Supplementary Material

Supplementary Figure 1. *ADNP* expression in various brain tissue across various timepoints in Allen Institute BrainSpan RNA-seq data. This dataset includes post-mortem samples of 16 brain regions ranging from fetus age eight post-conception weeks to adult age 40 years (n = 524). The data was normalized to RPKM (reads per kilobase per million) and a log base 2 transformation [log(RPKM + 1)]. ADNP expression was significantly greater in fetal compared to non-fetal brains ($p<0.001$, t-test). There is a 3.16-fold increase in *ADNP* fetal expression and a 68.3% decrease in expression in non-fetal brains. pcw=weeks post-conception, mos=postnatal months, yrs=postnatal years.

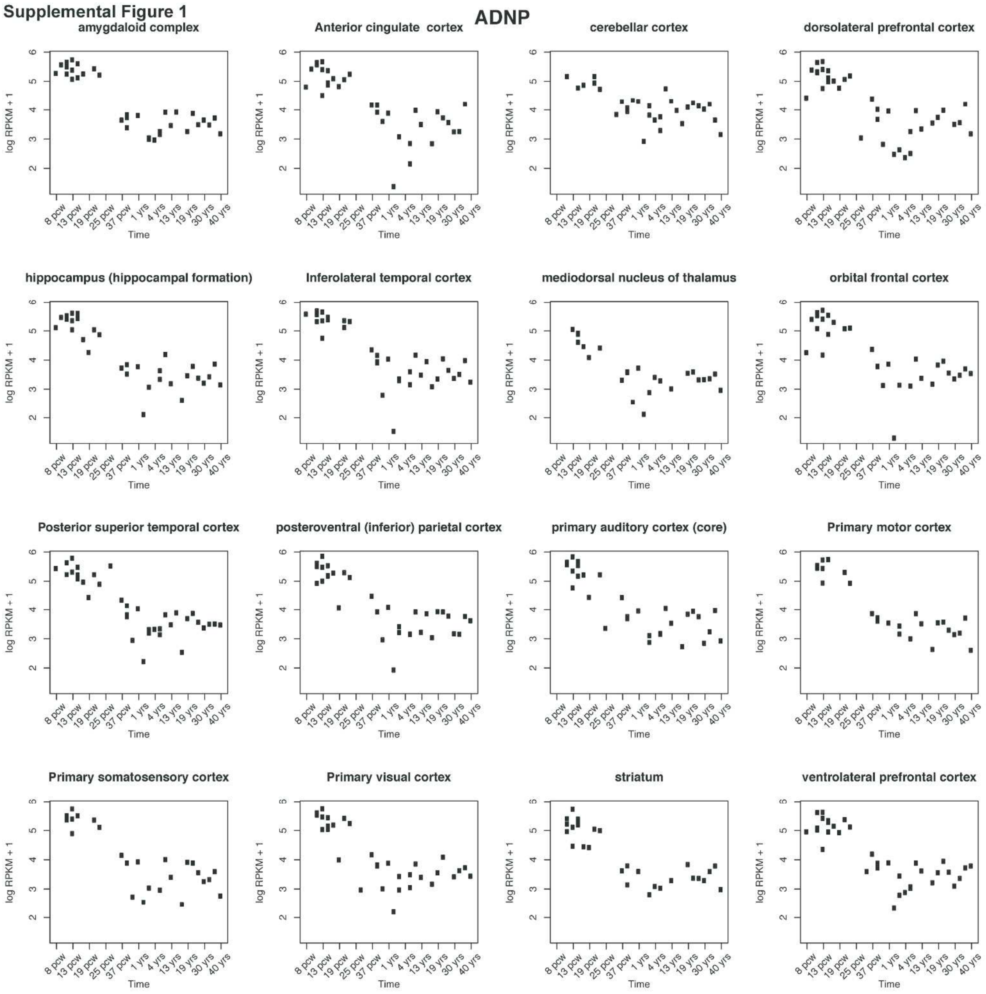
Supplementary Table 1. List of genetic variants (14 genes) identified in whole-exome sequencing (WES). Variants were filtered according to inclusion of those related to patient’s phenotype, removal of benign variants and exclusion of polymorphism/sequencing artifacts. Disease association was determined by reviewing the Online Mendelian Inheritance of Man (OMIM) and PubMed. Variants identified by Poly Phen and/or SIFT as damaging also include their genotype frequency from NHLBI GO Exome Sequencing Project (ESP), when possible.

Supplementary Table 2. List of genes positively correlated with ADNP (≥.9) from BrainSpan’s Developmental Transcriptome.

Supplementary Table 3. List of genes negatively correlated with ADNP (<-.8) from BrainSpan’s Developmental Transcriptome.

Supplementary Table 4. Significant biological processes of positively correlated gene pathway analysis. The 10 most highly enriched clusters are reported.

Supplementary Table 5. Significant biological processes of negatively correlated gene pathway analysis. The 10 most highly enriched clusters are reported.



Supplementary Figure 1. ADNP expression in various brain tissue across various timepoints in Allen Institute BrainSpan RNA-seq data. This dataset includes post-mortem samples of 16 brain regions ranging from fetus age eight post-conception weeks to adult age 40 years (n = 524). The data was normalized to RPKM (reads per kilobase per million) and a log base 2 transformation [log(RPKM + 1)]. ADNP expression was significantly greater in fetal compared to non-fetal brains ($p<0.001$, t-test). There is a 3.16-fold increase in ADNP fetal expression and a 68.3% decrease in expression in non-fetal brains. pcw=weeks post-conception, mos=postnatal months, yrs=postnatal years.

287x287mm (300 x 300 DPI)

Table S1

Gene	Locus	RefSeq	Variant	Proband	PolyPhen	SIFT	ESP Genotype #*	Disease Association	Disease Notes (OMIM)
ADNP	20q13.13	NM_015339	c.2157C>G p.Y719X	+/-	NR	NR	N/A	Autism	Multiple frameshift and nonsense mutations identified in individuals with autism (Helsmoortel et al 2014; O'Roak et al 2012a; O'Roak et al 2012b)
MYO9B	19p13.1	NM_004145	c.5567G>A p.R1856H	+/-	probably damaging	damaging	AA=0/AG=1/GG=6490	Schizophrenia, Celiac disease, Inflammatory bowel disease, Crohn's disease, Ulcerative colitis, Acute pancreatitis, Barrett's esophagus/ esophageal adenocarcinoma	**Schizophrenia:** rs1457092*A and rs2305767*A (Jungerius et al 2008); **Celiac disease**: rs2305764*A (Monsuur et al 2005), rs7259292 (Wolters et al 2007), rs1457092C/T (Loeff et al 2012); **Inflammatory bowel disease**: rs2305767 (Cooney et al 2009), rs962917 (van Bodegraven et al 2006, Latiano et al 2008), rs1545620 (van Bodegraven et al 2006, Latiano et al 2008), rs2305764 (van Bodegraven et al 2006, Latiano et al 2008), rs2279002 (van Bodegraven et al 2006); **Crohn's disease**: rs2305767 (Cooney et al 2009), rs1457092 (Wolters et al 2011), rs2305764 (Wolters et al 2011), rs962917 (Wolters et al 2011); **Ulcerative colitis**: rs1545620T/T (Shi et al 2011), rs2305767 (Nunez et al 2007), rs1457092 (Nunez et al 2007), rs2305764 (Nunez et al 2007); **Acute pancreatitis**: rs7259292 and rs1545620 (Nijmeijer et al 2013); **Barrett's esophagus/esophageal adenocarcinoma**: rs2305764G/G (Menke et al 2012)
MAML3	4q28	NM_018717	c.1526_1527insGCA p.Q509delinsRK	+/-	NR	NR	N/A	Congenital heart malformations, Biphenotypic sinonasal sarcoma	One SNP (rs1531070) was significantly associated with congenital heart malformations in a Han Chinese GWAS study (Hu et al 2013); Chromosomal translocation resulting in a PAX3-MAML3 fusion protein is associated with biphenotypic sinonasal sarcoma (Wang et al 2014). However, the direct role MAML3 plays in oncogenesis is unknown.
TEKT3	17p12	NM_031898	c.1272_1280del p.V424_E426del	+/-	NR	NR	N/A	No known disease association	N/A
CRIPAK	4p16.3	NM_175918	c.818_819insAT p.T273NfsX157	+/-	NR	NR	N/A	No known disease association	N/A
			c.826T>C p.C276R	+/-	benign	tolerated	N/A		N/A
KRTAP4-3	17q12-q21	NM_033187	c.302G>A p.R101H	+/-	benign	tolerated	N/A	No known disease association	N/A
			c.195_196ins15 p.C65X	+/-	NR	NR	N/A		N/A
KRTAP5-5	11p15.5	NM_001001480	c.87_158del p.G30_C52del	+/-	NR	NR	N/A	No known disease association	N/A
			c.130_138del p.G44_G46del	+/-	NR	NR	N/A		N/A

