

Supplementary material

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Supplementary table 1

Supplementary table 1. Primers designed in this study

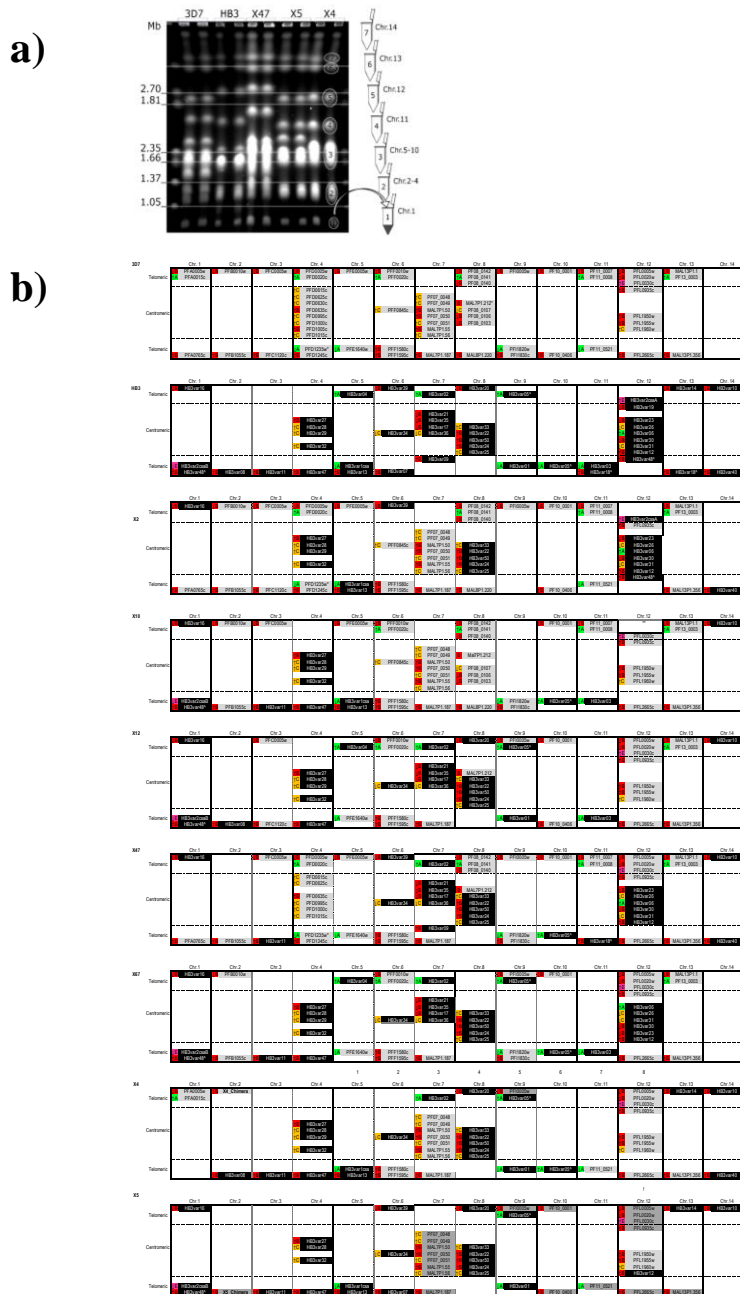
D) Quantitative real-time PCR primer pairs for chromosome mapping of var genes			
Chromosome	Gene name	Forward primer	Reverse primer
Chr.1	FA0590w	CAGTGGGTATGGTGAATGTA	CCTGATGAAGAAGGAGGATGC
Chr.2	FFB0490c	TCAAGCCOCCGCGA CGAT GT	CCAAAACCTCCAGTTGCTCC
Chr.3	PF02615w	GAACAACCTTCAAGGCA TCAAG CG	GTITTAATTCITTTTGAACAACA CG
Chr.4	FFE1640w	AATACGACGCGTGGTCTT	CTCTGATACCTGCTGCTT
Chr.5	FFE0330w	AATACGACGCGA GCA TAA TCC	TCCTTATCTCTTATGATTC
Chr.6	FF0565c	ACTCCAGAA TTTGAAAGTCCTTG	GTCTTGGGAAGCA TTTGGACCC
Chr.7	PF07_0073	AAATGACAGGCTCATCTGGTGT	TTGSSGCA CATCTTCCATCA
Chr.8	PF08_0118	GAACAACAAAGCA TCGA CGAC	GGCATTAATTTGATGTC TCCGCG
Chr.9	FF1590w	AACAGACGACCA TTA TTA TCG	TTGCTATTTTGGTATATCTCCCG
Chr.10	FF10_0027	ACTCAGGCA TTA TTA TCG	TTGGTGCCTTTTATCTCT
Chr.11	FF11_0481	AGCCCGA TGGCGGTGATGGTGT	CTGTGCA TAAACGAGCAAAAACCA
Chr.12	FFL1510c	TGCGCAATGCTTTTGGTGTCTG	ACATGATAAAAA TGA TCTCTCC
Chr.13	MAL13P1_151	AA TGGCGTGTGATGTCCTT	ACGATGCACTTGGTCTT
Chr.14	FF14_0425	TGTA CCAACA GCGCTACCGA	CTTCTGGCA TGTGTCATAT
	FFA0005w	CTCGTGTGATGATGCTGAGG	CCAGTAA TCGCTCAAAA TGTAT
	FFD1005c	CCATCA CGAAGA ACAA GAGCG	TGGGTGATGCTCTTGAAGC
	PF01245c	GGAT TGACTA TAA GGA TCGA AAGAC	GTGCGACTGTTCTCCACTGACA
	PF07_0048	CGGA AACA CTA GCGA CCGATG	ACGATGCACTGCGGCA ACGCG
	H3var2cSaB	AGTCAAGCACTATGTGATCA	TTCCATGAGTGAATTTGCTG

