

Table S1: Function ARegion StructureGene Chromosome Gene Type SNPBP Location

Region	Structures	Overlap genes	Annotations	Potential mechanism		
Limbic Region	Amygdala	NDUFAF3	MCI	assembly of mitochondrial complex		
		NOXRED1	-	NADP-dependent oxidoreductase		
		AHSA1	AD/MCI	cell growth, apoptosis and migration		
		MYL6B	-	cell adhesion, cell migration and tissue architecture, cargo transport and endocytosis		
	Hippocampus	VAPA	AD/MCI	vesicular neurotransmission, membrane fusion, protein complex assembly and cell motility		
		ME3	MCI	cell growth and cellular senescence		
		AGK	AD/MCI	function in the mitochondria		
		FAM162B	-	apoptosis		
		EPHA4	AD/MCI	synaptic plasticity		
		PTH1R	AD/MCI	regulate blood calcium homeostasis		
Basal ganglia Region	Accumbens.area	IPO7	AD	autonomous nuclear transport receptor or as an adapter-like protein		
		GTPBP8	AD	mitochondrial translation and mitochondrial bioenergetics		
	Caudate	RELCH	-	intracellular cholesterol distribution		
		IRX3	-	neural development		
		CLCNKB	MCI	cell volume, membrane potential stabilization, signal transduction and transepithelial transport		
		IL23A	AD/MCI	immune inflammatory		
		RELL1	-	inflammatory response		
		TMEM50A	-	unknown		
		SETD4	-	methyltransferase activity		
		ULBP3	AD	peptide antigen binding and natural killer cell lectin-like receptor binding		
	Putamen	TMEM253	-	unknown		
		ERCC4	AD/MCI	DNA repair		
		HPS3	-	biogenesis Of Lysosomal Organelles		
		SLC26A10	-	unknown		
		Cerebellum Region	Cerebellum.Cortex	SLC6A16	-	neurotransmitter transporter
				SLC10A5	-	solute carrier
ACAT2	AD/MCI			lipid metabolism		
ZFYVE9	MCI			neuronal migration		
ENSG00000272542	-			unknown		
ERBB2	AD/MCI			neuritic plaques		
LINC00958	-			unknown		
FCGRT	-			mediates the asymmetric transcytosis of IgG across the blood-brain barrier		
TRPM4	-	calcium-activated nonselective ion channel				

Table S2: Genomic locations of cis-eQTL SNPs,

Region	Structure	Gene	Chromosome	Gene Type	SNP	BP	Location
LimbicRegion	Amygdala	NDUFAF3	chr3	protein_coding	rs7100	49053219	3downstream,3utr
		NOXRED1	chr14	protein_coding	rs141260780	77890314	5upstream
		NOXRED1	chr14	protein_coding	rs11846861	77889546	intronic,5upstream
		AHSA1	chr14	protein_coding	rs11845345	77923783	5utr,intronic,non-coding intronic
		MYL6B	chr12	antisense	rs3809134	56546011	non-coding intronic
	Hippocampus	VAPA	chr18	protein_coding	rs4798889	9913930	3downstream
		ME3	chr11	protein_coding	rs670736	86383679	5upstream
		AGK	chr7	antisense	rs7790742	141250685	non-coding intronic
		AGK	chr7	antisense	rs7795885	141251044	5upstream,non-coding
		FAM162B	chr6	protein_coding	rs9387433	117077450	intronic

BasalGangliaRegion	AccumbensArea	FAM162B	chr6	protein_coding	rs641338	117086265	intronic
		EPHA4	chr2	protein_coding	rs14963619	222438915	5utr,5upstream
		PTH1R	chr3	protein_coding	rs2168442	46919379	intronic
		PTH1R	chr3	protein_coding	rs144645644	46934290	intronic,non-coding
		IPO7	chr11	protein_coding	rs75955853	9406129	3downstream
		IPO7	chr11	protein_coding	rs12363308	9409801	intronic
		GTPBP8	chr3	protein_coding	rs114429530	112710133	coding nonsyn,5upstream
		RELCH	chr18	protein_coding	rs3752091	59854253	5upstream,intronic,5utr,non-coding
		RELCH	chr18	protein_coding	rs9958695	59858801	intronic
		IRX3	chr16	antisense	rs191251428	54320835	non-coding intronic
	Putamen	CLCNKB	chr1	protein_coding	rs75909377	16370712	intronic
		IL23A	chr12	protein_coding	rs79824801	56728137	non-coding intronic
		RELL1	chr4	protein_coding	rs4832933	37688443	5upstream
		TMEM50A	chr1	protein_coding	rs3093586	25668826	5upstream,non-coding intronic,intronic
		TMEM50A	chr1	protein_coding	rs3091243	25669057	5upstream,non-coding intronic,intronic
		TMEM50A	chr1	protein_coding	rs8876	25687308	3utr,non-coding
		SETD4	chr21	protein_coding	rs2835263	37430245	5upstream,non-coding intronic,intronic
		SETD4	chr21	protein_coding	rs142847892	37451298	intronic
		ULBP3	chr6	protein_coding	rs1537648	150389924	intronic
		TMEM253	chr14	None	rs10872886	21574690	None
CerebellumRegion	Cerebellum	ERCC4	chr16	protein_coding	rs6498486	14013666	3downstream
		ERCC4	chr16	protein_coding	rs3136042	14014055	coding syn syn,non-coding
		ERCC4	chr16	protein_coding	rs1799798	14014278	intronic,non-coding intronic
		HPS3	chr3	protein_coding	rs13089410	148847441	non-coding,5utr,5upstream
		HPS3	chr3	protein_coding	rs7643410	148848073	non-coding intronic,intronic,non-coding
		SLC26A10	chr12	None	rs10747780	57980541	None
		SLC26A10	chr12	None	rs10437954	58003922	None
		SLC6A16	chr19	protein_coding	rs8102658	49828855	5upstream
		SLC10A5	chr8	TEC	rs2955002	82608878	non-coding
		SLC10A5	chr8	TEC	rs58379275	82609783	non-coding
	SLC10A5	chr8	protein_coding	rs75348453	82626146	intronic,non-coding intronic,3downstream	
	Cerebellum	ACAT2	chr6	protein_coding	rs2025187	160181435	intronic
		ZFYVE9	chr1	protein_coding	rs627011	52608109	non-coding intronic,intronic
		ENSG00000272542	chr13	transcribed_unprocessed_pseudogene	rs1886087	103535828	non-coding intronic
		ENSG00000272542	chr13	transcribed_unprocessed_pseudogene	rs9518861	103541616	5upstream,non-coding intronic
		ENSG00000272542	chr13	transcribed_unprocessed_pseudogene	rs9554903	103542220	non-coding intronic,5upstream
		ERBB2	chr17	protein_coding	rs2517955	37843681	non-coding intronic,intronic
		ERBB2	chr17	protein_coding	rs75849983	37843762	non-coding intronic,intronic
		LINC00958	chr11	lincRNA	rs4756736	13014898	5upstream
		FCGRT	chr19	protein_coding	rs2946865	50010378	non-coding intronic
FCGRT		chr19	protein_coding	rs1132990	50028163	3downstream,3utr,intronic,non-coding	
TRPM4	chr19	protein_coding	rs11882563	49661547	non-coding intronic,intronic,3utr		
TRPM4	chr19	protein_coding	rs11083963	49665340	non-coding intronic,intronic		
TRPM4	chr19	protein_coding	rs73048855	49669561	non-coding intronic,5upstream,intronic		

