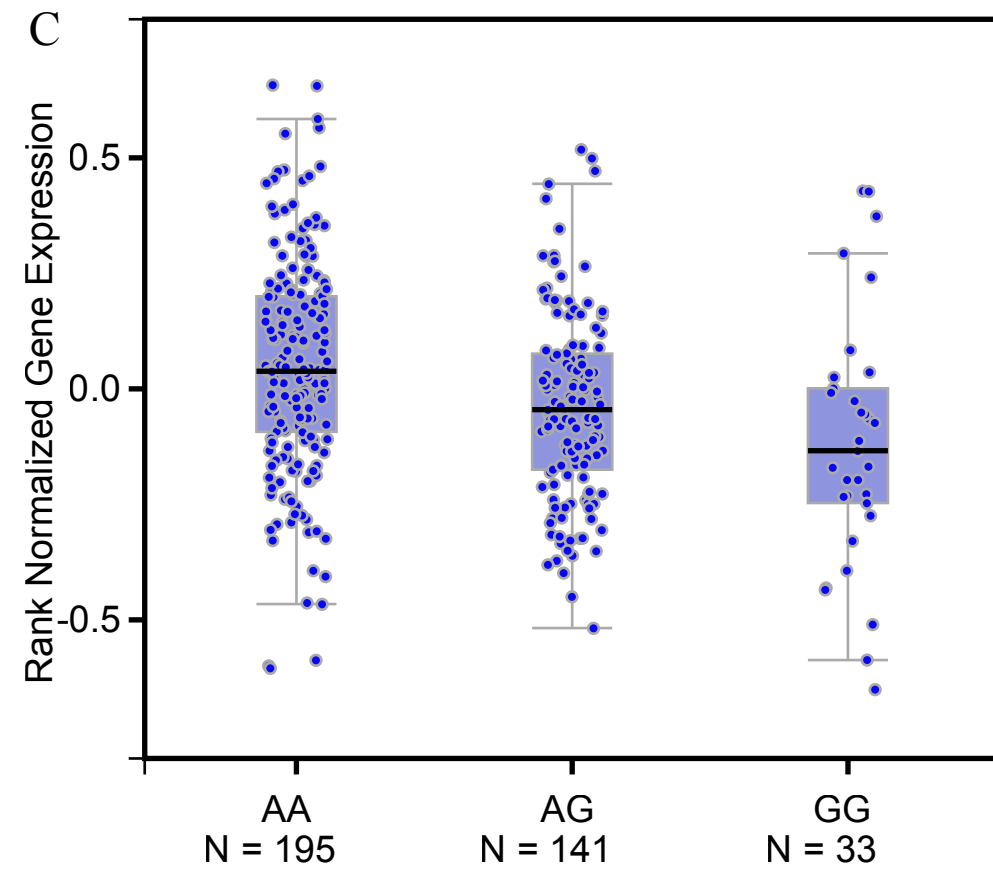
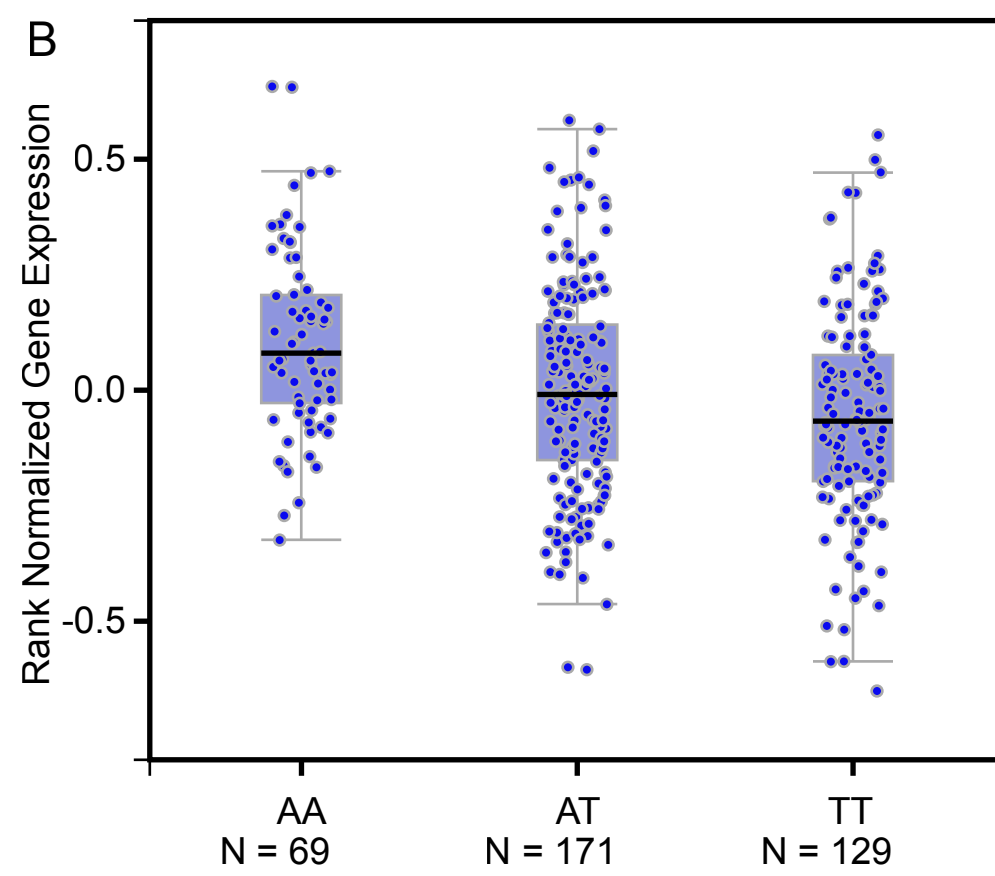
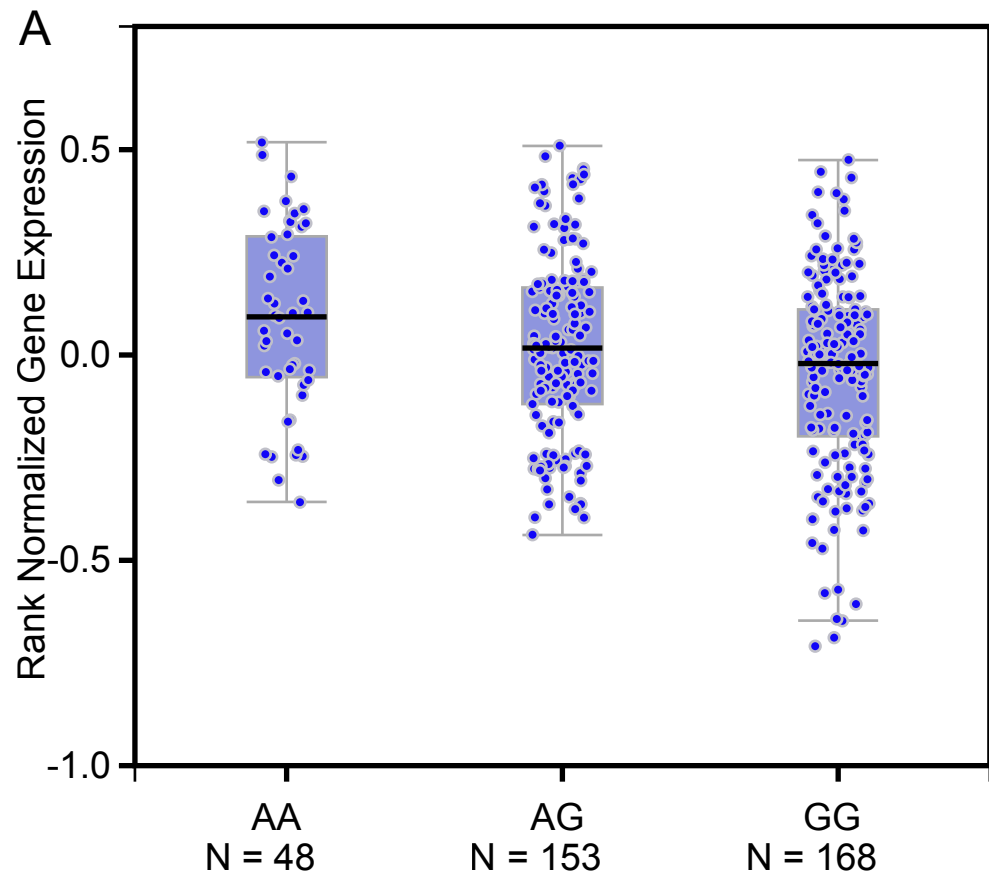


