Supplementary Material


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Pv42_vacc      1  EAPEILVPAGISDYDVVYLKPLAGMYKTIKKQLENHVNAFNTNITDMLDSRLKKRNYFLE
Pv19_vacc      1  -----------------------------------------------------------
Pv19_SalI      1  -----------------------------------------------------------
Pv19_PVP01     1  -----------------------------------------------------------
Pv19_Belem     1  -----------------------------------------------------------
Pv19_isolate   1  -----------------------------------------------------------

Pv42_vacc     61  VLNSDLNPFKYSPSGEYIIKDPYKLLDLEKKKKLLGSYKYIGASIDKDLATANDGVTYYN
Pv19_vacc      1  -----------------------------------------------------------
Pv19_SalI      1  -----------------------------------------------------------
Pv19_PVP01     1  -----------------------------------------------------------
Pv19_Belem     1  -----------------------------------------------------------
Pv19_isolate   1  -----------------------------------------------------------

Pv42_vacc    121  KMGELYKTHLTAVNEEVKKVEADIKAEDDKIKKIGSDSTKTTEKTQSMAKKAELEKYLPF
Pv19_vacc      1  -----------------------------------------------------------
Pv19_SalI      1  -----------------------------------------------------------
Pv19_PVP01     1  -----------------------------------------------------------
Pv19_Belem     1  -----------------------------------------------------------
Pv19_isolate   1  -----------------------------------------------------------

Pv42_vacc    181  LNSLQKEYESLVSKVNTYTDNLKKVINNCQLEKKEAEITVKKLQDYNKMDEKLEEYKKSE
Pv19_vacc      1  -----------------------------------------------------------
Pv19_SalI      1  -----------------------------------------------------------
Pv19_PVP01     1  -----------------------------------------------------------
Pv19_Belem     1  -----------------------------------------------------------
Pv19_isolate   1  -----------------------------------------------------------

Pv42_vacc    241  KKNEVKSSGLLEKLMKSKLIKENESKEILSQLLNVQTQLLTMSSEHTCIDTNVPDNAACY
Pv19_vacc      1  ---------------------------------------MSSEHTCIDTNVPDNAACY
Pv19_SalI      1  -----------------------------------------------CIDTNVPDNAACY
Pv19_PVP01     1  -----------------------------------------------CIDTNVPDNAACY
Pv19_Belem     1  -----------------------------------------------CIDTNVPDNAACY
Pv19_isolate   1  -----------------------------------------------CIDTNVPDNAACY

Pv42_vacc    301  RYLDGTEEWRCLLTFKEEGGKCVPASNVTCKDNNGGCAPEAECKMTDSNKIVCKCTKEGS
Pv19_vacc     20  RYLDGTEEWRCLLTFKEEGGKCVPASNVTCKDNNGGCAPEAECKMTDSNKIVCKCTKEGS
Pv19_SalI     14  RYLDGTEEWRCLLTFKEEGGKCVPASNVTCKDNNGGCAPEAECKMTDSNKIVCKCTKEGS
Pv19_PVP01    14  RYLDGTEEWRCLLTFKEEGGKCVPASNVTCKDNNGGCAPEAECKMTDSNEIVCKCTKEGS
Pv19_Belem    14  RYLDGTEEWRCLLTFKEEGGKCVPASNVTCKDNNGGCAPEAECKMTDSNKIVCKCTKEGS
Pv19_isolate  14  RYLDGTEEWRCLLTFKEEGGKCVPASNVTCKDNNGGCAPEAECKMTDSNKIVCKCTKEGS

Pv42_vacc    361  EPLFEGVFCS---------------------
Pv19_vacc     80  EPLFEGVFC----------------------
Pv19_SalI     74  EPLFEGVFCSSSSFLSLSFLLLMLLFLLCMEL
Pv19_PVP01    74  EPLFEGVFCSSSSFLSLSFLLLMLLFLLCMEL
Pv19_Belem    74  EPLFEGVFCSSSSFLSLSFLLLMLLFLLCMEL
Pv19_isolate  74  EPLFEGVFCSSSSFLSLSFLLLMLLFLLCMEL
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Supplementary Figure 1. Alignement of the *Pv*MSP1 amino acid sequences present in the αDEC-*Pv*MSP1$_{42}$ (Pv42_vacc) and all the MSP1$_{19}$ formulations (Pv19_vacc), compared to the *Pv*MSP1$_{19}$ amino acid sequences of the *P. vivax* strains SalI (PlasmoDB: PVX_099980), PVP01 (PlasmoDB: PVP01_0728900) and Belém (GenBank: AAN86208.1), as well as with the sequence obtained from a field isolate and used to generate the *P. berghei* hybrid parasites.

Supplementary Table 1.

Target	Primer name	Sequence 5'- 3'
Plasmid constructs		
hDHFR	hDhfr_Fw_EcoRI	GGG**GAATTC**TGCAGCCCAGCTTAATTCTTTTC
hDHFR	hDhfr_Rv_SmaI	AGT**CCCGGG**AAAATTGAAGGAAAAAACATCATTTGTG
P. berghei MSP1	Pb_Fw_KpnI	GGG**GGTACC**GCAATCGACAAATTAGAGAACTTAGTAT
P. berghei MSP1	Pb_Rv	TACATGCTTAGGGTCTATACCTAATAAATC
msp1 3'UTR	PbM3'_Fw_SmaI	ATG**CCCGGG**ATAAATTATTGAAATATTTGTTGGATT
msp1 3'UTR	PbM3'_Rv_NotI	GAT**GCGGCCGC**CAACAATATTTCCCCAAGCTTGTTAT
P. vivax MSP1$_{19}$	Pv_Fw	GGTATAGACCCTAAGCATGTATGTATAGACACCAATGTGCCTGAT
P. vivax MSP1$_{19}$	Pv_Rv_XhoI	GGG**CTCGAG**TTAAAGCTCCATGCACAGGAGGAAAAG
trap 3'UTR	trap3'_Fw_XhoI	GGG**CTCGAG**TTTTAATAAACATATATATCTAGATG
trap 3'UTR	trap3'_Rv_EcoRI	GGG**GAATTC**TTTTTGTTTCGTAAATTTTAAAATAAT
GFP cassette	Fw_GFP	AGT**CCCGGG**GGAAAATATACGTAATA
GFP cassette	Rv_GFP	ACT**CCCGGG**AAAATACCAATAATACC
Genotypic analysis		
MSP1	P1	GTGAAGAAGATATTCCTGCC
MSP1	P2	TCAAAGAGTGGCTCAGAACC

| *MSP1* | P3 | GCAGTTGGATCACATCCACC |

Restriction sites are highlighted in bold letters