

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

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Bachelor of Science (Hons.) (Biomedical Sciences)

Master of Science (Genetics)

*A thesis submitted for the Degree of Doctor of Philosophy*

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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  
<http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s3.xls>.

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

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

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

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

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

## 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:**

King-Hwa Ling (KHL), Chelsea A Hewitt (CAH), Tim Beissbarth (TB), Lavinia Hyde (LH), Kakoli Banerjee (KB), Pike-See Cheah (PSC), Ping Z Cannon (PZC), Christopher N Hahn (CNH), Paul Q Thomas (PQT), Gordon K Smyth (GKS), Seong-Seng Tan (SST), Tim Thomas (TT) and Hamish S Scott (HSS).

**Published in: *Genome Biology* 2009, 10(10): R104.**

**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.

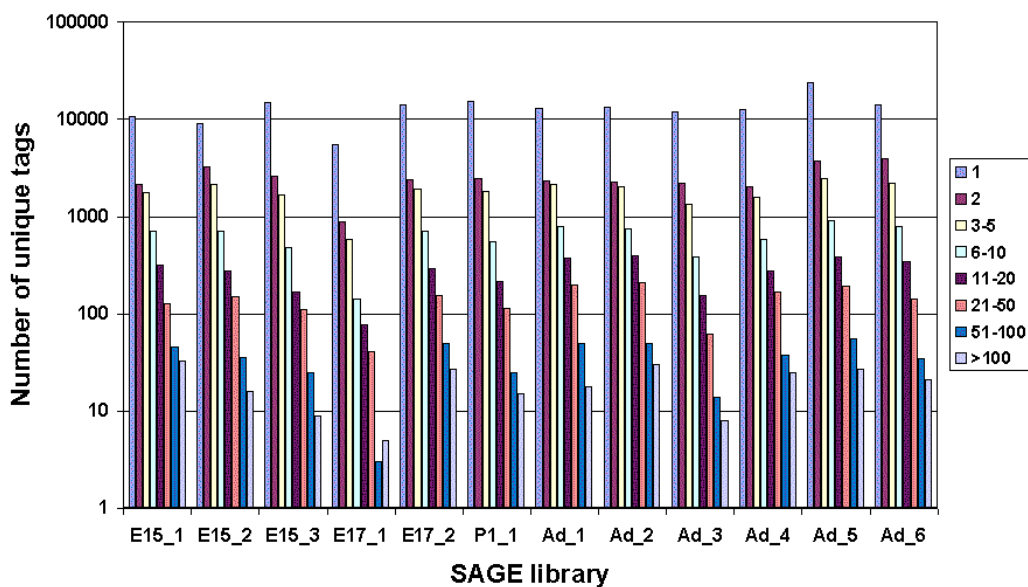
## A-2 Additional data file 1

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.

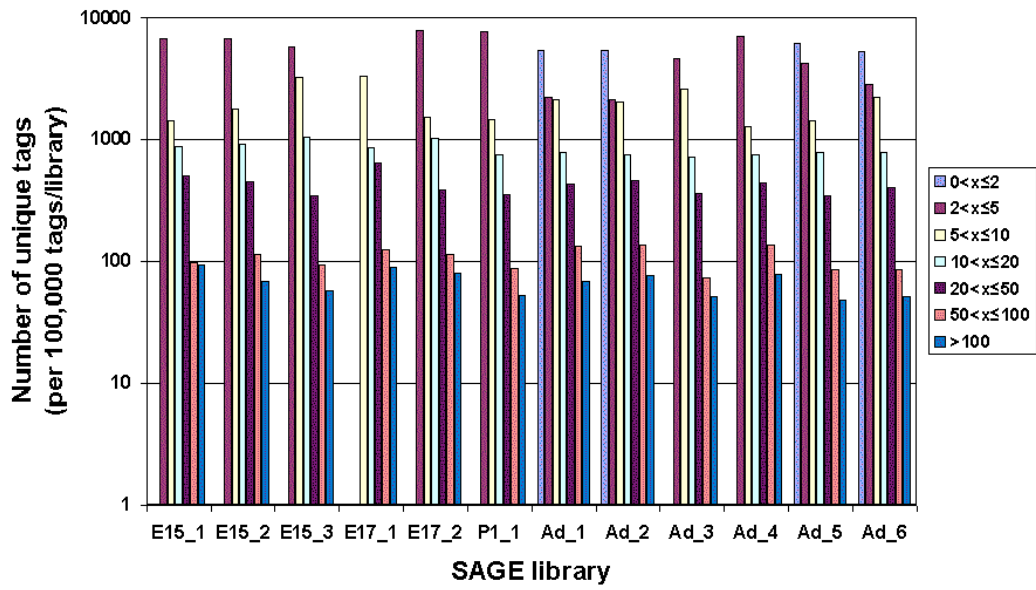
Original version of this data file can be accessible from at <http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s1.doc>.

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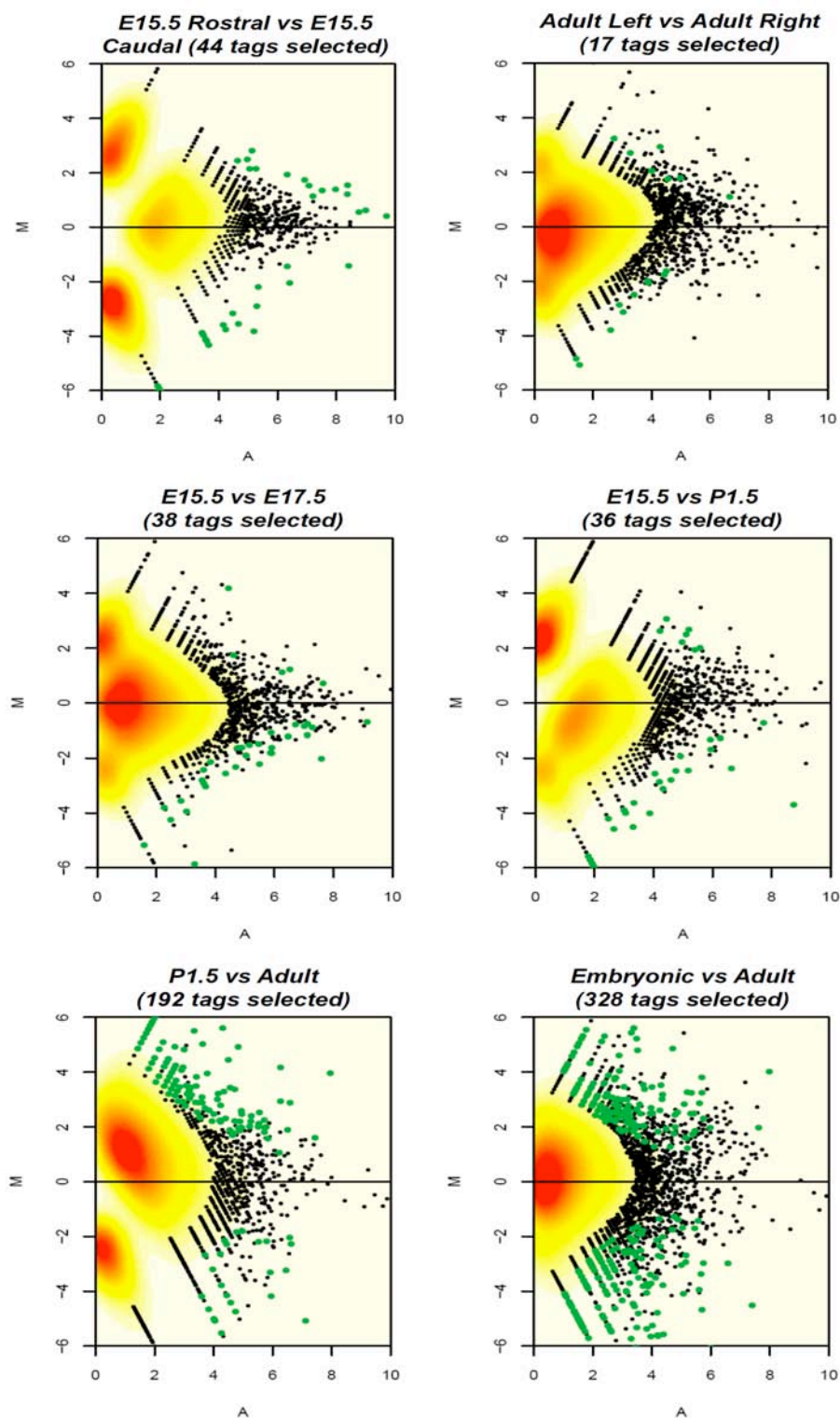
### SECTION A: SERIAL ANALYSIS OF GENE EXPRESSION



**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 ( $\log_2(P/Q)$ ) whereas the X-axis represents the A values, which is the mean ratio ( $1/2 \cdot \log_2(P \cdot Q)$ ). 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.

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

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 <sup>b</sup>
<b>No. of candidate DETs</b>	27	14	3	3	29	66	142
<b>No. of DETs with gene ID</b>	24 [8,3]	10 [4,0]	3 [0,3]	3 [2,1]	24 [21,16]	54 [44,42]	118 [79,65]
<b>No. of DETs with EST ID</b>	1 [0,0]	2 [0,0]	0 [0,0]	0	5 [4,3]	9 [8,7]	17 [12,10]
<b>No. of ambiguous DETs with ID</b>	2 [1,0]	2 [1,0]	0 [0,0]	0	0 [0,0]	3 [2,2]	7 [2,2]
<b>Failed RT-qPCR</b>	4/27	1/14	0/3	0/3	0/31	9/66	14/144
<b>Validation rate according to trend only</b>	9/27	5/14	3/3	3/3	25/31	54/66	99/144
<b>Validation rate according to trend with <math>p &lt; 0.05^a</math></b>	3/27	0/14	0/3	2/3	19/31	51/66	75/144

[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.

<sup>a</sup> based on empirical Bayesian moderated T-test with Benjamini-Hochberg correction for FDR.

<sup>b</sup> 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**

Gene clusters	Novel molecular networks			Score <sup>d</sup>	Canonical pathway <sup>e</sup>	p value
	Focus gene <sup>a</sup>	Other associated nodes <sup>b</sup>	Biological functions and/or diseases <sup>c</sup>			
<i>Embryonic specific gene clusters (1, 5 and 6)</i>	ALS2CR2, BTG1, H2AFY, <b>MARCKS</b> , <b>NEUROD1</b> , ROBO1, RPS4X, SFRP1, SOX4, SOX11, WSB1	BIK, CDX1, COTL1, CTNBN1, 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/ $\beta$ -catenin signaling	1.83E-03
	ACTB, 5031439G07Rik, CDK4, CDKN1C, CSRP2, DCX, EZH2, <b>MARCKS</b> , <b>NEUROD1</b> , 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	P53 signaling Tight junction signaling	8.13E-03 2.23E-02
<i>Adult specific gene clusters (4, 8 and 10)</i>	CAMK2A, EGRI, ITPR1, <b>MBP</b> , 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 GM-CSF Signaling	1.54E-05 9.60E-05 9.89E-04 1.30E-03 3.20E-03
	CRYAB, GRIA3, GSTM5 (GSTM1), <b>MBP</b> , 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	7.68E-03 1.78E-02 3.03E-02 4.60E-02
<i>Gene switching clusters (2 and 7)</i>	ACTL6B, APP, ATP7A, BCL11A, CLCN2, <b>CTSD</b> , HPRT1, MAPT, RBM9, <b>YWHAE</b>	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
	CALM1, CHGB, <b>CTSD</b> , NEDD8, UBE2E3, <b>YWHAE</b>	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

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

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

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

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

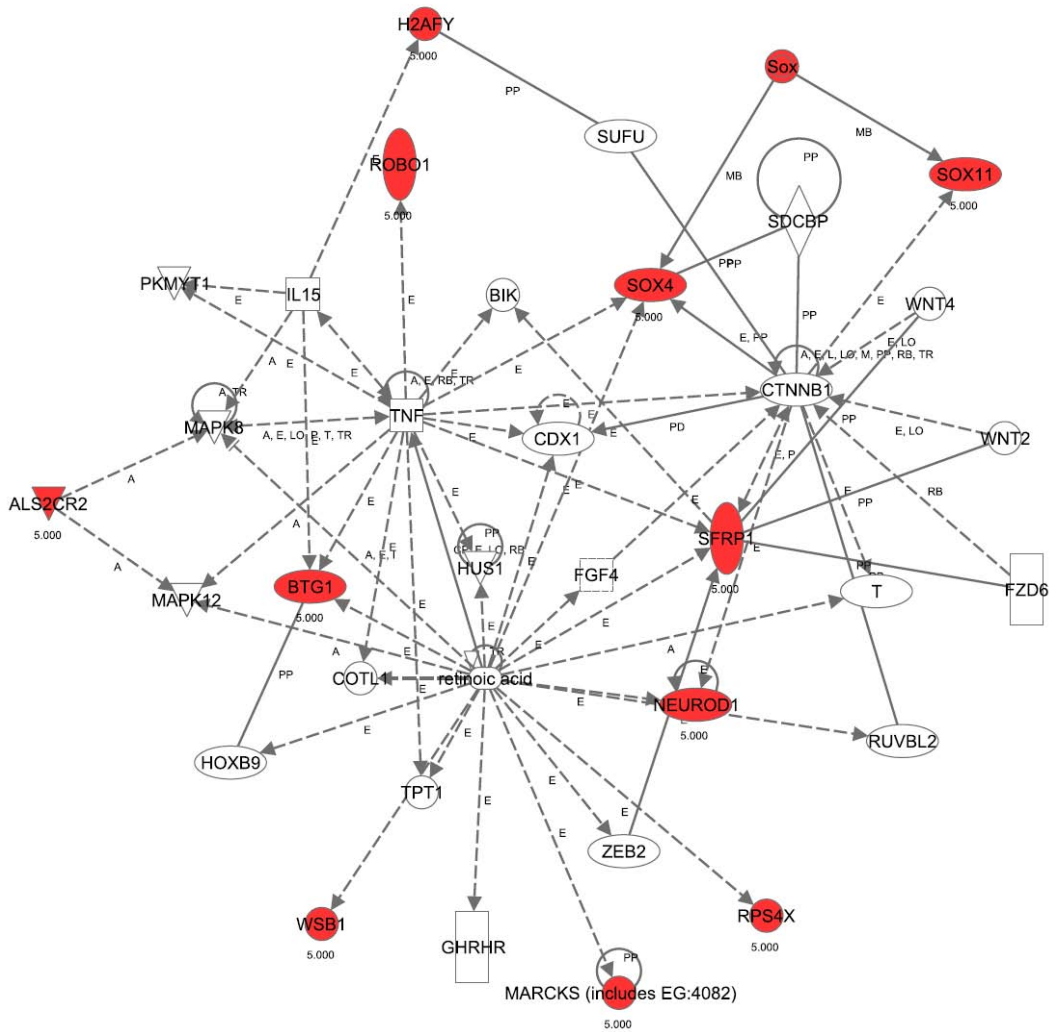
<sup>e</sup> Enriched canonical pathways were determined based only on focus genes and the related p values were calculated using Fisher's exact test.

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

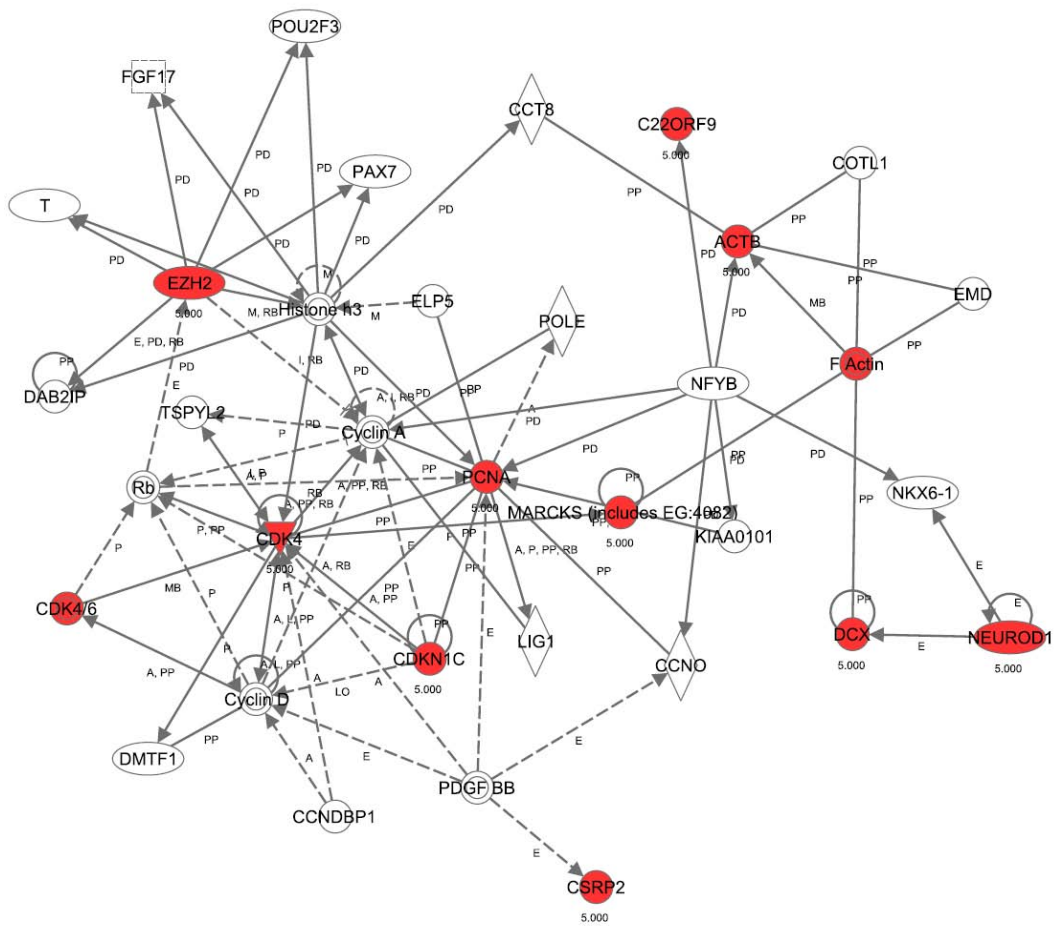
Gene clusters	<i>p</i> value	Canonical pathway <sup>a</sup>	Associated focus gene <sup>b</sup>
<i>Embryonic specific gene clusters (1, 5 and 6)</i>	1.83E-03	Wnt/ $\beta$ -catenin signaling	<i>Sox4, Sfrp1 and Sox11</i>
	8.13E-03	P53 signaling	<i>Cdk4 and Pcn</i>
	2.23E-02	Tight junction signaling	<i>Cdk4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

<sup>a</sup> Enriched canonical pathways were determined based only on focus genes and the related *p* values were calculated based on Fisher's exact test.

