

Supplementary Table 2. The 46 related SNPs from the GWAS of MetS involving 2,705 participants of the Guangzhou Biobank Cohort Study, 2003 to 2008

SNP	Nearest gene	Chr	Position	Risk/other allele	MAE, %	β	R^2	P value
rs662799	APOA5	11	116663707	G/A	28	0.4025	0.0467	1.67E-09
rs651821	APOA5	11	116662579	C/T	28	0.4011	0.0467	1.73E-09
rs7350481		11	116586283	T/C	28	0.3405	0.0385	6.82E-07
rs369326524		11	448280	C/A	1	1.3730	0.0019	7.44E-07
rs139017121	PTDSS2	11	468134	A/G	1	1.3730	0.0019	7.44E-07
rs6589566	ZNF259	11	116652423	G/A	23	0.3542	0.0334	9.17E-07
rs7483863	ZNF259	11	116652491	A/G	23	0.3542	0.0334	9.17E-07
rs2160669	ZNF259	11	116647607	C/T	22	0.3554	0.0324	9.17E-07
rs964184	ZNF259	11	116648917	G/C	23	0.3527	0.0333	1.02E-06
rs10750096	ZNF259	11	116656788	C/A	22	0.3530	0.0321	1.13E-06
rs10790162	BUD13	11	116639104	A/G	22	0.3494	0.0319	1.32E-06
rs6589565	BUD13	11	116640237	A/G	22	0.3494	0.0319	1.32E-06
rs9326246		11	116611733	C/G	23	0.3429	0.0328	1.44E-06
rs79605153		11	42820910	G/A	8	0.5446	0.0136	1.47E-06
rs138672212		11	42821674	T/G	8	0.5446	0.0136	1.47E-06
rs78160871		11	42824199	C/T	8	0.5446	0.0136	1.47E-06
rs2072560	APOA5	11	116661826	T/C	22	0.3484	0.0317	1.56E-06
rs146833250		11	42809333	G/A	8	0.5428	0.0136	1.59E-06
rs188079837		11	42812197	G/A	8	0.5428	0.0136	1.59E-06
rs187632323		11	42812408	G/A	8	0.5428	0.0136	1.59E-06
rs80036736		11	42799185	T/C	8	0.5420	0.0135	1.72E-06
rs140271395		11	42809205	C/T	8	0.5383	0.0135	1.91E-06
rs149979331		11	42790271	T/A	8	0.5375	0.0134	2.05E-06
rs76425601		11	42791477	C/T	8	0.5375	0.0134	2.05E-06
rs77699624		11	42798319	A/G	8	0.5375	0.0134	2.05E-06
rs74643618		11	42798127	T/G	8	0.5369	0.0134	2.10E-06
rs2266788	APOA5	11	116660686	G/A	23	0.3442	0.0323	2.12E-06
rs117738138		11	42802816	C/A	8	0.5363	0.0134	2.16E-06
rs1989154	HTR4	5	147848890	C/T	20	0.3837	0.0291	2.28E-06
rs74374343		11	42786965	G/A	8	0.5345	0.0134	2.32E-06
rs192379463		11	42804663	T/C	8	0.5337	0.0133	2.42E-06
rs3825041	BUD13	11	116631707	T/C	22	0.3422	0.0311	2.46E-06
rs1988819	HTR4	5	147849531	C/T	20	0.3814	0.0289	2.64E-06
rs10075211	HTR4	5	147839537	T/C	19	0.3863	0.0276	3.02E-06
rs12374521	HTR4	5	147836880	T/C	19	0.3883	0.0276	3.17E-06
rs80352262		7	47000652	A/G	0.6	1.6160	0.0011	3.26E-06
rs1558860		11	116607368	A/C	23	0.3296	0.0316	3.47E-06
rs4643960		5	84061741	T/C	24	-0.3576	-0.0324	3.73E-06

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Supplementary Table 2. Continued

SNP	Nearest gene	Chr	Position	Risk/other allele	MAF, %	β	R^2	<i>P</i> value
rs76187712		11	42799721	T/C	8	0.5209	0.0131	3.81E-06
rs1974718		11	116606766	G/A	23	0.3282	0.0315	3.82E-06
rs1558861		11	116607437	A/C	24	0.3266	0.0324	3.89E-06
rs4133436		5	84062058	C/T	24	-0.3548	-0.0324	3.91E-06
rs6887366	HTR4	5	147851270	A/T	20	0.3729	0.0284	4.03E-06
rs2075290	ZNF259	11	116653296	C/T	25	0.3168	0.0330	4.64E-06
rs149595528		11	42814083	G/A	9	0.5128	0.0144	4.99E-06
rs77173973		11	42816900	A/G	9	0.5128	0.0144	4.99E-06

$R^2 = 2 \times (1 - \text{MAF}) \times \text{MAF} \times \frac{\beta}{\text{SD}}$; $\text{SD} = \text{SE} \times \sqrt{n}$.

SNP, single nucleotide polymorphism; GWAS, genome-wide association study; MetS, metabolic syndrome; Chr, chromosome; MAF, minor allele frequency; APOA5, apolipoprotein A5; PTSS2, phosphatidylserine synthase 2; ZNF259, zinc finger protein 259; BUD13, BUD13 homolog; HTR4, 5-hydroxytryptamine receptor 4.