Supplementary materials

Susceptible genes and disease mechanisms identified in frontotemporal dementia and frontotemporal dementia with Amyotrophic Lateral Sclerosis by DNA-methylation and GWAS.

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The authors disclose no potential conflicts of interest

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SUPPLEMENTARY FILES

Fig.S1. Differential DNA-methylated genes and PCA for FTD. (A) P-value distribution plot for the comparison FTD versus Control using Student T-test. (B) Volcano plot depicting genes with the fold-difference on the x-axis and -log10(*P*-value) on the y-axis. (C) Principal Component analysis on the top 20% probes with highest variance.

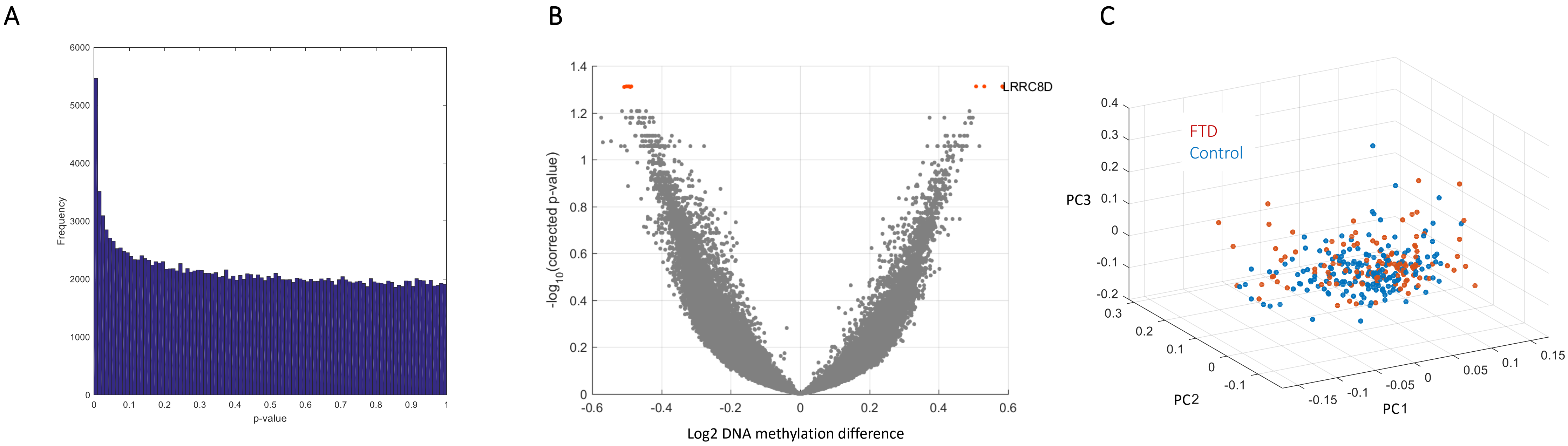
Fig.S2. Differential DNA-methylated genes and PCA for FTD-ALS. (A) P-value distribution plot for the comparison FTD-ALS versus Control using Student T-test. (B) Volcano plot depicting genes with the fold-difference on the x-axis and -log10(*P*-value) on the y-axis.

Fig.S3. GTEx tissue enrichment for the differential DNA-methylated genes in FTD-ALS. Tissue enrichment was computed by following the approach as outlined in Fig.2A. (A) Tissue enrichment for FTD-ALS with the 25 GTEx specific tissues. (B) Brain tissue enrichment for FTD-ALS with the 13 GTEx specific brain tissues. Genes are colored with the tissue specific color.

Fig.S4. Batch correction and differential DNA methylated genes after extending control data set. (A) batch effect of samples without correction. (B) Clustering of samples after batch-effect correction. (C) Differential DNA methylated probes for Controls (this study) vs. Non-smokers. (D) Differential DNA methylated probes for FTD vs. Non-smokers.

Fig.S5. Venn diagram depicting overlap of genes from the original meta-analysis. Genes from the meta-analysis from the original study were gathered and overlaid with the differential methylated that we detected in this study.

Figure S1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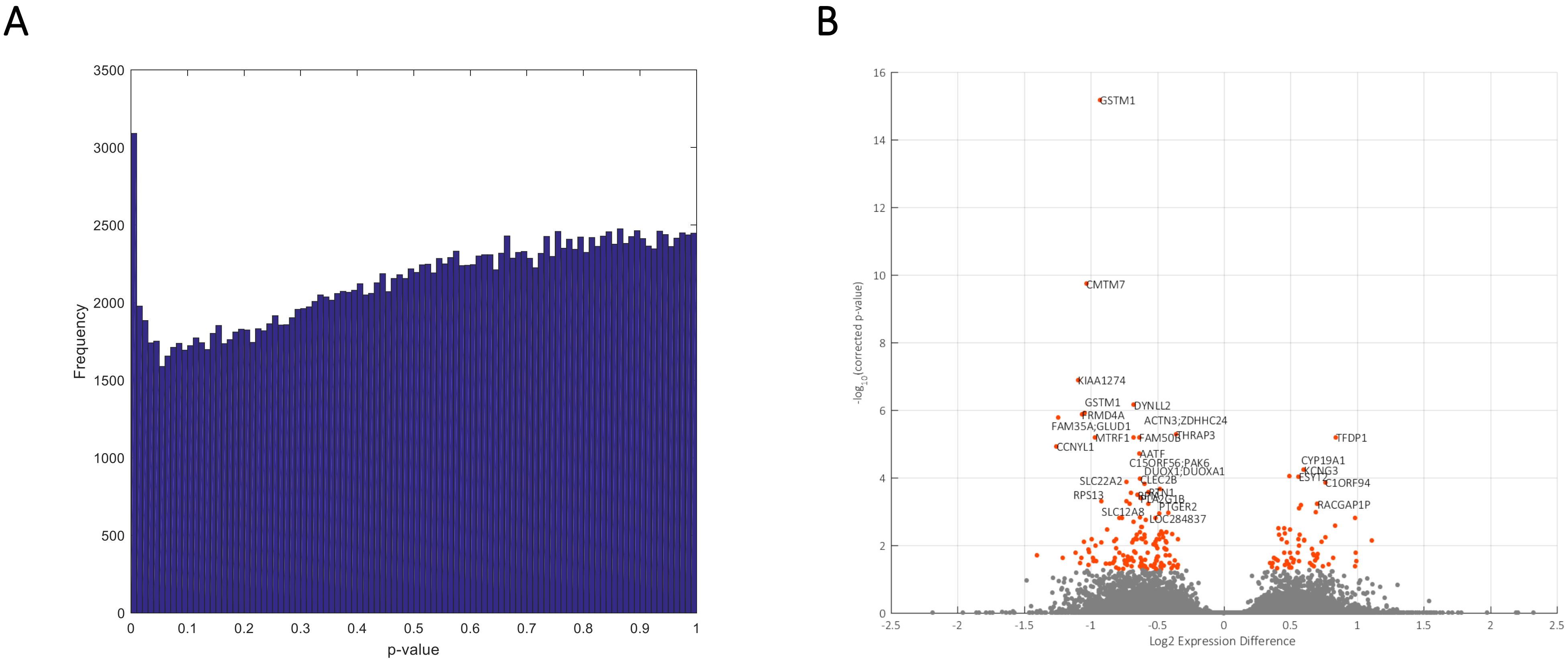
Frequency
6000
5000
4000
3000
2000
1000
0
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
p-value
B
$-\log_{10}$(corrected p-value)
1.4
1.2
1
0.8
0.6
0.4
0.2
0
-0.6
-0.4
-0.2
0
0.2
0.4
0.6
Log2 DNA methylation difference
LRRC8D
C
FTD
Control
PC3
0.4
0.3
0.2
0.1
0
-0.1
-0.2
PC2
0.3
0.2
0.1
0
-0.1
PC1
-0.15
-0.1
-0.05
0
0.05
0.1
0.15

