Transcriptome-wide association study, variant prioritization and colocalization analysis

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Table1: S-MultiXcan results for genes that were Bonferroni significant (1.79E-07) for cross-tissue QTL sharing (1,2)

GENE	GENE_NAME	PVALUE	N	N_INDEP	P_I_BEST	T_I_BEST	P_I_WORST	T_I_WORST	EIGEN_MAX	EIGEN_MIN	EIGEN_MIN_KEPT	Z_MIN	Z_MAX	Z_MEAN	Z_SD
ENSG00000185736.15	ADARB2	4.26E-07	6	5	3.86E-08	Brain_Amygdala	0.803900004	Brain_Cerebellum	2.337136	1.29E-18	0.169514	0.248303	5.497323	2.947977	2.12053
ENSG00000177352.9	CCDC71	2.87E-09	13	1	1.07E-10	Brain_Amygdala	0.0001064	Brain_Cortex	12.36216	2.26E-19	12.36216	3.875514	6.45714	5.774468	0.928683
ENSG00000124228.14	DDX27	6.76E-07	8	2	1.11E-07	Brain_Amygdala	0.006949999	Brain_Cerebellar_Hemisphere	7.203769	1.45E-33	0.796231	-2.69923	5.308057	1.675719	2.846354
ENSG00000170837.2	GPR27	4.25E-06	14	3	1.04E-07	Brain_Amygdala	0.549300019	Whole_Blood	10.814	3.29E-17	0.998184	0.598809	5.31872	4.352029	1.265387
ENSG00000233822.4	HIST1H2BN	7.45E-16	13	2	9.30E-17	Brain_Amygdala	0.349800002	Brain_Cerebellar_Hemisphere	7.379185	1.02E-32	5.620815	-0.93498	8.313411	4.423304	4.561427
ENSG00000185345.18	PARK2	3.16E-08	12	3	9.36E-09	Brain_Amygdala	0.805300002	Brain_Putamen_basal_ganglia	6.421233	1.08E-18	1.496722	-3.1928	5.741882	2.312451	3.747521
ENSG00000211450.9	SELENOH	4.89E-11	7	1	4.89E-11	Brain_Amygdala	4.89E-11	Brain_Nucleus_accumbens_basal_ganglia	7	1.89E-33	7	-6.57413	-6.57413	-6.57413	3.63E-16
ENSG00000100372.14	SLC25A17	3.34E-12	12	3	1.74E-13	Brain_Amygdala	0.118799987	Brain_Anterior_cingulate_cortex_BA24	8.398641	3.80E-18	0.48444	1.55983	7.367621	5.592848	2.484963
ENSG00000120896.13	SORBS3	7.15E-07	12	4	1.52E-07	Brain_Amygdala	0.857905438	Brain_Cerebellum	7.570772	1.76E-17	0.272294	-5.24965	-0.17904	-3.87927	1.562559
ENSG00000100380.13	ST13	2.60E-07	3	3	1.02E-08	Brain_Amygdala	0.091890003	Brain_Putamen_basal_ganglia	1.941039	0.153932	0.153932	1.685511	5.726871	3.955482	2.066298
ENSG00000187626.8	ZKSCAN4	8.66E-25	12	4	1.65E-12	Brain_Amygdala	0.540599996	Brain_Substantia_nigra	10.26168	3.83E-17	0.385879	-7.06126	-0.61191	-5.2116	2.751543
ENSG00000196653.11	ZNF502	8.67E-09	14	2	2.19E-09	Brain_Amygdala	3.39E-05	Brain_Spinal_cord_cervical_c-1	12.46654	1.18E-17	1.491818	-5.9829	-4.14559	-4.92231	0.81104
ENSG00000139567.12	ACVRL1	6.13E-07	4	3	9.85E-08	Brain_Anterior_cingulate_cortex_BA24	0.745681423	Brain_Caudate_basal_ganglia	2.561269	6.24E-18	0.472098	-5.32951	0.324339	-3.00467	2.806907
ENSG00000166165.12	CKB	5.57E-11	14	3	4.36E-12	Brain_Anterior_cingulate_cortex_BA24	0.658017149	Brain_Nucleus_accumbens_basal_ganglia	9.860498	1.65E-17	0.897398	-6.92501	6.311021	-3.78399	3.882756

ENSG00000077063.10	CTTNBP2	7.71E-10	11	5	2.48E-10	Brain_Anterior_cingulate_cortex_BA24	0.888400003	Brain_Amygdala	5.42763	3.84E-18	0.328584	-6.32804	5.720198	-0.961	4.010373
ENSG00000100395.14	L3MBTL2	7.00E-14	6	2	1.09E-14	Brain_Anterior_cingulate_cortex_BA24	0.457341302	Brain_Nucleus_accumbens_basal_ganglia	4.968836	0.00211	0.995825	-0.74323	7.727708	3.466047	2.824835
ENSG00000204410.14	MSH5	5.52E-08	13	4	8.77E-08	Brain_Anterior_cingulate_cortex_BA24	0.940976959	Whole_Blood	6.668273	1.84E-17	0.453258	0.074042	5.35054	3.335814	1.70869
ENSG00000204962.5	PCDHA8	4.48E-07	13	2	6.44E-08	Brain_Anterior_cingulate_cortex_BA24	0.033799998	Brain_Amygdala	10.98025	9.84E-18	1.743951	-5.40617	-2.12245	-4.76358	1.187356
ENSG00000049449.8	RCN1	7.67E-09	13	2	1.16E-09	Brain_Anterior_cingulate_cortex_BA24	0.819599996	Whole_Blood	12.00353	2.50E-17	0.99647	-0.22806	6.086092	5.600388	1.751231
ENSG00000283458.1	RP11-1I2.1	1.29E-06	8	2	4.17E-08	Brain_Anterior_cingulate_cortex_BA24	0.001180724	Brain_Caudate_basal_ganglia	7.063877	5.17E-18	0.792181	-5.48353	-3.2435	-4.88938	0.698099
ENSG00000279325.1	RP11-24H2.3	2.67E-11	2	2	2.64E-11	Brain_Anterior_cingulate_cortex_BA24	1.68E-07	Brain_Amygdala	1.52042	0.47958	0.47958	-6.66526	-5.23198	-5.94862	1.013478
ENSG00000225399.4	RP11-3B7.1	6.77E-12	4	2	3.93E-10	Brain_Anterior_cingulate_cortex_BA24	0.611200002	Brain_Cortex	2.851496	1.98E-17	1.148504	-6.25678	0.508361	-2.87421	3.905858
ENSG00000272468.1	RP1-86C11.7	6.46E-11	10	4	3.71E-10	Brain_Anterior_cingulate_cortex_BA24	0.769567752	Brain_Hypothalamus	5.849808	1.94E-18	0.502065	-6.26576	6.265765	1.706523	4.175685
ENSG00000115524.15	SF3B1	1.65E-07	10	1	1.65E-07	Brain_Anterior_cingulate_cortex_BA24	1.65E-07	Brain_Caudate_basal_ganglia	10	3.42E-33	10	5.234648	5.234648	5.234648	6.62E-16
ENSG00000168273.7	SMIM4	1.86E-06	12	3	1.40E-07	Brain_Anterior_cingulate_cortex_BA24	0.295700024	Whole_Blood	9.624278	7.92E-18	1.000014	-5.26536	1.239053	-3.88753	2.356024
ENSG00000120314.18	WDR55	7.08E-06	13	2	1.55E-07	Brain_Anterior_cingulate_cortex_BA24	0.6457	Brain_Frontal_Cortex_BA9	10.70791	5.07E-17	1.952286	-5.24641	-0.45974	-3.94851	1.521598
ENSG00000101489.19	CELF4	5.04E-14	12	6	1.13E-16	Brain_Caudate_basal_ganglia	0.706744282	Brain_Anterior_cingulate_cortex_BA24	6.104946	4.26E-17	0.426476	-7.61516	8.2907	3.206687	4.824023
ENSG00000100399.15	CHADL	1.45E-09	5	3	1.29E-10	Brain_Caudate_basal_ganglia	0.01347	Brain_Nucleus_accumbens_basal_ganglia	3.722216	4.14E-18	0.182316	2.471095	6.4287	4.916034	2.075036
ENSG00000119616.11	FCF1	9.15E-14	12	2	2.63E-14	Brain_Caudate_basal_ganglia	0.101199991	Brain_Hypothalamus	10.47387	2.67E-17	1.420002	1.639064	7.615143	3.560412	2.081913