Table S3: Annotations from HaploReg and RegulomeDB database,

		chr	pos (hg38)	variant	Promoter histone marks	Enhancer histone marks	DNase	Proteins bound	Motifs changed	RegulomeD B Rank
Limbic Region	Amygdala	3	4901578 6	rs7100		SKIN, BRST	SKIN, SKI N		Irf, SP1, SREBP	4
		14	7742397 1	rs141260 780					CACD, Isl2, Pax-4	7
		14	7742320 3	rs118468 61						5
		14	7745744 0	rs118453 45	24 tissues		46 tissues	9 bound proteins	AP-1	4
	Hippocampus	12	5615222 7	rs380913 4	24 tissues		52 tissues		5 altered motifs	4
		18	9913933 9	rs479888 9	24 tissues		53 tissues	17 bound proteins	BDP1, HEY1, Pax-5	4
		11	8667263 7	rs670736	22 tissues	7 tissues	26 tissues		4 altered motifs	4
		7	1415508 85	rs779074 2	24 tissues		30 tissues		PU.1	4
		7	1415512 44	rs779588 5	24 tissues		41 tissues	24 bound proteins	AP-2, Rad21, YY1	4
		6	1167562 87	rs938743 3					Nr2e3	5
		6	1167651 02	rs641338	21 tissues	BLD, GI, SPLN	6 tissues	SUZ12	7 altered motifs	2c
		2	2215741 91	rs149636 195	22 tissues	4 tissues	41 tissues			4
		3	4687788 9	rs216844 2		11 tissues			5 altered motifs	4
		3	4689280 0	rs144645 644	19 tissues	12 tissues	9 tissues			4
		11	9384582 53	rs759558 53	24 tissues	HRT	53 tissues	42 bound proteins	11 altered motifs	2a
		11	9388254 08	rs123633 08		ESDR, BLD, SKIN			6 altered motifs	4
		3	1129912 86	rs114429 530	24 tissues		52 tissues	30 bound proteins	6 altered motifs	2a
Basal ganglia Region	Accumbens area	18	6218702 0	rs375209 1	24 tissues		53 tissues	17 bound proteins	8 altered motifs	2b
		18	6219156 8	rs995869 5	ESDR	5 tissues	BLD		ELF1, Mef2, Spz1	7
		16	5428692 3	rs191251 428	22 tissues	9 tissues	38 tissues	POL24H8, HAE2F 1	9 altered motifs	2a
		1	1604421 7	rs759093 77		5 tissues			5 altered motifs	4
		12	5633435 3	rs798248 01	24 tissues		53 tissues	12 bound proteins	BCL, Ik-2	4
		4	3768640 5	rs383230 8	24 tissues		53 tissues	12 bound proteins	22 altered motifs	2a
		4	3768682 1	rs483293 3	24 tissues		53 tissues	5 bound proteins	4 altered motifs	2b
		1	2534233 5	rs309358 6		6 tissues			PLZF	7
		1	2534256 6	rs309124 3		6 tissues			E2F, Pou2f2	5
		1	2536081 7	rs8876		9 tissues	ESDR, LNC, BRN	CEBPB		4
	Caudate	21	3605794 7	rs283526 3		8 tissues	BLD, BLD		5 altered motifs	7
		21	3607900 0	rs142847 892	BLD, GI	8 tissues		STAT2	PLZF, ZBTB33	5
		6	1500687 88	rs153764 8	24 tissues		20 tissues		6 altered motifs	4
		14	2110653 1	rs108728 86			20 tissues	AP2ALPHA, BAF 155, BRG1		4

