Supplementary Table 2

Supplementary Table 2. Genotype frequencies for each SNP in *TIRAP* genotyped in the UK IPD and Gambian malaria case-control study groups.

Marker ID			**Population**			
			UK		**Gambian**	
Position relative to the start of Exon1	**dbSNP ID in NCBI**	**Genotype**	**Controls (%)**	**IPD cases (%)**	**Controls (%)**	**Malaria cases (%)**
-80708	rs480153	CC	63.1	68.7	74.8	76.1
		CT	35.2	27.0	24.3	20.4
		TT	1.7	4.3	0.9	3.5
-68168	rs588361	AA	30.7	30.8	16.9	15.2
		AG	52.5	52.3	50.8	50.6
		GG	16.8	16.8	32.3	34.2
-52070	rs618176	CC	64.0	69.3	82.5	88.7
		CT	34.2	28.1	17.5	11.3
		TT	1.8	2.6	0.0	0.0
-29144	rs670154	GG	32.9	36.7	23.1	22.1
		AG	50.0	36.7	46.2	47.1
		AA	17.1	26.6	30.7	30.9
-23852	rs631023	AA	54.1	52.8	12.1	9.0
		AC	38.6	33.3	51.6	44.9
		CC	7.3	13.9	36.3	46.1
-18304	rs638766	CC	58.0	56.1	32.9	27.7
		CT	35.6	36.0	46.6	47.9
		TT	6.4	7.9	20.5	24.5
-12534	rs478309	GG	57.9	54.5	34.3	29.6
		AG	36.0	35.7	46.5	43.5
		AA	6.1	9.8	19.2	26.9
-5289	rs594318	CC	60.9	60.9	75.8	80.7
		CG	35.3	36.4	22.0	18.2
		GG	3.8	2.7	2.2	1.1
-4570	rs591163	CC	58.4	55.9	35.1	33.0
		CT	35.5	35.5	32.0	34.1
		TT	6.1	8.6	33.0	33.0
-1580	rs563011	TT	55.8	59.6	94.6	94.1
		GT	35.5	33.9	5.4	5.9
		GG	8.6	6.4	0.0	0.0
-386	rs4937114	GG	94.0	94.9	91.7	92.6
		GT	6.0	3.8	8.3	7.4
		TT	0.0	1.3	0.0	0.0
-355	rs10893493	AA	78.7	79.2	81.6	81.1
		AG	20.9	18.9	15.8	18.9
		GG	0.4	1.9	2.6	0.0
+177	rs8177348	CC	59.9	62.6	31.7	27.2
		CT	34.9	29.7	47.6	45.6
		TT	5.2	7.7	20.7	27.2
+3977	rs595022	GG	61.0	59.5	94.6	95.8
		AG	33.4	36.7	4.3	4.2
		AA	5.6	3.8	1.1	0.0
+6032	rs646005	AA	40.2	43.3	28.4	22.3

		AG	45.8	35.1	33.7	39.3
		GG	14.0	21.6	37.9	38.4
+7685	rs1893352	AA	75.1	81.9	86.0	86.8
		AG	22.7	15.9	14.0	12.6
		GG	2.2	2.2	0.0	0.6
R13W	rs8177399	CC (RR)	95.9	95.8	97.1	99.7
		CT (RW)	4.1	4.2	2.4	0.3
		TT (WW)	0.0	0.0	0.5	0.0
S55N	rs3802813	GG (SS)	93.2	85.4	90.4	86.6
		AG (SN)	6.7	12.6	8.9	10.7
		AA (NN)	0.2	2.0	0.7	2.7
Q101Q	rs3802814	GG	73.9	77.6	97.0	98.7
		AG	24.2	20.1	3.0	1.2
		AA	1.9	2.3	0.0	0.1
S180L	rs8177374	CC (SS)	71.1	76.4	96.6	99.1
		CT (SL)	26.9	18.8	3.4	0.9
		TT (LL)	2.0	4.7	0.0	0.0
A186A	rs7932766	CC	46.7	46.0	75.8	80.6
		CT	40.0	39.0	21.2	17.4
		TT	13.3	15.0	3.0	2.0
V197I	rs7932976	GG (VV)	100.0	100.0	97.5	94.4
		AG (IV)	0.0	0.0	2.5	5.6
		AA (II)	0.0	0.0	0.0	0.0
+10122	rs609634	TT	61.8	64.6	41.6	32.6
		CT	34.5	27.8	32.6	42.1
		CC	3.6	7.6	25.8	25.3
+10610	rs8177376	TT	57.2	64.1	94.4	92.5
		TG	34.5	28.2	5.6	7.5
		GG	8.2	7.8	0.0	0.0
+11347	rs625413	CC	62.0	64.0	86.0	88.2
		CT	34.1	27.9	14.0	11.8
		TT	3.9	8.1	0.0	0.0
+13466	rs8177382	CC	74.8	80.2	70.0	78.9
		CA	24.8	18.9	30.0	21.1
		AA	0.5	0.9	0.0	0.0
+13955	rs8177385	CC	100.0	100.0	91.9	95.0
		CG	0.0	0.0	7.2	5.0
		GG	0.0	0.0	0.9	0.0
+14472	rs8177388	CC	74.6	81.7	82.0	83.2
		CT	25.0	18.3	18.0	16.8
		TT	0.4	0	0.0	0.0
+21162	rs695029	CC	66.8	66.7	77.5	78.7
		CT	30.1	31.7	20.6	19.3
		TT	3.1	1.7	1.9	2.0
+35464	rs611151	CC	53.0	53.4	37.1	30.8
		CT	40.7	36.4	37.1	48.1
		TT	6.4	10.2	25.8	21.1
+44402	rs645852	CC	52.6	57.7	69.5	70.8
		CG	37.0	34.6	25.6	25.5
		GG	10.4	7.7	4.8	3.7
+60339	rs240537	GG	53.7	55.8	71.7	80.2
		GT	35.8	39.0	25.0	16.7
		TT	10.5	5.2	3.3	3.2
+71446	rs7937122	CC	28.7	35.4	12.9	15.9
		CG	52.3	43.9	35.5	41.2
		GG	19.0	20.7	51.6	42.9