Identification and characterisation of novel transcripts involved in the proliferation, differentiation and developmental networks of the mouse cerebral cortex

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APPENDIX A

Additional information for Chapter 3.

A-1. Authors' declaration.

A-2. Additional data file 1. Original file is accessible at http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s1.doc.
A-3. Additional data file 2. Original file is accessible at

http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s2.xls.

A-4. Additional data file 3. Original file is accessible at <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s3.xls</u>.

A-5. Additional data file 4. Original file is accessible at <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s4.xls</u>.

A-6. Additional data file 5. Original file is accessible at <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s5.xls</u>.

A-7. Additional data file 6. Original file is accessible at <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s6.xls</u>.

A-8. Additional data file 7. Original file is accessible at <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s7.xls</u>.

A-9. Additional data file 8. Original file is accessible at <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s8.xls</u>.

A-1 Authors' declaration

DECLARATION OF INDIVIDUAL CONTRIBUTIONS TO THE PUBLISHED OR SUBMITTED MANUSCRIPTS

Title:

Molecular networks involved in mouse cerebral corticogenesis and spatio-temporal regulation of *Sox4* and *Sox11* novel antisense transcripts revealed by transcriptome profiling.

Authors:

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Declaration:

KHL performed all the SAGE validation experiments. CAH, PZC and SST procured the mouse cerebral cortex and constructed the SAGE libraries. KHL, TB, LH and GKS designed, performed and supervised the SAGE, RT-qPCR and IPA analyses. KHL and TT performed all the ISH studies. KHL, KB, PSC, CNH and PQT carried out the expression studies on *Sox4* and *Sox11* transcripts. CAH, GKS, TT and HSS conceived of the study, and participated in its design and coordination. All authors read and approved the final manuscript.

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NOTE:

Statements of authorship appear in the print copy of the thesis held in the University of Adelaide Library.

A-2 Additional data file 1

Analysis of SAGE, DETs, GO terms, Ingenuity Pathway Analysis, *Sox4* and *Sox11* genomic cluster analysis, additional description for Materials & Methods section and R script for implementing empirical Bayesian moderated T-test on multiple groups.

Original version of this data file can be accessible from at <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s1.doc</u>.



SECTION A: SERIAL ANALYSIS OF GENE EXPRESSION

Figure S1 Distribution of unique SAGE tags according to library type. The tag count represented by each bar is shown in the box on the right.



Figure S2 Distribution of normalized unique SAGE tags (per 100,000 tags/library) according to library type. The tag count represented by each bar is shown in the box on the right.



Figure S3 MA plots of various comparisons. The Y-axis represents the M values, which is the ratio (log2(P/Q)) whereas the X-axis represents the A values, which is the mean ratio (1/2*log2(P*Q)). P and Q represent the tag counts from the two libraries in the comparison. Tags are represented by black dots and those highlighted in green are significantly differentially expressed (see Table S1 for cutoff values). In dense regions the dots are replaced by a heatmap, where the colour (from yellow to red) represents the density of dots. E denotes 'embryonic days/stages'; P denotes 'postnatal days'.

Table S1: Statistical methods and cutoff values used in various comparison of
two developmental stages

No.	Comparison	Statistical method	Q or E value cutoff*	Number of DETs
1.	R vs C (E15.5)	Fisher's exact test	0.1	44
2.	L vs Ri (Adult)	Vencio et al, 2004	0.001	17
3.	E15.5 vs E17.5	Vencio et al, 2004	0.001	38
4.	E15.5 vs P1.5	Vencio et al, 2004	0.001	36
5.	P1.5 vs Ad	Vencio et al, 2004	0.001	192
6.	E vs Ad	Vencio et al, 2004	0.001	328

* Q indicates p-value cutoffs based on Fisher's exact test with multiple testing correction to control for the false-discovery rate [114]. E-value cutoffs were used in the Bayesian model as described previously [115]. R denotes 'rostral region'; C denotes 'caudal region'; L denotes ' adult left hemisphere'; Ri denotes 'adult right hemisphere'; E denotes 'embryonic days/stages'; P denotes 'postnatal days'; Ad denotes 'adult stage'

SECTION B: SUMMARY OF RT-qPCR VALIDATION ANALYSIS

RT-qPCR confirmed ~50% of SAGE expression profiles (p<0.05; Table S2). The majority of fold changes confirmed by RT-qPCR were lower than SAGE. These results indicate that at medium to high expression levels, SAGE provides a reliable estimation of differential gene expression. This is likely to be due to the normalization of libraries of various sizes to 100,000 tags, which could overcompensate the magnitude of differences between transcripts. In addition, technical differences between SAGE and RT-qPCR may also contribute to the fold change differences.

Items	E15.5 R vs C	Adult L vs Ri	E15.5 vs. E17.5	E15.5 vs. P1.5	P1.5 vs Ad	E vs Ad	Total ^b
No. of candidate DETs	27	14	3	3	29	66	142
No. of DETs with gene ID	24 [8,3]	10 [4,0]	3 [0,3]	3 [2,1]	24 [21,16]	54 [44,42]	118 [79,65]
No. of DETs with EST ID	1 [0,0]	2 [0,0]	0 [0,0]	0	5 [4,3]	9 [8,7]	17 [12,10]
No. of ambiguous DETs with ID	2 [1,0]	2 [1,0]	0 [0,0]	0	0 [0,0]	3 [2,2]	7 [2,2]
Failed RT-qPCR	4/27	1/14	0/3	0/3	0/31	9/66	14/144
Validation rate according to trend only	9/27	5/14	3/3	3/3	25/31	54/66	99/144
Validation rate according to trend with $p < 0.05^{a}$	3/27	0/14	0/3	2/3	19/31	51/66	75/144

Table S2: RT-qPCR validation of SAGE tags in various comparisons

[x,y] denotes x number of genes which were validated according to trend and y number of x genes were significantly different with a *p*<0.05 cutoff.

^a based on empirical Bayesian moderated T-test with Benjamini-Hochberg correction for FDR.

^b the final total values are higher than the one reported in the text because the calculation includes the same DETs that were differentially expressed in comparisons of various stages. The total number of unique DETs was 136 and the total number of unique DETs validated according to trend with an adjusted p<0.05 was 70.

Note: R - 'rostral region'; C - 'caudal region'; L - ' adult left hemisphere'; Ri - 'adult right hemisphere'; E - 'embryonic days/stages'; P - 'postnatal days'; Ad - 'adult stage'.

SECTION C: INGENUITY PATHWAY ANALYSIS OF VALIDATED DETS

Table S3: Novel molecular networks, related biological functions/diseases and canonical pathways based on Ingenuity Pathway Analysis

Como		Novel molecular networks				
clusters	Focus gene ^a	Other associated nodes ^b	Biological functions and/or diseases ^c	Score ^d	Canonical pathway ^e	p value
Embryonic specific gene	ALS2CR2, BTG1, H2AFY, MARCKS, NEUROD1, ROBO1, RPS4X, SFRP1, SOX4, SOX11, WSB1	BIK, CDX1, COTL1, CTNNB1, FGF4, FZD6, GHRHR, HOXB9, HUS1, IL15, MAPK8, MAPK12, PKMYT1, retinoic acid, RUVBL2, SDCBP, Sox, SUFU, T, TNF, TPT1, WNT2, WNT4, ZEB2	Cellular Development, Organismal Development, Cellular Growth and Proliferation	26	Wnt/β-catenin signaling	1.83E-03
clusters (1, 5 and 6)	ACTB, 5031439G07Rik, CDK4, CDKN1C, CSRP2, DCX, EZH2, MARCKS, NEUROD1, PCNA	CCNDBP1, CCNO, CCT8, CDK4/6, COTL1, Cyclin A, Cyclin D, DAB2IP, DMTF1, ELP5, EMD, F Actin, FGF17, Histone h3, KIAA0101, LIG1, NFYB, NKX6-1, PAX7, PDGF BB, POLE, POU2F3, Rb, T, TSPYL2	Cell Cycle, DNA Replication, Recombination, and Repair, Endocrine System Development and Function	23	Tight junction signaling	8.13E-03 2.23E-02
Adult specific	CAMK2A, EGR1, ITPR1, MBP, NRGN, PLP1, PPAP2B, PPP1R1B, PPP3CA, RGS4, SEPT4, SIRPA, SNCB	 AHCYL1, Akt, Alkaline Phosphatase, BMP2K (includes EG:55589), CABP1, Calmodulin, CAMK2N2, CCKAR, Cytokine Receptor, Jnk, MAD2L2, MAP4K2, Mapk, NPLOC4, P38 MAPK, PPP3R2, STK39, TAOK2 (includes EG:9344), TRHR, Ubiquitin, UFD1L 	Nervous System Development and Function, Neurological Disease, Cell Morphology	33	Synaptic Long Term Potentiation Calcium Signaling B Cell Receptor Signaling cAMP-mediated Signaling	1.54E-05 9.60E-05 9.89E-04 1.30E-03 2.20E.03
(4, 8 and 10)	CRYAB, GRIA3, GSTM5 (GSTM1), MBP , NPTXR, TSPAN7 (TM4SF2)	ACTN1, AGTR2, CHRM2, DYRK1A, EDN3, ELK3, EPOR, FGF2, Fgfr, FOSL1, HOXD3, HSPB1, HSPB2, MAPK14, MYC, NAB2, PAK3, PDGFB, PDGFC, PDK1, PF4, PITX2, PRKG1, RARG, SDCBP, SMN1, steroid, TGFB1, TIAM1	Cell Morphology, Cellular Development, Cellular Movement	12	Amyotrophic Lateral Sclerosis Signaling Synaptic Long Term Depression G-Protein Coupled Receptor Signaling Xenobiotic Metabolism Signaling	5.20E-03 7.68E-03 1.78E-02 3.03E-02 4.60E-02
Gene switching	ACTL6B, APP, ATP7A, BCL11A, CLCN2, CTSD , HPRT1, MAPT, RBM9, YWHAE	ACTB, APPBP2, ATP, CACNL MAPPED, CDK5R2, CLIP1, Cu+, DNMBP, DOCK3, ELAVL4, ESR1, Esr1- Estrogen-Sp1, FPRL1 (includes EG:2358), Hsp70, ICMT, IL4, IL1B, Insulin, KLC1, KLC2, S100P, SMARCD1, TFCP2, THOP1	Cell Morphology, Neurological Disease, Amino Acid Metabolism	25	Amyloid processing Aryl hydrocarbon receptor signaling	1.45E-03 1.01E-02
7)	CALM1, CHGB, CTSD , NEDD8, UBE2E3, YWHAE	AGER, CACNA1C, Calcineurin A, CAMK2G, CCL20, CHGA, CTSB, CUL2, EPB41, heme, IPO11, MARCKS (includes EG:4082), MT1E, MTPN, MYLK, NAE1, RAN, RCAN1, retinoic acid, S100B, SCARB1, SELL, SMPD1, SPHK1, TNF, TNFAIP2, UBE2M, VIP	Cell Death, Hematological Disease, Developmental Disorder	13	Cell cycle: G2/M DNA damage checkpoint regulation	4.22E-02

^a A focus gene is an input gene that matched an annotated (based on human, mouse and rat) node in the Ingenuity knowledge base.

^b Associated nodes are intermediate molecules/complexes that are belonged to a network but are not an input gene.

^c Biological functions and/or disease annotations were based on all nodes (focus genes and associated nodes) in a novel molecular network.

^d A score of 2 indicates that there was a 1/100 chance that these genes were connected in a network due to random chance.

^e Enriched canonical pathways were determined based only on focus genes and the related *p* values were calculated using Fisher's exact test.

Table S4: Novel molecular networks, related biological functions/diseases and canonical pathways based on Ingenuity Pathway Analysis

Gene clusters	p value	Canonical pathway ^a	Associated focus gene ^b
Embryonic specific gene clusters (1, 5 and 6)	1.83E-03 8.13E-03 2.23E-02	Wnt/β-catenin signaling P53 signaling Tight junction signaling	Sox4, Sfrp1 and Sox11 Cdk4 and Pcna Cdk4 and Actb
Adult specific gene clusters (4, 8 and 10)	1.54E-05 9.60E-05 9.89E-04 1.30E-03 3.20E-03 7.68E-03 1.78E-02 3.03E-02 4.60E-02	Synaptic Long Term Potentiation Calcium Signaling B Cell Receptor Signaling cAMP-mediated Signaling GM-CSF Signaling Amyotrophic Lateral Sclerosis Signaling Synaptic Long Term Depression G-Protein Coupled Receptor Signaling Xenobiotic Metabolism Signaling	Gria3, Itpr1, Ppp3ca and Camk2a Gria3, Itpr1, Ppp3ca and Camk2a Egr1, Ppp3ca and Camk2a Rgs4, Ppp3ca and Camk2a Ppp3ca and Camk2a Gria3 and Ppp3ca Gria3 and Itpr1 Rgs4 and Camk2a Gstm5 (Gstm1) and Camk2a
Gene switching clusters (2 and 7)	1.45E-03 1.01E-02 4.22E-02	Amyloid processing Aryl hydrocarbon receptor signaling Cell cycle: G2/M DNA damage checkpoint regulation	Mapt and App Nedd8 and Ctsd Ywhae

^a Enriched canonical pathways were determined based only on focus genes and the related p values were calculated based on Fisher's exact test.

^b Focus gene is an input gene that matched an annotated (based on human, mouse and rat) node in Ingenuity knowledge base.



Figure S4 Novel molecular network 1 (embryonic specific gene clusters 1, 5 and 6). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression'; PP='proteinprotein interaction'; LO='regulating the localization'; PD='protein-DNA interaction'.



Figure S5 Novel molecular network 2 (embryonic specific clusters 1, 5 and 6). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression'; PP='protein-protein interaction'; LO='regulating the localization'; PD='protein-DNA interaction'.



Figure S6 Novel molecular network 3 (adult specific gene clusters 4, 8 and 10). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression'; PP='protein-protein interaction'; LO='regulating the localization'; PD='protein-DNA interaction'.



Figure S7 Novel molecular network 4 (adult specific gene clusters 4, 8 and 10). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression'; PP='protein-protein interaction'; LO='regulating the localization'; PD='protein-DNA interaction'.



Figure S8 Novel molecular network 5 (gene-switching clusters 2 and 7). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression'; PP='protein-protein interaction'; LO='regulating the localization'; PD='protein-DNA interaction'.



Figure S9 Novel molecular network 6 (gene-switching clusters 2 and 7). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression'; PP='protein-protein interaction'; LO='regulating the localization'; PD='protein-DNA interaction'.

SECTION D: TABULATION OF CELLULAR EXPRESSION DATA FOR VALIDATED DETS BASED ON INFORMATION IN PUBLICLY AVAILABLE EXPRESSION DATABASES

Cellular expression of DETs were manually obtained from publicly available micrographs accessible from the Allen Institute for Brain Science website [32], Brain Gene Expression Map website [33] and Gene Expression Nervous System Atlas (GENSAT) website [34] and GenePaint website [35] (in descending order of database used). The cellular expression profiles of a small number of DETs not available on these databases were obtained from micrographs in the published literature. The expression intensity of each DET within the cerebral cortex was classified using a scale from 0-2 (Table S5). The expression intensities of one DET should not be compared to another DET based on this scale. However, the relative cellular expression of a DET within the cortical layers of a single timepoint is relatively comparable.

Classification of DETs into neuron (N), glia (G) or both (B) group was based on publicly available expression micrographs deposited in the Gene Expression Nervous System Atlas (GENSAT) website [34], IPA knowledgebase [118] and PubMed literature search (by using a combination of the following keywords "gene name", "neuron", "glial", cerebral cortex"). Only gene expression reported within the cerebral cortex of either mouse or rat was taken into consideration.

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		Embryonic development (E15.5) ^a									Af	terbir	th						Group			
No.	Gene	-	Empryo	inc uevei	opment	(E13.3)					Postn	atal ^ь						А	dult			(N, G
		SVZ/VZ	IZ	SP	СР	MZ	REF	6	5	4	2 or 3	1	CT ^d	REF	6	5	4	2 or 3	1	CT ^d	REF	or B) ^e
1	Camk2a	2	1	1	1	1	[33]	1	1	1	2	1	N	[33, 34]	1	1	1	2	1	Ν	[32, 34]	Ν
2	Egr1	1	1	2	1	1	[33, 34]	1	1	1	1	1	N,G	[33, 34]	2	1	2	2	1	Ν	[32, 34]	В
3	Plp1	0	0	0	0	0	[33]	0	0	0	0	0	-	[33]	2	1	1	1	1	G	[32, 52]	G
4	Camk2n1	0	0	0	1	1	IH	1	1	1	1	1	-	IH	0	0	1	2	1	N	[44],IH	N
5	Cryab	0	0	0	0	0	[33, 34]	2	2	1	0	0	-	[33]	2	2	2	1	1	G	[32, 34]	G
6	Nrgn	0	0	0	0	0	[32]	0	0	1	1	1	Ν	[33, 34]	2	2	2	2	1	N	[3]	N
7	BQ176089	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	В
8	Sept4	2	1	1	2	1	[33]	1	1	1	1	1	-	[33]	1	1	1	1	1	G	[32, 34]	G
9	Sncb	1	1	2	2	1	[33]	1	1	1	1	1	-	[33]	-	-	-	-	-	N	[45]	Ν
10	Nptxr	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	[46]	G
11	Ppp1r1b	0	1	1	2	1	[33, 34]	1	1	1	1	0	Ν	[33, 34]	2	1	1	2	1	Ν	[32, 34]	Ν
12	Gstm1	1	0	0	0	0	[33]	-	-	-	-	-	-	-	0	1	1	1	0	N,G	[32, 43]	В

Table S5 : Cellular expression of validated DETs based on publicly available micrographs or expression databases.

13	Chgb	0	1	1	2	1	[33, 34]	2	2	2	1	0	N,G	[33, 34]	1	1	1	1	1	N,G	[32, 34]	В
14	Itpr1	1	1	2	2	1	[33]	1	1	1	2	1	-	[33]	1	1	1	2	1	Ν	[32, 47]	Ν
15	Rgs4	0	1	2	1	1	[34]	1	1	1	1	1	Ν	[34]	1	2	1	2	0	N	[32, 34]	Ν
16	AK139402	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	В
17	Tspan7	2	2	2	1	1	[33]	1	1	2	2	1	G	[33, 34]	1	1	1	1	1	G	[32, 34]	G
18	Sirpa	2	1	1	2	2	[33]	1	1	1	1	1	N,G	[33, 34]	1	1	1	1	0	G	[32, 34]	В
19	AU258168	-	-	-	-	-	-	1	-	-	-	-	-	-	1	-	-	-	1	-	-	В
20	Ppp3ca	0	0	0	0	0	[33]	1	1	1	1	0	-	[32, 33]	1	1	1	2	0	Ν	[32, 48]	Ν
21	Арр	0	0	0	1	1	[35]	1	-	-	-	-	-	-	1	1	1	1	1	N,G	[32, 46, 55]	В
22	Hprt1	1	1	1	1	1	[33]	1	1	1	1	0	-	[33]	1	1	1	1	0	N	[32, 56]	Ν
23	Gria3	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	1	1	1	N,G	[32, 46, 49, 50]	В
24	Calm1	2	1	1	1	1	[33]	1	1	1	1	0	-	[33]	1	1	1	1	1	Ν	[32, 58]	Ν
25	Ctsd	2	1	1	1	1	[33]	1	1	1	1	0	-	[33]	1	1	1	1	1	N,G	[32, 46, 57]	В
26	Mbp	0	0	0	0	0	[33]	1	1	0	0	0	-	[33]	1	1	1	1	1	G	[32, 51]	G
27	Ppap2b	1	1	0	0	0	[35]	-	-	-	-	-	-	-	1	1	1	1	1	G	[32, 46]	G
28	AK138272	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	В
29	AK140219	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	В
30	Clcn2	1	1	1	1	1	[33]	1	1	1	1	0	-	[33]	1	2	1	1	0	-	[32]	В
31	AK154943	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	В
32	Als2cr2	1	1	1	2	1	[33]	1	1	1	1	0	-	[33]	0	0	0	0	0	-	[32]	-
33	Nedd8	2	1	1	2	1	[33]	1	1	1	1	0	Ν	[33, 34]	1	1	1	2	1	Ν	[32-34]	Ν
34	Ywhae	2	1	1	2	1	[33]	1	1	1	2	1	-	[33]	1	1	1	1	1	N	[32, 33, 59]	Ν
35	Ube2e3	0	0	0	0	0	[35]	-	-	-	-	-	-	-	0	0	0	0	0	-	[32]	В
36	Rps4x	2	1	1	1	1	[33]	1	1	1	1	1	-	[33]	1	1	1	1	1	-	[32, 33]	-
37	Pcna	2	1	0	0	0	[36]	I	-	-	-	-	-	-	0	0	0	0	0	N,G	[31, 32]	-
38	Cdkn1c	0	1	0	1	1	[33]	0	0	0	0	0	-	[33]	0	0	0	1	0	N	[32, 37]	-
39	5031439G07Ri k	0	0	0	1	1	[35]	-	-	-	-	-	-	-	1	2	1	1	0	-	[32]	-
40	Bcl11a	1	1	1	2	0	[54]	-	-	-	-	-	-	-	1	1	1	1	0	Ν	[32, 60]	Ν
41	H2afy	2	1	1	2	1	[33]	1	1	1	1	1	-	[33]	1	1	1	1	0	-	[32]	-
42	Neurod1	0	2	1	1	2	[34]	1	1	1	1	1	Ν	[34]	0	0	0	0	0	Ν	[32, 34]	-
43	Marcks	2	1	1	2	1	[33]	1	1	1	2	1	-	[33]	1	1	1	1	1	N,G	[32, 38, 39]	-
44	Rbm9	1	1	1	2	1	[35]	-	-	-	-	-	-	-	1	1	1	1	1	N	[32, 61]	Ν
45	Wsb1	1	2	1	1	1	[35]	-	-	-	-	-	-	-	1	1	1	1	1	-	[32]	-

46	Btg1	2	0	1	1	1	[33]	1	1	1	2	1	-	[33]	1	1	1	2	1	-	[32]	-
47	Robo1	0	0	0	1	0	[35]	-	-	-	-	-	-	-	0	1	0	0	0	Ν	[32, 40]	-
48	AA122503	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
49	Cdk4	2	1	1	1	1	[33]	1	1	1	1	0	N,G	[33, 34]	1	1	1	1	1	G	[32, 34]	-
50	Sfrp1	2	0	1	1	1	[33]	1	1	1	1	1	N,G	[33, 34]	1	1	1	2	1	N,G	[32, 34]	-
51	Ezh2	2	2	1	1	1	[35]	-	-	-	-	-	-	-	0	0	0	0	0	G	[32, 41]	-
52	Zfp57	0	0	0	2	1	[35]	-	-	-	-	-	-	-	0	0	0	1	0	-	[32]	-
53	Dcx	1	1	1	2	1	[33]	1	1	1	1	1	Ν	[33, 34]	0	0	0	0	0	Ν	[32, 34]	-
54	Sox11	1	2	1	2	1	[33]	1	1	1	1	1	Ν	[33, 34]	0	0	0	0	0	Ν	[32, 34]	-
55	Dr1	1	1	1	2	1	[42]	-	-	-	-	I	-	-	0	1	1	1	0	Ν	[32, 42]	-
56	Zswim4	-	-	-	-	-	-	-	-	-	-	-	-	-	0	1	1	1	0	-	[32]	-
57	Actl6b	0	1	1	2	1	[35]	-	-	-	-	I	-	-	1	1	1	1	1	-	[32]	В
58	Atp7a	2	1	1	1	1	[35]	-	-	-	-	I	-	-	0	0	0	0	0	N,G	[32, 53]	В
59	Hmgb3	1	1	1	1	0	[35]	-	-	-	-	1	-	-	0	1	1	1	0	-	[32]	В
60	BQ177886	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
61	Actb	1	2	1	2	1	[33]	1	1	1	2	1	-	[33]	1	1	1	2	1	N,G	[32]	-
62	Cand2	2	1	1	1	1	[35]	-	-	-	-	1	-	-	1	1	1	1	1	-	[32]	-
63	Sox4	1	1	1	2	1	[33]	1	1	1	2	1	N,G	[33, 34]	1	1	1	1	1	Ν	[33, 34]	-
64	Csrp2	0	1	0	1	0	[35]	-	-	-	-	-	-	-	0	0	0	0	0	-	[32]	-
65	Mapt	0	1	2	2	2	[33]	1	1	1	1	1	Ν	[33, 34]	1	1	1	1	1	Ν	[32, 34]	N
66	Blcap	0	0	0	0	1	[35]	-	-	-	-	-	-	-	1	1	1	1	0	-	[32]	-
67	CD802535	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
68	Tmsb4x	1	2	1	2	1	[33]	1	1	1	2	1	-	[33]	1	1	2	2	1	Ν	[32]	-

^a Based on E15.5 micrographs from [32-34] or E14.5 micrographs from [35]. ^b Based on P4 [32] or P7 [33] micrographs.

^c Based on P56 micrographs from [32, 33].

^d Based on micrographs from [34], IPA knowledgebase [118] and published literature. Only expression datasets generated from cortical neurons or glial cells of mouse and rat were considered.

^e Some of the DETs were not classified into the N-, G- or B-groups because they do not belong to the IPA Networks 3 to 6 in IPA analysis.

Note : IH denotes in-house experiment. A dash (-) denotes no expression information was found. The intensity of expression values range from 0-2 where 0 denotes 'no expression', 1 denotes 'relatively higher expression' and 2 denotes 'obvious expression'.



Figure S10 (A) IPA analysis of the qPCR-validated DETs from Networks 3 to 6 and their associated neurological disorders and cell death process. DETs were classified into three groups according to the origin of their expression; only expressed in cortical neurons (N-group), in cortical glia (G-group) or in both cell types (B-group). DETs without known cellular expression data were classified in B-group. Red coloured nodes = N-group DETs, green coloured nodes = G-group DETs and both grey and pink (DETs without cellular expression data) coloured nodes = B-group DETs. (B) Simplified Venn diagram to illustrate the association between N-, G- and B-group DETs according to (A). X-linked MR denotes 'X-linked mental retardation'.



Figure S11 Regionalization of *Sox4* transcripts. A-F are sagittal sections obtained from various developmental stages of the mouse cerebral cortex. Arrowheads show brain regions with higher *Sox4* sense expression. Both E15.5 and E17.5 brain sections show regionalized expression of *Sox4* in the cerebral cortex. Tel denotes telencephalon; VZ denotes ventricular zone; CP denotes cerebral cortex; C denotes caudal region; R denotes rostral region; IZ denotes intermediate zone; OB denotes olfactory bulb.



Figure S12 ISH of *Sox4* transcripts in E11.5 to P150 mouse brains. A-F show the expression of the sense transcript for *Sox4*. G-L show the expression of antisense transcripts for *Sox4*. Bright field micrographs show high magnification snapshots of the corresponding dark field micrographs. All micrographs were taken from coronal sections. Silver grains are seen as black dots under bright field. The silver grains confirm that the expression of both the sense and antisense transcripts are not due to background noise. PP=primordial plexiform layer; SVZ=subventricular zone; IZ=intermediate zone; CP=cortical plate; MZ=marginal zone.



Figure S13 A high magnification examination of *Sox4* transcript ISH. A and C show the expression of *Sox4* sense transcripts that are clearly detectable in both the nucleus and cytoplasm. B and D show the expression of *Sox4* antisense transcripts that are predominantly localized in the nucleus. All micrographs were taken of the P1.5 cerebral cortex. Both C and D are the enlarged micrographs corresponding to A and B, respectively.



Figure S14 ISH of the Hba-al transcript in E11.5 to P150 mouse brains. A-F show the expression of the sense transcript whereas G-L represent the expression of the antisense transcript for Hba-a1. Sense expression of Hba-al appeared 'dotted' because only specific haematopoetic cells such as reticulocytes that clump within vascular compartments expressed the transcript. There was no 'dotted'-like appearance in adult sections because adult mice were perfused with saline prior to fixation. We found no observable antisense expression for Hba-a1 at any developmental stages (10F.1-F.6). Therefore, Hba-a1 is not only a good candidate control gene for the spatio-temporal study of gene expression, it also provides quality assurance on technical issues such as tissue preparation.

Table S6: Mapped Paired End Di-tags (PETs) at the Sox4 gene locus.

FANTOM		Start	End		Size
PET ID	Chromosome	position ^a	position ^b	Strand	(nt) ^c
154342	chr13	29043154	29043961	+	807
153327	chr13	29042250	29045096	+	2846
87809	chr13	29041180	29045566	+	4386
31530	chr13	29041285	29044501	+	3216
32641	chr13	29041310	29043229	+	1919
154138	chr13	29043742	29045566	+	1824

^a Start position for the FANTOM PET left tag.

^b End position for the FANTOM PET right tag.

^c Size of the predicted transcript based on the left and right PETs presuming no splicing has occured.

^{a,b} FANTOM PET sequences were obtained from Ensembl website [64]. The ditag of PolyA+ RNA libraries were originally downloaded from the FANTOM consortium site and processed using code available in

http://www.ensembl.org/Mus_musculus/ditags/FANTOM_GSC_PET.html.

Table S7: miRNAs, which target Sox4 sense transcripts.

miDNA		Targeted position ^a											
IIIIKINA	Chromosome	Start position	End position	Strand									
mmu-miR-324-5p	chr13	29042673	29042695	-									
mmu-miR-331-3p	chr13	29042520	29042542	-									
mmu-miR-466a-3p	chr13	29041141	29041163	-									
mmu-miR-702	chr13	29043538	29043560	-									

^a Analysis was based on the miRanda 3.0 prediction created on 2007-11-1, which was downloaded from [103]. Only mouse miRNAs are shown. The targeted positions were re-mapped onto the NCBI build 37.1 mouse assembly database.



Figure S15 UCSC genome browser view of miRNAs, which target *Sox4* sense transcripts with corresponding SAGE tags and mouse mRNAs.

SECTION F: ANALYSIS OF THE SOX11 GENOMIC CLUSTER

Genomic cluster at the Sox11 locus

There were 14 SAGE tags situated within the Sox11 locus (Figure S16-A). Of these tags, 10 were located within the Sox11 canonical transcript. Only two DETs within the canonical transcript were identified by 3' RACE Southern blotting: sox11_tag11 and sox11_tag12. According to the SAGE analysis, both DETs were expressed highly in embryonic stages of development compared to P1.5 or Ad (Figure S16-B). RT-qPCR analysis using two different assays near to these tags confirmed the embryonic specific expression of sox11_tag11 and sox11_tag12 at P1.5 (with fold changes of -2.50 and -3.32 respectively; p<0.0001) and P150 (with fold changes of -140.10 and -139.80 respectively; p < 0.0001) compared to E15.5 (Figure S16-C). In agreement with the SAGE analysis, RT-qPCR showed consistently higher expression of the sox11_tag12 than the sox11_tag11 at all stages. Figure S16-D shows the strand specific 3' RACE-Southern blotting analysis of *Sox11*. The analysis confirms the existence of the multiple overlapping sense transcripts (Figure S16-D.1-D.3) within the Sox11 canonical transcript based on the SAGE expression profile. Figure S16-D.3 shows the sox11 tag11 amplicons, which range from 0.65kb-1.35kb. Amplicon sizes beyond 0.75kb are most likely to indicate the presence of alternative transcripts that contribute to the tags situated beyond the canonical mRNA; sox11_tag6, sox11_tag7 and sox11 tag9. In all cases, these transcripts were embryonic specific and expressed during cerebral cortical development. We also confirmed the existence of the sox11_tag12, which showed consistent expression throughout cortical development with only mild differences in expression between E15.5, P1.5 and P150. The same analysis with antisense specific probes confirmed the expression of antisense messages (sox11 tag16 and sox11 tag17) within this genomic locus (Figure S16-D.4). Sox11_tag16 and sox11_tag17 were expressed during the embryonic stages of development, and not at P1.5 or P150. The controls genes used in the 3' RACE-Southern blotting analysis were the same genes used in the Sox4 analysis, Psmb2 and Hmbs (Figure S16-D.5-D.6). In addition, we also performed Northern analysis on Sox11 using a ~1.0kb double stranded DNA probe spanning both sox11_tag16 and sox11_tag17. The Northern analysis showed only two prominent transcript variants ranging between ~7.0-8.0kb. Northern analysis of Sox11 (Figure S16-E) may not reflect the actual transcript variants that exist in the cluster for various reasons, these include: the probe does not span the relevant overlapping transcripts, or the overlapping region is limited.







Figure S17 ISH of Sox11 transcripts from E11.5 to P150 mouse brains. A-F show the expression of sense transcripts for Sox11. G-L show the ISH of antisense transcripts for Sox11. (A) At E11.5, Sox4 sense transcripts were confined to the primordial plexiform layer. (B-E) From E13.5 to P1.5, the sense transcripts were expressed throughout the cortical plate. Expression of sense transcripts at the subventricular zones was observed at E17.5 (D) and P1.5 (E) only. There was no observable expression of the sense transcript during the adult stage (F). The expression of the antisense transcript was not detected in all ISH sections (G-L).

Table S8: Mapped Paired End Di-tags (PETs) at the Sox11 gene locus.

FANTOM		Start	End		
PET ID	Chromosome	position ^a	position ^b	Strand	Size (nt) ^c
43777	chr12	28021261	28023139	+	1878
43643	chr12	28021321	28022447	+	1126
43286	chr12	28021782	28023532	+	1750
43573	chr12	28022508	28023136	+	628
43301	chr12	28022803	28025440	+	2637
43174	chr12	28023092	28024493	+	1401
168702	chr12	28023106	28024669	+	1563

^a Start position for the FANTOM PET left tag.

^b End position for the FANTOM PET right tag.

^c Size of the predicted transcript based on the left and right PETs presuming no splicing of transcript.

^{a,b} FANTOM PET sequences were obtained from EnsEMBL project website [64]. The ditag of PolyA+ RNA libraries were originally downloaded from the FANTOM consortium site and processed using code available in

http://www.ensembl.org/Mus_musculus/ditags/FANTOM_GSC_PET.html.

Table S9: miRNAs, which target Sox11 sense transcripts.

:DNA		Targeted po	osition ^a	
MIKINA	Chromosome	Start position	End position	Strand
mmu-let-7g*	chr12	28025175	28025196	-
mmu-miR-136*	chr12	28025967	28025988	-
mmu-miR-207	chr12	28026014	28026035	-
mmu-miR-20b*	chr12	28025454	28025475	-
mmu-miR-337-5p	chr12	28025682	28025701	-
mmu-miR-343	chr12	28025708	28025727	-
mmu-miR-378*	chr12	28026044	28026065	-
mmu-miR-409-5p	chr12	28025311	28025333	-
mmu-miR-453	chr12	28025325	28025348	-
mmu-miR-540-5p	chr12	28025633	28025652	-
mmu-miR-151-5p	chr12	28026067	28026088	-

^a Analysis was based on the miRanda 3.0 prediction created on 2007-11-1, which was downloaded from [103]. Only mouse miRNAs are shown. The targeted positions were re-mapped onto the NCBI build 37.1 mouse assembly database.

28027000 28026000 28026000 mmu-let-7g* mmu-miR-405 mmu-miR-20b* mmu-miR-30-5p mmu-miR-337-5p mmu-miR-334 mmu-miR-343 mmu-miR-345	28024000 28023000 28022000 miRNA targeting Sox11	28021000 28020000	:chr12
I mmu-mir-ca/ I mmu-mir-ca/ I mmu-mir-1376 I mmu-miR-151-5p Sox11_tag18	SAGE tags (sense only) Sox11_tag14 Sox11_tag15 RefSeq Genes	Sox11_tag11	Sox11_tag6 Sox11_tag7 Sox11_tag9
	Ensembl Gene Predictions	Sox11	
Kin Kin Kin Kin Kin Kin Kin Kin Kin	Mouse mRNAs from GenBank AK021300 AK021300 AK017690 AK018080	AK012222 AK012306	 ENSMUST00000079063 AK086326 AK004158

Figure S18 UCSC genome browser view for miRNAs, which target *Sox11* sense transcripts and corresponding SAGE tags and mouse mRNAs.

SECTION G: SUPPLEMENTARY MATERIALS AND METHODS

Total RNA isolation and first strand cDNA synthesis: An additional DNase I (Qiagen) treatment step was added prior to recovery of total RNA to remove traces of genomic DNA (gDNA) contamination. The concentration and quality of all isolated total RNA was determined using the 2100 Bioanalyzer (Agilent Technologies). Only total RNAs with an RNA Integrity Number [119] greater than 8.0 were considered for subsequent RT-qPCR analysis.

Primer design and RT-qPCR: The following parameters were applied to all primers designed; length between 18-27bp, GC% between 30-70, Tm between 59-60 and amplicon size between 50-250bp. All RT-qPCR reactions were prepared in 10µl volumes in a 384-well plate format with 1X LC480 Master Probe Mix (Roche Diagnostics), 250nM of forward and reverse primers (GeneWorks or Bioneer Corporation) and 100nM of Universal ProbeLibrary probe (Roche Diagnostics). RT-qPCRs were performed using the LightCycler® 480 System (Roche Diagnostics) with a pre-denaturing step of 95°C for 10 minutes, and 45 cycles of 95°C (10 seconds), 60°C (30 seconds) and 72°C (10 seconds) followed by a cooling step at 40°C for 1 minute.

Relative quantification using a standard curve method: The following criteria were adopted to define a successful PCR assay; PCR efficiency between 80-120%, R-squared>0.985 and a minimum of two successful housekeeping genes in each run. Based on a successful standard curve, the amount of starting RNA of both target and reference genes were calculated as a linear function of logarithmic concentration and Cp. All estimated starting amounts were in arbitrary values.

Strand specific RT-PCR: PCR amplifications were carried out in using FastStart PCR High Fidelity System (Roche Diagnostics) according to manufacturer's protocol. The cycling parameters were as follows; a pre-denaturing step at 95°C for 10 minutes, and 35 cycles of 95°C (30 seconds), 60°C (30 seconds) and 72°C (1 minute) followed by an additional extension at 72°C for 7 minutes.

3' Rapid Amplification of cDNA Ends (RACE): PCR amplifications were carried out in 40µl reaction using FastStart PCR High Fidelity System (Roche Diagnostics) at 95°C (10 minutes) initial denaturation, and 40 cycles of 95°C (30 seconds), 60°C (1 minute) and 72°C (1 minute) followed by a final extension at 72°C for 7 minutes (if necessary).

Southern blotting analysis: Prehybridization of blots was carried out at 42° C in 125μ l /cm² Rapid-Hyb buffer (GE Healthcare) for 20 minutes. Hybridizations were performed in the same solution and incubated for 2 hours at 42° C with $1-3x10^{6}$ dpm/ml of 5' end-labelled probe. Membranes were initially washed with 5X SSC (with 0.1% v/v SDS) for 20 minutes at 37°C followed by 1X SSC (with 0.1% v/v SDS) for 15 minutes with a gradual increase in washing temperature up to 65°C. A final wash (if needed) was performed using fresh 1X SSC (with 0.1% v/v SDS) at 65°C for an additional 15 minutes.

Synthetic oligonucleotides were 5' end-labelled using T4 polynucleotide kinase (T4-PNK) (Promega) and $[\gamma^{-32}P]ATP$ (Amersham). The reactions were prepared in a 25µl volume with 20U of T4-PNK, 0.05mCi of $[\gamma^{-32}P]ATP$ and 2.5ul of 10X kinase buffer (Promega). The reactions were incubated for 20 minutes at 37°C

before 2ul of 0.5M EDTA was added to stop the reaction. Unincorporated radionucleotides were separated from the labelled probe through a Sephadex G-25 column. See SI-7 for detailed primer sequences and oligonucleotides used for detection.

In situ RNA hybridization (ISH): All dissected embryonic and postnatal brains were fixed for 24-48 hours in cold 4% paraformaldehyde without cardiac perfusion. For E11.5 and E13.5, whole embryo heads were fixed. For adult mice, cardiac perfusion was performed using 4% paraformaldehyde prior to dissection. Dissected adult brains were then fixed in cold 4% paraformaldehyde for 48 hours. Brain sections were dewaxed, rehydrated through graded concentrations of ethanol, incubated for 30 minutes at room temperature in 10mg/ml proteinase K, followed by additional fixation in 4% paraformaldehyde for 10 minutes, then dehydrated through graded concentrations of ethanol. Pre-processed brain sections were air-dried, then hybridization solution containing 5×10^5 cts/minute/µl in vitro transcribed cRNA probes (Riboprobe® In Vitro Transcription System Kit by Promega) was placed over the section. Slides were incubated overnight at 56°C in a formamide-humidified chamber and then washed as described previously [123]. Washed slides were exposed to Kodak NTB-2 (Kodak) emulsion at 4°C for 7-21 days and then developed using Kodak Professional Developer Characteristics D-19 (Kodak).

Strand-specific RT-qPCR: Total RNA was extracted from harvested organs using the TRIzol®'s reagent (Invitrogen) according to the manufacturer's protocol. To avoid genomic DNA contamination, all isolated total RNA was treated with the recombinant DNAse I enzyme provided by the DNA-freeTM kit (Applied Biosystems) according to the manufacturer's protocol. The concentration and purity of all isolated total RNA was determined using the NanodropTM 1000 spectrophotometer (Thermo Scientific). First strand cDNA synthesis was carried out using strand-specific primers followed by qPCR analysis as described in above.

Embryonic neural stem cells grown as neurospheres: A neuroculture complete medium consists of: 1X NEUROBASALTM Medium (Cat number: 21103-049, Invitrogen) containing 2% (v/v) 50X B-27 serum-free supplement (Cat number: 17504-044, Invitrogen), 1% (v/v) 200mM L-glutamine, 1% (v/v) 200mM Glutamax (Cat number: 35050-061, Invitrogen), 100 units/ml penicillin, 100 μ g/ml streptomycin, 20ng/ml EGF (BD Biosciences) and 20ng/ml bFGF (R & D Systems).

P19 embryonal carcinoma (EC) cells: A P19GM complete medium consists of: Minimum Essential Medium Alpha (alpha-MEM; Cat number: 12571-071; Invitrogen) supplemented with 10% (v/v) heat-inactivated fetal calf serum (FCS; Cat number: 10438-026; Invitrogen), 100 units/ml penicillin, 100 μ g/ml streptomycin and 2 mM L-glutamine.

