

Differentiation of Oligodendrocyte Precursors is Impaired in the Prefrontal Cortex in Schizophrenia

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Table S1. qRT-PCR validation of microarray data

Table S2. Genes differentially expressed in oligodendrocytes in schizophrenia

Figure S1. Virtual gels of schizophrenia and normal control RNA samples showing the distribution of transcript lengths

Table S1. qRT-PCR validation of microarray data

Gene	qRT-PCR fold-change	Microarray fold-change
KBTBD11	1.34	1.890427899
PDGFRA	2.4	1.935126853
NCOR2	-2.95	-1.639546104
RGS1	-1.75	-2.616661871
FMNL1	-0.85	-0.627660814
COPG	1.34	1.076879269

Table S2. Genes differentially expressed in oligodendrocytes in schizophrenia

Gene	Gene symbol	Log2 Fold-change	FDR-adjusted P-value
acyl-CoA thioesterase 13	ACOT13	-1.923781757	0.013948217
acyl-CoA synthetase medium-chain family member 2A /// acyl-CoA synthetase medium-chain family member 2B	ACSM2A /// ACSM2B	-2.318142913	0.001881298
adenosine deaminase, tRNA-specific 1	ADAT1	-2.127937977	0.001753324
alcohol dehydrogenase 5 (class III), chi polypeptide	ADH5	1.416107999	0.03070861
ArfGAP with FG repeats 1	AGFG1	1.818372885	0.030353885
apoptosis-inducing factor, mitochondrion-associated, 2	AIFM2	1.687136644	0.005838414
anaphase promoting complex subunit 11	ANAPC11	1.139599771	0.011246383
ANKHD1-EIF4EBP3 readthrough	ANKHD1- EIF4EBP3	-1.772222419	0.043405372
ankyrin repeat domain 31	ANKRD31	-2.180879178	0.004653257
ankyrin repeat domain 35	ANKRD35	-1.856730612	0.012822249
ankyrin repeat domain 43	ANKRD43	1.292208224	0.05246083
acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	ANP32E	-1.712570785	0.040523973
anthrax toxin receptor 1	ANTXR1	1.857388641	0.016866282
adenomatosis polyposis coli 2	APC2	1.532765684	0.002700679
adenomatosis polyposis coli 2	APC2	-1.350544989	0.009392973
Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12	1.673344998	0.002786736
ADP-ribosylation factor-like 5A	ARL5A	3.048233409	0.000926709
armadillo repeat containing, X-linked 5	ARMCX5	0.993605366	0.010118639
arylsulfatase F	ARSF	-2.096424556	0.006326775
activating transcription factor 7	ATF7	1.254399876	0.005990469
activating transcription factor 7	ATF7	-1.828178868	0.006691991
atlastin GTPase 1	ATL1	-2.2868529	0.00912651
ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit s (factor B)	ATP5S	1.465581557	0.010805261
ATXN8 opposite strand (non-protein coding)	ATXN8OS	-1.599741055	0.039995453
UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	B3GALT6	-1.246953337	0.00308456
biliverdin reductase B (flavin reductase (NADPH))	BLVRB	-1.911114976	0.007035225
bromodomain containing 2	BRD2	-1.828391724	0.00981633
BTB (POZ) domain containing 3	BTBD3	2.104878068	0.002766694
chromosome 12 open reading frame 49	C12orf49	1.644509939	0.010843147
chromosome 13 open reading frame 36	C13orf36	-2.197407835	0.007727271
chromosome 14 open reading frame 104	C14orf104	-2.580030551	0.001139132
chromosome 14 open reading frame 167	C14orf167	-2.216565578	0.01465683
chromosome 14 open reading frame 182	C14orf182	-1.576754981	0.006342624
chromosome 14 open reading frame 64	C14orf64	-1.426845924	0.05200809
chromosome 15 open reading frame 55	C15orf55	-1.618923323	0.003401138
chromosome 17 open reading frame 85	C17orf85	2.080026521	0.01122615
chromosome 1 open reading frame 116	C1orf116	-1.518555301	0.029833869
chromosome 1 open reading frame 180	C1orf180	-2.646337646	0.004333549
chromosome 1 open reading frame 204	C1orf204	1.642594136	0.003622397
chromosome 20 open reading frame 194	C20orf194	1.431878349	0.021168344
C2 calcium-dependent domain containing 2	C2CD2	1.786659691	0.004629782
C2CD2-like	C2CD2L	-1.889818844	0.003984459