D) Quantitative real-time PCR primer pairs for var exon 1 extremities					
Gene	Gene name	5-end primer pairs	3-end primer pairs		
Qlone:	Gene name	Forward primer	Reverse primer	Forward primer	Reverse primer
3D7	PF10_0408	GTCCACCAAA GAAAGCACTCA	A CCA AAA CTCTCTGCCCA TT	GAT TGA TCGAT A TCCCTTGAA G	TTGTCCTCTCTGCTTCCAC
3D7	FFL0200w	TGCA TTA TGTGCGCGATGAT	TTCCGCTA GCA TGTGA TCCA	CATCGGCTCA GATCA CACTC	CAGATATGCGAT TGAACGGTT
3D7	MAL13P1_356	COGAA TAT TGTCCCTTCA CA	CATTTGCCCA CCA A GTGTA TC	ACCAA CA TAGCGCA A TCCAC	GTGGGCA TCTCCCA GAA TCTTC
3D7	PF01235w	AAACA GCGT TGA TGGCGCA TA	GA CGCGCA GGA GGTAAA TAG	ATCGA GGGGGGA GGTAAA AAC	ATCGA GTTCCGA CGGAT TTCC
3D7	PF01245c	AAAGAA GCGTCA CA TCC	CGTCTGCTGCTGCTGCTGCTG	TTCTGCTTTCA GCGA GGA C	ATCGA CA TAA CA TAGGCTG
3D7	PF08_0142	CTGTGTGGA AAA CGAA AAGT	TAT TCA TCCAGGGCCAAA AG	AAAGTGGGAAA ACAA CGCAT	AAAA CACTA TCGA AGTTA AGC
3D7	PF08_0107	CCTGAAA AAGGA CGGA GCGT	CGA GGA CA CTA CCA CCA GT	CCAGTGA GGA CCA AAA AAG C	AGTGA AACA GCGA AAA A C
3D7	PF08_0140	TCA TTA TGGGAAA GCA CGAT	TGAA TTTCTCA CTA TCGGAA CT	TGGAA CTA TCA TCGGAAA AAT C	CAAAA TAT TCCCTCTGGTATCC
3D7	PF08_0140	AT TGGTGGCA AACTTGTGAT	TTCAA TGGTCTCTGTA CA	ACA ACGA GAA ACAA CCGAAA C	TTCTCCGCA CATCTCTGTCT
3D7	FFA0005w	CTCGTGTGATGATGCTGAGG	CGA CCGTAA TCGCTGAT TGGT	AAC TCA GGA A GCGA GAA GAAC	GTGTGTGTTTGGTGGTGGTCCA
3D7	MAL7P1_212	CTCGTGTGTTGGGGATGACTAC	GATCTGTGTGCA CCA C GTCCCTG	GTA TGA C TCGT GAA AAA AAGTCCG	CTTTTTTCTTCA CCA CCGAC
3D7	PF02625c	CTA CGAAA AAGTCTTCTGGTGG	GGTCTCA C TCTCTTTCTGGTGG	CGTA CAA CA GAA CCA A AAG GG	AGTGA AACA GCGA AAA A C
3D7	FF11_0008	GGGTCA CAA CA TCA AAA ATTTTC	TTCCGA TCTCTGAAA TTTCCG	GA CGGCTCA CCA CA GAA GAA	CGTCA TCA TGGTGTGGTT
3D7	FF11_0008	CGTGGTGTGAT TGA CGA TCA CCG	CGTGGTGTGAT TGA CGA TCA CCG	CGTGGTGTGAT TGA CGA TCA CCG	AGGTTA TTTGTTGTA TGGT
3D7	FF00100w	CGCAAG TCTCTCA A CAG A GT	CGGCAAAA TGA TCGCTCTTC	ACTAA TGGCGCTGAAA AAGT	CGAA CCA A GCGA AAA A C
3D7	MAL7P1_55	GTGACGCTCTGAT TACTAA AC	CATTTTGA GCA TCTACTATGATC	GATCA CCGTCA CCA CCA TCT	GTGGGA TGGGTATTA AAGT
3D7	MAL7P1_55	CGCA CA GGA GTG AAGTGGTCTG	GTITGTGAG CCGCTGCTGTC	TAGA TGA CA CCGTCTGCAA	AA TAAA AAGCGCA A TGAAGTC
3D7	MAL7P1_58	TGCTGA TGGTACTG TAAA AAA TA	TTTA TTA TGGTCA TCTCTGTC	TCTGTGAA GAA A CCGCA CA	TAAA AAGCGCA A TGAAGTC
3D7	PF07_0048	CGGATGCA CTA GCGA CCGATG	CGA CCGTAA TCGCTGAT TGGT	TTCTGTTGTTTCCCA A GGGT	GTGTGTGTTTCCCA A GGGT
3D7	PF07_0050	GA TCTGGA GGGAAA AAT TTA G	CATCTTCTCA CTA CCGTCTG	CGGCA AAA C TCGTCA C TCA C	GA CAA A A C TCGTCA C TCA C
3D7	PF07_0051	CA CCGA TAA CCA TCGAA TTTGAT	GGCCCAAAA TCC TTA TAA TCG	GAA CA GAA GAAAA A CCA GAGG	GGGTTTTCTTGGTGGTCTTC
3D7	MAL7P1_187	TTTGGCA TAT ACTGCTGCA TC	GCTCTCTCA CTA TACTCA ATTC	TGGA CGA GAA TAA A TGGGAA GT	TTTGGTGGGA GGGG GT
3D7	PF08_0103	CGGCTCA GGA GCGTGTATC	GAA GAA TGA TGA TTTGGTGGG	GTGCA TTA TGA GAT TGA GATG	GGTGGTTTA CCA TCA TCTGTAT
3D7	PF08_0108	GTAA CCGTGT TTA CCGA CAGAC	GA CCGTGT TTA CCGA CAGAC	TTCTGCGA GAA GCA TGA C	CGAA CCA A GCGA AAA A C
3D7	PF11_0007	CGTGGCA GT TTA TGA AGCTTTCAC	TAAT TGGGAAA GCA GCA TCA TCC	AATGGA TGA CCA GCAA AACCA	TTCTGGTGA CAA TGGTGTGGT
3D7	FF11_0521	CGGA TCGCA A TCA CCA GCGACTC	CCTA TAA TCA GAA TCA CCA GGGCT	GATCA GA GAA A TGGCGGCT	TTCTGGTGA CAA TGGTGTGGT
3D7	MAL13P1_1	C TAA CAT TGGGCGCA C GAA GCGAC	GTGAGGTTGAT TACTGCTCA TGGT	ACA AAGGA A GCTGCA TCTCC	GGCAA TACTCCCA C TGA TGG
3D7	PF11_0521	AA TGA GAA TGA GCA TGA TGA GCG	AA TGA GAA CTTTAA TCGCTGAT	TTCTGCGA GAA GCA TGA C	CGAA CCA A GCGA AAA A C
3D7	FFA0785c	AA TGA TAA AAG TCCAAA AATGCG	ACTTCTCA C GAT TCGCTCTAC	ATGA C TGTG TGA CAA CAG	CGAA TGA A GCGA AAA A C
3D7	FFB0010w	TA TGGTGGGGGA TA GTTCA C	A TACTCTTGA CCAA AACA CCG	GATGTA TCA A C TGGGTA A G	CCACA CA TCGA TA TGA
3D7	PF00005w	GGAAA AATG TCA CGA AAA AAGC	TA T TCCCTGCTGTTTGTGGC	GAA GA TAGTGA TCGGAGGA	AA TAAA AAGCGCA A TGAAGTC
3D7	PF01220c	CGGMAA A GAA C TCGTCA TTAGT	TTGCTCGCA C GGA TCA AAT TGG	GA AAA GGGTGA A GGA TCA C	AA CCA A GCGTGA A AAGGGT
3D7	PF00005w	CTGGA TCGA GCA GGA GCGA CCGG	TA TGGT TAA TTA TTTGGTCTG	GA A A A CCGC CCGTCA CAG	GAT CCGGCTA CTTTCA
3D7	PF02002c	GA GCGGA TTTA TCA G A GCGA C	CGATGA CCGCTTA TTTA CCA TGT	AAA A GAG TCGCTCTCA C	TTTCTCA AAA A TAAA A GCGCA
3D7	PF02005c	GTGGTGA TGGTGGTGTACTGCTG	GCA TCGA CTTAA TGA C TGTG C	CGA C TGGGCTG TGA A TAG	TTTCTT TGA GAA A G T A C TCA C
3D7	PF02005w/MAL13P1_1	GGTAT TACTGCTG CCGA GGG	CCCGA TTTGGT TCGCA CCA AG	ACTGA TAA GCGA AAGCGTGG	CAGGGGTGAT TCTTCA GAC
3D7	PF02005w	CAATTTCA GGTGAT TGA C	CGCTTGGT TCGCA CCA AG	CGA TAA A GCGC CCA A A G C	ACTCGA C ATG TGGTGA A G C
3D7	FF11530c	ACGGA TAA GTA TAA AAT TCCCAAG	AGGCTGTA A C TTTTCCCTCG	GA C C TGGCTGCTGAA GAC	AA A CCGTGA C TCA C TCTC
3D7	FFL0030c	GTA TAA TCA GAT TGTCA A C	CATA GGA GGTGTAT TCTA	GATGA TCTTGA C TGA ATG	TTCA C TCA GAA A TCGCGAG