ENSG00000267325.1	LINC01415	6.38E-10	11	4	1.87E-09	Brain_Caudate_basal_ganglia	0.006034999	Brain_Putamen_basal_ganglia	6.319835	1.17E-18	0.251895	-6.00906	-2.74587	-4.56627	1.539704
ENSG00000250156.3	LINC02060	1.91E-09	10	1	1.91E-09	Brain_Caudate_basal_ganglia	1.91E-09	Brain_Nucleus_accumbens_basal_ganglia	10	2.69E-17	10	6.004858	6.004858	6.004858	1.32E-15
ENSG00000007372.21	PAX6	9.36E-12	12	1	9.36E-12	Brain_Caudate_basal_ganglia	9.36E-12	Brain_Amygdala	12	7.99E-17	12	6.816031	6.816031	6.816031	4.64E-16
ENSG00000041353.9	RAB27B	2.46E-08	10	3	1.44E-08	Brain_Caudate_basal_ganglia	0.8522	Brain_Anterior_cingulate_cortex_BA24	7.08631	2.30E-18	0.985783	-1.55184	5.668325	3.762557	3.089101
ENSG00000172575.11	RASGRP1	1.86E-06	10	2	1.63E-07	Brain_Caudate_basal_ganglia	0.791300003	Brain_Amygdala	8.865565	4.52E-17	1.07511	-5.23678	5.028085	0.49346	4.909751
ENSG00000096654.15	ZNF184	1.02E-15	11	2	1.85E-09	Brain_Caudate_basal_ganglia	0.0029	Brain_Hippocampus	10.60197	9.53E-18	0.398028	-6.01012	-2.97814	-3.80368	1.38953
ENSG00000112763.15	BTN2A1	3.94E-10	13	2	3.11E-09	Brain_Cerebellar_Hemisphere	0.113399986	Brain_Caudate_basal_ganglia	10.84433	2.73E-17	1.413134	-5.92584	-1.58309	-2.92613	1.672474
ENSG00000261353.1	CTA-14H9.5	3.24E-12	6	3	1.38E-12	Brain_Cerebellar_Hemisphere	3.92E-06	Brain_Caudate_basal_ganglia	3.932636	2.29E-17	0.486362	-4.61537	7.085944	2.898789	5.858451
ENSG00000250377.1	CTC-467M3.3	9.59E-11	5	2	5.55E-11	Brain_Cerebellar_Hemisphere	2.98E-09	Brain_Frontal_Cortex_BA9	4.573121	7.31E-17	0.426879	-6.55535	-5.93286	-6.05736	0.278384
ENSG00000281649.1	EBLN3P	2.36E-10	10	3	2.79E-08	Brain_Cerebellar_Hemisphere	0.020380006	Brain_Cortex	7.625815	1.38E-17	0.736006	-2.56413	5.553816	3.612867	3.301147
ENSG00000149485.18	FADS1	1.47E-06	14	2	4.33E-09	Brain_Cerebellar_Hemisphere	0.005198999	Brain_Spinal_cord_cervical_c-1	12.63439	9.13E-17	0.690862	-5.87098	5.760692	-4.0759	2.99274
ENSG00000228223.2	HCG11	7.66E-11	7	5	1.38E-12	Brain_Cerebellar_Hemisphere	0.534000007	Whole_Blood	2.888001	2.84E-17	0.617551	0.621912	7.085944	3.977141	2.602756
ENSG00000204389.9	HSPA1A	1.08E-07	3	1	1.08E-07	Brain_Cerebellar_Hemisphere	1.08E-07	Brain_Substantia_nigra	3	5.47E-48	3	5.31188	5.31188	5.31188	6.28E-16
ENSG00000204970.9	PCDHA1	9.37E-08	9	1	6.42E-08	Brain_Cerebellar_Hemisphere	1.05E-07	Brain_Anterior_cingulate_cortex_BA24	8.995428	2.90E-17	8.995428	-5.31733	5.40669	4.15556	3.552545
ENSG00000204969.6	PCDHA2	1.14E-06	6	1	6.17E-08	Brain_Cerebellar_Hemisphere	0.042230003	Brain_Frontal_Cortex_BA9	5.972292	3.96E-17	5.972292	-5.4138	5.413803	-1.24084	5.318537

ENSG00000255408.3	PCDHA3	1.50E-06	12	3	1.17E-07	Brain_Cerebellar_Hemisphere	0.590418874	Brain_Cortex	8.285453	6.52E-17	0.430401	-5.12624	5.298667	-0.53257	3.085417
ENSG00000137338.5	PGBD1	1.55E-12	13	5	1.67E-13	Brain_Cerebellar_Hemisphere	0.978935906	Brain_Nucleus_accumbens_basal_ganglia	5.549999	1.21E-17	0.290674	-7.37263	1.32612	-3.0449	3.35675
ENSG00000248483.6	POU5F2	4.11E-09	2	1	4.11E-09	Brain_Cerebellar_Hemisphere	4.11E-09	Brain_Cerebellar_Hemisphere	2	0	2	-5.87974	-5.87974	-5.87974	0
ENSG00000100387.8	RBX1	1.30E-08	10	2	4.34E-09	Brain_Cerebellar_Hemisphere	0.160400001	Brain_Spinal_cord_cervical_c-1	9.000067	7.65E-17	0.999933	-5.87065	1.403728	0.67629	2.300359
ENSG00000162367.11	TAL1	5.30E-07	10	2	9.01E-08	Brain_Cerebellar_Hemisphere	0.837599998	Brain_Cerebellum	8.745246	1.41E-17	0.976135	-5.29115	5.345656	3.67548	3.526309
ENSG00000182179.12	UBA7	5.49E-10	3	1	5.49E-10	Brain_Cerebellar_Hemisphere	5.49E-10	Brain_Cerebellum	3	0	3	-6.20436	-6.20436	-6.20436	8.88E-16
ENSG00000178917.15	ZNF852	9.97E-11	11	2	6.18E-10	Brain_Cerebellar_Hemisphere	7.18E-07	Brain_Anterior_cingulate_cortex_BA24	8.560703	1.86E-17	2.439297	-6.18564	5.749893	1.276386	5.922631
ENSG00000119682.16	AREL1	1.46E-13	10	2	2.63E-14	Brain_Cerebellum	0.0004835	Brain_Cortex	8.798951	9.66E-22	1.153419	-7.61514	-3.48973	-4.81375	1.748601
ENSG00000112249.13	ASCC3	2.77E-08	13	4	4.97E-09	Brain_Cerebellum	0.9911	Brain_Putamen_basal_ganglia	7.801973	2.08E-18	0.492841	-5.84819	0.080573	-2.13781	1.619107
ENSG00000164061.4	BSN	2.01E-10	2	2	1.23E-10	Brain_Cerebellum	2.71E-05	Brain_Cortex	1.39497	0.60503	0.60503	-6.43521	4.196811	-1.1192	7.517976
ENSG00000213047.12	DENND1B	3.67E-15	6	3	5.10E-16	Brain_Cerebellum	0.347000012	Brain_Cortex	4.344346	1.90E-19	0.734034	0.940424	8.1091	5.346974	3.34345
ENSG00000134824.13	FADS2	1.58E-07	8	2	1.01E-08	Brain_Cerebellum	0.570699987	Brain_Cortex	6.37226	1.22E-16	1.298069	-5.72854	5.373424	-0.68958	5.23938
ENSG00000126214.21	KLC1	4.06E-10	10	4	1.91E-12	Brain_Cerebellum	0.014800004	Brain_Hypothalamus	6.201084	2.18E-17	0.320961	-2.43724	7.040742	3.508421	2.635873
ENSG00000118263.14	KLF7	2.25E-10	7	3	2.17E-09	Brain_Cerebellum	0.265400017	Whole_Blood	4.53037	2.68E-17	0.33403	-5.98417	-1.11372	-3.75217	2.189727
ENSG00000155719.16	OTOA	1.55E-08	4	2	2.47E-09	Brain_Cerebellum	0.001577	Brain_Cortex	3.460284	1.03E-16	0.539716	3.160128	5.963494	5.262653	1.401683

ENSG00000112812.15	PRSS16	3.42E-14	11	6	3.87E-10	Brain_Cerebellum	0.899300002	Brain_Putamen_basal_ganglia	5.040955	2.25E-18	0.235869	-6.25909	2.743814	-3.32754	2.973102
ENSG00000102572.14	STK24	2.51E-07	12	3	1.16E-10	Brain_Cerebellum	0.062689997	Brain_Spinal_cord_cervical_c-1	8.223419	2.47E-17	0.42689	-5.22065	6.444105	1.688907	3.696381
ENSG00000169964.7	TMEM42	3.74E-10	14	3	2.79E-10	Brain_Cerebellum	0.437900002	Brain_Cerebellar_Hemisphere	10.83483	3.59E-17	0.722788	-6.30996	-0.77574	-2.53727	2.185663
ENSG00000196345.12	ZKSCAN7	1.44E-11	11	4	2.39E-11	Brain_Cerebellum	0.264900024	Brain_Frontal_Cortex_BA9	7.092933	8.81E-18	0.404935	-6.68023	1.114884	-5.36983	2.486557
ENSG00000186446.11	ZNF501	2.21E-08	14	2	6.27E-09	Brain_Cerebellum	0.002795001	Brain_Nucleus_accumbens_basal_ganglia	13.20588	6.41E-18	0.458661	-5.80944	-2.98943	-4.63418	0.819628
ENSG00000137185.11	ZSCAN9	1.40E-20	14	3	8.40E-17	Brain_Cerebellum	0.343020346	Whole_Blood	10.05555	5.12E-17	1.215407	-8.32548	-0.94821	-5.94954	2.377012
ENSG00000166170.9	BAG5	3.63E-11	10	4	6.67E-13	Brain_Cortex	0.9652	Brain_Hippocampus	6.35792	5.45E-18	0.231519	-0.04363	7.185997	5.139761	2.606918
ENSG00000134376.15	CRB1	1.66E-13	1	1	1.66E-13	Brain_Cortex	1.66E-13	Brain_Cortex	1	1	1	-7.37375	-7.37375	-7.37375	NA
ENSG00000258636.1	CTD-2298J14.2	3.32E-15	7	3	3.53E-16	Brain_Cortex	0.166799999	Brain_Anterior_cingulate_cortex_BA24	3.471243	9.15E-17	1.170157	-8.15379	-1.38256	-3.35956	3.275382
ENSG00000204390.9	HSPA1L	4.31E-07	8	4	1.08E-07	Brain_Cortex	0.671696397	Brain_Cerebellum	3.438814	3.95E-17	0.276405	-5.31188	5.31188	-0.31336	2.911133
ENSG00000187772.7	LIN28B	1.32E-10	8	2	3.36E-08	Brain_Cortex	0.014919996	Brain_Amygdala	5.365733	4.00E-18	2.634267	-5.5214	2.434315	-2.37482	3.294349
ENSG00000165379.13	LRFN5	2.64E-14	10	4	2.81E-16	Brain_Cortex	0.023240007	Brain_Caudate_basal_ganglia	7.502104	7.01E-17	0.575054	-7.95641	8.181342	0.454572	7.420767
ENSG00000119608.12	PROX2	1.40E-12	11	2	1.48E-13	Brain_Cortex	0.006690002	Brain_Anterior_cingulate_cortex_BA24	10.14095	9.85E-18	0.859046	-7.38858	-2.71189	-3.13705	1.410075
ENSG00000261839.1	RP1-265C24.8	9.11E-12	13	3	6.64E-10	Brain_Cortex	0.367800012	Brain_Cerebellar_Hemisphere	9.698419	7.03E-17	1.230748	-6.17436	3.850245	2.073283	3.726965