Cerebellum Region	Cerebellum	16	1391980 9	rs649848 6	23 tissues	5 tissues	52 tissues	16 bound proteins	CEBPB,Nanog	2b
		16	1392019 8	rs313604 2	24 tissues		53 tissues	20 bound proteins	Mxi1,SREBP	3a
		16	1392042 1	rs179979 8	24 tissues		40 tissues	POL2		4
		3	1491296 54	rs130894 10	24 tissues		53 tissues	35 bound proteins	4 altered motifs	4
		3	1491302 86	rs764341 0	23 tissues	SPLN	24 tissues		CEBPB,Zfp105	2b
		12	5758675 8	rs107477 80					7 altered motifs	4
		12	5761013 9	rs104379 54			10 tissues		NF- kappaB,Zfp161,Zn f143	4
		19	4932559 8	rs810265 8		BLD	BLD,BLD			5
		8	8169664 3	rs295500 2					5 altered motifs	1f
		8	8169754 8	rs583792 75					AP-1,BDP1,Maf	4
		8	8171391 1	rs753484 53					Mef2	5
		6	1597604 03	rs202518 7	4 tissues	18 tissues	ESC,KID	POL2	LUN-1,Osrf,Pitx2	3a
		1	5214243 7	rs627011	24 tissues		20 tissues	4 bound proteins	14 altered motifs	4
		13	1028834 78	rs188608 7					EWSR1- FLI1,HDAC2,Spde f	6
		13	1028892 66	rs951886 1						7
		13	1028898 70	rs955490 3					Foxp3	7
		17	3968742 8	rs251795 5	21 tissues	10 tissues	19 tissues	6 bound proteins	7 altered motifs	2a
		17	3968750 9	rs758499 83	21 tissues	10 tissues	21 tissues	4 bound proteins	LBP-1	4
		11	1298953 3	rs111880 988	6 tissues	ESDR, BLD	13 tissues	27 bound proteins	EWSR1- FLI1,PRDM1,TFII- I	4
		11	1299335 1	rs475673 6		BRST, SKIN, BLD			4 altered motifs	6
		19	4950712 1	rs294686 5	ESC, iPSC, BLD	6 tissues	iPSC,BLD, BLD		AhR,CHOP::CEBP alpha	5
		19	4952490 6	rs113299 0		iPSC, PLCNT, SPLN			Pbx3,Tgfb1,ZBTB33	3a
		19	4915829 0	rs118825 63	24 tissues	BLD	23 tissues	5 bound proteins	9 altered motifs	4
		19	4916208 3	rs110839 63		10 tissues	5 tissues	GATA2	21 altered motifs	3a
		19	4916630 4	rs730488 55	5 tissues	9 tissues	ESDR,KID, MUS		HNF4,LXR,VDR	2b
		Total		56	32 (57.1%)	29 (51.8%)		25 (44.6%)	49 (87.5%)	

Table S4: Annotations of promoters of cis-eQTL SNPs,

Region	Structure	Gene	SNP	BP	CHR	PromoterStart	PromoterEnd	Strand	Gene_name	Gene_id	Gene_type
LimbicRegion	Amygdala	NOXRED1	rs141260780	77890314	chr14	77887860	77890860	-	NOXRED1	ENSG00000165555	protein_coding
		NOXRED1	rs11846861	77889546	chr14	77887860	77890860	-	NOXRED1	ENSG00000165555	protein_coding

BasalGangliaRegion	Hippocampus	AHSA1	rs11845345	77923783	chr14	77922213	77925213	+	AHSA1	ENSG00000100591	protein_coding
		MYL6B	rs3809134	56546011	chr12	56544040	56547040	+	MYL6B	ENSG00000196465	protein_coding
		VAPA	rs4798889	9913930	chr18	9911999	9914999	+	VAPA	ENSG00000101558	protein_coding
		ME3	rs670736	86383679	chr11	86381678	86384678	-	ME3	ENSG00000151376	protein_coding
		AGK	rs7790742	141250685	chr7	1.41E+08	141252078	+	AGK	ENSG00000006530	protein_coding
		AGK	rs7795885	141251044	chr7	1.41E+08	141252078	+	AGK	ENSG00000006530	protein_coding
	AccumbensArea	FAM162B	rs641338	117086265	chr6	1.17E+08	117087882	-	FAM162B	ENSG00000183807	protein_coding
		EPHA4	rs149636195222438911	chr2	2.22E+08	222439922		-	EPHA4	ENSG00000116106	protein_coding
		PTH1R	rs2168442	46919379	chr3	46917211	46920211	+	PTH1R	ENSG00000160801	protein_coding
		IPO7	rs75955853	9406129	chr11	9404199	9407199	+	IPO7	ENSG00000205339	protein_coding
		GTPBP8	rs114429530112710133	chr3	1.13E+08	112710831		+	GTPBP8	ENSG00000163607	protein_coding
		RELCH	rs3752091	59854253	chr18	59852488	59855488	+	RELCH	ENSG00000134444	protein_coding
	Caudate	IRX3	rs191251428	54320835	chr16	54318699	54321699	-	IRX3	ENSG00000177508	protein_coding
		CLCNKB	rs75909377	16370712	chr1	16368231	16371231	+	CLCNKB	ENSG00000184908	protein_coding
		IL23A	rs79824801	56728137	chr12	56725958	56728958	+	IL23A	ENSG00000110944	protein_coding
		RELL1	rs4832933	37688443	chr4	37685998	37688998	-	RELL1	ENSG00000181826	protein_coding
		SETD4	rs142847892	37451298	chr21	37449687	37452687	-	SETD4	ENSG00000185917	protein_coding
		ULBP3	rs1537648	150389924	chr6	1.5E+08	150391257	-	ULBP3	ENSG00000131019	protein_coding
	Putamen	ERCC4	rs6498486	14013666	chr16	14012014	14015014	+	ERCC4	ENSG00000175595	protein_coding
		ERCC4	rs3136042	14014055	chr16	14012014	14015014	+	ERCC4	ENSG00000175595	protein_coding
		ERCC4	rs1799798	14014278	chr16	14012014	14015014	+	ERCC4	ENSG00000175595	protein_coding
		HPS3	rs13089410	148847441	chr3	1.49E+08	148848425	+	HPS3	ENSG00000163755	protein_coding
		HPS3	rs7643410	148848073	chr3	1.49E+08	148848425	+	HPS3	ENSG00000163755	protein_coding
		SLC6A16	rs8102658	49828855	chr19	49826472	49829472	-	SLC6A16	ENSG00000063127	protein_coding
CerebellumRegion	Cerebellum	ACAT2	rs2025187	160181435	chr6	1.6E+08	160184077	+	ACAT2	ENSG00000120437	protein_coding
		ZFYVE9	rs627011	52608109	chr1	52605766	52608766	+	ZFYVE9	ENSG00000157077	protein_coding
		ERBB2	rs2517955	37843681	chr17	37842167	37845167	+	ERBB2	ENSG00000141736	protein_coding
		ERBB2	rs75849983	37843762	chr17	37842167	37845167	+	ERBB2	ENSG00000141736	protein_coding
		FCGRT	rs2946865	50010378	chr19	50008073	50011073	+	FCGRT	ENSG00000104870	protein_coding
		TRPM4	rs11882563	49661547	chr19	49658998	49661998	+	TRPM4	ENSG00000130529	protein_coding

