SUPPLEMENTAL MATERIAL

Supplemental Tables

Supplementary Table I: Description of probands (cases/controls) in participating GWA studies:

Phenotype	Cohort name	N cases	N controls	%female	Mean age	Study design
Ischaemic stroke						
	ARIC	385	8,803	39.7/53.5	57.3/54.1	population-based
	ASGC	1,162	1,244	40.8/49.8	72.9/70.2	cross-sectional
	BRAINS	361	444	44.1/64.2	74.4/65.0	cross-sectional
	CHS	454	2,817	55.0/55.0	81.6/85.8	population-based
	deCODE	2,391	26,970	45.0/62.0	73.3/57.3	cross-sectional
	FHS	171	4,164	56.7/54.9	79.6/71.9	population-based
	MGH/GASROS	516	1,202	39.7/40.9	66.7/47.5	cross-sectional
	GEOS	448	498	38.6/43.4	41.0/39.5	cross-sectional
	HPS	578	468	25.0/33.0	64.9/59.2	cross-sectional
	HVH	566	1,290	66.3/52.3	69.2/66.6	cross-sectional
	MILANO	372	407	37.2/12.3	57.4/50.8	cross-sectional
	ROTTERDAM	367	5,396	54.8/59.7	70.8/69.0	population-based
	ISGS/SWISS	1,070	2,329	42.8/52.0	66.5/64.8	cross-sectional
	WTCCC2-D	1,174	797	38.1/48.6	66.7/62.7	cross-sectional
	WTCCC2-UK	2,374	5,175	46.2/50.5	72.2/52.0	cross-sectional
Large artery stroke						
	ARIC	31	8,803	41.9/53.5	57.8/54.1	population-based
	ASGC	421	1,244	31.3/49.8	73.2/70.2	cross-sectional
	BRAINS	120	444	47.5/64.2	77.7/65.0	cross-sectional
	deCODE	255	26,970	38.8/62.0	70.5/57.3	cross-sectional
	MGH/GASROS	95	1,202	41.1/40.9	66.8/47.5	cross-sectional
	GEOS	37	498	32.4/43.4	45.2/39.5	cross-sectional
	HVH	61	1,290	55.7/52.3	67.9/66.6	cross-sectional
	MILANO	74	407	24.0/12.3	63.5/50.8	cross-sectional
	ISGS/SWISS	229	2,329	40.8/52.0	69.1/64.8	cross-sectional
	WTCCC2-D	346	797	29.3/48.6	65.7/62.7	cross-sectional
	WTCCC2-UK	498	5,175	33.8/50.5	68.2/52.0	cross-sectional

(continued) Supplementary Table I:

Phenotype	Cohort name	N cases	N controls	%female	Mean age	Study design
Cardioembolic stroke						
	ARIC	93	8,803	41.9/53.5	57.8/54.1	population-based
	ASGC	240	1,244	31.3/49.8	73.2/70.2	cross-sectional
	BRAINS	29	444	47.5/64.2	77.7/65.0	cross-sectional
	CHS	147	2,817	55.0/55.0	81.6/85.8	population-based
	deCODE	399	26,970	38.8/62.0	70.5/57.3	cross-sectional
	FHS	48	4,164	56.7/54.9	79.6/71.9	population-based
	MGH/GASROS	169	1,202	41.1/40.9	66.8/47.5	cross-sectional
	GEOS	90	498	32.4/43.4	45.2/39.5	cross-sectional
	HVH	88	1,290	55.7/52.3	67.9/66.6	cross-sectional
	MILANO	25	407	24.0/12.3	63.5/50.8	cross-sectional
	ISGS/SWISS	247	2,329	40.8/52.0	69.1/64.8	cross-sectional
	WTCCC2-D	330	797	29.3/48.6	65.7/62.7	cross-sectional
	WTCCC2-UK	460	5,175	33.8/50.5	68.2/52.0	cross-sectional
Coronary artery disease						
	ADVANCE	278	312	57.9/ 59.0	45.8/45.3	cross-sectional
	CADomics	2,078	2,952	21.9/ 50.5	60.8/55.3	cross-sectional
	CHARGE	2,287	22,024	33.4/ 59.6	60.0/63.0	population-based
	deCODE	6,640	27,611	36.3/ 61.9	74.8/53.7	cross-sectional
	GERMIFS I	884	1,604	49.4/ 50.8	50.2/62.6	cross-sectional
	GERMIFS II	1,222	1,287	33.1/ 48.3	51.4/51.2	cross-sectional
	GERMIFS III (KORA)	1,157	1,748	20.1/ 48.9	58.6/55.9	population-based
	LURIC/ AtheroRemo 1	652	213	20.3/ 46.0	61.0/58.3	cross-sectional
	LURIC/ AtheroRemo 2	486	296	23.4/ 48.6	63.7/56.4	cross-sectional
	MedStar	874	447	33.0/ 54.6	48.9/59.7	cross-sectional
	MIGen	1,274	1,407	37.2/ 39.9	42.4/43.0	cross-sectional
	OHGS1	1,542	1,455	24.1/ 48.0	48.7/75.0	cross-sectional
	PennCATH	933	468	23.7/ 51.9	52.7/61.7	cross-sectional
	WTCCC	1,926	2,938	20.7/ 50.0	49.8/NA	cross-sectional
	HPS	2,704	2,887	20.0/49.0	64.1/NA	cross-sectional
	LOLIPOP	2,741	3,696	18.0/14.0	59.3/52.4	cross-sectional
	PROCARDIS	5,720	4,381	25.0/44.0	61.9/NA	cross-sectional

Both the METASTROKE and CARDIoGRAM/C4D cohorts have been previously described, including full details of case and control cohorts. Readers are referred to the following publications for full details: METASTROKE [1]; CARDIoGRAM [2]; C4D [3].

Supplementary Table II*: Association signals and directional consistency of effects of top variants for coronary artery disease, ischaemic stroke, and large artery stroke subtype. Results are shown for the CARDIoGRAM [2] and METASTROKE [1] samples. Heterogeneity is measured using I^2, non-significant heterogeneity values are underlined*

