SUPPLEMENTARY METHODS

Gene Set Assignment

Based on literature review, susceptibility genes were classified into groupings of 6 neuropsychiatric disorders and 12 gene sets based on genetic evidence for each disorder

(1) **Syndromal Neurodevelopmental Disorders**: As reported by Talkowsi et al, 2012 (1) in a cohort of 38 patients who presented with syndromal neurodevelopmental disorders of varying phenotypic type and severity, 33 potentially causal genes were identified to be disrupted in balanced chromosomal abnormalities by karyotypic analysis and sequencing of target breakpoints. **Of the 33 identified genes, microarray probes in the Brain Cloud data set mapped to 31 genes**.

(2) **Schizophrenia: Genes associated with Schizophrenia by meta-analysis**: The "Top Results" genes as reported in the Schizophrenia Research Forum meta-analysis as of October 2013 (http://www.szgene.org/) were identified (2). For genes with identical HuGENet/Venice grades, ranking is based on p value; for genes with identical grade and p value, ranking is based on effect size (odds ratio). **Of the 40 identified genes for schizophrenia, microarray probes in the Brain Cloud data set mapped to 36 genes**.

(3) **Schizophrenia: Genes associated with Schizophrenia by GWAS**: As reported by the Psychiatric Genomics Consortium (PGC), by Ripke et al 2013 (3),in a multistage genome-wide association study for schizophrenia, 22 loci associated at genome-wide significance ($p<10–8$) were reported. The reported genes containing the associated SNP or reported to be in LD region with the associated SNP were selected. Also, as reported by the Psychiatric Genomics Consortium (PGC), by Ripke et al, 2011 (4), in a genome-wide association study with stage 1 discovery sample of 21,856 individuals of European ancestry and a stage 2 replication sample of 29,839 independent subjects, highly significant genic regions with one or more SNPs achieving a Stage 1 $p<10^{-6}$ and/or a Combined Stages 1&2 $p<10–6$ were reported. The reported genes containing the associated SNP or in the LD region of the associated SNP (defined as r2 of 0.6 or greater, based on HapMap3) within 6MB of the associated SNP were selected. The MHC region on chromosome 6

was excluded from the present analysis due to strong LD within this region. **Of the 132 identified genes, microarray probes in the Brain Cloud data set mapped to 106 genes**.

(4) **Schizophrenia: Genes in CNV regions associated with schizophrenia**: We identified recurrent CNVs associated with schizophrenia from a series of genome-wide association studies from 2008 until the present (5–12). Each of the studies met the following criteria: standardized diagnosis, genome-wide detection, confirmed structural variations using at least two different methods for discovery and validation, and sufficient information to permit the identification of duplicate samples. Each identified CNV was rare (<1% frequency in the total sample) and autosomal, and met the study's proposed criteria for "high confidence". Recurrence was defined as identification in multiple cases across studies. CNVs regardless of size were included, 10–100kb, and>100kb. The following regions were identified: 1q21.1, 2p16.3, 3q29, 7q36.3, 15q11.2, 15q13.3, 16p11.2, and 22q11.21. Genomic regions that were initially reported using NCBI build 36 (hg18) coordinates were updated with RefSeq genes that populated to hg19 coordinates, if the region was better characterized in the latter version. **Of the 154 identified genes, microarray probes in the Brain Cloud data set mapped to 113 genes**.

(5) **Schizophrenia: Rare de novo Single nucleotide variants (SNVs)/Indels associated with schizophrenia:** From a series of exome capture high throughput sequencing studies of trios and/or quads, rare de novo mutations in probands with schizophrenia were identified, including missense, nonsense, frameshift and splice site mutations, as well as INDELs. The putative mutations in each study were validated by direct PCR amplification or Sanger sequencing within each study. The genes affected by the de novo mutations in the patient samples were selected. **Of the 240 identified genes, microarray probes in the Brain Cloud data set mapped to 212 genes** (13–16).

(6) **ASD: Genes in CNV regions associated with ASD**: We identified recurrent CNVs associated with ASD from a series of genome-wide association studies from 2007 until the present, as summarized by Sanders et al. (17–22) Each of these studies met the following criteria: standardized diagnosis, genome-wide detection, confirmed structural variations, and sufficient information to permit the identification of duplicate samples. Each identified CNV was rare (<1% frequency in the total sample) and autosomal, and met the study's proposed criteria for "high confidence". Recurrence was defined as identification in multiple cases across studies. CNVs regardless of size were included, 10–100kb, and>100kb. The

following regions were identified: 1q21.1, 2p16.3, 3p14.1, 5p15.2, 7q11.23, 7q31.1, 7q36.2, 8p23.3, 9p24.3, 10q11.23–21.1, 12q24.31, 15q11.2–13.1, 15q13.2–13.3, 15q23–24.1, 16p11.2, 16q23.3, 18q22.1, 20q13.33, 22q11.21, 22q13.33. **Of the 216 identified genes, microarray probes in the Brain Cloud data set mapped to 176 genes**.

(7) **Genes associated with ASD**: Genes associated with ASD were selected from a publicly available online database, SFARIgene, compiled by the Simons Foundation Autism Research Initiative, and most recently updated in June 2013 (http://sfari.org/resources/sfari-gene) (23). Genes labeled and cataloged in SFARIgene by "genetic association" and "functional" were included; that is, risk-conferring candidate genes with common polymorphisms identified from genetic association studies, and functional candidates relevant for ASD biology were included. The category of "rare single gene variant" was also included but only if did not contain genes analyzed in the CNV analysis above. The "syndromic" category of SFARIgene was excluded from current analysis due to the phenotypic heterogeneity of syndromic forms of autism. **Of the 262 identified genes, microarray probes in the Brain Cloud data set mapped to 242 genes**.

(8) **BPAD: Genes associated with Bipolar Disorder by GWAS**: As reported by the PGC meta-analysis, by Sklar et al, 2011 (24), in a genome-wide association study with stage 1 discovery sample of 7,481 individuals with BPAD and a stage 2 replication sample of 4,496 independent subjects with BPAD, highly significant genic regions with one or more SNPs achieving a Stage 1 $p<5\times10^{-5}$ and/or a Combined Stages 1&2 $p<5\times10^{-5}$ were included. Genes containing the associated SNP or genes in the LD region of the associated SNP within 20kb as reported by Sklar et al, 2011 were included. In addition, as reported in the large-scale BPAD association studies by Baum et al, 2008 (25), Cichon et al, 2011 (26), and Chen et al, 2013 (27), genes containing an associated SNP or in the LD region of an associated SNP, with a Phase 1 $p<10^{-8}$, or combined Phase I and II $p<p<10^{-8}$, that is GWAS significant, but not reported in the PGC 2011 meta-analysis, were included. **Of the 146 identified genes, microarray probes in the Brain Cloud data set mapped to 123 genes**.

(9) **Genes associated with Intellectual Disability**: Genes from a standardized clinical diagnostic genetic testing panel for intellectual disability were chosen, including 33 autosomal genes and 61 X-linked genes

(The University of Chicago Genetic Services Laboratories, Comprehensive Non-Syndromic Intellectual Disability Panel) (28). **Of the 94 identified genes, microarray probes in the Brain Cloud data set mapped to 88 genes**.

(10) **Genes Associated with Neurodegenerative Disorders**: The following neurodegenerative diseases were included: Alzheimer's Disease, Parkinson's Disease, Fronto-temporal Dementia, Amyotrophic Lateral Sclerosis, Huntington's Disease, and Multiple Sclerosis. For each disease, established Mendelian genes were included as well as genes from the "Top Results" list for each disease from a systematic meta-analysis of genome-wide association studies, reported as of October 2013 (www.alzgene.org (29), www.pdgene.org (30), www.msgene.org (31)). **Of the 59 identified genes, microarray probes in the Brain Cloud data set mapped to 46 genes**.

(11) **Genes that Overlap Diagnostic Categories**: A gene that was identified in more than 1 disease/diagnostic category in the current analysis was included. Genes that overlap the categories of NDD and ASD in the current analysis were not included in the Overlap category, since the NDD category was syndromal, containing some cases of patients with autism features. **A total of 62 genes overlapped multiple diagnostic categories and microarray probes in the Brain Cloud data set mapped to all 62 genes**.

(12) CNVs that Overlap Diagnostic Categories (SCZ and ASD): A gene that was identified to be affected by a recurrent CNV in ASD and SCZ was included. A total of 73 genes overlapped SCZ/ASD CNV regions in: 1q21.1, 2p16.3, 15q13.3, 16p11.2, and 22q11.21 and microarray probes in the Brain Cloud data set mapped to all 73 genes.

Supplementary Statistical Methods

The surrogate variables were estimated with the RUV-2 ("Remove Unwanted Variation 2-step") algorithm (32) which requires a set of "negative control" genes that are associated with the unwanted variation but not the biological variable on interest (e.g. the fetal effect). This adaptation of surrogate variable analysis (SVA), allowed for the decomposition of biological (fetal) and technical (genes associated with RNA quality) effects, as fetal samples tended to have higher RNA integrity numbers (RINs). We used 374 probes associated with RIN (acting as a

surrogate for unwanted biological variability) and unassociated with age, and used diagnostic plots from the algorithm to identify 30 surrogate variables.

Statistics from multiple probes mapping to the same gene by symbol were reduced into a single statistic. We did not include the 1,621 probes that were not annotated to a gene symbol in the present analysis. If a gene had expressed transcripts that annotated to more than one probe, the probe yielding the largest positive fetal effect was reported; if a gene had expressed transcripts that annotated to probes yielding only negative fetal effects (e.g. more expressed in postnatal samples), the most negative fetal effect was reported.

To investigate cellular and molecular functionality during prenatal neurodevelopment, prenatally enriched genes were subject to gene set enrichment analysis using the GOstats R package (33) for the hypergeometric test, and the limma R package for the Wilcoxon test (34). The genes that were preferentially fetally expressed within a disease-associated gene group were further subject to qualitative protein-protein interaction analysis using the IPA Ingenuity database (www.ingenuity.com) (35).

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SUPPLEMENTARY TABLES

Supplementary Table 1: **"Fetal Effect Analysis", by disease-associated gene set and gene**: Regression analysis results for each gene in a disease-associated gene set that mapped to a microarray probe (t-statistic, Regression Coefficient (i.e. "Fetal Effect), p-value, Adjusted R2)

Supplementary Table 2: Overlap Category: Of the 10 gene sets, the subset of 62 genes that overlapped more than one diagnostic category.

Supplementary Table 3: **Gene Set Enrichment Analysis**: Gene set enrichment analysis, indicating significant GO terms. Unadjusted p-values, corrected FDR and Bonferonni p-values are listed, and the size of a significant gene set and the count-number of genes enriched for a GO term.

Supplementary Table 4: Co-expression Analysis: Correlation analysis for disease-associated and pre-natally enriched genes (listed by gene set) assessed across 38 fetal samples, using a Pearson's correlation coefficient threshold of 0.8.

Supplementary Table 5: ASD/CNV Loci: Each gene investigated at an ASD and/or SCZ associated locus and its "fetal effect"/regression coefficient. Genes with a fetal effect greater than 0.5 are highlighted in red and genes with a fetal effect greater than 1 are shaded.

Supp Table 1 Gene Sets

Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
NDD	AUTS2	26053	autism susceptibility candidate 2	7q11.22	Balanced Chromosome Abnormality	3.12	33.97	4.92E-93	0.81	hHC003332	NM_015570
NDD	ANK3	288	ankyrin 3, node of Ranvier (ankyrin G)	10q21	Balanced Chromosome Abnormality	2.42	22.94	4.18E-62	0.65	hHA034365	NM_020987
NDD	SOX5	6660	SRY (sex determining region Y)-box 5	12p12.1	Balanced Chromosome Abnormality	2.23	20.12	3.37E-53	0.58	hHA035450	NM_006940
NDD	SATB2	23314	SATB homeobox 2	2q33	Balanced Chromosome Abnormality	2.02	20.69	5.02E-55	0.60	hHC001764	NM_015265
NDD	PDE10A	10846	phosphodiesterase 10A		Balanced Chromosome Abnormality	1.91	17.25	9.87E-44	0.50	hHE040838	NM_006661
NDD	SPAST	6683	spastin	2p24-p21	Balanced Chromosome Abnormality	1.44	22.92	4.52E-62	0.65	hHC004698	NM_014946
NDD	EHMT1	79813	euchromatic histone-lysine N-methyltransferase 1	9q34.3	Balanced Chromosome Abnormality	1.28	20.96	6.76E-56	0.60	hHC013184	AB058779
NDD	ITGB1	3688	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	10p11.2	Balanced Chromosome Abnormality	0.81	9.97	8.97E-20	0.20	hHC004253	NM_002211
NDD	ZBTB20	26137	zinc finger and BTB domain containing 20	3q13.2	Balanced Chromosome Abnormality	0.82	9.18	2.22E-17	0.17	hHC019897	NM_015642
NDD	METTL2B	55798	methyltransferase like 2B	7q32.1	Balanced Chromosome Abnormality	0.87	11.09	2.69E-23	0.26	hHR030073	NM_018396
NDD	FAM107B	83641	family with sequence similarity 107, member B	10p13	Balanced Chromosome Abnormality	0.58	4.19	3.88E-05	-0.05	hHC029691	NM_031453
NDD	TCF4	6925	transcription factor 4	18q21.1	Balanced Chromosome Abnormality	0.80	12.62	2.92E-28	0.32	hHC020459	NM_001083962
NDD	CDK5RAP2	55755	CDK5 regulatory subunit associated protein 2	9q33.2	Balanced Chromosome Abnormality	0.68	7.80	1.96E-13	0.10	hHC012789	NM_018249
NDD	MBD5	55777	methyl-CpG binding domain protein 5	2q23.1	Balanced Chromosome Abnormality	0.77	12.57	4.17E-28	0.32	hHC004339	NM_018328
NDD	SNTG2	54221	syntrophin, gamma 2	2p25.3	Balanced Chromosome Abnormality	0.58	4.29	2.56E-05	-0.05	hHR008345	NM_018968
NDD	ZNF804A	91752	zinc finger protein 804A	2q32.1	Balanced Chromosome Abnormality	0.54	4.35	2.06E-05	-0.05	hHC001802	NM_194250
NDD	SMG6	23293	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	17p13.3	Balanced Chromosome Abnormality	0.40	6.66	1.91E-10	0.05	hHC018992	NM_017575
NDD	ZNF507	22847	zinc finger protein 507	19q13.11	Balanced Chromosome Abnormality	0.21	2.64	8.96E-03	-0.10	hHC007828	NM_001136156
NDD	FOXP1	27086	forkhead box P1	3p14.1	Balanced Chromosome Abnormality	0.10	1.11	2.69E-01	-0.12	hHC002879	NM_032682
NDD	CHD8	57680	chromodomain helicase DNA binding protein 8	14q11.2	Balanced Chromosome Abnormality	0.26	5.23	3.66E-07	-0.01	hHR011006	NM_020920
NDD	GRIN2B	2904	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	12p12	Balanced Chromosome Abnormality	0.13	2.02	4.46E-02	-0.11	hHC022772	NM_000834
NDD	CDKL5	6792	cyclin-dependent kinase-like 5	Xp22	Balanced Chromosome Abnormality	0.13	1.57	1.18E-01	-0.12	hHC018635	NM_003159
NDD	SNRPN	6638	small nuclear ribonucleoprotein polypeptide N	15q11.2	Balanced Chromosome Abnormality	0.09	0.80	4.23E-01	-0.13	hHR008158	AF400501
NDD	PON3	5446	paraoxonase 3	7q21.3	Balanced Chromosome Abnormality	0.09	0.78	4.34E-01	-0.13	hHC013743	NM_000940
NDD	C18orf1	753	chromosome 18 open reading frame 1	18p11.2	Balanced Chromosome Abnormality	-0.04	-0.41	6.79E-01	-0.13	hHC001974	NM_001003674
NDD	ZNHIT6	54680	zinc finger, HIT type 6	1p22.3	Balanced Chromosome Abnormality	-0.07	-1.49	1.39E-01	-0.12	hHC008348	NM_017953
NDD	GTF2F1	2962	general transcription factor IIF, polypeptide 1, 74kDa	19p13.3	Balanced Chromosome Abnormality	-0.12	-2.93	3.77E-03	-0.09	hHC026723	NM_002096
NDD	UTRN	7402	utrophin	6q24	Balanced Chromosome Abnormality	-0.20	-2.69	7.63E-03	-0.10	hHR020245	NM_007124
NDD	NLRP1	22861	NLR family, pyrin domain containing 1	17p13.2	Balanced Chromosome Abnormality	-0.49	-5.82	1.88E-08	0.01	hHR021670	NM_033004
NDD	GNA14	9630	guanine nucleotide binding protein (G protein), alpha 14	9q21	Balanced Chromosome Abnormality	-1.38	-11.95	4.66E-26	0.29	hHC012888	NM_004297
NDD	SNURF	8926	SNRPN upstream reading frame	15q11.2	Balanced Chromosome Abnormality	-1.69	-25.02	1.84E-68	0.69	hHA033189	NM_005678
SCZ Meta-analysis	NRG1	3084	neuregulin 1	8p12	GWAS	2.34	17.10	2.91E-43	0.49	hHA033957	NM_004495
SCZ Meta-analysis	PLXNA2	5362	plexin A2	1q32.2	GWAS	1.31	9.14	2.93E-17	0.16	hHC010960	NM_025179
SCZ Meta-analysis	SRR	63826	serine racemase	17p13	GWAS	1.28	16.63	1.10E-41	0.48	hHC016218	NM_021947
SCZ Meta-analysis	AKT1	207	v-akt murine thymoma viral oncogene homolog 1	14q32.32|14q32.32	GWAS	0.95	15.83	5.46E-39	0.45	hHC010439	NM_005163
SCZ Meta-analysis	TCF4	6925	transcription factor 4	18q21.1	GWAS	0.80	12.62	2.92E-28	0.32	hHC020459	NM_001083962
SCZ Meta-analysis	DTNBP1	84062	dystrobrevin binding protein 1	6p22.3	GWAS	0.60	7.16	1.02E-11	0.07	hHA035123	NM_183040
SCZ Meta-analysis	ZNF804A	91752	zinc finger protein 804A	2q32.1	GWAS	0.54	4.35	2.06E-05	-0.05	hHC001802	NM_194250

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
SCZ Meta-analysis	MTHFR	4524	5,10-methylenetetrahydrofolate reductase (NADPH)	1p36.3	GWAS	0.54	5.23	3.69E-07	-0.01	hHC015904	NM_005957
SCZ Meta-analysis	PPP3CC	5533	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	8p21.3	GWAS	0.37	6.77	9.80E-11	0.05	hHC017654	NM_005605
SCZ Meta-analysis	RPP21	79897	ribonuclease P/MRP 21kDa subunit	6p21.33	GWAS	0.22	4.43	1.44E-05	-0.04	hHC023511	NM_024839
SCZ Meta-analysis	MDGA1	266727	MAM domain containing glycosylphosphatidylinositol anchor 1	6p21	GWAS	0.28	3.72	2.49E-04	-0.07	hHC011932	NM_153487
SCZ Meta-analysis	HIST1H2BJ	8970	histone cluster 1, H2bj	6p22.1	GWAS	0.18	1.97	4.98E-02	-0.11	hHC025199	NM_021058
SCZ Meta-analysis	RPGRIP1L	23322	RPGRIP1-like	16q12.2	GWAS	0.09	1.07	2.88E-01	-0.13	hHC011173	NM_015272
SCZ Meta-analysis	RELN	5649	reelin	7q22	GWAS	0.25	1.83	6.86E-02	-0.12	hHC004991	NM_005045
SCZ Meta-analysis	GRIN2B	2904	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	12p12	GWAS	0.13	2.02	4.46E-02	-0.11	hHC022772	NM_000834
SCZ Meta-analysis	DRD2	1813	dopamine receptor D2	11q23	GWAS	0.22	2.30	2.24E-02	-0.11	hHA035616	NM_000795
SCZ Meta-analysis	SLC18A1	6570	solute carrier family 18 (vesicular monoamine), member 1	8p21.3	GWAS	0.29	2.42	1.64E-02	-0.10	hHC007643	NM_001135691
SCZ Meta-analysis	DRD4	1815	dopamine receptor D4	11p15.5	GWAS	0.02	0.28	7.78E-01	-0.13	hHC024251	NM_000797
SCZ Meta-analysis	DAO	1610	D-amino-acid oxidase	12q24	GWAS	-0.02	-0.13	8.95E-01	-0.13	hHC016344	NM_001917
SCZ Meta-analysis	GABRB2	2561	gamma-aminobutyric acid (GABA) A receptor, beta 2	5q34	GWAS	-0.21	-1.75	8.18E-02	-0.12	hHC009761	NM_021911
SCZ Meta-analysis	TPH1	7166	tryptophan hydroxylase 1	11p15.3-p14	GWAS	-0.18	-2.06	4.03E-02	-0.11	hHC019590	NM_004179
SCZ Meta-analysis	CCKAR	886	cholecystokinin A receptor	4p15.1-p15.2	GWAS	-0.07	-0.76	4.51E-01	-0.13	hHC013516	NM_000730
SCZ Meta-analysis	IL10	3586	interleukin 10	1q31-q32	GWAS	-0.07	-0.46	6.49E-01	-0.13	hHC008663	NM_000572
SCZ Meta-analysis	DAOA	267012	D-amino acid oxidase activator	13q33.2|13q34	GWAS	-0.18	-2.61	9.55E-03	-0.10	hHC017573	NM_172370
SCZ Meta-analysis	GRIK3	2899	glutamate receptor, ionotropic, kainate 3	1p34-p33	GWAS	-0.06	-0.88	3.80E-01	-0.13	hHC015531	NM_000831
SCZ Meta-analysis	COMT	NA	catechol-O-methyltransferase	22q11.21-q11.23|22q11.21	GWAS	-0.28	-5.30	2.66E-07	-0.01	hHA032822	NM_000754
SCZ Meta-analysis	PDE4B	5142	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	1p31	GWAS	-0.49	-7.51	1.18E-12	0.09	hHC005298	NM_001037341
SCZ Meta-analysis	NOTCH4	4855	Notch homolog 4 (Drosophila)	6p21.3	GWAS	-0.58	-11.07	3.02E-23	0.25	hHC013731	NM_004557
SCZ Meta-analysis	PRSS16	10279	protease, serine, 16 (thymus)	6p21	GWAS	-0.55	-8.25	1.07E-14	0.12	hHC020074	NM_005865
SCZ Meta-analysis	AHI1	54806	Abelson helper integration site 1	6q23.3	GWAS	-1.06	-14.54	1.13E-34	0.40	hHR010594	NM_001134831
SCZ Meta-analysis	HP	3240	haptoglobin	16q22.1	GWAS	-0.68	-3.81	1.80E-04	-0.07	hHC027418	NM_005143
SCZ Meta-analysis	IL1B	3553	interleukin 1, beta	2q14	GWAS	-1.99	-10.47	2.40E-21	0.23	hHC022194	NM_000576
SCZ Meta-analysis	NRGN	4900	neurogranin (protein kinase C substrate, RC3)	11q24	GWAS	-2.49	-29.50	2.77E-81	0.76	hHC004291	NM_001126181
SCZ Meta-analysis	HTR2A	3356	5-hydroxytryptamine (serotonin) receptor 2A	13q14-q21	GWAS	-2.85	-25.58	4.00E-70	0.70	hHC015232	NM_000621
SCZ Meta-analysis	APOE	348	apolipoprotein E	19q13.2	GWAS	-2.54	-18.34	2.35E-47	0.53	hHC024278	NM_000041
SCZ Meta-analysis	RGS4	5999	regulator of G-protein signaling 4	1q23.3	GWAS	-5.57	-41.91	1.36E-111	0.87	hHC004006	NM_001102445
SCZ PGC GWAS	ABCB9	23457	ATP-binding cassette, sub-family B (MDR/TAP), member 9	12q24	GWAS	0.27	3.72	2.51E-04	-0.07	hHA038202	NM_203444
SCZ PGC GWAS	AK3	50808	adenylate kinase 3	9p24.1-p24.3	GWAS	0.42	5.66	4.26E-08	0.00	hHR021543	NM_016282
SCZ PGC GWAS	AKT3	10000	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	1q43-q44	GWAS	1.79	20.89	1.17E-55	0.60	hHC012518	NM_005465
SCZ PGC GWAS	ALAS1	211	aminolevulinate, delta-, synthase 1	3p21.1	GWAS	0.33	6.42	7.35E-10	0.04	hHA037941	NM_000688
SCZ PGC GWAS	ARL3	403	ADP-ribosylation factor-like 3	10q23.3	GWAS	0.72	12.12	1.28E-26	0.30	hHR006410	NM_004311
SCZ PGC GWAS	AS3MT	57412	arsenic (+3 oxidation state) methyltransferase	10q24.32	GWAS	1.16	13.66	1.04E-31	0.37	hHC010261	NM_020682
SCZ PGC GWAS	C10orf25	220979	chromosome 10 open reading frame 25	10q11.21	GWAS	0.66	6.92	4.15E-11	0.06	hHC005884	NM_001039380
SCZ PGC GWAS	C10orf26	54838	chromosome 10 open reading frame 26	10q24.32	GWAS	0.23	3.89	1.31E-04	-0.06	hHC025418	NM_017787

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
SCZ PGC GWAS	C12orf65	91574	chromosome 12 open reading frame 65	12q24.31	GWAS	0.56	5.05	8.67E-07	-0.02	hHC008880	NM_152269
SCZ PGC GWAS	C2orf47	79568	chromosome 2 open reading frame 47	2q33.1	GWAS	0.18	4.01	7.99E-05	-0.06	hHC012467	NM_024520
SCZ PGC GWAS	C2orf56	55471	chromosome 2 open reading frame 56	2p22.2	GWAS	0.28	5.33	2.29E-07	-0.01	hHC022081	NM_144736
SCZ PGC GWAS	C2orf60	129450	chromosome 2 open reading frame 60	2q33.1	GWAS	0.67	10.89	1.14E-22	0.25	hHC008533	NM_001039693
SCZ PGC GWAS	C2orf69	205327	chromosome 2 open reading frame 69	2q33.1	GWAS	0.03	0.59	5.58E-01	-0.13	hHC023780	NM_153689
SCZ PGC GWAS	CACNA1C	775	calcium channel, voltage-dependent, L type, alpha 1C subunit		GWAS	0.45	4.55	8.60E-06	-0.04	hHA037564	NM_001129840
SCZ PGC GWAS	CACNB2	783	calcium channel, voltage-dependent, beta 2 subunit	10p12	GWAS	0.08	1.14	2.56E-01	-0.12	hHA034894	NM_201590
SCZ PGC GWAS	CALHM3	119395	calcium homeostasis modulator 3	10q24.33	GWAS	0.38	4.13	5.05E-05	-0.05	hHC016032	NM_001129742
SCZ PGC GWAS	CDK2AP1	8099	cyclin-dependent kinase 2 associated protein 1	12q24.31	GWAS	0.13	1.63	1.03E-01	-0.12	hHC026423	NM_004642
SCZ PGC GWAS	CEBPZ	10153	CCAAT/enhancer binding protein (C/EBP), zeta	2p22.2	GWAS	0.48	8.88	1.67E-16	0.15	hHC017981	NM_005760
SCZ PGC GWAS	CEP170	9859	centrosomal protein 170kDa	1q44	GWAS	2.31	18.83	5.45E-49	0.55	hHR021294	NM_014812
SCZ PGC GWAS	CNNM2	54805	cyclin M2	10q24.32	GWAS	0.93	9.37	5.98E-18	0.17	hHA035949	NM_199077
SCZ PGC GWAS	FAM177A1	283635	family with sequence similarity 177, member A1	14q13.2	GWAS	0.08	1.11	2.70E-01	-0.13	hHC003086	NM_001079519
SCZ PGC GWAS	GATAD2A	54815	GATA zinc finger domain containing 2A	19p13.11	GWAS	0.48	4.45	1.31E-05	-0.04	hHA037609	AK125974
SCZ PGC GWAS	GIGYF2	26058	GRB10 interacting GYF protein 2	2q37.1	GWAS	0.46	11.41	2.56E-24	0.27	hHC020973	NM_015575
SCZ PGC GWAS	GLT8D1	55830	glycosyltransferase 8 domain containing 1	3p21.1	GWAS	0.52	9.52	2.18E-18	0.18	hHC017657	NM_001010983
SCZ PGC GWAS	GMIP	51291	GEM interacting protein	19p12-p11	GWAS	0.34	6.20	2.45E-09	0.03	hHC013414	NM_016573
SCZ PGC GWAS	INA	9118	internexin neuronal intermediate filament protein, alpha	10q24.33	GWAS	0.19	2.76	6.16E-03	-0.10	hHC003222	NM_032727
SCZ PGC GWAS	ITIH1	3697	inter-alpha (globulin) inhibitor H1	3p21.2-p21.1	GWAS	0.01	0.11	9.16E-01	-0.13	hHC022349	NM_002215
SCZ PGC GWAS	KIAA0391	9692	KIAA0391	14q13.2	GWAS	0.40	5.53	8.54E-08	0.00	hHR011807	AB002389
SCZ PGC GWAS	LPAR2	9170	lysophosphatidic acid receptor 2	19p12	GWAS	3.19	33.68	2.58E-92	0.80	hHC018912	NM_004720
SCZ PGC GWAS	MMP16	4325	matrix metallopeptidase 16 (membrane-inserted)	8q21.3	GWAS	1.33	15.78	7.95E-39	0.45	hHA035698	NM_005941
SCZ PGC GWAS	MPHOSPH9	10198	M-phase phosphoprotein 9	12q24.31	GWAS	1.09	8.35	5.78E-15	0.13	hHC002303	NM_022782
SCZ PGC GWAS	NCAN	1463	neurocan	19p12	GWAS	1.30	15.11	1.36E-36	0.42	hHC008161	NM_004386
SCZ PGC GWAS	NEK4	6787	NIMA (never in mitosis gene a)-related kinase 4	3p21.1	GWAS	0.40	7.44	1.88E-12	0.08	hHC006908	NM_003157
SCZ PGC GWAS	NT5C2	22978	5'-nucleotidase, cytosolic II		GWAS	1.26	12.56	4.46E-28	0.32	hHE041640	NM_012229
SCZ PGC GWAS	NT5DC2	64943	5'-nucleotidase domain containing 2	3p21.1	GWAS	1.62	17.99	3.39E-46	0.52	hHC024330	NM_022908
SCZ PGC GWAS	NUCB2	NA	nucleobindin 2	11p15.1-p14	GWAS	0.62	10.97	6.59E-23	0.25	hHC008716	AK097398
SCZ PGC GWAS	NUDT1	4521	nudix (nucleoside diphosphate linked moiety X)-type motif 1	7p22	GWAS	1.27	19.68	9.29E-52	0.57	hHC024103	NM_198949
SCZ PGC GWAS	PBRM1	55193	polybromo 1	3p21	GWAS	2.25	42.58	5.14E-113	0.87	hHC007983	NM_018313
SCZ PGC GWAS	PBX4	80714	pre-B-cell leukemia homeobox 4	19p12	GWAS	1.46	19.12	6.39E-50	0.56	hHC009226	NM_025245
SCZ PGC GWAS	PCGF6	84108	polycomb group ring finger 6	10q24.33	GWAS	0.55	6.55	3.50E-10	0.04	hHR027831	NM_001011663
SCZ PGC GWAS	PDCD11	22984	programmed cell death 11	10q24.33	GWAS	0.67	11.43	2.26E-24	0.27	hHR008588	NM_014976
SCZ PGC GWAS	PHF7	51533	PHD finger protein 7	3p21.1	GWAS	0.22	2.72	7.03E-03	-0.10	hHC012761	NM_016483
SCZ PGC GWAS	PIK3C2A	5286	phosphoinositide-3-kinase, class 2, alpha polypeptide	11p15.5-p14	GWAS	0.87	9.92	1.26E-19	0.20	hHC012392	NM_002645
SCZ PGC GWAS	PLCB2	5330	phospholipase C, beta 2	15q15	GWAS	0.15	3.72	2.50E-04	-0.07	hHC025905	NM_004573
SCZ PGC GWAS	PPP2R3C	55012	protein phosphatase 2 (formerly 2A), regulatory subunit B'', gamma	14q13.2	GWAS	1.06	8.53	1.74E-15	0.13	hHA034577	NM_017917
SCZ PGC GWAS	PRKD3	23683	protein kinase D3	2p22.2	GWAS	0.32	1.68	9.50E-02	-0.12	hHC007598	BU685552

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SCZ PGC GWAS	PSMA6	5687	proteasome (prosome, macropain) subunit, alpha type, 6	14q13	GWAS	0.31	4.18	4.05E-05	-0.05	hHC023230	AK302008
SCZ PGC GWAS	QPCTL	54814	glutaminyl-peptide cyclotransferase-like	19q13.32	GWAS	0.09	1.43	1.53E-01	-0.12	hHC023489	NM_017659
SCZ PGC GWAS	RFT1	91869	RFT1 homolog (S. cerevisiae)		GWAS	0.34	4.68	4.73E-06	-0.03	hHR013631	NM_052859
SCZ PGC GWAS	SDCCAG8	10806	serologically defined colon cancer antigen 8	1q43-q44	GWAS	0.65	10.07	4.28E-20	0.21	hHC002591	NM_006642
SCZ PGC GWAS	SETD8	387893	SET domain containing (lysine methyltransferase) 8	12q24.31	GWAS	0.24	4.30	2.55E-05	-0.05	hHC032155	NM_020382
SCZ PGC GWAS	SFMBT1	51460	Scm-like with four mbt domains 1	3p21.1	GWAS	0.49	7.89	1.08E-13	0.10	hHC019969	NM_001005159
SCZ PGC GWAS	SFXN2	118980	sideroflexin 2	10q24.32	GWAS	1.35	19.15	5.05E-50	0.56	hHC010043	NM_178858
SCZ PGC GWAS	SH3PXD2A	9644	SH3 and PX domains 2A	10q24.33	GWAS	0.09	1.21	2.29E-01	-0.12	hHC020707	NM_014631
SCZ PGC GWAS	STT3A	3703	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	11q23.3	GWAS	0.35	7.22	6.82E-12	0.07	hHC008282	NM_152713
SCZ PGC GWAS	TAF5	6877	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	10q24-q25.2	GWAS	1.35	19.44	5.55E-51	0.56	hHA034238	NM_006951
SCZ PGC GWAS	TCF4	6925	transcription factor 4	18q21.1	GWAS	0.80	12.62	2.92E-28	0.32	hHC020459	NM_001083962
SCZ PGC GWAS	TLR9	54106	toll-like receptor 9	3p21.3	GWAS	0.07	1.23	2.19E-01	-0.12	hHA039914	NM_017442
SCZ PGC GWAS	TM6SF2	53345	transmembrane 6 superfamily member 2	19p13.3-p12	GWAS	0.35	3.90	1.28E-04	-0.06	hHC015308	NM_001001524
SCZ PGC GWAS	WDR82	80335	WD repeat domain 82	3p21.1	GWAS	0.82	17.15	2.11E-43	0.50	hHC025830	NM_025222
SCZ PGC GWAS	ZEB2	9839	zinc finger E-box binding homeobox 2	2q22.3	GWAS	1.50	15.51	6.50E-38	0.44	hHR029739	NM_014795
SCZ PGC GWAS	ZSWIM6	57688	zinc finger, SWIM-type containing 6	5q12.1	GWAS	0.93	8.47	2.61E-15	0.13	hHR001783	NM_020928
SCZ PGC GWAS	ACRV1	56	acrosomal vesicle protein 1	11q23-q24	GWAS	-0.46	-4.13	5.00E-05	-0.05	hHC009898	NM_001612
SCZ PGC GWAS	ARL6IP4	51329	ADP-ribosylation-like factor 6 interacting protein 4	12q24.31	GWAS	-1.30	-20.93	8.67E-56	0.60	hHA038793	NM_001002252
SCZ PGC GWAS	BAP1	8314	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	3p21.31-p21.2	GWAS	-0.52	-8.90	1.49E-16	0.15	hHC018424	NM_004656
SCZ PGC GWAS	C10orf32	119032	chromosome 10 open reading frame 32	10q24.32	GWAS	-0.38	-6.25	1.92E-09	0.03	hHC008933	NM_001136200
SCZ PGC GWAS	C2orf82	389084	chromosome 2 open reading frame 82	2q37.1	GWAS	-0.20	-3.13	1.97E-03	-0.09	hHC025626	NM_206895
SCZ PGC GWAS	CALHM1	255022	calcium homeostasis modulator 1	10q24.33	GWAS	-0.58	-6.07	5.00E-09	0.02	hHC021341	NM_001001412
SCZ PGC GWAS	CALHM2	51063	calcium homeostasis modulator 2	10pter-q26.12	GWAS	-0.20	-2.92	3.85E-03	-0.09	hHA039430	NM_015916
SCZ PGC GWAS	CILP2	148113	cartilage intermediate layer protein 2	19p13.11	GWAS	-0.21	-4.72	3.96E-06	-0.03	hHC021470	NM_153221
SCZ PGC GWAS	CSMD1	64478	CUB and Sushi multiple domains 1	8p23.2	GWAS	-0.22	-3.55	4.59E-04	-0.07	hHR013460	NM_033225
SCZ PGC GWAS	CYP17A1	1586	cytochrome P450, family 17, subfamily A, polypeptide 1	10q24.3	GWAS	-0.16	-2.36	1.90E-02	-0.10	hHC025148	NM_000102
SCZ PGC GWAS	DNAH1	25981	dynein, axonemal, heavy chain 1		GWAS	-1.91	-16.91	1.26E-42	0.49	hHR017783	NM_015512
SCZ PGC GWAS	DPYD	1806	dihydropyrimidine dehydrogenase	1p22	GWAS	-0.42	-3.90	1.24E-04	-0.06	hHC002214	NM_000110
SCZ PGC GWAS	EI24	9538	etoposide induced 2.4 mRNA	11q24	GWAS	-0.06	-0.99	3.25E-01	-0.13	hHR016596	AF010313
SCZ PGC GWAS	FEZ1	9638	fasciculation and elongation protein zeta 1 (zygin I)	11q24.2	GWAS	-0.55	-8.40	4.06E-15	0.13	hHC021292	NM_005103
SCZ PGC GWAS	FTSJ2	29960	FtsJ homolog 2 (E. coli)	7p22	GWAS	-0.02	-0.40	6.90E-01	-0.13	hHC010873	NM_013393
SCZ PGC GWAS	GLYCTK	132158	glycerate kinase	3p21.1	GWAS	-0.32	-7.18	8.79E-12	0.07	hHC018008	NM_145262
SCZ PGC GWAS	GNL3	26354	guanine nucleotide binding protein-like 3 (nucleolar)	3p21.1	GWAS	-0.06	-0.50	6.15E-01	-0.13	hHA040707	NM_206825
SCZ PGC GWAS	ITIH3	3699	inter-alpha (globulin) inhibitor H3	3p21.2-p21.1	GWAS	-0.19	-2.38	1.79E-02	-0.10	hHC025527	NM_002217
SCZ PGC GWAS	ITIH4	3700	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	3p21-p14	GWAS	-0.59	-9.22	1.67E-17	0.17	hHC024955	NM_002218
SCZ PGC GWAS	MAD1L1	8379	MAD1 mitotic arrest deficient-like 1 (yeast)	7p22	GWAS	-0.67	-9.84	2.22E-19	0.20	hHR019802	NM_003550
SCZ PGC GWAS	MUSTN1	389125	musculoskeletal, embryonic nuclear protein 1	3p21.1	GWAS	-2.05	-13.74	5.32E-32	0.37	hHC019519	NM_205853

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SCZ PGC GWAS	NDUFA13	51079	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	19p13.2	GWAS	-0.97	-16.93	1.12E-42	0.49	hHC021546	NM_015965
SCZ PGC GWAS	NGEF	25791	neuronal guanine nucleotide exchange factor	2q37	GWAS	-2.54	-29.36	6.70E-81	0.76	hHC014574	NM_019850
SCZ PGC GWAS	NISCH	11188	nischarin	3p21.1	GWAS	-0.46	-6.97	3.17E-11	0.06	hHC014499	NM_007184
SCZ PGC GWAS	OGFOD2	NA	2-oxoglutarate and iron-dependent oxygenase domain containing 2	12q24.31	GWAS	-1.17	-15.41	1.42E-37	0.44	hHC021261	NM_024623
SCZ PGC GWAS	PITPNM2	57605	phosphatidylinositol transfer protein, membrane-associated 2	12q24.31	GWAS	-0.92	-16.09	7.13E-40	0.46	hHC012429	NM_020845
SCZ PGC GWAS	PKNOX2	63876	PBX/knotted 1 homeobox 2	-	GWAS	-1.04	-15.44	1.08E-37	0.44	hHA039708	NM_022062
SCZ PGC GWAS	PPM1M	132160	protein phosphatase 1M (PP2C domain containing)	3p21.1	GWAS	-0.42	-4.50	1.07E-05	-0.04	hHC011132	NM_144641
SCZ PGC GWAS	PTPRG	5793	protein tyrosine phosphatase, receptor type, G	3p21-p14	GWAS	-0.55	-6.74	1.19E-10	0.05	hHC004362	NM_002841
SCZ PGC GWAS	RILPL2	196383	Rab interacting lysosomal protein-like 2	12q24.31	GWAS	-1.56	-19.07	9.30E-50	0.55	hHR031019	NM_145058
SCZ PGC GWAS	SBNO1	55206	strawberry notch homolog 1 (Drosophila)	12q24.31	GWAS	-0.65	-7.39	2.50E-12	0.08	hHC011312	AK096864
SCZ PGC GWAS	SEMA3G	56920	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	3p21.1	GWAS	-0.92	-6.78	9.72E-11	0.05	hHC010991	NM_020163
SCZ PGC GWAS	SLCO6A1	133482	solute carrier organic anion transporter family, member 6A1	5q21.1	GWAS	-1.09	-9.65	8.43E-19	0.19	hHC004124	NM_173488
SCZ PGC GWAS	SNX19	399979	sorting nexin 19	11q25	GWAS	-0.25	-3.89	1.29E-04	-0.06	hHR003934	NM_014758
SCZ PGC GWAS	SPCS1	28972	signal peptidase complex subunit 1 homolog (S. cerevisiae)	3p21.1	GWAS	-0.73	-12.08	1.66E-26	0.30	hHC009782	NM_014041
SCZ PGC GWAS	SRP54	6729	signal recognition particle 54kDa	14q13.2	GWAS	-0.47	-8.77	3.61E-16	0.15	hHC002166	NM_003136
SCZ PGC GWAS	STAB1	23166	stabilin 1	3p21.1	GWAS	-0.06	-0.75	4.56E-01	-0.13	hHC025154	NM_015136
SCZ PGC GWAS	SF4	57794	splicing factor 4	19p13.11	GWAS	-0.24	-5.64	4.91E-08	0.00	hHC029084	NM_172231
SCZ PGC GWAS	SULT6B1	391365	sulfotransferase family, cytosolic, 6B, member 1	2p22.2	GWAS	-0.16	-1.75	8.10E-02	-0.12	hHR007924	NM_001032377
SCZ PGC GWAS	TNNC1	7134	troponin C type 1 (slow)	3p21.3-p14.3	GWAS	-0.27	-3.06	2.51E-03	-0.09	hHC020672	NM_003280
SCZ PGC GWAS	LBA1	9881	lupus brain antigen 1	3p22.2	GWAS	-0.43	-5.23	3.65E-07	-0.01	hHR016901	NM_014831
SCZ PGC GWAS	TWF2	11344	twinfilin, actin-binding protein, homolog 2 (Drosophila)	3p21.1	GWAS	-0.33	-7.41	2.26E-12	0.08	hHC020722	NM_007284
SCZ PGC GWAS	USMG5	84833	up-regulated during skeletal muscle growth 5 homolog (mouse)	10q24.33	GWAS	-0.72	-1.98	4.92E-02	-0.11	hHR011410	NM_032747
SCZ PGC GWAS	YJEFN3	374887	YjeF N-terminal domain containing 3	19p13.11	GWAS	-1.93	-23.55	5.18E-64	0.66	hHC026050	NM_198537
SCZ CNV	ALDOA	226	aldolase A, fructose-bisphosphate	16p11.2	CNV Association	0.32	5.01	1.08E-06	-0.02	hHA038102	NM_000034
SCZ CNV	ARVCF	421	armadillo repeat gene deletes in velocardiofacial syndrome	22q11.21	CNV Association	0.57	10.39	4.53E-21	0.22	hHC025769	NM_001670
SCZ CNV	ASPHD1	253982	aspartate beta-hydroxylase domain containing 1	16p11.2	CNV Association	0.74	8.54	1.69E-15	0.14	hHC008219	AF070642
SCZ CNV	BCL9	607	B-cell CLL/lymphoma 9	1q21	CNV Association	2.02	23.33	2.50E-63	0.66	hHC014098	NM_004326
SCZ CNV	C22orf29	79680	chromosome 22 open reading frame 29	22q11.21	CNV Association	0.07	1.38	1.70E-01	-0.12	hHC014745	NM_024627
SCZ CNV	C16orf53	79447	chromosome 16 open reading frame 53	16p11.2	CNV Association	1.29	19.62	1.49E-51	0.57	hHC013809	NM_024516
SCZ CNV	CDC45L	8318	CDC45 cell division cycle 45-like (S. cerevisiae)	22q11.21	CNV Association	3.89	25.04	1.59E-68	0.69	hHC004040	NM_003504
SCZ CNV	CHRNA7	1139	cholinergic receptor, nicotinic, alpha 7	15q14	CNV Association	0.83	5.64	4.76E-08	0.00	hHR025141	NM_000746
SCZ CNV	CLTCL1	8218	clathrin, heavy chain-like 1	22q11.2|22q11.21	CNV Association	0.90	9.68	7.00E-19	0.19	hHA036352	NM_007098
SCZ CNV	CRKL	1399	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	22q11|22q11.21	CNV Association	0.05	0.94	3.49E-01	-0.13	hHC019229	NM_005207
SCZ CNV	CYFIP1	NA	cytoplasmic FMR1 interacting protein 1	15q11	CNV Association	0.55	4.89	1.87E-06	-0.03	hHC003582	AY763579
SCZ CNV	DGCR10	26222	DiGeorge syndrome critical region gene 10	22q11	CNV Association	0.56	4.23	3.37E-05	-0.05	hHR005214	NR_026651
SCZ CNV	DGCR11	25786	DiGeorge syndrome critical region gene 11	22q11.21	CNV Association	0.00	0.03	9.72E-01	-0.13	hHR014573	NR_024157

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SCZ CNV	DGCR14	8220	DiGeorge syndrome critical region gene 14		CNV Association	0.45	5.40	1.60E-07	-0.01	hHR013003	NM_022719
SCZ CNV	DGCR5	NA	DiGeorge syndrome critical region gene 5 (non-protein coding)	22q11	CNV Association	0.65	7.67	4.41E-13	0.09	hHC030047	X91348
SCZ CNV	DGCR8	54487	DiGeorge syndrome critical region gene 8	22q11.2	CNV Association	0.82	6.25	1.92E-09	0.03	hHC018376	NM_022720
SCZ CNV	DLG1	1739	discs, large homolog 1 (Drosophila)	3q29	CNV Association	0.20	4.14	4.92E-05	-0.05	hHA038986	NM_004087
SCZ CNV	FAM57B	83723	family with sequence similarity 57, member B	16p11.2	CNV Association	0.88	12.37	1.94E-27	0.31	hHC021273	NM_031478
SCZ CNV	FBXO45	200933	F-box protein 45	3q29	CNV Association	0.05	1.09	2.77E-01	-0.13	hHR012604	NM_001105573
SCZ CNV	GDPD3	79153	glycerophosphodiester phosphodiesterase domain containing 3	16p11.2	CNV Association	0.24	4.35	2.03E-05	-0.05	hHC023507	NM_024307
SCZ CNV	GJA5	2702	gap junction protein, alpha 5, 40kDa	1q21.1	CNV Association	0.25	3.02	2.82E-03	-0.09	hHC014579	NM_005266
SCZ CNV	HFE2	148738	hemochromatosis type 2 (juvenile)	1q21.1	CNV Association	0.09	0.70	4.82E-01	-0.13	hHA039834	NM_213653
SCZ CNV	HIC2	23119	hypermethylated in cancer 2	22q11.21	CNV Association	2.32	31.79	1.95E-87	0.79	hHC029540	NM_015094
SCZ CNV	HIRA	7290	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	22q11.2|22q11.21	CNV Association	0.58	11.24	9.08E-24	0.26	hHC025127	NM_003325
SCZ CNV	HIRIP3	8479	HIRA interacting protein 3	16p11.2	CNV Association	0.16	2.28	2.33E-02	-0.11	hHA038020	NM_003609
SCZ CNV	KCTD13	253980	potassium channel tetramerisation domain containing 13	16p11.2	CNV Association	0.16	2.41	1.68E-02	-0.10	hHC015500	NM_178863
SCZ CNV	KIF22	3835	kinesin family member 22		CNV Association	0.22	3.55	4.67E-04	-0.07	hHC016722	AK294380
SCZ CNV	KLHL22	84861	kelch-like 22 (Drosophila)	22q11.21	CNV Association	0.38	8.72	5.11E-16	0.14	hHC021778	NM_032775
SCZ CNV	LIX1L	128077	Lix1 homolog (mouse)-like	1q21.1	CNV Association	1.38	21.92	6.15E-59	0.63	hHC005831	AK128733
SCZ CNV	LZTR1	8216	leucine-zipper-like transcription regulator 1	22q11.21|22q11.1-q11.2	CNV Association	0.56	10.82	1.98E-22	0.24	hHC019168	NM_006767
SCZ CNV	MFI2	4241	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	3q28-q29	CNV Association	0.07	0.92	3.59E-01	-0.13	hHA038525	NM_005929
SCZ CNV	MTMR15	NA	myotubularin related protein 15	15q13.2-q13.3	CNV Association	0.50	7.52	1.10E-12	0.09	hHC010102	NM_014967
SCZ CNV	NCBP2	22916	nuclear cap binding protein subunit 2, 20kDa	3q29	CNV Association	1.11	21.09	2.57E-56	0.61	hHC003863	NM_007362
SCZ CNV	NRXN1	9378	neurexin 1	2p16.3	CNV Association	1.31	14.33	6.02E-34	0.39	hHA035283	NM_001135659
SCZ CNV	P2RX6	9127	purinergic receptor P2X, ligand-gated ion channel, 6	22q11.21	CNV Association	0.16	3.13	2.00E-03	-0.09	hHC022715	AB002058
SCZ CNV	PAK2	5062	p21 protein (Cdc42/Rac)-activated kinase 2	3q29	CNV Association	1.74	24.02	1.95E-65	0.67	hHR008719	NM_002577
SCZ CNV	PDZK1	5174	PDZ domain containing 1	1q21	CNV Association	0.23	2.12	3.52E-02	-0.11	hHR023600	NM_002614
SCZ CNV	PI4KA	5297	phosphatidylinositol 4-kinase, catalytic, alpha	22q11.21	CNV Association	0.50	5.74	2.81E-08	0.01	hHA039366	NM_058004
SCZ CNV	PIAS3	NA	protein inhibitor of activated STAT, 3	1q21	CNV Association	0.07	1.46	1.46E-01	-0.12	hHC008914	NM_006099
SCZ CNV	POLR3C	10623	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	1q21.1	CNV Association	0.19	4.05	6.81E-05	-0.06	hHC015103	NM_006468
SCZ CNV	POLR3GL	84265	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	1q21.1	CNV Association	0.05	1.04	2.97E-01	-0.13	hHC005755	NM_032305
SCZ CNV	PPP4C	5531	protein phosphatase 4 (formerly X), catalytic subunit	16p12-p11	CNV Association	1.29	18.99	1.69E-49	0.55	hHC019979	NM_002720
SCZ CNV	PRKAB2	5565	protein kinase, AMP-activated, beta 2 non-catalytic subunit	1q21.1	CNV Association	1.39	21.24	8.97E-57	0.61	hHC007231	NM_005399
SCZ CNV	RANBP1	5902	RAN binding protein 1	22q11.21	CNV Association	0.40	8.73	4.51E-16	0.14	hHR030426	NM_002882
SCZ CNV	RBM8A	NA	RNA binding motif protein 8A	1q12	CNV Association	0.90	15.33	2.48E-37	0.43	hHR030321	NM_005105
SCZ CNV	RNF115	27246	ring finger protein 115	1q21.1	CNV Association	0.08	1.27	2.06E-01	-0.12	hHC007856	NM_014455
SCZ CNV	SERPIND1	3053	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	22q11.2|22q11.21	CNV Association	0.74	6.22	2.23E-09	0.03	hHC022493	NM_000185
SCZ CNV	SLC25A1	6576	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	22q11.21	CNV Association	0.48	8.50	2.19E-15	0.13	hHC024586	NM_005984
SCZ CNV	SPN	6693	sialophorin	16p11.2	CNV Association	0.15	3.40	7.88E-04	-0.08	hHC020872	NM_001030288

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SCZ CNV	TAOK2	9344	TAO kinase 2	16p11.2	CNV Association	0.50	5.08	7.67E-07	-0.02	hHA036912	NM_004783
SCZ CNV	TCTEX1D2	255758	Tctex1 domain containing 2	3q29	CNV Association	0.62	8.82	2.46E-16	0.15	hHC014256	NM_152773
SCZ CNV	TXNIP	10628	thioredoxin interacting protein	1q21.1	CNV Association	0.86	6.21	2.33E-09	0.03	hHC017503	NM_006472
SCZ CNV	UBXN7	26043	UBX domain protein 7	3q29	CNV Association	1.05	15.84	4.86E-39	0.45	hHR014260	NM_015562
SCZ CNV	UFD1L	7353	ubiquitin fusion degradation 1 like (yeast)	22q11.21	CNV Association	0.25	5.15	5.60E-07	-0.02	hHC030312	NM_005659
SCZ CNV	ZNF74	7625	zinc finger protein 74	22q11.2|22q11.21	CNV Association	1.57	23.04	2.05E-62	0.65	hHC014115	NM_003426
SCZ CNV	ANKRD34A	284615	ankyrin repeat domain 34A	1q21.1	CNV Association	-0.98	-14.04	5.24E-33	0.38	hHR014589	NM_001039888
SCZ CNV	ANKRD35	148741	ankyrin repeat domain 35	1q21.1	CNV Association	-0.61	-8.15	2.04E-14	0.12	hHC024169	NM_144698
SCZ CNV	C16orf54	283897	chromosome 16 open reading frame 54	16p11.2	CNV Association	-0.01	-0.11	9.09E-01	-0.13	hHC017288	NM_175900
SCZ CNV	C22orf25	128989	chromosome 22 open reading frame 25	22q11.21	CNV Association	-1.47	-23.16	8.40E-63	0.65	hHC014819	NM_152906
SCZ CNV	C3orf34	84984	chromosome 3 open reading frame 34	3q29	CNV Association	-0.09	-1.48	1.41E-01	-0.12	hHC017467	NM_032898
SCZ CNV	CD160	11126	CD160 molecule	1q21.1	CNV Association	-0.49	-8.59	1.18E-15	0.14	hHC014181	NM_007053
SCZ CNV	CDIPT	10423	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	16p11.2	CNV Association	-0.59	-13.67	9.04E-32	0.37	hHC022124	NM_006319
SCZ CNV	CHRFAM7A	89832	CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and FAM7A (family with sequence similarity 7A, exons A-E) fusion	15q13.1	CNV Association	-1.54	-13.74	5.29E-32	0.37	hHR031145	NM_139320
SCZ CNV	COMT	NA	catechol-O-methyltransferase	22q11.21-q11.23|22q11.21	CNV Association	-0.28	-5.30	2.66E-07	-0.01	hHA032822	NM_000754
SCZ CNV	CORO1A	11151	coronin, actin binding protein, 1A	16p11.2	CNV Association	-0.97	-16.13	5.34E-40	0.46	hHC026037	NM_007074
SCZ CNV	DGCR2	9993	DiGeorge syndrome critical region gene 2	22q11.21	CNV Association	-0.73	-12.66	2.09E-28	0.33	hHR017731	NM_005137
SCZ CNV	DGCR6	8214	DiGeorge syndrome critical region gene 6	22q11.21|22q11	CNV Association	-0.73	-13.54	2.53E-31	0.36	hHC031997	NM_005675
SCZ CNV	DGCR6L	85359	DiGeorge syndrome critical region gene 6-like	22q11	CNV Association	-0.74	-13.76	4.76E-32	0.37	hHC031931	NM_033257
SCZ CNV	DGCR9	25787	DiGeorge syndrome critical region gene 9	22q11.21	CNV Association	-0.60	-6.57	3.13E-10	0.04	hHR023893	NR_024159
SCZ CNV	DOC2A	8448	double C2-like domains, alpha	16p11.2	CNV Association	-0.64	-13.19	3.67E-30	0.35	hHC026830	NM_003586
SCZ CNV	FMO5	2330	flavin containing monooxygenase 5	1q21.1	CNV Association	-0.74	-9.65	8.54E-19	0.19	hHC015181	NM_001461
SCZ CNV	GJA8	2703	gap junction protein, alpha 8, 50kDa	1q21.1	CNV Association	-0.49	-6.30	1.40E-09	0.03	hHR032123	NM_005267
SCZ CNV	GNB1L	54584	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	22q11.2	CNV Association	-0.25	-3.92	1.14E-04	-0.06	hHC021043	NM_053004
SCZ CNV	GNRHR2	114814	gonadotropin-releasing hormone (type 2) receptor 2	1q12	CNV Association	-0.49	-5.22	3.85E-07	-0.01	hHR022874	NR_002328
SCZ CNV	INO80E	NA	INO80 complex subunit E	16p11.2	CNV Association	-0.03	-0.68	4.98E-01	-0.13	hHC019698	NM_173618
SCZ CNV	KLF13	51621	Kruppel-like factor 13	15q12	CNV Association	-0.53	-6.24	2.04E-09	0.03	hHC004305	NM_015995
SCZ CNV	MAPK3	5595	mitogen-activated protein kinase 3	16p11.2	CNV Association	-1.22	-20.77	2.91E-55	0.60	hHC016199	NM_001040056
SCZ CNV	MAZ	4150	MYC-associated zinc finger protein (purine-binding transcription factor)	16p11.2	CNV Association	-0.06	-1.78	7.63E-02	-0.12	hHC023211	NM_001042539
SCZ CNV	MED15	51586	mediator complex subunit 15	22q11.2	CNV Association	-0.49	-10.55	1.36E-21	0.23	hHC027374	NM_001003891
SCZ CNV	MRPL40	64976	mitochondrial ribosomal protein L40	22q11.21	CNV Association	-0.50	-7.82	1.74E-13	0.10	hHC015360	NM_003776
SCZ CNV	MVP	9961	major vault protein	16p13.1-p11.2	CNV Association	-1.16	-12.58	3.84E-28	0.32	hHC023971	NM_017458
SCZ CNV	NIPA1	123606	non imprinted in Prader-Willi/Angelman syndrome 1	15q11.2	CNV Association	-1.18	-13.19	3.66E-30	0.35	hHC009691	NM_144599
SCZ CNV	NIPA2	NA	non imprinted in Prader-Willi/Angelman syndrome 2	15q11.2	CNV Association	-0.03	-0.73	4.66E-01	-0.13	hHC014434	NM_030922
SCZ CNV	NUDT17	200035	nudix (nucleoside diphosphate linked moiety X)-type motif 17	1q21.1	CNV Association	-0.30	-5.72	3.23E-08	0.01	hHC018271	NM_001012758
SCZ CNV	OSTalpha	200931	organic solute transporter alpha	3q29	CNV Association	-0.01	-0.07	9.47E-01	-0.13	hHC018272	NM_152672
SCZ CNV	OTUD7A	161725	OTU domain containing 7A	15q13.3	CNV Association	-0.96	-10.35	6.01E-21	0.22	hHC013904	NM_130901

