

Supplementary Table 1. Detailed information including SNP genotype distribution and Hardy-Weinberg equilibrium (HWE) *p*-value

Gene	Chr	Fuction	SNP	Position	M/m	250 patients with IA		296 controls		
						MAF	MM/Mm/mm	MAF	MM/Mm/mm	HWE <i>p</i> -value
<i>BOLL</i>	2q33.1	Intron	rs700651	198631714	A/G	0.476	63/112/75	0.449	91/143/61	0.1826
<i>EDNRA</i>	4q31.22	Upstream	rs6841581	148401190	A/G	0.13	188/59/3	0.217	176/110/9	0.725
<i>LINC01344</i>	1q25.3	Intron	rs12033118	182229747	C/T	0.022	239/11/0	0.027	279/16/0	1
<i>RGPD4</i>	2q12.3	Downstream	rs328025	108355045	G/A	0.377	93/123/32	0.324	143/114/39	0.04597
<i>RGPD4</i>	2q12.3	Downstream	rs700855	108368694	T/C	0.372	94/125/30	0.328	139/120/37	0.1867
<i>MALL</i>	2q13	Intron	rs117802391	110862084	C/T	0.036	232/18/0	0.061	260/36/0	0.6112
<i>CXCR4</i>	2q22.1	Downstream	rs189432614	136809235	A/G	0.016	242/8/0	0.025	281/15/0	1
<i>RPRM</i>	2q23.3	Downstream	rs5005908	154003680	G/T	0.344	108/112/30	0.27	160/112/24	0.4642
<i>RBMS3</i>	3p24.1	Intron	rs1979271	29607405	T/A	0.406	86/125/39	0.39	107/147/42	0.5412
<i>FOXP1</i>	3p13	Intron	rs878118	71246228	T/G	0.238	144/93/13	0.255	166/109/21	0.6459
<i>LINC00879</i>	3q11.2	Upstream	rs4411883	94549686	T/G	0.09	206/43/1	0.111	231/61/2	0.5512
<i>RYK</i>	3q22.2	Downstream	rs74585958	133773362	G/A	0.054	222/27/0	0.041	272/24/0	1
<i>TNIK</i>	3q26.31	Intron	rs11925024	171014067	A/C	0.145	180/66/3	0.151	212/77/6	1
<i>TNIK</i>	3q26.31	Intron	rs1231	171031233	A/T	0.144	179/70/1	0.154	212/75/8	0.6551
<i>EIF2B5</i>	3q27.1	Intron	rs4350902	184352200	T/C	0.472	65/134/51	0.492	67/156/72	0.3527
<i>RUFY1</i>	5q35.3	Intron	rs4075890	178997373	T/C	0.216	154/84/12	0.2	190/92/13	0.7152
<i>Csorf60</i>	5q35.3	Intron	rs62405726	179069468	G/A	0.318	118/105/27	0.287	144/131/19	0.1554
<i>RREB1</i>	6p24.3	Intron	rs9505086	7232186	T/C	0.286	131/92/25	0.307	150/110/36	0.02932
<i>DST</i>	6p12.1	Intron	rs117021265	56628021	T/C	0.034	232/17/0	0.024	283/12/1	0.1456
<i>EIF4H</i>	7q11.23	Intron	rs150664966	73594157	T/C	0.016	242/8/0	0.022	283/13/0	1
<i>MPDZ</i>	9p23	Downstream	rs1332064	12942764	T/C	0.354	108/107/35	0.309	136/136/23	0.2186
<i>PTCH1</i>	9q22.32	Upstream	rs1105980	98113635	G/C	0.27	134/94/20	0.294	140/138/18	0.03663
<i>PFKP</i>	10p15.2	Upstream	rs58183624	3107217	C/T	0.066	220/27/3	0.044	272/22/2	0.09888
<i>CCDC3</i>	10p13	Downstream	rs12412014	12911725	G/C	0.281	123/108/15	0.291	152/116/28	0.3987
<i>CACUL1</i>	10q26.11	Upstream	rs11198727	120767097	A/G	0.382	101/106/42	0.429	92/153/50	0.3433
<i>PLEKHA1</i>	10q26.13	Downstream	rs10510110	124192430	C/T	0.399	81/136/31	0.372	123/126/47	0.1355
<i>TRIM22</i>	11p15.4	Intron	rs7480654	5722839	T/C	0.317	108/124/17	0.284	155/114/27	0.3907
<i>SAP18</i>	13q12.11	Upstream	rs9509543	21692404	C/T	0.346	101/125/24	0.356	130/121/45	0.05873
<i>LINC00457</i>	13q13.2	Intron	rs1536847	35106975	G/T	0.295	129/93/27	0.329	134/129/33	0.7937
<i>UNC13C</i>	15q21.3	Downstream	rs4774715	55140204	C/T	0.432	93/96/59	0.441	84/162/49	0.05915
<i>FTO</i>	16q12.2	Intron	rs9302654	54009545	C/T	0.114	197/49/4	0.144	218/69/8	0.3481
<i>CDH13</i>	16q23.3	Upstream	rs3848296	82550548	G/A	0.192	161/82/7	0.231	174/107/15	0.871
<i>SLFN11</i>	17q12	UTR-3	rs77814639	33678827	A/G	0.184	159/80/5	0.153	206/79/5	0.5034
<i>LINC01978</i>	17q25.3	Intron	rs57851800	77896371	A/C	0.345	104/117/27	0.326	131/137/28	0.4275
<i>METTL4</i>	18p11.32	Downstream	rs549315	2183055	G/A	0.378	90/130/29	0.429	91/156/49	0.2352
<i>SLC7A10</i>	19q13.11	Upstream	rs11672303	33726375	T/C	0.171	173/65/10	0.154	208/85/3	0.1135

SNP : single-nucleotide polymorphism, Chr : chromosome, M/m : major/minor allele, IA : intracranial aneurysm, MAF : minor allele frequency, MM : major/major allele, Mm : major/minor allele, mm : minor/minor allele