

Appendix

tRNA lysidinylation is essential for the minimal translation system in the *Plasmodium falciparum* apicoplast

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<i>PfTils</i>	MYLLCIFLYILSFLCFTICIKRKQNVSKRWQFFIPHINKEGLYNIMDKKIIIRVNKNKRFHRNVVCSNRLSEFIDRDININNMKNIKELKKKHIDNNILIKADIFSNIIEKKNNSNLFFKKFCSFINMEY	130
<i>SyTils</i>	-----	0
<i>AaTils</i>	-----	0
<i>MgTils</i>	-----	0
<i>EcTils</i>	-----	0
<i>GkTils</i>	-----	0
<i>AtRSY3</i>	-----	0
<i>PfTils</i>	DETTKDLEELKINKRLKNNNNNDNNNNNNNNMYDNKSNNIHNNNNNNSDNLKICKKNQD-----VLQVVEGYWLLTLKNKYMFSFLKKKKKIIIFSVS [★] SGVDSLCLLYSFIFVIYKILIS	244
<i>SyTils</i>	-----MAWTLHLSKHLHQNLR--FPQLQTRILVAVSGGQDSLCLLHLLNDLTKQWQ--	51
<i>AaTils</i>	-----MNPESRVIRKVLALQND--KIFSGERRVLIAFSGGVDSVVLTDVLLIKLNKYNFS--	52
<i>MgTils</i>	-----MASEKQYTAGVSGGSDSMLMLKLYQKKIA-----	29
<i>EcTils</i>	-----MTLTLN--RQLLTSRQILVAFSGGLDSTVLLHQLVQWRTEPN--	40
<i>GkTils</i>	-----MIDKVRAFIHRH--QLLSEGAIVGVSGGPDSTALLHVFLSRDEWK--	46
<i>AtRSY3</i>	-----MARGLSLCSN--GRKSSTLLSNSIPRVS--ISFSPKTLFTCSYPLQSRHPKFSQRLFCNHACVPETVDETRYKELFNKRMDMAGLKPHNRIALGVSGGPDSTALCVLTAKWKTEGL--	112
<i>PfTils</i>	MIYKNKSYFGFMNKINSVYSFTHEDIIDIIEKEYRYENNVSFFLSILSKIIVFYCHNTRKE-CTSEMYFLKNICKKFGIHFKSKKLTEKSIOQLNVINLTKKKKNYESNVNKKININMMKNKNFLLLAR	373
<i>SyTils</i>	-----W-----HL-AVAHCDHRWPTDAGIAD--HVQGLAC-----GY-----	80
<i>AaTils</i>	-----L-----KEVALAHFNMLRES-AERDEEFCKEFAKERNMKIFVVGKE-----	92
<i>MgTils</i>	-----CVVHVNYNTRST-SLRQKLVEQYCKLNIPLVVHTVDPDL-----	69
<i>EcTils</i>	-----G-----VALRAIHVHGLSAN-ADAWVTHCENVCCQWQVPLVVER-----	79
<i>GkTils</i>	-----L-----QV-IAAHVDHMFGRSESEEME [★] FVKRFQVERRILCETAQI-----	86
<i>AtRSY3</i>	-----SCVNK-----TDGFIDGLVAIVVDHCLRQESKDEAELVCSRVS-QMGIRCEIASC-----	161
<i>PfTils</i>	TWRRNIYVHLSNDILKRDMMNNIYHNNKMKDSHNNNNNDNNNTSMKDPLNMLDAYTYEKIYDINNYIKITNKKCITNVLIKKESFSKEYSNDSIMRKKKKECLLFNNIMNLQNNNIKIINNTCSNNIY	503
<i>SyTils</i>	-----KLP-----YFQR-----DAQDL-----PQTEA-----AAR	100
<i>AaTils</i>	-----DVR-----AFAK-----EN--R-----MSLEE-----AGR	110
<i>MgTils</i>	-----VWKK-----NFQN-----QAR	80
<i>EcTils</i>	-----VQ-----LAQEG-----LGIEA-----QAR	94
<i>GkTils</i>	-----DVP-----AFQR-----SA--G-----LGAQE-----AAR	104
<i>AtRSY3</i>	-----D-----WVD-----GRPKL-----GHLQE-----AAR	178
<i>PfTils</i>	NMKYTNVFLNKYICLKKKIKSIVFI [★] GHQNDNNETVLLQFFRGVFLKNLRGKFLTYK-----NCLLYRPFIKLNLHLRYMQLINKTNFDSNNNNMSISRNFIRNVVPIPNITHMLKD	619
<i>SyTils</i>	HWRYH--AL--TAIAKAENFPVVMTGHTQSDRAETLLFNLVIRGSGSDGLQAMNWRNLEE-----SGSDKSPIRLIRPLLEISRQETGDFCQQQLSVWEDVLNEKLTYYRRNRIRGELIPYLKKHFN	219
<i>AaTils</i>	FLRYK--FL--KEILESEGFDCIATAHHLNDLLETSLFFTRGTGLDGLIGFLPKEE-----VIRRPYYVVRSEIEEYAKFKGLRWVEDETNYEVSIPRNRIRHRVIBELKR-INE	217
<i>MgTils</i>	KIRFDQ--F--KKTAKLYOTNKLLLAHHRDDFIEQAKMQLDAKKR-AVYYGKTRCELY-----GLKIYRPLMKYWKDEIITLCRODHIPIYEIDETNKLPYIKRNEVRLEIEKWSKI-EKE	190
<i>EcTils</i>	QARYQ--AF--ARTILP--GEVLVTAQHLDQCETFLIALKRGSGPAGLSAMAEVSIFA-----GTRLIRPLLARTRGELVQWAQYDLRWIEDESNDQDSYDRNFLRLRVVPLLQQ-RWP	203
<i>GkTils</i>	ICRYR--FF--AELMEKHQAGYVAVGHHGDDQVETILMRLVRGSTSKGYAGIPVKRPFH-----GGYLIRPELAVSRAEIEAYCROMGLSPRODPSNEKDDYTRNRFRHHVPLLRQ-ENP	215
<i>AtRSY3</i>	EMRYE--MI--SNVCFRQIEVLIAAHADDQAEFLIRLSRSSGVILAGTAFASIFSRNLQLDAHKMNQSTRLVRLPLDLWKEDMYKICQWGRQDWVEDPTNRSQLFVRNRIRTSIGNLES----G	300
<i>PfTils</i>	KS [★] YKNRENHNIDKEINEKNDKHM [★] LDNVCVDYHDETPLHNKEMNKYDHVEISKNNIVNKNNELKNQHVVNTSLDRRLKNVLRCTTNLENYLNYYD-----NMFFTYLK [★] KKYKRCMSTTKKIT	739
<i>SyTils</i>	-QVEK---SLAQTVELLTAEVAYLEQVSGEIIYQTL [★] SQTDQ-----KSLNCR-----LS-----QK-PLALQRRIRQFLQSCQ-----SQ---SPNF-E	290
<i>AaTils</i>	-NLED---TFLKMVKVLAEREFLEE [★] EAQKLYKEVK-----KGNCLDVKK-----LK-----EK-PLALQRRVIRKFIGEKD-----VEK-VEL-----	285
<i>MgTils</i>	QFY-----AICAMNKTIAQKLFVLMKK-----AKK [★] WLLQPDVRELKRF [★] SIIDQKLIYSYLIYHKIN-----NGEKIDAILDFIQPSQKQYRLQNDIFLMVK-----NQCLALLYKS-	290
<i>EcTils</i>	-HFAE---ATARSAALCAEQESILDELADDLAHCQSPQ-----GTLOIVP-----ML-----AM-SDARRAAIRLRLAG-Q-----NAP-MESRDALV	276
<i>GkTils</i>	-RLHE---RFQQYSEMMAEDEQFLEETAAADALNKVMEKQHR---DAALISGP-----FL-----EL-ERPLQRRVQLLLLR-L-----VGG-VEPTLTSV	291
<i>AtRSY3</i>	-SFKS---ELQAVISECRRTSRVVDK [★] CTDLIHQTVTVTDK-----GYAILDLERLNPSGVKDICLSKYLFAVLQFISQR-QRPIRGNTSKLLN [★] YIR-----A-IPCRSLT	397