3D7	FFL0935c	CAAAA GGT TAA GTGAAA AATGGT	GA GCGGCA A CCA CCA AATG	GGGA GCGA ACAA AATATAG	AGCA CCA C TCA CAA ACG
3D7	FFL1960w	GGAA C A GGA A A GAA A GCGTTC	A TCA CTTAA TTT TTTTCTTCA C	CAA TA STGA CACA CAGCA	GTCCA GSTA TGA C TGTAG C
3D7	PF01245c	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	TAA AAA CCGC CCGTCA CAG	ATGA TCGTCA TCGTAA CCG
3D7	PF10_0001	AGG TAA A GGA GGT A AAGCTG	CGTGTGCA GAT TGA TGA AAG	TTG TAA A CCGA CAGCA GCA CCA	ATCGCA GCGCA TACTCTAA G
3D7	PF07_0049	TAT TATGGTGA TCTCTGCTTGG	TCTA TAT TGGGGA CAGGCTC	GA GGGAA C GAG TGA CAA GTG	TTTGGTGTGTTGTTGACT
3D7	PF08_0141	AACTGCTGGA TCA GCGGAT	CGA AACA TATTGGCTGCTC	CCTGAT TCCCAA TTTCTCT	TTTCTT TGA AAA AAG ACGCT
3D7	MAL13P1_220	GTCTCTCA TGGTGA TGA AAA GAA	AGTACGGT TACTCTGTTA TGG	CAAA A GCA TCGTGTGA A GATC	CTTCTCTT TGA CAA GGGTGTG
3D7	PF02005w	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CGCTGCA GAA A CTTTCA C	A TCTTTT TCGCA T TGA C TTTCT
H3B	H3Bvar16	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	GA A TAA A TGA TGT TGA TGG	A TCTTT TCGCA T TGA C TTTCT
H3B	H3Bvar18	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	TGACTTCA TGA A C A C TCTCTCA	CGAAA A C A C TGA C A A A G
H3B	H3Bvar2cSaB	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CCTA TGA A C TCTGGA GAA A C	GGAA C GGA A A GGA TGA A C T
H3B	H3Bvar18	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CAT TAT TGTAA CCA C TCTGAC	GA TGGTAA G A G A C TCTGAC
H3B	H3Bvar22	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CGAA A G TGTGAA A TGA C A G	GCTCA CTA C A C TGTG A A C
H3B	H3Bvar29	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CA TTTTGA TTA G TACTA C T A C	TTTCTGTAT CA CCGT TGA
H3B	H3Bvar13	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	GAA T TCTGCT TGGTAAA TCC	CGCTA TAA A C T T A A C GCGS
H3B	H3Bvar13a	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CA CCA C C T T A T A C G C C A C	TTTA CCA C A T T T T A C C T T A C
H3B	H3Bvar17	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	TC A T T T G T T T C T G A T C T	GT T T G A C T G T T G C C A C T
H3B	H3Bvar26	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CTGCA G T C C T G A A C T G A A	TTG T T G G A T T G G G G T
H3B	H3Bvar19	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CGA A C C A C T G G A A C A A A C	TTG T T G G A T T G G G G T
H3B	H3Bvar18	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	AGCTGCA GAA TCCCTGATAAA	TTG T T G G A T T G G G G T
H3B	H3Bvar10	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	TTGGA TGA A A T GCGTAA A G A G	AGG T T A A G G G T T G T G A T G
H3B	H3Bvar11	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CGA CCA C C T T A T A C G C C A C	TTTA CCA C A T T T T A C C T T A C
H3B	H3Bvar21	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	AG A TGA TGTGAAA A G T C A A A G	GT T T G A C T G T T G C C A C T
H3B	H3Bvar35	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CA G A A C C A C T G G S G A C C	TTG T T G G A T T G G G G T
H3B	H3Bvar2cSa A	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	AAA C G C G T G G A G G A G A C	CG T G G G T A C T C T G G T
H3B	H3Bvar31	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	AAA C G C G T G G A G G A G A C	AAA C C C C A G A C T A C A G
H3B	H3Bvar11	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	ACA T C T G G T T A T G T T G T G	GG C T T A A A C T T A T T C T G C
H3B	H3Bvar25	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	CGA A A T G T G A T G T G A T T C	TCA T G A C T G C T C T A C C G T
H3B	H3Bvar34	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	GA A C C A C G T T A T A T G A T T	T G A T T G G A A A G A G C
H3B	H3Bvar01	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	AAA A G G G G A T T G A A T G A A A	CG G T T G C A C T C T C A A C
H3B	H3Bvar27	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	C T T A C T G A T G A A C A C C G	T T C C T A C T G G T G G T G T G
H3B	H3Bvar02	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	T T T T A T T G C T C A T G A A G G	CG C C T G C A C A C T C T C T C
H3B	H3Bvar06	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	T G T C T C A C A C A C A C A A G	T G C C A C A C A A T C C A T C A C
H3B	H3Bvar30	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	C A C C A C A G A A C C G G A A A C	T A G G A T G T A G T G S A A A G T
H3B	H3Bvar12	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	G G T G T A T G T A G G G A T G C	T G A C C G G G A G A A G A T C C A
H3B	H3Bvar03	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	C C T C A G A A G G T A C T A A A C	T G C T G C A G A T C T G A A T T
H3B	H3Bvar36	CGTGTGCA GAT TGA TGA AAG	CGTGTGCA GAT TGA TGA AAG	AAA A G T T G T T T A T G A C T C A G	T T G A T G A C T G G G C A A A G G