ENSG00000124214.19	STAU1	8.25E-08	13	3	2.03E-08	Brain_Cortex	0.962499999	Brain_Cerebellar_Hemisphere	9.621344	3.66E-17	1.008888	-5.60925	0.069992	-3.02407	1.847893
ENSG00000179152.19	TCAIM	1.69E-09	14	4	4.21E-08	Brain_Cortex	0.685970603	Whole_Blood	6.125752	1.06E-17	0.412739	-5.48185	0.815825	-2.24947	2.280499
ENSG00000164180.13	TMEM161B	2.42E-15	7	2	1.84E-12	Brain_Cortex	0.104357766	Brain_Anterior_cingulate_cortex_BA24	5.312115	2.96E-35	1.687885	-7.0461	-1.62408	-5.52287	2.601945
ENSG00000119596.17	YLPM1	1.33E-12	5	2	1.41E-13	Brain_Cortex	0.079989999	Brain_Caudate_basal_ganglia	4.072072	1.78E-32	0.927928	1.750744	7.395667	6.266682	2.524486
ENSG00000164062.12	APEH	4.19E-10	10	3	4.71E-10	Brain_Frontal_Cortex_BA9	0.348299997	Brain_Amygdala	7.383822	4.45E-17	0.685339	-4.32174	6.228374	0.188368	3.028088
ENSG00000120334.15	CENPL	9.51E-10	1	1	9.51E-10	Brain_Frontal_Cortex_BA9	9.51E-10	Brain_Frontal_Cortex_BA9	1	1	1	6.117441	6.117441	6.117441	NA
ENSG00000134852.14	CLOCK	2.31E-06	12	3	9.89E-08	Brain_Frontal_Cortex_BA9	0.048659993	Brain_Substantia_nigra	6.364584	1.06E-17	1.310042	-1.97156	5.328652	3.041543	2.081927
ENSG00000048828.16	FAM120A	3.44E-11	7	3	3.25E-10	Brain_Frontal_Cortex_BA9	1.08E-06	Brain_Nucleus_accumbens_basal_ganglia	5.566305	4.59E-17	0.503154	-6.28655	6.286549	-2.41732	5.729832
ENSG00000204965.8	PCDHA5	2.09E-06	7	3	6.07E-08	Brain_Frontal_Cortex_BA9	0.073420003	Brain_Cerebellum	4.485626	5.19E-17	0.207165	-5.4167	5.416698	-0.64988	4.545191
ENSG00000120910.14	PPP3CC	4.38E-05	13	3	1.77E-07	Brain_Frontal_Cortex_BA9	0.224899991	Brain_Putamen_basal_ganglia	9.921608	6.20E-17	0.627881	1.213601	5.222315	3.63374	1.418124
ENSG00000157837.15	SPPL3	1.10E-10	11	3	9.32E-12	Brain_Frontal_Cortex_BA9	0.272775709	Whole_Blood	9.160607	1.17E-16	0.500319	-6.8166	1.096693	-5.3049	2.292288
ENSG00000166166.12	TRMT61A	5.90E-10	14	3	1.14E-10	Brain_Frontal_Cortex_BA9	0.259800005	Brain_Substantia_nigra	8.865914	1.01E-17	0.987933	1.126864	6.446981	2.721405	1.822599
ENSG00000156599.10	ZDHHC5	1.65E-10	14	3	5.01E-11	Brain_Frontal_Cortex_BA9	0.250300001	Brain_Hypothalamus	11.17146	6.39E-18	0.421035	-6.57061	6.499527	-1.20263	3.508481
ENSG00000182272.11	B4GALNT4	0.000133643	13	4	3.85E-08	Brain_Hippocampus	0.526047171	Brain_Cerebellar_Hemisphere	8.749351	1.53E-17	0.330391	-1.15084	5.497552	2.806018	1.778762
ENSG00000226913.1	BSN-AS2	3.53E-10	13	2	1.23E-10	Brain_Hippocampus	0.066689996	Brain_Amygdala	12.15891	3.73E-18	0.827092	1.833758	6.435214	2.357433	1.361371
ENSG00000245526.10	LINC00461	1.31E-10	5	2	1.55E-11	Brain_Hippocampus	5.42E-09	Brain_Nucleus_accumbens_basal_ganglia	4.766789	1.06E-16	0.227926	-6.74299	-5.83358	-6.05393	0.388185

ENSG00000076685.18	NT5C2	1.16E-06	13	5	4.42E-09	Brain_Hippocampus	0.766473638	Brain_Hypothalamus	7.107372	1.38E-16	0.433927	-5.86783	0.950054	-1.60929	2.011593
ENSG00000067560.10	RHOA	6.35E-11	11	2	4.96E-11	Brain_Hippocampus	0.063730006	Brain_Amygdala	7.9307	2.97E-18	3.061954	-1.85406	6.572102	1.697012	3.464067
ENSG00000271755.1	RP1-153G14.4	2.21E-15	13	4	3.82E-15	Brain_Hippocampus	0.045740003	Brain_Spinal_cord_cervical_c-1	9.043862	4.57E-17	0.476364	-2.13698	7.860829	3.502757	3.458909
ENSG00000124140.13	SLC12A5	4.55E-13	12	6	1.82E-12	Brain_Hippocampus	0.20449998	Brain_Nucleus_accumbens_basal_ganglia	5.740457	1.33E-17	0.282995	-2.08886	7.047853	3.331488	2.837392
ENSG00000221995.5	TIAF1	3.07E-05	14	2	1.79E-07	Brain_Hippocampus	0.747200001	Brain_Putamen_basal_ganglia	11.31803	5.73E-17	1.766909	-5.22001	0.477228	-3.76368	1.818707
ENSG00000158691.14	ZSCAN12	3.19E-20	14	5	1.14E-18	Brain_Hippocampus	0.849699994	Brain_Frontal_Cortex_BA9	6.153374	3.03E-17	0.85018	-1.54787	8.820546	1.12584	3.03877
ENSG00000124207.16	CSE1L	4.54E-07	14	3	3.29E-08	Brain_Hypothalamus	0.230800013	Brain_Amygdala	11.79445	1.75E-17	0.461612	-5.52537	-1.1983	-3.89394	1.546142
ENSG00000100393.12	EP300	1.25E-13	14	2	3.78E-13	Brain_Hypothalamus	0.015950005	Brain_Substantia_nigra	12.56503	4.03E-17	1.433701	2.410058	7.263197	5.098588	1.315038
ENSG00000140564.11	FURIN	2.27E-07	13	5	1.63E-09	Brain_Hypothalamus	0.836700005	Whole_Blood	8.367737	2.01E-17	0.512666	-6.03135	0.206116	-3.40558	1.738731
ENSG00000096433.10	ITPR3	2.72E-08	12	5	1.01E-07	Brain_Hypothalamus	0.595474198	Brain_Cerebellum	6.273661	6.66E-18	0.281793	-3.04536	5.324772	1.437199	2.857531
ENSG00000178053.17	MLF1	1.16E-09	14	4	3.90E-08	Brain_Hypothalamus	0.876841874	Brain_Frontal_Cortex_BA9	6.120224	4.05E-17	0.364634	-2.318	5.495111	2.232306	2.972995
ENSG00000172260.14	NEGR1	1.77E-25	13	1	3.19E-25	Brain_Hypothalamus	2.20E-23	Brain_Cortex	12.48403	1.09E-18	12.48403	9.963501	10.37591	10.22495	0.113901
ENSG00000145029.13	NICN1	3.46E-11	12	4	4.79E-11	Brain_Hypothalamus	0.502199985	Brain_Substantia_nigra	7.210438	2.34E-17	0.480935	-6.57729	5.505494	0.26495	4.443671
ENSG00000169760.17	NLGN1	1.21E-07	13	3	1.60E-09	Brain_Hypothalamus	0.676600003	Brain_Amygdala	8.914815	6.22E-19	1.470625	-4.0638	6.033633	-0.41577	2.595346
ENSG00000260100.1	RP11-220I1.5	2.79E-08	4	1	2.79E-08	Brain_Hypothalamus	2.79E-08	Brain_Amygdala	4	0	4	5.553816	5.553816	5.553816	7.25E-16
ENSG00000131323.14	TRAF3	2.48E-07	11	3	9.62E-08	Brain_Hypothalamus	0.48962568	Whole_Blood	8.994263	3.10E-17	0.353953	0.690904	5.333797	2.22112	1.601557