Lead SNPs	**Band**	**Gene in region**	**Minor Allele**	**Coronary Artery Disease**			**Ischaemic Stroke**			**Large Artery Stroke**		
				p-value	**Odds ratio (95%CI)**	**Effects go in same direction[1] (heterogeneity I^2)**	**p-value**	**Odds ratio (95%CI)**	**Effects go in same direction[2] (heterogeneity I^2)**	**p-value**	**Odds ratio (95%CI)**	**Effects go in same direction[2] (heterogeneity I^2)**
Top variants (known loci) for CAD/MI in the CARDIoGRAMplusC4D sample [4]												
rs17114036	1p32.2	PPAP2B	G	**9.78E-09**	0.87 [0.82-0.91]	-	0.1622	0.96 [0.90-1.01]	yes (86.1%)	0.1334	0.91 [0.81-1.02]	yes (0.0%)
rs1122608	19p13.2	LDLR/SMARCA4	T	**3.32E-11**	0.88 [0.85-0.92]	-	0.00235	0.94 [0.90-0.98]	yes (82.6%)	0.01682	0.91 [0.83-0.98]	yes (0.0%)
rs12413409	10q24.32	CYP17A1/CNNM2/NT5C2	A	**1.24E-06**	0.89 [0.84-0.93]	-	0.0603	0.95 [0.89-1.00]	yes (66.4%)	**0.00049**	0.80 [0.70-0.90]	yes (57.6%)
rs12190287	6q23.2	TCF21	G	**2.32E-09**	0.90 [0.87-0.93]	-	0.8241	1.00 [0.97-1.04]	no (94.7%)	0.8139	0.99 [0.91-1.07]	yes (77.7%)
rs264	8p21.3	LPL	A	**2.92E-07**	0.90 [0.87-0.94]	-	0.3092	0.98 [0.93-1.02]	yes (84.7%)	0.282	0.95 [0.86-1.05]	yes (0.0%)
rs602633	1p13.3	SORT1	T	**1.42E-08**	0.90 [0.87-0.93]	-	0.9639	1.00 [0.96-1.03]	yes (93.3%)	0.01718	0.90 [0.83-0.98]	yes (0.0%)
rs9369640	6p24.1	PHACTR1	C	**2.69E-11**	0.91 [0.88-0.93]	-	0.3374	1.02 [0.98-1.05]	no (96.2%)	0.1762	1.05 [0.98-1.12]	no (93.1%)
rs11556924	7q32.2	ZC3HC1	T	**2.55E-10**	0.91 [0.89-0.94]	-	0.2172	0.98 [0.94-1.01]	yes (87.3%)	0.1671	0.95 [0.87-1.02]	yes (0.0%)
rs501120	10q11.21	CXCL12	C	**1.54E-06**	0.92 [0.88-0.95]		0.6325	1.01 [0.96-1.06]	no (89.8%)	0.8433	0.99 [0.90-1.09]	yes (50.2%)
rs11206510	1p32.3	PCSK9	C	**2.03E-04**	0.92 [0.88-0.97]	-	0.48	1.02 [0.97-1.06]	no (88.5%)	0.365	1.04 [0.95-1.14]	no (82.4%)
rs7692387	4q32.1	GUCY1A3	A	**1.07E-05**	0.92 [0.89-0.96]	-	0.0459	0.96 [0.92-1.00]	yes (43.8%)	0.4768	1.03 [0.95-1.13]	no (81.0%)
rs9515203	13q34	COL4A1/COL4A2	C	**3.30E-05**	0.92 [0.89-0.96]	-	0.8864	1.00 [0.96-1.05]	no (85.1%)	0.0835	1.08 [0.99-1.18]	no (90.4%)
rs12936587	17p11.2	RAI1-PEMT-RASD1	A	**1.98E-07**	0.93 [0.90-0.96]	-	0.0051	0.95 [0.92-0.98]	yes (21.5%)	**2.7E-05**	0.86 [0.80-0.92]	yes (75.6%)
rs4252120	6q25.3	PLG	C	**2.73E-05**	0.93 [0.91-0.96]	-	0.5753	0.99 [0.96-1.03]	yes (83.4%)	0.8729	0.99 [0.92-1.07]	yes (55.2%)
rs7173743	15q25.1	ADAMTS7	C	**6.70E-08**	0.93 [0.90-0.95]	-	0.3965	0.99 [0.96-1.02]	yes (88.0%)	0.5462	1.02 [0.95-1.09]	no (85.1%)
rs12205331	6p21.31	ANKS1A	T	**6.39E-06**	0.93 [0.90-0.96]	-	0.052	0.96 [0.92-1.00]	yes (42.1%)	0.182	0.94 [0.87-1.03]	yes (0.0%)
rs515135	2p24.1	APOB	T	**9.12E-04**	0.94 [0.90-0.97]	-	0.8171	1.01 [0.96-1.05]	no (81.9%)	0.4072	1.04 [0.95-1.14]	no (76.0%)
rs10947789	6p21.2	KCNK5	C	**1.07E-03**	0.94 [0.91-0.97]	-	0.6972	0.99 [0.96-1.03]	yes (81.4%)	0.7174	0.99 [0.91-1.07]	yes (26.3%)
rs2954029	8q24.13	TRIB1	T	**1.28E-05**	0.94 [0.92-0.97]	-	0.1544	0.98 [0.95-1.01]	yes (62.0%)	0.1935	0.96 [0.89-1.02]	yes (0.0%)
rs15563	17q21.32	UBE2Z	A	**1.81E-05**	0.94 [0.91-0.96]	-	0.9662	1.00 [0.97-1.03]	yes (88.3%)	0.1373	0.98 [0.89-1.02]	yes (0.0%)
rs974819	11q22.3	PDGFD	T	**7.00E-04**	1.05 [1.02-1.08]	-	0.1196	0.97 [0.94-1.00]	no (90.8%)	0.1557	1.05 [0.98-1.13]	yes (0.0%)
rs11203042	10q23.31	LIPA	T	**6.51E-05**	1.06 [1.03-1.09]	-	0.6087	1.01 [0.98-1.04]	yes (79.2%)	0.3286	1.03 [0.97-1.11]	yes (0.0%)
rs2047009	10q11.21	CXCL12	T	**4.79E-06**	1.06 [1.03-1.09]	-	0.0705	1.03 [1.00-1.06]	yes (57.1%)	0.537	1.02 [0.96-1.09]	yes (15.5%)
rs4845625	1q21.3	IL6R	T	**1.93E-05**	1.06 [1.03-1.09]	-	0.2875	1.02 [0.99-1.05]	yes (72.0%)	0.9699	1.00 [0.94-1.07]	yes (56.4%)
rs2252641	2q22.3	ZEB2-AC074093.1	C	**1.19E-05**	1.06 [1.03-1.09]	-	0.4874	1.01 [0.98-1.04]	yes (80.6%)	0.1326	0.95 [0.89-1.02]	no (88.9%)
rs1561198	2p11.2	VAMP5-VAMP8- GGCX	T	**6.05E-04**	1.06 [1.03-1.09]	-	0.6505	0.99 [0.96-1.02]	no (88.3%)	0.8011	1.01 [0.94-1.08]	yes (33.3%)
rs9319428	13q12.2	FLT1	A	**4.47E-05**	1.06 [1.03-1.11]	-	0.3271	0.98 [0.95-1.01]	no (91.2%)	0.1348	1.06 [0.98-1.14]	yes (0.0%)
rs6544713	2p21	ABCG5-ABCG8	T	**5.20E-03**	1.06 [1.03-1.10]	-	0.5859	1.01 [0.97-1.05]	yes (77.1%)	0.4944	1.03 [0.95-1.11]	yes (0.0%)
rs2246833	10q23.31	LIPA	T	**5.28E-05**	1.07 [1.04-1.10]	-	0.0202	1.04 [1.01-1.08]	yes (20.5%)	0.1923	1.05 [0.98-1.13]	yes (0.0%)
rs2505083	10p11.23	KIAA1462	C	**2.40E-05**	1.07 [1.04-1.10]	-	0.073	1.03 [1.00-1.06]	yes (66.4%)	0.0975	1.06 [0.99-1.13]	yes (0.0%)
rs2048327	6q25.3	SLC22A3/LPAL2/LPA	C	**1.34E-06**	1.07 [1.05-1.10]	-	0.3984	0.99 [0.95-1.02]	no (93.5%)	0.1534	1.05 [0.98-1.13]	yes (0.0%)
rs3184504	12q24.12	chr12q24/SH2B3	T	**9.33E-07**	1.07 [1.04-1.11]	-	**1.01E-06**	1.08 [1.05-1.12]	yes (0.0%)	**0.00015**	1.14 [1.06-1.22]	yes (59.2%)
rs273909	5q31.1	SLC22A4-SLC22A5	G	**8.23E-03**	1.07 [1.02-1.11]	-	0.6286	0.99 [0.94-1.04]	no (80.5%)	0.0196	1.13 [1.02-1.26]	yes (8.2%)