C) Full exon 1 var PCR primer pairs and application of amplified fragment

Application	Gene name	Forward primer	Reverse primer	Amplified from (genome):
Sequencing	PF1_0008	AATGATCA TTTGCA GCGTGGTCT	CACTG TGGCCCATCTTGGCATATC	
Sequencing	PF08_0141	TAA TGGTGTG TGGCGA CCGCT	GGGGGTGAGGTTTGGTCTGAC	
Sequencing	PF01640w	ATCA TCA GAGGGGGCTAAAA TCC	CGTTGAACCTTAA CCGTGA A GATG	
Sequencing	PF13_0003	TAA CAGTGA GAGCCCAAAA CCGG	CGTGTCAAGGA TCAAGTGAATG	
Sequencing	PF01235w	CAT TGA GGGGGGAGGGTAAA CCG	C T C T A T T T G A T T G A C T C T G G	
Sequencing	PF02005w	GTA GCGCA TTTA TCA G A CCGA C	G T T C T G C T G C T G T G T G C T G	
Sequencing	PF11_0521	GAA TCGA A TCA GCGA CCGTCCG	TTCTGTGCA C A A C T T T T G G G T	
Sequencing	FF00100w	TTTTGGGGGAAA CCGA GCGAC	CACCTGCA GTCGAA CAA TGGCA	
Sequencing	FF1580c	TA GCGTGGTGA TGA C GCTGATG	GAA ACAA A GGGGTTCTA C TCGA C	
Sequencing	PF08_0140	TTCCCTGCTTCCCTTCCCTC	GAA TAA TGGTGA GGGGGGGTGG	
Sequencing	MAL7P1_187	CTCGTGTGATGATGCTGAGG	CGTGTGCA GAT TGA TGA AAG	
Sequencing	PF02005c	G T C A G G T G G G A T G A C T G T G C	T G C T A T T A C G T G C A C T G C	
Sequencing	PF02015c	CGCGGCAAA G T A TGGGGTATG	AA C A C T G A A A G T C A C A G G	
Sequencing	FFL0030c	CTTA CCGCA GAA A TGA AAGAG	G T T A C T T G A A A T T G A A C G	
Sequencing	H3B var2cSa B	CAGTTTGGTGGGGA TGA C TCA CAG	T T C A C T T G A A A T G C C A C G	
Sequencing	MAL7P1_212	GCTCTGCGATGATGCTGGTGA	GTGCGGGGGTGA TGA CAGAT	
Sequencing	PF02005w	CGCAA TTA TGGTGA GCA C GGA GGT A CCGG	GTG TGGT TGGG T T G T G T T C C A	
Sequencing	PF02005w	G T A A G A C T G A C T A A A G A T G C A T C	GGC CCG GCG G T G A T T G G G G T C T T C A T C	
Sequencing	PF13P1_356	GCTCTAGA CAA GGA GGT A GCGGTGA TCCG	GGCGGGCGCA C T C T C T G T T G T T G T T C A G	
Sequencing	MAL7P1_55	GCGA GGA GGT A GCGTGGTGG	TG T C A C T G T T G T C G C G G T T G C	
Sequencing	PF02005w	G A C T C A A T T T C A G G T T A T G A C	T G C G T T C T T G G C G C T T A T G	
Sequencing	PF10_0408	TGGA TCA CCA C T G C C A A C A C T G	TTTGA TCA CCGGGCTGGTCTTC	
Sequencing	PF08_0103	GTGACGCTAGGA GGTGATCTG	TTTTGGTCTTGGTCCACTTTGG	
Sequencing	PF02020c	GGA TCA GAT TAT TCGTCA CCA GGG	GGCTCGA A A C A A C T C T A C A A G	
Sequencing	MAL7P1_50	TGGA A A G T G T G A G A T G A C T G T C	A G T T C T G T G C T T G C A C C A C T	
Sequencing	MAL7P1_50	G T A A A G C A A G A G T A A G A G T C	G T T C T T G T G A A T T G T A A C G	
Sequencing	FFL0935c	A T G T T G C C A G C G C C A A G T C	G T T C T T G T G A A T T G T A A C G	
Sequencing	MAL13P1_1	GGGAA T TCA C T A A C T G G A G G G A C A A G C A C	G T T C G C G C G C A C C T C T T T G C C T C A C T A G	
Sequencing	PF08_0106	AGTAA GGGTGA TTTGA CAG A G A G	C C A C A C T G A T T G T G G T A T C	

