Genetic and Fetal Origins of Polycystic Ovary Syndrome

A thesis submitted in fulfilment of the requirement for

Doctor of Philosophy

by

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Dedication

This thesis is dedicated to

my lovely daughters, Maimoona & Musharrafa,

my dear husband, Abdullatif &

my cheerleaders mum, Saadetu and dad, Ismail.

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Abstract

Polycystic ovary syndrome (PCOS) is the most common endocrine disorder that affects women of reproductive age. Although the syndrome affects over 10 percent women worldwide, its cause(s) remains unknown. Numerous studies have focussed on the genetic and fetal origins of the syndrome. However, the outcomes of genome wide association studies and candidate gene studies towards defining PCOS have, arguably, had almost no impact on the definition, diagnosis and treatment of the syndrome. This could be attributed mainly to the divergence of PCOS studies, as these studies have not collectively defined the molecular mechanisms involved in PCOS phenotypes observed. This thesis examined the role of genes in loci associated with PCOS and TGFβ signalling molecules, as well as their upstream regulators and mechanisms in the pathogenesis of PCOS.

Genes in loci associated with PCOS (candidate genes) were shown to be dynamically expressed during bovine fetal ovary development. Notably, those genes expressed during the early stages of fetal development such as *C8H9orf3, TOX3, FBN3, GATA4, HMGA2* and *DENND1A* are co-expressed with genes involved in mitochondria function and are regulated upstream by *DAP3, MYC, PTEN, HNF4A, ESRRA/G, PSEN1, MYC,* mitochondrial *LONP1* and *TP53*. Those expressed in the second trimester or just after mid gestation such as *YAP1, INSR, THADA* and *TGFB1I1* were co-expressed with genes involved in stroma expansion and are regulated upstream by TGF-β signalling molecules including *TGFB1, TGFB2, TGFB3* and *TGFBR2,* coagulation factor II and fibroblast proliferation regulators including *FGF2.* Candidate genes expressed during the third trimester such as *FDFT1*, *LHCGR*, *AMH*, *FSHR, ZBTB16* and *PLGRKT* are co-expressed with genes involved with folliculogenesis and steroidogenesis and are regulated upstream by *SREBF2, INSIGI, TGFB1* and *RPTOR* among others. Thus, this study infers the possible role of these canonical pathways and upstream regulators in the pathogenesis of PCOS during fetal ovary development.

The role of TGFB signalling molecules in the aetiology of PCOS was further examined. These molecules were also found to be dynamically expressed during fetal ovary development and could regulate some PCOS candidate genes in bovine fetal ovary fibroblasts. Across gestation, *LTBP1/2/3/4, FBN1, TGFB2/3, TGFBR2/3* and *TGFB1I1* expression levels increased, while *FBN3, TGFBR3L, TGFBI* and *TGFB1* decreased and *TGFBRAP1, TGFBR1* and *FBN2* remained relatively constant. TGFβ1, but not androgens nor AMH, has previously been shown to inhibit expression of candidate genes (*AR, INSR, C8H9orf3* and *RAD50*) but stimulate expression of androgen receptor co-factor, *TGFB1I1*, in cultured fetal ovarian fibroblasts.

Additionally, we showed that expression of PCOS candidate genes *ERBB3, NEIL2, IRF1* and *ZBTB16* significantly decreased after TGFβ1 treatment in cultured fetal ovarian fibroblasts. These findings further confirm that TGFβ signalling could be involved in the pathogenesis of PCOS or at least in the establishment of polycystic ovaries.

The role of candidate genes and TGFβ signalling molecules in various tissues including non-ovarian tissues was assessed as PCOS does not only affect the ovary. Both were shown to be dynamically expressed in gonadal (ovary and testis), metabolic (heart, liver and kidney) and brain (brain and cerebellum) tissues during the first half of human fetal development and post-natally until adulthood. More so, some genes were significantly expressed in specific tissues at different time points pre-natally and/or post-natally. Notably, *HMGA2, FBN3* and *TOX3* were highly expressed during the early stages of fetal development in all tissues but least during adulthood. *DENND1A, THADA, MAPRE1, RAB5B, ARL14EP, KRR1, NEIL2* and *RAD50* were dynamically expressed in all postnatal tissues studied. Interestingly, correlation between expression of *HMGA2*/*YAP1* and *RAD50*/*YAP1* were significant in at least 5 of the 7 fetal tissues studied. Furthermore, *HMGA2, YAP1* and *RAD50* correlated significantly with most TGFβ signalling molecules in at least 4 tissues. We further showed that there is certainly a crosstalk within and between PCOS candidate genes and TGFβ signalling molecules during fetal development within each tissue. Considering the fact that *HMGA2* and *YAP1* are involved in the Hippo signalling pathway as well as epithelial mesenchymal transition (EMT) during embryogenesis through TGFβ signalling, their role in the aetiology of PCOS requires further studies.

In conclusion, these findings confirm that genes in loci associated with PCOS and TGFβ signalling molecules are actively involved in the genetic and fetal origins of the syndrome and that there is a possible crosstalk between both in the development of multiple organs. This also infers that dysregulation of PCOS candidate genes and TGFβ signalling molecules during fetal development could initiate/lead to a cascade of molecular events in various tissues accounting for the various phenotypes of PCOS observed in adulthood.

Thesis Declaration

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in my name, in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission in my name, for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree.

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List of Publications

Published:

1. Analysis of upstream regulators, networks and pathways associated with the expression patterns of polycystic ovary syndrome candidate genes during fetal ovary development; **Rafiatu Azumah**, Katja Hummitzsch, Monica D Hartanti, Justin C St. John, Richard A Anderson, Raymond J Rodgers; *Frontiers in Genetics*; 2022, 12:762177; doi.org/10.3389/fgene.2021.762177

2. Candidate genes for polycystic ovary syndrome are regulated by TGFβ in the bovine fetal ovary; **Rafiatu Azumah**, Menghe Liu, Katja Hummitzsch, Nicole A Bastian, Monica D Hartanti, Helen F Irving-Rodgers, Richard A Anderson, Raymond J Rodgers; *Human Reproduction*; 2022, 37 (6), 1244–1254; doi: 10.1093/humrep/deac049

3. Genes in loci genetically associated with polycystic ovary syndrome are dynamically expressed in human fetal gonadal, metabolic and brain tissues; **Rafiatu Azumah**, Katja Hummitzsch, Richard A. Anderson, Raymond J. Rodgers; Metabolism, *Frontiers in Endocrinology*, 2023, Volume 14 – 2023; https://doi.org/10.3389/fendo.2023.1149473

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1. TGFβ signalling molecules and genes for polycystic ovary syndrome in human tissues. **Rafiatu Azumah**, Katja Hummitzsch, Richard A. Anderson, Raymond J. Rodgers; *Journal of Molecular Endocrinology*, 2023

Poster Presentations

1. Expression of PCOS candidate genes in human fetal and adult gonadal, metabolic and brain tissues; **Rafiatu Azumah**, Katja Hummitzsch, Richard A Anderson, Raymond J Rodgers, Joint ESA/SRB/APEG/NZSE Annual Scientific Meeting, 2022
2. Could TGFβ signalling in the fetal ovary account for development of predisposition to Polycystic Ovary Syndrome (PCOS)?; **Rafiatu Azumah,** Menghe Liu, Katja Hummitzsch, Nicole A Bastian, Monica D Hartanti, Helen F Irving-Rodgers, Richard A Anderson, Raymond J Rodgers; Perinatal Society of Australia and New Zealand (PSANZ) Annual Congress, 2022
    - This was presented again at NHMRC Centre for Research Excellence in Women's Health in Reproductive Life (CRE WHiRL)/EMCR Network Annual General Meeting, 2023 and won the Best Poster Award
3. Upstream regulators and canonical pathways associated with PCOS candidate genes during fetal ovary development; **Rafiatu Azumah**, Katja Hummitzsch, Monica D Hartanti, Justin C St. John, Richard A Anderson, Raymond J Rodgers; Annual Scientific Meetings of ESA/SRB/ANZBMS, 2021
4. Analysis of polycystic ovary syndrome candidate genes and their upstream regulators using RNA sequencing data of the bovine fetal ovary; **Rafiatu Azumah**, Katja Hummitzsch, Raymond J Rodgers; Robinson Research Institute Symposium, 2020.
5. Analysis of polycystic ovary syndrome candidate genes and their upstream regulators using RNA sequencing data of the bovine fetal ovary; **Rafiatu Azumah**, Katja Hummitzsch, Raymond J Rodgers; Florey Postgraduate Conference, 2020

Abbreviations

AMH - Anti-Mullerian hormone
AR - Androgen receptor
AOPEP - Aminopeptidase
AIC - Akaike information criterion
ADIPOQ - Adiponectin, C1Q and collagen domain containing
DENND1A - DENN domain-containing 1A
CRL - crown-rump length
C8H9orf3 - Chromosome 9 open reading frame 3
DAVID - Database for annotation, visualization, and integrated discovery
ERBB3/4 - Erb-B2 receptor tyrosine kinase 3/4
GATA4 - GATA binding protein 4
GO - Gene ontology
GSA - Gene specific analysis
GWAS - Genome wide association studies
FBN1/2/3-Fibrillin 1/2/3
FDFT1 Farnesyl-diphosphate Farnesyltransferase 1
FSHB - Follicle stimulating hormone beta subunit
FSHR - Follicle stimulating hormone receptor
HBSS - Hank's balanced-salt solution
HCUP-NIS - Healthcare Cost and Utilization Project-Nationwide Inpatient Sample
HMGA2 - High mobility group AT-hook 2
INSR - Insulin receptor
IRF1 Interferon regulatory factor 1
IPA - Ingenuity pathway analysis
KRR1 - Ca2+/calmodulin-dependent protein kinase
KEGG - Kyoto encyclopedia of genes and genomes
LH - Luteinizing hormone
LHCGR - Luteinising hormone/chorionic gonadotrophin receptor
LTBP1/2/3/4 - Latent TGFβ binding proteins 1/2/3/4
MAPRE1 - Microtubule associated protein rp/eb family member 1
NEIL2 - Nei Like DNA gycosylase 2

PCOS- Polycystic ovary syndrome

PCOM – Polycystic ovary morphology

PI - Ponderal index

PLGRKT - Plasminogen receptor with a c-terminal lysine

PPIA - Peptidylprolyl isomerase A

RAD50 - DNA repair protein

RAB5B - Ras-related Protein

RQI - RNA quality index

RPL32 - Ribosomal protein L32

SUOX - Sulphite oxidase

SUMO1P1 - Small ubiquitin like modifier 1 pseudogene 1

TGFβ - Transforming growth factor beta

TGFB1I1 - Transforming growth factor beta 1 induced transcript 1

TGFB1/2/3 Transforming growth factor beta 1/2/3

TGFBR1/2/3 - Transforming growth factor beta receptor 1/2/3

TGFBR3L - Transforming growth factor beta receptor 3 Like

TGFBI - Transforming growth factor beta induced

TGFBRAP1 - Transforming growth factor beta receptor associated protein 1

THADA - Thyroid adenoma associated

TOX3 -TOX high mobility group box family member 3,

WnT - Wingless-type mouse mammary tumour virus integration site

YAP1 - Yes associated protein 1

ZBTB16 - Zinc Finger and BTB Domain Containing 16

Chapter 1

Literature Review

Background

Polycystic ovary syndrome (PCOS) is a polygenic disorder with reproductive, endocrine and metabolic features affecting 10% of women of reproductive age, with 72% of affected women suffering infertility due to anovulation (Joham et al. 2015). Unfortunately, the outcomes of genome wide association studies and candidate gene studies towards defining PCOS have, arguably, had almost no impact yet on the definition, diagnosis and treatment of the syndrome. This literature review discusses the role of candidate genes in the possible genetic and fetal origins of PCOS.

1.1 Polycystic Ovary Syndrome (PCOS)

According to Teede, Deeks and Moran (2010), ‘PCOS is a frustrating experience for women, often complex for managing clinicians and is a scientific challenge for researchers’. Thus, PCOS is a debilitating health problem that presents reproductive features such as menstrual irregularities, hirsutism, acne, alopecia, anovulatory infertility, recurrent miscarriages; metabolic features such as insulin resistance, obesity, lipid abnormalities; and endocrine features such as hyperandrogenism (Teede, Deeks & Moran 2010). Hyperandrogenism, oligo-/anovulation and presence of polycystic ovary morphology are cardinal features of the syndrome. However, hyperinsulinemia, type 2 diabetes mellitus, and obesity have also been associated with PCOS (Rodgers et al. 2019; Teede, Deeks & Moran 2010). Despite the relatively high prevalence of the syndrome, to date, a comprehensive mechanism elucidating its pathophysiology is still lacking. Divergent research outcomes from studies pertaining to the pathophysiology of PCOS have increased the scientific conundrum surrounding its aetiology.

The possible genetic and fetal predispositions of the syndrome have been discussed in literature. The multifactorial aetiology of PCOS (presented in Section 1.2) has been confirmed by numerous genomic studies ranging from candidate gene approaches to the Genome-Wide Association Studies (GWAS) [reviewed in detail by Hardy and Norman (2019)]. Previous studies have identified PCOS candidate genes including androgen receptor (*AR*) (Schüring et al. 2012), fibrillin 3 (*FBN3*) (Hatzirodos, Bayne, Irving-Rodgers, et al. 2011) and anti-Mullerian hormone (*AMH*) (Tata et al. 2018). GWAS have also identified 19 susceptibility loci among the Han Chinese, European and Korean ancestries related to PCOS [reviewed by Jones and Goodarzi (2016); McAllister et al. (2015); Hiam et al. (2019)]. Furthermore, the fetal origin of PCOS has been studied in humans and animals including mice (Sullivan & Moenter 2004), rats (Wu et al. 2010), sheep (Birch et al. 2003) and monkeys (Dumesic et al. 1997). The expression of genes in loci (candidate genes) associated with PCOS have been studied in bovine and human fetal ovaries; further confirming the possible fetal predisposition of the syndrome (Liu et al. 2020; Hartanti et al. 2020). Three distinct gene expression patterns were observed; genes expressed early in gestation, genes expressed late in gestation and genes expressed throughout gestation (Hartanti et al. 2020; Liu et al. 2020) as shown in Table 1. Although these studies have linked the possible genetic and fetal origins of the syndrome, the molecular mechanisms that associated with these genes during fetal development that lead to the expression of PCOS phenotypes (such as lean, obese, insulin resistant among others) during adulthood still remain elusive.

Table 1. The three distinct expression patterns of PCOS candidate genes observed during fetal ovary development according to Hartanti et al. (2020); Liu et al. (2020); early, late and throughout gestation.

Early	**Evidence of Choice**	**References**
Fibrillin 3 (*FBN3*)	Functional studies	(Prodoehl et al. 2009; Hatzirodos, Bayne, Irving-Rodgers, et al. 2011; Urbanek et al. 2007)
GATA binding protein 4 (*GATA4*)	GWAS	(Hayes et al. 2015)
High mobility group AT-hook 2 (*HMGA2*)	GWAS & Functional studies	(Shi et al. 2012; Li et al. 2019)
TOX high mobility group box family member 3 (*TOX3),*	GWAS & Functional studies	(Shi et al. 2012; Ning et al. 2017)
DENN domain-containing 1A (*DENND1A)*	GWAS & Functional studies	(Shi et al. 2012; Chen et al. 2011; McAllister et al. 2014)
Luteinising hormone/chorionic gonadotrophin receptor *(LHCGR*)	GWAS	(Chen et al. 2011; Zhang et al. 2019)
Follicle stimulating hormone beta subunit (*FSHB*)	GWAS & Functional studies	(Hayes et al. 2015; Day et al. 2015; Tian et al. 2016)
Erb-B2 receptor tyrosine kinase 3 (*ERBB3*)	GWAS	(Day et al. 2018)
Throughout		
Thyroid adenoma associated (*THADA*)	GWAS	(Shi et al. 2012; Day et al. 2015; Chen et al. 2011)
Erb-B2 receptor tyrosine kinase 4 (*ERBB4*)	GWAS & Functional studies	(Day et al. 2015; Peng et al. 2017)
DNA repair protein (*RAD50*)	GWAS	(Day et al. 2015)
Chromosome 9 open reading frame 3 (*C8H9orf3*)	GWAS	(Shi et al. 2012; Hayes et al. 2015)
Yes associated protein 1 (*YAP1*)	GWAS	(Shi et al. 2012; Day et al. 2015; Li et al. 2012)

Ras-related Protein (*RAB5B*)	GWAS	(Shi et al. 2012; Yu et al. 2019)
sulphite oxidase (*SUOX*)	GWAS	(Day et al. 2015)
Ca^{2+}/calmodulin-dependent protein kinase (*KRR1*)	GWAS	(Day et al. 2015)
ADP Ribosylation Factor Like GTPase 14 Effector Protein (*ARL14EP*)	GWAS	(Day et al. 2018)
Farnesyl-Diphosphate Farnesyltransferase 1 (*FDFT1*)	GWAS	(Hayes et al. 2015)
Nei Like DNA Glycosylase 2 (*NEIL2*)	GWAS	(Hayes et al. 2015)
Microtubule Associated Protein RP/EB Family Member 1 (*MAPRE1*)	GWAS	(Day et al. 2018)
Late		
Insulin receptor (*INSR*)	GWAS & functional studies	(Tucci et al. 2001; Goodarzi et al. 2011; Shi et al. 2012)
Follicle stimulating hormone receptor (*FSHR*)	GWAS	(Shi et al. 2012)
Plasminogen Receptor with a C-Terminal Lysine *(PLGRKT)*	GWAS	(Day et al. 2018)
Zinc Finger and BTB Domain Containing 16 (*ZBTB16*)	GWAS	(Day et al. 2018)
Interferon Regulatory Factor 1 (*IRF1*)	GWAS	(Day et al. 2018)
Transforming growth factor beta 1 induced transcript 1 (*TGFB1I1)*	Functional studies	(Hartanti et al. 2020)
Luteinizing Hormone/Choriogonadotropin Receptor (*LHCGR*)	GWAS	(Shi et al. 2012)
Anti-Mullerian hormone (*AMH)*	Functional studies	(Tata et al. 2018)
Androgen receptor (*AR*)	Functional studies	(Schüring et al. 2012)
Others included		
SUMO1 Pseudogene 1 (*SUMO1P1*)	GWAS	(Shi et al. 2012)

In an attempt to define the PCOS pathophysiology, the cells of the ovary, such as stromal (Hartanti et al. 2019), granulosa (Owens et al. 2019) and thecal cells (Fortune 1986), have been studied. However, understanding the role of tissues other than the ovary in PCOS aetiology as well as the expression profiles of candidate genes in different tissues such as brain and liver could be important to understand the varying PCOS phenotypes. For example, only a few studies have focused on the hepatic dysfunctions and risk of liver diseases in PCOS women as well as the health of their brothers or male offspring using animal models such as sheep (Siemienowicz et al. 2022; Saadat et al. 2022) and rats (Cui et al. 2021; Hogg et al. 2011; Vojnović Milutinović et al. 2021). Studies in metabolic tissues are limited, although studies focussed on understanding the metabolic phenotypes of PCOS such as insulin disorders have received some attention (Dumesic et al. 2019; Baillargeon & Carpentier 2007; Stepto et al. 2020; Attaoua et al. 2008; Macut et al. 2017). Additionally, the cellular, molecular and/or biochemical pathways that lead to the expression of these PCOS phenotypes are still not clear. Efforts to define the upstream regulators/pathways, particularly, the network of genes involved till the endpoint (phenotypes observed) are also scarce. Wood et al. (2004) proposed Wingless-type mouse mammary tumour virus integration site (WnT) signalling and the retinoic acid pathways to be involved in the upstream signalling of PCOS; yet, their relationship with PCOS has not been proven. The roles of transforming growth factor β (TGFβ) signalling pathways (Raja-Khan et al. 2014) and steroid signalling pathways such as the androgen signalling (Aflatounian et al. 2020) still remain a ‘chicken and egg story’ as knowledge on the pathogenesis of the disorder remain elusive.

1.2. Diversity of PCOS Phenotypes

The heterogeneity of PCOS phenotypes in women has had a great impact on the definition of the syndrome; leading to difficulties in diagnosis and management of the disorder. The prevalence of PCOS ranges between 6-21% depending on the diagnostic criteria used in the clinical settings (Lizneva et al. 2016). Notably, to date, the Rotterdam criterion for diagnosis has been the broadest and internationally accepted. It requires the presence of two of these three cardinal features of PCOS, hyperandrogenism, oligo/anovulation and polycystic ovary morphology (ESHRE & Group 2004; Norman & Teede 2018; Johnson et al. 2013). More so, of the numerous metabolic symptoms associated with PCOS, obesity and type 2 diabetes are considered to have a long-term consequences on PCOS patients (Conway et al. 2014). PCOS also affects the psychological health of the patients causing anxiety, depression and sleep disorders (Fernandez et al. 2018; Damone et al. 2019; Sadeeqa, Mustafa & Latif 2018). The disorder presents varying symptoms/phenotypes in different age groups; adolescents, peri- or post-menopausal women [reviewed in detail by Lizneva et al. (2016)]. These different phenotypes of PCOS are expressed in varying ratios across different stages of life, genotype, ethnicity and epigenetic factors including lifestyle and bodyweight, posing a huge economic burden on individual countries and the world at large (Teede, Deeks & Moran 2010). Together, these numerous phenotypes have made the definition of the syndrome a difficult challenge to researchers as the intrinsic mechanisms involved remain unclear. In an attempt to define the phenotypes involved, the pathophysiology of PCOS has been studied.

The numerous phenotypes expressed in PCOS are responsible for the multifaceted pathophysiology of the syndrome. Efforts to define the pathophysiology of PCOS have increased knowledge of the syndrome from being a mere reproductive disorder to a more complex endocrinopathy in women as well as brothers of the affected women (Urbanek et al. 2007). Increased androgen levels, follicular arrest and insulin resistance are the core components of its pathophysiology studied (Diamanti-Kandarakis 2008). In PCOS, aberration in hormones involved in folliculogenesis and ovarian steroidogenesis which interfere with the feedback mechanisms required to stabilise both processes are observed. Hormones such as LH, insulin, AMH and androgens are elevated whilst FSH levels are reduced. Specifically, hyperandrogenism, which is a requirement for PCOS diagnosis according to the Androgen Excess Society, has been studied the most [Abbott, Dumesic and Levine (2019)]. It impairs the feedback effects of ovarian steroids to the hypothalamus causing a persistent increase in gonadotrophin releasing hormone (GnRH) pulse frequency, hypersecretion of LH and a high LH/FSH ratio. The anomalous levels of these hormones further cause abnormal oocyte maturation and premature luteinisation of granulosa cells leading to ovarian dysfunction. This could be attributed to premature arrest of activated follicles at the antral stages, leading to the accumulation of small to medium antral follicles in polycystic ovaries as well as excess androgen production (Palomba, Daolio & La Sala 2017).

Insulin resistance has also been associated with increased androgen levels among PCOS patients. Majority of PCOS women experience up to a 30% decrease in insulin sensitivity and this could be exacerbated by obesity (Li et al. 2018). Thus, body-mass-index (BMI) was associated with insulin resistance with prevalence increasing from 34.5%, 80.2% to 98.7% in lean, overweight, and obese women with PCOS, respectively, of the Han Chinese ancestry (Li et al. 2018). Previous studies have also shown that insulin could further stimulate the accumulation of androgens in ovarian stroma of hyperandrogenic women *in vitro* (Barbieri et al. 1986). Thus, peripheral insulin resistance caused by either overexpression of insulin receptors (*INSR*) in the ovaries of non-obese patients or their under expression in metabolic tissues of obese patients, both result in a feedback mechanism leading to excess ovarian androgen production (Azziz et al. 2016).

The ovaries of women with PCOS tend to be more fibrous due to a more collagenous tunica, an increased thickness of cortical and subcortical stroma and increased ovarian stroma volume (Hughesdon 1982; Buckett et al. 1999). These features were among the earliest descriptions of the syndrome since 1935 (Stein 1935), however, it is still not known when and how this occurs. The increased stromal collagen and ovarian cortex expansion in PCOS patients have been associated with *FBN3* dysfunction, which is highly expressed in early stages of fetal development and were not expressed during late gestation nor in adult bovine ovaries (Hatzirodos, Bayne, Irving-Rodgers, et al.

2011). Fibrillins regulate TGF-β pathways, which stimulate fibroblast proliferation and collagen formation. TGFβ may also play significant roles in the cardiovascular and metabolic symptoms of PCOS as discussed in review by Raja-Khan et al. (2014). Nonetheless, attempts to delineate the molecular mechanism underpinning PCOS phenotypes towards defining the syndrome has resulted in the discovery of its genetic and fetal origins.

1.3. Genetic Origin of PCOS

The multifactorial aetiology of PCOS is underpinned by a complex genetic architecture that has only recently begun to be elucidated. Familial clustering and twin studies were the first evidence of genetic origin of PCOS (Lunde et al. 1989; Vink et al. 2006; Kahsar-Miller & Azziz 1998). Over 200 genes related to PCOS have since been identified through candidate gene studies and GWAS [reviewed in detail by Azziz et al. (2016); Hiam et al. (2019)]. Candidate gene studies are useful to discover the pathways involved as well as some of the cell types in which these genes are expressed (Franks, Gharani & McCarthy 2001). Also, these studies have attempted to explain the molecular mechanisms involved in some phenotypes observed in the syndrome, for instance those related to *AMH*, *AR*, *LH*, *FSH* and *INSR* [reviewed in detail by Kulkarni et al. (2019); McAllister et al. (2015)]. However, these studies are neither efficient, consistent nor conclusive due to the complex pathophysiology and the numerous phenotypes observed in PCOS (Azziz et al. 2016).

Furthermore, GWAS, which identifies the common genetic polymorphisms related to PCOS, has identified 19 loci among the Han Chinese, Korean and European ancestry (Jones & Goodarzi 2016). Collectively, the PCOS genes identified near/in these loci include *SUMO1P1*, *FBN3*, *NEIL2, GATA4*, *HMGA2*, *TOX3*, *DENND1A*, *LHCGR*, *INSR*, *FSHR*, *THADA, ERBB4, RAD50, C8H9orf3, YAP1, RAB5B, SUOX* and *KRR1* (Chen et al. 2011; Shi et al. 2012; Hayes et al. 2015). It is worth noting that GWAS only accounts for a small fraction of the estimated heritability and does not identify specific genes but merely provide information about the loci related to the syndrome (Azziz et al. 2016). This explains why certain crucial genes related to PCOS, like *AR,* were not identified by GWAS which is a limitation of this approach. Moreover, the loci identified by these studies could be located within or near a gene, having a role either functional or regulatory in PCOS which needs to be investigated further (Hiam et al. 2019).

Studies involving PCOS candidate genes including those identified in/near loci associated with the disorder have become the focus of genetic studies. Candidate gene studies in humans have been used to define the regulation of some of the genes identified in/near loci associated with PCOS with focus on steroid biosynthesis and actions [*DENND1A* isoforms (Tee et al. 2016), *AR* (Catteau-Jonard et al. 2008)], gonadotrophin secretion and action [*FSH* (Catteau-Jonard et al. 2008), *LHCGR* (Capalbo et al. 2012)], folliculogenesis [*AMH* (Tata et al. 2018)], weight and energy regulation [*ADIPOQ* (Ranjzad et al. 2012; Zhang et al. 2008), *FTO* (Attaoua et al. 2008; Barber et al. 2008)]; as well as insulin action [*INSR* (Lee et al. 2008), *IRS-1* (Baba et al. 2007) and *IRS-2* (El Mkadem et al. 2001)]. Some of the genes have regulatory roles in ovarian development, like transcription factors *GATA4,* which is required for the initial thickening and full development of the gonadal ridges (Efimenko et al. 2013; Hu, Okumura & Page 2013) and *FBN3* expression is involved in stromal compartmentalisation (Hatzirodos, Bayne, Irving-Rodgers, et al. 2011). However, their roles in establishing PCOS symptoms observed in the ovary and in non-ovarian tissues still remain unclear.

Studies to elucidate the roles of genes in loci associated to PCOS are still on-going. Genes nearest *FSHB* locus have been associated significantly with LH levels among women with Korean and European ancestries (Pau et al. 2017; Hong et al. 2020; Tian et al. 2016), and with free testosterone levels among the Korean ancestry (Hong et al. 2020). *THADA* has also been associated with these two hormones among the Han-Chinese ancestry (Cui et al. 2013). Tian et al. (2020) using a dominant model of genotype-phenotype studies proposed that *THADA*, *INSR, TOX3* and *DENND1A* could be involved in the metabolic disorder-related pathway of PCOS. Specifically, this study also associated *DENND1A* with insulin resistance (Tian et al. 2020). Also, previous candidate gene studies have shown some DENND1A isoforms regulate androgen biosynthesis in theca cells (McAllister et al. 2014) and are possibly associated significantly with reproductive subtype of PCOS according to Dapas et al. (2020). These findings collectively imply that these genes could be regulated upstream in a peculiar manner or are possibly upstream regulators of other genes leading to the PCOS phenotypes observed. Unfortunately, studies to delineate these mechanisms/pathways (both canonical and non-canonical) from fetal development through to adult life are very limited and difficult to achieve.

1.4. Fetal Origin of PCOS

PCOS animal models involving monkeys (Abbott, Tarantal & Dumesic 2009; Abbott et al. 2008; Dumesic et al. 2019; Abbott, Levine & Dumesic 2016), sheep (Cardoso & Padmanabhan 2019; Padmanabhan & Veiga-Lopez 2013; Cernea et al. 2015) and mice (van Houten et al. 2012; Aflatounian et al. 2020; van Houten & Visser 2014) as well as studies in PCOS women and their children (Mills et al. 2020; Tata et al. 2018) have confirmed the possible fetal predisposition to PCOS later in life. Most studies in animal-models have focussed on the effect of maternal hormones especially testosterone to comprehend the fetal predisposition to PCOS in mice (Sullivan & Moenter 2004), rats (Wu et al. 2010), sheep (Birch et al. 2003) and primates (Dumesic et al. 1997). Furthermore, peripheral exposure of AMH to mice during gestation have also been used to induce major cardinal PCOS neuroendocrine features such as hyperandrogenism, elevated LH levels, sporadic ovulation as well as fertility defects in mice (Tata et al. 2018). These neuroendocrine dysfunction were attributed to aberrant gonadotrophin receptor signalling (Tata et al. 2018). However, the AMH mouse model mainly represents the lean PCOS phenotype and the hormone when injected acts centrally by activating the neurons responsible for gonadotrophin-releasing hormone in the hypothalamus resulting in the features observed (Tata et al. 2018). Furthermore, Risal and colleagues developed a PCOS mouse model with similar complexity of the syndrome as observed in humans in an attempt to unravel the transgenerational inheritance involved in PCOS. To achieve this, pregnant mice were exposed to androgen (dihydrotestosterone) during late gestation (embryonic day 16.5-18.5) while altering their metabolic features including glucose homeostasis. This experiment resulted in PCOS-like reproductive and metabolic features in three generations of mice (Risal et al. 2019); providing more evidence on the impact of fetal programming on PCOS phenotypes observed. However, increased AMH levels, which is a common feature of PCOS, was not observed in F_1-F_3 generations. Also, F_2 offspring from obese and androgenised F_0 mothers died at weaning (Risal et al. 2019). Although with limitations, animal models are currently available that can mimic different PCOS phenotypes; further affirming the polygenic aetiology of the syndrome.

In a retrospective study of PCOS women at adulthood, anthropometric features at birth such as thinness as determined by low weight per cubic length (ponderal indices), have been associated with the likelihood of developing PCOS later in life (Davies et al. 2012). Specifically, every one unit increment of ponderal index (PI) at birth is associated with reduced risk of all three cardinal features of PCOS in women about 30-years-old, whereas a 100-g increase in birthweight is associated with increased risk of hyperandrogenism (Davies et al. 2012). This study highlights the relevance of anthropometric features in understanding the metabolic risk acquired at birth. A larger retrospective population-based cohort study using data collected over 11 years from Healthcare Cost and Utilization Project-Nationwide Inpatient Sample (HCUP-NIS) showed that PCOS mothers have higher likelihood of giving birth to infants with congenital anomalies compared to non-PCOS mothers (Mills et al. 2020). However, very few of such retrospective studies have been carried out and there is a need for more independent cohort studies.

Studies to understand differences between offspring exposed to PCOS and those not exposed are also becoming the focus of human studies attempting to define the fetal origin of the syndrome. In studies by Detti et al. (2019), AMH levels in PCOS pregnant mothers and umbilical cord blood samples of their offspring were statistically higher than in control healthy women, although increased testosterone and decreased FSH were observed only in maternal blood of PCOS women. In another study, AMH levels have been found to be higher in cord blood samples collected from obese PCOS mothers (n=60) than controls who were healthy pregnant women (n=60) (Far et al. 2019).

Furthermore, PCOS exposure *in utero* has been shown to affect the placental and umbilical cord morphology and changes in the expression of placental proteins observed (Sun et al. 2020). Other studies have also identified sex-dependent epigenetic changes in the promoter regions of metabolic and reproductive genes such as *AR*, leptin receptor and adiponectin receptor 1 and 2 in offspring from PCOS mothers to be associated with intrauterine exposure of the syndrome; although the sample size was low (n= 24) (Echiburú et al. 2020). A subsequent study involving a larger sample size (n=172), also showed that male offspring exposed to a PCOS environment *in utero* might be more susceptible to metabolic abnormalities in later life (Li et al. 2020). Additionally, women born with congenital adrenal hyperplasia have a higher incidence of PCOS at puberty than others (Barnes et al. 1994). Furthermore, children born to women with PCOS have a five-fold increased risk of developing the syndrome compared to those not exposed according to Risal et al. (2019). However, it has not been confirmed if this is due to a genetic or a fetal cause. Together, these findings not only confirm the possible fetal origin of PCOS, but also show that the syndrome is not only associated with the ovary as the name suggests. Thus, the need to study the possible upstream pathways/mechanisms as well as organs involved in PCOS, more especially during fetal development, has become necessary.

1.5. Relationships between Genetic and Fetal Origins

The scientific conundrum surrounding the aetiology of the disorder has increased the need to understand the roles/functions of candidate genes, identified both by candidate gene studies as well as those in/near GWAS loci, during fetal development that may lead to the predisposition of PCOS in adulthood. The genesis of such studies was from Hartanti et al. (2020) and Liu et al. (2020) who studied the expression of candidate genes in human and bovine fetal ovaries. Knowledge on the expression patterns of PCOS candidate genes during ovary development is essential in understanding the possible functionality of the genes at different time points of development.

The role of TGFβ signalling molecules in the predisposition of PCOS are limited, although the PCOM morphology (fibrous stroma) was the first feature discovered in women with PCOS (Stein 1935). These molecules include TGFβs and their receptors, latent TGFβ binding proteins (LTBP) and fibrillins, which are extracellular matrix proteins that bind LTBPs and are also expressed in fetal ovaries (Hatzirodos, Bayne, Irving-Rodgers, et al. 2011). Their expression levels were either constant (*TGFB1*, *TGFBR1*), increasing (*TGFB2*, *TGFB3*, *TGFBR2*, *TGFBR3*, *LTBP1*, *LTBP2*, *LTBP3*, *LTBP4*) or decreasing (*FBN2*, *FBN3*) across gestation (Hatzirodos et al. 2019; Hatzirodos, Bayne, Irving-Rodgers, et al. 2011). TGFβ1 has also been shown to inhibit expression of *AR* and 3 PCOS candidate genes (*INSR*, *C8H9orf3* and *RAD50*) and stimulated expression of *TGFB1I1* (Transforming Growth Factor Beta 1 Induced Transcript 1) in cultured fetal ovarian stroma cells (Hartanti et al. 2020). This suggests that TGFβ signalling is dynamic during fetal ovarian development and could be an important part of the aetiology of PCOS, providing a link between the genetic basis and fetal predisposition to PCOS. However, studies to discover the roles of these TGFβ signalling molecules in fetal development as well as the upstream mechanisms involved are limited. Also, the relationship between genes in loci associated with PCOS and TGFβ signalling molecules in various tissues during fetal development has not been studied.

1.6. Tissue and Organ Studies involving PCOS

The role of different tissues other than the ovary in the establishment of endocrine, metabolic, reproductive as well as psychological symptoms presented by women with PCOS has not received much attention over the years. Undoubtedly, the main causes of the various phenotypes observed in PCOS remain unknown. The role of various tissues involved in the common symptoms of PCOS are also elusive. A systematic and comparative study analysed different tissues in lean (BMI ≤ 23) and obese (BMI ≥ 23) women with PCOS using data from different studies available in the Gene Expression Omnibus (GEO) in a meta-analysis approach (Idicula-Thomas et al. 2020). The different tissues analysed were: ovarian including metaphase II oocyte, cumulus cells and lutein granulosa cells; endometrial cell types including epithelial, endothelial, stromal fibroblasts and mesenchymal stem cells; adipose made up of subcutaneous adipose tissue and omental adipose tissue; and skeletal muscle. Meta-analysis was achieved by normalising each study containing cases and controls, analysing them individually to identify differentially-expressed genes (DEGs) and enriched pathways and then comparing the results across studies. The study showed that most differentially-expressed genes were downregulated regardless of the type of the tissues or phenotype. The pathways associated with DEGs identified in the meta-analysis were grouped under four functional themes; (i) Mitochondrial related genes which were downregulated mainly in the cumulus cells of the obese PCOS samples but upregulated mainly in subcutaneous adipose tissues of lean PCOS samples; (ii) Cell-motility and immune response; (iii) FAK-related; (iv) ERBB1 and PDGFRB signalling were all upregulated in obese PCOS but downregulated in lean PCOS samples (Idicula-Thomas et al. 2020). It is worth noting that no commonly dysregulated genes were found between lean and obese phenotypes inferring that different mechanism could be involved in the development of PCOS in lean and obese women.

PCOS women or their brothers present various metabolic symptoms. Aside the hepatic dysfunctions and risk of liver diseases in PCOS women, their brothers and offspring (both male and female) studied in animal models mentioned earlier (Siemienowicz et al. 2022; Saadat et al. 2022; Cui et al. 2021; Hogg et al. 2011; Vojnović Milutinović et al. 2021), few other metabolic tissues have been studied. Morphological changes have been observed in the pancreatic islets of infant and adult monkeys exposed to pre-natal androgens, accounting for the metabolic symptoms associated with insulin resistance and glucose intolerance (Nicol et al. 2014). In skeletal muscle of overweight women with PCOS, high gene expression of collagens type IA2 and type IIIA1, decorin, lysyl oxidase and TGFβ receptor 2 was observed when compared to BMI-matched controls (Stepto et al. 2020). Also, administration of 12 weeks old female rats with testosterone caused hyperinsulinaemia, reduced whole-body insulin sensitivity and an inhibition of glycogen synthesis in skeletal muscle (Holmang et al. 1990). The mechanisms leading to insulin resistance in the skeletal muscle in PCOS have been discussed to be tissue-specific and presented in a review by Walters et al. (2022). These findings together infer the role of different metabolic tissues in the aetiology of PCOS; further confirming its multifactorial/polygenic nature.

The role of the central nervous system in PCOS pathophysiology has been investigated over the past decade (Silva, Prescott & Campbell 2018; Sverrisdottir et al. 2008; Maranon et al. 2015). Structural and functional brain disturbances have been associated with metabolic symptoms in PCOS women suggesting that the central nervous system could be playing a key role in PCOS development (Ozgen Saydam & Yildiz 2020). High sympathetic activity has also been associated with high blood pressure in PCOS (Sverrisdottir et al. 2008; Maranon et al. 2015). Notably, involvement of different tissues in the metabolic and reproductive symptoms observed in PCOS has not been studied. Thus, very little is known about the possible upstream or downstream mechanisms in various tissues that result in the metabolic or reproductive phenotypes observed in PCOS. Collectively, the role of candidate genes in various tissues, if known, could inform/guide further studies into delineating the possible mechanisms that are involved in PCOS predisposition from conception till adulthood.

1.7. Research Aims

The possible fetal and genetic predisposition of PCOS have been confirmed in numerous human and animal studies. Genes in loci associated with PCOS have been shown to be dynamically expressed during human and bovine fetal ovary development (Liu et al. 2020; Hartanti et al. 2020). However, upstream regulators and mechanisms associated with these genes during fetal ovary development have not been identified. A major focus has been on studies concerning the ovaries and fertility issues of women with PCOS. These ovaries are known to be more fibrous and have more tunica and stroma indicating a possible involvement of TGFβ signalling at some point. Our previous studies have also shown that TGFβ1, but not androgens or AMH, was able to regulate some PCOS candidate genes. Nonetheless, it has not been shown yet, how the members of the TGFβ family (TGFβs, LTBPs, fibrillins and associated molecules) are expressed during fetal development of ovaries as well as other organs involved in PCOS pathology, such as metabolic organs and the brain. The fact that male offspring from PCOS women tend to have metabolic abnormalities in adult shows that the syndrome is not only associated with the ovary as the name suggests. The role of metabolic, and brain tissues in the aetiology of the syndrome have been rarely studied. Understanding the possible relationship between genes in loci associated with PCOS and TGFβ signalling molecules in various tissues pre-natally and post-natally has become necessary in delineating the different phenotypes observed in PCOS. Thus, the aims of this study are:

I. To identify potential upstream regulators and pathways associated with PCOS candidate genes during fetal ovary development (Chapter 2).

II. To identify the expression of TGFβ signalling molecules during bovine fetal ovary development across gestation and their role in regulating more PCOS candidate genes (Chapter 3).

III. To examine the expression of PCOS candidate genes in gonadal, metabolic and brain tissues pre-natally and post-natally as well as their association with each other during fetal development (Chapter 4).

IV. To examine the expression of TGFβ signalling molecules in gonadal, metabolic and brain tissues pre-natally and post-natally as well as their relationship with genes in loci associated with PCOS (Chapter 5).

1.9. References

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Chapter 2

Analysis of Upstream Regulators, Networks, and Pathways Associated with the Expression Patterns of Polycystic Ovary Syndrome Candidate Genes During Fetal Ovary

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Analysis of Upstream Regulators, Networks, and Pathways Associated With the Expression Patterns of Polycystic Ovary Syndrome Candidate Genes During Fetal Ovary Development

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Polycystic Ovary Syndrome (PCOS) is a multifactorial syndrome with reproductive, endocrine, and metabolic symptoms, affecting about 10% women of reproductive age. Pathogenesis of the syndrome is poorly understood with genetic and fetal origins being the focus of the conundrum. Genetic predisposition of PCOS has been confirmed by candidate gene studies and Genome-Wide Association Studies (GWAS). Recently, the expression of PCOS candidate genes across gestation has been studied in human and bovine fetal ovaries. The current study sought to identify potential upstream regulators and mechanisms associated with PCOS candidate genes. Using RNA sequencing data of bovine fetal ovaries (62–276 days, $n = 19$), expression of PCOS candidate genes across gestation was analysed using Partek Flow. A supervised heatmap of the expression data of all 24,889 genes across gestation was generated. Most of the PCOS genes fell into one of four clusters according to their expression patterns. Some genes correlated negatively (early genes; *C8H9orf3*, *TOX3*, *FBN3*, *GATA4*, *HMGA2*, and *DENND1A*) and others positively (late genes; *FDFT1*, *LHCGR*, *AMH*, *FSHR*, *ZBTB16*, and *PLGRKT*) with gestational age. Pathways associated with PCOS candidate genes and genes co-expressed with them were determined using Ingenuity pathway analysis (IPA) software as well as DAVID Bioinformatics Resources for KEGG pathway analysis and Gene Ontology databases. Genes expressed in the early cluster were mainly involved in mitochondrial function and oxidative phosphorylation and their upstream regulators included *PTEN*, *ESRRG/A* and *MYC*. Genes in the late cluster were involved in stromal expansion, cholesterol biosynthesis and steroidogenesis and their upstream regulators included *TGFB1/2/3*, *TNF*, *ERBB2/3*, *VEGF*, *INSIG1*, *POR*, and *IL25*. These findings provide insight into ovarian development of relevance to the origins of PCOS, and suggest that multiple aetiological pathways might exist for the development of PCOS.

Keywords: polycystic ovary syndrome, mitochondrial dysfunction, stromal expansion, steroidogenesis, upstream regulators, fetal ovary

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INTRODUCTION

Polycystic Ovary syndrome (PCOS) is a debilitating syndrome with reproductive, endocrine and metabolic symptoms, affecting up to 10% women of reproductive age, with about 72% suffering infertility due to anovulation (Joham et al., 2015). Hyperandrogenism, oligo /anovulation and the presence of polycystic ovary morphology are the cardinal features of the syndrome. However, hyperinsulinemia, type 2 diabetes mellitus, and obesity are also associated with PCOS [reviewed in detail by Teede et al. (2010)]. Despite the high prevalence of the syndrome, a comprehensive mechanism elucidating its pathophysiology is still lacking. Research efforts to define the pathophysiology of PCOS have increased the scientific conundrum surrounding its developmental origin(s) due to the diverging nature of research outcomes.

The multifactorial aetiology of PCOS has been evident by numerous genomic studies ranging from candidate gene approaches to Genome Wide Association Studies (GWAS) confirming its genetic origin. Candidate gene studies have identified androgen receptor (*AR*) (Schüring et al., 2012), fibrillin 3 (*FBN3*) (Hatzirodos et al., 2011), and anti Mullerian hormone (*AMH*) (Tata et al., 2018) among others to be related to PCOS. GWAS have also identified 19 PCOS susceptibility loci among the Han Chinese, European and Korean ancestry [reviewed in detail by McAllister et al. (2015); Jones and Goodarzi (2016); Hiam et al. (2019)]. More so, the fetal origin of PCOS has been studied in human (Davies et al., 2012; Echiburú et al., 2020; Mills et al., 2020) and animal models including mice (Sullivan and Moenter 2004), rats (Wu et al., 2010), sheep (Birch et al., 2003), and monkeys (Dumesic et al., 1997). The possible fetal predisposition of the syndrome has also been studied further in bovine and human fetal ovaries using qRT PCR technique (Hartanti et al., 2020; Liu et al., 2020).

Hartanti, et al. (2020), Liu, et al. (2020) showed that all PCOS candidate genes in/near loci identified by GWAS, except small ubiquitin like modifier 1 pseudogene 1 (*SUMO1P1*), and three additional candidate genes *AR*, *AMH* and transforming growth factor beta 1 induced transcript 1 (*TGFB1I1*) were expressed in human and bovine fetal ovaries. Three distinct expression patterns were observed; some genes were highly expressed during early stages, others during late stages whilst others were expressed throughout gestation (**Table 1**). Notably, the mRNA levels of genes within the early and late groups significantly correlated with each other as well as mean age (Hartanti, et al., 2020; Liu, et al., 2020). The expression of these PCOS genes during fetal development has provided further insight to the fetal origin of the syndrome; necessitating further studies to delineate its pathophysiology. Thus, the molecular mechanisms and upstream regulators associated with PCOS candidate genes during fetal development that could probably lead to the expression of various phenotypes (such as lean, obese, insulin resistant) during adulthood still remain elusive.

Therefore, there is a need to identify the upstream regulators and pathways that operate when PCOS candidate genes are expressed during normal ovary development. This will provide more insight on the possible perturbations during fetal ovary development that could lead to PCOS in adulthood and also help clarify some of the conundra surrounding the genetic and fetal origins of the disorder. Although studies to delineate the roles of PCOS candidate genes during fetal development are on going, acquisition of human fetal ovary samples across gestation, especially from the third trimester, is a limitation. Considering the strong similarities between human and bovine ovaries in morphology and physiology, gestational length and the propensity for singleton pregnancies as well as the similarity in expression of PCOS candidate genes between human and

TABLE 1 | The three distinct expression patterns of PCOS candidate genes observed during fetal ovary development according to Hartanti, et al. (2020), Liu, et al. (2020); early, late and throughout gestation.

Early	Late	Throughout
Fibrillin 3 (*FBN3*)	Insulin receptor (*INSR*)	Thyroid adenoma associated (*THADA*)
GATA binding protein 4 (*GATA4*)	Follicle stimulating hormone receptor (*FSHR*)	Erb B2 receptor tyrosine kinase 4 (*ERBB4*)
High mobility group AT hook 2 (*HMGA2*)	Plasminogen receptor with a C terminal lysine *(PLGRKT)*	DNA repair protein (*RAD50*)
TOX high mobility group box family member 3 (*TOX3)*	Zinc finger and BTB domain containing 16 (*ZBTB16*)	Chromosome 9 open reading frame 3 (*C8H9orf3*)
DENN domain containing 1A (*DENND1A)*	Interferon regulatory factor 1 (*IRF1*)	Yes associated protein 1 (*YAP1*)
Luteinising hormone/chorionic gonadotrophin receptor *(LHCGR*)	Transforming growth factor beta 1 induced transcript 1 (*TGFB1I1)*	Ras related protein (*RAB5B*)
Follicle stimulating hormone beta subunit (*FSHB*)	Luteinizing hormone/choriogonadotropin receptor (*LHCGR*)	Sulphite oxidase (*SUOX*)
Erb B2 receptor tyrosine kinase 3 (*ERBB3*)	Anti mullerian hormone (*AMH)*	Ca^{2+}/calmodulin dependent protein kinase (*KRR1*)
	Androgen receptor (*AR*)	ADP ribosylation factor like GTPase 14 effector protein (*ARL14EP*)
		Farnesyl diphosphate farnesyltransferase 1 (*FDFT1*)
		Nei like DNA glycosylase 2 (*NEIL2*)
		Microtubule associated protein RP/EB family member 1 (*MAPRE1*)

TABLE 2 | Characteristics of bovine fetal ovaries and RNA quality index (RQI).

Sample ID	Identical samples	Crown-rump length [cm]	Gestational age [days]	Gestational period	RQI
15/R12t	Y	7.7	62	Early I	9.0
15/R85t	Y	9	66	Early I	8.5
15/R86t	N	12	76	Early I	8.9
15/R74t	Y	14	82	Early I	9.1
15/R41t	N	17	91	Early II	9.3
15/R57t	N	19	98	Early II	9.2
15/R42t	Y	24	113	Early II	9.6
15/R51t	Y	28	124	Early II	9.6
15/R43t	Y	32	135	Early II	9.5
15/R2t	Y	39	154	Late	9.8
15/R44t	Y	45	170	Late	9.3
15/R1t	Y	58	201	Late	9.5
15/R45t	Y	74	234	Late	9.6
15/R33t	Y	80	245	Late	9.6
15/R47t	N	86	255	Late	9.4
15/R35t	Y	88	258	Late	9.5
15/R38t	Y	91	263	Late	9.3
15/R49t	N	93	266	Late	9.7
15/R50t	Y	100	276	Late	9.5

Identical samples refer to samples also analysed in Hartanti, et al. (2020), Liu, et al. (2020).

bovine during early stages of fetal ovary development (Hartanti, et al., 2020; Liu, et al., 2020), this study seeks to define the upstream regulators and pathways that operate when PCOS candidate genes are expressed (Hartanti, et al., 2020; Liu, et al., 2020) using bovine fetal ovaries.

MATERIALS AND METHODS

Bovine Fetal Ovary Collection

Fetal ovarian pairs across gestation (62 276 days, $n = 19$) were collected from pregnant *Bos taurus* cows at the abattoir of Midfield Meat International, Warrnambool, Victoria, Australia and were immediately frozen on dry ice on site and later stored in the laboratory at −80°C. These ovaries were scavenged from animals that were being processed for human consumption and were not owned by the authors or their institutions. As such the University of Adelaide's Animal Ethics Committee only requires notification of this. To estimate the gestational age of fetal samples, the crown rump length (CRL) was measured (Russe 1983).

Sex Determination of Bovine Fetuses

Genomic DNA was extracted from the tail of fetuses with a CRL <10 cm using the Wizard SV Genomic DNA Purification System (Promega Australia, Alexandria, NSW, Australia) according to the manufacturer's instructions. Two pairs of primers specific for a region in the Sex determining region Y (SRY) sequence (sense primer: 5′ TCACTCCTGCAAAAGGAGCA 3′, antisense primer: 5′ TTATTGTGGCCCAGGCTTG 3′), and for the 18S ribosomal RNA (18S) gene sequence were used for amplifying the genomic DNA in individual reactions as previously described (Hummitzsch et al., 2013).

RNA Extraction and RNA Sequencing

Whole fetal bovine ovaries were homogenised in 1 ml Trizol® (Thermo Fisher Scientific, Waltham, MA, United States) using the Mo Bio Powerlyser 24 (Mo Bio Laboratories Inc., Carlsbad, CA, United States) and RNA extracted according to manufacturer's instructions. All samples were treated with DNase I (Promega/Thermo Fisher Scientific Australia Pty Ltd., Tullmarine, Vic, Australia). The RNA concentration and quality (RQI, **Table 2**) was then determined using the Experion™ RNA StdSens Analysis kit and the Experion™ Automated Electrophoresis System (Bio Rad Laboratories Pty., Ltd., Gladesville, NSW, Australia). 500 ng/50 µl per well (96 well plate) of total RNA of each sample was used for RNA seq.

RNA seq based transcriptome profiling was performed at the SAHMRI Genomics Facility (SAHMRI, Adelaide, SA, Australia). Briefly, Single end Poly A selection mRNA libraries (~35 M reads per sample) were created using the Nugen Universal Plus mRNA Seq library kit from Tecan (Mannedorf, Switzerland) and sequenced with an Illumina Nextseq 500 using single read 75 bp (v2.0) sequencing chemistry (Illumina Inc., San Diego, CA, United States). Two sequencing runs, with 10 samples per run, were performed and sample 15/R43t was used as internal control in both runs.

RNA-Seq Data Analysis Using Partek Flow®

The raw data containing FASTQ files were uploaded to Partek Flow® Software, version 8.0 (Partek Incorporated, St. Louis, Missouri, United States). All samples underwent a pre alignment quality assessment and showed Phred Quality Scores larger than 30. The reads were aligned and annotated to the bovine genome ARS UCD1.2 (bosTau9; https://www.ncbi.nlm.nih.gov/assembly/GCF 002263795.1/) using STAR 2.7.3a aligner (>97% alignment rate for all samples) and Partek

E/M, respectively. Transcript abundances were determined and expression levels presented as normalised counts per million (CPM). Initial comparison of gene expression profiles in the samples was then carried out using principal components analysis (PCA) (Hotelling 1933).

Analysis of PCOS Candidate Genes

Normalised RNA seq data of bovine fetal ovaries across gestation were analysed to study the expression of PCOS candidate genes as well as their associated upstream regulators and mechanisms. The expression of 27 PCOS candidate genes, most of which are located in/near the loci associated with PCOS from previous GWAS, and three additional candidate genes *AR*, *AMH*, and *TGFB1I1* were analysed using to Partek Flow® Software (version 8.0). Scatter plots showing the expression patterns for each candidate gene across gestation were also generated using GraphPad Prism version 8 (GraphPad Software Inc., La Jolla, Ca, United States). Pearson's correlation of the genes with each other as well as with gestational age were further analysed. Fold change and statistical significance of PCOS genes across gestation (comparing late versus early) were determined using the default parameters of Gene Specific Analysis (GSA); a multi model approach based on Akaike Information Criterion (AIC) in Partek Flow®.

A supervised hierarchical clustering (heatmap) of all 24,889 genes identified in the RNA seq data for all samples across gestation was then carried out; the location of PCOS genes on the heatmap was determined and clusters of PCOS genes as well as genes co expressed with them were identified. Four clusters associated with the PCOS candidate genes were further studied using the core analysis component of Ingenuity Pathway Analysis (IPA®, QIAGEN Redwood City, CA, United States). The canonical pathways, upstream regulators and networks associated with each cluster were analysed based on the statistical significance (*p* value) and fold change ($\log_2$ ratio) of its gene list, determined using the default parameters of GSA in Partek Flow®. *C9orf3,* also known as aminopeptidase *(AOPEP)* replaced its bovine variant, *C8H9orf3,* in IPA analysis. For a more in depth understanding of pathways associated with genes in each of the four clusters, the Database for Annotation, Visualization, and Integrated Discovery (DAVID) Bioinformatics Resources 6.8 (https://david.ncifcrf.gov/home.jsp, Frederick, MD 21702, United States) (Huang et al., 2009; Sherman and Lempicki 2009), was further used to analyse the pathway enrichment of genes for each cluster from Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases for bovine organisms.

Statistical Analyses

Expression of PCOS genes across gestation was plotted using GraphPad Prism version 8 (GraphPad Software Inc., La Jolla, CA, United States). PCA and hierarchical clustering were performed using the Euclidian algorithm for dissimilarity with average linkage. Pearson's correlation table and correlation coefficient (R) generated for scatterplots were determined in Partek Genomic Suite 7.0 (Partek Incorporated, St. Louis, Missouri, United States). The *p* value of overlap between a set of significant molecules in each cluster and a given process/pathway/upstream regulator is determined using the Right Tailed Fisher's Exact Test in IPA software. The z score, which considers the directional effect of one molecule on another molecule/process and the direction of change of molecules in the dataset, represents activation when ≥2 and inhibition when ≤ −2. R program, version 4.0.4 was used to plot GO graphs using data from DAVID bioinformatic resources.

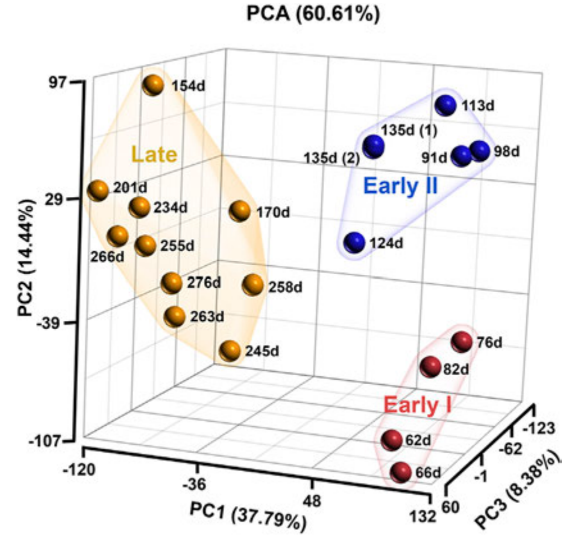


FIGURE 1 | Principal Component analysis of bovine ovarian samples analysed in the RNA sequencing. The samples are grouping into three stages; early I (red; 62 82 days, *n* = 4), early II (blue; 91 135 days, *n* = 5) and late (orange; 154 276 days, *n* = 10).

RESULTS

Expression of PCOS Candidate Genes

The normalised RNA seq data of bovine fetal ovaries identified 24,889 genes including uncharacterised and non coding RNA. Principal Component Analysis (PCA) of all the genes in the data clustered the samples into three groups/stages; early I (62 82 days, *n* = 4), early II (91 135 days, *n* = 5), and late (154 276 days, *n* = 10) (**Figure 1**). For the purposes of this study, the two early groups were combined as "early" (62 135 days, *n* = 9) and all comparisons across gestation involved late versus early samples.

The expression of the 27 PCOS candidate genes identified in the RNA seq data was studied across gestation. Using Pearson's correlation, the mRNA expression of these candidate genes across gestation showed three patterns; early, late, and throughout gestation. Thus, some PCOS candidate genes correlate significantly with gestational age negatively whilst others positively (**Table 3**). Genes that correlate negatively with gestational age, and therefore named "early" genes, correlate positively with each other, whilst those that correlate positively with gestational age, named "late" genes, correlate positively with each other but negatively with the "early" genes. Thus, according to this study, the "early" genes consist of *C8H9orf3, ARL14EP, MAPRE1, TOX3, FBN3, GATA4, HMGA2,* and *DENND1A*; the "late" genes include *YAP1, INSR, THADA, TGFB1I1, ZBTB16, IRF1, LHCGR, FSHR, AMH,* and *PLGRKT*; whilst genes expressed throughout gestation are *NEIL2, RAB5B, KRR1, SUOX, FDFT1, ERBB3, AR, ERBB4,* and *RAD50* (**Table 3**). Also, Gene Specific Analysis (GSA) comparing the expression of these candidate genes across gestation showed significant fold change across gestation; 14 of the genes were up regulated and 13 down regulated with significance at $p \leq 0.05$ for most candidate genes as shown in **Supplementary Table S1**. In addition to the "early" and "late" genes identified using Pearson's correlation, other genes that correlate significantly with gestational age according to GSA are; *ERBB3* (negatively) as well as *AR* and *ERBB4* (positively); see **Supplementary Table S1, Supplementary Figure S1**.

A supervised hierarchical clustering of all 24,889 genes showed that most PCOS candidate genes formed close clusters with each other according to the patterns earlier observed. Thus, most of the PCOS candidate genes that correlate significantly with each other in **Table 3** formed clusters closely with each other on the heatmap (**Figure 2**). Two strong clusters and two weak clusters were formed. The strong clusters contain "early" genes (cluster 1); *C8H9orf3, TOX3, FBN3, GATA4, HMGA2,* and *DENND1A* and "late" genes (cluster 4); *FDFT1, LHCGR, AMH, FSHR, ZBTB16* and *PLGRKT* (**Figure 2**). The two weak clusters comprised of "late" genes (cluster 2), *YAP1, INSR, THADA,* and *TGFB1I1* and genes expressed throughout gestation (cluster 3), *RAD50, NEIL2,* and *ERBB4*. It is worth noting that although *FDFT1* does not correlate significantly with gestational age, it correlates significantly with most of the genes in cluster 4 according to the Pearson's correlation (**Table 3**). Fold change and statistical significance were determined for the gene list of each of the clusters which were composed of PCOS candidate genes as well as the genes co expressed with them (**Supplementary Tables S2 S5**). They were mapped to the IPA knowledge base and DAVID bioinformatics database to identify the canonical pathways, upstream regulators and networks associated with each cluster.

The findings of this study were then aligned with the developmental stages of the ovary. Both IPA and GO

TABLE 3 | Pearson's correlation coefficients (R) between PCOS candidate genes mRNA expression levels and gestational age (n = 19) in bovine fetal ovaries.

Variable	Age (days)	*HMGA2*	*TOX3*	*FBN3*	*GATA4*	*MAPRE1*	*DENND1A*	*ARL14EP*	*C8H9orf3*	*NEIL2*	*SUOX*	*ERBB3*	*RAB5B*	*KRR1*	*RAD50*	*FDFT1*	*ERBB4*	*AR*	*LHCGR*	*IRF1*	*AMH*	*PLGRKT*	*ZBTB16*	*FSHR*	*YAP1*	*THADA*	*INSR*
HMGA2	-0.946^{d}																										
TOX3	-0.93^{d}	0.908^{d}																									
FBN3	-0.904^{d}	0.933^{d}	0.826^{d}																								
GATA4	-0.903^{d}	0.897^{d}	0.804^{d}	0.977^{d}																							
MAPRE1	-0.859^{d}	0.76^{c}	0.752^{c}	0.669^{b}	0.7^{c}																						
DENND1A	-0.728^{c}	0.747^{c}	0.744^{c}	0.74^{c}	0.728^{c}	0.452																					
ARL14EP	-0.716^{c}	0.547^{a}	0.664^{b}	0.397	0.444	0.869^{d}	0.298																				
C8H9orf3	-0.564^{a}	0.55^{a}	0.455	0.526^{a}	0.571^{a}	0.823^{d}	0.169	0.599^{b}																			
NEIL2	-0.431	0.328	0.441	0.198	0.2	0.331	0.596^{b}	0.448	-0.049																		
SUOX	-0.253	0.182	0.038	0.397	0.48^{a}	0.087	0.207	-0.031	0.072	-0.238																	
ERBB3	-0.250	0.262	0.143	0.303	0.312	0.523^{a}	0.089	0.263	0.745^{c}	-0.236	0.164																
RAB5B	-0.109	-0.07	0.173	-0.211	-0.199	0.117	0.085	0.536^{a}	-0.265	0.518^{a}	-0.171	-0.333															
KRR1	-0.081	0.228	0.292	0.084	0.001	-0.046	0.243	0.03	-0.089	0.097	-0.314	-0.081	0.237														
RAD50	0.055	-0.034	0.07	-0.208	-0.256	-0.186	0.23	-0.037	-0.461^{a}	0.701^{c}	-0.49^{a}	-0.492^{a}	0.349	0.393													
FDFT1	0.222	-0.233	-0.4	-0.058	-0.059	-0.159	-0.192	-0.412	-0.037	-0.271	0.261	0.238	-0.512^{a}	-0.678^{b}	-0.402												
ERBB4	0.377	-0.368	-0.273	-0.486^{a}	-0.531^{a}	-0.453	0.017	-0.289	-0.635^{b}	0.537^{a}	-0.501^{a}	-0.463^{a}	0.26	0.123	0.835^{d}	-0.076											
AR	0.446	-0.309	-0.364	-0.412	-0.464^{a}	-0.557^{a}	-0.195	-0.508^{a}	-0.603^{b}	-0.193	-0.126	-0.348	-0.112	0.288	0.361	-0.015	0.407										
LHCGR	0.526^{a}	-0.489^{a}	-0.561^{a}	-0.412	-0.434	-0.263	-0.41	-0.458^{a}	0.004	-0.453	-0.13	0.438	-0.423	-0.252	-0.314	0.639^{b}	0.023	0.106									
IRF1	0.602^{b}	-0.639^{b}	-0.466^{a}	-0.651^{b}	-0.651^{b}	-0.623^{b}	-0.232	-0.353	-0.676^{b}	0.08	-0.327	-0.525^{a}	0.306	-0.161	0.262	0.072	0.516^{a}	0.198	0.185								
AMH	0.643^{b}	-0.605^{b}	-0.684^{b}	-0.516^{a}	-0.524^{a}	-0.408	-0.481^{a}	-0.571^{a}	-0.153	-0.472^{a}	-0.138	0.158	-0.409	-0.29	-0.235	0.627^{b}	0.05	0.185	0.896^{d}	0.352							
PLGRKT	0.673^{b}	-0.588^{b}	-0.755^{c}	-0.454	-0.484^{a}	-0.568^{a}	-0.626^{b}	-0.661^{b}	-0.22	-0.642^{b}	0.115	0.167	-0.514^{a}	-0.351	-0.361	0.64^{b}	0.0003	0.254	0.694^{c}	0.275	0.701^{c}						
ZBTB16	0.674^{b}	-0.649^{b}	-0.656^{b}	-0.682^{b}	-0.7^{c}	-0.59^{b}	-0.547^{a}	-0.527^{a}	-0.532^{a}	-0.167	-0.293	-0.455	-0.113	-0.427	0.094	0.5^{a}	0.384	0.38	0.425	0.614^{b}	0.597^{b}	0.487^{a}					
FSHR	0.704^{c}	-0.666^{b}	-0.725^{c}	-0.588^{b}	-0.602^{b}	-0.48^{a}	-0.463^{a}	-0.605^{b}	-0.243	-0.4	-0.195	0.166	-0.347	-0.255	-0.141	0.604^{b}	0.2	0.245	0.932^{d}	0.418	0.97^{d}	0.71^{c}	0.591^{b}				
YAP1	0.71^{c}	-0.555^{a}	-0.557^{a}	-0.558^{a}	-0.619^{b}	-0.863^{d}	-0.313	-0.775^{d}	-0.748^{c}	-0.243	-0.219	-0.47^{a}	-0.117	0.435	0.435	-0.108	0.514^{a}	0.764^{c}	0.164	0.379	0.281	0.351	0.374	0.357			
THADA	0.783^{d}	-0.636^{b}	-0.664^{b}	-0.628^{b}	-0.701^{c}	-0.838^{d}	-0.361	-0.841^{d}	-0.702^{c}	-0.258	-0.263	-0.277	-0.245	0.198	0.37	0.226	0.568^{a}	0.721^{c}	0.47^{a}	0.472^{a}	0.566^{a}	0.578^{b}	0.56^{a}	0.64^{b}	0.895^{d}		
INSR	0.907^{d}	-0.816^{d}	-0.866^{d}	-0.777^{d}	-0.797^{d}	-0.811^{d}	-0.691^{b}	-0.807^{d}	-0.562^{a}	-0.494^{a}	-0.22	-0.261	-0.336	-0.182	0.023	0.459^{a}	0.342	0.569^{a}	0.628^{b}	0.492^{a}	0.756^{c}	0.734^{c}	0.819^{d}	0.783^{d}	0.698^{c}	0.84^{d}	
TGFB1I1	0.952^{d}	-0.904^{d}	-0.929^{d}	-0.822^{d}	-0.811^{d}	-0.848^{d}	-0.711^{c}	-0.747^{c}	-0.559^{a}	-0.496^{a}	-0.064	-0.268	-0.191	-0.254	-0.093	0.401	0.251	0.402	0.507^{a}	0.59^{b}	0.656^{b}	0.739^{c}	0.762^{c}	0.678^{b}	0.618^{b}	0.729^{c}	0.919^{d}

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. p *values: a <0.05; b < 0.01; c < 0.001; d < 0.0001.*

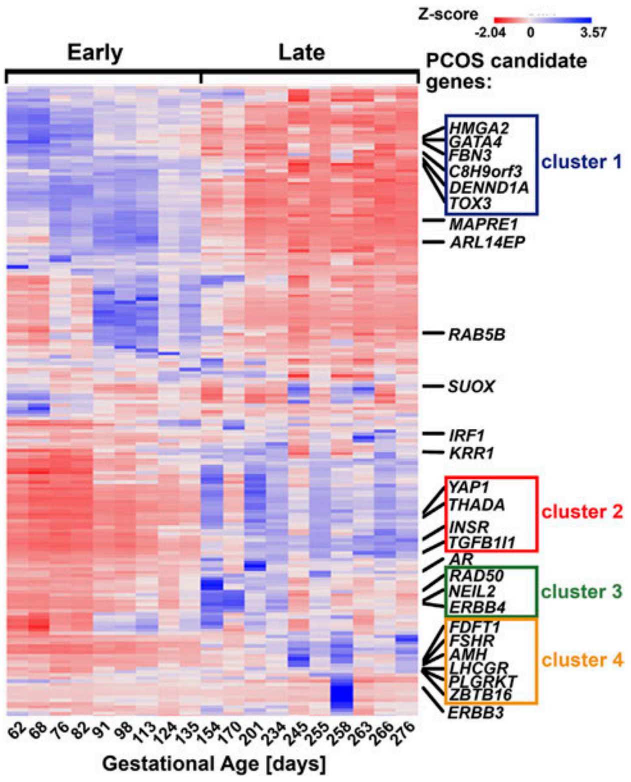


FIGURE 2 | Location of PCOS candidate genes and their respective clusters on the supervised heatmap of 24,889 genes identified in the fetal ovaries (62 276 days, $n = 19$) using RNA sequencing. Each cluster is made up of PCOS candidate genes as well as genes co expressed with them; detailed lists of each cluster can be found in **Supplementary Tables S2–S5**.

(biological processes) analyses of each cluster revealed relevant and similar canonical pathways to be associated with genes co expressed with PCOS candidate genes across gestation. The top canonical pathways associated with the "early" genes (cluster 1) are mainly involved in mitochondrial function (**Figure 3**) whilst "late" genes were involved in stromal development and expansion (cluster 2) and lipid biosynthesis/steroidogenesis (cluster 4) (**Figures 4**, **5**). Cluster 3, which consists of genes expressed throughout gestation, seems to be associated with a range of different pathways including central nervous system regulation and signalling among others (**Figure 6**). These pathways were also observed to some extent in the GO and KEGG pathway analysis for each cluster; with the strongest similarities to IPA observed in clusters 1 and 4 for mitochondrial function and steroidogenesis, respectively (**Supplementary Tables S6 S9**). Also, the number of genes extracted from each of these clusters as well as those that map to the IPA knowledge base and DAVID bioinformatic database for each cluster are shown in **Supplementary Table S10**.

Top biological upstream regulators associated with the strong clusters 1 and 4 and the weak clusters 2 and 3 were identified using IPA and are shown in **Tables 4**, **5**, respectively. Upstream regulators such as *TGFβ*, *TNF*, angiotensin, *ESR1*, among others were common to the "late" clusters 2 and 4. Upstream regulators such as *PTEN, HNF4A, ESRRA/G, PSEN1, MYC,* mitochondrial *LONP1,* and *TP53* among others were associated with cluster 1 whereas *HNF1A, GATA2, PSENEN, IL25, REST, OCT4 NANOG, APHIA,* and *AGRN* were associated with cluster 3. Chemical upstream regulators (including endogenous molecules) associated with each cluster was also studied. The list of the top chemical (including endogenous molecules) upstream regulators associated with each cluster are detailed in **Supplementary Tables S11, S12**. Estradiol is among the top chemical upstream regulators associated with certain genes in clusters 1, 2, and 4 while dexamethasone regulates some genes in cluster 2 and 4 among others.

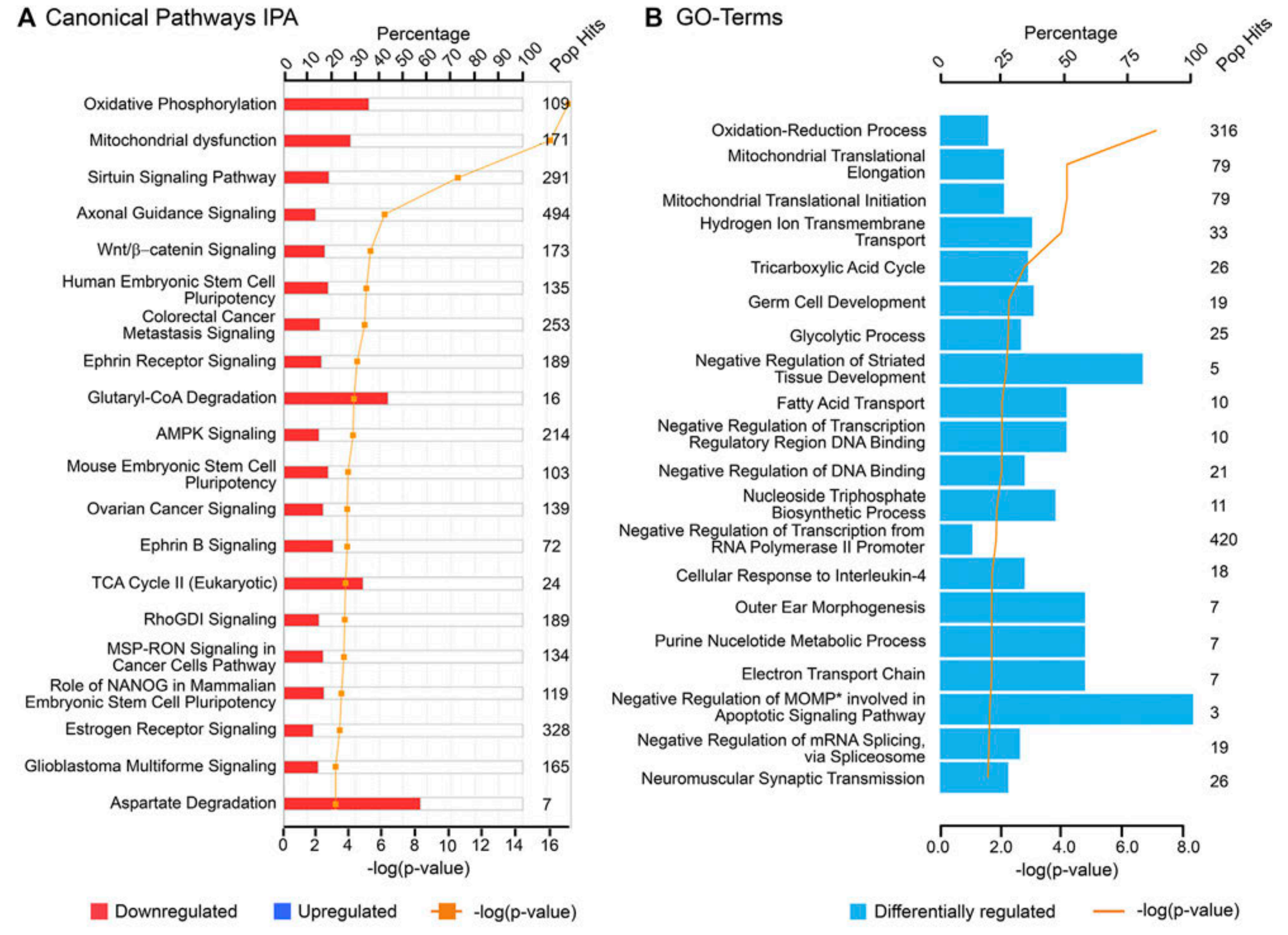
Additionally, 25 networks were generated by the IPA database for each cluster showing their functions and diseases. However, only those rated as important for fetal development and the role of PCOS candidate genes are shown in **Figures 7 9**. Specifically, mitochondrial function networks (1 and 3) of cluster 1 consisting of nuclear encoded and mitochondrial DNA encoded genes were downregulated during the second half of gestation (**Figure 7**). Networks associated with cluster 2, which were upregulated during the second half of gestation, consist of β catenin as the central player (network 16) interacting with other subunits of its kind, namely frizzled molecules and cadherins, which are cell adhesion molecules (CAM) (**Figure 8A**). The second network of cluster 2 (network 24) consists of extracellular matrix components including the different types of collagen with two central molecules, collagen, and fibronectin (**Figure 8B**). The top networks for cluster 4, which were also upregulated during the second half of gestation, are associated with the effects of the transcription factor *MYC* in metabolism (network 1) and steroidogenesis (network 2) (**Figure 9**). All other relevant networks are summarized in **Supplementary Figures S2 S5**.

Nuclear-Encoded Mitochondrial Genes and Mitochondrial-DNA Encoded Genes

Oxidative phosphorylation and mitochondrial dysfunction pathways are the top canonical pathways co expressed with the PCOS candidate genes expressed during early gestation (cluster 1). mRNA expression of nuclear encoded mitochondrial genes associated with these top pathways as well as genes encoded by mitochondrial DNA from the RNA seq are shown as scatterplots to outline their expression patterns across gestation (**Supplementary Figures S6, S7**, respectively). Similar patterns of expression were observed for both; thus, these genes are highly expressed during the early stages of gestation with expression decreasing gradually until 200 days of gestation, then the expression is maintained or increased slightly at that level in the third trimester.

DISCUSSION

Using RNA seq data from normal fetal ovaries collected across gestation, we examined the expression patterns of PCOS



*MOMP - Mitochondrial Outer Membrane Permeabilisation

FIGURE 3 | Top canonical pathways associated with cluster 1 ("early" genes) using **(A)** Ingenuity Pathway Analysis (IPA) and **(B)** Gene Ontology (GO) biological processes from DAVID database. "Pop Hits" refers to the total number of genes associated with each of the pathway in the database. The bar graphs represent the percentage of genes from the data set that map to each canonical pathway whilst the orange line shows the p value of overlap between genes in each cluster and a given pathway.

candidate genes and found that most belonged to one of four gene clusters. The expression patterns of most of the PCOS candidate genes in the RNA seq data were consistent with those previously identified by both Hartanti, et al. (2020) and Liu, et al. (2020). In addition to the PCOS candidate genes identified as expressed "early" or "late" in gestation in these previous studies, we found that *MAPRE1*, *ARL14EP*, and *C8H9orf3* were also "early" genes, whilst *YAP1* and *THADA* were "late" genes. The study then identified canonical pathways, biological and chemical upstream regulators and networks of genes that are co expressed in each of the clusters. This knowledge could be vital for understanding the mechanisms and identifying upstream regulators for delineating the fetal origin of PCOS.

During the early stages of fetal ovary development, primordial germ cells settle in the developing ovary as oogonia and start to proliferate between the proliferating Gonadal Ridge Epithelial Like (GREL) cells. Then stroma of the mesonephros, containing fibroblasts, fibres, and capillaries, penetrates into the gonadal ridge. This results in the formation of the ovigerous cords containing the GREL cells and proliferating oogonia. The ovigerous cords are separated from the penetrating stroma by a basal lamina and are open at the surface of the ovary during early gestation (Hummitzsch, et al., 2013; Hummitzsch et al., 2019). Interestingly, we found in cluster 1 that mitochondrial function is a key canonical pathway at this early stage of fetal ovary development. Expression patterns of nuclear encoded mitochondrial genes and mitochondrial DNA encoded genes across gestation showed that mitochondrial function and oxidative phosphorylation are at peak during stromal proliferation and penetration, specifically from the time of ovigerous cord formation until the cords begin to breakdown and primordial follicle formation occurs during fetal ovary development.

The relationship between mitochondrial dysfunction and the pathogenesis of PCOS remains unclear, although studies

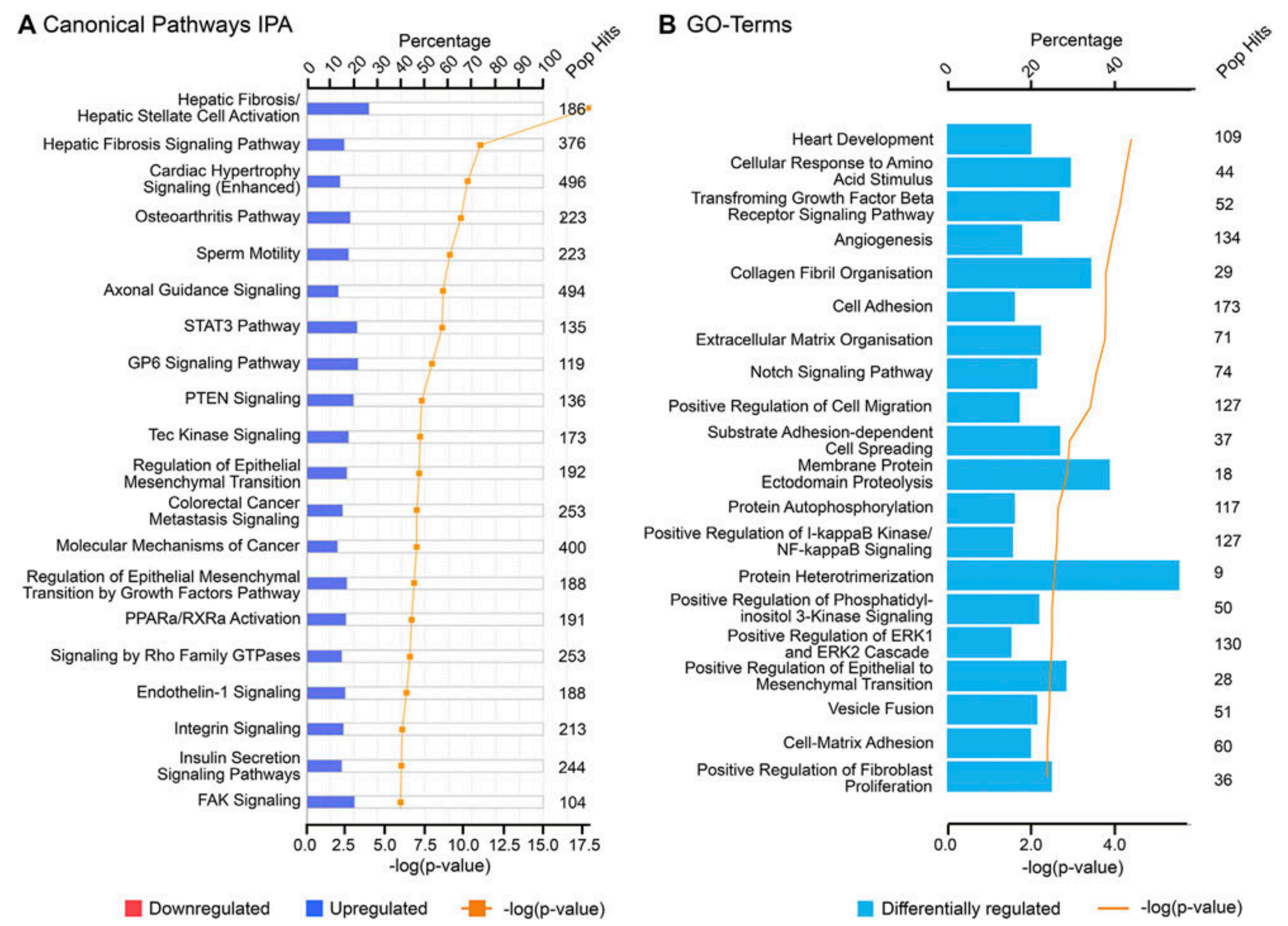


FIGURE 4 | Top canonical pathways associated with cluster 2 ("late" genes) using **(A)** Ingenuity Pathway Analysis (IPA) and **(B)** Gene Ontology (GO), biological processes from DAVID database. "Pop Hits" refers to the total number of genes associated with each of the pathway in the database. The bar graphs represent the percentage of genes from the data set that map to each canonical pathway whilst the orange line shows the *p* value of overlap between genes in each cluster and a given pathway.

focussed on this topic began over the last decade. Mitochondrial DNA copy number and abnormal reactive oxidative species have been associated with numerous phenotypes of PCOS (Hyderali and Mala 2015; Shukla et al., 2020). Thus, insulin resistance, obesity, hyperandrogenism among others have been linked directly/indirectly to mitochondrial dysfunction [see reviews (Ilie 2018; Zhang et al., 2019; Zeng et al., 2020)]. A meta analysis involving lean (BMI ≤ 23) and obese (BMI ≥ 23) PCOS patients using a systematic and comparative study by Idicula Thomas et al. (2020) showed that nuclear encoded mitochondrial genes were downregulated mainly in the cumulus cells of obese PCOS patients, but upregulated mainly in subcutaneous adipose tissues of lean PCOS patients. Furthermore, previous studies have shown that offspring of androgenised lean PCOS mice had impaired ovarian mitochondrial ultrastructure and function when compared to their controls (Chappell et al., 2020). Thus, mitochondrial ultrastructure in oocytes of androgenised offspring had disorganised cristae and swollen vacuoles without any electron dense content; a lower inner mitochondrial membrane potential of oocytes was also observed as compromised mitochondria function in the PCOS lean mice (Chappell, et al., 2020). This implies that *in utero* exposures to high androgen levels can significantly affect the development of the ovaries, most probably at the early stages of gestation, when germ cells undergo mitosis, ovigerous cords form, and stroma proliferates and migrates leading to the fetal programming of PCOS. More so, aberrant mitochondrial function was observed in oocytes at germinal vesicles stage of PCOS patients when compared to healthy controls in a study that compared the various stages of oocyte development in the two groups using single cell RNA sequencing (Qi et al., 2020). Additionally,

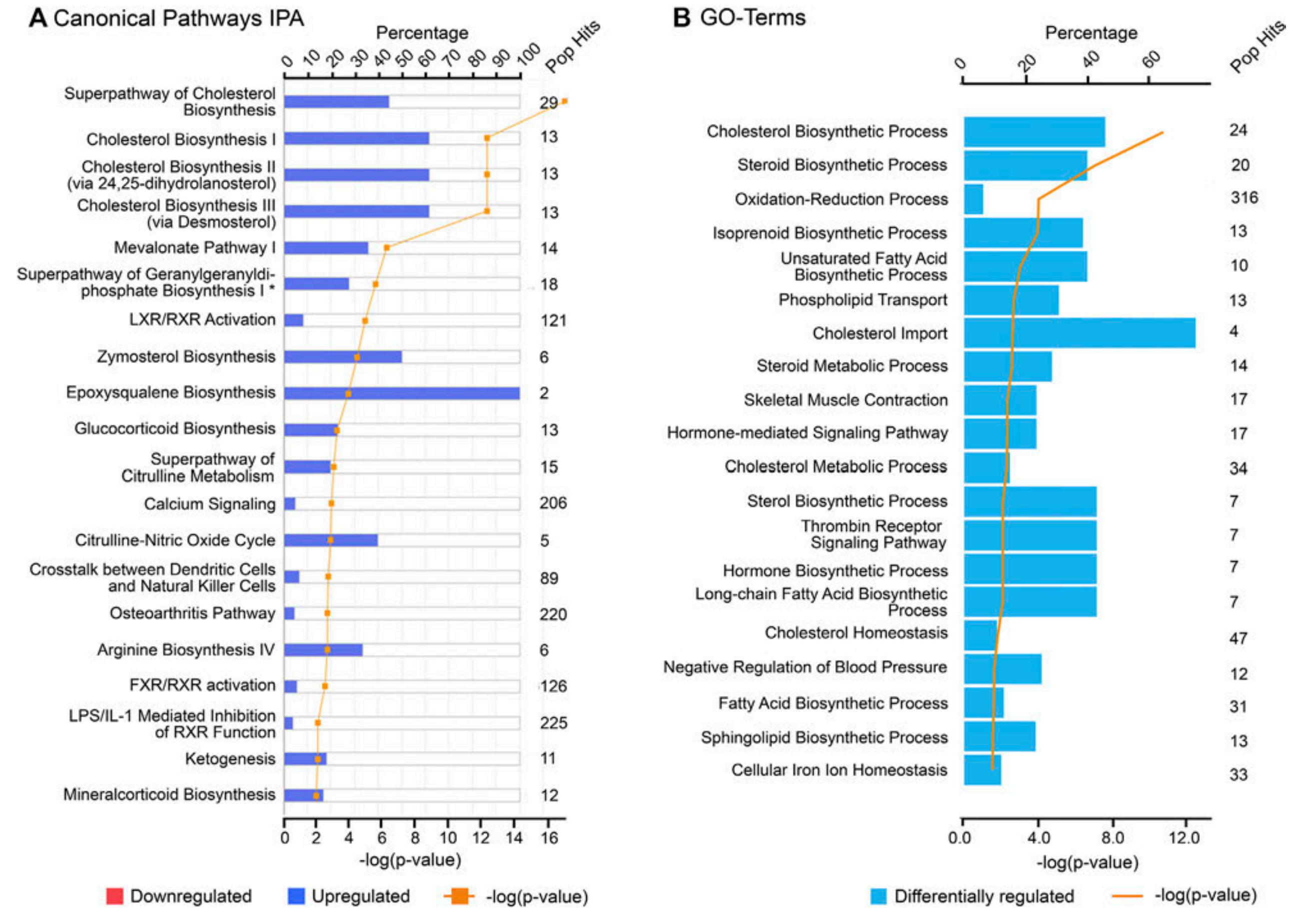


FIGURE 5 | Top canonical pathways associated with cluster 4 (“late” genes) using **(A)** Ingenuity Pathway Analysis (IPA) and **(B)** Gene Ontology (GO), biological processes from DAVID database. “Pop Hits” refers to the total number of genes associated with each of the pathway in the database. The bar graphs represent the percentage of genes from the data set that map to each canonical pathway whilst the orange line shows the *p* value of overlap between genes in each cluster and a given pathway.

studies focussed on the early stages of fetal ovary development in pig have also shown upregulation of mitochondrial activity and oxidative phosphorylation genes, inferred by higher expression of mitochondrial DNA encoded genes at early stages of development (E31). During this stage, extensive proliferation of primordial germ cells and the global waves of methylation and demethylation occur in the porcine ovary; requiring significant levels of energy to sustain the changes (Zhu et al., 2021). The high energy produced results in by products (e.g., alpha ketoglutarate) that are then used to establish various epigenetic marks and modulate demethylation by oxidising of 5 methylcytosine (5mC) to 5 hydroxymethylcytosine (5hmC) (Tahiliani et al., 2009; Wu and Zhang 2017). The findings together infer that mitochondrial function could play a significant role in the predisposition of PCOS; requiring further studies.

Furthermore, the identification of upstream regulators such as *DAP3,* which plays significant roles in mitochondrial respiration and apoptosis (Tang et al., 2009), and *MYC,* which is a regulator of mitochondrial biogenesis (Li et al., 2005), as well as the downregulation of nuclear and mitochondrial DNA encoded genes during the second half of gestation, in this study, implies that mitochondrial function is vital to the early stages of ovary development.

During mid gestation, compartmentalisation of the ovary into the cortex and medulla becomes apparent, where there are alternating ovigerous cords and stromal areas in the cortex and stroma from the mesonephros containing extracellular matrix, fibroblasts and vasculature in the medulla. The stroma starts to migrate laterally after reaching just below the ovarian surface resulting in the closing of the ovigerous cords on the surface and the establishment of an ovarian surface epithelium underlain by a basal lamina (Hummitzsch, et al.,

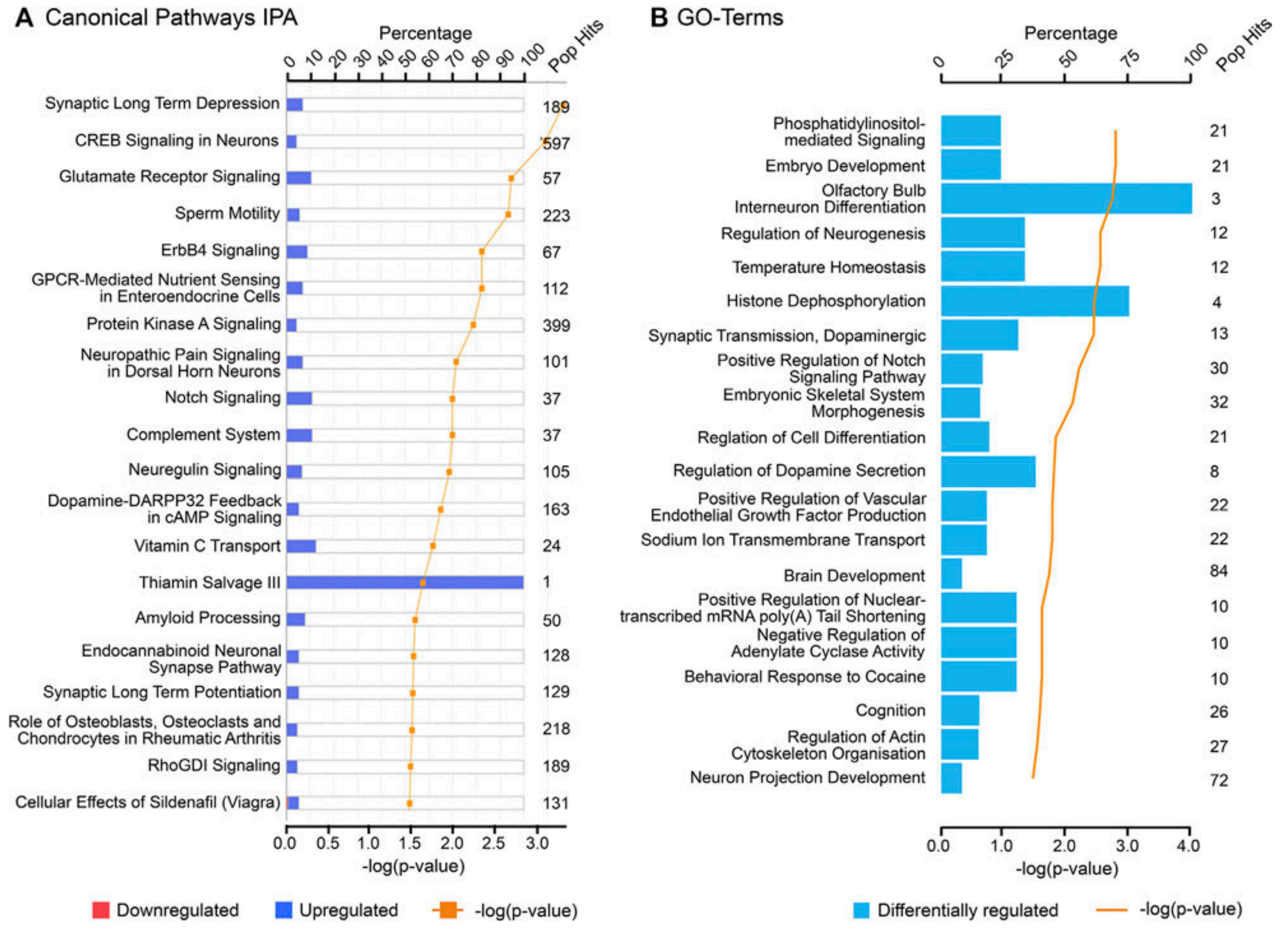


FIGURE 6 | Top canonical pathways associated with cluster 3 ("throughout" genes) using **(A)** Ingenuity Pathway Analysis (IPA) and **(B)** Gene Ontology (GO), biological processes from DAVID database. "Pop Hits" refers to the total number of genes associated with each of the pathway in the database. The bar graphs represent the percentage of genes from the data set that map to each canonical pathway whilst the orange line shows the *p* value of overlap between genes in each cluster and a given pathway.

2019; Hummitzsch, et al., 2013). This is, to some extent, consistent with our observations of genes connected with cluster 2, which includes genes involved in stromal expansion. Notably, the presence of elevated levels of fibrous tissues and collagen in the ovarian capsule or tunica albuginea resulting in denser ovarian stroma are common features of polycystic ovaries. Increased stromal collagen and ovarian cortex expansion in PCOS patients are associated with dysfunction of fibrillin 3 (*FBN3*) which is highly expressed in early stages of fetal development and not expressed late in gestation or adult ovaries (Hatzirodos, et al., 2011). *FBN3* regulates transforming growth factor β (TGF β) pathways, which stimulate fibroblast proliferation and collagen formation. TGF β may also play significant roles in the cardiovascular and metabolic symptoms of PCOS as discussed in review by Raja Khan et al. (2014). Upstream regulators involved in TGF β signalling pathways such as *TGFB1, TGFB2, TGFB3,* and *TGFBR2* and fibroblast proliferation regulators such as *FGF2*, coagulation factor II (*F2*) were consistent with findings of this study. In addition, networks associated with the components of extracellular matrix, such as collagen and fibronectin which are relevant to this stage of ovary development were associated with this cluster of genes.

Furthermore, *YAP1*, a PCOS candidate gene in cluster 2, is a critical regulator of granulosa cell proliferation, differentiation and survival by interaction with epidermal growth factor receptor, gonadotrophin, and TGF β signalling pathways (Lv et al., 2019). More so, *ERBB3,* which is an early gene according to our GSA analysis and Liu et al. (2020) and a member of the epidermal growth factor family, was identified as an upstream regulator for genes in cluster 2. Additionally, β catenin, which is a central molecule for one of the networks associated with this cluster, plays an essential role in Wnt signal

TABLE 4 | Top biological upstream regulators and their respective activation z score as well as *p* value of association for the strong clusters, cluster 1 and 4.

	Upstream regulator	Name	z-score	*p*-value
Cluster 1	*CLPP*	Caseinolytic mitochondrial matrix peptidase proteolytic subunit	4.899	1.11E 11
	PTEN	Phosphatase and tensin homolog	0.143	1.46E 10
	HNF4A	Hepatocyte nuclear factor 4 alpha	3.972	1.90E 10
	TLE3	TLE family member 3, Transcriptional corepressor		2.69E 10
	DAP3	Death associated protein 3	3.162	1.05E 09
	ARNT	Aryl hydrocarbon receptor nuclear translocator	3.689	2.98E 09
	LONP1	Lon peptidase 1, Mitochondrial	1.457	3.71E 09
	ESRRG	Estrogen related receptor gamma	2.006	6.71E 09
	Firre	Firre intergenic repeating RNA element	4.796	1.41E 08
	APP	Amyloid beta precursor protein	2.107	3.01E 08
	MYC	MYC proto oncogene, BHLH transcription factor	7.632	3.11E 08
	STK11	Serine/Threonine kinase 11	4.041	3.31E 08
	ALKBH1	AlkB homolog 1, Histone H2A dioxygenase	2.646	8.62E 08
	NSUN3	NOP2/Sun RNA methyltransferase 3	2.646	8.62E 08
	PSEN1	Presenilin 1	0.649	1.64E 07
	KDM5A	Lysine demethylase 5A	4.914	2.45E 07
	MAPT	Microtubule associated protein tau		3.58E 07
	RICTOR	RPTOR independent companion of MTOR complex 2	4.854	5.14E 07
	DDX5	DEAD box helicase 5	3.638	2.46E 06
	TP53	Tumor protein P53	1.511	2.90E 06
	Esrra	Estrogen related receptor alpha	1.849	3.18E 06
Cluster 4	*SREBF2*	Sterol regulatory element binding transcription factor 2	4.586	1.41E 22
	INSIG1	Insulin induced gene 1	4.447	5.74E 21
	MAP2K5	Mitogen activated protein kinase 5	4.088	3.78E 18
	SCAP	SREBF chaperone	4.269	9.03E 18
	POR	Cytochrome P450 oxidoreductase	3.776	4.93E 16
	SREBF1	Sterol regulatory element binding transcription factor 1	4.508	3.27E 14
	MFSD2A	Major facilitator superfamily domain containing 2A	3.138	8.14E 13
	ATP7B	ATPase copper transporting beta	3.464	1.46E 12
	MAPK7	Mitogen activated protein kinase 7	3.873	2.30E 12
	NPPB	Natriuretic peptide B	3.283	3.41E 12
	SH3TC2	SH3 domain and tetratricopeptide repeats 2	3.162	2.27E 11
	PROM1	Prominin 1	2.828	3.28E 11
	PPARA	Peroxisome proliferator activated receptor alpha	1.112	6.45E 11
	NR5A1	Nuclear receptor subfamily 5 group A member 1	3.446	7.22E 11
	C4BP	Complement component 4 binding protein	2.449	5.69E 10
	RPTOR	Regulatory associated protein of MTOR complex 1	3.2	1.43E 09
	KIF3A	Kinesin family member 3A	2.596	1.47E 09
	INSIG2	Insulin induced gene 2	2.586	1.97E 09
	TGFB1	Transforming growth factor beta 1	2.172	3.90E 09
	SIRT2	Sirtuin 2	1.913	6.77E 09

transduction and in intercellular adhesion by interacting with cadherin (Liu et al., 2009; Bush et al., 2019). Undoubtedly, the regulation of the PCOS candidate genes during this stage plays a substantial role in the cascade of events that occur later in fetal development.

During the late stages of ovary development, follicles consisting of oocytes and granulosa cells are formed from the differentiation of ovigerous cords (Hummitzsch, et al., 2013; Heeren et al., 2015). The first primordial follicles appear in the inner cortex medulla region, surrounded by a basal lamina. The surface epithelium, mostly single layered, then surrounds the ovary. Stroma beneath the surface epithelial basal lamina then develops into the tunica albuginea during the final developmental stages of the human and bovine ovary (Hummitzsch, et al., 2013; Heeren, et al., 2015; Hummitzsch, et al., 2019). Activation of some primordial follicles occurs leading to their development into primary and preantral follicles. Remarkably, the genes in cluster 4 (including the PCOS candidate genes), top canonical pathways, upstream regulators and networks were involved in folliculogenesis and ovarian steroidogenesis which is consistent with occurrence during this stage of development. *FDFT1,* which is an essential enzyme in the synthesis of sterols further leading to the synthesis of cholesterol, correlates significantly with genes involved in folliculogenesis such as *AMH, FSHR, LHCGR*. More so, upstream regulators involved in steroid synthesis such as *SREBF2, INSIG1, TGFB1, RPTOR*, and networks such as network 2 which has a central molecule, Mitogen Activated Protein Kinases, *ERK1/2*, interacting with other molecules of steroidogenesis such as FSH, LH, AMH, *CYP11A1* were also identified for this cluster.

Despite the increasing number of genetics studies to define the abnormalities associated with PCOS, the

TABLE 5 | Top biological upstream regulators and their respective activation z score as well as *p* value of association for the weak clusters, cluster 2 and cluster 3.

	Upstream regulator	Name	z-score	*p*-value
Cluster 2	*TGFB1*	Transforming growth factor beta 1	7.017	1.77E 21
	HRAS	HRas proto oncogene, GTPase	0.699	1.60E 14
	ERBB2	Erb B2 receptor tyrosine kinase 2	0.667	7.95E 13
	F2	Coagulation factor II, Thrombin	5.485	9.38E 13
	Alpha catenin	Alpha catenin group	5.256	1.76E 12
	TGFB2	Transforming growth factor beta 2	3.062	3.71E 12
	TNF	Tumor necrosis factor	3.597	1.00E 11
	Mek	Mitogen activated protein kinase 1	3.218	1.23E 11
	COLQ	Collagen like tail subunit of asymmetric acetylcholinesterase	1.511	1.29E 11
	MRTFB	Myocardin related transcription factor B	5.14	1.60E 11
	VEGF	Vascular endothelial growth factor	5.581	9.26E 11
	TP53	Tumor protein P53	4.493	9.90E 11
	Tgf beta	Transforming growth factor beta	4.093	2.28E 10
	AGT	Angiotensinogen	3.331	3.01E 10
	FGF2	Fibroblast growth factor 2	4.223	4.14E 10
	ITGB1	Integrin subunit beta 1	1.223	5.19E 10
	SP1	Sp1 transcription factor	5.601	1.01E 09
	ERBB3	Erb B2 receptor tyrosine kinase 3	0.325	1.71E 09
	TP63	Tumor protein P63	1.448	1.80E 09
	TGFBR2	Transforming growth factor beta receptor 2	3.079	3.79E 09
	TGFB3	Transforming growth factor beta 3	3.759	4.62E 09
Cluster 3	*ASCL1*	Achaete scute family BHLH transcription factor 1	2.543	7.44E 05
	FOXQ1	Forkhead box Q1		5.54E 04
	Dst	Dystonin		5.54E 04
	NOBOX	NOBOX oogenesis homeobox		9.83E 04
	HNF1A	HNF1 homeobox A	2.88	1.51E 03
	RSPO2	R spondin 2		3.22E 03
	TBPL1	TATA box binding protein like 1		3.22E 03
	ATOH1	Atonal BHLH transcription factor 1		3.48E 03
	GATA2	GATA binding protein 2	0.128	4.78E 03
	SNCA	Synuclein alpha	1.673	4.83E 03
	GRIN3A	Glutamate ionotropic receptor NMDA type subunit 3A	2.828	5.61E 03
	SAMD4A	Sterile alpha motif domain containing 4A		7.81E 03
	PSENEN	Presenilin enhancer, gamma secretase subunit		1.08E 02
	PTPN11	Protein tyrosine phosphatase non receptor type 11		1.09E 02
	REST	RE1 silencing transcription factor	2.19	1.14E 02
	OCT4 NANOG	POU class 5 homeobox 1 nanog homeobox		1.41E 02
	IL25	Interleukin 25	0.277	1.63E 02
	APH1A	Aph 1 homolog A, gamma secretase subunit		1.79E 02
	AGRN	Agrin		1.79E 02

pathogenesis of the syndrome still remains a challenge. Numerous studies to delineate the transgenerational susceptibility of PCOS in animals and human are on going (Tata, et al., 2018; Risal et al., 2019; Mimouni et al., 2021) and this study provides upstream regulators as well as canonical pathways that could be further studied to delineate the pathogenesis of the syndrome. Notably, genes co expressed with most PCOS candidate genes during both the early and late developmental stages of fetal development are involved in pathways that have previously been associated with PCOS, although mechanisms remain elusive. It would be very logical to infer that perturbations associated with mitochondrial function in the early stages of fetal ovary development lead to a cascade of events across gestation, some of which impact key canonical pathways such as stromal expansion and steroidogenesis, possibly, leading to PCOS in adulthood. The outcome of this study supports the need to further study the fetal origin of PCOS with the hope to, not only define the syndrome, but also towards the diagnosis, treatment and prevention of syndrome.

In summary, although this study is an *in silico* analysis of PCOS candidate genes and their co expressed genes from RNA seq data, it has shown significant consistency with the literature on ovarian development and PCOS. Additional studies to delineate the pathogenesis of the syndrome will be required based on these findings. The limitations of IPA software are also acknowledged as IPA is a knowledge based curated software.

CONCLUSION

These findings highlight the involvement of PCOS associated genes in mitochondrial function, stromal expansion and

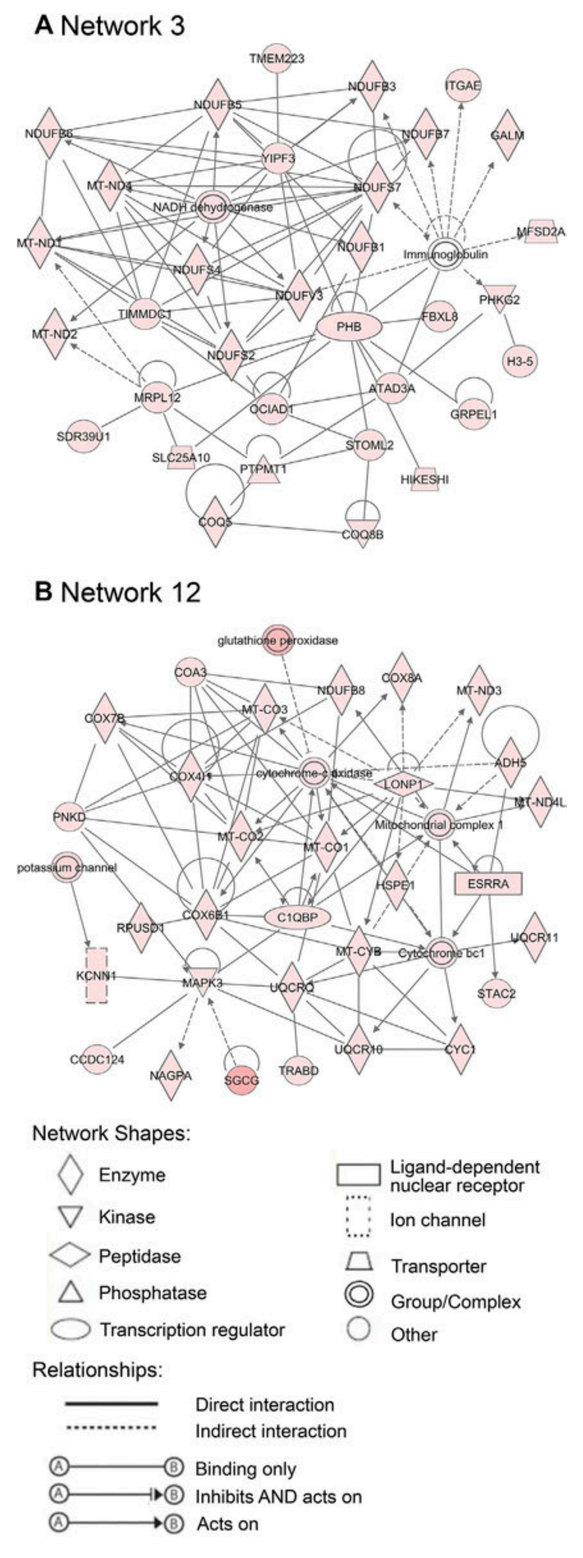


FIGURE 7 | Important networks connected with cluster 1. Network 3 **(A)** and network 12 **(B)** are associated with mitochondrial functions. Red color of molecules represents downregulation in the second half of gestation and the intensity of each color shows the strength of regulation.

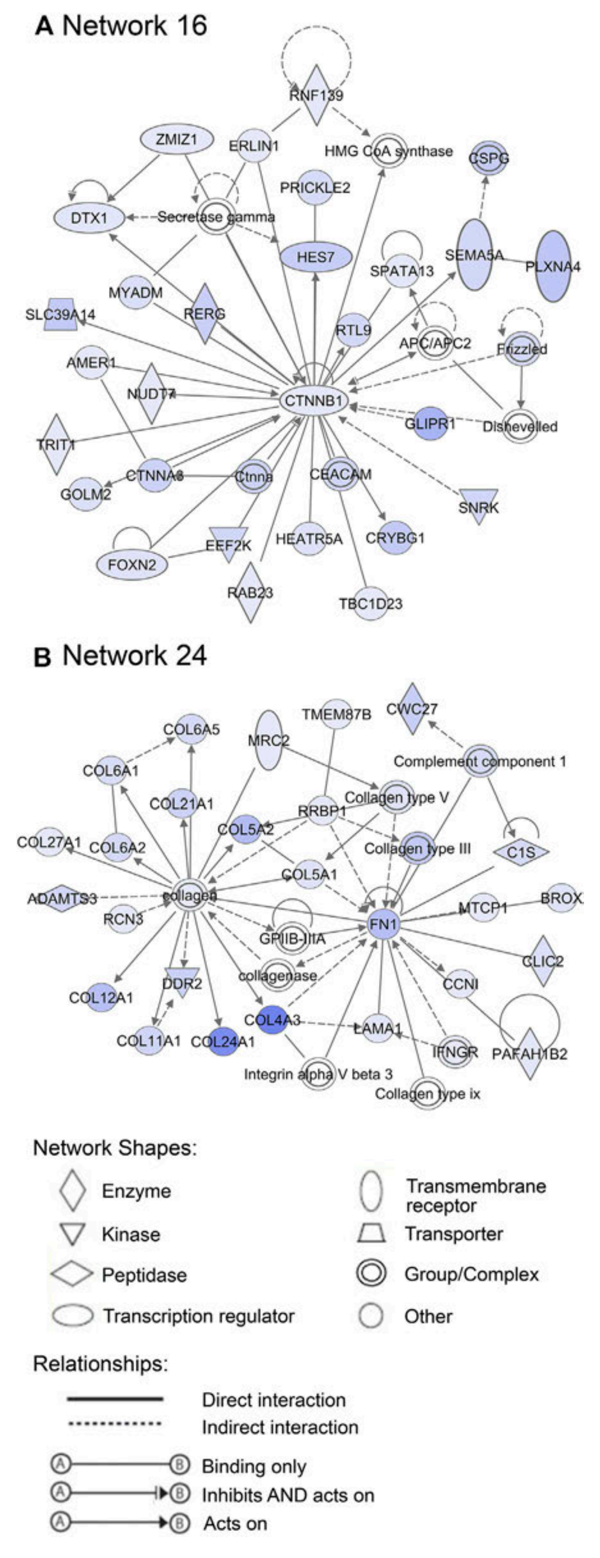


FIGURE 8 | Important networks associated with cluster 2. **(A)** Network 16 contains β catenin as central player, whereas **(B)** network 24 is associated with the components of extracellular matrix, such as collagens and fibronectin. Blue color of molecules represents upregulation in the second half of gestation and the intensity of each color shows the strength of regulation.

steroidogenesis during ovarian development. It could be speculated that perturbations during fetal ovary development resulting from dysregulation of these pathways could result in the different phenotypes of PCOS observed during adulthood. These perturbations could be genetic and/or environmental depending on maternal environment and fetal exposures associated with it. Further studies to delineate the role(s) of these pathways in the pathogenesis of PCOS are necessary. Notably, these findings infer a relationship between these major pathways, usually studied separately to define the syndrome and the need for studies investigating their interactions.

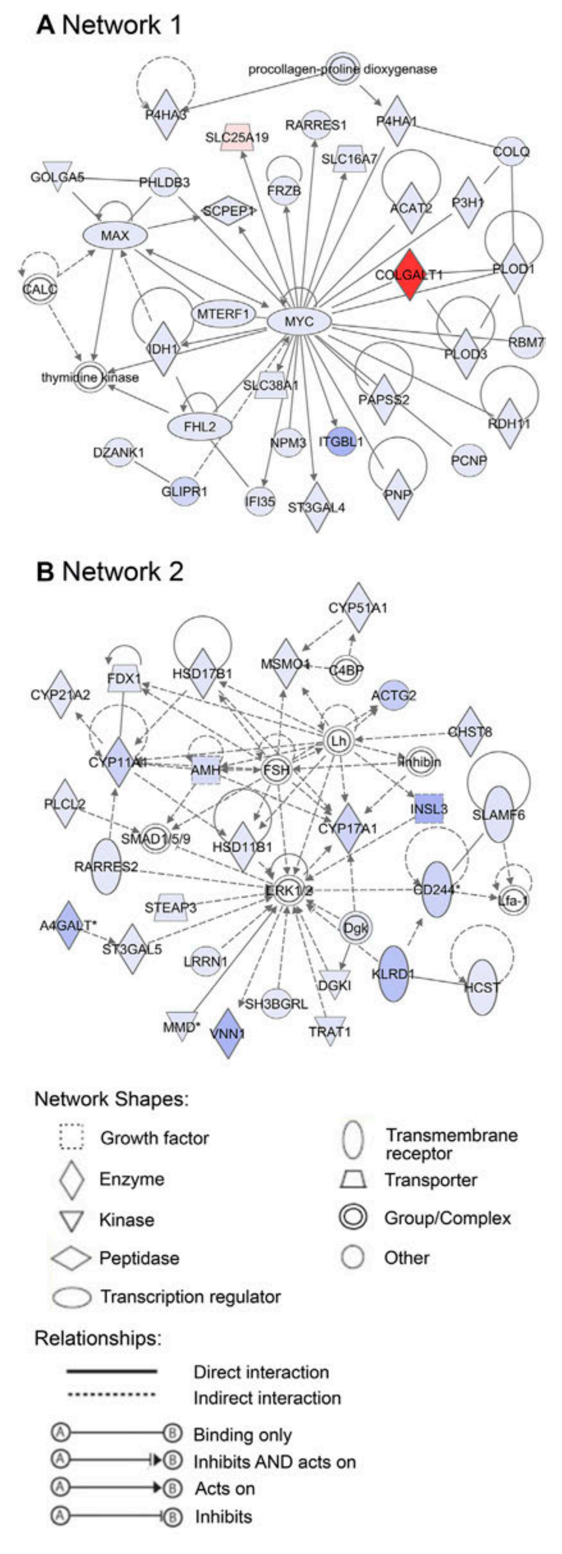


FIGURE 9 | Important networks of genes associated with cluster 4. **(A)** Network 1 is associated with the effects of the transcription factor MYC. **(B)** Network 2 is connected with steroidogenesis. Red represents downregulation and blue upregulation in the second half of gestation. The strength of regulation is shown by the intensity of each color.

DATA AVAILABILITY STATEMENT

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found below: https://www.ncbi.nlm.nih.gov/, GSE178450.

AUTHOR CONTRIBUTIONS

The authors contributions included Conceptualization (RA, KH, RJR), Formal analysis (RA, KH, RJR), Funding acquisition: KH, RJR, RAA, Investigation (RA), Analysis (RA, KH, RJR), Methodology (RA, KH, MDH, JCSJ, RJR), Project administration (KH, RJR), Resources (KH, RJR), Software (RA) Writing original draft (RA) and Writing review and editing (KH, JCSJ, RAA, RJR).

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fgene.2021.762177/full#supplementary material

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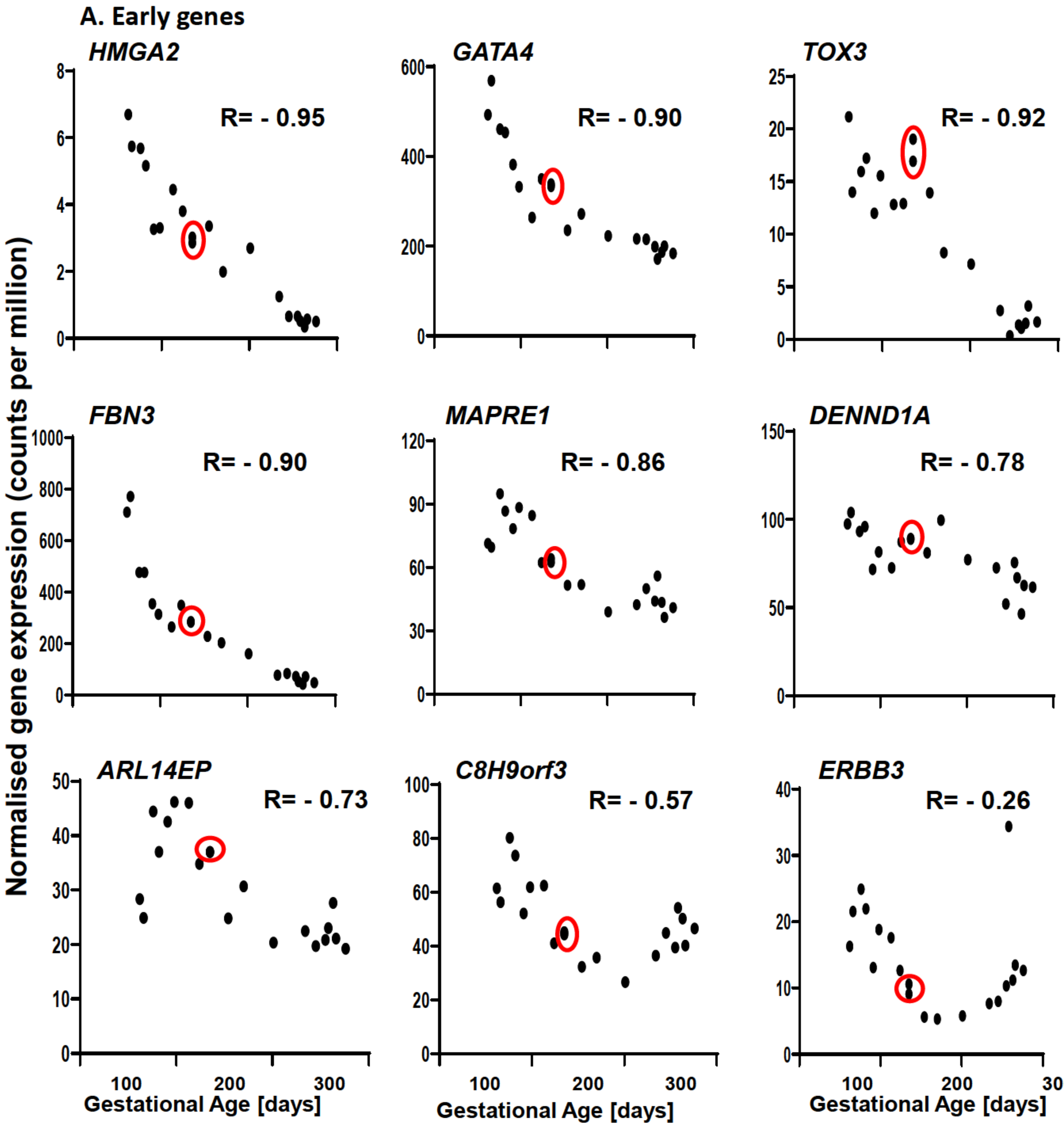
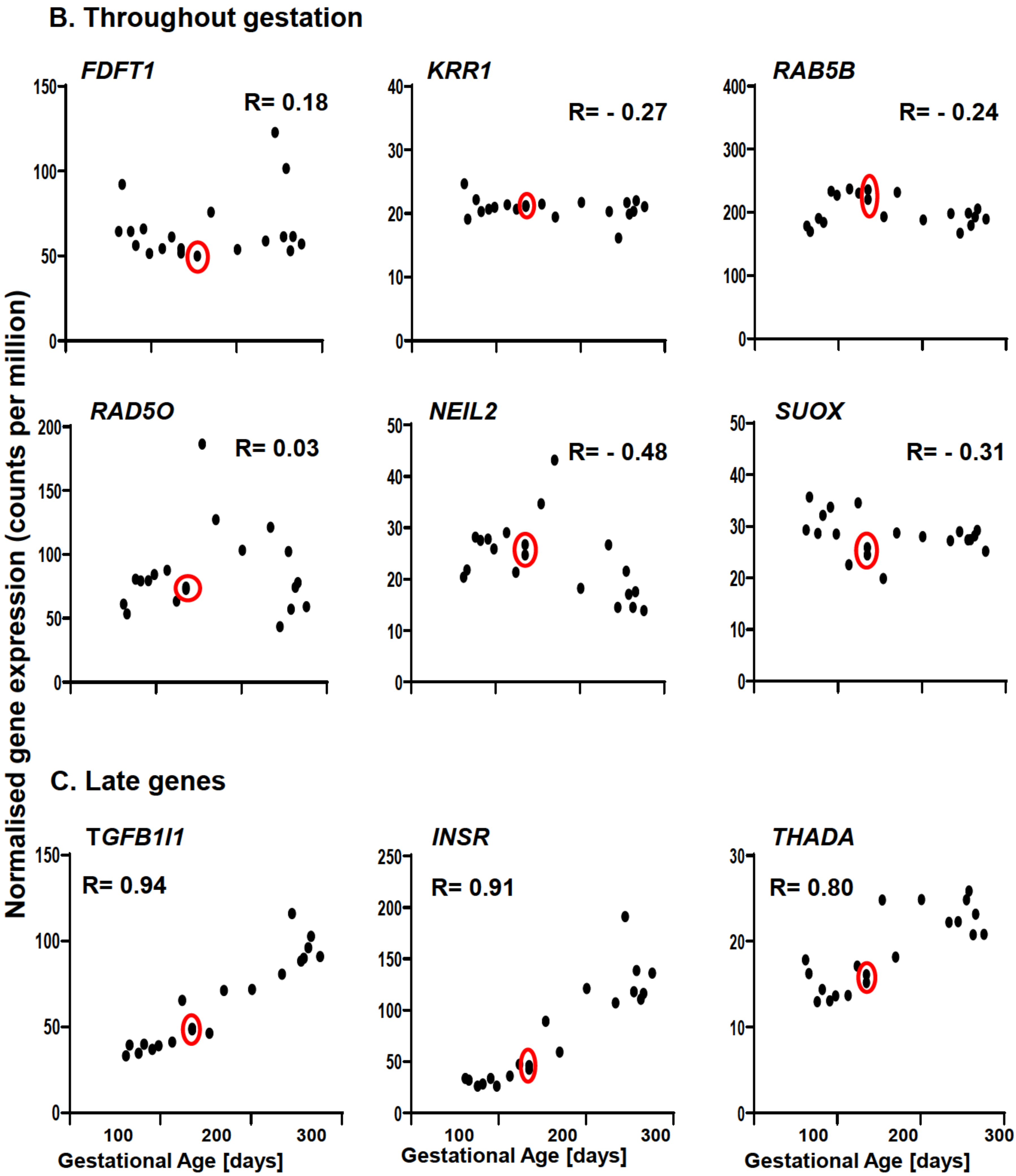
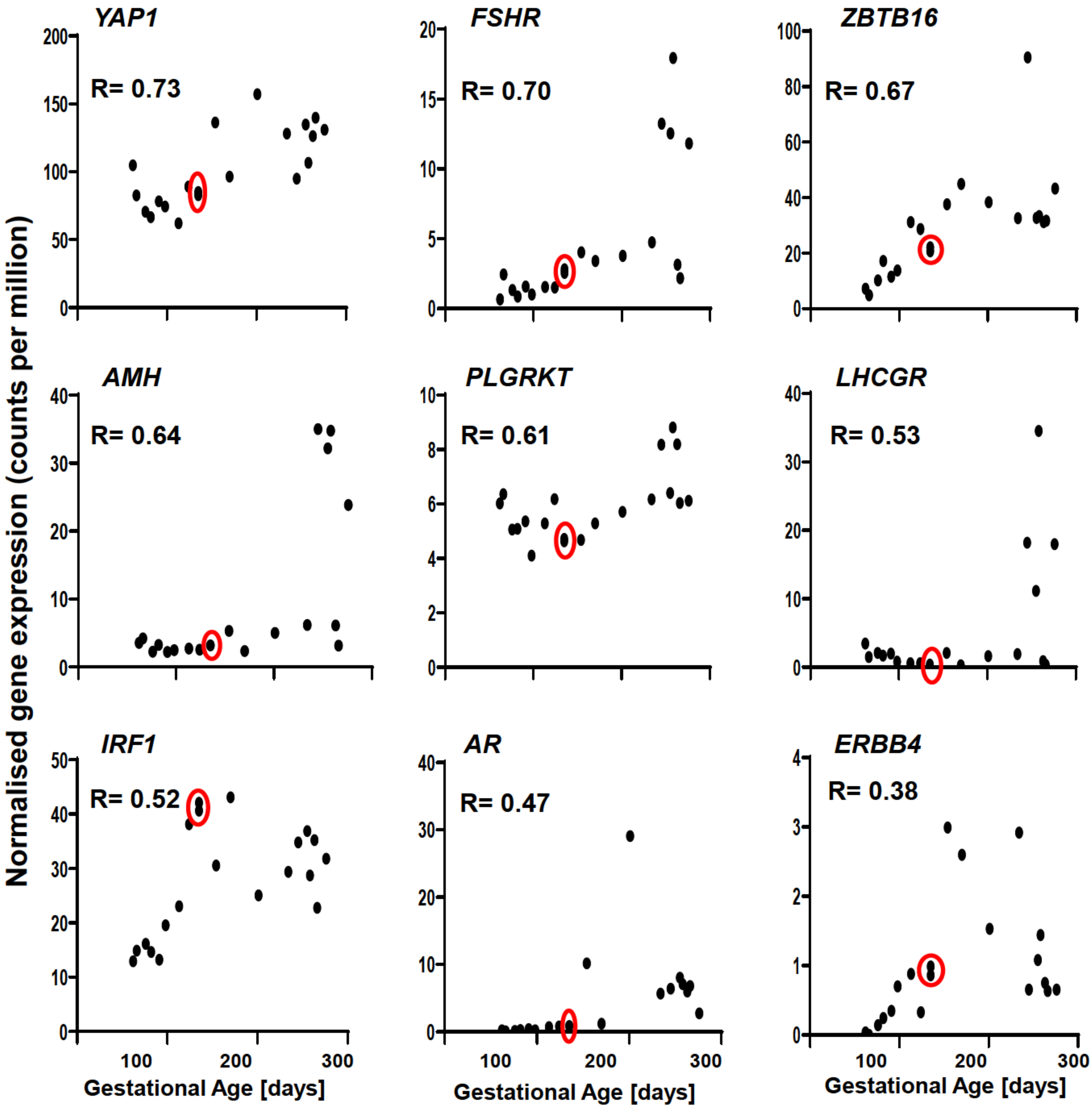
Conflict of Interest: Author RAA reports consultancy work for Ferring, Merck, IBSA, Roche Diagnostics, NeRRe Therapeutics and Sojournix Inc.

The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

S1 Fig. Scatterplots showing the expression of PCOS candidate genes across gestation. The expression patterns are in three groups according to Pearson's correlation and GSA outcomes;
A. early, B. throughout, and C. late genes. The red circle shows the results of two sequencing runs of the same sample.

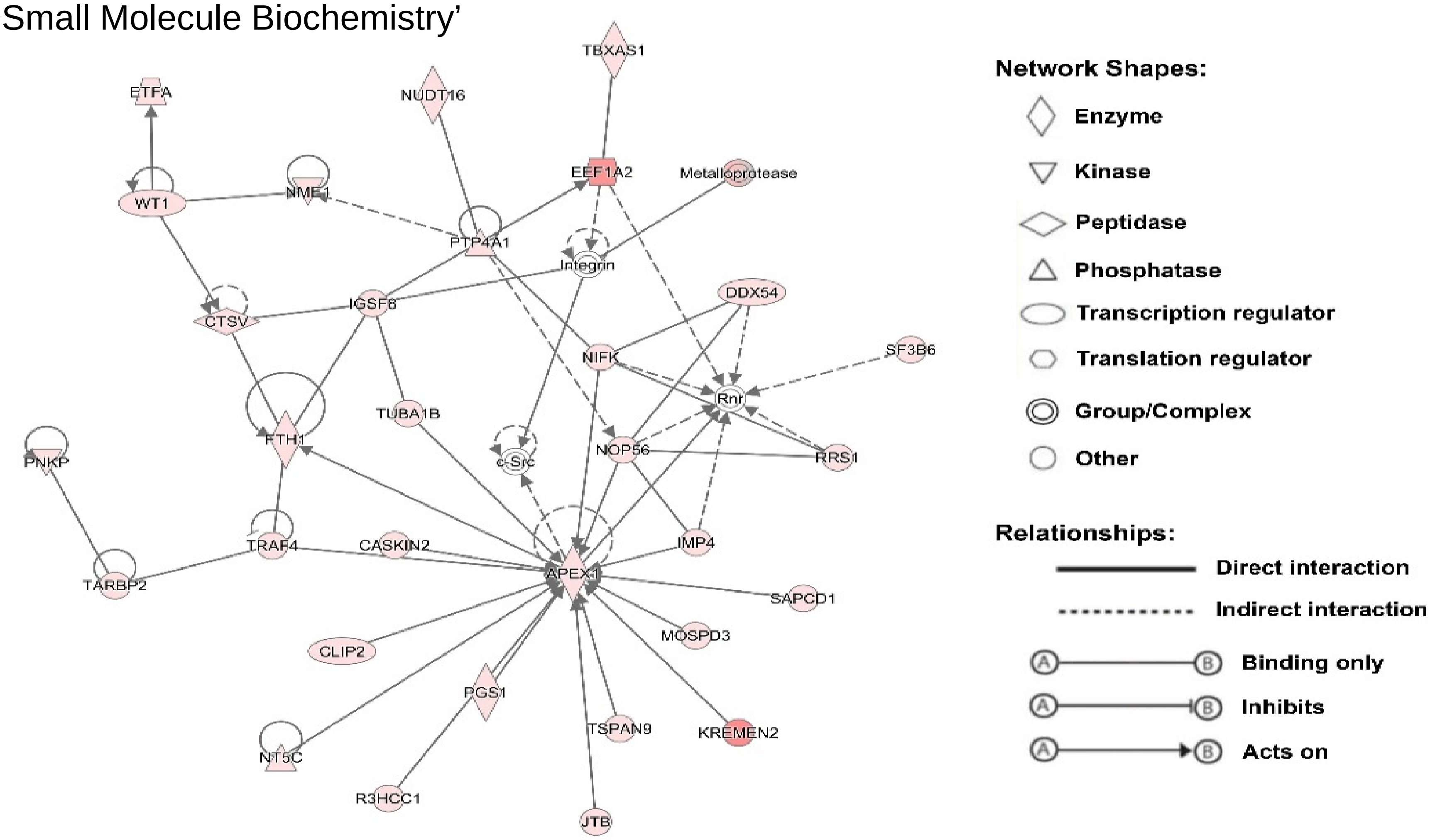



B. Throughout gestation
FDFT1
R= 0.18
KRR1
R= - 0.27
RAB5B
R= - 0.24
RAD5O
R= 0.03
NEIL2
R= - 0.48
SUOX
R= - 0.31
C. Late genes
TGFB1I1
R= 0.94
INSR
R= 0.91
THADA
R= 0.80
Normalised gene expression (counts per million)
Gestational Age [days]
0
50
100
150
200
250
300
400
10
20
30
40

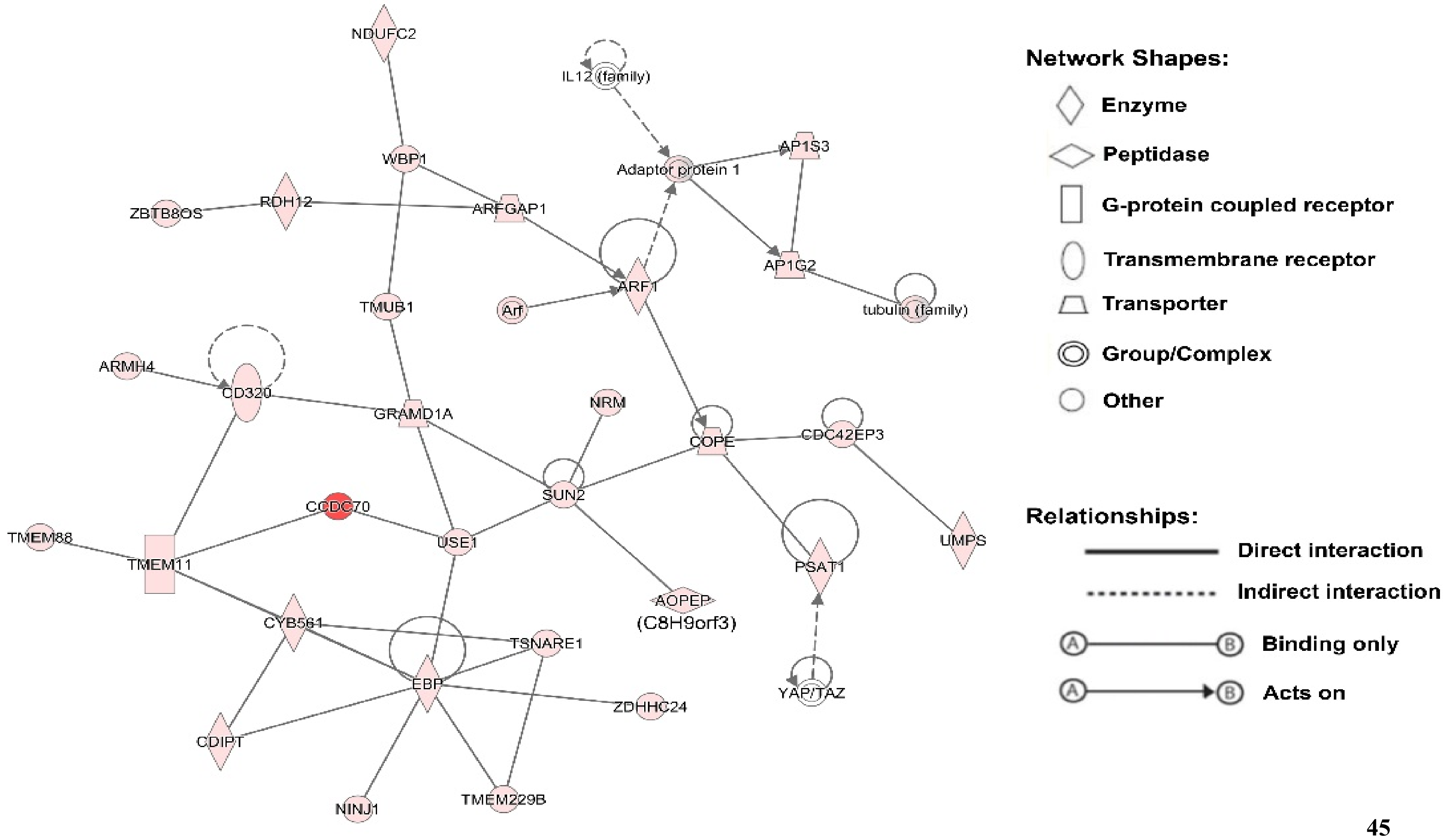

YAP1
R= 0.73
200
150
100
50
0
FSHR
R= 0.70
20
15
10
5
0
ZBTB16
R= 0.67
100
80
60
40
20
0
AMH
R= 0.64
40
30
20
10
0
PLGRKT
R= 0.61
10
8
6
4
2
0
LHCGR
R= 0.53
40
30
20
10
0
IRF1
R= 0.52
50
40
30
20
10
0
AR
R= 0.47
40
30
20
10
0
ERBB4
R= 0.38
4
3
2
1
0
100
200
300
Gestational Age [days]
Normalised gene expression (counts per million)

S2 Fig. Selected networks from cluster 1 and their respective functions and diseases. Red represents downregulation during the second half of gestation. The strength of regulation is shown by the intensity of each color.

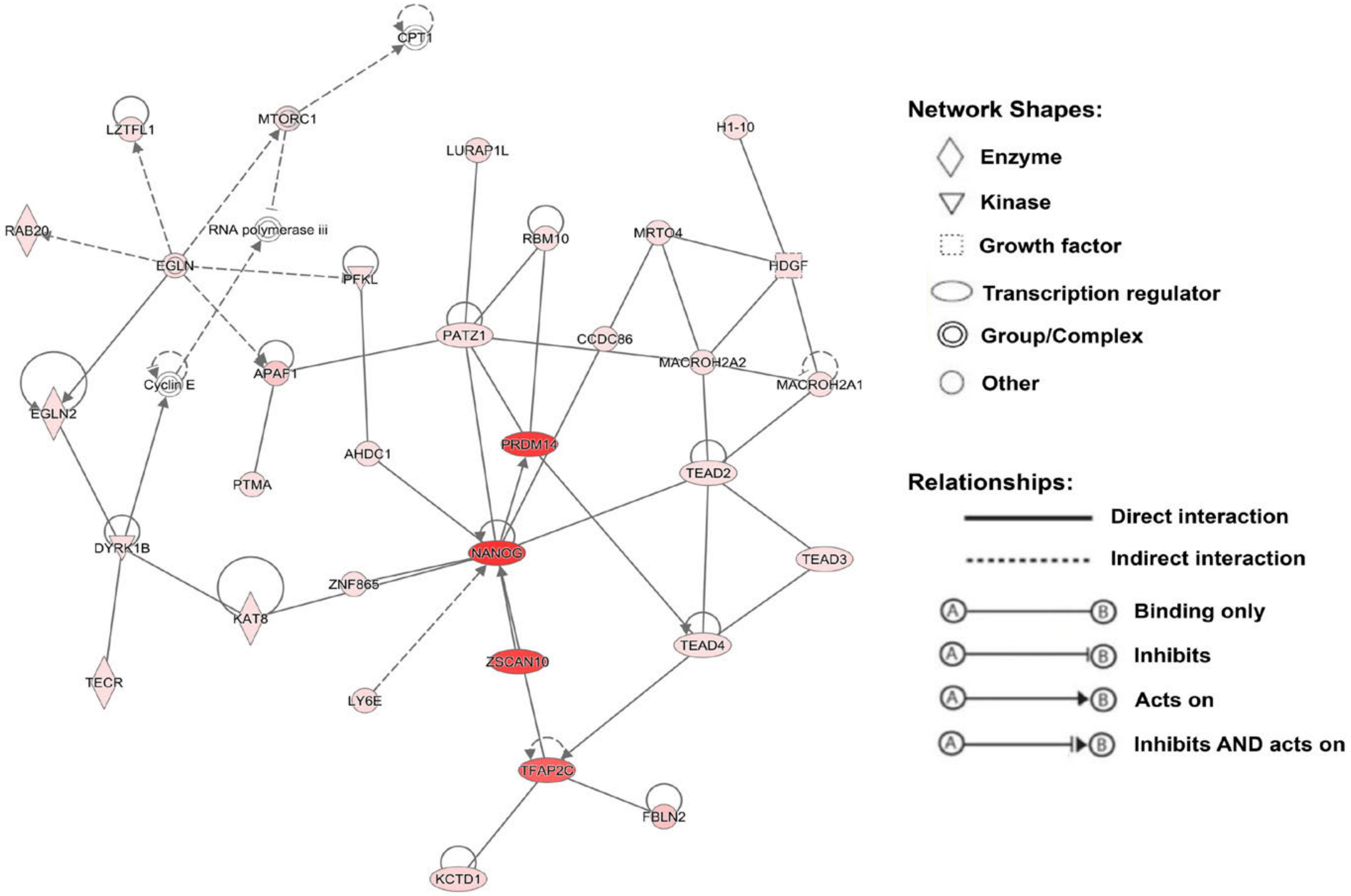
Network 11 ‘DNA Replication, Recombination, and Repair, Nucleic Acid Metabolism, Small Molecule Biochemistry’



Network 14 ‘Cardiovascular Disease, Cellular Assembly and Organization, Cellular Function and Maintenance’

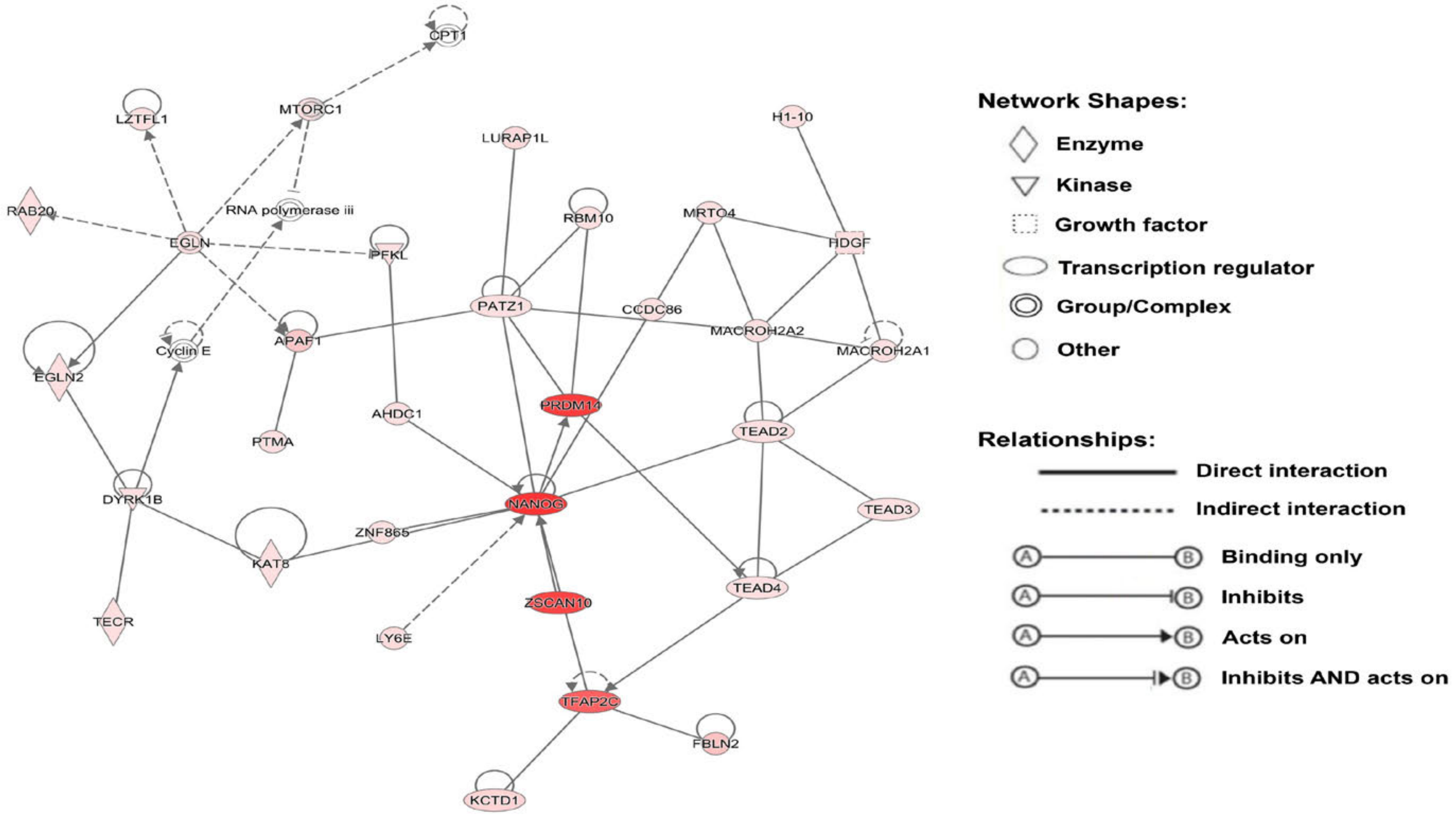


Network 18 ‘Endocrine System Disorders, Gene Expression, Hereditary Disorder’

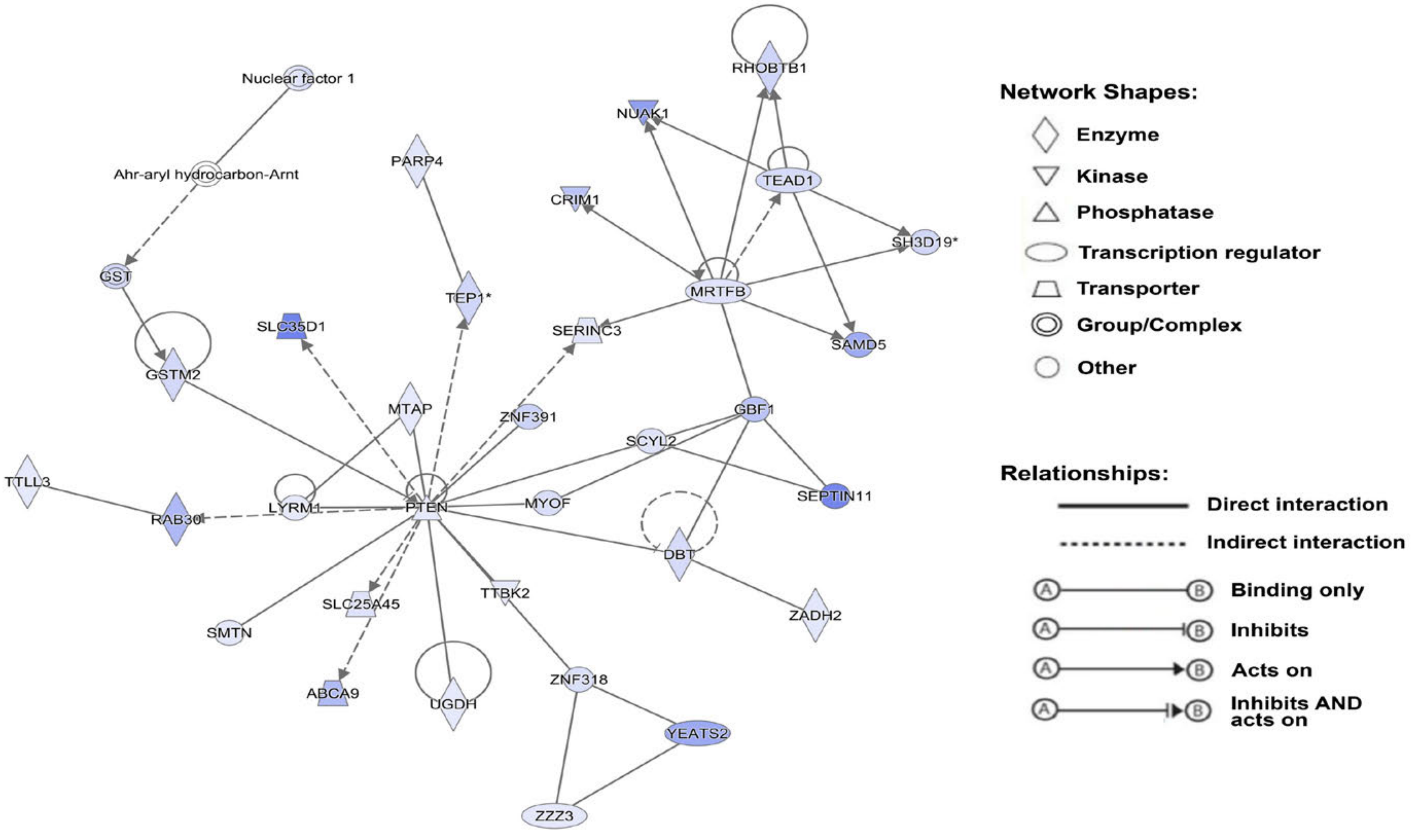


S3 Fig: Selected networks from cluster 2 and their respective functions and diseases. Red represents downregulation and blue represents upregulation during the second half of gestation. The strength of regulation is shown by the intensity of each color.

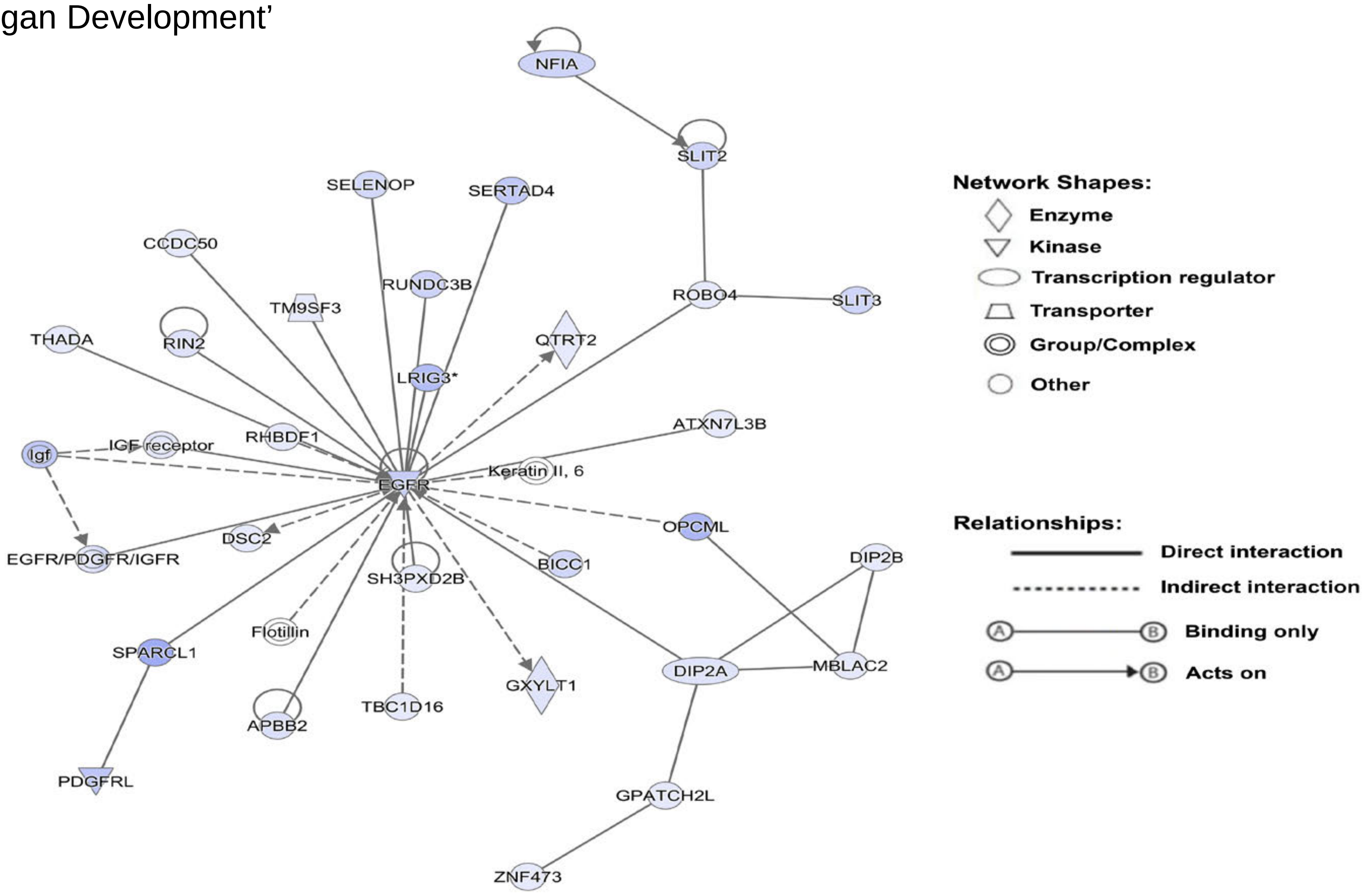
Network 1 ‘Cancer, Gastrointestinal Disease, Hepatic System Disease’



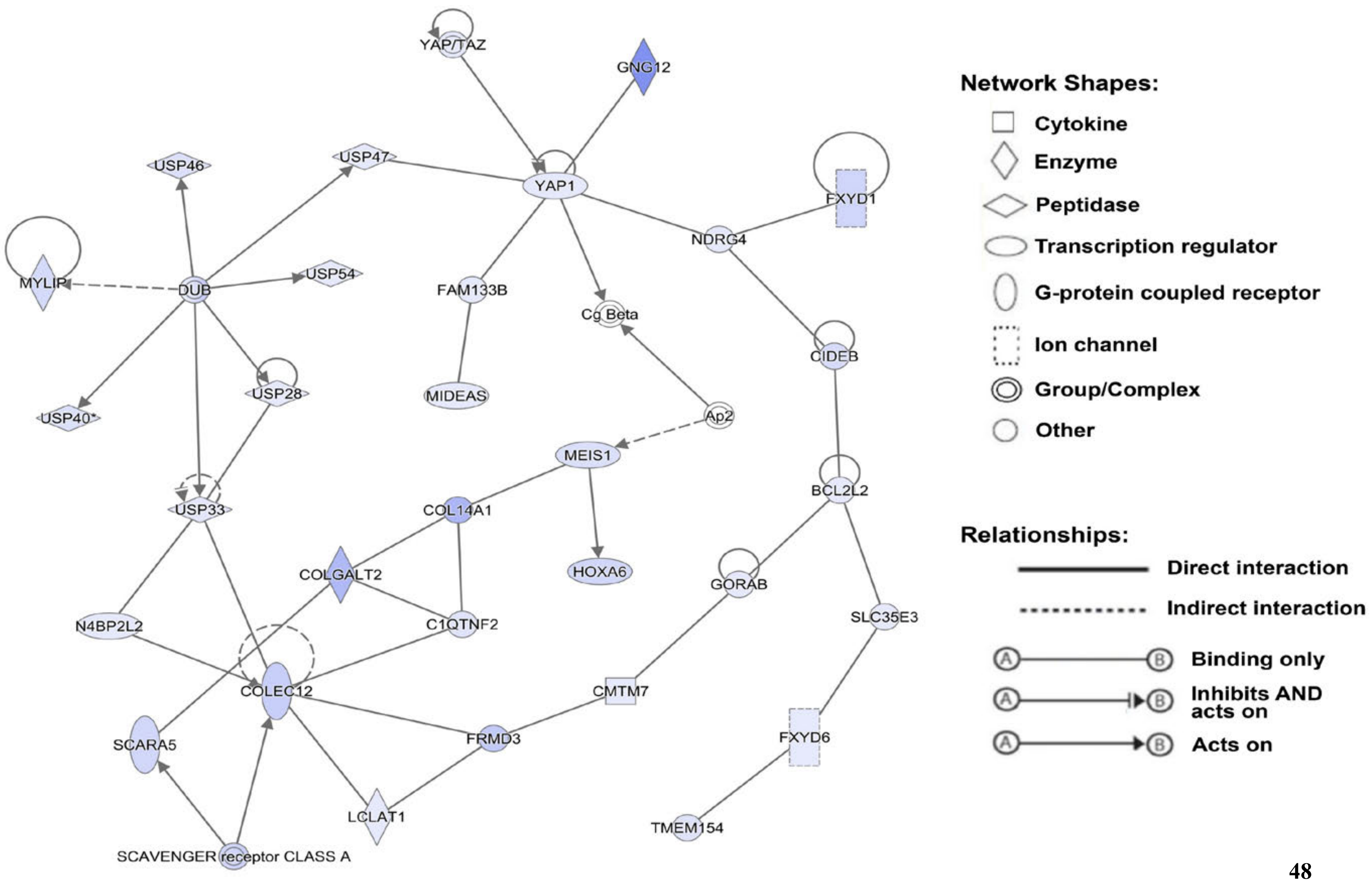
Network 4 ‘Carbohydrate Metabolism, Nucleic Acid Metabolism, Small Molecule Biochemistry’



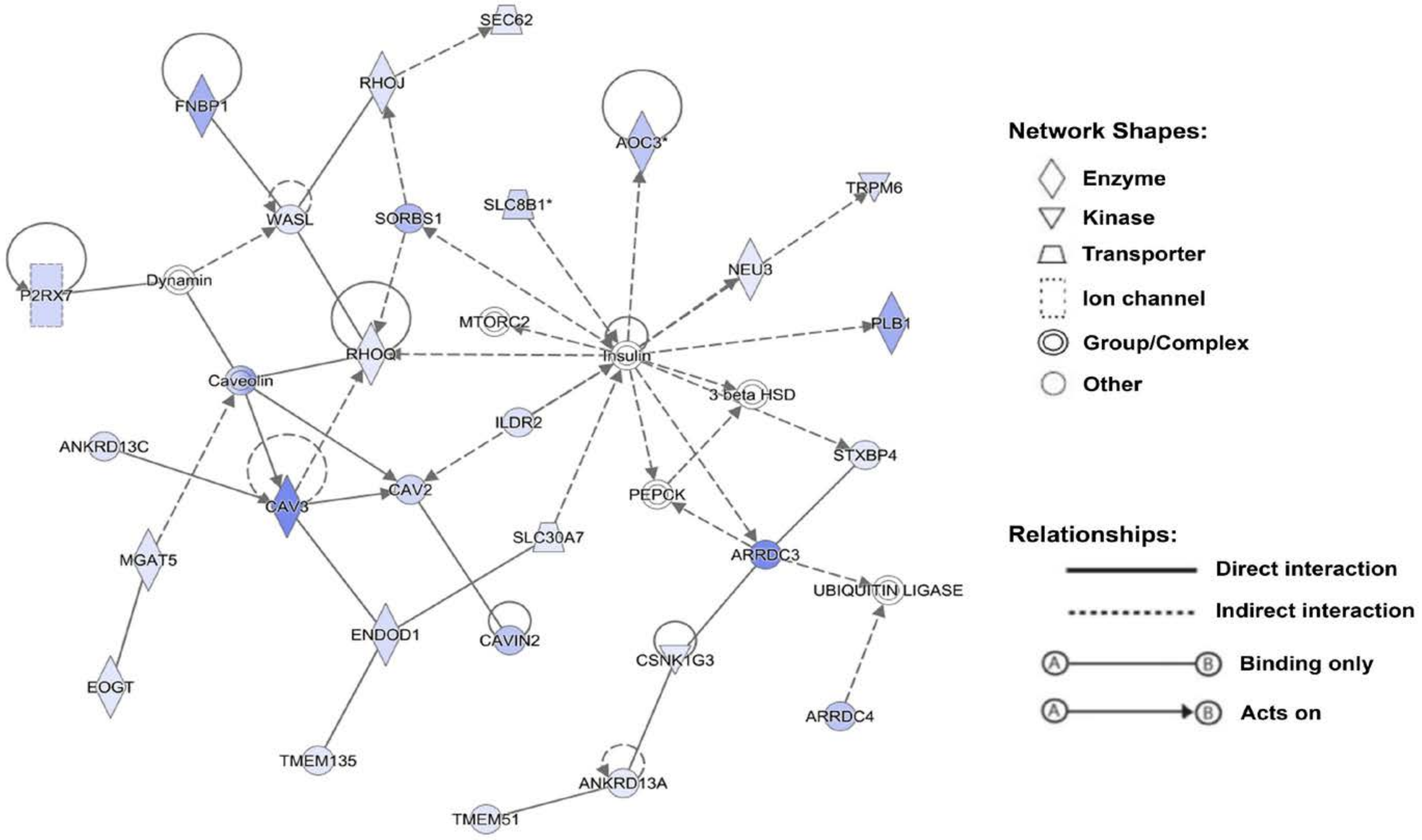
Network 8 ‘Embryonic Development, Nervous System Development and Function, Organ Development’



Network 10 ‘Cellular Development, Gene Expression, Tissue Development’

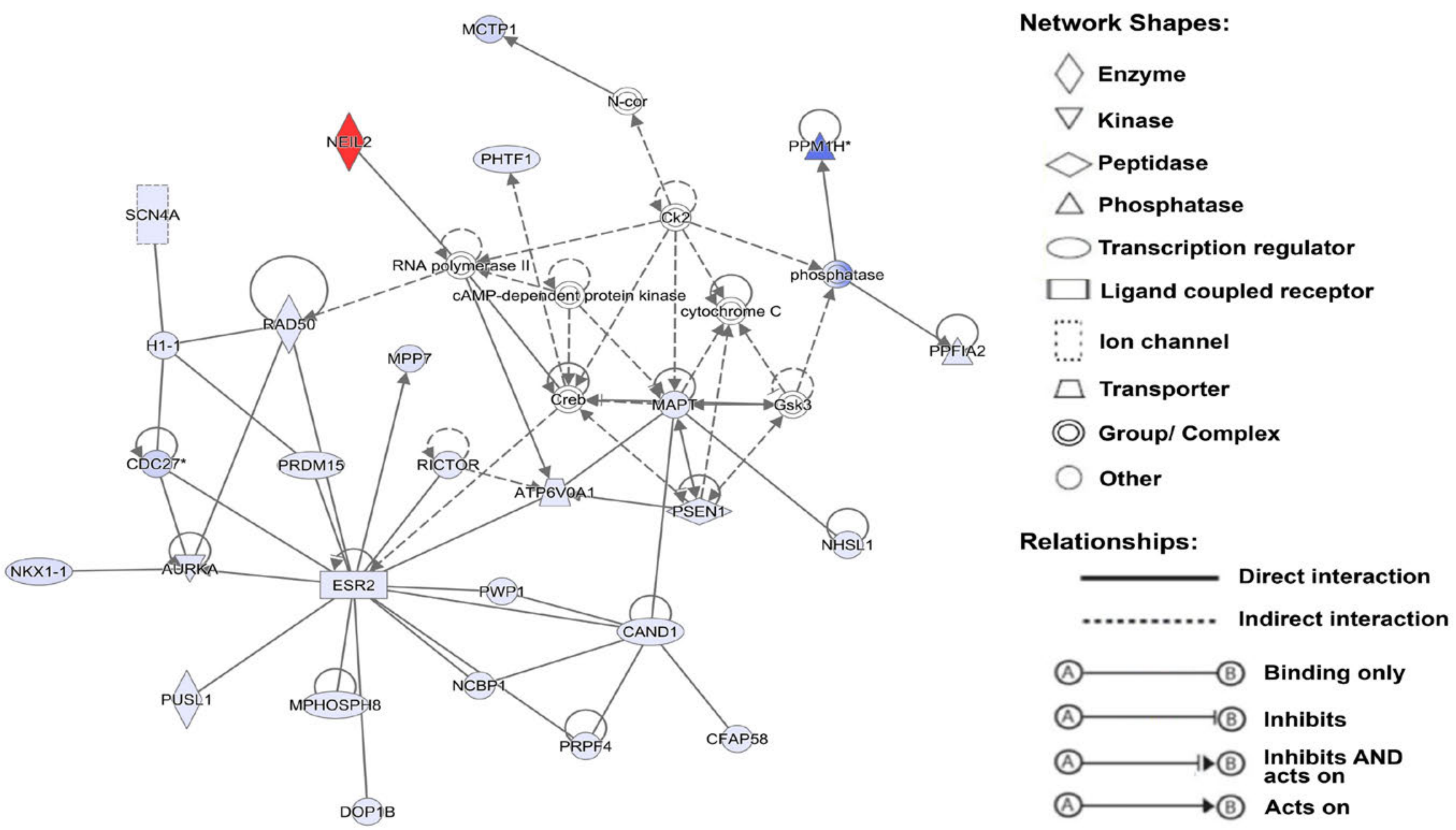


Network 14 ‘Cell Signalling, Cellular Assembly and Organization, Cellular Function and Maintenance’

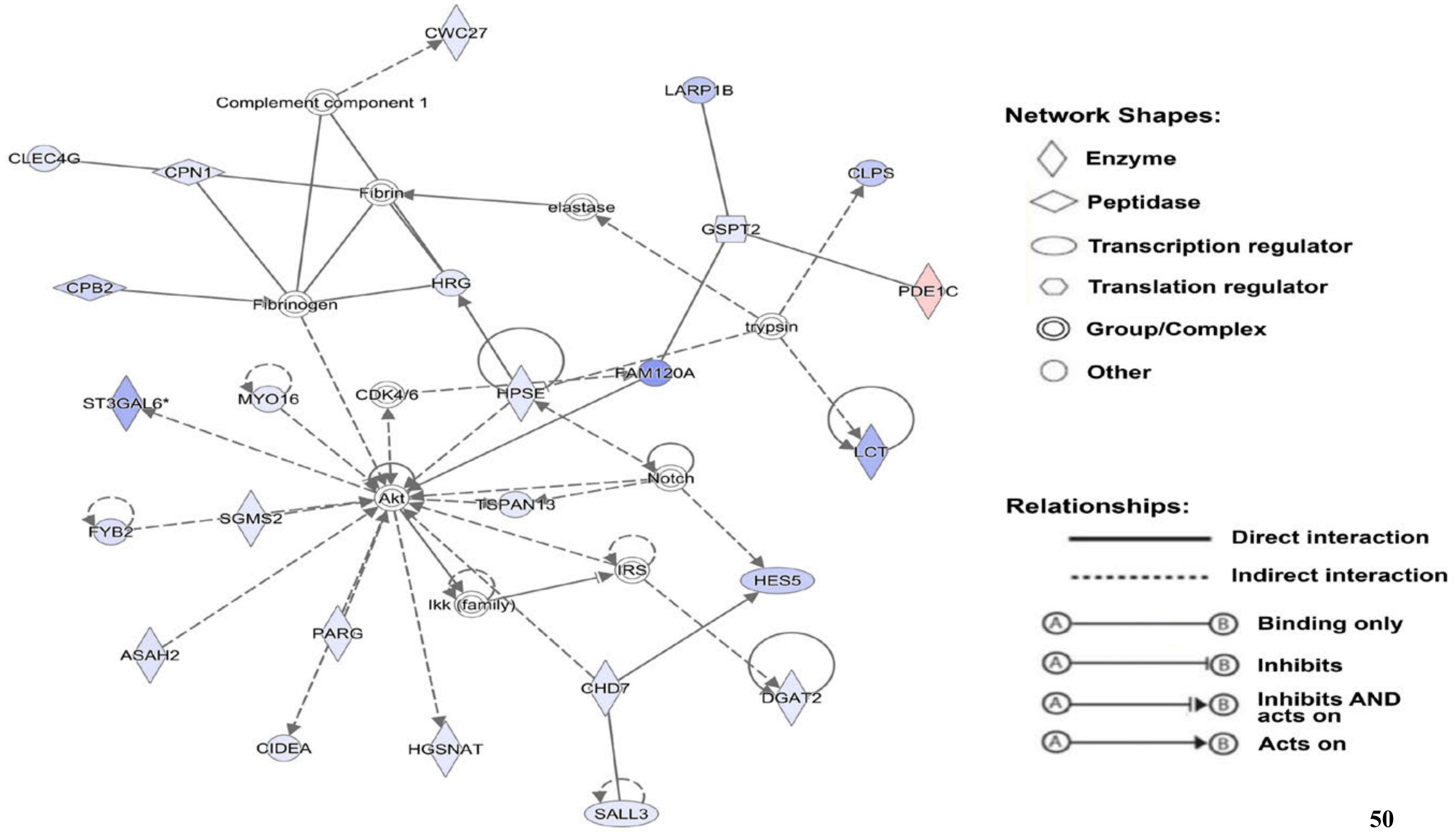


S4 Fig 4. Selected networks from cluster 3 and their respective functions and diseases. Red represents downregulation and blue represents upregulation during the second half of gestation. The strength of regulation is shown by the intensity of each color.

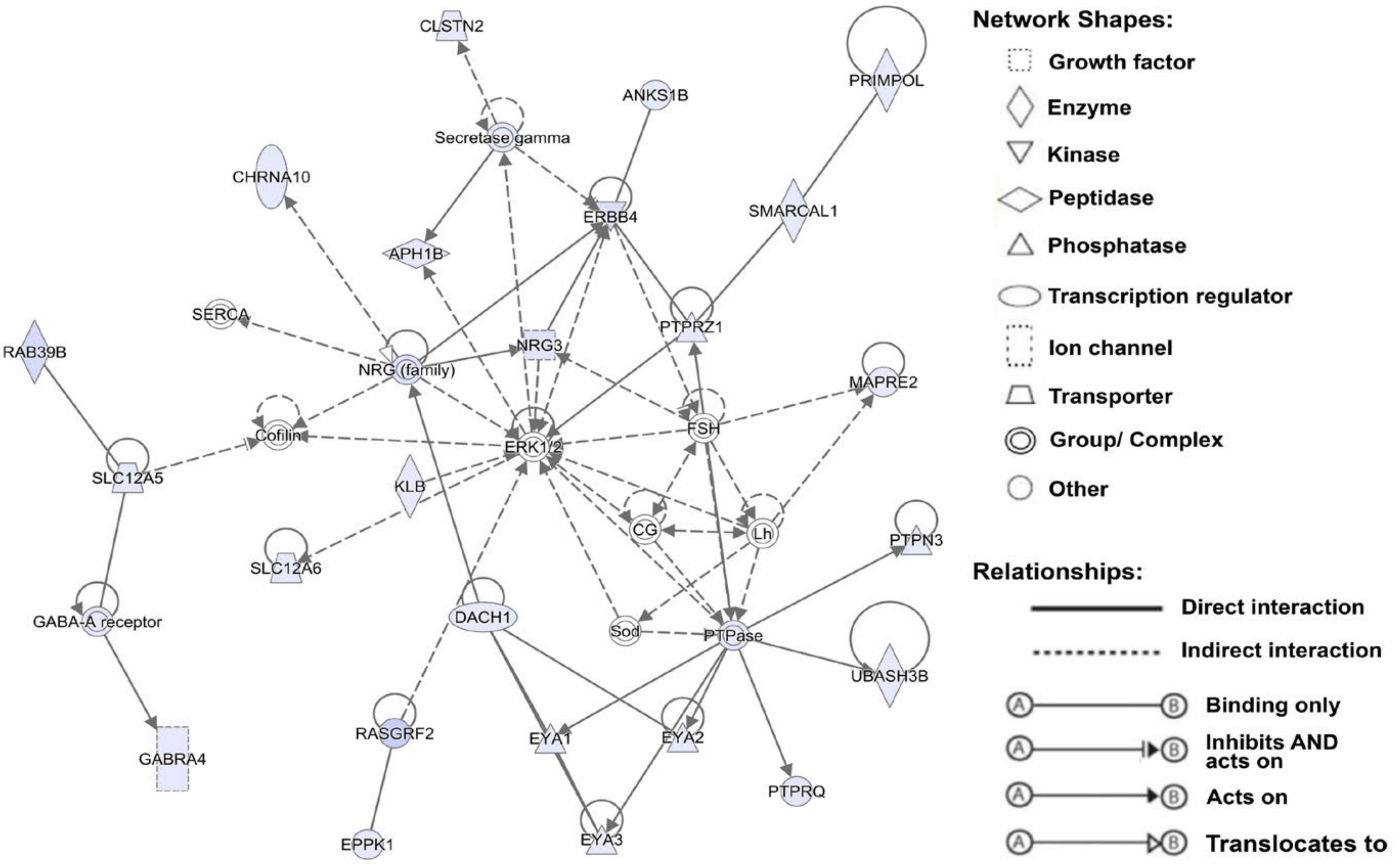
Network 3 ‘Cell-To-Cell Signaling and Interaction, Cellular Assembly and Organization, Cellular Function and Maintenance’



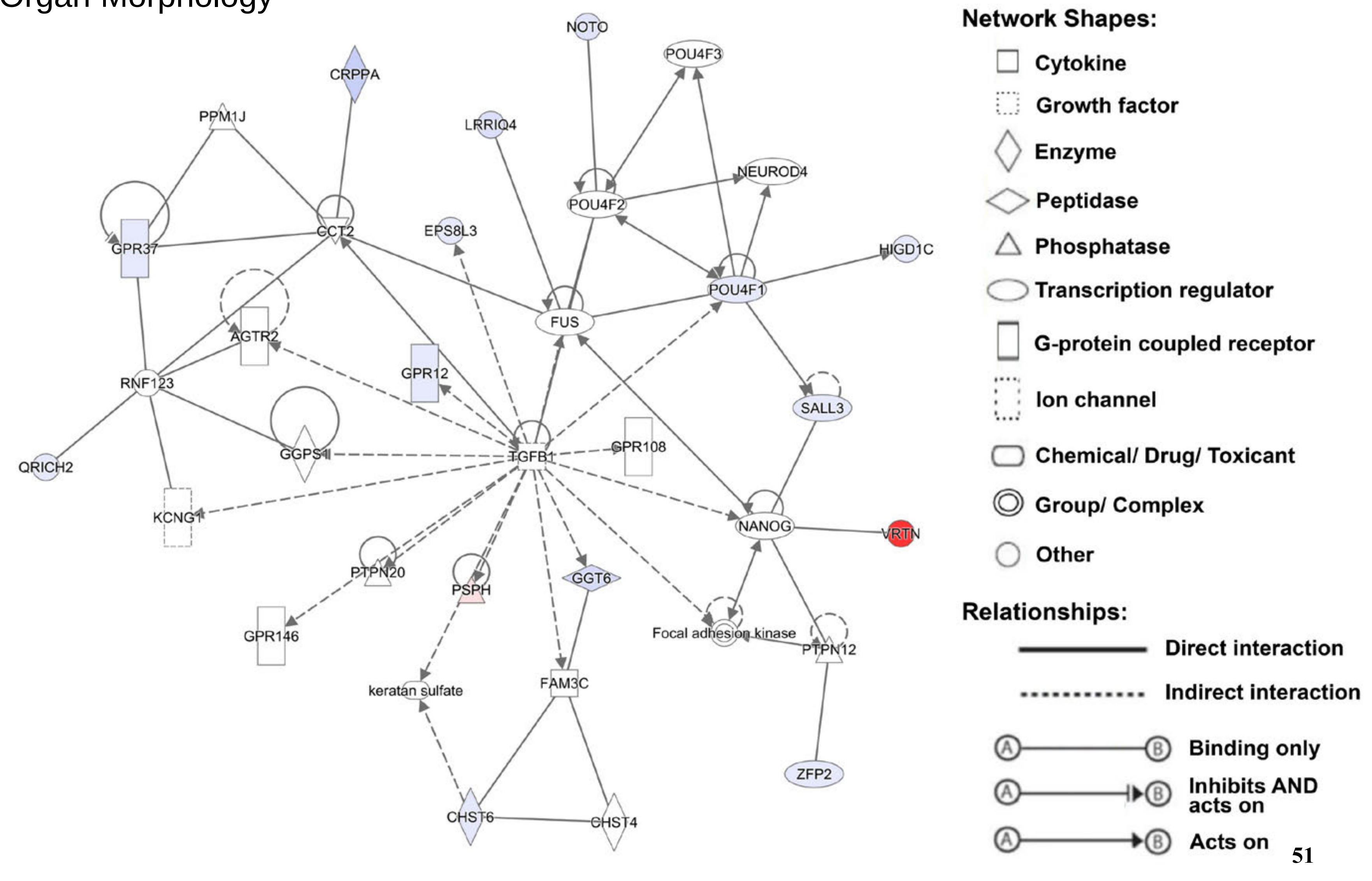
Network 5 ‘Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry’



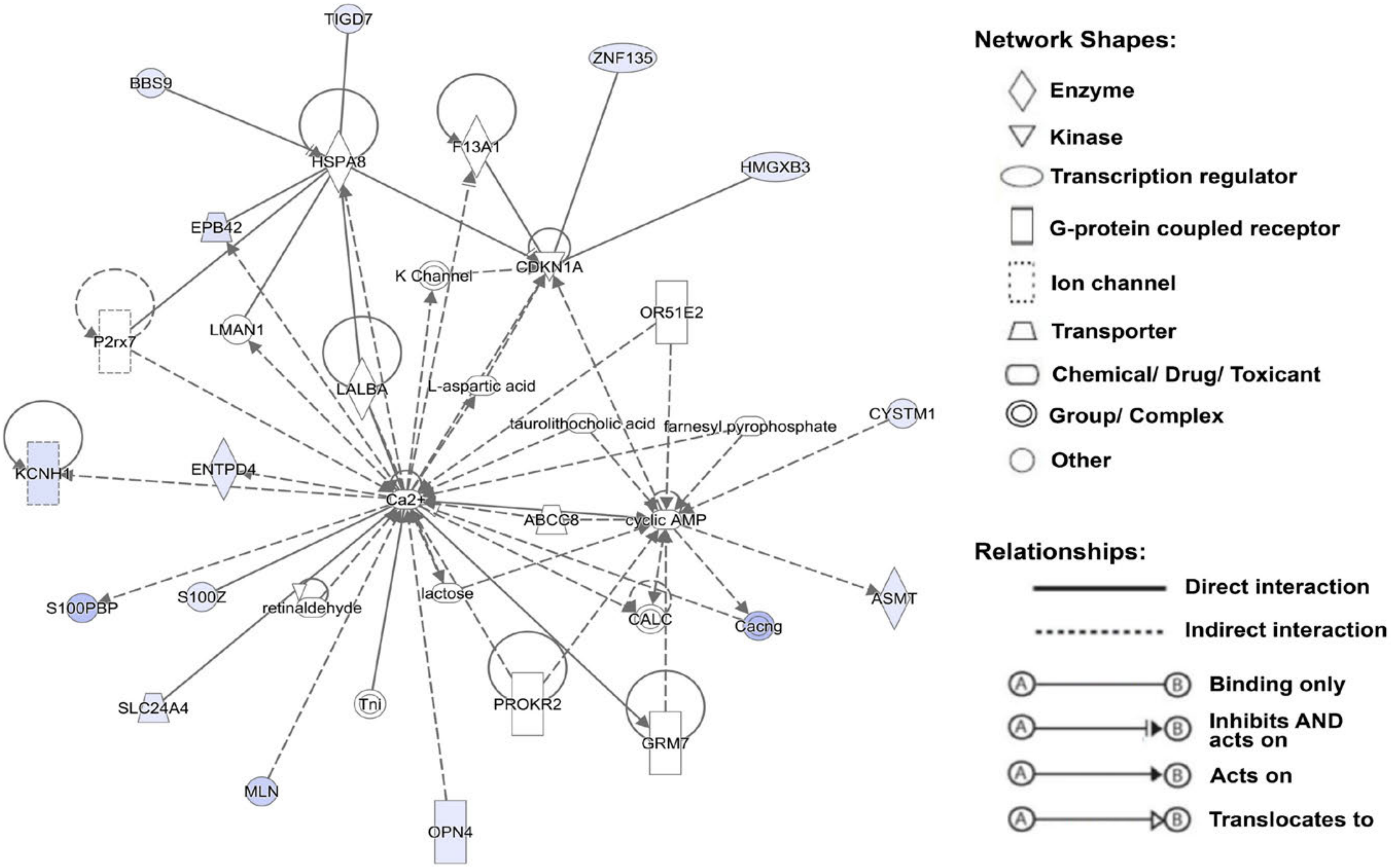
Network 6 ‘Cancer, Gastrointestinal Disease, Post-Translational Modification’



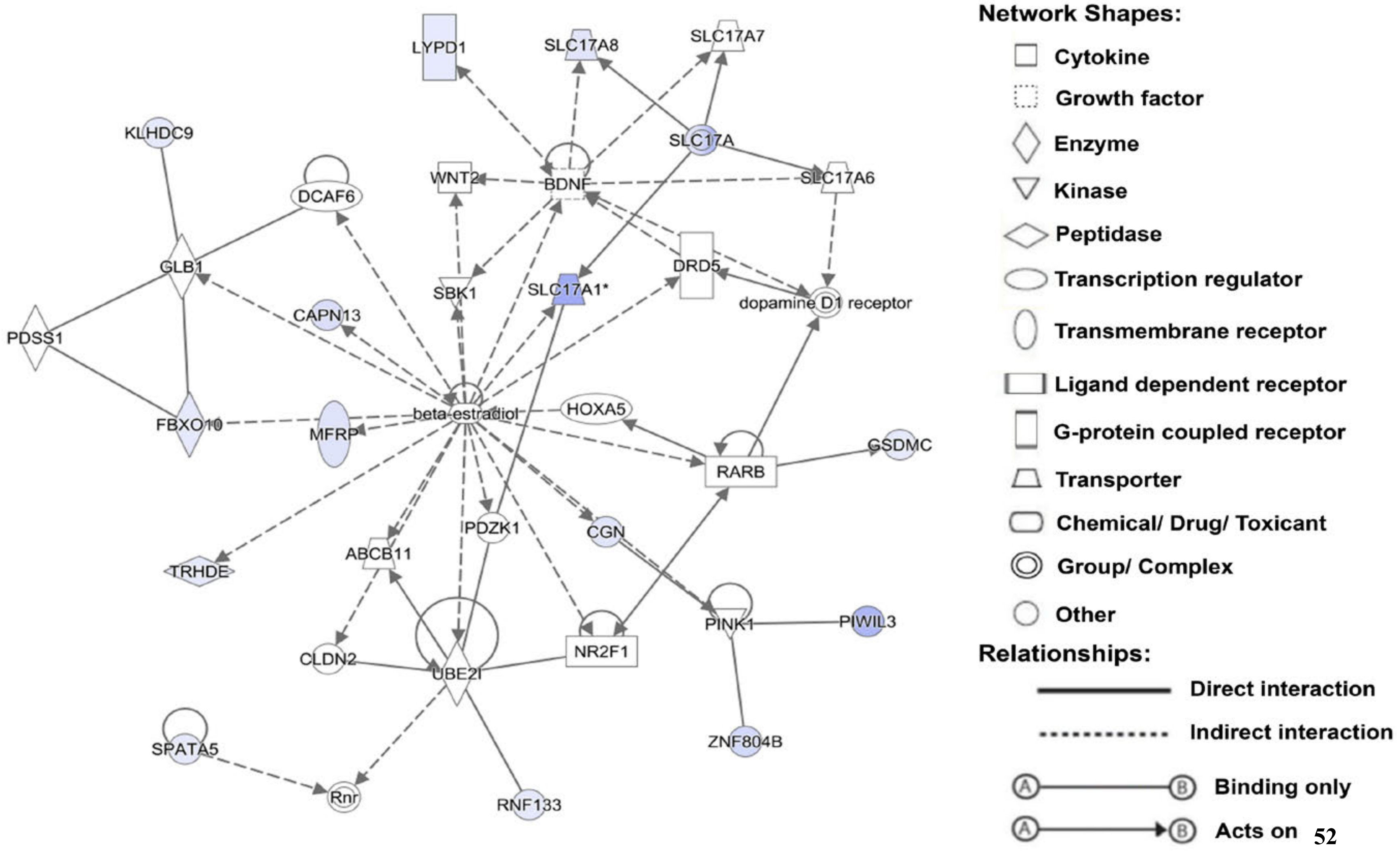
Network 20 ‘Nervous System Development and Function, Neurological Disease, Organ Morphology’



Network 21 ‘Cell Signaling, Molecular Transport, Vitamin and Mineral Metabolism’

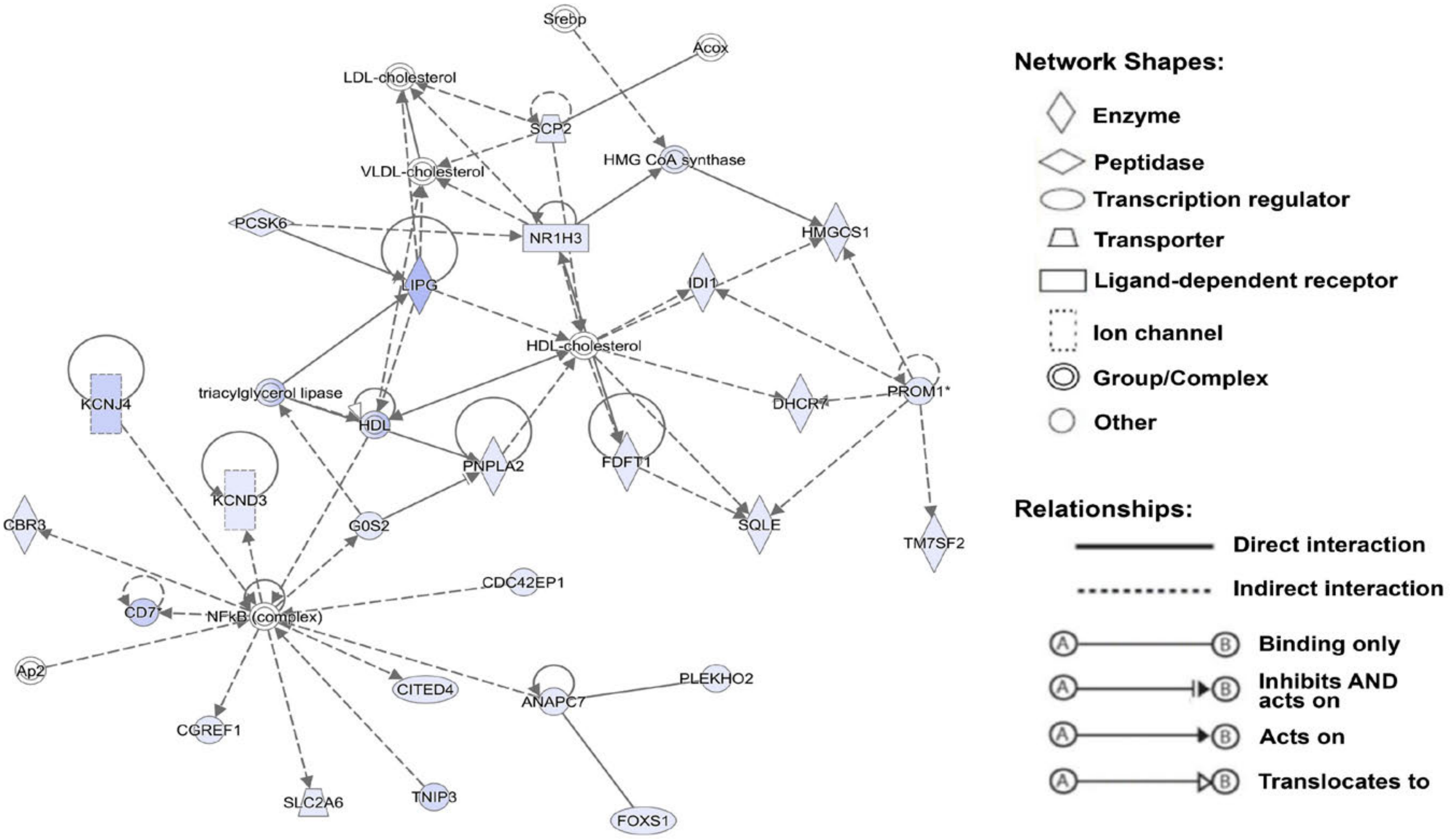


Network 22 ‘Amino Acid Metabolism, Molecular Transport, Small Molecule Biochemistry’

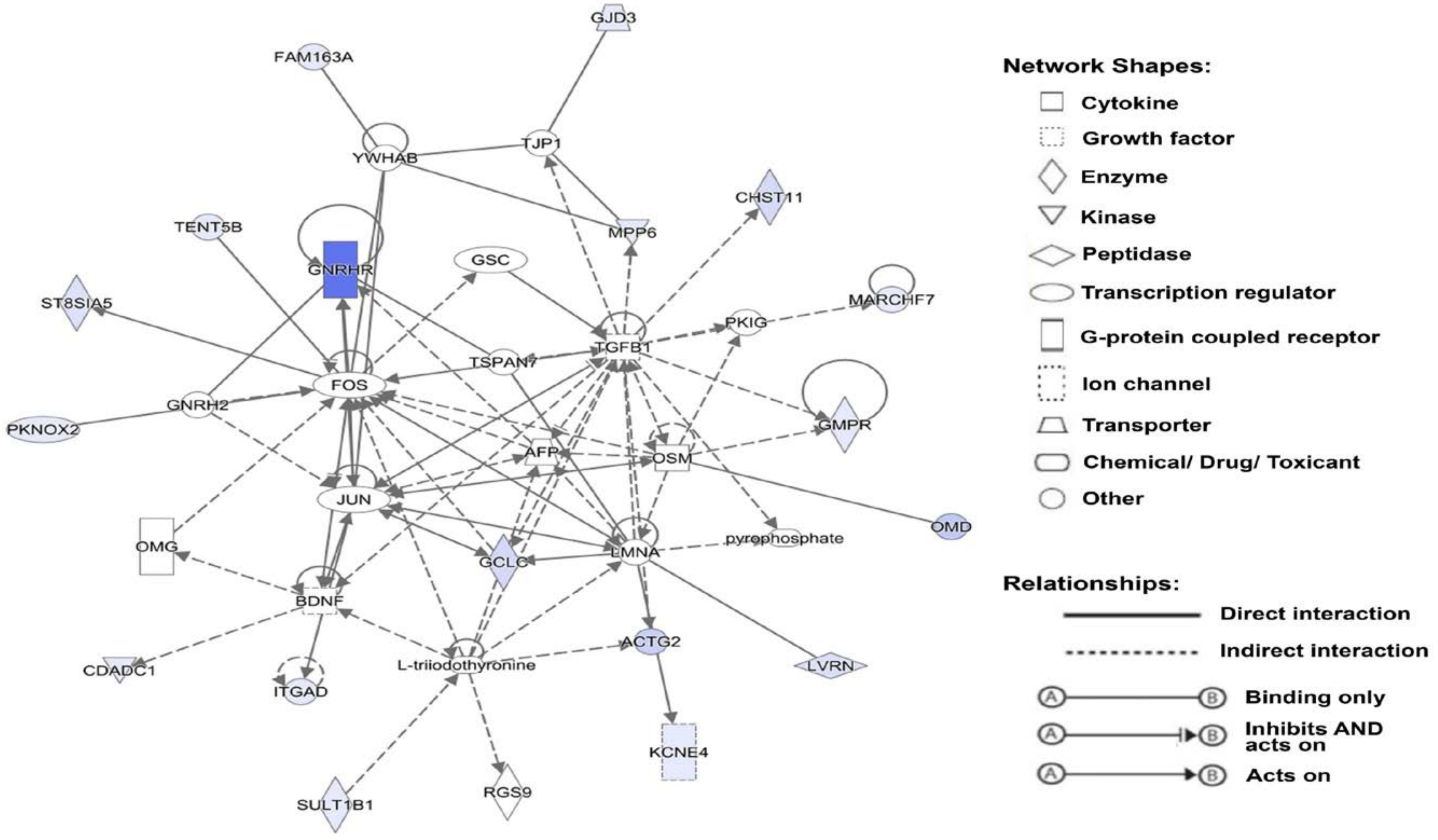


S5 Fig. Selected networks from cluster 4 and their respective functions and diseases. Blue represents upregulation during the second half of gestation. The strength of regulation is shown by the intensity of each color.

