

Supplementary Table 1: 148 genes associated with change in WMH volume over time

Symbol	Entrez Gene Name	p-value	Partial Corr %WMH change
ABHD12B	abhydrolase domain containing 12B	0.00961	-0.202
ABHD16A	abhydrolase domain containing 16A, phospholipase	0.00649	-0.212
ABT1	activator of basal transcription 1	0.00651	-0.212
ACTA1	actin alpha 1, skeletal muscle	0.00913	0.203
ADAM8	ADAM metalloproteinase domain 8	0.00888	-0.204
ADCK1	aarF domain containing kinase 1	0.000877	0.257
AMACR	alpha-methylacyl-CoA racemase	0.00935	-0.202
ANKDD1A	ankyrin repeat and death domain containing 1A	0.000299	-0.279
ANLN	anillin actin binding protein	0.00519	0.217
APBA1	amyloid beta precursor protein binding family A member 1	0.00391	0.224
APMAP	adipocyte plasma membrane associated protein	0.00225	-0.237
ARL6IP6	ADP ribosylation factor like GTPase 6 interacting protein 6	0.00656	-0.211
ATP5MC2P4	ATP synthase membrane subunit c locus 2 pseudogene 4	0.00447	-0.221
ATP6V1E2	ATPase H ⁺ transporting V1 subunit E2	0.00133	-0.248
BMP1	bone morphogenetic protein 1	0.0102	0.200
BTNL8	butyrophilin like 8	0.00699	-0.210
CAPN5	calpain 5	0.00851	-0.205
CASC15	cancer susceptibility 15	0.00797	0.207
CCDC71L	coiled-coil domain containing 71 like	0.00991	-0.201
CD9	CD9 molecule	0.0023	-0.236
CDAN1	codanin 1	0.00972	-0.201
CDH7	cadherin 7	0.00242	-0.235
CFD	complement factor D	0.00108	-0.253
CHMP4B	charged multivesicular body protein 4B	0.0094	-0.202
CLEC18A	C-type lectin domain family 18 member A	0.00829	-0.206
CNNM4	cyclin and CBS domain divalent metal cation transport mediator 4	0.0067	-0.211
CTHRC1	collagen triple helix repeat containing 1	0.000828	-0.259
CYB561D2	cytochrome b561 family member D2	0.00445	-0.221
CYSTM1	cysteine rich transmembrane module containing 1	0.00506	-0.218
DAB2	DAB adaptor protein 2	0.00974	0.201
DCAF4L1	DDB1 and CUL4 associated factor 4 like 1	0.00176	-0.242
DCP1B	decapping mRNA 1B	0.00486	-0.219
DHRS9	dehydrogenase/reductase 9	0.00306	-0.230
DNAJC3-DT	DNAJC3 divergent transcript	0.00377	-0.225
DNAL4	dynein axonemal light chain 4	0.00692	-0.210
DOC2B	double C2 domain beta	0.00133	0.249
DOLK	dolichol kinase	0.00761	-0.208
DPYD-IT1	DPYD intronic transcript 1	0.00466	-0.220
DUSP1	dual specificity phosphatase 1	0.00509	-0.218

DYNC1LI1	dynein cytoplasmic 1 light intermediate chain 1	0.00745	-0.208
EDC3	enhancer of mRNA decapping 3	0.00465	-0.220
EEF1A1P8	eukaryotic translation elongation factor 1 alpha 1 pseudogene 8	0.0045	0.221
EIF1AY	eukaryotic translation initiation factor 1A Y-linked	0.00175	-0.243
EPB41L2	erythrocyte membrane protein band 4.1 like 2	0.00602	0.214
EPHB4	EPH receptor B4	6.23E-06	-0.345
FPR2	formyl peptide receptor 2	0.00178	-0.242
FRAT2	FRAT regulator of WNT signaling pathway 2	0.00879	-0.204
GNB2	G protein subunit beta 2	0.000584	-0.266
GOLGA7	golgin A7	0.00725	-0.209
GRTP1	growth hormone regulated TBC protein 1	0.004	-0.224
GTF2IP4	general transcription factor Iii pseudogene 4	0.00578	-0.215
H1-12P	H1.12 linker histone, cluster member pseudogene	0.00107	-0.253
H2BC18	H2B clustered histone 18	0.00924	-0.203
HYAL3	hyaluronidase 3	0.000555	-0.267
IFNGR2	interferon gamma receptor 2	0.00132	-0.249
IPO13	importin 13	0.0091	0.203
ITM2B	integral membrane protein 2B	0.0062	-0.213
JTB	jumping translocation breakpoint	0.00472	-0.220
JUNB	JunB proto-oncogene, AP-1 transcription factor subunit	0.00329	-0.228
KBTBD7	kelch repeat and BTB domain containing 7	0.00116	-0.251
KDM5C-IT1	KDM5C intronic transcript 1	0.00548	-0.216
LHFPL6	LHFPL tetraspan subfamily member 6	0.00458	0.220
LOXL1-AS1	LOXL1 antisense RNA 1	0.0073	-0.209
MAX	MYC associated factor X	0.0087	-0.204
MCM4	minichromosome maintenance complex component 4	0.00078	0.260
MSRB1	methionine sulfoxide reductase B1	0.00735	-0.209
MTRNR2L6	MT-RNR2 like 6	0.00248	0.235
MTUS1	microtubule associated scaffold protein 1	0.000535	0.267
MX1	MX dynamin like GTPase 1	0.00754	0.208
MYBPC3	myosin binding protein C3	0.00943	-0.202
MYL12B	myosin light chain 12B	0.00553	-0.216
MYPN	myopalladin	0.00129	0.249
NAT14	N-acetyltransferase 14 (putative)	0.0043	-0.222
NEK7	NIMA related kinase 7	0.00276	-0.232
NEXN	nexilin F-actin binding protein	0.00573	0.215
NLRP2	NLR family pyrin domain containing 2	0.00304	-0.230
NOP10	NOP10 ribonucleoprotein	0.00558	-0.215
OAS2	2'-5'-oligoadenylate synthetase 2	0.00572	0.215
OAS3	2'-5'-oligoadenylate synthetase 3	0.00459	0.220
OAT	ornithine aminotransferase	0.00344	-0.227
OSER1	oxidative stress responsive serine rich 1	0.00223	-0.237
PCBP1-AS1	PCBP1 antisense RNA 1	0.00567	-0.215
PCBP3	poly(rC) binding protein 3	0.00867	-0.204

