Assay Number	SNP	Ch	Position	R/S Number	SNP Type	Degeneracy	Frame	Genes	Alleles	Parasites	MAF	Allele																			Number of Reads															Amino Acid														
												3D7_Reference	106_1	7G8	D10	D6	Dd2	FCB	FCC-2	FCR3	HB3	K1	Malayan Camp	RO-33	SantaLucia	Senegal P31.01	Senegal P34.04	Senegal P35.04	Senegal P51.02	VS/1	3D7_Reference	106_1	7G8	D10	D6	Dd2	FCB	FCC-2	FCR3	HB3	K1	Malayan Camp	RO-33	SantaLucia	Senegal P31.01	Senegal P34.04	Senegal P35.04	Senegal P51.02	VS/1	3D7_Reference	106_1	7G8	D10	D6	Dd2	FCB	FCC-2	FCR3	HB3	K1	Malayan Camp	RO-33	SantaLucia	Senegal P31.01	Senegal P34.04	Senegal P35.04	Senegal P51.02	VS/1
1	Pf_01_000130573	1	130573		N	ND	1	PFA0145c	C/T	10	0.4	C		C	T			C	T		T	C		C			C			T	1		1	2			1	2		1	1		1			4			2	A		A	T			A	T		T	A		A			A			T
2	Pf_01_000539044	1	539044		S	4	3	PFA0670c	A/G	10	0.4	G		A	A		A		G		G	G			A		A			A	1		2	1		1			2		1	1			2			2			2	S		S	S		S		S		S	S			S			S
3	Pf_02_000842803	2	842803		S	2	3	PFB0935w	T/C	10	0.5	C	C	C	T	C	T		T		C			T						T	1	1	2	2	2	9		1		1			2					1	N	N	N	N	N	N		N				N						N
4	Pf_04_000282592	4	282592		N	ND	2	PFD0250c	T/C	10	0.3	T			C		C		T		C	T		T	T		T			T	1			3		15		3		1	2		1	1		2			2	N			S		S		N		S	N		N	N		N			N
5	Pf_05_000931601	5	931601		N	ND	1	PFE1120w	C/G	10	0.3	C			C	C	C				C	C		G	G		G			C	1			1	2	47				1	1		1	1		4			2	P			P	P	P				P	P		A	A		A			P
6	Pf_06_000145472	6	145472	rs45343635	N	ND	2	PFF0175c	C/G	9	0.444	C		G	G	C	G				C	G					C			C	1		5	2	3	14				1	1					1			2	S		T	T	S	T				S	T					S			S
7	Pf_06_000937750	6	937750		S	4	3	PFF1105c	G/A	11	0.364	G		G	G	A	A		G		A	G			A		G			G	1		3	1	3	2		1		1	2			1			1			1	G		G	G	G	G		G			G				G			G
8	Pf_07_000277104	7	277104	rs45339742	S	4	3	MAL7P1_19	G/A	11	0.364	G		G		G	A		G		G	A		G	A		G			A	1		3		2	18		1		1	2		2	1		2			1	L		L		L	L		L			L	L		L	L		L			L
9	Pf_07_000490877	7	490877	rs45343970	S	4	3	PF07_0040	A/T	12	0.417	A		A	A	A	T	T			A	T		A	A		T			T	1		3	1	2	8	1			1	1		1	1		1			2	A		A	A	A	A	A			A	A		A	A		A			A
10	Pf_07_000545046	7	545046	rs45338103	S	4	3	PF07_0047	T/C	10	0.3	C				T	T		C	T	T	T		C			T			T	1				1	9		1	1	1	3		3			2			1	P				P	P		P	P		P	P	P	P		P			P
11	Pf_07_000657939	7	657939	rs45403113	S	2	3	MAL7P1_57	T/C	9	0.222	T			T	C			T		C	T		T			T			T	1				2	2				1		1	1		1			2	D			D	D			D			D	D		D			D			D
12	Pf_07_000671839	7	671839		N	ND	2	MAL7P1_65	A/G	10	0.2	G			G	A	A		A		A	A			A		A			A	1			1	1	1		2		1	3			3			4			4	S			S	N	N		N			N	N			N			N
13	Pf_07_000683772	7	683772	rs45339189	N	ND	1	PF07_0053	C/T	7	0.429	C			C		T	T			C						C			T	1			1		5	1			1						1			1	G			G		S	S			G						G			S
14	Pf_07_000792356	7	792356	rs45341962	S	4	3	PF07_0070	A/C	9	0.222	A	A		A	A					A			A	A		C			C	1	1		2	1					1			1	2		1			2	P	P		P	P					P			P	P		P			P
15	Pf_07_001415182	7	1415182	rs45403212	N	ND	1	MAL7P1_176	C/A	16	0.5	C	C	A		A	A	C	A	C	A	C		C	A	C	C	A	A		1	2	1		1	9	3	3	3	1	1		5	2	1	4	1	1		Q	Q	K		K	K	Q	K	Q	K	Q		Q	K	Q	Q	K	K	
16	Pf_08_000613716	8	613716	rs45405749	N	2	3	PF08_0089	C/A	8	0.375	C			C	C	A	A			C	C								A	1			1	1	6	1			1	1							3	F			F	F	L	L			F	F						L
17	Pf_09_000634010	9	634010	rs45408065	N	ND	2	PFI0725c	T/C	7	0.429	C			T	C	T				T	T								C	1			2	1	4				1	1							1	S			N	S	N				N	N						S
18	Pf_10_000082376	10	82376	rs45409692	I				T/A	4	0.5	A								T	A									T	1								1	1								1																		
19	Pf_10_001403751	10	1403751	rs45410415	N	ND	1	PF10_0344	A/C	9	0.333	A		A		A	C	C	A	C	A						A				1		1		1	13	1	2	1	1					2				T		T		T	P	P	T	P	T					T			
20	Pf_11_000117114	11	117114	rs45415497	N	ND	2	PF11_0037	G/A	7	0.429	G				A			A		G	G		G						A	1				2			1		1	1		2					2	S				F			F		S	S		S						F
21	Pf_11_000406215	11	406215		N	ND	1	PF11_0108	A/C	12	0.417	A	A	C	A	A	A		C		A	C		A			C			C	1	1	3	1	2	6		5		1	3		1			4			2	N	N	H	N	N	N		H			N	H			N			H
22	Pf_13_000158614	13	158614	rs45422484	S	4	3	MAL13P1_15	C/T	7	0.286	T		T		C	C		C	C							C				1		1		1	1		1	1						3				T		T		T	T		T	T						T			
23	Pf_13_001429265	13	1429265		N	ND	2	MAL13P1_176	T/G	12	0.417	T		T		T	G		G	G	T	G		T	T		T			G	1		1		1	1		1	1	1	1		2	2		2			3	N		N		N	T		T	T	N	T		N	N		N			T
24	Pf_14_000755729	14	755729		N	ND	2	PF14_0177	T/G	10	0.4	G		T	G	G	T	T	T		T						G			T	1		1	3	2	11	1	2		1						1			1	R		I	R	R	I	I	I			I				R			I