

Supplementary Table 1. Comparison of the MAF of the genotyped SNPs with 1000 Genome Project database

Gene	SNP	Chromosomal location	Minor allele	1000 Genomes MAF			MAF of this study	Functional consequence
				Global	EUR	SAS		
<i>COBLI1</i>	rs7607980	Chr 2:165551201	C	0.107	0.424	0.081	0.063	Missense variant
<i>GRB14</i>	rs3923113	Chr 2:165501849	C	0.385	0.154	0.211	0.154	-
<i>RBMS1</i>	rs7593730	Chr 2:161171454	T	0.247	0.408	0.214	0.210	Intron variant
<i>THADA</i>	rs7578597	Chr 2:43732823	C	0.137	0.090	0.132	0.107	Intron variant
<i>PPARG</i>	rs1801282	Chr 3:12393125	T	0.070	0.793	0.120	0.097	Missense variant
<i>ADAMTS9</i>	rs4607103	Chr 3:64711904	T	0.354	0.120	0.524	0.525	Intron variant
<i>IGF2BP2</i>	rs6769511	Chr 3:185530290	C	0.469	0.232	0.457	0.523	Intron variant
<i>IGF2BP2</i>	rs1470579	Chr 3:185529080	C	0.469	0.304	0.457	0.509	Intron variant
<i>IGF2BP2</i>	rs4402960	Chr 3:185511687	T	0.389	0.304	0.455	0.507	Intron variant
<i>CDKALI</i>	rs7754840	Chr 6:20661250	C	0.405	0.304	0.256	0.289	Intron variant
<i>CDKALI</i>	rs4712523	Chr 6:20657564	G	0.419	0.318	0.291	0.307	Intron variant
<i>CDKALI</i>	rs4712524	Chr 6:20657865	G	0.405	0.319	0.256	0.278	Intron variant
<i>JAZF1</i>	rs864745	Chr 7:28180556	C	0.303	0.318	0.237	0.241	Intron variant
<i>JAZF1</i>	rs849134	Chr 7:28196222	G	0.412	0.519	0.238	0.237	Intron variant
<i>SLC30A8</i>	rs13266634	Chr 8:118184783	T	0.265	0.514	0.255	0.209	Intron variant
<i>TP53INP1</i>	rs896854	Chr 8:95960511	C	0.516	0.283	0.610	0.409	Intron variant
<i>CDKN2A/B</i>	rs7020996	Chr 9:22129579	T	0.258	0.539	0.130	0.111	-
<i>CDKN2A/B</i>	rs2383208	Chr 9:22132076	G	0.210	0.130	0.134	0.126	-
<i>CDKN2A/2B</i>	rs564398	Chr 9:22029547	C	0.185	0.173	0.273	0.205	Intron variant
<i>HHEX</i>	rs1111875	Chr 10:94462882	T	0.456	0.413	0.644	0.425	-
<i>TCF7L2</i>	rs4506565	Chr 10:114756041	T	0.284	0.424	0.304	0.364	Intron variant
<i>CDC123</i>	rs10906115	Chr 10: 12314997	G	0.385	0.345	0.486	0.500	-
<i>HNF1A</i>	rs1800574	Chr 12: 121416864	T	0.020	0.371	0.061	0.087	Missense variant
<i>TSPAN8</i>	rs4760790	Chr 12: 71634794	G	0.236	0.027	0.326	0.385	-
<i>HNF4A</i>	rs4812829	Chr 20:42989267	A	0.255	0.703	0.301	0.358	Intron variant

MAF, minor allele frequency; SNP, single nucleotide polymorphism; EUR, European; SAS, South Asian; Chr, chromosome.