rs2281727	17p13.3	SMG6	G	**1.30E-07**	1.07 [1.04-1.10]	-	0.1164	1.03 [0.99-1.06]	yes (76.0%)	0.656	0.98 [0.92-1.06]	no (80.3%)
rs17514846	15q26.1	FURIN-FES	A	**7.49E-05**	1.07 [1.04-1.11]	-	0.1882	1.02 [0.99-1.05]	yes (76.3%)	0.1026	1.06 [0.99-1.13]	yes (0.0%)
rs4773144	13q34	COL4A1/COL4A2	G	**2.34E-06**	1.08 [1.05-1.12]	-	0.7407	1.01 [0.96-1.05]	yes (85.1%)	0.5777	0.97 [0.87-1.08]	no (73.2%)
rs2023938	7p21.1	HDAC9	C	**2.10E-03**	1.08 [1.03-1.13]	-	**1.65E-06**	1.14 [1.08-1.20]	yes (44.7%)	**2.33E-09**	1.38 [1.24-1.53]	yes (94.1%)
rs2895811	14q32.2	HHIPL1	C	**1.18E-05**	1.09 [1.06-1.13]	-	0.288	1.02 [0.99-1.05]	yes (88.4%)	0.149	1.05 [0.98-1.13]	yes (0.0%)
rs579459	9q34.2	ABO	C	**2.14E-07**	1.10 [1.06-1.14]	-	**0.00026**	1.08 [1.04-1.12]	yes (0.0%)	0.0054	1.13 [1.04-1.22]	yes (0.0%)
rs1878406	4q31.23	EDNRA	T	**1.02E-06**	1.10 [1.06-1.14]	-	0.1392	1.04 [0.99-1.08]	yes (72.8%)	0.00151	1.17 [1.06-1.29]	yes (23.9%)
rs9818870	3q22.3	MRAS	T	**1.24E-07**	1.11 [1.07-1.15]	-	0.7623	1.01 [0.97-1.05]	yes (90.7%)	0.4514	0.97 [0.88-1.06]	no (86.1%)
rs6725887	2q33.1	WDR12	C	**2.37E-08**	1.14 [1.10-1.19]	-	0.1435	0.96 [0.92-1.01]	no (96.2%)	0.9847	1.00 [0.90-1.11]	yes (81.4%)
rs9326246	11q23.3	ZNF259/APO5A/APOA1	C	**3.40E-07**	1.15 [1.09-1.21]	-	0.2928	1.04 [0.97-1.11]	yes (81.1%)	0.3523	0.93 [0.81-1.08]	no (85.3%)
rs3217992	9p21.3	CDKN2BAS	T	**2.21E-29**	1.17 [1.14-1.21]	-	0.0314	1.04 [1.00-1.07]	yes (96.6%)	0.0036	1.11 [1.03-1.19]	yes (56.0%)
rs9982601	21q22.11	gene_desert/KCNE2	T	**2.52E-10**	1.18 [1.12-1.24]	-	0.552	0.99 [0.94-1.03]	no (96.0%)	0.1801	0.93 [0.84-1.03]	no (93.5%)
rs1333049	9p21.3	CDKN2BAS	C	**2.96E-56**	1.24 [1.21-1.28]	-	0.0053	1.05 [1.01-1.09]	yes (98.2%)	**3.7E-06**	1.19 [1.11-1.28]	yes (3.2%)
Top variants ($p<10^{-5}$) for all ischaemic stroke in the METASTROKE sample												
rs225132	1p36.23	ERRFI1	G	0.3922	0.99 [0.96-1.03]	yes (93.2%)	**6.40E-08**	0.89 [0.86-0.93]	-	0.02563	0.90 [0.83-0.99]	yes (0.0%)
rs16851055	3q23	SPSB4	A	0.2321	0.98 [0.93-1.03]	yes (85.9%)	**7.01E-07**	0.90 [0.86-0.94]	-	0.00080	0.86 [0.78-0.94]	yes (0.0%)
rs161802	1p36.23	PARK7	T	0.2638	0.99 [0.95-1.02]	yes (91.9%)	**2.13E-07**	0.90 [0.86-0.93]	-	0.03699	0.91 [0.83-0.99]	yes (0.0%)
rs4792143	17p12	FLJ45455	T	0.3146	0.99 [0.95-1.02]	yes (88.6%)	**5.07E-06**	0.91 [0.87-0.95]	-	0.0092	0.89 [0.91-0.97]	yes (0.0%)
rs17696736	12q24.13	chr12q24/SH2B3	G	**6.56E-08**	1.07 [1.04-1.10]	yes (37.3%)	**5.96E-08**	1.10 [1.06-1.14]	-	0.0024	1.11 [1.04-1.20]	yes (0.0%)
rs12646447	4q25	PITX2	C	0.3897	1.02 [0.98-1.06]	yes (92.4%)	**3.19E-08**	1.14 [1.09-1.20]	-	0.0053	1.15 [1.04-1.28]	yes (0.0%)
Top variants ($p<10^{-5}$) for large artery stroke in the METASTROKE sample												
rs1005224	14q24.3	TTLL5	T	0.6857	0.99 [0.96-1.02]	yes (94.5%)	0.0616	0.97 [0.93-1.00]	yes (92.3%)	**1.47E-06**	0.83 [0.77-0.90]	-
rs1465330	14q24.3	ZDHHC22	A	0.9722	1.00 [0.97-1.03]	yes (94.3%)	0.0355	0.96 [0.93-1.00]	yes (90.9%)	**3.78E-06**	0.84 [0.78-0.91]	-
rs4304924	13q31.1	RNF219	G	0.4124	0.98 [0.94-1.02]	yes (91.8%)	3.9E-05	0.93 [0.91-0.97]	yes (83.1%)	**4.50E-06**	0.85 [0.79-0.91]	-
rs7791394	7q21.11	MAGI2	T	0.9297	0.99 [0.97-1.02]	no (94.5%)	0.00083	1.06 [1.02-1.09]	yes (85.2%)	**9.91E-06**	1.17 [1.09-1.26]	-
rs632728	6p21.1	SUPT3H	T	0.2024	0.99 [0.97-1.02]	no (95.4%)	0.1211	1.03 [0.99-1.07]	yes (92.1%)	**2.14E-06**	1.19 [1.11-1.28]	-
rs1333047	9p21.3	chr9p21	T	**1.44E-53**	1.24 [1.20-1.27]	yes (0.0%)	0.0063	1.05 [1.01-1.08]	yes (90.4%)	**1.64E-06**	1.20 [1.11-1.29]	-
rs2107595	7p21.1	HDAC9	A	0.0419	1.05 [1.01-1.09]	yes (96.8%)	4.4E-06	1.11 [1.06-1.16]	yes (94.5%)	**2.39E-12**	1.39 [1.27-1.52]	-
rs6792835	3q28	LPP	G	0.5078	1.01 [0.95-1.08]	yes (93.8%)	0.3355	1.04 [0.96-1.12]	yes (92.2%)	**1.16E-05**	1.46 [1.23-1.73]	-
rs7937106	11q22.3	ALKBH8	C	0.0884	1.09 [0.98-1.21]	yes (93.7%)	0.00136	1.18 [1.07-1.30]	yes (90.8%)	**5.74E-08**	1.69 [1.40-2.04]	-
rs10179686	2q21.2	TMEM163	T	0.7276	1.03 [0.93-1.13]	yes (93.4%)	0.4189	1.06 [0.93-1.20]	yes (91.8%)	**8.20E-06**	1.69 [1.34-2.13]	-
rs17167021	5q21.1	Chr5 gene desert	G	0.4010	1.08 [0.94-1.23]	yes (92.8%)	0.1733	1.11 [0.96-1.29]	yes (91.3%)	**1.37E-06**	1.81 [1.42-2.30]	-

[1]compared to IS or LAS respectively; [2]compared to CAD/MI; The ApoE-ApoC1 locus previously reported in [4]was not considered due to incomplete information in CARDIoGRAM; associations reaching study-wide significance ($p<0.00108$) are shown in bold. CAD=coronary artery disease; MI=myocardial infarction.

Supplementary Table III: *Influence of overlapping controls on meta-analysis results for the combined CAD/stroke phenotypes: results are shown for the same risk loci as in Table 2 and for two different scenarios.*