<u>SECTION H:</u> R-SCRIPT FOR REAL TIME PCR ANALYSIS (WITH MULTIPLE HOUSEKEEPING GENES NORMALIZATION AND MULTIPLE GROUP COMPARISONS)

#Realtime PCR Analysis

```
#(for multiple housekeeping genes normalization and multiple groups comparisons)
#The user needs to read the lines where there are 3 hashes and alter as advised
### Set this directory to suit your data
>dataDir <- "C:\"
#
>setwd(dataDir)
#Just as a check, list the files in this directory
>list.files()
#load the lima package
>library(limma)
### Set these value
>numTissues <- 4
>numRefGenes <- 1
>numReplicates <- 3
###Set the data filename
>dataFilename <- "data.txt"</pre>
# Assume the input files have row names in the first column...hence the
row.names=1 parameter
# read in the ratios of control to reference, treatment to reference
>ratios <- read.table(file=dataFilename, row.names=1, header=TRUE, sep="\t")</pre>
#creat a weights matrix of right dimensions and set all weights to 1
>weights <- matrix(1, nrow=dim(ratios)[1], ncol=dim(ratios)[2])</pre>
# if any data values = NA, set weight for that data value to 0
>weights[is.na(ratios)] <- 0</pre>
#
#
>tissue
              <- factor(rep(1:numTissues, each=numRefGenes*numReplicates))
# If there were 4 Tissues, 1 RefGene and 3 Replicates, then the tissue factor
would be
# [1] 1 1 1 1 2 2 2 2 3 3 3 3 4 4 4 4
# Levels: 1 2 3 4
#
>tissue
#
>referenceGene <- factor(rep(rep(1:numRefGenes, each=numReplicates), numTissues))</pre>
# If there were 1 refGenes and 3 Replicates and 4 Tissues, the factor
referenceGene would be
# [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
# Levels: 1 2 3
>referenceGene
# Make a design matrix. We want estimates of the mean ratio for control,
# and the mean ratio for treatment, so we won't fit an intercept term.
# We fit an effect for referenceGene, which is a nuisance parameter affecting
# our estimates of control and treatment, but which we don't really care about
>mm <- model.matrix(~ -1 + tissue)</pre>
### You need to enter abbreviations for each Tissue(Treatment), Tl to T4 in this
example
>colnames(mm) <- c("T1", "T2","T3", "T4")</pre>
# fit the model to the logged ratios
>fit <- lmFit((ratios), design=mm,weights=weights)</pre>
#
# now fit the all effects
# make a contrast matrix
### You need to enter all possible contrasts betweeen tissues
>contrastsMatrix <- makeContrasts("T1-T2","T1-T3","T1-T4","T2-T3","T2-T4","T3-T4",</pre>
levels=mm)
# fit the contrast
>fit2 <- contrasts.fit(fit, contr=contrastsMatrix)</pre>
>fit3 <- eBayes (fit2)</pre>
# calculate group-wise "means" and standard errors. Note: stderrs come
# from linear model, not from population
>estimates <- fit$coef[,1:numTissues]</pre>
>stdevs <- (fit$stdev*fit$sigma)[,1:numTissues]</pre>
>colnames(stdevs) <- paste(colnames(stdevs), "stdv")</pre>
```

#Create a toptable showing all contrasts. Use argument "genelist" of #topTable to get estimates and stdvs into table (this is a hack). >est <- data.frame(estimates, stdevs)</pre> >ttallc <- topTable(fit3, adjust="BH", number=nrow(fit3\$p.value), genelist=est)</pre> #create a topTable showing details for each contrast ###You need to modify these lines to suit your tissue contrasts >ttt1t2 <- topTable(fit3, adjust="BH", number=nrow(fit3\$p.value),coef=1) <- topTable(fit3, adjust="BH", number=nrow(fit3\$p.value),coef=2) >ttt1t3 >ttt1t4 <- topTable(fit3, adjust="BH", number=nrow(fit3\$p.value),coef=3) <- topTable(fit3, adjust="BH", number=nrow(fit3\$p.value),coef=4) >ttt2t3 <- topTable(fit3, adjust="BH", number=nrow(fit3\$p.value),coef=5) <- topTable(fit3, adjust="BH", number=nrow(fit3\$p.value),coef=6) >ttt2t4 >ttt3t4 # to write results to a file use something like >write.table(file="tlt2.xls", tttlt2, sep="\t", quote=F) >write.table(file="tlt3.xls", tttlt3, sep="\t", quote=F)
>write.table(file="tlt4.xls", tttlt4, sep="\t", quote=F) >write.table(file="t2t3.xls", ttt2t3, sep="\t", quote=F) >write.table(file="t2t4.xls", ttt2t4, sep="\t", quote=F)
>write.table(file="t3t4.xls", ttt3t4, sep="\t", quote=F) >write.table(file="means_std_allgroups.xls", est, sep="\t", quote=F) #

A-3 Additional data file 2

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SAGE tag information for 561 differentially expressed tags (DETs).

Full version of this data file is accessible at <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s2.xls</u>.

Note 1 Tags=refers to the tag sequence, which could be a short or long or a clusters of combined tags.

Note 2 ID=refers to the identifier assigned to each tag.

Note 3 Category est=when a tag matched a unique EST; gene=when a tag matched a unique GENE; ambiguousgene=when a tag was found matching to many genomic positions but only unique to a gene identifier (chromosome position was not provided); multiple=when a tag was found matching to many genomic positions but not any unique gene identifier (chromosome position was not provided); genomic=when a tag matched an unique genomic sequence without any annotations; nomatch=when a tag did not match any positions in genome.

Note 5 Please drag to the bottom of the table for the legend about the RED and GREEN backgrounds whereas R=E15.5 Rostral; C=CE15.5 caudal; L=adult left hemisphere; Ri=adult right hemisphere; E=embryonic stages (E15.5+E17.5); Ad=adult.

Note 6 Hierarchical clustering of log2 normalized count: the number indicates the cluster a particular tag belongs to.

- Note 7 Grouped normalized tag count: refers to the combined normalized tag counts when a particular stage of development consists of more than one SAGE library.
- Note 8Transcript signature: refers to the occurrence of each tag in every stages of development. Level of tag count was not taken into account.Please toggle 1 for presence and 0 for absence. This will let you know which tag is present in which development stages (*this information is only available in the excel form an therefore not presented in the Appendix*).

Note 4 Chromosome positions were based on mouse genome assembly release July 2007 (mm9).
					New genom:	c coordinate	(July	ffere	entia	11y Ex	presse	d Tags	(DET				Grou	ped norm	nalized tag	count		
No.	Tags	Accession Number	ID	Category	Chromosome	Start Coordinate	Strand	R vs C	L vs Ri	E15.5 VS E17.5	E15.5 VS PN1.5	PN1.5 VS Ad	E vs Ad	Hierarchical clustering of Log2 normalized count	E15.5	E17.5	PN1.5	Ad	E15.5 Rostral	E15.5 Caudal	Ad Right	Ad Left
1	cagactgetetgttete	NM 008696	Map4k4	gene	chrl	40082757	+	0	0	0	0	2	0	2	17.33	8.28	18.66	1.33	2.31	27.98	1.665	0.985
2	caccetgtgggagetea	NM 172656	Als2cr2	gene	chrl	59051929	+	0	0	0	0	0	2	1	11.03	12.88	7	1	9.23	2.54	0.725	1.9375
3	gatgtggetgettttaa	NM 018796	Eef1b2	gene	chrl	63226159	+	0	0	0	0	0	2	5	91.36	114.11	55.98	17.66	76,16	81.4	14.02	18.81
4	aaaacagtggccggtag	NM 009084	Rp137a	gene	chr1	72758767	+	0	0	0	0	2	0	5	69.31	57.97	97.97	32.65	87.71	61.05	30,855	35,4775
5	ctattaaaagtcaggtc	NM_009447	Tuba4a	gene	chrl	75211573	-	.0	0	0	0			4	0	2.76	0	35.32	0	0.0	27.53	39.5375
7	daaadaadaadaadaa	NM 009447	Dtore	gene	chrl	752/3012	-	0	0	0	0	0		9	18.9	0.92	0.33	32.00	0	61.05	39 405	0.90
8	gaattgatgatgeteac	NM 009129	Seg2	dene	chrl	79431449	-	0	0	0	0	0		8	1.58	0.92	9,33	9.66	2,31	2.54	9.035	9,91
9	gtagtggagcccttaaa	NM 022417	Itm2c	gene	chrl	87805169	+	0	0	0	0		1	7	14.18	12.88	4.67	46.98	6.92	12.72	45.305	49.5525
10	gttttgagaaaagcaaa	NM 019867	Ngef	gene	chr1	89373466	2 - 2 - 3	0	0	0	0	0		8	0	0.92	2.33	12	0	0	10.915	12,065
11	tcaaaactatcctctgg	NM 181750	R3hdm1	gene	chr1	130133789	+.	0	0	0	0	0		8	1.50	0.92	7	19.66	0	2.54	21.315	18.8125
12	ctaaaaggagataatat	NM 009227	Snrpe	gene	chrl	135500642	-	0	0	0	0	0	2	7	24.41	19.32	4.67	2.33	27.7	27.98	1.45	2.4775
13	tgttttcccttttcccc	NM 139438	Gpr3/11	gene	Chr1	137056957	-	0	0	0	0	.0	0	9	10 11	0	22.23	12.99	22.21	20.25	11.035	13.2125
15	ctgtacatttctgttct	NM 019962	Kif21b	dene	chrl	138074505	+	0	0	0	0	0	3	6	25.2	24.85	20,99	2.67	27.7	30.52	3.62	1.64
16	attteeegaggacgtet	NM 026369	Arpc5	gene	chr1	154622293	+	0	0	0	0	0	2	6	11.03	15.64	16.33	2.33	18.46	7.63	3.325	1.7775
17	tatagtatgttcggtta	NM 008131	Glul	gene	chr1	155756711	+	0	0	0	0			4	0.79	3.68	Ó	126.95	0	2.54	111.865	137.36
18	ttctagcatatgtaata	NM 009721	Atp1b1	gene	chr1	166367335	-	0	0	0		0	0	7	6.3	17.48	58.32	37.99	13.85	2.54	22,33	48.6625
19	gettgaaaaatgaccag	NM_138314	Nme7	gene	chrl	166368042	+	0	0	0	0	0	24	4	0.79	0	0	8.66	0	2.54	11.42	6.82
20	actttgagattgtacct	NM 009062	Rgs4	gene	chrl	171671897	-	0	0	0	0	0		8	1.58	0.92	7	19.33	0	2.54	25.145	15.33
21	aaggaagagatggctcg	NM 011701	Vim	gene	chr2	13501753	+	0	0	0	0	0		1	9.45	11.04	9.33	0.67	34.62	15.20	62.06	102.97
23	gccaccctctacagcag	NM 008963	Ptgds	gene	chr2	25323604		0	0	0	0	0		8	0.75	0.92	4.67	14,99	0	0	19.085	11.77
24	taactttaagacgetee	NM 019498	Olfml	gene	chr2	28069899	+	0	0	0	0			10	8.66	15.64	18.66	189.93	16.16	7.63	156.685	213.278
25	caatgetgtagttagga	NM 019498	Olfml	gene	chr2	28085938	+	0	2	0	0	0	Û	7	5.51	4.6	18,66	15.99	4.62	7.63	29.06	7.5375
26	cacacagcatacaaaaa	NM 021515	Ak1	gene	chr2	32490747	-	0	0	0	0	0	2	1	13.39	11.04	0	0.67	9.23	12.72	0.725	0
27	gtgtatgacatcaccag	NM_026697	Rab14	gene	chr2	35045436	-	0	2	0	0	0	0	2	7.88	0.92	4.67	22.66	13.85	7.63	38.17	11,7075
28	ccatttgagcaaataaa	AF513716	Fmn12	gene	chr2	52992807	+	0	0	0	0	0	- 2	6	15.75	16.56	14	2.33	25.39	15.26	1.665	2.745
29	teggagagagagagagtgattt	NM 010064	Duncli2	gene	chr2	71052508	- T	0	0	0	0	2	0	3	15.75	1.84	20.99	0.33	30	12 72	0.94	0.4925
31	ctcctgaaggcatagtt	NM 009454	Ube2e3	gene	chr2	78760729	+	ö	0	0	0	0	2	7	16.54	22.09	7	4	13.85	15.26	2.895	4.92
32	cagttgcaataaaaata	NM 010894	Neurodl	gene	chr2	79292826		0	0	0	0	0	2	1	12.6	8.28	4.67	1.67	13.85	12.72	0	1.05
33	ctggtacgttatgagga	NM_023850	Chstl	gene	chr2	92454236	+	0	0	0	0	0		8	1.58	0.92	7	19.33	2.31	2.54	22.195	16.8425
34	tetggttaeaetttgga	NM 030725	Syt13	gene	chr2	92795823	+	0	0	0	0	0		4	0	0	0	10	0	0	8.82	10.5975
35	ccaggttattaaagata	NM 025403	Nola3	gene	chr2	112102794	+	0	0	0	0	0	2	7	14.96	25.77	11.66	6	16.16	10.17	4.045	7.245
36	adgitttgtttaccagg	NM 146125	Rasgrp1	gene	chr2	11/105988	-	0	0	0	0	0		4	0	0	0	14.33	0	0	12.44	17 2075
38	tgtgactccctaacatt	NM 032393	Mtapla	dene	chr2	121134694		0	0	0	0	0		8	0	0	4.67	16.33	ő	0	22.84	12,005
39	tggaatgagcgtttagg	NM 009897	Ckmtl	gene	chr2	121188450	+	0	0	0	0	0		8	0	0	2.33	16.66	0	0	20.025	13.6675
40	ctgggtaagcactette	NM 010762	Mal	gene	chr2	127459418	-	0	0	0	0	Ũ		4	0	0	0	13.33	0	0	8.525	16.7125
41	tgggttgtgggtgctgt	NM_027192	Ttl	gene	chr2	128921862	+	0	0	0	0	2	0	2	7.88	5.52	20.99	2.33	6.92	2.54	0.94	3.9675
42	tgtatacacacacgggt	NM 007547	Sirpa	gene	chr2	129457646	+	0	0	0	0	0		8	0	0	2.33	18.66	0	0	18.955	16.825
43	tgactagegtgacctgt	NM 007694	Chgb 6320527006mik	gene	chr2	132620699	+	0	0	0	0	0			4.73	4.0	4.6/	15.66	6.92	0	44.715	32.04
45	tatattaaatcaaaaaa	AK078038	Snap25	gene	chr2	136608066	+	0	0	0	0			10	4.73	15.64	14	261.9	6,92	7.63	261.76	258.31
46	ccttgctcaaattaaaa	NM 009976	Cst3	gene	chr2	148697491	-	0	0	0	1	0	0	7	14.96	53.37	58.32	101.63	18.46	12.72	111.03	101.05
47	tgagtgaaga	NM_011438	Sox12	gene	chr2	152220781		0	0	0	0	0	2	1	7.88	8.28	0	0	11.54	15.26	0	0
48	ttogggttgetettttg	NM 025735	Map11c3a	gene	chr2	155103559	+	0	0	0	0	0		7	8.66	11.04	23.33	40.98	11.54	2.54	43.59	38.33
49	ctggctttcagttcttg	NM_010579	Eif6	gene	chr2	155645652	-	0	0	0	0	-2	2	2	8.66	11.96	16.33	1	6.92	2.54	0.725	0.985
50	agaactgtactateetg	NM 016916	Blcap	gene	chr2	157385929	+	0	0	0	0	0	0	2	21.26	5.52	20.99	+	39.24	22.89	0.725	1.3
52	agggggggggggggggggggggggggggggggggggggg	NM 010923	Nnat	dene	chr2	157387818	+		0	0	0	2	0	5	344,96	78,22	156.29	4.66	210.03	562.14	5.205	5.3675
53	cettaccgetgaaatga	NM 175692	A930034L06rik	gene	chr2	158211819	+	0	0	0	0	0		10	3.15	1.84	27.99	144.28	6.92	0	86.45	175.035
54	tgataaaagtetetgte	NM 015731	Atp9a	gene	chr2	168459959	-	0		0	0	0	0	7	1.58	5.52	2.33	15.66	4.62	5.09	7.8	30.41
55	gacaataaaatgcctct	NM 029761	Dok5	gene	chr2	170705247	+	0	0	1	Ő	0	0	2	3.94	35.89	2.33	3	6.92	0	1.665	3.595
56	tetgeaceteegeetgt	NM 007906	Eef1a2	gene	chr2	180882556	-	0	0	0	0	0		8	3.15	0	11.66	35.32	4.62	2.54	44.095	29.585
57	cctctgtttggtggcaa	NM 016775	Dnajc5	gene	chr2	181287541	+	0	0	0	0		0	7	37.0	23.01	39.66	8.33	2.31	15.26	9.035	6.8775
58	acoorcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	nn 025285	acquacaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	gene no match	chr3	8561180 nil	nil	0	0	0	0	2	0	6	37.8	18.4	20.99	2.67	16.16	7.63	19,945	3.35
60	agacaaactgaagtaac	NM 009801	Car2	gene	chr3	14900460	+	0	0	0	0	0		4	1.58	0	0	10.33	2.31	2.54	6.435	12,455
61	tgtgaaggettgggeae	NM 008802	Pde7a	gene	chr3	19126121	-	0	0	0	0	0	2	1	11.81	9.2	9.33	1.67	6.92	2.54	0	0.8075
62	gtgattttcccctcaaa	NM 027619	D3ertd789e	gene	chr3	33706365	+	0	0	0	0	2	0	3	1.58	0	14	0,67	2.31	2.54	1.665	0
63	etteaacetggetaaca	AK129248	Atplib	gene	chr3	35754916	+	0	0	0	0	2	0	2	3.15	2.76	18.66	1	6.92	0	0.94	1.3
64	tattttgacttgtatag	NM 013928	Schipl	gene	chr3	68430181	-	0	0	0	0	0		8	1.58	2.76	4.67	14.66	4.62	0	14.665	15.18
65	atgttaaaaaaaaaaaaaa	AK015737	AK015737	est	chr3	/3230219	-	0	0	0	0	0	2	1	14.18	10.12	2.33	1	11.54	12.72	0.725	1.05
00	cauggeteetataactt	NM 021896	Gucyias	dere	CHES	91990473	-	.0	U		Ų.	0.0	0	2	0.79	23.93	14	0 ·	0	.0	9.205	1.300

67	gagagaaaagottagga	BT202674	BT202674	ost.	chr3	88033745	+	0.1	0	0	0	0	2	6	21.26	18.4	11.66	2	18.46	12.72	1.875	2.2525
07	gagagaaaaccecacca	B1202074	51202074	000	one 2	00105405		0	0	0	0			2	23 53	21.12	11.00	0.22	16.16	20.00	2.005	2.165
68	cacagaaccagcagcoc	NM 009836	Cets	gene	Chr3	86123493		0	0		0	V	- ×	1	20.03	21.10	9.33	3.33	10.10	44.69	2.093	3.105
69	gttggagcagccaaaaa	NM 013604	Mtx1	gene	cnr3	89013062	-	0	0	0	.0.	0	12	(1 c	22.05	10.56	4.07	0	10.10	7.03	0	0.4775
70	ttacaageettgattaa	nil	TTACAAGCCTTGATTAA	multiple	nil	nil	nil	0	0	0	0	0	2	1	28.35	56.13	4.67	0	16.16	7.63	0	0.4925
71	cccattcgggcaaggaa	NM 011309	S100a1	gene	chr3	90316006	-	0	0	0	0	0		4	0	0	0	11.33	0	0	8.525	13.9825
72	gggtaggggtaccactc	NM 022030	Sv2a	gene	chr3	95998495	+	0	0	0	0	0		7	6.3	5.52	18,66	23.66	11.54	2.54	19,085	27,445
73	tagetgtaacggggggg	NM 144900	Atplal	Gene	chr3	101380326	-	0	0	0	- O		1	4	1.58	2.76	0	99.29	0	5.09	65 94	119 648
74	atagastttttattata	NTM 152562	62205 601222414	9.0110	ohu 2	107415506		0	0	0	0	-			14.10	12.0	1.4	3 32	0.22	15.96	2 225	2 1005
14	grggggtttttattgtg	NM 153565	6330369M22F1K	gene	Chrs	107415506	/	0	0		0	U	~	0	14.10	13.0	14	3.33	9.43	10.20	3.325	3.1025
75	geccettetteattgge	NM_010358	Gstml	gene	CDI 3	107815397	-	.0	0	0	0	0		8	.0	0	9.07	10	0	0	11.42	9.5425
76	ccctgcagetcaaaaaa	NM 008913	Ppp3ca	gene	chr3	136598228		0	2	0	0	0	0	4	3.94	1.84	0	11	0	5.09	24.85	2.6675
77	taagtgaaaacctgact	NM 145544	Rap1gds1	gene	chr3	138589053	-	0	0	0	0	0		2	2.36	4.6	2,33	21.66	2.31	2.54	13.59	25.8675
78	agcaattcaaaacaatt	NM 145545	Gbp6	gene	chr3	142212498	+	2	0	0	0	0	0	5	138.61	59.81	212.27	121.62	219.26	99.2	128.16	121,835
79	atctactgtgtgacacc	CJ251313	CJ251313	eat	chr3	146646906	+	0	0	0	0	0		8	0	3.68	4.67	20.33	0	0	18.58	21,6825
90	Essettatttaaaass	BV120215	Taba2	7000	mh r 2	140470051		0	0	0	0	-	0	2	11 01	10.12	10 66	2	26.20	7 63	2 30	1 64
00	Caaaccycccoaycaaa	ARIESEIS	Lpnnz	gene	GHLD	140470331	-	0			0	4		4	11.01	10.12	10.00	11.00	23.33	1.03	6.33	1.04
81	agtatttatgagttcag	NM 177274	Negri	gene	Chr3	150978233		0	0	0	0	0		8	0.79	1.84	2.33	11.00	0	0	9.545	12.8575
82	aagagagtgcgtgaage	NM 026989	Sfrsll	gene	chr3	157682324	-	0	2	0	0	0	0	2	10.24	1,84	2.33	9.33	20,77	10.17	19.3	2.3325
83	attetecetgtgacage	NM_172690	N28178	gene	chr4	42956931	+	0	0	0	0	0		8	0.79	4.6	2.33	12.66	0	0	10,915	14.25
84	gcgctgtttgtttcaga	NM 175201	Rnf38	gene	chr4	44139389	9 - 9	0	0	0	0	0	2	1.	18.9	14.72	2,33	2	4.62	10.17	0	0.4775
85	cagettttt	NM 018741	Igfbpll	gene	chr4	45824056		0	0	0.	0	0	2	1	18.9	24.85	4.67	1	16.16	5.09	0	0
86	gecagttttctacagag	NM 019535	Sh3g12	ciene	chr4	85034508	+	0	0	0	0	0		2	4.73	3,68	4.67	21.32	6.92	5.09	21.9	20,695
97	220020022222222222	AK044374	38044374	ost	chr4	05420033		0	0	0	õ	0	2	1	1 73	1.94	2 33	0.67	16.16	7 63	1 665	0.5725
	aaccagcaaaaaaaaaaaaaa	24044374	21.01.0	626	CIL 4	00420000		0		0		0	-	+	4.7.5	1.04	6+33	10.07	10.10	1.05	1.000	38 335
88	ttecactgtetgcatee	NM 172426	SICZ4aZ	gene	Chr4	86629140		U	U	0	0	0	-	. 8		0	2.33	18.33	0	0	21.095	15.715
89	tattaaatgtgottttt	NM_080555	Ppap2b	gene	chr4	104905324	+	0	0	0	Ū.	0		4	3.15	7.36	0	17.99	6.92	2.54	15.17	20.9725
90	acggagetggageagea	NM 024462	Ccdc23	gene	chr4	118873526	+	0	0	0	0	2	2	2	14.96	11.96	16.33	0.67	20.77	10.17	0	0.97
91	ctgcttctaatcgtgtt	NM_174998	Hpcal4	gene	chr4	122871845	+	0	0	0	0			8	0	3.68	2.33	50.98	0	0	48.12	53.33
92	gtggttgaaaacatttg	NM 026845	Ppill	gene	chr4	123123902	+	0	0	0	0	0	2	1	6.3	11.04	4.67	0.33	6.92	2.54	1.45	0.5725
93	gaatgatetg	AA590241	Rps28	est	chr4	126818482		0	0	1000	0	0	0	1	9.45	11.96	7	1	2,31	0	0	0
0.4	gagagt aacaggeet ga	NM 009030	Rhhn4	mene	chr4	128986810	-	0	0	0	0	2	0	2	7.09	10.12	23 33	1.33	11.54	2.54	3 325	0
05	tatetasettastssaa	NM 010907	Manahall	gene	onre	120102002		0	0	0	0		0		66.04	12.0	E2 65	1.00	02.22	71 22	A 045	2.025
.90	corocyactrigacaago	NH 010807	MATCKSII	gene	Chra	129193002		<u>v</u>	0	<u>v</u>	0			0	00.94	13.0	55.05		96.26	12.00	4.040	2.035
96	ggcgctcgtacacccct	NM 011520	Sdc3	gene	chr4	130382105	+	0	0	0	0		0	1	14.18	12,88	39.66	8	20.77	2.54	7.88	7.325
.97	agaaggaggtgccccag	NM_019641	Stmn1	gene	chr4	134028768	<u>t</u> 1	0	0	0	0	2	0	5	167.75	269.62	174.95	46.65	154.64	124.64	51.465	41.68
98	gtgactaatgagettee	NM 025411	1110049F12rik	gene	chr4	135531555	-	0		0	0	0	0	2	25.99	54.29	34,99	115.29	0	0	1.665	19.215
99	cggtctagtccagcttt	NM 025451	Camk2n1	gene	chr4	138013264	+	0	0	0	.0	0		B	3.15	0	7	172.27	4.62	5.09	241.175	138.65
100	caaaacaggcaactggc	NM 025451	Camk2n1	gene	chr4	138013846	-	0	0	0	0			8	1.58	2.76	2.33	129.95	0	2.54	185.02	88,735
101	gtatttgcaaaaaaaaa	NM 025451	Camk2n1	gene	chr4	138013851	+	0	0	0	0			8	1.58	1.84	4.67	109,96	2.31	2,54	122.395	101,293
102	agergentet	NM 008546	Mfan2	0000	ched	140571946	4	0	0	0	0	0		1	14 19	6 44	4.67	0.33	11.54	20.35	0	0
102	teetateeeeaataeea	NM 023051	Cletp1	gene	chrd	140072046		0	0	0	0			10	9.55	12 00	1.67	01.33	0.22	7 63	122 265	76 0575
103	toothoost a skithoot	NM 000142	Cischi	gene	chr.4	1640222000		0	0	0	0			+0	2.04	6.60	10.00	21.3	0.21	7.05	1.655	2 6026
104	cgettggetaetttget	NM 008142	GRDI	gene	Chr4	154932290	- T	0	0		0		0	6	3.94	5.52	13.00	10.00	2.31	5.09	1.005	2.5875
105	ttgaagcataatgagte	NM 011074	PICKI	gene	cnr5	4803538		U U	0	0	0	0		9	2.30	0	0	10.00	2.31	2.59	11.92	9.9025
106	ttaaactgtcaatcaat	NM 026448	Klh17	gene	chr5	23666556	+	0	0	0	0	0	2	1	16.54	11.96	2.33	3.67	18.46	12,72	1.665	2,6825
107	ctcggtgccgtgtggtg	NM 139153	Centg3	gene	chr5	23988721	*	0	0	0	.0	0		8	.0	0	2.33	8.66	0	0	7.88	9.1775
108	gecetatgetttggeca	NM 023047	Dpys15	gene	chr5	31101650	+	0	0	0	0	2	0	6	25.2	69.94	34.99	0.67	20.77	10.17	0	0.985
109	aaatatcgttgcatata	NM 013457	Add1	gene	chr5	34974847	+ 3	0	0	0	0	2	0	2	5.51	16.56	20.99	1.67	2.31	5.09	0.94	1.955
110	cactgttgageggegea	NM 010942	Nsgl	gene	chr5	38529469		0	0	0	0	2	0	7	12.6	12,88	46.65	9	6.92	12.72	7.455	9,6925
111	ccagtacctgaaaaaaa	NM 008453	K1f3	gene	chr5	65213593	4	0	0	0	0	0	2	1.	0	17.48	0	0.33	9.23	7.63	0.725	0.8075
442	aggaggagtaggaggagg	NN 011670	Hab11	gene	abat	67076042	-	-	0	0	0	0	0		0.0	26 27	42 22	23 62	A1 EA	172 07	E.C. A	E1 075
112	gegeeageceagaggae	111 011070	Ucnii	gene	chiro	24204014		0	0	0	0	0		4	0.70	0.07	40.05	33.05	41.04	112.51	30.4	10 445
115	ggucagagacaaccacc	NM 177561	USP46	gene	Unito	74334014		.0	0	0	.0				0.79	0.94	0	1.4	0	0	11.94	10.445
114	ttaaacctcaaataaat	NM 016690	Hnrpdl	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	7	25,99	17.48	11.66	5	32.31	27,98	7.08	3.48
					1.000 0.000					· · · ·				1							7.5.5.5.1	
115	ctgaggaagtaagatac	NM 010097	Sparcl1	gene	chr5	104508215	-	0	0	0	0	0		7	9.45	22.09	37.32	162.94	6.92	5.09	113.04	192.103
116	teccegteat	NM 026106	Drl	gene	chr5	108708695	- + - 9	0	0	0		2	0	3	1.58	0.92	32.66	0	4.62	0	0	0
117	ageetgteag	NM 024477	Ttc28	gene	chr5	111718784	+	0	0	0	0	0	2	1	14,18	8.28	0	0	18.46	10.17	0	0
118	cttgtagetgeetetgt	BY252337	BY252337	est	chr5	112642304		0	0	0	0	2	0	5	54.34	46.01	55,98	11.66	53.08	15.26	10.4	13,9775
119	gactgtgccaaacacac	NM 026504	D5ertd33e	gene	chrS	115748697		0	0	0	0		0	7	27.56	11.04	7	45.98	32,31	30.52	42,515	46,4375
120	atattttaaa	BC026510	BC026510	gene	chr5	115905596		õ.	0	0	ŏ	10	0	1.	0.70	0	0	2	6.92	12 72	0	0
120	gegetetgaa	D0020010	Butte	60 L	CHILD.	101200545	- T -	0	0	0	0	0	-	-	0.13	0.0	0.00	10.65	0.74	20.76	21.215	10.075
121	cecaetgeetttetteg	NM 011286	Rpn3a	gene	Chr5	121390565	-	0.	0	0	0	0		4	3.15	2.4	6.33	19.00	2.31	3+04	21.310	18.935
122	atttgatatttaggget	AV244322	2810407C02rik	est	chr5	124216321	-	0	0	0	.0	0		8	0.79	1.84	4.07	12	0	2.54	8.1	14.0775
123	cagatetttgtgaagae	NM 019639	Ubc	gene	chr5	125866576		2	0	0	0	0	0	5	46.47	46.93	58.32	36.32	73.86	12.72	19.38	45.0775
124	gaacgcaagttcagecc	NM_031404	Act16b	gene	chr5	138008524	+ 1	0	0	0	0	2	0	2	11.03	1.84	25.66	4.66	23.08	2.54	3.325	5.905
125	ggggtacetggtattga	NM 172412	Gpc2	gene	chr5	138715204	-	0	0	0	0	- 2	2	2	14.18	12.88	14	0.67	9.23	10.17	0.725	0.4775
126	tcccctggaataaagtg	NM 172723	Cental	gene	chr5	139747862	-	0	0	0	0	0		4	0	0.92	0	8.33	0	0	7.665	7.995
127	gacgcgaccatectect	NM 007393	Actb	gene	chr5	143665068	+		0	0	0	0	0	1	14,96	5.52	4.67	1	0	45.79	2.39	1.8575
128	gatacttggaatgacta	NM 007393	Actb	gene	chr5	143665145	+	2	0	0	0	2	0	5	238.63	129.75	326.58	17.66	408.52	155.16	27.53	13.5225
129	gtttttatctgagaagt	A.TI 33130	Ptprz1	gene	chr6	23002870		0	0	0	0	0	2	6	18,11	23.01	16.33	5	18.46	17.81	5.415	4.78
120	tacaactttetattess	MM 007971	Eab2	gene	chré	47492929	- T	0	0	0	0	0		1	21 26	11 04	7		16.16	5 09	0.725	0
130	egeagererergeteaa	MPI 00/9/1	EZRE	gene	Chro	47482928		0	0	0	0		-	4	21.20	11.04	22 55		10.10	5.09	0.125	0
131	agagcaaggaccacate	NM 026629	2410066E13rik	gene	Chr6	54653778	+	0	0	0	0	4	0	6	29.14	24.85	32.66	4	11.54	1.03	4.11	3.02
132	gttattttgggaaaaga	NM_025520	Lsm5	gene	chr6	56651137		0	0	0	0	0	2	1	9.45	14.72	0	2	9.23	2.54	1.875	2.1175
133	geegaeeeegagaagea	NM 021432	Nap115	gene	chr6	58856958	-	0	0	0	0	0		4	0.79	0	0	11	2.31	0	16.835	7.7825
134	cttaaggateecaaaca	NM_025814	Serbpl	gene	chr6	67234015	+	0	0	0	0	0	-2	7	44.1	34.05	18.66	5.66	73.86	27.98	2.6	7.705
135	actgettgeeetaagea	NM 145569	Mat2a	gene	chr6	72382913	-	0	0	0	0	0	2	6	11.03	17.48	16.33	2.67	4.62	17.81	3.11	2.57
136	ccacgaggtg	NM 025284	Tmsb10	gene	chr6	72907348	+	0	0	0	0	0	2	1	11.03	22.09	7	0	6.92	7.63	0	0
137	gettggaagt	NM 013458	Add2	dene	chr6	86059408	+	0	0	0	0	0	2	1	4.73	27.61	0	2	9.23	7.63	0	0
138	gagggaggtattetttat	NM 011585	Tial	gono	chré	86382732	- 1 -	0	0	0	0	0	- 3	1	11 02	A 6	2.33	0	6.92	10.17	1 975	2 51
130	tages and the state	NM 011000		gene	ohr C	00302733		0	0	0	0	0		-	0.30	0.00	a.33	10.23	0.74	10.17	11 625	10.205
139	rgagcarcgggggggggg	NM 011844	Mg11	gene	Chro	88778115	+	0	. U	0	.0	0		4	0.79	0.92	0	10.33	0	0	11.035	10.285
140	arragergreetttaat	NM_008881	Pixnal	gene	Chr6	89266558		0	0	0	0		0.		4.73	3.68	14	0.07	2.31	7.63	0.94	0.4775

141	agaaggaggg	NM 018815	Nup210	gene	chr6	90964167	+	0	0	0	0	2	0	3	0	0	18.66	0	0	0	0	0
142	gagttcagctttcaaat	NM 007697	Chl1	gene	chr6	103682990	+	0	0		0	0	0	6	25,99	73.62	23.33	2.67	25.39	15.26	1.45	2.94
143	atttetttetggatgg	NM_010585	Itprl	gene	chr6	108500912	+	0	0	0	0	0		4	0.79	1.84	0	11.33	2.31	0	12.145	10.64
144	ctggagatgtgacaaag	NM 013681	Syn2	gene	chr6	115226498	+	0	0	0	0	0		4	0.79	5.52	0	19.66	0	0	20,155	19.0725
145	ttttatgtttaaataaa	NM 172086	Bp132	ambiguousgene	nil	n11	nil.	0	0	0	n		0	5	97.66	126.99	111.97	18.99	108.48	165.34	18.79	17,9625
				and a group going											1000000		1000022				100000	101000
146	toccacagttgccacca	NM_013509	Eno2	gene	chro	124710449	-	0	0	0	0	0		4	0	0	0	16.99	0	0	19.865	16.975
147	aacccctgcccgcggac	NM 026988	Ptms	gene	Chro	124864200			0	0	0	0	0	5	92.15	27.61	60.65	37.99	48.47	132.27	48.57	31.89
148	citecaggigeteeegg	NM 009156	Sepwi	gene	cnr/	16502602	-	0	.0	0	0	0	.0	5	19.54	138.03	79.31	154.94	0.22	7 42	125.185	0 5725
150	taccotctcaageccag	NM 144921	Atrola3	gene	chr7	25764324			0	0	0	0	0	9	10.24	0	0	0.55	9.45	33.07	4.56	3 635
151	gtgacaactgaaaaaaa	NM 028166	1600014C10rik	gene	chr7	38980457	+	0	0	0	0	0	- 2	1	8,66	16.56	4.67	1.33	16,16	7.63	0	1.76
152	getgeeetgeaaggeet	NM 025368	Josd2	dene	chr7	51725858	+	0	0	0	0	0		8	0.79	0	7	12	2.31	0	13.81	11,0675
153	gtcgtcctctactagtt	NM 145954	Aldh16a1	gene	chr7	52430825	÷ +	0	0	0	0	0		8	2.36	0.92	2.33	47.65	2.31	5.09	60.505	39.3375
154	agggecactggetteag	NM 001005511	Lmtk3	gene	chr7	65326755	+	0	0	0	0	2	0	7	12.6	19.32	46.65	13.33	6.92	17.81	14.1	12.3775
155	gtgccatatttagctac	NM 173011	Idh2	gene	chr7	87239767		0	0	0	0	0	2	1	21.26	12.88	7	1	20.77	15.26	1.665	4.6275
156	gtcaaatact	NM_175366	Mex3b	gene	chr7	78793086	+	0	0	0	0	0	2	1	9.45	9.2	0	1.33	11.54	5.09	0	0
157	ggagegetatgtgetaa	NM 015814	Dkk3	gene	chr7	119259667	-	0	0	0	0	0		8	0	1.84	2.33	17,99	0	0	10.48	23.1025
158	gtcactctagccaggtc	NM_008855	Prkcb	gene	chr7	129772081	+	0	0	0	0	0		8	0	0	7	25.66	0	0	27.825	25.32
159	gaggettaga	NM 145587	Sbk1	gene	chr7	133437999	+		0	0	0	0	0	9	16.54	0.92	0	0	0	53.42	0	0
160	tgtttgtaaatactctg	NM_145587	Sbk1	gene	cnr/	133438425	+	0	0	0	0	0	10	0	25.2	32.21	30.32	4.00	30	22.89	1.45	0.0875
161	ggggcggggggggggg	NM 172748	BC059812	gene	chr7	134912748		0	0	0	0	6			17.33	0.44	10.00	1.07	13.00	5.09	0.725	2 6776
162	ctacgttetetacgaag	NM 023140	Glrv3	dene	chr7	144659817		0	0		0	0	0	7	16.54	51.53	2.33	17.99	16.16	10.17	11.85	21.63
164	cetcagectggggtaga	NM 009983	Ctsd	gene	chr7	149561941		0	0	0	0	0	- ×	7	8.66	14.72	14	29.99	6.92	5.09	25.52	33.015
165	cgtggatccctctgtca	NM 009876	Cdknlc	gene	chr7	150644541	-	0	0	0	0	0	2	1	22.84	11.96	2.33	1.67	11.54	10.17	0.725	0
166	cetttgagatcatecae	NM_009095	Rps5	gene	chr7	13510898	- 1	0	0	0	0	2	2	7	66.94	46.01	48.99	6.66	69.24	78.85	3.325	8.61
167	gcaaagaaaaacgtggt	NM 021324	Ttyhl	gene	chr7	4086425	+	0	0	0	0	0		8	2.36	0,92	2.33	15.66	2.31	0	16.11	16.035
168	categeeagtgggeaaa	NM_009696	Apoe	gene	chr7	20281818	+	0	0	0	0	0		10	4.73	4.6	20.99	58.31	2.31	2.54	61.545	55.65
169	cccgtgtgctcatccgc	NM 029767	Rps9	gene	chr7	3657491	+	0	0	0	0	0	2	5	63.79	46.93	41.99	23,66	60.01	76.31	21.82	25.7075
170	ctttccctgccaatgta	NM 013834	Sfrp1	gene	chr8	24560058	t	0	0	0	0	0	2	1	5.51	11.96	2.33	0	16.16	12.72	0	0.4925
171	atcacacactaaaaaaa	NM 144731	Galnt7	gene	chr8	60010446		0	0	0	0			7	7.09	7.36	14	51.31	9.23	12.72	51.015	53,7825
172	atcotggtaatgcactt	NM 013494	Cpe	gene	chr8	67071549		U	0	0		0	0	7	6.3	18.4	48.99	77.97	2.31	10.17	59.86	87.8925
173	ttetgagtatggaacet	NM 182991	Tmem591	gene	chr8	73007964	-	0	0	0	0	0	1.0	8	1.58	1.84	9.33	11 66	4.62	0	9.465	12.23
174	ggcaggaetegetgaag	NM 011563	Dudy2	gene	chr8	97497009	Ē	0	0		0	0	10	7	97.15	3.00	41.99	19.00	62 32	104 29	17 64	10.0375
175	ctccacagaaccagttg	NM 009142	Cx3cl1	gene	chr8	97306065	+	0	0	0	0	0		ß	0.79	0	2.33	21.66	2.31	104.25	25,945	18.71
177	aaggagattatgttgtg	NM 053246	Dok4	gene	chr8	97387814	-	0	0		0	0.	0	2	0.79	17.48	9,33	0.67	0	0	0.725	0.4925
178	ccgcccctttctgtaac	NM 145602	Ndrg4	gene	chr8	98238390	+	0	0	0	0	0		10	6.3	3.68	27.99	76.3	6.92	5.09	49.645	90.0025
179	caggataggtttctgta	NM 133206	Znrf1	gene	chr8	114147541	+	0	0	0	0	2	0	2	6.3	6.44	16.33	0.33	11.54	5.09	0	0.4775
180	acgaacatcacggacct	NM 019707	Cdh13	gene	chr8	121837965	+	0	0	0	.0	2	0	3	5.51	.0	18.66	2	6.92	10.17	0.94	2.8425
181	tgagtecacttggetet	NM 023279	Tubb3	gene	chr8	125945756	+	0	0	0	0	2	2	5	92,93	150	114.3	23.66	113.09	58.5	18.065	26.26
182	gtggccagtgcctgtaa	NM_139272	Galnt2	gene	chr8	126867769	+	0	0	0	0	2	0	3	5.51	0	16.33	0.33	6.92	10.17	0.725	0
183	gggaaactaagggagag	NM 172503	Zswim4	gene	chr8	90328313	+	0	0	0	0	2	0	3	0.79	0	14	0.33	2.31	0	0	0.4925
184	getgtgggtegetgtgg	NM 008319	Icam5	gene	chr9	20843089	+	0	0	0.	0	0		4	0	0	.0	13.99	0	0	15.465	14.53
185	ccagaaaataaaaagtt	(80177886)	Elav13	gene	chr9	21819476	-	0	0		0	0	0	7	14.96	46.93	34.99	15.99	16.16	10.17	9.035	19.0175
186	aaattggaggatgaagg	NM 178027	Vns26b	dene	chr9	26813166		0	0	0	Ô		0	3	0.79	4.6	1.4	0.67	0	2.54	0.725	0.8075
187	ttaccatactgggttgg	NM 022029	Nrgn	gene	chr9	37352126		0	0	0		0	- i	10	1.58	4.6	46.65	38.98	4.62	0	23.565	46.835
188	cagetetgecaccgcag	NM 022029	Nrgn	gene	chr9	37352617	-	0	0	0			1	10	0	3.68	44.32	216.25	0	0	223.535	216.248
189	ctgggcgcgtggacagg	NM 022029	Nrgn	gene	chr9	37352622	+	0	0	0	0	0		8	0	0.92	2.33	26.66	0	0	21.98	26.86
190	getttgaetgttetett	AA122503	AA122503	est	chr9	41400727	+	0	0	0	0	2	2	6	22.84	24.85	16.33	1.33	16,16	20.35	1.665	1.065
191	tataataccaccactac	NM_009382	Thyl	gene	chr9	43856589	+	0	0	0	0			8	0.79	5.52	2.33	95.3	0	0	67.07	109.125
192	gagacggtgctggtcct	NM 022004	Fxyd6	gene	chr9	45198079	+	0	0	0	0	2	2	6	16.54	15.64	25.66	4	16.16	10.17	3.11	4.935
193	ciggtettta	NM 001081445	Ncami	gene	chr9	49310606	+	0	0	0	0	2	0	5	1.58	5.52	14	10.55	0	0	0	12.02
194	getteateteeagggag	NM 009964	Elandi	gene	Chr9	50564407	+	0	0		0	0		9	4 32	0.92	2.22	22.22	6.02	2.54	22 105	17.50
196	cctggcactgcccttgg	NM 020270	Scamp5	gene	chr9	57289472		0	0	0	0	0		2	6.3	4.6	7	21.99	9.23	2.54	24.37	18,9975
197	tacttgtgttctgtgta	NM 009145	Nptn	multiple	chr9	58500597	+	0	0	0	ő			7	11.03	25.77	9.33	47.31	13.85	5.09	40,905	51,3275
198	gtggagattgatccagg	NM 029922	Parp6	gene	chr9	59497967	+	0	0	0	0	0	2	б	18.9	18.4	9.33	2	13.85	12.72	2.6	1.5425
199	tggtgacaaaaaaaaaa	NM_024212	Rp14	gene	chr9	64026317	+	0	0	0	0	0	2	5	8.9	141.71	27.99	11.33	64.62	58.5	9.975	11.41
200	atagetgggetteagte	NM 008927	Map2k1	gene	chr9	64033927	÷	0	0	0	0	0	1	4	2,36	0	0	14.66	0	5.09	14.745	14.62
201	tgacaagacactgtggc	AU258168	AU258168	est	chr9	69936640	-	0	0	0	0	0		8	0	0	4.67	10.66	0	0	10,56	10.1375
202	ggtctaagcgtttacct	NM 029784	6430514L14rik	gene	chr9	69938443		0	2	0	0	0	0	8	0	0	2.33	12.33	0	0	24.93	4.015
203	ttggtcaaacaataaac	NM 173781	Rab6b	gene	chr9	103087569		0	0	0	0	0		7	7.88	20.24	25.66	90.3	9.23	2.54	72.24	102.253
204	ccctgaggggttggggc	NM 133977	Trf	gene	chr9	103111295		0	0	0	0	0		4	1.58	0.92	0	26.99	0	0	15.765	33.465
205	teccetecatecetttg	NM 021567	Pobp4	gene	chr9	106366054		0	0	0	0	0		8	0.79	0.92	2.33	9.33	2.31	2 64	8.525	12.43
206	ttacttgatctcagage	MM 033264	LDa1	gene	chr9	111298088	+	0	0	0	0	0		6	0.79	1.84	1 67	34 65	2 31	2.54	20 50	12.43
208	tatgttgggggttaaca	NM 026892	Eiflb	gene	chr9	120404392	+	0	0	0	0	0	2	7	58,28	65.34	18.66	19.99	48.47	50.87	13,295	25.635
209	ggctggatggactttgg	NM 031161	Cck	gene	chr9	121399239		0	0	0	ő	0		B	1.58	1.84	7	60.98	0	2.54	71.145	50.9825
210	tttttcccaatccagtt	NR 024325	9130024F11rik	gene	chr1	57031883	+	0	0	0	0	0	2	1	8.66	5.52	0	0.33	16.16	7.63	1.665	0.4925
211	cctcatttcccctgttc	BQ176089	BQ176089	est	chr10	3460657	+	0	0	0	0	0		4	0	0	0	8.33	0	0	9.465	8.135
212	aagtttgcaagtctcca	NM 008538	Marcks	gene	chr10	36735458	-	0	0	0	0	2	2	6	33.08	15.64	18.66	1.33	36.93	22.89	0.725	1.4625
213	aactootaagaotatga	NM 008538	Marcks	gene	chr10	36735659	+	0	0	0	0	2	.0	6	27.56	11.04	137.63	2.33	36.93	43.24	4.77	0.4925