ENSG00000198315.10	ZKSCAN8	1.30E-08	14	2	2.55E-10	Brain_Hypothalamus	0.141866097	Whole_Blood	12.97274	8.99E-17	0.950432	1.468877	6.324208	5.431343	1.21054
ENSG00000111801.15	BTN3A3	7.47E-09	11	4	3.21E-10	Brain_Nucleus_accumbens_basal_ganglia	0.135299995	Brain_Caudate_basal_ganglia	7.154264	1.92E-18	0.584427	-6.2884	1.515286	-3.50585	3.481452
ENSG00000173421.16	CCDC36	2.23E-11	11	3	2.41E-10	Brain_Nucleus_accumbens_basal_ganglia	0.590900001	Brain_Cortex	9.185412	4.20E-18	0.80301	-6.33239	0.563786	-5.05465	2.77143
ENSG00000101017.13	CD40	5.08E-07	14	3	3.62E-08	Brain_Nucleus_accumbens_basal_ganglia	0.029285318	Brain_Cerebellar_Hemisphere	11.40295	2.97E-17	0.689815	-5.50852	-2.17962	-4.72003	0.891294
ENSG00000149295.13	DRD2	7.80E-19	12	7	1.87E-20	Brain_Nucleus_accumbens_basal_ganglia	0.915155539	Brain_Cerebellum	4.18993	6.51E-18	0.241998	-9.26968	5.281581	-0.70909	4.419129
ENSG00000156395.12	SORCS3	1.02E-10	22	2	5.77E-11	Brain_Nucleus_accumbens_basal_ganglia	0.0002888	Brain_Frontal_Cortex_BA9	1.295785	0.704215	0.704215	-6.54958	-3.62514	-5.08736	2.067887
ENSG00000106460.18	TMEM106B	3.76E-12	12	4	1.72E-13	Brain_Nucleus_accumbens_basal_ganglia	0.116000013	Brain_Hippocampus	8.855807	5.91E-17	0.553254	1.571787	7.369243	5.530825	1.742452
ENSG00000135655.15	USP15	8.14E-06	13	5	5.88E-08	Brain_Nucleus_accumbens_basal_ganglia	0.811600003	Brain_Amygdala	8.409019	5.29E-18	0.495232	-1.57206	5.422271	0.789667	2.142786
ENSG00000114316.12	USP4	2.84E-10	13	2	3.71E-11	Brain_Nucleus_accumbens_basal_ganglia	0.460434149	Brain_Frontal_Cortex_BA9	8.922654	3.71E-33	4.077346	-6.61522	6.61522	1.438795	5.293083
ENSG00000100403.11	ZC3H7B	1.50E-09	14	3	2.51E-11	Brain_Nucleus_accumbens_basal_ganglia	0.115876163	Whole_Blood	10.86176	1.44E-18	0.703643	-1.57232	6.672594	5.248187	2.515477
ENSG00000186448.14	ZNF197	3.11E-12	11	3	1.05E-14	Brain_Nucleus_accumbens_basal_ganglia	0.212899991	Brain_Spinal_cord_cervical_c-1	8.768395	4.08E-17	0.726055	-7.73333	-1.24563	-5.89294	1.942745
ENSG00000185219.16	ZNF445	1.17E-10	7	4	1.01E-09	Brain_Nucleus_accumbens_basal_ganglia	0.802800001	Brain_Cortex	4.032293	5.16E-17	0.616199	-6.10824	2.123763	-3.77288	3.434803
ENSG00000145020.15	AMT	9.47E-11	14	1	5.49E-12	Brain_Putamen_basal_ganglia	2.34E-08	Brain_Nucleus_accumbens_basal_ganglia	13.58524	4.96E-18	13.58524	-6.89233	-5.5847	-6.37773	0.37249
ENSG00000188938.15	FAM120AOS	2.62E-10	14	4	4.97E-09	Brain_Putamen_basal_ganglia	0.703366301	Brain_Cortex	7.625982	3.83E-17	0.743036	-5.84811	-0.38078	-4.2928	1.650213
ENSG00000233276.3	GPX1	1.22E-10	14	2	9.40E-12	Brain_Putamen_basal_ganglia	2.00E-05	Brain_Substantia_nigra	12.76948	1.58E-17	1.230518	4.264445	6.815465	6.247982	0.838306

ENSG00000203809.6	LIN28B-AS1	8.64E-11	10	3	2.13E-12	Brain_Putamen_basal_ganglia	1.67E-06	Brain_Cortex	9.232257	2.02E-19	0.342759	4.789446	7.025567	6.493217	0.671839
ENSG00000171206.13	TRIM8	2.71E-05	9	3	7.62E-08	Brain_Putamen_basal_ganglia	0.047530004	Brain_Cortex	6.10341	5.29E-17	0.755066	1.981547	5.375784	3.276428	1.263387
ENSG00000184357.4	HIST1H1B	2.90E-18	1	1	2.90E-18	Brain_Spinal_cord_cervical_c-1	2.90E-18	Brain_Spinal_cord_cervical_c-1	1	1	1	-8.71522	-8.71522	-8.71522	NA
ENSG00000274641.1	HIST1H2BO	2.36E-14	1	1	2.36E-14	Brain_Spinal_cord_cervical_c-1	2.36E-14	Brain_Spinal_cord_cervical_c-1	1	1	1	-7.62921	-7.62921	-7.62921	NA
ENSG00000163807.5	KIAA1143	4.83E-08	12	2	8.31E-09	Brain_Spinal_cord_cervical_c-1	0.701599989	Brain_Hypothalamus	8.802409	9.78E-18	2.990539	-0.38316	5.76201	3.141881	2.631822
ENSG00000185909.14	KLHDC8B	2.57E-13	14	2	6.66E-14	Brain_Spinal_cord_cervical_c-1	0.563400017	Brain_Hypothalamus	12.11752	3.41E-17	1.882483	-0.62724	7.494488	3.635879	2.249181
ENSG00000281332.1	LINC00997	2.38E-06	13	4	1.09E-09	Brain_Spinal_cord_cervical_c-1	1	Brain_Caudate_basal_ganglia	9.262604	5.58E-17	0.720728	-6.09535	0	-1.47684	1.694056
ENSG00000204963.5	PCDHA7	3.86E-08	12	2	1.20E-08	Brain_Spinal_cord_cervical_c-1	0.010439998	Brain_Nucleus_accumbens_basal_ganglia	10.73526	2.31E-17	0.700185	-5.70001	-2.5609	-4.80898	0.914645
ENSG00000270039.1	RP11-571M6.17	2.79E-06	11	1	5.09E-08	Brain_Spinal_cord_cervical_c-1	4.64E-06	Brain_Anterior_cingulate_cortex_BA24	10.84805	2.17E-17	10.84805	4.58053	5.448207	4.659409	0.261615
ENSG00000134825.15	TMEM258	1.06E-06	14	2	1.03E-08	Brain_Spinal_cord_cervical_c-1	0.041260336	Brain_Anterior_cingulate_cortex_BA24	12.15709	3.90E-17	1.638544	2.040904	5.725013	4.511588	0.845268
ENSG00000026950.16	BTN3A1	5.60E-09	14	4	6.90E-09	Brain_Substantia_nigra	0.68505847	Brain_Cerebellum	7.836423	1.44E-17	0.688631	-5.79324	1.26297	-2.43461	2.320232
ENSG00000260469.2	C15orf59-AS1	6.90E-09	12	2	2.11E-09	Brain_Substantia_nigra	0.000160585	Brain_Anterior_cingulate_cortex_BA24	10.46189	2.56E-18	0.850636	3.774102	5.989027	5.106102	0.652032
ENSG00000271904.1	CTC-498M16.4	4.94E-10	13	2	2.08E-12	Brain_Substantia_nigra	0.036889998	Brain_Caudate_basal_ganglia	11.44853	4.21E-18	1.252958	2.086979	7.028945	3.370863	1.639946
ENSG00000173402.11	DAG1	3.07E-10	6	2	7.15E-11	Brain_Substantia_nigra	0.322137869	Brain_Caudate_basal_ganglia	4.089192	1.14E-16	1.794059	-3.92293	6.517435	0.258213	3.993535
ENSG00000163412.12	EIF4E3	4.48E-05	12	6	1.26E-07	Brain_Substantia_nigra	0.9747	Brain_Caudate_basal_ganglia	6.322834	0.000277	0.417479	-1.38756	5.285007	0.546676	1.740576
ENSG00000227740.1	RP11-318C24.2	2.41E-11	6	3	5.48E-12	Brain_Substantia_nigra	0.002472	Brain_Cerebellar_Hemisphere	4.432767	0.004043	0.413114	-6.89242	-3.02675	-5.84577	1.411563