MUC5B	11p15.5	NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A	Idiopathic pulmonary fibrosis	An intronic minor allele (T) of SNP rs35705950 increases the susceptibility to pulmonary fibrosis (Seibold et al 2011; Zhang et al 2011; Hunninghake et al 2013)
			c.11357_11434del p.T3787_Q3811del	+/-	NR	NR	N/A		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.11309T>C p.F3770S	+/-	benign	tolerated	N/A		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.10246_10332del p.P3416_T3444del	+/-	NR	NR	N/A		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.9929C>G p.T3310S	+/-	benign	tolerated	N/A		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.9626G>A p.R3209K	+/-	benign	tolerated	N/A		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.8782C>G p.R2928G	+/-	benign	tolerated	N/A		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.8063C>T p.P2688L	+/-	benign	tolerated	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.13441_13442insTGC p.V4481_S4482insC	+/-	NR	NR	N/A		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.11855C>A p.T3952N	+/-	possibly damaging	tolerated	Not reported in ESP		
		NM_002458	c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
			c.13441_13442insTGC p.V4481_S4482insC	+/-	NR	NR	N/A		
		NM_002458	c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
			c.13441_13442insTGC p.V4481_S4482insC	+/-	NR	NR	N/A		
		NM_002458	c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
			c.11855C>A p.T3952N	+/-	possibly damaging	tolerated	Not reported in ESP		
		NM_002458	c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
			c.11357_11434del p.T3787_Q3811del	+/-	NR	NR	N/A		
		NM_002458	c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
			c.11309T>C p.F3770S	+/-	benign	tolerated	N/A		
		NM_002458	c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
			c.10246_10332del p.P3416_T3444del	+/-	NR	NR	N/A		
		NM_002458	c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
			c.9929C>G p.T3310S	+/-	benign	tolerated	N/A		
		NM_002458	c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
			c.9626G>A p.R3209K	+/-	benign	tolerated	N/A		
		NM_002458	c.8782C>G p.R2928G	+/-	benign	tolerated	N/A		
			c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
		NM_002458	c.8063C>T p.P2688L	+/-	benign	tolerated	N/A		
			c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.11855C>A p.T3952N	+/-	possibly damaging	tolerated	Not reported in ESP		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.11357_11434del p.T3787_Q3811del	+/-	NR	NR	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.11309T>C p.F3770S	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.10246_10332del p.P3416_T3444del	+/-	NR	NR	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.9929C>G p.T3310S	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.9626G>A p.R3209K	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.8782C>G p.R2928G	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.8063C>T p.P2688L	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.11357_11434del p.T3787_Q3811del	+/-	NR	NR	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.11855C>A p.T3952N	+/-	possibly damaging	tolerated	Not reported in ESP		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.11309T>C p.F3770S	+/-	benign	tolerated	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.10246_10332del p.P3416_T3444del	+/-	NR	NR	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.9929C>G p.T3310S	+/-	benign	tolerated	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.9626G>A p.R3209K	+/-	benign	tolerated	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.9353C>T p.A3118V	+/-	benign	tolerated	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.8782C>G p.R2928G	+/-	benign	tolerated	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.8063C>T p.P2688L	+/-	benign	tolerated	N/A		
		NM_002458	c.6875G>A p.R2292H	+/-	benign	tolerated	N/A		
			c.7744A>G p.T2582A	+/-	benign	tolerated	N/A		
		NM_002458	c.6845_6850del p.T2283_T2283del	+/-	NR	NR	N/A		
			c.13441_13442insTGC p.V4481_S4482insC	+/-	NR	NR	N/A		

PRAMEF1	1p36.21	NM_023013	c.1069G>A p.E357K	+/-	benign	tolerated	N/A	No known disease association	N/A
			c.1102G>A p.A368T	+/-	benign	tolerated	N/A		
PRAMEF11	1p36.21	NM_001146344	c.929C>T p.A310V	+/-	possibly damaging	damaging	Not reported in ESP	No known disease association	N/A
			c.458G>A p.R153H	+/-	benign	tolerated	N/A		
		NM_001146344	c.929C>T p.A310V	+/-	possibly damaging	damaging	Not reported in ESP		
			c.604A>G p.M202V	+/-	benign	tolerated	N/A		
		NM_001146344	c.929C>T p.A310V	+/-	possibly damaging	damaging	Not reported in ESP		
			c.640_642del p.K214del	+/-	NR	NR	N/A		
		NM_001146344	c.929C>T p.A310V	+/-	possibly damaging	damaging	Not reported in ESP		
			c.736G>A p.D246N	+/-	probably damaging	tolerated	Not reported in ESP		
PRAMEF2	1p36.21	NM_023014	c.878A>T p.N293I	+/-	benign	tolerated	N/A	No known disease association	N/A
			c.1158C>A p.S386R	+/-	benign	tolerated	N/A		
		NM_023014	c.879C>G p.N293K	+/-	possibly damaging	damaging	Not reported in ESP		
			c.1158C>A p.S386R	+/-	benign	tolerated	N/A		
		NM_023014	c.1102G>A p.A368T	+/-	benign	tolerated	N/A		
			c.1158C>A p.S386R	+/-	benign	tolerated	N/A		
RBM12	20q11.21	NM_006047	c.2504_2505ins6 p.P835_G836insAP	+/-	NR	NR	N/A	No known disease association	N/A
			c.1187G>C p.G396A	+/-	benign	tolerated	N/A		
VSIG10	12q24.23	NM_019086	c.1419_1421del p.E473del	+/-	NR	NR	N/A	No known disease association	N/A
			c.1046_1063del p.T349_I354del	+/-	NR	NR	N/A		
KRT76	12q13.13	NM_015848	c.1024A>T p.M342L	+/+	possibly damaging	damaging	AA=0/AT=6/TT=6497	No known disease association	N/A