chromosome 2 open reading frame 24	C2orf24	0.959682403	0.032456356
chromosome 3 open reading frame 67	C3orf67	-2.02113273	0.00136972
chromosome 4 open reading frame 3	C4orf3	1.991191166	0.009076333
chromosome 6 open reading frame 145	C6orf145	1.186187291	0.012049584
chromosome 6 open reading frame 165	C6orf165	-1.730078655	0.013236394
chromosome 6 open reading frame 218	C6orf218	-2.106166514	0.037935702
calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	CACNA1A	-1.485106659	0.016666298
Calcium channel, voltage-dependent, R type, alpha 1E subunit	CACNA1E	-2.025252332	0.011529326
calcium channel, voltage-dependent, L type, alpha 1F subunit	CACNA1F	-1.112030437	0.043605033
calcium channel, voltage-dependent, beta 1 subunit	CACNB1	-1.165539738	0.044181041
cullin-associated and neddylation-dissociated 1	CAND1	2.124976855	0.009482591
caspase recruitment domain family, member 14	CARD14	-2.434167054	0.001687491
collagen and calcium binding EGF domains 1	CCBE1	1.880910995	0.003523099
coiled-coil domain containing 13	CCDC13	-1.741044105	0.003021281
chemokine (C-C motif) ligand 24	CCL24	-1.260708936	0.039240951
CD209 molecule	CD209	-1.243701771	0.049122028
CD300a molecule	CD300A	-1.411924812	0.014775556
CD47 molecule	CD47	2.169314804	0.002629511
CD96 molecule	CD96	-2.197156685	0.003825296
CDC14 cell division cycle 14 homolog B (<i>S. cerevisiae</i>)	CDC14B	0.956431649	0.042575032
CDC42 binding protein kinase alpha (DMPK-like)	CDC42BPA	0.881931721	0.011442377
CCAAT/enhancer binding protein (C/EBP), beta	CEBPB	2.186859818	0.000352872
CUGBP, Elav-like family member 1	CELF1	2.106521086	0.024549037
Centrosomal protein 250kDa	CEP250	-2.011660385	0.001282057
centrosomal protein 350kDa	CEP350	2.197796233	0.018931652
centrosomal protein 57kDa	CEP57	1.563795005	0.012840618
centrosomal protein 70kDa	CEP70	1.452220986	0.03569254
centrosomal protein 97kDa	CEP97	1.812389537	0.005486699
Choline/ethanolamine phosphotransferase 1	CEPT1	-1.902271508	0.004661886
choline/ethanolamine phosphotransferase 1	CEPT1	1.774133124	0.005882454
chromodomain helicase DNA binding protein 9	CHD9	1.724040251	0.020606464
choline dehydrogenase	CHDH	2.046569322	0.026948909
cirrhosis, autosomal recessive 1A (cirhin)	CIRH1A	1.894157981	0.007548874
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	CITED2	-1.727538276	0.005048786
claudin 4	CLDN4	-1.639753796	0.003843161
chloride intracellular channel 1	CLIC1	2.306583945	0.007073497
chloride intracellular channel 4	CLIC4	-1.996529969	0.000651789
ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	CLN8	2.11828994	0.004536997
CKLF-like MARVEL transmembrane domain containing 3	CMTM3	-1.316738011	0.003969005
coatamer protein complex, subunit gamma	COPG	1.076879269	0.019429116
coenzyme Q10 homolog A (<i>S. cerevisiae</i>)	COQ10A	-1.841285568	0.04797491
coenzyme Q10 homolog B (<i>S. cerevisiae</i>)	COQ10B	2.081869701	0.008416919
cystatin A (stefin A)	CSTA	-1.453959731	0.004759876
chromosome X open reading frame 36	CXorf36	-2.034909497	0.013323425
cylindromatosis (turban tumor syndrome)	CYLD	1.95628538	0.012577542

cytochrome P450, family 4, subfamily F, polypeptide 3	CYP4F3	-2.25856678	0.00114959
cytochrome P450, family 4, subfamily V, polypeptide 2	CYP4V2	1.518438108	0.002369549
disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	DAB2	2.194042899	0.003024329
DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	DCUN1D4	1.037701778	0.048104507
DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	DDX25	1.614596551	0.052173581
DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	DDX3X	1.278488886	0.045980227
DiGeorge syndrome critical region gene 8	DGCR8	1.786224142	0.020936335
diaphanous homolog 1 (Drosophila)	DIAPH1	1.729895488	0.001081654
dickkopf homolog 4 (Xenopus laevis)	DKK4	-0.980876942	0.036756477
doublesex and mab-3 related transcription factor 1	DMRT1	-1.94201831	0.021276041
dynein, axonemal, heavy chain 11	DNAH11	-1.828610643	0.008225654
DnaJ (Hsp40) homolog, subfamily A, member 3	DNAJA3	2.160619782	0.013382921
dopey family member 2	DOPEY2	-1.707725754	0.002577427
deltex homolog 1 (Drosophila)	DTX1	2.006417914	0.005017446
deltex homolog 1 (Drosophila)	DTX1	1.988540476	0.007248929
dual specificity phosphatase 8	DUSP8	2.391284168	0.008644546
EGF-like repeats and discoidin I-like domains 3	EDIL3	-1.339551648	0.01297349
ephrin-A1	EFNA1	1.794080612	0.003081585
eukaryotic translation initiation factor 1A, Y-linked	EIF1AY	1.727918267	0.004421071
ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	ELOVL6	1.753699611	0.006632298
echinoderm microtubule associated protein like 1	EML1	1.433903504	0.035194824
endothelial PAS domain protein 1	EPAS1	1.619645628	0.013264682
ER lipid raft associated 1	ERLIN1	2.147754089	0.001232957
family with sequence similarity 108, member B1	FAM108B1	2.157371454	0.007125738
family with sequence similarity 160, member B1	FAM160B1	-2.46542646	0.00356508
family with sequence similarity 173, member A	FAM173A	-1.613686189	0.01478757
family with sequence similarity 200, member B	FAM200B	1.898163657	0.009664746
family with sequence similarity 21, member A ///	FAM21A ///		
family with sequence similarity 21, member B ///	FAM21B ///		
family with sequence similarity 21, member C ///	FAM21C ///	1.521608972	0.028963187
family with sequence similarity 21, member D	FAM21D		
family with sequence similarity 3, member A	FAM3A	-1.178360929	0.025388433
family with sequence similarity 55, member A	FAM55A	-2.441965168	0.003988946
family with sequence similarity 57, member A	FAM57A	2.473769404	0.012691819
Fanconi anemia, complementation group G	FANCG	2.363153262	0.004160794
F-box protein 33	FBXO33	2.239890789	0.052856686
fibroblast growth factor receptor 1	FGFR1	-2.456370853	0.003149392
fibroblast growth factor receptor 1	FGFR1	0.614033972	0.036231615
forkhead-associated (FHA) phosphopeptide binding domain 1	FHAD1	-1.872051293	0.004627825
FLT3-interacting zinc finger 1	FIZ1	-0.967210548	0.046141277
Friend leukemia virus integration 1	FLI1	-2.148419771	0.000412232
hypothetical LOC399876	FLJ13439	-1.511931678	0.020468356