rs_number	Band	Gene in region	Coronary Artery Disease & Stroke combined (p-value)	
			30,000 overlapping controls	**40,000 overlapping controls**
Ischemic Stroke				
rs1333049	9p21.3	9p21	1.00E-42	1.37E-41
rs11065987	12q24.12	chr12q24/SH2B3	7.80E-14	1.72E-13
rs10455872	6q25.3	SLC22A3/LPAL2/LPA	7.68E-10	1.31E-09
rs1122608	19p13.2	LDLR/SMARCA4	8.70E-12	1.69E-11
rs4714955	6p24.1	PHACTR1	1.56E-08	2.47E-08
rs11556924	7q32.2	ZC3HC1	2.82E-08	4.38E-08
rs964184	11q23.3	ZNF259	4.70E-08	8.18E-08
rs579459	9q34.2	ABO	1.35E-09	2.29E-09
rs2219939	15q25.1	ADAMTS7	1.03E-08	1.65E-08
rs7582720	2q33.1	WDR12	1.80E-08	2.84E-08
rs599839	1p13.3	SORT1	2.82E-07	3.83E-07
rs12190287	6q23.2	TCF21	2.53E-08	3.49E-08
rs12449964	17p11.2	RAI1-PEMT-RASD1	2.05E-08	3.22E-08
rs17114036	1p32.2	PPAP2B	2.06E-08	3.04E-08
rs9351814	6q13	C6orf155	5.80E-08	8.84E-08
Large Artery Stroke				
rs1333049	9p21.3	9p21	4.37E-59	1.65E-58
rs10455872	6q25.3	SLC22A3/LPAL2/LPA	2.62E-14	3.52E-14
rs2107595	7p21.1	HDAC9	7.43E-05	8.07E-05
rs1122608	19p13.2	LDLR/SMARCA4	6.86E-12	8.74E-12
rs4714955	6p24.1	PHACTR1	4.09E-12	5.24E-12
rs12936587	17p11.2	RAI1-PEMT-RASD1	4.53E-10	5.54E-10
rs11065987	12q24.12	chr12q24/SH2B3	2.08E-10	2.56E-10
rs11556924	7q32.2	ZC3HC1	2.16E-10	2.66E-10
rs599839	1p13.3	SORT1	1.59E-10	1.97E-10
rs964184	11q23.3	ZNF259	9.48E-10	1.15E-09
rs12190287	6q23.2	TCF21	1.28E-08	1.51E-08
rs12413409	10q24.32	CYP17A1-CNNM2-NT5C2	1.50E-08	1.77E-08
rs6841581	4q32.21	EDNRA	5.52E-09	6.58E-09
rs17114036	1p32.2	PPAP2B	2.43E-08	2.85E-08
rs899997	15q25.1	ADAMTS7	1.31E-08	1.55E-08
rs7582720	2q33.1	WDR12	8.59E-09	1.02E-08
rs579459	9q34.2	ABO	1.94E-08	2.29E-08

Supplemental Figures

Supplementary Figure I

(A)

		CAD/MI p-value	
		<0.01	>0.01
IS p-value	<0.01	205 (0.074%)	7,113 (2.57%)
	>0.01	4,113 (1.48%)	265,610 (95.87%)

p=3.59E-15

	CAD/MI p-value	
	<0.0001	>0.0001
<0.0001	5 (0.0018%)	137 (0.049%)
>0.0001	168 (0.061%)	276,731 (99.89%)

p=3.75E-08

(B)

		<0.01	>0.01
LAS p-value	<0.01	154 (0.056%)	7,268 (2.63%)
	>0.01	4,049 (1.46%)	265,114 (95.85%)

p=1.69E-04

	<0.0001	>0.0001
<0.0001	2 (0.0007%)	136 (0.049%)
>0.0001	169 (0.061%)	276,278 (99.89%)

p=3.40E-03

(C)

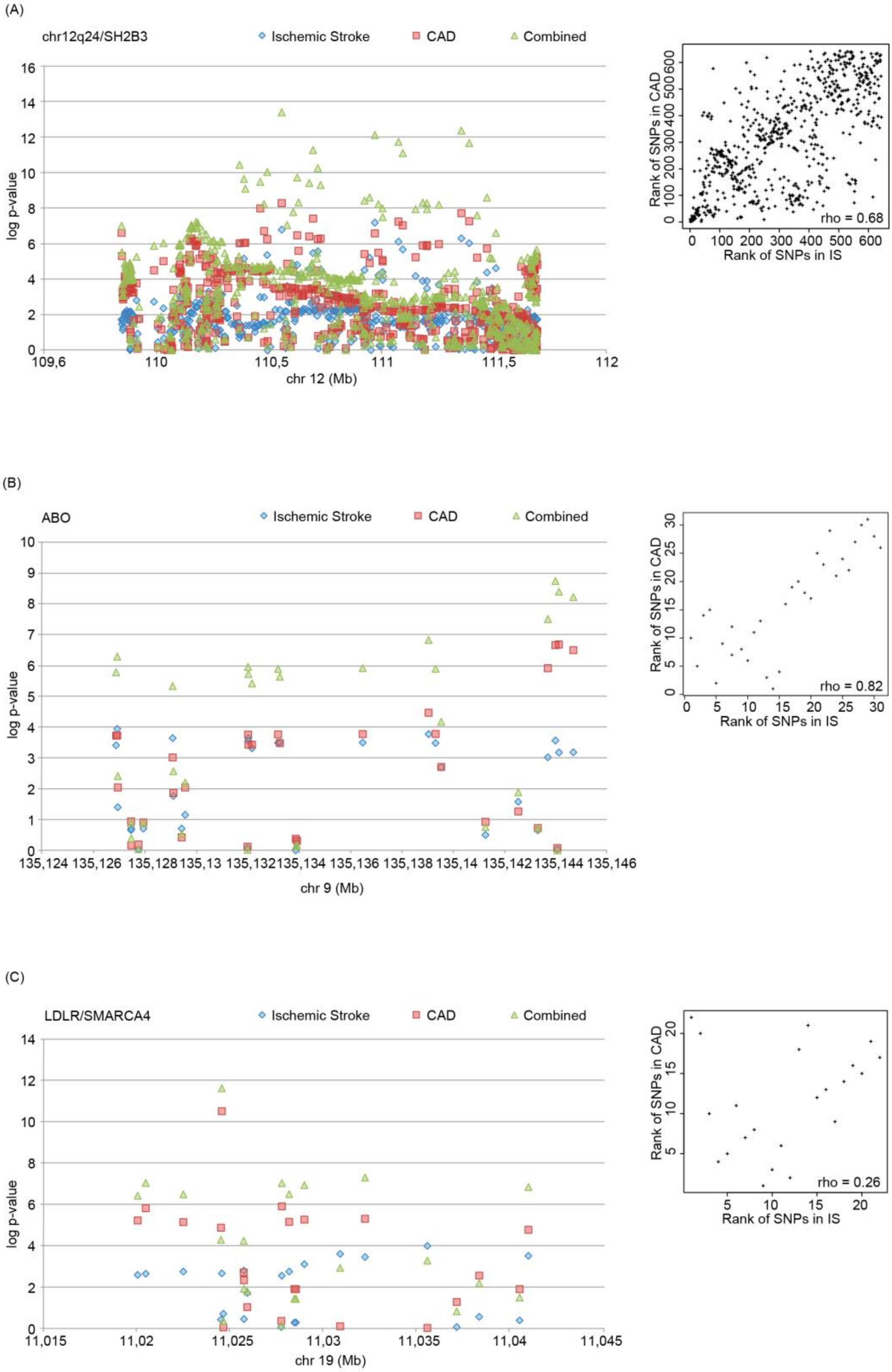
		<0.01	>0.01
CES p-value	<0.01	167 (0.060%)	7,578 (2.74%)
	>0.01	4,342 (1.57%)	264,750 (95.63%)

p=3.73E-04

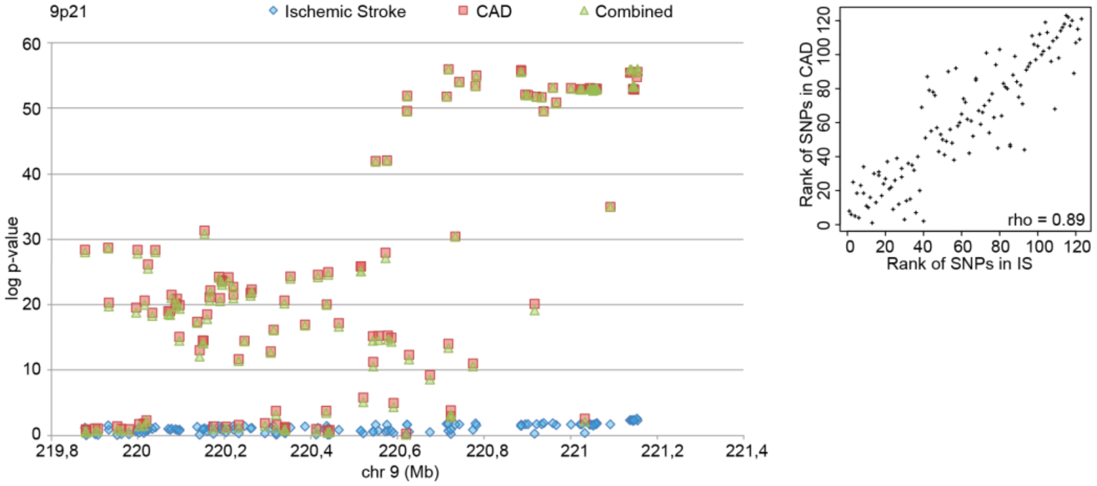
	<0.0001	>0.0001
<0.0001	0 (0%)	138 (0.050%)
>0.0001	161 (0.058%)	276,538 (99.89%)

