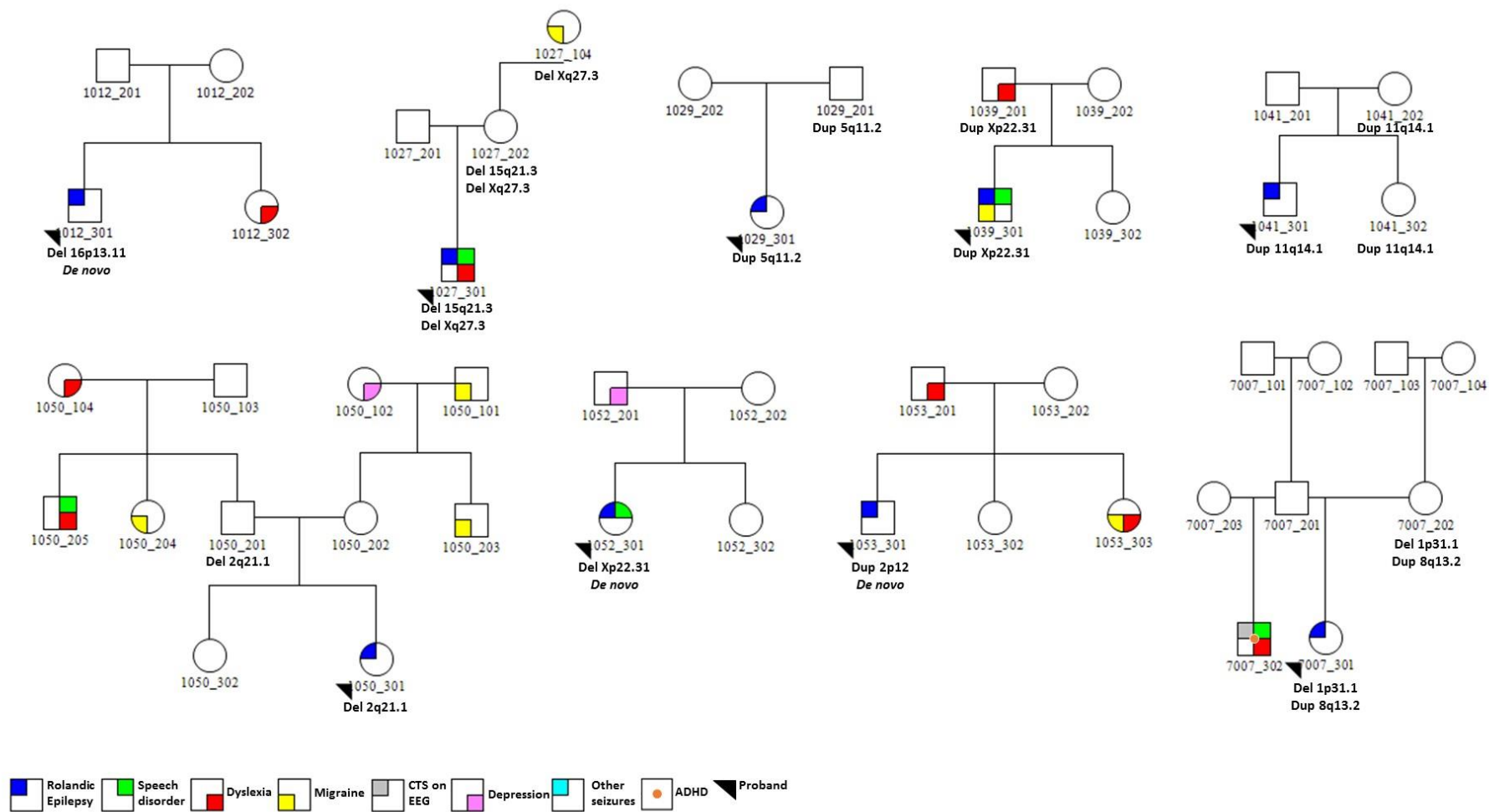
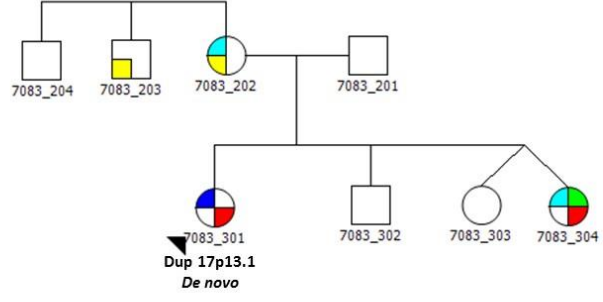
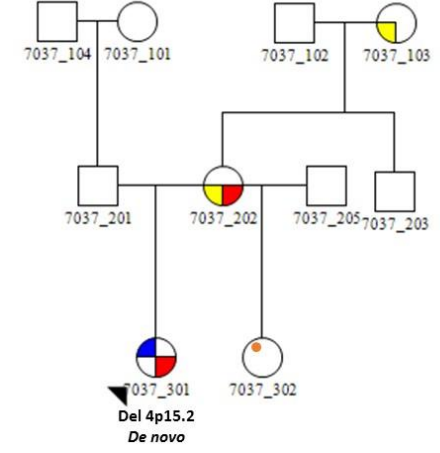
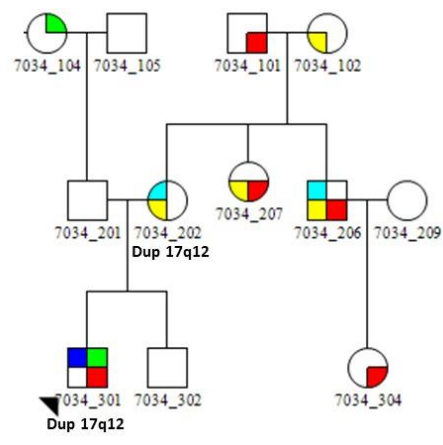
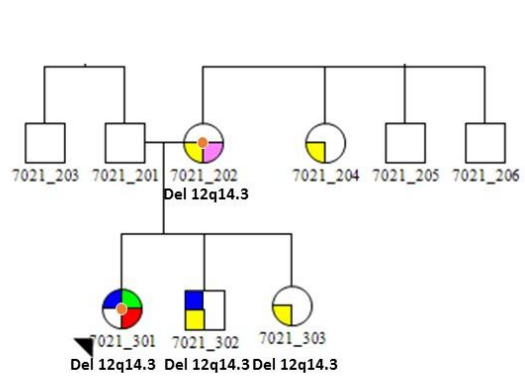