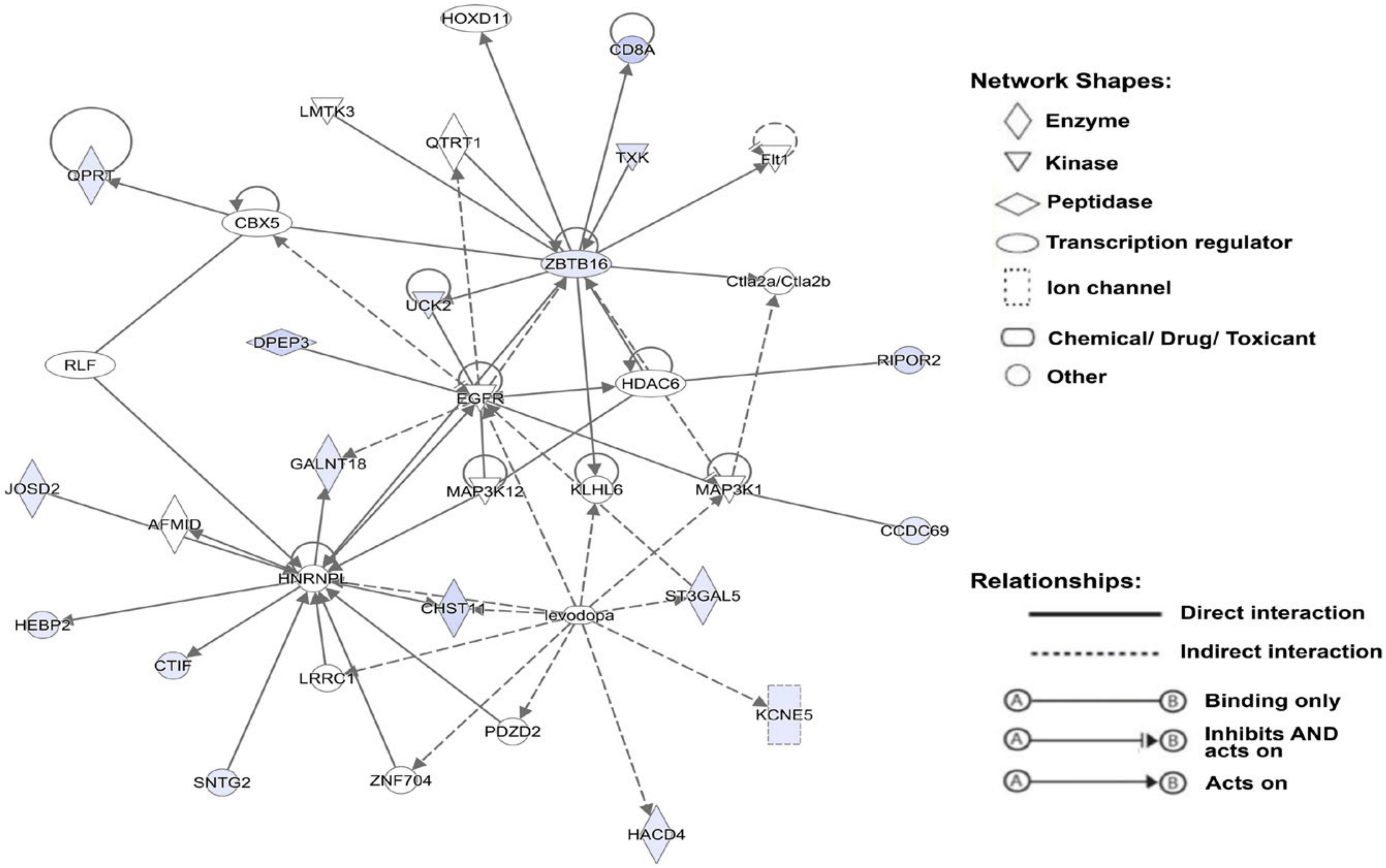
Network 4 ‘Lipid Metabolism, Small Molecule Biochemistry, Vitamin and Mineral Metabolism’



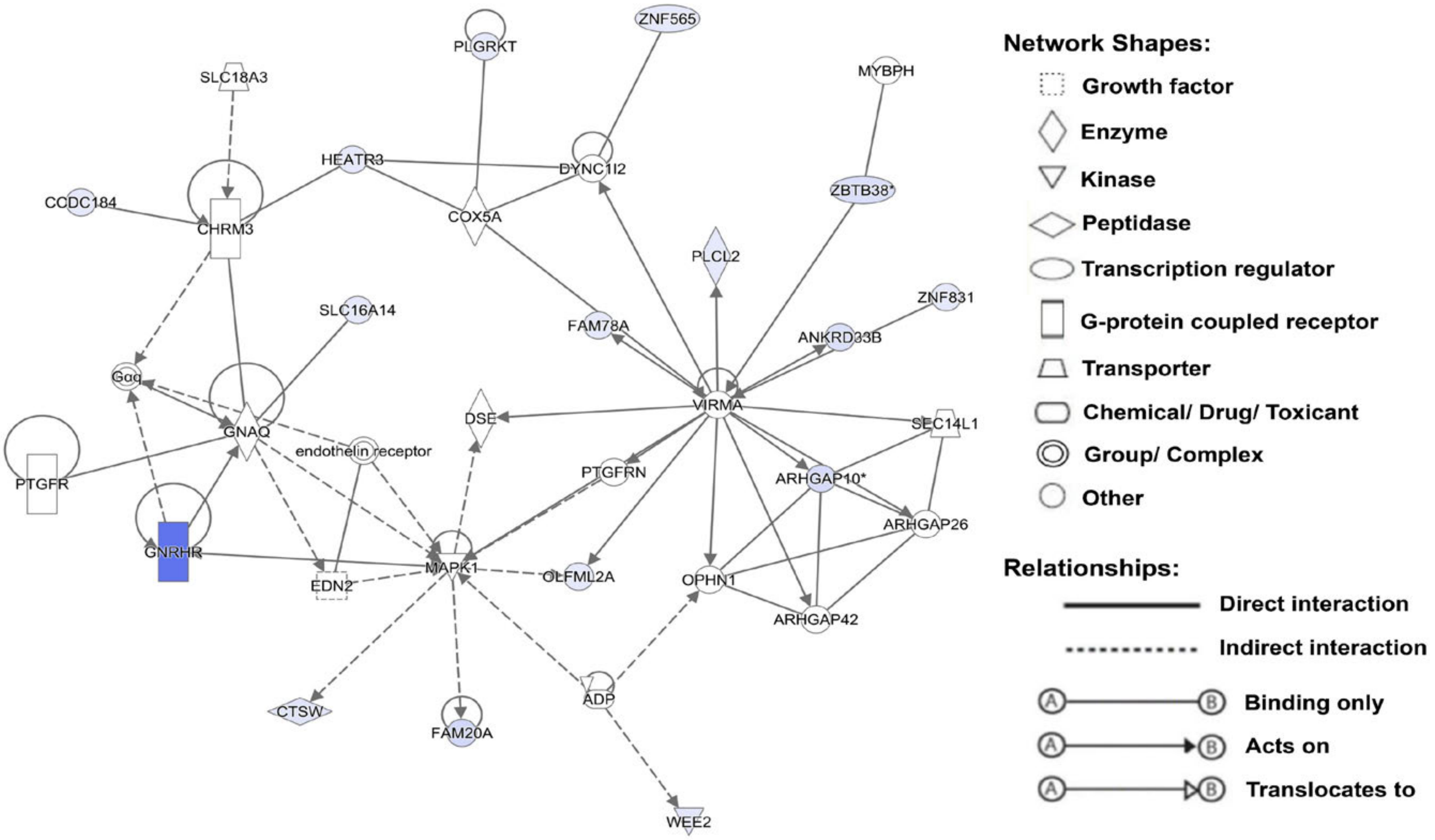
Network 9 ‘Carbohydrate Metabolism, Cell Cycle, Gene Expression’



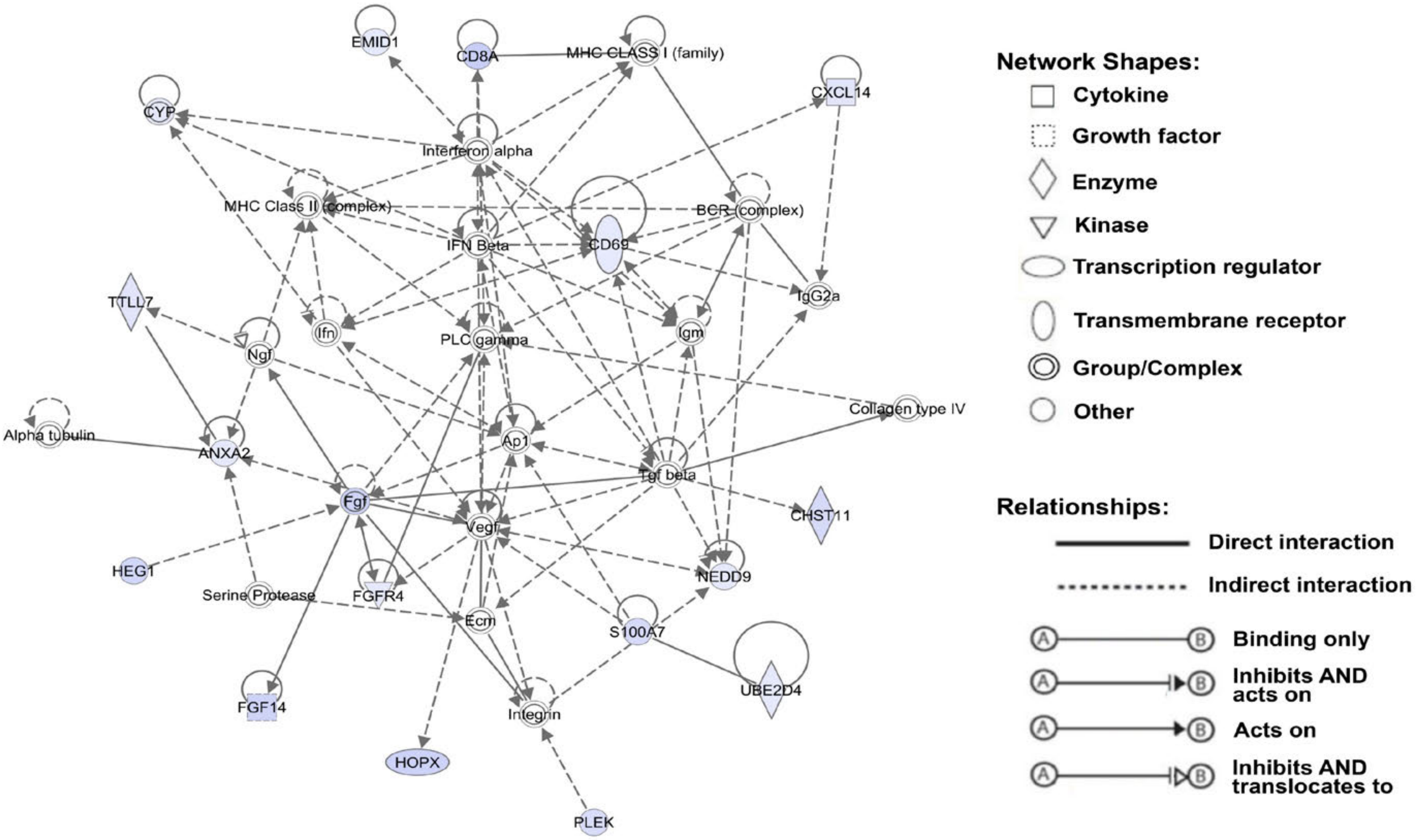
Network 12 ‘Cell Signaling, Connective Tissue Development and Function, Post-Translational Modification’



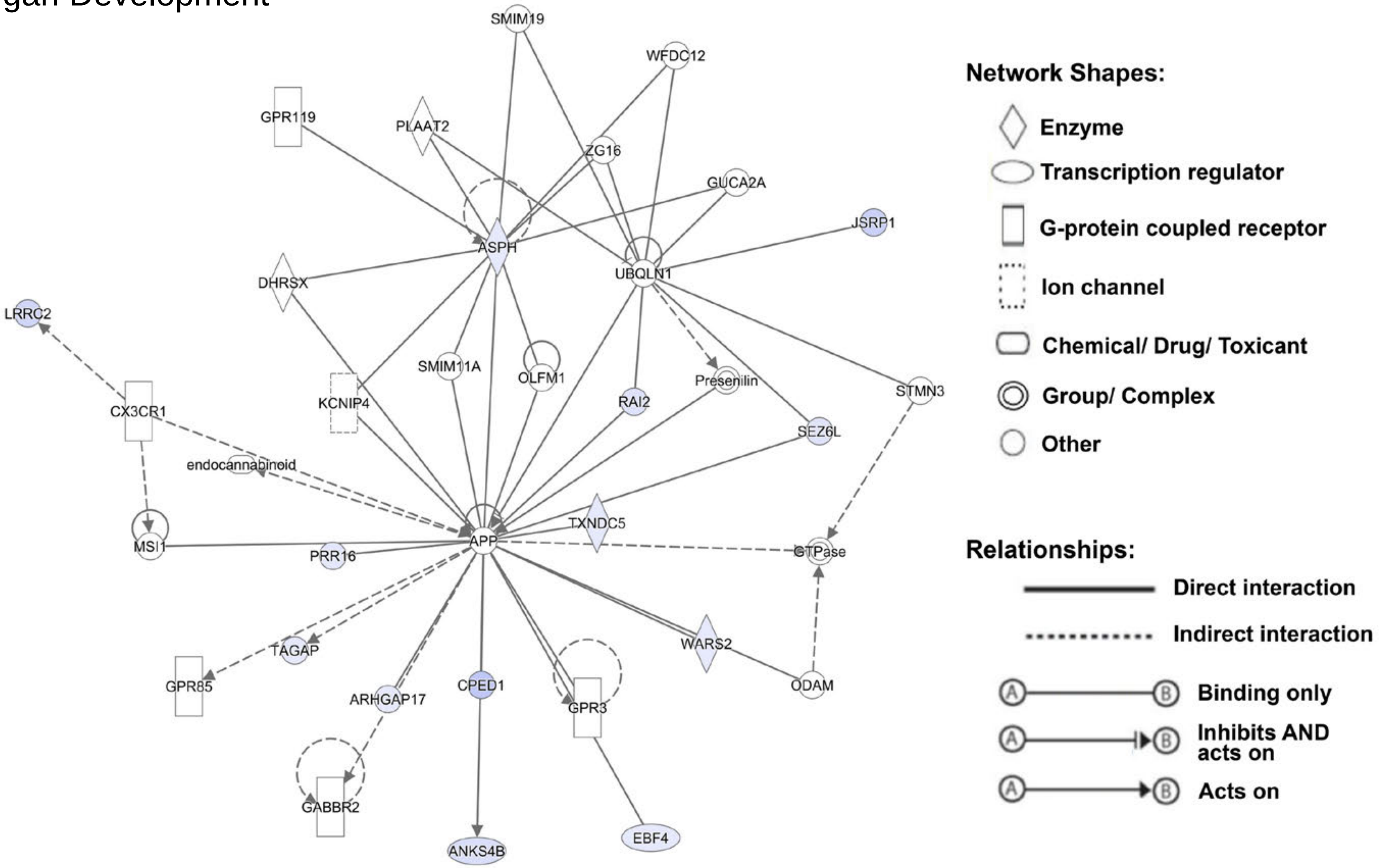
Network 14 ‘Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry’



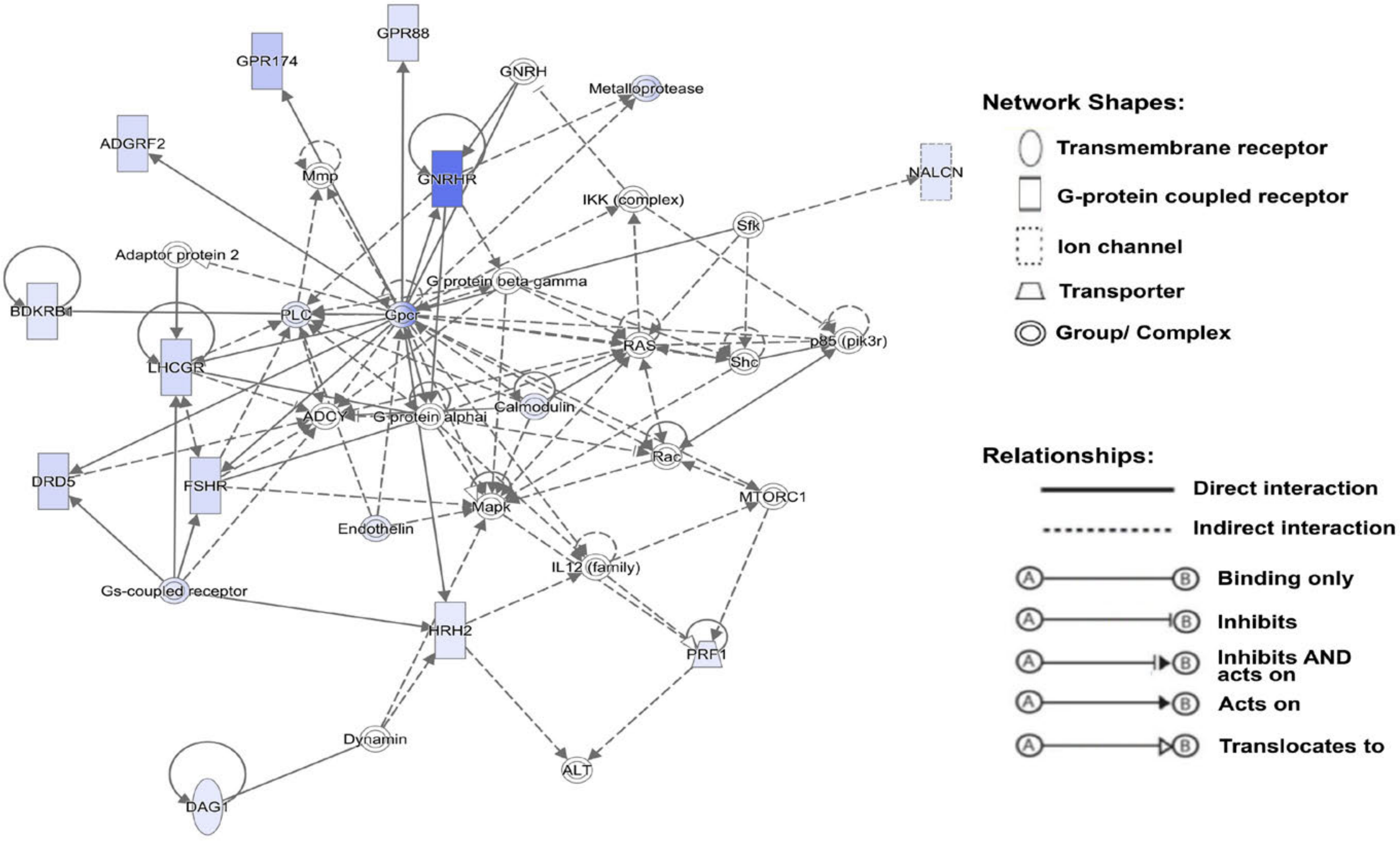
Network 16 ‘Cancer, Organismal Injury and Abnormalities, Tumor Morphology’



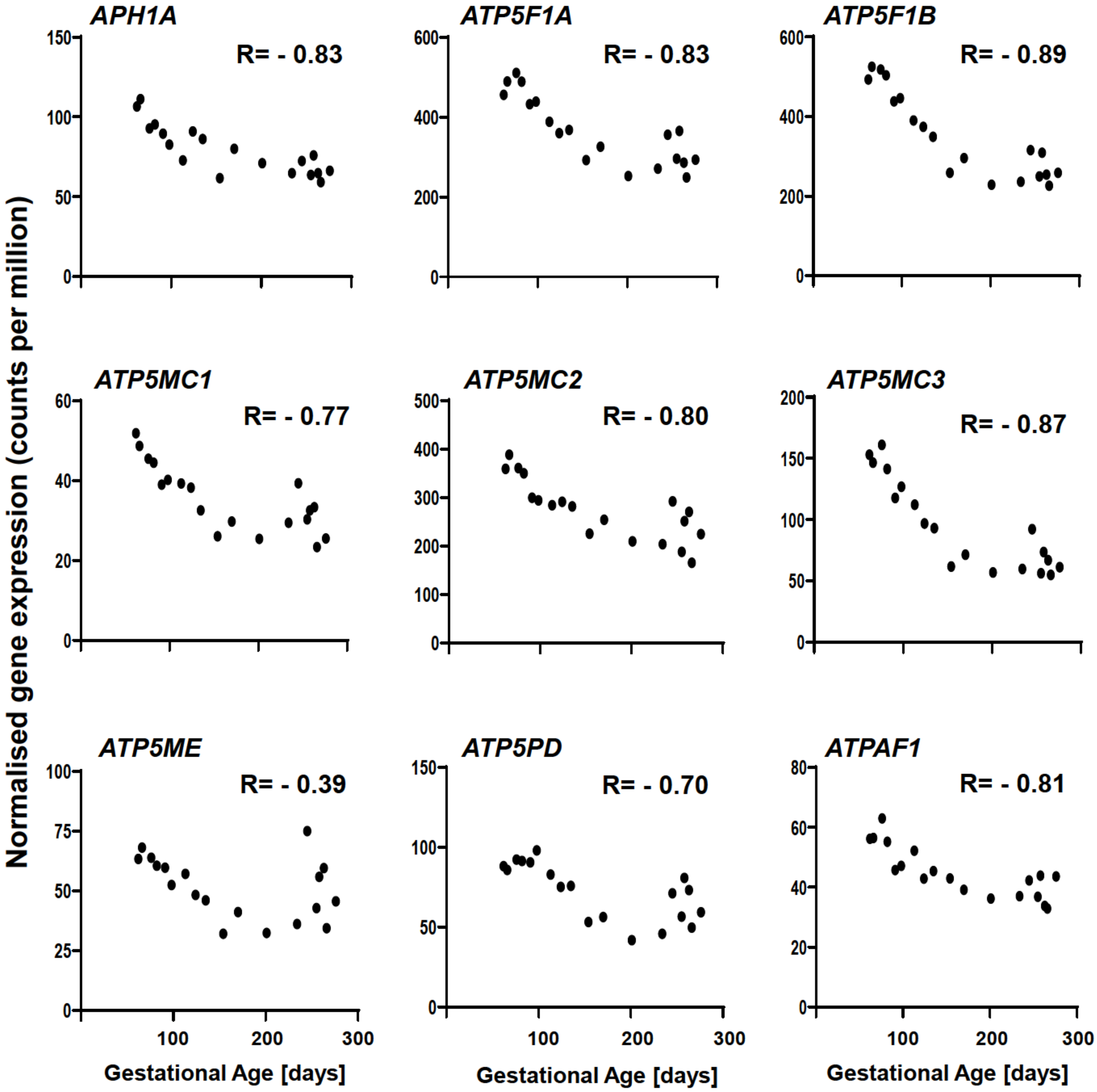
Network 20 ‘Embryonic Development, Nervous System Development and Function, Organ Development’

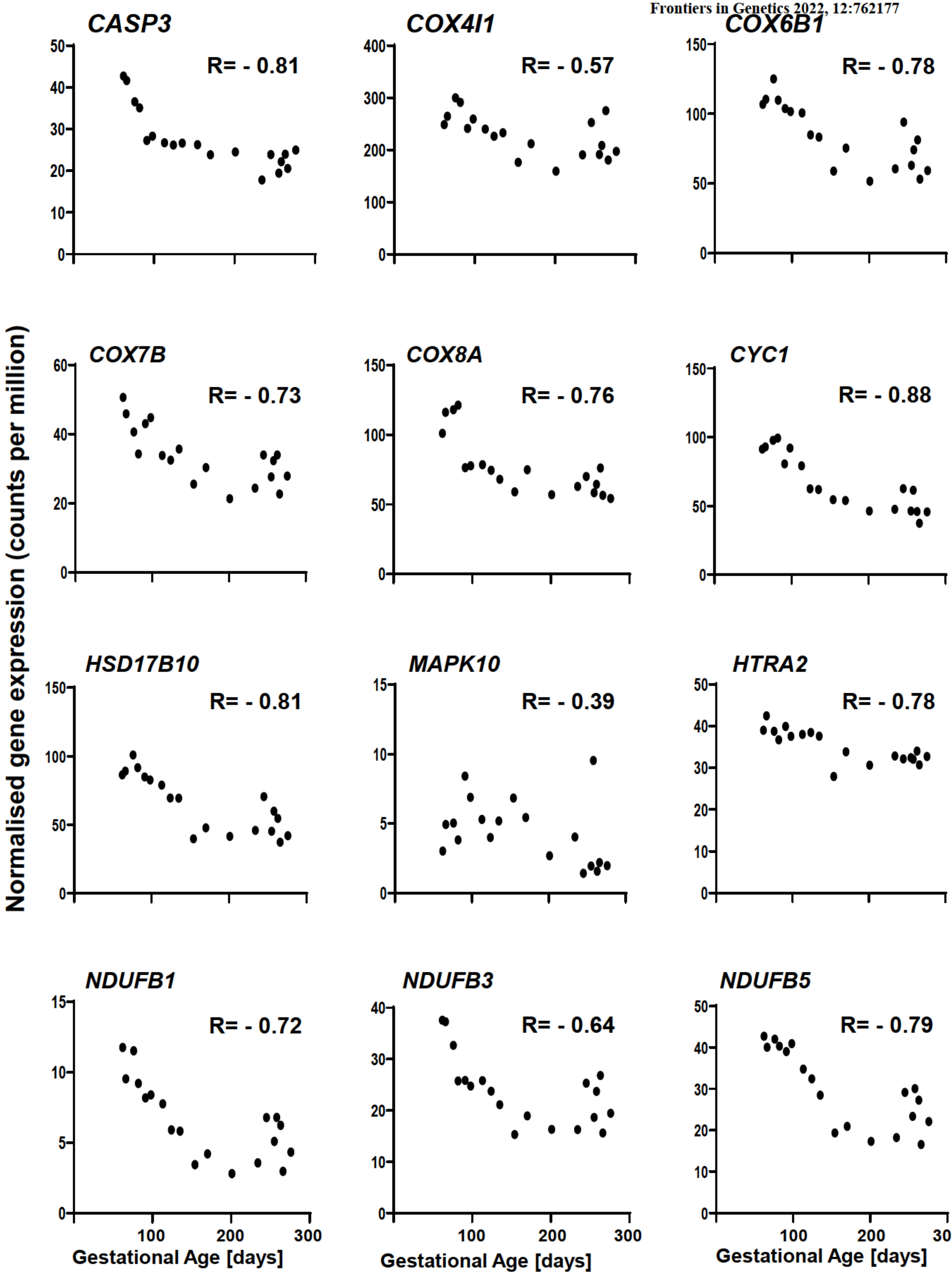


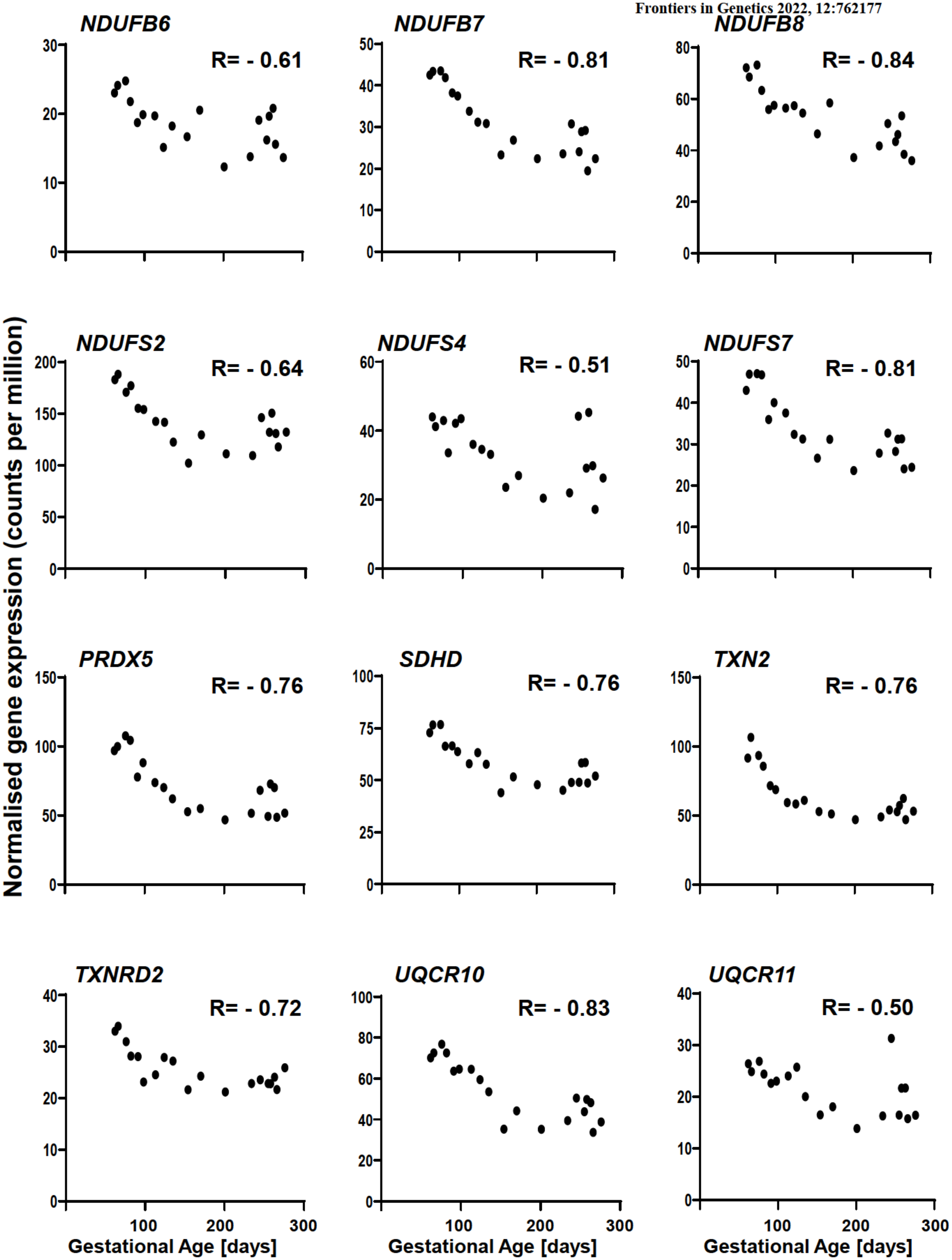
Network 21 ‘Endocrine System Disorders, Organismal Injury and Abnormalities, Reproductive System Disease’

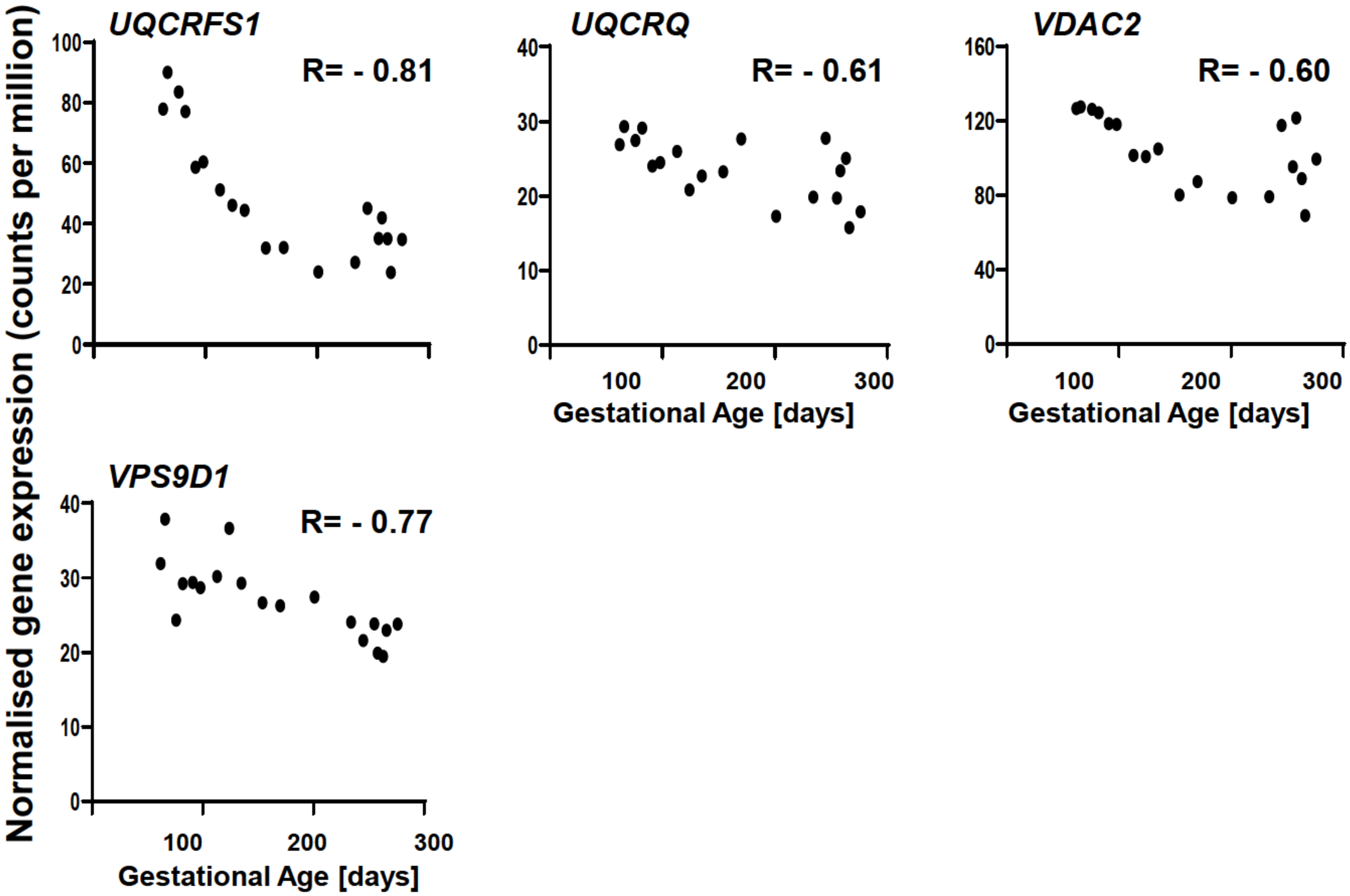


S6 Fig. Scatterplots showing the expression pattern of nuclear-encoded mitochondrial genes associated with the top canonical pathways 'oxidative phosphorylation' and 'mitochondrial dysfunction' identified in cluster 1.

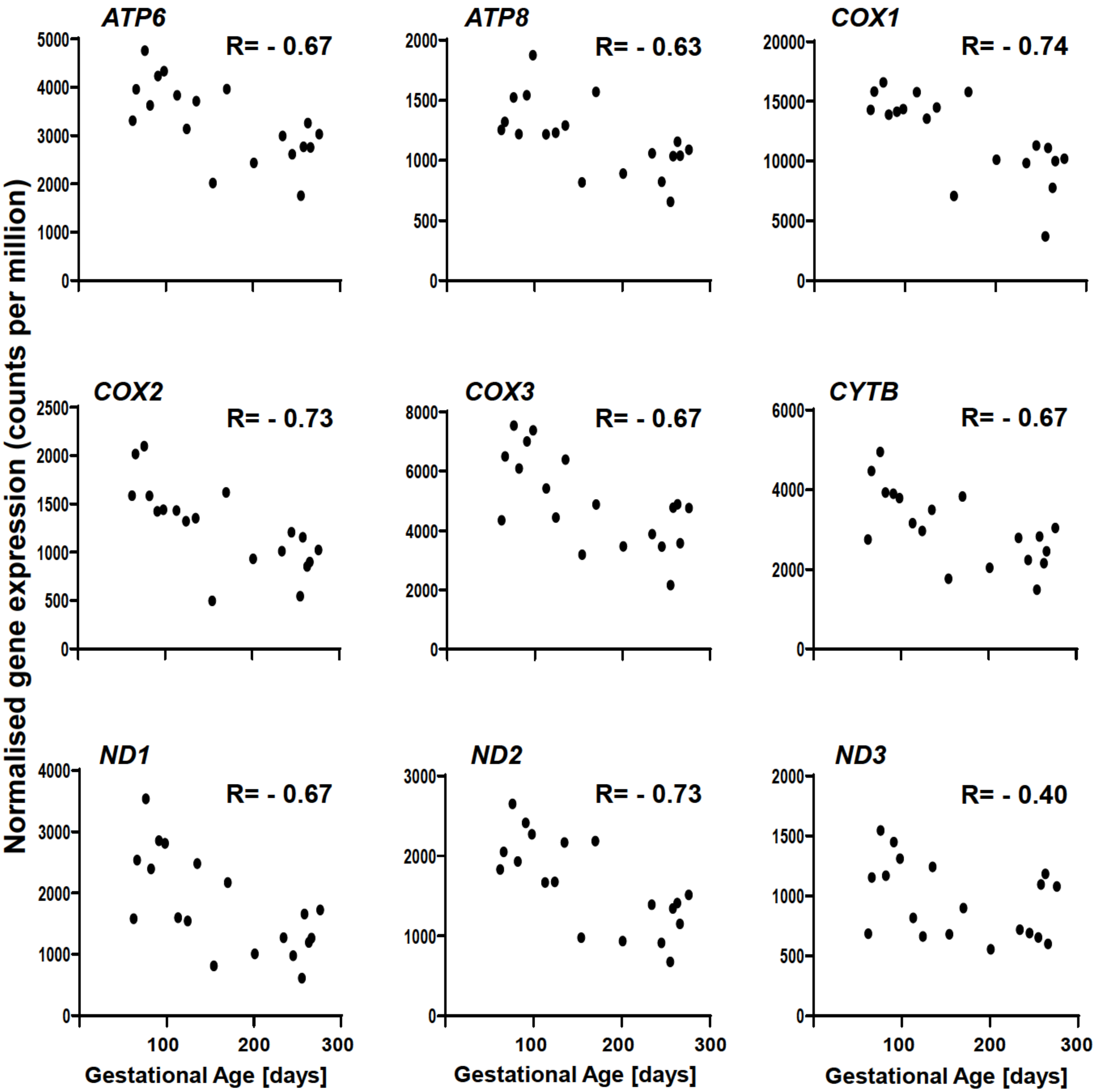


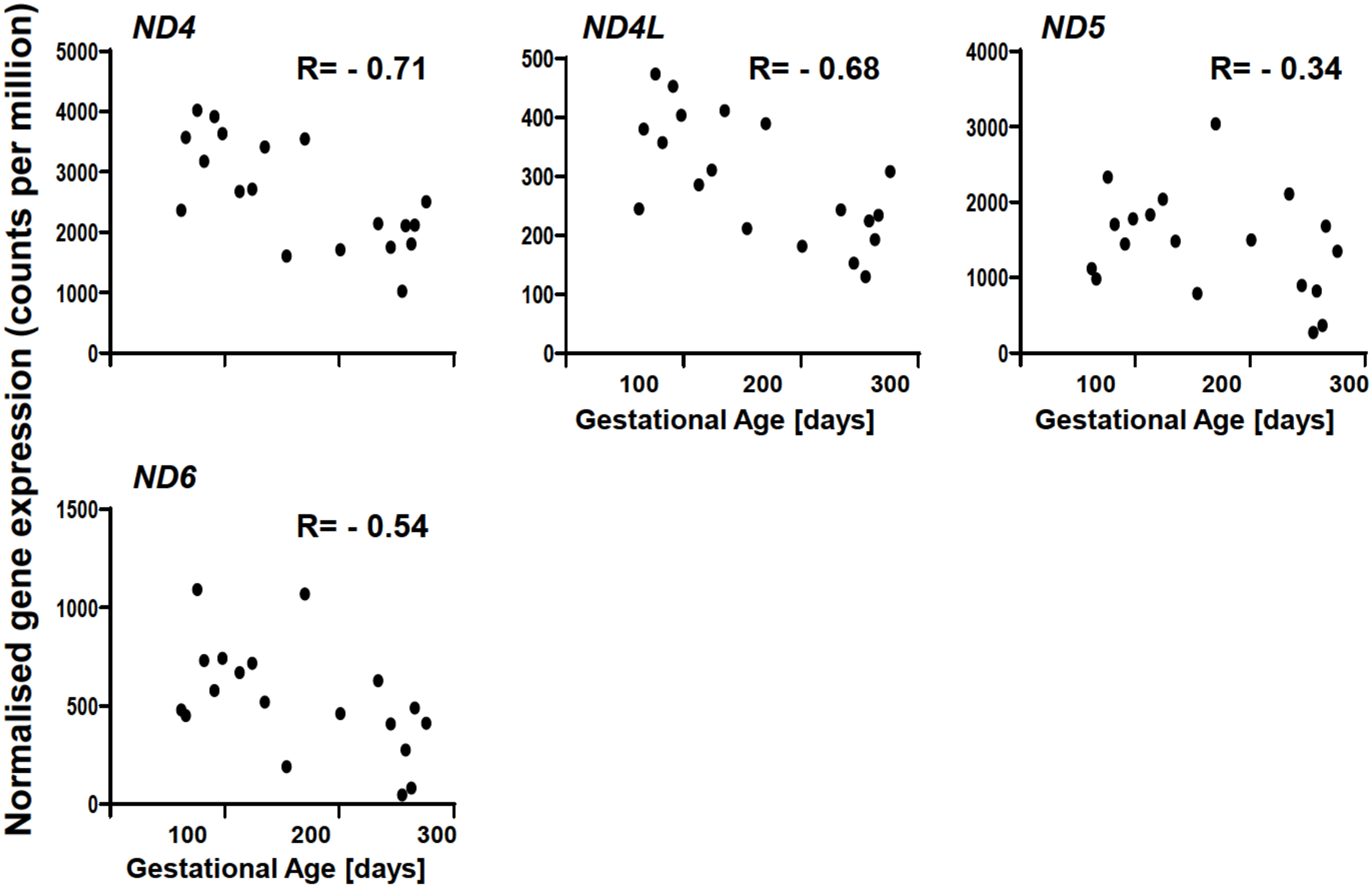

CASP3
R= - 0.81
COX4I1
R= - 0.57
COX6B1
R= - 0.78
COX7B
R= - 0.73
COX8A
R= - 0.76
CYC1
R= - 0.88
HSD17B10
R= - 0.81
MAPK10
R= - 0.39
HTRA2
R= - 0.78
NDUFB1
R= - 0.72
NDUFB3
R= - 0.64
NDUFB5
R= - 0.79
Normalised gene expression (counts per million)
Gestational Age [days]
100
200
300


NDUFB6
R= - 0.61
NDUFB7
R= - 0.81
NDUFB8
R= - 0.84
NDUFS2
R= - 0.64
NDUFS4
R= - 0.51
NDUFS7
R= - 0.81
PRDX5
R= - 0.76
SDHD
R= - 0.76
TXN2
R= - 0.76
TXNRD2
R= - 0.72
UQCR10
R= - 0.83
UQCR11
R= - 0.50
Normalised gene expression (counts per million)
Gestational Age [days]
0
100
200
300


Normalised gene expression (counts per million)
UQCRFS1
R= - 0.81
0
20
40
60
80
100
UQCRQ
R= - 0.61
0
10
20
30
40
100
200
300
Gestational Age [days]
VDAC2
R= - 0.60
0
40
80
120
160
100
200
300
Gestational Age [days]
VPS9D1
R= - 0.77
0
10
20
30
40
100
200
300
Gestational Age [days]

S7 Fig. Scatterplots showing the expression pattern of mitochondrial DNA-encoded genes across gestation in bovine fetal ovaries




Normalised gene expression (counts per million)
ND4
R= - 0.71
5000
4000
3000
2000
1000
0
ND4L
R= - 0.68
500
400
300
200
100
0
100
200
300
Gestational Age [days]
ND5
R= - 0.34
4000
3000
2000
1000
0
100
200
300
Gestational Age [days]
ND6
R= - 0.54
1500
1000
500
0
100
200
300
Gestational Age [days]

S1 Table. Gene Specific Analysis (late versus early gestation) of PCOS candidate genes. Shown are the fold change and its significance (p-value), log 2 ratio and False Discovery Rate (FDR) across gestation; least square (LS) mean (late and early gestation); total counts per million.

Gene symbol	Total counts	P-value	FDR step up	Ratio	Log2(Ratio)	Fold change	LSMean(Late)	LSMean(Early)
gene-INSR	1942.25	9.05E-10	2.44E-08	3.58	1.84	3.58	155.25	43.31
gene-AR	115.50	1.48E-07	2.00E-06	20.22	4.34	20.22	11.06	0.55
gene-MAPRE1	1480.03	4.16E-07	3.01E-06	0.61	-0.72	-1.65	59.56	98.27
gene-TGFB1I1	1593.22	4.46E-07	3.01E-06	2.09	1.06	2.09	111.35	53.30
gene-THADA	469.07	9.42E-07	4.33E-06	1.58	0.66	1.58	29.87	18.93
gene-GATA4	7348.90	1.07E-06	4.33E-06	0.54	-0.89	-1.86	275.16	510.81
gene-FBN3	6416.64	1.12E-06	4.33E-06	0.24	-2.03	-4.10	136.86	560.89
gene-YAP1	2543.69	5.58E-06	1.88E-05	1.64	0.71	1.64	164.20	100.19
gene-FSHR	117.47	3.24E-05	8.81E-05	5.23	2.39	5.23	10.02	1.92
gene-ARL14EP	732.89	3.26E-05	8.81E-05	0.63	-0.68	-1.60	30.06	48.03
gene-HMGA2	68.48	4.12E-05	1.01E-04	0.29	-1.79	-3.46	1.66	5.76
gene-ZBTB16	728.91	4.83E-05	1.09E-04	2.63	1.40	2.63	54.32	20.63
gene-TOX3	231.36	6.51E-05	1.35E-04	0.28	-1.84	-3.58	5.47	19.62
gene-C8H9orf3	1205.21	1.20E-03	2.30E-03	0.71	-0.50	-1.41	53.04	74.98
gene-AMH	233.84	1.37E-03	2.47E-03	5.42	2.44	5.42	20.05	3.70
gene-IRF1	662.25	2.54E-03	4.28E-03	1.52	0.60	1.52	41.59	27.38
gene-ERBB3	346.91	1.60E-02	2.53E-02	0.68	-0.56	-1.47	14.91	21.98
gene-DENND1A	1915.27	2.10E-02	3.08E-02	0.82	-0.29	-1.22	91.26	111.40
gene-ERBB4	24.70	2.17E-02	3.08E-02	3.93	1.97	3.93	2.01	0.51
gene-PLGRKT	146.53	2.70E-02	3.65E-02	1.26	0.34	1.26	8.56	6.77
gene-LHCGR	131.88	9.50E-02	1.22E-01	6.39	2.68	6.39	11.56	1.81
gene-RAD50	2093.91	1.72E-01	2.12E-01	1.35	0.43	1.35	125.48	93.23
gene-NEIL2	579.54	2.33E-01	2.73E-01	0.91	-0.14	-1.10	29.11	32.05
gene-SUOX	695.27	2.97E-01	3.35E-01	0.93	-0.10	-1.08	35.33	37.99
gene-FDFT1	1618.89	3.11E-01	3.35E-01	1.15	0.20	1.15	90.68	79.12
gene-RAB5B	4927.55	5.85E-01	6.07E-01	0.96	-0.06	-1.04	254.55	264.68
gene-KRR1	509.82	8.98E-01	8.98E-01	1.00	-0.01	-1.00	26.78	26.89

S2 Table . Gene Specific Analysis (late versus early gestation) of genes in cluster 1. Shown are the fold change and its significance (p-value), log 2 ratio and False Discovery Rate (FDR) across gestation; least square (LS) mean (late and early gestation); total counts per million.

Gene symbol	Total counts	P-value	FDR step up	Ratio	Log2(Ratio)	Fold change	LSMean(Late)	LSMean(Early)
ABCG4	1.63E+01	5.69E-05	1.05E-04	4.14E-01	-1.27E+00	-2.42E+00	5.15E-01	1.24E+00
ABHD12	1.64E+03	4.79E-06	1.29E-05	7.83E-01	-3.53E-01	-1.28E+00	7.67E+01	9.79E+01
ABHD17A	1.70E+03	1.41E-06	4.74E-06	7.48E-01	-4.19E-01	-1.34E+00	7.74E+01	1.04E+02
ABHD6	3.11E+02	2.87E-06	8.43E-06	5.16E-01	-9.56E-01	-1.94E+00	1.15E+01	2.24E+01
ABHD8	6.50E+02	1.03E-08	1.19E-07	6.97E-01	-5.22E-01	-1.44E+00	2.85E+01	4.10E+01
ABR	4.68E+03	2.30E-07	1.22E-06	6.30E-01	-6.66E-01	-1.59E+00	1.93E+02	3.07E+02
ABRACL	7.02E+01	1.60E-02	1.68E-02	7.01E-01	-5.12E-01	-1.43E+00	3.11E+00	4.44E+00
ACAA2	6.54E+02	7.30E-04	9.67E-04	7.73E-01	-3.71E-01	-1.29E+00	3.01E+01	3.90E+01
ACIN1	9.59E+03	2.86E-04	4.22E-04	8.36E-01	-2.59E-01	-1.20E+00	4.65E+02	5.56E+02
ACOT2-2	1.08E+01	5.31E-03	5.94E-03	1.50E-01	-2.74E+00	-6.69E+00	1.53E-01	1.02E+00
ACTG1	4.62E+04	1.22E-05	2.80E-05	7.68E-01	-3.81E-01	-1.30E+00	2.14E+03	2.79E+03
ACY1	2.40E+02	4.81E-03	5.42E-03	7.82E-01	-3.55E-01	-1.28E+00	1.13E+01	1.45E+01
ADAM11	1.54E+02	1.30E-06	4.47E-06	3.64E-01	-1.46E+00	-2.75E+00	4.47E+00	1.23E+01
ADAM8	5.58E+02	1.69E-06	5.46E-06	4.38E-01	-1.19E+00	-2.28E+00	1.85E+01	4.22E+01
ADAMTS13	2.17E+02	2.85E-05	5.72E-05	3.25E-01	-1.62E+00	-3.08E+00	5.83E+00	1.80E+01
ADCK1	2.16E+02	2.53E-05	5.17E-05	5.96E-01	-7.48E-01	-1.68E+00	8.71E+00	1.46E+01
ADD2	1.97E+02	3.90E-06	1.09E-05	4.40E-01	-1.18E+00	-2.27E+00	6.66E+00	1.51E+01
ADGRA1	9.67E+01	7.31E-03	7.99E-03	5.99E-01	-7.39E-01	-1.67E+00	3.89E+00	6.50E+00
ADGRB2	1.23E+03	7.72E-05	1.37E-04	6.46E-01	-6.31E-01	-1.55E+00	5.18E+01	8.02E+01
ADGRG1	2.40E+03	8.79E-07	3.31E-06	4.02E-01	-1.31E+00	-2.49E+00	7.56E+01	1.88E+02
ADH5	1.75E+03	2.00E-07	1.10E-06	6.66E-01	-5.87E-01	-1.50E+00	7.50E+01	1.13E+02
ADH6-2	2.28E+01	6.29E-07	2.58E-06	1.92E-01	-2.38E+00	-5.22E+00	4.16E-01	2.17E+00
ADK	3.78E+02	2.53E-03	3.02E-03	6.92E-01	-5.32E-01	-1.45E+00	1.64E+01	2.37E+01
ADRA2B	9.25E+01	4.11E-06	1.14E-05	5.23E-01	-9.34E-01	-1.91E+00	3.49E+00	6.66E+00
ADSSL1	3.78E+02	2.08E-08	2.04E-07	5.33E-01	-9.09E-01	-1.88E+00	1.42E+01	2.67E+01
AGA	7.43E+02	2.01E-03	2.43E-03	8.41E-01	-2.49E-01	-1.19E+00	3.58E+01	4.26E+01
AGAP2	1.48E+03	1.28E-06	4.45E-06	4.03E-01	-1.31E+00	-2.48E+00	4.63E+01	1.15E+02
AGAP3	1.85E+03	2.09E-07	1.14E-06	7.63E-01	-3.91E-01	-1.31E+00	8.52E+01	1.12E+02
AGER	2.82E+02	1.34E-03	1.68E-03	7.31E-01	-4.52E-01	-1.37E+00	1.27E+01	1.74E+01

AGPAT1	2.74E+03	1.09E-07	7.23E-07	7.35E-01	-4.45E-01	-1.36E+00	1.24E+02	1.68E+02
AGPAT4	2.72E+02	2.29E-07	1.22E-06	4.44E-01	-1.17E+00	-2.25E+00	9.26E+00	2.08E+01
AHCY	4.86E+03	8.15E-07	3.12E-06	5.98E-01	-7.42E-01	-1.67E+00	1.96E+02	3.27E+02
AHDC1	3.32E+03	4.32E-06	1.18E-05	5.39E-01	-8.92E-01	-1.86E+00	1.26E+02	2.33E+02
AIF1L	4.11E+02	7.71E-03	8.39E-03	5.90E-01	-7.62E-01	-1.70E+00	1.68E+01	2.85E+01
AIFM3	3.45E+03	5.58E-05	1.03E-04	3.36E-01	-1.57E+00	-2.98E+00	9.45E+01	2.81E+02
AIMP2	4.88E+02	2.41E-07	1.26E-06	6.28E-01	-6.72E-01	-1.59E+00	2.02E+01	3.22E+01
AJAP1	7.91E+01	1.24E-11	1.68E-09	3.55E-02	-4.82E+00	-2.82E+01	3.16E-01	8.92E+00
AK1	4.19E+02	1.12E-02	1.20E-02	7.40E-01	-4.33E-01	-1.35E+00	1.90E+01	2.57E+01
AK2	1.69E+03	1.06E-05	2.48E-05	7.56E-01	-4.04E-01	-1.32E+00	7.75E+01	1.03E+02
AKR1B1	2.74E+03	4.15E-05	7.99E-05	5.82E-01	-7.81E-01	-1.72E+00	1.10E+02	1.90E+02
AKT1	4.68E+03	2.30E-07	1.22E-06	7.36E-01	-4.42E-01	-1.36E+00	2.13E+02	2.89E+02
ALAS1	8.56E+02	8.34E-09	1.02E-07	6.28E-01	-6.70E-01	-1.59E+00	3.55E+01	5.64E+01
ALAS2	9.37E+01	4.86E-03	5.47E-03	3.92E-01	-1.35E+00	-2.55E+00	2.86E+00	7.31E+00
ALDH16A1	1.03E+03	1.76E-04	2.79E-04	7.93E-01	-3.35E-01	-1.26E+00	4.81E+01	6.07E+01
ALDH1A2	2.88E+03	3.10E-04	4.53E-04	4.71E-01	-1.09E+00	-2.12E+00	1.00E+02	2.13E+02
ALDH1L1	1.06E+02	1.75E-04	2.79E-04	4.61E-01	-1.12E+00	-2.17E+00	3.67E+00	7.96E+00
ALDH2	3.87E+03	9.53E-09	1.13E-07	6.48E-01	-6.27E-01	-1.54E+00	1.64E+02	2.54E+02
ALDH4A1	1.22E+03	5.87E-09	8.26E-08	5.85E-01	-7.74E-01	-1.71E+00	4.85E+01	8.30E+01
ALDOA	7.91E+03	2.22E-08	2.11E-07	5.03E-01	-9.90E-01	-1.99E+00	2.90E+02	5.76E+02
ALDOC	8.95E+02	1.79E-06	5.72E-06	6.30E-01	-6.68E-01	-1.59E+00	3.72E+01	5.90E+01
ALG14	4.30E+02	2.29E-03	2.74E-03	7.77E-01	-3.64E-01	-1.29E+00	2.00E+01	2.58E+01
ALG3	3.30E+02	3.58E-06	1.01E-05	6.69E-01	-5.80E-01	-1.49E+00	1.42E+01	2.12E+01
ALG5	2.33E+02	7.94E-07	3.08E-06	6.62E-01	-5.96E-01	-1.51E+00	9.93E+00	1.50E+01
ALKBH6	9.58E+01	8.92E-04	1.16E-03	7.54E-01	-4.07E-01	-1.33E+00	4.36E+00	5.78E+00
ALPL	2.90E+03	3.41E-08	2.97E-07	3.97E-01	-1.33E+00	-2.52E+00	9.02E+01	2.27E+02
ALX4	3.98E+01	2.04E-11	2.20E-09	2.53E-02	-5.30E+00	-3.95E+01	1.12E-01	4.44E+00
AMPD2	1.60E+03	1.68E-07	9.65E-07	6.71E-01	-5.75E-01	-1.49E+00	6.89E+01	1.03E+02
ANKRD2	4.18E+01	3.56E-06	1.01E-05	4.29E-01	-1.22E+00	-2.33E+00	1.37E+00	3.20E+00
ANKRD33	8.55E+01	9.31E-04	1.20E-03	6.34E-01	-6.58E-01	-1.58E+00	3.57E+00	5.64E+00
ANKRD55	2.62E+01	7.43E-06	1.86E-05	2.13E-01	-2.23E+00	-4.70E+00	5.26E-01	2.47E+00
ANP32A	2.62E+03	2.78E-10	1.22E-08	5.91E-01	-7.59E-01	-1.69E+00	1.05E+02	1.78E+02
ANP32B	6.01E+03	2.50E-06	7.48E-06	7.33E-01	-4.48E-01	-1.36E+00	2.71E+02	3.70E+02

ANXA6	6.51E+03	1.91E-05	4.07E-05	6.88E-01	-5.40E-01	-1.45E+00	2.85E+02	4.15E+02
AP1G2	8.53E+02	4.89E-05	9.23E-05	7.63E-01	-3.91E-01	-1.31E+00	3.94E+01	5.17E+01
AP1S3	7.08E+01	2.30E-04	3.50E-04	5.48E-01	-8.67E-01	-1.82E+00	2.65E+00	4.83E+00
AP2M1	5.54E+03	3.04E-04	4.46E-04	8.60E-01	-2.17E-01	-1.16E+00	2.72E+02	3.16E+02
AP4M1	6.97E+02	1.89E-07	1.06E-06	6.84E-01	-5.48E-01	-1.46E+00	3.04E+01	4.44E+01
APBB1	1.83E+03	7.32E-09	9.45E-08	6.44E-01	-6.36E-01	-1.55E+00	7.73E+01	1.20E+02
APCDD1	5.25E+03	1.67E-08	1.71E-07	3.30E-01	-1.60E+00	-3.03E+00	1.44E+02	4.37E+02
APEX1	2.49E+03	7.45E-09	9.50E-08	5.74E-01	-8.00E-01	-1.74E+00	9.85E+01	1.71E+02
APEX2	4.23E+02	1.34E-04	2.19E-04	7.54E-01	-4.08E-01	-1.33E+00	1.94E+01	2.58E+01
APH1A	1.51E+03	1.03E-06	3.74E-06	7.32E-01	-4.51E-01	-1.37E+00	6.80E+01	9.29E+01
APOA2	1.62E+00	1.65E-02	1.74E-02	3.62E-01	-1.46E+00	-2.76E+00	4.85E-02	1.34E-01
APOBEC3H	2.84E+02	9.90E-07	3.62E-06	5.60E-01	-8.37E-01	-1.79E+00	1.10E+01	1.97E+01
APOBEC3Z2	1.49E+02	7.27E-08	5.26E-07	4.53E-01	-1.14E+00	-2.21E+00	5.07E+00	1.12E+01
APOE	5.92E+03	6.69E-05	1.21E-04	4.92E-01	-1.02E+00	-2.03E+00	2.14E+02	4.36E+02
APOM	1.10E+02	4.87E-07	2.15E-06	3.39E-01	-1.56E+00	-2.95E+00	3.06E+00	9.02E+00
APOOL	2.35E+02	1.76E-04	2.79E-04	7.39E-01	-4.36E-01	-1.35E+00	1.07E+01	1.45E+01
AQP1	1.53E+03	1.55E-07	9.22E-07	5.11E-01	-9.67E-01	-1.96E+00	5.67E+01	1.11E+02
AQP5	1.45E+01	1.63E-03	2.00E-03	3.81E-01	-1.39E+00	-2.62E+00	4.21E-01	1.10E+00
ARC	1.83E+02	1.15E-09	3.00E-08	1.15E-01	-3.12E+00	-8.72E+00	2.15E+00	1.87E+01
ARF1	6.52E+03	1.91E-05	4.07E-05	8.38E-01	-2.55E-01	-1.19E+00	3.15E+02	3.76E+02
ARFGAP1	1.12E+03	9.29E-06	2.22E-05	8.42E-01	-2.48E-01	-1.19E+00	5.41E+01	6.43E+01
ARG2	1.27E+02	6.47E-11	5.11E-09	1.92E-01	-2.38E+00	-5.22E+00	2.28E+00	1.19E+01
ARHGAP45	8.65E+02	5.17E-09	7.66E-08	3.61E-01	-1.47E+00	-2.77E+00	2.51E+01	6.97E+01
ARHGAP9	6.02E+01	6.76E-04	9.06E-04	5.71E-01	-8.07E-01	-1.75E+00	2.34E+00	4.10E+00
ARHGDIA	5.13E+03	6.69E-05	1.21E-04	8.37E-01	-2.57E-01	-1.19E+00	2.48E+02	2.97E+02
ARHGEF18	1.71E+03	4.44E-04	6.24E-04	8.08E-01	-3.08E-01	-1.24E+00	8.08E+01	1.00E+02
ARL2	7.60E+02	3.98E-08	3.31E-07	6.09E-01	-7.17E-01	-1.64E+00	3.10E+01	5.09E+01
ARL2BP	8.86E+02	1.07E-03	1.37E-03	8.49E-01	-2.37E-01	-1.18E+00	4.30E+01	5.06E+01
ARL3	9.15E+02	7.75E-09	9.69E-08	6.00E-01	-7.38E-01	-1.67E+00	3.68E+01	6.14E+01
ARL6IP4	6.69E+02	6.23E-07	2.56E-06	7.39E-01	-4.37E-01	-1.35E+00	3.04E+01	4.12E+01
ARL8A	5.99E+02	7.40E-07	2.93E-06	7.79E-01	-3.60E-01	-1.28E+00	2.79E+01	3.58E+01
ARL9	8.72E+01	2.35E-07	1.23E-06	3.87E-01	-1.37E+00	-2.59E+00	2.64E+00	6.84E+00
ARMH4	2.98E+03	4.46E-04	6.26E-04	6.63E-01	-5.94E-01	-1.51E+00	1.27E+02	1.92E+02

ARPC3	1.27E+03	1.78E-04	2.82E-04	7.51E-01	-4.13E-01	-1.33E+00	5.81E+01	7.73E+01
ARPC4	1.27E+03	1.54E-06	5.10E-06	7.30E-01	-4.54E-01	-1.37E+00	5.70E+01	7.81E+01
ARPC5L	7.05E+02	3.85E-08	3.25E-07	5.33E-01	-9.08E-01	-1.88E+00	2.65E+01	4.97E+01
AS3MT	2.96E+02	4.18E-03	4.76E-03	6.98E-01	-5.20E-01	-1.43E+00	1.29E+01	1.84E+01
ASAP3	5.54E+02	1.16E-04	1.94E-04	6.12E-01	-7.08E-01	-1.63E+00	2.26E+01	3.70E+01
ASB16	2.35E+02	4.09E-09	6.70E-08	3.89E-01	-1.36E+00	-2.57E+00	7.18E+00	1.85E+01
ASCC1	4.20E+02	5.84E-06	1.53E-05	5.10E-01	-9.70E-01	-1.96E+00	1.53E+01	3.01E+01
ASCL4	1.20E+02	7.19E-05	1.28E-04	6.78E-01	-5.60E-01	-1.47E+00	5.19E+00	7.66E+00
ASIC4	3.04E+02	2.35E-06	7.09E-06	3.56E-01	-1.49E+00	-2.81E+00	8.72E+00	2.45E+01
ASMTL	1.25E+03	6.77E-06	1.72E-05	6.69E-01	-5.79E-01	-1.49E+00	5.37E+01	8.02E+01
ASNA1	1.22E+03	8.84E-07	3.31E-06	7.27E-01	-4.60E-01	-1.38E+00	5.49E+01	7.55E+01
ATAD3A	7.51E+02	1.10E-05	2.56E-05	5.80E-01	-7.85E-01	-1.72E+00	2.97E+01	5.12E+01
ATG10	1.16E+02	1.13E-04	1.89E-04	6.23E-01	-6.83E-01	-1.61E+00	4.78E+00	7.68E+00
ATOX1	3.91E+02	1.25E-03	1.58E-03	6.90E-01	-5.35E-01	-1.45E+00	1.71E+01	2.48E+01
ATP13A5	1.65E+00	4.99E-07	2.18E-06	4.73E-02	-4.40E+00	-2.11E+01	8.61E-03	1.82E-01
ATP1A3	3.78E+01	1.11E-04	1.86E-04	3.06E-01	-1.71E+00	-3.27E+00	9.67E-01	3.16E+00
ATP2A3	8.25E+02	7.80E-13	3.74E-10	2.06E-01	-2.28E+00	-4.84E+00	1.60E+01	7.73E+01
ATP5F1A	6.93E+03	2.73E-07	1.37E-06	6.76E-01	-5.65E-01	-1.48E+00	2.99E+02	4.42E+02
ATP5F1B	6.67E+03	9.25E-10	2.81E-08	5.79E-01	-7.89E-01	-1.73E+00	2.63E+02	4.55E+02
ATP5MC1	6.75E+02	4.57E-06	1.24E-05	6.91E-01	-5.34E-01	-1.45E+00	2.95E+01	4.28E+01
ATP5MC2	5.19E+03	6.14E-06	1.57E-05	6.98E-01	-5.19E-01	-1.43E+00	2.28E+02	3.27E+02
ATP5MC3	1.80E+03	9.88E-10	2.85E-08	5.04E-01	-9.88E-01	-1.98E+00	6.55E+01	1.30E+02
ATP5MD	2.69E+02	1.03E-04	1.75E-04	6.04E-01	-7.27E-01	-1.66E+00	1.09E+01	1.80E+01
ATP5ME	9.74E+02	9.02E-03	9.76E-03	7.80E-01	-3.59E-01	-1.28E+00	4.55E+01	5.83E+01
ATP5MPL	1.04E+03	8.60E-06	2.09E-05	6.27E-01	-6.74E-01	-1.60E+00	4.28E+01	6.82E+01
ATP5PD	1.37E+03	2.53E-05	5.17E-05	6.76E-01	-5.65E-01	-1.48E+00	5.88E+01	8.70E+01
ATP6	6.25E+04	9.00E-04	1.17E-03	7.11E-01	-4.93E-01	-1.41E+00	2.76E+03	3.88E+03
ATP6V1B1	1.65E+02	4.36E-04	6.15E-04	3.13E-01	-1.67E+00	-3.19E+00	4.22E+00	1.35E+01
ATP6V1C2	7.97E+01	1.28E-03	1.61E-03	3.99E-01	-1.32E+00	-2.51E+00	2.54E+00	6.37E+00
ATP8	2.26E+04	1.95E-03	2.37E-03	7.34E-01	-4.46E-01	-1.36E+00	1.01E+03	1.38E+03
ATP9B	1.14E+03	6.62E-03	7.29E-03	8.55E-01	-2.26E-01	-1.17E+00	5.57E+01	6.51E+01
ATPAF1	8.53E+02	2.53E-06	7.52E-06	7.44E-01	-4.26E-01	-1.34E+00	3.89E+01	5.22E+01
ATXN7L2	3.40E+02	3.43E-03	3.97E-03	8.17E-01	-2.92E-01	-1.22E+00	1.62E+01	1.99E+01

ATXN7L3	2.09E+03	1.18E-11	1.68E-09	5.71E-01	-8.08E-01	-1.75E+00	8.20E+01	1.44E+02
AURKAIP1	4.46E+02	8.21E-05	1.45E-04	7.58E-01	-4.00E-01	-1.32E+00	2.05E+01	2.71E+01
AURKB	4.90E+02	4.00E-08	3.31E-07	3.67E-01	-1.44E+00	-2.72E+00	1.46E+01	3.97E+01
AVIL	8.50E+01	4.41E-12	8.67E-10	1.44E-01	-2.80E+00	-6.94E+00	1.24E+00	8.63E+00
B3GALNT2	8.31E+02	2.54E-04	3.82E-04	7.71E-01	-3.75E-01	-1.30E+00	3.87E+01	5.01E+01
B3GALT4	3.47E+02	4.88E-06	1.31E-05	7.50E-01	-4.14E-01	-1.33E+00	1.59E+01	2.12E+01
B4GALNT3	2.05E+02	8.17E-10	2.62E-08	1.01E-01	-3.31E+00	-9.95E+00	2.16E+00	2.15E+01
B4GALT2	1.87E+03	3.53E-06	1.00E-05	7.57E-01	-4.03E-01	-1.32E+00	8.54E+01	1.13E+02
B4GALT3	7.54E+02	9.64E-05	1.65E-04	7.98E-01	-3.26E-01	-1.25E+00	3.56E+01	4.46E+01
B4GALT7	4.21E+02	2.26E-06	6.87E-06	7.49E-01	-4.17E-01	-1.33E+00	1.92E+01	2.56E+01
B9D1	2.88E+02	4.85E-06	1.30E-05	5.48E-01	-8.69E-01	-1.83E+00	1.10E+01	2.01E+01
B9D2	2.41E+02	6.37E-05	1.16E-04	6.73E-01	-5.71E-01	-1.49E+00	1.03E+01	1.54E+01
BAP1	2.10E+03	2.64E-09	5.11E-08	7.01E-01	-5.12E-01	-1.43E+00	9.25E+01	1.32E+02
BASP1	2.50E+03	2.62E-05	5.32E-05	5.31E-01	-9.13E-01	-1.88E+00	9.43E+01	1.78E+02
BAX	2.69E+02	5.73E-06	1.50E-05	6.46E-01	-6.31E-01	-1.55E+00	1.14E+01	1.76E+01
BCAR1	1.64E+03	4.66E-03	5.26E-03	8.76E-01	-1.90E-01	-1.14E+00	8.07E+01	9.21E+01
BCCIP	9.19E+02	7.66E-04	1.01E-03	7.57E-01	-4.01E-01	-1.32E+00	4.21E+01	5.56E+01
BCKDHB	2.75E+02	5.30E-05	9.87E-05	6.93E-01	-5.29E-01	-1.44E+00	1.21E+01	1.75E+01
BCKDK	8.81E+02	6.30E-07	2.58E-06	7.88E-01	-3.44E-01	-1.27E+00	4.12E+01	5.23E+01
BCL2L12	4.96E+02	4.18E-06	1.16E-05	7.33E-01	-4.48E-01	-1.36E+00	2.24E+01	3.06E+01
BCL3	4.01E+02	4.16E-06	1.15E-05	6.63E-01	-5.93E-01	-1.51E+00	1.72E+01	2.59E+01
BCO1	8.13E+00	2.40E-02	2.49E-02	2.24E-01	-2.16E+00	-4.47E+00	1.69E-01	7.57E-01
BDH1	7.15E+01	7.00E-04	9.33E-04	4.77E-01	-1.07E+00	-2.10E+00	2.52E+00	5.29E+00
BEAN1	1.40E+02	2.91E-05	5.81E-05	5.65E-01	-8.25E-01	-1.77E+00	5.43E+00	9.61E+00
BEND3	3.89E+02	4.85E-05	9.19E-05	6.96E-01	-5.22E-01	-1.44E+00	1.71E+01	2.46E+01
BEND5	3.69E+02	3.84E-03	4.42E-03	8.43E-01	-2.47E-01	-1.19E+00	1.78E+01	2.12E+01
BEX2-2	8.40E+02	2.47E-06	7.38E-06	5.68E-01	-8.17E-01	-1.76E+00	3.28E+01	5.77E+01
BEX5	9.11E+02	2.11E-05	4.42E-05	5.89E-01	-7.64E-01	-1.70E+00	3.64E+01	6.19E+01
BFAR	1.12E+03	5.44E-03	6.07E-03	8.50E-01	-2.34E-01	-1.18E+00	5.43E+01	6.39E+01
BFSP1	2.73E+02	6.06E-06	1.56E-05	4.53E-01	-1.14E+00	-2.21E+00	9.42E+00	2.08E+01
BIN1	1.32E+03	1.41E-07	8.58E-07	6.36E-01	-6.53E-01	-1.57E+00	5.53E+01	8.69E+01
BLVRA	1.23E+03	1.22E-08	1.34E-07	5.99E-01	-7.40E-01	-1.67E+00	5.00E+01	8.35E+01
BMP4	3.62E+02	3.76E-03	4.32E-03	6.74E-01	-5.68E-01	-1.48E+00	1.58E+01	2.34E+01

BORA	2.70E+02	2.76E-09	5.23E-08	4.76E-01	-1.07E+00	-2.10E+00	9.41E+00	1.98E+01
BORCS6	2.66E+02	4.80E-04	6.69E-04	7.43E-01	-4.29E-01	-1.35E+00	1.22E+01	1.64E+01
BORCS8	3.32E+02	1.08E-02	1.16E-02	8.15E-01	-2.95E-01	-1.23E+00	1.58E+01	1.94E+01
BPHL	4.62E+02	5.54E-03	6.16E-03	8.17E-01	-2.92E-01	-1.22E+00	2.22E+01	2.71E+01
BREH1	7.66E+01	2.01E-06	6.28E-06	2.50E-01	-2.00E+00	-3.99E+00	1.71E+00	6.82E+00
BRF2	3.37E+02	7.45E-05	1.32E-04	7.67E-01	-3.82E-01	-1.30E+00	1.56E+01	2.03E+01
BRICD5	1.77E+01	4.59E-03	5.19E-03	5.42E-01	-8.83E-01	-1.84E+00	6.65E-01	1.23E+00
BRINP1	1.81E+02	1.82E-03	2.22E-03	5.66E-01	-8.20E-01	-1.77E+00	7.10E+00	1.25E+01
BRMS1	7.16E+02	9.19E-09	1.11E-07	5.73E-01	-8.04E-01	-1.75E+00	2.82E+01	4.92E+01
BSCL2	6.23E+02	9.55E-03	1.03E-02	8.24E-01	-2.80E-01	-1.21E+00	2.96E+01	3.59E+01
BSG	6.90E+03	5.06E-04	7.01E-04	8.42E-01	-2.49E-01	-1.19E+00	3.35E+02	3.98E+02
BTD	2.41E+02	2.48E-03	2.95E-03	8.03E-01	-3.17E-01	-1.25E+00	1.13E+01	1.41E+01
C10H14orf119	6.12E+02	3.02E-05	6.01E-05	7.54E-01	-4.08E-01	-1.33E+00	2.79E+01	3.71E+01
C10H15orf59	8.32E+02	3.94E-07	1.82E-06	3.29E-01	-1.60E+00	-3.04E+00	2.29E+01	6.95E+01
C13H20orf27	9.93E+02	4.07E-06	1.14E-05	7.26E-01	-4.63E-01	-1.38E+00	4.44E+01	6.12E+01
C14H8orf82	3.49E+02	5.90E-04	8.01E-04	8.12E-01	-3.01E-01	-1.23E+00	1.67E+01	2.06E+01
C15H11orf49	5.24E+02	6.00E-06	1.56E-05	6.77E-01	-5.63E-01	-1.48E+00	2.26E+01	3.34E+01
C18H16orf74	1.64E+02	2.00E-08	1.98E-07	2.50E-01	-2.00E+00	-4.00E+00	3.69E+00	1.48E+01
C18H16orf78	1.23E+01	9.45E-09	1.13E-07	1.15E-02	-6.45E+00	-8.71E+01	1.66E-02	1.44E+00
C18H19orf33	5.51E+01	5.04E-08	3.94E-07	1.60E-01	-2.64E+00	-6.25E+00	8.89E-01	5.55E+00
C18H19orf48	7.86E+02	1.33E-04	2.18E-04	7.32E-01	-4.50E-01	-1.37E+00	3.55E+01	4.85E+01
C19H17orf49	9.45E+02	1.89E-04	2.96E-04	7.28E-01	-4.57E-01	-1.37E+00	4.25E+01	5.83E+01
C19H17orf67	4.33E+01	1.77E-09	3.98E-08	7.90E-02	-3.66E+00	-1.27E+01	3.74E-01	4.73E+00
C1QBP	1.23E+03	1.28E-04	2.11E-04	7.33E-01	-4.48E-01	-1.36E+00	5.60E+01	7.64E+01
C22H3orf62	1.92E+02	5.43E-03	6.06E-03	7.40E-01	-4.34E-01	-1.35E+00	8.68E+00	1.17E+01
C25H16orf45	2.10E+02	6.72E-07	2.70E-06	3.39E-01	-1.56E+00	-2.95E+00	5.84E+00	1.72E+01
C25H16orf91	4.57E+02	2.77E-05	5.58E-05	7.89E-01	-3.43E-01	-1.27E+00	2.14E+01	2.72E+01
C3H1orf210	4.06E+01	4.83E-04	6.73E-04	2.75E-01	-1.86E+00	-3.63E+00	1.01E+00	3.66E+00
C3H1orf226	3.20E+02	1.30E-05	2.94E-05	4.47E-01	-1.16E+00	-2.24E+00	1.09E+01	2.44E+01
C3H1orf94	2.25E+00	5.06E-04	7.01E-04	1.09E-01	-3.20E+00	-9.19E+00	2.51E-02	2.31E-01
C5H12orf73	3.49E+02	1.54E-05	3.37E-05	7.40E-01	-4.34E-01	-1.35E+00	1.58E+01	2.14E+01
C7H19orf25	3.92E+02	2.58E-04	3.86E-04	7.44E-01	-4.27E-01	-1.34E+00	1.78E+01	2.40E+01
C7H19orf53	1.54E+03	1.08E-04	1.81E-04	7.81E-01	-3.57E-01	-1.28E+00	7.21E+01	9.24E+01

C7H19orf70	3.23E+02	2.08E-03	2.51E-03	7.08E-01	-4.99E-01	-1.41E+00	1.43E+01	2.02E+01
C8H9orf3	1.21E+03	3.19E-04	4.65E-04	6.98E-01	-5.19E-01	-1.43E+00	5.30E+01	7.60E+01
C8H9orf40	2.55E+02	1.50E-04	2.43E-04	7.51E-01	-4.13E-01	-1.33E+00	1.16E+01	1.54E+01
C9H6orf203	2.95E+02	1.13E-04	1.88E-04	7.66E-01	-3.85E-01	-1.31E+00	1.36E+01	1.78E+01
CA11	4.39E+02	6.95E-04	9.30E-04	7.30E-01	-4.53E-01	-1.37E+00	1.97E+01	2.70E+01
CA14	3.84E+02	3.60E-04	5.18E-04	6.31E-01	-6.65E-01	-1.59E+00	1.60E+01	2.54E+01
CA8	2.96E+02	1.59E-04	2.56E-04	4.92E-01	-1.02E+00	-2.03E+00	1.07E+01	2.17E+01
CACFD1	8.07E+02	7.27E-08	5.26E-07	6.49E-01	-6.24E-01	-1.54E+00	3.42E+01	5.27E+01
CACNA1H	4.38E+03	4.13E-03	4.72E-03	6.88E-01	-5.39E-01	-1.45E+00	1.92E+02	2.79E+02
CACNG4	2.69E+02	1.91E-07	1.06E-06	3.69E-01	-1.44E+00	-2.71E+00	7.98E+00	2.16E+01
CACTIN	1.15E+03	1.34E-06	4.55E-06	7.79E-01	-3.59E-01	-1.28E+00	5.35E+01	6.86E+01
CADM4	7.15E+02	5.27E-09	7.66E-08	3.30E-01	-1.60E+00	-3.03E+00	1.96E+01	5.93E+01
CALB2	2.55E+02	1.80E-08	1.80E-07	1.40E-01	-2.84E+00	-7.14E+00	3.49E+00	2.50E+01
CAMKK1	1.49E+02	4.46E-08	3.62E-07	4.47E-01	-1.16E+00	-2.24E+00	5.02E+00	1.12E+01
CAMKV	2.92E+02	1.13E-10	6.64E-09	6.77E-02	-3.88E+00	-1.48E+01	2.16E+00	3.19E+01
CAPN10	7.36E+02	1.66E-06	5.40E-06	7.06E-01	-5.03E-01	-1.42E+00	3.25E+01	4.61E+01
CAPN12	7.63E+00	8.94E-02	9.01E-02	6.73E-01	-5.72E-01	-1.49E+00	3.31E-01	4.92E-01
CAPN14	2.44E+01	1.15E-06	4.10E-06	1.04E-01	-3.26E+00	-9.59E+00	2.71E-01	2.59E+00
CARHSP1	1.29E+03	4.86E-04	6.76E-04	7.90E-01	-3.41E-01	-1.27E+00	6.06E+01	7.68E+01
CASKIN2	2.41E+03	1.89E-07	1.06E-06	7.20E-01	-4.74E-01	-1.39E+00	1.08E+02	1.50E+02
CASP3	5.19E+02	7.71E-07	3.01E-06	6.89E-01	-5.37E-01	-1.45E+00	2.28E+01	3.30E+01
CBARP	2.38E+02	8.26E-08	5.82E-07	3.82E-01	-1.39E+00	-2.61E+00	7.19E+00	1.88E+01
CBLN4	1.43E+02	1.14E-03	1.45E-03	3.41E-01	-1.55E+00	-2.93E+00	4.07E+00	1.19E+01
CBS	8.57E+02	7.99E-07	3.10E-06	4.91E-01	-1.03E+00	-2.04E+00	3.07E+01	6.25E+01
CBX4	9.87E+02	6.25E-06	1.60E-05	7.33E-01	-4.49E-01	-1.36E+00	4.44E+01	6.06E+01
CBY1	9.88E+02	3.89E-05	7.54E-05	7.84E-01	-3.50E-01	-1.27E+00	4.63E+01	5.90E+01
CCDC124	6.66E+02	5.80E-03	6.43E-03	8.56E-01	-2.25E-01	-1.17E+00	3.26E+01	3.80E+01
CCDC148	7.84E+00	2.91E-02	3.01E-02	6.15E-01	-7.02E-01	-1.63E+00	3.15E-01	5.12E-01
CCDC173	5.11E+01	2.78E-03	3.28E-03	5.84E-01	-7.76E-01	-1.71E+00	1.99E+00	3.40E+00
CCDC189	4.67E+02	6.48E-04	8.70E-04	7.17E-01	-4.80E-01	-1.39E+00	2.09E+01	2.91E+01
CCDC28B	1.29E+03	2.43E-04	3.67E-04	7.19E-01	-4.77E-01	-1.39E+00	5.76E+01	8.02E+01
CCDC68	4.68E+01	3.98E-08	3.31E-07	1.98E-01	-2.34E+00	-5.05E+00	8.79E-01	4.44E+00
CCDC70	4.51E+00	2.50E-07	1.29E-06	1.21E-02	-6.37E+00	-8.25E+01	6.37E-03	5.26E-01

CCDC86	4.23E+02	4.25E-03	4.83E-03	7.89E-01	-3.42E-01	-1.27E+00	1.98E+01	2.51E+01
CCKBR	4.76E+02	1.23E-06	4.32E-06	2.05E-01	-2.29E+00	-4.88E+00	8.95E+00	4.37E+01
CCL25	1.25E+03	6.17E-08	4.68E-07	4.03E-01	-1.31E+00	-2.48E+00	3.93E+01	9.76E+01
CCNA2	2.99E+02	1.60E-06	5.24E-06	5.56E-01	-8.48E-01	-1.80E+00	1.16E+01	2.08E+01
CCNL2	1.45E+03	1.81E-06	5.76E-06	8.09E-01	-3.06E-01	-1.24E+00	6.93E+01	8.57E+01
CCRL2	2.12E+01	2.14E-02	2.23E-02	7.01E-01	-5.12E-01	-1.43E+00	9.32E-01	1.33E+00
CD19	9.22E+01	4.31E-04	6.08E-04	5.22E-01	-9.39E-01	-1.92E+00	3.39E+00	6.49E+00
CD24	3.09E+02	5.65E-11	4.67E-09	7.11E-02	-3.81E+00	-1.41E+01	2.45E+00	3.45E+01
CD2BP2	1.51E+03	7.28E-05	1.30E-04	8.11E-01	-3.03E-01	-1.23E+00	7.19E+01	8.87E+01
CD320	5.28E+02	7.51E-07	2.95E-06	5.93E-01	-7.55E-01	-1.69E+00	2.12E+01	3.57E+01
CD3G	1.53E+02	1.26E-08	1.38E-07	2.12E-01	-2.24E+00	-4.71E+00	2.94E+00	1.38E+01
CD79B	3.06E+01	1.28E-05	2.91E-05	1.48E-01	-2.75E+00	-6.75E+00	4.62E-01	3.12E+00
CD8B	8.62E+01	8.60E-08	6.00E-07	2.12E-01	-2.24E+00	-4.73E+00	1.71E+00	8.07E+00
CD9	1.92E+03	7.31E-08	5.26E-07	2.48E-01	-2.01E+00	-4.03E+00	4.31E+01	1.74E+02
CDC25B	4.74E+02	2.79E-04	4.13E-04	7.48E-01	-4.20E-01	-1.34E+00	2.16E+01	2.89E+01
CDC42EP3	4.67E+02	1.47E-05	3.25E-05	5.58E-01	-8.43E-01	-1.79E+00	1.84E+01	3.29E+01
CDCA3	3.63E+02	1.66E-07	9.57E-07	4.20E-01	-1.25E+00	-2.38E+00	1.17E+01	2.80E+01
CDCP1	2.80E+02	1.45E-02	1.53E-02	6.67E-01	-5.85E-01	-1.50E+00	1.18E+01	1.77E+01
CDH24	7.91E+02	5.69E-09	8.11E-08	4.55E-01	-1.14E+00	-2.20E+00	2.71E+01	5.96E+01
CDH4	4.84E+02	2.38E-03	2.84E-03	5.41E-01	-8.86E-01	-1.85E+00	1.85E+01	3.42E+01
CDH9	5.37E+01	4.44E-04	6.24E-04	2.82E-01	-1.82E+00	-3.54E+00	1.27E+00	4.49E+00
CDHR1	2.40E+01	5.67E-03	6.29E-03	1.29E-01	-2.96E+00	-7.76E+00	3.21E-01	2.49E+00
CDHR4	1.71E+01	5.46E-02	5.54E-02	4.33E-01	-1.21E+00	-2.31E+00	5.48E-01	1.26E+00
CDIP1	1.45E+03	4.78E-09	7.16E-08	6.73E-01	-5.72E-01	-1.49E+00	6.25E+01	9.30E+01
CDIPT	8.30E+02	3.73E-10	1.43E-08	6.35E-01	-6.54E-01	-1.57E+00	3.48E+01	5.48E+01
CDK18	3.83E+02	3.87E-04	5.51E-04	5.74E-01	-8.00E-01	-1.74E+00	1.52E+01	2.64E+01
CDK2	9.38E+02	1.60E-09	3.68E-08	5.95E-01	-7.49E-01	-1.68E+00	3.76E+01	6.31E+01
CDK20	9.54E+02	6.94E-09	9.01E-08	6.44E-01	-6.36E-01	-1.55E+00	3.99E+01	6.21E+01
CDK4	1.82E+03	3.63E-08	3.12E-07	6.47E-01	-6.28E-01	-1.55E+00	7.70E+01	1.19E+02
CDKN1C	1.34E+03	1.03E-07	6.93E-07	5.40E-01	-8.89E-01	-1.85E+00	5.09E+01	9.42E+01
CDKN2AIPNL	5.80E+02	3.24E-03	3.77E-03	8.32E-01	-2.65E-01	-1.20E+00	2.80E+01	3.37E+01
CDX1	2.78E+02	5.88E-09	8.26E-08	6.05E-02	-4.05E+00	-1.65E+01	1.87E+00	3.08E+01
CEP78	2.53E+02	6.62E-07	2.68E-06	7.05E-01	-5.04E-01	-1.42E+00	1.12E+01	1.58E+01

CERK	1.05E+03	1.96E-06	6.14E-06	7.16E-01	-4.81E-01	-1.40E+00	4.68E+01	6.54E+01
CERS4	1.07E+03	1.20E-03	1.52E-03	6.45E-01	-6.33E-01	-1.55E+00	4.51E+01	6.99E+01
CETN2	1.56E+03	2.39E-05	4.93E-05	6.89E-01	-5.38E-01	-1.45E+00	6.73E+01	9.78E+01
CETN4	4.45E+02	9.25E-06	2.22E-05	3.90E-01	-1.36E+00	-2.57E+00	1.32E+01	3.40E+01
CFAP161	1.29E+02	9.05E-06	2.19E-05	3.43E-01	-1.55E+00	-2.92E+00	3.68E+00	1.07E+01
CFL1	1.16E+04	6.63E-06	1.69E-05	7.28E-01	-4.59E-01	-1.37E+00	5.23E+02	7.19E+02
CHCHD1	5.32E+02	3.74E-06	1.05E-05	6.65E-01	-5.88E-01	-1.50E+00	2.26E+01	3.40E+01
CHCHD5	2.18E+02	6.46E-03	7.12E-03	7.77E-01	-3.65E-01	-1.29E+00	1.01E+01	1.30E+01
CHCHD8	1.98E+02	6.36E-05	1.16E-04	7.66E-01	-3.84E-01	-1.31E+00	9.13E+00	1.19E+01
CHD1L	4.99E+02	2.92E-03	3.43E-03	8.52E-01	-2.31E-01	-1.17E+00	2.44E+01	2.87E+01
hrM:1453..302	4.85E+03	5.36E-04	7.36E-04	5.07E-01	-9.79E-01	-1.97E+00	1.76E+02	3.47E+02
rM:15726..157	3.36E+00	7.34E-01	7.34E-01	4.30E-01	-1.22E+00	-2.33E+00	1.11E-01	2.58E-01
chrM:431..1385	1.93E+03	1.13E-02	1.21E-02	7.13E-01	-4.88E-01	-1.40E+00	8.59E+01	1.21E+02
CHRNA2	9.08E+01	6.11E-06	1.57E-05	1.50E-01	-2.74E+00	-6.68E+00	1.36E+00	9.11E+00
CHRNA5	6.92E+01	1.79E-05	3.86E-05	5.47E-01	-8.69E-01	-1.83E+00	2.64E+00	4.83E+00
CHRNB2	1.35E+01	2.73E-03	3.23E-03	4.68E-01	-1.09E+00	-2.14E+00	4.71E-01	1.01E+00
CHRNB4	1.95E+02	4.00E-06	1.12E-05	3.58E-01	-1.48E+00	-2.79E+00	5.57E+00	1.56E+01
CKM	1.29E+01	1.15E-07	7.49E-07	1.25E-01	-3.00E+00	-7.98E+00	1.62E-01	1.30E+00
CLBA1	8.44E+01	1.92E-04	3.00E-04	5.66E-01	-8.21E-01	-1.77E+00	3.24E+00	5.73E+00
CLDN6	9.63E+01	4.74E-12	8.67E-10	6.73E-03	-7.21E+00	-1.49E+02	7.82E-02	1.16E+01
CLIP2	2.92E+03	2.57E-07	1.32E-06	6.88E-01	-5.40E-01	-1.45E+00	1.28E+02	1.85E+02
CLN6	1.11E+03	5.76E-05	1.06E-04	6.88E-01	-5.40E-01	-1.45E+00	4.84E+01	7.04E+01
CLPP	6.01E+02	3.08E-03	3.60E-03	8.61E-01	-2.16E-01	-1.16E+00	2.96E+01	3.44E+01
CLSTN3	2.59E+03	7.59E-06	1.89E-05	4.04E-01	-1.31E+00	-2.47E+00	8.11E+01	2.01E+02
CLUH	1.66E+03	9.00E-05	1.56E-04	6.78E-01	-5.62E-01	-1.48E+00	7.23E+01	1.07E+02
CMIP	2.50E+03	2.54E-05	5.18E-05	6.91E-01	-5.33E-01	-1.45E+00	1.09E+02	1.58E+02
CMTM5	2.37E+01	1.94E-05	4.11E-05	4.36E-01	-1.20E+00	-2.29E+00	7.91E-01	1.81E+00
CNIH2	2.27E+02	1.33E-08	1.43E-07	3.51E-01	-1.51E+00	-2.85E+00	6.57E+00	1.87E+01
CNKSR1	6.41E+01	4.39E-05	8.42E-05	4.54E-01	-1.14E+00	-2.20E+00	2.18E+00	4.79E+00
CNNM1	4.62E+01	5.47E-05	1.01E-04	1.46E-02	-6.10E+00	-6.84E+01	8.03E-02	5.49E+00
CNPY3	9.70E+02	4.29E-06	1.17E-05	8.07E-01	-3.10E-01	-1.24E+00	4.60E+01	5.70E+01
CNTF	1.05E+01	1.22E-01	1.22E-01	7.02E-01	-5.10E-01	-1.42E+00	4.53E-01	6.45E-01
COA3	7.09E+02	1.27E-05	2.89E-05	6.86E-01	-5.43E-01	-1.46E+00	3.09E+01	4.50E+01

COASY	5.29E+02	5.33E-06	1.40E-05	7.50E-01	-4.15E-01	-1.33E+00	2.41E+01	3.22E+01
COL18A1	1.35E+04	1.62E-03	2.00E-03	7.02E-01	-5.11E-01	-1.43E+00	5.94E+02	8.46E+02
COL23A1	1.28E+02	5.04E-06	1.34E-05	3.40E-01	-1.56E+00	-2.94E+00	3.61E+00	1.06E+01
COL26A1	1.91E+03	2.30E-07	1.22E-06	1.97E-01	-2.34E+00	-5.08E+00	3.50E+01	1.78E+02
COMMD1	8.32E+02	1.28E-03	1.61E-03	7.93E-01	-3.34E-01	-1.26E+00	3.91E+01	4.93E+01
COMMD3	7.92E+02	6.14E-06	1.57E-05	7.37E-01	-4.40E-01	-1.36E+00	3.58E+01	4.86E+01
COMMD5	5.31E+02	6.57E-05	1.19E-04	8.16E-01	-2.94E-01	-1.23E+00	2.53E+01	3.10E+01
COMMD9	6.90E+02	8.00E-06	1.97E-05	7.40E-01	-4.35E-01	-1.35E+00	3.12E+01	4.22E+01
COPE	2.12E+03	6.39E-06	1.64E-05	7.39E-01	-4.36E-01	-1.35E+00	9.59E+01	1.30E+02
COPS4	1.02E+03	1.32E-03	1.65E-03	8.72E-01	-1.97E-01	-1.15E+00	5.05E+01	5.78E+01
COPS5	6.91E+02	7.84E-06	1.94E-05	7.52E-01	-4.10E-01	-1.33E+00	3.17E+01	4.22E+01
COQ5	2.35E+02	1.02E-02	1.09E-02	8.61E-01	-2.16E-01	-1.16E+00	1.15E+01	1.33E+01
COQ8B	2.73E+02	2.88E-05	5.76E-05	7.70E-01	-3.76E-01	-1.30E+00	1.26E+01	1.64E+01
COTL1	2.79E+03	4.96E-07	2.17E-06	6.31E-01	-6.64E-01	-1.58E+00	1.16E+02	1.84E+02
COX1	2.30E+05	2.23E-03	2.68E-03	6.55E-01	-6.10E-01	-1.53E+00	9.70E+03	1.48E+04
COX19	1.28E+03	1.13E-05	2.62E-05	7.88E-01	-3.43E-01	-1.27E+00	6.01E+01	7.62E+01
COX2	2.40E+04	2.12E-04	3.27E-04	6.06E-01	-7.23E-01	-1.65E+00	9.74E+02	1.61E+03
COX3	9.42E+04	4.98E-04	6.90E-04	6.37E-01	-6.50E-01	-1.57E+00	3.91E+03	6.13E+03
COX4I1	4.35E+03	6.13E-04	8.28E-04	7.92E-01	-3.36E-01	-1.26E+00	2.05E+02	2.58E+02
COX6B1	1.60E+03	3.71E-06	1.05E-05	6.46E-01	-6.30E-01	-1.55E+00	6.72E+01	1.04E+02
COX7B	6.41E+02	6.35E-05	1.16E-04	6.93E-01	-5.29E-01	-1.44E+00	2.80E+01	4.04E+01
COX8A	1.47E+03	1.35E-07	8.42E-07	6.70E-01	-5.77E-01	-1.49E+00	6.34E+01	9.46E+01
CPAMD8	1.12E+03	8.57E-07	3.26E-06	2.87E-01	-1.80E+00	-3.48E+00	2.75E+01	9.58E+01
CPLX3	4.13E+01	4.87E-03	5.47E-03	1.42E-01	-2.81E+00	-7.02E+00	5.90E-01	4.14E+00
CRABP2	5.33E+02	3.86E-04	5.51E-04	4.59E-01	-1.12E+00	-2.18E+00	1.85E+01	4.03E+01
CREB3	5.97E+02	7.03E-04	9.36E-04	8.28E-01	-2.73E-01	-1.21E+00	2.87E+01	3.46E+01
CRLF1	2.78E+02	2.00E-07	1.10E-06	5.14E-02	-4.28E+00	-1.95E+01	1.61E+00	3.13E+01
CRMP1	8.17E+02	8.97E-08	6.22E-07	3.92E-01	-1.35E+00	-2.55E+00	2.54E+01	6.49E+01
CRTAC1	9.47E+01	2.35E-06	7.09E-06	1.53E-01	-2.71E+00	-6.54E+00	1.39E+00	9.10E+00
CS	1.52E+03	1.07E-04	1.80E-04	7.90E-01	-3.41E-01	-1.27E+00	7.12E+01	9.02E+01
CSKMT	2.50E+02	1.24E-03	1.57E-03	4.74E-01	-1.08E+00	-2.11E+00	8.86E+00	1.87E+01
CSNK1G2	2.66E+03	7.89E-04	1.04E-03	7.40E-01	-4.34E-01	-1.35E+00	1.21E+02	1.63E+02
CSRNP1	3.27E+02	1.34E-06	4.55E-06	5.14E-01	-9.62E-01	-1.95E+00	1.21E+01	2.35E+01

CSTF2T	1.38E+03	4.10E-09	6.70E-08	6.27E-01	-6.74E-01	-1.60E+00	5.68E+01	9.07E+01
CT55	3.86E+01	5.55E-07	2.39E-06	1.19E-02	-6.39E+00	-8.40E+01	5.29E-02	4.44E+00
CTBP1	3.46E+03	3.82E-07	1.78E-06	7.61E-01	-3.94E-01	-1.31E+00	1.59E+02	2.09E+02
CTRC	1.82E+00	6.59E-02	6.65E-02	1.74E-01	-2.52E+00	-5.75E+00	2.98E-02	1.71E-01
CTSD	8.87E+03	3.90E-07	1.81E-06	6.14E-01	-7.04E-01	-1.63E+00	3.64E+02	5.92E+02
CTSV	2.32E+03	1.66E-07	9.57E-07	6.14E-01	-7.04E-01	-1.63E+00	9.54E+01	1.55E+02
CUTA	8.99E+02	1.20E-06	4.23E-06	6.68E-01	-5.83E-01	-1.50E+00	3.84E+01	5.76E+01
CXXC1	1.90E+03	2.88E-04	4.25E-04	8.59E-01	-2.19E-01	-1.16E+00	9.30E+01	1.08E+02
CYB561	1.55E+02	4.37E-02	4.46E-02	6.19E-01	-6.93E-01	-1.62E+00	6.19E+00	1.00E+01
CYB561A3	7.20E+02	1.72E-05	3.72E-05	6.41E-01	-6.41E-01	-1.56E+00	3.00E+01	4.69E+01
CYC1	1.26E+03	1.36E-07	8.43E-07	5.89E-01	-7.65E-01	-1.70E+00	5.02E+01	8.53E+01
CYP2S1	1.37E+02	5.62E-06	1.47E-05	1.39E-01	-2.85E+00	-7.20E+00	1.96E+00	1.41E+01
CYP4F2	4.02E+02	8.16E-06	2.00E-05	3.14E-01	-1.67E+00	-3.18E+00	1.05E+01	3.36E+01
CYTB	5.81E+04	7.14E-04	9.49E-04	6.58E-01	-6.03E-01	-1.52E+00	2.47E+03	3.75E+03
D2HGDH	7.05E+02	1.25E-06	4.37E-06	6.84E-01	-5.48E-01	-1.46E+00	3.06E+01	4.47E+01
DAD1	1.51E+03	5.23E-06	1.38E-05	7.26E-01	-4.62E-01	-1.38E+00	6.75E+01	9.30E+01
DBN1	4.18E+03	7.46E-10	2.43E-08	5.56E-01	-8.46E-01	-1.80E+00	1.62E+02	2.90E+02
DBNL	2.99E+03	2.99E-06	8.66E-06	7.89E-01	-3.42E-01	-1.27E+00	1.40E+02	1.78E+02
DCAF12L2	1.71E+02	1.56E-11	1.78E-09	4.05E-02	-4.62E+00	-2.47E+01	7.69E-01	1.90E+01
DDAH2	1.98E+03	7.03E-04	9.36E-04	7.62E-01	-3.93E-01	-1.31E+00	9.15E+01	1.20E+02
DDIT4	2.31E+03	8.52E-08	5.96E-07	3.96E-01	-1.34E+00	-2.53E+00	7.26E+01	1.83E+02
DDOST	4.43E+03	1.03E-06	3.75E-06	7.38E-01	-4.38E-01	-1.35E+00	2.00E+02	2.72E+02
DDT	3.84E+02	5.16E-05	9.67E-05	5.29E-01	-9.18E-01	-1.89E+00	1.46E+01	2.76E+01
DDX11	9.77E+02	2.34E-06	7.08E-06	5.02E-01	-9.95E-01	-1.99E+00	3.53E+01	7.03E+01
DDX19B	6.46E+02	7.20E-03	7.88E-03	8.46E-01	-2.42E-01	-1.18E+00	3.13E+01	3.70E+01
DDX51	8.18E+02	2.78E-07	1.39E-06	5.77E-01	-7.93E-01	-1.73E+00	3.23E+01	5.60E+01
DDX54	1.91E+03	1.47E-06	4.92E-06	6.09E-01	-7.15E-01	-1.64E+00	7.80E+01	1.28E+02
DECR2	4.24E+02	1.16E-07	7.49E-07	6.88E-01	-5.40E-01	-1.45E+00	1.84E+01	2.68E+01
DEF6	2.51E+02	3.51E-06	9.99E-06	5.08E-01	-9.76E-01	-1.97E+00	9.15E+00	1.80E+01
DEGS1	1.31E+03	1.63E-04	2.61E-04	8.13E-01	-2.99E-01	-1.23E+00	6.20E+01	7.63E+01
DEGS2	3.14E+01	7.81E-04	1.03E-03	4.37E-01	-1.19E+00	-2.29E+00	1.06E+00	2.41E+00
DENND1A	1.92E+03	1.10E-02	1.18E-02	8.11E-01	-3.02E-01	-1.23E+00	9.13E+01	1.12E+02
DENND3	3.73E+02	2.84E-02	2.93E-02	7.82E-01	-3.54E-01	-1.28E+00	1.73E+01	2.21E+01

DEUP1	2.83E+01	9.40E-04	1.21E-03	3.89E-01	-1.36E+00	-2.57E+00	8.43E-01	2.17E+00
DEXI	4.76E+02	8.40E-04	1.09E-03	8.02E-01	-3.18E-01	-1.25E+00	2.26E+01	2.81E+01
DGAT1	1.35E+03	1.70E-07	9.77E-07	6.08E-01	-7.18E-01	-1.65E+00	5.49E+01	9.03E+01
DGCR6L	1.11E+03	2.21E-05	4.59E-05	7.25E-01	-4.63E-01	-1.38E+00	4.97E+01	6.85E+01
DGKA	9.50E+02	6.48E-03	7.13E-03	8.37E-01	-2.57E-01	-1.20E+00	4.59E+01	5.49E+01
DGKQ	4.39E+02	1.16E-06	4.12E-06	5.70E-01	-8.11E-01	-1.75E+00	1.72E+01	3.01E+01
DGUOK	4.90E+02	2.17E-05	4.53E-05	7.73E-01	-3.71E-01	-1.29E+00	2.27E+01	2.94E+01
DHDH	1.76E+02	2.80E-06	8.26E-06	5.72E-01	-8.05E-01	-1.75E+00	6.92E+00	1.21E+01
DHRS11	7.60E+02	2.08E-09	4.39E-08	5.97E-01	-7.44E-01	-1.67E+00	3.08E+01	5.16E+01
DISP3	8.49E+01	5.33E-06	1.40E-05	1.29E-01	-2.95E+00	-7.74E+00	1.14E+00	8.84E+00
DKKL1	4.44E+02	4.12E-09	6.70E-08	4.06E-01	-1.30E+00	-2.46E+00	1.40E+01	3.44E+01
DLGAP4	3.68E+03	1.30E-05	2.93E-05	7.04E-01	-5.06E-01	-1.42E+00	1.62E+02	2.30E+02
DMTN	2.59E+02	9.98E-08	6.75E-07	3.82E-01	-1.39E+00	-2.62E+00	7.81E+00	2.05E+01
DNAI2	8.71E+02	2.33E-04	3.53E-04	5.15E-01	-9.57E-01	-1.94E+00	3.17E+01	6.15E+01
DNAJC19	1.37E+02	5.70E-07	2.42E-06	5.68E-01	-8.16E-01	-1.76E+00	5.37E+00	9.45E+00
DNAL4	4.04E+02	3.25E-04	4.72E-04	7.08E-01	-4.97E-01	-1.41E+00	1.80E+01	2.54E+01
DOC2A	5.07E+01	4.24E-09	6.76E-08	2.29E-01	-2.13E+00	-4.37E+00	1.06E+00	4.65E+00
DOCK6	1.69E+03	3.84E-07	1.79E-06	4.80E-01	-1.06E+00	-2.08E+00	6.04E+01	1.26E+02
DOHH	2.54E+02	3.77E-04	5.39E-04	7.85E-01	-3.48E-01	-1.27E+00	1.19E+01	1.51E+01
DOK4	9.38E+02	2.07E-06	6.41E-06	3.99E-01	-1.32E+00	-2.50E+00	2.97E+01	7.43E+01
DOLK	4.16E+02	1.00E-07	6.75E-07	6.71E-01	-5.75E-01	-1.49E+00	1.78E+01	2.66E+01
DPEP1	2.56E+02	2.43E-08	2.23E-07	1.78E-01	-2.49E+00	-5.61E+00	4.38E+00	2.45E+01
DPH7	4.71E+02	1.68E-04	2.68E-04	7.96E-01	-3.28E-01	-1.26E+00	2.22E+01	2.79E+01
DPP3	4.95E+02	4.77E-03	5.38E-03	7.92E-01	-3.37E-01	-1.26E+00	2.32E+01	2.94E+01
DPY30	6.05E+02	1.83E-05	3.92E-05	7.28E-01	-4.57E-01	-1.37E+00	2.72E+01	3.73E+01
DPYSL5	3.74E+02	7.24E-11	5.30E-09	8.60E-02	-3.54E+00	-1.16E+01	3.41E+00	3.96E+01
DSCAM	1.48E+01	4.10E-07	1.88E-06	9.59E-02	-3.38E+00	-1.04E+01	1.49E-01	1.55E+00
DSG2	4.95E+02	3.50E-04	5.05E-04	4.22E-01	-1.24E+00	-2.37E+00	1.61E+01	3.81E+01
DTD1	1.27E+03	1.71E-04	2.72E-04	8.14E-01	-2.97E-01	-1.23E+00	6.06E+01	7.45E+01
DTL	3.55E+02	1.84E-04	2.90E-04	6.72E-01	-5.74E-01	-1.49E+00	1.53E+01	2.28E+01
DUS2	1.60E+02	3.47E-05	6.82E-05	6.62E-01	-5.95E-01	-1.51E+00	6.73E+00	1.02E+01
DUS3L	5.86E+02	3.58E-06	1.01E-05	7.00E-01	-5.15E-01	-1.43E+00	2.58E+01	3.68E+01
DUSP15	3.85E+02	1.49E-04	2.40E-04	7.02E-01	-5.11E-01	-1.42E+00	1.69E+01	2.41E+01

DUSP26	2.93E+02	4.94E-04	6.86E-04	5.74E-01	-8.01E-01	-1.74E+00	1.16E+01	2.03E+01
DUSP4	7.71E+01	7.39E-04	9.77E-04	4.77E-01	-1.07E+00	-2.10E+00	2.74E+00	5.73E+00
DUT	9.42E+02	6.73E-06	1.71E-05	5.47E-01	-8.70E-01	-1.83E+00	3.61E+01	6.60E+01
DYRK1B	1.21E+03	6.64E-07	2.68E-06	7.01E-01	-5.13E-01	-1.43E+00	5.34E+01	7.62E+01
E2F8	1.18E+02	2.98E-05	5.94E-05	4.81E-01	-1.06E+00	-2.08E+00	4.17E+00	8.68E+00
EBP	2.51E+02	1.65E-02	1.74E-02	7.81E-01	-3.56E-01	-1.28E+00	1.18E+01	1.50E+01
ECI1	7.06E+02	4.45E-04	6.25E-04	7.15E-01	-4.84E-01	-1.40E+00	3.15E+01	4.40E+01
EDAR	5.68E+01	2.24E-05	4.66E-05	4.66E-01	-1.10E+00	-2.15E+00	1.97E+00	4.22E+00
EDF1	2.19E+03	9.22E-05	1.59E-04	7.43E-01	-4.29E-01	-1.35E+00	9.93E+01	1.34E+02
EEF1A2	2.93E+02	2.27E-08	2.15E-07	7.20E-02	-3.80E+00	-1.39E+01	2.23E+00	3.09E+01
EFCAB11	1.45E+02	1.49E-04	2.41E-04	6.02E-01	-7.33E-01	-1.66E+00	5.77E+00	9.59E+00
EFNA4	3.39E+02	3.98E-10	1.48E-08	3.75E-01	-1.42E+00	-2.67E+00	1.02E+01	2.72E+01
EFNB3	1.03E+03	5.19E-04	7.15E-04	6.88E-01	-5.39E-01	-1.45E+00	4.50E+01	6.54E+01
EFS	1.97E+03	4.94E-04	6.86E-04	6.85E-01	-5.45E-01	-1.46E+00	8.60E+01	1.25E+02
EGLN2	7.69E+02	1.22E-06	4.30E-06	6.58E-01	-6.03E-01	-1.52E+00	3.26E+01	4.95E+01
EHMT2	5.34E+03	1.82E-05	3.92E-05	7.04E-01	-5.05E-01	-1.42E+00	2.35E+02	3.34E+02
EID2	1.49E+02	9.06E-05	1.57E-04	7.31E-01	-4.52E-01	-1.37E+00	6.71E+00	9.18E+00
EIF1	3.64E+03	1.16E-03	1.47E-03	8.11E-01	-3.02E-01	-1.23E+00	1.74E+02	2.14E+02
EIF3D	5.53E+03	2.04E-03	2.47E-03	8.60E-01	-2.18E-01	-1.16E+00	2.71E+02	3.15E+02
EIF3I	2.10E+03	1.78E-05	3.84E-05	7.14E-01	-4.86E-01	-1.40E+00	9.32E+01	1.31E+02
EIF3M	6.22E+03	2.18E-04	3.34E-04	7.77E-01	-3.63E-01	-1.29E+00	2.90E+02	3.73E+02
EIF4A1	6.41E+03	1.54E-05	3.38E-05	6.40E-01	-6.44E-01	-1.56E+00	2.70E+02	4.22E+02
ELOB	1.32E+03	5.24E-09	7.66E-08	5.42E-01	-8.84E-01	-1.85E+00	5.01E+01	9.24E+01
EMC4	7.34E+02	8.80E-07	3.31E-06	7.39E-01	-4.36E-01	-1.35E+00	3.32E+01	4.48E+01
EMC6	3.66E+02	4.93E-07	2.17E-06	6.22E-01	-6.85E-01	-1.61E+00	1.51E+01	2.43E+01
EMG1	4.39E+02	6.05E-07	2.52E-06	5.79E-01	-7.89E-01	-1.73E+00	1.73E+01	2.99E+01
EMILIN3	6.27E+02	2.23E-04	3.41E-04	4.85E-01	-1.04E+00	-2.06E+00	2.23E+01	4.59E+01
ENDOU	1.14E+01	6.10E-03	6.73E-03	3.96E-01	-1.34E+00	-2.52E+00	3.62E-01	9.13E-01
ENO1	9.88E+03	3.05E-04	4.46E-04	6.65E-01	-5.89E-01	-1.50E+00	4.28E+02	6.43E+02
ENOX1	3.25E+02	3.92E-04	5.58E-04	6.87E-01	-5.42E-01	-1.46E+00	1.42E+01	2.07E+01
EPHA1	1.57E+02	5.94E-06	1.55E-05	4.62E-01	-1.11E+00	-2.16E+00	5.44E+00	1.18E+01
EPHA2	1.12E+03	1.06E-05	2.47E-05	7.08E-01	-4.98E-01	-1.41E+00	4.97E+01	7.02E+01
EPHB4	2.31E+03	5.27E-11	4.67E-09	6.21E-01	-6.86E-01	-1.61E+00	9.55E+01	1.54E+02

EPHX2	1.27E+03	8.88E-04	1.15E-03	6.88E-01	-5.41E-01	-1.45E+00	5.56E+01	8.08E+01
EPO	1.08E+01	2.07E-05	4.36E-05	2.80E-01	-1.84E+00	-3.57E+00	2.62E-01	9.38E-01
EPOR	1.70E+02	5.68E-07	2.42E-06	4.29E-01	-1.22E+00	-2.33E+00	5.54E+00	1.29E+01
ERF	1.42E+03	1.47E-10	7.92E-09	5.37E-01	-8.97E-01	-1.86E+00	5.40E+01	1.01E+02
ERI3	9.01E+02	1.57E-05	3.44E-05	8.35E-01	-2.60E-01	-1.20E+00	4.36E+01	5.22E+01
ERICH2	4.59E+01	2.37E-03	2.83E-03	3.96E-01	-1.34E+00	-2.53E+00	1.38E+00	3.48E+00
ESPN	4.31E+02	3.91E-09	6.58E-08	2.40E-01	-2.06E+00	-4.17E+00	9.28E+00	3.86E+01
ESRRA	3.80E+02	1.19E-09	3.02E-08	4.85E-01	-1.04E+00	-2.06E+00	1.35E+01	2.79E+01
ESRRB	3.15E+01	8.93E-06	2.16E-05	1.31E-02	-6.26E+00	-7.66E+01	4.84E-02	3.71E+00
ETFA	1.00E+03	1.11E-09	2.99E-08	5.35E-01	-9.02E-01	-1.87E+00	3.80E+01	7.10E+01
ETFB	1.87E+03	2.52E-07	1.30E-06	6.33E-01	-6.60E-01	-1.58E+00	7.79E+01	1.23E+02
ETNK2	7.92E+03	4.61E-08	3.72E-07	4.73E-01	-1.08E+00	-2.11E+00	2.76E+02	5.84E+02
ETV4	5.84E+02	7.11E-11	5.30E-09	8.11E-02	-3.62E+00	-1.23E+01	5.13E+00	6.32E+01
EVA1A	5.59E+01	2.90E-03	3.41E-03	7.00E-01	-5.15E-01	-1.43E+00	2.46E+00	3.51E+00
EVL	6.12E+03	1.00E-09	2.86E-08	6.39E-01	-6.45E-01	-1.56E+00	2.57E+02	4.02E+02
EVX1	6.73E+01	6.61E-04	8.87E-04	4.08E-02	-4.62E+00	-2.45E+01	3.06E-01	7.51E+00
EXO5	1.55E+02	2.23E-03	2.68E-03	8.03E-01	-3.17E-01	-1.25E+00	7.37E+00	9.19E+00
EXOC3L1	8.13E+02	4.58E-07	2.05E-06	4.56E-01	-1.13E+00	-2.19E+00	2.78E+01	6.10E+01
EXOC7	1.77E+03	3.53E-04	5.08E-04	8.42E-01	-2.47E-01	-1.19E+00	8.55E+01	1.02E+02
EXOSC4	4.79E+02	5.29E-06	1.39E-05	7.13E-01	-4.88E-01	-1.40E+00	2.13E+01	2.98E+01
EXOSC5	2.11E+02	2.76E-05	5.57E-05	5.97E-01	-7.44E-01	-1.67E+00	8.48E+00	1.42E+01
EXOSC6	3.70E+02	7.34E-04	9.71E-04	7.52E-01	-4.10E-01	-1.33E+00	1.70E+01	2.27E+01
EXTL1	1.99E+02	4.50E-07	2.02E-06	2.72E-01	-1.88E+00	-3.68E+00	4.72E+00	1.74E+01
F11	1.65E+01	5.81E-04	7.90E-04	3.93E-01	-1.35E+00	-2.55E+00	5.17E-01	1.31E+00
F11R	1.96E+03	3.55E-10	1.40E-08	4.71E-01	-1.09E+00	-2.12E+00	6.86E+01	1.46E+02
FAAP100	5.99E+02	5.87E-10	2.01E-08	6.03E-01	-7.31E-01	-1.66E+00	2.42E+01	4.02E+01
FAAP20	4.51E+02	6.61E-08	4.88E-07	6.59E-01	-6.02E-01	-1.52E+00	1.92E+01	2.91E+01
FABP7	2.59E+02	1.26E-07	7.96E-07	3.11E-01	-1.69E+00	-3.22E+00	6.94E+00	2.23E+01
FADD	4.13E+02	1.87E-02	1.96E-02	8.40E-01	-2.51E-01	-1.19E+00	2.00E+01	2.38E+01
FAIM	1.98E+02	2.30E-05	4.76E-05	7.28E-01	-4.59E-01	-1.37E+00	8.85E+00	1.22E+01
FAM107B	5.42E+02	5.76E-04	7.84E-04	7.09E-01	-4.96E-01	-1.41E+00	2.41E+01	3.40E+01
FAM110A	1.29E+02	5.04E-03	5.65E-03	7.64E-01	-3.88E-01	-1.31E+00	6.01E+00	7.86E+00
FAM131B	2.78E+01	2.72E-06	8.04E-06	3.98E-01	-1.33E+00	-2.51E+00	8.71E-01	2.19E+00

FAM19A5	2.96E+01	2.48E-08	2.27E-07	1.63E-01	-2.62E+00	-6.13E+00	4.66E-01	2.85E+00
FAM212A	3.18E+02	2.40E-03	2.87E-03	7.52E-01	-4.11E-01	-1.33E+00	1.46E+01	1.94E+01
FAM214B	5.65E+02	5.93E-06	1.55E-05	6.53E-01	-6.15E-01	-1.53E+00	2.39E+01	3.66E+01
FAM217A	4.53E+01	1.34E-05	3.00E-05	2.08E-01	-2.27E+00	-4.82E+00	8.72E-01	4.20E+00
FAM227A	2.53E+01	6.55E-04	8.80E-04	3.56E-01	-1.49E+00	-2.81E+00	7.22E-01	2.03E+00
FAM241B	3.72E+02	4.43E-10	1.62E-08	6.26E-01	-6.76E-01	-1.60E+00	1.54E+01	2.46E+01
FAM47E	2.00E+02	9.51E-03	1.03E-02	7.30E-01	-4.54E-01	-1.37E+00	9.04E+00	1.24E+01
FAM53A	1.39E+01	1.64E-06	5.33E-06	2.41E-01	-2.05E+00	-4.15E+00	3.02E-01	1.25E+00
FAM53B	1.91E+03	2.42E-05	4.98E-05	6.64E-01	-5.91E-01	-1.51E+00	8.24E+01	1.24E+02
FAM57A	6.16E+02	3.08E-04	4.51E-04	7.72E-01	-3.73E-01	-1.29E+00	2.86E+01	3.70E+01
FAM71F1	6.28E+00	1.66E-05	3.61E-05	2.02E-01	-2.31E+00	-4.95E+00	1.21E-01	5.96E-01
FAM89B	7.43E+02	2.46E-04	3.71E-04	8.16E-01	-2.93E-01	-1.23E+00	3.54E+01	4.34E+01
FAR2	1.56E+02	2.00E-05	4.22E-05	5.48E-01	-8.69E-01	-1.83E+00	5.98E+00	1.09E+01
FARS2	4.78E+02	4.51E-06	1.23E-05	7.44E-01	-4.27E-01	-1.34E+00	2.18E+01	2.93E+01
FASLG	2.75E+02	1.77E-07	1.01E-06	2.03E-01	-2.30E+00	-4.93E+00	5.23E+00	2.58E+01
FASN	7.56E+03	8.05E-05	1.42E-04	6.12E-01	-7.08E-01	-1.63E+00	3.09E+02	5.05E+02
FASTK	1.10E+03	2.31E-08	2.17E-07	7.19E-01	-4.76E-01	-1.39E+00	4.91E+01	6.83E+01
FBLN2	4.92E+03	1.11E-08	1.25E-07	2.31E-01	-2.12E+00	-4.34E+00	1.04E+02	4.50E+02
FBN3	6.42E+03	3.11E-07	1.52E-06	2.36E-01	-2.09E+00	-4.25E+00	1.37E+02	5.81E+02
FBXL15	2.45E+02	1.24E-05	2.84E-05	7.39E-01	-4.36E-01	-1.35E+00	1.11E+01	1.50E+01
FBXL19	1.16E+03	1.44E-06	4.80E-06	5.99E-01	-7.39E-01	-1.67E+00	4.69E+01	7.83E+01
FBXL21	9.91E+01	3.89E-04	5.55E-04	6.42E-01	-6.40E-01	-1.56E+00	4.16E+00	6.48E+00
FBXL8	2.41E+02	1.21E-02	1.28E-02	8.18E-01	-2.91E-01	-1.22E+00	1.15E+01	1.40E+01
FCRL3	3.28E+00	5.67E-03	6.29E-03	1.61E-01	-2.64E+00	-6.21E+00	5.06E-02	3.14E-01
FDXR	1.33E+03	8.14E-03	8.85E-03	6.90E-01	-5.35E-01	-1.45E+00	5.85E+01	8.48E+01
FEM1A	2.20E+03	1.35E-08	1.44E-07	7.23E-01	-4.68E-01	-1.38E+00	9.85E+01	1.36E+02
FETUB	4.35E+00	1.94E-04	3.03E-04	2.75E-01	-1.86E+00	-3.64E+00	1.04E-01	3.76E-01
FEZ1	5.51E+02	2.91E-04	4.28E-04	6.38E-01	-6.48E-01	-1.57E+00	2.32E+01	3.63E+01
FGD1	1.56E+03	1.27E-07	8.01E-07	6.52E-01	-6.17E-01	-1.53E+00	6.60E+01	1.01E+02
FGF11	1.89E+03	4.23E-04	5.99E-04	5.52E-01	-8.58E-01	-1.81E+00	7.21E+01	1.31E+02
FGF19	1.07E+02	7.90E-11	5.43E-09	1.07E-02	-6.55E+00	-9.36E+01	1.33E-01	1.25E+01
FGFR3	4.79E+02	2.72E-11	2.79E-09	9.90E-02	-3.34E+00	-1.01E+01	4.97E+00	5.02E+01
FGL1	1.24E+02	2.21E-05	4.61E-05	4.77E-01	-1.07E+00	-2.10E+00	4.32E+00	9.06E+00

FH	1.06E+03	6.37E-09	8.58E-08	7.09E-01	-4.95E-01	-1.41E+00	4.71E+01	6.64E+01
FITM1	8.87E+01	1.11E-04	1.86E-04	6.66E-01	-5.86E-01	-1.50E+00	3.78E+00	5.68E+00
FMNL1	3.45E+02	5.92E-03	6.55E-03	8.07E-01	-3.10E-01	-1.24E+00	1.64E+01	2.03E+01
FOLR1	1.36E+01	2.62E-04	3.93E-04	6.26E-02	-4.00E+00	-1.60E+01	9.35E-02	1.50E+00
FOXH1	4.74E+01	2.20E-08	2.10E-07	4.28E-02	-4.55E+00	-2.34E+01	2.30E-01	5.37E+00
FOXO6	4.32E+02	6.88E-08	5.04E-07	3.33E-01	-1.59E+00	-3.01E+00	1.20E+01	3.60E+01
FPGS	7.17E+02	4.55E-09	7.02E-08	6.23E-01	-6.83E-01	-1.61E+00	2.97E+01	4.77E+01
FRAT2	2.62E+02	1.62E-08	1.67E-07	4.51E-01	-1.15E+00	-2.22E+00	8.96E+00	1.99E+01
FRMD8	6.51E+02	1.34E-03	1.67E-03	8.19E-01	-2.89E-01	-1.22E+00	3.12E+01	3.81E+01
FSCN1	7.51E+03	1.32E-05	2.97E-05	7.14E-01	-4.86E-01	-1.40E+00	3.34E+02	4.68E+02
FTH1	2.39E+04	1.14E-06	4.05E-06	7.41E-01	-4.32E-01	-1.35E+00	1.09E+03	1.47E+03
FUS	9.65E+03	3.06E-08	2.71E-07	7.01E-01	-5.12E-01	-1.43E+00	4.26E+02	6.07E+02
FUT2	1.46E+01	7.84E-04	1.03E-03	6.92E-02	-3.85E+00	-1.44E+01	1.07E-01	1.54E+00
FUZ	3.68E+02	5.59E-07	2.39E-06	5.76E-01	-7.95E-01	-1.73E+00	1.45E+01	2.51E+01
FXN	6.22E+02	4.76E-08	3.79E-07	6.67E-01	-5.84E-01	-1.50E+00	2.67E+01	4.01E+01
FZD10	2.50E+02	1.03E-05	2.42E-05	3.48E-01	-1.52E+00	-2.88E+00	7.16E+00	2.06E+01
FZD2	1.08E+03	1.45E-03	1.80E-03	5.69E-01	-8.14E-01	-1.76E+00	4.23E+01	7.44E+01
G6PC3	1.02E+03	9.15E-09	1.11E-07	6.87E-01	-5.41E-01	-1.46E+00	4.46E+01	6.49E+01
G6PD	4.05E+03	6.44E-08	4.83E-07	4.97E-01	-1.01E+00	-2.01E+00	1.45E+02	2.92E+02
GADL1	1.01E+01	2.65E-05	5.37E-05	2.77E-01	-1.85E+00	-3.60E+00	2.34E-01	8.42E-01
GAL3ST2	1.13E+01	9.05E-06	2.19E-05	2.24E-01	-2.16E+00	-4.46E+00	2.30E-01	1.03E+00
GALE	2.74E+02	1.32E-08	1.42E-07	5.68E-01	-8.15E-01	-1.76E+00	1.08E+01	1.89E+01
GALM	5.04E+02	4.40E-04	6.20E-04	8.02E-01	-3.18E-01	-1.25E+00	2.39E+01	2.98E+01
GALNT16	5.70E+02	1.22E-04	2.02E-04	5.99E-01	-7.39E-01	-1.67E+00	2.31E+01	3.86E+01
GALT	5.40E+02	1.03E-08	1.19E-07	5.94E-01	-7.51E-01	-1.68E+00	2.16E+01	3.64E+01
GAP43	1.08E+02	3.29E-03	3.82E-03	3.41E-01	-1.55E+00	-2.93E+00	3.10E+00	9.10E+00
GAPDH	1.55E+04	2.46E-06	7.38E-06	6.56E-01	-6.09E-01	-1.53E+00	6.62E+02	1.01E+03
GAREM1	4.11E+02	2.26E-05	4.70E-05	6.71E-01	-5.76E-01	-1.49E+00	1.77E+01	2.64E+01
GARS	1.20E+03	2.87E-09	5.34E-08	4.93E-01	-1.02E+00	-2.03E+00	4.33E+01	8.80E+01
GAS2L1	9.08E+02	7.98E-04	1.05E-03	7.68E-01	-3.81E-01	-1.30E+00	4.20E+01	5.47E+01
GATA3	1.19E+02	5.04E-10	1.78E-08	1.78E-01	-2.49E+00	-5.63E+00	2.03E+00	1.14E+01
GATA4	7.35E+03	2.85E-09	5.34E-08	5.28E-01	-9.23E-01	-1.90E+00	2.75E+02	5.22E+02
GATD1	7.07E+02	1.23E-03	1.56E-03	7.84E-01	-3.51E-01	-1.28E+00	3.33E+01	4.24E+01

GATD3A	8.98E+02	1.11E-05	2.56E-05	7.29E-01	-4.56E-01	-1.37E+00	4.04E+01	5.54E+01
GCAT	3.39E+02	2.76E-05	5.56E-05	6.30E-01	-6.66E-01	-1.59E+00	1.41E+01	2.24E+01
GCDH	9.78E+02	1.24E-06	4.33E-06	7.29E-01	-4.55E-01	-1.37E+00	4.41E+01	6.04E+01
GCHFR	1.29E+02	1.81E-02	1.90E-02	7.38E-01	-4.38E-01	-1.36E+00	5.86E+00	7.95E+00
GDAP1L1	1.70E+02	6.45E-08	4.83E-07	3.22E-01	-1.63E+00	-3.10E+00	4.58E+00	1.42E+01
GDPD2	8.52E+01	9.90E-06	2.35E-05	2.73E-01	-1.87E+00	-3.66E+00	2.05E+00	7.49E+00
GDPD5	3.95E+02	1.22E-05	2.80E-05	3.91E-01	-1.36E+00	-2.56E+00	1.22E+01	3.13E+01
GDPGP1	1.71E+02	1.72E-04	2.74E-04	7.30E-01	-4.53E-01	-1.37E+00	7.76E+00	1.06E+01
GEMIN7	1.80E+02	1.36E-08	1.45E-07	5.05E-01	-9.85E-01	-1.98E+00	6.58E+00	1.30E+01
GFER	5.20E+02	1.34E-06	4.55E-06	6.31E-01	-6.65E-01	-1.59E+00	2.16E+01	3.43E+01
GFRA1	2.83E+02	2.26E-07	1.21E-06	3.82E-01	-1.39E+00	-2.62E+00	8.65E+00	2.26E+01
GINS3	2.39E+02	1.72E-04	2.74E-04	7.65E-01	-3.87E-01	-1.31E+00	1.11E+01	1.45E+01
GJB1	2.85E+01	3.38E-03	3.91E-03	4.36E-01	-1.20E+00	-2.30E+00	9.27E-01	2.13E+00
GLDC	8.52E+02	2.93E-05	5.83E-05	4.61E-01	-1.12E+00	-2.17E+00	2.92E+01	6.34E+01
GLOD4	9.54E+02	5.53E-06	1.45E-05	8.02E-01	-3.19E-01	-1.25E+00	4.52E+01	5.64E+01
GLRX5	8.93E+02	1.62E-03	1.99E-03	7.76E-01	-3.65E-01	-1.29E+00	4.17E+01	5.37E+01
GLYATL3	4.25E+01	5.79E-07	2.45E-06	1.67E-01	-2.58E+00	-5.97E+00	7.00E-01	4.18E+00
GMDS	7.25E+02	1.38E-05	3.08E-05	7.40E-01	-4.33E-01	-1.35E+00	3.28E+01	4.43E+01
GNAI2	8.78E+03	5.49E-05	1.02E-04	8.21E-01	-2.84E-01	-1.22E+00	4.21E+02	5.13E+02
GNAT1	2.70E+02	3.40E-07	1.64E-06	4.06E-01	-1.30E+00	-2.46E+00	8.58E+00	2.11E+01
GNB1L	2.01E+03	1.84E-03	2.23E-03	7.87E-01	-3.45E-01	-1.27E+00	9.42E+01	1.20E+02
GNB2	4.44E+03	5.89E-05	1.08E-04	7.79E-01	-3.60E-01	-1.28E+00	2.08E+02	2.67E+02
GNG13	1.68E+01	7.16E-06	1.81E-05	1.95E-01	-2.36E+00	-5.12E+00	3.04E-01	1.56E+00
GNG3	5.73E+01	1.59E-07	9.36E-07	3.48E-01	-1.52E+00	-2.87E+00	1.63E+00	4.69E+00
GNG5	1.08E+03	2.36E-05	4.88E-05	7.26E-01	-4.62E-01	-1.38E+00	4.83E+01	6.65E+01
GNMT	1.35E+02	4.31E-07	1.96E-06	5.59E-01	-8.40E-01	-1.79E+00	5.23E+00	9.36E+00
GOT1	7.61E+02	1.10E-03	1.41E-03	6.73E-01	-5.71E-01	-1.49E+00	3.28E+01	4.88E+01
GOT2	2.51E+03	1.42E-03	1.78E-03	8.33E-01	-2.64E-01	-1.20E+00	1.21E+02	1.45E+02
GPANK1	1.42E+03	4.63E-05	8.83E-05	7.90E-01	-3.41E-01	-1.27E+00	6.67E+01	8.45E+01
GPC2	1.43E+02	6.09E-08	4.64E-07	2.36E-01	-2.08E+00	-4.23E+00	3.04E+00	1.29E+01
GPC3	2.90E+03	6.55E-07	2.66E-06	4.70E-01	-1.09E+00	-2.13E+00	1.01E+02	2.16E+02
GPR1	7.80E+01	3.38E-06	9.66E-06	1.71E-01	-2.55E+00	-5.85E+00	1.33E+00	7.81E+00
GPR108	8.46E+02	1.54E-04	2.48E-04	8.16E-01	-2.94E-01	-1.23E+00	4.01E+01	4.92E+01

GPR153	1.66E+03	2.14E-06	6.58E-06	6.40E-01	-6.44E-01	-1.56E+00	6.92E+01	1.08E+02
GPR162	2.52E+02	2.10E-06	6.49E-06	5.85E-01	-7.72E-01	-1.71E+00	9.99E+00	1.71E+01
GPR3	1.21E+01	2.20E-04	3.37E-04	4.33E-01	-1.21E+00	-2.31E+00	3.98E-01	9.20E-01
GPR45	8.30E+01	4.13E-04	5.86E-04	6.84E-01	-5.49E-01	-1.46E+00	3.61E+00	5.28E+00
GPR61	6.66E+00	1.32E-03	1.66E-03	3.74E-01	-1.42E+00	-2.68E+00	1.92E-01	5.14E-01
GPR85	1.16E+01	6.13E-02	6.19E-02	5.85E-01	-7.73E-01	-1.71E+00	4.71E-01	8.05E-01
GPSM1	6.86E+03	8.32E-06	2.03E-05	6.82E-01	-5.52E-01	-1.47E+00	2.98E+02	4.38E+02
GPT	3.58E+02	4.27E-04	6.04E-04	6.49E-01	-6.24E-01	-1.54E+00	1.51E+01	2.33E+01
GRAMD1A	1.95E+03	5.64E-07	2.41E-06	7.37E-01	-4.40E-01	-1.36E+00	8.89E+01	1.21E+02
GRAMD4	9.03E+02	2.53E-04	3.80E-04	7.57E-01	-4.03E-01	-1.32E+00	4.16E+01	5.50E+01
GRIK5	1.06E+03	4.77E-04	6.65E-04	7.90E-01	-3.40E-01	-1.27E+00	4.99E+01	6.31E+01
GRIN1	2.85E+01	3.22E-04	4.69E-04	4.89E-01	-1.03E+00	-2.04E+00	9.94E-01	2.03E+00
GRK2	1.44E+03	8.54E-05	1.49E-04	8.42E-01	-2.48E-01	-1.19E+00	6.98E+01	8.29E+01
GRN	2.55E+03	2.03E-06	6.33E-06	7.89E-01	-3.42E-01	-1.27E+00	1.20E+02	1.52E+02
GRPEL1	9.06E+02	1.41E-05	3.13E-05	6.94E-01	-5.28E-01	-1.44E+00	3.97E+01	5.73E+01
GSS	3.82E+02	5.28E-05	9.83E-05	6.98E-01	-5.18E-01	-1.43E+00	1.69E+01	2.42E+01
GSTA4	1.35E+03	1.82E-04	2.87E-04	6.85E-01	-5.45E-01	-1.46E+00	5.90E+01	8.60E+01
GSTP1	1.33E+01	6.55E-08	4.88E-07	1.96E-01	-2.35E+00	-5.10E+00	2.50E-01	1.28E+00
GSTP1-2	2.82E+03	1.04E-07	6.94E-07	5.93E-01	-7.54E-01	-1.69E+00	1.14E+02	1.92E+02
GSTT1	1.20E+03	3.76E-10	1.43E-08	5.65E-01	-8.23E-01	-1.77E+00	4.69E+01	8.29E+01
GSTZ1	4.30E+02	1.69E-08	1.72E-07	6.29E-01	-6.68E-01	-1.59E+00	1.78E+01	2.83E+01
GTF2F1	1.73E+03	2.96E-06	8.59E-06	7.52E-01	-4.10E-01	-1.33E+00	7.92E+01	1.05E+02
GTF2H4	3.20E+02	1.76E-07	1.01E-06	6.85E-01	-5.46E-01	-1.46E+00	1.39E+01	2.03E+01
GTF2H5	3.62E+02	3.49E-03	4.03E-03	8.13E-01	-2.99E-01	-1.23E+00	1.73E+01	2.13E+01
GTF2IRD1	4.00E+02	3.20E-07	1.55E-06	5.82E-01	-7.82E-01	-1.72E+00	1.58E+01	2.72E+01
GTF3C2	1.37E+03	1.42E-04	2.31E-04	8.40E-01	-2.51E-01	-1.19E+00	6.64E+01	7.90E+01
GTPBP3	8.99E+02	8.88E-07	3.32E-06	7.67E-01	-3.83E-01	-1.30E+00	4.15E+01	5.42E+01
GUCA2A	1.70E+01	4.44E-07	2.00E-06	5.88E-02	-4.09E+00	-1.70E+01	1.11E-01	1.89E+00
GUCD1	1.07E+03	6.67E-07	2.69E-06	6.63E-01	-5.94E-01	-1.51E+00	4.57E+01	6.90E+01
GUK1	1.84E+03	3.71E-06	1.05E-05	7.24E-01	-4.65E-01	-1.38E+00	8.25E+01	1.14E+02
GYS1	9.24E+02	2.92E-06	8.53E-06	7.30E-01	-4.53E-01	-1.37E+00	4.16E+01	5.69E+01
H1FX	6.39E+03	2.58E-05	5.25E-05	7.78E-01	-3.63E-01	-1.29E+00	2.98E+02	3.84E+02
H2AFX	6.96E+02	4.51E-03	5.10E-03	7.45E-01	-4.26E-01	-1.34E+00	3.19E+01	4.29E+01

H2AFY	3.21E+03	7.33E-06	1.84E-05	7.70E-01	-3.77E-01	-1.30E+00	1.49E+02	1.93E+02
H2AFY2	1.34E+03	2.04E-07	1.12E-06	4.70E-01	-1.09E+00	-2.13E+00	4.69E+01	9.97E+01
H2AFZ	8.70E+02	2.59E-04	3.89E-04	6.16E-01	-6.98E-01	-1.62E+00	3.57E+01	5.79E+01
H3F3A	8.42E+03	7.90E-09	9.76E-08	5.17E-01	-9.53E-01	-1.94E+00	3.11E+02	6.02E+02
H3F3C	1.57E+02	9.25E-06	2.22E-05	6.84E-01	-5.47E-01	-1.46E+00	6.80E+00	9.94E+00
H4	2.44E+01	9.33E-06	2.23E-05	4.55E-01	-1.14E+00	-2.20E+00	8.34E-01	1.83E+00
HADH	1.84E+03	1.88E-05	4.02E-05	8.08E-01	-3.07E-01	-1.24E+00	8.75E+01	1.08E+02
HAGHL	3.50E+02	8.03E-07	3.10E-06	6.97E-01	-5.20E-01	-1.43E+00	1.54E+01	2.21E+01
HARS2	6.20E+02	8.25E-04	1.08E-03	7.92E-01	-3.37E-01	-1.26E+00	2.89E+01	3.65E+01
HBA	4.92E+03	3.15E-03	3.68E-03	3.62E-01	-1.47E+00	-2.76E+00	1.43E+02	3.95E+02
HBA1	4.72E+02	3.37E-03	3.90E-03	3.67E-01	-1.45E+00	-2.73E+00	1.38E+01	3.77E+01
HBG	2.49E+03	3.12E-03	3.64E-03	3.37E-01	-1.57E+00	-2.97E+00	6.88E+01	2.05E+02
HBM	5.44E+00	5.95E-03	6.58E-03	1.79E-01	-2.48E+00	-5.57E+00	9.48E-02	5.28E-01
HCRT	2.45E+00	1.08E-03	1.38E-03	2.12E-01	-2.24E+00	-4.72E+00	4.92E-02	2.32E-01
HDAC3	1.10E+03	1.45E-07	8.76E-07	7.51E-01	-4.14E-01	-1.33E+00	5.01E+01	6.68E+01
HDAC5	3.45E+03	2.57E-07	1.32E-06	7.68E-01	-3.81E-01	-1.30E+00	1.60E+02	2.08E+02
HDDC3	2.80E+02	1.33E-02	1.41E-02	8.20E-01	-2.86E-01	-1.22E+00	1.34E+01	1.64E+01
HDGF	4.08E+03	2.55E-09	5.03E-08	6.65E-01	-5.88E-01	-1.50E+00	1.75E+02	2.63E+02
HESX1	9.52E+01	2.94E-04	4.32E-04	6.87E-01	-5.42E-01	-1.46E+00	4.10E+00	5.96E+00
HEXDC	1.23E+03	3.12E-05	6.18E-05	7.06E-01	-5.03E-01	-1.42E+00	5.44E+01	7.71E+01
HEXIM1	1.87E+03	1.13E-02	1.21E-02	8.55E-01	-2.25E-01	-1.17E+00	9.15E+01	1.07E+02
HGFAC	2.86E+02	1.95E-04	3.04E-04	6.59E-01	-6.01E-01	-1.52E+00	1.22E+01	1.86E+01
HGH1	7.60E+02	3.30E-04	4.78E-04	7.74E-01	-3.69E-01	-1.29E+00	3.53E+01	4.56E+01
HHATL	8.19E+00	3.21E-03	3.73E-03	2.35E-01	-2.09E+00	-4.26E+00	1.69E-01	7.20E-01
HIBADH	1.20E+03	3.39E-08	2.96E-07	6.90E-01	-5.36E-01	-1.45E+00	5.23E+01	7.59E+01
HIGD2A	7.82E+02	5.64E-04	7.72E-04	7.59E-01	-3.98E-01	-1.32E+00	3.60E+01	4.74E+01
HIKESHI	4.10E+02	9.15E-06	2.21E-05	6.27E-01	-6.73E-01	-1.59E+00	1.70E+01	2.70E+01
HINT1	6.68E+02	2.90E-04	4.28E-04	7.40E-01	-4.35E-01	-1.35E+00	3.03E+01	4.10E+01
HJURP	6.17E+02	6.48E-05	1.17E-04	6.51E-01	-6.19E-01	-1.54E+00	2.60E+01	3.99E+01
HK1	5.65E+03	5.53E-06	1.45E-05	6.47E-01	-6.28E-01	-1.55E+00	2.38E+02	3.68E+02
HK2	4.70E+02	1.58E-03	1.95E-03	5.36E-01	-9.00E-01	-1.87E+00	1.80E+01	3.36E+01
HM13	1.32E+03	5.09E-03	5.70E-03	8.70E-01	-2.01E-01	-1.15E+00	6.51E+01	7.49E+01
HMGA2	6.85E+01	1.39E-05	3.10E-05	2.81E-01	-1.83E+00	-3.56E+00	1.66E+00	5.91E+00

HMGN1	4.04E+03	4.36E-06	1.19E-05	7.21E-01	-4.72E-01	-1.39E+00	1.81E+02	2.52E+02
HMGN3	1.73E+03	5.24E-08	4.04E-07	5.59E-01	-8.40E-01	-1.79E+00	6.71E+01	1.20E+02
HMOX1	1.74E+03	3.03E-03	3.55E-03	6.41E-01	-6.41E-01	-1.56E+00	7.42E+01	1.16E+02
HNF1A	4.43E+00	2.34E-06	7.08E-06	1.72E-01	-2.54E+00	-5.81E+00	7.20E-02	4.18E-01
HNF4A	1.31E+02	2.03E-06	6.33E-06	3.72E-03	-8.07E+00	-2.69E+02	5.86E-02	1.57E+01
HNRNPA0	4.69E+03	1.82E-12	5.81E-10	5.61E-01	-8.33E-01	-1.78E+00	1.82E+02	3.25E+02
HNRNPA1	1.70E+04	1.13E-05	2.61E-05	7.49E-01	-4.17E-01	-1.34E+00	7.79E+02	1.04E+03
HNRNPAB	4.13E+03	1.77E-10	8.85E-09	4.79E-01	-1.06E+00	-2.09E+00	1.45E+02	3.03E+02
HNRNPD	7.22E+03	2.49E-07	1.29E-06	7.43E-01	-4.29E-01	-1.35E+00	3.29E+02	4.42E+02
HOMER3	5.86E+02	1.56E-05	3.42E-05	7.20E-01	-4.74E-01	-1.39E+00	2.63E+01	3.65E+01
HOXA1	5.88E+01	2.72E-04	4.06E-04	5.31E-02	-4.23E+00	-1.88E+01	3.40E-01	6.41E+00
HOXC5	8.39E+01	3.66E-04	5.25E-04	5.00E-01	-1.00E+00	-2.00E+00	3.01E+00	6.02E+00
HPD	5.47E+00	1.27E-05	2.89E-05	3.31E-02	-4.92E+00	-3.02E+01	2.10E-02	6.36E-01
HPRT1	5.85E+02	2.09E-02	2.18E-02	7.97E-01	-3.28E-01	-1.25E+00	2.74E+01	3.44E+01
HPS6	2.06E+02	1.43E-07	8.66E-07	5.99E-01	-7.40E-01	-1.67E+00	8.29E+00	1.38E+01
HSD17B10	1.24E+03	1.41E-07	8.58E-07	5.73E-01	-8.02E-01	-1.74E+00	4.85E+01	8.46E+01
HSD17B14	6.93E+01	8.13E-06	2.00E-05	5.57E-01	-8.43E-01	-1.79E+00	2.68E+00	4.81E+00
HSD17B8	5.36E+02	1.31E-03	1.64E-03	7.87E-01	-3.46E-01	-1.27E+00	2.51E+01	3.19E+01
HSPBP1	6.40E+02	1.29E-04	2.13E-04	7.58E-01	-3.99E-01	-1.32E+00	2.95E+01	3.88E+01
HSPE1	2.47E+03	2.16E-06	6.64E-06	5.35E-01	-9.03E-01	-1.87E+00	9.29E+01	1.74E+02
HTRA2	6.68E+02	7.43E-06	1.86E-05	8.24E-01	-2.80E-01	-1.21E+00	3.19E+01	3.88E+01
HYAL2	1.26E+03	1.92E-08	1.92E-07	6.48E-01	-6.27E-01	-1.54E+00	5.30E+01	8.18E+01
IAH1	5.73E+02	1.01E-04	1.72E-04	7.31E-01	-4.52E-01	-1.37E+00	2.57E+01	3.51E+01
ICA1	5.19E+02	3.63E-05	7.09E-05	7.63E-01	-3.91E-01	-1.31E+00	2.40E+01	3.14E+01
ICAM5	1.89E+02	4.89E-06	1.31E-05	4.32E-01	-1.21E+00	-2.32E+00	6.25E+00	1.45E+01
IDH2	2.13E+03	8.76E-10	2.77E-08	5.94E-01	-7.51E-01	-1.68E+00	8.60E+01	1.45E+02
IDH3B	1.02E+03	1.90E-06	5.96E-06	7.33E-01	-4.48E-01	-1.36E+00	4.59E+01	6.27E+01
IFT122	1.25E+03	8.71E-05	1.52E-04	7.42E-01	-4.31E-01	-1.35E+00	5.62E+01	7.57E+01
IFT27	5.62E+02	8.10E-06	1.99E-05	7.32E-01	-4.51E-01	-1.37E+00	2.53E+01	3.46E+01
IFT46	6.44E+02	2.39E-02	2.48E-02	8.56E-01	-2.24E-01	-1.17E+00	3.15E+01	3.68E+01
IGBP1	1.01E+03	5.51E-04	7.56E-04	8.02E-01	-3.19E-01	-1.25E+00	4.78E+01	5.97E+01
IGF2	5.84E+04	2.18E-03	2.63E-03	7.95E-01	-3.32E-01	-1.26E+00	2.74E+03	3.45E+03
IGSF21	2.85E+01	1.67E-03	2.05E-03	9.17E-02	-3.45E+00	-1.09E+01	2.75E-01	2.99E+00

IGSF8	1.73E+03	1.10E-08	1.25E-07	5.70E-01	-8.11E-01	-1.75E+00	6.83E+01	1.20E+02
IGSF9	5.63E+02	2.69E-07	1.36E-06	3.14E-01	-1.67E+00	-3.19E+00	1.49E+01	4.76E+01
IL11RA	2.09E+03	2.08E-04	3.21E-04	5.79E-01	-7.88E-01	-1.73E+00	8.26E+01	1.43E+02
IL17RA	8.66E+02	1.81E-04	2.86E-04	7.32E-01	-4.51E-01	-1.37E+00	3.90E+01	5.34E+01
IL18BP	1.43E+01	6.28E-02	6.34E-02	2.49E-01	-2.01E+00	-4.02E+00	3.25E-01	1.31E+00
IL23A	1.35E+02	1.59E-07	9.36E-07	5.99E-01	-7.39E-01	-1.67E+00	5.41E+00	9.03E+00
IL27RA	1.22E+03	1.33E-04	2.17E-04	6.50E-01	-6.22E-01	-1.54E+00	5.17E+01	7.95E+01
ILVBL	1.10E+03	2.92E-08	2.61E-07	5.53E-01	-8.55E-01	-1.81E+00	4.26E+01	7.71E+01
IMP4	6.68E+02	3.56E-07	1.69E-06	6.67E-01	-5.84E-01	-1.50E+00	2.88E+01	4.31E+01
IMPDH2	2.14E+03	5.61E-05	1.03E-04	7.64E-01	-3.89E-01	-1.31E+00	9.88E+01	1.29E+02
INAVA	4.59E+01	6.32E-09	8.58E-08	1.14E-01	-3.13E+00	-8.78E+00	5.36E-01	4.70E+00
ING1	7.11E+02	1.36E-05	3.05E-05	7.26E-01	-4.62E-01	-1.38E+00	3.19E+01	4.39E+01
INO80B	8.10E+02	2.19E-07	1.19E-06	6.93E-01	-5.29E-01	-1.44E+00	3.54E+01	5.11E+01
INSRR	1.89E+02	1.59E-06	5.23E-06	4.80E-01	-1.06E+00	-2.08E+00	6.68E+00	1.39E+01
IP6K2	1.51E+03	3.37E-09	5.95E-08	6.68E-01	-5.82E-01	-1.50E+00	6.45E+01	9.65E+01
IQCG	1.11E+02	5.91E-04	8.02E-04	4.09E-01	-1.29E+00	-2.45E+00	3.39E+00	8.29E+00
IQGAP3	5.39E+02	3.75E-03	4.31E-03	7.03E-01	-5.08E-01	-1.42E+00	2.39E+01	3.40E+01
IQSEC2	1.36E+03	2.44E-03	2.92E-03	7.02E-01	-5.10E-01	-1.42E+00	5.97E+01	8.50E+01
IRAK1	1.38E+03	2.68E-03	3.17E-03	8.34E-01	-2.62E-01	-1.20E+00	6.67E+01	8.00E+01
IRF2BP1	1.47E+03	3.28E-02	3.38E-02	8.78E-01	-1.87E-01	-1.14E+00	7.31E+01	8.33E+01
IRX1	1.16E+02	9.23E-06	2.22E-05	7.91E-03	-6.98E+00	-1.26E+02	1.08E-01	1.37E+01
IRX3	3.20E+02	1.46E-07	8.76E-07	3.46E-01	-1.53E+00	-2.89E+00	8.98E+00	2.60E+01
ISG20L2	7.27E+02	1.68E-06	5.44E-06	7.57E-01	-4.02E-01	-1.32E+00	3.34E+01	4.41E+01
ISOC2	2.34E+02	1.07E-04	1.80E-04	6.46E-01	-6.30E-01	-1.55E+00	9.81E+00	1.52E+01
ISX	6.60E-01	8.68E-03	9.41E-03	1.21E-03	-9.69E+00	-8.24E+02	1.00E-04	8.24E-02
ISY1	5.92E+02	2.04E-07	1.12E-06	7.57E-01	-4.02E-01	-1.32E+00	2.72E+01	3.59E+01
ITGAE	5.27E+02	5.69E-04	7.77E-04	8.39E-01	-2.54E-01	-1.19E+00	2.55E+01	3.05E+01
ITGB1BP1	8.28E+02	4.07E-03	4.66E-03	8.62E-01	-2.14E-01	-1.16E+00	4.05E+01	4.70E+01
ITM2C	7.84E+03	2.08E-04	3.22E-04	7.98E-01	-3.26E-01	-1.25E+00	3.70E+02	4.64E+02
ITPA	4.59E+02	4.85E-05	9.19E-05	7.49E-01	-4.17E-01	-1.34E+00	2.09E+01	2.80E+01
ITPK1	1.01E+03	4.13E-03	4.72E-03	7.46E-01	-4.22E-01	-1.34E+00	4.67E+01	6.26E+01
JKAMP	8.05E+02	1.81E-04	2.86E-04	7.20E-01	-4.73E-01	-1.39E+00	3.62E+01	5.02E+01
JPT1	6.20E+02	4.18E-07	1.90E-06	5.37E-01	-8.96E-01	-1.86E+00	2.34E+01	4.35E+01

JTB	6.47E+02	4.32E-04	6.09E-04	8.52E-01	-2.31E-01	-1.17E+00	3.15E+01	3.70E+01
KANK4	1.46E+03	8.51E-05	1.49E-04	3.37E-01	-1.57E+00	-2.97E+00	4.02E+01	1.19E+02
KAT8	1.38E+03	1.95E-03	2.37E-03	9.04E-01	-1.46E-01	-1.11E+00	6.91E+01	7.64E+01
KCNA2	1.33E+01	2.66E-02	2.75E-02	5.65E-01	-8.23E-01	-1.77E+00	5.22E-01	9.24E-01
KCNAB3	4.29E+01	3.38E-04	4.89E-04	4.92E-01	-1.02E+00	-2.03E+00	1.50E+00	3.05E+00
KCND1	6.05E+02	8.10E-05	1.43E-04	7.65E-01	-3.86E-01	-1.31E+00	2.80E+01	3.66E+01
KCNG1	4.96E+01	1.06E-04	1.79E-04	4.53E-01	-1.14E+00	-2.21E+00	1.69E+00	3.74E+00
KCNH2	4.29E+03	2.18E-06	6.66E-06	5.52E-01	-8.57E-01	-1.81E+00	1.65E+02	2.99E+02
KCNJ5	4.02E+01	1.89E-06	5.95E-06	7.96E-02	-3.65E+00	-1.26E+01	3.48E-01	4.37E+00
KCNK1	1.95E+02	4.42E-11	4.32E-09	1.44E-01	-2.79E+00	-6.92E+00	2.79E+00	1.93E+01
KCNK15	1.44E+01	6.90E-04	9.23E-04	9.74E-02	-3.36E+00	-1.03E+01	1.45E-01	1.49E+00
KCNK5	1.23E+02	1.65E-04	2.65E-04	4.62E-01	-1.11E+00	-2.17E+00	4.20E+00	9.10E+00
KCNN1	1.49E+02	4.94E-03	5.55E-03	5.99E-01	-7.38E-01	-1.67E+00	6.03E+00	1.01E+01
KCNN4	8.00E+01	6.20E-04	8.37E-04	3.95E-01	-1.34E+00	-2.53E+00	2.48E+00	6.29E+00
KCTD1	8.07E+02	3.82E-08	3.24E-07	3.61E-01	-1.47E+00	-2.77E+00	2.36E+01	6.53E+01
KCTD17	9.10E+02	2.40E-09	4.88E-08	5.10E-01	-9.73E-01	-1.96E+00	3.35E+01	6.58E+01
KHNYN	1.67E+03	2.93E-07	1.45E-06	7.80E-01	-3.59E-01	-1.28E+00	7.81E+01	1.00E+02
KIAA0895L	1.26E+02	5.99E-04	8.11E-04	6.15E-01	-7.01E-01	-1.63E+00	5.13E+00	8.34E+00
KIAA1522	2.50E+03	5.87E-07	2.47E-06	5.13E-01	-9.63E-01	-1.95E+00	9.13E+01	1.78E+02
KIF17	2.61E+02	1.49E-03	1.85E-03	6.54E-01	-6.12E-01	-1.53E+00	1.10E+01	1.68E+01
KIF21B	3.07E+03	8.62E-04	1.12E-03	4.92E-01	-1.02E+00	-2.03E+00	1.11E+02	2.26E+02
KISS1	4.35E+01	1.37E-06	4.61E-06	8.66E-02	-3.53E+00	-1.16E+01	3.99E-01	4.61E+00
KLC2	2.69E+03	3.07E-10	1.28E-08	6.20E-01	-6.89E-01	-1.61E+00	1.11E+02	1.79E+02
KLF16	8.75E+02	7.17E-04	9.52E-04	7.75E-01	-3.69E-01	-1.29E+00	4.07E+01	5.26E+01
KLF17	3.68E+01	8.01E-06	1.97E-05	1.11E-02	-6.49E+00	-9.00E+01	4.80E-02	4.32E+00
KLHDC8B	5.77E+02	7.33E-03	8.00E-03	7.91E-01	-3.38E-01	-1.26E+00	2.72E+01	3.44E+01
KLHL26	2.26E+02	8.44E-08	5.93E-07	6.68E-01	-5.83E-01	-1.50E+00	9.65E+00	1.44E+01
KLHL29	8.27E+01	3.75E-05	7.31E-05	4.31E-01	-1.21E+00	-2.32E+00	2.72E+00	6.31E+00
KLK1	4.83E+02	3.22E-10	1.30E-08	2.30E-01	-2.12E+00	-4.35E+00	9.94E+00	4.32E+01
KLK12	2.14E+02	3.19E-07	1.55E-06	1.66E-01	-2.59E+00	-6.03E+00	3.52E+00	2.12E+01
KLK6	1.94E+02	1.11E-06	3.98E-06	3.83E-03	-8.03E+00	-2.61E+02	8.91E-02	2.33E+01
KLK7	4.77E+01	1.44E-04	2.34E-04	2.74E-02	-5.19E+00	-3.64E+01	1.50E-01	5.48E+00
KLK8	2.20E+01	1.03E-05	2.42E-05	1.17E-01	-3.09E+00	-8.54E+00	2.69E-01	2.30E+00

KMT5C	1.90E+03	4.37E-08	3.57E-07	4.12E-01	-1.28E+00	-2.43E+00	6.00E+01	1.45E+02
KREMEN1	1.45E+03	3.29E-04	4.78E-04	5.78E-01	-7.90E-01	-1.73E+00	5.62E+01	9.72E+01
KREMEN2	5.09E+01	9.67E-08	6.61E-07	6.01E-02	-4.06E+00	-1.66E+01	3.35E-01	5.58E+00
KRT7	4.99E+02	4.17E-03	4.76E-03	2.35E-01	-2.09E+00	-4.25E+00	1.09E+01	4.65E+01
KRTCAP2	6.80E+02	2.67E-05	5.41E-05	7.66E-01	-3.84E-01	-1.30E+00	3.14E+01	4.09E+01
KY	2.15E+01	3.51E-04	5.06E-04	3.13E-01	-1.67E+00	-3.19E+00	5.62E-01	1.79E+00
KYAT3	2.69E+02	5.42E-03	6.05E-03	5.42E-01	-8.83E-01	-1.84E+00	1.02E+01	1.89E+01
L1CAM	7.30E+02	3.05E-09	5.59E-08	1.54E-01	-2.70E+00	-6.50E+00	1.11E+01	7.25E+01
L3HYPDH	1.92E+02	4.87E-08	3.87E-07	4.43E-01	-1.17E+00	-2.26E+00	6.50E+00	1.47E+01
LAMTOR4	8.66E+02	9.50E-04	1.22E-03	8.29E-01	-2.71E-01	-1.21E+00	4.17E+01	5.04E+01
LBHD2	7.22E+01	7.61E-06	1.89E-05	1.44E-01	-2.80E+00	-6.94E+00	1.05E+00	7.29E+00
LCK	1.30E+02	1.80E-04	2.85E-04	5.59E-01	-8.40E-01	-1.79E+00	5.02E+00	8.99E+00
LCNL1	2.56E+01	2.20E-04	3.37E-04	4.79E-01	-1.06E+00	-2.09E+00	9.03E-01	1.88E+00
LDB1	6.22E+03	2.16E-08	2.08E-07	6.26E-01	-6.77E-01	-1.60E+00	2.57E+02	4.11E+02
LDHA	1.42E+03	1.89E-04	2.96E-04	5.76E-01	-7.95E-01	-1.74E+00	5.65E+01	9.81E+01
LDLRAP1	1.13E+03	9.89E-04	1.27E-03	8.75E-01	-1.92E-01	-1.14E+00	5.57E+01	6.36E+01
LEF1	1.66E+03	1.51E-05	3.33E-05	3.78E-01	-1.41E+00	-2.65E+00	4.95E+01	1.31E+02
LFNG	2.25E+02	7.05E-04	9.37E-04	6.09E-01	-7.14E-01	-1.64E+00	9.24E+00	1.52E+01
LGALS3BP	2.19E+03	1.61E-03	1.98E-03	7.66E-01	-3.84E-01	-1.30E+00	1.01E+02	1.32E+02
LGI2	8.11E+02	3.03E-07	1.49E-06	2.42E-01	-2.05E+00	-4.14E+00	1.78E+01	7.34E+01
LHFPL1	5.46E+01	8.41E-07	3.20E-06	2.54E-01	-1.98E+00	-3.94E+00	1.23E+00	4.84E+00
LHPP	9.35E+02	5.43E-07	2.36E-06	6.35E-01	-6.56E-01	-1.58E+00	3.92E+01	6.18E+01
LHX2	1.74E+02	4.86E-05	9.19E-05	2.75E-01	-1.86E+00	-3.64E+00	4.17E+00	1.52E+01
LIMD2	4.31E+02	7.38E-07	2.93E-06	6.14E-01	-7.03E-01	-1.63E+00	1.76E+01	2.86E+01
LIMK1	9.50E+02	7.41E-08	5.31E-07	6.61E-01	-5.97E-01	-1.51E+00	4.05E+01	6.13E+01
LIN28A	3.24E+01	1.31E-05	2.96E-05	1.39E-02	-6.17E+00	-7.22E+01	5.17E-02	3.73E+00
LIPH	1.82E+01	1.88E-04	2.95E-04	5.19E-02	-4.27E+00	-1.93E+01	1.05E-01	2.03E+00
LIPT1	1.13E+02	2.11E-03	2.55E-03	7.65E-01	-3.87E-01	-1.31E+00	5.21E+00	6.82E+00
LLGL2	7.34E+02	4.94E-03	5.55E-03	7.48E-01	-4.19E-01	-1.34E+00	3.36E+01	4.49E+01
LMAN1L	3.86E+01	1.94E-04	3.02E-04	5.27E-02	-4.25E+00	-1.90E+01	2.31E-01	4.38E+00
LMNB1	1.31E+03	2.52E-06	7.52E-06	6.38E-01	-6.49E-01	-1.57E+00	5.49E+01	8.61E+01
LMNB2	2.50E+03	1.04E-06	3.78E-06	6.32E-01	-6.61E-01	-1.58E+00	1.04E+02	1.64E+02
LMNTD2	2.95E+01	3.08E-06	8.90E-06	1.63E-01	-2.61E+00	-6.12E+00	4.70E-01	2.88E+00

LOC100139325	2.15E+02	1.40E-09	3.35E-08	2.78E-01	-1.85E+00	-3.60E+00	5.23E+00	1.89E+01
LOC100140550	5.01E+01	1.15E-05	2.66E-05	1.05E-02	-6.57E+00	-9.49E+01	6.28E-02	5.96E+00
LOC100141025	1.71E+02	1.30E-05	2.94E-05	5.29E-01	-9.19E-01	-1.89E+00	6.43E+00	1.22E+01
LOC100141117	1.72E+01	1.13E-02	1.21E-02	6.86E-01	-5.44E-01	-1.46E+00	7.39E-01	1.08E+00
LOC100295842	8.87E+00	3.22E-10	1.30E-08	3.88E-04	-1.13E+01	-2.57E+03	4.21E-04	1.08E+00
LOC100297725	4.05E+03	2.88E-12	7.32E-10	4.57E-01	-1.13E+00	-2.19E+00	1.38E+02	3.03E+02
LOC100298871	8.10E+01	9.76E-03	1.05E-02	8.09E-01	-3.05E-01	-1.24E+00	3.86E+00	4.77E+00
LOC100300760	4.64E+03	6.13E-07	2.54E-06	2.36E-01	-2.09E+00	-4.25E+00	9.84E+01	4.18E+02
LOC100336682	9.94E-01	1.68E-03	2.06E-03	2.22E-02	-5.49E+00	-4.50E+01	2.66E-03	1.20E-01
LOC100336980	1.39E+00	6.41E-01	6.41E-01	1.60E-01	-2.64E+00	-6.25E+00	2.21E-02	1.38E-01
LOC100847700	2.81E+02	9.67E-04	1.24E-03	6.39E-01	-6.46E-01	-1.57E+00	1.18E+01	1.85E+01
LOC100848253	2.22E+01	9.87E-05	1.69E-04	4.35E-01	-1.20E+00	-2.30E+00	7.35E-01	1.69E+00
LOC100848325	7.31E+01	1.43E-03	1.78E-03	4.39E-01	-1.19E+00	-2.28E+00	2.40E+00	5.47E+00
LOC100848353	1.39E+03	1.49E-02	1.57E-02	8.58E-01	-2.22E-01	-1.17E+00	6.84E+01	7.97E+01
LOC100849068	9.25E+00	3.69E-04	5.28E-04	7.19E-02	-3.80E+00	-1.39E+01	7.29E-02	1.01E+00
LOC100850808	1.33E+01	1.10E-03	1.40E-03	9.37E-02	-3.42E+00	-1.07E+01	1.37E-01	1.46E+00
LOC101902029	1.18E+01	1.06E-02	1.13E-02	5.33E-01	-9.08E-01	-1.88E+00	4.38E-01	8.23E-01
LOC101902937	1.01E+03	6.95E-05	1.25E-04	6.75E-01	-5.66E-01	-1.48E+00	4.32E+01	6.40E+01
LOC101903140	1.35E+01	2.36E-03	2.82E-03	5.97E-01	-7.44E-01	-1.67E+00	5.45E-01	9.12E-01
LOC101903991	1.61E+01	4.45E-03	5.05E-03	4.15E-01	-1.27E+00	-2.41E+00	5.06E-01	1.22E+00
LOC101904187	1.39E+02	3.91E-07	1.81E-06	3.13E-01	-1.68E+00	-3.20E+00	3.69E+00	1.18E+01
LOC101904275	2.76E+02	1.31E-03	1.65E-03	8.43E-01	-2.46E-01	-1.19E+00	1.33E+01	1.58E+01
LOC101904314	5.60E+01	1.33E-02	1.42E-02	7.37E-01	-4.40E-01	-1.36E+00	2.50E+00	3.39E+00
LOC101904810	6.76E+01	1.98E-05	4.18E-05	4.41E-01	-1.18E+00	-2.27E+00	2.25E+00	5.11E+00
LOC101905156	5.12E+02	2.33E-07	1.23E-06	6.78E-01	-5.60E-01	-1.47E+00	2.22E+01	3.28E+01
LOC101905222	8.68E+01	2.34E-09	4.81E-08	1.24E-01	-3.02E+00	-8.09E+00	1.10E+00	8.89E+00
LOC101905514	8.08E+02	5.51E-05	1.02E-04	6.86E-01	-5.43E-01	-1.46E+00	3.54E+01	5.16E+01
LOC101906010	1.57E+02	1.11E-06	3.99E-06	5.57E-01	-8.44E-01	-1.80E+00	6.00E+00	1.08E+01
LOC101906273	7.09E+01	4.76E-06	1.28E-05	5.67E-01	-8.18E-01	-1.76E+00	2.77E+00	4.89E+00
LOC101906280	1.34E+02	1.44E-04	2.34E-04	6.49E-01	-6.23E-01	-1.54E+00	5.66E+00	8.72E+00
LOC101906855	3.81E+02	4.93E-06	1.31E-05	6.84E-01	-5.48E-01	-1.46E+00	1.65E+01	2.41E+01
LOC101906916	2.14E+03	1.85E-06	5.86E-06	6.73E-01	-5.72E-01	-1.49E+00	9.21E+01	1.37E+02
LOC101906939	8.25E+01	1.02E-05	2.41E-05	6.00E-01	-7.38E-01	-1.67E+00	3.33E+00	5.55E+00

LOC101907000	8.88E+01	5.89E-05	1.08E-04	5.82E-01	-7.81E-01	-1.72E+00	3.52E+00	6.05E+00
LOC101907022	2.46E+01	9.47E-03	1.02E-02	5.83E-01	-7.78E-01	-1.71E+00	9.95E-01	1.71E+00
LOC101907127	6.49E+00	1.27E-03	1.60E-03	1.17E-01	-3.09E+00	-8.51E+00	7.86E-02	6.69E-01
LOC101907157	4.53E+01	3.70E-05	7.22E-05	3.35E-01	-1.58E+00	-2.99E+00	1.22E+00	3.66E+00
LOC101907294	5.01E+01	8.08E-04	1.06E-03	6.71E-01	-5.76E-01	-1.49E+00	2.16E+00	3.22E+00
LOC101907557	6.94E+01	4.59E-05	8.78E-05	5.89E-01	-7.64E-01	-1.70E+00	2.76E+00	4.68E+00
LOC101907853	9.49E+00	1.95E-04	3.03E-04	4.00E-01	-1.32E+00	-2.50E+00	2.99E-01	7.48E-01
LOC101907940	1.99E+01	5.26E-06	1.39E-05	4.62E-01	-1.11E+00	-2.17E+00	6.85E-01	1.48E+00
LOC104968964	1.76E+02	2.01E-04	3.11E-04	7.23E-01	-4.68E-01	-1.38E+00	7.87E+00	1.09E+01
LOC104969026	5.08E+00	1.14E-03	1.46E-03	8.58E-02	-3.54E+00	-1.17E+01	4.67E-02	5.45E-01
LOC104969408	3.57E+01	5.15E-04	7.10E-04	5.26E-01	-9.28E-01	-1.90E+00	1.34E+00	2.54E+00
LOC104970173	7.07E+02	2.21E-06	6.73E-06	7.36E-01	-4.42E-01	-1.36E+00	3.19E+01	4.34E+01
LOC104970930	6.36E+01	2.04E-04	3.16E-04	2.55E-01	-1.97E+00	-3.92E+00	1.45E+00	5.69E+00
LOC104970966	1.28E+01	1.27E-02	1.35E-02	6.49E-01	-6.23E-01	-1.54E+00	5.43E-01	8.35E-01
LOC104971292	6.68E+01	2.81E-06	8.28E-06	5.26E-01	-9.26E-01	-1.90E+00	2.48E+00	4.71E+00
LOC104971855	6.59E+00	1.39E-02	1.48E-02	6.00E-01	-7.37E-01	-1.67E+00	2.60E-01	4.33E-01
LOC104973427	4.26E+01	4.49E-03	5.09E-03	7.31E-01	-4.51E-01	-1.37E+00	1.91E+00	2.61E+00
LOC104973517	3.13E+02	1.73E-04	2.76E-04	6.77E-01	-5.63E-01	-1.48E+00	1.36E+01	2.01E+01
LOC104974770	4.16E+01	6.31E-04	8.50E-04	4.35E-01	-1.20E+00	-2.30E+00	1.37E+00	3.15E+00
LOC104975196	1.60E+03	3.20E-06	9.21E-06	7.03E-01	-5.09E-01	-1.42E+00	7.05E+01	1.00E+02
LOC107131293	8.66E+01	1.57E-06	5.18E-06	5.36E-01	-8.99E-01	-1.86E+00	3.26E+00	6.07E+00
LOC107131324	1.09E+02	1.66E-03	2.04E-03	7.64E-01	-3.89E-01	-1.31E+00	5.04E+00	6.60E+00
LOC107131465	8.45E+00	6.93E-03	7.61E-03	1.54E-01	-2.70E+00	-6.49E+00	1.32E-01	8.59E-01
LOC107131695	3.51E+01	1.91E-05	4.07E-05	5.46E-01	-8.74E-01	-1.83E+00	1.32E+00	2.42E+00
LOC107131728	1.22E+03	8.45E-06	2.06E-05	6.50E-01	-6.23E-01	-1.54E+00	5.14E+01	7.91E+01
LOC107132067	9.53E+01	1.55E-06	5.11E-06	5.84E-01	-7.77E-01	-1.71E+00	3.79E+00	6.49E+00
LOC107132075	2.39E+01	5.11E-05	9.58E-05	3.97E-02	-4.65E+00	-2.52E+01	1.07E-01	2.68E+00
LOC107132205	1.14E+00	6.01E-02	6.08E-02	9.58E-02	-3.38E+00	-1.04E+01	1.19E-02	1.24E-01
LOC107132228	2.59E+02	6.15E-05	1.12E-04	7.18E-01	-4.79E-01	-1.39E+00	1.16E+01	1.61E+01
LOC107132243	4.10E+02	7.87E-08	5.60E-07	6.76E-01	-5.64E-01	-1.48E+00	1.77E+01	2.62E+01
LOC107132247	4.16E+02	4.48E-07	2.02E-06	6.76E-01	-5.64E-01	-1.48E+00	1.80E+01	2.66E+01
LOC107132450	2.04E+02	4.29E-04	6.06E-04	7.11E-01	-4.92E-01	-1.41E+00	9.02E+00	1.27E+01
LOC107132556	8.51E+01	6.87E-05	1.23E-04	5.76E-01	-7.95E-01	-1.74E+00	3.33E+00	5.79E+00

LOC107132734	4.57E+01	1.42E-03	1.77E-03	6.43E-01	-6.37E-01	-1.56E+00	1.91E+00	2.97E+00
LOC107132856	1.16E+02	2.26E-02	2.35E-02	8.10E-01	-3.03E-01	-1.23E+00	5.50E+00	6.78E+00
LOC112441531	1.47E+00	1.79E-05	3.86E-05	8.99E-02	-3.48E+00	-1.11E+01	1.40E-02	1.56E-01
LOC112441539	9.10E+00	1.48E-03	1.83E-03	9.33E-02	-3.42E+00	-1.07E+01	9.17E-02	9.83E-01
LOC112441980	1.01E+02	1.29E-05	2.92E-05	3.03E-01	-1.72E+00	-3.30E+00	2.55E+00	8.41E+00
LOC112442207	1.34E+02	5.21E-09	7.66E-08	8.89E-03	-6.81E+00	-1.13E+02	1.42E-01	1.60E+01
LOC112442246	2.02E+02	3.34E-03	3.88E-03	7.49E-01	-4.17E-01	-1.34E+00	9.29E+00	1.24E+01
LOC112442288	8.93E+01	8.37E-07	3.19E-06	5.99E-01	-7.39E-01	-1.67E+00	3.63E+00	6.05E+00
LOC112442368	2.50E+00	3.44E-06	9.82E-06	8.18E-02	-3.61E+00	-1.22E+01	2.15E-02	2.63E-01
LOC112442373	4.71E+01	3.08E-07	1.51E-06	1.16E-01	-3.10E+00	-8.59E+00	5.64E-01	4.85E+00
LOC112442982	3.25E+01	4.22E-06	1.16E-05	5.30E-01	-9.16E-01	-1.89E+00	1.21E+00	2.28E+00
LOC112443216	8.09E+02	1.16E-07	7.49E-07	5.66E-01	-8.22E-01	-1.77E+00	3.16E+01	5.58E+01
LOC112444532	2.82E+00	2.21E-02	2.30E-02	3.76E-01	-1.41E+00	-2.66E+00	8.22E-02	2.18E-01
LOC112444733	5.15E+00	4.24E-02	4.33E-02	3.44E-01	-1.54E+00	-2.91E+00	1.50E-01	4.35E-01
LOC112445078	9.87E+02	1.10E-05	2.56E-05	5.95E-01	-7.48E-01	-1.68E+00	3.96E+01	6.65E+01
LOC112445127	7.59E+01	1.30E-04	2.14E-04	2.07E-02	-5.60E+00	-4.84E+01	1.85E-01	8.97E+00
LOC112445996	2.58E+03	2.63E-04	3.93E-04	7.98E-01	-3.26E-01	-1.25E+00	1.22E+02	1.53E+02
LOC112446393	1.23E+02	8.29E-06	2.03E-05	1.46E-02	-6.09E+00	-6.83E+01	2.11E-01	1.44E+01
LOC112446406	1.63E+03	1.30E-07	8.15E-07	5.99E-01	-7.40E-01	-1.67E+00	6.58E+01	1.10E+02
LOC112446645	6.39E+02	3.79E-07	1.77E-06	6.27E-01	-6.73E-01	-1.59E+00	2.65E+01	4.23E+01
LOC112446738	1.15E+01	5.94E-02	6.02E-02	7.30E-01	-4.54E-01	-1.37E+00	5.20E-01	7.13E-01
LOC112447018	3.28E+00	3.23E-01	3.23E-01	2.09E-01	-2.26E+00	-4.79E+00	6.45E-02	3.09E-01
LOC112447610	2.46E+01	1.64E-03	2.01E-03	6.79E-02	-3.88E+00	-1.47E+01	1.80E-01	2.65E+00
LOC112449049	2.77E+00	4.86E-02	4.95E-02	4.21E-01	-1.25E+00	-2.38E+00	8.66E-02	2.06E-01
LOC407163	2.88E+01	1.84E-03	2.23E-03	1.12E-01	-3.16E+00	-8.94E+00	3.37E-01	3.02E+00
LOC504861	1.77E+01	1.66E-05	3.61E-05	1.25E-02	-6.33E+00	-8.03E+01	2.57E-02	2.06E+00
LOC505183	4.94E+00	1.18E-03	1.50E-03	3.14E-01	-1.67E+00	-3.18E+00	1.30E-01	4.14E-01
LOC505972	8.55E+00	1.16E-04	1.93E-04	4.05E-02	-4.63E+00	-2.47E+01	3.84E-02	9.49E-01
LOC508098	5.23E+02	7.01E-05	1.26E-04	2.77E-01	-1.85E+00	-3.61E+00	1.30E+01	4.69E+01
LOC508455	3.08E+01	3.05E-04	4.46E-04	5.38E-01	-8.94E-01	-1.86E+00	1.15E+00	2.13E+00
LOC509911	7.71E+00	3.66E-04	5.25E-04	7.74E-02	-3.69E+00	-1.29E+01	6.44E-02	8.32E-01
LOC511130	1.05E+02	1.09E-03	1.39E-03	7.02E-01	-5.11E-01	-1.42E+00	4.67E+00	6.66E+00
LOC511386	4.08E+02	3.24E-05	6.42E-05	7.26E-01	-4.62E-01	-1.38E+00	1.83E+01	2.53E+01

LOC512175	5.56E+01	6.68E-03	7.35E-03	7.51E-01	-4.13E-01	-1.33E+00	2.52E+00	3.35E+00
LOC512953	1.63E+03	1.29E-06	4.45E-06	6.70E-01	-5.77E-01	-1.49E+00	7.01E+01	1.05E+02
LOC513322	1.13E+01	3.68E-05	7.18E-05	4.33E-01	-1.21E+00	-2.31E+00	3.78E-01	8.73E-01
LOC513690	7.84E+01	5.62E-03	6.25E-03	1.72E-01	-2.54E+00	-5.82E+00	1.26E+00	7.31E+00
LOC515042	2.83E+03	4.22E-05	8.13E-05	7.60E-01	-3.96E-01	-1.32E+00	1.31E+02	1.72E+02
LOC516108	4.79E+02	2.33E-03	2.79E-03	7.35E-01	-4.44E-01	-1.36E+00	2.16E+01	2.94E+01
LOC516378	2.99E+00	7.09E-05	1.27E-04	5.15E-02	-4.28E+00	-1.94E+01	1.71E-02	3.33E-01
LOC518080	1.27E+01	3.24E-02	3.34E-02	4.96E-01	-1.01E+00	-2.02E+00	4.43E-01	8.95E-01
LOC518961	1.31E+01	2.39E-03	2.85E-03	5.45E-01	-8.76E-01	-1.83E+00	4.98E-01	9.14E-01
LOC521224	1.96E+03	4.40E-07	1.99E-06	6.18E-01	-6.93E-01	-1.62E+00	8.04E+01	1.30E+02
LOC526230	5.27E+00	1.15E-03	1.46E-03	8.85E-02	-3.50E+00	-1.13E+01	4.86E-02	5.49E-01
LOC526769	6.88E+01	2.63E-05	5.35E-05	4.98E-01	-1.01E+00	-2.01E+00	2.46E+00	4.94E+00
LOC527388	1.91E+01	1.76E-03	2.15E-03	5.23E-01	-9.36E-01	-1.91E+00	7.12E-01	1.36E+00
LOC529657	1.67E+01	8.71E-03	9.43E-03	3.33E-01	-1.59E+00	-3.01E+00	4.32E-01	1.30E+00
LOC529823	1.37E+01	2.75E-04	4.09E-04	3.60E-01	-1.48E+00	-2.78E+00	3.92E-01	1.09E+00
LOC533307	5.34E+03	2.47E-07	1.29E-06	6.61E-01	-5.97E-01	-1.51E+00	2.29E+02	3.46E+02
LOC534391	2.11E+03	5.91E-03	6.54E-03	8.58E-01	-2.20E-01	-1.16E+00	1.04E+02	1.21E+02
LOC534967	1.33E+02	3.34E-06	9.59E-06	2.00E-01	-2.32E+00	-4.99E+00	2.55E+00	1.27E+01
LOC539705	6.90E+01	1.74E-10	8.85E-09	2.60E-02	-5.27E+00	-3.85E+01	2.06E-01	7.92E+00
LOC613345	5.94E+00	2.13E-03	2.57E-03	4.68E-01	-1.09E+00	-2.14E+00	2.05E-01	4.38E-01
LOC613364	2.88E+00	6.17E-02	6.23E-02	5.31E-01	-9.14E-01	-1.88E+00	1.09E-01	2.06E-01
LOC613401	8.30E+01	6.04E-06	1.56E-05	5.56E-01	-8.48E-01	-1.80E+00	3.20E+00	5.76E+00
LOC613660	1.63E+02	5.12E-03	5.73E-03	7.97E-01	-3.27E-01	-1.25E+00	7.72E+00	9.69E+00
LOC614423	1.87E+02	3.55E-02	3.65E-02	8.59E-01	-2.20E-01	-1.16E+00	9.19E+00	1.07E+01
LOC614748	1.72E+02	7.27E-06	1.83E-05	5.31E-01	-9.14E-01	-1.88E+00	6.56E+00	1.24E+01
LOC614882	2.51E+01	6.44E-07	2.63E-06	3.95E-01	-1.34E+00	-2.53E+00	7.78E-01	1.97E+00
LOC614922	4.60E+03	8.25E-05	1.45E-04	8.01E-01	-3.21E-01	-1.25E+00	2.18E+02	2.73E+02
LOC615002	2.60E+02	1.12E-05	2.59E-05	6.65E-01	-5.88E-01	-1.50E+00	1.12E+01	1.69E+01
LOC616199	1.05E+03	1.14E-04	1.91E-04	5.90E-01	-7.62E-01	-1.70E+00	4.26E+01	7.23E+01
LOC616200	3.68E+03	1.36E-05	3.04E-05	6.67E-01	-5.85E-01	-1.50E+00	1.59E+02	2.38E+02
LOC616281	2.20E+03	2.76E-06	8.13E-06	7.45E-01	-4.24E-01	-1.34E+00	1.00E+02	1.34E+02
LOC616860	9.92E+01	9.31E-10	2.81E-08	1.08E-03	-9.85E+00	-9.23E+02	1.29E-02	1.19E+01
LOC616995	3.19E+00	2.33E-04	3.53E-04	2.58E-01	-1.95E+00	-3.87E+00	7.29E-02	2.83E-01

