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Lhs1      1 MRNVLRLFLTAFAIGSL----AALGVYDYGQONIKAIIVSPOAPLELV 46
PFGRP170 1 MRPRFFLFLFIYIYNSLRKIKSSLLGIDFQNEYIKVYSVSPKGFNIL 50

Lhs1      47 LTPEAKRKEISGLSI-KRLPGYKGDONGIERIYGSAVGSLATRFQNTL 95
PFGRP170 51 LNNQSKRKITNSISFANKFRITYDEE----SKLY-----STKYPLTL 88

Lhs1      96 LHLKPLLGKLEDETTVLYSKQHPLEMVSTNRSTIAFLVDNVEPLLE 145
PFGRP170 89 LNSNILLGYNLFD----SLNKNEN-----FVIENYDENNEE 120

Lhs1      146 LVA-MVVOEIAN-----RANSLKDR-----DAR 168
PFGRP170 121 FYSIDINNYFSDNDFGSKYYSYDYYVDHKGRTINIKLDMNVISSSEVTAN 170

Lhs1      169 TEFVKNKHSFT-----IPDFDQHRRKALLDASS 197
PFGRP170 171 ILGVYKLLAYTHLNIDYKVRNINLNIGCVISVPCNFSQRKQDALINASK 220

Lhs1      198 ITTGEETLYLSEGMVAVNFKQRDFPPGEOQHYIVYDMGSGSIKASM 247
PFGRP170 221 I-AGLELLGIINGVTAALHNV---HDIPLNTKLTMYLDIGSKNINNGI 266

Lhs1      248 FSI-LQPEDTTQPVTFIEFEGYGNPHLGAKFTMDIGSLIENKFLETH-P 295
PFGRP170 267 ATISFVEKDKVRSRSVQVYACESLENISGNKIDMLAENLRKQFEKYNV 316

Lhs1      296 AIRDELHANPKALAKINQAEKAKILLSANSEASINIESLINDIFRTS 345
PFGRP170 317 SIENDK-----KAMRKLIVAANKAKILLSAKKSADVFIESLYNKSINES 361

Lhs1      346 ITRQFEFEFIADSLDVIKPINDAVTKQFGGYGNLPEINGVLAGGSSR 395
PFGRP170 362 VSRDFEELIOEVINMKIPINKALEK---GGF---QLKDIEALELIGSQR 407

Lhs1      396 IPIVODQLIKLVSEKVLRNWNADESAVNGVMRGIKLSNFKTKPLNVV 445
PFGRP170 408 VPKILNEVTEFFNPLKVGHLNSDEAVTMGSLYIAAYNSANFRKLDLYK 457

Lhs1      446 DRSVNTYSFKLSNESE-----LYDVFTRGSAYP-NKTSILNT 482
PFGRP170 458 DIVSNYHILVNTDEEENNTNEEKVNIKKELVYNSRYPIHNNVILT- 505

Lhs1      483 TDSIPNFTIDL FENGLFETITVNS---GAIKNYSY---SSDKCSSGVAYN 527
PFGRP170 506 ---YKDLKFSVYENGKIDNEYVLGNLDNAIKSKYEHLGTPK-----LV 546

Lhs1      528 ITFDLSORLSIQEVNCCI COSEND-IGNSKQIK-----LW 560
PFGRP170 547 LKFHLDFGLSLDKVLVYEEQKDGAGDTKNNKEGDEENNNNNNEEI 596

Lhs1      561 -----NKGR----- 565
PFGRP170 597 NKDDDTNNKSDDEQNKQGENKSNENKENEENKONGEKKQNDIHKHNP 646

Lhs1      566 LAFTSEDEVEIKRLSPSERLHEHIKLLDKQDKERFQFQENLVLESNLY 615
PFGRP170 647 IEFQTRNIKPLPTFEEIKEKKEILKNLDEHDIDIFLSEKKNLTESFY 696

Lhs1      616 DARNLLMDEVMONGPKSQVEELSEMVKVYLDWLEDASFDPDPEDIVSRI 665
PFGRP170 697 ETRSKMKQDIYQVTKETRNEYLNKLEEYEDWLYTEK-DEPLENVSNKI 745