NR = Not reported, N/A = Not applicable

*If variant denoted as damaging in Poly Phen and/or SIFT, then reported genotype frequency from NHLBI GO Exome Sequencing Project (ESP)

Table S2

Ensembl ID	Gene symbol	Entrez ID	Correlation
ENSG00000117139	KDM5B	10765	0.9561
ENSG00000181827	RFX7	64864	0.9536
ENSG00000163939	PBRM1	55193	0.9527
ENSG00000143702	CEP170	9859	0.9525
ENSG00000178163	ZNF518B	85460	0.9525
ENSG00000106346	USP42	84132	0.9517
ENSG00000138439	FAM117B	150864	0.9513
ENSG00000159579	RSPRY1	89970	0.9472
ENSG00000155592	ZKSCAN2	342357	0.9463
ENSG00000100426	ZBED4	9889	0.9444
ENSG00000134313	KIDINS220	57498	0.9443
ENSG00000197024	ZNF398	57541	0.9434
ENSG00000196632	WNK3	65267	0.9433
ENSG00000077097	TOP2B	7155	0.9432
ENSG00000198824	CHAMP1	283489	0.9432
ENSG00000160208	RRP1B	23076	0.9430
ENSG00000110066	SUV420H1	51111	0.9429
ENSG00000011007	TCEB3	6924	0.9418
ENSG00000089902	RCOR1	23186	0.9415
ENSG00000175087	PDIK1L	149420	0.9412
ENSG00000243943	ZNF512	84450	0.9411
ENSG00000089094	KDM2B	84678	0.9409
ENSG00000187607	ZNF286A	57335	0.9404
ENSG00000162613	FUBP1	8880	0.9398
ENSG00000183309	ZNF623	9831	0.9397
ENSG00000103160	HSDL1	83693	0.9388
ENSG00000169118	CSNK1G1	53944	0.9379
ENSG00000102974	CTCF	10664	0.9377
ENSG00000118263	KLF7	8609	0.9374
ENSG00000066135	KDM4A	9682	0.9372
ENSG00000120616	EPC1	80314	0.9370
ENSG00000124571	XPO5	57510	0.9367
ENSG00000163026	C2orf44	80304	0.9365
ENSG00000152443	ZNF776	284309	0.9358
ENSG00000144233	AMMECR1L	83607	0.9346
ENSG00000112182	BACH2	60468	0.9341
ENSG00000170558	CDH2	1000	0.9331
ENSG00000103194	USP10	9100	0.9331
ENSG00000172939	OXSR1	9943	0.9316
ENSG00000188994	ZNF292	23036	0.9314
ENSG00000125686	MED1	5469	0.9313
ENSG00000141424	SLC39A6	25800	0.9312
ENSG00000181007	ZFP82	284406	0.9306
ENSG00000171681	ATF7IP	55729	0.9304
ENSG00000163214	DHX57	90957	0.9298
ENSG00000198040	ZNF84	7637	0.9290
ENSG00000131023	LATS1	9113	0.9289

ENSG00000163104	SMARCAD1	56916	0.9286
ENSG00000122779	TRIM24	8805	0.9284
ENSG00000158636	C11orf30	56946	0.9282
ENSG00000100281	HMGXB4	10042	0.9282
ENSG00000004487	KDM1A	23028	0.9280
ENSG00000121406	ZNF549	256051	0.9279
ENSG00000213079	SCAF8	22828	0.9277
ENSG00000151458	ANKRD50	57182	0.9275
ENSG00000105866	SP4	6671	0.9272
ENSG00000121774	KHDRBS1	10657	0.9271
ENSG00000171456	ASXL1	171023	0.9268
ENSG00000164091	WDR82	80335	0.9266
ENSG00000143079	CTTNBP2NL	55917	0.9263
ENSG00000113300	CNOT6	57472	0.9263
ENSG00000011258	MBTD1	54799	0.9260
ENSG00000125944	HNRNPR	10236	0.9252
ENSG00000127483	HP1BP3	50809	0.9251
ENSG00000204611	ZNF616	90317	0.9248
ENSG00000244462	RBM12	10137	0.9245
ENSG00000143061	IGSF3	3321	0.9242
ENSG00000088930	XRN2	22803	0.9242
ENSG00000085721	RRN3	54700	0.9242
ENSG00000185219	ZNF445	353274	0.9240
ENSG00000147180	ZNF711	7552	0.9237
ENSG00000198553	KCNRG	283518	0.9236
ENSG00000242852	ZNF709	163051	0.9235
ENSG00000177932	ZNF354C	30832	0.9235
ENSG00000079387	SENP1	29843	0.9232
ENSG00000179837	RBM15B	29890	0.9231
ENSG00000204178	TMEM57	55219	0.9223
ENSG00000025293	PHF20	51230	0.9216
ENSG00000184675	FAM123B	139285	0.9216
ENSG00000109685	WHSC1	7468	0.9216
ENSG00000188636	LDOC1L	84247	0.9215
ENSG00000198492	YTHDF2	51441	0.9215
ENSG00000213799	ZNF845	91664	0.9214
ENSG00000198182	ZNF607	84775	0.9213
ENSG00000171843	MLLT3	4300	0.9211
ENSG00000131845	ZNF304	57343	0.9209
ENSG00000116128	BCL9	607	0.9203
ENSG00000186448	ZNF197	10168	0.9201
ENSG00000117000	RLF	6018	0.9200
ENSG00000130396	MLLT4	4301	0.9199
ENSG00000204519	ZNF551	90233	0.9198
ENSG00000177733	HNRNPA0	10949	0.9196
ENSG00000074054	CLASP1	23332	0.9192
ENSG00000162415	ZSWIM5	57643	0.9188
ENSG00000107341	UBE2R2	54926	0.9188
ENSG00000135999	EPC2	26122	0.9187

ENSG00000130803	ZNF317	57693	0.9187
ENSG00000136485	DCAF7	10238	0.9185
ENSG00000037749	MFAP3	4238	0.9181
ENSG00000145041	VPRBP	9730	0.9180
ENSG00000124459	ZNF45	7596	0.9179
ENSG00000168795	ZBTB5	9925	0.9179
ENSG00000125630	POLR1B	84172	0.9177
ENSG00000135387	CAPRIN1	4076	0.9176
ENSG00000186300	ZNF555	148254	0.9161
ENSG00000110218	PANX1	24145	0.9157
ENSG00000156531	PHF6	84295	0.9156
ENSG00000177125	ZBTB34	403341	0.9156
ENSG00000136381	IREB2	3658	0.9156
ENSG00000204977	TRIM13	10206	0.9151
ENSG00000073711	PPP2R3A	5523	0.9150
ENSG00000137574	TGS1	96764	0.9143
ENSG00000135747	ZNF670	93474	0.9141
ENSG00000101266	CSNK2A1	1457	0.9134
ENSG00000140598	EFTUD1	79631	0.9129
ENSG00000139990	DCAF5	8816	0.9129
ENSG00000196470	SIAH1	6477	0.9129
ENSG00000168246	UBTD2	92181	0.9127
ENSG00000166261	ZNF202	7753	0.9127
ENSG00000205268	PDE7A	5150	0.9126
ENSG00000114302	PRKAR2A	5576	0.9126
ENSG00000213762	ZNF134	7693	0.9126
ENSG00000152217	SETBP1	26040	0.9126
ENSG00000164244	PRRC1	133619	0.9125
ENSG00000197128	ZNF772	400720	0.9124
ENSG00000196150	ZNF250	58500	0.9123
ENSG00000196867	ZFP28	140612	0.9122
ENSG00000101193	C20orf11	54994	0.9121
ENSG00000184402	SS18L1	26039	0.9120
ENSG00000130559	CAMSAP1	157922	0.9119
ENSG00000143324	XPR1	9213	0.9119
ENSG00000092201	SUPT16H	11198	0.9117
ENSG00000147548	WHSC1L1	54904	0.9117
ENSG00000156853	ZNF689	115509	0.9116
ENSG00000110321	EIF4G2	1982	0.9113
ENSG00000174579	MSL2	55167	0.9110
ENSG00000135829	DHX9	1660	0.9109
ENSG00000176624	MEX3C	51320	0.9108
ENSG00000132436	FIGNL1	63979	0.9107
ENSG00000167785	ZNF558	148156	0.9107
ENSG00000176371	ZSCAN2	54993	0.9102
ENSG00000159131	GART	2618	0.9102
ENSG00000189091	SF3B3	23450	0.9101
ENSG00000179409	GEMIN4	50628	0.9100
ENSG00000113569	NUP155	9631	0.9099