ENSG00000124201.14	ZNFX1	1.30E-05	13	5	7.62E-08	Brain_Substantia_nigra	0.658389539	Brain_Caudate_basal_ganglia	5.9047	4.90E-17	0.333059	-5.37593	3.186477	-1.46238	3.305523
ENSG00000196812.4	ZSCAN16	1.64E-10	13	4	5.01E-11	Brain_Substantia_nigra	0.444256104	Brain_Putamen_basal_ganglia	7.745835	4.36E-18	0.28419	-6.50832	6.570712	2.50589	4.668538
ENSG00000170209.4	ANKK1	5.41E-13	8	6	1.05E-15	Whole_Blood	0.604400003	Brain_Cerebellum	4.100748	6.03E-18	0.230969	-8.02052	0.956143	-3.41872	2.878108
ENSG00000124508.16	BTN2A2	9.54E-06	14	4	6.68E-09	Whole_Blood	0.364099998	Brain_Spinal_cord_cervical_c-1	9.36286	6.92E-17	0.959308	-5.79876	-0.90758	-1.82856	1.41171
ENSG00000186470.13	BTN3A2	4.61E-12	14	1	3.28E-13	Whole_Blood	3.66E-06	Brain_Cerebellum	13.41296	3.58E-17	13.41296	4.629658	7.282489	6.753041	0.681908
ENSG00000273145.1	CITF22-92A6.1	1.04E-06	10	2	1.57E-07	Whole_Blood	0.0004368	Brain_Anterior_cingulate_cortex_BA24	9.433954	1.09E-17	0.566046	-5.24394	3.516789	1.234001	3.705575
ENSG00000172409.5	CLP1	1.69E-09	4	3	5.66E-11	Whole_Blood	0.009230997	Brain_Anterior_cingulate_cortex_BA24	2.49699	0.003764	0.099605	-2.60338	6.552452	2.728242	3.85645
ENSG00000172795.15	DCP2	5.06E-06	14	4	2.23E-08	Whole_Blood	0.350999985	Brain_Spinal_cord_cervical_c-1	8.704993	1.16E-17	0.458165	-5.59298	2.974256	-1.24982	2.300186
ENSG00000178342.4	KCNG2	4.32E-08	8	8	1.78E-07	Whole_Blood	0.577199983	Brain_Nucleus_accumbens_basal_ganglia	2.098009	0.147403	0.147403	-2.49207	5.220845	0.294343	2.431385
ENSG00000172037.13	LAMB2	8.39E-11	3	3	5.19E-10	Whole_Blood	0.005884001	Brain_Hippocampus	1.274752	0.673032	0.673032	2.754177	6.21328	4.288962	1.762144
ENSG00000185920.15	PTCH1	7.82E-07	7	3	1.29E-07	Whole_Blood	0.768699992	Brain_Amygdala	3.122573	2.02E-17	1.668824	-4.52575	5.279947	0.751148	3.538158
ENSG00000142599.17	RERE	1.03E-11	6	3	5.33E-11	Whole_Blood	0.081249998	Brain_Caudate_basal_ganglia	4.351609	0.003074	0.449385	-6.56133	-1.74348	-4.84358	1.734827
ENSG00000144306.14	SCRN3	3.41E-07	13	3	2.26E-08	Whole_Blood	0.972799999	Brain_Cerebellar_Hemisphere	8.123769	2.42E-18	0.69662	-5.59064	0.49438	-3.87156	1.904437
ENSG00000145022.4	TCTA	2.56E-11	14	3	1.28E-11	Whole_Blood	0.121457077	Brain_Frontal_Cortex_BA9	10.15422	2.70E-17	0.88345	-6.77112	2.370362	-3.72178	2.716382
ENSG00000175274.18	TP53I11	1.35E-05	10	7	7.84E-08	Whole_Blood	0.951575645	Brain_Cerebellar_Hemisphere	4.671072	7.63E-17	0.224006	-5.37077	4.568876	0.634057	2.608656

ENSG00000197279.3	ZNF165	3.10E-13	14	4	4.01E-11	Whole_Blood	0.95676415	Brain_Putamen_basal_ganglia	5.149643	8.91E-18	1.294564	-6.60368	6.251742	-0.66484	3.557102
ENSG00000144792.9	ZNF660	1.26E-08	14	2	1.42E-09	Whole_Blood	0.00365459	Brain_Cerebellum	13.13236	6.22E-18	0.62106	-6.0532	-2.90653	-3.77826	0.738443

Legend:

gene: gene id

gene_name: gene HUGO name

pvalue: p-value of S-MulTiXcan association

n: total number of single-tissue results for calculation

n_indep: number of components kept after SVD thresholding

p_i_best: best single-tissue p-value used

t_i_best: best single-tissue model used name

p_i_worst: worst single-tissue p-value used

t_i_worst: worst single-tissue model used name

eigen_max: Maximum eigenvalue in the covariance matrix

eigen_min: Minimum eigenvalue in the covariance matrix

eigen_min_kept: Minimum eigenvalue that survived thresholding

z_min: Minimum single-tissue zscore used

z_max: Maximum single-tissue zscore used

z_mean: mean of single-tissue zscores used

z_sd: standard deviation of single-tissue zscores

Table 2: SNPs that were prioritized using finemapping and functional annotation (CADD scores)(3)

SNP_ID	Causal_Post._Prob.	CHR	BP	P	PHRED
rs1021362	1	10	106611268	4.60E-19	12.76
rs1021362	1	10	106611268	4.60E-19	12.41
rs174546	0.837038	11	61569830	7.25E-09	12.71
rs11610143	0.368959	12	52349071	2.86E-09	17.63
rs11612312	0.631041	12	52349088	2.26E-09	16.06
rs904628	0.406742	12	121342084	4.35E-11	16.74
rs904628	0.406742	12	121342084	4.35E-11	16.44
rs9536381	0.499917	13	53860655	2.05E-15	11.74
rs7229	0.369216	14	64692825	2.75E-10	11.21
rs35641442	0.916466	14	75207263	1.63E-14	11.4
rs2896460	0.319206	14	103306106	1.05E-08	12.04
rs76119292	0.6267	17	27375598	3.18E-08	11.13
rs8066520	0.999646	17	27376591	5.29E-08	14.42
rs11082011	0.898497	18	35145122	2.72E-17	19.67
rs56960323	0.406804	18	39304625	2.49E-08	15.73
rs2717079	0.997559	2	58065936	8.01E-10	11.48
rs7617480	1	3	49210732	1.15E-14	15.13
rs75363979	0.734688	4	35934578	0.0001194	13.08
rs4626350	0.442219	5	30839451	1.52E-07	13.86
rs2431108	0.587126	5	103947968	4.67E-14	20.8
rs2408225	0.309848	5	124262051	2.20E-10	10.01

Legend

SNP_ID: SNP
Causal_Post._Prob.: Causal Posterior Probability
CHR: Chromosome
BP: Base pair position
P: p-value of the phenotype
PHRED: CADD score (Combined Annotation Dependent Depletion) : “a scaled C-score of greater of equal 10 indicates that these are predicted to be the 10% most deleterious substitutions that you can do to the human genome, a score of greater or equal 20 indicates the 1% most deleterious and so on”. Source: https://cadd.gs.washington.edu/info

Table 3: Positional gene annotation of prioritized SNPs using ± 100 kb window (4)

	Uploaded_variation	Location	Allele	Consequence	IMPACT	SYMBOL	Gene
1	rs1021362	10:106611268-106611268	A	intron_variant	MODIFIER	SORCS3	ENSG00000156395
2	rs174546	11:61569830-61569830	T	upstream_gene_variant	MODIFIER	RP11-467L20.10	ENSG00000124915
3	rs174546	11:61569830-61569830	T	downstream_gene_variant	MODIFIER	DAGLA	ENSG00000134780
4	rs174546	11:61569830-61569830	T	upstream_gene_variant	MODIFIER	FADS2	ENSG00000134824
5	rs174546	11:61569830-61569830	T	upstream_gene_variant	MODIFIER	TMEM258	ENSG00000134825
6	rs174546	11:61569830-61569830	T	downstream_gene_variant	MODIFIER	MYRF	ENSG00000124920
7	rs174546	11:61569830-61569830	T	downstream_gene_variant	MODIFIER	FADS3	ENSG00000221968
8	rs174546	11:61569830-61569830	T	downstream_gene_variant	MODIFIER	RAB3IL1	ENSG00000167994
9	rs174546	11:61569830-61569830	T	downstream_gene_variant	MODIFIER	FEN1	ENSG00000168496
10	rs174546	11:61569830-61569830	T	3_prime_UTR_variant	MODIFIER	FADS1	ENSG00000149485
11	rs174546	11:61569830-61569830	T	upstream_gene_variant	MODIFIER	MIR611	ENSG00000207601
12	rs174546	11:61569830-61569830	T	downstream_gene_variant	MODIFIER	MIR1908	ENSG00000222326
13	rs11610143	12:52349071-52349071	G	upstream_gene_variant	MODIFIER	NR4A1	ENSG00000123358
14	rs11610143	12:52349071-52349071	G	intron_variant	MODIFIER	ACVR1B	ENSG00000135503
15	rs11610143	12:52349071-52349071	G	upstream_gene_variant	MODIFIER	GRASP	ENSG00000161835
16	rs11610143	12:52349071-52349071	G	downstream_gene_variant	MODIFIER	ANKRD33	ENSG00000167612
17	rs11610143	12:52349071-52349071	G	upstream_gene_variant	MODIFIER	RNU6-574P	ENSG00000206992
18	rs11610143	12:52349071-52349071	G	downstream_gene_variant	MODIFIER	ACVRL1	ENSG00000139567
19	rs11610143	12:52349071-52349071	G	downstream_gene_variant	MODIFIER	RP11-1100L3.4	ENSG00000258021
20	rs11610143	12:52349071-52349071	G	regulatory_region_variant	MODIFIER	-	-
21	rs11612312	12:52349088-52349088	C	upstream_gene_variant	MODIFIER	NR4A1	ENSG00000123358
22	rs11612312	12:52349088-52349088	C	intron_variant	MODIFIER	ACVR1B	ENSG00000135503
23	rs11612312	12:52349088-52349088	C	upstream_gene_variant	MODIFIER	GRASP	ENSG00000161835

