

Table S3: List of all SNPs that were significant at p-value < 10⁻⁶ in regions with at least one SNP with GWAS threshold in mean platelet volume meta-analysis

SNP	Chr	Position	Gene	Role	Coded Allele	Allele Frequency	Effect Size (SE)	P Value	Het-P (I-square)	N
rs4727659	7	106144723			T	23.4%	0.122 (0.026)	2.84 x 10 ⁻⁶	0.20 (0)	3901
rs342293	7	106159455			G	61.5%	-0.155 (0.024)	5.84 x 10 ⁻¹¹	0.30 (0)	3904
Rs342294	7	106159858			T	61.4%	-0.162 (0.033)	7.37 x 10 ⁻⁷	0.99 (0)	1989
rs342295	7	106159996			C	37.6%	0.159 (0.024)	3.68 x 10 ⁻¹¹	0.20 (0.4)	3905
rs342296	7	106160139			G	37.2%	0.161 (0.024)	1.44 x 10 ⁻¹¹	0.25 (0)	3904
rs342298	7	106160882			C	37.3%	0.161 (0.024)	3.61 x 10 ⁻¹¹	0.33 (0)	3905
rs11653144	17	24699352	Near TAOK1		C	55.8%	0.132 (0.024)	4.17 x 10 ⁻⁸	0.48 (0)	3905
rs7213208	17	24756995			G	47.0%	-0.128 (0.024)	1.30 x 10 ⁻⁷	0.29 (0)	3905
rs7208363	17	24757534			T	45.9%	-0.131 (0.026)	5.31 x 10 ⁻⁷	0.18 (3.2)	3905
rs11655000	17	24791469			C	33.0%	-0.121 (0.027)	6.33 x 10 ⁻⁶	0.44 (0)	3905
rs9900280	17	24793724			G	64.3%	0.122 (0.025)	1.37 x 10 ⁻⁶	0.53 (0)	3905
rs12943131	17	24887832			G	64.4%	0.124 (0.025)	1.04 x 10 ⁻⁶	0.52 (0)	3905
rs8109288	19	16046559	TPM4	near gene-5'	G	8.4%	0.261 (0.044)	3.30 x 10 ⁻⁹	0.84 (0)	3905

I-square = a measure of heterogeneity among studies that cannot be explained by chance; Het-P = Cochran Q p-value to assess heterogeneity