ENSG00000162419	GMEB1	10691	0.9098
ENSG00000109171	SLAIN2	57606	0.9092
ENSG00000137942	FNBP1L	54874	0.9090
ENSG00000110987	BCL7A	605	0.9090
ENSG00000136709	WDR33	55339	0.9086
ENSG00000018699	TTC27	55622	0.9084
ENSG00000160062	ZBTB8A	653121	0.9078
ENSG00000143494	VASH2	79805	0.9076
ENSG00000171649	ZIK1	284307	0.9075
ENSG00000115421	PAPOLG	64895	0.9073
ENSG00000124214	STAU1	6780	0.9071
ENSG00000065183	WDR3	10885	0.9071
ENSG00000160199	PKNOX1	5316	0.9069
ENSG00000179151	EDC3	80153	0.9063
ENSG00000124789	NUP153	9972	0.9061
ENSG00000132155	RAF1	5894	0.9059
ENSG00000213551	DNAJC9	23234	0.9058
ENSG00000189079	ARID2	196528	0.9058
ENSG00000066117	SMARCD1	6602	0.9058
ENSG00000030066	NUP160	23279	0.9057
ENSG00000125484	GTF3C4	9329	0.9054
ENSG00000188295	ZNF669	79862	0.9052
ENSG00000196652	ZKSCAN5	23660	0.9051
ENSG00000112685	EXOC2	55770	0.9050
ENSG00000196267	ZNF836	162962	0.9048
ENSG00000056277	ZNF280C	55609	0.9048
ENSG00000147316	MCPH1	79648	0.9044
ENSG00000136866	ZFP37	7539	0.9041
ENSG00000142065	ZFP14	57677	0.9032
ENSG00000114742	WDR48	57599	0.9031
ENSG00000110880	CORO1C	23603	0.9030
ENSG00000079246	XRCC5	7520	0.9030
ENSG00000143379	SETDB1	9869	0.9029
ENSG00000198205	ZXDA	7789	0.9029
ENSG00000136891	TEX10	54881	0.9027
ENSG00000151846	PABPC3	5042	0.9026
ENSG00000158691	ZSCAN12	9753	0.9025
ENSG00000145725	PPIP5K2	23262	0.9019
ENSG00000131473	ACLY	47	0.9019
ENSG00000077279	DCX	1641	0.9016
ENSG00000129351	ILF3	3609	0.9014
ENSG00000166704	ZNF606	80095	0.9012
ENSG00000180370	PAK2	5062	0.9006
ENSG00000142556	ZNF614	80110	0.9004
ENSG00000086848	ALG9	79796	0.9003
ENSG00000081386	ZNF510	22869	0.9002
ENSG00000021574	SPAST	6683	0.9000

Table S3

Ensembl ID	Gene symbol	Entrez ID	Correlation
ENSG00000197971	MBP	4155	-0.9038
ENSG00000107902	LHPP	64077	-0.8995
ENSG00000160781	PAQR6	79957	-0.8984
ENSG00000090581	GNPTG	84572	-0.8977
ENSG00000159176	CSRP1	1465	-0.8928
ENSG00000105643	ARRDC2	27106	-0.8916
ENSG00000250479	CHCHD10	400916	-0.8899
ENSG00000116661	FBXO2	26232	-0.8896
ENSG00000021300	PLEKHB1	58473	-0.8873
ENSG00000189171	S100A13	6284	-0.8864
ENSG00000167641	PPP1R14A	94274	-0.8816
ENSG00000160307	S100B	6285	-0.8803
ENSG00000063180	CA11	770	-0.8801
ENSG00000100003	SEC14L2	23541	-0.8796
ENSG00000101400	SNTA1	6640	-0.8766
ENSG00000120306	C5orf32	84418	-0.8761
ENSG00000248871	TNFSF12-TNFSF13	407977	-0.8741
ENSG00000103740	ACSBG1	23205	-0.8740
ENSG00000173267	SNCG	6623	-0.8722
ENSG00000165795	NDRG2	57447	-0.8713
ENSG00000145198	VWA5B2	90113	-0.8706
ENSG00000102934	PLLP	51090	-0.8676
ENSG00000198892	SHISA4	149345	-0.8657
ENSG00000101439	CST3	1471	-0.8655
ENSG00000176485	PLA2G16	11145	-0.8654
ENSG00000109107	ALDOC	230	-0.8651
ENSG00000087250	MT3	4504	-0.8650
ENSG00000161955	TNFSF13	8741	-0.8639
ENSG00000131097	HIGD1B	51751	-0.8631
ENSG00000166091	CMTM5	116173	-0.8622
ENSG00000130303	BST2	684	-0.8619
ENSG00000244274	DBNDD2	55861	-0.8604
ENSG00000167705	RILP	83547	-0.8592
ENSG00000174939	ASPHD1	253982	-0.8565
ENSG00000163517	HDAC11	79885	-0.8564
ENSG00000239697	TNFSF12	8742	-0.8547
ENSG00000103811	CTSH	1512	-0.8545
ENSG00000160408	ST6GALNAC6	30815	-0.8535
ENSG00000124615	MOCS1	4337	-0.8519
ENSG00000189058	APOD	347	-0.8498
ENSG00000234745	HLA-B	3106	-0.8496
ENSG00000182902	SLC25A18	83733	-0.8484
ENSG00000166925	TSC22D4	81628	-0.8480
ENSG00000148120	C9orf3	84909	-0.8479
ENSG00000129250	KIF1C	10749	-0.8472
ENSG00000198835	GJC2	57165	-0.8468