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
SCZ CNV	PCYT1A	5130	phosphate cytidylyltransferase 1, choline, alpha	3q29	CNV Association	-0.45	-7.23	6.50E-12	0.07	hHC012756	NM_005017
SCZ CNV	PEX11B	8799	peroxisomal biogenesis factor 11 beta	1q21.1	CNV Association	-0.70	-15.11	1.44E-36	0.42	hHC006958	NM_003846
SCZ CNV	PIGX	54965	phosphatidylinositol glycan anchor biosynthesis, class X	3q29	CNV Association	-0.40	-4.72	4.00E-06	-0.03	hHC005676	NM_017861
SCZ CNV	PIGZ	80235	phosphatidylinositol glycan anchor biosynthesis, class Z	3q29	CNV Association	-1.19	-15.29	3.41E-37	0.43	hHC014426	NM_025163
SCZ CNV	PRODH	5625	proline dehydrogenase (oxidase) 1	22q11.21	CNV Association	-1.01	-9.02	6.36E-17	0.16	hHR022951	NM_016335
SCZ CNV	PRRT2	112476	proline-rich transmembrane protein 2	16p11.2	CNV Association	-0.57	-7.73	3.02E-13	0.10	hHC012542	NM_145239
SCZ CNV	QPRT	23475	quinolinate phosphoribosyltransferase	16p11.2	CNV Association	-0.86	-10.74	3.41E-22	0.24	hHC023172	NM_014298
SCZ CNV	RNF168	165918	ring finger protein 168	3q29	CNV Association	-0.13	-1.09	2.78E-01	-0.13	hHC014227	NM_152617
SCZ CNV	RTN4R	65078	reticulon 4 receptor	22q11.21	CNV Association	-0.81	-9.38	5.47E-18	0.18	hHC015361	NM_023004
SCZ CNV	SCARF2	91179	scavenger receptor class F, member 2	22q11.21	CNV Association	-0.17	-3.01	2.92E-03	-0.09	hHC025789	NM_153334
SCZ CNV	SENP5	205564	SUMO1/sentrin specific peptidase 5	3q29	CNV Association	-0.39	-5.55	7.65E-08	0.00	hHC019256	NM_152699
SCZ CNV	SEZ6L2	26470	seizure related 6 homolog (mouse)-like 2	16p11.2	CNV Association	-1.44	-16.87	1.83E-42	0.49	hHA039718	NM_201575
SCZ CNV	SLC7A4	6545	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	22q11.21	CNV Association	-0.83	-12.06	1.97E-26	0.30	hHC023947	NM_004173
SCZ CNV	SNAP29	9342	synaptosomal-associated protein, 29kDa	22q11.21	CNV Association	-0.69	-9.68	6.90E-19	0.19	hHC007354	NM_004782
SCZ CNV	TBX1	6899	T-box 1	22q11.21	CNV Association	-0.70	-11.59	6.57E-25	0.28	hHA037074	NM_080647
SCZ CNV	TBX6	6911	T-box 6	16p11.2	CNV Association	-0.78	-9.56	1.59E-18	0.18	hHA040492	NM_004608
SCZ CNV	TFRC	7037	transferrin receptor (p90, CD71)	3q29	CNV Association	-0.42	-3.88	1.33E-04	-0.06	hHC006485	NM_003234
SCZ CNV	THAP7	80764	THAP domain containing 7	22q11.2	CNV Association	-0.13	-3.41	7.74E-04	-0.08	hHC021948	CR605890
SCZ CNV	TM4SF19	116211	transmembrane 4 L six family member 19	3q29	CNV Association	-0.04	-0.58	5.60E-01	-0.13	hHC022595	NM_138461
SCZ CNV	TMEM219	124446	transmembrane protein 219	16p11.2	CNV Association	-0.95	-18.45	1.04E-47	0.54	hHR015749	NM_001083613
SCZ CNV	TRMT2A	27037	TRM2 tRNA methyltransferase 2 homolog A (S. cerevisiae)	22q11.1-22q13|22q11.21	CNV Association	-0.40	-5.92	1.14E-08	0.01	hHA038708	NM_022727
SCZ CNV	TSSK2	NA	testis-specific serine kinase 2	22q11.21	CNV Association	-0.55	-5.51	9.14E-08	0.00	hHC020559	NM_053006
SCZ CNV	TXNRD2	10587	thioredoxin reductase 2	22q11.21	CNV Association	-0.84	-16.35	9.34E-41	0.47	hHC023645	NM_006440
SCZ CNV	WDR53	348793	WD repeat domain 53		CNV Association	-0.40	-4.15	4.71E-05	-0.05	hHR008083	CA415142
SCZ CNV	YPEL3	83719	yippee-like 3 (Drosophila)	16p11.2	CNV Association	-0.95	-16.01	1.35E-39	0.46	hHC002415	NM_031477
SCZ CNV	ZDHHC19	131540	zinc finger, DHHC-type containing 19	3q29	CNV Association	-1.33	-14.96	4.47E-36	0.42	hHC023654	NM_001039617
SCZ CNV	ZDHHC8	29801	zinc finger, DHHC-type containing 8	22q11.21	CNV Association	-0.16	-3.59	4.09E-04	-0.07	hHC029138	NM_013373
SCZ SNV	ALS2CL	259173	ALS2 C-terminal like	3p21.31	Exome sequencing	0.19	2.31	2.20E-02	-0.11	hHA036014	AK126505
SCZ SNV	ARHGEF10	9639	Rho guanine nucleotide exchange factor (GEF) 10	8p23	Exome sequencing	0.49	4.69	4.52E-06	-0.03	hHA036494	NM_014629
SCZ SNV	ASAP2	8853	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	2p25|2p24	Exome sequencing	0.63	9.89	1.61E-19	0.20	hHC002182	NM_003887
SCZ SNV	ATP5O	539	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	21q22.1-q22.2|21q22.11	Exome sequencing	0.15	2.72	7.10E-03	-0.10	hHC028277	NM_001697
SCZ SNV	BCORL1	63035	BCL6 co-repressor-like 1	Xq25-q26.1	Exome sequencing	1.15	17.60	6.56E-45	0.51	hHC024980	NM_021946
SCZ SNV	BIRC6	57448	baculoviral IAP repeat-containing 6	2p22-p21	Exome sequencing	0.56	12.81	6.58E-29	0.33	hHC009547	NM_016252
SCZ SNV	BRPF1	7862	bromodomain and PHD finger containing, 1	3p26-p25	Exome sequencing	1.03	18.40	1.46E-47	0.53	hHC025318	NM_001003694
SCZ SNV	BSND	7809	Bartter syndrome, infantile, with sensorineural deafness (Barttin)	1p32.1	Exome sequencing	0.02	0.13	8.98E-01	-0.13	hHC022560	NM_057176
SCZ SNV	C11orf30	56946	chromosome 11 open reading frame 30	11q13.5	Exome sequencing	1.24	20.60	9.71E-55	0.59	hHC014706	NM_020193
SCZ SNV	C12orf72	NA	chromosome 12 open reading frame 72	12p11.21	Exome sequencing	0.24	2.73	6.72E-03	-0.10	hHC006714	AL832339
SCZ SNV	CARD6	84674	caspase recruitment domain family, member 6	5p13.1	Exome sequencing	0.01	0.15	8.78E-01	-0.13	hHC009976	NM_032587

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
SCZ SNV	CASP4	837	caspase 4, apoptosis-related cysteine peptidase	11q22.2-q22.3	Exome sequencing	0.14	1.91	5.76E-02	-0.11	hHA040399	NM_033306
SCZ SNV	CBX5	23468	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	12q13.13	Exome sequencing	0.78	7.03	2.19E-11	0.06	hHC010825	NM_001127322
SCZ SNV	CCDC108	255101	coiled-coil domain containing 108		Exome sequencing	0.04	0.37	7.12E-01	-0.13	hHR011130	NM_152389
SCZ SNV	CCDC137	339230	coiled-coil domain containing 137	17q25.3	Exome sequencing	0.14	2.53	1.19E-02	-0.10	hHC023195	NM_199287
SCZ SNV	CCDC84	338657	coiled-coil domain containing 84	11q23.3	Exome sequencing	0.54	7.87	1.24E-13	0.10	hHR016405	NM_198489
SCZ SNV	CHD4	1108	chromodomain helicase DNA binding protein 4	12p13	Exome sequencing	0.16	3.65	3.22E-04	-0.07	hHC022301	NM_001273
SCZ SNV	CHEK2	11200	CHK2 checkpoint homolog (S. pombe)	22q11|22q12.1	Exome sequencing	1.02	9.43	3.83E-18	0.18	hHA035671	NM_001005735
SCZ SNV	CLIC5	53405	chloride intracellular channel 5	6p21.1-p12.1	Exome sequencing	0.29	3.53	4.96E-04	-0.07	hHC008730	NM_001114086
SCZ SNV	CLTCL1	8218	clathrin, heavy chain-like 1	22q11.2|22q11.21	Exome sequencing	0.90	9.68	7.00E-19	0.19	hHA036352	NM_007098
SCZ SNV	COL3A1	1281	collagen, type III, alpha 1	2q31	Exome sequencing	2.87	12.11	1.33E-26	0.30	hHR008145	NM_000090
SCZ SNV	COMMD9	29099	COMM domain containing 9	11p13	Exome sequencing	0.36	5.31	2.47E-07	-0.01	hHA037644	NM_014186
SCZ SNV	CUGBP2	10659	CUG triplet repeat, RNA binding protein 2	10p13	Exome sequencing	1.27	17.75	2.14E-45	0.51	hHR003253	NM_001025077
SCZ SNV	DAB2IP	153090	DAB2 interacting protein	9q33.1-q33.3	Exome sequencing	0.10	2.04	4.24E-02	-0.11	hHC017247	NM_032552
SCZ SNV	DNAH6	1768	dynein, axonemal, heavy chain 6	2p11.2	Exome sequencing	0.26	2.66	8.25E-03	-0.10	hHC018025	NM_001370
SCZ SNV	DNMT1	1786	DNA (cytosine-5-)-methyltransferase 1	19p13.2	Exome sequencing	0.76	11.33	4.53E-24	0.27	hHC021326	NM_001130823
SCZ SNV	DSCAM	1826	Down syndrome cell adhesion molecule	21q22.2	Exome sequencing	0.43	6.22	2.20E-09	0.03	hHA036004	NM_001389
SCZ SNV	DTX1	1840	deltex homolog 1 (Drosophila)	12q24.13	Exome sequencing	0.40	6.78	9.65E-11	0.05	hHC016350	NM_004416
SCZ SNV	EDEM2	55741	ER degradation enhancer, mannosidase alpha-like 2	20q11.22	Exome sequencing	0.26	3.75	2.24E-04	-0.07	hHC019984	NM_018217
SCZ SNV	EIF5	1983	eukaryotic translation initiation factor 5	14q32.32	Exome sequencing	0.04	0.58	5.66E-01	-0.13	hHA039962	NM_001969
SCZ SNV	ESAM	90952	endothelial cell adhesion molecule	11q24.2	Exome sequencing	0.17	2.64	8.77E-03	-0.10	hHC021286	NM_138961
SCZ SNV	EVC2	132884	Ellis van Creveld syndrome 2	4p16.2-p16.1	Exome sequencing	0.54	5.16	5.15E-07	-0.02	hHC015130	NM_147127
SCZ SNV	FASTKD5	60493	FAST kinase domains 5	20p13	Exome sequencing	0.20	2.90	4.09E-03	-0.09	hHC007631	NM_021826
SCZ SNV	FBXL10	84678	F-box and leucine-rich repeat protein 10	12q24.31	Exome sequencing	1.48	28.92	1.10E-79	0.75	hHC010330	NM_032590
SCZ SNV	FCGBP	8857	Fc fragment of IgG binding protein	19q13.1	Exome sequencing	0.55	2.84	4.96E-03	-0.09	hHC015075	NM_003890
SCZ SNV	FLAD1	80308	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	1q21.3	Exome sequencing	0.98	10.99	5.57E-23	0.25	hHA034671	NM_025207
SCZ SNV	FLJ20184	54848	hypothetical protein FLJ20184	4q24	Exome sequencing	0.32	3.90	1.25E-04	-0.06	hHC022381	NM_017700
SCZ SNV	GIF	2694	gastric intrinsic factor (vitamin B synthesis)	11q13	Exome sequencing	0.20	3.55	4.67E-04	-0.07	hHC011933	NM_005142
SCZ SNV	GPR153	387509	G protein-coupled receptor 153	1p36.31	Exome sequencing	0.48	6.40	8.10E-10	0.04	hHC016431	AL540300
SCZ SNV	GPRIN3	285513	GPRIN family member 3	4q22.1	Exome sequencing	0.41	3.00	3.01E-03	-0.09	hHR003610	NM_198281
SCZ SNV	H2AFV	94239	H2A histone family, member V	7p13	Exome sequencing	1.35	21.74	2.29E-58	0.62	hHA033353	NM_138635
SCZ SNV	HIF1A	3091	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	14q21-q24	Exome sequencing	1.29	15.00	3.31E-36	0.42	hHC020587	NM_001530
SCZ SNV	HIST1H1E	3008	histone cluster 1, H1e	6p21.3	Exome sequencing	0.84	4.44	1.36E-05	-0.04	hHR016704	NM_005321
SCZ SNV	HIVEP1	3096	human immunodeficiency virus type I enhancer binding protein 1	6p24-p22.3	Exome sequencing	0.31	4.78	3.10E-06	-0.03	hHC002239	NM_002114
SCZ SNV	HMGCR	3156	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	5q13.3-q14	Exome sequencing	1.63	8.74	4.31E-16	0.14	hCT001342	NM_000859
SCZ SNV	HTR7	3363	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	10q21-q24	Exome sequencing	0.12	1.22	2.23E-01	-0.12	hHA036763	NM_019859
SCZ SNV	IFT140	9742	intraflagellar transport 140 homolog (Chlamydomonas)	16p13.3	Exome sequencing	0.38	5.67	4.19E-08	0.00	hHC022443	NM_014714
SCZ SNV	IFT81	28981	intraflagellar transport 81 homolog (Chlamydomonas)	12q24.13	Exome sequencing	1.83	27.21	7.41E-75	0.73	hHA034159	NM_014055

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SCZ SNV	INTS10	55174	integrator complex subunit 10	8p21.3	Exome sequencing	0.31	5.15	5.35E-07	-0.02	hHC009516	NM_018142
SCZ SNV	IRS1	3667	insulin receptor substrate 1	2q36	Exome sequencing	1.43	21.24	8.91E-57	0.61	hHC002137	NM_005544
SCZ SNV	KIAA0195	9772	KIAA0195	17q25.1	Exome sequencing	0.08	1.34	1.81E-01	-0.12	hHC025255	NM_014738
SCZ SNV	KLF12	11278	Kruppel-like factor 12	13q22	Exome sequencing	1.10	18.14	1.05E-46	0.53	hHR006221	NM_007249
SCZ SNV	KLK13	26085	kallikrein-related peptidase 13	19q13.3-q13.4	Exome sequencing	0.06	1.11	2.69E-01	-0.12	hHC015195	NM_015596
SCZ SNV	KPNA1	3836	karyopherin alpha 1 (importin alpha 5)	3q21	Exome sequencing	0.98	15.00	3.37E-36	0.42	hHE041382	NM_002264
SCZ SNV	KRT4	3851	keratin 4	12q12-q13	Exome sequencing	0.35	6.77	1.03E-10	0.05	hHC022916	NM_002272
SCZ SNV	LAMA1	284217	laminin, alpha 1	18p11.31	Exome sequencing	2.02	14.87	9.22E-36	0.41	hHC007864	NM_005559
SCZ SNV	LARP7	51574	La ribonucleoprotein domain family, member 7	4q25	Exome sequencing	0.26	4.36	1.97E-05	-0.05	hHC020835	NM_016648
SCZ SNV	LRIT2	340745	leucine-rich repeat, immunoglobulin-like and transmembrane domains 2	10q23.1	Exome sequencing	0.33	4.05	7.04E-05	-0.06	hHR005602	NM_001017924
SCZ SNV	LRP1	4035	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	12q13-q14	Exome sequencing	1.73	12.32	2.68E-27	0.31	hCT000695	NM_002332
SCZ SNV	MACF1	23499	microtubule-actin crosslinking factor 1	1p32-p31	Exome sequencing	1.99	22.61	4.19E-61	0.64	hHA035413	NM_012090
SCZ SNV	MBTPS1	8720	membrane-bound transcription factor peptidase, site 1	16|16q24	Exome sequencing	0.59	10.10	3.47E-20	0.21	hHA035034	NM_003791
SCZ SNV	MIOS	54468	missing oocyte, meiosis regulator, homolog (Drosophila)	7p22-p21	Exome sequencing	0.76	7.15	1.07E-11	0.07	hHC004314	AL136892
SCZ SNV	MKI67	4288	antigen identified by monoclonal antibody Ki-67	10q25-qter	Exome sequencing	2.68	22.97	3.37E-62	0.65	hHC010551	NM_002417
SCZ SNV	MUC5B	727897	mucin 5B, oligomeric mucus/gel-forming		Exome sequencing	0.43	4.23	3.34E-05	-0.05	hHR017878	NM_002458
SCZ SNV	MYH10	4628	myosin, heavy chain 10, non-muscle	17p13	Exome sequencing	0.02	0.30	7.61E-01	-0.13	hHC015906	NM_005964
SCZ SNV	MYH9	4627	myosin, heavy chain 9, non-muscle	22q13.1	Exome sequencing	0.05	1.26	2.08E-01	-0.12	hHC023712	NM_002473
SCZ SNV	N4BP2L2	10443	NEDD4 binding protein 2-like 2	13q13.1	Exome sequencing	0.90	11.98	3.68E-26	0.30	hHC016908	NM_014887
SCZ SNV	NCAN	1463	neurocan	19p12	Exome sequencing	1.30	15.11	1.36E-36	0.42	hHC008161	NM_004386
SCZ SNV	NFE2L3	9603	nuclear factor (erythroid-derived 2)-like 3	7p15-p14	Exome sequencing	1.12	7.54	9.84E-13	0.09	hHC028656	BC056142
SCZ SNV	NRIP1	8204	nuclear receptor interacting protein 1	21q11.2	Exome sequencing	0.01	0.09	9.31E-01	-0.13	hHC003199	NM_003489
SCZ SNV	NUP214	8021	nucleoporin 214kDa	9q34.1	Exome sequencing	0.59	11.37	3.45E-24	0.27	hHC009957	BC105998
SCZ SNV	NUP54	53371	nucleoporin 54kDa	4q21.1	Exome sequencing	1.19	15.99	1.56E-39	0.46	hHC012766	NM_017426
SCZ SNV	ODZ1	10178	odz, odd Oz/ten-m homolog 1(Drosophila)	Xq25	Exome sequencing	0.58	6.49	4.88E-10	0.04	hHC006993	NM_014253
SCZ SNV	PAG1	55824	phosphoprotein associated with glycosphingolipid microdomains 1	8q21.13	Exome sequencing	1.10	14.63	5.72E-35	0.41	hHC010986	NM_018440
SCZ SNV	PAPPA2	60676	pappalysin 2	1q23-q25	Exome sequencing	0.39	4.40	1.66E-05	-0.05	hHA039447	NM_020318
SCZ SNV	PHF23	79142	PHD finger protein 23	17p13.1	Exome sequencing	0.21	4.30	2.48E-05	-0.05	hHC011748	NM_024297
SCZ SNV	PLCL2	23228	phospholipase C-like 2	3p24.3	Exome sequencing	0.10	0.82	4.14E-01	-0.13	hHC011901	NM_015184
SCZ SNV	PLK3	1263	polo-like kinase 3 (Drosophila)	1p34.1	Exome sequencing	0.98	12.31	2.89E-27	0.31	hHC014816	NM_004073
SCZ SNV	PML	5371	promyelocytic leukemia	15q22	Exome sequencing	0.14	2.75	6.46E-03	-0.10	hHA038029	NM_033238
SCZ SNV	PPP1R14D	54866	protein phosphatase 1, regulatory (inhibitor) subunit 14D	15q15.1	Exome sequencing	0.08	0.91	3.64E-01	-0.13	hHC018153	NM_001130143
SCZ SNV	PSG1	5669	pregnancy specific beta-1-glycoprotein 1	19q13.2	Exome sequencing	0.54	5.71	3.37E-08	0.01	hHC031110	NM_006905
SCZ SNV	RAD54L2	23132	RAD54-like 2 (S. cerevisiae)	3p21.2	Exome sequencing	0.68	7.02	2.35E-11	0.06	hHC024061	NM_015106
SCZ SNV	RBBP5	5929	retinoblastoma binding protein 5	1q32	Exome sequencing	0.00	0.04	9.68E-01	-0.13	hHC015649	NM_005057
SCZ SNV	RECK	8434	reversion-inducing-cysteine-rich protein with kazal motifs	9p13.3	Exome sequencing	0.20	2.50	1.32E-02	-0.10	hHC004414	NM_021111
SCZ SNV	RFX3	5991	regulatory factor X, 3 (influences HLA class II expression)	9p24.2	Exome sequencing	1.11	8.63	8.85E-16	0.14	hHC006894	NM_134428
SCZ SNV	RGS12	6002	regulator of G-protein signaling 12	4p16.3	Exome sequencing	0.85	9.13	3.04E-17	0.16	hHA034713	BC118594

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
SCZ SNV	RRP1B	23076	ribosomal RNA processing 1 homolog B (S. cerevisiae)	21q22.3	Exome sequencing	1.19	17.71	2.71E-45	0.51	hHR002221	NM_015056
SCZ SNV	RUNX3	864	runt-related transcription factor 3	1p36	Exome sequencing	0.01	0.13	8.94E-01	-0.13	hHC017470	NM_001031680
SCZ SNV	SAP30BP	29115	SAP30 binding protein	17q25.1	Exome sequencing	0.25	4.86	2.12E-06	-0.03	hHC011964	NM_013260
SCZ SNV	SEC24B	10427	SEC24 family, member B (S. cerevisiae)	4q25	Exome sequencing	0.88	17.58	7.46E-45	0.51	hHC003807	NM_006323
SCZ SNV	SLC19A2	10560	solute carrier family 19 (thiamine transporter), member 2	1q23.3	Exome sequencing	1.31	14.10	3.36E-33	0.39	hHC006606	NM_006996
SCZ SNV	SLC25A1	6576	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	22q11.21	Exome sequencing	0.48	8.50	2.19E-15	0.13	hHC024586	NM_005984
SCZ SNV	SLC26A8	116369	solute carrier family 26, member 8	6p21	Exome sequencing	0.21	4.33	2.16E-05	-0.05	hHA036600	NM_052961
SCZ SNV	SLC38A2	54407	solute carrier family 38, member 2	12q	Exome sequencing	0.50	7.27	5.30E-12	0.08	hHC001832	NM_018976
SCZ SNV	SMCHD1	23347	structural maintenance of chromosomes flexible hinge domain containing 1	18p11.32	Exome sequencing	1.20	15.02	2.83E-36	0.42	hHR002326	NM_015295
SCZ SNV	SPATA22	84690	spermatogenesis associated 22	17p13.3	Exome sequencing	0.39	2.48	1.38E-02	-0.10	hHC011058	AK295299
SCZ SNV	SPATA5	166378	spermatogenesis associated 5		Exome sequencing	2.46	15.74	1.10E-38	0.45	hHE041009	NM_145207
SCZ SNV	SPIB	6689	Spi-B transcription factor (Spi-1/PU.1 related)	19q13.3-q13.4	Exome sequencing	0.28	3.28	1.21E-03	-0.08	hHC018407	NM_003121
SCZ SNV	ST3GAL6	10402	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	3q12.1	Exome sequencing	0.53	5.50	9.89E-08	0.00	hHC012897	AK001922
SCZ SNV	STAG1	10274	stromal antigen 1	3q22.3	Exome sequencing	1.79	24.09	1.19E-65	0.67	hHA037017	NM_005862
SCZ SNV	TBC1D14	NA	TBC1 domain family, member 14	4p16.1	Exome sequencing	1.47	24.56	4.43E-67	0.68	hHC006885	NM_020773
SCZ SNV	THBS1	7057	thrombospondin 1	15q15	Exome sequencing	2.94	13.79	3.63E-32	0.37	hHC004021	NM_003246
SCZ SNV	TLK2	11011	tousled-like kinase 2	17q23	Exome sequencing	0.66	11.43	2.13E-24	0.27	hHC030724	NM_006852
SCZ SNV	TRAK1	22906	trafficking protein, kinesin binding 1	3p25.3-p24.1	Exome sequencing	0.61	4.79	2.94E-06	-0.03	hHR003862	NM_014965
SCZ SNV	TUB	NA	tubby homolog (mouse)	11p15.5	Exome sequencing	0.39	5.47	1.15E-07	0.00	hHA038335	NM_003320
SCZ SNV	TUSC4	10641	tumor suppressor candidate 4	3p21.3	Exome sequencing	0.20	5.47	1.16E-07	0.00	hHC022724	NM_006545
SCZ SNV	UBQLN1	29979	ubiquilin 1	9q22|9q21.2-q21.3	Exome sequencing	0.40	6.31	1.39E-09	0.03	hHA035472	NM_013438
SCZ SNV	UBR5	NA	ubiquitin protein ligase E3 component n-recognin 5	8q22	Exome sequencing	1.53	15.90	3.02E-39	0.45	hHC001627	CD511402
SCZ SNV	UGT1A3	54659	UDP glucuronosyltransferase 1 family, polypeptide A3	2q37	Exome sequencing	0.43	4.92	1.61E-06	-0.03	hHC008744	NM_019093
SCZ SNV	URB2	9816	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	1q42.13	Exome sequencing	0.58	6.65	2.04E-10	0.05	hHC005092	NM_014777
SCZ SNV	XPR1	9213	xenotropic and polytropic retrovirus receptor	1q25.1	Exome sequencing	2.29	20.67	5.70E-55	0.60	hHR006568	NM_004736
SCZ SNV	YLPM1	56252	YLP motif containing 1	14q24.3	Exome sequencing	0.87	18.24	4.98E-47	0.53	hHC011709	NM_019589
SCZ SNV	ZBTB40	9923	zinc finger and BTB domain containing 40		Exome sequencing	1.16	19.24	2.58E-50	0.56	hHE042021	NM_001083621
SCZ SNV	ZNF14	7561	zinc finger protein 14	19p13.3-p13.2	Exome sequencing	0.97	18.12	1.23E-46	0.53	hHC019150	NM_021030
SCZ SNV	ZNF229	7772	zinc finger protein 229	19q13.31	Exome sequencing	0.74	6.66	1.92E-10	0.05	hHC016846	NM_014518
SCZ SNV	ZNF530	348327	zinc finger protein 530	19q13.43	Exome sequencing	0.87	9.69	6.44E-19	0.19	hHC015238	NM_020880
SCZ SNV	ABCG4	64137	ATP-binding cassette, sub-family G (WHITE), member 4	11q23.3	Exome sequencing	-0.77	-10.80	2.33E-22	0.24	hHC019774	NM_022169
SCZ SNV	ADAMTS17	170691	ADAM metallopeptidase with thrombospondin type 1 motif, 17	15q24	Exome sequencing	-0.95	-11.14	1.84E-23	0.26	hHE041152	NM_139057
SCZ SNV	ADAMTS3	9508	ADAM metallopeptidase with thrombospondin type 1 motif, 3	4q13.3	Exome sequencing	-0.14	-0.96	3.36E-01	-0.13	hHC006183	NM_014243
SCZ SNV	ADCY7	113	adenylate cyclase 7	16q12-q13	Exome sequencing	-1.01	-8.74	4.39E-16	0.14	hHC003521	NM_001114
SCZ SNV	ADCY9	115	adenylate cyclase 9	16p13.3	Exome sequencing	-0.12	-1.68	9.35E-02	-0.12	hHC016923	NM_001116
SCZ SNV	AHNAK2	113146	AHNAK nucleoprotein 2	14q32.33	Exome sequencing	-1.16	-13.65	1.08E-31	0.37	hHR010378	NM_138420
SCZ SNV	ANO9	338440	anoctamin 9	11p15.5	Exome sequencing	-0.06	-0.78	4.35E-01	-0.13	hHC024276	NM_001012302

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
SCZ SNV	AP2A2	161	adaptor-related protein complex 2, alpha 2 subunit	11p15.5	Exome sequencing	-0.52	-8.78	3.27E-16	0.15	hHC018021	NM_012305
SCZ SNV	BLNK	29760	B-cell linker	10q23.2-q23.33	Exome sequencing	-1.82	-9.29	1.01E-17	0.17	hHC005937	NM_013314
SCZ SNV	C16orf62	57020	chromosome 16 open reading frame 62	16p12.3	Exome sequencing	-0.73	-12.39	1.58E-27	0.31	hHC017915	NM_020314
SCZ SNV	C18orf1	753	chromosome 18 open reading frame 1	18p11.2	Exome sequencing	-0.04	-0.41	6.79E-01	-0.13	hHC001974	NM_001003674
SCZ SNV	C1orf185	284546	chromosome 1 open reading frame 185	1p32.3	Exome sequencing	-0.27	-4.21	3.68E-05	-0.05	hHR007866	NM_001136508
SCZ SNV	CACNA1I	8911	calcium channel, voltage-dependent, T type, alpha 1I subunit	22q13.1	Exome sequencing	-0.98	-10.96	6.96E-23	0.25	hHC014460	NM_021096
SCZ SNV	CAMK4	814	calcium/calmodulin-dependent protein kinase IV	5q21.3	Exome sequencing	-0.10	-1.00	3.20E-01	-0.13	hHC017173	NM_001744
SCZ SNV	CANX	821	calnexin	5q35	Exome sequencing	-0.15	-2.77	6.11E-03	-0.10	hHC012844	NM_001746
SCZ SNV	CCDC39	339829	coiled-coil domain containing 39	3q26.33	Exome sequencing	-1.66	-12.16	9.03E-27	0.30	hHR003101	NM_181426
SCZ SNV	CELSR2	1952	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	1p21	Exome sequencing	-0.26	-4.17	4.21E-05	-0.05	hHC005875	NM_001408
SCZ SNV	CIT	11113	citron (rho-interacting, serine/threonine kinase 21)	12q24	Exome sequencing	-2.55	-32.81	4.26E-90	0.80	hHR004773	NM_007174
SCZ SNV	COG1	NA	component of oligomeric golgi complex 1	17q25.1	Exome sequencing	-0.81	-11.80	1.40E-25	0.29	hHC015718	NM_018714
SCZ SNV	CRYBG3	NA	beta-gamma crystallin domain containing 3	3q11.2	Exome sequencing	-0.52	-6.45	6.25E-10	0.04	hHR008147	NM_153605
SCZ SNV	CSPG4	1464	chondroitin sulfate proteoglycan 4	15q24.2	Exome sequencing	-1.19	-10.74	3.43E-22	0.24	hHC015470	NM_001897
SCZ SNV	CYTH1	9267	cytohesin 1	17q25	Exome sequencing	-0.22	-2.99	3.05E-03	-0.09	hHC005431	NM_004762
SCZ SNV	DCDC5	196296	doublecortin domain containing 5	11p14.1-p13	Exome sequencing	-0.15	-1.89	5.97E-02	-0.11	hHC016351	AK128035
SCZ SNV	DDHD2	23259	DDHD domain containing 2	8p12	Exome sequencing	-0.37	-7.28	4.87E-12	0.08	hHC019481	NM_015214
SCZ SNV	DDX10	1662	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	11q22-q23	Exome sequencing	-0.30	-5.60	5.78E-08	0.00	hHC028052	NM_004398
SCZ SNV	DGCR2	9993	DiGeorge syndrome critical region gene 2	22q11.21	Exome sequencing	-0.73	-12.66	2.09E-28	0.33	hHR017731	NM_005137
SCZ SNV	DHX8	1659	DEAH (Asp-Glu-Ala-His) box polypeptide 8	17q21.31	Exome sequencing	-0.06	-1.07	2.84E-01	-0.13	hHC025611	NM_004941
SCZ SNV	DOCK1	1793	dedicator of cytokinesis 1	10q26.13-q26.3	Exome sequencing	-1.36	-14.12	2.98E-33	0.39	hHC001930	NM_001380
SCZ SNV	DPYD	1806	dihydropyrimidine dehydrogenase	1p22	Exome sequencing	-0.42	-3.90	1.24E-04	-0.06	hHC002214	NM_000110
SCZ SNV	EMR3	84658	egf-like module containing, mucin-like, hormone receptor-like 3	19p13.1	Exome sequencing	-0.36	-3.27	1.25E-03	-0.08	hHC010684	NM_032571
SCZ SNV	FAM13C	NA	family with sequence similarity 13, member C	10q21.1	Exome sequencing	-0.98	-10.74	3.57E-22	0.24	hHC001933	NM_198215
SCZ SNV	FBXO7	25793	F-box protein 7	22q12-q13	Exome sequencing	-0.84	-13.39	8.06E-31	0.36	hHC012997	NM_012179
SCZ SNV	FILIP1	27145	filamin A interacting protein 1	6q14.1	Exome sequencing	-1.46	-11.06	3.26E-23	0.25	hHC011197	NM_015687
SCZ SNV	FRY	10129	furry homolog (Drosophila)	13q13.1	Exome sequencing	-0.55	-9.11	3.53E-17	0.16	hHC002191	NM_023037
SCZ SNV	GLIPR1L2	144321	GLI pathogenesis-related 1 like 2	12q21.1-q21.2	Exome sequencing	-0.18	-1.05	2.93E-01	-0.13	hHC007031	BX640916
SCZ SNV	GLS	2744	glutaminase	2q32-q34	Exome sequencing	-2.19	-24.02	1.90E-65	0.67	hHR007488	AF327434
SCZ SNV	GNAO1	2775	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	16q13	Exome sequencing	-0.68	-9.57	1.48E-18	0.18	hHA035036	NM_020988
SCZ SNV	GPR115	221393	G protein-coupled receptor 115	6p12.3	Exome sequencing	-0.38	-4.27	2.87E-05	-0.05	hHC013926	NM_153838
SCZ SNV	HECTD1	25831	HECT domain containing 1	14q12	Exome sequencing	-0.20	-4.46	1.28E-05	-0.04	hHC027015	NM_015382
SCZ SNV	HLA-C	3107	major histocompatibility complex, class I, C	6p21.3	Exome sequencing	-0.88	-6.18	2.71E-09	0.03	hHC025166	NM_002117
SCZ SNV	INPP5A	3632	inositol polyphosphate-5-phosphatase, 40kDa	10q26.3	Exome sequencing	-1.02	-12.49	7.51E-28	0.32	hHC004252	NM_005539
SCZ SNV	INTS1	26173	integrator complex subunit 1	7p22.3	Exome sequencing	-0.34	-4.70	4.51E-06	-0.03	hHR017811	NM_001080453
SCZ SNV	ITGA3	3675	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	17q21.33	Exome sequencing	-0.24	-4.40	1.63E-05	-0.05	hHC024280	NM_002204
SCZ SNV	ITGA6	3655	integrin, alpha 6	2q31.1	Exome sequencing	-0.30	-3.27	1.23E-03	-0.08	hHC001949	NM_000210
SCZ SNV	KCNJ12	3768	potassium inwardly-rectifying channel, subfamily J, member 12		Exome sequencing	-2.94	-26.49	8.72E-73	0.71	hHR007348	NM_021012

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SCZ SNV	KIAA1109	84162	KIAA1109	4q27	Exome sequencing	-0.12	-1.94	5.31E-02	-0.11	hHC013197	NM_015312
SCZ SNV	LAMA2	3908	laminin, alpha 2	6q22-q23	Exome sequencing	-0.78	-7.68	4.06E-13	0.09	hHC020800	NM_000426
SCZ SNV	LRIT1	26103	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	10q23	Exome sequencing	-0.13	-1.87	6.30E-02	-0.11	hHC016679	NM_015613
SCZ SNV	NAPRT1	93100	nicotinate phosphoribosyltransferase domain containing 1	8q24.3	Exome sequencing	-0.31	-3.47	6.22E-04	-0.08	hHC025201	NM_145201
SCZ SNV	NCOR2	9612	nuclear receptor co-repressor 2	12q24	Exome sequencing	-0.67	-9.64	9.03E-19	0.19	hHR003503	NM_006312
SCZ SNV	NEB	4703	nebulin	2q22	Exome sequencing	-0.81	-8.35	5.82E-15	0.13	hHC002922	AK021567
SCZ SNV	NLRC5	84166	NLR family, CARD domain containing 5	16q13	Exome sequencing	-0.86	-7.06	1.82E-11	0.07	hHC011400	NM_032206
SCZ SNV	OPA3	80207	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)		Exome sequencing	-1.26	-15.03	2.63E-36	0.42	hHR026693	NM_001017989
SCZ SNV	OR4C46	119749	olfactory receptor, family 4, subfamily C, member 46	11p11.12	Exome sequencing	-0.07	-1.75	8.09E-02	-0.12	hHR030660	NM_001004703
SCZ SNV	P2RY2	5029	purinergic receptor P2Y, G-protein coupled, 2	11q13.5-q14.1	Exome sequencing	-0.15	-1.79	7.42E-02	-0.12	hHC015910	NM_176072
SCZ SNV	PDE4DIP	9659	phosphodiesterase 4D interacting protein	1q12	Exome sequencing	-1.60	-9.28	1.11E-17	0.17	hHC018232	NM_014644
SCZ SNV	PIK3CB	5291	phosphoinositide-3-kinase, catalytic, beta polypeptide	3q22.3	Exome sequencing	-0.58	-10.79	2.43E-22	0.24	hHC022373	NM_006219
SCZ SNV	PITPNM1	9600	phosphatidylinositol transfer protein, membrane-associated 1	11q13	Exome sequencing	-0.48	-9.08	4.43E-17	0.16	hHC019426	NM_004910
SCZ SNV	PLA2G12B	84647	phospholipase A2, group XIIB	10q22.1	Exome sequencing	-1.77	-16.19	3.37E-40	0.46	hHC008856	NM_032562
SCZ SNV	PRDX6	9588	peroxiredoxin 6	1q25.1	Exome sequencing	-0.89	-12.81	6.80E-29	0.33	hHC030001	NM_004905
SCZ SNV	PRKCB	5579	protein kinase C, beta	16p11.2	Exome sequencing	-3.02	-29.72	6.74E-82	0.76	hHC021733	NM_002738
SCZ SNV	PTPRM	5797	protein tyrosine phosphatase, receptor type, M	18p11.2	Exome sequencing	-0.54	-8.81	2.75E-16	0.15	hHC015648	NM_001105244
SCZ SNV	RARG	5916	retinoic acid receptor, gamma	12q13	Exome sequencing	-1.09	-10.48	2.29E-21	0.23	hHC019998	NM_000966
SCZ SNV	RASGRP1	10125	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	15q14	Exome sequencing	-2.03	-17.98	3.59E-46	0.52	hHC002998	NM_005739
SCZ SNV	RB1CC1	9821	RB1-inducible coiled-coil 1	8q11	Exome sequencing	-0.43	-4.36	1.92E-05	-0.05	hHC006191	NM_014781
SCZ SNV	RPH3A	22895	rabphilin 3A homolog (mouse)	12q24.13	Exome sequencing	-2.22	-16.33	1.11E-40	0.47	hHR012249	NM_014954
SCZ SNV	SBNO1	55206	strawberry notch homolog 1 (Drosophila)	12q24.31	Exome sequencing	-0.65	-7.39	2.50E-12	0.08	hHC011312	AK096864
SCZ SNV	SDF4	51150	stromal cell derived factor 4	1p36.33	Exome sequencing	-0.11	-1.22	2.23E-01	-0.12	hHA040703	NM_016547
SCZ SNV	SERPINI1	5274	serpin peptidase inhibitor, clade I (neuroserpin), member 1	3q26.1	Exome sequencing	-2.48	-22.05	2.46E-59	0.63	hHC002254	NM_005025
SCZ SNV	SETD1A	9739	SET domain containing 1A	16p11.2	Exome sequencing	-0.33	-7.76	2.52E-13	0.10	hHC024151	NM_014712
SCZ SNV	SLC17A1	6568	solute carrier family 17 (sodium phosphate), member 1	6p23-p21.3	Exome sequencing	-0.24	-4.34	2.08E-05	-0.05	hHC005716	NM_005074
SCZ SNV	SLC18A2	6571	solute carrier family 18 (vesicular monoamine), member 2	10q25	Exome sequencing	-0.02	-0.12	9.01E-01	-0.13	hHC006479	BC030593
SCZ SNV	SLC4A8	9498	solute carrier family 4, sodium bicarbonate cotransporter, member 8		Exome sequencing	-0.35	-4.70	4.49E-06	-0.03	hHC003605	NM_001039960
SCZ SNV	SLIT2	9353	slit homolog 2 (Drosophila)	4p15.2	Exome sequencing	-0.76	-7.97	6.89E-14	0.11	hHC003227	NM_004787
SCZ SNV	SLIT3	6586	slit homolog 3 (Drosophila)	5q35	Exome sequencing	-1.32	-11.99	3.37E-26	0.30	hHC020243	NM_003062
SCZ SNV	SMAP2	64744	small ArfGAP2	1p35.3-p34.1	Exome sequencing	-1.31	-17.08	3.47E-43	0.49	hHC011020	NM_022733
SCZ SNV	SPTLC2	9517	serine palmitoyltransferase, long chain base subunit 2	14q24.3-q31	Exome sequencing	-0.40	-4.20	3.73E-05	-0.05	hHC006581	NM_004863
SCZ SNV	SSBP3	23648	single stranded DNA binding protein 3	1p32.3	Exome sequencing	-0.62	-10.77	2.73E-22	0.24	hHC021338	NM_001009955
SCZ SNV	SSFA2	6744	sperm specific antigen 2	2q31.3	Exome sequencing	-0.87	-12.24	5.04E-27	0.31	hHC004019	NM_001130445
SCZ SNV	STAC2	342667	SH3 and cysteine rich domain 2	17q12	Exome sequencing	-1.01	-15.50	6.72E-38	0.44	hHC021697	NM_198993
SCZ SNV	STAP2	55620	signal transducing adaptor family member 2	19p13.3	Exome sequencing	-1.07	-12.85	4.83E-29	0.33	hHC023097	NM_017720

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
SCZ SNV	SYNGAP1	8831	synaptic Ras GTPase activating protein 1 homolog (rat)	6p21.3	Exome sequencing	-0.05	-0.57	5.67E-01	-0.13	hHC014146	NM_006772
SCZ SNV	SYNM	23336	synemin, intermediate filament protein	15q26.3	Exome sequencing	-2.31	-27.00	2.99E-74	0.72	hHC005198	NM_145728
SCZ SNV	TAF7L	54457	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa	Xq22.1	Exome sequencing	-0.46	-4.47	1.23E-05	-0.04	hHC015924	NM_024885
SCZ SNV	TEKT5	146279	tektin 5	16p13.13	Exome sequencing	-0.08	-0.82	4.12E-01	-0.13	hHC012570	NM_144674
SCZ SNV	TEP1	7011	telomerase-associated protein 1	14q11.2	Exome sequencing	-0.18	-1.80	7.30E-02	-0.12	hHC015032	NM_007110
SCZ SNV	TGM6	343641	transglutaminase 6	20p13	Exome sequencing	-0.27	-3.91	1.21E-04	-0.06	hHC022191	NM_198994
SCZ SNV	TOP3B	8940	topoisomerase (DNA) III beta	22q11.22	Exome sequencing	-0.40	-9.52	2.09E-18	0.18	hHR022284	NM_003935
SCZ SNV	TOR1AIP1	26092	torsin A interacting protein 1	1q24.2	Exome sequencing	-0.89	-17.47	1.84E-44	0.51	hHR003335	NM_015602
SCZ SNV	TREM2	54209	triggering receptor expressed on myeloid cells 2	6p21.1	Exome sequencing	-1.62	-7.35	3.20E-12	0.08	hHC011302	NM_018965
SCZ SNV	UNC13C	440279	unc-13 homolog C (C. elegans)	15q21.3	Exome sequencing	-2.56	-22.49	9.84E-61	0.64	hHC003835	NM_001080534
SCZ SNV	UPF2	26019	UPF2 regulator of nonsense transcripts homolog (yeast)	10p14-p13	Exome sequencing	-0.18	-3.73	2.37E-04	-0.07	hHC015194	NM_080599
SCZ SNV	VN1R4	317703	vomeronasal 1 receptor 4	19q13.41	Exome sequencing	-0.61	-5.81	2.02E-08	0.01	hHR029809	NM_173857
SCZ SNV	VPS11	55823	vacuolar protein sorting 11 homolog (S. cerevisiae)	11q23	Exome sequencing	-0.76	-15.28	3.80E-37	0.43	hHC013758	NM_021729
SCZ SNV	VPS35	55737	vacuolar protein sorting 35 homolog (S. cerevisiae)	16q12	Exome sequencing	-0.77	-13.16	4.65E-30	0.35	hHC011701	NM_018206
SCZ SNV	ZDHHC23	254887	zinc finger, DHHC-type containing 23	3q13.31	Exome sequencing	-2.11	-19.15	5.04E-50	0.56	hHC011184	NM_173570
ASD CNV	SEPT5	5413	septin 5	22q11.21-q11.23|22q11.21	CNV Association	0.11	1.38	1.69E-01	-0.12	hHC020572	NM_002688
ASD CNV	ABHD11	83451	abhydrolase domain containing 11	7q11.23	CNV Association	0.04	0.47	6.41E-01	-0.13	hHA039837	NR_026912
ASD CNV	ADM2	79924	adrenomedullin 2	22q13.33	CNV Association	0.43	9.65	8.34E-19	0.19	hHR024334	NM_024866
ASD CNV	ALDOA	226	aldolase A, fructose-bisphosphate	16p11.2	CNV Association	0.32	5.01	1.08E-06	-0.02	hHA038102	NM_000034
ASD CNV	ARIH1	25820	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	15q24	CNV Association	0.42	9.17	2.29E-17	0.17	hHR011923	NM_005744
ASD CNV	ARVCF	421	armadillo repeat gene deletes in velocardiofacial syndrome	22q11.21	CNV Association	0.57	10.39	4.53E-21	0.22	hHC025769	NM_001670
ASD CNV	ASPHD1	253982	aspartate beta-hydroxylase domain containing 1	16p11.2	CNV Association	0.74	8.54	1.69E-15	0.14	hHC008219	AF070642
ASD CNV	BAZ1B	9031	bromodomain adjacent to zinc finger domain, 1B	7q11.23	CNV Association	0.15	2.61	9.52E-03	-0.10	hHC018905	NM_032408
ASD CNV	BBS4	585	Bardet-Biedl syndrome 4	15q22.3-q23	CNV Association	0.02	0.21	8.32E-01	-0.13	hHC015344	NM_033028
ASD CNV	BCL7B	9275	B-cell CLL/lymphoma 7B	7q11.23	CNV Association	0.21	3.15	1.84E-03	-0.09	hHC028591	NM_001707
ASD CNV	BCL9	607	B-cell CLL/lymphoma 9	1q21	CNV Association	2.02	23.33	2.50E-63	0.66	hHC014098	NM_004326
ASD CNV	C16orf53	79447	chromosome 16 open reading frame 53	16p11.2	CNV Association	1.29	19.62	1.49E-51	0.57	hHC013809	NM_024516
ASD CNV	C20orf11	54994	chromosome 20 open reading frame 11	20q13.33	CNV Association	1.01	15.76	9.57E-39	0.45	hHC017116	NM_017896
ASD CNV	C22orf29	79680	chromosome 22 open reading frame 29	22q11.21	CNV Association	0.07	1.38	1.70E-01	-0.12	hHC014745	NM_024627
ASD CNV	CBWD1	55871	COBW domain containing 1	9p24.3	CNV Association	0.52	7.79	2.04E-13	0.10	hHC030237	NM_018491
ASD CNV	CD276	80381	CD276 molecule	15q23-q24	CNV Association	0.17	2.71	7.30E-03	-0.10	hHR022696	NM_001024736
ASD CNV	CDC45L	8318	CDC45 cell division cycle 45-like (S. cerevisiae)	22q11.21	CNV Association	3.89	25.04	1.59E-68	0.69	hHC004040	NM_003504
ASD CNV	CHKB	1120	choline kinase beta	22q13.33	CNV Association	0.60	9.55	1.66E-18	0.18	hHA040201	NM_005198
ASD CNV	CHRNA7	1139	cholinergic receptor, nicotinic, alpha 7	15q14	CNV Association	0.83	5.64	4.76E-08	0.00	hHR025141	NM_000746
ASD CNV	CLDN4	1364	claudin 4	7q11.23	CNV Association	0.02	0.14	8.86E-01	-0.13	hHC022740	NM_001305
ASD CNV	CLIP2	7461	CAP-GLY domain containing linker protein 2	7q11.23	CNV Association	0.18	2.69	7.63E-03	-0.10	hHC008431	NM_003388
ASD CNV	CLTCL1	8218	clathrin, heavy chain-like 1	22q11.2|22q11.21	CNV Association	0.90	9.68	7.00E-19	0.19	hHA036352	NM_007098
ASD CNV	CPT1B	1375	carnitine palmitoyltransferase 1B (muscle)	22q13.33	CNV Association	0.76	11.87	8.01E-26	0.29	hHA034492	NM_152247

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD CNV	CRKL	1399	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	22q11|22q11.21	CNV Association	0.05	0.94	3.49E-01	-0.13	hHC019229	NM_005207
ASD CNV	CSTF2T	23283	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	10q11	CNV Association	0.39	4.97	1.29E-06	-0.02	hHC003317	NM_015235
ASD CNV	DGCR10	26222	DiGeorge syndrome critical region gene 10	22q11	CNV Association	0.56	4.23	3.37E-05	-0.05	hHR005214	NR_026651
ASD CNV	DGCR11	25786	DiGeorge syndrome critical region gene 11	22q11.21	CNV Association	0.00	0.03	9.72E-01	-0.13	hHR014573	NR_024157
ASD CNV	DGCR14	8220	DiGeorge syndrome critical region gene 14		CNV Association	0.45	5.40	1.60E-07	-0.01	hHR013003	NM_022719
ASD CNV	DGCR5	NA	DiGeorge syndrome critical region gene 5 (non-protein coding)	22q11	CNV Association	0.65	7.67	4.41E-13	0.09	hHC030047	X91348
ASD CNV	DGCR8	54487	DiGeorge syndrome critical region gene 8	22q11.2	CNV Association	0.82	6.25	1.92E-09	0.03	hHC018376	NM_022720
ASD CNV	DIDO1	11083	death inducer-obliterator 1		CNV Association	1.04	8.76	3.80E-16	0.15	hHC005414	NM_033081
ASD CNV	DKK1	22943	dickkopf homolog 1 (Xenopus laevis)	10q11.2	CNV Association	0.01	0.11	9.12E-01	-0.13	hHC011527	NM_012242
ASD CNV	DNAJC30	84277	DnaJ (Hsp40) homolog, subfamily C, member 30	7q11.23	CNV Association	0.20	3.51	5.41E-04	-0.07	hHR012485	NM_032317
ASD CNV	DOCK4	9732	dedicator of cytokinesis 4	7q31.1	CNV Association	0.12	1.39	1.67E-01	-0.12	hHC005442	NM_014705
ASD CNV	FAM57B	83723	family with sequence similarity 57, member B	16p11.2	CNV Association	0.88	12.37	1.94E-27	0.31	hHC021273	NM_031478
ASD CNV	FOXD4L1	200350	forkhead box D4-like 1	2q14.1	CNV Association	0.03	0.40	6.90E-01	-0.13	hHC030644	NM_012184
ASD CNV	FRMD4B	23150	FERM domain containing 4B	3p14.1	CNV Association	1.78	14.47	1.97E-34	0.40	hHC004841	NM_015123
ASD CNV	GABRB3	2562	gamma-aminobutyric acid (GABA) A receptor, beta 3	15q11.2-q12	CNV Association	0.21	2.36	1.90E-02	-0.10	hHA040248	NM_021912
ASD CNV	GDPD3	79153	glycerophosphodiester phosphodiesterase domain containing 3	16p11.2	CNV Association	0.24	4.35	2.03E-05	-0.05	hHC023507	NM_024307
ASD CNV	GJA5	2702	gap junction protein, alpha 5, 40kDa	1q21.1	CNV Association	0.25	3.02	2.82E-03	-0.09	hHC014579	NM_005266
ASD CNV	GTF2IRD1	9569	GTF2I repeat domain containing 1	7q11.23	CNV Association	1.68	25.04	1.64E-68	0.69	hHC005789	NM_016328
ASD CNV	HCN4	10021	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	15q24-q25	CNV Association	0.39	8.56	1.40E-15	0.14	hHC024348	NM_005477
ASD CNV	HIRA	7290	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	22q11.2|22q11.21	CNV Association	0.58	11.24	9.08E-24	0.26	hHC025127	NM_003325
ASD CNV	HIRIP3	8479	HIRA interacting protein 3	16p11.2	CNV Association	0.16	2.28	2.33E-02	-0.11	hHA038020	NM_003609
ASD CNV	KCTD13	253980	potassium channel tetramerisation domain containing 13	16p11.2	CNV Association	0.16	2.41	1.68E-02	-0.10	hHC015500	NM_178863
ASD CNV	KIF22	3835	kinesin family member 22		CNV Association	0.22	3.55	4.67E-04	-0.07	hHC016722	AK294380
ASD CNV	KLHL22	84861	kelch-like 22 (Drosophila)	22q11.21	CNV Association	0.38	8.72	5.11E-16	0.14	hHC021778	NM_032775
ASD CNV	LZTR1	8216	leucine-zipper-like transcription regulator 1	22q11.21|22q11.1-q11.2	CNV Association	0.56	10.82	1.98E-22	0.24	hHC019168	NM_006767
ASD CNV	MAGI1	9223	membrane associated guanylate kinase, WW and PDZ domain containing 1	3p14.1	CNV Association	0.12	1.76	7.93E-02	-0.12	hHC022435	NM_015520
ASD CNV	MBL2	4153	mannose-binding lectin (protein C) 2, soluble (opsonic defect)	10q11.2-q21	CNV Association	0.23	2.28	2.37E-02	-0.11	hHC003939	NM_000242
ASD CNV	MBTPS1	8720	membrane-bound transcription factor peptidase, site 1	16|16q24	CNV Association	0.59	10.10	3.47E-20	0.21	hHA035034	NM_003791
ASD CNV	MITF	4286	microphthalmia-associated transcription factor	3p14.2-p14.1	CNV Association	0.17	2.09	3.79E-02	-0.11	hHA037127	NM_006722
ASD CNV	MKRN3	7681	makorin ring finger protein 3	15q11-q13	CNV Association	1.26	9.75	4.09E-19	0.19	hHC006923	NM_005664
ASD CNV	MTMR15	NA	myotubularin related protein 15	15q13.2-q13.3	CNV Association	0.50	7.52	1.10E-12	0.09	hHC010102	NM_014967
ASD CNV	MYO9A	4649	myosin IXA	15q22-q23	CNV Association	0.82	9.84	2.25E-19	0.20	hHC010565	NM_006901
ASD CNV	NBPF10	100132406	neuroblastoma breakpoint family, member 10		CNV Association	1.62	22.13	1.36E-59	0.63	hHR030655	AF419616
ASD CNV	NCAPH2	29781	non-SMC condensin II complex, subunit H2	22q13.33	CNV Association	0.20	3.14	1.88E-03	-0.09	hHA039435	NM_152299
ASD CNV	NEO1	4756	neogenin homolog 1 (chicken)	15q22.3-q23	CNV Association	1.35	15.02	2.86E-36	0.42	hHC014671	NM_002499
ASD CNV	NR2E3	10002	nuclear receptor subfamily 2, group E, member 3	15q22.32	CNV Association	0.04	0.32	7.47E-01	-0.13	hHA034458	NM_014249
ASD CNV	NRXN1	9378	neurexin 1	2p16.3	CNV Association	1.31	14.33	6.02E-34	0.39	hHA035283	NM_001135659