4

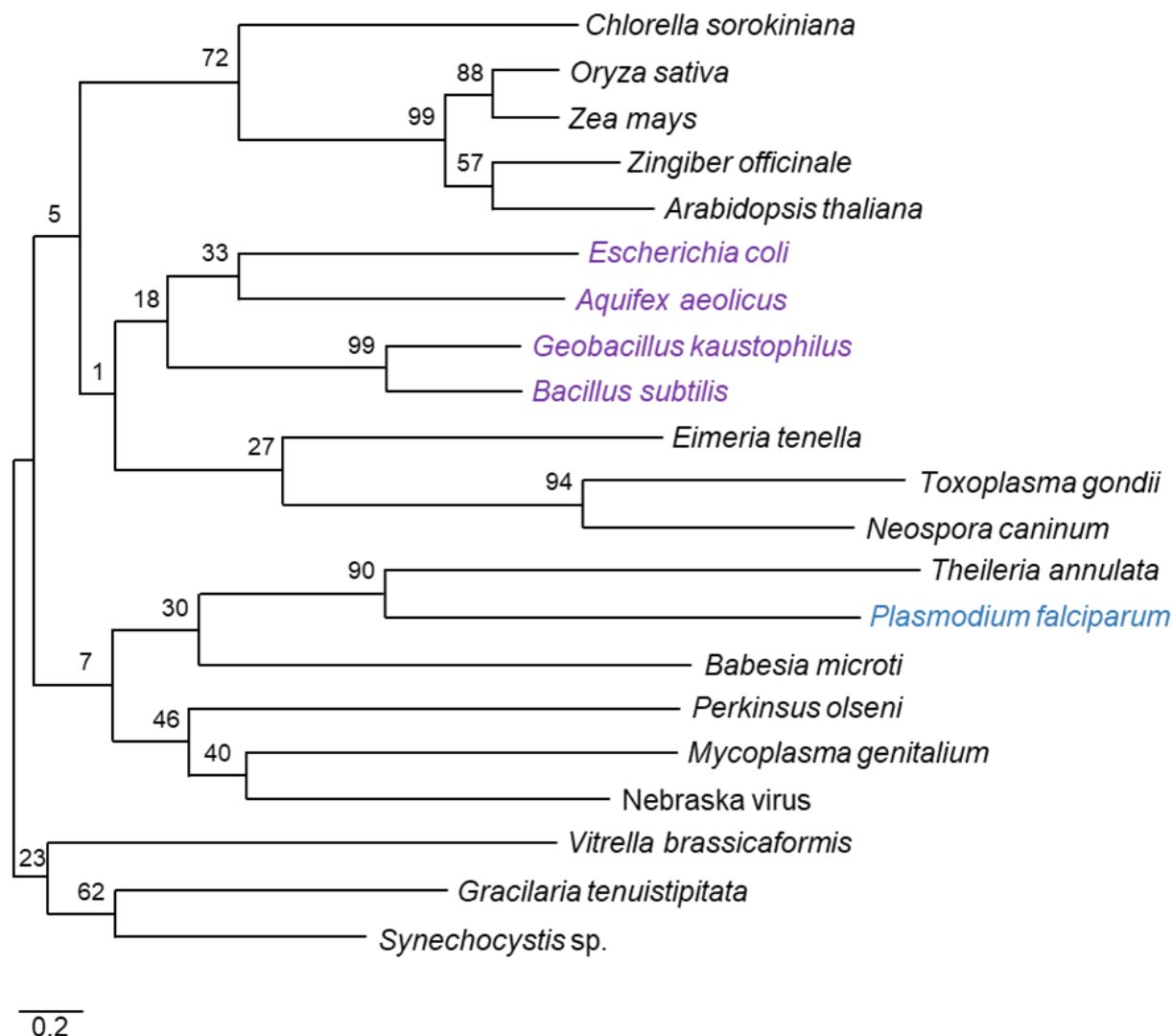
Apicomplexans	Gene ID	Identity to <i>Pf</i> TiS	E-value	Experimental localization
<i>Toxoplasma gondii</i>	TGME49_215100	30%	1e-8	Apicoplast*
<i>Eimeria tenella</i>	ETH2_0718500	23%	0.025	N.D.
<i>Neospora caninum</i>	NCLIV_052110	30%	8e-10	N.D.
<i>Babesia microti</i>	BMR1_01G01110	39%	1e-11	N.D.
<i>Theileria annulata</i>	TA03600	30%	2e-4	N.D.

* Identified in the apicoplast fraction from *T. gondii* via hyperLOPIT (Barylyuk *et al.*, 2020); N.D., not determined

Appendix Figure S2. Pathogenic apicomplexans have TiS orthologs. TiS orthologs were identified in pathogenic apicomplexans using *P. falciparum* TiS as the query.