214	ctqqcttctt	NM 008538	Marcks	gene	chr10	36738343	+	0	0	0	0	2	0	3	3.94	2.76	23.33	0	0	2.54	0	0
215	ttatggaattgatttgc	NM 009846	Cd24a	gene	chr10	43223422	+	0	0	-	0	2	2	6	106.32	180.36	102.64	0.67	120.02	86.48	0.94	0.4775
216	gactggctgtggcaatg	NM 178675	\$1c35f1	dene	chr10	52831359	+	0	.0	0	0	0	2	6	21.26	17.48	1.4	4.33	18.46	17.81	5.205	4.2275
217	taatatagacetageee	NM 010299	Gial	gono	chr10	56102485		0	0	0	0	0		4	0.70	1.94	0	23.66	0	2.54	20.75	26.16
218	ggatttttgatatggaaa	NM 021272	Fahn7	gene	chr10	57512507		0	0	0	0	2	2	6	50 20	61 65	20 03	1 67	36 03	35 61	2.6	0.97
210	the state to go a a	NN ODEADO	Paup/	gene	chulo	51126001		V.		<u>v</u> .	.0.	-		-	50.20	20.45	16 33	4.07	0.22	2 62	11 55	7 7225
219	cccaccgcgccaggaaa	NM 026438	Ppai	gene	chrio	01130081	+	0	0			.0	0	-	6.3	29.45	10.33	9	9.23	1.03	11.35	1.1225
220	cetttgtgacagtggee	NM 015635	Zwint	gene	chr10	72076802	*	V.	0	Q:	0			1	13.39	11.04	20.99	97.63	10.10	17.81	103.365	92.8725
221	ctcaataaatatttttt	NM 133182	Prmt2	gene	chrl0	75669981	-	0	0		0	0	0	2	1.58	23.93	9.33	2.67	0	0	1.45	2.9875
222	acctgcatctcagaaaa	NM_010925	Rrp1	gene	chr10	77863362	-	0	0	0	0	- 4	0	-2	9.45	3.68	30.32	2.33	4.62	15.26	2.815	2.2525
223	cetaccagttaceteac	NM 011789	Apc2	gene	chr10	79697044	. + .	0	0	0	0	0	2	1	11.81	13.8	9.33	1.	6,92	5.09	1.665	0
224	taccettgccetttgag	AK030708	Ckap4	gene	chr10	83661422	=	0	0	0	0	2	0	2	2.36	5.52	16.33	0.67	2.31	0	0	1.065
225	tgetetggagggtttgt	NM 026482	Atp2b1	gene	chr10	100813083	+	0	0	0	0	0		8	0	1.84	2.33	12.33	0	0	11.42	12.4375
226	ctcagtaatg	NM 007792	Csrp2	gene	chr10	112531795	+	0	0	0	0	2	2	1	13.39	7.36	0	1.67	4.62	17.81	0	0
227	getecetetgtttggat	NM 001033474	ENSMUSG00000074747	gene	chr10	112363784		0	0	0	0	0	2	7	31.5	41.41	11.66	6	43.85	25.44	3.325	7.705
228	cgtatcaatagaaaaaa	NM 182807	AI851790	gene	chr10	125620341	+	0	0		0	0	0	2	3,94	30.37	9.33	2,33	0	5,09	0.94	3,205
220	tagaacattagctatat	MM 009870	Cdk4	riene	chr10	129251273	- +	0	0	0	0	2	0	6	37.8	26 69	18 66	0 33	36.93	38 15	0 725	0
230	tattgattgggggggtt	NM 001106019	H2afy	gene	chr11	6328219		0	0	0	0	0	0	7	32.29	30.37	7	4	25.39	15.26	6.435	2,1325
200	etatacacacactaca	BB400103	DD499193	gene	chr11	24067807		0	0	0	0	0			10.24	22.01	0.33	0.22	13.05	20.35	3 325	0.0075
237	accentered	NM 016707	Ballia	1000	ohr11	24007007		0	0	0	0	0		7	23 63	16 56	7	2.55	22.00	20.35	3.323	2 555
232	acceetgaceeettgtt	NM 016707	BCIIIA	gene	CHLII	24073111	+	0	0	0	0	0		1	23.63	10.50		0.00	23.08	20.35	2.0	3.505
233	gtgetgaatatggaget	NM 008218	HDa-a1	gene	chrll	32183771	+		0	0	0	0	0	9	45.68	. 0	0	0.33	9.23	137.36	.0	0.4775
234	coettettetetetett	NM 008218	Hba-a1	gene	chrll	32184326	+	2	0	0.	0	0	0	T	123.65	150.92	7	25.32	156.95	40.7	17.775	29,0275
235	gtgetggtaattgteaa	NM 173784	Ubtd2	gene	chrl1	32418601	+	0	0	0	0	0	2	1	7.88	18.4	4.67	2	4.62	5.09	1.45	2.035
236	teteactgtattetatt	NM_010250	Gabral	gene	chrll	41944490	-	0	0	0.	0	0		8	0	0	4.67	11.33	0	0	10.775	11.44
237	tatagatatgtatagaa	NM 010250	Gabral	gene	chr11	41945025	-	0	0	0	0	0		8	0.79	0.92	2.33	22.99	0	2.54	15.385	28.61
238	getgeagttgatgegag	NM 008143	Gnb211	gene	chrll	48613964		0	0	0.	0	0	12	7	37.8	30.37	4.67	9.33	41.54	20.35	10.27	8.5475
239	tgcatcttatttaaaat	NM 010448	Hnrnpab	gene	chrll	51414800	-	0	0	0	0	0	2	6	25.99	28.53	9.33	2	34.62	20.35	1.665	2.05
240	tgggtgtcttccaacct	NM 011543	Skpla	gene	chrll	52059947	+	0	0	0	0	2	0	2	7.09	7.36	16.33	I	6.92	10.17	1.665	0.4775
241	ctcattataatcaagaa	CD802535	CD802535	est	chrll	53362906	+	0	0	0	0	0		4	0	0.92	0	8.33	0	0	7.88	8,165
242	teccentaca	AK144914	AK144914	pat	chrll	61211039	-	0	0	0	0	2	0	3	0.75	0.02	16.33	0	0	2.54	0	0.100
243	coasagaacacacacac	NM DODEAS	765170	000	abr11	61262261		0	0	0	0	0	- č		0.79	1.04	2.33	22.00	2.91	2104	22 625	24 105
24.3	coaaagaaccacaccec	M1 009540	2101/3	gene	GHLII	01202201	- 11	0	0	0	0	-		E	AE 20	P0+1	44 22	12 22	2:31	45.70	10.005	24,105
244	yaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	nii naanooo	GAAAAAAAA	mulcipie	BLL		nii	0	0	0	0	-		5	45.00	02.34	44.32	13.33	57.7	45.79	10.995	14.0
245	catagggtgcaaatagg	B0296899	BG296899	est	Chrii	67501041	-	U	-	0	0	0	0	8	3.15	0.92	9.33	9,66	4.02	2.59	21.9	1.285
246	cccccaattetgtggeg	NM 009497	Vamp2	gene	chr11	68905825	+	0	0	U.	0	1		/	17.33	18.4	10.33	58.31	23.08	5.09	55.785	00.44
247	ccagcetgaaagegtea	NM 013415	Atp1b2	gene	chrll	69413672	-	0	0	0	0	.0		8	2.36	1.84	4.67	12	2.31	2.54	11.5	12.485
248	aagaagacttettteta	NM 019749	Gabarap	gene	chr11	69807971	+	0	0	0	0	0	2	6	14.18	13.8	16.33	2	16.16	15.26	3.325	1.38
249	tctgatggaataaatca	NM 134022	6330403K07rik	gene	chr11	70845479	-	0	0		0	0	0	5	30.72	108.59	37.32	18.66	46.16	20.35	10.48	22.915
250	gaattaacattaaactt	NM_009536	Ywhae	gene	chr11	75579032	+	0	0		0	0	0	5	57.49	134.35	34.99	36.99	66.93	38.15	27.96	41.0675
251	cctccatcctttatact	NM 009536	Ywhae	gene	chr11	75579090	+	0	0	0	0	0	2	7	24.41	19.32	16.33	7.66	32.31	15.26	6.435	7.8475
252	aagaaaatagaggacaa	NM 207523	Rp123a	gene	chr11	77995043	-	0	0	0	0	2	0	5	47.25	57.97	60.65	14.99	64.62	48.33	9.25	18.57
253	tggacctttttcctgtc	NM 009657	Aldoc	gene	chrll	78140090	+	0		0	0	0	0	2	3.94	13.8	0	34.32	6.92	5.09	11.93	41.41
254	ggttttgtttgtttgac	NM 019653	Wsb1	gene	chr11	79053077	-	0	0	0	0	0	2	1	7.88	11,96	9.33	1	6.92	10.17	1.875	0.5725
255	accordctagtagtgaa	NM 011129	Sent4	dene	chr11	87403289	+	0	0	0	0	0		4	0.79	0.92	0	14.99	2.31	0	B.605	19.0975
256	ttttetteactataata	NM 172449	Bzrapl	gene	chrll	87599299	+	0	0	0	0	0		8	1.58	0	11.66	9.66	2.31	0	8.1	11,305
257	contatatttatacett	NM 016686	Verfl	gene	chr11	97807175	÷ ÷	0	0	0	0	0		1	5 51	10.12	1 67	0	11.54	5 09	0.94	0
0.30	ctotatageccgcgcocc	NM 17E322	F120012319+ik	gene	ohrll	07800700		0	0	0	0	0	-	Â	0.70	0.02	4.07	10		2.54	6.22	12 366
250	crycycygoccaadyor	111 110332	EISUOIZAIJIIK	gene	CHEIL	97400790	- <u>.</u>	0	0	0.	0	0		4	0.73	0.32	0.22	10	0	2.34	10.22	12.100
259	teeettagtatee	NM 144826	Pppirib	gene	Chrll	98218874	+	0	0	0	0	0.		8	0 70	0	2.33	21.00	0 31	0	12.05	27.7025
260	reegrgggrg	NM_028207	Dusp3	gene	chrll	101835090	-	0	0	0.	0	-	0	3	0.79	0	10.33	0	2.31	0	0	0
261	aattaatttatgtttet	NM 008740	Nsf	gene	chrll	103683222		0	0	0	0	0		8	0	0	7	13.33	0	0	17.13	11.3425
262	gagagaagagagagtga	NM_010838	Mapt	gene	chrll	104189531	+	0	0	0	0	- 2	0	5	60.64	85.58	104.97	20.32	76.16	63.59	21,095	29.62
263	atttctttggtgatttt	NM 010838	Mapt	gene	chr11	104193244	+	0	0	0		2	0		14.96	38.65	83.98	7.66	13.85	22.89	6.005	7.68
264	tggeetttgaetetgte	NM_019431	Cacng4	gene	chrll	107595339	-	0	0	0	0	2	0	2	12.6	7.36	27,99	2.33	20,77	15.26	1.665	3,08
265	teeceggaca	NM 021411	Rab37	gene	chr11	115015513		0	0	0	0	2	0	3	0	0	14	0	0	0	0	0
266	cttgggaactgcacage	NM 008258	Hnl	gene	chr11	115359414	-	0	0	0	0	0	12	7	19,69	23.93	7	3	27.7	15.26	2.39	3.1825
267	tetgtecegecaggece	NM 016852	Wbp2	gene	chrll	115940165	-	0	0	0	0	0		4	2.36	0.92	0	34.32	0	2.54	44.66	29.5675
268	ttcaaagagtgggcttt	NM 030723	Pum2	gene	chr12	8756555	+	0	0	0	0	2	0	7	11.81	8.28	48.99	5.66	18.46	15.26	8.82	3.9025
269	taatatttaaagaaaac	NM 012038	Vsnll	gene	chr12	11332143	-	0	0	0	0	0		8	0	0.92	9.33	40.65	0	0	30.855	45.3925
270	tttatgaaaa	NM 008709	Mycn	gene	chr12	12942932		0	0	0	0	0	2	1	6.3	13.8	4.67	1	4.62	7.63	0	0
271	gtgagtgtttgttgcat	NM 009234	Sox11	gene	chr12	28019499	-	0	0	0	0	0	2	6	18.11	40.49	2.33	0.33	39.24	30.52	0.725	0
272	cagagtgtagtgtgttg	NM 009234	Sox11	gene	chr12	28020368	-	0	0	0	0	0	2	1	9.45	13.8	0	0	6,92	25.44	0	0.4925
273	gractgttaacaagtgt	NM 009234	Sox11	gene	chr12	28020687		0	0	0	2	0	2	6	25.2	15.64	11.66	0.67	96.94	83.94	0	2.095
274	aaggeetteeagaagat	NM 025840	Brw2	zene	chr12	36830885	-	0	0	0	0	2	0	2	22.84	11.96	27.99	2	34.62	12.72	0.725	2,5275
275	aagt at ot dat daacd	NM 009241	Found	gene	obr12	E0407252		0	0	0	0	0	2	7	50 20	46.01	25 66	1 22	64 62	66 96	1.665	E 2625
276	gtttcattatgtaaata	NM 027349	Rhm25	gene	chr12	85023981		0	ő	0	0	0	2	1	17 33	15.64	A 67	1 33	4 62	20.35	3.6	1.065
270	togastttatacageanate	NN 026776	Trank J	gene	ohr12	05501534		0	0	0	0	2	-		11.22	2 60	1.07	0.67	9.04	20.35		1.065
277	cagagesterracadddet	NM 001030000	rmediv Sellil	gene	chr12	00001034		0	0	0	U		0	2	6.7	3.00	20 55	0.07	11 54	2 54	0	2.0175
278	cagacercaacceettg	NM 001039089	Selli	gene	Chriz	93045172		0	0	0	0	-	0	-	0.3	1.84	39.66	2.33	11.54	2.54	2.0	2.91/5
279	acteggagecaccagae	NM 009790	Calmi	gene	chr12	101445378	+	0	0	0	0		0	1	34.65	12.88	25.66	117.29	48.47	35.61	143.76	102.6
280	tecaacttgtaactata	NM_009790	Calml	gene	chr12	101447412	+	0	0	0	0	0		2	5.51	7.36	4.67	23.32	4.62	7.63	23.35	22,205
281	tgaccagetgecetgee	NM 010010	Cyp46a1	gene	chr12	109600318	+	0	0	0	0	0		8	0.79	0.92	2.33	11.33	2.31	0	9.035	12.03
282	gggatggccattcacta	NR 027651	Meg3	gene	chr12	110797236	+	0	0	0	0	0		8	0	2.76	4.67	17.33	0	0	11.205	20.6125
283	agettggcctacacett	NM 144513	Gt12	gene	chr12	110804976	+	0	0	0		0	0	8	3.15	0	58.32	38.65	6.92	2.54	64.39	30.26
284	atggggttggcttgaaa	NR_027651	Meg3	gène	chr12	110806729	+	0	0	0		0	0	8	1.58	1.84	30.32	5.33	2,31	0	6.355	5.445
285	catecttgatgattgca	NM 021273	Ckb	gene	chr12	112907708	-	0	0	0	0			10	33.87	33.13	27.99	268.23	32.31	25.44	292.295	248.178
286	ccggcccagaagtgaag	NM 021273	Ckb	gene	chr12	112907788	2 - 1	1	0	0	0	0	0	9	18.11	1.84	0	4.33	0	58.5	7.88	1.955
287	tatcatcttttgttatc	NM 134065	Epdr1	gene	chr13	19683800	-	0	0	0	0	0		4	0	0.92	0	12.99	0	0	9.465	15.38
288	taattttccattatgag	NM_009513	Vmp	gene	chr13	25343985	-	0	0	0	0			8	0.79	1.84	4.67	70.64	0	2.54	55.865	78.3975
and the second se	the second se	the second se								_												

289	ccagetaatcetgteeg	NM 009238	Sox4	gene	chr13	29040891	-	0	0	0	0	2	2	6	7.09	6.44	7	0	55.39	58.5	0	0.4775
200	acaddcacdaddacdcc	NM 009239	SovA	gene	chr13	29041126		0	0	0	- 0	2	2	6	0	5 52	0	0	110.79	71.22	0.94	0
200	deaggenegadgaegee	NM 000730	Coul	gene	ohr12	20041664		0	0	0	0	2		6	2.35	1.04	7 22	0	23.09	20.35	0.54	0
201	gagaaaccag	NH 000230	3084	gene	CHL13	20041004		V.	0	0	0		-	.0	2.30	4.04	6.23	0	23.00	20.33	0.755	0.07
292	gggaceregrggaagee	NM 009238	Sox4	gene	cnr13	29042712	-	0	0	0	0	-	U	0	2.30	0.92	0	0	120.02	13.11	0.125	0.97
293	gagaaactee	NM_009238	Sox4	gene	chr13	29042835			0	U.	.0.	0	0	.9	20.48	0	0	0	2.31	50.87	0	U.
294	teeetgggeagttteag	NM 009238	Sox4	gene	chr13	29043741		0	0	0	0	2	0	2	0.79	2.76	0	0	23.08	7.63	3.11	0.4925
295	getgaetaee	NM_009238	Sox4	gene	chr13	29044530	-		0	0.	0	0	0	9	7.09	7.36	0	0	4.62	61.05	0	0
296	ggttgtatgttttaact	BB801623	BB801623	est	chr13	41371887	+	0		0	0	0	0	2	3.94	10.12	4.67	12.33	0	2.54	3.325	23.31
297	aataaagccaatctgac	NM 033610	Sncb	gene	chr13	54860241	-	0	0	0	0	0		10	2.36	6.44	11.66	49.31	0	5.09	47.605	53.1125
298	contoteccccacetec	NM 012015	H2afy	gene	chr13	56175560		0	0	0	0	0	-2	1	7.09	9.2	4.67	0.33	23.08	17.81	1.665	1.5425
299	tcaagatgataagcaaa	BU511021	BU511021	est	chr13	58228017	+	0	0	0	0	2	0	2	7.09	6.44	14	0.67	6,92	2.54	0.725	0.4925
300	aatattetaacteaaaa	NM 182839	Topp	crana	chr13	74172951		0	0	0	0	0.		8	0	0	0.33	8 33	0	0	11 635	6.025
300	tappagaataatattt	NM 177100	C120071C02=ib	gene	chirl3	02000507	-	0	0	0	0	0		1	7 00	0.20		0.53	25.20	7.63	1 45	0.020
301	cocaggggegecatera	NPI 177100	CISOU/ICOSFIK	gene	CHEIS	02000207	+	0		0	0		-	-	7.09	0.40	1	0.67	20,00	1.05	1.45	V.27
302	caaattaaacttegeet	BX511708	BX511708	est	Chr13	92020038	-	0	0	0	0	0	-	4	0	0.92	0	9.00	0	0	0.435	11.1/15
303	tetgtatgttettgttt	NM_007930	Encl	gene	chr13	98022885	+	0	0		0	0	0	/	16.54	63.49	40.05	49.98	13.85	17.81	39.94	50.0
304	egecegecegeggeaac	NM 008634	Mtaplb	gene	chr13	100191731	-	0	0	2	0	0	0	7	44.1	12.88	81.64	16,99	57.7	27.98	21.77	14.685
305	atcaggagtg	NM_008634	MTAP1B	gene	chr13	100192599	+	0	0	0	0	- 2	0	3	0.79	0.92	20,99	0	0	2.54	0	0
306	aacggtgtatttgtttt	NM 010315	Gng2	gene	chr14	20691820		0	0		0	0	0	5	31.5	112.27	34.99	10.66	20.77	38,15	13.43	9,355
307	cetttattetegagtea	NM 010315	Gng2	gene	chr14	20691898	+	0	0	0.	0	2	0	2	3.94	10.12	25.66	1	2.31	5.09	1.45	0.5725
308	aacaaagcaaacttagt	BI693499	Ghitm	gene	chr14	37934258	2 - 1	0	0	0	0	0		4	1.58	0.92	0	15.66	2.31	0	17.21	13.885
309	taaaaagaaaggatgag	NM 013864	Ndrg2	dene	chr14	52525238		0	0	0	0	0		2	1.58	4.6	4.67	32,99	0	5,09	43.375	26,2075
									-	-												
310	attgccctgcgcctagt	NM_016884	Hnrnpc	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	1	11.81	11.96	4.67	0.67	20.77	12.72	1.45	2.3325
		111 000/02	W- 445	1	-1-14				0	0		0			24.27	13 25	1.02	7.00	22.00	25.44	5 0.25	0.0000
311	tgtgetteeetgtetta	NM 008683	Nedd8	gene	Chr14	56281156	-	0	0	0	0	0	- 2	1	34.65	61.05	4.67	7.33	23.08	25.44	5.925	8.0275
312	tetecaggegagtagae	NM_013492	Clu	gene	chr14	66600248	+	0	0	0.	0		-	8	0.79	0.92	2.33	70.97	0	2.54	53.21	79.165
313	agtgaatgcaaacatet	BE952212	BE952212	est	chr14	68707045	+	0	0	0	0	0		4	0.79	0.92	0	14.66	0	2.54	13.51	15.045
314	teccecacacagecece	NM_009366	Tgfbli4	gene	chrl4	76907498	+	0	0	0	0	0		4	1.58	5.52	0	54.65	4.62	0	39.16	62.3375
315	aggatetcagacaggac	NM 148938	Slc1a3	gene	chr15	8585450	-	0	2.	0	0	0	0	8	3.15	0	4.67	23.32	6.92	2.54	38.915	12.9975
316	tetetgaatgtgageag	NM 033521	Laptm4b	gene	chr15	34213966	+	0	0	0	0	0		4	0.79	0	0	12	2.31	0	8.605	13.3675
317	aatatgtgtggaggtaa	NM 053071	Cox6c	gene	chr15	35861788		0	0	0		0	0	5	48,83	69,94	118,97	80.63	50.78	43.24	69,965	87,5825
318	taagtggaataaaaaa	NM 011740	Ywhaz	gene	chr15	36701486	-	0	0	1	0	0	0	7	16.54	62.57	11.66	30.32	23.08	12.72	10,695	41.325
210	constant and and and and	NM 124004	Neeld	Gene	aba15	37206177		0	0	0	- č	0	- ×	0	0.70	0.001	22.22	34.00	2.21	10.15	EA 26	22.7725
319	ccccgggagecagagea	NP 134034	Neard	deue	CHIIS	57290177		0	0	0	-	0	-	0	0.79	0	23.33	34.99	2.31	0	34.30	22.1123
320	creagigigggiariaac	NM 178920	Maiz	gene	CHLID	54434095	+	0	0	0.	0	0		- 0	0		2.33	12.00	0	0	13.005	11.70
321	ttaaaactgaagcatac	NM 178718	Phf2011	gene	chrl5	66476586	+	0	0	0	0	.0	2	1	9.45	0.44	0	0.33	11.54	10.17	0	2.0175
322	gteetgacceageeece	NM_174991	Bail	gene	chr15	74419783	+	0	0	0	0	0		2	3.94	1.84	7	27.32	4.62	0	19.945	32.48
323	gacggacacgtgatgcc	NM 011838	Lynxl	gene	chr15	74578473	-	0	0	0	0	0	1	8	0	0	2.33	17.66	0	0	17.855	18.3325
324	aattototgt	AK010485	Ly6k	gene	chr15	74627356	1	0	0	0	0	2	0	3	11.81	2.76	16.33	0	11.54	25.44	0	0
325	gtgacagaggagggtgc	NM 019396	Cyhrl	gene	chr15	76498459	+	0	0	0	0	0	2	8	1.58	1.84	11.66	18.99	0	2.54	17.935	18.2275
326	aatcotgtggagcatco	NM 012053	Rp18	gene	chr15	76736398	+	0	0	0.	0	2.	2	5	56.7	39.57	55.98	13.99	41.54	71.22	14.1	12.6225
327	ttgctggcttttataaa	NM 053104	Rhm9	gene	chr15	76909517	-	0	0	Ő.	Ő.	0	2	7	24.41	31.29	11.66	4	18.46	27.98	0.94	5.715
328	actititattaccatete	NM 030699	Notyr	gene	chr15	79616847		0	0	0	0	0		10	3 15	4.6	20.99	56 31	10140	5.09	42 865	61 065
320	Geeelegelacoaleee	MA 030069	APCAL	dette	CHLIS	79010047		0	0	0	0	0		10	3.15	4.0	20.99	12.00	0	5.05	42.000	01.005
329	Laageaagageteeeae	NM 207708	Syngri	gene	Chris	79949442	+	0	0	0	V	0		ė.	0	0	1	13.99	0	0	15.98	12.83
330	gtgtacatacatacaca	NM_011889	Sept3	gene	chr15	82122452	*	0	.0	0	0	2	0		14.18	5.52	25.00	2.33	34.02	7.03	1.005	2.745
331	cagtettgagtgeeeta	NM 029787	Cyb5r3	gene	chr15	82984177	-	0	0	0	0	2	0	3	8.66	0.92	16.33	0.67	18.46	2.54	1.665	0
332	gaagecagtgggecate	NM_001033273	5031439g07rik	gene	chr15	84774543		0	0	0	0	0	2	1	9.45	10.12	4.67	1	2.31	10.17	0.725	1.8725
333	teettgaagtgataage	NM 009528	Wnt7b	gene	chr15	85365958	-	0	0	0	0	0	.2	1	9.45	11.96	9.33	1	18.46	5.09	0.725	1.7775
334	taggagcaaagtggccc	NM_133241	Mlcl	gene	chr15	88786703	-	0	0	0	0	0		4	0	0	0	8	0	0	7.665	8.12
335	attaatcaaaaaaaaaa	NM 175121	Slc38a2	gene	chr15	96517831	-	0	0	0	0	0	.2	-1	13.39	16.56	2.33	0	20.77	7.63	0.94	1.1475
336	tttaataacttgccttc	NM 007478	Arf3	gene	chr15	98568145		0	0	0	0	0		10	3.15	3.68	14	50.98	4.62	2.54	70.31	40.6925
337	tgacettggccaaatca	NM 001013741	Ddn	gene	chr15	98634389	-	0	0	Ö	0	0		8	0.79	0	2.33	38,65	0	0	43.64	37.1225
338	getgeectagaagaagg	NM 009448	Tuba6	gene	chr15	98780545		0	0	0	0	2	- 2	12	1172.69	832.8	977.4	62,31	1380.2	1220.94	77.955	47.6875
0.00	3	11120000110		giorna.	GHLLO	20100010	1000						-				21/11	Calles.	200012		1112.20	47,0010
339	gaggagggtgagttete	NM_011653	Tubala	ambiguousgene	nil	nil	nil	4	0	0	0	0	0	1	9.45	9.2	4.67	0	6.92	66,13	2.39	1.625
240	aettaetaee	NM 011652	Tubala	0000	abr15	00700000	-		0	0.	0	0	0	3	10.24	7.36	10	0	0	20.52	0	0
340	goeegee	NM 011055	Tubata	gene	CHIIS	30760002	-		0	0	0	0	0		10.24	7.30	75.00	10.00	0.21	30.52	0	111 1105
341	gacactggatgttECEE	WW 051391	Pppiria	gene	chrib	103301328		0	0	-	0	0	0	-	3.94	33.13	10.33	13.33	2.31	0	11.42	19.9925
342	rgarttteatttetgee	NM 001014226	Nacis	gene	CULTO	3904579	+	0	0	0	0	0	-	8	0.79	0.92	2.33	12.33	2.31	0	13.725	11.42
343	agtggctaattaggtgt	NM_009900	Clen2	gene	chrlo	20703050	+	0	0	0	0	0	-	2	1.58	5.52	2.33	22.99	2.31	0	14.745	27.6975
344	ttgaageteeaattget	NM 025693	Tmem41a	gene	chr16	21934470	-	0	0	0	0	0		2	2.36	1.84	7	33.65	0	5.09	26.46	38.0475
345	actgagatttgctgctg	NM_001164268	Kalrn	gene	chr16	34152182	-	0	0	0	0	0		4	0	0	0	8.66	0	0	10.48	7.56
346	taagaaacct	NM 019413	Robol	gene	chr16	73046239	+	0	0	0	0	0	2	1	9.45	5.52	2.33	0.33	18.46	2.54	0	0
347	atagetttetacacact	NM 007471	App	gene	chr16	84954736	1 e 1	0	0	0.	0	0		7	19.69	28.53	41.99	78.3	27.7	20.35	74.575	79.2325
348	attttttttttctgtcaaa	NM 024258	Usp16	gene	chr16	87483589	-	0	0	0	0	2	0	2	15.75	10,12	27.99	3.33	23.08	7.63	4.045	2.495
349	taataaaaattggaatg	NM 008251	Hmgm1	gene	chr16	96343256	-	0	0	0	0	0	2	7	18.11	20.24	7	5	18.46	17.81	2.39	6.2675
350	tagttagttagtagtet	NM 146073	Zdhhc14	gene	chr17	5753835	+	0	0	0	0	0.		7	21.26	15.64	27.99	149.94	18.46	35.61	116.74	170.283
351	ttttttatatata	NM 016891	Pnn2r1a	dene	chr17	21102793		0	0		0	0	0	7	20.49	59.81	58.32	21.90	25.30	10.17	34 31	15 8275
262	abaabaabaabababa	NM 022422	Cng13	gene	obr17	04333030		0	0	0	0	0		9	0,000	0	2.32	15 00	0	0	12.65	10 5675
352	gaggagegggaegtgee	NIN U22422	Gig15	gene	chill/	23033049		0	0	0	0	0	-	0	3.04	1.07	6.33	10.99	2.21	2.54	12.05	10,00/5
353	coordinaddroneaad	B1/3926/	FDX116	gene	chr1/	25957568	+	0	0	0	0	0		-	3.94	1.84	9.33	20.66	4.31	4+04	20.235	20.21
354	attgtgtaatttaaagg	NM 011861	Pacsin1	gene	chr17	27847959	+	0	0	0	0	0		4	0	0.92	0	12.66	0	0	9.035	14.165
355	ctectectgecettgge	NM_011655	Tubb5	gene	chr17	35970991		0	0	0	0	0	-2	6	18.11	21.16	14	3.67	13.85	10.17	4.045	3.4
356	gggcagaggtggtgaca	NM 011655	Tubb5	gene	chr17	35970996	+	0	0	0	0	2	0	2	17.33	11.96	23.33	1	32.31	12.72	0.725	1,285
357	cccagggtgtagaagga	NM 175934	Ppplr10	gene	chr17	36036969	2 -	0	0	0	0	0	2	1	17.33	4.6	0	2.33	27.7	17.81	1.45	0.5725
358	cacqacacceccacce	NM 009559	Zfp57	gene	chr17	37147491	+	0	0	0	0	2	2	.6	30.72	42.33	16.33	1	27.7	35.61	0.725	1.38
359	gaagaggtgg	NM 008302	Hsp90ab1	gene	chr17	45704978			0	0	0	0	0	9	15.75	1.84	0	0	0	45.79	0	0
360	toggaaagatggagaga	NM 011218	Ptors	gene	chr17	56552267	+	0	0	0	0	2	0	2	11.03	8.28	18.65	2	13,85	0	3,11	0.985
361	graatogtttttaaatg	NM 177630	Digani	gene	chr17	71168440	-	0	0	0	0	0		8	0.79	0.92	2 32	10 65	0	2 54	14 315	8.005
301	An owner prilitie propriet and provide a product of the	301_4770.32	Digapi	Jette	CHLA/	11100440	. T	. V.	- M.	v	U				U.12	N + 26	A 1 2 2	10100	V	See 8 62 14	- 4 + J 1 D	0.000