LOC617396	3.76E+01	5.83E-05	1.07E-04	5.68E-01	-8.16E-01	-1.76E+00	1.47E+00	2.58E+00
LOC618377	4.96E+02	1.63E-04	2.61E-04	5.63E-01	-8.29E-01	-1.78E+00	1.94E+01	3.44E+01
LOC780968	7.04E+02	6.40E-04	8.61E-04	8.12E-01	-3.00E-01	-1.23E+00	3.35E+01	4.13E+01
LOC781100	2.78E+02	8.85E-06	2.15E-05	6.44E-01	-6.34E-01	-1.55E+00	1.17E+01	1.82E+01
LOC781381	3.24E+03	8.80E-04	1.14E-03	8.13E-01	-2.98E-01	-1.23E+00	1.54E+02	1.90E+02
LOC782061	3.41E+01	1.94E-05	4.11E-05	1.20E-01	-3.06E+00	-8.35E+00	4.29E-01	3.58E+00
LOC782264	8.83E+02	8.11E-07	3.11E-06	5.64E-01	-8.26E-01	-1.77E+00	3.46E+01	6.14E+01
LOC782305	1.85E+01	2.25E-04	3.44E-04	5.96E-01	-7.46E-01	-1.68E+00	7.41E-01	1.24E+00
LOC782392	1.71E+01	9.54E-03	1.03E-02	6.94E-01	-5.27E-01	-1.44E+00	7.41E-01	1.07E+00
LOC782966	6.76E+02	4.65E-05	8.87E-05	6.79E-01	-5.58E-01	-1.47E+00	2.94E+01	4.32E+01
LOC783202	3.83E+02	8.99E-07	3.36E-06	6.62E-01	-5.95E-01	-1.51E+00	1.64E+01	2.48E+01
LOC783434	1.24E+01	1.69E-02	1.78E-02	6.85E-01	-5.45E-01	-1.46E+00	5.41E-01	7.89E-01
LOC783477	3.96E+00	6.08E-02	6.15E-02	3.72E-01	-1.43E+00	-2.69E+00	1.18E-01	3.17E-01
LOC783497	2.23E+01	2.09E-04	3.23E-04	3.40E-01	-1.55E+00	-2.94E+00	6.19E-01	1.82E+00
LOC783612	7.47E+02	5.36E-07	2.33E-06	6.20E-01	-6.90E-01	-1.61E+00	3.10E+01	5.00E+01
LOC783657	1.95E+03	4.78E-06	1.28E-05	7.26E-01	-4.62E-01	-1.38E+00	8.78E+01	1.21E+02
LOC783776	6.29E+01	4.28E-04	6.05E-04	7.17E-01	-4.79E-01	-1.39E+00	2.80E+00	3.91E+00
LOC783835	7.85E+01	6.98E-04	9.32E-04	6.78E-01	-5.61E-01	-1.48E+00	3.40E+00	5.01E+00
LOC784266	8.96E+01	4.80E-04	6.69E-04	6.93E-01	-5.29E-01	-1.44E+00	3.93E+00	5.67E+00
LOC784357	2.54E+00	3.33E-02	3.43E-02	3.95E-01	-1.34E+00	-2.53E+00	7.78E-02	1.97E-01
LOC784697	3.76E+01	1.60E-05	3.48E-05	5.23E-01	-9.34E-01	-1.91E+00	1.40E+00	2.67E+00
LOC784713	1.53E+02	2.21E-06	6.75E-06	6.59E-01	-6.02E-01	-1.52E+00	6.47E+00	9.82E+00
LOC785479	5.84E+01	3.26E-05	6.45E-05	6.35E-01	-6.56E-01	-1.58E+00	2.44E+00	3.84E+00
LOC785503	1.60E+03	4.17E-06	1.15E-05	8.33E-01	-2.64E-01	-1.20E+00	7.72E+01	9.27E+01
LOC785569	1.87E+02	2.50E-05	5.13E-05	6.87E-01	-5.41E-01	-1.45E+00	8.16E+00	1.19E+01
LOC785735	8.19E+00	2.88E-03	3.39E-03	3.79E-01	-1.40E+00	-2.64E+00	2.51E-01	6.63E-01
LOC785761	2.75E+03	2.77E-04	4.11E-04	7.93E-01	-3.34E-01	-1.26E+00	1.30E+02	1.64E+02
LOC785843	1.68E+02	1.36E-04	2.23E-04	7.54E-01	-4.07E-01	-1.33E+00	7.66E+00	1.01E+01
LOC786733	1.43E+02	2.12E-04	3.27E-04	6.55E-01	-6.11E-01	-1.53E+00	6.11E+00	9.33E+00
LOC786906	6.51E+01	8.56E-05	1.50E-04	5.94E-01	-7.51E-01	-1.68E+00	2.62E+00	4.41E+00
LOC789364	3.50E+00	2.20E-02	2.30E-02	2.94E-01	-1.77E+00	-3.40E+00	9.02E-02	3.07E-01
LOC790266	2.21E+03	1.11E-04	1.85E-04	8.18E-01	-2.90E-01	-1.22E+00	1.06E+02	1.30E+02
LONP1	1.85E+03	3.46E-07	1.66E-06	6.12E-01	-7.07E-01	-1.63E+00	7.57E+01	1.24E+02

LONP2	7.81E+02	1.38E-02	1.46E-02	8.62E-01	-2.14E-01	-1.16E+00	3.81E+01	4.42E+01
LPAR2	2.60E+02	1.14E-07	7.48E-07	5.17E-01	-9.51E-01	-1.93E+00	9.55E+00	1.85E+01
LRCH4	1.44E+03	1.32E-07	8.26E-07	6.83E-01	-5.50E-01	-1.46E+00	6.21E+01	9.09E+01
LRFN1	3.79E+02	1.97E-07	1.09E-06	5.64E-01	-8.27E-01	-1.77E+00	1.47E+01	2.61E+01
LRFN2	1.12E+02	6.04E-06	1.56E-05	3.04E-01	-1.72E+00	-3.29E+00	2.88E+00	9.48E+00
LRFN4	3.42E+02	2.38E-08	2.21E-07	5.54E-01	-8.53E-01	-1.81E+00	1.31E+01	2.37E+01
LRG1	3.08E+01	2.75E-06	8.12E-06	2.18E-01	-2.20E+00	-4.59E+00	6.27E-01	2.88E+00
LRP5	3.83E+03	2.79E-04	4.13E-04	7.39E-01	-4.37E-01	-1.35E+00	1.74E+02	2.35E+02
LRRC26	2.95E+00	2.16E-02	2.25E-02	3.49E-01	-1.52E+00	-2.87E+00	8.15E-02	2.33E-01
LRRC4	1.72E+02	1.93E-05	4.09E-05	4.46E-01	-1.16E+00	-2.24E+00	5.78E+00	1.30E+01
LRRC4B	9.60E+02	1.33E-06	4.54E-06	2.58E-01	-1.96E+00	-3.88E+00	2.15E+01	8.35E+01
LRRC4C	9.62E+01	5.48E-05	1.02E-04	4.13E-01	-1.27E+00	-2.42E+00	3.05E+00	7.38E+00
LRRC77	3.24E+00	3.32E-02	3.42E-02	3.56E-01	-1.49E+00	-2.81E+00	9.76E-02	2.75E-01
LRRN2	9.23E+02	1.09E-04	1.82E-04	7.18E-01	-4.79E-01	-1.39E+00	4.12E+01	5.74E+01
LSM6	4.81E+02	1.85E-04	2.91E-04	7.54E-01	-4.07E-01	-1.33E+00	2.21E+01	2.93E+01
LSM8	4.05E+02	1.50E-06	4.97E-06	6.77E-01	-5.63E-01	-1.48E+00	1.74E+01	2.58E+01
LTF	2.49E+02	8.84E-02	8.91E-02	6.95E-01	-5.25E-01	-1.44E+00	1.11E+01	1.60E+01
LUC7L	3.93E+03	2.31E-04	3.51E-04	8.68E-01	-2.04E-01	-1.15E+00	1.94E+02	2.23E+02
LURAP1L	1.77E+02	6.07E-05	1.11E-04	4.03E-01	-1.31E+00	-2.48E+00	5.73E+00	1.42E+01
LXN	5.04E+02	6.41E-06	1.64E-05	6.61E-01	-5.97E-01	-1.51E+00	2.16E+01	3.27E+01
LY6E	1.34E+03	3.68E-05	7.18E-05	4.26E-01	-1.23E+00	-2.34E+00	4.27E+01	1.00E+02
LYPD2	1.01E+01	1.02E-04	1.74E-04	7.47E-02	-3.74E+00	-1.34E+01	8.10E-02	1.08E+00
LYPLA1	4.77E+02	4.01E-03	4.60E-03	8.30E-01	-2.69E-01	-1.20E+00	2.29E+01	2.75E+01
LYPLA2	1.03E+03	3.87E-09	6.56E-08	5.64E-01	-8.25E-01	-1.77E+00	4.02E+01	7.13E+01
LYRM2	3.09E+02	5.53E-09	7.99E-08	5.32E-01	-9.09E-01	-1.88E+00	1.15E+01	2.17E+01
LYRM4	4.98E+02	9.82E-04	1.26E-03	7.76E-01	-3.66E-01	-1.29E+00	2.31E+01	2.98E+01
LZTFL1	6.17E+02	1.05E-05	2.46E-05	5.52E-01	-8.58E-01	-1.81E+00	2.33E+01	4.23E+01
LZTS1	2.88E+03	1.75E-06	5.61E-06	5.96E-01	-7.47E-01	-1.68E+00	1.16E+02	1.94E+02
LZTS3	1.79E+03	2.74E-07	1.38E-06	6.81E-01	-5.54E-01	-1.47E+00	7.80E+01	1.15E+02
MACROD1	5.17E+02	4.66E-07	2.07E-06	6.60E-01	-6.00E-01	-1.52E+00	2.20E+01	3.33E+01
MAD2L2	3.23E+02	6.29E-04	8.48E-04	7.96E-01	-3.30E-01	-1.26E+00	1.52E+01	1.91E+01
MAF1	2.21E+03	1.22E-06	4.29E-06	7.57E-01	-4.02E-01	-1.32E+00	1.01E+02	1.34E+02
MAFK	3.47E+02	2.41E-02	2.50E-02	7.53E-01	-4.09E-01	-1.33E+00	1.58E+01	2.10E+01

MAGED1	8.61E+03	1.87E-02	1.96E-02	8.87E-01	-1.73E-01	-1.13E+00	4.27E+02	4.81E+02
MAGED2	5.48E+03	4.88E-06	1.31E-05	7.12E-01	-4.90E-01	-1.40E+00	2.43E+02	3.42E+02
MAGED4B	4.15E+03	5.31E-04	7.30E-04	8.59E-01	-2.19E-01	-1.16E+00	2.03E+02	2.36E+02
MAGOHB	3.53E+02	7.23E-06	1.82E-05	6.98E-01	-5.18E-01	-1.43E+00	1.56E+01	2.23E+01
MAMDC4	1.99E+02	1.47E-02	1.55E-02	7.94E-01	-3.34E-01	-1.26E+00	9.35E+00	1.18E+01
MAN1B1	2.16E+03	1.81E-03	2.21E-03	7.80E-01	-3.58E-01	-1.28E+00	1.01E+02	1.29E+02
MANBAL	8.66E+02	6.97E-04	9.31E-04	8.73E-01	-1.96E-01	-1.15E+00	4.28E+01	4.90E+01
MAP3K11	1.27E+03	1.64E-07	9.55E-07	7.56E-01	-4.04E-01	-1.32E+00	5.83E+01	7.71E+01
MAP4K2	8.84E+02	1.71E-04	2.73E-04	6.24E-01	-6.80E-01	-1.60E+00	3.65E+01	5.85E+01
MAP6D1	3.10E+02	1.48E-03	1.84E-03	7.02E-01	-5.10E-01	-1.42E+00	1.36E+01	1.94E+01
MAPK10	8.44E+01	5.56E-02	5.64E-02	7.41E-01	-4.32E-01	-1.35E+00	3.77E+00	5.09E+00
MAPK13	4.09E+02	5.28E-05	9.83E-05	3.89E-01	-1.36E+00	-2.57E+00	1.26E+01	3.24E+01
MAPK3	2.05E+03	1.09E-05	2.54E-05	7.98E-01	-3.25E-01	-1.25E+00	9.65E+01	1.21E+02
MAPK4	2.47E+02	4.00E-05	7.74E-05	5.06E-01	-9.83E-01	-1.98E+00	9.10E+00	1.80E+01
MAPK8IP2	2.17E+02	2.28E-09	4.73E-08	8.15E-02	-3.62E+00	-1.23E+01	1.88E+00	2.30E+01
MARCKSL1	7.28E+03	7.84E-09	9.75E-08	5.59E-01	-8.38E-01	-1.79E+00	2.83E+02	5.06E+02
MARK4-2	5.11E+02	4.52E-05	8.65E-05	7.40E-01	-4.35E-01	-1.35E+00	2.32E+01	3.14E+01
MATN1	6.76E+01	9.69E-07	3.56E-06	1.92E-01	-2.38E+00	-5.20E+00	1.23E+00	6.40E+00
MB	5.10E+01	1.03E-02	1.10E-02	7.29E-01	-4.57E-01	-1.37E+00	2.28E+00	3.14E+00
MBD3	2.08E+03	6.64E-08	4.88E-07	6.98E-01	-5.18E-01	-1.43E+00	9.13E+01	1.31E+02
MBD4	4.35E+02	2.27E-04	3.46E-04	7.19E-01	-4.77E-01	-1.39E+00	1.93E+01	2.69E+01
MBNL3	7.38E+02	2.44E-05	5.01E-05	5.11E-01	-9.69E-01	-1.96E+00	2.72E+01	5.32E+01
MBOAT7	1.10E+03	2.29E-05	4.75E-05	6.80E-01	-5.57E-01	-1.47E+00	4.77E+01	7.02E+01
MCHR2	4.62E+01	2.14E-03	2.58E-03	7.00E-01	-5.15E-01	-1.43E+00	2.04E+00	2.91E+00
MCOLN3	1.10E+02	5.12E-06	1.36E-05	1.86E-01	-2.43E+00	-5.39E+00	1.99E+00	1.07E+01
MCRIP2	2.69E+02	1.55E-03	1.91E-03	6.65E-01	-5.88E-01	-1.50E+00	1.16E+01	1.74E+01
MDFI	1.22E+03	3.56E-04	5.12E-04	6.91E-01	-5.33E-01	-1.45E+00	5.31E+01	7.69E+01
MDH1	1.53E+03	1.10E-09	2.99E-08	4.80E-01	-1.06E+00	-2.08E+00	5.36E+01	1.12E+02
MDH2	3.03E+03	1.68E-06	5.45E-06	6.09E-01	-7.16E-01	-1.64E+00	1.23E+02	2.03E+02
MDK	9.90E+03	8.90E-05	1.55E-04	5.50E-01	-8.62E-01	-1.82E+00	3.81E+02	6.92E+02
MEA1	1.09E+03	1.25E-05	2.86E-05	6.29E-01	-6.69E-01	-1.59E+00	4.51E+01	7.16E+01
MECR	2.33E+02	2.06E-05	4.34E-05	6.83E-01	-5.50E-01	-1.46E+00	1.02E+01	1.49E+01
MED16	1.55E+03	4.32E-09	6.82E-08	6.56E-01	-6.09E-01	-1.52E+00	6.60E+01	1.01E+02

MED21	1.16E+03	3.75E-09	6.41E-08	5.40E-01	-8.88E-01	-1.85E+00	4.38E+01	8.11E+01
MED6	3.33E+02	8.07E-07	3.11E-06	6.75E-01	-5.67E-01	-1.48E+00	1.43E+01	2.12E+01
MEPCE	1.94E+03	8.72E-07	3.30E-06	7.49E-01	-4.17E-01	-1.34E+00	8.84E+01	1.18E+02
METRN	3.77E+02	1.21E-07	7.76E-07	5.38E-01	-8.95E-01	-1.86E+00	1.42E+01	2.64E+01
METTL23	3.03E+02	4.32E-03	4.91E-03	7.22E-01	-4.70E-01	-1.38E+00	1.35E+01	1.87E+01
METTL26	4.16E+02	1.09E-03	1.40E-03	7.51E-01	-4.13E-01	-1.33E+00	1.90E+01	2.53E+01
METTL27	9.52E+01	9.43E-05	1.62E-04	5.26E-01	-9.26E-01	-1.90E+00	3.53E+00	6.70E+00
METTL2A	4.91E+02	1.32E-03	1.66E-03	8.87E-01	-1.72E-01	-1.13E+00	2.45E+01	2.76E+01
MEX3D	1.55E+03	7.46E-07	2.94E-06	7.05E-01	-5.03E-01	-1.42E+00	6.90E+01	9.78E+01
MFAP3L	7.71E+01	1.20E-07	7.67E-07	2.84E-01	-1.82E+00	-3.52E+00	1.91E+00	6.71E+00
MFSD10	9.42E+02	2.88E-03	3.39E-03	8.59E-01	-2.19E-01	-1.16E+00	4.62E+01	5.38E+01
MFSD12	3.78E+02	2.42E-06	7.27E-06	6.45E-01	-6.32E-01	-1.55E+00	1.60E+01	2.48E+01
MFSD2A	1.94E+02	4.16E-02	4.25E-02	6.29E-01	-6.68E-01	-1.59E+00	8.25E+00	1.31E+01
MGAM	1.95E+02	6.96E-12	1.10E-09	6.27E-03	-7.32E+00	-1.59E+02	1.46E-01	2.33E+01
MGAT3	8.42E+02	6.62E-09	8.75E-08	3.28E-01	-1.61E+00	-3.05E+00	2.30E+01	7.01E+01
MIA	1.12E+02	5.20E-06	1.38E-05	5.36E-01	-9.00E-01	-1.87E+00	4.23E+00	7.89E+00
MIA2	5.08E+02	8.25E-03	8.95E-03	8.48E-01	-2.38E-01	-1.18E+00	2.46E+01	2.90E+01
MID1IP1	1.68E+03	1.86E-06	5.87E-06	7.36E-01	-4.43E-01	-1.36E+00	7.60E+01	1.03E+02
MIDN	2.23E+03	4.28E-08	3.51E-07	6.35E-01	-6.55E-01	-1.57E+00	9.32E+01	1.47E+02
MIF	1.93E+03	3.55E-05	6.96E-05	6.14E-01	-7.03E-01	-1.63E+00	7.93E+01	1.29E+02
MIF4GD	4.91E+02	3.69E-02	3.78E-02	8.97E-01	-1.57E-01	-1.12E+00	2.47E+01	2.75E+01
MLST8	7.48E+02	9.46E-05	1.62E-04	7.34E-01	-4.46E-01	-1.36E+00	3.38E+01	4.60E+01
MMADHC	1.09E+03	1.51E-05	3.32E-05	7.58E-01	-3.99E-01	-1.32E+00	5.00E+01	6.59E+01
MMP11	4.45E+02	2.66E-07	1.35E-06	4.94E-01	-1.02E+00	-2.02E+00	1.61E+01	3.27E+01
MMP17	6.76E+01	7.32E-05	1.30E-04	5.99E-01	-7.40E-01	-1.67E+00	2.74E+00	4.58E+00
MMP25	2.90E+02	8.11E-07	3.11E-06	2.15E-01	-2.22E+00	-4.65E+00	5.57E+00	2.59E+01
MNX1	8.17E+01	2.21E-07	1.20E-06	1.24E-01	-3.01E+00	-8.08E+00	1.03E+00	8.30E+00
MOGAT1	5.15E+01	2.06E-05	4.34E-05	4.16E-01	-1.26E+00	-2.40E+00	1.66E+00	3.98E+00
MOK	2.29E+02	1.69E-03	2.07E-03	6.76E-01	-5.64E-01	-1.48E+00	9.82E+00	1.45E+01
MORN4	3.50E+02	4.40E-03	4.99E-03	7.69E-01	-3.78E-01	-1.30E+00	1.60E+01	2.08E+01
MOSPD3	6.80E+02	9.69E-03	1.04E-02	8.42E-01	-2.48E-01	-1.19E+00	3.30E+01	3.92E+01
MOV10	2.17E+03	8.69E-13	3.74E-10	3.59E-01	-1.48E+00	-2.79E+00	6.38E+01	1.78E+02
MPC2	2.75E+02	2.84E-03	3.35E-03	7.89E-01	-3.42E-01	-1.27E+00	1.29E+01	1.63E+01

MPG	5.34E+02	3.16E-04	4.62E-04	7.35E-01	-4.43E-01	-1.36E+00	2.41E+01	3.27E+01
MPND	4.01E+02	1.66E-04	2.65E-04	8.10E-01	-3.03E-01	-1.23E+00	1.91E+01	2.36E+01
MPP1	1.18E+03	7.71E-05	1.37E-04	8.08E-01	-3.08E-01	-1.24E+00	5.62E+01	6.96E+01
MPV17	6.93E+02	1.66E-04	2.66E-04	8.02E-01	-3.19E-01	-1.25E+00	3.29E+01	4.11E+01
MPV17L2	1.48E+02	1.63E-05	3.56E-05	4.61E-01	-1.12E+00	-2.17E+00	5.07E+00	1.10E+01
MRAP	6.16E+00	1.39E-02	1.48E-02	5.61E-01	-8.34E-01	-1.78E+00	2.41E-01	4.30E-01
MRAS	1.31E+03	7.52E-06	1.88E-05	7.94E-01	-3.33E-01	-1.26E+00	6.17E+01	7.77E+01
MRI1	4.56E+02	4.28E-05	8.23E-05	7.69E-01	-3.79E-01	-1.30E+00	2.12E+01	2.76E+01
MRPL11	1.18E+03	2.26E-04	3.45E-04	7.07E-01	-5.00E-01	-1.41E+00	5.20E+01	7.35E+01
MRPL12	4.87E+02	9.63E-07	3.55E-06	5.55E-01	-8.50E-01	-1.80E+00	1.88E+01	3.39E+01
MRPL24	6.60E+02	1.78E-07	1.01E-06	6.02E-01	-7.31E-01	-1.66E+00	2.67E+01	4.42E+01
MRPL28	8.14E+02	1.35E-07	8.42E-07	7.08E-01	-4.98E-01	-1.41E+00	3.61E+01	5.10E+01
MRPL34	3.59E+02	1.80E-05	3.87E-05	7.04E-01	-5.06E-01	-1.42E+00	1.60E+01	2.27E+01
MRPL36	5.57E+02	3.72E-03	4.29E-03	8.07E-01	-3.09E-01	-1.24E+00	2.65E+01	3.28E+01
MRPL4	1.12E+03	1.09E-02	1.16E-02	8.70E-01	-2.01E-01	-1.15E+00	5.54E+01	6.37E+01
MRPL45	9.30E+02	8.02E-04	1.05E-03	8.05E-01	-3.13E-01	-1.24E+00	4.41E+01	5.47E+01
MRPL52	7.66E+02	6.90E-03	7.58E-03	8.58E-01	-2.21E-01	-1.17E+00	3.75E+01	4.37E+01
MRPL54	7.03E+02	9.95E-05	1.70E-04	7.87E-01	-3.45E-01	-1.27E+00	3.29E+01	4.18E+01
MRPL55	5.73E+02	4.01E-06	1.12E-05	6.28E-01	-6.72E-01	-1.59E+00	2.37E+01	3.78E+01
MRPL9	1.62E+03	1.35E-05	3.03E-05	7.21E-01	-4.73E-01	-1.39E+00	7.23E+01	1.00E+02
MRPS12	2.46E+02	5.39E-04	7.40E-04	7.24E-01	-4.65E-01	-1.38E+00	1.11E+01	1.53E+01
MRPS15	4.86E+02	4.09E-06	1.14E-05	5.91E-01	-7.59E-01	-1.69E+00	1.94E+01	3.28E+01
MRPS18A	7.13E+02	1.71E-02	1.80E-02	8.90E-01	-1.68E-01	-1.12E+00	3.57E+01	4.01E+01
MRPS24	2.62E+02	1.85E-06	5.86E-06	6.50E-01	-6.22E-01	-1.54E+00	1.10E+01	1.70E+01
MRPS27	9.54E+02	4.15E-05	7.99E-05	7.76E-01	-3.65E-01	-1.29E+00	4.43E+01	5.71E+01
MRPS28	1.72E+02	1.28E-06	4.45E-06	6.90E-01	-5.35E-01	-1.45E+00	7.49E+00	1.09E+01
MRPS33	6.99E+02	1.13E-03	1.44E-03	8.16E-01	-2.94E-01	-1.23E+00	3.33E+01	4.08E+01
MRPS35	5.64E+02	4.47E-05	8.57E-05	7.43E-01	-4.29E-01	-1.35E+00	2.54E+01	3.43E+01
MRPS9	8.81E+02	2.38E-08	2.21E-07	6.64E-01	-5.91E-01	-1.51E+00	3.78E+01	5.69E+01
MRTO4	1.41E+03	3.30E-05	6.52E-05	8.00E-01	-3.22E-01	-1.25E+00	6.65E+01	8.30E+01
MSH2	1.12E+03	3.68E-04	5.27E-04	7.73E-01	-3.71E-01	-1.29E+00	5.21E+01	6.74E+01
MSI1	7.89E+02	1.22E-07	7.76E-07	3.00E-01	-1.74E+00	-3.33E+00	1.99E+01	6.64E+01
MSLN	1.13E+03	2.35E-03	2.81E-03	3.81E-01	-1.39E+00	-2.62E+00	3.38E+01	8.86E+01

MSRA	3.06E+02	8.58E-05	1.50E-04	6.90E-01	-5.36E-01	-1.45E+00	1.34E+01	1.94E+01
MSX2	9.23E+01	8.84E-05	1.54E-04	2.06E-01	-2.28E+00	-4.86E+00	1.79E+00	8.72E+00
MTA1	8.34E+02	2.09E-05	4.40E-05	7.37E-01	-4.40E-01	-1.36E+00	3.77E+01	5.11E+01
MTA2	3.52E+03	1.12E-09	2.99E-08	6.48E-01	-6.26E-01	-1.54E+00	1.48E+02	2.29E+02
MTFR2	1.61E+02	4.49E-03	5.09E-03	5.92E-01	-7.56E-01	-1.69E+00	6.35E+00	1.07E+01
MTHFD1L	8.09E+02	1.02E-04	1.74E-04	5.75E-01	-7.98E-01	-1.74E+00	3.20E+01	5.57E+01
MTHFS	7.67E+02	2.15E-10	1.05E-08	5.39E-01	-8.93E-01	-1.86E+00	2.90E+01	5.39E+01
MTSS1L	5.88E+03	7.51E-07	2.95E-06	5.41E-01	-8.85E-01	-1.85E+00	2.23E+02	4.11E+02
MXD3	1.77E+02	5.10E-05	9.58E-05	5.47E-01	-8.72E-01	-1.83E+00	6.79E+00	1.24E+01
MYCBPAP	1.85E+02	1.01E-04	1.72E-04	5.19E-01	-9.45E-01	-1.93E+00	6.76E+00	1.30E+01
MYCN	5.57E+02	1.11E-06	3.98E-06	3.44E-01	-1.54E+00	-2.90E+00	1.57E+01	4.55E+01
MYH6	1.81E+02	1.04E-06	3.78E-06	3.11E-01	-1.68E+00	-3.21E+00	4.80E+00	1.54E+01
MYH8	6.30E+01	5.01E-05	9.43E-05	3.10E-01	-1.69E+00	-3.22E+00	1.62E+00	5.23E+00
MYL10	1.93E+00	1.57E-04	2.53E-04	1.29E-01	-2.95E+00	-7.74E+00	2.56E-02	1.99E-01
MYL6B	4.33E+02	2.94E-07	1.45E-06	5.21E-01	-9.40E-01	-1.92E+00	1.60E+01	3.07E+01
MYLK2	7.17E+00	1.89E-02	1.98E-02	5.42E-01	-8.82E-01	-1.84E+00	2.73E-01	5.03E-01
MYO19	3.39E+02	1.94E-04	3.03E-04	6.41E-01	-6.41E-01	-1.56E+00	1.43E+01	2.24E+01
MYO3B	1.86E+01	1.65E-06	5.38E-06	1.63E-01	-2.61E+00	-6.12E+00	2.98E-01	1.82E+00
MYOM3	3.04E+02	7.73E-04	1.02E-03	5.73E-01	-8.03E-01	-1.74E+00	1.20E+01	2.09E+01
MZB1	4.72E+01	4.49E-02	4.58E-02	7.22E-01	-4.69E-01	-1.38E+00	2.14E+00	2.96E+00
MZF1	3.02E+03	2.19E-05	4.56E-05	7.25E-01	-4.63E-01	-1.38E+00	1.35E+02	1.87E+02
N4BP3	2.43E+02	9.83E-06	2.33E-05	5.78E-01	-7.92E-01	-1.73E+00	9.61E+00	1.66E+01
NABP2	8.33E+02	1.16E-06	4.11E-06	7.39E-01	-4.36E-01	-1.35E+00	3.78E+01	5.11E+01
NACA	5.54E+03	1.50E-03	1.85E-03	8.61E-01	-2.16E-01	-1.16E+00	2.71E+02	3.15E+02
NAGPA	3.15E+02	1.93E-04	3.02E-04	8.09E-01	-3.06E-01	-1.24E+00	1.50E+01	1.86E+01
NAIF1	1.60E+02	5.47E-04	7.51E-04	7.23E-01	-4.68E-01	-1.38E+00	7.12E+00	9.85E+00
NANOG	2.63E+02	7.55E-09	9.50E-08	9.18E-04	-1.01E+01	-1.09E+03	2.91E-02	3.17E+01
NANP	1.61E+02	8.98E-02	9.05E-02	8.96E-01	-1.59E-01	-1.12E+00	8.00E+00	8.94E+00
NANS	4.54E+02	1.44E-03	1.79E-03	7.41E-01	-4.32E-01	-1.35E+00	2.07E+01	2.79E+01
NAP1L5	1.47E+02	9.63E-04	1.24E-03	6.67E-01	-5.85E-01	-1.50E+00	6.28E+00	9.41E+00
NAPA	1.50E+03	9.00E-05	1.56E-04	8.23E-01	-2.81E-01	-1.21E+00	7.19E+01	8.74E+01
NAT14	4.67E+02	5.75E-04	7.83E-04	8.04E-01	-3.15E-01	-1.24E+00	2.21E+01	2.75E+01
NAXD	9.98E+02	4.82E-05	9.14E-05	7.47E-01	-4.22E-01	-1.34E+00	4.54E+01	6.08E+01

NCKAP5L	2.79E+03	2.16E-04	3.33E-04	7.72E-01	-3.73E-01	-1.30E+00	1.30E+02	1.68E+02
NCR3LG1	1.35E+02	2.33E-06	7.06E-06	6.32E-01	-6.63E-01	-1.58E+00	5.60E+00	8.86E+00
NCS1	4.73E+02	7.95E-05	1.41E-04	6.46E-01	-6.31E-01	-1.55E+00	1.99E+01	3.08E+01
ND1	3.40E+04	3.61E-04	5.19E-04	5.32E-01	-9.10E-01	-1.88E+00	1.27E+03	2.39E+03
ND2	3.12E+04	1.88E-04	2.95E-04	6.02E-01	-7.33E-01	-1.66E+00	1.25E+03	2.08E+03
ND3	1.82E+04	2.96E-02	3.05E-02	7.30E-01	-4.54E-01	-1.37E+00	8.16E+02	1.12E+03
ND4	4.98E+04	4.58E-04	6.41E-04	6.20E-01	-6.89E-01	-1.61E+00	2.03E+03	3.28E+03
ND4L	5.60E+03	4.94E-04	6.86E-04	6.16E-01	-6.98E-01	-1.62E+00	2.28E+02	3.69E+02
NDC80	1.92E+02	1.17E-04	1.94E-04	6.26E-01	-6.75E-01	-1.60E+00	7.93E+00	1.27E+01
NDN	1.07E+03	4.20E-06	1.16E-05	7.07E-01	-5.01E-01	-1.42E+00	4.75E+01	6.73E+01
NDUFAF5	8.15E+01	5.80E-03	6.43E-03	7.43E-01	-4.28E-01	-1.35E+00	3.72E+00	5.00E+00
NDUFB1	1.25E+02	2.55E-05	5.20E-05	5.23E-01	-9.36E-01	-1.91E+00	4.64E+00	8.87E+00
NDUFB3	4.51E+02	1.19E-04	1.98E-04	6.82E-01	-5.52E-01	-1.47E+00	1.96E+01	2.88E+01
NDUFB5	5.65E+02	1.37E-06	4.61E-06	5.87E-01	-7.68E-01	-1.70E+00	2.24E+01	3.82E+01
NDUFB6	3.54E+02	5.40E-03	6.03E-03	8.06E-01	-3.11E-01	-1.24E+00	1.68E+01	2.09E+01
NDUFB7	5.94E+02	3.03E-07	1.49E-06	6.51E-01	-6.20E-01	-1.54E+00	2.51E+01	3.86E+01
NDUFB8	1.01E+03	9.72E-06	2.31E-05	7.20E-01	-4.75E-01	-1.39E+00	4.52E+01	6.28E+01
NDUFC2	1.04E+03	5.68E-05	1.05E-04	7.54E-01	-4.08E-01	-1.33E+00	4.76E+01	6.32E+01
NDUFS2	2.70E+03	8.59E-05	1.50E-04	7.82E-01	-3.54E-01	-1.28E+00	1.26E+02	1.61E+02
NDUFS4	6.37E+02	3.46E-03	3.99E-03	7.28E-01	-4.58E-01	-1.37E+00	2.85E+01	3.92E+01
NDUFS7	6.42E+02	7.59E-07	2.97E-06	6.91E-01	-5.33E-01	-1.45E+00	2.81E+01	4.07E+01
NDUFV3	1.32E+03	2.33E-05	4.83E-05	6.90E-01	-5.34E-01	-1.45E+00	5.78E+01	8.37E+01
NECAB2	4.74E+02	3.28E-05	6.48E-05	4.39E-01	-1.19E+00	-2.28E+00	1.60E+01	3.63E+01
NECAP2	1.25E+03	1.19E-05	2.74E-05	7.73E-01	-3.72E-01	-1.29E+00	5.76E+01	7.45E+01
NECTIN1	5.95E+02	3.45E-08	2.98E-07	3.21E-01	-1.64E+00	-3.12E+00	1.59E+01	4.96E+01
NECTIN2	3.92E+03	7.27E-08	5.26E-07	5.83E-01	-7.79E-01	-1.72E+00	1.56E+02	2.67E+02
NEK6	1.59E+03	7.24E-04	9.61E-04	8.23E-01	-2.82E-01	-1.22E+00	7.65E+01	9.30E+01
NFATC4	2.11E+03	6.11E-04	8.26E-04	7.80E-01	-3.58E-01	-1.28E+00	9.81E+01	1.26E+02
NFE2L3	3.42E+02	1.36E-03	1.70E-03	6.15E-01	-7.02E-01	-1.63E+00	1.38E+01	2.25E+01
NHLH1	7.24E+01	1.64E-03	2.01E-03	6.68E-01	-5.83E-01	-1.50E+00	3.09E+00	4.63E+00
NHP2	4.21E+02	2.51E-02	2.60E-02	8.32E-01	-2.65E-01	-1.20E+00	2.03E+01	2.44E+01
NIFK	8.31E+02	9.98E-07	3.64E-06	6.90E-01	-5.36E-01	-1.45E+00	3.63E+01	5.26E+01
NINJ1	3.69E+02	2.44E-04	3.69E-04	6.87E-01	-5.42E-01	-1.46E+00	1.61E+01	2.34E+01

NIPSNAP2	1.12E+03	4.72E-02	4.81E-02	9.24E-01	-1.14E-01	-1.08E+00	5.68E+01	6.15E+01
NIT1	3.14E+02	2.87E-08	2.59E-07	5.98E-01	-7.41E-01	-1.67E+00	1.26E+01	2.11E+01
NKD1	1.88E+03	1.54E-02	1.62E-02	6.17E-01	-6.97E-01	-1.62E+00	7.73E+01	1.25E+02
NKIRAS2	1.80E+03	2.22E-04	3.40E-04	8.29E-01	-2.70E-01	-1.21E+00	8.65E+01	1.04E+02
NLGN4X	3.66E+02	1.33E-04	2.17E-04	4.02E-01	-1.32E+00	-2.49E+00	1.17E+01	2.91E+01
NLRX1	4.32E+02	1.31E-11	1.68E-09	4.66E-01	-1.10E+00	-2.15E+00	1.50E+01	3.22E+01
NME1	4.19E+02	2.63E-07	1.34E-06	5.56E-01	-8.47E-01	-1.80E+00	1.61E+01	2.90E+01
NME3	8.29E+02	6.64E-03	7.30E-03	8.57E-01	-2.22E-01	-1.17E+00	4.06E+01	4.74E+01
NME4	2.13E+03	8.21E-11	5.43E-09	5.70E-01	-8.12E-01	-1.76E+00	8.37E+01	1.47E+02
NMUR2	4.53E+00	3.78E-07	1.77E-06	1.17E-01	-3.09E+00	-8.54E+00	5.45E-02	4.65E-01
NNAT	1.28E+03	7.75E-06	1.92E-05	5.87E-01	-7.68E-01	-1.70E+00	5.12E+01	8.72E+01
NOB1	8.96E+02	1.33E-05	2.99E-05	7.24E-01	-4.66E-01	-1.38E+00	4.02E+01	5.55E+01
NOC4L	5.89E+02	4.44E-08	3.61E-07	5.64E-01	-8.25E-01	-1.77E+00	2.29E+01	4.06E+01
NOG	2.67E+01	1.77E-01	1.78E-01	5.65E-01	-8.23E-01	-1.77E+00	1.07E+00	1.90E+00
NOL4L	2.33E+03	5.35E-04	7.35E-04	6.94E-01	-5.26E-01	-1.44E+00	1.02E+02	1.46E+02
NOP56	1.81E+03	4.38E-04	6.16E-04	7.89E-01	-3.43E-01	-1.27E+00	8.47E+01	1.07E+02
NOS1AP	6.70E+01	6.85E-05	1.23E-04	4.04E-01	-1.31E+00	-2.47E+00	2.11E+00	5.22E+00
NOSIP	1.26E+03	3.17E-03	3.69E-03	8.78E-01	-1.87E-01	-1.14E+00	6.26E+01	7.13E+01
NPFF	7.02E+00	2.40E-06	7.22E-06	1.01E-01	-3.30E+00	-9.87E+00	7.54E-02	7.45E-01
NPM1	7.53E+03	5.59E-07	2.39E-06	7.20E-01	-4.74E-01	-1.39E+00	3.37E+02	4.68E+02
NPSR1	2.11E+01	3.32E-03	3.85E-03	3.00E-01	-1.74E+00	-3.34E+00	5.54E-01	1.85E+00
NQO1	2.35E+02	1.03E-04	1.74E-04	4.98E-01	-1.00E+00	-2.01E+00	8.66E+00	1.74E+01
NR_001576.1	1.75E+01	1.29E-04	2.12E-04	4.53E-01	-1.14E+00	-2.21E+00	6.02E-01	1.33E+00
NR_024614.1	2.32E+02	1.32E-06	4.49E-06	5.46E-01	-8.73E-01	-1.83E+00	8.86E+00	1.62E+01
NR_028029.1	6.63E+02	3.95E-04	5.62E-04	7.59E-01	-3.98E-01	-1.32E+00	3.03E+01	3.99E+01
NR_031133.1	2.10E+00	1.95E-02	2.04E-02	2.65E-01	-1.92E+00	-3.78E+00	4.91E-02	1.85E-01
NR_036663.1	2.44E+02	7.34E-04	9.71E-04	6.11E-01	-7.11E-01	-1.64E+00	1.00E+01	1.64E+01
NR_046270.1	1.84E+02	1.40E-03	1.74E-03	7.93E-01	-3.35E-01	-1.26E+00	8.66E+00	1.09E+01
NR_104052.1	4.98E+00	9.70E-03	1.04E-02	3.58E-01	-1.48E+00	-2.80E+00	1.48E-01	4.13E-01
NR_110389.1	1.06E+02	2.25E-04	3.43E-04	5.21E-01	-9.42E-01	-1.92E+00	3.88E+00	7.45E+00
NR_120605.1	3.09E+02	2.54E-06	7.55E-06	5.25E-01	-9.30E-01	-1.91E+00	1.16E+01	2.21E+01
NR_131901.1	3.38E+03	8.34E-05	1.46E-04	6.46E-01	-6.29E-01	-1.55E+00	1.43E+02	2.22E+02
NR_131934.1	1.77E+02	6.38E-05	1.16E-04	3.00E-01	-1.73E+00	-3.33E+00	4.57E+00	1.52E+01

NR_132275.1	6.96E+01	9.82E-04	1.26E-03	6.50E-01	-6.22E-01	-1.54E+00	2.93E+00	4.51E+00
NR_137293.1	3.69E+02	8.49E-06	2.07E-05	4.23E-01	-1.24E+00	-2.36E+00	1.20E+01	2.83E+01
NR0B1	1.67E+02	2.07E-08	2.03E-07	3.98E-01	-1.33E+00	-2.51E+00	5.27E+00	1.33E+01
NR2C2AP	2.52E+02	9.52E-04	1.23E-03	7.65E-01	-3.86E-01	-1.31E+00	1.16E+01	1.52E+01
NR5A1	4.33E+03	4.96E-08	3.91E-07	5.26E-01	-9.27E-01	-1.90E+00	1.62E+02	3.08E+02
NRG1	3.13E+02	6.39E-05	1.16E-04	4.97E-01	-1.01E+00	-2.01E+00	1.14E+01	2.29E+01
NRGN	6.65E+01	1.66E-02	1.74E-02	6.68E-01	-5.83E-01	-1.50E+00	2.88E+00	4.31E+00
NRM	5.17E+02	1.43E-06	4.80E-06	6.11E-01	-7.10E-01	-1.64E+00	2.11E+01	3.45E+01
NRSN2	1.89E+02	1.37E-06	4.61E-06	3.68E-01	-1.44E+00	-2.71E+00	5.58E+00	1.52E+01
NSMF	2.60E+03	2.11E-05	4.42E-05	7.22E-01	-4.69E-01	-1.38E+00	1.17E+02	1.61E+02
NT5C	5.05E+02	1.63E-03	2.01E-03	6.76E-01	-5.66E-01	-1.48E+00	2.21E+01	3.27E+01
NTF4	1.13E+02	3.25E-04	4.72E-04	5.31E-01	-9.12E-01	-1.88E+00	4.21E+00	7.93E+00
NTRK1	1.69E+02	1.06E-04	1.79E-04	3.31E-01	-1.60E+00	-3.02E+00	4.72E+00	1.43E+01
NUDCD3	1.63E+03	5.63E-09	8.07E-08	7.23E-01	-4.69E-01	-1.38E+00	7.33E+01	1.01E+02
NUDT10	1.55E+02	3.35E-06	9.61E-06	4.98E-01	-1.01E+00	-2.01E+00	5.60E+00	1.13E+01
NUDT14	2.97E+02	8.01E-07	3.10E-06	5.65E-01	-8.24E-01	-1.77E+00	1.16E+01	2.05E+01
NUDT16	5.01E+02	3.16E-03	3.69E-03	7.46E-01	-4.22E-01	-1.34E+00	2.29E+01	3.08E+01
NUDT5	3.66E+02	3.71E-02	3.80E-02	8.90E-01	-1.68E-01	-1.12E+00	1.83E+01	2.05E+01
NUP35	3.39E+02	1.89E-03	2.30E-03	8.03E-01	-3.16E-01	-1.24E+00	1.60E+01	1.99E+01
NUTM1	1.03E+02	6.73E-10	2.23E-08	3.28E-02	-4.93E+00	-3.05E+01	3.76E-01	1.15E+01
NXPH3	2.16E+02	1.28E-02	1.36E-02	6.66E-01	-5.85E-01	-1.50E+00	9.37E+00	1.41E+01
NYNRIN	7.89E+03	1.23E-06	4.32E-06	5.37E-01	-8.98E-01	-1.86E+00	2.99E+02	5.58E+02
OAZ1	5.71E+03	1.31E-06	4.49E-06	6.83E-01	-5.50E-01	-1.46E+00	2.48E+02	3.62E+02
OAZ2	2.74E+03	6.23E-07	2.56E-06	7.68E-01	-3.82E-01	-1.30E+00	1.27E+02	1.65E+02
OBP	7.97E+00	1.95E-02	2.04E-02	2.60E-01	-1.94E+00	-3.85E+00	1.88E-01	7.24E-01
OCA2	3.28E+01	4.79E-05	9.11E-05	1.70E-01	-2.55E+00	-5.87E+00	5.49E-01	3.22E+00
OCIAD1	2.38E+03	7.46E-07	2.94E-06	7.19E-01	-4.76E-01	-1.39E+00	1.06E+02	1.48E+02
OLFM1	1.70E+01	1.75E-07	1.00E-06	1.14E-01	-3.13E+00	-8.78E+00	1.99E-01	1.74E+00
OLIG3	1.66E+01	1.06E-10	6.39E-09	1.52E-03	-9.36E+00	-6.59E+02	2.99E-03	1.97E+00
ORAI1	3.85E+02	8.96E-04	1.16E-03	8.40E-01	-2.51E-01	-1.19E+00	1.86E+01	2.22E+01
OSGEP	5.27E+02	2.16E-05	4.51E-05	7.41E-01	-4.33E-01	-1.35E+00	2.39E+01	3.23E+01
OSR1	3.29E+02	2.00E-09	4.27E-08	1.60E-01	-2.64E+00	-6.25E+00	5.24E+00	3.27E+01
OTUB2	1.61E+02	2.26E-04	3.45E-04	7.15E-01	-4.83E-01	-1.40E+00	7.17E+00	1.00E+01

OXA1L	1.99E+03	9.56E-07	3.54E-06	7.12E-01	-4.90E-01	-1.40E+00	8.85E+01	1.24E+02
OXLD1	1.35E+02	3.92E-08	3.29E-07	5.83E-01	-7.78E-01	-1.71E+00	5.35E+00	9.18E+00
P2RX3	7.81E+01	2.15E-05	4.50E-05	4.37E-01	-1.19E+00	-2.29E+00	2.61E+00	5.96E+00
P3H4	1.12E+03	6.18E-03	6.82E-03	8.43E-01	-2.47E-01	-1.19E+00	5.42E+01	6.43E+01
PABPC1L	1.51E+02	6.59E-05	1.19E-04	5.99E-01	-7.40E-01	-1.67E+00	6.10E+00	1.02E+01
PABPN1	4.37E+03	6.13E-07	2.54E-06	7.21E-01	-4.71E-01	-1.39E+00	1.96E+02	2.72E+02
PACS2	2.50E+03	2.93E-06	8.55E-06	7.61E-01	-3.95E-01	-1.31E+00	1.15E+02	1.51E+02
PAGR1	1.11E+03	5.22E-07	2.27E-06	7.50E-01	-4.14E-01	-1.33E+00	5.08E+01	6.76E+01
PAK4	1.52E+03	1.17E-07	7.52E-07	5.71E-01	-8.09E-01	-1.75E+00	5.98E+01	1.05E+02
PALD1	7.47E+02	1.81E-06	5.76E-06	6.66E-01	-5.87E-01	-1.50E+00	3.20E+01	4.81E+01
PAMR1	1.22E+02	2.35E-04	3.56E-04	2.78E-01	-1.85E+00	-3.59E+00	3.02E+00	1.08E+01
PANX3	7.66E+00	5.30E-03	5.93E-03	2.18E-01	-2.19E+00	-4.58E+00	1.54E-01	7.06E-01
PAPSS1	2.06E+03	4.54E-04	6.35E-04	8.15E-01	-2.96E-01	-1.23E+00	9.84E+01	1.21E+02
PARVB	3.55E+02	6.78E-05	1.22E-04	7.07E-01	-4.99E-01	-1.41E+00	1.57E+01	2.23E+01
PATZ1	2.05E+03	3.52E-09	6.12E-08	6.24E-01	-6.80E-01	-1.60E+00	8.45E+01	1.35E+02
PAX5	1.05E+01	1.45E-02	1.54E-02	2.73E-01	-1.87E+00	-3.66E+00	2.45E-01	8.97E-01
PAXX	4.63E+02	9.34E-05	1.61E-04	6.92E-01	-5.30E-01	-1.44E+00	2.03E+01	2.93E+01
PBX2	4.88E+03	6.18E-09	8.56E-08	5.25E-01	-9.30E-01	-1.91E+00	1.82E+02	3.47E+02
PCBP3	1.15E+02	4.74E-07	2.10E-06	3.03E-01	-1.72E+00	-3.30E+00	2.94E+00	9.69E+00
PCBP4	2.17E+03	1.93E-09	4.17E-08	5.18E-01	-9.49E-01	-1.93E+00	8.00E+01	1.54E+02
PCED1B	1.46E+03	7.51E-06	1.88E-05	5.89E-01	-7.63E-01	-1.70E+00	5.88E+01	9.98E+01
PCGF2	2.33E+03	2.04E-05	4.31E-05	7.63E-01	-3.89E-01	-1.31E+00	1.08E+02	1.41E+02
PCP4L1	6.81E+02	6.10E-06	1.57E-05	4.47E-01	-1.16E+00	-2.24E+00	2.28E+01	5.11E+01
PCSK4	8.13E+02	2.11E-06	6.49E-06	5.45E-01	-8.75E-01	-1.83E+00	3.07E+01	5.64E+01
PCYOX1L	5.04E+02	1.43E-05	3.17E-05	5.69E-01	-8.14E-01	-1.76E+00	1.97E+01	3.46E+01
PCYT2	9.29E+02	1.29E-04	2.12E-04	6.40E-01	-6.44E-01	-1.56E+00	3.89E+01	6.08E+01
PDCL3	5.85E+02	2.00E-04	3.11E-04	7.87E-01	-3.45E-01	-1.27E+00	2.75E+01	3.49E+01
PDE6G	2.91E+01	8.11E-05	1.43E-04	3.18E-01	-1.65E+00	-3.14E+00	7.59E-01	2.38E+00
PDE9A	4.47E+02	2.74E-04	4.07E-04	7.80E-01	-3.59E-01	-1.28E+00	2.09E+01	2.68E+01
PDF	1.10E+02	1.43E-03	1.78E-03	7.60E-01	-3.97E-01	-1.32E+00	5.09E+00	6.70E+00
PDGFA	1.13E+03	1.74E-08	1.77E-07	3.63E-01	-1.46E+00	-2.76E+00	3.28E+01	9.05E+01
PDIA4	6.00E+03	1.31E-06	4.49E-06	7.15E-01	-4.85E-01	-1.40E+00	2.67E+02	3.73E+02
PDIA5	1.06E+03	7.67E-03	8.35E-03	7.42E-01	-4.30E-01	-1.35E+00	4.81E+01	6.47E+01

PDZD4	1.88E+02	6.11E-09	8.53E-08	2.91E-01	-1.78E+00	-3.44E+00	4.74E+00	1.63E+01
PEBP4	1.41E+01	1.06E-02	1.13E-02	3.70E-01	-1.44E+00	-2.70E+00	4.31E-01	1.17E+00
PEPD	9.44E+02	3.50E-05	6.86E-05	7.64E-01	-3.89E-01	-1.31E+00	4.34E+01	5.68E+01
PEX10	1.39E+03	3.00E-05	5.97E-05	7.87E-01	-3.45E-01	-1.27E+00	6.52E+01	8.29E+01
PEX11G	5.39E+02	7.36E-03	8.03E-03	8.30E-01	-2.69E-01	-1.21E+00	2.60E+01	3.13E+01
PEX14	1.07E+03	3.85E-06	1.08E-05	7.31E-01	-4.52E-01	-1.37E+00	4.84E+01	6.62E+01
PEX2	3.16E+02	3.43E-04	4.95E-04	7.98E-01	-3.26E-01	-1.25E+00	1.49E+01	1.87E+01
PEX5	1.29E+03	4.60E-09	7.03E-08	6.13E-01	-7.06E-01	-1.63E+00	5.27E+01	8.59E+01
PFDN1	9.06E+02	6.30E-04	8.48E-04	7.51E-01	-4.14E-01	-1.33E+00	4.15E+01	5.52E+01
PFKFB3	1.16E+03	8.76E-07	3.31E-06	4.69E-01	-1.09E+00	-2.13E+00	4.06E+01	8.65E+01
PFKL	1.71E+03	1.85E-06	5.86E-06	5.90E-01	-7.62E-01	-1.70E+00	6.91E+01	1.17E+02
PFN1	5.32E+03	2.61E-05	5.32E-05	7.50E-01	-4.16E-01	-1.33E+00	2.44E+02	3.26E+02
PGLS	1.06E+03	4.51E-06	1.23E-05	6.93E-01	-5.29E-01	-1.44E+00	4.65E+01	6.71E+01
PHB	1.72E+03	7.02E-07	2.81E-06	6.86E-01	-5.44E-01	-1.46E+00	7.51E+01	1.09E+02
PHB2	2.29E+03	4.51E-04	6.32E-04	7.98E-01	-3.26E-01	-1.25E+00	1.08E+02	1.36E+02
PHC2	3.03E+03	6.06E-06	1.56E-05	8.22E-01	-2.83E-01	-1.22E+00	1.46E+02	1.77E+02
PHETA1	3.92E+02	3.25E-07	1.57E-06	7.38E-01	-4.39E-01	-1.36E+00	1.78E+01	2.41E+01
PHF21B	8.63E+01	3.51E-07	1.67E-06	2.12E-01	-2.24E+00	-4.72E+00	1.71E+00	8.09E+00
PHGDH	2.09E+03	3.34E-08	2.93E-07	3.88E-01	-1.37E+00	-2.58E+00	6.43E+01	1.66E+02
PHKG2	1.21E+03	4.98E-08	3.91E-07	6.46E-01	-6.31E-01	-1.55E+00	5.09E+01	7.88E+01
PHLDA1	8.27E+02	1.10E-05	2.56E-05	4.51E-01	-1.15E+00	-2.22E+00	2.81E+01	6.22E+01
PHLDB1	7.13E+03	3.70E-04	5.30E-04	7.21E-01	-4.71E-01	-1.39E+00	3.20E+02	4.44E+02
PHOSPHO1	9.29E+01	3.01E-14	6.17E-11	4.34E-02	-4.53E+00	-2.31E+01	4.56E-01	1.05E+01
PI3	3.03E+01	1.46E-04	2.38E-04	1.94E-01	-2.36E+00	-5.15E+00	5.63E-01	2.90E+00
PID1	1.98E+02	1.28E-02	1.37E-02	6.27E-01	-6.72E-01	-1.59E+00	8.37E+00	1.33E+01
PIDD1	9.90E+02	6.90E-04	9.23E-04	5.98E-01	-7.41E-01	-1.67E+00	3.99E+01	6.68E+01
PIGB	2.11E+02	1.24E-04	2.05E-04	7.01E-01	-5.12E-01	-1.43E+00	9.28E+00	1.32E+01
PIGC	1.27E+03	3.73E-04	5.34E-04	8.39E-01	-2.53E-01	-1.19E+00	6.17E+01	7.36E+01
PIGQ	1.19E+03	1.95E-05	4.14E-05	7.34E-01	-4.46E-01	-1.36E+00	5.40E+01	7.35E+01
PIH1D1	5.22E+02	4.47E-04	6.26E-04	7.71E-01	-3.75E-01	-1.30E+00	2.42E+01	3.14E+01
PIK3CD	4.95E+02	9.12E-13	3.74E-10	2.70E-01	-1.89E+00	-3.70E+00	1.17E+01	4.33E+01
PIK3R2	4.35E+03	2.25E-07	1.21E-06	6.36E-01	-6.52E-01	-1.57E+00	1.81E+02	2.85E+02
PIMREG	1.93E+02	8.13E-05	1.43E-04	5.48E-01	-8.67E-01	-1.82E+00	7.43E+00	1.36E+01

PIN1	2.26E+03	1.55E-05	3.39E-05	7.03E-01	-5.08E-01	-1.42E+00	9.97E+01	1.42E+02
PITPNM1	2.73E+02	4.63E-08	3.72E-07	5.18E-01	-9.50E-01	-1.93E+00	1.01E+01	1.95E+01
PKHD1	6.57E+00	3.18E-03	3.71E-03	3.04E-01	-1.72E+00	-3.28E+00	1.66E-01	5.46E-01
PKM	1.27E+04	6.45E-09	8.60E-08	5.30E-01	-9.17E-01	-1.89E+00	4.81E+02	9.08E+02
PLA2G5	9.44E+00	5.07E-04	7.01E-04	3.38E-01	-1.56E+00	-2.96E+00	2.66E-01	7.86E-01
PLCXD1	7.79E+01	4.53E-09	7.02E-08	1.51E-01	-2.72E+00	-6.61E+00	1.19E+00	7.86E+00
PLD3	8.21E+03	1.03E-05	2.43E-05	6.30E-01	-6.67E-01	-1.59E+00	3.41E+02	5.42E+02
PLEC	9.29E+03	2.58E-03	3.07E-03	7.69E-01	-3.79E-01	-1.30E+00	4.29E+02	5.58E+02
PLEK2	1.30E+02	2.70E-07	1.37E-06	3.69E-01	-1.44E+00	-2.71E+00	3.97E+00	1.08E+01
PLEKHG5	1.85E+03	2.72E-07	1.37E-06	6.44E-01	-6.34E-01	-1.55E+00	7.78E+01	1.21E+02
PLEKHM2	1.85E+03	1.42E-05	3.15E-05	8.36E-01	-2.59E-01	-1.20E+00	8.96E+01	1.07E+02
PLIN3	1.17E+03	9.61E-08	6.59E-07	5.77E-01	-7.94E-01	-1.73E+00	4.67E+01	8.10E+01
PLK3	2.19E+02	9.62E-03	1.04E-02	8.12E-01	-3.01E-01	-1.23E+00	1.04E+01	1.29E+01
PLPP7	4.36E+02	9.75E-05	1.67E-04	7.58E-01	-4.01E-01	-1.32E+00	2.00E+01	2.64E+01
PLVAP	2.21E+02	1.82E-03	2.21E-03	5.02E-01	-9.94E-01	-1.99E+00	8.07E+00	1.61E+01
PLXNA1	2.64E+03	2.87E-05	5.75E-05	6.39E-01	-6.45E-01	-1.56E+00	1.11E+02	1.73E+02
PLXNB1	1.20E+03	1.30E-06	4.47E-06	6.67E-01	-5.84E-01	-1.50E+00	5.14E+01	7.71E+01
PMM2	6.23E+02	1.67E-03	2.04E-03	8.39E-01	-2.54E-01	-1.19E+00	3.01E+01	3.60E+01
PNKD	7.67E+02	1.93E-07	1.07E-06	6.42E-01	-6.40E-01	-1.56E+00	3.21E+01	5.00E+01
PNKP	7.26E+02	4.29E-06	1.17E-05	7.11E-01	-4.91E-01	-1.41E+00	3.22E+01	4.53E+01
PNMT	3.56E+01	7.65E-06	1.90E-05	2.37E-01	-2.07E+00	-4.21E+00	7.79E-01	3.28E+00
POLR2D	3.68E+02	7.39E-07	2.93E-06	6.68E-01	-5.82E-01	-1.50E+00	1.57E+01	2.36E+01
POLR2E	1.93E+03	2.12E-08	2.06E-07	6.41E-01	-6.41E-01	-1.56E+00	8.08E+01	1.26E+02
POLR2L	4.70E+02	1.70E-04	2.71E-04	6.87E-01	-5.41E-01	-1.45E+00	2.05E+01	2.98E+01
POLR3E	6.82E+02	2.64E-04	3.94E-04	8.28E-01	-2.72E-01	-1.21E+00	3.29E+01	3.97E+01
POMGNT1	1.71E+03	1.27E-05	2.89E-05	7.73E-01	-3.72E-01	-1.29E+00	7.93E+01	1.03E+02
POP1	2.84E+02	8.38E-06	2.04E-05	6.47E-01	-6.28E-01	-1.55E+00	1.20E+01	1.86E+01
POP7	1.21E+03	2.64E-03	3.13E-03	8.03E-01	-3.16E-01	-1.24E+00	5.74E+01	7.15E+01
POU5F1	9.28E+02	2.90E-07	1.44E-06	6.58E-02	-3.93E+00	-1.52E+01	6.75E+00	1.03E+02
PPA2	2.95E+02	7.60E-03	8.28E-03	7.47E-01	-4.21E-01	-1.34E+00	1.34E+01	1.80E+01
PPCS	4.97E+02	8.57E-04	1.11E-03	7.90E-01	-3.39E-01	-1.27E+00	2.34E+01	2.96E+01
PPIA	5.14E+03	3.20E-06	9.21E-06	5.84E-01	-7.76E-01	-1.71E+00	2.04E+02	3.49E+02
PPIL1	6.12E+02	9.67E-07	3.56E-06	6.74E-01	-5.69E-01	-1.48E+00	2.64E+01	3.92E+01

PPM1F	1.45E+03	2.25E-03	2.70E-03	8.14E-01	-2.96E-01	-1.23E+00	6.96E+01	8.55E+01
PPP1CA	1.88E+03	3.76E-08	3.20E-07	5.96E-01	-7.47E-01	-1.68E+00	7.57E+01	1.27E+02
PPP1R12C	1.33E+03	4.09E-03	4.68E-03	8.74E-01	-1.95E-01	-1.14E+00	6.57E+01	7.52E+01
PPP1R14B	7.59E+02	9.19E-05	1.59E-04	6.82E-01	-5.51E-01	-1.47E+00	3.31E+01	4.85E+01
PPP1R14C	1.09E+02	1.09E-05	2.55E-05	2.90E-01	-1.78E+00	-3.44E+00	2.72E+00	9.36E+00
PPP1R16A	9.97E+02	1.80E-07	1.01E-06	5.47E-01	-8.72E-01	-1.83E+00	3.80E+01	6.96E+01
PPP1R1B	4.42E+02	1.26E-06	4.40E-06	3.13E-01	-1.68E+00	-3.20E+00	1.16E+01	3.72E+01
PPP2R1A	6.95E+03	6.23E-09	8.57E-08	6.54E-01	-6.14E-01	-1.53E+00	2.95E+02	4.52E+02
PPP2R2A	1.19E+03	3.34E-04	4.84E-04	8.76E-01	-1.91E-01	-1.14E+00	5.89E+01	6.73E+01
PPP4R1	1.94E+03	1.32E-08	1.42E-07	7.59E-01	-3.98E-01	-1.32E+00	8.91E+01	1.17E+02
PPP6R2	1.91E+03	7.11E-05	1.27E-04	7.20E-01	-4.74E-01	-1.39E+00	8.53E+01	1.18E+02
PPT2	6.07E+02	1.37E-08	1.45E-07	6.86E-01	-5.44E-01	-1.46E+00	2.64E+01	3.85E+01
PQBP1	9.82E+02	9.09E-05	1.57E-04	8.33E-01	-2.64E-01	-1.20E+00	4.76E+01	5.71E+01
PQLC3	9.76E+01	6.18E-05	1.13E-04	3.96E-01	-1.33E+00	-2.52E+00	3.06E+00	7.72E+00
PRDM1	6.41E+02	3.28E-08	2.90E-07	5.73E-01	-8.04E-01	-1.75E+00	2.54E+01	4.44E+01
PRDM14	1.60E+02	1.14E-06	4.05E-06	8.06E-03	-6.95E+00	-1.24E+02	1.47E-01	1.83E+01
PRDX1	4.47E+03	1.45E-11	1.74E-09	4.26E-01	-1.23E+00	-2.35E+00	1.46E+02	3.44E+02
PRDX2	4.56E+03	3.58E-05	7.01E-05	6.98E-01	-5.19E-01	-1.43E+00	2.01E+02	2.89E+02
PRDX5	1.35E+03	1.14E-06	4.05E-06	6.42E-01	-6.40E-01	-1.56E+00	5.67E+01	8.83E+01
PREB	8.06E+02	1.63E-06	5.33E-06	7.73E-01	-3.72E-01	-1.29E+00	3.74E+01	4.83E+01
PRELID1	1.38E+03	1.59E-04	2.56E-04	6.87E-01	-5.41E-01	-1.45E+00	6.03E+01	8.77E+01
PRELID3B	6.35E+02	2.33E-02	2.42E-02	8.51E-01	-2.32E-01	-1.17E+00	3.09E+01	3.63E+01
PRKAR1B	5.12E+02	1.65E-05	3.59E-05	7.07E-01	-5.00E-01	-1.41E+00	2.26E+01	3.20E+01
PRKRA	3.64E+02	1.46E-03	1.81E-03	8.31E-01	-2.68E-01	-1.20E+00	1.76E+01	2.11E+01
PRMT6	7.69E+02	1.84E-05	3.93E-05	6.74E-01	-5.69E-01	-1.48E+00	3.33E+01	4.94E+01
PRODH	2.67E+02	3.76E-13	3.74E-10	9.95E-02	-3.33E+00	-1.00E+01	2.79E+00	2.81E+01
PROSER3	2.97E+02	9.59E-07	3.54E-06	5.59E-01	-8.40E-01	-1.79E+00	1.15E+01	2.06E+01
PRPF19	2.27E+03	2.16E-08	2.08E-07	6.82E-01	-5.53E-01	-1.47E+00	9.87E+01	1.45E+02
PRR12	4.07E+03	2.50E-04	3.76E-04	6.94E-01	-5.26E-01	-1.44E+00	1.78E+02	2.56E+02
PRR13	4.41E+02	6.16E-04	8.31E-04	8.04E-01	-3.15E-01	-1.24E+00	2.07E+01	2.58E+01
PRR14	8.84E+02	2.13E-03	2.57E-03	8.44E-01	-2.44E-01	-1.18E+00	4.31E+01	5.10E+01
PRR3	9.17E+02	3.83E-05	7.44E-05	7.89E-01	-3.42E-01	-1.27E+00	4.30E+01	5.45E+01
PRR5	6.67E+02	1.27E-03	1.60E-03	6.91E-01	-5.34E-01	-1.45E+00	2.92E+01	4.23E+01

PRSS16	6.65E+00	3.61E-07	1.70E-06	1.18E-02	-6.40E+00	-8.44E+01	8.92E-03	7.53E-01
PRSS33	1.29E+01	7.91E-07	3.08E-06	2.90E-01	-1.79E+00	-3.45E+00	3.22E-01	1.11E+00
PRX	1.74E+02	1.25E-08	1.37E-07	3.93E-01	-1.35E+00	-2.55E+00	5.34E+00	1.36E+01
PSAT1	8.11E+02	3.09E-05	6.13E-05	4.64E-01	-1.11E+00	-2.15E+00	2.82E+01	6.07E+01
PSMA4	8.15E+02	3.78E-07	1.77E-06	5.33E-01	-9.09E-01	-1.88E+00	3.05E+01	5.73E+01
PSMB3	1.18E+03	2.03E-06	6.33E-06	6.35E-01	-6.55E-01	-1.57E+00	4.90E+01	7.71E+01
PSMB4	1.97E+03	3.50E-07	1.67E-06	6.14E-01	-7.04E-01	-1.63E+00	8.05E+01	1.31E+02
PSMB5	1.48E+03	1.27E-05	2.89E-05	6.58E-01	-6.03E-01	-1.52E+00	6.33E+01	9.61E+01
PSMC4	1.32E+03	1.41E-07	8.58E-07	6.73E-01	-5.72E-01	-1.49E+00	5.68E+01	8.45E+01
PSMD4	1.88E+03	5.86E-06	1.53E-05	7.12E-01	-4.91E-01	-1.40E+00	8.34E+01	1.17E+02
PSMD7	8.98E+02	2.50E-03	2.98E-03	8.47E-01	-2.39E-01	-1.18E+00	4.36E+01	5.15E+01
PSMD8	1.67E+03	2.20E-04	3.38E-04	7.68E-01	-3.81E-01	-1.30E+00	7.74E+01	1.01E+02
PSMD9	9.12E+02	3.30E-09	5.88E-08	4.24E-01	-1.24E+00	-2.36E+00	2.98E+01	7.02E+01
PSME3	1.90E+03	8.98E-08	6.22E-07	7.32E-01	-4.49E-01	-1.37E+00	8.55E+01	1.17E+02
PSMG3	3.07E+02	1.01E-04	1.72E-04	7.24E-01	-4.66E-01	-1.38E+00	1.37E+01	1.89E+01
PTBP1	8.21E+03	6.40E-09	8.58E-08	6.99E-01	-5.16E-01	-1.43E+00	3.63E+02	5.19E+02
PTDSS1	1.04E+03	2.63E-04	3.93E-04	7.47E-01	-4.21E-01	-1.34E+00	4.70E+01	6.30E+01
PTMA	3.61E+03	3.38E-05	6.66E-05	7.70E-01	-3.76E-01	-1.30E+00	1.67E+02	2.17E+02
PTMA-2	2.00E+04	2.01E-04	3.12E-04	7.94E-01	-3.32E-01	-1.26E+00	9.42E+02	1.19E+03
PTOV1	5.06E+03	3.95E-09	6.58E-08	6.58E-01	-6.03E-01	-1.52E+00	2.16E+02	3.28E+02
PTP4A1	1.42E+03	9.62E-04	1.24E-03	8.54E-01	-2.27E-01	-1.17E+00	6.91E+01	8.09E+01
PTPMT1	2.86E+02	4.50E-04	6.30E-04	6.94E-01	-5.26E-01	-1.44E+00	1.25E+01	1.80E+01
PTPRC	4.30E+02	5.53E-05	1.02E-04	5.47E-01	-8.70E-01	-1.83E+00	1.66E+01	3.04E+01
PTPRN2	5.54E+02	1.93E-08	1.92E-07	3.66E-01	-1.45E+00	-2.73E+00	1.62E+01	4.42E+01
PTRH2	1.64E+02	5.21E-05	9.75E-05	7.18E-01	-4.77E-01	-1.39E+00	7.32E+00	1.02E+01
PXDN	5.65E+03	9.06E-03	9.80E-03	8.00E-01	-3.22E-01	-1.25E+00	2.69E+02	3.36E+02
PXN	2.58E+03	5.81E-05	1.07E-04	6.46E-01	-6.31E-01	-1.55E+00	1.09E+02	1.68E+02
PYCR1	2.49E+03	1.86E-05	3.98E-05	6.43E-01	-6.38E-01	-1.56E+00	1.05E+02	1.63E+02
PYCR3	1.55E+03	4.01E-07	1.85E-06	6.67E-01	-5.84E-01	-1.50E+00	6.64E+01	9.96E+01
PYGO2	2.11E+03	1.56E-07	9.28E-07	6.50E-01	-6.22E-01	-1.54E+00	8.90E+01	1.37E+02
PYM1	3.56E+02	7.96E-03	8.65E-03	8.40E-01	-2.51E-01	-1.19E+00	1.73E+01	2.06E+01
QTRT1	7.45E+02	2.72E-05	5.50E-05	8.19E-01	-2.88E-01	-1.22E+00	3.58E+01	4.37E+01
R3HCC1	6.77E+02	6.85E-04	9.18E-04	8.13E-01	-2.99E-01	-1.23E+00	3.21E+01	3.95E+01

RAB11B	3.35E+03	6.11E-05	1.12E-04	8.12E-01	-3.00E-01	-1.23E+00	1.59E+02	1.96E+02
RAB15	6.68E+02	8.67E-05	1.51E-04	5.85E-01	-7.74E-01	-1.71E+00	2.66E+01	4.55E+01
RAB17	5.10E+01	1.36E-05	3.05E-05	1.72E-01	-2.54E+00	-5.82E+00	8.72E-01	5.07E+00
RAB19	1.70E+01	4.65E-03	5.26E-03	4.98E-01	-1.00E+00	-2.01E+00	5.96E-01	1.20E+00
RAB1B	3.46E+03	9.69E-10	2.84E-08	6.53E-01	-6.15E-01	-1.53E+00	1.47E+02	2.25E+02
RAB20	4.05E+01	4.23E-04	5.99E-04	5.23E-01	-9.34E-01	-1.91E+00	1.52E+00	2.90E+00
RAB34	2.26E+03	1.66E-07	9.57E-07	7.22E-01	-4.69E-01	-1.38E+00	1.01E+02	1.40E+02
RAB35	1.51E+03	1.27E-03	1.60E-03	8.79E-01	-1.87E-01	-1.14E+00	7.49E+01	8.52E+01
RAB38	1.89E+02	4.07E-03	4.66E-03	4.81E-01	-1.06E+00	-2.08E+00	6.81E+00	1.42E+01
RAB43	1.54E+03	6.56E-10	2.21E-08	5.74E-01	-8.02E-01	-1.74E+00	6.12E+01	1.07E+02
RAB7A	3.88E+03	1.61E-06	5.27E-06	8.03E-01	-3.16E-01	-1.24E+00	1.84E+02	2.29E+02
RABEP2	7.25E+02	4.37E-04	6.16E-04	8.10E-01	-3.05E-01	-1.24E+00	3.46E+01	4.28E+01
RABGGTA	3.90E+02	2.46E-04	3.70E-04	7.97E-01	-3.27E-01	-1.25E+00	1.84E+01	2.31E+01
RABGGTB	4.33E+02	1.09E-04	1.84E-04	7.48E-01	-4.19E-01	-1.34E+00	1.98E+01	2.64E+01
RAC3	5.73E+02	1.34E-06	4.55E-06	5.79E-01	-7.88E-01	-1.73E+00	2.27E+01	3.92E+01
RAD54L	5.64E+02	1.78E-05	3.84E-05	6.22E-01	-6.84E-01	-1.61E+00	2.33E+01	3.74E+01
RAD9A	5.44E+02	4.50E-09	7.02E-08	5.92E-01	-7.57E-01	-1.69E+00	2.19E+01	3.69E+01
RALY	5.21E+03	6.08E-07	2.52E-06	7.51E-01	-4.12E-01	-1.33E+00	2.38E+02	3.17E+02
RAMP1	3.03E+02	2.90E-06	8.51E-06	6.22E-01	-6.86E-01	-1.61E+00	1.24E+01	2.00E+01
RAMP3	4.01E+01	3.06E-03	3.58E-03	4.49E-01	-1.16E+00	-2.23E+00	1.37E+00	3.06E+00
RANBP1	2.14E+03	5.83E-07	2.46E-06	5.97E-01	-7.45E-01	-1.68E+00	8.62E+01	1.44E+02
RANBP3L	3.30E+01	3.23E-04	4.70E-04	3.88E-01	-1.36E+00	-2.58E+00	1.04E+00	2.67E+00
RANGAP1	1.01E+03	1.25E-07	7.89E-07	5.29E-01	-9.17E-01	-1.89E+00	3.80E+01	7.18E+01
RAP1GAP	6.83E+02	1.09E-06	3.93E-06	2.90E-01	-1.78E+00	-3.44E+00	1.69E+01	5.81E+01
RARA	2.87E+03	3.16E-03	3.69E-03	8.62E-01	-2.15E-01	-1.16E+00	1.41E+02	1.64E+02
RARS	1.24E+03	1.19E-05	2.75E-05	7.63E-01	-3.91E-01	-1.31E+00	5.75E+01	7.53E+01
RBFOX3	2.19E+02	2.57E-02	2.66E-02	6.96E-01	-5.24E-01	-1.44E+00	9.58E+00	1.38E+01
RBM10	6.01E+03	7.10E-07	2.83E-06	8.02E-01	-3.19E-01	-1.25E+00	2.84E+02	3.54E+02
RBM15B	1.61E+03	2.61E-09	5.09E-08	7.24E-01	-4.66E-01	-1.38E+00	7.22E+01	9.97E+01
RBM3	1.59E+03	1.07E-04	1.80E-04	6.85E-01	-5.47E-01	-1.46E+00	6.95E+01	1.02E+02
RBM4	3.32E+03	5.84E-07	2.46E-06	7.73E-01	-3.72E-01	-1.29E+00	1.54E+02	1.99E+02
RBP1	3.43E+03	1.45E-07	8.76E-07	5.77E-01	-7.92E-01	-1.73E+00	1.36E+02	2.35E+02
RBX1	1.50E+03	2.88E-04	4.25E-04	8.37E-01	-2.57E-01	-1.19E+00	7.25E+01	8.67E+01

RCC1L	7.91E+02	1.20E-08	1.33E-07	6.65E-01	-5.89E-01	-1.50E+00	3.38E+01	5.09E+01
RDH12	1.86E+01	1.96E-04	3.04E-04	4.39E-01	-1.19E+00	-2.28E+00	6.20E-01	1.41E+00
RELN	7.53E+02	4.42E-05	8.46E-05	4.75E-01	-1.07E+00	-2.11E+00	2.64E+01	5.55E+01
REM2	1.46E+01	1.47E-05	3.25E-05	4.37E-01	-1.20E+00	-2.29E+00	4.84E-01	1.11E+00
RENBP	1.20E+02	3.03E-03	3.55E-03	6.80E-01	-5.55E-01	-1.47E+00	5.22E+00	7.68E+00
REPIN1	2.33E+03	7.60E-06	1.89E-05	7.46E-01	-4.22E-01	-1.34E+00	1.06E+02	1.42E+02
RESP18	9.90E-01	5.73E-03	6.35E-03	1.65E-01	-2.60E+00	-6.05E+00	1.61E-02	9.72E-02
RFX4	7.92E+00	6.73E-04	9.03E-04	1.08E-01	-3.21E+00	-9.28E+00	8.44E-02	7.83E-01
RFXANK	1.12E+03	1.20E-08	1.33E-07	6.66E-01	-5.87E-01	-1.50E+00	4.80E+01	7.21E+01
RGL2	3.25E+03	2.34E-07	1.23E-06	7.76E-01	-3.66E-01	-1.29E+00	1.51E+02	1.95E+02
RGP1	2.21E+03	2.71E-03	3.21E-03	8.46E-01	-2.41E-01	-1.18E+00	1.08E+02	1.27E+02
RGS12	1.23E+03	4.00E-05	7.73E-05	7.37E-01	-4.40E-01	-1.36E+00	5.55E+01	7.54E+01
RGS20	3.27E+01	7.16E-05	1.28E-04	4.25E-01	-1.23E+00	-2.35E+00	1.08E+00	2.53E+00
RHBDD2	1.40E+03	6.63E-07	2.68E-06	6.92E-01	-5.30E-01	-1.44E+00	6.10E+01	8.81E+01
RHBG	2.40E+02	1.27E-03	1.60E-03	3.81E-01	-1.39E+00	-2.62E+00	7.43E+00	1.95E+01
RHEBL1	3.31E+01	1.60E-08	1.67E-07	1.49E-01	-2.75E+00	-6.73E+00	4.92E-01	3.31E+00
RHNO1	7.18E+02	9.22E-06	2.22E-05	7.22E-01	-4.70E-01	-1.38E+00	3.22E+01	4.45E+01
RHOD	1.40E+02	4.30E-02	4.39E-02	7.71E-01	-3.75E-01	-1.30E+00	6.54E+00	8.48E+00
RHPN1	8.35E+01	1.38E-03	1.73E-03	6.96E-01	-5.23E-01	-1.44E+00	3.62E+00	5.20E+00
RILPL2	7.39E+02	9.76E-07	3.58E-06	6.94E-01	-5.28E-01	-1.44E+00	3.25E+01	4.68E+01
RIN3	1.18E+03	2.24E-09	4.68E-08	4.85E-01	-1.04E+00	-2.06E+00	4.21E+01	8.67E+01
RING1	2.27E+03	9.74E-08	6.63E-07	7.81E-01	-3.56E-01	-1.28E+00	1.06E+02	1.36E+02
RNASEH2B	3.56E+02	5.23E-04	7.19E-04	8.28E-01	-2.72E-01	-1.21E+00	1.71E+01	2.07E+01
RND1	4.89E+02	4.81E-07	2.13E-06	4.62E-01	-1.11E+00	-2.17E+00	1.69E+01	3.66E+01
RNF10	2.12E+03	9.18E-08	6.34E-07	7.20E-01	-4.73E-01	-1.39E+00	9.47E+01	1.32E+02
RNF122	4.62E+02	1.38E-07	8.47E-07	5.37E-01	-8.98E-01	-1.86E+00	1.76E+01	3.27E+01
RNF126	7.66E+02	2.22E-07	1.20E-06	6.65E-01	-5.89E-01	-1.50E+00	3.27E+01	4.92E+01
RNF181	3.31E+02	3.83E-05	7.44E-05	7.22E-01	-4.70E-01	-1.38E+00	1.47E+01	2.03E+01
RNF215	7.07E+02	1.31E-03	1.64E-03	8.56E-01	-2.24E-01	-1.17E+00	3.46E+01	4.05E+01
RNF44	2.06E+03	9.46E-10	2.81E-08	4.93E-01	-1.02E+00	-2.03E+00	7.37E+01	1.50E+02
RNH1	1.59E+03	9.90E-07	3.62E-06	6.84E-01	-5.49E-01	-1.46E+00	6.94E+01	1.01E+02
RNPEP	1.00E+03	2.69E-04	4.01E-04	6.61E-01	-5.98E-01	-1.51E+00	4.22E+01	6.39E+01
RNPEPL1	1.20E+03	3.42E-03	3.96E-03	7.92E-01	-3.36E-01	-1.26E+00	5.64E+01	7.11E+01

ROGDI	1.24E+03	2.98E-07	1.47E-06	5.87E-01	-7.68E-01	-1.70E+00	4.96E+01	8.45E+01
RPL22L1	1.63E+03	2.05E-06	6.38E-06	6.58E-01	-6.03E-01	-1.52E+00	7.00E+01	1.06E+02
RPP25	9.06E+01	6.05E-07	2.52E-06	2.71E-01	-1.89E+00	-3.70E+00	2.12E+00	7.83E+00
RPP25L	4.82E+02	4.16E-07	1.90E-06	7.16E-01	-4.81E-01	-1.40E+00	2.14E+01	2.99E+01
RPP38	2.72E+02	3.72E-02	3.81E-02	9.03E-01	-1.47E-01	-1.11E+00	1.37E+01	1.51E+01
RPS6KA2	1.72E+03	7.31E-03	7.99E-03	8.11E-01	-3.02E-01	-1.23E+00	8.22E+01	1.01E+02
RPUSD1	3.80E+02	1.20E-06	4.23E-06	7.13E-01	-4.89E-01	-1.40E+00	1.69E+01	2.37E+01
RRM2	6.05E+02	5.16E-05	9.66E-05	6.32E-01	-6.63E-01	-1.58E+00	2.51E+01	3.97E+01
RRS1	3.71E+02	6.04E-02	6.11E-02	9.02E-01	-1.49E-01	-1.11E+00	1.86E+01	2.07E+01
RSPO1	7.73E+02	1.84E-04	2.90E-04	2.61E-01	-1.94E+00	-3.84E+00	1.76E+01	6.76E+01
RTL4	1.82E+01	2.23E-04	3.41E-04	3.31E-01	-1.59E+00	-3.02E+00	5.01E-01	1.51E+00
RTL6	1.70E+03	3.73E-06	1.05E-05	7.10E-01	-4.95E-01	-1.41E+00	7.53E+01	1.06E+02
RTN1	1.51E+02	3.28E-05	6.48E-05	2.43E-01	-2.04E+00	-4.11E+00	3.16E+00	1.30E+01
RTN4R	1.02E+02	1.25E-04	2.06E-04	4.33E-01	-1.21E+00	-2.31E+00	3.39E+00	7.82E+00
RTRAF	3.66E+03	6.99E-04	9.32E-04	7.84E-01	-3.51E-01	-1.28E+00	1.71E+02	2.18E+02
SALL1	1.77E+03	4.59E-04	6.41E-04	4.25E-01	-1.23E+00	-2.35E+00	5.75E+01	1.35E+02
SAMM50	1.52E+03	4.05E-04	5.75E-04	7.46E-01	-4.23E-01	-1.34E+00	6.89E+01	9.24E+01
SAP30BP	1.64E+03	2.82E-04	4.17E-04	8.28E-01	-2.72E-01	-1.21E+00	7.90E+01	9.54E+01
SAPCD1	4.41E+02	2.82E-04	4.17E-04	5.79E-01	-7.87E-01	-1.73E+00	1.71E+01	2.96E+01
SARAF	2.77E+03	2.33E-03	2.79E-03	7.68E-01	-3.81E-01	-1.30E+00	1.27E+02	1.66E+02
SARS2	6.16E+02	3.06E-06	8.85E-06	7.95E-01	-3.31E-01	-1.26E+00	2.90E+01	3.65E+01
SBK1	7.81E+02	1.05E-09	2.95E-08	3.71E-01	-1.43E+00	-2.69E+00	2.33E+01	6.26E+01
SBK2	5.14E+02	6.87E-06	1.74E-05	2.37E-01	-2.08E+00	-4.23E+00	1.12E+01	4.72E+01
SCAND1	2.06E+03	2.15E-06	6.61E-06	5.92E-01	-7.57E-01	-1.69E+00	8.30E+01	1.40E+02
SCCPDH	5.03E+02	2.66E-03	3.15E-03	8.02E-01	-3.19E-01	-1.25E+00	2.35E+01	2.93E+01
SCD5	1.44E+03	3.80E-02	3.89E-02	8.42E-01	-2.48E-01	-1.19E+00	7.00E+01	8.31E+01
SCG5	1.42E+03	4.65E-06	1.25E-05	6.29E-01	-6.69E-01	-1.59E+00	5.89E+01	9.36E+01
SCML4	9.89E+00	1.03E-04	1.74E-04	2.81E-01	-1.83E+00	-3.56E+00	2.44E-01	8.67E-01
SCNN1A	1.02E+03	3.71E-08	3.17E-07	1.28E-01	-2.97E+00	-7.84E+00	1.33E+01	1.04E+02
SCNN1G	2.18E+01	1.81E-03	2.21E-03	6.29E-02	-3.99E+00	-1.59E+01	1.53E-01	2.43E+00
SCRN2	6.39E+02	2.86E-03	3.37E-03	8.23E-01	-2.81E-01	-1.22E+00	3.07E+01	3.73E+01
SCUBE1	4.44E+02	5.06E-08	3.94E-07	1.84E-01	-2.44E+00	-5.43E+00	7.76E+00	4.22E+01
SDC1	5.31E+02	3.58E-07	1.69E-06	4.47E-01	-1.16E+00	-2.24E+00	1.80E+01	4.02E+01

SDE2	9.54E+02	4.79E-07	2.12E-06	4.46E-01	-1.16E+00	-2.24E+00	3.22E+01	7.22E+01
SDF2	5.84E+02	9.24E-06	2.22E-05	7.38E-01	-4.39E-01	-1.36E+00	2.64E+01	3.58E+01
SDHAF1	2.23E+02	9.53E-06	2.27E-05	6.65E-01	-5.89E-01	-1.50E+00	9.55E+00	1.44E+01
SDHAF2	6.56E+02	5.20E-08	4.03E-07	6.29E-01	-6.69E-01	-1.59E+00	2.71E+01	4.31E+01
SDHD	1.11E+03	8.77E-07	3.31E-06	7.47E-01	-4.21E-01	-1.34E+00	5.04E+01	6.75E+01
SDR39U1	3.71E+02	4.84E-03	5.45E-03	8.73E-01	-1.95E-01	-1.14E+00	1.83E+01	2.10E+01
SDR42E1	1.23E+02	1.00E-04	1.71E-04	5.12E-01	-9.67E-01	-1.95E+00	4.43E+00	8.66E+00
SEC14L1	2.43E+03	1.13E-07	7.43E-07	6.93E-01	-5.29E-01	-1.44E+00	1.07E+02	1.54E+02
SEC14L2	4.63E+02	3.95E-08	3.31E-07	2.96E-01	-1.76E+00	-3.38E+00	1.17E+01	3.96E+01
SEC14L4	6.49E+01	4.94E-04	6.86E-04	4.20E-01	-1.25E+00	-2.38E+00	2.12E+00	5.06E+00
SEC14L5	6.12E+01	1.19E-04	1.97E-04	2.40E-01	-2.06E+00	-4.16E+00	1.37E+00	5.69E+00
SEC14L6	6.49E+00	5.29E-03	5.91E-03	4.09E-02	-4.61E+00	-2.44E+01	3.09E-02	7.57E-01
SEC61G	7.97E+02	7.46E-06	1.87E-05	5.86E-01	-7.70E-01	-1.71E+00	3.16E+01	5.39E+01
SELENOF	1.44E+03	1.49E-06	4.96E-06	7.22E-01	-4.70E-01	-1.38E+00	6.45E+01	8.93E+01
SELENOO	1.09E+03	1.79E-06	5.71E-06	7.11E-01	-4.91E-01	-1.41E+00	4.84E+01	6.80E+01
SEMA3F	1.12E+03	1.65E-09	3.77E-08	4.77E-01	-1.07E+00	-2.10E+00	3.93E+01	8.25E+01
SEMA4B	1.31E+03	6.04E-06	1.56E-05	5.16E-01	-9.55E-01	-1.94E+00	4.80E+01	9.31E+01
SEMA4C	2.47E+03	5.56E-04	7.61E-04	8.34E-01	-2.62E-01	-1.20E+00	1.19E+02	1.43E+02
SEMA5B	6.27E+02	2.89E-05	5.78E-05	3.81E-01	-1.39E+00	-2.62E+00	1.91E+01	5.02E+01
SEPT9	7.84E+03	1.92E-09	4.17E-08	5.85E-01	-7.73E-01	-1.71E+00	3.13E+02	5.34E+02
SERINC2	3.70E+02	3.24E-09	5.83E-08	2.48E-01	-2.01E+00	-4.03E+00	8.21E+00	3.31E+01
SERPINA12	4.01E+00	3.11E-06	8.98E-06	2.67E-02	-5.23E+00	-3.75E+01	1.22E-02	4.58E-01
SERPINB6	3.60E+03	3.73E-07	1.75E-06	6.79E-01	-5.58E-01	-1.47E+00	1.56E+02	2.30E+02
SERPINC1	1.55E+01	1.36E-02	1.44E-02	6.32E-01	-6.63E-01	-1.58E+00	6.37E-01	1.01E+00
SERTM1	4.57E+01	1.73E-03	2.12E-03	4.47E-01	-1.16E+00	-2.24E+00	1.57E+00	3.51E+00
SESN2	9.69E+02	1.46E-09	3.39E-08	3.93E-01	-1.35E+00	-2.54E+00	2.98E+01	7.57E+01
SETD9	5.30E+01	4.39E-02	4.48E-02	7.79E-01	-3.61E-01	-1.28E+00	2.46E+00	3.15E+00
SF3B6	9.39E+02	1.09E-04	1.82E-04	7.70E-01	-3.76E-01	-1.30E+00	4.35E+01	5.65E+01
SGCG	9.73E+01	1.64E-07	9.55E-07	1.47E-01	-2.77E+00	-6.81E+00	1.38E+00	9.43E+00
SH3BP1	7.08E+02	2.06E-06	6.40E-06	5.87E-01	-7.68E-01	-1.70E+00	2.84E+01	4.83E+01
SH3GL1	4.29E+03	7.46E-07	2.94E-06	7.77E-01	-3.63E-01	-1.29E+00	2.00E+02	2.58E+02
SH3TC1	3.34E+02	1.28E-09	3.17E-08	4.09E-01	-1.29E+00	-2.44E+00	1.05E+01	2.57E+01
SHC4	3.59E+01	9.13E-04	1.18E-03	5.61E-01	-8.33E-01	-1.78E+00	1.40E+00	2.49E+00

SHF	8.85E+02	6.38E-04	8.59E-04	6.05E-01	-7.26E-01	-1.65E+00	3.64E+01	6.03E+01
SHISA3	7.27E+01	1.79E-09	3.99E-08	1.95E-01	-2.36E+00	-5.14E+00	1.34E+00	6.89E+00
SHISAL2A	7.29E+01	4.58E-06	1.24E-05	4.12E-01	-1.28E+00	-2.43E+00	2.34E+00	5.68E+00
SHROOM2	1.18E+03	6.64E-05	1.20E-04	6.12E-01	-7.07E-01	-1.63E+00	4.80E+01	7.84E+01
SIDT1	9.12E+01	1.01E-10	6.29E-09	5.44E-02	-4.20E+00	-1.84E+01	5.54E-01	1.02E+01
SIK1	8.33E+02	1.13E-02	1.21E-02	7.93E-01	-3.35E-01	-1.26E+00	3.95E+01	4.98E+01
SIRT5	8.17E+02	4.97E-03	5.58E-03	7.77E-01	-3.65E-01	-1.29E+00	3.79E+01	4.88E+01
SIRT6	2.90E+02	1.55E-06	5.11E-06	7.43E-01	-4.28E-01	-1.35E+00	1.32E+01	1.77E+01
SIT1	3.16E+01	3.95E-03	4.53E-03	5.89E-01	-7.64E-01	-1.70E+00	1.27E+00	2.16E+00
SIX5	2.81E+03	1.21E-05	2.77E-05	7.25E-01	-4.64E-01	-1.38E+00	1.26E+02	1.74E+02
SKA2	8.78E+02	1.62E-07	9.51E-07	6.98E-01	-5.18E-01	-1.43E+00	3.85E+01	5.51E+01
SLC17A9	6.33E+01	1.02E-04	1.73E-04	4.41E-01	-1.18E+00	-2.27E+00	2.12E+00	4.82E+00
SLC1A5	8.39E+02	7.02E-03	7.69E-03	7.71E-01	-3.74E-01	-1.30E+00	3.90E+01	5.05E+01
SLC20A1	1.49E+03	2.18E-08	2.09E-07	6.64E-01	-5.91E-01	-1.51E+00	6.38E+01	9.61E+01
SLC22A1	6.38E+01	6.28E-07	2.58E-06	6.81E-02	-3.88E+00	-1.47E+01	4.81E-01	7.06E+00
SLC22A17	4.77E+03	3.37E-06	9.66E-06	6.89E-01	-5.37E-01	-1.45E+00	2.09E+02	3.04E+02
SLC25A10	3.38E+03	1.00E-05	2.37E-05	4.49E-01	-1.15E+00	-2.23E+00	1.14E+02	2.54E+02
SLC25A11	1.08E+03	3.43E-05	6.75E-05	8.02E-01	-3.18E-01	-1.25E+00	5.10E+01	6.36E+01
SLC25A29	1.15E+03	2.74E-05	5.54E-05	6.90E-01	-5.35E-01	-1.45E+00	5.09E+01	7.37E+01
SLC25A3	2.08E+03	5.39E-05	1.00E-04	7.00E-01	-5.14E-01	-1.43E+00	9.21E+01	1.32E+02
SLC25A34	2.30E+02	5.19E-06	1.38E-05	6.40E-01	-6.44E-01	-1.56E+00	9.68E+00	1.51E+01
SLC25A35	1.45E+02	1.01E-10	6.29E-09	2.96E-01	-1.76E+00	-3.38E+00	3.63E+00	1.23E+01
SLC25A39	2.23E+03	2.07E-06	6.41E-06	6.75E-01	-5.66E-01	-1.48E+00	9.63E+01	1.43E+02
SLC25A5	1.90E+03	1.77E-10	8.85E-09	1.46E-01	-2.78E+00	-6.86E+00	2.79E+01	1.91E+02
SLC26A6	4.31E+02	8.22E-03	8.93E-03	8.42E-01	-2.48E-01	-1.19E+00	2.09E+01	2.48E+01
SLC27A1	2.98E+03	4.16E-03	4.75E-03	8.09E-01	-3.05E-01	-1.24E+00	1.42E+02	1.76E+02
SLC27A6	1.06E+02	7.09E-06	1.79E-05	1.02E-01	-3.30E+00	-9.83E+00	1.13E+00	1.12E+01
SLC28A1	2.60E+02	4.69E-08	3.76E-07	1.53E-01	-2.70E+00	-6.52E+00	3.98E+00	2.59E+01
SLC28A3	5.58E+00	2.82E-03	3.32E-03	4.05E-01	-1.30E+00	-2.47E+00	1.77E-01	4.38E-01
SLC29A4	9.10E+02	4.65E-06	1.25E-05	3.90E-01	-1.36E+00	-2.57E+00	2.81E+01	7.20E+01
SLC2A1	9.13E+02	1.86E-02	1.95E-02	8.07E-01	-3.09E-01	-1.24E+00	4.38E+01	5.43E+01
SLC2A4	6.94E+01	6.34E-09	8.58E-08	3.61E-01	-1.47E+00	-2.77E+00	2.02E+00	5.61E+00
SLC2A4RG	9.45E+02	6.02E-07	2.51E-06	6.78E-01	-5.62E-01	-1.48E+00	4.10E+01	6.04E+01

SLC2A8	3.16E+02	1.59E-05	3.47E-05	6.46E-01	-6.30E-01	-1.55E+00	1.33E+01	2.06E+01
SLC35F4	6.70E+01	4.15E-07	1.90E-06	4.66E-02	-4.42E+00	-2.14E+01	3.47E-01	7.44E+00
SLC35F6	6.33E+02	2.82E-05	5.67E-05	7.07E-01	-5.01E-01	-1.42E+00	2.82E+01	3.99E+01
SLC37A4	5.26E+02	3.43E-03	3.97E-03	8.36E-01	-2.58E-01	-1.20E+00	2.53E+01	3.03E+01
SLC39A4	5.78E+02	4.92E-11	4.59E-09	3.70E-02	-4.76E+00	-2.70E+01	2.49E+00	6.73E+01
SLC39A8	1.47E+02	4.79E-03	5.40E-03	4.95E-01	-1.01E+00	-2.02E+00	5.38E+00	1.09E+01
SLC3A2	1.99E+03	1.06E-09	2.95E-08	5.58E-01	-8.42E-01	-1.79E+00	7.74E+01	1.39E+02
SLC41A3	1.25E+03	5.24E-05	9.80E-05	7.66E-01	-3.85E-01	-1.31E+00	5.76E+01	7.52E+01
SLC43A3	2.63E+02	7.31E-08	5.26E-07	3.89E-01	-1.36E+00	-2.57E+00	8.21E+00	2.11E+01
SLC44A4	1.47E+02	7.70E-06	1.91E-05	1.75E-01	-2.52E+00	-5.73E+00	2.53E+00	1.45E+01
SLC45A4	7.35E+02	1.78E-07	1.01E-06	4.02E-01	-1.31E+00	-2.48E+00	2.32E+01	5.76E+01
SLC6A7	2.14E+01	9.32E-07	3.46E-06	1.86E-01	-2.42E+00	-5.37E+00	3.80E-01	2.04E+00
SLC6A9	1.58E+02	8.43E-04	1.10E-03	6.76E-01	-5.65E-01	-1.48E+00	6.87E+00	1.02E+01
SLC7A1	1.61E+03	3.58E-08	3.08E-07	5.28E-01	-9.20E-01	-1.89E+00	6.02E+01	1.14E+02
SLC7A7	5.63E+02	1.10E-04	1.84E-04	7.32E-01	-4.50E-01	-1.37E+00	2.54E+01	3.47E+01
SLC7A8	1.21E+03	2.52E-09	5.03E-08	2.14E-01	-2.23E+00	-4.68E+00	2.40E+01	1.12E+02
SLC8A3	3.38E+01	2.54E-03	3.02E-03	4.81E-01	-1.06E+00	-2.08E+00	1.20E+00	2.51E+00
SLC9A3R1	2.47E+03	4.73E-05	9.02E-05	4.80E-01	-1.06E+00	-2.08E+00	8.79E+01	1.83E+02
SLC9A5	1.01E+03	4.23E-06	1.16E-05	5.13E-01	-9.63E-01	-1.95E+00	3.72E+01	7.26E+01
SLIT1	4.52E+02	6.34E-08	4.80E-07	5.05E-02	-4.31E+00	-1.98E+01	2.57E+00	5.09E+01
SLITRK5	8.12E+01	3.95E-04	5.62E-04	5.80E-01	-7.86E-01	-1.72E+00	3.22E+00	5.55E+00
SLURP1	6.22E+00	1.32E-03	1.66E-03	1.13E-01	-3.15E+00	-8.88E+00	7.49E-02	6.66E-01
SMAD6	5.77E+02	2.64E-06	7.82E-06	6.38E-01	-6.48E-01	-1.57E+00	2.42E+01	3.80E+01
SMAD7	3.38E+02	4.21E-06	1.16E-05	6.23E-01	-6.84E-01	-1.61E+00	1.40E+01	2.25E+01
SMAGP	1.88E+02	6.65E-09	8.75E-08	4.14E-01	-1.27E+00	-2.41E+00	6.05E+00	1.46E+01
SMIM12	4.92E+02	2.27E-04	3.46E-04	7.69E-01	-3.78E-01	-1.30E+00	2.28E+01	2.96E+01
SMIM3	3.47E+02	8.38E-03	9.10E-03	7.50E-01	-4.15E-01	-1.33E+00	1.60E+01	2.13E+01
SMIM30	8.52E+01	3.96E-02	4.05E-02	8.13E-01	-3.00E-01	-1.23E+00	4.06E+00	5.00E+00
SMIM32	1.68E+02	1.25E-10	7.10E-09	4.86E-02	-4.36E+00	-2.06E+01	9.25E-01	1.90E+01
SMO	5.40E+03	2.40E-04	3.62E-04	7.98E-01	-3.26E-01	-1.25E+00	2.54E+02	3.19E+02
SMOC1	3.59E+03	2.39E-05	4.93E-05	3.82E-01	-1.39E+00	-2.62E+00	1.08E+02	2.82E+02
SMYD5	4.76E+02	1.30E-05	2.94E-05	7.47E-01	-4.20E-01	-1.34E+00	2.17E+01	2.90E+01
SNAPC4	3.19E+03	1.70E-05	3.70E-05	6.45E-01	-6.34E-01	-1.55E+00	1.34E+02	2.07E+02

SNN	2.14E+02	4.91E-06	1.31E-05	6.41E-01	-6.42E-01	-1.56E+00	8.95E+00	1.40E+01
SNRPB	1.98E+03	4.87E-10	1.75E-08	4.82E-01	-1.05E+00	-2.07E+00	6.98E+01	1.45E+02
SNX27	1.14E+01	7.97E-04	1.05E-03	2.98E-02	-5.07E+00	-3.35E+01	4.05E-02	1.36E+00
SNX7	2.59E+02	7.63E-04	1.01E-03	7.71E-01	-3.75E-01	-1.30E+00	1.20E+01	1.56E+01
SOCS1	1.24E+02	1.37E-05	3.05E-05	5.33E-01	-9.07E-01	-1.88E+00	4.69E+00	8.80E+00
SORD	1.70E+02	2.97E-07	1.47E-06	4.20E-01	-1.25E+00	-2.38E+00	5.51E+00	1.31E+01
SOSTDC1	3.89E+01	2.00E-02	2.09E-02	6.29E-01	-6.68E-01	-1.59E+00	1.64E+00	2.60E+00
SOX11	6.83E+02	1.52E-05	3.34E-05	5.74E-01	-8.02E-01	-1.74E+00	2.69E+01	4.69E+01
SOX12	4.88E+03	9.50E-05	1.63E-04	7.12E-01	-4.91E-01	-1.40E+00	2.16E+02	3.04E+02
SOX15	3.98E+02	8.00E-11	5.43E-09	2.01E-01	-2.32E+00	-4.99E+00	7.66E+00	3.82E+01
SOX17	3.16E+02	4.37E-07	1.99E-06	3.62E-01	-1.47E+00	-2.76E+00	9.40E+00	2.60E+01
SOX8	9.26E+01	8.81E-09	1.08E-07	2.28E-01	-2.13E+00	-4.38E+00	1.95E+00	8.56E+00
SPAG7	1.20E+03	1.48E-03	1.83E-03	8.23E-01	-2.82E-01	-1.22E+00	5.79E+01	7.04E+01
SPAG8	1.41E+02	2.98E-02	3.07E-02	7.64E-01	-3.89E-01	-1.31E+00	6.42E+00	8.41E+00
SPATA2L	1.75E+02	9.26E-06	2.22E-05	5.91E-01	-7.58E-01	-1.69E+00	7.02E+00	1.19E+01
SPC24	3.29E+02	2.87E-07	1.43E-06	3.64E-01	-1.46E+00	-2.75E+00	9.65E+00	2.65E+01
SPC25	3.80E+02	3.08E-06	8.90E-06	5.94E-01	-7.51E-01	-1.68E+00	1.53E+01	2.57E+01
SPIB	3.95E+01	2.86E-04	4.23E-04	4.09E-01	-1.29E+00	-2.44E+00	1.25E+00	3.06E+00
SPNS1	1.46E+03	2.36E-08	2.21E-07	7.47E-01	-4.20E-01	-1.34E+00	6.64E+01	8.89E+01
SPOCK1	7.01E+02	1.48E-04	2.40E-04	3.03E-01	-1.72E+00	-3.31E+00	1.82E+01	6.00E+01
SPOCK2	1.38E+03	1.23E-03	1.56E-03	4.42E-01	-1.18E+00	-2.26E+00	4.73E+01	1.07E+02
SPOP	1.17E+03	3.57E-09	6.15E-08	6.55E-01	-6.11E-01	-1.53E+00	4.98E+01	7.60E+01
SPRN	4.41E+02	3.37E-02	3.47E-02	6.50E-01	-6.21E-01	-1.54E+00	1.90E+01	2.92E+01
SPRY4	4.71E+02	1.92E-05	4.09E-05	5.28E-01	-9.20E-01	-1.89E+00	1.78E+01	3.38E+01
SPSB2	3.06E+02	8.41E-05	1.47E-04	6.72E-01	-5.74E-01	-1.49E+00	1.31E+01	1.95E+01
SPSB3	1.78E+03	1.43E-05	3.16E-05	7.90E-01	-3.40E-01	-1.27E+00	8.35E+01	1.06E+02
SPSB4	1.48E+02	2.80E-10	1.22E-08	1.75E-01	-2.51E+00	-5.70E+00	2.51E+00	1.43E+01
SRC	1.92E+03	7.49E-04	9.89E-04	7.92E-01	-3.36E-01	-1.26E+00	9.01E+01	1.14E+02
SRD5A1	2.24E+02	1.12E-04	1.88E-04	6.43E-01	-6.38E-01	-1.56E+00	9.32E+00	1.45E+01
SRI	7.20E+02	2.84E-03	3.35E-03	8.65E-01	-2.09E-01	-1.16E+00	3.54E+01	4.09E+01
SRSF1	3.62E+03	4.86E-03	5.47E-03	8.57E-01	-2.22E-01	-1.17E+00	1.77E+02	2.07E+02
SRSF3	1.81E+03	5.52E-05	1.02E-04	7.73E-01	-3.72E-01	-1.29E+00	8.40E+01	1.09E+02
SRSF4	4.37E+03	6.75E-05	1.22E-04	8.66E-01	-2.08E-01	-1.15E+00	2.15E+02	2.48E+02

SRSF7	2.38E+03	2.73E-09	5.23E-08	6.67E-01	-5.84E-01	-1.50E+00	1.02E+02	1.53E+02
SSBP3	1.54E+03	9.51E-04	1.23E-03	7.09E-01	-4.96E-01	-1.41E+00	6.82E+01	9.61E+01
SSLP1	2.77E+01	5.64E-03	6.27E-03	5.97E-01	-7.43E-01	-1.67E+00	1.09E+00	1.82E+00
SSTR2	3.61E+01	3.79E-04	5.40E-04	5.35E-01	-9.03E-01	-1.87E+00	1.37E+00	2.57E+00
SSTR3	2.93E+02	6.95E-07	2.79E-06	1.75E-01	-2.51E+00	-5.71E+00	4.86E+00	2.78E+01
ST14	1.26E+02	2.88E-05	5.77E-05	3.11E-01	-1.69E+00	-3.22E+00	3.31E+00	1.06E+01
STAC2	5.77E+01	2.10E-04	3.24E-04	4.70E-01	-1.09E+00	-2.13E+00	2.02E+00	4.29E+00
STARD3	1.03E+03	7.13E-05	1.27E-04	7.97E-01	-3.28E-01	-1.26E+00	4.85E+01	6.08E+01
STK32C	7.23E+01	1.42E-05	3.15E-05	4.95E-01	-1.02E+00	-2.02E+00	2.59E+00	5.24E+00
STK38	1.04E+03	8.22E-05	1.45E-04	8.26E-01	-2.76E-01	-1.21E+00	5.02E+01	6.07E+01
STK40	1.25E+03	2.94E-06	8.57E-06	7.71E-01	-3.75E-01	-1.30E+00	5.82E+01	7.55E+01
STMN2	7.52E+01	1.28E-06	4.45E-06	1.20E-01	-3.06E+00	-8.37E+00	9.29E-01	7.78E+00
STMN3	3.02E+01	1.10E-05	2.55E-05	2.27E-01	-2.14E+00	-4.41E+00	5.95E-01	2.62E+00
STOML2	1.50E+03	5.94E-07	2.49E-06	7.02E-01	-5.10E-01	-1.42E+00	6.61E+01	9.42E+01
STX3	1.20E+03	9.03E-07	3.37E-06	5.74E-01	-8.02E-01	-1.74E+00	4.73E+01	8.25E+01
STYXL1	5.76E+02	8.23E-08	5.82E-07	1.97E-01	-2.35E+00	-5.08E+00	1.06E+01	5.40E+01
SUCLA2	6.33E+02	6.39E-05	1.16E-04	7.90E-01	-3.39E-01	-1.27E+00	2.97E+01	3.75E+01
SUCLG1	1.71E+03	5.06E-06	1.34E-05	7.47E-01	-4.20E-01	-1.34E+00	7.76E+01	1.04E+02
SULT4A1	1.36E+02	5.48E-07	2.37E-06	2.10E-01	-2.25E+00	-4.75E+00	2.60E+00	1.23E+01
SUMO1	1.13E+03	5.11E-07	2.23E-06	6.90E-01	-5.35E-01	-1.45E+00	4.95E+01	7.18E+01
SUN2	5.83E+03	1.41E-05	3.13E-05	7.13E-01	-4.88E-01	-1.40E+00	2.61E+02	3.66E+02
SURF4	3.36E+03	6.49E-07	2.64E-06	7.97E-01	-3.28E-01	-1.25E+00	1.58E+02	1.98E+02
SYNDIG1L	9.86E+00	3.59E-05	7.03E-05	3.62E-01	-1.47E+00	-2.76E+00	2.91E-01	8.04E-01
SYNGR2	6.00E+02	5.07E-04	7.01E-04	6.75E-01	-5.68E-01	-1.48E+00	2.56E+01	3.80E+01
SZRD1	2.65E+03	1.19E-03	1.51E-03	8.24E-01	-2.79E-01	-1.21E+00	1.27E+02	1.55E+02
TADA3	2.74E+03	7.16E-04	9.51E-04	8.71E-01	-1.99E-01	-1.15E+00	1.35E+02	1.55E+02
TAF10	8.86E+02	1.93E-04	3.01E-04	7.78E-01	-3.62E-01	-1.28E+00	4.13E+01	5.30E+01
TAF6	2.42E+03	1.09E-08	1.25E-07	6.39E-01	-6.45E-01	-1.56E+00	1.01E+02	1.58E+02
TAF6L	4.97E+02	4.12E-08	3.40E-07	6.36E-01	-6.53E-01	-1.57E+00	2.07E+01	3.25E+01
TAF9	1.09E+03	6.39E-08	4.82E-07	6.36E-01	-6.53E-01	-1.57E+00	4.53E+01	7.13E+01
TAGLN2	2.80E+03	4.49E-02	4.58E-02	7.95E-01	-3.31E-01	-1.26E+00	1.33E+02	1.68E+02
TARBP2	6.93E+02	1.67E-06	5.40E-06	6.81E-01	-5.55E-01	-1.47E+00	3.00E+01	4.41E+01
TBC1D2	2.51E+02	1.22E-04	2.01E-04	7.15E-01	-4.83E-01	-1.40E+00	1.11E+01	1.55E+01

TBXAS1	2.55E+01	7.28E-04	9.66E-04	6.11E-01	-7.10E-01	-1.64E+00	1.05E+00	1.71E+00
TBXT	4.96E+01	5.07E-12	8.67E-10	5.80E-04	-1.08E+01	-1.72E+03	3.39E-03	5.84E+00
TCEA3	5.65E+02	4.16E-06	1.15E-05	5.82E-01	-7.82E-01	-1.72E+00	2.25E+01	3.86E+01
TCEAL4	1.80E+03	1.77E-06	5.66E-06	7.23E-01	-4.67E-01	-1.38E+00	8.07E+01	1.12E+02
TCF3	2.37E+03	1.19E-08	1.33E-07	6.04E-01	-7.27E-01	-1.65E+00	9.58E+01	1.59E+02
TCF7	8.61E+02	2.54E-09	5.03E-08	3.39E-01	-1.56E+00	-2.95E+00	2.38E+01	7.03E+01
TCL1A	7.13E+01	3.47E-03	4.01E-03	4.51E-01	-1.15E+00	-2.22E+00	2.45E+00	5.43E+00
TCL1B	4.63E+01	1.10E-02	1.17E-02	5.70E-01	-8.11E-01	-1.75E+00	1.82E+00	3.19E+00
TCTN1	7.53E+02	7.41E-05	1.32E-04	7.33E-01	-4.48E-01	-1.36E+00	3.40E+01	4.64E+01
TDH	2.55E+01	2.75E-04	4.09E-04	4.28E-01	-1.22E+00	-2.34E+00	8.25E-01	1.93E+00
TDRP	5.29E+02	1.23E-04	2.02E-04	6.14E-01	-7.03E-01	-1.63E+00	2.11E+01	3.44E+01
TEAD2	2.19E+03	4.65E-09	7.04E-08	5.38E-01	-8.95E-01	-1.86E+00	8.32E+01	1.55E+02
TEAD3	1.76E+03	4.02E-05	7.76E-05	8.02E-01	-3.18E-01	-1.25E+00	8.33E+01	1.04E+02
TEAD4	4.09E+02	3.31E-04	4.80E-04	6.69E-01	-5.80E-01	-1.50E+00	1.76E+01	2.63E+01
TECR	2.44E+03	1.12E-07	7.41E-07	6.00E-01	-7.37E-01	-1.67E+00	9.89E+01	1.65E+02
TELO2	7.05E+02	2.17E-06	6.64E-06	6.88E-01	-5.39E-01	-1.45E+00	3.07E+01	4.47E+01
TEN1	3.75E+02	4.17E-03	4.76E-03	8.35E-01	-2.60E-01	-1.20E+00	1.82E+01	2.18E+01
TEPSIN	8.00E+02	2.49E-08	2.27E-07	6.73E-01	-5.71E-01	-1.49E+00	3.44E+01	5.12E+01
TFAP2C	3.62E+02	5.13E-10	1.78E-08	2.05E-02	-5.61E+00	-4.88E+01	8.62E-01	4.21E+01
TFAP4	4.96E+02	5.18E-04	7.15E-04	7.58E-01	-3.99E-01	-1.32E+00	2.29E+01	3.02E+01
TFCP2L1	3.27E+02	1.66E-08	1.71E-07	3.34E-02	-4.91E+00	-3.00E+01	1.23E+00	3.67E+01
TFG	2.36E+03	3.00E-09	5.54E-08	6.17E-01	-6.97E-01	-1.62E+00	9.64E+01	1.56E+02
TFPT	4.26E+02	1.57E-07	9.28E-07	6.80E-01	-5.56E-01	-1.47E+00	1.84E+01	2.71E+01
TFR2	9.48E+01	5.51E-07	2.38E-06	4.01E-01	-1.32E+00	-2.50E+00	2.98E+00	7.45E+00
TGFBI	1.88E+03	7.17E-07	2.85E-06	4.49E-01	-1.15E+00	-2.23E+00	6.43E+01	1.43E+02
TGFBR3L	7.00E+01	1.91E-04	2.99E-04	5.82E-01	-7.82E-01	-1.72E+00	2.77E+00	4.77E+00
TGM3	3.08E+01	3.85E-06	1.08E-05	1.75E-01	-2.52E+00	-5.72E+00	5.25E-01	3.00E+00
THAP7	5.09E+02	1.47E-05	3.25E-05	7.85E-01	-3.49E-01	-1.27E+00	2.38E+01	3.03E+01
THBS3	2.07E+03	1.21E-06	4.26E-06	3.99E-01	-1.33E+00	-2.51E+00	6.40E+01	1.60E+02
THEM6	1.26E+02	1.49E-06	4.97E-06	3.23E-01	-1.63E+00	-3.10E+00	3.43E+00	1.06E+01
TIGD5	1.59E+03	4.86E-05	9.19E-05	7.18E-01	-4.78E-01	-1.39E+00	7.12E+01	9.92E+01
TIMM17A	4.67E+02	1.57E-04	2.53E-04	6.50E-01	-6.22E-01	-1.54E+00	1.98E+01	3.04E+01
TIMM44	6.81E+02	2.93E-06	8.55E-06	7.84E-01	-3.51E-01	-1.28E+00	3.18E+01	4.06E+01

TIMM8B	4.00E+02	2.67E-04	3.98E-04	7.43E-01	-4.28E-01	-1.35E+00	1.82E+01	2.46E+01
TIMM9	2.80E+02	2.80E-02	2.89E-02	8.71E-01	-2.00E-01	-1.15E+00	1.38E+01	1.59E+01
TIMMDC1	1.02E+02	1.43E-04	2.32E-04	6.47E-01	-6.28E-01	-1.55E+00	4.23E+00	6.53E+00
TK1	5.58E+02	1.31E-09	3.20E-08	3.58E-01	-1.48E+00	-2.79E+00	1.62E+01	4.51E+01
TLE2	1.92E+03	9.52E-09	1.13E-07	4.81E-01	-1.05E+00	-2.08E+00	6.79E+01	1.41E+02
TMA7	9.37E+02	1.30E-06	4.47E-06	6.18E-01	-6.95E-01	-1.62E+00	3.85E+01	6.23E+01
TMBIM7	1.11E+01	1.40E-02	1.48E-02	5.32E-01	-9.11E-01	-1.88E+00	4.11E-01	7.73E-01
TMCC2	8.37E+02	1.06E-08	1.21E-07	4.51E-01	-1.15E+00	-2.22E+00	2.82E+01	6.26E+01
TMEM102	6.96E+01	1.29E-05	2.92E-05	4.73E-01	-1.08E+00	-2.12E+00	2.42E+00	5.12E+00
TMEM11	7.04E+02	6.51E-05	1.18E-04	7.45E-01	-4.25E-01	-1.34E+00	3.21E+01	4.30E+01
TMEM115	1.21E+03	1.20E-05	2.77E-05	7.79E-01	-3.60E-01	-1.28E+00	5.63E+01	7.22E+01
TMEM120A	8.66E+02	8.02E-04	1.05E-03	6.70E-01	-5.79E-01	-1.49E+00	3.73E+01	5.58E+01
TMEM121B	6.35E+01	1.58E-07	9.34E-07	3.83E-01	-1.39E+00	-2.61E+00	1.92E+00	5.01E+00
TMEM126A	2.85E+02	9.61E-08	6.59E-07	4.73E-01	-1.08E+00	-2.11E+00	9.91E+00	2.09E+01
TMEM132A	1.46E+03	1.45E-08	1.53E-07	4.80E-01	-1.06E+00	-2.08E+00	5.15E+01	1.07E+02
TMEM139	2.45E+01	1.87E-04	2.94E-04	2.94E-01	-1.77E+00	-3.40E+00	6.28E-01	2.13E+00
TMEM141	1.20E+02	2.94E-04	4.32E-04	6.34E-01	-6.57E-01	-1.58E+00	5.01E+00	7.90E+00
TMEM147	1.74E+03	7.39E-03	8.05E-03	8.65E-01	-2.10E-01	-1.16E+00	8.52E+01	9.86E+01
TMEM150A	5.26E+02	4.98E-05	9.37E-05	6.67E-01	-5.85E-01	-1.50E+00	2.27E+01	3.40E+01
TMEM169	1.63E+02	2.16E-02	2.25E-02	7.61E-01	-3.94E-01	-1.31E+00	7.51E+00	9.86E+00
TMEM175	1.52E+03	7.56E-07	2.96E-06	7.78E-01	-3.62E-01	-1.28E+00	7.09E+01	9.11E+01
TMEM176A	6.19E+02	1.75E-05	3.78E-05	5.14E-01	-9.61E-01	-1.95E+00	2.28E+01	4.44E+01
TMEM179	1.23E+01	4.99E-03	5.60E-03	4.49E-01	-1.15E+00	-2.23E+00	4.14E-01	9.22E-01
TMEM182	3.19E+01	5.67E-03	6.29E-03	5.69E-01	-8.13E-01	-1.76E+00	1.23E+00	2.16E+00
TMEM183A	9.54E+02	8.75E-05	1.52E-04	8.01E-01	-3.21E-01	-1.25E+00	4.51E+01	5.63E+01
TMEM185B	3.06E+02	2.47E-05	5.07E-05	7.85E-01	-3.50E-01	-1.27E+00	1.44E+01	1.83E+01
TMEM190	1.43E+03	6.64E-08	4.88E-07	1.09E-01	-3.20E+00	-9.17E+00	1.60E+01	1.47E+02
TMEM200C	2.95E+01	2.78E-03	3.28E-03	4.11E-01	-1.28E+00	-2.43E+00	9.43E-01	2.29E+00
TMEM208	3.57E+02	1.17E-04	1.94E-04	7.52E-01	-4.12E-01	-1.33E+00	1.63E+01	2.16E+01
TMEM221	5.76E+01	8.51E-05	1.49E-04	5.08E-01	-9.78E-01	-1.97E+00	2.11E+00	4.16E+00
TMEM222	7.52E+02	3.05E-08	2.71E-07	7.21E-01	-4.72E-01	-1.39E+00	3.36E+01	4.66E+01
TMEM223	3.82E+02	4.22E-06	1.16E-05	6.90E-01	-5.36E-01	-1.45E+00	1.67E+01	2.42E+01
TMEM229B	8.97E+02	3.89E-03	4.47E-03	6.60E-01	-5.99E-01	-1.51E+00	3.81E+01	5.77E+01

TMEM231	5.58E+02	8.32E-06	2.03E-05	5.97E-01	-7.44E-01	-1.68E+00	2.22E+01	3.71E+01
TMEM238	7.97E+01	6.51E-03	7.16E-03	7.43E-01	-4.29E-01	-1.35E+00	3.60E+00	4.85E+00
TMEM25	8.68E+02	2.31E-04	3.51E-04	7.50E-01	-4.15E-01	-1.33E+00	3.97E+01	5.29E+01
TMEM265	1.46E+02	3.94E-05	7.64E-05	6.80E-01	-5.56E-01	-1.47E+00	6.34E+00	9.32E+00
TMEM30C	4.77E+00	1.30E-02	1.38E-02	5.18E-01	-9.50E-01	-1.93E+00	1.73E-01	3.34E-01
TMEM37	1.53E+02	4.88E-07	2.15E-06	4.72E-01	-1.08E+00	-2.12E+00	5.38E+00	1.14E+01
TMEM39B	5.28E+02	6.09E-06	1.57E-05	7.63E-01	-3.90E-01	-1.31E+00	2.44E+01	3.20E+01
TMEM53	2.37E+02	2.12E-06	6.54E-06	6.41E-01	-6.43E-01	-1.56E+00	9.91E+00	1.55E+01
TMEM59L	2.10E+03	1.75E-08	1.77E-07	9.72E-02	-3.36E+00	-1.03E+01	2.11E+01	2.18E+02
TMEM63C	3.00E+01	7.25E-06	1.83E-05	2.50E-01	-2.00E+00	-4.00E+00	6.58E-01	2.63E+00
TMEM88	3.58E+02	6.42E-06	1.64E-05	6.40E-01	-6.43E-01	-1.56E+00	1.51E+01	2.35E+01
TMEM8A	1.30E+03	2.91E-10	1.24E-08	2.85E-01	-1.81E+00	-3.51E+00	3.19E+01	1.12E+02
TMEM9	2.33E+03	1.62E-08	1.67E-07	5.79E-01	-7.87E-01	-1.73E+00	9.21E+01	1.59E+02
TMEM94	5.60E+03	4.17E-07	1.90E-06	5.70E-01	-8.10E-01	-1.75E+00	2.18E+02	3.83E+02
TMEM97	1.51E+03	3.11E-03	3.64E-03	7.61E-01	-3.93E-01	-1.31E+00	6.96E+01	9.15E+01
TMEM98	1.26E+03	4.71E-03	5.31E-03	8.43E-01	-2.47E-01	-1.19E+00	6.12E+01	7.27E+01
TMPRSS2	8.34E+01	1.40E-09	3.35E-08	8.08E-02	-3.63E+00	-1.24E+01	7.22E-01	8.94E+00
TMSB10	1.70E+04	4.64E-06	1.25E-05	6.76E-01	-5.66E-01	-1.48E+00	7.31E+02	1.08E+03
TMUB1	5.08E+02	2.78E-05	5.59E-05	7.26E-01	-4.61E-01	-1.38E+00	2.28E+01	3.14E+01
TNKS1BP1	8.09E+03	4.82E-05	9.14E-05	7.08E-01	-4.99E-01	-1.41E+00	3.60E+02	5.09E+02
TOE1	5.77E+02	3.70E-04	5.30E-04	8.51E-01	-2.33E-01	-1.17E+00	2.81E+01	3.30E+01
TOM1	1.03E+03	2.39E-07	1.25E-06	7.69E-01	-3.80E-01	-1.30E+00	4.78E+01	6.22E+01
TOMM40	1.08E+03	6.63E-08	4.88E-07	5.52E-01	-8.57E-01	-1.81E+00	4.15E+01	7.51E+01
TOR4A	1.18E+02	2.43E-06	7.28E-06	4.72E-01	-1.08E+00	-2.12E+00	4.18E+00	8.86E+00
TP53	2.11E+03	5.71E-07	2.42E-06	7.02E-01	-5.11E-01	-1.43E+00	9.37E+01	1.33E+02
TP53I11	2.22E+03	9.19E-06	2.21E-05	6.48E-01	-6.25E-01	-1.54E+00	9.37E+01	1.44E+02
TPC3	4.92E+01	2.85E-06	8.39E-06	2.95E-01	-1.76E+00	-3.39E+00	1.26E+00	4.27E+00
TPI1	4.12E+03	1.19E-04	1.97E-04	7.23E-01	-4.67E-01	-1.38E+00	1.86E+02	2.58E+02
TPM3	5.71E+03	1.01E-05	2.39E-05	7.48E-01	-4.19E-01	-1.34E+00	2.61E+02	3.49E+02
TPPP	3.97E+02	9.14E-07	3.40E-06	2.48E-01	-2.01E+00	-4.03E+00	8.93E+00	3.60E+01
TRABD	1.89E+03	4.61E-05	8.81E-05	8.27E-01	-2.74E-01	-1.21E+00	9.08E+01	1.10E+02
TRAF3IP2	4.53E+02	1.00E-07	6.75E-07	6.04E-01	-7.27E-01	-1.65E+00	1.85E+01	3.07E+01
TRAF4	9.36E+02	2.89E-08	2.60E-07	4.79E-01	-1.06E+00	-2.09E+00	3.31E+01	6.90E+01

TRAPPC12	1.12E+03	9.88E-09	1.16E-07	5.56E-01	-8.48E-01	-1.80E+00	4.31E+01	7.76E+01
TRAPPC6A	1.17E+02	2.19E-03	2.64E-03	6.82E-01	-5.52E-01	-1.47E+00	5.07E+00	7.43E+00
TRIAP1	3.97E+02	2.82E-03	3.32E-03	8.19E-01	-2.89E-01	-1.22E+00	1.91E+01	2.33E+01
TRIM13	5.50E+02	7.54E-08	5.39E-07	6.15E-01	-7.01E-01	-1.63E+00	2.25E+01	3.66E+01
TRIM32	6.98E+02	2.80E-03	3.30E-03	7.56E-01	-4.03E-01	-1.32E+00	3.19E+01	4.22E+01
TRIM46	2.35E+02	1.53E-07	9.17E-07	2.60E-01	-1.94E+00	-3.84E+00	5.37E+00	2.06E+01
TRIM8	1.27E+03	3.52E-07	1.67E-06	6.77E-01	-5.62E-01	-1.48E+00	5.54E+01	8.18E+01
TRIML2	3.34E+01	9.04E-06	2.19E-05	1.66E-02	-5.91E+00	-6.03E+01	6.24E-02	3.76E+00
TRIP6	1.34E+03	3.48E-04	5.03E-04	8.08E-01	-3.07E-01	-1.24E+00	6.39E+01	7.91E+01
TRIR	1.99E+03	1.83E-06	5.81E-06	7.29E-01	-4.55E-01	-1.37E+00	8.97E+01	1.23E+02
TRMT61A	5.48E+02	6.31E-02	6.37E-02	9.06E-01	-1.42E-01	-1.10E+00	2.76E+01	3.05E+01
TRMU	7.77E+02	2.10E-04	3.24E-04	7.67E-01	-3.83E-01	-1.30E+00	3.60E+01	4.69E+01
TROAP	6.89E+02	3.43E-05	6.75E-05	5.72E-01	-8.05E-01	-1.75E+00	2.71E+01	4.74E+01
TSC22D4	2.05E+03	8.43E-03	9.14E-03	9.06E-01	-1.43E-01	-1.10E+00	1.03E+02	1.14E+02
TSEN54	6.78E+02	2.34E-05	4.83E-05	7.43E-01	-4.29E-01	-1.35E+00	3.08E+01	4.14E+01
TSNARE1	5.88E+02	5.90E-07	2.48E-06	6.12E-01	-7.08E-01	-1.63E+00	2.40E+01	3.92E+01
TSPAN11	6.62E+02	6.05E-06	1.56E-05	6.35E-01	-6.55E-01	-1.57E+00	2.76E+01	4.34E+01
TSPAN14	1.69E+03	2.13E-04	3.27E-04	7.70E-01	-3.77E-01	-1.30E+00	7.84E+01	1.02E+02
TSPAN15	3.62E+02	2.63E-03	3.12E-03	7.17E-01	-4.81E-01	-1.40E+00	1.62E+01	2.26E+01
TSPAN31	1.24E+03	2.74E-05	5.54E-05	7.97E-01	-3.26E-01	-1.25E+00	5.88E+01	7.37E+01
TSPAN6	1.82E+03	9.85E-09	1.16E-07	5.00E-01	-9.99E-01	-2.00E+00	6.56E+01	1.31E+02
TSPAN9	2.19E+03	1.27E-03	1.60E-03	8.45E-01	-2.43E-01	-1.18E+00	1.07E+02	1.26E+02
TSR3	3.56E+02	7.56E-04	9.97E-04	7.90E-01	-3.39E-01	-1.27E+00	1.67E+01	2.12E+01
TSSC4	5.03E+02	2.33E-04	3.53E-04	7.62E-01	-3.92E-01	-1.31E+00	2.31E+01	3.04E+01
TSTD1	1.60E+02	2.29E-05	4.75E-05	5.95E-01	-7.49E-01	-1.68E+00	6.41E+00	1.08E+01
TTC30B	5.99E+01	2.63E-03	3.12E-03	6.44E-01	-6.35E-01	-1.55E+00	2.47E+00	3.83E+00
TTC36	7.45E+01	1.04E-06	3.78E-06	3.76E-01	-1.41E+00	-2.66E+00	2.21E+00	5.87E+00
TTC6	1.81E+01	3.33E-03	3.87E-03	3.62E-01	-1.47E+00	-2.76E+00	5.06E-01	1.40E+00
TTC9C	7.79E+02	2.25E-04	3.44E-04	6.61E-01	-5.98E-01	-1.51E+00	3.34E+01	5.05E+01
TTYH2	4.64E+02	6.18E-05	1.13E-04	4.59E-01	-1.12E+00	-2.18E+00	1.62E+01	3.52E+01
TTYH3	8.72E+03	2.13E-05	4.45E-05	6.38E-01	-6.47E-01	-1.57E+00	3.64E+02	5.71E+02
TUBA1B	2.17E+04	1.00E-07	6.75E-07	6.09E-01	-7.14E-01	-1.64E+00	8.84E+02	1.45E+03
TUBB	2.51E+04	2.13E-07	1.16E-06	6.67E-01	-5.85E-01	-1.50E+00	1.08E+03	1.62E+03

TUFT1	4.81E+02	1.45E-03	1.80E-03	7.23E-01	-4.68E-01	-1.38E+00	2.17E+01	3.00E+01
TXN	1.18E+03	9.14E-05	1.58E-04	6.42E-01	-6.39E-01	-1.56E+00	4.94E+01	7.69E+01
TXN2	1.22E+03	2.41E-08	2.23E-07	6.66E-01	-5.87E-01	-1.50E+00	5.26E+01	7.90E+01
TXNDC17	1.94E+02	6.90E-09	9.01E-08	4.19E-01	-1.25E+00	-2.39E+00	6.27E+00	1.49E+01
TXNRD2	4.88E+02	2.85E-05	5.72E-05	8.00E-01	-3.22E-01	-1.25E+00	2.31E+01	2.89E+01
TYRO3	3.02E+03	2.42E-06	7.27E-06	6.04E-01	-7.27E-01	-1.66E+00	1.22E+02	2.02E+02
UAP1L1	1.03E+03	2.06E-05	4.34E-05	6.64E-01	-5.90E-01	-1.51E+00	4.44E+01	6.68E+01
UBALD2	6.79E+02	6.10E-04	8.26E-04	7.51E-01	-4.13E-01	-1.33E+00	3.13E+01	4.16E+01
UBE2C	7.19E+02	8.36E-07	3.19E-06	4.25E-01	-1.24E+00	-2.36E+00	2.35E+01	5.54E+01
UBE2E2	5.98E+02	4.58E-07	2.05E-06	6.77E-01	-5.63E-01	-1.48E+00	2.60E+01	3.84E+01
UBIAD1	3.98E+02	1.94E-04	3.03E-04	7.66E-01	-3.85E-01	-1.31E+00	1.83E+01	2.39E+01
UBL5	1.01E+03	1.43E-06	4.80E-06	6.89E-01	-5.37E-01	-1.45E+00	4.39E+01	6.36E+01
UBL7	9.87E+02	1.18E-05	2.73E-05	8.00E-01	-3.22E-01	-1.25E+00	4.66E+01	5.82E+01
UCKL1	1.22E+03	2.55E-04	3.83E-04	8.65E-01	-2.09E-01	-1.16E+00	6.03E+01	6.97E+01
UGT1A1	1.22E+01	2.81E-04	4.16E-04	1.82E-01	-2.46E+00	-5.49E+00	2.22E-01	1.22E+00
UGT1A6	3.07E+00	5.27E-05	9.83E-05	2.66E-04	-1.19E+01	-3.76E+03	1.00E-04	3.76E-01
UHRF1	9.68E+02	1.14E-06	4.07E-06	4.84E-01	-1.05E+00	-2.06E+00	3.41E+01	7.05E+01
ULK1	2.85E+03	7.52E-09	9.50E-08	6.28E-01	-6.71E-01	-1.59E+00	1.18E+02	1.88E+02
UMPS	4.83E+02	5.09E-05	9.58E-05	7.99E-01	-3.25E-01	-1.25E+00	2.27E+01	2.85E+01
UNC119	2.56E+03	2.58E-07	1.32E-06	5.44E-01	-8.79E-01	-1.84E+00	9.78E+01	1.80E+02
UNC13D	4.01E+02	5.71E-04	7.79E-04	6.09E-01	-7.16E-01	-1.64E+00	1.65E+01	2.71E+01
UNC93B1	9.15E+02	1.83E-05	3.93E-05	7.67E-01	-3.83E-01	-1.30E+00	4.22E+01	5.51E+01
UPK1A	1.88E+01	4.87E-05	9.19E-05	4.66E-01	-1.10E+00	-2.14E+00	6.53E-01	1.40E+00
UQCR10	1.02E+03	5.55E-08	4.26E-07	6.25E-01	-6.79E-01	-1.60E+00	4.19E+01	6.71E+01
UQCR11	4.06E+02	2.67E-03	3.16E-03	7.72E-01	-3.72E-01	-1.29E+00	1.88E+01	2.44E+01
UQCRFS1	9.21E+02	2.85E-08	2.59E-07	4.93E-01	-1.02E+00	-2.03E+00	3.31E+01	6.72E+01
UQCRQ	4.48E+02	1.69E-02	1.78E-02	8.40E-01	-2.51E-01	-1.19E+00	2.18E+01	2.59E+01
USE1	7.55E+02	7.34E-04	9.71E-04	8.11E-01	-3.02E-01	-1.23E+00	3.59E+01	4.43E+01
USF1	1.25E+03	8.12E-07	3.11E-06	7.78E-01	-3.62E-01	-1.28E+00	5.84E+01	7.51E+01
USP43	1.15E+03	4.66E-07	2.07E-06	2.55E-01	-1.97E+00	-3.92E+00	2.57E+01	1.01E+02
UXT	2.59E+02	1.04E-02	1.12E-02	8.10E-01	-3.04E-01	-1.23E+00	1.23E+01	1.52E+01
VANGL2	1.12E+03	7.51E-05	1.33E-04	6.27E-01	-6.74E-01	-1.60E+00	4.63E+01	7.39E+01
VAPB	1.48E+03	1.41E-07	8.58E-07	7.55E-01	-4.05E-01	-1.32E+00	6.80E+01	9.00E+01

VASH1	2.71E+03	1.53E-04	2.47E-04	7.46E-01	-4.22E-01	-1.34E+00	1.23E+02	1.65E+02
VASP	2.17E+03	5.70E-11	4.67E-09	5.46E-01	-8.73E-01	-1.83E+00	8.31E+01	1.52E+02
VDAC2	1.97E+03	5.94E-04	8.06E-04	7.81E-01	-3.57E-01	-1.28E+00	9.18E+01	1.18E+02
VEGFB	1.19E+03	6.82E-06	1.73E-05	8.11E-01	-3.03E-01	-1.23E+00	5.67E+01	6.99E+01
VEGFC	4.93E+02	1.98E-06	6.19E-06	4.35E-01	-1.20E+00	-2.30E+00	1.63E+01	3.73E+01
VIL1	3.85E+01	1.06E-04	1.79E-04	2.25E-01	-2.15E+00	-4.44E+00	8.21E-01	3.64E+00
VPS18	5.88E+02	1.86E-03	2.26E-03	8.30E-01	-2.68E-01	-1.20E+00	2.82E+01	3.40E+01
VPS25	2.19E+03	3.43E-07	1.65E-06	6.86E-01	-5.43E-01	-1.46E+00	9.55E+01	1.39E+02
VPS72	8.68E+02	9.12E-03	9.86E-03	8.72E-01	-1.97E-01	-1.15E+00	4.30E+01	4.93E+01
VPS9D1	5.13E+02	2.91E-04	4.28E-04	7.65E-01	-3.87E-01	-1.31E+00	2.36E+01	3.08E+01
VSX2	2.66E+01	3.67E-06	1.04E-05	1.05E-02	-6.58E+00	-9.56E+01	3.16E-02	3.03E+00
VWCE	2.45E+02	1.21E-09	3.02E-08	3.14E-01	-1.67E+00	-3.18E+00	6.53E+00	2.08E+01
WBP1	1.67E+03	1.84E-09	4.05E-08	5.37E-01	-8.96E-01	-1.86E+00	6.35E+01	1.18E+02
WBP2	2.44E+03	8.33E-06	2.03E-05	7.81E-01	-3.56E-01	-1.28E+00	1.14E+02	1.46E+02
WC1.3	3.77E+00	4.96E-02	5.04E-02	3.07E-01	-1.70E+00	-3.25E+00	1.00E-01	3.26E-01
WDR13	2.41E+03	1.55E-06	5.11E-06	7.75E-01	-3.67E-01	-1.29E+00	1.12E+02	1.45E+02
WDR6	7.60E+03	4.25E-09	6.76E-08	5.35E-01	-9.02E-01	-1.87E+00	2.87E+02	5.36E+02
WDR83	3.68E+02	1.28E-05	2.90E-05	7.26E-01	-4.63E-01	-1.38E+00	1.65E+01	2.27E+01
WFDC3	9.28E+01	4.37E-05	8.39E-05	4.67E-01	-1.10E+00	-2.14E+00	3.11E+00	6.67E+00
WFIKKN1	4.15E+01	1.24E-07	7.87E-07	3.10E-01	-1.69E+00	-3.23E+00	1.07E+00	3.46E+00
WIZ	2.88E+03	4.89E-08	3.88E-07	6.82E-01	-5.52E-01	-1.47E+00	1.25E+02	1.83E+02
WNK4	1.31E+03	1.35E-05	3.02E-05	4.65E-01	-1.11E+00	-2.15E+00	4.49E+01	9.66E+01
WNT10A	2.82E+02	9.60E-06	2.29E-05	1.66E-01	-2.59E+00	-6.04E+00	4.53E+00	2.74E+01
WNT5B	1.44E+02	8.95E-10	2.78E-08	2.29E-01	-2.13E+00	-4.37E+00	3.00E+00	1.31E+01
WNT6	1.80E+03	5.75E-08	4.40E-07	2.34E-01	-2.10E+00	-4.27E+00	3.77E+01	1.61E+02
WNT9B	4.96E+01	2.07E-08	2.03E-07	1.38E-01	-2.86E+00	-7.25E+00	6.90E-01	5.00E+00
WRAP53	5.53E+02	2.59E-07	1.32E-06	7.31E-01	-4.52E-01	-1.37E+00	2.50E+01	3.42E+01
WT1	5.42E+03	3.01E-02	3.11E-02	7.68E-01	-3.80E-01	-1.30E+00	2.51E+02	3.26E+02
XKR4	2.89E+01	7.20E-05	1.28E-04	2.11E-01	-2.25E+00	-4.74E+00	5.82E-01	2.76E+00
XKR7	4.81E+00	7.03E-03	7.70E-03	1.66E-01	-2.59E+00	-6.01E+00	7.82E-02	4.70E-01
XPNPEP1	1.06E+03	1.45E-09	3.39E-08	6.36E-01	-6.52E-01	-1.57E+00	4.42E+01	6.94E+01
XPNPEP2	2.55E+02	1.02E-08	1.19E-07	2.07E-01	-2.27E+00	-4.83E+00	5.01E+00	2.42E+01
XR_001494160.	5.63E+01	1.59E-03	1.96E-03	6.80E-01	-5.56E-01	-1.47E+00	2.43E+00	3.58E+00

R_001494187.	1.48E+02	1.31E-04	2.15E-04	5.96E-01	-7.47E-01	-1.68E+00	5.95E+00	9.98E+00
R_001494238.	3.30E+00	4.26E-01	4.27E-01	2.89E-01	-1.79E+00	-3.45E+00	8.51E-02	2.94E-01
R_001494285.	8.67E+00	1.88E-01	1.89E-01	2.29E-01	-2.12E+00	-4.36E+00	1.90E-01	8.29E-01
R_001494523.	4.25E+00	3.76E-02	3.86E-02	3.59E-01	-1.48E+00	-2.78E+00	1.22E-01	3.40E-01
R_001495283.	2.43E+00	3.80E-02	3.89E-02	3.88E-01	-1.37E+00	-2.58E+00	7.55E-02	1.94E-01
R_001495345.	4.22E+02	1.01E-01	1.02E-01	8.72E-01	-1.97E-01	-1.15E+00	2.09E+01	2.40E+01
R_001495359.	6.51E+01	6.31E-03	6.96E-03	8.21E-01	-2.85E-01	-1.22E+00	3.12E+00	3.80E+00
R_001500534.	2.35E+03	1.91E-06	6.01E-06	6.51E-01	-6.19E-01	-1.54E+00	9.97E+01	1.53E+02
R_001500577.	3.02E+01	2.59E-03	3.08E-03	5.72E-01	-8.07E-01	-1.75E+00	1.19E+00	2.09E+00
R_001501856.	1.78E+01	4.92E-05	9.27E-05	3.17E-01	-1.66E+00	-3.16E+00	4.67E-01	1.47E+00
R_003029376.	1.63E+00	2.05E-03	2.48E-03	2.71E-01	-1.88E+00	-3.68E+00	3.98E-02	1.47E-01
R_003029471.	2.36E+01	9.42E-03	1.02E-02	4.40E-01	-1.19E+00	-2.28E+00	7.85E-01	1.79E+00
R_003029479.	3.48E+01	9.39E-04	1.21E-03	6.51E-01	-6.19E-01	-1.54E+00	1.46E+00	2.25E+00
R_003029507.	4.19E+00	1.07E-01	1.07E-01	4.72E-01	-1.08E+00	-2.12E+00	1.50E-01	3.17E-01
R_003029761.	1.72E+02	4.35E-02	4.44E-02	7.93E-01	-3.34E-01	-1.26E+00	8.06E+00	1.02E+01
R_003029836.	6.10E+00	1.86E-07	1.05E-06	1.11E-02	-6.49E+00	-9.00E+01	8.11E-03	7.30E-01
R_003029934.	5.97E+02	5.52E-07	2.38E-06	5.84E-01	-7.75E-01	-1.71E+00	2.37E+01	4.06E+01
R_003030031.	5.24E+01	5.73E-04	7.80E-04	5.19E-01	-9.46E-01	-1.93E+00	1.90E+00	3.65E+00
R_003030051.	1.02E+01	1.81E-03	2.21E-03	1.18E-01	-3.08E+00	-8.46E+00	1.25E-01	1.06E+00
R_003030120.	1.34E+01	2.73E-04	4.07E-04	2.82E-01	-1.83E+00	-3.55E+00	3.18E-01	1.13E+00
R_003030162.	1.32E+02	2.37E-04	3.59E-04	7.54E-01	-4.07E-01	-1.33E+00	6.07E+00	8.05E+00
R_003030168.	1.02E+02	3.46E-06	9.86E-06	4.40E-01	-1.18E+00	-2.27E+00	3.43E+00	7.79E+00
R_003030238.	2.59E+02	1.38E-03	1.72E-03	6.77E-01	-5.62E-01	-1.48E+00	1.12E+01	1.65E+01
R_003030302.	2.27E+01	1.77E-07	1.01E-06	8.75E-02	-3.51E+00	-1.14E+01	2.13E-01	2.43E+00
R_003030324.	2.42E+02	3.44E-09	6.02E-08	1.97E-01	-2.35E+00	-5.08E+00	4.62E+00	2.35E+01
R_003030341.	1.47E+02	1.02E-04	1.74E-04	3.73E-01	-1.42E+00	-2.68E+00	4.39E+00	1.18E+01
R_003030429.	5.29E+01	1.80E-04	2.85E-04	4.67E-01	-1.10E+00	-2.14E+00	1.83E+00	3.92E+00
R_003030478.	6.40E+00	1.61E-03	1.98E-03	3.33E-01	-1.59E+00	-3.01E+00	1.73E-01	5.20E-01
R_003030498.	2.63E+01	7.14E-03	7.82E-03	7.19E-01	-4.76E-01	-1.39E+00	1.18E+00	1.64E+00
R_003030651.	6.82E+01	1.76E-03	2.15E-03	2.86E-01	-1.81E+00	-3.50E+00	1.72E+00	6.03E+00
R_003030652.	1.16E+02	2.50E-03	2.98E-03	2.57E-01	-1.96E+00	-3.89E+00	2.74E+00	1.07E+01
R_003030653.	2.40E+02	7.59E-04	1.00E-03	1.94E-01	-2.37E+00	-5.16E+00	4.52E+00	2.33E+01
R_003030744.	2.61E+01	8.28E-04	1.08E-03	3.67E-01	-1.45E+00	-2.73E+00	7.70E-01	2.10E+00

XR_003030817.1	3.78E+01	1.37E-04	2.23E-04	5.59E-01	-8.39E-01	-1.79E+00	1.46E+00	2.62E+00
XR_003030820.1	4.17E+01	1.15E-07	7.49E-07	3.42E-01	-1.55E+00	-2.93E+00	1.17E+00	3.43E+00
XR_003030867.1	9.34E+02	7.17E-05	1.28E-04	7.36E-01	-4.42E-01	-1.36E+00	4.23E+01	5.75E+01
XR_003030868.1	1.60E+02	1.77E-05	3.82E-05	5.90E-01	-7.61E-01	-1.69E+00	6.37E+00	1.08E+01
XR_003030928.1	6.40E+01	5.89E-04	8.01E-04	6.44E-01	-6.34E-01	-1.55E+00	2.68E+00	4.15E+00
XR_003030959.1	1.41E+02	3.20E-03	3.72E-03	7.64E-01	-3.89E-01	-1.31E+00	6.48E+00	8.48E+00
XR_003030982.1	2.16E+01	5.08E-02	5.16E-02	6.63E-01	-5.94E-01	-1.51E+00	9.00E-01	1.36E+00
XR_003031000.1	2.35E+01	7.24E-03	7.92E-03	2.55E-01	-1.97E+00	-3.93E+00	5.04E-01	1.98E+00
XR_003031003.1	2.91E+00	3.52E-02	3.62E-02	3.79E-01	-1.40E+00	-2.64E+00	8.32E-02	2.19E-01
XR_003031018.1	3.67E+00	4.18E-03	4.76E-03	1.73E-01	-2.54E+00	-5.80E+00	6.12E-02	3.55E-01
XR_003031179.1	7.08E+01	8.53E-04	1.11E-03	6.38E-01	-6.48E-01	-1.57E+00	2.98E+00	4.67E+00
XR_003031266.1	5.01E+01	1.06E-04	1.79E-04	4.99E-01	-1.00E+00	-2.00E+00	1.78E+00	3.57E+00
XR_003031361.1	3.67E+01	5.54E-03	6.16E-03	2.31E-01	-2.12E+00	-4.33E+00	7.78E-01	3.37E+00
XR_003031495.1	3.29E+00	8.09E-06	1.99E-05	4.29E-02	-4.54E+00	-2.33E+01	1.53E-02	3.56E-01
XR_003031543.1	7.89E+00	5.53E-04	7.57E-04	2.89E-01	-1.79E+00	-3.47E+00	1.96E-01	6.81E-01
XR_003031596.1	1.34E+01	3.18E-04	4.63E-04	3.39E-01	-1.56E+00	-2.95E+00	3.66E-01	1.08E+00
XR_003031713.1	1.34E+02	9.61E-06	2.29E-05	2.70E-02	-5.21E+00	-3.71E+01	4.07E-01	1.51E+01
XR_003031756.1	2.96E+01	7.11E-05	1.27E-04	4.98E-01	-1.01E+00	-2.01E+00	1.09E+00	2.18E+00
XR_003031802.1	3.25E+01	9.84E-04	1.26E-03	3.16E-01	-1.66E+00	-3.17E+00	8.54E-01	2.70E+00
XR_003031863.1	1.83E+01	7.09E-07	2.83E-06	7.97E-03	-6.97E+00	-1.25E+02	1.68E-02	2.11E+00
XR_003031970.1	5.53E+00	1.41E-02	1.50E-02	4.81E-01	-1.06E+00	-2.08E+00	1.94E-01	4.04E-01
XR_003032146.1	1.64E+01	2.52E-05	5.16E-05	3.87E-01	-1.37E+00	-2.58E+00	5.00E-01	1.29E+00
XR_003032451.1	1.42E+01	1.30E-03	1.63E-03	1.70E-01	-2.56E+00	-5.89E+00	2.35E-01	1.38E+00
XR_003032531.1	6.82E+01	1.10E-03	1.40E-03	5.28E-01	-9.21E-01	-1.89E+00	2.53E+00	4.79E+00
XR_003032593.1	1.39E+01	2.53E-04	3.80E-04	3.87E-01	-1.37E+00	-2.59E+00	4.19E-01	1.08E+00
XR_003032648.1	3.03E+01	5.66E-03	6.29E-03	6.74E-01	-5.68E-01	-1.48E+00	1.31E+00	1.94E+00
XR_003032672.1	6.16E+02	1.55E-03	1.92E-03	7.70E-01	-3.77E-01	-1.30E+00	2.85E+01	3.71E+01
XR_003032689.1	1.80E+02	1.31E-06	4.49E-06	5.76E-01	-7.96E-01	-1.74E+00	7.08E+00	1.23E+01
XR_003032753.1	7.19E+01	3.50E-04	5.04E-04	4.84E-01	-1.05E+00	-2.07E+00	2.54E+00	5.26E+00
XR_003032844.1	8.85E+00	9.07E-05	1.57E-04	4.86E-02	-4.36E+00	-2.06E+01	4.80E-02	9.88E-01
XR_003032957.1	4.00E+00	1.24E-02	1.32E-02	1.71E-01	-2.54E+00	-5.83E+00	6.85E-02	4.00E-01
XR_003032984.1	2.22E+01	5.34E-03	5.97E-03	1.00E-01	-3.32E+00	-9.97E+00	2.39E-01	2.38E+00
XR_003033023.1	1.34E+01	3.18E-04	4.63E-04	3.39E-01	-1.56E+00	-2.95E+00	3.66E-01	1.08E+00

XR_003033053.	9.71E+01	5.72E-04	7.80E-04	6.29E-01	-6.68E-01	-1.59E+00	3.98E+00	6.33E+00
XR_003033069.	8.54E+00	8.33E-04	1.08E-03	1.71E-01	-2.55E+00	-5.86E+00	1.40E-01	8.19E-01
XR_003033139.	8.18E+01	4.04E-03	4.63E-03	8.21E-01	-2.85E-01	-1.22E+00	3.92E+00	4.77E+00
XR_003033185.	9.71E+02	3.88E-05	7.53E-05	6.21E-01	-6.88E-01	-1.61E+00	4.02E+01	6.48E+01
XR_003033257.	1.85E+02	9.27E-04	1.20E-03	7.08E-01	-4.98E-01	-1.41E+00	8.24E+00	1.16E+01
XR_003033315.	4.77E+00	3.55E-03	4.09E-03	1.75E-01	-2.51E+00	-5.70E+00	8.46E-02	4.82E-01
XR_003033363.	8.49E+00	5.40E-02	5.48E-02	7.34E-01	-4.45E-01	-1.36E+00	3.86E-01	5.26E-01
XR_003033364.	8.49E+00	5.40E-02	5.48E-02	7.34E-01	-4.45E-01	-1.36E+00	3.86E-01	5.26E-01
XR_003033405.	5.10E+02	1.13E-07	7.45E-07	3.83E-01	-1.39E+00	-2.61E+00	1.54E+01	4.02E+01
XR_003033429.	2.35E+01	8.64E-07	3.28E-06	1.83E-01	-2.45E+00	-5.48E+00	4.11E-01	2.25E+00
XR_003033454.	1.88E+00	2.31E-10	1.08E-08	4.45E-04	-1.11E+01	-2.25E+03	1.00E-04	2.25E-01
XR_003033463.	1.58E+01	1.43E-04	2.32E-04	5.01E-01	-9.97E-01	-2.00E+00	5.63E-01	1.12E+00
XR_003033464.	2.76E+00	2.26E-03	2.71E-03	1.41E-01	-2.82E+00	-7.08E+00	3.96E-02	2.80E-01
XR_003033525.	4.65E+00	1.12E-01	1.13E-01	5.12E-01	-9.67E-01	-1.95E+00	1.71E-01	3.35E-01
XR_003033542.	1.42E+01	1.75E-04	2.79E-04	4.34E-02	-4.53E+00	-2.31E+01	7.00E-02	1.61E+00
XR_003033843.	1.85E+03	5.21E-08	4.03E-07	5.19E-01	-9.46E-01	-1.93E+00	6.82E+01	1.31E+02
XR_003034286.	6.43E+00	3.18E-03	3.71E-03	4.47E-01	-1.16E+00	-2.24E+00	2.12E-01	4.74E-01
XR_003034564.	5.61E+02	4.58E-07	2.05E-06	6.12E-01	-7.08E-01	-1.63E+00	2.28E+01	3.73E+01
XR_003034596.	1.57E+01	3.35E-04	4.86E-04	2.52E-01	-1.99E+00	-3.96E+00	3.50E-01	1.39E+00
XR_003034612.	5.14E+01	1.46E-03	1.82E-03	5.30E-01	-9.17E-01	-1.89E+00	1.89E+00	3.56E+00
XR_003034749.	2.04E+01	1.52E-07	9.10E-07	2.55E-01	-1.97E+00	-3.92E+00	4.60E-01	1.81E+00
XR_003034902.	2.99E+01	1.04E-05	2.44E-05	9.64E-03	-6.70E+00	-1.04E+02	3.41E-02	3.53E+00
XR_003035004.	2.12E+02	8.94E-03	9.68E-03	8.12E-01	-3.01E-01	-1.23E+00	1.01E+01	1.24E+01
XR_003035342.	1.98E+02	1.37E-04	2.24E-04	6.70E-01	-5.78E-01	-1.49E+00	8.58E+00	1.28E+01
XR_003035343.	1.53E+02	1.41E-04	2.29E-04	6.71E-01	-5.75E-01	-1.49E+00	6.58E+00	9.81E+00
XR_003035344.	1.77E+03	1.19E-07	7.63E-07	6.03E-01	-7.30E-01	-1.66E+00	7.18E+01	1.19E+02
XR_003035393.	1.02E+02	1.05E-06	3.81E-06	3.53E-01	-1.50E+00	-2.83E+00	2.90E+00	8.22E+00
XR_003035427.	2.00E+02	7.63E-06	1.89E-05	6.40E-01	-6.44E-01	-1.56E+00	8.37E+00	1.31E+01
XR_003035429.	4.84E+01	2.38E-04	3.60E-04	6.59E-01	-6.01E-01	-1.52E+00	2.06E+00	3.13E+00
XR_003035460.	2.69E+01	1.36E-10	7.55E-09	4.01E-02	-4.64E+00	-2.49E+01	1.22E-01	3.05E+00
XR_003035476.	6.83E+01	5.95E-02	6.03E-02	5.34E-01	-9.04E-01	-1.87E+00	2.61E+00	4.88E+00
XR_003035604.	2.45E+01	2.29E-02	2.39E-02	6.77E-01	-5.62E-01	-1.48E+00	1.05E+00	1.55E+00
XR_003035797.	8.49E+00	5.40E-02	5.48E-02	7.34E-01	-4.45E-01	-1.36E+00	3.86E-01	5.26E-01

R_003036083.	1.49E+01	9.76E-03	1.05E-02	1.83E-01	-2.45E+00	-5.47E+00	2.63E-01	1.44E+00
R_003036085.	2.69E+01	1.90E-03	2.30E-03	3.88E-01	-1.37E+00	-2.58E+00	8.10E-01	2.09E+00
R_003036141.	6.83E+01	2.94E-06	8.57E-06	3.42E-01	-1.55E+00	-2.92E+00	1.93E+00	5.62E+00
R_003036235.	5.23E+00	3.05E-03	3.57E-03	2.22E-01	-2.17E+00	-4.50E+00	1.02E-01	4.59E-01
R_003036500.	4.14E+01	1.60E-04	2.58E-04	5.93E-01	-7.54E-01	-1.69E+00	1.63E+00	2.75E+00
R_003036857.	5.63E+01	3.52E-07	1.67E-06	4.10E-01	-1.29E+00	-2.44E+00	1.79E+00	4.37E+00
R_003037052.	5.30E+02	6.76E-03	7.43E-03	7.54E-01	-4.07E-01	-1.33E+00	2.42E+01	3.21E+01
R_003037101.	1.00E+01	4.01E-04	5.70E-04	3.89E-01	-1.36E+00	-2.57E+00	3.08E-01	7.91E-01
R_003037273.	1.45E+01	2.37E-02	2.46E-02	6.75E-01	-5.67E-01	-1.48E+00	6.19E-01	9.18E-01
R_003037281.	2.68E+01	5.26E-05	9.82E-05	5.32E-01	-9.09E-01	-1.88E+00	1.01E+00	1.89E+00
R_003037285.	1.45E+01	1.71E-02	1.80E-02	6.45E-01	-6.32E-01	-1.55E+00	6.15E-01	9.53E-01
R_003037308.	5.55E+00	7.99E-04	1.05E-03	3.65E-01	-1.45E+00	-2.74E+00	1.60E-01	4.39E-01
R_003037317.	3.07E+02	1.68E-02	1.77E-02	8.42E-01	-2.48E-01	-1.19E+00	1.49E+01	1.77E+01
R_003037474.	3.54E+02	3.20E-07	1.55E-06	2.67E-01	-1.91E+00	-3.75E+00	8.40E+00	3.15E+01
R_003037594.	4.11E+01	5.08E-04	7.01E-04	4.17E-01	-1.26E+00	-2.40E+00	1.32E+00	3.17E+00
R_003037691.	4.38E+02	4.79E-05	9.11E-05	7.12E-01	-4.90E-01	-1.40E+00	1.95E+01	2.74E+01
R_003037718.	1.38E+01	7.54E-09	9.50E-08	3.65E-03	-8.10E+00	-2.74E+02	5.91E-03	1.62E+00
R_003037729.	9.73E+01	1.73E-06	5.55E-06	4.33E-02	-4.53E+00	-2.31E+01	4.69E-01	1.08E+01
R_003037801.	1.09E+01	1.50E-04	2.42E-04	3.62E-02	-4.79E+00	-2.76E+01	4.56E-02	1.26E+00
R_003037806.	7.47E+01	4.72E-03	5.33E-03	7.46E-01	-4.23E-01	-1.34E+00	3.39E+00	4.54E+00
R_003037808.	3.00E+01	3.76E-05	7.31E-05	2.26E-02	-5.47E+00	-4.43E+01	8.01E-02	3.55E+00
R_003037816.	5.49E+00	5.94E-04	8.05E-04	1.03E-01	-3.28E+00	-9.69E+00	5.95E-02	5.77E-01
R_003037828.	1.81E+00	2.77E-04	4.11E-04	2.50E-01	-2.00E+00	-4.00E+00	3.97E-02	1.59E-01
R_003037846.	1.36E+01	5.31E-02	5.40E-02	4.06E-01	-1.30E+00	-2.46E+00	4.45E-01	1.10E+00
R_003037929.	1.93E+00	3.12E-01	3.13E-01	3.34E-01	-1.58E+00	-2.99E+00	5.45E-02	1.63E-01
R_003038009.	3.60E+00	1.18E-01	1.19E-01	6.75E-01	-5.67E-01	-1.48E+00	1.55E-01	2.29E-01
R_003038056.	2.52E+00	1.53E-06	5.07E-06	2.58E-02	-5.28E+00	-3.87E+01	7.32E-03	2.84E-01
R_003038178.	8.02E+00	1.48E-04	2.39E-04	6.37E-02	-3.97E+00	-1.57E+01	5.65E-02	8.87E-01
R_003038179.	3.98E+01	1.20E-09	3.02E-08	1.22E-01	-3.03E+00	-8.18E+00	4.91E-01	4.02E+00
R_003038180.	3.02E+01	8.14E-08	5.78E-07	1.33E-01	-2.91E+00	-7.53E+00	4.10E-01	3.09E+00
XR_083674.4	1.27E+03	2.63E-06	7.81E-06	6.65E-01	-5.88E-01	-1.50E+00	5.48E+01	8.23E+01
XR_084136.4	3.94E+03	1.01E-05	2.39E-05	7.56E-01	-4.03E-01	-1.32E+00	1.81E+02	2.39E+02
XR_139212.4	8.38E+01	6.02E-03	6.64E-03	7.35E-01	-4.45E-01	-1.36E+00	3.80E+00	5.17E+00

XR_139625.4	5.24E+00	5.08E-04	7.01E-04	3.47E-01	-1.53E+00	-2.88E+00	1.49E-01	4.29E-01
XR_233379.4	6.55E+00	7.61E-03	8.29E-03	4.91E-01	-1.03E+00	-2.04E+00	2.34E-01	4.76E-01
XR_234350.2	6.88E+01	3.86E-02	3.96E-02	7.93E-01	-3.34E-01	-1.26E+00	3.25E+00	4.09E+00
XR_234970.4	3.47E+01	7.82E-04	1.03E-03	5.36E-01	-9.01E-01	-1.87E+00	1.30E+00	2.42E+00
XR_234993.3	1.15E+02	2.62E-03	3.11E-03	5.00E-01	-9.99E-01	-2.00E+00	4.02E+00	8.03E+00
XR_235101.4	5.01E+00	6.98E-04	9.32E-04	3.36E-01	-1.57E+00	-2.97E+00	1.42E-01	4.21E-01
XR_235867.4	1.68E+02	6.05E-04	8.19E-04	6.99E-01	-5.17E-01	-1.43E+00	7.43E+00	1.06E+01
XR_235954.4	2.40E+00	1.75E-04	2.79E-04	5.53E-02	-4.18E+00	-1.81E+01	1.48E-02	2.68E-01
XR_236319.2	1.51E+02	2.34E-02	2.43E-02	8.02E-01	-3.18E-01	-1.25E+00	7.15E+00	8.91E+00
XR_236839.4	4.30E+00	5.66E-04	7.73E-04	3.57E-01	-1.49E+00	-2.80E+00	1.24E-01	3.48E-01
XR_237014.4	1.46E+01	8.06E-04	1.05E-03	5.46E-01	-8.73E-01	-1.83E+00	5.60E-01	1.03E+00
XR_237209.4	7.74E+01	3.74E-03	4.30E-03	5.31E-01	-9.12E-01	-1.88E+00	2.86E+00	5.38E+00
XR_237845.3	3.60E+02	4.61E-03	5.22E-03	7.42E-01	-4.31E-01	-1.35E+00	1.64E+01	2.22E+01
XR_238808.3	3.06E+02	1.26E-03	1.59E-03	6.62E-01	-5.94E-01	-1.51E+00	1.30E+01	1.97E+01
XR_238819.3	1.38E+02	1.82E-03	2.22E-03	7.40E-01	-4.34E-01	-1.35E+00	6.27E+00	8.47E+00
XR_238838.4	2.95E+01	1.69E-06	5.46E-06	2.62E-01	-1.93E+00	-3.81E+00	6.78E-01	2.59E+00
XR_239260.4	8.85E+00	3.47E-04	5.02E-04	4.35E-01	-1.20E+00	-2.30E+00	2.93E-01	6.73E-01
XR_239333.4	2.51E+01	3.24E-03	3.77E-03	6.62E-01	-5.95E-01	-1.51E+00	1.07E+00	1.62E+00
XR_239539.4	2.43E+02	1.69E-05	3.67E-05	5.97E-01	-7.44E-01	-1.67E+00	9.74E+00	1.63E+01
XR_239770.4	1.56E+01	1.83E-02	1.91E-02	5.11E-01	-9.68E-01	-1.96E+00	5.67E-01	1.11E+00
XR_239936.3	2.31E+02	1.13E-03	1.44E-03	7.75E-01	-3.68E-01	-1.29E+00	1.07E+01	1.38E+01
XR_239937.4	8.47E+02	9.15E-04	1.18E-03	8.40E-01	-2.51E-01	-1.19E+00	4.10E+01	4.88E+01
XR_240083.4	1.39E+02	3.34E-04	4.83E-04	6.72E-01	-5.74E-01	-1.49E+00	6.01E+00	8.95E+00
XR_240196.4	1.07E+02	1.98E-12	5.81E-10	3.51E-02	-4.83E+00	-2.85E+01	4.23E-01	1.20E+01
XR_240634.4	3.63E+01	1.59E-06	5.21E-06	3.75E-01	-1.41E+00	-2.67E+00	1.09E+00	2.90E+00
XR_240655.4	8.27E+00	2.10E-03	2.54E-03	5.16E-01	-9.55E-01	-1.94E+00	3.06E-01	5.93E-01
XR_240730.3	2.61E+01	7.96E-05	1.41E-04	3.16E-01	-1.66E+00	-3.16E+00	6.91E-01	2.18E+00
XR_805221.3	4.68E+01	1.04E-07	6.94E-07	4.49E-03	-7.80E+00	-2.23E+02	2.50E-02	5.58E+00
XR_805447.3	8.55E+02	4.15E-09	6.71E-08	4.08E-01	-1.29E+00	-2.45E+00	2.74E+01	6.72E+01
XR_806416.2	8.53E+01	8.23E-04	1.07E-03	5.86E-01	-7.72E-01	-1.71E+00	3.39E+00	5.79E+00
XR_806651.3	7.91E+01	3.10E-09	5.63E-08	2.37E-01	-2.08E+00	-4.21E+00	1.74E+00	7.32E+00
XR_806820.3	1.71E+00	1.02E-02	1.10E-02	1.19E-01	-3.07E+00	-8.42E+00	2.19E-02	1.84E-01
XR_806995.3	2.10E+01	1.12E-01	1.12E-01	5.24E-01	-9.33E-01	-1.91E+00	7.78E-01	1.48E+00

XR_807571.3	4.82E+02	4.19E-03	4.77E-03	7.69E-01	-3.79E-01	-1.30E+00	2.24E+01	2.91E+01
XR_807592.3	4.23E+02	9.48E-07	3.51E-06	3.02E-01	-1.73E+00	-3.31E+00	1.08E+01	3.58E+01
XR_807685.3	1.06E+02	2.35E-03	2.81E-03	7.18E-01	-4.77E-01	-1.39E+00	4.72E+00	6.57E+00
XR_807866.3	3.35E+02	2.11E-07	1.15E-06	7.51E-02	-3.74E+00	-1.33E+01	2.75E+00	3.67E+01
XR_809071.1	1.64E+03	2.54E-07	1.31E-06	5.96E-01	-7.46E-01	-1.68E+00	6.67E+01	1.12E+02
XR_809153.2	2.19E+03	1.76E-06	5.65E-06	6.01E-01	-7.33E-01	-1.66E+00	8.84E+01	1.47E+02
XR_809928.3	1.70E+00	2.45E-02	2.54E-02	1.38E-01	-2.85E+00	-7.23E+00	2.45E-02	1.77E-01
XR_810193.3	1.54E+01	1.18E-03	1.50E-03	2.73E-01	-1.88E+00	-3.67E+00	3.64E-01	1.34E+00
XR_810407.3	2.62E+01	3.52E-06	1.00E-05	1.87E-01	-2.42E+00	-5.36E+00	4.63E-01	2.48E+00
XR_810408.3	3.00E+01	1.72E-06	5.53E-06	1.89E-01	-2.40E+00	-5.29E+00	5.38E-01	2.85E+00
XR_810409.3	2.69E+01	1.46E-03	1.81E-03	3.29E-01	-1.60E+00	-3.04E+00	7.21E-01	2.19E+00
XR_810468.3	1.02E+01	4.62E-04	6.45E-04	3.42E-01	-1.55E+00	-2.92E+00	2.90E-01	8.49E-01
XR_810885.3	1.16E+02	4.35E-03	4.94E-03	6.15E-01	-7.02E-01	-1.63E+00	4.73E+00	7.69E+00
XR_811112.3	4.77E+01	1.37E-07	8.47E-07	3.01E-01	-1.73E+00	-3.33E+00	1.21E+00	4.02E+00
XR_811114.3	7.66E+00	6.30E-07	2.58E-06	2.01E-01	-2.31E+00	-4.98E+00	1.45E-01	7.22E-01
XR_811148.3	2.26E+02	1.46E-02	1.54E-02	7.73E-01	-3.72E-01	-1.29E+00	1.05E+01	1.36E+01
XR_811391.3	2.23E+01	3.45E-05	6.78E-05	3.90E-01	-1.36E+00	-2.57E+00	6.77E-01	1.74E+00
XR_811484.3	1.82E+01	3.59E-02	3.69E-02	7.00E-01	-5.15E-01	-1.43E+00	8.08E-01	1.15E+00
XR_811713.3	3.07E+01	2.66E-02	2.75E-02	7.26E-01	-4.62E-01	-1.38E+00	1.38E+00	1.90E+00
XR_811837.3	2.50E+00	1.09E-02	1.17E-02	1.02E-01	-3.29E+00	-9.79E+00	2.68E-02	2.62E-01
XR_812569.3	1.43E+00	1.47E-02	1.56E-02	1.35E-01	-2.89E+00	-7.41E+00	1.99E-02	1.47E-01
XR_812916.3	1.18E+02	3.61E-03	4.16E-03	6.39E-01	-6.45E-01	-1.56E+00	4.90E+00	7.67E+00
XR_813062.2	3.72E+01	2.74E-03	3.24E-03	6.81E-01	-5.53E-01	-1.47E+00	1.59E+00	2.33E+00
XR_813149.3	1.62E+01	7.44E-04	9.83E-04	1.35E-01	-2.88E+00	-7.38E+00	2.28E-01	1.68E+00
XR_813476.3	1.42E+01	3.46E-03	3.99E-03	5.56E-01	-8.46E-01	-1.80E+00	5.44E-01	9.78E-01
XR_813537.3	4.33E+01	1.98E-05	4.18E-05	1.44E-01	-2.80E+00	-6.95E+00	6.43E-01	4.47E+00
XR_814326.1	5.52E+00	7.28E-03	7.95E-03	5.31E-01	-9.13E-01	-1.88E+00	2.09E-01	3.93E-01
XR_814368.3	2.56E+02	5.38E-05	1.00E-04	6.75E-01	-5.66E-01	-1.48E+00	1.11E+01	1.64E+01
XR_814548.3	2.40E+02	4.21E-03	4.79E-03	6.96E-01	-5.23E-01	-1.44E+00	1.04E+01	1.50E+01
XR_814962.3	4.53E+02	5.15E-04	7.10E-04	7.32E-01	-4.50E-01	-1.37E+00	2.06E+01	2.81E+01
XR_814975.3	9.87E+00	3.83E-01	3.83E-01	4.70E-01	-1.09E+00	-2.13E+00	3.40E-01	7.24E-01
XR_815135.3	6.24E+00	2.71E-01	2.72E-01	5.09E-01	-9.76E-01	-1.97E+00	2.36E-01	4.64E-01
XR_815259.2	1.31E+01	9.20E-05	1.59E-04	7.20E-02	-3.80E+00	-1.39E+01	1.01E-01	1.40E+00

XR_815718.3	2.91E+01	5.99E-03	6.62E-03	4.65E-01	-1.10E+00	-2.15E+00	1.01E+00	2.17E+00
XR_815719.3	1.94E+01	5.62E-04	7.69E-04	4.61E-01	-1.12E+00	-2.17E+00	6.66E-01	1.44E+00
XR_816495.3	7.56E+00	4.12E-03	4.71E-03	4.58E-01	-1.13E+00	-2.18E+00	2.64E-01	5.77E-01
XR_816506.3	1.21E+02	5.53E-03	6.16E-03	7.58E-01	-4.01E-01	-1.32E+00	5.58E+00	7.36E+00
XR_816816.3	4.18E+01	1.49E-02	1.57E-02	6.48E-01	-6.26E-01	-1.54E+00	1.78E+00	2.75E+00
YIF1B	4.90E+02	2.22E-07	1.20E-06	5.88E-01	-7.65E-01	-1.70E+00	1.95E+01	3.32E+01
YIPF3	2.84E+03	2.68E-05	5.43E-05	8.11E-01	-3.02E-01	-1.23E+00	1.35E+02	1.67E+02
YJEFN3	1.30E+01	1.97E-02	2.06E-02	6.56E-01	-6.09E-01	-1.52E+00	5.43E-01	8.28E-01
YPEL1	1.02E+03	7.57E-06	1.89E-05	6.51E-01	-6.20E-01	-1.54E+00	4.30E+01	6.61E+01
YPEL4	1.38E+02	3.86E-03	4.44E-03	6.86E-01	-5.43E-01	-1.46E+00	6.08E+00	8.85E+00
ZBTB12	8.53E+02	2.99E-04	4.38E-04	7.03E-01	-5.09E-01	-1.42E+00	3.77E+01	5.36E+01
ZBTB8OS	5.08E+02	2.50E-05	5.12E-05	7.20E-01	-4.74E-01	-1.39E+00	2.24E+01	3.11E+01
ZC3H7B	3.67E+03	1.92E-04	3.00E-04	7.67E-01	-3.83E-01	-1.30E+00	1.70E+02	2.21E+02
ZCCHC3	2.40E+03	4.56E-06	1.24E-05	7.29E-01	-4.57E-01	-1.37E+00	1.08E+02	1.48E+02
ZDHHC24	3.66E+02	6.84E-03	7.51E-03	8.34E-01	-2.61E-01	-1.20E+00	1.75E+01	2.10E+01
ZDHHC5	1.95E+03	2.65E-10	1.21E-08	6.02E-01	-7.33E-01	-1.66E+00	7.87E+01	1.31E+02
ZDHHC7	1.48E+03	6.00E-07	2.51E-06	7.05E-01	-5.03E-01	-1.42E+00	6.58E+01	9.32E+01
ZFP42	1.11E+01	4.67E-09	7.04E-08	4.98E-03	-7.65E+00	-2.01E+02	6.68E-03	1.34E+00
ZFPM1	9.37E+02	4.22E-06	1.16E-05	6.10E-01	-7.14E-01	-1.64E+00	3.82E+01	6.27E+01
ZIM3	6.64E+01	4.51E-06	1.23E-05	1.39E-02	-6.17E+00	-7.21E+01	1.09E-01	7.87E+00
ZNF114	1.21E+01	9.11E-05	1.57E-04	2.99E-02	-5.06E+00	-3.34E+01	4.13E-02	1.38E+00
ZNF219	7.33E+02	1.43E-03	1.78E-03	7.51E-01	-4.13E-01	-1.33E+00	3.31E+01	4.41E+01
ZNF282	1.59E+03	4.08E-04	5.79E-04	8.43E-01	-2.46E-01	-1.19E+00	7.70E+01	9.13E+01
ZNF296	8.84E+01	3.21E-12	7.32E-10	6.17E-02	-4.02E+00	-1.62E+01	5.98E-01	9.70E+00
ZNF362	2.65E+03	2.30E-06	6.98E-06	6.42E-01	-6.39E-01	-1.56E+00	1.11E+02	1.73E+02
ZNF382	2.13E+02	1.02E-05	2.41E-05	7.40E-01	-4.34E-01	-1.35E+00	9.69E+00	1.31E+01
ZNF423	1.13E+03	2.89E-04	4.26E-04	6.56E-01	-6.08E-01	-1.52E+00	4.80E+01	7.32E+01
ZNF428	1.40E+03	2.80E-07	1.40E-06	6.86E-01	-5.44E-01	-1.46E+00	6.15E+01	8.96E+01
ZNF444	1.29E+03	3.33E-08	2.93E-07	6.06E-01	-7.22E-01	-1.65E+00	5.26E+01	8.67E+01
ZNF446	4.42E+02	2.34E-07	1.23E-06	4.69E-01	-1.09E+00	-2.13E+00	1.53E+01	3.26E+01
ZNF488	2.34E+01	1.06E-04	1.79E-04	4.66E-01	-1.10E+00	-2.14E+00	8.06E-01	1.73E+00
ZNF579	9.72E+02	6.49E-06	1.65E-05	6.40E-01	-6.45E-01	-1.56E+00	4.09E+01	6.40E+01
ZNF582	8.80E+01	5.25E-03	5.87E-03	7.62E-01	-3.93E-01	-1.31E+00	4.03E+00	5.30E+00

ZNF703	8.28E+02	1.15E-09	3.00E-08	3.83E-01	-1.39E+00	-2.61E+00	2.53E+01	6.61E+01
ZNF710	9.76E+02	1.98E-03	2.40E-03	7.92E-01	-3.37E-01	-1.26E+00	4.59E+01	5.79E+01
ZNF740	1.79E+03	9.59E-05	1.64E-04	7.36E-01	-4.41E-01	-1.36E+00	8.07E+01	1.10E+02
ZNF768	1.87E+03	4.32E-05	8.31E-05	7.78E-01	-3.62E-01	-1.29E+00	8.71E+01	1.12E+02
ZNF789	6.74E+01	1.76E-04	2.79E-04	6.34E-01	-6.57E-01	-1.58E+00	2.78E+00	4.39E+00
ZNF865	6.21E+02	8.22E-05	1.45E-04	7.40E-01	-4.35E-01	-1.35E+00	2.82E+01	3.81E+01
ZNHIT1	4.70E+02	1.16E-04	1.93E-04	6.76E-01	-5.64E-01	-1.48E+00	2.04E+01	3.01E+01
ZSCAN10	1.16E+02	2.28E-10	1.08E-08	1.00E-02	-6.64E+00	-9.95E+01	1.42E-01	1.41E+01
ZSWIM1	1.85E+02	1.29E-06	4.45E-06	5.78E-01	-7.90E-01	-1.73E+00	7.30E+00	1.26E+01
C9orf3	1.21E+03	3.19E-04	4.65E-04	6.98E-01	-5.19E-01	-1.43E+00	5.30E+01	7.60E+01

S3 Table. Gene Specific Analysis (late versus early gestation) for genes in cluster 2. Shown are the fold change and its significance (p-value), log 2 ratio and False Discovery Rate (FDR) across gestation; least square (LS) mean (late and early gestation); total counts per million.