Lhs1      666 REIGILKXKIELYMDSAKEPLNSQFKG-MLEEGHKLQ-AIETHKNTVE 713
PFGRP170 746 HELQ-----DIY-NPIKERAEELOVRDKIIEETNKKIQEMTEKID- 785

Lhs1      714 EFLSQFETEFADIDNVREEFKIKOPAYVSKALSTWEETLTSFKNSISE 763
PFGRP170 786 --LSEKKPAAETIKMVKDS-----LQKEVQNNHAQEEQK---K 820

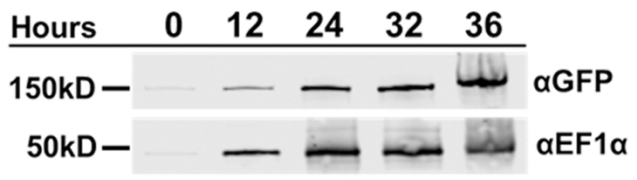
Lhs1      764 IEKFLAKNLFGEDELREHLFETKLFQDMYRTKLEEKRLIKSGDESRLNEI 813
PFGRP170 821 LQNYTAPFFKHKD-----VOLKFSIQ-----MLIKTLDKLKKPVE 856

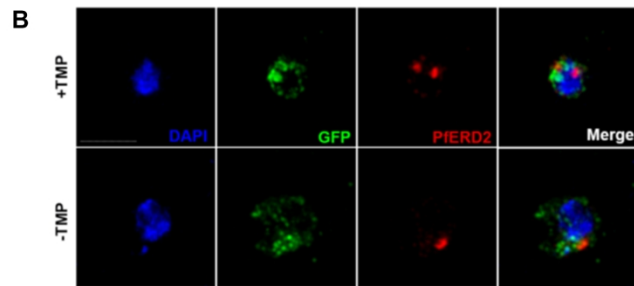
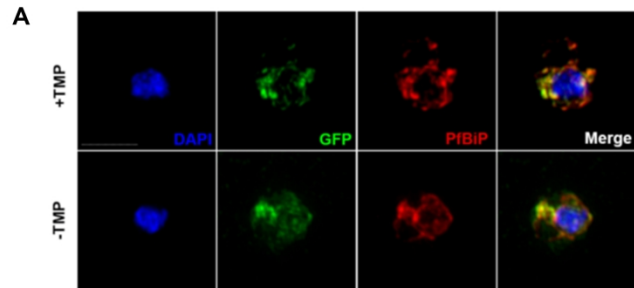
Lhs1      814 KKLHLRNFRLQKRKEEK-----LKRKLEQESRNNETESTVIN 852
PFGRP170 857 KKEKKNNTDNQENTSKQDAGADKNHNTTENQNEQSAQNNENNDQNN 906

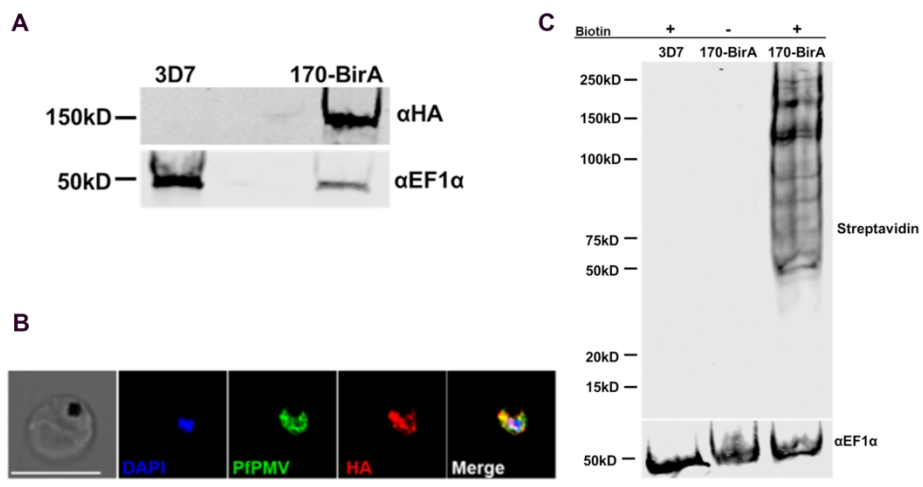
Lhs1      853 SADDKTTIVNDKTTESNPSSEEDILHDEL 881
PFGRP170 907 NEHDANQSNDEQNNNDGASQ---KDEL 932