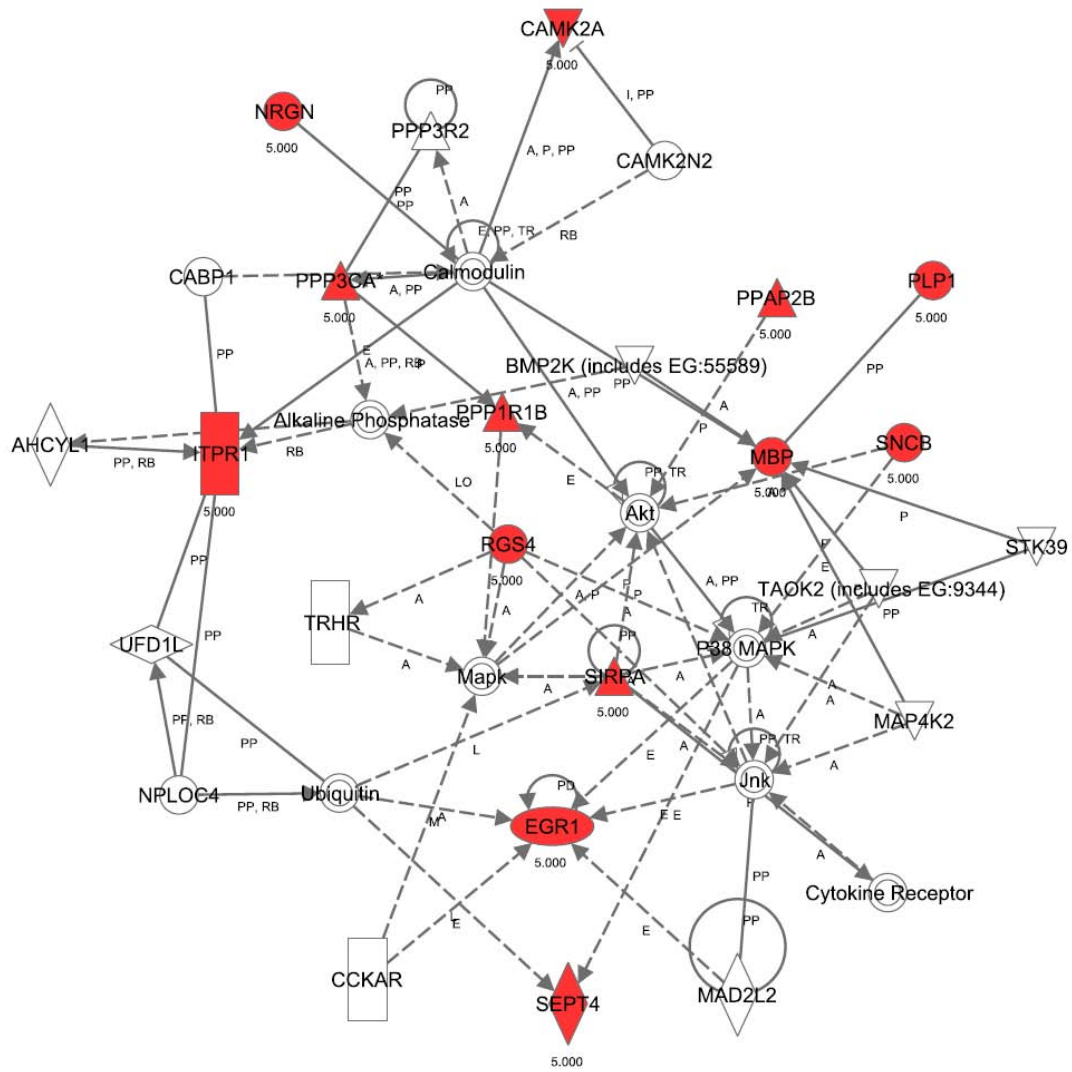
<sup>b</sup> Focus gene is an input gene that matched an annotated (based on human, mouse and rat) node in Ingenuity knowledge base.



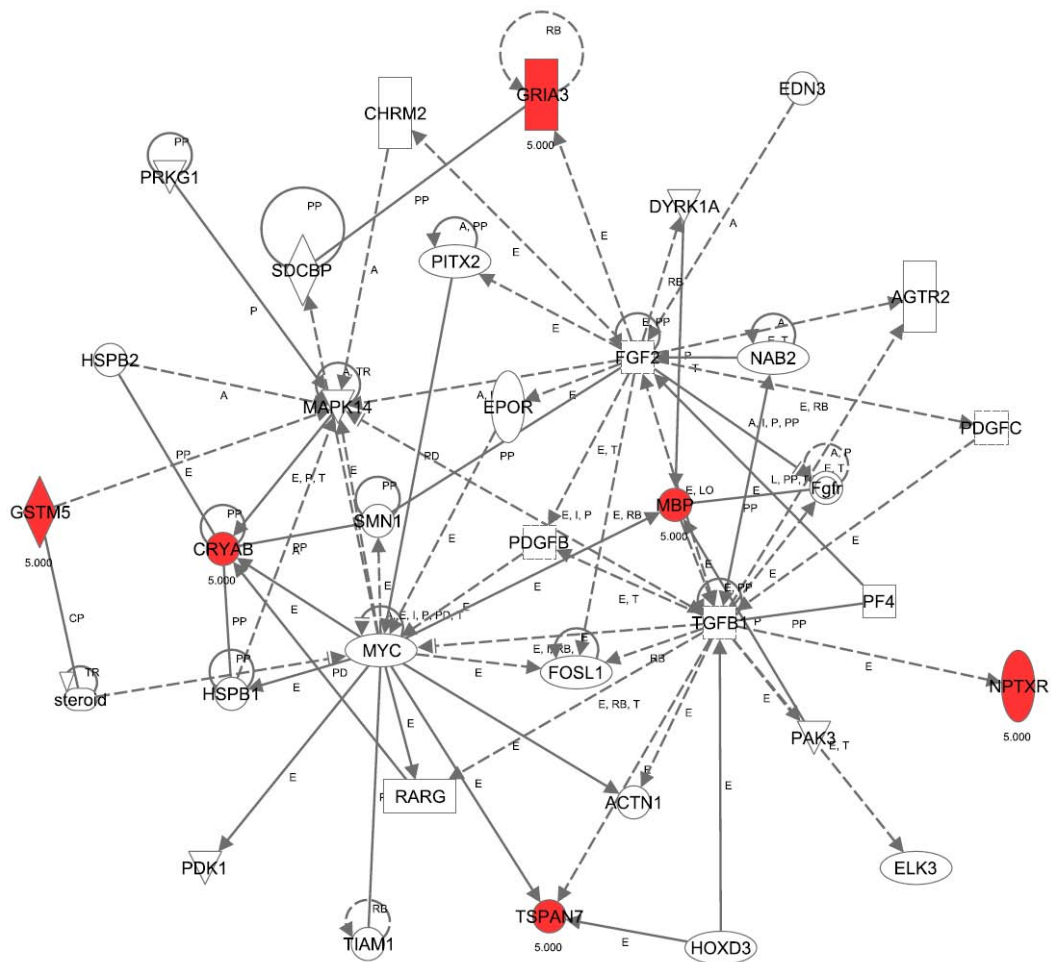
**Figure S4** Novel molecular network 1 (embryonic specific gene clusters 1, 5 and 6). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression';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



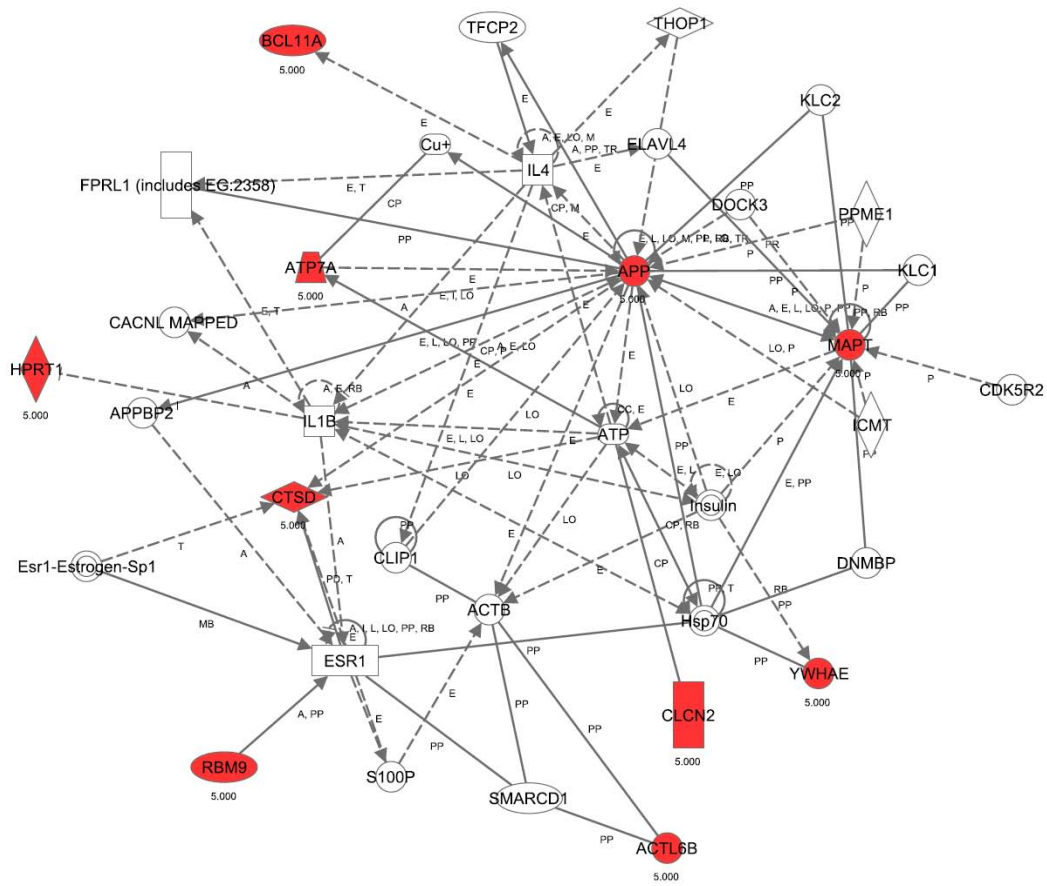
**Figure S5** Novel molecular network 2 (embryonic specific clusters 1, 5 and 6). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression'; PP='protein-protein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



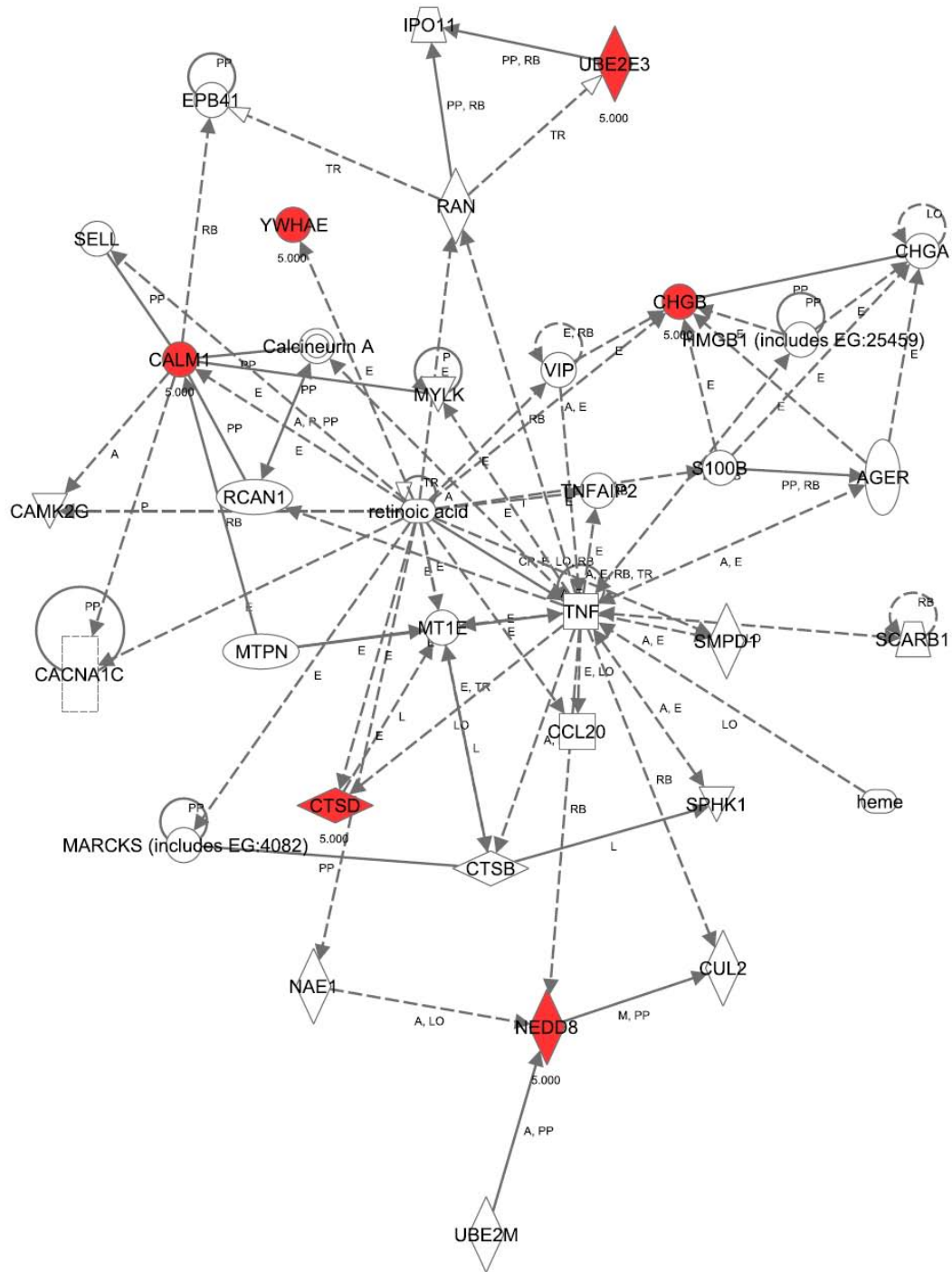
**Figure S6** Novel molecular network 3 (adult specific gene clusters 4, 8 and 10). Red coloured nodes=focus gene; non-coloured nodes = associated molecules; solid line='directly interact with'; dotted line='indirectly interact with'; A='activation'; I='inhibition'; E='regulating the expression'; PP='protein-protein 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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**Table S5 : Cellular expression of validated DETs based on publicly available micrographs or expression databases.**

No.	Gene	Embryonic development (E15.5) <sup>a</sup>						Afterbirth														Group (N, G or B) <sup>e</sup>
								Postnatal <sup>b</sup>							Adult <sup>c</sup>							
		SVZ/VZ	IZ	SP	CP	MZ	REF	6	5	4	2 or 3	1	CT <sup>d</sup>	REF	6	5	4	2 or 3	1	CT <sup>d</sup>	REF	
1	Camk2a	2	1	1	1	1	[33]	1	1	1	2	1	N	[33, 34]	1	1	1	2	1	N	[32, 34]	N
2	Egr1	1	1	2	1	1	[33, 34]	1	1	1	1	1	N,G	[33, 34]	2	1	2	2	1	N	[32, 34]	B
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	N	[33, 34]	2	2	2	2	1	N	[3]	N
7	BQ176089	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B
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]	N
10	Nptxr	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	[46]	G
11	Ppp1r1b	0	1	1	2	1	[33, 34]	1	1	1	1	0	N	[33, 34]	2	1	1	2	1	N	[32, 34]	N
12	Gstm1	1	0	0	0	0	[33]	-	-	-	-	-	-	-	0	1	1	1	0	N,G	[32, 43]	B

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]	B
14	Itrp1	1	1	2	2	1	[33]	1	1	1	2	1	-	[33]	1	1	1	2	1	N	[32, 47]	N
15	Rgs4	0	1	2	1	1	[34]	1	1	1	1	1	N	[34]	1	2	1	2	0	N	[32, 34]	N
16	AK139402	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B
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]	B
19	AU258168	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B
20	Ppp3ca	0	0	0	0	0	[33]	1	1	1	1	0	-	[32, 33]	1	1	1	2	0	N	[32, 48]	N
21	App	0	0	0	1	1	[35]	-	-	-	-	-	-	-	1	1	1	1	1	N,G	[32, 46, 55]	B
22	Hprt1	1	1	1	1	1	[33]	1	1	1	1	0	-	[33]	1	1	1	1	0	N	[32, 56]	N
23	Gria3	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	1	1	1	N,G	[32, 46, 49, 50]	B
24	Calm1	2	1	1	1	1	[33]	1	1	1	1	0	-	[33]	1	1	1	1	1	N	[32, 58]	N
25	Ctsd	2	1	1	1	1	[33]	1	1	1	1	0	-	[33]	1	1	1	1	1	N,G	[32, 46, 57]	B
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	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B
29	AK140219	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B
30	Cln2	1	1	1	1	1	[33]	1	1	1	1	0	-	[33]	1	2	1	1	0	-	[32]	B
31	AK154943	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	B
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	N	[33, 34]	1	1	1	2	1	N	[32-34]	N
34	Ywhae	2	1	1	2	1	[33]	1	1	1	2	1	-	[33]	1	1	1	1	1	N	[32, 33, 59]	N
35	Ube2e3	0	0	0	0	0	[35]	-	-	-	-	-	-	-	0	0	0	0	0	-	[32]	B
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]	-	-	-	-	-	-	-	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	5031439G07Rik	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	N	[32, 60]	N
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	N	[34]	0	0	0	0	0	N	[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]	N
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	N	[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	N	[33, 34]	0	0	0	0	0	N	[32, 34]	-
54	Sox11	1	2	1	2	1	[33]	1	1	1	1	1	N	[33, 34]	0	0	0	0	0	N	[32, 34]	-
55	Dr1	1	1	1	2	1	[42]	-	-	-	-	-	-	-	0	1	1	1	0	N	[32, 42]	-
56	Zswim4	-	-	-	-	-	-	-	-	-	-	-	-	-	0	1	1	1	0	-	[32]	-
57	Actl6b	0	1	1	2	1	[35]	-	-	-	-	-	-	-	1	1	1	1	1	-	[32]	B
58	Atp7a	2	1	1	1	1	[35]	-	-	-	-	-	-	-	0	0	0	0	0	N,G	[32, 53]	B
59	Hmgb3	1	1	1	1	0	[35]	-	-	-	-	-	-	-	0	1	1	1	0	-	[32]	B
60	BQ177886	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
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	-	[32]	-
63	Sox4	1	1	1	2	1	[33]	1	1	1	2	1	N,G	[33, 34]	1	1	1	1	1	N	[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	N	[33, 34]	1	1	1	1	1	N	[32, 34]	N
66	Bicap	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	N	[32]	-

<sup>a</sup> Based on E15.5 micrographs from [32-34] or E14.5 micrographs from [35].