Gene symbol	Total counts	P-value	FDR step up	Ratio	Log2(Ratio)	Fold change	LSMean(Late)	LSMean(Early)
FLT1	7.30E+02	2.30E-16	4.10E-13	3.99E+00	2.00E+00	3.99E+00	5.94E+01	1.49E+01
EBF1	1.64E+02	1.07E-14	9.57E-12	8.53E+00	3.09E+00	8.53E+00	1.48E+01	1.73E+00
CNNM2	5.57E+02	6.44E-14	3.82E-11	3.30E+00	1.72E+00	3.30E+00	4.34E+01	1.32E+01
JAZF1	2.23E+02	9.10E-14	4.05E-11	6.68E+00	2.74E+00	6.68E+00	1.95E+01	2.92E+00
JAG1	1.48E+03	1.53E-13	4.57E-11	5.18E+00	2.37E+00	5.18E+00	1.25E+02	2.41E+01
DSE	1.18E+03	1.54E-13	4.57E-11	3.54E+00	1.83E+00	3.54E+00	9.38E+01	2.65E+01
EDIL3	3.68E+02	2.83E-13	7.20E-11	1.08E+01	3.44E+00	1.08E+01	3.39E+01	3.13E+00
FBXO32-2	2.09E+02	6.18E-13	1.38E-10	2.41E+01	4.59E+00	2.41E+01	2.01E+01	8.34E-01
CRIM1	9.40E+02	8.83E-13	1.60E-10	4.09E+00	2.03E+00	4.09E+00	7.66E+01	1.88E+01
SLC40A1	1.08E+03	9.00E-13	1.60E-10	2.53E+00	1.34E+00	2.53E+00	7.89E+01	3.12E+01
TMTC2	6.60E+02	1.35E-12	2.07E-10	4.78E+00	2.26E+00	4.78E+00	5.54E+01	1.16E+01
MRVI1	1.41E+03	1.40E-12	2.07E-10	1.24E+01	3.63E+00	1.24E+01	1.31E+02	1.06E+01
ARHGEF6	5.91E+02	2.22E-12	3.05E-10	3.44E+00	1.78E+00	3.44E+00	4.65E+01	1.35E+01
COL5A2	5.58E+03	2.79E-12	3.55E-10	4.78E+00	2.26E+00	4.78E+00	4.68E+02	9.80E+01
SORBS1	1.16E+03	3.48E-12	3.69E-10	5.08E+00	2.35E+00	5.08E+00	9.83E+01	1.93E+01
EPAS1	6.79E+02	3.86E-12	3.69E-10	7.33E+00	2.87E+00	7.33E+00	6.01E+01	8.20E+00
MDFIC	4.39E+02	3.86E-12	3.69E-10	3.94E+00	1.98E+00	3.94E+00	3.56E+01	9.03E+00
KLF6	2.32E+03	4.06E-12	3.69E-10	3.38E+00	1.76E+00	3.38E+00	1.82E+02	5.39E+01
ITPR1	1.73E+03	4.10E-12	3.69E-10	4.52E+00	2.18E+00	4.52E+00	1.44E+02	3.18E+01
ELF1	3.63E+02	4.61E-12	3.69E-10	2.94E+00	1.55E+00	2.94E+00	2.75E+01	9.36E+00
ECM2	2.18E+03	4.69E-12	3.69E-10	4.81E+00	2.27E+00	4.81E+00	1.83E+02	3.79E+01
FOXP1	1.41E+03	4.70E-12	3.69E-10	2.28E+00	1.19E+00	2.28E+00	1.01E+02	4.43E+01
PTGS2	5.32E+01	4.77E-12	3.69E-10	7.13E+00	2.83E+00	7.13E+00	4.70E+00	6.59E-01
RAB30	3.96E+02	5.77E-12	4.28E-10	5.32E+00	2.41E+00	5.32E+00	3.38E+01	6.35E+00
CRYBG1	4.00E+02	6.66E-12	4.74E-10	3.38E+00	1.76E+00	3.38E+00	3.13E+01	9.25E+00
TGFB2	3.83E+02	7.68E-12	4.74E-10	4.91E+00	2.30E+00	4.91E+00	3.23E+01	6.58E+00
DKK3	9.80E+02	7.68E-12	4.74E-10	3.64E+00	1.87E+00	3.64E+00	7.78E+01	2.13E+01
TGFBR2	2.27E+03	7.73E-12	4.74E-10	2.64E+00	1.40E+00	2.64E+00	1.67E+02	6.34E+01
MYO1D	1.07E+03	7.89E-12	4.74E-10	3.40E+00	1.76E+00	3.40E+00	8.44E+01	2.48E+01

IQGAP1	2.52E+03	8.14E-12	4.74E-10	3.15E+00	1.65E+00	3.15E+00	1.96E+02	6.22E+01
GGTA1	3.29E+02	8.39E-12	4.74E-10	4.84E+00	2.28E+00	4.84E+00	2.75E+01	5.69E+00
SYTL2	3.94E+02	8.52E-12	4.74E-10	6.23E+00	2.64E+00	6.23E+00	3.43E+01	5.51E+00
MTURN	1.56E+03	1.05E-11	5.53E-10	2.88E+00	1.53E+00	2.88E+00	1.18E+02	4.11E+01
JPH1	4.74E+02	1.06E-11	5.53E-10	7.40E+00	2.89E+00	7.40E+00	4.19E+01	5.67E+00
DDAH1	1.04E+03	1.10E-11	5.59E-10	6.20E+00	2.63E+00	6.20E+00	9.00E+01	1.45E+01
ADAMTSL1	2.80E+02	1.17E-11	5.77E-10	6.03E+00	2.59E+00	6.03E+00	2.41E+01	4.00E+00
RAB33B	2.67E+02	1.21E-11	5.84E-10	3.01E+00	1.59E+00	3.01E+00	2.04E+01	6.80E+00
CARD6	3.17E+02	1.28E-11	6.00E-10	2.53E+00	1.34E+00	2.53E+00	2.32E+01	9.18E+00
ANTXR1	7.63E+02	1.47E-11	6.73E-10	8.16E+00	3.03E+00	8.16E+00	6.86E+01	8.41E+00
RNF19A	1.45E+03	1.54E-11	6.76E-10	2.77E+00	1.47E+00	2.77E+00	1.09E+02	3.94E+01
PARD3B	7.11E+02	1.57E-11	6.76E-10	3.49E+00	1.80E+00	3.49E+00	5.62E+01	1.61E+01
SYNM	1.20E+03	1.59E-11	6.76E-10	5.43E+00	2.44E+00	5.43E+00	1.02E+02	1.88E+01
PLCL1	1.21E+02	1.69E-11	6.77E-10	7.00E+00	2.81E+00	7.00E+00	1.07E+01	1.52E+00
IL6ST	1.49E+03	1.72E-11	6.77E-10	3.21E+00	1.68E+00	3.21E+00	1.16E+02	3.60E+01
FRY	3.82E+02	1.72E-11	6.77E-10	3.20E+00	1.68E+00	3.20E+00	2.96E+01	9.27E+00
MYLK	8.43E+03	1.75E-11	6.77E-10	7.80E+00	2.96E+00	7.80E+00	7.52E+02	9.65E+01
GUCY1B1	8.43E+02	1.81E-11	6.85E-10	2.97E+00	1.57E+00	2.97E+00	6.42E+01	2.16E+01
MFHAS1	1.24E+03	1.95E-11	7.21E-10	3.03E+00	1.60E+00	3.03E+00	9.53E+01	3.14E+01
NFIA	1.95E+03	1.98E-11	7.21E-10	2.76E+00	1.46E+00	2.76E+00	1.47E+02	5.32E+01
CAMK2D	7.89E+02	2.05E-11	7.32E-10	2.48E+00	1.31E+00	2.48E+00	5.76E+01	2.33E+01
SNRK	1.05E+03	2.16E-11	7.54E-10	2.54E+00	1.35E+00	2.54E+00	7.75E+01	3.05E+01
FBN1	2.45E+03	2.24E-11	7.68E-10	3.81E+00	1.93E+00	3.81E+00	1.98E+02	5.19E+01
GUCY1A1	9.40E+02	2.33E-11	7.83E-10	3.68E+00	1.88E+00	3.68E+00	7.52E+01	2.04E+01
ETV6	4.49E+02	2.47E-11	8.16E-10	6.48E+00	2.70E+00	6.48E+00	3.92E+01	6.05E+00
TIMP3	2.02E+03	2.52E-11	8.16E-10	3.82E+00	1.93E+00	3.82E+00	1.63E+02	4.27E+01
CYBRD1	9.26E+02	2.58E-11	8.20E-10	3.48E+00	1.80E+00	3.48E+00	7.31E+01	2.10E+01
PDP2	3.54E+02	2.98E-11	9.30E-10	2.56E+00	1.36E+00	2.56E+00	2.61E+01	1.02E+01
GDAP1	1.20E+02	3.07E-11	9.44E-10	4.39E+00	2.13E+00	4.39E+00	9.88E+00	2.25E+00
TENM2	1.70E+03	3.18E-11	9.61E-10	8.94E+00	3.16E+00	8.94E+00	1.53E+02	1.71E+01
SMAD3	8.38E+02	3.25E-11	9.64E-10	5.35E+00	2.42E+00	5.35E+00	7.12E+01	1.33E+01
PDGFD	2.02E+02	3.34E-11	9.75E-10	2.11E+01	4.40E+00	2.11E+01	1.93E+01	9.17E-01
FUT11	7.25E+02	3.96E-11	1.13E-09	2.75E+00	1.46E+00	2.75E+00	5.44E+01	1.98E+01

MAN1A1	8.18E+02	4.21E-11	1.13E-09	3.10E+00	1.63E+00	3.10E+00	6.31E+01	2.04E+01
ROR1	4.77E+02	4.24E-11	1.13E-09	5.03E+00	2.33E+00	5.03E+00	4.03E+01	8.01E+00
COL24A1	1.50E+02	4.24E-11	1.13E-09	1.54E+01	3.95E+00	1.54E+01	1.42E+01	9.17E-01
MYH11	1.36E+04	4.25E-11	1.13E-09	1.07E+01	3.42E+00	1.07E+01	1.25E+03	1.16E+02
TWSG1	1.38E+03	4.26E-11	1.13E-09	3.07E+00	1.62E+00	3.07E+00	1.06E+02	3.46E+01
SGMS1	6.67E+02	4.42E-11	1.16E-09	3.27E+00	1.71E+00	3.27E+00	5.20E+01	1.59E+01
CALCRL	4.72E+02	4.84E-11	1.25E-09	5.77E+00	2.53E+00	5.77E+00	4.07E+01	7.05E+00
ANO6	7.64E+02	5.04E-11	1.27E-09	3.70E+00	1.89E+00	3.70E+00	6.13E+01	1.66E+01
ARCN1	1.92E+03	5.06E-11	1.27E-09	2.28E+00	1.19E+00	2.28E+00	1.36E+02	5.96E+01
SPON1	1.53E+04	5.17E-11	1.28E-09	6.49E+00	2.70E+00	6.49E+00	1.34E+03	2.06E+02
CRYBG3	4.88E+02	5.38E-11	1.31E-09	2.33E+00	1.22E+00	2.33E+00	3.49E+01	1.50E+01
CAVIN2	1.04E+03	5.68E-11	1.37E-09	4.01E+00	2.01E+00	4.01E+00	8.44E+01	2.10E+01
PRKAR2A	1.80E+03	5.80E-11	1.38E-09	1.89E+00	9.18E-01	1.89E+00	1.22E+02	6.44E+01
AFAP1L2	2.00E+03	6.19E-11	1.45E-09	5.04E+00	2.33E+00	5.04E+00	1.68E+02	3.34E+01
MYOCD	1.31E+03	6.39E-11	1.48E-09	5.72E+00	2.52E+00	5.72E+00	1.13E+02	1.97E+01
SMAD9	6.98E+02	7.15E-11	1.63E-09	3.35E+00	1.75E+00	3.35E+00	5.46E+01	1.63E+01
SYNPO2	2.29E+03	7.21E-11	1.63E-09	8.69E+00	3.12E+00	8.69E+00	2.06E+02	2.38E+01
LAMA4	1.56E+03	7.55E-11	1.68E-09	5.48E+00	2.45E+00	5.48E+00	1.34E+02	2.44E+01
CALD1	7.36E+03	7.84E-11	1.72E-09	4.39E+00	2.13E+00	4.39E+00	6.10E+02	1.39E+02
FRMD6	5.85E+02	8.18E-11	1.78E-09	5.36E+00	2.42E+00	5.36E+00	4.98E+01	9.29E+00
MTMR11	3.36E+02	8.53E-11	1.82E-09	2.53E+00	1.34E+00	2.53E+00	2.46E+01	9.73E+00
SERINC5	2.30E+03	8.61E-11	1.82E-09	3.86E+00	1.95E+00	3.86E+00	1.85E+02	4.80E+01
FNBP1	2.14E+03	8.75E-11	1.82E-09	6.75E+00	2.75E+00	6.75E+00	1.87E+02	2.78E+01
DGKH	4.99E+02	8.79E-11	1.82E-09	3.05E+00	1.61E+00	3.05E+00	3.83E+01	1.26E+01
TMEM170B	4.22E+02	9.29E-11	1.90E-09	2.12E+00	1.09E+00	2.12E+00	2.94E+01	1.39E+01
ACTA2	1.10E+04	9.43E-11	1.90E-09	8.34E+00	3.06E+00	8.34E+00	9.87E+02	1.18E+02
FAM198B	1.25E+02	9.50E-11	1.90E-09	1.74E+01	4.12E+00	1.74E+01	1.19E+01	6.82E-01
USP46	9.33E+02	9.83E-11	1.95E-09	2.05E+00	1.04E+00	2.05E+00	6.45E+01	3.15E+01
EIF2AK3	5.30E+02	1.02E-10	2.00E-09	2.30E+00	1.20E+00	2.30E+00	3.80E+01	1.65E+01
ACSL5	2.74E+02	1.07E-10	2.07E-09	4.07E+00	2.03E+00	4.07E+00	2.22E+01	5.45E+00
SSPN	1.20E+03	1.11E-10	2.11E-09	2.54E+00	1.34E+00	2.54E+00	8.89E+01	3.50E+01
DPYD	6.33E+02	1.11E-10	2.11E-09	4.41E+00	2.14E+00	4.41E+00	5.25E+01	1.19E+01
ITGA4	8.65E+01	1.13E-10	2.12E-09	9.21E+00	3.20E+00	9.21E+00	7.84E+00	8.52E-01

FYCO1	1.93E+03	1.14E-10	2.12E-09	2.95E+00	1.56E+00	2.95E+00	1.47E+02	4.98E+01
FOSL2	3.99E+03	1.17E-10	2.16E-09	4.65E+00	2.22E+00	4.65E+00	3.33E+02	7.16E+01
CHN2	2.20E+02	1.19E-10	2.17E-09	4.00E+00	2.00E+00	4.00E+00	1.79E+01	4.48E+00
MBNL2	8.99E+02	1.23E-10	2.22E-09	3.15E+00	1.66E+00	3.15E+00	6.98E+01	2.21E+01
RIMS1	3.75E+02	1.30E-10	2.31E-09	1.51E+01	3.92E+00	1.51E+01	3.53E+01	2.34E+00
GPM6B	1.05E+03	1.36E-10	2.37E-09	2.61E+00	1.38E+00	2.61E+00	7.82E+01	3.00E+01
FAM172A	6.23E+02	1.37E-10	2.37E-09	2.24E+00	1.16E+00	2.24E+00	4.43E+01	1.98E+01
SUDS3	3.56E+02	1.38E-10	2.37E-09	3.32E+00	1.73E+00	3.32E+00	2.78E+01	8.37E+00
TOR1AIP1	1.22E+02	1.39E-10	2.37E-09	4.54E+00	2.18E+00	4.54E+00	1.01E+01	2.22E+00
PDE1A	3.57E+02	1.39E-10	2.37E-09	5.16E+00	2.37E+00	5.16E+00	3.02E+01	5.85E+00
CXHXorf36	1.08E+03	1.42E-10	2.38E-09	2.90E+00	1.53E+00	2.90E+00	8.22E+01	2.84E+01
GNA14	3.88E+02	1.47E-10	2.44E-09	8.30E+00	3.05E+00	8.30E+00	3.48E+01	4.19E+00
EHD4	3.07E+02	1.48E-10	2.44E-09	3.36E+00	1.75E+00	3.36E+00	2.39E+01	7.10E+00
PCMTD2	8.33E+02	1.49E-10	2.44E-09	1.88E+00	9.11E-01	1.88E+00	5.60E+01	2.98E+01
UNC13C	9.14E+01	1.62E-10	2.62E-09	7.83E+00	2.97E+00	7.83E+00	8.15E+00	1.04E+00
PCMTD1	1.88E+03	1.67E-10	2.69E-09	1.99E+00	9.94E-01	1.99E+00	1.29E+02	6.47E+01
FBXO30	4.82E+02	1.74E-10	2.77E-09	2.26E+00	1.17E+00	2.26E+00	3.42E+01	1.51E+01
IGF1	6.89E+02	1.91E-10	2.98E-09	3.65E+00	1.87E+00	3.65E+00	5.51E+01	1.51E+01
CAST	9.89E+02	1.93E-10	2.98E-09	3.20E+00	1.68E+00	3.20E+00	7.70E+01	2.40E+01
GPR107	2.22E+02	1.94E-10	2.98E-09	4.40E+00	2.14E+00	4.40E+00	1.82E+01	4.13E+00
TBC1D15	3.46E+02	1.94E-10	2.98E-09	2.00E+00	9.97E-01	2.00E+00	2.37E+01	1.19E+01
PRKG1	2.35E+02	1.98E-10	3.00E-09	3.44E+00	1.78E+00	3.44E+00	1.86E+01	5.40E+00
FAM120A	2.24E+03	1.99E-10	3.00E-09	2.10E+00	1.07E+00	2.10E+00	1.56E+02	7.45E+01
COL14A1	9.93E+03	2.02E-10	3.03E-09	5.70E+00	2.51E+00	5.70E+00	8.53E+02	1.50E+02
ADAM33	1.43E+03	2.05E-10	3.05E-09	5.98E+00	2.58E+00	5.98E+00	1.24E+02	2.07E+01
ATP8B4	8.71E+01	2.10E-10	3.08E-09	7.21E+00	2.85E+00	7.21E+00	7.68E+00	1.06E+00
ADAMTS12	7.24E+02	2.12E-10	3.09E-09	6.45E+00	2.69E+00	6.45E+00	6.32E+01	9.81E+00
PRDM8	2.31E+02	2.17E-10	3.11E-09	4.33E+00	2.11E+00	4.33E+00	1.89E+01	4.37E+00
SLC25A37-2	1.85E+03	2.20E-10	3.11E-09	2.12E+00	1.09E+00	2.12E+00	1.30E+02	6.11E+01
MBNL1	1.06E+03	2.21E-10	3.11E-09	2.81E+00	1.49E+00	2.81E+00	8.03E+01	2.86E+01
GBF1	8.12E+01	2.22E-10	3.11E-09	4.16E+00	2.06E+00	4.16E+00	6.57E+00	1.58E+00
TMEM47	1.87E+02	2.23E-10	3.11E-09	7.43E+00	2.89E+00	7.43E+00	1.67E+01	2.24E+00
XR_234157.4	3.02E+02	2.24E-10	3.11E-09	2.68E+00	1.42E+00	2.68E+00	2.25E+01	8.38E+00

DST	5.50E+03	2.33E-10	3.22E-09	3.47E+00	1.80E+00	3.47E+00	4.36E+02	1.26E+02
COLEC12	2.65E+03	2.35E-10	3.22E-09	3.18E+00	1.67E+00	3.18E+00	2.05E+02	6.45E+01
ADAMTSL4	7.35E+02	2.37E-10	3.22E-09	3.91E+00	1.97E+00	3.91E+00	5.94E+01	1.52E+01
SH3D19	2.55E+03	2.52E-10	3.40E-09	2.13E+00	1.09E+00	2.13E+00	1.79E+02	8.40E+01
COL4A3	5.61E+02	2.61E-10	3.47E-09	2.03E+01	4.35E+00	2.03E+01	5.37E+01	2.64E+00
FIGN	1.63E+02	2.61E-10	3.47E-09	2.96E+00	1.57E+00	2.96E+00	1.25E+01	4.22E+00
ADAMTS2	8.40E+02	2.63E-10	3.47E-09	5.42E+00	2.44E+00	5.42E+00	7.18E+01	1.33E+01
SAMD4A	4.67E+02	2.66E-10	3.48E-09	3.49E+00	1.80E+00	3.49E+00	3.70E+01	1.06E+01
SYT11	5.56E+02	2.81E-10	3.65E-09	3.51E+00	1.81E+00	3.51E+00	4.40E+01	1.25E+01
SNX31	9.32E+01	2.93E-10	3.75E-09	8.87E+00	3.15E+00	8.87E+00	8.41E+00	9.48E-01
TBL2	4.25E+02	2.93E-10	3.75E-09	2.09E+00	1.06E+00	2.09E+00	2.94E+01	1.41E+01
VSTM4	5.86E+02	2.99E-10	3.75E-09	5.20E+00	2.38E+00	5.20E+00	4.96E+01	9.52E+00
PELI2	5.42E+02	2.99E-10	3.75E-09	3.32E+00	1.73E+00	3.32E+00	4.25E+01	1.28E+01
R_003030698.	7.60E+01	3.00E-10	3.75E-09	2.23E+01	4.48E+00	2.23E+01	7.30E+00	3.27E-01
SPARCL1	1.24E+04	3.01E-10	3.75E-09	7.46E+00	2.90E+00	7.46E+00	1.10E+03	1.47E+02
TRIM2	8.80E+02	3.05E-10	3.77E-09	2.89E+00	1.53E+00	2.89E+00	6.71E+01	2.33E+01
ANO4	5.69E+02	3.07E-10	3.77E-09	3.86E+00	1.95E+00	3.86E+00	4.58E+01	1.19E+01
ABLIM1	5.72E+03	3.10E-10	3.78E-09	2.79E+00	1.48E+00	2.79E+00	4.31E+02	1.54E+02
R_003034559.	2.28E+02	3.19E-10	3.87E-09	4.99E+00	2.32E+00	4.99E+00	1.92E+01	3.84E+00
LOC101904642	1.83E+02	3.39E-10	4.08E-09	4.08E+00	2.03E+00	4.08E+00	1.48E+01	3.64E+00
LRRK1	6.47E+02	3.42E-10	4.08E-09	2.61E+00	1.39E+00	2.61E+00	4.75E+01	1.82E+01
SULF2	4.30E+03	3.43E-10	4.08E-09	5.36E+00	2.42E+00	5.36E+00	3.66E+02	6.83E+01
R_003036136.	3.40E+02	3.52E-10	4.14E-09	3.11E+00	1.64E+00	3.11E+00	2.59E+01	8.32E+00
LRRK2	2.46E+02	3.54E-10	4.14E-09	4.17E+00	2.06E+00	4.17E+00	2.02E+01	4.83E+00
ADGRF5	8.77E+02	3.69E-10	4.25E-09	3.59E+00	1.85E+00	3.59E+00	6.99E+01	1.95E+01
RFTN2	4.68E+02	3.72E-10	4.25E-09	2.98E+00	1.58E+00	2.98E+00	3.58E+01	1.20E+01
SLC10A7	1.77E+02	3.73E-10	4.25E-09	2.73E+00	1.45E+00	2.73E+00	1.32E+01	4.84E+00
FOS	2.84E+03	3.73E-10	4.25E-09	8.82E+00	3.14E+00	8.82E+00	2.59E+02	2.93E+01
INSR	1.94E+03	3.75E-10	4.25E-09	3.63E+00	1.86E+00	3.63E+00	1.55E+02	4.27E+01
NUAK1	1.13E+02	3.79E-10	4.27E-09	1.01E+01	3.33E+00	1.01E+01	1.03E+01	1.02E+00
NTRK2	3.03E+03	3.83E-10	4.29E-09	1.34E+01	3.75E+00	1.34E+01	2.82E+02	2.10E+01
STUM	4.18E+02	3.87E-10	4.31E-09	3.22E+00	1.69E+00	3.22E+00	3.23E+01	1.01E+01
ENPP1	4.55E+02	3.92E-10	4.33E-09	3.78E+00	1.92E+00	3.78E+00	3.67E+01	9.71E+00

FGF2	2.99E+02	4.03E-10	4.39E-09	2.72E+00	1.44E+00	2.72E+00	2.23E+01	8.20E+00
FN1	2.12E+04	4.04E-10	4.39E-09	4.46E+00	2.16E+00	4.46E+00	1.75E+03	3.93E+02
PRKG2	4.98E+01	4.05E-10	4.39E-09	5.45E+00	2.45E+00	5.45E+00	4.24E+00	7.78E-01
CHSY1	8.81E+02	4.07E-10	4.39E-09	2.84E+00	1.50E+00	2.84E+00	6.66E+01	2.35E+01
PEAK1	1.17E+03	4.11E-10	4.41E-09	3.38E+00	1.76E+00	3.38E+00	9.22E+01	2.73E+01
CD302	4.37E+02	4.32E-10	4.60E-09	3.12E+00	1.64E+00	3.12E+00	3.38E+01	1.08E+01
IL13RA1	1.93E+03	4.39E-10	4.65E-09	2.54E+00	1.34E+00	2.54E+00	1.41E+02	5.56E+01
THBS2	9.10E+02	4.44E-10	4.68E-09	1.58E+01	3.98E+00	1.58E+01	8.60E+01	5.44E+00
LRP12	3.85E+02	4.50E-10	4.71E-09	2.46E+00	1.30E+00	2.46E+00	2.80E+01	1.14E+01
EDNRB	3.78E+02	4.55E-10	4.74E-09	9.05E+00	3.18E+00	9.05E+00	3.42E+01	3.78E+00
XR_003036597.1	3.24E+02	4.59E-10	4.75E-09	2.78E+01	4.80E+00	2.78E+01	3.14E+01	1.13E+00
CCDC142	1.73E+02	4.63E-10	4.76E-09	2.40E+00	1.26E+00	2.40E+00	1.24E+01	5.19E+00
APBB2	1.05E+03	4.86E-10	4.97E-09	2.08E+00	1.06E+00	2.08E+00	7.32E+01	3.51E+01
TIRAP	3.58E+02	4.90E-10	4.99E-09	2.89E+00	1.53E+00	2.89E+00	2.71E+01	9.35E+00
ITGB8	1.27E+02	4.99E-10	5.05E-09	4.21E+00	2.07E+00	4.21E+00	1.04E+01	2.48E+00
AOC3	2.05E+03	5.03E-10	5.05E-09	3.87E+00	1.95E+00	3.87E+00	1.65E+02	4.26E+01
SLC7A2	5.61E+02	5.05E-10	5.05E-09	2.89E+00	1.53E+00	2.89E+00	4.24E+01	1.46E+01
RIOK3	6.62E+02	5.11E-10	5.06E-09	1.70E+00	7.65E-01	1.70E+00	4.30E+01	2.53E+01
GDA	8.45E+01	5.13E-10	5.06E-09	7.19E+00	2.85E+00	7.19E+00	7.46E+00	1.04E+00
RUNX1T1	8.02E+02	5.18E-10	5.06E-09	2.91E+00	1.54E+00	2.91E+00	6.09E+01	2.09E+01
SCUBE2	1.18E+03	5.18E-10	5.06E-09	5.76E+00	2.53E+00	5.76E+00	1.01E+02	1.75E+01
C28H1orf198	6.72E+02	5.20E-10	5.06E-09	3.11E+00	1.63E+00	3.11E+00	5.16E+01	1.66E+01
ZFYVE26	7.85E+02	5.34E-10	5.16E-09	2.52E+00	1.33E+00	2.52E+00	5.75E+01	2.28E+01
IPO5	9.55E+02	5.36E-10	5.16E-09	4.77E+00	2.25E+00	4.77E+00	7.95E+01	1.67E+01
XYLT1	1.14E+03	5.51E-10	5.27E-09	4.79E+00	2.26E+00	4.79E+00	9.54E+01	1.99E+01
ZEB1	1.34E+03	5.69E-10	5.41E-09	4.25E+00	2.09E+00	4.25E+00	1.10E+02	2.58E+01
ZFP36	9.75E+02	5.71E-10	5.41E-09	3.24E+00	1.70E+00	3.24E+00	7.60E+01	2.34E+01
RAPGEF4	1.07E+02	5.81E-10	5.48E-09	4.37E+00	2.13E+00	4.37E+00	8.85E+00	2.03E+00
RNASEL	6.14E+01	5.86E-10	5.49E-09	9.21E+00	3.20E+00	9.21E+00	5.55E+00	6.03E-01
COL12A1	8.73E+03	5.90E-10	5.50E-09	4.41E+00	2.14E+00	4.41E+00	7.17E+02	1.62E+02
ANOS1	1.06E+02	6.01E-10	5.57E-09	3.47E+00	1.80E+00	3.47E+00	8.40E+00	2.42E+00
SASH1	1.04E+03	6.08E-10	5.61E-09	3.45E+00	1.79E+00	3.45E+00	8.25E+01	2.39E+01
SAP30L	2.83E+02	6.19E-10	5.65E-09	7.32E+00	2.87E+00	7.32E+00	2.50E+01	3.42E+00

LOC784451	1.18E+02	6.19E-10	5.65E-09	4.20E+00	2.07E+00	4.20E+00	9.67E+00	2.30E+00
HSPA12A	4.41E+02	6.26E-10	5.69E-09	9.62E+00	3.27E+00	9.62E+00	4.02E+01	4.18E+00
PHLDB2	1.22E+03	6.38E-10	5.74E-09	3.50E+00	1.81E+00	3.50E+00	9.72E+01	2.78E+01
THBS1	1.94E+03	6.40E-10	5.74E-09	1.04E+01	3.38E+00	1.04E+01	1.78E+02	1.70E+01
IFNAR1	3.95E+02	6.43E-10	5.74E-09	3.26E+00	1.71E+00	3.26E+00	3.07E+01	9.40E+00
KIAA0040	1.88E+02	6.48E-10	5.74E-09	4.53E+00	2.18E+00	4.53E+00	1.56E+01	3.44E+00
EGFR	1.03E+03	6.48E-10	5.74E-09	3.30E+00	1.72E+00	3.30E+00	8.08E+01	2.44E+01
GGCX	8.53E+02	6.57E-10	5.79E-09	2.57E+00	1.36E+00	2.57E+00	6.25E+01	2.43E+01
TMOD2	1.37E+02	6.63E-10	5.82E-09	3.09E+00	1.63E+00	3.09E+00	1.05E+01	3.40E+00
LOC784007	5.59E+03	6.66E-10	5.82E-09	3.23E+00	1.69E+00	3.23E+00	4.35E+02	1.35E+02
CD200	1.17E+02	6.76E-10	5.88E-09	2.45E+00	1.29E+00	2.45E+00	8.51E+00	3.47E+00
DCAF7	4.53E+02	6.81E-10	5.89E-09	2.65E+00	1.41E+00	2.65E+00	3.35E+01	1.26E+01
COL3A1	8.71E+04	7.15E-10	6.15E-09	4.09E+00	2.03E+00	4.09E+00	7.10E+03	1.74E+03
CCBE1	7.28E+01	7.29E-10	6.24E-09	5.41E+00	2.44E+00	5.41E+00	6.24E+00	1.15E+00
FLRT2	1.01E+03	7.45E-10	6.35E-09	2.22E+00	1.15E+00	2.22E+00	7.19E+01	3.24E+01
PARP8	2.83E+02	7.52E-10	6.36E-09	3.30E+00	1.72E+00	3.30E+00	2.21E+01	6.70E+00
ABCA6	3.41E+02	7.55E-10	6.36E-09	4.79E+00	2.26E+00	4.79E+00	2.85E+01	5.94E+00
CLIC4	1.36E+03	7.58E-10	6.36E-09	4.54E+00	2.18E+00	4.54E+00	1.13E+02	2.48E+01
MGAT5	8.41E+02	7.90E-10	6.60E-09	1.85E+00	8.85E-01	1.85E+00	5.67E+01	3.07E+01
DHRS12	1.66E+02	8.17E-10	6.80E-09	2.10E+00	1.07E+00	2.10E+00	1.16E+01	5.51E+00
COL1A1	1.63E+05	8.57E-10	7.06E-09	3.86E+00	1.95E+00	3.86E+00	1.31E+04	3.41E+03
MAML2	4.09E+02	8.60E-10	7.06E-09	4.30E+00	2.10E+00	4.30E+00	3.37E+01	7.83E+00
PGM5	1.59E+03	8.60E-10	7.06E-09	3.21E+00	1.68E+00	3.21E+00	1.23E+02	3.84E+01
TRIO	3.13E+03	8.69E-10	7.09E-09	2.42E+00	1.28E+00	2.42E+00	2.27E+02	9.36E+01
INPP4B	9.90E+01	8.72E-10	7.09E-09	3.10E+00	1.63E+00	3.10E+00	7.66E+00	2.47E+00
PLEKHG1	5.29E+02	8.79E-10	7.09E-09	2.94E+00	1.56E+00	2.94E+00	4.04E+01	1.37E+01
PRRG3	1.07E+03	8.80E-10	7.09E-09	2.37E+00	1.25E+00	2.37E+00	7.69E+01	3.24E+01
PDE3A	2.11E+02	9.21E-10	7.39E-09	4.24E+00	2.08E+00	4.24E+00	1.74E+01	4.11E+00
SGCD	2.33E+02	9.30E-10	7.40E-09	4.22E+00	2.08E+00	4.22E+00	1.91E+01	4.54E+00
RECK	6.24E+02	9.31E-10	7.40E-09	2.80E+00	1.48E+00	2.80E+00	4.70E+01	1.68E+01
PLEKHA2	1.57E+03	9.52E-10	7.46E-09	2.38E+00	1.25E+00	2.38E+00	1.14E+02	4.77E+01
ADGRL4	2.86E+02	9.53E-10	7.46E-09	4.19E+00	2.07E+00	4.19E+00	2.34E+01	5.59E+00
USP6NL	4.90E+02	9.54E-10	7.46E-09	1.76E+00	8.18E-01	1.76E+00	3.25E+01	1.84E+01

PARVA	2.89E+03	9.57E-10	7.46E-09	1.87E+00	9.05E-01	1.87E+00	1.94E+02	1.04E+02
ARRDC4	6.19E+02	9.59E-10	7.46E-09	4.00E+00	2.00E+00	4.00E+00	5.01E+01	1.25E+01
TM4SF1	6.84E+02	9.75E-10	7.55E-09	3.60E+00	1.85E+00	3.60E+00	5.44E+01	1.51E+01
COLGALT2	6.73E+01	9.80E-10	7.56E-09	5.35E+00	2.42E+00	5.35E+00	5.71E+00	1.07E+00
LOC789192	8.46E+02	9.97E-10	7.64E-09	1.77E+00	8.23E-01	1.77E+00	5.57E+01	3.15E+01
TGFBR3	5.26E+03	9.99E-10	7.64E-09	5.24E+00	2.39E+00	5.24E+00	4.48E+02	8.54E+01
EDEM3	5.50E+02	1.02E-09	7.77E-09	2.09E+00	1.06E+00	2.09E+00	3.83E+01	1.83E+01
FRMD4A	1.11E+03	1.04E-09	7.90E-09	2.04E+00	1.03E+00	2.04E+00	7.63E+01	3.74E+01
DKK2	5.77E+01	1.05E-09	7.90E-09	6.36E+00	2.67E+00	6.36E+00	5.03E+00	7.91E-01
MTMR10	3.84E+02	1.06E-09	7.93E-09	3.00E+00	1.58E+00	3.00E+00	2.94E+01	9.80E+00
WIPF1	4.82E+02	1.08E-09	8.07E-09	3.04E+00	1.60E+00	3.04E+00	3.69E+01	1.21E+01
LPP	2.76E+03	1.12E-09	8.32E-09	3.03E+00	1.60E+00	3.03E+00	2.13E+02	7.02E+01
ACTN1	3.78E+03	1.14E-09	8.32E-09	2.05E+00	1.04E+00	2.05E+00	2.63E+02	1.28E+02
NAPEPLD	2.65E+02	1.14E-09	8.32E-09	6.63E+00	2.73E+00	6.63E+00	2.32E+01	3.50E+00
ITGB1	8.82E+03	1.14E-09	8.32E-09	1.98E+00	9.83E-01	1.98E+00	6.05E+02	3.06E+02
GREB1	4.66E+03	1.14E-09	8.32E-09	3.35E+00	1.74E+00	3.35E+00	3.65E+02	1.09E+02
XR_805198.3	1.55E+02	1.14E-09	8.32E-09	4.13E+00	2.04E+00	4.13E+00	1.27E+01	3.08E+00
MID2	2.34E+02	1.14E-09	8.32E-09	2.74E+00	1.45E+00	2.74E+00	1.75E+01	6.39E+00
XR_003035396.1	7.99E+02	1.15E-09	8.35E-09	1.70E+01	4.08E+00	1.70E+01	7.56E+01	4.46E+00
DMD	5.46E+02	1.16E-09	8.35E-09	2.62E+00	1.39E+00	2.62E+00	4.06E+01	1.55E+01
MSN	3.93E+03	1.17E-09	8.40E-09	1.88E+00	9.14E-01	1.88E+00	2.64E+02	1.40E+02
ARMCX3	1.49E+03	1.18E-09	8.42E-09	2.26E+00	1.18E+00	2.26E+00	1.06E+02	4.70E+01
STARD9	1.39E+03	1.18E-09	8.42E-09	3.33E+00	1.74E+00	3.33E+00	1.09E+02	3.26E+01
TBC1D12	3.85E+02	1.19E-09	8.42E-09	1.88E+00	9.09E-01	1.88E+00	2.58E+01	1.37E+01
FBXL7	1.52E+03	1.21E-09	8.50E-09	2.34E+00	1.23E+00	2.34E+00	1.09E+02	4.65E+01
DBT	3.07E+02	1.21E-09	8.50E-09	2.34E+00	1.23E+00	2.34E+00	2.22E+01	9.47E+00
COL21A1	2.81E+03	1.23E-09	8.66E-09	2.86E+00	1.52E+00	2.86E+00	2.13E+02	7.42E+01
ATG4A	7.74E+01	1.25E-09	8.76E-09	2.99E+00	1.58E+00	2.99E+00	5.89E+00	1.97E+00
MECOM	2.46E+02	1.30E-09	9.03E-09	3.85E+00	1.94E+00	3.85E+00	1.99E+01	5.16E+00
CFAP97	3.55E+02	1.30E-09	9.03E-09	2.49E+00	1.31E+00	2.49E+00	2.60E+01	1.05E+01
NID1	9.52E+03	1.31E-09	9.05E-09	3.50E+00	1.81E+00	3.50E+00	7.51E+02	2.15E+02
NEURL1B	2.13E+03	1.37E-09	9.42E-09	3.35E+00	1.74E+00	3.35E+00	1.66E+02	4.97E+01
LAMB1	8.78E+03	1.42E-09	9.73E-09	2.94E+00	1.56E+00	2.94E+00	6.71E+02	2.28E+02

LAMB2	3.39E+03	1.43E-09	9.73E-09	1.75E+00	8.04E-01	1.75E+00	2.23E+02	1.28E+02
GCNT2	2.59E+01	1.46E-09	9.94E-09	5.62E+00	2.49E+00	5.62E+00	2.22E+00	3.96E-01
PTPRB	4.65E+02	1.47E-09	9.99E-09	4.28E+00	2.10E+00	4.28E+00	3.83E+01	8.95E+00
TMOD3	5.51E+02	1.48E-09	1.00E-08	2.86E+00	1.52E+00	2.86E+00	4.18E+01	1.46E+01
ADAM19	1.27E+03	1.53E-09	1.02E-08	1.84E+00	8.78E-01	1.84E+00	8.51E+01	4.63E+01
BACE1	1.25E+03	1.53E-09	1.02E-08	2.35E+00	1.23E+00	2.35E+00	9.02E+01	3.83E+01
EML1	5.18E+02	1.57E-09	1.04E-08	2.07E+00	1.05E+00	2.07E+00	3.60E+01	1.74E+01
MLLT3	6.41E+02	1.58E-09	1.05E-08	1.97E+00	9.80E-01	1.97E+00	4.38E+01	2.22E+01
R_003029755.	3.38E+02	1.70E-09	1.12E-08	4.38E+00	2.13E+00	4.38E+00	2.79E+01	6.37E+00
PDE8B	9.85E+02	1.71E-09	1.13E-08	3.11E+00	1.64E+00	3.11E+00	7.57E+01	2.44E+01
PARD3	1.97E+03	1.72E-09	1.13E-08	2.07E+00	1.05E+00	2.07E+00	1.37E+02	6.61E+01
CALHM5	4.77E+01	1.73E-09	1.13E-08	1.17E+01	3.54E+00	1.17E+01	4.40E+00	3.78E-01
SYT1	9.25E+02	1.74E-09	1.14E-08	5.46E+00	2.45E+00	5.46E+00	7.91E+01	1.45E+01
R_003035418.	1.68E+02	1.76E-09	1.14E-08	3.83E+00	1.94E+00	3.83E+00	1.35E+01	3.53E+00
CD99	6.16E+03	1.78E-09	1.16E-08	1.95E+00	9.64E-01	1.95E+00	4.18E+02	2.14E+02
R_003030575.	3.83E+02	1.84E-09	1.19E-08	3.89E+00	1.96E+00	3.89E+00	3.09E+01	7.93E+00
ARHGEF3	5.70E+02	1.87E-09	1.20E-08	2.43E+00	1.28E+00	2.43E+00	4.15E+01	1.71E+01
PTPN21	1.40E+03	1.87E-09	1.20E-08	2.34E+00	1.23E+00	2.34E+00	1.01E+02	4.29E+01
ABCB1	8.21E+02	1.89E-09	1.21E-08	2.68E+00	1.42E+00	2.68E+00	6.15E+01	2.29E+01
R_003032007.	8.46E+00	1.91E-09	1.21E-08	1.35E+01	3.76E+00	1.35E+01	7.89E-01	5.84E-02
CDON	1.45E+03	1.92E-09	1.21E-08	2.24E+00	1.17E+00	2.24E+00	1.03E+02	4.58E+01
SCN2A	8.16E+01	1.93E-09	1.21E-08	2.54E+00	1.35E+00	2.54E+00	6.03E+00	2.37E+00
SCUBE3	7.72E+02	1.93E-09	1.21E-08	8.14E+00	3.03E+00	8.14E+00	6.94E+01	8.53E+00
ITGA9	6.02E+02	1.94E-09	1.21E-08	5.54E+00	2.47E+00	5.54E+00	5.15E+01	9.30E+00
SP140L	4.41E+01	1.94E-09	1.21E-08	6.55E+00	2.71E+00	6.55E+00	3.85E+00	5.87E-01
NNT	6.78E+02	1.98E-09	1.23E-08	2.25E+00	1.17E+00	2.25E+00	4.82E+01	2.15E+01
MICU3	1.67E+02	1.98E-09	1.23E-08	2.67E+00	1.42E+00	2.67E+00	1.23E+01	4.61E+00
HSPB6	2.63E+03	1.98E-09	1.23E-08	2.80E+00	1.48E+00	2.80E+00	1.98E+02	7.06E+01
FAM124B	1.23E+02	2.01E-09	1.24E-08	3.07E+00	1.62E+00	3.07E+00	9.52E+00	3.10E+00
COL1A2	7.73E+04	2.04E-09	1.25E-08	3.44E+00	1.78E+00	3.44E+00	6.10E+03	1.78E+03
GRK3	3.62E+02	2.04E-09	1.25E-08	2.40E+00	1.26E+00	2.40E+00	2.61E+01	1.09E+01
FZD4	2.59E+02	2.06E-09	1.26E-08	4.90E+00	2.29E+00	4.90E+00	2.19E+01	4.46E+00
SNX18	7.78E+02	2.14E-09	1.30E-08	2.47E+00	1.31E+00	2.47E+00	5.70E+01	2.31E+01

CCDC141	1.26E+02	2.15E-09	1.30E-08	3.66E+00	1.87E+00	3.66E+00	1.00E+01	2.74E+00
IKBIP	9.61E+02	2.16E-09	1.30E-08	1.83E+00	8.75E-01	1.83E+00	6.43E+01	3.51E+01
ABCA9	5.41E+02	2.21E-09	1.33E-08	5.13E+00	2.36E+00	5.13E+00	4.56E+01	8.89E+00
TCF4	1.15E+03	2.26E-09	1.35E-08	2.35E+00	1.23E+00	2.35E+00	8.28E+01	3.53E+01
EEF2K	1.76E+03	2.26E-09	1.35E-08	2.52E+00	1.34E+00	2.52E+00	1.29E+02	5.12E+01
NLRP1	4.93E+01	2.27E-09	1.35E-08	5.24E+00	2.39E+00	5.24E+00	4.19E+00	8.01E-01
MTPN	8.01E+02	2.28E-09	1.35E-08	3.83E+00	1.94E+00	3.83E+00	6.41E+01	1.67E+01
FBXL3	8.57E+02	2.33E-09	1.37E-08	2.13E+00	1.09E+00	2.13E+00	5.99E+01	2.81E+01
ZNF366	5.90E+01	2.33E-09	1.37E-08	9.75E+00	3.29E+00	9.75E+00	5.36E+00	5.50E-01
CC2D2A	4.63E+02	2.35E-09	1.38E-08	2.40E+00	1.27E+00	2.40E+00	3.37E+01	1.40E+01
MTMR12	4.14E+02	2.39E-09	1.40E-08	2.19E+00	1.13E+00	2.19E+00	2.92E+01	1.34E+01
VPS13B	1.09E+03	2.41E-09	1.40E-08	2.14E+00	1.09E+00	2.14E+00	7.65E+01	3.58E+01
IGSF3	2.84E+02	2.42E-09	1.41E-08	6.10E+00	2.61E+00	6.10E+00	2.46E+01	4.03E+00
PER3	4.16E+02	2.45E-09	1.42E-08	2.53E+00	1.34E+00	2.53E+00	3.05E+01	1.21E+01
GPC5	1.51E+03	2.48E-09	1.44E-08	2.80E+00	1.48E+00	2.80E+00	1.13E+02	4.05E+01
NKAIN3	7.96E+01	2.52E-09	1.45E-08	2.77E+00	1.47E+00	2.77E+00	5.98E+00	2.16E+00
ACER2	3.06E+02	2.58E-09	1.48E-08	2.27E+00	1.18E+00	2.27E+00	2.18E+01	9.61E+00
ZNF391	4.06E+01	2.62E-09	1.50E-08	2.85E+00	1.51E+00	2.85E+00	3.06E+00	1.07E+00
B3GNT3	2.23E+02	2.63E-09	1.50E-08	2.27E+00	1.18E+00	2.27E+00	1.60E+01	7.05E+00
ANKRD27	9.05E+02	2.69E-09	1.53E-08	1.72E+00	7.83E-01	1.72E+00	5.92E+01	3.44E+01
TMEM140	1.34E+02	2.72E-09	1.54E-08	3.06E+00	1.61E+00	3.06E+00	1.03E+01	3.36E+00
CLCC1	1.40E+03	2.72E-09	1.54E-08	1.88E+00	9.11E-01	1.88E+00	9.43E+01	5.01E+01
ZNF318	6.70E+02	2.74E-09	1.54E-08	2.11E+00	1.08E+00	2.11E+00	4.69E+01	2.23E+01
RNF152	1.59E+02	2.75E-09	1.54E-08	3.36E+00	1.75E+00	3.36E+00	1.26E+01	3.74E+00
AFAP1L1	4.08E+02	2.79E-09	1.56E-08	2.57E+00	1.36E+00	2.57E+00	3.00E+01	1.17E+01
MYLIP	9.94E+02	2.79E-09	1.56E-08	2.40E+00	1.26E+00	2.40E+00	7.16E+01	2.98E+01
OSBPL6	4.63E+02	2.81E-09	1.56E-08	1.72E+00	7.86E-01	1.72E+00	3.04E+01	1.76E+01
VCL	4.43E+03	2.82E-09	1.56E-08	2.46E+00	1.30E+00	2.46E+00	3.23E+02	1.32E+02
KR_003038221.1	2.83E+00	2.82E-09	1.56E-08	6.78E+00	2.76E+00	6.78E+00	2.47E-01	3.64E-02
CP	1.55E+02	2.82E-09	1.56E-08	2.58E+00	1.37E+00	2.58E+00	1.14E+01	4.40E+00
MOB3B	6.78E+02	2.83E-09	1.56E-08	2.63E+00	1.40E+00	2.63E+00	5.03E+01	1.91E+01
ZNF697	6.50E+02	2.85E-09	1.56E-08	2.38E+00	1.25E+00	2.38E+00	4.70E+01	1.97E+01
SERINC3	1.19E+03	2.86E-09	1.56E-08	1.83E+00	8.74E-01	1.83E+00	7.90E+01	4.31E+01

HRH1	1.59E+02	2.90E-09	1.58E-08	3.08E+00	1.62E+00	3.08E+00	1.22E+01	3.96E+00
PDZRN3	1.24E+03	2.93E-09	1.59E-08	2.53E+00	1.34E+00	2.53E+00	9.13E+01	3.61E+01
FXYD1	6.05E+02	2.98E-09	1.61E-08	2.72E+00	1.45E+00	2.72E+00	4.51E+01	1.66E+01
XR_001495344.	5.19E+02	2.99E-09	1.62E-08	2.52E+00	1.33E+00	2.52E+00	3.78E+01	1.50E+01
JAM2	9.07E+02	3.05E-09	1.64E-08	3.10E+00	1.63E+00	3.10E+00	7.00E+01	2.26E+01
SLC39A14	1.10E+03	3.06E-09	1.64E-08	3.43E+00	1.78E+00	3.43E+00	8.68E+01	2.53E+01
XR_003029634.	1.51E+02	3.24E-09	1.73E-08	1.25E+01	3.64E+00	1.25E+01	1.40E+01	1.12E+00
MCL1	2.68E+03	3.28E-09	1.75E-08	1.97E+00	9.76E-01	1.97E+00	1.84E+02	9.36E+01
PCYT1A	7.72E+02	3.30E-09	1.76E-08	1.99E+00	9.89E-01	1.99E+00	5.28E+01	2.66E+01
MEF2C	8.16E+02	3.32E-09	1.76E-08	2.06E+00	1.04E+00	2.06E+00	5.66E+01	2.76E+01
ATP7A	2.43E+02	3.33E-09	1.76E-08	2.50E+00	1.32E+00	2.50E+00	1.78E+01	7.12E+00
LOC112441542	5.78E+01	3.40E-09	1.79E-08	5.98E+00	2.58E+00	5.98E+00	5.00E+00	8.36E-01
MITF	3.97E+02	3.43E-09	1.80E-08	5.25E+00	2.39E+00	5.25E+00	3.38E+01	6.44E+00
LOC101902366	4.53E+02	3.46E-09	1.81E-08	1.77E+00	8.27E-01	1.77E+00	2.98E+01	1.68E+01
PCOLCE2	2.45E+02	3.50E-09	1.83E-08	2.87E+00	1.52E+00	2.87E+00	1.85E+01	6.46E+00
CCDC80	3.03E+03	3.55E-09	1.85E-08	4.24E+00	2.08E+00	4.24E+00	2.49E+02	5.87E+01
PECAM1	1.39E+03	3.83E-09	1.99E-08	2.38E+00	1.25E+00	2.38E+00	1.00E+02	4.21E+01
UTRN	1.56E+03	3.86E-09	2.00E-08	2.26E+00	1.18E+00	2.26E+00	1.12E+02	4.95E+01
NR1H4	1.84E+02	4.01E-09	2.07E-08	4.42E+00	2.14E+00	4.42E+00	1.51E+01	3.42E+00
SREK1IP1	4.58E+02	4.04E-09	2.08E-08	1.90E+00	9.25E-01	1.90E+00	3.10E+01	1.63E+01
CDK14	9.05E+02	4.21E-09	2.16E-08	2.33E+00	1.22E+00	2.33E+00	6.52E+01	2.80E+01
ITGA1	7.83E+02	4.26E-09	2.18E-08	7.14E+00	2.84E+00	7.14E+00	6.93E+01	9.72E+00
XR_233332.4	5.96E+01	4.33E-09	2.21E-08	9.54E+00	3.25E+00	9.54E+00	5.42E+00	5.68E-01
MTCL1	6.92E+02	4.34E-09	2.21E-08	2.88E+00	1.53E+00	2.88E+00	5.24E+01	1.82E+01
CEACAM1	3.60E+02	4.40E-09	2.23E-08	2.59E+00	1.38E+00	2.59E+00	2.65E+01	1.02E+01
RNF169	7.10E+02	4.46E-09	2.25E-08	1.75E+00	8.08E-01	1.75E+00	4.68E+01	2.67E+01
LPGAT1	8.14E+02	4.47E-09	2.25E-08	2.30E+00	1.20E+00	2.30E+00	5.81E+01	2.53E+01
CASC4	1.44E+03	4.50E-09	2.26E-08	2.02E+00	1.02E+00	2.02E+00	9.89E+01	4.89E+01
Sep-08	1.99E+03	4.54E-09	2.27E-08	1.94E+00	9.56E-01	1.94E+00	1.35E+02	6.95E+01
ZNF704	4.29E+02	4.55E-09	2.27E-08	2.41E+00	1.27E+00	2.41E+00	3.11E+01	1.29E+01
XR_235579.4	7.55E+01	4.56E-09	2.27E-08	3.07E+00	1.62E+00	3.07E+00	5.78E+00	1.88E+00
GHR	1.53E+02	4.69E-09	2.33E-08	8.06E+00	3.01E+00	8.06E+00	1.38E+01	1.71E+00
ECHDC3	3.39E+03	4.76E-09	2.36E-08	1.92E+00	9.45E-01	1.92E+00	2.30E+02	1.20E+02

LOC507055	8.63E+01	4.80E-09	2.37E-08	4.23E+00	2.08E+00	4.23E+00	7.06E+00	1.67E+00
ITSN1	1.41E+03	4.81E-09	2.37E-08	2.05E+00	1.04E+00	2.05E+00	9.75E+01	4.75E+01
FILIP1	4.81E+02	4.92E-09	2.42E-08	3.25E+00	1.70E+00	3.25E+00	3.77E+01	1.16E+01
XR_003029603.	6.87E+01	4.98E-09	2.44E-08	6.09E+01	5.93E+00	6.09E+01	6.76E+00	1.11E-01
CAMSAP2	1.45E+03	5.02E-09	2.45E-08	2.68E+00	1.42E+00	2.68E+00	1.08E+02	4.04E+01
MB21D2	8.52E+01	5.03E-09	2.45E-08	3.31E+00	1.73E+00	3.31E+00	6.66E+00	2.01E+00
RHOBTB1	8.01E+02	5.04E-09	2.45E-08	2.69E+00	1.43E+00	2.69E+00	5.96E+01	2.22E+01
ZNF226	1.28E+03	5.07E-09	2.46E-08	1.89E+00	9.15E-01	1.89E+00	8.63E+01	4.58E+01
XR_813933.3	4.36E+01	5.15E-09	2.49E-08	7.28E+00	2.86E+00	7.28E+00	3.87E+00	5.32E-01
ERLIN2	3.10E+03	5.16E-09	2.49E-08	1.93E+00	9.48E-01	1.93E+00	2.09E+02	1.09E+02
GLI2	1.41E+03	5.40E-09	2.60E-08	2.57E+00	1.36E+00	2.57E+00	1.04E+02	4.05E+01
BROX	5.70E+02	5.52E-09	2.65E-08	1.88E+00	9.11E-01	1.88E+00	3.83E+01	2.04E+01
CPNE8	6.08E+01	5.72E-09	2.74E-08	6.18E+00	2.63E+00	6.18E+00	5.27E+00	8.53E-01
NEK7	7.36E+02	5.79E-09	2.76E-08	1.75E+00	8.07E-01	1.75E+00	4.83E+01	2.76E+01
SVEP1	3.50E+02	5.80E-09	2.76E-08	4.77E+00	2.25E+00	4.77E+00	2.93E+01	6.15E+00
PIK3CA	5.33E+02	5.83E-09	2.77E-08	1.71E+00	7.70E-01	1.71E+00	3.48E+01	2.04E+01
SMIM14	5.54E+02	5.85E-09	2.77E-08	2.05E+00	1.03E+00	2.05E+00	3.84E+01	1.87E+01
ADAMTS18	4.60E+01	5.93E-09	2.80E-08	3.99E+00	2.00E+00	3.99E+00	3.73E+00	9.35E-01
SELENOP	5.31E+03	5.97E-09	2.81E-08	2.53E+00	1.34E+00	2.53E+00	3.89E+02	1.54E+02
PRNP	1.07E+03	5.97E-09	2.81E-08	2.03E+00	1.02E+00	2.03E+00	7.37E+01	3.63E+01
XR_813947.3	3.15E+02	6.10E-09	2.86E-08	5.17E+00	2.37E+00	5.17E+00	2.68E+01	5.18E+00
B3GNT5	1.06E+02	6.14E-09	2.87E-08	3.52E+00	1.81E+00	3.52E+00	8.49E+00	2.41E+00
OPHN1	5.48E+02	6.33E-09	2.95E-08	2.55E+00	1.35E+00	2.55E+00	4.04E+01	1.58E+01
SDC2	4.12E+03	6.34E-09	2.95E-08	3.40E+00	1.77E+00	3.40E+00	3.25E+02	9.55E+01
TMEM100	1.54E+03	6.52E-09	3.02E-08	4.12E+00	2.04E+00	4.12E+00	1.24E+02	3.02E+01
TTC37	7.99E+02	6.52E-09	3.02E-08	1.97E+00	9.77E-01	1.97E+00	5.46E+01	2.77E+01
SH3PXD2A	7.90E+03	6.54E-09	3.02E-08	3.21E+00	1.68E+00	3.21E+00	6.13E+02	1.91E+02
PCOLCE	2.04E+03	6.58E-09	3.03E-08	2.63E+00	1.39E+00	2.63E+00	1.51E+02	5.76E+01
SETMAR	3.90E+02	6.77E-09	3.11E-08	2.22E+00	1.15E+00	2.22E+00	2.75E+01	1.24E+01
ANTXR2	1.53E+03	6.85E-09	3.14E-08	3.10E+00	1.63E+00	3.10E+00	1.18E+02	3.81E+01
PLCB1	2.68E+02	6.90E-09	3.15E-08	3.50E+00	1.81E+00	3.50E+00	2.13E+01	6.08E+00
TTL	2.28E+02	7.06E-09	3.21E-08	2.57E+00	1.36E+00	2.57E+00	1.67E+01	6.51E+00
SLC30A5	5.32E+02	7.07E-09	3.21E-08	2.06E+00	1.04E+00	2.06E+00	3.70E+01	1.80E+01

POC1B	3.05E+02	7.09E-09	3.21E-08	1.85E+00	8.90E-01	1.85E+00	2.04E+01	1.10E+01
HIPK3	7.80E+02	7.14E-09	3.23E-08	2.05E+00	1.04E+00	2.05E+00	5.41E+01	2.63E+01
FAM185A	1.53E+02	7.25E-09	3.27E-08	3.36E+00	1.75E+00	3.36E+00	1.20E+01	3.58E+00
HIPK1	1.57E+03	7.32E-09	3.29E-08	2.57E+00	1.36E+00	2.57E+00	1.16E+02	4.53E+01
CYP4V2	9.36E+02	7.38E-09	3.31E-08	2.18E+00	1.12E+00	2.18E+00	6.60E+01	3.03E+01
CFH	2.18E+03	7.39E-09	3.31E-08	1.27E+01	3.67E+00	1.27E+01	2.03E+02	1.60E+01
MAP3K21	2.46E+02	7.63E-09	3.41E-08	3.57E+00	1.84E+00	3.57E+00	1.95E+01	5.46E+00
PTPN14	1.12E+03	7.80E-09	3.47E-08	2.74E+00	1.46E+00	2.74E+00	8.42E+01	3.07E+01
CRTC3	1.76E+03	7.85E-09	3.49E-08	1.85E+00	8.86E-01	1.85E+00	1.18E+02	6.37E+01
PSD3	1.23E+03	8.22E-09	3.64E-08	2.12E+00	1.09E+00	2.12E+00	8.57E+01	4.04E+01
PRKACB	8.30E+02	8.24E-09	3.64E-08	1.90E+00	9.29E-01	1.90E+00	5.63E+01	2.95E+01
DDR2	9.66E+02	8.26E-09	3.64E-08	2.91E+00	1.54E+00	2.91E+00	7.38E+01	2.53E+01
LRRC8B	2.74E+02	8.29E-09	3.65E-08	1.98E+00	9.88E-01	1.98E+00	1.88E+01	9.46E+00
SYTL4	3.58E+02	8.50E-09	3.73E-08	1.69E+00	7.59E-01	1.69E+00	2.32E+01	1.37E+01
STON1	3.96E+02	8.54E-09	3.74E-08	2.74E+00	1.45E+00	2.74E+00	2.98E+01	1.09E+01
LOC101906235	3.17E+01	8.57E-09	3.74E-08	3.87E+00	1.95E+00	3.87E+00	2.56E+00	6.62E-01
LOC527414	9.96E+00	8.61E-09	3.75E-08	1.04E+02	6.70E+00	1.04E+02	9.87E-01	9.52E-03
MYCT1	2.18E+02	8.63E-09	3.75E-08	3.02E+00	1.59E+00	3.02E+00	1.67E+01	5.53E+00
SPARC	6.06E+04	8.89E-09	3.85E-08	2.56E+00	1.36E+00	2.56E+00	4.47E+03	1.74E+03
RAB8B	5.76E+02	8.90E-09	3.85E-08	2.23E+00	1.16E+00	2.23E+00	4.08E+01	1.83E+01
ZEB2	7.02E+01	8.98E-09	3.87E-08	3.02E+01	4.92E+00	3.02E+01	6.81E+00	2.26E-01
DIP2A	1.03E+03	9.15E-09	3.94E-08	1.92E+00	9.43E-01	1.92E+00	7.03E+01	3.65E+01
R_003030590.	2.54E+02	9.21E-09	3.95E-08	2.05E+00	1.04E+00	2.05E+00	1.76E+01	8.59E+00
EPS8	3.23E+02	9.25E-09	3.96E-08	2.15E+00	1.11E+00	2.15E+00	2.26E+01	1.05E+01
ADAMTS1	3.69E+03	9.27E-09	3.96E-08	6.64E+00	2.73E+00	6.64E+00	3.24E+02	4.88E+01
PRRG1	2.64E+02	9.33E-09	3.98E-08	2.21E+00	1.14E+00	2.21E+00	1.87E+01	8.45E+00
DENND6A	5.13E+02	9.40E-09	3.99E-08	1.98E+00	9.83E-01	1.98E+00	3.51E+01	1.78E+01
SRP72	8.30E+02	9.47E-09	4.01E-08	1.87E+00	9.01E-01	1.87E+00	5.57E+01	2.98E+01
LOC100848991	1.75E+02	9.48E-09	4.01E-08	2.32E+00	1.21E+00	2.32E+00	1.25E+01	5.39E+00
R_003029636.	1.85E+02	9.62E-09	4.06E-08	4.09E+00	2.03E+00	4.09E+00	1.51E+01	3.68E+00
GFOD1	2.21E+02	9.65E-09	4.06E-08	2.34E+00	1.23E+00	2.34E+00	1.59E+01	6.79E+00
LMCD1	1.51E+03	9.82E-09	4.13E-08	3.81E+00	1.93E+00	3.81E+00	1.22E+02	3.20E+01
MFN1	7.41E+02	9.95E-09	4.17E-08	2.01E+00	1.01E+00	2.01E+00	5.09E+01	2.53E+01

XR_003037702.1	2.33E+02	1.01E-08	4.23E-08	5.10E+00	2.35E+00	5.10E+00	1.97E+01	3.85E+00
XR_003032005.1	1.07E+01	1.02E-08	4.26E-08	8.98E+00	3.17E+00	8.98E+00	9.69E-01	1.08E-01
L3MBTL3	6.07E+02	1.03E-08	4.29E-08	1.86E+00	8.93E-01	1.86E+00	4.06E+01	2.19E+01
CCDC102B	2.53E+01	1.06E-08	4.41E-08	7.02E+00	2.81E+00	7.02E+00	2.22E+00	3.17E-01
NOTCH2	7.22E+03	1.09E-08	4.51E-08	3.13E+00	1.64E+00	3.13E+00	5.60E+02	1.79E+02
SSFA2	7.45E+02	1.10E-08	4.55E-08	2.50E+00	1.32E+00	2.50E+00	5.44E+01	2.18E+01
ZSCAN30	6.27E+01	1.10E-08	4.55E-08	3.46E+00	1.79E+00	3.46E+00	4.93E+00	1.43E+00
LRRC8C	7.25E+01	1.13E-08	4.65E-08	3.33E+00	1.74E+00	3.33E+00	5.68E+00	1.70E+00
SSR3	2.22E+03	1.14E-08	4.66E-08	1.58E+00	6.62E-01	1.58E+00	1.41E+02	8.95E+01
SLAIN2	7.42E+02	1.15E-08	4.69E-08	1.92E+00	9.42E-01	1.92E+00	5.03E+01	2.62E+01
ERAP1	3.07E+02	1.17E-08	4.77E-08	3.47E+00	1.80E+00	3.47E+00	2.42E+01	6.96E+00
OLFML1	1.31E+03	1.18E-08	4.80E-08	2.06E+00	1.04E+00	2.06E+00	9.05E+01	4.40E+01
C19H17orf75	5.32E+02	1.19E-08	4.84E-08	1.71E+00	7.75E-01	1.71E+00	3.47E+01	2.03E+01
XR_235055.4	1.77E+02	1.20E-08	4.86E-08	3.54E+00	1.82E+00	3.54E+00	1.40E+01	3.95E+00
GSN	9.17E+03	1.21E-08	4.89E-08	3.07E+00	1.62E+00	3.07E+00	7.06E+02	2.30E+02
ZFP36L2	3.28E+03	1.21E-08	4.89E-08	1.97E+00	9.78E-01	1.97E+00	2.24E+02	1.14E+02
ATL3	1.19E+03	1.22E-08	4.91E-08	1.73E+00	7.93E-01	1.73E+00	7.82E+01	4.51E+01
XR_003036004.1	1.87E+02	1.22E-08	4.92E-08	5.08E+00	2.34E+00	5.08E+00	1.58E+01	3.11E+00
CD46	2.23E+03	1.25E-08	5.02E-08	1.80E+00	8.51E-01	1.80E+00	1.48E+02	8.22E+01
SPART	1.44E+03	1.26E-08	5.04E-08	1.81E+00	8.55E-01	1.81E+00	9.55E+01	5.28E+01
LOC100298868	6.48E+01	1.26E-08	5.04E-08	3.08E+00	1.62E+00	3.08E+00	4.97E+00	1.62E+00
C23H6orf89	2.27E+03	1.27E-08	5.05E-08	1.61E+00	6.90E-01	1.61E+00	1.45E+02	8.98E+01
POFUT1	1.31E+03	1.33E-08	5.27E-08	1.70E+00	7.66E-01	1.70E+00	8.49E+01	4.99E+01
SLC44A1	9.37E+02	1.36E-08	5.36E-08	2.05E+00	1.04E+00	2.05E+00	6.52E+01	3.18E+01
LOC521981	1.27E+02	1.36E-08	5.36E-08	5.35E+00	2.42E+00	5.35E+00	1.09E+01	2.03E+00
CNTN1	1.99E+02	1.36E-08	5.36E-08	5.58E+00	2.48E+00	5.58E+00	1.70E+01	3.05E+00
DOCK9	1.09E+03	1.37E-08	5.42E-08	2.19E+00	1.13E+00	2.19E+00	7.68E+01	3.51E+01
CCDC47	6.49E+02	1.39E-08	5.48E-08	1.72E+00	7.81E-01	1.72E+00	4.24E+01	2.47E+01
NRIP2	3.05E+02	1.40E-08	5.50E-08	4.23E+00	2.08E+00	4.23E+00	2.49E+01	5.90E+00
ABI1	1.19E+03	1.41E-08	5.53E-08	1.46E+00	5.42E-01	1.46E+00	7.31E+01	5.02E+01
C7	2.03E+03	1.43E-08	5.60E-08	4.00E+00	2.00E+00	4.00E+00	1.64E+02	4.11E+01
SP140	5.99E+02	1.48E-08	5.76E-08	1.68E+00	7.52E-01	1.68E+00	3.87E+01	2.30E+01
CHRM3	3.40E+01	1.49E-08	5.78E-08	4.78E+00	2.26E+00	4.78E+00	2.85E+00	5.96E-01

XR_003032918.1	1.36E+02	1.50E-08	5.83E-08	3.00E+00	1.58E+00	3.00E+00	1.04E+01	3.46E+00
XR_003029971.1	1.23E+02	1.54E-08	5.95E-08	2.59E+00	1.37E+00	2.59E+00	9.10E+00	3.51E+00
MYOF	2.20E+03	1.54E-08	5.96E-08	2.17E+00	1.12E+00	2.17E+00	1.56E+02	7.18E+01
FRYL	5.48E+02	1.55E-08	5.97E-08	1.84E+00	8.77E-01	1.84E+00	3.68E+01	2.00E+01
DLC1	1.47E+03	1.58E-08	6.07E-08	3.01E+00	1.59E+00	3.01E+00	1.13E+02	3.76E+01
HACD2	2.28E+02	1.59E-08	6.11E-08	2.04E+00	1.03E+00	2.04E+00	1.57E+01	7.70E+00
WWC3	1.17E+03	1.60E-08	6.13E-08	1.77E+00	8.24E-01	1.77E+00	7.71E+01	4.35E+01
C2CD5	7.03E+02	1.61E-08	6.14E-08	1.90E+00	9.27E-01	1.90E+00	4.77E+01	2.51E+01
ARHGAP28	1.44E+03	1.63E-08	6.23E-08	2.60E+00	1.38E+00	2.60E+00	1.07E+02	4.11E+01
MAP3K20	8.49E+02	1.65E-08	6.26E-08	2.71E+00	1.44E+00	2.71E+00	6.36E+01	2.35E+01
JDP2	3.66E+02	1.65E-08	6.28E-08	2.62E+00	1.39E+00	2.62E+00	2.71E+01	1.04E+01
VSIG10	5.30E+02	1.69E-08	6.42E-08	1.73E+00	7.93E-01	1.73E+00	3.48E+01	2.01E+01
GANC	9.69E+01	1.71E-08	6.46E-08	2.52E+00	1.33E+00	2.52E+00	7.05E+00	2.80E+00
LOC100139670	1.16E+02	1.74E-08	6.57E-08	2.97E+00	1.57E+00	2.97E+00	8.73E+00	2.94E+00
C1QTNF9	2.50E+01	1.75E-08	6.57E-08	1.04E+01	3.37E+00	1.04E+01	2.29E+00	2.21E-01
MEOX2	5.97E+01	1.77E-08	6.66E-08	8.36E+00	3.06E+00	8.36E+00	5.39E+00	6.46E-01
TEAD1	1.71E+03	1.79E-08	6.70E-08	2.30E+00	1.20E+00	2.30E+00	1.22E+02	5.31E+01
SEMA3C	2.25E+02	1.81E-08	6.76E-08	3.64E+00	1.86E+00	3.64E+00	1.80E+01	4.94E+00
LOC100138922	2.96E+01	1.81E-08	6.76E-08	5.80E+00	2.54E+00	5.80E+00	2.54E+00	4.38E-01
CALU	4.18E+03	1.83E-08	6.81E-08	1.53E+00	6.11E-01	1.53E+00	2.62E+02	1.72E+02
XR_003036623.1	6.32E+02	1.87E-08	6.96E-08	1.97E+00	9.81E-01	1.97E+00	4.34E+01	2.20E+01
XR_003037048.1	4.50E+01	1.92E-08	7.11E-08	1.35E+01	3.76E+00	1.35E+01	4.21E+00	3.11E-01
MYO18A	1.36E+03	1.94E-08	7.20E-08	2.16E+00	1.11E+00	2.16E+00	9.53E+01	4.41E+01
TCP11L2	3.65E+02	1.98E-08	7.32E-08	1.98E+00	9.86E-01	1.98E+00	2.50E+01	1.26E+01
PARP4	4.46E+02	1.99E-08	7.32E-08	1.83E+00	8.73E-01	1.83E+00	2.97E+01	1.62E+01
ITGA2	3.37E+02	2.01E-08	7.38E-08	3.38E+00	1.76E+00	3.38E+00	2.66E+01	7.86E+00
CRK	1.42E+03	2.01E-08	7.39E-08	1.63E+00	7.00E-01	1.63E+00	9.09E+01	5.60E+01
IFNAR2	4.12E+02	2.04E-08	7.49E-08	1.68E+00	7.46E-01	1.68E+00	2.67E+01	1.59E+01
FOXN3	1.77E+03	2.05E-08	7.49E-08	1.80E+00	8.46E-01	1.80E+00	1.18E+02	6.56E+01
IL1RAP	1.16E+02	2.06E-08	7.52E-08	2.69E+00	1.43E+00	2.69E+00	8.75E+00	3.25E+00
PMEPA1	3.45E+03	2.08E-08	7.57E-08	2.79E+00	1.48E+00	2.79E+00	2.59E+02	9.30E+01
KDELC2	8.34E+02	2.15E-08	7.82E-08	1.84E+00	8.82E-01	1.84E+00	5.60E+01	3.04E+01
CADM1	8.80E+02	2.16E-08	7.82E-08	2.73E+00	1.45E+00	2.73E+00	6.63E+01	2.43E+01

DIAPH2-2	3.53E+02	2.24E-08	8.09E-08	1.78E+00	8.29E-01	1.78E+00	2.34E+01	1.32E+01
FBXO33	7.49E+01	2.30E-08	8.31E-08	2.98E+00	1.58E+00	2.98E+00	5.69E+00	1.91E+00
RABGAP1L-2	5.13E+02	2.33E-08	8.40E-08	1.62E+00	6.99E-01	1.62E+00	3.30E+01	2.03E+01
RECQL	3.01E+02	2.34E-08	8.41E-08	1.81E+00	8.56E-01	1.81E+00	1.99E+01	1.10E+01
LOC107131134	2.12E+02	2.35E-08	8.43E-08	3.67E+00	1.88E+00	3.67E+00	1.69E+01	4.60E+00
GBE1	6.27E+02	2.40E-08	8.59E-08	1.96E+00	9.70E-01	1.96E+00	4.30E+01	2.20E+01
ETS1	2.25E+03	2.43E-08	8.67E-08	1.98E+00	9.88E-01	1.98E+00	1.54E+02	7.79E+01
SGPL1	9.82E+02	2.45E-08	8.74E-08	1.60E+00	6.79E-01	1.60E+00	6.24E+01	3.90E+01
PDE7B	6.46E+02	2.45E-08	8.74E-08	2.35E+00	1.23E+00	2.35E+00	4.67E+01	1.99E+01
TGM2	5.57E+03	2.49E-08	8.86E-08	2.68E+00	1.42E+00	2.68E+00	4.13E+02	1.54E+02
FLI1	5.62E+02	2.50E-08	8.86E-08	2.09E+00	1.07E+00	2.09E+00	3.91E+01	1.87E+01
ANK2	6.55E+02	2.50E-08	8.86E-08	2.61E+00	1.38E+00	2.61E+00	4.85E+01	1.86E+01
ADAMTS5	4.37E+01	2.52E-08	8.91E-08	9.40E+00	3.23E+00	9.40E+00	3.98E+00	4.23E-01
PAQR8	3.29E+02	2.54E-08	8.95E-08	1.75E+00	8.08E-01	1.75E+00	2.17E+01	1.24E+01
LOC101907642	1.12E+02	2.56E-08	9.02E-08	5.25E+00	2.39E+00	5.25E+00	9.52E+00	1.81E+00
SAMD5	1.99E+01	2.59E-08	9.11E-08	7.45E+00	2.90E+00	7.45E+00	1.78E+00	2.38E-01
VPS4B	7.46E+02	2.62E-08	9.17E-08	1.49E+00	5.72E-01	1.49E+00	4.62E+01	3.11E+01
SMTN	2.62E+03	2.63E-08	9.19E-08	1.68E+00	7.49E-01	1.68E+00	1.70E+02	1.01E+02
TEK	6.93E+02	2.67E-08	9.33E-08	1.94E+00	9.59E-01	1.94E+00	4.74E+01	2.44E+01
CDH11	4.22E+03	2.74E-08	9.54E-08	2.80E+00	1.48E+00	2.80E+00	3.18E+02	1.14E+02
RAB27B	3.03E+01	2.77E-08	9.62E-08	3.44E+00	1.78E+00	3.44E+00	2.40E+00	6.98E-01
CAV2	1.30E+02	2.77E-08	9.62E-08	2.60E+00	1.38E+00	2.60E+00	9.64E+00	3.71E+00
FHDC1	2.25E+02	2.80E-08	9.69E-08	2.96E+00	1.56E+00	2.96E+00	1.71E+01	5.79E+00
MIER1	7.91E+02	2.82E-08	9.75E-08	1.90E+00	9.22E-01	1.90E+00	5.34E+01	2.82E+01
RPS6KA5	5.96E+02	2.92E-08	1.01E-07	1.73E+00	7.93E-01	1.73E+00	3.90E+01	2.25E+01
XR_810543.3	3.60E+01	2.93E-08	1.01E-07	4.09E+00	2.03E+00	4.09E+00	2.93E+00	7.18E-01
XR_003030695.1	3.06E+01	2.94E-08	1.01E-07	5.01E+00	2.33E+00	5.01E+00	2.59E+00	5.17E-01
ERCC5	1.18E+03	2.98E-08	1.02E-07	1.58E+00	6.56E-01	1.58E+00	7.46E+01	4.74E+01
MAP3K7CL	7.62E+01	3.05E-08	1.05E-07	7.60E+00	2.93E+00	7.60E+00	6.77E+00	8.92E-01
WDFY4	2.72E+02	3.07E-08	1.05E-07	3.95E+00	1.98E+00	3.95E+00	2.20E+01	5.56E+00
AFF2	8.21E+02	3.15E-08	1.07E-07	3.34E+00	1.74E+00	3.34E+00	6.44E+01	1.93E+01
DSEL	1.02E+03	3.16E-08	1.07E-07	2.07E+00	1.05E+00	2.07E+00	7.07E+01	3.41E+01
RAB23	5.78E+02	3.19E-08	1.08E-07	1.63E+00	7.06E-01	1.63E+00	3.72E+01	2.28E+01

RERG	2.41E+02	3.21E-08	1.09E-07	3.01E+00	1.59E+00	3.01E+00	1.85E+01	6.13E+00
MAP1B	1.65E+03	3.24E-08	1.10E-07	1.86E+00	8.96E-01	1.86E+00	1.11E+02	5.97E+01
CSGALNACT1	1.12E+03	3.25E-08	1.10E-07	2.44E+00	1.29E+00	2.44E+00	8.17E+01	3.35E+01
XR_003029640.	3.29E+02	3.25E-08	1.10E-07	2.38E+00	1.25E+00	2.38E+00	2.38E+01	1.00E+01
PDGFRA	7.16E+03	3.26E-08	1.10E-07	3.19E+00	1.67E+00	3.19E+00	5.57E+02	1.75E+02
GOLM1	3.46E+03	3.29E-08	1.10E-07	1.61E+00	6.88E-01	1.61E+00	2.20E+02	1.37E+02
XR_003038029.	5.38E+02	3.30E-08	1.11E-07	2.36E+00	1.24E+00	2.36E+00	3.88E+01	1.65E+01
GPR17	3.49E+01	3.32E-08	1.11E-07	4.00E+00	2.00E+00	4.00E+00	2.82E+00	7.04E-01
C5AR2	2.41E+01	3.37E-08	1.12E-07	9.70E+00	3.28E+00	9.70E+00	2.19E+00	2.26E-01
MFAP3	5.37E+02	3.51E-08	1.17E-07	1.83E+00	8.71E-01	1.83E+00	3.60E+01	1.97E+01
LOC101902991	4.13E+01	3.51E-08	1.17E-07	3.10E+00	1.63E+00	3.10E+00	3.19E+00	1.03E+00
COPA	5.27E+03	3.58E-08	1.19E-07	1.56E+00	6.42E-01	1.56E+00	3.32E+02	2.13E+02
ERBIN	1.34E+03	3.60E-08	1.19E-07	2.02E+00	1.01E+00	2.02E+00	9.25E+01	4.59E+01
ADAP2	5.40E+01	3.64E-08	1.21E-07	5.53E+00	2.47E+00	5.53E+00	4.63E+00	8.37E-01
MFAP4	3.95E+03	3.77E-08	1.25E-07	2.85E+00	1.51E+00	2.85E+00	2.98E+02	1.05E+02
TYK2	1.70E+03	3.80E-08	1.25E-07	1.80E+00	8.46E-01	1.80E+00	1.13E+02	6.29E+01
ZNF185	2.28E+02	3.83E-08	1.26E-07	3.88E+00	1.96E+00	3.88E+00	1.84E+01	4.74E+00
CAPN2	3.07E+03	3.85E-08	1.26E-07	1.66E+00	7.32E-01	1.66E+00	1.99E+02	1.20E+02
GNE	9.20E+02	3.85E-08	1.26E-07	1.82E+00	8.66E-01	1.82E+00	6.14E+01	3.37E+01
TP53BP2	1.97E+03	3.85E-08	1.26E-07	1.58E+00	6.59E-01	1.58E+00	1.26E+02	7.96E+01
XR_003032575.	1.05E+02	3.90E-08	1.27E-07	3.83E+00	1.94E+00	3.83E+00	8.45E+00	2.21E+00
ITGA8	9.90E+02	3.94E-08	1.28E-07	3.54E+00	1.82E+00	3.54E+00	7.90E+01	2.23E+01
ANK3	5.06E+02	3.97E-08	1.29E-07	2.62E+00	1.39E+00	2.62E+00	3.77E+01	1.44E+01
NGF	2.69E+02	3.97E-08	1.29E-07	3.10E+00	1.63E+00	3.10E+00	2.06E+01	6.64E+00
TANC2	1.32E+03	4.04E-08	1.31E-07	2.68E+00	1.42E+00	2.68E+00	9.81E+01	3.66E+01
IGF2R	8.61E+03	4.21E-08	1.36E-07	1.72E+00	7.86E-01	1.72E+00	5.63E+02	3.26E+02
FRMD3	1.22E+02	4.22E-08	1.36E-07	3.57E+00	1.84E+00	3.57E+00	9.70E+00	2.72E+00
FOCAD	4.58E+02	4.32E-08	1.39E-07	1.97E+00	9.82E-01	1.97E+00	3.13E+01	1.59E+01
XR_001495001.	2.81E+01	4.33E-08	1.40E-07	8.85E+00	3.15E+00	8.85E+00	2.54E+00	2.87E-01
PRKAR2B	1.19E+03	4.41E-08	1.42E-07	3.05E+00	1.61E+00	3.05E+00	9.19E+01	3.01E+01
TMX3	8.09E+02	4.42E-08	1.42E-07	1.70E+00	7.65E-01	1.70E+00	5.28E+01	3.11E+01
CRISPLD2	1.46E+03	4.43E-08	1.42E-07	3.49E+00	1.80E+00	3.49E+00	1.15E+02	3.30E+01
GXYLT2	6.55E+02	4.44E-08	1.42E-07	3.79E+00	1.92E+00	3.79E+00	5.26E+01	1.39E+01

XR_815453.3	4.07E+02	4.44E-08	1.42E-07	1.78E+00	8.33E-01	1.78E+00	2.69E+01	1.51E+01
PDGFRL	7.98E+01	4.44E-08	1.42E-07	3.93E+00	1.97E+00	3.93E+00	6.47E+00	1.65E+00
CBLB	3.85E+02	4.47E-08	1.42E-07	1.71E+00	7.74E-01	1.71E+00	2.52E+01	1.47E+01
PPP1R12A	1.08E+03	4.47E-08	1.42E-07	2.02E+00	1.01E+00	2.02E+00	7.46E+01	3.70E+01
ADAMTS14	1.96E+02	4.58E-08	1.45E-07	2.76E+00	1.46E+00	2.76E+00	1.48E+01	5.36E+00
ZBTB25	8.83E+01	4.71E-08	1.49E-07	2.47E+00	1.30E+00	2.47E+00	6.41E+00	2.60E+00
ELK3	1.44E+03	4.72E-08	1.49E-07	1.89E+00	9.19E-01	1.89E+00	9.76E+01	5.16E+01
GPD2	4.47E+02	4.79E-08	1.51E-07	3.39E+00	1.76E+00	3.39E+00	3.52E+01	1.04E+01
LOC515240	1.62E+01	4.81E-08	1.51E-07	4.64E+00	2.21E+00	4.64E+00	1.35E+00	2.91E-01
DDX21	6.32E+02	4.84E-08	1.52E-07	2.43E+00	1.28E+00	2.43E+00	4.60E+01	1.89E+01
FSTL1	8.07E+03	4.86E-08	1.52E-07	1.93E+00	9.48E-01	1.93E+00	5.48E+02	2.84E+02
XR_003031732.	4.63E+02	4.86E-08	1.52E-07	2.32E+00	1.21E+00	2.32E+00	3.33E+01	1.43E+01
PGM2	1.30E+02	4.92E-08	1.54E-07	2.47E+01	4.63E+00	2.47E+01	1.25E+01	5.06E-01
PER2	2.81E+02	4.96E-08	1.55E-07	2.66E+00	1.41E+00	2.66E+00	2.09E+01	7.84E+00
AMER1	3.90E+02	4.99E-08	1.55E-07	1.65E+00	7.25E-01	1.65E+00	2.52E+01	1.52E+01
SREK1	1.66E+03	5.06E-08	1.57E-07	1.87E+00	9.05E-01	1.87E+00	1.12E+02	5.99E+01
DAB2	1.97E+03	5.08E-08	1.58E-07	1.91E+00	9.30E-01	1.91E+00	1.34E+02	7.01E+01
RHOBTB3	1.59E+03	5.15E-08	1.60E-07	2.29E+00	1.19E+00	2.29E+00	1.14E+02	5.00E+01
EIF2A	1.48E+03	5.24E-08	1.62E-07	1.44E+00	5.22E-01	1.44E+00	9.07E+01	6.32E+01
ATG16L2	7.78E+02	5.50E-08	1.70E-07	2.19E+00	1.13E+00	2.19E+00	5.46E+01	2.49E+01
HIVEP2	2.54E+02	5.51E-08	1.70E-07	2.88E+00	1.53E+00	2.88E+00	1.93E+01	6.71E+00
LRRC32	7.28E+02	5.59E-08	1.72E-07	2.52E+00	1.33E+00	2.52E+00	5.34E+01	2.12E+01
KLHL7	2.87E+02	5.60E-08	1.72E-07	1.70E+00	7.63E-01	1.70E+00	1.86E+01	1.10E+01
XR_003030731.	1.60E+02	5.64E-08	1.73E-07	2.11E+00	1.08E+00	2.11E+00	1.10E+01	5.20E+00
CACNA2D1	3.32E+02	5.78E-08	1.77E-07	2.45E+00	1.29E+00	2.45E+00	2.43E+01	9.92E+00
GSTM2	1.50E+03	5.88E-08	1.80E-07	2.49E+00	1.32E+00	2.49E+00	1.10E+02	4.41E+01
DTNA	3.68E+02	5.89E-08	1.80E-07	2.20E+00	1.14E+00	2.20E+00	2.61E+01	1.18E+01
RCOR3	6.40E+02	5.92E-08	1.80E-07	1.78E+00	8.34E-01	1.78E+00	4.22E+01	2.37E+01
ITGA7	6.05E+02	5.97E-08	1.81E-07	2.63E+00	1.39E+00	2.63E+00	4.47E+01	1.70E+01
PI4K2B	2.35E+02	6.01E-08	1.82E-07	1.87E+00	9.02E-01	1.87E+00	1.58E+01	8.44E+00
CTDSPL	1.33E+03	6.20E-08	1.88E-07	1.60E+00	6.74E-01	1.60E+00	8.43E+01	5.28E+01
CH25H	2.59E+02	6.38E-08	1.93E-07	9.34E+00	3.22E+00	9.34E+00	2.35E+01	2.52E+00
STX6	1.03E+03	6.45E-08	1.95E-07	1.66E+00	7.30E-01	1.66E+00	6.65E+01	4.01E+01

FOXN2	1.79E+02	6.46E-08	1.95E-07	1.89E+00	9.20E-01	1.89E+00	1.20E+01	6.36E+00
ABCC9	2.67E+02	6.49E-08	1.95E-07	3.21E+00	1.68E+00	3.21E+00	2.08E+01	6.47E+00
ADAMTS3	4.31E+02	6.64E-08	1.99E-07	2.55E+00	1.35E+00	2.55E+00	3.18E+01	1.25E+01
LGI4	3.22E+02	6.68E-08	2.00E-07	2.89E+00	1.53E+00	2.89E+00	2.43E+01	8.41E+00
CCDC6	1.27E+03	6.71E-08	2.01E-07	1.50E+00	5.83E-01	1.50E+00	7.93E+01	5.30E+01
TMEM65	3.83E+02	6.81E-08	2.03E-07	1.79E+00	8.41E-01	1.79E+00	2.53E+01	1.41E+01
SEMA5A	3.18E+03	6.87E-08	2.05E-07	2.48E+00	1.31E+00	2.48E+00	2.33E+02	9.37E+01
FAM76A	1.34E+02	7.05E-08	2.10E-07	3.01E+00	1.59E+00	3.01E+00	1.02E+01	3.40E+00
RHOJ	3.96E+02	7.06E-08	2.10E-07	1.94E+00	9.56E-01	1.94E+00	2.68E+01	1.38E+01
CPE	2.54E+03	7.08E-08	2.10E-07	1.83E+00	8.75E-01	1.83E+00	1.69E+02	9.22E+01
AKAP13	3.21E+03	7.09E-08	2.10E-07	1.80E+00	8.45E-01	1.80E+00	2.13E+02	1.19E+02
PRKAA1	3.76E+02	7.12E-08	2.11E-07	1.90E+00	9.23E-01	1.90E+00	2.55E+01	1.34E+01
MN1	6.89E+02	7.24E-08	2.14E-07	3.02E+00	1.59E+00	3.02E+00	5.27E+01	1.75E+01
R_003029468.	2.41E+02	7.27E-08	2.14E-07	5.15E+00	2.37E+00	5.15E+00	2.04E+01	3.97E+00
CCDC93	3.67E+02	7.33E-08	2.16E-07	2.00E+00	1.00E+00	2.00E+00	2.51E+01	1.26E+01
XR_815171.3	1.99E+01	7.36E-08	2.16E-07	5.39E+00	2.43E+00	5.39E+00	1.69E+00	3.13E-01
CCNG1	4.04E+03	7.39E-08	2.17E-07	1.50E+00	5.89E-01	1.50E+00	2.52E+02	1.67E+02
USP33	6.06E+02	7.44E-08	2.18E-07	1.77E+00	8.26E-01	1.77E+00	4.01E+01	2.26E+01
LTBP1	1.34E+04	7.60E-08	2.22E-07	3.09E+00	1.63E+00	3.09E+00	1.03E+03	3.35E+02
CYYR1	6.72E+02	7.77E-08	2.27E-07	2.26E+00	1.17E+00	2.26E+00	4.80E+01	2.13E+01
IPO7	1.06E+03	7.79E-08	2.27E-07	2.00E+00	1.00E+00	2.00E+00	7.32E+01	3.65E+01
ADAM9	4.29E+02	7.80E-08	2.27E-07	2.44E+00	1.29E+00	2.44E+00	3.13E+01	1.28E+01
MAP4K5	6.94E+02	7.85E-08	2.28E-07	1.75E+00	8.04E-01	1.75E+00	4.57E+01	2.61E+01
AEBP1	4.42E+03	8.08E-08	2.34E-07	1.95E+00	9.65E-01	1.95E+00	3.01E+02	1.54E+02
CDH19	8.18E+00	8.09E-08	2.34E-07	4.74E+01	5.57E+00	4.74E+01	8.01E-01	1.69E-02
KANSL1L	4.91E+02	8.09E-08	2.34E-07	1.89E+00	9.15E-01	1.89E+00	3.32E+01	1.76E+01
FAM171B	7.23E+02	8.10E-08	2.34E-07	2.93E+00	1.55E+00	2.93E+00	5.51E+01	1.88E+01
HEPH	3.92E+02	8.19E-08	2.36E-07	2.98E+00	1.58E+00	2.98E+00	3.01E+01	1.01E+01
R_003029589.	3.04E+01	8.20E-08	2.36E-07	2.82E+00	1.50E+00	2.82E+00	2.29E+00	8.11E-01
CTNNB1	4.06E+03	8.32E-08	2.39E-07	1.46E+00	5.49E-01	1.46E+00	2.50E+02	1.71E+02
SLC26A10	3.32E+02	8.35E-08	2.40E-07	2.45E+00	1.29E+00	2.45E+00	2.42E+01	9.88E+00
TOGARAM1	3.95E+02	8.46E-08	2.42E-07	2.09E+00	1.06E+00	2.09E+00	2.75E+01	1.32E+01
TRAK1	1.13E+03	8.46E-08	2.42E-07	1.58E+00	6.63E-01	1.58E+00	7.18E+01	4.54E+01

NOTCH4	3.20E+02	8.49E-08	2.42E-07	2.03E+00	1.02E+00	2.03E+00	2.21E+01	1.09E+01
RGS6	5.78E+02	8.52E-08	2.43E-07	3.11E+00	1.64E+00	3.11E+00	4.46E+01	1.43E+01
ATP10D	5.38E+02	8.59E-08	2.44E-07	2.21E+00	1.14E+00	2.21E+00	3.82E+01	1.73E+01
KIAA0355	2.29E+03	8.63E-08	2.45E-07	1.68E+00	7.50E-01	1.68E+00	1.48E+02	8.79E+01
NR4A1	3.44E+03	8.66E-08	2.46E-07	1.02E+01	3.35E+00	1.02E+01	3.16E+02	3.09E+01
SLC46A2	5.58E+01	8.71E-08	2.47E-07	3.23E+00	1.69E+00	3.23E+00	4.34E+00	1.35E+00
LOC107131398	1.61E+02	8.81E-08	2.49E-07	3.26E+00	1.71E+00	3.26E+00	1.24E+01	3.81E+00
ARMC10	1.69E+03	8.90E-08	2.51E-07	1.35E+00	4.36E-01	1.35E+00	1.01E+02	7.49E+01
LOC101902475	1.38E+02	8.95E-08	2.52E-07	2.72E+00	1.44E+00	2.72E+00	1.03E+01	3.80E+00
PABPC5	8.95E+01	9.03E-08	2.54E-07	2.80E+00	1.48E+00	2.80E+00	6.76E+00	2.42E+00
XR_239392.4	5.93E+02	9.11E-08	2.56E-07	1.65E+00	7.20E-01	1.65E+00	3.83E+01	2.33E+01
CASP8	1.75E+02	9.22E-08	2.59E-07	2.31E+00	1.21E+00	2.31E+00	1.25E+01	5.42E+00
PLA2G12A	5.82E+02	9.32E-08	2.61E-07	1.41E+00	4.93E-01	1.41E+00	3.56E+01	2.53E+01
LRIG3	3.33E+02	9.40E-08	2.63E-07	2.41E+00	1.27E+00	2.41E+00	2.41E+01	9.96E+00
F8	1.71E+02	9.41E-08	2.63E-07	1.86E+00	8.94E-01	1.86E+00	1.15E+01	6.17E+00
FXYD5	3.53E+02	9.55E-08	2.66E-07	2.24E+00	1.17E+00	2.24E+00	2.50E+01	1.12E+01
MKL2	1.26E+03	9.56E-08	2.66E-07	1.96E+00	9.70E-01	1.96E+00	8.67E+01	4.43E+01
TOR1AIP2	1.03E+03	9.69E-08	2.69E-07	1.47E+00	5.51E-01	1.47E+00	6.35E+01	4.33E+01
PHKB	4.51E+02	9.82E-08	2.72E-07	1.65E+00	7.24E-01	1.65E+00	2.91E+01	1.76E+01
GLG1	8.57E+03	1.01E-07	2.80E-07	1.70E+00	7.62E-01	1.70E+00	5.57E+02	3.29E+02
JAML	3.77E+01	1.02E-07	2.81E-07	4.05E+00	2.02E+00	4.05E+00	3.06E+00	7.55E-01
GPC6	6.25E+01	1.03E-07	2.83E-07	9.94E+00	3.31E+00	9.94E+00	5.74E+00	5.77E-01
FRMD4B	5.20E+02	1.03E-07	2.84E-07	1.89E+00	9.15E-01	1.89E+00	3.51E+01	1.86E+01
DYSF	1.32E+03	1.05E-07	2.89E-07	2.50E+00	1.32E+00	2.50E+00	9.69E+01	3.87E+01
MMRN2	3.12E+02	1.06E-07	2.90E-07	3.23E+00	1.69E+00	3.23E+00	2.43E+01	7.52E+00
DRAM2	3.64E+02	1.06E-07	2.92E-07	1.77E+00	8.20E-01	1.77E+00	2.41E+01	1.36E+01
FAM13C	5.03E+02	1.07E-07	2.94E-07	1.86E+00	8.97E-01	1.86E+00	3.37E+01	1.81E+01
SGCB	1.09E+03	1.09E-07	2.99E-07	1.77E+00	8.20E-01	1.77E+00	7.18E+01	4.07E+01
PAPD5	3.15E+02	1.09E-07	2.99E-07	1.90E+00	9.29E-01	1.90E+00	2.13E+01	1.12E+01
RBPJ	1.86E+03	1.12E-07	3.06E-07	2.06E+00	1.04E+00	2.06E+00	1.29E+02	6.27E+01
ACVR1	7.58E+02	1.13E-07	3.08E-07	1.49E+00	5.77E-01	1.49E+00	4.73E+01	3.17E+01
MS4A2	4.97E+00	1.15E-07	3.13E-07	4.97E+01	5.64E+00	4.97E+01	4.89E-01	9.83E-03
SERPINB9	1.65E+02	1.20E-07	3.25E-07	2.33E+00	1.22E+00	2.33E+00	1.18E+01	5.05E+00

BNIP1	1.43E+02	1.21E-07	3.29E-07	1.73E+00	7.89E-01	1.73E+00	9.31E+00	5.39E+00
RNASE4	5.04E+02	1.24E-07	3.35E-07	3.20E+00	1.68E+00	3.20E+00	3.91E+01	1.22E+01
ACOX1	1.23E+03	1.24E-07	3.36E-07	1.63E+00	7.08E-01	1.63E+00	7.90E+01	4.83E+01
XR_003033573.1	6.98E+02	1.25E-07	3.37E-07	1.54E+00	6.23E-01	1.54E+00	4.38E+01	2.85E+01
ALPK1	2.31E+02	1.25E-07	3.38E-07	2.50E+00	1.32E+00	2.50E+00	1.69E+01	6.77E+00
RIN2	1.94E+03	1.27E-07	3.42E-07	1.99E+00	9.96E-01	1.99E+00	1.33E+02	6.69E+01
RNASE10	1.60E+02	1.27E-07	3.42E-07	2.48E+00	1.31E+00	2.48E+00	1.18E+01	4.75E+00
DAPK1	1.07E+03	1.29E-07	3.46E-07	2.33E+00	1.22E+00	2.33E+00	7.69E+01	3.30E+01
LBR	5.81E+02	1.30E-07	3.49E-07	1.59E+00	6.70E-01	1.59E+00	3.70E+01	2.33E+01
DCTN4	1.90E+03	1.32E-07	3.53E-07	1.54E+00	6.25E-01	1.54E+00	1.20E+02	7.77E+01
FAM168A	1.99E+03	1.33E-07	3.56E-07	1.66E+00	7.28E-01	1.66E+00	1.28E+02	7.75E+01
XR_003031013.1	2.61E+02	1.34E-07	3.56E-07	2.13E+00	1.09E+00	2.13E+00	1.82E+01	8.50E+00
PPFIBP1	1.18E+03	1.35E-07	3.59E-07	2.12E+00	1.08E+00	2.12E+00	8.30E+01	3.92E+01
TGFB1I1	1.59E+03	1.35E-07	3.59E-07	2.12E+00	1.08E+00	2.12E+00	1.11E+02	5.26E+01
XR_003032607.1	2.18E+01	1.36E-07	3.62E-07	4.17E+00	2.06E+00	4.17E+00	1.78E+00	4.27E-01
GAS6	2.35E+03	1.37E-07	3.63E-07	2.62E+00	1.39E+00	2.62E+00	1.75E+02	6.68E+01
NRIP1	1.13E+03	1.41E-07	3.73E-07	2.37E+00	1.25E+00	2.37E+00	8.16E+01	3.44E+01
XR_003035005.1	1.79E+01	1.44E-07	3.80E-07	1.00E+01	3.32E+00	1.00E+01	1.64E+00	1.64E-01
S100A4	5.33E+01	1.45E-07	3.83E-07	4.37E+00	2.13E+00	4.37E+00	4.41E+00	1.01E+00
ACBD3	1.19E+03	1.50E-07	3.96E-07	1.59E+00	6.65E-01	1.59E+00	7.55E+01	4.76E+01
TMC7	1.98E+01	1.52E-07	4.00E-07	3.25E+00	1.70E+00	3.25E+00	1.54E+00	4.73E-01
COL11A1	9.08E+02	1.53E-07	4.01E-07	2.63E+00	1.39E+00	2.63E+00	6.75E+01	2.57E+01
BCL6B	4.86E+02	1.54E-07	4.04E-07	1.71E+00	7.71E-01	1.71E+00	3.17E+01	1.86E+01
PDE4A	1.02E+03	1.54E-07	4.04E-07	1.90E+00	9.27E-01	1.90E+00	6.80E+01	3.58E+01
GPCPD1	1.67E+03	1.54E-07	4.04E-07	1.74E+00	7.99E-01	1.74E+00	1.10E+02	6.31E+01
ELP6	2.05E+02	1.56E-07	4.06E-07	2.34E+00	1.23E+00	2.34E+00	1.47E+01	6.30E+00
PGR	3.03E+02	1.56E-07	4.07E-07	2.84E+00	1.51E+00	2.84E+00	2.27E+01	8.00E+00
PLEKHH2	6.72E+02	1.56E-07	4.07E-07	2.44E+00	1.29E+00	2.44E+00	4.90E+01	2.01E+01
RNF168	4.97E+02	1.58E-07	4.12E-07	1.70E+00	7.63E-01	1.70E+00	3.24E+01	1.91E+01
PLOD2	1.01E+03	1.59E-07	4.14E-07	1.90E+00	9.28E-01	1.90E+00	6.85E+01	3.60E+01
LOC789091	2.02E+01	1.60E-07	4.16E-07	3.13E+00	1.65E+00	3.13E+00	1.56E+00	4.99E-01
TMPO	2.07E+03	1.61E-07	4.18E-07	1.50E+00	5.83E-01	1.50E+00	1.29E+02	8.62E+01
LMNA	4.01E+03	1.62E-07	4.19E-07	1.87E+00	9.04E-01	1.87E+00	2.70E+02	1.44E+02

DIXDC1	4.12E+02	1.63E-07	4.20E-07	1.95E+00	9.61E-01	1.95E+00	2.81E+01	1.44E+01
HSPG2	1.97E+04	1.63E-07	4.20E-07	1.83E+00	8.74E-01	1.83E+00	1.33E+03	7.23E+02
DOCK7	7.76E+02	1.64E-07	4.23E-07	1.67E+00	7.38E-01	1.67E+00	5.05E+01	3.03E+01
XR_809167.3	2.83E+02	1.66E-07	4.26E-07	2.63E+00	1.40E+00	2.63E+00	2.09E+01	7.94E+00
CCR8	4.80E+01	1.71E-07	4.38E-07	3.37E+00	1.75E+00	3.37E+00	3.75E+00	1.12E+00
EPC2	6.78E+02	1.71E-07	4.39E-07	1.74E+00	7.97E-01	1.74E+00	4.44E+01	2.56E+01
TCF21	3.02E+03	1.72E-07	4.40E-07	2.92E+00	1.55E+00	2.92E+00	2.29E+02	7.84E+01
LIG4	2.11E+02	1.73E-07	4.43E-07	2.02E+00	1.01E+00	2.02E+00	1.45E+01	7.19E+00
MED23	5.01E+02	1.75E-07	4.47E-07	1.94E+00	9.58E-01	1.94E+00	3.42E+01	1.76E+01
BMPR1A	1.04E+03	1.78E-07	4.53E-07	2.32E+00	1.21E+00	2.32E+00	7.45E+01	3.21E+01
LOC112448856	2.03E+01	1.82E-07	4.63E-07	8.01E+00	3.00E+00	8.01E+00	1.82E+00	2.27E-01
SETBP1	4.73E+02	1.84E-07	4.68E-07	3.20E+00	1.68E+00	3.20E+00	3.68E+01	1.15E+01
ZNF606	3.80E+02	1.87E-07	4.75E-07	2.46E+00	1.30E+00	2.46E+00	2.78E+01	1.13E+01
KCNMB1	4.13E+01	1.88E-07	4.76E-07	1.21E+01	3.59E+00	1.21E+01	3.84E+00	3.18E-01
TIPRL	5.31E+02	1.88E-07	4.76E-07	1.46E+00	5.49E-01	1.46E+00	3.27E+01	2.23E+01
LITAF	1.30E+03	1.92E-07	4.85E-07	1.77E+00	8.26E-01	1.77E+00	8.60E+01	4.85E+01
IPO8	7.40E+02	1.94E-07	4.89E-07	1.62E+00	6.99E-01	1.62E+00	4.76E+01	2.93E+01
EPC1	1.50E+03	1.94E-07	4.89E-07	1.44E+00	5.21E-01	1.44E+00	9.20E+01	6.41E+01
RCAN2	2.50E+02	2.01E-07	5.05E-07	3.52E+00	1.81E+00	3.52E+00	1.98E+01	5.63E+00
LIN7C	6.32E+02	2.02E-07	5.06E-07	1.75E+00	8.06E-01	1.75E+00	4.17E+01	2.38E+01
ANKRD13C	1.03E+02	2.04E-07	5.11E-07	1.99E+00	9.92E-01	1.99E+00	7.06E+00	3.55E+00
ADCY3	9.95E+02	2.04E-07	5.11E-07	2.02E+00	1.02E+00	2.02E+00	6.83E+01	3.37E+01
ZNF112	2.03E+02	2.07E-07	5.17E-07	2.12E+00	1.08E+00	2.12E+00	1.43E+01	6.73E+00
GLCE	9.28E+02	2.07E-07	5.17E-07	1.97E+00	9.77E-01	1.97E+00	6.35E+01	3.23E+01
RTL9	4.67E+01	2.09E-07	5.20E-07	2.43E+00	1.28E+00	2.43E+00	3.41E+00	1.40E+00
PDK1	1.03E+03	2.10E-07	5.24E-07	1.75E+00	8.05E-01	1.75E+00	6.78E+01	3.88E+01
R_003032993.	3.88E+01	2.13E-07	5.31E-07	3.01E+00	1.59E+00	3.01E+00	2.97E+00	9.84E-01
TRIM44	8.30E+02	2.14E-07	5.31E-07	1.72E+00	7.85E-01	1.72E+00	5.43E+01	3.15E+01
LOC101903572	1.07E+02	2.22E-07	5.51E-07	1.81E+01	4.18E+00	1.81E+01	1.02E+01	5.64E-01
SENP7	2.58E+02	2.25E-07	5.56E-07	2.13E+00	1.09E+00	2.13E+00	1.81E+01	8.51E+00
ANGPTL2	2.96E+03	2.25E-07	5.57E-07	2.26E+00	1.17E+00	2.26E+00	2.11E+02	9.35E+01
MMP23	1.47E+03	2.33E-07	5.76E-07	1.98E+00	9.89E-01	1.98E+00	1.01E+02	5.09E+01
ZNF383	1.08E+02	2.35E-07	5.81E-07	1.76E+00	8.20E-01	1.76E+00	7.11E+00	4.03E+00

FAM162B	2.67E+01	2.36E-07	5.82E-07	3.60E+00	1.85E+00	3.60E+00	2.11E+00	5.86E-01
CDH5	2.30E+03	2.38E-07	5.85E-07	1.65E+00	7.26E-01	1.65E+00	1.48E+02	8.95E+01
CDKN1B	9.59E+02	2.44E-07	5.99E-07	1.49E+00	5.79E-01	1.49E+00	5.95E+01	3.99E+01
PDE5A	4.76E+02	2.45E-07	6.01E-07	2.45E+00	1.30E+00	2.45E+00	3.46E+01	1.41E+01
R_001494670.	4.03E+01	2.46E-07	6.03E-07	2.88E+00	1.53E+00	2.88E+00	3.07E+00	1.06E+00
LRRFIP1	7.85E+02	2.46E-07	6.03E-07	1.98E+00	9.84E-01	1.98E+00	5.39E+01	2.72E+01
MTM1	1.23E+02	2.49E-07	6.08E-07	1.86E+00	8.92E-01	1.86E+00	8.17E+00	4.41E+00
TLR3	4.49E+02	2.50E-07	6.09E-07	2.11E+00	1.08E+00	2.11E+00	3.12E+01	1.48E+01
PLXNA4	1.11E+03	2.51E-07	6.11E-07	3.76E+00	1.91E+00	3.76E+00	8.96E+01	2.38E+01
CCR2	2.04E+01	2.51E-07	6.11E-07	6.01E+00	2.59E+00	6.01E+00	1.76E+00	2.92E-01
ERLIN1	9.15E+02	2.52E-07	6.12E-07	1.40E+00	4.83E-01	1.40E+00	5.54E+01	3.96E+01
MIGA1	1.65E+02	2.52E-07	6.12E-07	2.00E+00	1.00E+00	2.00E+00	1.14E+01	5.67E+00
OGA	1.74E+03	2.53E-07	6.14E-07	1.66E+00	7.28E-01	1.66E+00	1.13E+02	6.79E+01
MBLAC2	1.81E+02	2.55E-07	6.18E-07	1.70E+00	7.62E-01	1.70E+00	1.18E+01	6.96E+00
R_003032359.	1.10E+02	2.58E-07	6.24E-07	3.75E+00	1.91E+00	3.75E+00	8.74E+00	2.33E+00
R_003038036.	1.01E+02	2.58E-07	6.24E-07	3.40E+00	1.77E+00	3.40E+00	7.90E+00	2.32E+00
R_003033144.	1.09E+01	2.62E-07	6.32E-07	9.17E+00	3.20E+00	9.17E+00	9.86E-01	1.07E-01
LOC101902435	8.47E+01	2.64E-07	6.36E-07	2.43E+00	1.28E+00	2.43E+00	6.11E+00	2.52E+00
PALMD	1.47E+02	2.66E-07	6.40E-07	2.99E+00	1.58E+00	2.99E+00	1.13E+01	3.76E+00
TMED10	5.79E+03	2.67E-07	6.42E-07	1.52E+00	6.05E-01	1.52E+00	3.63E+02	2.39E+02
SH3BGRL2	5.93E+02	2.70E-07	6.48E-07	2.17E+00	1.12E+00	2.17E+00	4.15E+01	1.91E+01
R_003037059.	2.59E+01	2.71E-07	6.49E-07	4.06E+00	2.02E+00	4.06E+00	2.10E+00	5.17E-01
GULP1	9.03E+01	2.71E-07	6.49E-07	3.01E+00	1.59E+00	3.01E+00	6.93E+00	2.30E+00
MYCBP2	1.48E+03	2.72E-07	6.49E-07	2.17E+00	1.12E+00	2.17E+00	1.04E+02	4.81E+01
ATXN1	1.69E+02	2.73E-07	6.52E-07	3.01E+00	1.59E+00	3.01E+00	1.29E+01	4.30E+00
TCAF1	4.29E+03	2.76E-07	6.56E-07	2.00E+00	1.00E+00	2.00E+00	2.96E+02	1.48E+02
ZZZ3	9.18E+02	2.76E-07	6.56E-07	1.68E+00	7.45E-01	1.68E+00	5.96E+01	3.55E+01
LURAP1	3.60E+02	2.79E-07	6.63E-07	2.56E+00	1.35E+00	2.56E+00	2.65E+01	1.04E+01
CLMN	7.00E+02	2.80E-07	6.63E-07	2.23E+00	1.16E+00	2.23E+00	4.97E+01	2.23E+01
STAM	5.25E+02	2.83E-07	6.69E-07	1.56E+00	6.40E-01	1.56E+00	3.32E+01	2.13E+01
PUM1	1.87E+03	2.87E-07	6.79E-07	1.87E+00	9.05E-01	1.87E+00	1.26E+02	6.73E+01
PRICKLE2	7.88E+02	2.88E-07	6.79E-07	2.22E+00	1.15E+00	2.22E+00	5.59E+01	2.51E+01
RNF217	2.62E+02	2.89E-07	6.83E-07	1.62E+00	6.99E-01	1.62E+00	1.68E+01	1.04E+01

ZNF557	3.99E+02	2.91E-07	6.85E-07	1.69E+00	7.53E-01	1.69E+00	2.59E+01	1.54E+01
CLEC2B	5.11E+01	2.97E-07	6.98E-07	5.01E+00	2.33E+00	5.01E+00	4.30E+00	8.57E-01
AIDA	2.65E+02	2.97E-07	6.98E-07	1.78E+00	8.32E-01	1.78E+00	1.75E+01	9.83E+00
USP28	1.13E+03	2.98E-07	6.98E-07	1.46E+00	5.43E-01	1.46E+00	6.98E+01	4.79E+01
WISP2	2.12E+01	2.98E-07	6.99E-07	1.47E+01	3.88E+00	1.47E+01	1.99E+00	1.35E-01
CDC40	3.61E+02	2.99E-07	6.99E-07	1.57E+00	6.55E-01	1.57E+00	2.29E+01	1.46E+01
SHPK	6.18E+01	3.00E-07	7.00E-07	2.19E+00	1.13E+00	2.19E+00	4.34E+00	1.98E+00
PBX1	3.56E+03	3.02E-07	7.04E-07	2.30E+00	1.20E+00	2.30E+00	2.55E+02	1.11E+02
CAMKK2	1.46E+03	3.06E-07	7.12E-07	1.75E+00	8.05E-01	1.75E+00	9.54E+01	5.46E+01
RPS6KC1	6.20E+02	3.14E-07	7.32E-07	1.60E+00	6.75E-01	1.60E+00	3.97E+01	2.49E+01
DAAM2	1.46E+03	3.17E-07	7.37E-07	1.87E+00	9.01E-01	1.87E+00	9.85E+01	5.27E+01
OXR1	6.89E+02	3.18E-07	7.39E-07	1.89E+00	9.17E-01	1.89E+00	4.62E+01	2.45E+01
BICC1	8.29E+02	3.19E-07	7.39E-07	2.62E+00	1.39E+00	2.62E+00	6.15E+01	2.35E+01
PWWP2A	7.33E+02	3.19E-07	7.39E-07	1.48E+00	5.67E-01	1.48E+00	4.54E+01	3.07E+01
CACNB2	3.08E+02	3.28E-07	7.60E-07	2.03E+00	1.02E+00	2.03E+00	2.12E+01	1.04E+01
LIMA1	1.06E+03	3.31E-07	7.65E-07	1.83E+00	8.68E-01	1.83E+00	7.09E+01	3.88E+01
ADAM10	9.14E+02	3.33E-07	7.69E-07	1.89E+00	9.19E-01	1.89E+00	6.20E+01	3.28E+01
R_003031941.	1.44E+01	3.34E-07	7.69E-07	4.76E+00	2.25E+00	4.76E+00	1.20E+00	2.53E-01
DHX36	5.28E+02	3.34E-07	7.69E-07	1.87E+00	9.05E-01	1.87E+00	3.56E+01	1.90E+01
THSD4	9.20E+01	3.36E-07	7.72E-07	3.36E+01	5.07E+00	3.36E+01	8.93E+00	2.66E-01
ZFP3	9.91E+01	3.38E-07	7.76E-07	2.83E+00	1.50E+00	2.83E+00	7.47E+00	2.63E+00
RCN1	7.07E+03	3.40E-07	7.79E-07	1.60E+00	6.80E-01	1.60E+00	4.52E+02	2.82E+02
R_003030279.	1.03E+01	3.41E-07	7.80E-07	1.84E+01	4.20E+00	1.84E+01	9.81E-01	5.34E-02
DBX1	4.47E+00	3.41E-07	7.80E-07	5.68E+00	2.51E+00	5.68E+00	3.84E-01	6.75E-02
MOG	2.17E+02	3.42E-07	7.81E-07	3.30E+00	1.72E+00	3.30E+00	1.70E+01	5.14E+00
R_003031257.	6.03E+01	3.43E-07	7.83E-07	9.91E+00	3.31E+00	9.91E+00	5.53E+00	5.58E-01
LOC781318	3.71E+01	3.46E-07	7.88E-07	2.40E+00	1.26E+00	2.40E+00	2.67E+00	1.11E+00
ZNF550	2.21E+02	3.47E-07	7.89E-07	2.44E+00	1.29E+00	2.44E+00	1.61E+01	6.60E+00
PAFAH1B2	7.93E+02	3.53E-07	8.01E-07	1.73E+00	7.92E-01	1.73E+00	5.19E+01	3.00E+01
VWF	2.17E+03	3.53E-07	8.01E-07	4.15E+00	2.05E+00	4.15E+00	1.78E+02	4.28E+01
KLHL5	7.64E+02	3.56E-07	8.06E-07	1.53E+00	6.11E-01	1.53E+00	4.79E+01	3.14E+01
TRIT1	3.53E+02	3.57E-07	8.06E-07	1.61E+00	6.85E-01	1.61E+00	2.25E+01	1.40E+01
APLP2	1.05E+04	3.57E-07	8.06E-07	1.47E+00	5.54E-01	1.47E+00	6.49E+02	4.42E+02

ENG	4.41E+03	3.59E-07	8.11E-07	1.86E+00	8.99E-01	1.86E+00	2.96E+02	1.59E+02
TSPOAP1	1.08E+03	3.63E-07	8.19E-07	1.66E+00	7.34E-01	1.66E+00	6.93E+01	4.17E+01
ZNF175	4.50E+02	3.66E-07	8.24E-07	1.82E+00	8.66E-01	1.82E+00	3.01E+01	1.65E+01
GALNT7	5.22E+02	3.67E-07	8.26E-07	1.80E+00	8.51E-01	1.80E+00	3.48E+01	1.93E+01
SLC36A4	4.93E+02	3.69E-07	8.27E-07	1.92E+00	9.41E-01	1.92E+00	3.33E+01	1.74E+01
LTBP3	6.20E+03	3.69E-07	8.27E-07	1.91E+00	9.36E-01	1.91E+00	4.17E+02	2.18E+02
LOC781280	2.05E+02	3.70E-07	8.29E-07	1.85E+00	8.88E-01	1.85E+00	1.37E+01	7.39E+00
PTGDR	4.82E+01	3.70E-07	8.29E-07	4.99E+00	2.32E+00	4.99E+00	4.05E+00	8.11E-01
IL17B	4.11E+01	3.72E-07	8.31E-07	4.84E+00	2.28E+00	4.84E+00	3.47E+00	7.18E-01
MARK1	1.36E+03	3.75E-07	8.36E-07	1.61E+00	6.86E-01	1.61E+00	8.68E+01	5.40E+01
ID4	3.34E+02	3.88E-07	8.64E-07	2.78E+00	1.48E+00	2.78E+00	2.53E+01	9.10E+00
AEBP2	5.73E+02	3.92E-07	8.72E-07	1.64E+00	7.10E-01	1.64E+00	3.67E+01	2.24E+01
HECA	6.89E+02	3.92E-07	8.72E-07	1.70E+00	7.66E-01	1.70E+00	4.47E+01	2.63E+01
HECTD4	2.47E+03	3.93E-07	8.73E-07	1.75E+00	8.07E-01	1.75E+00	1.61E+02	9.21E+01
GPATCH2L	1.41E+03	3.94E-07	8.73E-07	1.68E+00	7.48E-01	1.68E+00	9.14E+01	5.44E+01
TNFSF10	6.16E+01	4.00E-07	8.87E-07	3.01E+01	4.91E+00	3.01E+01	5.97E+00	1.98E-01
ATP2B4	2.68E+03	4.01E-07	8.88E-07	1.93E+00	9.49E-01	1.93E+00	1.83E+02	9.46E+01
VANGL1	4.93E+02	4.11E-07	9.09E-07	1.70E+00	7.68E-01	1.70E+00	3.22E+01	1.89E+01
TRPM6	3.36E+01	4.15E-07	9.16E-07	2.35E+00	1.23E+00	2.35E+00	2.41E+00	1.03E+00
R_003029618.	2.53E+01	4.21E-07	9.29E-07	8.72E+00	3.12E+00	8.72E+00	2.29E+00	2.63E-01
RUNDC3B	2.43E+02	4.24E-07	9.33E-07	2.80E+00	1.49E+00	2.80E+00	1.82E+01	6.49E+00
R_003029474.	3.77E+01	4.30E-07	9.45E-07	6.01E+00	2.59E+00	6.01E+00	3.26E+00	5.42E-01
C19H17orf100	1.04E+02	4.39E-07	9.64E-07	1.99E+00	9.96E-01	1.99E+00	7.09E+00	3.55E+00
Mar-07	7.18E+02	4.41E-07	9.66E-07	1.95E+00	9.62E-01	1.95E+00	4.92E+01	2.52E+01
DNMBP	1.17E+03	4.45E-07	9.76E-07	2.49E+00	1.31E+00	2.49E+00	8.54E+01	3.44E+01
SPRED2	1.50E+03	4.47E-07	9.79E-07	1.63E+00	7.05E-01	1.63E+00	9.65E+01	5.92E+01
LOC510362	3.56E+02	4.49E-07	9.81E-07	1.73E+00	7.89E-01	1.73E+00	2.33E+01	1.35E+01
ZC3HAV1	1.71E+03	4.49E-07	9.81E-07	1.53E+00	6.16E-01	1.53E+00	1.08E+02	7.07E+01
R_003030148.	1.30E+02	4.50E-07	9.82E-07	2.09E+00	1.06E+00	2.09E+00	8.97E+00	4.30E+00
ADCY4	3.19E+02	4.51E-07	9.82E-07	2.03E+00	1.02E+00	2.03E+00	2.20E+01	1.08E+01
GLIPR1	1.52E+02	4.58E-07	9.97E-07	5.89E+00	2.56E+00	5.89E+00	1.31E+01	2.23E+00
CHST1	2.13E+03	4.68E-07	1.02E-06	2.41E+00	1.27E+00	2.41E+00	1.54E+02	6.38E+01
PTPRK	6.53E+02	4.78E-07	1.04E-06	1.98E+00	9.82E-01	1.98E+00	4.49E+01	2.27E+01

XR_003033993.1	1.23E+01	4.88E-07	1.06E-06	3.36E+00	1.75E+00	3.36E+00	9.58E-01	2.85E-01
TMEM181	1.22E+03	5.00E-07	1.08E-06	1.47E+00	5.56E-01	1.47E+00	7.52E+01	5.11E+01
ZNF608	5.28E+02	5.02E-07	1.08E-06	1.96E+00	9.69E-01	1.96E+00	3.62E+01	1.85E+01
PTGFRN	4.98E+03	5.02E-07	1.08E-06	1.78E+00	8.32E-01	1.78E+00	3.31E+02	1.86E+02
GNAI1	4.98E+02	5.07E-07	1.09E-06	1.72E+00	7.86E-01	1.72E+00	3.27E+01	1.90E+01
RNF150	7.81E+02	5.11E-07	1.10E-06	1.94E+00	9.58E-01	1.94E+00	5.32E+01	2.74E+01
C1R	3.76E+03	5.16E-07	1.11E-06	2.37E+00	1.25E+00	2.37E+00	2.70E+02	1.14E+02
KCTD12	1.60E+03	5.16E-07	1.11E-06	2.71E+00	1.44E+00	2.71E+00	1.19E+02	4.40E+01
DFFB	3.97E+02	5.20E-07	1.12E-06	1.57E+00	6.51E-01	1.57E+00	2.51E+01	1.60E+01
COL6A2	2.55E+04	5.23E-07	1.12E-06	2.38E+00	1.25E+00	2.38E+00	1.84E+03	7.70E+02
INVS	6.61E+02	5.24E-07	1.12E-06	1.46E+00	5.42E-01	1.46E+00	4.07E+01	2.79E+01
LOC782545	1.50E+01	5.24E-07	1.12E-06	1.55E+01	3.95E+00	1.55E+01	1.42E+00	9.18E-02
LOC534742	5.01E+02	5.26E-07	1.12E-06	1.74E+00	7.96E-01	1.74E+00	3.30E+01	1.90E+01
PHF8	6.38E+03	5.34E-07	1.14E-06	1.50E+00	5.86E-01	1.50E+00	3.97E+02	2.64E+02
ZFP37	1.93E+02	5.36E-07	1.14E-06	1.97E+00	9.76E-01	1.97E+00	1.32E+01	6.71E+00
AAED1	5.68E+02	5.37E-07	1.14E-06	1.55E+00	6.35E-01	1.55E+00	3.59E+01	2.31E+01
PTEN	1.37E+03	5.39E-07	1.15E-06	1.46E+00	5.42E-01	1.46E+00	8.41E+01	5.78E+01
CCDC50	1.22E+03	5.41E-07	1.15E-06	1.47E+00	5.52E-01	1.47E+00	7.57E+01	5.16E+01
C21H14orf28	1.37E+02	5.65E-07	1.20E-06	1.67E+00	7.36E-01	1.67E+00	8.83E+00	5.30E+00
FAM241A	6.20E+01	5.73E-07	1.21E-06	2.27E+00	1.18E+00	2.27E+00	4.39E+00	1.93E+00
XR_003034780.1	2.20E+02	5.73E-07	1.21E-06	3.00E+00	1.59E+00	3.00E+00	1.68E+01	5.60E+00
PPM1D	4.93E+02	5.83E-07	1.23E-06	1.44E+00	5.22E-01	1.44E+00	3.02E+01	2.10E+01
HECW2	1.31E+02	5.83E-07	1.23E-06	2.15E+00	1.10E+00	2.15E+00	9.21E+00	4.28E+00
ENDOD1	2.43E+02	5.85E-07	1.23E-06	2.32E+00	1.21E+00	2.32E+00	1.74E+01	7.51E+00
LOC782470	4.98E+02	5.87E-07	1.24E-06	1.74E+00	8.01E-01	1.74E+00	3.27E+01	1.88E+01
PCDH7	7.47E+02	5.94E-07	1.25E-06	2.66E+00	1.41E+00	2.66E+00	5.60E+01	2.10E+01
CANX	7.05E+03	6.04E-07	1.27E-06	1.44E+00	5.27E-01	1.44E+00	4.32E+02	3.00E+02
KPNA1	6.70E+02	6.06E-07	1.27E-06	1.80E+00	8.46E-01	1.80E+00	4.44E+01	2.47E+01
DZIP1	2.26E+03	6.08E-07	1.27E-06	1.89E+00	9.15E-01	1.89E+00	1.53E+02	8.10E+01
P2RX7	5.38E+01	6.18E-07	1.29E-06	2.59E+00	1.37E+00	2.59E+00	3.96E+00	1.53E+00
THADA	4.69E+02	6.20E-07	1.30E-06	1.57E+00	6.55E-01	1.57E+00	2.99E+01	1.90E+01
CSNK1B	6.36E+02	6.26E-07	1.31E-06	1.71E+00	7.77E-01	1.71E+00	4.18E+01	2.44E+01
SMARCA1	1.51E+03	6.36E-07	1.33E-06	1.69E+00	7.57E-01	1.69E+00	9.84E+01	5.83E+01

KLHL4	3.36E+01	6.38E-07	1.33E-06	2.82E+00	1.50E+00	2.82E+00	2.54E+00	9.01E-01
HEATR5A	3.10E+02	6.66E-07	1.38E-06	1.95E+00	9.63E-01	1.95E+00	2.12E+01	1.09E+01
R_003031718.	4.41E+01	6.68E-07	1.39E-06	4.36E+00	2.13E+00	4.36E+00	3.64E+00	8.35E-01
CEMIP2	2.65E+02	6.80E-07	1.41E-06	1.87E+00	9.04E-01	1.87E+00	1.79E+01	9.56E+00
DENND4C	5.66E+02	6.84E-07	1.42E-06	1.65E+00	7.25E-01	1.65E+00	3.65E+01	2.21E+01
TRIM56	1.37E+03	7.12E-07	1.48E-06	1.58E+00	6.63E-01	1.58E+00	8.72E+01	5.51E+01
PLN	8.58E+01	7.26E-07	1.50E-06	1.33E+01	3.73E+00	1.33E+01	8.02E+00	6.03E-01
RBMS2	2.17E+03	7.27E-07	1.50E-06	1.55E+00	6.33E-01	1.55E+00	1.37E+02	8.82E+01
TMEM173	2.24E+02	7.32E-07	1.51E-06	1.99E+00	9.90E-01	1.99E+00	1.53E+01	7.69E+00
SLC35D1	5.61E+01	7.33E-07	1.51E-06	1.98E+01	4.31E+00	1.98E+01	5.36E+00	2.70E-01
ZKSCAN5	1.04E+03	7.41E-07	1.52E-06	1.47E+00	5.58E-01	1.47E+00	6.43E+01	4.37E+01
SLITRK6	1.02E+02	7.42E-07	1.53E-06	2.59E+00	1.37E+00	2.59E+00	7.51E+00	2.90E+00
FYN	1.34E+03	7.48E-07	1.54E-06	1.48E+00	5.62E-01	1.48E+00	8.32E+01	5.64E+01
R_003031804.	6.51E+01	7.50E-07	1.54E-06	4.87E+00	2.28E+00	4.87E+00	5.46E+00	1.12E+00
PNPLA8	6.00E+02	7.55E-07	1.55E-06	1.52E+00	6.05E-01	1.52E+00	3.76E+01	2.48E+01
PIK3R1	2.43E+03	7.61E-07	1.56E-06	1.69E+00	7.60E-01	1.69E+00	1.59E+02	9.38E+01
ZNF770	2.31E+02	7.69E-07	1.57E-06	1.53E+00	6.16E-01	1.53E+00	1.45E+01	9.45E+00
EHBP1L1	1.75E+03	7.70E-07	1.57E-06	1.66E+00	7.34E-01	1.66E+00	1.13E+02	6.78E+01
DYRK2	7.62E+02	7.74E-07	1.58E-06	1.64E+00	7.14E-01	1.64E+00	4.92E+01	3.00E+01
R_003034585.	6.87E+01	7.86E-07	1.60E-06	5.22E+00	2.39E+00	5.22E+00	5.84E+00	1.12E+00
N4BP2L2	5.99E+02	8.15E-07	1.66E-06	1.54E+00	6.23E-01	1.54E+00	3.78E+01	2.45E+01
NCOA4	1.26E+03	8.20E-07	1.67E-06	1.39E+00	4.76E-01	1.39E+00	7.61E+01	5.47E+01
IGFBP6	4.19E+03	8.24E-07	1.67E-06	2.11E+00	1.08E+00	2.11E+00	2.92E+02	1.38E+02
CNST	2.05E+02	8.32E-07	1.69E-06	1.91E+00	9.33E-01	1.91E+00	1.40E+01	7.31E+00
RILP	1.44E+02	8.35E-07	1.69E-06	1.60E+00	6.77E-01	1.60E+00	9.09E+00	5.68E+00
R_003037447.	2.84E+00	8.39E-07	1.70E-06	1.39E+01	3.79E+00	1.39E+01	2.66E-01	1.92E-02
MSS51	1.94E+02	8.66E-07	1.75E-06	1.72E+00	7.86E-01	1.72E+00	1.27E+01	7.35E+00
UBQLN2	8.45E+02	8.73E-07	1.76E-06	1.55E+00	6.29E-01	1.55E+00	5.31E+01	3.44E+01
ASCC3	3.43E+02	8.74E-07	1.76E-06	1.57E+00	6.53E-01	1.57E+00	2.17E+01	1.38E+01
PTPRJ	5.41E+02	8.76E-07	1.76E-06	2.24E+00	1.16E+00	2.24E+00	3.86E+01	1.72E+01
ANXA5	6.18E+03	8.77E-07	1.76E-06	1.67E+00	7.43E-01	1.67E+00	4.00E+02	2.39E+02
LOC515551	1.05E+03	8.83E-07	1.77E-06	1.38E+00	4.68E-01	1.38E+00	6.35E+01	4.59E+01
SERTAD4	2.56E+02	8.91E-07	1.79E-06	3.68E+00	1.88E+00	3.68E+00	2.06E+01	5.61E+00

NEDD4	3.66E+02	8.93E-07	1.79E-06	1.65E+00	7.22E-01	1.65E+00	2.37E+01	1.44E+01
XR_003031806.	2.60E+02	8.94E-07	1.79E-06	3.15E+00	1.66E+00	3.15E+00	2.00E+01	6.35E+00
LOC514507	1.30E+02	8.96E-07	1.79E-06	2.00E+00	1.00E+00	2.00E+00	8.89E+00	4.44E+00
IBTK	8.41E+02	9.00E-07	1.80E-06	1.52E+00	6.04E-01	1.52E+00	5.26E+01	3.46E+01
POGZ	2.60E+03	9.05E-07	1.81E-06	1.55E+00	6.31E-01	1.55E+00	1.64E+02	1.06E+02
PICALM	2.71E+03	9.06E-07	1.81E-06	1.38E+00	4.60E-01	1.38E+00	1.63E+02	1.19E+02
PHACTR4	1.27E+03	9.09E-07	1.81E-06	1.61E+00	6.91E-01	1.61E+00	8.13E+01	5.04E+01
XR_003030700.	6.16E+01	9.11E-07	1.81E-06	4.96E+00	2.31E+00	4.96E+00	5.18E+00	1.04E+00
EVC2	8.23E+02	9.15E-07	1.82E-06	1.59E+00	6.68E-01	1.59E+00	5.20E+01	3.27E+01
ANG2	7.67E+01	9.22E-07	1.83E-06	2.56E+00	1.36E+00	2.56E+00	5.63E+00	2.20E+00
PODXL	2.79E+03	9.34E-07	1.85E-06	1.97E+00	9.76E-01	1.97E+00	1.92E+02	9.76E+01
MAGT1	9.09E+02	9.47E-07	1.88E-06	1.42E+00	5.08E-01	1.42E+00	5.54E+01	3.89E+01
SIK2	1.56E+03	9.59E-07	1.90E-06	1.71E+00	7.71E-01	1.71E+00	1.02E+02	5.96E+01
ZNF25	1.09E+03	9.65E-07	1.91E-06	1.97E+00	9.76E-01	1.97E+00	7.47E+01	3.80E+01
XR_239281.4	4.57E+02	9.72E-07	1.92E-06	1.99E+00	9.91E-01	1.99E+00	3.14E+01	1.58E+01
KIF13A	1.16E+03	9.90E-07	1.95E-06	1.80E+00	8.48E-01	1.80E+00	7.73E+01	4.30E+01
SNRNP48	9.14E+02	9.93E-07	1.96E-06	1.39E+00	4.70E-01	1.39E+00	5.51E+01	3.98E+01
PSMD10	6.60E+02	9.97E-07	1.96E-06	1.43E+00	5.13E-01	1.43E+00	4.04E+01	2.83E+01
XR_233909.4	3.21E+00	1.02E-06	2.00E-06	3.60E+00	1.85E+00	3.60E+00	2.52E-01	6.99E-02
LOC784108	4.09E+00	1.03E-06	2.02E-06	1.86E+01	4.22E+00	1.86E+01	3.89E-01	2.09E-02
PLAT	2.76E+03	1.05E-06	2.06E-06	2.48E+00	1.31E+00	2.48E+00	2.03E+02	8.17E+01
NUDT7	4.90E+02	1.06E-06	2.08E-06	1.54E+00	6.23E-01	1.54E+00	3.08E+01	2.00E+01
LOC107133024	1.95E+01	1.08E-06	2.11E-06	3.14E+00	1.65E+00	3.14E+00	1.52E+00	4.83E-01
PIGN	5.40E+02	1.08E-06	2.11E-06	1.49E+00	5.74E-01	1.49E+00	3.36E+01	2.26E+01
ZADH2	9.59E+02	1.11E-06	2.16E-06	1.75E+00	8.07E-01	1.75E+00	6.35E+01	3.63E+01
PCDHA13	4.44E+02	1.14E-06	2.23E-06	1.86E+00	8.93E-01	1.86E+00	2.98E+01	1.60E+01
ACE2	9.94E+01	1.14E-06	2.23E-06	1.40E+01	3.81E+00	1.40E+01	9.32E+00	6.66E-01
MXRA7	2.34E+03	1.14E-06	2.23E-06	1.61E+00	6.90E-01	1.61E+00	1.50E+02	9.28E+01
GXYLT1	6.34E+02	1.19E-06	2.31E-06	1.90E+00	9.26E-01	1.90E+00	4.29E+01	2.26E+01
WASL	1.18E+03	1.22E-06	2.37E-06	1.70E+00	7.67E-01	1.70E+00	7.69E+01	4.52E+01
XR_003031719.	6.88E+01	1.24E-06	2.41E-06	3.05E+00	1.61E+00	3.05E+00	5.29E+00	1.73E+00
ZNF317	4.49E+02	1.26E-06	2.44E-06	1.50E+00	5.85E-01	1.50E+00	2.80E+01	1.86E+01
FXYD6	4.45E+03	1.31E-06	2.53E-06	1.57E+00	6.55E-01	1.57E+00	2.84E+02	1.80E+02

SETD6	3.60E+02	1.31E-06	2.53E-06	1.49E+00	5.72E-01	1.49E+00	2.23E+01	1.50E+01
FAM13B	6.66E+02	1.32E-06	2.55E-06	1.70E+00	7.68E-01	1.70E+00	4.35E+01	2.55E+01
TMEM263	1.82E+03	1.32E-06	2.55E-06	1.52E+00	6.03E-01	1.52E+00	1.14E+02	7.48E+01
PLK2	9.17E+02	1.38E-06	2.65E-06	1.66E+00	7.31E-01	1.66E+00	5.93E+01	3.57E+01
JUNB	6.38E+02	1.38E-06	2.65E-06	2.50E+00	1.32E+00	2.50E+00	4.69E+01	1.87E+01
XR_003037466.1	1.69E+01	1.42E-06	2.73E-06	6.67E+00	2.74E+00	6.67E+00	1.47E+00	2.21E-01
LOC101908048	2.47E+01	1.43E-06	2.74E-06	3.27E+00	1.71E+00	3.27E+00	1.93E+00	5.91E-01
YES1	8.16E+02	1.45E-06	2.78E-06	1.90E+00	9.26E-01	1.90E+00	5.53E+01	2.91E+01
SCARA5	1.79E+03	1.49E-06	2.85E-06	2.60E+00	1.38E+00	2.60E+00	1.32E+02	5.09E+01
KCNN3	1.95E+02	1.53E-06	2.92E-06	2.25E+00	1.17E+00	2.25E+00	1.40E+01	6.22E+00
EDNRA	8.04E+02	1.54E-06	2.95E-06	2.00E+00	9.97E-01	2.00E+00	5.53E+01	2.77E+01
XR_814565.3	1.19E+03	1.55E-06	2.96E-06	1.56E+00	6.39E-01	1.56E+00	7.56E+01	4.85E+01
IRAK4	6.56E+02	1.55E-06	2.96E-06	1.43E+00	5.13E-01	1.43E+00	4.02E+01	2.82E+01
REM1	1.07E+03	1.60E-06	3.06E-06	1.86E+00	8.98E-01	1.86E+00	7.15E+01	3.84E+01
KLF2	6.52E+02	1.61E-06	3.07E-06	2.35E+00	1.23E+00	2.35E+00	4.70E+01	2.00E+01
CYFIP1	2.19E+03	1.61E-06	3.07E-06	1.46E+00	5.48E-01	1.46E+00	1.35E+02	9.23E+01
ITIH4	2.40E+02	1.62E-06	3.08E-06	3.44E+00	1.78E+00	3.44E+00	1.89E+01	5.48E+00
F5	2.46E+01	1.65E-06	3.13E-06	2.71E+00	1.44E+00	2.71E+00	1.84E+00	6.80E-01
TACC1	1.54E+03	1.65E-06	3.14E-06	1.82E+00	8.62E-01	1.82E+00	1.02E+02	5.63E+01
CCL16	5.74E+01	1.67E-06	3.17E-06	3.25E+00	1.70E+00	3.25E+00	4.47E+00	1.38E+00
MAP2K1	7.39E+02	1.70E-06	3.21E-06	1.33E+00	4.14E-01	1.33E+00	4.41E+01	3.31E+01
TLR4	8.24E+01	1.71E-06	3.23E-06	6.11E+00	2.61E+00	6.11E+00	7.15E+00	1.17E+00
XR_001501236.2	8.97E+00	1.71E-06	3.23E-06	4.10E+00	2.04E+00	4.10E+00	7.35E-01	1.79E-01
SLC25A16	1.80E+02	1.73E-06	3.27E-06	1.62E+00	6.95E-01	1.62E+00	1.15E+01	7.09E+00
XR_003032719.1	4.32E+01	1.74E-06	3.28E-06	3.70E+00	1.89E+00	3.70E+00	3.47E+00	9.39E-01
DUSP16	5.42E+02	1.74E-06	3.28E-06	1.93E+00	9.48E-01	1.93E+00	3.69E+01	1.92E+01
CSNK1G3	6.45E+02	1.76E-06	3.30E-06	1.61E+00	6.88E-01	1.61E+00	4.13E+01	2.57E+01
PLAGL1	1.73E+03	1.78E-06	3.34E-06	2.19E+00	1.13E+00	2.19E+00	1.21E+02	5.55E+01
XR_003035941.1	5.37E+01	1.80E-06	3.37E-06	2.81E+00	1.49E+00	2.81E+00	4.06E+00	1.45E+00
TMEM252	3.58E+01	1.82E-06	3.41E-06	3.33E+00	1.73E+00	3.33E+00	2.80E+00	8.41E-01
EDEM1	3.35E+01	1.82E-06	3.41E-06	2.48E+01	4.64E+00	2.48E+01	3.22E+00	1.30E-01
SYNDIG1	1.43E+02	1.82E-06	3.41E-06	6.88E+00	2.78E+00	6.88E+00	1.26E+01	1.84E+00
CD164	3.26E+03	1.87E-06	3.50E-06	1.47E+00	5.51E-01	1.47E+00	2.01E+02	1.37E+02

XR_236232.4	2.11E+02	1.89E-06	3.53E-06	2.20E+00	1.14E+00	2.20E+00	1.49E+01	6.77E+00
COL6A1	3.58E+04	1.92E-06	3.58E-06	2.16E+00	1.11E+00	2.16E+00	2.51E+03	1.16E+03
XR_003029913.	3.00E+01	1.95E-06	3.63E-06	2.65E+00	1.41E+00	2.65E+00	2.23E+00	8.40E-01
XR_003031554.	4.12E+01	1.96E-06	3.64E-06	3.90E+00	1.96E+00	3.90E+00	3.35E+00	8.59E-01
ZSWIM6	4.54E+02	1.98E-06	3.68E-06	1.87E+00	9.04E-01	1.87E+00	3.05E+01	1.63E+01
KCNJ8	3.33E+02	1.99E-06	3.69E-06	2.79E+00	1.48E+00	2.79E+00	2.50E+01	8.97E+00
POT1	2.51E+02	1.99E-06	3.69E-06	1.58E+00	6.61E-01	1.58E+00	1.60E+01	1.01E+01
CD300LG	8.07E+02	1.99E-06	3.69E-06	2.75E+00	1.46E+00	2.75E+00	6.05E+01	2.20E+01
BICD2	1.42E+03	2.01E-06	3.72E-06	1.45E+00	5.38E-01	1.45E+00	8.72E+01	6.01E+01
PMVK	5.80E+02	2.01E-06	3.72E-06	1.73E+00	7.94E-01	1.73E+00	3.79E+01	2.19E+01
SEL1L3	4.56E+02	2.04E-06	3.76E-06	2.41E+00	1.27E+00	2.41E+00	3.31E+01	1.37E+01
CLK4	1.10E+03	2.04E-06	3.76E-06	1.46E+00	5.48E-01	1.46E+00	6.81E+01	4.66E+01
EIF4G2	1.22E+04	2.06E-06	3.81E-06	1.48E+00	5.64E-01	1.48E+00	7.55E+02	5.11E+02
XR_003029437.	1.80E+01	2.12E-06	3.91E-06	3.98E+00	1.99E+00	3.98E+00	1.46E+00	3.67E-01
XR_001494399.	2.43E+01	2.14E-06	3.93E-06	3.16E+00	1.66E+00	3.16E+00	1.88E+00	5.94E-01
XR_003034233.	4.53E+03	2.15E-06	3.95E-06	1.93E+00	9.48E-01	1.93E+00	3.08E+02	1.60E+02
XR_003032538.	4.93E+01	2.15E-06	3.96E-06	7.95E+00	2.99E+00	7.95E+00	4.44E+00	5.58E-01
SYT4	6.80E+02	2.16E-06	3.96E-06	2.74E+00	1.45E+00	2.74E+00	5.12E+01	1.87E+01
SLC9B2	1.23E+02	2.18E-06	3.99E-06	1.98E+00	9.89E-01	1.98E+00	8.48E+00	4.27E+00
F2R	5.86E+02	2.19E-06	4.01E-06	1.86E+00	8.99E-01	1.86E+00	3.92E+01	2.10E+01
LOC505918	2.55E+02	2.21E-06	4.03E-06	1.61E+00	6.83E-01	1.61E+00	1.63E+01	1.02E+01
TMLHE	9.89E+01	2.21E-06	4.03E-06	1.54E+00	6.19E-01	1.54E+00	6.22E+00	4.05E+00
KIAA1211	7.57E+01	2.23E-06	4.06E-06	3.41E+00	1.77E+00	3.41E+00	6.00E+00	1.76E+00
CCNI	6.73E+03	2.25E-06	4.10E-06	1.39E+00	4.72E-01	1.39E+00	4.07E+02	2.93E+02
LCLAT1	3.73E+02	2.25E-06	4.10E-06	1.62E+00	6.96E-01	1.62E+00	2.40E+01	1.48E+01
QTRT2	2.22E+02	2.29E-06	4.17E-06	1.49E+00	5.79E-01	1.49E+00	1.38E+01	9.27E+00
DCUN1D1	8.19E+02	2.31E-06	4.21E-06	1.52E+00	6.07E-01	1.52E+00	5.14E+01	3.37E+01
UGDH	7.56E+02	2.32E-06	4.21E-06	1.43E+00	5.20E-01	1.43E+00	4.64E+01	3.24E+01
TMEM135	2.15E+02	2.35E-06	4.27E-06	1.73E+00	7.91E-01	1.73E+00	1.42E+01	8.20E+00
TNS1	9.08E+03	2.37E-06	4.30E-06	1.63E+00	7.07E-01	1.63E+00	5.81E+02	3.56E+02
FAM20B	1.10E+03	2.40E-06	4.33E-06	1.66E+00	7.35E-01	1.66E+00	7.09E+01	4.26E+01
XR_003033202.	7.87E+00	2.40E-06	4.34E-06	2.48E+01	4.63E+00	2.48E+01	7.59E-01	3.06E-02
LOC112445980	3.61E+01	2.42E-06	4.37E-06	2.70E+00	1.43E+00	2.70E+00	2.68E+00	9.92E-01

LOC112445906	9.81E+00	2.45E-06	4.43E-06	2.51E+03	1.13E+01	2.51E+03	9.81E-01	3.90E-04
TBC1D23	1.16E+03	2.46E-06	4.43E-06	1.42E+00	5.02E-01	1.42E+00	7.04E+01	4.97E+01
CARNMT1	1.90E+02	2.52E-06	4.53E-06	1.53E+00	6.14E-01	1.53E+00	1.19E+01	7.78E+00
KCTD6	3.86E+02	2.54E-06	4.56E-06	1.46E+00	5.44E-01	1.46E+00	2.38E+01	1.63E+01
LOC107132952	1.71E+01	2.59E-06	4.66E-06	3.23E+00	1.69E+00	3.23E+00	1.32E+00	4.08E-01
CSRP1	3.97E+03	2.60E-06	4.66E-06	1.74E+00	7.98E-01	1.74E+00	2.61E+02	1.50E+02
ST8SIA4	5.30E+01	2.60E-06	4.66E-06	5.30E+00	2.41E+00	5.30E+00	4.52E+00	8.53E-01
RYBP	1.30E+03	2.66E-06	4.76E-06	1.72E+00	7.82E-01	1.72E+00	8.51E+01	4.95E+01
PELI1	4.56E+02	2.71E-06	4.85E-06	1.44E+00	5.29E-01	1.44E+00	2.79E+01	1.94E+01
GOLT1B	1.49E+02	2.71E-06	4.85E-06	1.71E+00	7.70E-01	1.71E+00	9.64E+00	5.65E+00
SLC12A4	2.49E+03	2.77E-06	4.95E-06	1.43E+00	5.20E-01	1.43E+00	1.52E+02	1.06E+02
COL5A1	2.72E+04	2.80E-06	5.00E-06	1.90E+00	9.29E-01	1.90E+00	1.83E+03	9.63E+02
EHD2	3.92E+03	2.81E-06	5.01E-06	1.88E+00	9.08E-01	1.88E+00	2.65E+02	1.41E+02
JADE2	1.85E+03	2.87E-06	5.12E-06	1.76E+00	8.15E-01	1.76E+00	1.22E+02	6.91E+01
R_003029914.	1.10E+02	2.89E-06	5.14E-06	2.37E+00	1.24E+00	2.37E+00	7.90E+00	3.34E+00
APOL3	4.38E+02	2.90E-06	5.15E-06	1.72E+00	7.85E-01	1.72E+00	2.86E+01	1.66E+01
SLC39A9	8.37E+02	2.90E-06	5.15E-06	1.59E+00	6.68E-01	1.59E+00	5.33E+01	3.36E+01
LYL1	1.77E+03	2.90E-06	5.15E-06	1.75E+00	8.09E-01	1.75E+00	1.16E+02	6.60E+01
PCNX4	4.84E+02	2.93E-06	5.19E-06	1.78E+00	8.29E-01	1.78E+00	3.21E+01	1.81E+01
R_003036865.	3.40E+00	2.96E-06	5.24E-06	6.32E+00	2.66E+00	6.32E+00	2.94E-01	4.65E-02
MYADM	2.57E+03	2.98E-06	5.27E-06	2.04E+00	1.03E+00	2.04E+00	1.78E+02	8.73E+01
ITPR2	3.52E+02	2.99E-06	5.28E-06	2.01E+00	1.01E+00	2.01E+00	2.44E+01	1.21E+01
R_003030645.	5.48E+02	3.01E-06	5.32E-06	1.88E+00	9.14E-01	1.88E+00	3.66E+01	1.94E+01
BMP5	2.37E+01	3.02E-06	5.33E-06	2.97E+00	1.57E+00	2.97E+00	1.80E+00	6.06E-01
USP8	1.49E+03	3.13E-06	5.52E-06	1.48E+00	5.70E-01	1.48E+00	9.30E+01	6.27E+01
LYSMD3	2.54E+02	3.14E-06	5.52E-06	1.72E+00	7.84E-01	1.72E+00	1.66E+01	9.66E+00
ADAMTS9	7.29E+02	3.16E-06	5.56E-06	2.11E+00	1.08E+00	2.11E+00	5.12E+01	2.42E+01
MSH3	5.89E+02	3.18E-06	5.58E-06	1.41E+00	4.96E-01	1.41E+00	3.59E+01	2.55E+01
BIVM	7.35E+02	3.21E-06	5.63E-06	1.42E+00	5.09E-01	1.42E+00	4.49E+01	3.16E+01
LOC112445030	6.06E+02	3.23E-06	5.66E-06	1.98E+00	9.85E-01	1.98E+00	4.13E+01	2.09E+01
PHACTR2	4.99E+02	3.24E-06	5.67E-06	1.68E+00	7.49E-01	1.68E+00	3.24E+01	1.93E+01
MR1	6.77E+01	3.29E-06	5.76E-06	2.24E+00	1.16E+00	2.24E+00	4.76E+00	2.12E+00
ARL4C	1.88E+02	3.30E-06	5.77E-06	1.65E+00	7.19E-01	1.65E+00	1.22E+01	7.39E+00

STXBP4	4.70E+02	3.31E-06	5.79E-06	1.68E+00	7.50E-01	1.68E+00	3.06E+01	1.82E+01
MEIS1	1.24E+03	3.38E-06	5.89E-06	2.11E+00	1.08E+00	2.11E+00	8.70E+01	4.13E+01
CTNNA3	2.79E+01	3.43E-06	5.97E-06	2.79E+00	1.48E+00	2.79E+00	2.09E+00	7.51E-01
LOC787074	3.52E+02	3.44E-06	6.00E-06	1.85E+00	8.91E-01	1.85E+00	2.37E+01	1.28E+01
FAM19A3	1.48E+02	3.45E-06	6.00E-06	2.89E+00	1.53E+00	2.89E+00	1.12E+01	3.86E+00
RGS9	2.40E+02	3.46E-06	6.02E-06	2.37E+00	1.24E+00	2.37E+00	1.72E+01	7.28E+00
ENAH	2.13E+03	3.47E-06	6.03E-06	1.92E+00	9.43E-01	1.92E+00	1.45E+02	7.53E+01
STAU2	8.75E+02	3.53E-06	6.13E-06	1.39E+00	4.76E-01	1.39E+00	5.30E+01	3.81E+01
XR_816906.3	3.55E+02	3.55E-06	6.15E-06	3.72E+00	1.89E+00	3.72E+00	2.85E+01	7.67E+00
R_003037047.	1.55E+02	3.56E-06	6.15E-06	4.48E+00	2.16E+00	4.48E+00	1.29E+01	2.88E+00
NOL9	1.58E+01	3.62E-06	6.26E-06	9.24E+00	3.21E+00	9.24E+00	1.43E+00	1.55E-01
XR_237771.4	9.95E+01	3.64E-06	6.28E-06	4.35E+00	2.12E+00	4.35E+00	8.21E+00	1.89E+00
FSD1L	2.23E+02	3.72E-06	6.42E-06	1.56E+00	6.40E-01	1.56E+00	1.41E+01	9.02E+00
TIMP2	9.81E+03	3.73E-06	6.43E-06	1.66E+00	7.30E-01	1.66E+00	6.34E+02	3.82E+02
TINAGL1	8.64E+02	3.75E-06	6.46E-06	2.15E+00	1.10E+00	2.15E+00	6.11E+01	2.84E+01
METTL24	2.53E+01	3.78E-06	6.51E-06	2.70E+00	1.43E+00	2.70E+00	1.88E+00	6.96E-01
R_001501953.	2.70E+01	3.82E-06	6.56E-06	5.06E+00	2.34E+00	5.06E+00	2.30E+00	4.54E-01
AFG1L	4.26E+01	3.82E-06	6.56E-06	2.03E+00	1.02E+00	2.03E+00	2.95E+00	1.45E+00
PAN3	1.28E+03	3.89E-06	6.67E-06	1.66E+00	7.31E-01	1.66E+00	8.26E+01	4.98E+01
R_003035736.	3.88E+01	3.90E-06	6.69E-06	4.71E+00	2.24E+00	4.71E+00	3.25E+00	6.89E-01
RBM18	2.44E+02	3.93E-06	6.73E-06	1.45E+00	5.39E-01	1.45E+00	1.50E+01	1.03E+01
MXRA8	5.00E+03	3.95E-06	6.77E-06	1.97E+00	9.76E-01	1.97E+00	3.42E+02	1.74E+02
ARHGAP17	1.36E+03	3.99E-06	6.82E-06	1.39E+00	4.73E-01	1.39E+00	8.27E+01	5.96E+01
MTDH	1.78E+03	4.00E-06	6.82E-06	1.40E+00	4.88E-01	1.40E+00	1.08E+02	7.72E+01
AGO4	5.52E+02	4.04E-06	6.89E-06	1.48E+00	5.63E-01	1.48E+00	3.42E+01	2.32E+01
MGC139164	1.38E+02	4.04E-06	6.89E-06	1.94E+00	9.60E-01	1.94E+00	9.41E+00	4.84E+00
ZNF8	7.06E+02	4.07E-06	6.93E-06	1.96E+00	9.73E-01	1.96E+00	4.80E+01	2.45E+01
PRPF38B	1.46E+03	4.14E-06	7.04E-06	1.30E+00	3.80E-01	1.30E+00	8.64E+01	6.64E+01
PEG3	1.29E+04	4.20E-06	7.13E-06	1.92E+00	9.44E-01	1.92E+00	8.80E+02	4.57E+02
AKAP12	4.91E+03	4.20E-06	7.13E-06	2.75E+00	1.46E+00	2.75E+00	3.69E+02	1.34E+02
ATP6V1A	6.54E+02	4.22E-06	7.15E-06	1.53E+00	6.13E-01	1.53E+00	4.11E+01	2.69E+01
OTUD6B	5.02E+02	4.22E-06	7.15E-06	1.38E+00	4.60E-01	1.38E+00	3.03E+01	2.20E+01
KANK2	5.02E+03	4.23E-06	7.17E-06	1.55E+00	6.34E-01	1.55E+00	3.16E+02	2.04E+02

KR_003037543.	5.97E+01	4.24E-06	7.18E-06	2.49E+00	1.31E+00	2.49E+00	4.33E+00	1.74E+00
EPB41L1	8.27E+03	4.29E-06	7.24E-06	1.55E+00	6.34E-01	1.55E+00	5.23E+02	3.37E+02
DCN	2.27E+04	4.31E-06	7.27E-06	1.70E+00	7.68E-01	1.70E+00	1.48E+03	8.70E+02
LOC615521	1.06E+01	4.31E-06	7.27E-06	3.01E+00	1.59E+00	3.01E+00	8.10E-01	2.69E-01
CD93	1.80E+03	4.32E-06	7.27E-06	1.82E+00	8.65E-01	1.82E+00	1.20E+02	6.59E+01
Sep-11	2.19E+03	4.44E-06	7.48E-06	1.62E+00	6.98E-01	1.62E+00	1.41E+02	8.70E+01
LOC616063	9.56E+02	4.46E-06	7.50E-06	2.48E+00	1.31E+00	2.48E+00	6.96E+01	2.80E+01
TM9SF3	2.59E+03	4.50E-06	7.56E-06	1.35E+00	4.29E-01	1.35E+00	1.55E+02	1.15E+02
KR_001501425.	1.02E+01	4.52E-06	7.59E-06	3.31E+00	1.73E+00	3.31E+00	7.94E-01	2.40E-01
HLF	4.81E+02	4.53E-06	7.59E-06	1.94E+00	9.56E-01	1.94E+00	3.28E+01	1.69E+01
GADD45A	6.88E+02	4.54E-06	7.61E-06	2.36E+00	1.24E+00	2.36E+00	4.97E+01	2.11E+01
KR_003030701.	1.63E+01	4.58E-06	7.67E-06	7.58E+00	2.92E+00	7.58E+00	1.46E+00	1.92E-01
LOC511847	1.69E+02	4.70E-06	7.86E-06	1.64E+00	7.12E-01	1.64E+00	1.09E+01	6.63E+00
MAST2	4.03E+03	4.72E-06	7.88E-06	1.66E+00	7.30E-01	1.66E+00	2.61E+02	1.57E+02
TRPS1	5.40E+02	4.89E-06	8.16E-06	1.62E+00	6.94E-01	1.62E+00	3.47E+01	2.15E+01
PPARA	8.95E+02	4.97E-06	8.29E-06	1.82E+00	8.64E-01	1.82E+00	6.02E+01	3.31E+01
CNN1	5.64E+02	5.02E-06	8.36E-06	5.37E+00	2.43E+00	5.37E+00	4.82E+01	8.96E+00
KR_001500650.	2.14E+02	5.05E-06	8.41E-06	5.21E+00	2.38E+00	5.21E+00	1.82E+01	3.49E+00
LOC104973175	4.22E+01	5.07E-06	8.43E-06	2.09E+00	1.06E+00	2.09E+00	2.93E+00	1.40E+00
KR_003037449.	4.29E+00	5.10E-06	8.47E-06	9.84E+00	3.30E+00	9.84E+00	3.91E-01	3.98E-02
RORA	3.13E+02	5.28E-06	8.76E-06	1.68E+00	7.48E-01	1.68E+00	2.04E+01	1.22E+01
PIP4K2A	7.96E+02	5.33E-06	8.84E-06	1.39E+00	4.73E-01	1.39E+00	4.83E+01	3.48E+01
HES7	1.64E+01	5.64E-06	9.34E-06	3.09E+00	1.63E+00	3.09E+00	1.26E+00	4.08E-01
YAP1	2.54E+03	5.72E-06	9.47E-06	1.64E+00	7.11E-01	1.64E+00	1.64E+02	1.00E+02
GALNT15	9.89E+01	5.95E-06	9.84E-06	6.43E+00	2.69E+00	6.43E+00	8.63E+00	1.34E+00
KR_003032576.	2.83E+01	5.95E-06	9.84E-06	2.57E+00	1.36E+00	2.57E+00	2.09E+00	8.11E-01
CLN5	1.56E+02	5.97E-06	9.86E-06	1.64E+00	7.18E-01	1.64E+00	1.01E+01	6.12E+00
CPT1A	9.22E+02	6.08E-06	1.00E-05	1.74E+00	7.98E-01	1.74E+00	6.07E+01	3.49E+01
KR_003032722.	5.61E+00	6.14E-06	1.01E-05	6.26E+00	2.65E+00	6.26E+00	4.90E-01	7.83E-02
LOC511531	1.32E+02	6.14E-06	1.01E-05	2.18E+00	1.13E+00	2.18E+00	9.20E+00	4.22E+00
DEPTOR	6.22E+02	6.17E-06	1.01E-05	1.71E+00	7.71E-01	1.71E+00	4.08E+01	2.39E+01
ARHGEF38	1.91E+01	6.17E-06	1.01E-05	4.86E+00	2.28E+00	4.86E+00	1.61E+00	3.30E-01
KR_003035193.	3.63E+01	6.28E-06	1.03E-05	3.12E+00	1.64E+00	3.12E+00	2.78E+00	8.93E-01

TMEM260	7.56E+02	6.33E-06	1.04E-05	1.54E+00	6.19E-01	1.54E+00	4.76E+01	3.10E+01
SNX33	3.13E+02	6.36E-06	1.04E-05	1.62E+00	6.99E-01	1.62E+00	2.01E+01	1.24E+01
TMEM63A	1.94E+03	6.40E-06	1.05E-05	1.54E+00	6.26E-01	1.54E+00	1.22E+02	7.92E+01
GATAD1	9.97E+01	6.41E-06	1.05E-05	2.51E+00	1.33E+00	2.51E+00	7.29E+00	2.90E+00
XR_234534.4	1.84E+00	6.45E-06	1.05E-05	1.14E+01	3.51E+00	1.14E+01	1.69E-01	1.48E-02
NCEH1	1.93E+02	6.45E-06	1.05E-05	1.85E+00	8.85E-01	1.85E+00	1.29E+01	7.00E+00
PSME4	7.73E+02	6.63E-06	1.08E-05	1.49E+00	5.75E-01	1.49E+00	4.81E+01	3.23E+01
R_003037458.	1.15E+01	6.63E-06	1.08E-05	4.99E+00	2.32E+00	4.99E+00	9.68E-01	1.94E-01
LIX1L	1.36E+03	6.65E-06	1.08E-05	1.59E+00	6.68E-01	1.59E+00	8.65E+01	5.44E+01
RBMS1	8.44E+02	6.74E-06	1.10E-05	1.47E+00	5.52E-01	1.47E+00	5.26E+01	3.59E+01
KDR	2.50E+03	6.79E-06	1.10E-05	1.83E+00	8.73E-01	1.83E+00	1.69E+02	9.21E+01
R_003034845.	3.56E+01	6.80E-06	1.10E-05	2.47E+00	1.30E+00	2.47E+00	2.58E+00	1.04E+00
TBC1D16	1.73E+03	7.01E-06	1.14E-05	1.43E+00	5.17E-01	1.43E+00	1.06E+02	7.42E+01
CHAD	1.70E+02	7.04E-06	1.14E-05	2.36E+00	1.24E+00	2.36E+00	1.22E+01	5.16E+00
CHST3	2.00E+03	7.09E-06	1.15E-05	1.91E+00	9.37E-01	1.91E+00	1.36E+02	7.09E+01
TOPORS	8.01E+02	7.16E-06	1.16E-05	1.35E+00	4.28E-01	1.35E+00	4.77E+01	3.55E+01
LOC112449111	1.56E+02	7.18E-06	1.16E-05	2.54E+00	1.34E+00	2.54E+00	1.14E+01	4.49E+00
SLIT2	3.26E+02	7.20E-06	1.16E-05	2.69E+00	1.43E+00	2.69E+00	2.45E+01	9.10E+00
ELMSAN1	1.48E+03	7.21E-06	1.16E-05	1.63E+00	7.04E-01	1.63E+00	9.49E+01	5.83E+01
HOMER1	1.94E+02	7.22E-06	1.16E-05	1.84E+00	8.78E-01	1.84E+00	1.29E+01	7.04E+00
EOGT	3.12E+02	7.23E-06	1.16E-05	1.75E+00	8.08E-01	1.75E+00	2.05E+01	1.17E+01
RASAL2	3.67E+02	7.28E-06	1.17E-05	1.70E+00	7.67E-01	1.70E+00	2.39E+01	1.40E+01
PUS10	4.34E+02	7.51E-06	1.21E-05	1.33E+00	4.11E-01	1.33E+00	2.58E+01	1.94E+01
LOC112449284	5.79E+01	7.55E-06	1.21E-05	1.85E+00	8.89E-01	1.85E+00	3.89E+00	2.10E+00
ABCE1	8.17E+02	7.60E-06	1.22E-05	1.34E+00	4.19E-01	1.34E+00	4.88E+01	3.65E+01
R_003033508.	1.17E+01	7.61E-06	1.22E-05	2.82E+00	1.49E+00	2.82E+00	8.80E-01	3.12E-01
DBP	5.77E+02	7.63E-06	1.22E-05	1.56E+00	6.41E-01	1.56E+00	3.66E+01	2.34E+01
RXFP1	5.26E+01	7.78E-06	1.24E-05	1.07E+02	6.73E+00	1.07E+02	5.21E+00	4.90E-02
ZNF367	2.24E+02	7.80E-06	1.25E-05	1.49E+00	5.77E-01	1.49E+00	1.38E+01	9.28E+00
EHHADH	1.84E+02	7.88E-06	1.26E-05	1.62E+00	6.94E-01	1.62E+00	1.18E+01	7.27E+00
ZBTB4	2.82E+03	7.88E-06	1.26E-05	1.60E+00	6.80E-01	1.60E+00	1.79E+02	1.12E+02
R_003031377.	6.68E+01	7.89E-06	1.26E-05	2.41E+00	1.27E+00	2.41E+00	4.87E+00	2.02E+00
R_003037720.	1.95E+01	8.24E-06	1.31E-05	1.80E+00	8.47E-01	1.80E+00	1.29E+00	7.18E-01

PRDM16	8.71E+01	8.74E-06	1.39E-05	2.25E+00	1.17E+00	2.25E+00	6.18E+00	2.75E+00
XR_003034366.1	8.92E+00	8.80E-06	1.40E-05	6.72E+00	2.75E+00	6.72E+00	7.80E-01	1.16E-01
ZFP62	4.51E+02	8.81E-06	1.40E-05	1.57E+00	6.54E-01	1.57E+00	2.86E+01	1.82E+01
NUCB1	9.48E+03	8.85E-06	1.40E-05	1.40E+00	4.86E-01	1.40E+00	5.75E+02	4.11E+02
NPY1R	3.66E+01	8.87E-06	1.41E-05	2.47E+00	1.31E+00	2.47E+00	2.69E+00	1.09E+00
FGR	1.63E+02	8.95E-06	1.42E-05	1.72E+00	7.86E-01	1.72E+00	1.06E+01	6.17E+00
C26H10orf82	6.14E+00	9.16E-06	1.45E-05	4.34E+00	2.12E+00	4.34E+00	5.05E-01	1.17E-01
KLHL18	7.17E+02	9.22E-06	1.46E-05	1.36E+00	4.43E-01	1.36E+00	4.31E+01	3.17E+01
PNISR	2.81E+03	9.33E-06	1.47E-05	1.58E+00	6.60E-01	1.58E+00	1.79E+02	1.13E+02
TDG	4.13E+02	9.34E-06	1.47E-05	1.56E+00	6.42E-01	1.56E+00	2.62E+01	1.68E+01
LOC509283	1.36E+03	9.44E-06	1.49E-05	1.68E+00	7.47E-01	1.68E+00	8.83E+01	5.26E+01
RALA	1.35E+03	9.45E-06	1.49E-05	1.30E+00	3.84E-01	1.30E+00	7.98E+01	6.11E+01
LOC101905725	6.05E+00	9.97E-06	1.57E-05	3.45E+00	1.79E+00	3.45E+00	4.71E-01	1.37E-01
FGF10	1.97E+02	9.98E-06	1.57E-05	3.04E+00	1.60E+00	3.04E+00	1.51E+01	4.97E+00
CLIC2	9.63E+01	1.00E-05	1.57E-05	2.05E+00	1.03E+00	2.05E+00	6.66E+00	3.25E+00
XR_003037739.1	1.61E+01	1.00E-05	1.57E-05	2.50E+00	1.32E+00	2.50E+00	1.18E+00	4.70E-01
PPP2R5E	9.16E+02	1.02E-05	1.60E-05	1.34E+00	4.22E-01	1.34E+00	5.48E+01	4.09E+01
XR_811487.3	2.41E+03	1.02E-05	1.60E-05	1.62E+00	6.99E-01	1.62E+00	1.54E+02	9.51E+01
LHFPL6	2.01E+03	1.03E-05	1.61E-05	2.06E+00	1.04E+00	2.06E+00	1.39E+02	6.76E+01
MFSD14B	8.11E+02	1.08E-05	1.69E-05	1.42E+00	5.07E-01	1.42E+00	4.96E+01	3.49E+01
XR_003030579.1	3.11E+02	1.11E-05	1.73E-05	2.53E+00	1.34E+00	2.53E+00	2.26E+01	8.96E+00
LY96	4.53E+01	1.14E-05	1.77E-05	3.22E+00	1.69E+00	3.22E+00	3.52E+00	1.09E+00
LOC112444773	1.47E+01	1.14E-05	1.78E-05	3.06E+00	1.62E+00	3.06E+00	1.13E+00	3.70E-01
ANXA4	1.12E+03	1.15E-05	1.79E-05	1.60E+00	6.82E-01	1.60E+00	7.15E+01	4.46E+01
SLC25A53	7.87E+01	1.15E-05	1.80E-05	1.80E+00	8.51E-01	1.80E+00	5.22E+00	2.90E+00
FBXL4	1.79E+02	1.16E-05	1.81E-05	1.45E+00	5.40E-01	1.45E+00	1.10E+01	7.54E+00
LOC104969678	2.58E+02	1.17E-05	1.82E-05	2.13E+00	1.09E+00	2.13E+00	1.81E+01	8.50E+00
ADRA1A	4.48E+01	1.20E-05	1.87E-05	3.39E+00	1.76E+00	3.39E+00	3.53E+00	1.04E+00
XR_003033178.1	7.41E+01	1.20E-05	1.87E-05	3.43E+00	1.78E+00	3.43E+00	5.85E+00	1.71E+00
XR_003033054.1	1.66E+02	1.22E-05	1.89E-05	2.30E+00	1.20E+00	2.30E+00	1.19E+01	5.16E+00
SCYL2	7.53E+02	1.23E-05	1.91E-05	1.92E+00	9.39E-01	1.92E+00	5.11E+01	2.66E+01
C1S	2.71E+03	1.24E-05	1.92E-05	2.28E+00	1.19E+00	2.28E+00	1.92E+02	8.41E+01
XR_816437.3	1.20E+01	1.24E-05	1.92E-05	2.41E+00	1.27E+00	2.41E+00	8.70E-01	3.61E-01

UFL1	1.94E+02	1.24E-05	1.92E-05	2.53E+00	1.34E+00	2.53E+00	1.42E+01	5.61E+00
LAMA1	9.25E+03	1.25E-05	1.92E-05	1.75E+00	8.06E-01	1.75E+00	6.08E+02	3.48E+02
DESI2	7.46E+02	1.25E-05	1.93E-05	1.50E+00	5.84E-01	1.50E+00	4.67E+01	3.11E+01
ETNK1	8.05E+02	1.25E-05	1.93E-05	1.74E+00	8.00E-01	1.74E+00	5.31E+01	3.05E+01
LOC784297	1.81E+03	1.26E-05	1.95E-05	1.85E+00	8.91E-01	1.85E+00	1.22E+02	6.57E+01
STRN	4.52E+02	1.27E-05	1.96E-05	1.50E+00	5.81E-01	1.50E+00	2.81E+01	1.88E+01
TPM4	6.62E+03	1.27E-05	1.96E-05	1.56E+00	6.41E-01	1.56E+00	4.18E+02	2.68E+02
CDKAL1	3.78E+02	1.28E-05	1.96E-05	1.36E+00	4.45E-01	1.36E+00	2.27E+01	1.67E+01
FGF7	7.68E+01	1.31E-05	2.02E-05	6.37E+00	2.67E+00	6.37E+00	6.68E+00	1.05E+00
R_001500478.	1.77E+00	1.32E-05	2.02E-05	4.63E+00	2.21E+00	4.63E+00	1.45E-01	3.14E-02
R_003036761.	3.74E+02	1.33E-05	2.04E-05	1.41E+00	5.00E-01	1.41E+00	2.28E+01	1.61E+01
R_003033302.	1.18E+02	1.33E-05	2.04E-05	2.10E+00	1.07E+00	2.10E+00	8.24E+00	3.92E+00
LCAT	6.47E+02	1.34E-05	2.05E-05	1.40E+00	4.85E-01	1.40E+00	3.93E+01	2.81E+01
R_003038219.	2.64E+01	1.34E-05	2.05E-05	5.24E+00	2.39E+00	5.24E+00	2.24E+00	4.26E-01
VIT	1.54E+01	1.35E-05	2.07E-05	1.23E+01	3.63E+00	1.23E+01	1.43E+00	1.16E-01
R_003029448.	2.26E+02	1.37E-05	2.09E-05	1.98E+00	9.84E-01	1.98E+00	1.55E+01	7.83E+00
R_003031256.	8.41E+01	1.38E-05	2.10E-05	2.74E+00	1.45E+00	2.74E+00	6.26E+00	2.29E+00
R_001500250.	1.85E+01	1.38E-05	2.10E-05	2.84E+00	1.51E+00	2.84E+00	1.40E+00	4.92E-01
TMEM87B	6.90E+02	1.38E-05	2.10E-05	1.37E+00	4.52E-01	1.37E+00	4.16E+01	3.04E+01
HIP1	3.05E+03	1.38E-05	2.10E-05	1.55E+00	6.30E-01	1.55E+00	1.92E+02	1.24E+02
GORAB	1.99E+02	1.39E-05	2.12E-05	1.57E+00	6.52E-01	1.57E+00	1.26E+01	8.03E+00
LOC112442256	3.16E+00	1.40E-05	2.12E-05	1.06E+02	6.72E+00	1.06E+02	3.13E-01	2.96E-03
R_003032760.	4.78E+01	1.41E-05	2.14E-05	2.57E+00	1.36E+00	2.57E+00	3.51E+00	1.37E+00
R_003030697.	4.17E+01	1.42E-05	2.15E-05	3.53E+00	1.82E+00	3.53E+00	3.30E+00	9.34E-01
SLFNL1	4.17E+01	1.43E-05	2.17E-05	2.62E+00	1.39E+00	2.62E+00	3.08E+00	1.18E+00
XR_233910.4	2.70E+00	1.44E-05	2.18E-05	4.35E+00	2.12E+00	4.35E+00	2.20E-01	5.06E-02
XR_816330.2	2.53E+02	1.44E-05	2.18E-05	2.67E+00	1.42E+00	2.67E+00	1.89E+01	7.07E+00
EPRS	2.35E+03	1.45E-05	2.19E-05	1.41E+00	4.98E-01	1.41E+00	1.44E+02	1.02E+02
LOC104975635	1.06E+03	1.47E-05	2.22E-05	1.35E+00	4.28E-01	1.35E+00	6.36E+01	4.73E+01
KHDC4	1.13E+03	1.47E-05	2.22E-05	1.32E+00	3.95E-01	1.32E+00	6.73E+01	5.12E+01
B4GALT1	8.34E+02	1.48E-05	2.23E-05	1.55E+00	6.31E-01	1.55E+00	5.24E+01	3.39E+01
GSTCD	1.40E+02	1.48E-05	2.23E-05	1.49E+00	5.79E-01	1.49E+00	8.74E+00	5.85E+00
TNS3	3.68E+03	1.50E-05	2.26E-05	1.47E+00	5.58E-01	1.47E+00	2.27E+02	1.54E+02

XR_003037456.1	2.91E+01	1.51E-05	2.27E-05	5.63E+00	2.49E+00	5.63E+00	2.48E+00	4.41E-01
STAT6	1.64E+03	1.54E-05	2.31E-05	1.43E+00	5.17E-01	1.43E+00	1.01E+02	7.02E+01
CIDEB	1.04E+02	1.54E-05	2.31E-05	2.36E+00	1.24E+00	2.36E+00	7.49E+00	3.18E+00
BRD8	1.92E+03	1.57E-05	2.35E-05	1.28E+00	3.54E-01	1.28E+00	1.12E+02	8.80E+01
RHBDF1	9.34E+02	1.57E-05	2.35E-05	1.39E+00	4.75E-01	1.39E+00	5.66E+01	4.07E+01
MSRB3	2.29E+03	1.58E-05	2.36E-05	1.71E+00	7.73E-01	1.71E+00	1.49E+02	8.74E+01
XR_003034852.1	1.38E+01	1.58E-05	2.36E-05	3.07E+00	1.62E+00	3.07E+00	1.06E+00	3.44E-01
IKBKB	6.61E+02	1.59E-05	2.38E-05	1.33E+00	4.10E-01	1.33E+00	3.92E+01	2.95E+01
PLPP3	9.05E+02	1.62E-05	2.42E-05	2.09E+00	1.06E+00	2.09E+00	6.32E+01	3.02E+01
GRIK3	3.91E+01	1.63E-05	2.43E-05	6.46E+00	2.69E+00	6.46E+00	3.42E+00	5.29E-01
WDR19	2.25E+03	1.64E-05	2.44E-05	1.44E+00	5.23E-01	1.44E+00	1.37E+02	9.57E+01
FAM171A1	1.88E+03	1.66E-05	2.47E-05	1.41E+00	4.95E-01	1.41E+00	1.14E+02	8.12E+01
GNG12	2.78E+01	1.67E-05	2.49E-05	1.44E+01	3.85E+00	1.44E+01	2.60E+00	1.81E-01
XR_003032006.1	2.99E+01	1.70E-05	2.53E-05	3.04E+00	1.60E+00	3.04E+00	2.29E+00	7.54E-01
CCDC149	3.60E+02	1.70E-05	2.53E-05	1.50E+00	5.87E-01	1.50E+00	2.24E+01	1.49E+01
XR_003037782.1	8.74E+01	1.74E-05	2.58E-05	2.70E+00	1.43E+00	2.70E+00	6.48E+00	2.40E+00
ALG10	2.15E+02	1.77E-05	2.62E-05	1.47E+00	5.53E-01	1.47E+00	1.33E+01	9.06E+00
XR_003031269.1	3.53E+02	1.81E-05	2.68E-05	2.25E+00	1.17E+00	2.25E+00	2.50E+01	1.11E+01
SLC8A2	2.02E+02	1.81E-05	2.68E-05	2.14E+00	1.10E+00	2.14E+00	1.40E+01	6.56E+00
ATF7	2.84E+03	1.87E-05	2.76E-05	1.65E+00	7.18E-01	1.65E+00	1.82E+02	1.10E+02
ASAP1	9.06E+02	1.89E-05	2.79E-05	1.66E+00	7.28E-01	1.66E+00	5.88E+01	3.55E+01
XR_003030182.1	2.51E+01	1.90E-05	2.81E-05	3.36E+00	1.75E+00	3.36E+00	1.97E+00	5.87E-01
UHRF2	8.50E+02	1.92E-05	2.84E-05	1.31E+00	3.94E-01	1.31E+00	5.04E+01	3.84E+01
CREB3L1	8.18E+02	1.95E-05	2.88E-05	1.59E+00	6.66E-01	1.59E+00	5.21E+01	3.28E+01
TMEM67	2.12E+02	1.98E-05	2.92E-05	1.81E+00	8.53E-01	1.81E+00	1.40E+01	7.77E+00
SMCO3	1.29E+01	2.01E-05	2.96E-05	1.06E+01	3.40E+00	1.06E+01	1.18E+00	1.12E-01
ELF4	1.05E+03	2.05E-05	3.02E-05	1.61E+00	6.91E-01	1.61E+00	6.65E+01	4.12E+01
CASK	1.06E+03	2.08E-05	3.06E-05	1.41E+00	4.97E-01	1.41E+00	6.48E+01	4.59E+01
NIPAL3	1.15E+03	2.12E-05	3.11E-05	1.38E+00	4.61E-01	1.38E+00	6.93E+01	5.04E+01
LOC101905866	1.83E+01	2.13E-05	3.12E-05	4.69E+00	2.23E+00	4.69E+00	1.53E+00	3.27E-01
DTX1	3.90E+02	2.21E-05	3.23E-05	1.75E+00	8.09E-01	1.75E+00	2.56E+01	1.46E+01
LOC782904	2.94E+01	2.21E-05	3.24E-05	1.97E+00	9.77E-01	1.97E+00	2.01E+00	1.02E+00
NR1I3	1.32E+01	2.21E-05	3.24E-05	2.94E+00	1.55E+00	2.94E+00	1.01E+00	3.42E-01

XR_003036089.	1.87E+01	2.24E-05	3.28E-05	2.36E+00	1.24E+00	2.36E+00	1.34E+00	5.70E-01
CLU	1.34E+04	2.29E-05	3.35E-05	1.76E+00	8.15E-01	1.76E+00	8.86E+02	5.04E+02
SH3BGR	5.11E+02	2.35E-05	3.43E-05	2.44E+00	1.29E+00	2.44E+00	3.71E+01	1.52E+01
XR_003037537.	1.60E+01	2.35E-05	3.43E-05	6.61E+00	2.73E+00	6.61E+00	1.39E+00	2.10E-01
SUMF1	1.65E+03	2.37E-05	3.46E-05	1.28E+00	3.59E-01	1.28E+00	9.67E+01	7.54E+01
GFRA4	1.08E+02	2.53E-05	3.68E-05	1.79E+00	8.36E-01	1.79E+00	7.19E+00	4.02E+00
LOC790009	3.06E+02	2.53E-05	3.68E-05	1.54E+00	6.28E-01	1.54E+00	1.93E+01	1.25E+01
EPM2AIP1	4.64E+03	2.53E-05	3.68E-05	1.55E+00	6.35E-01	1.55E+00	2.93E+02	1.89E+02
LOC101907802	1.32E+01	2.55E-05	3.70E-05	2.36E+00	1.24E+00	2.36E+00	9.53E-01	4.04E-01
VAMP8	3.76E+02	2.60E-05	3.78E-05	1.36E+00	4.42E-01	1.36E+00	2.26E+01	1.67E+01
TRABD2B	1.22E+02	2.61E-05	3.79E-05	2.27E+00	1.18E+00	2.27E+00	8.73E+00	3.85E+00
ZNF473	4.73E+02	2.62E-05	3.79E-05	1.46E+00	5.42E-01	1.46E+00	2.92E+01	2.00E+01
COL16A1	9.67E+03	2.66E-05	3.85E-05	1.52E+00	6.02E-01	1.52E+00	6.08E+02	4.01E+02
XR_003034240.	2.80E+01	2.66E-05	3.85E-05	2.66E+00	1.41E+00	2.66E+00	2.08E+00	7.82E-01
N4BP2L1	7.08E+02	2.67E-05	3.86E-05	1.37E+00	4.56E-01	1.37E+00	4.26E+01	3.11E+01
ME3	1.72E+02	2.68E-05	3.87E-05	2.01E+00	1.01E+00	2.01E+00	1.18E+01	5.87E+00
XR_815660.3	3.99E+02	2.70E-05	3.90E-05	1.64E+00	7.09E-01	1.64E+00	2.57E+01	1.57E+01
GLI3	1.26E+03	2.70E-05	3.90E-05	1.90E+00	9.26E-01	1.90E+00	8.58E+01	4.52E+01
XR_003030699.	1.04E+01	2.71E-05	3.91E-05	4.53E+00	2.18E+00	4.53E+00	8.66E-01	1.91E-01
XR_003030150.	2.12E+01	2.73E-05	3.94E-05	1.12E+01	3.49E+00	1.12E+01	1.95E+00	1.74E-01
XR_003034633.	1.12E+01	2.83E-05	4.07E-05	5.57E+00	2.48E+00	5.57E+00	9.54E-01	1.71E-01
XR_003031747.	2.24E+01	2.85E-05	4.09E-05	2.13E+00	1.09E+00	2.13E+00	1.56E+00	7.35E-01
XR_808699.3	5.28E+01	2.93E-05	4.21E-05	8.50E+00	3.09E+00	8.50E+00	4.77E+00	5.60E-01
AGO1	1.46E+03	2.97E-05	4.26E-05	1.44E+00	5.26E-01	1.44E+00	9.03E+01	6.27E+01
XR_003029617.	2.14E+02	3.02E-05	4.33E-05	2.24E+00	1.16E+00	2.24E+00	1.53E+01	6.82E+00
FGF1	3.91E+02	3.04E-05	4.35E-05	2.17E+00	1.12E+00	2.17E+00	2.76E+01	1.27E+01
TMC5	5.93E+01	3.04E-05	4.35E-05	6.09E+00	2.61E+00	6.09E+00	5.18E+00	8.51E-01
BBS7	2.14E+02	3.20E-05	4.58E-05	1.48E+00	5.70E-01	1.48E+00	1.32E+01	8.92E+00
XR_003033859.	3.33E+02	3.21E-05	4.59E-05	1.45E+00	5.33E-01	1.45E+00	2.05E+01	1.42E+01
MAOB	4.06E+02	3.36E-05	4.79E-05	3.25E+00	1.70E+00	3.25E+00	3.18E+01	9.78E+00
EMC1	4.67E+03	3.37E-05	4.81E-05	1.31E+00	3.90E-01	1.31E+00	2.76E+02	2.10E+02
NR_131898.1	3.83E+03	3.43E-05	4.89E-05	1.33E+00	4.11E-01	1.33E+00	2.29E+02	1.72E+02
AFAP1	1.08E+03	3.44E-05	4.89E-05	1.55E+00	6.35E-01	1.55E+00	6.83E+01	4.40E+01

BTBD7	7.84E+02	3.45E-05	4.92E-05	1.59E+00	6.66E-01	1.59E+00	4.99E+01	3.14E+01
R_003029614.	4.53E+00	3.47E-05	4.94E-05	5.78E+00	2.53E+00	5.78E+00	3.88E-01	6.71E-02
JAKMIP3	1.62E+02	3.49E-05	4.97E-05	1.94E+00	9.59E-01	1.94E+00	1.09E+01	5.62E+00
R_003035051.	1.29E+01	3.50E-05	4.97E-05	2.76E+00	1.46E+00	2.76E+00	9.62E-01	3.49E-01
CLEC5A	7.04E+00	3.50E-05	4.97E-05	1.59E+01	3.99E+00	1.59E+01	6.64E-01	4.19E-02
TNFSF12	4.38E+02	3.60E-05	5.10E-05	1.46E+00	5.43E-01	1.46E+00	2.70E+01	1.85E+01
R_003031288.	6.48E+00	3.63E-05	5.15E-05	1.09E+01	3.45E+00	1.09E+01	5.96E-01	5.45E-02
LOC100297540	1.31E+01	3.63E-05	5.15E-05	4.06E+00	2.02E+00	4.06E+00	1.07E+00	2.64E-01
ZNF484	9.64E+02	3.64E-05	5.15E-05	1.37E+00	4.54E-01	1.37E+00	5.83E+01	4.25E+01
RCN3	3.35E+03	3.66E-05	5.17E-05	1.38E+00	4.61E-01	1.38E+00	2.02E+02	1.47E+02
R_003030578.	8.60E+02	3.69E-05	5.21E-05	2.01E+00	1.01E+00	2.01E+00	5.88E+01	2.92E+01
LOC101902656	1.70E+01	3.74E-05	5.28E-05	2.27E+00	1.18E+00	2.27E+00	1.21E+00	5.31E-01
XR_807235.3	2.29E+02	3.74E-05	5.28E-05	2.49E+00	1.32E+00	2.49E+00	1.69E+01	6.79E+00
ZCCHC10	1.15E+02	3.80E-05	5.35E-05	1.42E+00	5.05E-01	1.42E+00	6.99E+00	4.93E+00
OSR2	1.17E+03	3.88E-05	5.46E-05	1.68E+00	7.47E-01	1.68E+00	7.60E+01	4.53E+01
R_003031737.	4.48E+02	3.96E-05	5.57E-05	1.64E+00	7.09E-01	1.64E+00	2.87E+01	1.76E+01
RHOQ	7.02E+02	4.00E-05	5.62E-05	1.47E+00	5.61E-01	1.47E+00	4.37E+01	2.96E+01
CREBZF	1.51E+03	4.00E-05	5.62E-05	1.37E+00	4.49E-01	1.37E+00	9.06E+01	6.63E+01
LOC787234	7.70E+00	4.04E-05	5.67E-05	2.58E+00	1.37E+00	2.58E+00	5.65E-01	2.19E-01
GPR180	5.01E+01	4.05E-05	5.68E-05	1.89E+00	9.15E-01	1.89E+00	3.34E+00	1.77E+00
R_001495596.	1.84E+03	4.11E-05	5.76E-05	1.84E+00	8.78E-01	1.84E+00	1.23E+02	6.72E+01
TMEM68	2.75E+02	4.29E-05	6.01E-05	1.41E+00	4.94E-01	1.41E+00	1.67E+01	1.19E+01
R_001498246.	1.29E+01	4.31E-05	6.04E-05	1.62E+01	4.02E+00	1.62E+01	1.21E+00	7.49E-02
PCDH11X	2.38E+01	4.32E-05	6.04E-05	4.83E+00	2.27E+00	4.83E+00	2.00E+00	4.14E-01
EIF4EBP2	2.54E+02	4.35E-05	6.07E-05	3.65E+00	1.87E+00	3.65E+00	2.03E+01	5.55E+00
B4GALT6	3.61E+02	4.36E-05	6.08E-05	1.87E+00	9.00E-01	1.87E+00	2.42E+01	1.30E+01
ZRANB3	2.52E+02	4.37E-05	6.09E-05	1.43E+00	5.21E-01	1.43E+00	1.55E+01	1.08E+01
BLOC1S5	4.47E+02	4.39E-05	6.11E-05	1.31E+00	3.86E-01	1.31E+00	2.64E+01	2.02E+01
MYO1C	3.27E+03	4.39E-05	6.11E-05	1.34E+00	4.20E-01	1.34E+00	1.95E+02	1.46E+02
PUS7L	1.47E+02	4.42E-05	6.15E-05	1.62E+00	6.98E-01	1.62E+00	9.41E+00	5.80E+00
HIGD1B	1.84E+01	4.42E-05	6.15E-05	4.74E+00	2.25E+00	4.74E+00	1.55E+00	3.26E-01
XR_139535.5	1.03E+02	4.51E-05	6.26E-05	1.63E+00	7.02E-01	1.63E+00	6.59E+00	4.05E+00
LOC107131225	1.24E+02	4.68E-05	6.49E-05	1.92E+00	9.38E-01	1.92E+00	8.36E+00	4.36E+00

C1QTNF2	1.37E+02	4.68E-05	6.49E-05	1.88E+00	9.09E-01	1.88E+00	9.24E+00	4.92E+00
XR_003037481.1	3.93E+00	4.85E-05	6.73E-05	8.36E+00	3.06E+00	8.36E+00	3.55E-01	4.24E-02
PRPF18	4.65E+02	4.88E-05	6.76E-05	1.33E+00	4.17E-01	1.33E+00	2.77E+01	2.07E+01
RRAD	1.56E+03	4.91E-05	6.79E-05	1.90E+00	9.29E-01	1.90E+00	1.05E+02	5.54E+01
GCNT4	4.13E+01	4.99E-05	6.91E-05	2.23E+00	1.16E+00	2.23E+00	2.92E+00	1.31E+00
DSC2	4.50E+02	5.01E-05	6.93E-05	1.59E+00	6.71E-01	1.59E+00	2.87E+01	1.80E+01
ATAD2	2.78E+01	5.03E-05	6.94E-05	5.74E+00	2.52E+00	5.74E+00	2.39E+00	4.17E-01
PARM1	1.26E+02	5.04E-05	6.96E-05	2.69E+00	1.43E+00	2.69E+00	9.43E+00	3.50E+00
XR_003034894.1	1.38E+02	5.08E-05	7.00E-05	2.03E+00	1.02E+00	2.03E+00	9.44E+00	4.65E+00
XR_003034801.1	3.38E+00	5.19E-05	7.15E-05	2.64E+01	4.72E+00	2.64E+01	3.26E-01	1.23E-02
XR_003035381.1	1.80E+01	5.20E-05	7.16E-05	2.34E+00	1.23E+00	2.34E+00	1.29E+00	5.50E-01
RNF139	5.85E+02	5.41E-05	7.44E-05	1.22E+00	2.90E-01	1.22E+00	3.36E+01	2.74E+01
GNAO1	2.45E+02	5.44E-05	7.48E-05	3.11E+00	1.64E+00	3.11E+00	1.88E+01	6.05E+00
NTF3	6.27E+01	5.53E-05	7.59E-05	2.64E+00	1.40E+00	2.64E+00	4.64E+00	1.76E+00
BMX	1.40E+01	5.62E-05	7.71E-05	7.18E+00	2.84E+00	7.18E+00	1.24E+00	1.72E-01
QRFPR	4.89E+02	5.77E-05	7.91E-05	2.68E+00	1.42E+00	2.68E+00	3.65E+01	1.36E+01
LOC101903835	2.53E+00	5.87E-05	8.04E-05	4.34E+00	2.12E+00	4.34E+00	2.07E-01	4.76E-02
LTBR	1.50E+03	5.92E-05	8.10E-05	1.37E+00	4.52E-01	1.37E+00	9.07E+01	6.63E+01
IGFBP4	8.61E+03	5.96E-05	8.14E-05	1.51E+00	5.92E-01	1.51E+00	5.37E+02	3.56E+02
MAPK9	5.80E+02	5.96E-05	8.14E-05	1.42E+00	5.02E-01	1.42E+00	3.55E+01	2.50E+01
C1QTNF7	3.25E+02	6.08E-05	8.31E-05	1.86E+00	8.97E-01	1.86E+00	2.17E+01	1.16E+01
C5H12orf45	1.74E+02	6.13E-05	8.37E-05	1.52E+00	6.04E-01	1.52E+00	1.09E+01	7.14E+00
MAVS	8.85E+02	6.16E-05	8.40E-05	1.46E+00	5.50E-01	1.46E+00	5.46E+01	3.73E+01
LOC107131526	2.54E+00	6.21E-05	8.47E-05	1.00E+01	3.32E+00	1.00E+01	2.32E-01	2.32E-02
XR_003035852.1	2.44E+02	6.25E-05	8.51E-05	1.44E+00	5.21E-01	1.44E+00	1.49E+01	1.04E+01
POU6F1	9.17E+02	6.35E-05	8.64E-05	1.61E+00	6.86E-01	1.61E+00	5.82E+01	3.62E+01
LOC107131684	7.11E+01	6.38E-05	8.67E-05	1.83E+00	8.70E-01	1.83E+00	4.76E+00	2.60E+00
PRKAB2	8.88E+02	6.58E-05	8.95E-05	1.37E+00	4.53E-01	1.37E+00	5.37E+01	3.92E+01
XR_001501515.2	1.52E+02	6.62E-05	8.99E-05	1.40E+00	4.88E-01	1.40E+00	9.22E+00	6.58E+00
SLIT3	6.28E+02	6.71E-05	9.10E-05	2.72E+00	1.44E+00	2.72E+00	4.71E+01	1.73E+01
DEK	2.62E+03	6.72E-05	9.11E-05	1.31E+00	3.85E-01	1.31E+00	1.55E+02	1.19E+02
XR_003036885.1	7.44E+00	6.73E-05	9.12E-05	7.99E+00	3.00E+00	7.99E+00	6.64E-01	8.31E-02
SUPT7L	3.60E+02	6.78E-05	9.18E-05	1.27E+00	3.40E-01	1.27E+00	2.10E+01	1.66E+01