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ASD CNV	OSGIN1	29948	oxidative stress induced growth inhibitor 1	16q23.3	CNV Association	0.10	1.90	5.83E-02	-0.11	hHA040418	NM_013370
ASD CNV	P2RX6	9127	purinergic receptor P2X, ligand-gated ion channel, 6	22q11.21	CNV Association	0.16	3.13	2.00E-03	-0.09	hHC022715	AB002058
ASD CNV	PAR4	347745	Prader-Willi/Angelman region gene 4	15q11.2	CNV Association	0.05	0.81	4.20E-01	-0.13	hHR028566	NR_022010
ASD CNV	PAR5	8123	Prader-Willi/Angelman syndrome-5	15q11-q13	CNV Association	0.69	5.76	2.60E-08	0.01	hHR005044	NR_022008
ASD CNV	PARP6	56965	poly (ADP-ribose) polymerase family, member 6	15q23	CNV Association	0.69	12.73	1.21E-28	0.33	hHA036630	NM_020214
ASD CNV	PAR-SN	347746	paternally expressed transcript PAR-SN		CNV Association	0.67	6.57	3.21E-10	0.04	hHO047740	NR_022011
ASD CNV	PI4KA	5297	phosphatidylinositol 4-kinase, catalytic, alpha	22q11.21	CNV Association	0.50	5.74	2.81E-08	0.01	hHA039366	NM_058004
ASD CNV	PKM2	5315	pyruvate kinase, muscle	15q22	CNV Association	0.05	0.61	5.41E-01	-0.13	hHA033204	NM_002654
ASD CNV	PPP4C	5531	protein phosphatase 4 (formerly X), catalytic subunit	16p12-p11	CNV Association	1.29	18.99	1.69E-49	0.55	hHC019979	NM_002720
ASD CNV	PRKAB2	5565	protein kinase, AMP-activated, beta 2 non-catalytic subunit	1q21.1	CNV Association	1.39	21.24	8.97E-57	0.61	hHC007231	NM_005399
ASD CNV	PSMD9	5715	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	12q24.31-q24.32	CNV Association	0.18	2.56	1.09E-02	-0.10	hHC002728	NM_002813
ASD CNV	RANBP1	5902	RAN binding protein 1	22q11.21	CNV Association	0.40	8.73	4.51E-16	0.14	hHR030426	NM_002882
ASD CNV	RFC2	5982	replication factor C (activator 1) 2, 40kDa	7q11.23	CNV Association	0.83	15.90	3.10E-39	0.45	hHC021061	NM_181471
ASD CNV	SERPIND1	3053	serpin peptidase inhibitor, clade D (heparin cofactor), member 1	22q11.2|22q11.21	CNV Association	0.74	6.22	2.23E-09	0.03	hHC022493	NM_000185
ASD CNV	SETD1B	23067	SET domain containing 1B	12q24.31	CNV Association	1.30	21.60	6.47E-58	0.62	hHR005194	NM_015048
ASD CNV	SHANK3	85358	SH3 and multiple ankyrin repeat domains 3	22q13.3	CNV Association	0.69	7.85	1.42E-13	0.10	hHR018776	NM_001080420
ASD CNV	SLC25A1	6576	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	22q11.21	CNV Association	0.48	8.50	2.19E-15	0.13	hHC024586	NM_005984
ASD CNV	SNRPN	6638	small nuclear ribonucleoprotein polypeptide N	15q11.2	CNV Association	0.09	0.80	4.23E-01	-0.13	hHR008158	AF400501
ASD CNV	SPN	6693	sialophorin	16p11.2	CNV Association	0.15	3.40	7.88E-04	-0.08	hHC020872	NM_001030288
ASD CNV	TAOK2	9344	TAO kinase 2	16p11.2	CNV Association	0.50	5.08	7.67E-07	-0.02	hHA036912	NM_004783
ASD CNV	TBL2	26608	transducin (beta)-like 2	7q11.23	CNV Association	0.17	2.61	9.66E-03	-0.10	hHC022487	NM_012453
ASD CNV	TMF1	7110	TATA element modulatory factor 1	3p21-p12	CNV Association	0.24	1.64	1.03E-01	-0.12	hHR006487	NM_007114
ASD CNV	UBA3	9039	ubiquitin-like modifier activating enzyme 3	3p24.3-p13	CNV Association	1.38	21.13	2.01E-56	0.61	hHA037337	NM_003968
ASD CNV	UBE3A	7337	ubiquitin protein ligase E3A	15q11-q13	CNV Association	0.71	6.01	7.11E-09	0.02	hHA033034	NM_130839
ASD CNV	UFD1L	7353	ubiquitin fusion degradation 1 like (yeast)	22q11.21	CNV Association	0.25	5.15	5.60E-07	-0.02	hHC030312	NM_005659
ASD CNV	VPS37D	155382	vacuolar protein sorting 37 homolog D (S. cerevisiae)	7q11.23	CNV Association	0.81	11.86	8.78E-26	0.29	hHC021811	NM_001077621
ASD CNV	WBSCR28	135886	Williams-Beuren syndrome chromosome region 28	7q11.23	CNV Association	0.19	2.53	1.21E-02	-0.10	hHC016628	NM_182504
ASD CNV	ZNF74	7625	zinc finger protein 74	22q11.2|22q11.21	CNV Association	1.57	23.04	2.05E-62	0.65	hHC014115	NM_003426
ASD CNV	ADPGK	83440	ADP-dependent glucokinase	15q24.1	CNV Association	-0.36	-6.44	6.77E-10	0.04	hHC014133	NR_023318
ASD CNV	ARL6IP5	10550	ADP-ribosylation-like factor 6 interacting protein 5	3p14	CNV Association	-1.02	-16.17	4.03E-40	0.46	hHC023865	NM_006407
ASD CNV	ATP10A	57194	ATPase, class V, type 10A	15q11.2	CNV Association	-1.50	-10.73	3.76E-22	0.24	hHC013443	NM_024490
ASD CNV	BHLHE23	128408	basic helix-loop-helix family, member e23	20q13.33	CNV Association	-0.16	-3.59	4.09E-04	-0.07	hHR024544	NM_080606
ASD CNV	BRUNOL6	60677	bruno-like 6, RNA binding protein (Drosophila)	15q24	CNV Association	-0.05	-0.76	4.49E-01	-0.13	hHR008016	NM_052840
ASD CNV	C15orf2	23742	chromosome 15 open reading frame 2	15q11-q13	CNV Association	-1.90	-19.39	7.92E-51	0.56	hHR013304	NM_018958
ASD CNV	C15orf34	80072	chromosome 15 open reading frame 34	15q24.1	CNV Association	0.00	0.00	9.97E-01	-0.13	hHR008445	BC068211
ASD CNV	C15orf59	388135	chromosome 15 open reading frame 59	15q24.1	CNV Association	-0.85	-12.87	4.29E-29	0.33	hHR021371	NM_001039614
ASD CNV	C16orf54	283897	chromosome 16 open reading frame 54	16p11.2	CNV Association	-0.01	-0.11	9.09E-01	-0.13	hHC017288	NM_175900
ASD CNV	C22orf25	128989	chromosome 22 open reading frame 25	22q11.21	CNV Association	-1.47	-23.16	8.40E-63	0.65	hHC014819	NM_152906

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD CNV	C3orf64	285203	chromosome 3 open reading frame 64	3p14.1	CNV Association	-1.01	-8.82	2.57E-16	0.15	hHC010483	NM_173654
ASD CNV	C9orf66	157983	chromosome 9 open reading frame 66	9p24.3	CNV Association	-0.38	-5.36	2.01E-07	-0.01	hHC008964	NM_152569
ASD CNV	CCDC102B	79839	coiled-coil domain containing 102B	18q22.1	CNV Association	-0.42	-2.23	2.68E-02	-0.11	hHC002972	NM_001093729
ASD CNV	CDIPT	10423	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	16p11.2	CNV Association	-0.59	-13.67	9.04E-32	0.37	hHC022124	NM_006319
ASD CNV	CLDN3	1365	claudin 3	7q11.23	CNV Association	-0.27	-4.75	3.53E-06	-0.03	hHC022882	NM_001306
ASD CNV	COMT	NA	catechol-O-methyltransferase	22q11.21-q11.23|22q11.21	CNV Association	-0.28	-5.30	2.66E-07	-0.01	hHA032822	NM_000754
ASD CNV	CTNND2	1501	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	5p15.2	CNV Association	-0.07	-0.96	3.37E-01	-0.13	hHC005854	NM_001332
ASD CNV	DGCR2	9993	DiGeorge syndrome critical region gene 2	22q11.21	CNV Association	-0.73	-12.66	2.09E-28	0.33	hHR017731	NM_005137
ASD CNV	DGCR6	8214	DiGeorge syndrome critical region gene 6	22q11.21|22q11	CNV Association	-0.73	-13.54	2.53E-31	0.36	hHC031997	NM_005675
ASD CNV	DGCR6L	85359	DiGeorge syndrome critical region gene 6-like	22q11	CNV Association	-0.74	-13.76	4.76E-32	0.37	hHC031931	NM_033257
ASD CNV	DGCR9	25787	DiGeorge syndrome critical region gene 9	22q11.21	CNV Association	-0.60	-6.57	3.13E-10	0.04	hHR023893	NR_024159
ASD CNV	DLGAP2	9228	discs, large (Drosophila) homolog-associated protein 2	8p23	CNV Association	-2.22	-24.35	1.96E-66	0.68	hHC002789	NM_004745
ASD CNV	DOC2A	8448	double C2-like domains, alpha	16p11.2	CNV Association	-0.64	-13.19	3.67E-30	0.35	hHC026830	NM_003586
ASD CNV	DOCK8	81704	dedicator of cytokinesis 8	9p24.3	CNV Association	-1.52	-9.42	4.19E-18	0.18	hHR007689	NM_203447
ASD CNV	ELN	2006	elastin	7q11.23	CNV Association	-0.03	-0.36	7.20E-01	-0.13	hHC023027	NM_000501
ASD CNV	FMO5	2330	flavin containing monooxygenase 5	1q21.1	CNV Association	-0.74	-9.65	8.54E-19	0.19	hHC015181	NM_001461
ASD CNV	FZD9	8326	frizzled homolog 9 (Drosophila)	7q11.23	CNV Association	-0.41	-4.23	3.34E-05	-0.05	hHC020473	U82169
ASD CNV	GABRA5	NA	gamma-aminobutyric acid (GABA) A receptor, alpha 5	15q11.2-q12	CNV Association	-2.43	-27.43	1.71E-75	0.73	hHC009760	BC011403
ASD CNV	GABRG3	2567	gamma-aminobutyric acid (GABA) A receptor, gamma 3	15q12	CNV Association	-0.44	-4.38	1.81E-05	-0.05	hHC022899	NM_033223
ASD CNV	GJA8	2703	gap junction protein, alpha 8, 50kDa	1q21.1	CNV Association	-0.49	-6.30	1.40E-09	0.03	hHR032123	NM_005267
ASD CNV	GNB1L	54584	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	22q11.2	CNV Association	-0.25	-3.92	1.14E-04	-0.06	hHC021043	NM_053004
ASD CNV	GRAMD2	196996	GRAM domain containing 2	15q23	CNV Association	-1.04	-9.05	5.38E-17	0.16	hHC011872	NM_001012642
ASD CNV	HERC2	8924	hect domain and RLD 2	15q13	CNV Association	-0.40	-5.52	8.70E-08	0.00	hHC002570	NM_004667
ASD CNV	HIGD2B	123346	HIG1 hypoxia inducible domain family, member 2B (pseudogene)	15q24.1	CNV Association	-0.31	-5.05	9.00E-07	-0.02	hHR027193	NR_002780
ASD CNV	HPD	3242	4-hydroxyphenylpyruvate dioxygenase	12q24-qter	CNV Association	-0.12	-1.69	9.20E-02	-0.12	hHC019295	NM_002150
ASD CNV	INO80E	NA	INO80 complex subunit E	16p11.2	CNV Association	-0.03	-0.68	4.98E-01	-0.13	hHC019698	NM_173618
ASD CNV	IPW	3653	imprinted in Prader-Willi syndrome (non-protein coding)	15q11-q12	CNV Association	-0.06	-0.64	5.21E-01	-0.13	hHR003918	NR_023915
ASD CNV	KLF13	51621	Kruppel-like factor 13	15q12	CNV Association	-0.53	-6.24	2.04E-09	0.03	hHC004305	NM_015995
ASD CNV	KLHDC7B	113730	kelch domain containing 7B	22q13.33	CNV Association	-0.02	-0.32	7.49E-01	-0.13	hHC019446	NM_138433
ASD CNV	LAT2	7462	linker for activation of T cells family, member 2	7q11.23	CNV Association	-1.22	-8.35	5.75E-15	0.13	hHC014111	NM_032464
ASD CNV	LIMK1	3984	LIM domain kinase 1	7q11.23	CNV Association	-0.50	-6.61	2.58E-10	0.05	hHC007551	NM_002314
ASD CNV	LMF2	91289	lipase maturation factor 2	22q13.33	CNV Association	-0.08	-1.97	5.01E-02	-0.11	hHC025977	NM_033200
ASD CNV	LMOD3	56203	leiomodin 3 (fetal)	3p14.1	CNV Association	-0.35	-2.75	6.50E-03	-0.10	hHC007604	NM_198271
ASD CNV	MAGEL2	54551	MAGE-like 2	15q11-q12	CNV Association	-0.45	-5.28	2.92E-07	-0.01	hHC009144	NM_019066
ASD CNV	MAPK3	5595	mitogen-activated protein kinase 3	16p11.2	CNV Association	-1.22	-20.77	2.91E-55	0.60	hHC016199	NM_001040056
ASD CNV	MAPK8IP2	23542	mitogen-activated protein kinase 8 interacting protein 2	22q13.33	CNV Association	-1.04	-19.21	3.20E-50	0.56	hHC024365	NM_012324

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD CNV	MAZ	4150	MYC-associated zinc finger protein (purine-binding transcription factor)	16p11.2	CNV Association	-0.06	-1.78	7.63E-02	-0.12	hHC023211	NM_001042539
ASD CNV	MED15	51586	mediator complex subunit 15	22q11.2	CNV Association	-0.49	-10.55	1.36E-21	0.23	hHC027374	NM_001003891
ASD CNV	MIOX	55586	myo-inositol oxygenase	22q13.3	CNV Association	-0.52	-9.44	3.55E-18	0.18	hHC021730	NM_017584
ASD CNV	MRPL40	64976	mitochondrial ribosomal protein L40	22q11.21	CNV Association	-0.50	-7.82	1.74E-13	0.10	hHC015360	NM_003776
ASD CNV	MVP	9961	major vault protein	16p13.1-p11.2	CNV Association	-1.16	-12.58	3.84E-28	0.32	hHC023971	NM_017458
ASD CNV	NDN	4692	necdin homolog (mouse)	15q11.2-q12	CNV Association	-0.01	-0.10	9.18E-01	-0.13	hHC023479	NM_002487
ASD CNV	NECAB2	54550	N-terminal EF-hand calcium binding protein 2	16q23.3	CNV Association	-2.30	-17.89	7.29E-46	0.52	hHC021220	NM_019065
ASD CNV	NPTN	27020	neuroplastin	15q22	CNV Association	-1.30	-23.00	2.56E-62	0.65	hHC018056	NM_012428
ASD CNV	OCA2	4948	oculocutaneous albinism II	15q11.2-q12	CNV Association	-0.54	-4.48	1.17E-05	-0.04	hHC004293	NM_000275
ASD CNV	ODF3B	440836	outer dense fiber of sperm tails 3B	22q13|22q13.33	CNV Association	-0.29	-5.44	1.30E-07	-0.01	hHA038946	NM_001014440
ASD CNV	OTUD7A	161725	OTU domain containing 7A	15q13.3	CNV Association	-0.96	-10.35	6.01E-21	0.22	hHC013904	NM_130901
ASD CNV	PAR1	145624	Prader-Willi/Angelman region-1	15q11.2	CNV Association	-0.39	-3.59	4.03E-04	-0.07	hHR012219	NR_022009
ASD CNV	PRODH	5625	proline dehydrogenase (oxidase) 1	22q11.21	CNV Association	-1.01	-9.02	6.36E-17	0.16	hHR022951	NM_016335
ASD CNV	PRRT2	112476	proline-rich transmembrane protein 2	16p11.2	CNV Association	-0.57	-7.73	3.02E-13	0.10	hHC012542	NM_145239
ASD CNV	QPRT	23475	quinolinate phosphoribosyltransferase	16p11.2	CNV Association	-0.86	-10.74	3.41E-22	0.24	hHC023172	NM_014298
ASD CNV	RHOF	NA	ras homolog gene family, member F (in filopodia)	12q24.31	CNV Association	-1.58	-23.39	1.67E-63	0.66	hHR019557	NM_019034
ASD CNV	RTN4R	65078	reticulon 4 receptor	22q11.21	CNV Association	-0.81	-9.38	5.47E-18	0.18	hHC015361	NM_023004
ASD CNV	SBF1	6305	SET binding factor 1	22q13.33	CNV Association	-0.41	-6.04	5.82E-09	0.02	hHC030360	NM_002972
ASD CNV	SCARF2	91179	scavenger receptor class F, member 2	22q11.21	CNV Association	-0.17	-3.01	2.92E-03	-0.09	hHC025789	NM_153334
ASD CNV	SCO2	9997	SCO cytochrome oxidase deficient homolog 2 (yeast)	22q13.33	CNV Association	-0.57	-9.18	2.20E-17	0.17	hHC017980	NM_005138
ASD CNV	SEZ6L2	26470	seizure related 6 homolog (mouse)-like 2	16p11.2	CNV Association	-1.44	-16.87	1.83E-42	0.49	hHA039718	NM_201575
ASD CNV	SLC17A9	63910	solute carrier family 17, member 9	20q13.33	CNV Association	-1.65	-10.49	2.08E-21	0.23	hHC020002	NM_022082
ASD CNV	SLC38A8	146167	solute carrier family 38, member 8	16q23.3	CNV Association	-0.45	-2.82	5.17E-03	-0.09	hHR017767	NM_001080442
ASD CNV	SLC7A4	6545	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	22q11.21	CNV Association	-0.83	-12.06	1.97E-26	0.30	hHC023947	NM_004173
ASD CNV	SNAP29	9342	synaptosomal-associated protein, 29kDa	22q11.21	CNV Association	-0.69	-9.68	6.90E-19	0.19	hHC007354	NM_004782
ASD CNV	SNURF	8926	SNRPN upstream reading frame	15q11.2	CNV Association	-1.69	-25.02	1.84E-68	0.69	hHA033189	NM_005678
ASD CNV	STX1A	6804	syntaxin 1A (brain)	7q11.23	CNV Association	-1.52	-18.84	5.20E-49	0.55	hHC022261	NM_004603
ASD CNV	SUCLG2	8801	succinate-CoA ligase, GDP-forming, beta subunit	3p14.1	CNV Association	-0.60	-8.90	1.49E-16	0.15	hHR027954	NM_003848
ASD CNV	TBX1	6899	T-box 1	22q11.21	CNV Association	-0.70	-11.59	6.57E-25	0.28	hHA037074	NM_080647
ASD CNV	TBX6	6911	T-box 6	16p11.2	CNV Association	-0.78	-9.56	1.59E-18	0.18	hHA040492	NM_004608
ASD CNV	TCFL5	10732	transcription factor-like 5 (basic helix-loop-helix)	20q13.3-qter	CNV Association	-1.11	-12.39	1.62E-27	0.31	hHC005107	NM_006602
ASD CNV	THAP7	80764	THAP domain containing 7	22q11.2	CNV Association	-0.13	-3.41	7.74E-04	-0.08	hHC021948	CR605890
ASD CNV	TMEM219	124446	transmembrane protein 219	16p11.2	CNV Association	-0.95	-18.45	1.04E-47	0.54	hHR015749	NM_001083613
ASD CNV	TRMT2A	27037	TRM2 tRNA methyltransferase 2 homolog A (S. cerevisiae)	22q11.1-22q13|22q11.21	CNV Association	-0.40	-5.92	1.14E-08	0.01	hHA038708	NM_022727
ASD CNV	TSSK2	NA	testis-specific serine kinase 2	22q11.21	CNV Association	-0.55	-5.51	9.14E-08	0.00	hHC020559	NM_053006
ASD CNV	TXNRD2	10587	thioredoxin reductase 2	22q11.21	CNV Association	-0.84	-16.35	9.34E-41	0.47	hHC023645	NM_006440
ASD CNV	TYMP	1890	thymidine phosphorylase	22q13|22q13.33	CNV Association	-0.59	-4.52	9.87E-06	-0.04	hHC023665	NM_001113755
ASD CNV	WBSCR22	114049	Williams Beuren syndrome chromosome region 22	-	CNV Association	-0.37	-8.11	2.77E-14	0.11	hHR005117	NM_017528
ASD CNV	WBSCR27	155368	Williams Beuren syndrome chromosome region 27	7q11.23	CNV Association	-0.29	-2.22	2.74E-02	-0.11	hHC012588	NM_152559

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD CNV	WDR66	144406	WD repeat domain 66	12q24.31	CNV Association	-0.58	-6.48	5.32E-10	0.04	hHC007415	NM_144668
ASD CNV	YPEL3	83719	yippee-like 3 (Drosophila)	16p11.2	CNV Association	-0.95	-16.01	1.35E-39	0.46	hHC002415	NM_031477
ASD CNV	ZDHHC8	29801	zinc finger, DHHC-type containing 8	22q11.21	CNV Association	-0.16	-3.59	4.09E-04	-0.07	hHC029138	NM_013373
ASD DATABASE	AUTS2	26053	autism susceptibility candidate 2	7q11.22	Rare Single Gene variant	3.12	33.97	4.92E-93	0.81	hHC003332	NM_015570
ASD DATABASE	DAB1	1600	disabled homolog 1 (Drosophila)	1p32-p31	Functional	2.96	33.92	6.42E-93	0.81	hHE041224	AB210012
ASD DATABASE	ANK3	288	ankyrin 3, node of Ranvier (ankyrin G)	10q21	Genetic Association	2.42	22.94	4.18E-62	0.65	hHA034365	NM_020987
ASD DATABASE	NFIA	4774	nuclear factor I/A	1p31.3-p31.2	Rare Single Gene variant	2.40	28.64	6.55E-79	0.75	hHC001484	NM_001134673
ASD DATABASE	ROBO1	6091	roundabout, axon guidance receptor, homolog 1 (Drosophila)	3p12	Genetic Association	2.40	29.38	5.67E-81	0.76	hHC002741	NM_133631
ASD DATABASE	SOX5	6660	SRY (sex determining region Y)-box 5	12p12.1	Rare single gene variant	2.23	20.12	3.37E-53	0.58	hHA035450	NM_006940
ASD DATABASE	POGZ	23126	pogo transposable element with ZNF domain	1q21.3	Rare single gene variant	2.23	21.62	5.63E-58	0.62	hHA034135	NM_145796
ASD DATABASE	ZSWIM5	57643	zinc finger, SWIM-type containing 5	1p34.1	Rare Single Gene variant	2.20	30.43	8.08E-84	0.77	hHR019994	NM_020883
ASD DATABASE	DLX2	1746	distal-less homeobox 2	2q32	Genetic Association	2.11	14.79	1.69E-35	0.41	hHC006280	NM_004405
ASD DATABASE	CACNA1H	8912	calcium channel, voltage-dependent, T type, alpha 1H subunit	16p13.3	Rare Single Gene variant	2.06	21.73	2.49E-58	0.62	hHC005422	NM_021098
ASD DATABASE	FEZF2	55079	FEZ family zinc finger 2	3p14.2	Genetic Association	2.04	16.43	5.27E-41	0.47	hHC017900	NM_018008
ASD DATABASE	LAMA1	284217	laminin, alpha 1	18p11.31	Genetic association	2.02	14.87	9.22E-36	0.41	hHC007864	NM_005559
ASD DATABASE	HMGN1	3150	high-mobility group nucleosome binding domain 1	21q22.3|21q22.2	Genetic Association	2.02	23.73	1.44E-64	0.67	hHR030827	NM_004965
ASD DATABASE	BCL2	596	B-cell CLL/lymphoma 2	18q21.33|18q21.3	Functional	1.97	19.05	1.03E-49	0.55	hHA033818	NM_000633
ASD DATABASE	BRCA2	675	breast cancer 2, early onset	13q12.3	Rare Single Gene variant	1.89	11.56	8.44E-25	0.28	hHC005360	NM_000059
ASD DATABASE	VASH1	22846	vasohibin 1	14q24.3	Genetic Association	1.87	24.78	9.58E-68	0.69	hHC015490	NM_014909
ASD DATABASE	ADNP	23394	activity-dependent neuroprotector homeobox	20q13.13	Rare Single Gene variant	1.85	23.34	2.27E-63	0.66	hHA037442	NM_015339
ASD DATABASE	CTTNBP2	83992	cortactin binding protein 2	7q31	Rare Single Gene variant	1.84	21.69	3.31E-58	0.62	hHC004724	NM_033427
ASD DATABASE	LRRC7	57554	leucine rich repeat containing 7	1p31.1	Functional	1.78	21.18	1.36E-56	0.61	hHC003436	NM_020794
ASD DATABASE	GRIK2	2898	glutamate receptor, ionotropic, kainate 2	6q16.3-q21	Genetic Association	1.76	22.53	7.68E-61	0.64	hHC019020	NM_175768
ASD DATABASE	GRIP1	23426	glutamate receptor interacting protein 1	12q14.3	Rare Single Gene variant, Genetic Association	1.69	21.90	7.36E-59	0.63	hHR016670	NM_021150
ASD DATABASE	SETDB1	9869	SET domain, bifurcated 1	1q21	Rare single gene variant	1.68	27.38	2.43E-75	0.73	hHC006984	BC028671
ASD DATABASE	SUV420H1	51111	suppressor of variegation 4-20 homolog 1 (Drosophila)	11q13.2	Rare Single Gene variant	1.68	25.50	6.94E-70	0.70	hHA033920	NM_017635
ASD DATABASE	JMJD1C	221037	jumonji domain containing 1C	10q21.2-q21.3	Rare single gene variant	1.67	21.97	4.21E-59	0.63	hHC023549	NM_032776
ASD DATABASE	CNTN4	152330	contactin 4	3p26-p25	Rare Single Gene variant	1.57	12.93	2.75E-29	0.34	hHA040420	NM_175607
ASD DATABASE	OTX1	5013	orthodenticle homeobox 1	2p13	Genetic association	1.54	13.46	4.58E-31	0.36	hHC011290	NM_014562
ASD DATABASE	UBR5	NA	ubiquitin protein ligase E3 component n-recognin 5	8q22	Rare single gene variant	1.53	15.90	3.02E-39	0.45	hHC001627	CD511402
ASD DATABASE	EPHB2	2048	EPH receptor B2	1p36.1-p35	Rare single gene variant	1.49	21.44	2.07E-57	0.62	hHC020957	NM_004442
ASD DATABASE	LRRC1	55227	leucine rich repeat containing 1	6p12.1	Genetic Association	1.33	12.30	3.17E-27	0.31	hHA037417	NM_018214
ASD DATABASE	NBEA	26960	neurobeachin	13q13	Rare single gene variant	1.31	25.39	1.52E-69	0.70	hHC002233	NM_015678
ASD DATABASE	UBA6	55236	ubiquitin-like modifier activating enzyme 6	4q13.2	Functional	1.29	22.24	6.13E-60	0.63	hHC003689	NM_018227
ASD DATABASE	NRP2	8828	neuropilin 2	2q33.3	Genetic Association	1.29	11.84	1.01E-25	0.29	hHC009632	NM_201266
ASD DATABASE	MARK1	4139	MAP/microtubule affinity-regulating kinase 1	1q41	Genetic association/Functional	1.26	18.60	3.11E-48	0.54	hHC007557	NM_018650
ASD DATABASE	SLC25A24	29957	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	1p13.3	Functional	1.25	12.20	6.92E-27	0.31	hHC003620	NM_013386
ASD DATABASE	ST7	7982	suppression of tumorigenicity 7	7q31.1-q31.3	Rare Single Gene variant	1.16	20.39	4.81E-54	0.59	hHC008055	NM_018412
ASD DATABASE	MACROD2	140733	MACRO domain containing 2	20p12.1	Genetic Association	1.12	12.11	1.38E-26	0.30	hHR007786	BC128036

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD DATABASE	ST8SIA2	8128	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	15q26	Genetic Association	1.12	10.38	4.76E-21	0.22	hHC017702	NM_006011
ASD DATABASE	DIAPH3	81624	diaphanous homolog 3 (Drosophila)	13q21.2	Rare Single Gene variant	1.12	8.02	4.98E-14	0.11	hHC016253	NM_030932
ASD DATABASE	CNTNAP3	79937	contactin associated protein-like 3	9p13.1	Rare Single Gene variant	1.11	9.93	1.22E-19	0.20	hHR030569	NM_033655
ASD DATABASE	KIAA1586	57691	KIAA1586	6p12.1	Rare Single Gene variant	1.10	10.99	5.56E-23	0.25	hHC008010	NM_020931
ASD DATABASE	PSD3	23362	pleckstrin and Sec7 domain containing 3	8pter-p23.3	Rare Single Gene variant	1.09	10.33	6.62E-21	0.22	hHA036085	NM_015310
ASD DATABASE	JARID2	3720	jumonji, AT rich interactive domain 2	6p24-p23	Genetic association	1.08	16.74	4.66E-42	0.48	hHC009434	NM_004973
ASD DATABASE	HS3ST5	222537	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	6q22.31	Genetic Association	1.02	9.69	6.38E-19	0.19	hHR004521	NM_153612
ASD DATABASE	NRCAM	4897	neuronal cell adhesion molecule	7q31.1-q31.2	Genetic Association	1.02	11.78	1.66E-25	0.29	hHA035333	NM_001037132
ASD DATABASE	EIF4EBP2	1979	eukaryotic translation initiation factor 4E binding protein 2	10q21-q22	Functional	1.02	19.07	9.46E-50	0.55	hHR029057	NM_004096
ASD DATABASE	RAI1	10743	retinoic acid induced 1	17p11.2	Rare Single Gene variant	0.99	15.41	1.40E-37	0.44	hHC011816	NM_030665
ASD DATABASE	TBR1	10716	T-box, brain, 1	2q24	Rare Single Gene variant	0.99	9.31	8.89E-18	0.17	hHC005106	NM_006593
ASD DATABASE	TAF1C	9013	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	16q24	Genetic association	0.97	15.11	1.40E-36	0.42	hHC014149	NM_005679
ASD DATABASE	YEATS2	55689	YEATS domain containing 2	3q27.1	Genetic association	0.97	18.26	4.32E-47	0.53	hHC002724	NM_018023
ASD DATABASE	SETD2	29072	SET domain containing 2	3p21.31	Rare Single Gene variant	0.96	20.38	5.06E-54	0.59	hHC017824	NM_014159
ASD DATABASE	SHANK2	22941	SH3 and multiple ankyrin repeat domains 2	11q13.3	Rare Single Gene variant	0.94	10.27	1.06E-20	0.22	hHA034077	NM_012309
ASD DATABASE	MTR	4548	5-methyltetrahydrofolate-homocysteine methyltransferase		Functional	0.94	13.86	2.23E-32	0.38	hHC007040	NM_000254
ASD DATABASE	APC	324	adenomatous polyposis coli	5q21-q22	Genetic Association	0.94	8.68	6.67E-16	0.14	hHA034118	NM_001127511
ASD DATABASE	XPO1	7514	exportin 1 (CRM1 homolog, yeast)	2p16	Genetic association	0.92	17.48	1.65E-44	0.51	hHC005732	NM_003400
ASD DATABASE	CLTCL1	8218	clathrin, heavy chain-like 1	22q11.2|22q11.21	Rare single gene variant	0.90	9.68	7.00E-19	0.19	hHA036352	NM_007098
ASD DATABASE	A2BP1	54715	ataxin 2-binding protein 1	16p13.3	Genetic Association	0.90	13.45	5.14E-31	0.36	hHC022670	NM_018723
ASD DATABASE	EP400	57634	E1A binding protein p400	12q24.33	Rare single gene variant	0.90	14.40	3.44E-34	0.40	hHR012430	NM_015409
ASD DATABASE	MAPK1	5594	mitogen-activated protein kinase 1	22q11.2|22q11.21	Functional	0.89	11.80	1.34E-25	0.29	hHA035377	NM_138957
ASD DATABASE	CNTN3	5067	contactin 3 (plasmacytoma associated)	3p26	Rare Single Gene variant	0.89	8.06	3.71E-14	0.11	hHR004942	NM_020872
ASD DATABASE	AFF4	27125	AF4/FMR2 family, member 4	5q31	Rare Single Gene variant	0.88	3.83	1.66E-04	-0.06	hHC002880	NM_014423
ASD DATABASE	EP300	2033	E1A binding protein p300	22q13.2	Rare Single Gene variant	0.88	12.68	1.76E-28	0.33	hHC012239	NM_001429
ASD DATABASE	CHRNA7	1139	cholinergic receptor, nicotinic, alpha 7	15q14	Rare single gene variant	0.83	5.64	4.76E-08	0.00	hHR025141	NM_000746
ASD DATABASE	MAP2	4133	microtubule-associated protein 2	2q34-q35	Rare Single Gene variant	0.83	8.08	3.24E-14	0.11	hHC022926	NM_002374
ASD DATABASE	DCTN5	84516	dynactin 5 (p25)	16p12.1	Rare Single Gene variant	0.81	11.51	1.24E-24	0.27	hHR027462	NM_032486
ASD DATABASE	CADM1	23705	cell adhesion molecule 1	11q23.2	Rare Single Gene variant	0.80	7.20	7.70E-12	0.07	hHR011178	NM_014333
ASD DATABASE	GUCY1A2	2977	guanylate cyclase 1, soluble, alpha 2	11q21-q22	Genetic association	0.77	8.67	6.84E-16	0.14	hHC011966	NM_000855
ASD DATABASE	MBD5	55777	methyl-CpG binding domain protein 5	2q23.1	Rare single gene variant	0.77	12.57	4.17E-28	0.32	hHC004339	NM_018328
ASD DATABASE	SLC30A5	64924	solute carrier family 30 (zinc transporter), member 5	5q12.1	Rare Single Gene variant	0.76	9.73	4.71E-19	0.19	hHA033870	NM_022902
ASD DATABASE	DLX1	1745	distal-less homeobox 1	2q32	Genetic Association	0.74	5.04	9.24E-07	-0.02	hHC006676	NM_178120
ASD DATABASE	KHDRBS2	202559	KH domain containing, RNA binding, signal transduction associated 2	6q11.1	Rare Single Gene variant	0.72	8.55	1.49E-15	0.14	hHC008977	NM_152688
ASD DATABASE	UBE3A	7337	ubiquitin protein ligase E3A	15q11-q13	Genetic Association	0.71	6.01	7.11E-09	0.02	hHA033034	NM_130839
ASD DATABASE	EIF4E	1977	eukaryotic translation initiation factor 4E	4q21-q25	Rare single gene variant	0.70	8.47	2.68E-15	0.13	hHC030864	NM_001130679
ASD DATABASE	HDAC4	9759	histone deacetylase 4	2q37.3	Genetic Association	0.70	5.88	1.38E-08	0.01	hHC005088	NM_006037
ASD DATABASE	SHANK3	85358	SH3 and multiple ankyrin repeat domains 3	22q13.3	Rare Single Gene variant	0.69	7.85	1.42E-13	0.10	hHR018776	NM_001080420

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD DATABASE	ITGB3BP	23421	integrin beta 3 binding protein (beta3-endonexin)	1p31.3	Genetic Association	0.69	4.82	2.52E-06	-0.03	hHA035416	NM_014288
ASD DATABASE	TLK2	11011	tousled-like kinase 2	17q23	Rare Single Gene variant	0.66	11.43	2.13E-24	0.27	hHC030724	NM_006852
ASD DATABASE	YTHDC2	64848	YTH domain containing 2	5q22.2	Rare Single Gene variant	0.66	7.26	5.38E-12	0.08	hHC004011	NM_022828
ASD DATABASE	GSK3B	2932	glycogen synthase kinase 3 beta	3q13.3	Functional	0.66	9.27	1.19E-17	0.17	hHR024272	NM_002093
ASD DATABASE	PLAUR	5329	plasminogen activator, urokinase receptor	19q13	Genetic association	0.64	7.12	1.27E-11	0.07	hHC020214	NM_002659
ASD DATABASE	TSN	7247	translin	2q21.1	Functional	0.64	7.85	1.47E-13	0.10	hHA040599	NM_004622
ASD DATABASE	ZNF18	7566	zinc finger protein 18	17p11.2	Rare single gene variant	0.63	6.74	1.17E-10	0.05	hHC019788	NM_144680
ASD DATABASE	DAPK1	1612	death-associated protein kinase 1	9q34.1	Genetic Association	0.57	8.42	3.73E-15	0.13	hHC008562	NM_004938
ASD DATABASE	RORA	6095	RAR-related orphan receptor A	15q21.3	Functional	0.56	4.71	4.13E-06	-0.03	hHA033097	NM_134260
ASD DATABASE	UBE2H	7328	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	7q32	Genetic Association	0.55	9.12	3.40E-17	0.16	hHC029382	NM_003344
ASD DATABASE	MBD6	114785	methyl-CpG binding domain protein 6	-	Rare single gene variant	0.55	8.69	5.92E-16	0.14	hHC020288	NM_052897
ASD DATABASE	MTHFR	4524	5,10-methylenetetrahydrofolate reductase (NADPH)	1p36.3	Genetic Association	0.54	5.23	3.69E-07	-0.01	hHC015904	NM_005957
ASD DATABASE	GPD2	2820	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	2q24.1	Rare single gene variant	0.52	5.73	3.11E-08	0.01	hHC030717	NM_001083112
ASD DATABASE	MBD1	4152	methyl-CpG binding domain protein 1	18q21	Rare Single Gene variant	0.48	9.16	2.51E-17	0.16	hHR003120	NM_015846
ASD DATABASE	TTN	7273	titin	2q31	Rare Single Gene variant	0.47	3.87	1.39E-04	-0.06	hHA035073	NM_133378
ASD DATABASE	ADSL	158	adenylosuccinate lyase	22q13.1|22q13.2	Rare Single Gene variant	0.47	11.13	2.05E-23	0.26	hHA037287	NM_000026
ASD DATABASE	PCDHA1	56147	protocadherin alpha 1	5q31	Rare single gene variant	0.47	7.18	8.68E-12	0.07	hHR006046	NM_018900
ASD DATABASE	MCPH1	79648	microcephalin 1	8p23.1	Rare Single Gene variant	0.47	5.25	3.40E-07	-0.01	hHC008828	NM_024596
ASD DATABASE	MEF2C	4208	myocyte enhancer factor 2C	5q14	Rare Single Gene variant	0.45	3.85	1.50E-04	-0.06	hHR007934	NM_002397
ASD DATABASE	C4BPB	725	complement component 4 binding protein, beta	1q32	Genetic Association	0.42	4.57	7.95E-06	-0.04	hHC022556	NM_000716
ASD DATABASE	NTRK3	4916	neurotrophic tyrosine kinase, receptor, type 3	15q25	Rare Single Gene variant, Genetic Association	0.41	5.83	1.83E-08	0.01	hHC013101	NM_001012338
ASD DATABASE	NRXN3	9369	neurexin 3	14q31	Rare Single Gene variant	0.40	4.04	7.22E-05	-0.06	hHA036677	NM_004796
ASD DATABASE	CMIP	80790	c-Maf-inducing protein		Genetic Association	0.40	6.04	5.95E-09	0.02	hHA039536	NM_030629
ASD DATABASE	MTF1	4520	metal-regulatory transcription factor 1	1p33	Genetic Association	0.36	5.95	9.49E-09	0.02	hHR018133	NM_005955
ASD DATABASE	RAB19	401409	RAB19, member RAS oncogene family		Rare single gene variant	0.35	3.62	3.63E-04	-0.07	hHR012361	NM_001008749
ASD DATABASE	ADK	132	adenosine kinase	10q22|10q11-q24	Rare Single Gene variant	0.34	4.71	4.30E-06	-0.03	hHA038719	NM_001123
ASD DATABASE	YWHAE	7531	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	17p13.3	Rare single gene variant	0.33	5.16	5.21E-07	-0.02	hHC028280	NR_024058
ASD DATABASE	PCDHGA11	56105	protocadherin gamma subfamily A, 11		Rare single gene variant	0.33	3.69	2.77E-04	-0.07	hHA034119	NM_032091
ASD DATABASE	LAMB1	3912	laminin, beta 1	7q22	Genetic Association	0.33	3.02	2.81E-03	-0.09	hHC004268	NM_002291
ASD DATABASE	HTR3A	3359	5-hydroxytryptamine (serotonin) receptor 3A	11q23.1	Functional	0.33	7.23	6.61E-12	0.07	hHA040524	NM_213621
ASD DATABASE	NF1	4763	neurofibromin 1	17q11.2	Rare Single Gene variant, Genetic Association	0.32	4.18	4.07E-05	-0.05	hHC019086	NM_001042492
ASD DATABASE	TBC1D7	51256	TBC1 domain family, member 7	6p24.1	Functional	0.28	3.50	5.47E-04	-0.08	hHA036695	NM_016495
ASD DATABASE	AVPR1A	552	arginine vasopressin receptor 1A	12q14-q15	Rare Single Gene variant, Genetic Association	0.27	2.31	2.19E-02	-0.11	hHC009154	NM_000706
ASD DATABASE	CHD8	57680	chromodomain helicase DNA binding protein 8	14q11.2	Rare Single Gene variant	0.26	5.23	3.66E-07	-0.01	hHR011006	NM_020920
ASD DATABASE	ARHGAP15	55843	Rho GTPase activating protein 15	2q22.2	Rare Single Gene variant	0.26	1.94	5.31E-02	-0.11	hHC010987	NM_018460
ASD DATABASE	IL1R2	7850	interleukin 1 receptor, type II	2q12-q22	Rare Single Gene variant	0.26	3.90	1.23E-04	-0.06	hHA038212	NM_004633
ASD DATABASE	UBR7	55148	ubiquitin protein ligase E3 component n-recognin 7 (putative)	14q32.12	Rare Single Gene variant	0.25	4.87	2.02E-06	-0.03	hHA033800	NM_175748
ASD DATABASE	KIAA1602	57701	KIAA1602	12q13.13	Rare single gene variant	0.25	5.25	3.39E-07	-0.01	hHR024402	NM_001037806
ASD DATABASE	RELN	5649	reelin	7q22	Genetic Association	0.25	1.83	6.86E-02	-0.12	hHC004991	NM_005045

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD DATABASE	CACNA1G	8913	calcium channel, voltage-dependent, T type, alpha 1G subunit	17q22	Genetic Association	0.23	2.33	2.05E-02	-0.11	hHA039581	NM_198396
ASD DATABASE	TBL1XR1	79718	transducin (beta)-like 1 X-linked receptor 1	3q26.32	Rare Single Gene variant	0.22	3.08	2.33E-03	-0.09	hHC018417	NM_024665
ASD DATABASE	DRD2	1813	dopamine receptor D2	11q23	Rare single gene variant	0.22	2.30	2.24E-02	-0.11	hHA035616	NM_000795
ASD DATABASE	GABRB3	2562	gamma-aminobutyric acid (GABA) A receptor, beta 3	15q11.2-q12	Genetic Association	0.21	2.36	1.90E-02	-0.10	hHA040248	NM_021912
ASD DATABASE	CA6	765	carbonic anhydrase VI	1p36.2	Rare Single Gene variant	0.20	3.14	1.91E-03	-0.09	hHC019151	NM_001215
ASD DATABASE	PDE4A	5141	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	19p13.2	Functional	0.17	2.19	2.96E-02	-0.11	hHA038823	NM_001111307
ASD DATABASE	NTRK1	4914	neurotrophic tyrosine kinase, receptor, type 1	1q21-q22	Rare Single Gene variant	0.15	1.51	1.33E-01	-0.12	hHC022368	NM_002529
ASD DATABASE	GRIN2B	2904	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	12p12	Genetic Association	0.13	2.02	4.46E-02	-0.11	hHC022772	NM_000834
ASD DATABASE	GPX1	2876	glutathione peroxidase 1	3p21.3	Genetic Association	0.13	1.15	2.50E-01	-0.12	hHR012671	NM_201397
ASD DATABASE	CCDC64	92558	coiled-coil domain containing 64	12q24.23	Genetic Association	0.11	0.90	3.67E-01	-0.13	hHR014469	AK129960
ASD DATABASE	CADPS2	93664	Ca++-dependent secretion activator 2	7q31.3	Rare Single Gene variant	0.10	1.22	2.24E-01	-0.12	hHA036220	NM_017954
ASD DATABASE	FOXP1	27086	forkhead box P1	3p14.1	Rare Single Gene variant	0.10	1.11	2.69E-01	-0.12	hHC002879	NM_032682
ASD DATABASE	DMPK	1760	dystrophia myotonica-protein kinase	19q13.3	Genetic Association	0.10	1.26	2.10E-01	-0.12	hHC016348	NM_001081563
ASD DATABASE	LRPPRC	10128	leucine-rich PPR-motif containing	2p21	Functional	0.10	1.82	7.02E-02	-0.12	hHC010016	NM_133259
ASD DATABASE	TSC2	7249	tuberous sclerosis 2	16p13.3	Genetic Association	0.08	1.48	1.40E-01	-0.12	hHC023736	NM_000548
ASD DATABASE	CAMTA1	23261	calmodulin binding transcription activator 1	1p36.31-p36.23	Rare single gene variant	0.05	0.60	5.50E-01	-0.13	hHA032936	NM_015215
ASD DATABASE	MYO1A	4640	myosin IA	12q13-q14	Rare Single Gene variant	0.04	0.47	6.37E-01	-0.13	hHC024205	NM_005379
ASD DATABASE	POT1	25913	POT1 protection of telomeres 1 homolog (S. pombe)	7q31.33	Rare single gene variant	0.02	0.27	7.89E-01	-0.13	hHC003328	NR_003102
ASD DATABASE	CD44	960	CD44 molecule (Indian blood group)	11p13	Genetic Association	0.00	0.06	9.48E-01	-0.13	hHA036604	NM_000610
ASD DATABASE	HOXA1	3198	homeobox A1	7p15.3	Genetic Association	0.00	0.01	9.92E-01	-0.13	hHA039747	NM_005522
ASD DATABASE	MSR1	4481	macrophage scavenger receptor 1	8p22	Rare Single Gene variant	0.00	0.00	9.96E-01	-0.13	hHA037301	NM_138715
ASD DATABASE	OXTR	5021	oxytocin receptor	3p25	Genetic Association	-0.01	-0.06	9.55E-01	-0.13	hHR017882	NM_000916
ASD DATABASE	MDGA2	161357	MAM domain containing glycosylphosphatidylinositol anchor 2	14q21.3	Genetic Association	-0.01	-0.08	9.34E-01	-0.13	hHC004809	NM_001113498
ASD DATABASE	SYNGAP1	8831	synaptic Ras GTPase activating protein 1 homolog (rat)	6p21.3	Rare Single Gene variant	-0.05	-0.57	5.67E-01	-0.13	hHC014146	NM_006772
ASD DATABASE	FOXP2	93986	forkhead box P2	7q31	Rare single gene variant	-0.06	-0.47	6.35E-01	-0.13	hHC010005	NM_148898
ASD DATABASE	AMT	275	aminomethyltransferase	3p21.2-p21.1	Rare single gene variant	-0.07	-1.25	2.12E-01	-0.12	hHC025760	NM_000481
ASD DATABASE	TPO	7173	thyroid peroxidase	2p25	Genetic association	-0.08	-1.33	1.84E-01	-0.12	hHC018189	NM_000547
ASD DATABASE	PITX1	5307	paired-like homeodomain 1	5q31	Genetic Association	-0.09	-1.73	8.52E-02	-0.12	hHC024311	NM_002653
ASD DATABASE	MBD3	53615	methyl-CpG binding domain protein 3	19p13.3	Rare Single Gene variant, Genetic Association	-0.09	-1.36	1.75E-01	-0.12	hHR026224	NM_003926
ASD DATABASE	CACNA1D	776	calcium channel, voltage-dependent, L type, alpha 1D subunit	3p14.3	Functional	-0.11	-1.32	1.89E-01	-0.12	hHC016540	NM_000720
ASD DATABASE	ADARB1	104	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	21q22.3	Functional	-0.12	-1.65	1.01E-01	-0.12	hHA038018	NM_001112
ASD DATABASE	AGAP1	116987	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1	2q37	Rare Single Gene variant, Genetic Association	-0.13	-1.37	1.73E-01	-0.12	hHC021643	NM_001037131
ASD DATABASE	TYR	7299	tyrosinase (oculocutaneous albinism IA)	11q14-q21	Functional	-0.13	-2.03	4.37E-02	-0.11	hHR017154	NM_000372
ASD DATABASE	CACNA1B	774	calcium channel, voltage-dependent, N type, alpha 1B subunit	9q34	Genetic association	-0.13	-2.08	3.88E-02	-0.11	hHC019378	NM_000718
ASD DATABASE	HOXB1	3211	homeobox B1	17q21.3	Genetic Association	-0.16	-1.89	6.00E-02	-0.11	hHC024275	NM_002144

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ASD DATABASE	SERPINE1	5054	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	7q21.3-q22	Genetic association	-0.18	-0.93	3.55E-01	-0.13	hHR017883	NM_000602
ASD DATABASE	DNM1L	10059	dynamin 1-like	12p11.21	Functional	-0.20	-4.74	3.70E-06	-0.03	hHA040566	NM_012062
ASD DATABASE	EN2	2020	engrailed homeobox 2	7q36	Genetic Association	-0.21	-1.05	2.95E-01	-0.13	hHR003567	NM_001427
ASD DATABASE	ESRRB	2103	estrogen-related receptor beta	14q24.3	Genetic Association	-0.21	-3.30	1.13E-03	-0.08	hHC020118	NM_004452
ASD DATABASE	TAF1L	138474	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210kDa-like	9p21.1	Rare Single Gene variant	-0.22	-1.94	5.41E-02	-0.11	hHC026675	NM_153809
ASD DATABASE	MTX2	10651	metaxin 2	2q31.1	Functional	-0.23	-4.48	1.14E-05	-0.04	hHC004105	NM_001006635
ASD DATABASE	DRD3	1814	dopamine receptor D3	3q13.3	Genetic Association	-0.24	-3.71	2.56E-04	-0.07	hHC011871	NM_000796
ASD DATABASE	GAP43	2596	growth associated protein 43	3q13.1-q13.2	Functional	-0.25	-2.73	6.91E-03	-0.10	hHC021492	NM_001130064
ASD DATABASE	LZTS2	84445	leucine zipper, putative tumor suppressor 2	10q24	Genetic Association	-0.26	-4.37	1.88E-05	-0.05	hHC022109	NM_032429
ASD DATABASE	MBD4	8930	methyl-CpG binding domain protein 4	3q21-q22	Rare Single Gene variant, Genetic Association	-0.26	-5.53	8.52E-08	0.00	hHC013517	NM_003925
ASD DATABASE	CUL3	8452	cullin 3	2q36.2	Rare single gene variant	-0.27	-4.19	3.97E-05	-0.05	hHC002562	NM_003590
ASD DATABASE	PARD3B	117583	par-3 partitioning defective 3 homolog B (C. elegans)	2q33.3	Genetic association	-0.32	-5.94	1.00E-08	0.02	hHR017747	NM_152526
ASD DATABASE	SND1	27044	staphylococcal nuclease and tudor domain containing 1	7q31.3	Genetic Association	-0.32	-7.79	2.08E-13	0.10	hHC015809	NM_014390
ASD DATABASE	HTR3C	170572	5-hydroxytryptamine (serotonin) receptor 3, family member C	3q27.1	Genetic Association	-0.32	-5.72	3.12E-08	0.01	hHC012593	NM_130770
ASD DATABASE	LAMC3	10319	laminin, gamma 3	9q31-q34	Rare Single Gene variant	-0.34	-3.98	9.12E-05	-0.06	hHC021119	NM_006059
ASD DATABASE	AR	367	androgen receptor	Xq11.2-q12	Genetic Association	-0.38	-3.80	1.87E-04	-0.07	hHC019711	NM_000044
ASD DATABASE	GSTM1	2944	glutathione S-transferase mu 1	1p13.3	Genetic Association	-0.39	-2.45	1.51E-02	-0.10	hHA033255	NM_000561
ASD DATABASE	CHST5	23563	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	16q22.3	Rare Single Gene variant	-0.40	-6.55	3.47E-10	0.04	hHA034690	NM_024533
ASD DATABASE	HERC2	8924	hect domain and RLD 2	15q13	Rare single gene variant	-0.40	-5.52	8.70E-08	0.00	hHC002570	NM_004667
ASD DATABASE	DLG4	1742	discs, large homolog 4 (Drosophila)	17p13.1	Functional	-0.41	-7.50	1.27E-12	0.09	hHA040671	NM_001365
ASD DATABASE	ADRB2	154	adrenergic, beta-2-, receptor, surface	5q31-q32	Genetic Association	-0.44	-4.72	3.96E-06	-0.03	hHC010417	NM_000024
ASD DATABASE	DDX11	1663	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)	12p11	Genetic Association	-0.44	-6.64	2.10E-10	0.05	hHA033471	U75968
ASD DATABASE	PER1	5187	period homolog 1 (Drosophila)	17p13.1-p12	Genetic Association	-0.44	-5.06	8.26E-07	-0.02	hHC014060	NM_002616
ASD DATABASE	PCDHAC2	56134	protocadherin alpha subfamily C, 2		Genetic association	-0.45	-5.26	3.24E-07	-0.01	hHA040138	NM_018899
ASD DATABASE	CDH22	64405	cadherin-like 22	20q13.1	Genetic Association	-0.45	-5.36	1.93E-07	-0.01	hHC022550	NM_021248
ASD DATABASE	ADCY5	111	adenylate cyclase 5	3q13.2-q21	Rare Single Gene variant	-0.45	-5.80	2.13E-08	0.01	hHR020929	NM_183357
ASD DATABASE	DLX6	1750	distal-less homeobox 6	7q22	Rare Single Gene variant	-0.45	-3.92	1.18E-04	-0.06	hHR004816	NM_005222
ASD DATABASE	PPP1R1B	84152	protein phosphatase 1, regulatory (inhibitor) subunit 1B	17q12	Genetic association	-0.46	-8.09	3.15E-14	0.11	hHA040375	NM_032192
ASD DATABASE	PDE4B	5142	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	1p31	Functional	-0.49	-7.51	1.18E-12	0.09	hHC005298	NM_001037341
ASD DATABASE	BZRAP1	9256	benzodiazapine receptor (peripheral) associated protein 1	17q22-q23	Rare Single Gene variant	-0.49	-10.51	1.84E-21	0.23	hHC025747	NM_004758
ASD DATABASE	GALNT14	79623	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	2p23.1	Genetic association	-0.53	-5.92	1.14E-08	0.01	hHC020467	NM_024572
ASD DATABASE	DNER	92737	delta/notch-like EGF repeat containing	2q36.3	Genetic association	-0.54	-6.61	2.47E-10	0.05	hHC010355	NM_139072
ASD DATABASE	BCKDK	10295	branched chain ketoacid dehydrogenase kinase	16p11.2	Rare single gene variant	-0.56	-8.12	2.56E-14	0.12	hHA036422	NM_001122957
ASD DATABASE	PCDHAC1	56135	protocadherin alpha subfamily C, 1	5q31	Genetic association	-0.61	-7.79	2.11E-13	0.10	hHC015008	NM_018898

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD DATABASE	LMX1B	4010	LIM homeobox transcription factor 1, beta		Genetic Association	-0.63	-9.42	4.08E-18	0.18	hHE040758	NM_002316
ASD DATABASE	CDH10	1008	cadherin 10, type 2 (T2-cadherin)	5p14-p13	Genetic Association	-0.67	-8.42	3.65E-15	0.13	hHC005100	NM_006727
ASD DATABASE	FLT1	2321	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	13q12	Genetic Association	-0.68	-5.27	3.08E-07	-0.01	hHC021672	NM_002019
ASD DATABASE	SLC25A14	9016	solute carrier family 25 (mitochondrial carrier, brain), member 14	Xq24	Functional	-0.72	-12.97	2.04E-29	0.34	hHC028296	NM_003951
ASD DATABASE	ARHGAP24	83478	Rho GTPase activating protein 24	4q21.23-q21.3	Rare single gene variant	-0.73	-15.63	2.47E-38	0.44	hHC011396	NM_001025616
ASD DATABASE	SLC25A27	9481	solute carrier family 25, member 27	6p11.2-q12	Genetic association/functional	-0.73	-9.98	8.57E-20	0.20	hHR003234	NM_004277
ASD DATABASE	TBL1X	6907	transducin (beta)-like 1X-linked	Xp22.3	Genetic Association	-0.74	-9.07	4.77E-17	0.16	hHC017932	NM_005647
ASD DATABASE	PCDH10	57575	protocadherin 10	4q28.3	Rare Single Gene variant	-0.75	-10.31	7.79E-21	0.22	hHA034716	NM_020815
ASD DATABASE	NDUFA5	4698	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	7q32	Genetic Association	-0.78	-9.84	2.26E-19	0.20	hHR022224	NM_005000
ASD DATABASE	DDC	1644	dopa decarboxylase (aromatic L-amino acid decarboxylase)	7p12.2	Genetic association	-0.80	-6.86	5.83E-11	0.06	hHC005505	NM_001082971
ASD DATABASE	GALNT13	114805	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	2q23.3-q24.1	Rare Single Gene variant	-0.82	-11.32	5.09E-24	0.27	hHC004472	NM_052917
ASD DATABASE	ABAT	18	4-aminobutyrate aminotransferase	16p13.2	Genetic Association	-0.83	-12.75	1.09E-28	0.33	hHR002012	NM_000663
ASD DATABASE	INPP1	3628	inositol polyphosphate-1-phosphatase	2q32	Genetic Association	-0.83	-12.89	3.60E-29	0.34	hHC010890	NM_001128928
ASD DATABASE	APBA2	321	amyloid beta (A4) precursor protein-binding, family A, member 2	15q11-q12	Rare Single Gene variant	-0.84	-13.15	4.87E-30	0.35	hHC002497	NM_005503
ASD DATABASE	TGM3	7053	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	20q11.2	Rare Single Gene variant	-0.85	-10.36	5.61E-21	0.22	hHC019588	NM_003245
ASD DATABASE	LRFN5	145581	leucine rich repeat and fibronectin type III domain containing 5	14q21.2	Genetic Association	-0.86	-11.06	3.33E-23	0.25	hHC020529	NM_152447
ASD DATABASE	SLC39A11	201266	solute carrier family 39 (metal ion transporter), member 11	17q24.3-q25.1	Genetic association	-0.87	-11.89	7.12E-26	0.29	hHC012606	NM_139177
ASD DATABASE	PCDH15	65217	protocadherin 15		Genetic association	-0.91	-12.91	3.13E-29	0.34	hHR010523	NM_001142771
ASD DATABASE	RPP25	54913	ribonuclease P/MRP 25kDa subunit	15q24.1	Functional	-0.95	-18.31	2.95E-47	0.53	hHC018851	NM_017793
ASD DATABASE	EGR2	1959	early growth response 2 (Krox-20 homolog, Drosophila)	10q21.1	Genetic Association	-0.97	-5.82	1.89E-08	0.01	hHC017547	NM_000399
ASD DATABASE	CACNA1I	8911	calcium channel, voltage-dependent, T type, alpha 1I subunit	22q13.1	Genetic association	-0.98	-10.96	6.96E-23	0.25	hHC014460	NM_021096
ASD DATABASE	HOMER1	9456	homer homolog 1 (Drosophila)	5q14.2	Rare single gene variant	-0.98	-9.46	3.13E-18	0.18	hHC012166	NM_004272
ASD DATABASE	PEX7	5191	peroxisomal biogenesis factor 7	6q23.3	Genetic Association	-1.02	-10.43	3.24E-21	0.23	hHC002373	NM_000288
ASD DATABASE	MAPK8IP2	23542	mitogen-activated protein kinase 8 interacting protein 2	22q13.33	Functional	-1.04	-19.21	3.20E-50	0.56	hHC024365	NM_012324
ASD DATABASE	ALOX5AP	241	arachidonate 5-lipoxygenase-activating protein	13q12	Genetic Association	-1.12	-5.45	1.26E-07	0.00	hHC019682	NM_001629
ASD DATABASE	CD38	952	CD38 molecule	4p15	Genetic Association	-1.16	-7.38	2.61E-12	0.08	hHC011804	NM_001775
ASD DATABASE	REEP3	NA	receptor accessory protein 3	10q21.3	Rare single gene variant	-1.19	-11.02	4.44E-23	0.25	hHE041048	BC018658
ASD DATABASE	ADA	100	adenosine deaminase	20q12-q13.11	Genetic Association	-1.21	-10.95	7.62E-23	0.25	hHC016014	AK123988
ASD DATABASE	DNAJC19	131118	DnaJ (Hsp40) homolog, subfamily C, member 19	3q26.33	Functional	-1.21	-16.93	1.14E-42	0.49	hHC004483	NM_145261
ASD DATABASE	BAIAP2	10458	BAI1-associated protein 2	17q25	Genetic Association	-1.21	-15.92	2.65E-39	0.45	hHA036123	NM_017450
ASD DATABASE	MAPK3	5595	mitogen-activated protein kinase 3	16p11.2	Rare Single Gene variant	-1.22	-20.77	2.91E-55	0.60	hHC016199	NM_001040056
ASD DATABASE	USP9Y	8287	ubiquitin specific peptidase 9, Y-linked	Yq11.2	Genetic Association	-1.22	-1.97	4.99E-02	-0.11	hHC008068	NM_004654
ASD DATABASE	CACNA1F	778	calcium channel, voltage-dependent, L type, alpha 1F subunit	Xp11.23	Genetic Association	-1.23	-21.57	8.09E-58	0.62	hHC022101	NM_005183