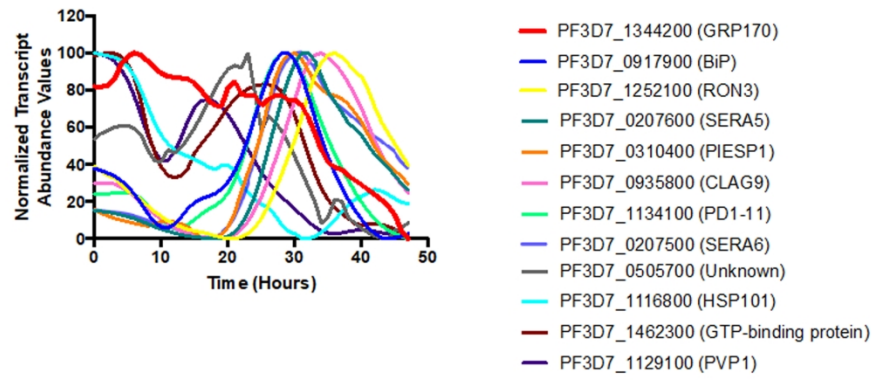
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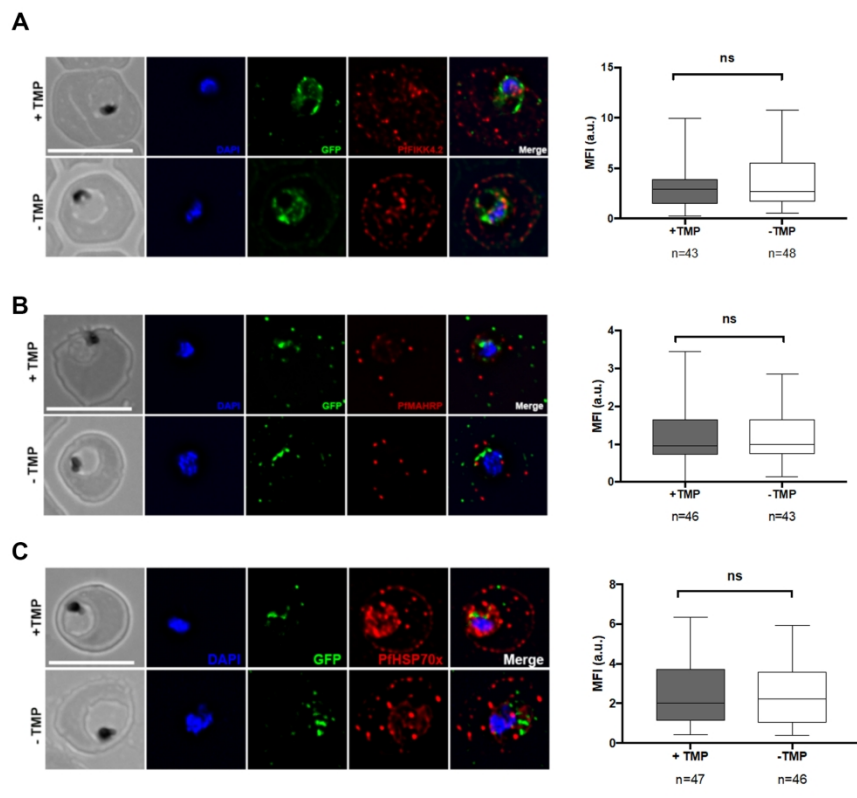
Organism	% Identity	% Homology
<i>P. vivax</i>	62.6	78.6
<i>P. malariae</i>	65.5	81.7
<i>P. ovale</i>	61.7	77.5
<i>P. berghei</i>	59.6	77.5
<i>T. gondii</i>	26.2	45.5
<i>S. cerevisiae</i>	22.4	40.1
<i>H. sapiens</i>	23.6	42.1