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362	tgacaattttcaaagta	NM 029239	Prkcn	gene	chr17	79348865	-	0	0	0	0	0	-2	6	25.2	34.97	14	1.33	30	12.72	0	2.3325
363	attttatatatatatat	NM 008378	Impact	dene	chr18	13151324		0	0	0	0	0		4	0.79	0.92	0	20.99	0	0	23.13	18.74
000	accedenceeddeo	101 0000000	ampace	guasa	1 10	232020404	- A - A	-			0				7.00	10 77	0.70	10.00	C 0.0	7 40	4 0 45	10 1705
364	aataaactgetgetttt	NM 009308	Syta	gene	CUL18	3139/484	-	0	.0		0	0	0		1.88	48.11	9.33	10.00	0.94	1.03	4.045	10.4725
365	gaacctgtggagettgg	NM 009308	Syt4	gene	chr18	31598083		0	0	0	0	2	0	2	4.73	4.6	25.66	2.67	6.92	5.09	2.39	2.925
366	cactotecetetteact	NM 053078	D0H4S114	gene	chr18	33596937		0	0	0	0	2	2	7	58.28	76.38	53.65	5 33	60.01	38.15	5.205	5.6125
000	sasegeeseeseesee	141 000010	DONIGITAL	gene	0112.2.0	21500207								-	NOTIO -	10120	30100	3.00	00104	20120	01100	DIVANU.
367	ctagggacagtggcaca	NM 007874	Reep5	gene	CUL18	34506722		0	0	0	0	1	0		5.51	1.30	20.99	1.33	.0	0	0.94	1.4025
368	ggatatgtggtgtgtac	NM 007913	Egrl	gene	chr18	35024589	+	0	0	0.	0	0		4	0	0.92	0	28.66	0	0	24.07	31,7075
360	creaseseseseses to	NM 172626	Phm27	crene	chr18	42498607	-	0	0		0	0	0	5	40.17	85 58	34 00	21 00	43.85	38 15	17 905	04 395
309	ycaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	WP 172020	RDIII2 /	gene	0111.1.0	42490007				_	0	0	<u> </u>		40.17	00.00	39.22	44.00	43.00	30.20	11.305	64.360
370	gtgtgtggggtgtteagt	NM 009468	Dpys13	gene	chr18	43480872	-	0	0	0	0	4	- 2	6	70.88	57.05	67.65	1.	62.32	40.7	0.94	0.9525
371	tatgatggac	NM 009468	Dpvs13	gene	chr18	43485508	-	0	0	0	0	2	0	6	57,49	16.56	118,97	0	92,32	83,94	0	0
070	an a back has a sound door	104 022110	Prove 1		ab = 1.0	40200000		0	-	0	0	0	0	7	7 00	2 44	2.22	20.20	20.24	16 26	70 625	140.005
312	caaaaataaaageegea	NP 023119	Enor	gene	CULT9	40208009	Ŧ	0		U.	0	0		1	1.00	0.44	2.33	30.32	39.44	10.20	10:005	142.905
373	gettecccaccccctt	NM 177407	Camk2a	gene	chr18	61147366	+	0	0	0	0	0		8	0	0	2.33	44.65	0	0	51.015	41.5325
374	ttgtgcttgtttatgct	BY689428	BY689428	est	chr18	69846520		0	0	0	0		0	3	7.09	0	18.66	2	13.85	2.54	0.725	2.495
01.4		101 010205			OTTA & C	20010010								-	21.00	F 5 0.0		3.00	20100	121.01	4 0.45	
375	accgttctgtagcaata	NM 013685	Tcf4	gene	chr18	69847544	· · ·	0	0	0.	0	0	1.1	0	31.5	58.89	14	3.33	34.62	17.81	4.045	3.3375
376	gettegtecacacageg	NM 010777	Mbp	gene	chr18	82754936	+	0	0	0	0			4	0.79	0.92	0	159.94	0	0	177.245	155.598
377	asagetateesagaase	MM 00100100E	man 151a	and a	abat 0	EGGOREG		0	0	0	0	0		4	0	0	0	1.0	0	0	0 1	10.04
3/1	gageergreeagggggae	NM 001001885	Imemibia	gene	Chris	2080863		U	0	0	0	0	-	9	0	0	0	10	0	.0	0.1	10.84
378	geetgaceceaceetgg	NM 008451	Klc2	gene	chr19	5107921	-	0	0	0	0	0		8	0.79	1.84	7	16.99	0	0	21.045	13.1675
379	etetettetadttadta	NM 024176	Dranl	gene	chr19	5422891	· - /	0	0	0	0	0	- 5	7	19.69	33.13	16.33	6	16.16	20.35	9.465	3.715
0.00		101 007/07	Drup x	10 10 2 2 10	011110	6402050		-		-	0	-	-		200 80	244 20	103 61	107.05	202.12	20100	20.01	1.00 2.1
380	gaagcaggaccagcaag	NM 007687	Cf11	gene	chr19	5493958	+	- <u>2</u>	0	U.	0	0	.0	5	268.56	244.78	193.01	127.95	293.12	114.40	08.81	102.11
381	cagaagetgactgtggt	NM 008874	Plcb3	gene	chr19	7051511	+		0	0.	0	0	0	9	13.39	1.84	0	0.33	2.31	40.7	0	0.8075
	0.000			0.00	2.55		1000			100	32.1						1000 C.153		200223		2012	
382	ageagggatecceqtge	NM 008889	Ppp1r14b	ambiguousgene	nil	nil	nil	0	0	0	0	- 2	2	7	43.32	42.33	34.99	3.67	43.85	25.44	3.325	3.625
						2 Sterrit		1.000										a second a	x (2) 25 (2) (2) (2)	The second second	1.0000000000	10000
383	cactacacgggaaaget	NM 008020	Fkbp2	gene	chr19	7053471		0	0	0	0	0		8	2,36	0	4.67	12.99	0	5.09	10.27	14,0225
204	Faggatates	NM 134150	Otobl	00000	about 6	7070722		0	0	6	6	0			2 64	A	8 279	10 00	5 34	0 54	1.4 1	21 65
384	-AAAAArereadeeeadd	mm 134150	OCUDI	gene	CHE19	1412100		0	. V	0	0	0			5.94	9.0	9.07	70.33	6.31	2.54	1911	44.95
385	gtgccaggaagccaaag	NM_016813	Nxfl	gene	chr19	8845281	+	0	0	0	0	0	2	6	16.54	14.72	11.66	2.33	13.85	10.17	0.94	3.555
386	gcagtgtacttcccttc	NM 144872	BC022146	gene	chr19	9026537	9 <u> </u>	0	0	0	0	2	0	3	0	0	3.4	0.67	0	0	0	0.97
207	han a state to be to be to be	100000		1910110	street 6	10050400		0		0	~	-	~		50.07	02.7*	16.65	100.00	40.47	26.52	170.25	200.002
387	teaggetgeeeteatet	NM_010239	Fth1	gene	chr19	10059488	+	0	0	0	0		0	5	59.07	83.74	40.65	192.92	48.47	30.52	179.36	200.803
388	agccaagagagaccagt	NM 019699	Fads2	gene	chr19	10137385	-	0	0	0.	0	2	0	7	11.81	23.01	34.99	5.33	2.31	5.09	4.045	5.7575
				521			1 555			- 27									V000000			and the second se
389	ggetttggagteetett	NM 026919	1810006K21rik	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	7	23,63	16.56	4.67	6	25.39	15.26	4.045	7,7825
							1.									Contraction of the local data	A0414-02-00	-	100000		1.2.3.5.5.5.5.	in the second
390	attagaaacaacgaagg	nil	GTTGGAAACA	multiple	nil	nil	nil	0	0	0	0	2	0	3	3.15	0	14	0.67	2.31	7,63	ö	1,285
201	ant act statk to a act	334 134126	D10		about 0	10070900		-	0	0	Č.	0	10		10.0	22.04	1.4		40.47	0	6.06	0 2025
391	congenergenergen	NPI 134129	Prpis	gene	CULTA	10919890	+		0		0		V	1	10.9	11.04	4.4	9	40.47	.0.	0.00	9.1015
392	ttcaaaaaaaaaaaaaaa	NM 153808	Smc511	gene	chr19	23281340	-	0	0	0	0	0	.2	7	19.69	16.56	4.67	3.67	27.7	20.35	3.325	3.715
303	ttetgggtaggggaggt	NM 026061	Ndufb8	gene	chr19	44627226	· - ·	0	0	0	0	2	0	2	4.73	10.12	32.66	4.66	2.31	5.09	4.045	5.145
000		101 1021001	102050.0007.11	9010	1	20040024		0	-	-	~	-	-	2	12 26	20.00	25 55	3 23	11.54	1 22	2.015	2 2625
394	gggaattaaaacgcgat	NM 175172	4930506M0/F1K	gene	Chr19	59048014	-	0	0	0	0			0	13.39	22.09	25.00	2.01	11.54	1.03	2.815	2.7625
395	getgecetecaaaaaaa	AW214344	AW214344	est	chr2	22443678		2	0	0	0	0	0	12	851.36	359.8	594.84	829.34	969.37	730.02	1388.54	552.93
306	attacctcagatttect	NM 008913	Ppp 3ca	dene	ch+3	136599994	+	0	0	0	0	0		8	0	1.9.4	2 33	10	0	0	11 205	8 5475
	cccacccaggcccccc	NP1 000515	rppsca	gene	Ones	130330034	T		0	0			-	0	0	1.04	6.33	10	0	V	11.200	0.0475
397	egecetggeteegeeee	NM 001039385	Vgf	gene	chr5	137508805	+	0	0	0	0	0		8	0	0	2.33	10.33	0	0	13.81	7.7775
308	accactgatatgtaata	NM 025816	Tax1bn1	dene	chr6	52716449		0	0	0	0	0	2	6	14.18	28.53	18.66	3.67	11.54	10.17	3, 325	3.675
000		104 144000		3	1	2000000		-	~	-	-		-			14 75		0.22	0.00	10.12		1.05
399	gcacctettatcaggaa	NM 144922	Hnrnpull	gene	cnr/	26506200	-	0	0	0	0	0	- 64	4	0	19.12	0	0.33	9.23	10.17	0	1.05
400	gtgactgaageteteaa	NM 008155	Gpi1	gene	chr7	35005767		0	0		0	0	0	1	12.6	11.04	7.	0.67	0	0	0.725	0
401	atatetaataataataaaaa	NM 000031	Coldal	0000	ab x2	11100073		0	0	0	0	2	0		0.79	KO T	1.4	0 67	0	5 E.A	0.725	0.5725
401	gegeocgacaacgagoo	NR 003331	COI441	Gene	CHLO	11130363				0	V		<u>v</u>		0.72	1.04	1.9	0.07		6+94	0.120	0.0160
402	acagtetatgttggagg	NM 010487	Elav13	gene	chr9	21819663	-	0	0	0	0		0	6	18.9	21.16	41.99	2 - 1	41.54	7.63	0	1.8725
403	aataaaatta	NM 015806	Mank6	gene	chr9	75234731	-	0	0	0	0	0	-0	1	9.45	12.88	9.33	2	4.62	7.63	0	0
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404	Caaacetteaaaaacea	MR140219	AR140219	63C	CHIM	113	- T	0	0	0	.0.			10	27.00	40.20	23.33	805.35	£1.1	43.64	181.100	110.210
405	accaatgaacaaaaaaa	CJ072466	CJ072466	est	chrM	1077	+	0	0	0	0			10	4.73	10.12	4.67	517.46	4.62	5.09	338.855	621.403
406	acaaaaaattacteece	AK153847	AK153847	ont	chrM	4312		0	0	0.	0	0		8	0.79	0	2 33	13 33	0	2.54	8.82	15.005
400	deddddddeegoebbbb	241200047		600	- HAR	1040		~	-		-	0		0	0.72	2.04	0.00	10.00	6.00	5.00	22.045	10.000
407	ctcttgttataaatttc	AK159675	AK159675	est	cnrM	5512	+	0	0	0	0	0		2	3.94	1.84	9.33	57.31	6.92	5.09	11.845	40.05
408	aaacccccagaaaaaaa	AK159675	AK159675	est	chrM	5841	+	0	0	0	0			7	11.81	3.68	9.33	43.32	9.23	17.81	52.03	38.08
400	aaccetaataaaaaaaaaa	AV132099	AK132098	ost	chrM	9130	-	1.1	0	0	0	0	0	7	17.33	11.96	40 00	34 99	2 31	49 33	32 675	36 336
400		AL152020	hus races	000	GHLPI	11040	T	10	12		- č	N.		-	11103	120.20	0.77 0.7	442 45	100.00	120.07	541913	30.333
410	atgactgataacaacte	AK157367	AK157367	est	ChrM	11240	*	0	-0.1			0	-0		104.0	109.32	212.92	442.49	180.03	172.97	558.32	363.215
	and the second second second	NC 005089		42,765	1.1.1.1.1.1.1.1	1 Sec. 9 See 5	- W		_	~			_		the second s			10/06/02/22	14	No.	10.07	
411	cutatectcacctcage		and AND C	and the second		10107		60									0.00	10 00			12.87	29.51
-		(AK138272)	mt-ND6	est	chrM	12126	+	0	0	0	0	0	1	8	0	0	2.33	19.66	0	0		
	A A A A A A A A A A A A A A A A A A A	(AK138272)	mt-ND6	est	chrM	12126	+	0	0	0	0	0	4	8	0	0	2.33	19.66	0	0	151 205	1000 0000
412	tcattggtcgaaaaaaa	(AK138272) AK140457	mt-ND6 AK140457	est.	chrM chrM	12126	+	0	0	0	0	0	1	8	0 7.09	0 8.28	2.33	19.66 137.95	9.23	0	154.325	133.643
412	tcattggtcgaaaaaaa aataattagccttaggt	(AK138272) AK140457 AK139402	mt-ND6 AK140457 AK139402	est est	chrM chrM chrM	12126 14123 16041	+	0	0	0	0	0	1	8 10 4	0 7.09 0	0 8.28 0	2.33 4.67 0	19.66 137.95 16.99	9.23	0 10.17 0	154.325	133.643
412 413 414	tcattggtcgaaaaaaa aataattagccttaggt	(AK138272) AK140457 AK139402	mt-ND6 AK140457 AK139402	est est	chrM chrM chrM	12126 14123 16041	+	0	0	0	0	0	-	8 10 4	0 7.09 0 7.09	0 8.28 0	2.33 4.67 0	19.66 137.95 16.99	9.23 0	0 10.17 0	154.325 11.635	133.643 21.0125 35 4225
412 413 414	tcattggtcgaaaaaaa aataattagcettaggt tteegtgaaccaaaact	(AK138272) AK140457 AK139402 AK154943	mt-ND6 AK140457 AK139402 AK154943	est est est est	chrM chrM chrM chrM	12126 14123 16041 16248	+	0 0 0 0	0 0 0 0	0	0	0		8 10 4 4	0 7.09 0 7.09	0 8.28 0 9.2	2.33 4.67 0 0	19.66 137.95 16.99 36.99	0 9.23 0 9.23	0 10.17 0 0	154.325 11.635 36.565	133.643 21.0125 35.4225
412 413 414 415	tcattggtcgaaaaaaa aataattagcottaggt ttoogtgaaccaaaaot taagateettgccagtg	(AK138272) AK140457 AK139402 AK154943 NM_009838	mt-ND6 AK140457 AK139402 AK154943 Cct6a	est est est gene	chrM chrM chrM chrM chr5	12126 14123 16041 16248 130322157	+	0 0 0 0 0 0	0 0 0 0 0 0	0	0 0 0 0	0	1. Water and	8 10 4 4 7	0 7.09 0 7.09 30.72	0 8.28 0 9.2 46.01	2.33 4.67 0 16.33	19.66 137.95 16.99 36.99 15.33	0 9.23 0 9.23 36.93	0 10.17 0 0 27.98	154.325 11.635 36.565 18.065	133.643 21.0125 35.4225 13.1875
412 413 414 415 416	tcattggtcgaaaaaaa aataattagccttaggt ttccgtgaaccaaaact taagatccttgccagtg ataatacataaaaaaaa	(AK138272) AK140457 AK139402 AK154943 NM_009838 NM_007807	mt-ND6 AK140457 AK139402 AK154943 Cet6a Cobb	est est est gene gene	chrM chrM chrM chrS chr5 chrX	12126 14123 16041 16248 130322157 9014274	+	0 0 0 0 0 2	0 0 0 0 0 0 0 0	0	0 0 0 0 0 0 0 0 0	0	0	8 10 4 7 12	0 7.09 0 7.09 30.72 393	0 8.28 0 9.2 46.01 702.13	2.33 4.67 0 16.33 699.81	19.66 137.95 16.99 36.99 15.33 518.8	0 9.23 0 9.23 36.93 639.32	0 10.17 0 27.98 414.61	154.325 11.635 36.565 18.065 468.87	133.643 21.0125 35.4225 13.1875 556.203
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412 413 414 415 416 417 418 419 420 421 422	tcattggtcgaaaaaaa aataattagcttaggt Ltcogtgaaccaaact taagatcattgccagtg ataatacataaaaaaa ctagacagaggcatta tattaataacagagga tagtgaacagtggtcgt aggtagtacaaagttt Lttcagcagtgttggc aagaaacatttaatta	(AK138272) AK139402 AK154943 NM 009838 NM 007807 NM 019634 NM 019634 NM 009457 NM 016886 NM 013556 NM 012010	mt-ND6 AK140457 AK139402 AK154943 Cct6a Cybb Tspan7 Tm4sf2 Ubal Gria3 Hprt1 Eif2s3x	est est est gene gene gene gene gene gene	chrM chrM chrM chr5 chr5 chrX chrX chrX chrX chrX chrX chrX	12126 14123 16041 16248 130322157 9014274 10173655 10173702 20259554 39031727 50374749 91434084	+ + + + + + + + + + + + + + + + + + + +	0 0 0 0 0 0 0 0 0 0 0			0 0 0 0 0 0 0 0 0 0 0 0 0 0			8 10 4 7 12 4 10 9 4 2 1	0 7.09 0 7.09 30.72 393 0.79 0.79 0.79 14.18 3.15 4.73 10.24	0 8.28 0 9.2 46.01 702.13 1.84 23.93 0.92 1.84 3.68 13.8	2.33 4.67 0 16.33 699.81 0 14 0 0 4.67 9.33	19.66 137.95 16.99 36.99 15.33 518.8 10.33 197.59 0.33 15.66 32.65 1.33	0 9.23 0 9.23 36.93 639.32 0 2.31 0 4.62 6.92 6.92	0 10.17 0 27.98 414.61 0 0 414.61 0 0 45.79 2.54 2.54 7.63	154.325 11.635 36.565 18.065 468.87 12.145 120.975 0.725 10.48 29.195 0.94	133.643 21.0125 35.4225 13.1875 556.203 8.61 240.608 0 18.9025 34.41 2.745
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412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429	tcattggtcgaaaaaaa aataattagccttaggt ttcogtgaaccaaact taagatocttgcoagtg ataatacataaaaaaaa ctagacaggcatta tattaataaacaggcatta tagtagtgcatggtgct dggtatgtacaaagtt ttcogogactggtgct ttcagcagtgttggaa ggaactaggtgcctot aaattattgggaaatc tggtgaaggaaaaaaaaaaa	(AK138272) AK140457 AK139402 AK154943 NM 009838 NM 019634 NM 019634 NM 019634 NM 019634 NM 019634 NM 013556 NM 012010 NM 010210 NM 009094 NM 025379 NM 011123 NM 011025 NM 0121278 NM 0121278	mt-ND6 AK140457 AK139402 AK154943 Cct6a Cybb Tspan7 Tm4sf2 Uba1 Gria3 Hprt1 Eif233x Efnb1 Rps4x Cox7b Flp1 Dcx Tmab4x Bagagcagagagagaga	est est est gene gene gene gene gene gene gene gen	chrM chrM chrM chrM chrS chrX chrX chrX chrX chrX chrX chrX chrX	12126 14123 16041 16248 130322157 9014274 9014274 20259554 10173702 20259554 39031727 50374749 91334084 96343700 99380289 103214976 133371868 140290568 140290568 140290568	+ + + + + + + + + + + + + + + - - - - + + + + + 					0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		8 10 4 7 12 4 10 9 4 10 9 4 1 9 5 2 8 6 5 1 1	0 7.09 0 7.09 30.72 393 0.79 14.18 3.15 4.73 10.24 8.66 139.4 5.51 3.9.4 5.51 3.9.4 5.51 3.9.4 5.50 380.47 8.66	0 8.28 0 9.2 46.01 702.13 1.84 23.93 0.92 1.84 3.68 13.8 0.92 255.82 4.6 0 78.22 283.43 8.28 0	2.33 4.67 0 16.33 699.81 0 14 0 4.67 9.33 0 62.98 23.33 2.33 32.66 277.59 4.67	19.66 137.95 16.99 36.99 15.33 518.8 10.33 197.59 0.33 15.66 32.65 1.33 0 13.33 1.67 90.63 1.33 141.61 0.67	0 9.23 0 9.23 36.93 639.32 0 2.31 0 2.31 0 4.62 6.92 0 71.55 0 6.92 0 6.92 48.47 507.77 4.62	0 10.17 0 27.98 414.61 0 0 45.79 2.54 7.63 27.98 117.01 2.54 2.54 45.79 218.75 10.17	$\begin{array}{c} 154.325\\ 11.635\\ 36.565\\ 18.065\\ 18.068\\ 468.07\\ 12.145\\ 120.975\\ 0.725\\ 10.48\\ 29.195\\ 0.94\\ 0\\ 17.05\\ 2.39\\ 116.365\\ 0\\ 61.225\\ 0.94 \end{array}$	133.643 21.0125 35.4225 13.1875 556.203 8.61 240.608 0 18.9025 34.41 2.745 0 10.855 1.065 78.1425 2.365 187.383 1.4625
412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429	tcattggtcgaaaaaaa aataattagcttaggt tLcogtgaaccaaast taagtcttgccagtg ataatcattaaaaaaa tgggggcattat tattaataacagggattat tattaataacaggg tggggtggag gggggtggag ggggaactaaaaaaaaa gaactagtggcoct aagtaattggaaatco tggggagtggag gtgaactaaaaaaaaaa gaactagtggcoct tgggaggggag aastattgggaaaaaa tagggaaaaaa aaaaacaaaaaaaaaa	(AK138272) AK140457 AK139402 AK154943 NM 009838 NM 019634 NM 019634 NM 019634 NM 019634 NM 019634 NM 019634 NM 0126356 NM 012010 NM 012010 NM 012010 NM 012010 NM 012010 NM 012010 NM 012010 NM 012010 NM 012025 NM 01123 NM 01025 NM 0121278	mt-ND6 AK140457 AK139402 AK154943 Cct6a Cybb Tspan7 Tm4sf2 Ubal Gria3 Hprt1 Eif2s3x Efnb1 Rps4x Cox7b Flp1 Dcx Tmb4x aaaacaaaaaaaaaa	est est est gene gene gene gene gene gene gene gen	chrM chrM chrM chrM chrS chrS chrS chrX chrX chrX chrX chrX chrX chrX chrX	12126 14123 16041 16248 130322157 9014274 10173702 20259554 39031727 50374749 91434084 96343700 95380289 103214976 133371868 140290568 140290560 111	+ + + + + + + + + + + - - + + - - - - - - - -					0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		8 10 4 7 12 4 10 9 4 10 9 4 2 2 8 6 5 1 1	0 7.09 0 30.72 393 0.79 0.79 0.79 0.79 0.79 0.79 0.79 0.79	0 8.28 0 9.2 46.01 702.13 1.84 23.93 0.92 1.86 13.8 0.92 255.82 4.6 0 78.22 283.43 8.28	$\begin{array}{c} 2.33\\ 4.67\\ 0\\ 0\\ 16.33\\ 699.81\\ 0\\ 0\\ 1.4\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\ 0\\$	$\begin{array}{c} 19.66\\ 137.95\\ 16.99\\ 36.99\\ 15.33\\ 518.8\\ 10.33\\ 197.59\\ 0.33\\ 15.66\\ 32.65\\ 1.33\\ 0\\ 1.33\\ 1.67\\ 90.63\\ 1.33\\ 1.67\\ 10.67\\ 141.61\\ 0.67\\ \end{array}$	0 9.23 0 9.23 639.32 0 2.31 0 4.62 6.92 6.92 6.92 71.55 0 71.55 0 6.92 48.47 48.47 48.47 4.62	0 10.17 0 27.98 414.61 0 0 45.79 2.54 2.54 2.54 2.79 117.01 2.54	$\begin{array}{c} 154.325\\ 11.635\\ 36.565\\ 18.065\\ 468.07\\ 12.145\\ 120.975\\ 10.48\\ 29.195\\ 10.48\\ 29.195\\ 0.94\\ 0\\ 17.05\\ 2.39\\ 116.365\\ 0.94\\ 0\\ 61.225\\ 0.94 \end{array}$	$\begin{array}{c} 133,643\\ 21,0125\\ 35,4225\\ 13,1875\\ 556,203\\ 8,61\\ 240,608\\ 0\\ 18,9025\\ 34,41\\ 2,745\\ 0\\ 10,855\\ 1,065\\ 78,1425\\ 2,365\\ 187,383\\ 1,4625\\ \end{array}$
412 413 414 415 416 417 418 417 418 420 421 422 423 424 425 426 427 428 429 430	tcattggtcgaaaaaaa aataattagccttaggt ttcogtgaaccaaact taagtottgcoagtg ataatactataaaaaaa ctagacgagggcattat tattaataacagagga tttcagtggtagtgttggt ttcagtgtgtggt gtggaactggtgggg gtggaactaaaaaaaaa gggagtggga gtgaactagaactaaaaaaaaa gaaactagggaaatco taattattgggaaaacc ttggtgaagtgtcttgt aaaacaacaaaaaaaaaa	(AKI 38272) AKI 40457 AKI 39402 AKI 54943 NM 009838 NM 019634 NM 019635 NM 010110 NM 025379 NM 011025 NM 021278 NM 01025 NM 0212762	mt-ND6 AK140457 AK139402 AK154943 Cct5a Cybb Tspan7 Tm4sf2 Ubal Gria3 Hprt1 Eif2s3x Efnb1 Rps4x Cox7b Plp1 Dcx Tmsb4x aaaacaaaaaaaa Ato5h	est est est gene gene gene gene gene gene gene gen	chrM chrM chrM chrS chrX chrX chrX chrX chrX chrX chrX chrX	12126 14123 16041 16248 130322157 9014274 10173655 10173702 20259554 10173702 20259554 39031727 50374749 91434084 96343700 99380289 9133214976 133371868 1402990588 163645205 nl1 ni1	+ + + + + + + + + + + - - - - - - -							8 10 4 7 12 4 10 9 4 10 9 4 2 1 9 5 2 8 6 5 1 2	0 7.09 0 30.72 393 0.79 0.79 0.79 14.18 3.15 4.73 10.24 8.66 139.4 5.51 3.15 5.51 3.15 5.51 3.15 5.9.07 350.47 8.66	0 8.28 0 9.2 46.01 702.13 1.84 23.93 0.92 1.84 3.68 13.8 0.92 255.82 4.6 0 78.22 283.43 8,129 31.29	2.33 4.67 0 0 16.33 699.81 0 14 0 0 0 4.67 9.33 0 62.98 23.33 32.66 277.59 4.67 9.33	19.66 137.95 16.99 36.99 15.33 518.8 10.33 197.59 0.33 15.66 32.65 1.33 0 13.33 1.67 90.63 1.33 141.61 0.67 14.99	0 9.23 0 9.23 639.32 0 2.31 0 2.31 0 4.62 6.92 6.92 0 711.55 0 6.92 48.47 507.77 4.62	0 10.17 0 0 27.98 414.61 0 414.61 0 45.79 2.54 2.54 2.54 2.54 2.7.98 117.01 2.54 0.17 0 0 0 0 0 0 0 0 0 0 0 0 0	$\begin{array}{c} 154.325\\ 11.635\\ 36.565\\ 18.065\\ 18.068\\ 468.87\\ 12.145\\ 120.975\\ 0.725\\ 10.48\\ 29.195\\ 0.94\\ 0\\ 17.05\\ 2.39\\ 116.365\\ 0\\ 61.225\\ 0.94\\ 11.34\\ \end{array}$	133.643 21.0125 35.4225 13.1875 556.203 8.61 240.608 0 10.9025 34.41 2.745 0 10.855 1.065 78.1425 2.365 187.383 1.4625 19.455
412 413 414 415 416 417 418 419 420 421 422 423 424 422 423 424 425 426 425 426 429 430	tcattggtcgaaaaaaa aataattagcttaggt ttcogtgaaccaaaat taagatcattacaaaaaaa ctagacagaggcatta tattaataaacagagca tagtagtactggtgct aggtagtgtaga ggggaactaaaaaaaa gaaactagtggcgct tggggaagtgtagga ttggtgaagtgaa	(AKI 38272) AKI 40457 AKI 39402 AKI 39402 AKI 39402 NM 009838 NM 019634 NM 019634 NM 019634 NM 019634 NM 019634 NM 013566 NM 013566 NM 0132010 NM 029094 NM 011123 NM 029094 NM 011123 NM 020278 NM 021278 NM 021278	mt-ND6 AK140457 AK139402 AK139403 Cct6a Cybb Tspan7 Tm4sf2 Ubal Gria3 Hprt1 Eif223x Efnbl Rps4x Cox7b Plp1 Dcx Tmab4x agagacaasaagagagaga	est est est gene gene gene gene gene gene gene gen	chrM chrM chrM chrS chrS chrS chrS chrX chrX chrX chrX chrX chrX chrX chrX	12126 14123 16041 16248 130322157 9014274 10173702 20259554 39031727 50374749 91434084 96343700 99380289 103214976 133371868 140290568 163645205 n11 n11	+ + + + + + + + - - + + - - - - - -					0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		8 10 4 7 12 4 10 9 4 2 1 9 5 2 8 8 8 6 5 1 2 2	0 7.09 0 30.72 393 0.79 0.79 14.18 3.15 4.73 10.24 8.66 139.4 5.51 3.15 5.9.07 350.47 8.66 1.58	0 8.28 0 9.2 46.01 702.13 1.84 3.68 13.8 0.92 255.82 4.6 0 78.22 283.43 8.28 31.29	$\begin{array}{c} 2.33\\ 4.67\\ 0\\ 0\\ 699.81\\ 699.81\\ 699.81\\ 14\\ 0\\ 0\\ 0\\ 4.67\\ 9.33\\ 32.66\\ 2.73\\ 32.66\\ 277.59\\ 4.67\\ 9.33\\ \end{array}$	$\begin{array}{c} 19.66\\ 137.95\\ 16.99\\ 36.99\\ 15.33\\ 518.8\\ 10.33\\ 197.59\\ 0.33\\ 15.66\\ 32.65\\ 1.33\\ 0\\ 13.33\\ 1.67\\ 90.63\\ 1.33\\ 1.67\\ 141.61\\ 0.67\\ 144.99 \end{array}$	$\begin{array}{c} 0\\ 9,23\\ 0\\ 9,23\\ 36,99\\ 639,32\\ 0\\ 2,31\\ 4,62\\ 6,92\\ 0\\ 0\\ 71,55\\ 0\\ 6,92\\ 48,47\\ 507,77\\ 4,62\\ 4,62\\ \end{array}$	$\begin{array}{c} 0\\ 10.17\\ 0\\ 27.90\\ 414.61\\ 0\\ 0\\ 45.79\\ 2.54\\ 2.54\\ 2.54\\ 7.63\\ 27.98\\ 117.01\\ 2.54\\ 117.01\\ 2.54\\ 45.79\\ 218.75\\ 10.17\\ 0\\ \end{array}$	$\begin{array}{c} 154.325\\ 11.635\\ 36.565\\ 18.065\\ 18.065\\ 12.145\\ 12.145\\ 12.145\\ 12.145\\ 12.19,10,42\\ 29.195\\ 0.94\\ 0\\ 17.05\\ 2.39\\ 116.365\\ 0\\ 0.94\\ 11.34\\ \end{array}$	$\begin{array}{c} 133.643\\ 21.0125\\ 35.4225\\ 13.1875\\ 556.203\\ 8.61\\ 240.608\\ 0\\ 18.9025\\ 34.41\\ 2.745\\ 0\\ 10.855\\ 1.065\\ 78.1425\\ 2.365\\ 187.343\\ 1.4625\\ 19.45\\ \end{array}$

432	aagaaaccagaatcctt	NM_008705	Nme2	ambiguousgene	nil	nil	nil	0	0	0	0	2	2	7	33.08	44.17	37.32	6.33	27.7	15.26	4.265	7.5175
433	aagaggcaagacgaaaa	nil	AAGAGGCAAG	multiple	nil	nil	nil	0	0	0	0	0	2	5	92.15	89.26	23.33	12.33	66.93	68.68	6.22	15.9275
434	aaggtggaagagattgc	NM_029751	Rp118a	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	5	106.32	79.14	44.32	16.33	94.63	71.22	11.85	18.59
435	aatgacctggtgtctga	NM_023716	Tubb2b	ambiguousgene	nil	nil	nil	0	0	0	0	2	.2	5	166.18	109.51	104.97	4.33	99.25	188.23	5.71	3.2225
436	aatgtttctgctttaca	NM_011045	Pcna	ambiguousgene	nil	nil	nil	0	0	0	0	0	.2	1	18.9	11.04	4.67	1.33	18.46	12.72	0.725	0.97
437	aatttcaaaacaccacg	NM_009092	Rps17	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	5	51.98	77.3	44.32	11.33	43.85	45.79	13.215	10.1525
438	accattaactggagcot	nil	accattaactggagcct	no match	nil	nil	nil	0	0	0	0	0		8	0	3.68	7	17.33	0	0	19.865	17.185
439	accotattaa	NM 009342	Dvnlt1	no match	nil	nil	nil	0	0	0	0		2	5	21.26	15.64	9,33	2,33	0	22,89	0.94	3,3175
441	agaaataaatactgtaa	nil	AGAAATAAATACTGTAA	multiple	nil	nil	nil	0	0		0	0	0	1	12.6	17.48	0	2.67	2,31	2.54	1.875	2.35
442	agaagtgtttggagttt	NM_008253	Hmgb3	ambiguousgene	nil	nil	nil	0	0	0	0	2	0	2	16.54	11.96	20.99	1	18.46	5.09	0	1.625
443	agagcagagaagcagca	nil	AGAGCAGAGA	multiple	nil	nil	nil	0	2	0	0	0	0	2	11.81	1.84	4.67	6.66	11.54	22.89	15.545	0
444	agagegaagtggeggaa	nil	AGAGCGAAGTGGCGGAA	multiple	nil	nil	nil	0	0	0	0	2	0	5	92.15	99.38	212.27	27.32	120.02	50.87	24.875	26.685
445	agagtaatcaaaaaaaa	nil	agagtaatcaaaaaaaa	no match	nil	nil	nil	0	0	0	0	0		7	8.66	4.6	9.33	46.98	4.62	7.63	37.8	52.615
447	agcagecectecctagg	nil	agcagecectecctagg	no match	nil	nil	nil	0	0	0	0	2	0	3	1.58	0	27.99	0.33	4.62	0	0.94	0
448	aggcagacagtagctgt	nil	AGGCAGACAG	multiple	nil	nil	nil	0	0	0	0	2	2	5	436.31	333.12	300.92	98.63	380.82	333.21	116.605	88.87
449	aggecaagaaactagec	nil	AGGCCAAGAA	multiple	nil	nil	nil	0	0	0	0	2	0	2	6.3	4.6	18.66	1	11.54	5.09	0.94	0.97
450	agggaaaaaaaaaaaaaa	nil	agggaaaaaaaaaaaaaa	no match	nil	níl	nil	0	0	0	0	0	2	6	13.39	23.01	16.33	3	20.77	10.17	5.205	1.445
451	ataatggatacataagc	nil	ATAATGGATACATAAGC	multiple	nil	n11	nil		0	0	0	0	0	6	35.44	12.88	16.33	8.	18.40	80.48	12.145	4.73
452	atactgaagccccactt	NM_016738	Rp113	ambiguousgene	nil	nil	nil	0	0	0	0	2	0	5	61.43	64.42	81.64	17.33	90.01	30.52	18.15	15.92
454	atactgacatattgtag	nil	atactgacat	no match	nil	nil	nil	2	0		0	0	0	12	445.76	720.53	758,12	1170.9	530,85	361.19	1085,97	1208.16
455	atacttgaca	nil	atacttgaca	no match	nil	nil	nil	0	0	0	ő	2	0	3	9.45	0	18.66	0	11.54	17.81	0	0
456	atccgaaagaacaagga	nil	ATCCGAAAGA	multiple	nil	nil	nil	0	0	0	0	2	2	5	87.42	61.65	90.97	22.32	103.86	76.31	20.67	23.905
457	atcctgacattttgtag	nil	atcctgacattttgtag	no match	nil	nil	nil	0	0	0		. 2	0	3	0	0	23.33	1.33	0	0	1.665	1.3
458	atettectec	NM_009080	Rp126	ambiguousgene	nil	nil	nil	0	0	0	0	2	0	3	1.58	1.84	14	0	2.31	2.54	0	0
459	atgatggtagaggacat	nil	ATGATGGTAGAGGACAT	multiple	nil	nil	nil	0	2	0	0	0	0	2	9.45	3.68	7	5.66	18.46	10.17	14.235	0
460	atggettaataaatttt	NM 011830	Impdh2	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	1	16.54	9.2	2.33	2	13.85	12.72	0.725	0.4775
462	attetgaacaggataat	nil	ATTCTGAACA	multiple	nil	nil	nil	0	0	0	0	0		2	1.58	6.44	7	27.66	0	5.09	26.67	27.0825
463	attgettagagatgttt	nil	ATTGCTTAGAGATGTTT	multiple	nil	nil	nil	0	0	0	0	0	2	7	29.14	22.09	30.32	10.33	32.31	27.98	6.65	12.965
464	attgtttatgaaaagaa	NM_016957	Hmgn2	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	7	55.13	69.02	23.33	6.33	73.86	61.05	6.65	6.3275
465	atttgattagccccaaa	nil	atttgattagccccaaa	no match	nil	nil	nil	0	0	0	0	2	0	6	18.11	34.97	30.32	3.67	27.7	12.72	5.415	3.175
466	attttcagttttcttgc	nil	ATTTTCAGTTTTCTTGC	multiple	nil	nil	nil		0	0	0	0	0	2	37.8	0.92	2.33	4.66	13.85	106.83	9.035	1.7925
468	caacaacaagggagace	nil	CAACTATTACT	multiple	nil	n11	n11 n11	-	0	0	0	0	0	9	25.7	3.69	0	0.35	4.62	69.69	0	0.4775
469	caattetta	nil	CAATTCTTTA	multiple	nil	nil	nil	0	0	0	0	2	0	3	0.79	1.84	14	0	2.31	00.00	0	ŏ
470	cacaaacggtactcttg	NM_027015	Rps27	ambiguousgene	nil	nil	nil	0	0	0	0	2	0	5	141.76	147.23	107.3	50.98	66.93	78.85	46.03	55.0125
471	caccaccacaggatcaa	nil	CACCACCACAGGATCAA	multiple	nil	nil	nil	0	0	Ŭ.	0	0	2	7	49.62	35.89	23.33	11	66,93	38.15	8.31	13
472	caccaccgttgccttca	nil	CACCACCGTT	multiple	nil	nil	nil	0	0	0	0	0	2	5	98.45	65.34	44.32	22.66	129.25	55.96	17.64	25.6225
473	cagaacccacgacagta	NM_011296	Rps18	ambiguousgene	nil	nil	nil	0	0	0	2	0	0	7	66.94	42.33	14	16.99	73.86	53.42	9.545	21.625
474	caggagcatcaaaaaaa	nil	caggagcatc	no match	nil	nil	nil	0	0	0	0	0		2	3.94	1.84	4.67	30.99	2.31	2.54	23.855	33.98
475	cagttattaatttatta	NM_175752	Chn1	ambiguousgene	nil	nil	nil	0		0	0	0	0	4	4.73	33.13	11.66	21.99	2.31	0	6.65	51.8825
476	cagttgggttttagctg	NM 010447	Hnrnpal	gene	chr15	103077034	+	0	0	0	0	0	2	6	17.33	24.85	18.66	3.33	11.54	12.72	1.665	4.07
477	cecacaaget	nil	CCCACAAGCT	multiple	nil	nil	nil		0	0	0	0	0	9	29.14	0	0	0	6.92	86.48	0	0
478	cccctattaa	nil	cccctattaa	no match	nil	nil	nil	0	0	0	0	2	.0	3	5.51	1.84	27.99	0.	2.31	7.63	0	0
479	ccctgattttatatact	NM_013507	Eif4g2	ambiguousgene	nil	nil	nil	2	0	0	0	0	0	7	36.23	25.77	25,66	7.66	69.24	15.26	5.495	8.7575
480	ccctgggttcagcccgc	nil	CCCTGGGTTC	multiple	nil	nil	nil	0	0	2	0	0	0	5	140.19	59.81	95.64	26.99	126.94	127.18	37.235	21,9575
481	congagaccet	nil	CCTGCAACCA	multiple	nil	nil	nil	0	0	0	0	0		2	5.51	7.36	14	24.99	6.92	2.54	28,495	21.7475
402		-113_044796		anorguousgene	104.4	314.4	11.4.4		100		×.,		-		44.193	11.30	M	0.00	, 2M <u>0</u>	44+44	×	
483	ctaataaagccaccgtg	nil	CTAATAAAGC	multiple	nil	nil	nil	0	0		0	0	0	5	96.08	173	81.64	49.65	110.79	81.4	36.485	57.6225
484	ctgcacttttttattet	NM 008568	Mcm7	mutcibie	chr5	138605867		0	0	0	0	0	-	1	12.6	8.28	9.33	0.33	9,23	7.63	13.085	1.38
486	ctgcatcgttgctgtca	nil	CTGCATCGTTGCTGTCA	multiple	nil	ni1	nil	0	0	0	0	2	0	6	22.84	31.29	34.99	2.67	11.54	7.63	0.725	3.91
487	ctgccccaca	NM_009438	Rp113a	ambiguousgene	nil	nil	nil	1.1	0	0	0	0	0	9	18.11	0.92	.0	0	2.31	55.96	0	0
488	ctggggtgggcattggt	nil	CTGGGGTGGG	multiple	nil	nil	nil	2	0	0	0	0	0	7	29.14	12.88	23.33	22.99	57.7	10.17	19.22	25.5325
489	ctgtaggtgaaatteet	nil	CTGTAGGTGA	multiple	nil	nil	nil	2	0	0	0	0	0	5	122.07	144.47	97.97	44.32	228,49	78.85	31.23	49.475

490	gaagtcaaaaaaaaaaa	nil	gaagtcaaaaaaaaaaa	no match	nil	nil	nil	0	0	0	0	0	-2	1	0.79	27.61	0	0.67	13.85	5.09	1.665	0,985
491	gagaaactgaccaatct	NM_010864	Муо5а	ambiguousgene	nil	nil	nil	0	0	Ö.	1	0	0	3	0	0	23.33	3.33	0	0	7.375	0.8075
492	gatgctgccaattttga	NM_009079	Rp122	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	6	22.84	15.64	18.66	4.33	30	17.81	4.77	3.8275
493	gcaaaaaaaaaaaaaaaa	nil	GCAAAAAAAAAAAAAAAAA	multiple	nil	nil	nil	0	0	0	0	0	2	1	14.18	23.01	2.33	2.33	16.16	5.09	0.94	2.035
494	gccaagggtcagagget	nil	GCCAAGGGTCAGAGGCT	multiple	nil	nil	nil	0	0	0	- 2	0	0	5	81.91	55.21	20.99	32.65	80.78	63.59	34.42	29.8225
495	gcetecaaggagtaaaa	nil	GCCTCCAAGG	multiple	nil	nil	nil	2	0	0	0	0	0	5	185.87	114.11	174.95	126.62	221.57	66.13	119.8	133.323
496	gcetttatgagaagaaa	NM_011297	Rps24	ambiguousgene	nil	nil	nil	0	0	0	0	0	12	5	121,29	127.91	67.65	31.32	124.63	109.38	27.315	32.89
497	geggtgaateaegggtg	nil	GCGGTGAATCACGGGTG	multiple	nil	nil	nil	0	0	0	0	0	2	1	25.2	5.52	2.33	2	16.16	2.54	0.94	0.4775
498	getgeetagagaaggat	n11	gctgcctagagaaggat	no match	nil	nil	nil	0	0	0	0	2	0	3	13.39	0	16.33	0.33	6,92	33.07	0	0.4775
499	gettgeeeta	nil	gettgeeeta	no match	n1.1	n11	n11	0	0	0	.0	- 4	0	3	7.09	0	14	0	9.23	12.72	0	0
500	ggggaaategeagette	NM_025284	TMSB10	ambiguousgene	nil	nil	nil	0	0	2	0	2	0	5	256.75	156.44	261.26	34.99	237.73	269.62	39.885	33.9575
501	ggggeteacaaceatet	n11	GGGGCTCACAACCATCT	multiple	n11	n11	n11	0	0	0	0		0	3	14.96	52.27	27.99	11 66	101.55	17.81	0 31	1.8725
502	ggtaaacaat	nil	GGTAAACAAT	multiple	nil	nil	nil	0	0	0	0	0	2	1	10.24	14.72	2.33	1.67	20.77	7.63	0.54	14.0170
504	gtaagcataaaaaaaaaa	NR 002856	LOC218963	ambiquousgene	nil	nil	nil	0	0		0	0	0	5	92.15	207.05	62.98	40.65	80.78	89.03	27,395	46.4225
505	gtcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	nil	gtcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	no match	nil	nil	nil	0	0	0	0	0	2	6	18.9	29.45	16.33	3	20.77	20.35	0.725	4.27
506	gtcacaccacaagtaaa	nil	GTCACACCACAAGTAAA	multiple	nil	nil	nil	0	0	0.	0	2	0	2	8.66	10.12	30.32	1.33	6.92	2.54	0.94	1.625
507	gtcatagetgttetgtg	NM_146219	BC025816	ambiguousgene	nil	nil	nil	4	0	0	0	0	0	9	12.6	0.92	0	0.33	0	38.15	0	0.4925
508	gtctgctgatggccaga	NM_008143	Gnb211	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	5	118.14	147.23	41.99	17.66	85.4	66.13	15.12	17.81
509	gtggctcacaaaaatat	nil	GTGGCTCACA	multiple	nil	nil	nil	2	0	0	0	0	0	12	1045.89	528.2	625.16	1162.2	1375.59	1040.34	1049.76	1239.57
510	gtgggcgtgtacaaagg	NM_009091	Rps15	ambiguousgene	nil	nil	nil	0	0	2	0	0	0	5	112.62	51.53	58.32	76.3	101.55	124.64	62.11	80.365
511	gtgttaaccagctgaaa	nil	GTGTTAACCAGCTGAAA	multiple	nil	nil	nil	0	0	0	0	2	0	7	70.88	42.33	76.98	6.66	99.25	35.61	3.325	9.47
512	gttgetgagaagegget	nil	GTTGCTGAGAAGCGGCT	multiple	nil	nil	nil	0	0	0	0	2	0	5	145.7	110.43	97.97	27.66	143.1	76.31	16.19	34.825
513	taatttttttagatcat	nil	TAATTTTTTT	multiple	nil	nil	nil	0	0	0.	0	2	0	7	9.45	18.4	32.66	6.66	13.85	5.09	5.925	6.485
514	taccogtaca	nil	taccogtaca	no match	nil	nil	nil	0	0	0	0	2	0	3	1.58	0	14	0	2.31	2.54	0	Ö
515	tactgctgataaagcct	NM_017367	Ccni	ambiguousgene	nil	nil	nil	0	0	0	2	0	0	7	45.68	34.05	7	29.99	48.47	38.15	27.53	30.705
516	tagatataggettacta	nil	TAGATATAGGCTTACTA	multiple	nil	nil	nil	0	0	0		0	0	5	43.32	108.59	226.27	239.91	48.47	40.7	65.115	335.975
517	tatattgattgtggcaa	NM_007569	Btgl	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	1	10.24	11.04	2.33	0.67	9.23	5.09	0.725	1.3
518	tcaagaacaaaataaaa	nil	TCAAGAACAA	multiple	nil	nil	nil	0	0	0	0	0		4	0.79	0.92	0	9.66	0	2.54	11.34	8.74
519	tcaataaagccadtgaa	nil	TCAATAAAGC	multiple	nil	nil	nil	0	0	0	0	2	0	7	14.96	51.53	55.98	14.99	27.7	0	15.465	13.7625
520	teacegtaca	nil	tcaccgtaca	no match	nil	nil	nil	0	0	0	0	2	0	3	0	0	16.33	0	0	0	0	0
521	tecccegtacagteccc	nil	tecccegtacagtecce	no match	nil	nil	nil	0	0	0	0	2	0	3	1.58	0.92	23.33	0.33	2.31	2.54	0.725	0
522	teeecgacat	n11	teccegacat	no match	nil	nil	nil	0	0	0	0		0	3	1.58	0.92	27.99	0	4.62	0	0	0
523	topcogguat	nil	tecceggtac	no match	nil	n11	nii	0	0	0.			0	3	3.94	1.94	23.00	0	4.02	7.03	0	0
525	teccegtaca	nil	teccegtaca	no match	nil	nil	nil		0	0	0		0	11	268.56	202.45	1229.33	0	572,39	195.86	0	0
526	tecceqtact	nil	teccegtact	no match	nil	nil	nil	0	0	0	Ö	2	0	3	4.73	0	16.33	0	9,23	5.09	0	0
527	tecceqttea	nil	teccegttea	no match	nil	nil	nil	0	0	0	0	2	0	3	0	0	20,99	0	0	0	0	0
528	teeectacat	nil	tcccctacat	no match	nil	nil	nil	0	0	Ö		2	0	3	8,66	0.92	62.98	Ŭ.	11.54	10.17	0	0
529	teccetatta	nil	teccetatta	no match	nil	nil	nil	0	0	0.	0	2	0	3	1.58	0.92	30.32	0	0	5.09	0	0
530	tecegtacat	nil	tecegtacat	no match	nil	nil	nil	2	0	Ő	0	2	0	6	37.02	19.32	123.63	0	92.32	12.72	0	.0
531	teeetattaa	nil	tccctattaa	no match	nil	nil	nil	0	0	0		2	2	11	118.92	240.18	1551.24	0	136.17	178.05	0	0
532	teectattag	nil	tecctattag	no match	nil	nil	nil	0	0	0	0	2	0	3	1.58	1.84	16.33	0	0	5.09	0	0
533	tecctattat	nil	tccctattat	no match	nil	nil	nil	0	0	0	0	2	0	3	0.79	0.92	14	0	0	2.54	0	0
534	teectattga	nil	teectattga	no match	nil	nil	nil	0	0	0		2	0	3	0	0	27,99	0	0	0	0	0
535	teectattta	nil	tecctattta	no match	n1.1	n11		0	0	0	U		0	3	0	0	14	0	0	0	0	0
536	teectgtaca	n11	tccctgtaca	no match	n11	n11	nil	0	0	0	-	-	0	3	0.79	1.04	30.32	0	2.31	0	0	0
629	tootattaad	nil	teecttatta	no match	nil	n11	n11 n11	0	0	0	0		0	3	7.00	1.04	27.99	0	12.05	7.62	0	0
530	teettattaa	nil	teettattaa	no match	nil	n11	nil	0	0	0		2	0	3	0	0.92	30.32	0	0	0	ő	ő
540	tegcegtaca	nil	tegeegtaca	no match	nil	nil	nil	0	0	Û		2	0	3	0	0	23.33	0	0	0	0	0
541	tetetetgttgteegte	NM 001039147	Morf411	ambiguousgene	nil	nil	nil	0	0	0		2	0	3	0	1.84	25.66	0.67	0	0	0	1,05
542	tetgeceteteaggeet	nil	TCTGCCCTCT	multiple	nil	nil	nil	0	0	0	0	0		7	13.39	21.16	37.32	41.65	16.16	10.17	36.265	45.0475
543	tetgetaaagaaaagga	NM_010439	HMGB1	ambiguousgene	nil	nil	nil	0	2	0	0	0	0	2	37.8	1.84	4.67	15.66	41.54	76.31	28.76	6.98
544	tetgttagetatteata	NM_145556	Tardbp	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	1	12.6	12.88	14	0	9.23	10.17	0.725	2,3325
545	tettaatgaagtttgaa	NM_013506	Eif4a2	ambiguousgene	nil	nil	nil	0	0	1	0	0	0	7	20.48	96.62	27.99	42.65	25.39	10.17	33.67	47.51
546	toctotoaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	nil	TGCTGTGAAA	multiple	nil	nil	nil	0		0	0	0	0	7	14,95	33.13	23.33	40.98	9,23	12.72	16.405	57.045
547	tggaggetee	nil	TGGAGGCTCC	multiple	nil	nil	nil	0	0	0	2	0	2	6	62.22	34.05	7	0	60,01	58.5	0	0
548	tggatcaagt	nil	TGGATCAAGT	multiple	nil	nil	nil	0	0	0	0	2	0	3	5.51	0	14	0	11.54	5,09	0	0
549	tgtactcaataaacgac	nil	TGTACTCAAT	multiple	nil	nil	nil	0	0		0	2	2	5	114.2	212.57	88.64	16.33	120.02	104.29	12.145	18.295

550	tgtagtgtaacaaaggt	NM_009098	Rps8	ambiguousgene	nil	nil	nil	0	0	(Taxin)	0	0	0	5	95.3	388.33	97.97	93.96	96.94	58.5	38.465	124.025
551	tgtataaaaaaaaaaaa	nil	TGTATAAAAA	multiple	nil	nil	nil	0	0		1	2	0	5	33.87	104.9	109.64	26.99	46.16	33.07	16.62	34.4775
552	tgtgccaagtgtgtccg	NM_026724	Rp134	ambiguousgene	nil	nil	nil	0	0	0	0	2	0	5	88.21	92.94	74.65	17,99	64.62	30.52	11.635	22.49
553	tgtgtcaaccagtgtca	nil	TGTGTCAACC	multiple	nil	nil	nil	0	0	0	0	0	1	7	25.99	31.29	34.99	77.3	23.08	20.35	68.515	82.5075
554	tgtgttgagagettete	nil	TGTGTTGAGAGCTTCTC	multiple	nil	nil	nil		0	0	0	0	0	1	0.79	74.54	0	0	2.31	43.24	4.77	0.5725
555	ttcagctcgagcgccaa	NM_011300	Rps7	ambiguousgene	nil	nil	nil	0	0	0	0	2	0	5	65.37	48.77	74.65	12	78.47	43.24	10,995	11.9775
556	tteccgtaca	nil	ttcccgtaca	no match	nil	nil	nil	0	0	0	0	2	0	3	1.58	3.68	16.33	0	4.62	0	0	0
557	ttcctattaa	níl	ttcctattaa	no match	nil	nil	nil	0	0	0		2	0	3	2.36	0	34.99	0	0	5.09	0	0
558	ttgagaatgataactet	nil	TTGAGAATGATAACTCT	multiple	nil	nil	nil	0	0	0	0	0	2	1	7.88	10.12	0	0	6.92	5.09	0.94	0,8075
559	tttctgtatgttaaata	nil	TTTCTGTATG	multiple	nil	nil	nil	0	0	0	0	2	0	6	20.48	22.09	27.99	2.67	25.39	35.61	3.835	2.11
560	tttgttaattotaaatt	NM_021510	Hnrnphl	ambiguousgene	nil	nil	nil	0	0	0	0	2	0	7	33.08	25.77	37.32	6.33	34.62	53.42	6.14	6.64
561	tttttggtgtgottata	NM_024173	Atp6v1g1	ambiguousgene	nil	nil	nil	0	0	0	0	0	2	7	20.48	33,13	18,66	6	23.08	10.17	5,205	6.17



A-4 Additional data file 3

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Functional annotations clustering analysis using DAVID.