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ASD DATABASE	LRP2	4036	low density lipoprotein-related protein 2	2q24-q31	Rare single gene variant	-1.24	-7.92	9.38E-14	0.11	hHC010917	NM_004525
ASD DATABASE	C3orf58	205428	chromosome 3 open reading frame 58	3q24	Rare Single Gene variant	-1.29	-15.26	4.41E-37	0.43	hHC007820	NM_173552
ASD DATABASE	TDO2	6999	tryptophan 2,3-dioxygenase	4q31-q32	Genetic Association	-1.33	-9.84	2.17E-19	0.20	hHC006104	NM_005651
ASD DATABASE	STK39	27347	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	2q24.3	Genetic Association	-1.34	-19.27	2.09E-50	0.56	hHC006733	NM_013233
ASD DATABASE	BRUNOL4	56853	bruno-like 4, RNA binding protein (Drosophila)		Functional	-1.34	-18.40	1.43E-47	0.53	hHE041886	NM_020180
ASD DATABASE	PTGS2	5743	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	1q25.2-q25.3	Genetic Association	-1.38	-7.07	1.74E-11	0.07	hHR007248	NM_000963
ASD DATABASE	NOS2	4843	nitric oxide synthase 2, inducible	17q11.2-q12	Genetic Association	-1.45	-14.89	7.86E-36	0.42	hHC030645	NM_000625
ASD DATABASE	ATP10A	57194	ATPase, class V, type 10A	15q11.2	Genetic Association	-1.50	-10.73	3.76E-22	0.24	hHC013443	NM_024490
ASD DATABASE	CNTNAP5	129684	contactin associated protein-like 5	2q14.3	Genetic Association	-1.55	-13.90	1.54E-32	0.38	hHR010052	NM_130773
ASD DATABASE	SCN2A	6326	sodium channel, voltage-gated, type II, alpha subunit	2q23-q24	Rare Single Gene variant	-1.58	-20.89	1.20E-55	0.60	hHC014396	NM_021007
ASD DATABASE	SLC22A15	55356	solute carrier family 22, member 15	1p13.1	Genetic association	-1.65	-18.47	8.39E-48	0.54	hHC006443	NM_018420
ASD DATABASE	GRM8	2918	glutamate receptor, metabotropic 8	7q31.3-q32.1	Genetic Association	-1.66	-16.47	3.83E-41	0.47	hHC019914	NM_001127323
ASD DATABASE	ASS1	445	argininosuccinate synthetase 1	9q34.1	Genetic Association	-1.71	-18.84	5.12E-49	0.55	hHC030607	NM_000050
ASD DATABASE	PTPRC	5788	protein tyrosine phosphatase, receptor type, C	1q31-q32	Genetic Association	-1.74	-10.58	1.13E-21	0.23	hHC002057	NM_002838
ASD DATABASE	MKL2	57496	MKL/myocardin-like 2	16p13.12	Genetic Association	-1.97	-28.21	1.02E-77	0.74	hHC012802	NM_014048
ASD DATABASE	ATP2B2	491	ATPase, Ca++ transporting, plasma membrane 2	3p25.3	Genetic Association	-2.02	-23.71	1.69E-64	0.66	hHC001957	NM_001001331
ASD DATABASE	ZBTB16	7704	zinc finger and BTB domain containing 16	11q23.1	Genetic association	-2.10	-23.54	5.86E-64	0.66	hHC017436	NM_006006
ASD DATABASE	GABRA4	2557	gamma-aminobutyric acid (GABA) A receptor, alpha 4	4p12	Genetic Association	-2.26	-18.08	1.73E-46	0.52	hHC002869	NM_000809
ASD DATABASE	FOLH1	2346	folate hydrolase (prostate-specific membrane antigen) 1	11p11.2	Functional	-2.29	-11.48	1.49E-24	0.27	hHR028477	NM_004476
ASD DATABASE	SYT17	51760	synaptotagmin XVII	16p12.3	Genetic Association	-2.35	-24.20	5.52E-66	0.67	hHC019342	NM_016524
ASD DATABASE	CDH8	1006	cadherin 8, type 2	16q22.1	Rare Single Gene variant	-2.59	-22.06	2.25E-59	0.63	hHC009663	NM_001796
ASD DATABASE	MET	4233	met proto-oncogene (hepatocyte growth factor receptor)	7q31	Genetic Association	-2.86	-16.24	2.21E-40	0.46	hHR003121	NM_001127500
ASD DATABASE	PAH	5053	phenylalanine hydroxylase	12q22-q24.2	Rare single gene variant	-2.90	-19.08	8.66E-50	0.55	hHC005995	NM_000277
ASD DATABASE	PRKCB	5579	protein kinase C, beta	16p11.2	Genetic Association	-3.02	-29.72	6.74E-82	0.76	hHC021733	NM_002738
ASD DATABASE	NEFL	4747	neurofilament, light polypeptide	8p21	Genetic association/functional	-3.43	-25.34	2.15E-69	0.70	hHC005656	NM_006158
ASD DATABASE	CDH9	1007	cadherin 9, type 2 (T1-cadherin)	5p14	Genetic Association	-3.45	-27.28	4.67E-75	0.73	hHC005099	NM_016279
BPAD GWAS	AK5	26289	adenylate kinase 5	1p31	GWAS	0.33	3.76	2.17E-04	-0.07	hHA035503	NM_012093
BPAD GWAS	ALAS1	211	aminolevulinate, delta-, synthase 1	3p21.1	GWAS	0.33	6.42	7.35E-10	0.04	hHA037941	NM_000688
BPAD GWAS	ANK3	288	ankyrin 3, node of Ranvier (ankyrin G)	10q21	GWAS	2.42	22.94	4.18E-62	0.65	hHA034365	NM_020987
BPAD GWAS	BRMS1	25855	breast cancer metastasis suppressor 1	11q13-q13.2	GWAS	0.53	7.86	1.36E-13	0.10	hHC022165	NM_015399
BPAD GWAS	CACNA1C	775	calcium channel, voltage-dependent, L type, alpha 1C subunit		GWAS	0.45	4.55	8.60E-06	-0.04	hHA037564	NM_001129840
BPAD GWAS	CCS	9973	copper chaperone for superoxide dismutase	11q13	GWAS	0.25	4.85	2.23E-06	-0.03	hHC021118	NM_005125
BPAD GWAS	CNNM4	26504	cyclin M4	2p12-p11.2	GWAS	0.40	5.13	6.13E-07	-0.02	hHC003338	NM_020184
BPAD GWAS	DDX23	9416	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	12q13.12	GWAS	0.63	6.96	3.22E-11	0.06	hHR025792	NM_004818
BPAD GWAS	DGKH	160851	diacylglycerol kinase, eta		GWAS	0.01	0.07	9.45E-01	-0.13	hHR027242	BC044822
BPAD GWAS	DPP3	10072	dipeptidyl-peptidase 3	11q12-q13.1	GWAS	0.63	6.15	3.18E-09	0.03	hHR013854	NM_130443
BPAD GWAS	FAM83E	54854	family with sequence similarity 83, member E	19q13.32-q13.33	GWAS	0.01	0.22	8.26E-01	-0.13	hHC025861	NM_017708
BPAD GWAS	FSTL5	56884	follistatin-like 5	4q32.3	GWAS	0.61	5.95	9.73E-09	0.02	hHC008371	NM_020116

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BPAD GWAS	FUBP1	8880	far upstream element (FUSE) binding protein 1	1p31.1	GWAS	1.86	29.54	2.08E-81	0.76	hHC011066	AB209366
BPAD GWAS	GLT8D1	55830	glycosyltransferase 8 domain containing 1	3p21.1	GWAS	0.52	9.52	2.18E-18	0.18	hHC017657	NM_001010983
BPAD GWAS	GPR20	2843	G protein-coupled receptor 20	8q24.2-q24.3	GWAS	0.29	4.53	9.23E-06	-0.04	hHR010856	NM_005293
BPAD GWAS	ITIH1	3697	inter-alpha (globulin) inhibitor H1	3p21.2-p21.1	GWAS	0.01	0.11	9.16E-01	-0.13	hHC022349	NM_002215
BPAD GWAS	LMAN2L	81562	lectin, mannose-binding 2-like	2q11.2	GWAS	0.59	8.16	1.96E-14	0.12	hHC012128	NM_001142292
BPAD GWAS	LMBR1L	55716	limb region 1 homolog (mouse)-like	12q13.12	GWAS	1.33	26.01	2.27E-71	0.71	hHC022245	NM_018113
BPAD GWAS	LRFN4	78999	leucine rich repeat and fibronectin type III domain containing 4	11q13.1	GWAS	0.32	5.08	7.50E-07	-0.02	hHC021087	NM_024036
BPAD GWAS	LYG1	129530	lysozyme G-like 1	2q11.2	GWAS	0.57	4.50	1.07E-05	-0.04	hHC009312	NM_174898
BPAD GWAS	MAPK10	5602	mitogen-activated protein kinase 10	4q22.1-q23	GWAS	0.08	0.86	3.91E-01	-0.13	hHA032930	AK294125
BPAD GWAS	MGC27382	NA	hypothetical MGC27382	1p31.1	GWAS	0.09	1.18	2.38E-01	-0.12	hHC013898	AK091757
BPAD GWAS	MITD1	129531	MIT, microtubule interacting and transport, domain containing 1	2q11.2	GWAS	0.58	10.25	1.19E-20	0.22	hHC014516	NM_138798
BPAD GWAS	MLL2	8085	myeloid/lymphoid or mixed-lineage leukemia 2		GWAS	0.83	8.98	8.71E-17	0.16	hHE041849	NM_003482
BPAD GWAS	MRPL11	65003	mitochondrial ribosomal protein L11	11q13.3	GWAS	0.59	5.17	4.99E-07	-0.02	hHA035129	NM_170739
BPAD GWAS	MRPL30	51263	mitochondrial ribosomal protein L30	2q11.2	GWAS	0.26	4.21	3.62E-05	-0.05	hHR024911	NM_145212
BPAD GWAS	NCAN	1463	neurocan	19p12	GWAS	1.30	15.11	1.36E-36	0.42	hHC008161	NM_004386
BPAD GWAS	NEK4	6787	NIMA (never in mitosis gene a)-related kinase 4	3p21.1	GWAS	0.40	7.44	1.88E-12	0.08	hHC006908	NM_003157
BPAD GWAS	NFIX	4784	nuclear factor I/X (CCAAT-binding transcription factor)	19p13.3	GWAS	0.09	2.23	2.65E-02	-0.11	hHA040029	AK295290
BPAD GWAS	NPAS4	266743	neuronal PAS domain protein 4	11q13	GWAS	0.04	0.54	5.89E-01	-0.13	hHA037215	NM_178864
BPAD GWAS	NT5DC2	64943	5'-nucleotidase domain containing 2	3p21.1	GWAS	1.62	17.99	3.39E-46	0.52	hHC024330	NM_022908
BPAD GWAS	NUDT1	4521	nudix (nucleoside diphosphate linked moiety X)-type motif 1	7p22	GWAS	1.27	19.68	9.29E-52	0.57	hHC024103	NM_198949
BPAD GWAS	ODZ4	26011	odz, odd Oz/ten-m homolog 4 (Drosophila)	11q14.1	GWAS	0.74	6.92	4.23E-11	0.06	hHC008608	NM_001098816
BPAD GWAS	PACS1	55690	phosphofurin acidic cluster sorting protein 1	11q13.1	GWAS	0.10	1.83	6.89E-02	-0.12	hHC016796	NM_018026
BPAD GWAS	PBRM1	55193	polybromo 1	3p21	GWAS	2.25	42.58	5.14E-113	0.87	hHC007983	NM_018313
BPAD GWAS	PHF7	51533	PHD finger protein 7	3p21.1	GWAS	0.22	2.72	7.03E-03	-0.10	hHC012761	NM_016483
BPAD GWAS	PLK1	5347	polo-like kinase 1 (Drosophila)	16p12.1	GWAS	0.11	2.02	4.42E-02	-0.11	hHR026450	NM_005030
BPAD GWAS	PTGFR	5737	prostaglandin F receptor (FP)	1p31.1	GWAS	1.08	8.00	5.47E-14	0.11	hHC002159	NM_001039585
BPAD GWAS	RAB1B	81876	RAB1B, member RAS oncogene family	11q12	GWAS	0.39	6.18	2.76E-09	0.03	hHA033303	NM_030981
BPAD GWAS	RBM14	10432	RNA binding motif protein 14		GWAS	1.52	13.31	1.48E-30	0.35	hHC002778	NM_006328
BPAD GWAS	RBM4	5936	RNA binding motif protein 4	11q13	GWAS	2.17	38.34	1.38E-103	0.84	hHA033137	NM_002896
BPAD GWAS	RBM4B	83759	RNA binding motif protein 4B	11q13	GWAS	1.15	21.36	3.72E-57	0.61	hHC026961	NM_031492
BPAD GWAS	RCE1	9986	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	11q13	GWAS	1.15	18.66	2.10E-48	0.54	hHC014793	NM_005133
BPAD GWAS	REV1	51455	REV1 homolog (S. cerevisiae)	2q11.1-q11.2	GWAS	1.11	14.39	3.68E-34	0.40	hHC004303	NM_016316
BPAD GWAS	RFT1	91869	RFT1 homolog (S. cerevisiae)		GWAS	0.34	4.68	4.73E-06	-0.03	hHR013631	NM_052859
BPAD GWAS	RPL18	6141	ribosomal protein L18	19q13	GWAS	0.67	9.58	1.43E-18	0.18	hHR029076	NM_000979
BPAD GWAS	SF3B2	10992	splicing factor 3b, subunit 2, 145kDa	11q13.1	GWAS	0.02	0.43	6.68E-01	-0.13	hHC011819	NM_006842
BPAD GWAS	SFMBT1	51460	Scm-like with four mbt domains 1	3p21.1	GWAS	0.49	7.89	1.08E-13	0.10	hHC019969	NM_001005159
BPAD GWAS	SH3PXD2A	9644	SH3 and PX domains 2A	10q24.33	GWAS	0.09	1.21	2.29E-01	-0.12	hHC020707	NM_014631
BPAD GWAS	SLC29A2	3177	solute carrier family 29 (nucleoside transporters), member 2	11q13	GWAS	0.13	2.47	1.42E-02	-0.10	hHC019291	NM_001532
BPAD GWAS	SYNE1	23345	spectrin repeat containing, nuclear envelope 1	6q25	GWAS	0.69	5.34	2.23E-07	-0.01	hHA033917	NM_133650

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
BPAD GWAS	TLR9	54106	toll-like receptor 9	3p21.3	GWAS	0.07	1.23	2.19E-01	-0.12	hHA039914	NM_017442
BPAD GWAS	TRIM9	114088	tripartite motif-containing 9	14q22.1	GWAS	0.09	1.09	2.75E-01	-0.13	hHA037601	NM_015163
BPAD GWAS	TUBA1A	7846	tubulin, alpha 1a	12q12-q14.3	GWAS	0.75	11.21	1.12E-23	0.26	hHC025916	NM_006009
BPAD GWAS	USP33	23032	ubiquitin specific peptidase 33	1p31.1	GWAS	1.00	8.21	1.46E-14	0.12	hHA033914	NM_201626
BPAD GWAS	WDR82	80335	WD repeat domain 82	3p21.1	GWAS	0.82	17.15	2.11E-43	0.50	hHC025830	NM_025222
BPAD GWAS	ZMIZ1	57178	zinc finger, MIZ-type containing 1	10q22.3	GWAS	1.96	28.57	1.03E-78	0.75	hHC003709	NM_020338
BPAD GWAS	ZZZ3	26009	zinc finger, ZZ-type containing 3	1p31.1	GWAS	0.42	7.15	1.09E-11	0.07	hHC005208	NM_015534
BPAD GWAS	B3GNT1	11041	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	11q13.1	GWAS	-2.12	-23.82	8.16E-65	0.67	hHC006616	NM_006876
BPAD GWAS	BAP1	8314	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	3p21.31-p21.2	GWAS	-0.52	-8.90	1.49E-16	0.15	hHC018424	NM_004656
BPAD GWAS	BBS1	582	Bardet-Biedl syndrome 1	11q13.1	GWAS	-0.18	-2.95	3.46E-03	-0.09	hHC010268	NM_024649
BPAD GWAS	C2orf55	343990	chromosome 2 open reading frame 55	2q11.2	GWAS	-4.72	-45.96	4.80E-120	0.89	hHC013040	NM_207362
BPAD GWAS	CA11	770	carbonic anhydrase XI	19q13.3	GWAS	-2.77	-33.89	7.40E-93	0.81	hHC020247	NM_001217
BPAD GWAS	CACNA1D	776	calcium channel, voltage-dependent, L type, alpha 1D subunit	3p14.3	GWAS	-0.11	-1.32	1.89E-01	-0.12	hHC016540	NM_000720
BPAD GWAS	CACNB3	784	calcium channel, voltage-dependent, beta 3 subunit	12q13	GWAS	-0.01	-0.21	8.34E-01	-0.13	hHC016238	NM_000725
BPAD GWAS	CCDC87	55231	coiled-coil domain containing 87	11q13.1	GWAS	-1.34	-11.53	1.01E-24	0.28	hHC008764	NM_018219
BPAD GWAS	CHDH	55349	choline dehydrogenase	3p21.1	GWAS	-1.14	-12.28	3.71E-27	0.31	hHC013130	NM_018397
BPAD GWAS	CNIH2	254263	cornichon homolog 2 (Drosophila)	11q13.1	GWAS	-0.10	-1.21	2.29E-01	-0.12	hHC026434	NM_182553
BPAD GWAS	DBP	1628	D site of albumin promoter (albumin D-box) binding protein	19q13.3	GWAS	-1.42	-16.59	1.53E-41	0.48	hHC024359	NM_001352
BPAD GWAS	DDN	23109	dendrin	12q13.12	GWAS	-2.08	-20.06	5.29E-53	0.58	hHC022008	NM_015086
BPAD GWAS	DHH	50846	desert hedgehog homolog (Drosophila)	12q12-q13.1	GWAS	-0.12	-1.53	1.27E-01	-0.12	hHC014677	NM_021044
BPAD GWAS	DNAH1	25981	dynein, axonemal, heavy chain 1		GWAS	-1.91	-16.91	1.26E-42	0.49	hHR017783	NM_015512
BPAD GWAS	DNAJB4	11080	DnaJ (Hsp40) homolog, subfamily B, member 4	1p31.1	GWAS	-0.72	-9.00	7.34E-17	0.16	hHC002810	NM_007034
BPAD GWAS	EIF5B	9669	eukaryotic translation initiation factor 5B	2q11.2	GWAS	-0.01	-0.17	8.66E-01	-0.13	hHC001642	NM_015904
BPAD GWAS	FAM73A	374986	family with sequence similarity 73, member A	1p31.1	GWAS	-1.57	-16.93	1.11E-42	0.49	hHC001773	NM_198549
BPAD GWAS	FER1L5	90342	fer-1-like 5 (C. elegans)		GWAS	-0.02	-0.26	7.98E-01	-0.13	hHR016466	NM_001113382
BPAD GWAS	FGF21	26291	fibroblast growth factor 21	19q13.1-qter	GWAS	-0.13	-2.09	3.75E-02	-0.11	hHC024366	NM_019113
BPAD GWAS	FTSJ2	29960	FtsJ homolog 2 (E. coli)	7p22	GWAS	-0.02	-0.40	6.90E-01	-0.13	hHC010873	NM_013393
BPAD GWAS	FUT1	2523	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)	19q13.3	GWAS	-0.78	-8.32	6.97E-15	0.12	hHC012990	NM_000148
BPAD GWAS	FUT2	2524	fucosyltransferase 2 (secretor status included)	19q13.3	GWAS	-0.47	-8.05	3.90E-14	0.11	hHR018998	NM_000511
BPAD GWAS	GAL3ST3	89792	galactose-3-O-sulfotransferase 3	11q13.1	GWAS	-0.24	-4.11	5.48E-05	-0.06	hHC016890	NM_033036
BPAD GWAS	GLYCTK	132158	glycerate kinase	3p21.1	GWAS	-0.32	-7.18	8.79E-12	0.07	hHC018008	NM_145262
BPAD GWAS	GNL3	26354	guanine nucleotide binding protein-like 3 (nucleolar)	3p21.1	GWAS	-0.06	-0.50	6.15E-01	-0.13	hHA040707	NM_206825
BPAD GWAS	ITIH3	3699	inter-alpha (globulin) inhibitor H3	3p21.2-p21.1	GWAS	-0.19	-2.38	1.79E-02	-0.10	hHC025527	NM_002217
BPAD GWAS	ITIH4	3700	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	3p21-p14	GWAS	-0.59	-9.22	1.67E-17	0.17	hHC024955	NM_002218
BPAD GWAS	IZUMO1	284359	izumo sperm-egg fusion 1	19q13.33	GWAS	-1.06	-9.51	2.24E-18	0.18	hHC021500	NM_182575
BPAD GWAS	KLC2	64837	kinesin light chain 2	11q13.1	GWAS	-0.41	-8.03	4.55E-14	0.11	hHC023734	NM_001134775
BPAD GWAS	LBA1	9881	lupus brain antigen 1	3p22.2	GWAS	-0.43	-5.23	3.65E-07	-0.01	hHR016901	NM_014831
BPAD GWAS	LIPT1	51601	lipoyltransferase 1	2q11.2	GWAS	-0.41	-4.09	5.99E-05	-0.06	hHA034041	NM_145197

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Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
BPAD GWAS	MAD1L1	8379	MAD1 mitotic arrest deficient-like 1 (yeast)	7p22	GWAS	-0.67	-9.84	2.22E-19	0.20	hHR019802	NM_003550
BPAD GWAS	MGAT4A	11320	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	2q12	GWAS	-0.79	-9.20	1.97E-17	0.17	hHC020284	NM_012214
BPAD GWAS	MUSTN1	389125	musculoskeletal, embryonic nuclear protein 1	3p21.1	GWAS	-2.05	-13.74	5.32E-32	0.37	hHC019519	NM_205853
BPAD GWAS	NISCH	11188	nischarin	3p21.1	GWAS	-0.46	-6.97	3.17E-11	0.06	hHC014499	NM_007184
BPAD GWAS	NEXN	91624	nexilin (F actin binding protein)	1p31.1	GWAS	-0.71	-5.02	1.01E-06	-0.02	hHA035504	NM_144573
BPAD GWAS	NGF	4803	nerve growth factor (beta polypeptide)	1p13.1	GWAS	-0.16	-2.01	4.52E-02	-0.11	hHC009122	NM_002506
BPAD GWAS	NTN5	126147	netrin 5	19q13.33	GWAS	-1.29	-15.00	3.37E-36	0.42	hHC001505	NM_145807
BPAD GWAS	PC	5091	pyruvate carboxylase	11q13.4-q13.5	GWAS	-1.27	-19.63	1.34E-51	0.57	hHC009859	NM_001040716
BPAD GWAS	PELI3	246330	pellino homolog 3 (Drosophila)	11q13.1	GWAS	-2.30	-30.01	1.11E-82	0.76	hHC015800	NM_145065
BPAD GWAS	PPM1M	132160	protein phosphatase 1M (PP2C domain containing)	3p21.1	GWAS	-0.42	-4.50	1.07E-05	-0.04	hHC011132	NM_144641
BPAD GWAS	PRKAG1	5571	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	12q12-q14	GWAS	-0.55	-10.00	7.26E-20	0.20	hHC003989	NM_212461
BPAD GWAS	PRKCD	5580	protein kinase C, delta	3p21.31	GWAS	-1.86	-16.95	9.47E-43	0.49	hHC009892	NM_006254
BPAD GWAS	PTPRT	11122	protein tyrosine phosphatase, receptor type, T	20q12-q13	GWAS	-1.81	-19.43	6.29E-51	0.56	hHC008506	NM_133170
BPAD GWAS	RASIP1	54922	Ras interacting protein 1	19q13.33	GWAS	-1.20	-14.71	2.98E-35	0.41	hHC005312	NM_017805
BPAD GWAS	RHEBL1	121268	Ras homolog enriched in brain like 1	12q13.12	GWAS	-1.58	-17.30	6.67E-44	0.50	hHC024613	NM_144593
BPAD GWAS	RIN1	9610	Ras and Rab interactor 1	11q13.1	GWAS	-1.95	-26.11	1.12E-71	0.71	hHC023969	NM_004292
BPAD GWAS	RND1	27289	Rho family GTPase 1	12q12-q13	GWAS	-0.46	-5.74	2.91E-08	0.01	hHC023788	NM_014470
BPAD GWAS	SEMA3G	56920	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	3p21.1	GWAS	-0.92	-6.78	9.72E-11	0.05	hHC010991	NM_020163
BPAD GWAS	SPCS1	28972	signal peptidase complex subunit 1 homolog (S. cerevisiae)	3p21.1	GWAS	-0.73	-12.08	1.66E-26	0.30	hHC009782	NM_014041
BPAD GWAS	SPHK2	NA	sphingosine kinase 2	19q13.2	GWAS	-0.62	-11.71	2.76E-25	0.28	hHC026145	NM_020126
BPAD GWAS	SPRED1	161742	sprouty-related, EVH1 domain containing 1	15q14	GWAS	-0.46	-6.00	7.22E-09	0.02	hHC009720	NM_152594
BPAD GWAS	SPTBN2	6712	spectrin, beta, non-erythrocytic 2	11q13	GWAS	-0.22	-4.09	5.93E-05	-0.06	hHC021077	NM_006946
BPAD GWAS	STAB1	23166	stabilin 1	3p21.1	GWAS	-0.06	-0.75	4.56E-01	-0.13	hHC025154	NM_015136
BPAD GWAS	STK39	27347	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	2q24.3	GWAS	-1.34	-19.27	2.09E-50	0.56	hHC006733	NM_013233
BPAD GWAS	SYT12	91683	synaptotagmin XII	11q13.1	GWAS	-1.36	-16.68	7.49E-42	0.48	hHC023402	NM_177963
BPAD GWAS	TMEM151A	256472	transmembrane protein 151A	11q13.1	GWAS	-1.64	-21.69	3.22E-58	0.62	hHC023557	NM_153266
BPAD GWAS	TNNC1	7134	troponin C type 1 (slow)	3p21.3-p14.3	GWAS	-0.27	-3.06	2.51E-03	-0.09	hHC020672	NM_003280
BPAD GWAS	TNR	7143	tenascin R (restrictin, janusin)	1q24	GWAS	-0.17	-2.34	2.03E-02	-0.11	hHC015964	NM_003285
BPAD GWAS	TSGA10	80705	testis specific, 10	2q11.2	GWAS	-1.20	-8.72	5.01E-16	0.14	hHC009599	NM_025244
BPAD GWAS	TUBA1B	10376	tubulin, alpha 1b	12q13.12	GWAS	-0.37	-7.07	1.77E-11	0.07	hHR029243	NM_006082
BPAD GWAS	TWF2	11344	twinfilin, actin-binding protein, homolog 2 (Drosophila)	3p21.1	GWAS	-0.33	-7.41	2.26E-12	0.08	hHC020722	NM_007284
BPAD GWAS	TXNDC9	10190	thioredoxin domain containing 9	2q11.2	GWAS	-0.07	-1.23	2.19E-01	-0.12	hHC002433	NM_005783
BPAD GWAS	YIF1A	10897	Yip1 interacting factor homolog A (S. cerevisiae)	11q13	GWAS	-0.65	-11.99	3.34E-26	0.30	hHC023148	NM_020470
BPAD GWAS	ZDHHC24	254359	zinc finger, DHHC-type containing 24	11q13.1	GWAS	-1.55	-24.06	1.44E-65	0.67	hHC018753	NM_207340
ID	DCX	1641	doublecortin	Xq22.3-q23		4.28	40.18	8.85E-108	0.86	hHC004157	NM_000555
ID	FOXG1	2290	forkhead box G1			2.81	35.69	2.62E-97	0.82	hHC007076	NM_005249
ID	ZNF711	7552	zinc finger protein 711	Xq21.1-q21.2		2.14	18.43	1.15E-47	0.54	hHC007660	NM_021998
ID	AFF2	2334	AF4/FMR2 family, member 2	Xq28		2.34	26.87	6.79E-74	0.72	hHC005898	NM_002025
ID	BCOR	54880	BCL6 co-repressor	Xp21.2-p11.4		2.25	20.73	3.74E-55	0.60	hHA033656	AB046795

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ID	MID1	4281	midline 1 (Opitz/BBB syndrome)	Xp22		2.11	21.07	3.17E-56	0.61	hHR002515	NM_000381
ID	GRIK2	2898	glutamate receptor, ionotropic, kainate 2	6q16.3-q21		1.76	22.53	7.68E-61	0.64	hHC019020	NM_175768
ID	PRSS12	8492	protease, serine, 12 (neurotrypsin, motopsin)	4q28.1		1.55	11.40	2.73E-24	0.27	hHC015067	NM_003619
ID	ZEB2	9839	zinc finger E-box binding homeobox 2	2q22.3		1.50	15.51	6.50E-38	0.44	hHR029739	NM_014795
ID	CASK	8573	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	Xp11.4		1.58	15.94	2.28E-39	0.45	hHR002782	NM_003688
ID	PHF6	84295	PHD finger protein 6	Xq26.3		1.53	24.92	3.68E-68	0.69	hHR002178	NM_032458
ID	NRXN1	9378	neurexin 1	2p16.3		1.31	14.33	6.02E-34	0.39	hHA035283	NM_001135659
ID	ATRX	546	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	Xq13.1-q21.1		1.10	10.75	3.29E-22	0.24	hHC031675	NM_000489
ID	ZC3H14	79882	zinc finger CCCH-type containing 14	14q31.3		1.35	15.99	1.58E-39	0.46	hHA035687	NM_024824
ID	SOBP	55084	sine oculis binding protein homolog (Drosophila)	6q21		1.20	14.01	6.70E-33	0.38	hHC010973	NM_018013
ID	ST3GAL3	6487	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	1p34.1		0.03	0.42	6.75E-01	-0.13	hHC011729	NM_174963
ID	UBE2A	7319	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	Xq24-q25		0.97	9.70	5.85E-19	0.19	hHA034036	NM_181777
ID	CUL4B	8450	cullin 4B	Xq23		1.03	17.06	4.11E-43	0.49	hHR004728	NM_003588
ID	UPF3B	65109	UPF3 regulator of nonsense transcripts homolog B (yeast)	Xq25-q26		1.10	19.36	1.03E-50	0.56	hHC025870	NM_080632
ID	BRWD3	254065	bromodomain and WD repeat domain containing 3	Xq21.1		0.87	8.48	2.51E-15	0.13	hHC011183	NM_153252
ID	AP4B1	10717	adaptor-related protein complex 4, beta 1 subunit	1p13.2		0.96	18.28	3.73E-47	0.53	hHC019207	NM_006594
ID	ZNF81	347344	zinc finger protein 81	Xp11.23		0.92	11.05	3.72E-23	0.25	hHR008276	NM_007137
ID	TUSC3	7991	tumor suppressor candidate 3	8p22		1.00	13.96	1.02E-32	0.38	hHC024693	NM_006765
ID	RAI1	10743	retinoic acid induced 1	17p11.2		0.99	15.41	1.40E-37	0.44	hHC011816	NM_030665
ID	VLDLR	NA	very low density lipoprotein receptor	9p24		1.45	14.53	1.25E-34	0.40	hHA035290	NM_003383
ID	UBE3A	7337	ubiquitin protein ligase E3A	15q11-q13		0.71	6.01	7.11E-09	0.02	hHA033034	NM_130839
ID	AP4M1	9179	adaptor-related protein complex 4, mu 1 subunit	7q22.1		0.81	12.80	7.22E-29	0.33	hHR012502	NM_004722
ID	TCF4	6925	transcription factor 4	18q21.1		0.80	12.62	2.92E-28	0.32	hHC020459	NM_001083962
ID	FTSJ1	24140	FtsJ homolog 1 (E. coli)	Xp11.23		0.75	15.25	4.79E-37	0.43	hHC013601	NM_177439
ID	OCRL	4952	oculocerebrorenal syndrome of Lowe	Xq25-q26.1		0.73	13.77	4.22E-32	0.37	hCT001285	NM_000276
ID	SLC16A2	6567	solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	Xq13.2		0.87	14.11	3.27E-33	0.39	hHC009198	NM_006517
ID	OFD1	8481	oral-facial-digital syndrome 1	Xp22		0.73	11.02	4.47E-23	0.25	hHC027610	NM_003611
ID	NSDHL	50814	NAD(P) dependent steroid dehydrogenase-like	Xq28		0.48	4.49	1.11E-05	-0.04	hHC008330	AK026549
ID	DLG3	1741	discs, large homolog 3 (Drosophila)	Xq13.1		0.67	8.25	1.07E-14	0.12	hHA034468	NM_020730
ID	SLC9A6	10479	solute carrier family 9 (sodium/hydrogen exchanger), member 6	Xq26.3		0.31	3.20	1.56E-03	-0.08	hHA036834	NM_001042537
ID	OPHN1	4983	oligophrenin 1	Xq12		0.58	6.06	5.34E-09	0.02	hHC002925	NM_002547
ID	HSD17B10	3028	hydroxysteroid (17-beta) dehydrogenase 10	Xp11.2		0.43	8.44	3.10E-15	0.13	hHC024075	NM_004493
ID	MECP2	4204	methyl CpG binding protein 2 (Rett syndrome)	Xq28		0.36	3.15	1.86E-03	-0.09	hHA035057	NM_004992
ID	FLNA	2316	filamin A, alpha (actin binding protein 280)	Xq28		0.53	7.42	2.05E-12	0.08	hHC016668	NM_001110556
ID	ERLIN2	11160	ER lipid raft associated 2	8p11.2		0.51	6.52	4.21E-10	0.04	hHA037813	NM_007175
ID	CRBN	51185	cereblon	3p26.3		0.30	4.65	5.57E-06	-0.04	hHA036013	NM_016302

Supp Table 1 Gene Sets

Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ID	ARX	170302	aristaless related homeobox	Xp21		0.21	3.19	1.62E-03	-0.08	hHC020322	NM_139058
ID	SHROOM4	57477	shroom family member 4	Xp11.22		0.29	1.96	5.09E-02	-0.11	hHC015016	NM_020717
ID	AP1S2	8905	adaptor-related protein complex 1, sigma 2 subunit	Xp22.2		0.32	4.39	1.70E-05	-0.05	hHR009633	NM_003916
ID	FOXP1	27086	forkhead box P1	3p14.1		0.10	1.11	2.69E-01	-0.12	hHC002879	NM_032682
ID	MEF2C	4208	myocyte enhancer factor 2C	5q14		0.45	3.85	1.50E-04	-0.06	hHR007934	NM_002397
ID	ZNF41	7592	zinc finger protein 41	Xp11.23		0.31	4.17	4.22E-05	-0.05	hHC007289	NM_007130
ID	PCDH19	57526	protocadherin 19	Xq13.3		0.28	3.12	2.01E-03	-0.09	hHC004670	NM_001105243
ID	HUWE1	10075	HECT, UBA and WWE domain containing 1	Xp11.22		0.24	3.27	1.24E-03	-0.08	hHR001757	NM_031407
ID	PHF8	23133	PHD finger protein 8	Xp11.22		0.19	3.35	9.49E-04	-0.08	hHC005894	NM_015107
ID	GRIA3	2892	glutamate receptor, ionotrophic, AMPA 3	Xq25-q26		0.12	1.48	1.39E-01	-0.12	hHA033134	NM_007325
ID	CDKL5	6792	cyclin-dependent kinase-like 5	Xp22		0.13	1.57	1.18E-01	-0.12	hHC018635	NM_003159
ID	MED12	9968	mediator complex subunit 12	Xq13		0.13	3.58	4.13E-04	-0.07	hHC023972	NM_005120
ID	ACSL4	2182	acyl-CoA synthetase long-chain family member 4	Xq22.3-q23		0.02	0.16	8.69E-01	-0.13	hHA034712	NM_022977
ID	PQBP1	10084	polyglutamine binding protein 1	Xp11.23		0.04	0.98	3.29E-01	-0.13	hHC024350	NM_005710
ID	ZNF526	116115	zinc finger protein 526	19q13.2		0.08	1.39	1.65E-01	-0.12	hHC025378	NM_133444
ID	SRPX2	27286	sushi-repeat-containing protein, X-linked 2	Xq21.33-q23		0.17	2.08	3.85E-02	-0.11	hHC012279	NM_014467
ID	MAN1B1	11253	mannosidase, alpha, class 1B, member 1	9q34		0.03	0.57	5.71E-01	-0.13	hHC022873	NM_016219
ID	CDH15	1013	cadherin 15, type 1, M-cadherin (myotubule)	16q24.3		0.16	1.43	1.55E-01	-0.12	hHC019200	NM_004933
ID	NHS	4810	Nance-Horan syndrome (congenital cataracts and dental anomalies)	Xp22.13		0.03	0.31	7.54E-01	-0.13	hHC007570	NM_198270
ID	MAGT1	84061	magnesium transporter 1	Xq21.1		-0.87	-9.21	1.74E-17	0.17	hHC031167	NM_032121
ID	ZDHHC9	51114	zinc finger, DHHC-type containing 9	Xq26.1		-0.11	-1.10	2.73E-01	-0.13	hHC012373	NM_016032
ID	PAK3	5063	p21 protein (Cdc42/Rac)-activated kinase 3	Xq22.3		0.00	-0.08	9.34E-01	-0.13	hHC020632	NM_002578
ID	RPS6KA3	6197	ribosomal protein S6 kinase, 90kDa, polypeptide 3	Xp22.2-p22.1		-0.17	-3.14	1.91E-03	-0.09	hHC016215	NM_004586
ID	FMR1	2332	fragile X mental retardation 1	Xq27.3		-0.15	-2.98	3.15E-03	-0.09	hHC006309	NM_002024
ID	GDI1	2664	GDP dissociation inhibitor 1	Xq28		-0.10	-1.53	1.27E-01	-0.12	hHC017813	NM_001493
ID	SYNGAP1	8831	synaptic Ras GTPase activating protein 1 homolog (rat)	6p21.3		-0.05	-0.57	5.67E-01	-0.13	hHC014146	NM_006772
ID	CC2D1A	54862	coiled-coil and C2 domain containing 1A	19p13.12		-0.23	-4.92	1.65E-06	-0.03	hHC024755	AF536205
ID	IQSEC2	23096	IQ motif and Sec7 domain 2	Xp11.22		-0.32	-5.00	1.11E-06	-0.02	hHC019479	NM_001111125
ID	PTCHD1	139411	patched domain containing 1	Xp22.11		-0.31	-3.19	1.61E-03	-0.08	hHC004792	NM_173495
ID	RAB39B	116442	RAB39B, member RAS oncogene family	Xq28		-0.33	-5.51	9.31E-08	0.00	hHC004780	NM_171998
ID	DYNC1H1	1778	dynein, cytoplasmic 1, heavy chain 1	14q32.3-qter|14q32		-0.45	-6.91	4.46E-11	0.06	hHR011150	NM_001376
ID	AP4S1	11154	adaptor-related protein complex 4, sigma 1 subunit	14q12		-0.53	-8.63	9.09E-16	0.14	hHC017225	NM_007077
ID	ATP6AP2	10159	ATPase, H+ transporting, lysosomal accessory protein 2	Xp11.4		-0.60	-10.51	1.82E-21	0.23	hHC031215	NM_005765
ID	CNTNAP2	26047	contactin associated protein-like 2	7q35-q36		-1.05	-6.98	3.01E-11	0.06	hHC008609	NM_014141
ID	TRAPPC9	83696	trafficking protein particle complex 9	8q24.3		-0.71	-13.29	1.74E-30	0.35	hHC021094	NM_031466
ID	PRPS1	5631	phosphoribosyl pyrophosphate synthetase 1	Xq21.32-q24		-0.91	-18.09	1.57E-46	0.52	hHC023493	NM_002764
ID	CA8	767	carbonic anhydrase VIII	8q11-q12		-0.83	-8.66	7.48E-16	0.14	hHC011745	NM_004056
ID	STXBP1	6812	syntaxin binding protein 1	9q34.1		-1.08	-16.32	1.24E-40	0.47	hHA037879	NM_003165
ID	ARHGEF9	23229	Cdc42 guanine nucleotide exchange factor (GEF) 9	Xq11.1		-1.14	-18.43	1.20E-47	0.54	hHC009004	NM_015185

Supp Table 1 Gene Sets

Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
ID	HCCS	3052	holocytochrome c synthase (cytochrome c heme-lyase)	Xp22.3		-0.97	-17.57	8.49E-45	0.51	hHC007513	NM_005333
ID	SLC6A8	6535	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Xq28		-1.15	-17.03	5.18E-43	0.49	hHR029029	NM_005629
ID	ARHGEF6	9459	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	Xq26.3		-1.17	-15.87	4.06E-39	0.45	hHC007361	NM_004840
ID	IL1RAPL1	11141	interleukin 1 receptor accessory protein-like 1	Xp22.1-p21.3		-1.16	-16.10	6.47E-40	0.46	hHC014183	AJ243874
ID	SYN1	6853	synapsin I	Xp11.23		-1.35	-15.31	2.90E-37	0.43	hHC023953	NM_006950
ID	TSPAN7	7102	tetraspanin 7	Xp11.4		-1.99	-26.84	8.25E-74	0.72	hHC005367	NM_004615
ID	SYP	6855	synaptophysin	Xp11.23-p11.22		-2.22	-29.72	6.79E-82	0.76	hHC023248	NM_003179
ID	PLP1	5354	proteolipid protein 1	Xq22		-4.47	-22.11	1.61E-59	0.63	hHA036342	NM_001128834
Neurodegenerative	ABCA7	10347	ATP-binding cassette, sub-family A (ABC1), member 7	19p13.3	GWAS	0.31	3.33	1.01E-03	-0.08	hHA038953	NM_019112
Neurodegenerative	ANG	283	angiogenin, ribonuclease, RNase A family, 5	14q11.1-q11.2	`	0.28	6.68	1.69E-10	0.05	hHA038640	NM_001145
Neurodegenerative	APP	351	amyloid beta (A4) precursor protein	21q21.2|21q21.3	"Mendelian" Gene	0.96	11.91	6.16E-26	0.29	hCT001336	NM_000484
Neurodegenerative	BST1	683	bone marrow stromal cell antigen 1	4p15	GWAS	0.29	3.13	1.95E-03	-0.09	hHC006909	NM_004334
Neurodegenerative	C9orf72	203228	chromosome 9 open reading frame 72	9p21.2	GWAS	1.22	13.73	5.83E-32	0.37	hHA034733	NM_018325
Neurodegenerative	CCDC62	84660	coiled-coil domain containing 62	12q24.31	GWAS	0.42	4.60	6.81E-06	-0.04	hHA034710	NM_201435
Neurodegenerative	CD2AP	23607	CD2-associated protein	6p12	GWAS	1.32	20.76	3.11E-55	0.60	hHC007088	NM_012120
Neurodegenerative	CLEC16A	23274	C-type lectin domain family 16, member A	16p13.13	GWAS	0.44	8.10	2.98E-14	0.11	hHC009748	NM_015226
Neurodegenerative	FUS	2521	fusion (involved in t(12;16) in malignant liposarcoma)	16p11.2	"Mendelian" Gene	0.65	12.88	3.97E-29	0.33	hHC024724	NM_004960
Neurodegenerative	HTT	3064	huntingtin	4p16.3	"Mendelian" Gene/Linkage Analysis	0.15	2.40	1.70E-02	-0.10	hHC016403	NM_002111
Neurodegenerative	MAPT	4137	microtubule-associated protein tau	17q21.1	"Mendelian" Gene/Linkage Analysis	0.67	8.69	6.14E-16	0.14	hHR012346	NM_001123066
Neurodegenerative	MCCC1	56922	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	3q27	GWAS	0.01	0.24	8.07E-01	-0.13	hHC004347	NM_020166
Neurodegenerative	PICALM	8301	phosphatidylinositol binding clathrin assembly protein	11q14	GWAS	0.04	0.60	5.50E-01	-0.13	hHC003477	NM_007166
Neurodegenerative	PSEN1	5663	presenilin 1	14q24.3	"Mendelian" Gene	0.21	2.48	1.39E-02	-0.10	hHA037604	NM_000021
Neurodegenerative	TARDBP	23435	TAR DNA binding protein	1p36.22	"Mendelian" Gene	0.34	5.67	4.23E-08	0.00	hHR007838	NM_007375
Neurodegenerative	AHI1	54806	Abelson helper integration site 1	6q23.3	GWAS	-1.06	-14.54	1.13E-34	0.40	hHR010594	NM_001134831
Neurodegenerative	APOE	348	apolipoprotein E	19q13.2	"Mendelian" Gene/Linkage Analysis	-2.54	-18.34	2.35E-47	0.53	hHC024278	NM_000041
Neurodegenerative	BIN1	274	bridging integrator 1	2q14	GWAS	-1.44	-22.62	3.91E-61	0.64	hHC021831	NM_139343
Neurodegenerative	CD226	10666	CD226 molecule	18q22.3	GWAS	-0.25	-1.58	1.15E-01	-0.12	hHC006609	NM_006566
Neurodegenerative	CD33	945	CD33 molecule	19q13.3	GWAS	-0.70	-9.63	9.73E-19	0.19	hHC026914	NM_001772
Neurodegenerative	CD5	921	CD5 molecule	11q13	GWAS	-0.06	-0.88	3.79E-01	-0.13	hHC015713	NM_014207
Neurodegenerative	CHMP2B	25978	chromatin modifying protein 2B	3p11.2	"Mendelian" Gene/Linkage Analysis	-0.51	-8.23	1.24E-14	0.12	hHC003076	NM_014043
Neurodegenerative	CLU	1191	clusterin	8p21-p12	GWAS	-1.68	-23.69	1.94E-64	0.66	hHC017231	NM_203339
Neurodegenerative	CR1	1378	complement component (3b/4b) receptor 1 (Knops blood group)	1q32	GWAS	-0.04	-0.46	6.45E-01	-0.13	hHA033522	NM_000651
Neurodegenerative	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma, 1	3q27-qter	"Mendelian" Gene/Linkage Analysis	-0.17	-1.83	6.81E-02	-0.11	hHA039850	D12686
Neurodegenerative	EVI5	7813	ecotropic viral integration site 5	1p22.1	GWAS	-0.60	-10.18	2.02E-20	0.21	hHC006925	NM_005665
Neurodegenerative	GAK	2580	cyclin G associated kinase	4p16	GWAS	-0.47	-8.43	3.32E-15	0.13	hHC015505	NM_005255
Neurodegenerative	GBA	2629	glucosidase, beta; acid (includes glucosylceramidase)	1q21	GWAS	-1.54	-21.61	5.82E-58	0.62	hHR023044	NM_001005749
Neurodegenerative	GPNMB	10457	glycoprotein (transmembrane) nmb	7p15	GWAS	-0.33	-1.78	7.63E-02	-0.12	hHA035795	NM_001005340

Supp Table 1 Gene Sets

Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Genetic Evidence	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe ID	Ref Seq Accession
Neurodegenerative	GRN	2896	granulin	17q21.32	"Mendelian" Gene/Linkage Analysis	-0.66	-8.48	2.38E-15	0.13	hHC020152	NM_002087
Neurodegenerative	IL7R	3575	interleukin 7 receptor	5p13	"Mendelian" Gene/Linkage Analysis	-1.16	-7.04	2.01E-11	0.06	hHC010514	AL713738
Neurodegenerative	LRRK2	120892	leucine-rich repeat kinase 2	12q12	"Mendelian" Gene/Linkage Analysis	-2.56	-30.72	1.33E-84	0.77	hHC001998	NM_198578
Neurodegenerative	MS4A6A	64231	membrane-spanning 4-domains, subfamily A, member 6A	11q12.1	GWAS	-0.38	-2.72	6.95E-03	-0.10	hHA039975	NM_022349
Neurodegenerative	OPTN	10133	optineurin	10p13	"Mendelian" Gene/Linkage Analysis	-0.97	-15.14	1.11E-36	0.43	hHC006197	NM_001008211
Neurodegenerative	PARK7	11315	Parkinson disease (autosomal recessive, early onset) 7	1p36.23	"Mendelian" Gene/Linkage Analysis	-0.28	-5.28	2.88E-07	-0.01	hHC020515	NM_007262
Neurodegenerative	PINK1	65018	PTEN induced putative kinase 1	1p36	"Mendelian" Gene/Linkage Analysis	-2.22	-32.69	8.64E-90	0.79	hHC008411	NM_032409
Neurodegenerative	PSEN2	5664	presenilin 2 (Alzheimer disease 4)	1q31-q42	"Mendelian" Gene/Linkage Analysis	-1.15	-20.11	3.69E-53	0.58	hHC024320	NM_000447
Neurodegenerative	RAB25	57111	RAB25, member RAS oncogene family	1q22	GWAS	-0.02	-0.19	8.50E-01	-0.13	hHC023607	NM_020387
Neurodegenerative	SETD1A	9739	SET domain containing 1A	16p11.2	GWAS	-0.33	-7.76	2.52E-13	0.10	hHC024151	NM_014712
Neurodegenerative	SNCA	6622	synuclein, alpha (non A4 component of amyloid precursor)	4q21	"Mendelian" Gene/Linkage Analysis	-1.86	-16.66	9.07E-42	0.48	hHC003453	NM_000345
Neurodegenerative	SOD1	6647	superoxide dismutase 1, soluble	21q22.1|21q22.11	"Mendelian" Gene/Linkage Analysis	-0.41	-6.53	4.06E-10	0.04	hHC020010	NM_000454
Neurodegenerative	STK39	27347	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	2q24.3	GWAS	-1.34	-19.27	2.09E-50	0.56	hHC006733	NM_013233
Neurodegenerative	TAGAP	117289	T-cell activation RhoGTPase activating protein	6q25.3	GWAS	-0.11	-1.05	2.96E-01	-0.13	hHA034514	NM_138810
Neurodegenerative	UBQLN2	29978	ubiquilin 2	Xp11.23-p11.1	"Mendelian" Gene/Linkage Analysis	-0.49	-7.81	1.87E-13	0.10	hHC003359	NM_013444
Neurodegenerative	VAPB	9217	VAMP (vesicle-associated membrane protein)-associated protein B and C	20q13.33	"Mendelian" Gene/Linkage Analysis	-0.68	-6.25	1.89E-09	0.03	hHR011073	NM_004738
Neurodegenerative	VPS35	55737	vacuolar protein sorting 35 homolog (S. cerevisiae)	16q12	"Mendelian" Gene/Linkage Analysis	-0.77	-13.16	4.65E-30	0.35	hHC011701	NM_018206

Supp Table 2 Overlap

Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe	Ref Seq Accession
SCZ (Meta-analysis), NDG	AHI1	54806	Abelson helper integration site 1	6q23.3	-1.06	-14.54	1.13E-34	0.40	hHR010594	NM_001134831
SCZ (PGC GWAS), BPAD GWAS	ALAS1	211	aminolevulinate, delta-, synthase 1	3p21.1	0.33	6.42	7.35E-10	0.04	hHA037941	NM_000688
ASD (Database), BPAD GWAS, NDD	ANK3	288	ankyrin 3, node of Ranvier (ankyrin G)	10q21	2.42	22.94	4.18E-62	0.65	hHA034365	NM_020987
SCZ (Meta-analysis), NDG	APOE	348	apolipoprotein E	19q13.2	-2.54	-18.34	2.35E-47	0.53	hHC024278	NM_000041
SCZ (PGC GWAS), BPAD GWAS	BAP1	8314	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	3p21.31-p21.2	-0.52	-8.90	1.49E-16	0.15	hHC018424	NM_004656
NDD, SCZ SNV	C18orf1	753	chromosome 18 open reading frame 1	18p11.2	-0.04	-0.41	6.79E-01	-0.13	hHC001974	NM_001003674
SCZ (PGC GWAS), BPAD GWAS	CACNA1C	775	calcium channel, voltage-dependent, L type, alpha 1C subunit		0.45	4.55	8.60E-06	-0.04	hHA037564	NM_001129840
ASD (Database), BPAD GWAS	CACNA1D	776	calcium channel, voltage-dependent, L type, alpha 1D subunit	3p14.3	-0.11	-1.32	1.89E-01	-0.12	hHC016540	NM_000720
SCZ (SNV), ASD (Database)	CACNA1I	8911	calcium channel, voltage-dependent, T type, alpha 1I subunit	22q13.1	-0.98	-10.96	6.96E-23	0.25	hHC014460	NM_021096
ID, NDD	CDKL5	6792	cyclin-dependent kinase-like 5	Xp22	0.13	1.57	1.18E-01	-0.12	hHC018635	NM_003159
SCZ (PGC GWAS), BPAD GWAS	DNAH1	25981	dynein, axonemal, heavy chain 1		-1.91	-16.91	1.26E-42	0.49	hHR017783	NM_015512
SCZ (Meta-analysis), ASD (Database)	DRD2	1813	dopamine receptor D2	11q23	0.22	2.30	2.24E-02	-0.11	hHA035616	NM_000795
NDD, ASD (Database),ID	FOXP1	27086	forkhead box P1	3p14.1	0.10	1.11	2.69E-01	-0.12	hHC002879	NM_032682
SCZ (PGC GWAS), BPAD GWAS	FTSJ2	29960	FtsJ homolog 2 (E. coli)	7p22	-0.02	-0.40	6.90E-01	-0.13	hHC010873	NM_013393
SCZ (PGC GWAS), BPAD GWAS	GLT8D1	55830	glycosyltransferase 8 domain containing 1	3p21.1	0.52	9.52	2.18E-18	0.18	hHC017657	NM_001010983
SCZ (PGC GWAS), BPAD GWAS	GLYCTK	132158	glycerate kinase	3p21.1	-0.32	-7.18	8.79E-12	0.07	hHC018008	NM_145262
SCZ (PGC GWAS), BPAD GWAS	GNL3	26354	guanine nucleotide binding protein-like 3 (nucleolar)	3p21.1	-0.06	-0.50	6.15E-01	-0.13	hHA040707	NM_206825
ID, ASD (Databse)	GRIK2	2898	glutamate receptor, ionotropic, kainate 2	6q16.3-q21	1.76	22.53	7.68E-61	0.64	hHC019020	NM_175768
NDD, SCZ (Meta-analysis), ASD Database	GRIN2B	2904	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	12p12	0.13	2.02	4.46E-02	-0.11	hHC022772	NM_000834
SCZ (PGC GWAS), BPAD GWAS	ITIH1	3697	inter-alpha (globulin) inhibitor H1	3p21.2-p21.1	0.01	0.11	9.16E-01	-0.13	hHC022349	NM_002215
SCZ (PGC GWAS), BPAD GWAS	ITIH3	3699	inter-alpha (globulin) inhibitor H3	3p21.2-p21.1	-0.19	-2.38	1.79E-02	-0.10	hHC025527	NM_002217
SCZ (PGC GWAS), BPAD GWAS	ITIH4	3700	inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein)	3p21-p14	-0.59	-9.22	1.67E-17	0.17	hHC024955	NM_002218
SCZ (SNV), ASD (Database)	LAMA1	284217	laminin, alpha 1	18p11.31	2.02	14.87	9.22E-36	0.41	hHC007864	NM_005559
SCZ (PGC GWAS), BPAD GWAS	LBA1	9881	lupus brain antigen 1	3p22.2	-0.43	-5.23	3.65E-07	-0.01	hHR016901	NM_014831
SCZ (PGC GWAS), BPAD GWAS	MAD1L1	8379	MAD1 mitotic arrest deficient-like 1 (yeast)	7p22	-0.67	-9.84	2.22E-19	0.20	hHR019802	NM_003550
ASD CNV, SCZ SNV	MBTPS1	8720	membrane-bound transcription factor peptidase, site 1	16|16q24	0.59	10.10	3.47E-20	0.21	hHA035034	NM_003791
ID, ASD (Databse)	MEF2C	4208	myocyte enhancer factor 2C	5q14	0.45	3.85	1.50E-04	-0.06	hHR007934	NM_002397
SCZ (Meta-analysis), ASD (Database)	MTHFR	4524	5,10-methylenetetrahydrofolate reductase (NADPH)	1p36.3	0.54	5.23	3.69E-07	-0.01	hHC015904	NM_005957
SCZ (PGC GWAS), BPAD GWAS	MUSTN1	389125	musculoskeletal, embryonic nuclear protein 1	3p21.1	-2.05	-13.74	5.32E-32	0.37	hHC019519	NM_205853
SCZ (PGC GWAS, SNV), BPAD GWAS	NCAN	1463	neurocan	19p12	1.30	15.11	1.36E-36	0.42	hHC008161	NM_004386
SCZ (PGC GWAS), BPAD GWAS	NEK4	6787	NIMA (never in mitosis gene a)-related kinase 4	3p21.1	0.40	7.44	1.88E-12	0.08	hHC006908	NM_003157
SCZ (PGC GWAS), BPAD GWAS	NISCH	11188	nischarin	3p21.1	-0.46	-6.97	3.17E-11	0.06	hHC014499	NM_007184
ID, SCZ (CNV), ASD (CNV)	NRXN1	9378	neurexin 1	2p16.3	1.31	14.33	6.02E-34	0.39	hHA035283	NM_001135659
SCZ (PGC GWAS), BPAD GWAS	NT5DC2	64943	5'-nucleotidase domain containing 2	3p21.1	1.62	17.99	3.39E-46	0.52	hHC024330	NM_022908
SCZ (PGC GWAS), SCZ (CNV), BPAD GWAS	NUDT1	4521	nudix (nucleoside diphosphate linked moiety X)-type motif 1	7p22	1.27	19.68	9.29E-52	0.57	hHC024103	NM_198949
SCZ (PGC GWAS), BPAD GWAS	PBRM1	55193	polybromo 1	3p21	2.25	42.58	5.14E-113	0.87	hHC007983	NM_018313
SCZ (Meta-analysis), ASD (Database)	PDE4B	5142	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	1p31	-0.49	-7.51	1.18E-12	0.09	hHC005298	NM_001037341
SCZ (PGC GWAS), BPAD GWAS	PHF7	51533	PHD finger protein 7	3p21.1	0.22	2.72	7.03E-03	-0.10	hHC012761	NM_016483
SCZ (PGC GWAS), BPAD GWAS	PPM1M	132160	protein phosphatase 1M (PP2C domain containing)	3p21.1	-0.42	-4.50	1.07E-05	-0.04	hHC011132	NM_144641
SCZ (SNV), ASD (Database)	PRKCB	5579	protein kinase C, beta	16p11.2	-3.02	-29.72	6.74E-82	0.76	hHC021733	NM_002738
ID, ASD (Databse)	RAI1	10743	retinoic acid induced 1	17p11.2	0.99	15.41	1.40E-37	0.44	hHC011816	NM_030665

