

Supplementary Table 2. Significant MVP discovery loci.

Significant genomic risk loci from individual MVP European (EUR), admixed African (AFR), and Hispanic/Latino (HIS) cohorts.

Genomic coordinates correspond to GRCh38. EA, effect allele; NEA, non-effect allele; EAF, effect allele frequency;

SE, standard error; OR [L95, U95], odds ratio with lower and upper bounds of 95% confidence interval.

Cohort	rsID	CHR	POS (GRCh38)	EA	NEA	EAF	Ncase	N	BETA	SE	OR [L95, U95]	P-value
MVP EUR	rs11590557	1	54,324,099	A	G	0.040	2,251	254,596	0.465	0.071	1.59, [1.39, 1.83]	2.68E-11
MVP EUR	rs79742895	1	62,317,189	C	T	0.043	2,251	254,596	0.510	0.067	1.67, [1.46, 1.90]	1.11E-14
MVP EUR	rs1200114	1	169,091,251	A	G	0.651	2,251	254,596	####	0.031	0.74, [0.69, 0.78]	1.26E-22
MVP EUR	rs34278601	1	183,146,193	C	CA	0.548	2,251	254,596	####	0.031	0.81, [0.76, 0.86]	1.38E-12
MVP EUR	rs74882680	7	11,700,254	G	A	0.024	2,251	254,596	0.587	0.087	1.80, [1.52, 2.14]	9.48E-12
MVP EUR	rs6597981	11	803,017	G	A	0.511	2,251	254,596	0.180	0.031	1.20, [1.13, 1.27]	4.56E-09
MVP EUR	rs11659764	18	55,668,281	A	T	0.047	2,251	254,596	1.858	0.046	6.41, [5.86, 7.01]	9.40E-360
MVP AFR	rs11659764	18	55,668,281	A	T	0.009	315	79,200	2.024	0.225	7.57, [4.87, 11.75]	1.10E-19
MVP HIS	rs11659764	18	55,668,281	A	T	0.022	80	26,448	1.968	0.306	7.16, [3.93, 13.04]	6.19E-11