Original version of this data file is accessible <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s3.xls</u>.

- **Note 1** Only GeneOntology databases were considered in the functional annotation clustering analysis.
- **Note 2** Functional clustering was performed using high stringency classification with a kappa similarity threshold of 0.85 and a minimum term overlap of 3. Classification was carried out using a multiple linkage threshold of 0.5 with both numbers of initial and final group members set to 3.
- **Note 3** A GO term was considered statistically significant when the computed p value was <0.05.
- **Note 4** Only functional group with equal or more than 3 statistically significant GO terms are shown here.
- **Note 5** Total number of DETs from embryonic-specific gene clusters (1, 5 and 6) mapped to DAVID ID = 127.
- **Note 6** Total number of DETs from adult-specific gene clusters (4, 8 and 10) mapped to DAVID ID = 113.
- **Note 7** Total number of DETs from gene-switching gene clusters (2 and 7) mapped to DAVID ID = 118.

EMBRYONIC-SPECIFIC GENE CLUSTERS: 1, 5 and 6

Functional Group 1	Median: 9.82E-14	Geo: 9.01E-14	Rps8, Rpl2 Mapt, Actb	2, Rps24, Rp ,	s4x, Rps9, Rps27, Rps17, Rps28, Rpl32, Rpl13, Rpl8, Rps15, Rps7,	RpI37a, Rp	14, RpI34, F	pl23a, Rpl1	8a, Ppil1, Hnrnpa1	, Hnrnpc, Ls	m5, Uchl1,	Tmsb4x,
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_ALL	GO:0005830~cytosolic ribosome (sensu Eukaryota)	14	11.02%	5.53E-18	Rps8, Rpl22, Rps24, Rps4x, Rps9, Rps27, Rps17, Rps28, Rpl32, Rpl13, Rpl8, Rps15, Rps7, Rpl37a,	105	50	15845	42.25333333	4.34E-15	4.34E-15	8.47E-15
GOTERM_MF_ALL	GO:0003735~structural constituent of ribosome	18	14.17%	4.63E-15	Rps8, Rpl22, Rps24, Rps4x, Rps9, Rps27, Rpl4, Rpl34, Rps17, Rps28, Rpl32, Rpl23a, Rpl13, Rpl8, Rps15, Rpl18a, Rps7, Rpl37a,	109	186	16377	14.54010062	1.26E-11	1.26E-11	8.30E-12
GOTERM_CC_ALL	GO:0005840~ribosome	18	14.17%	9.90E-15	Rps8, Rpl22, Rps24, Rps4x, Rps9, Rps27, Rpl4, Rpl34, Rps17, Rps28, Rpl32, Rpl23a, Rpl13, Rpl8, Rps15, Rpl18a, Rps7, Rpl37a,	105	196	15845	13.85860058	7.75E-12	3.87E-12	1.51E-11
GOTERM_CC_ALL	GO:0044445~cytosolic part	14	11.02%	1.87E-13	Rps8, Rpl22, Rps24, Rps4x, Rps9, Rps27, Rps17, Rps28, Rpl32, Rpl13, Rpl8, Rps15, Rps7, Rpl37a,	105	106	15845	19.93081761	1.46E-10	2.44E-11	2.86E-10
GOTERM_CC_ALL	GO:0030529~ribonucleoprotein complex	22	17.32%	4.67E-12	Ppi11, Rps8, Rpl22, Rps24, Rps4x, Hnmpa1, Rps9, Hnmpc, Lsm5, Rps27, Rpl4, Rpl34, Rps28, Rps17, Rpl32, Rpl23a, Rpl13, Rpl8, Rps15, Rpl18a, Rps7, Rpl37a,	105	483	15845	6.873508824	3.66E-09	5.23E-10	7.14E-09
GOTERM_CC_ALL	GO:0005829~cytosol	18	14.17%	2.43E-09	Rps8, Rpl22, Uchl1, Rps24, Rps4x, Tmsb4x, Rps9, Rps27, Rps28, Rps17, Rpl32, Mapt, Rpl13, Rpl8, Rps15, Actb, Rps7, Rpl37a,	105	427	15845	6.361324858	1.91E-06	1.91E-07	3.72E-06

Functional Group 2	Median: 2.12E-7	Geo: 1.51E-7	RpI22, Ptn	ns, Rps24, Rµ	os4x, Rps9, Eif2s3x, Rps27, Rpl4, Rpl34, Tia1, Rps28, Rps17, Rpl32	, Rpl23a, Rp	ol13, Rpl8, F	Rps15, Rpl1	8a, Rps7, Eef1b2,	Rpl37a, Gpi1	, Impdh2, N	lat2a,
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0006412~translation	21	16.54%	4.64E-10	Rpl22, Ptms, Rps24, Rps4x, Rps9, Eif2s3x, Rps27, Rpl4, Rpl34, Tia1, Rps28, Rps17, Rpl32, Rpl23a, Rpl13, Rpl8, Rps15, Rpl18a, Rps7, Eef1b2, Rpl37a,	108	510	14977	5.710185185	2.41E-06	2.41E-06	8.86E-07
GOTERM_BP_ALL	GO:0009059~macromolecule biosynthetic process	22	17.32%	6.85E-08	Rpl22, Ptms, Rps24, Rps4x, Rps9, Gpi1, Eif2s3x, Rps27, Rpl4, Rpl34, Tia1, Rps28, Rps17, Rpl32, Rpl23a, Rpl13, Rpl8, Rps15, Rpl18a, Rps7, Eef1b2, Rpl37a,	108	754	14977	4.046247176	3.55E-04	1.78E-04	1.31E-04
GOTERM_BP_ALL	GO:0044249~cellular biosynthetic process	24	18.90%	3.55E-07	Rpl22, Ptms, Rps24, Rps4x, Rps9, Gpi1, Impdh2, Eif2s3x, Rps27, Rpl4, Rpl34, Tia1, Rps28, Rps17, Mat2a, Rpl32, Rpl23a, Rpl13, Rpl8, Rps15, Rpl18a, Rps7, Eef1b2, Rpl37a,	108	985	14977	3.378905809	0.0018425	4.61E-04	6.79E-04
GOTERM_BP_ALL	GO:0009058~biosynthetic process	24	18.90%	4.57E-05	Rpl22, Ptms, Rps24, Rps4x, Rps9, Gpi1, Impdh2, Ett2s3x, Rps27, Rpl4, Rpl34, Tia1, Rps28, Rps17, Mat2a, Rpl32, Rpl23a, Rpl13, Rpl8, Rps15, Rpl18a, Rps7, Eef1b2, Rpl37a,	108	1318	14977	2.525206542	0.2111883	0.016802	0.087259

Eunctional Group 3	Median: 2.13E.6	Geo:	Rpl22, Uc	hl1, Ptms, Rp	s24, Mapk6, Rps4x, Rps9, Tubb3, Eif2s3x, Rpl4, Cfl1, Ubc, Ptprz1, F	ps28, Rps1	7, Tubb5, F	RpI32, Ubtd.	2, Arpc5, Rpl13, Rp	ol8, Prkcn, N	lex3b, Btg1	, Rpl18a,
T directorial Group o	Median. 2.15E-0	2.53E-6	Cdk4, Rps	s7, Eef1b2, Pp	uil1, Sbk1, Ezh2, Tubb2b, Stmn1, Rps27, Rpl34, Tia1, Tuba1a, Als2ci	[.] 2, Rpl23a, I	Mapt, Wsb1	l, Cd24a, Rr	1538, Rps15, Rpl37	a,		
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0044267~cellular protein metabolic process	45	35.43%	1.46E-06	Rpl22, Uchl1, Ptms, Rps24, Mapk6, Rps4x, Rps9, Tubb3, Eif2s3x, Rpl4, Cf11, Ubc, Ptpr21, Rps28, Rps17, Tubb5, Rpl32, Ubtd2, Arpc5, Rpl13, Rpl8, Prkcn, Mex3b, Btg1, Rpl18a, Cdk4, Rps7, Eef1b2, Ppil1, Sbk1, Ezh2, Tubb2b, Stmn1, Rps27, Rpl34, Tia1, Tuba1a, Als2cr2, Rpl23a, Mapt, Wsb1, Cd24a, Rnf38, Rps15, Rpl37a,	108	3123	14977	1.998212189	0.007557	9.48E-04	0.002791
GOTERM_BP_ALL	GO:0044260~cellular macromolecule metabolic process	45	35.43%	2.13E-06	RpI22, Uchi1, Ptms, Rps24, Mapk6, Rps4x, Rps9, Tubb3, Eif2s3x, RpI4, Cf11, Ubc, Ptpr21, Rps28, Rps17, Tubb5, RpI32, Ubtd2, Arpc5, RpI13, RpI8, Prkcn, Mex3b, Btg1, RpI18a, Cdk4, Rps7, Eef1b2, Ppi11, Sbk1, Ezh2, Tubb2b, Stmn1, Rps27, RpI34, Tia1, Tuba1a, Als2cr2, RpI23a, Mapt, Wsb1, Cd24a, Rnf38, Rps15, RpI37a,	108	3165	14977	1.971695629	0.0109988	0.001228	0.00407
GOTERM_BP_ALL	GO:0019538~protein metabolic process	45	35.43%	5.18E-06	RpI22, Uchl1, Ptms, Rps24, Mapk6, Rps4x, Rps9, Tubb3, Eif2s3x, RpI4, Cf11, Ubc, Ptprz1, Rps28, Rps17, Tubb5, RpI32, Ubtd2, Arpc5, RpI13, RpI8, Prkcn, Mex3b, Btg1, RpI18a, Cdk4, Rps7, Eef1b2, Ppil1, Sbk1, Ezh2, Tubb2b, Stmn1, Rps27, RpI34, Tia1, Tuba1a, Als2cr2, RpI23a, Mapt, Wsb1, Cd24a, Rnf38, Rps15, RpI37a,	108	3268	14977	1.909552224	0.0265473	0.002687	0.009901

Functional Group 4	Median: 3.16E-4	Geo: 4.29E-4	Ptprz1, Uc	hl1, Cdkn1c,	Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Dcx, Cfl1, Igfbpl1, Als2d	er2, Btg1, Wi	nt7b, Vezf1,	Mycn,				
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0048666~neuron	10	7.87%	5.50E-05	Ptprz1, Uchl1, Cdkn1c, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5,	108	240	14977	5.77816358	0.2483063	0.017681	0.104979
	development				Dcx,							
GOTERM_BP_ALL	GO:0031175~neurite development	9	7.09%	1.43E-04	Ptprz1, Uchl1, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Dcx,	108	213	14977	5.859546166	0.5245989	0.042798	0.273262
GOTERM_BP_ALL	GO:0007409~axonogenesis	8	6.30%	2.16E-04	Ptprz1, Uchl1, Robo1, Chl1, Mapt, Stmn1, Dpysl5, Dcx,	108	170	14977	6.525925926	0.6739078	0.057272	0.411512
GOTERM_BP_ALL	GO:0032990~cell part morphogenesis	10	7.87%	2.75E-04	Ptprz1, Uchl1, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Cfl1, Dcx,	108	297	14977	4.669223095	0.7606276	0.065817	0.524747

GOTERM_BP_ALL	GO:0048858~cell projection morphogenesis	10	7.87%	2.75E-04	Ptprz1, Uchl1, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Cfl1, Dcx,	108	297	14977	4.669223095	0.7606276	0.065817	0.524747
GOTERM_BP_ALL	GO:0030030~cell projection organization and biogenesis	10	7.87%	2.75E-04	Ptprz1, Uchl1, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Cfl1, Dcx,	108	297	14977	4.669223095	0.7606276	0.065817	0.524747
GOTERM_BP_ALL	GO:0048667~neuron morphogenesis during differentiation	8	6.30%	3.16E-04	Ptprz1, Uchl1, Robo1, Chl1, Mapt, Stmn1, Dpysl5, Dcx,	108	181	14977	6.129322693	0.8065873	0.06894	0.602758
GOTERM_BP_ALL	GO:0048812~neurite morphogenesis	8	6.30%	3.16E-04	Ptprz1, Uchl1, Robo1, Chl1, Mapt, Stmn1, Dpysl5, Dcx,	108	181	14977	6.129322693	0.8065873	0.06894	0.602758
GOTERM_BP_ALL	GO:0030182~neuron differentiation	10	7.87%	3.27E-04	Ptprz1, Uchl1, Cdkn1c, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Dcx,	108	304	14977	4.56170809	0.8167392	0.065622	0.622477
GOTERM_BP_ALL	GO:0000902~cell morphogenesis	13	10.24%	4.04E-04	Uchl1, Stmn1, Dcx, Igfbpl1, Cfl1, Ptprz1, Robo1, Als2cr2, Chl1, Mapt, Cd24a, Dpysl5, Btg1,	108	531	14977	3.395079166	0.8770696	0.077456	0.768391
GOTERM_BP_ALL	GO:0032989~cellular structure morphogenesis	13	10.24%	4.04E-04	Uchl1, Stmn1, Dcx, Igfbpl1, Cfl1, Ptprz1, Robo1, Als2cr2, Chl1, Mapt, Cd24a, Dpysl5, Btg1,	108	531	14977	3.395079166	0.8770696	0.077456	0.768391
GOTERM_BP_ALL	GO:0000904~cellular morphogenesis during differentiation	8	6.30%	6.48E-04	Ptprz1, Uchl1, Robo1, Chl1, Mapt, Stmn1, Dpysl5, Dcx,	108	204	14977	5.438271605	0.9654702	0.113267	1.230992
GOTERM_BP_ALL	GO:0048699~generation of neurons	10	7.87%	8.13E-04	Ptprz1, Uchl1, Cdkn1c, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Dcx,	108	345	14977	4.019592056	0.9853443	0.135512	1.541984
GOTERM_BP_ALL	GO:0022008~neurogenesis	10	7.87%	0.00140287	Ptprz1, Uchl1, Cdkn1c, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Dcx,	108	373	14977	3.717853242	0.9993169	0.187997	2.646558
GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	16	12.60%	0.02198447	Uchl1, Stmn1, Cfl1, Dcx, Igfbpl1, Ptprz1, Wnt7b, Robo1, Als2cr2, Chl1, Mapt, Vezf1, Cd24a, Btg1, Dpysl5, Mycn,	108	1191	14977	1.862984731	1	0.918655	34.6049

Functional Group 5	Median: 8 95E-4	Geo:	Ptms, Rps	24, Rps4x, So	ox4, Hnrnpa1, Tubb3, Gpi1, Eif2s3x, Klf3, Rbm25, Ubc, Tubb5, Rps	17, Rps28, Io	dh2, H2afy,	Arpc5, Rpl	8, Prkcn, Neurod1,	Mycn, Cdk4	, Ppil1, Tarc	dbp,
r unocional oroup o		0.0012	Tubb2b, S	tmn1, Rpl34,	Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, M	apk6, Rps9,	Hnrnpc, Rp	014, Cfl1, Pt	prz1, Rpl32, Ubtd2	Rpl13, Mex	3b, Btg1, Po	cna,
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0043170~macromolecule metabolic process	65	51.18%	1.55E-04	Ptms, Rps24, Rps4x, Sox4, Hnrnpa1, Tubb3, Gpi1, Eif2s3x, Klf3, Rbm25, Ubc, Tubb5, Rps17, Rps28, Idh2, H2afy, Arpc5, Rpl8, Prkcn, Neurod1, Mycn, Cdk4, Ppi11, Tardbp, Tubb2b, Stmn1, Rpl34, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uch11, Mapk6, Rps9, Hnrnpc, Rpl4, Cf11, Ptprz1, Rpl32, Ubtd2, Rpl13, Mex3b, Btg1, Pcna, Rpl18a, Rps7, Eef1b2, Ybx1, Cdkn1c, Sbk1, Mcm7, Sox12, Ezh2, Lsm5, Rps27, Tia1, Tuba1a, Wsb1, Cd24a, Sox11, Rps15,	108	6299	14977	1.431010507	0.5518833	0.043615	0.294951
GOTERM_BP_ALL	GO:0044238~primary metabolic process	69	54.33%	8.93E-04	Ptms, Rps24, Rps4x, Sox4, Hnrnpa1, Tubb3, Gpi1, Eif2s3x, Klf3, Rbm25, Ubc, Tubb5, Rps17, Rps28, Idh2, H2afy, Arpc5, Rpl8, Prkcn, Mycn, Neurod1, Cdk4, Ppi1, Tardbp, Tubb2b, Stmn1, Rpl34, Ppp1r10, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, Mapk6, Ak1, Rps9, Hnrnpc, Impdh2, Rpl4, Cfl1, Ptpr21, Rpl32, Ubtd2, Rpl13, Mex3b, Btg1, Pcna, Rpl18a, Rps7, Eef1b2, Ybx1, Cdkn1c, Sbk1, Mcm7, Sox12, Ezh2, Lsm5, Rps27, Tia1, Tuba1a, Mat2a, Wsb1, Cd24a, Sox11, Rps15,	108	7204	14977	1.328239713	0.9903202	0.143234	1.692153
GOTERM_BP_ALL	GO:0044237~cellular metabolic process	69	54.33%	8.97E-04	Ptms, Rps24, Rps4x, Sox4, Hnrnpa1, Tubb3, Gpi1, Eif2s3x, Klf3, Rbm25, Ubc, Tubb5, Rps17, Rps28, Idh2, H2afy, Arpc5, Rpl8, Prkcn, Mycn, Neurod1, Cdk4, Ppi11, Tardbp, Tubb2b, Stmn1, Rpl34, Ppp1r10, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, Mapk6, Ak1, Rps9, Hnrnpc, Impdh2, Rpl4, Cfl1, Ptpr21, Rpl32, Ubtd2, Rpl13, Mex3b, Btg1, Pcna, Rpl18a, Rps7, Eef1b2, Ybx1, Cdkn1c, Sbk1, Mcm7, Sox12, Ezh2, Lsm5, Rps27, Tia1, Tuba1a, Mat2a, Wsb1, Cd24a, Sox11, Rps15,	108	7205	14977	1.328055363	0.9905298	0.139559	1.700072
GOTERM_BP_ALL	GO:0008152~metabolic process	70	55.12%	0.01491178	Ptms, Rps24, Rps4x, Sox4, Hnrnpa1, Tubb3, Gpi1, Eif2s3x, Klf3, Rbm25, Ubc, Tubb5, Rps17, Rps28, Idh2, H2afy, Arpc5, Rpl8, Prkcn, Mycn, Neurod1, Cdk4, Ppi1, Tardbp, Tubb2b, Stmn1, Rpl34, Ppp1r10, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, Mapk6, Ak1, Rps9, Hnrnpc, Impdh2, Rpl4, Cfl1, Ptprz1, Rpl32, Ubtd2, Rpl13, Mex3b, Btg1, Pcna, Rpl18a, Rps7, Eef1b2, Ybx1, Cdkn1c, Sbk1, Mcm7, Sox12, Ezh2, Lsm5, Rps27, Tia1, Tuba1a, Mat2a, Wsb1, Cd24a, Cox6c, Sox11, Rps15,	108	8036	14977	1.207978449	1	0.843901	24.95266

Functional Group 6	Median: 0.0012	Geo: 0.0020	Tmsb4x, R	obo1, Chl1, A	rpc5, Cd24a, Btg1, Stmn1, Dpysl5, Cfl1, Dcx,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0051674~localization of cell	10	7.87%	0.00118437	Tmsb4x, Robo1, Chl1, Arpc5, Cd24a, Btg1, Stmn1, Dpysl5, Cfl1, Dcx,	108	364	14977	3.809778185	0.9978727	0.165538	2.238773
GOTERM_BP_ALL	GO:0006928~cell motility	10	7.87%	0.00118437	Tmsb4x, Robo1, Chl1, Arpc5, Cd24a, Btg1, Stmn1, Dpysl5, Cfl1, Dcx,	108	364	14977	3.809778185	0.9978727	0.165538	2.238773
GOTERM_BP_ALL	GO:0016477~cell migration	8	6.30%	0.00592416	Tmsb4x, Robo1, Chl1, Cd24a, Btg1, Dpysl5, Cfl1, Dcx,	108	302	14977	3.673534462	1	0.546617	10.73173

Functional Group 7	Median: 0.0351	Geo: 0.0099	Tubb5, Gn	g2, Tubb3, G	nb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a, Mcm7,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_ALL	GO:0003924~GTPase activity	8	6.30%	6.58E-05	Tubb5, Gng2, Tubb3, Gnb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	152	16377	7.907774022	0.1630826	0.03498	0.117077
GOTERM_MF_ALL	GO:0017111~nucleoside- triphosphatase activity	9	7.09%	0.02820823	Tubb5, Gng2, Mcm7, Tubb3, Gnb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	547	16377	2.472082921	1	0.992073	39.90837
GOTERM_MF_ALL	GO:0016462~pyrophosphatase activity	9	7.09%	0.0350734	Tubb5, Gng2, Mcm7, Tubb3, Gnb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	571	16377	2.368177509	1	0.995324	47.03224
GOTERM_MF_ALL	GO:0016818~hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	9	7.09%	0.03663521	Tubb5, Gng2, Mcm7, Tubb3, Gnb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	576	16377	2.347620413	1	0.995076	48.53764
GOTERM_MF_ALL	GO:0016817~hydrolase activity, acting on acid anhydrides	9	7.09%	0.03890012	Tubb5, Gng2, Mcm7, Tubb3, Gnb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	583	16377	2.319432861	1	0.995329	50.64915

Functional Group 8	Median: 0.0748	Geo: 0.0130	Tubb5, Gn	g2, Tubb3, G	nb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_ALL	GO:0003924~GTPase activity	8	6.30%	6.58E-05	Tubb5, Gng2, Tubb3, Gnb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	152	16377	7.907774022	0.1630826	0.03498	0.117077
GOTERM_MF_ALL	GO:0005525~GTP binding	6	4.72%	0.07153823	Tubb5, Tubb3, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	336	16377	2.682994758	1	0.999838	73.31744
GOTERM_MF_ALL	GO:0032561~guanyl ribonucleotide binding	6	4.72%	0.07810209	Tubb5, Tubb3, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	345	16377	2.61300359	1	0.999895	76.48283
GOTERM_MF_ALL	GO:0019001~guanyl nucleotide binding	6	4.72%	0.07885095	Tubb5, Tubb3, Tubb2b, Eif2s3x, Gbp6, Tuba1a,	109	346	16377	2.605451556	1	0.999862	76.82054

Functional Group 9	Median: 0.0450	Geo: 0.0537	Ppil1, Hnri	npa1, Hnrnpc, Lsm5, Rbm25, Ybx1,							
Category	Term	Count	%	PValue Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0006397~mRNA processing	6	4.72%	0.02795747 Ppil1, Hnrnpa1, Hnrnpc, Lsm5, Rbm25, Ybx1,	108	238	14977	3.496031746	1	0.947369	41.82802
GOTERM_BP_ALL	GO:0016071~mRNA metabolic process	6	4.72%	0.04486508 Ppil1, Hnrnpa1, Hnrnpc, Lsm5, Rbm25, Ybx1,	108	271	14977	3.070315703	1	0.982393	58.39791
GOTERM_BP_ALL	GO:0008380~RNA splicing	5	3.94%	0.04505871 Ppil1, Hnrnpa1, Hnrnpc, Lsm5, Ybx1,	108	187	14977	3.707912458	1	0.981494	58.55875
GOTERM_BP_ALL	GO:0006396~RNA processing	6	4.72%	0.14700059 Ppil1, Hnrnpa1, Hnrnpc, Lsm5, Rbm25, Ybx1,	108	390	14977	2.133475783	1	0.999994	95.20596

ADULT-SPECIFIC GENE CLUSTERS: 4, 8 and 10

Functional Group 1	Median: 1.35E-6	Geo: 7.52E-5	Apoe, Sna	p25, Clstn1,	Mbp, Ppp3ca, Camk2a, Lynx1, Digap1, Gabra1, Sncb, Syn2, Pip1, Gj	a1, Gng13,	Atp1a1, Mt	tap1a,				
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0019226~transmission of nerve impulse	12	10.62%	2.14E-07	Apoe, Snap25, Clstn1, Mbp, Ppp3ca, Camk2a, Lynx1, Dlgap1, Gabra1, Sncb, Syn2, Plp1,	87	254	14977	8.133043714	0.001111	0.001111	4.09E-04
GOTERM_BP_ALL	GO:0007268~synaptic transmission	11	9.73%	3.47E-07	Apoe, Snap25, Clstn1, Ppp3ca, Camk2a, Lynx1, Dlgap1, Gabra1, Sncb, Syn2, Plp1,	87	211	14977	8.974614588	0.0018	9.00E-04	6.63E-04
GOTERM_BP_ALL	GO:0007267~cell-cell signaling	13	11.50%	1.35E-06	Snap25, Apoe, Camk2a, Ppp3ca, Lynx1, Gja1, Sncb, Syn2, Mbp, Clstn1, Dlgap1, Gabra1, Plp1,	87	372	14977	6.01597454	0.006986	0.002334	0.00258
GOTERM_BP_ALL	GO:0003008~system process	16	14.16%	0.12136378	Apoe, Snap25, Gng13, Camk2a, Ppp3ca, Lynx1, Gja1, Atp1a1, Sncb, Syn2, Mbp, Clstn1, Dlgap1, Gabra1, Plp1, Mtap1a,	87	1894	14977	1.454271808	1	0.999994	91.55863
GOTERM_BP_ALL	GO:0050877~neurological system process	14	12.39%	0.1977012	Snap25, Apoe, Gng13, Camk2a, Ppp3ca, Lynx1, Sncb, Syn2, Mbp, Clstn1, Dlgap1, Gabra1, Plp1, Mtap1a,	87	1745	14977	1.381141521	1	1	98.51324

Functional Group 2	Median: 0.0025	Geo: 0.0016	Slc1a3, So Laptm4b,	cg2, Atp1b2, Klc2, Ncald,	Tuba4a, Mlc1, Thy1, Car2, Ptgds, Camk2n1, Syt13, Apoe, Itpr1, Syng Cck, Pacsin1, Kcnj3, Trf, Gabra1, Arf3,	r1, Snap25	i, Camk2a, I	Ppp3ca, Gri	a3, Gja1, Atp2b1,	Atp1a1, Sir	rpa, Nsf, Sy	n2,
Category	Term	Count	%	PValue ■	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0051179~localization	32	28.32%	4.48E-04	SIc1a3, Scg2, Atp1b2, Tuba4a, MIc1, Thy1, Car2, Ptgds, Camk2n1, Syt13, Apoe, Itpr1, Syngr1, Snap25, Camk2a, Ppp3ca, Gria3, Gja1, Atp2b1, Atp1a1, Sirpa, Nsf, Syn2, Laptm4b, KIc2, Ncald, Cck, Pacsin1, Kcnj3, Trf, Gabra1, Arf3,	87	3021	14977	1.823496064	0.902294	0.440912	0.852219
GOTERM_BP_ALL	GO:0006810~transport	27	23.89%	0.00248859	Sic1a3, Atp1b2, Tuba4a, Mic1, Car2, Ptgds, Syt13, Itpr1, Syngr1, 9 Snap25, Apoe, Camk2a, Ppp3ca, Gria3, Atp2b1, Atp1a1, Sirpa, Nsf, Syn2, Laptm4b, Kic2, Ncald, Pacsin1, Kcnj3, Trf, Gabra1, Arf3,	87	2613	14977	1.778811513	0.999998	0.924783	4.649106
GOTERM_BP_ALL	GO:0051234~establishment of localization	27	23.89%	0.00365748	Sic1a3, Atp1b2, Tuba4a, Mic1, Car2, Ptgds, Syt13, Itpr1, Syngr1, 3 Snap25, Apoe, Camk2a, Ppp3ca, Gria3, Atp2b1, Atp1a1, Sirpa, Nsf, Syn2, Laptm4b, Kic2, Ncald, Pacsin1, Kcnj3, Trf, Gabra1, Arf3,	87	2685	14977	1.731111539	1	0.958028	6.761382

Functional Group 3	Median: 0.0122	Geo: 0.0125	Apoe, Scg	g2, Lynx1, Ch	st1, Sirpa, Tmem59I, Epdr1, Ptprn, Ckmt1, Dkk3, Cx3cl1, Negr1, Cls	tn1, Ptgds,	Fkbp2, Cck	, Nptxr, Trf	, Gabra1, Cyp46a	1, Vgf, Syt1	3, Clu, Olfn	n1,
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_ALL	GO:0005576~extracellular region	24	21.24%	0.00697976	Apoe, Scg2, Lynx1, Chst1, Sirpa, Tmem59I, Epdr1, Ptprn, Ckmt1, Dkk3, Cx3cl1, Negr1, Clstn1, Ptgds, Fkbp2, Cck, Nptxr, Trf, Gabra1, Cyp46a1, Vgf, Syt13, Clu, Olfm1,	92	2375	15845	1.740411899	0.995878	0.422549	10.16808
GOTERM_CC_ALL	GO:0005615~extracellular space	21	18.58%	0.01219032	Apoe, Scg2, Lynx1, Chst1, Sirpa, Tmem59I, Epdr1, Ptpm, Ckmt1, Dkk3, Cx3c11, Negr1, Fkbp2, Cck, Nptxr, Trf, Gabra1, Cyp46a1, Syt13, Clu, Olfm1,	92	2064	15845	1.752322422	0.999933	0.522737	17.11964
GOTERM_CC_ALL	GO:0044421~extracellular region part	21	18.58%	0.0226895	Apoe, Scg2, Lynx1, Chst1, Sirpa, Tmem59I, Epdr1, Ptprn, Ckmt1, Dkk3, Cx3c1, Negr1, Fkbp2, Cck, Nptxr, Trf, Gabra1, Cyp46a1, Syt13, Clu, Olfm1,	92	2195	15845	1.647741904	1	0.675215	29.62707

Functional Group 4	Median: 0.0140	Geo: 0.0198	Syngr1, N	cald, Pacsin1	, Syt13, Syn2, Trf,							
Category	Term	Count	%	PValue ■	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_ALL	GO:0030135~coated vesicle	5	4.42%	0.00581693	Syngr1, Ncald, Pacsin1, Syt13, Syn2,	92	125	15845	6.889130435	0.989681	0.479725	8.544083
GOTERM_CC_ALL	GO:0016023~cytoplasmic membrane-bound vesicle	6	5.31%	0.01366611	Syngr1, Ncald, Pacsin1, Trf, Syt13, Syn2,	92	246	15845	4.20068929	0.999979	0.537255	18.99515
GOTERM_CC_ALL	GO:0031988~membrane-bound vesicle	6	5.31%	0.0159822	Syngr1, Ncald, Pacsin1, Trf, Syt13, Syn2,	92	256	15845	4.036599864	0.999997	0.569188	21.85877
GOTERM CC ALL	GO:0031410~cytoplasmic vesicle	6	5.31%	0.04704287	Syngr1, Ncald, Pacsin1, Trf, Syt13, Syn2,	92	342	15845	3.021548436	1	0.792797	52.17797
GOTERM_CC_ALL	GO:0031982~vesicle	6	5.31%	0.05153873	Syngr1, Ncald, Pacsin1, Trf, Syt13, Syn2,	92	351	15845	2.944072835	1	0.809746	55.51779

Functional Group 5	Median: 0.0242	Geo: 0.0238	Apoe, Cls	tn1, Trf, Atp1	a1, Thy1, 2810407C02rik, Mbp, Plp1,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM BP ALL	GO:0030003~cellular cation homeostasis	5	4.42%	0.00547871	Apoe, Clstn1, Trf, Atp1a1, Thy1,	87	123	14977	6.997944117	1	0.983004	9.964335
GOTERM_BP_ALL	GO:0055080~cation homeostasis	5	4.42%	0.00579821	Apoe, Clstn1, Trf, Atp1a1, Thy1,	87	125	14977	6.885977011	1	0.97704	10.51537
GOTERM_BP_ALL	GO:0019725~cellular homeostasis	6	5.31%	0.01716587	Apoe, Clstn1, 2810407C02rik, Trf, Atp1a1, Thy1,	87	261	14977	3.957458053	1	0.997505	28.16655
GOTERM_BP_ALL	GO:0055082~cellular chemical homeostasis	5	4.42%	0.01926314	Apoe, Clstn1, Trf, Atp1a1, Thy1,	87	178	14977	4.835658014	1	0.995084	31.03934
GOTERM BP ALL	GO:0006873~cellular ion homeostasis	5	4.42%	0.01926314	Apoe, Clstn1, Trf, Atp1a1, Thy1,	87	178	14977	4.835658014	1	0.995084	31.03934

GOTERM_BP_ALL	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	4	3.54%	0.02422939	Apoe, Clstn1, Trf, Thy1,	87	108	14977	6.37590464	1	0.996938	37.41402
GOTERM_BP_ALL	GO:0055066~di-, tri-valent inorganic cation homeostasis	4	3.54%	0.02540658	Apoe, Clstn1, Trf, Thy1,	87	110	14977	6.259979101	1	0.997001	38.84098
GOTERM_BP_ALL	GO:0050801~ion homeostasis	5	4.42%	0.02805437	Apoe, Clstn1, Trf, Atp1a1, Thy1,	87	200	14977	4.303735632	1	0.997879	41.93871
GOTERM_BP_ALL	GO:0048878~chemical homeostasis	5	4.42%	0.05058167	Apoe, Clstn1, Trf, Atp1a1, Thy1,	87	242	14977	3.556806308	1	0.999874	62.906
GOTERM_BP_ALL	GO:0042592~homeostatic process	6	5.31%	0.06455195	Apoe, Clstn1, 2810407C02rik, Trf, Atp1a1, Thy1,	87	375	14977	2.754390805	1	0.999914	72.05527
GOTERM BP ALL	GO:0065008~regulation of biological quality	8	7.08%	0.12064177	Apoe, Clstn1, Mbp, 2810407C02rik, Trf, Atp1a1, Thy1, Plp1,	87	722	14977	1.907472856	1	0.999995	91.42511

Functional Group 6	Median: 0.0190	Geo: 0.0243	Camk2a, E	Eef1a2, Kalrı	n, Zfp179, Itpka, Tuba4a, Atp1a1, Atp2b1, Nsf, Nme7, Pftk1, Ckmt1, St	ept4, Syn2,	Map2k1, Cl	kb, Centg3,	Arf3,			
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_ALL	GO:0032555~purine ribonucleotide binding	18	15.93%	0.01561772	Camk2a, Eef1a2, Kalrn, Zfp179, Itpka, Tuba4a, Atp1a1, Atp2b1, Nsf, Nme7, Pftk1, Ckmt1, Sept4, Syn2, Map2k1, Ckb, Centg3, Arf3,	92	1754	16377	1.826793416	1	0.999999	24.43488
GOTERM_MF_ALL	GO:0032553~ribonucleotide binding	18	15.93%	0.01561772	Camk2a, Eef1a2, Kalrn, Zfp179, Itpka, Tuba4a, Atp1a1, Atp2b1, Nsf, Nme7, Pftk1, Ckmt1, Sept4, Syn2, Map2k1, Ckb, Centg3, Arf3,	92	1754	16377	1.826793416	1	0.999999	24.43488
GOTERM_MF_ALL	GO:0017076~purine nucleotide binding	18	15.93%	0.02236065	Camk2a, Eef1a2, Kalrn, Zfp179, Itpka, Tuba4a, Atp1a1, Atp2b1, Nsf, Nme7, Pftk1, Ckmt1, Sept4, Syn2, Map2k1, Ckb, Centg3, Arf3,	92	1826	16377	1.754762132	1	0.999963	33.13654
GOTERM_MF_ALL	GO:0000166~nucleotide binding	18	15.93%	0.0635773	Camk2a, Eef1a2, Kalrn, Zfp179, Itpka, Tuba4a, Atp1a1, Atp2b1, Nsf, Nme7, Pftk1, Ckmt1, Sept4, Syn2, Map2k1, Ckb, Centg3, Arf3,	92	2075	16377	1.544190676	1	0.999689	68.93831

Functional Group 7	Median: 0.0404	Geo: 0.0390	Gng13, Ee	ef1a2, Zfp179,	Atp1b2, Tuba4a, Atp2b1, Atp1a1, Nsf,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_ALL	GO:0017111~nucleoside-triphosphatase activity	8	7.08%	0.03251187	Gng13, Eef1a2, Zfp179, Atp1b2, Tuba4a, Atp2b1, Atp1a1, Nsf,	92	547	16377	2.603449646	1	0.999986	44.47291
GOTERM_MF_ALL	GO:0016462~pyrophosphatase activity	8	7.08%	0.03957795	Gng13, Eef1a2, Zfp179, Atp1b2, Tuba4a, Atp2b1, Atp1a1, Nsf,	92	571	16377	2.494022691	1	0.999889	51.26501
GOTERM_MF_ALL	GO:0016818~hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	8	7.08%	0.04116788	Gng13, Eef1a2, Zfp179, Atp1b2, Tuba4a, Atp2b1, Atp1a1, Nsf,	92	576	16377	2.472373188	1	0.999703	52.68121
GOTERM_MF_ALL	GO:0016817~hydrolase activity, acting on acid anhydrides	8	7.08%	0.04346338	Gng13, Eef1a2, Zfp179, Atp1b2, Tuba4a, Atp2b1, Atp1a1, Nsf,	92	583	16377	2.442687747	1	0.999454	54.65753

Functional Group 8	Median: 0.0432	Geo: 0.0420	Eef1a2, Zf	p179, Tuba4a	n, Centg3, Arf3, Sept4,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM MF ALL	GO:0005525~GTP binding	6	5.31%	0.03926778	Eef1a2, Zfp179, Tuba4a, Centg3, Arf3, Sept4,	92	336	16377	3.178765528	1	0.999947	50.9841
GOTERM_MF_ALL	GO:0032561~guanyl ribonucleotide binding	6	5.31%	0.04317176	Eef1a2, Zfp179, Tuba4a, Centg3, Arf3, Sept4,	92	345	16377	3.09584121	1	0.99965	54.41085
GOTERM_MF_ALL	GO:0019001~guanyl nucleotide binding	6	5.31%	0.04361952	Eef1a2, Zfp179, Tuba4a, Centg3, Arf3, Sept4,	92	346	16377	3.086893692	1	0.999172	54.78909

GENE-SWITCHING GENE CLUSTERS: 2 and 7

Functional Group 1	Median: 7.64E-5	Geo: 9.11E-5	Rab6b, Gn	g2, Gnb1, (Gnb2l1, Eif4a2, Rbbp4, Atp6v1g1, Tubb5, Atp9a, Ppa1, Atp5h, Atp1b1,	Nav1, Atp1	1b,					
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_ALL	GO:0016462~pyrophosphatase activity	14	11.86%	6.56E-05	Rab6b, Gng2, Gnb1, Gnb2l1, Eif4a2, Rbbp4, Atp6v1g1, Tubb5, Atp9a, Ppa1, Atp5h, Atp1b1, Nav1, Atp11b,	105	571	16377	3.824168126	0.162706	0.162706	0.116781
GOTERM_MF_ALL	GO:0016818~hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	14	11.86%	7.17E-05	Rab6b, Gng2, Gnb1, Gnb2l1, Eif4a2, Rbbp4, Atp6v1g1, Tubb5, Atp9a, Ppa1, Atp5h, Atp1b1, Nav1, Atp11b,	105	576	16377	3.790972222	0.176322	0.092433	0.127557
GOTERM_MF_ALL	GO:0016817~hydrolase activity, acting on acid anhydrides	14	11.86%	8.10E-05	Rab6b, Gng2, Gnb1, Gnb2l1, Eif4a2, Rbbp4, Atp6v1g1, Tubb5, Atp9a, Ppa1, Atp5h, Atp1b1, Nav1, Atp11b,	105	583	16377	3.745454545	0.196788	0.070441	0.14409
GOTERM_MF_ALL	GO:0017111~nucleoside-triphosphatase activity	13	11.02%	1.80E-04	Rab6b, Gng2, Gnb1, Gnb2l1, Eif4a2, Rbbp4, Tubb5, Atp9a, Atp6v1g1, Atp5h, Atp1b1, Nav1, Atp11b,	105	547	16377	3.706816401	0.38609	0.092971	0.320532

Functional Group 2	Median: 0.0064	Geo: 0.0031	Atp6v1g1,	Scamp5, S	v2a, Rph3a, Syt4, Vamp2, Map1lc3a, App,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_ALL	GO:0008021~synaptic vesicle	6	5.08%	3.46E-05	Atp6v1g1, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	59	15845	15.95401913	0.026759	0.026759	0.052951
GOTERM_CC_ALL	GO:0030136~clathrin-coated vesicle	6	5.08%	5.79E-04	Atp6v1g1, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	107	15845	8.797075969	0.36478	0.107248	0.882197
GOTERM CC ALL	GO:0030135~coated vesicle	6	5.08%	0.001168	Atp6v1g1, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	125	15845	7.53029703	0.599866	0.108183	1.772699
GOTERM_CC_ALL	GO:0031410~cytoplasmic vesicle	8	6.78%	0.005919	Atp6v1g1, Map1lc3a, App, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	342	15845	3.669735395	0.990476	0.372112	8.687098
GOTERM_CC_ALL	GO:0031982~vesicle	8	6.78%	0.006793	Atp6v1g1, Map1lc3a, App, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	351	15845	3.575639615	0.995221	0.359368	9.908603
GOTERM_CC_ALL	GO:0045202~synapse	6	5.08%	0.018	App, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	240	15845	3.922029703	0.999999	0.613018	24.27636
COTERM CC ALL	GO:0016023~cytoplasmic membrane-	6	5.00%	0.010700	Atabulat Scompt Sula Babla Sutt Vamal	101	246	15945	2 926270442	1	0.602269	26 27106
GOTERM_CC_ALL	bound vesicle	0	3.00 %	0.019799	Alpovirgi, Scamps, Svza, Rpnsa, Syl4, Vampz,	101	240	13043	3.020370442	1	0.002300	20.57 190
GOTERM_CC_ALL	GO:0031988~membrane-bound vesicle	6	5.08%	0.023052	Atp6v1g1, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	256	15845	3.676902847	1	0.617997	30.02542