24	rs11612312	12:52349088-52349088	C	downstream_gene_variant	MODIFIER	ANKRD33	ENSG00000167612
25	rs11612312	12:52349088-52349088	C	upstream_gene_variant	MODIFIER	RNU6-574P	ENSG00000206992
26	rs11612312	12:52349088-52349088	C	downstream_gene_variant	MODIFIER	ACVRL1	ENSG00000139567
27	rs11612312	12:52349088-52349088	C	downstream_gene_variant	MODIFIER	RP11-1100L3.4	ENSG00000258021
28	rs11612312	12:52349088-52349088	C	regulatory_region_variant	MODIFIER	-	-
29	rs904628	12:121342084-121342084	A	upstream_gene_variant	MODIFIER	HNF1A	ENSG00000135100
30	rs904628	12:121342084-121342084	A	downstream_gene_variant	MODIFIER	C12orf43	ENSG00000157895
31	rs904628	12:121342084-121342084	A	5_prime_UTR_variant	MODIFIER	SPPL3	ENSG00000157837
32	rs904628	12:121342084-121342084	A	upstream_gene_variant	MODIFIER	ARF1P2	ENSG00000213137
33	rs904628	12:121342084-121342084	A	upstream_gene_variant	MODIFIER	CLIC1P1	ENSG00000231313
34	rs904628	12:121342084-121342084	A	downstream_gene_variant	MODIFIER	HNF1A-AS1	ENSG00000241388
35	rs904628	12:121342084-121342084	A	upstream_gene_variant	MODIFIER	RPL12P33	ENSG00000244585
36	rs904628	12:121342084-121342084	A	downstream_gene_variant	MODIFIER	AC079602.1	ENSG00000272214
37	rs904628	12:121342084-121342084	A	downstream_gene_variant	MODIFIER	RP11-216P16.2	ENSG00000271769
38	rs904628	12:121342084-121342084	A	regulatory_region_variant	MODIFIER	-	-
39	rs9536381	13:53860655-53860655	T	downstream_gene_variant	MODIFIER	AL450423.1	ENSG00000220990
40	rs9536381	13:53860655-53860655	T	downstream_gene_variant	MODIFIER	PCDH8P1	ENSG00000225510
41	rs9536381	13:53860655-53860655	T	downstream_gene_variant	MODIFIER	RN7SL618P	ENSG00000241613
42	rs7229	14:64692825-64692825	A	downstream_gene_variant	MODIFIER	ESR2	ENSG00000140009
43	rs7229	14:64692825-64692825	A	3_prime_UTR_variant	MODIFIER	SYNE2	ENSG00000054654
44	rs35641442	14:75207263-75207263	A	upstream_gene_variant	MODIFIER	YLPM1	ENSG00000119596
45	rs35641442	14:75207263-75207263	A	upstream_gene_variant	MODIFIER	AC007956.1	ENSG00000214670
46	rs35641442	14:75207263-75207263	A	downstream_gene_variant	MODIFIER	FCF1	ENSG00000119616
47	rs35641442	14:75207263-75207263	A	upstream_gene_variant	MODIFIER	AREL1	ENSG00000119682
48	rs35641442	14:75207263-75207263	A	downstream_gene_variant	MODIFIER	SNORA7	ENSG00000222604

49	rs35641442	14:75207263-75207263	A	downstream_gene_variant	MODIFIER	RP11-173A8.2	ENSG00000258439
50	rs2896460	14:103306106-103306106	T	upstream_gene_variant	MODIFIER	AMN	ENSG00000166126
51	rs2896460	14:103306106-103306106	T	intron_variant	MODIFIER	TRAF3	ENSG00000131323
52	rs2896460	14:103306106-103306106	T	downstream_gene_variant	MODIFIER	CDC42BPB	ENSG00000198752
53	rs2896460	14:103306106-103306106	T	upstream_gene_variant	MODIFIER	RNU6-1316P	ENSG00000206969
54	rs2896460	14:103306106-103306106	T	upstream_gene_variant	MODIFIER	AL117209.1	ENSG00000211990
55	rs2896460	14:103306106-103306106	T	upstream_gene_variant	MODIFIER	snoU13	ENSG00000238853
56	rs2896460	14:103306106-103306106	T	upstream_gene_variant	MODIFIER	RP11-661D19.3	ENSG00000259508
57	rs2896460	14:103306106-103306106	T	upstream_gene_variant	MODIFIER	RP11-365N19.2	ENSG00000259515
58	rs76119292	17:27375598-27375598	G	upstream_gene_variant	MODIFIER	PHF12	ENSG00000109118
59	rs76119292	17:27375598-27375598	G	upstream_gene_variant	MODIFIER	SEZ6	ENSG00000063015
60	rs76119292	17:27375598-27375598	G	intron_variant	MODIFIER	PIPOX	ENSG00000179761
61	rs76119292	17:27375598-27375598	G	downstream_gene_variant	MODIFIER	MYO18A	ENSG00000196535
62	rs76119292	17:27375598-27375598	G	downstream_gene_variant	MODIFIER	TIAF1	ENSG00000221995
63	rs76119292	17:27375598-27375598	G	downstream_gene_variant	MODIFIER	AC024619.2	ENSG00000238007
64	rs76119292	17:27375598-27375598	G	upstream_gene_variant	MODIFIER	RP11-321A17.3	ENSG00000263781
65	rs76119292	17:27375598-27375598	G	upstream_gene_variant	MODIFIER	RP11-321A17.5	ENSG00000263613
66	rs76119292	17:27375598-27375598	G	upstream_gene_variant	MODIFIER	RP11-321A17.4	ENSG00000263709
67	rs76119292	17:27375598-27375598	G	regulatory_region_variant	MODIFIER	-	-
68	rs8066520	17:27376591-27376591	A	upstream_gene_variant	MODIFIER	PHF12	ENSG00000109118
69	rs8066520	17:27376591-27376591	A	upstream_gene_variant	MODIFIER	SEZ6	ENSG00000063015
70	rs8066520	17:27376591-27376591	A	intron_variant	MODIFIER	PIPOX	ENSG00000179761
71	rs8066520	17:27376591-27376591	A	downstream_gene_variant	MODIFIER	MYO18A	ENSG00000196535
72	rs8066520	17:27376591-27376591	A	downstream_gene_variant	MODIFIER	TIAF1	ENSG00000221995
73	rs8066520	17:27376591-27376591	A	downstream_gene_variant	MODIFIER	AC024619.2	ENSG00000238007

74	rs8066520	17:27376591-27376591	A	upstream_gene_variant	MODIFIER	RP11-321A17.3	ENSG00000263781
75	rs8066520	17:27376591-27376591	A	upstream_gene_variant	MODIFIER	RP11-321A17.5	ENSG00000263613
76	rs8066520	17:27376591-27376591	A	upstream_gene_variant	MODIFIER	RP11-321A17.4	ENSG00000263709
77	rs8066520	17:27376591-27376591	A	regulatory_region_variant	MODIFIER	-	-
78	rs11082011	18:35145122-35145122	T	intron_variant	MODIFIER	CELF4	ENSG00000101489
79	rs11082011	18:35145122-35145122	T	upstream_gene_variant	MODIFIER	MIR4318	ENSG00000266530
80	rs11082011	18:35145122-35145122	T	regulatory_region_variant	MODIFIER	-	-
81	rs56960323	18:39304625-39304625	C	upstream_gene_variant	MODIFIER	AC011225.1	ENSG00000225253
82	rs56960323	18:39304625-39304625	C	downstream_gene_variant	MODIFIER	RP11-188I24.1	ENSG00000267652
83	rs56960323	18:39304625-39304625	C	upstream_gene_variant	MODIFIER	RP11-142I20.1	ENSG00000267313
84	rs2717079	2:58065936-58065936	A	upstream_gene_variant	MODIFIER	VRK2	ENSG00000028116
85	rs2717079	2:58065936-58065936	A	downstream_gene_variant	MODIFIER	CTD-2026C7.1	ENSG00000271615
86	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	CCDC36	ENSG00000173421
87	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	LAMB2	ENSG00000172037
88	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	USP19	ENSG00000172046
89	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	QARS	ENSG00000172053
90	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	CCDC71	ENSG00000177352
91	rs7617480	3:49210732-49210732	C	intron_variant	MODIFIER	KLHDC8B	ENSG00000185909
92	rs7617480	3:49210732-49210732	C	downstream_gene_variant	MODIFIER	C3orf62	ENSG00000188315
93	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	QRICH1	ENSG00000198218
94	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	Y_RNA	ENSG00000199546
95	rs7617480	3:49210732-49210732	C	downstream_gene_variant	MODIFIER	C3orf84	ENSG00000236980
96	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	RP11-3B7.1	ENSG00000225399
97	rs7617480	3:49210732-49210732	C	downstream_gene_variant	MODIFIER	RN7SL182P	ENSG00000241461
98	rs7617480	3:49210732-49210732	C	upstream_gene_variant	MODIFIER	RP11-694I15.7	ENSG00000270441