Table S5: Annotations of super enhancers of cis-eQTL SNPs,

Region	Structure	GE	SN	BP	Chr	En ha nc er Sta rt	En ha nc er En t d	Ra nk	Co Ele me nt	mm on SN P	Ris eQ TL SN P	TF _cas9_ t se_ val	Crisps ites	Ca trol _val	Con trol _val	Overlap_ gene	Proximal_gene	Clo sest _ge ne	Close st _act ive	Data _so urce	Biosam ple_ type	Tissue_type	Biosample_name
LimbicRegion	Amygdala	M	rs38565	chr12	YL0914606B3411	5655653685609378202	5655653725618505186	3	209	11	1	132	1726	25762.29	2124.232	MYL6B,S MARCC2, ESYT1,MYL6	ESYT1,RPL41,PA2G4,SMA	MYL6B	ENCODE	Tissue	Adrenal gland	adrenal-gland	
		M	rs38565	chr12	YL0914606B3411	5655653725618505186	5655653725618505186	2	209	11	1	129	1675	20538.79	1897.287	MYL6B,S MARCC2, ESYT1,MYL6	ESYT1,RPL41,PA2G4,SMA	MYL6B	ENCODE	Tissue	Peyers patch	Peyers-patch	
		M	rs38565	chr12	YL0914606B3411	5655653645707289720	5655653645707289720	2	220	11	1	143	1962	24549.61	3326.778	MYL6B,S MARCC2, ESYT1,MYL6	ESYT1,RPL41,PA2G4,SMA	MYL6B	NCBI GEO/SRA	Cell line	Umbilical vein	HUVEC_VEGF_4h	
		M	rs38565	chr12	YL0914606B3411	5655652597241851807	5655652597241851807	10	486	30	2	363	4242	43634.58	7201.146	MYL6B,S MARCC2, ESYT1,MYL6	ESYT1,RPL41,PA2G4,SMA	MYL6B	NCBI GEO/SRA	Cell line	Other	90-8TL_DMSO	
		M	rs38565	chr12	YL0914606B3411	5655653685841166	5655653685841166	1052	4	228	11	1	185	2182	7503.458	1847.172	MYL6B,S MARCC2, ESYT1,MYL6	ESYT1,RPL41,PA2G4,SMA	MYL6B	NCBI GEO/SRA	Other	Skin	NHEK_scramble
		M	rs38565	chr12	YL0914606B3411	5655653665426259136	5655653665426259136	3	189	10	0	118	1459	23826.11	2844.045	MYL6B,E SYT1,MYL6	ESYT1,RPL41,PA2G4,SMA	MYL6B	NCBI GEO/SRA	Cell line	Colon	V456	
		M	rs38565	chr12	YL0914606B3411	5655653825524527491	5655653825524527491	3	192	11	1	119	1378	33567.73	2084.583	MYL6B,E SYT1,MYL6	ESYT1,RPL41,PA2G4,SMA	MYL6B	NCBI GEO/SRA	Cell line	Colon	V481	
Hippocampus	VAMPAs	rs47991	988393	chr18	99199126271286	99199126271286	1145	1	64	8	0	34	196	10373.74	767.3588	VAPA	TXNDC2,VAPA	VAPA	ENCODE	In vitro differentiated cells	Liver	hepatocyte	