Supplementary Figure S1(A) The first two principal components were calculated combining HapMap 3 individuals with the RE (Case) and NL4 (Control) datasets. **(B)** Individuals of non-European ancestry were removed if they were ± 10 s.d. from the HapMap CEU mean considering

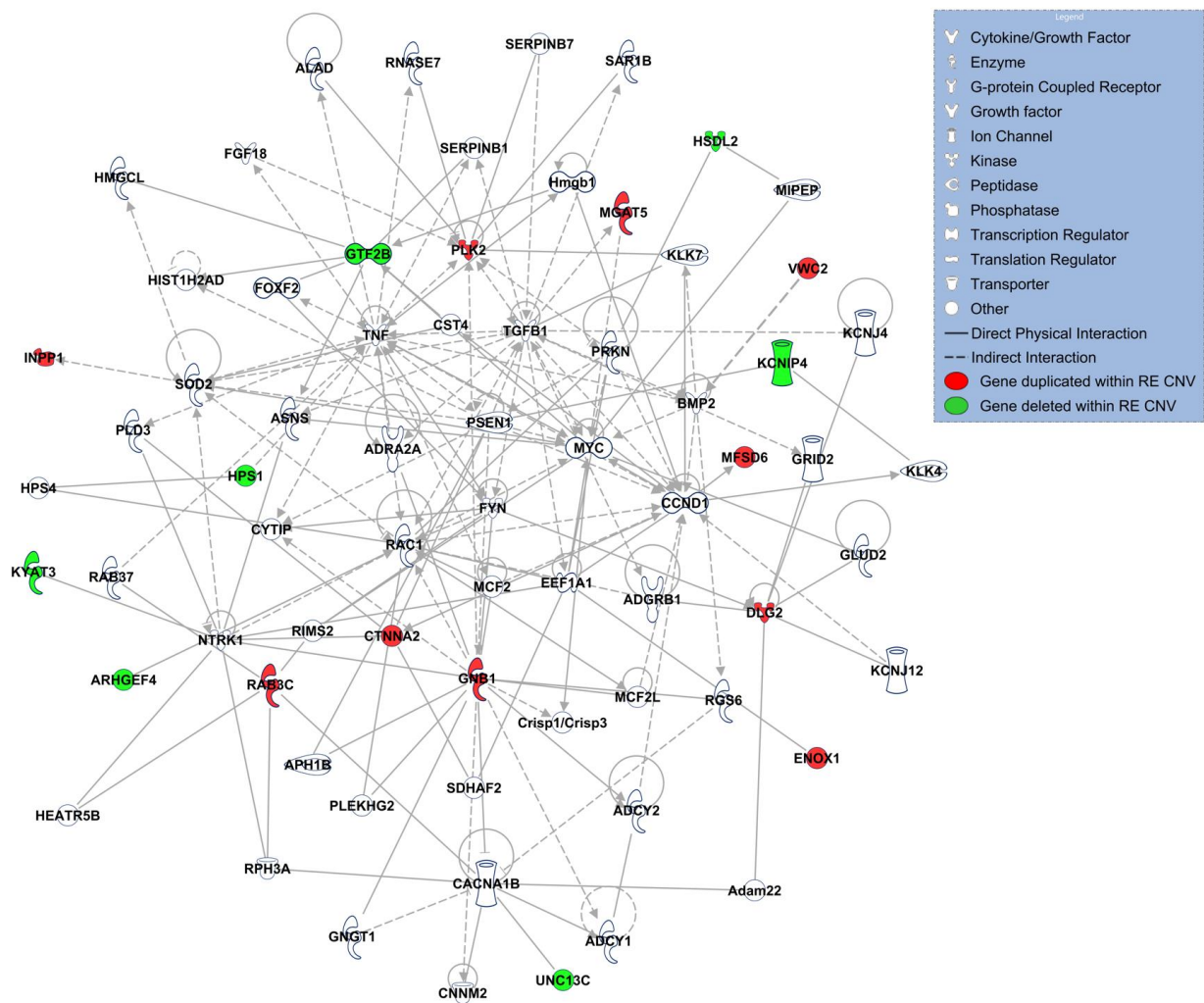
the first four Principal Components (PCs). A subsequent removal of samples deviating by more than 5 s.d. from the stratum mean of the first two PCs was also performed (Calculated on Genotyped data only). **(C)** Individuals remaining after removing population outliers resulted in a homogenous European sample. **(D)** Individuals remaining after removing population outliers resulting in a homogenous group between the RE cases and NL4 datasets.



Supplementary Figure S2 (cont. on next page). Pedigree diagrams of families with RE and hotpost or rare CNVs where inheritance information was available. Circles indicate females, and squares males. Details of CNVs are found below individuals that carry that CNV.

