



SUPPLEMENTAL FIGURE 1. Linkage disequilibrium map of tagging SNPs in interferon-alpha receptor 1 (IFNAR1) gene from the Yoruba, Nigeria (YRI) HapMap database for malaria disease association analysis. Linkage disequilibrium plot representing pairwise R^2 in a grayscale. We selected 16 tagging SNPs found in the YRI population HapMap dataset within the IFNAR1 coding and noncoding sequences (including 2 kb upstream of the transcription start site).

SUPPLEMENTAL TABLE 1

Cerebral malaria-associated IFNAR1 variants are associated with alterations in expression levels of IFNAR1 and IL10RB by expression quantitative trait loci data extracted from Westra et al.³⁶

SNP	SNP Chr:Pos	SNP alleles	Minor allele	Gene name	Z-score	P value	FDR	Probe	Probe Chr:Pos
rs914142	21:33647677	A/G	G	IFNAR1	-14.75	3.01E-49	0	7550181	21:33653663
rs914142	21:33647677	A/G	G	IL10RB	-5	5.63E-07	0	5050368	21:33590465
rs12626750	21:33620255	C/A	A	IFNAR1	11	3.80E-28	0	7550181	21:33653663
rs12626750	21:33620255	C/A	A	IL10RB	8.48	2.23E-17	0	5670719	21:33591282
rs12626750	21:33620255	C/A	A	IL10RB	4.88	1.06E-06	0	5050368	21:33590465
rs1041867	21:33649122	T/G	T	IL10RB	6.44	1.17E-10	0	5670719	21:33591282

FDR = false discovery rate; IFNAR1 = interferon-alpha receptor 1. A positive Z score indicates an increased gene expression. In some cases, multiple probes are used for the same gene. Associations with false discovery rate $P < 0.01$ are reported.