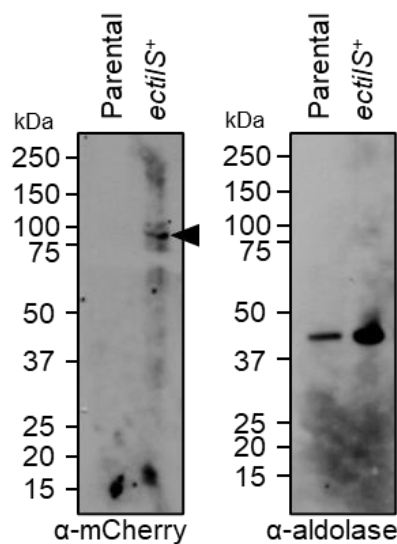
Reference:

Barylyuk K, Koreny L, Ke H, Butterworth S, Crook OM, Lassadi I, Gupta V, Tromer E, Mourier T, Stevens TJ *et al* (2020) A comprehensive subcellular atlas of the *Toxoplasma* proteome via hyperLOPIT provides spatial context for protein functions. *Cell Host Microbe* 28: 752-766.e759



Appendix Figure S3. The phylogenetic relationship among TilS orthologs.

Phylogenetic analysis revealed a distant relationship between the TilS proteins of *P. falciparum* and *E. coli*. Bootstrap analyses (1000 replicates) were employed to assess the robustness of the branching patterns. The percentage of replicate trees in which the associated taxa clustered together is indicated adjacent to each branch. The phylogenetic tree is drawn to scale, with branch lengths representing the estimated number of substitutions per site. Refer to **Appendix Table S2** for the accession IDs of the proteins used in this analysis.



Appendix Figure S4. Uncropped image of immunoblot shown in Fig. 4D.

Immunoblot of saponin-isolated PfMev^{attB} (parental) and *ecti/S*⁺ parasite lysates with anti-mCherry antibodies (left panel) confirms expression of EcTilS-mCherry fusion protein (expected molecular weight 91 kDa, black arrowhead). Anti-aldolase immunoblot shows relative loading levels (right panel). Protein markers are in kilodaltons (kDa).

AfTiaS	-----	0
PfTilS	MYLLCIFLYILSFLCFTICIKRKQNVSKRWQFFIPHINKEGLYNIMDKKIIRVNKNKRFHRNVVCSNRLSEFIDRDININ	80
AfTiaS	-----	0
PfTilS	NKMKNIKELKKKHIDNNILIKADIFSNIIEKKNSNLFKKFCFSFINMEYDETTKDLEELKINKRLKNNNDNNNNNNNN	160
AfTiaS	-----	0
PfTilS	MYDNKSNNIHNNNNNSDNLKCIKKNQDVLQLVEGYWLLTLKNKYMFSFLKKKKKIIFSVS SGVDSLCLLYSFIFVIYK	240
AfTiaS	-----	0
PfTilS	ILISMIYKNKSYFGFMNKINSVYSFTHEDIIDIIEKYRYENNVSFSLSKIIIVYCHHNTRKECTSEMYFLKNICKKF	320
AfTiaS	-----	0
PfTilS	GIHFKS KKLTEKSIQKLNVINLKTKKKNYESNVNKKININMMKNKNFLLARTWRNIYVHLSNDILKRDMMNNIYHNN	400
AfTiaS	-----	0
PfTilS	KMKDSHNNNNNDNNNTSMKDPLNMLDAYTYEKYIYDINNYIKITNKKCITNVLIKKEFSKEYSNDSIMRKKKKEGLLF	480
AfTiaS	-----MRVWVGIDDDSSRGM-----	16
PfTilS	NNIMNLQNNNIKIINNTCSNNIYNMKYTNVFLNKYILKKKIKSIVFLGHHQNDNETVLLQFFRGVFLKNLRGKIFLTY	560
AfTiaS	---CTTYLAVLAMER-----VERELGKVGIFERLIRLNPTIPYKTRGNGAVSFLVEVDDVG	69
PfTilS	YKNCLLYRPFIKLNKLHLYRYMQLINKTNWFDSSNNNMSISRNFI RNVVIEINITHMLKDKSYKKNRENHNIDKEINEKNDK	640
AfTiaS	ELV-----DVVNEVII-----EH-----AML-DDEKTNPGAVFVDEELAVKLKPFADKAIKDVIQIDE-----AL	123
PfTilS	HMLDDNVCVYHDETPLHNKKEMNKYDHVEISKNNIVNKNNELKNQHVVNTSLDR-----LKNVLRQTNTLENYL	712
AfTiaS	FVIGKYFIPHHRHKKGRGLIGALAAVGALEED-----FTLELIA	162
PfTilS	NYYDNMFETYLKKKYKRCMSTTKKITHETTYTNVHDTHNGNIKNKRNI TKIHKS YNTYKNSDINLRNVHLKKNIKC	792
AfTiaS	YRYPERFGTEREYDEESFEDMDYELYPQTFDNVDWCN-----DV-----VVCIPN--TPCPVLYGIRGE-	219
PfTilS	YNYQDA---HNIFMNEYFRMNNLYNIFPRYNMETLIKINKLYEKNIYLKIFNFFELLLLSKLIRLEILYNIIRKY	868
AfTiaS	-----SVEALYKAMESVKTEPVDRRMIFVTNHATDMHLIGEEVHRLNYSYRLRGRVTL-EPYDIEGGHVFFEID	290
PfTilS	VKVNIKYAKIERIYEQMIAYINE-----YIKRDKTKYGTTSQSFHQSHIFNDDD	916
AfTiaS	TKFGSVKCAAEPTQFRNVIRLLRKGDVVEVYGS MKKDTINLEKIQIVELAEIWEKNPICPS-----CRR--	358
PfTilS	TMFDNKMVRQNKSKKEN---KILNVKIKDLFGDTKIEEVNFVVINITKSKSLLQNNLFRIERDMIEDITKGRKRLH	991
AfTiaS	MESAGRGQGFRCKKC-----RTKAEKLR-----EKVE-----R-----ELQ-----	390
PfTilS	MDDNKRDDNKRDDNKRDDNKRDDNKRDDNKRDDNKRDDNKRDDNKRDDNKRDDNKRDDNKRDDKDKDTHIQHDKDI	1071
AfTiaS	--PGFYEVPSP-----ARRHLSKPLIRMNVEGRHILR-----	420
PfTilS	TSQTEFPHNKITIANEKCIKNDEYIDNSLVCFKEKSANIEVHNNISTEVSRLKKYDITKNDKKNIFLLIKRKKKKKEK	1151
AfTiaS	-----	420
PfTilS	FHIHIRYIKKNDYVYLEKKKISVNKFLTLHKIPYIYQTALPVIEIINFNNNHILFFYLFPEVKSPYFTLREKTFPQKYMN	1231
AfTiaS	-----	420
PfTilS	THFVYSIKFKGIRD	1245