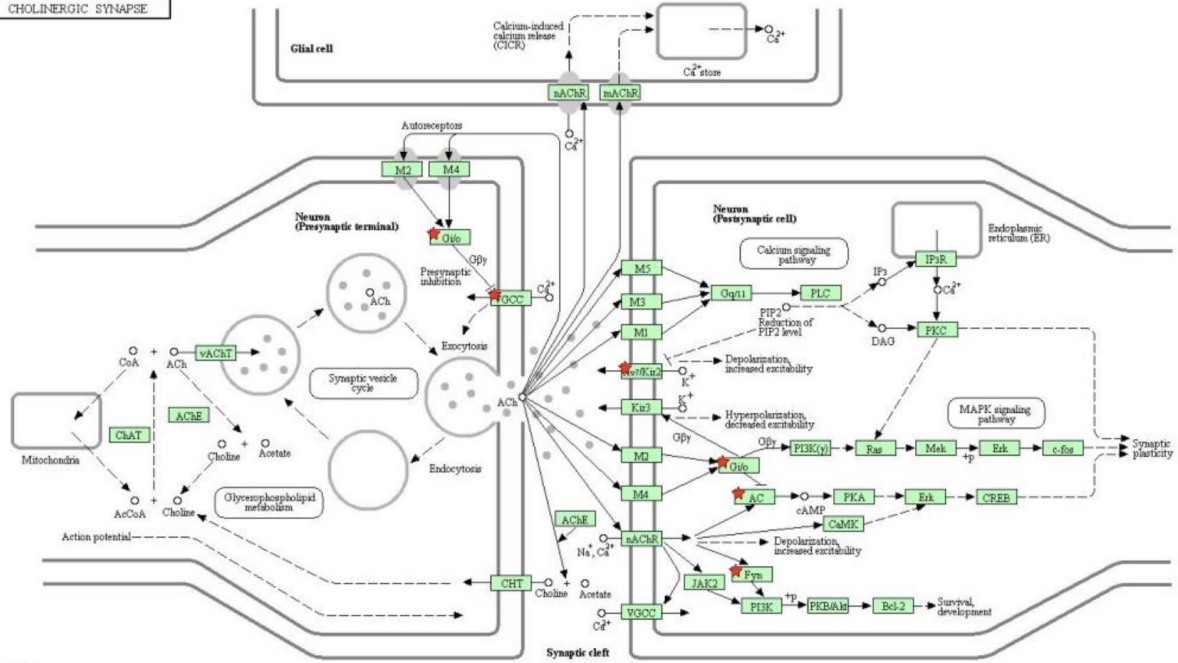


- Rolandic Epilepsy
- Speech disorder
- Dyslexia
- Migraine
- CTS on EEG
- Depression
- Other seizures
- ADHD
- Proband



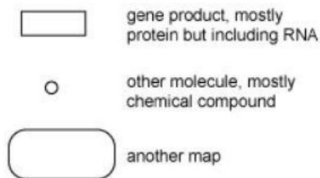
Supplementary Figure S3. Ingenuity Pathway Analysis of genes disrupted by CNV from European RE cases with high brain expression, creating a network of up to 70 genes. White symbols are genes added by IPA during network generation due to direct physical, or indirect (e.g. via activation) interactions with the input list.

CHOLINERGIC SYNAPSE

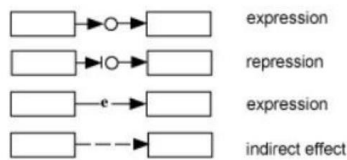


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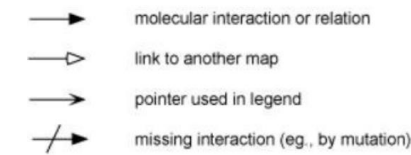
Objects



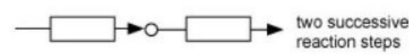
Gene expression relations



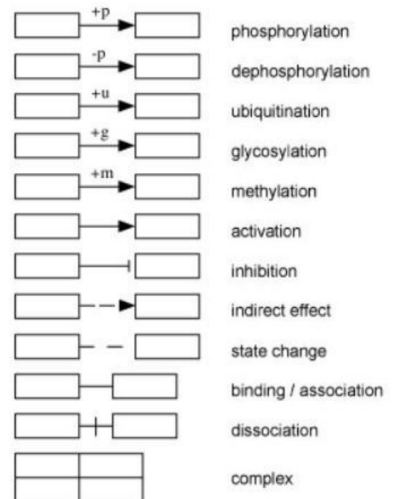
Arrows



Enzyme-enzyme relations



Protein-protein interactions



Supplementary Figure S4. KEGG pathway of cholinergic synapse from <http://www.kegg.jp/>. Red stars indicate genes that are from the IPA in Supplementary Figure 2. Enrichment analysis carried out within Enrichr <http://amp.pharm.mssm.edu/Enrichr/>.

Supplementary Table S1

Cohort	Sample Source	Original Sample (N)	Family Members (N)	Cases (N)	Controls (N)
RE	UK	537	412	125	-
NL4	The Netherlands	800	-	-	800

The original Dutch cohort included 2,262 controls (dataset NL4)¹. 800 controls from this dataset were randomly selected and used in the present study.

Supplementary Table S2

Cohort	Individuals after QC			SNPs	
	Samples (N)	Cases (N)	Controls (N)	Before QC (N)	After QC (N)
RE	76	76	-	538,448	227,632
NL4	795	-	795	719,665	612,666

After Quality Control, a total of 222,612 SNPs overlapped between the two datasets. Only affected individuals from the RE dataset were included in the QC to determine the population structure.