ZDHHC1	1.48E+02	6.87E-05	9.28E-05	1.56E+00	6.40E-01	1.56E+00	9.34E+00	5.99E+00
R_003030358.1	7.55E+02	6.87E-05	9.29E-05	1.93E+00	9.47E-01	1.93E+00	5.10E+01	2.65E+01
R_003037292.1	3.44E+00	6.89E-05	9.31E-05	7.76E+00	2.96E+00	7.76E+00	3.06E-01	3.94E-02
R_003033479.1	1.30E+01	6.95E-05	9.37E-05	3.01E+00	1.59E+00	3.01E+00	9.99E-01	3.32E-01
TIA1	3.69E+03	6.95E-05	9.37E-05	1.49E+00	5.74E-01	1.49E+00	2.30E+02	1.54E+02
FZD8	7.77E+02	7.02E-05	9.45E-05	2.44E+00	1.29E+00	2.44E+00	5.63E+01	2.31E+01
R_003034241.1	2.61E+01	7.13E-05	9.59E-05	2.03E+00	1.02E+00	2.03E+00	1.80E+00	8.86E-01
RGL1	1.20E+03	7.14E-05	9.60E-05	1.72E+00	7.82E-01	1.72E+00	7.78E+01	4.53E+01
NFE2L2	1.62E+03	7.20E-05	9.67E-05	1.29E+00	3.68E-01	1.29E+00	9.52E+01	7.38E+01
PRKCE	4.84E+02	7.35E-05	9.87E-05	1.61E+00	6.83E-01	1.61E+00	3.10E+01	1.93E+01
R_003034239.1	1.91E+01	7.47E-05	1.00E-04	2.39E+00	1.26E+00	2.39E+00	1.38E+00	5.79E-01
LOC531090	1.15E+02	7.57E-05	1.01E-04	1.14E+01	3.51E+00	1.14E+01	1.07E+01	9.34E-01
EMCN	7.02E+02	7.60E-05	1.02E-04	1.43E+00	5.19E-01	1.43E+00	4.31E+01	3.01E+01
ANKMY2	5.18E+02	7.62E-05	1.02E-04	1.28E+00	3.59E-01	1.28E+00	3.04E+01	2.37E+01
TMEM51	4.60E+02	7.65E-05	1.02E-04	1.83E+00	8.71E-01	1.83E+00	3.05E+01	1.67E+01
BCL2	8.88E+01	7.73E-05	1.03E-04	3.05E+00	1.61E+00	3.05E+00	6.87E+00	2.25E+00
CLK1	3.47E+03	7.93E-05	1.06E-04	1.36E+00	4.48E-01	1.36E+00	2.10E+02	1.54E+02
BCL2L2	1.48E+03	7.99E-05	1.07E-04	1.34E+00	4.23E-01	1.34E+00	8.82E+01	6.58E+01
R_003037689.1	1.86E+01	8.11E-05	1.08E-04	8.50E+00	3.09E+00	8.50E+00	1.67E+00	1.96E-01
R_003034464.1	4.31E+00	8.37E-05	1.12E-04	7.67E+00	2.94E+00	7.67E+00	3.84E-01	5.01E-02
SLC16A2	7.92E+02	8.50E-05	1.13E-04	1.80E+00	8.45E-01	1.80E+00	5.24E+01	2.92E+01
TBX18	8.16E+00	8.58E-05	1.14E-04	4.03E+00	2.01E+00	4.03E+00	6.61E-01	1.64E-01
PCNX2	7.67E+01	8.71E-05	1.16E-04	2.04E+00	1.03E+00	2.04E+00	5.30E+00	2.60E+00
ZNF180	1.71E+02	8.92E-05	1.19E-04	1.36E+00	4.45E-01	1.36E+00	1.02E+01	7.53E+00
NR_129534.1	4.74E+01	8.96E-05	1.19E-04	1.66E+00	7.35E-01	1.66E+00	3.08E+00	1.85E+00
TMEM241	3.00E+02	9.01E-05	1.20E-04	1.43E+00	5.12E-01	1.43E+00	1.83E+01	1.28E+01
RBM5	4.83E+03	9.19E-05	1.22E-04	1.32E+00	3.99E-01	1.32E+00	2.86E+02	2.17E+02
MED28	3.76E+02	9.31E-05	1.23E-04	1.51E+00	5.95E-01	1.51E+00	2.34E+01	1.55E+01
XR_815545.3	5.18E+00	9.31E-05	1.23E-04	4.01E+00	2.00E+00	4.01E+00	4.19E-01	1.04E-01
R_003031871.1	5.53E+01	9.39E-05	1.24E-04	2.33E+00	1.22E+00	2.33E+00	3.94E+00	1.69E+00
IZUMO2	6.88E+00	9.41E-05	1.24E-04	3.50E+00	1.81E+00	3.50E+00	5.43E-01	1.55E-01
ZNF146	1.53E+03	9.54E-05	1.26E-04	1.36E+00	4.40E-01	1.36E+00	9.20E+01	6.78E+01
LOC788150	5.38E+00	9.72E-05	1.28E-04	3.48E+00	1.80E+00	3.48E+00	4.26E-01	1.22E-01

ILDR2	4.27E+02	9.82E-05	1.30E-04	2.02E+00	1.01E+00	2.02E+00	2.94E+01	1.46E+01
GALNT1	1.08E+03	9.89E-05	1.30E-04	1.26E+00	3.36E-01	1.26E+00	6.30E+01	4.99E+01
SPATA13	7.11E+02	9.96E-05	1.31E-04	1.70E+00	7.65E-01	1.70E+00	4.62E+01	2.72E+01
CCDC188	3.05E+02	1.01E-04	1.32E-04	1.75E+00	8.10E-01	1.75E+00	2.00E+01	1.14E+01
ATG5	4.36E+02	1.02E-04	1.34E-04	1.23E+00	3.00E-01	1.23E+00	2.52E+01	2.04E+01
ERGIC2	5.53E+02	1.04E-04	1.37E-04	1.27E+00	3.50E-01	1.27E+00	3.24E+01	2.54E+01
XR_003030605.1	3.17E+00	1.05E-04	1.38E-04	5.46E+00	2.45E+00	5.46E+00	2.70E-01	4.95E-02
ZFP90	5.55E+02	1.06E-04	1.39E-04	1.30E+00	3.80E-01	1.30E+00	3.28E+01	2.52E+01
TFPI	1.60E+02	1.07E-04	1.41E-04	2.16E+00	1.11E+00	2.16E+00	1.12E+01	5.20E+00
ITIH5	1.95E+03	1.07E-04	1.41E-04	3.31E+00	1.73E+00	3.31E+00	1.51E+02	4.56E+01
RBFOX2	4.64E+03	1.09E-04	1.43E-04	1.34E+00	4.18E-01	1.34E+00	2.77E+02	2.08E+02
ROBO4	1.33E+03	1.10E-04	1.43E-04	1.67E+00	7.36E-01	1.67E+00	8.68E+01	5.21E+01
NBDY	7.65E+02	1.15E-04	1.50E-04	1.35E+00	4.30E-01	1.35E+00	4.60E+01	3.42E+01
C5H12orf56	7.04E+01	1.15E-04	1.50E-04	2.34E+00	1.23E+00	2.34E+00	5.10E+00	2.18E+00
XR_001500449.2	2.41E+02	1.17E-04	1.53E-04	1.57E+00	6.54E-01	1.57E+00	1.53E+01	9.70E+00
FECH	5.33E+02	1.18E-04	1.54E-04	1.61E+00	6.87E-01	1.61E+00	3.42E+01	2.13E+01
LOC112442967	2.12E+01	1.18E-04	1.54E-04	2.13E+00	1.09E+00	2.13E+00	1.49E+00	7.01E-01
XR_814213.2	1.86E+01	1.19E-04	1.54E-04	3.19E+00	1.67E+00	3.19E+00	1.43E+00	4.49E-01
XR_236306.4	3.30E+02	1.19E-04	1.55E-04	1.32E+00	4.01E-01	1.32E+00	1.95E+01	1.48E+01
C17H4orf46	2.79E+02	1.19E-04	1.55E-04	1.45E+00	5.38E-01	1.45E+00	1.72E+01	1.18E+01
LOC616948	2.21E+02	1.19E-04	1.55E-04	1.63E+00	7.09E-01	1.63E+00	1.42E+01	8.71E+00
GLUD1	2.29E+03	1.20E-04	1.56E-04	1.30E+00	3.75E-01	1.30E+00	1.35E+02	1.04E+02
XR_003034114.1	3.20E+02	1.20E-04	1.56E-04	1.97E+00	9.76E-01	1.97E+00	2.19E+01	1.11E+01
KIAA1841	2.07E+02	1.21E-04	1.57E-04	1.52E+00	6.01E-01	1.52E+00	1.29E+01	8.51E+00
PMP22	2.95E+03	1.23E-04	1.60E-04	1.61E+00	6.88E-01	1.61E+00	1.88E+02	1.17E+02
DNAJB4	4.97E+02	1.26E-04	1.64E-04	1.38E+00	4.62E-01	1.38E+00	3.01E+01	2.18E+01
XR_805374.3	2.87E+02	1.28E-04	1.66E-04	1.35E+00	4.35E-01	1.35E+00	1.72E+01	1.27E+01
XR_003031981.1	1.96E+02	1.30E-04	1.68E-04	1.70E+00	7.69E-01	1.70E+00	1.28E+01	7.51E+00
RCSD1	4.09E+02	1.31E-04	1.69E-04	1.50E+00	5.82E-01	1.50E+00	2.54E+01	1.70E+01
XR_003029449.1	4.46E+00	1.36E-04	1.76E-04	2.79E+00	1.48E+00	2.79E+00	3.34E-01	1.20E-01
LOC101902154	1.74E+01	1.38E-04	1.77E-04	2.11E+00	1.07E+00	2.11E+00	1.20E+00	5.69E-01
LOC539893	8.31E+01	1.39E-04	1.79E-04	1.50E+00	5.89E-01	1.50E+00	5.20E+00	3.46E+00
EXT2	2.05E+03	1.39E-04	1.79E-04	1.27E+00	3.47E-01	1.27E+00	1.19E+02	9.40E+01

CTSB	6.92E+03	1.40E-04	1.80E-04	1.35E+00	4.38E-01	1.35E+00	4.15E+02	3.06E+02
DISC1	2.44E+02	1.43E-04	1.84E-04	1.51E+00	5.98E-01	1.51E+00	1.52E+01	1.01E+01
LOC112448743	7.20E+01	1.44E-04	1.85E-04	2.32E+00	1.21E+00	2.32E+00	5.17E+00	2.23E+00
XR_808566.3	7.60E+00	1.44E-04	1.85E-04	3.07E+00	1.62E+00	3.07E+00	5.85E-01	1.91E-01
LOC100140039	2.58E+01	1.46E-04	1.88E-04	2.22E+00	1.15E+00	2.22E+00	1.80E+00	8.13E-01
INPP4A	1.22E+03	1.49E-04	1.92E-04	1.43E+00	5.17E-01	1.43E+00	7.47E+01	5.22E+01
MFSD8	2.21E+02	1.50E-04	1.92E-04	1.36E+00	4.43E-01	1.36E+00	1.33E+01	9.76E+00
R_003035435.	8.96E+00	1.50E-04	1.92E-04	2.57E+00	1.36E+00	2.57E+00	6.59E-01	2.57E-01
R_003036889.	4.08E+01	1.52E-04	1.95E-04	1.79E+00	8.41E-01	1.79E+00	2.72E+00	1.52E+00
IPMK	8.91E+01	1.53E-04	1.95E-04	1.52E+00	6.06E-01	1.52E+00	5.61E+00	3.69E+00
R_003033130.	2.17E+02	1.53E-04	1.95E-04	2.94E+00	1.55E+00	2.94E+00	1.63E+01	5.55E+00
TMEM106B	9.77E+02	1.53E-04	1.96E-04	1.36E+00	4.44E-01	1.36E+00	5.88E+01	4.32E+01
PDLIM7	4.37E+03	1.54E-04	1.96E-04	1.36E+00	4.45E-01	1.36E+00	2.63E+02	1.93E+02
NFX1	7.20E+02	1.62E-04	2.07E-04	1.40E+00	4.82E-01	1.40E+00	4.35E+01	3.12E+01
FAM69A	9.51E+01	1.65E-04	2.11E-04	1.78E+00	8.33E-01	1.78E+00	6.29E+00	3.53E+00
R_003034390.	3.39E+02	1.65E-04	2.11E-04	1.61E+00	6.90E-01	1.61E+00	2.16E+01	1.34E+01
XR_808734.3	1.94E+00	1.66E-04	2.11E-04	1.67E+02	7.38E+00	1.67E+02	1.93E-01	1.16E-03
R_003031268.	2.11E+02	1.67E-04	2.12E-04	1.80E+00	8.48E-01	1.80E+00	1.40E+01	7.76E+00
KIF27	3.31E+02	1.67E-04	2.13E-04	1.75E+00	8.08E-01	1.75E+00	2.18E+01	1.24E+01
DIO2	9.28E+00	1.68E-04	2.14E-04	4.17E+00	2.06E+00	4.17E+00	7.61E-01	1.83E-01
PGRMC2	1.23E+03	1.70E-04	2.16E-04	1.19E+00	2.57E-01	1.19E+00	6.99E+01	5.85E+01
R_001495102.	7.79E+01	1.71E-04	2.17E-04	1.94E+00	9.56E-01	1.94E+00	5.29E+00	2.73E+00
ZNF184	6.26E+02	1.73E-04	2.19E-04	1.41E+00	4.94E-01	1.41E+00	3.80E+01	2.70E+01
RC3H1	8.87E+02	1.74E-04	2.20E-04	1.30E+00	3.81E-01	1.30E+00	5.23E+01	4.01E+01
NUDT12	1.48E+02	1.77E-04	2.24E-04	1.57E+00	6.49E-01	1.57E+00	9.39E+00	5.99E+00
R_003029746.	2.47E+01	1.79E-04	2.27E-04	1.77E+00	8.27E-01	1.77E+00	1.62E+00	9.12E-01
RPP14	1.04E+03	1.81E-04	2.29E-04	1.23E+00	2.99E-01	1.23E+00	6.01E+01	4.88E+01
R_003036487.	2.93E+00	1.85E-04	2.33E-04	2.84E+00	1.50E+00	2.84E+00	2.17E-01	7.64E-02
R_003036126.	2.94E+01	1.86E-04	2.34E-04	1.60E+00	6.82E-01	1.60E+00	1.88E+00	1.17E+00
EPHA3	1.80E+01	1.86E-04	2.34E-04	2.35E+01	4.56E+00	2.35E+01	1.74E+00	7.38E-02
ZNF326	9.53E+02	1.86E-04	2.34E-04	1.29E+00	3.65E-01	1.29E+00	5.60E+01	4.35E+01
MCAM	1.44E+03	1.87E-04	2.36E-04	1.64E+00	7.16E-01	1.64E+00	9.28E+01	5.65E+01
R_003032351.	7.13E+01	1.89E-04	2.38E-04	2.96E+00	1.57E+00	2.96E+00	5.45E+00	1.84E+00

XR_003034394.1	8.43E+01	1.90E-04	2.38E-04	1.77E+00	8.26E-01	1.77E+00	5.56E+00	3.14E+00
PLD2	1.55E+03	1.91E-04	2.41E-04	1.41E+00	4.99E-01	1.41E+00	9.45E+01	6.69E+01
XR_003035894.1	1.66E+00	1.92E-04	2.42E-04	7.00E+00	2.81E+00	7.00E+00	1.46E-01	2.08E-02
XR_003034580.1	1.11E+02	1.93E-04	2.42E-04	2.06E+00	1.04E+00	2.06E+00	7.63E+00	3.71E+00
LOC104974678	8.57E+00	1.96E-04	2.46E-04	2.43E+00	1.28E+00	2.43E+00	6.23E-01	2.56E-01
COL6A5	2.03E+02	1.96E-04	2.46E-04	2.34E+00	1.23E+00	2.34E+00	1.46E+01	6.23E+00
FCHO2	3.27E+01	1.97E-04	2.47E-04	9.68E+00	3.27E+00	9.68E+00	2.98E+00	3.08E-01
SEMA3B	1.37E+03	1.98E-04	2.48E-04	1.49E+00	5.76E-01	1.49E+00	8.56E+01	5.74E+01
SCO1	9.68E+02	2.01E-04	2.52E-04	1.22E+00	2.87E-01	1.22E+00	5.56E+01	4.55E+01
XR_003030467.1	1.24E+01	2.04E-04	2.54E-04	1.68E+01	4.07E+00	1.68E+01	1.18E+00	7.04E-02
XR_003035030.1	5.47E+00	2.07E-04	2.59E-04	1.87E+01	4.22E+00	1.87E+01	5.22E-01	2.79E-02
PRR16	8.46E+01	2.11E-04	2.63E-04	8.45E+00	3.08E+00	8.45E+00	7.61E+00	9.01E-01
LRRTM3	9.87E+00	2.15E-04	2.68E-04	2.80E+00	1.49E+00	2.80E+00	7.38E-01	2.63E-01
SYNE2	3.55E+03	2.15E-04	2.68E-04	1.47E+00	5.52E-01	1.47E+00	2.19E+02	1.49E+02
MSI2	1.91E+03	2.16E-04	2.68E-04	1.52E+00	6.08E-01	1.52E+00	1.20E+02	7.89E+01
RBM39	5.66E+03	2.16E-04	2.69E-04	1.22E+00	2.83E-01	1.22E+00	3.26E+02	2.68E+02
XR_806610.3	1.04E+03	2.17E-04	2.70E-04	1.35E+00	4.36E-01	1.35E+00	6.27E+01	4.64E+01
XR_003034762.1	1.07E+01	2.17E-04	2.70E-04	2.93E+00	1.55E+00	2.93E+00	8.20E-01	2.80E-01
EHD3	5.36E+02	2.17E-04	2.70E-04	1.69E+00	7.54E-01	1.69E+00	3.48E+01	2.06E+01
SSBP2	1.37E+03	2.18E-04	2.70E-04	1.36E+00	4.41E-01	1.36E+00	8.20E+01	6.04E+01
XR_003036088.1	2.19E+01	2.23E-04	2.77E-04	5.42E+00	2.44E+00	5.42E+00	1.86E+00	3.43E-01
PIK3R6	1.32E+02	2.24E-04	2.77E-04	1.47E+00	5.52E-01	1.47E+00	8.11E+00	5.53E+00
PLPP6	2.80E+01	2.28E-04	2.82E-04	1.85E+00	8.86E-01	1.85E+00	1.88E+00	1.02E+00
LOC107132868	2.01E+00	2.28E-04	2.82E-04	2.23E+01	4.48E+00	2.23E+01	1.92E-01	8.61E-03
NFYA	5.59E+02	2.30E-04	2.84E-04	1.35E+00	4.38E-01	1.35E+00	3.35E+01	2.48E+01
CCL1	5.02E+00	2.31E-04	2.86E-04	9.65E+00	3.27E+00	9.65E+00	4.58E-01	4.75E-02
MTCP1	6.64E+01	2.32E-04	2.86E-04	1.49E+00	5.79E-01	1.49E+00	4.13E+00	2.76E+00
GDF10	4.47E+02	2.41E-04	2.98E-04	2.90E+00	1.54E+00	2.90E+00	3.40E+01	1.17E+01
XR_003036746.1	3.72E+00	2.43E-04	3.00E-04	9.72E+00	3.28E+00	9.72E+00	3.39E-01	3.49E-02
LOC107131940	7.22E+00	2.44E-04	3.01E-04	2.26E+00	1.18E+00	2.26E+00	5.13E-01	2.27E-01
XR_003036365.1	1.62E+01	2.51E-04	3.09E-04	2.30E+00	1.20E+00	2.30E+00	1.16E+00	5.04E-01
CRISPLD1	5.56E+02	2.51E-04	3.09E-04	1.62E+00	6.98E-01	1.62E+00	3.55E+01	2.19E+01
KYNU	5.40E+00	2.51E-04	3.09E-04	2.53E+00	1.34E+00	2.53E+00	3.94E-01	1.56E-01

XR_003032631.	5.79E+01	2.56E-04	3.15E-04	2.08E+00	1.06E+00	2.08E+00	4.01E+00	1.93E+00
LRP1	2.29E+04	2.59E-04	3.18E-04	1.61E+00	6.89E-01	1.61E+00	1.46E+03	9.08E+02
XR_003037488.	3.87E+00	2.63E-04	3.23E-04	5.85E+00	2.55E+00	5.85E+00	3.36E-01	5.74E-02
LOC104972581	7.27E+00	2.64E-04	3.23E-04	3.96E+00	1.98E+00	3.96E+00	5.93E-01	1.50E-01
XR_001494799.	7.58E+01	2.64E-04	3.23E-04	1.73E+00	7.93E-01	1.73E+00	4.95E+00	2.85E+00
IFNGR1	1.19E+03	2.84E-04	3.48E-04	1.35E+00	4.36E-01	1.35E+00	7.10E+01	5.25E+01
SNED1	9.64E+02	2.84E-04	3.48E-04	1.91E+00	9.34E-01	1.91E+00	6.49E+01	3.40E+01
XR_001500471.	7.28E+00	2.92E-04	3.57E-04	3.35E+00	1.74E+00	3.35E+00	5.69E-01	1.70E-01
XR_001494474.	6.28E+01	2.92E-04	3.57E-04	1.47E+00	5.53E-01	1.47E+00	3.87E+00	2.64E+00
XR_003031034.	6.03E+00	2.96E-04	3.62E-04	1.22E+01	3.60E+00	1.22E+01	5.60E-01	4.61E-02
LOC100298573	6.83E+00	2.98E-04	3.64E-04	5.06E+00	2.34E+00	5.06E+00	5.73E-01	1.13E-01
XR_003033297.	6.20E+01	3.03E-04	3.69E-04	1.58E+00	6.61E-01	1.58E+00	3.94E+00	2.49E+00
SLC25A45	2.98E+01	3.21E-04	3.91E-04	1.95E+00	9.61E-01	1.95E+00	2.02E+00	1.04E+00
XR_003030781.	1.33E+01	3.23E-04	3.94E-04	1.51E+01	3.92E+00	1.51E+01	1.25E+00	8.30E-02
C11H2orf42	2.91E+02	3.23E-04	3.94E-04	1.32E+00	4.01E-01	1.32E+00	1.73E+01	1.31E+01
MYOZ3	4.02E+01	3.33E-04	4.05E-04	1.89E+00	9.21E-01	1.89E+00	2.72E+00	1.44E+00
XR_003037518.	5.36E+01	3.48E-04	4.22E-04	2.19E+00	1.13E+00	2.19E+00	3.77E+00	1.72E+00
XR_003037599.	1.08E+02	3.48E-04	4.22E-04	2.23E+00	1.15E+00	2.23E+00	7.69E+00	3.45E+00
NFIX	3.56E+03	3.48E-04	4.22E-04	1.67E+00	7.39E-01	1.67E+00	2.28E+02	1.37E+02
SLC18B1	2.57E+02	3.51E-04	4.26E-04	1.34E+00	4.25E-01	1.34E+00	1.53E+01	1.14E+01
XR_003033394.	4.99E+01	3.51E-04	4.26E-04	1.56E+00	6.38E-01	1.56E+00	3.14E+00	2.02E+00
LOC100140085	1.21E+01	3.70E-04	4.49E-04	2.15E+00	1.10E+00	2.15E+00	8.40E-01	3.91E-01
ZNF260	7.05E+02	3.73E-04	4.51E-04	1.29E+00	3.64E-01	1.29E+00	4.15E+01	3.23E+01
LOC112446390	4.05E+01	3.87E-04	4.68E-04	1.75E+00	8.10E-01	1.75E+00	2.65E+00	1.51E+00
SEC62	2.65E+03	3.93E-04	4.76E-04	1.24E+00	3.16E-01	1.24E+00	1.54E+02	1.23E+02
CAV3	5.47E+00	3.99E-04	4.83E-04	1.75E+01	4.13E+00	1.75E+01	5.19E-01	2.96E-02
XR_003029487.	6.59E+01	4.00E-04	4.83E-04	1.52E+00	6.01E-01	1.52E+00	4.12E+00	2.72E+00
LRP3	4.36E+02	4.16E-04	5.02E-04	1.36E+00	4.40E-01	1.36E+00	2.61E+01	1.92E+01
ZBTB21	3.93E+02	4.17E-04	5.03E-04	1.75E+00	8.11E-01	1.75E+00	2.58E+01	1.47E+01
XR_236157.4	8.28E+00	4.27E-04	5.15E-04	2.70E+00	1.43E+00	2.70E+00	6.14E-01	2.27E-01
XR_236815.3	4.28E+01	4.28E-04	5.15E-04	1.61E+00	6.87E-01	1.61E+00	2.74E+00	1.70E+00
MARVELD1	3.35E+03	4.44E-04	5.34E-04	1.25E+00	3.18E-01	1.25E+00	1.94E+02	1.56E+02
RASL11A	1.45E+02	4.48E-04	5.38E-04	2.08E+00	1.06E+00	2.08E+00	1.02E+01	4.89E+00

GK	5.80E+01	4.56E-04	5.47E-04	1.46E+00	5.49E-01	1.46E+00	3.57E+00	2.44E+00
LOC104970812	1.14E+01	4.56E-04	5.47E-04	2.07E+00	1.05E+00	2.07E+00	7.86E-01	3.79E-01
USP47	1.83E+03	4.63E-04	5.56E-04	1.27E+00	3.48E-01	1.27E+00	1.07E+02	8.44E+01
COL27A1	9.42E+03	4.71E-04	5.65E-04	1.53E+00	6.12E-01	1.53E+00	5.92E+02	3.87E+02
XR_001500965.2	4.33E+01	4.73E-04	5.67E-04	3.93E+00	1.97E+00	3.93E+00	3.51E+00	8.93E-01
XR_003036642.1	6.98E+01	4.76E-04	5.71E-04	1.74E+00	8.02E-01	1.74E+00	4.61E+00	2.65E+00
TNFSF15	4.58E+00	4.80E-04	5.74E-04	1.31E+01	3.71E+00	1.31E+01	4.27E-01	3.26E-02
GPR137B	1.10E+02	4.88E-04	5.83E-04	1.52E+00	6.02E-01	1.52E+00	6.87E+00	4.53E+00
LOC101903205	4.52E+02	4.89E-04	5.84E-04	1.46E+00	5.49E-01	1.46E+00	2.80E+01	1.91E+01
XR_003033186.1	7.93E+00	4.95E-04	5.91E-04	1.28E+01	3.68E+00	1.28E+01	7.43E-01	5.79E-02
LOC112444193	3.92E+00	5.00E-04	5.96E-04	5.54E+00	2.47E+00	5.54E+00	3.33E-01	6.02E-02
TMEM154	2.09E+02	5.12E-04	6.11E-04	1.90E+00	9.23E-01	1.90E+00	1.41E+01	7.45E+00
XR_003030684.1	1.11E+02	5.13E-04	6.11E-04	1.49E+00	5.73E-01	1.49E+00	6.87E+00	4.61E+00
XR_239312.4	2.10E+02	5.18E-04	6.17E-04	1.48E+00	5.61E-01	1.48E+00	1.30E+01	8.79E+00
XR_003029544.1	6.21E+00	5.23E-04	6.22E-04	2.97E+00	1.57E+00	2.97E+00	4.75E-01	1.60E-01
YAF2	3.15E+02	5.24E-04	6.23E-04	1.31E+00	3.93E-01	1.31E+00	1.87E+01	1.42E+01
RINT1	4.24E+02	5.28E-04	6.28E-04	1.25E+00	3.17E-01	1.25E+00	2.47E+01	1.98E+01
PKD1	6.03E+03	5.36E-04	6.36E-04	1.42E+00	5.08E-01	1.42E+00	3.68E+02	2.59E+02
LYZ2	4.45E+00	5.50E-04	6.53E-04	4.79E+00	2.26E+00	4.79E+00	3.70E-01	7.73E-02
SORCS2	7.35E+02	5.54E-04	6.58E-04	1.82E+00	8.61E-01	1.82E+00	4.87E+01	2.68E+01
XR_805792.3	2.07E+01	5.66E-04	6.71E-04	1.36E+01	3.77E+00	1.36E+01	1.94E+00	1.42E-01
SLC25A41	1.79E+01	5.67E-04	6.72E-04	1.84E+00	8.79E-01	1.84E+00	1.19E+00	6.48E-01
AMMECR1	4.73E+01	5.69E-04	6.74E-04	1.36E+01	3.76E+00	1.36E+01	4.43E+00	3.26E-01
LOC100848799	5.36E+01	5.84E-04	6.91E-04	1.76E+00	8.18E-01	1.76E+00	3.54E+00	2.01E+00
FAM46A	9.98E+02	5.88E-04	6.96E-04	1.89E+00	9.17E-01	1.89E+00	6.77E+01	3.58E+01
LST1	8.04E+01	6.08E-04	7.18E-04	1.81E+00	8.55E-01	1.81E+00	5.32E+00	2.94E+00
XR_003037770.1	4.47E+00	6.12E-04	7.22E-04	5.19E+00	2.37E+00	5.19E+00	3.76E-01	7.26E-02
CTCF	2.26E+03	6.12E-04	7.23E-04	1.21E+00	2.76E-01	1.21E+00	1.29E+02	1.07E+02
ZYG11B	7.10E+02	6.54E-04	7.71E-04	1.25E+00	3.23E-01	1.25E+00	4.14E+01	3.31E+01
CCDC71L	4.32E+02	6.67E-04	7.86E-04	1.52E+00	6.03E-01	1.52E+00	2.70E+01	1.78E+01
XR_003030810.1	1.83E+02	6.78E-04	7.98E-04	1.46E+00	5.41E-01	1.46E+00	1.13E+01	7.79E+00
XR_001494366.2	1.16E+01	6.78E-04	7.99E-04	2.70E+00	1.43E+00	2.70E+00	8.63E-01	3.20E-01
CA4	4.53E+01	6.96E-04	8.19E-04	1.08E+01	3.44E+00	1.08E+01	4.20E+00	3.88E-01

KCTD18	2.86E+02	7.01E-04	8.24E-04	1.29E+00	3.64E-01	1.29E+00	1.68E+01	1.30E+01
TTC14	8.21E+02	7.01E-04	8.24E-04	1.27E+00	3.46E-01	1.27E+00	4.81E+01	3.78E+01
XR_815663.3	9.06E+00	7.17E-04	8.42E-04	1.16E+01	3.54E+00	1.16E+01	8.40E-01	7.22E-02
R_003030780.	4.31E+01	7.32E-04	8.59E-04	1.95E+00	9.65E-01	1.95E+00	2.95E+00	1.51E+00
R_003034594.	9.32E+01	7.43E-04	8.72E-04	1.47E+00	5.57E-01	1.47E+00	5.77E+00	3.92E+00
R_003029776.	1.21E+01	7.48E-04	8.77E-04	3.36E+00	1.75E+00	3.36E+00	9.49E-01	2.83E-01
XR_236050.4	1.82E+02	7.63E-04	8.94E-04	1.37E+00	4.53E-01	1.37E+00	1.09E+01	7.98E+00
GAPVD1	5.98E+02	7.65E-04	8.95E-04	1.37E+00	4.53E-01	1.37E+00	3.61E+01	2.63E+01
R_003029526.	4.13E+01	7.87E-04	9.20E-04	2.03E+00	1.02E+00	2.03E+00	2.83E+00	1.39E+00
R_003029816.	8.83E+00	7.91E-04	9.24E-04	7.01E+00	2.81E+00	7.01E+00	7.84E-01	1.12E-01
LOC112443452	2.60E+03	8.09E-04	9.45E-04	1.28E+00	3.58E-01	1.28E+00	1.53E+02	1.19E+02
MTAP	4.64E+02	8.18E-04	9.54E-04	1.21E+00	2.72E-01	1.21E+00	2.66E+01	2.20E+01
R_003035399.	3.56E+00	8.25E-04	9.62E-04	7.03E+00	2.81E+00	7.03E+00	3.13E-01	4.45E-02
R_003030885.	1.29E+01	8.34E-04	9.73E-04	2.42E+00	1.27E+00	2.42E+00	9.47E-01	3.91E-01
MEIS3	1.25E+03	8.37E-04	9.75E-04	1.43E+00	5.15E-01	1.43E+00	7.65E+01	5.35E+01
LOC101905723	6.63E+00	8.44E-04	9.82E-04	2.52E+00	1.33E+00	2.52E+00	4.85E-01	1.92E-01
R_003034308.	1.99E+00	8.51E-04	9.90E-04	6.24E+00	2.64E+00	6.24E+00	1.71E-01	2.75E-02
R_003030580.	1.29E+01	8.52E-04	9.91E-04	7.40E+00	2.89E+00	7.40E+00	1.14E+00	1.55E-01
CAPRIN1	6.20E+03	8.61E-04	1.00E-03	1.24E+00	3.14E-01	1.24E+00	3.60E+02	2.90E+02
R_003034186.	2.25E+00	8.67E-04	1.01E-03	7.81E+00	2.97E+00	7.81E+00	2.03E-01	2.59E-02
ACAN	1.08E+02	8.73E-04	1.01E-03	3.30E+00	1.72E+00	3.30E+00	8.39E+00	2.54E+00
XR_814919.2	1.75E+02	8.79E-04	1.02E-03	2.32E+00	1.21E+00	2.32E+00	1.25E+01	5.41E+00
ZBED5	9.94E+02	8.96E-04	1.04E-03	1.26E+00	3.38E-01	1.26E+00	5.80E+01	4.59E+01
EPHB3	9.32E+02	9.07E-04	1.05E-03	1.60E+00	6.76E-01	1.60E+00	5.98E+01	3.74E+01
METAP1	2.77E+02	9.15E-04	1.06E-03	1.63E+00	7.02E-01	1.63E+00	1.78E+01	1.09E+01
CYSLTR2	9.93E+00	9.60E-04	1.11E-03	7.72E+00	2.95E+00	7.72E+00	8.92E-01	1.16E-01
R_003030074.	6.17E+01	9.66E-04	1.12E-03	3.20E+00	1.68E+00	3.20E+00	4.71E+00	1.47E+00
LOC789799	1.29E+00	9.76E-04	1.13E-03	1.85E+01	4.21E+00	1.85E+01	1.23E-01	6.64E-03
HGF	1.59E+02	9.93E-04	1.15E-03	2.57E+00	1.36E+00	2.57E+00	1.17E+01	4.57E+00
GTF2IRD2	9.89E+02	1.01E-03	1.17E-03	1.20E+00	2.68E-01	1.20E+00	5.67E+01	4.71E+01
LOC100849050	2.75E+01	1.04E-03	1.19E-03	1.59E+00	6.65E-01	1.59E+00	1.75E+00	1.10E+00
XR_240630.4	3.38E+01	1.05E-03	1.21E-03	3.66E+00	1.87E+00	3.66E+00	2.72E+00	7.43E-01
CPNE6	7.76E+00	1.06E-03	1.22E-03	4.91E+00	2.30E+00	4.91E+00	6.54E-01	1.33E-01

KIAA1614	7.00E+02	1.08E-03	1.24E-03	1.35E+00	4.35E-01	1.35E+00	4.19E+01	3.10E+01
ENOSF1	2.11E+02	1.08E-03	1.24E-03	1.29E+00	3.64E-01	1.29E+00	1.23E+01	9.55E+00
XR_003036622.	2.69E+01	1.08E-03	1.24E-03	9.59E+00	3.26E+00	9.59E+00	2.45E+00	2.55E-01
TOP2B	3.60E+03	1.09E-03	1.25E-03	1.28E+00	3.57E-01	1.28E+00	2.12E+02	1.65E+02
XR_003029837.	3.86E+00	1.10E-03	1.26E-03	3.16E+00	1.66E+00	3.16E+00	3.01E-01	9.53E-02
UNKL	7.60E+02	1.11E-03	1.28E-03	1.44E+00	5.31E-01	1.44E+00	4.66E+01	3.22E+01
LOC112447863	1.31E+00	1.13E-03	1.30E-03	1.26E+01	3.66E+00	1.26E+01	1.21E-01	9.62E-03
XR_813886.3	1.25E+01	1.13E-03	1.30E-03	4.40E+00	2.14E+00	4.40E+00	1.03E+00	2.34E-01
RNF14	6.44E+02	1.17E-03	1.34E-03	1.22E+00	2.85E-01	1.22E+00	3.68E+01	3.02E+01
XR_003029580.	1.09E+02	1.17E-03	1.34E-03	8.35E+00	3.06E+00	8.35E+00	9.82E+00	1.18E+00
USP54	7.50E+02	1.20E-03	1.37E-03	1.26E+00	3.32E-01	1.26E+00	4.37E+01	3.47E+01
XR_003037505.	3.83E+01	1.22E-03	1.39E-03	2.93E+00	1.55E+00	2.93E+00	2.93E+00	9.98E-01
LOC112444775	2.90E+01	1.24E-03	1.41E-03	1.74E+00	7.95E-01	1.74E+00	1.90E+00	1.10E+00
SMUG1	1.19E+03	1.24E-03	1.42E-03	1.20E+00	2.62E-01	1.20E+00	6.81E+01	5.68E+01
NRAS	9.42E+02	1.26E-03	1.44E-03	1.22E+00	2.84E-01	1.22E+00	5.42E+01	4.45E+01
MYH9	1.66E+04	1.27E-03	1.45E-03	1.28E+00	3.52E-01	1.28E+00	9.72E+02	7.61E+02
XR_003037516.	6.82E+01	1.28E-03	1.46E-03	1.86E+00	8.97E-01	1.86E+00	4.55E+00	2.44E+00
RBM43	5.99E+02	1.37E-03	1.56E-03	1.34E+00	4.20E-01	1.34E+00	3.57E+01	2.67E+01
GPR141	2.52E+00	1.37E-03	1.56E-03	5.31E+00	2.41E+00	5.31E+00	2.14E-01	4.03E-02
XR_003030194.	1.10E+02	1.38E-03	1.56E-03	1.67E+00	7.41E-01	1.67E+00	7.09E+00	4.24E+00
NDRG4	5.14E+02	1.42E-03	1.61E-03	1.70E+00	7.63E-01	1.70E+00	3.36E+01	1.98E+01
XR_236092.4	1.54E+03	1.43E-03	1.62E-03	1.25E+00	3.20E-01	1.25E+00	8.91E+01	7.14E+01
BCLAF1	2.47E+03	1.43E-03	1.62E-03	1.28E+00	3.58E-01	1.28E+00	1.45E+02	1.13E+02
ZBED3	3.57E+03	1.46E-03	1.65E-03	1.65E+00	7.24E-01	1.65E+00	2.30E+02	1.39E+02
FUT10	1.44E+02	1.46E-03	1.66E-03	1.35E+00	4.31E-01	1.35E+00	8.59E+00	6.37E+00
XR_003030043.	2.09E+01	1.47E-03	1.67E-03	2.13E+00	1.09E+00	2.13E+00	1.45E+00	6.83E-01
XR_805839.3	1.09E+01	1.48E-03	1.67E-03	2.00E+00	9.98E-01	2.00E+00	7.47E-01	3.74E-01
LOC783920	4.04E+01	1.55E-03	1.75E-03	2.90E+00	1.54E+00	2.90E+00	3.01E+00	1.04E+00
XR_808417.3	4.14E+00	1.56E-03	1.76E-03	2.24E+00	1.17E+00	2.24E+00	2.93E-01	1.30E-01
XR_001495436.	2.48E+00	1.57E-03	1.77E-03	5.71E+00	2.51E+00	5.71E+00	2.13E-01	3.73E-02
SMIM33	2.10E+01	1.57E-03	1.78E-03	1.94E+00	9.59E-01	1.94E+00	1.44E+00	7.38E-01
XR_236236.4	4.30E+02	1.57E-03	1.78E-03	1.25E+00	3.20E-01	1.25E+00	2.50E+01	2.00E+01
GAS2	7.27E+01	1.62E-03	1.82E-03	1.56E+00	6.43E-01	1.56E+00	4.58E+00	2.93E+00

SYNJ2BP	3.76E+02	1.65E-03	1.86E-03	1.18E+00	2.44E-01	1.18E+00	2.14E+01	1.80E+01
LOC112445190	1.54E+01	1.66E-03	1.87E-03	2.36E+00	1.24E+00	2.36E+00	1.10E+00	4.67E-01
SERINC1	2.64E+03	1.72E-03	1.93E-03	1.21E+00	2.72E-01	1.21E+00	1.51E+02	1.25E+02
AMN1	6.41E+02	1.76E-03	1.98E-03	1.34E+00	4.24E-01	1.34E+00	3.83E+01	2.85E+01
FBXW7	7.93E+02	1.76E-03	1.98E-03	1.37E+00	4.52E-01	1.37E+00	4.75E+01	3.47E+01
XR_813457.3	8.85E+01	1.77E-03	1.99E-03	2.17E+00	1.12E+00	2.17E+00	6.21E+00	2.86E+00
TTLL3	5.84E+02	1.78E-03	2.00E-03	1.28E+00	3.61E-01	1.28E+00	3.42E+01	2.66E+01
XR_003032003.	1.41E+01	1.85E-03	2.07E-03	2.39E+00	1.26E+00	2.39E+00	1.02E+00	4.27E-01
TTBK2	5.65E+02	1.85E-03	2.08E-03	1.26E+00	3.30E-01	1.26E+00	3.29E+01	2.61E+01
LOC519309	1.38E+01	1.87E-03	2.10E-03	1.79E+00	8.41E-01	1.79E+00	9.15E-01	5.11E-01
XR_233395.4	3.47E+01	1.91E-03	2.14E-03	1.92E+00	9.41E-01	1.92E+00	2.35E+00	1.23E+00
XR_240511.4	2.94E+01	1.92E-03	2.15E-03	1.97E+00	9.77E-01	1.97E+00	2.01E+00	1.02E+00
RGS18	6.69E+00	1.94E-03	2.17E-03	2.11E+00	1.08E+00	2.11E+00	4.66E-01	2.21E-01
FAM133B	4.39E+02	1.97E-03	2.20E-03	1.21E+00	2.72E-01	1.21E+00	2.51E+01	2.08E+01
SH3PXD2B	3.08E+03	1.99E-03	2.23E-03	1.35E+00	4.33E-01	1.35E+00	1.85E+02	1.37E+02
NEU3	4.25E+02	2.02E-03	2.25E-03	1.27E+00	3.46E-01	1.27E+00	2.47E+01	1.94E+01
DDX42	2.97E+03	2.09E-03	2.33E-03	1.15E+00	1.99E-01	1.15E+00	1.66E+02	1.45E+02
LOC112442704	1.04E+01	2.11E-03	2.35E-03	6.75E+00	2.76E+00	6.75E+00	9.16E-01	1.36E-01
CEBPZ	1.76E+03	2.13E-03	2.38E-03	1.16E+00	2.12E-01	1.16E+00	9.94E+01	8.59E+01
LOC101907083	5.01E+02	2.14E-03	2.39E-03	1.24E+00	3.14E-01	1.24E+00	2.91E+01	2.34E+01
PLXND1	4.80E+03	2.16E-03	2.40E-03	1.28E+00	3.51E-01	1.28E+00	2.82E+02	2.21E+02
EMP2	2.61E+03	2.18E-03	2.43E-03	1.28E+00	3.58E-01	1.28E+00	1.53E+02	1.20E+02
GPLD1	1.38E+01	2.19E-03	2.43E-03	4.43E+00	2.15E+00	4.43E+00	1.13E+00	2.56E-01
OPCML	1.28E+02	2.21E-03	2.45E-03	5.62E+00	2.49E+00	5.62E+00	1.10E+01	1.95E+00
PCDHB8	1.23E+02	2.22E-03	2.46E-03	1.55E+00	6.33E-01	1.55E+00	7.78E+00	5.01E+00
GRIP2	2.01E+02	2.22E-03	2.46E-03	2.10E+00	1.07E+00	2.10E+00	1.40E+01	6.67E+00
DUSP3	5.82E+02	2.23E-03	2.47E-03	1.22E+00	2.90E-01	1.22E+00	3.35E+01	2.74E+01
RAB2B	5.83E+02	2.23E-03	2.47E-03	1.19E+00	2.50E-01	1.19E+00	3.30E+01	2.78E+01
XR_233521.4	1.02E+02	2.26E-03	2.50E-03	1.70E+00	7.69E-01	1.70E+00	6.64E+00	3.89E+00
NFIC	4.84E+03	2.31E-03	2.55E-03	1.33E+00	4.16E-01	1.33E+00	2.88E+02	2.16E+02
XR_003030102.	1.62E+01	2.32E-03	2.56E-03	1.83E+00	8.71E-01	1.83E+00	1.08E+00	5.89E-01
XR_003031758.	4.87E+02	2.43E-03	2.69E-03	1.28E+00	3.55E-01	1.28E+00	2.85E+01	2.23E+01
EML3	1.59E+03	2.45E-03	2.70E-03	1.18E+00	2.34E-01	1.18E+00	8.98E+01	7.64E+01

IL1RL1	6.75E+00	2.50E-03	2.75E-03	2.42E+00	1.27E+00	2.42E+00	4.94E-01	2.04E-01
XR_003030756.1	4.12E+01	2.51E-03	2.77E-03	1.75E+00	8.05E-01	1.75E+00	2.71E+00	1.55E+00
MRC2	1.37E+04	2.53E-03	2.79E-03	1.32E+00	3.97E-01	1.32E+00	8.15E+02	6.19E+02
C19H17orf113	1.99E+02	2.56E-03	2.82E-03	1.29E+00	3.62E-01	1.29E+00	1.17E+01	9.07E+00
XR_003033860.1	1.76E+01	2.62E-03	2.89E-03	4.11E+00	2.04E+00	4.11E+00	1.43E+00	3.47E-01
XR_814092.3	6.58E+01	2.72E-03	2.99E-03	1.49E+00	5.77E-01	1.49E+00	4.08E+00	2.74E+00
GNAT2	1.38E+01	2.75E-03	3.02E-03	1.98E+00	9.86E-01	1.98E+00	9.48E-01	4.79E-01
LOC112448540	1.61E+01	2.77E-03	3.04E-03	4.51E+00	2.17E+00	4.51E+00	1.33E+00	2.96E-01
XR_234798.4	2.24E+01	2.78E-03	3.05E-03	3.94E+00	1.98E+00	3.94E+00	1.80E+00	4.58E-01
XR_003037247.1	4.12E+01	2.81E-03	3.08E-03	1.64E+00	7.13E-01	1.64E+00	2.65E+00	1.62E+00
XR_001494379.1	2.06E+02	2.87E-03	3.15E-03	1.43E+00	5.11E-01	1.43E+00	1.26E+01	8.81E+00
XR_003035349.1	2.07E+01	2.94E-03	3.22E-03	1.74E+00	7.98E-01	1.74E+00	1.36E+00	7.83E-01
XR_003031251.1	5.11E+00	2.98E-03	3.26E-03	2.12E+00	1.09E+00	2.12E+00	3.59E-01	1.69E-01
FAM170B	7.59E+00	3.01E-03	3.29E-03	4.78E+00	2.26E+00	4.78E+00	6.33E-01	1.32E-01
CCDC174	4.78E+02	3.02E-03	3.30E-03	1.20E+00	2.58E-01	1.20E+00	2.73E+01	2.28E+01
XR_003037207.1	2.46E+00	3.05E-03	3.33E-03	1.26E+01	3.65E+00	1.26E+01	2.29E-01	1.82E-02
XR_003038092.1	2.04E+01	3.10E-03	3.39E-03	1.86E+00	8.99E-01	1.86E+00	1.37E+00	7.36E-01
XR_003033129.1	1.70E+01	3.11E-03	3.39E-03	6.56E+00	2.71E+00	6.56E+00	1.48E+00	2.26E-01
HOXA6	2.47E+02	3.12E-03	3.40E-03	2.55E+00	1.35E+00	2.55E+00	1.82E+01	7.13E+00
NDRG2	2.25E+03	3.21E-03	3.50E-03	1.35E+00	4.35E-01	1.35E+00	1.35E+02	9.95E+01
XR_003029542.1	2.81E+00	3.23E-03	3.52E-03	5.95E+00	2.57E+00	5.95E+00	2.44E-01	4.10E-02
LARGE1	9.37E+02	3.30E-03	3.59E-03	1.17E+00	2.22E-01	1.17E+00	5.26E+01	4.51E+01
XR_003037763.1	5.66E+00	3.41E-03	3.71E-03	2.13E+00	1.09E+00	2.13E+00	3.98E-01	1.87E-01
IL1RAPL1	2.58E+00	3.51E-03	3.82E-03	2.79E+00	1.48E+00	2.79E+00	1.94E-01	6.96E-02
XR_239993.4	3.33E+01	3.61E-03	3.93E-03	1.66E+00	7.34E-01	1.66E+00	2.16E+00	1.30E+00
PARD6G	3.30E+02	3.62E-03	3.94E-03	1.29E+00	3.64E-01	1.29E+00	1.94E+01	1.51E+01
LOC101906315	1.16E+01	3.64E-03	3.95E-03	1.96E+00	9.71E-01	1.96E+00	7.89E-01	4.03E-01
XR_810846.3	5.34E+00	3.65E-03	3.96E-03	5.28E+00	2.40E+00	5.28E+00	4.54E-01	8.60E-02
LOC100300896	4.87E+02	3.67E-03	3.98E-03	2.21E+00	1.14E+00	2.21E+00	3.43E+01	1.55E+01
MPZL1	2.66E+03	3.68E-03	3.99E-03	1.17E+00	2.22E-01	1.17E+00	1.50E+02	1.28E+02
XR_003036097.1	4.77E+01	3.77E-03	4.08E-03	2.08E+00	1.05E+00	2.08E+00	3.32E+00	1.60E+00
LOC789035	5.98E+00	3.79E-03	4.10E-03	4.12E+00	2.04E+00	4.12E+00	4.89E-01	1.18E-01
XR_814093.3	9.30E+01	3.89E-03	4.21E-03	1.39E+00	4.73E-01	1.39E+00	5.60E+00	4.04E+00

XR_003032809.1	7.44E+00	3.91E-03	4.22E-03	3.64E+00	1.87E+00	3.64E+00	5.93E-01	1.63E-01
TEP1	7.34E+02	4.04E-03	4.37E-03	1.34E+00	4.21E-01	1.34E+00	4.39E+01	3.28E+01
RIT1	1.05E+03	4.07E-03	4.39E-03	1.15E+00	2.05E-01	1.15E+00	5.88E+01	5.10E+01
XR_003035990.1	7.62E+00	4.20E-03	4.53E-03	7.25E+00	2.86E+00	7.25E+00	6.76E-01	9.32E-02
MXRA5	7.06E+03	4.20E-03	4.53E-03	1.87E+00	9.06E-01	1.87E+00	4.73E+02	2.53E+02
MEIS2	8.33E+02	4.32E-03	4.66E-03	1.54E+00	6.24E-01	1.54E+00	5.25E+01	3.41E+01
XR_806997.3	1.34E+01	4.36E-03	4.69E-03	1.74E+00	8.01E-01	1.74E+00	8.71E-01	5.00E-01
XR_003036120.1	2.35E+01	4.37E-03	4.71E-03	1.42E+00	5.10E-01	1.42E+00	1.44E+00	1.01E+00
VIRMA	2.31E+03	4.42E-03	4.76E-03	1.17E+00	2.30E-01	1.17E+00	1.30E+02	1.11E+02
XR_003036064.1	5.76E+00	4.53E-03	4.87E-03	3.05E+00	1.61E+00	3.05E+00	4.39E-01	1.44E-01
XR_003033866.1	1.75E+02	4.55E-03	4.89E-03	1.42E+00	5.03E-01	1.42E+00	1.07E+01	7.55E+00
XR_003029505.1	6.53E+00	4.70E-03	5.05E-03	1.30E+01	3.70E+00	1.30E+01	6.11E-01	4.71E-02
PDGFRB	6.72E+03	4.73E-03	5.08E-03	1.33E+00	4.06E-01	1.33E+00	4.00E+02	3.02E+02
ANKRD42	2.21E+02	4.83E-03	5.18E-03	1.38E+00	4.69E-01	1.38E+00	1.33E+01	9.60E+00
MYEF2	1.33E+03	4.92E-03	5.27E-03	1.22E+00	2.84E-01	1.22E+00	7.63E+01	6.26E+01
XR_003032941.1	6.06E+00	4.99E-03	5.35E-03	4.47E+00	2.16E+00	4.47E+00	4.98E-01	1.11E-01
XR_003031472.1	2.28E+00	5.32E-03	5.69E-03	2.63E+00	1.40E+00	2.63E+00	1.67E-01	6.36E-02
ANKRD13A	1.17E+03	5.32E-03	5.69E-03	1.16E+00	2.11E-01	1.16E+00	6.57E+01	5.67E+01
XR_003035229.1	3.59E+00	5.49E-03	5.87E-03	4.56E+00	2.19E+00	4.56E+00	3.00E-01	6.58E-02
GCSAML	3.66E+00	5.58E-03	5.97E-03	1.00E+01	3.33E+00	1.00E+01	3.36E-01	3.35E-02
LOC616094	6.26E+00	5.60E-03	5.99E-03	2.67E+00	1.42E+00	2.67E+00	4.65E-01	1.74E-01
XR_808632.3	6.00E+00	5.94E-03	6.34E-03	4.22E+00	2.08E+00	4.22E+00	4.90E-01	1.16E-01
LOC112447438	5.65E+00	5.97E-03	6.37E-03	2.91E+00	1.54E+00	2.91E+00	4.24E-01	1.46E-01
XR_813935.3	3.79E+01	6.06E-03	6.46E-03	2.00E+00	1.00E+00	2.00E+00	2.64E+00	1.32E+00
C1H21orf91	6.85E+02	6.15E-03	6.55E-03	1.34E+00	4.24E-01	1.34E+00	4.12E+01	3.07E+01
MMP16	7.42E+02	6.25E-03	6.66E-03	1.99E+00	9.94E-01	1.99E+00	5.08E+01	2.55E+01
IFT52	4.93E+02	6.28E-03	6.69E-03	1.15E+00	1.99E-01	1.15E+00	2.75E+01	2.40E+01
NEURL3	3.24E+01	6.32E-03	6.73E-03	1.66E+00	7.35E-01	1.66E+00	2.08E+00	1.25E+00
LOC107131660	2.88E+01	6.38E-03	6.78E-03	3.11E+00	1.64E+00	3.11E+00	2.21E+00	7.11E-01
DACT3	6.58E+02	6.38E-03	6.78E-03	1.30E+00	3.75E-01	1.30E+00	3.89E+01	3.00E+01
XR_003029509.1	2.55E+00	6.49E-03	6.89E-03	3.76E+00	1.91E+00	3.76E+00	2.04E-01	5.44E-02
GPALPP1	6.23E+02	6.56E-03	6.97E-03	1.21E+00	2.72E-01	1.21E+00	3.56E+01	2.95E+01
OTOP1	3.49E+01	6.71E-03	7.12E-03	1.81E+00	8.55E-01	1.81E+00	2.32E+00	1.28E+00

ACAD10	7.44E+02	6.76E-03	7.17E-03	1.19E+00	2.51E-01	1.19E+00	4.23E+01	3.55E+01
TMEM138	7.30E+02	6.80E-03	7.20E-03	1.27E+00	3.42E-01	1.27E+00	4.27E+01	3.37E+01
NR_031314.1	5.83E+00	6.86E-03	7.27E-03	1.07E+01	3.42E+00	1.07E+01	5.35E-01	5.01E-02
KR_003030613.	3.26E+00	7.05E-03	7.46E-03	2.38E+00	1.25E+00	2.38E+00	2.35E-01	9.89E-02
RAB44	4.69E+00	7.17E-03	7.59E-03	3.59E+00	1.85E+00	3.59E+00	3.78E-01	1.05E-01
KR_003029600.	2.86E+02	7.19E-03	7.60E-03	1.63E+00	7.09E-01	1.63E+00	1.84E+01	1.12E+01
KR_001502300.	6.62E+00	7.30E-03	7.71E-03	4.17E+00	2.06E+00	4.17E+00	5.41E-01	1.30E-01
KR_003033489.	4.27E+00	7.42E-03	7.83E-03	4.57E+00	2.19E+00	4.57E+00	3.56E-01	7.79E-02
LOC100847546	1.46E+01	7.52E-03	7.93E-03	1.65E+00	7.21E-01	1.65E+00	9.44E-01	5.73E-01
XR_238184.4	3.31E+00	7.70E-03	8.12E-03	5.77E+00	2.53E+00	5.77E+00	2.83E-01	4.90E-02
LOC781778	9.48E+00	7.71E-03	8.12E-03	1.93E+00	9.48E-01	1.93E+00	6.42E-01	3.33E-01
NOVA2	1.13E+02	7.83E-03	8.25E-03	1.29E+00	3.69E-01	1.29E+00	6.66E+00	5.16E+00
KR_003033961.	3.16E+00	7.84E-03	8.25E-03	2.94E+00	1.55E+00	2.94E+00	2.40E-01	8.16E-02
ATXN7L3B	2.46E+03	7.98E-03	8.40E-03	1.18E+00	2.34E-01	1.18E+00	1.39E+02	1.18E+02
DIP2B	6.60E+02	8.04E-03	8.45E-03	1.34E+00	4.20E-01	1.34E+00	3.95E+01	2.95E+01
KR_003037126.	1.07E+01	8.35E-03	8.78E-03	3.11E+00	1.63E+00	3.11E+00	8.22E-01	2.65E-01
JCAD	1.95E+03	8.51E-03	8.94E-03	1.32E+00	4.01E-01	1.32E+00	1.16E+02	8.76E+01
PRELP	8.02E+03	8.54E-03	8.96E-03	1.72E+00	7.85E-01	1.72E+00	5.23E+02	3.03E+02
FAM196A	1.62E+02	8.70E-03	9.12E-03	1.43E+00	5.14E-01	1.43E+00	9.90E+00	6.93E+00
FBLN1	2.27E+04	8.84E-03	9.27E-03	1.64E+00	7.12E-01	1.64E+00	1.46E+03	8.89E+02
ZBED8	5.06E+02	9.15E-03	9.58E-03	1.17E+00	2.22E-01	1.17E+00	2.86E+01	2.45E+01
KRT24	1.66E+01	9.26E-03	9.69E-03	3.77E+00	1.92E+00	3.77E+00	1.33E+00	3.52E-01
DYRK1A	1.76E+03	9.39E-03	9.83E-03	1.21E+00	2.71E-01	1.21E+00	1.01E+02	8.37E+01
ZNF614	1.94E+02	9.44E-03	9.87E-03	1.26E+00	3.38E-01	1.26E+00	1.13E+01	8.95E+00
KR_003031776.	1.17E+01	9.44E-03	9.87E-03	1.90E+00	9.27E-01	1.90E+00	7.99E-01	4.20E-01
METTL15	1.55E+02	9.71E-03	1.01E-02	1.21E+00	2.76E-01	1.21E+00	8.86E+00	7.32E+00
KR_003035129.	3.13E+01	9.98E-03	1.04E-02	1.66E+00	7.32E-01	1.66E+00	2.02E+00	1.22E+00
ARHGEF12-2	8.83E+02	1.03E-02	1.08E-02	1.27E+00	3.47E-01	1.27E+00	5.17E+01	4.07E+01
ZNF81	8.02E+00	1.10E-02	1.14E-02	1.85E+00	8.88E-01	1.85E+00	5.34E-01	2.89E-01
MOB1B	8.04E+02	1.10E-02	1.14E-02	1.20E+00	2.59E-01	1.20E+00	4.58E+01	3.83E+01
KR_003030365.	1.37E+01	1.21E-02	1.26E-02	3.02E+00	1.59E+00	3.02E+00	1.05E+00	3.47E-01
KR_003035726.	1.84E+01	1.22E-02	1.26E-02	2.96E+00	1.57E+00	2.96E+00	1.41E+00	4.75E-01
KR_003037504.	7.35E+00	1.22E-02	1.26E-02	3.74E+00	1.90E+00	3.74E+00	5.85E-01	1.56E-01

LOC101910094	4.50E+00	1.27E-02	1.32E-02	3.54E+00	1.83E+00	3.54E+00	3.58E-01	1.01E-01
OR13J1	2.49E+00	1.29E-02	1.34E-02	7.84E+00	2.97E+00	7.84E+00	2.20E-01	2.81E-02
STOML1	3.04E+02	1.32E-02	1.37E-02	1.26E+00	3.31E-01	1.26E+00	1.76E+01	1.40E+01
ACAP3	3.89E+03	1.35E-02	1.40E-02	1.22E+00	2.86E-01	1.22E+00	2.24E+02	1.84E+02
XR_003035059.1	1.85E+00	1.41E-02	1.46E-02	2.42E+00	1.28E+00	2.42E+00	1.34E-01	5.55E-02
RERE	6.28E+03	1.44E-02	1.49E-02	1.37E+00	4.53E-01	1.37E+00	3.77E+02	2.75E+02
FXYD7	9.04E+00	1.45E-02	1.50E-02	1.64E+00	7.12E-01	1.64E+00	5.81E-01	3.55E-01
XR_003037685.1	1.20E+00	1.49E-02	1.54E-02	2.31E+01	4.53E+00	2.31E+01	1.15E-01	4.96E-03
RCBTB2	1.49E+03	1.49E-02	1.54E-02	1.13E+00	1.79E-01	1.13E+00	8.27E+01	7.31E+01
SLC27A5	1.75E+02	1.52E-02	1.57E-02	1.27E+00	3.41E-01	1.27E+00	1.02E+01	8.06E+00
FTO	1.53E+03	1.54E-02	1.59E-02	1.17E+00	2.23E-01	1.17E+00	8.61E+01	7.37E+01
XR_001501102.2	2.93E+00	1.57E-02	1.62E-02	2.94E+00	1.56E+00	2.94E+00	2.22E-01	7.55E-02
SH3BP5	1.37E+03	1.58E-02	1.63E-02	1.35E+00	4.38E-01	1.35E+00	8.24E+01	6.08E+01
LOC112448773	6.51E+00	1.58E-02	1.63E-02	2.90E+00	1.54E+00	2.90E+00	4.96E-01	1.71E-01
RNF145	1.43E+03	1.61E-02	1.66E-02	1.12E+00	1.64E-01	1.12E+00	7.91E+01	7.06E+01
URGCP	5.75E+02	1.63E-02	1.68E-02	1.12E+00	1.65E-01	1.12E+00	3.18E+01	2.84E+01
PGAM2	1.15E+01	1.64E-02	1.69E-02	1.50E+00	5.81E-01	1.50E+00	7.13E-01	4.77E-01
TMEM18	1.98E+02	1.66E-02	1.71E-02	1.20E+00	2.67E-01	1.20E+00	1.13E+01	9.39E+00
XR_805838.3	3.60E+00	1.73E-02	1.78E-02	2.02E+00	1.01E+00	2.02E+00	2.47E-01	1.22E-01
SLC35E3	7.17E+02	1.78E-02	1.83E-02	1.29E+00	3.62E-01	1.29E+00	4.19E+01	3.26E+01
DACT1	1.84E+03	1.86E-02	1.91E-02	1.30E+00	3.80E-01	1.30E+00	1.08E+02	8.34E+01
XR_003029590.1	2.06E+01	1.90E-02	1.95E-02	3.47E+00	1.80E+00	3.47E+00	1.63E+00	4.68E-01
FUBP3	8.25E+02	1.90E-02	1.95E-02	1.16E+00	2.14E-01	1.16E+00	4.65E+01	4.00E+01
LOC786512	7.81E+01	1.94E-02	1.99E-02	1.39E+00	4.79E-01	1.39E+00	4.70E+00	3.37E+00
HTR2A	3.28E+00	2.02E-02	2.07E-02	2.55E+00	1.35E+00	2.55E+00	2.41E-01	9.46E-02
SP7	3.63E+01	2.18E-02	2.23E-02	1.49E+00	5.77E-01	1.49E+00	2.27E+00	1.52E+00
LOC787328	3.74E+00	2.29E-02	2.35E-02	5.27E+00	2.40E+00	5.27E+00	3.17E-01	6.03E-02
XR_813683.3	1.08E+01	2.32E-02	2.37E-02	3.06E+00	1.61E+00	3.06E+00	8.35E-01	2.73E-01
RRBP1	1.22E+04	2.33E-02	2.38E-02	1.16E+00	2.10E-01	1.16E+00	6.89E+02	5.96E+02
XR_003033176.1	1.84E+03	2.41E-02	2.47E-02	1.27E+00	3.50E-01	1.27E+00	1.07E+02	8.41E+01
XR_810077.2	3.28E+01	2.48E-02	2.53E-02	1.65E+00	7.19E-01	1.65E+00	2.11E+00	1.28E+00
SLC37A3	7.08E+02	2.50E-02	2.55E-02	1.13E+00	1.73E-01	1.13E+00	3.93E+01	3.48E+01
C21H14orf132	1.80E+00	2.50E-02	2.55E-02	6.89E+00	2.78E+00	6.89E+00	1.59E-01	2.31E-02

XR_003034598.	1.95E+00	2.52E-02	2.57E-02	4.61E+00	2.21E+00	4.61E+00	1.62E-01	3.52E-02
ADAMTS20	4.72E+00	2.56E-02	2.61E-02	1.94E+00	9.56E-01	1.94E+00	3.18E-01	1.64E-01
LOC100140533	1.61E+02	2.76E-02	2.81E-02	1.16E+00	2.19E-01	1.16E+00	9.07E+00	7.79E+00
XR_003033835.	3.88E+01	2.83E-02	2.88E-02	1.87E+00	9.04E-01	1.87E+00	2.58E+00	1.38E+00
NAV1	3.80E+03	2.97E-02	3.02E-02	1.25E+00	3.22E-01	1.25E+00	2.20E+02	1.76E+02
XR_003037293.	2.00E+00	3.09E-02	3.14E-02	7.34E+00	2.88E+00	7.34E+00	1.78E-01	2.43E-02
LOC112447439	3.18E+00	3.12E-02	3.17E-02	2.47E+00	1.31E+00	2.47E+00	2.30E-01	9.31E-02
XR_003032625.	4.62E+02	3.16E-02	3.21E-02	1.38E+00	4.65E-01	1.38E+00	2.79E+01	2.02E+01
TGFB3	2.46E+03	3.19E-02	3.24E-02	1.50E+00	5.85E-01	1.50E+00	1.53E+02	1.02E+02
XR_003029373.	2.86E+00	3.23E-02	3.28E-02	7.33E+00	2.87E+00	7.33E+00	2.53E-01	3.46E-02
XR_003034248.	2.38E+00	3.44E-02	3.49E-02	4.21E+00	2.07E+00	4.21E+00	1.96E-01	4.65E-02
LOC100335642	6.04E+01	3.59E-02	3.63E-02	1.50E+00	5.81E-01	1.50E+00	3.77E+00	2.52E+00
CLCA3	2.49E+00	3.81E-02	3.86E-02	3.12E+00	1.64E+00	3.12E+00	1.92E-01	6.15E-02
STX17	6.65E+02	4.28E-02	4.33E-02	1.23E+00	2.96E-01	1.23E+00	3.82E+01	3.11E+01
PTPRS	1.06E+04	4.91E-02	4.97E-02	1.17E+00	2.22E-01	1.17E+00	6.01E+02	5.15E+02
XR_003034005.	9.24E+00	5.43E-02	5.49E-02	2.86E+00	1.52E+00	2.86E+00	6.99E-01	2.44E-01
XR_003034438.	1.64E+00	5.56E-02	5.62E-02	1.29E+01	3.68E+00	1.29E+01	1.53E-01	1.19E-02
NAMPT	5.75E+02	6.18E-02	6.25E-02	1.11E+00	1.55E-01	1.11E+00	3.17E+01	2.85E+01
XR_812723.3	3.62E+01	6.21E-02	6.27E-02	1.37E+00	4.52E-01	1.37E+00	2.18E+00	1.59E+00
VAT1L	2.13E+02	6.27E-02	6.32E-02	1.56E+00	6.39E-01	1.56E+00	1.33E+01	8.57E+00
XR_003031808.	3.46E+00	6.56E-02	6.62E-02	4.57E+00	2.19E+00	4.57E+00	2.89E-01	6.32E-02
LOC101905975	5.73E+00	6.59E-02	6.65E-02	1.69E+00	7.54E-01	1.69E+00	3.68E-01	2.18E-01
XR_003030727.	3.60E+02	7.44E-02	7.49E-02	1.32E+00	3.97E-01	1.32E+00	2.13E+01	1.62E+01
C26H10orf62	8.67E+00	7.51E-02	7.56E-02	1.43E+00	5.12E-01	1.43E+00	5.30E-01	3.71E-01
ZMIZ1	3.82E+03	7.98E-02	8.03E-02	1.24E+00	3.05E-01	1.24E+00	2.21E+02	1.79E+02
XR_001501363.	1.09E+01	9.03E-02	9.08E-02	7.16E+00	2.84E+00	7.16E+00	9.60E-01	1.34E-01
XR_813169.3	2.88E+00	9.25E-02	9.30E-02	6.97E+00	2.80E+00	6.97E+00	2.54E-01	3.64E-02
XR_003032060.	2.46E+02	9.25E-02	9.30E-02	1.21E+00	2.73E-01	1.21E+00	1.41E+01	1.17E+01
XR_003030726.	4.81E+02	9.29E-02	9.33E-02	1.27E+00	3.44E-01	1.27E+00	2.80E+01	2.21E+01
CAVIN4	1.51E+02	9.69E-02	9.72E-02	1.17E+00	2.31E-01	1.17E+00	8.53E+00	7.27E+00
XR_003033122.	2.75E+02	1.09E-01	1.09E-01	1.16E+00	2.16E-01	1.16E+00	1.54E+01	1.33E+01
ZCCHC24	2.09E+03	1.67E-01	1.67E-01	1.20E+00	2.68E-01	1.20E+00	1.19E+02	9.91E+01
LOC101903326	4.74E+02	2.61E-01	2.62E-01	1.08E+00	1.17E-01	1.08E+00	2.58E+01	2.38E+01

XR_003034251.1	2.88E+00	2.66E-01	2.66E-01	8.40E+00	3.07E+00	8.40E+00	2.59E-01	3.08E-02
XR_807452.3	7.88E+00	3.19E-01	3.19E-01	3.22E+00	1.69E+00	3.22E+00	6.14E-01	1.91E-01
XR_003030423.1	3.68E+00	8.70E-01	8.70E-01	1.90E+00	9.27E-01	1.90E+00	2.48E-01	1.30E-01

S4 Table. Gene Specific Analysis (late versus early gestation) for genes in cluster 3. Shown are the fold change and its significance (p-value), log 2 ratio and False Discovery Rate (FDR) across gestation; least square (LS) mean (late and early gestation); total counts per million.

Gene symbol	Total counts	P-value	FDR step up	Ratio	Log2(Ratio)	Fold change	LSMean(Late)	LSMean(Early)
PPM1H	1.96E+01	1.78E-10	1.55E-07	1.95E+04	1.43E+01	1.95E+04	1.96E+00	1.00E-04
XR_003036541.1	3.19E+00	8.55E-08	3.72E-05	3.87E+01	5.27E+00	3.87E+01	3.11E-01	8.05E-03
XR_003035353.1	6.62E+01	3.94E-07	1.14E-04	1.14E+01	3.51E+00	1.14E+01	6.14E+00	5.38E-01
LCT	3.67E+01	8.73E-07	1.73E-04	2.16E+01	4.43E+00	2.16E+01	3.52E+00	1.63E-01
LOC104969177	3.23E+01	9.94E-07	1.73E-04	4.98E+00	2.32E+00	4.98E+00	2.74E+00	5.50E-01
XR_804252.1	1.95E+00	1.24E-06	1.80E-04	3.93E+02	8.62E+00	3.93E+02	1.95E-01	4.95E-04
LOC781927	1.73E+00	1.79E-06	1.89E-04	2.63E+01	4.72E+00	2.63E+01	1.67E-01	6.35E-03
XR_003037470.1	6.77E+00	1.88E-06	1.89E-04	2.06E+01	4.36E+00	2.06E+01	6.48E-01	3.15E-02
BMP15	1.92E+02	2.33E-06	1.89E-04	3.95E+01	5.30E+00	3.95E+01	1.88E+01	4.76E-01
GPR179	3.21E+01	2.36E-06	1.89E-04	8.92E+00	3.16E+00	8.92E+00	2.92E+00	3.27E-01
XR_003036766.1	5.31E+00	2.39E-06	1.89E-04	2.31E+01	4.53E+00	2.31E+01	5.12E-01	2.21E-02
id-IGHM	4.49E+02	2.60E-06	1.89E-04	1.11E+01	3.47E+00	1.11E+01	4.16E+01	3.75E+00
ABCC2	1.71E+02	3.17E-06	2.10E-04	1.11E+01	3.47E+00	1.11E+01	1.58E+01	1.43E+00
ZP3	1.21E+03	3.38E-06	2.10E-04	1.54E+01	3.94E+00	1.54E+01	1.15E+02	7.46E+00
KHDC3L	3.86E+02	4.75E-06	2.76E-04	7.98E+00	3.00E+00	7.98E+00	3.47E+01	4.35E+00
TREH	1.26E+02	5.11E-06	2.78E-04	1.55E+01	3.95E+00	1.55E+01	1.19E+01	7.69E-01
LOC101904481	2.40E+02	5.88E-06	3.01E-04	9.59E+00	3.26E+00	9.59E+00	2.19E+01	2.28E+00
XR_003031564.1	5.53E+00	8.63E-06	3.76E-04	2.36E+01	4.56E+00	2.36E+01	5.32E-01	2.26E-02
XR_003032366.1	4.15E+01	8.81E-06	3.76E-04	5.41E+00	2.44E+00	5.41E+00	3.56E+00	6.58E-01
KPNA7	1.25E+02	9.36E-06	3.76E-04	5.28E+00	2.40E+00	5.28E+00	1.07E+01	2.02E+00
CNTD2	1.80E+02	9.66E-06	3.76E-04	8.31E+00	3.05E+00	8.31E+00	1.62E+01	1.96E+00
ARHGDIG	3.59E+01	1.05E-05	3.76E-04	4.39E+00	2.13E+00	4.39E+00	2.98E+00	6.79E-01
XR_003035912.1	1.29E+00	1.06E-05	3.76E-04	2.60E+01	4.70E+00	2.60E+01	1.24E-01	4.78E-03
FAM170A	1.28E+00	1.06E-05	3.76E-04	1.25E+01	3.64E+00	1.25E+01	1.20E-01	9.60E-03
SLCO3A1	2.71E+02	1.08E-05	3.76E-04	2.16E+00	1.11E+00	2.16E+00	1.91E+01	8.84E+00
OLFM4	5.44E+01	1.41E-05	4.72E-04	7.17E+00	2.84E+00	7.17E+00	4.84E+00	6.75E-01
MCF2	1.87E+01	1.47E-05	4.73E-04	3.16E+00	1.66E+00	3.16E+00	1.46E+00	4.61E-01
DRD3	4.87E+00	1.53E-05	4.74E-04	2.21E+01	4.46E+00	2.21E+01	4.68E-01	2.12E-02
XR_003033896.1	7.12E+01	1.77E-05	5.28E-04	2.77E+01	4.79E+00	2.77E+01	6.90E+00	2.49E-01

LOC522174	3.55E+01	1.84E-05	5.28E-04	5.27E+00	2.40E+00	5.27E+00	3.04E+00	5.76E-01
LOC104970698	2.06E+01	1.88E-05	5.28E-04	4.65E+00	2.22E+00	4.65E+00	1.72E+00	3.71E-01
SLBP2	6.57E+01	2.08E-05	5.65E-04	5.50E+00	2.46E+00	5.50E+00	5.65E+00	1.03E+00
NPM2	3.66E+02	2.19E-05	5.78E-04	1.11E+01	3.48E+00	1.11E+01	3.39E+01	3.04E+00
XR_001501628.2	3.94E+01	2.68E-05	6.86E-04	3.34E+01	5.06E+00	3.34E+01	3.83E+00	1.15E-01
XR_003033142.1	1.43E+00	2.85E-05	7.10E-04	2.85E+01	4.83E+00	2.85E+01	1.39E-01	4.87E-03
d-LOC101902461	3.92E+02	3.06E-05	7.36E-04	5.91E+00	2.56E+00	5.91E+00	3.40E+01	5.76E+00
SELP	2.22E+02	3.18E-05	7.36E-04	2.71E+00	1.44E+00	2.71E+00	1.66E+01	6.13E+00
EGR3	1.40E+02	3.24E-05	7.36E-04	3.99E+00	2.00E+00	3.99E+00	1.14E+01	2.86E+00
MPIG6B	6.19E+02	3.29E-05	7.36E-04	9.77E+00	3.29E+00	9.77E+00	5.67E+01	5.80E+00
MOS	9.91E+01	3.63E-05	7.77E-04	1.78E+01	4.15E+00	1.78E+01	9.43E+00	5.30E-01
TBPL2	3.50E+00	3.66E-05	7.77E-04	1.18E+01	3.56E+00	1.18E+01	3.25E-01	2.75E-02
XR_003031851.1	4.23E+00	5.16E-05	1.07E-03	1.04E+01	3.38E+00	1.04E+01	3.89E-01	3.74E-02
MYO1H	3.32E+01	5.30E-05	1.07E-03	6.45E+00	2.69E+00	6.45E+00	2.91E+00	4.52E-01
XR_003029820.1	3.26E+00	7.08E-05	1.39E-03	1.17E+01	3.55E+00	1.17E+01	3.03E-01	2.58E-02
XR_003035869.1	1.90E+00	7.26E-05	1.39E-03	7.45E+01	6.22E+00	7.45E+01	1.87E-01	2.52E-03
LOC783811	3.26E+01	7.32E-05	1.39E-03	3.81E+01	5.25E+00	3.81E+01	3.18E+00	8.35E-02
XR_811475.3	4.63E+00	7.78E-05	1.44E-03	1.55E+01	3.95E+00	1.55E+01	4.38E-01	2.82E-02
XR_003036902.1	2.65E+01	8.19E-05	1.49E-03	4.37E+00	2.13E+00	4.37E+00	2.20E+00	5.03E-01
MAPRE2	2.51E+03	8.59E-05	1.53E-03	1.97E+00	9.78E-01	1.97E+00	1.72E+02	8.73E+01
XR_003036075.1	2.09E+01	9.15E-05	1.59E-03	2.45E+00	1.29E+00	2.45E+00	1.53E+00	6.26E-01
LOC618696	1.21E+01	9.82E-05	1.68E-03	8.12E+00	3.02E+00	8.12E+00	1.09E+00	1.34E-01
SLC6A5	1.71E+01	1.01E-04	1.69E-03	3.24E+00	1.70E+00	3.24E+00	1.34E+00	4.14E-01
TSPAN7	1.14E+03	1.06E-04	1.73E-03	2.62E+00	1.39E+00	2.62E+00	8.52E+01	3.25E+01
DSCAML1	1.52E+02	1.08E-04	1.73E-03	6.51E+00	2.70E+00	6.51E+00	1.33E+01	2.05E+00
SAXO1	3.10E+02	1.12E-04	1.73E-03	7.79E+00	2.96E+00	7.79E+00	2.78E+01	3.56E+00
CACNG3	1.09E+01	1.14E-04	1.73E-03	1.50E+01	3.91E+00	1.50E+01	1.03E+00	6.85E-02
XR_003030793.1	1.01E+00	1.15E-04	1.73E-03	3.19E+01	5.00E+00	3.19E+01	9.83E-02	3.08E-03
XR_003029444.1	1.69E+00	1.15E-04	1.73E-03	4.18E+01	5.39E+00	4.18E+01	1.65E-01	3.94E-03
XR_001495546.2	3.42E+00	1.29E-04	1.90E-03	1.97E+01	4.30E+00	1.97E+01	3.27E-01	1.66E-02
PLEKHG7	1.99E+02	1.43E-04	2.08E-03	5.46E+00	2.45E+00	5.46E+00	1.71E+01	3.13E+00
PANX1	6.31E+02	1.47E-04	2.10E-03	2.35E+00	1.23E+00	2.35E+00	4.56E+01	1.94E+01
KCTD16	1.03E+01	1.54E-04	2.17E-03	6.98E+00	2.80E+00	6.98E+00	9.16E-01	1.31E-01

XR_001494959.2	5.03E+00	1.61E-04	2.23E-03	5.24E+01	5.71E+00	5.24E+01	4.95E-01	9.44E-03
PIWIL3	2.80E+01	1.66E-04	2.24E-03	2.08E+01	4.38E+00	2.08E+01	2.68E+00	1.29E-01
XR_811073.3	6.32E+01	1.67E-04	2.24E-03	1.83E+01	4.20E+00	1.83E+01	6.02E+00	3.28E-01
PATL2	1.59E+02	1.85E-04	2.44E-03	6.60E+00	2.72E+00	6.60E+00	1.40E+01	2.13E+00
BCL2L10	5.28E+01	1.91E-04	2.49E-03	2.87E+00	1.52E+00	2.87E+00	4.02E+00	1.40E+00
MYO1E	9.67E+02	1.98E-04	2.54E-03	1.55E+00	6.30E-01	1.55E+00	6.11E+01	3.95E+01
MPP7	8.57E+01	2.16E-04	2.73E-03	3.32E+00	1.73E+00	3.32E+00	6.74E+00	2.03E+00
AURKA	1.08E+03	2.31E-04	2.87E-03	2.73E+00	1.45E+00	2.73E+00	8.14E+01	2.98E+01
XR_003033062.1	1.44E+00	2.37E-04	2.91E-03	7.01E+00	2.81E+00	7.01E+00	1.27E-01	1.82E-02
TRIM77	1.77E+01	2.42E-04	2.93E-03	1.50E+01	3.90E+00	1.50E+01	1.67E+00	1.11E-01
ILDR1	3.69E+01	2.53E-04	3.00E-03	4.30E+00	2.10E+00	4.30E+00	3.05E+00	7.09E-01
SLC17A1	5.65E+01	2.62E-04	3.00E-03	1.24E+01	3.63E+00	1.24E+01	5.26E+00	4.26E-01
XR_003035013.1	3.91E+00	2.62E-04	3.00E-03	1.13E+01	3.49E+00	1.13E+01	3.62E-01	3.21E-02
GLRA1	1.79E+01	2.65E-04	3.00E-03	1.04E+01	3.37E+00	1.04E+01	1.65E+00	1.59E-01
LYPD1	2.46E+02	2.65E-04	3.00E-03	1.91E+00	9.34E-01	1.91E+00	1.68E+01	8.77E+00
XR_003031039.1	9.47E+00	2.90E-04	3.21E-03	5.08E+00	2.34E+00	5.08E+00	8.04E-01	1.58E-01
SLC17A3	1.29E+01	2.91E-04	3.21E-03	1.56E+01	3.96E+00	1.56E+01	1.22E+00	7.79E-02
ARHGEF26	3.22E+02	3.02E-04	3.23E-03	1.65E+00	7.18E-01	1.65E+00	2.08E+01	1.26E+01
LOC100337390	8.73E+01	3.03E-04	3.23E-03	3.00E+00	1.59E+00	3.00E+00	6.72E+00	2.24E+00
XR_001501757.2	5.06E+00	3.04E-04	3.23E-03	1.19E+01	3.57E+00	1.19E+01	4.70E-01	3.95E-02
LOC104972713	1.64E+01	3.13E-04	3.29E-03	4.95E+00	2.31E+00	4.95E+00	1.39E+00	2.81E-01
XR_003035686.1	4.96E+00	3.32E-04	3.40E-03	9.00E+00	3.17E+00	9.00E+00	4.51E-01	5.01E-02
PAK5	1.94E+01	3.32E-04	3.40E-03	2.52E+00	1.33E+00	2.52E+00	1.43E+00	5.68E-01
CCNO	8.18E+01	3.46E-04	3.51E-03	4.85E+00	2.28E+00	4.85E+00	6.90E+00	1.42E+00
SPATA5	2.60E+02	3.63E-04	3.56E-03	1.57E+00	6.55E-01	1.57E+00	1.66E+01	1.05E+01
CACNA1E	1.10E+02	3.66E-04	3.56E-03	3.38E+00	1.76E+00	3.38E+00	8.71E+00	2.58E+00
C15H11orf52	1.35E+01	3.66E-04	3.56E-03	4.64E+00	2.21E+00	4.64E+00	1.13E+00	2.44E-01
ITGB4	7.13E+02	3.68E-04	3.56E-03	2.52E+00	1.33E+00	2.52E+00	5.26E+01	2.08E+01
XR_240539.4	5.09E+01	3.81E-04	3.63E-03	2.96E+00	1.57E+00	2.96E+00	3.90E+00	1.32E+00
CD27	3.62E+01	3.83E-04	3.63E-03	2.21E+00	1.14E+00	2.21E+00	2.58E+00	1.17E+00
MAP2	9.80E+02	3.89E-04	3.64E-03	1.52E+00	6.08E-01	1.52E+00	6.16E+01	4.04E+01
HEATR1	1.94E+01	3.93E-04	3.64E-03	4.07E+00	2.03E+00	4.07E+00	1.59E+00	3.90E-01
XR_003030871.1	1.25E+01	4.05E-04	3.71E-03	4.61E+00	2.21E+00	4.61E+00	1.04E+00	2.26E-01

CEACAM20	9.66E+00	4.12E-04	3.73E-03	4.23E+00	2.08E+00	4.23E+00	7.96E-01	1.88E-01
KRT33A	3.24E+00	4.17E-04	3.75E-03	1.58E+01	3.98E+00	1.58E+01	3.06E-01	1.94E-02
XR_003036726.1	1.16E+01	4.27E-04	3.79E-03	2.55E+00	1.35E+00	2.55E+00	8.56E-01	3.36E-01
CLPS	1.28E+00	4.44E-04	3.90E-03	9.19E+00	3.20E+00	9.19E+00	1.17E-01	1.27E-02
LOC518980	4.76E+01	4.81E-04	4.19E-03	1.94E+00	9.54E-01	1.94E+00	3.25E+00	1.68E+00
RAB39B	1.76E+01	4.95E-04	4.27E-03	4.57E+00	2.19E+00	4.57E+00	1.47E+00	3.21E-01
FAM19A2	2.92E+01	5.01E-04	4.28E-03	4.30E+00	2.10E+00	4.30E+00	2.41E+00	5.62E-01
XR_003036006.1	3.33E+00	5.19E-04	4.34E-03	1.02E+01	3.35E+00	1.02E+01	3.06E-01	3.01E-02
LY6G6C	1.98E+01	5.26E-04	4.34E-03	4.92E+00	2.30E+00	4.92E+00	1.67E+00	3.40E-01
UCP3	3.16E+01	5.27E-04	4.34E-03	1.04E+01	3.38E+00	1.04E+01	2.91E+00	2.79E-01
LRMP	2.53E+01	5.28E-04	4.34E-03	2.46E+00	1.30E+00	2.46E+00	1.85E+00	7.55E-01
XR_811466.3	9.60E+00	5.39E-04	4.37E-03	3.18E+00	1.67E+00	3.18E+00	7.49E-01	2.35E-01
XR_003034297.1	3.27E+00	5.42E-04	4.37E-03	7.34E+00	2.88E+00	7.34E+00	2.91E-01	3.96E-02
OGDHL	1.83E+02	5.59E-04	4.46E-03	4.60E+00	2.20E+00	4.60E+00	1.53E+01	3.34E+00
SPICE1	5.54E+02	5.64E-04	4.46E-03	1.32E+00	4.01E-01	1.32E+00	3.29E+01	2.49E+01
SYTL5	1.53E+01	6.04E-04	4.74E-03	1.17E+01	3.55E+00	1.17E+01	1.42E+00	1.22E-01
LOC787740	1.48E+01	6.18E-04	4.81E-03	5.95E+00	2.57E+00	5.95E+00	1.28E+00	2.15E-01
BTN3A3	2.69E+00	6.79E-04	5.17E-03	3.84E+00	1.94E+00	3.84E+00	2.18E-01	5.67E-02
DOPEY2	2.93E+02	6.81E-04	5.17E-03	2.11E+00	1.08E+00	2.11E+00	2.05E+01	9.75E+00
LOC112447758	2.16E+00	6.83E-04	5.17E-03	7.17E+00	2.84E+00	7.17E+00	1.92E-01	2.68E-02
SGMS2	2.84E+02	7.55E-04	5.67E-03	1.73E+00	7.92E-01	1.73E+00	1.87E+01	1.08E+01
XR_001494794.2	1.48E+01	7.87E-04	5.86E-03	6.64E+00	2.73E+00	6.64E+00	1.30E+00	1.96E-01
LOC100298309	6.91E+00	7.93E-04	5.86E-03	5.96E+00	2.58E+00	5.96E+00	6.00E-01	1.01E-01
DTNBP1	4.42E+02	8.04E-04	5.89E-03	1.38E+00	4.69E-01	1.38E+00	2.68E+01	1.93E+01
TDRD10	1.65E+02	8.49E-04	6.16E-03	4.51E+00	2.17E+00	4.51E+00	1.37E+01	3.04E+00
XR_003032801.1	3.02E+00	8.96E-04	6.41E-03	1.26E+01	3.65E+00	1.26E+01	2.82E-01	2.24E-02
SNX10	6.72E+01	9.02E-04	6.41E-03	1.85E+00	8.84E-01	1.85E+00	4.52E+00	2.45E+00
XR_003031821.1	1.79E+01	9.10E-04	6.41E-03	4.32E+00	2.11E+00	4.32E+00	1.48E+00	3.43E-01
ENTPD4	7.77E+02	9.13E-04	6.41E-03	1.47E+00	5.60E-01	1.47E+00	4.82E+01	3.27E+01
PRKCQ	2.47E+02	9.19E-04	6.41E-03	3.74E+00	1.90E+00	3.74E+00	1.99E+01	5.33E+00
XR_003029452.1	5.48E+00	9.34E-04	6.46E-03	1.39E+01	3.80E+00	1.39E+01	5.15E-01	3.69E-02
PLCH1	1.97E+02	1.06E-03	7.29E-03	2.83E+00	1.50E+00	2.83E+00	1.49E+01	5.28E+00
COLEC10	1.09E+01	1.07E-03	7.31E-03	3.22E+00	1.69E+00	3.22E+00	8.54E-01	2.65E-01

XR_003035363.1	1.64E+01	1.16E-03	7.77E-03	7.36E+00	2.88E+00	7.36E+00	1.46E+00	1.98E-01
LOC101901970	5.80E+00	1.16E-03	7.77E-03	5.87E+00	2.55E+00	5.87E+00	5.03E-01	8.56E-02
XR_003036137.1	9.84E+01	1.22E-03	8.13E-03	5.02E+00	2.33E+00	5.02E+00	8.35E+00	1.66E+00
PLA2G4D	4.22E+01	1.24E-03	8.17E-03	2.68E+00	1.42E+00	2.68E+00	3.16E+00	1.18E+00
TECTB	1.73E+01	1.28E-03	8.37E-03	1.02E+01	3.35E+00	1.02E+01	1.59E+00	1.56E-01
ZNF804B	1.57E+01	1.39E-03	9.04E-03	4.90E+00	2.29E+00	4.90E+00	1.33E+00	2.71E-01
LOC617633	9.01E+00	1.40E-03	9.06E-03	7.11E+00	2.83E+00	7.11E+00	8.00E-01	1.12E-01
BBS9	1.74E+02	1.43E-03	9.17E-03	1.55E+00	6.28E-01	1.55E+00	1.10E+01	7.10E+00
XR_814925.3	2.16E+01	1.47E-03	9.30E-03	3.38E+00	1.76E+00	3.38E+00	1.71E+00	5.05E-01
XR_003032350.1	4.91E+01	1.47E-03	9.30E-03	2.05E+00	1.04E+00	2.05E+00	3.41E+00	1.66E+00
XR_003030656.1	1.05E+02	1.53E-03	9.53E-03	2.28E+00	1.19E+00	2.28E+00	7.54E+00	3.31E+00
ASAH2	1.42E+01	1.54E-03	9.53E-03	3.24E+00	1.70E+00	3.24E+00	1.11E+00	3.42E-01
XR_003031027.1	2.32E+00	1.54E-03	9.53E-03	1.39E+01	3.79E+00	1.39E+01	2.18E-01	1.57E-02
XR_003034304.1	1.14E+01	1.57E-03	9.62E-03	2.95E+00	1.56E+00	2.95E+00	8.76E-01	2.97E-01
LOC100296257	3.91E+01	1.60E-03	9.71E-03	4.85E+00	2.28E+00	4.85E+00	3.30E+00	6.79E-01
XR_003037432.1	1.10E+00	1.60E-03	9.71E-03	7.11E+00	2.83E+00	7.11E+00	9.72E-02	1.37E-02
CSF1R	8.65E+02	1.71E-03	1.03E-02	1.96E+00	9.71E-01	1.96E+00	5.93E+01	3.02E+01
XR_810104.3	2.48E+01	1.72E-03	1.03E-02	2.53E+00	1.34E+00	2.53E+00	1.83E+00	7.25E-01
ARMC2	1.08E+02	1.75E-03	1.04E-02	1.84E+00	8.82E-01	1.84E+00	7.25E+00	3.93E+00
BTG2	1.47E+03	1.77E-03	1.04E-02	1.52E+00	6.03E-01	1.52E+00	9.26E+01	6.09E+01
HHAT	5.60E+01	1.83E-03	1.07E-02	2.02E+00	1.02E+00	2.02E+00	3.87E+00	1.91E+00
XR_003032686.1	3.78E+00	1.87E-03	1.08E-02	3.59E+01	5.17E+00	3.59E+01	3.68E-01	1.03E-02
CAPN13	1.68E+01	1.87E-03	1.08E-02	3.80E+00	1.93E+00	3.80E+00	1.36E+00	3.58E-01
XR_003030060.1	1.31E+01	1.96E-03	1.11E-02	5.81E+00	2.54E+00	5.81E+00	1.13E+00	1.95E-01
BSPRY	9.81E+01	1.97E-03	1.11E-02	2.52E+00	1.34E+00	2.52E+00	7.23E+00	2.86E+00
LOC782385	1.55E+02	1.97E-03	1.11E-02	2.20E+00	1.14E+00	2.20E+00	1.10E+01	5.01E+00
CRNKL1	7.49E+02	1.99E-03	1.12E-02	1.28E+00	3.59E-01	1.28E+00	4.40E+01	3.43E+01
LINGO3	6.04E+01	2.01E-03	1.12E-02	3.87E+00	1.95E+00	3.87E+00	4.90E+00	1.27E+00
LOC112446768	4.70E+01	2.02E-03	1.12E-02	2.51E+00	1.33E+00	2.51E+00	3.46E+00	1.38E+00
ZNF177	4.27E+02	2.12E-03	1.16E-02	1.39E+00	4.72E-01	1.39E+00	2.59E+01	1.87E+01
PRPF4	1.00E+03	2.12E-03	1.16E-02	1.36E+00	4.43E-01	1.36E+00	6.02E+01	4.43E+01
CADM2	4.75E+01	2.12E-03	1.16E-02	1.89E+00	9.18E-01	1.89E+00	3.22E+00	1.70E+00
XR_003030812.1	6.23E+00	2.19E-03	1.18E-02	3.52E+00	1.82E+00	3.52E+00	4.96E-01	1.41E-01

AQP3	4.07E+01	2.21E-03	1.19E-02	3.01E+00	1.59E+00	3.01E+00	3.13E+00	1.04E+00
TMCC3	2.57E+02	2.23E-03	1.19E-02	1.77E+00	8.23E-01	1.77E+00	1.70E+01	9.62E+00
TSR1	1.04E+03	2.28E-03	1.21E-02	1.27E+00	3.47E-01	1.27E+00	6.08E+01	4.78E+01
LOC787257	3.18E+02	2.31E-03	1.22E-02	1.25E+00	3.17E-01	1.25E+00	1.85E+01	1.48E+01
XR_003031395.1	4.19E+01	2.34E-03	1.23E-02	4.56E+00	2.19E+00	4.56E+00	3.50E+00	7.67E-01
POU3F2	6.02E+00	2.41E-03	1.26E-02	6.67E+00	2.74E+00	6.67E+00	5.30E-01	7.95E-02
C6H4orf17	5.81E+00	2.43E-03	1.26E-02	7.07E+00	2.82E+00	7.07E+00	5.16E-01	7.29E-02
XR_003036065.1	1.36E+01	2.44E-03	1.26E-02	2.48E+00	1.31E+00	2.48E+00	9.99E-01	4.03E-01
XR_003032804.1	2.45E+00	2.47E-03	1.26E-02	5.75E+00	2.52E+00	5.75E+00	2.12E-01	3.69E-02
XR_003030981.1	1.41E+01	2.53E-03	1.29E-02	3.21E+00	1.68E+00	3.21E+00	1.10E+00	3.42E-01
XR_808313.3	7.42E+00	2.54E-03	1.29E-02	9.45E+00	3.24E+00	9.45E+00	6.77E-01	7.17E-02
LOC112447410	2.00E+00	2.62E-03	1.32E-02	4.22E+00	2.08E+00	4.22E+00	1.65E-01	3.91E-02
LOC107131273	1.51E+01	2.70E-03	1.35E-02	3.37E+00	1.75E+00	3.37E+00	1.19E+00	3.54E-01
HES5	5.88E+01	2.74E-03	1.37E-02	7.28E+00	2.86E+00	7.28E+00	5.24E+00	7.19E-01
MLN	3.28E+00	2.78E-03	1.37E-02	6.84E+00	2.77E+00	6.84E+00	2.90E-01	4.24E-02
XR_003033380.1	1.97E+01	2.93E-03	1.44E-02	5.16E+00	2.37E+00	5.16E+00	1.67E+00	3.24E-01
NRG3	2.73E+01	2.96E-03	1.45E-02	3.25E+00	1.70E+00	3.25E+00	2.13E+00	6.57E-01
XR_813704.3	6.22E+00	3.01E-03	1.46E-02	3.02E+00	1.59E+00	3.02E+00	4.79E-01	1.59E-01
XR_003037159.1	1.13E+00	3.07E-03	1.49E-02	1.67E+01	4.06E+00	1.67E+01	1.07E-01	6.42E-03
ABCG5	1.56E+01	3.11E-03	1.50E-02	5.93E+00	2.57E+00	5.93E+00	1.35E+00	2.28E-01
KCNH1	6.15E+01	3.15E-03	1.51E-02	3.46E+00	1.79E+00	3.46E+00	4.88E+00	1.41E+00
XR_003036542.1	1.43E+00	3.19E-03	1.51E-02	1.43E+01	3.83E+00	1.43E+01	1.34E-01	9.42E-03
CHST6	7.78E+01	3.20E-03	1.51E-02	2.54E+00	1.35E+00	2.54E+00	5.75E+00	2.26E+00
XR_003036054.1	5.79E+00	3.36E-03	1.58E-02	4.95E+00	2.31E+00	4.95E+00	4.90E-01	9.89E-02
LOC107132048	2.05E+02	3.36E-03	1.58E-02	2.13E+00	1.09E+00	2.13E+00	1.44E+01	6.77E+00
FBLL1	3.36E+01	3.45E-03	1.61E-02	1.76E+00	8.15E-01	1.76E+00	2.22E+00	1.26E+00
NRXN3	6.97E+01	3.50E-03	1.62E-02	2.59E+00	1.37E+00	2.59E+00	5.18E+00	2.00E+00
LOC107131851	5.39E+00	3.62E-03	1.67E-02	4.80E+00	2.26E+00	4.80E+00	4.54E-01	9.45E-02
HGSNAT	2.35E+03	3.81E-03	1.75E-02	1.16E+00	2.10E-01	1.16E+00	1.32E+02	1.14E+02
XR_003032065.1	5.15E+01	3.83E-03	1.75E-02	2.19E+00	1.13E+00	2.19E+00	3.65E+00	1.67E+00
LOC100140216	2.49E+00	4.08E-03	1.84E-02	4.93E+00	2.30E+00	4.93E+00	2.10E-01	4.27E-02
NOTO	2.53E+01	4.09E-03	1.84E-02	2.96E+00	1.57E+00	2.96E+00	1.94E+00	6.55E-01
XR_001501286.2	2.95E+00	4.09E-03	1.84E-02	1.25E+01	3.64E+00	1.25E+01	2.75E-01	2.21E-02

XR_003036313.1	1.10E+00	4.15E-03	1.85E-02	1.30E+01	3.70E+00	1.30E+01	1.03E-01	7.97E-03
LOC525426	1.31E+02	4.16E-03	1.85E-02	1.95E+00	9.67E-01	1.95E+00	8.94E+00	4.57E+00
NSMAF	4.61E+02	4.21E-03	1.86E-02	1.21E+00	2.72E-01	1.21E+00	2.64E+01	2.19E+01
SENP8	1.93E+02	4.43E-03	1.95E-02	1.96E+00	9.73E-01	1.96E+00	1.32E+01	6.73E+00
C15H11orf91	2.74E+00	4.45E-03	1.95E-02	7.29E+00	2.87E+00	7.29E+00	2.44E-01	3.34E-02
LOC616149	1.93E+00	4.58E-03	2.00E-02	3.96E+00	1.99E+00	3.96E+00	1.57E-01	3.97E-02
XR_003032748.1	2.01E+00	4.65E-03	2.02E-02	4.09E+00	2.03E+00	4.09E+00	1.65E-01	4.04E-02
NCF2	1.35E+02	4.80E-03	2.07E-02	2.11E+00	1.08E+00	2.11E+00	9.46E+00	4.48E+00
SHTN1	3.88E+02	5.21E-03	2.24E-02	1.45E+00	5.41E-01	1.45E+00	2.40E+01	1.65E+01
LOC112444524	8.02E+00	5.26E-03	2.25E-02	2.28E+00	1.19E+00	2.28E+00	5.75E-01	2.52E-01
MED14OS	1.69E+00	5.33E-03	2.27E-02	4.94E+00	2.30E+00	4.94E+00	1.43E-01	2.89E-02
CSDE1	8.26E+03	5.36E-03	2.27E-02	1.21E+00	2.77E-01	1.21E+00	4.74E+02	3.91E+02
KLHDC9	5.81E+01	5.42E-03	2.27E-02	1.89E+00	9.20E-01	1.89E+00	3.93E+00	2.08E+00
USP49	1.88E+02	5.43E-03	2.27E-02	1.86E+00	8.98E-01	1.86E+00	1.27E+01	6.79E+00
MCTP1	4.24E+00	5.54E-03	2.30E-02	5.82E+00	2.54E+00	5.82E+00	3.68E-01	6.32E-02
XR_003032264.1	3.02E+00	5.56E-03	2.30E-02	4.81E+00	2.26E+00	4.81E+00	2.55E-01	5.30E-02
A1BG	2.00E+01	5.63E-03	2.32E-02	7.06E+00	2.82E+00	7.06E+00	1.77E+00	2.51E-01
XR_003034418.1	3.21E+00	5.67E-03	2.33E-02	4.16E+00	2.05E+00	4.16E+00	2.63E-01	6.34E-02
MED12L	1.14E+02	5.77E-03	2.36E-02	2.56E+00	1.36E+00	2.56E+00	8.47E+00	3.30E+00
XR_003030108.1	2.02E+01	5.90E-03	2.39E-02	2.44E+00	1.29E+00	2.44E+00	1.47E+00	6.05E-01
XR_003031890.1	9.77E+00	5.91E-03	2.39E-02	4.49E+00	2.17E+00	4.49E+00	8.14E-01	1.81E-01
SLC34A1	2.70E+00	6.04E-03	2.44E-02	6.74E+00	2.75E+00	6.74E+00	2.38E-01	3.53E-02
CD58	2.46E+03	6.20E-03	2.49E-02	1.22E+00	2.86E-01	1.22E+00	1.42E+02	1.16E+02
ULK4	4.22E+02	6.27E-03	2.50E-02	1.81E+00	8.60E-01	1.81E+00	2.82E+01	1.56E+01
CPB2	6.73E+00	6.44E-03	2.56E-02	5.58E+00	2.48E+00	5.58E+00	5.80E-01	1.04E-01
XR_001502178.2	7.28E+00	6.70E-03	2.65E-02	1.06E+01	3.40E+00	1.06E+01	6.71E-01	6.33E-02
TSPAN5	3.80E+02	7.31E-03	2.88E-02	1.55E+00	6.35E-01	1.55E+00	2.41E+01	1.55E+01
XR_003031860.1	1.81E+02	7.43E-03	2.91E-02	1.65E+00	7.25E-01	1.65E+00	1.17E+01	7.11E+00
MAP3K8	1.11E+02	7.45E-03	2.91E-02	2.53E+00	1.34E+00	2.53E+00	8.22E+00	3.25E+00
PPFIA2	4.05E+01	7.51E-03	2.92E-02	2.57E+00	1.36E+00	2.57E+00	3.00E+00	1.17E+00
SOX7	4.15E+02	7.61E-03	2.93E-02	1.44E+00	5.29E-01	1.44E+00	2.56E+01	1.77E+01
XR_003037742.1	1.28E+01	7.61E-03	2.93E-02	6.51E+00	2.70E+00	6.51E+00	1.13E+00	1.73E-01
XR_003029493.1	1.79E+01	7.71E-03	2.96E-02	5.71E+00	2.51E+00	5.71E+00	1.55E+00	2.71E-01

SLC6A20	2.30E+02	7.79E-03	2.96E-02	2.23E+00	1.16E+00	2.23E+00	1.64E+01	7.35E+00
KNG1	2.77E+00	7.81E-03	2.96E-02	5.45E+00	2.45E+00	5.45E+00	2.38E-01	4.37E-02
LOC101904994	5.99E+00	7.82E-03	2.96E-02	3.74E+00	1.90E+00	3.74E+00	4.83E-01	1.29E-01
NLRC5	9.07E+01	7.88E-03	2.97E-02	2.21E+00	1.14E+00	2.21E+00	6.44E+00	2.92E+00
FGD6	1.33E+02	8.43E-03	3.17E-02	1.50E+00	5.87E-01	1.50E+00	8.33E+00	5.55E+00
DERL1	1.73E+03	8.52E-03	3.19E-02	1.14E+00	1.92E-01	1.14E+00	9.67E+01	8.46E+01
LOC112449365	1.66E+00	8.58E-03	3.19E-02	2.83E+00	1.50E+00	2.83E+00	1.26E-01	4.45E-02
ACTL7B	4.68E+00	8.80E-03	3.24E-02	2.77E+00	1.47E+00	2.77E+00	3.53E-01	1.27E-01
C1H3orf38	6.99E+02	8.84E-03	3.24E-02	1.18E+00	2.34E-01	1.18E+00	3.96E+01	3.37E+01
XR_003032239.1	1.34E+00	8.85E-03	3.24E-02	3.37E+01	5.07E+00	3.37E+01	1.30E-01	3.87E-03
MPHOSPH8	1.58E+03	8.85E-03	3.24E-02	1.27E+00	3.46E-01	1.27E+00	9.25E+01	7.28E+01
ALX1	5.07E+01	8.90E-03	3.24E-02	2.04E+00	1.03E+00	2.04E+00	3.52E+00	1.72E+00
MYF5	3.37E+00	9.16E-03	3.33E-02	4.00E+00	2.00E+00	4.00E+00	2.75E-01	6.88E-02
XR_003037904.1	1.79E+01	9.32E-03	3.37E-02	4.66E+00	2.22E+00	4.66E+00	1.50E+00	3.22E-01
XR_003030623.1	3.15E+01	9.40E-03	3.38E-02	1.59E+00	6.65E-01	1.59E+00	2.01E+00	1.27E+00
TTI2	1.04E+02	9.43E-03	3.38E-02	1.51E+00	5.90E-01	1.51E+00	6.48E+00	4.30E+00
XR_003032243.1	4.63E+00	9.53E-03	3.40E-02	1.59E+01	3.99E+00	1.59E+01	4.38E-01	2.76E-02
XR_001501955.2	2.73E+00	9.59E-03	3.41E-02	4.11E+00	2.04E+00	4.11E+00	2.24E-01	5.46E-02
SORCS1	5.52E+01	9.74E-03	3.45E-02	3.37E+00	1.75E+00	3.37E+00	4.36E+00	1.29E+00
SLC47A1	6.95E+01	9.86E-03	3.48E-02	2.67E+00	1.42E+00	2.67E+00	5.20E+00	1.94E+00
SYNRG	1.09E+03	1.01E-02	3.54E-02	1.37E+00	4.55E-01	1.37E+00	6.59E+01	4.81E+01
TMEM225B	6.30E+02	1.02E-02	3.55E-02	1.25E+00	3.18E-01	1.25E+00	3.66E+01	2.94E+01
EPB42	1.62E+01	1.02E-02	3.55E-02	3.34E+00	1.74E+00	3.34E+00	1.28E+00	3.82E-01
FYB2	2.27E+02	1.02E-02	3.55E-02	3.52E+00	1.81E+00	3.52E+00	1.81E+01	5.14E+00
XR_003033982.1	7.16E+00	1.04E-02	3.60E-02	2.43E+00	1.28E+00	2.43E+00	5.23E-01	2.15E-01
GDF9	1.12E+02	1.05E-02	3.63E-02	2.37E+00	1.25E+00	2.37E+00	8.11E+00	3.42E+00
XR_003032739.1	1.68E+01	1.06E-02	3.65E-02	2.34E+00	1.23E+00	2.34E+00	1.22E+00	5.20E-01
XR_812138.3	1.19E+01	1.08E-02	3.68E-02	4.98E+00	2.32E+00	4.98E+00	1.01E+00	2.02E-01
SLC7A9	2.11E+01	1.09E-02	3.70E-02	4.05E+00	2.02E+00	4.05E+00	1.73E+00	4.26E-01
DGAT2	2.63E+02	1.14E-02	3.87E-02	1.87E+00	9.01E-01	1.87E+00	1.77E+01	9.50E+00
XR_812731.3	4.64E+01	1.18E-02	3.99E-02	1.58E+00	6.64E-01	1.58E+00	2.96E+00	1.87E+00
CPN1	5.93E+01	1.20E-02	4.05E-02	2.59E+00	1.37E+00	2.59E+00	4.40E+00	1.70E+00
ICA1L	1.81E+02	1.21E-02	4.05E-02	3.82E+00	1.93E+00	3.82E+00	1.46E+01	3.82E+00

XR_003033104.1	7.76E+00	1.22E-02	4.07E-02	4.07E+00	2.03E+00	4.07E+00	6.36E-01	1.56E-01
XR_003032983.1	3.40E+01	1.24E-02	4.12E-02	2.02E+00	1.02E+00	2.02E+00	2.36E+00	1.17E+00
LOC509267	7.31E+00	1.25E-02	4.12E-02	2.31E+00	1.21E+00	2.31E+00	5.26E-01	2.27E-01
HPSE	1.31E+02	1.25E-02	4.12E-02	2.17E+00	1.12E+00	2.17E+00	9.28E+00	4.28E+00
PLCG2	7.06E+02	1.25E-02	4.12E-02	1.59E+00	6.72E-01	1.59E+00	4.51E+01	2.83E+01
XR_003029623.1	1.56E+01	1.27E-02	4.14E-02	2.07E+00	1.05E+00	2.07E+00	1.09E+00	5.24E-01
LOC526787	6.15E+00	1.29E-02	4.21E-02	3.57E+00	1.84E+00	3.57E+00	4.91E-01	1.38E-01
XR_001496995.2	2.10E+00	1.34E-02	4.35E-02	4.58E+00	2.20E+00	4.58E+00	1.75E-01	3.83E-02
GRM5	2.80E+01	1.36E-02	4.42E-02	3.12E+00	1.64E+00	3.12E+00	2.17E+00	6.96E-01
MYLK4	4.32E+01	1.39E-02	4.49E-02	2.09E+00	1.07E+00	2.09E+00	3.02E+00	1.44E+00
ERBB4	2.47E+01	1.41E-02	4.52E-02	3.93E+00	1.97E+00	3.93E+00	2.01E+00	5.11E-01
QRICH2	1.27E+02	1.41E-02	4.52E-02	1.62E+00	6.94E-01	1.62E+00	8.19E+00	5.06E+00
KRT31	2.00E+00	1.42E-02	4.52E-02	5.43E+00	2.44E+00	5.43E+00	1.72E-01	3.16E-02
TPST2	6.36E+02	1.46E-02	4.63E-02	1.30E+00	3.74E-01	1.30E+00	3.75E+01	2.90E+01
LOC107132928	1.45E+00	1.47E-02	4.64E-02	1.02E+01	3.35E+00	1.02E+01	1.33E-01	1.30E-02
RPH3AL	3.02E+02	1.48E-02	4.66E-02	1.94E+00	9.59E-01	1.94E+00	2.06E+01	1.06E+01
XR_003033103.1	1.00E+01	1.49E-02	4.68E-02	4.12E+00	2.04E+00	4.12E+00	8.23E-01	2.00E-01
XR_003034796.1	2.44E+00	1.50E-02	4.69E-02	1.36E+01	3.77E+00	1.36E+01	2.29E-01	1.68E-02
XR_003033061.1	2.91E+00	1.55E-02	4.84E-02	2.89E+03	1.15E+01	2.89E+03	2.91E-01	1.01E-04
LOC616427	1.81E+01	1.59E-02	4.94E-02	1.78E+00	8.35E-01	1.78E+00	1.20E+00	6.74E-01
XR_808518.3	2.05E+01	1.59E-02	4.94E-02	1.95E+00	9.65E-01	1.95E+00	1.40E+00	7.17E-01
SERPINA14	6.68E+00	1.60E-02	4.95E-02	3.36E+00	1.75E+00	3.36E+00	5.27E-01	1.57E-01
XR_003035712.1	3.75E+00	1.61E-02	4.95E-02	2.11E+00	1.08E+00	2.11E+00	2.63E-01	1.25E-01
XR_001494795.2	1.51E+01	1.63E-02	4.99E-02	2.24E+00	1.16E+00	2.24E+00	1.08E+00	4.82E-01
LRRIQ4	8.50E+00	1.63E-02	5.00E-02	3.68E+00	1.88E+00	3.68E+00	6.83E-01	1.86E-01
C8B	2.72E+01	1.67E-02	5.07E-02	2.54E+00	1.35E+00	2.54E+00	2.01E+00	7.91E-01
XR_003036937.1	8.25E+00	1.67E-02	5.07E-02	1.81E+00	8.58E-01	1.81E+00	5.51E-01	3.04E-01
SYCP2L	3.28E+01	1.69E-02	5.12E-02	4.10E+00	2.04E+00	4.10E+00	2.69E+00	6.56E-01
XR_812040.3	5.54E+00	1.70E-02	5.12E-02	3.25E+00	1.70E+00	3.25E+00	4.34E-01	1.34E-01
XR_804131.3	1.74E+01	1.72E-02	5.16E-02	4.79E+00	2.26E+00	4.79E+00	1.47E+00	3.07E-01
HERC3	3.57E+02	1.73E-02	5.17E-02	1.32E+00	4.01E-01	1.32E+00	2.12E+01	1.61E+01
MFSD4B	1.34E+02	1.78E-02	5.31E-02	1.55E+00	6.35E-01	1.55E+00	8.48E+00	5.46E+00
MAP7	2.73E+02	1.81E-02	5.38E-02	1.82E+00	8.63E-01	1.82E+00	1.83E+01	1.00E+01

LOC504207	1.27E+00	1.83E-02	5.42E-02	6.83E+00	2.77E+00	6.83E+00	1.12E-01	1.64E-02
C15H11orf16	2.02E+02	1.85E-02	5.45E-02	2.27E+00	1.18E+00	2.27E+00	1.45E+01	6.37E+00
SH2D2A	4.14E+01	1.85E-02	5.45E-02	1.60E+00	6.75E-01	1.60E+00	2.65E+00	1.66E+00
TIGD7	1.06E+02	1.87E-02	5.48E-02	1.36E+00	4.43E-01	1.36E+00	6.38E+00	4.70E+00
LOC107132300	2.23E+00	1.88E-02	5.49E-02	6.22E+00	2.64E+00	6.22E+00	1.95E-01	3.13E-02
EFCAB10	4.30E+01	2.02E-02	5.88E-02	2.27E+00	1.19E+00	2.27E+00	3.08E+00	1.35E+00
XR_003031394.1	2.28E+01	2.03E-02	5.88E-02	6.39E+00	2.68E+00	6.39E+00	1.99E+00	3.12E-01
XR_003037756.1	1.91E+00	2.03E-02	5.88E-02	2.24E+00	1.16E+00	2.24E+00	1.36E-01	6.08E-02
PRDM15	3.20E+02	2.04E-02	5.89E-02	1.43E+00	5.21E-01	1.43E+00	1.96E+01	1.37E+01
LOC104974272	7.25E+00	2.07E-02	5.94E-02	1.95E+00	9.63E-01	1.95E+00	4.96E-01	2.55E-01
LOC527981	2.00E+02	2.07E-02	5.94E-02	2.32E+00	1.22E+00	2.32E+00	1.44E+01	6.20E+00
RICTOR	3.95E+02	2.08E-02	5.94E-02	1.40E+00	4.83E-01	1.40E+00	2.40E+01	1.72E+01
XR_806817.3	2.36E+00	2.09E-02	5.94E-02	4.77E+00	2.25E+00	4.77E+00	1.98E-01	4.16E-02
XR_001494570.2	1.25E+00	2.12E-02	6.01E-02	4.92E+00	2.30E+00	4.92E+00	1.05E-01	2.14E-02
GGT6	1.72E+01	2.13E-02	6.01E-02	4.43E+00	2.15E+00	4.43E+00	1.43E+00	3.23E-01
ANKRD53	2.26E+01	2.15E-02	6.05E-02	1.67E+00	7.40E-01	1.67E+00	1.47E+00	8.80E-01
XR_003030037.1	2.16E+00	2.17E-02	6.09E-02	5.74E+00	2.52E+00	5.74E+00	1.87E-01	3.25E-02
CWC25	9.33E+01	2.17E-02	6.09E-02	1.35E+00	4.37E-01	1.35E+00	5.61E+00	4.14E+00
BHLHA9	4.46E+00	2.20E-02	6.13E-02	2.79E+00	1.48E+00	2.79E+00	3.37E-01	1.21E-01
LOC101906472	1.13E+01	2.20E-02	6.13E-02	4.30E+00	2.10E+00	4.30E+00	9.34E-01	2.17E-01
XR_003037448.1	1.24E+01	2.23E-02	6.17E-02	6.01E+00	2.59E+00	6.01E+00	1.08E+00	1.79E-01
XR_003030941.1	5.99E+01	2.23E-02	6.17E-02	1.59E+00	6.69E-01	1.59E+00	3.83E+00	2.41E+00
SNAI3	4.05E+01	2.29E-02	6.31E-02	2.41E+00	1.27E+00	2.41E+00	2.95E+00	1.22E+00
LOC112447087	3.27E+02	2.30E-02	6.31E-02	1.79E+00	8.44E-01	1.79E+00	2.18E+01	1.21E+01
PUSL1	1.22E+02	2.32E-02	6.34E-02	1.32E+00	4.04E-01	1.32E+00	7.27E+00	5.49E+00
XR_003031397.1	8.17E+01	2.33E-02	6.36E-02	2.12E+00	1.08E+00	2.12E+00	5.73E+00	2.70E+00
CARMIL2	1.76E+02	2.33E-02	6.36E-02	2.07E+00	1.05E+00	2.07E+00	1.23E+01	5.93E+00
C6H4orf50	2.05E+01	2.35E-02	6.36E-02	1.99E+00	9.93E-01	1.99E+00	1.41E+00	7.08E-01
UNC13B	1.05E+03	2.45E-02	6.62E-02	1.48E+00	5.70E-01	1.48E+00	6.54E+01	4.40E+01
NR_038195.1	1.99E+01	2.51E-02	6.77E-02	2.23E+00	1.16E+00	2.23E+00	1.42E+00	6.35E-01
XR_003030045.1	3.44E+00	2.56E-02	6.88E-02	2.12E+00	1.09E+00	2.12E+00	2.42E-01	1.14E-01
XR_003030705.1	6.81E+00	2.58E-02	6.89E-02	2.41E+00	1.27E+00	2.41E+00	4.96E-01	2.06E-01
TRAPPC8	8.18E+02	2.58E-02	6.89E-02	1.22E+00	2.89E-01	1.22E+00	4.71E+01	3.86E+01

ELP1	7.76E+02	2.60E-02	6.92E-02	1.34E+00	4.26E-01	1.34E+00	4.65E+01	3.46E+01
RBP7	2.76E+00	2.61E-02	6.92E-02	3.02E+00	1.59E+00	3.02E+00	2.12E-01	7.04E-02
LOC509884	1.14E+00	2.69E-02	7.12E-02	2.09E+01	4.38E+00	2.09E+01	1.09E-01	5.22E-03
XR_001494342.2	2.78E+00	2.70E-02	7.12E-02	6.23E+00	2.64E+00	6.23E+00	2.43E-01	3.90E-02
EXOC4	1.11E+03	2.71E-02	7.14E-02	1.20E+00	2.59E-01	1.20E+00	6.31E+01	5.27E+01
LOC112442545	1.98E+01	2.72E-02	7.14E-02	1.66E+00	7.29E-01	1.66E+00	1.28E+00	7.73E-01
GJA8	6.10E+00	2.73E-02	7.15E-02	2.36E+00	1.24E+00	2.36E+00	4.42E-01	1.87E-01
NOS1	1.47E+02	2.76E-02	7.18E-02	2.74E+00	1.46E+00	2.74E+00	1.10E+01	4.03E+00
COBL	6.94E+01	2.76E-02	7.19E-02	1.73E+00	7.94E-01	1.73E+00	4.57E+00	2.63E+00
SCEL	6.40E+00	2.78E-02	7.21E-02	3.76E+00	1.91E+00	3.76E+00	5.17E-01	1.37E-01
NHSL1	3.44E+02	2.84E-02	7.33E-02	1.51E+00	5.95E-01	1.51E+00	2.15E+01	1.43E+01
XR_003035705.1	8.30E+00	2.84E-02	7.33E-02	7.59E+00	2.92E+00	7.59E+00	7.42E-01	9.78E-02
LOC107131950	1.95E+00	2.86E-02	7.35E-02	3.18E+00	1.67E+00	3.18E+00	1.52E-01	4.78E-02
NAT10	1.51E+03	2.89E-02	7.38E-02	1.31E+00	3.95E-01	1.31E+00	8.96E+01	6.82E+01
MTNR1A	4.26E+00	2.89E-02	7.38E-02	8.98E+00	3.17E+00	8.98E+00	3.87E-01	4.31E-02
TRIM64	4.08E+00	2.96E-02	7.51E-02	7.74E+00	2.95E+00	7.74E+00	3.66E-01	4.72E-02
XR_003035190.1	1.68E+01	2.97E-02	7.51E-02	2.55E+00	1.35E+00	2.55E+00	1.24E+00	4.87E-01
KLHL3	2.36E+02	2.97E-02	7.51E-02	1.52E+00	6.04E-01	1.52E+00	1.48E+01	9.74E+00
HTR1B	1.12E+01	2.98E-02	7.51E-02	2.24E+00	1.16E+00	2.24E+00	8.00E-01	3.57E-01
MRS2	2.95E+02	2.98E-02	7.51E-02	1.24E+00	3.07E-01	1.24E+00	1.71E+01	1.38E+01
GPR84	7.59E+00	3.00E-02	7.54E-02	2.25E+00	1.17E+00	2.25E+00	5.42E-01	2.41E-01
XR_003032263.1	1.04E+01	3.03E-02	7.58E-02	2.06E+00	1.04E+00	2.06E+00	7.25E-01	3.53E-01
KDM4C	2.85E+02	3.06E-02	7.64E-02	1.18E+00	2.36E-01	1.18E+00	1.61E+01	1.37E+01
XR_003037892.1	5.04E+00	3.10E-02	7.72E-02	2.75E+00	1.46E+00	2.75E+00	3.79E-01	1.38E-01
SLC23A1	9.18E+01	3.15E-02	7.81E-02	1.61E+00	6.83E-01	1.61E+00	5.88E+00	3.66E+00
XR_003033448.1	2.95E+01	3.16E-02	7.81E-02	2.94E+00	1.56E+00	2.94E+00	2.26E+00	7.66E-01
FNDC7	6.07E+00	3.21E-02	7.90E-02	2.92E+00	1.55E+00	2.92E+00	4.64E-01	1.59E-01
RNF133	5.60E+00	3.21E-02	7.90E-02	1.77E+00	8.21E-01	1.77E+00	3.71E-01	2.10E-01
XR_003037547.1	9.64E+00	3.27E-02	8.03E-02	2.56E+00	1.36E+00	2.56E+00	7.14E-01	2.78E-01
CAND1	2.43E+03	3.31E-02	8.07E-02	1.18E+00	2.38E-01	1.18E+00	1.38E+02	1.17E+02
SLC28A2	3.59E+01	3.31E-02	8.07E-02	1.77E+00	8.23E-01	1.77E+00	2.38E+00	1.34E+00
LOC529036	1.20E+01	3.35E-02	8.16E-02	6.11E+00	2.61E+00	6.11E+00	1.05E+00	1.72E-01
ZACN	1.77E+00	3.36E-02	8.16E-02	2.50E+00	1.32E+00	2.50E+00	1.30E-01	5.20E-02

LOC112445019	1.30E+00	3.37E-02	8.16E-02	2.74E+00	1.45E+00	2.74E+00	9.77E-02	3.57E-02
LOC506121	1.31E+00	3.41E-02	8.22E-02	7.58E+00	2.92E+00	7.58E+00	1.17E-01	1.55E-02
SLC1A1	1.86E+01	3.42E-02	8.22E-02	2.55E+00	1.35E+00	2.55E+00	1.37E+00	5.39E-01
RWDD2A	1.76E+02	3.49E-02	8.36E-02	1.28E+00	3.57E-01	1.28E+00	1.04E+01	8.09E+00
GLRX	3.71E+02	3.51E-02	8.40E-02	1.47E+00	5.54E-01	1.47E+00	2.30E+01	1.57E+01
XR_003030796.1	5.89E+01	3.55E-02	8.46E-02	2.02E+00	1.02E+00	2.02E+00	4.08E+00	2.02E+00
HSH2D	2.17E+01	3.56E-02	8.47E-02	1.66E+00	7.33E-01	1.66E+00	1.40E+00	8.45E-01
SUPT3H	6.59E+02	3.60E-02	8.54E-02	1.18E+00	2.37E-01	1.18E+00	3.74E+01	3.17E+01
ERMP1	6.91E+02	3.63E-02	8.59E-02	1.32E+00	4.06E-01	1.32E+00	4.11E+01	3.11E+01
USP13	4.12E+02	3.64E-02	8.59E-02	1.25E+00	3.24E-01	1.25E+00	2.39E+01	1.91E+01
XR_001495971.2	2.70E+00	3.67E-02	8.63E-02	5.44E+00	2.44E+00	5.44E+00	2.32E-01	4.26E-02
CCDC42	2.09E+02	3.68E-02	8.63E-02	2.07E+00	1.05E+00	2.07E+00	1.45E+01	7.04E+00
XR_003034336.1	5.24E+00	3.68E-02	8.63E-02	1.70E+00	7.68E-01	1.70E+00	3.43E-01	2.01E-01
DDHD1	4.55E+02	3.70E-02	8.63E-02	1.27E+00	3.39E-01	1.27E+00	2.66E+01	2.10E+01
XR_812060.3	4.21E+00	3.75E-02	8.73E-02	1.84E+00	8.79E-01	1.84E+00	2.83E-01	1.54E-01
XR_003032242.1	1.80E+00	3.77E-02	8.75E-02	6.85E+00	2.78E+00	6.85E+00	1.60E-01	2.33E-02
NF1	5.25E+00	3.78E-02	8.75E-02	2.40E+00	1.26E+00	2.40E+00	3.81E-01	1.59E-01
XR_812473.3	1.85E+00	3.85E-02	8.91E-02	2.50E+00	1.32E+00	2.50E+00	1.36E-01	5.45E-02
ANO10	6.09E+02	3.88E-02	8.93E-02	1.23E+00	3.02E-01	1.23E+00	3.52E+01	2.86E+01
SMURF1	1.35E+03	3.96E-02	9.08E-02	1.45E+00	5.41E-01	1.45E+00	8.34E+01	5.74E+01
CCDC171	1.21E+02	3.96E-02	9.08E-02	1.42E+00	5.02E-01	1.42E+00	7.43E+00	5.24E+00
XR_003030709.1	1.19E+00	4.15E-02	9.49E-02	4.51E+00	2.17E+00	4.51E+00	9.92E-02	2.20E-02
XR_806191.2	2.22E+00	4.21E-02	9.61E-02	4.37E+00	2.13E+00	4.37E+00	1.84E-01	4.21E-02
STK3	8.12E+02	4.23E-02	9.62E-02	1.20E+00	2.60E-01	1.20E+00	4.64E+01	3.87E+01
LOC523431	4.61E+00	4.25E-02	9.64E-02	2.92E+00	1.54E+00	2.92E+00	3.53E-01	1.21E-01
RAPH1	7.19E+02	4.34E-02	9.79E-02	1.35E+00	4.28E-01	1.35E+00	4.31E+01	3.20E+01
MTHFD1	1.53E+03	4.34E-02	9.79E-02	1.19E+00	2.56E-01	1.19E+00	8.71E+01	7.29E+01
GSX2	4.06E+00	4.35E-02	9.79E-02	3.25E+00	1.70E+00	3.25E+00	3.18E-01	9.77E-02
AKNAD1	1.81E+01	4.37E-02	9.81E-02	3.24E+00	1.70E+00	3.24E+00	1.42E+00	4.37E-01
GPR52	2.84E+00	4.39E-02	9.82E-02	2.57E+00	1.36E+00	2.57E+00	2.10E-01	8.18E-02
XR_001500112.2	1.04E+01	4.41E-02	9.85E-02	1.94E+00	9.58E-01	1.94E+00	7.14E-01	3.67E-01
LOC101903953	1.05E+01	4.45E-02	9.90E-02	2.63E+00	1.40E+00	2.63E+00	7.82E-01	2.97E-01
XR_001501639.2	2.27E+00	4.54E-02	1.01E-01	3.11E+00	1.64E+00	3.11E+00	1.76E-01	5.66E-02

LOC100138454	1.98E+00	4.54E-02	1.01E-01	1.85E+00	8.87E-01	1.85E+00	1.33E-01	7.22E-02
LOC101906595	2.11E+00	4.55E-02	1.01E-01	3.20E+00	1.68E+00	3.20E+00	1.65E-01	5.14E-02
IL1R2	6.55E+00	4.60E-02	1.01E-01	2.23E+00	1.16E+00	2.23E+00	4.67E-01	2.09E-01
XR_003035679.1	2.35E+00	4.61E-02	1.01E-01	3.00E+00	1.58E+00	3.00E+00	1.81E-01	6.03E-02
LOC785036	1.85E+00	4.66E-02	1.02E-01	1.64E+01	4.03E+00	1.64E+01	1.75E-01	1.07E-02
SERPINA6	6.84E+00	4.68E-02	1.02E-01	1.35E+00	4.30E-01	1.35E+00	4.10E-01	3.04E-01
XR_003035851.1	8.74E+00	4.75E-02	1.04E-01	2.73E+00	1.45E+00	2.73E+00	6.57E-01	2.41E-01
GDI2	6.87E+03	4.77E-02	1.04E-01	1.11E+00	1.50E-01	1.11E+00	3.79E+02	3.42E+02
CLIP4	9.49E+01	4.79E-02	1.04E-01	1.60E+00	6.82E-01	1.60E+00	6.08E+00	3.79E+00
LOC618124	1.15E+00	4.82E-02	1.04E-01	9.24E+00	3.21E+00	9.24E+00	1.04E-01	1.13E-02
PLA2G12B	4.07E+00	4.84E-02	1.05E-01	2.23E+00	1.15E+00	2.23E+00	2.90E-01	1.30E-01
DAPK2	2.23E+02	4.89E-02	1.06E-01	1.25E+00	3.17E-01	1.25E+00	1.30E+01	1.04E+01
ADAD1	2.52E+02	4.91E-02	1.06E-01	2.11E+00	1.08E+00	2.11E+00	1.77E+01	8.38E+00
GPR39	5.86E+01	4.92E-02	1.06E-01	1.72E+00	7.80E-01	1.72E+00	3.85E+00	2.24E+00
XR_003034709.1	3.55E+00	5.04E-02	1.08E-01	2.53E+00	1.34E+00	2.53E+00	2.62E-01	1.03E-01
FAM21A	1.51E+03	5.09E-02	1.08E-01	1.16E+00	2.13E-01	1.16E+00	8.49E+01	7.32E+01
LOC100337053	1.52E+01	5.09E-02	1.08E-01	2.40E+00	1.26E+00	2.40E+00	1.10E+00	4.59E-01
XR_003035120.1	1.55E+00	5.10E-02	1.08E-01	2.60E+01	4.70E+00	2.60E+01	1.50E-01	5.76E-03
XR_003037120.1	2.55E+00	5.11E-02	1.08E-01	4.32E+00	2.11E+00	4.32E+00	2.11E-01	4.87E-02
XR_001500662.2	1.08E+01	5.11E-02	1.08E-01	6.73E+00	2.75E+00	6.73E+00	9.56E-01	1.42E-01
XR_003038077.1	5.21E+00	5.12E-02	1.08E-01	2.07E+00	1.05E+00	2.07E+00	3.63E-01	1.76E-01
XR_003037237.1	2.17E+00	5.20E-02	1.09E-01	5.08E+00	2.35E+00	5.08E+00	1.84E-01	3.62E-02
XR_003037220.1	9.76E+00	5.23E-02	1.10E-01	4.32E+00	2.11E+00	4.32E+00	8.07E-01	1.87E-01
TTC39C	2.02E+02	5.35E-02	1.12E-01	1.35E+00	4.37E-01	1.35E+00	1.21E+01	8.95E+00
LOC107132230	3.29E+00	5.36E-02	1.12E-01	2.51E+00	1.33E+00	2.51E+00	2.42E-01	9.65E-02
XR_003036833.1	3.43E+00	5.46E-02	1.14E-01	3.55E+00	1.83E+00	3.55E+00	2.73E-01	7.71E-02
HIGD1C	6.93E+00	5.49E-02	1.14E-01	2.23E+00	1.15E+00	2.23E+00	4.94E-01	2.22E-01
LOC112445104	8.59E+00	5.71E-02	1.18E-01	1.11E+00	1.54E-01	1.11E+00	4.75E-01	4.27E-01
HRCT1	1.65E+02	5.75E-02	1.19E-01	1.31E+00	3.88E-01	1.31E+00	9.75E+00	7.45E+00
XR_237971.4	2.18E+01	5.76E-02	1.19E-01	1.52E+00	6.06E-01	1.52E+00	1.37E+00	9.02E-01
SLC17A4	2.69E+00	5.77E-02	1.19E-01	1.21E+01	3.60E+00	1.21E+01	2.50E-01	2.07E-02
MEX3C	1.87E+03	5.84E-02	1.20E-01	1.21E+00	2.76E-01	1.21E+00	1.07E+02	8.86E+01
CLDN23	1.29E+01	5.90E-02	1.21E-01	2.52E+00	1.33E+00	2.52E+00	9.51E-01	3.77E-01

XR_001500630.2	2.30E+00	5.99E-02	1.23E-01	1.65E+00	7.24E-01	1.65E+00	1.49E-01	9.02E-02
APBA1	7.30E+02	6.12E-02	1.25E-01	1.50E+00	5.83E-01	1.50E+00	4.56E+01	3.04E+01
XR_003029667.1	2.55E+00	6.14E-02	1.25E-01	1.80E+00	8.51E-01	1.80E+00	1.70E-01	9.45E-02
CPEB3	2.36E+02	6.17E-02	1.25E-01	1.49E+00	5.78E-01	1.49E+00	1.48E+01	9.88E+00
PTPRQ	1.73E+01	6.22E-02	1.26E-01	2.73E+00	1.45E+00	2.73E+00	1.30E+00	4.77E-01
XR_003030783.1	3.24E+00	6.25E-02	1.26E-01	3.16E+00	1.66E+00	3.16E+00	2.52E-01	8.00E-02
XR_001494442.2	1.97E+00	6.29E-02	1.27E-01	4.09E+00	2.03E+00	4.09E+00	1.62E-01	3.95E-02
CFAP58	1.81E+01	6.43E-02	1.29E-01	2.10E+00	1.07E+00	2.10E+00	1.27E+00	6.04E-01
SLC36A1	3.49E+02	6.53E-02	1.31E-01	1.33E+00	4.06E-01	1.33E+00	2.08E+01	1.57E+01
XR_003030235.1	2.48E+00	6.55E-02	1.31E-01	2.37E+01	4.57E+00	2.37E+01	2.39E-01	1.00E-02
XR_001498507.2	4.97E+00	6.59E-02	1.32E-01	3.09E+00	1.63E+00	3.09E+00	3.85E-01	1.25E-01
LOC100337152	1.10E+01	6.62E-02	1.32E-01	1.49E+00	5.76E-01	1.49E+00	6.88E-01	4.61E-01
XR_003034667.1	2.38E+00	6.65E-02	1.32E-01	1.82E+00	8.63E-01	1.82E+00	1.59E-01	8.74E-02
TENM1	1.54E+02	6.66E-02	1.32E-01	1.72E+00	7.82E-01	1.72E+00	1.01E+01	5.86E+00
ZNF182	1.75E+02	6.73E-02	1.33E-01	1.23E+00	2.96E-01	1.23E+00	1.01E+01	8.24E+00
LOC785617	7.60E+00	6.73E-02	1.33E-01	2.16E+00	1.11E+00	2.16E+00	5.36E-01	2.49E-01
CRH	5.46E+01	6.80E-02	1.34E-01	1.58E+00	6.60E-01	1.58E+00	3.48E+00	2.20E+00
ZNF648	1.46E+00	6.80E-02	1.34E-01	2.98E+00	1.58E+00	2.98E+00	1.12E-01	3.76E-02
B3GALT2	1.50E+02	6.84E-02	1.34E-01	1.37E+00	4.52E-01	1.37E+00	9.07E+00	6.63E+00
ASMT	2.35E+01	6.85E-02	1.34E-01	1.52E+00	6.06E-01	1.52E+00	1.48E+00	9.71E-01
C16H1orf105	9.46E+01	6.88E-02	1.34E-01	1.45E+00	5.36E-01	1.45E+00	5.83E+00	4.02E+00
C7H19orf67	4.90E+01	7.01E-02	1.37E-01	1.70E+00	7.61E-01	1.70E+00	3.20E+00	1.89E+00
PARG	7.70E+02	7.04E-02	1.37E-01	1.16E+00	2.09E-01	1.16E+00	4.33E+01	3.75E+01
TRIM45	3.70E+02	7.06E-02	1.37E-01	1.29E+00	3.72E-01	1.29E+00	2.18E+01	1.69E+01
ZNF304	3.87E+02	7.32E-02	1.42E-01	1.16E+00	2.14E-01	1.16E+00	2.18E+01	1.88E+01
LOC615183	3.03E+01	7.46E-02	1.44E-01	2.07E+00	1.05E+00	2.07E+00	2.11E+00	1.02E+00
LOC112449108	1.31E+01	7.54E-02	1.45E-01	1.88E+00	9.12E-01	1.88E+00	8.86E-01	4.71E-01
LOC788599	6.21E+01	7.62E-02	1.47E-01	1.35E+00	4.36E-01	1.35E+00	3.73E+00	2.76E+00
PHTF1	4.37E+02	7.75E-02	1.48E-01	1.19E+00	2.50E-01	1.19E+00	2.49E+01	2.09E+01
XR_233302.4	3.27E+00	7.75E-02	1.48E-01	2.84E+00	1.51E+00	2.84E+00	2.48E-01	8.73E-02
XR_003036862.1	1.04E+01	7.77E-02	1.48E-01	1.47E+00	5.60E-01	1.47E+00	6.48E-01	4.39E-01
XR_003037246.1	4.26E+00	7.77E-02	1.48E-01	2.36E+00	1.24E+00	2.36E+00	3.09E-01	1.30E-01
XR_003030782.1	7.18E+00	7.92E-02	1.50E-01	4.77E+00	2.25E+00	4.77E+00	6.04E-01	1.27E-01

NKX1-1	2.61E+00	7.92E-02	1.50E-01	3.64E+00	1.86E+00	3.64E+00	2.09E-01	5.75E-02
XR_003035096.1	3.46E-01	7.97E-02	1.51E-01	7.04E+01	6.14E+00	7.04E+01	3.42E-02	4.86E-04
ATRNL1	7.31E+02	8.01E-02	1.51E-01	1.28E+00	3.52E-01	1.28E+00	4.29E+01	3.36E+01
LOC112443761	8.02E+00	8.05E-02	1.51E-01	2.07E+00	1.05E+00	2.07E+00	5.59E-01	2.70E-01
TP63	4.35E+01	8.05E-02	1.51E-01	2.72E+00	1.44E+00	2.72E+00	3.27E+00	1.20E+00
XR_003035121.1	2.25E+00	8.09E-02	1.52E-01	4.71E+01	5.56E+00	4.71E+01	2.20E-01	4.68E-03
LOC100336282	9.69E+01	8.24E-02	1.54E-01	1.61E+00	6.89E-01	1.61E+00	6.22E+00	3.86E+00
TDRD15	4.52E+01	8.34E-02	1.56E-01	1.91E+00	9.37E-01	1.91E+00	3.08E+00	1.61E+00
CCL17	5.07E+00	8.62E-02	1.61E-01	1.68E+00	7.50E-01	1.68E+00	3.30E-01	1.96E-01
XR_003031463.1	2.05E+00	8.71E-02	1.62E-01	5.14E+00	2.36E+00	5.14E+00	1.74E-01	3.39E-02
LRRC51	1.24E+02	8.76E-02	1.63E-01	1.60E+00	6.80E-01	1.60E+00	7.97E+00	4.97E+00
CHL1	4.70E+02	8.90E-02	1.65E-01	2.10E+00	1.07E+00	2.10E+00	3.29E+01	1.56E+01
XR_001494316.2	1.59E+01	8.94E-02	1.65E-01	1.57E+00	6.53E-01	1.57E+00	1.01E+00	6.44E-01
XR_003035103.1	5.22E+00	8.94E-02	1.65E-01	2.32E+00	1.21E+00	2.32E+00	3.76E-01	1.62E-01
SLC17A8	8.57E+00	8.98E-02	1.65E-01	2.93E+00	1.55E+00	2.93E+00	6.56E-01	2.24E-01
DRD2	3.85E+00	9.04E-02	1.66E-01	2.21E+00	1.15E+00	2.21E+00	2.74E-01	1.24E-01
XR_001500537.2	1.93E+00	9.05E-02	1.66E-01	4.84E+00	2.27E+00	4.84E+00	1.63E-01	3.36E-02
LOC112444595	4.03E+01	9.18E-02	1.68E-01	7.86E-01	-3.48E-01	-1.27E+00	1.88E+00	2.39E+00
TMEM131	2.12E+03	9.25E-02	1.69E-01	1.14E+00	1.91E-01	1.14E+00	1.19E+02	1.04E+02
PCDHB1	1.28E+01	9.27E-02	1.69E-01	2.30E+00	1.20E+00	2.30E+00	9.20E-01	4.00E-01
NELL1	3.53E+01	9.33E-02	1.70E-01	2.23E+00	1.16E+00	2.23E+00	2.52E+00	1.13E+00
GRHPR	7.78E+02	9.38E-02	1.70E-01	1.26E+00	3.29E-01	1.26E+00	4.53E+01	3.61E+01
CCDC88A	9.87E+02	9.38E-02	1.70E-01	1.16E+00	2.15E-01	1.16E+00	5.56E+01	4.79E+01
XR_003030447.1	7.05E+00	9.41E-02	1.70E-01	1.86E+00	8.96E-01	1.86E+00	4.75E-01	2.55E-01
MALRD1	5.59E+01	9.56E-02	1.72E-01	2.69E+00	1.43E+00	2.69E+00	4.19E+00	1.56E+00
LRMDA	3.72E+01	9.57E-02	1.72E-01	1.36E+00	4.47E-01	1.36E+00	2.24E+00	1.64E+00
SCG3	1.54E+01	9.64E-02	1.73E-01	1.78E+00	8.30E-01	1.78E+00	1.03E+00	5.77E-01
B3GNT4	7.94E+01	9.81E-02	1.76E-01	1.78E+00	8.28E-01	1.78E+00	5.27E+00	2.97E+00
TOR2A	2.61E+02	9.87E-02	1.76E-01	1.31E+00	3.85E-01	1.31E+00	1.54E+01	1.18E+01
XR_233990.4	3.48E+00	9.89E-02	1.77E-01	1.72E+00	7.84E-01	1.72E+00	2.29E-01	1.33E-01
CD177	1.67E+01	1.00E-01	1.78E-01	2.01E+00	1.01E+00	2.01E+00	1.15E+00	5.73E-01
XR_003034451.1	5.46E+01	1.01E-01	1.79E-01	1.33E+00	4.10E-01	1.33E+00	3.26E+00	2.45E+00
XR_003036476.1	2.30E+01	1.01E-01	1.80E-01	2.12E+00	1.08E+00	2.12E+00	1.62E+00	7.64E-01

KIF28	4.65E+00	1.04E-01	1.85E-01	1.61E+00	6.87E-01	1.61E+00	2.98E-01	1.85E-01
MAATS1	6.87E+01	1.05E-01	1.85E-01	1.65E+00	7.21E-01	1.65E+00	4.44E+00	2.70E+00
RASGRP1	1.38E+02	1.05E-01	1.85E-01	1.59E+00	6.66E-01	1.59E+00	8.79E+00	5.54E+00
LOC530211	3.62E+01	1.05E-01	1.85E-01	1.32E+00	3.97E-01	1.32E+00	2.15E+00	1.63E+00
MFRP	1.16E+01	1.06E-01	1.85E-01	3.16E+00	1.66E+00	3.16E+00	9.04E-01	2.86E-01
MGC137454	1.57E+00	1.06E-01	1.85E-01	2.19E+00	1.13E+00	2.19E+00	1.11E-01	5.08E-02
MBOAT1	2.41E+02	1.07E-01	1.86E-01	1.24E+00	3.15E-01	1.24E+00	1.40E+01	1.12E+01
XR_003033848.1	3.75E+01	1.07E-01	1.86E-01	2.89E+00	1.53E+00	2.89E+00	2.86E+00	9.89E-01
XR_003037318.1	1.43E+00	1.08E-01	1.88E-01	6.63E+01	6.05E+00	6.63E+01	1.41E-01	2.13E-03
XR_003037750.1	9.87E+00	1.09E-01	1.89E-01	1.87E+00	9.04E-01	1.87E+00	6.67E-01	3.56E-01
EYA2	4.70E+01	1.10E-01	1.91E-01	2.05E+00	1.04E+00	2.05E+00	3.27E+00	1.59E+00
KALRN	9.15E+02	1.11E-01	1.92E-01	1.21E+00	2.76E-01	1.21E+00	5.25E+01	4.33E+01
LOC107132735	1.07E+01	1.13E-01	1.95E-01	1.43E+00	5.19E-01	1.43E+00	6.59E-01	4.60E-01
XR_003031396.1	6.66E+00	1.17E-01	2.01E-01	2.75E+00	1.46E+00	2.75E+00	5.02E-01	1.83E-01
KIF2A	3.58E+02	1.17E-01	2.02E-01	1.20E+00	2.67E-01	1.20E+00	2.05E+01	1.70E+01
ARHGEF33	3.99E+01	1.21E-01	2.07E-01	1.89E+00	9.15E-01	1.89E+00	2.70E+00	1.43E+00
XR_001494879.2	1.01E+01	1.22E-01	2.09E-01	2.24E+00	1.16E+00	2.24E+00	7.23E-01	3.23E-01
TTLL4	7.92E+02	1.23E-01	2.11E-01	1.26E+00	3.31E-01	1.26E+00	4.62E+01	3.67E+01
ATOH7	5.75E+00	1.24E-01	2.11E-01	2.18E+00	1.12E+00	2.18E+00	4.07E-01	1.87E-01
SETD2	2.35E+03	1.26E-01	2.15E-01	1.17E+00	2.26E-01	1.17E+00	1.33E+02	1.13E+02
XR_814952.3	5.04E-01	1.26E-01	2.15E-01	1.03E+02	6.68E+00	1.03E+02	5.00E-02	4.86E-04
XR_003033532.1	3.20E+00	1.28E-01	2.17E-01	2.84E+00	1.51E+00	2.84E+00	2.43E-01	8.56E-02
XR_003037902.1	1.30E+00	1.29E-01	2.18E-01	2.47E+00	1.30E+00	2.47E+00	9.55E-02	3.87E-02
VRTN	1.85E+02	1.32E-01	2.23E-01	9.05E-01	-1.45E-01	-1.11E+00	9.29E+00	1.03E+01
SLC12A2	2.73E+02	1.32E-01	2.23E-01	1.25E+00	3.26E-01	1.25E+00	1.59E+01	1.27E+01
GSDMC	3.25E+00	1.34E-01	2.25E-01	2.18E+00	1.13E+00	2.18E+00	2.30E-01	1.06E-01
SHISA9	5.79E+01	1.36E-01	2.29E-01	1.99E+00	9.90E-01	1.99E+00	3.98E+00	2.01E+00
XR_003031258.1	3.13E+00	1.37E-01	2.30E-01	1.71E+00	7.78E-01	1.71E+00	2.05E-01	1.20E-01
XR_001502079.2	2.83E+01	1.38E-01	2.30E-01	1.46E+00	5.46E-01	1.46E+00	1.75E+00	1.20E+00
LOC785712	8.17E-01	1.38E-01	2.31E-01	2.34E+00	1.23E+00	2.34E+00	5.90E-02	2.52E-02
CIT	1.25E+03	1.39E-01	2.31E-01	1.20E+00	2.64E-01	1.20E+00	7.15E+01	5.95E+01
CDH26	2.37E+00	1.42E-01	2.37E-01	4.49E+00	2.17E+00	4.49E+00	1.97E-01	4.39E-02
HRG	3.22E+00	1.43E-01	2.38E-01	1.85E+00	8.90E-01	1.85E+00	2.17E-01	1.17E-01

THSD7B	4.68E+01	1.44E-01	2.38E-01	1.67E+00	7.38E-01	1.67E+00	3.04E+00	1.82E+00
SLC45A1	1.34E+01	1.46E-01	2.41E-01	1.51E+00	5.93E-01	1.51E+00	8.36E-01	5.54E-01
XR_816662.3	1.65E+01	1.46E-01	2.41E-01	5.20E+00	2.38E+00	5.20E+00	1.40E+00	2.70E-01
PRKDC	8.83E+02	1.46E-01	2.41E-01	1.19E+00	2.52E-01	1.19E+00	5.03E+01	4.22E+01
RAB27A	2.39E+02	1.46E-01	2.41E-01	1.20E+00	2.58E-01	1.20E+00	1.36E+01	1.14E+01
LYPD6B	3.19E+01	1.48E-01	2.42E-01	2.04E+00	1.03E+00	2.04E+00	2.21E+00	1.09E+00
SMARCAL1	1.70E+03	1.48E-01	2.44E-01	1.19E+00	2.53E-01	1.19E+00	9.71E+01	8.15E+01
MGC138914	1.97E+00	1.49E-01	2.44E-01	8.86E-01	-1.74E-01	-1.13E+00	9.75E-02	1.10E-01
XR_003031815.1	2.29E+00	1.50E-01	2.45E-01	2.13E+00	1.09E+00	2.13E+00	1.61E-01	7.58E-02
TRIM24	1.48E+03	1.54E-01	2.51E-01	1.19E+00	2.50E-01	1.19E+00	8.40E+01	7.07E+01
GDAP2	2.24E+02	1.56E-01	2.54E-01	1.14E+00	1.93E-01	1.14E+00	1.25E+01	1.10E+01
XR_003032559.1	9.74E+00	1.57E-01	2.55E-01	1.71E+00	7.76E-01	1.71E+00	6.38E-01	3.73E-01
XR_003031850.1	1.57E+00	1.57E-01	2.55E-01	3.12E+00	1.64E+00	3.12E+00	1.22E-01	3.90E-02
XR_234317.4	1.48E+01	1.59E-01	2.56E-01	1.62E+00	6.93E-01	1.62E+00	9.52E-01	5.89E-01
SCLT1	1.49E+02	1.59E-01	2.56E-01	1.21E+00	2.74E-01	1.21E+00	8.55E+00	7.07E+00
XR_003032471.1	2.91E+00	1.59E-01	2.56E-01	1.68E+00	7.50E-01	1.68E+00	1.90E-01	1.13E-01
STXBP6	5.29E+02	1.59E-01	2.57E-01	1.26E+00	3.38E-01	1.26E+00	3.09E+01	2.45E+01
ADORA2B	7.85E+01	1.60E-01	2.57E-01	1.22E+00	2.84E-01	1.22E+00	4.51E+00	3.71E+00
XR_003038209.1	5.55E+00	1.60E-01	2.57E-01	4.26E+00	2.09E+00	4.26E+00	4.58E-01	1.07E-01
USH2A	4.30E+01	1.62E-01	2.59E-01	1.49E+00	5.79E-01	1.49E+00	2.68E+00	1.80E+00
PRSS38	1.30E+01	1.63E-01	2.61E-01	1.55E+00	6.31E-01	1.55E+00	8.23E-01	5.31E-01
XR_003030353.1	7.81E+01	1.67E-01	2.66E-01	1.33E+00	4.17E-01	1.33E+00	4.67E+00	3.50E+00
RAD50	2.09E+03	1.68E-01	2.67E-01	1.35E+00	4.29E-01	1.35E+00	1.25E+02	9.32E+01
MFN2	1.63E+03	1.68E-01	2.67E-01	1.14E+00	1.87E-01	1.14E+00	9.08E+01	7.97E+01
GPR12	9.27E+00	1.69E-01	2.67E-01	2.42E+00	1.27E+00	2.42E+00	6.75E-01	2.79E-01
XR_003038187.1	8.21E+00	1.69E-01	2.67E-01	6.26E+00	2.65E+00	6.26E+00	7.18E-01	1.15E-01
PDCD6IP	3.66E+03	1.69E-01	2.67E-01	1.17E+00	2.25E-01	1.17E+00	2.07E+02	1.77E+02
ZDHHC15	1.06E+02	1.70E-01	2.68E-01	1.19E+00	2.52E-01	1.19E+00	6.02E+00	5.05E+00
XR_814551.3	6.10E+00	1.72E-01	2.72E-01	3.41E+00	1.77E+00	3.41E+00	4.83E-01	1.42E-01
XR_235188.4	1.63E+01	1.73E-01	2.72E-01	1.63E+00	7.07E-01	1.63E+00	1.05E+00	6.44E-01
NCBP1	1.06E+03	1.75E-01	2.74E-01	1.12E+00	1.62E-01	1.12E+00	5.89E+01	5.26E+01
DYNC1I2	1.89E+03	1.77E-01	2.77E-01	1.08E+00	1.05E-01	1.08E+00	1.03E+02	9.57E+01
LOC100140356	3.13E+00	1.77E-01	2.77E-01	1.66E+00	7.30E-01	1.66E+00	2.03E-01	1.22E-01

GRAMD2A	3.06E+01	1.81E-01	2.82E-01	1.90E+00	9.25E-01	1.90E+00	2.07E+00	1.09E+00
LOC112447011	3.03E+02	1.83E-01	2.84E-01	1.49E+00	5.80E-01	1.49E+00	1.89E+01	1.27E+01
MSX1	9.12E+01	1.83E-01	2.85E-01	1.22E+00	2.84E-01	1.22E+00	5.24E+00	4.31E+00
XR_003033925.1	1.43E+00	1.86E-01	2.88E-01	9.47E-01	-7.82E-02	-1.06E+00	7.33E-02	7.74E-02
XR_003033279.1	1.10E+00	1.86E-01	2.88E-01	2.77E+00	1.47E+00	2.77E+00	8.29E-02	2.99E-02
XR_003036888.1	9.04E-01	1.88E-01	2.92E-01	5.05E+00	2.34E+00	5.05E+00	7.67E-02	1.52E-02
TBC1D9	1.51E+03	1.90E-01	2.93E-01	1.34E+00	4.21E-01	1.34E+00	9.01E+01	6.73E+01
LOC407145	1.78E+00	1.90E-01	2.93E-01	2.52E+00	1.33E+00	2.52E+00	1.31E-01	5.20E-02
C5	6.99E+00	1.91E-01	2.94E-01	1.34E+00	4.27E-01	1.34E+00	4.19E-01	3.12E-01
ATP6V0A1	1.20E+03	1.93E-01	2.97E-01	1.15E+00	1.99E-01	1.15E+00	6.73E+01	5.86E+01
PTCHD1	2.31E+00	1.95E-01	3.00E-01	8.69E-01	-2.03E-01	-1.15E+00	1.14E-01	1.31E-01
B3GALNT1	3.84E+02	1.96E-01	3.00E-01	1.14E+00	1.88E-01	1.14E+00	2.15E+01	1.88E+01
LOC616002	6.34E+00	1.96E-01	3.00E-01	3.12E+00	1.64E+00	3.12E+00	4.92E-01	1.58E-01
CD164L2	2.09E+01	1.96E-01	3.00E-01	1.41E+00	5.00E-01	1.41E+00	1.28E+00	9.05E-01
C3	2.22E+03	2.00E-01	3.05E-01	1.88E+00	9.09E-01	1.88E+00	1.50E+02	7.98E+01
TRIP12	3.81E+03	2.01E-01	3.05E-01	1.14E+00	1.92E-01	1.14E+00	2.13E+02	1.87E+02
GFI1	5.22E+01	2.01E-01	3.05E-01	1.26E+00	3.29E-01	1.26E+00	3.04E+00	2.42E+00
XR_003033233.1	1.70E+01	2.02E-01	3.05E-01	1.51E+00	5.94E-01	1.51E+00	1.06E+00	7.05E-01
CIDEA	4.47E+01	2.02E-01	3.05E-01	1.21E+00	2.72E-01	1.21E+00	2.56E+00	2.12E+00
CFHR5	2.70E+00	2.02E-01	3.05E-01	1.58E+00	6.56E-01	1.58E+00	1.72E-01	1.09E-01
TBC1D1	1.53E+03	2.03E-01	3.06E-01	1.11E+00	1.46E-01	1.11E+00	8.42E+01	7.61E+01
CENPJ	3.17E+02	2.04E-01	3.06E-01	1.21E+00	2.81E-01	1.21E+00	1.82E+01	1.50E+01
XR_003037903.1	3.93E+00	2.05E-01	3.07E-01	4.11E+00	2.04E+00	4.11E+00	3.23E-01	7.86E-02
ZFP69	4.50E+02	2.05E-01	3.08E-01	1.13E+00	1.74E-01	1.13E+00	2.51E+01	2.22E+01
LOC788414	1.14E+02	2.08E-01	3.11E-01	1.55E+00	6.28E-01	1.55E+00	7.17E+00	4.64E+00
CDH7	2.35E+02	2.08E-01	3.11E-01	2.56E+00	1.36E+00	2.56E+00	1.74E+01	6.78E+00
XR_003029478.1	1.94E+00	2.09E-01	3.12E-01	2.76E+00	1.46E+00	2.76E+00	1.46E-01	5.30E-02
CAPRIN2	2.04E+03	2.10E-01	3.13E-01	1.18E+00	2.38E-01	1.18E+00	1.15E+02	9.79E+01
LOC112449110	1.00E+01	2.12E-01	3.15E-01	2.73E+00	1.45E+00	2.73E+00	7.53E-01	2.76E-01
XR_003029901.1	1.15E+00	2.13E-01	3.17E-01	1.32E+01	3.72E+00	1.32E+01	1.08E-01	8.19E-03
FAM71F2	6.44E+00	2.15E-01	3.18E-01	1.58E+00	6.62E-01	1.58E+00	4.10E-01	2.59E-01
ABCA3	7.20E+02	2.15E-01	3.18E-01	1.31E+00	3.91E-01	1.31E+00	4.27E+01	3.25E+01
GRAP2	1.64E+01	2.19E-01	3.24E-01	1.45E+00	5.40E-01	1.45E+00	1.01E+00	6.98E-01

XR_003035449.1	2.79E+00	2.21E-01	3.25E-01	1.86E+00	8.97E-01	1.86E+00	1.88E-01	1.01E-01
LOC100336903	1.44E+01	2.21E-01	3.26E-01	2.09E+00	1.07E+00	2.09E+00	1.00E+00	4.80E-01
LOC101904580	5.62E+00	2.24E-01	3.29E-01	4.65E+00	2.22E+00	4.65E+00	4.71E-01	1.01E-01
XR_003035607.1	2.81E+01	2.25E-01	3.29E-01	1.25E+00	3.25E-01	1.25E+00	1.63E+00	1.30E+00
KIAA0556	1.17E+03	2.26E-01	3.31E-01	1.18E+00	2.38E-01	1.18E+00	6.61E+01	5.61E+01
PHYHD1	4.92E+02	2.33E-01	3.40E-01	1.11E+00	1.48E-01	1.11E+00	2.72E+01	2.45E+01
XR_816450.3	1.56E+01	2.33E-01	3.40E-01	1.25E+00	3.19E-01	1.25E+00	9.06E-01	7.26E-01
NEIL2	5.80E+02	2.35E-01	3.42E-01	9.08E-01	-1.39E-01	-1.10E+00	2.91E+01	3.21E+01
APH1B	4.64E+02	2.38E-01	3.46E-01	1.37E+00	4.51E-01	1.37E+00	2.80E+01	2.05E+01
LOC100138519	1.59E+00	2.40E-01	3.48E-01	2.80E+00	1.48E+00	2.80E+00	1.20E-01	4.30E-02
XR_807447.3	1.30E+01	2.42E-01	3.50E-01	2.27E+00	1.18E+00	2.27E+00	9.34E-01	4.11E-01
AKAIN1	7.88E-01	2.43E-01	3.52E-01	8.41E+01	6.39E+00	8.41E+01	7.80E-02	9.27E-04
CNOT1	3.08E+03	2.46E-01	3.55E-01	1.17E+00	2.24E-01	1.17E+00	1.74E+02	1.49E+02
NUP133	1.03E+03	2.47E-01	3.55E-01	1.18E+00	2.42E-01	1.18E+00	5.86E+01	4.96E+01
NUBPL	5.27E+01	2.47E-01	3.55E-01	1.17E+00	2.27E-01	1.17E+00	2.98E+00	2.54E+00
EIF4ENIF1	2.02E+03	2.47E-01	3.55E-01	1.20E+00	2.62E-01	1.20E+00	1.16E+02	9.64E+01
CHRNA3-2	3.69E+02	2.47E-01	3.55E-01	1.19E+00	2.54E-01	1.19E+00	2.10E+01	1.76E+01
ZNF181	3.69E+02	2.51E-01	3.59E-01	1.09E+00	1.24E-01	1.09E+00	2.02E+01	1.85E+01
XR_003035965.1	3.73E+00	2.51E-01	3.60E-01	8.86E-01	-1.75E-01	-1.13E+00	1.85E-01	2.09E-01
XR_003031166.1	1.65E+00	2.52E-01	3.60E-01	2.37E+00	1.25E+00	2.37E+00	1.19E-01	5.03E-02
XR_003032403.1	3.11E+00	2.52E-01	3.60E-01	1.58E+00	6.61E-01	1.58E+00	1.98E-01	1.25E-01
UBE2U	4.40E+01	2.53E-01	3.60E-01	1.55E+00	6.33E-01	1.55E+00	2.79E+00	1.80E+00
CFI	4.25E+02	2.54E-01	3.61E-01	1.42E+00	5.05E-01	1.42E+00	2.60E+01	1.83E+01
AGBL2	2.24E+02	2.56E-01	3.63E-01	1.35E+00	4.29E-01	1.35E+00	1.34E+01	9.98E+00
GJB2	7.32E+01	2.57E-01	3.64E-01	1.63E+00	7.08E-01	1.63E+00	4.72E+00	2.89E+00
FAM184A	3.23E+02	2.58E-01	3.65E-01	1.26E+00	3.35E-01	1.26E+00	1.88E+01	1.49E+01
FAM19A1	7.77E+00	2.61E-01	3.69E-01	3.51E+00	1.81E+00	3.51E+00	6.18E-01	1.76E-01
LINGO2	1.15E+02	2.62E-01	3.69E-01	1.41E+00	4.96E-01	1.41E+00	7.02E+00	4.98E+00
C10H15orf61	6.06E+01	2.63E-01	3.70E-01	1.26E+00	3.30E-01	1.26E+00	3.53E+00	2.81E+00
EYA3	1.45E+03	2.65E-01	3.72E-01	1.10E+00	1.36E-01	1.10E+00	7.97E+01	7.25E+01
XR_003030628.1	7.60E+02	2.67E-01	3.75E-01	1.11E+00	1.56E-01	1.11E+00	4.20E+01	3.77E+01
CLEC4G	8.64E+00	2.69E-01	3.77E-01	1.31E+00	3.85E-01	1.31E+00	5.12E-01	3.92E-01
RAI14	1.13E+03	2.70E-01	3.78E-01	1.22E+00	2.91E-01	1.22E+00	6.52E+01	5.33E+01

MAPT	1.31E+02	2.72E-01	3.79E-01	1.32E+00	3.97E-01	1.32E+00	7.76E+00	5.89E+00
XR_003036255.1	2.50E+00	2.76E-01	3.84E-01	7.00E+00	2.81E+00	7.00E+00	2.22E-01	3.17E-02
XR_003034271.1	6.05E+01	2.76E-01	3.84E-01	1.64E+00	7.10E-01	1.64E+00	3.90E+00	2.39E+00
LOC107132775	2.21E+01	2.78E-01	3.86E-01	2.07E+00	1.05E+00	2.07E+00	1.54E+00	7.45E-01
C23H6orf10	5.76E-01	2.79E-01	3.87E-01	1.50E+01	3.91E+00	1.50E+01	5.44E-02	3.63E-03
LOC100296379	1.16E+00	2.81E-01	3.89E-01	6.26E+00	2.65E+00	6.26E+00	1.02E-01	1.63E-02
XR_003031547.1	7.81E+00	2.82E-01	3.90E-01	1.48E+00	5.63E-01	1.48E+00	4.86E-01	3.29E-01
HIST1H1A	3.75E+00	2.83E-01	3.91E-01	1.61E+00	6.90E-01	1.61E+00	2.40E-01	1.49E-01
TAS1R3	2.91E+01	2.85E-01	3.92E-01	1.25E+00	3.21E-01	1.25E+00	1.69E+00	1.35E+00
XR_003029787.1	2.33E+00	2.86E-01	3.94E-01	2.44E+00	1.29E+00	2.44E+00	1.70E-01	6.98E-02
SPATC1L	7.81E+00	2.92E-01	4.02E-01	1.58E+00	6.62E-01	1.58E+00	4.98E-01	3.15E-01
MYRFL	9.32E+00	2.93E-01	4.02E-01	1.71E+00	7.71E-01	1.71E+00	6.10E-01	3.58E-01
CYP3A5-2	4.32E+00	2.95E-01	4.03E-01	2.38E+00	1.25E+00	2.38E+00	3.13E-01	1.32E-01
OPN4	3.65E+00	2.95E-01	4.03E-01	2.45E+00	1.29E+00	2.45E+00	2.67E-01	1.09E-01
SALL3	1.10E+02	2.99E-01	4.09E-01	1.97E+00	9.81E-01	1.97E+00	7.57E+00	3.83E+00
TMEM255B	5.26E+01	3.01E-01	4.10E-01	1.54E+00	6.23E-01	1.54E+00	3.32E+00	2.16E+00
RALGAPA2	5.16E+02	3.03E-01	4.12E-01	1.19E+00	2.48E-01	1.19E+00	2.94E+01	2.47E+01
TPK1	6.48E+02	3.04E-01	4.12E-01	1.17E+00	2.22E-01	1.17E+00	3.66E+01	3.14E+01
NRSN1	1.04E+01	3.04E-01	4.12E-01	1.65E+00	7.24E-01	1.65E+00	6.76E-01	4.09E-01
XR_003032358.1	2.68E+00	3.05E-01	4.12E-01	1.19E+01	3.57E+00	1.19E+01	2.49E-01	2.10E-02
XR_003033250.1	4.63E+00	3.05E-01	4.12E-01	1.49E+00	5.75E-01	1.49E+00	2.89E-01	1.94E-01
PPEF1	2.02E+02	3.07E-01	4.14E-01	1.25E+00	3.25E-01	1.25E+00	1.18E+01	9.38E+00
XR_003035884.1	4.06E-01	3.07E-01	4.14E-01	3.83E+02	8.58E+00	3.83E+02	4.05E-02	1.06E-04
XR_001494446.2	7.70E+00	3.07E-01	4.14E-01	1.47E+00	5.56E-01	1.47E+00	4.78E-01	3.25E-01
XR_814612.3	9.90E+00	3.09E-01	4.15E-01	1.62E+00	6.92E-01	1.62E+00	6.36E-01	3.94E-01
RASGEF1A	1.91E+02	3.09E-01	4.15E-01	1.35E+00	4.35E-01	1.35E+00	1.15E+01	8.49E+00
LOC112446361	3.87E+00	3.12E-01	4.18E-01	1.67E+00	7.44E-01	1.67E+00	2.52E-01	1.50E-01
XR_003037564.1	1.23E+00	3.16E-01	4.23E-01	1.64E+00	7.15E-01	1.64E+00	7.95E-02	4.84E-02
CDK5R1	1.30E+02	3.16E-01	4.23E-01	1.46E+00	5.50E-01	1.46E+00	8.06E+00	5.50E+00
PDE1C	1.61E+02	3.20E-01	4.27E-01	9.78E-01	-3.15E-02	-1.02E+00	8.41E+00	8.59E+00
XR_001500699.2	4.51E+00	3.20E-01	4.27E-01	1.74E+00	8.03E-01	1.74E+00	2.98E-01	1.71E-01
HBQ1	1.30E+02	3.21E-01	4.27E-01	1.10E+00	1.37E-01	1.10E+00	7.17E+00	6.52E+00
XR_003030389.1	6.91E+00	3.22E-01	4.28E-01	2.05E+00	1.03E+00	2.05E+00	4.80E-01	2.35E-01

GCKR	7.27E+00	3.26E-01	4.32E-01	1.38E+00	4.65E-01	1.38E+00	4.40E-01	3.19E-01
CCR9	1.24E+01	3.27E-01	4.33E-01	1.06E+00	8.61E-02	1.06E+00	6.71E-01	6.33E-01
XR_003037141.1	2.56E+00	3.28E-01	4.34E-01	2.24E+00	1.16E+00	2.24E+00	1.82E-01	8.15E-02
HAAO	3.44E+01	3.30E-01	4.35E-01	1.40E+00	4.80E-01	1.40E+00	2.09E+00	1.50E+00
LOC112448731	9.99E+00	3.34E-01	4.41E-01	1.31E+00	3.87E-01	1.31E+00	5.92E-01	4.53E-01
HMGXB3	1.47E+03	3.35E-01	4.41E-01	1.13E+00	1.72E-01	1.13E+00	8.17E+01	7.25E+01
ZFP2	7.41E+02	3.40E-01	4.47E-01	1.09E+00	1.29E-01	1.09E+00	4.06E+01	3.71E+01
TEX29	2.23E+01	3.43E-01	4.50E-01	1.40E+00	4.82E-01	1.40E+00	1.35E+00	9.70E-01
ALOX12	5.52E+01	3.47E-01	4.54E-01	1.33E+00	4.06E-01	1.33E+00	3.29E+00	2.48E+00
TLE4	7.18E+02	3.61E-01	4.72E-01	1.21E+00	2.73E-01	1.21E+00	4.12E+01	3.41E+01
NOX3	9.25E-01	3.61E-01	4.72E-01	2.65E+00	1.41E+00	2.65E+00	6.90E-02	2.60E-02
WDR76	6.08E+02	3.64E-01	4.75E-01	1.19E+00	2.45E-01	1.19E+00	3.45E+01	2.91E+01
SGF29	4.59E+02	3.65E-01	4.76E-01	1.20E+00	2.61E-01	1.20E+00	2.62E+01	2.19E+01
XR_003036159.1	5.47E+00	3.68E-01	4.78E-01	1.10E+00	1.32E-01	1.10E+00	3.00E-01	2.74E-01
CHRNA10	2.23E+01	3.69E-01	4.80E-01	1.43E+00	5.15E-01	1.43E+00	1.37E+00	9.59E-01
WIF1	1.27E+02	3.72E-01	4.83E-01	1.52E+00	6.08E-01	1.52E+00	7.97E+00	5.23E+00
XR_003032642.1	8.55E+00	3.78E-01	4.90E-01	1.52E+00	6.01E-01	1.52E+00	5.37E-01	3.54E-01
XR_003033863.1	4.05E+00	3.81E-01	4.93E-01	2.48E+00	1.31E+00	2.48E+00	2.97E-01	1.20E-01
DYM	1.64E+03	3.83E-01	4.94E-01	1.08E+00	1.17E-01	1.08E+00	8.97E+01	8.27E+01
FBXO10	7.68E+02	3.87E-01	4.99E-01	1.21E+00	2.81E-01	1.21E+00	4.41E+01	3.63E+01
XR_804250.3	2.45E+00	3.95E-01	5.08E-01	1.27E+00	3.50E-01	1.27E+00	1.44E-01	1.13E-01
HID1	8.00E+02	3.96E-01	5.09E-01	1.12E+00	1.61E-01	1.12E+00	4.43E+01	3.96E+01
MYO7A	1.12E+02	3.99E-01	5.11E-01	1.36E+00	4.44E-01	1.36E+00	6.72E+00	4.94E+00
LOC112441554	2.35E+00	4.01E-01	5.14E-01	1.33E+00	4.09E-01	1.33E+00	1.40E-01	1.05E-01
XR_003037900.1	2.07E+00	4.04E-01	5.16E-01	2.95E+00	1.56E+00	2.95E+00	1.58E-01	5.37E-02
LOC112442380	1.58E+01	4.05E-01	5.18E-01	1.35E+00	4.29E-01	1.35E+00	9.49E-01	7.05E-01
OS9	4.28E+03	4.07E-01	5.19E-01	1.04E+00	5.46E-02	1.04E+00	2.29E+02	2.21E+02
LOC781830	5.45E+00	4.12E-01	5.24E-01	1.45E+00	5.36E-01	1.45E+00	3.36E-01	2.32E-01
PWP1	1.41E+03	4.20E-01	5.34E-01	1.10E+00	1.44E-01	1.10E+00	7.79E+01	7.05E+01
C2H2orf66	1.69E+00	4.25E-01	5.39E-01	2.83E+00	1.50E+00	2.83E+00	1.28E-01	4.54E-02
XR_003035656.1	1.99E+01	4.25E-01	5.39E-01	1.41E+00	4.99E-01	1.41E+00	1.21E+00	8.60E-01
UNC5D	7.59E+01	4.26E-01	5.39E-01	1.62E+00	7.00E-01	1.62E+00	4.89E+00	3.01E+00
ESR2	2.60E+02	4.26E-01	5.39E-01	1.34E+00	4.21E-01	1.34E+00	1.55E+01	1.16E+01

XR_813019.3	5.58E+01	4.34E-01	5.48E-01	1.43E+00	5.21E-01	1.43E+00	3.43E+00	2.39E+00
BMP3	6.12E+01	4.35E-01	5.48E-01	1.63E+00	7.08E-01	1.63E+00	3.95E+00	2.42E+00
CEL	6.71E+00	4.36E-01	5.48E-01	1.26E+00	3.31E-01	1.26E+00	3.91E-01	3.11E-01
OR12D2	6.62E+00	4.37E-01	5.48E-01	2.64E+00	1.40E+00	2.64E+00	4.94E-01	1.87E-01
XR_003037869.1	5.06E+01	4.37E-01	5.48E-01	1.23E+00	2.96E-01	1.23E+00	2.92E+00	2.38E+00
SCGB1A1	2.33E+01	4.39E-01	5.50E-01	1.23E+00	2.96E-01	1.23E+00	1.34E+00	1.09E+00
XR_003035657.1	9.02E-01	4.42E-01	5.53E-01	2.67E+01	4.74E+00	2.67E+01	8.72E-02	3.27E-03
LOC112445942	1.20E+01	4.43E-01	5.53E-01	1.23E+00	2.94E-01	1.23E+00	6.91E-01	5.64E-01
PIF1	1.21E+02	4.44E-01	5.53E-01	1.46E+00	5.48E-01	1.46E+00	7.50E+00	5.13E+00
OMA1	1.37E+02	4.44E-01	5.53E-01	1.10E+00	1.43E-01	1.10E+00	7.53E+00	6.82E+00
PRIMPOL	2.50E+02	4.47E-01	5.56E-01	1.17E+00	2.22E-01	1.17E+00	1.41E+01	1.21E+01
XR_003032215.1	9.04E+00	4.47E-01	5.56E-01	2.50E+00	1.32E+00	2.50E+00	6.65E-01	2.66E-01
XR_003035888.1	1.84E+00	4.50E-01	5.59E-01	3.18E+00	1.67E+00	3.18E+00	1.44E-01	4.51E-02
TTC1	1.02E+03	4.53E-01	5.61E-01	9.62E-01	-5.53E-02	-1.04E+00	5.28E+01	5.49E+01
LOC112445014	4.50E+00	4.66E-01	5.76E-01	1.34E+00	4.26E-01	1.34E+00	2.70E-01	2.01E-01
GALK2	2.22E+02	4.69E-01	5.79E-01	1.11E+00	1.55E-01	1.11E+00	1.23E+01	1.10E+01
MLXIPL	1.32E+02	4.70E-01	5.80E-01	1.43E+00	5.19E-01	1.43E+00	8.14E+00	5.68E+00
C19H17orf97	6.84E+01	4.72E-01	5.82E-01	1.43E+00	5.17E-01	1.43E+00	4.20E+00	2.93E+00
DPCD	4.17E+02	4.81E-01	5.92E-01	1.16E+00	2.11E-01	1.16E+00	2.35E+01	2.03E+01
MCOLN1	6.69E+02	4.85E-01	5.96E-01	1.04E+00	5.87E-02	1.04E+00	3.59E+01	3.44E+01
XR_003034384.1	2.39E+00	4.86E-01	5.96E-01	1.60E+00	6.77E-01	1.60E+00	1.53E-01	9.57E-02
ABI2	1.43E+03	4.87E-01	5.97E-01	1.09E+00	1.29E-01	1.09E+00	7.84E+01	7.17E+01
LOC107132761	1.60E+00	4.96E-01	6.06E-01	1.28E+00	3.55E-01	1.28E+00	9.40E-02	7.35E-02
XR_003033548.1	4.05E+00	5.00E-01	6.11E-01	1.72E+00	7.87E-01	1.72E+00	2.66E-01	1.54E-01
AMHR2	6.63E+02	5.01E-01	6.11E-01	1.00E+00	3.30E-03	1.00E+00	3.49E+01	3.49E+01
TBX19	6.81E+01	5.08E-01	6.19E-01	1.12E+00	1.61E-01	1.12E+00	3.77E+00	3.38E+00
STK10	8.19E+02	5.16E-01	6.28E-01	1.06E+00	7.77E-02	1.06E+00	4.42E+01	4.19E+01
XR_003037271.1	9.43E-01	5.21E-01	6.32E-01	4.09E+00	2.03E+00	4.09E+00	7.73E-02	1.89E-02
XR_003030974.1	1.20E+00	5.21E-01	6.33E-01	1.90E+00	9.27E-01	1.90E+00	8.12E-02	4.27E-02
UNCX	1.93E+01	5.24E-01	6.34E-01	1.25E+00	3.23E-01	1.25E+00	1.12E+00	8.96E-01
XR_235065.4	5.29E+01	5.30E-01	6.41E-01	1.08E+00	1.09E-01	1.08E+00	2.88E+00	2.67E+00
PPP1R9A	6.43E+02	5.30E-01	6.41E-01	1.11E+00	1.48E-01	1.11E+00	3.55E+01	3.20E+01
ARHGAP22	4.06E+02	5.34E-01	6.44E-01	1.12E+00	1.64E-01	1.12E+00	2.25E+01	2.01E+01

XR_003032635.1	1.75E+00	5.36E-01	6.46E-01	1.52E+00	6.01E-01	1.52E+00	1.10E-01	7.23E-02
NR_003052.2	1.55E+00	5.37E-01	6.46E-01	1.62E+00	6.96E-01	1.62E+00	9.96E-02	6.15E-02
LOC785156	1.52E+00	5.41E-01	6.50E-01	2.74E+00	1.46E+00	2.74E+00	1.15E-01	4.18E-02
GABRA4	7.30E+00	5.56E-01	6.67E-01	1.50E+00	5.90E-01	1.50E+00	4.57E-01	3.04E-01
LOC783740	2.99E+00	5.57E-01	6.67E-01	1.33E+00	4.13E-01	1.33E+00	1.79E-01	1.34E-01
SCN4A	2.13E+01	5.59E-01	6.69E-01	1.61E+00	6.89E-01	1.61E+00	1.36E+00	8.46E-01
AKAP7	1.52E+02	5.64E-01	6.73E-01	1.07E+00	9.16E-02	1.07E+00	8.26E+00	7.75E+00
POU4F1	7.83E+01	5.64E-01	6.73E-01	1.19E+00	2.47E-01	1.19E+00	4.45E+00	3.75E+00
XR_003035538.1	1.46E+01	5.68E-01	6.77E-01	1.27E+00	3.50E-01	1.27E+00	8.57E-01	6.73E-01
XR_003030284.1	1.18E+01	5.72E-01	6.81E-01	1.22E+00	2.86E-01	1.22E+00	6.80E-01	5.58E-01
XR_003030938.1	1.67E+01	5.76E-01	6.84E-01	1.40E+00	4.86E-01	1.40E+00	1.02E+00	7.26E-01
XR_815375.3	6.01E+00	5.77E-01	6.85E-01	2.29E+00	1.20E+00	2.29E+00	4.32E-01	1.88E-01
PLEKHF1	4.00E+02	5.80E-01	6.87E-01	1.23E+00	2.99E-01	1.23E+00	2.31E+01	1.88E+01
GNG4	2.38E+02	5.81E-01	6.87E-01	1.35E+00	4.36E-01	1.35E+00	1.43E+01	1.06E+01
SLC24A1	1.02E+02	5.84E-01	6.90E-01	1.29E+00	3.72E-01	1.29E+00	6.02E+00	4.65E+00
TMPRSS9	1.57E+02	5.85E-01	6.90E-01	1.20E+00	2.63E-01	1.20E+00	8.99E+00	7.49E+00
SLC10A4	8.52E+01	5.86E-01	6.90E-01	1.08E+00	1.05E-01	1.08E+00	4.64E+00	4.31E+00
GPR37	2.78E+01	5.88E-01	6.92E-01	1.22E+00	2.91E-01	1.22E+00	1.60E+00	1.31E+00
XR_003035907.1	6.76E-01	5.93E-01	6.97E-01	1.67E+00	7.37E-01	1.67E+00	4.39E-02	2.63E-02
TSPAN13	4.55E+02	5.94E-01	6.97E-01	1.09E+00	1.21E-01	1.09E+00	2.49E+01	2.29E+01
PGS1	6.11E+02	5.97E-01	7.00E-01	1.11E+00	1.46E-01	1.11E+00	3.37E+01	3.04E+01
LOC100848912	1.26E+01	6.03E-01	7.04E-01	1.51E+00	5.94E-01	1.51E+00	7.86E-01	5.21E-01
CHD7	7.47E+02	6.03E-01	7.04E-01	1.18E+00	2.35E-01	1.18E+00	4.23E+01	3.60E+01
EZR	4.92E+03	6.04E-01	7.05E-01	1.01E+00	1.82E-02	1.01E+00	2.60E+02	2.57E+02
XR_003032139.1	4.29E+01	6.08E-01	7.09E-01	1.25E+00	3.26E-01	1.25E+00	2.50E+00	1.99E+00
EYA1	1.00E+02	6.14E-01	7.15E-01	1.33E+00	4.11E-01	1.33E+00	5.97E+00	4.49E+00
GSPT2	5.50E+02	6.15E-01	7.15E-01	1.04E+00	5.59E-02	1.04E+00	2.95E+01	2.84E+01
LOC112446429	1.51E+00	6.18E-01	7.17E-01	2.77E+00	1.47E+00	2.77E+00	1.14E-01	4.13E-02
LOC511713	1.47E+02	6.18E-01	7.17E-01	9.71E-01	-4.21E-02	-1.03E+00	7.65E+00	7.88E+00
SLC12A6	8.81E+02	6.20E-01	7.18E-01	1.09E+00	1.27E-01	1.09E+00	4.83E+01	4.42E+01
XR_001501641.2	1.03E+01	6.22E-01	7.19E-01	1.25E+00	3.21E-01	1.25E+00	6.00E-01	4.80E-01
S100Z	7.54E+00	6.31E-01	7.29E-01	1.51E+00	5.98E-01	1.51E+00	4.73E-01	3.12E-01
XR_003031979.1	1.49E+02	6.33E-01	7.31E-01	1.24E+00	3.16E-01	1.24E+00	8.62E+00	6.93E+00

PNOC	9.41E+00	6.34E-01	7.31E-01	1.41E+00	5.00E-01	1.41E+00	5.75E-01	4.06E-01
RPP21	1.79E+02	6.38E-01	7.34E-01	1.11E+00	1.47E-01	1.11E+00	9.86E+00	8.90E+00
LOC112449240	2.76E+01	6.38E-01	7.34E-01	1.08E+00	1.10E-01	1.08E+00	1.51E+00	1.39E+00
GLS2	1.57E+02	6.44E-01	7.39E-01	1.21E+00	2.78E-01	1.21E+00	9.01E+00	7.43E+00
SPERT	8.39E+00	6.45E-01	7.39E-01	3.08E+00	1.63E+00	3.08E+00	6.50E-01	2.11E-01
APC2	2.37E+02	6.47E-01	7.40E-01	1.11E+00	1.57E-01	1.11E+00	1.31E+01	1.18E+01
LOC522128	2.35E+01	6.49E-01	7.42E-01	1.71E+00	7.78E-01	1.71E+00	1.54E+00	8.98E-01
LOC104970608	1.28E+00	6.50E-01	7.42E-01	3.24E+00	1.69E+00	3.24E+00	1.00E-01	3.09E-02
XR_003032511.1	1.57E+01	6.51E-01	7.43E-01	2.14E+00	1.10E+00	2.14E+00	1.11E+00	5.17E-01
XR_003034346.1	6.28E-01	6.53E-01	7.43E-01	1.84E+00	8.81E-01	1.84E+00	4.22E-02	2.29E-02
XR_815227.3	3.80E+01	6.55E-01	7.44E-01	1.21E+00	2.79E-01	1.21E+00	2.18E+00	1.80E+00
DACH1	4.98E+02	6.55E-01	7.44E-01	1.14E+00	1.91E-01	1.14E+00	2.79E+01	2.44E+01
XR_003030253.1	1.03E+01	6.60E-01	7.48E-01	3.22E+00	1.69E+00	3.22E+00	8.09E-01	2.51E-01
PPP1R17	2.49E+00	6.60E-01	7.48E-01	6.75E+00	2.76E+00	6.75E+00	2.20E-01	3.25E-02
FAM192A	1.07E+03	6.66E-01	7.54E-01	9.93E-01	-1.06E-02	-1.01E+00	5.61E+01	5.65E+01
ARHGAP44	4.88E+02	6.69E-01	7.55E-01	1.19E+00	2.51E-01	1.19E+00	2.78E+01	2.34E+01
GRIA3	1.83E+02	6.70E-01	7.56E-01	1.07E+00	9.11E-02	1.07E+00	9.92E+00	9.31E+00
XR_003037218.1	3.07E+00	6.74E-01	7.59E-01	1.79E+00	8.38E-01	1.79E+00	2.04E-01	1.14E-01
KIAA1324L	1.01E+02	6.76E-01	7.60E-01	1.42E+00	5.05E-01	1.42E+00	6.19E+00	4.36E+00
HEPHL1	7.09E+00	6.77E-01	7.60E-01	1.17E+00	2.27E-01	1.17E+00	4.01E-01	3.43E-01
ANKS1B	4.44E+01	6.91E-01	7.75E-01	1.02E+00	2.58E-02	1.02E+00	2.36E+00	2.32E+00
CASZ1	5.09E+02	6.92E-01	7.75E-01	1.09E+00	1.29E-01	1.09E+00	2.79E+01	2.55E+01
MYO16	4.85E+01	6.93E-01	7.76E-01	1.52E+00	6.00E-01	1.52E+00	3.04E+00	2.01E+00
XR_003032619.1	5.67E+00	6.94E-01	7.76E-01	3.76E+00	1.91E+00	3.76E+00	4.57E-01	1.22E-01
CATSPERG	5.84E+02	7.00E-01	7.81E-01	1.07E+00	1.02E-01	1.07E+00	3.17E+01	2.96E+01
XR_003035629.1	6.10E+01	7.02E-01	7.82E-01	1.12E+00	1.62E-01	1.12E+00	3.38E+00	3.02E+00
XR_003031581.1	5.70E+00	7.02E-01	7.82E-01	1.93E+00	9.45E-01	1.93E+00	3.88E-01	2.02E-01
SLC12A5	4.04E+01	7.08E-01	7.88E-01	1.12E+00	1.67E-01	1.12E+00	2.24E+00	2.00E+00
EPPK1	1.03E+03	7.10E-01	7.89E-01	1.11E+00	1.48E-01	1.11E+00	5.70E+01	5.15E+01
LOC107132994	3.69E+00	7.11E-01	7.89E-01	1.58E+00	6.59E-01	1.58E+00	2.35E-01	1.49E-01
ZFAND5	1.52E+03	7.20E-01	7.98E-01	1.02E+00	3.14E-02	1.02E+00	8.08E+01	7.90E+01
TRHDE	5.92E+01	7.26E-01	8.04E-01	1.38E+00	4.64E-01	1.38E+00	3.59E+00	2.60E+00
LOC104969340	4.00E+02	7.29E-01	8.06E-01	1.05E+00	6.39E-02	1.05E+00	2.15E+01	2.05E+01

USP29	3.40E+00	7.38E-01	8.15E-01	1.35E+00	4.35E-01	1.35E+00	2.04E-01	1.51E-01
XR_003035572.1	1.77E+00	7.39E-01	8.15E-01	1.32E+00	4.03E-01	1.32E+00	1.05E-01	7.97E-02
DSTYK	9.97E+02	7.41E-01	8.16E-01	1.07E+00	9.22E-02	1.07E+00	5.41E+01	5.07E+01
DHX58	9.39E+02	7.45E-01	8.19E-01	1.04E+00	6.02E-02	1.04E+00	5.04E+01	4.83E+01
XR_809755.3	4.33E+00	7.47E-01	8.19E-01	1.96E+00	9.67E-01	1.96E+00	2.97E-01	1.52E-01
PSEN1	1.33E+03	7.47E-01	8.19E-01	1.03E+00	3.80E-02	1.03E+00	7.09E+01	6.91E+01
LOC516904	6.54E-01	7.48E-01	8.19E-01	6.52E+00	2.71E+00	6.52E+00	5.75E-02	8.81E-03
XR_003031875.1	2.33E+00	7.49E-01	8.19E-01	1.67E+00	7.40E-01	1.67E+00	1.51E-01	9.07E-02
XR_003032544.1	4.96E+02	7.52E-01	8.22E-01	9.87E-01	-1.87E-02	-1.01E+00	2.59E+01	2.63E+01
CHP1	1.60E+03	7.53E-01	8.22E-01	1.06E+00	8.00E-02	1.06E+00	8.64E+01	8.18E+01
XR_813547.3	4.34E+01	7.60E-01	8.28E-01	1.56E+00	6.44E-01	1.56E+00	2.75E+00	1.76E+00
XR_003031750.1	4.71E-01	7.64E-01	8.31E-01	1.43E+00	5.13E-01	1.43E+00	2.89E-02	2.02E-02
XR_001501375.2	6.23E+00	7.64E-01	8.31E-01	2.89E+00	1.53E+00	2.89E+00	4.75E-01	1.64E-01
LOC518561	2.23E+00	7.69E-01	8.34E-01	1.90E+00	9.28E-01	1.90E+00	1.51E-01	7.96E-02
XR_003033430.1	3.18E+01	7.69E-01	8.34E-01	1.14E+00	1.91E-01	1.14E+00	1.78E+00	1.56E+00
LOC619014	1.30E+01	7.76E-01	8.40E-01	2.72E+00	1.44E+00	2.72E+00	9.78E-01	3.60E-01
SV2C	3.61E+00	7.78E-01	8.41E-01	1.42E+00	5.06E-01	1.42E+00	2.21E-01	1.56E-01
LOC112442305	3.25E+00	7.78E-01	8.41E-01	1.80E+00	8.48E-01	1.80E+00	2.17E-01	1.20E-01
PSPH	8.21E+01	7.85E-01	8.46E-01	9.99E-01	-1.71E-03	-1.00E+00	4.32E+00	4.32E+00
PHEX	2.27E+02	7.85E-01	8.46E-01	1.24E+00	3.05E-01	1.24E+00	1.31E+01	1.06E+01
XR_003029443.1	4.02E+00	7.86E-01	8.46E-01	1.53E+00	6.13E-01	1.53E+00	2.53E-01	1.66E-01
WNT9A	3.22E+02	7.92E-01	8.51E-01	1.04E+00	4.99E-02	1.04E+00	1.72E+01	1.67E+01
XR_003035879.1	1.55E+00	7.96E-01	8.55E-01	1.44E+00	5.29E-01	1.44E+00	9.54E-02	6.61E-02
HSPA4L	2.29E+02	7.98E-01	8.55E-01	1.14E+00	1.92E-01	1.14E+00	1.28E+01	1.12E+01
XR_003037233.1	6.33E-01	7.98E-01	8.55E-01	3.73E+00	1.90E+00	3.73E+00	5.10E-02	1.37E-02
GPR87	1.68E+00	7.99E-01	8.55E-01	1.50E+00	5.87E-01	1.50E+00	1.05E-01	7.01E-02
MAPKAP1	1.05E+03	8.03E-01	8.58E-01	1.03E+00	3.77E-02	1.03E+00	5.61E+01	5.47E+01
XR_003036864.1	2.24E+00	8.04E-01	8.59E-01	1.31E+00	3.91E-01	1.31E+00	1.33E-01	1.01E-01
CHADL	3.25E+01	8.06E-01	8.59E-01	1.24E+00	3.08E-01	1.24E+00	1.88E+00	1.52E+00
ZNF135	2.91E+02	8.07E-01	8.59E-01	1.04E+00	6.32E-02	1.04E+00	1.56E+01	1.50E+01
TRIM50	9.47E+01	8.08E-01	8.60E-01	1.03E+00	4.37E-02	1.03E+00	5.06E+00	4.90E+00
UBASH3B	1.73E+02	8.16E-01	8.67E-01	1.21E+00	2.76E-01	1.21E+00	9.94E+00	8.21E+00
IFNT2	9.96E+00	8.22E-01	8.71E-01	1.19E+00	2.52E-01	1.19E+00	5.67E-01	4.76E-01

CYSTM1	4.79E+02	8.22E-01	8.71E-01	1.06E+00	8.68E-02	1.06E+00	2.59E+01	2.44E+01
NPAS3	9.07E+01	8.25E-01	8.73E-01	1.30E+00	3.81E-01	1.30E+00	5.36E+00	4.12E+00
GRIK1	2.25E+01	8.28E-01	8.75E-01	1.72E+00	7.83E-01	1.72E+00	1.48E+00	8.60E-01
XR_001501583.2	8.09E+00	8.29E-01	8.76E-01	1.60E+00	6.74E-01	1.60E+00	5.18E-01	3.24E-01
PLK5	4.24E+01	8.31E-01	8.76E-01	1.15E+00	2.04E-01	1.15E+00	2.38E+00	2.07E+00
SKIDA1	1.17E+02	8.33E-01	8.77E-01	1.04E+00	6.01E-02	1.04E+00	6.31E+00	6.05E+00
XR_003034017.1	1.50E+01	8.33E-01	8.77E-01	1.07E+00	9.82E-02	1.07E+00	8.13E-01	7.59E-01
XR_003031513.1	2.08E+00	8.40E-01	8.83E-01	1.69E+00	7.57E-01	1.69E+00	1.36E-01	8.03E-02
PTPN3	3.59E+02	8.42E-01	8.84E-01	1.16E+00	2.09E-01	1.16E+00	2.02E+01	1.75E+01
GPR160	7.17E+01	8.50E-01	8.91E-01	1.38E+00	4.68E-01	1.38E+00	4.34E+00	3.14E+00
PAX3	1.65E+01	8.52E-01	8.92E-01	1.18E+00	2.41E-01	1.18E+00	9.37E-01	7.93E-01
P2RY6	7.09E+01	8.61E-01	9.00E-01	1.12E+00	1.69E-01	1.12E+00	3.94E+00	3.50E+00
XR_003029730.1	1.57E+00	8.65E-01	9.03E-01	2.50E+00	1.32E+00	2.50E+00	1.15E-01	4.61E-02
GPER1	1.04E+02	8.76E-01	9.14E-01	1.35E+00	4.37E-01	1.35E+00	6.24E+00	4.61E+00
XR_003038202.1	9.26E+00	8.79E-01	9.15E-01	1.15E+00	2.07E-01	1.15E+00	5.20E-01	4.51E-01
SLC24A4	2.96E+01	8.84E-01	9.20E-01	1.34E+00	4.24E-01	1.34E+00	1.77E+00	1.32E+00
SLC38A8	1.97E+02	8.85E-01	9.20E-01	1.23E+00	2.98E-01	1.23E+00	1.14E+01	9.23E+00
SHANK2	5.51E+02	8.88E-01	9.21E-01	1.05E+00	7.35E-02	1.05E+00	2.97E+01	2.82E+01
LOC112444897	8.49E+01	8.88E-01	9.21E-01	1.17E+00	2.29E-01	1.17E+00	4.80E+00	4.10E+00
CCDC129	9.66E-01	8.94E-01	9.24E-01	1.54E+00	6.24E-01	1.54E+00	6.10E-02	3.96E-02
ANKRD6	3.63E+02	8.94E-01	9.24E-01	1.10E+00	1.32E-01	1.10E+00	1.99E+01	1.82E+01
XR_003037275.1	2.90E+00	8.94E-01	9.24E-01	1.36E+00	4.46E-01	1.36E+00	1.74E-01	1.28E-01
SLC22A20P	2.21E+00	8.95E-01	9.24E-01	1.72E+00	7.80E-01	1.72E+00	1.45E-01	8.46E-02
OLAH	3.36E+00	8.97E-01	9.24E-01	2.00E+00	1.00E+00	2.00E+00	2.32E-01	1.16E-01
GZMM	1.28E+01	9.06E-01	9.33E-01	1.09E+00	1.23E-01	1.09E+00	7.01E-01	6.44E-01
XR_234571.4	4.42E+02	9.16E-01	9.41E-01	1.05E+00	6.55E-02	1.05E+00	2.37E+01	2.27E+01
RIMBP2	6.09E+01	9.16E-01	9.41E-01	1.06E+00	8.73E-02	1.06E+00	3.30E+00	3.10E+00
KIAA1147	4.67E+02	9.32E-01	9.56E-01	1.02E+00	2.16E-02	1.02E+00	2.47E+01	2.44E+01
EPS8L3	3.89E+00	9.39E-01	9.62E-01	1.37E+00	4.58E-01	1.37E+00	2.35E-01	1.71E-01
XR_001494431.2	2.35E+00	9.40E-01	9.62E-01	1.68E+00	7.46E-01	1.68E+00	1.53E-01	9.11E-02
LOC100336843	2.86E+00	9.44E-01	9.65E-01	1.44E+00	5.27E-01	1.44E+00	1.76E-01	1.22E-01
DTX2	1.03E+03	9.47E-01	9.67E-01	1.09E+00	1.30E-01	1.09E+00	5.65E+01	5.16E+01
XR_003033412.1	1.12E+00	9.49E-01	9.67E-01	1.72E+00	7.85E-01	1.72E+00	7.36E-02	4.27E-02

LOC112442972	1.77E+01	9.50E-01	9.67E-01	1.57E+00	6.49E-01	1.57E+00	1.12E+00	7.15E-01
PTPRZ1	2.18E+02	9.51E-01	9.68E-01	1.49E+00	5.71E-01	1.49E+00	1.36E+01	9.12E+00
XR_003037094.1	1.02E+00	9.59E-01	9.74E-01	1.60E+00	6.78E-01	1.60E+00	6.50E-02	4.06E-02
XR_814259.3	4.76E+00	9.60E-01	9.74E-01	1.21E+00	2.74E-01	1.21E+00	2.73E-01	2.25E-01
LOC104973965	1.31E+01	9.62E-01	9.76E-01	1.20E+00	2.59E-01	1.20E+00	7.46E-01	6.23E-01
XR_139422.5	3.40E+00	9.67E-01	9.78E-01	2.12E+00	1.08E+00	2.12E+00	2.39E-01	1.13E-01
TPCN1	9.54E+02	9.67E-01	9.78E-01	1.04E+00	5.69E-02	1.04E+00	5.12E+01	4.92E+01
XR_003037344.1	1.53E+00	9.68E-01	9.78E-01	1.15E+00	2.08E-01	1.15E+00	8.57E-02	7.42E-02
KLB	2.43E+01	9.69E-01	9.78E-01	1.06E+00	7.93E-02	1.06E+00	1.31E+00	1.24E+00
XR_001501795.2	2.47E+01	9.75E-01	9.83E-01	1.64E+00	7.16E-01	1.64E+00	1.60E+00	9.73E-01
ME1	6.34E+02	9.76E-01	9.83E-01	1.04E+00	6.07E-02	1.04E+00	3.40E+01	3.26E+01
NLRP13	1.42E+02	9.77E-01	9.83E-01	1.28E+00	3.54E-01	1.28E+00	8.34E+00	6.53E+00
UBE2Q1	2.89E+03	9.78E-01	9.83E-01	1.07E+00	9.86E-02	1.07E+00	1.57E+02	1.46E+02
DHODH	2.68E+02	9.79E-01	9.83E-01	1.09E+00	1.20E-01	1.09E+00	1.46E+01	1.35E+01
CLSTN2	2.87E+02	9.86E-01	9.88E-01	1.23E+00	3.03E-01	1.23E+00	1.66E+01	1.34E+01
EXD1	4.46E+01	9.93E-01	9.94E-01	1.08E+00	1.14E-01	1.08E+00	2.43E+00	2.25E+00
ZNF235	5.87E+02	1.00E+00	1.00E+00	1.01E+00	1.60E-02	1.01E+00	3.11E+01	3.07E+01

S5 Table. Gene Specific Analysis (late versus early gestation) for genes in cluster 4. Shown are the fold change and its significance (p-value), log 2 ratio and False Discovery Rate (FDR) across gestation; least square (LS) mean (late and early gestation); total counts per million.