Figure S2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Frequency
3500
3000
2500
2000
1500
1000
500
0
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
p-value
B
-log10(corrected p-value)
16
14
12
10
8
6
4
2
0
-2.5
-2
-1.5
-1
-0.5
0
0.5
1
1.5
2
2.5
Log2 Expression Difference
GSTM1
CMTM7
KIAA1274
GSTM1
DYNLL2
FRMD4A
ACTN3;ZDHHC24
FAM35A;GLUD1
MTRF1
FAM50B
THRAP3
CCNYL1
AATF
C15ORF56;PAK6
DUOX1;DUOXA1
SLC22A2
CLEC2B
RTN1
RPS13
PLA2G1B
PTGER2
SLC12A8
LOC284837
TFDP1
CYP19A1
KCNG3
ESYT2
C1ORF94
RACGAP1P

Figure S3

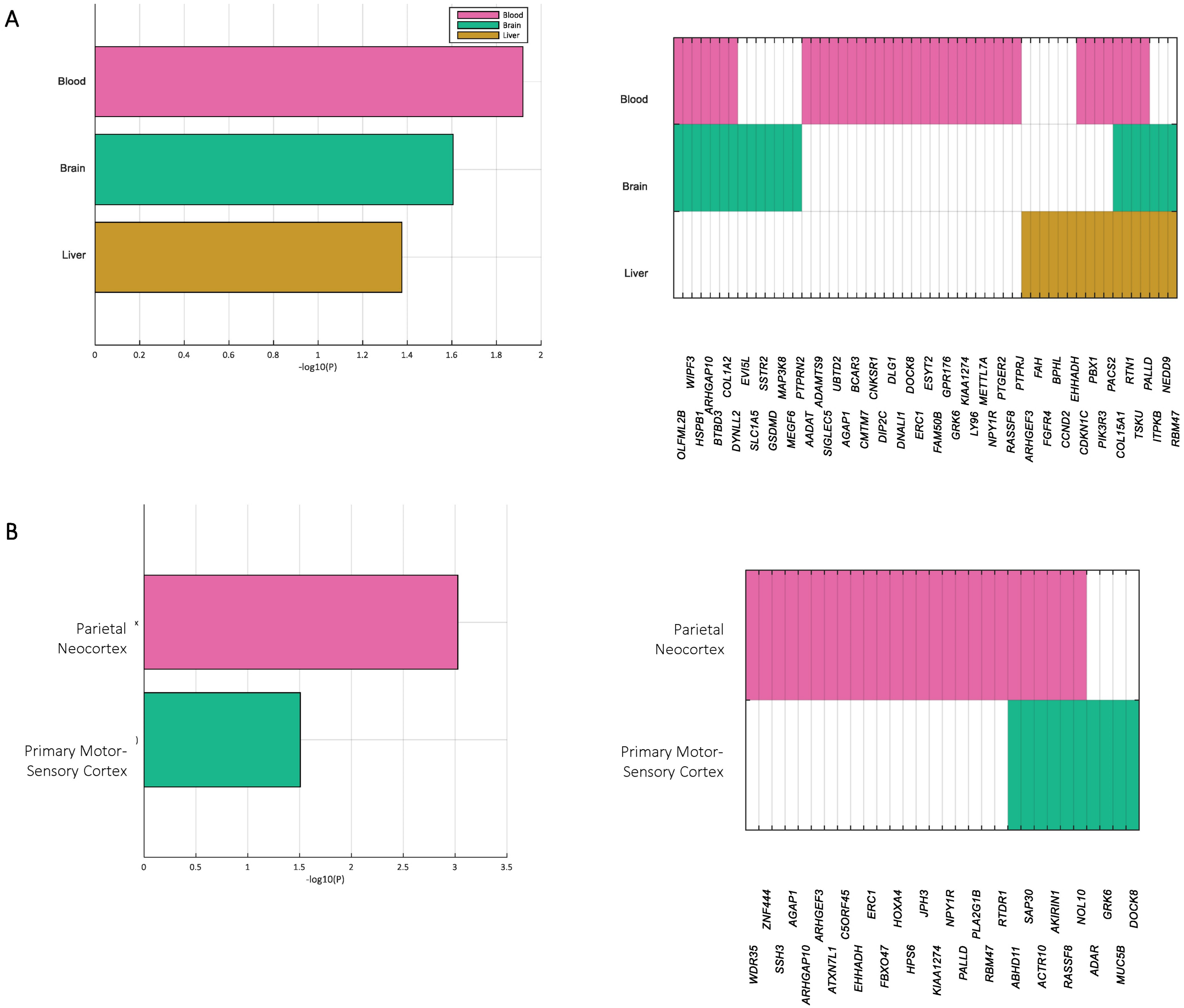
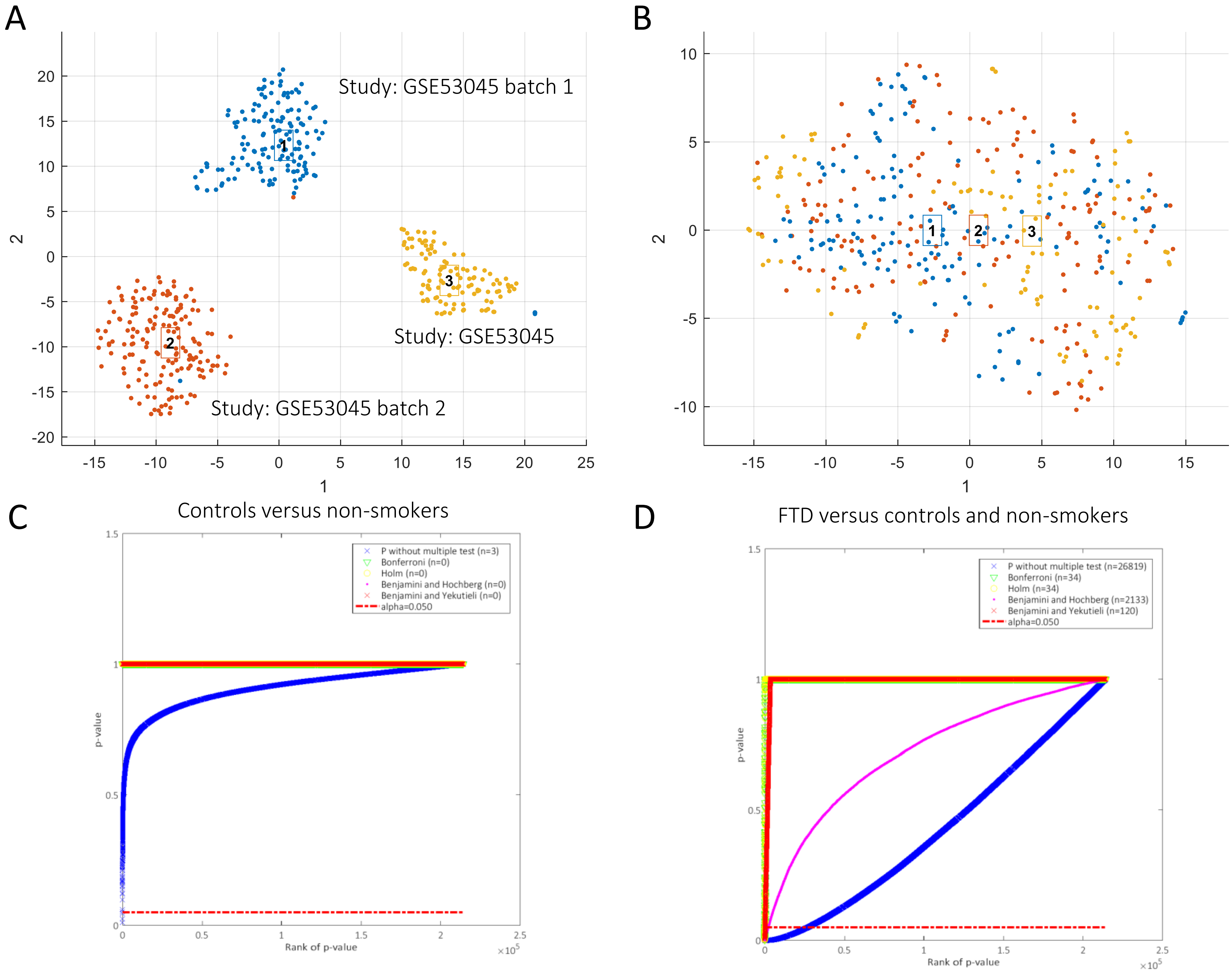

A
Blood
Brain
Liver
Blood
Brain
Liver
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6
1.8
2