Supplementary Table S3

Case and Gene ID/hotspot	References
S218, <i>KLHL17</i>	2 3
SFR, 1q21.1	4 5
1050-301, <i>ARHGEF4</i>	6
RK044, <i>KCTD7</i>	7
RK011, <i>GRIN2A</i>	8-10
1012-301, 16p13.11	11-13
7083-301, <i>ARHGEF15</i>	14
All with Xp22.31 CNV	2 10 15-21
7007-301, <i>PTGER3</i>	22
RK029, <i>ASH1L</i>	23
1053-301, <i>CTNNA2</i>	24
S218, <i>ERBB4</i>	25 26
7037-301, <i>KCNIP4</i>	27
S52, <i>GRID2</i>	28
1029-301, <i>PLK2</i>	29 30
7007-301, <i>ARFGEF1</i>	31 32
SSM, <i>CTNNA3</i>	33 34
S38, <i>NRG3</i>	35
1041-301, <i>DLG2</i>	36
7021-301, <i>GRIP1</i>	37 38
1027-301, <i>UNC13</i>	39
SMJ, <i>SMAD3</i>	40
7034-301, <i>ASIC2</i>	41
NVH, <i>PTPRT</i>	42
1027-301, <i>SLITRK2</i>	43

Additional references for genes and regions disrupted by RE CNV and detailed in Tables 1 and 2 in the main text.

Term	Overlap	P-value	Adjusted P-value	Z-score	Combined Score	Genes
Cholinergic synapse_Homo sapiens_hsa04725	8/111	5.55E-09	9.60E-07	-2.06	39.18	GNGT1;KCNJ4;KCNJ12;GNB1;CACNA1B;ADCY2;FYN;ADCY1
Pathways in cancer_Homo sapiens_hsa05200	12/397	1.41E-08	1.22E-06	-2.08	37.65	NTRK1;GNGT1;BMP2;TGFB1;CCND1;MYC;FGF18;GNB1;ADCY2;ADCY1;CTNNA2;RAC1
GABAergic synapse_Homo sapiens_hsa04727	5/88	1.52E-05	6.20E-04	-1.80	19.92	GNGT1;GNB1;CACNA1B;ADCY2;ADCY1
Morphine addiction_Homo sapiens_hsa05032	5/91	1.79E-05	6.20E-04	-1.75	19.07	GNGT1;GNB1;CACNA1B;ADCY2;ADCY1
Hippo signaling pathway_Homo sapiens_hsa04390	6/153	1.73E-05	6.20E-04	-1.66	18.25	BMP2;TGFB1;DLG2;CCND1;MYC;CTNNA2
MAPK signaling pathway_Homo sapiens_hsa04010	7/255	3.35E-05	8.27E-04	-1.85	19.01	NTRK1;TGFB1;MYC;FGF18;CACNA1B;RAC1;TNF
Retrograde endocannabinoid signaling_Homo sapiens_hsa04723	5/101	2.97E-05	8.27E-04	-1.80	18.74	GNGT1;GNB1;CACNA1B;ADCY2;ADCY1
Colorectal cancer_Homo sapiens_hsa05210	4/62	6.96E-05	1.51E-03	-1.73	16.55	TGFB1;CCND1;MYC;RAC1
Thyroid cancer_Homo sapiens_hsa05216	3/29	1.47E-04	2.82E-03	-1.36	11.98	NTRK1;CCND1;MYC
Oxytocin signaling pathway_Homo sapiens_hsa04921	5/158	2.47E-04	3.88E-03	-1.71	14.20	KCNJ4;CCND1;KCNJ12;ADCY2;ADCY1
TGF-beta signaling pathway_Homo sapiens_hsa04350	4/84	2.27E-04	3.88E-03	-1.60	13.44	BMP2;TGFB1;MYC;TNF
HTLV-I infection_Homo sapiens_hsa05166	6/258	3.09E-04	4.11E-03	-1.64	13.28	TGFB1;CCND1;MYC;ADCY2;ADCY1;TNF
Dilated cardiomyopathy_Homo sapiens_hsa05414	4/90	2.96E-04	4.11E-03	-1.56	12.71	TGFB1;ADCY2;ADCY1;TNF
Circadian entrainment_Homo sapiens_hsa04713	4/95	3.64E-04	4.50E-03	-1.57	12.40	GNGT1;GNB1;ADCY2;ADCY1
AGE-RAGE signaling pathway in diabetic complications_Homo sapiens_hsa04933	4/101	4.59E-04	4.97E-03	-1.63	12.55	TGFB1;CCND1;RAC1;TNF
Amoebiasis_Homo sapiens_hsa05146	4/100	4.42E-04	4.97E-03	-1.48	11.44	SERPINB1;TGFB1;ADCY1;TNF
Chemokine signaling pathway_Homo sapiens_hsa04062	5/187	5.35E-04	5.45E-03	-1.51	11.40	GNGT1;GNB1;ADCY2;ADCY1;RAC1

Supplementary Table S4: Output table from Enricher of enriched KEGG pathways from IPA analysis of CNV-disrupted genes with high brain expression in European cases.

