

Supplementary table S4: Maximum likelihood estimates of single allele and haplotype frequencies from health centre samples

SNP	Sigimaru HC (Karimui) (N=97)		Kunjingini HC (South Wosera) (N=112)	
	\hat{p}	95%CI	\hat{p}	95%CI
<i>pfmdr1</i> N86Y	0.69	(0.60, 0.77)	0.99	(0.98, 1.00)
<i>pfmdr1</i> Y184F	0.05	(0.01, 0.09)	0.00	
<i>pfmdr1</i> N1042D	0.01	(0.00, 0.03)	0.00	
<i>pfcr1</i> K76T	0.91	(0.85, 0.96)	0.92	(0.86, 0.97)
<i>pfcr1</i> S163R	0.01	(0.00, 0.03)	0.01	(0.00, 0.02)
<i>pfcr1</i> A220S	0.80	(0.72, 0.87)	0.55	(0.45, 0.66)
<i>pfcr1</i> N326D	0.87	(0.80, 0.93)	0.90	(0.84, 0.96)
<i>pfcr1</i> I356L	0.87	(0.80, 0.93)	0.91	(0.84, 0.96)
<i>pfdhfr</i> S108N	0.85	(0.79, 0.90)	0.87	(0.81, 0.92)
<i>pfdhfr</i> C59R	0.79	(0.71, 0.86)	0.80	(0.72, 0.88)
<i>pfdhps</i> A437G	0.02	(0.00, 0.05)	0.23	(0.15, 0.32)
<i>pfdhps</i> K540E	0.03	(0.00, 0.07)	0.01	(0.00, 0.03)
Haplotype				
<i>pfmdr1</i> N86Y+Y184F+N1042D	\hat{h}	95%CI	\hat{h}	95%CI
000	0.006	(0.0, 0.026)	0.261	(0.203, 0.325)
001	0.0	(0.0, 0.012)	0.0	(0.0, 0.010)
010	0.994	(0.974, 0.999)	0.687	(0.620, 0.749)
011	0.0	(0.0, 0.011)	0.005	(0.0, 0.021)
100	0.0	(0.0, 0.012)	0.038	(0.017, 0.071)
101	0.0	(0.0, 0.012)	0.010	(0.001, 0.030)
110	0.0	(0.0, 0.011)	0.0	(0.0, 0.010)
111	0.0	(0.0, 0.012)	0.0	(0.0, 0.010)
<i>pfcr1</i> K76T+A220S+I356L				
000	0.072	(0.038, 0.119)	0.090	(0.055, 0.135)
001	0.0	(0.0, 0.013)	0.0	(0.0, 0.010)
010	0.0	(0.0, 0.013)	0.0	(0.0, 0.010)
011	0.0	(0.0, 0.013)	0.0	(0.0, 0.010)
100	0.019	(0.004, 0.048)	0.030	(0.011, 0.061)
101	0.343	(0.272, 0.418)	0.082	(0.049, 0.126)
110	0.0	(0.0, 0.013)	0.005	(0.0, 0.022)
111	0.566	(0.488, 0.642)	0.793	(0.732, 0.845)
<i>pfdhfr</i> C59R+S108N				
00	0.135	(0.089, 0.191)	0.152	(0.106, 0.206)
01	0.062	(0.032, 0.105)	0.056	(0.029, 0.095)
10	0.0	(0.0, 0.012)	0.0	(0.0, 0.011)
11	0.803	(0.740, 0.859)	0.792	(0.733, 0.845)
<i>pfdhps</i> A437G+K540E				
00	0.753	(0.684, 0.815)	0.951	(0.915, 0.976)
01	0.006	(0.0, 0.026)	0.029	(0.011, 0.059)
10	0.235	(0.175, 0.304)	0.020	(0.005, 0.045)
11	0.006	(0.0, 0.026)	0.0	(0.0, 0.010)

N, number of samples analyzed; SNP, single nucleotide polymorphism; \hat{p} , mutant allele frequency; \hat{h} , estimated haplotype frequency; 0 wild-type allele; 1, mutated allele; CI, confidence intervals determined from 10,000 bootstrap samples.