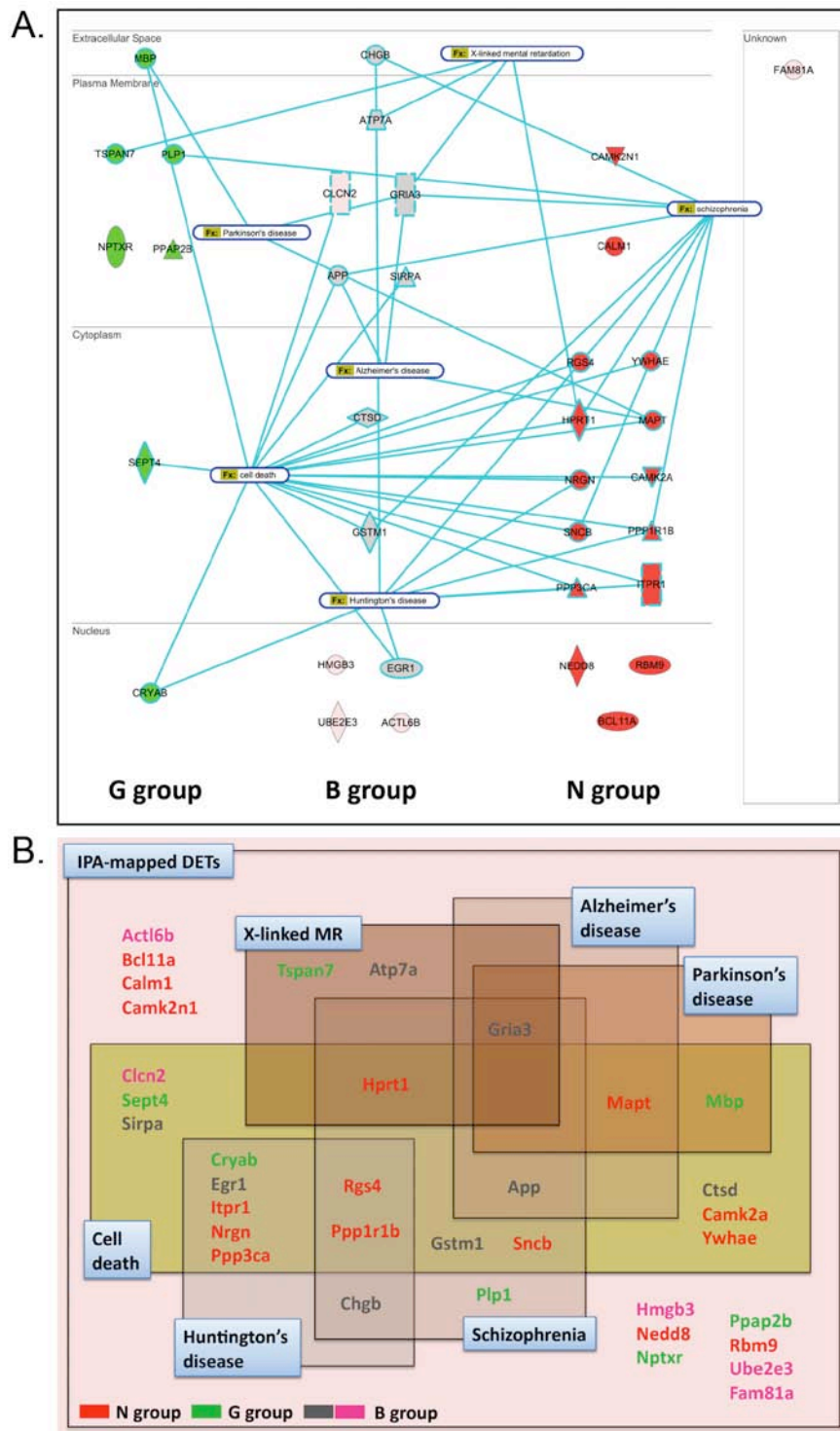
<sup>b</sup> Based on P4 [32] or P7 [33] micrographs.

<sup>c</sup> Based on P56 micrographs from [32, 33].

<sup>d</sup> 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.

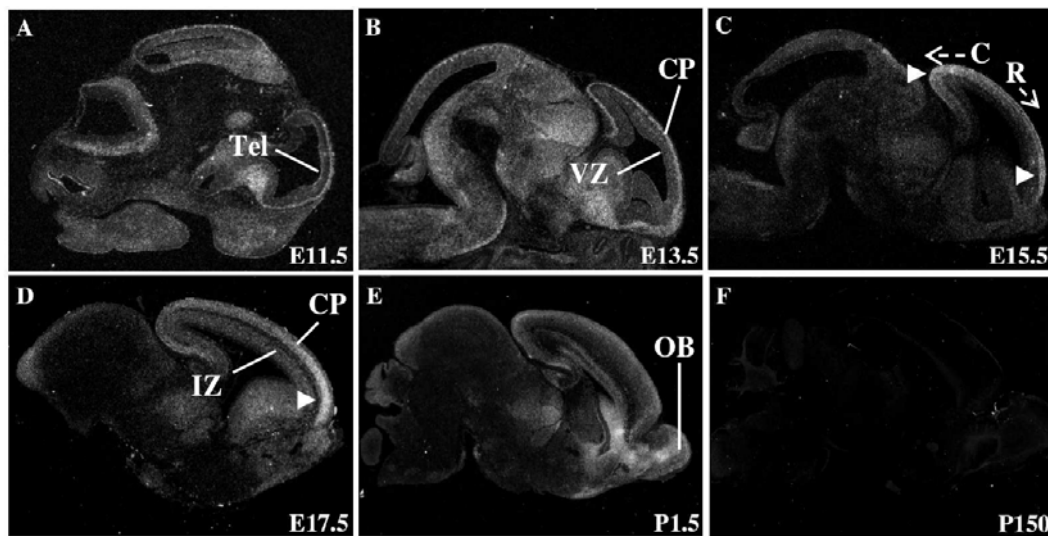
<sup>e</sup> Some of the DETs were not classified into the N-, G- or B-groups because they do not belong to the IPA Networks 3 to 6 in IPA analysis.

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'.

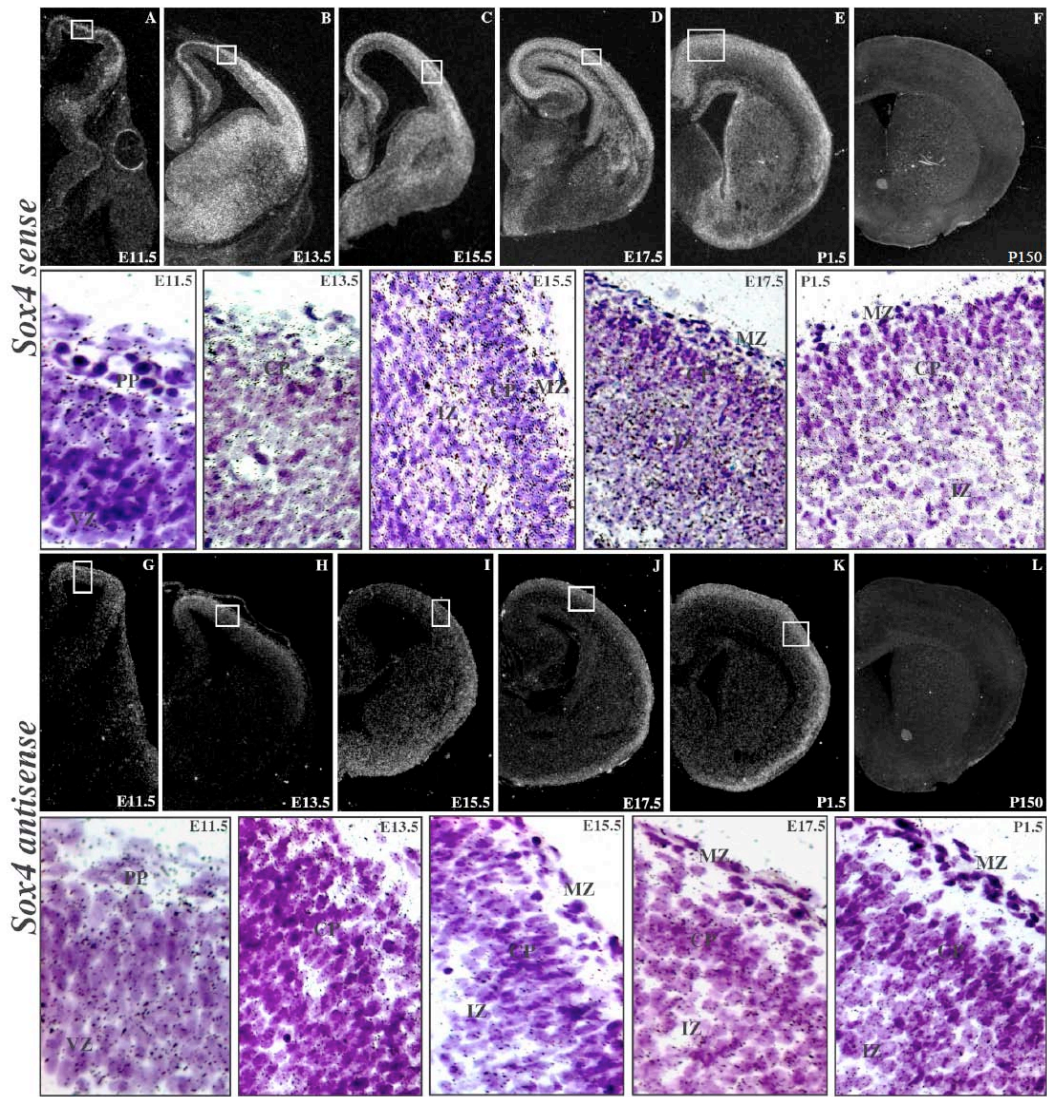


**Figure S10** (A) IPA analysis of the qPCR-validated DETs from Networks 3 to 6 and their associated neurological disorders and cell death process. DETs were classified into three groups according to the origin of their expression; only expressed in cortical neurons (N-group), in cortical glia (G-group) 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'.

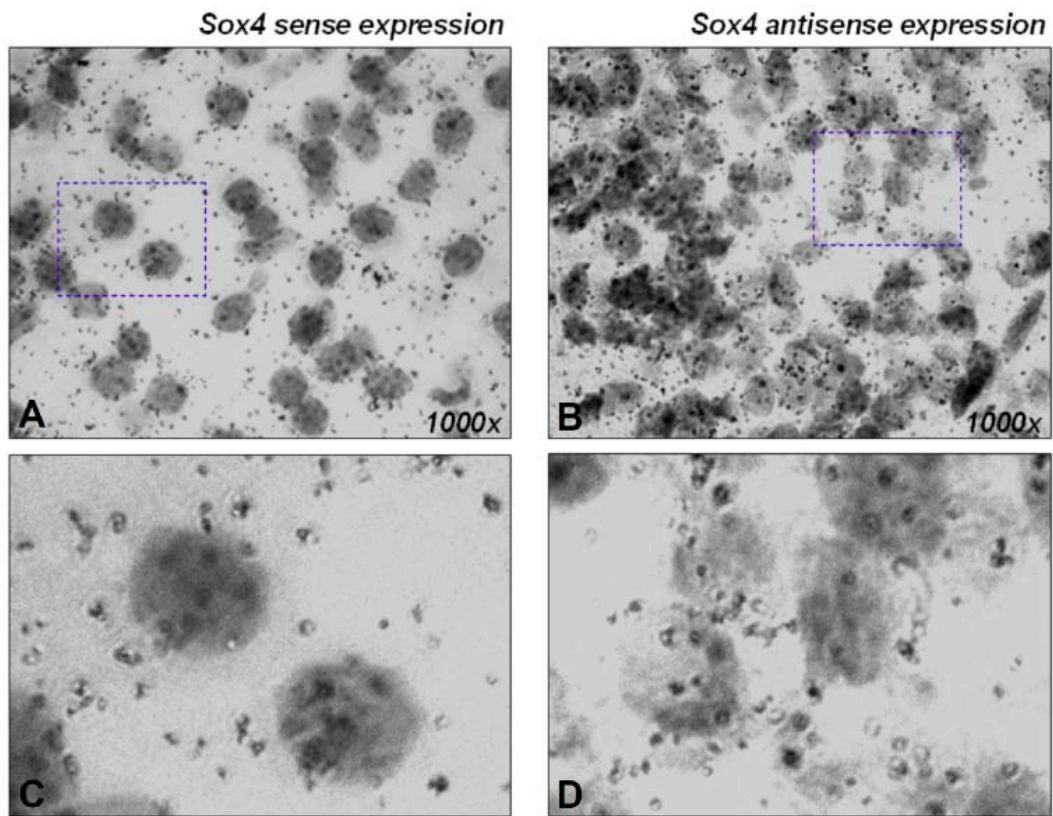
**SECTION E: ANALYSIS OF THE *SOX4* GENOMIC CLUSTER**



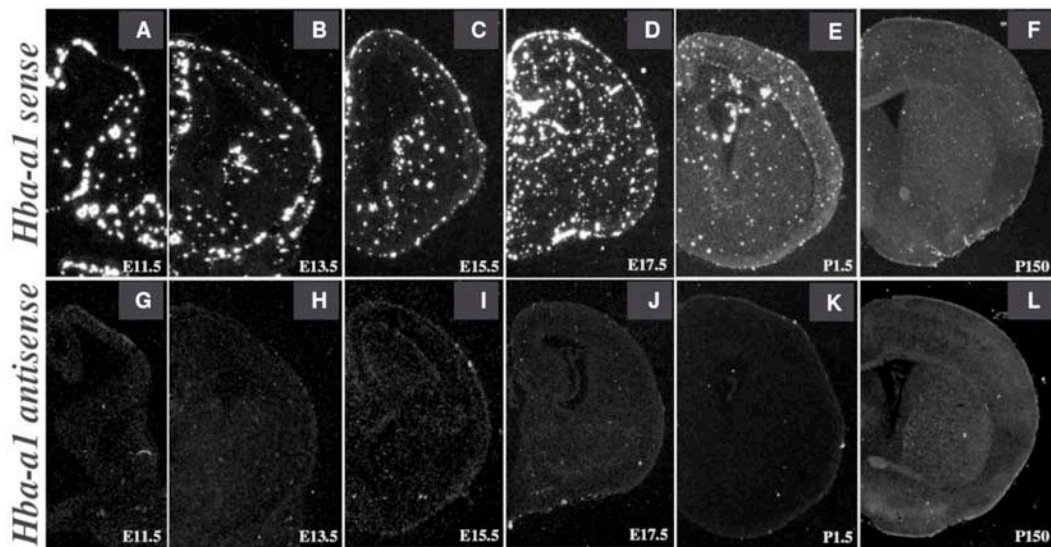
**Figure S11** Regionalization of *Sox4* transcripts. A-F are sagittal sections obtained from various developmental stages of the mouse cerebral cortex. Arrowheads show brain regions with higher *Sox4* sense expression. Both E15.5 and E17.5 brain sections show regionalized expression of *Sox4* in the 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-a1* 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-a1* appeared ‘dotted’ because only specific haematopoietic 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 PET ID	Chromosome	Start position <sup>a</sup>	End position <sup>b</sup>	Strand	Size (nt) <sup>c</sup>
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

<sup>a</sup> Start position for the FANTOM PET left tag.

<sup>b</sup> End position for the FANTOM PET right tag.

<sup>c</sup> Size of the predicted transcript based on the left and right PETs presuming no splicing has occurred.