Functional Group 3	Median: 0.0089	Geo: 0.0075	Eif4g2, Bz	w2, Eif1b, E	Eif4a2, Eif6,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_ALL	GO:0003743~translation initiation factor activity	5	4.24%	0.00192	Eif4g2, Bzw2, Eif1b, Eif4a2, Eif6,	105	83	16377	9.395869191	0.994474	0.57953	3.362679
GOTERM_MF_ALL	GO:0008135~translation factor activity, nucleic acid binding	5	4.24%	0.008045	Eif4g2, Bzw2, Eif1b, Eif4a2, Eif6,	105	124	16377	6.289170507	1	0.911758	13.3912
GOTERM_MF_ALL	GO:0045182~translation regulator activity	5	4.24%	0.009716	Eif4g2, Bzw2, Eif1b, Eif4a2, Eif6,	105	131	16377	5.953107961	1	0.909362	15.95165
GOTERM_BP_ALL	GO:0022618~protein-RNA complex assembly	4	3.39%	0.021278	Eif4g2, Bzw2, Eif1b, Eif6,	96	93	14977	6.710125448	1	0.988515	33.69642

Functional Group 4	Median: 0.0092	Geo:	Ube2e3, M	ap4k4, Gali	nt7, Map1lc3a, Pum2, Fbxl16, Ttl, Bzw2, Cct3, Otub1, Eif4a2, Usp16, C	tsd, Tubb5	, Cct6a, Neo	dd8, Znrf1,	Ppp1r1a, Dnajc5,	Rps18, Cp	e, Ptprs, Eif	б, Арр,
r unocionar oroup 4		0.0080	Lmtk3, Eif	1b, Skp1a, I	Rps5, Eif4g2, Enc1, Mapt, Syt4, Olfm1,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0044260~cellular macromolecule metabolic process	32	27.12%	0.005925	Ube2e3, Map4k4, Galnt7, Map1lc3a, Pum2, Fbx116, Ttl, Bzw2, Cct3, Otub1, Eif4a2, Usp16, Ctsd, Tubb5, Cct6a, Nedd8, Znf1, Ppp1r1a, Dnajc5, Rps18, Cpe, Ptprs, Eif6, App, Lmtk3, Eif1b, Skp1a, Rps5, Eif4g2, Enc1, Mapt, Syt4,	96	3165	14977	1.577356503	1	0.978863	10.73303
GOTERM_BP_ALL	GO:0044267~cellular protein metabolic process	31	26.27%	0.009192	Ube2e3, Map4k4, Galnt7, Map1lc3a, Pum2, Fbx116, Ttl, Bzw2, Cct3, Otub1, Eif4a2, Usp16, Ctsd, Tubb5, Cct6a, Nedd8, Znrf1, Dnajc5, Rps18, Cpe, Ptprs, Eif6, App, Lmtk3, Eif1b, Skp1a, Rps5, Eif4g2, Enc1, Mapt, Syt4,	96	3123	14977	1.548614447	1	0.991726	16.17488
GOTERM_BP_ALL	GO:0019538~protein metabolic process	32	27.12%	0.009544	Ube2e3, Map4k4, Galnt7, Map1lc3a, Pum2, Fbx116, Ttl, Bzw2, Cct3, Otub1, Eif4a2, Usp16, Ctsd, Tubb5, Cct6a, Nedd8, Znrf1, Dnajc5, Rps18, Cpe, Ptprs, Eif6, App, Lmtk3, Eif1b, Skp1a, Rps5, Eif4g2, Enc1, Mapt, Syt4, Olfm1,	96	3268	14977	1.527641779	1	0.989179	16.74149

Functional Group 5	Median: 0.0173	Geo: 0.0153	Map4k4, G Nedd8, Zn H2afv, Cts	alnt7, Map rf1, Atp5h, d. Cct6a, Fe	1163a, Pum2, Sox4, Hnrpdl, Bzw2, Ttl, Fads2, Fbx116, Actl6b, Rrp1, Nr Ppp1r1a, HMGB1, Hmgn1, Atpr1b, Eif6, Hpr11, Skp1a, Rps5, Ppa1, Er oxa1, Snrpe, Dnajc5, Rps18, Coe, Nduf08, Ptprs, App. Lmtk3, Eif1b, C	ne2, Bcl11a, nc1, Hmgb3, Gucv1a3, At	Eif4a2, Rb Nav1, Map o6v1q1, Eif	bp4, Usp16 t, Syt4, Olfi 4g2, Rbm9.	, Nola3, Drap1, T m1, Ube2e3, Prm	ubb5, Atp9: 2, Prdx2, N	i, Aldoc, Gli fix, Cct3, Oi	rx3, tub1,
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0008152~metabolic process	64	54.24%	0.008171	Map4k4, Galnt7, Map1Ic3a, Pum2, Sox4, Hnrpdl, Bzw2, Ttl, Fads2, Fbx116, Actl6b, Rrp1, Nme2, Bc111a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Atp9a, Aldoc, Glrx3, Nedd8, Znrf1, Atp5h, Ppp1r1a, HMGB1, Hmgn1, Atp11b, Eif6, Hprt1, Skp1a, Rps5, Ppa1, Enc1, Hmgb3, Nav1, Mapt, Syt4, Olfm1, Ube2e3, Prmt2, Prdx2, Nfix, Cct3, Otub1, H2afv, Ctsd, Cct6a, Foxg1, Snrpe, Dnajc5, Rps18, Cpe, Ndufb8, Ptbrs, App, Lmtk3, Eif1b, Gucy1a3, Atp6v1a1, Eif4a2, Rbm9,	96	8036	14977	1.242492119	1	0.991199	14.50806
GOTERM_BP_ALL	GO:0044237~cellular metabolic process	58	49.15%	0.012975	Map4k4, Galnt7, Map1lc3a, Pum2, Sox4, Hnrpdl, Bzw2, Ttl, Fads2, Fbx116, Actl6b, Rrp1, Nme2, Bc111a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Aldoc, Nedd8, Znrt1, Atp5h, Pop1r1a, HMGB1, Hmgn1, Eif6, Hprt1, Skp1a, Rps5, Enc1, Ppa1, Hmgb3, Mapt, Syt4, Ube2e3, Prdx2, Prmt2, Nfix, Cct3, Otub1, H2afv, Ctsd, Cct6a, Foxg1, Snrpe, Dnajc5, Rps18, Cpe, Ptprs, App, Lmtk3, Eif1b, Gucy1a3, Atp6v1g1, Eif4Q2, Rbm9,	96	7205	14977	1.255878441	1	0.985561	22.0822
GOTERM_BP_ALL	GO:0044238~primary metabolic process	57	48.31%	0.021632	Map4k4, Galnt7, Map1Ic3a, Pum2, Sox4, Hnrpdl, Bzw2, Ttl, Fads2, Fbx116, Actl6b, Rrp1, Nme2, Bc111a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Aldoc, Nedd8, Znrf1, Atp5h, Ppp1r1a, HMGB1, Hmgn1, Eif6, Hprt1, Skp1a, Rps5, Enc1, Hmgb3, Mapt, Syt4, Olfm1, Ube2e3, Prmt2, Nfix, Cct3, Otub1, H2afv, Ctsd, Cct6a, Foxg1, Snrpe, Dnajc5, Rps18, Cpe, Ptprs, App, Lmtk3, Eif1b, Gucy1a3, Atp6v1g1, Eif4g2, Rbm9,	96	7204	14977	1.234396689	1	0.987313	34.15309
GOTERM_BP_ALL	GO:0043170~macromolecule metabolic process	51	43.22%	0.023892	Map4k4, Galnt7, Map1Ic3a, Pum2, Sox4, Hnrpdl, Bzw2, Ttl, Fbx116, Actl6b, Rrp1, Bc111a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Aldoc, Nedd8, Ppp1r1a, Znrf1, HMGB1, Hmgn1, Eif6, Skp1a, Rps5, Enc1, Hmgb3, Mapt, Syt4, Olfm1, Ube2e3, Prmt2, Nfix, Otub1, H2afv, Cct3, Ctsd, Cct6a, Snrpe, Foxg1, Dnajc5, Rps18, Cpe, Ptprs, App, Lmtk3, Eif1b, Eif4g2, Rbm9,	96	6299	14977	1.263141967	1	0.984778	36.99872

Functional Group 6	Median: 0.0179	Geo: 0.02136	Mtap1b, T	ubb5, Ttl, N	av1, Mapt, Map1lc3a, App, Eif6,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0000226~microtubule cytoskeleton organization and biogenesis	5	4.24%	0.001587	Mtap1b, Tubb5, Ttl, Nav1, Mapt,	96	79	14977	9.874077004	0.999738	0.872739	2.988895
GOTERM CC ALL	GO:0005874~microtubule	6	5.08%	0.009834	Mtap1b, Tubb5, Map1lc3a, Ttl, Nav1, Mapt,	101	206	15845	4.569354994	0.999568	0.425026	14.04074
GOTERM_BP_ALL	GO:0007017~microtubule-based process	6	5.08%	0.013017	Mtap1b, Tubb5, App, Ttl, Nav1, Mapt,	96	220	14977	4.254829545	1	0.981715	22.14635
GOTERM_CC_ALL	GO:0015630~microtubule cytoskeleton	7	5.93%	0.022868	Mtap1b, Tubb5, Map1lc3a, App, Ttl, Nav1, Mapt,	101	348	15845	3.155656083	1	0.6349	29.82336
GOTERM CC ALL	GO:0044430~cytoskeletal part	8	6.78%	0.078838	Mtap1b, Tubb5, Map1lc3a, App, Ttl, Nav1, Mapt, Eif6,	101	589	15845	2.1308141	1	0.874673	71.55478
GOTERM_BP_ALL	GO:0007010~cytoskeleton organization and biogenesis	6	5.08%	0.254538	Mtap1b, Tubb5, App, Ttl, Nav1, Mapt,	96	537	14977	1.743133147	1	1	99.63478

Functional Group 7	Median: 0.0164	Geo: 0.0222	Atp6v1g1,	Atp9a, Atp	5h, Atp1b1, Atp11b, Reep5, Cacng4,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_ALL	GO:0042625~ATPase activity, coupled to transmembrane movement of ions	5	4.24%	0.004645	Atp6v1g1, Atp9a, Atp5h, Atp1b1, Atp11b,	105	106	16377	7.357142857	0.999997	0.792833	7.952796
GOTERM_MF_ALL	GO:0015662~ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism	4	3.39%	0.010807	Atp6v1g1, Atp9a, Atp1b1, Atp11b,	105	72	16377	8.665079365	1	0.913651	17.58512
GOTERM_MF_ALL	GO:0042626~ATPase activity, coupled to transmembrane movement of substances	5	4.24%	0.014019	Atp6v1g1, Atp9a, Atp5h, Atp1b1, Atp11b,	105	146	16377	5.34148728	1	0.947009	22.2202
GOTERM_MF_ALL	GO:0043492~ATPase activity, coupled to movement of substances	5	4.24%	0.014019	Atp6v1g1, Atp9a, Atp5h, Atp1b1, Atp11b,	105	146	16377	5.34148728	1	0.947009	22.2202
GOTERM_MF_ALL	GO:0016820~hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	5	4.24%	0.016383	Atp6v1g1, Atp9a, Atp5h, Atp1b1, Atp11b,	105	153	16377	5.097105509	1	0.938739	25.47306
GOTERM_MF_ALL	GO:0015399~primary active transmembrane transporter activity	5	4.24%	0.018983	Atp6v1g1, Atp9a, Atp5h, Atp1b1, Atp11b,	105	160	16377	4.874107143	1	0.94387	28.90283

GOTERM_MF_ALL	GO:0015405~P-P-bond-hydrolysis-driven transmembrane transporter activity	5	4.24%	0.018983	Atp6v1g1, Atp9a, Atp5h, Atp1b1, Atp11b,	105	160	16377	4.874107143	1	0.94387	28.90283
GOTERM_MF_ALL	GO:0022804~active transmembrane transporter activity	6	5.08%	0.086725	Atp6v1g1, Atp9a, Atp5h, Atp1b1, Reep5, Atp11b,	105	370	16377	2.529266409	1	0.99992	80.10512
GOTERM_BP_ALL	GO:0006812~cation transport	6	5.08%	0.258141	Atp6v1g1, Atp9a, Atp5h, Atp1b1, Cacng4, Atp11b,	96	540	14977	1.733449074	1	1	99.66707

Functional Group 8	Median: 0.0225	Geo: 0.0274	Atp6v1g1,	Hprt1, Atp5	Hprt1, Atp5h, Nme2, Gucy1a3,										
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR			
GOTERM_BP_ALL	GO:0009165~nucleotide biosynthetic process	5	4.24%	0.014568	Atp6v1g1, Hprt1, Atp5h, Nme2, Gucy1a3,	96	148	14977	5.270622185	1	0.977843	24.45033			
GOTERM_BP_ALL	GO:0006164~purine nucleotide biosynthetic process	4	3.39%	0.016271	Atp6v1g1, Hprt1, Atp5h, Nme2,	96	84	14977	7.42906746	1	0.979176	26.90709			
GOTERM_BP_ALL	GO:0006163~purine nucleotide metabolic process	4	3.39%	0.022493	Atp6v1g1, Hprt1, Atp5h, Nme2,	96	95	14977	6.568859649	1	0.985278	35.25106			
GOTERM_BP_ALL	GO:0009117~nucleotide metabolic process	5	4.24%	0.049239	Atp6v1g1, Hprt1, Atp5h, Nme2, Gucy1a3,	96	217	14977	3.594710061	1	0.997415	61.89111			
GOTERM_BP_ALL	GO:0055086~nucleobase, nucleoside and nucleotide metabolic process	5	4.24%	0.059318	Atp6v1g1, Hprt1, Atp5h, Nme2, Gucy1a3,	96	231	14977	3.376848846	1	0.998465	68.91191			

Functional Group 9	Median: 0.04189	Geo: 0.0430	Sox4, Hmg	b3, HMGB [,]	1, H2afv, Hmgn1, Zwint,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_ALL	GO:0000785~chromatin	5	4.24%	0.024851	Sox4, Hmgb3, HMGB1, H2afv, Hmgn1,	101	175	15845	4.482319661	1	0.609181	31.97302
GOTERM_CC_ALL	GO:0044427~chromosomal part	6	5.08%	0.041889	Sox4, Zwint, Hmgb3, HMGB1, H2afv, Hmgn1,	101	301	15845	3.127199763	1	0.752875	48.06149
GOTERM CC ALL	GO:0005694~chromosome	6	5.08%	0.076187	Sox4, Zwint, Hmgb3, HMGB1, H2afv, Hmgn1,	101	358	15845	2.629293656	1	0.873935	70.27549

Functional Group 10	Median: 0.0503	Geo: 0.0464	Gng2, Gnb	1, Gnb2l1,								
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_ALL	GO:0005834~heterotrimeric G-protein complex	3	2.54%	0.02392	Gng2, Gnb1, Gnb2l1,	101	38	15845	12.38535696	1	0.6129	30.97167
GOTERM_CC_ALL	GO:0019897~extrinsic to plasma membrane	3	2.54%	0.050291	Gng2, Gnb1, Gnb2l1,	101	57	15845	8.256904638	1	0.801735	54.61314
GOTERM CC ALL	GO:0019898~extrinsic to membrane	3	2.54%	0.083227	Gng2, Gnb1, Gnb2l1,	101	76	15845	6.192678478	1	0.881037	73.56049

Functional Group 11	Median: 0.0583	Geo: 0.0528	Rab6b, Sh Atp1b1, Na	13gl2, Fads2, Reep5, Hba-a1, Ywhaz, Tubb5, Atp9a, Foxg1, Nedd8, Atp5h, Cacng4, HMGB1, Atp11b, Vamp2, App, Sv2a, Rab14, Gnb2l1, Atp6v1g1, Ywhae, Scar Jav1, Rph3a, Clcn2, Elmod1, Syt4,								
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0051179~localization	28	23.73%	0.033675	Rab6b, Sh3gl2, Fads2, Reep5, Hba-a1, Ywhaz, Tubb5, Atp9a, Foxg1, Nedd8, Atp5h, Cacng4, HMGB1, Atp11b, Vamp2, App, Sv2a, Rab14, Gnb2l1, Atp6v1g1, Ywhae, Scamp5, Atp1b1, Nav1, Rph3a, Clcn2, Elmod1, Syt4,	96	3021	14977	1.445975394	1	0.990724	48.02911
GOTERM_BP_ALL	GO:0006810~transport	24	20.34%	0.058301	Rab6b, Sh3gl2, App, Fads2, Sv2a, Rab14, Reep5, Hba-a1, Ywhaz, Atp6v1g1, Tubb5, Atp9a, Ywhae, Scamp5, Atp5h, Atp1b1, Cacng4, Rph3a, HMGB1, Clcn2, Atp11b, Elmod1, Syt4, Vamp2,	96	2613	14977	1.432931496	1	0.998493	68.26332
GOTERM_BP_ALL	GO:0051234~establishment of localization	24	20.34%	0.074862	Rab6b, Sh3gl2, App, Fads2, Sv2a, Rab14, Reep5, Hba-a1, Ywhaz, Atp6v1g1, Tubb5, Atp9a, Ywhae, Scamp5, Atp5h, Atp1b1, Cacng4, Rph3a, HMGB1, Clcn2, Atp11b, Elmod1, Syt4, Vamp2,	96	2685	14977	1.394506518	1	0.998938	77.38813

Functional Group 12	Median: 0.0406	Geo: 0.0538	Mtap1b, A	op, Foxg1, I	Hprt1, Ttl, Mapt, Nav1, Ube2e3, Bai1, Gucy1a3, Eif4g2, Prdx2,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM BP ALL	GO:0031175~neurite development	6	5.08%	0.011444	Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt,	96	213	14977	4.394659624	1	0.981386	19.74035
GOTERM_BP_ALL	GO:0048666~neuron development	6	5.08%	0.018305	Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt,	96	240	14977	3.900260417	1	0.984555	29.74083
GOTERM_BP_ALL	GO:0048699~generation of neurons	7	5.93%	0.022436	Mtap1b, App, Foxg1, Hprt1, Ttl, Nav1, Mapt,	96	345	14977	3.165428744	1	0.987267	35.17987
GOTERM_BP_ALL	GO:0048667~neuron morphogenesis during differentiation	5	4.24%	0.028078	App, Foxg1, Hprt1, Ttl, Mapt,	96	181	14977	4.309680018	1	0.990156	41.96603
GOTERM BP ALL	GO:0048812~neurite morphogenesis	5	4.24%	0.028078	App, Foxg1, Hprt1, Ttl, Mapt,	96	181	14977	4.309680018	1	0.990156	41.96603
GOTERM_BP_ALL	GO:0022008~neurogenesis	7	5.93%	0.031277	Mtap1b, App, Foxg1, Hprt1, Ttl, Nav1, Mapt,	96	373	14977	2.927809428	1	0.99103	45.50892
GOTERM_BP_ALL	GO:0048858~cell projection morphogenesis	6	5.08%	0.040569	Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt,	96	297	14977	3.151725589	1	0.994724	54.67346

GOTERM_BP_ALL	GO:0032990~cell part morphogenesis	6	5.08%	0.040569	Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt,	96	297	14977	3.151725589	1	0.994724	54.67346
GOTERM_BP_ALL	GO:0030030~cell projection organization and biogenesis	6	5.08%	0.040569	Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt,	96	297	14977	3.151725589	1	0.994724	54.67346
GOTERM_BP_ALL	GO:0000904~cellular morphogenesis during differentiation	5	4.24%	0.040807	App, Foxg1, Hprt1, Ttl, Mapt,	96	204	14977	3.823784722	1	0.994202	54.88763
GOTERM_BP_ALL	GO:0030182~neuron differentiation	6	5.08%	0.044094	Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt,	96	304	14977	3.079152961	1	0.995682	57.75149
GOTERM_BP_ALL	GO:0007409~axonogenesis	4	3.39%	0.093624	App, Foxg1, Ttl, Mapt,	96	170	14977	3.670833333	1	0.999562	84.71279
GOTERM BP ALL	GO:0000902~cell morphogenesis	7	5.93%	0.12111	Ube2e3, Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt,	96	531	14977	2.056634495	1	0.999897	91.51197
GOTERM_BP_ALL	GO:0032989~cellular structure morphogenesis	7	5.93%	0.12111	Ube2e3, Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt,	96	531	14977	2.056634495	1	0.999897	91.51197
GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	9	7.63%	0.486914	Ube2e3, Mtap1b, App, Foxg1, Hprt1, Ttl, Bai1, Mapt, Gucy1a3,	96	1191	14977	1.178920025	1	1	99.99971
GOTERM BP ALL	GO:0048468~cell development	9	7.63%	0.527178	Mtap1b, Eif4g2, App, Foxg1, Prdx2, Hprt1, Ttl, Nav1, Mapt,	96	1233	14977	1.138762165	1	1	99.99994

Functional Group 13	Median: 0.0729	Geo: 0.06447	Atp6v1g1,	v1g1, Hprt1, Atp5h, Nme2,									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR	
GOTERM_BP_ALL	GO:0006164~purine nucleotide biosynthetic process	4	3.39%	0.016271	Atp6v1g1, Hprt1, Atp5h, Nme2,	96	84	14977	7.42906746	1	0.979176	26.90709	
GOTERM_BP_ALL	GO:0006163~purine nucleotide metabolic process	4	3.39%	0.022493	Atp6v1g1, Hprt1, Atp5h, Nme2,	96	95	14977	6.568859649	1	0.985278	35.25106	
GOTERM_BP_ALL	GO:0009145~purine nucleoside triphosphate biosynthetic process	3	2.54%	0.060591	Atp6v1g1, Atp5h, Nme2,	96	63	14977	7.42906746	1	0.998482	69.70586	
GOTERM_BP_ALL	GO:0009206~purine ribonucleoside triphosphate biosynthetic process	3	2.54%	0.060591	Atp6v1g1, Atp5h, Nme2,	96	63	14977	7.42906746	1	0.998482	69.70586	
GOTERM_BP_ALL	GO:0009201~ribonucleoside triphosphate biosynthetic process	3	2.54%	0.062294	Atp6v1g1, Atp5h, Nme2,	96	64	14977	7.312988281	1	0.998375	70.73826	
GOTERM_BP_ALL	GO:0009142~nucleoside triphosphate biosynthetic process	3	2.54%	0.067501	Atp6v1g1, Atp5h, Nme2,	96	67	14977	6.985541045	1	0.998793	73.69111	
GOTERM_BP_ALL	GO:0009205~purine ribonucleoside triphosphate metabolic process	3	2.54%	0.071049	Atp6v1g1, Atp5h, Nme2,	96	69	14977	6.783061594	1	0.998922	75.53942	
GOTERM_BP_ALL	GO:0009144~purine nucleoside triphosphate metabolic process	3	2.54%	0.074657	Atp6v1g1, Atp5h, Nme2,	96	71	14977	6.591989437	1	0.999037	77.29222	
GOTERM_BP_ALL	GO:0009199~ribonucleoside triphosphate metabolic process	3	2.54%	0.074657	Atp6v1g1, Atp5h, Nme2,	96	71	14977	6.591989437	1	0.999037	77.29222	
GOTERM_BP_ALL	GO:0009152~purine ribonucleotide biosynthetic process	3	2.54%	0.083926	Atp6v1g1, Atp5h, Nme2,	96	76	14977	6.158305921	1	0.999351	81.26537	
GOTERM_BP_ALL	GO:0009141~nucleoside triphosphate metabolic process	3	2.54%	0.093524	Atp6v1g1, Atp5h, Nme2,	96	81	14977	5.77816358	1	0.999608	84.68036	
GOTERM_BP_ALL	GO:0009260~ribonucleotide biosynthetic process	3	2.54%	0.097449	Atp6v1g1, Atp5h, Nme2,	96	83	14977	5.638930723	1	0.999554	85.89924	
GOTERM_BP_ALL	GO:0009150~purine ribonucleotide metabolic process	3	2.54%	0.10142	Atp6v1g1, Atp5h, Nme2,	96	85	14977	5.50625	1	0.999641	87.03859	
GOTERM_BP_ALL	GO:0009259~ribonucleotide metabolic process	3	2.54%	0.121909	Atp6v1g1, Atp5h, Nme2,	96	95	14977	4.926644737	1	0.999861	91.65821	

Functional Group 14	Median: 0.0309	Geo: 0.0696	App, Hprt1	l, Sv2a, Cac	ng4, Rph3a, Syt4, Vamp2, Gnb1, Gucy1a3,							
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0019226~transmission of nerve impulse	7	5.93%	0.005546	App, Hprt1, Sv2a, Cacng4, Rph3a, Syt4, Vamp2,	96	254	14977	4.299499672	1	0.983834	10.08035
GOTERM BP ALL	GO:0007268~synaptic transmission	6	5.08%	0.08% 0.011019 App, Hprt1, Sv2a, Rph3a, Syt4, Vamp2, 96 211 14977 4.436315166 1							0.988029	19.07931
GOTERM_BP_ALL	GO:0007267~cell-cell signaling	7	5.93%	0.030928	App, Hprt1, Sv2a, Cacng4, Rph3a, Syt4, Vamp2,	96	372	14977	2.935679884	1	0.991749	45.13168
GOTERM_BP_ALL	GO:0003008~system process	9	7.63%	0.92579	App, Hprt1, Sv2a, Cacng4, Gnb1, Rph3a, Syt4, Gucy1a3, Vamp2,	96	1894	14977	0.741337777	1	1	100
GOTERM BP ALL	GO:0050877~neurological system process	8	6.78% 0.936652 App, Hprt1, Sv2a, Cacng4, Gnb1, Rph3a, Syt4, Vamp2, 96 1745 14977 0.715234002 1 1							100		

A-5 Additional data file 4

RT-qPCR validation of DETs based on multiple comparisons between two developmental stages (E vs. Ad, PN1.5 vs. Ad and E15.5 vs. PN1.5). Original version of this data file is accessible <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s4.xls</u>.

- **Note 1** Any fold changes/enrichments less than 1 are presented in "negative fold changes/enrichements" format.
- **Note 2** Adjusted p values were based on empirical bayesian moderated t-test with BH correction.
- **Note 3** Grey background denotes disagreement between RT-qPCR and SAGE analyses.

RT-qPCR results for EvAd cerebral cortex analysis (based on canonical/reference gene)												
SAGE tag	Refseq accession	Gene ID	E15.5/100,000 tags (SAGE)	E17.5/100,000 tags (SAGE)	Adult/100,000 tags (SAGE)	Fold-enrichment in adult/E15.5 (SAGE)	Fold-enrichment in adult/E17.5 (SAGE)	Fold-enrichment in adult/E15.5 (RT-qPCR)	Adjusted p value (RT- qPCR)	Fold- enrichment in adult/E17.5 (RT-qPCR)	Adjusted p value (RT-qPCR)	Specificity
gcttccccaccccctt	NM_177407	calcium/calmodulin-dependent protein kinase II alpha, Camk2a	0.00	0.00	44.65	Adult specific	Adult specific	111.59	1.16E-13	54.74	5.90E-13	Adult
ggatatgtggtgtgtac	NM 007913	early growth response 1, Egr1	0.00	0.00	28.66	Adult specific	Adult specific	108.47	1.22E-10	38.93	2.74E-09	Adult
aaattattgggaaatcc	NM 011123	proteolipid protein (myelin) 1, Plp1	3.15	0.00	90.63	28.77	Adult specific	103.15	5.16E-12	89.13	8.20E-12	Adult
gtatttgcaaaaaaaaa	NM_025451	calcium/calmodulin-dependent protein kinase II inhibitor 1, Camk2n1	1.58	1.84	109.96	69.59	59.76	40.08	1.83E-13	21.46	1.77E-12	Adult
gcttcatctccagggag	NM 009964	crystallin, alpha B, Cryab	0.00	0.92	10.66	Adult specific	11.59	30.47	1.07E-10	20.58	6.73E-10	Adult
ttaccatactgggttgg	NM 022029	neurogranin, Nrgn	1.58	4.60	38.98	24.67	8.47	43.67	9.30E-10	17.00	8.43E-09	Adult
cctcatttcccctgttc	BQ176089	and postrema tissues	0.00	0.00	8.33	Adult specific	Adult specific	23.01	2.98E-08	8.91	1.66E-06	Adult
acccggctagtagtgaa	NM 011129	septin 4, Sept4	0.79	0.92	14.99	18.97	16.29	22.38	6.50E-12	12.96	9.51E-11	Adult
ctcattataatcaagaa	CD802535	tissue	0.00	0.92	8.33	Adult specific	9.05	22.03	6.50E-12	13.25	9.27E-11	Adult
aataaagccaatctgac	NM 033610	synuclein, beta, Sncb	2.36	6.44	49.31	20.89	7.66	18.20	6.28E-08	15.83	1.18E-08	Adult
getttgttaccatete	NM 030689	protein phosphatase 1 regulatory	3.15	4.60	56.31	17.88	12.24	15.02	3.29E-11	10.93	2.09E-10	Adult
tccctcccttagtatcc	NM_144828	(inhibitor) subunit 18, Ppp1r1b	0.00	0.00	21.66	Adult specific	Adult specific	10.47	1.82E-08	6.88	1.64E-07	Adult
geccettetteattgge	NM 010358	chromogranin B. Chub	4.73	4.60	28.99	Adult specific	Adult specific	9.87	2.07E-10	7 22	2.08E-09	Adult
atttcttttctggatgg	NM 010585	inositol 1,4,5-triphosphate receptor 1,	0.79	1.84	11.33	14.34	6.16	9.29	5.08E-10	6.12	7.92E-09	Adult
	-	Itpr1	4.50		10.00	10.00			0.507.00	5.00	6 4 4 7 00	
actttgagattgtacct	NM 009062	regulator of G-protein signaling 4, Rgs4	1.58	0.92	19.33	12.23	21.01	8.84	2.52E-09	5.32	6.14E-08	Adult
ctagacagaggcattat	NM 019634	tetraspanin 7 Tspan7	0.00	1.84	10.33	13.08	5 61	7 99	9 31F-11	5 38	1 17F-09	Adult
tgtatacacacagggt	NM 007547	signal-regulatory protein alpha, Sirpa	0.00	0.00	18.66	Adult specific	Adult specific	7.18	3.71E-09	4.63	7.29E-08	Adult
tgacaagacactgtggc	AU258168	EST from mouse brain	0.00	0.00	10.66	Adult specific	Adult specific	6.49	1.37E-07	4.58	1.47E-06	Adult
cttacctcaggtttcct	NM_008913	protein phosphatase 3, catalytic subunit, alpha isoform, Ppp3ca	0.00	1.84	10.00	Adult specific	5.43	5.48	3.51E-08	3.45	1.30E-06	Adult
atagetttetacacact	NM 007471	amyloid beta (A4) precursor protein, App	19.69	28.53	78.30	3.98	2.74	4.56	4.18E-09	3.49	4.97E-08	Adult
tttcagcagtgttggct	NM_013556	hypoxanthine guanine phosphoribosyl transferase 1, Hprt1	4.73	3.68	32.65	6.90	8.87	3.45	1.71E-07	2.85	1.28E-06	Adult
aggtatgtacaaagttt	NM_016886	glutamate receptor, ionotropic, AMPA3 (alpha 3), Gria3	3.15	1.84	15.66	4.97	8.51	3.40	2.65E-06	1.81	2.68E-03	Adult
tccaacttgtaactata	NM 009790	calmodulin 1, Calm1	5.51	7.36	23.32	4.23	3.17	3.24	6.38E-08	2.27	3.92E-06	Adult
cctcagcctggggtaga	NM 009983	cathepsin D, Ctsd	8.66	14.72	29.99	3.46	2.04	3.22	2.94E-07	3.84	7.05E-08	Adult
gcttcgtccacacagcg	NM 010777	myelin basic protein, Mbp	0.79	0.92	159.94	202.46	173.85	3.19	1.92E-07	2.05	3.94E-05	Adult
tattaaatgtgcttttt	NM_080555	phosphatidic acid phosphatase type 2B, Ppap2b	3.15	7.36	17.99	5.71	2.44	3.02	1.96E-06	2.76	5.37E-06	Adult
cttatcctcacctcagc	NC 005089	NADH dehydrogenase 6, mitochondrial, mt-ND6	0.00	0.00	19.66	Adult specific	Adult specific	2.65	6.99E-06	2.13	9.73E-05	Adult
caaacctccaaaaacca	AK140219	Mus musculus adult male corpora	27.56	43.25	805.35	29.22	18.62	2.63	1.04E-05	2.03	2.47E-04	Adult
agtggctaattaggtgt	NM 009900	chloride channel 2. Clcn2	1.58	5.52	22 - 99	14.55	4.16	2.23	3.83E-04	2.18	5-05E-04	Adult
		Mus musculus NOD-derived CD11c +ve	2.00	0.01	0.000				0.000 01	4 95 979	0.000 00	
ttccgtgaaccaaaact	AK154943	dendritic cells cDNA	7.09	9.2	36.99	5.22	4.02	1.76	3.19E-03	1.35 (NS)	8.63E-02	Adult
ccagtacctgaaaaaaa	NM 008453	Kruppel-like factor 3 (basic), Klf3	0.00	17.48	0.33	Adult specific	-52.97	-1.47	6.47E-02	-1.27 (NS)	2.42E-01	Adult
aagaaaacatttaaata	NM_012010	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked,	10.24	13.80	1.33	-7.70	-10.38	-1.72	3.50E-03	-1.74	3.20E-03	Adult
		Eif2s3x amyotrophic lateral sclerosis 2 (juvenile)										
caccctgtgggagctca	NM_172656	chromosome region, candidate 2 (human), Als2cr2	11.03	12.88	1.00	-11.03	-12.88	-1.75	2.14E-03	-2.48	2.81E-05	Embryonic
cctccatcctttatact	NM 009536	tyrosine 3-monooxygenase/tryptophan 5- monooxygenase activation protein, epsilon	24.41	19.32	7.66	-3.19	-2.52	-1.82	1.27E-03	-2.66	1.41E-05	Embryonic
	-	polypeptide, Ywhae										-
tgtgcttccctgtctta	NM_008683	developmentally down-regulated gene 8,	34.65	61.65	7.33	-4.73	-8.41	-1.83	7.59E-05	-1.86	5.63E-05	Embryonic
		Nedd8 ubiguitin-conjugating enzyme E2E 3, UBC4/5										
ctcctgaaggcatagtt	NM_009454	homolog (yeast), Ube2e3	16.54	22.09	4.00	-4.14	-5.52	-2.51	1.81E-06	-3.22	1.28E-07	Embryonic
gtgaaactaaaaaaaaa	NM 009094	ribosomal protein S4, X-linked, Rps4x	139.40	255.82	13.33	-10.46	-19.19	-2.76	1.76E-06	-3.35	2.63E-07	Embryonic
aatgtttctgctttaca	NM 011045	proliferating cell nuclear antigen, Pcna	18.90	11.04	1.33	-14.21	-8.30	-3.09	6.28E-08	-2.62	4.00E-07	Embryonic
cgtggatccctctgtca	NM_009876	cyclin-dependent kinase inhibitor 1C (P57), Cdkn1c	22.84	11.96	1.67	-13.68	-7.16	-3.39	1.13E-03	-3.30	1.36E-03	Embryonic
cctttgtgacagtggcc	NM 025635	ZW10 interactor, Zwint	13.39	11.04	97.63	7.29	8.84	-3.47	9.38E-06	-4.80	8.40E-07	Embryonic
gaagccagtgggccatc	NM 001033273	RIKEN cDNA 5031439G07 gene, 5031439G07Rik	9.45	10.12	1	-9.10	-10.00	-4.13	4.02E-07	-3.65	1.28E-06	Embryonic
gctgtgggtcgctgtgg	NM 010561	Interleukin enhancer binding factor 3, Ilf3	0.00	0.00	13.99	Adult specific	Adult specific	-4.15	6.84-E08	-2.97	1.48E-06	Embryonic
acccctgaccccttgtt	NM_016707	protein), Bcl11a	23.63	16.56	3.00	-7.88	-5.52	-4.42	3.76E-08	-4.78	2.61E-08	Embryonic
cggtgtcccccacctcc	NM 012015	HZA histone family, member Y, H2afy	7.09	9.20	0.33	-21.48	-27.88	-4.62	1.40E-08	-3.70	8.18E-08	Embryonic
cayttycaataaaddta	MPI 010094	myristovlated alanine rich protein kinger C	12.00	0.20	1.0/	-7.51	-4.90	-3.02	2.702-08	-5.10	3.93E-08	Empryonite
aagtttgcaagtctcca	NM_008538	substrate, Marcks	33.08	15.64	1.33	-24.87	-11.76	-5.72	3.26E-100	-5.56	4.63E-97	Embryonic

ttgctggcttttataaa	NM 053104	RNA binding motif protein 9, Rbm9	24.41	31.29	4.00	-6.10	-7.82	-6.50	2.70E-08	-5.97	5.22E-08	Embryonic
ggttttgtttgtttgac	NM 019653	WD repeat and SOCS box-containing 1, Wsb1	7.88	11.96	1.00	-7.88	-11.96	-6.54	3.76E-08	-7.00	3.12E-08	Embryonic
tatattgattgtggcaa	NM_007569	B-cell translocation gene 1, anti- proliferative, Btg1	10.24	11.04	0.67	-15.28	-16.48	-6.93	1.72E-10	-5.58	9.31E-10	Embryonic
taagaaacct	NM 019413	roundabout homolog 1 (Drosophila), Robol	9.45	5.52	0.33	-28.64	-16.73	-8.23	1.72E-08	-11.35	3.40E-09	Embryonic
gctttgactgttctctt	AA122503	EST from M2 cells of skin melanoma	22.84	24.85	1.33	-17.17	-18.68	-9.88	1.17E-07	-10.15	1.13E-07	Embryonic
tggagcgttggctgtat	NM 009870	cyclin-dependent kinase 4, Cdk4	37.80	26.69	0.33	-114.55	-80.88	-14.77	2.77E-11	-10.00	3.12E-08	Embryonic
ctttccctgccaatgta	NM 013834	secreted frizzled-related protein 1, Sfrp1	5.51	11.96	0.00	Embryonic specific	Embryonic specific	-16.48	5.08E-10	-16.37	7.80E-10	Embryonic
tgcagctttctgttcaa	NM_007971	enhancer of zeste homolog 2 (Drosophila), Ezh2	21.26	11.04	2.00	-10.63	-5.52	-21.36	2.14E-10	-17.59	7.41E-10	Embryonic
cacgacacccccaccc	NM 009559	zinc finger protein 57, Zfp57	30.72	42.33	1.00	-30.72	-42.33	-29.13	1.07E-10	-44.46	4.99E-11	Embryonic
tgtgtgaggtgttgtga	NM_010025	doublecortin, Dcx	59.07	78.22	1.33	-44.41	-58.81	-73.76	1.46E-13	-91.10	1.48E-13	Embryonic
cagagtgtagtgtgttg	NM 009234	SRY-box containing gene 11, Sox11	9.45	13.80	0.00	Embryonic specific	Embryonic specific	-140.05	1.38E-14	-120.35	2.14E-14	Embryonic

RT-qPCR results for PN1.5vAd cerebral cortex analysis (based on canonical/reference gene)													
SACE tag	Manageion	Cone /RST ID	PN1.5/100,000 tags	Adult/100,000	Fold-enrichment in	Fold-enrichment in	Adjusted p value	Specificity					
Shub tay	ACCESSION		(SAGE)	tags (SAGE)	adult (SAGE)	adult (RT-qPCR)	(RT-qPCR)	Specificity					
aaattattgggaaatcc	NM 011123	proteolipid protein (myelin) 1, Plp1	2.33	90.63	38.9	43.33	7.49E-11	Adult					
tttcagcagtgttggct	NM_013556	hypoxanthine guanine phosphoribosyl transferase 1, Hprt1	4.67	32.65	6.99	2.26	2.28E-05	Adult					
actcggagccaccagac	NM 009790	calmodulin 1, Calm1	25.66	117.29	4.57	1.83	1.00E-04	Adult					
gcttcgtccacacagcg	NM 010777	myelin basic protein, Mbp	0	159.94	Adult specific	1.79	3.10E-04	Adult					
tccccgtcat	NM 026106	down-regulator of transcription 1, Dr1	32.66	0	PN1.5 specific	-1.46	1.38E-02	PN1.5					
gggaaactaagggagag	NM 172503	zinc finger, SWIM domain containing 4, Zswim4	14	0.33	-42.42	-1.96	3.63E-03	PN1.5					
gaacgcaagttcagccc	NM 031404	actin-like 6B, Act16b	25.66	4.66	-5.51	-2.26	1.00E-04	PN1.5					
gtgaaactaaaaaaaaa	NM 009094	ribosomal protein S4, X-linked, Rps4x	62.98	13.33	-4.72	-2.27	2.25E-05	PN1.5					
Nil	NM 009726	ATPase, Cu++ transporting, alpha polypeptide, Atp7a	Nil	Nil	Nil	-2.91	1.24E-05	PN1.5					
agaagtgtttggagttt	NM 008253	high mobility group box 3, Hmgb3	20.99	1	-20.99	-3.53	4.88-e07	PN1.5					
cctttgtgacagtggcc	NM 025635	ZW10 interactor, Zwint	20.99	97.63	4.65	-4.04	4.06E-06	PN1.5					
acagtctatgttggagg	BQ177886 / NM_010487	C57BL/6 whole brain E15.5 (also known as embryonic lethal, abnormal vision, Drosophila-like 3 (Hu antigen C), Elav13)	41.99	1	-41.99	-4.06	1.04E-07	PN1.5					
gatacttggaatgacta	NM 007393	actin, beta, cytoplasmic, Actb	326.58	17.66	-18.49	-4.35	1.00E-04	PN1.5					
ctggcttctt	NM_008538	myristoylated alanine rich protein kinase C substrate, Marcks	23.33	0	PN1.5 specific	-4.76	6.52E-81	PN1.5					
Nil	NM_025958	cullin-associated and neddylation-dissociated 2 (putative), Cand2	Nil	Nil	Nil	-5.62	1.53E-08	PN1.5					
tggagcgttggctgtat	NM 009870	cyclin-dependent kinase 4, Cdk4	18.66	0.33	-56.55	-5.77	7.91E-09	PN1.5					
gctttgactgttctctt	AA122503	EST from M2 cells of skin melanoma	16.33	1.33	-12.28	-11.12	1.00E-07	PN1.5					
gggacctcgtggaagcc	NM_009238	SRY-box containing gene 4, Sox4	27.99	0.89	-31.51	-11.74	1.35E-07	PN1.5					
ctcagtaatg	NM 007792	cysteine and glycine-rich protein 2, Csrp2	14	0	PN1.5 specific	-26.10	1.48E-11	PN1.5					
cacgacaccccccaccc	NM 009559	zinc finger protein 57, Zfp57	16.33	1	-16.33	-32.74	1.60E-10	PN1.5					
tgtgtgaggtgttgtga	NM 010025	doublecortin, Dcx	32.66	1.33	-24.56	-82.11	2.06E-13	PN1.5					

RT-qPCR results for E15.5vPN1.5 cerebral cortex analysis (based on canonical/reference gene)													
SAGE tag	Accession	Gene/EST ID	E15.5/100,000 tags (SAGE)	PN1.5/100,000 tags (SAGE)	Fold-enrichment in E15.5 (SAGE)	Fold-enrichment in PN1.5 (RT-qPCR)	Adjusted p value (RT-qPCR)	Specificity					
atttctttggtgatttt	NM_010838	Microtubule-associated protein tau, Mapt	15.25	83.98	5.51	1.53	1.11E-02	PN1.5					
gcactgttaacaagtgt	NM_009234	SRY-box containing gene 11, Sox11	25.2	11.66	0.46	-3.32	1.14E-06	E15.5					

A-6 Additional data file 5

RT-qPCR validation of gene clusters based on hierarchical clustering analysis. Original version of this data file is accessible <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s5.xls</u>.