ENSG00000198624	CCDC69	26112	-0.8462
ENSG00000183401	CCDC159	126075	-0.8460
ENSG00000109846	CRYAB	1410	-0.8452
ENSG00000175482	POLD4	57804	-0.8451
ENSG00000108387	5-Sep	5414	-0.8440
ENSG00000120885	CLU	1191	-0.8435
ENSG00000131730	CKMT2	1160	-0.8433
ENSG00000170634	ACYP2	98	-0.8427
ENSG00000102760	C13orf15	28984	-0.8425
ENSG00000149489	ROM1	6094	-0.8406
ENSG00000091513	TF	7018	-0.8399
ENSG00000244187	TMEM141	85014	-0.8398
ENSG00000244607	CCDC13	152206	-0.8394
ENSG00000135525	MAP7	9053	-0.8391
ENSG00000078804	TP53INP2	58476	-0.8390
ENSG00000161835	GRASP	160622	-0.8372
ENSG00000183628	DGCR6	8214	-0.8371
ENSG00000146122	DAAM2	23500	-0.8371
ENSG00000158526	TSR2	90121	-0.8354
ENSG00000128805	ARHGAP22	58504	-0.8353
ENSG00000100399	CHADL	150356	-0.8352
ENSG00000172216	CEBPB	1051	-0.8331
ENSG00000139192	TAPBPL	55080	-0.8330
ENSG00000180155	LYNX1	66004	-0.8327
ENSG00000204592	HLA-E	3133	-0.8327
ENSG00000211584	SLC48A1	55652	-0.8326
ENSG00000175602	CCDC85B	11007	-0.8325
ENSG00000166710	B2M	567	-0.8322
ENSG00000164403	SHROOM1	134549	-0.8317
ENSG00000160801	PTH1R	5745	-0.8307
ENSG00000198832	RP3-412A9.11	140606	-0.8305
ENSG00000172458	IL17D	53342	-0.8301
ENSG00000100033	PRODH	5625	-0.8300
ENSG00000135926	TMBIM1	64114	-0.8282
ENSG00000245937	CTC-228N24.3	644873	-0.8277
ENSG00000091428	RAPGEF4	11069	-0.8273
ENSG00000114993	RTKN	6242	-0.8265
ENSG00000189283	FHIT	2272	-0.8264
ENSG00000125148	MT2A	4502	-0.8260
ENSG00000164402	9-Sep	23176	-0.8254
ENSG00000105518	TMEM205	374882	-0.8252
ENSG00000078814	MYH7B	57644	-0.8249
ENSG00000130988	RGN	9104	-0.8243
ENSG00000167106	FAM102A	399665	-0.8242
ENSG00000134873	CLDN10	9071	-0.8241
ENSG00000236830	AP000689.8	100506428	-0.8235
ENSG00000240065	PSMB9	5698	-0.8229
ENSG00000112561	TFEB	7942	-0.8228
ENSG00000102032	RENBP	5973	-0.8228

ENSG00000084453	SLCO1A2	6579	-0.8228
ENSG00000198121	LPAR1	1902	-0.8225
ENSG00000123560	PLP1	5354	-0.8222
ENSG00000175197	DDIT3	1649	-0.8221
ENSG00000087076	HSD17B14	51171	-0.8215
ENSG00000160685	ZBTB7B	51043	-0.8211
ENSG00000148411	NACC2	138151	-0.8211
ENSG00000149090	PAMR1	25891	-0.8197
ENSG00000158315	RHBDL2	54933	-0.8192
ENSG00000157873	TNFRSF14	8764	-0.8192
ENSG00000159228	CBR1	873	-0.8192
ENSG00000072952	MRVI1	10335	-0.8192
ENSG00000196502	SULT1A1	6817	-0.8192
ENSG00000104267	CA2	760	-0.8188
ENSG00000037042	TUBG2	27175	-0.8186
ENSG00000166411	IDH3A	3419	-0.8181
ENSG00000012171	SEMA3B	7869	-0.8177
ENSG00000182600	C2orf82	389084	-0.8177
ENSG00000239382	ALKBH6	84964	-0.8171
ENSG00000129538	RNASE1	6035	-0.8169
ENSG00000067113	PPAP2A	8611	-0.8169
ENSG00000182700	IGIP	492311	-0.8155
ENSG00000127824	TUBA4A	7277	-0.8146
ENSG00000130203	APOE	348	-0.8145
ENSG00000161281	COX7A1	1346	-0.8144
ENSG00000101335	MYL9	10398	-0.8143
ENSG00000149091	DGKZ	8525	-0.8139
ENSG00000126709	IFI6	2537	-0.8137
ENSG00000010278	CD9	928	-0.8135
ENSG00000152583	SPARCL1	8404	-0.8133
ENSG00000129473	BCL2L2	599	-0.8131
ENSG00000174080	CTSF	8722	-0.8117
ENSG00000144040	SFXN5	94097	-0.8110
ENSG00000184524	CEND1	51286	-0.8105
ENSG00000100307	CBX7	23492	-0.8104
ENSG00000013364	MVP	9961	-0.8101
ENSG00000178980	SEPW1	6415	-0.8101
ENSG00000106351	AGFG2	3268	-0.8101
ENSG00000161714	PLCD3	113026	-0.8095
ENSG00000042445	RETSAT	54884	-0.8085
ENSG00000155324	GRAMD3	65983	-0.8083
ENSG00000224877	C17orf89	284184	-0.8083
ENSG00000036530	CYP46A1	10858	-0.8080
ENSG00000156381	ANKRD9	122416	-0.8073
ENSG00000137825	ITPKA	3706	-0.8072
ENSG00000161642	ZNF385A	25946	-0.8060
ENSG00000068079	IFI35	3430	-0.8059
ENSG00000117691	NENF	29937	-0.8055
ENSG00000080573	COL5A3	50509	-0.8052

ENSG00000122359	ANXA11	311	-0.8047
ENSG00000184221	OLIG1	116448	-0.8043
ENSG00000126860	EVI2A	2123	-0.8041
ENSG00000198753	PLXNB3	5365	-0.8035
ENSG00000135916	ITM2C	81618	-0.8035
ENSG00000117266	CDK18	5129	-0.8033
ENSG00000087842	PIR	8544	-0.8029
ENSG00000100116	GCAT	23464	-0.8027
ENSG00000182196	ARL6IP4	51329	-0.8025
ENSG00000166033	HTRA1	5654	-0.8025
ENSG00000105516	DBP	1628	-0.8022
ENSG00000147576	ADHFE1	137872	-0.8017
ENSG00000135929	CYP27A1	1593	-0.8014
ENSG00000185043	CIB1	10519	-0.8013
ENSG00000198171	DDRGK1	65992	-0.8005
ENSG00000104825	NFKBIB	4793	-0.8002