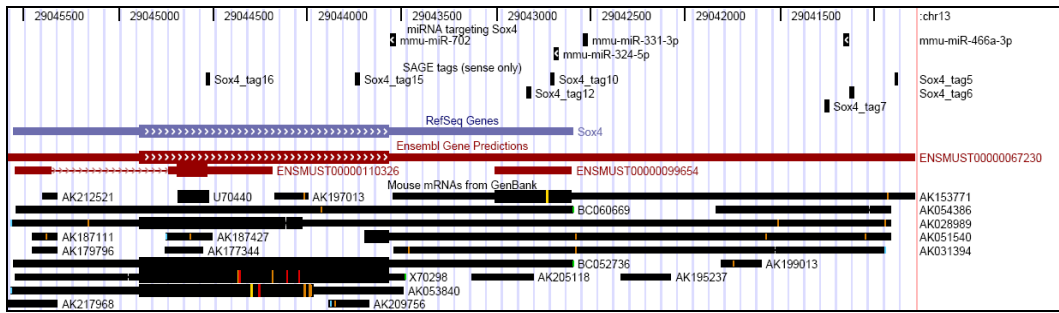
<sup>a,b</sup> FANTOM PET sequences were obtained from Ensembl website [64]. The ditag of PolyA+ RNA libraries were originally downloaded from the FANTOM consortium site and processed using code available in

[http://www.ensembl.org/Mus\\_musculus/ditags/FANTOM\\_GSC\\_PET.html](http://www.ensembl.org/Mus_musculus/ditags/FANTOM_GSC_PET.html).

**Table S7: miRNAs, which target *Sox4* sense transcripts.**

miRNA	Targeted position <sup>a</sup>			
	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	-

<sup>a</sup> 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.

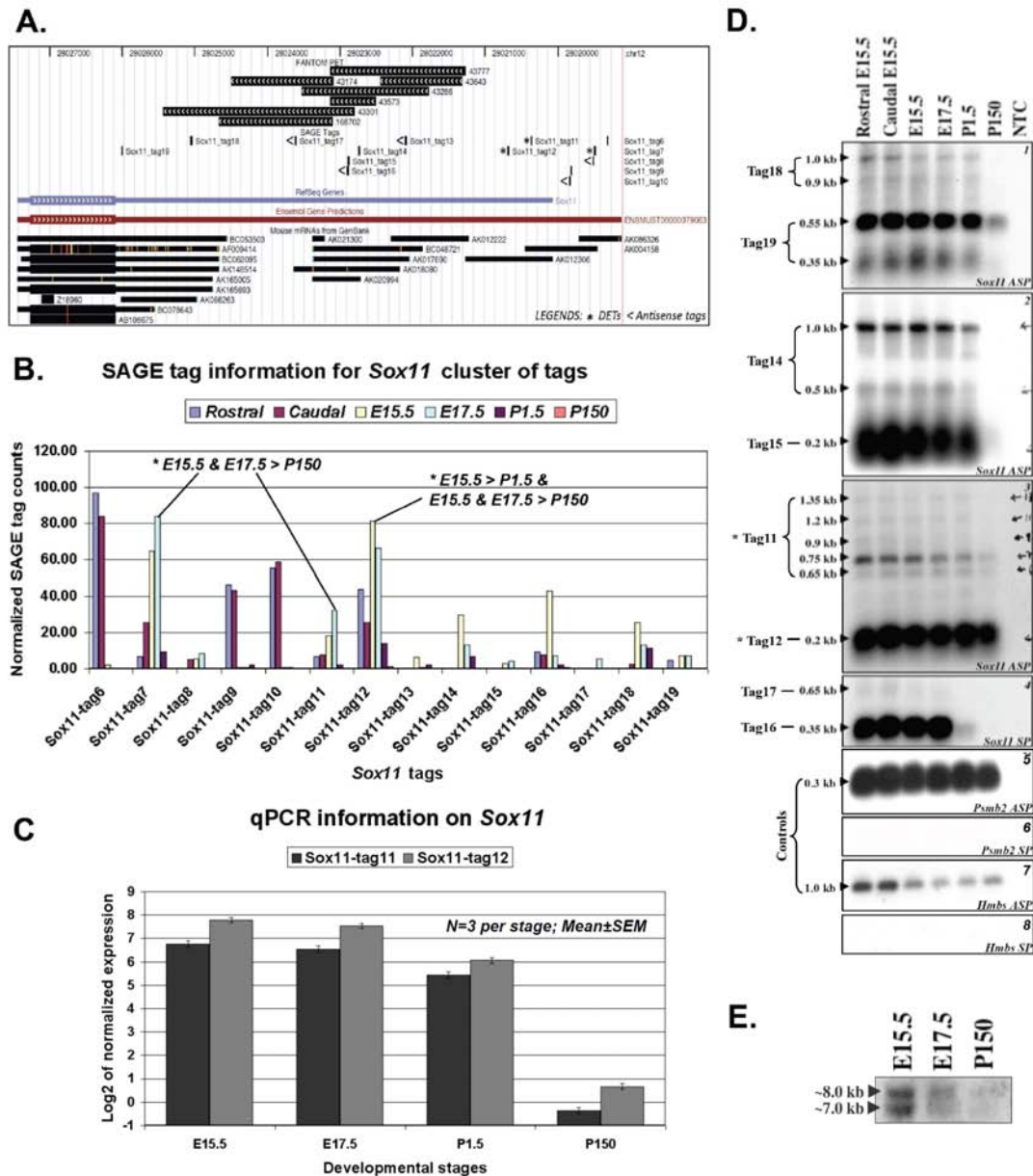
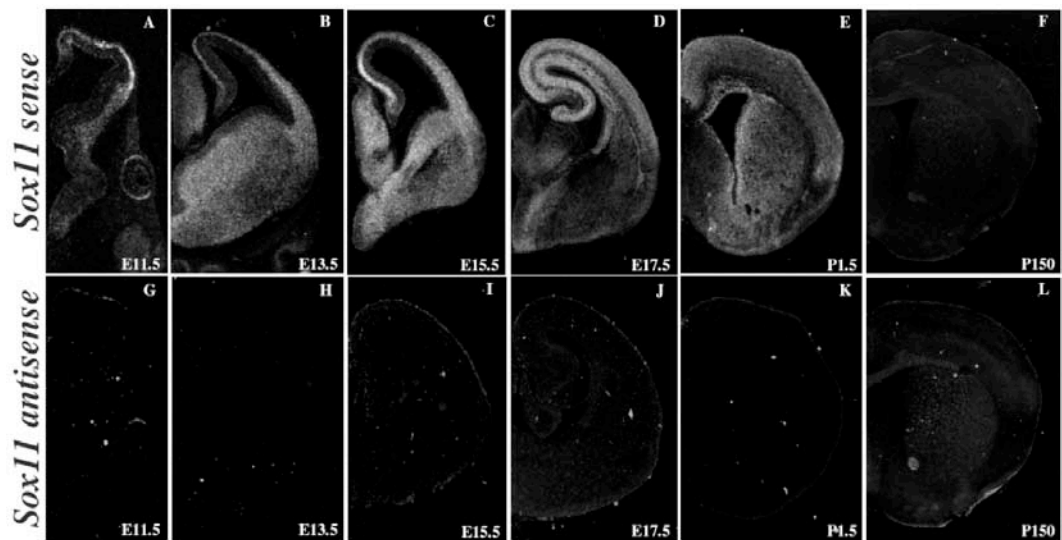


Figure S16

Diagram A shows the UCSC genome browser at the *Sox11* genomic locus. SAGE tags are found in both directions within the *Sox11* reference gene. B shows the SAGE expression profiles for each tag in the *Sox11* locus. C shows the RT-qPCR validations of selected DETs at various loci within the *Sox11* canonical gene whereas D shows the 3' RACE-Southern blotting analysis. D.1-D.3 show the amplification of *Sox11* sense transcripts whereas D.4 represents the amplifications of *Sox11* antisense transcripts. Tags with asterisks (\*) are DETs. Both D.5 and D.7 are positive controls exclusively generated from the sense strand of *Pomb2* and *Hmbs* endogenous genes. The corresponding D.6 and D.8 show the antisense expression (negative control) of *Pomb2* and *Hmbs*, respectively. E shows a Northern analysis of total RNA isolated from pooled mouse cerebral cortices (n=7).



**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, *Sox11* 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 PET ID	Chromosome	Start position <sup>a</sup>	End position <sup>b</sup>	Strand	Size (nt) <sup>c</sup>
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

<sup>a</sup> Start position for the FANTOM PET left tag.

<sup>b</sup> End position for the FANTOM PET right tag.

<sup>c</sup> Size of the predicted transcript based on the left and right PETs presuming no splicing of transcript.

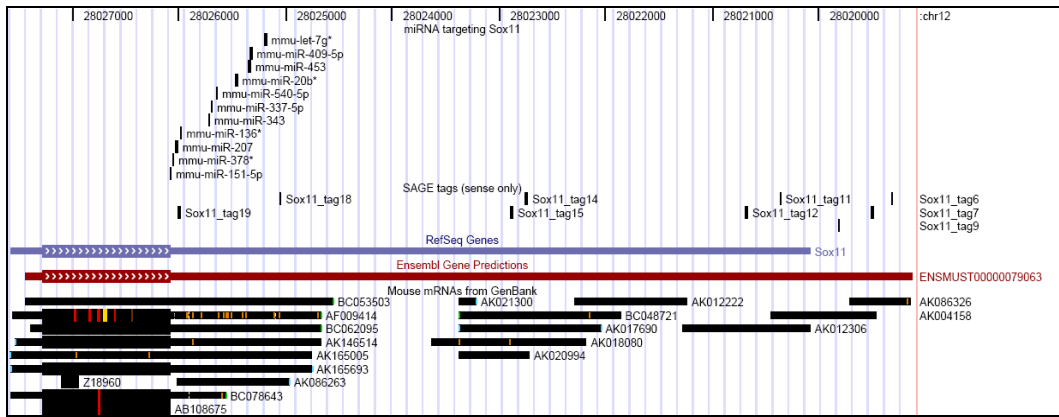
<sup>a,b</sup> FANTOM PET sequences were obtained from Ensembl project website [64]. The ditag of PolyA+ RNA libraries were originally downloaded from the FANTOM consortium site and processed using code available in

[http://www.ensembl.org/Mus\\_musculus/ditags/FANTOM\\_GSC\\_PET.html](http://www.ensembl.org/Mus_musculus/ditags/FANTOM_GSC_PET.html).

**Table S9: miRNAs, which target *Sox11* sense transcripts.**

miRNA	Targeted position <sup>a</sup>			
	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	-

<sup>a</sup> 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 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, T<sub>m</sub> 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 C<sub>p</sub>. 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 125µl /cm<sup>2</sup> 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<sup>6</sup> 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 [ $\gamma$ -<sup>32</sup>P]ATP (Amersham). The reactions were prepared in a 25µl volume with 20U of T4-PNK, 0.05mCi of [ $\gamma$ -<sup>32</sup>P]ATP and 2.5µl 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  $5 \times 10^5$  cts/minute/ $\mu$ l *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-free™ kit (Applied Biosystems) according to the manufacturer's protocol. The concentration and purity of all isolated total RNA was determined using the Nanodrop™ 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 NEUROBASAL™ 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  $\mu$ 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  $\mu$ g/ml streptomycin and 2 mM L-glutamine.

## **SECTION H: 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"
# 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")
#
#creat a weights matrix of right dimensions and set all weights to 1
>weights <- matrix(1, nrow=dim(ratios)[1], ncol=dim(ratios)[2])
# if any data values = NA, set weight for that data value to 0
>weights[is.na(ratios)] <- 0
#
#
>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))
# 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)
#
### You need to enter abbreviations for each Tissue(Treatment), T1 to T4 in this
example
>colnames(mm) <- c("T1", "T2", "T3", "T4")
#
# fit the model to the logged ratios
#
>fit <- lmFit((ratios), design=mm, weights=weights)
#
# now fit the all effects
# make a contrast matrix
### You need to enter all possible contrasts between tissues
>contrastsMatrix <- makeContrasts("T1-T2", "T1-T3", "T1-T4", "T2-T3", "T2-T4", "T3-T4",
levels=mm)
# fit the contrast
>fit2 <- contrasts.fit(fit, contr=contrastsMatrix)
>fit3 <- eBayes (fit2)
# calculate group-wise "means" and standard errors. Note: stderrs come
# from linear model, not from population
>estimates <- fit$coef[,1:numTissues]
>stdevs <- (fit$stdev*fit$sigma)[,1:numTissues]
>colnames(stdevs) <- paste(colnames(stdevs), "stdv")
```