★ tRNA binding residue ★ ATP coordinating residue CXXC motif

Appendix Figure S5. Sequence alignment between *Archaeoglobus fulgidus* TiaS (AfTiaS) and *P. falciparum* TilS (PfTilS). Threonine18 (Bold purple T) of AfTiaS is subject to autophosphorylation. Alignment output was visualized using Boxshade to highlight conserved residues. AfTiaS and PfTilS accession IDs are provided in the Methods section.

pftiS-3xV5

CCTAGGATGTACCTGCTGTGCATTTTCCTGTATATCTTGAGCTTTTTTATGTTTTACAATTTGTATTAAACGTAAACAGAACG
TCTCGAAGCGTTGGCAGTTTTTTCATTCCGCATATTAACAAGGAAGGCCCTTTACAATATCATGGATAAGAAAATCATCCGGGT
CAACAAAAACAACCGTTCCATCGTAACGTTGTATGCAGCAACCGGCTGAGTGAATTCATCGATCGCGATATCAACATTAAC
AACAAGATGAAGAATATCAAGGAACGAAAAAACAACATTGATAACAACATTTTGATTAAAGCAGACATTTTCAGCAACA
TAATCGAGAAAAAACAATTCAAACCTATTTTTTAAAAAATTTTGCTCTTTTATTAACATGGAATATGACGAAACCACCAA
AGATTTAGAAGAGTTAAAAATCAACAACGATTGAAAAACAATAACAATGATAATAACAACAATAACAACAACATGTAT
GATAACAAAAGCAATAATATTCATAACAACAACAATAACAATAGCGATAATTTGATTAAATGTATCAAAAAAGAAATCAGGATG
TGCTGCAGTTGGTAGAAGGATACTGGCTGTTAACGCTGAAAAACAATATATGTTTTCTTTCTGAAAAAAGAAAAAAT
TATCTTCAGCGTGTCAAGTGGGGTGGACTCTTTGTGCCTTCTTTATAGCTTCATCTTTGTTATCTATAAAATCTGATCAGC
ATGATTTACAAAAATAAAGTTATTTTGGCTTTATGAATAAAATCAACAGCGTGTATAGCTTTACTCATGAAGATATTATTG
ATCATCATCAAGAATACCGTTATGAAAAAATGTCTGAGCTTCTTTCTGTCGATCCTGAGCAAAATTCGTGATTTACTGTCA
TCATAATACCGGTAAAGAATGTACCTCAGAAATGTATTTTCTTAAAAAATTTGCAAAAAATTCGGTATCCACTTTAAATCC
AAAAAATGACGGAAAAAGAGTATTCAGAACTGAATGTAATAAATTTAAAAACGAAAAAGAAAAATTACGAAAGCAATGTGA
ATAAGAAAAATTAATATTAACATGATGAAGAATAAAAAAATTTTCTGCTGCTAGCACGAACCTGGCGTCGTAACATCTACGT
GCACCTCTCCAACGATATTTTGAACGGGACATGAACAACAATATTTATCACAACAACAAAATGAAAGATTCCCATAACAAC
AACAACAATAACGATAATAACAACACGAGCATGAAGGACCCCTGAATATGTTAGATGCTTATACCTACGAAAAATATATTT
ACGATATTAACAATTATATCAAAATCACCAACAAAAATGCATCACCAACGTCCTGATTAAGAAAGAAATCATTCAGTAAGGA
GTACTCCAACGATTTCGATCATGCGCAAGAAGAAAAAGGAAGGTCTGCTTTTCAATAATATTATGAACCTGCAGAATAATAAC
ATTAATATTAACAACACTTGCAGCAATAATATTTACAATATGAAATATACTAATGTTTTTCTGAACAAATATTGCATCC
TGAAAAAAGATTAAATCAATCGTGTTCCTCGGCCACCACCAGAACGACAACAACGAAACGGTGCTGCTTCAGTTCTTCCG
TGGTGTTTTTTTAAAAAACCTGCGCGGCATTAAATTTCTCACCTACTATAAAAAATTGTCTGCTGTATCGTCCGTTTCATCAA
CTGAACAACTCCATTTGTATCGCTACATGCAGCTTATCAACAAACTTGAATTTTCGATTCCTCTAACAACAATATGTCTA
TTTCGCGTAACCTTCATCCGCAATGTGGTGATCCCAACATAACCCATATGTTGAAAGATAAAAGCTATAAAAAATCGTGAGAA
CCACAATATTGACAAAGAGATTAATGAGAAGAAATGATAAGCACATGCTGGATGATAACGTGTGCGTTGATTACCATGATGAA
ACACCCCTTCATAATAAGAAAGAAATGAATAAATATGATCATGTGCAAAATTTTCGAAAAATAACATCGTTAACAAAAACAATG
AACTGAAAAACCAGCATGTATATGTCAATACCTCTCTGGATCGTTCGCTGAAAAACGTTCTGCGCCAGACCACGAACCTGGA
AAATTACCTGAATTATTATGACAATATGTTCTTTACCTATCTGAAAAAGAAATATTACAAACGCTGCATGTCAACCACAAAA
AAGATTACGCATGAAGAAGAGACGTACACTAACGTCCATGATACCCATAACGGCAACATCAAAAAATAACGCAACATCACCA
AAATTCACAAAAGTTATAACACCTATAAAAACTCCGATATAAATTTAATCAATCGTAACGTGCATTTGAAAAAACAATTAA
ATGCTACAACATATCAGGATGCGCATAACATCTTTATGAACGAATACCTTTAAATGCAAAACAATCTGTATAACATCTTTTTT
CCGCGTTACAACATGGAACACTGATCAAAATTAACAAAAAATGTACGAGAAAAACATTTACCTGAAAAATTTTAACTTCT
TCGAACCTCTGCTGCTGCCTTCTAACTCATCCGCTCGAAATTCGTATAACATCATCCGTAAATATGTCAAGGTAAACAT
TAAATATGCCAAGATAGAACGGATTTATGAACAAATGATTGCGTACATTAATGAATATATCAACGTGATAAAACAAAATAC
GGTACCACGCAATCGTTTCATCAATCGCATATATTCAACGATGATGATACTATGTTTCGACAATAAAATGCGTGTTTCAGATA
AAAGCAAAAAGGAAAAATAAAATCCTGAACGTGAAAATTAAGGATTTGTTGGGGATACCAAAATGAGGAGGTGAACCTTTGT
GGTGATTAATATTACTAAAGTAAGTCAATCCTTCTCCAAACAACCTGTTCCGGATTATTGAACGCGATATGATCGAAGAT
ATTACCAAAGGACGCAACGCCTCCACATGGACGATAAACAACGCGACGATAATAAACGCGACGATAACAACGCGACGATA
ACAAACGCGACGATAACAACGCGGACGATAATAAACGCGACGATAACAACGCGTACGATAATAAACGCGACGATAATAAACG
CGACGATAACAACGCGTACGACAACAACGCGGACGATAACAACGCGGACGATAATAAACGCGGATGATAAAAAAGATACCCAC
ATTCAGCACGATAAGGATATTACATCACAACCTTTTTTCCCTCACAACAAAATTACAATTGCCAACGAGAAATGTATTAAAA
ACGATGAATACATTGACAACAGCCTGGTCTGTTTTAAAGAAAAAAGCGCCAATATCTTTGTCCATAATAATATTTCCACGGA
GGTGTCTCGCCTGAAAAAATATGATATCACGAAAAAGAACGATAAAAAAGAACATCTTTCTTCTAATCAAAAAAGCGGAAAAA
AAAAAAGAAAAAATTTACATTCACATTCGATACATTAAAAAATGATTATGTTTATCTGGAAAAAATATCTCCG
TTAATAAATTTCTGACCTTTCACAAGATCCCGTATATTTATCAGACCGCGCTGCCGTTATTGAAATTATCAATTTTAATAA
TAACCATATTCTGTTTTTTTATTTGTTCCCGAAGTGAAAAGCCCGTATTTCACTCTGCGAGAAAAACGTTTCCACAAAAA
TATATGAATACACATTTTGTATTATAGTATCAAATTCAGGGGATCCGTGACCGTACGGACGTCGGAAACCAATACCAATC
CTTTGTTAGGTTTAGACAGTACAGGAGGTAAACCTATACCTAATCCTTTATTGGGTCTTGATTCAACTGGTGGAAACCTAT
TCCAAATCCATTATTAGGATTAGATTCTACATAAGGGCCC