hypothetical LOC402483 /// hypothetical LOC399744 /// hypothetical LOC401357 /// hypothetical protein LOC729021 /// hypothetical LOC729218	FLJ45340 /// LOC399744 /// LOC401357 /// LOC729021 /// LOC729218		
formin-like 1	FMNL1	-0.627660814	0.05156197
Fibronectin type III domain containing 3B	FNDC3B	-1.8868294	0.028632616
folliculin-like 1	FSTL1	2.274981955	0.002361778
GTPase activating protein (SH3 domain) binding protein 2	G3BP2	-1.310946168	0.046378331
GRB2-associated binding protein 3	GAB3	-2.41131328	0.00016526
GATA binding protein 2	GATA2	2.750130454	0.000400838
glucosidase, beta (bile acid) 2	GBA2	-1.437395846	0.027828361
golgi-associated, gamma adaptin ear containing, ARF binding protein 2	GGA2	1.808649213	0.024783647
gamma-glutamyl hydrolase (conjugase, folic polyglutamate hydrolase)	GGH	-2.273649336	0.013273696
geranylgeranyl diphosphate synthase 1	GGPS1	-1.824200775	0.011365199
gamma-glutamyltransferase 1	GGT1	-0.870762544	0.012985393
gap junction protein, delta 4, 40.1kDa	GJD4	-1.704339971	0.003349209
glucuronic acid epimerase	GLCE	1.914032981	0.004869985
glycerate kinase	GLYCK	-1.216229064	0.004889698
guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	GNA11	1.32084553	0.007965659
guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	GNA11	-1.616161704	0.043343596
guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	GNAI1	1.603934746	0.049408905
G protein-coupled receptor 68	GPR68	-1.667638573	0.002932456
G protein regulated inducer of neurite outgrowth 2	GPRIN2	-1.609995102	0.017907965
glycogen synthase kinase 3 beta	GSK3B	-1.741191799	0.022828576
Glutathione S-transferase theta 1	GSTT1	1.833831727	0.018918938
general transcription factor Iii	GTF2I	-1.435114964	0.030811119
hepatitis B virus x interacting protein	HBXIP	1.713669957	0.023254532
holocytochrome c synthase	HCCS	-1.503130209	0.026637588
HEAT repeat containing 1	HEATR1	-2.139213887	0.036669667
helicase with zinc finger	HELZ	1.351594982	0.036783059
homogentisate 1,2-dioxygenase	HGD	-2.256040109	0.00153587
histone cluster 1, H1d	HIST1H1D	-1.212445997	0.032910387
histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	HIST2H2AA3 /// HIST2H2AA4	-1.63142419	0.002243966
heterogeneous nuclear ribonucleoprotein C (C1/C2)	HNRNPC	-1.75067978	0.006093378
heterogeneous nuclear ribonucleoprotein U-like 1	HNRNPUL1	1.05896344	0.02315213
heterogeneous nuclear ribonucleoprotein D-like	HNRPDL	2.317994826	0.007426184
HORMA domain containing 2	HORMAD2	-2.085323773	0.006629671
homeobox D3	HOXD3	1.957794903	0.016845489
heterochromatin protein 1, binding protein 3	HP1BP3	-2.228269178	0.035996687
Hermansky-Pudlak syndrome 4	HPS4	-0.891085868	0.006721789
heparan sulfate 6-O-sulfotransferase 3	HS6ST3	-1.338471959	0.048998052
hydroxysteroid (17-beta) dehydrogenase 7 /// pseudogene 2	HSD17B7 /// HSD17B7P2	-1.946858523	0.012463223

isopentenyl-diphosphate delta isomerase 2	IDI2	-1.60443483	0.013943988
immediate early response 3	IER3	2.353255533	0.008436659
insulin-like growth factor binding protein-like 1	IGFBPL1	-1.818456087	0.012504559
immunoglobulin heavy constant mu	IGHM	-1.954107237	0.003821931
Immunoglobulin kappa constant	IGKC	-1.411167269	0.014870297
interleukin 17B	IL17B	1.19212667	0.007179999
Interleukin 4 receptor	IL4R	-1.82702191	0.028208449
inositol polyphosphate-4-phosphatase, type I, 107kDa	INPP4A	1.210449418	0.052922957
integrator complex subunit 5	INTS5	-1.827004242	0.015858591
integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	ITGB3	-2.648153153	0.000393075
integrin, beta-like 1 (with EGF-like repeat domains)	ITGBL1	-1.857638443	0.016417382
inter-alpha (globulin) inhibitor H5	ITIH5	-2.415309492	0.003323432
integral membrane protein 2C	ITM2C	0.751395169	0.013336292
jumonji domain containing 7	JMJD7	-1.679232343	0.014111175
jerky homolog (mouse)	JRK	-1.093723721	0.00471313
jun proto-oncogene	JUN	-1.451839093	0.008039344
Katanin p80 (WD repeat containing) subunit B 1	KATNB1	-1.488730163	0.015561555
kelch repeat and BTB (POZ) domain containing 11	KBTBD11	1.890427899	0.0062759
potassium channel modulatory factor 1	KCMF1	1.868923542	0.003861465
potassium large conductance calcium-activated channel, subfamily M, alpha member 1	KCNMA1	2.703413947	0.014349863
potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1	KCNS1	-1.793283088	0.013701313
KIAA0182	KIAA0182	1.654024252	0.033435203
KIAA0368	KIAA0368	1.873343654	0.003147379
KIAA0664-like 3	KIAA0664L3	1.446266386	0.010567733
KIAA1267	KIAA1267	2.026138726	0.018899796
KIAA1267 /// hypothetical LOC100294337	KIAA1267 /// LOC100294337	-1.71483368	0.008153374
kelch domain containing 1	KLHDC1	-1.700084214	0.008304861
kelch domain containing 10	KLHDC10	-2.437749974	0.007263004
kelch-like 36 (Drosophila)	KLHL36	1.431108118	0.054397597
kelch-like 4 (Drosophila)	KLHL4	-1.59499603	0.003949899
KRR1, small subunit (SSU) processome component, homolog (yeast)	KRR1	2.04206037	0.022351245
keratin 79	KRT79	-1.166347239	0.006417514
keratin 80	KRT80	-1.702817956	0.003413384
laminin, alpha 2	LAMA2	-1.747737586	0.000394995
leucyl-tRNA synthetase 2, mitochondrial	LARS2	1.724088975	0.005656377
late cornified envelope 3D	LCE3D	-1.031405327	0.007479417
leukocyte receptor cluster (LRC) member 1	LENG1	-1.267296623	0.002824358
LIM homeobox 9	LHX9	-1.6854513	0.005375823
Lectin, mannose-binding 2	LMAN2	-1.560180222	0.023576841
leishmanolysin-like (metallopeptidase M8 family)	LMLN	2.232009446	0.000690385
hypothetical LOC100128175	LOC100128175	1.939249051	0.00358423
succinate dehydrogenase cytochrome b560 subunit, mitochondrial-like /// succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	LOC100128302 /// SDHC	-1.478009081	0.036627459
hypothetical LOC100130357	LOC100130357	1.595094019	0.011126192