-log10(P)
Blood
Brain
Liver
OLFML2B
WIPF3
HSPB1
ARHGAP10
BTBD3
COL1A2
DYNLL2
EVI5L
SLC1A5
SSTR2
GSDMD
MAP3K8
MEGF6
PTPRN2
AADAT
ADAMTS9
SIGLEC5
UBTD2
AGAP1
BCAR3
CMTM7
CNKSR1
DIP2C
DLG1
DNALI1
DOCK8
ERC1
ESYT2
FAM50B
GPR176
GRK6
KIAA1274
LY96
METTL7A
NPY1R
PTGER2
RASSF8
PTPRJ
ARHGEF3
FAH
FGFR4
BPHL
CCND2
EHHADH
CDKN1C
PBX1
PIK3R3
PACS2
COL15A1
RTN1
TSKU
PALLD
ITPKB
NEDD9
RBM47
B
Parietal Neocortex
Primary Motor-Sensory Cortex
0
0.5
1
1.5
2
2.5
3
3.5
-log10(P)
Parietal Neocortex
Primary Motor-Sensory Cortex
WDR35
ZNF444
SSH3
AGAP1
ARHGAP10
ARHGEF3
ATXN7L1
C5ORF45
EHHADH
ERC1
FBXO47
HOXA4
HPS6
JPH3
KIAA1274
NPY1R
PALLD
PLA2G1B
RBM47
RTDR1
ABHD11
SAP30
ACTR10
AKIRIN1
RASSF8
NOL10
ADAR
GRK6
MUC5B
DOCK8

