

Table S6. Primers for qRT-PCR, RT-PCR and generation of *pbmisfit* transgenic parasites

Primer name	Sequence (5' to 3')	Description
<i>misfit</i> QRT-PCR F	CAAATGATTTCGGAAATGTTGC	
<i>misfit</i> QRT-PCR R	CAATTTGCTATCATCGCCCT	
<i>misfit</i> RT-PCR F	GATGAAGAAAAGGACAAAGAAATTTTC	
<i>misfit</i> RT-PCR R	AAGGGATACATATTCACAATCAAG	
<i>gfp</i> QRT-PCR F	CCTGTCTCTTTTACCAGACAACCA	
<i>gfp</i> QRT-PCR R	GGTCTCTCTTTTTCGTTGGGATCT	
<i>p28</i> RT-PCR F	AATGCACAGGTACAGGAGAACTAAAT	
<i>p28</i> RT-PCR R	CACACTCATAATGTTTTCCAGTCAATT	
<i>amal</i> RT-PCR F	TATGGGTCCAAGATATTGTAGTAATAA	
<i>amal</i> RT-PCR R	GAATTAGCTTTACCATAAATATCTGC	
<i>chit</i> RT-PCR F	GCCCGCCAGATGTAATTATA	
<i>chit</i> RT-PCR R	TGCCAAATTCTACACCATCG	
<i>ctrp</i> RT-PCR F	AGAGAAGAAGATTGCCCAACAG	
<i>ctrp</i> RT-PCR R	ATCGGATCATTTCGATCGATAAC	
<i>soap</i> RT-PCR F	TCGAAGGAGCAAGGAAAAATTCC	
<i>soap</i> RT-PCR R	ATGAACAGCTACATTCTTCGGTC	
<i>warp</i> RT-PCR F	ATGAAGAGTGTTAAAAGGAATAACATATAT	
<i>warp</i> RT-PCR R	CAGACGTCAGTGAAGAAGGATT	
<i>maebl</i> RT-PCR F	GAATTGAAGAAGCTAAGAAAGCAG	
<i>maebl</i> RT-PCR R	TTCTTCGTACCATCTTCCTCC	
<i>misfit</i> A F	<u>TTGGGCCCAAGATGATAGTAATTATAAAGAATTAGAAG</u>	Disruption upstream target (A) <i>Apal</i>
<i>misfit</i> A R	<u>CCAAGCTTGAACAATAACTGTTACTAGTGG</u>	Disruption upstream target (A) <i>HindIII</i>
<i>misfit</i> B F	<u>TGAATTCTTGTTCATATTTAGCAGTGAATTAG</u>	Disruption downstream target (B) <i>EcoRI</i>
<i>misfit</i> B R	<u>GGGGATCCGAATCAAATCTGCTTCATCCATG</u>	Disruption downstream target (B) <i>BamHI</i>
<i>misfit</i> A INT F	CATAAATTTTTACGATGAGGTA	38 bp upstream of <i>misfit A</i>
<i>misfit</i> WT R	GCCTGATCAACATATGAATCATTG	332 bp downstream of <i>misfit A</i>
<i>tgdhfr-ts</i> 5'UTR R	GATGTGTTATGTGATTAATTCATACAC	200 bp into the 5'UTR of <i>tgdhfr-ts</i>
<i>misfit-myc</i> F	<u>GGGGTACCCAGAAGGAAGATTAAGTTGTATGG</u>	Tagging 3' target <i>pbmisfit Apal</i>
<i>misfit-myc</i> R	<u>TTGGGCCCCAGCAGAAGAATCAAATTCCTGC</u>	Tagging 3' target <i>pbmisfit KpnI</i>
<i>Misfit-myc</i> Seq F(1)	CAACAGTTCACCTTTCAAAAACCTG	Sequencing (Tagging construct)
<i>misfit-myc</i> Seq F(2)	TGGAAACAAACCTAATTACGAAGTT	Sequencing (Tagging construct)

Where appropriate, target restriction sites are shown as underlined italics and restriction site overhangs (to ensure efficient cutting) are in italics. The appropriate restriction enzyme is presented in the description column. F, forward; R, reverse. All primers are listed in a 5' to 3' direction.