Gene symbol	Total counts	P-value	FDR step up	Ratio	Log2(Ratio)	Fold change	LSMean(Late)	LSMean(Early)
RIPOR2	1.29E+02	9.15E-12	4.72E-09	4.90E+00	2.29E+00	4.90E+00	1.08E+01	2.21E+00
ZFP57	8.72E+02	9.47E-11	2.29E-08	2.48E+00	1.31E+00	2.48E+00	6.33E+01	2.56E+01
GNRHR	1.70E+00	1.33E-10	2.29E-08	1.70E+03	1.07E+01	1.70E+03	1.70E-01	1.00E-04
HOPX	3.24E+02	2.13E-10	2.74E-08	8.41E+00	3.07E+00	8.41E+00	2.92E+01	3.48E+00
ACCSL	1.21E+02	8.58E-10	8.85E-08	1.40E+01	3.81E+00	1.40E+01	1.14E+01	8.11E-01
HEG1	1.20E+03	1.22E-09	1.05E-07	7.07E+00	2.82E+00	7.07E+00	1.06E+02	1.51E+01
NLRP8	5.22E+01	2.77E-09	2.04E-07	2.46E+01	4.62E+00	2.46E+01	5.02E+00	2.04E-01
NPR3	2.37E+02	4.56E-09	2.94E-07	8.46E+00	3.08E+00	8.46E+00	2.13E+01	2.52E+00
KRT2	1.85E+02	5.41E-09	3.10E-07	1.09E+03	1.01E+01	1.09E+03	1.85E+01	1.69E-02
MPP6	6.08E+02	6.29E-09	3.25E-07	2.01E+00	1.01E+00	2.01E+00	4.14E+01	2.06E+01
ARSB	1.08E+03	9.94E-09	4.66E-07	1.83E+00	8.70E-01	1.83E+00	7.20E+01	3.94E+01
TRAM2	1.75E+03	1.32E-08	5.66E-07	1.94E+00	9.58E-01	1.94E+00	1.19E+02	6.12E+01
ACTG2	1.89E+03	2.06E-08	8.19E-07	1.03E+01	3.36E+00	1.03E+01	1.73E+02	1.68E+01
NEDD9	1.18E+03	2.38E-08	8.78E-07	2.20E+00	1.14E+00	2.20E+00	8.30E+01	3.78E+01
EIF4B	1.55E+04	4.70E-08	1.60E-06	1.68E+00	7.45E-01	1.68E+00	1.00E+03	5.98E+02
OLFML2A	3.24E+03	5.18E-08	1.60E-06	1.91E+00	9.37E-01	1.91E+00	2.18E+02	1.14E+02
SERP1	4.76E+02	5.27E-08	1.60E-06	1.65E+00	7.25E-01	1.65E+00	3.05E+01	1.85E+01
MOCOS	4.65E+02	6.56E-08	1.88E-06	5.43E+00	2.44E+00	5.43E+00	3.95E+01	7.27E+00
LRCH1	6.17E+02	7.76E-08	2.11E-06	1.66E+00	7.32E-01	1.66E+00	3.99E+01	2.40E+01
RGMB	1.55E+03	9.50E-08	2.45E-06	1.92E+00	9.41E-01	1.92E+00	1.05E+02	5.44E+01
TAL1	2.00E+02	1.03E-07	2.52E-06	1.71E+00	7.75E-01	1.71E+00	1.30E+01	7.58E+00
ERRFI1	3.72E+03	1.12E-07	2.52E-06	3.82E+00	1.94E+00	3.82E+00	2.99E+02	7.83E+01
ATP13A3	2.82E+02	1.13E-07	2.52E-06	2.34E+00	1.23E+00	2.34E+00	2.01E+01	8.61E+00
APOD	1.16E+03	1.30E-07	2.73E-06	2.81E+01	4.81E+00	2.81E+01	1.12E+02	4.01E+00
LOC101909718	2.17E+01	1.34E-07	2.73E-06	8.99E+01	6.49E+00	8.99E+01	2.15E+00	2.39E-02
P4HA1	1.07E+03	1.38E-07	2.73E-06	1.67E+00	7.42E-01	1.67E+00	6.90E+01	4.13E+01
ANKRD33B	1.00E+02	1.45E-07	2.74E-06	4.46E+00	2.16E+00	4.46E+00	8.36E+00	1.88E+00
LOC100336869	6.24E+00	1.49E-07	2.74E-06	1.41E+02	7.14E+00	1.41E+02	6.19E-01	4.40E-03
REEP5	1.05E+03	1.58E-07	2.80E-06	2.49E+00	1.32E+00	2.49E+00	7.63E+01	3.06E+01

CHST11	5.47E+02	1.80E-07	3.03E-06	5.90E+00	2.56E+00	5.90E+00	4.74E+01	8.04E+00
TLL2	8.70E+02	1.82E-07	3.03E-06	7.46E+00	2.90E+00	7.46E+00	7.77E+01	1.04E+01
TNNI3	6.17E+02	2.99E-07	4.82E-06	6.50E+00	2.70E+00	6.50E+00	5.41E+01	8.32E+00
CDK5R2	8.08E+01	3.65E-07	5.71E-06	5.94E+00	2.57E+00	5.94E+00	6.99E+00	1.18E+00
RAI2	1.91E+02	3.94E-07	5.98E-06	4.02E+00	2.01E+00	4.02E+00	1.55E+01	3.87E+00
CPED1	1.84E+02	4.47E-07	6.58E-06	1.51E+01	3.92E+00	1.51E+01	1.73E+01	1.15E+00
R_001502153.	8.77E+01	4.67E-07	6.69E-06	5.64E+00	2.50E+00	5.64E+00	7.53E+00	1.33E+00
TPM2	2.65E+03	4.87E-07	6.80E-06	4.10E+00	2.04E+00	4.10E+00	2.16E+02	5.27E+01
LOC782043	2.16E+00	5.03E-07	6.82E-06	4.36E+01	5.45E+00	4.36E+01	2.11E-01	4.83E-03
LOC786303	8.15E+00	5.40E-07	7.15E-06	2.90E+00	1.53E+00	2.90E+00	6.12E-01	2.11E-01
LATS2	5.87E+02	6.88E-07	8.87E-06	1.50E+00	5.83E-01	1.50E+00	3.65E+01	2.44E+01
GCLC	1.15E+03	7.99E-07	1.00E-05	6.15E+00	2.62E+00	6.15E+00	1.00E+02	1.63E+01
LOC508153	1.54E+02	1.05E-06	1.29E-05	2.81E+00	1.49E+00	2.81E+00	1.15E+01	4.10E+00
XR_808585.3	2.75E+00	1.32E-06	1.57E-05	1.10E+01	3.46E+00	1.10E+01	2.52E-01	2.29E-02
LVRN	2.21E+02	1.34E-06	1.57E-05	4.69E+00	2.23E+00	4.69E+00	1.85E+01	3.94E+00
MGAT4C	2.58E+01	1.50E-06	1.72E-05	1.30E+01	3.70E+00	1.30E+01	2.41E+00	1.86E-01
LRRC2	1.41E+02	1.65E-06	1.85E-05	7.30E+00	2.87E+00	7.30E+00	1.25E+01	1.71E+00
GMPR	1.47E+02	1.97E-06	2.17E-05	2.59E+00	1.37E+00	2.59E+00	1.08E+01	4.18E+00
TNFAIP3	2.01E+02	2.34E-06	2.48E-05	1.89E+00	9.18E-01	1.89E+00	1.35E+01	7.14E+00
FGF14	2.89E+01	2.36E-06	2.48E-05	8.16E+00	3.03E+00	8.16E+00	2.60E+00	3.19E-01
PABPC1	2.08E+04	2.63E-06	2.72E-05	1.38E+00	4.63E-01	1.38E+00	1.25E+03	9.07E+02
TAGAP	1.76E+02	2.95E-06	2.99E-05	1.81E+00	8.57E-01	1.81E+00	1.16E+01	6.40E+00
R_003035865.	4.35E+02	3.08E-06	3.06E-05	3.55E+00	1.83E+00	3.55E+00	3.45E+01	9.73E+00
ZBTB16	7.29E+02	3.28E-06	3.19E-05	2.74E+00	1.46E+00	2.74E+00	5.43E+01	1.98E+01
TNIP3	2.25E+01	3.34E-06	3.20E-05	6.06E+00	2.60E+00	6.06E+00	1.97E+00	3.24E-01
LOC112449619	1.11E+01	3.56E-06	3.34E-05	3.30E+00	1.72E+00	3.30E+00	8.70E-01	2.64E-01
PLEK	7.49E+01	3.87E-06	3.56E-05	5.17E+00	2.37E+00	5.17E+00	6.33E+00	1.22E+00
KCNK6	9.35E+00	4.11E-06	3.72E-05	3.49E+00	1.80E+00	3.49E+00	7.34E-01	2.11E-01
P4HA3	1.17E+02	4.61E-06	4.10E-05	3.04E+00	1.61E+00	3.04E+00	9.01E+00	2.96E+00
R_003035984.	2.44E+01	4.93E-06	4.31E-05	2.50E+00	1.32E+00	2.50E+00	1.78E+00	7.13E-01
KLF15	1.84E+02	5.02E-06	4.32E-05	2.22E+00	1.15E+00	2.22E+00	1.31E+01	5.90E+00
HHIPL1	5.61E+02	5.24E-06	4.42E-05	2.54E+00	1.35E+00	2.54E+00	4.12E+01	1.62E+01
SMAD4	2.18E+03	5.31E-06	4.42E-05	1.36E+00	4.39E-01	1.36E+00	1.31E+02	9.64E+01

R_001500496.	2.23E+00	5.68E-06	4.65E-05	5.93E+00	2.57E+00	5.93E+00	1.97E-01	3.32E-02
ARHGAP10	1.56E+03	6.63E-06	5.35E-05	3.23E+00	1.69E+00	3.23E+00	1.21E+02	3.76E+01
MYL9	3.61E+03	7.38E-06	5.81E-05	2.78E+00	1.47E+00	2.78E+00	2.72E+02	9.79E+01
TTLL7	2.71E+01	7.43E-06	5.81E-05	3.55E+00	1.83E+00	3.55E+00	2.15E+00	6.06E-01
MMD	2.03E+03	7.73E-06	5.96E-05	1.53E+00	6.16E-01	1.53E+00	1.28E+02	8.38E+01
OMD	8.38E+01	7.93E-06	6.02E-05	1.49E+01	3.90E+00	1.49E+01	7.89E+00	5.30E-01
TPM1	9.66E+03	9.97E-06	7.46E-05	2.29E+00	1.19E+00	2.29E+00	6.95E+02	3.04E+02
LOC100335205	2.43E+01	1.03E-05	7.57E-05	7.02E+00	2.81E+00	7.02E+00	2.13E+00	3.04E-01
VNN1	1.31E+02	1.07E-05	7.78E-05	3.61E+01	5.18E+00	3.61E+01	1.28E+01	3.54E-01
CLCA2	7.45E+00	1.10E-05	7.92E-05	1.19E+01	3.57E+00	1.19E+01	6.88E-01	5.78E-02
RGS11	1.47E+02	1.17E-05	8.11E-05	2.68E+00	1.42E+00	2.68E+00	1.09E+01	4.07E+00
R_003030154.	7.05E+00	1.17E-05	8.11E-05	5.10E+00	2.35E+00	5.10E+00	6.02E-01	1.18E-01
GOLGA5	5.74E+02	1.18E-05	8.11E-05	1.30E+00	3.76E-01	1.30E+00	3.37E+01	2.60E+01
ABCC1	1.29E+03	1.22E-05	8.28E-05	1.38E+00	4.68E-01	1.38E+00	7.78E+01	5.62E+01
EIF4E1B	1.35E+01	1.26E-05	8.45E-05	3.40E+01	5.09E+00	3.40E+01	1.31E+00	3.86E-02
HEYL	1.66E+03	1.86E-05	1.23E-04	1.70E+00	7.68E-01	1.70E+00	1.07E+02	6.31E+01
CITED4	2.39E+02	1.94E-05	1.27E-04	2.66E+00	1.41E+00	2.66E+00	1.78E+01	6.70E+00
R_003035533.	2.32E+01	2.24E-05	1.45E-04	8.42E+01	6.40E+00	8.42E+01	2.29E+00	2.73E-02
CD244	8.94E+00	2.43E-05	1.55E-04	8.16E+00	3.03E+00	8.16E+00	8.00E-01	9.80E-02
ADAMDEC1	6.19E+01	2.65E-05	1.67E-04	1.48E+01	3.89E+00	1.48E+01	5.83E+00	3.94E-01
GALNT18	3.38E+02	2.90E-05	1.80E-04	1.98E+00	9.85E-01	1.98E+00	2.31E+01	1.17E+01
FSHR	1.17E+02	2.93E-05	1.80E-04	5.30E+00	2.41E+00	5.30E+00	1.00E+01	1.89E+00
TXK	1.91E+01	3.10E-05	1.88E-04	3.72E+00	1.90E+00	3.72E+00	1.54E+00	4.13E-01
HSPB7	1.31E+02	3.40E-05	2.03E-04	1.07E+01	3.42E+00	1.07E+01	1.21E+01	1.13E+00
FAT3	1.63E+02	3.42E-05	2.03E-04	4.69E+00	2.23E+00	4.69E+00	1.37E+01	2.92E+00
UPK1B	3.27E+02	3.60E-05	2.11E-04	1.98E+01	4.31E+00	1.98E+01	3.12E+01	1.58E+00
SPSB1	2.91E+03	3.64E-05	2.11E-04	1.43E+00	5.14E-01	1.43E+00	1.78E+02	1.24E+02
FOXS1	3.18E+02	3.76E-05	2.16E-04	2.52E+00	1.33E+00	2.52E+00	2.32E+01	9.20E+00
MYC	2.18E+03	3.90E-05	2.21E-04	2.58E+00	1.37E+00	2.58E+00	1.61E+02	6.26E+01
CHMP2B	4.19E+02	4.08E-05	2.29E-04	1.35E+00	4.35E-01	1.35E+00	2.51E+01	1.86E+01
EDN3	5.53E+02	4.22E-05	2.34E-04	1.62E+00	6.99E-01	1.62E+00	3.53E+01	2.17E+01
ARSK	1.30E+02	4.30E-05	2.36E-04	1.90E+00	9.24E-01	1.90E+00	8.76E+00	4.62E+00
R_003035529.	2.67E+00	4.39E-05	2.39E-04	3.32E+01	5.05E+00	3.32E+01	2.60E-01	7.81E-03

R_001500346.	2.66E+01	4.53E-05	2.44E-04	2.20E+00	1.14E+00	2.20E+00	1.88E+00	8.55E-01
XR_235225.4	1.04E+01	4.95E-05	2.64E-04	6.16E+00	2.62E+00	6.16E+00	8.97E-01	1.46E-01
ST8SIA5	3.57E+01	5.19E-05	2.73E-04	4.06E+00	2.02E+00	4.06E+00	2.92E+00	7.18E-01
FHL2	9.92E+02	5.33E-05	2.78E-04	2.62E+00	1.39E+00	2.62E+00	7.37E+01	2.82E+01
CGREF1	7.57E+01	5.52E-05	2.85E-04	2.77E+00	1.47E+00	2.77E+00	5.71E+00	2.06E+00
LOC614781	3.03E+00	7.01E-05	3.58E-04	3.74E+01	5.23E+00	3.74E+01	2.95E-01	7.87E-03
LIPG	1.15E+02	9.56E-05	4.84E-04	2.97E+01	4.89E+00	2.97E+01	1.12E+01	3.76E-01
PCNP	1.69E+03	1.12E-04	5.62E-04	1.27E+00	3.42E-01	1.27E+00	9.88E+01	7.80E+01
-LOC10190801	5.48E+01	1.15E-04	5.69E-04	6.62E+00	2.73E+00	6.62E+00	4.81E+00	7.26E-01
FAM20A	6.50E+01	1.24E-04	6.09E-04	6.61E+00	2.73E+00	6.61E+00	5.70E+00	8.62E-01
GPR174	1.85E+01	1.25E-04	6.09E-04	1.64E+01	4.03E+00	1.64E+01	1.74E+00	1.07E-01
CD8A	1.52E+01	1.30E-04	6.28E-04	1.04E+01	3.37E+00	1.04E+01	1.39E+00	1.34E-01
STX7	6.68E+02	1.34E-04	6.40E-04	1.26E+00	3.34E-01	1.26E+00	3.89E+01	3.09E+01
R_003033125.	4.86E+00	1.35E-04	6.40E-04	3.67E+00	1.88E+00	3.67E+00	3.82E-01	1.04E-01
ADAM23	7.82E+01	1.39E-04	6.47E-04	2.71E+00	1.44E+00	2.71E+00	5.80E+00	2.14E+00
ITGBL1	2.08E+02	1.39E-04	6.47E-04	3.83E+01	5.26E+00	3.83E+01	2.04E+01	5.33E-01
LPIN1	4.66E+02	1.50E-04	6.85E-04	1.69E+00	7.57E-01	1.69E+00	3.04E+01	1.80E+01
R_003036309.	1.72E+00	1.51E-04	6.85E-04	1.62E+01	4.02E+00	1.62E+01	1.63E-01	1.01E-02
IHH	1.17E+02	1.51E-04	6.85E-04	5.24E+01	5.71E+00	5.24E+01	1.15E+01	2.19E-01
R_003036828.	3.94E+01	1.57E-04	7.05E-04	4.13E+00	2.04E+00	4.13E+00	3.25E+00	7.87E-01
PTGES	3.99E+01	1.64E-04	7.28E-04	7.22E+00	2.85E+00	7.22E+00	3.56E+00	4.93E-01
KCNS3	1.14E+02	1.75E-04	7.72E-04	2.49E+00	1.32E+00	2.49E+00	8.34E+00	3.34E+00
R_001500638.	7.68E+01	2.16E-04	9.46E-04	3.08E+00	1.62E+00	3.08E+00	5.90E+00	1.92E+00
FAM46B	8.01E+01	2.20E-04	9.55E-04	2.06E+00	1.04E+00	2.06E+00	5.49E+00	2.66E+00
TNFSF14	1.09E+01	2.24E-04	9.62E-04	2.92E+00	1.55E+00	2.92E+00	8.18E-01	2.80E-01
SCD	2.50E+03	2.32E-04	9.88E-04	3.56E+00	1.83E+00	3.56E+00	1.99E+02	5.60E+01
CD69	3.37E+00	2.35E-04	9.96E-04	2.80E+00	1.49E+00	2.80E+00	2.49E-01	8.89E-02
RND3	4.78E+02	2.48E-04	1.04E-03	1.56E+00	6.42E-01	1.56E+00	3.04E+01	1.95E+01
TM6SF1	2.13E+02	2.54E-04	1.06E-03	1.44E+00	5.29E-01	1.44E+00	1.31E+01	9.06E+00
id-TRGC6	4.96E+00	2.61E-04	1.08E-03	1.70E+01	4.09E+00	1.70E+01	4.73E-01	2.78E-02
ZNF683	4.15E+01	2.84E-04	1.16E-03	6.37E+00	2.67E+00	6.37E+00	3.59E+00	5.64E-01
ARFGAP3	1.53E+03	3.02E-04	1.23E-03	2.39E+00	1.25E+00	2.39E+00	1.11E+02	4.65E+01
TNNT1	4.44E+01	3.12E-04	1.26E-03	2.44E+00	1.29E+00	2.44E+00	3.24E+00	1.33E+00

CD7	1.01E+01	3.20E-04	1.28E-03	6.95E+00	2.80E+00	6.95E+00	8.84E-01	1.27E-01
NR_003096.1	3.28E+01	3.29E-04	1.30E-03	7.40E+00	2.89E+00	7.40E+00	2.90E+00	3.92E-01
ERP44	8.97E+02	3.34E-04	1.32E-03	1.22E+00	2.88E-01	1.22E+00	5.16E+01	4.23E+01
PTCH1	1.11E+03	3.37E-04	1.32E-03	2.75E+00	1.46E+00	2.75E+00	8.36E+01	3.03E+01
NR_038087.1	7.03E+01	3.69E-04	1.43E-03	1.79E+00	8.39E-01	1.79E+00	4.68E+00	2.62E+00
COLQ	1.63E+02	3.70E-04	1.43E-03	1.74E+00	7.96E-01	1.74E+00	1.08E+01	6.23E+00
NR5A2	3.05E+02	3.85E-04	1.47E-03	5.78E+00	2.53E+00	5.78E+00	2.64E+01	4.56E+00
R_001502098.	8.78E+01	4.07E-04	1.54E-03	1.81E+00	8.57E-01	1.81E+00	5.81E+00	3.21E+00
NOS2	4.10E+02	4.43E-04	1.66E-03	2.24E+00	1.16E+00	2.24E+00	2.93E+01	1.31E+01
HIF1A	1.47E+03	4.45E-04	1.66E-03	1.97E+00	9.75E-01	1.97E+00	1.01E+02	5.12E+01
R_003034833.	9.61E+00	4.57E-04	1.70E-03	2.33E+01	4.54E+00	2.33E+01	9.24E-01	3.96E-02
GPR88	1.87E+01	4.73E-04	1.74E-03	3.92E+00	1.97E+00	3.92E+00	1.53E+00	3.90E-01
KCNE5	4.05E+02	4.78E-04	1.74E-03	2.29E+00	1.20E+00	2.29E+00	2.90E+01	1.27E+01
OR10AD1	1.34E+00	4.80E-04	1.74E-03	4.98E+00	2.32E+00	4.98E+00	1.12E-01	2.26E-02
PAPSS2	5.55E+02	4.95E-04	1.79E-03	2.96E+00	1.57E+00	2.96E+00	4.27E+01	1.44E+01
HACD4	1.21E+02	5.47E-04	1.96E-03	2.49E+00	1.32E+00	2.49E+00	8.80E+00	3.54E+00
G0S2	2.96E+02	5.54E-04	1.97E-03	1.60E+00	6.78E-01	1.60E+00	1.90E+01	1.19E+01
HMGCS1	1.74E+03	5.59E-04	1.97E-03	2.93E+00	1.55E+00	2.93E+00	1.33E+02	4.55E+01
SLC16A14	2.02E+02	5.61E-04	1.97E-03	1.67E+00	7.42E-01	1.67E+00	1.32E+01	7.90E+00
LOC101907857	3.26E+02	5.99E-04	2.09E-03	6.10E+00	2.61E+00	6.10E+00	2.81E+01	4.61E+00
FAM167B	3.45E+01	6.07E-04	2.09E-03	2.08E+00	1.06E+00	2.08E+00	2.39E+00	1.15E+00
LOC112442215	6.61E+00	6.09E-04	2.09E-03	3.26E+00	1.71E+00	3.26E+00	5.08E-01	1.56E-01
KLRD1	9.38E+00	6.60E-04	2.25E-03	1.86E+01	4.22E+00	1.86E+01	8.93E-01	4.80E-02
XR_233092.4	3.89E+00	6.72E-04	2.28E-03	1.75E+01	4.13E+00	1.75E+01	3.71E-01	2.12E-02
FAM163A	6.01E+02	7.17E-04	2.42E-03	2.07E+00	1.05E+00	2.07E+00	4.15E+01	2.01E+01
XR_815109.3	7.51E+01	7.36E-04	2.46E-03	3.54E+00	1.83E+00	3.54E+00	5.90E+00	1.67E+00
CDH3	1.66E+03	8.67E-04	2.89E-03	1.44E+00	5.31E-01	1.44E+00	1.02E+02	7.04E+01
SEZ6L	3.86E+01	8.80E-04	2.91E-03	3.66E+00	1.87E+00	3.66E+00	3.08E+00	8.42E-01
R_003032574.	7.00E+01	9.10E-04	2.97E-03	1.88E+00	9.13E-01	1.88E+00	4.72E+00	2.50E+00
CTPS1	1.16E+03	9.11E-04	2.97E-03	1.57E+00	6.47E-01	1.57E+00	7.40E+01	4.72E+01
LOC100848575	6.52E+00	9.16E-04	2.97E-03	1.30E+01	3.70E+00	1.30E+01	6.07E-01	4.67E-02
NAT1	1.58E+02	9.25E-04	2.98E-03	1.44E+00	5.28E-01	1.44E+00	9.72E+00	6.74E+00
LOC104972370	3.62E+00	9.78E-04	3.13E-03	8.05E+00	3.01E+00	8.05E+00	3.22E-01	4.00E-02

RPE	1.93E+02	9.89E-04	3.15E-03	1.30E+00	3.77E-01	1.30E+00	1.14E+01	8.78E+00
DZANK1	1.16E+03	1.02E-03	3.24E-03	1.41E+00	4.93E-01	1.41E+00	7.04E+01	5.00E+01
VLDLR	2.41E+02	1.04E-03	3.28E-03	1.50E+00	5.84E-01	1.50E+00	1.49E+01	9.95E+00
APOLD1	1.40E+02	1.07E-03	3.31E-03	1.82E+00	8.62E-01	1.82E+00	9.46E+00	5.20E+00
R_003030385.	2.95E+00	1.07E-03	3.31E-03	4.82E+00	2.27E+00	4.82E+00	2.46E-01	5.10E-02
TMEM200A	4.70E+02	1.07E-03	3.31E-03	1.79E+00	8.44E-01	1.79E+00	3.14E+01	1.75E+01
LRRC8D	7.55E+02	1.13E-03	3.46E-03	1.54E+00	6.20E-01	1.54E+00	4.78E+01	3.11E+01
R_001494808.	2.55E+01	1.15E-03	3.50E-03	3.18E+00	1.67E+00	3.18E+00	1.98E+00	6.22E-01
ST3GAL5	3.08E+02	1.17E-03	3.56E-03	1.63E+00	7.06E-01	1.63E+00	1.97E+01	1.21E+01
FAM83A	2.80E+01	1.20E-03	3.63E-03	3.11E+00	1.64E+00	3.11E+00	2.17E+00	6.98E-01
JSRP1	4.88E+01	1.24E-03	3.73E-03	9.55E+00	3.26E+00	9.55E+00	4.46E+00	4.66E-01
WIPF3	9.26E+02	1.34E-03	3.99E-03	1.35E+00	4.38E-01	1.35E+00	5.54E+01	4.09E+01
LOC100848188	2.10E+01	1.41E-03	4.19E-03	2.22E+00	1.15E+00	2.22E+00	1.49E+00	6.70E-01
LOC513767	1.23E+02	1.42E-03	4.19E-03	1.39E+00	4.72E-01	1.39E+00	7.47E+00	5.39E+00
JOSD2	2.44E+02	1.47E-03	4.32E-03	1.52E+00	6.08E-01	1.52E+00	1.53E+01	1.00E+01
DRD5	1.52E+01	1.51E-03	4.42E-03	6.47E+00	2.69E+00	6.47E+00	1.32E+00	2.04E-01
IQGAP2	8.19E+02	1.63E-03	4.71E-03	1.92E+00	9.40E-01	1.92E+00	5.57E+01	2.90E+01
LAIR1	1.92E+02	1.65E-03	4.76E-03	2.20E+00	1.13E+00	2.20E+00	1.34E+01	6.10E+00
HSD17B1	3.94E+02	1.67E-03	4.79E-03	3.34E+00	1.74E+00	3.34E+00	3.10E+01	9.29E+00
RARRES1	6.44E+02	1.73E-03	4.94E-03	2.20E+00	1.14E+00	2.20E+00	4.58E+01	2.08E+01
RANGRF	2.12E+02	1.75E-03	4.96E-03	1.29E+00	3.69E-01	1.29E+00	1.25E+01	9.64E+00
LOC511617	1.55E+01	1.82E-03	5.12E-03	4.04E+00	2.01E+00	4.04E+00	1.24E+00	3.08E-01
R_003035035.	4.55E+01	1.86E-03	5.22E-03	3.34E+00	1.74E+00	3.34E+00	3.60E+00	1.08E+00
CITED2	2.03E+03	1.87E-03	5.23E-03	1.68E+00	7.49E-01	1.68E+00	1.33E+02	7.92E+01
CD52	1.04E+02	1.90E-03	5.27E-03	2.55E+00	1.35E+00	2.55E+00	7.58E+00	2.97E+00
GDNF	4.62E+01	1.91E-03	5.27E-03	1.98E+00	9.82E-01	1.98E+00	3.14E+00	1.59E+00
MOSPD1	1.20E+02	1.92E-03	5.27E-03	1.37E+00	4.51E-01	1.37E+00	7.23E+00	5.29E+00
AMH	2.34E+02	1.95E-03	5.32E-03	5.35E+00	2.42E+00	5.35E+00	2.01E+01	3.75E+00
SNX24	2.68E+02	2.00E-03	5.40E-03	1.25E+00	3.21E-01	1.25E+00	1.56E+01	1.25E+01
XR_813808.3	2.86E+00	2.00E-03	5.40E-03	7.74E+00	2.95E+00	7.74E+00	2.55E-01	3.30E-02
S100A7	2.16E+00	2.13E-03	5.69E-03	5.71E+00	2.51E+00	5.71E+00	1.85E-01	3.24E-02
GRB14	4.85E+02	2.13E-03	5.69E-03	2.57E+00	1.36E+00	2.57E+00	3.58E+01	1.39E+01
MCFD2	7.45E+02	2.22E-03	5.91E-03	1.20E+00	2.63E-01	1.20E+00	4.25E+01	3.54E+01

CALM1	7.00E+03	2.25E-03	5.94E-03	1.47E+00	5.55E-01	1.47E+00	4.32E+02	2.94E+02
OTOS	6.75E+01	2.26E-03	5.95E-03	3.82E+01	5.26E+00	3.82E+01	6.60E+00	1.73E-01
XR_814835.3	2.72E+01	2.35E-03	6.14E-03	5.84E+00	2.55E+00	5.84E+00	2.33E+00	3.98E-01
FRZB	4.82E+02	2.43E-03	6.34E-03	2.07E+00	1.05E+00	2.07E+00	3.38E+01	1.63E+01
LRRN1	4.38E+02	2.61E-03	6.76E-03	2.08E+00	1.06E+00	2.08E+00	3.04E+01	1.46E+01
MTERF1	2.97E+02	2.80E-03	7.22E-03	1.24E+00	3.08E-01	1.24E+00	1.72E+01	1.39E+01
FNDC4	2.06E+02	2.81E-03	7.22E-03	1.52E+00	6.03E-01	1.52E+00	1.28E+01	8.41E+00
ZBTB24	2.35E+02	2.85E-03	7.29E-03	1.21E+00	2.78E-01	1.21E+00	1.35E+01	1.11E+01
CYP21	6.48E+01	3.04E-03	7.73E-03	2.10E+00	1.07E+00	2.10E+00	4.58E+00	2.18E+00
INSL3	6.04E+03	3.11E-03	7.87E-03	4.19E+01	5.39E+00	4.19E+01	5.92E+02	1.41E+01
R_003031551.	1.87E+00	3.20E-03	8.05E-03	4.02E+01	5.33E+00	4.02E+01	1.82E-01	4.53E-03
CBR3	1.10E+02	3.33E-03	8.33E-03	1.64E+00	7.11E-01	1.64E+00	7.09E+00	4.33E+00
KCNJ6	5.26E+00	3.41E-03	8.50E-03	9.72E+00	3.28E+00	9.72E+00	4.81E-01	4.95E-02
LOC101908581	1.11E+00	3.52E-03	8.72E-03	1.62E+01	4.02E+00	1.62E+01	1.05E-01	6.45E-03
R_003031414.	2.48E+02	3.60E-03	8.88E-03	1.91E+00	9.32E-01	1.91E+00	1.69E+01	8.87E+00
R_001498619.	9.35E+00	3.64E-03	8.95E-03	2.39E+01	4.58E+00	2.39E+01	9.02E-01	3.78E-02
PTPN22	8.96E+00	3.69E-03	9.02E-03	2.71E+00	1.44E+00	2.71E+00	6.67E-01	2.46E-01
SCP2	1.03E+03	3.74E-03	9.09E-03	1.21E+00	2.73E-01	1.21E+00	5.93E+01	4.91E+01
NPM3	1.56E+02	3.81E-03	9.23E-03	1.39E+00	4.70E-01	1.39E+00	9.46E+00	6.83E+00
R_003036118.	7.20E+00	3.89E-03	9.39E-03	4.08E+00	2.03E+00	4.08E+00	5.94E-01	1.46E-01
LOC101902742	1.82E+00	3.97E-03	9.52E-03	1.44E+01	3.84E+00	1.44E+01	1.70E-01	1.19E-02
SLC5A6	6.54E+02	4.03E-03	9.64E-03	1.28E+00	3.58E-01	1.28E+00	3.81E+01	2.97E+01
CCDC38	1.37E+01	4.06E-03	9.64E-03	1.94E+00	9.58E-01	1.94E+00	9.33E-01	4.81E-01
KRT77	2.02E+00	4.09E-03	9.67E-03	8.71E+00	3.12E+00	8.71E+00	1.85E-01	2.12E-02
R_003034730.	2.15E+02	4.10E-03	9.67E-03	1.57E+00	6.47E-01	1.57E+00	1.37E+01	8.72E+00
APOA1	1.49E+03	4.19E-03	9.83E-03	3.39E+00	1.76E+00	3.39E+00	1.19E+02	3.49E+01
GJD3	7.90E+00	4.38E-03	1.02E-02	2.03E+00	1.02E+00	2.03E+00	5.41E-01	2.66E-01
XR_808026.3	2.53E+00	4.40E-03	1.02E-02	7.76E+00	2.96E+00	7.76E+00	2.27E-01	2.93E-02
TRAT1	3.43E+00	4.40E-03	1.02E-02	3.56E+00	1.83E+00	3.56E+00	2.70E-01	7.59E-02
ELOVL5	1.38E+03	4.57E-03	1.05E-02	1.27E+00	3.42E-01	1.27E+00	8.06E+01	6.36E+01
SH3BGRL	8.36E+02	4.63E-03	1.06E-02	1.25E+00	3.22E-01	1.25E+00	4.86E+01	3.89E+01
CPXM1	2.38E+03	4.71E-03	1.08E-02	1.43E+00	5.16E-01	1.43E+00	1.47E+02	1.03E+02
HSD11B1	1.23E+01	4.84E-03	1.10E-02	2.02E+00	1.01E+00	2.02E+00	8.47E-01	4.19E-01

LOC101904824	6.28E+00	4.86E-03	1.10E-02	2.97E+00	1.57E+00	2.97E+00	4.80E-01	1.61E-01
ALOX5AP	2.13E+01	4.90E-03	1.10E-02	1.68E+00	7.52E-01	1.68E+00	1.38E+00	8.23E-01
R_003031734.	1.45E+01	4.91E-03	1.10E-02	2.88E+00	1.52E+00	2.88E+00	1.11E+00	3.86E-01
LOC100852061	1.55E+00	5.31E-03	1.19E-02	4.08E+01	5.35E+00	4.08E+01	1.51E-01	3.72E-03
ANKS4B	2.12E+00	6.01E-03	1.33E-02	4.93E+00	2.30E+00	4.93E+00	1.80E-01	3.66E-02
LOC514686	1.60E+00	6.03E-03	1.33E-02	3.55E+00	1.83E+00	3.55E+00	1.26E-01	3.55E-02
DAG1	7.56E+03	6.05E-03	1.33E-02	1.58E+00	6.60E-01	1.58E+00	4.81E+02	3.04E+02
LOC100141014	1.78E+00	6.06E-03	1.33E-02	3.10E+00	1.63E+00	3.10E+00	1.37E-01	4.42E-02
UCK2	1.64E+02	6.92E-03	1.51E-02	1.62E+00	7.00E-01	1.62E+00	1.06E+01	6.53E+00
GALNT13	3.80E+01	6.96E-03	1.51E-02	1.78E+00	8.35E-01	1.78E+00	2.54E+00	1.42E+00
R_001500092.	3.18E+00	7.94E-03	1.72E-02	9.97E+00	3.32E+00	9.97E+00	2.89E-01	2.90E-02
PTX3	1.85E+02	8.19E-03	1.76E-02	2.26E+00	1.18E+00	2.26E+00	1.32E+01	5.83E+00
RHBDD1	5.74E+02	8.23E-03	1.76E-02	1.22E+00	2.86E-01	1.22E+00	3.30E+01	2.71E+01
NIPAL4	2.27E+01	8.23E-03	1.76E-02	4.32E+00	2.11E+00	4.32E+00	1.86E+00	4.30E-01
SCPEP1	1.31E+03	8.57E-03	1.83E-02	1.20E+00	2.67E-01	1.20E+00	7.48E+01	6.21E+01
DBIL5	1.02E+01	1.01E-02	2.15E-02	1.67E+00	7.39E-01	1.67E+00	6.61E-01	3.96E-01
DGKI	9.03E+01	1.05E-02	2.23E-02	1.71E+00	7.73E-01	1.71E+00	5.89E+00	3.45E+00
HEATR3	3.11E+02	1.09E-02	2.31E-02	1.19E+00	2.55E-01	1.19E+00	1.77E+01	1.48E+01
LOC112442378	3.88E+00	1.11E-02	2.31E-02	4.50E+00	2.17E+00	4.50E+00	3.22E-01	7.16E-02
TXNDC5	4.30E+03	1.11E-02	2.31E-02	1.24E+00	3.15E-01	1.24E+00	2.49E+02	2.00E+02
LOC751811	5.38E+00	1.11E-02	2.31E-02	4.62E+00	2.21E+00	4.62E+00	4.48E-01	9.71E-02
R_003037450.	5.87E+01	1.15E-02	2.38E-02	2.82E+00	1.49E+00	2.82E+00	4.45E+00	1.58E+00
EGFL7	1.11E+03	1.19E-02	2.45E-02	1.35E+00	4.34E-01	1.35E+00	6.65E+01	4.92E+01
LOC112441481	1.85E+00	1.21E-02	2.49E-02	2.74E+01	4.78E+00	2.74E+01	1.79E-01	6.52E-03
BDKRB1	3.66E+00	1.23E-02	2.53E-02	3.26E+00	1.70E+00	3.26E+00	2.86E-01	8.77E-02
KCNF1	7.07E+01	1.24E-02	2.53E-02	8.06E+00	3.01E+00	8.06E+00	6.38E+00	7.91E-01
ANXA1	8.52E+02	1.25E-02	2.55E-02	1.45E+00	5.35E-01	1.45E+00	5.27E+01	3.64E+01
CTSC	8.73E+02	1.27E-02	2.57E-02	1.70E+00	7.63E-01	1.70E+00	5.73E+01	3.37E+01
RBM7	2.75E+02	1.28E-02	2.57E-02	1.20E+00	2.68E-01	1.20E+00	1.57E+01	1.30E+01
CYP11A1	1.26E+03	1.28E-02	2.57E-02	8.03E+00	3.01E+00	8.03E+00	1.13E+02	1.41E+01
KLRF1	1.37E+00	1.28E-02	2.57E-02	1.27E+01	3.67E+00	1.27E+01	1.28E-01	1.00E-02
CDC42EP1	2.36E+03	1.33E-02	2.65E-02	1.23E+00	2.95E-01	1.23E+00	1.37E+02	1.12E+02
CCDC184	4.42E+01	1.35E-02	2.68E-02	1.57E+00	6.51E-01	1.57E+00	2.79E+00	1.78E+00

CASS4	1.26E+01	1.36E-02	2.68E-02	1.96E+00	9.68E-01	1.96E+00	8.52E-01	4.36E-01
IL18RAP	2.75E+00	1.37E-02	2.69E-02	4.27E+00	2.09E+00	4.27E+00	2.24E-01	5.26E-02
SNTG2	1.83E+01	1.38E-02	2.70E-02	2.06E+00	1.04E+00	2.06E+00	1.27E+00	6.17E-01
OAT	1.58E+03	1.38E-02	2.70E-02	1.18E+00	2.44E-01	1.18E+00	8.99E+01	7.59E+01
ST3GAL4	1.65E+03	1.40E-02	2.72E-02	1.92E+00	9.41E-01	1.92E+00	1.12E+02	5.83E+01
R_003030242.	4.21E+00	1.45E-02	2.82E-02	4.58E+00	2.19E+00	4.58E+00	3.46E-01	7.55E-02
R_003035554.	1.77E+01	1.46E-02	2.82E-02	2.71E+00	1.44E+00	2.71E+00	1.32E+00	4.88E-01
FAM78A	6.34E+02	1.47E-02	2.83E-02	2.84E+00	1.51E+00	2.84E+00	4.83E+01	1.70E+01
LOC100848495	2.18E+01	1.49E-02	2.86E-02	1.43E+00	5.19E-01	1.43E+00	1.33E+00	9.32E-01
ZNF831	5.44E+00	1.55E-02	2.95E-02	2.13E+00	1.09E+00	2.13E+00	3.79E-01	1.78E-01
PNP	1.08E+03	1.60E-02	3.05E-02	1.41E+00	4.91E-01	1.41E+00	6.66E+01	4.74E+01
LOC107132002	5.11E+00	1.70E-02	3.22E-02	1.98E+00	9.86E-01	1.98E+00	3.52E-01	1.78E-01
R_003037185.	1.06E+00	1.75E-02	3.30E-02	3.53E+01	5.14E+00	3.53E+01	1.03E-01	2.93E-03
SULT1B1	1.39E+02	1.78E-02	3.35E-02	1.41E+00	4.97E-01	1.41E+00	8.51E+00	6.03E+00
GAT	2.49E+00	1.82E-02	3.41E-02	2.41E+01	4.59E+00	2.41E+01	2.39E-01	9.94E-03
ZNF565	1.17E+02	1.92E-02	3.58E-02	1.19E+00	2.46E-01	1.19E+00	6.62E+00	5.58E+00
R_003030631.	1.70E+00	1.98E-02	3.66E-02	3.31E+00	1.73E+00	3.31E+00	1.33E-01	4.02E-02
DHCR24	1.68E+03	1.99E-02	3.66E-02	1.66E+00	7.29E-01	1.66E+00	1.08E+02	6.53E+01
R_003036304.	2.05E+00	2.00E-02	3.66E-02	9.13E+00	3.19E+00	9.13E+00	1.87E-01	2.05E-02
SH3GL3	1.73E+02	2.00E-02	3.66E-02	1.93E+00	9.49E-01	1.93E+00	1.19E+01	6.14E+00
XR_806886.3	4.09E+00	2.00E-02	3.66E-02	2.73E+00	1.45E+00	2.73E+00	3.06E-01	1.12E-01
CYP51A1	7.52E+02	2.00E-02	3.66E-02	1.53E+00	6.09E-01	1.53E+00	4.71E+01	3.09E+01
PHLDB3	3.12E+02	2.02E-02	3.68E-02	1.68E+00	7.48E-01	1.68E+00	2.02E+01	1.21E+01
NALCN	8.06E+01	2.08E-02	3.78E-02	3.27E+00	1.71E+00	3.27E+00	6.23E+00	1.90E+00
PLGRKT	1.47E+02	2.09E-02	3.78E-02	1.26E+00	3.32E-01	1.26E+00	8.56E+00	6.80E+00
TMPRSS6	3.43E+01	2.13E-02	3.83E-02	1.51E+00	5.94E-01	1.51E+00	2.17E+00	1.44E+00
SQLE	1.17E+03	2.15E-02	3.87E-02	1.52E+00	6.01E-01	1.52E+00	7.27E+01	4.79E+01
KCND3	1.99E+02	2.16E-02	3.87E-02	2.37E+00	1.25E+00	2.37E+00	1.44E+01	6.07E+00
NR_103815.1	2.54E+02	2.20E-02	3.93E-02	1.91E+00	9.34E-01	1.91E+00	1.71E+01	8.95E+00
SPTSSA	3.72E+02	2.28E-02	4.05E-02	1.25E+00	3.22E-01	1.25E+00	2.16E+01	1.73E+01
P3H1	2.39E+03	2.32E-02	4.12E-02	1.17E+00	2.30E-01	1.17E+00	1.35E+02	1.15E+02
KIR2DL5A	1.72E+00	2.34E-02	4.12E-02	2.29E+01	4.52E+00	2.29E+01	1.65E-01	7.20E-03
OTULINL	3.47E+03	2.34E-02	4.12E-02	1.23E+00	2.99E-01	1.23E+00	2.00E+02	1.62E+02

SAMD3	7.37E+00	2.35E-02	4.13E-02	1.66E+00	7.35E-01	1.66E+00	4.77E-01	2.87E-01
R_003036829.	1.16E+03	2.46E-02	4.30E-02	1.40E+00	4.83E-01	1.40E+00	7.09E+01	5.07E+01
MSMO1	1.46E+03	2.49E-02	4.34E-02	1.45E+00	5.35E-01	1.45E+00	8.98E+01	6.20E+01
ZNF330	3.75E+02	2.50E-02	4.34E-02	1.28E+00	3.52E-01	1.28E+00	2.20E+01	1.72E+01
R_001500342.	3.03E+00	2.53E-02	4.37E-02	3.75E+00	1.91E+00	3.75E+00	2.41E-01	6.41E-02
ARAF	1.17E+03	2.56E-02	4.41E-02	1.15E+00	2.00E-01	1.15E+00	6.54E+01	5.69E+01
SRGN	3.38E+03	2.57E-02	4.42E-02	2.52E+00	1.33E+00	2.52E+00	2.50E+02	9.93E+01
C6H4orf3	1.59E+03	2.61E-02	4.48E-02	1.20E+00	2.63E-01	1.20E+00	9.12E+01	7.60E+01
R_003037434.	3.25E+01	2.67E-02	4.57E-02	2.12E+00	1.08E+00	2.12E+00	2.28E+00	1.08E+00
GRAMD1B	1.01E+03	2.68E-02	4.57E-02	1.92E+00	9.44E-01	1.92E+00	6.88E+01	3.58E+01
XR_235161.2	2.10E+02	2.70E-02	4.59E-02	2.73E+00	1.45E+00	2.73E+00	1.58E+01	5.77E+00
R_003038026.	9.90E+00	2.71E-02	4.59E-02	2.27E+00	1.18E+00	2.27E+00	7.16E-01	3.16E-01
R_001500581.	9.29E+01	2.76E-02	4.66E-02	1.47E+00	5.58E-01	1.47E+00	5.75E+00	3.91E+00
CTSW	8.30E+01	2.81E-02	4.73E-02	3.46E+00	1.79E+00	3.46E+00	6.56E+00	1.90E+00
XR_233810.4	2.06E+01	2.82E-02	4.73E-02	1.88E+00	9.13E-01	1.88E+00	1.40E+00	7.42E-01
SCARB1	2.30E+03	2.84E-02	4.74E-02	1.78E+00	8.33E-01	1.78E+00	1.53E+02	8.60E+01
PODNL1	1.41E+02	3.01E-02	5.00E-02	1.48E+00	5.62E-01	1.48E+00	8.79E+00	5.95E+00
HEBP2	2.43E+02	3.09E-02	5.13E-02	1.68E+00	7.47E-01	1.68E+00	1.59E+01	9.46E+00
XR_804520.3	1.30E+00	3.11E-02	5.14E-02	4.70E+00	2.23E+00	4.70E+00	1.09E-01	2.31E-02
R_003034727.	5.61E+00	3.15E-02	5.19E-02	1.04E+01	3.38E+00	1.04E+01	5.15E-01	4.93E-02
XR_236197.4	5.47E+01	3.18E-02	5.22E-02	1.60E+00	6.76E-01	1.60E+00	3.51E+00	2.20E+00
RGN	2.09E+02	3.34E-02	5.46E-02	1.40E+00	4.85E-01	1.40E+00	1.28E+01	9.12E+00
EIF4EBP1	8.28E+02	3.45E-02	5.64E-02	1.34E+00	4.26E-01	1.34E+00	4.96E+01	3.69E+01
PEAK3	6.92E+00	3.46E-02	5.64E-02	1.58E+00	6.62E-01	1.58E+00	4.36E-01	2.76E-01
R_001501284.	1.49E+00	3.50E-02	5.66E-02	2.74E+00	1.45E+00	2.74E+00	1.11E-01	4.06E-02
WEE2	1.06E+01	3.50E-02	5.66E-02	3.24E+00	1.70E+00	3.24E+00	8.29E-01	2.56E-01
WARS2	1.75E+02	3.55E-02	5.72E-02	1.19E+00	2.50E-01	1.19E+00	9.97E+00	8.38E+00
R_003037968.	2.71E+00	3.66E-02	5.87E-02	2.09E+00	1.06E+00	2.09E+00	1.88E-01	9.01E-02
SCG2	3.98E+02	3.66E-02	5.87E-02	8.36E+00	3.06E+00	8.36E+00	3.58E+01	4.29E+00
PNPLA2	4.64E+02	3.68E-02	5.88E-02	1.21E+00	2.72E-01	1.21E+00	2.66E+01	2.20E+01
TOR1B	4.13E+02	3.78E-02	6.02E-02	1.18E+00	2.40E-01	1.18E+00	2.34E+01	1.99E+01
TARBP1	3.56E+02	3.82E-02	6.07E-02	1.29E+00	3.66E-01	1.29E+00	2.09E+01	1.63E+01
ANGPTL5	1.76E+01	3.89E-02	6.16E-02	8.38E+00	3.07E+00	8.38E+00	1.58E+00	1.89E-01

ANXA2	3.56E+03	3.92E-02	6.19E-02	1.18E+00	2.39E-01	1.18E+00	2.02E+02	1.72E+02
HSD17B12	7.61E+02	3.97E-02	6.25E-02	1.35E+00	4.30E-01	1.35E+00	4.55E+01	3.38E+01
R_003029390.	2.39E+01	3.99E-02	6.26E-02	1.86E+00	8.95E-01	1.86E+00	1.62E+00	8.68E-01
VAMP5	2.88E+02	4.13E-02	6.45E-02	1.35E+00	4.31E-01	1.35E+00	1.73E+01	1.29E+01
LOC112446743	1.45E+00	4.18E-02	6.52E-02	1.45E+03	1.05E+01	1.45E+03	1.45E-01	1.00E-04
LOC100847738	1.55E+00	4.25E-02	6.61E-02	1.55E+03	1.06E+01	1.55E+03	1.55E-01	1.00E-04
LOC511161	3.91E+00	4.29E-02	6.65E-02	2.36E+00	1.24E+00	2.36E+00	2.84E-01	1.20E-01
DLL1	2.98E+02	4.31E-02	6.66E-02	1.21E+00	2.71E-01	1.21E+00	1.71E+01	1.41E+01
CYP17A1	1.26E+01	4.33E-02	6.68E-02	7.32E+00	2.87E+00	7.32E+00	1.13E+00	1.54E-01
GJB5	3.65E+01	4.39E-02	6.74E-02	4.50E+00	2.17E+00	4.50E+00	3.06E+00	6.80E-01
STAR	9.10E+02	4.54E-02	6.94E-02	4.02E+00	2.01E+00	4.02E+00	7.49E+01	1.87E+01
LOC101902413	3.56E+00	4.55E-02	6.95E-02	2.28E+00	1.19E+00	2.28E+00	2.56E-01	1.12E-01
FCAR	7.94E-01	4.82E-02	7.34E-02	7.94E+02	9.63E+00	7.94E+02	7.94E-02	1.00E-04
STYK1	8.59E+00	4.96E-02	7.53E-02	6.23E+00	2.64E+00	6.23E+00	7.51E-01	1.21E-01
FKBP5	7.91E+02	5.05E-02	7.64E-02	2.62E+00	1.39E+00	2.62E+00	5.86E+01	2.24E+01
IDI1	7.39E+02	5.31E-02	8.00E-02	1.34E+00	4.24E-01	1.34E+00	4.39E+01	3.27E+01
HCST	3.05E+00	5.42E-02	8.15E-02	2.31E+00	1.21E+00	2.31E+00	2.17E-01	9.43E-02
MYL6	6.74E+03	5.62E-02	8.42E-02	1.25E+00	3.23E-01	1.25E+00	3.94E+02	3.15E+02
LDLR	1.62E+03	5.64E-02	8.44E-02	1.54E+00	6.20E-01	1.54E+00	1.02E+02	6.62E+01
LOC112442745	1.93E+01	5.66E-02	8.44E-02	1.67E+00	7.42E-01	1.67E+00	1.23E+00	7.36E-01
C10H14orf1	1.60E+02	5.83E-02	8.68E-02	1.30E+00	3.82E-01	1.30E+00	9.49E+00	7.28E+00
R_003030234.	1.81E+00	6.00E-02	8.87E-02	6.17E+00	2.63E+00	6.17E+00	1.56E-01	2.52E-02
R_003030005.	1.26E+00	6.02E-02	8.87E-02	1.37E+01	3.78E+00	1.37E+01	1.18E-01	8.59E-03
HMGCR	1.15E+03	6.02E-02	8.87E-02	1.79E+00	8.43E-01	1.79E+00	7.68E+01	4.28E+01
R_003032548.	2.86E+01	6.06E-02	8.91E-02	1.43E+00	5.14E-01	1.43E+00	1.75E+00	1.23E+00
R_003035042.	1.13E+02	6.10E-02	8.95E-02	1.44E+00	5.27E-01	1.44E+00	6.89E+00	4.78E+00
RORB	2.00E+01	6.30E-02	9.20E-02	2.79E+00	1.48E+00	2.79E+00	1.50E+00	5.39E-01
LOC112441470	2.21E+03	6.31E-02	9.20E-02	1.68E+01	4.07E+00	1.68E+01	2.10E+02	1.25E+01
LOC104973382	2.96E+00	6.52E-02	9.48E-02	2.34E+00	1.22E+00	2.34E+00	2.14E-01	9.14E-02
XR_810083.3	6.84E+01	6.62E-02	9.60E-02	1.32E+00	3.99E-01	1.32E+00	4.06E+00	3.08E+00
LOC100336984	5.92E+00	7.33E-02	1.06E-01	1.25E+01	3.64E+00	1.25E+01	5.51E-01	4.41E-02
XR_815239.3	1.60E+01	7.46E-02	1.08E-01	1.39E+00	4.77E-01	1.39E+00	9.73E-01	6.99E-01
R_003030615.	2.08E+00	7.67E-02	1.10E-01	1.01E+01	3.34E+00	1.01E+01	1.89E-01	1.87E-02

METTL9	1.43E+03	7.87E-02	1.13E-01	1.16E+00	2.16E-01	1.16E+00	8.08E+01	6.96E+01
PANK1	2.69E+02	7.99E-02	1.14E-01	1.21E+00	2.77E-01	1.21E+00	1.55E+01	1.28E+01
ANAPC7	1.11E+03	8.06E-02	1.15E-01	1.08E+00	1.11E-01	1.08E+00	6.02E+01	5.58E+01
FDX1	3.54E+02	8.07E-02	1.15E-01	1.32E+00	3.96E-01	1.32E+00	2.10E+01	1.59E+01
R_003032747.	7.34E+00	8.35E-02	1.18E-01	6.15E+00	2.62E+00	6.15E+00	6.46E-01	1.05E-01
R_003034434.	5.49E-01	8.75E-02	1.24E-01	1.44E+01	3.85E+00	1.44E+01	5.14E-02	3.57E-03
LOC100138641	1.06E+02	8.95E-02	1.26E-01	2.51E+00	1.33E+00	2.51E+00	7.85E+00	3.13E+00
R_003035956.	5.86E+00	9.21E-02	1.30E-01	1.87E+00	9.01E-01	1.87E+00	3.92E-01	2.10E-01
S100A11	2.24E+03	9.33E-02	1.31E-01	1.21E+00	2.76E-01	1.21E+00	1.29E+02	1.06E+02
ELOVL6	3.51E+02	9.63E-02	1.34E-01	1.27E+00	3.46E-01	1.27E+00	2.06E+01	1.62E+01
QPRT	3.25E+02	9.63E-02	1.34E-01	1.18E+00	2.44E-01	1.18E+00	1.85E+01	1.56E+01
R_003034037.	1.84E+00	9.80E-02	1.36E-01	9.91E+00	3.31E+00	9.91E+00	1.71E-01	1.72E-02
R_003031416.	2.57E+01	9.93E-02	1.38E-01	2.55E+00	1.35E+00	2.55E+00	1.90E+00	7.44E-01
KCNE4	1.93E+02	1.05E-01	1.45E-01	2.55E+00	1.35E+00	2.55E+00	1.43E+01	5.61E+00
LHCGR	1.32E+02	1.08E-01	1.49E-01	6.08E+00	2.60E+00	6.08E+00	1.16E+01	1.90E+00
INSIG1	7.50E+02	1.08E-01	1.49E-01	1.49E+00	5.74E-01	1.49E+00	4.64E+01	3.12E+01
LRP11	2.06E+02	1.09E-01	1.50E-01	1.43E+00	5.20E-01	1.43E+00	1.27E+01	8.83E+00
R_001500563.	1.87E+00	1.11E-01	1.52E-01	1.84E+00	8.81E-01	1.84E+00	1.21E-01	6.58E-02
NDNF	6.63E+01	1.15E-01	1.57E-01	1.47E+00	5.58E-01	1.47E+00	4.13E+00	2.80E+00
LOC781813	1.39E+02	1.17E-01	1.59E-01	1.20E+00	2.62E-01	1.20E+00	7.97E+00	6.65E+00
TDGF1	6.65E+00	1.19E-01	1.62E-01	2.61E+00	1.38E+00	2.61E+00	4.94E-01	1.90E-01
R_001501446.	3.43E+00	1.21E-01	1.63E-01	1.94E+00	9.53E-01	1.94E+00	2.33E-01	1.20E-01
R_001494888.	4.31E-01	1.24E-01	1.68E-01	4.30E+02	8.75E+00	4.30E+02	4.30E-02	1.00E-04
FKBP11	7.11E+02	1.26E-01	1.70E-01	1.18E+00	2.39E-01	1.18E+00	4.03E+01	3.42E+01
SLC35C2	6.06E+02	1.27E-01	1.70E-01	1.10E+00	1.34E-01	1.10E+00	3.33E+01	3.04E+01
XR_812966.3	1.01E+02	1.27E-01	1.70E-01	4.04E+00	2.01E+00	4.04E+00	8.37E+00	2.07E+00
TEX45	3.86E+00	1.32E-01	1.77E-01	2.67E+00	1.42E+00	2.67E+00	2.90E-01	1.09E-01
GSTA1	2.95E+03	1.32E-01	1.77E-01	2.62E+00	1.39E+00	2.62E+00	2.21E+02	8.44E+01
NR_038147.1	2.47E+02	1.37E-01	1.82E-01	1.27E+00	3.50E-01	1.27E+00	1.45E+01	1.14E+01
PCSK6	6.50E+02	1.41E-01	1.88E-01	1.28E+00	3.60E-01	1.28E+00	3.77E+01	2.94E+01
IFI35	2.12E+02	1.46E-01	1.94E-01	1.16E+00	2.13E-01	1.16E+00	1.19E+01	1.03E+01
GRAMD2B	3.96E+02	1.48E-01	1.95E-01	1.29E+00	3.65E-01	1.29E+00	2.33E+01	1.81E+01
CC2D2B	4.27E+02	1.61E-01	2.12E-01	1.20E+00	2.64E-01	1.20E+00	2.44E+01	2.03E+01

id-TRGC3	1.39E+01	1.65E-01	2.16E-01	2.28E+00	1.19E+00	2.28E+00	1.00E+00	4.40E-01
R_003034613.	1.62E+00	1.65E-01	2.17E-01	6.66E+00	2.73E+00	6.66E+00	1.43E-01	2.15E-02
id-LOC407201	6.16E-01	1.67E-01	2.18E-01	5.21E+00	2.38E+00	5.21E+00	5.17E-02	9.92E-03
XR_236208.4	5.07E+00	1.67E-01	2.18E-01	3.91E+00	1.97E+00	3.91E+00	4.10E-01	1.05E-01
PRF1	1.15E+01	1.76E-01	2.28E-01	2.61E+00	1.38E+00	2.61E+00	8.64E-01	3.31E-01
NR_132744.1	2.62E+02	1.76E-01	2.29E-01	1.13E+00	1.80E-01	1.13E+00	1.47E+01	1.29E+01
TSC22D3	1.49E+03	1.77E-01	2.29E-01	1.18E+00	2.36E-01	1.18E+00	8.44E+01	7.16E+01
EMID1	1.38E+03	1.80E-01	2.32E-01	1.80E+00	8.50E-01	1.80E+00	9.20E+01	5.10E+01
FADS2	9.38E+02	1.86E-01	2.39E-01	1.25E+00	3.22E-01	1.25E+00	5.46E+01	4.37E+01
BCDIN3D	1.33E+02	1.89E-01	2.43E-01	1.10E+00	1.38E-01	1.10E+00	7.33E+00	6.67E+00
-LOC11244641	6.53E-01	1.91E-01	2.44E-01	5.55E+00	2.47E+00	5.55E+00	5.60E-02	1.01E-02
PPP1R14A	1.66E+02	1.93E-01	2.47E-01	1.50E+00	5.85E-01	1.50E+00	1.05E+01	6.97E+00
CTIF	5.48E+02	1.97E-01	2.50E-01	1.22E+00	2.86E-01	1.22E+00	3.16E+01	2.59E+01
LOC107132529	6.26E+00	1.97E-01	2.50E-01	1.47E+00	5.52E-01	1.47E+00	3.91E-01	2.66E-01
RDH11	4.51E+02	1.99E-01	2.52E-01	1.26E+00	3.33E-01	1.26E+00	2.64E+01	2.09E+01
XR_233298.4	4.03E-01	2.01E-01	2.54E-01	4.02E+02	8.65E+00	4.02E+02	4.02E-02	1.00E-04
NOP53	4.46E+03	2.02E-01	2.54E-01	1.16E+00	2.11E-01	1.16E+00	2.52E+02	2.18E+02
ABAT	8.51E+02	2.02E-01	2.55E-01	1.23E+00	3.03E-01	1.23E+00	4.93E+01	3.99E+01
ACLY	2.92E+03	2.06E-01	2.58E-01	1.15E+00	1.99E-01	1.15E+00	1.63E+02	1.42E+02
TSKU	1.51E+03	2.12E-01	2.66E-01	1.19E+00	2.54E-01	1.19E+00	8.62E+01	7.23E+01
PRORSD1	1.99E+02	2.13E-01	2.66E-01	1.31E+00	3.89E-01	1.31E+00	1.19E+01	9.09E+00
KIR3DL2	1.23E+00	2.19E-01	2.73E-01	7.91E+00	2.98E+00	7.91E+00	1.10E-01	1.39E-02
KRT1	9.97E-01	2.25E-01	2.80E-01	1.80E+00	8.51E-01	1.80E+00	6.41E-02	3.56E-02
ADGRF2	2.94E+00	2.26E-01	2.80E-01	5.43E+00	2.44E+00	5.43E+00	2.50E-01	4.61E-02
R_001500425.	1.39E+00	2.27E-01	2.80E-01	2.17E+01	4.44E+00	2.17E+01	1.33E-01	6.14E-03
STBD1	4.12E+02	2.37E-01	2.92E-01	1.13E+00	1.78E-01	1.13E+00	2.31E+01	2.04E+01
PLOD1	5.08E+03	2.38E-01	2.93E-01	1.08E+00	1.16E-01	1.08E+00	2.77E+02	2.55E+02
R_001501097.	2.81E+01	2.40E-01	2.95E-01	2.19E+00	1.13E+00	2.19E+00	2.01E+00	9.18E-01
XR_815563.3	5.50E+02	2.42E-01	2.96E-01	1.13E+00	1.72E-01	1.13E+00	3.06E+01	2.72E+01
R_003029940.	1.13E+00	2.42E-01	2.96E-01	4.55E+00	2.19E+00	4.55E+00	9.61E-02	2.11E-02
R_003030041.	5.15E+00	2.44E-01	2.97E-01	1.57E+00	6.49E-01	1.57E+00	3.27E-01	2.09E-01
RBBP9	3.31E+02	2.56E-01	3.11E-01	1.11E+00	1.55E-01	1.11E+00	1.83E+01	1.64E+01
PKNOX2	7.69E+02	2.61E-01	3.17E-01	1.15E+00	1.99E-01	1.15E+00	4.32E+01	3.76E+01

A4GALT	1.50E+03	2.64E-01	3.20E-01	2.20E+00	1.14E+00	2.20E+00	1.07E+02	4.84E+01
RARRES2	3.99E+03	2.64E-01	3.20E-01	1.34E+00	4.25E-01	1.34E+00	2.40E+02	1.79E+02
R_003033396.	1.06E+00	2.81E-01	3.38E-01	5.99E+00	2.58E+00	5.99E+00	9.17E-02	1.53E-02
CAPZA2	6.04E+02	2.85E-01	3.43E-01	1.06E+00	8.69E-02	1.06E+00	3.27E+01	3.08E+01
SERBP1	4.61E+03	2.89E-01	3.47E-01	1.05E+00	6.44E-02	1.05E+00	2.48E+02	2.37E+02
MT1E-2	2.88E+01	2.92E-01	3.49E-01	1.77E+00	8.24E-01	1.77E+00	1.92E+00	1.09E+00
R_003032455.	2.52E+01	2.93E-01	3.50E-01	1.19E+00	2.56E-01	1.19E+00	1.43E+00	1.19E+00
R_003034854.	1.64E+00	2.97E-01	3.54E-01	3.20E+00	1.68E+00	3.20E+00	1.27E-01	3.97E-02
CD96	9.25E+00	3.07E-01	3.64E-01	1.72E+00	7.84E-01	1.72E+00	6.10E-01	3.54E-01
ASS1	9.78E+01	3.07E-01	3.64E-01	1.40E+00	4.84E-01	1.40E+00	5.98E+00	4.27E+00
XR_809763.3	2.88E+00	3.08E-01	3.65E-01	5.26E+00	2.39E+00	5.26E+00	2.44E-01	4.64E-02
R_003034435.	3.65E+00	3.09E-01	3.65E-01	3.92E+00	1.97E+00	3.92E+00	2.96E-01	7.56E-02
RIN1	2.78E+01	3.20E-01	3.77E-01	2.40E+00	1.26E+00	2.40E+00	2.01E+00	8.39E-01
FAM3A	2.56E+02	3.21E-01	3.77E-01	1.10E+00	1.36E-01	1.10E+00	1.41E+01	1.28E+01
PTCH2	8.95E+02	3.27E-01	3.84E-01	1.73E+00	7.87E-01	1.73E+00	5.95E+01	3.45E+01
PLCL2	9.76E+02	3.38E-01	3.95E-01	1.17E+00	2.30E-01	1.17E+00	5.52E+01	4.70E+01
LOC780982	2.98E+01	3.48E-01	4.06E-01	1.19E+00	2.49E-01	1.19E+00	1.69E+00	1.42E+00
R_001501206.	1.54E+00	3.48E-01	4.06E-01	4.29E+00	2.10E+00	4.29E+00	1.28E-01	2.98E-02
SLC2A6	4.84E+01	3.50E-01	4.07E-01	1.45E+00	5.37E-01	1.45E+00	2.96E+00	2.04E+00
FDFT1	1.62E+03	3.54E-01	4.10E-01	1.14E+00	1.83E-01	1.14E+00	9.07E+01	7.99E+01
XR_238288.4	1.77E+00	3.54E-01	4.10E-01	4.50E+00	2.17E+00	4.50E+00	1.48E-01	3.28E-02
RGS17	2.53E+01	3.57E-01	4.12E-01	1.61E+00	6.87E-01	1.61E+00	1.64E+00	1.02E+00
TM7SF2	2.49E+02	3.62E-01	4.17E-01	1.30E+00	3.77E-01	1.30E+00	1.47E+01	1.13E+01
C16H1orf167	3.90E+01	3.86E-01	4.44E-01	9.58E-01	-6.14E-02	-1.04E+00	2.02E+00	2.10E+00
PITPNB	1.49E+03	4.08E-01	4.68E-01	1.04E+00	5.62E-02	1.04E+00	7.99E+01	7.69E+01
MBD2	7.44E+02	4.19E-01	4.79E-01	1.06E+00	8.35E-02	1.06E+00	4.04E+01	3.81E+01
BHMT2	8.96E+00	4.21E-01	4.81E-01	1.43E+00	5.11E-01	1.43E+00	5.46E-01	3.83E-01
id-LOC781951	4.96E+00	4.23E-01	4.82E-01	9.09E-01	-1.37E-01	-1.10E+00	2.45E-01	2.69E-01
HPGD	8.53E+01	4.40E-01	5.00E-01	1.57E+00	6.48E-01	1.57E+00	5.41E+00	3.45E+00
PLA2G3	9.70E+00	4.41E-01	5.01E-01	1.41E+00	4.92E-01	1.41E+00	5.96E-01	4.23E-01
LOC100139916	1.29E+01	4.48E-01	5.07E-01	2.69E+00	1.43E+00	2.69E+00	9.62E-01	3.57E-01
CENPM	3.53E+02	4.54E-01	5.12E-01	1.08E+00	1.08E-01	1.08E+00	1.92E+01	1.78E+01
PLEKHO2	7.22E+02	4.55E-01	5.12E-01	1.09E+00	1.26E-01	1.09E+00	3.96E+01	3.62E+01

TNNI1	7.05E+01	4.57E-01	5.14E-01	2.42E+00	1.27E+00	2.42E+00	5.19E+00	2.15E+00
MVK	1.59E+03	4.65E-01	5.22E-01	1.17E+00	2.26E-01	1.17E+00	8.98E+01	7.67E+01
STEAP3	2.48E+02	4.70E-01	5.27E-01	1.11E+00	1.49E-01	1.11E+00	1.37E+01	1.23E+01
MTHFD2	1.64E+02	4.75E-01	5.31E-01	1.08E+00	1.07E-01	1.08E+00	8.92E+00	8.28E+00
NR1H3	4.51E+02	4.77E-01	5.32E-01	1.07E+00	9.50E-02	1.07E+00	2.44E+01	2.28E+01
MTCH1	5.90E+03	4.94E-01	5.49E-01	1.05E+00	6.45E-02	1.05E+00	3.18E+02	3.04E+02
CRTAM	4.08E+00	4.98E-01	5.52E-01	3.65E+00	1.87E+00	3.65E+00	3.22E-01	8.81E-02
GRIA2	7.77E+00	5.09E-01	5.64E-01	1.35E+00	4.28E-01	1.35E+00	4.78E-01	3.55E-01
LOC112445109	2.17E+00	5.15E-01	5.69E-01	1.22E+00	2.92E-01	1.22E+00	1.26E-01	1.03E-01
SLC5A11	1.01E+01	5.22E-01	5.76E-01	5.73E+00	2.52E+00	5.73E+00	8.79E-01	1.53E-01
CCND3	1.50E+03	5.31E-01	5.85E-01	1.10E+00	1.40E-01	1.10E+00	8.27E+01	7.51E+01
CYB5R3	6.56E+03	5.40E-01	5.93E-01	1.10E+00	1.32E-01	1.10E+00	3.60E+02	3.29E+02
KCNK3	6.37E+01	5.44E-01	5.96E-01	1.78E+00	8.33E-01	1.78E+00	4.29E+00	2.41E+00
CLCNKA	3.46E+00	5.49E-01	6.00E-01	1.50E+00	5.88E-01	1.50E+00	2.13E-01	1.42E-01
GALNT10	1.61E+03	5.58E-01	6.09E-01	1.06E+00	7.88E-02	1.06E+00	8.67E+01	8.21E+01
R_001494305.	5.76E+01	5.61E-01	6.10E-01	1.16E+00	2.08E-01	1.16E+00	3.22E+00	2.79E+00
CCDC69	3.61E+02	5.79E-01	6.29E-01	1.28E+00	3.56E-01	1.28E+00	2.12E+01	1.66E+01
SLC35F2	5.25E+01	5.81E-01	6.30E-01	1.20E+00	2.66E-01	1.20E+00	3.00E+00	2.50E+00
FKBP10	4.96E+03	5.83E-01	6.31E-01	1.04E+00	6.04E-02	1.04E+00	2.66E+02	2.55E+02
LOC112449109	3.12E+00	5.89E-01	6.36E-01	2.63E+00	1.39E+00	2.63E+00	2.31E-01	8.80E-02
STEAP1	9.77E+00	5.98E-01	6.44E-01	1.54E+00	6.26E-01	1.54E+00	6.20E-01	4.02E-01
FGFR4	7.49E+01	6.07E-01	6.52E-01	1.04E+00	5.76E-02	1.04E+00	4.01E+00	3.85E+00
R_003034136.	5.72E+00	6.14E-01	6.58E-01	3.64E+00	1.86E+00	3.64E+00	4.61E-01	1.27E-01
XR_809117.3	1.34E+00	6.23E-01	6.67E-01	1.42E+00	5.05E-01	1.42E+00	8.02E-02	5.65E-02
FSTL3	2.65E+02	6.50E-01	6.94E-01	9.58E-01	-6.26E-02	-1.04E+00	1.36E+01	1.42E+01
LOC100139931	4.27E+00	6.65E-01	7.09E-01	1.88E+00	9.13E-01	1.88E+00	2.86E-01	1.52E-01
LARGE2	5.42E+02	6.69E-01	7.12E-01	1.44E+00	5.25E-01	1.44E+00	3.32E+01	2.31E+01
ACAT2	9.40E+02	6.87E-01	7.29E-01	1.10E+00	1.35E-01	1.10E+00	5.18E+01	4.71E+01
LOC107131588	2.66E+00	6.95E-01	7.37E-01	1.47E+00	5.53E-01	1.47E+00	1.63E-01	1.11E-01
PLOD3	1.88E+03	7.09E-01	7.49E-01	1.03E+00	4.24E-02	1.03E+00	1.00E+02	9.73E+01
KCNJ4	2.66E+01	7.15E-01	7.55E-01	9.33E+00	3.22E+00	9.33E+00	2.42E+00	2.60E-01
R_003037291.	1.14E+02	7.20E-01	7.58E-01	1.00E+00	6.31E-05	1.00E+00	6.00E+00	6.00E+00
R_003036488.	2.01E+00	7.26E-01	7.61E-01	1.64E+00	7.14E-01	1.64E+00	1.27E-01	7.73E-02

LOC614050	1.83E+00	7.26E-01	7.61E-01	2.00E+00	1.00E+00	2.00E+00	1.23E-01	6.14E-02
IDH1	1.51E+03	7.27E-01	7.61E-01	1.00E+00	3.76E-03	1.00E+00	7.98E+01	7.96E+01
LOC781773	3.99E+00	7.65E-01	7.99E-01	1.09E+00	1.23E-01	1.09E+00	2.19E-01	2.01E-01
XR_003033942.	8.39E+00	7.82E-01	8.15E-01	2.46E+00	1.30E+00	2.46E+00	6.08E-01	2.47E-01
XR_003030361.	4.01E-01	7.86E-01	8.17E-01	7.11E+00	2.83E+00	7.11E+00	3.52E-02	4.96E-03
ITGAD	3.76E+00	8.00E-01	8.30E-01	2.00E+00	1.00E+00	2.00E+00	2.56E-01	1.28E-01
XR_814656.3	3.24E+00	8.27E-01	8.57E-01	1.60E+00	6.81E-01	1.60E+00	2.06E-01	1.28E-01
COLGALT1	2.93E+03	8.38E-01	8.65E-01	9.94E-01	-8.03E-03	-1.01E+00	1.54E+02	1.54E+02
CXCL14	1.20E+02	8.38E-01	8.65E-01	3.38E+00	1.76E+00	3.38E+00	9.47E+00	2.80E+00
CHST8	1.82E+02	8.43E-01	8.69E-01	3.82E+00	1.93E+00	3.82E+00	1.48E+01	3.88E+00
FITM2	4.65E+02	8.46E-01	8.70E-01	1.00E+00	-3.75E-04	-1.00E+00	2.44E+01	2.44E+01
REG4	7.29E+00	8.61E-01	8.84E-01	6.79E+00	2.76E+00	6.79E+00	6.44E-01	9.49E-02
LRPAP1	1.81E+03	8.73E-01	8.94E-01	1.02E+00	2.70E-02	1.02E+00	9.62E+01	9.45E+01
SLC25A19	3.42E+02	8.87E-01	9.06E-01	9.99E-01	-9.38E-04	-1.00E+00	1.79E+01	1.79E+01
XR_003036663.	1.70E+00	9.02E-01	9.20E-01	1.74E+00	7.98E-01	1.74E+00	1.08E-01	6.23E-02
XR_003033094.	4.99E+01	9.11E-01	9.27E-01	1.17E+00	2.29E-01	1.17E+00	2.79E+00	2.38E+00
LSS	1.40E+03	9.17E-01	9.30E-01	1.06E+00	8.77E-02	1.06E+00	7.58E+01	7.13E+01
EBF4	9.13E+02	9.17E-01	9.30E-01	1.00E+00	4.50E-03	1.00E+00	4.82E+01	4.80E+01
DHCR7	1.17E+03	9.25E-01	9.36E-01	1.20E+00	2.66E-01	1.20E+00	6.71E+01	5.58E+01
LOC107132995	3.56E+00	9.26E-01	9.36E-01	1.12E+00	1.69E-01	1.12E+00	1.98E-01	1.76E-01
XR_003031849.	1.91E+02	9.32E-01	9.40E-01	1.02E+00	2.73E-02	1.02E+00	1.01E+01	9.96E+00
C5H12orf75	6.81E+01	9.46E-01	9.51E-01	1.31E+00	3.93E-01	1.31E+00	4.04E+00	3.08E+00
RSPO4	1.24E+01	9.83E-01	9.87E-01	1.63E+00	7.02E-01	1.63E+00	7.98E-01	4.90E-01
SLC16A7	7.43E+01	9.95E-01	9.97E-01	1.18E+00	2.38E-01	1.18E+00	4.20E+00	3.56E+00
ARTN	5.29E+00	9.98E-01	9.98E-01	1.02E+00	3.17E-02	1.02E+00	2.78E-01	2.72E-01

S6 Table. Top 20 pathways enriched for the early genes in cluster 1. Pathways were identified from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis using Database for Annotation, Visualization, and Integrated Discovery (DAVID) knowledgebase.

KEGG Term	Count	P-value	Pop Hits	Percentage
bta01100:Metabolic pathways	185	7.35E-15	1235	14.98
bta05012:Parkinson's disease	40	4.83E-10	152	26.32
bta00190:Oxidative phosphorylation	38	5.51E-10	140	27.14
bta01130:Biosynthesis of antibiotics	48	5.86E-10	206	23.30
bta05010:Alzheimer's disease	41	1.84E-08	178	23.03
bta05016:Huntington's disease	43	5.54E-08	199	21.61
bta04932:Non-alcoholic fatty liver disease (NAFLD)	36	2.92E-07	160	22.50
bta01200:Carbon metabolism	28	5.10E-07	109	25.69
bta01230:Biosynthesis of amino acids	20	7.49E-06	71	28.17
bta04260:Cardiac muscle contraction	20	4.70E-05	80	25.00
bta04360:Axon guidance	25	1.94E-04	125	20.00
bta00051:Fructose and mannose metabolism	11	2.11E-04	31	35.48
bta05230:Central carbon metabolism in cancer	15	7.93E-04	62	24.19
bta00010:Glycolysis / Gluconeogenesis	15	9.39E-04	63	23.81
bta00052:Galactose metabolism	10	0.001035	31	32.26
bta01210:2-Oxocarboxylic acid metabolism	7	0.003367	18	38.89
bta00020:Citrate cycle (TCA cycle)	9	0.003534	30	30.00
bta00230:Purine metabolism	26	0.011116	176	14.77
bta05210:Colorectal cancer	13	0.011599	66	19.70
bta05200:Pathways in cancer	49	0.014493	398	12.31

S7 Table. Top 20 pathways enriched for the late genes in cluster 2. Pathways were identified from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis using Database for Annotation, Visualization, and Integrated Discovery (DAVID) knowledgebase.

KEGG Term	Count	P-value	Pop Hits	Percentage
bta04510:Focal adhesion	54	5.83E-19	208	25.96
bta04151:PI3K-Akt signaling pathway	64	1.90E-14	347	18.44
bta04512:ECM-receptor interaction	30	4.27E-14	87	34.48
bta05200:Pathways in cancer	60	8.22E-10	398	15.08
bta04810:Regulation of actin cytoskeleton	37	6.40E-08	212	17.45
bta04611:Platelet activation	27	1.04E-07	127	21.26
bta05146:Amoebiasis	25	1.32E-07	112	22.32
bta05414:Dilated cardiomyopathy	21	3.67E-07	86	24.42
bta05205:Proteoglycans in cancer	33	1.94E-06	203	16.26
bta05410:Hypertrophic cardiomyopathy (HCM)	19	2.36E-06	80	23.75
bta04015:Rap1 signaling pathway	33	6.17E-06	214	15.42
bta05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	16	1.18E-05	65	24.62
bta04520:Adherens junction	16	2.12E-05	68	23.53
bta04022:cGMP-PKG signaling pathway	26	2.72E-05	159	16.35
bta05218:Melanoma	16	4.33E-05	72	22.22
bta04974:Protein digestion and absorption	17	7.68E-05	84	20.24
bta04068:FoxO signaling pathway	22	1.00E-04	132	16.67
bta04921:Oxytocin signaling pathway	23	1.41E-04	145	15.86
bta04725:Cholinergic synapse	19	2.16E-04	110	17.27
bta04020:Calcium signaling pathway	26	4.60E-04	189	13.76

S8 Table. The pathways enriched for the genes in cluster 3. Pathways were identified from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis using Database for Annotation, Visualization, and Integrated Discovery (DAVID) knowledgebase.

KEGG Term	Count	P-value	Pop Hits	Percentage
bta04724:Glutamatergic synapse	9	0.004596	113	7.96460177
bta04610:Complement and coagulation cascades	7	0.007168	74	9.45945946
bta04975:Fat digestion and absorption	5	0.01985	45	11.1111111
bta04730:Long-term depression	5	0.047364	59	8.47457627
bta04080:Neuroactive ligand-receptor interaction	12	0.076422	292	4.10958904
bta04330:Notch signaling pathway	4	0.094725	47	8.5106383

S9 Table. Top 20 pathways enriched for the late genes in cluster 4. Pathways were identified from Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis using Database for Annotation, Visualization, and Integrated Discovery (DAVID) knowledgebase.

KEGG Term	Count	P-value	Pop Hits	Percentage
bta01100:Metabolic pathways	56	1.75E-09	1235	4.53441296
bta00100:Steroid biosynthesis	8	7.27E-08	20	40
bta01130:Biosynthesis of antibiotics	18	7.09E-07	206	8.73786408
bta04913:Ovarian steroidogenesis	8	5.64E-05	50	16
bta01040:Biosynthesis of unsaturated fatty acids	6	9.66E-05	24	25
bta01212:Fatty acid metabolism	7	3.68E-04	48	14.5833333
bta00900:Terpenoid backbone biosynthesis	5	8.71E-04	22	22.7272727
bta04925:Aldosterone synthesis and secretion	7	0.005008	79	8.86075949
bta00140:Steroid hormone biosynthesis	6	0.005587	57	10.5263158
bta04977:Vitamin digestion and absorption	4	0.009304	22	18.1818182
bta00062:Fatty acid elongation	4	0.014816	26	15.3846154
bta04270:Vascular smooth muscle contraction	7	0.032633	119	5.88235294
bta03320:PPAR signaling pathway	5	0.05209	70	7.14285714
bta00330:Arginine and proline metabolism	4	0.079019	50	8
bta04650:Natural killer cell mediated cytotoxicity	6	0.086757	117	5.12820513
bta04340:Hedgehog signaling pathway	3	0.089385	25	12
bta00310:Lysine degradation	4	0.094478	54	7.40740741

S10 Table. The number of genes extracted from the heatmap and those from the list that mapped onto IPA and DAVID knowledge bases for each cluster.

Cluster	**Number of genes**			
	Heatmap	**Mapped to IPA**	**DAVID (*Homo sapiens*)**	**DAVID (*Bos taurus*)**
1	2052	1654	1589	1773
2	1781	1402	1290	1415
3	871	534	477	576
4	516	376	350	393

S11 Table. Chemical upstream regulators (including endogenous molecules) associated with the strong clusters (clusters 1 and 4).

Cluster 1	Upstream Regulator	Molecule Type	Activation z-score	p-value of overlap
	GSKJ4	chemical reagent	5.048	7.57E-18
	CD 437	chemical drug	6.173	1.69E-12
	ST1926	chemical drug	5.799	6.37E-12
	metribolone	chemical reagent	-7.648	1.87E-10
	actinonin	chemical reagent	3.317	2.70E-09
	IND S1	chemical - kinase inhibitor	0.302	1.09E-07
	5-fluorouracil	chemical drug	2.671	1.56E-08
	trichostatin A	chemical drug	-3.257	8.85E-07
	PCGEM1	other	-3.696	9.53E-07
	1,2-dithiol-3-thione	chemical reagent	-4.967	1.28E-06
	decitabine	chemical drug	-3.542	2.35E-06
	beta-estradiol	chemical - endogenous mammalian	-7.079	2.93E-06
	mono-(2-ethylhexyl)phthalate	chemical toxicant	-5.073	3.01E-06
	tazemetostat	chemical drug	1.121	3.88E-06
	SP2509	chemical reagent	1.254	4.47E-06
	torin1	chemical reagent	5.339	9.53E-06
	D-glucose	chemical - endogenous mammalian	0.006	1.18E-05
	MEL S3	chemical - kinase inhibitor	0.632	2.47E-05
	miR-127 prodrug	chemical reagent	2.234	3.96E-05
	MEL T1	chemical - kinase inhibitor	-0.378	7.27E-05
Cluster 4	dexamethasone	chemical drug	2.675	1.30E-19
	chloropromazine	chemical drug	2.207	3.00E-18
	(-)-norephedrine	chemical drug	3.317	3.15E-17
	lysophosphatidylcholine	chemical - other	3.873	2.52E-15
	beta-estradiol	chemical - endogenous mammalian	3.597	1.19E-13
	elaidic acid	chemical - endogenous mammalian	4.084	2.33E-13
	isoquercitrin	chemical drug	2.985	4.22E-13
	25-hydroxycholesterol	chemical reagent	-1.444	4.82E-11
	pitavastatin	chemical drug	2.937	6.13E-11
	atorvastatin	chemical drug	2.456	3.97E-10
	ezetimibe	chemical drug	2.81	1.47E-09
	rosuvastatin	chemical drug	2.345	1.84E-09
	dihydrotestosterone	chemical - endogenous mammalian	2.503	2.52E-09
	lithium chloride	chemical drug	2.557	2.86E-09
	PD98059	chemical - kinase inhibitor	-3.495	3.64E-09
	3-deoxy-2-octulosonic acid(2)-lipid A	chemical - endogenous non-mammalian	-0.378	5.79E-09
	Gm35986	other	-2.216	7.50E-09

	TO-901317	chemical reagent	1.295	3.87E-09
	sterol	chemical - endogenous mammalian	-2.587	1.31E-08
	bucladesine	chemical toxicant	4.579	1.33E-08

Activation z-scores were not generated for most of the upstream regulators in Cluster 3. These could be due to the fact that these genes are expressed throughout gestation and are not differentially expressed.

S12 Table. Chemical upstream regulators (including endogenous molecules) associated with the weak clusters (clusters 2 and 3).

Cluster 2	**Upstream Regulator**	**Molecule Type**	**Activation z-score**	**p-value of overlap**
	beta-estradiol	chemical - endogenous mammalian	6.994	2.34E-13
	dexamethasone	chemical drug	4.76	4.53E-13
	8-bromo-cAMP	chemical reagent	7.755	1.33E-12
	thioacetamide	chemical toxicant	4.372	1.54E-11
	medroxyprogesterone acetate	chemical drug	7.159	1.05E-10
	trans-hydroxytamoxifen	chemical drug	-2.135	5.21E-10
	halofuginone	chemical drug	-2.216	7.47E-10
	triptolide	chemical drug	-5.053	1.08E-09
	lipopolysaccharide	chemical drug	6.225	1.47E-09
	D-glucose	chemical - endogenous mammalian	5.076	7.70E-09
	trichostatin A	chemical drug	1.985	1.41E-08
	estrogen	chemical drug	2.554	1.23E-07
	2-amino-5-phosphonovaleric acid	chemical - other	-0.482	2.60E-07
	branched chain amino acids	chemical drug	-3	2.88E-07
	prednisolone	chemical drug	-1.147	7.09E-07
	thapsigargin	chemical toxicant	2.22	9.11E-07
	ramipril	chemical drug	-1.943	1.46E-06
	dihydrotestosterone	chemical - endogenous mammalian	3.025	1.60E-06
	aspirin	chemical drug	-4.891	1.78E-06
	levodopa	chemical - endogenous mammalian	0.472	1.83E-06
	MM-589	chemical reagent	-1.69	2.47E-06
	PTC-209	chemical reagent	-1.69	2.47E-06
Cluster 3	AMP	chemical - endogenous mammalian		3.22E-03
	sulpiride	chemical drug		7.81E-03
	Congo Red	chemical toxicant		7.81E-03
	2-(3-hydroxypropoxy)calcitriol	chemical drug		1.41E-02
	tetrodotoxin	chemical drug		1.67E-02
	6-amino-4-(4-phenoxyphenylethylamino)quinazoline	chemical reagent		1.79E-02
	ziprasidone	chemical drug		1.79E-02
	tolbutamide	chemical drug		2.20E-02

	CGP 42112	chemical reagent		2.20E-02
	formononetin	chemical - endogenous non-mammalian		2.20E-02
	5'-adenylyl (beta,gamma-methylene)diphosphonate	chemical reagent		2.36E-02
	pregnanolone	chemical - endogenous mammalian		2.36E-02
	taurolithocholate-3-sulfate	chemical - endogenous mammalian		2.36E-02
	soraphen-A1alpha	chemical - endogenous non-mammalian		2.36E-02
	A-443654	chemical reagent		2.36E-02
	tiapride	chemical drug		2.36E-02
	ATP-gamma-S	chemical reagent		2.08E-02
	CORT-108297	chemical reagent		2.36E-02
	betel quid extract	chemical reagent		2.36E-02
	RECTAS	chemical reagent		2.36E-02

Activation z-scores were not generated for most of the upstream regulators in Cluster 3. These could be due to the fact that these genes are expressed throughout gestation and are not differentially expressed.

Chapter 3

Candidate Genes for Polycystic Ovary Syndrome are Regulated by TGFβ in the Bovine Foetal Ovary

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Title of Paper	Candidate genes for polycystic ovary syndrome are regulated by TGFβ in the fetal ovary		
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Principal Author

Name of Principal Author (Candidate)	Rafiatu Azumah		
Contribution to the Paper	acquired part of the data, conducted the statistical analysis, interpreted the data, drafted the manuscript.		
Overall percentage (%)	50 %		
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.		
Signature		Date	27/11/2022

Co-Author Contributions

By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

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Contribution to the Paper	acquired part of the data, conducted the statistical analysis, interpreted the data, drafted the manuscript.		
Signature		Date	

Name of Co-Author	Katja Hummitzsch		
Contribution to the Paper	initiated the conception and design of the study, acquired the data, interpreted the data, supervised and conducted critical revision of manuscript.		
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human reproduction **ORIGINAL ARTICLE** ***Reproductive biology***

Candidate genes for polycystic ovary syndrome are regulated by TGFβ in the bovine foetal ovary

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STUDY QUESTION: Could changes in transforming growth factor β (TGFβ) signalling during foetal ovary development alter the expression of polycystic ovary syndrome (PCOS) candidate genes leading to a predisposition to PCOS?

SUMMARY ANSWER: TGFβ signalling molecules are dynamically expressed during foetal ovary development and TGFβ1 inhibits expression of the androgen receptor (*AR*) and 7 (*INSR*, *C8H9orf3*, *RAD50*, *ERBB3*, *NEIL2*, *IRF1* and *ZBTB16*) of the 25 PCOS candidate genes in foetal ovarian fibroblasts *in vitro*, whilst increasing expression of the AR cofactor TGFβ induced transcript 1 (*TGFB1I1* or Hic5).

WHAT IS KNOWN ALREADY: The ovarian stroma arises from the mesonephros during foetal ovary development. Changes in the morphology of the ovarian stroma are cardinal features of PCOS. The ovary is more fibrous and has more tunica and cortical and subcortical stroma. It is not known why this is and when this arises. PCOS has a foetal origin and perhaps ovarian stroma development is altered during foetal life to determine the formation of a polycystic ovary later in life. PCOS also has a genetic origin with 19 loci containing 25 PCOS candidate genes. In many adult tissues, TGFβ is known to stimulate fibroblast replication and collagen deposition in stroma, though it has the opposite effect in the non scaring foetal tissues. Our previous studies showed that TGFβ signalling molecules [TGFβs and their receptors, latent TGFβ binding proteins (LTBPs) and fibrillins, which are extracellular matrix proteins that bind LTBPs] are expressed in foetal ovaries. Also, we previously showed that TGFβ1 inhibited expression of *AR* and 3 PCOS candidate genes (*INSR*, *C8H9orf3* and *RAD50*) and stimulated expression of *TGFB1I1* in cultured foetal ovarian fibroblasts.

STUDY DESIGN, SIZE, DURATION: We used *Bos taurus* for this study as we can ethically collect foetal ovaries from across the full 9 month gestational period. Foetal ovaries (62 276 days, n = 19) from across gestation were collected from pregnant *B. taurus* cows for RNA sequencing (RNA seq) analyses. Foetal ovaries from *B. taurus* cows were collected (160 198 days, n = 6) for culture of ovarian fibroblasts.

PARTICIPANTS/MATERIALS, SETTING, METHODS: RNA seq transcriptome profiling was performed on foetal ovaries and the data on genes involved in TGFβ signalling were extracted. Cells were dispersed from foetal ovaries and fibroblasts cultured and treated with TGFβ1. The effects of TGFβ regulation on the remaining eight PCOS candidate genes not previously studied (*ERBB3*, *MAPRE1*, *FDFT1*, *NEIL2*, *ARL14EP*, *PLGRKT*, *IRF1* and *ZBTB16*) were examined.

MAIN RESULTS AND THE ROLE OF CHANCE: Many TGFβ signalling molecules are expressed in the foetal ovary, and for most, their expression levels increased accross gestation (*LTBP1/2/3/4*, *FBN1*, *TGFB2/3*, *TGFBR2/3* and *TGFB1I1*), while a few decreased (*FBN3*, *TGFBR3L*, *TGFBI* and *TGFB1*) and others remained relatively constant (*TGFBRAP1*, *TGFBR1* and *FBN2*). TGFβ1 significantly decreased expression of PCOS candidate genes *ERBB3*, *NEIL2*, *IRF1* and *ZBTB16* in cultured foetal ovarian fibroblasts.

LARGE SCALE DATA: The FASTQ files, normalized data and experimental information have been deposited in the Gene Expression Omnibus (GEO) accessible by accession number GSE178450.

[†]The first two authors contributed equally as first authors.

LIMITATIONS, REASONS FOR CAUTION: Regulation of PCOS candidate genes by TGFβ was carried out *in vitro* and further studies *in vivo* are required. This study was carried out in bovine where foetal ovaries from across all of the 9 month gestational period were available, unlike in the human where it is not ethically possible to obtain ovaries from the second half of gestation.

WIDER IMPLICATIONS OF THE FINDINGS: From our current and previous results we speculate that inhibition of TGFβ signalling in the foetal ovary is likely to (i) increase androgen sensitivity by enhancing expression of *AR*, (ii) increase stromal activity by stimulating expression of *COL1A1* and *COL3A1* and (iii) increase the expression of 7 of the 25 PCOS candidate genes. Thus inhibition of TGFβ signalling could be part of the aetiology of PCOS or at least the aetiology of polycystic ovaries.

STUDY FUNDING/COMPETING INTEREST(S): Funding was received from Adelaide University China Fee Scholarship (M.L.), Australian Research Training Program (R.A.) and the Faculty of Health and Medical Science Divisional Scholarship (R.A.), Adelaide Graduate Research Scholarships (R.A. and N.A.B.), Australia Awards Scholarship (M.D.H.), Robinson Research Institute Career Development Fellowship (K.H.) and Building On Ideas Grant (K.H.), National Health and Medical Research Council of Australia Centre for Research Excellence in the Evaluation, Management and Health Care Needs of Polycystic Ovary Syndrome (N.A.B., M.D.H. and R.J.R.; GTN1078444) and the Centre for Research Excellence on Women's Health in Reproductive life (R.A., R.J.R. and K.H.; GTN1171592) and the UK Medical Research Council (R.A.A.; grant no. G1100357). The funders did not play any role in the study design, data collection and analysis, decision to publish or preparation of the manuscript. The authors of this manuscript have nothing to declare and no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

Key words: PCOS / stroma TGFβ signalling molecules / ovary development / PCOS candidate genes / regulation / extracellular matrix / RNA seq / gene expression

Introduction

Polycystic ovary syndrome (PCOS) is a complex reproductive and metabolic disorder with multiple clinical symptoms including psychological consequences (Teede *et al.*, 2010). The syndrome affects around 1 in 10 women, presenting with symptoms associated with excess androgen, reproductive dysfunction and metabolic complications such as insulin resistance, gestational diabetes, central adiposity, obesity, non-alcoholic fatty liver disease, dyslipidaemia and cerebro- and cardiovascular diseases among others (Norman *et al.*, 2007; March *et al.*, 2010; Azziz *et al.*, 2016; Rodgers *et al.*, 2019; Stepto *et al.*, 2019; Berni *et al.*, 2021).

The aetiology of PCOS is not well established. However, a possible foetal predisposition has been observed in numerous studies over the past decades. For example, babies born with congenital adrenal hyperplasia, which causes elevated androgen exposure in foetal life, develop some of the features of PCOS in adulthood (Barnes *et al.*, 1994). Androgen treatment of pregnant animals also produces a phenotype of PCOS features in the offspring (Abbott *et al.*, 2006; Walters, 2016; Tata *et al.*, 2018; Risal *et al.*, 2019; Aflatounian *et al.*, 2020; Stener-Victorin *et al.*, 2020). More so, a low ponderal index (kg/m^3) of children at birth has also been associated with the risk of all three cardinal PCOS symptoms (menstrual dysfunction, hyperandrogenism and polycystic ovaries) in later life (Davies *et al.*, 2012).

PCOS also has a genetic predisposition with large genome-wide association studies and familial microsatellite linkage studies having identified a number of loci associated with PCOS (Legro *et al.*, 1998; Urbanek, 2007; Chen *et al.*, 2011; Goodarzi *et al.*, 2012; Shi *et al.*, 2012; Kosova and Urbanek, 2013; Louwers *et al.*, 2013). There are about 25 genes in or near these loci. We recently identified that PCOS candidate genes in these loci were not differentially expressed in adult human PCOS ovaries (Liu *et al.*, 2020) but were dynamically expressed in developing human and bovine foetal ovaries (Hartanti *et al.*, 2020; Liu *et al.*, 2020). We concluded that expression of PCOS candidate genes in foetal ovaries if perturbed or dysregulated may underpin development of PCOS (Hartanti *et al.*, 2020; Liu *et al.*, 2020).

There are some other unique features of PCOS. PCOS ovaries not only have many antral follicles but they have an expanded and very fibrous stroma (Stein and Leventhal, 1935; Hughesdon, 1982). During foetal development, the ovarian stroma is initially derived from stroma that penetrates into the ovarian primordium from the mesonephros during the first trimester (Hummitzsch *et al.*, 2013, 2015, 2018). It expands the most during early gestation due to high levels of stromal cell replication (Hartanti *et al.*, 2019; Hummitzsch *et al.*, 2019). The causes or consequences of expanded fibrous stroma in PCOS ovaries are still unknown. It is possible that either the stroma is altered in a peculiar way during development of the ovary to enable it to expand and become fibrous in later life or that the adult PCOS ovaries have just became fibrotic due to fibrosis. Fibrosis is usually a wound healing event where death of specialized cells occurs and replaced by stroma and collagen.

Growth of stroma in many organs is usually driven by the growth factor transforming growth factor β (TGFβ) (Hatzirodos *et al.*, 2011). In adult tissues TGFβ stimulates replication and production and deposition of collagen in stroma, particularly in fibrotic tissues (Verrecchia and Mauviel, 2004). In stroma, TGFβ activity is regulated by the extracellular matrix fibrillins (Kielty *et al.*, 2002). Fibrillins achieve this by binding the latent TGFβ binding proteins (LTBPs). There are three fibrillin genes, four LTBPs, three TGFβs and three TGFβ receptors. We previously found that TGFβ signalling molecules (TGFβs, LTBPs, fibrillins and TGFβ receptors) are expressed in foetal ovaries (Hatzirodos *et al.*, 2011, 2019). Their levels of expression were either constant (*TGFB1*, *TGFBR1*), increasing (*TGFB2*, *TGFB3*, *TGFBR2*, *TGFBR3*, *LTBP1*, *LTBP2*, *LTBP3*, *LTBP4*) or decreasing (*FBN2*, *FBN3*) across gestation (Hatzirodos *et al.*, 2011, 2019). We also showed that TGFβ inhibited expression of androgen receptor (*AR*) and 3 PCOS candidate genes (*INSR*, *C8H9orf3* and *RAD50*) and stimulated expression of *TGFBI11* (transforming growth factor beta 1 induced transcript 1) in cultured foetal ovarian stroma cells (Hartanti *et al.*, 2020). This suggests that TGFβ signalling is dynamic during foetal ovarian development and could be an important part of the aetiology of PCOS, providing a link between the genetic basis and foetal predisposition to PCOS.

Circulating levels of TGFβ2 were found to be correlated with androgen levels in women (Raja Khan *et al.*, 2014) and skeletal muscles in adult women with PCOS have higher expression levels of genes controlled by TGFβ and they produce more collagens (Stepto *et al.*, 2020). In adipose tissue of PCOS women, TGFβ1 was identified as the master upstream regulator (Dumesic *et al.*, 2019). In order to further our knowledge of TGFβ and foetal ovary development, we examined the regulation of eight additional PCOS candidate genes and the expression of TGFβ signalling molecules during foetal ovary development using RNA sequencing (RNA seq) analysis.

Materials and methods

Ethical approval for the study

Ethical approval was not required for this study, as foetuses and foetal ovaries were scavenged from animals being processed for human consumption and were not owned by the authors or their institutions. As such the University of Adelaide's Animal Ethics Committee only requires notification of this.

Collection of bovine foetal ovaries

For RNA seq, foetal ovarian pairs across gestation (62 276 days, n = 19) were collected from pregnant *Bos taurus* cows at the abattoir of Midfield Meat International, Warrnambool, Victoria, Australia and were immediately frozen on dry ice on site and later stored in the laboratory at 80°C.

For TGFβ1 treatment, foetuses from pregnant *B. taurus* cows were collected at local abattoirs (Thomas Foods International, Murray Bridge, SA, Australia and Strath Meats, Strathalbyn, SA, Australia) and transported on ice in Hank's balanced salt solution (HBSS) with calcium and magnesium (HBSS$^{+/+}$) to the laboratory. The gestational ages of all foetuses were estimated from the crown rump length (CRL) (Russe, 1983). Foetuses with a CRL <8 cm underwent sex determination as previously reported by Hummitzsch *et al.* (2013).

RNA extraction and RNA-seq

Using the Mo Bio Powerlyser 24 (Mo Bio Laboratories Inc., Carlsbad, CA, USA) and 1 ml Trizol® (Thermo Fisher Scientific, Waltham, MA, USA), whole foetal bovine ovaries were homogenized and RNA extracted according to manufacturer's instructions. DNase I (Promega/Thermo Fisher Scientific Australia Pty Ltd, Tullamarine, VIC, Australia) was used to treat all samples. The RNA concentration and quality were then determined using the Experion™ RNA StdSens Analysis kit and the Experion™ Automated Electrophoresis System (Bio Rad Laboratories Pty., Ltd., Gladesville, NSW, Australia). Of total RNA, 500 ng/50 µl per well (96 well plate) of each sample was used for RNA seq.

RNA seq based transcriptome profiling was performed at the SAHMRI Genomics Facility (SAHMRI, Adelaide, SA, Australia). Briefly, single end poly A selection mRNA libraries (∼35 M reads per sample) were created using the Nugen Universal Plus mRNA Seq library kit from Tecan (Mannedorf, Switzerland) and sequenced with an Illumina Nextseq 500 using single read 75 bp (v2.0) sequencing chemistry (Illumina Inc., San Diego, CA, USA). Two sequencing runs, with 10 samples per run, were performed and a sample (15/R43t, 135 days gestational age) was used as internal control in both runs.

RNA-seq data analysis using Partek flow

The raw data containing FASTQ files were uploaded to Partek Flow® Software, version 8.0 (Partek Incorporated, St. Louis, MO, USA). All samples underwent a pre alignment quality assessment and showed Phred Quality Scores larger than 30. The reads were aligned and annotated to the bovine genome ARS UCD1.2 (bosTau9; https://www.ncbi.nlm nih.gov/assembly/GCF 002263795.1/) using STAR 2.7.3a aligner (>97% alignment rate for all samples) and Partek E/M, respectively. The FASTQ files, normalised data and experimental information have been deposited in the Gene Expression Omnibus (GEO) (Barrett *et al.*, 2009), accessible by accession number GSE178450. The expression of TGFβs, LTBPs, fibrillins and TGFβ receptors were analysed using Partek Flow® Software (version 8.0). Scatter plots showing the expression patterns for fibrillins, LTBPs, TGFβs and TGFβ receptors across gestation were generated using GraphPad Prism version 8 (GraphPad Software Inc., La Jolla, CA, USA). Pearson's correlation of the genes with gestational age as well as with each other were further analysed.

Treatment of bovine foetal fibroblasts with TGFβ1

Foetal fibroblasts (160 198 days, n = 6) were cultured and treated with 5 ng/ml or 20 ng/ml TGFβ1 (R&D Systems) as previously described by Bastian *et al.* (2016). Briefly, bovine foetal fibroblasts were seeded at 30 000 cells/well in 24 well plates in DMEM/F12 medium containing 5% (v/v) foetal calf serum, 100 IU/ml penicillin, 0.01% streptomycin sulfate (GIBCO, Carlsbad, CA, USA, 15140122) and 0.1% fungizone at 38.5°C and 5% CO$_2$. At 60 70% confluency, cells were treated with 5 ng/ml or 20 ng/ml of TGFβ1 for 18 h in DMEM/F12 medium containing 1% foetal calf serum and then harvested and stored at 80°C for analysis.

RNA isolation, cDNA synthesis and quantitative real-time PCR

Bovine foetal fibroblasts were homogenized in 1 ml Trizol® (Thermo Fisher Scientific, Waltham, MA, USA) using the Mo Bio Powerlyser 24 (Mo Bio Laboratories Inc., Carlsbad, CA, USA) and RNA extracted according to manufacturer's instructions as reported previously (Bastian *et al.*, 2016). Complementary DNA was then synthesized from 200 ng of DNase treated RNA using random hexamers (Sigma, Adelaide, SA, Australia) and 200 U Superscript Reverse Transcriptase III (Thermo Fisher Scientific, Waltham, MA, USA) as previously described (Hartanti *et al.*, 2020). Based on available RNA sequences in NCBI, PCR primers for eight newly discovered PCOS candidate genes (*ERBB3*, *MAPRE1*, *FDFT1*, *NEIL2*, *ARL14EP*, *PLGRKT*, *IRF1* and *ZBTB16*) were designed to span introns using Primer3 plus and Net primer software (PREMIER Biosoft Palo Alto, CA, USA) and primers are listed in Table I. Primer combinations were tested as previously described (Hummitzsch *et al.*, 2013; Liu *et al.*, 2020). The amplification conditions were 95°C for 15 s, then 60°C for 60 s for 40 cycles using Rotor

Table I List of genes and primers used for qRT-PCR.

Gene name	Gene symbol	Primers (5′→3′) (F = forward, R = reverse)	Accession number	Size (bp)
Ribosomal protein L32	*RPL32*	F: GCCATCAGAATCACCAATCC R: AAATGTGCACACGAGCTGTC	NM 001034783.2	73
Peptidylprolyl isomerase A (cyclophilin A)	*PPIA*	F: CTGGCATCTTGTCCATGGCAAA R: CCACAGTCAGCAATGGTGATCTTC	NM 178320.2	202
ADP ribosylation factor like GTPase 14 effector protein	*ARL14EP*	F: ACCTGGTTGGAAGCTTTGTC R: TTCTGCCGGTCTTCAGAATC	NM 001031761.3	78
Erb B2 receptor tyrosine kinase 3	*ERBB3*	F: TGGTCATGGTCAAGTGTTGG R: CATCCTGGTGAACTCATTGG	NM 001103105.1	80
Farnesyl diphosphate farnesyltransferase 1	*FDFT1*	F: CAAGGAAAAGGACCGACAAG R: ACGCGCTTATCCAGAAACTC	NM 001013004.1	144
Interferon regulatory factor 1	*IRF1*	F: AAGGATGCCTGTCTGTTTCG R: CAATATCTGGCAGCGAGTTC	NM 001191261.2	127
Microtubule associated protein RP/EB family member 1	*MAPRE1*	F: AGGCCCATTACAACACACAG R: TTCAGCTGCTTCGTCATCTC	NM 001075334.2	102
Nei like DNA glycosylase 2	*NEIL2*	F: CGAAGAAGGCAAACAAGAGG R: AAGAGAAGCGCCATGTCATC	NM 001013003.1	117
Plasminogen receptor with a C terminal lysine	*PLGRKT*	F: TCCCGACTTCAGTTGGAAAG R: ACCAAGCAATCTGCATAGCC	NM 001034426.2	79
Zinc finger and BTB domain containing 16	*ZBTB16*	F: CACTCAGCGGGTGCCAAAG R: TTCCCACACAGCAGACAGAAG	NM 001037476.2	131

Gene 6000 cycler (Q series, Qiagen GmbH, Hilden, Germany). Ct values were determined using Rotor Gene 6000 software at a threshold of 0.05 normalized fluorescent unit. Gene expression values were determined using $2^{-\Delta Ct}$ method and ribosomal protein L32 (*RPL32*) and peptidylprolyl isomerase A (*PPIA*) were used as housekeeping genes. The fold change of gene expression in foetal fibroblasts treated with the two different concentrations of TGFβ1 were presented as $2^{-\Delta\Delta Ct}$ data with the same housekeeping genes in $2^{-\Delta Ct}$ method.

Statistical analysis

All statistical analyses were carried out using Microsoft Office Excel 365 (Microsoft Redmond, WA, USA) and IBM SPSS Statistics for Windows, version 25 (IBM Corp., Armonk, NY, USA). Scatter plots and columns were made using GraphPad Prism version 8.00 (GraphPad Software Inc., La Jolla, CA, USA). One way ANOVA with Dunnett's *post hoc* tests were conducted to compare the difference between the control and the TGFβ1 treatments of foetal fibroblasts.

Results

Expression of TGFβs, LTBPs, fibrillins, TGFβ receptors other molecules involved in TGFβ signalling

The expression of the TGFβ signalling molecules in foetal ovaries showed dynamic differences across gestation. The expression levels of most TGFβ signalling molecules significantly correlated with gestational age either positively (*LTBP1*, *LTBP2*, *LTBP3*, *LTBP4*, *FBN1*, *TGFB2*, *TGFB3*, *TGFBR2*, *TGFBR3* and *TGFB1I1*) or negatively (*FBN3*, *TGFBR3L*, *TGFBI* and *TGFB1*), while few showed no significant correlation with gestational age (*TGFBRAP1*, *TGFBR1* and *FBN2*). Also, almost all the TGFβ signalling molecules, with the major exception being *TGFBRAP1*, correlated either positively or negatively with each other (Table II), consistent with there being a regulated network.

The expression of all four *LTBP* genes increased across gestation (Fig. 1D G). *LTBP3* and *LTBP4* expression levels plateaued at the second half of gestation or at the start of the third trimester, respectively. *FBN1* expression (Fig. 1A) increased across gestation and *FBN3* decreased significantly across gestation (Fig. 1C). *FBN2* also increased slightly across gestation (Fig. 1B).

Notably, *TGFB1* expression decreased across gestation until about the end of the second trimester and gradually increased during the third semester. The expression patterns of *TGFB2* and *TGFB3* increased across gestation (Fig. 2B and C). Although *TGFB3* expression increased across gestation, the expression levels were variable in the third trimester (Fig. 2C). The levels of *TGFBR1* expression increased gradually until about the end of the second semester and decreased during the third semester. *TGFBR2* and *TGFBR3* expression both increased across gestation without any decline in the third trimester (Fig. 2E and F).

The expression of other molecules involved in TGFB signalling such as *TGFBRAP1* (transforming growth factor beta receptor associated protein 1), *TGFBR3L* (transforming growth factor beta receptor 3 like), *TGFBI* (transforming growth factor beta induced protein or βig H3) and *TGFB1I1* were also studied. While *TGFBR3L* and *TGFBI* expression

Table II **Pearson's correlation coefficients (R) between TGFβ signalling molecules mRNA expression levels and gestational age (62–276 days, n = 19) in bovine foetal ovaries.**

	Mean Age	*FBN3*	*TGFBR3L*	*TGFBI*	*TGFB1*	*TGFBRAP1*	*TGFBR1*	*FBN2*	*TGFB3*	*LTBP4*	*LTBP1*	*LTBP3*	*FBN1*	*LTBP2*	*TGFBR3*	*TGFB2*	*TGFB1I1*	*TGFBR2*
FBN3	-0.90^{d}																	
TGFBR3L	-0.86^{d}	0.87^{d}																
TGFBI	-0.78^{d}	0.82^{d}	0.72^{c}															
TGFB1	-0.66^{b}	0.52^{a}	0.45	0.71^{c}														
TGFBRAP1	0.36	-0.58^{b}	-0.48^{a}	-0.60^{b}	0.01													
TGFBR1	0.41	-0.43	-0.31	-0.52^{a}	-0.80^{d}	-0.04												
FBN2	0.41	-0.38	-0.41	-0.50^{a}	-0.61^{b}	0.12	0.66^{b}											
TGFB3	0.52^{a}	-0.49^{a}	-0.37	-0.51^{a}	-0.57^{a}	-0.05	0.47^{a}	0.08										
LTBP4	0.53^{a}	-0.53^{a}	-0.36	-0.66^{b}	-0.70^{c}	0.13	0.63^{b}	0.38	0.82^{d}									
LTBP1	0.61^{b}	-0.57^{a}	-0.52^{a}	-0.59^{b}	-0.68^{b}	0.05	0.72^{c}	0.61^{b}	0.61^{b}	0.66^{b}								
LTBP3	0.78^{d}	-0.79^{d}	-0.58^{b}	-0.73^{c}	-0.74^{c}	0.28	0.65^{b}	0.37	0.79^{d}	0.87^{d}	0.66^{b}							
FBN1	0.89^{d}	-0.77^{c}	-0.76^{c}	-0.71^{c}	-0.77^{c}	0.17	0.66^{b}	0.70^{c}	0.49^{a}	0.54^{a}	0.82^{d}	0.71^{c}						
LTBP2	0.90^{d}	-0.76^{c}	-0.81^{d}	-0.65^{b}	-0.53^{a}	0.34	0.23	0.54^{a}	0.22	0.26	0.44	0.52^{a}	0.83^{d}					
TGFBR3	0.91^{d}	-0.77^{c}	-0.78^{d}	-0.69^{b}	-0.71^{c}	0.14	0.54^{a}	0.46^{a}	0.69^{b}	0.62^{b}	0.78^{d}	0.77^{c}	0.93^{d}	0.77^{b}				
TGFB2	0.93^{d}	-0.80^{d}	-0.80^{d}	-0.72^{c}	-0.76^{c}	0.2	0.60^{b}	0.63^{b}	0.51^{a}	0.54^{a}	0.74^{c}	0.74^{c}	0.98^{d}	0.86^{d}	0.95^{d}			
TGFB1I1	0.95^{d}	-0.82^{d}	-0.83^{d}	-0.75^{c}	-0.64^{b}	0.34	0.3	0.48^{a}	0.46^{a}	0.52^{a}	0.55^{a}	0.71^{c}	0.84^{d}	0.92^{d}	0.86^{d}	0.90^{d}		
TGFBR2	0.97^{d}	-0.90^{d}	-0.84^{d}	-0.85^{d}	-0.74^{c}	0.41	0.54^{a}	0.50^{a}	0.563^{a}	0.64^{b}	0.65^{b}	0.84^{d}	0.89^{d}	0.85^{d}	0.91^{d}	0.94^{d}	0.92^{d}	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: ^{a}<0.05; ^{b}<0.01; ^{c}<0.001; ^{d}<0.0001.

decreased across gestation (Fig. 3B and C), expression of *TGFB1I1* increased across gestation (Fig. 3D). Expression of *TGFBRAP1* was relatively constant across gestation (Fig 3A).

Regulation of PCOS candidate genes in foetal fibroblast

We also examined the effects of TGFβ1 on the PCOS genes in cultured foetal fibroblasts. Treatment with TGFβ1 had an effect on half of the eight genes (*ERBB3*, *MAPRE1*, *FDFT1*, *NEIL2*, *ARL14EP*, *PLGRKT*, *IRF1* and *ZBTB16*) studied. Significantly, TGFβ1 (20 ng/ml) decreased the expression of *ERBB3* (Fig. 4A), *NEIL2*, *IRF1* and *ZBTB16* (Fig. 4D, G and H), with the latter three also decreased by treatment with 5 ng/ml TGFβ1.

Discussion

In this study, we explored the expression of TGFβ signalling molecules (TGFβs, LTBPs, fibrillins and TGFβ receptors and other associated proteins) in bovine foetal ovaries across gestation using RNA seq analysis. We also analysed the effects of TGFβ1 in regulating expression of PCOS candidate genes in cultured bovine foetal ovarian fibroblasts. Our results indicate that TGFβ signalling pathways operating in the foetal ovary should be considered contenders for involvement in at least some aspects of the aetiology of PCOS, especially the development of polycystic ovaries.

The current theories on the aetiology of PCOS strongly implicate androgens or androgen signalling during foetal development (Abbott *et al.*, 2006; Walters, 2016; Tata *et al.*, 2018; Risal *et al.*, 2019; Aflatounian *et al.*, 2020; Stener Victorin *et al.*, 2020) and in particular androgen signalling in the brain (Cox *et al.*, 2020). The question has remained what would stimulate or initiate enhanced androgen signalling *in vivo*. As far as we are aware, there are no environmental androgens, if anything, many are anti androgens. Recently, it has been suggested that AMH, which is elevated in PCOS women during pregnancy by about 2 fold, could elevate the levels of androgens and hence initiate the PCOS phenotype in their offspring (Tata *et al.*, 2018). However, AMH and androgens do not alter expression of any of the PCOS candidate genes in cultured foetal fibroblasts (Hartanti *et al.*, 2020; Liu *et al.*, unpublished results), but in contrast, TGFβ1 alters the expression of 7 out of 25 PCOS candidate genes as shown previously (Hartanti *et al.*, 2020) and in this study. Importantly, TGFβ also regulates the expression of *AR* and one of its cofactors, *TGFβ1I1* (Hartanti *et al.*, 2020). Members of the TGFβ signalling pathways are operative before and when the AR is expressed in the foetal ovary. The concept that TGFβ is involved in PCOS not only links the foetal and genetic predispositions to PCOS but it specifically links to the ovarian morphology of PCOS (Hatzirodos *et al.*, 2011). In adult tissues in general, TGFβ stimulates stromal fibroblast replication and collagen deposition but in foetal tissues, which do not scar in wound healing, it has the opposite effect (Rolfe *et al.*, 2007; Rolfe and Grobbelaar, 2012). This has also been demonstrated in the foetal ovarian fibroblasts where TGFβ inhibited *COL1A1* and *COL3A1* expression (Liu *et al.*, unpublished results). TGFβ also inhibited expression of *AR*. Thus, we speculate that inhibition of TGFβ signalling in the foetal ovary is likely to increase androgen sensitivity and stromal activity and thus this mechanism could be part of the aetiology of PCOS. It is also possible that such mechanisms act in other organs affected by PCOS such as skeletal muscle where in PCOS women expression levels of genes controlled by TGFβ are elevated, including collagens (Stepto *et al.*, 2020).

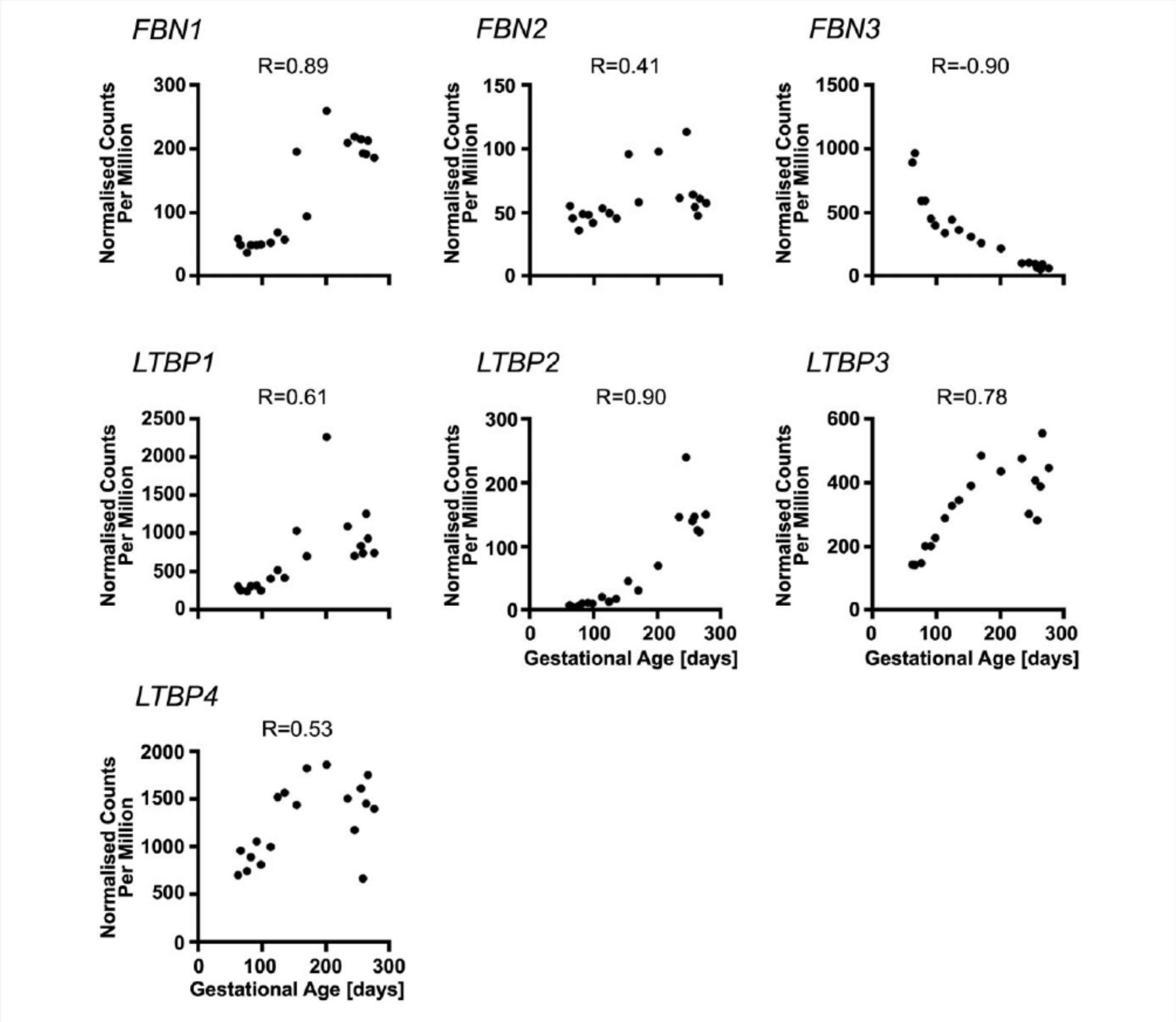

Figure 1. Scatter plots showing the expression patterns of *FBN*s and *LTBP*s across gestation.

In this study, we found that most of TGFβ signalling molecules significantly correlated negatively or positively with gestational age similar to our previous studies of bovine foetal ovaries using qRT PCR (Hatzirodos *et al.*, 2011, 2019; Hartanti *et al.*, 2019). The expression of TGFβ signalling molecules in foetal and adult ovaries have also been studied in various species now including human, goat, sheep, pig and cattle (Chegini and Flanders, 1992; Nilsson *et al.*, 2003; Sriperumbudur *et al.*, 2010; Hatzirodos *et al.*, 2011, 2019; Rodrigues *et al.*, 2014; Hartanti *et al.*, 2019). Stromal growth factors play significant roles in embryonic gonadal development via extracellular matrix contributing significantly to cell growth, differentiation and development (Ingman and Robertson, 2002; Memon *et al.*, 2008). TGFβ signalling molecules are also known to contribute significantly to ovarian function in later life including follicle development (Oliver, 2016), granulosa proliferation (Dodson and Schomberg, 1987), differentiation of thecal interstitial cells (Magoffin *et al.*, 1989) and antral follicle growth and follicle selection (Knight and Glister, 2006), among others.

The relationship between TGFβ and androgen signalling in general is complex as their regulation could be negative or positive depending on the various signals or environmental conditions (Qi *et al.*, 2008). Although TGFβ is positively regulated by androgen in certain cancer cell lines (Rosas *et al.*, 2021), TGFβ is known to inhibit androgen through interaction with Smad3 in different cells including thecal interstitial cells, prostate and prostate epithelial cells (Kyprianou and Isaacs, 1988, 1989; Magoffin *et al.*, 1989; Chipuk *et al.*, 2002). Furthermore, studies focused on TGFβ1 deficiency in reproduction have received significant attention and have been reviewed in detail by Ingman and Robertson (2009). TGFβ1 is a ligand of the TGFβ super family, which is essential in development and cell differentiation (Wu and Hill, 2009; Zinski *et al.*, 2018). In adult bovine ovaries, TGFβ1

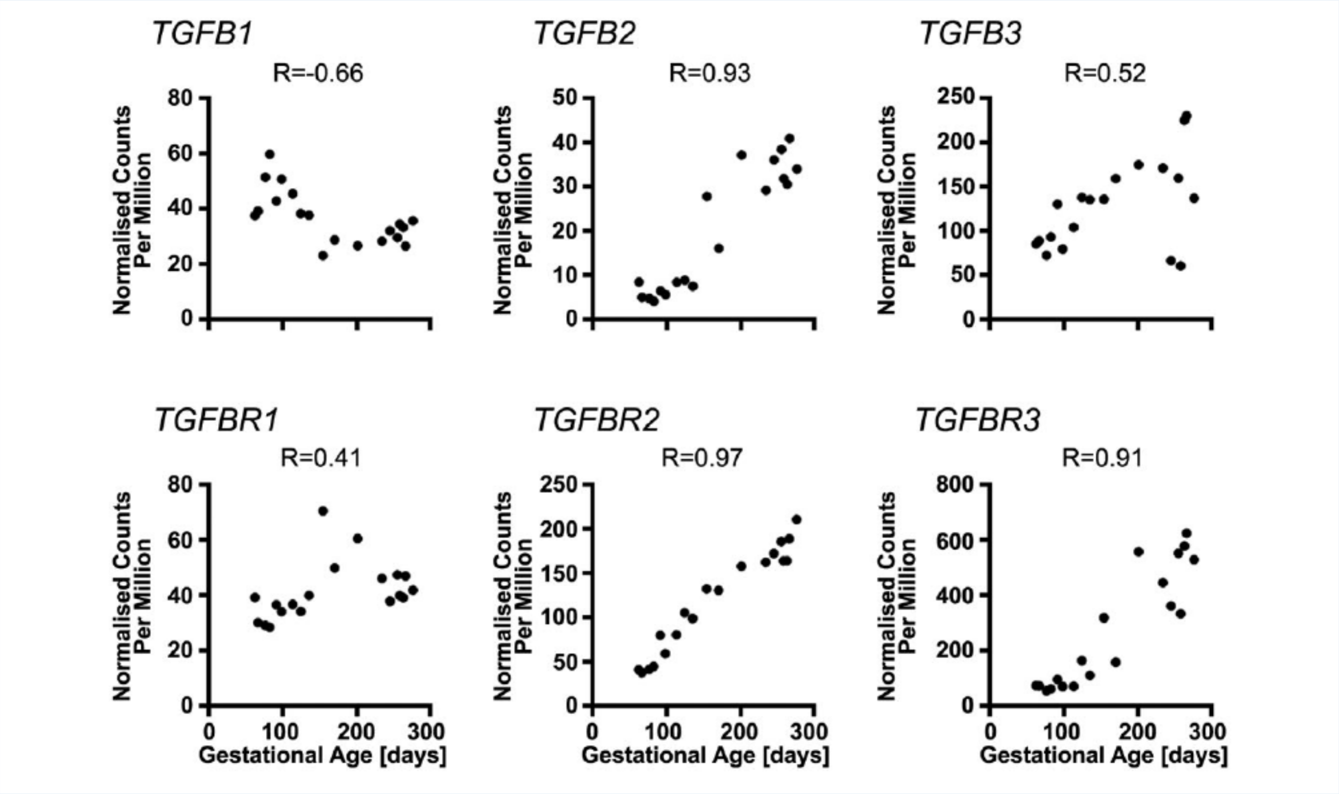

Figure 2. Scatter plots showing the expression patterns of *TGFBs* and *TGFBRs* across gestation.

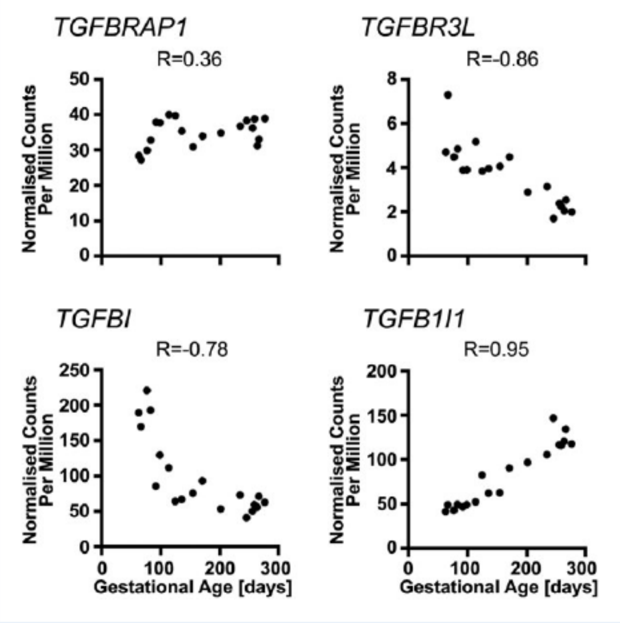

Figure 3. Scatter plots showing the expression patterns of other molecules involved in TGFβ signalling across gestation.

protein was detected in the granulosa cells of early pre antral and early antral follicles (1 2 cm) but was not observed after these stages (Nilsson *et al.*, 2003). *TGFB1* null mice have perturbed hypothalamic pituitary gonadal axis function, which results in reduction in LH levels, further resulting in reduced serum androstenedione and testosterone production in males and oestrous cycle abnormalities in female mice (Ingman *et al.*, 2006; Ingman and Robertson, 2007). Notably, oocyte developmental incompetence due to a TGFβ1 deficient follicular environment has also been associated with the early embryo arrest in these mice (Ingman *et al.*, 2006; Ingman and Robertson, 2009). These observations further affirm the significance of TGFβ1 in ovarian functions and their possible association with PCOS.

Dysregulation of TGFβ signalling during foetal ovary development could involve a number of different members of the pathways and could vary across gestation. *FBN3*, *TGFBR3L*, *TGFBI* and *TGFB1* were highly expressed at the early stages of foetal ovary development and their levels significantly dropped as the ovary developed. It is during the early stages of ovarian development that stroma expansion predominantly occurs (Hartanti *et al.*, 2019). Thus, these genes are mostly expressed when the stroma of the mesonephros, containing fibroblasts, fibres and capillaries, penetrates into the gonadal ridge resulting in the formation of the ovigerous cords containing the gonadal ridge epithelial like (GREL) cells and oogonia. *TGFBR3L* was recently shown to bind inhibin B and null mice were found to have elevated levels of

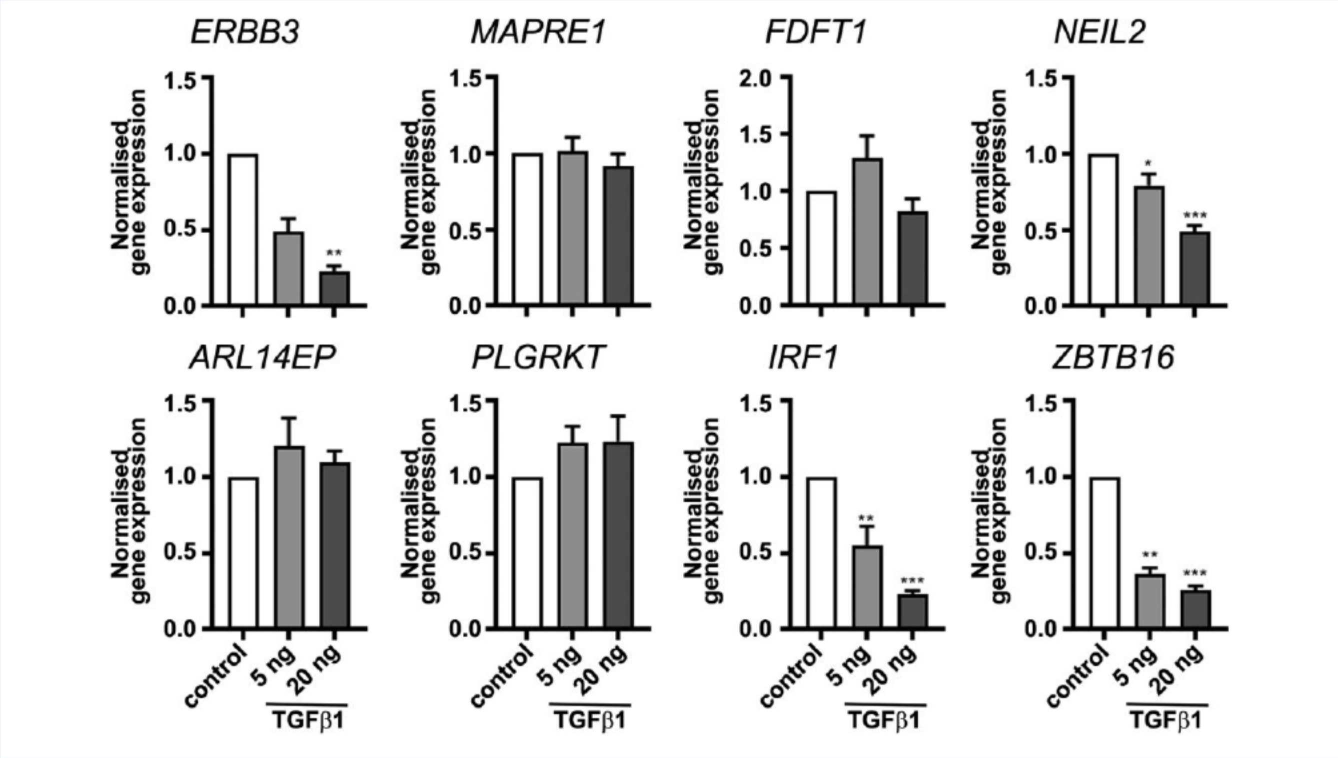

Figure 4. Normalized gene expression of eight newly studied polycystic ovary syndrome (PCOS) candidate genes in cultured foetal fibroblasts treated with transforming growth factor β-1 (TGFβ1). Fibroblasts from foetal ovaries (160 198 days, n 6) were cultured in the presence of 5 or 20 ng/ml of TGFβ1 for 18 h. Fold changes of gene expression to the control groups are presented as mean ± SEM (normalized to *PPIA* and *RPL32*). Significant differences among groups were determined by one way ANOVA with Dunnett's *post hoc* test. $^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$.

FSH, antral follicles and corpora lutea (Brûlé *et al.*, 2021). *TGFBI*, previously named Beta Ig H3 (*βig H3*), has been studied over the past two decades. *TGFBI* is a secreted extracellular matrix protein, expressed in collagen rich tissues in response to TGFβ. *TGFBI* is known to play significant roles in numerous physiological processes such as morphogenesis, extracellular matrix interactions, cell adhesion/migration and angiogenesis required for development; however, its functional contribution is poorly understood (Ferguson *et al.*, 2003; Thapa *et al.*, 2007). *TGFBI* polymorphisms have also been associated with levels of insulin and BMI (Park *et al.*, 2005) and its roles in physiological and pathological conditions including diabetes and tumourigenesis have been reviewed (Ween *et al.*, 2012). Recent studies have also shown that *TGFBI* regulates adipose angiogenesis and stimulates the angiogenic capacity of endothelial cells (Lee *et al.*, 2021).

During the later stages of ovary development, the expression of TGFβ signalling molecules such as *TGFB2*, *TGFB3*, *LTBP1*, *LTBP2*, *LTBP3*, *LTBP4*, *FBN1*, *TGFBR2*, *TGFBR3* and *TGFB1I1* increases. During this stage of ovary development, folliculogenesis and ovarian steroidogenesis occur and stroma beneath the surface epithelial basal lamina develops into the tunica albuginea in human and bovine ovaries (Hummitzsch *et al.*, 2013, 2019; Heeren *et al.*, 2015). Activation of some primordial follicles occurs leading to their development into primary and preantral follicles. LTBPs, whose genes are expressed the most during the third trimester, are well known for their ability to bind to FBN1 and FBN2 to modulate TGFβ availability. They also act as structural components of extracellular matrix (Todorovic *et al.*, 2005). Notably in adult bovine ovaries, TGFβ2 and TGFβ3 levels increase as follicles develop into large antral stage, while TGFβ1 levels decrease during this stage (Nilsson *et al.*, 2003). *TGFB1* and *TGFBR3* were downregulated in cumulus cells isolated from matured metaphase II oocytes of PCOS women (Haouzi *et al.*, 2012). *TGFBR1* and *TGFBR3* expression were dysregulated in ovaries of cows with cystic ovarian disease (Matiller *et al.*, 2019). It is unclear if these dysregulations are of foetal origin given that *TGFBR1* is expressed more in foetal fibroblasts than adult fibroblasts of the ovary (Liu *et al.*, unpublished results).

TGFB1I1, also known as hic 5, is a transcription factor and a co-activator of the AR (Fujimoto *et al.*, 1999). It regulates proliferation and apoptosis via Wnt/β catenin signal pathway (Sha *et al.*, 2020) and suppresses cell migration and invasion by inhibition of the TGFβ pathway and epithelial mesenchymal transition (Ruan *et al.*, 2020). Also, expression of *TGFB1I1* is increased in the presence of TGFβ1 (Hartanti *et al.*, 2020). *TGFB1I1* was also among the TGFβ signalling molecules downregulated in cumulus cells isolated from matured metaphase II oocytes of PCOS women (Haouzi *et al.*, 2012).

In conclusion, we consider the following data support the hypothesis that altered TGFβ signalling could be involved in the foetal predisposition to PCOS or at least in the development of polycystic ovaries: (i) TGFβ is linked to the development of fibrous stroma, which is a hallmark of polycystic ovaries, (ii) in foetal ovarian fibroblasts TGFβ1 can regulate seven genes genetically associated with PCOS, (iii) in foetal ovarian fibroblasts TGFβ1 can alter the expression of *AR* and an AR cofactor and androgen signalling has been shown to be very likely involved in the foetal development of an adult PCOS phenotype, (iv) in foetal ovarian fibroblasts TGFβ1 can regulate expression of *COL1A1* and *COL3A1* thus regulating collagen synthesis and (v) many of the components of TGFβ signalling are dynamically expressed in foetal ovaries across gestation as are the PCOS candidate genes. The implications of these findings for the function of other organ systems associated with PCOS, like the skeletal muscle, should also be explored.

Data availability

The FASTQ files, normalised data and experimental information have been deposited in the Gene Expression Omnibus (GEO) accessible by accession number GSE178450. Data used to create Figs 1 4 can be found at FigShare.

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Authors' roles

R.J.R. and K.H. initiated the conception and design of the study. R.A., M.L., N.A.B., M.D.H. and K.H. acquired the data. R.A. and M.L. conducted the statistical analysis. R.A., M.L., K.H., H.F.I R. and R.J.R. interpreted the data. R.A., M.L. and R.J.R. drafted the manuscript. K.H., H.F.I R., R.A.A. and R.J.R. supervised and conducted critical revision of manuscript. All authors read and approved the final version to be published.

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Conflict of interest

The authors of this manuscript have nothing to declare and no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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Chapter 4

Genes in Loci Genetically associated with Polycystic Ovary Syndrome are Dynamically Expressed in Human Fetal Gonadal, Metabolic and Brain Tissues

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i. the candidate's stated contribution to the publication is accurate (as detailed above);

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Genes in loci genetically associated with polycystic ovary syndrome are dynamically expressed in human fetal gonadal, metabolic and brain tissues

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Background: Polycystic ovary syndrome (PCOS) is a heterogeneous disorder, affecting around 10% of women of reproductive age, with infertility, depression or anxiety, obesity, insulin resistance and type 2 diabetes as risk factors. The cause of PCOS is not known but there is a predisposition to developing PCOS in adult life that arises during fetal or perinatal life. PCOS also has a genetic predisposition and a number of genetic loci associated with PCOS have been identified. These loci contain 25 candidate genes which are currently being studied to define the syndrome. Although the name PCOS suggests a syndrome of the ovary, PCOS has also been associated with the central nervous system and other organ systems in the body due to the wide variety of symptoms it presents.

Methods: Here, we examined the expression patterns of PCOS candidate genes in gonadal (ovary and testis), metabolic (heart, liver and kidney) and brain (brain and cerebellum) tissues during the first half of human fetal development and postnatally until adulthood using public RNA sequencing data. This study is an initial step for more comprehensive and translational studies to define PCOS.

Results: We found that the genes were dynamically expressed in the fetal tissues studied. Some genes were significantly expressed in gonadal tissues, whilst others were expressed in metabolic or brain tissues at different time points prenatally and/or postnatally. *HMGA2*, *FBN3* and *TOX3* were highly expressed during the early stages of fetal development in all tissues but least during adulthood. Interestingly, correlation between expression of *HMGA2/YAP1* and *RAD50/YAP1* were significant in at least 5 of the 7 fetal tissues studied. Notably, *DENND1A*, *THADA*, *MAPRE1*, *RAB5B*, *ARL14EP*, *KRR1*, *NEIL2* and *RAD50* were dynamically expressed in all postnatal tissues studied.

Conclusions: These findings suggest that these genes have tissue- or development-specific roles in multiple organs, possibly resulting in the various symptoms associated with PCOS. Thus the fetal origin of a predisposition to PCOS in adulthood could arise *via* the effects of PCOS candidate genes in the development of multiple organs.

KEYWORDS

fetus, ovary, testis, kidney, liver, heart, brain, PCOS (polycystic ovarian syndrome)

Introduction

Polycystic ovary syndrome (PCOS) is a heterogeneous disorder that affects 10% women of reproductive age of which 72% suffer infertility due to anovulation (1). The disorder has become a public health concern presenting long term complications in women, notwithstanding challenges of diagnosis to clinicians and researchers. The syndrome presents varying symptoms ranging from endocrine features including hyperandrogenism (hirsutism, acne, alopecia); reproductive features including menstrual irregularities and infertility; metabolic features such as insulin resistance, obesity, hyperinsulinemia, type 2 diabetes mellitus; and cardiovascular features including atherogenic dyslipidaemia, a prothrombotic state, elevated blood pressure and increased circulation proinflammatory markers (2 9). The syndrome also affects the psychological health of patients causing anxiety and sleep disturbances as well as sleep disorders (10). Aside from the challenges of delayed diagnosis and lack of treatment options, these symptoms collectively worsen the psychological health of PCOS women.

Some of the metabolic symptoms of PCOS have also been observed in male offspring of PCOS mothers in both human and animal studies (11 16). However, the cause of the syndrome still remains unclear. The genetic and fetal origins of the disorder have become the focus of current studies. Previous studies have shown that PCOS candidate genes including those in loci identified in GWAS and microsatellite genotyping are dynamically expressed in human and bovine fetal ovaries (17 19). Also, these genes are co expressed with genes involved in mitochondrial function, stromal expansion and steroidogenesis during fetal ovary development (18). Even though, it is not clear how these genes further regulate canonical pathways during fetal development leading to PCOS predisposition later in life, numerous theories in the literature have associated these pathways to the aetiology of PCOS. Interestingly, these candidate genes were not differentially expressed in the ovaries of adult women with PCOS when compared with controls (19), further supporting the possible fetal origin of the syndrome.

Although the name PCOS suggests a syndrome of the ovary, the disorder presents symptoms associated with other organs of the body. The majority of PCOS studies have focussed on the role of the ovary in understanding the disorder, however, most of these studies have increased the conundrum surrounding the syndrome. Currently, animal studies, including genetic knock out studies, are focussing on the role of genes in or near loci associated with PCOS; towards delineating the disorder. However, studies delineating the expression patterns of these candidate genes during fetal and adult development in different tissues/organs, other than the ovary, are lacking. Thus, this study seeks to delineate the expression patterns of genes in loci associated with PCOS (17 19) in gonadal, metabolic and brain tissues during fetal development as well as postnatally until adulthood using publicly available human RNA sequencing data. For the purpose of presentation and discussion, the PCOS candidate genes were grouped based on their known basic functions; DNA/RNA regulation/processing (*HMGA2*, *TOX3*, *GATA4*, *YAP1*, *ZBTB16*, *IRF1*, *NEIL2*, *RAD50*, *KRR1*), cellular functions (*RAB5B*, *ARL14EP*, *DENND1A*, *THADA*, *MAPRE1*), enzymatic reactions (*C9orf3/AOPEP*, *SUOX*, *SUMO1P1*), cell surface receptors (*ERBB3*, *ERBB4*, *PLGRKT*), extracellular matrix regulation (*FBN3*), metabolism (*INSR*, *FDFT1*), and reproduction (*FSHB*, *FSHR*, *LHCGR*, *AR*, *AMH*).

Materials and methods

We analysed normalised human RNA sequencing data (counts per million) deposited in Array Express (E MTAB 6814) from the '*Gene expression across mammalian organ development*' project, which sampled seven organs collected from males and females. The prenatal samples in that project were provided by the MRC Wellcome Trust Human Developmental Biology Resource based in the United Kingdom. They were from elective abortions with normal karyotypes. Postnatal samples were provided by the NICHD Brain and Tissue Bank for Developmental Disorders at the University of Maryland, USA, and by the Chinese Brain Bank Center in Wuhan, China. They originated from individuals with diverse causes of death that, given the information available, were not associated with the organ sampled. The patient information provided in this project was gender and age or developmental status (Tables S1 S3). The status regarding any PCOS is unknown but it is possible that some samples are from such women. The organs in this project represent the three germ layers: the ectoderm consisting of brain (forebrain/cerebrum) and cerebellum (hindbrain/cerebellum); the mesoderm of heart, kidney, ovary and testis; and the endoderm of the liver (20). The expression of PCOS candidate genes was studied in all 7 tissues in fetuses 4 20 weeks post conception (wpc) and from birth till adulthood. Fetal ovary samples were available only up to 18 wpc and no postpartum samples were available, while kidney samples were collected only up to 8 years. Postnatally, we grouped the samples as prepubertal (from birth till 9 years), pubertal (13 19 years) and adulthood (each decade until 65 years of age). In testis samples, 13 14 years were considered as early puberty, and 15 19 as late puberty as grouped in the original study (20).

The tissues were grouped according to function; gonads (ovary and testis), metabolic tissues (liver, kidney, and heart), and brain tissues (brain and cerebellum). Expression data of PCOS candidate genes studied previously (17 19) were extracted from normalised data and further analysed. The possible influence of transcriptional and post transcriptional mechanisms such as mRNA stability/ degradation, storage in stress granules, translational control was not the focus of this study. Specifically, time course scatterplots were generated for each gene as grouped for all samples available using ggplot2 package in R (21). Tables S1 3 show the sex and specific time points (gestational age/years postnatally) of samples plotted for each gene. Pearson's correlation was then carried out for each fetal tissue separately using IBM SPSS Statistics for Windows, version 25 (IBM Corp., Armonk, NY, USA). The correlation of each gene with others within each tissue was then compared with that in the other tissues and the output collated based on all significant correlations ($P < 0.01$). No further statistical analysis was conducted as this study, from a basic science perspective, provides an initial set of results for more comprehensive and translational studies.

Results

Expression in fetal tissues

Gene expression in the context of this study refers to the steady state mRNA levels measured. The expression of PCOS candidate genes was studied in 7 fetal tissues (ovary, testis, heart, liver, kidney, brain and cerebellum) from early till mid gestation (4 20 wpc). All genes were dynamically expressed across all tissues, with few exceptions. Although there were fewer female samples than males, there was no difference in gene expression observed between the two sexes in the same tissues, excluding the gonads. We compared gene expression among different tissues and found that some genes were significantly expressed in gonadal tissues, whilst others were expressed in the metabolic or brain tissues at different time points prenatally and/or postnatally.

DNA and RNA regulation/processing genes (*HMGA2*, *TOX3*, *GATA4*, *YAP1*, *ZBTB16*, *IRF1*, *NEIL2*, *RAD50*, *KRR1*) were dynamically expressed across gestation. *HMGA2* was highly expressed at 4 weeks and expression decreased significantly till mid gestation in all tissues (Figure 1). This expression pattern was also observed in *YAP1* (Figure 2) and *ZBTB16* (Figure S1A) in both brain tissues. *IRF1* and *GATA4* were not detected in the brain and cerebellum (Figures S1B, C). Levels of all other genes in this group are very consistently expressed in the two brain tissues during the 20 weeks. The expression of *YAP1* also declined in the liver and ovary, whereas it had a U shaped distribution in the testis and was highly expressed throughout gestation in heart and kidney (Figure 2). Furthermore, *GATA4* expression increased significantly until 13 weeks in gonadal tissues and levels drastically decreased thereafter (Figure S1C). A similar steep increase in expression with a decline after 10 weeks was observed for *TOX3* in the fetal ovary, whereas levels in the testis were always low (Figure S1D). In metabolic tissues, *GATA4* was highly expressed in heart tissues throughout gestation, whereas the expression in the liver was highest at 4 weeks and then declined, however, only low levels of expression were observed in fetal kidneys. *TOX3*, on the other hand, was least expressed in metabolic tissues with a slight increase in expression in kidney tissues towards mid gestation (Figure S1D). *ZBTB16* expression was low and remained relatively constant in most of the fetal tissues (Figure S1A). *IRF1* levels increased slightly as the fetus developed in both gonadal and metabolic tissues (Figure S1B). *NEIL2* was moderately expressed in the metabolic and brain tissues, however, the levels increased slightly after 14 weeks in the brain tissues (Figure S1E). In addition, *NEIL2* expression increased significantly in the gonadal tissues, especially the ovary, as the fetus developed. *RAD50* was expressed highest at 12 weeks in the ovary, but remained relatively constant in all tissues studied

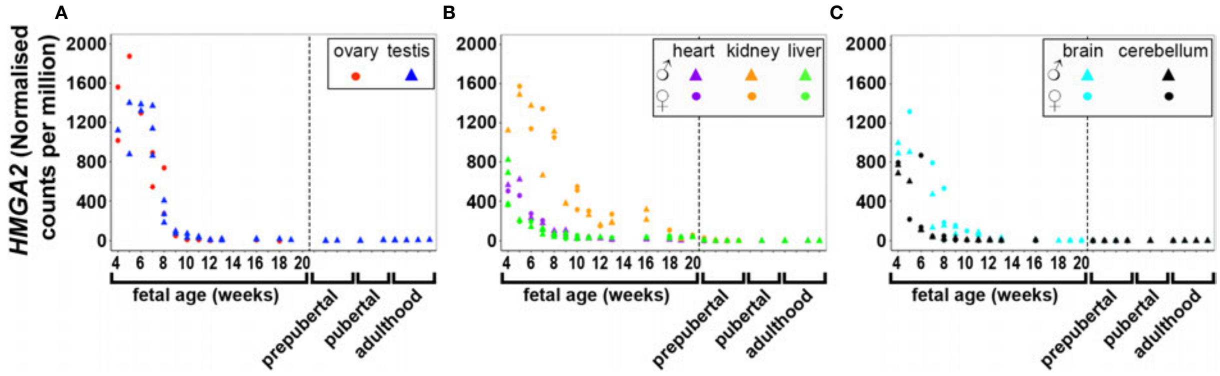

FIGURE 1
Expression of *HMGA2* in gonadal **(A)**, metabolic **(B)** and brain tissues **(C)** during the first half of fetal development and postnatally. Short dashes distinguish fetal samples from postnatal ones.

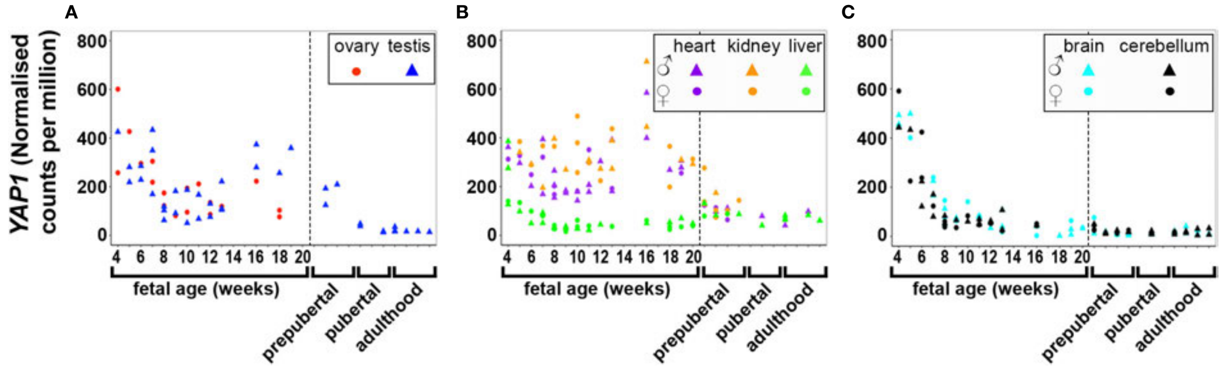

FIGURE 2
Expression of *YAP1* in gonadal **(A)**, metabolic **(B)** and brain tissues **(C)** during the first half of fetal development and during lifetime. Short dashes distinguish fetal samples from postnatal ones.

(Figure 3). *KRR1* was dynamically expressed in all tissues with levels remaining relatively constant throughout the first half of gestation (Figure S1F).

Cell function genes (*RAB5B, ARL14EP, DENND1A, THADA, MAPRE1*), were expressed at relatively constant levels in most tissues with very few exceptions (Figure S2). In brain tissues, expression levels of *THADA* and *MAPRE1* decreased significantly towards 20 weeks. The expression of the genes for the enzymes *C9orf3/AOPEP, SUOX* and *SUMO1P1* was relatively low or absent in most fetal tissues (Figure S3).

Cell surface receptor genes (*ERBB3, ERBB4, PLGRKT*) were dynamically expressed in the tissues studied. *ERBB3* was least expressed in the ovary, heart and brain (brain and cerebellum) tissues, but highly in testis from week 7 up until week 14 before declining. *ERBB3* was also highly expressed in the fetal kidney and liver throughout the 20 weeks (Figure S4A). Although, *ERBB4* was least expressed in the liver and both gonadal tissues, it was highly expressed in the kidney, heart, and both brain tissues during early to mid stage fetal development (Figure S4B). *PLGRKT* was evenly expressed in all fetal tissues throughout the 20 weeks of gestation (Figure S4C). Like *GATA4*, *FBN3* levels increased until 8 weeks and levels decreased thereafter in gonadal, kidney and heart tissues (Figure S5). However, *FBN3* was least expressed in the liver and heart tissues whilst levels remained relatively constant in the brain tissues.

Metabolic genes (*INSR, FDFT1*) were expressed significantly in all tissues during fetal development. *INSR* expression remained relatively constant in all fetal tissues throughout the 20 weeks of gestation (Figure S6A). *FDFT1* was expressed higher in the first weeks of fetal liver development, but decreased significantly thereafter. In the fetal testis, *FDFT1* showed a steep increase in expression between 8 13 weeks before dramatically declining towards 20 weeks. *FDFT1* was least expressed in the kidney and heart during the early stages of fetal development (Figure S6B). Notably, genes involved in reproduction (*FSHB*, *FSHR*, *LHCGR*, *AR*, *AMH*) were not expressed in most of the fetal tissues before mid gestation, as expected. *FSHB* was only detected in three kidney and one cerebellum samples during mid gestation, but not in all other fetal samples throughout the 20 weeks (Figure S7B). *FSHR, LHCGR* and *AMH* levels showed a steep increase after 7 8 weeks gestation in the fetal testis, whereas levels remained relatively low in the fetal ovary (Figures S7B, C, E). An increasing expression of *FSHR* and *AR* were observed in ovary tissues at low levels till mid gestation (Figure S7).

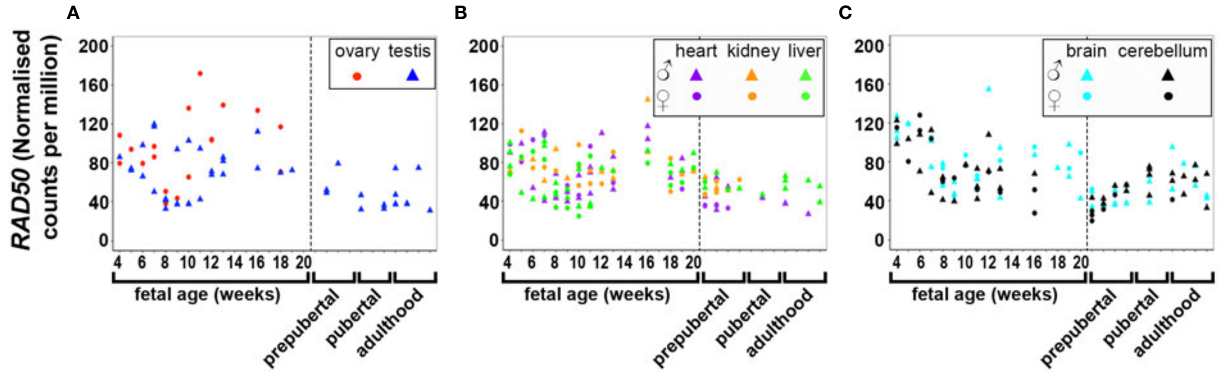

FIGURE 3
Expression of *RAD50* in gonadal **(A)**, metabolic **(B)** and brain tissues **(C)** during the first half of fetal development and during lifetime. Short dashes distinguish fetal samples from postnatal ones.

Relationships of gene expression in fetal tissues

Pearson's correlation of candidate genes with each other as well as with gestational age was carried out for each tissue separately and the outcome of all significant correlations ($P < 0.01$) for all tissues collated into a table for each gene. All PCOS candidate genes showed a significant ($P < 0.01$) correlation with gestational age (days) in at least one tissue studied except for *FSHB, SUOX* and *SUMO1P1* (Table 1). Selected gene expression relationships are reported here, however, detailed data on other genes not mentioned here can be found in supplementary tables (Tables S4 28). Interestingly, the correlation of *HMGA2/YAP1* and *RAD50/YAP1* were significant in at least 5 of the 7 fetal tissues studied.

While *HMGA2* significantly correlated negatively with gestational age in all tissues studied, *IRF1* correlated with gestational age in 5 tissues including gonads and cerebellum but not heart and brain tissues (Table 1). *FBN3* expression correlated negatively with gestational age in testis and all metabolic tissues while *GATA4* correlated negatively with gestational age in all metabolic tissues. *AR* correlated positively with gestational age in the gonads and the liver but negatively in brain tissues. *LHCGR, YAP1, ZBTB16, THADA*, and *MAPRE1* correlated negatively with gestational age in brain tissues but positively with *NEIL2* (Table 1).

Interestingly, RNA/DNA regulation/processing genes correlated with each other and other candidate gene significantly in at least 3 tissues studied. For instance, *HMGA2* expression significantly correlated positively with *FSHR, ERBB3/4, TOX3, YAP1, THADA, MAPRE1*, and *FBN3*, but negatively with *INSR*, and *IRF1* in at least 3 tissues studied (Table 2). *YAP1* expression significantly correlated positively with *FSHR, LHCGR, ERBB4, HMGA2, RAD50, KRR1, ARL14EP, THADA*, and *MAPRE1*, but negatively with *INSR* and *DENND1A* in at least 3 tissues studied (Table 3). *ZBTB16* expression significantly correlated positively with *AR, RAD50, THADA* and *MAPRE1* in at least 3 tissues studied (Table S6). *RAD50* expression significantly correlated with *THADA* in all tissues, with *YAP1, KRR1, MAPRE1* in 6 tissues and with *AR, AMH, ZBTB16, RAB5B, ARL14EP, DENND1A* and *AOPEP* in at least 3 tissues (Table 4). *KRR1* expression significantly correlated positively with *YAP1, ZBTB16, RAD50, THADA* and *MAPRE1* but negatively with *AMH* and *SUOX* in at least 3 tissues (Table S9).

More so, genes involved in cell function (*RAB5B, ARL14EP, DENND1A, THADA*, and *MAPRE1)* significantly correlated with *RAD50* in at least 4 tissues (Tables S10 14). *THADA* and *MAPRE1* significantly correlated positively with each other in 5 tissues and both genes correlated positively with *FDFT1, HMGA2, ZBTB16, KRR1*, and *THADA* in at least 3 tissues. More so, *ERBB3* significantly correlated with *FSHR, LHCGR, HMGA2, NEIL2, THADA*, and *AOPEP* in at least 3 tissues (Table S18). *ERBB4* significantly correlated with *HMGA2, TOX3, YAP1*, and *RAB5B* in at least 3 tissues studied (Table S19).

In testis tissues, *INSR* and *FDFT1* expression significantly correlated with each other positively; both genes also significantly correlated positively with *FSHR, LHCGR, AMH, GATA4*, and *NEIL2*, but negatively with *HMGA2* and *YAP1* (Tables S22, S23). *FSHB* expression did not correlate with other reproductive genes, but correlated significantly with *ZBTB16* and *IRF1* in the kidney (Table S24). *FSHR* significantly correlated positively with other genes including *LHCGR, AR, ERBB3, HMGA2*, and *GATA4* in at least 4 tissues (Table S25). *LHCGR* expression significantly correlated positively with *AMH, INSR, FDFT1, ERBB3, NEIL2*, and *MAPRE1*, but negatively with *HMGA2* and *YAP1* in the testis (Table S26). Detailed correlation relationships on other genes are in Supplementary Tables S4 S28.

Postnatal gene expression

The expression of PCOS candidate genes was studied in 5 tissues (testis, heart, liver, brain, and cerebellum) from birth till adulthood and in kidney samples till 8 years old. No data from postnatal ovary samples were available. We compared the levels of gene expression in the fetal tissues to those in the corresponding postnatal tissues. We found that *RAD50* (Figure 3), *KRR1, NEIL2* (Figure S4), and *DENND1A, THADA, MAPRE1, RAB5B*, and *ARL14EP* (Figure S5) were dynamically expressed in all postnatal tissues studied.

HMGA2 (Figure 1) and *TOX3* (Figure S1D, except for prepubertal kidney), were not expressed in any tissue postnatally. *RAD50, NEIL2*, and *KRR1* (Figure 3 and Figures S1E, F respectively) were expressed in all tissues studied. *YAP1* expression was high in testis, kidney and heart during fetal life, but decreased to very low levels towards adulthood (Figure 2). The expression levels in liver, brain and cerebellum remained low postnatally similar to fetal levels. *ZBTB16* expression levels in the metabolic tissues increased during the prepubertal stage and then slowly declined towards adulthood (Figure S1A), whereas levels in the two brain tissues increased with age. Expression levels in the testis remained relatively constant postnatally at levels similar to those of mid gestation. *IRF1* expression increased dramatically from birth until adulthood in all three metabolic tissues (Figure S1B). *GATA4* was only significantly expressed in the heart tissues and slightly in testis samples after puberty, whereas all other tissues showed low to nil expression (Figure S1C). Even the expression levels in the brain tissues were slightly higher after birth and throughout lifetime. On the other hand, in testis *IRF1* expression was dramatically higher during prepuberty, and then declined again towards adulthood to levels comparable to mid gestation.

All genes involved in cell function (*RAB5B, ARL14EP, DENND1A, THADA, MAPRE1*) were dynamically expressed in all tissues studied (Figure S2). Notably, *RAB5B* levels increased slightly from birth till the end of puberty in the brain tissues where they remained relatively constant thereafter (Figure S2A). *ARL14EP* and *DENND1A* levels remained relatively constant in all tissues postnatally and at similar levels as during fetal life (Figures S2B, C). *THADA* and *MAPRE1* levels decreased slightly after birth in all tissues compared to fetal life (Figures S2D, E).

C9orf3/AOPEP and *SUOX* showed increased expression during prepuberty in testis compared to fetal life (Figure S3). However, this expression declined to very low levels at puberty and in adulthood. In the metabolic tissues, *C9orf3/AOPEP* and *SUOX* expression

TABLE 1 Pearson's correlation coefficients (R) between PCOS candidate genes mRNA expression levels and gestational age across individual tissues.

Genes	Ovary	Testis	Heart	Kidney	Liver	Cerebellum	Brain	
FSHB	-	-	-	0.46^{a}	–	0.35^{a}	–	
FSHR	0.24	0.16	-0.41^{a}	-0.50^{b}	-0.28	-0.30	-0.45^{b}	2-
LHCGR	-0.42	0.20	-0.03	-0.12	-0.46^{b}	-0.37^{a}	-0.61^{c}	2-
AR	0.51^{a}	0.85^{d}	0.16	0.09	0.64^{d}	-0.58^{c}	-0.75^{d}	2+, 2-
AMH	-0.17	0.00	-0.33	-0.56^{b}	-0.25	0.04	-0.34	1-
INSR	-0.14	0.36	0.29	0.31	0.52^{b}	0.20	0.74^{d}	2+
FDFT1	0.20	0.17	-0.26	-0.57^{b}	-0.42^{a}	-0.72^{d}	-0.14	2-
ERBB3	-0.31	0.05	-0.39^{a}	0.52^{b}	-0.04	-0.34	-0.38^{a}	1+
ERBB4	-0.61^{b}	-0.47^{a}	0.12	0.79^{d}	-0.29	0.23	0.29	1+, 1-
PLGRKT	-0.72^{c}	-0.32	0.53^{b}	0.52^{b}	0.14	-0.48^{b}	-0.15	2+, 2-
HMGA2	-0.77^{c}	-0.75^{d}	-0.69^{d}	-0.85^{d}	-0.55^{c}	-0.64^{d}	-0.72^{d}	7-
TOX3	0.34	-0.50^{b}	-0.31	0.68^{d}	-0.51^{b}	-0.60^{c}	-0.07	1+, 3-
GATA4	0.45	-0.15	-0.51^{b}	-0.53^{b}	-0.66^{d}	-0.03	-0.22	3-
YAP1	-0.65^{b}	-0.02	0.21	0.12	-0.47^{b}	-0.72^{d}	-0.74^{d}	4-
ZBTB16	0.43	0.62^{c}	0.43^{a}	0.25	0.15	-0.66^{d}	-0.57^{c}	1+, 2-
IRF1	0.69^{b}	0.84^{d}	0.11	0.67^{c}	0.82^{d}	0.54^{b}	0.04	5+
NEIL2	0.75^{c}	0.31	-0.42^{a}	-0.56^{b}	0.27	0.75^{d}	0.67^{d}	3+, 1-
RAD50	0.31	0.04	0.01	-0.04	0.05	-0.61^{c}	-0.28	1-
KRR1	0.01	0.29	0.34	0.30	0.36^{a}	-0.58^{c}	-0.28	1-
RAB5B	-0.04	0.27	0.33	0.54^{b}	0.32	0.06	0.25	1+
ARL14EP	-0.39	0.30	0.53^{b}	0.32	-0.03	-0.02	0.30	1+
DENND1A	0.33	-0.14	-0.35^{a}	0.01	-0.22	0.66^{d}	0.09	1+
THADA	0.21	-0.12	-0.11	0.01	-0.36^{a}	-0.79^{d}	-0.78^{d}	2-
MAPRE1	0.06	-0.19	-0.41^{a}	-0.61^{c}	0.16	-0.78^{d}	-0.69^{d}	3-
AOPEP	0.02	0.11	0.28	0.57^{b}	-0.20	-0.41^{a}	-0.65^{d}	1+, 1-
SUOX	-0.26	-0.41^{a}	-0.27	0.12	-0.34^{a}	0.16	-0.13	
SUMO1P1	0.09	0.10	-0.18	0.06	0.00	–	0.22	
FBN3	-0.44	-0.73^{d}	-0.77^{d}	-0.73^{d}	-0.46^{b}	-0.17	0.43^{a}	4-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: $^{a} < 0.05$; $^{b} < 0.01$; $^{c} < 0.001$; $^{d} < 0.0001$. Tissues with $P < 0.01$ were regarded as significant. †Number of organs with significant ($P < 0.01$), positive (+) or negative (-) correlations. (-) for no gene expression.

increased significantly after birth (Figures S3A, B). *C9orf3/AOPEP* expression increase slightly in the brain tissues towards adulthood (Figure S3A). *SUMO1P1* expression was undetectable until puberty and then increased dramatically towards adulthood in testis, whereas no expression was detected in any other postnatal tissues (Figure S3C).

Cell surface receptor genes (*ERBB3, ERBB4, PLGRKT*) were dynamically expressed postnatally (Figure S4). *ERBB3* expression levels remained low and constant in the heart, kidney and brain tissues while levels increased with age in the liver and kidney. In the testis, *ERBB3* expression was high during prepuberty, but levels declined significantly at puberty where it remained low during late puberty and adult life (Figure S4A). *ERBB4* expression was least in the liver and testis tissues, but levels remained constant in the brain. Compared to fetal life, *ERBB4* expression decreased during prepuberty in heart and kidney samples but levels remained low and constant thereafter in the heart (Figure S4B). *PLGRKT* was highest expressed in heart tissues postnatally and the expression increased with age. Levels also increased slightly from birth till prepuberty in kidney samples whilst expression remained relatively constant in testis, liver and brain tissues (Figure S4C). Postnatally *FBN3* was not expressed in any tissues (Figure S5).

TABLE 2 Pearson's correlation coefficients (R) between PCOS candidate genes mRNA expression levels and *HMGA2* across individual tissues.

Genes	Ovary	Testis	Heart	Kidney	Liver	Cerebellum	Brain	
FSHB	-	-	-	-0.34	-	-0.09	-	
FSHR	-0.61^b	-0.37	0.67^d	0.64^c	0.82^d	0.59^c	0.45^b	5+, 1-
LHCGR	0.52^a	-0.58^b	0.18	0.13	0.41^a	0.68^d	0.68^d	2+, 1-
AR	-0.31	-0.49^a	-0.03	0.19	-0.050	0.92^d	0.85^d	2+
AMH	-0.16	-0.55^b	-0.12	0.53^b	-0.03	-0.330	-0.044	1+, 1-
INSR	-0.16	-0.71^d	-0.33	-0.22	-0.61^d	-0.42^a	-0.65^d	3-
FDFT1	-0.07	-0.50^b	0.75^d	0.57^b	0.15	0.41^a	-0.176	2+, 1-
ERBB3	0.05	-0.37	0.82^d	-0.68^d	0.10	0.68^d	0.60^c	3+, 1-
ERBB4	0.77^c	0.60^c	0.11	-0.74^d	0.78^d	-0.32	-0.22	3+, 1-
PLGRKT	0.63^b	-0.09	-0.60^c	-0.42^a	-0.22	0.19	-0.10	1+, 1-
HMGA2	*	*	*	*	*	*	*	
TOX3	-0.59^a	0.86^d	0.58^c	-0.54^b	0.62^d	0.11	0.05	3+, 1-
GATA4	-0.82^d	-0.25	0.33	0.70^d	0.94^d	-0.14	-0.08	2+
YAP1	0.86^d	0.53^b	0.20	0.06	0.97^d	0.96^d	0.92^d	5+
ZBTB16	-0.40	-0.26	-0.14	-0.27	0.20	0.86^d	0.76^d	2+
IRF1	-0.62^b	-0.72^d	0.19	-0.71^d	-0.42^b	0.02	0.25	4-
NEIL2	-0.78^c	-0.60^b	0.53^b	0.67^c	-0.17	-0.30	-0.34	2+, 2-
RAD50	-0.20	0.29	0.35^a	0.28	0.39^a	0.67^d	0.53^b	2+
KRR1	-0.12	0.09	-0.05	-0.09	-0.08	0.54^b	0.50^b	2+
RAB5B	0.33	-0.05	0.12	-0.44^a	0.24	0.11	-0.03	
ARL14EP	0.48^a	-0.01	-0.34	-0.11	0.35^a	-0.11	-0.18	
DENND1A	-0.70^b	0.09	0.62^c	-0.05	0.18	-0.38^a	0.01	1+, 1-
THADA	-0.23	0.21	0.53^b	0.02	0.52^b	0.87^d	0.89^d	4+
MAPRE1	-0.10	-0.03	0.54^c	0.61^c	0.26	0.50^b	0.58^c	4+
AOPEP	-0.06	-0.20	-0.59^c	-0.58^b	-0.25	0.67^d	0.85^d	2+, 2-
SUOX	0.12	0.20	-0.04	-0.23	-0.06	-0.01	0.26	
SUMO1P1	-0.45	-0.08	0.35^a	-0.01	-0.13	–	-0.10	
FBN3	-0.02	0.75^d	0.87^d	0.73d	0.95^d	0.26	-0.01	4+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with P < 0.01 were regarded as significant. †Number of organs with significant (P < 0.01), positive (+) or negative (-) correlations. '-' and '*' were for no gene expression and correlation between same gene, respectively.

Metabolic genes (*INSR, FDFT1*) were expressed dynamically from birth throughout lifetime in all tissues (Figure S6). In the testis, *INSR* levels decreased from birth until adulthood, while *FDFT1* levels increased. The expression of both genes remained constant during prepuberty, puberty and adulthood. The levels of *INSR* expression in the liver appeared slightly higher postnatally compared to fetal life, whereas those in kidney and heart were relatively unchanged. Relative to fetal expression, *FDFT1* declined towards puberty/adulthood more in the liver, and only slightly in the brain tissues.

The expression of all reproductive genes (*FSHB, FSHR, LHCGR, AMH* and *AR*) was very low or nil at the postnatal stages for both brain tissues and the three metabolic tissues, except for high *FSHB* expression in prepubertal kidney and high *AR* expression in the liver (Figure S7). *AMH* level was also low or not detected in postnatal testes (Figure S7E). *FSHB* showed an increased expression in the testis during puberty followed by a decline during adulthood, whereas *FSHR* was low prepubertally, then increased expression at puberty and the levels remained high throughout adulthood (Figures S7A, B). Contrary to this,

TABLE 3 Pearson's correlation coefficients (R) between PCOS candidate genes mRNA expression levels and *YAP1* across individual tissues.

