Chr	rs_ID	Genes (within/ close to)	Position (GRCh37)	EA	AA	EAF	OR(95%Cl)	P_value
1	rs116279952	*LOC124904156*	56826428	A	G	0.013	2.64(2.39-2.88)	3.66×10^{-7}
12	rs10879942	*LOC105369844*	76017475	T	G	0.210	1.29(1.22-1.36)	4.27×10^{-6}
13	rs9589807	*GPC6*	94309026	G	A	0.197	1.30(1.23-1.38)	4.46×10^{-6}
17	rs7220255	*LINC01993*	76289418	T	C	0.386	0.81(0.75-0.87)	4.47×10^{-6}
6	rs62413399	*SH3BGRL2*	80297080	T	C	0.046	1.64(1.50-1.78)	6.04×10^{-6}
2	rs116356815	*EPHA4*	222298536	A	G	0.126	1.36(1.27-1.45)	6.13×10^{-6}
5	rs10070308	*FBXL17*	107281621	T	C	0.262	1.25(1.19-1.32)	8.44×10^{-6}
3	rs1580082	*LINC00971*	84843143	C	A	0.243	0.79(0.72-0.86)	8.71×10^{-6}
10	rs1171728	*C10orf143*	131907568	A	G	0.037	1.70(1.54-1.85)	9.15×10^{-6}
8	rs138831048	*SLCO5A1*	70726388	T	C	0.039	1.67(1.52-1.82)	9.28×10^{-6}
1	rs2797179	*NHLH2*	116357654	T	G	0.394	1.23(1.17-1.28)	9.35×10^{-6}

Chr = chromosome number, rs_ID = SNP identifier, EA = effect allele, AA = alternate allele, EAF = effect allele frequency, OR= odds ratio,95%CI= 95% confidence interval, OR calculated with reference to EA