

Additional File 3. SNPs in *n*-, *o*-, *pfmc-2tm* and *q*-gene found in different *P.f.* strains

Gene	Reference Gene / remarks	start	end	bp surveyed	SNP Position	NS	S	3D7	FCR3	TM180	7G8	UAS39	UAS31	7G8*	Dd2*	D10*	HB3*			
<i>n-gene</i>	PFA0055c	69594	70343	749	69760	+		T/C	C	C	T/C	T/C	T/C	C	C	C	C			
					69761	+		A/G	G	G	G	A/G	G							
					69779	+		T/G	G	T/G	G	G	G	G	G	G	G	G	G	G
					69947	+		A	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A	A
<i>o-gene</i>	no SNP detected			560																
<i>pfmc-2tm</i>	variant gene family			544																
<i>q-gene</i>	PF07_0002	127855	128703	746	127990	+		G/A	G	G	G/A	G/A	G							
					128383	+		A/G	A/G	A	A	A	A/G							
					128396	+		A/G	A/G	A	A	A	A/G							
					127872		+	T	-	-	-	-	-	-	-	-	-	C		T
					127880	+		A/G	-	-	-	-	-	-	-	-	-	A		A
					127897		+	A/G	-	-	-	-	-	-	-	-	-	A		A

Sequences were manually curated by visualization of the chromatograms. Criteria for true SNPs are: (1) SNP present in at least two parasites. (2) At least two sequences showing the particular SNP in one of the parasites.

NS, non-synonymous; S, synonymous; * information acquired from [39]; - sequenced area not covered