```

#
#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)
>tallc <- topTable(fit3, adjust="BH", number=nrow(fit3$p.value), genelist=est)
#
#create a topTable showing details for each contrast
###You need to modify these lines to suit your tissue contrasts
>t1t2 <- topTable(fit3, adjust="BH", number=nrow(fit3$p.value),coef=1)
>t1t3 <- topTable(fit3, adjust="BH", number=nrow(fit3$p.value),coef=2)
>t1t4 <- topTable(fit3, adjust="BH", number=nrow(fit3$p.value),coef=3)
>t2t3 <- topTable(fit3, adjust="BH", number=nrow(fit3$p.value),coef=4)
>t2t4 <- topTable(fit3, adjust="BH", number=nrow(fit3$p.value),coef=5)
>t3t4 <- topTable(fit3, adjust="BH", number=nrow(fit3$p.value),coef=6)
#
# to write results to a file use something like
>write.table(file="t1t2.xls", t1t2, sep="\t", quote=F)
>write.table(file="t1t3.xls", t1t3, sep="\t", quote=F)
>write.table(file="t1t4.xls", t1t4, sep="\t", quote=F)
>write.table(file="t2t3.xls", t2t3, sep="\t", quote=F)
>write.table(file="t2t4.xls", t2t4, sep="\t", quote=F)
>write.table(file="t3t4.xls", t3t4, sep="\t", quote=F)
>write.table(file="means_std_allgroups.xls", est, sep="\t", quote=F)
#

```

## A-3 Additional data file 2

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

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

---

- 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 4** Chromosome positions were based on mouse genome assembly release July 2007 (mm9).
- 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 log<sub>2</sub> 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 8** Transcript 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*).



















550	tgtagtgtacaagggt	NM_009098	<b>Rps8</b>	ambiguousgene	nil	nil	nil	0	0	0	0	0	0	5	95.3	388.33	97.97	93.96	96.94	58.5	38.465	124.025
551	tgtataaaaaaaaaaa	nil	<b>TGTATAAAA</b>	multiple	nil	nil	nil	0	0	0	0	0	0	5	33.87	104.9	109.64	26.99	46.16	33.07	16.62	34.4775
552	tgtgccaagtgtgtcoo	NM_026724	<b>Rp134</b>	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	tgtgtcaaccagtgtoa	nil	<b>TGTGTCAACC</b>	multiple	nil	nil	nil	0	0	0	0	0	0	7	25.99	31.29	34.99	77.3	23.08	20.35	68.515	82.5075
554	tgtgttgagagcttctc	nil	<b>TGTGTTGAGAGCTTCTC</b>	multiple	nil	nil	nil	0	0	0	0	0	0	1	0.79	74.54	0	0	2.31	43.24	4.77	0.5725
555	ttcagotogagcgccaa	NM_011300	<b>Rps7</b>	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	ttcccgta	nil	<b>ttcccgta</b>	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	nil	<b>ttcctattaa</b>	no match	nil	nil	nil	0	0	0	0	2	0	3	2.36	0	34.99	0	0	5.09	0	0
558	ttgagaatgataactct	nil	<b>TTGAGAATGATAACTCT</b>	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	tttctgtatgtaaata	nil	<b>TTTCTGTATG</b>	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	tttgtaattctaaatt	NM_021510	<b>Hnrnph1</b>	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	tttttgggtgtgottata	NM_024173	<b>Atp6v1g1</b>	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

1 Enriched in R	1 Enriched in R	1 Enriched in E15.5	1 Enriched in PBL5	1 Enriched in Ad.	1 Enriched in Ad.
2 Enriched in R	2 Enriched in R	2 Enriched in E15.5	2 Enriched in PBL5	2 Enriched in PBL5	2 Enriched in E

## A-4 Additional data file 3

### Functional annotations clustering analysis using DAVID.

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

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- 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	<i>Rps8, Rpl22, Rps24, Rps4x, Rps9, Rps27, Rps17, Rps28, Rpl32, Rpl13, Rpl8, Rps15, Rps7, Rpl37a, Rpl4, Rpl34, Rpl23a, Rpl18a, Ppil1, Hnrnpa1, Hnrnpc, Lsm5, Uchl1, Tmsb4x, Mapt, Actb.</i>									
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	Ppil1, Rps8, Rpl22, Rps24, Rps4x, Hnrnpa1, Rps9, Hnrnpc, 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	<i>Rpl22, Ptms, Rps24, Rps4x, Rps9, Eif2s3x, Rps27, Rpl4, Rpl34, Tia1, Rps28, Rps17, Rpl32, Rpl23a, Rpl13, Rpl8, Rps15, Rpl18a, Rps7, Eef1b2, Rpl37a, Gpi1, Impdh2, Mat2a.</i>									
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, Eif2s3x, 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

Functional Group 3	Median: 2.13E-6	Geo: 2.53E-6	<i>Rpl22, Uchl1, Ptms, Rps24, Mapk6, Rps4x, Rps9, Tubb3, Eif2s3x, Rpl4, Cfl1, Ubc, Ptptr1, Rps28, Rps17, Tubb5, Rpl32, Ubt2, Arpc5, Rpl13, Rpl8, Prkc, Mex3b, Btg1, Rpl18a, Cdk4, Rps7, Eef1b2, Ppil1, Sbk1, Ezh2, Tubb2b, Stmn1, Rps27, Rpl34, Tia1, Tuba1a, Als2cr2, Rpl23a, Mapt, Wsb1, Cd24a, Rnf38, Rps15, Rpl37a.</i>									
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, Cfl1, Ubc, Ptptr1, Rps28, Rps17, Tubb5, Rpl32, Ubt2, Arpc5, Rpl13, Rpl8, Prkc, 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	Rpl22, Uchl1, Ptms, Rps24, Mapk6, Rps4x, Rps9, Tubb3, Eif2s3x, Rpl4, Cfl1, Ubc, Ptptr1, Rps28, Rps17, Tubb5, Rpl32, Ubt2, Arpc5, Rpl13, Rpl8, Prkc, Mex3b, Btg1, Rpl18a, Cdk4, Rps7, Eef1b2, Ppil1, Sbk1, Ezh2, Tubb2b, Stmn1, Rps27, Rpl34, Tia1, Tuba1a, Als2cr2, Rpl23a, Mapt, Wsb1, Cd24a, Rnf38, Rps15, Rpl37a	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	Rpl22, Uchl1, Ptms, Rps24, Mapk6, Rps4x, Rps9, Tubb3, Eif2s3x, Rpl4, Cfl1, Ubc, Ptptr1, Rps28, Rps17, Tubb5, Rpl32, Ubt2, Arpc5, Rpl13, Rpl8, Prkc, Mex3b, Btg1, Rpl18a, Cdk4, Rps7, Eef1b2, Ppil1, Sbk1, Ezh2, Tubb2b, Stmn1, Rps27, Rpl34, Tia1, Tuba1a, Als2cr2, Rpl23a, Mapt, Wsb1, Cd24a, Rnf38, Rps15, Rpl37a	108	3268	14977	1.909552224	0.0265473	0.002687	0.009901

Functional Group 4	Median: 3.16E-4	Geo: 4.29E-4	<i>Ptptr1, Uchl1, Cdkn1c, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Dcx, Cfl1, Igfbp1, Als2cr2, Btg1, Wnt7b, Vezf1, Mycn.</i>									
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_ALL	GO:0048666~neuron development	10	7.87%	5.50E-05	Ptptr1, Uchl1, Cdkn1c, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, Dcx	108	240	14977	5.77816358	0.2483063	0.017681	0.104979
GOTERM_BP_ALL	GO:0031175~neurite development	9	7.09%	1.43E-04	Ptptr1, 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	Ptptr1, 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	Ptptr1, Uchl1, Robo1, Chl1, Mapt, Cd24a, Stmn1, Dpysl5, 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, Igfbp1, 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, Igfbp1, 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, Igfbp1, 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: 0.0012	<b>Ptms, Rps24, Rps4x, Sox4, Hnrnpa1, Tubb3, Gpi1, Eif2s3x, Klf3, Rbm25, Ubc, Tubb5, Rps17, Rps28, Idh2, H2afy, Arpc5, Rpl8, Prkc, Neurod1, Mycn, Cdk4, Ppil1, Tardbp, Tubb2b, Stmn1, Rpl34, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, Mapk6, Rps9, Hnrnp, Rpl4, Cfl1, Ptprz1, Rpl32, Ubt2, Rpl13, Mex3b, Btg1, Pdna, Rpl18a, Rps7, Eef1b2, Ybx1, Cdkn1c, Sbk1, Mcm7, Sox12, Ezh2, Lsm5, Rps27, Tia1, Tuba1a, Wsb1, Cd24a, Sox11, Rps15,</b>									
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, Prkc, Neurod1, Mycn, Cdk4, Ppil1, Tardbp, Tubb2b, Stmn1, Rpl34, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, Mapk6, Rps9, Hnrnp, Rpl4, Cfl1, Ptprz1, Rpl32, Ubt2, Rpl13, Mex3b, Btg1, Pdna, 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, Prkc, Mycn, Neurod1, Cdk4, Ppil1, Tardbp, Tubb2b, Stmn1, Rpl34, Ppp1r10, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, Mapk6, Ak1, Rps9, Hnrnp, Impdh2, Rpl4, Cfl1, Ptprz1, Rpl32, Ubt2, Rpl13, Mex3b, Btg1, Pdna, 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, Prkc, Mycn, Neurod1, Cdk4, Ppil1, Tardbp, Tubb2b, Stmn1, Rpl34, Ppp1r10, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, Mapk6, Ak1, Rps9, Hnrnp, Impdh2, Rpl4, Cfl1, Ptprz1, Rpl32, Ubt2, Rpl13, Mex3b, Btg1, Pdna, 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, Prkc, Mycn, Neurod1, Cdk4, Ppil1, Tardbp, Tubb2b, Stmn1, Rpl34, Ppp1r10, Tcf4, Als2cr2, Rpl23a, Mapt, Zfp57, Rnf38, Rpl37a, Rpl22, Uchl1, Mapk6, Ak1, Rps9, Hnrnp, Impdh2, Rpl4, Cfl1, Ptprz1, Rpl32, Ubt2, Rpl13, Mex3b, Btg1, Pdna, 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	<i>Tmsb4x, Robo1, Chl1, Arpc5, Cd24a, Btg1, Stmn1, Dpysl5, Cfl1, Dcx,</i>								
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	<i>Tubb5, Gng2, Tubb3, Gnb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a, Mcm7,</i>								
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	<i>Tubb5, Gng2, Tubb3, Gnb2l1, Tubb2b, Eif2s3x, Gbp6, Tuba1a,</i>								
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	<i>Ppil1, Hnrnpa1, Hnrnpc, Lsm5, Rbm25, Ybx1,</i>								
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	<i>Apoe, Snap25, Clstn1, Mbp, Ppp3ca, Camk2a, Lynx1, Dlgap1, Gabra1, Sncb, Syn2, Plp1, Gja1, Gng13, Atp1a1, Mtap1a,</i>									
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	<i>Apoe, Snap25, Clstn1, Mbp, Ppp3ca, Camk2a, Lynx1, Dlgap1, Gabra1, Sncb, Syn2, Plp1,</i>	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	<i>Apoe, Snap25, Clstn1, Ppp3ca, Camk2a, Lynx1, Dlgap1, Gabra1, Sncb, Syn2, Plp1,</i>	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	<i>Snap25, Apoe, Camk2a, Ppp3ca, Lynx1, Gja1, Sncb, Syn2, Mbp, Clstn1, Dlgap1, Gabra1, Plp1,</i>	87	372	14977	6.01597454	0.006986	0.002334	0.00258
GOTERM_BP_ALL	GO:0003008--system process	16	14.16%	0.12136378	<i>Apoe, Snap25, Gng13, Camk2a, Ppp3ca, Lynx1, Gja1, Atp1a1, Sncb, Syn2, Mbp, Clstn1, Dlgap1, Gabra1, Plp1, Mtap1a,</i>	87	1894	14977	1.454271808	1	0.999994	91.55863
GOTERM_BP_ALL	GO:0050877--neurological system process	14	12.39%	0.1977012	<i>Snap25, Apoe, Gng13, Camk2a, Ppp3ca, Lynx1, Sncb, Syn2, Mbp, Clstn1, Dlgap1, Gabra1, Plp1, Mtap1a,</i>	87	1745	14977	1.381141521	1	1	98.51324

Functional Group 2	Median: 0.0025	Geo: 0.0016	<i>Slc1a3, Scg2, Atp1b2, Tuba4a, Mlc1, Thy1, Car2, Ptgs, Camk2n1, Syt13, Apoe, Itpr1, Syng1, Snap25, Camk2a, Ppp3ca, Gria3, Gja1, Atp2b1, Atp1a1, Sirpa, Nsf, Syn2, Laptm4b, Klc2, Ncald, Cck, Pacsin1, Kcnj3, Trf, Gabra1, Arf3,</i>									
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	<i>Slc1a3, Scg2, Atp1b2, Tuba4a, Mlc1, Thy1, Car2, Ptgs, Camk2n1, Syt13, Apoe, Itpr1, Syng1, Snap25, Camk2a, Ppp3ca, Gria3, Gja1, Atp2b1, Atp1a1, Sirpa, Nsf, Syn2, Laptm4b, Klc2, Ncald, Cck, Pacsin1, Kcnj3, Trf, Gabra1, Arf3,</i>	87	3021	14977	1.823496064	0.902294	0.440912	0.852219
GOTERM_BP_ALL	GO:0006810--transport	27	23.89%	0.00248859	<i>Slc1a3, Atp1b2, Tuba4a, Mlc1, Car2, Ptgs, Syt13, Itpr1, Syng1, Snap25, Apoe, Camk2a, Ppp3ca, Gria3, Atp2b1, Atp1a1, Sirpa, Nsf, Syn2, Laptm4b, Klc2, Ncald, Pacsin1, Kcnj3, Trf, Gabra1, Arf3,</i>	87	2613	14977	1.778811513	0.999998	0.924783	4.649106
GOTERM_BP_ALL	GO:0051234--establishment of localization	27	23.89%	0.00365748	<i>Slc1a3, Atp1b2, Tuba4a, Mlc1, Car2, Ptgs, Syt13, Itpr1, Syng1, Snap25, Apoe, Camk2a, Ppp3ca, Gria3, Atp2b1, Atp1a1, Sirpa, Nsf, Syn2, Laptm4b, Klc2, Ncald, Pacsin1, Kcnj3, Trf, Gabra1, Arf3,</i>	87	2685	14977	1.731111539	1	0.958028	6.761382

Functional Group 3	Median: 0.0122	Geo: 0.0125	<i>Apoe, Scg2, Lynx1, Chst1, Sirpa, Tmem59l, Epdr1, Ptpn, Ckmt1, Dkk3, Cx3cl1, Negr1, Clstn1, Ptgs, Fkbp2, Cck, Nptxr, Trf, Gabra1, Cyp46a1, Vgf, Syt13, Clu, Olfm1,</i>									
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	<i>Apoe, Scg2, Lynx1, Chst1, Sirpa, Tmem59l, Epdr1, Ptpn, Ckmt1, Dkk3, Cx3cl1, Negr1, Clstn1, Ptgs, Fkbp2, Cck, Nptxr, Trf, Gabra1, Cyp46a1, Vgf, Syt13, Clu, Olfm1,</i>	92	2375	15845	1.740411899	0.995878	0.422549	10.16808
GOTERM_CC_ALL	GO:0005615--extracellular space	21	18.58%	0.01219032	<i>Apoe, Scg2, Lynx1, Chst1, Sirpa, Tmem59l, Epdr1, Ptpn, Ckmt1, Dkk3, Cx3cl1, Negr1, Fkbp2, Cck, Nptxr, Trf, Gabra1, Cyp46a1, Syt13, Clu, Olfm1,</i>	92	2064	15845	1.752322422	0.999933	0.522737	17.11964
GOTERM_CC_ALL	GO:0044421--extracellular region part	21	18.58%	0.0226895	<i>Apoe, Scg2, Lynx1, Chst1, Sirpa, Tmem59l, Epdr1, Ptpn, Ckmt1, Dkk3, Cx3cl1, Negr1, Fkbp2, Cck, Nptxr, Trf, Gabra1, Cyp46a1, Syt13, Clu, Olfm1,</i>	92	2195	15845	1.647741904	1	0.675215	29.62707

Functional Group 4	Median: 0.0140	Geo: 0.0198	<i>Syng1, Ncald, Pacsin1, Syt13, Syn2, Trf,</i>									
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	<i>Syng1, Ncald, Pacsin1, Syt13, Syn2,</i>	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	<i>Syng1, Ncald, Pacsin1, Trf, Syt13, Syn2,</i>	92	246	15845	4.20068929	0.999979	0.537255	18.99515
GOTERM_CC_ALL	GO:0031988--membrane-bound vesicle	6	5.31%	0.0159822	<i>Syng1, Ncald, Pacsin1, Trf, Syt13, Syn2,</i>	92	256	15845	4.036599864	0.999997	0.569188	21.85877
GOTERM_CC_ALL	GO:0031410--cytoplasmic vesicle	6	5.31%	0.04704287	<i>Syng1, Ncald, Pacsin1, Trf, Syt13, Syn2,</i>	92	342	15845	3.021548436	1	0.792797	52.17797
GOTERM_CC_ALL	GO:0031982--vesicle	6	5.31%	0.05153873	<i>Syng1, Ncald, Pacsin1, Trf, Syt13, Syn2,</i>	92	351	15845	2.944072835	1	0.809746	55.51779

Functional Group 5	Median: 0.0242	Geo: 0.0238	<i>Apoe, Clstn1, Trf, Atp1a1, Thy1, 2810407C02rik, Mbp, Plp1,</i>									
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	<i>Apoe, Clstn1, Trf, Atp1a1, Thy1,</i>	87	123	14977	6.997944117	1	0.983004	9.964335
GOTERM_BP_ALL	GO:0055080--cation homeostasis	5	4.42%	0.00579821	<i>Apoe, Clstn1, Trf, Atp1a1, Thy1,</i>	87	125	14977	6.885977011	1	0.97704	10.51537
GOTERM_BP_ALL	GO:0019725--cellular homeostasis	6	5.31%	0.01716587	<i>Apoe, Clstn1, 2810407C02rik, Trf, Atp1a1, Thy1,</i>	87	261	14977	3.957458053	1	0.997505	28.16655
GOTERM_BP_ALL	GO:0055082--cellular chemical homeostasis	5	4.42%	0.01926314	<i>Apoe, Clstn1, Trf, Atp1a1, Thy1,</i>	87	178	14977	4.835658014	1	0.995084	31.03934