p=1

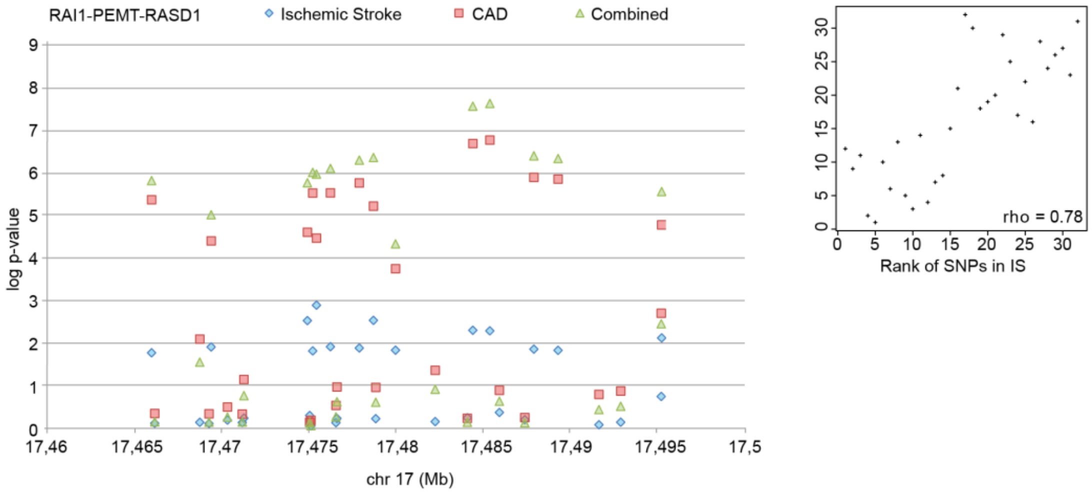
Supplementary Figure II



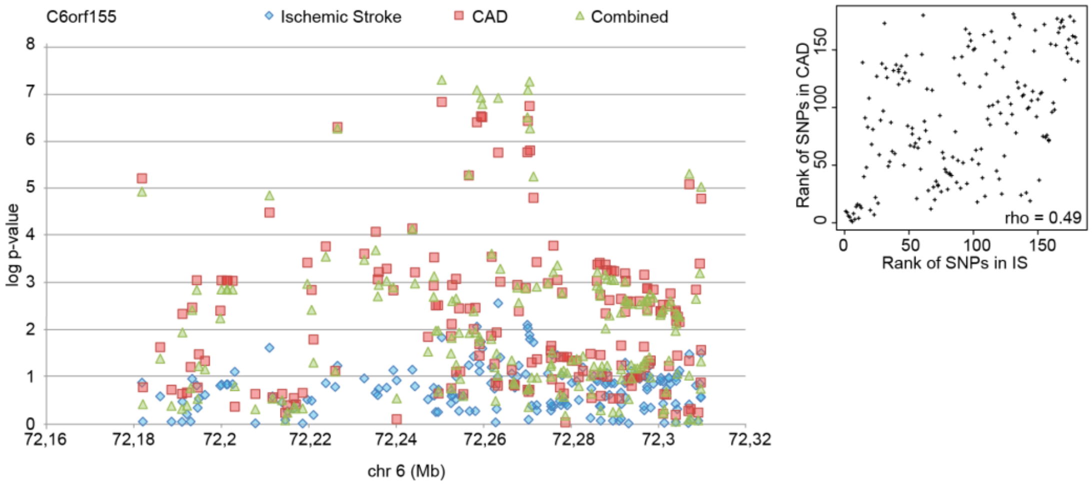
(D)


9p21
Ischemic Stroke
CAD
Combined
log p-value
0
10
20
30
40
50
60
219,8
220
220,2
220,4
220,6
220,8
221
221,2
221,4
chr 9 (Mb)
Rank of SNPs in CAD
Rank of SNPs in IS
0
20
40
60
80
100
120
rho = 0.89

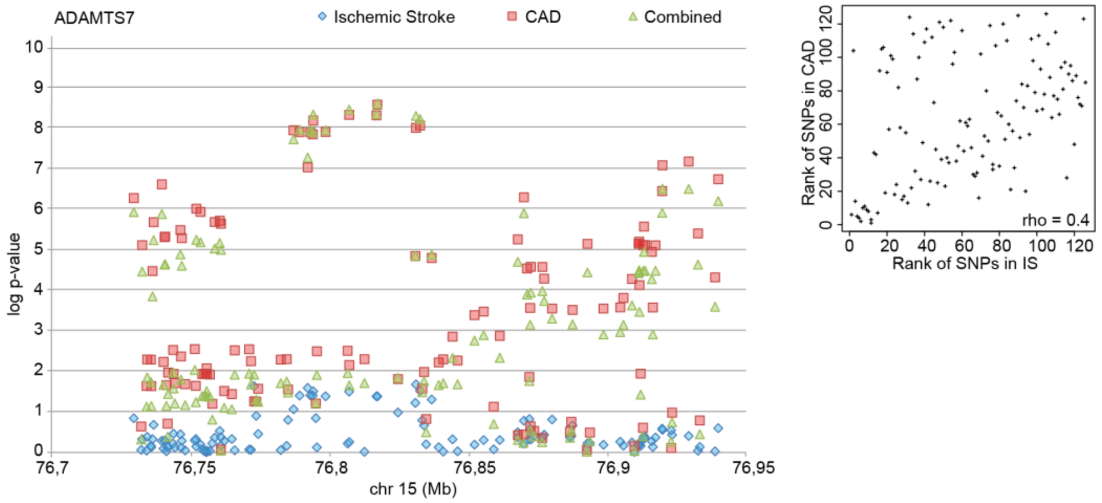
(E)


RAI1-PEMT-RASD1
Ischemic Stroke
CAD
Combined
log p-value
0
1
2
3
4
5
6
7
8
9
17,46
17,465
17,47
17,475
17,48
17,485
17,49
17,495
17,5
chr 17 (Mb)
Rank of SNPs in IS
0
5
10
15
20
25
30
rho = 0.78

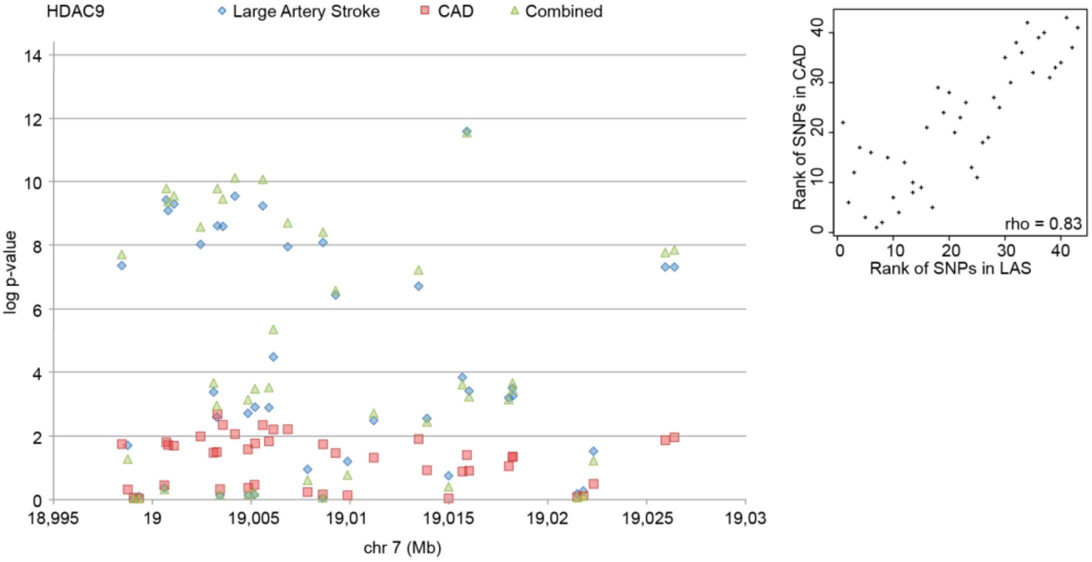
(F)