Appendix Figure S6. Sequence of codon-modified full-length *pftiS* (in blue font) as synthesized. AvrII (CCTAGG) and *Psp*OMI (GGGCCC) sites are underlined. The 3xV5 sequence is in magenta.

trpftilS-3xV5

CCTAGGATGATTAAATGTATCAAAAAGAATCAGGATGTGCTGCAGTTGGTAGAAGGATACTGGCTGTTAACGCTGAAAAACA
 AATATATGTTTTCTTTCTGAAAAAAGAAAAAATTATCTTCAGCGTGTCAAGTGGGGTGGACTCTTTGTGCCTTCTTTA
 TAGCTTCATCTTTGTTATCTATAAAATTCTGATCAGCATGATTTACAAAAATAAAAGTTATTTTGGCTTTATGAATAAAATC
 AACAGCGTGTATAGCTTTACTCATGAAGATATTATTGATATCATCAAAGAATACCGTTATGAAAACAATGTCAGCTTCTTTC
 TGTGATCCTGAGCAAAATTATCGTGATTTACTGTCATCATAATACCGTAAAGAATGTACCTCAGAAATGATTTTTCTTAA
 AAACATTTGCAAAAAATTCGGTATCCACTTTAAATCCAAAAAAGTACGCGAAAAGAGTATTGAGAACTGAATGTAATAAAC
 TTAAAAACGAAAAAGAAAAATTACGAAAGCAATGTGAATAAGAAAATTAATATTAACATGATGAAGAATAAAAAAATTTCC
 TGCTGCTAGCACGAACCTGGCGTCGTAACATCTACGTGCACCTCTCCAACGATATTTTGAAACGGGACATGAACAACAATAT
 TTATCACAACAACAAAATGAAAGATTCCCATATAACAACAACAATAACGATAATAACAACACGAGCATGAAGGACCCCTG
 AATATGTTAGATGCTTATACCTACGAAAAATATATTTACGATATTAACAATTATATCAAAATCACCAACAAAAAATGCATCA
 CCAACGTCCTGATTAAAGAAAGAATCATTTCAGTAAGGAGTACTCCAACGATTCGATCATGCGCAAGAAGAAAAAGGAAGGTCT
 GCTTTTCAATAATATTATGAACCTGCAGAATAATAACATTAATAATTATCAACAACACTTGCAGCAATAATATTTACAATATG
 AAATATACTAATGTTTTTCTGAACAAATATTGCATCCTGAAAAAAGATTAAATCAATCGTGTTCCTCGGCCACCACCAGA
 ACGACAACAACGAAACGGTGTGCTTTCAGTTCTTCCGTGGTGTTTTTTAAAAAACCTGCGCGGCATTAAATTTCTCACCTA
 CTATAAAAAATTGTCTGCTGTATCGTCCGTTTCATCAAACCTGAACAACTCCATTTGTATCGCTACATGCAGCTTATCAACAAA
 ACTTGGAAATTCGATTCTCTAACAACAATATGTCTATTTTCGCGTAACCTTCATCCGCAATGTGGTGATCCCAACATAACCC
 ATATGTTGAAAGATAAAAGCTATAAAAAATCGTGAGAACCACAATATTGACAAAGAGATTAATGAGAAGAATGATAAGCACAT
 GCTGGATGATAACGTGTGCGTTGATTACCATGATGAAACACCCCTTCATAATAAGAAAGAAATGAATAAATATGATCATGTG
 GAAATTTTCGAAAAATAACATCGTTAACAAAAACAATGAACCTGAAAAACAGCATGTATATGTCAATACCTCTCTGGATCGTC
 GCCTGAAAAACGTTCTGCGCCAGACCAGAACCTGGAAAAATTACCTGAATTATTATGACAATATGTTCTTTACCTATCTGAA
 AAAGAAATATTACAAACGCTGCATGTCAACCACAAAAAAGATTACGCATGAAGAAGAGACGTACACTAACGTCCATGATACC
 CATAACGGCAACATCAAAAAATAAACGCAACATCACCAAAATTCACAAAAAGTTATAACACCTATAAAAACTCCGATATAAATT
 TAATCAATCGTAACGTGCATTTGAAAAAACAATTAATGCTACAACCTATCAGGATGCGCATAACATCTTTATGAACGAATA
 CTTTAAATGCAAAACAATCTGTATAACATCTTTTTCCCGCGTTACAACATGGAAACACTGATCAAAATTAACAAAAAAGT
 TACGAGAAAAACATTTACCTGAAAATTTTTAACTTCTTCGAACTCCTGCTGCTGCCTTCTAACTCATCCGCCTCGAAATTC
 TGTATAACATCATCCGTAAATATGTCAAGGTAAACATTAATATGCCAAGATAGAACGGATTTATGAACAAATGATTGCGTA
 CATTAATGAATATATCAAACGTGATAAAACAAAAATACGGTACCACGCAATCGTTTCATCAATCGCATATATTCAACGATGAT
 GATACTATGTTTCGACAATAAAATGCGTGTTCAGAATAAAAGCAAAAAGGAAAAATAAAATCCTGAACGTGAAAATTAAGGATT
 TGTTTGGGGATACCAAAATTGAGGAGGTGAACCTTTGTGGTGATTAATATTACTAAAAGTAAGTCAATCCTTCTCCAAAACAA
 CCTGTTCCGGATTATTGAACGCGATATGATCGAAGATATTACCAAAGGACGCAACGCCTCCACATGGACGATAACAAACGC
 GACGATAATAAACGCGACGATAACAAACGCGACGATAACAAACGCGACGATAACAAACGGGACGATAATAACGCGACGATA
 ACAAACGTGACGATAATAAACGTGACGATAATAAACGCGACGATAACAAACGTGACGACAACAAACGGGACGATAACAAACG
 GGACGATAATAAACGGGATGATAAAAAAGATACCCACATTCAGCAGCATTAAGGATATTACATCACAAACCTTTTTCCCTCAC
 AACAAAATTACAATTGCCAACGAGAAATGTATTAATAACGATGAATACATTGACAACAGCCTGGTCTGTTTTAAAGAAAAA
 GCGCCAATATCTTTGTCCATAATAATATTTCCACGGAGGTGTCTCGCCTGAAAAAATATGATATCACGAAAAAGAACGATAA
 AAAGAACATCTTTCTTCTAATCAAAAAGCGGAAAAAAGAAAAAATTTACATTCACATTCGATACATTAAAAAA
 AATGATTATGTTTATCTGGAATAAAAAAATCTCCGTTAATAAATTTCTGACCCTTCACAAGATCCCGTATATTTATCAGA
 CCGCGCTGCCGGTTATTGAAATTATCAATTTTAATAATAACCATATTCTGTTTTTTTATTTGTTCCCGGAAGTGAAAAGCCC
 GTATTTCACTCTGCGAGAAAAACGTTTCACAAAAATATATGAATACATTTTGTATTATAGTATCAAAATCAAGGGGATC
 CGTGACCGTACGGACGTCGGAAACCAATACCAATCCTTTGTTAGGTTTAGACAGTACAGGAGGTAAACCTATACCTAATC
 CTTTATTGGGTCTTGATTCAACTGGTGGAAACCTATTCCAAATCCATTATTAGGATTAGATTCTACATAAGGGCCC