Table S4

Enrichment Score: 22.21679332120849

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
nucleus	6.55E-38	2.970245353	1.15E-35	1.15E-35	8.03E-35
Transcription	1.85E-34	4.275328995	3.24E-32	1.62E-32	2.27E-31
transcription regulation	1.86E-33	4.269822989	3.25E-31	1.08E-31	2.28E-30
GO:0006350~transcription	3.37E-30	3.545436471	2.15E-27	2.15E-27	5.02E-27
zinc-finger	6.14E-30	4.44291997	1.07E-27	2.68E-28	7.52E-27
zinc finger region:C2H2-type 9	9.39E-29	10.7581898	5.88E-26	5.88E-26	1.40E-25
zinc finger region:C2H2-type 8	3.58E-28	9.942940885	2.24E-25	1.12E-25	5.32E-25
zinc finger region:C2H2-type 7	5.85E-28	9.41759054	3.66E-25	1.22E-25	8.69E-25
zinc finger region:C2H2-type 6	1.08E-27	8.910779339	6.79E-25	1.70E-25	1.61E-24
IPR007087:Zinc finger, C2H2-type	1.99E-27	6.291521776	6.09E-25	6.09E-25	2.67E-24
GO:0045449~regulation of transcription	3.43E-27	3.028474929	2.18E-24	1.09E-24	5.10E-24
IPR015880:Zinc finger, C2H2-like	4.34E-27	6.188899715	1.33E-24	6.64E-25	5.82E-24
zinc finger region:C2H2-type 4	6.67E-27	7.914285714	4.17E-24	8.35E-25	9.91E-24
zinc finger region:C2H2-type 3	1.68E-26	7.478844485	1.05E-23	1.76E-24	2.50E-23
zinc finger region:C2H2-type 5	5.54E-25	7.894671623	3.47E-22	4.96E-23	8.23E-22
GO:0003677~DNA binding	6.08E-25	3.128194731	1.42E-22	1.42E-22	7.81E-22
zinc	8.28E-25	3.579936721	1.45E-22	2.90E-23	1.02E-21
IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding	3.13E-24	6.743988341	9.59E-22	3.20E-22	4.20E-21
zinc finger region:C2H2-type 2	6.22E-24	7.152072891	3.89E-21	4.86E-22	9.23E-21
zinc finger region:C2H2-type 1	7.48E-24	7.649827213	4.68E-21	5.20E-22	1.11E-20
domain:KRAB	9.03E-24	10.35637789	5.65E-21	5.65E-22	1.34E-20
dna-binding	9.21E-24	3.813744151	1.61E-21	2.69E-22	1.13E-20
zinc finger region:C2H2-type 10	1.09E-23	10.29436365	6.84E-21	6.22E-22	1.62E-20
GO:0008270~zinc ion binding	6.44E-23	3.039830353	1.51E-20	7.53E-21	8.28E-20
IPR001909:Krueppel-associated box	6.81E-23	9.175623574	2.08E-20	5.21E-21	9.13E-20
SM00355:ZnF_C2H2	4.61E-22	4.539457175	4.06E-20	4.06E-20	4.99E-19
metal-binding	3.81E-21	2.876476746	6.66E-19	9.52E-20	4.67E-18
zinc finger region:C2H2-type 11	8.36E-20	10.00915543	5.24E-17	4.36E-18	1.24E-16
SM00349:KRAB	3.24E-19	6.730170497	2.85E-17	1.42E-17	3.51E-16
GO:0046914~transition metal ion binding	3.97E-19	2.586318585	9.29E-17	3.10E-17	5.11E-16
zinc finger region:C2H2-type 12	4.55E-17	10.0324389	2.85E-14	2.19E-15	6.77E-14
zinc finger region:C2H2-type 13	5.15E-17	11.57174445	3.22E-14	2.30E-15	7.65E-14
GO:0051252~regulation of RNA metabolic process	2.79E-13	2.73909249	1.77E-10	5.91E-11	4.15E-10
GO:0006355~regulation of transcription, DNA-dependent	1.55E-12	2.704305797	9.89E-10	2.47E-10	2.31E-09
GO:0046872~metal ion binding	2.41E-12	1.890185957	5.64E-10	1.41E-10	3.10E-09
zinc finger region:C2H2-type 14	3.56E-12	10.95005561	2.23E-09	1.48E-10	5.29E-09

GO:0043169~cation binding	4.28E-12	1.872546031	1.00E-09	2.00E-10	5.50E-09
GO:0043167~ion binding	1.04E-11	1.845170918	2.44E-09	4.07E-10	1.34E-08
zinc finger region:C2H2-type 15	8.94E-08	9.056147832	5.60E-05	3.50E-06	1.33E-04

Enrichment Score: 7.901711245751855

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0031981~nuclear lumen	5.67E-11	3.547569386	8.95E-09	8.95E-09	6.83E-08
GO:0043228~non-membrane-bounded organelle	4.58E-09	2.461864407	7.24E-07	3.62E-07	5.52E-06
GO:0043232~intracellular non-membrane-bounded organelle	4.58E-09	2.461864407	7.24E-07	3.62E-07	5.52E-06
GO:0070013~intracellular organelle lumen	1.05E-08	2.891498375	1.66E-06	5.53E-07	1.27E-05
GO:0043233~organelle lumen	1.84E-08	2.826360225	2.91E-06	7.27E-07	2.22E-05
GO:0031974~membrane-enclosed lumen	2.97E-08	2.771538583	4.69E-06	9.38E-07	3.58E-05
GO:0005730~nucleolus	4.94E-08	4.466419736	7.80E-06	1.30E-06	5.95E-05
GO:0005654~nucleoplasm	1.82E-06	3.534649632	2.87E-04	4.10E-05	0.002187243

Enrichment Score: 7.222013089662222

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
chromatin regulator	3.27E-10	8.122686738	5.73E-08	6.36E-09	4.01E-07
GO:0016568~chromatin modification	1.19E-07	5.312205488	7.56E-05	1.51E-05	1.77E-04
GO:0006325~chromatin organization	3.95E-07	4.303663519	2.52E-04	4.19E-05	5.88E-04
GO:0051276~chromosome organization	8.44E-07	3.707268694	5.37E-04	7.68E-05	0.001256098

Enrichment Score: 7.160509555746129

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
zinc finger region:C2H2-type 12	4.55E-17	10.0324389	2.85E-14	2.19E-15	6.77E-14
zinc finger region:C2H2-type 13	5.15E-17	11.57174445	3.22E-14	2.30E-15	7.65E-14
zinc finger region:C2H2-type 14	3.56E-12	10.95005561	2.23E-09	1.48E-10	5.29E-09
zinc finger region:C2H2-type 15	8.94E-08	9.056147832	5.60E-05	3.50E-06	1.33E-04
zinc finger region:C2H2-type 16	8.06E-07	9.818153799	5.05E-04	2.97E-05	0.001197551
zinc finger region:C2H2-type 19	1.62E-05	12.87070707	0.010116411	5.65E-04	0.02412557
zinc finger region:C2H2-type 17	1.76E-05	9.747179193	0.010960886	5.80E-04	0.026150343
zinc finger region:C2H2-type 18	4.65E-05	10.72558923	0.028719093	0.001455917	0.069124222
zinc finger region:C2H2-type 20	4.18E-04	14.04541446	0.230039257	0.010402149	0.618419055
zinc finger region:C2H2-type 21	0.002061302	15.55799756	0.725198611	0.046714641	3.018716537
zinc finger region:C2H2-type 22	0.02489012	12.1352381	0.99999986	0.325956132	31.23128575

Enrichment Score: 3.3107824634939407

Term	PValue	Fold	Bonferroni	Benjamini	FDR

		Enrichment			
domain:SCAN box	2.42E-04	10.6449457	0.140325717	0.006552426	0.358158493
IPR003309:Transcriptional regulator SCAN	3.52E-04	9.796530432	0.102036025	0.013363077	0.470309493
SM00431:SCAN	0.001375961	7.185595568	0.11411481	0.029837776	1.480343682

Enrichment Score: 3.2230796608798102

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0005694~chromosome	3.03E-05	4.405249205	0.004776254	5.98E-04	0.036503859
GO:0044427~chromosomal part	1.56E-04	4.442120561	0.024344546	0.002734673	0.187769831
GO:0000228~nuclear chromosome	0.003629998	5.773261066	0.437060511	0.050894038	4.287106481
GO:0044454~nuclear chromosome part	0.007468967	6.388444622	0.694108852	0.087089455	8.63711235