C6orf155
Ischemic Stroke
CAD
Combined
log p-value
0
1
2
3
4
5
6
7
8
72,16
72,18
72,2
72,22
72,24
72,26
72,28
72,3
72,32
chr 6 (Mb)
Rank of SNPs in CAD
Rank of SNPs in IS
0
50
100
150
rho = 0.49

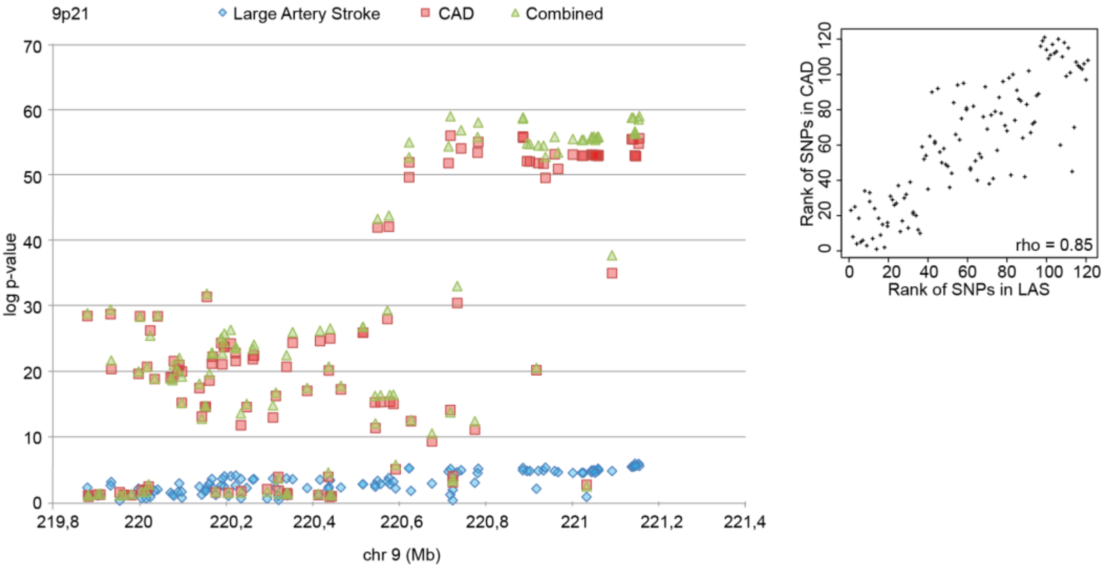
(G)


ADAMTS7
◆ Ischemic Stroke
■ CAD
▲ Combined
log p-value
0
1
2
3
4
5
6
7
8
9
10
76,7
76,75
76,8
76,85
76,9
76,95
chr 15 (Mb)
Rank of SNPs in CAD
0
20
40
60
80
100
120
Rank of SNPs in IS
rho = 0.4

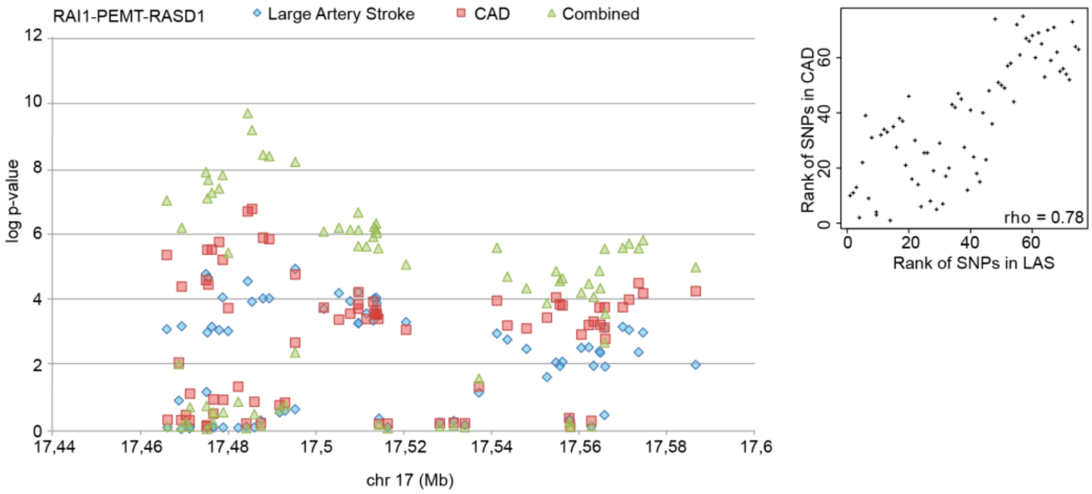
(H)


HDAC9
◆ Large Artery Stroke
■ CAD
▲ Combined
log p-value
0
2
4
6
8
10
12
14
18,995
19
19,005
19,01
19,015
19,02
19,025
19,03
chr 7 (Mb)
Rank of SNPs in CAD
0
10
20
30
40
Rank of SNPs in LAS
rho = 0.83

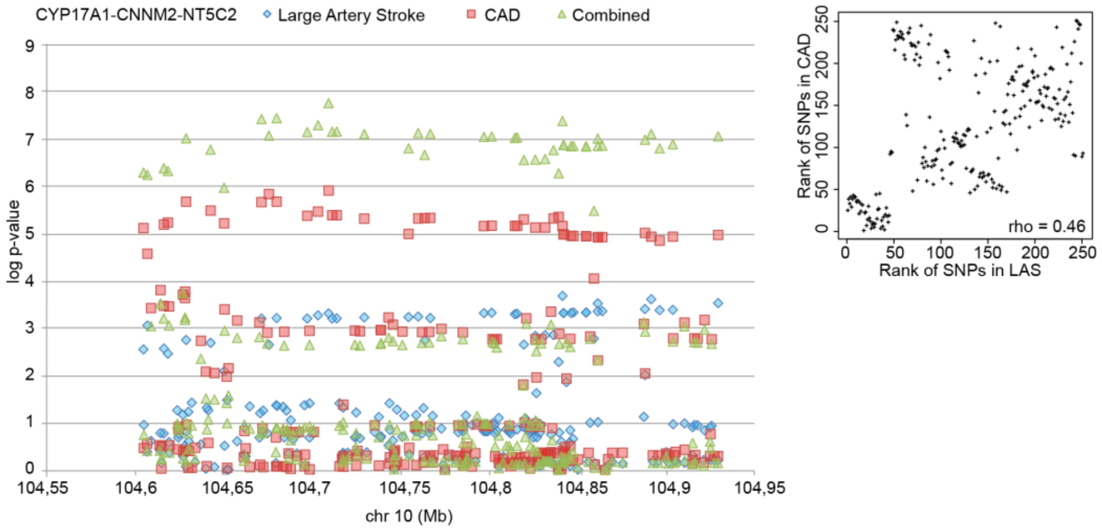
(I)


9p21
◆ Large Artery Stroke
■ CAD
▲ Combined
log p-value
0
10
20
30
40
50
60
70
219,8
220
220,2
220,4
220,6
220,8
221
221,2
221,4
chr 9 (Mb)
Rank of SNPs in CAD
0
20
40
60
80
100
120
Rank of SNPs in LAS
rho = 0.85