Figure S4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Study: GSE53045 batch 1
Study: GSE53045
Study: GSE53045 batch 2
1
2
3
20
15
10
5
0
-5
-10
-15
-20
-15
-10
-5
0
5
10
15
20
25
1
2
B
10
5
0
-5
-10
-15
-10
-5
0
5
10
15
1
2
C
Controls versus non-smokers
P without multiple test (n=3)
Bonferroni (n=0)
Holm (n=0)
Benjamini and Hochberg (n=0)
Benjamini and Yekutieli (n=0)
alpha=0.050
p-value
Rank of p-value
1.5
1
0.5
0
0
0.5
1
1.5
2
2.5
×10⁵
D
FTD versus controls and non-smokers
P without multiple test (n=26819)
Bonferroni (n=34)
Holm (n=34)
Benjamini and Hochberg (n=2133)
Benjamini and Yekutieli (n=120)
alpha=0.050
p-value
Rank of p-value
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1
0.5
0
0
0.5
1
1.5
2
2.5
×10⁵

Figure S5

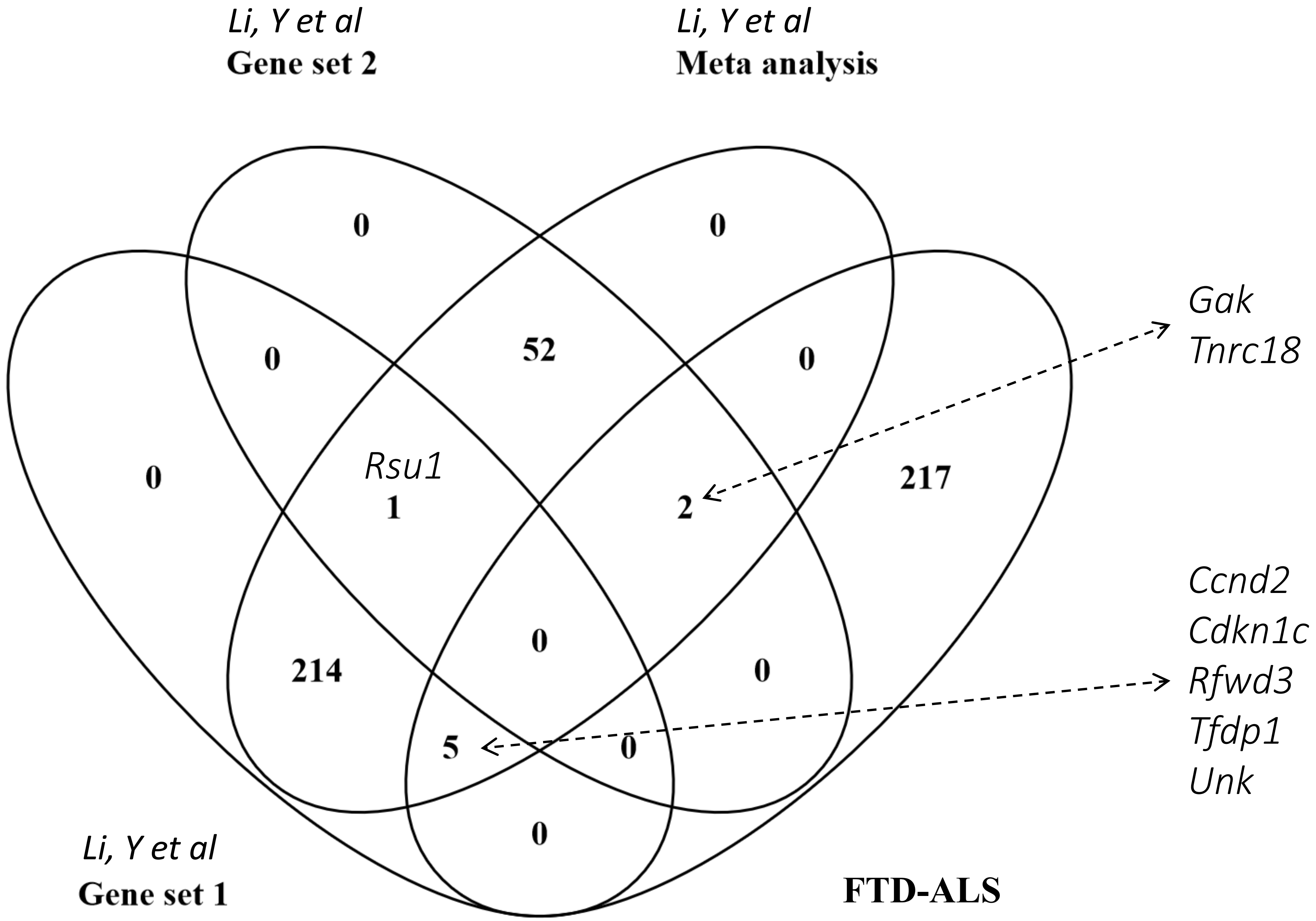
Li, Y et al
Gene set 2
Li, Y et al
Meta analysis
0
0
0
52
0
Gak
Tnrc18
0
Rsu1
1
2
217
0
Ccnd2
Cdkn1c
Rfwd3
Tfdp1
Unk
214
0
5
0
0
Li, Y et al
Gene set 1
FTD-ALS

Table S1

Genesymbol	Chr	Strand	GWAS SNPs						DNA-methylation probes					Description		Validated by gene-expression
			Id	P	Location	Mutation type	CADD score	Min(P)	Id	P_{BH}	Location	T-stat	Hyper/hypo	Phenotype	Wikigene	
ELP2/ SLC39A6	chr18	.	rs16967474	0.03221	exonic	nonsynonymous SNV	25.3	0.03221	cg12339809	0.0486004	Island	-5.0795263	Hypomethylation	.	.	Yes
ZMIZ1	chr10	.	rs12571751	0.03573	intronic	.	.	0.03573	cg19168578	0.0486004	Island	-4.9091067	Hypomethylation	.	.	
AP3M1	chr10	-	exm954373	0.01207	intronic	.	.	0.01207	cg04760117	0.0486004	.	4.9137135	Hypermethylation	.	adaptor-related protein complex 3, mu 1 subunit	
ZNF808,ZNF701	chr19	+	exm2216491	0.02767	intergenic	.	.	0.02767	cg10782349	0.0489753	Island	4.9227971	Hypermethylation	.	zinc finger protein 701	
TPK1	chr7	-	.	.	.	.	.	.	cg16316507	0.0486004	Island	-4.9587098	Hypomethylation	THIAMINE METABOLISM DYSFUNCTION SYNDROME 5	thiamin pyrophosphokinase 1	
STK39	chr2	-	.	.	.	.	.	.	cg03159329	0.0486004	Island	-4.9394391	Hypomethylation	.	serine threonine kinase 39	
BMS1P4	chr10	-	.	.	.	.	.	.	cg26771998	0.0489753	Island	-4.8163424	Hypomethylation	.	BMS1 pseudogene 4	
NCRNA00188;SNORD49A;SNORD4	chr17	.	.	.	.	.	.	.	cg02830903	0.0489753	Island	-4.8184838	Hypomethylation	.	.	
LRRC8D	chr1	+	.	.	.	.	.	.	cg01533966	0.0486004	.	4.9315597	Hypermethylation	.	leucine rich repeat containing 8 family, member D	
RAI1	chr17	+	.	.	.	.	.	.	cg19285752	0.0486004	N_Shore	4.8937517	Hypermethylation	Smith-Magenis syndrome (SMS)	retinoic acid induced 1	