VA PA	rs47991	chr9	991993	2860085	102	4	214	32	0	40	196	247	1812	VAPA	TXNDC2,VAPA	VA PA	VAP A	EN CO DE	Primary cell	Skin	keratinocyte																									
	988393	18	5	0	5	4	214	32	0	40	196	22.46	74																																	
	rs47991	chr9	991993	283434	729	6	271	43	1	45	236	299	2715									VAPA	TXNDC2,VAPA	VA PA	VAP A	EN CO DE	Tissue	Adrenal gland	adrenal-gland																	
	988393	18	8	2	2	6	271	43	1	45	236	78.73	955																																	
	rs47991	chr9	991991	281693	945	1	60	8	0	34	196	295	535.																	VAPA	TXNDC2,VAPA	VA PA	VAP A	EN CO DE	Tissue	Spleen	spleen									
	988393	18	1	2	2	1	60	8	0	34	196	24.9	3179																																	
	rs47991	chr9	991992	284831	126	7	4	195	28	0	40	196	177																									1889	VAPA	TXNDC2,VAPA	VA PA	VAP A	EN CO DE	Tissue	Tibial nerve	tibial-nerve
	988393	18	8	3	7	4	195	28	0	40	196	33.72	823																																	
	rs47991	chr9	989991	790819	503	2	281	35	0	38	196	248	2416																									VAPA								
988393	18	7	5	5	2	281	35	0	38	196	06.14	301																																		
rs47991	chr9	990991	476667	633	2	167	19	0	35	196	895	1271	VAPA	TXNDC2,VAPA	VA PA	VAP A	NC BI GE O/S RA	Stem cell	Umbilical cord	umbilical-cord-derived-mesenchymal-stem-cells_Control_cycle_6																										
988393	18	9	7	7	2	167	19	0	35	196	1.244	774																																		
rs47991	chr9	991991	294661	448	1	54	8	0	31	196	388	563.									VAPA	TXNDC2,VAPA	VA PA	VAP A	NC BI GE O/S RA	Cell line	Pancreatic	L3-6_4SC-202																		
988393	18	8	1	1	1	54	8	0	31	196	14.98	0031																																		
rs47991	chr9	991995	252402	549	6	568	100	3	80	400	311	3331																	VAPA	TXNDC2,VAPA	VA PA	VAP A	NC BI GE O/S RA	Cell line	Pancreatic	L3-6_DMSO										
988393	18	7	0	0	6	568	100	3	80	400	11.45	888																																		
rs47991	chr9	991991	294678	613	1	58	8	0	31	196	390	2377																									VAPA		TXNDC2,VAPA	VA PA	VAP A	NC BI GE O/S RA	Cell line	Peripheral blood	CUTLL1_dimer-mutant	
988393	18	1	1	1	1	58	8	0	31	196	58.18	344																																		
rs47991	chr9	986993	744453	236	8	966	152	7	80	715	840	6212																										VAPA,TX NDC2								TXNDC2,VAPA
988393	18	4	3	3	8	966	152	7	80	715	55.81	441																																		
rs67863	chr11	863864	747188	564	6	585	105	10	104	282	237	5093	ME3	ME3	ME3	NC BI GE	Tissue	Pancreas	pancreatic-islets-F																											
073836	11	54	16	6	585	105	10	104	282	71.45	567																																			

[illegible]

Basal Accu Gangl mbe iaReg nsAr ion ea	PT rs21469 H1 684 193 R 42 79	chr 3	469469 018356984 5 354 44 4 377 867	216 21. .644	8335 MYL3,PT H1R	PRSS42	PT H1 R	PTH1 R	Roa dma p	Tissue	Right cardiac atrium	right-cardiac- atrium
	PT rs21469 H1 684 193 R 42 79	chr 3	469469 077358 92 2 297 36 4 317 581	259 97. .566	5614 PTH1R	PRSS42,MYL3	PT H1 R	PTH1 R	NC BI GE O/S RA NC	Tissue	Kidney	Patient_x750N
	PT rs21469 H1 684 193 R 42 79	chr 3	469469 081422397 6 365 45 3 398 1132	211 02. .533	4535 PTH1R	PRSS42,MYL3	PT H1 R	PTH1 R	BI GE O/S RA NC	Tissue	Skeletal muscle	RMS008
	PT rs21469 H1 684 193 R 42 79	chr 3	468469 990363625 3 385 52 4 387 1173	304 20. .661	5344 MYL3,PT H1R	PRSS42	PT H1 R	PTH1 R	BI GE O/S RA	Primar y cell	Heart	purified cardiomyocyte G296S mutants
	PT rs14 H1 464 342 R 564 90 4	chr 3	469469 018356984 5 354 44 4 377 867	216 21. .644	8335 MYL3,PT H1R	PRSS42	PT H1 R	PTH1 R	Roa dma p	Tissue	Right cardiac atrium	right-cardiac- atrium
	PT rs14 H1 464 342 R 564 90 4	chr 3	469469 077358 92 2 297 36 4 317 581	259 97. .566	5614 PTH1R	PRSS42,MYL3	PT H1 R	PTH1 R	NC BI GE O/S RA NC	Tissue	Kidney	Patient_x750N
	PT rs14 H1 464 342 R 564 90 4	chr 3	469469 081422397 6 365 45 3 398 1132	211 02. .533	4535 PTH1R	PRSS42,MYL3	PT H1 R	PTH1 R	BI GE O/S RA NC	Tissue	Skeletal muscle	RMS008
	PT rs14 H1 464 342 R 564 90 4	chr 3	468469 990363625 3 385 52 4 387 1173	304 20. .661	5344 MYL3,PT H1R	PRSS42	PT H1 R	PTH1 R	BI GE O/S RA NC	Primar y cell	Heart	purified cardiomyocyte G296S mutants
	IP O7	rs75940 955 612 853 9 11	932942 805010 21 12 1482209 3 66 321	667 88. .326	9057 TMEM41 B,IPO7	SNORA23,DENND5A	IPO 7	IPO7	NC BI GE O/S RA NC	Stem cell	Embryo	Embryonic-stem- cells_Naive
	IP O7	rs75940 955 612 853 9 11	938942 271798976 6 605 70 3 44 167	260 67. .046	4518 IPO7	SNORA23,TMEM41B	IPO 7	IPO7	NC BI GE	Cell line	Lung	IMR- 90_proliferating

[illegible]