Term	Overlap	P-value	Adjusted P-value	Z-score	Combined Score	Genes
GTPase activity, coupled (GO:0061745)	6/151	1.6E-05	3.8E-03	-2.57	28.38	EEF1A1;GNGT1;RAB3C;SAR1B;GNB1;RAC1
GTPase activity (GO:0003924)	6/157	2.0E-05	3.8E-03	-2.61	28.23	EEF1A1;GNGT1;RAB3C;SAR1B;GNB1;RAC1
GTPase motor activity (GO:0061791)	6/169	3.0E-05	3.8E-03	-2.57	26.79	EEF1A1;GNGT1;RAB3C;SAR1B;GNB1;RAC1
Rho guanyl-nucleotide exchange factor activity (GO:0005089)	4/52	3.5E-05	3.8E-03	-1.96	20.11	PLEKHG2;MCF2L;MCF2;ARHGEF4
Rac guanyl-nucleotide exchange factor activity (GO:0030676)	4/56	4.7E-05	4.1E-03	-2.05	20.49	PLEKHG2;MCF2L;MCF2;ARHGEF4
PDZ domain binding (GO:0030165)	4/62	7.0E-05	5.0E-03	-2.04	19.57	PRKN;KCNJ4;GRID2;PSEN1

Supplementary Table S5: Output table from Enricher of enriched GO Molecular Functions from IPA analysis of CNV-disrupted genes with high brain expression in European cases.