Table S2

			GWAS SNPs						DNA-methylation probes				Validated by gene-expression
Genesymbol	Chr	Strand	Id	*P*	Location	Mutation type	CADD score	min(*P*) for gene	Id	P_{BY}	Location	Tstat	
PCDHA4	chr5		rs59233330	1.92E-04	exonic	nonsynonymous SNV	0	1.92E-04	cg02357321	3.348E-02	N_Shore	-6.43	
DLG1	chr3	-	rs74674649	6.01E-04	exonic	nonsynonymous SNV	28	6.01E-04	cg12594803	2.879E-02	.	-7.04	Yes
KIAA1147	chr7	-	rs201876806	9.13E-04	exonic	nonsynonymous SNV	23	9.13E-04	cg24662653	2.890E-03	Island	-6.51	Yes
HPS6	chr10	+	rs36078476	1.07E-03	exonic	nonsynonymous SNV	0	1.07E-03	cg02840794	3.383E-03	Island	-7.36	
GPN3	chr12		rs143166802	1.69E-03	exonic	nonsynonymous SNV	2	1.69E-03	cg00558990	1.524E-02	N_Shore	-5.99	
GGA1	chr22	+	rs143909159	2.91E-03	exonic	nonsynonymous SNV	34	2.91E-03	cg21268578	2.796E-02	.	-7.16	
PTPRN2	chr7	-	rs142437536	3.02E-03	exonic	nonsynonymous SNV	0	3.02E-03	cg05135176	7.528E-03	S_Shore	-5.52	Yes
PPP1R36,PLEKHG3	chr14	+	rs117300689	3.29E-03	intergenic	.	.	3.29E-03	cg26763365	4.418E-02	Island	-5.55	
MRPL21	chr11		rs200690672	3.96E-03	exonic	nonsynonymous SNV	9	3.96E-03	cg26065952	2.314E-02	N_Shore	-5.70	Yes
IGHMBP2	chr11		rs201692151	4.00E-03	exonic	nonsynonymous SNV	23	4.00E-03	cg26065952	2.314E-02	N_Shore	-5.70	Yes
MTRF1	chr13	-	rs9532758	5.25E-03	exonic	nonsynonymous SNV	7	5.25E-03	cg21446692	6.388E+08	.	-10.38	
ASPM	chr1	-	rs150125249	5.78E-03	exonic	nonsynonymous SNV	34	5.78E-03	cg11336294	2.729E-02	.	-5.59	
NEDD9	chr6	-	rs112742585	5.85E-03	exonic	nonsynonymous SNV	13	5.85E-03	cg05917225	9.185E-03	.	-5.79	
PRSS36	chr16	-	rs145749002	6.04E-03	exonic	nonsynonymous SNV	33	6.04E-03	cg14301190	4.949E-03	Island	-6.68	
PPP1R36,PLEKHG3	chr14	+	rs117434243	6.48E-03	intergenic	.	.	3.29E-03	cg26763365	4.418E-02	Island	-5.55	
IGHMBP2	chr11		rs622082	7.05E-03	exonic	nonsynonymous SNV	0	4.00E-03	cg26065952	2.314E-02	N_Shore	-5.70	Yes
PKNOX1	chr21	+	rs2839627	8.18E-03	intronic	.	.	8.18E-03	cg04193427	4.013E-02	Island	-5.38	Yes
CNKSR1	chr1	+	rs144396219	8.32E-03	exonic	nonsynonymous SNV	28	8.32E-03	cg09890400	1.962E-02	.	-8.83	Yes
UBTD2	chr5	-	rs17074452	9.54E-03	exonic	nonsynonymous SNV	18	9.54E-03	ch.5.3268483F	4.949E-03	.	-5.84	Yes
GGA1	chr22	+	rs138525343	9.76E-03	exonic	nonsynonymous SNV	27	2.91E-03	cg21268578	2.796E-02	.	-7.16	
IGHMBP2	chr11		rs145226920	0.01001	exonic	stopgain	35	4.00E-03	cg26065952	2.314E-02	N_Shore	-5.70	Yes
FAH	chr15	+	rs144234072	1.07E-02	exonic	nonsynonymous SNV	27	0.01066	cg06856840	1.648E-02	.	-6.95	
RBM14	chr11	+	rs148119991	1.28E-02	exonic	nonsynonymous SNV	5	0.01281	cg03249986	1.005E-02	Island	-5.46	
NEDD9	chr6	-	rs34044517	1.63E-02	exonic	nonsynonymous SNV	24	5.85E-03	cg05917225	9.185E-03	.	-5.79	
FAH	chr15	+	rs34749737	0.01663	exonic	nonsynonymous SNV	6	0.01066	cg06856840	1.648E-02	.	-6.95	
BPHL	chr6	+	rs2231365	0.01671	splicing	.	24	0.01671	cg22799902	6.218E-03	Island	-6.43	
ARHGAP10	chr4	+	rs144604709	0.0183	exonic	nonsynonymous SNV	0	0.0183	ch.4.2714611R	2.836E-02	.	-4.78	
ACTN3	chr11		rs201576110	0.02133	exonic	nonsynonymous SNV	32	0.02133	cg25117505	6.388E+08	Island	-8.39	
FGD6	chr12		rs143773760	0.02322	exonic	nonsynonymous SNV	9	0.02322	cg02688710	2.339E-02	Island	-6.09	Yes
WDR66	chr12	+	rs77422261	0.02336	exonic	nonsynonymous SNV	30	0.02336	cg21016266	1.331E-02	Island	-4.89	
RBM47	chr4	-	rs1688939	0.02571	intronic	.	.	0.02571	cg00802478	4.080E-02	.	-5.98	Yes
IQSEC1	chr3	-	rs144790333	0.02763	exonic	nonsynonymous SNV	23	0.02763	cg02559896	6.666E-03	Island	-5.14	
DLG1	chr3	-	rs141544348	0.03024	exonic	nonsynonymous SNV	35	6.01E-04	cg12594803	2.879E-02	.	-7.04	Yes
