Appendix 1 – Height thresholds for automated microsatellite analysis

Marker	%OfHighest <sup>*</sup>	%OfMinus3 <sup>*</sup>	%OfPlus3 <sup>*</sup>	%Of(Minus3 + Plus3)*	%OfPlus6 <sup>*</sup>
TA40	2.5	5	7	10	-
TA60	2.5	-	11	8	-
TA81	2.5	3	15	9	3
PfPK2	2.5	-	16	4	4

<sup>\*</sup> Each threshold defines the relative height a given peak must attain compared to other peaks in the sample. If a peak is below any threshold, it is filtered out. %OfHighest = height as a percentage of the height of the highest peak in the sample; %OfMinus3 = height as a percentage of the height of a peak located 3 bases shorter, if present; %OfPlus3 = height as a percentage of the height of a peak located 3 bases longer, if present; %Of(Minus3+Plus3) = height as a percentage of the total of the heights of peaks located 3 bases shorter and 3 bases longer, if both are present; %OfPlus6 = height as a percentage of the height of a peak located 6 bases longer, if present.

Appendix 2 - Detailed results for detection of laboratory clones

	Labo	ratory cl	ones pre	sent in s	ample (	oarasites	s/µl) <sup>*</sup>	Clones	s missed b	y geno	typing	at each	locus <sup>†</sup>
#	3D7	FCR3	HB3	K1	W2	V1/S	<sup>'</sup> Total	msp1	msp2	TA40	TA60	TA81	PfPK2
1			Negative	Control			0		-				
2	50						50						
3		50					50						
4			50				50						
5				50			50						
6					50		50						
<u>7</u> 8						50	50						
8	500						500						
9		500					500						
10			500				500						
11				500			500						
12					500		500						
13						500	500						
14	5,000						5,000						
15		5,000					5,000						
16			5,000				5,000						
17				5,000			5,000						
18					5,000		5,000						
19						5,000	5,000						
20	50,000						50,000						
21			50,000				50,000						
22					50,000		50,000						
23			2,000		1,000	7,000	10,000						
24			1,000		2,000	7,000	10,000	1440					
25			7,000		1,000	2,000	10,000	W2					
26			7,000		2,000	1,000	10,000	W2					
27			1,000		7,000	2,000	10,000						1.100
28			2,000		7,000	1,000	10,000						HB3
29			10,000		5,000	35,000	50,000					LIDO	1.100
30			5,000		10,000	35,000	50,000	14/0				HB3	HB3
31			35,000		5,000	10,000	50,000	W2					
32			35,000		10,000	5,000	50,000	W2					LIDO
33			5,000 10,000		35,000	10,000	50,000						HB3
34					35,000	5,000	50,000	207	ECD2				HB3
35	50 500	50 500	50 500	50 500	50 500	50 500	300	3D7	FCR3				
36	500 5.000	500 5.000	500 5.000	500 5.000	500 5.000	500 5.000	3,000		FCR3				
37	5,000	5,000	5,000	5,000	5,000	5,000	30,000	FCR3	FCR3				
38 39	10,000 15,000	2,500 2,500	10,000	2,500 2,500	2,500	2,500	30,000	FURS	FCR3,K1				
	2,500		5,000 30,000	2,500 10,000	10,000 2,500	15,000 2,500	50,000 50,000	FCR3	FCR3,K1 FCR3,W2	3D7			
40 41	2,500 5,000	2,500 5,000	25,000	5,000	2,500 5,000	2,500 5,000	50,000	FCR3	FCR3,W2 K1	307			
41 42	5,000 5,000	25,000	10,000	2,500	5,000	2,500	50,000	FURS	K1 K1			K1	HB3
42	2,500	25,000	2,500	10,000	2,500	30,000	50,000	3D7	FCR3	3D7		HB3	HB3
43 44	2,500	2,500	2,500	30,000	2,500	10,000	50,000	3D7 3D7	I CR3	3D7	3D7	пвз 3D7	HB3
44	2,500	2,500	2,500	30,000	2,500	10,000	50,000	307		301	307	307	пвэ

<sup>\*</sup>For each sample #1--44, the composition of laboratory clones is denoted by listing the parasite density for each clone present in the appropriate column, with total parasite density indicated in the last column

<sup>&</sup>lt;sup>†</sup>If alleles of laboratory clones present in a sample were not detected by a particular locus, the names of the corresponding missed clones are indicated

Appendix 3 - Detailed results for detection of false positive alleles

	Laboratory clones present in sample (parasites/µl)*							Number of false positive alleles <sup>†</sup>					
#	3D7	FCR3	HB3	K1	W2	V1/S	Total	msp1	msp2	TA40	TA60	TA81	PfPK2
1		Negative Control 0											
2	50						50						
3		50					50						
4			50				50						
5				50			50			1			
6					50		50		1	1			
. 7						50	50			1			
8	500						500						
9		500					500						
10			500				500						
11				500			500		2				
12					500		500		1				
13						500	500						
14	5,000						5,000						
15		5,000	<b>5</b> 000				5,000						
16			5,000	F 000			5,000		0				
17				5,000	F 000		5,000		2 2				
18					5,000	E 000	5,000 5,000		2				
19	50,000					5,000	50,000						
20 21	50,000		50,000				50,000						
22			30,000		50,000		50,000		2				
23			2,000		1,000	7,000	10,000		2				
24			1,000		2,000	7,000	10,000	1	3				
25			7,000		1,000	2,000	10,000	'	2	1			2
26			7,000		2,000	1,000	10,000		1				3
27			1,000		7,000	2,000	10,000	1	3				Ü
28			2,000		7,000	1,000	10,000	1	2				
29			10,000		5,000	35,000	50,000		3				
30			5,000		10,000	35,000	50,000	1	3				
31			35,000		5,000	10,000	50,000		3				3
32			35,000		10,000	5,000	50,000		3	1			3
33			5,000		35,000	10,000	50,000	1	3				
34			10,000		35,000	5,000	50,000	1	3	1			
35	50	50	50	50	50	50	300		3				1
36	500	500	500	500	500	500	3,000	1	3				
37	5,000	5,000	5,000	5,000	5,000	5,000	30,000	1	3				
38	10,000	2,500	10,000	2,500	2,500	2,500	30,000		2	2			3
39	15,000	2,500	5,000	2,500	10,000	15,000	50,000	1	2				
40	2,500	2,500	30,000	10,000	2,500	2,500	50,000		1	1			4
41	5,000	5,000	25,000	5,000	5,000	5,000	50,000		2	1			4
42	5,000	25,000	10,000	2,500	5,000	2,500	50,000		2				
43	2,500	2,500	2,500	10,000	2,500	30,000	50,000		2				
44	2,500	2,500	2,500	30,000	2,500	10,000	50,000		2				

\*For each sample #1--44, the composition of laboratory clones is denoted by listing the parasite density for each clone present in the appropriate column, with total parasite density indicated in the last column

<sup>&</sup>lt;sup>†</sup>If alleles were detected not corresponding to laboratory clones present in a sample, the number of false positive alleles are indicated