Term	Overlap	P-value	Adjusted P-value	Z-score	Combined Score	Genes
positive regulation of apoptotic process (GO:0043065)	12/374	7.28E-09	9.95E-06	-4.87	91.24	NTRK1;BMP2;TGFB1;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;FYN;RAC1;HMGB1;TNF
canonical Wnt signaling pathway involved in positive regulation of apoptotic process (GO:0044337)	11/279	3.90E-09	9.95E-06	-4.36	84.39	BMP2;APH1B;PLEKHG2;MYC;MCF2;MCF2L;ARHGEF4;RAC1;PSEN1;HMGB1;TNF
positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO:0043280)	10/258	2.48E-08	2.26E-05	-4.13	72.31	BMP2;APH1B;PLEKHG2;MYC;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of neuron apoptotic process (GO:0043525)	10/270	3.81E-08	2.60E-05	-4.25	72.68	BMP2;GRID2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of leukocyte apoptotic process (GO:2000108)	9/234	1.40E-07	2.64E-05	-3.97	62.61	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of fat cell apoptotic process (GO:1904651)	9/234	1.40E-07	2.64E-05	-3.97	62.60	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of myofibroblast cell apoptotic process (GO:1904522)	9/234	1.40E-07	2.64E-05	-3.96	62.58	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of muscle cell apoptotic process (GO:0010661)	9/234	1.40E-07	2.64E-05	-3.96	62.50	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of epithelial cell apoptotic process (GO:1904037)	9/234	1.40E-07	2.64E-05	-3.96	62.50	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of myeloid cell apoptotic process (GO:0033034)	9/235	1.45E-07	2.64E-05	-3.96	62.42	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of glial cell apoptotic process (GO:0034352)	9/234	1.40E-07	2.64E-05	-3.95	62.42	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of mesenchymal cell apoptotic process (GO:2001055)	9/234	1.40E-07	2.64E-05	-3.95	62.41	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of apoptotic process involved in development (GO:1904747)	9/234	1.40E-07	2.64E-05	-3.95	62.37	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of apoptotic process in other organism (GO:0044533)	9/234	1.40E-07	2.64E-05	-3.95	62.34	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of compound eye retinal cell apoptotic process (GO:1901694)	9/234	1.40E-07	2.64E-05	-3.95	62.31	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of execution phase of apoptosis (GO:1900119)	9/241	1.79E-07	2.72E-05	-4.03	62.62	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of anoikis (GO:2000210)	9/240	1.73E-07	2.72E-05	-3.98	62.01	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of fibroblast apoptotic process (GO:2000271)	9/238	1.61E-07	2.72E-05	-3.94	61.69	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
positive regulation of apoptotic signaling pathway (GO:2001235)	9/248	2.29E-07	3.29E-05	-4.09	62.51	BMP2;APH1B;PLEKHG2;MCF2;MCF2L;ARHGEF4;RAC1;HMGB1;TNF
cellular response to forskolin (GO:1904322)	4/19	5.43E-07	7.41E-05	-3.42	49.30	TGFB1;ADCY2;ADCY1;TNF