Supplementary figure 1

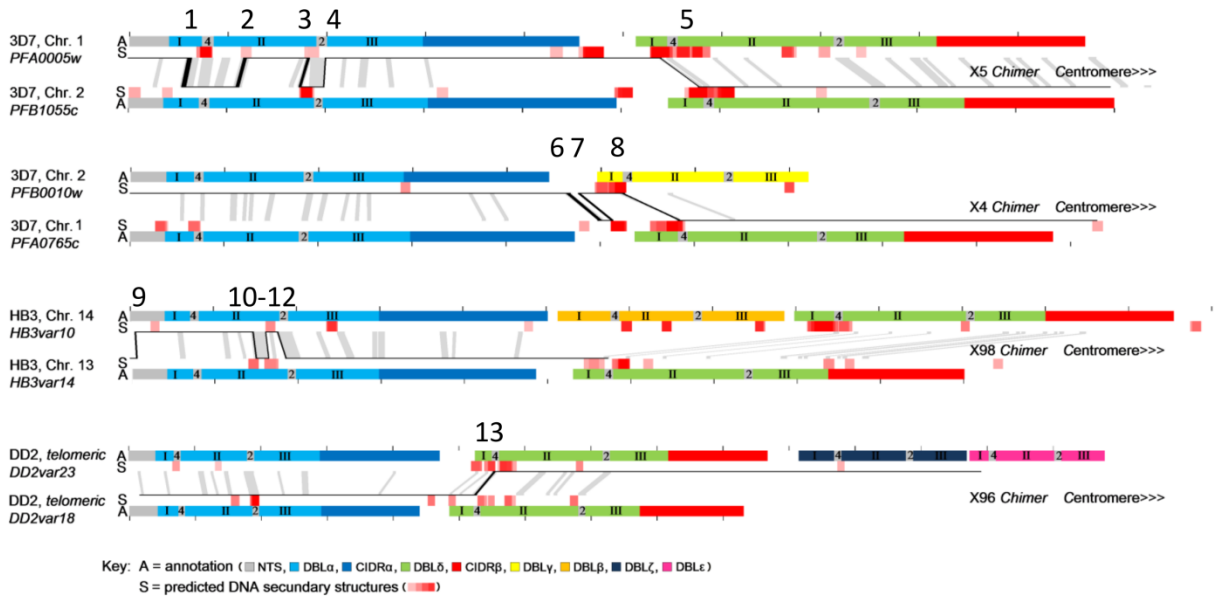


Supplementary Figure 1 | Parent and progeny karyotype and chromosomal positions of *var* gene repertoires of the parental and seven progeny clones

a) Pulsed Field Gel Electrophoresis (PFGE) karyotypes of parent (3D7 & HB3) and three progeny clones (X47, X5 & X4). For illustration chromosome excisions used for X4 *var* mapping using QPCR are shown. **b)** Chromosomal positions of 3D7 (gray) and HB3 (black) *var* genes and their inheritance in seven progeny clones X4, X5, X2, X10, X12, X47 and X67. The chromosomal orientation (arrows) and *ups* promoter type (*upsA*: green; *upsB*: red; *upsC*: yellow) is shown for each gene. Solid black vertical lines indicate chromosomes within each PFGE separated chromosomal excision. Horizontal dashed lines delimit the centromere and telomere-proximal chromosome regions. Mapping estimates are based on QPCR data and chromosomal locations and orientations of specific genes and *ups*-types from 3D7 and HB3 genome assemblies (PlasmODB and Broad institute [6,12]). The analysis of the *var* gene segregation in progeny clones illustrates the plasticity of *P. falciparum*'s telomeric regions and that meiosis imposes a Mendelian inheritance of *var* repertoires.

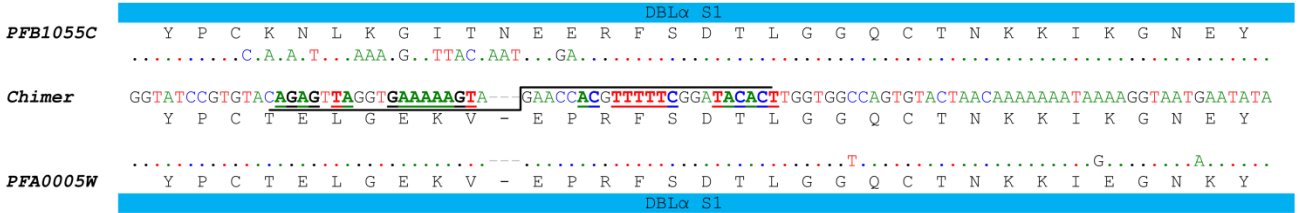
Supplementary figure 2

a

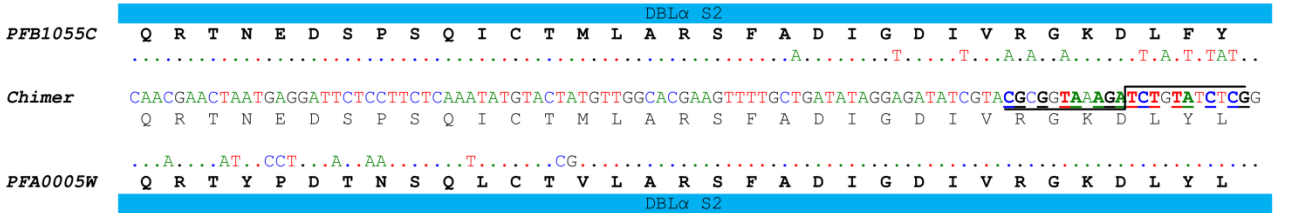


b

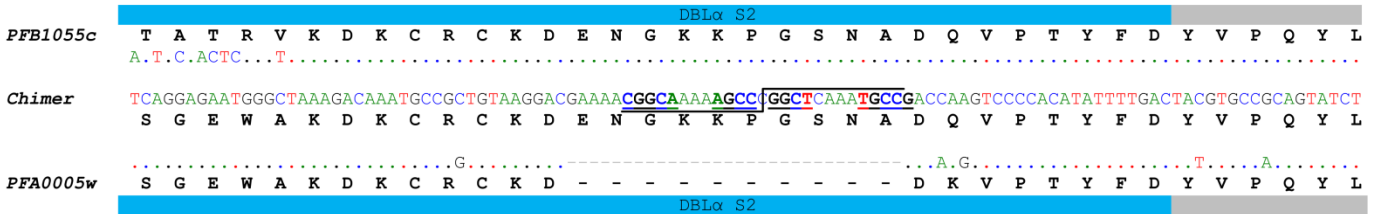
Recombination Site 1



Recombination Site 2



Recombination Sites 3 & 4



HB2 DBL α S3
PFB1055c R W F E E W A E D F C R K K K K K L E K L E Q Q C R
GAA..AA...A.G.....G..A.GTTGG..C.AC.G.....C
Chimer TCGCTGGTTCGAGGAATGGGCAGAAGACTTTGTAGATTAAGGAAACATAAATAAAAAGATGCTAAAAACAAATGTCGT
 R W F E E W A E D F C R L R K H K L K D A K N K C R
C.....T.....
PFA0005w R W F E E W A E D F C R L R K H K L K D A K N K C R
 HB2 DBL α S3