99	rs7617480	3:49210732-49210732	C	downstream_gene_variant	MODIFIER	RP11-3B7.7	ENSG00000270538
100	rs7617480	3:49210732-49210732	C	regulatory_region_variant	MODIFIER	-	-
101	rs75363979	4:35934578-35934578	C	downstream_gene_variant	MODIFIER	ARAP2	ENSG00000047365
102	rs4626350	5:30839451-30839451	A	regulatory_region_variant	MODIFIER	-	-
103	rs2431108	5:103947968-103947968	C	intron_variant,non_coding_transcript_variant	MODIFIER	RP11-6N13.1	ENSG00000251574
104	rs2431108	5:103947968-103947968	C	regulatory_region_variant	MODIFIER	-	-
105	rs2408225	5:124262051-124262051	C	downstream_gene_variant	MODIFIER	RP11-284A20.1	ENSG00000249423
106	rs2408225	5:124262051-124262051	C	upstream_gene_variant	MODIFIER	RP11-284A20.2	ENSG00000249261
107	rs2408225	5:124262051-124262051	C	downstream_gene_variant	MODIFIER	RP11-284A20.3	ENSG00000248443

Table 4: Colocalization analysis of genes and their specific tissue pairs (as reported from MetaXcan) which overlapped with genes identified from variant prioritization (5)

GENE	GENE NAME	PVALUE	N	N_INDE	P_I_BEST	T_I_BEST	PP.H0.ABF	PP.H1.ABF	PP.H2.ABF	PP.H3.ABF	PP.H4.ABF	
ENSG00000177352.9	*CCDC71*	2.87E-09	13	1	1.07E-10	Brain_Amygdala	1.78E-09	6.19E-02	2.20E-10	6.75E-03	9.31E-01	[1] "PP abf for shared variant: 93.1%"
ENSG00000139567.12	*ACVRL1*	6.13E-07	4	3	9.85E-08	Brain_Anterior_cingulate_cortex_BA24	N/A					
ENSG00000225399.4	*RP11-3B7.1*	6.77E-12	4	2	3.93E-10	Brain_Anterior_cingulate_cortex_BA24	6.55E-09	1.83E-01	4.01E-09	1.12E-01	7.05E-01	[1] "PP abf for shared variant: 70.5%"
ENSG00000101489.19	*CELF4*	5.04E-14	12	6	1.13E-16	Brain_Caudate_basal_ganglia	N/A					
ENSG00000119616.11	*FCF1*	9.15E-14	12	2	2.63E-14	Brain_Caudate_basal_ganglia	N/A					
ENSG00000149485.18	*FADS1*	1.47E-06	14	2	4.33E-09	Brain_Cerebellar_Hemisphere	3.78E-15	2.35E-12	5.63E-05	3.40E-02	9.66E-01	[1] "PP abf for shared variant: 96.6%"
ENSG00000119682.16	*AREL1*	1.46E-13	10	2	2.63E-14	Brain_Cerebellum	N/A					
ENSG00000134824.13	*FADS2*	1.58E-07	8	2	1.01E-08	Brain_Cerebellum	N/A					
ENSG00000119596.17	*YLPM1*	1.33E-12	5	2	1.41E-13	Brain_Cortex	N/A					
ENSG00000157837.15	*SPPL3*	1.10E-10	11	3	9.32E-12	Brain_Frontal_Cortex_BA9	1.07E-07	1.05E-02	1.55E-06	1.50E-01	8.39E-01	[1] "PP abf for shared variant: 83.9%"
ENSG00000221995.5	*TIAF1*	3.07E-05	14	2	1.79E-07	Brain_Hippocampus	2.68E-06	8.17E-04	1.78E-03	5.42E-01	4.55E-01	[1] "PP abf for shared variant: 45.5%"
ENSG00000131323.14	*TRAF3*	2.48E-07	11	3	9.62E-08	Brain_Hypothalamus	2.73E-06	1.59E-03	8.18E-05	4.67E-02	9.52E-01	[1] "PP abf for shared variant: 95.2%"
ENSG00000173421.16	*CCDC36*	2.23E-11	11	3	2.41E-10	Brain_Nucleus_accumbens_basal_ganglia	N/A					
ENSG00000156395.12	*SORCS3*	1.02E-10	2	2	5.77E-11	Brain_Nucleus_accumbens_basal_ganglia	N/A					
ENSG00000185909.14	*KLHDC8B*	2.57E-13	14	2	6.66E-14	Brain_Spinal_cord_cervical_c-1	N/A					
ENSG00000134825.15	*TMEM258*	1.06E-06	14	2	1.03E-08	Brain_Spinal_cord_cervical_c-1	N/A					

ENSG00000172037.13	*LAMB2*	8.39E-11	3	3	5.19E-10	Whole_Blood	3.71E-07	8.55E-02	5.05E-07	1.16E-01	7.99E-01	[1] "PP abf for shared variant: 79.9%"

Legend

#H0: neither trait has a genetic association in the region
#H1: only trait 1 has a genetic association in the region
#H2: only trait 2 has a genetic association in the region
#H3: both traits are associated, but with different causal variants
#H4: both traits are associated and share a single causal variant
gene: Ensembl id
gene_name: HUGO name
pvalue: p-value of the S-MultiXcan association
n number of S-PrediXcan results available for the gene
n_indep number of independent components surviving SVD
p_i_best best p-value of S-PrediXcan
t_i_best tissue that presented best S-PrediXcan result

Figures of genes with H_4 probability of >~80%

Each figure has three panels: Left-panel shows p-value of tissue eQTL on y-axis and GWAS on x-axis. The right panel shows the (top) GWAS-p-value (y-axis) and (bottom) eQTL-value (y-axis) and genomic position of the locus (x-axis). The most significant variant for GWAS and eQTL is annotated [LocusCompare].