Supp Table 2 Overlap

Gene Set	Gene Symbol	EntrezGene ID	Description	Location	Beta Coefficient ("Fetal Effect")	t-statistic	p-value	Adjusted R2	Probe	Ref Seq Accession
SCZ (Meta-analysis), ASD (Database)	RELN	5649	reelin	7q22	0.25	1.83	6.86E-02	-0.12	hHC004991	NM_005045
SCZ (PGC GWAS), BPAD GWAS	RFT1	91869	RFT1 homolog (S. cerevisiae)		0.34	4.68	4.73E-06	-0.03	hHR013631	NM_052859
SCZ (PGC GWAS), BPAD GWAS	SEMA3G	56920	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	3p21.1	-0.92	-6.78	9.72E-11	0.05	hHC010991	NM_020163
SCZ (SNV), NDG	SETD1A	9739	SET domain containing 1A	16p11.2	-0.33	-7.76	2.52E-13	0.10	hHC024151	NM_014712
SCZ (PGC GWAS), BPAD GWAS	SFMBT1	51460	Scm-like with four mbt domains 1	3p21.1	0.49	7.89	1.08E-13	0.10	hHC019969	NM_001005159
SCZ (PGC GWAS), BPAD GWAS	SH3PXD2A	9644	SH3 and PX domains 2A	10q24.33	0.09	1.21	2.29E-01	-0.12	hHC020707	NM_014631
SCZ (PGC GWAS), BPAD GWAS	SPCS1	28972	signal peptidase complex subunit 1 homolog (S. cerevisiae)	3p21.1	-0.73	-12.08	1.66E-26	0.30	hHC009782	NM_014041
SCZ (PGC GWAS), BPAD GWAS	STAB1	23166	stabilin 1	3p21.1	-0.06	-0.75	4.56E-01	-0.13	hHC025154	NM_015136
ASD(Database), BPAD GWAS, NDG	STK39	27347	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	2q24.3	-1.34	-19.27	2.09E-50	0.56	hHC006733	NM_013233
SCZ (SNV), ASD (Database), ID	SYNGAP1	8831	synaptic Ras GTPase activating protein 1 homolog (rat)	6p21.3	-0.05	-0.57	5.67E-01	-0.13	hHC014146	NM_006772
NDD, SCZ (Meta-analysis, GWAS), ID	TCF4	6925	transcription factor 4	18q21.1	0.80	12.62	2.92E-28	0.32	hHC020459	NM_001083962
SCZ (SNV), ASD (Database)	TLK2	11011	tousled-like kinase 2	17q23	0.66	11.43	2.13E-24	0.27	hHC030724	NM_006852
SCZ (PGC GWAS), BPAD GWAS	TLR9	54106	toll-like receptor 9	3p21.3	0.07	1.23	2.19E-01	-0.12	hHA039914	NM_017442
SCZ (PGC GWAS), BPAD GWAS	TNNC1	7134	troponin C type 1 (slow)	3p21.3-p14.3	-0.27	-3.06	2.51E-03	-0.09	hHC020672	NM_003280
SCZ (PGC GWAS), BPAD GWAS	TWF2	11344	twinfilin, actin-binding protein, homolog 2 (Drosophila)	3p21.1	-0.33	-7.41	2.26E-12	0.08	hHC020722	NM_007284
ID, ASD (Database)	UBE3A	7337	ubiquitin protein ligase E3A	15q11-q13	0.71	6.01	7.11E-09	0.02	hHA033034	NM_130839
SCZ (SNV), ASD (Database)	UBR5	NA	ubiquitin protein ligase E3 component n-recognin 5	8q22	1.53	15.90	3.02E-39	0.45	hHC001627	CD511402
SCZ (SNV), NDG	VPS35	55737	vacuolar protein sorting 35 homolog (S. cerevisiae)	16q12	-0.77	-13.16	4.65E-30	0.35	hHC011701	NM_018206
SCZ (PGC GWAS), BPAD GWAS	WDR82	80335	WD repeat domain 82	3p21.1	0.82	17.15	2.11E-43	0.50	hHC025830	NM_025222
SCZ (PGC GWAS), ID	ZEB2	9839	zinc finger E-box binding homeobox 2	2q22.3	1.50	15.51	6.50E-38	0.44	hHR029739	NM_014795
NDD, SCZ (Meta-analysis)	ZNF804A	91752	zinc finger protein 804A	2q32.1	0.54	4.35	2.06E-05	-0.05	hHC001802	NM_194250

Supp Table 3 GO Enrichment

Set	Gene Set Size (Mapping to probe)	Fetally Expressed Genes (Fetal Effect>0.5)	Gene Set Size used for enrichment analysis	Background Universe n (Unique genes)	Background Universe n (transcripts)	GO Type	GOBPID	Pvalue	OddsRatio	Count	Size	Term	ID	FDR	Bon
NDD	33	16	15	15802	30160	BP	GO:0007399	8.59E-05	12.6	7	1456	nervous system development	5;NM_014946;NM_002211;NM_001083962;N	4.03E-02	4.82E-02
NDD	33	16	15	15802	30160	BP	GO:0001578	2.12E-04	119.7	2	24	microtubule bundle formation	NM_014946;NM_018249	4.03E-02	1.19E-01
NDD	33	16	15	15802	30160	BP	GO:0071559	2.50E-04	109.8	2	26	response to transforming growth factor beta stimulus	NM_006940;NM_002211	4.03E-02	1.40E-01
NDD	33	16	15	15802	30160	BP	GO:0048731	6.74E-04	8.9	8	2749	system development	015265;NM_014946;NM_002211;NM_00108	4.03E-02	3.78E-01
NDD	33	16	15	15802	30160	BP	GO:0048699	7.53E-04	10.3	5	895	generation of neurons	7;NM_015265;NM_002211;NM_001083962;N	4.03E-02	4.22E-01
NDD	33	16	15	15802	30160	BP	GO:0045665	8.58E-04	57.2	2	48	negative regulation of neuron differentiation	NM_002211;NM_018249	4.03E-02	4.81E-01
NDD	33	16	15	15802	30160	BP	GO:0022008	9.85E-04	9.7	5	949	neurogenesis	7;NM_015265;NM_002211;NM_001083962;N	4.03E-02	5.53E-01
NDD	33	16	15	15802	30160	BP	GO:0030154	9.89E-04	8.0	7	2131	cell differentiation	0;NM_015265;NM_014946;NM_002211;NM_	4.03E-02	5.55E-01
NDD	33	16	15	15802	30160	BP	GO:0045666	1.01E-03	52.6	2	52	positive regulation of neuron differentiation	NM_002211;NM_001083962	4.03E-02	5.65E-01
NDD	33	16	15	15802	30160	BP	GO:0048869	1.46E-03	7.4	7	2268	cellular developmental process	0;NM_015265;NM_014946;NM_002211;NM_	4.51E-02	8.19E-01
NDD	33	16	15	15802	30160	BP	GO:0045664	1.53E-03	16.8	3	262	regulation of neuron differentiation	NM_002211;NM_001083962;NM_018249	4.51E-02	8.59E-01
NDD	33	16	15	15802	30160	CC	GO:0042383	4.91E-05	54.3	3	77	sarcolemma	NM_020987;NM_002211;NM_018968	6.08E-03	6.08E-03
NDD	33	16	15	15802	30160	CC	GO:0014704	2.34E-04	111.2	2	24	intercalated disc	NM_020987;NM_002211	9.90E-03	2.90E-02
NDD	33	16	15	15802	30160	CC	GO:0044291	2.54E-04	106.4	2	25	cell-cell contact zone	NM_020987;NM_002211	9.90E-03	3.15E-02
NDD	33	16	15	15802	30160	CC	GO:0009925	3.19E-04	94.1	2	28	basal plasma membrane	NM_020987;NM_002211	9.90E-03	3.96E-02
NDD	33	16	15	15802	30160	CC	GO:0045178	4.73E-04	76.4	2	34	basal part of cell	NM_020987;NM_002211	1.17E-02	5.86E-02
NDD	33	16	15	15802	30160	CC	GO:0034678	1.93E-03	1123.1	1	2	alpha8-beta1 integrin complex	NM_002211	2.65E-02	2.39E-01
NDD	33	16	15	15802	30160	CC	GO:0034679	1.93E-03	1123.1	1	2	alpha9-beta1 integrin complex	NM_002211	2.65E-02	2.39E-01
NDD	33	16	15	15802	30160	CC	GO:0035748	2.89E-03	561.5	1	3	myelin sheath abaxonal region	NM_002211	3.58E-02	3.58E-01
NDD	33	16	15	15802	30160	MF	GO:0008092	2.13E-04	12.4	5	528	cytoskeletal protein binding	087;NM_014946;NM_002211;NM_018249;NM	2.14E-02	2.39E-02
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0007399	2.10E-05	43.2	6	1456	nervous system development	025179;NM_021947;NM_005163;NM_00108	1.46E-02	1.46E-02
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0048468	1.70E-04	22.8	5	1181	cell development	5;NM_025179;NM_005163;NM_001083962;N	4.81E-02	1.18E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0030182	6.83E-04	17.9	4	826	neuron differentiation	025179;NM_005163;NM_001083962;NM_18	4.81E-02	4.75E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0030307	7.87E-04	65.6	2	74	positive regulation of cell growth	NM_004495;NM_005163	4.81E-02	5.47E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0048731	8.55E-04	20.0	6	2749	system development	025179;NM_021947;NM_005163;NM_00108	4.81E-02	5.94E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0048699	9.29E-04	16.4	4	895	generation of neurons	025179;NM_005163;NM_001083962;NM_18	4.81E-02	6.45E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0032501	1.06E-03		7	4470	multicellular organismal process	9;NM_021947;NM_005163;NM_001083962;N	4.81E-02	7.36E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0008652	1.09E-03	55.5	2	87	cellular amino acid biosynthetic process	NM_021947;NM_005957	4.81E-02	7.55E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0045597	1.10E-03	22.3	3	389	positive regulation of cell differentiation	NM_004495;NM_005163;NM_001083962	4.81E-02	7.67E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0022008	1.16E-03	15.4	4	949	neurogenesis	025179;NM_005163;NM_001083962;NM_18	4.81E-02	8.07E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0021934	1.18E-03	1980.0	1	2	hindbrain tangential cell migration	NM_025179	4.81E-02	8.18E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0031999	1.18E-03	1980.0	1	2	negative regulation of fatty acid beta-oxidation	NM_005163	4.81E-02	8.18E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:0070178	1.18E-03	1980.0	1	2	D-serine metabolic process	NM_021947	4.81E-02	8.18E-01
SCZ GWAS Meta	36	8	8	15802	30168	BP	GO:2001047	1.18E-03	1980.0	1	2	regulation of G1/S transition checkpoint	NM_005163	4.81E-02	8.18E-01
SCZ (PGC) GWAS	106	30	29	15802	30146	CC	GO:0005814	1.15E-03	38.9	3	48	centriole	NM_014812;NM_022782;NM_006642	1.10E-02	1.10E-02
SCZ (PGC) GWAS	106	30	29	15802	30146	CC	GO:0005813	1.15E-03	9.8	5	325	centrosome	311;NM_014812;NM_022782;NM_017917;NM	1.38E-02	3.62E-02
SCZ (PGC) GWAS	106	30	29	15802	30146	CC	GO:0044450	1.15E-03	24.3	3	75	microtubule organizing center part	NM_014812;NM_022782;NM_006642	1.38E-02	4.15E-02
SCZ (PGC) GWAS	106	30	29	15802	30146	CC	GO:0005815	1.15E-03	7.6	5	414	microtubule organizing center	311;NM_014812;NM_022782;NM_017917;NM	2.72E-02	1.09E-01
SCZ CNV	113	29	25	15802	30147	MF	GO:0005515	1.15E-03	6.8	20	6046	protein binding	003325;NM_014967;NM_007362;NM_00113	2.62E-02	2.62E-02
SCZ SNV	212	62	56	15802	30114	CC	GO:0005694	1.15E-03	5.0	9	511	chromosome	1130823;NM_138635;NM_005321;NM_0024	2.68E-02	3.74E-02
SCZ SNV	212	62	56	15802	30114	CC	GO:0044427	1.15E-03	5.2	8	431	chromosomal part	M_001130823;NM_138635;NM_005321;NM	2.68E-02	6.17E-02
SCZ SNV	212	62	56	15802	30114	CC	GO:0000785	1.15E-03	6.8	6	244	chromatin	M_001130823;NM_138635;NM_005321;NM_1	2.68E-02	8.46E-02
SCZ SNV	212	62	56	15802	30114	CC	GO:0005721	5.77E-04	72.4	2	9	centromeric heterochromatin	NM_001127322;NM_001130823	2.68E-02	1.07E-01
SCZ SNV	212	62	56	15802	30114	CC	GO:0005634	7.89E-04	2.4	32	4906	nucleus	7249;NM_002264;NM_002332;NM_002417;N	2.93E-02	1.47E-01
SCZ SNV	212	62	56	15802	30114	MF	GO:0005515	2.00E-04	6.8	20	6046	protein binding	003325;NM_014967;NM_007362;NM_00113	2.62E-02	2.62E-02
ASD CNV	176	41	38	15802	30135	BP	GO:0097114	1.15E-03		2	2	N-methyl-D-aspartate receptor clustering	NM_001135659;NM_001080420	2.32E-03	4.64E-03
ASD CNV	176	41	38	15802	30135	BP	GO:0097117	1.15E-03		2	2	guanylate kinase-associated protein clustering	NM_001135659;NM_001080420	2.32E-03	4.64E-03
ASD CNV	176	41	38	15802	30135	BP	GO:0072578	1.15E-03	423.4	2	4	neurotransmitter-gated ion channel clustering	NM_001135659;NM_001080420	9.25E-03	2.78E-02
ASD CNV	176	41	38	15802	30135	BP	GO:0071625	1.15E-03	282.3	2	5	vocalization behavior	NM_001135659;NM_001080420	1.16E-02	4.62E-02
ASD CNV	176	41	38	15802	30135	BP	GO:0006853	1.15E-03	211.7	2	6	carnitine shuttle	NM_152247;NM_005399	1.38E-02	6.92E-02
ASD CNV	176	41	38	15802	30135	BP	GO:0001941	1.15E-03	105.8	2	10	postsynaptic membrane organization	NM_001135659;NM_001080420	2.58E-02	2.06E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0015838	2.75E-04	105.5	2	10	amino-acid betaine transport	NM_152247;NM_005399	2.60E-02	2.08E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0015879	2.75E-04	105.5	2	10	carnitine transport	NM_152247;NM_005399	2.60E-02	2.08E-01
ASD CNV	176	41	38	15802	30135	BP	GO:2000463	3.36E-04	93.7	2	11	positive regulation of excitatory postsynaptic membrane potential	NM_001135659;NM_001080420	2.81E-02	2.53E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0051968	4.03E-04	84.4	2	12	positive regulation of synaptic transmission, glutamatergic	NM_001135659;NM_001080420	2.98E-02	3.04E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0003333	4.75E-04	76.7	2	13	amino acid transmembrane transport	NM_152247;NM_005399	2.98E-02	3.58E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0015697	4.75E-04	76.7	2	13	quaternary ammonium group transport	NM_152247;NM_005399	2.98E-02	3.58E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0032365	6.37E-04	64.9	2	15	intracellular lipid transport	NM_152247;NM_005399	3.43E-02	4.81E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0045838	6.37E-04	64.9	2	15	positive regulation of membrane potential	NM_001135659;NM_001080420	3.43E-02	4.81E-01
ASD CNV	176	41	38	15802	30135	BP	GO:2000311	7.27E-04	60.2	2	16	of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate rece	NM_001135659;NM_001080420	3.66E-02	5.48E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0043113	1.03E-03	49.6	2	19	receptor clustering	NM_001135659;NM_001080420	4.86E-02	7.78E-01
ASD CNV	176	41	38	15802	30135	BP	GO:0015695	1.14E-03	46.8	2	20	organic cation transport	NM_152247;NM_005399	5.08E-02	8.63E-01
ASD CNV	176	41	38	15802	30135	BP	GO:1900449	1.26E-03	44.4	2	21	regulation of glutamate receptor signaling pathway	NM_001135659;NM_001080420	5.29E-02	9.52E-01
ASD DB	242	88	84	15802	30088	BP	GO:0007399	1.15E-03	6.2	34	1456	nervous system development	002093;NM_006037;NM_004973;NM_00555	1.44E-09	1.44E-09
ASD DB	242	88	84	15802	30088	BP	GO:0048667	1.15E-03	8.9	20	494	cell morphogenesis involved in neuron differentiation	004442;NM_018008;NM_002093;NM_00555	1.07E-08	2.50E-08
ASD DB	242	88	84	15802	30088	BP	GO:0048812	1.15E-03	8.7	20	501	neuron projection morphogenesis	004442;NM_018008;NM_002093;NM_00555	1.07E-08	3.22E-08

Supp Table 3 GO Enrichment

Set	Gene Set Size (Mapping to probe)	Fetally Expressed Genes (Fetal Effect>0.5)	Gene Set Size used for enrichment analysis	Background Universe n (Unique genes)	Background Universe n (transcripts)	GO Type	GOBPID	Pvalue	OddsRatio	Count	Size	Term	ID	FDR	Bon
ASD DB	242	88	84	15802	30088	BP	GO:0007409	1.15E-03	9.1	19	453	axonogenesis	429;NM_004442;NM_018008;NM_002093;NM	1.23E-08	4.92E-08
ASD DB	242	88	84	15802	30088	BP	GO:0048699	1.15E-03	6.4	25	895	generation of neurons	2;NM_018008;NM_002093;NM_005559;NM_	2.51E-08	1.25E-07
ASD DB	242	88	84	15802	30088	BP	GO:0030182	1.15E-03	6.6	24	826	neuron differentiation	_004442;NM_018008;NM_002093;NM_00555	2.54E-08	1.52E-07
ASD DB	242	88	84	15802	30088	BP	GO:0007417	1.15E-03	7.8	20	554	central nervous system development	02093;NM_004973;NM_002374;NM_001037	2.81E-08	1.97E-07
ASD DB	242	88	84	15802	30088	BP	GO:0022008	1.15E-03	6.0	25	949	neurogenesis	2;NM_018008;NM_002093;NM_005559;NM_	5.08E-08	4.39E-07
ASD DB	242	88	84	15802	30088	BP	GO:0048858	1.15E-03	7.4	20	583	cell projection morphogenesis	_004442;NM_018008;NM_002093;NM_00555	5.08E-08	4.88E-07
ASD DB	242	88	84	15802	30088	BP	GO:0031175	1.15E-03	7.4	20	586	neuron projection development	_004442;NM_018008;NM_002093;NM_00555	5.08E-08	5.34E-07
ASD DB	242	88	84	15802	30088	BP	GO:0000904	1.15E-03	7.3	20	588	cell morphogenesis involved in differentiation	_004442;NM_018008;NM_002093;NM_00555	5.08E-08	5.67E-07
ASD DB	242	88	84	15802	30088	BP	GO:0007420	1.15E-03	8.8	17	403	brain development	2;NM_018008;NM_002093;NM_014562;NM_	5.08E-08	6.10E-07
ASD DB	242	88	84	15802	30088	BP	GO:0032990	1.15E-03	7.3	20	594	cell part morphogenesis	_004442;NM_018008;NM_002093;NM_00555	5.22E-08	6.78E-07
ASD DB	242	88	84	15802	30088	BP	GO:0048666	1.15E-03	6.4	20	670	neuron development	_004442;NM_018008;NM_002093;NM_00555	3.96E-07	5.54E-06
ASD DB	242	88	84	15802	30088	BP	GO:0048468	1.15E-03	5.0	26	1181	cell development	_001429;NM_004442;NM_018008;NM_00209	5.48E-07	8.22E-06
ASD DB	242	88	84	15802	30088	BP	GO:0030030	1.15E-03	5.5	20	771	cell projection organization	_004442;NM_018008;NM_002093;NM_00555	3.75E-06	6.02E-05
ASD DB	242	88	84	15802	30088	BP	GO:0048731	1.15E-03	3.7	39	2749	system development	7;NM_004973;NM_005559;NM_002374;NM_	3.75E-06	6.37E-05
ASD DB	242	88	84	15802	30088	BP	GO:0000902	1.15E-03	5.3	20	788	cell morphogenesis	_004442;NM_018008;NM_002093;NM_00555	4.81E-06	8.66E-05
ASD DB	242	88	84	15802	30088	BP	GO:0009653	1.15E-03	4.0	29	1661	anatomical structure morphogenesis	2;NM_018008;NM_002093;NM_005559;NM_	7.61E-06	1.45E-04
ASD DB	242	88	84	15802	30088	BP	GO:0008037	1.15E-03	23.2	7	60	cell recognition	7;NM_033655;NM_004442;NM_018008;NM_	8.52E-06	1.70E-04
ASD DB	242	88	84	15802	30088	BP	GO:0032989	1.15E-03	5.1	20	824	cellular component morphogenesis	_004442;NM_018008;NM_002093;NM_00555	8.64E-06	1.81E-04
ASD DB	242	88	84	15802	30088	BP	GO:0030154	1.15E-03	3.7	33	2131	cell differentiation	8;NM_002093;NM_006037;NM_004973;NM_	9.33E-06	2.05E-04
ASD DB	242	88	84	15802	30088	BP	GO:0048856	1.15E-03	3.5	41	3163	anatomical structure development	3;NM_006037;NM_004973;NM_005559;NM_	1.29E-05	2.98E-04
ASD DB	242	88	84	15802	30088	BP	GO:0048869	1.15E-03	3.4	33	2268	cellular developmental process	8;NM_002093;NM_006037;NM_004973;NM_	3.90E-05	9.36E-04
ASD DB	242	88	84	15802	30088	BP	GO:0008038	1.15E-03	40.7	5	26	neuron recognition	7;NM_004442;NM_018008;NM_001037132;N	4.10E-05	1.03E-03
ASD DB	242	88	84	15802	30088	BP	GO:0007411	1.15E-03	7.3	12	316	axon guidance	_018008;NM_002093;NM_005559;NM_13895	4.13E-05	1.07E-03
ASD DB	242	88	84	15802	30088	BP	GO:0051239	1.15E-03	3.8	25	1417	regulation of multicellular organismal process	9;NM_004442;NM_175768;NM_002093;NM_	5.32E-05	1.44E-03
ASD DB	242	88	84	15802	30088	BP	GO:0007275	1.15E-03	3.2	40	3227	multicellular organismal development	_006037;NM_004973;NM_005559;NM_00237	6.43E-05	1.80E-03
ASD DB	242	88	84	15802	30088	BP	GO:2000026	1.15E-03	4.5	19	868	regulation of multicellular organismal development	5;NM_001429;NM_004442;NM_002093;NM_	6.99E-05	2.03E-03
ASD DB	242	88	84	15802	30088	BP	GO:0030900	1.15E-03	8.6	10	222	forebrain development	_018008;NM_002093;NM_014562;NM_00031	7.44E-05	2.26E-03
ASD DB	242	88	84	15802	30088	BP	GO:0071842	1.15E-03	3.2	36	2729	cellular component organization at cellular level	_006037;NM_014288;NM_004973;NM_03277	7.44E-05	2.30E-03
ASD DB	242	88	84	15802	30088	BP	GO:0021537	1.15E-03	11.2	8	134	telencephalon development	_004442;NM_018008;NM_002093;NM_00031	1.10E-04	3.61E-03
ASD DB	242	88	84	15802	30088	BP	GO:0032501	1.15E-03	3.1	48	4470	multicellular organismal process	_000855;NM_006037;NM_153612;NM_00497	1.10E-04	3.64E-03
ASD DB	242	88	84	15802	30088	BP	GO:0007413	1.15E-03	61.3	4	15	axonal fasciculation	175607;NM_004442;NM_018008;NM_00103	1.12E-04	3.80E-03
ASD DB	242	88	84	15802	30088	BP	GO:0032502	1.15E-03	3.0	42	3603	developmental process	_002093;NM_006037;NM_004973;NM_00555	1.18E-04	4.14E-03
ASD DB	242	88	84	15802	30088	BP	GO:0071841	1.15E-03	3.1	36	2818	cellular component organization or biogenesis at cellular level	_006037;NM_014288;NM_004973;NM_03277	1.44E-04	5.17E-03
ASD DB	242	88	84	15802	30088	BP	GO:0040011	1.15E-03	4.0	20	1021	locomotion	M_153612;NM_005559;NM_138957;NM_018	1.50E-04	5.55E-03
ASD DB	242	88	84	15802	30088	BP	GO:0060284	1.15E-03	5.8	12	394	regulation of cell development	04405;NM_001429;NM_002093;NM_006037	2.84E-04	1.08E-02
ASD DB	242	88	84	15802	30088	BP	GO:0018193	1.15E-03	5.0	14	544	peptidyl-amino acid modification	M_015409;NM_004442;NM_002093;NM_006	2.93E-04	1.14E-02
ASD DB	242	88	84	15802	30088	BP	GO:0048732	1.15E-03	7.9	9	213	gland development	0059;NM_005559;NM_138957;NM_002659;N	3.43E-04	1.37E-02
ASD DB	242	88	84	15802	30088	BP	GO:0048589	1.15E-03	7.7	9	217	developmental growth	9;NM_001429;NM_001037132;NM_002659;N	3.89E-04	1.60E-02
ASD DB	242	88	84	15802	30088	BP	GO:0021766	1.15E-03	20.3	5	47	hippocampus development	120;NM_004405;NM_018008;NM_002093;NM	5.15E-04	2.16E-02
ASD DB	242	88	84	15802	30088	BP	GO:0051960	1.15E-03	5.9	11	353	regulation of nervous system development	NM_004405;NM_001429;NM_004442;NM_0	5.22E-04	2.25E-02
ASD DB	242	88	84	15802	30088	BP	GO:0006935	1.15E-03	4.9	13	502	chemotaxis	8;NM_002093;NM_005559;NM_138957;NM_	5.40E-04	2.43E-02
ASD DB	242	88	84	15802	30088	BP	GO:0042330	1.15E-03	4.9	13	502	taxis	8;NM_002093;NM_005559;NM_138957;NM_	5.40E-04	2.43E-02
ASD DB	242	88	84	15802	30088	BP	GO:0050793	1.15E-03	3.6	20	1127	regulation of developmental process	_001429;NM_004442;NM_002093;NM_00603	5.40E-04	2.48E-02
ASD DB	242	88	84	15802	30088	BP	GO:0048513	1.15E-03	3.1	27	1895	organ development	093;NM_006037;NM_004973;NM_005559;NM	5.90E-04	2.82E-02
ASD DB	242	88	84	15802	30088	BP	GO:0018205	1.15E-03	10.2	7	127	peptidyl-lysine modification	429;NM_015409;NM_006037;NM_014159;NM	5.90E-04	2.83E-02
ASD DB	242	88	84	15802	30088	BP	GO:0021543	1.15E-03	12.9	6	86	pallium development	M_004405;NM_018008;NM_002093;NM_0003	6.49E-04	3.18E-02
ASD DB	242	88	84	15802	30088	BP	GO:0016568	1.15E-03	5.4	11	378	chromatin modification	037;NM_014288;NM_004973;NM_032776;NM	8.51E-04	4.26E-02
ASD DB	242	88	84	15802	30088	CC	GO:0043005	1.15E-03	6.7	16	505	neuron projection	020794;NM_002374;NM_138957;NM_00103	7.35E-06	7.35E-06
ASD DB	242	88	84	15802	30088	CC	GO:0030424	1.15E-03	8.9	10	226	axon	M_175607;NM_004442;NM_175768;NM_138	9.62E-05	1.92E-04
ASD DB	242	88	84	15802	30088	CC	GO:0045202	1.15E-03	6.0	12	403	synapse	175768;NM_021150;NM_006037;NM_02079	3.08E-04	9.24E-04
ASD DB	242	88	84	15802	30088	CC	GO:0045211	1.15E-03	9.0	7	150	postsynaptic membrane	8;NM_021150;NM_020794;NM_015310;NM_	1.56E-03	6.96E-03
ASD DB	242	88	84	15802	30088	CC	GO:0033267	1.15E-03	11.3	6	103	axon part	01127511;NM_175768;NM_138957;NM_0010	1.56E-03	7.78E-03
ASD DB	242	88	84	15802	30088	CC	GO:0030425	1.15E-03	6.1	9	286	dendrite	8;NM_020794;NM_002374;NM_138957;NM_	1.83E-03	1.10E-02
ASD DB	242	88	84	15802	30088	CC	GO:0030054	1.15E-03	4.2	13	620	cell junction	8;NM_021150;NM_005559;NM_020794;NM_	2.12E-03	1.49E-02
ASD DB	242	88	84	15802	30088	CC	GO:0097060	1.15E-03	7.7	7	174	synaptic membrane	8;NM_021150;NM_020794;NM_015310;NM_	2.24E-03	1.79E-02
ASD DB	242	88	84	15802	30088	CC	GO:0042995	1.15E-03	3.3	16	987	cell projection	020794;NM_002374;NM_138957;NM_00103	4.58E-03	4.12E-02
ASD DB	242	88	84	15802	30088	CC	GO:0044456	3.78E-04	5.0	8	302	synapse part	175768;NM_021150;NM_020794;NM_01531	8.42E-03	9.71E-02
ASD DB	242	88	84	15802	30088	CC	GO:0043228	4.26E-04	2.4	28	2567	non-membrane-bounded organelle	NM_014288;NM_020794;NM_002374;NM_13	8.42E-03	1.09E-01
ASD DB	242	88	84	15802	30088	CC	GO:0043232	4.26E-04	2.4	28	2567	intracellular non-membrane-bounded organelle	NM_014288;NM_020794;NM_002374;NM_13	8.42E-03	1.09E-01
ASD DB	242	88	84	15802	30088	CC	GO:0030877	5.00E-04	87.1	2	6	beta-catenin destruction complex	NM_001127511;NM_002093	9.18E-03	1.29E-01
ASD DB	242	88	84	15802	30088	CC	GO:0034747	6.98E-04	69.6	2	7	Axin-APC-beta-catenin-GSK3B complex	NM_001127511;NM_002093	1.17E-02	1.79E-01
ASD DB	242	88	84	15802	30088	CC	GO:0005694	7.67E-04	3.7	10	511	chromosome	NM_014288;NM_018328;NM_052897;NM_14	1.17E-02	1.97E-01
ASD DB	242	88	84	15802	30088	CC	GO:0044304	7.72E-04	18.9	3	31	main axon	NM_020987;NM_001037132;NM_133631	1.17E-02	1.98E-01
ASD DB	242	88	84	15802	30088	CC	GO:0043194	9.27E-04	58.0	2	8	axon initial segment	NM_020987;NM_001037132	1.32E-02	2.38E-01
ASD DB	242	88	84	15802	30088	CC	GO:0032839	1.80E-03	38.7	2	11	dendrite cytoplasm	NM_175768;NM_138957	2.38E-02	4.62E-01
ASD DB	242	88	84	15802	30088	CC	GO:0043025	1.86E-03	5.0	6	221	neuronal cell body	001127511;NM_175768;NM_002374;NM_13	2.38E-02	4.77E-01

Supp Table 3 GO Enrichment

Set	Gene Set Size (Mapping to probe)	Fetally Expressed Genes (Fetal Effect>0.5)	Gene Set Size used for enrichment analysis	Background Universe n (Unique genes)	Background Universe n (transcripts)	GO Type	GOBPID	Pvalue	OddsRatio	Count	Size	Term	ID	FDR	Bon
ASD DB	242	88	84	15802	30088	CC	GO:0014069	2.06E-03	8.1	4	92	postsynaptic density	020794;NM_015310;NM_012309;NM_00108	2.41E-02	5.29E-01
ASD DB	242	88	84	15802	30088	CC	GO:0044327	2.06E-03	8.1	4	92	dendritic spine head	020794;NM_015310;NM_012309;NM_00108	2.41E-02	5.29E-01
ASD DB	242	88	84	15802	30088	CC	GO:0044430	2.68E-03	2.6	14	1042	cytoskeletal part	M_002093;NM_006037;NM_020794;NM_002	2.94E-02	6.89E-01
ASD DB	242	88	84	15802	30088	CC	GO:0044297	2.75E-03	4.6	6	239	cell body	001127511;NM_175768;NM_002374;NM_13	2.94E-02	7.06E-01
ASD DB	242	88	84	15802	30088	MF	GO:0003682	6.16E-05	6.7	8	216	chromatin binding	M_004405;NM_001429;NM_004965;NM_004	2.05E-02	2.17E-02
ASD DB	242	88	84	15802	30088	MF	GO:0005488	1.81E-04	4.7	73	9746	binding	688;NM_020931;NM_005559;NM_002374;NI	2.05E-02	6.35E-02
ASD DB	242	88	84	15802	30088	MF	GO:0030159	2.17E-04	30.7	3	19	receptor signaling complex scaffold activity	NM_021150;NM_012309;NM_001080420	2.05E-02	7.62E-02
ASD DB	242	88	84	15802	30088	MF	GO:0030160	2.33E-04	161.9	2	4	GKAP/Homer scaffold activity	NM_012309;NM_001080420	2.05E-02	8.20E-02
ASD DB	242	88	84	15802	30088	MF	GO:0008013	3.62E-04	13.3	4	54	beta-catenin binding	001127511;NM_001429;NM_021150;NM_00	2.55E-02	1.28E-01
BPAD	123	30	29	15802	30146	BP	GO:0043153	1.15E-03	988.4	2	3	entrainment of circadian clock by photoperiod	NM_002896;NM_031492	7.70E-03	7.70E-03
BPAD	123	30	29	15802	30146	BP	GO:0009648	1.15E-03	329.4	2	5	photoperiodism	NM_002896;NM_031492	1.28E-02	2.56E-02
BPAD	123	30	29	15802	30146	BP	GO:0009649	1.28E-04	164.7	2	8	entrainment of circadian clock	NM_002896;NM_031492	2.38E-02	7.14E-02
BPAD	123	30	29	15802	30146	BP	GO:0032922	2.50E-04	109.8	2	11	circadian regulation of gene expression	NM_002896;NM_031492	3.49E-02	1.40E-01
ID	94	35	34	15802	30141	BP	GO:0043113	1.15E-03	74.0	3	19	receptor clustering	NM_175768;NM_001135659;NM_001110556	1.01E-02	1.72E-02
ID	94	35	34	15802	30141	BP	GO:0042384	1.15E-03	29.1	4	60	cilium assembly	005249;NM_000276;NM_003611;NM_00111	1.01E-02	2.02E-02
ID	94	35	34	15802	30141	BP	GO:0051966	1.15E-03	51.4	3	26	regulation of synaptic transmission, glutamatergic	NM_175768;NM_001135659;NM_002547	1.52E-02	4.56E-02
ID	94	35	34	15802	30141	BP	GO:0060271	7.04E-05	21.1	4	81	cilium morphogenesis	005249;NM_000276;NM_003611;NM_00111	1.52E-02	6.61E-02
ID	94	35	34	15802	30141	BP	GO:0030031	8.16E-05	13.1	5	164	cell projection assembly	9;NM_000276;NM_003611;NM_002547;NM_	1.52E-02	7.66E-02
ID	94	35	34	15802	30141	BP	GO:0007420	9.72E-05	7.8	7	403	brain development	249;NM_002025;NM_014795;NM_000489;NM	1.52E-02	9.13E-02
ID	94	35	34	15802	30141	BP	GO:0048858	1.49E-04	6.3	8	583	cell projection morphogenesis	01135659;NM_000276;NM_003611;NM_020	1.65E-02	1.40E-01
ID	94	35	34	15802	30141	BP	GO:0032990	1.69E-04	6.2	8	594	cell part morphogenesis	01135659;NM_000276;NM_003611;NM_020	1.65E-02	1.59E-01
ID	94	35	34	15802	30141	BP	GO:0010927	1.79E-04	16.4	4	103	cellular component assembly involved in morphogenesis	005249;NM_000276;NM_003611;NM_00111	1.65E-02	1.68E-01
ID	94	35	34	15802	30141	BP	GO:0030030	1.82E-04	5.5	9	771	cell projection organization	559;NM_003383;NM_000276;NM_003611;NM	1.65E-02	1.71E-01
ID	94	35	34	15802	30141	BP	GO:0035249	1.93E-04	31.1	3	41	synaptic transmission, glutamatergic	NM_175768;NM_001135659;NM_002547	1.65E-02	1.82E-01
ID	94	35	34	15802	30141	BP	GO:0000902	2.14E-04	5.3	9	788	cell morphogenesis	559;NM_153252;NM_000276;NM_003611;NM	1.68E-02	2.01E-01
ID	94	35	34	15802	30141	BP	GO:0032989	3.00E-04	5.1	9	824	cellular component morphogenesis	559;NM_153252;NM_000276;NM_003611;NM	2.16E-02	2.81E-01
ID	94	35	34	15802	30141	BP	GO:0050890	5.63E-04	12.0	4	139	cognition	002025;NM_001135659;NM_006765;NM_00	3.78E-02	5.29E-01
ID	94	35	34	15802	30141	BP	GO:0048856	6.06E-04	3.3	18	3163	anatomical structure development	181777;NM_153252;NM_030665;NM_00338	3.79E-02	5.69E-01
ID	94	35	34	15802	30141	BP	GO:0007417	6.81E-04	5.6	7	554	central nervous system development	249;NM_002025;NM_014795;NM_000489;NM	4.00E-02	6.39E-01
ID	94	35	34	15802	30141	CC	GO:0044456	5.50E-05	10.7	6	302	synapse part	003619;NM_003688;NM_001135659;NM_02	4.04E-03	9.24E-03
ID	94	35	34	15802	30141	CC	GO:0043195	6.26E-05	46.4	3	34	terminal button	NM_175768;NM_003619;NM_002547	4.04E-03	1.05E-02
ID	94	35	34	15802	30141	CC	GO:0033267	8.60E-05	20.0	4	103	axon part	175768;NM_003619;NM_001135659;NM_00	4.04E-03	1.45E-02
ID	94	35	34	15802	30141	CC	GO:0042734	1.37E-04	35.1	3	44	presynaptic membrane	NM_175768;NM_003688;NM_001135659	4.04E-03	2.29E-02
ID	94	35	34	15802	30141	CC	GO:0044463	1.37E-04	7.4	7	517	cell projection part	9;NM_003688;NM_001135659;NM_003611;N	4.04E-03	2.31E-02
ID	94	35	34	15802	30141	CC	GO:0043229	1.64E-04	8.2	29	8641	intracellular organelle	7;NM_003588;NM_080632;NM_006594;NM_	4.04E-03	2.75E-02
ID	94	35	34	15802	30141	CC	GO:0043226	1.68E-04	8.1	29	8651	organelle	7;NM_003588;NM_080632;NM_006594;NM_	4.04E-03	2.83E-02
ID	94	35	34	15802	30141	CC	GO:0043679	2.52E-04	28.2	3	54	axon terminus	NM_175768;NM_003619;NM_002547	4.09E-03	4.23E-02
ID	94	35	34	15802	30141	CC	GO:0005905	2.66E-04	27.6	3	55	coated pit	NM_003383;NM_004722;NM_000276	4.09E-03	4.47E-02
ID	94	35	34	15802	30141	CC	GO:0045202	2.67E-04	7.9	6	403	synapse	003619;NM_003688;NM_001135659;NM_02	4.09E-03	4.49E-02
ID	94	35	34	15802	30141	CC	GO:0042995	2.68E-04	5.2	9	987	cell projection	9;NM_003688;NM_001135659;NM_000276;N	4.09E-03	4.50E-02
ID	94	35	34	15802	30141	CC	GO:0044306	3.44E-04	25.2	3	60	neuron projection terminus	NM_175768;NM_003619;NM_002547	4.82E-03	5.78E-02
ID	94	35	34	15802	30141	MF	GO:0004385	3.83E-04	87.3	2	11	guanylate kinase activity	NM_003688;NM_020730	2.43E-02	8.12E-02
ID	94	35	34	15802	30141	MF	GO:0031625	4.29E-04	12.9	4	133	ubiquitin protein ligase binding	M_000381;NM_175768;NM_181777;NM_003	2.43E-02	9.09E-02
ID	94	35	34	15802	30141	MF	GO:0044389	4.29E-04	12.9	4	133	small conjugating protein ligase binding	M_000381;NM_175768;NM_181777;NM_003	2.43E-02	9.09E-02
ID	94	35	34	15802	30141	MF	GO:0035255	4.59E-04	78.6	2	12	ionotropic glutamate receptor binding	NM_020730;NM_002547	2.43E-02	9.72E-02
ID	94	35	34	15802	30141	MF	GO:0035254	9.37E-04	52.4	2	17	glutamate receptor binding	NM_020730;NM_002547	3.97E-02	1.99E-01
ID	94	35	34	15802	30141	MF	GO:0019201	1.44E-03	41.3	2	21	nucleotide kinase activity	NM_003688;NM_020730	4.77E-02	3.05E-01
NDG	46	5	5	15802	30171	CC	GO:0045298	1.11E-03	1685.5	1	3	tubulin complex	NM_001123066	4.50E-02	9.00E-02
NDG	46	5	5	15802	30171	CC	GO:0030424	2.70E-03	39.5	2	226	axon	NM_000484;NM_001123066	4.50E-02	2.19E-01
NDG	46	5	5	15802	30171	CC	GO:0035253	2.96E-03	481.4	1	8	ciliary rootlet	NM_000484	4.50E-02	2.40E-01
NDG	46	5	5	15802	30171	CC	GO:0043233	3.24E-03	20.2	4	2231	organelle lumen	000484;NM_012120;NM_004960;NM_00112	4.50E-02	2.62E-01
NDG	46	5	5	15802	30171	CC	GO:0031974	3.46E-03	19.8	4	2270	membrane-enclosed lumen	000484;NM_012120;NM_004960;NM_00112	4.50E-02	2.80E-01
NDG	46	5	5	15802	30171	CC	GO:0042995	3.49E-03	19.1	3	987	cell projection	NM_000484;NM_012120;NM_001123066	4.50E-02	2.83E-01
NDG	46	5	5	15802	30171	CC	GO:0044430	4.08E-03	18.0	3	1042	cytoskeletal part	NM_000484;NM_012120;NM_001123066	4.50E-02	3.31E-01
NDG	46	5	5	15802	30171	CC	GO:0051233	4.44E-03	306.3	1	12	spindle midzone	NM_000484	4.50E-02	3.60E-01
NDG	46	5	5	15802	30171	CC	GO:0004385	3.83E-04	87.3	2	11	guanylate kinase activity	NM_003688;NM_020730	2.43E-02	8.12E-02
NDG	46	5	5	15802	30171	CC	GO:0031625	4.29E-04	12.9	4	133	ubiquitin protein ligase binding	M_000381;NM_175768;NM_181777;NM_003	2.43E-02	9.09E-02
NDG	46	5	5	15802	30171	CC	GO:0044389	4.29E-04	12.9	4	133	small conjugating protein ligase binding	M_000381;NM_175768;NM_181777;NM_003	2.43E-02	9.09E-02
NDG	46	5	5	15802	30171	CC	GO:0035255	4.59E-04	78.6	2	12	ionotropic glutamate receptor binding	NM_020730;NM_002547	2.43E-02	9.72E-02
NDG	46	5	5	15802	30171	CC	GO:0035254	9.37E-04	52.4	2	17	glutamate receptor binding	NM_020730;NM_002547	3.97E-02	1.99E-01
NDG	46	5	5	15802	30171	CC	GO:0019201	1.44E-03	41.3	2	21	nucleotide kinase activity	NM_003688;NM_020730	4.77E-02	3.05E-01
NDG	46	5	5	15802	30171	CC	GO:0005200	1.76E-04	187.0	2	67	structural constituent of cytoskeleton	NM_012120;NM_001123066	4.69E-03	7.58E-03
NDG	46	5	5	15802	30171	CC	GO:0019904	2.18E-04	75.7	3	469	protein domain specific binding	NM_000484;NM_012120;NM_001123066	4.69E-03	9.38E-03
NDG	46	5	5	15802	30171	CC	GO:0017124	4.59E-04	114.3	2	108	SH3 domain binding	NM_012120;NM_001123066	6.57E-03	1.97E-02
NDG	46	5	5	15802	30171	CC	GO:0033130	1.31E-03	1357.6	1	4	acetylcholine receptor binding	NM_000484	1.13E-02	5.63E-02
NDG	46	5	5	15802	30171	CC	GO:0051425	1.31E-03	1357.6	1	4	PTB domain binding	NM_000484	1.13E-02	5.63E-02

Supp Table 3 GO Enrichment

Set	Gene Set Size (Mapping to probe)	Fetally Expressed Genes (Fetal Effect>0.5)	Gene Set Size used for enrichment analysis	Background Universe n (Unique genes)	Background Universe n (transcripts)	GO Type	GOBPID	Pvalue	OddsRatio	Count	Size	Term	ID	FDR	Bon
NDG	46	5	5	15802	30171	CC	GO:0034185	4.25E-03	339.1	1	13	apolipoprotein binding	NM_001123066	3.04E-02	1.83E-01
NDG	46	5	5	15802	30171	CC	GO:0071813	6.53E-03	214.1	1	20	lipoprotein particle binding	NM_001123066	3.51E-02	2.81E-01
NDG	46	5	5	15802	30171	CC	GO:0071814	6.53E-03	214.1	1	20	protein-lipid complex binding	NM_001123066	3.51E-02	2.81E-01
NDG	46	5	5	15802	30171	CC	GO:0005198	9.56E-03	23.4	2	502	structural molecule activity	NM_012120;NM_001123066	4.35E-02	4.11E-01
NDG	46	5	5	15802	30171	CC	GO:0016504	1.01E-02	135.5	1	31	peptidase activator activity	NM_000484	4.35E-02	4.35E-01

Note: Not displayed in the table above are the gene sets with a gene set size of 1

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
NDD	hHC003332	AUTS2	hHR030827	HMGN1	NM_004965	0.80
			hHC030775	RPS24	NM_001142285	0.83
			hHC005526	FDFT1	NM_004462	0.83
			hHC007037	VCAN	NM_004385	0.86
			hHR029537	BTF3	NM_001037637	0.82
			hHC029645	HNRPDL	NR_003249	0.81
			hHC029931	HMGN1	NM_004965	0.81
			hHR030086	HNRPA1L-2	NR_002944	0.80
			hHR009745	FOXG1	NM_005249	0.82
			hHC031741	EEF1B2	NM_001959	0.83
NDD	hHA034365	ANK3	hHA034403	NRXN1	NM_001135659	0.85
			hHA036742	NRXN1	NM_001135659	0.80
			hHC002037	APC	NM_001127511	0.84
			hHA035661	NRXN1	NM_001135659	0.87
			hHC014372	PCDHA1	NM_018900	0.81
			hHC009631	CDKL1	NM_004196	0.81
			hHC014371	PCDHA1	NM_018900	0.83
			hHA035369	NRXN1	NM_001135659	0.81
NDD	hHA035450	SOX5	hHR003716	MIB1	NM_020774	0.80
			hHA037290	SYNE2	NM_182914	0.84
			hHA036869	SYNE2	NM_182914	0.83
			hHA034421	SYNE2	NM_182914	0.81
			hHA034061	SYNE2	NM_182914	0.84
			hHA035103	SYNE2	NM_182914	0.85
NDD	hHC001764	SATB2	hHC005100	CDH10	NM_006727	0.84
			hHC008844	PPP1R14C	NM_030949	0.86
			hHC010008	GPRASP1	NM_014710	0.83
			hHC002436	SEMA3C	NM_006379	0.82
			hHC009936	TMOD1	NM_003275	0.87
			hHC005064	LMO4	NM_006769	0.87
			hHC028284	ACSL4	NM_022977	0.83
			hHA033852	ARPP-21	NM_016300	0.87
			hHC013140	NLN	AB033052	0.87
			hHC018263	LOC150568	AK126958	0.86
			hHC011075	NRXN1	NM_001135659	0.81
			hHC003515	CHL1	NM_006614	0.85
			hHR004667	KIAA1211	NM_020722	0.80
			hHR003071	FLRT2	NM_013231	0.82
			hHC008950	CCBE1	NM_133459	0.82
			hHR009994	KALRN	NM_003947	0.82
			hHA033934	PCDH10	NM_032961	0.82
			hHC019546	OAT	NM_000274	0.82
			hHR002770	THSD7B	NM_001080427	0.88
			hHC017266	CUX2	NM_015267	0.83

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC017458	NCALD	NM_001040630	0.85
			hHC005289	NAP1L3	NM_004538	0.82
			hHC003777	NAV3	NM_014903	0.88
			hHR004557	ATRNL1	NM_207303	0.80
			hHC015105	ARPP-21	NM_016300	0.85
			hHC016833	SRD5A1	NM_001047	0.83
			hHC008901	ELMO1	NM_014800	0.81
			hHC013509	RSPO3	NM_032784	0.84
			hHC018609	STK32B	NM_018401	0.82
			hHA035912	GRM7	BC136458	0.86
			hHC008960	NKAIN2	NM_001040214	0.93
			hHC010412	DB519783	DB519783	0.89
			hHC004100	UST	NM_005715	0.83
			hHC002576	DCLK1	NM_004734	0.87
			hHR006055	PCDHA1	NM_018900	0.80
			hHC018655	CXXC4	NM_025212	0.84
			hHC006295	JAZF1	NM_175061	0.80
			hHC008995	RIMS1	BC036608	0.83
			hHE041335	DCLK1	NM_004734	0.89
			hHC002299	AKAP7	NM_016377	0.88
			hHC005898	AFF2	NM_002025	0.82
			hHC007530	KCNK2	NM_001017424	0.88
			hHC024318	DOK4	NM_018110	0.82
			hHC003222	INA	NM_032727	0.81
			hHC005154	C1orf52	NR_024113	0.81
			hHC015330	RPRM	NM_019845	0.84
			hHR002609	LOC150568	NR_015399	0.86
			hHC004805	RUNDC3B	NM_138290	0.83
			hHR006053	PCDHA1	NM_018900	0.80
			hHR001757	HUWE1	NM_031407	0.81
			hHC004361	LRRC4C	NM_020929	0.80
			hHR010109	TBC1D30	AB023201	0.84
			hHR005537	LPHN3	NM_015236	0.89
			hHR008897	PLCH2	NM_014638	0.82
			hHE040949	EY892390	EY892390	0.84
			hHC001625	SCN3A	NM_006922	0.80
			hHC008260	GRM7	NM_181874	0.88
			hHC005116	CHRM2	AL832585	0.86
			hHC004792	PTCHD1	NM_173495	0.87
			hHC009615	L3MBTL3	NM_032438	0.85
			hHR002139	AK096649	AK096649	0.94
			hHC003711	ADAMTSL3	NM_207517	0.83
			hHC004959	CPVL	NM_019029	0.80
			hHC006519	CXXC4	AK127778	0.86

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC019179	RSPO3	NM_032784	0.82
			hHR006050	PCDHA1	NM_018900	0.80
			hHR011906	RIMBP2	NM_015347	0.86
			hHC014222	C3orf59	NM_178496	0.85
			hHC009926	SH3GL3	NM_003027	0.86
			hHC003698	FRMD4A	NM_018027	0.82
			hHR001898	KIAA1239	NM_001144990	0.90
			hHC002666	ITPR1	NM_001099952	0.89
			hHC001741	CCDC113	NM_014157	0.81
			hHC008737	GNG2	NM_053064	0.81
			hHC008929	ARAP2	NM_015230	0.84
			hHA034669	CDC42	NM_044472	0.81
			hHA034861	ARPP-21	NM_016300	0.81
			hHE041473	BQ189296	BQ189296	0.85
			hHC004537	LRRC8B	NM_015350	0.85
NDD	hHC004698	SPAST	hHC004698	SPAST	NM_014946	1.00
NDD	hHC013184	EHMT1	hHC013184	EHMT1	AB058779	1.00
NDD	hHC004253	ITGB1	hHR015907	SEPT2	NM_001008491	0.84
			hHC004253	ITGB1	NM_002211	1.00
			hHR013673	ITGB1	NM_002211	0.96
			hHC008033	SLC1A3	NM_004172	0.80
			hHR005523	REEP3	NM_001001330	0.82
			hHA036351	AGFG1	NM_001135187	0.82
NDD	hHC019897	ZBTB20	hHC019897	ZBTB20	NM_015642	1.00
NDD	hHR030073	METTL2B	hHC029890	METTL2B	NM_018396	0.85
			hHA034001	FAM178A	NM_018121	0.82
			hHA033363	TTC3	NM_003316	0.84
			hHR030073	METTL2B	NM_018396	1.00
			hHA033181	DHX9	NM_001357	0.82
NDD	hHC029691	FAM107B	hHC029691	FAM107B	NM_031453	1.00
NDD	hHC020459	TCF4	hHC020459	TCF4	NM_001083962	1.00
NDD	hHC012789	CDK5RAP2	hHC027600	C10orf7	NM_145247	0.84
			hHC012789	CDK5RAP2	NM_018249	1.00
			hHC015033	TFAM	NM_003201	0.83
NDD	hHC004339	MBD5	hHC004339	MBD5	NM_018328	1.00
			hHR027830	TAF9	NM_001015892	0.80
NDD	hHR008345	SNTG2	hHR008345	SNTG2	NM_018968	1.00
NDD	hHC001802	ZNF804A	hHC001802	ZNF804A	NM_194250	1.00
CZ (SRF) Meta-analysi	hHA033957	NRG1	hHA033957	NRG1	NM_004495	1.00
CZ (SRF) Meta-analysi	hHC010960	PLXNA2	hHA033168	ZFP106	NM_022473	0.85
			hHA036720	MAP4	NM_002375	0.82
			hHR017820	LOC285178	AK091571	0.80
			hHC021227	KIF21A	NM_017641	0.85
			hHC020447	BBS4	NM_033028	0.82

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHA032831	TFAM	NM_003201	0.83
			hHA037235	MAP4	NM_002375	0.83
			hHC031882	EPN2	NM_014964	0.88
			hHC009658	LPGAT1	NM_014873	0.82
			hHA037234	MAP4	NM_002375	0.85
			hHE042165	DB275830	DB275830	0.87
			hHE042537	CHD9	NM_025134	0.83
			hHC017133	ANKRD50	NM_020337	0.83
			hHA039933	ILF3	NM_017620	0.84
			hHC022472	ERC1	NM_178037	0.83
			hHA036500	MACF1	NM_012090	0.81
			hHC014876	GABRA3	NM_000808	0.85
			hHA034951	ZFP106	NM_022473	0.83
			hHA036019	LSAMP	NM_002338	0.81
			hHC021702	ILF3	NM_017620	0.83
			hHC014922	ANKRD32	NM_032290	0.84
			hHA033054	CDC27	NM_001114091	0.81
			hHA034481	KCNH7	NM_033272	0.83
			hHC027005	THRAP3	NM_005119	0.85
			hHC006628	SLC36A4	NM_152313	0.82
			hHR013252	C20orf94	NM_001009608	0.82
			hHC020751	SWAP70	NM_015055	0.81
			hHC008475	KCNH7	NM_033272	0.85
			hHA038715	NARG1L	NM_024561	0.82
			hHR004083	H2AFV	NM_012412	0.88
			hHC004659	PCDHB9	NM_019119	0.82
			hHA032979	TFAM	NM_003201	0.84
			hHA034359	TFAM	NM_003201	0.82
			hHC008174	CXorf38	AK095710	0.83
			hHA033806	ARID4B	NM_016374	0.85
			hHC007262	BRUNOL6	NM_052840	0.82
			hHR005617	AAK1	NM_014911	0.84
			hHC016573	LDB1	NM_003893	0.82
			hHA035197	RAD50	NM_005732	0.81
			hHC010825	CBX5	NM_001127322	0.82
CZ (SRF) Meta-analysi	hHC016218	SRR	hHC016218	SRR	NM_021947	1.00
CZ (SRF) Meta-analysi	hHC010439	AKT1	hHC010439	AKT1	NM_005163	1.00
CZ (SRF) Meta-analysi	hHC020459	TCF4	hHC020459	TCF4	NM_001083962	1.00
CZ (SRF) Meta-analysi	hHA035123	DTNBP1	hHA035123	DTNBP1	NM_183040	1.00
CZ (SRF) Meta-analysi	hHC001802	ZNF804A	hHC001802	ZNF804A	NM_194250	1.00
CZ (SRF) Meta-analysi	hHC015904	MTHFR	hHC015904	MTHFR	NM_005957	1.00
SCZ (PGC) GWAS	hHC012518	AKT3	hHC012518	AKT3	NM_005465	1.00
SCZ (PGC) GWAS	hHR006410	ARL3	hHR030183	RABL2B	NM_001130921	0.81
SCZ (PGC) GWAS	ARL3	NM_004311	hHR006410	ARL3	NM_004311	1.00

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
SCZ (PGC) GWAS	hHC010261	AS3MT	hHC029136	PTTG1	NM_004219	0.82
			hHC003228	WDR67	NM_145647	0.80
			hHC009468	MCM3	NM_002388	0.85
			hHR001920	SOX21	NM_007084	0.83
			hHC022115	TP53I13	NM_138349	0.82
			hHC014134	BCL2L12	NM_138639	0.83
			hHC010030	MTMR11	NM_181873	0.80
			hHC006214	NMU	NM_006681	0.83
			hHC004018	BRCA1	NM_007295	0.81
			hHC007762	CDCA5	NM_080668	0.85
			hHR016126	RGAG4	NM_001024455	0.80
			hHC020830	GMNN	NM_015895	0.86
			hHC009225	AKNA	NM_030767	0.82
			hHR004929	SMAD5	NM_001001419	0.83
			hHR028665	CR625830	CR625830	0.83
			hHR014301	C9orf119	NM_001040011	0.86
			hHC008264	H2AFX	NM_002105	0.88
			hHR019400	RNASEH2C	NM_032193	0.87
			hHC007628	RFX2	NM_000635	0.85
			hHC009920	RFC4	NM_181573	0.81
			hHC022400	SMO	NM_005631	0.80
			hHC015044	C17orf101	NM_175902	0.83
			hHC027620	RNASEH2C	NM_032193	0.85
			hHE041072	STK17B	NM_004226	0.81
			hHC018835	NDUFA7	NM_005001	0.81
			hHC024103	NUDT1	NM_198949	0.80
			hHC004459	CLGN	NM_001130675	0.82
			hHC009559	FAM111A	NM_001142520	0.82
			hHC026275	DCI	NM_001919	0.83
			hHC004699	TCF7L2	BX648364	0.84
			hHC004014	BMP7	NM_001719	0.84
			hHR018234	CHAF1A	NM_005483	0.81
			hHC018426	IFI27L2	NM_032036	0.84
			hHC009617	TUBB6	NM_032525	0.83
			hHE042545	CENPN	NM_001100624	0.85
			hHC023741	SHFM1	NM_006304	0.81
			hHC004289	NOTCH2	NM_024408	0.83
			hHC015605	NAGA	NM_000262	0.81
			hHC016577	CCNB1	NM_031966	0.84
			hHC020993	HADH	NM_005327	0.82
			hHC013913	EPHB4	NM_004444	0.81
			hHC015353	XYLT2	NM_022167	0.82
			hHC006208	SPAG5	NM_006461	0.82
			hHC008212	DNMBP	NM_015221	0.90

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC020032	REEP4	NM_025232	0.88
			hHC011224	ZNRD1	NM_170783	0.86
			hHC009603	FAM83D	NM_030919	0.84
			hHE042447	BX097999	BX097999	0.82
			hHC023847	CASP7	NM_033338	0.83
			hHC027387	TULP3	NM_003324	0.85
			hHC004851	ITGB3BP	NM_014288	0.84
			hHR018207	HINT2	NM_032593	0.83
			hHC006135	FAM117A	NM_030802	0.80
			hHC026199	CDKN3	NM_005192	0.84
			hHC028599	RPA3	NM_002947	0.82
			hHR003398	NOTCH1	NM_017617	0.81
			hHC029222	CKS2	NM_001827	0.86
			hHC013214	ATPAF2	NM_145691	0.87
			hHC007178	MCM6	NM_005915	0.80
			hHC017366	MTCP1	NM_014221	0.85
			hHR003949	MYBL1	NM_001080416	0.83
			hHC015961	TRIM21	NM_003141	0.83
			hHC007261	RNASE4	NM_002937	0.81
			hHC009265	SLC9A3R1	NM_004252	0.87
			hHC012913	CHST14	NM_130468	0.87
			hHC015229	HMGB2	NM_002129	0.82
			hHC016861	TRIM56	NM_030961	0.82
			hHC027997	PTTG3	NR_002734	0.86
			hHC030397	SAP30	NM_003864	0.84
			hHC002281	NR2E1	NM_003269	0.84
			hHC004117	PPIL5	NM_152329	0.82
			hHC006025	FGGY	NM_001113411	0.82
			hHC006313	CRB1	NM_201253	0.81
			hHC010261	AS3MT	NM_020682	1.00
			hHR011689	KCTD9	NM_017634	0.84
			hHC027913	CDYL	NM_004824	0.86
SCZ (PGC) GWAS	hHC005884	C10orf25	hHC005884	C10orf25	NM_001039380	1.00
SCZ (PGC) GWAS	hHC008880	C12orf65	hHC008880	C12orf65	NM_152269	1.00
SCZ (PGC) GWAS	hHC008533	C2orf60	hHC008533	C2orf60	NM_001039693	1.00
SCZ (PGC) GWAS	hHR021294	CEP170	hHR021294	CEP170	NM_014812	1.00
SCZ (PGC) GWAS	hHA035949	CNNM2	hHR010176	DLGAP1	AK316099	0.82
			hHR001762	LOC158301	AK057958	0.84
			hHA035949	CNNM2	NM_199077	1.00
			hHR016299	RTN3	NM_201428	0.82
			hHR009542	SPTBN1	AB209551	0.87
SCZ (PGC) GWAS	hHC017657	GLT8D1	hHA037103	ZNF3	NM_032924	0.80
			hHA035253	USP14	NM_005151	0.80
			hHA039140	SNX2	NM_003100	0.88

