

**Supplementary Table 2.** Result of meat-analysis with our data and genome-wide association study catalog

Chr	BP	SNP	A1	A2	P.FE	OR.FE	Q	I
6	20688121	rs10440833	A	T	3.29E-27	1.2497	0.9853	0
10	114754088	rs7901695	G	A	5.00E-25	1.3531	0.1672	47.59
6	20657564	rs4712523	G	A	6.86E-23	1.2552	0.5603	0
6	20661250	rs7754840	C	G	1.37E-18	1.1991	0.2851	12.49
6	20657865	rs4712524	G	A	2.20E-16	1.2281	0.7947	0
11	2857194	rs2237895	C	A	1.25E-14	1.2626	0.6013	0
3	185529080	rs1470579	C	A	1.72E-14	1.1644	0.4303	0
6	20661034	rs10946398	C	A	2.45E-14	1.1923	0.1729	46.17
6	20652717	rs9295474	G	C	6.98E-13	1.197	0.2171	34.36
13	33554302	rs576674	G	A	3.96E-12	1.0715	0.5165	0
2	161171454	rs7593730	A	G	8.85E-12	1.1041	0.2747	16.19
11	17409572	rs5219	A	G	1.16E-11	1.1277	0.2851	12.47
10	94465559	rs5015480	G	A	6.70E-11	1.1767	0.7479	0
11	92673828	rs1387153	A	G	1.27E-09	1.0891	0.8863	0
17 <sup>a</sup>	36098040	rs4430796	G	A	3.65E-09	1.132	0.1743	45.82
15 <sup>a</sup>	80432222	rs11634397	G	A	3.95E-09	1.061	0.5825	0
2 <sup>a</sup>	227093745	rs2943641	A	G	1.20E-08	1.1753	0.2832	13.18
9 <sup>a</sup>	136155000	rs635634	A	G	1.34E-08	1.0843	0.4732	0
3 <sup>a</sup>	185511687	rs4402960	A	C	3.40E-08	1.1404	0.9856	0
9 <sup>a</sup>	4292083	rs10758593	A	G	5.40E-08	1.0795	0.9431	0
12 <sup>a</sup>	55098996	rs1153188	A	T	4.87E-07	1.0794	0.762	0
11 <sup>a</sup>	17418477	rs757110	C	A	5.15E-07	1.0731	0.6318	0
15 <sup>a</sup>	77832762	rs7177055	A	G	6.74E-07	1.0724	0.2404	27.45

Chr, chromosome; BP, base position; SNP, single nucleotide polymorphism; A1, minor allele; A2, major allele; P.FE, *P* value of fixed effect model; OR.FE, odds ratio of fixed effect model; Q, *P* value of Cochran Q statistic; I, *I*<sup>2</sup> heterogeneity index.

<sup>a</sup>Chromosome indicates that the variant is significant in exome-wide association analysis.