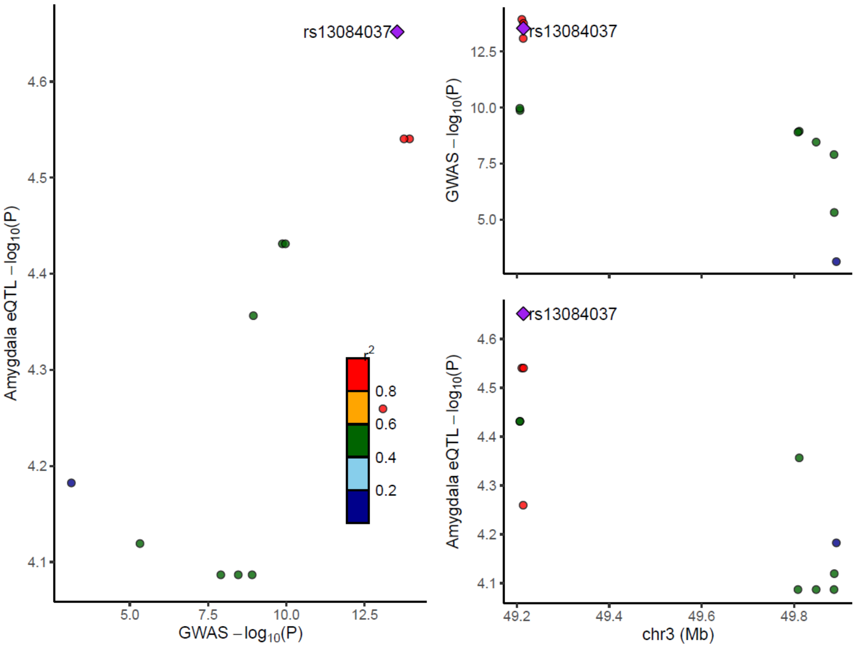

Figure 1: *CCDC71* - Amygdala

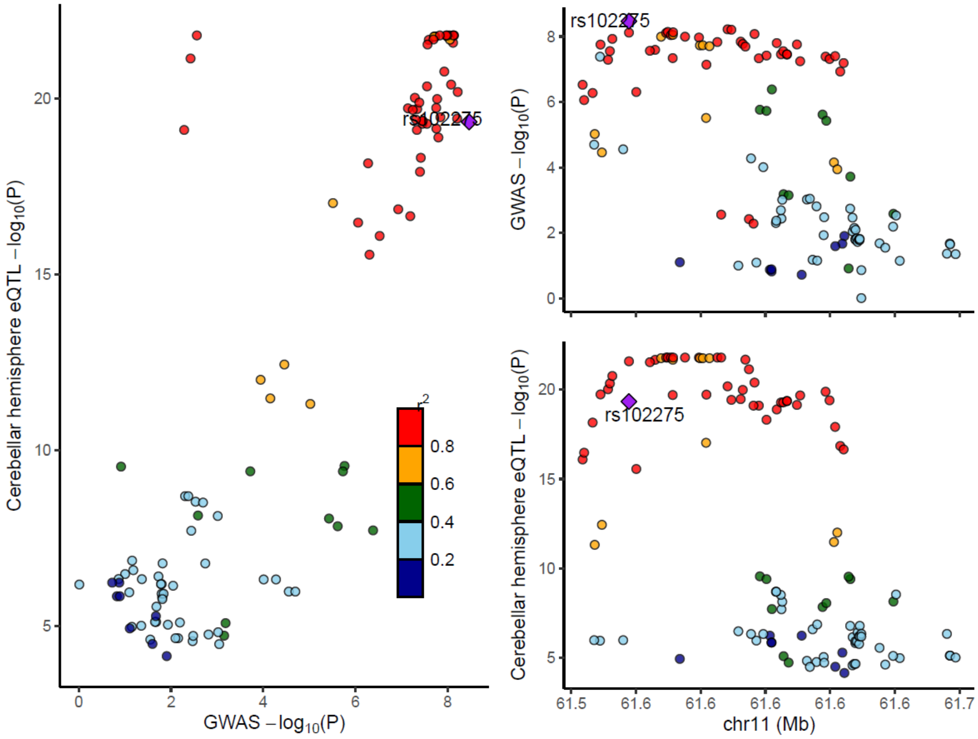

Figure 2: *FADS1* - Cerebellar hemisphere

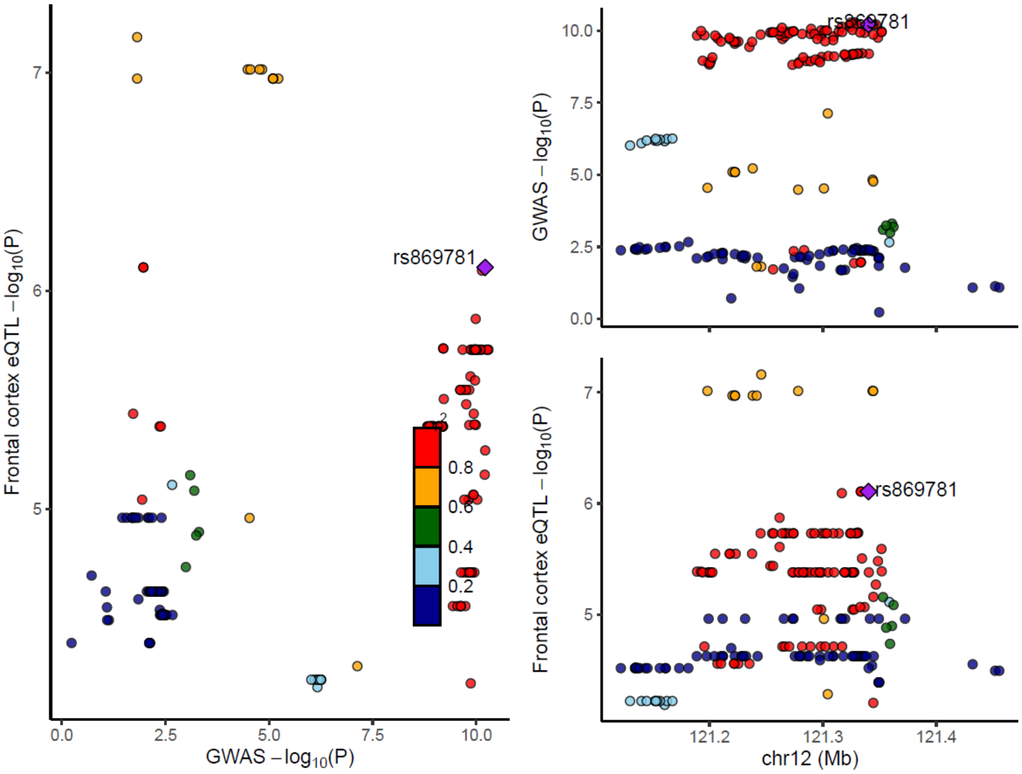

Figure 3: *SPPL3* - Frontal Cortex

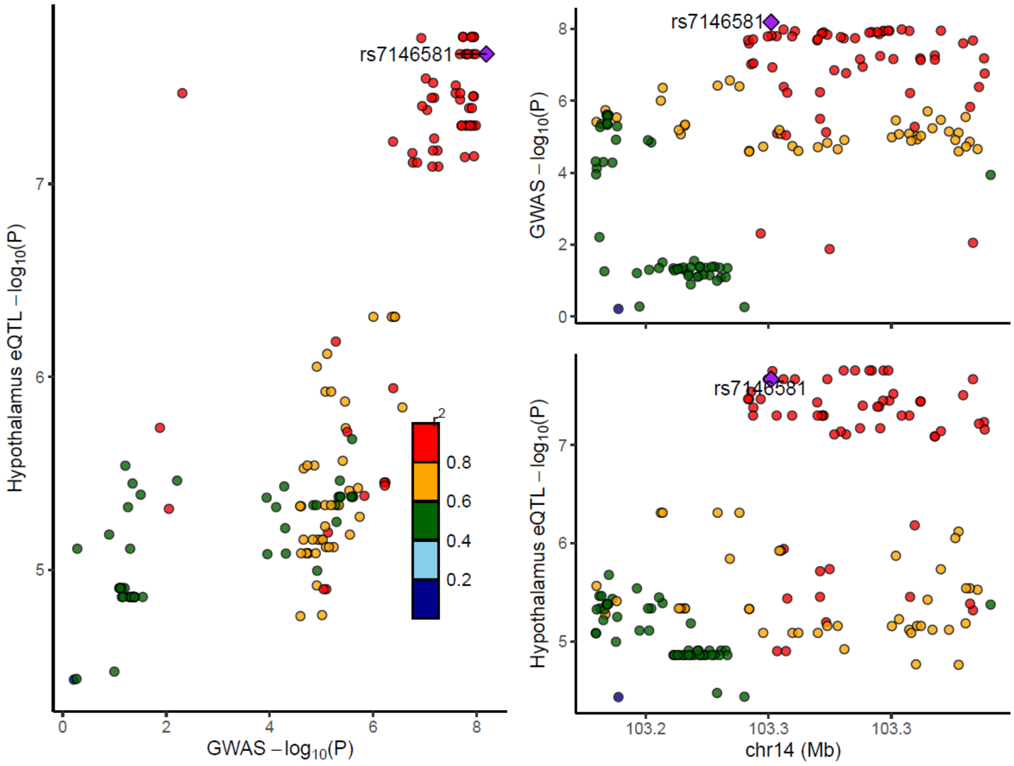

Figure 4: *TRAF3* – Hypothalamus

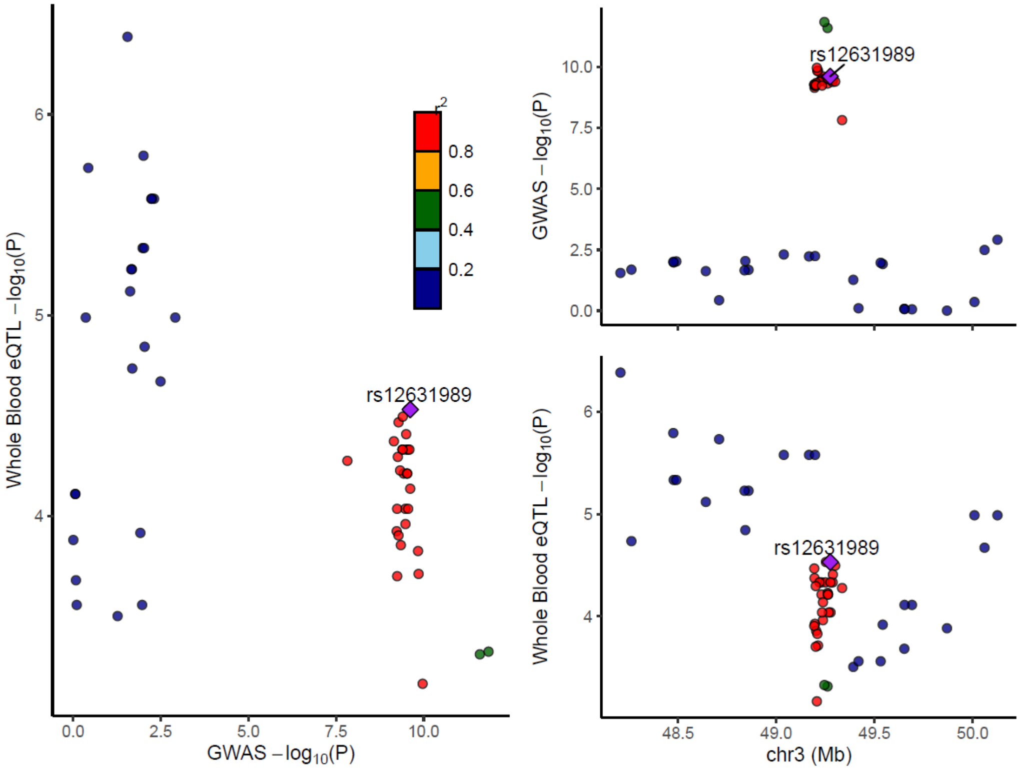

Figure 5: *LAMB2* - Whole blood

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