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHA039847	CNOT1	NM_016284	0.81
			hHA035947	SPTLC1	NM_006415	0.87
			hHA036547	TRO	NM_001039705	0.83
			hHA034363	YME1L1	NM_139312	0.85
			hHA037435	GART	NM_001136005	0.81
			hHC017657	GLT8D1	NM_001010983	1.00
			hCT001156	OCRL	NM_000276	0.81
			hCT001287	OCRL	AK226116	0.82
			hHC017161	ZNF226	NM_001032372	0.84
SCZ (PGC) GWAS	hHC018912	LPAR2	hHC018912	LPAR2	NM_004720	1.00
SCZ (PGC) GWAS	hHA035698	MMP16	hHA038808	ERBB2IP	NM_018695	0.81
			hHA033948	INPP5F	NM_014937	0.82
			hHA035698	MMP16	NM_005941	1.00
			hHC012775	FAM120C	NM_017848	0.82
			hHC024247	PRRC1	NM_130809	0.81
			hHC019374	TGFBR1	NM_004612	0.82
SCZ (PGC) GWAS	hHC002303	MPHOSPH9	hHC015671	WHSC1	NM_133330	0.81
			hHC002303	MPHOSPH9	NM_022782	1.00
			hHC003923	KIF11	NM_004523	0.84
			hHC008266	HMMR	NM_001142556	0.84
			hHR011637	AK095498	AK095498	0.81
			hHC029781	NEK2	NM_002497	0.84
			hHR030128	OSTCL	NM_145303	0.81
			hHA036737	UBE2C	NM_181799	0.83
			hHC014681	DTL	NM_016448	0.80
			hHA035403	SYNE2	NM_182914	0.81
			hHA039446	NUF2	NM_145697	0.84
SCZ (PGC) GWAS	hHC008161	NCAN	hHC008161	NCAN	NM_004386	1.00
SCZ (PGC) GWAS	hHE041640	NT5C2	hHE041640	NT5C2	NM_012229	1.00
SCZ (PGC) GWAS	hHC024330	NT5DC2	hHC024330	NT5DC2	NM_022908	1.00
SCZ (PGC) GWAS	hHC008716	NUCB2	hHC008716	NUCB2	AK097398	1.00
SCZ (PGC) GWAS	hHC024103	NUDT1	hHC014134	BCL2L12	NM_138639	0.82
			hHR019400	RNASEH2C	NM_032193	0.86
			hHC027620	RNASEH2C	NM_032193	0.84
			hHC024103	NUDT1	NM_198949	1.00
			hHC020863	PXMP2	NM_018663	0.81
			hHC026275	DCI	NM_001919	0.83
			hHC021775	CHCHD5	NM_032309	0.84
			hHC014490	SSSCA1	NM_006396	0.82
			hHR021317	CYBA	NM_000101	0.80
			hHC019133	FKBPL	NM_022110	0.85
			hHC023741	SHFM1	NM_006304	0.83
			hHC022169	C1orf144	NM_001114600	0.85
			hHC032284	DTYMK	NM_012145	0.85

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC020032	REEP4	NM_025232	0.80
			hHC011224	ZNRD1	NM_170783	0.86
			hHC018782	DCPS	NM_014026	0.82
			hHC012266	WDR51A	NM_015426	0.81
			hHC017366	MTCP1	NM_014221	0.82
			hHA039530	TRPT1	NM_001033678	0.85
			hHA035545	CDK4	NM_000075	0.85
			hHC010261	AS3MT	NM_020682	0.80
SCZ (PGC) GWAS	hHC007983	PBRM1	hHC007983	PBRM1	NM_018313	1.00
SCZ (PGC) GWAS	hHC009226	PBX4	hHC009226	PBX4	NM_025245	1.00
SCZ (PGC) GWAS	hHR027831	PCGF6	hHR027831	PCGF6	NM_001011663	1.00
SCZ (PGC) GWAS	hHR008588	PDCD11	hHR008588	PDCD11	NM_014976	1.00
SCZ (PGC) GWAS	hHC012392	PIK3C2A	hHC010032	CHD2	NM_001271	0.83
			hCT001500	RB1	NM_000321	0.80
			hHC001918	KIAA0528	NM_014802	0.83
			hHC012392	PIK3C2A	NM_002645	1.00
SCZ (PGC) GWAS	hHA034577	PPP2R3C	hHA034577	PPP2R3C	NM_017917	1.00
SCZ (PGC) GWAS	hHC002591	SDCCAG8	hHC002591	SDCCAG8	NM_006642	1.00
SCZ (PGC) GWAS	hHC010043	SFXN2	hHR003000	CDK6	NM_001259	0.82
			hHC031104	CDC20	NM_001255	0.85
			hHC007043	ARL6IP6	NM_152522	0.84
			hHC010043	SFXN2	NM_178858	1.00
			hHE041914	AK123765	AK123765	0.85
			hHC004018	BRCA1	NM_007295	0.82
			hHC003297	DACH1	NM_080759	0.85
			hHR029265	CDC20	BE836833	0.80
			hHC018812	MCM2	NM_004526	0.82
			hHR007303	FLJ11710	AK021772	0.84
			hHC023143	TRAIP	NM_005879	0.84
			hHC024931	TJAP1	NM_080604	0.80
			hHC027319	TGIF2	NM_021809	0.82
			hHC008143	ZNF491	AK096593	0.83
			hHC011874	IGF2BP1	NM_006546	0.81
			hHC006929	MLF1IP	NM_024629	0.84
			hHA038801	DACH1	NM_080759	0.83
			hHA039557	DACH1	NM_080759	0.85
			hHC015197	PHF19	NM_015651	0.84
			hHC004469	PHF21B	NM_138415	0.81
			hHC006509	E2F8	NM_024680	0.83
			hHA036365	DACH1	NM_080759	0.82
			hHC003148	CEP55	NM_018131	0.81
			hHR016888	CBX2	NM_005189	0.82
			hHC003267	COL9A1	NM_001851	0.81
			hHC008847	NUF2	NM_145697	0.82

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC027267	STIL	NM_001048166	0.85
			hHR029571	C9orf140	NM_178448	0.81
			hHC023199	IMPA2	NM_014214	0.81
			hHR015831	EPR1	NM_001012271	0.82
			hHC002402	BUB1B	NM_001211	0.80
			hHC009506	POLE2	NM_002692	0.84
			hHR006230	FOXN4	NM_213596	0.81
			hHC007597	HJURP	NM_018410	0.81
			hHA036721	CEP192	NM_032142	0.81
SCZ (PGC) GWAS	hHA034238	TAF5	hHA034238	TAF5	NM_006951	1.00
SCZ (PGC) GWAS	hHC020459	TCF4	hHC020459	TCF4	NM_001083962	1.00
SCZ (PGC) GWAS	hHC025830	WDR82	hHC017134	NDRG3	NM_032013	0.81
			hHC025830	WDR82	NM_025222	1.00
			hHA040084	PCDHA1	NM_018900	0.81
SCZ (PGC) GWAS	hHR029739	ZEB2	hHR029739	ZEB2	NM_014795	1.00
SCZ (PGC) GWAS	hHR001783	ZSWIM6	hHC001966	ZSWIM6	NM_020928	0.91
			hHR003490	EIF3J	NM_003758	0.84
			hHC006549	DOCK7	NM_033407	0.81
			hHC005313	UCKL1	NM_017859	0.84
			hHC002924	CNOT4	NM_013316	0.87
			hHC004063	EIF3J	NM_003758	0.81
			hHR029131	UBE2E4P	AF136176	0.85
			hHR001783	ZSWIM6	NM_020928	1.00
			hHC003810	ZBTB6	NM_006626	0.82
			hHC002837	KIAA2026	NM_001017969	0.81
			hHC002260	C14orf104	NM_018139	0.82
			hHR030412	BZW1	NM_014670	0.83
			hHC004443	PHF14	NM_001007157	0.81
			hHC030387	NDUFAF2	NM_174889	0.81
			hHC005101	YAF2	NM_005748	0.83
SCZ CNV	hHC025769	ARVCF	hHC025769	ARVCF	NM_001670	1.00
SCZ CNV	hHC008219	ASPHD1	hHC008219	ASPHD1	AF070642	1.00
			hHC011324	MAPK4	NM_002747	0.84
			hHC028147	PTPN2	NM_080422	0.85
			hHC004854	ABHD7	NM_173567	0.83
			hHA034525	ASPHD1	AF070642	0.85
SCZ CNV	hHC014098	BCL9	hHC014098	BCL9	NM_004326	1.00
SCZ CNV	hHC013809	C16orf53	hHR016547	AK027209	AK027209	0.80
			hHC013809	C16orf53	NM_024516	1.00
			hHC013455	RPGR	NM_000328	0.83
			hHC006601	EFS	NM_005864	0.82
SCZ CNV	hHC004040	CDC45L	hHC003564	ZNF367	NM_153695	0.85
			hHC014412	TGIF1	NM_170695	0.81
			hHC021144	TPX2	NM_012112	0.83

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC025176	SLMO2	NM_016045	0.81
			hHC029136	PTTG1	NM_004219	0.85
			hHA034980	CDC2	NM_001130829	0.88
			hHC031104	CDC20	NM_001255	0.81
			hHA038688	NUSAP1	NM_016359	0.88
			hHC014123	CENPO	NM_024322	0.83
			hHC026699	RRM2	NM_001034	0.81
			hHC028811	UBE2C	NM_181802	0.91
			hHA038027	TYMS	NM_001071	0.90
			hHC007043	ARL6IP6	NM_152522	0.84
			hHC013295	FOXM1	NM_202002	0.89
			hHC020495	PRC1	NM_003981	0.87
			hHC023951	AURKA	NM_198433	0.90
			hHC004775	FAM54A	NM_001099286	0.83
			hHC007271	CENPK	NM_022145	0.84
			hHC014459	CCNA2	NM_001237	0.88
			hHC024347	CDC25C	NM_001790	0.87
			hHA037019	RAD51	NM_002875	0.87
			hHC002195	STON1	NM_006873	0.85
			hHR002122	CEP152	NM_014985	0.88
			hHC002314	FAM122C	NM_138819	0.83
			hHC004534	NCAPD3	NM_015261	0.85
			hHR014122	CENPO	NM_024322	0.82
			hHC029674	FAM64A	NM_019013	0.93
			hHC005794	KIAA0101	NM_014736	0.94
			hHC015970	CENPM	NM_024053	0.89
			hHR020686	MXD3	NM_031300	0.85
			hHA039586	TYMS	NM_001071	0.91
			hHC011686	C21orf58	NM_058180	0.81
			hHA038554	RGS3	NM_144488	0.80
			hHC002590	CENPF	NM_016343	0.86
			hHC004018	BRCA1	NM_007295	0.86
			hHC007762	CDCA5	NM_080668	0.86
			hHC016905	CDK2	NM_001798	0.84
			hHC021045	CDCA8	NM_018101	0.95
			hHC025653	MND1	NM_032117	0.87
			hHR012993	FZD2	NM_001466	0.85
			hHC024705	KNTC1	NM_014708	0.85
			hHR025293	RPSAP58	NR_003662	0.81
			hHC004389	WEE1	NM_003390	0.81
			hHC006489	TYMS	NM_001071	0.83
			hHR017349	MAD2L1	NM_002358	0.90
			hHR025605	CDC25A	NM_001789	0.86
			hHC007965	C21orf45	NM_018944	0.85

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC027729	DLGAP5	NM_014750	0.86
			hHR029265	(CDC20),	BE836833	0.92
			hHC002420	CDC14A	NM_003672	0.84
			hHR003572	RTKN2	NM_145307	0.92
			hHC004040	CDC45L	NM_003504	1.00
			hHC008264	H2AFX	NM_002105	0.82
			hHC008876	C15orf42	NM_152259	0.89
			hHC014252	POLA2	NM_002689	0.84
			hHC022400	SMO	NM_005631	0.85
			hHA034304	CDKN3	NM_005192	0.86
			hHC016868	CDCA7	NM_031942	0.87
			hHR026084	NCRNA00095	NR_024348	0.83
			hHC029252	IGF2BP3	NM_006547	0.82
			hHR002672	KIF11	NM_004523	0.90
			hHC009680	ZWINT	NM_032997	0.83
			hHC018812	MCM2	NM_004526	0.88
			hHC025244	MXD3	NM_031300	0.83
			hHC014803	RNASEH2A	NM_006397	0.84
			hHC014791	CDC2	NM_001130829	0.88
			hHC024295	MCM5	NM_006739	0.87
			hHC027187	CTDSP2	NM_005730	0.80
			hHC031507	UHRF1	NM_013282	0.86
			hHC003499	LIPG	NM_006033	0.82
			hHC004255	C5orf34	NM_198566	0.87
			hHC007903	KIF24	NM_194313	0.85
			hHC009163	C1orf112	NM_018186	0.92
			hHC009931	TCF19	NM_007109	0.84
			hHC021451	TROAP	NM_005480	0.86
			hHC022591	OIP5	NM_007280	0.92
			hHC009559	FAM111A	NM_001142520	0.84
			hHR017719	CCNB2	NM_004701	0.88
			hHC027319	TGIF2	NM_021809	0.84
			hHR030487	FAM60A	NM_001135811	0.85
			hHA035671	CHEK2	NM_001005735	0.85
			hHC003451	SFRP2	NM_003013	0.85
			hHA037339	ACAA2	NM_006111	0.81
			hHR013734	DTL	NM_016448	0.91
			hHR026706	SAP30	NM_003864	0.81
			hHC006558	DLEU2	CR625878	0.84
			hHC011850	EME1	NM_152463	0.90
			hHA034122	PPIL5	NM_152329	0.88
			hHC001986	IL33	NM_033439	0.86
			hHR004098	SMC4	NM_005496	0.88
			hHR001818	C11orf82	NM_145018	0.85

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC011418	TIMELESS	NM_003920	0.86
			hHC018606	C12orf48	NM_017915	0.87
			hHA039066	CDCA4	NM_017955	0.85
			hHR005105	RAD51AP1	NM_001130862	0.92
			hHC006929	MLF1IP	NM_024629	0.88
			hHC006917	TTK	NM_003318	0.91
			hHC020837	GINS2	NM_016095	0.87
			hHA033713	ARHGAP11A	NM_014783	0.87
			hHA035921	RAD51	NM_002875	0.90
			hHA036485	CDC25C	NM_001790	0.89
			hHC003593	C6orf167	NM_198468	0.93
			hHC027497	GINS4	NM_032336	0.88
			hHA033053	C14orf94	NM_017815	0.80
			hHC006593	SMC4	NM_005496	0.92
			hHC016577	CCNB1	NM_031966	0.84
			hHA033857	NUSAP1	NM_016359	0.93
			hHA035585	FST	NM_006350	0.82
			hHA036737	UBE2C	NM_181799	0.80
			hHC007277	STK33	NM_030906	0.82
			hHC014681	DTL	NM_016448	0.81
			hHC014704	CENPN	NM_001100624	0.89
			hHR017092	NEK2	NM_002497	0.91
			hHC001792	NUP37	NM_024057	0.83
			hHC014176	CENPE	NM_001813	0.90
			hHC003160	KIF15	NM_020242	0.85
			hHC003148	CEP55	NM_018131	0.88
			hHC021592	TK1	NM_003258	0.90
			hHA035416	ITGB3BP	NM_014288	0.85
			hHC001935	ORC6L	NM_014321	0.81
			hHC008847	NUF2	NM_145697	0.97
			hHC009603	FAM83D	NM_030919	0.90
			hHC022563	PIF1	NM_025049	0.81
			hHC027267	STIL	NM_001048166	0.90
			hHR017511	CKS2	NM_001827	0.93
			hHC021243	KRI1	NM_023008	0.82
			hHA035259	OIP5	NM_007280	0.89
			hHC003603	INTU	NM_015693	0.82
			hHC003795	MELK	NM_014791	0.90
			hHC004851	ITGB3BP	NM_014288	0.87
			hHC011295	NUSAP1	NM_016359	0.91
			hHR017427	SMO	NM_005631	0.80
			hHA038355	CDCA3	NM_031299	0.86
			hHC010551	MKI67	NM_002417	0.85
			hHC012087	RAD51	NM_002875	0.87

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHR015831	EPR1	NM_001012271	0.92
			hHC026199	CDKN3	NM_005192	0.80
			hHC002402	BUB1B	NM_001211	0.86
			hHC003746	VRK1	NM_003384	0.81
			hHC006926	NSBP1	NM_030763	0.84
			hHC009506	POLE2	NM_002692	0.85
			hHC005690	DEPDC1	NM_001114120	0.83
			hHC018470	PPIL5	NM_152329	0.81
			hHC020474	CDCA3	NM_031299	0.89
			hHC027578	CCNB2	NM_004701	0.92
			hHC029222	CKS2	NM_001827	0.81
			hHC031718	CDC20	NM_001255	0.92
			hHR003986	MCM10	NM_182751	0.95
			hHC016862	KIF18A	NM_031217	0.92
			hHC019742	PLCE1	NM_016341	0.82
			hHC025682	MTA3	NM_020744	0.80
			hHC026750	BTG3	NM_001130914	0.82
			hHC029426	DBF4	NM_006716	0.89
			hHR006230	FOXN4	NM_213596	0.92
			hHC010346	PIF1	NM_025049	0.85
			hHC023882	SPC24	AK075287	0.85
			hHC007597	HJURP	NM_018410	0.94
			hHC020461	TK1	NM_003258	0.82
			hHR028333	PTTG3	NR_002734	0.90
			hHC005509	TRDMT1	NM_004412	0.82
			hHC016069	E2F2	NM_004091	0.89
			hHC019417	LOC91431	NM_001099776	0.85
			hHC004849	NCAPH	NM_015341	0.95
			hHC005725	BUB1	NM_004336	0.94
			hHC012913	CHST14	NM_130468	0.85
			hHC016789	SEMA5B	NM_001031702	0.80
SCZ CNV	hHR025141	CHRNA7	hHR025141	CHRNA7	NM_000746	1.00
SCZ CNV	hHA036352	CLTCL1	hHA036352	CLTCL1	NM_007098	1.00
SCZ CNV	hHC003582	CYFIP1	hHC003582	CYFIP1	AY763579	1.00
SCZ CNV	hHR005214	DGCR10	hHR005214	DGCR10	NR_026651	1.00
SCZ CNV	hHC030047	DGCR5	hHC029747	PDXDC2	NR_003610	0.81
			hHC030047	DGCR5	X91348	1.00
			hHC022670	A2BP1	NM_018723	0.83
SCZ CNV	hHC018376	DGCR8	hHC018376	DGCR8	NM_022720	1.00
SCZ CNV	hHC021273	FAM57B	hHC021273	FAM57B	NM_031478	1.00
			hHR026756	TTLL12	NM_015140	0.85
			hHC021087	LRFN4	NM_024036	0.84
SCZ CNV	hHC029540	HIC2	hHC029540	HIC2	NM_015094	1.00
SCZ CNV	hHC025127	HIRA	hHC025127	HIRA	NM_003325	1.00

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
SCZ CNV	hHC005831	LIX1L	hHC005831	LIX1L	AK128733	1.00
SCZ CNV	hHC019168	LZTR1	hHC019168	LZTR1	NM_006767	1.00
			hHC020896	RP3-402G11.5	NM_031454	0.81
SCZ CNV	hHC010102	MTMR15	hHC010102	MTMR15	NM_014967	1.00
SCZ CNV	hHC003863	NCBP2	hHC003863	NCBP2	NM_007362	1.00
SCZ CNV	hHA035283	NRXN1	hHC009943	CACNA2D1	NM_000722	0.81
			hHC014427	SLC35F5	NM_025181	0.82
			hHA034405	USP34	NM_014709	0.85
			hHC019261	ANKRD28	NM_015199	0.80
			hHC029833	GNAQ	NM_002072	0.80
SCZ CNV	hHR008719	PAK2	hHR008719	PAK2	NM_002577	1.00
SCZ CNV	hHA039366	PI4KA	hHA039366	PI4KA	NM_058004	1.00
SCZ CNV	hHC019979	PPP4C	hHC018696	KDELR1	NM_006801	0.80
			hHA034332	MBNL1	NM_021038	0.80
			hHC019979	PPP4C	NM_002720	1.00
			hHC014351	TMED7	NM_181836	0.81
			hHA033755	HERPUD2	NM_022373	0.80
			hHA036513	FYN	NM_002037	0.84
			hHC030932	NONO	NM_007363	0.85
			hCT000607	ACTB	NM_001101	0.85
			hHA033126	CASC4	NM_138423	0.83
			hHA034506	MACF1	NM_012090	0.83
			hHC013157	SEL1L	NM_005065	0.83
			hHR023273	TOMM20	NM_014765	0.82
			hHC017813	GDI1	NM_001493	0.83
SCZ CNV	hHC007231	PRKAB2	hHC004824	TAPT1	NM_153365	0.81
			hHC005100	CDH10	NM_006727	0.88
			hHC001872	CNRIP1	NM_015463	0.80
			hHC006408	LPL	NM_000237	0.82
			hHC028284	ACSL4	NM_022977	0.80
			hHR006048	PCDHA1	NM_018900	0.83
			hHE040931	CB242912	CB242912	0.80
			hHR020135	CHD5	NM_015557	0.87
			hHR006047	PCDHA1	NM_018900	0.84
			hHR007103	FAM169A	NM_015566	0.85
			hHC012083	KIAA1377	NM_020802	0.85
			hHC008950	CCBE1	NM_133459	0.84
			hHR009994	KALRN	NM_003947	0.83
			hHA034678	MYLIP	NM_013262	0.86
			hHC008506	PTPRT	NM_133170	0.88
			hHR030586	PCDH11X	NM_032968	0.83
			hHR006046	PCDHA1	NM_018900	0.84
			hHC009694	FBXO27	NM_178820	0.86
			hHC017266	CUX2	NM_015267	0.84

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC006933	BAALC	NM_024812	0.81
			hHR009129	ZNF706	NM_001042510	0.82
			hHC003777	NAV3	NM_014903	0.86
			hHC009741	FGF9	NM_002010	0.82
			hHC005253	KCND2	NM_012281	0.86
			hHR004605	THRB	NM_001128177	0.88
			hHC004689	NECAB1	NM_022351	0.86
			hHR006045	PCDHA1	NM_018900	0.85
			hHC007220	ELOVL2	NM_017770	0.79
			hHC025160	C17orf58	NM_181656	0.82
			hHA035912	GRM7	BC136458	0.85
			hHC008960	NKAIN2	NM_001040214	0.83
			hHC010412	DB519783	DB519783	0.87
			hHR006055	PCDHA1	NM_018900	0.84
			hHC017683	SUOX	NM_000456	0.84
			hHC005695	AJAP1	NM_018836	0.81
			hHC007231	PRKAB2	NM_005399	1.00
			hHE040843	CD678534	CD678534	0.84
			hHC006295	JAZF1	NM_175061	0.82
			hHC008995	RIMS1	BC036608	0.85
			hHC027511	FABP3	NM_004102	0.81
			hHC002299	AKAP7	NM_016377	0.80
			hHR006043	PCDHA1	NM_018900	0.85
			hHC002214	DPYD	NM_000110	0.82
			hHC004902	FAM19A2	NM_178539	0.84
			hHR006054	PCDHA1	NM_018900	0.81
			hHR006738	LOC283070	BC073155	0.85
			hHC005898	AFF2	NM_002025	0.81
			hHC013950	CHD5	NM_015557	0.81
			hHA033834	HDAC9	NM_014707	0.80
			hHR005850	BEAN	NM_001136106	0.83
			hHR006042	PCDHA1	NM_018900	0.82
			hHR008046	DERL1	AY358818	0.82
			hHC010734	MMP24	NM_006690	0.81
			hHR006053	PCDHA1	NM_018900	0.85
			hHA033893	KLHL4	NM_019117	0.88
			hHC001865	RBM24	NM_153020	0.82
			hHC002429	DNAJC6	NM_014787	0.84
			hHC004361	LRRC4C	NM_020929	0.90
			hHR028841	USP6	NM_004505	0.80
			hHR005537	LPHN3	NM_015236	0.82
			hHR008897	PLCH2	NM_014638	0.91
			hHE040949	EY892390	EY892390	0.87
			hHA033869	NEBL	NM_006393	0.86

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC008260	GRM7	NM_181874	0.86
			hHC007240	KLHL4	NM_019117	0.83
			hHC004792	PTCHD1	NM_173495	0.88
			hHR006051	PCDHA1	NM_018900	0.84
			hHC009615	L3MBTL3	NM_032438	0.81
			hHR002763	CACNA1C	NM_199460	0.81
			hHC001634	BACE1	NM_012104	0.80
			hHR006050	PCDHA1	NM_018900	0.84
			hHR011906	RIMBP2	NM_015347	0.83
			hHR002630	KIAA1107	NM_015237	0.80
			hHC003290	LOC153364	NM_203406	0.81
			hHC009926	SH3GL3	NM_003027	0.80
			hHC003698	FRMD4A	NM_018027	0.83
			hHR001898	KIAA1239	NM_001144990	0.84
			hHC003050	ALCAM	NM_001627	0.87
			hHC008234	LHX6	NM_014368	0.81
			hHC018506	WWC1	NM_015238	0.81
			hHC002797	CDH11	NM_001797	0.82
			hHR006049	PCDHA1	NM_018900	0.83
			hHE040993	SAMD5	NM_001030060	0.90
			hHC004537	LRRC8B	NM_015350	0.84
			hHC005689	SLC30A10	NM_018713	0.82
			hHC006757	MYLIP	NM_013262	0.82
			hHA035269	KLHL4	NM_019117	0.82
			hHE040789	SCN9A	NM_002977	0.87
SCZ CNV	hHR030321	RBM8A	hHR030321	RBM8A	NM_005105	1.00
SCZ CNV	hHC022493	SERPIND1	hHC022493	SERPIND1	NM_000185	1.00
SCZ CNV	hHC014256	TCTEX1D2	hHC014256	TCTEX1D2	NM_152773	1.00
SCZ CNV	hHC017503	TXNIP	hHC017503	TXNIP	NM_006472	1.00
SCZ CNV	hHR014260	UBXN7	hHR014260	UBXN7	NM_015562	1.00
SCZ CNV	hHC014115	ZNF74	hHC014115	ZNF74	NM_003426	1.00
SCZ SNV	hHC002182	ASAP2	hHC002182	ASAP2	NM_003887	1.00
			hHC002121	NAPEPLD	NM_001122838	0.85
			hHC003758	C9orf82	NM_024828	0.82
			hHR001994	SPTLC1	NM_006415	0.81
SCZ SNV	hHC024980	BCORL1	hHC011844	FAM123B	NM_152424	0.81
			hHC019619	ABCC10	NM_033450	0.80
			hHC024980	BCORL1	NM_021946	1.00
SCZ SNV	hHC009547	BIRC6	hHC009547	BIRC6	NM_016252	1.00
SCZ SNV	hHC025318	BRPF1	hHC025318	BRPF1	NM_001003694	1.00
SCZ SNV	hHC014706	C11orf30	hHC014706	C11orf30	NM_020193	1.00
SCZ SNV	hHC010825	CBX5	hHA033084	PRKRIR	AV706361	0.81
			hHA037235	MAP4	NM_002375	0.82
			hHA037234	MAP4	NM_002375	0.83

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC003596	BOD1L	NM_148894	0.82
			hHA034951	ZFP106	NM_022473	0.82
			hHA036019	LSAMP	NM_002338	0.84
			hHA033054	CDC27	NM_001114091	0.86
			hHA034481	KCNH7	NM_033272	0.81
			hHC010960	PLXNA2	NM_025179	0.82
			hHC017776	THAP6	NM_144721	0.81
			hHR010912	(ENC1),	DA181535	0.82
			hHC008475	KCNH7	NM_033272	0.90
			hHR004083	H2AFV	NM_012412	0.86
			hHC003794	BU071960	BU071960	0.87
			hHR011989	C6orf174	NM_001012279	0.81
SCZ SNV	hHR016405	CCDC84	hHR016405	CCDC84	NM_198489	1.00
SCZ SNV	hHA035671	CHEK2	hHC003564	ZNF367	NM_153695	0.84
			hHC006552	PPAP2B	NM_003713	0.81
			hHC014412	TGIF1	NM_170695	0.80
			hHC029136	PTTG1	NM_004219	0.89
			hHA034980	CDC2	NM_001130829	0.82
			hHC029940	ADH5	NM_000671	0.83
			hHC004439	STK17B	NM_004226	0.81
			hHC028811	UBE2C	NM_181802	0.83
			hHA038027	TYMS	NM_001071	0.84
			hHC003887	MAT2B	NM_182796	0.82
			hHC020495	PRC1	NM_003981	0.82
			hHC023951	AURKA	NM_198433	0.90
			hHC007271	CENPK	NM_022145	0.89
			hHR012539	CHEK2	NM_001005735	0.82
			hHC014459	CCNA2	NM_001237	0.92
			hHA037019	RAD51	NM_002875	0.80
			hHC002195	STON1	NM_006873	0.83
			hHC002314	FAM122C	NM_138819	0.84
			hHC029674	FAM64A	NM_019013	0.80
			hHC005794	KIAA0101	NM_014736	0.84
			hHC009634	C15orf23	NM_001142761	0.82
			hHC015970	CENPM	NM_024053	0.84
			hHA039586	TYMS	NM_001071	0.80
			hHC003418	C14orf106	NM_018353	0.85
			hHC011686	C21orf58	NM_058180	0.85
			hHE041914	AK123765	AK123765	0.90
			hHC002590	CENPF	NM_016343	0.81
			hHC004018	BRCA1	NM_007295	0.86
			hHC007762	CDCA5	NM_080668	0.86
			hHC020830	GMNN	NM_015895	0.82
			hHC016905	CDK2	NM_001798	0.89

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC021045	CDCA8	NM_018101	0.86
			hHC003297	DACH1	NM_080759	0.86
			hHR012993	FZD2	NM_001466	0.82
			hHC004389	WEE1	NM_003390	0.85
			hHC006489	TYMS	NM_001071	0.86
			hHC010341	ACTL6A	NM_178042	0.85
			hHR017349	MAD2L1	NM_002358	0.90
			hHR025605	CDC25A	NM_001789	0.84
			hHR028857	RACGAP1	NM_001126103	0.87
			hHC002420	CDC14A	NM_003672	0.87
			hHR003572	RTKN2	NM_145307	0.88
			hHC004040	CDC45L	NM_003504	0.85
			hHC010568	NFATC3	NM_004555	0.84
			hHA032936	CAMTA1	NM_015215	0.82
			hHC014252	POLA2	NM_002689	0.82
			hHA033836	CDC14A	NM_003672	0.83
			hHA034304	CDKN3	NM_005192	0.85
			hHR008024	PRDM16	NM_022114	0.84
			hHC016868	CDCA7	NM_031942	0.83
			hHR002672	KIF11	NM_004523	0.86
			hHC009680	ZWINT	NM_032997	0.84
			hHC024295	MCM5	NM_006739	0.85
			hHC031507	UHRF1	NM_013282	0.83
			hHC003499	LIPG	NM_006033	0.87
			hHC004255	C5orf34	NM_198566	0.86
			hHC009163	C1orf112	NM_018186	0.81
			hHC009931	TCF19	NM_007109	0.81
			hHC009559	FAM111A	NM_001142520	0.83
			hHA035671	CHEK2	NM_001005735	1.00
			hHC003451	SFRP2	NM_003013	0.83
			hHR026706	SAP30	NM_003864	0.82
			hHA034122	PPIL5	NM_152329	0.82
			hHC001986	IL33	NM_033439	0.81
			hHR004098	SMC4	NM_005496	0.89
			hHC008214	TMEM194A	NM_001130963	0.87
			hHR023394	FAM96A	NM_032231	0.82
			hHA039906	PCNA	NM_182649	0.80
			hHC003354	ATAD2	NM_014109	0.82
			hHC018606	C12orf48	NM_017915	0.83
			hHR005105	RAD51AP1	NM_001130862	0.87
			hHC009617	TUBB6	NM_032525	0.85
			hHA035921	RAD51	NM_002875	0.81
			hHE042545	CENPN	NM_001100624	0.86
			hHC003593	C6orf167	NM_198468	0.84

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC027497	GINS4	NM_032336	0.83
			hHC002849	ECT2	NM_018098	0.83
			hHC004469	PHF21B	NM_138415	0.81
			hHC006593	SMC4	NM_005496	0.87
			hHC008801	SFRP1	NM_003012	0.85
			hHC016577	CCNB1	NM_031966	0.88
			hHA033857	NUSAP1	NM_016359	0.87
			hHC006905	CENPH	NM_022909	0.82
			hHC014176	CENPE	NM_001813	0.80
			hHC021592	TK1	NM_003258	0.83
			hHC001935	ORC6L	NM_014321	0.84
			hHC008847	NUF2	NM_145697	0.87
			hHC009603	FAM83D	NM_030919	0.91
			hHC003795	MELK	NM_014791	0.82
			hHC011295	NUSAP1	NM_016359	0.87
			hHC028467	10-Sep	NM_144710	0.82
			hHA038355	CDCA3	NM_031299	0.85
			hHC009591	ZFHX4	NM_024721	0.83
			hHC012087	RAD51	NM_002875	0.84
			hHC026199	CDKN3	NM_005192	0.88
			hHC002402	BUB1B	NM_001211	0.90
			hHC006926	NSBP1	NM_030763	0.81
			hHC009506	POLE2	NM_002692	0.83
			hHC005690	DEPDC1	NM_001114120	0.85
			hHC020474	CDCA3	NM_031299	0.83
			hHC031718	CDC20	NM_001255	0.83
			hHR003986	MCM10	NM_182751	0.86
			hHC016862	KIF18A	NM_031217	0.84
			hHC019742	PLCE1	NM_016341	0.82
			hHC023870	EXOSC8	AK096810	0.82
			hHC025682	MTA3	NM_020744	0.85
			hHC026750	BTG3	NM_001130914	0.82
			hHC029426	DBF4	NM_006716	0.84
			hHC030398	TMEM98	NM_015544	0.81
			hHA038450	RAD51	NM_002875	0.85
			hHC010346	PIF1	NM_025049	0.90
			hHC007597	HJURP	NM_018410	0.84
			hHC020461	TK1	NM_003258	0.81
			hHR028333	PTTG3	NR_002734	0.86
			hHR031105	CKS1B	X54941	0.83
			hHC019417	LOC91431	NM_001099776	0.86
			hHC004849	NCAPH	NM_015341	0.90
			hHC005725	BUB1	NM_004336	0.83
			hHC027997	PTTG3	NR_002734	0.85

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC002281	NR2E1	NM_003269	0.85
			hHC004117	PPIL5	NM_152329	0.88
SCZ SNV	hHA036352	CLTCL1	hHA036352	CLTCL1	NM_007098	1.00
SCZ SNV	hHR008145	COL3A1	hHR005136	COL1A1	NM_000088	0.80
0			hHC007632	CCL2	NM_002982	0.83
			hHC015300	MS4A4A	NM_024021	0.82
			hHC002304	MPZL2	NM_005797	0.86
			hHR009600	COL18A1	NM_130444	0.90
			hHC015348	ACTA2	NM_001141945	0.84
			hHC002807	LYVE1	NM_006691	0.84
			hHC004751	CD163	NM_004244	0.83
			hHC009359	F13A1	NM_000129	0.84
			hHC003035	DSP	NM_004415	0.83
			hHC021119	LAMC3	NM_006059	0.84
			hHA035807	CTSC	NM_148170	0.87
			hHC002758	TGFBR3	NM_003243	0.89
			hHC004306	EMCN	NM_016242	0.86
			hHC003681	ASPN	NM_017680	0.85
			hHA034053	CXCL12	NM_199168	0.83
			hHC006513	C7orf58	NM_024913	0.90
			hHR008145	COL3A1	NM_000090	1.00
			hHC012669	SCARA5	NM_173833	0.85
			hHR012212	COL5A1	NM_000093	0.85
			hHC005636	LUM	NM_002345	0.84
			hHC007832	FOXD1	NM_004472	0.94
			hHC012248	NID2	NM_007361	0.90
			hHC001532	CLDN11	NM_005602	0.81
			hHC014131	COLEC12	NM_130386	0.93
			hHC002143	NID1	NM_002508	0.87
			hHC028998	GJA1	NM_000165	0.81
			hHR015546	INS-IGF2	NR_003512	0.87
			hHC015773	DCN	NM_001920	0.89
			hHC003664	OGN	NM_033014	0.82
			hHC022528	PCOLCE	NM_002593	0.82
			hHC015351	RNASE1	NM_198235	0.83
			hHC017835	ISLR	NM_005545	0.86
			hHR026571	GJA1	NM_000165	0.81
			hHC013442	OLFML3	NM_020190	0.94
			hHR008102	TMEM132C	NM_001136103	0.82
			hHC003038	EDNRA	NM_001957	0.85
			hHC011606	ID3	NM_002167	0.85
			hHR003865	FOXC1	NM_001453	0.86
			hHC016645	DCN	NM_001920	0.91
			hHC031057	CFH	NM_000186	0.84

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
SCZ SNV	hHR003253	CUGBP2	hHR003253	CUGBP2	NM_001025077	1.00
SCZ SNV	hHC021326	DNMT1	hHC021326	DNMT1	NM_001130823	1.00
SCZ SNV	hHC015130	EVC2	hHC015130	EVC2	NM_147127	1.00
SCZ SNV	hHC010330	FBXL10	hHC010330	FBXL10	NM_032590	1.00
SCZ SNV	hHC015075	FCGBP	hHC015075	FCGBP	NM_003890	1.00
SCZ SNV	hHA034671	FLAD1	hHA034671	FLAD1	NM_025207	1.00
SCZ SNV	hHA033353	H2AFV	hHC003564	ZNF367	NM_153695	0.82
			hHC023628	ANP32E	NM_030920	0.85
			hHR026820	MRPL51	NM_016497	0.80
			hHC029136	PTTG1	NM_004219	0.90
			hHC009468	MCM3	NM_002388	0.81
			hHR001920	SOX21	NM_007084	0.81
			hHC028811	UBE2C	NM_181802	0.88
			hHA038027	TYMS	NM_001071	0.82
			hHC003875	MCM9	NM_153255	0.81
			hHC023951	AURKA	NM_198433	0.86
			hHR012539	CHEK2	NM_001005735	0.81
			hHC014459	CCNA2	NM_001237	0.83
			hHC029674	FAM64A	NM_019013	0.80
			hHC005794	KIAA0101	NM_014736	0.82
			hHC009634	C15orf23	NM_001142761	0.88
			hHC015970	CENPM	NM_024053	0.92
			hHR020686	MXD3	NM_031300	0.80
			hHR024910	PCNA	NM_002592	0.92
			hHA039586	TYMS	NM_001071	0.85
			hHC003418	C14orf106	NM_018353	0.84
			hHC006214	NMU	NM_006681	0.88
			hHC011686	C21orf58	NM_058180	0.82
			hHC011962	UBE2T	NM_014176	0.86
			hHC007762	CDCA5	NM_080668	0.84
			hHC020830	GMNN	NM_015895	0.87
			hHC016905	CDK2	NM_001798	0.82
			hHC003297	DACH1	NM_080759	0.85
			hHR012993	FZD2	NM_001466	0.83
			hHC022125	PECI	NM_206836	0.82
			hHR029325	KPNA2	BC067848	0.85
			hHC004389	WEE1	NM_003390	0.83
			hHC006489	TYMS	NM_001071	0.91
			hHC010341	ACTL6A	NM_178042	0.88
			hHR025605	CDC25A	NM_001789	0.82
			hHR028665	CR625830	CR625830	0.89
			hHR028857	RACGAP1	NM_001126103	0.90
			hHC015069	HAT1	NM_003642	0.81
			hHR029265	(CDC20),	BE836833	0.82

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHR029469	THOC4	NM_005782	0.84
			hHR019400	RNASEH2C	NM_032193	0.81
			hHA032936	CAMTA1	NM_015215	0.84
			hHC007628	RFX2	NM_000635	0.80
			hHC009920	RFC4	NM_181573	0.83
			hHA034304	CDKN3	NM_005192	0.82
			hHC016868	CDCA7	NM_031942	0.84
			hHR026084	NCRNA00095	NR_024348	0.81
			hHR002672	KIF11	NM_004523	0.85
			hHC009680	ZWINT	NM_032997	0.92
			hHC016400	GYPC	NM_002101	0.81
			hHC018812	MCM2	NM_004526	0.87
			hHA039836	CNIH4	NM_014184	0.82
			hHE041072	STK17B	NM_004226	0.87
			hHC014803	RNASEH2A	NM_006397	0.84
			hHC024295	MCM5	NM_006739	0.80
			hHC004255	C5orf34	NM_198566	0.85
			hHC004459	CLGN	NM_001130675	0.87
			hHC009931	TCF19	NM_007109	0.82
			hHC022591	OIP5	NM_007280	0.81
			hHC031243	SNRPG	NM_003096	0.80
			hHC009559	FAM111A	NM_001142520	0.88
			hHC026275	DCI	NM_001919	0.81
			hHC030307	SEPHS1	NM_012247	0.83
			hHC030499	EEF1D	NM_032378	0.86
			hHC003451	SFRP2	NM_003013	0.84
			hHR016603	CDK4	NM_000075	0.85
			hHA037339	ACAA2	NM_006111	0.83
			hHC027006	CLIC1	NM_001288	0.82
			hHR004098	SMC4	NM_005496	0.86
			hHC005430	C20orf72	NM_052865	0.82
			hHC012822	SNRPD3	NM_004175	0.83
			hHC016578	MBD2	NM_003927	0.85
			hHR023394	FAM96A	NM_032231	0.81
			hHC030102	SLC25A5	NM_001152	0.82
			hHA039906	PCNA	NM_182649	0.82
			hHC003354	ATAD2	NM_014109	0.82
			hHC006906	SNAPC3	BC036031	0.81
			hHR018234	CHAF1A	NM_005483	0.84
			hHC031290	FEN1	NM_004111	0.82
			hHR005105	RAD51AP1	NM_001130862	0.85
			hHC009617	TUBB6	NM_032525	0.83
			hHC020837	GINS2	NM_016095	0.81
			hHA035921	RAD51	NM_002875	0.85

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHE042545	CENPN	NM_001100624	0.82
			hHC009833	MCM7	NM_182776	0.81
			hHC015197	PHF19	NM_015651	0.84
			hHC027497	GINS4	NM_032336	0.86
			hHC029309	PCNA	NM_002592	0.94
			hHA033053	C14orf94	NM_017815	0.83
			hHA033353	H2AFV	NM_138635	1.00
			hHC002849	ECT2	NM_018098	0.82
			hHC008801	SFRP1	NM_003012	0.83
			hHC016577	CCNB1	NM_031966	0.91
			hHC020993	HADH	NM_005327	0.86
			hHA033857	NUSAP1	NM_016359	0.86
			hHC006905	CENPH	NM_022909	0.88
			hHC009869	CPSF3	NM_016207	0.81
			hHC016505	PTBP1	NM_002819	0.82
			hHC004240	ID4	NM_001546	0.81
			hHC014704	CENPN	NM_001100624	0.84
			hHR017092	NEK2	NM_002497	0.81
			hHC006208	SPAG5	NM_006461	0.87
			hHC021592	TK1	NM_003258	0.84
			hHC003267	COL9A1	NM_001851	0.81
			hHC008847	NUF2	NM_145697	0.82
			hHC009603	FAM83D	NM_030919	0.85
			hHC007719	CTNNAL1	NM_003798	0.81
			hHR017511	CKS2	NM_001827	0.83
			hHC004851	ITGB3BP	NM_014288	0.81
			hHC011295	NUSAP1	NM_016359	0.89
			hHC023199	IMPA2	NM_014214	0.85
			hHC031347	ALDH7A1	NM_001182	0.81
			hHA038163	CDKN2C	NM_001262	0.84
			hHC009591	ZFHX4	NM_024721	0.81
			hHR015831	EPR1	NM_001012271	0.82
			hHC026199	CDKN3	NM_005192	0.86
			hHC002402	BUB1B	NM_001211	0.84
			hHC006926	NSBP1	NM_030763	0.84
			hHC011042	DSN1	NM_024918	0.88
			hHC014402	SHMT2	NM_005412	0.83
			hHC010490	CNIH4	NM_014184	0.80
			hHC018470	PPIL5	NM_152329	0.81
			hHC020474	CDCA3	NM_031299	0.87
			hHC029222	CKS2	NM_001827	0.85
			hHC031718	CDC20	NM_001255	0.85
			hHR003986	MCM10	NM_182751	0.82
			hHR004658	NXT2	NM_018698	0.83

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC012446	SNRPD3	NM_004175	0.83
			hHC013214	ATPAF2	NM_145691	0.83
			hHC026750	BTG3	NM_001130914	0.87
			hHC030398	TMEM98	NM_015544	0.88
			hHA038450	RAD51	NM_002875	0.86
			hHC010346	PIF1	NM_025049	0.82
			hHC023882	SPC24	AK075287	0.85
			hHC007597	HJURP	NM_018410	0.81
			hHC020461	TK1	NM_003258	0.84
			hHR028333	PTTG3	NR_002734	0.86
			hHR031105	CKS1B	X54941	0.83
			hHC004849	NCAPH	NM_015341	0.84
			hHC007825	C6orf130	NM_145063	0.89
			hHC015229	HMGB2	NM_002129	0.86
			hHC019069	MPST	NR_024038	0.81
			hHC027997	PTTG3	NR_002734	0.82
			hHC030397	SAP30	NM_003864	0.86
			hHC002281	NR2E1	NM_003269	0.83
			hHC004117	PPIL5	NM_152329	0.89
			hHC006313	CRB1	NM_201253	0.84
			hHC013429	RBM23	NM_001077351	0.82
			hHR030613	DHFR	NM_000791	0.81
			hHA039049	SHMT2	NM_005412	0.80
			hHA040105	CDK4	NM_000075	0.83
SCZ SNV	hHC020587	HIF1A	hHA032988	HIF1A	NM_001530	0.86
			hHC006599	ADAM10	NM_001110	0.79
			hHC020587	HIF1A	NM_001530	1.00
			hHC031002	DYNC1I2	NM_001378	0.81
SCZ SNV	hHR016704	HIST1H1E	hHR016704	HIST1H1E	NM_005321	1.00
SCZ SNV	hCT001342	HMGCR	hCT001234	HMGCR	NM_000859	0.93
			hCT001342	HMGCR	NM_000859	1.00
			hHR006622	PWWP2A	NM_052927	0.85
			hCT001245	RB1	M15400	0.84
			hCT001341	HMGCR	NM_000859	0.84
			hHA033002	MATR3	NM_199189	0.82
SCZ SNV	hHA034159	IFT81	hHA034159	IFT81	NM_014055	1.00
SCZ SNV	hHC002137	IRS1	hHE041500	NFASC	NM_015090	0.80
			hHC002137	IRS1	NM_005544	1.00
SCZ SNV	hHR006221	KLF12	hHC005215	SACS	NM_014363	0.89
			hHR006221	KLF12	NM_007249	1.00
SCZ SNV	hHE041382	KPNA1	hHE041382	KPNA1	NM_002264	1.00
SCZ SNV	hHC007864	LAMA1	hHR006282	S1PR3	NM_005226	0.83
			hHC007864	LAMA1	NM_005559	1.00
			hHC012913	CHST14	NM_130468	0.87

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
SCZ SNV	hCT000695	LRP1	hCT000695	LRP1	NM_002332	1.00
			hHR031067	COL4A5	NM_033380	0.87
			hHC016882	COL27A1	AB058773	0.82
			hCT000593	VIM	NM_003380	0.84
SCZ SNV	hHA035413	MACF1	hHA034754	MACF1	NM_012090	0.81
			hHA035413	MACF1	NM_012090	1.00
SCZ SNV	hHA035034	MBTPS1	hHR027288	BAT2D1	NM_015172	0.81
			hHA035034	MBTPS1	NM_003791	1.00
SCZ SNV	hHC004314	MIOS	hHC004314	MIOS	AL136892	1.00
SCZ SNV	hHC010551	MKI67	hHR003000	CDK6	NM_001259	0.83
			hHC003564	ZNF367	NM_153695	0.81
			hHC021144	TPX2	NM_012112	0.80
			hHC024216	POLD1	NM_002691	0.83
			hHC029136	PTTG1	NM_004219	0.82
			hHC003228	WDR67	NM_145647	0.84
			hHR001920	SOX21	NM_007084	0.82
			hHA038688	NUSAP1	NM_016359	0.86
			hHC015671	WHSC1	NM_133330	0.82
			hHC028811	UBE2C	NM_181802	0.88
			hHA038027	TYMS	NM_001071	0.83
			hHC007043	ARL6IP6	NM_152522	0.86
			hHC013295	FOXM1	NM_202002	0.91
			hHC023951	AURKA	NM_198433	0.85
			hHC014459	CCNA2	NM_001237	0.88
			hHC024347	CDC25C	NM_001790	0.83
			hHA037019	RAD51	NM_002875	0.83
			hHC002195	STON1	NM_006873	0.81
			hHC004534	NCAPD3	NM_015261	0.81
			hHC005590	MSH6	NM_000179	0.81
			hHC029674	FAM64A	NM_019013	0.85
			hHC005794	KIAA0101	NM_014736	0.88
			hHC015970	CENPM	NM_024053	0.83
			hHR020686	MXD3	NM_031300	0.83
			hHA039586	TYMS	NM_001071	0.82
			hHE041914	AK123765	AK123765	0.81
			hHC002590	CENPF	NM_016343	0.84
			hHC004018	BRCA1	NM_007295	0.83
			hHC004690	GINS3	NM_001126129	0.85
			hHC007762	CDCA5	NM_080668	0.85
			hHR018046	LOC254559	NR_015411	0.85
			hHC021045	CDCA8	NM_018101	0.85
			hHC025653	MND1	NM_032117	0.80
			hHC003297	DACH1	NM_080759	0.82
			hHR012993	FZD2	NM_001466	0.83

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC024705	KNTC1	NM_014708	0.84
			hHC004389	WEE1	NM_003390	0.83
			hHR017349	MAD2L1	NM_002358	0.82
			hHR025605	CDC25A	NM_001789	0.82
			hHC007965	C21orf45	NM_018944	0.83
			hHC021789	CENPF	NM_016343	0.82
			hHC027729	DLGAP5	NM_014750	0.85
			hHR029265	(CDC20),	BE836833	0.88
			hHR003572	RTKN2	NM_145307	0.87
			hHC004040	CDC45L	NM_003504	0.85
			hHC008876	C15orf42	NM_152259	0.84
			hHC022400	SMO	NM_005631	0.84
			hHC016868	CDCA7	NM_031942	0.85
			hHR026084	NCRNA00095	NR_024348	0.82
			hHR002672	KIF11	NM_004523	0.86
			hHC006896	MUTED	NM_201280	0.81
			hHC009680	ZWINT	NM_032997	0.82
			hHC018812	MCM2	NM_004526	0.84
			hHC025244	MXD3	NM_031300	0.83
			hHC031507	UHRF1	NM_013282	0.84
			hHC003499	LIPG	NM_006033	0.81
			hHC007903	KIF24	NM_194313	0.82
			hHC009163	C1orf112	NM_018186	0.80
			hHC021451	TROAP	NM_005480	0.84
			hHC022591	OIP5	NM_007280	0.86
			hHR017719	CCNB2	NM_004701	0.83
			hHC027319	TGIF2	NM_021809	0.80
			hHC003451	SFRP2	NM_003013	0.81
			hHR013734	DTL	NM_016448	0.80
			hHC011850	EME1	NM_152463	0.81
			hHC001986	IL33	NM_033439	0.83
			hHR001818	C11orf82	NM_145018	0.86
			hHC011418	TIMELESS	NM_003920	0.87
			hHC018606	C12orf48	NM_017915	0.88
			hHA039066	CDCA4	NM_017955	0.87
			hHR005105	RAD51AP1	NM_001130862	0.86
			hHC006929	MLF1IP	NM_024629	0.80
			hHC006917	TTK	NM_003318	0.88
			hHC020837	GINS2	NM_016095	0.83
			hHA036485	CDC25C	NM_001790	0.80
			hHC003593	C6orf167	NM_198468	0.84
			hHC027497	GINS4	NM_032336	0.83
			hHC006593	SMC4	NM_005496	0.85
			hHA033857	NUSAP1	NM_016359	0.87

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHA035585	FST	NM_006350	0.80
			hHC007277	STK33	NM_030906	0.82
			hHC014681	DTL	NM_016448	0.82
			hHC014704	CENPN	NM_001100624	0.82
			hHR017092	NEK2	NM_002497	0.85
			hHC024976	ASF1B	NM_018154	0.82
			hHC014176	CENPE	NM_001813	0.86
			hHC003160	KIF15	NM_020242	0.85
			hHC003148	CEP55	NM_018131	0.89
			hHC008344	POLA1	NM_016937	0.80
			hHR016888	CBX2	NM_005189	0.83
			hHC021592	TK1	NM_003258	0.84
			hHC023416	KIF2C	NM_006845	0.81
			hHC008847	NUF2	NM_145697	0.91
			hHC009603	FAM83D	NM_030919	0.86
			hHC027267	STIL	NM_001048166	0.87
			hHR029571	C9orf140	NM_178448	0.82
			hHR017511	CKS2	NM_001827	0.89
			hHA035259	OIP5	NM_007280	0.84
			hHC004851	ITGB3BP	NM_014288	0.81
			hHC011295	NUSAP1	NM_016359	0.87
			hHR017427	SMO	NM_005631	0.81
			hHA038355	CDCA3	NM_031299	0.84
			hHC010551	MKI67	NM_002417	1.00
			hHC012087	RAD51	NM_002875	0.94
			hHR015831	EPR1	NM_001012271	0.92
			hHC026199	CDKN3	NM_005192	0.80
			hHC009506	POLE2	NM_002692	0.83
			hHC018470	PPIL5	NM_152329	0.83
			hHC020474	CDCA3	NM_031299	0.86
			hHC027578	CCNB2	NM_004701	0.88
			hHC031718	CDC20	NM_001255	0.83
			hHR003986	MCM10	NM_182751	0.88
			hHC016862	KIF18A	NM_031217	0.83
			hHC025682	MTA3	NM_020744	0.81
			hHR006230	FOXN4	NM_213596	0.88
			hHC010346	PIF1	NM_025049	0.81
			hHC023882	SPC24	AK075287	0.86
			hHC007597	HJURP	NM_018410	0.89
			hHR028333	PTTG3	NR_002734	0.87
			hHC016069	E2F2	NM_004091	0.87
			hHC004849	NCAPH	NM_015341	0.86
			hHC005725	BUB1	NM_004336	0.88
			hHR009085	ZNF788	AK128700	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC004117	PPIL5	NM_152329	0.81
			hHC016789	SEMA5B	NM_001031702	0.81
SCZ SNV	hHC016908	N4BP2L2	hHC016908	N4BP2L2	NM_014887	1.00
SCZ SNV	hHC008161	NCAN	hHC008161	NCAN	NM_004386	1.00
SCZ SNV	hHC028656	NFE2L3	hHR030156	NFE2L3	NM_004289	0.83
			hHC028656	NFE2L3	BC056142	1.00
SCZ SNV	hHC009957	NUP214	hHC009957	NUP214	BC105998	1.00
			hHC021306	AGAP3	NM_031946	0.81
SCZ SNV	hHC012766	NUP54	hHC012766	NUP54	NM_017426	1.00
SCZ SNV	hHC006993	ODZ1	hHC006993	ODZ1	NM_014253	1.00
SCZ SNV	hHC010986	PAG1	hHC010919	LTBP1	NM_206943	0.81
			hHC010986	PAG1	NM_018440	1.00
			hHC007804	CCDC147	NM_001008723	0.83
SCZ SNV	hHC014816	PLK3	hHC014816	PLK3	NM_004073	1.00
SCZ SNV	hHC031110	PSG1	hHC031110	PSG1	NM_006905	1.00
SCZ SNV	hHC024061	RAD54L2	hHC022553	SNAPC4	NM_003086	0.82
			hHC024061	RAD54L2	NM_015106	1.00
SCZ SNV	hHC006894	RFX3	hHA036647	MAP2	NM_002374	0.82
			hHC006894	RFX3	NM_134428	1.00
SCZ SNV	hHA034713	RGS12	hHA034713	RGS12	BC118594	1.00
SCZ SNV	hHR002221	RRP1B	hHR002221	RRP1B	NM_015056	1.00
SCZ SNV	hHC003807	SEC24B	hHC003807	SEC24B	NM_006323	1.00
SCZ SNV	hHC006606	SLC19A2	hHA033756	ZNF644	NM_201269	0.82
			hCT001199	RB1	NM_000321	0.80
			hCT001475	RB1	NM_000321	0.80
			hHC001918	KIAA0528	NM_014802	0.81
			hHA037592	FAM178A	NM_018121	0.81
			hHA038142	C9orf72	NM_018325	0.80
SCZ SNV	hHC001832	SLC38A2	hHC001832	SLC38A2	NM_018976	1.00
SCZ SNV	hHR002326	SMCHD1	hHR002326	SMCHD1	NM_015295	1.00
			hHC004846	ZCCHC11	NM_001009881	0.84
SCZ SNV	hHE041009	SPATA5	hHE041009	SPATA5	NM_145207	1.00
SCZ SNV	hHC012897	ST3GAL6	hHC011157	LOC202451	BC022980	0.81
			hHC012897	ST3GAL6	AK001922	1.00
			hHA034003	SORBS1	NM_001034954	0.81
			hHA035251	EPHA3	NM_005233	0.83
			hHR022370	RRM2B	NM_015713	0.84
SCZ SNV	hHA037017	STAG1	hCT001452	RB1	NM_000321	0.80
			hHA033036	DHX9	NM_001357	0.81
			hHC013212	SPAG9	NM_001130528	0.85
			hCT001175	RB1	NM_000321	0.80
			hHA034415	NKHD1-EIF4EBP	NM_020690	0.86
			hHA038075	KIAA1429	NM_015496	0.80
			hHC009525	PRKAA1	NM_206907	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHA033237	DHX9	NM_001357	0.85
			hHA037017	STAG1	NM_005862	1.00
			hHA035143	CNOT1	NM_016284	0.82
			hCT001205	OCRL	NM_000276	0.80
SCZ SNV	hHC006885	TBC1D14	hHC006885	TBC1D14	NM_020773	1.00
SCZ SNV	hHC004021	THBS1	hHC004021	THBS1	NM_003246	1.00
SCZ SNV	hHC030724	TLK2	hHC030724	TLK2	NM_006852	1.00
SCZ SNV	hHR003862	TRAK1	hHR003862	TRAK1	NM_014965	1.00
SCZ SNV	hHC001627	UBR5	hHR001980	USP38	NM_032557	0.82
			hHC001627	UBR5	CD511402	1.00
SCZ SNV	hHC005092	URB2	hHC005092	URB2	NM_014777	1.00
SCZ SNV	hHR006568	XPR1	hHR006568	XPR1	NM_004736	1.00
			hHA034190	DST	NM_020388	0.82
SCZ SNV	hHC011709	YLPM1	hHC011709	YLPM1	NM_019589	1.00
SCZ SNV	hHE042021	XPR1	hHE042021	XPR1	NM_004736	1.00
SCZ SNV	hHC019150	ZNF14	hHC019150	ZNF14	NM_021030	1.00
SCZ SNV	hHC016846	ZNF229	hHC016846	ZNF229	NM_014518	1.00
			hHR025990	ZNF780B	NM_001005851	0.85
SCZ SNV	hHC015238	ZNF530	hHC015238	ZNF530	NM_020880	1.00
ASD CNV	hHC025769	ARVCF	hHC025769	ARVCF	NM_001670	1.00
ASD CNV	hHC008219	ASPHD1	hHC008219	ASPHD1	AF070642	1.00
			hHC011324	MAPK4	NM_002747	0.84
			hHC028147	PTPN2	NM_080422	0.85
			hHC004854	ABHD7	NM_173567	0.83
			hHA034525	ASPHD1	AF070642	0.85
ASD CNV	hHC014098	BCL9	hHC014098	BCL9	NM_004326	1.00
ASD CNV	hHC013809	C16orf53	hHC013809	C16orf53	NM_024516	1.00
			hHC013455	RPGR	NM_000328	0.83
			hHC006601	EFS	NM_005864	0.82
ASD CNV	hHC017116	C20orf11	hHC017116	C20orf11	NM_017896	1.00
ASD CNV	hHC030237	CBWD1	hHC030237	CBWD1	NM_018491	1.00
ASD CNV	hHC004040	CDC45L	hHC003564	ZNF367	NM_153695	0.85
			hHC014412	TGIF1	NM_170695	0.81
			hHC021144	TPX2	NM_012112	0.83
			hHC025176	SLMO2	NM_016045	0.81
			hHC029136	PTTG1	NM_004219	0.85
			hHA034980	CDC2	NM_001130829	0.88
			hHC031104	CDC20	NM_001255	0.81
			hHA038688	NUSAP1	NM_016359	0.88
			hHC014123	CENPO	NM_024322	0.83
			hHC026699	RRM2	NM_001034	0.81
			hHC028811	UBE2C	NM_181802	0.91
			hHA038027	TYMS	NM_001071	0.90
			hHC007043	ARL6IP6	NM_152522	0.84