hypothetical LOC100130581	LOC100130581	-2.365367833	0.000818251
Hypothetical protein LOC100131180	LOC100131180	-1.983756237	0.008163399
Hypothetical LOC100132147	LOC100132147	-1.260181915	0.004977375
hypothetical LOC100132354	LOC100132354	-1.907390258	0.014206018
hypothetical LOC100133039	LOC100133039	1.796293152	0.003420414
hypothetical LOC100169752	LOC100169752	-0.912502803	0.007533527
hypothetical LOC100272216	LOC100272216	2.324446381	0.003066251
hypothetical LOC100272217	LOC100272217	2.144488186	0.007103334
Similar to hCG2024922	LOC100287911	-1.477312154	0.004350168
hypothetical LOC100288271	LOC100288271	-2.281475156	0.001105129
Hypothetical protein LOC100289070	LOC100289070	-1.987079072	0.002179802
hypothetical LOC100506556	LOC100506556	2.289974339	0.004759256
hypothetical LOC100506882	LOC100506882	-1.609437163	0.003297271
hypothetical LOC100506941	LOC100506941	-1.369257211	0.012868409
hypothetical LOC100506992	LOC100506992	-2.439090254	0.000551744
hypothetical LOC100506995	LOC100506995	-2.4781647	0.008766246
hypothetical LOC100507007	LOC100507007	-1.597185823	0.039153094
hypothetical LOC100507164	LOC100507164	-2.470782897	0.001249143
hypothetical LOC100507168	LOC100507168	-1.482188795	0.004422307
hypothetical LOC100507466	LOC100507466	-1.544526751	0.040244612
hypothetical LOC115110	LOC115110	-1.675226166	0.022881609
hypothetical protein LOC257152	LOC257152	-1.17546414	0.01611722
hypothetical LOC282997	LOC282997	-1.395415835	0.023088295
hypothetical protein LOC283270	LOC283270	1.556767493	0.022604268
hypothetical LOC283335	LOC283335	-1.421136337	0.021224888
hypothetical LOC286114	LOC286114	-1.57947941	0.01990937
hypothetical LOC344595	LOC344595	-2.459972236	0.001693686
hypothetical LOC388796 /// small nucleolar RNA, H/ACA box 71B	LOC388796 /// SNORA71B	-1.283518389	0.046858466
hypothetical LOC401588	LOC401588	-1.701978343	0.025218924
RAB guanine nucleotide exchange factor (GEF) 1 pseudogene	LOC493754	-1.135634625	0.006088326
Hypothetical protein LOC574538	LOC574538	-3.222678129	0.001968485
hypothetical LOC644450	LOC644450	-1.584892689	0.006921041
Hypothetical LOC644620	LOC644620	-1.463319191	0.042818505
p21 protein (Cdc42/Rac)-activated kinase 2 pseudogene	LOC646214	-2.020761941	0.015183481
hypothetical LOC729852	LOC729852	1.965818756	0.01190498
lysophosphatidic acid receptor 4	LPAR4	-1.249572208	0.007691133
leucine-rich PPR-motif containing	LRPPRC	2.575690107	0.028402906
leucine rich repeat containing 27	LRRC27	-1.786878348	7.24E-05
leucine rich repeat containing 8 family, member A	LRRC8A	1.908042011	0.008841949
leucine zipper protein 1	LUZP1	-2.141739914	0.005224197
LYR motif containing 5	LYRM5	1.965775026	0.016019259
v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	MAFG	1.593979978	0.053671471
mastermind-like 2 (Drosophila)	MAML2	1.77560605	0.012438685
mitogen-activated protein kinase kinase kinase 4	MAP4K4	1.916869136	0.004468281
MAP7 domain containing 2	MAP7D2	-1.86261178	0.00956376
MAP7 domain containing 3	MAP7D3	-1.206717182	0.035013756
mitogen-activated protein kinase 8	MAPK8	-1.818112335	0.014327518
mitogen-activated protein kinase 8 interacting protein 1	MAPK8IP1	-1.362082782	0.003772316