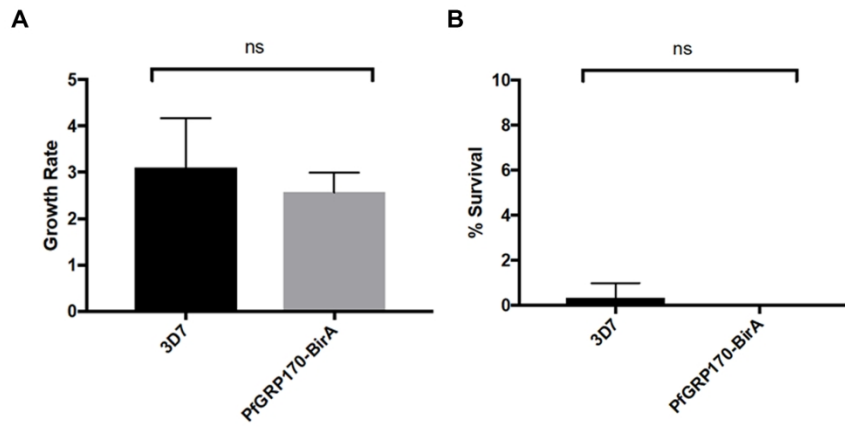


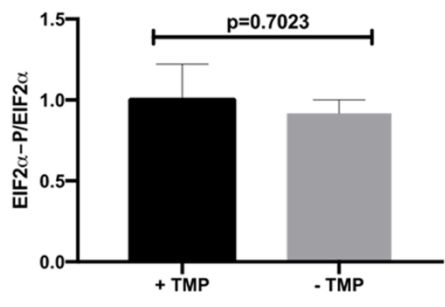
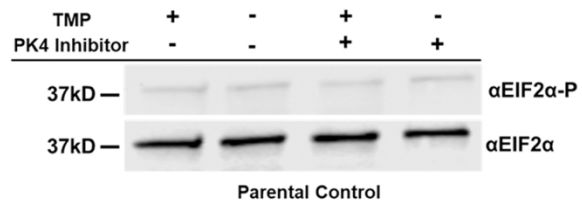












Primer	Sequence
P1	cataaatatattatataactcgacgcggccgtcaaagttcatcactagcgtaatctggaacatcgatggg
P2	cccatac gatgtccagattacgctagtgatgaacttgacggccgctcgagttatataatataatg
P3	CACTATAGA AACTCGAGGATAAAGTTCTTGTTGTTTATGAAGAACA AAAAAGATGGAGCTGG
P4	CTGCACCTGGCCTAGGTTGATCTGATGCTCCATCATTTTTATTTTGCTCATCGTTGG
P5	AAAAACTCACGCTAGCATGAGACCTCGTTTTTTTTGTTTCTACTTTTTATAATATATATATAATAG
P6	GACGTCGTACGGGTACCTAGGTTGATCTGATGCTCCATCATTTTTATTTTGCTCATCGTTG
P7	GGAGCATCAGATCAACCTAGGTACCCGTACGACGTCCCGGACTACGCTGGCTATCCCTATG
P8	GAACAATAATAGATCTttataattcatctttCTTCTCTGCGCTTCTCAGGGAGATTTCTCCGCCATCCAG
P9	TCTTCTCCTTTACTGACGTCACCTCTTTTATGATCTACTACATAATCATATGAATAATAC
P10	TAAAAGAGGTGACGTCAGTAAAGGAGAAGAATTATTTACTGGAGTTGTCCCAATTCTTG
P11	GAACAATAATAGATCTTTATTTGTATAGTTCATCCATGCCATGTGTAATCCCAGCAGCTG
P12	ATGAGACCTCGTTTTTTTTGTTTCTACTTTTTATAATATATATATAATAGTTTAAAG
P13	gtgccattaacatcaccatctaattcaacaagaattggg

Supplemental Table 2: Primers used in this study