Notch receptor processing, ligand-dependent (GO:0035333)	5/59	2.11E-06	2.74E-04	-2.57	33.62	BMP2;TGFB1;APH1B;MYC;PSEN1
positive regulation of I-kappaB phosphorylation (GO:1903721)	8/252	3.05E-06	3.47E-04	-4.03	51.22	PRKN;NTRK1;BMP2;TGFB1;CCND1;PLK2;RAC1;TNF
induction by virus of host protein phosphorylation (GO:0039614)	6/113	3.02E-06	3.47E-04	-2.90	36.80	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of inhibitory G-protein coupled receptor phosphorylation (GO:1904325)	6/113	3.02E-06	3.47E-04	-2.89	36.77	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of MAP kinase activity (GO:0043406)	6/118	3.89E-06	4.25E-04	-3.06	38.16	BMP2;TGFB1;FGF18;HMGB1;TNF;ADRA2A
positive regulation of histone phosphorylation (GO:0033129)	6/120	4.29E-06	4.50E-04	-2.88	35.54	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of phosphorylation of RNA polymerase II C-terminal domain (GO:1901409)	6/122	4.72E-06	4.77E-04	-2.95	36.17	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of MAPK cascade (GO:0043410)	7/194	5.71E-06	5.57E-04	-3.41	41.19	NTRK1;BMP2;TGFB1;CCND1;RAC1;HMGB1;TNF
positive regulation of protein autophosphorylation (GO:0031954)	6/128	6.22E-06	5.86E-04	-3.05	36.54	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of peptidyl-threonine phosphorylation (GO:0010800)	6/131	7.11E-06	6.48E-04	-3.10	36.73	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
activation of MAPKK activity (GO:0000186)	5/86	1.36E-05	1.20E-03	-3.03	33.92	NTRK1;TGFB1;FGF18;TNF;ADRA2A
positive regulation of ERK1 and ERK2 cascade via TNFSF11-mediated signaling (GO:0071848)	6/151	1.60E-05	1.33E-03	-3.28	36.26	NTRK1;BMP2;TGFB1;FGF18;HMGB1;TNF
positive regulation of protein phosphorylation (GO:0001934)	6/151	1.60E-05	1.33E-03	-3.26	36.03	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of pathway-restricted SMAD protein phosphorylation (GO:0010862)	6/155	1.86E-05	1.49E-03	-3.21	34.94	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of peptidyl-serine phosphorylation (GO:0033138)	6/160	2.22E-05	1.74E-03	-3.46	37.11	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of peptidyl-tyrosine phosphorylation (GO:0050731)	6/169	3.03E-05	2.30E-03	-3.40	35.41	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
cellular response to catecholamine stimulus (GO:0071870)	3/18	3.37E-05	2.49E-03	-2.96	30.49	TGFB1;GNB1;TNF
positive regulation of protein kinase activity (GO:0045860)	6/176	3.80E-05	2.66E-03	-3.40	34.62	NTRK1;BMP2;TGFB1;CCND1;RAC1;TNF
positive regulation of JUN kinase activity (GO:0043507)	5/106	3.75E-05	2.66E-03	-2.87	29.22	TGFB1;FGF18;HMGB1;TNF;ADRA2A
cAMP-mediated signaling (GO:0019933)	3/23	7.22E-05	4.93E-03	-2.94	28.04	RIMS2;ADCY2;ADCY1
negative regulation of neuron apoptotic process (GO:0043524)	8/399	8.31E-05	5.40E-03	-5.02	47.19	NTRK1;PRKN;GRID2;MYC;PLK2;ASNS;PSEN1;SOD2

Supplementary Table S6: Output table from Enricher of enriched GO Biological Processes from IPA analysis of CNV-disrupted genes with high brain expression in European cases.