Note 1 The fold enrichment in SAGE was calculated by using the formula (X+0.5)/(Y+0.5), where X and Y represent the normalized combined tag counts of groups that are being compared.

- **Note 2** Adjusted p values were based on empirical bayesian moderated t-test with BH correction.
- **Note 3** Sky-blue background denotes SAGE data.
- **Note 4** Yellow background denotes RT-qPCR data.
- **Note 5** Bold p values denote a particular comparison is significant at p<0.05 level.

	RT-qPCR results for RvC analysis of E15.5 cerebral cortex quadrants																				
				Comb	oined no	rmalized	l tag	Log2 norm	alized expr	ession (agai	inst 3 house	keeping		Fold-enr	ichment afte	r normalized	to 815.5	cerebral cor	tex (linear	r scale)	
	Pofeor			CO	unts (pe	er 100,0	00)	Normalized	Normalized	genes)	Normalized	Standard	Rold	Rold	Rold	Fold		Fold		Rold	
SAGE tag	accession	Gene ID	Cluster	E15.5	E17.5	PN1.5	Adult	expression	expression	expression	expression	error of	enrichment	enrichment	enrichment	enrichment	Adjusted	enrichment	Adjusted	enrichment	Adjusted p
				(SAGE)	(SAGE)	(SAGE)	(SAGE)	for E15.5	for E17.5	for PN1.5	for Adult	coefficie	in E17.5	in EP1.5	in Adult	in E17.5	p value (RT- σPCR)	in PN1.5	(RT-gPCR)	in Adult	value (RT- gPCR)
		amustrophig latoral						(RT-qPCR)	(RT-qPCR)	(RT-qPCR)	(RT-qPCR)	nt	(SAGE)	(SAGE)	(SAGE)	(RT-qPCR)		(RT-qPCR)		(RT-qPCR)	,
caccctgtgggagctca	NM_172656	sclerosis 2 (juvenile) chromosome region, candidate 2 (human), Als2cr2	1	11.03	12.88	7	1	2.1244	2.6335	2.8639	1.3210	0.1511	1.1605	0.6505	0.1301	1.4231	8.75E-02	1.6696	7.90E-03	0.5730	2.14E-03
tatattgattgtggcaa	NM 007569	B-cell translocation gene	1	10.24	11.04	2.33	0.67	4.5243	4.2125	4.0420	1.7311	0.0716	1.0745	0.2635	0.1089	0.8057	1.43E-01	0.7158	1.53E-02	0.1443	1.72E-10
cgtggatccctctgtca		cyclin-dependent kinase	1	22.84	11.96	2.33	1.67	3.7967	3.7602	3.5940	2.0375	0.3770	0.5338	0.1213	0.0930	0.9750	9.56E-01	0.8690	6.89E-01	0.2954	1.13E-03
ctcagtaatg	NM_007792	cysteine and glycine-rich protein 2. Carp2	1	13.39	7.36	0	1.67	4.1050	4.1457	4.0421	-0.6637	0.1331	0.5659	0.0360	0.1562	1.0286	9.19E-01	0.9573	7.52E-01	0.0367	6.50B-12
tgcagctttctgttcaa	NM_007971	enhancer of zeste homolog 2 (Drosophila), Ezh2	1	21.26	11.04	7	2	4.7558	4.4760	3.5977	0.3390	0.2010	0.5303	0.3447	0.1149	0.8237	4.23E-01	0.4481	1.27E-03	0.0468	2.14E-10
cggtgtcccccacctcc	NM_012015	H2A histone family, member Y, H2afy	1	7.09	9.2	4.67	0.33	2.5224	2.2015	1.2976	0.3146	0.1072	1.2780	0.6812	0.1094	0.8006	1.82E-01	0.4278	5.02E-05	0.2165	1.40E-08
cagttgcaataaaaata	NM_010894	neurogenic differentiation 1, Neurod1	1	12.6	8.28	4.67	1.67	0.3379	0.1979	-0.4781	-2.1540	0.1544	0.6702	0.3947	0.1656	0.9075	6.68E-01	0.5680	4.77E-03	0.1778	2.70E-08
aatgtttctgctttaca	NM_011045	proliferating cell nuclear antigen, Pcna	1	18.9	11.04	4.67	1.33	2.0093	1.7744	1.2033	0.3828	0.0606	0.5948	0.2665	0.0943	0.8498	2.43E-01	0.5720	4.37E-04	0.3239	6.28E-08
gaagccagtgggccatc	NM_0010332 73	RIKEN cDNA 5031439G07 gene, 5031439G07Rik	1	9.45	10.12	4.67	1	-0.0391	-0.2176	-1.2283	-2.0868	0.1681	1.0673	0.5196	0.1508	0.8836	5.94E-01	0.4386	4.50E-04	0.2419	4.028-07
taagaaacct	NM_019413	roundabout homolog 1 (Drosophila), Robol	1	9.45	5.52	2.33	0.33	3.5569	4.0201	3.1720	0.5159	0.1966	0.6050	0.2844	0.0834	1.3786	1.74E-01	0.7658	1.88E-01	0.1215	1.72E-08
ctttccctgccaatgta	NM_013834	secreted frizzled-related protein 1, Sfrp1	1	5.51	11.96	2.33	0	4.2489	4.2392	3.4998	0.2061	0.1965	2.0732	0.4709	0.0832	0.9933	9.69E-01	0.5950	1.68E-02	0.0607	5.08E-10
cagagtgtagtgtgttg	NM_009234	SRY-box containing gene 11, Sox11	1	18.31	32.51	2.33	0.33	6.7563	6.5376	5.4361	-0.3735	0.1371	1.7552	0.1505	0.0440	0.8593	4.59E-01	0.4005	2.63E-05	0.0071	1.388-14
ggttttgtttgtttgac	NM_019653	WD repeat and SOCS box- containing 1, Wsb1	1	7.88	11.96	9.33	1	3.0108	3.1096	2.1393	0.3023	0.1861	1.4869	1.1730	0.1790	1.0709	7.62E-01	0.5466	6.63E-03	0.1530	3.76E-08
gaacgcaagttcagccc	NM 031404	ATPase, Cu++ transporting,	2	11.03	1.84	25.66	4.66	1.6220	1.9737	1.7109	0.5320	0.1535	0.2029	2.2689	0.4475	1.2760	2.15E-01	1.0635	7.26E-01	0.4698	1.87E-04
Nil	NM_009726	alpha polypeptide, Atp7a	2	Nil 5 51	Nil	Nil	Nil	3.0221	3.2890	2.8290	1.2889	0.1664	Nil 1 3078	Nil 0.8602	Nil 3 9634	1.2032	3.76E-01	0.8747	4.84E-01	0.3008	2.41E-06
agtggctaattaggtgt	NM 009900	chloride channel 2, Clcn2	2	1.58	5.52	2.33	22.99	0.1516	0.1846	0.8915	1.3065	0.1912	2.8942	1.3606	11.2933	1.0231	9.41E-01	1.6700	1.65E-02	2.2267	3.83E-04
tgactagcgtgacctgt	NM 007694	chromogranin B, Chgb	2	4.73	4.6	4.67	28.99	-3.8800	-3.4940	-2.5643	-0.6429	0.1168	0.9751	0.9885	5.6386	1.3068	1.26E-01	2.4893	3.77E-05	9.4292	2.07E-10
agaagtgtttggagttt	NM_008253	high mobility group box 3, Hmgb3	2	16.54	11.96	20.99	1	3.7721	3.6355	3.8398	2.0204	0.1330	0.7312	1.2612	0.0880	0.9096	6.51E-01	1.0480	7.44E-01	0.2970	5.13E-07
tttcagcagtgttggct	NM_013556	hypoxanthine guanine phosphoribosyl transferase 1, Hprt1	2	4.73	3.68	4.67	32.65	-1.0870	-0.8138	-0.4744	0.6987	0.1128	0.7992	0.9885	6.3384	1.2085	2.54E-01	1.5290	9.828-03	3.4478	1.71E-07
tccccgtcat	NM_026106	down-regulator of transcription 1 , Dr1	3	1.58	0.92	32.66	0	1.5061	1.3192	1.2784	0.7307	0.1224	0.6827	15.9423	0.2404	0.8785	4.71E-01	0.8540	3.06E-01	0.5842	1.22E-03
gggaaactaagggagag	NM_172503	zinc finger, SWIM domain containing 4, Zswim4	3	0.79	0	14	0.33	2.0056	1.2838	1.5983	0.6255	0.2204	0.3876	11.2403	0.6434	0.6063	6.48E-02	0.7541	1.97E-01	0.3842	1.95E-04
aataattagccttaggt	AK139402	AK139402 B0176089	4	0	0	0	16.99	-2.9847	-2.8527	-0.9637	0.0642	0.2263	1.0000	1.0000	34.9800	1.0958	7.30E-01	4.0588	3.20E-05	8.2759	4.84E-08
ctcattataatcaagaa	CD802535	CD802535	4	0	0.92	0	8.33	-3.9262	-3.1924	-2.4421	0.5354	0.1198	2.8400	1.0000	17.6600	1.6630	1.39E-02	2.7974	1.92E-05	22.0330	6.50E-12
gcttcatctccagggag	NM 009964	crystallin, alpha B, Cryab	4	0	0.92	0	10.66	-4.7473	-4.1813	-1.2528	0.1819	0.2124	2.8400	1.0000	22.3200	1.4804	1.18E-01	11.2704	1.48E-07	30.4674	1.07E-10
ggatatgtggtgtgtac	NM_007913	early growth response 1, Egr1	4	0	0.92	0	28.66	-1.5593	-0.0810	0.8635	5.2019	0.3210	2.8400	1.0000	58.3200	2.7861	1.39E-02	5.3622	6.54E-05	108.4736	1.22B-10
aggtatgtacaaagttt	NM_016886	glutamate receptor, ionotropic, AMPA3 (alpha 3)	4	3.15	1.84	0	15.66	0.1469	1.0594	0.8645	1.9136	0.1741	0.6411	0.1370	4.4274	1.8824	1.39E-02	1.6445	1.46B-02	3.4029	2.658-06
atttcttttctggatgg	NM_010585	inositol 1,4,5-triphosphate receptor 1, Itpr1	4	0.79	1.84	0	11.33	-3.0283	-2.4257	-2.0953	0.1878	0.1362	1.8140	0.3876	9.1705	1.5185	3.60E-02	1.9093	1.06E-03	9.2928	5.08E-10
gcttcgtccacacagcg	NM 010777	myelin basic protein, Mbp	4	0.79	0.92	0	159.94	-0.9078	-0.2710	-0.0766	0.7665	0.0989	1.1008	0.3876	124.3721	1.5548	1.63E-02	1.7791	9.18E-04	3.1916	1.92E-07
tattaaatgtgcttttt	NM_080555	phosphatidic acid phosphatase type 2B, Ppap2b	4	3.15	7.36	0	17.99	-1.2052	-1.0749	-0.9390	0.3889	0.1394	2.1534	0.1370	5.0658	1.0945	6.68E-01	1.2027	2.60E-01	3.0191	1.96B-06
ccctgcagctcaaaaaa	NM_008913	protein phosphatase 3, catalytic subunit, alpha isoform, Ppp3ca	4	3.94	1.84	0	11	-0.6816	-0.0134	0.1942	1.7724	0.1569	0.5270	0.1126	2.5901	1.5892	3.48E-02	1.8351	3.17E-03	5.4795	3.51E-08
acccggctagtagtgaa	NM 011129	septin 4, Sept4	4	0.79	0.92	0	14.99	-4.2001	-3.4119	-3.0548	0.2842	0.1210	1.1008	0.3876	12.0078	1.7270	1.39E-02	2.2120	1.33E-04	22.3825	6.50E-12
clagacagaggcattat	NM 019634	actin, beta, cytoplasmic.	4	0.79	1.84	0	10.33	-2.9839	-2.4136	-2.0821	0.0140	0.0727	1.8140	0.3876	8.3953	1.4849	1.685-02	1.8684	2.205-04	7.9883	9.318-11
gatacttggaatgacta	NM_007393	Actb	5	238.63	129.75	326.58	17.66	5.2309	5.1727	6.0578	3.9376	0.3369	0.5447	1.3678	0.0759	0.9604	9.39E-01	1.7739	7.90E-02	0.4080	4.94E-03
Nil	NM_025958	neddylation-dissociated 2 (putative), Cand2	5	Nil	Nil	Nil	Nil	6.6907	6.1651	5.8919	3.4002	0.1314	#VALUE !	#VALUE !	#VALUE !	0.6947	6.42E-02	0.5748	3.12E-03	0.1022	3.208-10
gtgaaactaaaaaaaa	NM_009094	ribosomal protein S4, X- linked, Rps4x	5	139.4	255.82	62.98	13.33	1.6573	1.9364	1.3754	0.1926	0.1141	1.8322	0.4538	0.0989	1.2134	2.49E-01	0.8225	1.88E-01	0.3623	1.76E-06
ttggtgaaggaaaaaac	NM_021278	thymosin, beta 4, X chromosome, Tmsb4x	5	350.47	283.43	277.59	141.61	-1.0195	-0.3970	-0.5403	-0.1306	0.2552	0.8090	0.7923	0.4049	1.5396	1.33E-01	1.3940	1.82E-01	1.8517	1.20E-02
gctttgactgttctctt	AA122503	AA122503	6	22.84	24.85	16.33	1.33	2.4560	2.4943	2.6264	-0.8485	0.2771	1.0861	0.7211	0.0784	1.0269	9.43E-01	1.1254	6.75E-01	0.1012	1.17E-07

acagtctatgttggagg	BQ177886 / NM_010487	C57BL/6 whole brain E15.5 (also known as embryonic lethal, abnormal vision, Drosophila-like 3 (Hu antigen C), Elavl3)	6	18.9	21.16	41.99	1	0.3771	0.7871	0.7179	-1.3032	0.1250	1.1165	2.1902	0.0773	1.3287	1.18E-01	1.2665	1.31E-01	0.3120	5.71E-07
tggagcgttggctgtat	NM_009870	cyclin-dependent kinase 4, Cdk4 devblocertin Day	6	37.8	26.69	18.66	0.33	4.2613	3.6983	2.9051	0.3768	0.1133	0.7099	0.5003	0.0217	0.6769	3.48E-02	0.3906	2.96E-05	0.0677	2.77E-11
aagtttgcaagtctcca	NM_008538	myristoylated alanine rich protein kinase C substrate, Marcks	6	32.72	12.61	18.66	1.33	1.4250	1.3845	1.3374	-1.0905	0.0608	0.3945	0.5767	0.0517	0.9723	9.47E-01	0.9411	6.88E-01	0.1749	3.26E-100
gggacctcgtggaagcc	NM_009238	SRY-box containing gene 4, Sox4	6	69.11	30.95	27.99	0.89	5.1089	4.2920	3.2133	-0.3397	0.3209	0.4518	0.4093	0.0199	0.57	9.80E-02	0.27	2.10E-04	0.02	4.98E-10
cacgacaccccccaccc	NM_009559	zinc finger protein 57, 2fp57	6	30.72	42.33	16.33	1	4.8674	5.4775	5.0360	0.0031	0.2069	1.3719	0.5391	0.0480	1.5263	9.26E-02	1.1239	5.98E-01	0.0343	1.07E-10
atagctttctacacact	NM_007471	amyloid beta (A4) precursor protein, App	7	19.69	28.53	41.99	78.3	0.3366	0.7228	0.9108	2.5261	0.0793	1.4378	2.1045	3.9029	1.3069	8.75E-02	1.4889	7.09E-03	4.5613	4.18E-09
acccctgaccccttgtt	NM_016707	B-cell CLL/lymphoma 11A (zinc finger protein), Bcl11a	7	23.63	16.56	7	3	4.4328	4.5481	3.9757	2.2898	0.1245	0.7070	0.3108	0.1450	1.0832	6.69E-01	0.7284	5.03E-02	0.2264	3.76E-08
cctcagcctggggtaga	NM 009983	cathepsin D. Ctsd	7	8.66	14.72	14	29.99	-1.1254	-1.3798	-0.7925	0.5616	0.1103	1.6616	1.5830	3.3286	0.8383	2.89E-01	1.2595	1.22E-01	3.2199	2.94E-07
atttctttggtgatttt	NM_010838	microtubule-associated protein tau, Mapt	7	14.96	38.65	83.98	7.66	6.1984	6.6246	6.8133	4.3586	0.1206	2.5323	5.4644	0.5278	1.3437	1.05E-01	1.5314	1.11E-02	0.2794	1.71E-07
tgtgcttccctgtctta	NM_008683	neural precursor cell expressed, developmentally down-regulated gene 8, Nedd8	7	34.65	61.65	4.67	7.33	1.1480	1.1769	1.2288	0.2791	0.0680	1.7681	0.1471	0.2228	1.0202	9.23E-01	1.0576	6.75E-01	0.5476	7.59E-05
ttgctggcttttataaa	NM_053104	RNA binding motif protein 9, Rbm9	7	24.41	31.29	11.66	4	4.4245	4.3023	3.7870	1.7241	0.1754	1.2762	0.4882	0.1807	0.9188	7.19E-01	0.6429	2.62E-02	0.1539	2.70E-08
cctccatcctttatact	NM_009536	tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation protein, epsilon polypeptide, Ywhae	7	24.41	19.32	16.33	7.66	2.3229	2.8669	2.4051	1.4580	0.1525	0.7957	0.6756	0.3276	1.4580	7.49E-02	1.0586	7.32E-01	0.5491	1.27E-03
ctcctgaaggcatagtt	NM_009454	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (veast), Ube2e3	7	16.54	22.09	7	4	1.4535	1.8128	1.9607	0.1252	0.0892	1.3257	0.4401	0.2641	1.2828	1.18E-01	1.4213	1.608-02	0.3983	1.81E-06
tgacaagacactgtggc	AU258168	AU258168	8	0	0	4.67	10.66	-2.7713	-2.2700	-1.9205	-0.0731	0.2180	1.0000	10.3400	22.3200	1.4155	1.74E-01	1.8035	1.37E-02	6.4901	1.37E-07
gcttccccaccccctt	NM_177407	calcium/calmodulin- dependent protein kinase II alpha, Camk2a	8	0	0	2.33	44.65	-3.4525	-2.4250	-1.6261	3.3496	0.1194	1.0000	5.6600	90.3000	2.0384	2.69E-03	3.5466	2.42E-06	111.5941	1.168-13
gtatttgcaaaaaaaaa,	NM_025451	calcium/calmodulin- dependent protein kinase II inhibitor 1, Camk2n1	8	1.62	0.00	4.67	108.33	-4.2087	-3.3072	-2.6872	1.1163	0.1246	0.2362	2.4425	51.4142	1.8681	3.68E-03	2.8709	5.30E-06	40.0845	1.83E-13
gccccttcttcattggc	NM_010358	glutathione S-transferase, mu 1, Gstm1	8	0	0	4.67	10	-2.0706	-1.2468	-0.9544	1.2331	0.0924	1.0000	10.3400	21.0000	1.7700	5.64E-03	2.1677	6.54E-05	9.8743	7.00E-11
cttatcctcacctcagc	NC_005089 (AK138272)	NADH dehydrogenase 6, mitochondrial, mt-ND6	8	0	0	2.33	19.66	-2.2899	-1.9774	-1.2902	-0.8833	0.1368	1.0000	5.6600	40.3200	1.2419	2.43E-01	1.9995	6.79E-04	2.6511	6.99B-06
tccctcccttagtatcc	NM_144828	protein phosphatase 1, regulatory (inhibitor) subunit 1B, Ppp1r1b	8	0	0	2.33	21.66	2.5125	3.1178	2.6143	5.9001	0.2300	1.0000	5.6600	44.3200	1.5214	1.18E-01	1.0731	7.39E-01	10.4658	1.82E-08
cttacctcaggtttcct	NM_008913	protein phosphatase 3, catalytic subunit, alpha isoform, Ppp3ca	8	0	1.84	2.33	10	-0.6816	-0.0134	0.1942	1.7724	0.1569	4.6800	5.6600	21.0000	1.5892	3.488-02	1.8351	3.17E-03	5.4795	3.51E-08
aaattattgggaaatcc	NM_011123	proteolipid protein (myelin) 1, Plp1	8	3.15	0	2.33	90.63	-5.5861	-5.3754	-4.3350	1.1025	0.2088	0.1370	0.7753	24.9671	1.1573	5.92E-01	2.3803	9.18E-04	103.1484	5.16E-12
actttgagattgtacct	NM_009062	regulator of G-protein signaling 4, Rgs4	8	1.58	0.92	7	19.33	-1.2477	-0.5141	-0.8612	1.8961	0.1629	0.6827	3.6058	9.5337	1.6628	2.69E-02	1.3072	1.37E-01	8.8388	2.52E-09
tgtatacacacacgggt	NM_007547	signal-regulatory protein alpha, Sirpa	8	0	0	2.33	18.66	-1.1699	-0.5368	-0.4853	1.6741	0.1452	1.0000	5.6600	38.3200	1.5509	3.48E-02	1.6072	1.05E-02	7.1800	3.71E-09
caaacctccaaaaacca	AK140219	AK140219	10	27.56	43.25	23.33	517 46	-1.4382	-1.0636	-0.6668	-0.0434	0.1445	2.0306	0.8493	28.7188	1.2965	1.80E-01	1.7069	5.30E-03	2.6296	1.04E-05
ttaccatactgggttgg	NM 022029	Neurogranin, Nrgn	10	1.58	4.6	46.65	39.08	-2.2899	-1.9774	-1.2902	-0.8833	0.1368	2.4519	22.6683	19.0280	1.2419	2.43E-01	1.9995	6.79E-04	2.6511	6.99E-06
gcttttgttaccatctc	NM_030689	neuronal pentraxin receptor, Nptxr	10	3.15	4.6	20.99	56.31	5.2414	5.7004	7.0775	9.1500	0.1203	1.3973	5.8877	15.5644	1.3746	8.61E-02	3.5703	2.42E-06	15.0181	3.29E-11
aataaagccaatctgac	NM 033610	synuclein, beta, Sncb	10	2.36	6.44	11.66	49.31	3.1351	3.3361	3.5811	7.3206	0.3429	2.4266	4.2517	17.4161	1.1495	7.19E-01	1.3623	3.30E-01	18.1964	6.28E-08

A-7 Additional data file 6

RT-qPCR validation of DETs based on the Rostral vs. Caudal E15.5 cerebral cortex comparison. Original version of this data file is accessible <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s6.xls</u>.

- **Note 1** Any fold changes/enrichments less than 1 are presented in "negative fold changes/enrichements" format.
- **Note 2** Adjusted p values were based on empirical bayesian moderated t-test with BH correction.
- **Note 3** Grey background denotes selected control genes based on published data or genes of interest.
- **Note 4** Bold p values denote a particular comparison is significant at p<0.05 level.
- **Note 5** SAGE expression profile is considered validated by RT-qPCR when both fold change value is in the same direction and has a magnitude of > 1.3.

	RT-qPCR results for RvC analysis of E15.5 cerebral contex E15.5 E15.5 Fold-enrichment Fold-enrichment Adjusted														
SAGE tag	Refseq accession	Gene ID	E15.5 rostral/100,000 tags (SAGE)	E15.5 caudal/100,000 tags (SAGE)	Fold-enrichment in E15.5 caudal (SAGE)	Fold-enrichment in E15.5 caudal (RT-qPCR)	Adjusted p value (RT-qPCR)	Specificity							
NII	NM_010151	nuclear receptor subfamily 2, group F, member 1, Nr2f1 (Coup- tf1)	NII	NII	Caudal specific	2.44	2.53E-02	Caudal							
gttgttcttccagtcgg	NM_016916	bladder cancer associated protein homolog (human), Blcap	4.62	5.09	1.10	1.43	1.17E-01	Caudal							
gatacttggaatgacta	NM 007393	actin, beta, cytoplasmic, Actb	408.52	155.16	-2.63	-1.32	1.32E-01	Rostral							
Nil	NM_001043354 / NM 146095	RAR-related orphan receptor beta, Rorb	Nil	Nil	Rostral specific	-1.65	8.97E-02	Rostral							
ttggtgaaggaaaaaac	NM_021278	thymosin, beta 4, X chromosome, Tmsb4x	507.77	218.75	-2.33	-2.14	7.33E-03	Rostral							
gtcatagctgttctgtg	BC025816	EST sequence BC025816	0	38.15	Caudal specific	1.31	3.17E-01	Caudal							
aagettgacatttggaa	NM_026187	ankyrin repeat and zinc finger domain containing 1, Ankzfl	2.31	0.00	Rostral specific	1.17	4.16E-01	Not validated							

	RT-qPCR results for RvC analysis of E15.5 cerebral cortex quadrants Log2 normalized expression for E15.5 cerebral cortex (against 3															
						Log2 norm	alized express hou	ion for E15.5 sekeeping ge	cerebral cortex nes)	c (against 3	Fold-enr	ichment after	normalized to) E15.5 rostro	lateral cerebra	al cortex
SAGE tag	Refseq accession	Gene ID	E15.5 rostral/100,000 tags (SAGE)	E15.5 caudal/100,000 tags (SAGE)	Fold-enrichment in E15.5 caudal (SAGE)	Normalized expression for E15.5 rostro- lateral (RT qPCR)	Normalized expression for E15.5 rostro- medial (RT-qPCR)	Normalized expression for E15.5 caudo- lateral (RT-qPCR)	Normalized expression for E15.5 caudo- medial (RT-qPCR)	Standard error of coefficient	Fold- enrichment in E15.5 rostro- medial (RT-qPCR)	Adjusted p value (RT-qPCR)	Fold- enrichment in E15.5 caudo- lateral (RT-qPCR)	Adjusted p value (RT- qPCR)	Fold- enrichment in E15.5 caudo- medial (RT-qPCR)	Adjusted p value (RT-qPCR)
Nil	NM_001043354 / NM 146095	RAR-related orphan receptor beta, Rorb	Nil	Nil	Rostral specific	0.46	0.09	-0.37	-0.53	0.34	-1.30	7.42E-01	-1.78	1.42E-01	-1.99	8.57E-02
gatacttggaatgacta	NM 007393	actin, beta, cytoplasmic, Actb	408.52	155.16	-2.63	3.85	3.79	3.37	3.47	0.18	-1.04	8.82E-01	-1.39	3.37E-01	-1.30	3.41E-01
ttggtgaaggaaaaaac	NM_021278	thymosin, beta 4, X chromosome, Tmsb4x	507.77	218.75	-2.33	-2.57	-2.73	-3.97	-3.53	0.26	-1.12	8.49E-01	-2.64	1.50E-02	-1.95	8.57E-02
ataatacataaaaaaaa	NM_007807	Cybb cytochrome b-245, beta polypeptide, Cybb	639.32	414.61	-1.54	-1.11	-3.57	-2.40	-1.97	0.42	-5.53	6.36E-05	-2.45	7.84E-02	-1.83	1.05E-01
Nil	NM_010151	<pre>nuclear receptor subfamily 2, group F, member 1, Nr2f1 (Coup- tf1)</pre>	Nil	Nil	Caudal specific	-0.76	-0.37	0.24	1.21	0.42	1.31	7.42E-01	2.00	1.21E-01	3.91	1.69E-03
gttgttcttccagtcgg	NM_016916	bladder cancer associated protein homolog (human), Blcap	4.62	5.09	1.10	0.03	0.40	0.69	0.78	0.24	1.30	7.42E-01	1.58	1.98E-01	1.69	1.05E-01
gtcatagctgttctgtg	BC025816	EST sequence BC025816	0	38.15	Caudal specific	-1.74	-1.31	-1.33	-0.94	0.32	1.34	7.42E-01	1.33	4.47E-01	1.74	1.05E-01
aagcttgacatttggaa	NM_026187	ankyrin repeat and zinc finger domain containing 1, Ankzf1	2.31	0.00	Rostral specific	-0.42	-0.21	-0.25	0.08	0.19	1.16	8.49E-01	1.12	6.80E-01	1.41	2.76E-01
aaccctaataaaaaaaa	AK132098 / X55780	mRNA for cytochrome c oxidase subunit I, Cox1	2.31	48.33	20.92	-1.17	-1.04	-1.00	-0.74	0.29	1.10	8.49E-01	1.13	6.80E-01	1.35	3.41E-01

A-8 Additional data file 7

Significantly represented genomic loci based on genomic clustering of tags. Original version of this data file is accessible <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s7.xls</u>.

Note 1	Chromosome	positions	presented here	e were based	on mouse assembly	y release 1	February	y 2006.
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- **Note 2** Adjusted p values were based on empirical bayesian moderated t-test with BH correction.
- **Note 3** Grey background denotes no RT-qPCRs were performed on these tags.
- Note 4 N.A.=Not determined.
- **Note 5** Bold p values denote a particular comparison is significant at p<0.05 level.
- **Note 6** The background colour for each cluster is meant to aid visualization of data across the table.

Ganomia	New (Jul	coordinate v 2007. mm9)					Hierarchical		S7	AGE		1	RT-qPCR	(Log2 expres	of norm sion)	alized	Fo	ld-enrich	ment af	ter normal ral cortex	ized to	E15.5	
Tag	Genomic cluster	Chromosome	Start coordinate	Strand	. Chromosome position (May 2004, mm5)	Tag orientation	Tag ID	DETS	clustering of log2 normalized expression	E15.5	E17.5	PN1.5	Adult	E15.5	E17.5	PN1.5	Adult	SE of coefficien	In E17.5	Adjusted p value	In PN1.5	Adjusted p value	In Adult	Adjusted p value
ttgtgatttgtactcta	Sox11	chr12	26991815	-	chr12:021263120:-	N.A.	Sox11-tag1	0	0	0.85	4.73	0	2.05											
cgcacgtgcacacgtag	Sox11	chr12	26991985	-	chr12:021263290:-	N.A.	Sox11-tag2	0	0	2.39	0	0	1.86											
tggctcacacactctga	Sox11	chr12	26994454	-	chr12:021265759:-	N.A.	Sox11-tag3	0	0	2.47	0	0	0.32											
aaacctgacagtgaata	Sox11	chr12	27164665	+	chr12:021435316:+	N.A.	Sox11-tag4	0	0	2.45	1.045	0	0.65											
ggagcaaaggtetetgg	Sox11	chr12	27825946	-	chr12:022104837:-	N.A.	Sox11-tag5	0	0	0.00	3.685	0	1.32											
tgttggacag	Sox11	chr12	28019322	-	chr12:022297492:-	Sense	Sox11-tag6	0	0	2.39	0.00	0.00	0.00											
gtgagtgtttgttgcat	Sox11	chr12	28019499	-	chr12:022297669:-	Sense	Sox11-tag7	1	6	64.61	83.91	9.33	0.24											
taaacacatc	Sox11	chr12	28019504	+	chr12:022297674:+	Antisense	Sox11-tag8	0	0	5.62	8.38	0.00	0.00											
gtgatcgtgt	Sox11	chr12	28019821	-	chr12:022297991:-	Sense	Sox11-tag9	0	0	0.75	1.05	2.33	0.00											
cttattccac	50x11	chr12	28019826	+	chr12:022297996:+	Antisense	Sox11-tag10	0	0	0.85	1.05	0.00	0.00	6.86			0.05							
cagagtgtagtgtgttg	Sox11	chr12	28020368	-	chr12:022298538:-	Sense	Sox11-tag11	1	1	18.31	32.51	2.33	0.33	6.76	6.54	5.44	-0.37	0.14	-1.16	4.59E-01	-2.50	2.63E-05	-140.05	1.38E-14
gcactgttaacaagtgt	Sox11	chr12	28020687	-	Chr12:022298857:-	Sense	Sox11-tag12	1	6	81.35	1.05	14.00	1.40	1.19	7.54	6.06	0.67	0.12	-1.19	3.80E-01	-3.32	1.145-06	-139.76	9.188-15
taaggeteagteetgte	50X11	chr12	28022089	+	chr12:022300259:+	Antisense	Sox11-tag13	0	0	6.55	1.05	2.33	0.48											
ctcttagcagtcaggat	Sout1	chr12	28022745	-	chr12:022300915:-	Sense	Sox11-tag14	0	0	29.80	13.11	7.00	0.32											
tatttgcaaaaaaatgc,ta	Sox11	chr12	28022890	+	chr12:022301055:-	Antisense	Sox11-tag16	0	0	42.92	7.37	2.33	0.87											
caaatottaa	Sov11	chr12	28023608	+	chr12.022301778.+	Antisense	Sox11-tag17	0	0	0.00	5 78	0.00	0.00		<u> </u>									
caaatatottootacot	Sox11	chr12	28025050	_	chr12:022303220:-	Sense	Sox11-tag18	0	0	25.35	13.11	11.66	0.63						-					
gtcagagaga	Sov11	chr12	28026005	_	chr12:022304175:-	Sense	Sox11-tag19	0	0	7 09	7 36	0	0.00		<u> </u>									
gcaaaggtactggcaga	Sox4	chr13	25344545	+	chr13:024632613:+	N.A.	Sox4-tag1	0	0	0.00	1.045	0	0.72											
tattectagaattacaa	Sox4	chr13	25344818	_	chr13:024632886:-	N.A.	Sox4-tag2	0	0	0.00	0	0	2.46											
gaagtgtaaacttttaa,ga	Sox4	chr13	28501982	-	chr13:027789795:-	N.A.	Sox4-tag3	0	0	0.75	1.045	2.33	1.08											
tatcetetat	Sox4	chr13	28552777	-	chr13:027840590:-	N.A.	Sox4-tag4	0	0	1.70	1.045	0	0.00											
ccagetaatectgtccg	Sox4	chr13	29040891	+	chr13:028328704+	Antisense	Sox4-tag5	1	6	71.05	19,40	27.99	0.32											
acaggcacgaggacgcc	Sox4	chr13	29041126	+	chr13:028328939+	Antisense	Sox4-tag6	1	6	94.51	56.67	23.33	0.31											
gtgatagcat	Sox4	chr13	29041258	-	chr13:028329071:-	Sense	Sox4-tag7	0	0	2.45	4.19	0.00	0.00											
ccataggact	Sox4	chr13	29041263	+	chr13:028329076:+	Antisense	Sox4-tag8	0	0	7.39	2.10	7.00	0.00											
gagaaaccag	Sox4	chr13	29041664	+	chr13:028329477:+	Antisense	Sox4-tag9	1	6	24.25	20.48	23.33	0.00											
gggacctcgtggaagcc	Sox4	chr13	29042712	-	chr13:028330525:-	Sense	Sox4-tag10	1	6	69.11	30.95	27.99	0.89	5.11	4.29	3.21	-0.34	0.32	-1.76	9.80E-02	-3.72	2.10E-04	-43.67	4.98E-10
tccatttccg	Sox4	chr13	29042717	+	chr13:028330530:+	Antisense	Sox4-tag11	0	0	1.70	1.05	0.00	0.00											
gagaaactcc	Sox4	chr13	29042835	-	chr13:028330648:-	Sense	Sox4-tag12	1	9	17.73	1.05	0.00	0.00	6.34	6.27	5.34	-0.02	0.14	-1.05	8.42E-01	-2.00	3.31E-04	-82.08	3.88E-14
ccaatgctcc	Sox4	chr13	29042840	+	chr13:028330653:+	Antisense	Sox4-tag13	0	0	5.76	4.73	0.00	0.00											
aggcaaaatcaaacaag	Sox4	chr13	29043013	+	chr13:028330826:+	Antisense	Sox4-tag14	0	0	5.09	0.00	2.33	0.56											
tccctgggcagtttcag	Sox4	chr13	29043741	-	chr13:028331554:-	Sense	Sox4-tag15	1	2	10.99	6.29	20.99	1.37	6.46	6.40	5.81	0.35	0.20	-1.04	8.42E-01	-1.57	2.53E-02	-68.92	8.95E-13
gctgactacc	Sox4	chr13	29044530	-	chr13:028332343:-	Sense	Sox4-tag16	1	9	21.89	0.00	0.00	0.00	8.45	8.28	7.57	2.34	0.21	-1.13	4.79E-01	-1.84	4.37E-04	-69.41	2.82E-14
tgtgggcccccaggtca	Sox4	chr13	29128016	+	chr13:028415829:+	N.A.	Sox4-tag17	0	0	0.00	0	0	0.72											
tacgacagaaaaaaaaa	Sox4	chr13	29998919	+	chr13:029286732:+	N.A.	Sox4-tag18	0	0	0.00	0	0	0.24											
ggtcacactatgacgcc	Sox4	chr13	30632706	-	chr13:029920519:-	N.A.	Sox4-tag19	0	0	6.03	5.235	9.33	14.13											
tctcttggtgtgtgttt	Sox4	chr13	30803002	+	chr13:030090815:+	N.A.	Sox4-tag20	0	0	0.00	0	0	2.22											
		New coord	inate (July	2007,					Hierarchical	9	AGE	I	T-qPCR	(Log2	of norm	alized	express	ion) F	old-enri	chment af	ter nor	malized to	E15.5 r	ostro-
Tag	Genomic cluster	Chromosome	Start coordinate	Strand	Chromosome position (May 2004, mm5)	Tag orientation	Tag ID	DETS	clustering of log2 normalized expression	Rostra	1 Caud	E: al ros lat	15.5 stro- r teral r	E15.5 costro- medial	E15.5 caudo- lateral	E15.5 caudo media	Coeff	of icient medi	.5 ro- ial	usted p value	E15.5 caudo- Lateral	Adjusted p value	E15.5 caudo- medial	Adjusted p value
gggacctcgtggaagcc	SOX4	chr13	29042712	-	chr13:028330525:-	Sense	Sox4-tag10	1	6	120.02	73.	77 5	.47	5.62	5,59	5.55	0.	39 1.	.0 7.	69E-01	1.08	8.19E-01	1.06	8.72E-01
gagaaactcc	SOX4	chr13	29042835	-	chr13:028330648:-	Sense	Sox4-tag12	1	9	2.31	50.8	87 6	.48	6.31	6.26	6.24	0	15 -1	12 6	62E-01	-1.16	5.56E-01	-1.18	7.63E-01
tccctgggcagtttcag	SOX4	chr13	29043741	-	chr13:028331554:-	Sense	Sox4-tag15	1	2	23.08	7.6	3 6	. 40	6.02	6.08	6.21	0.	16 -1.	30 5	54E-01	-1.25	5.56E-01	-1.14	7.63E-01
gctgactacc	SOX4	chr13	29044530	-	chr13:028332343:-	Sense	Sox4-tag16	1	9	4.62	61.0	05 7	.75	7.43	7.51	7.58	0.	20 -1.	24 5.	54E-01	-1.18	5.56E-01	-1.12	7.63E-01

A-9 Additional data file 8

List of primers, probes, clones and assays designed for RT-qPCR, RACE, Southern, Northern and ISH analysis. Original version of this data file is accessible <u>http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s8.xls</u>.

SECTION A: LIST OF RT-qPCR ASSAYS DESIGNED FOR GENOMIC CLUSTERS

- **Note 1** Primer sets are listed according to the SAGE tag position.
- Note 2 NISP=Non-intron spanning primer; ISP=intron-spanning primer
- **Note 3** "F" in the primer name denotes forward primer whereas "R" denotes reverse primer.
- **Note 4** "SAGE tags" column provides information on genomic cluster tags where the corresponding primers were used to performed qPCR.
- Note 5 UPL Probe # refers to the Mouse Universal ProbeLibrary (Roche) Cat. No.: 04683641001 (4683641).
- Note 6 Tm calculations were based on Breslauer et al, Proc Natl Acad Sci U S A 83 (1986) 3746-50.

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Primer set	Gene ID	Primer Name	Notes	SAGE tags	Length (mer)	UPL Probe #	Sequence 5'-3'	%GC	Tm (°C)	Amplicon size	Amplicon sequence
1	Sox4	sox4_t4_F	NISP	covi tegio	18	99	GTTGGGGATGCAGAAGGA	56	60	73nt	gttggggatgcagaaggacccggagcacagagggcgttgg
	Sox4	sox4_t4_R	NISP	SUX4_tay10	22	99	TTTGCACAGACCCCAGGCGGAG	64	73	7.511	ggttcccgggcctccgcctggggtctgtgcaaa
2	Sox4	3671s4-3tgF	NISP	covi tool2	18	78	AGGCTGGCCTGCTACTCC	67	60	Rent	gcaaggacaaggggaaaaaaggtgggggggggggggggg
4	Sox4	3672s4-3tgR	NISP	SOX4_tag12	18	78	GCTGGGCTTTCTCCTCCT	67	59	0011	aagcccagcccgggacttcgccagcgtggagtttctccatgcc
2	Sox4	3673s4-5F	NISP	covi togit	20	17	CTGAACCCCAGCTCAAACTT	50	59	Otot	ctgaaccccagctcaaactttgagagcatgtccctgggcagttt
3	Sox4	3674s4-5R	NISP	SOX4_tag15	23	17	GGTTCGAAGTTAAAATCCAGGTC	50	60	9211	cagctcctcatcggcgctcgatcgggacctggattttaacttcg
4	Sox4	3675s4-10F	NISP	covi togic	20	79	ACAGCGACAAGATTCCGTTC	50	60	COnt	acagcgacaagattccgttcatccaggaggcggagcggctg
4	Sox4	3676s4-10R	NISP	SOX4_lag16	19	79	GTCAGCCATGTGCTTGAGG	58	60	0211	cgcctcaagcacatggctgac
5	Sox11	sox11_t16_F	NISP	covil togil	23	6	GTTGAATTCATACACTCCAATGT	35	56	07nt	gttgaattcatacactccaatgtctctttttgcaggagtttttcaca
5	Sox11	sox11_t16_R	NISP	sox n_tagn	20	6	GGAGATTGATCACACGATTT	40	55	9/11	gaggaatacatttgttcaaaagaccaataaaaatcgtgtgatc
c	Sox11	sox11_t3_F	NISP	could togdo	20	21	ATCCCGTGATGCTTTGTTTC	45	59	ZEnt	atcccgtgatgctttgtttcccgggacagagccacctgaagtct
0	Sox11	sox11_t3_R	NISP	sox11_tag12	21	21	TGTTAACAGTGCCATGCTGAT	45	59	/ / Shi	gagagtagttatcagcatggcactgttaaca
-	Hmbs	3843_hmbs_F	ISP	endogenous	20	42	AAAGTTCCCCAACCTGGAAT	45	59	00-1	aaagttccccaacctggaattcaagagtattcggggaaacctc
1	Hmbs	3844_hmbs_R	ISP	control	20	42	CCAGGACAATGGCACTGAAT	50	60	John	aacacccgccttcggaagctggatgagctgcaggaattcagt
0	Psmb2	3367_psmb2_F	ISP	endogenous	20	25	GAGGGCAGTGGAGCTTCTTA	55	59	74	gagggcagtggagcttcttaggaagtgtctggaggagctcca
0	Psmb2	3368_psmb2_R	ISP	control	21	25	AGGTGGGCAGATTCAAGATG	50	60	1 /111	gaagcgcttcatcttgaatctgcccacct
0	Pgk1	3365_pgk1_F	ISP	endogenous	18	108	TACCTGCTGGCTGGATGG	61	60	05-1	tacctgctggctggatgggcttggactgtggtactgagagcag
9 Pgk1	3366_pgk1_R	ISP	control	20	108	CACAGCCTCGGCATATTTCT	50	60	bont	caagaaatatgccgaggctgtg	

SECTION B: LIST OF PRIMERS AND OLIGONUCLEOTIDE PROBES USED IN 3' RACE AND SOUTHERN BLOTTING

- **Note 1** Primers are listed according to the Southern blot figure in the manuscript.
- **Note 2** Adaptor primer sequence is TACGACGTCTGCTAGGACTG.
- **Note 3** "SAGE tags" column provides information on genomic cluster tags where the corresponding primers were used to perform 3' RACE.
- **Note 4** Oligonucleotide probes were end-labeled prior to hybridization (see manuscript for more information).