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC013295	FOXM1	NM_202002	0.89
			hHC020495	PRC1	NM_003981	0.87
			hHC023951	AURKA	NM_198433	0.90
			hHC004775	FAM54A	NM_001099286	0.83
			hHC007271	CENPK	NM_022145	0.84
			hHC014459	CCNA2	NM_001237	0.88
			hHC024347	CDC25C	NM_001790	0.87
			hHA037019	RAD51	NM_002875	0.87
			hHC002195	STON1	NM_006873	0.85
			hHR002122	CEP152	NM_014985	0.88
			hHC002314	FAM122C	NM_138819	0.83
			hHC004534	NCAPD3	NM_015261	0.85
			hHR014122	CENPO	NM_024322	0.82
			hHC029674	FAM64A	NM_019013	0.93
			hHC005794	KIAA0101	NM_014736	0.94
			hHC015970	CENPM	NM_024053	0.89
			hHR020686	MXD3	NM_031300	0.85
			hHA039586	TYMS	NM_001071	0.91
			hHC011686	C21orf58	NM_058180	0.81
			hHA038554	RGS3	NM_144488	0.80
			hHC002590	CENPF	NM_016343	0.86
			hHC004018	BRCA1	NM_007295	0.86
			hHC007762	CDCA5	NM_080668	0.86
			hHC016905	CDK2	NM_001798	0.84
			hHC021045	CDCA8	NM_018101	0.95
			hHC025653	MND1	NM_032117	0.87
			hHR012993	FZD2	NM_001466	0.85
			hHC024705	KNTC1	NM_014708	0.85
			hHR025293	RPSAP58	NR_003662	0.81
			hHC004389	WEE1	NM_003390	0.81
			hHC006489	TYMS	NM_001071	0.83
			hHR017349	MAD2L1	NM_002358	0.90
			hHR025605	CDC25A	NM_001789	0.86
			hHC007965	C21orf45	NM_018944	0.85
			hHC027729	DLGAP5	NM_014750	0.86
			hHR029265	(CDC20),	BE836833	0.92
			hHC002420	CDC14A	NM_003672	0.84
			hHR003572	RTKN2	NM_145307	0.92
			hHC004040	CDC45L	NM_003504	1.00
			hHC008264	H2AFX	NM_002105	0.82
			hHC008876	C15orf42	NM_152259	0.89
			hHC014252	POLA2	NM_002689	0.84
			hHC022400	SMO	NM_005631	0.85
			hHA034304	CDKN3	NM_005192	0.86

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC016868	CDCA7	NM_031942	0.87
			hHR026084	NCRNA00095	NR_024348	0.83
			hHC029252	IGF2BP3	NM_006547	0.82
			hHR002672	KIF11	NM_004523	0.90
			hHC009680	ZWINT	NM_032997	0.83
			hHC018812	MCM2	NM_004526	0.88
			hHC025244	MXD3	NM_031300	0.83
			hHC014803	RNASEH2A	NM_006397	0.84
			hHC014791	CDC2	NM_001130829	0.88
			hHC024295	MCM5	NM_006739	0.87
			hHC027187	CTDSP2	NM_005730	0.80
			hHC031507	UHRF1	NM_013282	0.86
			hHC003499	LIPG	NM_006033	0.82
			hHC004255	C5orf34	NM_198566	0.87
			hHC007903	KIF24	NM_194313	0.85
			hHC009163	C1orf112	NM_018186	0.92
			hHC009931	TCF19	NM_007109	0.84
			hHC021451	TROAP	NM_005480	0.86
			hHC022591	OIP5	NM_007280	0.92
			hHC009559	FAM111A	NM_001142520	0.84
			hHR017719	CCNB2	NM_004701	0.88
			hHC027319	TGIF2	NM_021809	0.84
			hHR030487	FAM60A	NM_001135811	0.85
			hHA035671	CHEK2	NM_001005735	0.85
			hHC003451	SFRP2	NM_003013	0.85
			hHA037339	ACAA2	NM_006111	0.81
			hHR013734	DTL	NM_016448	0.91
			hHR026706	SAP30	NM_003864	0.81
			hHC006558	DLEU2	CR625878	0.84
			hHC011850	EME1	NM_152463	0.90
			hHA034122	PPIL5	NM_152329	0.88
			hHC001986	IL33	NM_033439	0.86
			hHR004098	SMC4	NM_005496	0.88
			hHR001818	C11orf82	NM_145018	0.85
			hHC011418	TIMELESS	NM_003920	0.86
			hHC018606	C12orf48	NM_017915	0.87
			hHA039066	CDCA4	NM_017955	0.85
			hHR005105	RAD51AP1	NM_001130862	0.92
			hHC006929	MLF1IP	NM_024629	0.88
			hHC006917	TTK	NM_003318	0.91
			hHC020837	GINS2	NM_016095	0.87
			hHA033713	ARHGAP11A	NM_014783	0.87
			hHA035921	RAD51	NM_002875	0.90
			hHA036485	CDC25C	NM_001790	0.89

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC003593	C6orf167	NM_198468	0.93
			hHC027497	GINS4	NM_032336	0.88
			hHA033053	C14orf94	NM_017815	0.80
			hHC006593	SMC4	NM_005496	0.92
			hHC016577	CCNB1	NM_031966	0.84
			hHA033857	NUSAP1	NM_016359	0.93
			hHA035585	FST	NM_006350	0.82
			hHA036737	UBE2C	NM_181799	0.80
			hHC007277	STK33	NM_030906	0.82
			hHC014681	DTL	NM_016448	0.81
			hHC014704	CENPN	NM_001100624	0.89
			hHR017092	NEK2	NM_002497	0.91
			hHC001792	NUP37	NM_024057	0.83
			hHC014176	CENPE	NM_001813	0.90
			hHC003160	KIF15	NM_020242	0.85
			hHC003148	CEP55	NM_018131	0.88
			hHC021592	TK1	NM_003258	0.90
			hHA035416	ITGB3BP	NM_014288	0.85
			hHC001935	ORC6L	NM_014321	0.81
			hHC008847	NUF2	NM_145697	0.97
			hHC009603	FAM83D	NM_030919	0.90
			hHC022563	PIF1	NM_025049	0.81
			hHC027267	STIL	NM_001048166	0.90
			hHR017511	CKS2	NM_001827	0.93
			hHC021243	KRI1	NM_023008	0.82
			hHA035259	OIP5	NM_007280	0.89
			hHC003603	INTU	NM_015693	0.82
			hHC003795	MELK	NM_014791	0.90
			hHC004851	ITGB3BP	NM_014288	0.87
			hHC011295	NUSAP1	NM_016359	0.91
			hHR017427	SMO	NM_005631	0.80
			hHA038355	CDCA3	NM_031299	0.86
			hHC010551	MKI67	NM_002417	0.85
			hHC012087	RAD51	NM_002875	0.87
			hHR015831	EPR1	NM_001012271	0.92
			hHC026199	CDKN3	NM_005192	0.80
			hHC002402	BUB1B	NM_001211	0.86
			hHC003746	VRK1	NM_003384	0.81
			hHC006926	NSBP1	NM_030763	0.84
			hHC009506	POLE2	NM_002692	0.85
			hHC005690	DEPDC1	NM_001114120	0.83
			hHC018470	PPIL5	NM_152329	0.81
			hHC020474	CDCA3	NM_031299	0.89
			hHC027578	CCNB2	NM_004701	0.92

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC029222	CKS2	NM_001827	0.81
			hHC031718	CDC20	NM_001255	0.92
			hHR003986	MCM10	NM_182751	0.95
			hHC016862	KIF18A	NM_031217	0.92
			hHC019742	PLCE1	NM_016341	0.82
			hHC025682	MTA3	NM_020744	0.80
			hHC026750	BTG3	NM_001130914	0.82
			hHC029426	DBF4	NM_006716	0.89
			hHR006230	FOXN4	NM_213596	0.92
			hHC010346	PIF1	NM_025049	0.85
			hHC023882	SPC24	AK075287	0.85
			hHC007597	HJURP	NM_018410	0.94
			hHC020461	TK1	NM_003258	0.82
			hHR028333	PTTG3	NR_002734	0.90
			hHC005509	TRDMT1	NM_004412	0.82
			hHC016069	E2F2	NM_004091	0.89
			hHC019417	LOC91431	NM_001099776	0.85
			hHC004849	NCAPH	NM_015341	0.95
			hHC005725	BUB1	NM_004336	0.94
			hHC012913	CHST14	NM_130468	0.85
			hHC016789	SEMA5B	NM_001031702	0.80
ASD CNV	hHA040201	CHKB	hHA040201	CHKB	NM_005198	1.00
ASD CNV	hHR025141	CHRNA7	hHR025141	CHRNA7	NM_000746	1.00
ASD CNV	hHA036352	CLTCL1	hHA036352	CLTCL1	NM_007098	1.00
ASD CNV	hHA034492	CPT1B	hHA034492	CPT1B	NM_152247	1.00
ASD CNV	hHR005214	DGCR10	hHR005214	DGCR10	NR_026651	1.00
ASD CNV	hHC030047	DGCR5	hHC029747	PDXDC2	NR_003610	0.81
			hHC030047	DGCR5	X91348	1.00
			hHC022670	A2BP1	NM_018723	0.83
ASD CNV	hHC018376	DGCR8	hHC018376	DGCR8	NM_022720	1.00
ASD CNV	hHC005414	DIDO1	hHC003670	DBR1	NM_016216	0.81
			hHR001870	SHPRH	NM_001042683	0.80
			hHC005008	ARID4A	NM_002892	0.81
			hHC005414	DIDO1	NM_033081	1.00
ASD CNV	hHC021273	FAM57B	hHC021273	FAM57B	NM_031478	1.00
			hHR026756	TTLL12	NM_015140	0.85
			hHC021087	LRFN4	NM_024036	0.84
ASD CNV	hHC004841	FRMD4B	hHC004841	FRMD4B	NM_015123	1.00
ASD CNV	hHC005789	GTF2IRD1	hHC005789	GTF2IRD1	NM_016328	1.00
ASD CNV	hHC025127	HIRA	hHC025127	HIRA	NM_016328	1.00
ASD CNV	hHC019168	LZTR1	hHC019168	LZTR1	NM_006767	1.00
			hHC020896	RP3-402G11.5	NM_031454	0.81
ASD CNV	hHA035034	MBTPS1	hHR027288	BAT2D1	NM_015172	0.81
			hHA035034	MBTPS1	NM_003791	1.00

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
ASD CNV	hHC006923	MKRN3	hHC006923	MKRN3	NM_005664	1.00
ASD CNV	hHC010102	MTMR15	hHC010102	MTMR15	NM_014967	1.00
ASD CNV	hHC010565	MYO9A	hHC010565	MYO9A	NM_006901	1.00
ASD CNV	hHR030655	NBPF10	hHR030655	NBPF10	AF419616	1.00
ASD CNV	hHC014671	NEO1	hHC004738	ACTN2	NM_001103	0.83
			hHC011157	LOC202451	BC022980	0.85
			hHR009236	FAM172A	NM_032042	0.80
			hHC002156	CSGALNACT1	NM_001130518	0.80
			hHC007963	PIK3R1	NM_181523	0.80
			hHC014671	NEO1	NM_002499	1.00
			hHC003282	FAM81A	NM_152450	0.80
			hHR011106	GPR176	NM_007223	0.81
			hHC017058	LGALS8	NM_006499	0.82
			hHC002930	SERPINE2	NM_001136529	0.84
ASD CNV	hHA035283	NRXN1	hHC009943	CACNA2D1	NM_000722	0.81
			hHC014427	SLC35F5	NM_025181	0.82
			hHA035283	NRXN1	NM_001135659	1.00
			hHA034405	USP34	NM_014709	0.85
			hHC019261	ANKRD28	NM_015199	0.80
			hHC029833	GNAQ	NM_002072	0.80
ASD CNV	hHR005044	PAR5	hHC010704	ZMYM5	NM_001142684	0.80
			hHR011700	PEX26	AK000702	0.81
			hHC011135	TTBK2	NM_173500	0.80
			hHE040918	TNRC6B	NM_015088	0.82
			hHA036789	DST	NM_183380	0.80
			hHC017133	ANKRD50	NM_020337	0.84
			hHA032997	GRIA1	NM_000827	0.80
			hHE041033	BF347758	BF347758	0.80
			hHR004048	C14orf153	BC007412	0.84
			hHR005044	PAR5	NR_022008	1.00
			hHR006112	ZKSCAN1	NM_003439	0.85
			hHC030027	ANKRD36B	NM_025190	0.82
			hHR027157	ANKRD36B	NM_025190	0.83
			hHA035701	MACF1	NM_012090	0.83
ASD CNV	hHA036630	PARP6	hHC019891	ZNF346	NM_012279	0.80
			hHA036630	PARP6	NM_020214	1.00
ASD CNV	hHO047740	PAR-SN	hHR017972	PAR-SN	NR_022011	0.86
			hHO047740	PAR-SN	NR_022011	1.00
ASD CNV	hHA039366	PI4KA	hHA039366	PI4KA	NM_058004	1.00
ASD CNV	hHC019979	PPP4C	hHC018696	KDELR1	NM_006801	0.80
			hHA034332	MBNL1	NM_021038	0.80
			hHC019979	PPP4C	NM_002720	1.00
			hHC014351	TMED7	NM_181836	0.81
			hHA033755	HERPUD2	NM_022373	0.80

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHA036513	FYN	NM_002037	0.84
			hHC030932	NONO	NM_007363	0.85
			hCT000607	ACTB	NM_001101	0.85
			hHA033126	CASC4	NM_138423	0.83
			hHA034506	MACF1	NM_012090	0.83
			hHC013157	SEL1L	NM_005065	0.83
			hHR023273	TOMM20	NM_014765	0.82
			hHC017813	GDI1	NM_001493	0.83
ASD CNV	hHC007231	PRKAB2	hHC004824	TAPT1	NM_153365	0.81
			hHC005100	CDH10	NM_006727	0.88
			hHC001872	CNRIP1	NM_015463	0.80
			hHC006408	LPL	NM_000237	0.82
			hHC028284	ACSL4	NM_022977	0.80
			hHR006048	PCDHA1	NM_018900	0.83
			hHE040931	CB242912	CB242912	0.80
			hHR020135	CHD5	NM_015557	0.87
			hHR006047	PCDHA1	NM_018900	0.84
			hHR007103	FAM169A	NM_015566	0.85
			hHC012083	KIAA1377	NM_020802	0.85
			hHC008950	CCBE1	NM_133459	0.84
			hHR009994	KALRN	NM_003947	0.83
			hHA034678	MYLIP	NM_013262	0.86
			hHC008506	PTPRT	NM_133170	0.88
			hHR030586	PCDH11X	NM_032968	0.83
			hHR006046	PCDHA1	NM_018900	0.84
			hHC009694	FBXO27	NM_178820	0.86
			hHC017266	CUX2	NM_015267	0.84
			hHC006933	BAALC	NM_024812	0.81
			hHR009129	ZNF706	NM_001042510	0.82
			hHC003777	NAV3	NM_014903	0.86
			hHC009741	FGF9	NM_002010	0.82
			hHC005253	KCND2	NM_012281	0.86
			hHR004605	THRB	NM_001128177	0.88
			hHC004689	NECAB1	NM_022351	0.86
			hHR006045	PCDHA1	NM_018900	0.85
			hHC007220	ELOVL2	NM_017770	0.79
			hHC025160	C17orf58	NM_181656	0.82
			hHA035912	GRM7	BC136458	0.85
			hHC008960	NKAIN2	NM_001040214	0.83
			hHC010412	DB519783	DB519783	0.87
			hHR006055	PCDHA1	NM_018900	0.84
			hHC017683	SUOX	NM_000456	0.84
			hHC005695	AJAP1	NM_018836	0.81
			hHC007231	PRKAB2	NM_005399	1.00

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHE040843	CD678534	CD678534	0.84
			hHC006295	JAZF1	NM_175061	0.82
			hHC008995	RIMS1	BC036608	0.85
			hHC027511	FABP3	NM_004102	0.81
			hHC002299	AKAP7	NM_016377	0.80
			hHR006043	PCDHA1	NM_018900	0.85
			hHC002214	DPYD	NM_000110	0.82
			hHC004902	FAM19A2	NM_178539	0.84
			hHR006054	PCDHA1	NM_018900	0.81
			hHR006738	LOC283070	BC073155	0.85
			hHC005898	AFF2	NM_002025	0.81
			hHC013950	CHD5	NM_015557	0.81
			hHA033834	HDAC9	NM_014707	0.80
			hHR005850	BEAN	NM_001136106	0.83
			hHR006042	PCDHA1	NM_018900	0.82
			hHR008046	DERL1	AY358818	0.82
			hHC010734	MMP24	NM_006690	0.81
			hHR006053	PCDHA1	NM_018900	0.85
			hHA033893	KLHL4	NM_019117	0.88
			hHC001865	RBM24	NM_153020	0.82
			hHC002429	DNAJC6	NM_014787	0.84
			hHC004361	LRRC4C	NM_020929	0.90
			hHR028841	USP6	NM_004505	0.80
			hHR005537	LPHN3	NM_015236	0.82
			hHR008897	PLCH2	NM_014638	0.91
			hHE040949	EY892390	EY892390	0.87
			hHA033869	NEBL	NM_006393	0.86
			hHC008260	GRM7	NM_181874	0.86
			hHC007240	KLHL4	NM_019117	0.83
			hHC004792	PTCHD1	NM_173495	0.88
			hHR006051	PCDHA1	NM_018900	0.84
			hHC009615	L3MBTL3	NM_032438	0.81
			hHR002763	CACNA1C	NM_199460	0.81
			hHC001634	BACE1	NM_012104	0.80
			hHR006050	PCDHA1	NM_018900	0.84
			hHR011906	RIMBP2	NM_015347	0.83
			hHR002630	KIAA1107	NM_015237	0.80
			hHC003290	LOC153364	NM_203406	0.81
			hHC009926	SH3GL3	NM_003027	0.80
			hHC003698	FRMD4A	NM_018027	0.83
			hHR001898	KIAA1239	NM_001144990	0.84
			hHC003050	ALCAM	NM_001627	0.87
			hHC008234	LHX6	NM_014368	0.81
			hHC018506	WWC1	NM_015238	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC002797	CDH11	NM_001797	0.82
			hHR006049	PCDHA1	NM_018900	0.83
			hHE040993	SAMD5	NM_001030060	0.90
			hHC004537	LRRC8B	NM_015350	0.84
			hHC005689	SLC30A10	NM_018713	0.82
			hHC006757	MYLIP	NM_013262	0.82
			hHA035269	KLHL4	NM_019117	0.82
			hHE040789	SCN9A	NM_002977	0.87
ASD CNV	hHC021061	RFC2	hHC014803	RNASEH2A	NM_006397	0.84
			hHA037339	ACAA2	NM_006111	0.83
			hHR026706	SAP30	NM_003864	0.84
			hHA038450	RAD51	NM_002875	0.82
			hHC021061	RFC2	NM_181471	1.00
			hHA039049	SHMT2	NM_005412	0.82
			hHA040105	CDK4	NM_000075	0.82
ASD CNV	hHC022493	SERPIND1	hHC022493	SERPIND1	NM_000185	1.00
ASD CNV	hHR005194	SETD1B	hHR005194	SETD1B	NM_015048	1.00
ASD CNV	hHR018776	SHANK3	hHR018776	SHANK3	NM_001080420	1.00
ASD CNV	hHA037337	UBA3	hHA034151	TM7SF3	NM_016551	0.85
			hHA033395	CCT6A	NM_001762	0.83
			hHA033154	SAE1	NM_005500	0.82
			hHR026984	DNAJA1	L08069	0.81
			hHA039547	ATP6AP2	NM_005765	0.80
			hHA037337	UBA3	NM_003968	1.00
			hHA033231	TCP1	NM_030752	0.84
			hHR026558	BZW1	NM_014670	0.80
			hHA032990	ATP6AP2	NM_005765	0.80
			hHA036074	TTC33	NM_012382	0.82
ASD CNV	hHA033034	UBE3A	hHA037464	CREB1	NM_134442	0.85
			hCT001104	OCRL	NM_000276	0.83
			hCT001188	HMGCR	NM_000859	0.86
			hHA033936	CSE1L	NM_001316	0.82
			hHA034020	UBE2J1	NM_016021	0.83
			hHA035472	UBQLN1	NM_013438	0.82
			hHA039504	UBE3A	NM_130839	0.83
			hHC013212	SPAG9	NM_001130528	0.82
			hHA034344	CSE1L	NM_001316	0.84
			hHA034332	MBNL1	NM_021038	0.81
			hHC017280	UBXN7	NM_015562	0.84
			hHA035988	CNR1	NM_016083	0.85
			hCT001175	RB1	NM_000321	0.85
			hCT001163	HMGCR	NM_000859	0.92
			hCT001451	RB1	NM_000321	0.85
			hHC005015	SP4	NM_003112	0.84

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHR007991	PPP1R9A	NM_017650	0.82
			hHC009995	CCNH	AK094534	0.88
			hHC024011	LRRC49	NM_017691	0.81
			hHC026327	GMFB	NM_004124	0.85
			hHA035927	USP15	AF153604	0.85
			hHA036779	KIF1B	NM_015074	0.81
			hCT001187	HMGCR	NM_000859	0.90
			hCT001295	HMGCR	NM_000859	0.82
			hCT001475	RB1	NM_000321	0.80
			hHR003683	FNBP1L	AK000282	0.84
			hHR008195	LOC221710	NM_001135575	0.88
			hHC014351	TMED7	NM_181836	0.83
			hHA035279	PPP1CB	NM_002709	0.83
			hHA036431	RNF138	NM_016271	0.84
			hCT001211	HMGCR	NM_000859	0.91
			hCT001499	RB1	NM_000321	0.81
			hHA033083	GTF2H1	NM_001142307	0.87
			hHA037511	NEDD9	NM_001142393	0.82
			hHA034739	INPP5F	NM_014937	0.84
			hHA037811	DPYSL2	NM_001386	0.83
			hCT001174	RB1	NM_000321	0.80
			hCT001162	HMGCR	NM_000859	0.88
			hCT001270	HMGCR	NM_000859	0.87
			hHR017590	SNX12	NM_013346	0.80
			hHR018634	SRP72	NM_006947	0.85
			hHA033034	UBE3A	NM_130839	1.00
			hHA033322	GNAQ	NM_002072	0.81
			hHA037078	SETD3	NM_032233	0.80
			hHA038794	G3BP2	NM_203505	0.83
			hCT001198	RB1	NM_000321	0.83
			hCT001186	HMGCR	NM_000859	0.91
			hCT001294	HMGCR	NM_000859	0.93
			hHC020782	SNX12	NM_013346	0.81
			hCT001210	HMGCR	NM_000859	0.94
			hCT001318	HMGCR	NM_000859	0.92
			hHA035578	ZMYND11	NM_006624	0.83
			hCT001234	HMGCR	NM_000859	0.85
			hCT001342	HMGCR	NM_000859	0.80
			hCT001161	HMGCR	NM_000859	0.94
			hCT001269	HMGCR	NM_000859	0.95
			hHC004341	MAP2K6	U39657	0.85
			hHR027573	ENST00000332119	ENST00000332119	0.81
			hHA035253	USP14	NM_005151	0.83
			hHA035337	SPAG9	NM_001130528	0.85

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHA038613	WDR17	NM_170710	0.83
			hHA040713	UHRF2	NM_152896	0.81
			hCT001197	RB1	NM_000321	0.83
			hCT001293	HMGCR	NM_000859	0.88
			hCT001281	OCRL	NM_000276	0.83
			hCT001473	RB1	NM_000321	0.82
			hHA037869	USP46	NM_001134223	0.84
			hCT001317	HMGCR	NM_000859	0.84
			hHC016293	ZEB2	NM_014795	0.84
			hHA033381	NCOA4	NM_005437	0.87
			hHA035193	INPP5F	NM_014937	0.83
			hCT001245	RB1	M15400	0.81
			hCT001341	HMGCR	NM_000859	0.90
			hHA035601	ZMYM6	NM_007167	0.83
			hCT001268	HMGCR	NM_000859	0.94
			hCT001448	RB1	NM_000321	0.87
			hHR025556	API5	NR_024625	0.80
			hHA037652	SPAG9	AK024068	0.84
			hHE041108	CSNK1A1	CN267058	0.84
			hCT001196	RB1	NM_000321	0.84
			hHA037964	ATF2	NM_001880	0.84
			hCT001316	HMGCR	NM_000859	0.92
			hHC015992	CUL2	NM_003591	0.80
			hCT001340	HMGCR	NM_000859	0.88
			hCT001520	RB1	NM_000321	0.85
			hHC002588	NCOA2	NM_006540	0.81
			hCT001171	RB1	NM_000321	0.80
			hHC009223	WDR26	NM_025160	0.84
			hHA034567	HECTD2	NM_182765	0.85
			hHC005983	ATXN3	NM_004993	0.85
			hHA039691	SLC30A5	NM_022902	0.88
			hHC009943	CACNA2D1	NM_000722	0.83
			hHC010327	PHF6	NM_032458	0.88
			hHA034363	YME1L1	NM_139312	0.81
			hHC020934	CHUK	NM_001278	0.81
			hHA038142	C9orf72	NM_018325	0.84
			hHR007254	ZBTB26	NM_020924	0.82
			hHA033942	MBOAT2	NM_138799	0.83
			hHA035670	C9orf72	NM_018325	0.84
			hHA033870	SLC30A5	NM_022902	0.85
			hHA035514	SNX14	NM_153816	0.83
			hHR014321	CK818803	CK818803	0.85
			hHC025829	ZKSCAN1	NM_003439	0.82
			hHC021053	MAPK8	NM_139046	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC024053	CSNK1G3	NM_001044723	0.85
			hHC027940	ZNF770	NM_014106	0.83
			hHA035440	MBTPS1	NM_003791	0.82
			hHC014703	11-Sep	NM_018243	0.86
			hHA034347	OSBPL6	NM_032523	0.80
			hHA034443	MTMR2	NR_023356	0.84
			hCT001262	OCRL	NM_000276	0.81
			hHA036770	PPP2R5C	NM_002719	0.80
			hHA035654	WDR17	NM_170710	0.85
			hHA039302	C9orf72	NM_018325	0.84
			hCT001334	OCRL	NM_000276	0.81
			hHA033002	MATR3	NM_199189	0.85
			hCT001189	HMGCR	NM_000859	0.83
			hHC007333	BM312210	BM312210	0.81
			hHC008377	GOPC	NM_020399	0.83
			hHA036025	TCF12	NM_207037	0.82
			hHA037573	CSE1L	NM_001316	0.82
			hCT001213	HMGCR	NM_000859	0.83
			hHA035677	INPP5F	NM_014937	0.88
			hCT001237	HMGCR	NM_000859	0.80
			hCT001333	OCRL	NM_000276	0.84
ASD CNV	hHC021811	VPS37D	hHC020015	TESK1	NM_006285	0.80
			hHC020445	MKL1	NM_020831	0.80
			hHC021811	VPS37D	NM_001077621	1.00
ASD CNV	hHC014115	ZNF74	hHC014115	ZNF74	NM_003426	1.00
ASD DB	hHC017702	ST8SIA2	hHA033838	C1orf103	NM_018372	0.83
			hHC028514	ALG10B	NM_001013620	0.81
			hHC017702	ST8SIA2	NM_006011	1.00
			hHA038941	DDX17	NM_001098504	0.81
ASD DB	hHC022670	A2BP1	hHC001488	TP63	NM_003722	0.82
			hHC030047	DGCR5	X91348	0.83
			hHA036525	GGA2	AF323754	0.84
			hHC022670	A2BP1	NM_018723	1.00
ASD DB	hHA037442	ADNP	hHA037442	ADNP	NM_015339	1.00
ASD DB	hHC002880	AFF4	hHC010692	STX16	NM_001001433	0.80
			hHC002880	AFF4	NM_014423	1.00
			hHC012960	TMTC2	NM_152588	0.81
			hHC005015	SP4	NM_003112	0.83
			hHR008704	BG292040	BG292040	0.80
ASD DB	hHA034365	ANK3	hHA034403	NRXN1	NM_001135659	0.85
			hHA036742	NRXN1	NM_001135659	0.80
			hHC002037	APC	NM_001127511	0.84
			hHA035661	NRXN1	NM_001135659	0.87
			hHA034365	ANK3	NM_020987	1.00

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC014372	PCDHA1	NM_018900	0.81
			hHC009631	CDKL1	NM_004196	0.81
			hHC014371	PCDHA1	NM_018900	0.83
			hHA035369	NRXN1	NM_001135659	0.81
ASD DB	hHA034118	APC	hHC015725	JMJD2A	NM_014663	0.81
			hHA034118	APC	NM_001127511	1.00
			hHA035870	ANK3	NM_020987	0.82
			hHA035701	MACF1	NM_012090	0.80
ASD DB	hHC003332	AUTS2	hHR030827	HMGN1	NM_004965	0.80
			hHC003332	AUTS2	NM_015570	1.00
			hHC030775	RPS24	NM_001142285	0.83
			hHC005526	FDFT1	NM_004462	0.83
			hHC007037	VCAN	NM_004385	0.86
			hHR029537	BTF3	NM_001037637	0.82
			hHC029645	HNRPDL	NR_003249	0.81
			hHC029931	HMGN1	NM_004965	0.81
			hHR030086	HNRPA1L-2	NR_002944	0.80
			hHR009745	FOXG1	NM_005249	0.82
			hHC031741	EEF1B2	NM_001959	0.83
ASD DB	hHA033818	BCL2	hHC002540	BCL2	NM_000633	0.91
			hHA033818	BCL2	NM_000633	1.00
ASD DB	hHC005360	BRCA2	hHC005360	BRCA2	NM_000059	1.00
			hHR015258	ZNF90	CR593334	0.84
ASD DB	hHC005422	CACNA1H	hHC005422	CACNA1H	NM_021098	1.00
ASD DB	hHR011178	CADM1	hHR011178	CADM1	NM_014333	1.00
ASD DB	hHR025141	CHRNA7	hHR025141	CHRNA7	NM_000746	1.00
ASD DB	hHA036352	CLTCL1	hHA036352	CLTCL1	NM_007098	1.00
ASD DB	hHR004942	CNTN3	hHR004942	CNTN3	NM_020872	1.00
			hHC004915	KCNC2	NM_139136	0.87
			hHC007949	CNTN3	NM_020872	0.88
ASD DB	hHA040420	CNTN4	hHC004824	TAPT1	NM_153365	0.80
			hHC014076	FBXW7	NM_033632	0.84
			hHC013140	NLN	AB033052	0.82
			hHA040128	FGF12	NM_004113	0.84
			hHC018263	LOC150568	AK126958	0.86
			hHC008950	CCBE1	NM_133459	0.80
			hHE040906	PDE4D	NM_001104631	0.81
			hHC016930	ANO4	NM_178826	0.84
			hHC003081	TNFRSF21	NM_014452	0.85
			hHR004521	HS3ST5	NM_153612	0.87
			hHC003777	NAV3	NM_014903	0.80
			hHC008097	LDB2	NM_001130834	0.81
			hHC014625	IL7	NM_000880	0.81
			hHC015105	ARPP-21	NM_016300	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC020013	TAL2	BC126375	0.83
			hHC013509	RSPO3	NM_032784	0.83
			hHC027321	SRM	NM_003132	0.85
			hHC011889	HS3ST5	NM_153612	0.86
			hHC018609	STK32B	NM_018401	0.86
			hHC005000	KLHL14	NM_020805	0.86
			hHC010964	FAM134B	NM_001034850	0.81
			hHC007616	RNF150	NM_020724	0.82
			hHC008960	NKAIN2	NM_001040214	0.83
			hHC004100	UST	NM_005715	0.85
			hHA038780	FGF12	NM_004113	0.81
			hHC008455	CALN1	NM_001017440	0.84
			hHA035634	CNTN4	NM_175607	0.86
			hHC015330	RPRM	NM_019845	0.80
			hHR002609	LOC150568	NR_015399	0.81
			hHR028841	USP6	NM_004505	0.81
			hHA040420	CNTN4	NM_175607	1.00
			hHC011932	MDGA1	NM_153487	0.86
			hHR012315	AV727085	AV727085	0.81
			hHC003711	ADAMTSL3	NM_207517	0.88
			hHC019179	RSPO3	NM_032784	0.82
			hHC020919	UST	NM_005715	0.86
			hHR011906	RIMBP2	NM_015347	0.81
			hHC025730	NHSL1	NM_001144060	0.84
			hHC009926	SH3GL3	NM_003027	0.86
			hHC020666	SLN	NM_003063	0.82
			hHR001898	KIAA1239	NM_001144990	0.83
			hHC002666	ITPR1	NM_001099952	0.82
			hHC004537	LRRC8B	NM_015350	0.84
			hHA036049	FBXW7	NM_018315	0.84
ASD DB	hHR030569	CNTNAP3	hHR030569	CNTNAP3	NM_033655	1.00
ASD DB	hHC004724		hHC004724	CTTNBP2	NM_033427	1.00
			hHC009653	ST18	NM_014682	0.81
ASD DB	hHE041224	DAB1	hHE041224	DAB1	AB210012	1.00
ASD DB	hHC008562		hHC008562	DAPK1	NM_004938	1.00
			hHC007012	OLIG1	NM_138983	0.80
			hHR003231	NRXN3	NM_004796	0.85
			hHC010359	NRXN3	NM_004796	0.85
			hHC006218	RAPGEF4	NM_007023	0.82
ASD DB	hHR027462	DCTN5	hHR027462	DCTN5	NM_032486	1.00
ASD DB	hHC016253	DIAPH3	hHC016253	DIAPH3	NM_030932	1.00
ASD DB	hHC006676	DLX1	hHA034101	GAD1	NM_000817	0.81
			hHR012667	FLJ34048	AK095619	0.84
			hHC005550	GAD1	NM_000817	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC006280	DLX2	NM_004405	0.86
			hHC006676	DLX1	NM_178120	1.00
			hHC003820	SLAIN1	NM_001040153	0.83
			hHC009410	FLJ34048	AK055423	0.84
			hHC013969	FLJ34048	AK095619	0.84
ASD DB	hHC006280	DLX2	hHC006356	LOC285084	AL833646	0.85
			hHR012667	FLJ34048	AK095619	0.88
			hHC006280	DLX2	NM_004405	1.00
			hHC006676	DLX1	NM_178120	0.86
			hHC010359	NRXN3	NM_004796	0.83
			hHC009410	FLJ34048	AK055423	0.84
			hHA034226	GAD1	NM_000817	0.82
			hHC013969	FLJ34048	AK095619	0.91
ASD DB	hHC030864	EIF4E	hHC030864	EIF4E	NM_001130679	1.00
ASD DB	hHR029057	EIF4EBP2	hHR029057	EIF4EBP2	NM_004096	1.00
ASD DB	hHC012239	EP300	hHC012239	EP300	NM_001429	1.00
ASD DB	hHR012430	EP400	hHA036816	(KIAA0174),	DA947565	0.82
			hHA038436	DIP2A	NM_015151	0.81
			hHC015828	GTF3C2	NM_001521	0.86
			hCT001175	RB1	NM_000321	0.81
			hHC022487	TBL2	NM_012453	0.82
			hHA035555	SEC24B	NM_006323	0.89
			hHR012430	EP400	NM_015409	1.00
			hHA039105	PBRM1	NM_018313	0.80
			hHA037592	FAM178A	NM_018121	0.82
			hHC015187	PATZ1	NM_014323	0.82
			hHC024247	PRRC1	NM_130809	0.84
			hHC025829	ZKSCAN1	NM_003439	0.84
ASD DB	hHC020957	EPHB2	hHC020957	EPHB2	NM_004442	1.00
ASD DB	hHC017900		hHC017900	FEZF2	NM_018008	1.00
			hHR008287	C14orf23	NR_026731	0.83
			hHC009653	ST18	NM_014682	0.82
ASD DB	hHC030717	GPD2	hHC030717	GPD2	NM_001083112	1.00
ASD DB	hHC019020	GRIK2	hHC019020	GRIK2	NM_175768	1.00
			hCT001188	HMGCR	NM_000859	0.80
			hHA038748	MACF1	NM_012090	0.82
			hCT001271	HMGCR	NM_000859	0.84
			hHA038079	MACF1	NM_012090	0.82
			hCT001189	HMGCR	NM_000859	0.80
ASD DB	hHR016670	GRIP1	hHR017492	ZEB2	NM_014795	0.80
			hHC024017	SETMAR	NR_024022	0.82
			hHA037157	MAP4K4	BC064691	0.82
			hHR016670	GRIP1	NM_021150	1.00
			hHC027553	ZNF486	NM_052852	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
ASD DB	hHR024272	GSK3B	hHR024272	GSK3B	NM_002093	1.00
ASD DB	hHC011966	GUCY1A2	hHC011966	GUCY1A2	NM_000855	1.00
ASD DB	hHC005088	HDAC4	hHC005088	HDAC4	NM_006037	1.00
ASD DB	hHR030827	HMGN1	hHR030827	HMGN1	NM_004965	1.00
			hHC009743	FOXG1	NM_005249	0.81
			hHC003332	AUTS2	NM_015570	0.80
			hHC030775	RPS24	NM_001142285	0.81
			hHC029645	HNRPDL	NR_003249	0.82
			hHC029931	HMGN1	NM_004965	0.82
			hHR030086	HNRPA1L-2	NR_002944	0.86
ASD DB	hHR004521	HS3ST5	hHA040128	FGF12	NM_004113	0.81
			hHC013931	FGF12	NM_021032	0.86
			hHC008950	CCBE1	NM_133459	0.82
			hHC016930	ANO4	NM_178826	0.84
			hHC003081	TNFRSF21	NM_014452	0.84
			hHR004521	HS3ST5	NM_153612	1.00
			hHC003777	NAV3	NM_014903	0.82
			hHC008097	LDB2	NM_001130834	0.82
			hHC020013	TAL2	BC126375	0.88
			hHC027321	SRM	NM_003132	0.85
			hHC011889	HS3ST5	NM_153612	0.94
			hHC005000	KLHL14	NM_020805	0.87
			hHA035912	GRM7	BC136458	0.81
			hHC004100	UST	NM_005715	0.83
			hHA038780	FGF12	NM_004113	0.82
			hHC008455	CALN1	NM_001017440	0.85
			hHC011395	FZD4	NM_012193	0.82
			hHR010109	TBC1D30	AB023201	0.81
			hHR028841	USP6	NM_004505	0.86
			hHA040420	CNTN4	NM_175607	0.87
			hHC011932	MDGA1	NM_153487	0.82
			hHR012315	AV727085	AV727085	0.81
			hHC020919	UST	NM_005715	0.88
			hHC020666	SLN	NM_003063	0.81
ASD DB	hHA035416	ITGB3BP	hHC029136	PTTG1	NM_004219	0.83
			hHC022115	TP53I13	NM_138349	0.83
			hHC023951	AURKA	NM_198433	0.83
			hHC014459	CCNA2	NM_001237	0.81
			hHA033311	ITGB1	NM_002211	0.82
			hHC011818	RAB32	NM_006834	0.85
			hHC005794	KIAA0101	NM_014736	0.86
			hHC015970	CENPM	NM_024053	0.84
			hHC004018	BRCA1	NM_007295	0.84
			hHC007762	CDCA5	NM_080668	0.85

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC010473	AP3M1	NM_207012	0.81
			hHR012993	FZD2	NM_001466	0.82
			hHC004389	WEE1	NM_003390	0.81
			hHC006489	TYMS	NM_001071	0.83
			hHR017349	MAD2L1	NM_002358	0.88
			hHR025605	CDC25A	NM_001789	0.84
			hHR028665	CR625830	CR625830	0.84
			hHC030981	GMPS	NM_003875	0.83
			hHC007965	C21orf45	NM_018944	0.84
			hHR003572	RTKN2	NM_145307	0.82
			hHC004040	CDC45L	NM_003504	0.85
			hHC008264	H2AFX	NM_002105	0.84
			hHC007628	RFX2	NM_000635	0.84
			hHC009920	RFC4	NM_181573	0.83
			hHA034304	CDKN3	NM_005192	0.80
			hHR002672	KIF11	NM_004523	0.86
			hHC004255	C5orf34	NM_198566	0.89
			hHC004459	CLGN	NM_001130675	0.83
			hHC009163	C1orf112	NM_018186	0.90
			hHC009931	TCF19	NM_007109	0.86
			hHC020863	PXMP2	NM_018663	0.81
			hHE041995	C6orf173	NM_001012507	0.81
			hHC009559	FAM111A	NM_001142520	0.85
			hHC003451	SFRP2	NM_003013	0.81
			hHA038287	EEF1B2	NM_001959	0.82
			hHC001986	IL33	NM_033439	0.84
			hHR004098	SMC4	NM_005496	0.82
			hHC006690	GPC4	NM_001448	0.83
			hHR023394	FAM96A	NM_032231	0.80
			hHA039906	PCNA	NM_182649	0.83
			hHC003354	ATAD2	NM_014109	0.83
			hHC004014	BMP7	NM_001719	0.83
			hHR005105	RAD51AP1	NM_001130862	0.85
			hHA033701	SLC30A5	NM_024055	0.80
			hHC003593	C6orf167	NM_198468	0.86
			hHC027497	GINS4	NM_032336	0.82
			hHC006593	SMC4	NM_005496	0.86
			hHC016577	CCNB1	NM_031966	0.87
			hHA033857	NUSAP1	NM_016359	0.84
			hHC007277	STK33	NM_030906	0.84
			hHC013913	EPHB4	NM_004444	0.86
			hHR017092	NEK2	NM_002497	0.85
			hHA034312	PRDM2	NM_015866	0.83
			hHC001792	NUP37	NM_024057	0.82

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHR006016	ENST0000036848	ENST00000368484	0.84
			hHC006208	SPAG5	NM_006461	0.86
			hHC008212	DNMBP	NM_015221	0.84
			hHC014176	CENPE	NM_001813	0.90
			hHC011224	ZNRD1	NM_170783	0.81
			hHC021592	TK1	NM_003258	0.85
			hHC008847	NUF2	NM_145697	0.83
			hHC009603	FAM83D	NM_030919	0.86
			hHC027267	STIL	NM_001048166	0.86
			hHR017511	CKS2	NM_001827	0.86
			hHC027387	TULP3	NM_003324	0.85
			hHC002547	TPR	NM_003292	0.83
			hHC004851	ITGB3BP	NM_014288	0.94
			hHR010899	LOC388588	NR_024432	0.84
			hHC011295	NUSAP1	NM_016359	0.84
			hHC028467	10-Sep	NM_144710	0.82
			hHC012087	RAD51	NM_002875	0.82
			hHR015831	EPR1	NM_001012271	0.81
			hHC026199	CDKN3	NM_005192	0.81
			hHC002402	BUB1B	NM_001211	0.82
			hHC006926	NSBP1	NM_030763	0.85
			hHR011618	C6orf173	NM_001012507	0.82
			hHC020474	CDCA3	NM_031299	0.81
			hHC027578	CCNB2	NM_004701	0.82
			hHC029222	CKS2	NM_001827	0.86
			hHR003986	MCM10	NM_182751	0.87
			hHC013502	SLC7A6OS	AK091674	0.80
			hHC016862	KIF18A	NM_031217	0.84
			hHC019742	PLCE1	NM_016341	0.81
			hHC025682	MTA3	NM_020744	0.84
			hHC026750	BTG3	NM_001130914	0.81
			hHC029426	DBF4	NM_006716	0.86
			hHA038450	RAD51	NM_002875	0.80
			hHC004849	NCAPH	NM_015341	0.89
			hHC012913	CHST14	NM_130468	0.88
			hHC015229	HMGB2	NM_002129	0.83
			hHR017137	RIT1	NM_006912	0.82
			hHC027997	PTTG3	NR_002734	0.80
			hHC030397	SAP30	NM_003864	0.87
			hHC002281	NR2E1	NM_003269	0.86
			hHC007189	NCK1	NM_006153	0.82
ASD DB	hHC009434	JARID2	hHC013206	JRK	NM_003724	0.81
			hHC009434	JARID2	NM_004973	1.00
ASD DB	hHC023549	JMJD1C	hHA036996	KCNH2	NM_172056	0.82

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC023549	JMJD1C	NM_032776	1.00
			hHR002918	JMJD1C	AA358573	0.88
ASD DB	hHC008977	KHDRBS2	hHC005416	SLC25A12	NM_003705	0.81
			hHC005437	AKAP6	NM_004274	0.84
			hHC008977	KHDRBS2	NM_152688	1.00
ASD DB	hHC008010	KIAA1586	hHC008010	KIAA1586	NM_020931	1.00
ASD DB	hHC007864	LAMA1	hHR006282	S1PR3	NM_005226	0.83
			hHC007864	LAMA1	NM_005559	1.00
			hHC012913	CHST14	NM_130468	0.87
ASD DB	hHA037417	LRRC1	hHA034320	LRRC1	NM_018214	0.81
			hHC005448	AASS	NM_005763	0.84
			hHC010822	THSD7A	NM_015204	0.84
			hHR010821	THSD7A	NM_015204	0.82
			hHE042017	AK129971	AK129971	0.81
			hHA036365	DACH1	NM_080759	0.83
			hHC018854	PHIP	NM_017934	0.82
			hHC026725	RBPJ	NM_203284	0.85
			hHA035989	LRRC1	NM_018214	0.83
			hHA037417	LRRC1	NM_018214	1.00
ASD DB	hHC003436	LRRC7	hHC011244	KIF5C	NM_004522	0.81
			hHC013114	PIK3CA	NM_006218	0.80
			hHC011157	LOC202451	BC022980	0.82
			hHA034003	SORBS1	NM_001034954	0.80
			hHC002058	PTPRK	NM_001135648	0.81
			hHC003436	LRRC7	NM_020794	1.00
ASD DB	hHR007786	MACROD2	hHC011904	GRIP1	NM_021150	0.80
			hHR007786	MACROD2	BC128036	1.00
			hHC017203	ACVR2A	NM_001616	0.81
ASD DB	hHC022926	MAP2	hHC022926	MAP2	NM_002374	1.00
			hHA033006	DHX9	NM_001357	0.85
			hHA036558	BAZ2B	NM_013450	0.83
ASD DB	hHA035377	MAPK1	hHA035377	MAPK1	NM_138957	1.00
ASD DB	hHC007557	MARK1	hHC006083	RRAGD	NM_021244	0.82
			hHC001978	FAM172A	NM_032042	0.81
			hHC006586	RHOBTB1	NR_024556	0.80
			hHC007557	MARK1	NM_018650	1.00
			hHR009236	FAM172A	NM_032042	0.82
			hHC002058	PTPRK	NM_001135648	0.82
ASD DB	hHC004339	MBD5	hHC004339	MBD5	NM_018328	1.00
			hHR027830	TAF9	NM_001015892	0.80
ASD DB	hHC020288	MBD6	hHC030274	GNG5	NM_005274	0.82
			hHC020288	MBD6	NM_052897	1.00
			hHC022400	SMO	NM_005631	0.80
			hHC015005	ASAP3	NM_017707	0.84

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
ASD DB	hHC015904	MTHFR	hHC015904	MTHFR	NM_005957	1.00
ASD DB	hHC007040	MTR	hHC007040	MTR	NM_000254	1.00
			hHC011332	ASPHD2	NM_020437	0.81
			hHR004141	MTR	NM_000254	0.80
ASD DB	hHC002233		hHR009129	ZNF706	NM_001042510	0.81
			hHC002156	CSGALNACT1	NM_001130518	0.83
			hHC004525	DAAM1	NM_014992	0.83
			hHC008737	GNG2	NM_053064	0.85
			hHC002233	NBEA	NM_015678	1.00
			hHR026185	SNX7	NM_015976	0.84
			hHC027817	SNX7	NM_015976	0.85
ASD DB	hHC001484	NFIA	hHC016978	ASTN2	NM_198187	0.86
			hHC001484	NFIA	NM_001134673	1.00
ASD DB	hHA035333	NRCAM	hHA035333	NRCAM	NM_001037132	1.00
ASD DB	hHC009632	NRP2	hHC009632	NRP2	NM_001037132	1.00
ASD DB	hHC011290	OTX1	hHC011290	OTX1	NM_014562	1.00
			hHC019448	PARD3B	NM_152526	0.81
			hHA035860	LMO7	NM_015842	0.81
ASD DB	hHC020214	PLAUR	hHC027319	TGIF2	NM_021809	0.81
			hHC020214	PLAUR	NM_002659	1.00
ASD DB	hHA034135	POGZ	hHA034135	POGZ	NM_145796	1.00
ASD DB	hHA036085	PSD3	hHA036647	MAP2	NM_002374	0.82
			hHA037707	ANK3	NM_020987	0.81
			hHA036085	PSD3	NM_015310	1.00
ASD DB	hHR010614	PTEN	hHR010614	PTEN	NM_000314	1.00
ASD DB	hHC011816	RAI1	hHC011816	RAI1	NM_030665	1.00
ASD DB	hHC002741	ROBO1	hHC002741	ROBO1	NM_13363	1.00
ASD DB	hHA033097	RORA	hHA033097	RORA	NM_134260	1.00
ASD DB	hHC017824	SETD2	hHC017824	SETD2	NM_014159	1.00
ASD DB	hHC006984	SETDB1	hHC006984	SETDB1	BC028671	1.00
ASD DB	hHA034077	SHANK2	hHA034077	SHANK2	NM_012309	1.00
ASD DB	hHR018776	SHANK3	hHR018776	SHANK3	NM_001080420	1.00
ASD DB	hHC003620	SLC25A24	hHC006021	CCDC99	NM_017785	0.83
			hHC011961	MRPL42	NM_014050	0.83
			hHC003620	SLC25A24	NM_013386	1.00
ASD DB	hHA033870	SLC30A5	hHA037464	CREB1	NM_134442	0.81
			hHC010692	STX16	NM_001001433	0.88
			hHR025872	ZNF12	NM_016265	0.86
			hHA033252	G3BP1	NM_005754	0.81
			hHA038436	DIP2A	NM_015151	0.80
			hHA039504	UBE3A	NM_130839	0.85
			hHA033372	ZNF532	NM_018181	0.82
			hHA034332	MBNL1	NM_021038	0.86
			hCT001175	RB1	NM_000321	0.84

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hCT001163	HMGCR	NM_000859	0.83
			hCT001451	RB1	NM_000321	0.83
			hHC005015	SP4	NM_003112	0.83
			hHC026327	GMFB	NM_004124	0.81
			hCT001187	HMGCR	NM_000859	0.81
			hCT001295	HMGCR	NM_000859	0.81
			hHA034991	HNRNPC	AK126950	0.80
			hHA035279	PPP1CB	NM_002709	0.86
			hHA036431	RNF138	NM_016271	0.80
			hHA040739	RNF138	NM_016271	0.86
			hCT001211	HMGCR	NM_000859	0.85
			hCT001499	RB1	NM_000321	0.83
			hHA033083	GTF2H1	NM_001142307	0.85
			hCT001162	HMGCR	NM_000859	0.85
			hHA033034	UBE3A	NM_130839	0.85
			hCT001186	HMGCR	NM_000859	0.85
			hCT001294	HMGCR	NM_000859	0.84
			hHC007714	CGGBP1	NM_001008390	0.80
			hHC018478	MAPK14	NM_139012	0.79
			hCT001210	HMGCR	NM_000859	0.89
			hCT001318	HMGCR	NM_000859	0.84
			hHC022246	CXorf15	NM_018360	0.81
			hHA035482	ATE1	NM_007041	0.80
			hCT001161	HMGCR	NM_000859	0.84
			hCT001269	HMGCR	NM_000859	0.86
			hHA035253	USP14	NM_005151	0.80
			hCT001293	HMGCR	NM_000859	0.85
			hCT001473	RB1	NM_000321	0.81
			hHA037869	USP46	NM_001134223	0.82
			hHA033273	LYPLA1	NM_006330	0.80
			hHA038265	RBM12	NM_006047	0.89
			hHA039993	NKHD1-EIF4EBP	NM_020690	0.82
			hCT001341	HMGCR	NM_000859	0.85
			hHA035601	ZMYM6	NM_007167	0.80
			hHA036561	UBQLN1	NM_013438	0.80
			hCT001268	HMGCR	NM_000859	0.85
			hCT001448	RB1	NM_000321	0.80
			hHA037652	SPAG9	AK024068	0.81
			hCT001196	RB1	NM_000321	0.83
			hHA037964	ATF2	NM_001880	0.82
			hCT001316	HMGCR	NM_000859	0.90
			hCT001496	RB1	NM_000321	0.84
			hHA037508	CSDE1	NM_001130523	0.84
			hHA037592	FAM178A	NM_018121	0.83

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hCT001520	RB1	NM_000321	0.84
			hHA034567	HECTD2	NM_182765	0.85
			hHA038215	ABI2	NM_005759	0.83
			hHC005983	ATXN3	NM_004993	0.87
			hHA035851	FAM126B	NM_173822	0.81
			hHA035947	SPTLC1	NM_006415	0.85
			hHA039691	SLC30A5	NM_022902	0.86
			hHC007255	ZBTB26	NM_020924	0.86
			hHC010327	PHF6	NM_032458	0.83
			hHA036547	TRO	NM_001039705	0.82
			hHA038142	C9orf72	NM_018325	0.81
			hHR007254	ZBTB26	NM_020924	0.85
			hHC011478	NANP	AK055472	0.80
			hHA036834	SLC9A6	NM_001042537	0.84
			hHA034842	ZMYM6	NM_007167	0.83
			hHR014321	CK818803	CK818803	0.83
			hHC025829	ZKSCAN1	NM_003439	0.90
			hHA035177	CCNT2	NM_058241	0.89
			hHC010037	PB41L4A),(C5orf2	BI086626	0.81
			hHC024053	CSNK1G3	NM_001044723	0.87
			hHA034241	PTPN12	NM_002835	0.81
			hHA035297	HECTD2	NM_182765	0.89
			hHA038453	ANKS1B	NM_152788	0.82
			hCT001156	OCRL	NM_000276	0.80
			hHA038656	PHC2	NM_198040	0.82
			hCT000856	LRP1	NM_002332	0.80
			hHC020643	TRIT1	NM_017646	0.80
			hCT001287	OCRL	AK226116	0.83
			hHA040743	SLC30A5	NM_022902	0.80
			hCT001262	OCRL	NM_000276	0.81
			hHA036770	PPP2R5C	NM_002719	0.83
			hCT001286	OCRL	NM_001587	0.80
			hHA039302	C9orf72	NM_018325	0.83
			hHC008377	GOPC	NM_020399	0.84
			hHC014521	ZNF664	NM_152437	0.81
			hHA037573	CSE1L	NM_001316	0.84
			hHC017161	ZNF226	NM_001032372	0.82
ASD DB	hHA035450	SOX5	hHR003716	MIB1	NM_020774	0.80
			hHA037290	SYNE2	NM_182914	0.84
			hHA036869	SYNE2	NM_182914	0.83
			hHA034421	SYNE2	NM_182914	0.81
			hHA034061	SYNE2	NM_182914	0.84
			hHA035103	SYNE2	NM_182914	0.85
			hHA035450	SOX5	NM_006940	1.00

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
ASD DB	hHC008055	ST7	hHA036774	ST7	NM_018412	0.80
			hHC006702	DB549992	DB549992	0.87
			hHC003245	AKAP9	NM_005751	0.80
			hHC008055	ST7	NM_018412	1.00
			hHC001717	ELOVL5	NM_021814	0.86
ASD DB	hHA033920	SUV420H1	hHA033036	DHX9	NM_001357	0.81
			hCT001284	OCRL	NM_000276	0.87
			hHC007559	MFAP3	NR_024152	0.80
			hHC004341	MAP2K6	U39657	0.81
			hHA033237	DHX9	NM_001357	0.81
			hHC008805	BMI1	NM_005180	0.81
			hCT001196	RB1	NM_000321	0.81
			hHA033920	SUV420H1	NM_017635	1.00
			hHA037592	FAM178A	NM_018121	0.83
			hHC009223	WDR26	NM_025160	0.83
			hHC016805	SMEK2	NM_001122964	0.82
			hHC024053	CSNK1G3	NM_001044723	0.83
			hHA038079	MACF1	NM_012090	0.81
			hHA037273	RBM26	BC111739	0.80
ASD DB	hHC014149	TAF1C	hHC014149	TAF1C	NM_005679	1.00
ASD DB	hHC005106	TBR1	hHC005106	TBR1	NM_006593	1.00
ASD DB	hHC030724	TLK2	hHC030724	TLK2	NM_006852	1.00
ASD DB	hHA040599	TSN	hHA040599	TSN	NM_004622	1.00
ASD DB	hHC003689	UBA6	hHC003689	UBA6	NM_018227	1.00
ASD DB	hHC029382	UBE2H	hHA032974	SCAMP1	NM_004866	0.85
			hCT001185	HMGCR	NM_000859	0.80
			hHA040005	CSDE1	NM_001007553	0.84
			hHC010196	MARK3	NM_001128918	0.81
			hHA035144	MBTPS1	NM_003791	0.82
			hHR026924	CSNK1A1	NM_001025105	0.79
			hHA033080	DHX9	NM_001357	0.83
			hHA034279	XRN2	NM_012255	0.84
			hHA033067	DHX9	NM_001357	0.81
			hHC006930	TTLL7	NM_024686	0.83
			hHC016038	ZBTB8	NM_001040441	0.80
			hHC029382	UBE2H	NM_003344	1.00
			hHA035849	NRXN1	NM_001135659	0.80
			hHC009268	SCAMP1	NM_004866	0.82
			hHA033723	ZNF644	NM_201269	0.83
			hHR027385	HSP90B1	NM_003299	0.82
			hHA035557	ANKRD17	NM_032217	0.81
ASD DB	hHA033034	UBE3A	hHA037464	CREB1	NM_134442	0.85
			hCT001104	OCRL	NM_000276	0.83
			hCT001188	HMGCR	NM_000859	0.86