DUOX1	chr15		rs143304688	0.03047	exonic	stopgain	44	0.03047	cg10496082	1.526E-04	Island	-6.61	
RTDR1	chr22		rs3788337	0.03193	intronic	.	.	0.03193	cg21100191	3.904E-02	Island	-5.23	
CCR5,CCRL2	chr3	+	.	0.03194	intergenic	.	.	0.03194	cg10952220	1.002E-02	.	-7.39	
CCRL2	chr3	+	.	0.03355	downstream	.	.	0.03194	cg10952220	1.002E-02	.	-7.39	
PCDHA3	chr5		rs146951816	0.0354	exonic	nonsynonymous SNV	15	0.0354	cg02357321	3.348E-02	N_Shore	-6.43	
PARP11,CCND2	chr12	+	rs11063069	0.03845	intergenic	.	.	0.01055	cg05987650	8.273E-03	Island	-6.49	
C6orf70	chr6		rs140632188	0.04056	exonic	nonsynonymous SNV	23	0.04056	cg22807378	1.211E-02	Island	-7.15	
IGHMBP2	chr11		rs17612126	0.04126	exonic	nonsynonymous SNV	1	4.00E-03	cg26065952	2.314E-02	N_Shore	-5.70	Yes
TCTE3	chr6		rs116980543	0.04138	exonic	nonsynonymous SNV	10	0.04138	cg22807378	1.211E-02	Island	-7.15	
HERV-Fb1,PKNOX1	chr21	+	.	0.04328	intergenic	.	.	8.18E-03	cg04193427	4.013E-02	Island	-5.38	
FGFR4	chr5	+	.	0.04391	exonic	synonymous SNV	.	0.04391	cg21042539	4.943E-02	Island	-5.63	
CLRN2	chr4	+	rs201124485	0.04711	exonic	nonsynonymous SNV	21	0.04711	cg16760587	1.143E-03	S_Shelf	-6.06	
COL15A1	chr9	+	rs199906142	3.62E-03	exonic	nonsynonymous SNV	23	0.003618	cg18115656	3.656E-02	Island	5.37	
TNRC18	chr7	-	rs112785272	6.27E-03	exonic	nonsynonymous SNV	19	6.27E-03	cg10546562	1.010E-02	N_Shore	5.91	
SLC26A7	chr8	+	rs200788056	9.04E-03	exonic	nonsynonymous SNV	23	9.04E-03	cg25481252	2.582E-03	.	7.38	
DOCK8	chr9	+	rs77399114	9.95E-03	exonic	nonsynonymous SNV	9	9.95E-03	cg13876553	2.938E-02	.	5.41	
PCNX	chr14	+	rs200261097	0.01309	exonic	nonsynonymous SNV	32	0.01309	cg10066683	4.218E-02	.	5.34	Yes
PRICKLE2,ADAMTS9	chr3	-	rs7648640	0.01701	intergenic	.	.	0.01701	cg11044162	2.539E-02	N_Shore	4.75	
WDR35	chr2	-	rs148436608	0.02293	exonic	nonsynonymous SNV	16	0.02293	cg13734338	2.796E-02	.	6.00	Yes
SLC1A5	chr19	-	rs3027961	0.02329	exonic	nonsynonymous SNV	7	0.02329	cg08533710	1.634E-02	S_Shore	5.00	
ATXN7L1	chr7	-	rs10435352	0.03096	intronic	.	.	0.03096	cg05424831	3.142E-03	.	5.46	
MEGF6	chr1	-	rs61910697	0.03109	exonic	nonsynonymous SNV	20	0.03109	cg04391135	3.451E-03	Island	6.21	
DOCK8	chr9	+	rs12347078	0.03557	intronic	.	.	9.95E-03	cg13876553	2.938E-02	.	5.41	
PCNX	chr14	+	rs151313378	0.03622	exonic	nonsynonymous SNV	15	0.01309	cg10066683	4.218E-02	.	5.34	Yes
MEGF6	chr1	-	rs12075570	0.0367	exonic	nonsynonymous SNV	9	0.03109	cg04391135	3.451E-03	Island	6.21	
AGAP1	chr2	+	rs2292708	0.03677	exonic	synonymous SNV	.	0.03677	cg00834223	4.423E-03	.	6.19	
ARHGAP8,PRR5-ARH	chr22	+	rs55849456	0.03933	exonic	nonsynonymous SNV	25	0.03933	cg06647930	4.418E-02	S_Shelf	4.26	Yes
C1orf94	chr1	+	rs61741807	0.04033	exonic	nonsynonymous SNV	0	0.04033	cg15098077	1.363E-04	N_Shore	7.96	
PBX1,LMX1A	chr1	+	.	0.04041	intergenic	.	.	0.04041	cg20682146	4.200E-02	Island	6.22	
COL1A2	chr7	+	.	0.04129	exonic	synonymous SNV	.	0.04129	cg12563520	3.706E-02	.	6.05	
HS6ST3	chr13	+	rs4771948	0.04256	intronic	.	.	0.04256	cg09122588	4.527E-02	.	5.11	
ARHGAP8,PRR5-ARH	chr22	+	rs16992915	0.04662	exonic	nonsynonymous SNV	19	0.03933	cg06647930	4.418E-02	S_Shelf	4.26	Yes
ESYT2	chr7	-	rs2305475	0.04728	exonic	nonsynonymous SNV	23	0.04728	cg19584649	9.356E+09	.	6.66	Yes
AHRR	chr5	+	rs201569850	0.04754	exonic	nonsynonymous SNV	12	0.04754	cg16577724	3.796E-02	.	5.86	Yes
ESYT2	chr7	-	rs2305473	0.04755	exonic	nonsynonymous SNV	14	0.04728	cg19584649	9.356E+09	.	6.66	Yes
ESYT2	chr7	-	rs13233513	0.0479	exonic	nonsynonymous SNV	13	0.04728	cg19584649	9.356E+09	.	6.66	Yes