Southern blot number	Gene ID	Primer used for 3' RACE with adaptor primer	Orientation of targeted mRNA	SAGE tags	Length (mer)	Sequence 5'-3'	%GC	Тт (°С)	Oligonucleotide probe used for hybridization during Southern blotting (sequence 5'-3')
Fig. 7D.1	Sox4	3675s4-10F	Sense	Sox4_tag10, tag15, tag16	20	ACAGCGACAAGATTCCGTTC	50	60	GTCAGCCATGTGCTTGAGG
Fig. 7D.2	Sox4	3673s4-5F	Sense	Sox4_tag10, tag12, tag15	20	CTGAACCCCAGCTCAAACTT	50	59	GGTTCGAAGTTAAAATCCAGGTC
Fig. 7D.3	Sox4	s4_tg4_ota	Sense	Sox4_tag10	20	TGATGTTGGTGGTGGCTAAA	45	60	GCTGGGCTTTCTCCTCCT
Fig. 7D.4	Sox4	sox4_t4_R	Antisense	Sox4_tag11, tag13, tag14	22	TTTGCACAGACCCCAGGCGGAG	64	73	AGGCTGGCCTGCTACTCC
Fig. 8D.1	Sox11	3665s11-8F	Sense	Sox11_tag18, tag19	20	GTGGCGGTCAGGATAAAGAG	55	59	TCTCAGCGCCACATCTCTC
Fig. 8D.2	Sox11	3669s11-4tgF	Sense	Sox11_tag14, tag15	20	GCGTTGTGTGCATAGCAGTC	55	60	GCACTCGAGTCTGTGAACTAGG
Fig. 8D.3	Sox11	sox11_t3_F	Sense	Sox11_tag11, tag12	20	ATCCCGTGATGCTTTGTTTC	45	59	TGTTAACAGTGCCATGCTGAT
Fig. 8D.4	Sox11	3670s11-4tgR	Antisense	Sox11_tag16, tag17	22	GCACTCGAGTCTGTGAACTAGG	55	59	GCGTTGTGTGCATAGCAGTC
Failed	Sox11	s11_tg5_ota	Antisense	Sox11_tag13	21	GCCAACTCTCAGAGAAACACG	52	60	TTCCTGTTCGGACACATGTAAG
Failed	Sox11	3663s11-9F	Antisense	Sox11_tag17	19	GGCCAAGGACTTTGCAACT	53	60	AGGTTGCTCTCGGCTTCC
Fig. 7D.5 & Fig. 8D.5	Psmb2	3367_psmb2_F	Sense	N.A.	20	GAGGGCAGTGGAGCTTCTTA	55	<mark>5</mark> 9	AGGTGGGCAGATTCAAGATG
Fig. 7D.6 & Fig. 8D.6	Psmb2	3368_psmb2_R	Antisense	N.A.	21	AGGTGGGCAGATTCAAGATG	50	60	GAGGGCAGTGGAGCTTCTTA
Fig. 7D.7 & Fig. 8D.7	Hmbs	3843_hmbs_F	Sense	N.A.	20	AAAGTTCCCCAACCTGGAAT	45	59	CCAGGACAATGGCACTGAAT
Fig. 7D.8 & Fig. 8D.8	Hmbs	3844_hmbs_R	Antisense	N.A.	20	CCAGGACAATGGCACTGAAT	50	60	AAAGTTCCCCAACCTGGAAT

SECTION C: LIST OF DOUBLE-STRANDED DNA PROBE USED IN NORTHERN BLOTTING

These probes were double-digested from pGEMT clone, gel purified and sequenced prior to random labeling. The position of the probe is based on the RefSeq canonical mRNA sequence. Note 1

Note 2

Name of probe	Size of probe	Probe sequence	Target sequence (Refseq)	The position of the probe on target mRNA
Sox4 (C1)	614	TTGATGTTGGTGGTGGCTAAAAAAGCTACTTCGAGTTTCCTCCCCAATTTTGCTTGAAGAGACTCCCCCCCACCCCACCCTTCCAACGAGCT TCCGGACTTGGTGCACCCCCAGCAAGAAAAGAA	Sox4 (NM_009238)	2330-2943bp
Sox11 (C10)	950	CACCTGAACCAGCGTTCTCTTATTCTTTAAGCTGTGGAAATAATTTCCAGTTTCTACATTCTCGATATGCATCCTTATTAAAAAGATAATACGAAT GAAAGGCAGTGTGCTTAAAGTGTGCTTTGCAAATACATGTTATGAATGA	Sox11 (NM_009234)	4558-5507ър

SECTION D: LIST OF CLONES USED TO GENERATE RIBOPROBE FOR IN SITU RNA HYBRIDIZATION (ISH

Note 1 Clones were either obtained from NIA mouse 15k cDNA clone set or through PCR amplification and cloning procedure.

Note 2 The restriction enzymes used were from Promega and their relevant buffer systems.

Note 3 "Comment" describes the position of the clone within the canonical mRNA transcript.

	Gene Vector	Promoter region	Restriction	-	Entimated		-	NUA moura dek aDNA
Gene	Vector	used to generate the	enzyme used for	Sequencing result	Esumated	Probe	Comment	NIA mouse 15K CDNA
		riboprobe	linearization		size			cione accession
Actb	pSPORT1	T7	Mlul/Buff. D	Confirmed +/-	1580bp	Sense	Full length	H3018D10
Actb	pSPORT1	SP6	EcoRI/Buff. H	Confirmed +/-	1580bp	Antisense	Full length	H3016D10
BC025816	pGEMT	T7	Sacl/Buff. J	Confirmed +/-	911bp	Antisense	Mid BC02	Amplification by PCR
BC025816	pGEMT	SP6	Aatll/Buff. J	Confirmed +/-	911bp	Sense	Mid BC02	followed by cloning
Blcap	pSPORT1	T7	Mlul/Buff. D	Confirmed - only	965bp	Sense	1/2 of Blcap till 3'	112008010
Blcap	pSPORT1	SP6	EcoRI/Buff. H	Confirmed - only	965bp	Antisense	1/2 of Blcap till 3'	HSUUGTU
Coup-tf1	pSPORT1	T7	Mlul/Buff. D	Confirmed +/-	375bp	Sense	3' of Ctf1	H2007D07
Coup-tf1	pSPORT1	SP6	EcoRI/Buff. H	Confirmed +/-	375bp	Antisense	3' of Ctf1	H3097D07
Cybb	pSPORT1	T7	Mlul/Buff. D	Confirmed +/-	1492bp	Sense	Mid Cybb	LI2060E11
Cybb	pSPORT1	SP6	Kpnl/Buff. J	Confirmed +/-	1492bp	Antisense	Mid Cybb	HSUGUFTI
D1ertd161e	pSPORT1	T7	BamHI/Buff. E	Confirmed +/-	2460bp	Sense	Full length	H2024H07
D1ertd161e	pSPORT1	SP6	Kpnl/Buff. J	Confirmed +/-	2460bp	Antisense	Full length	H3024H07
Hba-a1	pSPORT1	T7	Mlul/Buff. D	Confirmed +/-	>500bp	Sense	Full length	H2045412
Hba-a1	pSPORT1	SP6	Kpnl/Buff. J	Confirmed +/-	>500bp	Antisense	Full length	HSU45A12
Rorb	pGEMT	T7	Spel/Buff. B	Confirmed +/-	935bp	Sense	Mid Rorb	Amplification by PCR
Rorb	pGEMT	SP6	Apal/Buff. A	Confirmed +/-	935bp	Antisense	Mid Rorb	followed by cloning
Sox11 (C10)	pGEMT	T7	Spel/Buff. B	Confirmed +/-	950bp	Antisense	Mid Sox11 (3' UTR)	Amplification by PCR
Sox11 (C10)	pGEMT	SP6	Aatll/Buff. J	Confirmed +/-	950bp	Sense	Mid Sox11 (3' UTR)	followed by cloning
Sox4 (C1)	pGEMT	T7	Spel/Buff. B	Confirmed +/-	614bp	Antisense	3' of Sox4 (3' UTR)	Amplification by PCR
Sox4 (C1)	pGEMT	SP6	Aatll/Buff. J	Confirmed +/-	614bp	Sense	3' of Sox4 (3' UTR)	followed by cloning
Tmsb4x	pSPORT1	T7	Mlul/Buff. D	Confirmed - only	~500bp	Sense	Full length	H3143A02
Tmsb4x	pSPORT1	SP6	EcoRI/Buff. H	Confirmed - only	~500bp	Antisense	Full length	H3143A02

SECTION E: LIST OF PRIMERS USED IN STRAND SPECIFIC RT-PCR

- **Note 1** Please correspond the gel lane positions in the table with Figure 6.
- **Note 2** For sense mRNA=primer used to synthesize the first strand cDNA using sense mRNA as template.
- **Note 3** For antisense mRNA=primer used to synthesize the first strand cDNA using antisense mRNA as template.
- Note 4 Tm calculations were based on Breslauer et al, Proc Natl Acad Sci U S A 83 (1986) 3746-50.

Gel Iane	Gene ID	Primer Name	Notes	Length (mer)	Sequence 5'-3'	%GC	Tm (°C)	Amplicon size	Amplicon sequence
4	Sox4	3675s4-10F	For antisense mRNA	20	ACAGCGACAAGATTCCGTTC	50	60		acagcgacaagattccgttcatccaggaggcggagcggctg
1	Sox4	3676s4-10R	For sense mRNA	19	GTCAGCCATGTGCTTGAGG	58	60	62nt	cgcctcaagcacatggctgac
2	Sox4	sox4_t4_F	For antisense mRNA	18	GTTGGGGATGCAGAAGGA	56	60	72nt	gttggggatgcagaaggacccggagcacagagggcgttgg
2	Sox4	sox4_t4_R	For sense mRNA	22	TTTGCACAGACCCCAGGCGGAG	64	73	7511	ggttcccgggcctccgcctggggtctgtgcaaa
2	Sox4	3673s4-5F	For antisense mRNA	20	CTGAACCCCAGCTCAAACTT	50	59	02nt	ctgaaccccagctcaaactttgagagcatgtccctgggcagttt
5	Sox4	3674s4-5R	For sense mRNA	23	GGTTCGAAGTTAAAATCCAGGTC	50	60 ^{9,}	- 5 2111	cageteetcateggegetegategggaeetggattttaaetteg
1	Sox11	3665s11-8F	For antisense mRNA	20	GTGGCGGTCAGGATAAAGAG	55	59	75nt	gtggcggtcaggataaagaggatggtggggggggggggg
-	Sox11	3666s11-8R	For sense mRNA	19	TCTCAGCGCCACATCTCTC	55	60	7.511	aagatgctcatggtcagagagatgtggcgctgaga
5	Sox11	sox11_t16_F	For antisense mRNA	23	GTTGAATTCATACACTCCAATGT	35	56	97nt	gttgaattcatacactccaatgtctctttttgcaggagtttttcaca
5	Sox11	sox11_t16_R	For sense mRNA	20	GGAGATTGATCACACGATTT	40	55	5711	gaggaatacatttgttcaaaagaccaataaaaatcgtgtgatc
6	Sox11	3669s11-4tgF	For antisense mRNA	20	GCGTTGTGTGCATAGCAGTC	55	60	60nt	gcgttgtgtgcatagcagtctagccggttgggtaccctgctcctg
0	Sox11	3670s11-4tgR	For sense mRNA	22	GCACTCGAGTCTGTGAACTAGG	55	59	6911	tacctagttcacagactcgagtgc
7 and 8	Hmbs	3843_hmbs_F	For antisense mRNA	20	AAAGTTCCCCAACCTGGAAT	45	59	Oget	aaagttccccaacctggaattcaagagtattcggggaaacct
	Hmbs	3844_hmbs_R	For sense mRNA	20	CCAGGACAATGGCACTGAAT	50	60	3011	caacacccgccttcggaagctggatgagctgcaggaattcag

SECTION F: LIST OF RT-qPCR ASSAYS DESIGNED

- **Note 1** Primer sets are listed in alphabetical order.
- **Note 2** NISP=Non-intron spanning primer; ISP=intron-spanning primer.
- **Note 3** "F" in the primer name denotes forward primer whereas "R" denotes reverse primer.
- Note 4 UPL Probe # refers to the Mouse Universal ProbeLibrary (Roche) Cat. No.: 04683641001 (4683641).
- Note 5 Tm calculations were based on Breslauer et al, Proc Natl Acad Sci U S A 83 (1986) 3746-50.

Primer	0		Duine au Manaa	Length	UPL	Comucines El 21	*/00	Tm	Amplicon	A
set	Gene ID	Notes	Filler Name	(mer)	Probe #	Sequence 5-5	/ /// ////////////////////////////////	(°C)	size	Amplicon sequence
4	AA122503	NISP	AA122503 F	22	25	AGATGCTGCACACAGGTATCTC	50	59	00-1	
1	AA122503	NISP	AA122503 R	25	25	TCTAGTTTGGTTTAGGTGACATTCG	50	60	60nt	agatgctgcacacaggtatctcccctcctccaccccgaatgtcacctaaaccaaactaga
2	Actb	ISP	3361_actb_F	20	56	AAGGCCAACCGTGAAAAGAT	45	60	110nt	aaggccaaccgtgaaaagatgacccagatcatgtttgagaccttcaacaccccagccatgtacgtagccatc
	Actb	ISP	3362 actb R	21	56	GTGGTACGACCAGAGGCATAC	57	59		caggetgtgetgtccctgtatgcctctggtcgtaccac
3	Actl6b	ISP	actl6b_F	19	104	AAGTTCAGCCCCTGGATTG	53	60	71.nt	
	Actl6b	ISP	actl6b_R	20	104	TTGGAGATCCACATCTGCTG	53	59	7 111	aagiicageeeelggallggaggeleealellggeeleaclgggeacalleeageagalgiggaleleeaa
4	AK138272	NISP	AK138272_F	20	102	GTTCGTCCGTACCATCATCC	55	60	105nt	gttcgtccgtaccatcatccaattagtaggaaagatataattcccaccccttctcagccaatgaaaagttgaaat
4	AK138272	NISP	AK138272_R	21	102	CATGCTTATCCTCACCTCAGC	55	59	10511	atgttgttggctgaggtgaggataagcatg
5	AK139402	NISP	AK139402_F	20	56	TCTTCACCGTAGGTGCGTCT	55	60	63nt	tetteacentaggiaggiaggiaggiaggiaggiaggiaggiaggiagg
5	AK139402	NISP	AK139402_R	20	56	CATCAACATAGCCGTCAAGG	55	59	0.511	เขาะสุราร์ เล่าสาราย เล่าสารา สาราย สาราย เล่าสารา สาราย สาราย เล่าสาราย เล่าสาราย เล่าสารา สาราย สารา สารา
6	AK140219	NISP	AK140219_F	23	83	CCTCTTAGGGTTGGTAAATTTCG	43	60	69nt	cctcttagggttggtaaatttcgtgccagccaccgcggtcatacgattaacccaaactaattatcttcg
	AK140219	NISP	AK140219_R	26	83	CGAAGATAATTAGTTTGGGTTAATCG	43	60		
7	AK154943	NISP	AK154943_F	19	69	GGCCCTAGCAATCGTTCAC	58	60	60nt	ggccctagcaatcgttcacctcctcttcctccacgaaacaggatcaaacaacccaacagg
	AK154943	NISP	AK154943_R	20	69	CCTGTTGGGTTGTTTGATCC	58	60		
8	Als2cr2	ISP	als2cr2_F	20	17	TCTCCATTTATGGCCTACGG	50	59	69nt	tctccatttatggcctacggttcagcaagtcagctcctaaggacctactttcctgatggaatgagtgag
	Als2cr2	ISP	als2cr2_R	23	17	CTCACTCATTCCATCAGGAAAGT	50	59		
9	Арр	ISP	app_F	20	34	AGCACCGAGAGAGAATGTCC	55	59	69nt	ancaccuananantateccannteatnananatunnaananneananenteaaneeaanaaettue
	Арр	ISP	app_R	19	34	GCAAGTTCTTGGCTTGACG	55	59		agoaoogagagagagaagoooaggioalgagagagggaagagggaagagogloaagooaagaaoligo
10	Atp7a	ISP	atp7a_F	23	17	GAGCAGCTGTAACCAAATATTGC	43	60	64nt	
	Atp7a	ISP	atp7a_R	22	17	TCTGTACAGGTACCCAGGGTTT	43	59		gagoagoigiaaooaaaiaiigoaaaaaggagoiggaoaoigaaaoooigggiaooigiaoaga
11	AU258168	NISP	AU258168_F	19	62	CTTGGGAGGAGGAGACAGG	63	59	72nt	cttgggaggaggagacaggggacacctgctgaccctggcctagcaggtgatgtaagcaggtgacacagct
	AU258168	NISP	AU258168_R	20	62	GCAGCTGTGTCACCTGCTTA	63	60		gc
12	BC025816	ISP	3433cdnap1_F	19	83	CGCCGTAAACAGTGGATCA	53	60	122nt	cgccgtaaacagtggatcaaggtggcgtccatgaaccagcgccgtgtggatttctacctagcttccattgaaga
	BC025816	ISP	3434cdnap1_R	20	83	GAAGACAGCGCTCCATTCTC	55	60		catgctggtggctgtcggtggccggaacgagaatggagcgctgtcttc
13	Bcl11a	ISP	bcl11a_F	18	3	CCCCGCAGGGTATTTGTA	56	59	65nt	concentrational and the
	Bcl11a	ISP	bcl11a_R	21	3	GAATGGCTGTTTGCAAGTTGT	56	60		
14	Blcap	ISP	3435blcap_F	19	74	AGCTAAGGTGGAGGCAAGC	58	59	116nt	agctaaggtggaggcaagcagcggcggcgacggcgacagtggcggcagtgccatggtggggctcgcag
	Blcap	ISP	3436blcap_R	19	74	GCTGTGCTCTCTGGCTGTC	63	59		gatccctgctgccttggtgatcccgggctgacagccagagagcacagc
15	Blcap	NISP	3517blcap_F	20	32	GGACTCCAAGGTGGTTCAGA	55	60	62nt	ggactccaaggtggttcagacaagacccaggggagcagtcgccatcatcctcccaccaggag
	Blcap	NISP	3518blcap_R	19	32	CTCCTGGTGGGAGGATGAT	58	59		
16 17 18 19	BQ1/6089	NISP	BQ1/6089_F	23	99		35	60	62nt 71nt 107nt 65nt	ttctttttaaatgcagggtctgatttcctgtgctccatgtgatatggtgtgattgagaaggt cacttcaagttgcgttagacatttcttaccgagccccaggcctggccgcggtaactgacttttacatggga caagttcctccgcaccaagggggctcacgagcgacggcgacagctgcaggactttcagccagagcctgcaggag
	BQ1/6089	NISP	BQ1/6089_R	24	99	ACCITCICAATCACACCATATCAC	35	60		
	BQ177886	NISP	BQ177886_F	24	45	CACTTCAAGTTGCGTTAGACATTT	38	59		
	BQ1//886	NISP	BQ1//886_R	23	45	ICCCAIGIAAAAGICAGIIACCG	38	60		
	Btg1	ISP	btg1_F	18	17		56	60		
	Btg1	ISP	btg1_R	21	17		50	59		ctgctggcagaacattacaaacatcactggttcccag
	Calm1	ISP	caim1_F	20	89	GCTGCAGGATATGATCAACG	50	59		actacaggatatgatcaacgaagtggatgctgatggcaatggcaccattgacttcccagagttct
	Caimi	15P		22	89	AGAACTCTGGGAAGTCAATGGT	50	59		
20 21 22	Camk2a	ISP	camk2a_F	20	75		55	60	97nt	
		15P	camk2a_R	20	75	GGULAGUAAUAGATTUTUAG	50	60		
	Camk2n1	NISP	camk2n1_t2_F	20	21		20	62	112nt	
	Camk2n1		2510cond2 E	21	21		40	03 50		amgcaaaaaangccicmgcgigaggaan
	Cand2		2520cond2_P	10	39		40	09	60nt	ctggcagaaacctcaatatgctgcgagcacaggtgcccctagtgataaaggccctgcagc
23		NICD		25	00		30	60	75nt	
	CD802535	NISP	CD802535_F	20	90	COTTECCTETTCTETETETAA	44	60		ู่รูปอาหาร์ เกิดสาราย เกิดสาราย เกิดสาราย เกิดสาราย เกิดสาราย เกิดสาราย เกิดสาราย เกิดสาราย เกิดสาราย เกิดสาราย สาราย เกิดสาราย เกิดส
	Cdk4			20	13		55	59		y taocananatanaanaatatanaacacaatactactactacaatataacottaacottaacocaataaacaaatata
24	Cdk4	ISP	cdk4 R	20	13	TTGTGCAGGTAGGAGTCCTC	55	60	109nt	yooayayayayayooyyayoyoayooyoaciyyaaaiyoiyacoiiiaacooadaayoyaalolo
25	Cdkn1c	ISP	cdkn1c_F	20	17	CAGGACGAGAATCAAGAGCA	50	59	110nt	caggacgagaatcaagagcagcgggccaggagctgaaggaccagcctctctcggggattccaggacgt
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25	Cdkn1c	ISP	cdk1nc_R	18	17	GCTTGGCGAAGAAGTCGT	50	59	TION	cctgcacccgggactgctgcggccaatgcgaacgacttcttcgccaagc
26	Chgb	ISP	chgb_F	19	79	ACGACTCGGAGGAGCAGAT	58	59	110nt	acgactcggaggagcagatggggcctcaccaggaggcaaacgatgaaaaggccagggctgaccagag
20	Chgb	ISP	chgb_R	20	79	GCAGCCAAGTTCTCCAGTTC	58	59	112ni	agttctgacggcggaagaaaaaggaactggagaacttggctgc
27	Chn1	ISP	3490chn1_R	21	9	TGGAGTTGGCATATGGTATGG	48	60	88nt	gccattggtttctgatgcttgcacacacacacacacataagcagtgccctggctgttacatcaccatccccatacca
	Chn1	ISP	3489chn1_F	20	9	GCCATTGGTTTCTGATGCTT	45	60		tatgccaactcca
28 29 30	Clcn2	ISP	clcn2_F	20	103	AAAACCATCAACCGCTTCCT	45	60	71.nt	
	Clcn2	ISP	clcn2_R	21	103	GTGGAGATGAGCAGAGTCACC	45	59	7 111	aaaaccalcaaccycliccicalyayyaaacyyclyclolloccyycaclyylyaclolycloalolocac
	Coup-tf1	ISP	3379_couptf1_F	20	89	CAAAGCCATCGTGCTATTCA	45	59	71nt	
	Coup-tf1	ISP	3380_couptf1_R	19	89	CCTGCAGGCTTTCGATGT	56	59	7.110	
	Cox1	ISP	3475cox1_F	21	46	TCGAATGTGTGATATGGTGGA	43	59	94nt	tcgaatgtgtgatatggtggagggcagccatgaagtcattctaaatttgttgaggtatatgatactgatattacttct
	Cox1	ISP	3476cox1_R	22	46	CCTTTGCTTCAAAACGAGAAGT	41	59	34m	cgttttgaagcaaagg
31	Cryab	ISP	cryab_F	18	80	ACGGCAAGCACGAAGAAC	56	59	60nt	
51	Cryab	ISP	cryab_R	20	80	TCCGGTACTTCCTGTGGAAC	56	59	oant	acygcaagtacyaagaacyctaggacyaataiggciitaicittagggagiittataggaagiactyga
32	Csrp2	ISP	csrp2_F	18	106	GACCGCGGTGAGAGACTG	67	60	61nt	asconominananactanacestessaccesasatactessectesesanacetscases
52	Csrp2	ISP	csrp2_R	20	106	TTGTCGTAGGCCTGTGAGGT	67	60	om	yaccycygigagagacigggcaicaagccagagagigcicaaccicacaggcciacgacaa
33	Ctsd	ISP	ctsd_F	20	64	TGAGCCAGGACACTGTATCG	55	59	125nt	tgagccaggacactgtatcggttccatgtaagtctgaccagtcaaaggcaagaggtatcaaggtggagaaac
55	Ctsd	ISP	ctsd_R	20	64	CTTGGCTGCAACAAATACGA	55	59	12.511	agatctttggagaagccaccaagcagcctggaatcgtatttgttgcagccaag
34	Cybb	ISP	3441cybb_F	20	20	TGCCAACTTCCTCAGCTACA	50	59	73nt	tappaanttootaaantapaatatataonttaotaantaaataaataaataaaata
54	Cybb	ISP	3442cybb_R	20	20	GTGCACAGCAAAGTGATTGG	50	60	7511	igocaaciicolagolacaalaiciacollaciggolgggalgaaloloaggocaaloaciilgolgigoac
35	Cybb	ISP	3515cybb_F	19	108	CTGATCCTGCTGCCAGTGT	58	59	83nt	ctgatcctgctgccagtgtgtcgaaatctgctctcctttctcaggggttccagtgcgtgttgctcgacaaggattcg
00	Cybb	ISP	3516cybb_R	21	108	TGTCTTCGAATCCTTGTCGAG	48	60	oom	aagaca
36	D1Ertd161e	ISP	3443dier_F	20	71	CTCAGTGACCGGGAGAAGAG	60	59	69nt	cteantnacennnanaananetetnaetneananeneenaettnetneeeanttnunaneeetane
50	D1Ertd161e	ISP	3444dier_R	18	71	GCTAGGGGCTCCCAACTG	67	60	UUIII	0039192009992323239292019990190392909209201900391190039119993900001890
37	D1Ertd161e	ISP	3507dier_F	23	81	GGAGAAGAATCTTGATGCCTATG	43	59	74nt	ggagaagaatcttgatgcctatgattacaacaaggctcgggtgccagggccattgactcaagaaatggaggc
51	D1Ertd161e	ISP	3508dier_R	20	81	GGGCCTCCATTTCTTGAGTC	55	60	7410	20
38	Dcx	ISP	dcx_F	20	9	ACACCCTTGATGGAAAGCAG	50	60	77nt 138nt	
	Dcx	ISP	dcx_R	20	9	AGGACCACAAGCAATGAACA	50	59		494999194199444994991949919499194194199194194
39	Dr1	ISP	dr1_F	23	102	CAACAGGAATTATTTGCAAAAGC	35	60		caacaggaattatttgcaaaagctagacagcaacaagcagaattggcccaacaggaatggcttcaaatgca
	Dr1	ISP	dr1_R	21	102	TGAAGATCCTGCTTGAGTGGA	35	60		gcaagcagctcaacaagcccagctggctgcagcctcagccagc
40	Egr1	ISP	egr1_F	20	22	CCTATGAGCACCTGACCACA	55	59	90nt	cctatgagcacctgaccacagagtccttttctgacatcgctctgaataatgagaaggcgatggtggagacgagt
	Egr1	ISP	egr1_R	20	22	ICGIIIGGCIGGGAIAACIC	55	60		tatcccagccaaacga
41	Eif2s3x	ISP	eif2s3x_F	18	76	GAGCCCCGTCTCATTGTC	61	59	76nt	gagccccgtctcattgtcatcaggtcatttgatgtcaacaaacctggctgtgaagtcgatgaccttaagggaggt
	Eif2s3x	ISP	eif2s3x_R	20	76	CACCTCCCTTAAGGTCATCG	61	59		g
42	Ezh2	ISP	ezh2_F	21	38	GCTCTTCTGTCGACGATGTTT	48	59	66nt	octettetotegacgatgttttaagtatgactgetteetacatecetteeatgeaacaeceaacae
	Ezh2	ISP	ezh2_R	18	38	GIGIIGGGIGIIGCAIGG	48	59		· · · · · · · · · · · · · · · · · · ·
43	Foxg1	ISP	toxg1_F	18	26	GAAGGCCTCCACAGAACG	61	59	114nt	gaaggeeteeacagaacgeaceecacegeteageegeeeteageegeeteageegeeteagee
	Foxg1	ISP	toxg1_R	21	26	CAAGGCATGTAGCAAAAGAGC	61	60		gagetegeegegggeegeaggaagetettttgetacatgeettg
44	Gria3	ISP	gria3_F	20	31	AGCCGTGTGATACGATGAAA	45	59	99nt 77nt 77nt 98nt	agccgtgtgatacgatgaaagttggtggaaatctggattccaaaggctatggtgtggcaacccctaaaggctc
	Gria3	ISP	gria3_R	20	31		45	59		agcattaggaacgccigtaaaccttg
45	Gstm1	15P	gstm1_F	20	100	GCAGCICATCATGCICIGII	50	59		gcagcicaicaigcicigiiacaacccigaciiigagaagcagaagccagagiiciigaagaccaicccigaga
	Gstm1	15P	gstm1_R	21	100		00	59		
46	HZary	15P	nzary_F	24	47		38	59		
	Hzary	15P	nzary_r	23	47		38	59		
47	HIMDS		3643_NMDS_F	20	42		40	28		
-		IOP	5044_NINDS_K	20	42		60	60		
48	Hmgb3		hmgb3_P	20	04 94		60	50	108nt	
	Hort1		3363 hprt1 E	10	04	TCCTCCTCAGACCGCTTT	53	59		
49	Hort1		3364 hprt1 P	21	95		18	50	90nt	
	i ipiti	IOF	5504_IIPILI_R	∠ 1	30	JUI DO I DAI DAI DO I AAI D	1 40	J9		yuyaiyaattayy

50	llf3	ISP	ilf3_F	19	40	TGGGTACAGCAGCAATTCG	53	60	61nt	taataaaaaaaataaaaaaaaaaaaaaaaaaaaaaaaaa	
	llf3	ISP	ilf3_R	20	40	ATGCCCTCCATTGCTGTAGA	53	60		เข้าสุดการการการการการการการการการการการการการก	
51	ltpr1	ISP	itpr1_F	20	88	TGGCCAGCTGTCAGAACTAA	50	59	105nt	tggccagctgtcagaactaaaggaccagatgacagaacagaggaagcagaaacaaagaatcggccttct	
	ltpr1	ISP	itpr1_R	20	88	TGCTGTGGGTTGACATTCAT	50	59		aggacatectectcacatgaatgtcaacecacagca	
50	Klf3	ISP	klf3_F	19	2	TCGCACTTGAAAGCACACA	47	60	62nt	· · · · · · · · · · · · · · · · · · ·	
52	Klf3	ISP	klf3_R	19	2	TCCCAGGTGCATTTGTACG	47	60		tcgcactigaaagcacacagaagaactcatacaggagaaaagccgtacaaatgcacciggga	
50	Mapt	ISP	3521mapt_F	18	79	AGCAGGCATCGGAGACAC	61	59	02-4	agcaggcatcggagacaccccgaaccaggaggaccaagccgctgggcatgtgactcaagctcgtgtggcc	
55	Mapt	ISP	3522mapt_R	21	79	CATTTCCTGTCCTGTCTTTGC	48	59	92ht	agcaaagacaggacaggaaatg	
E 4	Marcks	NISP	marcks_t2_F	21	25	GCATCTCGTCTCCGTGTTTT	48	59	76 mt		
54	Marcks	NISP	marcks_t2_R	21	25	GCAACGTTACATTCCAGCTCT	48	59	7011	gcatctcgtctctcgtgttttgtaaatactggaggagctttgaccaatttgacatagagctggaatgtaacgttgc	
FF	Mbp	ISP	mbp_F	22	16	CAGAGGACAGTGATGTGTTTGG	50	60	90nt	cagaggacagtgatgtgtttggggaggcagatgcgatccagaacaatgggacctcggctgaggacacg	
55	Mbp	ISP	mbp_R	20	16	TGTGCTTGGAGTCTGTCACC	50	59		ggtgacagactccaagcaca	
FC	Nedd8	ISP	nedd8_F	20	12	CAACCTGGGAAGAAGATGCT	50	59	72-4	caacctgggaagaagatgctaattaaagtgaagacgctgactgggaaggagattgagatagacatcgaac	
90	Nedd8	ISP	nedd8_R	23	12	TGGGTTCGATGTCTATCTCAATC	50	60	7 Shi	cca	
57	Neurod1	NISP	neurod1_F	19	104	CGATAGCCATTCGCATCAT	47	59	74.04		
57	Neurod1	NISP	neurod1_R	20	104	TGACGTGCCTCTAATCGTGA	47	60	7411	cgatagccattcgcatcatgagcgagtcatgagtgcccagcttaatgccatctttcacgattagaggcacgtca	
E0	Nptxr	ISP	nptxr_F	20	89	GTGGAGAAGGAGCTGAATGC	55	59	124-4	gtggagaaggagctgaatgccctgcagggtcgcgtggccgagctggagcacgggtcctcggcctacagtcc	
50	Nptxr	ISP	nptxr_R	21	89	GGGCGTACATGTAGTTGTTGC	55	60	12401	ccctgatgccttcaaggtcagcatccccatccgcaacaactacatgtacgccc	
50	Nrgn	NISP	nrgn_t7_F	18	97/5/11	ATAGCCTCTCCCCCGTTG	61	60	60nt		
59	Nrgn	NISP	nrgn_t7_R	20	97/5/11	AACATGCACACGCAGAGATT	61	59	ooni		
60	Olfm1	ISP	3493olfm1_F	19	91	CACCGAACTCACCCAAGTG	58	60	71.nt	caccgaactcacccaagtgttgcccaccaaccccgaggagagctggcaggtgtacagctctgcccaggac	
00	Olfm1	ISP	3494olfm1_R	19	91	TGTCCTGGGCAGAGCTGTA	58	60	7 mu	а	
61	Pcna	ISP	pcna_F	18	41	CTAGCCATGGGCGTGAAC	61	60	11 (nt	ctagccatgggcgtgaacctcaccagcatgtccaaaattctaaaatgtgctggtaatgaagacatcattacatta	
01	Pcna	ISP	pcna_R	26	41	GAATACTAGTGCTAAGGTGTCTGCAT	61	59	114nu	agggctgaagataatgcagacaccttagcactagtattc	
60	Plp1	ISP	plp1_F	22	53	TCAGTCTATTGCCTTCCCTAGC	50	59	01-+	tcagtctattgccttccctagcaagacctctgccagtataggcagtctctgcgctgatgccagaatgtatggtgttc	
02	Plp1	ISP	plp1_R	20	53	AGCATTCCATGGGAGAACAC	50	59	Sint	tcccatggaatgct	
62	Ppap2b	ISP	ppap2b_F	18	40	CAGGATTTGCCCAAGGAG	56	59	60pt		
03	Ppap2b	ISP	ppap2b_R	20	40	AGAGGTCGGACACGAAGAAC	56	59	oon	cayyalligeccaayyayeleyyiggeelgelgealayigilelleyigleegaeelei	
64	Ppp1r1b	ISP	ppp1r1b_F	20	98	CCACCCAAAGTCGAAGAGAC	55	59	92mt	ccacccaaagtcgaagagacccaacccctgtgcctatacgcccccatcactgaaagctgtgcagcacctgc	
04	Ppp1r1b	ISP	ppp1r1b_R	20	98	GCTAATGGTCTGCAGGTGCT	55	60	0211	agaccattagc	
65	Ppp3ca	ISP	3497ppp3ca_F	20	4	CACAGTCAGAGGCTGTTCGT	55	59	86nt	cacagt cag agg ctg ttcg tactt ctacagt tacccag ctg tg tg tg acttcctg cag caca at a atttg ttg tccat	
05	Ppp3ca	ISP	3498ppp3ca_R	19	4	CGCGGAGTATGGACAACAA	53	60		actccgcg	
66	Psmb2	ISP	3367_psmb2(+)	20	25	GAGGGCAGTGGAGCTTCTTA	55	59	71nt	aaaaacaataaaaattettaaaaaatatetaaaaaaacteeaaaaaacteeatettaaatetaaceaact	
00	Psmb2	ISP	3368_psmb2(-)	21	25	AGGTGGGCAGATTCAAGATG	50	60	7 110	yayyycayiyyayciiciiayyaayiyiciyyayyayciccayaaycyciicaiciiyaaiciycccacci	
67	Rbm9	ISP	rbm9_F	20	5	ACGGTGCTGACCTCTATGGT	55	59	113nt	acggtgctgacctctatggtggatatgcagcctacagatatgcacagcctgctactgcaaccgcagccacagc	
07	Rbm9	ISP	rbm9_R	18	5	GCCGTAACCGTCGCTGTA	55	60	TISH	tgctgcagccgctgcagccgcttacagcgacggttacggc	
68	Rgs4	ISP	rgs4_F	23	4	TCCCTCAGTTAAACAAGATGTGC	43	60	78nt	78nt	tccctcagttaaacaagatgtgcaaaggacttgcaggtctgccggcttcctgcctg
00	Rgs4	ISP	rgs4_R	21	4	GTTTCATGTCCTTTGCACTCC	43	59		gaaac	
69	Robo1	ISP	robo1_F	19	98	AGGGAAGCCTACGCAGATG	58	60	106nt	agggaagcctacgcagatgatcttccaccccctccagtgccaccacctgctataaaatcgcccactgtccagt	
00	Robo1	ISP	robo1_R	18	98	CCATGACAGGCCGTACCT	58	59	Toolic	ccaaggcacagctggaggtacggcctgtcatgg	
70	Rorb	ISP	3381_rorb_F	18	63	CACGTGTGAAGGCTGCAA	56	60	65nt	cacatatasagagtasagagattetteaggagagagagagagagagagagataetettasteetaee	
10	Rorb	ISP	3382_rorb_R	20	63	GGCAGGAGTAAGAGGCATTG	55	59	00110	cacylylydadygelycadygydliciicagyddygagecageagaacaalyeelellaeleelyee	
71	Rps4x	ISP	rps4x_F	19	34	GTTGACTGGCGTGTTTGCT	53	59	114nt	gttgactggcgtgtttgctcctcgtccatccactggtcctcacaagctgagggaatgcctgcc	
	Rps4x	ISP	rps4x_R	21	34	TCATCTCCAGTCAGGGCATAC	53	60	11410		aaggaacagacttaagtatgccctgactggagatga
72	Sept4	ISP	sept4_F	20	11	GGGATGCAGTCAACAACACA	50	60	61nt	nggatgcagtcaacaacagagggggggggggggggggggg	
12	Sept4	ISP	sept4_R	21	11	AACTGCTGGTCGATGTATTCG	50	60	Unit	ลลละเลืองสังกรรกรรรกรุกรุสสุขภาณิสุขรุสุภภาณิเดิลการสุขกรุสุกษณิกษณิเ	
73	Sfrp1	ISP	sfrp1_F	20	45	CCTCAGAGCTCATGGTTGGT	55	60	72nt	72nt	
	Sfrp1	ISP	sfrp1_R	20	45	AAGCCTGGAACTGGGCTTAG	55	60	7211		
74	Sirpa	ISP	sirpa_F	19	46	AGGGAGCATGCAAACCTTC	53	60	127nt	agggagcatgcaaaccttccctgataataatgctacccacaactggaatgtcttcatcggtgtgggcgtggcgt	
	Sirpa	ISP	sirpa R	20	46	TTTGATCCGGAGGAGGTAGA	53	59	12111	gtgctttgctcgtagtcctgctgatggctgctctctacctcctggatcaaa	

75	Sncb	ISP	sncb_F	19	84	TGGCTGCAGCTGAGAAAAC	53	60	94nt	tggctgcagctgagaaaaccaagcagggggtcaccgaggcagcagagaagaccaaggaagg
15	Sncb	ISP	sncb_R	20	84	ACTCCACTGGTCTTGCTTCC	53	59		tatgtcggaagcaagaccagtggagt
76	Sox11	NISP	sox11_t16_F	23	6	GTTGAATTCATACACTCCAATGT	35	56	97nt	gttgaattcatacactccaatgtctctttttgcaggagtttttcacagaggaatacatttgttcaaaagaccaataaa
10	Sox11	NISP	sox11_t16_R	20	6	GGAGATTGATCACACGATTT	40	55		aatcgtgtgatcaatctcc
77	Sox4	NISP	sox4_t4_F	18	99	GTTGGGGATGCAGAAGGA	56	60	73nt	gttggggatgcagaaggacccggagcacagagggcgttggggttcccgggcctccgcctggggtctgtgca
· · ·	Sox4	NISP	sox4_t4_R	22	99	TTTGCACAGACCCCAGGCGGAG	64	73		aa
70	Tmsb4x	ISP	3463tmsb4x_F	19	91	CACACATAAAGCGGCGTTC	53	60	110nt	cacacataaagcggcgttcgccgcgcccctcccgacaatccgcagcggcttctgagcagatcagactctcct
10	Tmsb4x	ISP	3464tmsb4x_R	20	91	GACATGGTTGCTGGAAGGAG	55	60	112nt	cgttcgcgcagctcgctcggctccttccagcaaccatgtc
70	Tspan7	ISP	tspan7_F	20	89	TTGGATGCTTTGCTACATGC	45	59	66nt	ttagataetttaataaataataataataataataataataaaaatata
19	Tspan7	ISP	tspan7_R	20	89	GGGACAGGAACATGGCATAC	45	60		
90	Ube2e3	ISP	ube2e3_F	20	109	GGGAGTCATCTGCCTGGATA	55	60	126nt	gggagt catctgcctggatattctgaaagacaactggagtcctgctttgactatttcaaaggttttgctctctatttgtt
00	Ube2e3	ISP	ube2e3_R	19	109	ATGCTTCCGACCAGAGGAT	55	59	12011	cccttttgacagattgcaaccctgcggatcctctggtcggaagcat
91	Usp16	ISP	usp16_F	19	94	TTTGGTGGCGAGCTGACTA	53	60	77nt	tttaataacaaataataataataataataataataaata
01	Usp16	ISP	usp16_R	20	94	TCAAGGAACGATTCATGCAC	53	59	· / //tt	แม่งให้ก็กลุ่มการกลมารกลุ่มการการกลมารกมามการการกา
92	Wsb1	ISP	wsb1_F	18	11	GGCGCCAGTAAAGCAGTT	56	59	94nt	ggcgccagtaaagcagttttcctttggaatatggataaatacaccatgattaggaagctggaaggtcatcacca
02	Wsb1	ISP	wsb1_R	23	11	AGTCACAAGCTACAACATCATGG	56	59		tgatgttgtagcttgtgact
83	Ywhae	ISP	ywhae_F	20	102	GGCGAGTCCAAGGTTTTCTA	50	59	00nt	ggcgagtccaaggttttctattataaaatgaaaggggactaccacaggtatctggctgagtttgccacaggaaa
05	Ywhae	ISP	ywhae_R	20	102	TGCCTCCTTCCTGTCATTTC	50	60	John	tgacaggaaggaggca
94	Zfp57	ISP	zfp57_F	21	64	TGGCTAGAAGCAGTCTGGAAT	48	59	96nt	tggctagaagcagtctggaatagaagtcaaacgcctaggaccagcctggcattaccaaacaatggcagcta
04	Zfp57	ISP	zfp57_R	19	64	CTGGATGGCTGGGAAGACT	48	60		ggaaacagtcttcccagccatccag
85	Zswim4	ISP	zswim4_F	18	3	TGCAAGACAGCCACTCCA	56	60	112nt	tg caga at a agctg g t cat ct ct g agg g ca agg ct g agg a ca a ag at g t g a a agg g c g ag c c ct t a c ag c c a a g a g a g a g a g a g a
00	Zswim4	ISP	zswim4_R	18	3	TGTCATCCGCATCACCTG	56	60		aaatccaaatctccttaaagggtgaaaacattgatgggtga
86	Zwint	ISP	zwint_F	22	73	TGCAGAATAAGCTGGTCATCTC	45	59	90nt	tgcaagacagccactccagccagcgcaccgccagacaccgtgctgctgcggcatcgcgctggagctcggcct
- 50	Zwint	ISP	zwint_R	21	73	TCACCCATCAATGTTTTCACC	45	60	3011	gcaggtgatgcggatgaca