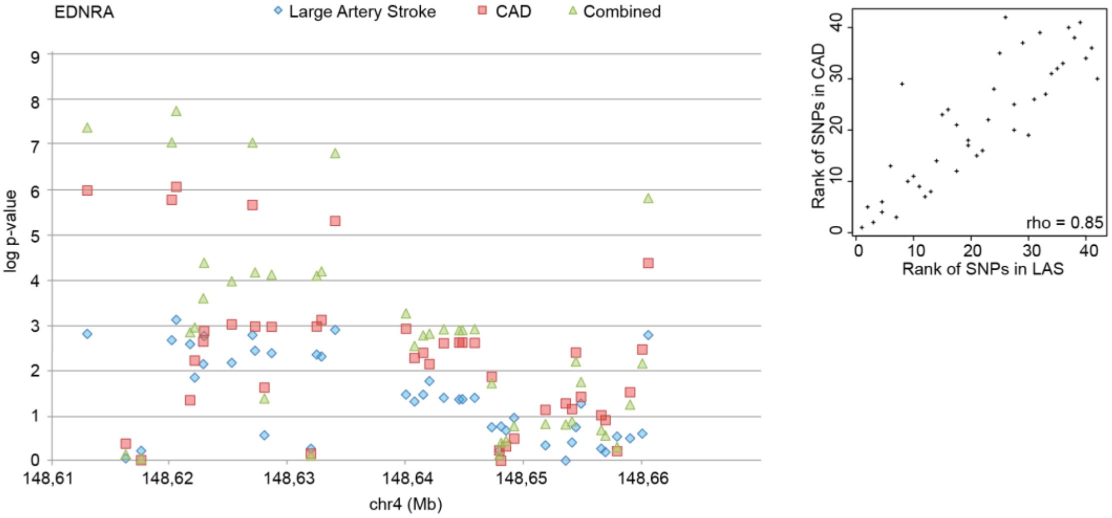
(J)


RAI1-PEMT-RASD1
Large Artery Stroke
CAD
Combined
log p-value
0
2
4
6
8
10
12
17,44
17,46
17,48
17,5
17,52
17,54
17,56
17,58
17,6
chr 17 (Mb)
Rank of SNPs in CAD
0
20
40
60
Rank of SNPs in LAS
rho = 0.78

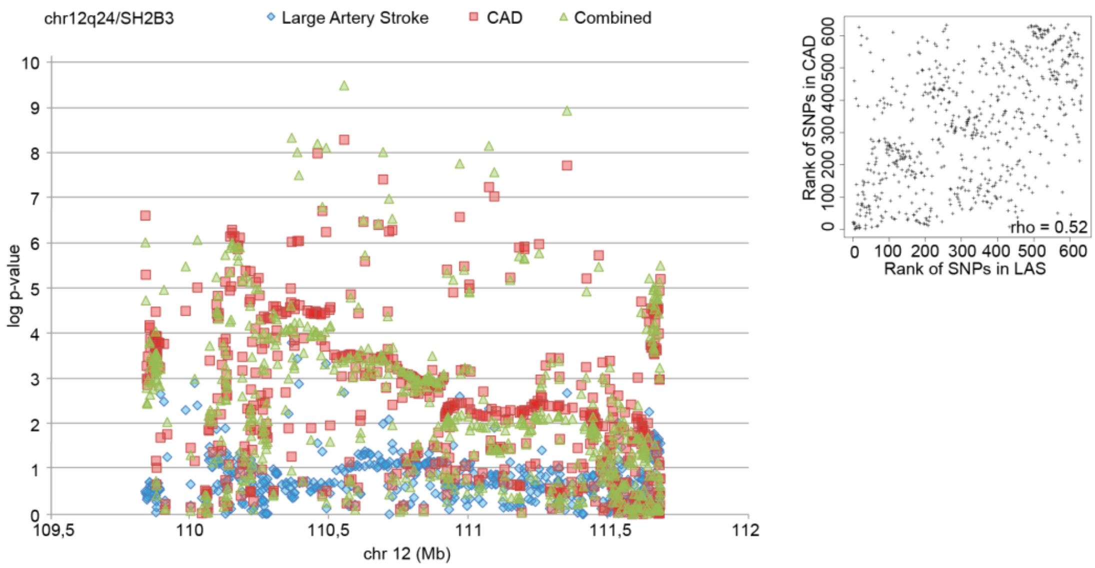
(K)


CYP17A1-CNNM2-NT5C2
Large Artery Stroke
CAD
Combined
log p-value
0
1
2
3
4
5
6
7
8
9
104,55
104,6
104,65
104,7
104,75
104,8
104,85
104,9
104,95
chr 10 (Mb)
Rank of SNPs in CAD
0
50
100
150
200
250
Rank of SNPs in LAS
rho = 0.46

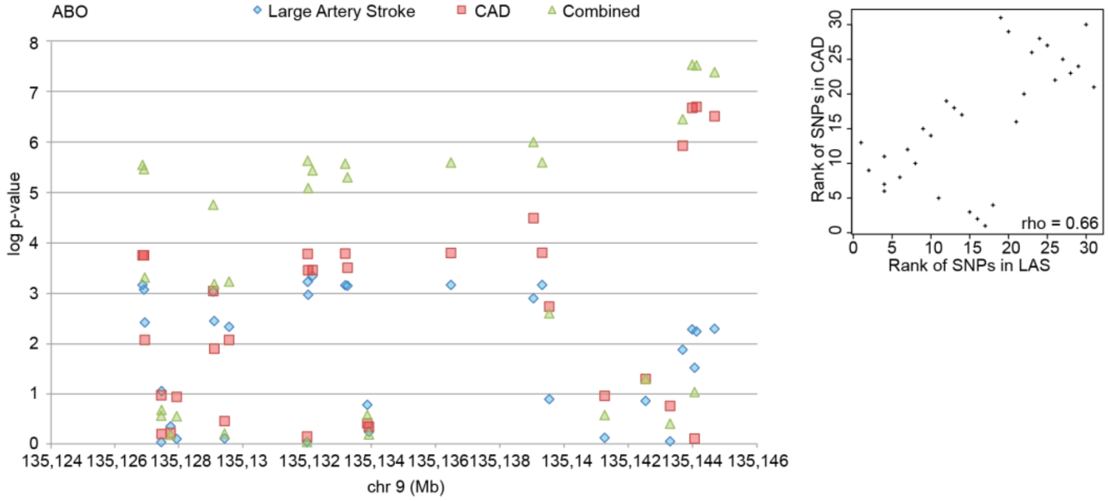
(L)


EDNRA
Large Artery Stroke
CAD
Combined
log p-value
0
1
2
3
4
5
6
7
8
9
148,61
148,62
148,63
148,64
148,65
148,66
chr4 (Mb)
Rank of SNPs in CAD
0
10
20
30
40
Rank of SNPs in LAS
rho = 0.85

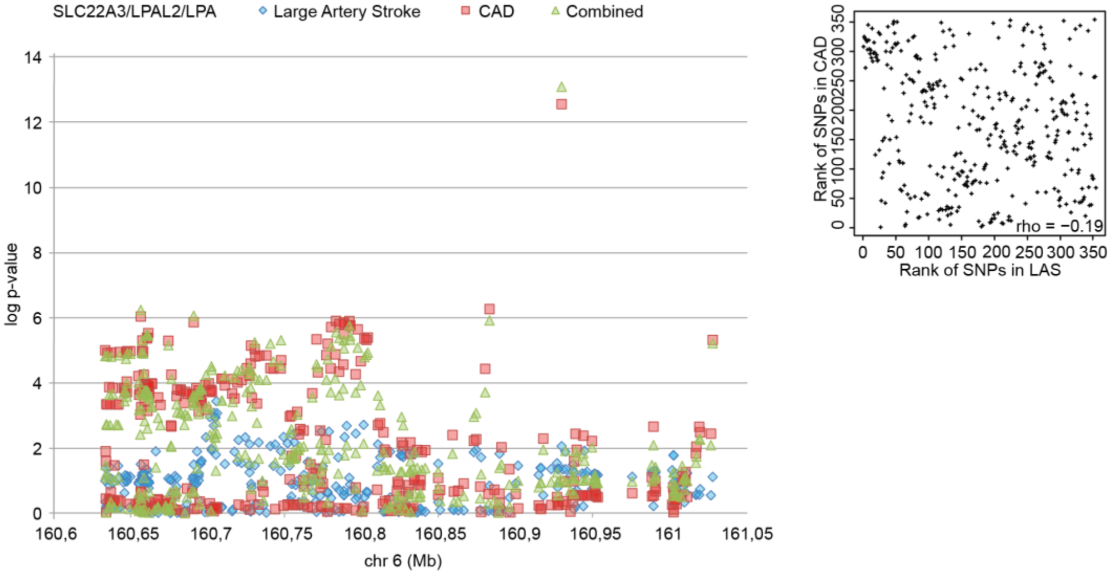
(M)


chr12q24/SH2B3
Large Artery Stroke
CAD
Combined
log p-value
0
1
2
3
4
5
6
7
8
9
10
109,5
110
110,5
111
111,5
112
chr 12 (Mb)
Rank of SNPs in CAD
0
100
200
300
400
500
600
Rank of SNPs in LAS
rho = 0.52