PCDHGA8	protocadherin gamma subfamily A, 8	0.00678	-0.211
PGAP1	post-GPI attachment to proteins inositol deacylase 1	0.00309	0.230
PGM2	phosphoglucomutase 2	0.000598	-0.265
PIGFP2	phosphatidylinositol glycan anchor biosynthesis class F pseudogene 2	0.0043	0.222
PIP4K2C	phosphatidylinositol-5-phosphate 4-kinase type 2 gamma	0.00178	-0.242
PIPSL	PIP5K1A and PSMD4 like (pseudogene)	0.00441	-0.221
PLGLB1	plasminogen like B2	0.00157	-0.245
PLP2	proteolipid protein 2	0.00857	-0.205
POLB	DNA polymerase beta	0.00255	-0.234
POLQ	DNA polymerase theta	0.00602	0.214
PPP1R3F	protein phosphatase 1 regulatory subunit 3F	0.0066	-0.211
PPTC7	protein phosphatase targeting COQ7	0.0064	-0.212
PROK2	prokineticin 2	0.00522	-0.217
PRPH2	peripherin 2	0.00743	-0.208
PRRG1	proline rich and Gla domain 1	0.000389	0.274
PRRG4	proline rich and Gla domain 4	0.00921	-0.203
PSMA8	proteasome 20S subunit alpha 8	0.00625	-0.213
PSMB3	proteasome 20S subunit beta 3	0.0017	-0.243
PSMD8P1	proteasome 26S subunit, non-ATPase, 8 pseudogene 1	0.00425	-0.222
PTK2	protein tyrosine kinase 2	0.00506	0.218
QPCT	glutamyl-peptide cyclotransferase	0.00906	-0.203
RAB11A	RAB11A, member RAS oncogene family	0.00548	-0.216
RAB2A	RAB2A, member RAS oncogene family	0.0101	-0.200
RARRES1	retinoic acid receptor responder 1	0.0102	-0.200
RDH10-AS1	RDH10 antisense RNA 1	0.0015	-0.246
RGL4	ral guanine nucleotide dissociation stimulator like 4	0.00215	-0.238
RGS14	regulator of G protein signaling 14	0.000494	-0.269
RHOB	ras homolog family member B	0.000341	-0.276
RHOQP3	ras homolog family member Q pseudogene 3	0.00575	-0.215
RRAGC	Ras related GTP binding C	0.00371	-0.225
S100P	S100 calcium binding protein P	0.00531	-0.217
SAMD13	sterile alpha motif domain containing 13	0.00727	0.209
SCN9A	sodium voltage-gated channel alpha subunit 9	0.00498	-0.218
SCNN1A	sodium channel epithelial 1 subunit alpha	0.0007	-0.262
SDCBP	syndecan binding protein	0.00295	-0.231
SDHAF4	succinate dehydrogenase complex assembly factor 4	0.00456	-0.220
SERTAD3	SERTA domain containing 3	0.00473	-0.220
SIGLEC1	sialic acid binding Ig like lectin 1	0.00292	0.231
SLC19A1	solute carrier family 19 member 1	0.00719	-0.209
SND1-IT1	SND1 intronic transcript 1	0.00599	-0.214
SPACA6	sperm acrosome associated 6	0.00244	-0.235
SRXN1	sulfiredoxin 1	0.00352	-0.227
ST20	suppressor of tumorigenicity 20	0.00967	-0.202
STAC3	SH3 and cysteine rich domain 3	0.00761	0.208

STOX2	storkhead box 2	0.00934	0.202
TBC1D20	TBC1 domain family member 20	0.00904	-0.203
TM2D3	TM2 domain containing 3	0.00486	-0.219
TM6SF1	transmembrane 6 superfamily member 1	0.000551	-0.267
TMEM154	transmembrane protein 154	0.00149	-0.246
TMEM43	transmembrane protein 43	0.000831	-0.259
TMEM69	transmembrane protein 69	0.00075	-0.261
TOPORS	TOP1 binding arginine/serine rich protein, E3 ubiquitin ligase	0.0087	-0.204
TRADD	TNFRSF1A associated via death domain	0.00284	-0.232
TRPC4AP	transient receptor potential cation channel subfamily C member 4 associated protein	0.00385	-0.224
TSPAN2	tetraspanin 2	0.000682	-0.263
TTC9	tetratricopeptide repeat domain 9	0.00986	-0.201
UBE2B	ubiquitin conjugating enzyme E2 B	0.00274	-0.232
UTY	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	0.00595	-0.214
VLDLR	very low density lipoprotein receptor	0.00285	-0.232
VSIG8	V-set and immunoglobulin domain containing 8	0.00731	-0.209
WLS	Wnt ligand secretion mediator	0.00716	-0.209
ZBED3-AS1	ZBED3 antisense RNA 1	0.00895	-0.204
ZNF180	zinc finger protein 180	0.00613	-0.213
ZNF404	zinc finger protein 404	0.00688	0.210
ZNF561-AS1	ZNF561 antisense RNA 1 (head to head)	0.00796	-0.207