Enrichment Score: 2.3130380263222956

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0044427~chromosomal part	1.56E-04	4.442120561	0.024344546	0.002734673	0.187769831
GO:0000775~chromosome, centromeric region	0.001127328	7.542486231	0.163240251	0.017663959	1.349882119
GO:0000793~condensed chromosome	0.048527052	4.833427869	0.999613955	0.353797258	45.08382775
GO:0000779~condensed chromosome, centromeric region	0.065578614	7.085365854	0.99997783	0.431094842	55.83564827

Enrichment Score: 1.9942403821216887

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0006730~one-carbon metabolic process	0.001932511	5.351265823	0.708349823	0.142749434	2.839237976
GO:0043414~biopolymer methylation	0.008414554	6.204366171	0.995404831	0.450135455	11.82301673
GO:0032259~methylation	0.011735525	5.632911392	0.999457726	0.495209975	16.11952629
methyltransferase	0.055256448	3.485359136	0.999952144	0.407581843	50.18492728

Enrichment Score: 1.9292045235495077

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
hsa00310:Lysine degradation	0.001367962	17.12121212	0.072524979	0.072524979	1.337401931
GO:0018024~histone-lysine N-methyltransferase activity	0.00533937	11.11558219	0.714284898	0.117746643	6.651022219
GO:0016278~lysine N-methyltransferase activity	0.00533937	11.11558219	0.714284898	0.117746643	6.651022219
GO:0016279~protein-lysine N-methyltransferase activity	0.00533937	11.11558219	0.714284898	0.117746643	6.651022219
GO:0042054~histone methyltransferase activity	0.009295436	9.120477696	0.887556518	0.166489278	11.31312122
domain:Post-SET	0.010547965	18.96130952	0.998690483	0.182213892	14.57419346
domain:SET	0.012385353	8.25526401	0.999590938	0.205037338	16.90061692
IPR003616:Post-SET zinc-binding region	0.013895822	16.42359514	0.986184186	0.378594396	17.10181228
IPR001214:SET	0.015422278	7.597309315	0.991399939	0.351025833	18.80536576

GO:0008276~protein methyltransferase activity	0.0182432	7.113972603	0.986543973	0.264891907	21.0767893
GO:0008170~N-methyltransferase activity	0.021285153	6.711294908	0.993490535	0.285114721	24.16344823
SM00508:PostSET	0.024737543	12.04643963	0.889670275	0.356514882	23.76250072
SM00317:SET	0.034063996	5.572502685	0.952635261	0.398490454	31.29841131
methyltransferase	0.055256448	3.485359136	0.999952144	0.407581843	50.18492728

Enrichment Score: 1.8300576056858162

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
IPR019786:Zinc finger, PHD-type, conserved site	6.82E-06	9.006487655	0.002085425	4.17E-04	0.009143667
IPR001965:Zinc finger, PHD-type	5.01E-05	8.272625698	0.015199861	0.002549505	0.067066893
IPR019787:Zinc finger, PHD-finger	2.98E-04	7.664344397	0.087026693	0.012922723	0.398015745
SM00249:PHD	3.21E-04	6.067836257	0.027866551	0.009376494	0.347264263
GO:0032452~histone demethylase activity	0.001211765	53.35479452	0.247026288	0.034844085	1.54666813
zinc finger region:PHD-type 2	0.003127356	13.48359788	0.859253173	0.067632572	4.546367355
zinc finger region:PHD-type 3	0.004111709	30.33809524	0.924168093	0.085098781	5.93698306
zinc finger region:PHD-type 1	0.004112952	12.25781626	0.924227289	0.082406291	5.938726185
GO:0032451~demethylase activity	0.005256475	26.67739726	0.708658534	0.128054894	6.550958771
IPR013129:Transcription factor jumonji	0.026859363	11.63337989	0.999759156	0.473168162	30.57540997
domain:JmjC	0.034957495	10.11269841	1	0.404303634	41.05623778
IPR003347:Transcription factor jumonji/aspartyl beta-hydroxylase	0.043113413	9.006487655	0.999998609	0.52725392	44.60560967
SM00558:JmjC	0.074197614	6.606112054	0.998868616	0.492587686	56.61496085
zinc finger region:PHD-type	0.092751415	5.834249084	1	0.697231248	76.44812883
dioxygenase	0.136146605	4.626022126	1	0.574172612	83.3740831
GO:0016702~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	0.168029077	4.042029888	1	0.846118205	90.60419375
GO:0016701~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	0.172001719	3.981701084	1	0.84122322	91.16491495
iron	0.529790313	1.428385779	1	0.93977053	99.99039599
GO:0005506~iron ion binding	0.672693158	1.154865682	1	0.995680773	99.99994187
oxidoreductase	0.915406538	0.724359336	1	0.999256298	100
GO:0055114~oxidation reduction	0.942781936	0.669955033	1	0.999999091	100

Table S5

Enrichment Score: 2.05520653893013

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0019725~cellular homeostasis	2.43E-05	3.922978773	0.025459257	0.025459257	0.03865368
GO:0006873~cellular ion homeostasis	5.13E-05	4.236257648	0.053053764	0.026888374	0.081688971
GO:0055082~cellular chemical homeostasis	5.98E-05	4.169369369	0.061564435	0.020957632	0.095211386
GO:0050801~ion homeostasis	1.20E-04	3.873741712	0.119986644	0.031449397	0.191433421
GO:0042552~myelination	2.47E-04	16.03603604	0.230648636	0.05109017	0.392313208
GO:0008366~axon ensheathment	3.65E-04	14.50879451	0.321463586	0.053895686	0.579703918
GO:0007272~ensheathment of neurons	3.65E-04	14.50879451	0.321463586	0.053895686	0.579703918
GO:0043218~compact myelin	4.51E-04	84.83628319	0.086337655	0.086337655	0.564274133
GO:0048878~chemical homeostasis	9.18E-04	3.094453829	0.622745017	0.114722609	1.4507822
GO:0019228~regulation of action potential in neuron	9.57E-04	11.28461795	0.638356043	0.106858777	1.513198461
GO:0001508~regulation of action potential	0.002259673	8.961314255	0.909507496	0.196202594	3.537569297
GO:0042592~homeostatic process	0.003032565	2.434231835	0.960263194	0.235696093	4.720384985
GO:0042391~regulation of membrane potential	0.004722187	5.457039129	0.9934405	0.284749697	7.258969351
GO:0043209~myelin sheath	0.006464551	24.23893805	0.726678723	0.35103021	7.807323496
GO:0030003~cellular cation homeostasis	0.017490709	3.358728808	0.999999993	0.667901423	24.49192749
GO:0055080~cation homeostasis	0.029210562	2.982926983	1	0.760948925	37.6236393
GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	0.037761529	3.221335873	1	0.830917913	45.81899971
GO:0055066~di-, tri-valent inorganic cation homeostasis	0.045424144	3.05959516	1	0.861213338	52.29481365
GO:0006875~cellular metal ion homeostasis	0.075750771	3.109027395	1	0.94960014	71.46787402
GO:0055065~metal ion homeostasis	0.086014806	2.972533509	1	0.949456141	76.11533618
GO:0051336~regulation of hydrolase activity	0.139911289	2.169861256	1	0.989675831	90.92442057
GO:0019226~transmission of nerve impulse	0.156357284	2.089266409	1	0.991363732	93.32604578
GO:0006874~cellular calcium ion homeostasis	0.186732685	2.663909811	1	0.993186681	96.27745303
GO:0055074~calcium ion homeostasis	0.197036228	2.593061146	1	0.992976816	96.96134967
GO:0043085~positive regulation of catalytic activity	0.248403167	1.640609841	1	0.994142275	98.9393363
GO:0044093~positive regulation of molecular function	0.341718263	1.455831258	1	0.996870335	99.87148146
GO:0051345~positive regulation of hydrolase activity	0.428818501	2.042578892	1	0.998213244	99.98658338
GO:0007268~synaptic transmission	0.701197799	1.226918193	1	0.999817699	99.99999956
GO:0050877~neurological system process	0.872256558	0.805777679	1	0.999998367	100