Genes	Ovary	Testis	Heart	Kidney	Liver	Cerebellum	Brain	
FSHB	-	-	-	-0.19	-	-0.12	-	
FSHR	-0.45	-0.35	0.41^{a}	0.01	0.85^{d}	0.62^{c}	0.63^{b}	3+
LHCGR	0.71^{c}	-0.57^{b}	0.21	0.05	0.41^{a}	0.69^{d}	0.80^{d}	3+, 1-
AR	-0.15	0.27	0.40^{a}	0.11	0.01	0.94^{d}	0.93^{d}	2+
AMH	-0.39	-0.86^{d}	-0.60^{c}	-0.46^{a}	-0.11	-0.40^{a}	-0.10	2-
INSR	-0.10	-0.58^{b}	0.10	-0.07	-0.50^{b}	-0.39^{a}	-0.68^{b}	3-
FDFT1	0.17	-0.53^{b}	0.36^{a}	-0.05	0.15	0.52^{b}	-0.09	1+, 1-
ERBB3	0.22	-0.44^{a}	0.37^{a}	0.03	0.09	0.65^{d}	0.73^{c}	2+
ERBB4	0.93^{d}	0.67^{c}	0.82^{d}	0.49^{b}	0.83^{d}	-0.25	-0.08	5+
PLGRKT	0.51^{a}	-0.59^{b}	-0.03	0.54^{b}	-0.24	0.25	-0.21	1+, 1-
HMGA2	0.86^{d}	0.53^{b}	0.20	0.06	0.97^{d}	0.96^{d}	0.92^{d}	5+
TOX3	-0.31	0.63^{c}	0.04	0.31	0.67^{d}	0.25	0.16	2+
GATA4	-0.77^{c}	-0.60^{b}	-0.08	-0.04	0.86^{d}	-0.10	-0.05	1+, 2-
YAP1	*	*	*	*	*	*	*	
ZBTB16	-0.10	0.40^{a}	0.22	-0.42^{a}	0.30	0.87^{d}	0.92^{d}	2+
IRF1	-0.56^{a}	-0.16	0.14	-0.42^{a}	-0.36^{a}	-0.05	0.17	
NEIL2	-0.61^{b}	-0.63^{c}	0.13	-0.42^{a}	-0.14	-0.35^{a}	-0.35	2-
RAD50	0.18	0.72^{d}	0.83^{d}	0.90^{d}	0.52^{b}	0.75^{d}	0.58^{c}	6+
KRR1	0.23	0.61^{c}	0.86^{d}	0.91^{d}	0.07	0.65^{d}	0.57^{c}	5+
RAB5B	0.50^{a}	0.40^{a}	0.64^{d}	-0.12	0.36^{a}	0.18	0.06	1+
ARL14EP	0.72^{c}	0.50^{a}	0.56^{c}	0.84^{d}	0.47^{b}	0.00	-0.20	4+
DENND1A	-0.60^{b}	-0.04	0.18	-0.57^{b}	0.18	-0.53^{b}	0.00	3-
THADA	0.13	0.36	0.74^{d}	0.67^{c}	0.53^{c}	0.93^{d}	0.94^{d}	5+
MAPRE1	0.22	-0.06	0.60^{c}	0.47^{a}	0.37^{a}	0.63^{d}	0.62^{c}	3+
AOPEP	-0.26	-0.34	-0.47^{b}	-0.14	-0.32	0.63^{d}	0.91^{d}	2+, 1-
SUOX	-0.04	-0.37	-0.60^{c}	-0.51^{b}	-0.15	-0.08	0.27	2-
SUMO1P1	-0.42	0.05	0.40^{a}	-0.06	-0.14	–	-0.16	
FBN3	-0.20	0.13	-0.02	-0.29	0.92^{d}	0.08	0.02	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with P < 0.01 were regarded as significant. †Number of organs with significant (P < 0.01), positive (+) or negative (-) correlations. '-' and '*' were for no gene expression and correlation between same gene, respectively.

expression of *AR* in the testis had been increased towards mid gestation, remained high during prepuberty, but then declined during puberty and adulthood (Figure S7D). *LHCGR* expression levels were slightly higher in some pubertal and adult testis samples than in others, but generally low (Figure S7C).

Discussion

In this study, we analysed the expression patterns of genes in loci associated with PCOS (candidate genes) from 4 20 weeks of gestation as an index of their potential roles in the development of PCOS at different stages of postnatal human life in gonadal, metabolic and brain tissues. We found that candidate genes such as *HMGA2, TOX3* and *FBN3* were mainly expressed in fetal tissues, while *DENND1A, THADA, MAPRE1, RAB5B, ARL14EP, KRR1, NEIL2*, and *RAD50* were dynamically expressed in all postnatal tissues studied. Notably, the expression patterns of PCOS candidate genes observed in the human ovary were consistent to our previous findings in bovine ovaries at the same timeframe (17 19). However, due to the limitation of obtaining human fetal tissues after mid gestation, it was not prudent to cluster or group the PCOS candidate genes into expressed early, late or throughout gestation as previously done for bovine fetal ovaries (17 19). We therefore

TABLE 4 Pearson's correlation coefficients (R) between PCOS candidate genes mRNA expression levels and *RAD50* across individual tissues.

Genes	Ovary	Testis	Heart	Kidney	Liver	Cerebellum	Brain	
FSHB	-	–	–	-0.19	–	-0.16	–	
FSHR	0.10	0.21	0.57^{c}	0.31	0.32	0.41^{a}	0.38^{a}	1+
LHCGR	0.05	0.00	0.29	0.20	0.04	0.39^{a}	0.37^{a}	
AR	0.59^{b}	0.21	0.42^{a}	0.35	0.27	0.69^{d}	0.51^{b}	3+
AMH	-0.67^{b}	-0.56^{b}	-0.64^{d}	-0.33	-0.55^{c}	-0.6^{c}	-0.44^{a}	5-
INSR	-0.06	-0.10	0.01	0.00	-0.14	0.17	0.09	
FDFT1	0.42	0.03	0.47^{b}	0.05	0.21	0.36^{a}	-0.13	1+
ERBB3	0.32	-0.01	0.50^{b}	-0.21	0.12	0.40^{a}	0.42^{a}	1+
ERBB4	0.11	0.53^{b}	0.66^{d}	0.30	0.31	0.25	0.02	2+
PLGRKT	-0.39	-0.50^{b}	-0.17	0.31	-0.08	-0.02	-0.43^{a}	1-
HMGA2	-0.20	0.29	0.35^{a}	0.28	0.40^{a}	0.67^{d}	0.53^{b}	2+
TOX3	0.55^{a}	0.53^{b}	0.21	0.16	0.37^{a}	0.50^{b}	0.21	2+
GATA4	0.03	-0.09	0.01	0.24	0.30	0.11	-0.18	
YAP1	0.18	0.72^{d}	0.83^{d}	0.90^{d}	0.52^{b}	0.75^{d}	0.58^{c}	6+
ZBTB16	0.71^{c}	0.09	0.31	-0.42^{a}	0.70^{d}	0.69^{d}	0.56^{c}	4+
IRF1	0.41	0.14	0.17	-0.51^{b}	-0.02	-0.14	-0.04	1-
NEIL2	0.48^{a}	-0.23	0.18	-0.18	0.01	-0.50^{b}	-0.29	
RAD50	*	*	*	*	*	*	*	
KRR1	0.52^{a}	0.63^{c}	0.71^{d}	0.85^{d}	0.44^{b}	0.90^{d}	0.70^{d}	6+
RAB5B	0.59^{a}	0.77^{d}	0.80^{d}	-0.22	0.86^{d}	0.54^{b}	0.49^{b}	5+
ARL14EP	0.36	0.53^{b}	0.30	0.83^{d}	0.37^{a}	0.47^{b}	0.41^{a}	3+
DENND1A	0.03	0.11	0.44^{b}	-0.62^{c}	0.44^{b}	-0.45^{b}	0.03	2+, 2-
THADA	0.83^{d}	0.60^{b}	0.90^{d}	0.56^{b}	0.64^{d}	0.82^{d}	0.65^{d}	7+
MAPRE1	0.78^{c}	0.51^{b}	0.69^{d}	0.48^{a}	0.75^{d}	0.65^{d}	0.52^{b}	6+
AOPEP	-0.58^{a}	-0.59^{b}	-0.63^{d}	-0.41^{a}	-0.80^{d}	0.38^{a}	0.45^{b}	2+, 2-
SUOX	-0.12	-0.40^{a}	-0.58^{c}	-0.54^{b}	-0.29	-0.37^{a}	-0.13	2-
SUMO1P1	-0.18	0.15	0.33	0.05	-0.08	–	-0.24	
FBN3	-0.62^{b}	-0.10	0.14	-0.17	0.33^{a}	-0.16	0.20	1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with P < 0.01 were regarded as significant. †Number of organs with significant (P < 0.01), positive (+) or negative (-) correlations. '-' and '*' were for no gene expression and correlation between same gene, respectively.

grouped these genes based on their functionality, while we focussed on the differences and similarities in each group. Although, postnatal ovary samples were not available and postnatal kidney samples were only available up to 8 years of age, the findings of this study infer that other fetal tissues, in addition to the ovary, could also be involved in the manifestation of the syndrome in adulthood.

It is important to recognise that GWAS findings only account for a small fraction of the estimated heritability of PCOS and do not identify specific genes but rather loci related to the syndrome (22). Genes within or near these loci could either have a causal or regulatory role in PCOS, which needs to be investigated further (23). This may be addressed by Mendelian randomisation studies and transcriptome wide association studies in the future. Numerous human and animal studies have focussed on defining the possible causal or regulatory roles of these genes. For instance, recent animal studies have associated *THADA* and *RAD50* with ovarian folliculogenesis, steroidogenesis, and female fertility (24 26). However, studies comparing PCOS adult tissues with controls rarely identify PCOS candidate genes to be differentially expressed (19, 27). A study comparing the ovaries of PCOS women with controls showed no significant difference in the expression of these candidate genes except for *RAD50* (19). A meta analysis involving lean (BMI ≤ 23) and obese (BMI ≥ 23) PCOS patients identified *ZBTB16, FSHR, GATA4* and *AR* to be downregulated in cumulus cells of lean PCOS women, while *INSR, THADA, PLGRKT* were downregulated in endometrial tissues of obese women with PCOS (27). These findings not only suggest roles for the different organs other than the ovary in the pathophysiology of PCOS, but could also imply that most of these candidate genes could be dysregulated during early stages of fetal development when some are mostly expressed. Thus, further understanding of the effects of androgens, AMH, TGFβ and other regulatory factors (18) on fetal programming of candidate genes during development is required.

The expression patterns as well as the roles/mechanisms of these candidate genes during normal fetal development and postnatally could be of value in identifying abnormalities that could lead to PCOS in adulthood. Considering the limitation of collecting human fetal samples after mid gestation and also the strong similarities between human and bovine ovaries in morphology and physiology, gestational length and the propensity for singleton pregnancies, implications can be drawn from bovine data. In addition, the expression level of a candidate gene in a particular tissue at birth could inform to some extent the level of expression for this gene during the final days of gestation. For instance, it can be inferred that *HMGA2* levels might be consistently very low during the third trimester in all human tissues as the levels at birth were the same as those at mid gestation, consistent with previous bovine studies (17 19). More so, the correlation between candidate genes within a tissue during fetal development suggests a possible co regulation between these genes, which needs to be further investigated. This has become necessary as some loci identified in GWAS contain up to three candidate genes in/near it, requiring more studies to understand their possible association with the syndrome. For instance, although the possible role of *FDFT1* in PCOS aetiology remains unknown, it is located in GWAS loci 8p32.1 in proximity to *GATA4* and *NEIL2*; it is not clear if all these genes are causal or regulatory in PCOS (28).

Correlation studies provide preliminary knowledge about the relationships between candidate genes, their possible co regulation (either co activation/ inhibition) and affirm that the genes do not necessarily operate in isolation. In this study, correlation of *HMGA2/YAP1* and *YAP1/RAD50* was significant in at least 5 out of the 7 tissues studied. *HMGA2* plays a crucial role in proliferation and differentiation of mesenchymal cells and is also involved in adipogenesis, stem cell development as well as spermatogenesis (29 32). It also increases the proliferation of cancer cells by promoting cell cycle entry and apoptosis inhibition (33). *HMGA2* has been associated with the Hippo YAP pathway as it regulates *YAP1* stability and possibly inhibits its ubiquitination (34). Although these genes have been studied individually in PCOS, the co expression of *HMGA2* and *YAP1* in PCOS has yet to be studied. *HMGA2* has been associated with polycystic ovary morphology (PCOM) phenotype in PCOS patients of Han Chinese ancestry, potentially functioning to promote the proliferation of ovarian granulosa cells *via* the HMGA2/IMP2 pathway, thereby underpinning the increased proliferation of early growing follicles and decreased apoptosis in granulosa cells in PCOS (35 37). *HMGA2* has also been significantly associated with both hyperandrogenism and oligo/amenorrhea in women with PCOS in Saudi Arabia (38). More so, *YAP1* is highly expressed in mammalian oocytes and preimplantation embryos, consistent with our finding in 4 week fetal tissues (39). *YAP1* is a core component of the Hippo signalling pathway, essential for cell proliferation and apoptosis during early developmental events, promoting organ size and tumorigenesis (40 43). The gene is also important for normal ovarian development and function, and is required for proliferation of granulosa cells (44). Furthermore, maternal accumulation of *YAP1* in the oocyte is crucial for zygotic genome activation, which occurs 2 3 days after fertilisation (39). In ovarian granulosa cells in PCOS, a significant decrease in methylation level was observed in the promoter region of *YAP1*, accounting for a significant increase in the mRNA and protein expression levels of YAP1 (45). Treatment of granulosa cells from control women with testosterone, but not luteinizing hormone (LH) or follicle stimulating hormone (FSH) reduced *YAP1* methylation in a dose dependent manner (45); implying regulatory roles of androgens on the gene. Together, these findings and the co regulatory effects of *HMGA2* and *YAP1* identified in this study, require further exploration towards delineating their roles in the pathogenesis of PCOS.

Although the cause of PCOS remains unclear, it is well known that aberration in most hormones involved in folliculogenesis and ovarian steroidogenesis interfere with the feedback mechanisms that regulate both processes. Hormones such as LH, insulin, AMH and androgens are elevated whilst FSH levels are reduced. This, in addition to hyperandrogenism in most women with PCOS, disrupted hypothalamo pituitary function leading to increased LH pulse frequency, increased LH/FSH ratio and a persistently rapid frequency of gonadotropin releasing hormone (GnRH) pulse secretion, suggests an impaired feedback mechanism between gonads and the brain (46). The anomalous levels of these hormones further cause abnormal oocyte maturation and premature luteinisation of granulosa cells leading to premature arrest of activated follicles at the antral stage. This then results in the accumulation of small to medium antral follicles in polycystic ovaries as well as excess androgen production (47). In this study we observed, as expected, that mRNA of reproductive genes (*FSHB*, *FSHR*, *LHCGR*, *AR*, *AMH*) were not detected during the first half of fetal development in the tissues studied except for *LHCGR* and *AMH* in the testis. These genes are usually expressed during the second half of gestation in the ovary and are associated with folliculogenesis and steroidogenesis (17, 18); the lack of *AMH* in the ovary in first half of gestation is consistent with its known function in regulating Mullerian tract regression and the lack of *AMH* and *LHCGR* with the absence of follicles at early stages of ovary development (48).

Furthermore, the increased risk of metabolic disorders such as obesity, chronic hypertension and pre gestational diabetes in pregnant women with PCOS (49) implies that dysregulation of candidate genes in metabolic tissues could certainly play a role in the aetiology of the syndrome. Thus, insulin receptor signalling has also been associated with GnRH dysregulation leading to LH secretion and reproductive dysfunction in obesity (50). Insulin resistance has also been linked with increased androgen levels among PCOS patients. Specifically, both overexpression of insulin receptor (INSR) in the ovaries of non obese PCOS patients and its underexpression in metabolic tissues of obese PCOS patients results in feedback mechanisms for excess ovarian androgen production (22). Moreover, offspring of women with PCOS are more likely to have metabolic and congenital anomalies compared to those from healthy women (49, 51, 52). Notably, brothers/sons of women with PCOS have elevated androgen levels (53), increased total cholesterol and low density lipoproteins levels at puberty (16), decreased insulin sensitivity (independent of obesity) and glucose tolerance (12), among other symptoms. Also, hepatic dysfunctions and risk of liver diseases have been observed in PCOS models in male sheep (11), female sheep (54, 55), and rats (56, 57), together affirming the roles of these organs in the pathophysiology of the syndrome. Although transcriptional and post transcriptional factors were not evaluated, *INSR* and *FDFT1* were dynamically expressed in all tissues examined in this study. However, it is not clear how dysregulation of these and other genes during fetal development are involved in the metabolic symptoms observed in PCOS. Thus, understanding the roles of PCOS candidate genes in these metabolic tissues and their possible dysregulation in PCOS will improve understanding of the pathogenesis of disorder.

Association studies as well as co localisation studies have been carried out on genes in loci genetically associated with PCOS with the hope to map the role of these candidate genes to the phenotypes or symptoms observed in women with PCOS [reviewed in (38, 58 67)]. Specifically, *FSHB* and *FHSR* loci have been associated with gonadotropin levels, while *LHCGR, FSHR, DENND1A, RAB5/SUOX, HMGA2, C9orf3, YAP1, TOX3, RAD50, FBN3*, and *AMH* have been associated with gonadotropin action and ovarian function (61, 62, 64). *THADA, GATA/NEIL2, ERBB4, SUMO1P1, INSR, KRR1* and *RAB5B* have been associated with metabolic function (61, 62, 64, 65). However, most of these studies, including GWAS, were carried out in adult women with confirmed diagnosis, mostly several years after presenting their first symptoms. Considering the increasing evidence on the fetal origin of PCOS, studies monitoring high risk children from birth until adulthood where phenotypes are observed, should be the focus of current studies for delineating this polygenic disorder. This supports the recommendations of the International Guidelines which have emphasised the metabolic nature of PCOS (68).

It is tempting to infer that dysregulation of genes expressed in particular tissues could have relevant functions or mechanisms contributing to the predisposition of the syndrome in these tissues. The metabolic abnormalities observed particularly in male offspring or brothers of women with PCOS also present empirical evidence that PCOS is not only a syndrome of the ovary. Collectively, the role of candidate genes in various tissues, if clearly defined, could inform/guide further studies into delineating the possible mechanisms that are involved in PCOS predisposition in different tissues from conception till adulthood.

Conclusions

Although, Mendelian randomisation studies and transcriptome wide association studies were not included in this study, they may be addressed in future studies. Also, the influence of transcriptional and post transcriptional mechanisms such as mRNA stability/degradation, storage in stress granules, translational control on gene expression should be considered. That notwithstanding, this study further confirms that PCOS is a polygenic syndrome involving multiple organs of the body. This study identified expression of PCOS candidate genes during fetal development of many organs in humans. Thus, the fetal origin of a predisposition to PCOS in adulthood could arise *via* the effects of PCOS candidate genes in the development of multiple organs.

Data availability statement

The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found in the article/Supplementary Material.

Author contributions

RA, KH and RR designed the study. RA performed statistical analysis. RA, KH and RR interpreted the data and contributed to discussion. RA, KH, RAA and RR wrote the manuscript. RR is the guarantor of this work, had full access to all the data in the study, and assumes full responsibility for the integrity of the data and the accuracy of the data analysis. All authors contributed to the article and approved the submitted version.

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Conflict of interest

RAA reports consultancy work for Ferring Merck, IBSA, Roche Diagnostics. The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

Supplementary material

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fendo.2023.1149473/full#supplementary material

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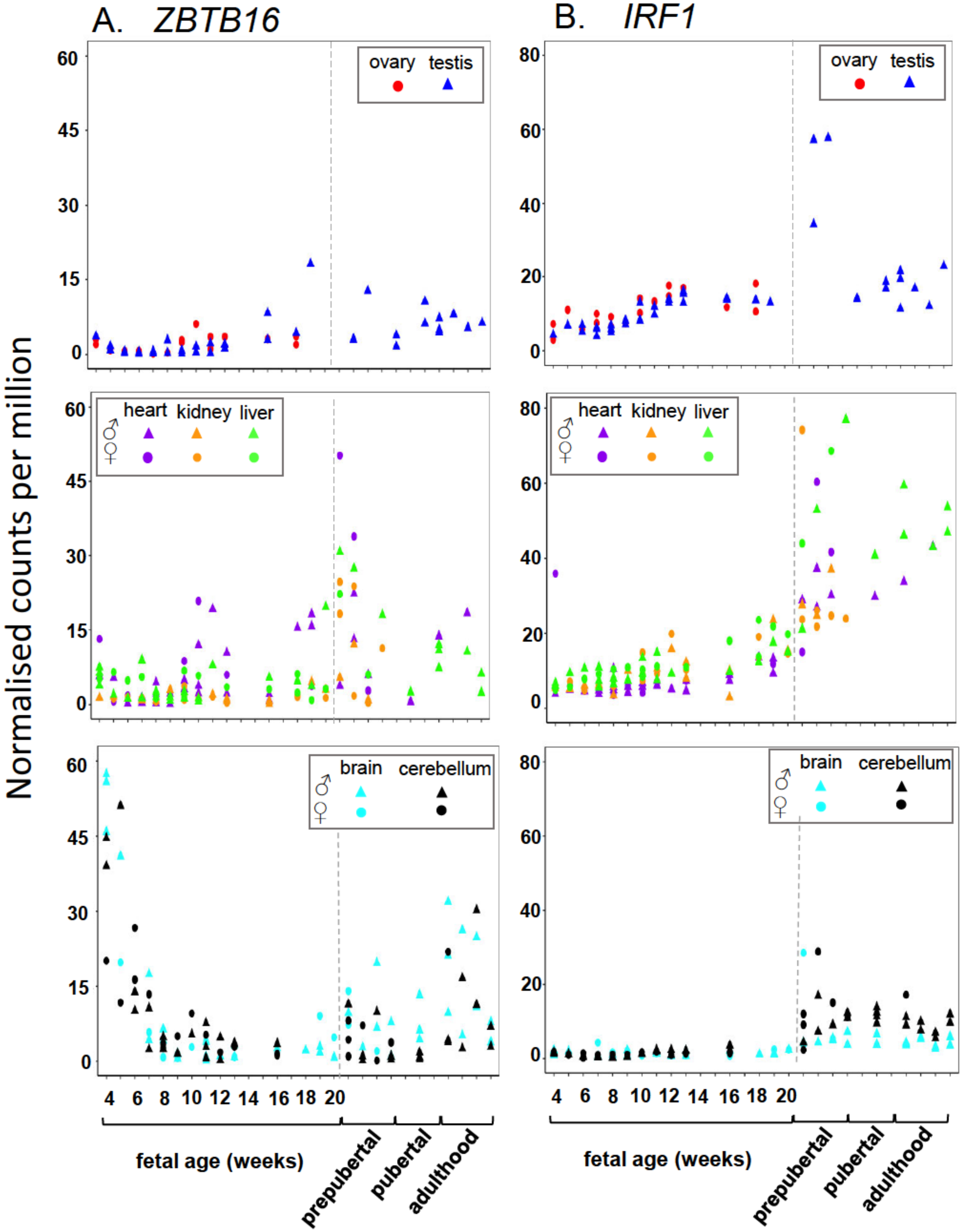
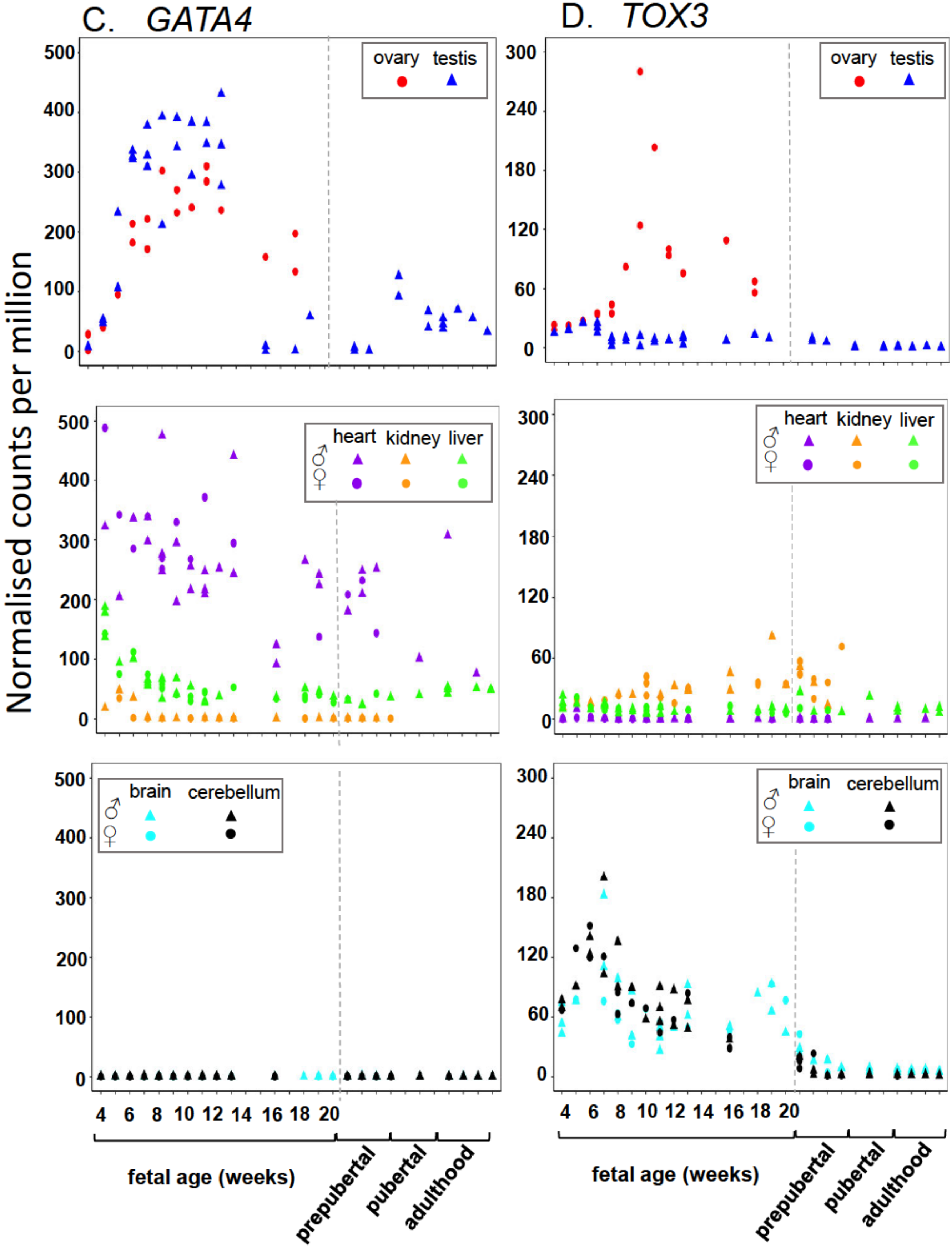
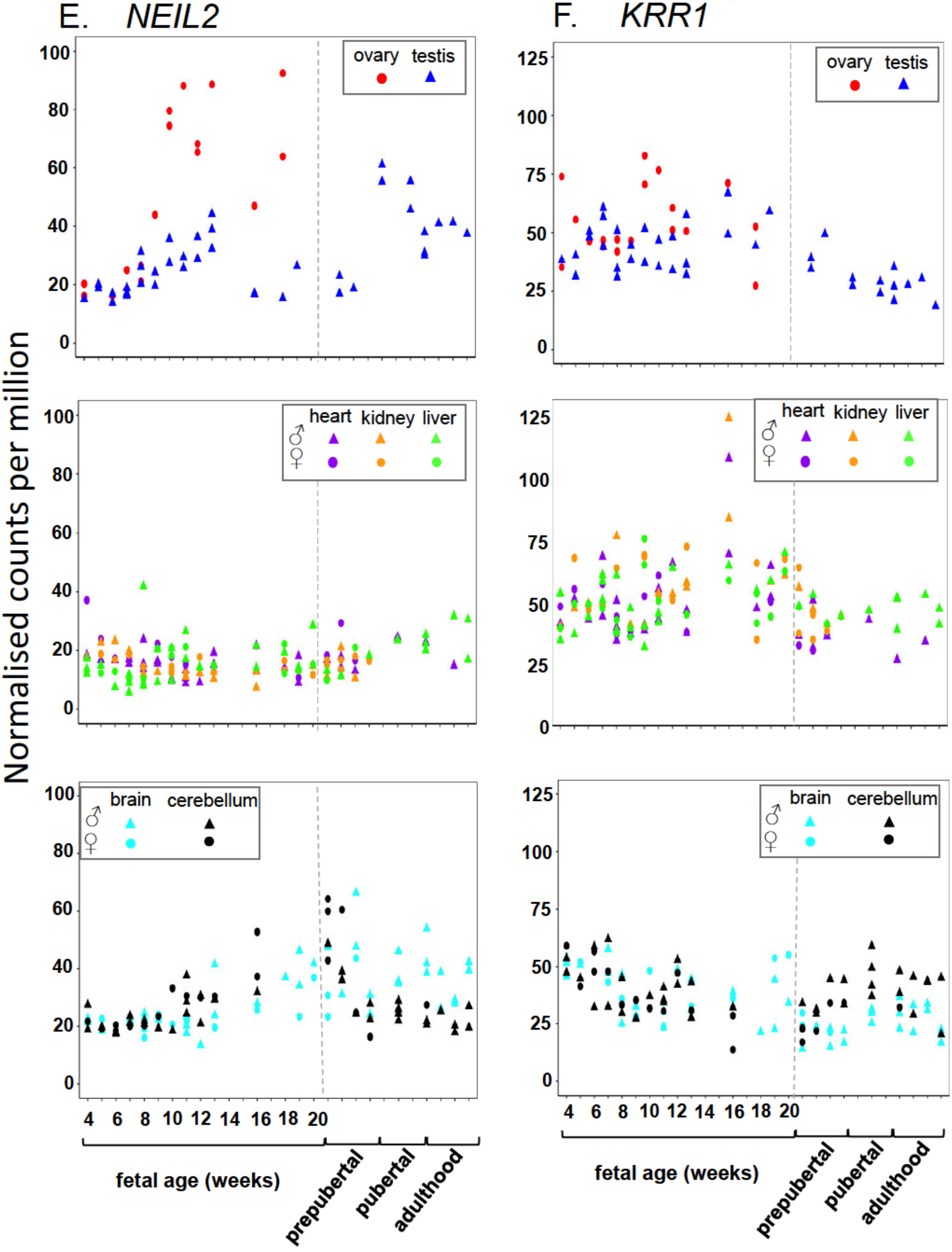
Suppl Fig 1 showing expression (CPM) of RNA/DNA regulation or processing PCOS candidate genes in gonadal, metabolic and brain tissues.



Short dashes distinguish fetal samples from the postnatal ones

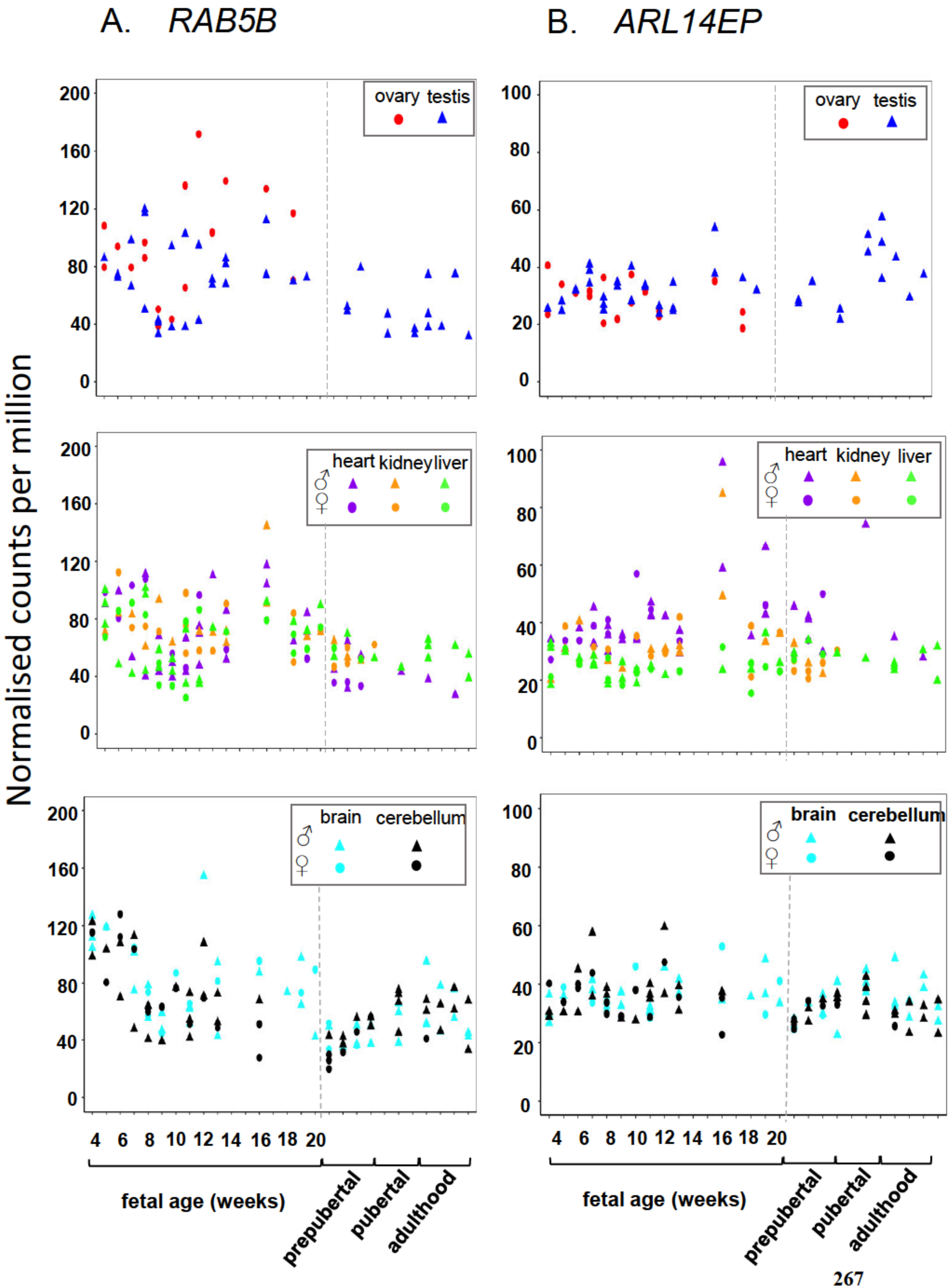


Short dashes distinguish fetal samples from the postnatal ones



Short dashes distinguish fetal samples from the postnatal ones

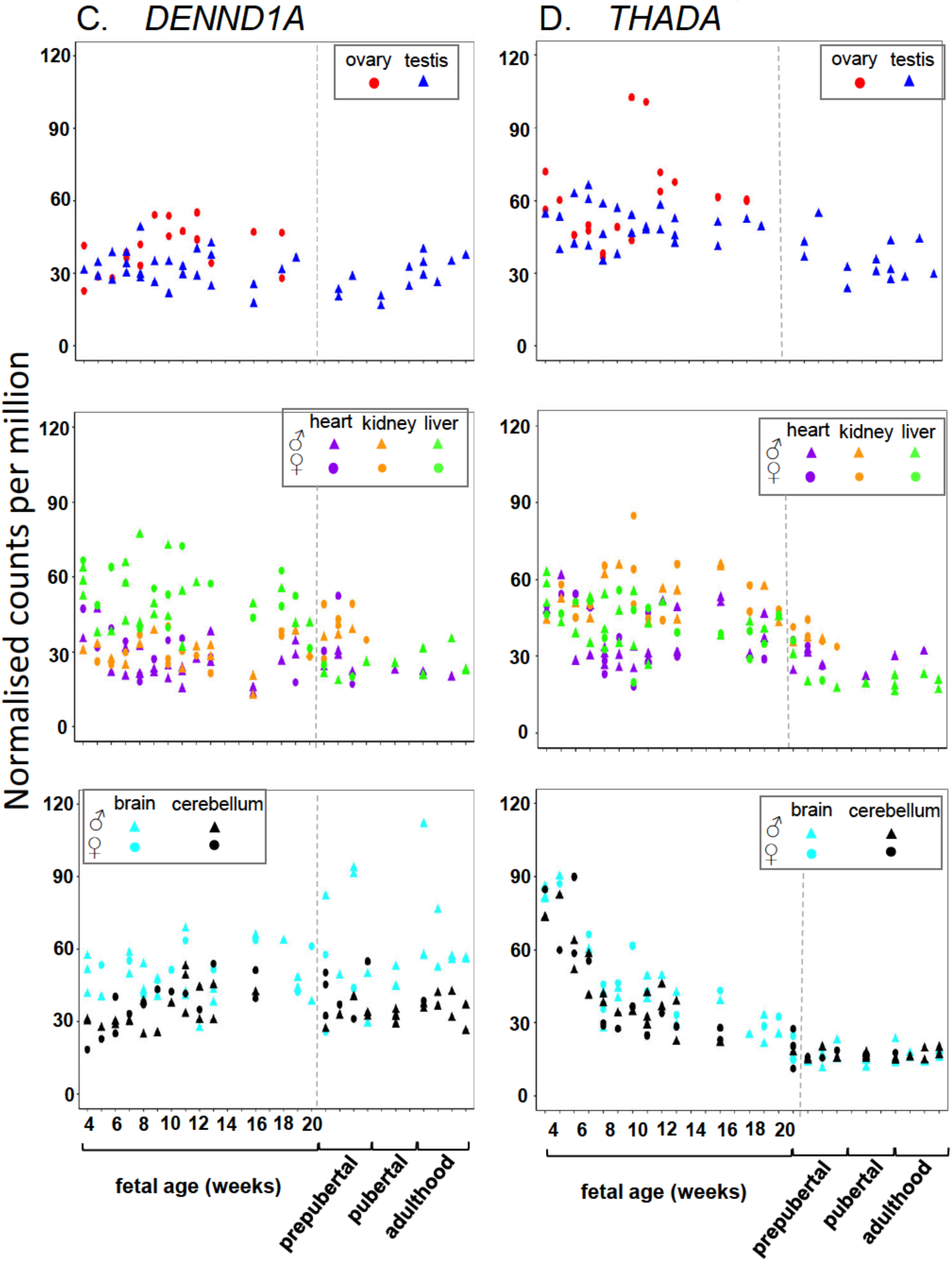
Suppl Fig 2 showing expression of candidate genes involved in cell functions in gonadal, metabolic and brain tissues.



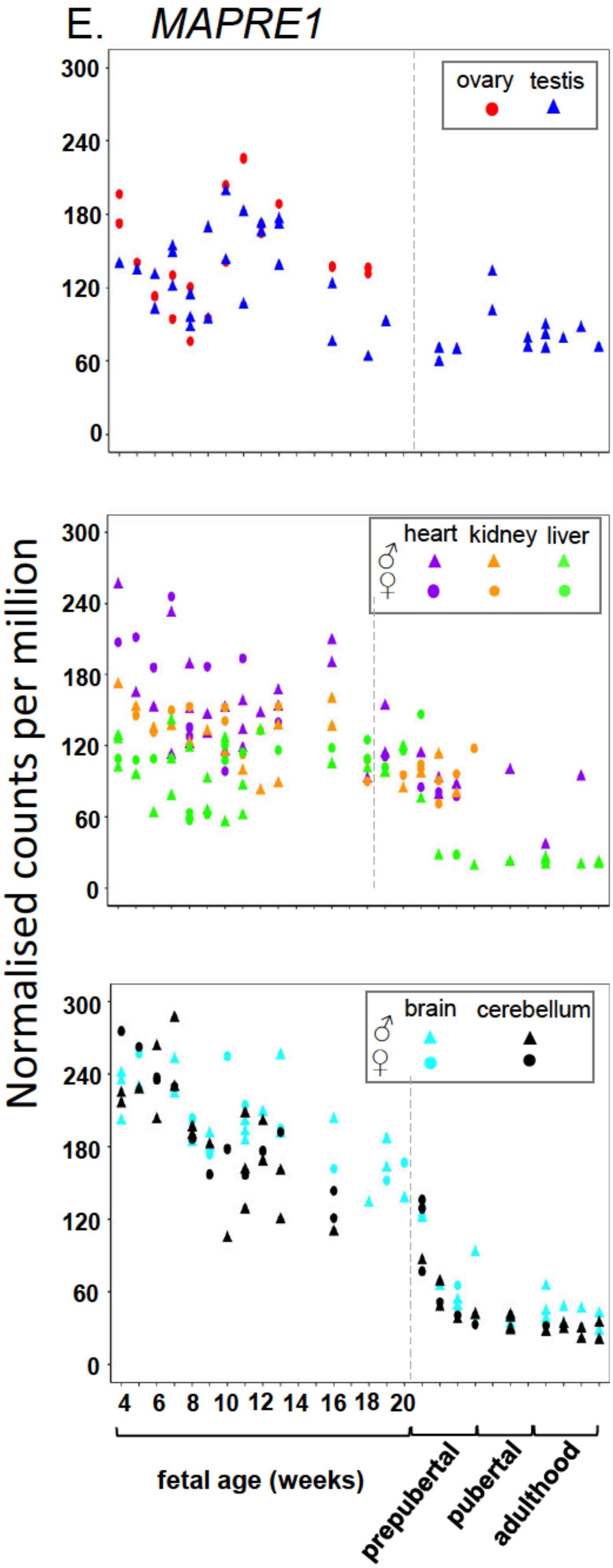
A. *RAB5B*

B. *ARL14EP*

Short dashes distinguish fetal samples from the postnatal ones

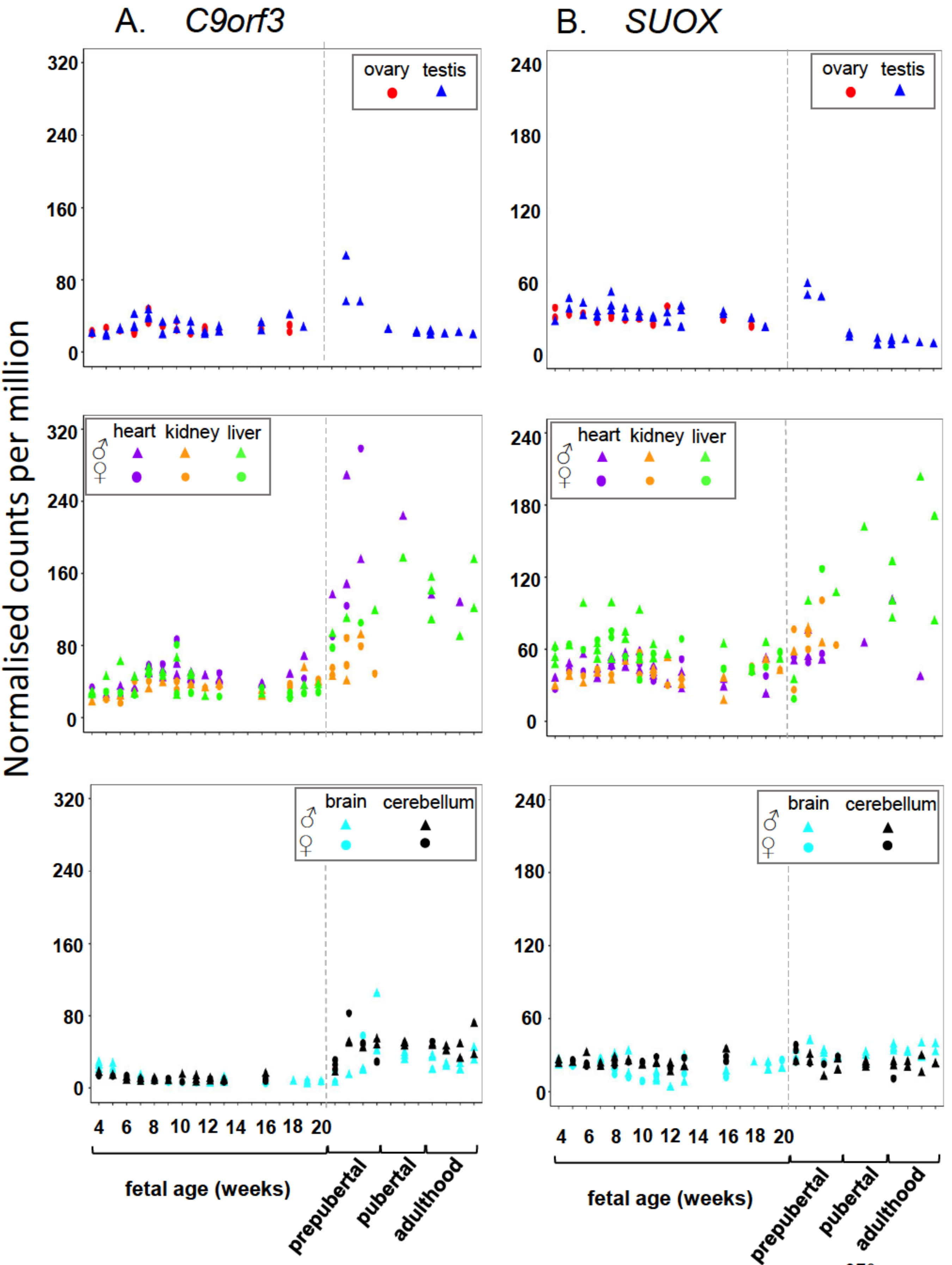


Short dashes distinguish fetal samples from the postnatal ones

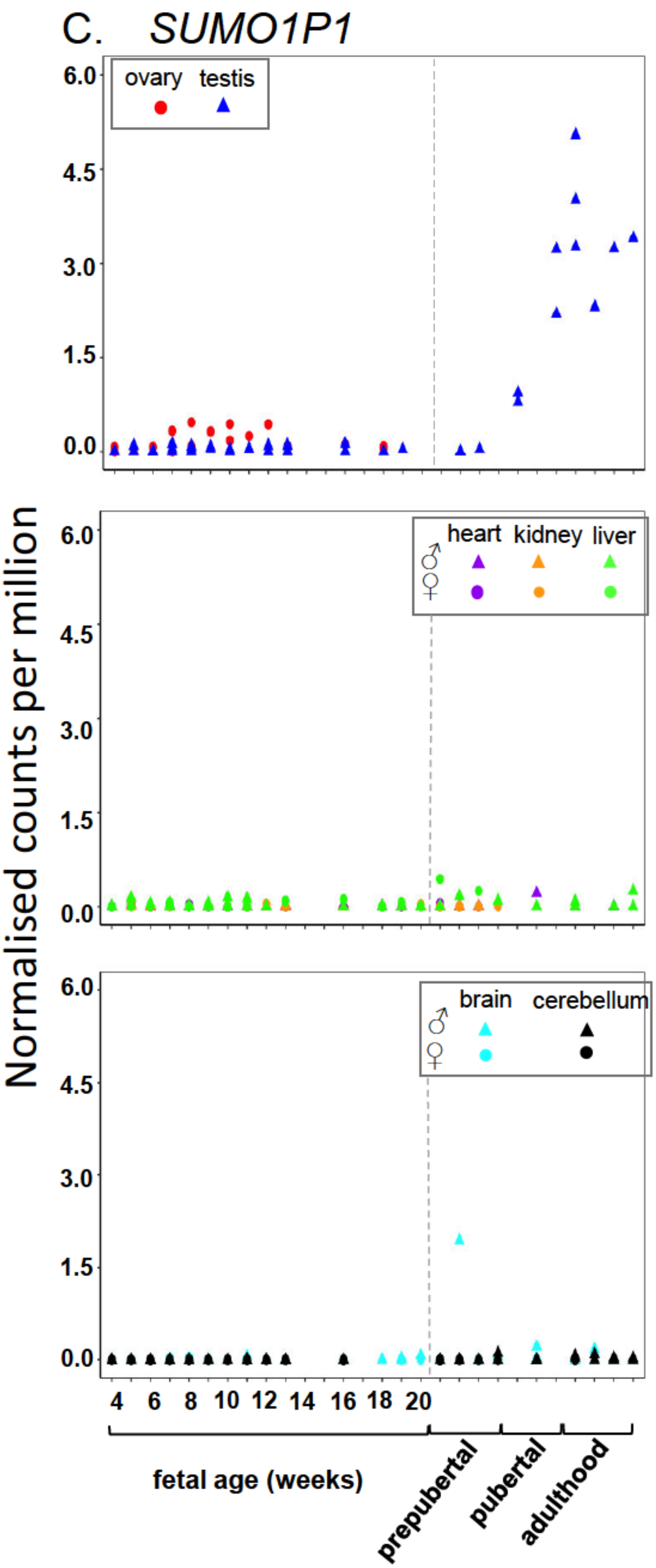


Short dashes distinguish fetal samples from the postnatal ones

Suppl Fig 3 showing expression (CPM) of enzyme-related candidate genes in gonadal, metabolic and brain tissues.

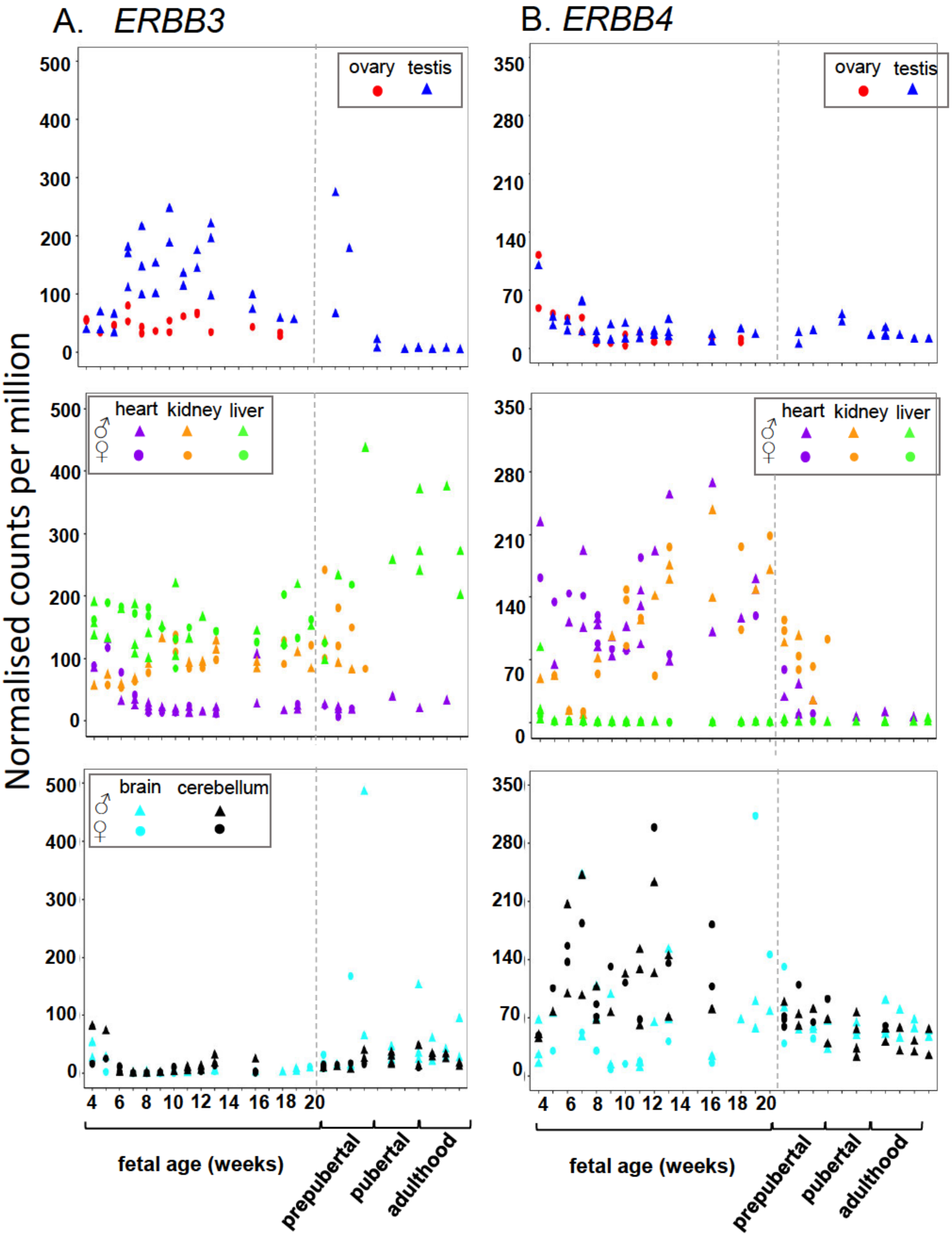


Short dashes distinguish fetal samples from the postnatal ones



Short dashes distinguish fetal samples from the postnatal ones

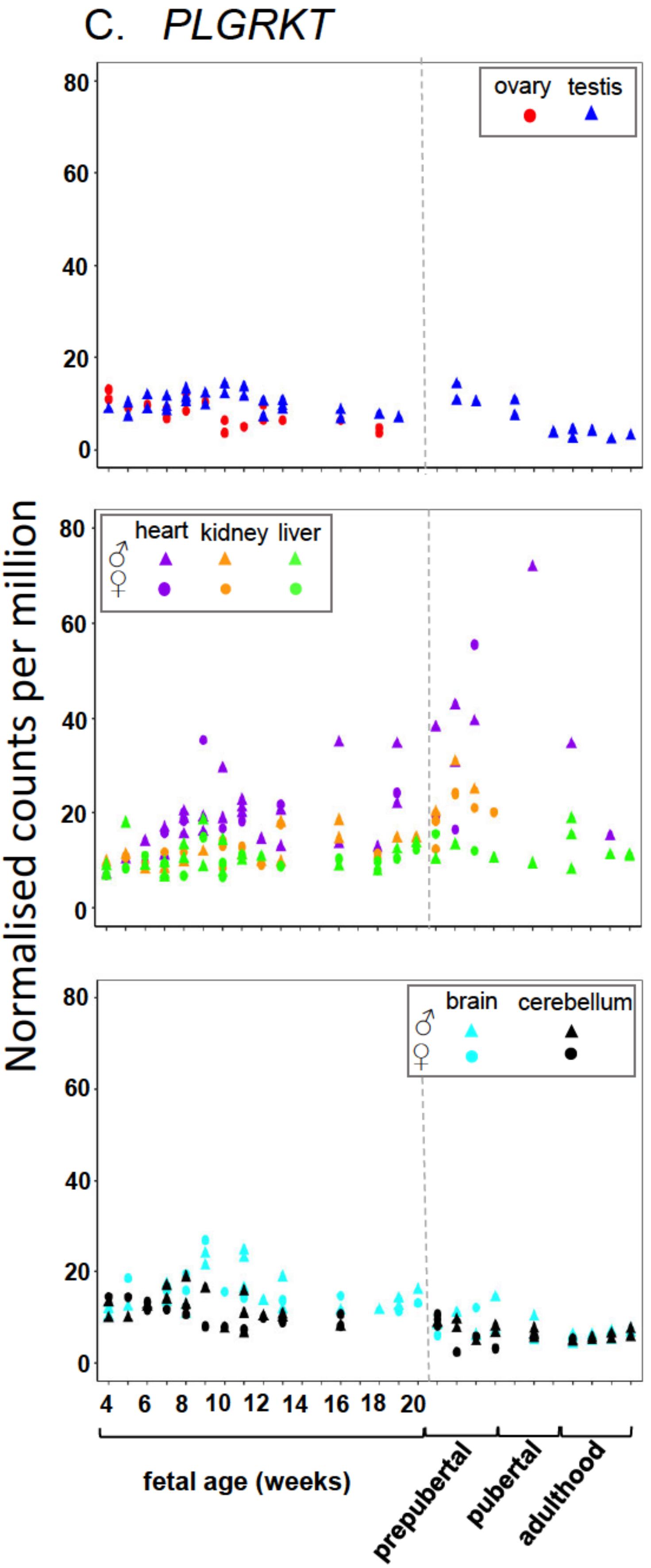
Suppl Fig 4 showing expression of cell surface receptors PCOS candidate genes in gonadal, metabolic and brain tissues.



A. *ERBB3*

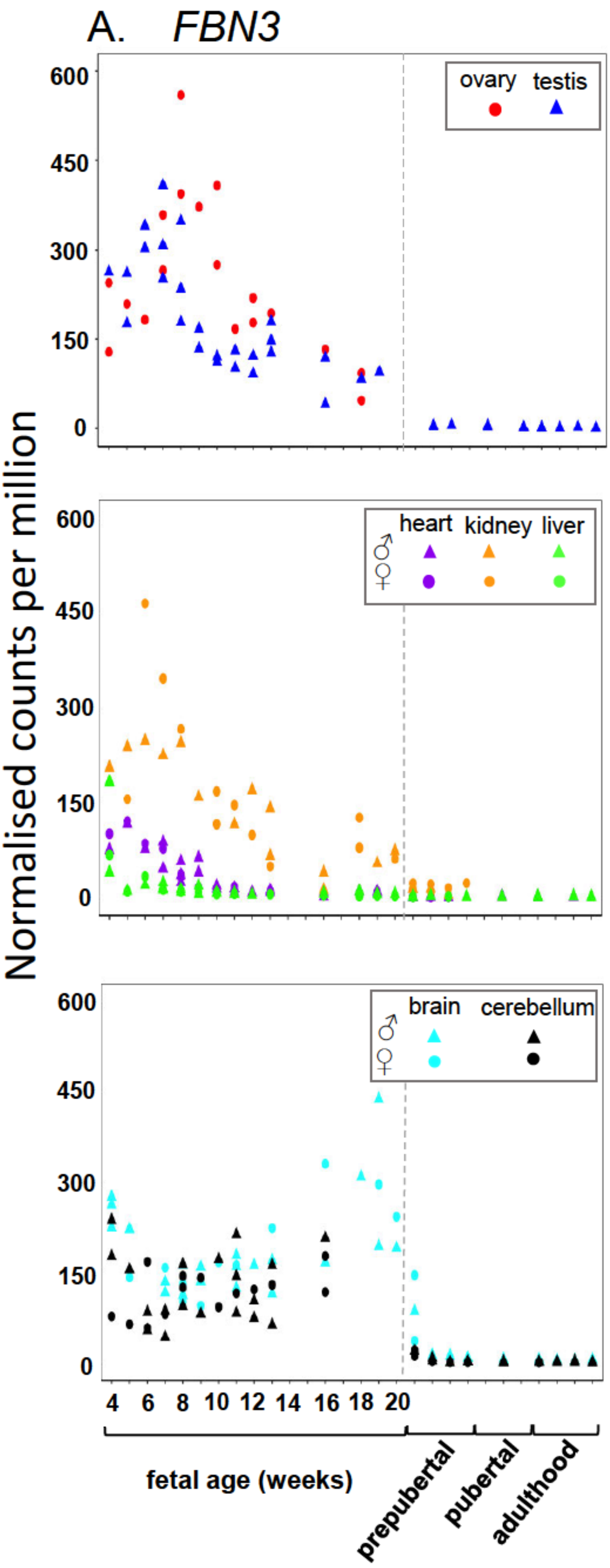
B. *ERBB4*

Short dashes distinguish fetal samples from the postnatal ones



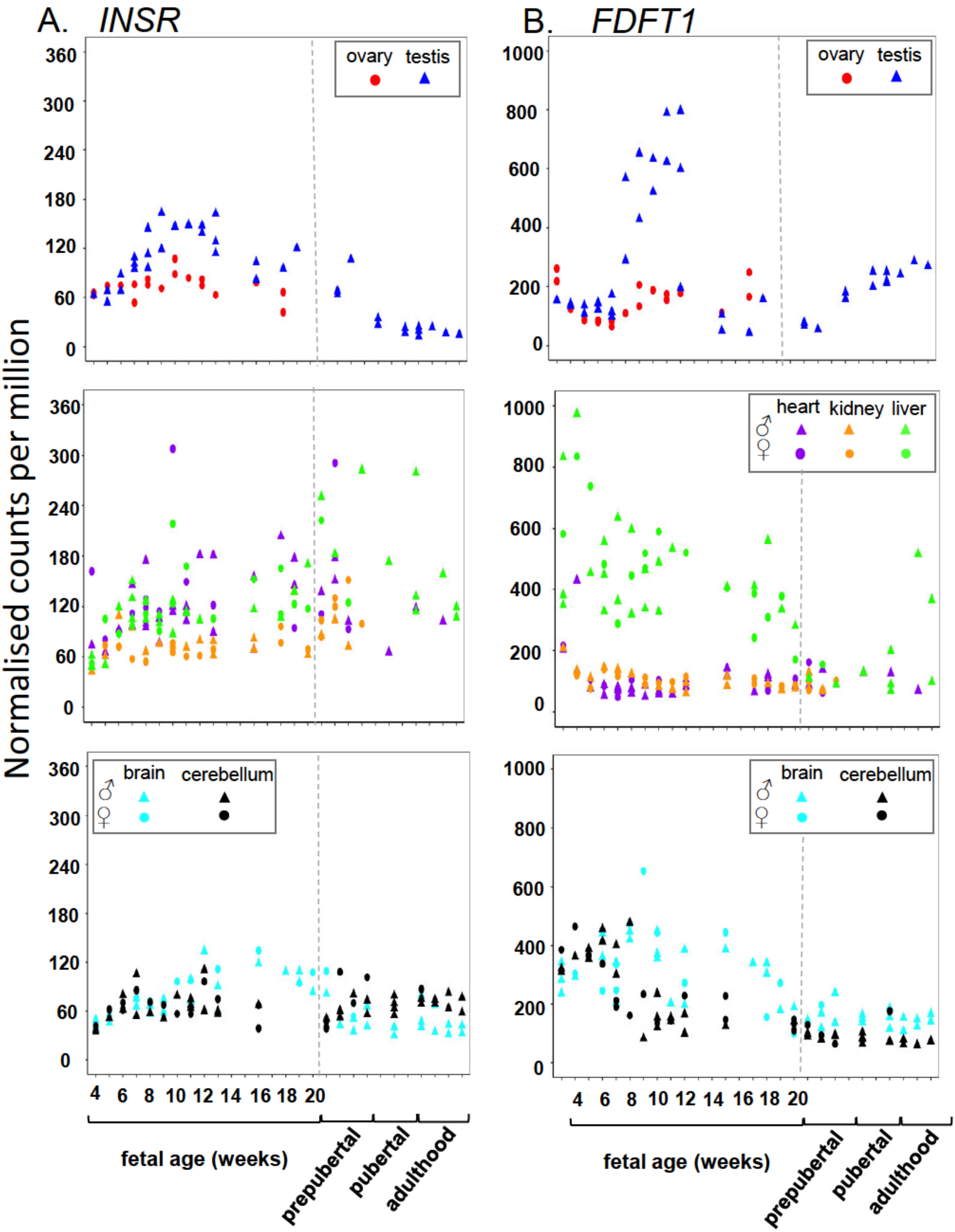
Short dashes distinguish fetal samples from the postnatal ones

Suppl Fig 5 showing expression of matrix-related PCOS candidate genes in gonadal, metabolic and brain tissues.



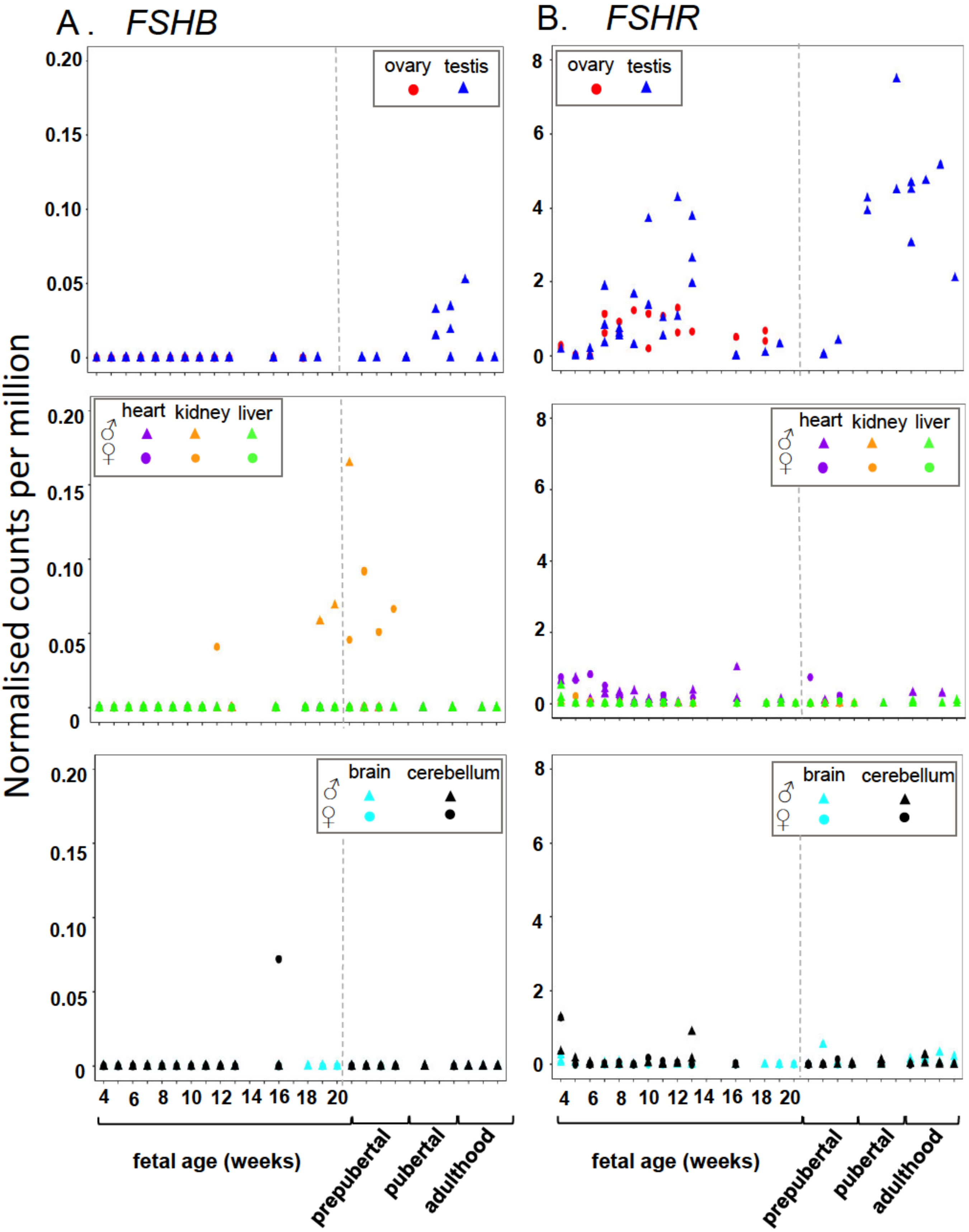
Short dashes distinguish fetal samples from the postnatal ones

Suppl Fig 6 showing expression of PCOS candidate genes involved in metabolism in gonadal, metabolic and brain tissues.

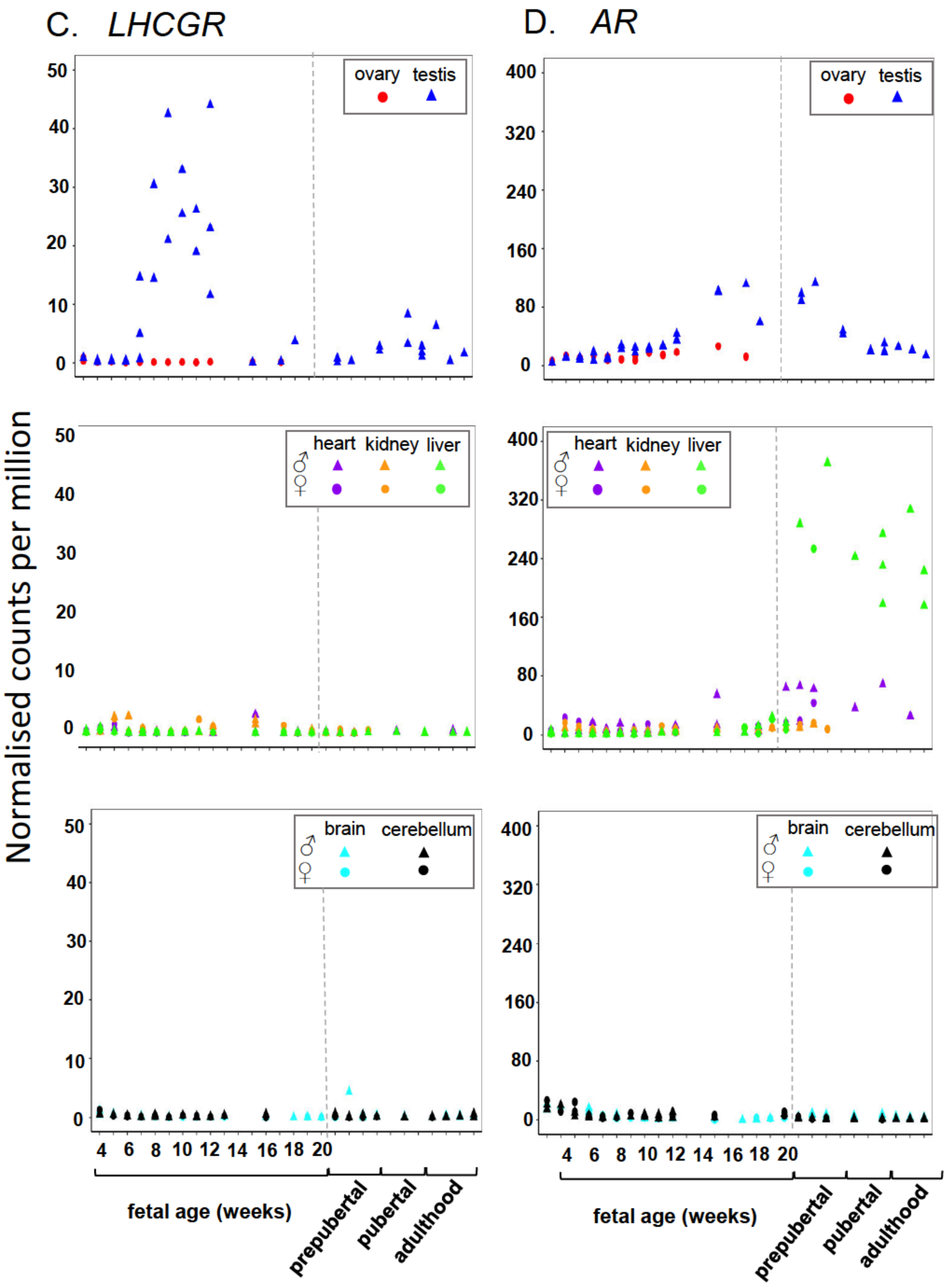


Short dashes distinguish fetal samples from the postnatal ones

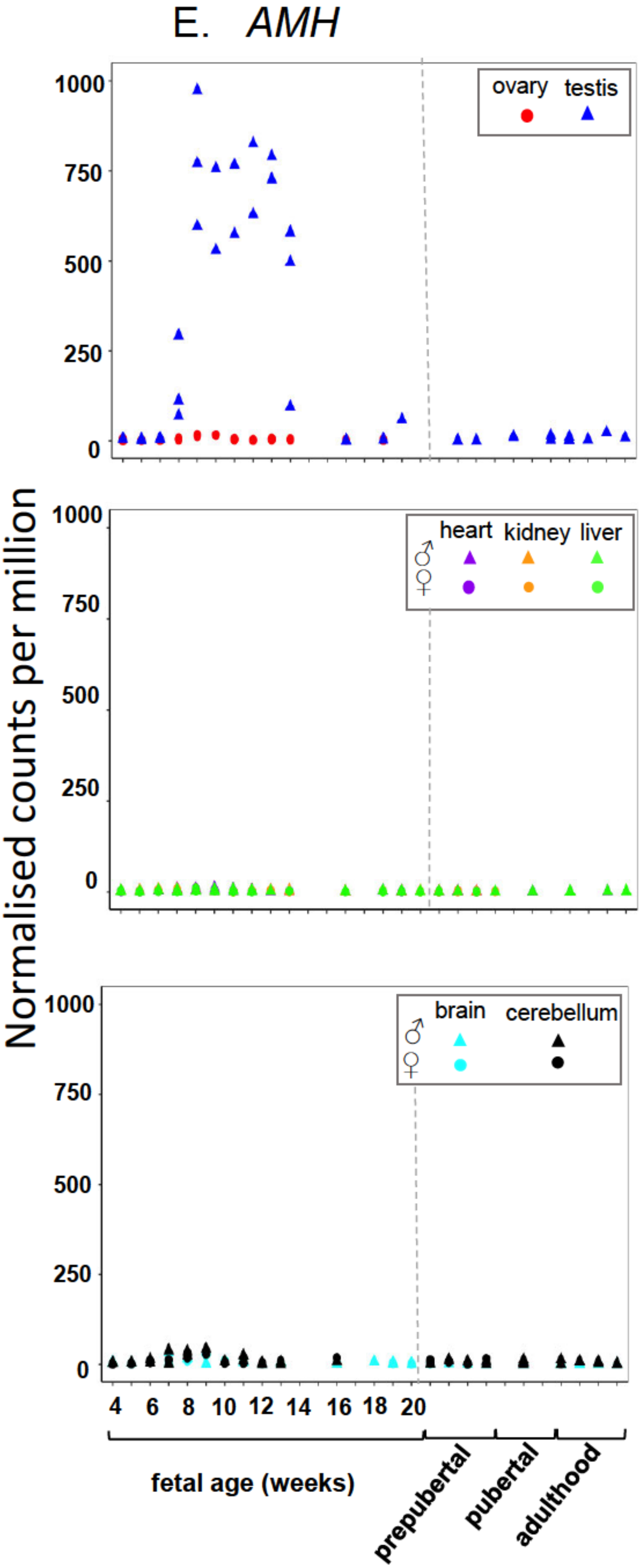
Suppl Fig 7 showing expression of reproduction-related PCOS candidate genes in gonadal, metabolic and brain tissues.



Short dashes distinguish fetal samples from the postnatal ones



Short dashes distinguish fetal samples from the postnatal ones



Short dashes distinguish fetal samples from the postnatal ones

Table S1. Characteristics (age and gender) of gonadal tissues analysed in this study.

Sample	Tissue	age	age_days	Sex
Ovary.4wpc.1	Ovary	4	28	Female
Ovary.4wpc.2	Ovary	4	28	Female
Ovary.5wpc.3	Ovary	5	35	Female
Ovary.6wpc.4	Ovary	6	42	Female
Ovary.7wpc.5	Ovary	7	49	Female
Ovary.7wpc.6	Ovary	7	49	Female
Ovary.8wpc.7	Ovary	8	56	Female
Ovary.8wpc.8	Ovary	8	56	Female
Ovary.9wpc.9	Ovary	9	63	Female
Ovary.10wpc.10	Ovary	10	70	Female
Ovary.10wpc.11	Ovary	10	70	Female
Ovary.11wpc.12	Ovary	11	77	Female
Ovary.12wpc.13	Ovary	12	84	Female
Ovary.12wpc.14	Ovary	12	84	Female
Ovary.13wpc.15	Ovary	13	91	Female
Ovary.16wpc.16	Ovary	16	112	Female
Ovary.18wpc.17	Ovary	18	126	Female
Ovary.18wpc.18	Ovary	18	126	Female
Testis.4wpc.1	Testis	4	28	Male
Testis.5wpc.2	Testis	5	35	Male
Testis.5wpc.3	Testis	5	35	Male
Testis.6wpc.4	Testis	6	42	Male
Testis.6wpc.5	Testis	6	42	Male
Testis.7wpc.6	Testis	7	49	Male
Testis.7wpc.7	Testis	7	49	Male
Testis.7wpc.8	Testis	7	49	Male
Testis.8wpc.9	Testis	8	56	Male
Testis.8wpc.10	Testis	8	56	Male
Testis.8wpc.11	Testis	8	56	Male
Testis.9wpc.12	Testis	9	63	Male
Testis.9wpc.13	Testis	9	63	Male
Testis.10wpc.14	Testis	10	70	Male
Testis.10wpc.15	Testis	10	70	Male
Testis.11wpc.16	Testis	11	77	Male
Testis.11wpc.17	Testis	11	77	Male
Testis.12wpc.18	Testis	12	84	Male
Testis.12wpc.19	Testis	12	84	Male
Testis.13wpc.20	Testis	13	91	Male
Testis.13wpc.21	Testis	13	91	Male
Testis.13wpc.22	Testis	13	91	Male
Testis.16wpc.23	Testis	16	112	Male
Testis.16wpc.24	Testis	16	112	Male
Testis.18wpc.26	Testis	18	126	Male
Testis.19wpc.27	Testis	19	133	Male
Testis.infant.28	Testis	infant	463	Male
Testis.infant.29	Testis	infant	463	Male
Testis.toddler.31	Testis	toddler	1375	Male

Testis.youngTeenager.32	Testis	youngTeenager	5025	Male
Testis.youngTeenager.33	Testis	youngTeenager	5025	Male
Testis.oldTeenager.34	Testis	oldTeenager	6485	Male
Testis.oldTeenager.35	Testis	oldTeenager	6485	Male
Testis.youngAdult.36	Testis	youngAdult	11230	Male
Testis.youngAdult.37	Testis	youngAdult	11230	Male
Testis.youngAdult.38	Testis	youngAdult	11230	Male
Testis.youngMidAge.39	Testis	youngMidAge	14880	Male
Testis.olderMidAge.40	Testis	olderMidAge	18530	Male
Testis.Senior.41	Testis	Senior	22180	Male

Table S2. Characteristics (age and gender) of metabolic tissues analysed in this study.

Sample	Tissue	age	age (days)	Sex
Heart.4wpc.1	Heart	4	28	Female
Heart.4wpc.2	Heart	4	28	Male
Heart.5wpc.3	Heart	5	35	Female
Heart.5wpc.4	Heart	5	35	Male
Heart.6wpc.5	Heart	6	42	Female
Heart.6wpc.6	Heart	6	42	Male
Heart.7wpc.7	Heart	7	49	Female
Heart.7wpc.8	Heart	7	49	Male
Heart.7wpc.9	Heart	7	49	Male
Heart.8wpc.10	Heart	8	56	Female
Heart.8wpc.11	Heart	8	56	Female
Heart.8wpc.12	Heart	8	56	Male
Heart.8wpc.13	Heart	8	56	Male
Heart.8wpc.14	Heart	8	56	Male
Heart.9wpc.15	Heart	9	63	Female
Heart.9wpc.16	Heart	9	63	Male
Heart.9wpc.17	Heart	9	63	Male
Heart.10wpc.19	Heart	10	70	Female
Heart.10wpc.20	Heart	10	70	Male
Heart.10wpc.21	Heart	10	70	Male
Heart.11wpc.22	Heart	11	77	Female
Heart.11wpc.23	Heart	11	77	Male
Heart.11wpc.24	Heart	11	77	Male
Heart.11wpc.25	Heart	11	77	Male
Heart.12wpc.27	Heart	12	84	Male
Heart.13wpc.28	Heart	13	91	Female
Heart.13wpc.30	Heart	13	91	Male
Heart.13wpc.31	Heart	13	91	Male
Heart.16wpc.33	Heart	16	112	Male
Heart.16wpc.34	Heart	16	112	Male
Heart.18wpc.36	Heart	18	126	Male
Heart.19wpc.35	Heart	19	133	Female
Heart.19wpc.37	Heart	19	133	Male
Heart.19wpc.38	Heart	19	133	Male
Heart.newborn.39	Heart	newborn	280	Female
Heart.newborn.41	Heart	newborn	280	Male
Heart.infant.43	Heart	infant	463	Female
Heart.infant.44	Heart	infant	463	Male
Heart.infant.45	Heart	infant	463	Male
Heart.toddler.46	Heart	toddler	1375	Female
Heart.toddler.47	Heart	toddler	1375	Male
Heart.teenager.48	Heart	teenager	5755	Male
Heart.youngAdult.49	Heart	youngAdult	11230	Male
Heart.olderMidAge.50	Heart	olderMidAge	18530	Male
Kidney.4wpc.1	Kidney	04	28	Male
Kidney.5wpc.2	Kidney	05	35	Female
Kidney.5wpc.3	Kidney	05	35	Male

Kidney.6wpc.4	Kidney	06	42	Female
Kidney.6wpc.5	Kidney	06	42	Male
Kidney.7wpc.6	Kidney	07	49	Female
Kidney.7wpc.7	Kidney	07	49	Male
Kidney.8wpc.8	Kidney	08	56	Female
Kidney.8wpc.9	Kidney	08	56	Male
Kidney.9wpc.11	Kidney	09	63	Male
Kidney.10wpc.12	Kidney	10	70	Female
Kidney.10wpc.13	Kidney	10	70	Female
Kidney.10wpc.14	Kidney	10	70	Female
Kidney.11wpc.15	Kidney	11	77	Female
Kidney.11wpc.16	Kidney	11	77	Male
Kidney.12wpc.17	Kidney	12	84	Female
Kidney.12wpc.18	Kidney	12	84	Male
Kidney.13wpc.19	Kidney	13	91	Female
Kidney.13wpc.20	Kidney	13	91	Male
Kidney.13wpc.21	Kidney	13	91	Male
Kidney.16wpc.23	Kidney	16	112	Male
Kidney.16wpc.24	Kidney	16	112	Male
Kidney.18wpc.25	Kidney	18	126	Female
Kidney.18wpc.26	Kidney	18	126	Female
Kidney.19wpc.30	Kidney	19	133	Male
Kidney.20wpc.28	Kidney	20	140	Female
Kidney.20wpc.29	Kidney	20	140	Male
Kidney.newborn.31	Kidney	newborn	280	Female
Kidney.newborn.32	Kidney	newborn	280	Female
Kidney.newborn.33	Kidney	newborn	280	Male
Kidney.infant.34	Kidney	infant	463	Female
Kidney.infant.36	Kidney	infant	463	Female
Kidney.infant.37	Kidney	infant	463	Male
Kidney.toddler.38	Kidney	toddler	1375	Female
Kidney.toddler.39	Kidney	toddler	1375	Male
Kidney.school.40	Kidney	school	3200	Female
Liver.4wpc.1	Liver	04	28	Female
Liver.4wpc.2	Liver	04	28	Male
Liver.4wpc.3	Liver	04	28	Male
Liver.4wpc.4	Liver	04	28	Male
Liver.5wpc.5	Liver	05	35	Female
Liver.5wpc.6	Liver	05	35	Male
Liver.6wpc.7	Liver	06	42	Female
Liver.6wpc.8	Liver	06	42	Male
Liver.7wpc.9	Liver	07	49	Female
Liver.7wpc.10	Liver	07	49	Male
Liver.7wpc.11	Liver	07	49	Male
Liver.7wpc.12	Liver	07	49	Male
Liver.8wpc.13	Liver	08	56	Female
Liver.8wpc.14	Liver	08	56	Female
Liver.8wpc.15	Liver	08	56	Male
Liver.8wpc.16	Liver	08	56	Male
Liver.9wpc.17	Liver	09	63	Female

Liver.9wpc.18	Liver	09	63	Male
Liver.9wpc.19	Liver	09	63	Male
Liver.10wpc.20	Liver	10	70	Female
Liver.10wpc.21	Liver	10	70	Female
Liver.10wpc.22	Liver	10	70	Male
Liver.10wpc.23	Liver	10	70	Male
Liver.11wpc.24	Liver	11	77	Female
Liver.11wpc.25	Liver	11	77	Male
Liver.11wpc.26	Liver	11	77	Male
Liver.12wpc.27	Liver	12	84	Male
Liver.13wpc.28	Liver	13	91	Female
Liver.16wpc.29	Liver	16	112	Female
Liver.16wpc.30	Liver	16	112	Male
Liver.18wpc.31	Liver	18	126	Female
Liver.18wpc.32	Liver	18	126	Female
Liver.18wpc.33	Liver	18	126	Male
Liver.19wpc.34	Liver	19	133	Female
Liver.19wpc.36	Liver	19	133	Male
Liver.20wpc.35	Liver	20	140	Female
Liver.20wpc.37	Liver	20	140	Male
Liver.newborn.38	Liver	newborn	280	Female
Liver.newborn.39	Liver	newborn	280	Male
Liver.infant.40	Liver	infant	463	Male
Liver.toddler.42	Liver	toddler	1375	Female
Liver.school.43	Liver	school	3200	Male
Liver.teenager.44	Liver	teenager	5755	Male
Liver.youngAdult.45	Liver	youngAdult	11230	Male
Liver.youngAdult.46	Liver	youngAdult	11230	Male
Liver.youngAdult.47	Liver	youngAdult	11230	Male
Liver.olderMidAge.48	Liver	olderMidAge	18530	Male
Liver.senior.49	Liver	senior	22180	Male
Liver.senior.50	Liver	senior	22180	Male

Table S3. Characteristics (age and gender) of metabolic tissues analysed in this study.

Sample	Tissue	age	age (days)	Sex
Brain.5wpc.4	Brain	5	35	Female
Brain.7wpc.6	Brain	7	49	Female
Brain.8wpc.9	Brain	8	56	Female
Brain.8wpc.10	Brain	8	56	Female
Brain.9wpc.13	Brain	9	63	Female
Brain.10wpc.16	Brain	10	70	Female
Brain.11wpc.17	Brain	11	77	Female
Brain.13wpc.22	Brain	13	91	Female
Brain.16wpc.25	Brain	16	112	Female
Brain.19wpc.28	Brain	19	133	Female
Brain.20wpc.32	Brain	20	140	Female
Brain.newborn.34	Brain	newborn	280	Female
Brain.newborn.35	Brain	newborn	280	Female
Brain.toddler.38	Brain	toddler	1375	Female
Cerebellum.4wpc.1	Cerebellum	4	28	Female
Cerebellum.5wpc.4	Cerebellum	5	35	Female
Cerebellum.6wpc.6	Cerebellum	6	42	Female
Cerebellum.6wpc.7	Cerebellum	6	42	Female
Cerebellum.7wpc.10	Cerebellum	7	49	Female
Cerebellum.8wpc.13	Cerebellum	8	56	Female
Cerebellum.8wpc.14	Cerebellum	8	56	Female
Cerebellum.9wpc.17	Cerebellum	9	63	Female
Cerebellum.10wpc.19	Cerebellum	10	70	Female
Cerebellum.11wpc.21	Cerebellum	11	77	Female
Cerebellum.12wpc.25	Cerebellum	12	84	Female
Cerebellum.13wpc.28	Cerebellum	13	91	Female
Cerebellum.16wpc.31	Cerebellum	16	112	Female
Cerebellum.16wpc.32	Cerebellum	16	112	Female
Cerebellum.newborn.34	Cerebellum	newborn	280	Female
Cerebellum.newborn.35	Cerebellum	newborn	280	Female
Cerebellum.newborn.37	Cerebellum	newborn	280	Female
Cerebellum.infant.39	Cerebellum	infant	463	Female
Cerebellum.toddler.42	Cerebellum	toddler	1375	Female
Cerebellum.school.44	Cerebellum	school	3200	Female
Cerebellum.youngAdult.51	Cerebellum	youngAdult	11230	Female
Brain.4wpc.1	Brain	4	28	Male
Brain.4wpc.2	Brain	4	28	Male
Brain.4wpc.3	Brain	4	28	Male
Brain.5wpc.5	Brain	5	35	Male
Brain.7wpc.7	Brain	7	49	Male
Brain.7wpc.8	Brain	7	49	Male
Brain.8wpc.11	Brain	8	56	Male
Brain.8wpc.12	Brain	8	56	Male
Brain.9wpc.14	Brain	9	63	Male
Brain.9wpc.15	Brain	9	63	Male
Brain.11wpc.18	Brain	11	77	Male
Brain.11wpc.19	Brain	11	77	Male

Brain.11wpc.20	Brain	11	77	Male
Brain.12wpc.21	Brain	12	84	Male
Brain.13wpc.23	Brain	13	91	Male
Brain.13wpc.24	Brain	13	91	Male
Brain.16wpc.26	Brain	16	112	Male
Brain.18wpc.27	Brain	18	126	Male
Brain.19wpc.29	Brain	19	133	Male
Brain.19wpc.30	Brain	19	133	Male
Brain.20wpc.31	Brain	20	140	Male
Brain.newborn.33	Brain	newborn	280	Male
Brain.infant.37	Brain	infant	463	Male
Brain.toddler.39	Brain	toddler	1375	Male
Brain.toddler.40	Brain	toddler	1375	Male
Brain.school.41	Brain	school	3200	Male
Brain.school.42	Brain	school	3200	Male
Brain.teenager.43	Brain	teenager	5755	Male
Brain.teenager.44	Brain	teenager	5755	Male
Brain.teenager.45	Brain	teenager	5755	Male
Brain.youngAdult.47	Brain	youngAdult	11230	Male
Brain.youngAdult.48	Brain	youngAdult	11230	Male
Brain.youngAdult.49	Brain	youngAdult	11230	Male
Brain.youngMidAge.50	Brain	youngMidAge	14880	Male
Brain.youngMidAge.51	Brain	youngMidAge	14880	Male
Brain.olderMidAge.52	Brain	olderMidAge	18530	Male
Brain.olderMidAge.53	Brain	olderMidAge	18530	Male
Brain.senior.54	Brain	senior	22180	Male
Brain.senior.55	Brain	senior	22180	Male
Cerebellum.4wpc.2	Cerebellum	4	28	Male
Cerebellum.4wpc.3	Cerebellum	4	28	Male
Cerebellum.5wpc.5	Cerebellum	5	35	Male
Cerebellum.6wpc.8	Cerebellum	6	42	Male
Cerebellum.6wpc.9	Cerebellum	6	42	Male
Cerebellum.7wpc.11	Cerebellum	7	49	Male
Cerebellum.7wpc.12	Cerebellum	7	49	Male
Cerebellum.8wpc.15	Cerebellum	8	56	Male
Cerebellum.8wpc.16	Cerebellum	8	56	Male
Cerebellum.9wpc.18	Cerebellum	9	63	Male
Cerebellum.10wpc.20	Cerebellum	10	70	Male
Cerebellum.11wpc.22	Cerebellum	11	77	Male
Cerebellum.11wpc.23	Cerebellum	11	77	Male
Cerebellum.11wpc.24	Cerebellum	11	77	Male
Cerebellum.12wpc.26	Cerebellum	12	84	Male
Cerebellum.12wpc.27	Cerebellum	12	84	Male
Cerebellum.13wpc.29	Cerebellum	13	91	Male
Cerebellum.13wpc.30	Cerebellum	13	91	Male
Cerebellum.16wpc.33	Cerebellum	16	112	Male
Cerebellum.newborn.36	Cerebellum	newborn	280	Male
Cerebellum.infant.40	Cerebellum	infant	463	Male
Cerebellum.infant.41	Cerebellum	infant	463	Male
Cerebellum.toddler.43	Cerebellum	toddler	1375	Male

Cerebellum.school.45	Cerebellum	school	3200	Male
Cerebellum.school.46	Cerebellum	school	3200	Male
Cerebellum.teenager.47	Cerebellum	teenager	5755	Male
Cerebellum.teenager.48	Cerebellum	teenager	5755	Male
Cerebellum.teenager.49	Cerebellum	teenager	5755	Male
Cerebellum.teenager.50	Cerebellum	teenager	5755	Male
Cerebellum.youngAdult.52	Cerebellum	youngAdult	11230	Male
Cerebellum.youngAdult.53	Cerebellum	youngAdult	11230	Male
Cerebellum.youngMidAge.54	Cerebellum	youngMidAge	14880	Male
Cerebellum.youngMidAge.55	Cerebellum	youngMidAge	14880	Male
Cerebellum.olderMidAge.56	Cerebellum	olderMidAge	18530	Male
Cerebellum.olderMidAge.57	Cerebellum	olderMidAge	18530	Male
Cerebellum.senior.58	Cerebellum	senior	22180	Male
Cerebellum.senior.59	Cerebellum	senior	22180	Male

Table S4

Pearson's correlation coefficients (R) between mRNA expression levels of *GATA4* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[†]
age (days)	0.45	-0.15	-0.51^{b}	-0.53^{b}	-0.66^{d}	-0.03	-0.22	3-
FSHB	-	-	-	-0.14	-	-0.11	-	
FSHR	0.79^{d}	0.63^{c}	0.20	0.59^{b}	0.66^{d}	-0.14	0.03	4+
LHCGR	-0.64^{b}	0.66^{c}	-0.19	0.05	0.42^{a}	-0.19	0.05	1+, 1-
AR	0.25	-0.49^{a}	-0.24	0.39^{a}	-0.17	-0.12	0.02	
AMH	0.34	0.72^{d}	0.09	0.18	0.11	-0.06	0.34	1+
INSR	0.35	0.73^{d}	0.24	0.01	-0.68^{d}	0.23	-0.17	1+, 1-
FDFT1	-0.18	0.65^{c}	0.04	0.38^{a}	0.24	0.06	-0.02	1+
ERBB3	0.15	0.76^{d}	0.07	-0.48^{a}	0.18	-0.09	-0.10	1+
ERBB4	-0.77^{c}	-0.20	0.18	-0.43^{a}	0.63^{d}	0.21	0.02	1+, 1-
PLGRKT	-0.41	0.45^{a}	-0.42^{a}	-0.28	-0.24	-0.14	0.07	
HMGA2	-0.82^{d}	-0.25	0.33	0.70^{d}	0.94^{d}	-0.14	-0.08	2+, 1-
TOX3	0.56^{a}	-0.23	-0.10	-0.35	0.59^{c}	0.32	0.12	1+
GATA4	*	*	*	*	*	*	*	
YAP1	-0.77^{c}	-0.60^{b}	-0.08	-0.04	0.86^{d}	-0.10	-0.05	1+, 2-
ZBTB16	0.13	-0.47^{a}	0.16	-0.07	0.11	-0.02	-0.05	
IRF1	0.57^{a}	0.02	0.28	-0.33	-0.50^{b}	0.09	-0.18	1-
NEIL2	0.61^{b}	0.62^{c}	0.57^{c}	0.71^{d}	-0.32	0.08	-0.22	4+
RAD50	0.03	-0.09	0.01	0.24	0.30	0.11	-0.18	
KRR1	0.07	-0.22	-0.33	-0.18	-0.26	0.23	-0.11	
RAB5B	-0.43	0.06	0.00	-0.17	0.14	0.20	-0.23	
ARL14EP	-0.40	-0.24	-0.58^{c}	0.00	0.28	0.29	-0.19	1-
DENND1A	0.76^{c}	0.35	0.60^{c}	-0.01	0.19	0.21	-0.23	2+
THADA	0.17	0.14	0.11	-0.11	0.45^{b}	-0.04	-0.13	1+
MAPRE1	-0.02	0.56^{b}	0.22	0.35	0.11	0.19	-0.03	1+
AOPEP	0.15	0.10	-0.08	-0.56^{b}	-0.18	-0.27	-0.01	1-
SUOX	0.04	0.07	-0.08	-0.20	0.12	-0.21	0.01	
SUMO1P1	0.66^{b}	0.09	-0.11	0.15	-0.10	-	0.23	1+
FBN3	0.30	0.09	0.39^{a}	0.25	0.86^{d}	-0.20	-0.09	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S5

Pearson’s correlation coefficients (R) between mRNA expression levels of *TOX3* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	0.34	-0.50^{b}	-0.31	0.68^{d}	-0.51^{b}	-0.60^{c}	-0.07	1+, 3-
FSHB	-	-	-	0.45^{a}	-	-0.22	-	
FSHR	0.47^{a}	-0.21	0.37^{a}	-0.31	0.34^{a}	-0.17	0.08	
LHCGR	-0.27	-0.45^{a}	0.06	-0.30	0.54^{c}	-0.22	0.01	1+
AR	0.28	-0.25	-0.08	-0.08	-0.13	0.15	0.36^{a}	
AMH	-0.13	-0.70^{d}	-0.05	-0.60^{c}	-0.19	-0.04	0.08	2-
INSR	0.50^{a}	-0.55^{b}	-0.26	0.62^{c}	-0.24	0.33	-0.10	1+, 1-
FDFT1	0.27	-0.41^{a}	0.81^{d}	-0.38^{a}	0.31	0.72^{d}	0.05	2+
ERBB3	0.16	-0.36	0.55^{c}	0.51^{b}	0.07	-0.14	-0.14	2+
ERBB4	-0.35	0.56^{b}	-0.23	0.63^{c}	0.32	0.33	0.65^{d}	3+
PLGRKT	-0.47^{a}	-0.29	-0.26	0.44^{a}	-0.17	0.44^{b}	-0.30	1+
HMGA2	-0.59^{a}	0.86^{d}	0.58^{c}	-0.54^{b}	0.62^{d}	0.11	0.05	3+, 1-
TOX3	*	*	*	*	*	*	*	
GATA4	0.56^{a}	-0.23	-0.10	-0.35	0.59^{c}	0.32	0.12	1+
YAP1	-0.31	0.63^{c}	0.04	0.31	0.67^{d}	0.25	0.16	2+
ZBTB16	0.55^{a}	-0.13	-0.06	0.45^{a}	0.28	0.20	0.09	
IRF1	0.47^{a}	-0.47^{a}	-0.11	0.52^{b}	-0.44^{b}	-0.66^{d}	-0.25	1+, 2-
NEIL2	0.69^{b}	-0.62^{c}	0.05	-0.49^{a}	-0.28	-0.58^{c}	0.05	1+, 2-
RAD50	0.55^{a}	0.53^{b}	0.21	0.16	0.37^{a}	0.50^{b}	0.21	2+
KRR1	0.58^{a}	0.32	0.00	0.35	0.12	0.58^{c}	0.43^{a}	1+
RAB5B	-0.06	0.26	0.01	0.56^{b}	0.23	0.18	0.45^{b}	2+
ARL14EP	0.19	0.17	-0.18	0.33	0.60^{d}	0.49^{b}	0.21	2+
DENND1A	0.63^{b}	0.15	0.45^{b}	0.09	-0.06	-0.43^{a}	0.13	2+
THADA	0.76^{c}	0.35	0.40^{a}	0.38	0.26	0.50^{b}	0.10	2+
MAPRE1	0.56^{a}	0.06	0.06	-0.34	0.20	0.77^{d}	0.23	1+
AOPEP	-0.09	-0.28	-0.32	0.60^{b}	-0.16	-0.08	0.02	1+
SUOX	-0.20	0.03	0.12	0.23	-0.09	-0.25	0.45^{b}	1+
SUMO1P1	0.27	-0.08	0.29	-0.13	0.03	-	-0.21	
FBN3	-0.05	0.62^{c}	0.52^{b}	-0.58^{b}	0.56^{c}	-0.51^{b}	0.02	3+, 2-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. ‘-’ and ‘*’ indicate no gene expression and correlation between same gene, respectively.

Table S6

Pearson's correlation coefficients (R) between mRNA expression levels of *ZBTB16* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	0.43	0.62^c	0.43^a	0.25	0.15	-0.66^d	-0.57^c	1+, 2-
FSHB	-	-	-	0.58^b	-	-0.12	-	1+
FSHR	0.15	-0.21	-0.17	-0.12	0.14	0.47^b	0.77^d	2+
LHCGR	0.03	-0.17	-0.25	-0.39^a	0.04	0.53^b	0.88^d	2+
AR	0.32	0.52^b	-0.22	-0.07	0.52^c	0.80^d	0.84^d	4+
AMH	-0.52^a	-0.35	-0.42^a	-0.12	-0.38^a	-0.38^a	-0.19	
INSR	0.15	-0.02	0.55^c	0.43^a	0.16	-0.40^a	-0.57^c	1+, 1-
FDFT1	0.67^b	-0.16	0.12	-0.19	0.05	0.40^a	-0.18	1+
ERBB3	0.06	-0.36	-0.15	0.37	0.14	0.83^d	0.88^d	2+
ERBB4	-0.06	-0.07	0.36^a	-0.01	0.14	-0.26	0.01	
PLGRKT	-0.54^a	-0.55^b	0.02	-0.07	-0.01	0.02	-0.38^a	1-
HMGA2	-0.40	-0.26	-0.14	-0.27	0.20	0.86^d	0.76^d	2+
TOX3	0.55^a	-0.13	-0.06	0.45^a	0.28	0.20	0.09	
GATA4	0.13	-0.47^a	0.16	-0.07	0.11	-0.02	-0.05	
YAP1	-0.10	0.40^a	0.22	-0.42^a	0.30	0.87^d	0.91^d	2+
ZBTB16	*	*	*	*	*	*	*	
IRF1	0.56^a	0.37	0.39^a	0.64^c	0.02	-0.04	0.14	1+
NEIL2	0.70^b	-0.03	-0.10	0.01	0.18	-0.31	-0.20	1+
RAD50	0.71^c	0.09	0.31	-0.43^a	0.70^d	0.69^d	0.56^c	4+
KRR1	0.34	0.29	0.19	-0.46^a	0.52^b	-0.51^b	0.50^b	2+, 1-
RAB5B	0.43	0.34	0.52^b	0.53^b	0.70^d	0.19	0.11	3+
ARL14EP	-0.02	0.08	0.09	-0.37	0.17	-0.13	-0.24	
DENND1A	0.35	0.05	0.41^a	0.62^c	0.22	-0.36^a	0.04	1+
THADA	0.74^c	-0.02	0.21	-0.10	0.39^a	0.82^d	0.79^d	3+
MAPRE1	0.76^c	-0.32	-0.17	-0.47^a	0.59^c	0.48^b	0.38^a	3+
AOPEP	-0.33	-0.07	0.11	0.47^a	-0.48^b	0.61^c	0.91^d	2+, 1-
SUOX	-0.05	-0.41^a	-0.47^b	0.66^c	-0.26	-0.03	0.32	1+, 1-
SUMO1P1	-0.06	0.06	-0.26	-0.13	-0.22	-	-0.20	
FBN3	-0.50^a	-0.36	-0.33	-0.07	0.18	0.23	0.24	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S7

Pearson's correlation coefficients (R) between mRNA expression levels of *IRF1* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	0.69^{b}	0.84^{d}	0.11	0.67^{c}	0.82^{d}	0.54^{b}	0.04	5+
FSHB	-	-	-	0.60^{c}	-	0.01	-	1+
FSHR	0.39	0.42^{a}	0.18	-0.30	-0.21	0.20	0.11	
LHCGR	-0.53^{a}	0.48^{a}	-0.01	-0.28	-0.24	0.29	0.07	
AR	0.52^{a}	0.67^{c}	-0.01	0.10	0.52^{c}	0.10	0.17	2+
AMH	-0.25	0.09	-0.31	-0.32	-0.29	-0.34	-0.23	
INSR	0.08	0.42^{a}	0.21	0.42^{a}	0.46^{b}	-0.21	-0.14	1+
FDFT1	0.32	0.51^{b}	0.24	-0.41^{a}	-0.27	-0.59^{c}	-0.35^{a}	1+, 1-
ERBB3	0.01	0.14	0.20	0.48^{a}	0.06	0.26	0.13	
ERBB4	-0.60^{b}	-0.44^{a}	0.11	0.32	-0.23	-0.25	0.08	1-
PLGRKT	-0.59^{a}	-0.29	-0.11	0.17	0.22	-0.49^{b}	-0.04	1-
HMGA2	-0.62^{b}	-0.72^{d}	0.19	-0.71^{d}	-0.42^{b}	0.02	0.25	3-
TOX3	0.47^{a}	-0.47^{a}	-0.11	0.52^{b}	-0.44^{b}	-0.66^{d}	-0.25	2+, 1-
GATA4	0.57^{a}	0.02	0.28	-0.33	-0.50^{b}	0.09	-0.18	1-
YAP1	-0.56^{a}	-0.16	0.14	-0.42^{a}	-0.36^{a}	-0.05	0.17	
ZBTB16	0.56^{a}	0.37	0.39^{a}	0.64^{c}	0.02	-0.04	0.14	1+
IRF1	*	*	*	*	*	*	*	
NEIL2	0.83^{d}	0.55^{b}	0.59^{c}	-0.16	0.23	0.59^{c}	0.13	4+
RAD50	0.41	0.14	0.17	-0.51^{b}	-0.02	-0.14	-0.04	1-
KRR1	-0.02	0.08	0.06	-0.31	0.12	-0.21	0.03	
RAB5B	0.21	0.48^{a}	0.27	0.65^{c}	0.29	0.21	0.09	1+
ARL14EP	-0.33	0.12	-0.06	-0.23	-0.02	-0.17	-0.40^{a}	
DENND1A	0.49^{a}	-0.02	0.34	0.44^{a}	-0.12	0.51^{b}	0.07	1+
THADA	0.44	-0.09	0.15	-0.20	-0.29	-0.25	0.10	
MAPRE1	0.39	0.18	0.02	-0.64^{c}	0.21	-0.50^{b}	-0.13	2-
AOPEP	-0.02	-0.19	-0.10	0.62^{c}	-0.19	0.19	0.14	1+
SUOX	0.21	-0.34	-0.33	0.49^{b}	-0.30	0.27	0.11	1+
SUMO1P1	0.11	0.06	-0.11	0.26	0.14	-	0.27	
FBN3	-0.35	-0.75^{d}	0.09	-0.51^{b}	-0.38^{a}	0.42^{a}	-0.02	2-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S8

Pearson's correlation coefficients (R) between mRNA expression levels of *NEIL2* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	0.75^{c}	0.31	-0.42^{a}	-0.55^{b}	0.27	0.75^{d}	0.67^{d}	3+, 1-
FSHB	-	-	-	0.04	-	0.28	-	-
FSHR	0.36	0.63^{c}	0.58^{c}	0.41^{a}	0.05	-0.09	-0.12	2+
LHCGR	-0.34	0.73^{d}	0.30	0.26	-0.10	-0.19	-0.20	1+
AR	0.31	-0.11	0.28	0.39^{a}	0.20	-0.22	-0.33	
AMH	-0.24	0.63^{c}	-0.08	0.56^{b}	-0.31	-0.07	-0.23	2+
INSR	0.19	0.71^{d}	0.00	0.06	0.28	-0.22	0.22	1+
FDFT1	0.47^{a}	0.76^{d}	0.37^{a}	0.49^{b}	0.16	-0.45^{b}	-0.18	2+, 1-
ERBB3	-0.13	0.62^{c}	0.56^{c}	-0.60^{c}	-0.39^{a}	-0.06	-0.05	2+, 1-
ERBB4	-0.55^{a}	-0.39^{a}	0.00	-0.76^{d}	0.01	0.03	0.26	1-
PLGRKT	-0.71^{c}	0.20	-0.43^{a}	-0.51^{b}	0.47^{b}	-0.40^{a}	-0.25	1+, 2-
HMGA2	-0.78^{c}	-0.60^{b}	0.53^{b}	0.67^{c}	-0.17	-0.30	-0.34	2+, 2-
TOX3	0.69^{b}	-0.62^{c}	0.05	-0.49^{a}	-0.28	-0.58^{c}	0.05	1+, 2-
GATA4	0.61^{b}	0.62^{c}	0.57^{c}	0.71^{d}	-0.32	0.08	-0.22	4+
YAP1	-0.61^{b}	-0.63^{c}	0.13	-0.42^{a}	-0.14	-0.35^{a}	-0.35	2+
ZBTB16	0.70^{b}	-0.03	-0.10	0.01	0.18	-0.31	-0.20	1-
IRF1	0.83^{d}	0.55^{b}	0.59^{c}	-0.16	0.23	0.59^{c}	0.13	4-
NEIL2	*	*	*	*	*	*	*	
RAD50	0.48^{a}	-0.23	0.18	-0.18	0.01	-0.50^{b}	-0.29	1-
KRR1	0.26	-0.36	-0.07	-0.49^{b}	0.31	-0.54^{b}	-0.21	2-
RAB5B	-0.01	0.24	0.09	-0.18	0.02	0.18	0.12	
ARL14EP	-0.32	-0.47^{a}	-0.29	-0.33	-0.16	-0.20	0.22	
DENND1A	0.51^{a}	0.25	0.52^{b}	0.13	0.38^{a}	0.68^{d}	0.12	2+
THADA	0.56^{a}	-0.04	0.33	-0.31	0.16	-0.49^{b}	-0.48^{b}	2-
MAPRE1	0.50^{a}	0.48^{a}	0.39^{a}	0.32	0.36^{a}	-0.48^{b}	-0.50^{b}	2-
AOPEP	-0.05	-0.08	-0.28	-0.41^{a}	0.07	-0.26	-0.20	
SUOX	-0.08	-0.10	-0.10	-0.04	-0.49^{b}	0.22	0.35	1-
SUMO1P1	0.21	0.02	0.11	0.10	0.03	-	0.25	
FBN3	-0.33	-0.43^{a}	0.52^{b}	0.52^{b}	-0.12	0.18	0.27	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S9

Pearson's correlation coefficients (R) between mRNA expression levels of *KRR1* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[†]
age (days)	0.01	0.29	0.34	0.30	0.36^{a}	-0.58^{c}	-0.28	1-
FSHB	-	-	-	-0.04	-	-0.18	-	
FSHR	-0.06	0.06	0.17	-0.06	0.04	0.38^{a}	0.27	
LHCGR	0.23	-0.21	0.19	0.20	-0.19	0.28	0.37^{a}	
AR	0.16	0.39	0.40^{a}	0.16	0.41^{a}	0.56^{c}	0.56^{c}	1+, 1-
AMH	-0.33	-0.48^{a}	-0.53^{b}	-0.42^{a}	-0.43^{b}	-0.53^{b}	-0.27	3-
INSR	0.51^{a}	-0.05	0.24	-0.02	0.51^{b}	0.32	-0.19	1+
FDFT1	0.14	-0.31	0.18	-0.17	-0.08	0.36^{a}	-0.14	
ERBB3	0.19	-0.05	0.18	-0.02	-0.33^{a}	0.26	0.38^{a}	
ERBB4	0.15	0.18	0.63^{d}	0.54^{b}	0.04	0.38^{a}	0.39^{a}	4+
PLGRKT	-0.20	-0.25	0.24	0.53^{b}	-0.06	0.14	-0.30	1+
HMGA2	-0.12	0.09	-0.05	-0.09	-0.08	0.54^{b}	0.50^{b}	2+
TOX3	0.58^{a}	0.32	0.00	0.35	0.12	0.58^{c}	0.43^{a}	1+
GATA4	0.07	-0.22	-0.33	-0.18	-0.26	0.23	-0.11	
YAP1	0.23	0.61^{c}	0.86^{d}	0.91^{d}	0.07	0.65^{d}	0.57^{c}	5+
ZBTB16	0.34	0.29	0.19	-0.46^{a}	0.52^{b}	0.51^{b}	0.50^{b}	3+
IRF1	-0.02	0.08	0.06	-0.31	0.12	-0.21	0.03	
NEIL2	0.26	-0.36	-0.07	-0.49^{b}	0.31	-0.54^{b}	-0.21	2-
RAD50	0.52^{a}	0.63^{c}	0.71^{d}	0.85^{d}	0.44^{b}	0.90^{d}	0.70^{d}	6+
KRR1	*	*	*	*	*	*	*	
RAB5B	-0.08	0.34	0.51^{b}	-0.20	0.44^{b}	0.44^{a}	0.45^{a}	2+
ARL14EP	0.56^{a}	0.73^{d}	0.87^{d}	0.90^{d}	0.28	0.65^{d}	0.32	4+
DENND1A	0.07	-0.13	-0.06	-0.65^{c}	-0.04	-0.47^{b}	-0.11	2-
THADA	0.48^{a}	0.30	0.56^{c}	0.52^{b}	0.06	0.75^{d}	0.58^{c}	4+
MAPRE1	0.53^{a}	0.06	0.39^{a}	0.27	0.58^{c}	0.70^{d}	0.50^{b}	3+
AOPEP	-0.08	-0.08	-0.20	-0.05	-0.12	0.25	0.44^{a}	
SUOX	-0.22	-0.46^{a}	-0.50^{b}	-0.49^{b}	-0.50^{b}	-0.48^{b}	0.09	4+
SUMO1P1	0.23	0.29	0.42^{a}	0.03	-0.22	-	-0.10	
FBN3	-0.10	-0.12	-0.17	-0.39^{a}	-0.02	-0.22	-0.01	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S10

Pearson's correlation coefficients (R) between mRNA expression levels of *RAB5B* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs‡
age (days)	-0.04	0.27	0.33	0.54^b	0.32	0.06	0.25	1+
FSHB	-	-	-	0.27	-	-0.15	-	
FSHR	-0.17	0.48^a	0.39^a	-0.11	0.19	0.09	0.05	
LHCGR	0.29	0.33	0.19	-0.46^a	0.03	0.01	0.02	
AR	0.29	0.20	0.36^a	0.07	0.49^b	0.26	0.09	1+
AMH	-0.76^c	-0.34	-0.71^d	-0.54^b	-0.58^c	-0.76^d	-0.51^b	6-
INSR	-0.39	0.17	0.13	0.36	0.01	0.26	0.40^a	
FDFT1	0.55^a	0.40^a	0.29	-0.14	0.20	-0.05	-0.22	
ERBB3	0.43	0.08	0.33	0.63^c	0.25	0.08	0.05	1+
ERBB4	0.51^a	0.27	0.53^b	0.41^a	0.18	0.54^b	0.51^b	3+
PLGRKT	0.05	-0.59^b	-0.11	0.23	-0.07	-0.47^b	-0.66^d	3-
HMGA2	0.33	-0.05	0.12	-0.44^a	0.24	0.11	-0.03	
TOX3	-0.06	0.26	0.01	0.56^b	0.23	0.18	0.45^b	2+
GATA4	-0.43	0.06	0.00	-0.17	0.14	0.20	-0.23	
YAP1	0.50^a	0.40^a	0.64^d	-0.12	0.36^a	0.18	0.06	1+
ZBTB16	0.43	0.34	0.52^b	0.53^b	0.70^d	0.19	0.11	3+
IRF1	0.21	0.48^a	0.27	0.65^c	0.29	0.21	0.09	1+
NEIL2	-0.01	0.24	0.09	-0.18	0.02	0.18	0.12	
RAD50	0.59^a	0.77^d	0.80^d	-0.22	0.86^d	0.54^b	0.49^b	5+
KRR1	-0.08	0.34	0.51^b	-0.20	0.44^b	0.44^a	0.45^a	2+
RAB5B	*	*	*	*	*	*	*	
ARL14EP	0.24	0.10	0.18	-0.24	0.26	0.48^b	0.30	1+
DENND1A	-0.22	0.27	0.43^a	0.51^b	0.32	0.11	0.33	1+
THADA	0.49^a	0.41^a	0.70^d	0.24	0.39^a	0.25	0.04	1+
MAPRE1	0.54^a	0.64^c	0.38^a	-0.34	0.78^d	0.27	0.23	2+
AOPEP	-0.66^b	-0.71^d	-0.50^b	0.48^a	-0.82^d	-0.11	-0.01	4-
SUOX	0.22	-0.40^a	-0.47^b	0.38	-0.39^a	-0.24	0.05	1-
SUMO1P1	-0.52^a	0.15	0.13	0.17	-0.12	-	-0.23	
FBN3	-0.71^b	-0.30	-0.11	-0.43^a	0.16	-0.36^a	0.23	1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. ‡Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S11

Pearson's correlation coefficients (R) between mRNA expression levels of *ARL14EP* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	-0.39	0.30	0.53^b	0.32	-0.03	-0.02	0.30	1+
FSHB	-	-	-	-0.01	-	-0.03	-	
FSHR	-0.21	-0.13	-0.16	-0.04	0.32	-0.05	-0.26	
LHCGR	0.45	-0.20	0.13	0.35	0.42^a	-0.15	-0.28	
AR	0.18	0.53^b	0.27	0.31	0.15	-0.06	-0.21	1+
AMH	-0.23	-0.38	-0.31	-0.40^a	-0.15	-0.37^a	-0.33	
INSR	0.18	-0.13	0.27	0.14	-0.08	0.74^d	0.53^b	2+
FDFT1	-0.01	-0.31	-0.05	-0.24	0.13	0.12	0.21	
ERBB3	0.27	-0.02	-0.12	-0.07	-0.01	-0.25	-0.20	
ERBB4	0.55^a	0.03	0.37^a	0.52^b	0.33^a	0.74^d	0.04	2+
PLGRKT	0.30	-0.05	0.55^c	0.54^b	0.06	0.09	-0.15	2
HMGA2	0.48^a	-0.01	-0.34	-0.11	0.35^a	-0.11	-0.18	
TOX3	0.19	0.17	-0.18	0.33	0.60^d	0.49^b	0.21	2+
GATA4	-0.40	-0.24	-0.58^c	0.00	0.28	0.29	-0.19	1-
YAP1	0.72^c	0.50^a	0.56^c	0.84^d	0.47^b	0.00	-0.20	4+
ZBTB16	-0.02	0.08	0.09	-0.37	0.17	-0.13	-0.24	
IRF1	-0.33	0.12	-0.06	-0.23	-0.02	-0.17	-0.40^a	
NEIL2	-0.32	-0.47^a	-0.29	-0.33	-0.16	-0.20	0.22	
RAD50	0.36	0.53^b	0.30	0.83^d	0.37^a	0.47^b	0.41^a	3+
KRR1	0.56^a	0.73^d	0.82^d	0.90^d	0.28	0.65^d	0.32	4+
RAB5B	0.24	0.10	0.18	-0.24	0.26	0.48^b	0.30	1+
ARL14EP	*	*	*	*	*	*	*	
DENND1A	-0.35	-0.45^a	-0.39^a	-0.70^d	-0.26	-0.22	0.03	1-
THADA	0.29	0.08	0.11	0.39^a	0.19	0.19	-0.03	
MAPRE1	0.32	-0.07	0.10	0.25	0.21	0.43^a	0.13	
AOPEP	0.04	0.02	0.18	-0.15	-0.17	-0.33	-0.24	
SUOX	-0.26	-0.25	-0.35^a	-0.53^b	-0.11	-0.47^b	-0.22	2-
SUMO1P1	-0.35	0.06	0.28	0.01	0.22	-	-0.09	
FBN3	-0.10	-0.18	-0.44^b	-0.43^a	0.33^a	-0.45^b	0.16	2-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S12

Pearson's correlation coefficients (R) between mRNA expression levels of *DENND1A* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	0.33	-0.14	-0.35[a]	0.01	-0.22	0.66[d]	0.09	1+
FSHB	-	-	-	0.14	-	0.07	-	
FSHR	0.68[b]	0.14	0.50[b]	-0.09	0.20	-0.34	-0.10	2+
LHCGR	-0.51[a]	0.24	-0.06	-0.49[b]	-0.08	-0.37[a]	0.00	1-
AR	0.19	-0.30	-0.12	-0.28	-0.29	-0.36[a]	-0.02	
AMH	0.24	0.15	-0.32	0.15	-0.22	0.02	-0.18	
INSR	0.49[a]	0.26	0.23	0.13	-0.15	0.07	0.28	
FDFT1	0.07	0.28	0.64[d]	0.09	0.33[a]	-0.62[d]	0.32	1+, 1-
ERBB3	0.12	-0.07	0.48[b]	0.34	-0.10	-0.19	0.01	1+
ERBB4	-0.58[a]	0.09	0.20	-0.20	0.13	0.01	-0.13	
PLGRKT	-0.36	-0.31	-0.47[b]	-0.23	0.05	-0.55[c]	-0.26	2-
HMGA2	-0.70[b]	0.09	0.62[c]	-0.05	0.18	-0.38[a]	0.01	1+, 1-
TOX3	0.63[b]	0.15	0.45[b]	0.09	-0.06	-0.43[a]	0.13	2+
GATA4	0.76[c]	0.35	0.60[c]	-0.01	0.19	0.21	-0.23	2+
YAP1	-0.60[b]	-0.04	0.18	-0.57[b]	0.18	-0.52[b]	0.00	2-
ZBTB16	0.35	0.05	0.41[a]	0.62[c]	0.22	-0.36[a]	0.04	1+
IRF1	0.49[a]	-0.02	0.34	0.44[a]	-0.12	0.51[b]	0.07	1+
NEIL2	0.51[a]	0.25	0.52[b]	0.13	0.38[a]	0.68[d]	0.12	2+
RAD50	0.03	0.11	0.44[b]	-0.62[c]	0.44[b]	-0.45[b]	0.03	2+, 2-
KRR1	0.07	-0.13	-0.06	-0.65[c]	-0.04	-0.47[b]	-0.11	2-
RAB5B	-0.22	0.27	0.43[a]	0.51[b]	0.32	0.11	0.33	1+
ARL14EP	-0.35	-0.45[a]	-0.39[a]	-0.70[d]	-0.26	-0.22	0.03	1-
DENND1A	*	*	*	*	*	*	*	
THADA	0.30	0.57[b]	0.55[c]	-0.10	0.58[c]	-0.56[c]	0.08	3+, 1-
MAPRE1	0.09	0.16	0.32	-0.33	0.55[c]	-0.55[c]	-0.02	1+, 1-
AOPEP	0.04	0.03	-0.31	0.45[a]	-0.46[b]	-0.26	-0.03	1-
SUOX	0.07	-0.10	-0.22	0.59[b]	-0.28	0.14	0.08	1+
SUMO1P1	0.54[a]	0.08	0.05	-0.06	-0.10	-	-0.29	
FBN3	0.24	0.18	0.47[b]	0.17	0.16	0.39[a]	0.21	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S13

Pearson's correlation coefficients (R) between mRNA expression levels of *THADA* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs‡
age (days)	0.21	-0.12	-0.11	0.01	-0.36^{a}	-0.79^{d}	-0.78^{d}	2-
FSHB	-	-	-	-0.22	-	-0.20	-	
FSHR	0.32	0.14	0.69^{d}	-0.05	0.42^{b}	0.43^{a}	0.47^{b}	3+
LHCGR	0.09	0.09	0.33	-0.16	0.23	0.47^{b}	0.68^{d}	2+
AR	0.27	-0.06	0.42^{a}	-0.16	0.03	0.87^{d}	0.86^{d}	2+
AMH	-0.51^{a}	-0.13	-0.59^{c}	-0.46^{a}	-0.27	-0.38^{a}	-0.07	1-
INSR	0.11	0.16	-0.17	0.09	-0.52^{c}	-0.16	-0.54^{b}	2-
FDFT1	0.64^{b}	0.14	0.63^{d}	0.07	0.34^{a}	0.64^{d}	0.10	3+
ERBB3	0.31	0.11	0.68^{d}	0.33	0.02	0.51^{b}	0.60^{c}	3+
ERBB4	0.13	0.41^{a}	0.56^{c}	0.33	0.40^{a}	-0.06	-0.22	1+
PLGRKT	-0.29	-0.40^{a}	-0.26	0.23	0.27	0.37^{a}	-0.07	
HMGA2	-0.23	0.21	0.53^{b}	0.02	0.52^{b}	0.87^{d}	0.89^{d}	4+
TOX3	0.76^{c}	0.35	0.40^{a}	0.38	0.26	0.50^{b}	0.10	2+
GATA4	0.17	0.14	0.11	-0.11	0.45^{b}	-0.04	-0.13	1-
YAP1	0.13	0.36	0.74^{d}	0.68^{c}	0.53^{c}	0.93^{d}	0.94^{d}	5+
ZBTB16	0.74^{c}	-0.02	0.21	-0.10	0.39^{a}	0.82^{d}	0.79^{d}	3+
IRF1	0.44	-0.09	0.15	-0.20	-0.29	-0.25	0.10	
NEIL2	0.56^{a}	-0.04	0.33	-0.31	0.16	-0.49^{b}	-0.48^{b}	2-
RAD50	0.83^{d}	0.60^{b}	0.90^{d}	0.56^{b}	0.64^{d}	0.82^{d}	0.65^{d}	7+
KRR1	0.48^{a}	0.30	0.56^{c}	0.52^{b}	0.06	0.75^{d}	0.58^{c}	4+
RAB5B	0.49^{a}	0.41^{a}	0.70^{d}	0.24	0.39^{a}	0.25	0.04	1+
ARL14EP	0.29	0.08	0.11	0.39^{a}	0.19	0.19	-0.03	
DENND1A	0.30	0.57^{b}	0.55^{c}	-0.10	0.58^{c}	-0.56^{c}	0.08	3+, 1-
THADA	*	*	*	*	*	*	*	
MAPRE1	0.85^{d}	0.36	0.68^{d}	0.42^{a}	0.48^{b}	0.77^{d}	0.73^{d}	5+
AOPEP	-0.48^{a}	-0.19	-0.72^{d}	0.09	-0.50^{b}	0.54^{b}	0.81^{d}	2+, 2-
SUOX	-0.08	-0.39^{a}	-0.50^{b}	-0.03	-0.09	-0.20	0.08	1-
SUMO1P1	-0.05	-0.08	0.40^{a}	-0.13	-0.07	-	-0.23	
FBN3	-0.48^{a}	-0.02	0.36^{a}	-0.24	0.47^{b}	-0.08	-0.09	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. ‡Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S14

Pearson's correlation coefficients (R) between mRNA expression levels of *MAPRE1* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	0.06	-0.19	-0.41[a]	-0.61[c]	0.16	-0.78[d]	-0.69[d]	3-
FSHB	-	-	-	-0.35	-	-0.26	-	
FSHR	0.08	0.70[d]	0.58[c]	0.33	0.26	0.22	0.26	2+
LHCGR	0.34	0.62[c]	0.23	0.22	0.05	0.19	0.35	1+
AR	0.13	-0.35	0.38[a]	0.09	0.28	0.53[b]	0.59[c]	2+
AMH	-0.55[a]	0.19	-0.31	0.05	-0.65[d]	-0.22	0.03	1-
INSR	0.06	0.42[a]	-0.32	-0.30	0.06	0.05	-0.34	
FDFT1	0.74[c]	0.67[c]	0.37[a]	0.66[c]	0.27	0.82[d]	0.27	4+
ERBB3	0.39	0.55[b]	0.52[b]	-0.38	-0.21	0.16	0.19	2+
ERBB4	0.26	0.28	0.47[b]	-0.32	0.21	0.15	-0.24	1+
PLGRKT	-0.12	0.09	-0.13	0.06	0.09	0.49[b]	0.03	1+
HMGA2	-0.10	-0.03	0.54[c]	0.61[c]	0.26	0.50[b]	0.58[c]	4+
TOX3	0.56[a]	0.06	0.06	-0.34	0.20	0.77[d]	0.23	1+
GATA4	-0.02	0.56[b]	0.22	0.35	0.11	0.19	-0.03	
YAP1	0.22	-0.06	0.60[c]	0.47[a]	0.37[a]	0.63[d]	0.62[c]	2+, 1-
ZBTB16	0.76[c]	-0.32	-0.17	-0.47[a]	0.59[c]	0.48[b]	0.38[a]	3+
IRF1	0.39	0.18	0.02	-0.64[c]	0.21	-0.50[b]	-0.13	2-
NEIL2	0.50[a]	0.48[a]	0.39[a]	0.32	0.36[a]	-0.48[b]	-0.50[b]	2-
RAD50	0.78[c]	0.51[b]	0.69[d]	0.48[a]	0.75[d]	0.65[d]	0.52[b]	6+
KRR1	0.53[a]	0.06	0.39[a]	0.27	0.58[c]	0.70[d]	0.50[b]	3+
RAB5B	0.54[a]	0.64[c]	0.39[a]	-0.34	0.78[d]	0.27	0.23	2+
ARL14EP	0.32	-0.07	0.10	0.25	0.21	0.43[a]	0.13	
DENND1A	0.09	0.16	0.32	-0.33	0.55[c]	-0.55[c]	-0.02	1+, 1-
THADA	0.85[d]	0.36	0.68[d]	0.42[a]	0.48[b]	0.78[d]	0.73[d]	5+
MAPRE1	*	*	*	*	*	*	*	
AOPEP	-0.38	-0.61[c]	-0.60[c]	-0.49[b]	-0.66[d]	0.08	0.43[a]	4-
SUOX	0.16	-0.28	-0.35[a]	-0.53[b]	-0.63[d]	-0.25	-0.12	2-
SUMO1P1	-0.18	0.05	0.38[a]	0.04	0.02	-	-0.23	
FBN3	-0.52[a]	-0.17	0.40[a]	0.24	0.23	-0.50[b]	-0.37[a]	1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S15

Pearson's correlation coefficients (R) between mRNA expression levels of *AOPEP* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[†]
age (days)	0.02	0.11	0.28	0.57^b	-0.20	-0.41^a	-0.65^d	1+, 1-
FSHB	-	-	-	0.40^a	-	-0.15	-	
FSHR	-0.01	-0.24	-0.66^d	-0.55^b	-0.18	0.35^a	0.57^c	1+, 2-
LHCGR	-0.06	-0.16	-0.33	-0.46^a	0.01	0.51^b	0.91^d	2+
AR	-0.16	0.09	-0.39^a	-0.36	-0.23	0.57^c	0.83^d	2+
AMH	0.67^b	0.32	0.39^a	-0.24	0.51^b	-0.19	-0.04	2+
INSR	0.37	0.13	0.60^c	0.25	0.31	-0.39^a	-0.67^d	1+, 1-
FDFT1	-0.32	-0.33	-0.44^b	-0.38^a	-0.12	0.12	-0.26	1+
ERBB3	-0.43	0.12	-0.65^d	0.60^c	-0.15	0.61^c	0.84^d	3+, 1-
ERBB4	-0.32	-0.37	-0.34^a	0.39^a	-0.16	-0.43^a	-0.08	
PLGRKT	0.16	0.33	0.45^b	0.36	0.01	0.12	-0.30	1+
HMGA2	-0.06	-0.20	-0.59^c	-0.58^b	-0.25	0.67^d	0.85^d	2+, 2-
TOX3	-0.09	-0.28	-0.32	0.60^b	-0.16	-0.08	0.02	1+
GATA4	0.15	0.10	-0.08	-0.56^b	-0.18	-0.27	-0.01	1-
YAP1	-0.26	-0.34	-0.47^b	-0.14	-0.32	0.63^d	0.91^d	2+, 1-
ZBTB16	-0.33	-0.07	0.11	0.47^a	-0.48^b	0.61^c	0.91^d	2+, 1-
IRF1	-0.02	-0.19	-0.10	0.62^c	-0.19	0.19	0.14	1+
NEIL2	-0.05	-0.08	-0.28	-0.41^a	0.07	-0.26	-0.20	
RAD50	-0.58^a	-0.59^b	-0.63^d	-0.41^a	-0.80^d	0.38^a	0.45^b	1+, 3-
KRR1	-0.08	-0.08	-0.20	-0.05	-0.12	0.25	0.44^a	
RAB5B	-0.66^b	-0.71^d	-0.50^b	0.48^a	-0.82^d	-0.11	-0.01	3-
ARL14EP	0.04	0.02	0.18	-0.15	-0.17	-0.33	-0.24	
DENND1A	0.04	0.03	-0.31	0.45^a	-0.46^b	-0.26	-0.03	1-
THADA	-0.48^a	-0.19	-0.72^d	0.09	-0.50^b	0.54^b	0.81^d	2+, 2-
MAPRE1	-0.38	-0.61^c	-0.60^c	-0.49^b	-0.66^d	0.08	0.43^a	4-
AOPEP	*	*	*	*	*	*	*	
SUOX	-0.02	0.22	0.21	0.56^b	0.35^a	0.19	0.41^a	1+
SUMO1P1	0.18	-0.13	-0.35^a	-0.03	-0.06	-	-0.17	
FBN3	0.52^a	0.23	-0.54^b	-0.38^a	-0.20	0.55^c	0.11	1+, 1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [†] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S16

Pearson's correlation coefficients (R) between mRNA expression levels of *SUOX* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	-0.26	-0.41^{a}	-0.26766	0.12	-0.33^{a}	0.16	-0.13	
FSHB	-	-	-	0.11	-	0.25	-	
FSHR	-0.08	-0.12	-0.32	-0.11	-0.20	-0.14	0.30	
LHCGR	0.04	-0.12	-0.17	-0.53^{b}	0.02	0.22	0.34	1-
AR	-0.09	-0.31	-0.32	-0.26	-0.21	-0.08	0.43^{a}	
AMH	0.00	0.17	0.63^{d}	-0.04	0.44^{b}	0.18	0.24	2+
INSR	0.09	-0.27	-0.20	0.21	-0.20	-0.39^{a}	-0.47^{b}	1-
FDFT1	0.09	-0.16	-0.18	-0.26	0.02	0.04	-0.35^{a}	
ERBB3	0.23	0.00	-0.21	0.39^{a}	0.50^{b}	0.07	0.26	1+
ERBB4	0.02	-0.28	-0.58^{c}	-0.05	-0.16	-0.45^{b}	0.44^{a}	2-
PLGRKT	0.37	0.23	0.03	-0.13	-0.04	-0.04	-0.35	
HMGA2	0.12	0.20	-0.04	-0.23	-0.06	-0.01	0.26	
TOX3	-0.20	0.03	0.12	0.23	-0.09	-0.25	0.45^{b}	1+
GATA4	0.04	0.07	-0.08	-0.20	0.12	-0.21	0.01	
YAP1	-0.04	-0.37	-0.60^{c}	-0.51^{b}	-0.15	-0.08	0.27	2-
ZBTB16	-0.05	-0.41^{a}	-0.47^{b}	0.66^{c}	-0.26	-0.03	0.32	1+, 1-
IRF1	0.21	-0.34	-0.33	0.49^{b}	-0.30	0.27	0.11	1+
NEIL2	-0.08	-0.10	-0.10	-0.04	-0.49^{b}	0.22	0.35	1-
RAD50	-0.12	-0.40^{a}	-0.58^{c}	-0.55^{b}	-0.29	-0.37^{a}	-0.13	2-
KRR1	-0.22	-0.46^{a}	-0.50^{b}	-0.49^{b}	-0.50^{b}	-0.48^{b}	0.09	4-
RAB5B	0.22	-0.40^{a}	-0.47^{b}	0.38	-0.39^{a}	-0.24	0.05	1-
ARL14EP	-0.26	-0.25	-0.35^{a}	-0.53^{b}	-0.11	-0.46^{b}	-0.22	2-
DENND1A	0.07	-0.10	-0.22	0.59^{b}	-0.28	0.14	0.08	1+
THADA	-0.08	-0.39^{a}	-0.50^{b}	-0.03	-0.09	-0.20	0.08	1-
MAPRE1	0.16	-0.28	-0.35^{a}	-0.53^{b}	-0.63^{d}	-0.25	-0.12	2-
AOPEP	-0.02	0.22	0.21	0.56^{b}	0.35^{a}	0.19	0.41^{a}	1-
SUOX	*	*	*	*	*	*	*	
SUMO1P1	0.16	-0.11	-0.02	-0.19	-0.05	-	-0.18	
FBN3	0.08	0.48^{a}	0.14	0.06	-0.11	0.30	0.10	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S17

Pearson’s correlation coefficients (R) between mRNA expression levels of *SUMO1P1* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[†]
age (days)	0.09	0.10	-0.18	0.06	0.00	-	0.22	
FSHB	-	-	-	0.12	-	-	-	
FSHR	0.38	0.27	0.23	0.40[a]	-0.13	-	-0.15	
LHCGR	-0.33	0.01	0.03	0.00	0.30	-	-0.18	
AR	-0.08	0.10	0.17	0.59[b]	-0.20	-	-0.15	1+
AMH	0.32	-0.05	-0.03	-0.16	-0.27	-	-0.01	
INSR	0.62[b]	0.13	-0.15	-0.08	-0.15	-	0.00	1+
FDFT1	-0.26	-0.04	0.30	-0.08	0.15	-	-0.22	
ERBB3	0.05	0.05	0.39[a]	0.03	-0.25	-	-0.10	
ERBB4	-0.40	0.03	0.16	0.04	-0.11	-	-0.08	
PLGRKT	-0.23	-0.13	0.01	0.09	0.38[a]	-	0.22	
HMGA2	-0.45	-0.08	0.35[a]	-0.01	-0.13	-	-0.10	
TOX3	0.27	-0.08	0.29	-0.13	0.03	-	-0.21	
GATA4	0.66[b]	0.09	-0.11	0.15	-0.10	-	0.23	1+
YAP1	-0.42	0.05	0.40[a]	-0.06	-0.14	-	-0.16	
ZBTB16	-0.06	0.06	-0.26	-0.13	-0.22	-	-0.20	
IRF1	0.11	0.06	-0.11	0.26	0.14	-	0.27	
NEIL2	0.21	0.02	0.11	0.10	0.03	-	0.25	
RAD50	-0.18	0.15	0.33	0.05	-0.08	-	-0.24	
KRR1	0.23	0.29	0.42[a]	0.03	-0.22	-	-0.10	
RAB5B	-0.52[a]	0.15	0.13	0.17	-0.12	-	-0.23	
ARL14EP	-0.35	0.06	0.28	0.01	0.22	-	-0.09	
DENND1A	0.54[a]	0.08	0.05	-0.06	-0.10	-	-0.29	
THADA	-0.05	-0.08	0.40[a]	-0.13	-0.07	-	-0.23	
MAPRE1	-0.18	0.05	0.38[a]	0.04	0.02	-	-0.23	
AOPEP	0.18	-0.13	-0.35[a]	-0.03	-0.06	-	-0.17	
SUOX	0.16	-0.11	-0.02	-0.19	-0.05	-	-0.18	
SUMO1P1	*	*	*	*	*	*	*	
FBN3	0.53[a]	-0.14	0.37[a]	-0.23	-0.18	-	-0.12	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. ‘-’ and ‘*’ indicate no gene expression and correlation between same gene, respectively.

Table S18

Pearson's correlation coefficients (R) between mRNA expression levels of *ERBB3* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	-0.31	0.05	-0.40^{a}	0.52^{b}	-0.04	-0.34	-0.38^{a}	1+
FSHB	-	-	-	0.00	-	-0.08	-	
FSHR	0.36	0.68^{c}	0.88^{d}	-0.53^{b}	-0.10	0.56^{c}	0.54^{b}	4+, 1-
LHCGR	0.08	0.53^{b}	0.60^{c}	-0.45^{a}	0.01	0.52^{b}	0.87^{d}	4+
AR	0.08	-0.18	0.49^{b}	-0.36	0.17	0.59^{c}	0.58^{c}	3+
AMH	-0.22	0.59^{b}	-0.34^{a}	-0.55^{b}	0.09	-0.38^{a}	-0.22	1+, 1-
INSR	-0.06	0.67^{c}	-0.40^{a}	0.20	-0.12	-0.49^{b}	-0.44^{a}	1+, 1-
FDFT1	0.05	0.46^{a}	0.74^{d}	-0.40^{a}	0.12	0.11	-0.28	1+
ERBB3		*	*	*	*	*	*	
ERBB4	0.22	-0.15	0.05	0.59^{b}	-0.06	-0.39^{a}	-0.08	1+
PLGRKT	0.28	0.41^{a}	-0.54^{c}	0.35	-0.12	-0.09	-0.37^{a}	1-
HMGA2	0.05	-0.37	0.82^{d}	-0.68^{d}	0.10	0.68^{d}	0.60^{c}	3+, 1-
TOX3	0.16	-0.36	0.55^{c}	0.51^{b}	0.07	-0.14	-0.14	2+
GATA4	0.15	0.76^{d}	0.07	-0.48^{a}	0.18	-0.09	-0.10	1+
YAP1	0.22	-0.45^{a}	0.37^{a}	0.03	0.09	0.65^{d}	0.73^{d}	2+
ZBTB16	0.06	-0.36	-0.15	0.37	0.14	0.83^{d}	0.88^{d}	2+
IRF1	0.01	0.14	0.20	0.48^{a}	0.06	0.26	0.13	
NEIL2	-0.13	0.62^{c}	0.56^{c}	-0.60^{c}	-0.39^{a}	-0.06	-0.05	2+,1-
RAD50	0.32	-0.01	0.50^{b}	-0.21	0.12	0.40^{a}	0.42^{a}	1+
KRR1	0.19	-0.05	0.18	-0.02	-0.33^{a}	0.26	0.38^{a}	
RAB5B	0.43	0.08	0.33	0.63^{c}	0.25	0.08	0.05	1+
ARL14EP	0.27	-0.02	-0.12	-0.07	-0.01	-0.25	-0.20	
DENND1A	0.12	-0.07	0.48^{b}	0.34	-0.10	-0.19	0.01	1+
THADA	0.31	0.11	0.68^{d}	0.33	0.02	0.51^{b}	0.60^{c}	3+
MAPRE1	0.39	0.55^{b}	0.52^{b}	-0.38	-0.21	0.16	0.19	2+
AOPEP	-0.43	0.12	-0.65^{d}	0.60^{c}	-0.15	0.61^{c}	0.86^{d}	3+, 1-
SUOX	0.23	0.00	-0.21	0.39^{a}	0.50^{b}	0.07	0.26	1+
SUMO1P1	0.05	0.05	0.39^{a}	0.03	-0.25	-	-0.10	
FBN3	-0.12	-0.17	0.70^{d}	-0.57^{b}	0.01	0.43^{a}	0.35	1+, 1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S19

Pearson's correlation coefficients (R) between mRNA expression levels of *ERBB4* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	**Ovary (N=18)**	**Testis (N=27)**	**Heart (N=38)**	**Kidney (N=29)**	**Liver (N=37)**	**Cerebellum (N=33)**	**Brain (N=32)**	**Number of organs[‡]**
age (days)	-0.61^{b}	-0.47^{a}	0.12	0.80^{d}	-0.27	0.23	0.29	1+, 1-
FSHB	-	-	-	0.13	-	0.18	-	
FSHR	-0.45	-0.01	0.17	-0.40^{a}	0.97^{d}	-0.29	0.02	1+
LHCGR	0.87^{d}	-0.27	-0.08	-0.24	0.27	-0.49^{b}	-0.07	1+,1-
AR	-0.35	-0.27	0.04	-0.06	0.05	-0.27	0.09	
AMH	-0.37	-0.48^{a}	-0.43^{a}	-0.77^{d}	0.04	-0.31	-0.14	1-
INSR	-0.21	-0.40^{a}	0.25	0.08	-0.33^{a}	0.78^{d}	0.03	1+
FDFT1	0.37	-0.23	0.09	-0.51^{b}	-0.11	-0.08	-0.35^{a}	1+
ERBB3	0.22	-0.15	0.05	0.59^{b}	-0.06	-0.39^{a}	-0.08	1+
ERBB4	*	*	*	*	*	*	*	
PLGRKT	0.55^{a}	-0.23	-0.05	0.69^{d}	-0.21	-0.21	-0.37^{a}	1+
HMGA2	0.77^{c}	0.61^{c}	0.11	-0.74^{d}	0.78^{d}	-0.32	-0.22	2+, 2-
TOX3	-0.35	0.56^{b}	-0.23	0.63^{c}	0.32	0.33	0.65^{d}	3+
GATA4	-0.77^{c}	-0.20	0.18	-0.43^{a}	0.63^{d}	0.21	0.02	1+, 1-
YAP1	0.93^{d}	0.67^{c}	0.82^{d}	0.49^{b}	0.83^{d}	-0.25	-0.08	4+
ZBTB16	-0.06	-0.07	0.36^{a}	-0.01	0.14	-0.26	0.01	
IRF1	-0.60^{b}	-0.44^{a}	0.11	0.32	-0.23	-0.25	0.08	1-
NEIL2	-0.55^{a}	-0.39^{a}	0.00	-0.77^{d}	0.01	0.03	0.26	1-
RAD50	0.11	0.53^{b}	0.66^{d}	0.30	0.31	0.25	0.02	2+
KRR1	0.15	0.18	0.63^{d}	0.54^{b}	0.04	0.38^{a}	0.39^{a}	2+
RAB5B	0.51^{a}	0.27	0.53^{b}	0.40^{a}	0.18	0.54^{b}	0.50^{b}	3+
ARL14EP	0.55^{a}	0.03	0.37^{a}	0.52^{b}	0.33^{a}	0.74^{d}	0.04	2+
DENND1A	-0.58^{a}	0.09	0.20	-0.20	0.13	0.01	-0.13	
THADA	0.13	0.41^{a}	0.56^{c}	0.33	0.40^{a}	-0.06	-0.22	1+
MAPRE1	0.26	0.28	0.47^{b}	-0.32	0.21	0.15	-0.24	1+
AOPEP	-0.32	-0.37	-0.34^{a}	0.39^{a}	-0.16	-0.43^{a}	-0.08	
SUOX	0.02	-0.28	-0.58^{c}	-0.05	-0.16	-0.45^{b}	0.44^{a}	2-
SUMO1P1	-0.40	0.03	0.16	0.04	-0.11	-	-0.08	
FBN3	-0.26	0.33	-0.08	-0.79^{d}	0.78^{d}	-0.42^{a}	0.10	1+, 1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S20

Pearson's correlation coefficients (R) between mRNA expression levels of *PLGRKT* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[†]
age (days)	-0.72^{c}	-0.32	0.53^{b}	0.52^{b}	0.14	-0.48^{b}	-0.15	2+, 2-
FSHB	-	-	-	0.16	-	-0.19	-	
FSHR	-0.15	0.14	-0.59^{c}	-0.25	-0.20	0.00	-0.31	1-
LHCGR	0.57^{a}	0.32	-0.31	-0.21	0.25	0.03	-0.34	
AR	-0.37	-0.48^{a}	-0.11	0.04	0.19	0.16	-0.19	
AMH	0.37	0.61^{c}	-0.02	-0.67^{c}	-0.35^{a}	0.45^{b}	0.48^{b}	3+, 1-
INSR	-0.19	0.29	0.10	0.03	-0.11	-0.11	-0.18	
FDFT1	-0.11	0.16	-0.27	-0.28	0.41^{a}	0.70^{d}	0.46^{b}	2+
ERBB3	0.28	0.41^{a}	-0.54^{c}	0.35	-0.12	-0.09	-0.37^{a}	1-
ERBB4	0.55^{a}	-0.23	-0.05	0.69^{d}	-0.21	-0.21	-0.37^{a}	1+
PLGRKT	*	*	*	*	*	*	*	
HMGA2	0.63^{b}	-0.09	-0.60^{c}	-0.42^{a}	-0.22	0.19	-0.10	1+, 1-
TOX3	-0.47^{a}	-0.29	-0.26	0.44^{a}	-0.17	0.44^{b}	-0.30	1+
GATA4	-0.41	0.45^{a}	-0.42^{a}	-0.28	-0.24	-0.14	0.07	
YAP1	0.51^{a}	-0.59^{b}	-0.03	0.54^{b}	-0.24	0.25	-0.21	1+, 1-
ZBTB16	-0.54^{a}	-0.55^{b}	0.02	-0.07	-0.01	0.02	-0.38^{a}	1-
IRF1	-0.59^{a}	-0.29	-0.11	0.17	0.22	-0.49^{b}	-0.04	1-
NEIL2	-0.72^{c}	0.20	-0.43^{a}	-0.51^{b}	0.47^{b}	-0.40^{a}	-0.25	1+, 2-
RAD50	-0.39	-0.50^{b}	-0.17	0.31	-0.08	-0.02	-0.43^{a}	1-
KRR1	-0.20	-0.25	0.24	0.53^{b}	-0.06	0.14	-0.30	1+
RAB5B	0.05	-0.59^{b}	-0.11	0.23	-0.07	-0.47^{b}	-0.66^{d}	3-
ARL14EP	0.30	-0.05	0.55^{c}	0.54^{b}	0.06	0.09	-0.15	2+
DENND1A	-0.36	-0.31	-0.47^{b}	-0.23	0.05	-0.56^{c}	-0.26	2-
THADA	-0.29	-0.40^{a}	-0.26	0.23	0.27	0.37^{a}	-0.07	
MAPRE1	-0.12	0.09	-0.13	0.06	0.09	0.49^{b}	0.03	1+
AOPEP	0.16	0.33	0.45^{b}	0.36	0.01	0.12	-0.30	1+
SUOX	0.37	0.23	0.03	-0.13	-0.04	-0.04	-0.35	
SUMO1P1	-0.23	-0.13	0.01	0.09	0.38^{a}	-	0.22	
FBN3	0.20	0.11	-0.63^{d}	-0.59^{b}	-0.25	-0.21	-0.43^{a}	2-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S21

Pearson's correlation coefficients (R) between mRNA expression levels of *FBN3* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs‡
age (days)	-0.44	-0.73^{d}	-0.77^{d}	-0.73^{d}	-0.46^{b}	0.17	0.43^{a}	4-
FSHB	-	-	-	-0.28	-	0.20	-	
FSHR	0.24	-0.25	0.62^{d}	0.32	0.85^{d}	0.01	0.10	2+
LHCGR	-0.22	-0.44^{a}	0.21	0.22	0.28	0.20	0.12	
AR	-0.34	-0.62^{c}	0.03	-0.02	-0.02	0.07	-0.07	1-
AMH	0.74^{c}	-0.21	0.13	0.80^{d}	0.07	0.09	-0.38^{a}	2+
INSR	0.50^{a}	-0.45^{a}	-0.40^{a}	-0.21	-0.52^{c}	-0.25	0.28	
FDFT1	-0.60^{b}	-0.42^{a}	0.50^{b}	0.28	-0.06	-0.45^{b}	-0.16	1+, 2-
ERBB3	-0.12	-0.17	0.70^{d}	-0.57^{b}	0.01	0.43^{a}	0.35	1+, 1-
ERBB4	-0.26	0.33	-0.08	-0.79^{d}	0.78^{d}	-0.42^{a}	0.10	1+, 1-
PLGRKT	0.20	0.11	-0.63^{d}	-0.59^{b}	-0.25	-0.21	-0.43^{a}	2-
HMGA2	-0.02	0.75^{d}	0.87^{d}	0.73^{d}	0.95^{d}	0.26	-0.01	4+
TOX3	-0.05	0.62^{c}	0.51^{b}	-0.58^{b}	0.56^{c}	-0.51^{b}	0.02	3+, 2-
GATA4	0.30	0.09	0.39^{a}	0.25	0.86^{d}	-0.20	-0.09	1+
YAP1	-0.20	0.13	-0.02	-0.29	0.92^{d}	0.08	0.02	1+
ZBTB16	-0.50^{a}	-0.36	-0.33	-0.07	0.18	0.23	0.24	
IRF1	-0.35	-0.75^{d}	0.09	-0.51^{b}	-0.38^{a}	0.42^{a}	-0.02	2-
NEIL2	-0.33	-0.43^{a}	0.52^{b}	0.52^{b}	-0.12	0.18	0.27	2+
RAD50	-0.62^{b}	-0.10	0.14	-0.17	0.33^{a}	-0.16	0.20	1-
KRR1	-0.10	-0.12	-0.17	-0.39^{a}	-0.02	-0.22	-0.01	
RAB5B	-0.71^{b}	-0.30	-0.11	-0.43^{a}	0.16	-0.36^{a}	0.23	1-
ARL14EP	-0.10	-0.18	-0.44^{b}	-0.43^{a}	0.33^{a}	-0.45^{b}	0.16	2-
DENND1A	0.24	0.18	0.47^{b}	0.17	0.16	0.39^{a}	0.21	1+
THADA	-0.48^{a}	-0.02	0.36^{a}	-0.24	0.47^{b}	-0.08	-0.09	1+
MAPRE1	-0.52^{a}	-0.17	0.40^{a}	0.24	0.23	-0.50^{b}	-0.37^{a}	1-
AOPEP	0.52^{a}	0.23	-0.54^{b}	-0.38^{a}	-0.20	0.55^{c}	0.11	1+, 1-
SUOX	0.08	0.48^{a}	0.14	0.06	-0.11	0.30	0.10	
SUMO1P1	0.53^{a}	-0.14	0.37^{a}	-0.23	-0.18		-0.12	
FBN3	*	*	*	*	*	*	*	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. ‡Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S22

Pearson's correlation coefficients (R) between mRNA expression levels of *INSR* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	-0.14	0.36	0.29	0.31	0.52^{b}	0.20	0.74^{d}	2+
FSHB	-	-	-	0.28	-	0.02	-	
FSHR	0.07	0.65^{c}	-0.35^{a}	-0.12	-0.34^{a}	-0.44^{a}	-0.46^{b}	1+, 1-
LHCGR	-0.18	0.84^{d}	-0.32	0.17	-0.36^{a}	-0.45^{b}	-0.61^{c}	1+, 2-
AR	0.01	-0.01	-0.31	0.15	0.24	-0.42^{a}	-0.69^{d}	1-
AMH	0.12	0.73^{d}	-0.12	-0.16	-0.03	-0.170	-0.37^{a}	1+
INSR	1.00	*	*	*	*	*	*	
FDFT1	-0.15	0.75^{d}	-0.17	-0.23	-0.30	-0.20	0.09	1+
ERBB3	-0.06	0.67^{c}	-0.40^{a}	0.20	-0.12	-0.49^{b}	-0.44^{a}	1+, 1-
ERBB4	-0.21	-0.40^{a}	0.25	0.08	-0.33^{a}	0.78^{d}	0.03	1+
PLGRKT	-0.19	0.29	0.10	0.03	-0.11	-0.11	-0.18	
HMGA2	-0.16	-0.71^{d}	-0.33	-0.22	-0.61^{d}	-0.42^{a}	-0.65^{d}	3+
TOX3	050^{a}	-0.55^{b}	-0.26	0.62^{c}	-0.24	0.33	-0.10	1+, 1-
GATA4	0.35	0.73^{d}	0.24	0.01	-0.68^{d}	0.23	-0.17	1+, 1-
YAP1	-0.10	-0.58^{b}	0.10	-0.07	-0.50^{b}	-0.39^{a}	-0.68^{d}	3-
ZBTB16	0.15	-0.02	0.55^{c}	0.43^{a}	0.16	-0.39^{a}	-0.57^{c}	1+, 1-
IRF1	0.08	0.42^{a}	0.21	0.42^{a}	0.46^{b}	-0.21	-0.14	1+
NEIL2	0.19	0.71^{d}	0.00	0.06	0.28	-0.22	0.22	1+
RAD50	-0.06	-0.10	0.01	0.00	-0.14	0.17	0.09	
KRR1	0.51^{a}	-0.05	0.24	-0.02	0.51^{b}	0.32	-0.19	1+
RAB5B	-0.39	0.17	0.13	0.36	0.01	0.26	0.40^{a}	
ARL14EP	0.18	-0.13	0.27	0.14	-0.08	0.74^{d}	0.53^{b}	2+
DENND1A	0.49^{a}	0.26	0.23	0.13	-0.15	0.07	0.28	
THADA	0.11	0.16	-0.17	0.09	-0.52^{c}	-0.16	-0.54^{b}	2-
MAPRE1	0.06	0.42^{a}	-0.32	-0.30	0.06	0.05	-0.34	
AOPEP	0.37	0.13	0.60^{c}	0.25	0.31	-0.39^{a}	-0.67^{d}	1+, 1-
SUOX	0.09	-0.27	-0.20	0.21	-0.20	-0.39^{a}	-0.47^{b}	1-
SUMO1P1	0.62^{b}	0.13	-0.15	-0.08	-0.15	-	0.00	1+
FBN3	0.50^{a}	-0.45^{a}	-0.40^{a}	-0.21	-0.52^{c}	-0.25	0.28	1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S23

Pearson's correlation coefficients (R) between mRNA expression levels of *FDFT1* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	0.20	0.17	-0.26	-0.57^{b}	-0.42^{a}	-0.72^{d}	-0.14	2-
FSHB	-	-		-0.25	-	-0.17	-	
FSHR	-0.04	0.69^{c}	0.56^{c}	0.27	-0.13	0.08	-0.10	2+
LHCGR	0.50^{a}	0.92^{d}	0.14	-0.04	0.52^{b}	0.11	-0.25	2+
AR	-0.18	-0.16	0.02	-0.13	-0.26	0.42^{a}	-0.11	
AMH	-0.50^{a}	0.61^{c}	-0.33	0.23	-0.41^{a}	0.14	0.27	1+
INSR	-0.15	0.75^{d}	-0.17	-0.23	-0.30	-0.20	0.09	1+
FDFT1	*	*	*	*	*	*	*	
ERBB3	0.05	0.47^{a}	0.74^{d}	-0.40^{a}	0.12	0.11	-0.28	1+
ERBB4	0.37	-0.23	0.09	-0.52^{b}	-0.11	-0.08	-0.35^{a}	1-
PLGRKT	-0.11	0.16	-0.27	-0.28	0.41^{a}	0.70^{d}	0.46^{b}	2+
HMGA2	-0.07	-0.50^{b}	0.75^{d}	0.57^{b}	0.15	0.41^{a}	-0.18	2+, 1-
TOX3	0.27	-0.41^{a}	0.81^{d}	-0.38^{a}	0.31	0.72^{d}	0.05	2+
GATA4	-0.18	0.65^{c}	0.04	0.38^{a}	0.24	0.06	-0.02	1+
YAP1	0.17	-0.53^{b}	0.36^{a}	-0.05	0.15	0.52^{b}	-0.09	1+, 1-
ZBTB16	0.67^{b}	-0.16	0.12	-0.19	0.05	0.40^{a}	-0.18	1+
IRF1	0.32	0.51^{b}	0.24	-0.41^{a}	-0.27	-0.59^{c}	-0.35^{a}	1+, 1-
NEIL2	0.47^{a}	0.76^{d}	0.37^{a}	0.49^{b}	0.16	-0.45^{b}	-0.18	2+, 1-
RAD50	0.42	0.03	0.47^{b}	0.05	0.21	0.36^{a}	-0.13	1+
KRR1	0.14	-0.31	0.18	-0.17	-0.08	0.36^{a}	-0.14	
RAB5B	0.55^{a}	0.40^{a}	0.29	-0.14	0.20	-0.05	-0.22	
ARL14EP	-0.01	-0.31	-0.05	-0.24	0.13	0.12	0.21	
DENND1A	0.07	0.28	0.64^{d}	0.09	0.33^{a}	-0.63^{d}	0.32	1+, 1-
THADA	0.64^{b}	0.14	0.63^{d}	0.07	0.34^{a}	0.64^{d}	0.10	3+
MAPRE1	0.74^{c}	0.67^{c}	0.37^{a}	0.66^{c}	0.27	0.82^{d}	0.27	4+
AOPEP	-0.32	-0.33	-0.44^{b}	-0.38^{a}	-0.12	0.12	-0.26	1-
SUOX	0.09	-0.16	-0.18	-0.26	0.02	0.04	-0.35^{a}	
SUMO1P1	-0.26	-0.04	0.30	-0.08	0.15	-	-0.22	
FBN3	-0.60^{b}	-0.42^{a}	0.50^{b}	0.28	-0.06	-0.45^{b}	-0.16	1+, 2-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S24

Pearson's correlation coefficients (R) between mRNA expression levels of *FSHB* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	-	-	-	0.46^{a}	-	0.35^{a}	-	
FSHB	*	*	*	*	*	*	*	
FSHR	-	-	-	-0.14	-	-0.06	-	
LHCGR	-	-	-	-0.03	-	-0.11	-	
AR	-	-	-	0.22	-	-0.12	-	
AMH	-	-	-	-0.11	-	0.07	-	
INSR	-	-	-	0.28	-	0.02	-	
FDFT1	-	-	-	-0.25	-	-0.17	-	
ERBB3	-	-	-	0.00	-	-0.08	-	
ERBB4	-	-	-	0.13	-	0.18	-	
PLGRKT	-	-	-	0.16	-	-0.19	-	
HMGA2	-	-	-	-0.34	-	-0.09	-	
TOX3	-	-	-	0.45^{a}	-	-0.22	-	
GATA4	-	-	-	-0.14	-	-0.11	-	
YAP1	-	-	-	-0.19	-	-0.12	-	
ZBTB16	-	-	-	0.58^{b}	-	-0.12	-	1+
IRF1	-	-	-	0.60^{c}	-	0.01	-	1+
NEIL2	-	-	-	0.04	-	0.28	-	
RAD50	-	-	-	-0.19	-	-0.16	-	
KRR1	-	-	-	-0.04	-	-0.18	-	
RAB5B	-	-	-	0.27	-	-0.15	-	
ARL14EP	-	-	-	-0.01	-	-0.03	-	
DENND1A	-	-	-	0.14	-	0.08	-	
THADA	-	-	-	-0.22	-	-0.20	-	
MAPRE1	-	-	-	-0.35	-	-0.27	-	
AOPEP	-	-	-	0.40^{a}	-	-0.15	-	
SUOX	-	-	-	0.11	-	0.25	-	
SUMO1P1	-	-	-	0.12	-	-	-	
FBN3	-	-	-	-0.28	-	0.20	-	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S25

Pearson's correlation coefficients (R) between mRNA expression levels of *FSHR* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[ǂ]
age (days)	0.24	0.16	-0.41^{a}	-0.50^{b}	-0.28	-0.30	-0.45^{b}	2-
FSHB	-	-	-	-0.14	-	-0.06	-	-
FSHR	*	*	*	*	*	*	*	
LHCGR	-0.39	0.74^{d}	0.68^{d}	0.00	0.26	0.73^{d}	0.59^{c}	4+
AR	0.16	-0.11	0.61^{c}	0.56^{b}	0.03	0.64^{d}	0.67^{d}	4+
AMH	0.35	0.40^{a}	-0.35^{a}	0.05	0.03	-0.35^{a}	-0.08	
INSR	0.07	0.64^{c}	-0.35^{a}	-0.12	-0.34^{a}	-0.44^{a}	-0.46^{b}	1+, 1-
FDFT1	-0.04	0.69^{c}	0.56^{c}	0.27	-0.13	0.08	-0.10	2+
ERBB3	0.36	0.68^{c}	0.88^{d}	-0.53^{b}	-0.10	0.56^{c}	0.54^{b}	4+, 1-
ERBB4	-0.45	-0.01	0.17	-0.40^{a}	0.97^{d}	-0.29	0.02	1+
PLGRKT	-0.15	0.14	-0.59^{c}	-0.25	-0.20	0.00	-0.31	1-
HMGA2	-0.61^{b}	-0.37	0.67^{d}	0.64^{c}	0.82^{d}	0.59^{c}	0.45^{b}	5+, 1-
TOX3	0.47^{a}	-0.21	0.37^{a}	-0.31	0.34^{a}	-0.17	0.08	
GATA4	0.79^{d}	0.64^{c}	0.20	0.59^{b}	0.66^{d}	-0.14	0.03	4+
YAP1	-0.45	-0.35	0.41^{a}	0.01	0.85^{d}	0.62^{c}	0.63^{c}	3+
ZBTB16	0.15	-0.21	-0.17	-0.12	0.14	0.47^{b}	0.77^{d}	2+
IRF1	0.39	0.42^{a}	0.18	-0.30	-0.21	0.20	0.11	
NEIL2	0.36	0.63^{c}	0.58^{c}	0.41^{a}	0.05	-0.09	-0.12	2+
RAD50	0.10	0.21	0.57^{c}	0.31	0.32	0.41^{a}	0.38^{a}	1+
KRR1	-0.06	0.06	0.17	-0.06	0.04	0.38^{a}	0.27	
RAB5B	-0.17	0.48^{a}	0.39^{a}	-0.11	0.19	0.09	0.05	
ARL14EP	-0.21	-0.13	-0.16	-0.04	0.32	-0.05	-0.26	
DENND1A	0.68^{b}	0.14	0.50^{b}	-0.09	0.20	-0.34	-0.10	2+
THADA	0.32	0.14	0.69^{d}	-0.05	0.42^{b}	0.43^{a}	0.47^{b}	3+
MAPRE1	0.08	0.70^{d}	0.58^{c}	0.33	0.26	0.22	0.26	2+
AOPEP	-0.01	-0.24	-0.66^{d}	-0.55^{b}	-0.18	0.35^{a}	0.57^{c}	1+, 2-
SUOX	-0.08	-0.12	-0.32	-0.11	-0.20	-0.14	0.30	
SUMO1P1	0.38	0.27	0.23	0.40^{a}	-0.13	-	-0.15	
FBN3	0.24	-0.25	0.62^{d}	0.32	0.85^{d}	0.01	0.10	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S26

Pearson's correlation coefficients (R) between mRNA expression levels of *LHCGR* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	-0.42	0.20	-0.03	-0.12	-0.46[b]	-0.37[a]	-0.61[c]	2-
FSHB	-	-	-	-0.03	-	-0.110	-	
FSHR	-0.39	0.74[d]	0.68[d]	0.00	0.26435	0.732[d]	0.58[c]	4+
LHCGR	*	*	*	*	*	*	*	
AR	-0.43	-0.12	0.81[d]	0.36	-0.18	0.65[d]	0.70[d]	3+
AMH	-0.17	0.65[c]	-0.20	0.36	-0.05	-0.34	-0.02	1+
INSR	-0.18	0.84[d]	-0.32	0.17	-0.36[a]	-0.45[b]	-0.61[c]	1+, 2-
FDFT1	0.50[a]	0.92[d]	0.14	-0.04	0.52[b]	0.11	-0.25	2+
ERBB3	0.08	0.53[b]	0.60[c]	-0.45[a]	0.01	0.52[b]	0.87[d]	4+
ERBB4	0.87[d]	-0.27	-0.08	-0.24	0.27	-0.49[b]	-0.07	1+, 1-
PLGRKT	0.57[a]	0.32	-0.31	-0.21	0.25	0.03	-0.34	
HMGA2	0.52[a]	-0.58[b]	0.18	0.13	0.41[a]	0.68[d]	0.68[d]	2+, 1-
TOX3	-0.27	-0.45[a]	0.06	-0.30	0.54[c]	-0.22	0.01	1+
GATA4	-0.64[b]	0.66[c]	-0.19	0.05	0.42[a]	-0.19	0.05	1+, 1-
YAP1	0.71[c]	-0.57[b]	0.21	0.05	0.41[a]	0.69[d]	0.80[d]	3+, 1-
ZBTB16	0.03	-0.17	-0.25	-0.39[a]	0.04	0.53[b]	0.89[d]	2+
IRF1	-0.53[a]	0.48[a]	-0.01	-0.28	-0.24	0.29	0.07	
NEIL2	-0.34	0.73[d]	0.30	0.26	-0.10	-0.19	-0.20	1+
RAD50	0.05	0.00	0.29	0.20	0.04	0.39[a]	0.38[a]	
KRR1	0.23	-0.21	0.19	0.20	-0.19	0.28	0.37[a]	
RAB5B	0.29	0.33	0.19	-0.46[a]	0.03	0.01	0.02	
ARL14EP	0.45	-0.20	0.13	0.35	0.42[a]	-0.15	-0.28	
DENND1A	-0.51[a]	0.24	-0.06	-0.49[b]	-0.08	-0.37[a]	0.00	1-
THADA	0.09	0.09	0.33	-0.16	0.23	0.47[b]	0.68[d]	2+
MAPRE1	0.34	0.62[c]	0.23	0.22	0.05	0.19	0.35	1+
AOPEP	-0.06	-0.16	-0.33	-0.46[a]	0.01	0.51[b]	0.91[d]	2+
SUOX	0.04	-0.12	-0.17	-0.53[b]	0.02	0.22	0.34	1-
SUMO1P1	-0.33	0.01	0.03	0.00	0.30	-	-0.18	
FBN3	-0.22	-0.44[a]	0.21	0.22	0.28	0.20	0.12	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S27

Pearson's correlation coefficients (R) between mRNA expression levels of *AR* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	Ovary (N=18)	Testis (N=27)	Heart (N=38)	Kidney (N=29)	Liver (N=37)	Cerebellum (N=33)	Brain (N=32)	Number of organs[‡]
age (days)	0.51^{a}	0.85^{d}	0.16	0.09	0.65^{d}	-0.58^{c}	-0.75^{d}	2+, 2-
FSHB	-	-	-	0.22	-	-0.16	-	
FSHR	0.16	-0.11	0.61^{c}	0.56^{b}	0.03	0.64^{d}	0.67^{d}	4+
LHCGR	-0.43	-0.12	0.81^{d}	0.36	-0.18	0.65^{d}	0.70^{d}	3+
AR	*	*	*	*	*	*	*	
AMH	-0.26	-0.34	-0.36^{a}	-0.06	-0.27	-0.43^{a}	0.03	
INSR	0.01	-0.01	-0.31	0.15	0.24	-0.42^{a}	-0.69^{d}	1-
FDFT1	-0.18	-0.16	0.02	-0.13	-0.26	0.42^{a}	-0.11	
ERBB3	0.08	-0.18	0.49^{b}	-0.36	0.17	0.59^{c}	0.58^{c}	3+
ERBB4	-0.35	-0.27	0.04	-0.06	0.05	-0.27	0.09	
PLGRKT	-0.37	-0.48^{a}	-0.11	0.04	0.19	0.16	-0.19	
HMGA2	-0.31	-0.49^{a}	-0.03	0.19	-0.05	0.92^{d}	0.85^{d}	2+
TOX3	0.28	-0.25	-0.08	-0.08	-0.13	0.15	0.36^{a}	
GATA4	0.25	-0.49^{a}	-0.24	0.39^{a}	-0.17	-0.12	0.02	
YAP1	-0.15	0.27	0.40^{a}	0.11	0.01	0.94^{d}	0.93^{d}	2+
ZBTB16	0.32	0.52^{b}	-0.22	-0.07	0.52^{c}	0.80^{d}	0.84^{d}	4+
IRF1	0.52^{a}	0.67^{c}	-0.01	0.10	0.52^{c}	0.10	0.17	2+
NEIL2	0.31	-0.11	0.28	0.39^{a}	0.20	-0.22	-0.33	
RAD50	0.59^{b}	0.21	0.42^{a}	0.35	0.27	0.69^{d}	0.51^{b}	3+
KRR1	0.16	0.39	0.40^{a}	0.16	0.41^{a}	0.56^{c}	0.56^{c}	2+
RAB5B	0.29	0.20	0.36^{a}	0.07	0.49^{b}	0.26	0.09	1+
ARL14EP	0.18	0.53^{b}	0.27	0.31	0.15	-0.06	-0.21	1+
DENND1A	0.19	-0.30	-0.12	-0.28	-0.29	-0.36^{a}	-0.02	
THADA	0.27	-0.06	0.42^{a}	-0.16	0.03	0.87^{d}	0.86^{d}	2+
MAPRE1	0.13	-0.35	0.38^{a}	0.09	0.28	0.53^{b}	0.59^{c}	2+
AOPEP	-0.16	0.09	-0.39^{a}	-0.36	-0.23	0.57^{c}	0.83^{d}	2+
SUOX	-0.09	-0.31	-0.32	-0.26	-0.21	-0.08	0.45^{a}	
SUMO1P1	-0.08	0.10	0.17	0.59^{b}	-0.20	-	-0.15	1+
FBN3	-0.34	-0.62^{c}	0.03	-0.02	-0.02	0.07	-0.07	1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Table S28

Pearson's correlation coefficients (R) between mRNA expression levels of *AMH* and PCOS candidate genes in fetal organs and the number of organs with significant ($P < 0.01$) correlations.

Genes	**Ovary (N=18)**	**Testis (N=27)**	**Heart (N=38)**	**Kidney (N=29)**	**Liver (N=37)**	**Cerebellum (N=33)**	**Brain (N=32)**	**Number of organs**[†]
age (days)	-0.17	0.00	-0.33	-0.55[b]	-0.25	0.04	-0.34	1-
FSHB	-	-	-	-0.11	-	0.07	-	
FSHR	0.35	0.40[a]	-0.35[a]	0.05	0.03	-0.35[a]	-0.08	
LHCGR	-0.17	0.65[c]	-0.2	0.36	-0.05	-0.34	-0.02	2+
AR	-0.26	-0.34	-0.36[a]	-0.06	-0.27	-0.43[a]	0.07	
AMH	*	*	*	*	*	*	*	
INSR	0.12	0.73[d]	-0.13	-0.16	-0.03	-0.17	-0.37[a]	1+
FDFT1	-0.50[a]	0.61[c]	-0.33	0.23	-0.41[a]	0.14	0.27	1+
ERBB3	-0.22	0.59[b]	-0.34[a]	-0.55[b]	0.09	-0.38[a]	-0.22	1+, 1-
ERBB4	-0.37	-0.48[a]	-0.43[a]	-0.77[d]	0.04	-0.31	-0.14	1-
PLGRKT	0.37	0.61[c]	-0.02	-0.67[c]	-0.35[a]	0.45[b]	0.48[b]	3+, 1-
HMGA2	-0.16	-0.55[b]	-0.12	0.53[b]	-0.03	-0.33	-0.04	1+, 1-
TOX3	-0.13	-0.69[d]	-0.05	-0.60[c]	-0.19	-0.04	0.08	2-
GATA4	0.34	0.72[d]	0.09	0.18	0.11	-0.06	0.34	1+
YAP1	-0.39	-0.86[d]	-0.60[c]	-0.46[a]	-0.11	-0.40[a]	-0.10	2-
ZBTB16	-0.52[a]	-0.35	-0.42[a]	-0.12	-0.38[a]	-0.38[a]	-0.19	
IRF1	-0.25	0.09	-0.31	-0.32	-0.29	-0.34	-0.23	
NEIL2	-0.24	0.63[c]	-0.08	0.56[b]	-0.31	-0.07	-0.23	2+
RAD50	-0.67[b]	-0.56[b]	-0.64[d]	-0.33	-0.55[c]	-0.62[c]	-0.45[a]	5-
KRR1	-0.33	-0.48[a]	-0.53[b]	-0.42[a]	-0.43[b]	-0.53[b]	-0.27	3-
RAB5B	-0.76[c]	-0.34	-0.71[d]	-0.54[b]	-0.58[c]	-0.76[d]	-0.51[b]	6-
ARL14EP	-0.23	-0.38	-0.31	-0.40[a]	-0.15	-0.37[a]	-0.33	
DENND1A	0.24	0.15	-0.32	0.15	-0.22	0.02	-0.18	
THADA	-0.51[a]	-0.13	-0.59[c]	-0.46[a]	-0.27	-0.38[a]	-0.07	1-
MAPRE1	-0.55[a]	0.19	-0.31	0.05	-0.65[d]	-0.22	0.03	1-
AOPEP	0.67[b]	0.32	0.39[a]	-0.24	0.51[b]	-0.19	-0.04	2+
SUOX	0.00	0.17	0.63[d]	-0.04	0.44[b]	0.18	0.24	2+
SUMO1P1	0.32	-0.05	-0.03	-0.16	-0.27	-	-0.01	
FBN3	0.74[c]	-0.21	0.13	0.80[d]	0.07	0.09	-0.38[a]	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '-' and '*' indicate no gene expression and correlation between same gene, respectively.

Chapter 5

Expression of TGFβ Signalling Molecules and Candidate Genes for Polycystic Ovary Syndrome in Human Fetal and Adult Gonadal, Metabolic and Brain Tissues

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Contribution to the Paper	Took part in study designed performed data and statistical analyses, data interpretation and discussion as well as manuscript writing.		
Overall percentage (%)	70 %		
Certification:	This paper reports on original research I conducted during the period of my Higher Degree by Research candidature and is not subject to any obligations or contractual agreements with a third party that would constrain its inclusion in this thesis. I am the primary author of this paper.		
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By signing the Statement of Authorship, each author certifies that:

i. the candidate's stated contribution to the publication is accurate (as detailed above);

ii. permission is granted for the candidate in include the publication in the thesis; and

iii. the sum of all co-author contributions is equal to 100% less the candidate's stated contribution.

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TGFβ signalling molecules and genes for polycystic ovary syndrome in human tissues.

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Abstract

Polycystic Ovary Syndrome (PCOS) patients present with varying symptoms including reproductive, endocrine, metabolic and sometimes psychological symptoms. Current theories have attributed high levels of androgens or anti-Mullerian hormone (AMH) during fetal development to the establishment of PCOS phenotypes in later life. Our previous studies showed that TGFβ1, rather than these hormones, altered expression in cultured fetal ovarian fibroblasts of 7 of 25 genes in loci associated with PCOS. However, the relationship between TGFβ signalling molecules and PCOS candidate genes is still unknown. Here, we examined the expression patterns of TGFβ signalling molecules in gonadal, metabolic and brain tissues, and examined relationships with expression of PCOS candidate genes during the first half of human fetal development and postnatally until adulthood, using publicly available RNA sequencing data. Generally, the TGFβ signalling molecules were dynamically expressed in most tissues during prenatal or/and postnatal development. *FBN3* was only expressed during fetal development in all tissues. Genes in loci associated with PCOS such as *HMGA2, YAP1* and *RAD50* correlated significantly with most TGFβ signalling molecules in at least 4 fetal tissues and specifically with *TGFBR1* in 6 out of 7 tissues. The findings of this study suggest that possible crosstalk between genes in loci associated with PCOS and TGFβ signalling molecules occurs in various tissues particularly during fetal development.

Introduction

Polycystic Ovary Syndrome (PCOS) is a polygenic reproductive/endocrine disorder that affects 10% women of reproductive age of which 72% suffer infertility due to anovulation (Joham, et al. 2015). The syndrome presents varying symptoms ranging from endocrine features including hyperandrogenism leading to hirsutism, acne or alopecia; reproductive features including menstrual irregularities and infertility; metabolic features such as insulin resistance, obesity, hyperinsulinaemia, type 2 diabetes mellitus; and cardiovascular features including atherogenic dyslipidaemia, elevated blood pressure and increased circulating proinflammatory markers (Anagnostis, et al. 2018; Comerford, et al. 2012; Echiburú, et al. 2016; Glueck and Goldenberg 2019; Hart, et al. 2004; Hart, et al. 2011; Stuckey, et al. 2014; Teede, et al. 2010). The syndrome also affects the psychological health of patients, causing anxiety and depression as well as sleep disorders (Fernandez, et al. 2018). More so, the ovaries of PCOS women are morphologically distinct, having numerous antral follicles and more fibrous stroma (Buckett, et al. 1999; Hughesdon 1982; Stein 1935). Despite the many non-reproductive aspects, PCOS is currently diagnosed using reproductive symptoms. The key criteria for PCOS diagnosis commonly used, the Rotterdam criteria, require two of the following three: hyperandrogenism (biochemical or clinical), polycystic ovarian morphology (PCOM) or oligo/anovulation observed on ultrasound, after exclusion of all other differential diagnoses (Teede, et al. 2018).

The heterogeneity of PCOS phenotypes in women has had a great impact on the definition, diagnosis and treatment of the syndrome. The disorder presents varying symptoms/phenotypes in different age groups (adolescents, peri- or post-menopausal women) as reviewed in detail by Lizneva, et al. (2016). Furthermore, of the numerous metabolic symptoms associated with PCOS, obesity and type 2 diabetes have long-term consequences for patients (Conway, et al. 2014; Macut, et al. 2017). More so, over 50% of women with PCOS of Chinese Han ancestry had up to a 30% decrease in insulin sensitivity and this was exacerbated by obesity (Li, et al. 2018). Thus, BMI was associated with insulin resistance in these PCOS women with prevalence increasing from 34.5%, 80.2% to 98.7% in lean, overweight and obese women with PCOS, respectively (Li et al. 2018). Previous studies have also shown that insulin could further stimulate the accumulation of androgens in ovarian stromal cells from hyperandrogenic women (Barbieri, et al. 1986). However, it is not entirely clear when and how these phenotypes develop as the disorder progresses.

Although recent studies have focused on the genetics of PCOS, it is also evident from animal studies that fetal exposures such as to hormones (androgens and AMH) and diet during pregnancy play a role in PCOS (Birch, et al. 2003; Dumesic, et al. 1997; Risal, et al. 2019; Sullivan and Moenter 2004; Tata, et al. 2018; Wu, et al. 2010). A link between the genetic and fetal predisposition became evident when studies identified that PCOS candidate genes including those in loci identified in GWAS and microsatellite genotyping are dynamically expressed in human and bovine fetal ovaries (Azumah, et al. 2022a; Hartanti, et al. 2020; Hatzirodos, et al. 2011; Liu, et al. 2020). A recent study in the developing bovine fetal ovary found that PCOS candidate genes were co-expressed with genes involved in mitochondrial function (*C8H9orf3, TOX3, FBN3, GATA4, HMGA2* and *DENND1A*), stroma expansion (*YAP1, INSR, THADA* and *TGFB1I1*) and steroidogenesis (*FDFT1, LHCGR, AMH, FSHR, ZBTB16* and *PLGRKT*) (Azumah et al. 2022a). Studies on the fetal origins of PCOS have focused on the effects of androgens (Birch et al. 2003; Dumesic et al. 1997; Risal et al. 2019; Sullivan and Moenter 2004; Wu et al. 2010) and more recently AMH (Tata et al. 2018) and transforming growth factor beta (TGFβ). TGFβ is a good candidate as it regulates stroma and its collagen content (Raja-Khan, et al. 2014; Walters, et al. 2022) and the adult polycystic ovary has more stroma and is more collagen rich (Buckett et al. 1999; Hughesdon 1982; Lesnoy 1928; Stein 1935).

TGFβ1 is not only essential in development and cell differentiation (Wu & Hill, 2009; Zinski et al, 2018) but it is important for reproduction. TGFβ1 protein was detected in bovine granulosa cells of early pre-antral and antral follicles (1-2 cm) but was not observed in later stages (Nilsson, et al. 2003). *TGFB1* null mice had perturbed function of the hypothalamic–pituitary–gonadal axis, which resulted in a reduction in luteinising hormone levels, further resulting in reduced serum androstenedione and testosterone production in males and abnormalities of the oestrous cycle in females (Ingman and Robertson 2007; Ingman, et al. 2006). Notably, oocyte developmental incompetence due to a TGFβ1 deficient follicular environment has also been associated with early embryo arrest in mice (Ingman and Robertson 2009; Ingman et al. 2006). TGFβ signalling molecules are known to be expressed during the development of the ovary and have been postulated to be involved in the aetiology of PCOS, thus linking the possible genetic and fetal disposition to PCOS in adulthood and additionally to the PCOS ovarian phenotype (Azumah et al. 2022a; Azumah, et al. 2022b; Hartanti et al. 2020; Hatzirodos et al. 2011; Liu et al. 2020). TGFβ signalling molecules including *TGFB1/2/3* appear to be upstream regulators during stroma expansion of the developing fetal ovary (Azumah et al. 2022a). TGFβ1, but not AMH nor androgen, has been shown to regulate a proportion of PCOS candidate genes in fetal ovarian cells (Azumah et al. 2022b; Hartanti et al. 2020). Thus, expression of some genes in loci associated with PCOS including *INSR, C8H9orf3, RAD50, ERBB3, NEIL2, IRF1* and *ZBTB16,* were inhibited by TGFβ1 in fetal ovarian fibroblasts *in vitro* (Azumah et al. 2022b; Hartanti et al. 2020). Notably, androgen receptor (*AR*) expression was also inhibited, while its cofactor TGFβ induced transcript 1 (*TGFB1I1*) was stimulated by TGFβ1 in cultured fetal ovarian stromal cells (Azumah et al. 2022b; Hartanti et al. 2020). These observations further affirm the significance of TGFβ in PCOS pathogenesis.

Not surprisingly many of the fetal studies have focused on the ovary. Only more recently with the use of tissue specific knock outs (Cox, et al. 2020; Roy, et al. 2022) and direct examination of PCOS candidate genes in other fetal organs (Azumah, et al. 2023) have other organs involved in the non-reproductive symptoms of PCOS been specifically examined. We hypothesise that TGFβ signalling molecules could be regulating genes in loci associated with PCOS, not only in the fetal ovary, but also in other developing fetal tissues and organs likely involved in non-reproductive symptoms of PCOS. Additionally, TGFβ signalling molecules could be regulating other downstream genes/pathways leading to PCOS later in life. The current study seeks to understand the patterns of expression of TGFβ signalling molecules in different tissues. Although some of these have been previously studied such as in the fetal ovary (Azumah et al. 2022a; Azumah et al. 2022b; Hartanti et al. 2020; Hatzirodos et al. 2011; Liu et al. 2020) their expression relationships with PCOS candidate genes has not been examined. To achieve this, we used publicly available RNA sequencing data from various human fetal and adult tissues. The TGFβ signalling molecules examined included TGFβs, of which there are three (TGFB1 to 3), their latent TGFβ binding proteins of which there are four (LTBP1 to 4), the fibrillins that they bind to, of which there are three (FBN1 to 3) and TGFβ receptors of which there are three different types (TGFBR1 to 3), and other related genes [Transforming Growth Factor Beta 1 Induced Transcript 1 (*TGFB1I1*), Transforming Growth Factor Beta Receptor 3 Like (*TGFBR3L*), Transforming Growth Factor Beta Induced (*TGFBI*), Transforming Growth Factor Beta Receptor Associated Protein 1 (*TGFBRAP1*)]. The expression levels of the PCOS candidate genes are published elsewhere (Azumah et al. 2023).

Materials and methods

Data extraction and analysis

We analysed normalised (counts per million) human RNA-seq data deposited in Array Express (E-MTAB-6814) from the ‘*Gene expression across mammalian organ development*’ project (Cardoso-Moreira, et al. 2019). The prenatal samples in that project were provided by the MRC Wellcome Trust Human Developmental Biology Resource based in the United Kingdom. They were from elective abortions with normal karyotypes. Postnatal samples were provided by the NICHD Brain and Tissue Bank for Developmental Disorders at the University of Maryland, USA, and by the Chinese Brain Bank Center in Wuhan, China. They originated from individuals with diverse causes of death that, given the information available, were not associated with the organ sampled. The organs in this project were sampled from the three germ layers: the ectoderm made up of brain (forebrain/cerebrum) and cerebellum (hindbrain/cerebellum); the mesoderm made up of heart, kidney, ovary and testis; and the endoderm consisting of the liver. The expression of TGFβ family genes (*TGFB1*, *TGFB2*, *TGFB3*, *LTBP1*, *LTBP2*, *LTBP3*, *LTBP4*, *FBN1*, *FBN2*, *FBN3*, *TGFBR1*, *TGFBR2*, *TGFBR3*, *TGFB1I1*, *TGFBR3L*, *TGFBI*, *TGFBRAP1*) was studied in all 7 tissues from fetuses [4-20 weeks post conception (wpc); but missing 14, 15 and 17 wpc], from 5 tissues at birth until adulthood, and for kidney until 8 years. There were no postnatal ovary tissues available. Postnatally, we grouped the samples as prepubertal (from birth until 9 years), pubertal (13-19 years) and adulthood (each decade until 65 years of age). For testis samples, 13-14 years were considered as early puberty, and 15-19 years as late puberty as grouped in the original study (Cardoso-Moreira et al. 2019). Supplementary Table S1-3 shows the specific details for each tissue sample used.

The tissues were grouped according to function; gonads (ovary and testis), metabolic tissues (liver, kidney, and heart), and brain tissues (brain and cerebellum). The TGFβ family was grouped functionally: TGFβs, (*TGFB1*, *TGFB2*, *TGFB3*), latent TGFβ binding proteins (LTBPs) (*LTBP1*, *LTBP2*, *LTBP3*, *LTBP4)*, fibrillins (*FBN1*, *FBN2*, *FBN3*), TGFβ receptors (*TGFBR1*, *TGFBR2*, *TGFBR3*) and others (*TGFB1I1*, *TGFBR3L*, *TGFBI*, *TGFBRAP1*). Expression levels of TGFβ family genes studied previously (Azumah et al. 2022b) were extracted from normalised counts and further analysed. Specifically, time-course scatterplots were generated for TGFβ signalling molecules using ggplot2 package in R (Wickham, et al. 2016). Pearson's correlation was then carried out for fetal samples of each tissue separately for firstly, TGFβ signalling molecules with each other and secondly with PCOS candidate genes [IBM SPSS Statistics for Windows, version 25 (IBM Corp., Armonk, NY, USA)]. The correlation of each gene with each other within each tissue was then compared with that in the other tissues and the output collated based on all significant correlations (*P* <0.01).

Results

TGFβ Signalling Molecules: Expression in Fetal Tissues

The expression of the TGFβ family of genes was studied in 7 tissues (ovary, testis, heart, liver, kidney, brain and cerebellum) in fetal tissues until mid-gestation (4-20 wpc). All the genes were dynamically expressed across all tissues with few exceptions as stated below. Although, there were fewer female samples than males, there was no difference in gene expression observed between the two sexes in the same tissues, excluding the gonads. We compared the gene expression among different tissues and found that some genes were significantly expressed in gonadal tissues, whilst others were expressed in the metabolic or brain tissues at different time points prenatally.