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHA033936	CSE1L	NM_001316	0.82
			hHA034020	UBE2J1	NM_016021	0.83
			hHA035472	UBQLN1	NM_013438	0.82
			hHA039504	UBE3A	NM_130839	0.83
			hHC013212	SPAG9	NM_001130528	0.82
			hHA034344	CSE1L	NM_001316	0.84
			hHA034332	MBNL1	NM_021038	0.81
			hHC017280	UBXN7	NM_015562	0.84
			hHA035988	CNR1	NM_016083	0.85
			hCT001175	RB1	NM_000321	0.85
			hCT001163	HMGCR	NM_000859	0.92
			hCT001451	RB1	NM_000321	0.85
			hHC005015	SP4	NM_003112	0.84
			hHR007991	PPP1R9A	NM_017650	0.82
			hHC009995	CCNH	AK094534	0.88
			hHC024011	LRRC49	NM_017691	0.81
			hHC026327	GMFB	NM_004124	0.85
			hHA035927	USP15	AF153604	0.85
			hHA036779	KIF1B	NM_015074	0.81
			hCT001187	HMGCR	NM_000859	0.90
			hCT001295	HMGCR	NM_000859	0.82
			hCT001475	RB1	NM_000321	0.80
			hHR003683	FNBP1L	AK000282	0.84
			hHR008195	LOC221710	NM_001135575	0.88
			hHC014351	TMED7	NM_181836	0.83
			hHA035279	PPP1CB	NM_002709	0.83
			hHA036431	RNF138	NM_016271	0.84
			hCT001211	HMGCR	NM_000859	0.91
			hCT001499	RB1	NM_000321	0.81
			hHA033083	GTF2H1	NM_001142307	0.87
			hHA037511	NEDD9	NM_001142393	0.82
			hHA034739	INPP5F	NM_014937	0.84
			hHA037811	DPYSL2	NM_001386	0.83
			hCT001174	RB1	NM_000321	0.80
			hCT001162	HMGCR	NM_000859	0.88
			hCT001270	HMGCR	NM_000859	0.87
			hHR017590	SNX12	NM_013346	0.80
			hHR018634	SRP72	NM_006947	0.85
			hHA033034	UBE3A	NM_130839	1.00
			hHA033322	GNAQ	NM_002072	0.81
			hHA037078	SETD3	NM_032233	0.80
			hHA038794	G3BP2	NM_203505	0.83
			hCT001198	RB1	NM_000321	0.83
			hCT001186	HMGCR	NM_000859	0.91

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hCT001294	HMGCR	NM_000859	0.93
			hHC020782	SNX12	NM_013346	0.81
			hCT001210	HMGCR	NM_000859	0.94
			hCT001318	HMGCR	NM_000859	0.92
			hHA035578	ZMYND11	NM_006624	0.83
			hCT001234	HMGCR	NM_000859	0.85
			hCT001342	HMGCR	NM_000859	0.80
			hCT001161	HMGCR	NM_000859	0.94
			hCT001269	HMGCR	NM_000859	0.95
			hHC004341	MAP2K6	U39657	0.85
			hHR027573	ENST00000332111	ENST00000332119	0.81
			hHA035253	USP14	NM_005151	0.83
			hHA035337	SPAG9	NM_001130528	0.85
			hHA038613	WDR17	NM_170710	0.83
			hHA040713	UHRF2	NM_152896	0.81
			hCT001197	RB1	NM_000321	0.83
			hCT001293	HMGCR	NM_000859	0.88
			hCT001281	OCRL	NM_000276	0.83
			hCT001473	RB1	NM_000321	0.82
			hHA037869	USP46	NM_001134223	0.84
			hCT001317	HMGCR	NM_000859	0.84
			hHC016293	ZEB2	NM_014795	0.84
			hHA033381	NCOA4	NM_005437	0.87
			hHA035193	INPP5F	NM_014937	0.83
			hCT001245	RB1	M15400	0.81
			hCT001341	HMGCR	NM_000859	0.90
			hHA035601	ZMYM6	NM_007167	0.83
			hCT001268	HMGCR	NM_000859	0.94
			hCT001448	RB1	NM_000321	0.87
			hHR025556	API5	NR_024625	0.80
			hHA037652	SPAG9	AK024068	0.84
			hHE041108	(CSNK1A1),	CN267058	0.84
			hCT001196	RB1	NM_000321	0.84
			hHA037964	ATF2	NM_001880	0.84
			hCT001316	HMGCR	NM_000859	0.92
			hHC015992	CUL2	NM_003591	0.80
			hCT001340	HMGCR	NM_000859	0.88
			hCT001520	RB1	NM_000321	0.85
			hHC002588	NCOA2	NM_006540	0.81
			hCT001171	RB1	NM_000321	0.80
			hHC009223	WDR26	NM_025160	0.84
			hHA034567	HECTD2	NM_182765	0.85
			hHC005983	ATXN3	NM_004993	0.85
			hHA039691	SLC30A5	NM_022902	0.88

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC009943	CACNA2D1	NM_000722	0.83
			hHC010327	PHF6	NM_032458	0.88
			hHA034363	YME1L1	NM_139312	0.81
			hHC020934	CHUK	NM_001278	0.81
			hHA038142	C9orf72	NM_018325	0.84
			hHR007254	ZBTB26	NM_020924	0.82
			hHA033942	MBOAT2	NM_138799	0.83
			hHA035670	C9orf72	NM_018325	0.84
			hHA033870	SLC30A5	NM_022902	0.85
			hHA035514	SNX14	NM_153816	0.83
			hHR014321	CK818803	CK818803	0.85
			hHC025829	ZKSCAN1	NM_003439	0.82
			hHC021053	MAPK8	NM_139046	0.81
			hHC024053	CSNK1G3	NM_001044723	0.85
			hHC027940	ZNF770	NM_014106	0.83
			hHA035440	MBTPS1	NM_003791	0.82
			hHC014703	11-Sep	NM_018243	0.86
			hHA034347	OSBPL6	NM_032523	0.80
			hHA034443	MTMR2	NR_023356	0.84
			hCT001262	OCRL	NM_000276	0.81
			hHA036770	PPP2R5C	NM_002719	0.80
			hHA035654	WDR17	NM_170710	0.85
			hHA039302	C9orf72	NM_018325	0.84
			hCT001334	OCRL	NM_000276	0.81
			hHA033002	MATR3	NM_199189	0.85
			hCT001189	HMGCR	NM_000859	0.83
			hHC007333	BM312210	BM312210	0.81
			hHC008377	GOPC	NM_020399	0.83
			hHA036025	TCF12	NM_207037	0.82
			hHA037573	CSE1L	NM_001316	0.82
			hCT001213	HMGCR	NM_000859	0.83
			hHA035677	INPP5F	NM_014937	0.88
			hCT001237	HMGCR	NM_000859	0.80
			hCT001333	OCRL	NM_000276	0.84
ASD DB	hHC001627		hHR001980	USP38	NM_032557	0.82
			hHC001627	UBR5	CD511402	1.00
ASD DB	hHC015490	VASH1	hHC015490	VASH1	NM_014909	1.00
ASD DB	hHC005732	XPO1	hHC005732	XPO1	NM_003400	1.00
ASD DB	hHC002724	YEATS2	hHC002724	YEATS2	NM_018023	1.00
ASD DB	hHC004011	YTHDC2	hHC004011	YTHDC2	NM_022828	1.00
ASD DB	hHC019788	ZNF18	hHC019788	ZNF18	NM_144680	1.00
ASD DB	hHR019994	ZSWIM5	hHR019994	ZSWIM5	NM_020883	1.00
BPAD	hHA034365	ANK3	hHA034403	NRXN1	NM_001135659	0.85
			hHA036742	NRXN1	NM_001135659	0.80

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC002037	APC	NM_001127511	0.84
			hHA035661	NRXN1	NM_001135659	0.87
			hHA034365	ANK3	NM_020987	1.00
			hHC014372	PCDHA1	NM_018900	0.81
			hHC009631	CDKL1	NM_004196	0.81
			hHC014371	PCDHA1	NM_018900	0.83
			hHA035369	NRXN1	NM_001135659	0.81
BPAD	hHC022165	BRMS1	hHC022165	BRMS1	NM_015399	1.00
BPAD	hHR025792	DDX23	hHC011368	ZNF3	NM_032924	0.91
			hHC020296	MORN4	NM_178832	0.86
			hHA038248	HERPUD2	NM_022373	0.81
			hHR025792	DDX23	NM_004818	1.00
BPAD	hHR013854		hHC016530	SMARCB1	NM_003073	0.83
			hHR013854	DPP3	NM_130443	1.00
BPAD	hHC008371	FSTL5	hHC008371	FSTL5	NM_020116	1.00
BPAD	hHC011066	FUBP1	hHC011066	FUBP1	AB209366	1.00
BPAD	hHC017657	GLT8D1	hHA037103	ZNF3	NM_032924	0.80
			hHA035253	USP14	NM_005151	0.80
			hHA039140	SNX2	NM_003100	0.88
			hHA039847	CNOT1	NM_016284	0.81
			hHA035947	SPTLC1	NM_006415	0.87
			hHC031063	SMU1	NM_018225	0.78
			hHA036547	TRO	NM_001039705	0.83
			hHA034363	YME1L1	NM_139312	0.85
			hHA037435	GART	NM_001136005	0.81
			hHA037673	GLT8D1	NM_001010983	0.79
			hHC017657	GLT8D1	NM_001010983	1.00
			hCT001156	OCRL	NM_000276	0.81
			hCT001287	OCRL	AK226116	0.82
			hHA032833	RBM5	NM_005778	0.79
			hHC017161	ZNF226	NM_001032372	0.84
BPAD	hHC012128	LMAN2L	hHC012128	LMAN2L	NM_001142292	1.00
BPAD	hHC022245	LMBR1L	hHC022245	LMBR1L	NM_018113	1.00
BPAD	hHC009312	LYG1	hHC009312	LYG1	NM_174898	1.00
BPAD	hHC014516	MITD1	hHC014516	MITD1	NM_138798	1.00
BPAD	hHE041849	MLL2	hHE041849	MLL2	NM_003482	1.00
BPAD	hHA035129	MRPL11	hHA035129	MRPL11	NM_170739	1.00
BPAD	hHC008161	NCAN	hHC008161	NCAN	NM_004386	1.00
BPAD	hHC024330	NT5DC2	hHC024330	NT5DC2	NM_022908	1.00
BPAD	hHC024103	NUDT1	hHC014134	BCL2L12	NM_138639	0.82
			hHR019400	RNASEH2C	NM_032193	0.86
			hHC027620	RNASEH2C	NM_032193	0.84
			hHC024103	NUDT1	NM_198949	0.81
			hHC020863	PXMP2	NM_018663	1.00

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC026275	DCI	NM_001919	0.83
			hHC021775	CHCHD5	NM_032309	0.84
			hHC014490	SSSCA1	NM_006396	0.82
			hHR021317	CYBA	NM_000101	0.80
			hHC019133	FKBPL	NM_022110	0.85
			hHC023741	SHFM1	NM_006304	0.83
			hHC022169	C1orf144	NM_001114600	0.85
			hHC032284	DTYMK	NM_012145	0.85
			hHC020032	REEP4	NM_025232	0.80
			hHC011224	ZNRD1	NM_170783	0.86
			hHC018782	DCPS	NM_014026	0.82
			hHC012266	WDR51A	NM_015426	0.81
			hHC017366	MTCP1	NM_014221	0.82
			hHA039530	TRPT1	NM_001033678	0.85
			hHA035545	CDK4	NM_000075	0.85
			hHC010261	AS3MT	NM_020682	0.80
BPAD	hHC008608	ODZ4	hHC008608	ODZ4	NM_001098816	1.00
BPAD	hHC007983	PBRM1	hHC007983	PBRM1	NM_018313	1.00
BPAD	hHC002159	PTGFR	hHC002159	PTGFR	NM_001039585	1.00
BPAD	hHC002778	RBM14	hHC002778	RBM14	NM_006328	1.00
BPAD	hHA033137	RBM4	hHA033137	RBM4	NM_002896	1.00
BPAD	hHC026961	RBM4B	hHC026961	RBM4B	NM_031492	1.00
BPAD	hHC014793	RCE1	hHC014793	RCE1	NM_005133	1.00
BPAD	hHC004303	REV1	hHC004580	MRPS28	NM_014018	0.82
			hHC004303	REV1	NM_016316	1.00
			hHC027685	PDCD7	NM_005707	0.80
BPAD	hHR029076	RPL18	hHR029076	RPL18	NM_000979	1.00
BPAD	hHA033917	SYNE1	hHA033917	SYNE1	NM_133650	1.00
BPAD	hHC025916	TUBA1A	hHC025916	TUBA1A	NM_006009	1.00
BPAD	hHA033914	USP33	hHA033914	USP33	NM_201626	1.00
BPAD	hHC025830	WDR82	hHC017134	NDRG3	NM_032013	0.81
			hHC025830	WDR82	NM_025222	1.00
			hHA040084	PCDHA1	NM_018900	0.81
BPAD	hHC003709	ZMIZ1	hHC003709	ZMIZ1	NM_020338	1.00
ID	hHC004157	DCX	hHC004157	DCX	NM_000555	1.00
			hHR028947	ZNF91	NM_003430	0.83
ID	hHC007076	FOXG1	hHC007076	FOXG1	NM_005249	1.00
ID	hHC007660	ZNF711	hHA038080	MACF1	NM_012090	0.82
			hHC007660	ZNF711	NM_021998	1.00
			hHC009196	TMEM135	NM_022918	0.87
			hHC015340	GPR107	NM_001136557	0.82
ID	hHC005898	AFF2	hHC004824	TAPT1	NM_153365	0.81
			hHC005100	CDH10	NM_006727	0.82
			hHC008844	PPP1R14C	NM_030949	0.83

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC001764	SATB2	NM_015265	0.82
			hHC018263	LOC150568	AK126958	0.82
			hHC012083	KIAA1377	NM_020802	0.81
			hHC008950	CCBE1	NM_133459	0.85
			hHC003310	ETV6	NM_001987	0.82
			hHC004558	SLITRK5	NM_015567	0.80
			hHA033934	PCDH10	NM_032961	0.91
			hHR002770	THSD7B	NM_001080427	0.82
			hHC009694	FBXO27	NM_178820	0.80
			hHC009741	FGF9	NM_002010	0.82
			hHC016833	SRD5A1	NM_001047	0.84
			hHC013509	RSPO3	NM_032784	0.84
			hHC004689	NECAB1	NM_022351	0.84
			hHC004797	C13orf31	NM_001128303	0.85
			hHC018609	STK32B	NM_018401	0.83
			hHC002996	SEMA3E	NM_012431	0.84
			hHC005000	KLHL14	NM_020805	0.81
			hHC007220	ELOVL2	NM_017770	0.80
			hHA035912	GRM7	BC136458	0.90
			hHC003116	SHC4	NM_203349	0.86
			hHC008960	NKAIN2	NM_001040214	0.86
			hHC010412	DB519783	DB519783	0.88
			hHC003704	PCDHB4	NM_018938	0.84
			hHC004100	UST	NM_005715	0.82
			hHC018704	ADCY8	NM_001115	0.83
			hHC005695	AJAP1	NM_018836	0.81
			hHC007231	PRKAB2	NM_005399	0.81
			hHC018655	CXXC4	NM_025212	0.88
			hHC008995	RIMS1	BC036608	0.84
			hHC009655	HDAC9	NM_178423	0.89
			hHC002299	AKAP7	NM_016377	0.87
			hHC005898	AFF2	NM_002025	
			hHC007530	KCNK2	NM_001017424	0.82
			hHC024318	DOK4	NM_018110	0.85
			hHA033834	HDAC9	NM_014707	0.81
			hHC007074	MRAS	NM_012219	0.80
			hHR002609	LOC150568	NR_015399	0.86
			hHC004901	CHSY3	NM_175856	0.84
			hHA033893	KLHL4	NM_019117	0.80
			hHC004361	LRRC4C	NM_020929	0.82
			hHR028841	USP6	NM_004505	0.83
			hHR005537	LPHN3	NM_015236	0.83
			hHR008897	PLCH2	NM_014638	0.85
			hHE040949	EY892390	EY892390	0.87

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC001625	SCN3A	NM_006922	0.80
			hHA033869	NEBL	NM_006393	0.82
			hHC008260	GRM7	NM_181874	0.88
			hHC002620	EPHA3	NM_005233	0.80
			hHC004792	PTCHD1	NM_173495	0.81
			hHC030459	LOC162632	NR_003190	0.83
			hHC001971	GREM2	NM_022469	0.83
			hHC003711	ADAMTSL3	NM_207517	0.85
			hHC004671	PCDH10	NM_032961	0.88
			hHC004959	CPVL	NM_019029	0.84
			hHC006519	CXXC4	AK127778	0.87
			hHC019179	RSPO3	NM_032784	0.80
			hHR011906	RIMBP2	NM_015347	0.82
			hHC014222	C3orf59	NM_178496	0.88
			hHC009926	SH3GL3	NM_003027	0.84
			hHR001898	KIAA1239	NM_001144990	0.86
			hHC002666	ITPR1	NM_001099952	0.85
			hHC005654	NAP1L2	NM_021963	0.80
			hHC002797	CDH11	NM_001797	0.86
			hHC004537	LRRC8B	NM_015350	0.85
			hHC009277	LPPR4	NM_014839	0.81
			hHE040789	SCN9A	NM_002977	0.80
ID	hHA033656	BCOR	hHA033656	BCOR	AB046795	1.00
ID	hHR002515	MID1	hHR013860	PAICS	NM_006452	0.81
			hHA034320	LRRC1	NM_018214	0.80
			hHC004680	RFX4	NM_213594	0.81
			hHC009468	MCM3	NM_002388	0.84
			hHC027720	YAP1	NM_001130145	0.85
			hHR001920	SOX21	NM_007084	0.80
			hHC018731	ABHD3	NM_138340	0.84
			hHC028715	LAPTM4B	NM_018407	0.80
			hHC024419	RFXANK	NM_003721	0.81
			hHR031067	COL4A5	NM_033380	0.82
			hHC007295	DHX40	NM_024612	0.80
			hHC030274	GNG5	NM_005274	0.80
			hHA036094	BCAN	NM_198427	0.87
			hHC003297	DACH1	NM_080759	0.86
			hHC007569	NAB1	NM_005966	0.86
			hHC009021	LRIG1	NM_015541	0.84
			hHR002515	MID1	NM_000381	1.00
			hHC003499	LIPG	NM_006033	0.82
			hHR006559	CPNE3	NM_003909	0.80
			hHC024931	TJAP1	NM_080604	0.85
			hHC015727	TLK1	NM_012290	0.83

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC027439	ODC1	NM_002539	0.81
			hHC016518	DNAJC1	NM_022365	0.83
			hHC006582	CREB5	NM_182898	0.86
			hHC006690	GPC4	NM_001448	0.89
			hHC002081	MPDZ	NM_003829	0.80
			hHC004289	NOTCH2	NM_024408	0.84
			hHR006017	ANKHD1	NM_017747	0.81
			hHC008801	SFRP1	NM_003012	0.81
			hHR004084	QKI	NM_206855	0.80
			hHC003267	COL9A1	NM_001851	0.81
			hHR002103	LOC145474	AK023718	0.82
			hHR010263	HEG1	NM_020733	0.82
			hHR003398	NOTCH1	NM_017617	0.86
			hHC019742	PLCE1	NM_016341	0.81
			hHC004586	HES1	NM_005524	0.81
			hHC013189	TMPRSS5	NM_030770	0.81
			hHC004957	PLAG1	NM_002655	0.80
ID	hHC019020	GRIK2	hHC019020	GRIK2	NM_175768	1.00
			hCT001188	HMGCR	NM_000859	0.80
			hHA038748	MACF1	NM_012090	0.82
			hCT001271	HMGCR	NM_000859	0.84
			hHC029543	HMGCS1	NM_001098272	0.79
			hHA038079	MACF1	NM_012090	0.82
			hCT001189	HMGCR	NM_000859	0.80
ID	hHC015067	PRSS12	hHC015067	PRSS12	NM_003619	1.00
			hHC010695	NRP1	NM_003873	0.80
ID	hHR029739	ZEB2	hHR029739	ZEB2	NM_014795	1.00
ID	hHR002782	CASK	hHR002782	CASK	NM_003688	1.00
ID	hHR002178	PHF6	hHR002178	PHF6	NM_032458	1.00
ID	hHA035283	NRXN1	hHA035988	CNR1	NM_016083	0.79
			hHC009943	CACNA2D1	NM_000722	0.81
			hHC010327	PHF6	NM_032458	0.79
			hHC014427	SLC35F5	NM_025181	0.82
			hHA035283	NRXN1	NM_001135659	1.00
			hCT001189	HMGCR	NM_000859	0.79
			hHA034405	USP34	NM_014709	0.85
			hHA036025	TCF12	NM_207037	0.79
			hHC019261	ANKRD28	NM_015199	0.80
			hHC029833	GNAQ	NM_002072	0.80
ID	hHC031675	ATRX	hCT001188	HMGCR	NM_000859	0.81
			hCT001271	HMGCR	NM_000859	0.82
			hHR007991	PPP1R9A	NM_017650	0.82
			hCT001295	HMGCR	NM_000859	0.81
			hHC026531	CDC42EP3	NM_006449	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHC029543	HMGCS1	NM_001098272	0.81
			hHA035301	TTC33	NM_012382	0.78
			hHC031675	ATRX	NM_000489	1.00
			hHA035670	C9orf72	NM_018325	0.79
			hHA035514	SNX14	NM_153816	0.86
			hCT001189	HMGCR	NM_000859	0.83
			hCT001213	HMGCR	NM_000859	0.83
			hCT001237	HMGCR	NM_000859	0.80
ID	hHA035687	ZC3H14	hHA035687	ZC3H14	NM_024824	1.00
			hHA035396	PTPN12	NM_002835	0.82
			hHC009031	GNB1	NM_002074	0.83
			hHA037387	RBM25	AK094697	0.83
			hHA033126	CASC4	NM_138423	0.86
			hHA034947	METTL6	NM_152396	0.83
			hHC010971	FBXO34	NM_017943	0.80
			hHC013970	C9orf126	NM_173690	0.80
ID	hHC010973	SOBP	hHC006884	SRGAP1	NM_020762	0.80
			hHC010973	SOBP	NM_018013	1.00
			hHC025730	NHSL1	NM_001144060	0.81
ID	hHA034036	UBE2A	hHA034036	UBE2A	NM_181777	1.00
ID	hHR004728	CUL4B	hHR004728	CUL4B	NM_003588	1.00
			hHC022092	AASDHPPT	NM_015423	0.81
			hHA034020	UBE2J1	NM_016021	0.82
			hHR008796	GUF1	NM_021927	0.84
			hHA032988	HIF1A	NM_001530	0.80
			hCT001271	HMGCR	NM_000859	0.83
			hHR007991	PPP1R9A	NM_017650	0.83
			hHC026327	GMFB	NM_004124	0.81
			hCT001295	HMGCR	NM_000859	0.81
			hHC014351	TMED7	NM_181836	0.80
			hHC006599	ADAM10	NM_001110	0.83
			hHC007559	MFAP3	NR_024152	0.80
			hHR030407	ZNF322A	NM_024639	0.81
			hHA032999	ARMC8	NM_015396	0.80
			hHA037811	DPYSL2	NM_001386	0.84
			hCT001270	HMGCR	NM_000859	0.82
			hHA037774	KIAA0528	BC143859	0.80
			hHR013798	TOP1	NM_003286	0.80
			hHC009165	TMEM30A	NM_018247	0.80
			hHC008805	BMI1	NM_005180	0.84
			hHE041108	(CSNK1A1),	CN267058	0.81
			hHC009223	WDR26	NM_025160	0.88
			hHC013157	SEL1L	NM_005065	0.80
			hHC016805	SMEK2	NM_001122964	0.82

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHR023273	TOMM20	NM_014765	0.81
			hHC023439	BAT2D1	NM_015172	0.80
			hCT001189	HMGCR	NM_000859	0.85
			hCT001213	HMGCR	NM_000859	0.82
			hCT001237	HMGCR	NM_000859	0.80
ID	hHC025870	UPF3B	hHC025870	UPF3B	NM_080632	1.00
ID	hHC011183	BRWD3	hHC011183	BRWD3	NM_153252	1.00
			hHA034773	EZH2	NM_004456	0.84
			hHC008765	NEIL3	NM_018248	0.82
ID	hHC019207	AP4B1	hHA034020	UBE2J1	NM_016021	0.80
			hHC030874	BMPR1A	NM_004329	0.84
			hHC019207	AP4B1	NM_006594	1.00
ID	hHR008276	ZNF81	hHC006767	HPX	NM_000613	0.80
			hHR008276	ZNF81	NM_007137	1.00
			hHC022100	ZNF70	NM_021916	0.82
			hHA037064	CDH23	NM_022124	0.83
ID	hHC024693		hHC018672	PPFIA2	NM_003625	0.80
			hHC024693	TUSC3	NM_006765	1.00
ID	hHC011816	RAI1	hHC011816	RAI1	NM_030665	1.00
ID	hHA035290	VLDLR	hHA035290	VLDLR	NM_003383	1.00
			hHC005950	HTR1A	NM_000524	0.83
			hHR027435	BM927052	BM927052	0.84
ID	hHA033034	UBE3A	hHA037464	CREB1	NM_134442	0.85
			hCT001104	OCRL	NM_000276	0.83
			hCT001188	HMGCR	NM_000859	0.86
			hHA033936	CSE1L	NM_001316	0.82
			hHA034020	UBE2J1	NM_016021	0.83
			hHA035472	UBQLN1	NM_013438	0.82
			hHA039504	UBE3A	NM_130839	0.83
			hHC013212	SPAG9	NM_001130528	0.82
			hHA034344	CSE1L	NM_001316	0.84
			hHA034332	MBNL1	NM_021038	0.81
			hHC017280	UBXN7	NM_015562	0.84
			hHA035988	CNR1	NM_016083	0.85
			hCT001175	RB1	NM_000321	0.85
			hCT001163	HMGCR	NM_000859	0.92
			hCT001451	RB1	NM_000321	0.85
			hHC005015	SP4	NM_003112	0.84
			hHR007991	PPP1R9A	NM_017650	0.82
			hHC009995	CCNH	AK094534	0.88
			hHC024011	LRRC49	NM_017691	0.81
			hHC026327	GMFB	NM_004124	0.85
			hHA035927	USP15	AF153604	0.85
			hHA036779	KIF1B	NM_015074	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hCT001187	HMGCR	NM_000859	0.90
			hCT001295	HMGCR	NM_000859	0.82
			hCT001475	RB1	NM_000321	0.80
			hHR003683	FNBP1L	AK000282	0.84
			hHR008195	LOC221710	NM_001135575	0.88
			hHC014351	TMED7	NM_181836	0.83
			hHA035279	PPP1CB	NM_002709	0.83
			hHA036431	RNF138	NM_016271	0.84
			hCT001211	HMGCR	NM_000859	0.91
			hCT001499	RB1	NM_000321	0.81
			hHA033083	GTF2H1	NM_001142307	0.87
			hHA037511	NEDD9	NM_001142393	0.82
			hHA034739	INPP5F	NM_014937	0.84
			hHA037811	DPYSL2	NM_001386	0.83
			hCT001174	RB1	NM_000321	0.80
			hCT001162	HMGCR	NM_000859	0.88
			hCT001270	HMGCR	NM_000859	0.87
			hHR017590	SNX12	NM_013346	0.80
			hHR018634	SRP72	NM_006947	0.85
			hHA033034	UBE3A	NM_130839	1.00
			hHA033322	GNAQ	NM_002072	0.81
			hHA037078	SETD3	NM_032233	0.80
			hHA038794	G3BP2	NM_203505	0.83
			hCT001198	RB1	NM_000321	0.83
			hCT001186	HMGCR	NM_000859	0.91
			hCT001294	HMGCR	NM_000859	0.93
			hHC020782	SNX12	NM_013346	0.81
			hCT001210	HMGCR	NM_000859	0.94
			hCT001318	HMGCR	NM_000859	0.92
			hHA035578	ZMYND11	NM_006624	0.83
			hCT001234	HMGCR	NM_000859	0.85
			hCT001342	HMGCR	NM_000859	0.80
			hCT001161	HMGCR	NM_000859	0.94
			hCT001269	HMGCR	NM_000859	0.95
			hHC004341	MAP2K6	U39657	0.85
			hHR027573	ENST00000332111	ENST00000332119	0.81
			hHA035253	USP14	NM_005151	0.83
			hHA035337	SPAG9	NM_001130528	0.85
			hHA038613	WDR17	NM_170710	0.83
			hHA040713	UHRF2	NM_152896	0.81
			hCT001197	RB1	NM_000321	0.83
			hCT001293	HMGCR	NM_000859	0.88
			hCT001281	OCRL	NM_000276	0.83
			hCT001473	RB1	NM_000321	0.82

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hHA037869	USP46	NM_001134223	0.84
			hCT001317	HMGCR	NM_000859	0.84
			hHC016293	ZEB2	NM_014795	0.84
			hHA033381	NCOA4	NM_005437	0.87
			hHA035193	INPP5F	NM_014937	0.83
			hCT001245	RB1	M15400	0.81
			hCT001341	HMGCR	NM_000859	0.90
			hHA035601	ZMYM6	NM_007167	0.83
			hCT001268	HMGCR	NM_000859	0.94
			hCT001448	RB1	NM_000321	0.87
			hHR025556	API5	NR_024625	0.80
			hHA037652	SPAG9	AK024068	0.84
			hHE041108	(CSNK1A1),	CN267058	0.84
			hCT001196	RB1	NM_000321	0.84
			hHA037964	ATF2	NM_001880	0.84
			hCT001316	HMGCR	NM_000859	0.92
			hHC015992	CUL2	NM_003591	0.80
			hCT001340	HMGCR	NM_000859	0.88
			hCT001520	RB1	NM_000321	0.85
			hHC002588	NCOA2	NM_006540	0.81
			hCT001171	RB1	NM_000321	0.80
			hHC009223	WDR26	NM_025160	0.84
			hHA034567	HECTD2	NM_182765	0.85
			hHC005983	ATXN3	NM_004993	0.85
			hHA039691	SLC30A5	NM_022902	0.88
			hHC009943	CACNA2D1	NM_000722	0.83
			hHC010327	PHF6	NM_032458	0.88
			hHA034363	YME1L1	NM_139312	0.81
			hHC020934	CHUK	NM_001278	0.81
			hHA038142	C9orf72	NM_018325	0.84
			hHR007254	ZBTB26	NM_020924	0.82
			hHA033942	MBOAT2	NM_138799	0.83
			hHA035670	C9orf72	NM_018325	0.84
			hHA033870	SLC30A5	NM_022902	0.85
			hHA035514	SNX14	NM_153816	0.83
			hHR014321	CK818803	CK818803	0.85
			hHC025829	ZKSCAN1	NM_003439	0.82
			hHC021053	MAPK8	NM_139046	0.81
			hHC024053	CSNK1G3	NM_001044723	0.85
			hHC027940	ZNF770	NM_014106	0.83
			hHA035440	MBTPS1	NM_003791	0.82
			hHC014703	11-Sep	NM_018243	0.86
			hHA034347	OSBPL6	NM_032523	0.80
			hHA034443	MTMR2	NR_023356	0.84

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
			hCT001262	OCRL	NM_000276	0.81
			hHA036770	PPP2R5C	NM_002719	0.80
			hHA035654	WDR17	NM_170710	0.85
			hHA039302	C9orf72	NM_018325	0.84
			hCT001334	OCRL	NM_000276	0.81
			hHA033002	MATR3	NM_199189	0.85
			hCT001189	HMGCR	NM_000859	0.83
			hHC007333	BM312210	BM312210	0.81
			hHC008377	GOPC	NM_020399	0.83
			hHA036025	TCF12	NM_207037	0.82
			hHA037573	CSE1L	NM_001316	0.82
			hCT001213	HMGCR	NM_000859	0.83
			hHA035677	INPP5F	NM_014937	0.88
			hCT001237	HMGCR	NM_000859	0.80
			hCT001333	OCRL	NM_000276	0.84
ID	hHR012502	AP4M1	hHR012502	AP4M1	NM_004722	1.00
ID	hHC020459	TCF4	hHC020459	TCF4	NM_001083962	1.00
ID	hHC013601	FTSJ1	hHC013601	FTSJ1	NM_177439	1.00
ID	hCT001285	OCRL	hHA036996	KCNH2	NM_172056	0.81
			hHR027299	CR602880	CR602880	0.87
			hHA039898	TNXB	NM_019105	0.80
			hHR014709	RGL3	AK096811	0.81
			hHC011781	SKAP1	NM_003726	0.84
			hHC016029	CLC	NM_001828	0.87
			hHA037245	PPFIBP1	NM_003622	0.82
			hCT001256	OCRL	NM_000276	0.83
			hHC023252	ATAD4	NM_024320	0.86
			hHO048776	EU427377	EU427377	0.82
			hCT000848	TLN1	NM_006289	0.82
			hHC024691	TP73	NM_005427	0.81
			hHR027199	C9orf44	AK023662	0.81
			hHR023046	TCL6	NM_014418	0.81
			hHC026214	GFRA3	NM_001496	0.82
			hHR028686	IFNA6	NM_021002	0.81
			hHA037433	ABCG1	AY048757	0.81
			hHA032908	SLC23A2	NM_005116	0.83
			hHR010191	DMTF1	NM_021145	0.83
			hHR023907	HMX3	NM_001105574	0.80
			hHA038799	OTOF	NM_194248	0.82
			hHC025887	C21orf88	NR_026542	0.80
			hHC020270	RAB3D	NM_004283	0.85
			hCT000806	LRP1	NM_002332	0.80
			hHC026785	LINGO1	CN295335	0.89
			hCT001285	OCRL	NM_000276	1.00

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
ID	hHC009198	SLC16A2	hHC009198	SLC16A2	NM_006517	1.00
ID	hHC027610	OFD1	hHC027610	OFD1	NM_003611	1.00
ID	hHA034468	DLG3	hHA034468	DLG3	NM_020730	1.00
ID	hHC002925	OPHN1	hHC002925	OPHN1	NM_002547	1.00
ID	hHC016668	FLNA	hHC016668	FLNA	NM_001110556	1.00
ID	hHA037813	ERLIN2	hHA037813	ERLIN2	NM_007175	1.00
NDG	hCT001336	APP	hHA034332	MBNL1	NM_021038	0.81
			hHA035375	LANCL1	NM_006055	0.84
			hHR027419	HSPA9	NM_004134	0.85
			hHA034151	TM7SF3	NM_016551	0.82
			hHC006515	PHC3	NM_024947	0.83
			hHA033395	CCT6A	NM_001762	0.80
			hHC008805	BMI1	NM_005180	0.80
			hHR025556	API5	NR_024625	0.84
			hHA037136	HDHD2	NM_032124	0.83
			hCT001183	APP	NM_000484	0.86
			hCT001231	APP	NM_000484	0.82
			hCT001158	APP	NM_000484	0.84
			hHC008454	CASP3	NM_004346	0.85
			hHA033126	CASC4	NM_138423	0.81
			hHA036978	TMEM66	NM_016127	0.88
			hCT001182	APP	NM_000484	0.87
			hCT001206	APP	NM_000484	0.87
			hCT001230	APP	NM_000484	0.91
			hHC028698	CSNK1A1	NM_001025105	0.81
			hHA033306	GOT2	NM_002080	0.83
			hHC013157	SEL1L	NM_005065	0.80
			hCT001289	APP	NM_000484	0.85
			hHR023273	TOMM20	NM_014765	0.85
			hHC028925	NAP1L4	NM_005969	0.83
			hHC031625	LOC100131998	AK055742	0.82
			hHA034781	UQCC	NM_018244	0.81
			hCT001313	APP	NM_000484	0.84
			hHA034241	PTPN12	NM_002835	0.85
			hCT001337	APP	NM_000484	0.90
			hCT001264	APP	NM_000484	0.84
			hCT001288	APP	NM_000484	0.90
			hCT001312	APP	NM_000484	0.92
			hHC031215	ATP6AP2	NM_005765	0.81
			hHA033231	TCP1	NM_030752	0.82
			hHA040743	SLC30A5	NM_022902	0.81
			hHA034443	MTMR2	NR_023356	0.82
			hHR012818	RFWD2	NM_022457	0.80
			hHR026558	BZW1	NM_014670	0.81

Table S4 Coexpression

Gene Set	Probe	Pre-natally enriched Disease-associated Gene	Correlated Probe	Gene	Accession	Pearson's Correlation Coefficient (RIN Adjusted)
NDG	hHA034733	C9orf72	hHA034733	C9orf72	NM_018325	1.00
NDG	hHC007088	CD2AP	hHC007088	CD2AP	NM_012120	1.00
NDG	hHC024724	FUS	hHC024724	FUS	NM_004960	1.00
NDG	hHR012346	MAPT	hHC013920	FASN	NM_004104	0.83
			hHA037044	SPTBN1	NM_003128	0.80
			hHC010607	ANKH	NM_054027	0.85
			hHC011075	NRXN1	NM_001135659	0.83
			hHC017927	PDIA2	NM_006849	0.85
			hHR001582	GNAZ	NM_002073	0.84
			hHC007234	PRKCE	NM_005400	0.81
			hHC017710	RAB11FIP4	NM_032932	0.90
			hHR012346	MAPT	NM_001123066	1.00
			hHC013318	GNAZ	NM_002073	0.83
			hHR015934	DOK4	NM_018110	0.83
			hHC008119	ADCY1	NM_021116	0.88
			hHC008431	CLIP2	NM_003388	0.80
			hHA034861	ARPP-21	NM_016300	0.81

CNV LOCI ASSOCIATED WITH SCZ AND ASD

Band		Gene	Fetal Effect	t statistic	p-value
1q21.1	Dup/Del	NBPF13P	n/a		
		PRKAB2	1.39	21.24	8.97E-57
		FMO5			
		CHD1L	n/a		
		BCL9	2.02	23.33	2.50E-63
		ACP6	n/a		
		GJA5	0.25	3.02	2.82E-03
		GJA8	-0.49	-6.30	1.40E-09
		GPR89B	n/a		
		GPR89C	n/a		
		PDZK1P1	n/a		
		NBPF8	n/a		
		NBPF24	n/a		
		NBPF11	n/a		
		NBPF10			
2p16.3	Dup/Del	NRXN1	1.31	14.33	6.02E-34
15q13.3	Del/Dup	MTMR15	0.50	7.52	1.10E-12
		MTMR10	n/a		
		TRPM1	n/a		
		MIR211	n/a		
		KLF13	-0.53	-6.24	2.04E-09
		OTUD7A	-0.96	-10.35	6.01E-21
		CHRNA7	0.83	5.64	4.76E-08
16p11.2	Del/Dup	SPN	0.15	3.40	7.88E-04
		QPRT	-0.86	-10.74	3.41E-22
		C16orf54	-0.01	-0.11	9.09E-01
		ZG16	n/a		
		KIF22	0.22	3.55	4.67E-04
		MAZ	-0.06	-1.78	7.63E-02
		PRRT2	-0.57	-7.73	3.02E-13
		PAGR1 (C16orf53)	1.29	19.62	1.49E-51
		MVP	-1.16	-12.58	3.84E-28
		CDIPT	-0.59	-13.67	9.04E-32
		SEZ6L2	-1.44	-16.87	1.83E-42
		ASPHD1	0.74	8.54	1.69E-15
		KCTD13	0.16	2.41	1.68E-02
		TMEM219	-0.95	-18.45	1.04E-47
		TAOK2	0.50	5.08	7.67E-07
		HIRIP3	0.16	2.28	2.33E-02
		INO80E	-0.03	-0.68	4.98E-01
		DOC2A	-0.64	-13.19	3.67E-30
		C16orf92	n/a		
		FAM57B	-0.64	-13.19	3.67E-30
		ALDOA	0.32	5.01	1.08E-06
		PPP4C	1.29	18.99	1.69E-49
		TBX6	-0.78	-9.56	1.59E-18
		YPEL3	-0.95	-16.01	1.35E-39
		GDPD3	0.24	4.35	2.03E-05
		MAPK3	-1.22	-20.77	2.91E-55
22q11.21	Del/Dup	DGCR6	-0.73	-13.54	2.53E-31
		PRODH	-1.01	-9.02	6.36E-17
		DGCR5	0.65	7.67	4.41E-13
		DGCR9	-0.60	-6.57	3.13E-10
		DGCR10	0.56	4.23	3.37E-05
		DGCR2	-0.73	-12.66	2.09E-28
		DGCR11	0.00	0.03	9.72E-01
		DGCR14	0.45	5.40	1.60E-07
		TSSK2	-0.55	-5.51	9.14E-08
		GSC2	n/a		
		SLC25A1	0.48	8.50	2.19E-15
		CLTCL1	0.48	8.50	2.19E-15
		HIRA	0.58	11.24	9.08E-24
		MRPL40	-0.50	-7.82	1.74E-13
		C22orf39	n/a		
		UFD1L	0.25	5.15	5.60E-07
		CDC45L	3.89	25.04	1.59E-68
		CLDN5	n/a		
		SEPT5			
		GP1BB	n/a		

OTHER CNV LOCI ASSOCIATED WITH SCZ

Locus	CNV Type	Genes	Fetal Effect	t-statistic	p-value
1q21.1	Del	HFE2	0.09	0.70	4.82E-01
		TXNIP	0.86	6.21	2.33E-09
		POLR3GL	0.05	1.04	2.97E-01
		ANKRD34A	-0.98	-14.04	5.24E-33
		LIX1L	1.38	21.92	6.15E-59
		RBM8A	0.90	15.33	2.48E-37
		GNRHR2	-0.49	-5.22	3.85E-07
		PEX11B	-0.70	-15.11	1.44E-36
		ITGA10	n/a		
		ANKRD35	-0.61	-8.15	2.04E-14
		PIAS3	0.07	1.46	1.46E-01
		NUDT17	-0.30	-5.72	3.23E-08
		POLR3C	0.19	4.05	6.81E-05
		RNF115	0.08	1.27	2.06E-01
		CD160	-0.49	-8.59	1.18E-15
		PDZK1	0.23	2.12	3.52E-02
		GPR89A	n/a		
3q29	Del	TFRC	-0.42	-3.88	1.33E-04
		ZDHHC19	-0.16	-3.59	4.09E-04
		OSTalpha	-0.01	-0.07	9.47E-01
		PCYT1A	-0.45	-7.23	6.50E-12
		TCTEX1D2	0.62	8.82	2.46E-16
		TM4SF19	-0.04	-0.58	5.60E-01
		UBXD7	1.05	15.84	4.86E-39
		RNF168	-0.13	-1.09	2.78E-01
		SMCO1	n/a		
		WDR53	-0.40	-4.15	4.71E-05
		FBXO45	0.05	1.09	2.77E-01
		NRROS	n/a		
		CEP19	n/a		
		PIGX	-0.40	-4.72	4.00E-06
		PAK2	1.74	24.02	1.95E-65
		SENP5	-0.39	-5.55	7.65E-08
		NCBP2	1.11	21.09	2.57E-56
		PIGZ	-1.19	-15.29	3.41E-37
		MFI2	0.07	0.92	3.59E-01
		DLG1	0.20	4.14	4.92E-05
7q36.3	Dup	VIPR2	n/a		
15q11.2	Del	CYFIP1	0.55	4.89	1.87E-06
		NIPA2	-0.03	-0.73	4.66E-01
		NIPA1	-1.18	-13.19	3.66E-30
		TUBGCP5	n/a		
15q13.3	Del/Dup	CHRFAM7A	-1.54	-13.74	5.29E-32
		ARHGAP11B	n/a		
		MTMR15	0.50	7.52	1.10E-12
		MTMR10	n/a		
		TRPM1	n/a		
		MIR211	n/a		
		KLF13	-0.53	-6.24	2.04E-09
		OTUD7A	-0.96	-10.35	6.01E-21
		CHRNA7	0.83	5.64	4.76E-08
16p11.2	Dup	SPN	0.15	3.40	7.88E-04
		QPRT	-0.86	-10.74	3.41E-22
		C16orf54	-0.01	-0.11	9.09E-01
		ZG16	n/a		
		KIF22	0.22	3.55	4.67E-04
		MAZ	-0.06	-1.78	7.63E-02
		PRRT2	-0.57	-7.73	3.02E-13
		PAGR1 (C16orf53)	1.29	19.62	1.49E-51
		MVP	-1.16	-12.58	3.84E-28
		CDIPT	-0.59	-13.67	9.04E-32
		SEZ6L2	-1.44	-16.87	1.83E-42
		ASPHD1	0.74	8.54	1.69E-15
		KCTD13	0.16	2.41	1.68E-02
		TMEM219	-0.95	-18.45	1.04E-47
		TAOK2	0.50	5.08	7.67E-07
		HIRIP3	0.16	2.28	2.33E-02
		INO80E	-0.03	-0.68	4.98E-01
		DOC2A	-0.64	-13.19	3.67E-30
		C16orf92	n/a		

OTHER CNV LOCI ASSOCIATED WITH ASD

Band		Gene	Fetal Effect	t statistic	p-value
3p14.1	Del	MAGI1	0.12	1.76	7.93E-02
3p14.1	Del	SUCLG2	-0.60	-8.90	1.49E-16
		FAM19A1	n/a		
		FAM19A4	n/a		
		C3orf64			
		MIR3136	n/a		
		TMF1	0.24	1.64	1.03E-01
		UBA3	1.38	21.13	2.01E-56
		ARL6IP5	-1.02	-16.17	4.03E-40
		LMOD3	-0.35	-2.75	6.50E-03
		FRMD4B	1.78	14.47	1.97E-34
		MITF	0.17	2.09	3.79E-02
5p15.2	Del	CTNND2	-0.07	-0.96	3.37E-01
7q11.23	Dup	FZD9	-0.41	-4.23	3.34E-05
		BAZ1B	0.15	2.61	9.52E-03
		BCL7B	0.21	3.15	1.84E-03
		TBL2	0.17	2.61	9.66E-03
		MLXIPL	n/a		
		VPS37D	0.81	11.86	8.78E-26
		DNAJC30	0.20	3.51	5.41E-04
		WBSCR22	-0.37	-8.11	2.77E-14
		STX1A	-1.52	-18.84	5.20E-49
		MIR4284	n/a		
		ABHD11	0.04	0.47	6.41E-01
		CLDN3	-0.27	-4.75	3.53E-06
		CLDN4	0.02	0.14	8.86E-01
		WBSCR27	-0.29	-2.22	2.74E-02
		WBSCR28	0.19	2.53	1.21E-02
		ELN	-0.03	-0.36	7.20E-01
		LIMK1	-0.50	-6.61	2.58E-10
		MIR590	n/a		
		LAT2	-1.22	-8.35	5.75E-15
		RFC2	0.83	15.90	3.10E-39
		CLIP2	0.18	2.69	7.63E-03
		GTF2IRD1	1.68	25.04	1.64E-68
		GTF2I	n/a		
7q31.1	Del/Dup	C7orf66	n/a		
7q31.1	Del/Dup	DOCK4	0.12	1.39	1.67E-01
7q36.2	Del	DPP6	n/a		
8p23.3	Dup	DLGAP2	-2.22	-24.35	1.96E-66
9p24.3	Del/Dup	FOXD4	n/a		
		CBWD1	0.52	7.79	2.04E-13
		C9orf66	-0.38	-5.36	2.01E-07
		DOCK8	-1.52	-9.42	4.19E-18
10q11.23-21.1	Dup	PRKG1	n/a		
		MIR605	n/a		
		CSTF2T	0.39	4.97	1.29E-06
		DKK1	0.01	0.11	9.12E-01
		MBL2	0.23	2.28	2.37E-02
12q24.31	Dup	TMEM120B	n/a		
		RHOF	-1.58	-23.39	1.67E-63
		SETD1B	1.30	21.60	6.47E-58
		HPD	-0.12	-1.69	9.20E-02
		PSMD9	0.18	2.56	1.09E-02
		WDR66	-0.58	-6.48	5.32E-10
15q11.2-13.1	Dup	MKRN3	1.26	9.75	4.09E-19
		MAGEL2	-0.45	-5.28	2.92E-07
		NDN	-0.01	-0.10	9.18E-01
		PWRN2	n/a		
		PWRN1	n/a		
		C15orf2	-1.90	-19.39	7.92E-51
		SNURF	-1.69	-25.02	1.84E-68
		SNRPN	0.09	0.80	4.23E-01

CNV LOCI ASSOCIATED WITH SCZ AND ASD

		TBX1	-0.70	-11.59	6.57E-25
		GNB1L	-0.25	-3.92	1.14E-04
		C22orf29	0.07	1.38	1.70E-01
		TXNRD2	-0.84	-16.35	9.34E-41
		COMT	-0.28	-5.30	2.66E-07
		ARVCF	0.57	10.39	4.53E-21
		C22orf25	-1.47	-23.16	8.40E-63
		MIR185	n/a		
		DGCR8	0.82	6.25	1.92E-09
		MIR3618	n/a		
		MIR1306	n/a		
		TRMT2A	-0.40	-5.92	1.14E-08
		RANBP1	0.40	8.73	4.51E-16
		ZDHHC8	-0.16	-3.59	4.09E-04
		RTN4R	-0.81	-9.38	5.47E-18
		MIR1286	n/a		
		DGCR6L	-0.74	-13.76	4.76E-32
		TMEM191B	n/a		
		RIMBP3	n/a		
		ZNF74	1.57	23.04	2.05E-62
		SCARF2	-0.17	-3.01	2.92E-03
		KLHL22	0.38	8.72	5.11E-16
		MED15	-0.49	-10.55	1.36E-21
		PI4KA	0.50	5.74	2.81E-08
		SERPIND1	0.74	6.22	2.23E-09
		SNAP29	-0.69	-9.68	6.90E-19
		CRKL	0.05	0.94	3.49E-01
		AIFM3	n/a		
		LZTR1	0.56	10.82	1.98E-22
		THAP7	-0.13	-3.41	7.74E-04
		P2RX6	0.16	3.13	2.00E-03
		SLC7A4	-0.83	-12.06	1.97E-26
		RIMBP3C	n/a		
		RIMBP3B	n/a		
		HIC2	2.32	31.79	1.95E-87

OTHER CNV LOCI ASSOCIATED WITH SCZ

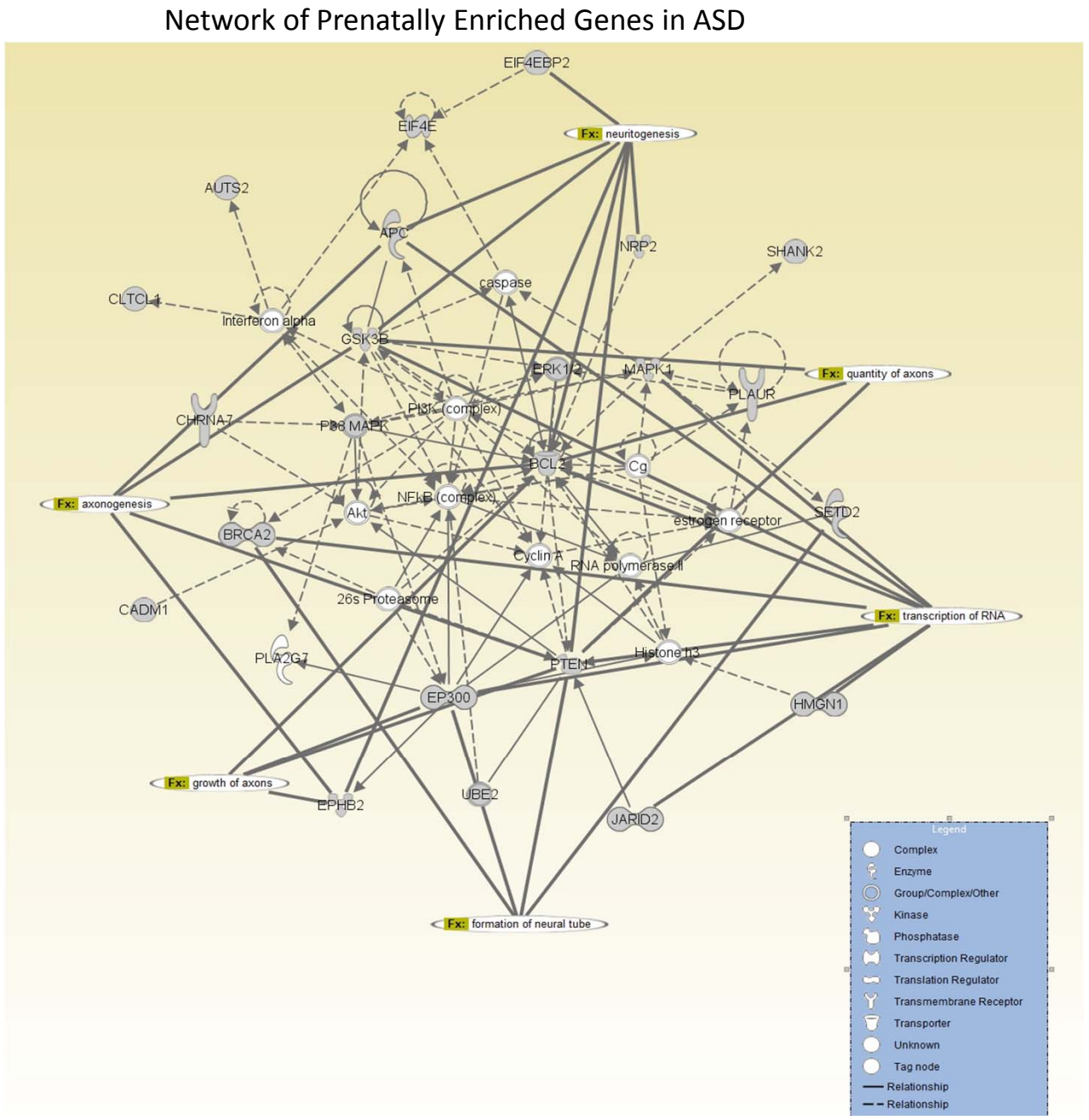
FAM57B	-0.64	-13.19	3.67E-30
ALDOA	0.32	5.01	1.08E-06
PPP4C	1.29	18.99	1.69E-49
TBX6	-0.78	-9.56	1.59E-18
YPEL3	-0.95	-16.01	1.35E-39
GDPD3	0.24	4.35	2.03E-05
MAPK3	-1.22	-20.77	2.91E-55
CORO1A	-0.97	-16.13	5.34E-40
BOLA2B	n/a		
BOLA2	n/a		
SLX1A	n/a		
SLX1B	n/a		
SULT1A4	n/a		
SULT1A3	n/a		

OTHER CNV LOCI ASSOCIATED WITH ASD

		PWARSN	0.67	6.57	3.21E-10
		PWAR5	0.69	5.76	2.60E-08
		IPW	-0.06	-0.64	5.21E-01
		PWAR1	-0.39	-3.59	4.03E-04
		PWAR4	0.05	0.81	4.20E-01
		UBE3A	0.71	6.01	7.11E-09
		ATP10A	-1.50	-10.73	3.76E-22
		MIR4715	n/a		
		GABRB3	0.21	2.36	1.90E-02
		GABRA5	-2.43	-27.43	1.71E-75
		GABRG3	-0.44	-4.38	1.81E-05
		OCA2	-0.54	-4.48	1.17E-05
		HERC2	-0.40	-5.52	8.70E-08
15q23-24.1	Del	THSD4	n/a		
		NR2E3	0.04	0.32	7.47E-01
		MYO9A	0.82	9.84	2.25E-19
		SENP8	n/a		
		GRAMD2	-1.04	-9.05	5.38E-17
		PKM	0.05	0.61	5.41E-01
		PARP6	0.69	12.73	1.21E-28
		CELF6	-0.05	-0.76	4.49E-01
		HEXA	n/a		
		HEXA-AS1	n/a		
		TMEM202	n/a		
		ARIH1	0.42	9.17	2.29E-17
		MIR630	n/a		
		GOLGA6B	n/a		
		HIGD2BP	-0.31	-5.05	9.00E-07
		BBS4	0.02	0.21	8.32E-01
		ADPGK	-0.36	-6.44	6.77E-10
		NEO1	1.35	15.02	2.86E-36
		HCN4	0.39	8.56	1.40E-15
		C15orf60	n/a		
		NPTN	-1.30	-23.00	2.56E-62
		CD276	-1.30	-23.00	2.56E-62
		C15orf59	-0.01	-0.11	9.09E-01
16q23.3	Del	OSGIN1	0.10	1.90	5.83E-02
		NECAB2	-2.30	-17.89	7.29E-46
		SLC38A8	-0.45	-2.82	5.17E-03
		MBTPS1	0.59	10.10	3.47E-20
18q22.1	Del	CCDC102B	-0.42	-2.23	0.026808138
20q13.33	Del/Dup	TCFL5	-1.11	-12.39	1.62E-27
		DIDO1	1.04	8.76	3.80E-16
		GID8 (C20orf11)	1.01	15.76	9.57E-39
		SLC17A9	-1.65	-10.49	2.08E-21
		BHLHE23	-0.16	-3.59	0.000408524
		HAR1B	n/a		
		HAR1A	n/a		
22q13.33	Del	SBF1	-0.41	-6.04	5.82E-09
		ADM2	0.43	9.65	8.34E-19
		MIOX	-0.52	-9.44	3.55E-18
		LMF2	-0.08	-1.97	0.050122583
		NCAPH2	0.82	9.84	2.25E-19
		SCO2	-0.57	-9.18	2.20E-17
		TYMP	-0.59	-4.52	9.87E-06
		ODF3B	-0.29	-5.44	1.30E-07
		KLHDC7B	-0.02	-0.32	0.749222246
		SYCE3	n/a		
		CPT1B	0.76	11.87	8.01E-26
		CHKB	0.60	9.55	1.66E-18
		MAPK8IP2	-1.04	-19.21	3.20E-50
		ARSA	n/a		
		SHANK3	0.69	7.85	1.42E-13

Note: Genes with a fetal effect greater than 0.5 are highlighted in red and genes with a fetal effect greater than 1 are shadea

Supplementary Figure 1a: Network of Prenatally Enriched Genes in ASD: Top scoring interaction network using the Ingenuity algorithm indicating direct (solid line) and indirect (dashed line) interactions , as well as directionality. Gray shading indicates genes/gene products in the prenatally enriched ASD gene set.



Supplementary Figure 1b: Network of Prenatally Enriched Genes in SCZ (GWAS, CNV, SNV): Top scoring interaction network using the Ingenuity algorithm indicating direct (solid line) and indirect (dashed line) interactions , as well as directionality. Gray shading indicates genes/gene products in the prenatally enriched SCZ gene sets.

Network of Prenatally Enriched Genes in SCZ (GWAS, CNV, SNV)