membrane-associated ring finger (C3HC4) 10	MARCH10	-1.801576406	8.30E-05
MCF.2 cell line derived transforming sequence	MCF2	-2.46548925	0.005860416
Mdm1 nuclear protein homolog (mouse)	MDM1	2.265661348	0.009991643
Mediator complex subunit 13	MED13	-1.888003362	0.016760458
mediator complex subunit 28	MED28	2.799437607	0.000430196
mediator complex subunit 28	MED28	-1.517478215	0.018709715
methyltransferase 11 domain containing 1	METT11D1	2.387063123	0.001106245
microfibrillar-associated protein 3-like	MFAP3L	2.212921696	0.005261276
major facilitator superfamily domain containing 4	MFSD4	-1.766079688	0.002277426
MAP kinase interacting serine/threonine kinase 2	MKNK2	1.757862073	0.003566982
MAP kinase interacting serine/threonine kinase 2	MKNK2	1.23985052	0.032164014
myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	MLL	-1.370011059	0.014429638
major histocompatibility complex, class I-related	MR1	-0.864714938	0.047872728
mitochondrial ribosomal protein L2	MRPL2	-2.268659943	0.000562097
mitochondrial ribosomal protein L9	MRPL9	-1.473411436	0.012450867
msh homeobox 2	MSX2	-1.654307082	0.018751661
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	MTHFD2L	-1.766127304	0.005224676
mitochondrial translational release factor 1	MTRF1	-3.40886833	1.80E-07
metastasis suppressor 1	MTSS1	1.763366395	0.016109176
mucin 5AC, oligomeric mucus/gel-forming	MUC5AC	1.252904056	0.026563795
myeloid-associated differentiation marker	MYADM	-2.112916996	0.00052162
myosin, heavy chain 8, skeletal muscle, perinatal	MYH8	-2.226120612	0.000972652
myoferlin	MYOF	-1.537121166	0.033532061
Myb-like, SWIRM and MPN domains 1	MYSM1	-1.387142448	0.023281344
nuclear cap binding protein subunit 1, 80kDa	NCBP1	-0.955662507	0.001833535
neutral cholesterol ester hydrolase 1	NCEH1	-1.607792447	0.027810923
nuclear receptor corepressor 1	NCOR1	1.430887271	0.005028979
nuclear receptor corepressor 2	NCOR2	-1.639546104	0.00820626
non-protein coding RNA 102	NCRNA00102	-2.005607149	0.011523766
non-protein coding RNA 107	NCRNA00107	1.789190327	0.050566524
non-protein coding RNA 188	NCRNA00188	-1.648794425	0.018391145
NIMA (never in mitosis gene a)- related kinase 11	NEK11	-2.454979305	0.007789592
NEL-like 1 (chicken)	NELL1	-2.282135473	0.003463382
nuclear factor I/A	NFIA	-2.283436204	0.002212056
nuclear factor I/A	NFIA	1.808503755	0.003994386
nescient helix loop helix 2	NHLH2	2.325017403	0.002792833
nescient helix loop helix 2	NHLH2	1.739648666	0.011327974
ninein-like	NINL	1.573417911	0.029398289
NLR family, pyrin domain containing 12	NLRP12	-1.461181341	0.008922641
NMD3 homolog (S. cerevisiae)	NMD3	-2.503440961	0.005436676
notch 2	NOTCH2	-1.307654818	0.022620206
nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NR3C1	1.526015261	0.042090167
5'-nucleotidase domain containing 2	NT5DC2	-1.745628556	0.010477016
5',3'-nucleotidase, mitochondrial	NT5M	-1.663663467	0.013263594
nuclear VCP-like	NVL	3.329494152	0.00078915
oral-facial-digital syndrome 1	OFD1	2.617818121	0.002536412
osteoglycin	OGN	-2.107570331	0.001074635
olfactory receptor, family 1, subfamily E, member 1	OR1E1	-1.730346585	0.020459938
olfactory receptor, family 2, subfamily L, member 2	OR2L2	-1.515354999	0.01179742

olfactory receptor, family 2, subfamily S, member 2	OR2S2	-1.566869984	0.028254874
olfactory receptor, family 5, subfamily V, member 1	OR5V1	-1.937567047	0.029985648
olfactory receptor, family 9, subfamily A, member 1 pseudogene	OR9A1P	-1.310905959	0.035179354
ORAI calcium release-activated calcium modulator 2	ORAI2	-2.136702172	0.000821389
orosomuroid 1 /// orosomuroid 2	ORM1 /// ORM2	-1.160081008	0.001659592
oxidation resistance 1	OXR1	-2.098818364	0.004047149
platelet-activating factor acetylhydrolase 2, 40kDa	PAFAH2	-0.959191788	0.011010042
Palladin, cytoskeletal associated protein	PALLD	-1.200683924	0.017301233
parvin, alpha	PARVA	-1.60063743	0.046601279
PRKC, apoptosis, WT1, regulator	PAWR	2.109517407	0.00449821
phosphodiesterase 7A	PDE7A	0.972354038	0.031180191
platelet-derived growth factor receptor, alpha polypeptide	PDGFRA	1.935126853	0.028282159
PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	PDS5A	1.754617084	0.007769419
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	PFKFB2	2.370167303	0.000951935
progesterone receptor membrane component 2	PGRMC2	1.338443698	0.024111438
phosphorylated adaptor for RNA export	PHAX	-1.35095859	0.005338234
PHD finger protein 15	PHF15	2.421430989	0.002725952
PHD finger protein 15	PHF15	2.901601455	0.019727518
PHD finger protein 17	PHF17	1.674119672	0.006757104
PHD finger protein 8	PHF8	1.596392129	0.028936903
phytanoyl-CoA 2-hydroxylase interacting protein	PHYHIP	-1.119499206	0.000817755
phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	1.681566587	0.006922502
phospholipase A2, group XIIA	PLA2G12A	2.803929806	0.006205703
phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	PLA2G7	-1.196056764	0.054031845
polo-like kinase 1 substrate 1	PLK1S1	1.584696782	0.029056846
polo-like kinase 3	PLK3	-1.424543388	0.011278168
polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	POLR3A	1.642209335	0.025799614
hypothetical LOC100128046	PP13439	-2.064239132	0.006501181
protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	PPFIA1	1.809825953	0.001718653
peptidylprolyl isomerase G (cyclophilin G)	PPIG	-1.699438084	0.020634328
protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1B	PPM1B	0.590369891	0.012272291
protein phosphatase 1, regulatory (inhibitor) subunit 3E	PPP1R3E	2.977047587	0.002579784
peroxisomal proliferator-activated receptor A interacting complex 285	PRIC285	-0.875311281	0.039119959
protein kinase, cAMP-dependent, regulatory, type II, alpha	PRKAR2A	2.131309864	0.024441839
protein kinase D1	PRKD1	1.659810448	0.039854808
protein kinase, Y-linked	PRKY	-1.121699717	0.006366022
prolactin receptor	PRLR	-1.613036481	0.006048558
protamine 3	PRM3	-1.638639224	0.020266155