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[illegible]

																			positive, alpha-beta T cell
IL2 3A	rs79567	chr12	567567	261361369	2	73	12	0	130	757	276	1559	IL23A,ST	CNPY2,APOF,PAN2,CS	IL2 3A	Roa dma p	Primar y cell	Blood	CD4-positive- alpha-beta- memory-T-cell
IL2 3A	rs79567	chr12	567567	261346441	2	60	11	0	126	631	274	1004	IL23A,PA	CNPY2,STAT2,APOF,PAN2	IL2 3A	Roa dma p	Primar y cell	Blood	CD8-positive- alpha-beta-T-cell
IL2 3A	rs79567	chr12	567567	262358370	2	68	11	0	130	717	291	1046	IL23A,ST	CNPY2,APOF,PAN2,CS	IL2 3A	Roa dma p	Primar y cell	Cord blood	T-cell
IL2 3A	rs79567	chr12	567567	264356602	5	61	9	0	130	698	145	999	IL23A,ST	CNPY2,APOF,PAN2,CS	IL2 3A	BI GE O/S RA NC	Primar y cell	Blood	CD8donorA
IL2 3A	rs79567	chr12	567567	262342926	1	55	11	0	126	618	235	988	IL23A,PA	CNPY2,STAT2,APOF,PAN2	IL2 3A	BI GE O/S RA NC	Cell line	Peripheral blood	MV411
RE LL 1	rs48376	chr4	376377	486025905	9	781	37	6	104	291	307	7720	RELL1		REL L1	Roa dma p	Tissue	Large intestine	large- intestine_108d
RE LL 1	rs48376	chr4	376377	662024	127	6	505	16	1	77	222	4682	RELL1		REL L1	Roa dma p	Tissue	Small intestine	small- intestine_108days
RE LL 1	rs48376	chr4	376377	630026835	9	548	17	1	83	191	122	3310	RELL1		REL L1	Roa dma p	Tissue	Stomach	stomach_3y
RE LL 1	rs48376	chr4	376377	332047550	8	1047	61	9	128	422	374	7284	RELL1	C4orf19	REL L1	EN CO DE	Tissue	Stomach	stomach
M E M50A	rs30256	chr1	256257	347106207	14	815	116	2	31	1148	760	8338	RHD,TM	RHD,TMEM57,RHCE	TM EM 50A	TME M50A DE	Cell line	Submandibular Salivary Gland	ACC112
M E M50A	rs30256	chr1	256256	344712495	5	412	74	0	18	741	292	7612	RHD,TM	RHD	TM EM 50A	TME M50A O/S RA NC	Cell line	Endometrium	EEC16
M E M50A	rs30256	chr1	256257	349106	105	12	808	113	2	31	316	1114	RHD,TM	RHD,TMEM57,RHCE	TM EM 50A	TME M50A GE	Cell line	Lung	IMR- 90_proliferating

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ER rs25378	chr17	378378	BB 179 436 2 55 81	434476546 40 41	1	37	5	2	1	211	134 82.27	379.3503	ERBB2,P GAP3	C17orf37,GRB7,PNMT,ERB B2,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Stem cell	Embryo	H7
ER rs25378	chr17	378378	BB 179 436 2 55 81	434473413 18 80	1	35	5	2	1	211	958 7.2 48	746.837	ERBB2,P GAP3	C17orf37,GRB7,PNMT,ERB B2,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Cell line	Embryo endodermal	CyT49_ES_D0
ER rs25378	chr17	378378	BB 179 436 2 55 81	426694 67 90	1	2	244	26	6	142	1358 464 821.1	1192 20.2	ERBB2,P GAP3	STARD3,C17orf37,GRB7,PNMT,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Cell line	Lung	Calu-3
ER rs25378	chr17	378378	BB 179 436 2 55 81	432623672 03 27	3	186	21	4	99	633	892 1.3 46	1474.46	ERBB2,P GAP3	STARD3,C17orf37,GRB7,PNMT,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Stem cell	Embryo	Embryonic-stem-cells_Primed
ER rs25378	chr17	378378	BB 179 436 2 55 81	281637141 49 77	4	344	72	10	117	1581	335 25.95	3131.701	ERBB2,P GAP3	PPP1R1B,STARD3,GRB7,C17orf37,PNMT,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Cell line	Mammary Gland	ZR-75-1_2
ER rs75378	chr17	378378	BB 849 437 2 983 62	434476546 40 41	1	37	5	2	1	211	134 82.27	379.3503	ERBB2,P GAP3	C17orf37,GRB7,PNMT,ERB B2,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Stem cell	Embryo	H7
ER rs75378	chr17	378378	BB 849 437 2 983 62	434473413 18 80	1	35	5	2	1	211	958 7.2 48	746.837	ERBB2,P GAP3	C17orf37,GRB7,PNMT,ERB B2,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Cell line	Embryo endodermal	CyT49_ES_D0
ER rs75378	chr17	378378	BB 849 437 2 983 62	426694 67 90	1	2	244	26	6	142	1358 464 821.1	1192 20.2	ERBB2,P GAP3	STARD3,C17orf37,GRB7,PNMT,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Cell line	Lung	Calu-3
ER rs75378	chr17	378378	BB 849 437 2 983 62	432623672 03 27	3	186	21	4	99	633	892 1.3 46	1474.46	ERBB2,P GAP3	STARD3,C17orf37,GRB7,PNMT,TCAP	ERB B2	ERBB 2	NC BI GE O/S RA NC	Stem cell	Embryo	Embryonic-stem-cells_Primed

