

S1 Table. Weighted polygenic risk scores from the genome-wide association study

Gene	Chr	SNP	NR ^a R ^a	ln(OR) ^b	OR ^b	P ^b
GWA $p < 5 \times 10^{-8}$						
<i>PRDM2</i>	1p36.21	rs61775135	A C	1.153597	0.3155	3.59×10^{13}
<i>GBA</i>	1q22	rs75822236	C T	5.083886	161.4	1.09×10^{-19}
<i>FMO4</i>	1q24.3	rs3737926	T C	1.014731	0.3625	1.83×10^{-10}
<i>RNF144A</i>	2p25.1	rs6741819	T C	1.382302	0.251	4.05×10^{-14}
<i>FLJ45964</i>	2q37.3	rs59626274	T C	1.342852	0.2611	5.78×10^{-14}
<i>LINC01237</i>	2q37.3	rs78458145	A G	1.407722	0.2447	3.14×10^{-15}
<i>SPCS3</i>	4q34.2	rs17688188	A G	1.312301	0.2692	5.99×10^{-13}
<i>TCF24</i>	8q13.1	rs112859779	T C	1.686319	0.1852	3.33×10^{-16}
<i>C9orf92</i>	9p22.3	rs12350582	A G	0.888714	2.432	1.49×10^{-8}
<i>LINGO2</i>	9p21.1	rs56942085	G A	1.809108	6.105	3.90×10^{-8}
<i>TMOD1</i>	9q22.33	rs1052270	T C	0.893063	0.4094	2.71×10^{-8}
<i>SUSD1</i>	9q31.3	rs79461840	T C	1.933693	6.915	1.40×10^{-8}
<i>LINC00474</i>	9q33.1	rs4979583	C T	0.896496	2.451	4.61×10^{-9}
<i>OLFML2A</i>	9q33.3	rs79134766	A G	1.972562	0.1391	1.70×10^{-19}
<i>MYEOV</i>	11q13.3	rs76855873	T C	1.107451	0.3304	1.23×10^{-11}
<i>ARHGAP32</i>	11q24.3	rs371331393	G A	3.774369	43.57	9.32×10^{-27}
<i>CD163L1</i>	12p13.31	rs138525217	C T	4.33047	75.98	6.20×10^{-23}
<i>SLC2A14</i>	12p13.31	rs118107419	A C	1.395537	0.2477	1.44×10^{-14}
<i>DRAM1</i>	12q23.2	rs7964241	A G	0.910675	2.486	1.95×10^{-8}
<i>CUL4A</i>	13q34	rs74115822	G A	1.831781	6.245	1.12×10^{-10}
<i>LINC02130</i>	16p13.12	rs11646803	T C	0.790319	0.4537	4.76×10^{-10}

<i>LOC102724084</i>	16q23.2	rs75861150	C	T	1.934476	0.1445	1.27×10 ⁻⁸
<i>SCARF1</i>	17p13.3	rs3744644	C	G	0.943405	0.3893	6.02×10 ⁻⁹
<i>MINK1</i>	17p13.2	rs72835045	A	G	1.382701	0.2509	1.69×10 ⁻¹²
<i>SLC47A1</i>	17p11.2	rs2440154	G	A	0.981704	2.669	1.42×10 ⁻⁸
<i>NAPA-ASI</i>	19q13.32	rs55800589	C	G	0.963644	0.3815	3.35×10 ⁻¹³
<i>DSCAM</i>	21q22.2	rs727333	A	C	1.364533	0.2555	3.69×10 ⁻¹⁴
<i>LRRC3</i>	21q22.3	rs116969723	A	G	1.447744	0.2351	3.83×10 ⁻¹⁵
<i>SLC5A4-ASI</i>	22q12.3	rs117398778	T	C	1.318818	3.739	2.00×10 ⁻⁹
Reported <i>p</i> < 0.05							
<i>BOLL</i>	2q33.1	rs700651	A	G	0.34713	1.415	0.00789
<i>EDNRA</i>	4q31.22	rs6841581	A	G	0.630548	0.5323	0.00065

OR, odds ratio; SNP, single-nucleotide polymorphism.

^aNon-risk (NR) and risk (R) allele were described.

^bThe values that indicates beta coefficient were computed by the natural log transformed OR (i.e., ln(OR)).

^cOR and *p*-value were estimated by the multivariate logistic regression model after adjusting for age, gender, hypertension, diabetes, hyperlipidemia, smoking status, and four genetic ancestry values.