Table 1

Term	Overlap	P-value	Adjusted P-value	Z-score	Combined Score	Genes
mRNA binding (GO:0003729)	18/1230	1.52E-07	6.78E-06	-3.87	60.74	YWHAE;EIF4A2;LRRC59;SF3B2;RFX3;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
RNA binding (GO:0003723)	17/1199	5.68E-07	6.78E-06	-3.68	52.90	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
base pairing with RNA (GO:0000498)	17/1199	5.68E-07	6.78E-06	-3.67	52.81	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
N6-methyladenosine-containing RNA binding (GO:1990247)	17/1199	5.68E-07	6.78E-06	-3.67	52.73	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
pre-mRNA binding (GO:0036002)	17/1200	5.75E-07	6.78E-06	-3.67	52.68	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
7S RNA binding (GO:0008312)	17/1200	5.75E-07	6.78E-06	-3.66	52.58	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
misfolded RNA binding (GO:0034336)	17/1199	5.68E-07	6.78E-06	-3.66	52.56	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
G-quadruplex RNA binding (GO:0002151)	17/1201	5.82E-07	6.78E-06	-3.66	52.53	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
histone pre-mRNA DCP binding (GO:0071208)	17/1200	5.75E-07	6.78E-06	-3.65	52.50	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
alpha-aminoacyl-tRNA binding (GO:1904678)	17/1199	5.68E-07	6.78E-06	-3.65	52.50	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
snRNA binding (GO:0017069)	17/1202	5.89E-07	6.78E-06	-3.66	52.48	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
AU-rich element binding (GO:0017091)	17/1203	5.95E-07	6.78E-06	-3.66	52.42	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
miRNA binding (GO:0035198)	17/1203	5.95E-07	6.78E-06	-3.65	52.38	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
21U-RNA binding (GO:0034583)	17/1199	5.68E-07	6.78E-06	-3.64	52.37	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
pre-miRNA binding (GO:0070883)	17/1201	5.82E-07	6.78E-06	-3.65	52.37	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
telomeric repeat-containing RNA binding (GO:0061752)	17/1200	5.75E-07	6.78E-06	-3.64	52.36	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
RNA stem-loop binding (GO:0035613)	17/1200	5.75E-07	6.78E-06	-3.64	52.30	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
GU repeat RNA binding (GO:1990605)	17/1199	5.68E-07	6.78E-06	-3.63	52.26	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
RNA cap binding (GO:0000339)	17/1201	5.82E-07	6.78E-06	-3.64	52.24	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
piRNA binding (GO:0034584)	17/1202	5.89E-07	6.78E-06	-3.64	52.22	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
BRE binding (GO:0042835)	17/1200	5.75E-07	6.78E-06	-3.63	52.20	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
ribonuclease P RNA binding (GO:0033204)	17/1199	5.68E-07	6.78E-06	-3.63	52.20	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
telomerase RNA binding (GO:0070034)	17/1205	6.09E-07	6.78E-06	-3.64	52.15	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
snoRNA binding (GO:0030515)	17/1206	6.16E-07	6.78E-06	-3.65	52.14	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
primary miRNA binding (GO:0070878)	17/1204	6.02E-07	6.78E-06	-3.64	52.13	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
regulatory region RNA binding (GO:0001069)	17/1199	5.68E-07	6.78E-06	-3.62	52.10	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
rRNA binding (GO:0019843)	17/1205	6.09E-07	6.78E-06	-3.64	52.04	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
siRNA binding (GO:0035197)	17/1203	5.95E-07	6.78E-06	-3.63	52.04	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
translation factor activity, RNA binding (GO:0008135)	17/1210	6.46E-07	6.86E-06	-3.65	52.06	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
single-stranded RNA binding (GO:0003727)	17/1216	6.92E-07	7.10E-06	-3.66	51.88	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
tRNA binding (GO:0000049)	17/1219	7.16E-07	7.11E-06	-3.65	51.62	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
double-stranded RNA binding (GO:0003725)	17/1223	7.49E-07	7.21E-06	-3.62	51.04	YWHAE;EIF4A2;LRRC59;SF3B2;LARP4B;APEH;C14ORF93;GTPBP4;AKAP1;MOV10;S100A16;KYAT3;LUC7L3;RP9;METTL16;SRSF7;FAM50A
death receptor binding (GO:0005123)	2/14	1.07E-03	9.98E-03	-1.03	7.07	TMBIM1;TNFSF11

Supplementary Table S7: Output table from Enricher of enriched GO Molecular Functions from IPA analysis of CNV-disrupted genes with high brain expression in European controls.

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