ER rs75378	chr17	378378	281637141	4	344	72	10	117	1581	335	3131	ERBB2,P	PPP1R1B,STARD3,GRB7,C1ERB	ERBB	NC	BI	Cell line	Mammary Gland	ZR-75-1_2
BB 849 437	2	983 62	49 77							25	.701	GAP3	7orf37,PNMT,TCAP	B2	2	GE			
FC rs29500	chr19	500500	021320901	4	427	70	2	74	1719	267	2861	FCGRT,R	RPL13AP5,SNORD33,SNO	FC	FCGR	Roa	Tissue	Spleen	spleen_30y
GR 468 103	T	65 78	67 71							13	.813	PS11,MIR	RD34,SNORD32A,ALDH16	GR	T	dma			
										24		150,RCN3	A1,PIH1D1,SNORD35A,FLT3LG,SNORD35B	T		p			
FC rs29500	chr19	500500	099208179	1	141	27	1	23	733	335	808	FCGRT	RPL13AP5,SNORD33,SNO	FC	FCGR	EN	Cell line	Brain: derived from metastatic site: supra-orbital area	SK-N-MC
GR 468 103	T	65 78	69 33							06	2816		RD34,SNORD32A,RPS11,RCN3,SNORD35A,FLT3LG,MIR150,SNORD35B	GR	T	CO			
										75				T		DE			
FC rs11500	chr19	500500	021320901	4	427	70	2	74	1719	267	2861	FCGRT,R	RPL13AP5,SNORD33,SNO	FC	FCGR	Roa	Tissue	Spleen	spleen_30y
GR 329 281	T	90 63	67 71							13	.813	PS11,MIR	RD34,SNORD32A,ALDH16	GR	T	dma			
										24		150,RCN3	A1,PIH1D1,SNORD35A,FLT3LG,SNORD35B	T		p			
TR rs11496	chr19	496496	510703451	2	313	41	0	114	2028	295	4527	HRC,TRP	RPL13AP5,SNORD33,SNO	TRP	TRPM	Roa	Tissue	Lung	lung_3y
PM 882 615	4	563 47	32 98							60	.771	M4,PPFIA	LIN7B,C19orf73,TRPM4	M4	4	dma			
										26		3				p			
TR rs11496	chr19	496496	515711550	3	332	43	0	105	1980	918	1996	HRC,TRP	RPL13AP5,SNORD33,SNO	TRP	TRPM	EN	Tissue	Prostate	prostate
PM 882 615	4	563 47	89 99							1.4	.298	M4,PPFIA	LIN7B,C19orf73,TRPM4	M4	4	CO			
										02		3				DE			
																NC			
TR rs11496	chr19	496496	518696255	3	299	39	0	105	1895	147	2429	HRC,TRP	RPL13AP5,SNORD33,SNO	TRP	TRPM	BI	Cell line	Prostate	C4-2B_vehicle_24h
PM 882 615	4	563 47	20 48							99	.956	M4,PPFIA	LIN7B,C19orf73,TRPM4	M4	4	GE			
										02		3				O/S			
																RA			
																NC			
TR rs11496	chr19	496496	514747292	4	385	50	0	142	2322	423	501	HRC,TRP	RPL13AP5,SNORD33,SNO	TRP	TRPM	BI	Tissue	Endometrioid	endometrioid_ade
PM 882 615	4	563 47	04 33							93	.5735	M4,PPFIA	LIN7B,C19orf73,TRPM4	M4	4	GE			
										46		3				O/S			nocarcinoma_TumorA
																RA			
																NC			
TR rs11496	chr19	496496	526723431	2	342	46	0	129	1968	328	1829	HRC,TRP	RPL13AP5,SNORD33,SNO	TRP	TRPM	BI	Primar y cell	Heart	purified cardiomyocyte WT
PM 882 615	4	563 47	96 29							38	.796	M4,PPFIA	LIN7B,C19orf73,TRPM4	M4	4	GE			
										16		3				O/S			
																RA			
																NC			
TR rs11496	chr19	496496	509725505	3	362	50	0	147	2313	306	2233	HRC,TRP	RPL13AP5,SNORD33,SNO	TRP	TRPM	BI	Primar y cell	Heart	purified cardiomyocyte G296S mutants
PM 882 615	4	563 47	75 59							57	.944	M4,PPFIA	LIN7B,C19orf73,TRPM4	M4	4	GE			
										91		3				O/S			
																RA			
TR rs11496	chr19	496496	510703451	2	313	41	0	114	2028	295	4527	HRC,TRP	RPL13AP5,SNORD33,SNO	TRP	TRPM	Roa	Tissue	Lung	lung_3y
PM 083 653	4	963 40	32 98							60	.771	M4,PPFIA	LIN7B,C19orf73,TRPM4	M4	4	dma			
										26		3				p			