GOTERM_BP_ALL	GO:0006873--cellular ion homeostasis	5	4.42%	0.01926314	<i>Apoe, Clstn1, Trf, Atp1a1, Thy1,</i>	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	<i>Camk2a, Eef1a2, Kalrn, Zfp179, Itpka, Tuba4a, Atp1a1, Atp2b1, Nsf, Nme7, Pftk1, Ckmt1, Sept4, Syn2, Map2k1, Ckb, Centg3, Arf3,</i>									
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	<i>Gng13, Eef1a2, Zfp179, Atp1b2, Tuba4a, Atp2b1, Atp1a1, Nsf,</i>									
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	<i>Eef1a2, Zfp179, Tuba4a, Centg3, Arf3, Sept4,</i>									
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	<i>Rab6b, Gng2, Gnb1, Gnb2l1, Eif4a2, Rbbp4, Atp6v1g1, Tubb5, Atp9a, Ppa1, Atp5h, Atp1b1, Nav1, Atp11b,</i>									
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	<i>Atp6v1g1, Scamp5, Sv2a, Rph3a, Syt4, Vamp2, Map1lc3a, App,</i>									
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
GOTERM_CC_ALL	GO:0016023-cytoplasmic membrane-bound vesicle	6	5.08%	0.019799	Atp6v1g1, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	246	15845	3.826370442	1	0.602368	26.37196
GOTERM_CC_ALL	GO:0031988-membrane-bound vesicle	6	5.08%	0.023052	Atp6v1g1, Scamp5, Sv2a, Rph3a, Syt4, Vamp2,	101	256	15845	3.678902847	1	0.617997	30.02542

Functional Group 3	Median: 0.0089	Geo: 0.0075	<i>Eif4g2, Bzw2, Eif1b, Eif4a2, Eif6,</i>									
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: 0.0080	<i>Ube2e3, Map4k4, Galnt7, Map1lc3a, Pum2, Fbxl16, Ttl, Bzw2, Cct3, Otub1, Eif4a2, Usp16, Cttd, Tubb5, Cct6a, Nedd8, Znr1, Ppp1r1a, Dnajc5, Rps18, Cpe, Ptpns, Eif6, App, Lmtk3, Eif1b, Skp1a, Rps5, Eif4g2, Enc1, Mapt, Syt4, Olfm1,</i>									
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, Fbxl16, Ttl, Bzw2, Cct3, Otub1, Eif4a2, Usp16, Cttd, Tubb5, Cct6a, Nedd8, Znr1, Ppp1r1a, Dnajc5, Rps18, Cpe, Ptpns, 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, Fbxl16, Ttl, Bzw2, Cct3, Otub1, Eif4a2, Usp16, Cttd, Tubb5, Cct6a, Nedd8, Znr1, Dnajc5, Rps18, Cpe, Ptpns, 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, Fbxl16, Ttl, Bzw2, Cct3, Otub1, Eif4a2, Usp16, Cttd, Tubb5, Cct6a, Nedd8, Znr1, Dnajc5, Rps18, Cpe, Ptpns, 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	<i>Map4k4, Galnt7, Map1lc3a, Pum2, Sox4, Hnrpd1, Bzw2, Ttl, Fads2, Fbxl16, Actl6b, Rrp1, Nme2, Bcl11a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Atp9a, Aldoc, Glrx3, Nedd8, Znrfl, 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, Ptprs, App, Lmtk3, Eif1b, Gucy1a3, Atp6v1g1, Eif4g2, Rbm9.</i>								
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, Map1lc3a, Pum2, Sox4, Hnrpd1, Bzw2, Ttl, Fads2, Fbxl16, Actl6b, Rrp1, Nme2, Bcl11a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Atp9a, Aldoc, Glrx3, Nedd8, Znrfl, 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, Ptprs, App, Lmtk3, Eif1b, Gucy1a3, Atp6v1g1, Eif4g2, 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, Hnrpd1, Bzw2, Ttl, Fads2, Fbxl16, Actl6b, Rrp1, Nme2, Bcl11a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Aldoc, Nedd8, Znrfl, Atp5h, Ppp1r1a, 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, Eif4g2, 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, Map1lc3a, Pum2, Sox4, Hnrpd1, Bzw2, Ttl, Fads2, Fbxl16, Actl6b, Rrp1, Nme2, Bcl11a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Aldoc, Nedd8, Znrfl, 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, Map1lc3a, Pum2, Sox4, Hnrpd1, Bzw2, Ttl, Fbxl16, Actl6b, Rrp1, Bcl11a, Eif4a2, Rbbp4, Usp16, Nola3, Drap1, Tubb5, Aldoc, Nedd8, Ppp1r1a, Znrfl, HMGB1, Hmgn1, Eif6, Skp1a, Rps5, Enc1, Hmgb3, Mapt, Syt4, Olfm1, Ube2e3, Prmt2, Nfix, 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	<i>Mtap1b, Tubb5, Ttl, Nav1, Mapt, Map1lc3a, App, Eif6.</i>								
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	<i>Atp6v1g1, Atp9a, Atp5h, Atp1b1, Atp11b, Reep5, Cacng4.</i>								
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	<i>Atp6v1g1, Hprt1, Atp5h, Nme2, Gucy1a3,</i>									
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	<i>Sox4, Hmgb3, HMGB1, H2afv, Hmgn1, Zwint,</i>									
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	<i>Gng2, Gnb1, Gnb211,</i>									
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, Gnb211,	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, Gnb211,	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, Gnb211,	101	76	15845	6.192678478	1	0.881037	73.56049

Functional Group 11	Median: 0.0583	Geo: 0.0528	<i>Rab6b, Sh3gl2, Fads2, Reep5, Hba-a1, Ywhaz, Tubb5, Atp9a, Foxg1, Nedd8, Atp5h, Cacng4, HMGB1, Atp11b, Vamp2, App, Sv2a, Rab14, Gnb211, Atp6v1g1, Ywhae, Scamp5, Atp1b1, Nav1, Rph3a, Clcn2, Elmod1, Syt4,</i>									
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, Gnb211, 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	<i>Mtap1b, App, Foxg1, Hprt1, Ttl, Mapt, Nav1, Ube2e3, Bai1, Gucy1a3, Eif4g2, Prdx2,</i>									
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, Eif4q2, 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	<i>Atp6v1g1, Hprt1, Atp5h, Nme2,</i>									
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	<i>App, Hprt1, Sv2a, Cacng4, Rph3a, Syt4, Vamp2, Gnb1, Gucy1a3,</i>									
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%	0.011019	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 <http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s4.xls>.*

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- Note 1** Any fold changes/enrichments less than 1 are presented in "negative fold changes/enrichments" 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
gcttcccccccccctt	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
ggatgatgggtgtgtac	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
aaattattgggaatcc	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
gtatttgcacaaaaaa	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
gcttcctccccaggag	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
cctcatttccctgtttc	BQ176089	EST from adult C57BL/6 subfornical organ and postrema tissues	0.00	0.00	8.33	Adult specific	Adult specific	23.01	2.98E-08	8.91	1.66E-06	Adult
accggctagtgtgaa	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
ctcattataacaaagaa	CD802535	EST from 27-32 days C57BL/6 hippocampus tissue	0.00	0.92	8.33	Adult specific	9.05	22.03	6.50E-12	13.25	9.27E-11	Adult
ataaaagcaactgtac	NM_033610	synuclein, beta, Snca	2.36	6.44	49.31	20.89	7.66	18.20	6.28E-08	15.83	1.18E-08	Adult
gctttttgtaccatctc	NM_030689	neuronal pentraxin receptor, Nptxr	3.15	4.60	56.31	17.88	12.24	15.02	3.29E-11	10.93	2.09E-10	Adult
tcctcccttagtatcc	NM_144828	protein phosphatase 1, regulatory (inhibitor) subunit 1B, Ppp1rb	0.00	0.00	21.66	Adult specific	Adult specific	10.47	1.82E-08	6.88	1.64E-07	Adult
gccttctctctatggc	NM_010358	glutathione S-transferase, mu 1, Gstm1	0.00	0.00	10.00	Adult specific	Adult specific	9.87	7.00E-11	5.58	2.08E-09	Adult
tgactagcgtgactggt	NM_007694	chromogranin B, Chgb	4.73	4.60	28.99	6.13	6.30	9.43	2.07E-10	7.22	1.17E-09	Adult
attctttcttggtggtg	NM_010585	inositol 1,4,5-triphosphate receptor 1, Itpr1	0.79	1.84	11.33	14.34	6.16	9.29	5.08E-10	6.12	7.92E-09	Adult
actttgagatgtacct	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
ataaattagccttaggt	AK139402	Mus musculus 10 days neonate cortex cDNA	0.00	0.00	16.99	Adult specific	Adult specific	8.28	4.84E-08	7.55	8.56E-08	Adult
ctagacagagcattat	NM_019634	tetraspanin 7, Tspan7	0.79	1.84	10.33	13.08	5.61	7.99	9.31E-11	5.38	1.17E-09	Adult
tgatacaacaacagctg	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
tgacaagacactgtggt	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
cttactctaggttctct	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
atagctttctcacact	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
ttcagcaggtgttggct	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
aggtatgtacaagttt	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
tccaactgttaactata	NM_008790	calmodulin 1, Calm1	5.51	7.36	23.32	4.23	3.17	3.24	6.38E-08	2.27	3.92E-06	Adult
cctcagctggggtaga	NM_009983	cathepsin D, Ctscd	8.66	14.72	29.99	3.46	2.04	3.22	2.94E-07	3.84	7.05E-08	Adult
gcttctgtccacaacagc	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
tattaaatgtctttttt	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
cttattctcactctcagc	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 quadrigemina cDNA	27.56	43.25	805.35	29.22	18.62	2.63	1.04E-05	2.03	2.47E-04	Adult
agtggtctaattaggtgt	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
ttccgtgaacaaaaact	AK154943	Mus musculus NOD-derived CD11c +ve 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
ccagtcactgaaaaaaa	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
aagaaaacatttaata	NM_012010	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked, Eif2s3x	10.24	13.80	1.33	-7.70	-10.38	-1.72	3.50E-03	-1.74	3.20E-03	Adult
caccctgtggagactca	NM_172656	amyotrophic lateral sclerosis 2 (juvenile) 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
ccttcactctttatact	NM_009536	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide, Ywhae	24.41	19.32	7.66	-3.19	-2.52	-1.82	1.27E-03	-2.66	1.41E-05	Embryonic
tgtgtcttccctgtctta	NM_008683	neural precursor cell expressed, developmentally down-regulated gene 8, Nedd8	34.65	61.65	7.33	-4.73	-8.41	-1.83	7.59E-05	-1.86	5.63E-05	Embryonic
ctcctgaaggcatagtt	NM_009454	ubiquitin-conjugating enzyme E2E 3, Ubc4/5 homolog (yeast), Ube2e3	16.54	22.09	4.00	-4.14	-5.52	-2.51	1.81E-06	-3.22	1.28E-07	Embryonic
gtgaaactcaaaaaaaa	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
aatgtttctgcttttaca	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
ctttgtgacagtggtgc	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
gaagcagctggcgcctc	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
gctgtggctcgtgtggg	NM_010561	interleukin enhancer binding factor 3, Ilf3	0.00	0.00	13.99	Adult specific	Adult specific	-4.15	6.84E-08	-2.97	1.48E-06	Embryonic
accctgtaccctctgtt	NM_016707	B-cell CLL/lymphoma 11A (zinc finger protein), Bcl11a	23.63	16.56	3.00	-7.88	-5.52	-4.42	3.76E-08	-4.78	2.61E-08	Embryonic
cggtgtgtccccaccttc	NM_012015	H2A 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
caagtgcataaaaaata	NM_010894	neurogenic differentiation 1, Neurod1	12.60	8.28	1.67	-7.54	-4.96	-5.62	2.70E-08	-5.10	5.93E-08	Embryonic
aagttgtcaagttctcca	NM_008538	myristoylated alanine rich protein kinase C substrate, Marcks	33.08	15.64	1.33	-24.87	-11.76	-5.72	3.26E-100	-5.56	4.63E-97	Embryonic

ttgtgcttttataaa	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, Wsbl	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), Robo1	9.45	5.52	0.33	-28.64	-16.73	-8.23	1.72E-08	-11.35	3.40E-09	Embryonic
gctttgactgtttctctt	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
tggagcgttggtgtat	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
tgtgtgagtggtgtgta	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
caagtgtagtggtgtg	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)											
SAGE tag	Accession	Gene/EST ID	PN1.5/100,000 tags (SAGE)	Adult/100,000 tags (SAGE)	Fold-enrichment in adult (SAGE)	Fold-enrichment in adult (RT-qPCR)	Adjusted p value (RT-qPCR)	Specificity			
aaattattgggaaatcc	NM_011123	proteolipid protein (myelin) 1, Plp1	2.33	90.63	38.9	43.33	7.49E-11	Adult			
tttcagcagtggtgct	NM_013556	hypoxanthine guanine phosphoribosyl transferase 1, Hprt1	4.67	32.65	6.99	2.26	2.28E-05	Adult			
actcgagcaccacagac	NM_009790	calmodulin 1, Calm1	25.66	117.29	4.57	1.83	1.00E-04	Adult			
gcttgctccacacagcg	NM_010777	myelin basic protein, Mbp	0	159.94	Adult specific	1.79	3.10E-04	Adult			
tcccctcat	NM_026106	down-regulator of transcription 1, Drl1	32.66	0	PN1.5 specific	-1.46	1.38E-02	PN1.5			
gggaaactaaggagag	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, Actl6b	25.66	4.66	-5.51	-2.26	1.00E-04	PN1.5			
gtgaaactaaaaaa	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	4.88E-07	PN1.5			
ctttgtgacagtgccc	NM_025635	ZW10 interactor, Zwint	20.99	97.63	4.65	-4.04	4.06E-06	PN1.5			
acagtctatgttgagg	BQ177886 / NM_010487	C57BL/6 whole brain E15.5 (also known as embryonic lethal, abnormal vision, Drosophila-like 3 (Hu antigen C), Elavl3)	41.99	1	-41.99	-4.06	1.04E-07	PN1.5			
gatacttggagtgacta	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			
tggagcgttggtgtat	NM_009870	cyclin-dependent kinase 4, Cdk4	18.66	0.33	-56.55	-5.77	7.91E-09	PN1.5			
gctttgactgtttctctt	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			
cacgacacccccaccc	NM_009559	zinc finger protein 57, Zfp57	16.33	1	-16.33	-32.74	1.60E-10	PN1.5			
tgtgtgagtggtgtgta	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 <http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s5.xls>.*

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- 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.



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
tgagcgttgctgtat	NM_009870	cyclin-dependent kinase 4, Cdk4	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
tgtgtgaggtgtgtga	NM_010025	doublecortin, Dcx	6	59.07	78.22	32.66	1.33	7.7633	8.0678	7.9180	1.5585	0.1124	1.3215	0.5567	0.0307	1.2350	2.11E-01	1.1132	4.84E-01	0.0136	1.46E-13
aagtttgaagtctcca	NM_008538	myristoylated alanine rich protein kinase C substrate, Marcks	6	32.72	12.61	18.66	1.22	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
gggacctctgtgaagcc	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
cacgacacccccacc	NM_009559	zinc finger protein 57, Zfp57	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
