

Supplementary table 4. Analysis of allelic association.

Chr	SNP	Gene/Location	A1	A2	P	OR	L95	U95	
19	rs2545771	<i>CYP2F2P</i>	A	G	8.83E-22	0.104	0.05986	0.1806	
10	rs7098158	<i>VCL</i>	A	G	0.0001181	0.1015	0.02429	0.4238	
9	rs10780946	<i>TRPM3</i>	A	G	0.0001934	0.6192	0.4806	0.7977	
4	rs13109426	<i>LOC105377462</i>	G	A	0.0006167	1.437	1.167	1.768	
18	rs17084708	<i>LINC01541</i>	G	A	0.0006484	0.6048	0.4521	0.8091	
18	rs8086262	<i>LINC01541</i>	G	A	0.0006759	0.6178	0.4672	0.8169	
18	rs11660297	<i>LINC01541</i>	C	A	0.0006817	0.6058	0.4527	0.8106	
18	rs11151679	<i>LINC01541</i>	G	A	0.0006858	0.6124	0.4605	0.8143	
10	rs7088944	<i>ADK</i>	A	G	0.0007208	0.2268	0.08877	0.5793	
9	rs3181358	<i>TNFSF8</i>	A	C	0.0007773	0.07245	0.009776	0.5369	
11	rs11827713	<i>LOC105369452</i>	A	G	0.00084	0.1676	0.05102	0.5506	
3	rs1511532	<i>LOC105377164</i>	A	G	0.000976	1.403	1.147	1.716	↑ p<0.001
18	rs11151678	<i>LINC01541</i>	C	G	0.001025	0.6139	0.4579	0.823	
1	rs10914228	<i>LOC101929406</i>	A	C	0.001588	0.7177	0.584	0.882	
2	rs6712954	<i>SERPINE2</i>	A	G	0.001812	0.7003	0.5595	0.8764	
1	rs2893225	<i>FAM69A</i>	G	C	0.001882	0.6997	0.5583	0.8769	
7	rs10230391	<i>HIP1</i>	A	C	0.002772	0.477	0.2909	0.7823	
6	rs3179003	<i>NCR3</i>	A	C	0.002974	0.2629	0.1021	0.6771	
7	rs2069835	<i>IL6</i>	G	A	0.003788	0.4365	0.2454	0.7764	
12	rs16947426	<i>NOS1</i>	G	C	0.005251	0.2495	0.0871	0.7148	
4	rs10013495	<i>LOC105377462</i>	A	G	0.005855	0.7438	0.6024	0.9183	
6	rs1475080	<i>LOC105374951</i>	T	A	0.00629	0.7474	0.6063	0.9212	
7	rs995043	<i>PLEKHA8</i>	A	G	0.007857	1.665	1.14	2.433	
2	rs6732835	<i>GNLY</i>	G	A	0.008072	0.1748	0.04072	0.7506	
19	rs2291287	<i>CYP2B6</i>	G	A	0.008284	0.3691	0.1711	0.7966	
2	rs6738983	<i>SERPINE2</i>	A	G	0.008937	0.7646	0.6252	0.9352	
19	rs1056854	<i>HNRNPUL1</i>	G	A	0.009332	0.7387	0.5877	0.9286	
20	rs6041817	<i>SPTLC3</i>	G	A	0.009463	0.6984	0.5321	0.9167	
2	rs7597791	<i>XRCC5</i>	C	A	0.009485	0.4498	0.2423	0.835	↑ p<0.01

P values before Bonferroni correction.