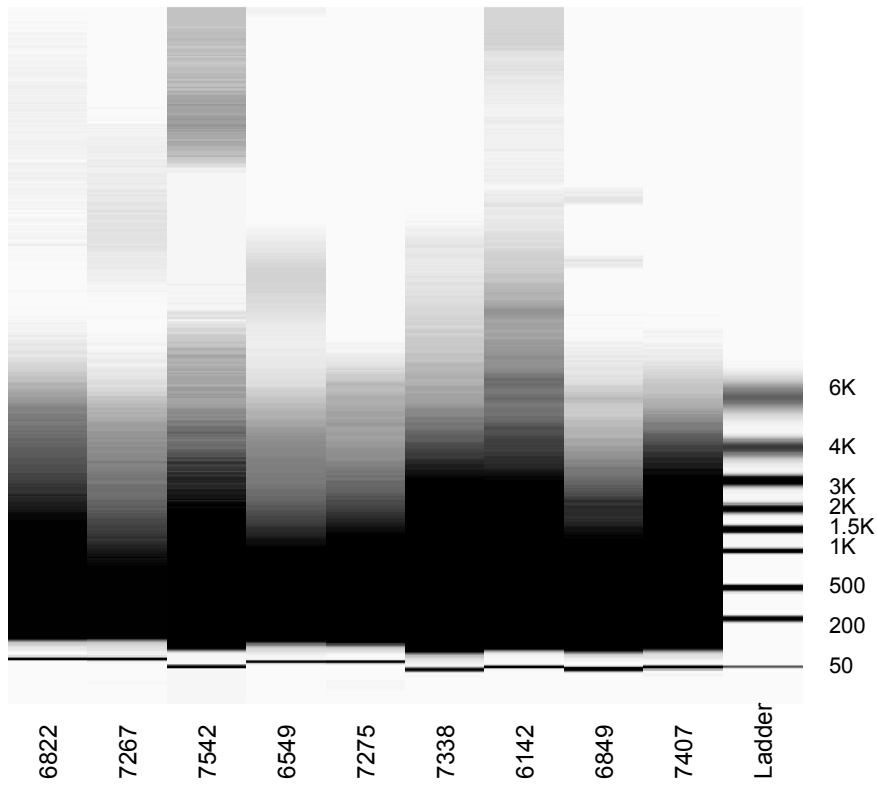
hypothetical protein PRO2949	PRO2949	-1.362306203	0.003312296
PSMC3 interacting protein	PSMC3IP	1.330124293	0.048196655
polypyrimidine tract binding protein 1	PTBP1	-1.729592465	0.004238948
prostaglandin reductase 2	PTGR2	-2.269827623	0.008459491
parathyroid hormone 2	PTH2	-1.00977801	0.022902417
parathyroid hormone-like hormone	PTHLH	-1.694821963	0.02052041
protein tyrosine phosphatase domain containing 1	PTPDC1	1.321365734	0.032145391
Protein tyrosine phosphatase, non-receptor type 9	PTPN9	-2.222593714	0.000533207
pituitary tumor-transforming 1	PTTG1	1.997121745	0.01379026
pumilio homolog 1 (Drosophila)	PUM1	0.961668058	0.006127485
poliovirus receptor	PVR	1.199197874	0.015909269
Pvt1 oncogene (non-protein coding)	PVT1	-2.139905823	0.009610305
RAB30, member RAS oncogene family	RAB30	1.028817748	0.041808333
RAB5C, member RAS oncogene family	RAB5C	-2.130888993	0.002020749
RAD23 homolog A (S. cerevisiae)	RAD23A	-1.405791744	0.006609832
Ral GEF with PH domain and SH3 binding motif 1	RALGPS1	1.169141698	0.054428345
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	RAPH1	-1.342633909	0.046658343
Ras association (RalGDS/AF-6) domain family member 6	RASSF6	-1.956186111	0.000867459
Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	RASSF8	2.265668336	0.00280088
RNA binding motif protein 23	RBM23	1.752427041	0.008836646
RNA binding motif protein 33	RBM33	1.568155676	0.013445794
retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	RDH14	1.314123834	0.037713283
replication factor C (activator 1) 5, 36.5kDa	RFC5	-2.589080514	5.67E-05
regulator of G-protein signaling 1	RGS1	-2.616661871	0.00186756
Rho-related BTB domain containing 2	RHOBTB2	-1.346290398	0.052936158
ring finger protein 126	RNF126	-1.301130026	0.011350291
ring finger protein 213	RNF213	1.815452219	0.013728683
Ring finger protein 31	RNF31	-1.062695451	0.006962925
RNA (guanine-7-) methyltransferase	RNMT	-2.008185784	0.006317329
retinitis pigmentosa GTPase regulator	RPGR	-1.735013639	0.027329674
ribosomal RNA processing 15 homolog (S. cerevisiae)	RRP15	2.014960143	0.003409456
runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	RUNX1T1	-2.398388144	0.000580142
sarcoma antigen 1	SAGE1	-2.367149701	0.001445319
SAR1 homolog A (S. cerevisiae)	SAR1A	1.541800042	0.017590116
sodium channel, voltage-gated, type XI, alpha subunit	SCN11A	-2.361925576	0.004164986
Sec23 homolog B (S. cerevisiae)	SEC23B	1.943209786	0.010253037
sel-1 suppressor of lin-12-like 3 (C. elegans)	SEL1L3	-1.9497525	0.002275016
SET domain, bifurcated 2	SETDB2	-2.538368061	0.001979599
senataxin	SETX	1.460557692	0.003275429
senataxin	SETX	1.725538535	0.030492283
SHC (Src homology 2 domain containing) transforming protein 3	SHC3	-1.379431704	0.041822744
seven in absentia homolog 1 (Drosophila)	SIAH1	2.425511012	8.98E-05
SIN3 homolog B, transcription regulator (yeast)	SIN3B	-2.377227209	0.003652938