Recombination Sites 5

DBL δ S1 HB4
PFB1055c W K C V S S G E K S V A T A G S S G A T G K S G D K G A I C V P P
A.....AT..AGTGGTGA AAAAGTGTGTG..C.C..CCGGT.GT.....GTG.....
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T.....C.CCACC.GTGG.A..A.TTGTGTG
PFA0005w W K C V T - - - - - P S G N T S D T T V K S G D T T G G S I C V
 DBL δ S1 HB4

RECOMBINATION SITES 6 & 7

inter domain region
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A.....C.GC.-----C.GCCG..G.AA...ACG..ACAGGG.....
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A...TG.GG.T...A..CCG.AGAAGAC..A.....
PFA0765C N T E D D D A E E D E E D E E E E E E E E E K E N A D A G G E D G K E E K
 inter domain region

PFB0010W S E S K E

Chimer GTCGGAGTCCAGGAG
 S E S K E
GAA.....
PFA0765C S E E K E

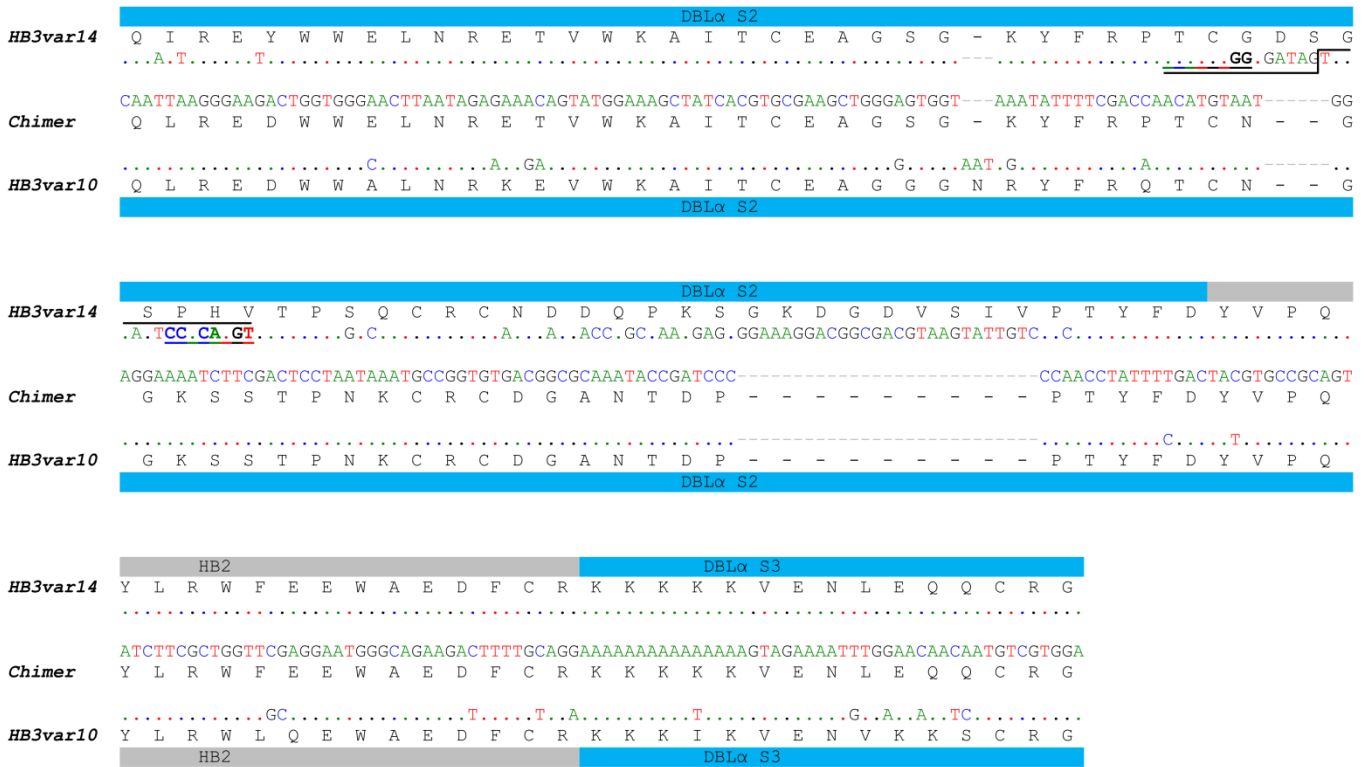
RECOMBINATION SITE 8

DBL γ S1 HB4 S2
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Chimer TATCGCACCTAGTGGTACCCTAGTGGAAAAGACGGTGCTATATGTGTGCCACCCAGGAGACGAAAAC TATACATACAGAAACTACCAGACGTGCAATTT
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 C.C.C.....T---.CC.G....C.....
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 DBL δ S1 HB4 S2

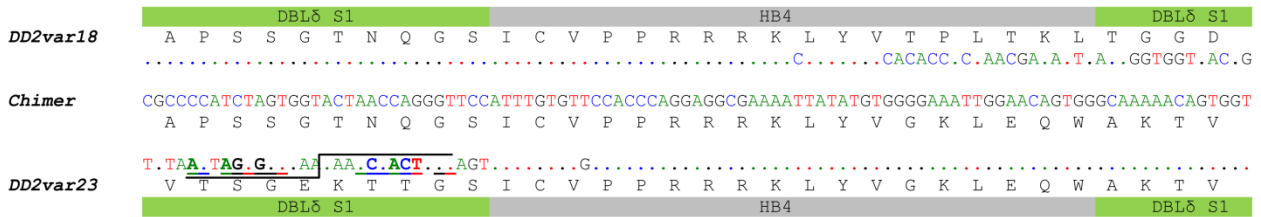
RECOMBINATION SITE 9

NTS
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Chimer ATGGTGACCTAGGAGGTGGTGGTGGAAAGTAGTGGTGGTGAGGATGATATTGATAAAAACA---AGTGC AAAACTTTTATTTGGATAGCATAGGAAAATAG
 M V T L G G G G G S S G G E D D I D K T - S A K H L L D S I G K I
A.A.T.....CTG.....
HB3var10 M V T Q S G G G A G S G G E D D I D K T - S A K H L L D S I G K I
 NTS