Appendix Figure S7. Sequence of codon-modified N-terminally truncated *pftils* (in blue font) as synthesized. *AvrII* (CCTAGG) and *PspOMI* (GGGCCC) sites are underlined. The 3xV5 sequence is in magenta.

Appendix Table S1. Primers used in this study. Restriction enzyme sites are underlined.

Primer name	Sequence (5'→3')	Primer description
Primers to amplify homology arms (HA) and guide RNA (gRNA) annealing for <i>pftiS</i> knockout		
TiIS.HA1F	GTGCCACGAGCGGCCGCAGGTTCCAT AGAAATGTTGTGTG	Forward for HA1 amplification
TiIS.HA1R	AAGCGCAGCGGCCGCGTAAAACATCT TGATTCTTTTAAATACA	Reverse for HA1 amplification
TiIS.HA2F	TTCGACAGACGCCGGCAAAGGATATA TGAACAGATGATAGCA	Forward for HA2 amplification
TiIS.HA2R	TGGCCACCAGCCGGCATCATGTTGTA TATGTGTATCTTTTT	Reverse for HA2 amplification
TiIS.gRNA.pF	/5Phos/TATTTCAAGATGTTTTACA ACTTG	5'-phosphorylated guide RNA forward oligo
TiIS.gRNA.pR	/5Phos/AAACCAAGTTGTAAAACAT CTTGA	5'-phosphorylated guide RNA reverse oligo
Primers for <i>pftiS</i> gene knockout confirmation		
TiIS.5.F	ATGTGTCGAAGAGATGGCAATTTTTC ATACCACAT	Forward for 5' and Δ5' PCR
TiIS.5.WT.R	TATGAATGAATAAAGTAGACACAAAG AATCTACCCCTGA	Reverse for 5' PCR
TiIS.3.WT.F	TGAACTTTTATTATTACCCTCTAAAC TAATTAGACTAGAAAT	Forward for 3' PCR
TiIS.3.R	TACAAAAATGTTAGCACTTTTTTCTT TAAAGCACACTAATG	Reverse for 3' and Δ3' PCR
pRS.F	CATATTTATTAAATCTAGAATTTCGAC AGACGCCG	Forward for Δ3' PCR
pRS.R	TACAAAATGCTTAAGCGCAGCGGCC	Reverse for Δ5' PCR

Primers to amplify representative genes from nuclear and organellar genome		
LDH.F	GGAGATGTAGTTTTGTTTCGATATTG	Forward for PCR
LDH.R	CTTGTAAGGGATACCACCTACAG	Reverse for PCR
SufB.F	CATGTAGCTATAGTAGAAATAATAGT AAAAGATTATGG	Forward for PCR
SufB.R	GACTCTGAAATACTTAAACCACGTTG C	Reverse for PCR
Cox1.F	CTTCATCTTTAAGAATAATTGCACAA GAAATGTAAATC	Forward for PCR
Cox1.R	GTACATATGATGTACCCATACTAAGC TTCC	Reverse for PCR
Primers for generation of pCLD- <i>ectilS-mcherry-10xapt</i> plasmid		
EcTils.InF F	GTTAGAAGGTTCGGGAATGACACTCA CGCTCAATAGACAAC	Forward for <i>ectilS</i> amplification
EcTils.InF R	GCCCTTGCTCGTACGACTAAGCGTTT TCTGCCAGACAAAAC	Reverse for <i>ectilS</i> amplification
Primers for confirmation of gene knock-in		
P230p.out.HA. F	GGTTGTGATTTTTTCAGGTGATTCC	Forward for attL and attB PCR
P230p.out.HA. R	GAAAATTGTAGGGGAGCTAAATCCG AC	Reverse for attR and attB PCR
attB.Int.F	GCAGTGTGGAATTCCCTGCA	Reverse for attL PCR
attB.Int.R	TTAAGTGTAGTTAATTCATCAAATAG CATGC	Forward for attR PCR
Primers for sequencing		
pRS.R	TACAAAATGCTTAAGCGCAGCGGCC	For HA1 insertion in pRSng- <i>pftilS</i>