Enrichment Score: 1.6774356195641622

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	3.27E-04	28.67620562	0.293709198	0.056307308	0.519935621

GO:0048002~antigen processing and presentation of peptide antigen	0.00147787	17.41055341	0.792091774	0.145352223	2.327125998
mhc i	0.002643424	37.96381579	0.513229958	0.513229958	3.424202808
domain:Ig-like C1-type	0.003855531	12.57434211	0.853378699	0.61708839	5.40650517
GO:0019882~antigen processing and presentation	0.004646526	7.341799631	0.99288899	0.297629083	7.146661526
immune response	0.008593187	3.954564145	0.90438709	0.690786627	10.7387509
heterodimer	0.008851814	6.143012264	0.910937142	0.453708861	11.04477624
SM00407:IGc1	0.009243444	9.051844467	0.477980351	0.477980351	9.163282854
IPR003597:Immunoglobulin C1-set	0.018487766	7.101023018	0.997352487	0.94854601	22.24283252
GO:0042612~MHC class I protein complex	0.02479911	12.11946903	0.993411026	0.633761865	27.00288516
IPR003006:Immunoglobulin/major histocompatibility complex, conserved site	0.034967396	5.550224888	0.999987856	0.940967942	38.11297818
GO:0042611~MHC protein complex	0.089019731	5.953423381	0.999999992	0.666085754	68.91958152
hsa04612:Antigen processing and presentation	0.178339897	3.829066265	0.999999279	0.99103371	87.05651982
IPR007110:Immunoglobulin-like	0.593744737	1.204764384	1	0.999999999	99.99946796
IPR013783:Immunoglobulin-like fold	0.67108928	1.091477317	1	1	99.99996914
Immunoglobulin domain	0.886851993	0.807740761	1	0.999789747	100

Enrichment Score: 1.422597126082399

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0006706~steroid catabolic process	0.012439646	17.41055341	0.999998315	0.564325584	18.0689046
GO:0016042~lipid catabolic process	0.052581996	3.522366297	1	0.88989274	57.6821684
GO:0008202~steroid metabolic process	0.082520822	3.016680046	1	0.957317715	74.61946123

Enrichment Score: 1.3734763560145584

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
SM00280:KAZAL	0.034690381	10.0357406	0.915537413	0.709375522	30.60746334
domain:Kazal-like	0.039766725	9.430756579	0.999999998	0.993538827	44.22588955
IPR002350:Proteinase inhibitor I1, Kazal	0.054934104	7.872873346	0.999999984	0.949940001	53.31395407

Enrichment Score: 1.094223868313612

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
steroid metabolism	0.05460337	7.909128289	0.999999767	0.750539402	52.24678483
GO:0008202~steroid metabolic process	0.082520822	3.016680046	1	0.957317715	74.61946123
lipid metabolism	0.115756504	3.352213315	1	0.844173379	80.19775816

Enrichment Score: 0.997470634770057

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR

GO:0015630~microtubule cytoskeleton	0.022155154	2.266421652	0.988676251	0.673789785	24.48314254
microtubule	0.108940683	2.739092048	1	0.859261646	78.09162005
GO:0044430~cytoskeletal part	0.128734802	1.544638209	1	0.747940152	82.22347776
GO:0007017~microtubule-based process	0.150950395	2.408574582	1	0.990875966	92.61151135
GO:0005874~microtubule	0.219508703	2.064143143	1	0.84051259	95.5234329

Enrichment Score: 0.9827211085507533

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
oxidoreductase	0.033448787	2.251709122	0.999904244	0.685481941	36.09838067
Secondary metabolites biosynthesis, transport, and catabolism	0.076953622	6	0.429093934	0.429093934	33.82174085
nadp	0.124408406	3.24477058	1	0.835827076	82.60182777
GO:0055114~oxidation reduction	0.14880303	1.716533435	1	0.991372459	92.30832673
GO:0009055~electron carrier activity	0.256049255	2.259484859	1	0.999401689	97.98032133

Enrichment Score: 0.9643760199606757

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
iron	0.025176738	3.108148661	0.99902761	0.628728605	28.51266864
GO:0005506~iron ion binding	0.035802532	2.837194056	0.99995736	0.99995736	38.18386548
heme	0.245668498	3.137505437	1	0.93534462	97.55473392
GO:0020037~heme binding	0.249364063	3.095120788	1	0.999635372	97.72731459
GO:0046906~tetrapyrrole binding	0.272912452	2.903175313	1	0.998132413	98.50750363

Enrichment Score: 0.9529608825552933

Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0031967~organelle envelope	0.04525387	2.006879817	0.999905031	0.733701473	44.03510045
GO:0031975~envelope	0.046078933	2.000426828	0.999920111	0.692524157	44.63827132
GO:0005743~mitochondrial inner membrane	0.052223996	2.587599051	0.999978065	0.69636692	48.94595328
GO:0031090~organelle membrane	0.05510773	1.651314515	0.999988075	0.678155628	50.85916168
GO:0031966~mitochondrial membrane	0.057889259	2.296752167	0.999993387	0.661836709	52.64184028
GO:0019866~organelle inner membrane	0.069138326	2.406703069	0.999999402	0.667868557	59.26126348
GO:0005740~mitochondrial envelope	0.075067963	2.159714449	0.999999833	0.67201453	62.39706864
transit peptide:Mitochondrion	0.077581033	2.154062887	1	0.998755806	68.71189696
transit peptide	0.08171978	2.126824414	1	0.809163428	67.44368997
mitochondrion	0.119706799	1.67308483	1	0.838825339	81.33112491
GO:0044429~mitochondrial part	0.150825708	1.710983863	1	0.773787443	87.1160551
GO:0005739~mitochondrion	0.15519041	1.456863495	1	0.769261372	87.92192257
mitochondrion inner membrane	0.448304308	1.967037088	1	0.982479067	99.96019501
GO:0031980~mitochondrial lumen	0.594606831	1.494912479	1	0.964706846	99.99878343

GO:0005759~mitochondrial matrix	0.594606831	1.494912479	1	0.964706846	99.99878343
Enrichment Score: 0.9372789408800029					
Term	PValue	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0000302~response to reactive oxygen species	0.023139848	6.49993994	1	0.748747001	31.11521524
GO:0010035~response to inorganic substance	0.025916446	3.567040211	1	0.769543897	34.16721209
GO:0006979~response to oxidative stress	0.044751832	3.715666886	1	0.868131083	51.75707056
GO:0007568~aging	0.060463982	4.431777232	1	0.913980868	62.95245262
GO:0033554~cellular response to stress	0.490048042	1.291949193	1	0.998586087	99.99779391
GO:0010033~response to organic substance	0.536459289	1.183241494	1	0.999068666	99.99951712
GO:0009719~response to endogenous stimulus	0.644211486	1.203692581	1	0.999687149	99.99999285