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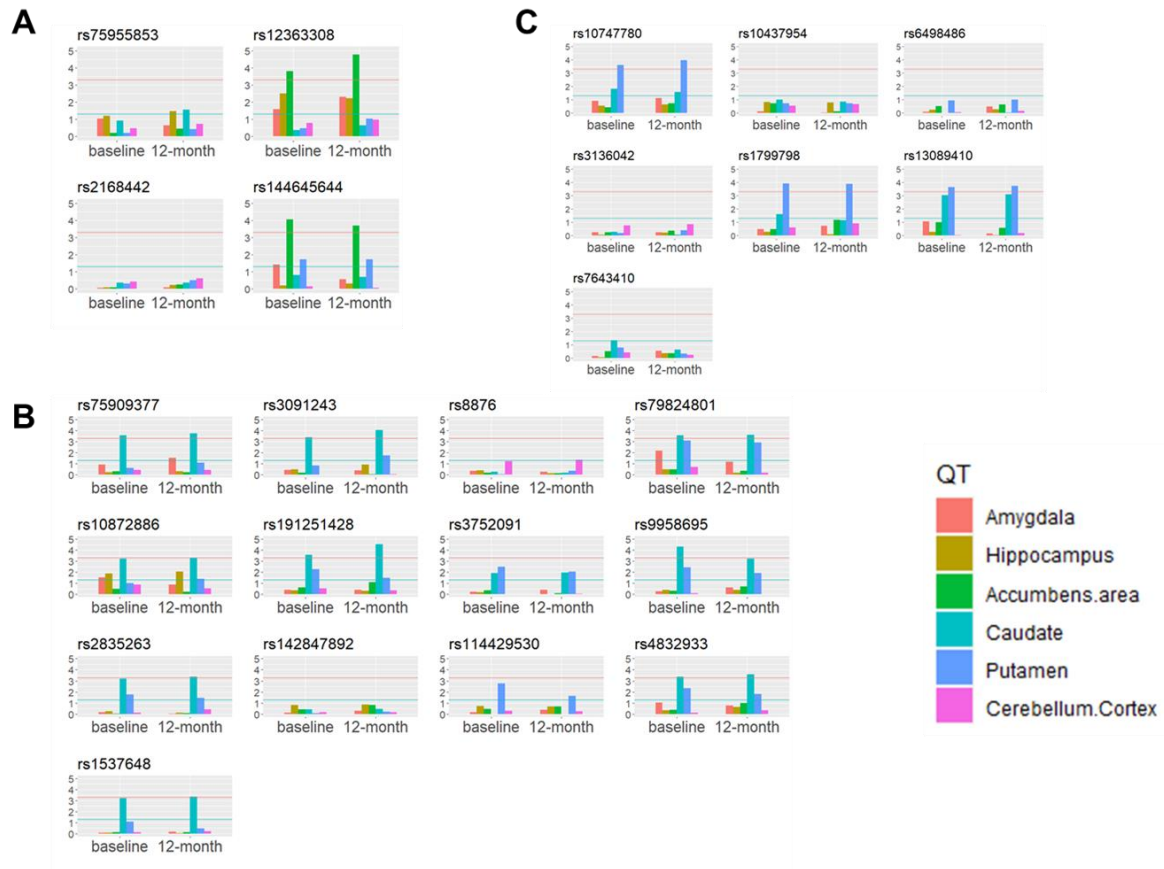


Figure S1. Bar plots of associations between 26 SNPs in basal ganglia region and 6 subcortical structures. (A) 4 SNPs derived from previous step in accumbens area. (B) 13 SNPs derived from previous step in caudate. (C) 7 SNPs derived from previous step in putamen. X-axial presents six subcortical structures (amygdala, hippocampus, accumbens area, caudate, putamen and cerebellum cortex) at baseline and 12-month's follow-up. Y-axial presents the p-value ($-\log_{10}$) of association based on QT-GWAS. Blue horizontal line represents $-\log_{10}(0.05)$ while red horizontal line represents $-\log_{10}(5e-4)$.

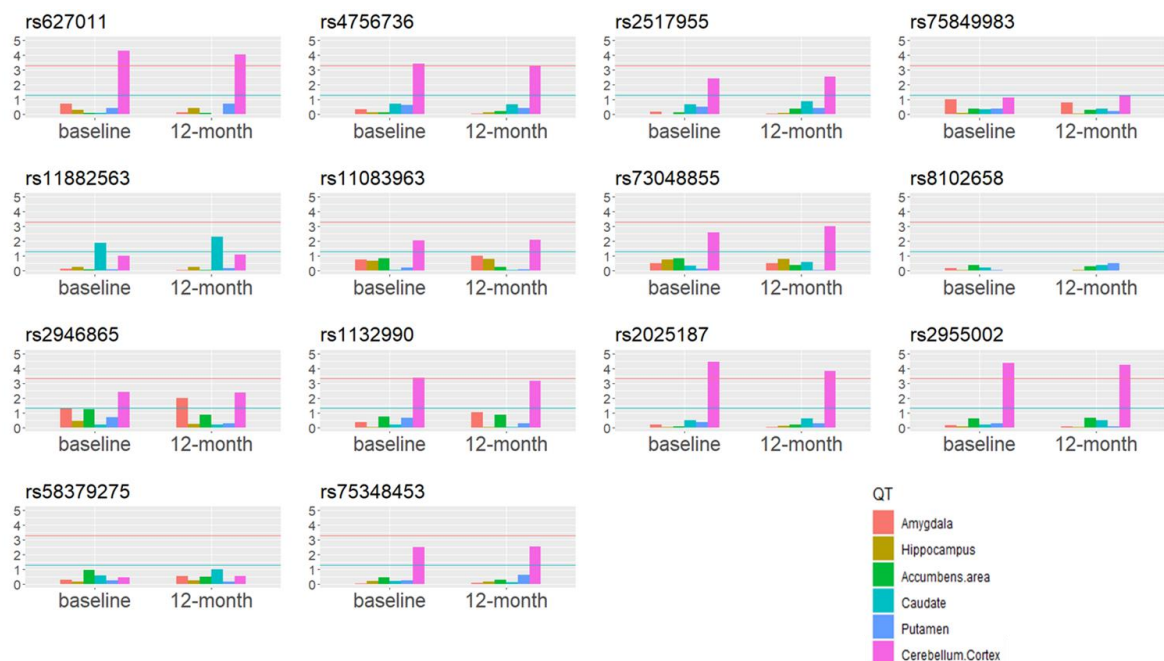


Figure S2. Bar plots of associations between 14 SNPs in cerebellum region and 6 subcortical structures. X-axial presents six subcortical structures (amygdala, hippocampus, accumbens area, caudate, putamen and cerebellum cortex) at baseline and 12-month's follow-up. Y-axial presents the p-value ($-\log_{10}$) of association based on QT-GWAS. Blue horizontal line represents $-\log_{10}(0.05)$ while red horizontal line represents $-\log_{10}(5e-4)$.