pRS.F	CATATTTATTAAATCTAGAATTCGAC AGACGCCG	For HA2 insertion in pRSng- <i>pftilS</i>
pL6.gRNA.F	GGGTAAATTATTATTAAAAAATGTAT ATGTTATG	For guide RNA insertion in pCasG-LacZ
CLD2.F	ACAACCTAGGATGAAGATCTTATTAC	Forward for <i>ectilS</i> insertion in pCLD- <i>ectilS</i> - <i>mcherry</i> - 10xapt
RFP.R	GAGGGCTCCGTGAACGGC	Reverse for <i>ectilS</i> insertion in pCLD- <i>ectilS</i> - <i>mcherry</i> - 10xapt
Cre.Ins.Seq.F	CAACCTAGATAACTTCGTATAGCATA CATTATACG	Forward for <i>pftilS</i> (full- length or truncated) insertion in pCre- <i>tr/pftilS</i> - 3xV5
TilS.Seq.F1	GGATGTGCTGCAGTTGGTAGAAGGA	Forward for <i>pftilS</i> (full- length or truncated) insertion in pCre- <i>tr/pftilS</i> - 3xV5
TilS.Seq.F2	CAGTAAGGAGTACTCCAACGATTCG	Forward for <i>pftilS</i> (full- length or truncated) insertion in pCre- <i>tr/pftilS</i> - 3xV5
TilS.Seq.F3	GACCACGAACCTGGAAAATTACC	Forward for <i>pftilS</i> (full- length or truncated) insertion in pCre- <i>tr/pftilS</i> - 3xV5
NewApt.5R	CTCGCTATCAAGGAATCGAGTCC	Reverse for <i>pftilS</i> (full- length or truncated) insertion in pCre- <i>tr/pftilS</i> - 3xV5

Appendix Table S2. Proteins used for phylogenetic analysis presented in Appendix Fig. S3. ^aUniprot ID, ^bPlasmoDB ID, ^cToxoDB ID, ^dPiroplasmaDB ID.

Species	Accession	Gene name
Only Syngen Nebraska virus 5 (Nv) (Chlorovirus)	A0A1J0F9X6 ^a	OS5_287L
<i>Chlorella sorokiniana</i> (Freshwater green alga)	A0A2P6TQ55 ^a	C2E21_4934
<i>Gracilaria tenuistipitata</i> var. <i>liui</i> (Red alga)	Q6B8L1 ^a	tiIS, ycf62, Grc000193
<i>Oryza sativa</i> (Monocot)	B8AFB7 ^a	Osl_06667
<i>Zea mays</i> (Monocot)	A0A804PGD6 ^a	tiIS
<i>Zingiber officinale</i> (Monocot root plant)	A0A8J5GGP9 ^a	ZIOFF_041066
<i>Arabidopsis thaliana</i> (Dicot)	F4J7P7 ^a	RSY3
<i>Perkinsus olseni</i> (Dinoflagellate)	A0A7J6UN02 ^a	FOZ63_029171
<i>Synechocystis</i> sp, PCC 6803 (Freshwater cyanobacteria)	P74192 ^a	tiIS, slr1278
<i>Vitrella brassicaformis</i> CCMP3155 (Dinoflagellate)	A0A0G4FYP9 ^a	Vbra_16478
<i>Escherichia coli</i> (Gram-negative bacteria)	P52097 ^a	tiIS, mesJ
<i>Geobacillus kaustophilus</i> (Thermophilic Gram-positive bacteria)	Q5L3T3 ^a	tiIS, GK0060
<i>Bacillus subtilis</i> (Gram-positive bacteria)	P37563 ^a	tiIS, yacA
<i>Aquifex aeolicus</i> (chemolithoautotrophic Gram-negative bacteria)	O67728 ^a	tiIS, aq_1887
<i>Mycoplasma genitalium</i> (Gram-negative bacteria)	P47330 ^a	tiIS, MG084
<i>Plasmodium falciparum</i> (Apicomplexan)	PF3D7_0411200 ^b	tiIS, PP-loop family protein
<i>Toxoplasma gondii</i> (Apicomplexan)	TGME49_215100 ^c	tiIS, PP-loop family protein
<i>Neospora caninum</i> (Apicomplexan)	NCLIV_052110 ^c	tiIS, hypothetical protein

<i>Eimeria tenella</i> (Apicomplexan)	ETH2_0718500 ^c	tiIS, PP-loop family protein
<i>Babesia microti</i> (Apicomplexan)	BMR1_01G01110 ^d	tiIS, PP-loop family protein
<i>Theileria annulata</i> (Apicomplexan)	TA03600 ^d	tiIS, hypothetical protein

Appendix Table S3. tRNAs used for phylogenetic analysis presented in Fig. EV2.

Accession ID for apicoplast-genome-encoded tRNAs are provided. *Pfal*, *Plasmodium falciparum*; *Tgon*, *Toxoplasma gondii*; *Eten*, *Eimeria tenella*; *Bmic*, *Babesia microti*; *Tpar*, *Theileria parva*; *Hmar*, *Haloarcula marismortui*; *Mmob*, *Mycoplasma mobile*; *Bsub*, *Bacillus subtilis*; *Ecol*, *Escherichia coli*; *Cpan*, *Cycas panzhihuaensis*; *Slyc*, *Solanum lycopersicum*; *Scer*, *Saccharomyces cerevisiae*.