Additional file 2 Figure S1.

eQTL analysis of mRNA expression in whole blood and genotype data. A: *TLR4* rs1927911, p-value=0.000016; B: *TGF-BRI* rs6478974, p-value=6.5e-7, and C: rs334348, p-value= 0.0000029.



Additional file 2 Figure S2. Results from the Haploreg website for the *TGF-BRI* rs10512263

Query SNP: **rs10512263** and variants with $r^2 \geq 0.8$

chr	pos (hg38)	LD (r ²)	LD (D')	variant	Ref	Alt	AFR freq	AMR freq	ASN freq	EUR freq	SiPhy cons	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	dbSNP func annot
9	99123789	1	1	rs10512263	T	C	0.02	0.11	0.26	0.07				BLD		Ik-1,STAT				TGFBR1	intronic

Regulatory motifs altered

Position Weight Matrix ID (Library from Kheradpour and Kellis, 2013)	Strand	Ref	Alt	Match on:
Ik-1_2	+	12.9	9.8	Ref: ATTCTACAGTGGAAATTTGTCACTACTTTTGGGAAGAAGTTTACCTTTGGTGGCCTACG Alt: ATTCTACAGTGGAAATTTGTCACTACTTTGGGAAGAAGTTTACCTTTGGTGGCCTACG
STAT_known10	-	-5.5	6.4	KYTRGGRRR BDBVAHTCCSGGAADTRRSR