Table S3

Genesymbol	Chr	Strand	GWAS SNPs						DNA-methylation probes				Validated by gene-expression
			Id	*P*	Location	Mutation type	CADD score	min(*P*) for gene	Id	P_{BY}	Location	Tstat	
AP3M1	chr21			0.0121	intronic			0.0121	cg04760117	0.0486004	NaN	4.913713	
ZMIZ1/LOC283050	chr11		rs12571751	0.0357	intronic			0.0357	cg19168578	0.0486004	Island	-4.90911	
ELP2/SLC39A6	chr11	-	rs16967474	0.0322	exonic	nonsynonymous SNV	25.3	0.0322	cg12339809	0.0486004	Island	-5.07953	Yes

Table S4

Gene-symbol	Degree
THRAP3	33
C5orf45	33
ANKRD17	32
ATXN7L1	32
GPR176	32
IGHMBP2	31
PCNX	31
ADAR	30
GAK	30
ZNF544	30
BOP1	29
RTN1	29
POLR2A	29
SSTR2	29
TNRC18	28
PKNOX1	28
SDF4	27
RAB1A	26
TRIM23	26
UNC45A	26
GNL3	24
DIP2C	24
ARHGEF3	23
PBRM1	22
ERC1	22
RFWD3	22
UNK	22
TGOLN2	21
GGA1	21
PTP4A2	20
ACTR10	18
FAM110B	17
IQSEC1	16
FAM50B	16
ESYT2	15
RBM14	15
RAB6A	15
HPS6	14
GSDMD	13
MTRF1	13
HP1BP3	12
C5orf44	12
UBTD2	12
FUCA2	12
PTPRN2	12
MAP3K8	12
CNKSR1	11
GRK6	11
lists continues (1)	
MDGA1	11
SLC1A5	11
B3GALT6	10
C2orf63	10
DOCK8	10
DCLK1	10
LSM14A	10
RBM47	9
CAMLG	9
SSH3	9
CMIP	9
PALLD	8
FAM35A	8
CLEC2B	8
VEZT	8
GPN3	8
BTBD3	8
BCAR3	7
ITPKB	7
RPIA	7
LY96	7
GLUD1	7
NINJ2	7
METTL7A	7
TFDP1	7
ZNF444	7
CCRL2	6
ADAMTS9	6
DLG1	6
FGD4	6
SAP18	6
JMJD6	6
PIK3R3	5
PBX1	5
LRRC2	5
EHHADH	5
FGFR4	5
WIPF3	5
CDKN1C	5
C12orf29	5
HAR1A	5
AKIRIN1	4
NPY1R	4
AHRR	4
RNASEH2C	4
ZDHHC24	4
CCND2	4
FGD6	4
lists continues (2)	
PACS2	4
DUOX1	4
EVI5L	4
PPP1R8	3
FYN	3
TATDN1	3
UBE2D1	3
WDR66	3
PLEKHG3	3
TMC7	3
DYNLL2	3
SIGLEC5	3
RABGGTB	2
CCNYL1	2
CMTM7	2
AADAT	2
BPHL	2
NEDD9	2
KIAA1147	2
RPS13	2
PTPRJ	2
FAH	2
RNF220	1
NOL10	1
LMAN2	1
GMNN	1
C6orf70	1
COL1A2	1
KIAA1274	1
POLR2G	1
RASSF8	1
PRSS36	1
AATF	1
MEGF6	0
DNALI1	0
GSTM1	0
OLFML2B	0
WDR35	0
AGAP1	0
ARHGAP10	0
SAP30	0
ARL15	0
PEX7	0
TCTE3	0
ABHD11	0
HSPB1	0
C8orf44	0
NDUFB9	0
lists continues (3)	
COL15A1	0
FRMD4A	0
MRPL21	0
TSKU	0
PTGER2	0
MPV17L	0

Table S5

Gene-symbol	GSE18632	GSE13162	GSE68605	GSE40438	Overlap with differential DNA-methylated genes in FTD-ALS
AATF	TRUE				TRUE
ABHD11					TRUE
ADAMTS9					TRUE
ADAR					TRUE
AGAP1					TRUE
AHRR	TRUE				TRUE
AKIRIN1	TRUE				TRUE
ANKRD17	TRUE				TRUE
APOB		TRUE			TRUE
ARHGEF3	TRUE				TRUE
ARL15	TRUE				TRUE
BCAR3					TRUE
BOP1					TRUE
BTBD3					TRUE
C1ORF61	TRUE				TRUE
CCND2	TRUE	TRUE			TRUE
CCNYL1					TRUE
CCRL2					TRUE
CDKN1C		TRUE			TRUE
CLEC2B					TRUE
CMIP					TRUE
CNKSR1		TRUE			TRUE
COL15A1					TRUE
COL1A2					TRUE
DCLK1					TRUE
DIP2C					TRUE
DLG1		TRUE			TRUE
DUOX1					TRUE
DYNLL2	TRUE				TRUE
ERC1	TRUE				TRUE
ESYT2	TRUE				TRUE
EVI5L					TRUE
FAH					TRUE
FAM110B					TRUE
FAM24B	TRUE				TRUE
FGD6	TRUE				TRUE
FGFR4					TRUE
FYN		TRUE			TRUE
GABRG2					TRUE
GAK	TRUE				TRUE
GLUD1					TRUE
GNL3					TRUE
GPR176					TRUE
GRK6	TRUE				TRUE
GSDMD					TRUE
GSTM1					TRUE