RECOMBINATION SITES 10, 11 & 12



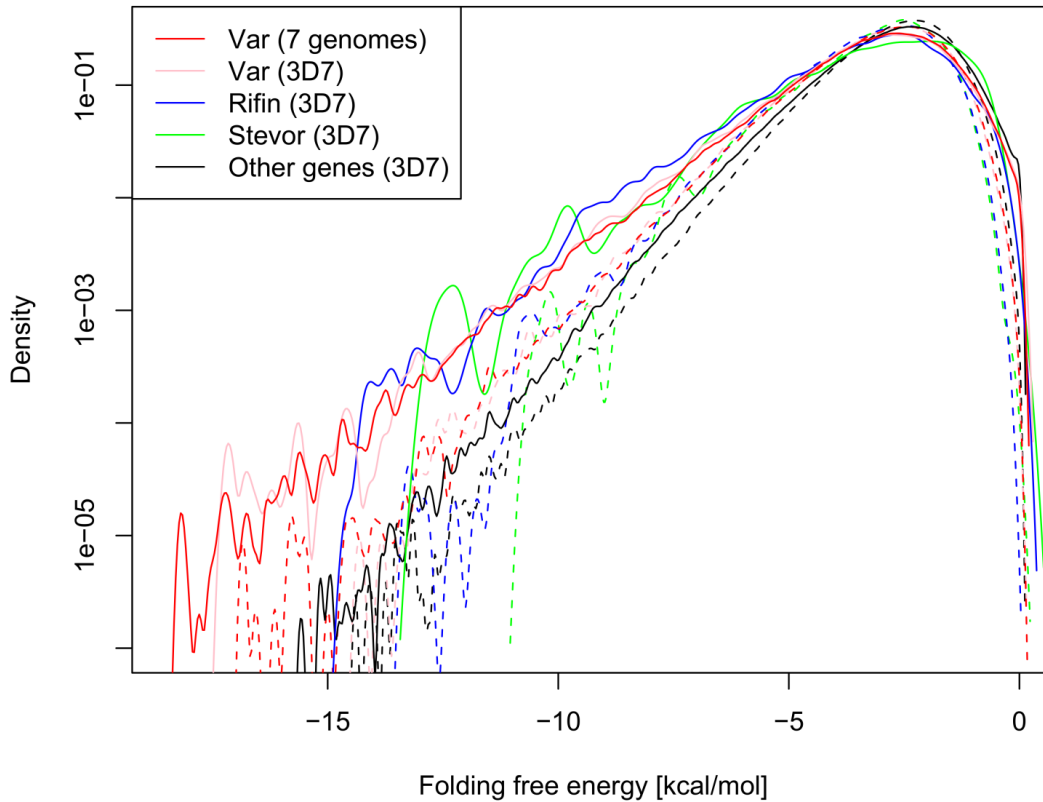
RECOMBINATION SITE 13



Supplementary Figure 2 | Alignments of donor and chimer sequence regions containing recombination sites

a) Schematic presentation of Figure 1 showing numbered recombination sites. **b)** Alignments of DNA sequence regions surrounding each of the 13 observed recombination sites with annotated domains of the encoded protein. Dots indicate base pairs identical to the chimeric sequence. Examples of quasi-palindromic sequences are highlighted by bold and under/over-lined formatted nucleotides.

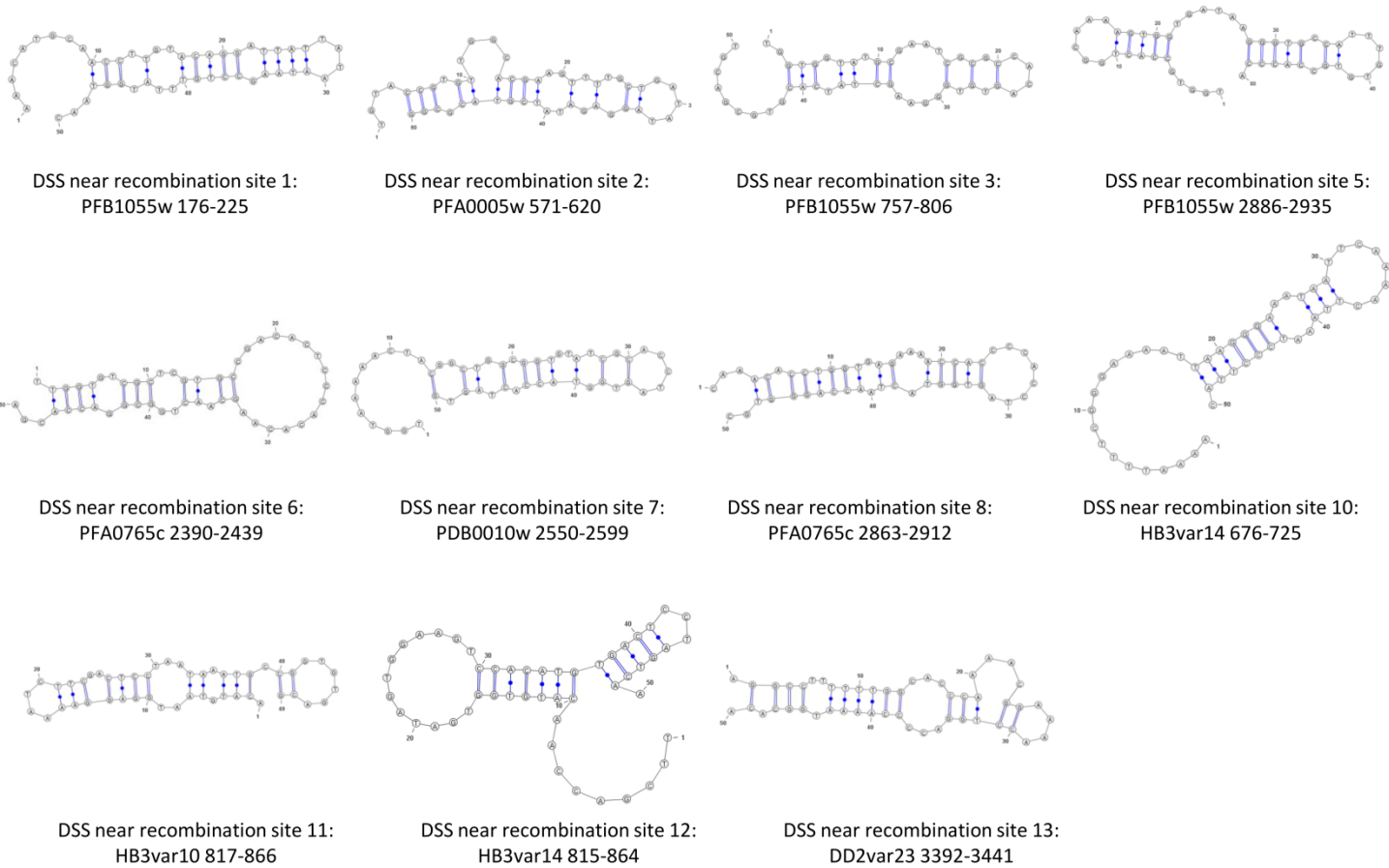
Supplementary figure 3



Supplementary figure 3 | Density distribution of 50-mer DNA folding energies in *P. falciparum* real and shuffled genes