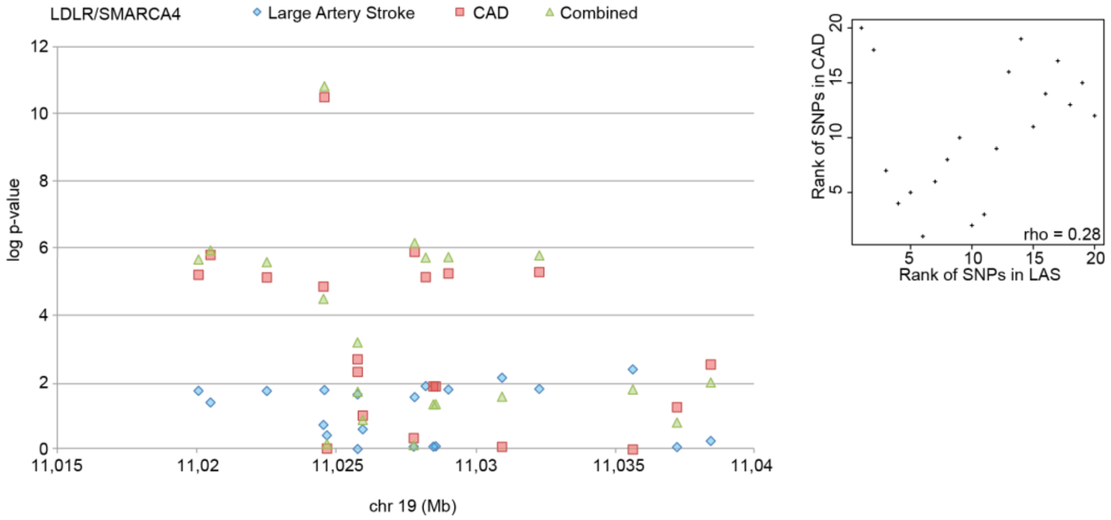
(N)


ABO
Large Artery Stroke
CAD
Combined
log p-value
0
1
2
3
4
5
6
7
8
135,124
135,126
135,128
135,13
135,132
135,134
135,136
135,138
135,14
135,142
135,144
135,146
chr 9 (Mb)
Rank of SNPs in CAD
0
5
10
15
20
25
30
Rank of SNPs in LAS
rho = 0.66

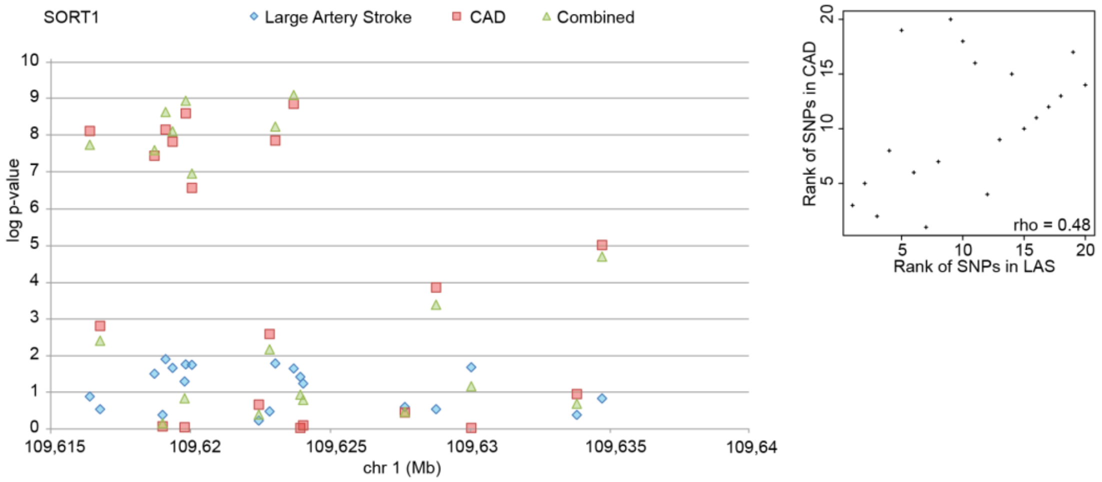
(O)


SLC22A3/LPAL2/LPA
Large Artery Stroke
CAD
Combined
log p-value
0
2
4
6
8
10
12
14
160,6
160,65
160,7
160,75
160,8
160,85
160,9
160,95
161
161,05
chr 6 (Mb)
Rank of SNPs in CAD
0
50
100
150
200
250
300
350
Rank of SNPs in LAS
rho = −0.19

(P)


LDLR/SMARCA4
Large Artery Stroke
CAD
Combined
log p-value
0
2
4
6
8
10
12
11,015
11,02
11,025
11,03
11,035
11,04
chr 19 (Mb)
Rank of SNPs in CAD
5
10
15
20
Rank of SNPs in LAS
rho = 0.28

(Q)


SORT1
Large Artery Stroke
CAD
Combined
log p-value
0
1
2
3
4
5
6
7
8
9
10
109,615
109,62
109,625
109,63
109,635
109,64
chr 1 (Mb)
Rank of SNPs in CAD
5
10
15
20
Rank of SNPs in LAS
rho = 0.48

Supplemental Figure Legends

Supplementary Figure I: Contingency tables for IS and CAD (**A**), LAS and CAD (**B**), and CES and CAD (**C**) for the number of variants showing a p-value above/below 0.01 (**left**) and above/below 0.0001 (**right**). For each table, LD-pruned data with $r^2<0.3$ was used and the SNP with the lowest p-value in the original sample was retained. Similar results were obtained when using an $r^2<0.1$ (data not shown).

Supplementary Figure II: Regional association plots **(left)** and corresponding Spearman correlation plots of p-values **(right)** for individual variants between IS and CAD **(A-G)** and LAS and CAD **(H-Q)** at the 10 loci that showed independent contributions from CAD and stroke in the phenotype-differentiated meta-analysis: **(A)** chr12q24/SH2B3; **(B)** ABO; **(C)** LDLR/SMARCA4; **(D)** 9p21; **(E)** RAI1-PEMT-RASD1; **(F)** C6orf155; **(G)** ADAMTS7; **(H)** HDAC9; **(I)** 9p21; **(J)** RAI1-PEMT-RASD1; **(K)** CYP17A1-CNNM2-NT5C2; **(L)** EDNRA; **(M)** chr12q24/SH2B3; **(N)** ABO; **(O)** SLC22A3/LPAL2/LPA; **(P)** LDLR/SMARCA4; **(Q)** SORT1. Data were drawn from METASTROKE and CARDIoGRAM.

Supplemental References

1. Traylor M, Farrall M, Holliday EG, Sudlow C, Hopewell JC, Cheng YC, et al. Genetic risk factors for ischaemic stroke and its subtypes (the metastroke collaboration): A meta-analysis of genome-wide association studies. *Lancet neurology*. 2012;11:951-962
2. Schunkert H, Konig IR, Kathiresan S, Reilly MP, Assimes TL, Holm H, et al. Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature genetics*. 2011;43:333-338
3. Coronary Artery Disease (C4D) Genetics Consortium. A genome-wide association study in europeans and south asians identifies five new loci for coronary artery disease. *Nature genetics*. 2011;43:339-344
4. CARDIoGRAMplusC4D Consortium, Deloukas P, Kanoni S, Willenborg C, Farrall M, Assimes TL, et al. Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature genetics*. 2013;45:25-33