HOXA4		TRUE			TRUE
HP1BP3					TRUE
HSPB1	TRUE				TRUE
IGHMBP2		TRUE			TRUE
ITPKB		TRUE			TRUE
JPH3	TRUE				TRUE
KCNQ2		TRUE			TRUE
KIAA1147	TRUE				TRUE
LAMP3	TRUE				TRUE
LMAN2		TRUE			TRUE
LRRC2					TRUE
LSM14A	TRUE				TRUE
LY96					TRUE
MDGA1					TRUE
MEGF6					TRUE
MEOX1		TRUE			TRUE
METTL7A	TRUE	TRUE			TRUE
MPV17L					TRUE
MRPL21	TRUE				TRUE
MYF6					TRUE
NDUFB9					TRUE
NINJ2		TRUE			TRUE
OLFML2B					TRUE
PACS2					TRUE
PALLD	TRUE	TRUE			TRUE
PBRM1	TRUE				TRUE
PBX1					TRUE
PCDHA2					TRUE
PCDHA3					TRUE
PCDHA5					TRUE
PCNX	TRUE	TRUE			TRUE
PEX7					TRUE
PIK3R3	TRUE				TRUE
PKNOX1		TRUE			TRUE
PLEKHG3		TRUE			TRUE
POLR2A					TRUE
POLR2G					TRUE
PRR5-ARHGAP8	TRUE				TRUE
PTGER2					TRUE
PTP4A2	TRUE	TRUE			TRUE
PTPRJ	TRUE				TRUE
PTPRN2		TRUE			TRUE
RAB1A	TRUE				TRUE
RAB6A		TRUE			TRUE
RABGGTB					TRUE
RASSF8					TRUE
RBM14					TRUE
RBM47	TRUE				TRUE
RPIA					TRUE
RPS13		TRUE			TRUE

RTN1					TRUE
SAP18					TRUE
SAP30		TRUE			TRUE
SHANK1		TRUE			TRUE
SLC1A5					TRUE
SLC26A7					TRUE
SSH3					TRUE
SSTR2		TRUE			TRUE
TCTE3					TRUE
TFDP1	TRUE				TRUE
TGOLN2					TRUE
THRAP3					TRUE
TLX3		TRUE			TRUE
TNRC18					TRUE
TRIM23	TRUE				TRUE
TRIM61					TRUE
UBE2D1		TRUE			TRUE
UBTD2	TRUE				TRUE
UNK					TRUE
VEZT		TRUE			TRUE
WDR35	TRUE				TRUE
WIPF3	TRUE				TRUE
ZNF444		TRUE			TRUE

Table S6

Data set	GEO accesion nr.	#Genes with $P_{BH} \leq 0.05$	#Genes in overlap with FTD-ALS	*P*	#Genes in overlap with FTD	*P*
1	GSE18632	4407	36	0.0276*	1	0.7666
2	GSE13162	2572	29	0.0445*	0	1
3	GSE68605	7	0	1	0	1
4	GSE40438	0	-	-	-	-
4						

Table S7

Data used in our study	Genesymbol	Probe id	chr	Location (range)	Marie-Laure Caillet-Boudin et al, 2015	*Daniela Galimberti et al, 2013*	Russ, J. et al, 2012
					MAPT - extended CpG regions	*GRN - (entire open reading frame)*	*C9orf72 - (2KB upstream promoter region)*
					44060543-44061296 ($\text{CpG}_{21)}$ 43972053-44039685 ($\text{CpG}_{27)}$ 43971747-43972052 ($\text{CpG}_{300)}$	43971748-44105699	27573864-27575864
Li, Y et al	*Mapt*	cg05533539	chr17	44104521-44104571			
Li, Y et al	*Grn*	cg19107120	chr17	42430376-42430426			
Li, Y et al	*Grn*	cg11999384	chr17	42422811-42422861			
Li, Y et al	*Grn*	cg12837296	chr17	42426483-42426533			
Li, Y et al	*Grn*	cg20679560	chr17	42423025-42423075			
Li, Y et al	*Grn*	cg23570245	chr17	42426011-42426061			
Li, Y et al	*Grn*	cg24420717	chr17	42426506-42426556			
Li, Y et al	*Grn*	cg17714154	chr17	42422247-42422297			
Li, Y et al	*Grn*	cg18872749	chr17	42421993-42422043			
Li, Y et al	*Grn*	cg01146514	chr17	42422409-42422459			
Li, Y et al	*Grn*	cg04269641	chr17	42422442-42422492			
Li, Y et al	*Grn*	cg07777378	chr17	42422412-42422462			
Li, Y et al	*Grn*	cg17101358	chr17	42422688-42422738			
Li, Y et al	*C9orf72*	cg13958452	chr9	27571484-27571534			
Li, Y et al	*C9orf72*	cg05990720	chr9	27573650-27573700			
Li, Y et al	*C9orf72*	cg11613875	chr9	27573889-27573939			X
Li, Y et al	*C9orf72*	cg14363787	chr9	27573986-27574036			X

Table S8

Padjusted	Probe id	Genesymbol
0.0007	cg16316507	tpk1
0.0010	cg21369679	dnaja2
0.0015	cg08312369	cdkn2d
0.0015	cg19285752	rai1
0.0018	cg12339809	elp2;slc39a6
0.0037	cg06358566	rpia
0.0047	cg04760117	ap3m1
0.0062	cg26771998	bms1p4
0.0083	cg14948912	gatad2a
0.0083	cg01533966	lrrc8d
0.0087	cg11759644	rnf138
0.0098	cg18562663	bcl6
0.0128	cg19576806	dhrs12
0.0135	cg03431064	tubb2c
0.0156	cg11457817	stc2
0.0180	cg26840318	irf2bp2
0.0195	cg03511282	ntan1
0.0204	cg01404182	c6orf120;wdr27
0.0206	cg17222196	efna3
0.0208	cg03159329	stk39
0.0213	cg06951969	smad6
0.0227	cg14325160	rad23b
0.0246	cg08090063	plcd1
0.0262	cg11952315	nags
0.0268	cg11342046	ing5
0.0275	cg02988046	egln1
0.0285	cg11760861	adat3;scamp4
0.0308	cg02504384	tsc2
0.0327	cg12588699	c1orf96
0.0358	cg19168578	loc283050;zmiz1
0.0411	cg19791630	vav1
0.0437	cg13714039	znf14
0.0446	cg05554039	map6
0.0457	cg08797483	calcr

APPENDIX A

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APPENDIX B

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