spindle and kinetochore associated complex subunit 2	SKA2	-2.601670966	0.00568977
solute carrier family 25 (mitochondrial carrier, brain), member 14	SLC25A14	2.472471119	0.000576853
solute carrier family 26 (sulfate transporter), member 2	SLC26A2	2.074382164	0.003145485
solute carrier family 2 (facilitated glucose transporter), member 1	SLC2A1	1.544108206	0.025454861
solute carrier family 35, member A4	SLC35A4	-1.504601415	0.01272245
solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	SLC35D1	-2.067783059	0.006885697
solute carrier family 9 (sodium/hydrogen exchanger), member 5	SLC9A5	-1.253165048	0.006329982
SMAD family member 2	SMAD2	-1.581149219	0.038286276
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	SMARCA1	-1.297240048	0.035431733
structural maintenance of chromosomes 2	SMC2	2.500826277	4.29E-05
SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	SNF8	2.002783057	0.000605843
small nucleolar RNA host gene 10 (non-protein coding)	SNHG10	1.427835861	0.041493594
small nuclear ribonucleoprotein 27kDa (U4/U6.U5)	SNRNP27	1.940798481	0.003704401
SNW domain containing 1	SNW1	1.899918696	0.034664783
sorting nexin 2	SNX2	1.957270771	0.022093178
sorting nexin 22	SNX22	-1.325975143	0.010888669
sorbin and SH3 domain containing 1	SORBS1	3.1656514	4.77E-05
SRY (sex determining region Y)-box 6	SOX6	-1.789593325	0.029901042
sperm associated antigen 5	SPAG5	1.219118635	0.019027182
spermatogenesis associated 19	SPATA19	1.659772347	0.004770328
spermatogenesis associated, serine-rich 2	SPATS2	-1.363641953	0.008702852
serine peptidase inhibitor, Kazal type 4	SPINK4	-1.79437552	0.000591941
speckle-type POZ protein-like	SPOPL	1.206078851	0.022952804
Snf2-related CREBBP activator protein	SRCAP	-0.809964237	0.050307509
slingshot homolog 1 (Drosophila)	SSH1	-1.819686613	0.01857738
signal sequence receptor, gamma (translocon-associated protein gamma)	SSR3	0.97423878	0.037411746
synovial sarcoma, X breakpoint 2 /// synovial sarcoma, X breakpoint 2B	SSX2 /// SSX2B	-1.274417434	0.019863504
synovial sarcoma, X breakpoint 2 interacting protein	SSX2IP	1.913359595	0.012698243
suppression of tumorigenicity 7	ST7	-2.090676315	0.007522863
staufer, RNA binding protein, homolog 2 (Drosophila)	STAU2	-2.140417604	0.003351642
serine/threonine kinase 36	STK36	-1.14906968	0.014579003
syntaxin 6	STX6	1.927749666	0.008782402
suppressor of Ty 16 homolog (S. cerevisiae)	SUPT16H	-1.762552104	0.037005058
synapsin I	SYN1	-2.190196166	0.003017236
SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	SYS1	-1.775295342	0.006454992
synaptotagmin XV	SYT15	-1.456271488	0.009024538

TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	TAF4B	-1.325459859	0.043284082
TANK-binding kinase 1	TBK1	-1.168493645	0.005432759
transcription elongation factor A (SII) N-terminal and central domain containing	TCEANC	-1.140290571	0.031431543
transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	TCEB1	1.395875118	0.01578964
transcription factor 12	TCF12	1.986270721	0.018625183
testis expressed 13B	TEX13B	-1.248710619	0.005466337
transcription factor AP-4 (activating enhancer binding protein 4)	TFAP4	1.776675814	0.001677112
transcription factor Dp-1	TFDP1	-1.66751551	0.030664227
thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	THRB	-1.426761142	0.003768353
T cell immunoreceptor with Ig and ITIM domains	TIGIT	-1.036691774	0.053030679
translocase of inner mitochondrial membrane 8 homolog A (yeast)	TIMM8A	-1.955344462	0.00527223
transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	TLE4	-2.006332764	0.01961207
transmembrane protein 106C	TMEM106C	-1.43649337	0.014980129
transmembrane protein 18	TMEM18	1.753258875	0.001085338
transmembrane protein 198	TMEM198	1.637449217	0.008597806
transmembrane protein 218	TMEM218	1.965034085	0.004134009
transmembrane protein 64	TMEM64	-1.402751087	0.007482381
TMEM9 domain family, member B	TMEM9B	1.585927384	0.004162305
thioredoxin-related transmembrane protein 4	TMX4	1.92730926	0.002286309
transition protein 2 (during histone to protamine replacement)	TNP2	-1.615523007	0.005686633
T cell receptor alpha constant /// T cell receptor alpha joining 17 /// T cell receptor alpha variable 20	TRAC /// TRAJ17 /// TRAV20	-2.65031686	0.002715363
TNF receptor-associated factor 3	TRAF3	-1.948884888	0.004402883
TRAF3 interacting protein 3	TRAF3IP3	-1.970346371	0.000482277
tripartite motif-containing 2	TRIM2	-1.982412312	0.005226112
tripartite motif-containing 46	TRIM46	1.294763067	0.01131572
tripartite motif-containing 9	TRIM9	-1.587399106	0.022467195
TruB pseudouridine (psi) synthase homolog 2 (E. coli)	TRUB2	-1.800946253	0.00215984
tetraspanin 31	TSPAN31	2.975798389	0.000699631
tetratricopeptide repeat domain 31	TTC31	1.725118081	0.001047
tocopherol (alpha) transfer protein-like	TTPAL	1.662041747	0.022951187
testis-specific transcript, Y-linked 13 (non-protein coding)	TTYT13	-1.480595973	0.001848697
tubulin, gamma 2	TUBG2	1.966918829	0.026862669
Tu translation elongation factor, mitochondrial	TUFM	-1.691825249	0.007882064
thymidine phosphorylase	TYMP	-1.595133069	0.013812509
ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	UBE2E2	2.704964988	0.004526747
ubiquitin-conjugating enzyme E2N-like	UBE2NL	-2.660371675	0.000946591
U-box domain containing 5	UBOX5	1.888416492	0.019581453
UBX domain protein 8	UBXN8	-2.329553217	0.001732837
UPF3 regulator of nonsense transcripts homolog B (yeast)	UPF3B	2.110698011	0.030582292