TGFB1 (Supplementary Fig. S1A) and *TGFB2* (Fig. 1) expression was highest at 4 weeks in both gonadal and metabolic tissues and in general, levels in all tissues decreased as the fetuses developed. *TGFB2* and *TGFB3* (Fig. 1 and Supplementary Fig. S1B) expression increased at 16 wpc in the testis until 20 wpc; and at 16 weeks in the heart. *TGFB1* expression was low in both brain tissues and levels decreased and remained low until mid-gestation. *TGFB2* expression increased with gestational age in the cerebellum but remained low in the brain. *TGFB3* was least expressed in both brain tissues. *TGFB2* was only expressed early in fetal liver development but *TGFB3* was not expressed in the fetal tissues.

LTBP1/2/3/4 (Fig. 2 and Supplementary Fig. S2) were dynamically expressed in most tissues with least expression in the fetal brain tissues. *LTBP1* (Supplementary Fig. 2) expression was expressed highest in the heart early in gestation and then slowly declined. In all other tissues, its expression was relatively constant. The expression of *LTBP2* (Supplementary Fig. S2A) increased in the ovary, testis and heart during gestation, but remained relatively constant and quite low in kidney, and both brain tissues. *LTBP3* and *4* (Supplementary Fig. S2B and C) were the most highly expressed LTBPs in the fetal testis and their expression increased throughout the gestational period studied. The expression of both these genes in the ovary remained steady, similar to heart and liver. The expression in the liver was the lowest of the metabolic tissues and remained constant. *LTBP3* expression increased in both brain tissues, whereas *LTBP4* was constantly low. *LTBP2/4* were not expressed in the fetal liver tissues.

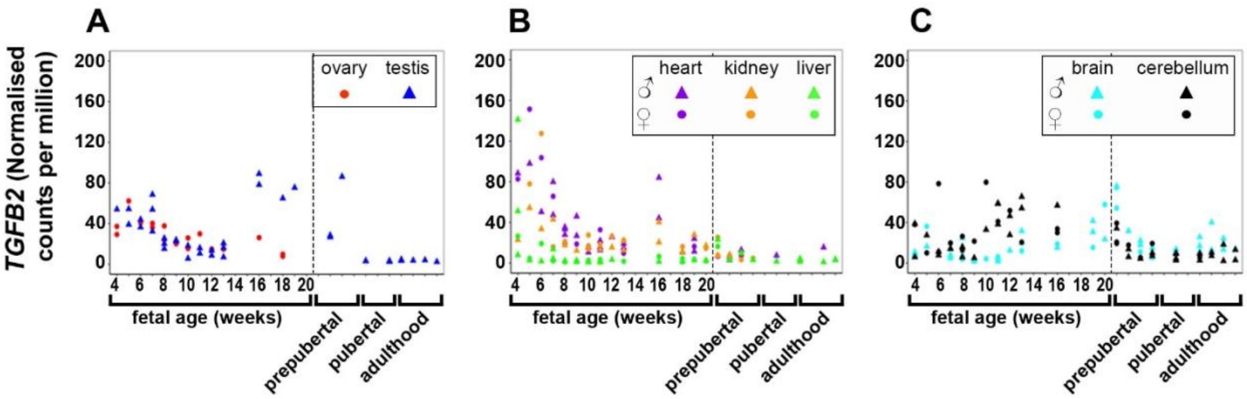

Fig. 1. Expression of *TGFB2* in gonadal, metabolic and brain tissues during the first half of fetal development and during lifetime. Short dashes distinguish fetal samples from the postnatal one.

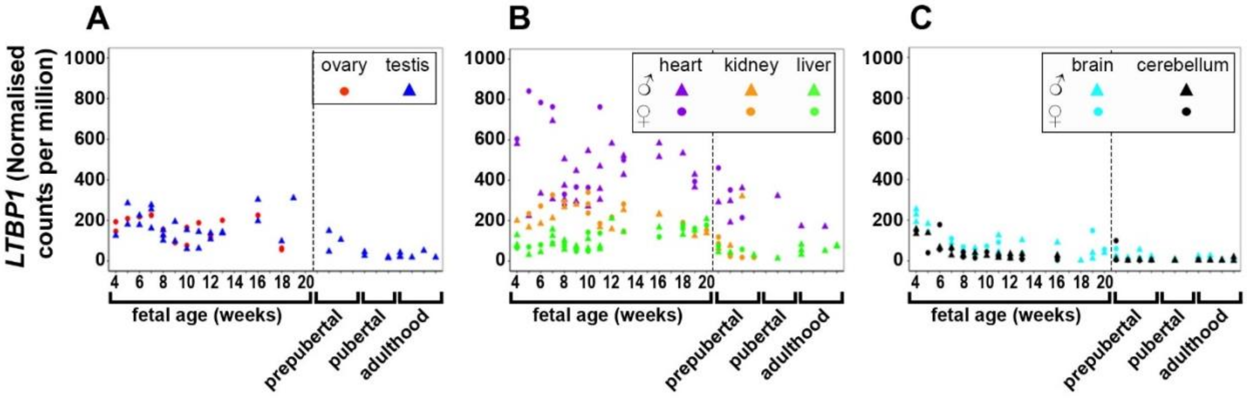

Fig. 2. Expression of *LTBP1* in gonadal, metabolic and brain tissues during the first half of fetal development and during lifetime. Short dashes distinguish fetal samples from the postnatal one.

FBN1/2/3 were dynamically across many fetal tissues with the least expression in the fetal liver. *FBN1* (Supplementary Fig. S3A) expression remained constant in the ovary, kidney, liver tissues and both brain tissues although levels decreased until 6 wpc in both brain tissues. The expression of *FBN1* in the heart was constant except for one male heart sample at 16 wpc, which showed an extremely high level. Expression of *FBN1* and *FBN2* increased in testis until 16 wpc and levels decreased thereafter. *FBN2* (Supplementary Fig. S3B) expression remained constant in the ovary tissues and both brain tissues but levels decreased until 8 wpc in both brain tissues. While *FBN2* was not expressed in the liver tissues prenatally, it was most expressed in the early stages (first trimester) in heart tissues after which levels decreased towards mid-gestation. Both *FBN1* and *FBN2* were least expressed in the liver and both brain tissues. However, *FBN3* (Fig. 3) was highest early in gestation in all tissues except in the brain tissues and then decreased towards mid-gestation. Expression was the same in both cerebellum and brain tissues during the earlier stages but increased towards mid-gestation in only brain tissues; although there were no cerebellum tissues at this stage. Notably, *FBN3* is the fibrillin which is most expressed in brain tissues.

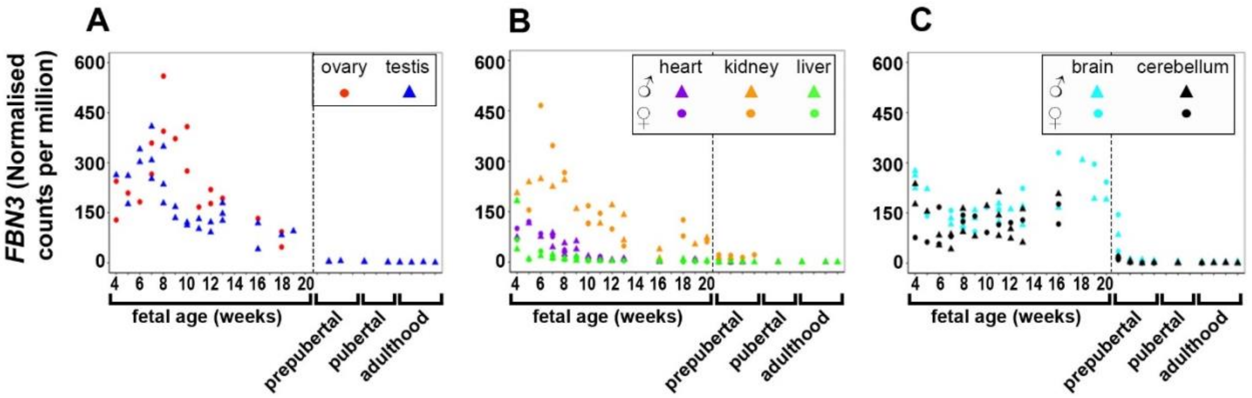

Fig. 3. Expression of *FBN3* in gonadal, metabolic and brain tissues during the first half of fetal development and during lifetime. Short dashes distinguish fetal samples from the postnatal one.

TGFBR1 (Fig. 4) expression was highest early in gestation across all tissues, the brain tissues having the highest levels, and then declined towards mid-gestation. *TGFBR2* (Supplementary Fig. S4A) expression increased across gestation in the testis and metabolic tissues, but remained very low and constant in the brain tissues and the ovary tissues. *TGFBR3* (Supplementary Fig. S4B) expression increased in the testis and kidney, decreased in the ovary and liver but remained constant in the heart and both brain tissues.

In most tissues, expression of *TGFB1I1* (Supplementary Fig. S5A) remained relatively constant and low, except for testis where it increased towards mid-gestation and for heart where the expression drastically increased towards 10 wpc and then dropped at 16 wpc to increase again at 18 and 20 wpc. *TGFB1I1* was not expressed in the fetal liver. *TGFBR3L* (Supplementary Fig. S5B) expression was either very low or nil in all fetal. *TGFBI* (Supplementary Fig. S5C) expression was high at early gestation in heart and brain tissues and then declined. In the ovary and testis, a small increase up to 8 wpc could be observed, which then declined and stayed low in the ovary and increased in the testis from 16 wpc onwards again. *TGFBI* was constantly expressed in liver and kidney, whereby an increase towards 20 wpc occurred. *TGFBRAP1* (Supplementary Fig. S5D) was dynamically expressed with levels remaining constant across all tissues.

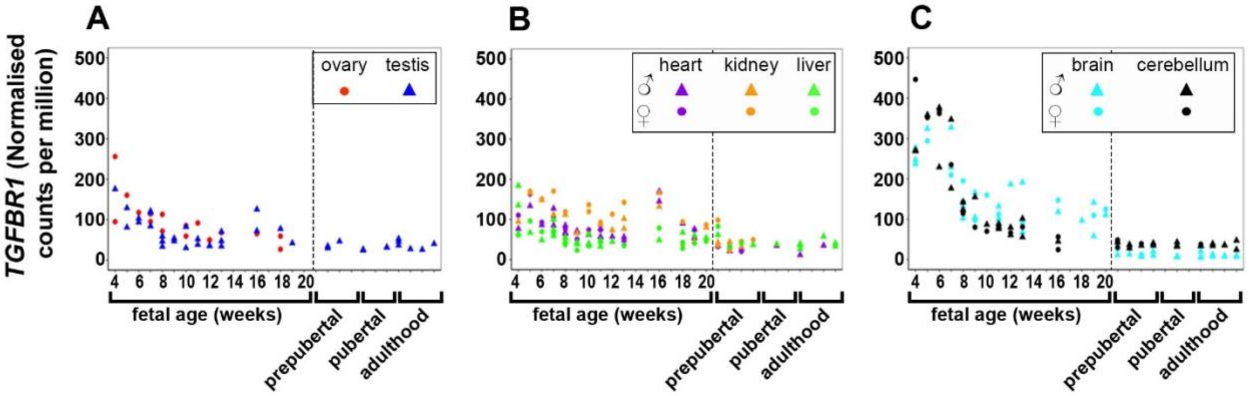

Fig. 4. Expression of *TGFBR1* in gonadal, metabolic and brain tissues during the first half of fetal development and during lifetime. Short dashes distinguish fetal samples from the postnatal one.

TGFβ Signalling Molecules: Relationships in Fetal Tissues

Pearson's correlations of the expression of genes within each fetal tissue were carried out between the genes and gestational age and the outcomes were tabulated in Tables 1-5 and Supplementary Tables S4-S16. Where description of significance involved more than two tissues or genes, the direction of correlation (negative or positive) are generally omitted from the text here, to minimise the complexity in the presentation of the results. However, these details can be observed in the respective tables for each gene.

In the ovary only *LTBP2* significantly correlated positively with gestational age (Table 1), while *TGFB1/2*, *LTBP1*, *FBN2*, *TGFBR1/2* correlated negatively. In the testis samples *FBN3* significantly correlated negatively with gestational age, whilst *TGFB3*, *LTBP2/3/4*, *FBN1/2*, *TGFBR2/3* and *TGFB1I1* correlated positively (Table 1). In the heart, *TGFB1/2*, and *FBN2/3* significantly correlated negatively with gestational age, while *FBN1* and *TGFBR1/2* correlated positively. In the kidney *LTBP2* and *TGFBR2* significantly correlated positively with gestational age, while *TGFB2/3, LTBP1, FBN2/3,* and *TGFBR1/3* correlated negatively. In the liver *LTBP1/2, TGFBR2, TGFBI, TGFBRAP1* significantly correlated with gestational age and *TGFB2, FBN1/2/3* and *TGFBR3* negatively. For brain and cerebellum tissues, *LTBP1*, *FBN1/2*, *TGFBR1/3* significantly correlated negatively with gestational age while *TGBFB2,* and *LTBP3* correlated positively. However, *TGFB3*, *FBN3* and *TGFBRAP1* significantly correlated positively, and *LTBP4* and *TGFBI* negatively with gestational age in brain only. *TGFBR3L* only positively correlated with gestational age in cerebellum. Thus, *LTBP1/2/3*, *FBN2/3,* and *TGFBR1/2/3* correlated significantly (P < 0.01) in at least three tissues.

TGFB1 (Supplementary Table S4) expression correlated with expression of most other genes in the brain tissues; *LTBP1/2/4*, *FBN1/2/3*, *TGFBR2/3* and *TGFBI* in cerebellum and *LTBP1*, *FBN1/2*, *TGFBR2/3*, *TGFB1I1* and *TGFBI* in brain. No correlations were observed in gonadal tissues. *TGFB2* (Table 2) correlated with *TGFB3, FBN1/2/3, TGFBR1* and *TGFBI* in at least three tissues. It correlated significantly with *LTBP1*, *FBN1/2,* and *TGFBR1/2* in both gonadal tissues, but with *TGFBR3* and *TGFBRAP1* in only the ovary and *TGFB3* and *TGFBR3L* in only the testis. *TGFB2* correlated with *LTBP2* negatively in the ovary, but positively in the testis. *TGFB3* (Supplementary Table S5) expression correlated significantly with *TGFB2, LTBP2/3/4, FBN1/2/3, TGFBR2/3, TGFB1I1,* and *TGFBI* in at least three tissues.

LTBP1 (Table 3) expression correlated significantly (P < 0.01) with *FBN1/2, TGFBR2,* and *TGFBI* in five out of seven tissues and with *TGFB2, LTBP2, TGFBR3,* and *TGFBRAP1* in at least three tissues. *LTBP2* (Supplementary Table S6) expression positively correlated with *TGFBR2* in all tissues except the ovary, where the correlation was negative, and with *TGFB3, LTBP2, FBN1/2,* and *TGFBI* in at least three tissues. *LTBP3* (Supplementary Table S7) correlated significantly with *TGFB1I1* in all tissues and *TGBFR3L* in at least five tissues and with *LTBP4,* and *TGFBI* in at least three tissues. *LTBP4* (Supplementary Table S8) expression correlated significantly ($P < 0.01$) with *TGFB1I1* in five tissues and with *TGFB3, LTBP3,* and *TGFBR1* in at least three tissues.

Table 1

Pearson's correlation coefficients (R) between mRNA expression levels of TGFβ signalling molecules and gestational age in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[ǂ]
TGFB1	-0.53[a]	-0.30	-0.61[c]	0.01	-0.29	-0.32	-0.25	1-
TGFB2	-0.75[c]	0.22	-0.54[c]	-0.42[a]	-0.34[a]	0.42[a]	0.50[b]	1+, 2-
TGFB3	-0.18	0.64[c]	0.18	-0.39[a]	-0.08	0.32	0.61[c]	2+
LTBP1	-0.48[a]	0.03	-0.11	-0.45[a]	0.70[d]	-0.71[d]	-0.54[b]	1+, 2-
LTBP2	0.55[a]	0.61[c]	0.22	0.69[d]	0.75[d]	-0.14	0.25	3+
LTBP3	0.03	0.61[c]	-0.22	0.03	-0.28	0.62[c]	0.48[b]	3+
LTBP4	0.25	0.69[c]	0.02	0.20	-0.32	-0.22	-0.60[c]	1+, 1-
FBN1	-0.49[a]	0.77[d]	0.35[a]	0.06	-0.23	-0.39[a]	-0.56[c]	1+, 1-
FBN2	-0.70[b]	0.56[b]	-0.38[a]	-0.22	-0.34[a]	-0.59[c]	-0.60[c]	1+, 3-
FBN3	-0.44	-0.73[d]	-0.77[d]	-0.73[d]	-0.46[b]	0.17	0.43[a]	4-
TGFBR1	-0.69[b]	-0.41[a]	-0.16	-0.51[b]	-0.40[a]	-0.84[d]	-0.66[d]	4-
TGFBR2	-0.62[b]	0.65[c]	0.63[d]	0.67[c]	0.51[b]	-0.21	-0.14	4+, 1-
TGFBR3	-0.46	0.62[c]	0.45[b]	0.55[b]	-0.59[c]	-0.49[b]	-0.60[c]	2+, 4-
TGFB1I1	-0.09	0.57[b]	0.25	0.29	-0.29	0.07	0.08	1+
TGFBR3L	-0.02	-0.17	-0.18	0.15	-0.01	0.54[b]	0.12	1+
TGFBI	-0.39	0.31	-0.12	0.13	0.63[d]	-0.29	-0.57[c]	1+, 1-
TGFBRAP1	-0.46	-0.07	-0.17	-0.27	0.39[a]	-0.02	0.35[a]	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

No *FBNs* were expressed in the liver. *FBN1* and *FBN2* (Supplementary Table S9 and S10, respectively) correlated significantly with each other in all other tissues except the heart. Both genes correlated with *LTBP1/2, TGBF1/2/3* and *TGFBI*, while *FBN2* only with *TGFB2* in at least three tissues. *FBN3* (Table 4) expression significantly correlated with *FBN1/2* and *TGFBR3* in the testis, with *TGFB1/2, TGFBR1/2* and *TGFBI* in the heart, and with *TGFB2/3, LTBP2*, and *TGFBR2/3* in the kidney.

Table 2

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFB2* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**Number of organs‡**
TGFB1	0.28	-0.07	0.60^c	-0.03	-0.05	0.16	-0.28	1+
TGFB2	*	*	*	*	*	*	*	
TGFB3	0.27	0.76^d	0.07	0.70^d	0.37^a	0.664^d	0.29	3+
LTBP1	0.69^b	0.70^d	0.54^c	0.14	0.00	0.05	-0.26	3+
LTBP2	-0.51^a	0.57^b	0.01	-0.25	-0.10	0.39^a	0.40^a	1+
LTBP3	-0.15	0.37	-0.14	0.27	-0.01	0.44^a	-0.09	
LTBP4	-0.12	0.11	-0.28	-0.30	0.67^d	-0.07	-0.45^b	1+, 1-
FBN1	0.75^c	0.62^c	0.38^a	0.23	0.85^d	0.37^a	-0.05	3+
FBN2	0.65^b	0.62^c	0.46^b	0.36	0.98^d	0.10	-0.11	4+
FBN3	0.13	0.00	0.79^d	0.54^b	0.89^d	0.23	0.40^a	3+
TGFBR1	0.72^c	0.64^c	0.76^d	0.54^b	0.82^d	-0.32	-0.18	5+
TGFBR2	0.80^d	0.73^d	0.01	-0.33	-0.05	0.44^a	-0.08	2+
TGFBR3	0.65^b	0.25	0.11	-0.17	0.74^d	0.23	-0.19	2+
TGFB1I1	0.18	-0.04	-0.76^d	-0.36	0.02	0.28	-0.36^a	1-
TGFBR3L	-0.18	-0.57^b	-0.27	-0.15	-0.31	0.30	-0.14	1-
TGFBI	0.47^a	0.77^d	0.72^d	0.32	0.07	0.40^a	-0.10	2+
TGFBRAP1	0.66^b	0.38	0.50^b	0.03	0.22	0.16	0.33	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. ‡Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

TGFBR1/2/3 (Table 5, Supplementary Tables S11 and S12, respectively) correlated significantly with *FBN1/2* in at least four tissues. *TGFBR1* (Table 5) correlated significantly ($P < 0.01$) with *TGFB2, LTBP4, TGFBR3,* and *TGFBR3L,* while *TGFBR2* (Supplementary Table S11) correlated with *LTBP1/2, TGFBR3,* and *TGFBI* in at least four tissues. *TGFBR3* (Supplementary Table S12) expression showed predominantly significant correlations in the brain tissues; with *TGFB1*, *LTBP1, FBN1/2, TGFBR1/2* and *TGFBI* in brain and cerebellum, and additionally with *LTBP2* in cerebellum only.

Table 3

Pearson's correlation coefficients (R) between mRNA expression levels of *LTBP1* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	Number of organs[ǂ]
TGFB1	0.35	0.17	0.33	-0.41[a]	-0.12	0.70[d]	0.52[b]	2+
TGFB2	0.69[b]	0.70[d]	0.54[c]	0.14	0.00	0.05	-0.26	3+
TGFB3	0.36	0.52[b]	0.16	0.32	-0.05	0.10	-0.28	1+
LTBP1	*	*	*	*	*	*	*	
LTBP2	-0.09	0.58[b]	0.23	-0.31	0.66[d]	0.49[b]	0.16	3+
LTBP3	-0.17	0.11	0.00	-0.48[a]	-0.28	-0.39[a]	-0.13	
LTBP4	0.14	0.09	0.08	-0.25	-0.06	0.32	0.17	
FBN1	0.84[d]	0.55[b]	0.47[b]	0.22	0.17	0.81[d]	0.79[d]	5+
FBN2	0.41	0.60[b]	0.71[d]	0.67[c]	0.02	0.93[d]	0.87[d]	5+
FBN3	-0.01	0.13	0.18	0.34	-0.14	0.16	0.11	
TGFBR1	0.40	0.44[a]	0.40[a]	0.46[a]	0.02	0.78[d]	0.63[c]	2+
TGFBR2	0.71[c]	0.576[b]	0.39[a]	-0.12	0.75[d]	0.58[c]	0.51[b]	5+
TGFBR3	0.63[b]	0.39[a]	0.07	-0.25	-0.16	0.86[d]	0.70[d]	3+
TGFB1I1	0.27	-0.12	-0.22	-0.14	-0.25	0.15	0.07	
TGFBR3L	-0.42	-0.60[b]	-0.32	-0.45[a]	-0.38[a]	-0.36[a]	-0.30	1-
TGFBI	0.33	0.72[d]	0.47[b]	0.03	0.62[d]	0.79[d]	0.84[d]	5+
TGFBRAP1	0.71[b]	0.49[a]	0.612[c]	0.63[c]	0.81[d]	0.06	0.14	4+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

TGFB1I1 (Supplementary Table S13) expression correlated significantly with *LTBP3/4* in at least five tissues and with *TGFBR1* and *TGFBI* in at least three tissues, whereby the correlations with *TGFBR1* in testis, heart and kidney were all negative. *TGFBR3L* (Supplementary Table S14) correlated significantly with *LTBP3* and *TGFBR1* in five out of seven tissues. *TGFBI* (Supplementary Table S15) correlated significantly ($P < 0.01$) and predominantly positively with *TGFB1/3, LTBP1/2/3, FBN1/2, TGFBR2,* and *TGFB1I1* in at least three tissues while *TGFBRAP1* (Supplementary Table S16) correlated with *LTBP1, TGFBR2,* and *TGFBR3L* in at least three tissues.

Table 4

Pearson's correlation coefficients (R) between mRNA expression levels of *FBN3* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	Number of organs[ǂ]
TGFB1	0.20	0.23	0.71[d]	-0.01	-0.06	0.47[b]	0.00	1+
TGFB2	0.13	0.00	0.79[d]	0.54[b]	0.89[d]	0.23	0.40[a]	3+
TGFB3	0.54[a]	-0.23	-0.26	0.69[d]	0.24	0.28	0.49[b]	2+
LTBP1	-0.01	0.13	0.18	0.34	-0.14	0.16	0.11	
LTBP2	0.19	-0.19	-0.27	-0.55[b]	-0.20	0.38[a]	0.23	1-
LTBP3	0.80[d]	-0.19	0.08	0.34	0.00	0.38[a]	0.00	1+
LTBP4	0.44	-0.38	-0.13	0.08	0.69[d]	0.59[c]	-0.44[a]	2+
FBN1	-0.24	-0.53[b]	-0.14	-0.21	0.84[d]	0.28	0.18	1+, 1-
FBN2	-0.13	-0.54[b]	0.31	0.05	0.92[d]	0.27	0.21	1+, 1-
FBN3	*	*	*	*	*	*	*	
TGFBR1	-0.09	0.36	0.46[b]	0.35	0.81[d]	-0.29	-0.12	2+
TGFBR2	-0.12	-0.48[a]	-0.46[b]	-0.79[d]	-0.11	0.07	-0.03	2-
TGFBR3	-0.10	-0.63[c]	-0.13	-0.77[d]	0.86[d]	0.26	0.02	1+, 2-
TGFB1I1	0.55[a]	-0.35	-0.54[c]	-0.04	-0.04	0.22	-0.30	1-
TGFBR3L	0.79[c]	0.08	-0.01	-0.03	-0.31	0.41[a]	-0.21	1+
TGFBI	0.54[a]	-0.04	0.50[b]	0.20	-0.06	0.30	0.25	1+
TGFBRAP1	-0.38	0.00	0.28	0.40[a]	0.18	-0.12	0.43[a]	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

TGFβ Signalling Molecules: Relationships with PCOS candidate genes in Fetal Tissues

The correlation of PCOS candidate genes with TGFβ signalling molecules within each fetal tissue were examined (Tables 6-8, Supplementary Tables S17-S40). Significant correlations of TGFβ signalling molecules within tissues were observed for *HMGA2* (Table 6)*, YAP1* (Table 7) and *RAD50* (Table 8). The least number of correlations with TGFβ signalling molecules in the different fetal tissues occurred with *FSHB, NEIL2, SUOX* and *SUMO1P1* (Supplementary Table S17, S31, S39 and S40, respectively).

Table 5

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFBR1* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	Number of organs[†]
TGFB1	0.04	-0.10	0.20	-0.55[b]	-0.04	0.31	0.15	1-
TGFB2	0.72[c]	0.64[c]	0.76[d]	0.54[b]	0.82[d]	-0.32	-0.18	5+
TGFB3	-0.05	0.05	0.11	0.35	0.37[a]	-0.26	-0.32	
LTBP1	0.40	0.44[a]	0.40[a]	0.46[a]	0.02	0.78[d]	0.63[c]	2+
LTBP2	-0.63[b]	-0.03	0.03	-0.30	-0.10	0.15	0.01	1-
LTBP3	-0.49[a]	-0.36	-0.38[a]	-0.42[a]	-0.11	-0.60[c]	-0.50[b]	2-
LTBP4	-0.45	-0.51[b]	-0.48[b]	-0.75[d]	0.52[c]	0.06	0.18	1+, 3-
FBN1	0.56[a]	-0.02	0.54[b]	0.11	0.86[d]	0.46[b]	0.71[d]	4+
FBN2	0.91[d]	0.20	0.21	0.45[a]	0.85[d]	0.65[d]	0.68[d]	4+
FBN3	-0.09	0.36	0.46[b]	0.35	0.81[d]	-0.29	-0.12	2+
TGFBR1	*	*	*	*	*	*	*	
TGFBR2	0.58[a]	0.21	0.39[a]	-0.37	0.18	0.33	0.29	
TGFBR3	0.43	-0.12	0.50[b]	-0.20	0.85[d]	0.55[c]	0.62[c]	4+
TGFB1I1	-0.24	-0.70[d]	-0.78[d]	-0.77[d]	-0.19	-0.01	-0.30	3-
TGFBR3L	-0.32	-0.57[b]	-0.37[a]	-0.58[b]	-0.50[b]	-0.54[b]	-0.47[b]	5-
TGFBI	0.14	0.18	0.61[c]	-0.29	-0.01	0.41[a]	0.60[c]	2+
TGFBRAP1	0.68[b]	0.52[b]	0.37[a]	0.26	0.36[a]	0.10	0.03	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

HMGA2, YAP1 and *RAD50* (Tables 6-8) correlated significantly with *TGFBR1* in at least six out of the seven tissues studied. The three genes also correlated significantly with *FBN1/2* and *TGFBR2/3* in at least four fetal tissues. *HMGA2* and *YAP1* expression significantly correlated with *TGFB2* in at least four tissues. While *YAP1* and *RAD50* correlated significantly with *LTBP1/3* in at least four tissues, *RAD50* expression additionally significantly ($P < 0.01$) correlated with *TGFBR3L* and *TGFBRAP1* in five tissues.

FSHR (Supplementary Table S18) showed strong correlations with some of the TGFβ signalling molecules in liver and brain. Despite this relationship it should be noted that *FSHR* expression levels were very low for most tissues except for the ovary and testis, as expected (Azumah et al. 2023). *LHCGR* and *AR* also showed low expression except for the ovary and testis, and *AMH* showed low expression except only for the testis (Azumah et al. 2023). *LHCGR* (Supplementary Table S19) and *AR* (Supplementary Table S20) expression correlated with several TGFβ molecules particularly in the brain tissues. However, *LHCGR* significantly and negatively correlated with *TGFB2, TGFBR1* and *TGFBI* in the testis.

Table 6

Pearson's correlation coefficients (R) between mRNA expression levels of *HMGA2* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**Number of organs**[‡]
TGFB1	0.37	0.26	0.79^{d}	-0.04	0.01	0.74^{d}	0.38^{a}	2+
TGFB2	0.85^{d}	0.33	0.80^{d}	0.53^{b}	0.87^{d}	0.07	-0.15	4+
TGFB3	0.01	-0.12	-0.34	0.39^{a}	0.29	0.08	-0.35	
LTBP1	0.47^{a}	0.38	0.24	0.36	-0.18	0.96^{d}	0.75^{d}	2+
LTBP2	-0.79^{c}	-0.11	-0.31	-0.61^{c}	-0.25	0.57^{c}	0.08	3-
LTBP3	-0.30	-0.35	-0.23	-0.08	-0.09	-0.39^{a}	-0.45^{b}	1-
LTBP4	-0.32	-0.50^{b}	-0.30	-0.35	0.68^{d}	0.29	0.31	1+, 1-
FBN1	0.75^{c}	-0.37	-0.10	-0.19	0.87^{d}	0.88^{d}	0.83^{d}	4+
FBN2	0.88^{d}	-0.26	0.43^{a}	0.15	0.91^{d}	0.98^{d}	0.84^{d}	4+
FBN3	-0.02	0.75^{d}	0.87^{d}	0.73d	0.95^{d}	0.26	-0.01	4+
TGFBR1	0.84^{d}	0.73^{d}	0.48^{b}	0.68^{d}	0.85^{d}	0.71^{d}	0.76^{d}	7+
TGFBR2	0.84^{d}	-0.16	-0.33	-0.77^{d}	-0.04	0.61^{c}	0.47^{b}	3+, 1-
TGFBR3	0.56^{a}	-0.42^{a}	0.08	-0.53^{b}	0.95^{d}	0.90^{d}	0.74^{d}	3+, 1-
TGFB1I1	0.00	-0.58^{b}	-0.63^{d}	-0.42^{a}	-0.09	0.15	-0.18	2-
TGFBR3L	-0.28	-0.28	-0.15	-0.23	-0.42^{b}	-0.34	-0.36^{a}	1-
TGFBI	0.30	0.07	0.56^{c}	-0.09	-0.06	0.82^{d}	0.79^{d}	3+
TGFBRAP1	0.67^{b}	0.38	0.42^{a}	0.31	0.18	0.08	0.01	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. Tissues with $P < 0.01$ were regarded as significant. [‡]Number of organs with significant ($P < 0.01$), positive (+) or negative (-) correlations.

AR expression correlated significantly with *TGFB2/3, LTBP2, FBN1* and *TGFBR2* in both heart and testis, with *LTBP2/3, FBN3, TGFBR3* in testis only and *LTBP1, TGFBR1*, and *TGFB1I1* in heart only. *AMH* (Supplementary Table S21) expression correlated significantly and negatively with *TGFB2/3, LTBP1, TGFBR1/2,* and *TGFBRAP1*, and positively with *TGFBR3L* in testis. It also correlated positively with *TGFB3*, *LTBP3*, *FBN3*, *TGFB1/1*, *TGFBR3L* and *TGFBI* in fetal ovary.

INSR (Supplementary Table S22) showed significant negative correlations with *FBN2, TGFBR3* and *TGFBI,* and positive correlations with *TGFBRAP1* in brain and cerebellum, and additionally positively with *TGFB3* and negatively with *LTBP1, FBN1* and *TGFBR1* in the brain. *FDFT1* (Supplementary Table S23) did not correlate with many of TGFβ signalling molecules in any of the tissues.

Table 7

Pearson's correlation coefficients (R) between mRNA expression levels of *YAP1* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**Number of organs[†]**
TGFB1	0.11	-0.05	0.02	-0.49[b]	0.00	0.65[d]	0.49[b]	2+, 1-
TGFB2	0.75[c]	0.86[d]	0.40[a]	0.07	0.90[d]	-0.03	-0.21	3+
TGFB3	-0.12	0.51[b]	0.18	-0.19	0.34[a]	0.01	-0.40[a]	1+
LTBP1	0.51[a]	0.73[d]	0.56[c]	0.36	-0.05	0.95[d]	0.87[d]	4+
LTBP2	-0.60[b]	0.45[a]	0.18	0.00	-0.17	0.49[b]	0.13	1+, 1-
LTBP3	-0.53[a]	-0.02	-0.46[b]	-0.77[d]	-0.14	-0.45[b]	-0.46[b]	4-
LTBP4	-0.44	-0.08	-0.41[a]	-0.70[d]	0.63[d]	0.17	0.24	1+, 1-
FBN1	0.69[b]	0.44[a]	0.55[c]	0.01	0.92[d]	0.82[d]	0.92[d]	5+
FBN2	0.89[d]	0.49[a]	0.34	0.36	0.93[d]	0.95[d]	0.94[d]	4+
FBN3	-0.20	0.13	-0.02	-0.29	0.92[d]	0.08	0.02	1+
TGFBR1	0.96[d]	0.83[d]	0.68[d]	0.56[b]	0.94[d]	0.83[d]	0.84[d]	7+
TGFBR2	0.67[b]	0.57[b]	0.65[d]	0.20	0.10	0.61[c]	0.48[b]	5+
TGFBR3	0.57[a]	0.23	0.67[d]	0.33	0.93[d]	0.89[d]	0.84[d]	4+
TGFB1I1	-0.27	-0.35	-0.55[c]	-0.60[b]	-0.15	0.03	-0.17	2-
TGFBR3L	-0.48[a]	-0.73[d]	-0.36[a]	-0.49[a]	-0.50[b]	-0.44[a]	-0.40[a]	2-
TGFBI	0.04	0.52[b]	0.36[a]	-0.18	0.01	0.77[d]	0.89[d]	3+
TGFBRAP1	0.80[d]	0.60[b]	0.52[b]	-0.05	0.30	0.10	0.00	3+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$), positive (+) or negative (-) correlations.

ERBB3 (Supplementary Table S24) significantly correlated with *TGFB1/2, FBN3, TGFB1, TGFB1I1, TGFBI* and *TGFBRAP1* in the heart. The positive correlations with TGFβ signalling molecules in the brain and cerebellum whilst statistically significant were a result of very low levels expression in these tissues (Azumah et al. 2023). *ERBB4* (Supplementary Table S25) correlated significantly with *LTBP3*, *TGFBR1* and *TGFBRAP1* in testis and ovary, but only with *LTBP2* and *FBN2* in the ovary and with *TGFB1I1* in the testis. The observed correlations in the liver were also related to very low expression of *ERBB4* (Azumah et al. 2023) and the TGFβ signalling molecules (Figs 1 and 2; Supplementary Figs 2,3,4) in this tissue. *PLGRKT* (Supplementary Table S26) expression correlated significantly and negatively with genes in testis including *TGFB2/3, LTBP2, FBN1/2*, *TGFBR2/3* and *TGFBRAP1*, whereas it correlated positively with *TGFBR3L*. *TOX3* (Supplementary Table S27) expression significantly correlated with *FBN3* in five out of seven tissues and with *TGFBR1/3* and *TGFBR3L* in at least three tissues. *GATA4* (Supplementary Table S28) expression correlated significantly positively with *TGFB2*, *LTBP4*, *FBN1/2/3* and *TGBFBR1/3* in liver and with *LTBP2* positively in the ovaries, and negatively with *FBN2* and *TGFBR1/2* in both gonads, *TGFBI* in testis and *TGFBRAP1* in ovary. *ZBTB16* (Supplementary Table S29) significantly correlated with *TGFB1*, *LTBP1*, *FBN1/2, TGFBR1/2/3* and *TGFBI* in at least three tissues, most of which were in the testis, liver and brain and cerebellum. *IRF1* (Supplementary Table S30) expression correlated significantly with *LTBP4, FBN1/2/3* and *TGFBR2/3* in the testis, with *LTBP2/4, FBN3, TGFBR1/2* and *TGFB1/1* in kidneys, with *TGFB2/3* and *TGFBR3L* in cerebellum and with *TGFB1* and *TGFBR2* in brain. *KRRI* (Supplementary Table S32) expression correlated significantly with *LTPB1/3, FBN1* and *TGFBR1/2* in at least three tissues. The strongest positive correlations were with *TGFBR1/2/3* in the heart and *TGFBR1* in brain and cerebellum.

RAB5B (Supplementary Table S33) significantly correlated positively with *TGFBRAP1* in all tissues except the kidney and with *FBN1, TGFBR2/3* and *TGFBR3L* in at least three tissues. *ARL14EP* (Supplementary Table S34) expression showed significant correlations ($P < 0.01$) with *LTBP3, FBN3* and *TGFBR2/3* in the heart, while *DENND1A* (Supplementary Table S35) correlated significantly with *TGFB2/3, LTBP3, TGFBR1,* and *TGFBR3L* in cerebellum, with *TGFB1* in heart and *TGFB1/1* in kidney. *THADA* (Supplementary Table S36) showed the most significant correlations in heart (*TGFB2*, *LTBP1*, *FBN1/2, TGFBR1/3, TGFB1/1, TGFBI* and *TGFBRAP1*) and the brain and cerebellum (*LTBP1/3, FBN1/2, TGFBR1/3* and *TGFBI)*. *MAPRE1* (Supplementary Table S37) expression correlated significantly with *LTBP1* and *TGFBR1* in five out of seven tissues, and with *LTBP3* and *TGFB1I1* in at least three tissues. *AOPEP* (Supplementary Table S38) expression correlated significantly with *LTBP1/3, FBN1/2, TGFBR1, TGFBI* and *TGFBRAP1* in at least three tissues. In the metabolic tissues, the correlations were predominantly negative, except for *LTBP3, TGFB1I1* and *TGFBR3L.*

Table 8

Pearson's correlation coefficients (R) between mRNA expression levels of *RAD50* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**Testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**Number of organs**[‡]
TGFB1	-0.32	-0.22	0.28	-0.45[a]	0.04	0.27	0.06	
TGFB2	-0.05	0.46[a]	0.53[b]	0.29	0.35[a]	0.04	0.03	1-
TGFB3	-0.34	0.17	0.14	-0.07	0.14	-0.15	-0.03	
LTBP1	0.34	0.64[c]	0.71[d]	0.25	0.56[c]	0.74[d]	0.48[b]	5+
LTBP2	0.24	0.27	0.15	-0.04	0.19	0.26	0.24	
LTBP3	-0.63[b]	-0.38	-0.42[a]	-0.62[c]	-0.32[a]	-0.61[c]	-0.46[b]	4-
LTBP4	-0.30	-0.20	-0.29	-0.76[d]	0.22	-0.14	-0.18	1-
FBN1	0.21	0.29	0.55[c]	0.02	0.63[d]	0.62[c]	0.65[d]	4+
FBN2	-0.04	0.44[a]	0.52[b]	0.32	0.41[a]	0.63[d]	0.57[c]	3+
FBN3	-0.62[b]	-0.10	0.14	-0.17	0.33[a]	-0.16	0.20	1-
TGFBR1	0.08	0.58[b]	0.56[c]	0.68[c]	0.60[d]	0.75[d]	0.71[d]	6+
TGFBR2	-0.06	0.50[b]	0.54[b]	0.00	0.72[d]	0.49[b]	0.46[b]	5+
TGFBR3	0.23	0.52[b]	0.54[b]	0.22	0.50[b]	0.62[c]	0.59[c]	5+
TGFB1I1	-0.53[a]	-0.47[a]	-0.53[b]	-0.72[d]	-0.35[a]	-0.23	-0.40[a]	2-
TGFBR3L	-0.74[c]	-0.79[d]	-0.40[a]	-0.44[a]	-0.72[d]	-0.52[b]	-0.60[c]	5-
TGFBI	-0.55[a]	0.16	0.40[a]	-0.24	0.25	0.43[a]	0.50[b]	1+
TGFBRAP1	0.52[a]	0.79[d]	0.68[d]	-0.05	0.85[d]	0.49[b]	0.53[b]	5+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

TGFβ Signalling Molecules: Postnatal Gene Expression

The expression of TGFβ family genes was studied in five postnatal tissues (testis, heart, liver, kidney, brain, and cerebellum) at birth until adulthood, except kidney samples which were only up to 8 years of age. There were no postnatal ovary samples. We also compared the levels of expression in the adult tissues to expression in fetal tissues. Expression of TGFβ signalling molecules were generally lower during adulthood compared to expression in fetal tissues.

The expression of *TGFB1/2/3* (Fig. 1, Supplementary Figs S1A and B, respectively) postnatally decreased significantly from birth throughout life in all tissues except for *TGFB1/3* in the heart, where expression increased. In most cases, expression levels were similar to those in fetal tissues, except *TGFB3* in the cerebellum where expression levels were very high at birth after which levels decreased substantially.

LTBP1/2/4 (Fig. 2 and Supplementary Figs S2A and C, respectively) levels were very low and constant in brain tissues, whereas *LTBP3* (Supplementary Fig. S2B) levels were relatively high. Expression of all four genes decreased from birth until adulthood in the testis and were dynamically expressed in the metabolic tissues with the least expression in the liver. *LTBP2/3/4* levels increased with age while *LTBP1* levels decreased in heart tissues.

FBN1/2/3 (Fig. 3, Supplementary Figs. S3A and B) expression declined after birth and remained low throughout adulthood in all tissues studied. *TGFBR1/2/3* (Fig. 4, Supplementary Figs. S4A and B) levels remained constant postnatally in most tissues with few exceptions. *TGFBR2* levels increased after birth until before puberty in kidney and testis, and before adulthood in the heart. The same patterns were observed in kidney and testis for *TGFBR3*.

TGFB1I1 (Supplementary Fig. S5A) and *TGFBI* (Supplementary Fig. S5C) expression had similar patterns in the testis; higher expression during prepubertal stages and lower expression during the rest of life. Their levels in the brain and cerebellum were low and constant from birth. Both genes were dynamically expressed in metabolic tissues. However, *TGFBR3L* (Supplementary Fig. S5B) expression was low and constant in all tissues except in the brain, where its expression increased significantly from birth until adulthood in both tissues. *TGFBRAP1* (Supplementary Fig. S5D) levels remained constant in metabolic tissues and brain and cerebellum, similar to their expression in the respective fetal tissues. However in the testis, the levels decreased during late puberty and remained low and constant during adulthood.

Discussion

In this study we examined the expression patterns and levels of TGFβ signalling molecules from 4-20 weeks of gestation and at different stages of postnatal human life. Seven different tissues were included. The relationships between the expression of these genes in fetal tissues to each other and to age of gestation, and prenatal or/and postnatal levels of expression were compared. The expression of TGFβ signalling molecules was also related to expression of PCOS candidate genes within each fetal tissue. While some of the expression patterns observed in the human fetal ovary were consistent to our previous findings in bovine fetal ovaries during 8-18 wpc (Azumah et al. 2022a; Hatzirodos, et al. 2019; Hatzirodos et al. 2011), others could not be inferred as human samples after mid gestation were not available in the current study whereas they were previously for bovine tissues (Azumah et al. 2022a; Hatzirodos et al. 2019; Hatzirodos et al. 2011). Here we highlight from this plethora of information what we perceive are the most significant findings.

Studies on the role of androgens, insulin, AMH and TGFβ1 in the signalling pathways associated with PCOS have recently been reviewed (Walters et al. 2022). In particular, TGFβ signalling molecules have been associated with fibrosis in various tissues including the heart, kidney, lung, liver and ovary, and the mechanisms involved have been reviewed (Biernacka, et al. 2011; Gressner, et al. 2002; Zhou, et al. 2017). Interestingly, these regulators have been previously associated with the development of fibrous ovarian stroma observed in PCOS women as well as its predisposition to PCOS (Hatzirodos et al. 2011). Skeletal muscle of women with PCOS tend to have higher expression of genes controlled by TGFβ and produce more collagens (Stepto, et al. 2020). Also, TGFβ2 levels in circulation correlate with androgen levels in women (Raja-Khan et al. 2014), clearly showing a connection between TGFβs and androgens. Recent studies have shown that TGFβ1 could regulate some genes in loci associated with PCOS in cultured fetal ovarian fibroblasts (Azumah et al. 2022b; Hartanti et al. 2020). Specifically, TGFβ1 inhibited expression of genes including *INSR*, *C8H9orf3*, *RAD50*, *ERBB3*, *NEIL2*, *IRF1* and *ZBTB16* in fetal ovarian fibroblasts *in vitro* (Azumah et al. 2022b; Hartanti et al. 2020). Note that androgens and AMH, which have been used to induce PCOS in animals previously (Abbott, et al. 2006; Dumesic et al. 1997; Hartanti et al. 2020; Risal et al. 2019; Stener-Victorin, et al. 2020; Tata et al. 2018; Walters 2016), did not regulate any of the PCOS candidate genes in fetal ovarian fibroblasts *in vitro* (Azumah et al. 2022b; Hartanti et al. 2020). TGFβ1 also inhibited the expression of the androgen receptor (*AR*) and stimulated expression of its cofactor TGFβ induced transcript 1 (*TGFB1I1*) (Azumah et al. 2022b; Hartanti et al. 2020). These findings further infer crosstalk between TGFβ signalling pathways with androgen signalling. Collectively all these results further affirm TGFβ's possible role in the aetiology of PCOS.

Examining genes in loci associated with PCOS also shed light on the aetiology of PCOS. We had previously found these genes to be dynamically expressed during fetal ovary development (Azumah et al. 2022a; Hartanti et al. 2020; Liu et al. 2020) whereas in adult ovarian stroma there was no difference in the expression of these genes between control and PCOS (Liu et al. 2020). We also found recently that many of the PCOS genes were dynamically expressed across gestation in many other fetal tissues (Azumah et al. 2023). In the fetal bovine ovary, we found PCOS expression patterns across gestation could be divided into similarly-expressed groups and that genes in these groups were co-expressed with genes involved either in mitochondria function, stroma expansion or steroidogenesis (Azumah et al. 2022a). The mitochondrial genes were both nuclear and mitochondrially encoded (Azumah et al. 2022a). Upstream regulators associated with these pathways according to Ingenuity Pathway Analyses and KEGG analyses showed that TGFβ1/2/3 among others regulate the stroma expansion (Azumah et al. 2022a). Furthermore, meta-analysis involving lean (BMI ≤ 23) and obese (BMI ≥ 23) PCOS patients in a systematic and comparative study by Idicula-Thomas, et al. (2020), showed that some PCOS candidate genes were differentially expressed in different tissues. *ZBTB16, FSHR, GATA4, TGFB1I1, AR* and *LTBP4* were downregulated in cumulus cells and *TGFB2* in subcutaneous adipose tissue of lean PCOS women while *INSR, THADA, PLGRKT, TGFBI, FBN1* and *LTBP1* were downregulated in endometrial tissues in obese PCOS women (Idicula-Thomas et al. (2020). A recent study showed that correlation between the expressions of *HMGA2/YAP1* and *RAD50/YAP1* were significant in at least 5 of the 7 fetal tissues analysed (ovary, testis, kidney, liver, heart, cerebellum and brain) during the first half of human fetal development (Azumah et al. 2023). Thus clearly there is a real possibility that mis-regulation of genes in loci associated with PCOS during fetal development could be involved in the aetiology of PCOS.

In the current study, the expression of 3 PCOS candidate genes (*HMGA2, YAP1* and *RAD50*) in particular correlated significantly with many TGFβ signalling molecules during the first half of human fetal development in most tissues. Although the specific roles of the 3 genes in the aetiology of PCOS remain unknown, their functional roles are intriguingly associated directly or indirectly with some phenotypes of the syndrome. In numerous studies *HMGA2* has been associated with birthweight as well as adult and childhood height (Beaumont, et al. 2018; Horikoshi, et al. 2013; Weedon, et al. 2007). Birthweight has been associated with the risk of hyperandrogenism and obesity, while ponderal index (weight per cubic length) at birth has been independently associated with some symptoms of PCOS in adulthood (Davies, et al. 2012; Yu, et al. 2011). Low birthweight, for instance, has been associated with coronary artery disease, hypertension, obesity and insulin resistance among others [see review by Calkins and Devaskar (2011)]. Understanding the role of *HMGA2* in the fetal onset of adult disorders/symptoms observed in PCOS will enhance the understanding of the aetiology of the syndrome.

HMGA2 and *YAP1* are involved in epithelial mesenchymal transition (EMT) during embryogenesis through TGFβ signalling (Martínez Traverso, et al. 2022; Thuault, et al. 2006; Vignali and Marracci 2020). Both *HMGA2* and *YAP1* are also involved in the Hippo signalling pathway, which regulates organ size by regulating cell differentiation and apoptosis (Huang, et al. 2005; Shen, et al. 2015; Varelas 2014; Xu, et al. 2021; Zhang, et al. 2014) including in the ovary (Clark, et al. 2022). Interaction between TGFβ and Hippo signalling pathways has been shown to stimulate hepatocytes to undergo an EMT-like response in a TGFβ-enriched microenvironment (Oh, et al. 2018). *HMGA2* regulates *YAP1* stability via the Hippo-YAP signalling pathway and possibly inhibits its ubiquitination, which has been shown to regulate the progression of EMT in human breast cancer cell lines (Xu et al. 2021). Additionally, *YAP1* has also been shown to regulate fibrosis in liver (Martin, et al. 2016), lung (Chen, et al. 2019) and heart (Li, et al. 2022), contributing to numerous diseases including cardiovascular diseases, diabetes and cancers (Salloum, et al. 2021). It is not known if the exposure to high androgens and AMH during pregnancy in PCOS women leads to dysregulation of some of the genes in loci associated with PCOS, such as *YAP1* and *HMGA2,* as well as TGFβ signalling molecules during fetal development. Could this lead to the development of a polycystic ovary morphology and the various phenotypes observed in adulthood?

Although most genes in loci associated with PCOS have been studied individually, studies of their regulatory roles on each other are limited. *HMGA2* has been associated with the Polycystic Ovary Morphology (PCOM) phenotype in PCOS patients of Han Chinese ancestry, potentially functioning to promote the proliferation of ovarian granulosa cells via the HMGA2/IMP2 pathway (Li, et al. 2019). This could possibly account for the increased proliferation of early preantral follicles and decreased apoptosis in granulosa cells in PCOS (Das, et al. 2008; Li et al. 2019; Stubbs, et al. 2007). *HMGA2* has also been significantly associated with both hyperandrogenism and oligo/amenorrhea in women with PCOS in Saudi Arabia (Bakhashab and Ahmed 2019). More so, *YAP1*, which is highly expressed in mammalian oocytes and preimplantation embryos, is essential for normal ovarian development and function, as well as granulosa cell proliferation (Ji, et al. 2017; Yu, et al. 2016). *YAP1* is also regulated by gonadotrophins and hormones including oestrogen, follicle stimulating hormone (FSH), and luteinising hormone (LH) (de Andrade, et al. 2022; Ji et al. 2017;

Moon, et al. 2022; Sun and Diaz 2019); however the consequences of this regulation in PCOS women has not been studied. In granulosa cells of women with PCOS, a significant decrease in DNA methylation levels were observed in the promoter region of *YAP1*, accounting for a significant increase in the mRNA and protein expression levels of YAP1 (Jiang, et al. 2017). Treatment of granulosa cells from healthy women with testosterone, but not LH or FSH, reduced *YAP1* methylation in a dose-dependent manner (Jiang et al. 2017); implying regulatory roles of androgens on this gene. Together, these findings confirm the possible co-regulatory effects between some PCOS candidate genes, *HMGA2* and *YAP1*, as well as with some TGFβ signalling molecules.

Considering the fact that *HMGA2* is mainly expressed during the early stages of fetal development, one could argue that some or most of these interactions occur mainly during this time. Thus, exposure of fetuses to a PCOS environment such as high levels of androgens or AMH could possibly lead to an initiation of mechanisms which possibly leads to a cascade of events during and after fetal development; accounting for the phenotypes observed. It could also be said that the dynamic expression of both TGFβ signalling molecules and PCOS candidate genes during fetal and postnatal development in gonadal, metabolic and brain tissues could account for the variations in age of onset as well as the phenotypes observed in PCOS. Postnatal exposures could also influence time of onset of some of these symptoms observed.

Together the current study confirms that some genes in loci associated with PCOS including *HMGA2* and *YAP1* could be interacting with TGFβ signalling molecules, resulting in cascades of events downstream, possibly accounting for the different phenotypes observed. Specifically, this relationship could underpin the PCOM phenotype, as well as contributing to non-reproductive aspects of the condition.

Conclusion

The influence of transcriptional and post-transcriptional mechanisms such as mRNA stability/degradation, storage in stress granules, translational control on gene expression were not considered in this study. Also, Mendelian randomisation studies and transcriptome-wide association studies may be addressed in future studies.

Notably, most TGFβ signalling molecules were actively expressed in all tissues studied except in the liver and some were co-expressed with PCOS candidate genes. The findings and interpretations of this study thus confirms possible relationships between TGFβ signalling molecules and genes in loci associated with PCOS in various tissues, providing an early step towards understanding the multiple aspects of this condition.

Credit authorship contribution statement

R.A., K.H and R.J.R designed the study. R.A. performed statistical analysis. R.A., K.H and R.J.R interpreted the data and contributed to discussion. R.A., K.H, R.A.A and R.J.R wrote the manuscript. R.J.R is the guarantor of this work, had full access to all the data in the study, and assumes full responsibility for the integrity of the data and the accuracy of the data analysis.

Declaration of competing interest

R.A.A. reports consultancy work for Ferring Merck, IBSA, Roche Diagnostics. The other authors of this manuscript have nothing to declare and no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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Data sharing statement

All data generated or analysed during this study are included in this published article and its supplementary information files.

Supplementary data

Supplementary data to this article can be found online.

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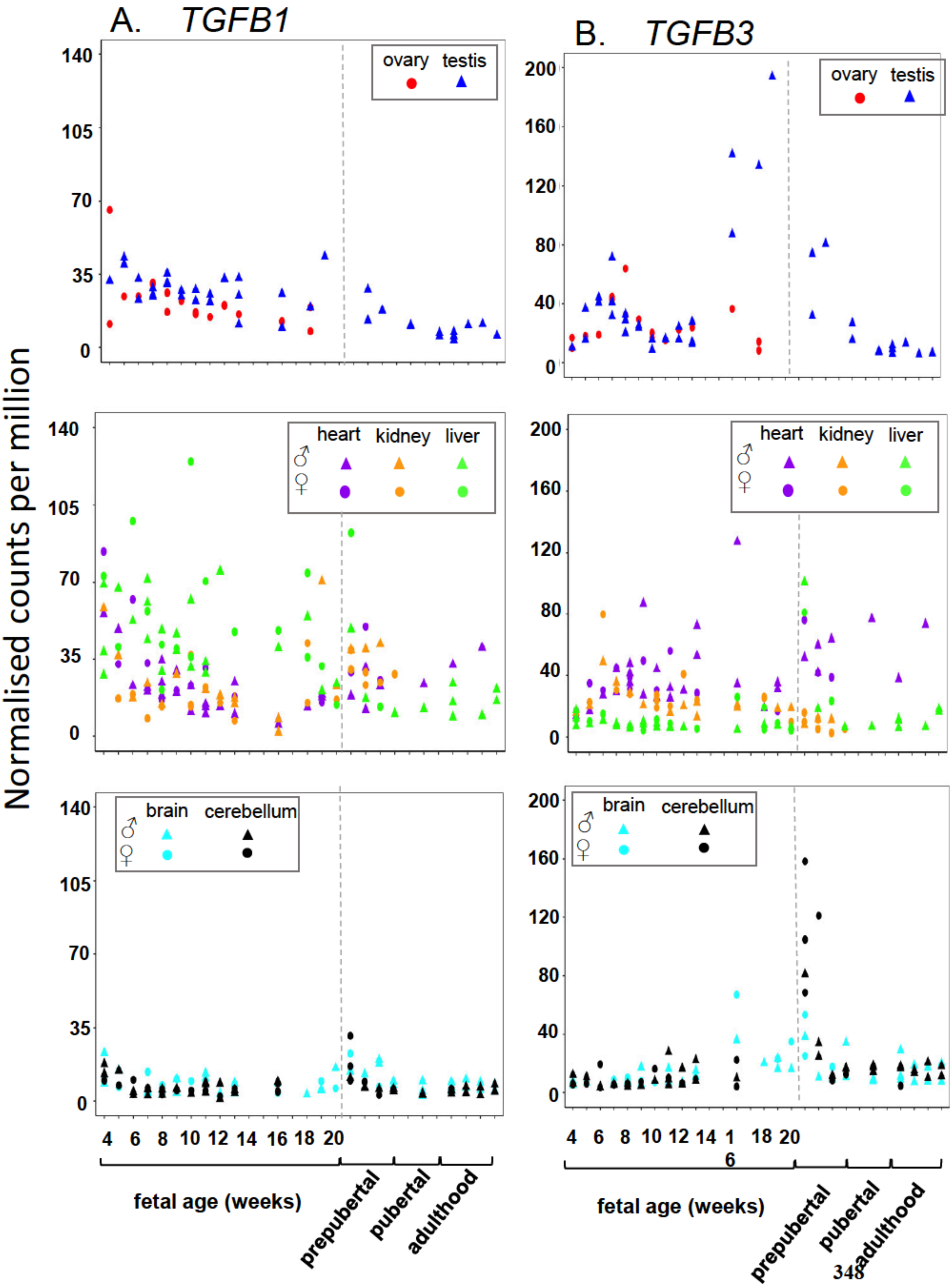
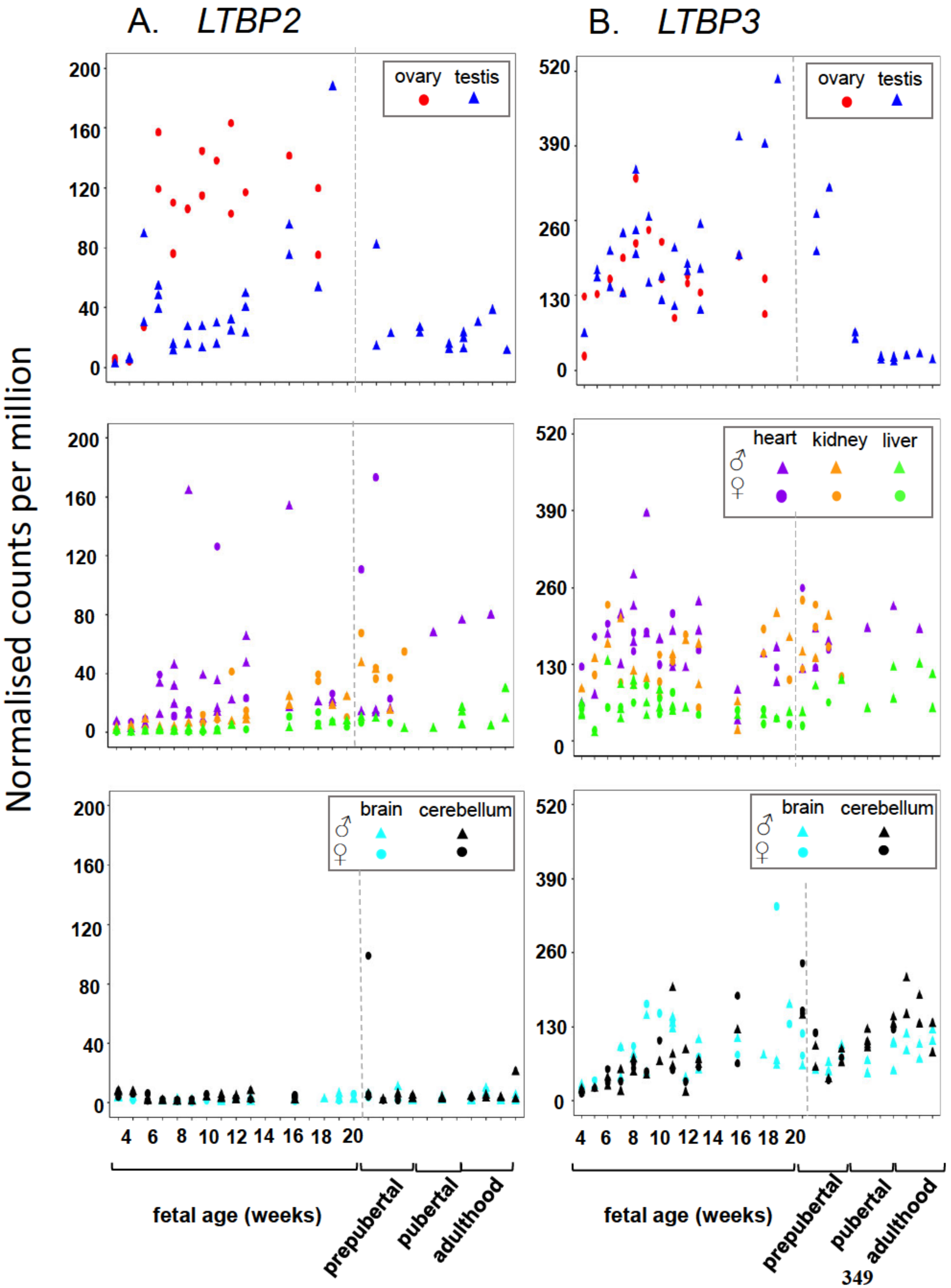
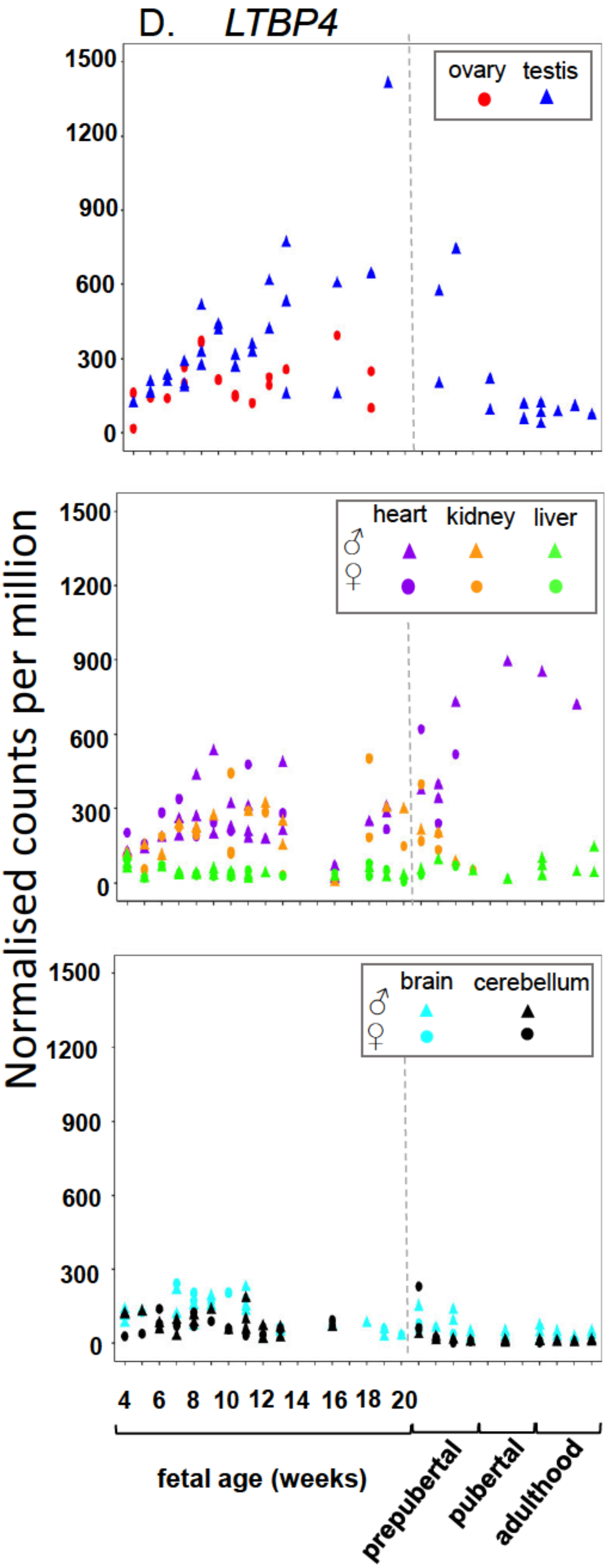
Suppl Fig 1 showing expression of *TGFB* signalling molecules in gonadal, metabolic and brain tissues

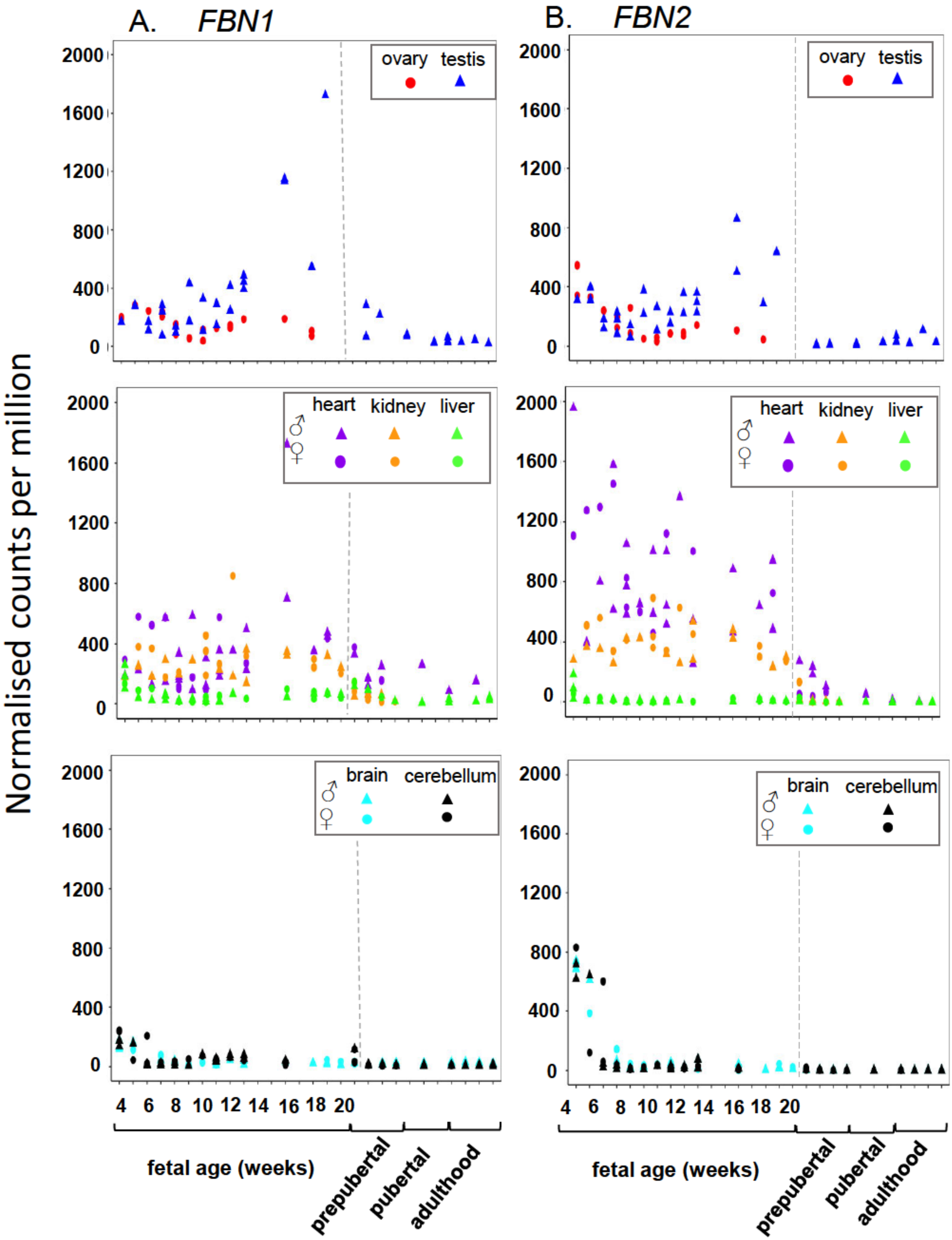


Suppl Fig 2 showing expression of latent-transforming growth factor beta-binding protein in gonadal, metabolic and brain tissues

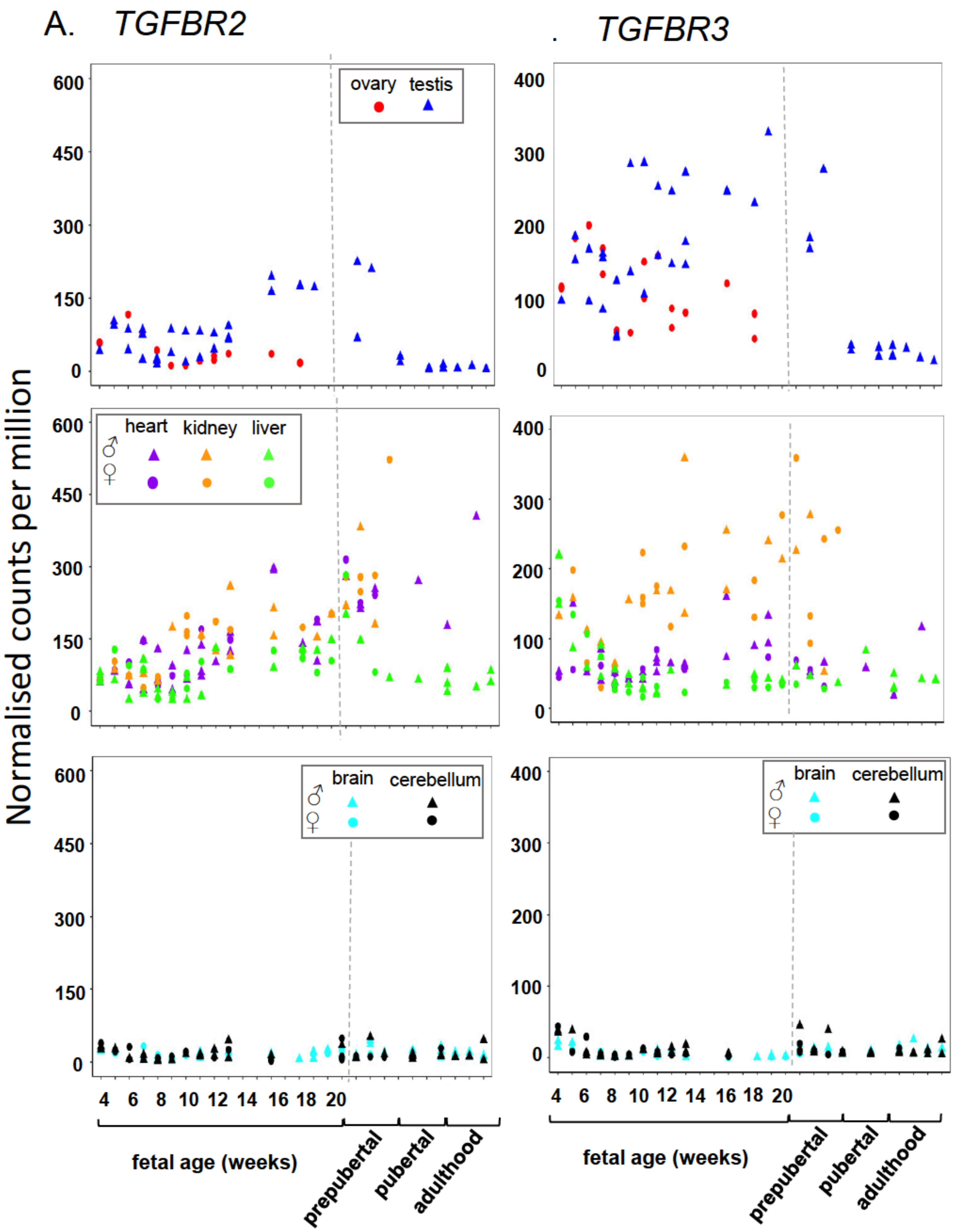



D. *LTBP4*
ovary
testis
heart
kidney
liver
♂
♀
brain
cerebellum
Normalised counts per million
1500
1200
900
600
300
0
4
6
8
10
12
14
16
18
20
fetal age (weeks)
prepubertal
pubertal
adulthood

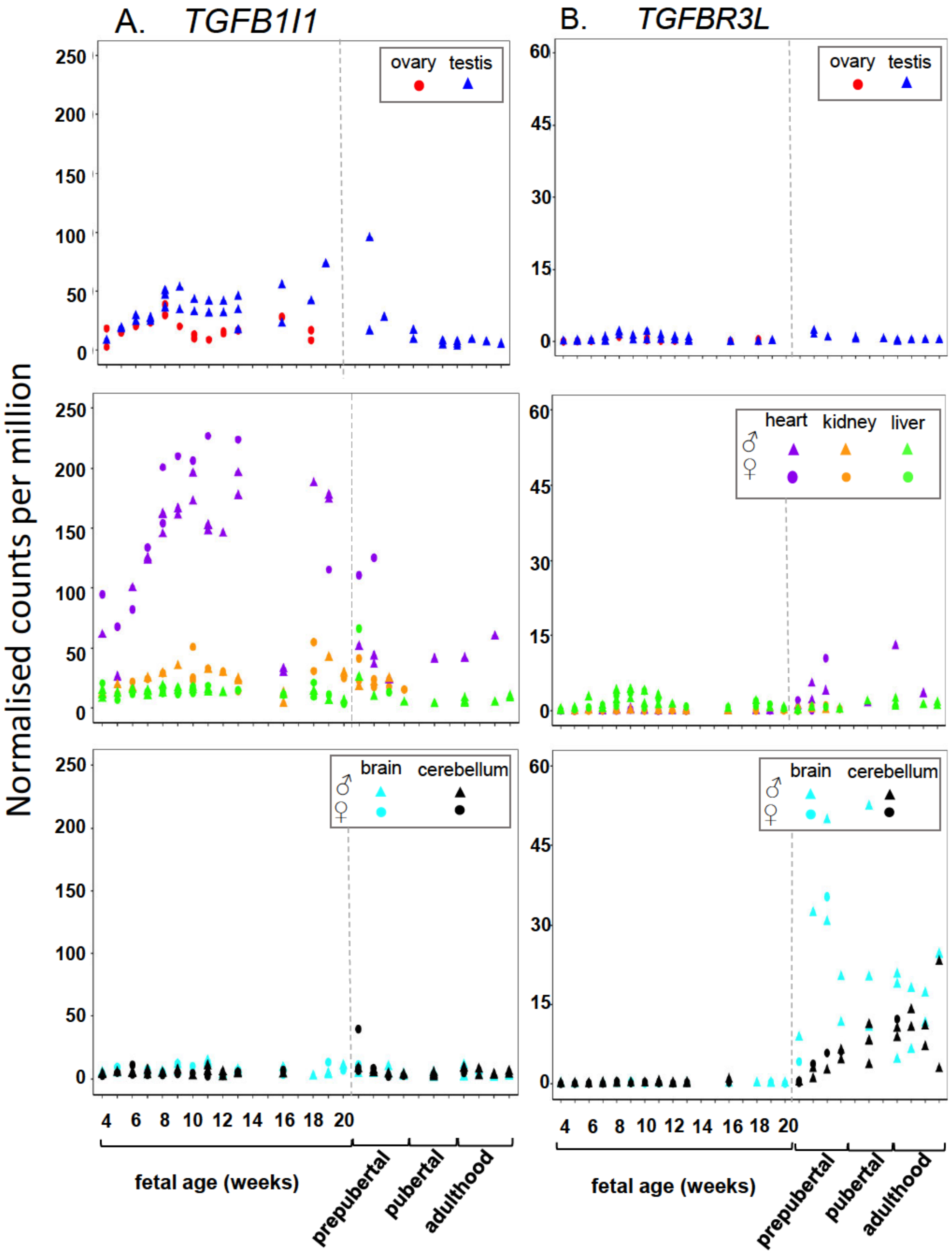
Suppl Fig 3 showing expression of fibrillins in gonadal, metabolic and brain tissues



Suppl Fig 4 showing expression of TGFB receptors in gonadal, metabolic and brain tissues



Suppl Fig 5 showing expression of other TGFP signalling molecules in gonadal, metabolic and brain tissues



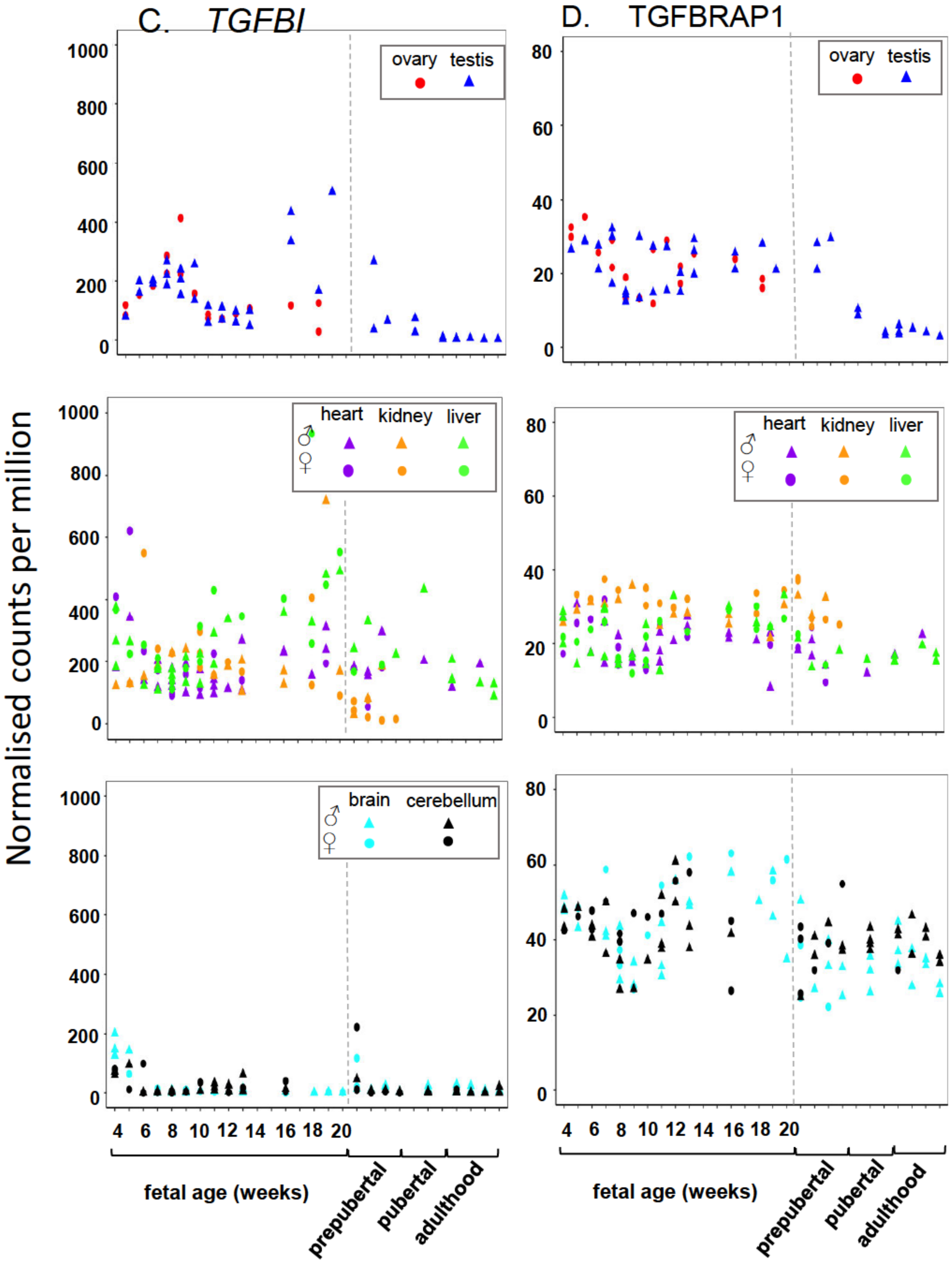

C. TGFBI
D. TGFBRAP1
Normalised counts per million
ovary
testis
heart
kidney
liver
brain
cerebellum
♂
♀
1000
800
600
400
200
0
80
60
40
20
0
4
6
8
10
12
14
16
18
20
fetal age (weeks)
prepubertal
pubertal
adulthood

Table S1. Characteristics (age and gender) of gonadal tissues analysed in this study.

Sample	Tissue	age	age_days	Sex
Ovary.4wpc.1	Ovary	4	28	Female
Ovary.4wpc.2	Ovary	4	28	Female
Ovary.5wpc.3	Ovary	5	35	Female
Ovary.6wpc.4	Ovary	6	42	Female
Ovary.7wpc.5	Ovary	7	49	Female
Ovary.7wpc.6	Ovary	7	49	Female
Ovary.8wpc.7	Ovary	8	56	Female
Ovary.8wpc.8	Ovary	8	56	Female
Ovary.9wpc.9	Ovary	9	63	Female
Ovary.10wpc.10	Ovary	10	70	Female
Ovary.10wpc.11	Ovary	10	70	Female
Ovary.11wpc.12	Ovary	11	77	Female
Ovary.12wpc.13	Ovary	12	84	Female
Ovary.12wpc.14	Ovary	12	84	Female
Ovary.13wpc.15	Ovary	13	91	Female
Ovary.16wpc.16	Ovary	16	112	Female
Ovary.18wpc.17	Ovary	18	126	Female
Ovary.18wpc.18	Ovary	18	126	Female
Testis.4wpc.1	Testis	4	28	Male
Testis.5wpc.2	Testis	5	35	Male
Testis.5wpc.3	Testis	5	35	Male
Testis.6wpc.4	Testis	6	42	Male
Testis.6wpc.5	Testis	6	42	Male
Testis.7wpc.6	Testis	7	49	Male
Testis.7wpc.7	Testis	7	49	Male
Testis.7wpc.8	Testis	7	49	Male
Testis.8wpc.9	Testis	8	56	Male
Testis.8wpc.10	Testis	8	56	Male
Testis.8wpc.11	Testis	8	56	Male
Testis.9wpc.12	Testis	9	63	Male
Testis.9wpc.13	Testis	9	63	Male
Testis.10wpc.14	Testis	10	70	Male
Testis.10wpc.15	Testis	10	70	Male
Testis.11wpc.16	Testis	11	77	Male
Testis.11wpc.17	Testis	11	77	Male
Testis.12wpc.18	Testis	12	84	Male
Testis.12wpc.19	Testis	12	84	Male
Testis.13wpc.20	Testis	13	91	Male
Testis.13wpc.21	Testis	13	91	Male
Testis.13wpc.22	Testis	13	91	Male
Testis.16wpc.23	Testis	16	112	Male
Testis.16wpc.24	Testis	16	112	Male
Testis.18wpc.26	Testis	18	126	Male
Testis.19wpc.27	Testis	19	133	Male
Testis.infant.28	Testis	infant	463	Male
Testis.infant.29	Testis	infant	463	Male
Testis.toddler.31	Testis	toddler	1375	Male

Testis.youngTeenager.32	Testis	youngTeenager	5025	Male
Testis.youngTeenager.33	Testis	youngTeenager	5025	Male
Testis.oldTeenager.34	Testis	oldTeenager	6485	Male
Testis.oldTeenager.35	Testis	oldTeenager	6485	Male
Testis.youngAdult.36	Testis	youngAdult	11230	Male
Testis.youngAdult.37	Testis	youngAdult	11230	Male
Testis.youngAdult.38	Testis	youngAdult	11230	Male
Testis.youngMidAge.39	Testis	youngMidAge	14880	Male
Testis.olderMidAge.40	Testis	olderMidAge	18530	Male
Testis.Senior.41	Testis	Senior	22180	Male

Table S2. Characteristics (age and gender) of metabolic tissues analysed in this study.

Sample	Tissue	age	age (days)	Sex
Heart.4wpc.1	Heart	4	28	Female
Heart.4wpc.2	Heart	4	28	Male
Heart.5wpc.3	Heart	5	35	Female
Heart.5wpc.4	Heart	5	35	Male
Heart.6wpc.5	Heart	6	42	Female
Heart.6wpc.6	Heart	6	42	Male
Heart.7wpc.7	Heart	7	49	Female
Heart.7wpc.8	Heart	7	49	Male
Heart.7wpc.9	Heart	7	49	Male
Heart.8wpc.10	Heart	8	56	Female
Heart.8wpc.11	Heart	8	56	Female
Heart.8wpc.12	Heart	8	56	Male
Heart.8wpc.13	Heart	8	56	Male
Heart.8wpc.14	Heart	8	56	Male
Heart.9wpc.15	Heart	9	63	Female
Heart.9wpc.16	Heart	9	63	Male
Heart.9wpc.17	Heart	9	63	Male
Heart.10wpc.19	Heart	10	70	Female
Heart.10wpc.20	Heart	10	70	Male
Heart.10wpc.21	Heart	10	70	Male
Heart.11wpc.22	Heart	11	77	Female
Heart.11wpc.23	Heart	11	77	Male
Heart.11wpc.24	Heart	11	77	Male
Heart.11wpc.25	Heart	11	77	Male
Heart.12wpc.27	Heart	12	84	Male
Heart.13wpc.28	Heart	13	91	Female
Heart.13wpc.30	Heart	13	91	Male
Heart.13wpc.31	Heart	13	91	Male
Heart.16wpc.33	Heart	16	112	Male
Heart.16wpc.34	Heart	16	112	Male
Heart.18wpc.36	Heart	18	126	Male
Heart.19wpc.35	Heart	19	133	Female
Heart.19wpc.37	Heart	19	133	Male
Heart.19wpc.38	Heart	19	133	Male
Heart.newborn.39	Heart	newborn	280	Female
Heart.newborn.41	Heart	newborn	280	Male
Heart.infant.43	Heart	infant	463	Female
Heart.infant.44	Heart	infant	463	Male
Heart.infant.45	Heart	infant	463	Male
Heart.toddler.46	Heart	toddler	1375	Female
Heart.toddler.47	Heart	toddler	1375	Male
Heart.teenager.48	Heart	teenager	5755	Male
Heart.youngAdult.49	Heart	youngAdult	11230	Male
Heart.olderMidAge.50	Heart	olderMidAge	18530	Male
Kidney.4wpc.1	Kidney	04	28	Male
Kidney.5wpc.2	Kidney	05	35	Female
Kidney.5wpc.3	Kidney	05	35	Male

Kidney.6wpc.4	Kidney	06	42	Female
Kidney.6wpc.5	Kidney	06	42	Male
Kidney.7wpc.6	Kidney	07	49	Female
Kidney.7wpc.7	Kidney	07	49	Male
Kidney.8wpc.8	Kidney	08	56	Female
Kidney.8wpc.9	Kidney	08	56	Male
Kidney.9wpc.11	Kidney	09	63	Male
Kidney.10wpc.12	Kidney	10	70	Female
Kidney.10wpc.13	Kidney	10	70	Female
Kidney.10wpc.14	Kidney	10	70	Female
Kidney.11wpc.15	Kidney	11	77	Female
Kidney.11wpc.16	Kidney	11	77	Male
Kidney.12wpc.17	Kidney	12	84	Female
Kidney.12wpc.18	Kidney	12	84	Male
Kidney.13wpc.19	Kidney	13	91	Female
Kidney.13wpc.20	Kidney	13	91	Male
Kidney.13wpc.21	Kidney	13	91	Male
Kidney.16wpc.23	Kidney	16	112	Male
Kidney.16wpc.24	Kidney	16	112	Male
Kidney.18wpc.25	Kidney	18	126	Female
Kidney.18wpc.26	Kidney	18	126	Female
Kidney.19wpc.30	Kidney	19	133	Male
Kidney.20wpc.28	Kidney	20	140	Female
Kidney.20wpc.29	Kidney	20	140	Male
Kidney.newborn.31	Kidney	newborn	280	Female
Kidney.newborn.32	Kidney	newborn	280	Female
Kidney.newborn.33	Kidney	newborn	280	Male
Kidney.infant.34	Kidney	infant	463	Female
Kidney.infant.36	Kidney	infant	463	Female
Kidney.infant.37	Kidney	infant	463	Male
Kidney.toddler.38	Kidney	toddler	1375	Female
Kidney.toddler.39	Kidney	toddler	1375	Male
Kidney.school.40	Kidney	school	3200	Female
Liver.4wpc.1	Liver	04	28	Female
Liver.4wpc.2	Liver	04	28	Male
Liver.4wpc.3	Liver	04	28	Male
Liver.4wpc.4	Liver	04	28	Male
Liver.5wpc.5	Liver	05	35	Female
Liver.5wpc.6	Liver	05	35	Male
Liver.6wpc.7	Liver	06	42	Female
Liver.6wpc.8	Liver	06	42	Male
Liver.7wpc.9	Liver	07	49	Female
Liver.7wpc.10	Liver	07	49	Male
Liver.7wpc.11	Liver	07	49	Male
Liver.7wpc.12	Liver	07	49	Male
Liver.8wpc.13	Liver	08	56	Female
Liver.8wpc.14	Liver	08	56	Female
Liver.8wpc.15	Liver	08	56	Male
Liver.8wpc.16	Liver	08	56	Male
Liver.9wpc.17	Liver	09	63	Female

Liver.9wpc.18	Liver	09	63	Male
Liver.9wpc.19	Liver	09	63	Male
Liver.10wpc.20	Liver	10	70	Female
Liver.10wpc.21	Liver	10	70	Female
Liver.10wpc.22	Liver	10	70	Male
Liver.10wpc.23	Liver	10	70	Male
Liver.11wpc.24	Liver	11	77	Female
Liver.11wpc.25	Liver	11	77	Male
Liver.11wpc.26	Liver	11	77	Male
Liver.12wpc.27	Liver	12	84	Male
Liver.13wpc.28	Liver	13	91	Female
Liver.16wpc.29	Liver	16	112	Female
Liver.16wpc.30	Liver	16	112	Male
Liver.18wpc.31	Liver	18	126	Female
Liver.18wpc.32	Liver	18	126	Female
Liver.18wpc.33	Liver	18	126	Male
Liver.19wpc.34	Liver	19	133	Female
Liver.19wpc.36	Liver	19	133	Male
Liver.20wpc.35	Liver	20	140	Female
Liver.20wpc.37	Liver	20	140	Male
Liver.newborn.38	Liver	newborn	280	Female
Liver.newborn.39	Liver	newborn	280	Male
Liver.infant.40	Liver	infant	463	Male
Liver.toddler.42	Liver	toddler	1375	Female
Liver.school.43	Liver	school	3200	Male
Liver.teenager.44	Liver	teenager	5755	Male
Liver.youngAdult.45	Liver	youngAdult	11230	Male
Liver.youngAdult.46	Liver	youngAdult	11230	Male
Liver.youngAdult.47	Liver	youngAdult	11230	Male
Liver.olderMidAge.48	Liver	olderMidAge	18530	Male
Liver.senior.49	Liver	senior	22180	Male
Liver.senior.50	Liver	senior	22180	Male

Table S3 Characteristics (age and gender) of brain tissues analysed in this study.

Sample	Tissue	age	age (days)	Sex
Brain.5wpc.4	Brain	5	35	Female
Brain.7wpc.6	Brain	7	49	Female
Brain.8wpc.9	Brain	8	56	Female
Brain.8wpc.10	Brain	8	56	Female
Brain.9wpc.13	Brain	9	63	Female
Brain.10wpc.16	Brain	10	70	Female
Brain.11wpc.17	Brain	11	77	Female
Brain.13wpc.22	Brain	13	91	Female
Brain.16wpc.25	Brain	16	112	Female
Brain.19wpc.28	Brain	19	133	Female
Brain.20wpc.32	Brain	20	140	Female
Brain.newborn.34	Brain	newborn	280	Female
Brain.newborn.35	Brain	newborn	280	Female
Brain.toddler.38	Brain	toddler	1375	Female
Cerebellum.4wpc.1	Cerebellum	4	28	Female
Cerebellum.5wpc.4	Cerebellum	5	35	Female
Cerebellum.6wpc.6	Cerebellum	6	42	Female
Cerebellum.6wpc.7	Cerebellum	6	42	Female
Cerebellum.7wpc.10	Cerebellum	7	49	Female
Cerebellum.8wpc.13	Cerebellum	8	56	Female
Cerebellum.8wpc.14	Cerebellum	8	56	Female
Cerebellum.9wpc.17	Cerebellum	9	63	Female
Cerebellum.10wpc.19	Cerebellum	10	70	Female
Cerebellum.11wpc.21	Cerebellum	11	77	Female
Cerebellum.12wpc.25	Cerebellum	12	84	Female
Cerebellum.13wpc.28	Cerebellum	13	91	Female
Cerebellum.16wpc.31	Cerebellum	16	112	Female
Cerebellum.16wpc.32	Cerebellum	16	112	Female
Cerebellum.newborn.34	Cerebellum	newborn	280	Female
Cerebellum.newborn.35	Cerebellum	newborn	280	Female
Cerebellum.newborn.37	Cerebellum	newborn	280	Female
Cerebellum.infant.39	Cerebellum	infant	463	Female
Cerebellum.toddler.42	Cerebellum	toddler	1375	Female
Cerebellum.school.44	Cerebellum	school	3200	Female
Cerebellum.youngAdult.51	Cerebellum	youngAdult	11230	Female
Brain.4wpc.1	Brain	4	28	Male
Brain.4wpc.2	Brain	4	28	Male
Brain.4wpc.3	Brain	4	28	Male
Brain.5wpc.5	Brain	5	35	Male
Brain.7wpc.7	Brain	7	49	Male
Brain.7wpc.8	Brain	7	49	Male
Brain.8wpc.11	Brain	8	56	Male
Brain.8wpc.12	Brain	8	56	Male
Brain.9wpc.14	Brain	9	63	Male
Brain.9wpc.15	Brain	9	63	Male
Brain.11wpc.18	Brain	11	77	Male
Brain.11wpc.19	Brain	11	77	Male

Brain.11wpc.20	Brain	11	77	Male
Brain.12wpc.21	Brain	12	84	Male
Brain.13wpc.23	Brain	13	91	Male
Brain.13wpc.24	Brain	13	91	Male
Brain.16wpc.26	Brain	16	112	Male
Brain.18wpc.27	Brain	18	126	Male
Brain.19wpc.29	Brain	19	133	Male
Brain.19wpc.30	Brain	19	133	Male
Brain.20wpc.31	Brain	20	140	Male
Brain.newborn.33	Brain	newborn	280	Male
Brain.infant.37	Brain	infant	463	Male
Brain.toddler.39	Brain	toddler	1375	Male
Brain.toddler.40	Brain	toddler	1375	Male
Brain.school.41	Brain	school	3200	Male
Brain.school.42	Brain	school	3200	Male
Brain.teenager.43	Brain	teenager	5755	Male
Brain.teenager.44	Brain	teenager	5755	Male
Brain.teenager.45	Brain	teenager	5755	Male
Brain.youngAdult.47	Brain	youngAdult	11230	Male
Brain.youngAdult.48	Brain	youngAdult	11230	Male
Brain.youngAdult.49	Brain	youngAdult	11230	Male
Brain.youngMidAge.50	Brain	youngMidAge	14880	Male
Brain.youngMidAge.51	Brain	youngMidAge	14880	Male
Brain.olderMidAge.52	Brain	olderMidAge	18530	Male
Brain.olderMidAge.53	Brain	olderMidAge	18530	Male
Brain.senior.54	Brain	senior	22180	Male
Brain.senior.55	Brain	senior	22180	Male
Cerebellum.4wpc.2	Cerebellum	4	28	Male
Cerebellum.4wpc.3	Cerebellum	4	28	Male
Cerebellum.5wpc.5	Cerebellum	5	35	Male
Cerebellum.6wpc.8	Cerebellum	6	42	Male
Cerebellum.6wpc.9	Cerebellum	6	42	Male
Cerebellum.7wpc.11	Cerebellum	7	49	Male
Cerebellum.7wpc.12	Cerebellum	7	49	Male
Cerebellum.8wpc.15	Cerebellum	8	56	Male
Cerebellum.8wpc.16	Cerebellum	8	56	Male
Cerebellum.9wpc.18	Cerebellum	9	63	Male
Cerebellum.10wpc.20	Cerebellum	10	70	Male
Cerebellum.11wpc.22	Cerebellum	11	77	Male
Cerebellum.11wpc.23	Cerebellum	11	77	Male
Cerebellum.11wpc.24	Cerebellum	11	77	Male
Cerebellum.12wpc.26	Cerebellum	12	84	Male
Cerebellum.12wpc.27	Cerebellum	12	84	Male
Cerebellum.13wpc.29	Cerebellum	13	91	Male
Cerebellum.13wpc.30	Cerebellum	13	91	Male
Cerebellum.16wpc.33	Cerebellum	16	112	Male
Cerebellum.newborn.36	Cerebellum	newborn	280	Male
Cerebellum.infant.40	Cerebellum	infant	463	Male
Cerebellum.infant.41	Cerebellum	infant	463	Male
Cerebellum.toddler.43	Cerebellum	toddler	1375	Male

Cerebellum.school.45	Cerebellum	school	3200	Male
Cerebellum.school.46	Cerebellum	school	3200	Male
Cerebellum.teenager.47	Cerebellum	teenager	5755	Male
Cerebellum.teenager.48	Cerebellum	teenager	5755	Male
Cerebellum.teenager.49	Cerebellum	teenager	5755	Male
Cerebellum.teenager.50	Cerebellum	teenager	5755	Male
Cerebellum.youngAdult.52	Cerebellum	youngAdult	11230	Male
Cerebellum.youngAdult.53	Cerebellum	youngAdult	11230	Male
Cerebellum.youngMidAge.54	Cerebellum	youngMidAge	14880	Male
Cerebellum.youngMidAge.55	Cerebellum	youngMidAge	14880	Male
Cerebellum.olderMidAge.56	Cerebellum	olderMidAge	18530	Male
Cerebellum.olderMidAge.57	Cerebellum	olderMidAge	18530	Male
Cerebellum.senior.58	Cerebellum	senior	22180	Male
Cerebellum.senior.59	Cerebellum	senior	22180	Male

Supplementary Tables S4 to S16

Table S4

Pearson's correlation coefficients (R) between mRNA expression levels *TGFB1* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[†]
TGFB1	*	*	*	*	*	*	*	
TGFB2	0.28	-0.07	0.60[c]	-0.03	-0.05	0.16	-0.28	1+
TGFB3	0.18	0.05	-0.25	-0.13	0.35[a]	0.33	-0.19	
LTBP1	0.35	0.17	0.33	-0.41[a]	-0.12	0.70[d]	0.52[b]	2+
LTBP2	-0.35	0.11	-0.14	0.01	-0.08	0.67[d]	0.13	1+
LTBP3	0.02	0.18	0.05	0.44[a]	0.13	0.04	0.11	
LTBP4	0.03	0.34	0.13	0.46[a]	0.34[a]	0.47[b]	0.23	1+
FBN1	0.38	-0.02	-0.10	-0.07	0.05	0.62[c]	0.57[c]	2+
FBN2	0.34	-0.09	0.42[a]	-0.41[a]	-0.02	0.77[d]	0.55[b]	2+
FBN3	0.20	0.23	0.71[d]	-0.01	-0.06	0.47[b]	0.00	2+
TGFBR1	0.04	-0.10	0.20	-0.55[b]	-0.04	0.31	0.15	1-
TGFBR2	0.38	-0.11	-0.33	-0.06	0.12	0.522[b]	0.65[d]	2+
TGFBR3	0.19	-0.02	-0.12	0.07	0.09	0.73[d]	0.64[d]	2+
TGFB1I1	0.28	0.20	-0.33	0.46[a]	0.52[c]	0.32	0.38[a]	1+
TGFBR3L	-0.07	0.10	-0.08	0.68[d]	0.11	0.11	0.04	1+
TGFBI	0.30	0.09	0.49[b]	0.54[b]	0.10	0.73[d]	0.47[b]	4+
TGFBRAP1	0.27	0.07	0.25	-0.43[a]	0.05	-0.01	0.00	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S5

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFB3* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	0.18	0.05	-0.25	-0.13	0.35[a]	0.33	-0.19	
TGFB2	0.27	0.76[d]	0.07	0.70[d]	0.37[a]	0.66[d]	0.29	3+
TGFB3	*	*	*	*	*	*	*	
LTBP1	0.36	0.52[b]	0.16	0.32	-0.05	0.10	-0.28	1+
LTBP2	0.30	0.85[d]	0.86[d]	-0.05	0.44[b]	0.29	0.11	3+
LTBP3	0.52[a]	0.79[d]	0.35[a]	0.45[a]	0.02	0.70[d]	0.20	2+
LTBP4	0.74[c]	0.64[c]	0.21	0.02	0.56[c]	0.26	-0.34	3+
FBN1	0.18	0.83[d]	0.71[d]	0.30	0.50[b]	0.22	-0.21	3+
FBN2	-0.03	0.57[b]	-0.25	0.40[a]	0.42[b]	0.11	-0.28	2+
FBN3	0.54[a]	-0.23	-0.26	0.70[d]	0.24	0.28	0.49[b]	2+
TGFBR1	-0.05	0.05	0.11	0.35	0.37[a]	-0.26	-0.32	
TGFBR2	0.14	0.80[d]	0.45[b]	-0.37	0.17	0.43[a]	-0.18	2+
TGFBR3	-0.12	0.47[a]	-0.10	-0.50[b]	0.31	0.22	-0.36[a]	1-
TGFB1I1	0.87[d]	0.51[b]	0.00	-0.03	0.23	0.56[c]	-0.11	3+
TGFBR3L	0.46	-0.37	0.10	-0.10	-0.11	0.22	0.04	
TGFBI	0.88[d]	0.78[d]	0.01	0.41[a]	0.36[a]	0.52[b]	-0.26	3+
TGFBRAP1	-0.16	0.16	0.10	0.23	0.14	-0.17	0.48[b]	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S6

Pearson's correlation coefficients (R) between mRNA expression levels of *LTBP2* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs†**
TGFB1	-0.35	0.11	-0.14	0.01	-0.08	0.67^{d}	0.13	1+
TGFB2	-0.51^{a}	0.57^{b}	0.01	-0.25	-0.10	0.39^{a}	0.40^{a}	
TGFB3	0.30	0.85^{d}	0.86^{d}	-0.05	0.44^{b}	0.29	0.11	3+
LTBP1	-0.09	0.58^{b}	0.23	-0.31	0.66^{d}	0.49^{b}	0.16	3+
LTBP2	*	*	*	*	*	*	*	
LTBP3	0.36	0.63^{c}	0.44^{b}	0.14	-0.25	-0.02	-0.25	2+
LTBP4	0.44	0.69^{d}	0.44^{b}	0.23	0.08	0.12	-0.45^{a}	2+
FBN1	-0.40	0.83^{d}	0.66^{d}	0.50^{b}	0.14	0.59^{c}	0.31	4+
FBN2	-0.78^{c}	0.54^{b}	-0.12	0.09	-0.04	0.59^{c}	0.26	2+, 1-
FBN3	0.19	-0.19	-0.27	-0.55^{b}	-0.20	0.39^{a}	0.23	1-
TGFBR1	-0.63^{b}	-0.03	0.03	-0.30	-0.10	0.15	0.01	1-
TGFBR2	-0.52^{a}	0.67^{c}	0.46^{b}	0.50^{b}	0.60^{d}	0.470^{b}	0.50^{b}	6+
TGFBR3	-0.21	0.55^{b}	-0.05	0.23	-0.23	0.64^{d}	0.27	2+
TGFB1I1	0.15	0.49^{a}	0.07	0.27	-0.11	0.12	-0.34	
TGFBR3L	0.25	-0.37	-0.06	-0.02	-0.17	-0.11	-0.38^{a}	
TGFBI	-0.04	0.71^{d}	0.01	0.07	0.78^{d}	0.62^{c}	0.31	3+
TGFBRAP1	-0.39	0.16	0.15	-0.23	0.50^{b}	0.19	0.46^{b}	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. †Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S7

Pearson's correlation coefficients (R) between mRNA expression levels of *LTBP3* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs[ǂ]**
TGFB1	0.02	0.18	0.05	0.44[a]	0.13	0.04	0.11	
TGFB2	-0.15	0.37	-0.14	0.27	-0.01	0.44[a]	-0.09	
TGFB3	0.52[a]	0.79[d]	0.35[a]	0.45[a]	0.02	0.70[d]	0.20	2+
LTBP1	-0.17	0.11	0.00	-0.48[a]	-0.28	-0.39[a]	-0.13	
LTBP2	0.36	0.63[c]	0.44[b]	0.14	-0.25	-0.02	-0.25	2+
LTBP3	*	*	*	*	*	*	*	
LTBP4	0.74[c]	0.80[d]	0.77[d]	0.65[c]	0.21	0.32	0.07	4+
FBN1	-0.37	0.60[b]	-0.16	0.09	-0.23	-0.30	-0.46[b]	1+, 1-
FBN2	-0.46	0.29	-0.14	-0.29	-0.05	-0.36[a]	-0.46[b]	1-
FBN3	0.80[d]	-0.19	0.08	0.34	0.00	0.379[a]	0.00	1+
TGFBR1	-0.49[a]	-0.36	-0.38[a]	-0.42[a]	-0.11	-0.60[c]	-0.50[b]	2-
TGFBR2	-0.27	0.45[a]	-0.33	-0.22	-0.49[b]	-0.19	-0.12	1-
TGFBR3	-0.27	0.24	-0.55[c]	-0.30	-0.14	-0.32	-0.44[a]	1-
TGFB1I1	0.71[b]	0.81[d]	0.43[a]	0.54[b]	0.47[b]	0.51[b]	0.71[d]	6+
TGFBR3L	0.79[d]	0.12	0.37[a]	0.59[b]	0.59[c]	0.68[d]	0.47[b]	5+
TGFBI	0.44	0.61[c]	-0.15	0.51[b]	-0.32	-0.02	-0.46[b]	2+, 1-
TGFBRAP1	-0.63[b]	-0.26	-0.10	-0.17	-0.32	-0.41[a]	-0.06	1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S8

Pearson's correlation coefficients (R) between mRNA expression levels of *LTBP4* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	0.03	0.34	0.13	0.46[a]	0.34[a]	0.47[b]	0.23	1+
TGFB2	-0.12	0.11	-0.28	-0.30	0.67[d]	-0.07	-0.45[b]	1-
TGFB3	0.74[c]	0.64[c]	0.21	0.02	0.56[c]	0.26	-0.34	3+
LTBP1	0.14	0.09	0.08	-0.25	-0.06	0.32	0.17	
LTBP2	0.44	0.69[d]	0.44[b]	0.23	0.08	0.12	-0.44[a]	2+
LTBP3	0.74[c]	0.80[d]	0.77[d]	0.65[c]	0.21	0.32	0.07	4+
LTBP4	*	*	*	*	*	*	*	
FBN1	-0.04	0.65[c]	-0.08	0.03	0.72[d]	0.07	0.01	2+
FBN2	-0.33	0.35	-0.03	-0.32	0.74[d]	0.23	0.03	1+
FBN3	0.44	-0.38	-0.13	0.08	0.69[d]	0.59[c]	-0.44[a]	2+
TGFBR1	-0.45	-0.51[b]	-0.48[b]	-0.75[d]	0.52[c]	0.06	0.18	1+, 3-
TGFBR2	-0.18	0.40[a]	-0.12	0.11	-0.02	-0.12	-0.12	
TGFBR3	-0.34	0.52[b]	-0.29	-0.19	0.64[d]	0.12	0.09	2+
TGFB1I1	0.87[d]	0.82[d]	0.59[c]	0.92[d]	0.41[a]	0.66[d]	0.29	5+
TGFBR3L	0.50[a]	0.00	0.03	0.49[b]	-0.09	0.22	0.19	1+
TGFBI	0.56[a]	0.38	-0.04	0.40[a]	0.21	0.26	-0.03	
TGFBRAP1	-0.37	-0.09	-0.03	-0.02	0.18	-0.37[a]	-0.45[a]	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S9

Pearson's correlation coefficients (R) between mRNA expression levels of *FBN1* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	0.38	-0.02	-0.10	-0.07	0.05	0.62[c]	0.57[c]	2+
TGFB2	0.75[c]	0.62[c]	0.38[a]	0.23	0.85[d]	0.37[a]	-0.05	3+
TGFB3	0.18	0.83[d]	0.71[d]	0.30	0.50[b]	0.22	-0.21	3+
LTBP1	0.84[d]	0.55[b]	0.47[b]	0.22	0.17	0.81[d]	0.79[d]	5+
LTBP2	-0.40	0.83[d]	0.66[d]	0.50[b]	0.14	0.59[c]	0.31	4+
LTBP3	-0.37	0.60[b]	-0.16	0.09	-0.23	-0.30	-0.46[b]	1+, 1-
LTBP4	-0.04	0.65[c]	-0.08	0.03	0.72[d]	0.07	0.01	2+
FBN1	*	*	*	*	*	*	*	
FBN2	0.65[b]	0.85[d]	0.08	0.71[d]	0.91[d]	0.92[d]	0.94[d]	6+
FBN3	-0.24	-0.53[b]	-0.14	-0.21	0.84[d]	0.28	0.18	1+, 1-
TGFBR1	0.56[a]	-0.02	0.54[b]	0.11	0.86[d]	0.461[b]	0.71[d]	4+
TGFBR2	0.90[d]	0.84[d]	0.80[d]	0.38	0.34[a]	0.77[d]	0.63[c]	5+
TGFBR3	0.63[b]	0.69[d]	0.31	0.14	0.87[d]	0.93[d]	0.91[d]	5+
TGFB1I1	0.13	0.44[a]	-0.42[a]	0.05	-0.13	0.01	-0.24	
TGFBR3L	-0.57[a]	-0.45[a]	-0.40[a]	-0.13	0.56[c]	-0.31	-0.38[a]	1+
TGFBI	0.28	0.69[d]	0.36[a]	0.18	0.28	0.85[d]	0.88[d]	3+
TGFBRAP1	0.81[d]	0.17	0.35[a]	-0.01	0.49[b]	0.22	0.24	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001 [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S10

Pearson's correlation coefficients (R) between mRNA expression levels of *FBN2* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs[ǂ]**
TGFB1	0.34	-0.09	0.42[a]	-0.41[a]	-0.02	0.77[d]	0.55[b]	2+
TGFB2	0.65[b]	0.62[c]	0.46[b]	0.36	0.98[d]	0.10	-0.11	4+
TGFB3	-0.03	0.57[b]	-0.25	0.40[a]	0.42[b]	0.11	-0.28	2+
LTBP1	0.41	0.60[b]	0.71[d]	0.67[c]	0.02	0.93[d]	0.87[d]	5+
LTBP2	-0.78[c]	0.54[b]	-0.12	0.09	-0.04	0.59[c]	0.26	2+, 1-
LTBP3	-0.46	0.29	-0.14	-0.29	-0.05	-0.36[a]	-0.46[b]	1-
LTBP4	-0.33	0.35	-0.03	-0.32	0.74[d]	0.23	0.03	1+
FBN1	0.65[b]	0.85[d]	0.08	0.71[d]	0.91[d]	0.92[d]	0.94[d]	6+
FBN2	*	*	*	*	*	*	*	
FBN3	-0.13	-0.54[b]	0.31	0.05	0.92[d]	0.27	0.21	1+, 1-
TGFBR1	0.91[d]	0.20	0.21	0.45[a]	0.85[d]	0.65[d]	0.68[d]	4+
TGFBR2	0.63[b]	0.77[d]	0.04	0.20	0.03	0.68[d]	0.54[b]	4+
TGFBR3	0.33	0.70[d]	-0.08	0.07	0.81[d]	0.95[d]	0.88[d]	4+
TGFB1I1	-0.10	0.10	-0.25	-0.22	0.03	0.06	-0.21	
TGFBR3L	-0.36	-0.56[b]	-0.35[a]	-0.58[b]	-0.36[a]	-0.33	-0.39[a]	2-
TGFBI	0.19	0.58[b]	0.21	0.01	0.11	0.86[d]	0.97[d]	3+
TGFBRAP1	0.69[b]	0.30	0.48[b]	0.33	0.29	0.10	0.11	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S11

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFBR2* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[†]
TGFB1	0.38	-0.11	-0.33	-0.06	0.12	0.52^{b}	0.65^{d}	2+
TGFB2	0.80^{d}	0.73^{d}	0.01	-0.33	-0.05	0.44^{a}	-0.08	2+
TGFB3	0.14	0.80^{d}	0.45^{b}	-0.37	0.17	0.43^{a}	-0.18	2+
LTBP1	0.71^{c}	0.57^{b}	0.39^{a}	-0.12	0.75^{d}	0.58^{c}	0.51^{b}	5+
LTBP2	-0.52^{a}	0.67^{c}	0.46^{b}	0.50^{b}	0.60^{d}	0.47^{b}	0.50^{b}	6+
LTBP3	-0.27	0.45^{a}	-0.33	-0.22	-0.49^{b}	-0.19	-0.12	1-
LTBP4	-0.18	0.40^{a}	-0.12	0.11	-0.02	-0.12	-0.12	
FBN1	0.90^{d}	0.84^{d}	0.80^{d}	0.38	0.34^{a}	0.78^{d}	0.63^{c}	5+
FBN2	0.63^{b}	0.77^{d}	0.04	0.20	0.03	0.68^{d}	0.54^{b}	4+
FBN3	-0.12	-0.48^{a}	-0.46^{b}	-0.79^{d}	-0.11	0.07	-0.03	2-
TGFBR1	0.58^{a}	0.21	0.39^{a}	-0.37	0.18	0.33	0.29	
TGFBR2	*	*	*	*	*	*	*	
TGFBR3	0.72^{c}	0.72^{d}	0.53^{b}	0.82^{d}	0.11	0.80^{d}	0.71^{d}	6+
TGFB1I1	0.14	0.16	-0.24	0.21	-0.40^{a}	0.04	0.06	
TGFBR3L	-0.39	-0.70^{d}	-0.37^{a}	-0.16	-0.58^{c}	-0.27	-0.29	2-
TGFBI	0.37	0.56^{b}	0.16	-0.02	0.58^{c}	0.78^{d}	0.51^{b}	4+
TGFBRAP1	0.63^{b}	0.50^{b}	0.39^{a}	-0.18	0.82^{d}	0.28	0.36^{a}	3+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S12

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFBR3* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[ǂ]
TGFB1	0.19	-0.02	-0.12	0.07	0.09	0.73^{d}	0.64^{d}	2+
TGFB2	0.65^{b}	0.25	0.11	-0.17	0.74^{d}	0.23	-0.19	2+
TGFB3	-0.12	0.47^{a}	-0.10	-0.49^{b}	0.31	0.22	-0.36^{a}	1-
LTBP1	0.63^{b}	0.39^{a}	0.07	-0.25	-0.16	0.86^{d}	0.70^{d}	3+
LTBP2	-0.21	0.55^{b}	-0.05	0.23	-0.23	0.64^{d}	0.27	2+
LTBP3	-0.27	0.24	-0.55^{c}	-0.30	-0.14	-0.32	-0.44^{a}	1-
LTBP4	-0.34	0.52^{b}	-0.29	-0.19	0.64^{d}	0.12	0.09	2+
FBN1	0.63^{b}	0.69^{d}	0.31	0.14	0.87^{d}	0.93^{d}	0.91^{d}	5+
FBN2	0.33	0.70^{d}	-0.08	0.07	0.81^{d}	0.95^{d}	0.87^{d}	4+
FBN3	-0.10	-0.63^{c}	-0.13	-0.77^{d}	0.86^{d}	0.26	0.02	1+, 2-
TGFBR1	0.43	-0.12	0.50^{b}	-0.20	0.85^{d}	0.55^{c}	0.62^{c}	4+
TGFBR2	0.72^{c}	0.72^{d}	0.53^{b}	0.82^{d}	0.11	0.80^{d}	0.71^{d}	6+
TGFBR3	*	*	*	*	*	*	*	
TGFB1I1	-0.16	0.26	-0.37^{a}	-0.07	-0.14	-0.02	-0.10	
TGFBR3L	-0.41	-0.56^{b}	-0.42^{a}	-0.06	-0.51^{b}	-0.34	-0.34	2-
TGFBI	-0.01	0.26	0.32	-0.05	-0.06	0.90^{d}	0.83^{d}	2+
TGFBRAP1	0.61^{b}	0.51^{b}	0.26	-0.34	0.24	0.15	0.07	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S13

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFB1I1* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[†]
TGFB1	0.28	0.20	-0.33	0.46[a]	0.52[c]	0.32	0.38[a]	1+
TGFB2	0.18	-0.04	-0.76[d]	-0.36	0.02	0.28	-0.36[a]	1-
TGFB3	0.87[d]	0.51[b]	0.00	-0.03	0.23	0.56[c]	-0.11	3+
LTBP1	0.27	-0.12	-0.22	-0.14	-0.25	0.15	0.07	
LTBP2	0.15	0.49[a]	0.07	0.27	-0.11	0.12	-0.34	
LTBP3	0.71[b]	0.81[d]	0.43[a]	0.54[b]	0.47[b]	0.51[b]	0.71[d]	6+
LTBP4	0.87[d]	0.82[d]	0.59[c]	0.92[d]	0.41[a]	0.66[d]	0.29	5+
FBN1	0.13	0.44[a]	-0.42[a]	0.05	-0.13	0.01	-0.24	
FBN2	-0.10	0.10	-0.25	-0.22	0.03	0.06	-0.21	
FBN3	0.55[a]	-0.35	-0.54[c]	-0.04	-0.04	0.22	-0.30	1-
TGFBR1	-0.24	-0.70[d]	-0.78[d]	-0.77[d]	-0.19	-0.01	-0.30	3-
TGFBR2	0.14	0.16	-0.24	0.21	-0.40[a]	0.04	0.06	
TGFBR3	-0.16	0.26	-0.37[a]	-0.07	-0.14	-0.02	-0.10	
TGFB1I1	*	*	*	*	*	*	*	
TGFBR3L	0.55[a]	0.40[a]	0.26	0.43[a]	0.50[b]	0.25	0.36[a]	1+
TGFBI	0.84[d]	0.40[a]	-0.45[b]	0.49[b]	0.01	0.30	-0.24	2+, 1-
TGFBRAP1	-0.30	-0.40[a]	-0.39[a]	0.08	-0.33[a]	-0.32	-0.23	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S14

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFBR3L* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[ǂ]
TGFB1	-0.07	0.10	-0.08	0.68^{d}	0.11	0.11	0.04	1+
TGFB2	-0.18	-0.57^{b}	-0.27	-0.15	-0.31	0.30	-0.14	1-
TGFB3	0.46	-0.37	0.10	-0.10	-0.11	0.22	0.04	
LTBP1	-0.42	-0.60^{b}	-0.32	-0.45^{a}	-0.38^{a}	-0.36^{a}	-0.30	1-
LTBP2	0.25	-0.37	-0.06	-0.02	-0.17	-0.11	-0.38^{a}	
LTBP3	0.79^{d}	0.12	0.37^{a}	0.59^{b}	0.59^{c}	0.68^{d}	0.47^{b}	5+
LTBP4	0.50^{a}	0.00	0.03	0.49^{b}	-0.09	0.22	0.19	1+
FBN1	-0.57^{a}	-0.45^{a}	-0.39^{a}	-0.13	-0.56^{c}	-0.31	-0.38^{a}	1-
FBN2	-0.36	-0.56^{b}	-0.35^{a}	-0.58^{b}	-0.36^{a}	-0.33	-0.39^{a}	2-
FBN3	0.79^{c}	0.08	-0.01	-0.03	-0.31	0.41^{a}	-0.21	1+
TGFBR1	-0.32	-0.57^{b}	-0.37^{a}	-0.58^{b}	-0.50^{b}	-0.54^{b}	-0.47^{b}	5-
TGFBR2	-0.39	-0.70^{d}	-0.37^{a}	-0.16	-0.58^{c}	-0.27	-0.29	2-
TGFBR3	-0.41	-0.56^{b}	-0.42^{a}	-0.06	-0.51^{b}	-0.34	-0.34	2-
TGFB1I1	0.55^{a}	0.40^{a}	0.26	0.43^{a}	0.50^{b}	0.25	0.36^{a}	1+
TGFBR3L	*	*	*	*	*	*	*	
TGFBI	0.53^{a}	-0.20	-0.36^{a}	0.52^{b}	-0.23	-0.19	-0.40^{a}	1+
TGFBRAP1	-0.73^{c}	-0.77^{d}	-0.26	-0.45^{a}	-0.60^{d}	-0.22	-0.32	3-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S15

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFBI* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[†]
TGFB1	0.30	0.09	0.49[b]	0.54[b]	0.10	0.73[d]	0.47[b]	3+, 1-
TGFB2	0.47[a]	0.77[d]	0.72[d]	0.32	0.07	0.40[a]	-0.10	2+
TGFB3	0.88[d]	0.78[d]	0.01	0.41[a]	0.36[a]	0.52[b]	-0.26	3+
LTBP1	0.33	0.72[d]	0.47[b]	0.03	0.62[d]	0.79[d]	0.84[d]	5+
LTBP2	-0.04	0.71[d]	0.01	0.07	0.78[d]	0.62[c]	0.31	3+
LTBP3	0.44	0.61[c]	-0.15	0.51[b]	-0.32	-0.02	-0.46[b]	2+, 1-
LTBP4	0.56[a]	0.38	-0.04	0.40[a]	0.21	0.26	-0.03	
FBN1	0.28	0.70[d]	0.36[a]	0.18	0.28	0.85[d]	0.88[d]	3+
FBN2	0.19	0.58[b]	0.21	0.01	0.11	0.85[d]	0.97[d]	3+
FBN3	0.54[a]	-0.04	0.50[b]	0.20	-0.06	0.30	0.25	1+
TGFBR1	0.14	0.18	0.61[c]	-0.29	-0.01	0.41[a]	0.60[c]	2+
TGFBR2	0.37	0.56[b]	0.16	-0.02	0.58[c]	0.78[d]	0.51[b]	3+
TGFBR3	-0.01	0.26	0.32	-0.05	-0.06	0.90[d]	0.83[d]	2+
TGFB1I1	0.84[d]	0.40[a]	-0.45[b]	0.49[b]	0.01	0.30	-0.24	2+, 1-
TGFBR3L	0.53[a]	-0.20	-0.36[a]	0.52[b]	-0.23	-0.19	-0.40[a]	1+
TGFBI	*	*	*	*	*	*	*	
TGFBRAP1	-0.08	-0.01	0.29	-0.22	0.44[b]	-0.01	0.08	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Table S16

Pearson's correlation coefficients (R) between mRNA expression levels of *TGFBRAP1* and TGFβ signalling molecules in different fetal tissues/organs and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[†]
TGFB1	0.25	0.27	0.07	-0.43^{a}	0.05	-0.01	0.00	
TGFB2	0.50^{b}	0.66^{b}	0.38	0.03	0.22	0.16	0.33	2+
TGFB3	0.10	-0.16	0.16	0.23	0.14	-0.17	0.48^{b}	1+
LTBP1	0.61^{c}	0.71^{b}	0.49^{a}	0.63^{c}	0.81^{d}	0.06	0.14	4+
LTBP2	0.15	-0.39	0.16	-0.23	0.50^{b}	0.19	0.46^{b}	2+
LTBP3	-0.10	-0.63^{b}	-0.26	-0.17	-0.32	-0.41^{a}	-0.06	1-
LTBP4	-0.03	-0.37	-0.09	-0.02	0.18	-0.37^{a}	-0.44^{a}	
FBN1	0.35^{a}	0.81^{d}	0.17	-0.01	0.49^{b}	0.22	0.24	2+
FBN2	0.48^{b}	0.69^{b}	0.30	0.33	0.29	0.10	0.11	2+
FBN3	0.28	-0.38	0.00	0.40^{a}	0.18	-0.12	0.43^{a}	
TGFBR1	0.37^{a}	0.68^{b}	0.52^{b}	0.26	0.36^{a}	0.10	0.03	2+
TGFBR2	0.39^{a}	0.63^{b}	0.50^{b}	-0.18	0.82^{d}	0.28	0.36^{a}	3+
TGFBR3	0.26	0.61^{b}	0.51^{b}	-0.34	0.24	0.15	0.07	2+
TGFB1I1	-0.39^{a}	-0.30	-0.40^{a}	0.08	-0.33^{a}	-0.32	-0.23	
TGFBR3L	-0.26	-0.73^{c}	-0.77^{d}	-0.45^{a}	-0.60^{d}	-0.22	-0.32	3-
TGFBI	0.29	-0.08	-0.01	-0.22	0.44^{b}	-0.01	0.08	1+
TGFBRAP1	*	*	*	*	*	*	*	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations. '*' was for the correlation between the same gene.

Supplementary Tables S17 to S40

Table S17

Pearson's correlation coefficients (R) between mRNA expression levels of *FSHB* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[‡]
TGFB1	-	-	-	0.36	-	-0.09	-	
TGFB2	-	-	-	-0.07	-	-0.02	-	
TGFB3	-	-	-	-0.05	-	-0.15	-	
LTBP1	-	-	-	-0.40[a]	-	-0.17	-	
LTBP2	-	-	-	0.43[a]	-	0.00	-	
LTBP3	-	-	-	0.40[a]	-	0.02	-	
LTBP4	-	-	-	0.27	-	0.07	-	
FBN1	-	-	-	0.33	-	-0.09	-	
FBN2	-	-	-	-0.11	-	-0.09	-	
FBN3	-	-	-	-0.28	-	0.20	-	
TGFBR1	-	-	-	-0.31	-	-0.16	-	
TGFBR2	-	-	-	0.27	-	-0.13	-	
TGFBR3	-	-	-	0.17	-	-0.13	-	
TGFB1I1	-	-	-	0.24	-	0.07	-	
TGFBR3L	-	-	-	0.42[a]	-	0.04	-	
TGFBI	-	-	-	0.38	-	-0.11	-	
TGFBRAP1	-	-	-	-0.31	-	0.04	-	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S18

Pearson's correlation coefficients (R) between mRNA expression of *FSHR* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[†]
TGFB1	-0.19	-0.12	0.62[c]	0.07	-0.09	0.48[b]	0.59[c]	3+
TGFB2	-0.34	-0.54[b]	0.85[d]	0.65[c]	0.97[d]	0.21	-0.08	3+, 1-
TGFB3	0.27	-0.38	0.32	0.23	0.30	0.16	-0.21	
LTBP1	-0.12	-0.25	0.48[b]	0.08	0.04	0.55[c]	0.52[b]	3+
LTBP2	0.73[c]	-0.17	0.26	-0.31	-0.09	0.32	0.19	1+
LTBP3	0.23	-0.34	-0.06	0.01	0.04	-0.27	-0.36[a]	
LTBP4	0.24	0.02	-0.21	-0.32	0.65[d]	-0.13	-0.01	1+
FBN1	-0.41	-0.11	0.52[b]	0.06	0.80[d]	0.68[d]	0.72[d]	4+
FBN2	-0.55[a]	-0.12	0.31	0.21	0.95[d]	0.69[d]	0.71[d]	3+
FBN3	0.24	-0.25	0.62[d]	0.32	0.85[d]	0.01	0.10	2+
TGFBR1	-0.50[a]	-0.31	0.59[c]	0.41[a]	0.77[d]	0.32	0.45[b]	3+
TGFBR2	-0.42	-0.19	0.16	-0.37	-0.07	0.69[d]	0.36[a]	1+
TGFBR3	-0.44	0.22	0.06	-0.10	0.67[d]	0.71[d]	0.68[d]	3+
TGFB1I1	0.09	-0.08	-0.70[d]	-0.36	0.08	-0.23	-0.22	1-
TGFBR3L	0.33	0.02	-0.18	-0.20	-0.23	-0.28	-0.08	
TGFBI	0.09	-0.53[b]	0.54[b]	-0.02	0.10	0.56[c]	0.61[c]	3+, 1-
TGFBRAP1	-0.30	0.07	0.54[b]	0.11	0.21	0.04	0.09	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S19

Pearson's correlation coefficients (R) between mRNA expression of *LHCGR* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[†]
TGFB1	0.03	-0.10	0.11	-0.37	0.16	0.52[b]	0.33	1+
TGFB2	0.22	-0.69[d]	0.53[b]	0.42[a]	0.28	0.13	-0.14	1+, 1-
TGFB3	-0.26	-0.44[a]	0.54[b]	0.64[c]	0.08	-0.07	-0.30	2+
LTBP1	0.03	-0.43[a]	0.19	0.03	-0.31	0.62[c]	0.75[d]	2+
LTBP2	-0.62[b]	-0.23	0.35[a]	0.20	-0.27	0.36[a]	0.24	1-
LTBP3	-0.52[a]	-0.25	-0.16	0.20	-0.14	-0.29	-0.45[b]	1-
LTBP4	-0.45	0.15	-0.34	-0.29	0.09	-0.10	0.01	
FBN1	0.19	-0.13	0.71[d]	0.30	0.25	0.75[d]	0.76[d]	3+
FBN2	0.82[d]	-0.07	-0.05	0.20	0.28	0.76[d]	0.85[d]	3+
FBN3	-0.22	-0.44[a]	0.21	0.22	0.28	0.20	0.12	
TGFBR1	0.79[c]	-0.54[b]	0.47[b]	0.40[a]	0.37[a]	0.42[a]	0.58[c]	3+, 1-
TGFBR2	0.18	-0.25	0.33	-0.21	-0.03	0.60[c]	0.35	1+
TGFBR3	0.04	0.41[a]	-0.01	-0.31	0.41[a]	0.77[d]	0.67[d]	2+
TGFB1I1	-0.36	0.15	-0.55[c]	-0.39[a]	-0.06	-0.27	-0.30	1-
TGFBR3L	-0.27	0.19	-0.07	-0.05	-0.20	-0.06	-0.34	
TGFBI	-0.12	-0.54[b]	0.28	-0.05	-0.12	0.59[c]	0.84[d]	2+, 1-
TGFBRAP1	0.41	0.00	0.15	-0.02	-0.11	-0.02	0.01	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S20

Pearson's correlation coefficients (R) between mRNA expression levels of *AR* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[‡]
TGFB1	-0.28	-0.43[a]	-0.04	-0.15	-0.38[a]	0.68[d]	0.46[b]	2+
TGFB2	-0.02	0.56[b]	0.49[b]	0.59[b]	0.04	0.21	-0.23	3+
TGFB3	0.28	0.72[d]	0.74[d]	0.35	-0.08	0.26	-0.42[a]	2+
LTBP1	0.45	0.19	0.44[b]	-0.10	0.61[d]	0.92[d]	0.76[d]	4+
LTBP2	0.52[a]	0.53[b]	0.63[d]	0.37	0.52[c]	0.53[b]	0.10	4+
LTBP3	-0.02	0.55[b]	-0.03	0.15	-0.30	-0.26	-0.48[b]	1+, 1-
LTBP4	0.47[a]	0.39[a]	-0.08	-0.26	-0.16	0.19	0.29	
FBN1	0.29	0.74[d]	0.94[d]	0.47[a]	0.13	0.85[d]	0.85[d]	4+
FBN2	-0.31	0.67[c]	0.07	0.32	0.04	0.92[d]	0.83[d]	3+
FBN3	-0.34	-0.62[c]	0.03	-0.02	-0.02	0.07	-0.07	1-
TGFBR1	-0.29	-0.02	0.54[c]	0.44[a]	0.01	0.74[d]	0.87[d]	3+
TGFBR2	0.01	0.84[d]	0.65[d]	0.08	0.53[c]	0.72[d]	0.40[a]	4+
TGFBR3	0.12	0.56[b]	0.09	0.17	-0.07	0.89[d]	0.74[d]	3+
TGFB1I1	0.23	0.31	-0.44[b]	-0.28	-0.55[c]	0.20	-0.23	2-
TGFBR3L	-0.35	-0.38	-0.24	-0.29	-0.29	-0.36[a]	-0.33	
TGFBI	-0.02	0.44[a]	0.38[a]	0.04	0.57[c]	0.86	0.75[d]	2+
TGFBRAP1	0.19	0.15	0.32	0.07	0.48[b]	0.08	-0.02	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S21

Pearson's correlation coefficients (R) between mRNA expression levels of *AMH* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[†]
TGFB1	0.16	0.06	-0.13	-0.09	-0.14	-0.14	-0.19	
TGFB2	-0.06	-0.81[d]	-0.29	0.19	0.03	-0.39[a]	-0.25	1-
TGFB3	0.64[b]	-0.51[b]	-0.16	0.53[b]	-0.09	-0.14	-0.32	2+, 1-
LTBP1	-0.24	-0.67[c]	-0.53[b]	0.10	-0.39[a]	-0.32	-0.24	2-
LTBP2	0.12	-0.41[a]	-0.29	-0.29	-0.30	-0.47[b]	-0.31	1-
LTBP3	0.72[c]	-0.08	0.26	0.45[a]	0.45[b]	0.26	-0.05	2+
LTBP4	0.55[a]	0.09	0.04	0.27	0.13	0.56[c]	0.48[b]	2+
FBN1	-0.38	-0.40[a]	-0.52[b]	-0.12	-0.23	-0.49[b]	-0.26	2-
FBN2	-0.16	-0.44[a]	-0.26	-0.13	0.00	-0.36[a]	-0.20	
FBN3	0.74[c]	-0.21	0.13	0.80[d]	0.07	0.09	-0.38[a]	2+
TGFBR1	-0.23	-0.75[d]	-0.32	0.21	-0.15	-0.28	-0.06	1-
TGFBR2	-0.29	-0.64[c]	-0.55[c]	-0.71[d]	-0.61[d]	-0.60[c]	-0.49[b]	6-
TGFBR3	-0.52[a]	-0.17	-0.51[b]	-0.80[d]	-0.12	-0.49[b]	-0.24	3-
TGFB1I1	0.67[b]	0.39[a]	0.36[a]	0.05	0.25	0.36[a]	-0.10	1+
TGFBR3L	0.78[c]	0.78[d]	0.48[b]	0.14	0.58[c]	0.33	0.34	4+
TGFBI	0.63[b]	-0.42[a]	-0.50[b]	0.00	-0.47[b]	-0.38[a]	-0.17	1+, 2-
TGFBRAP1	-0.54[a]	-0.60[b]	-0.40[a]	0.28	-0.45[b]	-0.62[c]	-0.56[c]	4-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S22

Pearson's correlation coefficients (R) between mRNA expression levels of *INSR* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	-0.15	-0.19	-0.14	0.37	0.18	-0.62[c]	-0.37[a]	1-
TGFB2	0.00	-0.62[c]	-0.39[a]	0.07	-0.40[a]	0.00	0.30	1-
TGFB3	0.07	-0.21	-0.14	0.13	0.10	-0.20	0.62[c]	1+
LTBP1	-0.02	-0.38	0.03	-0.29	0.34[a]	-0.35[a]	-0.51[b]	1-
LTBP2	0.33	-0.03	-0.15	0.21	0.41[a]	-0.44[a]	0.07	
LTBP3	0.44	-0.01	-0.09	0.41[a]	0.24	-0.14	0.28	
LTBP4	0.15	0.30	0.00	0.18	-0.29	-0.33	-0.37[a]	
FBN1	-0.23	-0.01	-0.21	0.05	-0.42[a]	-0.29	-0.51[b]	1-
FBN2	-0.22	-0.13	-0.13	-0.20	-0.43[b]	-0.46[b]	-0.60[c]	3-
FBN3	0.50[a]	-0.45[a]	-0.40[a]	-0.21	-0.52[c]	-0.25	0.28	1-
TGFBR1	-0.10	-0.72[d]	-0.14	-0.26	-0.36[a]	-0.11	-0.45[b]	2-
TGFBR2	-0.22	-0.20	0.00	0.13	0.19	-0.24	-0.15	
TGFBR3	0.29	0.36	0.16	0.26	-0.62[d]	-0.45[b]	-0.50[b]	3-
TGFB1I1	0.06	0.42[a]	0.42[a]	0.29	0.12	-0.21	0.02	
TGFBR3L	0.32	0.35	0.05	0.59[b]	0.37[a]	-0.07	-0.02	1+
TGFBI	-0.05	-0.34	-0.17	0.60[b]	0.31	-0.47[b]	-0.58[c]	1+, 2-
TGFBRAP1	-0.12	-0.22	-0.30	-0.35	0.10	0.49[b]	0.57[c]	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S23

Pearson's correlation coefficients (R) between mRNA expression levels of *FDFT1* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[ǂ]
TGFB1	-0.02	0.01	0.56[c]	0.29	0.45[b]	0.20	-0.07	2+
TGFB2	-0.34	-0.68[c]	0.54[b]	0.00	-0.09	-0.52[b]	-0.20	1+, 2-
TGFB3	-0.69[b]	-0.45[a]	-0.14	-0.03	0.09	-0.31	0.02	1-
LTBP1	-0.30	-0.38	0.03	0.30	-0.25	0.50[b]	-0.14	1+
LTBP2	-0.17	-0.20	-0.11	-0.32	-0.29	-0.07	-0.36[a]	
LTBP3	-0.67[b]	-0.30	-0.39[a]	-0.27	-0.20	-0.46[b]	0.04	2-
LTBP4	-0.55[a]	0.18	-0.28	-0.24	-0.05	0.15	0.47[b]	1+
FBN1	-0.13	-0.13	0.08	-0.10	0.12	0.06	-0.27	
FBN2	0.21	-0.02	0.05	-0.02	-0.07	0.34	-0.17	
FBN3	-0.60[b]	-0.42[a]	0.50[b]	0.28	-0.06	-0.45[b]	-0.16	1+, 2-
TGFBR1	0.14	-0.52[b]	0.45[b]	0.25	0.15	0.78[d]	0.01	2+, 1-
TGFBR2	-0.30	-0.24	0.03	-0.51[b]	0.19	0.01	-0.48[b]	2-
TGFBR3	-0.14	0.41[a]	0.53[b]	-0.32	0.31	0.19	-0.14	1+
TGFB1I1	-0.73[c]	0.10	-0.57[c]	-0.26	0.02	0.18	0.26	2-
TGFBR3L	-0.45	0.10	-0.18	0.08	-0.21	-0.39[a]	0.04	
TGFBI	-0.64[b]	-0.57[b]	0.53[b]	-0.15	-0.02	0.15	-0.20	1+, 2-
TGFBRAP1	0.31	0.03	0.43[a]	0.09	-0.11	-0.18	-0.29	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [ǂ]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S24

Pearson's correlation coefficients (R) between mRNA expression levels of *ERBB3* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs‡
TGFB1	0.24	-0.28	0.62^{c}	0.09	-0.17	0.81^{d}	0.40^{a}	2+
TGFB2	0.19	-0.57^{b}	0.89^{d}	-0.53^{b}	-0.04	0.07	-0.05	1+, 2-
TGFB3	0.15	-0.42^{a}	0.07	-0.44^{a}	0.12	0.18	-0.16	
LTBP1	0.40	-0.30	0.34^{a}	0.05	0.02	0.63^{d}	0.78^{d}	2+
LTBP2	0.16	-0.28	0.03	0.24	0.15	0.69^{d}	0.42^{a}	1+
LTBP3	-0.38	-0.39	-0.30	-0.14	-0.07	-0.23	-0.37^{a}	
LTBP4	-0.23	-0.19	-0.34^{a}	0.36	0.08	0.24	-0.18	
FBN1	0.28	-0.25	0.41^{a}	0.09	0.14	0.61^{c}	0.74^{d}	2+
FBN2	0.14	-0.31	0.26	0.07	0.00	0.74^{d}	0.87^{d}	2+
FBN3	-0.12	-0.17	0.70^{d}	-0.57^{b}	0.01	0.43^{a}	0.35	1+, 1-
TGFBR1	0.19	-0.42^{a}	0.69^{d}	-0.59^{b}	0.01	0.31	0.45^{b}	2+, 1-
TGFBR2	0.23	-0.37	0.09	0.71^{d}	0.12	0.61^{c}	0.49^{b}	3+
TGFBR3	0.18	-0.06	0.22	0.54^{b}	0.19	0.78^{d}	0.67^{d}	3+
TGFB1I1	-0.13	0.02	-0.78^{d}	0.54^{b}	-0.24	-0.05	-0.27	1+, 1-
TGFBR3L	-0.31	0.37	-0.28	0.08	-0.14	-0.14	-0.41^{a}	
TGFBI	0.07	-0.41^{a}	0.72^{d}	0.13	0.18	0.69^{d}	0.93^{d}	3+
TGFBRAP1	0.28	-0.17	0.49^{b}	0.04	0.05	0.17	0.16	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. ‡Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S25

Pearson's correlation coefficients (R) between mRNA expression levels of *ERBB4* and TGFβ signalling molecules in different fetal organs/tissues s and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs‡
TGFB1	0.17	0.05	0.04	-0.19	-0.07	-0.57[c]	-0.15	1-
TGFB2	0.53[a]	0.30	0.17	-0.40[a]	0.97[d]	0.04	0.17	1+
TGFB3	-0.27	-0.15	-0.04	-0.58[b]	0.33[a]	-0.20	0.05	1-
LTBP1	0.30	0.21	0.52[b]	-0.25	0.04	-0.28	0.02	1+
LTBP2	-0.66[b]	-0.17	-0.01	0.42[a]	-0.10	-0.29	0.17	1-
LTBP3	-0.60[b]	-0.51[b]	-0.29	-0.40[a]	0.02	-0.25	0.30	2-
LTBP4	-0.55[a]	-0.40[a]	-0.30	-0.18	0.60[d]	-0.47[b]	-0.37[a]	1+, 1-
FBN1	0.52[a]	-0.18	0.16	-0.06	0.77[d]	-0.23	-0.01	1+
FBN2	0.91[d]	-0.04	0.45[b]	-0.06	0.93[d]	-0.36[a]	-0.14	3+
FBN3	-0.26	0.33	-0.08	-0.79[d]	0.78[d]	-0.42[a]	0.10	1+, 1-
TGFBR1	0.92[d]	0.80[d]	0.29	-0.27	0.77[d]	-0.03	0.09	3+
TGFBR2	0.52[a]	-0.04	0.32	0.72[d]	-0.06	-0.17	-0.03	1+
TGFBR3	0.39	-0.15	0.39[a]	0.74[d]	0.64[d]	-0.34	-0.19	2+
TGFB1I1	-0.39	-0.65[c]	-0.29	-0.06	0.05	-0.21	-0.05	1-
TGFBR3L	-0.47[a]	-0.44[a]	-0.18	-0.14	-0.24	-0.30	0.01	
TGFBI	-0.09	-0.16	0.11	-0.16	0.08	-0.35[a]	-0.16	
TGFBRAP1	0.69[b]	0.50[b]	0.35[a]	-0.24	0.20	0.51[b]	0.17	3+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. ‡Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S26

Pearson's correlation coefficients (R) between mRNA expression levels of *PLGRKT* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[†]
TGFB1	0.41	-0.23	-0.53^{b}	-0.14	-0.07	0.03	-0.03	1-
TGFB2	0.53^{a}	-0.60^{b}	-0.54^{b}	-0.21	-0.24	-0.45^{b}	-0.34	3-
TGFB3	0.32	-0.59^{b}	0.07	-0.39^{a}	-0.19	-0.07	-0.22	1-
LTBP1	0.29	-0.63^{c}	-0.23	0.02	0.00	0.25	-0.27	1-
LTBP2	-0.60^{b}	-0.53^{b}	0.01	0.21	0.09	-0.27	-0.42^{a}	2-
LTBP3	-0.04	-0.31	-0.10	-0.51^{b}	-0.10	-0.11	0.21	1-
LTBP4	0.01	-0.37	0.09	-0.29	-0.34^{a}	0.33	0.40^{a}	
FBN1	0.40	-0.60^{b}	0.01	-0.02	-0.21	-0.07	-0.38^{a}	1-
FBN2	0.73^{c}	-0.63^{c}	-0.27	-0.01	-0.25	0.13	-0.28	1+, 1-
FBN3	0.20	0.11	-0.63^{d}	-0.59^{b}	-0.25	-0.21	-0.43^{a}	2-
TGFBR1	0.60^{b}	-0.30	-0.23	0.01	-0.23	0.44^{b}	-0.15	2+
TGFBR2	0.44	-0.74^{d}	0.31	0.66^{c}	0.04	-0.11	-0.29	1+, 1-
TGFBR3	-0.04	-0.54^{b}	0.28	0.67^{c}	-0.22	0.00	-0.19	1+, 1-
TGFB1I1	0.28	-0.01	0.34	-0.15	-0.08	0.33	0.49^{b}	1+
TGFBR3L	0.06	0.71^{d}	0.12	-0.25	0.07	-0.21	0.40^{a}	1+
TGFBI	0.50^{a}	-0.40^{a}	-0.16	0.00	0.13	0.05	-0.28	
TGFBRAP1	0.27	-0.57^{b}	-0.40^{a}	-0.18	-0.12	-0.48^{b}	-0.61^{c}	3-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [†]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S27

Pearson's correlation coefficients (R) between mRNA expression levels of *TOX3* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs[‡]**
TGFB1	-0.37	0.08	0.33	0.30	0.10	-0.22	-0.33	
TGFB2	-0.30	0.40[a]	0.41[a]	-0.26	0.42[b]	-0.44[b]	0.14	1+, 1-
TGFB3	-0.19	0.07	-0.18	-0.39[a]	0.24	-0.34[a]	-0.13	
LTBP1	-0.10	0.51[b]	-0.19	-0.27	-0.25	0.26	0.06	1+
LTBP2	0.56[a]	0.08	-0.13	0.32	-0.22	-0.29	-0.07	
LTBP3	-0.03	-0.28	-0.16	-0.01	-0.22	-0.48[b]	-0.15	1-
LTBP4	-0.10	-0.37	-0.14	0.07	0.23	-0.02	0.01	
FBN1	-0.42	-0.18	-0.08	-0.02	0.56[c]	-0.15	0.04	1+
FBN2	-0.52[a]	-0.12	-0.15	-0.19	0.49[b]	0.00	-0.04	1+
FBN3	-0.05	0.62[c]	0.52[b]	-0.58[b]	0.56[c]	-0.51[b]	0.02	3+, 2-
TGFBR1	-0.32	0.68[c]	0.33	-0.38	0.68[d]	0.66[d]	0.46[b]	4+
TGFBR2	-0.55[a]	0.11	-0.15	0.42[a]	0.14	-0.09	-0.29	
TGFBR3	-0.04	-0.08	0.45[b]	0.52[b]	0.70[d]	-0.09	-0.15	3+
TGFB1I1	-0.34	-0.55[b]	-0.41[a]	0.24	-0.26	0.02	-0.34	1-
TGFBR3L	-0.05	-0.59[b]	-0.09	0.44[a]	-0.49[b]	-0.48[b]	-0.15	3-
TGFBI	-0.41	0.10	0.29	0.50[b]	-0.18	-0.14	-0.11	1-
TGFBRAP1	-0.05	0.56[b]	0.35[a]	-0.41[a]	0.13	0.14	0.03	1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. P-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S28

Pearson's correlation coefficients (R) between mRNA expression of *GATA4* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	-0.32	-0.04	0.51^{b}	0.20	0.13	-0.04	-0.13	1+
TGFB2	-0.58^{a}	-0.78^{d}	0.17	0.38	0.73^{d}	0.06	-0.19	1+, 1-
TGFB3	0.22	-0.58^{b}	-0.09	0.07	0.30	-0.14	-0.14	1-
LTBP1	-0.31	-0.37	0.28	-0.19	-0.34^{a}	-0.07	-0.18	
LTBP2	0.85^{d}	-0.31	-0.11	-0.27	-0.34^{a}	0.00	-0.18	1+
LTBP3	0.45	-0.37	0.37^{a}	0.02	0.02	-0.07	-0.16	
LTBP4	0.34	-0.07	0.27	-0.31	0.73^{d}	-0.12	0.09	1+
FBN1	-0.58^{a}	-0.47^{a}	-0.36^{a}	-0.10	0.77^{d}	-0.14	-0.09	1+
FBN2	-0.83^{d}	-0.54^{b}	0.26	-0.02	0.78^{d}	-0.13	-0.09	1+, 2-
FBN3	0.30	0.09	0.39^{a}	0.25	0.86^{d}	-0.20	-0.09	1+
TGFBR1	-0.72^{c}	-0.52^{b}	-0.15	0.46^{a}	0.72^{d}	0.02	-0.04	1+, 2-
TGFBR2	-0.62^{b}	-0.61^{b}	-0.48^{b}	-0.40^{a}	-0.12	-0.05	-0.31	3-
TGFBR3	-0.40	-0.09	-0.39^{a}	-0.07	0.92^{d}	-0.11	-0.10	1+
TGFB1I1	0.12	0.06	0.22	-0.37	0.00	0.03	-0.14	
TGFBR3L	0.42	0.43^{a}	0.26	-0.16	-0.36^{a}	0.06	0.29	
TGFBI	-0.04	-0.53^{b}	0.14	-0.24	-0.17	-0.15	-0.07	1-
TGFBRAP1	-0.60^{b}	-0.17	0.06	-0.03	0.07	0.18	-0.26	1-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S29

Pearson's correlation coefficients (R) between mRNA expression levels of *ZBTB16* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[‡]
TGFB1	-0.14	0.27	0.05	0.69[d]	0.03	0.760[d]	0.51[b]	3+
TGFB2	-0.37	0.53[b]	-0.26	-0.11	0.17	-0.04	-0.10	1+
TGFB3	-0.49[a]	0.83[d]	-0.14	-0.07	0.02	0.01	-0.25	1+
LTBP1	-0.02	0.42[a]	0.18	-0.23	0.58[c]	0.88[d]	0.86[d]	3+
LTBP2	0.28	0.82[d]	0.08	0.15	0.27	0.62[c]	0.27	2+
LTBP3	-0.46	0.68[c]	-0.17	0.50[b]	-0.17	-0.43[a]	-0.44[a]	2+
LTBP4	-0.25	0.79[d]	0.16	0.61[c]	0.12	0.29	0.00	2+
FBN1	-0.14	0.89[d]	-0.01	0.10	0.40[a]	0.70[d]	0.92[d]	3+
FBN2	-0.19	0.63[c]	0.04	-0.18	0.22	0.86[d]	0.97[d]	3+
FBN3	-0.50[a]	-0.36	-0.33	-0.07	0.18	0.23	0.24	
TGFBR1	-0.20	-0.07	-0.24	-0.60[b]	0.37[a]	0.67[d]	0.69[d]	2+, 1-
TGFBR2	-0.37	0.67[c]	0.10	0.20	0.65[d]	0.51[b]	0.47[b]	4+
TGFBR3	0.09	0.57[b]	0.34[a]	0.10	0.30	0.83[d]	0.81[d]	3+
TGFB1I1	-0.51[a]	0.55[b]	0.31	0.65[c]	-0.29	0.00	-0.25	2+
TGFBR3L	-0.43	-0.33	-0.29	0.52[b]	-0.47[b]	-0.36[a]	-0.37[a]	1+, 1-
TGFBI	-0.63[b]	0.62[c]	0.10	0.59[b]	0.32	0.72[d]	0.93[d]	4+, 1-
TGFBRAP1	0.26	0.13	-0.04	-0.06	0.70[d]	0.20	0.12	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S30

Pearson's correlation coefficients (R) between mRNA expression levels of *IRF1* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[‡]
TGFB1	-0.25	-0.23	0.48[b]	0.43[a]	-0.15	0.37[a]	0.63[c]	2+
TGFB2	-0.51[a]	-0.04	0.05	-0.36	-0.27	0.70[d]	-0.03	1+
TGFB3	-0.14	0.30	-0.18	-0.21	0.16	0.51[b]	0.06	1+
LTBP1	-0.18	-0.08	0.13	-0.45[a]	0.52[c]	-0.04	0.28	1+
LTBP2	0.56[a]	0.38	-0.06	0.63[c]	0.80[d]	0.40[a]	0.20	2+
LTBP3	-0.08	0.28	-0.14	0.43[a]	-0.16	0.51[b]	0.30	1+
LTBP4	0.17	0.51[b]	0.02	0.58[b]	-0.14	-0.09	0.17	2+
FBN1	-0.19	0.57[b]	0.07	0.34	-0.14	0.26	0.27	1+
FBN2	-0.59[a]	0.52[b]	0.02	-0.17	-0.26	0.10	0.18	1+
FBN3	-0.35	-0.75[d]	0.09	-0.51[b]	-0.38[a]	0.42[a]	-0.02	2-
TGFBR1	-0.62[b]	-0.41[a]	0.12	-0.70[d]	-0.29	-0.40[a]	-0.05	2-
TGFBR2	-0.42	0.52[b]	0.10	0.54[b]	0.41[a]	0.39[a]	0.63[c]	3+
TGFBR3	-0.25	0.67[c]	0.07	0.37	-0.45[b]	0.25	0.24	1+, 1-
TGFB1I1	-0.14	0.33	-0.09	0.65[c]	-0.16	0.12	0.32	1+
TGFBR3L	-0.13	-0.25	-0.18	0.41[a]	-0.01	0.56[c]	0.12	1+
TGFBI	-0.31	-0.02	0.41[a]	0.39[a]	0.73[d]	0.33	0.12	1+
TGFBRAP1	-0.12	0.08	-0.13	-0.26	0.29	0.08	0.18	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S31

Pearson's correlation coefficients (R) between mRNA expression levels of *NEIL2* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	-0.44	0.05	0.67[d]	0.23	0.09	0.07	-0.05	1+
TGFB2	-0.72[c]	-0.69[d]	0.53[b]	0.39[a]	-0.03	0.44[a]	0.61[c]	2+, 2-
TGFB3	-0.38	-0.34	0.14	0.44[a]	0.03	0.45[b]	0.36[a]	1+
LTBP1	-0.44	-0.41[a]	0.27	-0.02	0.20	-0.39[a]	-0.30	
LTBP2	0.56[a]	-0.10	0.05	-0.17	0.22	0.25	0.57[c]	1+
LTBP3	-0.12	-0.09	0.09	0.37	0.09	0.64[d]	0.05	1+
LTBP4	-0.06	0.32	0.02	-0.03	-0.07	-0.14	-0.53[b]	1-
FBN1	-0.55[a]	-0.02	0.16	0.07	-0.04	-0.17	-0.23	
FBN2	-0.66[b]	-0.08	0.16	-0.01	-0.05	-0.24	-0.23	1-
FBN3	-0.33	-0.43[a]	0.52[b]	0.52[b]	-0.12	0.18	0.27	2+
TGFBR1	-0.61[b]	-0.69[d]	0.36[a]	0.37	-0.08	-0.60[c]	-0.39[a]	3-
TGFBR2	-0.70[b]	-0.26	-0.08	-0.55[b]	0.15	-0.06	0.05	2-
TGFBR3	-0.29	0.21	-0.19	-0.41[a]	-0.22	-0.17	-0.32	
TGFB1I1	-0.40	0.29	-0.27	-0.11	0.25	0.21	-0.18	
TGFBR3L	-0.05	0.35	0.05	0.07	0.28	0.46[b]	-0.05	1+
TGFBI	-0.56[a]	-0.47[a]	0.54[c]	0.01	0.34[a]	0.05	-0.20	1+
TGFBRAP1	-0.29	-0.19	0.14	0.16	0.00	-0.06	0.22	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S32

Pearson's correlation coefficients (R) between mRNA expression levels of *KRR1* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs[‡]
TGFB1	-0.51[a]	-0.43[a]	-0.19	-0.56[b]	0.14	0.11	0.04	1-
TGFB2	0.05	0.59[b]	0.25	0.00	0.05	-0.01	-0.16	1+
TGFB3	-0.24	0.46[a]	0.13	-0.22	-0.04	-0.17	-0.10	
LTBP1	0.03	0.60[b]	0.43[a]	0.17	0.56[c]	0.62[c]	0.54[b]	4+
LTBP2	0.12	0.51[b]	0.11	0.13	0.21	0.06	0.20	1+
LTBP3	-0.25	0.10	-0.51[b]	-0.64[c]	-0.13	-0.62[c]	-0.12	3-
LTBP4	-0.33	0.02	-0.41[a]	-0.64[c]	-0.17	-0.17	-0.09	1-
FBN1	-0.18	0.50[b]	0.56[c]	0.02	0.12	0.53[b]	0.50[b]	4+
FBN2	0.00	0.41[a]	0.21	0.20	0.03	0.52[b]	0.46[b]	2+
FBN3	-0.10	-0.12	-0.17	-0.39[a]	-0.02	-0.22	-0.01	
TGFBR1	0.26	0.38	0.68[d]	0.46[a]	0.20	0.71[d]	0.74[d]	3+
TGFBR2	-0.22	0.49[a]	0.70[d]	0.21	0.52[c]	0.45[b]	0.33	3+
TGFBR3	0.26	0.32	0.73[d]	0.28	-0.06	0.51[b]	0.40[a]	2+
TGFB1I1	-0.44	-0.07	-0.47[b]	-0.58[b]	-0.29	-0.22	-0.20	2-
TGFBR3L	-0.21	-0.43[a]	-0.42[a]	-0.35	-0.23	-0.59[c]	-0.48[b]	2-
TGFBI	-0.43	0.54[b]	0.27	-0.23	0.23	0.32	0.41[a]	1+
TGFBRAP1	0.11	0.19	0.25	-0.11	0.56[c]	0.47[b]	0.22	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S33

Pearson's correlation coefficients (R) between mRNA expression of *RAB5B* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	0.24	0.08	0.14	0.40[a]	0.10	-0.03	-0.08	
TGFB2	0.21	0.15	0.26	-0.24	0.21	0.37[a]	0.14	
TGFB3	-0.32	0.16	0.08	-0.24	0.21	0.10	0.21	
LTBP1	0.48[a]	0.49[a]	0.68[d]	-0.08	0.74[d]	0.14	0.26	2+
LTBP2	-0.19	0.35	0.16	0.34	0.48[b]	0.24	0.29	1+
LTBP3	-0.75[c]	-0.21	-0.37[a]	0.08	-0.45[b]	-0.18	0.08	2-
LTBP4	-0.33	0.21	-0.11	0.25	0.19	-0.52[b]	-0.29	1-
FBN1	0.66[b]	0.45[a]	0.52[b]	0.13	0.57[c]	0.23	0.16	3+
FBN2	0.43	0.50[b]	0.47[b]	0.08	0.29	0.10	0.04	2+
FBN3	-0.71[b]	-0.30	-0.11	-0.43[a]	0.16	-0.36[a]	0.23	1-
TGFBR1	0.33	0.16	0.26	-0.51[b]	0.40[a]	0.16	0.18	1-
TGFBR2	0.44	0.52[b]	0.62[c]	0.45[a]	0.90[d]	0.355[a]	0.23	3+
TGFBR3	0.35	0.75[d]	0.45[b]	0.50[b]	0.36[a]	0.20	-0.03	3+
TGFB1I1	-0.39	-0.21	-0.22	0.48[a]	-0.37[a]	-0.20	-0.12	
TGFBR3L	-0.83[d]	-0.75[d]	-0.47[b]	0.18	-0.71[d]	-0.21	-0.29	4-
TGFBI	-0.29	0.00	0.38[a]	0.39[a]	0.60[d]	0.19	-0.03	1+
TGFBRAP1	0.78[c]	0.71[d]	0.63[d]	0.04	0.88[d]	0.64[d]	0.78[d]	6+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S34

Pearson's correlation coefficients (R) between mRNA expression levels of *ARL14EP* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	-0.17	-0.64^{c}	-0.42^{a}	-0.48^{a}	-0.18	-0.43^{a}	-0.49^{b}	2-
TGFB2	0.64^{b}	0.58^{b}	-0.09	0.07	0.36^{a}	0.06	0.21	2+
TGFB3	0.21	0.38	0.14	-0.15	0.15	-0.21	0.44^{a}	
LTBP1	0.53^{a}	0.43^{a}	0.05	0.01	0.04	-0.04	-0.32	
LTBP2	-0.20	0.33	0.09	0.25	0.04	-0.33	0.22	
LTBP3	-0.37	0.03	-0.51^{b}	-0.54^{b}	-0.29	-0.34	-0.22	2-
LTBP4	-0.20	-0.18	-0.36^{a}	-0.62^{c}	-0.01	-0.45^{b}	-0.33	2-
FBN1	0.46	0.39	0.43^{a}	0.07	0.41^{a}	-0.01	-0.17	
FBN2	0.54^{a}	0.42^{a}	-0.10	0.13	0.38^{a}	-0.12	-0.23	
FBN3	-0.10	-0.18	-0.44^{b}	-0.43^{a}	0.33^{a}	-0.45^{b}	0.16	2-
TGFBR1	0.73^{c}	0.38	0.41^{a}	0.47^{a}	0.56^{c}	0.20	0.14	2+
TGFBR2	0.40	0.48^{a}	0.63^{d}	0.29	0.29	0.04	-0.11	1+
TGFBR3	0.46	0.28	0.63^{d}	0.36	0.34^{a}	-0.10	-0.17	1+
TGFB1I1	-0.07	-0.10	-0.23	-0.60^{b}	-0.44^{b}	-0.25	-0.41^{a}	2-
TGFBR3L	-0.32	-0.38	-0.27	-0.34	-0.46^{b}	-0.29	-0.42^{a}	1-
TGFBI	0.18	0.51^{b}	0.03	-0.22	-0.06	-0.17	-0.21	1+
TGFBRAP1	0.60^{b}	0.18	-0.16	-0.21	0.30	0.53^{b}	0.38^{a}	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡] Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S35

Pearson's correlation coefficients (R) between mRNA expression levels *DENND1A* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	0.02	0.48^{a}	0.74^{d}	0.57^{b}	0.43^{b}	0.00	-0.06	3+
TGFB2	-0.50^{a}	-0.19	0.43^{a}	-0.29	0.15	0.49^{b}	0.24	1+
TGFB3	0.05	-0.03	-0.18	-0.07	0.09	0.45^{b}	0.43^{a}	1+
LTBP1	-0.23	0.13	0.38^{a}	-0.05	0.19	-0.43^{a}	0.15	
LTBP2	0.71^{c}	0.10	-0.11	0.05	-0.02	0.15	0.01	1+
LTBP3	0.41	0.11	0.02	0.39^{a}	0.17	0.67^{d}	0.03	1+
LTBP4	0.29	0.35	0.15	0.67^{c}	0.42^{b}	0.11	0.21	2+
FBN1	-0.50^{a}	-0.12	-0.11	-0.10	0.29	-0.23	-0.02	
FBN2	-0.68^{b}	-0.18	0.28	-0.18	0.20	-0.37^{a}	-0.02	1-
FBN3	0.24	0.18	0.47^{b}	0.17	0.16	0.39^{a}	0.21	1+
TGFBR1	-0.68^{b}	-0.16	0.10	-0.60^{c}	0.18	-0.68^{d}	-0.04	3-
TGFBR2	-0.62^{b}	-0.12	-0.20	-0.07	0.22	-0.13	-0.16	1-
TGFBR3	-0.25	0.21	0.15	-0.15	0.25	-0.32	-0.18	
TGFB1I1	0.05	0.19	-0.10	0.77^{d}	0.48^{b}	0.33	0.09	2+
TGFBR3L	0.27	0.03	-0.06	0.34	-0.02	0.56^{c}	-0.05	1+
TGFBI	-0.20	-0.08	0.46^{b}	0.35	0.12	-0.12	-0.03	1+
TGFBRAP1	-0.36	0.25	0.44^{b}	0.23	0.28	0.14	0.35^{a}	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S36

Pearson's correlation coefficients (R) between mRNA expression levels of *THADA* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant (*P* < 0.01) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs[‡]**
TGFB1	-0.28	0.05	0.40[a]	-0.30	-0.04	0.51[b]	0.40[a]	1+
TGFB2	-0.11	0.13	0.68[d]	-0.08	0.43[b]	-0.10	-0.30	2+
TGFB3	-0.48[a]	0.03	0.15	-0.17	-0.10	0.00	-0.35	
LTBP1	0.09	0.38	0.64[d]	0.57[b]	0.12	0.91[d]	0.79[d]	4+
LTBP2	0.23	0.12	0.12	-0.10	-0.24	0.35[a]	0.03	
LTBP3	-0.56[a]	-0.25	-0.30	-0.61[c]	0.01	-0.49[b]	-0.45[b]	3-
LTBP4	-0.43	-0.06	-0.26	-0.46[a]	0.23	0.17	0.36[a]	
FBN1	-0.03	0.00	0.49[b]	0.08	0.51[b]	0.69[d]	0.82[d]	4+
FBN2	-0.08	0.09	0.44[b]	0.49[a]	0.46[b]	0.82[d]	0.84[d]	4+
FBN3	-0.48[a]	-0.02	0.36[a]	-0.24	0.47[b]	-0.08	-0.09	1+
TGFBR1	0.07	0.25	0.59[c]	0.28	0.56[c]	0.90[d]	0.86[d]	4+
TGFBR2	-0.26	0.13	0.39[a]	0.13	0.22	0.52[b]	0.43[a]	1+
TGFBR3	0.08	0.34	0.50[b]	0.21	0.56[c]	0.76[d]	0.80[d]	4+
TGFB1I1	-0.67[b]	-0.18	-0.61[c]	-0.23	-0.17	0.11	-0.11	2-
TGFBR3L	-0.54[a]	-0.28	-0.33	-0.27	-0.35[a]	-0.56[c]	-0.44[a]	1-
TGFBI	-0.60[b]	0.03	0.59[c]	0.00	-0.14	0.67[d]	0.79[d]	3+, 1-
TGFBRAP1	0.46	0.49[a]	0.71[d]	0.23	0.38[a]	0.16	0.02	1+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant (*P* < 0.01) positive (+) or negative (-) correlations.

Table S37

Pearson's correlation coefficients (R) between mRNA expression levels of *MAPRE1* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	-0.09	-0.06	0.44^{b}	-0.18	0.33^{a}	0.16	0.14	1+
TGFB2	-0.09	-0.44^{a}	0.67^{d}	0.31	0.25	-0.36^{a}	-0.42^{a}	1+
TGFB3	-0.48^{a}	-0.57^{b}	0.17	0.19	0.18	-0.28	-0.47^{b}	2-
LTBP1	0.12	0.01	0.67^{d}	0.64^{c}	0.63^{d}	0.57^{c}	0.51^{b}	5+
LTBP2	-0.01	-0.28	0.13	-0.32	0.34^{a}	0.01	-0.11	
LTBP3	-0.72^{c}	-0.76^{d}	-0.20	-0.58^{b}	-0.31	-0.60^{c}	-0.37^{a}	4-
LTBP4	-0.52^{a}	-0.31	-0.15	-0.67^{c}	0.22	-0.08	0.41^{a}	1-
FBN1	0.05	-0.21	0.39^{a}	0.18	0.51^{b}	0.27	0.44^{a}	1+
FBN2	0.16	-0.03	0.67^{d}	0.47^{a}	0.31	0.45^{b}	0.45^{a}	2+
FBN3	-0.52^{a}	-0.17	0.40^{a}	0.24	0.23	-0.50^{b}	-0.37^{a}	1-
TGFBR1	0.20	0.03	0.52^{b}	0.73^{d}	0.43^{b}	0.86^{d}	0.67^{d}	5+
TGFBR2	-0.18	-0.19	0.24	-0.28	0.72^{d}	0.23	0.22	1+
TGFBR3	0.10	0.27	0.14	-0.14	0.33^{a}	0.34	0.50^{b}	1+
TGFB1I1	-0.66^{b}	-0.47^{a}	-0.48^{b}	-0.62^{c}	-0.05	-0.02	-0.05	3-
TGFBR3L	-0.58^{a}	-0.22	-0.19	-0.40^{a}	-0.51^{b}	-0.53^{b}	-0.34	2-
TGFBI	-0.55^{a}	-0.53^{b}	0.43^{a}	-0.19	0.49^{b}	0.23	0.38^{a}	1+, 1-
TGFBRAP1	0.48^{a}	0.35	0.59^{c}	0.20	0.76^{d}	0.27	0.05	2+

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S38

Pearson's correlation coefficients (R) between mRNA expression levels of *AOPEP* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P <$ 0.01) correlations.

	ovary	testis	heart	kidney	liver	cerebellum	brain	number of organs‡
TGFB1	-0.13	-0.16	-0.42^{a}	0.15	0.05	0.66^{d}	0.42^{a}	1+
TGFB2	-0.03	-0.06	-0.69^{d}	-0.63^{c}	-0.21	0.00	-0.08	2-
TGFB3	0.52^{a}	0.18	-0.03	-0.43^{a}	-0.07	0.15	-0.32	
LTBP1	-0.34	-0.35	-0.55^{c}	-0.11	-0.62^{d}	0.62^{c}	0.80^{d}	2+, 2-
LTBP2	0.03	0.00	-0.11	0.21	-0.36^{a}	0.42^{a}	0.29	
LTBP3	0.56^{a}	0.51^{b}	0.09	0.08	0.51^{b}	-0.02	-0.50^{b}	2+, 1-
LTBP4	0.49^{a}	0.13	0.13	0.43^{a}	-0.22	0.38^{a}	0.06	
FBN1	-0.31	-0.17	-0.37^{a}	-0.09	-0.52^{c}	0.55^{c}	0.88^{d}	2+, 1-
FBN2	-0.06	-0.42^{a}	-0.51^{b}	-0.28	-0.29	0.65^{d}	0.93^{d}	2+, 1-
FBN3	0.52^{a}	0.23	-0.54^{b}	-0.38^{a}	-0.20	0.55^{c}	0.11	1+, 1-
TGFBR1	-0.10	-0.31	-0.48^{b}	-0.58^{b}	-0.34^{a}	0.40^{a}	0.68^{d}	1+, 2-
TGFBR2	-0.24	-0.24	-0.25	0.39^{a}	-0.70^{d}	0.36^{a}	0.45^{a}	1-
TGFBR3	-0.34	-0.39	-0.17	0.21	-0.36^{a}	0.61^{c}	0.78^{d}	2+
TGFB1I1	0.57^{a}	0.46^{a}	0.64^{d}	0.60^{c}	0.24	0.09	-0.30	2+
TGFBR3L	0.71^{c}	0.63^{c}	0.30	0.33	0.74^{d}	-0.01	-0.42^{a}	3+
TGFBI	0.57^{a}	0.15	-0.48^{b}	0.27	-0.42^{a}	0.50^{b}	0.93^{d}	2+, 1-
TGFBRAP1	-0.46	-0.54^{b}	-0.77^{d}	0.06	-0.75^{d}	-0.12	0.05	3-

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. ‡Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S39

Pearson's correlation coefficients (R) between mRNA expression levels of *SUOX* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	0.39	0.23	-0.13	0.35	-0.29	0.23	0.00	
TGFB2	-0.05	-0.20	-0.21	-0.22	-0.19	-0.10	0.26	
TGFB3	-0.05	-0.28	-0.27	-0.14	-0.19	-0.06	-0.07	
LTBP1	0.15	-0.09	-0.43[a]	-0.08	-0.43[b]	-0.05	0.20	1-
LTBP2	-0.20	-0.40[a]	-0.30	-0.11	-0.39[a]	-0.07	0.37[a]	
LTBP3	0.05	-0.02	0.31	0.41[a]	0.38[a]	0.24	-0.25	
LTBP4	0.09	-0.28	0.13	0.61[c]	-0.13	0.15	-0.08	1+
FBN1	0.26	-0.41[a]	-0.46[b]	-0.22	-0.30	-0.14	0.30	1-
FBN2	0.20	-0.29	-0.12	-0.31	-0.22	-0.03	0.25	
FBN3	0.08	0.48[a]	0.14	0.06	-0.11	0.30	0.10	
TGFBR1	-0.06	-0.10	-0.25	-0.54[b]	-0.18	-0.13	0.19	1-
TGFBR2	0.16	-0.36	-0.37[a]	0.03	-0.49[b]	-0.09	0.00	1-
TGFBR3	-0.10	-0.46[a]	-0.34[a]	-0.10	-0.05	-0.08	0.07	
TGFB1I1	0.07	-0.06	0.26	0.71[d]	0.00	0.15	-0.40[a]	1+
TGFBR3L	-0.14	0.35	0.34[a]	0.34	0.21	0.47[b]	-0.14	1+
TGFBI	-0.03	-0.05	-0.32	0.33	-0.43[b]	-0.02	0.27	1-
TGFBRAP1	0.10	-0.17	-0.15	0.24	-0.41[a]	-0.27	-0.01	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Table S40

Pearson's correlation coefficients (R) between mRNA expression levels of *SUMO1P1* and TGFβ signalling molecules in different fetal organs/tissues and the number of organs with significant ($P < 0.01$) correlations.

	ovary	**testis**	**heart**	**kidney**	**liver**	**cerebellum**	**brain**	**number of organs**[‡]
TGFB1	-0.26	-0.01	0.04	-0.15	0.04	-	0.22	
TGFB2	-0.41	0.07	0.47^{b}	0.15	-0.14	-	-0.04	1+
TGFB3	0.05	0.05	-0.06	-0.03	0.10	-	-0.07	
LTBP1	-0.38	0.08	0.29	-0.04	-0.14	-	-0.19	
LTBP2	0.53^{a}	0.02	-0.17	0.18	0.07	-	0.08	
LTBP3	0.55^{a}	0.12	-0.21	-0.05	-0.21	-	0.14	
LTBP4	0.20	0.11	-0.30	-0.16	-0.22	-	-0.07	
FBN1	-0.52^{a}	0.15	0.16	0.54^{b}	-0.14	-	-0.17	1+
FBN2	-0.48^{a}	0.00	0.15	0.36	-0.13	-	-0.16	
FBN3	0.53^{a}	-0.14	0.37^{a}	-0.23	-0.18	-	-0.12	
TGFBR1	-0.38	-0.04	0.63^{d}	0.12	-0.12	-	-0.13	1+
TGFBR2	-0.48^{a}	0.17	0.17	0.33	-0.06	-	0.31	
TGFBR3	-0.21	0.04	0.33	0.37	-0.17	-	-0.04	
TGFB1I1	0.01	0.11	-0.41^{a}	-0.13	0.08	-	0.16	
TGFBR3L	0.42	-0.06	-0.19	-0.24	-0.17	-	0.19	
TGFBI	-0.16	0.02	0.47^{b}	-0.19	-0.06	-	-0.16	1+
TGFBRAP1	-0.51	0.11	0.35^{a}	0.10	-0.06	-	-0.17	

Positive and negative correlations are marked in pink and blue, respectively. The colour intensity corresponds with the strength of the correlation. *P*-values: a < 0.05; b < 0.01; c < 0.001; d < 0.0001. [‡]Number of organs with significant ($P < 0.01$) positive (+) or negative (-) correlations.

Chapter 6

General Discussion and Conclusions

6.1. Significance of the Research Findings

The diagnosis of PCOS often leads to a frustrating experience for women, as there are currently no syndrome-specific treatments or prevention strategies available. Clinicians simply manage the symptoms presented. Research efforts have confirmed possible genetic and fetal origins of the disorder. Since the discovery of loci associated with PCOS by GWAS, scientific efforts to delineate the possible roles of genes in/near these loci became the focus of PCOS studies. However, these findings have increased the scientific challenges surrounding the disorder. In an attempt to unravel the aetiology of PCOS, this thesis examined how genes in loci associated with PCOS and TGFβ signalling molecules and their upstream regulators results in predisposition of PCOS in various tissues pre-natally and post-natally.

In Chapter 2 of this thesis, we identified the upstream regulators and pathways associated with PCOS candidate genes during fetal bovine ovary development and this has been published in Azumah, Hummitzsch, et al. (2022). Notably, we demonstrated that PCOS candidate genes expressed during the early stages of fetal development such as *C8H9orf3, TOX3, FBN3, GATA4, HMGA2* and *DENND1A* are co-expressed with genes involved in mitochondria function and are regulated upstream by *DAP3, MYC, PTEN, HNF4A, ESRRA/G, PSEN1,* mitochondrial *LONP1* and *TP53*. Those expressed in the second trimester or just after mid gestation, such as *YAP1, INSR, THADA* and *TGFB1I1,* were co-expressed with genes involved in stroma expansion and are regulated upstream by TGF-β signalling molecules such as *TGFB1, TGFB2, TGFB3* and *TGFBR2* and fibroblast proliferation regulators such as *FGF2,* and coagulation factor II. This could account for the fibrous nature of PCOS ovaries and might also affect stroma in other organs such as pancreas or heart resulting in altered organ-specific function. PCOS candidate genes expressed during the third trimester such as *FDFT1*, *LHCGR*, *AMH*, *FSHR, ZBTB16* and *PLGRKT* are co-expressed with genes involved with folliculogenesis and steroidogenesis and are regulated upstream by SREBF2, INSIG1 TGFB1, RPTOR (Azumah, Hummitzsch, et al. 2022). The role of mitochondria (Zhang et al. 2019; Zeng et al. 2020; Ilie 2018), stroma expansion (Hatzirodos, Bayne, Irving-Rodgers, et al. 2011; Raja-Khan et al. 2014) and steroidogenesis (de Medeiros, Rodgers & Norman 2021) in the aetiology of PCOS have been studied. However, the possible fetal dysregulation of these pathways that could lead to phenotypes observed in adulthood has not been investigated yet. These findings infer that dysregulation of PCOS candidate genes during fetal development could possibly lead to a cascade of molecular events from the early stages of fetal development until adulthood where the various phenotypes are observed; requiring further studies.

Furthermore, genetic linkage between the stroma and the pathogenesis of PCOS, especially in defining the PCOM which is common in women with the disorder, is gradually becoming the research focus in PCOS. Also, the roles of TGFβ signalling molecules in the PCOS phenotypes observed have not been discussed in much detail but have been shown to be expressed in fetal ovaries (Hatzirodos, Bayne, Irving-Rodgers, et al. 2011). TGFβ1, but not androgens nor AMH, has been shown to inhibit the expression of PCOS candidate genes, *AR, INSR, C8H9orf3* and *RAD50* but stimulate expression of androgen receptor co-factor, *TGFB1I1*, in cultured fetal ovarian fibroblasts (Hartanti et al. 2020).

In Chapter 3 of this thesis, we showed the role of TGFβ signalling molecules in the possible predisposition of PCOS and the findings have been published in Azumah, Liu, et al. (2022). TGFβ signalling molecules are expressed dynamically in the fetal ovary. Levels of expression of genes such as *LTBP1/2/3/4, FBN1, TGFB2/3* and *TGFBR2/3* were increased, while *FBN3, TGFBR3L, TGFBI* and *TGFB1* levels were decreased and *TGFBRAP1, TGFBR1* and *FBN2* remained relatively constant across gestation. The role of TGFβ signalling molecules in regulating more PCOS candidate genes during fetal ovary development was also examined. Expression of PCOS candidate genes *ERBB3, NEIL2, IRF1* and *ZBTB16* was shown to be significantly decreased after TGFβ1 treatment of cultured fetal ovarian fibroblasts (Azumah, Liu, et al. 2022). However, TGFβ is known to have different effects in stroma of adult and fetal tissues. Thus, it stimulates stromal fibroblast replication and collagen deposition in the former but stimulates wound healing in the latter, which do not scar (Rolfe et al. 2007; Rolfe & Grobbelaar 2012). This was also confirmed in fetal ovarian fibroblasts where TGFβ inhibited *COL1A1* and *COL3A1* expression (Liu et al. 2022). TGFβ also inhibited expression of *AR*. Thus, we speculate that inhibition of TGFβ signalling in the fetal ovary is likely to increase androgen sensitivity and stromal activity and this mechanism could be part of the aetiology of PCOS. It is also possible that these mechanisms act in other organs affected by PCOS such as skeletal muscle where expression levels of genes controlled by TGFβ are elevated, including collagens (Stepto et al. 2020). Together, the conclusions of this chapter were that inhibition of TGFβ signalling in the fetal ovary is likely to (i) increase androgen sensitivity by enhancing expression of *AR*, (ii) increase stromal activity by stimulating expression of *COL1A1* and *COL3A1* resulting in the fibrotic appearance of polycystic ovaries and (iii) increase the expression of 7 of the 25 PCOS candidate genes. These findings further suggest that TGFβ signalling could be part of the aetiology of PCOS or at least the aetiology of polycystic ovaries.

PCOS presents various symptoms ranging from endocrine, metabolic, reproductive and psychological. Offspring including males from PCOS mothers present varying symptoms including congenital abnormalities (Mills et al. 2020). In Chapters 4 and 5 of this thesis, genes in loci associated with PCOS and TGFβ signalling molecules, respectively, were shown to be dynamically expressed in gonadal (ovary and testis), metabolic (heart, liver and kidney) and brain (brain and cerebellum) tissues during the first half of human fetal development and post-natally until adulthood. Notably, some genes were significantly expressed in specific tissues at different time points pre-natally and/or post-natally. Specifically, *HMGA2, FBN3* and *TOX3* were highly expressed during the early stages of fetal development in all tissues but least during adulthood while *DENND1A, THADA, MAPRE1, RAB5B, ARL14EP, KRR1, NEIL2* and *RAD50* were dynamically expressed in all post-natal tissues studied. Interestingly, the correlation between expression of *HMGA2*/*YAP1* and *RAD50*/*YAP1* were significant in at least 5 of the 7 fetal tissues studied (Chapter 4). Also, genes in loci associated with PCOS such as *HMGA2, YAP1* and *RAD50* correlated significantly with most TGFβ signalling molecules in at least different 4 tissues (Chapter 5). The fact that *HMGA2* and *YAP1* correlate with each other as well as with most TGFβ signalling molecules in most tissues is intriguing.

Both *HMGA2* and *YAP1* are involved in the Hippo signalling pathway, which regulates organ size by regulating cell differentiation and apoptosis (Varelas 2014; Huang et al. 2005; Shen et al. 2015; Zhang et al. 2014; Xu et al. 2021), as well as epithelial mesenchymal transition (EMT) during embryogenesis through TGFβ signalling (Thuault et al. 2006; Martínez Traverso et al. 2022; Vignali & Marracci 2020). Interaction between the TGFβ and Hippo signalling pathways have been shown to stimulate hepatocytes to undergo an EMT-like response in a TGFβ-enriched microenvironment (Oh et al. 2018). In PCOS women, *HMGA2* has been associated with PCOM phenotype among Han Chinese ancestry, potentially promoting the proliferation of ovarian granulosa cells via the HMGA2/IMP2 pathway (Das et al. 2008; Li et al. 2019; Stubbs et al. 2007). *HMGA2* has also been significantly associated with hyperandrogenism and oligo/amenorrhea in women with PCOS in Saudi Arabia (Bakhashab & Ahmed 2019). More so, *YAP1*, which is highly expressed in mammalian oocytes and preimplantation embryos, is also essential for normal ovarian development and function, as well as granulosa cell proliferation (Yu et al. 2016; Ji et al. 2017). *YAP1* is also regulated by gonadotrophins and hormones including oestrogen, follicle-stimulating hormone, and luteinising hormone (Moon et al. 2022; Sun & Diaz 2019; Ji et al. 2017; de Andrade et al. 2022). However, the role of these genes in the pathogenesis of PCOS still remains elusive. It could be possible that exposure of offspring to abnormal levels of hormones such as androgens, AMH due to PCOS during pregnancy dysregulates some of the genes in loci associated with PCOS, such as *YAP1* and *HMGA2,* as well as TGFβ signalling molecules during fetal development leading to the various phenotypes observed in adulthood. Together, these findings confirm possible crosstalk between genes in loci associated with PCOS and TGFβ signalling molecules in various tissues. It also suggests that these genes have tissue- or development-specific roles in multiple organs, possibly resulting in the various symptoms associated with PCOS. Thus, the fetal origin of a predisposition to PCOS in adulthood could arise via the effects of PCOS candidate genes and TGFβ signalling molecules in the development of multiple organs.

6.2. Limitations of the Study

In a basic researcher's ideal world, one would study human tissues from fetuses known to subsequently develop PCOS or not in later life. However, studying human fetal development including ovaries is limited to the first and second trimester as samples after mid-gestation are rare due to ethical and legal considerations. Those that are available result from terminations of unhealthy fetuses or mothers. Additionally the earliest time point in development where a predisposition to PCOS in later life is discernible is post-natally. Therefore, in the current studies bovine fetal ovaries were used in addition to human fetal ovaries to complete the gestational period based on previous findings. Previous studies have identified strong similarities between human and bovine in morphology and physiology of fetal and adult ovaries (Hatzirodos, Bayne, Irving-Rodgers, et al. 2011; Hummitzsch et al. 2013; Heeren et al. 2015), gestational length and the propensity for singleton pregnancies as well as the similarity in expression of PCOS candidate genes during early stages of fetal ovary development (Hartanti, et al. 2020, Liu, et al. 2020).

Chapter 2 is based on in-silico analysis of PCOS candidate genes and their co-expressed genes from bovine RNA-sequencing data. Limitations associated with the use of IPA software are acknowledged as it is a knowledge-based curated software, mainly using rodent and human data. However, to further confirm our results, Database for Annotation, Visualization, and Integrated Discovery (DAVID) Bioinformatics Resources 6.8, was used to analyse the pathway enrichment of genes from Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases for bovine organisms. Also, Chapter 3 which involves the regulation of PCOS candidate genes by TGFβ *in vitro* using bovine fetal ovarian fibroblasts and further studies *in vivo* or with human ovarian cells are required for further validation of our findings. In Chapters 4 and 5, the results were interpreted based on the expression profiles obtained from RNA sequencing output. The influence of transcriptional and post-transcriptional mechanisms such as mRNA stability/degradation, storage in stress granules, translational control on gene expression were not considered in this study. Also, Mendelian randomisation studies and transcriptome-wide association studies were not addressed in these studies.

6.3. Future Directions

The outcome of this thesis provides fundamental knowledge required for further studies specifically translational and clinical studies involving PCOS candidate genes and TGFβ signalling molecules. The upstream regulators identified in Chapter 2 should be studied further in different tissues, which are functionally affected by PCOS, in both human and animal models to delineate their possible role in the aetiology of the syndrome. Specifically, the expression/translation of the upstream regulators that are identifiable in blood should be studied by assessing their levels in cord blood samples as well as determine their possible association with anthropometric features associated with PCOS such as ponderal indices at birth.

Further studies *in vivo* and *in utero* are required to confirm the role of TGFβ signalling molecules in the regulation of PCOS candidate genes to account for their role in the establishment of the different phenotypes of PCOS. This will further confirm their role in the genetic and fetal origins of PCOS. As this project also informs on the expression of PCOS candidate genes and TGFβ signalling molecules pre-natally and post-natally, future studies involving knock-out models of candidate genes, either at organ or whole organism level, at different time points will be required to delineate the pathogenesis of PCOS. Furthermore, the possible role of environmental and *in utero* exposomes in the regulation of upstream regulators and candidate genes studied could enhance knowledge on the aetiology of PCOS; possibly towards early diagnosis, treatment or prevention of the syndrome.

6.4. Concluding Remarks

This project is the first of its kind in understanding the aetiology of PCOS as it unravels the roles of and relationships between the genes studied during fetal development as a fundamental step for further translational studies in defining the syndrome. The findings of this study also confirm the possible genetic and fetal origins of PCOS. Thus, this study identified the canonical pathways that could be disturbed when genes in loci associated with PCOS are dysregulated during fetal ovary development. It also confirmed that TGFβ signalling in the fetal ovary could account for the various phenotypes observed in PCOS or at least the development of the polycystic ovaries. Also, PCOS candidate genes and TGFβ signalling molecules, are shown to be dynamically expressed in gonadal, metabolic and brain tissues pre-natally and post-natally, inferring their possible role in the predisposition of PCOS. This project further showed that there is certainly crosstalk within and between PCOS candidate genes and TGFβ signalling molecules during fetal development in many tissues. Together, these findings infer that exposures *in utero* could initiate dysregulation of genes leading to a cascade of events downstream possibly resulting in PCOS in adulthood. Undoubtedly, post-natal environmental exposures could also enhance/trigger some candidate genes associated with PCOS resulting in the predisposition of the syndrome. Nevertheless, there is still a lot more research work required in women with PCOS and their offspring as well as animal models of PCOS to understand fully, which cause(s) lead to the development of PCOS as well as the phenotypes observed in female and male offspring of PCOS women.

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