acccttgaacccctgtt	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
cctcagctgggtaga	NM_009983	cathepsin D, Ctcd	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
attctctgtgtattt	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
tgtgtctccctgtctta	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
ttgctggctttataaa	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
ctctcgaagcatagtt	NM_009454	ubiquitin-conjugating enzyme E2E 3, Ubc4/5 homolog (yeast), 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	1.60E-02	0.3983	1.81E-06
tgacaagacactgtggc	AU258168	calcium/calmodulin-dependent protein kinase II alpha, Camk2a	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
gcttccccccccctt	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	1.16E-13
gtatttgcaaaaaaaa	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
gcccctctctctggc	NM_010358	glutathione S-transferase, mu 1, Gstmu	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
cttactcctcactcagc	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	6.99E-06
tcctcctctagatcc	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
cttactcctaggttctc	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	3.48E-02	1.8351	3.17E-03	5.4795	3.51E-08
aaattattgggaatcc	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
caaacctcnaaaaccca	AK140219	AK140219	10	27.56	43.25	23.33	805.35	-1.4382	-1.0636	-0.6668	-0.0434	0.1445	1.5592	0.8493	28.7188	1.2965	1.80E-01	1.7069	5.30E-03	2.6296	1.04E-05
accatgacnaaaaaaa	AK154943	AK154943	10	4.73	10.12	4.67	517.46	-1.6172	-1.2325	-0.8269	-0.8010	0.1698	2.0306	0.9885	99.0363	1.3055	2.08E-01	1.7294	7.91E-03	1.7607	3.19E-03
ttaccatactgggttg	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
gctttgttaccatctc	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
aataagccaatttgac	NM_033610	synuclein, beta, Snca	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 <http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s6.xls>.*

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- Note 1** Any fold changes/enrichments less than 1 are presented in "negative fold changes/enrichments" 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 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)	Fold-enrichment in E15.5 caudal (RT-qPCR)	Adjusted p value (RT-qPCR)	Specificity
<i>Nil</i>	NM_010151	nuclear receptor subfamily 2, group F, member 1, Nr2f1 (Couptf1)	<i>Nil</i>	<i>Nil</i>	<i>Caudal specific</i>	<b>2.44</b>	<b>2.53E-02</b>	Caudal
gttgttcttccagtcgg	NM_016916	bladder cancer associated protein homolog (human), Blcap	4.62	5.09	1.10	<b>1.43</b>	1.17E-01	Caudal
gataactggaatgacta	NM_007393	actin, beta, cytoplasmic, Actb	408.52	155.16	-2.63	<b>-1.32</b>	1.32E-01	Rostral
<i>Nil</i>	NM_001043354 / NM_146095	RAR-related orphan receptor beta, Rorb	<i>Nil</i>	<i>Nil</i>	<i>Rostral specific</i>	<b>-1.65</b>	8.97E-02	Rostral
ttggtgaaggaaaaaac	NM_021278	thymosin, beta 4, X chromosome, Tmsb4x	507.77	218.75	-2.33	<b>-2.14</b>	<b>7.33E-03</b>	Rostral
gtcatagctgttctgtg	BC025816	EST sequence BC025816	0	38.15	<i>Caudal specific</i>	<b>1.31</b>	3.17E-01	Caudal
aagcttgacatttgaa	NM_026187	ankyrin repeat and zinc finger domain containing 1, Ankzf1	2.31	0.00	<i>Rostral specific</i>	1.17	4.16E-01	Not validated

RT-qPCR results for RvC analysis of E15.5 cerebral cortex quadrants																
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)	Log2 normalized expression for E15.5 cerebral cortex (against 3 housekeeping genes)					Fold-enrichment after normalized to E15.5 rostro-lateral cerebral cortex					
						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)
						<i>Nil</i>	NM_001043354 / NM_146095	RAR-related orphan receptor beta, Rorb	<i>Nil</i>	<i>Nil</i>	<i>Rostral specific</i>	0.46	0.09	-0.37	-0.53	0.34
gataactggaatgacta	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	<b>1.50E-02</b>	-1.95	<b>8.57E-02</b>
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	<b>6.36E-05</b>	-2.45	7.84E-02	-1.83	1.05E-01
<i>Nil</i>	NM_010151	nuclear receptor subfamily 2, group F, member 1, Nr2f1 (Couptf1)	<i>Nil</i>	<i>Nil</i>	<i>Caudal specific</i>	-0.76	-0.37	0.24	1.21	0.42	1.31	7.42E-01	2.00	1.21E-01	<b>3.91</b>	<b>1.69E-03</b>
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	<b>1.69</b>	1.05E-01
gtcatagctgttctgtg	BC025816	EST sequence BC025816	0	38.15	<i>Caudal specific</i>	-1.74	-1.31	-1.33	-0.94	0.32	<b>1.34</b>	7.42E-01	<b>1.33</b>	4.47E-01	<b>1.74</b>	1.05E-01
aagcttgacatttgaa	NM_026187	ankyrin repeat and zinc finger domain containing 1, Ankzf1	2.31	0.00	<i>Rostral specific</i>	-0.42	-0.21	-0.25	0.08	0.19	1.16	8.49E-01	1.12	6.80E-01	<b>1.41</b>	2.76E-01
aaccctaataaaaaaaa	AK132098 / X55780	mRNA for cytochrome c oxidase subunit 1, 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	<b>1.35</b>	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 <http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s7.xls>.*

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- Note 1** Chromosome positions presented here were based on mouse assembly release February 2006.
- 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.





## 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 <http://genomebiology.com/content/supplementary/gb-2009-10-10-r104-s8.xls>.

### 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.

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	sox4_tag10	18	99	GTTGGGGATGCAGAAGGA	56	60	73nt	gtggggatgcagaaggaccggagcacagagggcggtgg
	Sox4	sox4_t4_R	NISP		22	99	TTTGCACAGACCCAGGCGGAG	64	73		ggttccgggctccgctgggctgtgcaaa
2	Sox4	3671s4-3tgF	NISP	sox4_tag12	18	78	AGGCTGGCCTGCTACTCC	67	60	86nt	gcaaggacaaggggaaaaagtgggggaggaggaga
	Sox4	3672s4-3tgR	NISP		18	78	GCTGGGCTTTCTCCTCT	67	59		aagcccagcccgggactcgcagcgtggagtttccatgcc
3	Sox4	3673s4-5F	NISP	sox4_tag15	20	17	CTGAACCCAGCTCAAATT	50	59	92nt	ctgaacccagctcaacttgagagcatgcccgggagtt
	Sox4	3674s4-5R	NISP		23	17	GGTTCGAAGTTAAATCCAGGTC	50	60		cagctcctcatcggcctcagcgggacctggatttaactcg
4	Sox4	3675s4-10F	NISP	sox4_tag16	20	79	ACAGCGACAAGATCCGTTT	50	60	62nt	acagcgacaagattccgttcaccaggaggcggagcggtg
	Sox4	3676s4-10R	NISP		19	79	GTCAGCCATGTGCTTGAGG	58	60		cgccctcaagcacatggctgac
5	Sox11	sox11_t16_F	NISP	sox11_tag11	23	6	GTTGAATTCATACACTCCAATGT	35	56	97nt	gttgaattcatacactccaatgctcttttcaggagttttcaca
	Sox11	sox11_t16_R	NISP		20	6	GGAGATTGATCACACGATTT	40	55		gaggaatacattgttcaaaagaccaataaaaatcgtgtgac
6	Sox11	sox11_t3_F	NISP	sox11_tag12	20	21	ATCCCCTGATGCTTTGTTTC	45	59	75nt	atcccgtgatgcttggttccgggacagagccacctgaagct
	Sox11	sox11_t3_R	NISP		21	21	TGTTAACAGTGCCATGCTGAT	45	59		gagagtagttatcagcatggcactgtaaca
7	Hmbs	3843_hmbs_F	ISP	endogenous control	20	42	AAAGTTCCCCAACCTGGAAT	45	59	98nt	aaagttcccaacctggaattcaagagatcggggaaacctc
	Hmbs	3844_hmbs_R	ISP		20	42	CCAGGACAATGGCACTGAAT	50	60		aacacccgctcgggaagctgagctgagctgaggaattcagt
8	Psmb2	3367_psmb2_F	ISP	endogenous control	20	25	GAGGGCAGTGGAGCTTCTTA	55	59	71nt	gagggcagtgagctcttaggaagtgtctgaggagctcca
	Psmb2	3368_psmb2_R	ISP		21	25	AGTGGGCAGATTCAGATG	50	60		gaagcctcatctgaaatctgccacct
9	Pgk1	3365_pgk1_F	ISP	endogenous control	18	108	TACCTGCTGGCTGGATGG	61	60	65nt	tacctgctggctggatggcctggactgtgttactgagagcag
	Pgk1	3366_pgk1_R	ISP		20	108	CACAGCCTCGGCATATTTCT	50	60		caagaaatgccgaggctgtg

## 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).

<i>Southern blot number</i>	<i>Gene ID</i>	<i>Primer used for 3' RACE with adaptor primer</i>	<i>Orientation of targeted mRNA</i>	<i>SAGE tags</i>	<i>Length (mer)</i>	<i>Sequence 5'-3'</i>	<i>%GC</i>	<i>Tm (°C)</i>	<i>Oligonucleotide probe used for hybridization during Southern blotting (sequence 5'-3')</i>
Fig. 7D.1	Sox4	3675s4-10F	Sense	Sox4_tag10, tag15, tag16	20	ACAGCGACAAGATTCCGTC	50	60	GTCAGCCATGTGCTTGAGG
Fig. 7D.2	Sox4	3673s4-5F	Sense	Sox4_tag10, tag12, tag15	20	CTGAACCCAGCTCAAATT	50	59	GGTTCGAAGTAAAATCCAGGTC
Fig. 7D.3	Sox4	s4_tg4_ota	Sense	Sox4_tag10	20	TGATGTTGGTGGTGGCTAAA	45	60	GCTGGGCTTTCTCCTCT
Fig. 7D.4	Sox4	sox4_t4_R	Antisense	Sox4_tag11, tag13, tag14	22	TTTGACAGACCCCAGGCGGAG	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	TTCCTGTTCCGGACACATGTAAG
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	59	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	AAAGTCCCCAACCTGGAAT	45	59	CCAGGACAATGGCACTGAAT
Fig. 7D.8 & Fig. 8D.8	Hmbs	3844_hmbs_R	Antisense	N.A.	20	CCAGGACAATGGCACTGAAT	50	60	AAAGTCCCCAACCTGGAAT

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

**Note 1** These probes were double-digested from pGEMT clone, gel purified and sequenced prior to random labeling.

**Note 2** The position of the probe is based on the RefSeq canonical mRNA sequence.

<i>Name of probe</i>	<i>Size of probe</i>	<i>Probe sequence</i>	<i>Target sequence (Refseq)</i>	<i>The position of the probe on target mRNA</i>
Sox4 (C1)	614	TTGATGTTGGTGGTGGCTAAAAAGCTACTTCGAGTTTCTCCCAATTTGCTTGAAGAGACTCCCCCACCACCCCTTCCAACGAGCT TCCGGACTTGGTTGCACCCCCAGCAAGAAAAGAAGCCAAGCAAAGCTTCTAAAGACCGAAGGAATCTTCCCTCACCCCCACCCCTCGC CTTGGTGATTTCTTGTGATTTTGCCTCATGGTCAAGAAAGGAGGGGAAAATCCAGCGTGCCCATCTCCTACCCACCCCTCTTTGTATT CTCTTTGATTTTTCCCTTCTTAAATTTCTTTTTCTGCAATGAAGACAGAAAAGAAGCTCTGGGGTGATGCGTTTGGCATTGTGTTGAGCT TAGGGGAGCATTGGCATGGAGAACTCCACGCTGGCGAAGTCCCGGGCTGGGCTTTCTCCTCCTCCCCACCTTTTTCCCTTGCCTT GCAGCTGGAGATGTGCTGGGAGTAGCAGGCCAGCCTCGAAAATGGACATGGGGACCTCGTGAAGCCACAGCAACCTGGTTGGGGATGC AGAAGGACCCGGAGCACAGAGGGCGTTGGGGTCCCGGGCTCCGCCTGGGGTCTGTGCAAAAAT	Sox4 (NM_009238)	2330-2943bp
Sox11 (C10)	950	CACCTGAACCAGCGTTCTTATTCTTTAAGCTGTGAAATAATTTCCAGTTTCTACATTCTCGATATGCATCCTTATTA AAAAGATAATACGAAT GAAAGGCAGTGTGCTTAAAGTGTGCTTTGCAAATACATGTTATGAATGACTACGGTCACTGGGCAAATATTTGTAGAATGATTAGCCTTTAGC TAGAAAAAAAATCATTGCAGCTCTTTGGGCCTGGATGGTTCTTTTTAATGTTAATGGAGGGGAAGTGATTTAAATATGCATGCTTTAGCA GTCAGGATCTGACTTAGTTGTTTTGAGAGAAAAAAAATCAAAAGGCAAGGTCTACTTTTTTCTCTGGAATTGAAACCACAATCATCTTGAT ACTAGAACAGTGAAGAAATGAACATTTGTTCTTCACTTCAGAATTCAAATGAGTTTGGCCCAAGGAATCTGGGAAATAAGGCAAATAAGTTGC TCAATTTTCAAGTAGTCATTCAATAGAAATATACTCCATCACTCGGCTTTCTTATTCTCTGATGGGGTATTCTGTATAGTCTCACTGTTTTCTCT AATGGGCATATGTATCTTTGTGGACACTTGAAGAGAGGTTTTCTGTACTCTCTCATTCTAGAATCTTTATACTTTTTCTGCAAGGTTCT CTGCTTTTAAACAGATTTCTGAGGCAACTATATTTGTGCTTTTTCTTATGTAGGAAGACCAGCGAAACTAGCTTACTGAGTTGTGATTTTATCA GTAGATAAAGAACTTTGTTTATTACAGTTTCAGGGAAGGTTTTCTAGGATATTTCTCAGTTATTCTAAGGGCCAAATTTTATATATAAAAAAAA AAAACCTCATTAGGAATGTCAGTTTCAGATACCCTTTGTATAGCCTGTGGCCTGCAAGCACGACAGGACTGAGCCTTACATGTGTCGAACA GGAA	Sox11 (NM_009234)	4558-5507bp

**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 used to generate the riboprobe	Restriction enzyme used for linearization	Sequencing result	Estimated size	Probe	Comment	NIA mouse 15K cDNA clone accession
Actb	pSPORT1	T7	MluI/Buf. D	Confirmed +/-	1580bp	Sense	Full length	H3018D10
Actb	pSPORT1	SP6	EcoRI/Buf. H	Confirmed +/-	1580bp	Antisense	Full length	
BC025816	pGEMT	T7	SacI/Buf. J	Confirmed +/-	911bp	Antisense	Mid BC02	Amplification by PCR followed by cloning
BC025816	pGEMT	SP6	AatII/Buf. J	Confirmed +/-	911bp	Sense	Mid BC02	
Bicap	pSPORT1	T7	MluI/Buf. D	Confirmed - only	965bp	Sense	1/2 of Bicap till 3'	H3008G10
Bicap	pSPORT1	SP6	EcoRI/Buf. H	Confirmed - only	965bp	Antisense	1/2 of Bicap till 3'	
Coup-tf1	pSPORT1	T7	MluI/Buf. D	Confirmed +/-	375bp	Sense	3' of Ctf1	H3097D07
Coup-tf1	pSPORT1	SP6	EcoRI/Buf. H	Confirmed +/-	375bp	Antisense	3' of Ctf1	
Cybb	pSPORT1	T7	MluI/Buf. D	Confirmed +/-	1492bp	Sense	Mid Cybb	H3060F11
Cybb	pSPORT1	SP6	KpnI/Buf. J	Confirmed +/-	1492bp	Antisense	Mid Cybb	
D1ertd161e	pSPORT1	T7	BamHI/Buf. E	Confirmed +/-	2460bp	Sense	Full length	H3024H07
D1ertd161e	pSPORT1	SP6	KpnI/Buf. J	Confirmed +/-	2460bp	Antisense	Full length	
Hba-a1	pSPORT1	T7	MluI/Buf. D	Confirmed +/-	>500bp	Sense	Full length	H3045A12
Hba-a1	pSPORT1	SP6	KpnI/Buf. J	Confirmed +/-	>500bp	Antisense	Full length	
Rorb	pGEMT	T7	SpeI/Buf. B	Confirmed +/-	935bp	Sense	Mid Rorb	Amplification by PCR followed by cloning
Rorb	pGEMT	SP6	Apal/Buf. A	Confirmed +/-	935bp	Antisense	Mid Rorb	
Sox11 (C10)	pGEMT	T7	SpeI/Buf. B	Confirmed +/-	950bp	Antisense	Mid Sox11 (3' UTR)	Amplification by PCR followed by cloning
Sox11 (C10)	pGEMT	SP6	AatII/Buf. J	Confirmed +/-	950bp	Sense	Mid Sox11 (3' UTR)	
Sox4 (C1)	pGEMT	T7	SpeI/Buf. B	Confirmed +/-	614bp	Antisense	3' of Sox4 (3' UTR)	Amplification by PCR followed by cloning
Sox4 (C1)	pGEMT	SP6	AatII/Buf. J	Confirmed +/-	614bp	Sense	3' of Sox4 (3' UTR)	
Tmsb4x	pSPORT1	T7	MluI/Buf. D	Confirmed - only	~500bp	Sense	Full length	H3143A02
Tmsb4x	pSPORT1	SP6	EcoRI/Buf. H	Confirmed - only	~500bp	Antisense	Full length	

## 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** T<sub>m</sub> calculations were based on Breslauer et al, Proc Natl Acad Sci U S A 83 (1986) 3746-50.

Gel lane	Gene ID	Primer Name	Notes	Length (mer)	Sequence 5'-3'	%GC	T <sub>m</sub> (°C)	Amplicon size	Amplicon sequence
1	Sox4	3675s4-10F	For antisense mRNA	20	ACAGCGACAAGATTCCGTTTC	50	60	62nt	acagcgacaagattccgttcatccaggaggcggagcggcgtg cgcctcaagcacatggctgac
	Sox4	3676s4-10R	For sense mRNA	19	GTCAGCCATGTGCTTGAGG	58	60		
2	Sox4	sox4_t4_F	For antisense mRNA	18	GTTGGGGATGCAGAAGGA	56	60	73nt	gttgggatgcagaaggacccggagcacagagggcgttgg ggtcccggcctccgctgggtctgtgcaaa
	Sox4	sox4_t4_R	For sense mRNA	22	TTGCACAGACCCAGGCGGAG	64	73		
3	Sox4	3673s4-5F	For antisense mRNA	20	CTGAACCCAGCTCAAACCTT	50	59	92nt	ctgaaccccagctcaactttgagagcatgtccctggcagttt cagctcctcatcggcgtcgtatcgggacctggatttaactcg
	Sox4	3674s4-5R	For sense mRNA	23	GGTTCGAAGTTAAAATCCAGGTC	50	60		