ubiquitin specific peptidase 19	USP19	1.651380324	0.043357642
ubiquitin specific peptidase 2	USP2	-2.213688616	0.000273064
ubiquitin specific peptidase 33	USP33	1.524696202	0.033510123
ubiquitin specific peptidase 34	USP34	-2.01951521	0.008375098
pre-B lymphocyte 1	VPREB1	-1.67241459	0.024473453
vacuolar protein sorting 39 homolog (S. cerevisiae)	VPS39	1.366990205	0.006636035
vacuolar protein sorting 39 homolog (S. cerevisiae)	VPS39	1.364303996	0.011756772
WW domain binding protein 5	WBP5	1.729994219	0.007520719
WD repeat domain 66	WDR66	-1.542297285	0.01397923
WD repeat domain 90	WDR90	-0.538246092	0.046140206
WD and tetratricopeptide repeats 1	WDTC1	2.612838936	0.001855751
Yip1 interacting factor homolog B (S. cerevisiae)	YIF1B	-0.903775828	0.005265459
yippee-like 4 (Drosophila)	YPEL4	1.287404684	0.018743698
yrdC domain containing (E. coli)	YRDC	1.134460703	0.01495258
YTH domain family, member 2	YTHDF2	-2.195665588	0.007736222
YY2 transcription factor	YY2	-2.127024156	0.000514878
Zinc finger, AN1-type domain 6	ZFAND6	-1.731305801	0.008076044
zinc finger protein 10	ZNF10	-1.970045688	0.001096795
Zinc finger protein 117	ZNF117	-2.603483817	0.003059113
Zinc finger protein 131	ZNF131	-2.073792796	0.003160802
zinc finger protein 131	ZNF131	1.859210685	0.031487888
zinc finger protein 189	ZNF189	1.901792011	0.008075307
zinc finger protein 263	ZNF263	1.711155662	0.017380837
zinc finger protein 282	ZNF282	1.642105204	0.007876143
zinc finger protein 343	ZNF343	-1.340970131	0.026452431
zinc finger protein 430	ZNF430	-1.35496225	0.024419221
zinc finger protein 441	ZNF441	-2.355139073	0.000335024
zinc finger protein 512B	ZNF512B	-2.174937225	0.011007183
zinc finger protein 587	ZNF587	-2.15880446	0.012489022
zinc finger protein 599	ZNF599	1.483916458	0.00558898
zinc finger protein 667	ZNF667	-1.131847403	0.00337552
zinc finger protein 697	ZNF697	2.108817766	0.0136406
zinc finger protein 77	ZNF77	-1.014310584	0.01532253
zinc finger protein 846	ZNF846	-1.612087755	0.001094848
zinc finger, NFX1-type containing 1	ZNFX1	2.0629443	0.008257172
zinc finger and SCAN domain containing 21	ZSCAN21	-1.856286235	0.014865884

Schizophrenia samples



Control samples

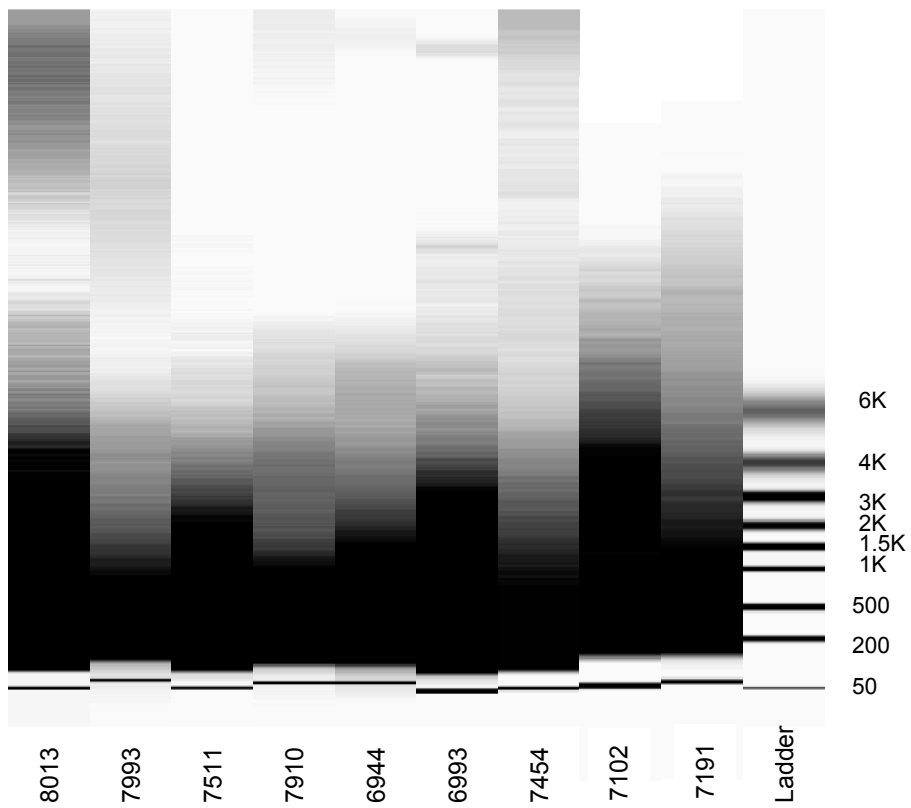


Figure S1