The distribution of 50-mer folding free energies in each of five *P. falciparum* gene groups is plotted with solid lines, while dashed lines show the distribution of 50-mer folding free energies in the same gene groups with each gene sequence randomly shuffled. The folding free energy reflects the probability of a DNA 50-mer to form a DNA secondary structure (DSS); with lower folding free energy 50-mers having higher likelihood of forming DSS. The *var* genes contain the 50-mers with the lowest folding free energies, but all telomeric antigen gene families (*var*, *rif* and *stevor*) contain significantly higher proportions of 50-mers predicted to form DSS (folding free energy cut-off set at <-6.27 kcal/mol) compared to the group of all other *P. falciparum* genes ($p < 2e-16$ for all comparisons). In *var*, *rif* and *stevor* genes, the proportion of 50-mers with folding free energy <-6.27 kcal/mol is 5.6%, 8.2% and 5.6%, respectively. For comparison the proportion of the group of all other *P. falciparum* genes is 2.1%. In all *P. falciparum* gene groups the folding free energy of 50-mers is lower than would be expected from the nucleotide composition alone.

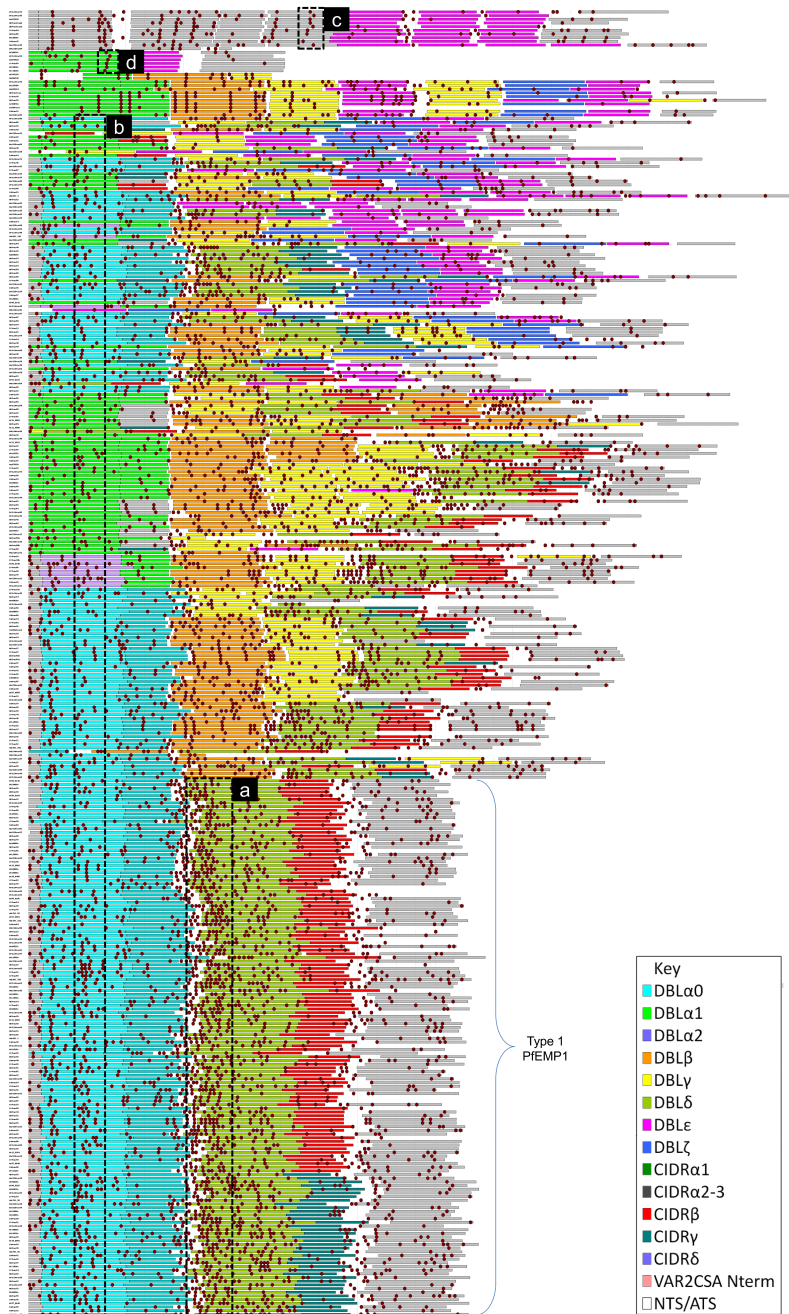
Supplementary figure 4



Supplementary figure 4 | Examples of *var* 50-mer DNA secondary structures

Examples of minimum free energy structures of *var* 50-mers predicted by RNAfold. 50-mers, which are located near recombination sites, and that have a high propensity of forming secondary structures are shown.

Supplementary figure 5



Supplementary Figure 5 | Location of low folding free energy DNA 50-mers in *P. falciparum* var genes

The DNA 50-mers in var genes with the highest potential to form DNA secondary structures (DSS) (folding free energy < -6.27 kcal/mol) are shown as brown dots superimposed onto of 366 domain annotated PfEMP1 sequences from seven different *P. falciparum* genomes (31) originating from Central America (HB3), Africa (PFCLIN, IT/FCR3) and Asia (RAJ116, IGH, DD2). 3D7 is the Schiphol airport canal isolate. For simplicity, only non-overlapping 50-mers are plotted. PfEMP1 are aligned by composition of phylogenetically distinct DBL and CIDR domain sub-classes flanked by N-terminal (NTS) and C-terminal acidic segments (ATS) (see colour code). Frames indicate previously identified recombination hotspots, which are particularly enriched for DSS. These include hotspots in 'mid var gene inter-domain region' (a) [6,7], the boundary between DBL subdomain 2 and 3 (b) (31), DBL3 of var2csa (c) (47) and (d) the first DBL of var3 (31). Plots using varying folding free energy thresholds yield similar results as those presented here.

Supplementary data file 1

Fasta file with chimeric *var* sequences

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