4	Sox11	3665s11-8F	For antisense mRNA	20	GTGGCGGTCAGGATAAAGAG	55	59	75nt	gtggcgtcaggataaagaggatgggtggggagggggag aagatgctcatggtcagagagatgtggcgtgaga
	Sox11	3666s11-8R	For sense mRNA	19	TCTCAGCGCCACATCTCTC	55	60		
5	Sox11	sox11_t16_F	For antisense mRNA	23	GTTGAATTCATACACTCCAATGT	35	56	97nt	gttgaattcatacactccaatgtctcttttgcaggagttttcaca gaggaatacattgttcaaaagaccaataaaaatcgtgtgatc
	Sox11	sox11_t16_R	For sense mRNA	20	GGAGATTGATCACACGATTT	40	55		
6	Sox11	3669s11-4tgF	For antisense mRNA	20	GCGTTGTGTGCATAGCAGTC	55	60	69nt	gctgtgtgcatagcagctagccggtgggtacctctctctg tacctagttcacagactcagatgc
	Sox11	3670s11-4tgR	For sense mRNA	22	GCACTCGAGTCTGTGAAC TAGG	55	59		
7 and 8	Hmbs	3843_hmbs_F	For antisense mRNA	20	AAAGTTCCCAACCTGGAAT	45	59	98nt	aaagtccccaacctggaattcaagagattcggggaaacct caacaccgccttggagactggatgagctgcaggaattcag
	Hmbs	3844_hmbs_R	For sense mRNA	20	CCAGGACAATGGCACTGAAT	50	60		

## **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** T<sub>m</sub> calculations were based on Breslauer et al, Proc Natl Acad Sci U S A 83 (1986) 3746-50.

Primer set	Gene ID	Notes	Primer Name	Length (mer)	UPL Probe #	Sequence 5'-3'	%GC	Tm (°C)	Amplicon size	Amplicon sequence
1	AA122503	NISP	AA122503_F	22	25	AGATGCTGCACACAGGTATCTC	50	59	60nt	agatgctgcacacaggtatctcccctccacccccgaatgtcacctaaacaaactaga
	AA122503	NISP	AA122503_R	25	25	TCTAGTTTGGTTTAGGTGACATTCG	50	60		
2	Actb	ISP	3361_actb_F	20	56	AAGCCCAACCGTGAAAGAT	45	60	110nt	aaggccaaccgtgaaaagatgaccagatcatgtttgagacctcaacacccagcatgtacgttagccatc caggctgtgctgcctgtatgcctctggtgtaccac
	Actb	ISP	3362_actb_R	21	56	GTGGTACGACCAGAGGCATAC	57	59		
3	Actl6b	ISP	actl6b_F	19	104	AAGTTCAGCCCCTGGATTG	53	60	71nt	aagttcagccccgtgattggaggctccatctggcctcactgggcacattccagcagatgtggatctccaa
	Actl6b	ISP	actl6b_R	20	104	TTGGAGATCCACATCTGCTG	53	59		
4	AK138272	NISP	AK138272_F	20	102	GTTTCGTCCTACCATCATCC	55	60	105nt	gttctgctgtaccatccaatagtaggaaagataataatcccacccctctcagccaatgaaaagttgaaat atgttggctgaggtggagataagcatg
	AK138272	NISP	AK138272_R	21	102	CATGCTTATCCTCACCTCAGC	55	59		
5	AK139402	NISP	AK139402_F	20	56	TCTTACCCTAGGTGCGTCT	55	60	63nt	tcttcaccgtaggctgctgtagactgtgtgctcttcatgacctgacggctatgtgatg
	AK139402	NISP	AK139402_R	20	56	CATCAACATAGCCGTCAAGG	55	59		
6	AK140219	NISP	AK140219_F	23	83	CCTCTTAGGGTTGGTAAATTCG	43	60	69nt	cctctagggttgtaaattctgtccagccaccggtcatacagtaacccaaactaattctctg
	AK140219	NISP	AK140219_R	26	83	CGAAGATAATTAGTTTGGGTTAATCG	43	60		
7	AK154943	NISP	AK154943_F	19	69	GGCCCTAGCAATCGTTCAC	58	60	60nt	ggccctagcaatgttccctctctctccacgaacaggatcaaacacccaacacagg
	AK154943	NISP	AK154943_R	20	69	CCTGTTGGTTGTTTGATCC	58	60		
8	Als2cr2	ISP	als2cr2_F	20	17	TCTCCATTTATGGCCTACGG	50	59	69nt	tctccattatggcctacggtcagcaagtcatgctcctaaggacctcttctgatggaatgagtgag
	Als2cr2	ISP	als2cr2_R	23	17	CTCACTCAITTCATCAGGAAAGT	50	59		
9	App	ISP	app_F	20	34	AGCACCAGAGAGAAATGTCC	55	59	69nt	agcaccgagagagaatgtcccaggctagagagaatgggaagaggcagagcgtaagccaagaacttc
	App	ISP	app_R	19	34	GCAAGTCTTGGCTTGACG	55	59		
10	Atp7a	ISP	atp7a_F	23	17	GAGCAGCTGTAACCAAATATTGC	43	60	64nt	gagcagctgtaacaaaattgcaaaaaggagctggacactgaaacccctgggtactgtacaga
	Atp7a	ISP	atp7a_R	22	17	TCTGTACAGGTACCCAGGGTTT	43	59		
11	AU258168	NISP	AU258168_F	19	62	CTTGGGAGGAGGACAGG	63	59	72nt	ctggaggaggagacaggggacacctgctgacctggcctagcaggtgatgtaagcaggtgacacagct gc
	AU258168	NISP	AU258168_R	20	62	GCAGCTGTGTACCTGCTTA	63	60		
12	BC025816	ISP	3433cdnap1_F	19	83	CGCCGTAACAGTGGATCA	53	60	122nt	cgccgtaaacagtgatcaagggtgctcctgaaccagcgcctgtggtattctacctgactcattgaaga catgctggtgctgctggtggccggaacgagaatggagcgctgcttc
	BC025816	ISP	3434cdnap1_R	20	83	GAAGACAGCGTCCATCTC	55	60		
13	Bcl11a	ISP	bcl11a_F	18	3	CCCCGCAGGGTATTTGTA	56	59	65nt	ccccgcaggtattgtaaagatgagcccagcagctacacatgtaacaactgcaaacagcattc
	Bcl11a	ISP	bcl11a_R	21	3	GAATGGCTGTTTGCAAGTTGT	56	60		
14	Bicap	ISP	3435bicap_F	19	74	AGCTAAGGTGGAGGCAAGC	58	59	116nt	agctaaggtggaggcaagcagcggcgagcggcagcagtgccagtgccagtggtggctcgcag gatccctgctgctggtgatcccggtgacagccagagagacagc
	Bicap	ISP	3436bicap_R	19	74	GCTGTGCTCTCTGGCTGTC	63	59		
15	Bicap	NISP	3517bicap_F	20	32	GGACTCCAAGGTGGTTCAGA	55	60	62nt	ggactccaaggtggttcagacaagaccaggggagcagctgccaatcatctcccaccaggag
	Bicap	NISP	3518bicap_R	19	32	CTCCTGGTGGGAGGATGAT	58	59		
16	BQ176089	NISP	BQ176089_F	23	99	TTCTTTTAAATGCAGGGTCTGA	35	60	62nt	ttcttttaaatgcagggctgatttctgtgctcctatgtgatggtgtgattgagaaggt
	BQ176089	NISP	BQ176089_R	24	99	ACCTTCTCAATCACACCATATCAC	35	60		
17	BQ177886	NISP	BQ177886_F	24	45	CACCTCAAGTTGCGTTAGACATTT	38	59	71nt	cacttcaagttgcttagacatttctaccagccccaggcctggccggttaactgactttacatggga
	BQ177886	NISP	BQ177886_R	23	45	TCCCATGTAAGTCAAGTACCG	38	60		
18	Btg1	ISP	btg1_F	18	17	CAAGTTCCTCCGCACCAA	56	60	107nt	caagttctccgcaccaaggggtcacgagcagcagcagctgagacttccagcagagcctgaggag ctgctggcagaacattacaacatcactggttccag
	Btg1	ISP	btg1_R	21	17	CTGGGAACCAAGTGTGTTTGT	56	59		
19	Calm1	ISP	calm1_F	20	89	GCTGCAGGATAGATCAACG	50	59	65nt	gctgcaggatgatcaacgaagtgatgctgagcaatggcaccattgactcccagagttct
	Calm1	ISP	calm1_R	22	89	AGAACTCTGGGAAGTCAATGGT	50	59		
20	Camk2a	ISP	camk2a_F	20	75	CAGCCACTGTATCCAGCAGA	55	60	97nt	cagccactgtatccagcagatctggaggctgtgctcactgtcaccagatgggggtggtcatcgtgacctga agcctgagaatctgtgtggcc
	Camk2a	ISP	camk2a_R	20	75	GGCCAGCAACAGATTCTCAG	55	60		
21	Camk2n1	NISP	camk2n1_t2_F	20	27	TGTGTGGGAACACTGGAGA	50	60	112nt	tgtgtgggaacactggagcttcttctgttattataggggtctcttaaggctcgccagctgctgtttgcatggt attgcacaaaaaatgcctctgctgaggaat
	Camk2n1	NISP	camk2n1_t2_R	21	27	ATTCTCACGCAAGGAGCATT	48	63		
22	Cand2	ISP	3519cand2_F	21	99	CTGGCAGAACTCAATATGC	48	59	60nt	ctggcagaaacctaatatgctgagcagcaggtgcccctagtataaaggccctgcagc
	Cand2	ISP	3520cand2_R	19	99	GCTGCAGGGCCTTTATCAC	58	60		
23	CD802535	NISP	CD802535_F	25	98	GCATGAGTTATAGAGTCTCCCTGA	44	60	75nt	gcatgagttatagagctccctgagactgctgtgcttggacagctgtttacaacacagaacaggcaag g
	CD802535	NISP	CD802535_R	22	98	CCTTGCCTGTCTGTGTTGTAA	44	60		
24	Cdk4	ISP	cdk4_F	20	13	TGCCAGAGATGGAGGAGTCT	55	59	109nt	tgccagagatggaggagctggagcagctgctactgaaatgctgaccttaacccacataagcgaatctc tgccctcagagccctgacagcactcctgacaa
	Cdk4	ISP	cdk4_R	20	13	TTGTGCAGGTAGGAGTGCTG	55	60		



25	Cdkn1c	ISP	cdkn1c_F	20	17	CAGGACGAGAATCAAGAGCA	50	59	118nt	caggacgagaatcaagagcagcgccaggagctgaaggaccgctctctcgggattccaggacgt cctgcacccgggactgtcggccaatgcgaacgactctctcgccaagc
	Cdkn1c	ISP	cdk1nc_R	18	17	GCTTGGCGAAGAAGTCGT	50	59		
26	Chgb	ISP	chgb_F	19	79	ACGACTCGGAGGAGCAGAT	58	59	112nt	acgactcggaggagcagatgggcccaccaggaggcaaacgatgaaaagccagggtgaccagag agttctgcgcggaagagaaaaaggaaactggagaactggctgc
	Chgb	ISP	chgb_R	20	79	GCAGCCAAGTTCTCCAGITC	58	59		
27	Chn1	ISP	3490chn1_R	21	9	TGGAGTTGGCATATGGTATGG	48	60	88nt	gccattggttctgatctgtcacacacacacataagcagtgccctggctgttacatcaccatccccatacca tatgccaactcca
	Chn1	ISP	3489chn1_F	20	9	GCCATTGGTTTTCTGATGCTT	45	60		
28	Clcn2	ISP	clcn2_F	20	103	AAAACCATCAACCGCTTCCT	45	60	71nt	aaaaccatcaaccgctctcatgaggaaacggctgtctctccggcactggtgactctgctcatctccac
	Clcn2	ISP	clcn2_R	21	103	GTGGAGATGAGCAGAGTCACC	45	59		
29	Coup-tf1	ISP	3379_couptf1_F	20	89	CAAAGCCATCGTCTATTCA	45	59	71nt	caaagccatcgtgtattcacgtcagatgctgtggcctgtcgatgctgccacatcgaaagcctgcagg
	Coup-tf1	ISP	3380_couptf1_R	19	89	CCTGCAGGCTTTCGATGT	56	59		
30	Cox1	ISP	3475cox1_F	21	46	TCGAATGTGTATATGGTGGGA	43	59	94nt	tcgaatgtgatgatgtgggaggccagccatgaagtcattcaaatgtgtgaggtatatactgatactactct cgttttgaagcaagg
	Cox1	ISP	3476cox1_R	22	46	CCTTTGCTTCAAACGAGAAGT	41	59		
31	Cryab	ISP	cryab_F	18	80	ACGGCAAGCAGGAAGAAC	56	59	69nt	acggcaagcacgaagacgcccaggacgaacatggctcatctccagggttccacaggaagtaccgga
	Cryab	ISP	cryab_R	20	80	TCCGGTACTTCTGTGGAAC	56	59		
32	Csrp2	ISP	csr2_F	18	106	GACC CGGTGAGAGACTG	67	60	61nt	gaccggtgagagactgggcatcaagccagagagtgctcaacctcacaggcctacgacaa
	Csrp2	ISP	csr2_R	20	106	TTGTCGTAGGCCTGTGAGGT	67	60		
33	Ctsd	ISP	ctsd_F	20	64	TGAGCCAGGACACTGTATCG	55	59	125nt	tgaccaggacactgtatcggttccatgtaagtctgaccagtaaaaggcaagaggtatcaaggtggagaaac agatctttggagaagccaccaagcagcctggaatcgtattgttgacccaag
	Ctsd	ISP	ctsd_R	20	64	CTTGGCTGCAACAAATACGA	55	59		
34	Cybb	ISP	3441cybb_F	20	20	TGCCAACTTCTCAGCTACA	50	59	73nt	tgccaactctcagctacaatatctactctggtgggtaaatcaggccaatcacttctgtgtgac
	Cybb	ISP	3442cybb_R	20	20	GTGCACAGCAAAGTGATTGG	50	60		
35	Cybb	ISP	3515cybb_F	19	108	CTGATCCTGTGCCAGTGT	58	59	83nt	ctgatctgtccagctgtgtcgaatctgctctcttctcagggttccagtgctgtgtcgcacaaggtcg aagaca
	Cybb	ISP	3516cybb_R	21	108	TGTCTCGAATCCTTGTGCGAG	48	60		
36	D1Erd161e	ISP	3443dier_F	20	71	CTCAGTGACCGGGAGAAGAG	60	59	69nt	ctcagtgaccgggagaagagagctctggctgcagagcgccgactgctgccagttgggagcccctagc
	D1Erd161e	ISP	3444dier_R	18	71	GCTAGGGCTCCCAACTG	67	60		
37	D1Erd161e	ISP	3507dier_F	23	81	GGAGAAGAATCTTGATGCCTATG	43	59	74nt	ggagaagaatctgatgctgatgattacaacaaggctgggtgccaggccattgactcaagaaatggaggc cc
	D1Erd161e	ISP	3508dier_R	20	81	GGCCTCCATTTCTTGAGTC	55	60		
38	Dcx	ISP	dcx_F	20	9	ACACCCTTGATGGAAGCAG	50	60	77nt	acaccctgatgaaagcaggtcacctgtctcatgattcttggatgatgatgttcttctgtgtgtct
	Dcx	ISP	dcx_R	20	9	AGGACCAAGCAATGAACA	50	59		
39	Dr1	ISP	dr1_F	23	102	CAACAGGAATTATTGCAAAAAGC	35	60	138nt	caacaggaattattgtcaaaagctagacagcaacaagcagaattggcccaacaggaatggctcaaatgca gcaagcagctcaacaagcccagctggctgcagcctcagccagcgctccactcaagcaggtctca
	Dr1	ISP	dr1_R	21	102	TGAAGATCCTGCTTGAGTGGA	35	60		
40	Egr1	ISP	egr1_F	20	22	CCTATGAGCACCTGACCACA	55	59	90nt	cctatgagcactgaccacagagctctttctgacatcgtctgtaataatgagaagcggatggtggagcaggt tatccagccaacga
	Egr1	ISP	egr1_R	20	22	TCGTTTGGCTGGGATAACTC	55	60		
41	Eif2s3x	ISP	eif2s3x_F	18	76	GAGCCCGTCTCATTGTC	61	59	76nt	gagccccgtctattgtatcaggtcattgtatgtaacaacacctggctgtaagtgatgacctaaagggaggt g
	Eif2s3x	ISP	eif2s3x_R	20	76	CACCTCCCTTAAGTCTATCG	61	59		
42	Ezh2	ISP	ezh2_F	21	38	GCTCTTCTGTCGCAATGTTT	48	59	66nt	gctctctgacagatgtttaagatgactgctctctacatccctccatgcaacaccaaacac
	Ezh2	ISP	ezh2_R	18	38	GTGTTGGGTGTTGCATGG	48	59		
43	Foxg1	ISP	foxg1_F	18	26	GAAGGCCTCCACAGAACG	61	59	114nt	gaaggcctccacagaacgcacccagcctcagccgccccgctcgccctcagccagcttcacagcc gagctgcgcccggggccgaggaagcttttctacatgcctg
	Foxg1	ISP	foxg1_R	21	26	CAAGGCATGTAGCAAAGAGC	61	60		
44	Gria3	ISP	gria3_F	20	31	AGCCGTGTGATACGATGAAA	45	59	99nt	agccgtgtgatacagatgaaagttggtggaatctgattccaaaggtatggtgtggcaaccctaaaggctc agcattaggaacgctgtaaacctg
	Gria3	ISP	gria3_R	20	31	CAAGGTTTACAGGCGTTTCT	45	59		
45	Gstm1	ISP	gstm1_F	20	106	GCAGCTCATCATGCTCTGTT	50	59	77nt	gcagctcatgctctgttacaacacctgactttgagaagcagaagccagaggtcttgaagacctccctgaga aaa
	Gstm1	ISP	gstm1_R	21	106	TTTTCTCAGGGATGGTCTTCA	50	59		
46	H2afy	ISP	h2afy_F	24	47	TGACATTGACCTTAAAGATGACCT	38	59	77nt	tgacattgacctaaagatgacctaggaacaacactggagaagaagggcggcaagggtttgtagaagctg ttctgg
	H2afy	ISP	h2afy_R	23	47	CCAGAACAGCTTCTACAAACTCC	38	59		
47	Hmbs	ISP	3843_hmbs_F	20	42	AAAGTCCCCAACCTGGAAT	45	59	98nt	aaagttcccaacctggaattcaagagatattcggggaaacctcaacaccgctcgggaagctggatgagct gcaggaattcagtcattgtctctg
	Hmbs	ISP	3844_hmbs_R	20	42	CCAGGACAAATGGCACTGAAT	50	60		
48	Hmgb3	ISP	hmgb3_F	20	84	ACCACTCTGGGTGTCTCCAC	60	60	108nt	accactctggtctcactcccgcctctgcccctctctctctgctctaggtggccaagaaggaa gacgcaattcagtcaggatggctaagggtgacc
	Hmgb3	ISP	hmgb3_R	20	84	GGTCACCTTTAGCCATCCTG	60	59		
49	Hprt1	ISP	3363_hprt1_F	19	95	TCCTCCTCAGACCGCTTTT	53	59	90nt	tctctcagaccgcttttgcgcgagccgaccggtcccctcatgccacccagctccagcgtctgatta gcatgatgaaccagg
	Hprt1	ISP	3364_hprt1_R	21	95	CCTGGTTCATCATCGCTAATC	48	59		



75	Sncb	ISP	sncb_F	19	84	TGGCTGCAGCTGAGAAAAC	53	60	94nt	tggctgcagctgagaaaaccaagcaggggggtaccgaggcagcagagaagaccaaggaaggcgtctct tatgtcgggaagcaagaccagtgaggat
	Sncb	ISP	sncb_R	20	84	ACTCCACTGGTCTTGCTTCC	53	59		
76	Sox11	NISP	sox11_t16_F	23	6	GTTGAATTCATACACTCCAATGT	35	56	97nt	gttgaaitcatacactccaatgtctcttttgcaggagttttcacagaggaatacattgttcaaaagaccaataaa aatcgtgtgatcaatctcc
	Sox11	NISP	sox11_t16_R	20	6	GGAGATTGATCACACGATTT	40	55		
77	Sox4	NISP	sox4_t4_F	18	99	GTTGGGGATGCAGAAGGA	56	60	73nt	gttggggatgcagaaggaccggagcacagagggcggtgggggtcccgggctccgctggggtctgtgca aa
	Sox4	NISP	sox4_t4_R	22	99	TTTGACACAGACCCAGGCGGAG	64	73		
78	Tmsb4x	ISP	3463tmsb4x_F	19	91	CACACATAAAGCGGCGTTC	53	60	112nt	cacacataaagcggcggttcgcccgcgccctccgacaatccgagcggctctgagcagatcagactctct cgttcgcgcagctcgtcggctcctccagcaacctatgc
	Tmsb4x	ISP	3464tmsb4x_R	20	91	GACATGGTTGCTGGAAGGAG	55	60		
79	Tspan7	ISP	tspan7_F	20	89	TTGGATGCTTTGCTACATGC	45	59	66nt	ttggatgctttgctacatgccgtggtatccatggatgctgaaactgtatgccatgttctgtccc
	Tspan7	ISP	tspan7_R	20	89	GGGACAGGAACATGGCATAAC	45	60		
80	Ube2e3	ISP	ube2e3_F	20	109	GGGAGTCATCTGCCTGGATA	55	60	126nt	gggagtcatctgcctggatattcgaagacaactggagtcctgcttgaactattcaagggttgcctctattgtt ccctttgacagattgcaacctgcgatcctctggtcgggaagcat
	Ube2e3	ISP	ube2e3_R	19	109	ATGCTTCCGACCAGAGGAT	55	59		
81	Usp16	ISP	usp16_F	19	94	TTTGGTGGCGAGCTGACTA	53	60	77nt	tttggcggagctgactagtagcatgtgtgatgaatgaggactgtctccttagtgcataatcgttcttga
	Usp16	ISP	usp16_R	20	94	TCAAGGAACGATTCATGCAC	53	59		
82	Wsb1	ISP	wsb1_F	18	11	GGCGCCAGTAAAGCAGTT	56	59	94nt	ggcgcagtaaagcagtttcttggataggataaatacccatgattaggaagctggaaggtcatcacca tgatgttagctgtgact
	Wsb1	ISP	wsb1_R	23	11	AGTCACAAGCTACAACATCATGG	56	59		
83	Ywhae	ISP	ywhae_F	20	102	GGCGAGTCCAAGGTTTTCTA	50	59	90nt	ggcagtcacaaggtttctattataaaatgaaaggggactaccacaggtatctggctgagttgccacagaaa tgacaggaaggaggca
	Ywhae	ISP	ywhae_R	20	102	TGCCTCCTTCTGTCATTTTC	50	60		
84	Zfp57	ISP	zfp57_F	21	64	TGGCTAGAAGCAGTCTGGAAT	48	59	96nt	tggctagaagcagctctggaatagaagtcaaacgcctaggaccagcctggcattaccaacaatggcagcta ggaacagcttcccagccatccag
	Zfp57	ISP	zfp57_R	19	64	CTGGATGGCTGGGAAGACT	48	60		
85	Zswim4	ISP	zswim4_F	18	3	TGCAAGACAGCCACTCCA	56	60	112nt	tgcagaataagctggtcatctctgagggaaggctgaggacaagaatgtgaaagggcgagcccttacagcc aaatccaaatctcctaaagggtgaaaacattgatgggtga
	Zswim4	ISP	zswim4_R	18	3	TGTCATCCGCATCACCTG	56	60		
86	Zwint	ISP	zwint_F	22	73	TGCAGAATAAGCTGGTCATCTC	45	59	90nt	tgcaagacagccactccagccagcaccggcagacacogtctgctgggcatcgctggagctggcct gcagggtatcggtatgaca
	Zwint	ISP	zwint_R	21	73	TCACCCATCAATGTTTTACC	45	60		