tRNA	Accession ID	Sequence (5' → 3')
<i>Pfal</i> _trnM-CAU1	PF3D7_API06600	AGCGAAAUAGAGCAUAAGGAAAGUUCGUCGGAUUC AUGCUCCGAAGGUAAUCGGUUCAAUUCGUAUUUUC GCUUA
<i>Pfal</i> _trnM-CAU2	PF3D7_API00600	AACAUUUUAUAGCUAAGUGGUCGAAAGCAAUGGACU CAUAAUUCAUUUUCAUAUAUUGAUCAGUAGUU CGAAUCUACUUAUAUGU
<i>Pfal</i> _trnM-CAU3	PF3D7_API05000	AGCGAAAUAGAGCAUAAGGAAAGUUCGUCGGAUUC AUGCUCCGAAGGUAAUCGGUUCAAUUCGUAUUUUC GCUU
<i>Pfal</i> _trnI-GAU	PF3D7_API05800	AUAGGUUUUAGUUUAAUGGUUAAAACAUACUCUU GAUAAGGGUAAAAUUUAGUUCAAUUCUAAAAUAA CC
<i>Tgon</i> _trnM-CAU1	TGME49_355180	AGCGGGGUAGAGCAGGUUGGUAGCUCGUCGGGCUC AUGACCCGAAGGUCAGCGGUUCAAUCCGCUCCUC GUUU
<i>Tgon</i> _trnM-CAU2	TGME49_355060	AUACUUGUGGCUGAGUGGGCAAAGCAGUGAGCUC AUAACUCAUAUAAAACGAAAGUUCGAAUCUUUUCA AGUUA
<i>Tgon</i> _trnI-GAU1	TGME49_355100	AGGCUAGUAGCUCAACGGUAGAGCACGCUUUUGAU AAGGGCGUGGUUUCUGGUUCGAUUCAGGGUGGCC UA
<i>Tgon</i> _trnI-GAU2	TGME49_355110	AGGCUAGUAGCUCAACGGUAGAGCACGCUUUUGAU AAGGGCGUGGUUUCUGGUUCGAUUCAGGGUGGCC UA
<i>Eten</i> _trnM-CAU1	ETH2_API00800	AAACGGAGUAGAGCAGUCUGGUUAGCUCAUCGGGC UCAUGAUCCGAAGGUCAACGGUUCAAUCCGUUCU CCGUUUU
<i>Eten</i> _trnM-CAU2	ETH2_API01500	UGUACCUGUGGCUGAGUGGUCAAAAGCGGUGGGCU CAUAAUCCAUUUUUUUUCAAAAGUCAAUCUUUU CAGGUUAUA
<i>Eten</i> _trnM-CAU3	ETH2_API05600	AAACGGAGUAGAGCAGUCUGGUUAGCUCAUCGGGC UCAUGAUCCGAAGGUCAACGGUUCAAUCCGUUCU CCGUUUU

<i>Eten_trnI</i> -GAU1	ETH2_API00100	GGGCUGUUAGCUCAUCGGUAGAGCGCGCCCCUGAU AAGGGCGAGGUACCUGGUUCAACCCCAGGACGGCC UA
<i>Eten_trnI</i> -GAU2	ETH2_API06300	GGGCUGUUAGCUCAUCGGUAGAGCGCGCCCCUGAU AAGGGCGAGGUACCUGGUUCAACCCCAGGACGGCC UA
<i>Bmic_trnM</i> -CAU1	BmR1_api00060	AAUAAGAUUAGUAAUAAGGAAACUUACCAGCUUC AUGGUCUGGAGAUUGCAGUUCGAGUCUGCAUCUUA UUU
<i>Bmic_trnM</i> -CAU2	BmR1_api00070	AUAUCUGUAGCUUAGUGGUUAUAGCAAUGGGCCCA UGACUCAUUAUUUCAGUAGUUCAAAUCUACUCAG AUAUA
<i>Bmic_trnM</i> -UAU	BmR1_api00200	AAUAAUUUAUUUUUUUAUAUAUAUAUAUAUAUAU AUAUAAAAUAAUAAUAUUU
<i>Bmic_trnI</i> -GAU	BmR1_api00090	AGAUUUUUAGUUUACUGGUAAAACAUUCUUUGAU AAGGAUAAAAUAUUUGGUUCAAUUCCAAAAAAAU UA
<i>Tpar_trnM</i> -CAU	TpMuguga_05g00051	GUAUCUAUAGCUUAGAGGCUAAAGCGAUGAGUUCA UACCUCAUGUACAGUAGUUCAAAUCUACUUAGAUA UA
<i>Tpar_trnI</i> -GAU	TpMuguga_05g00069	GGACUUUUAGCUUAAUUGUUAAGUUUACAUGUGA UAUAUGUGAGAGUUUUGGUUAAAAUCCAAAAAGU CCA
<i>Hmar_trnM</i> -CAU		GCCCGGGUGGCUUAGCUGGACAUAGCGCCGCACUC AUAAUGCGGAGAUUCGAGGGUUCGGA
<i>Hmar_trnI</i> -M-CAU		AGCGGGAUGGGAUAGCCAGGAGAUUCCGGCGGGCU CAUAACCCGCAGAUUCGGUAGUUCAAAUCUACCUCC CGCUA
<i>Hmar_trnI</i> -CAU		GGGCCCUIAGCUUAGUCUGGUUAAAGCGAUCGGCU CAUAACCGAUUGAGCGCUGGUUCAAAUCCGGCAGG GCCCA
<i>Hmar_trnI</i> -GAU		GGGCCAAUAGCUCAAUCAGGUUGAGCGCUCGGCUG AUAACCGGGAGGUUCGCGGUUCAAAUCCGCGUUGG CCCA
<i>Mmob_trnM</i> -CAU		GGCUCUGUAGCUCAGCUGGUUAGAGCAUUCGGUUC AUACCCGAAAGGUCAAGAGUUCGACUCUCUUCGGA GCUACCA
<i>Mmob_trnI</i> -GAU		GGGAGCGUAGCUCAGCUGGUUAGAGCACACGACUG AUAUUCGUGAGGUCAUGGUUCGAGUCCAUUCGUU CCCACCA

<i>Mmob_trnI</i> -UAU		GGUCCUAUAGCUCAGUCGGUUAGAGCACACGACUU AUAUUCGUGAGGUCGCUGGUUCAAUCCCAGCUAGG ACUACCA
<i>Bsub_trnM</i> -CAU1		GGCGGUGUAGCUCAGCUGGCUAGAGCGUACGGUUC AUACCCGUGAGGUCGGGGGUUCGAUCCCCUCCGCC GCUACCA
<i>Bsub_trnM</i> -CAU2		GGCGGUGUAGCUCAGCUGGCUAGAGCGUACGGUUC AUACCCGUGAGGUCGGGGGUUCGAUCCCCUCCGCC GCUACCA
<i>Bsub_trnf</i> M-CAU1		CGCGGGGUGGAGCAGUUCGGUAGCUCGUCGGGCUC AUAACCCGAAGGUCGCAGGUUCAAUCCUGCCCCC GCAACCA
<i>Bsub_trnf</i> M-CAU2		CGCGGGGUGGAGCAGUUCGGUAGCUCGUCGGGCUC AUAACCCGAAGGUCGCAGGUUCAAUCCUGCCCCC GCAACCA
<i>Bsub_trnf</i> M-CAU3		CGCGGGGUGGAGCAGUUCGGUAGCUCGUCGGGCUC AUAACCCGAAGGUCGCAGGUUCAAUCCUGCCCCC GCAACCA
<i>Bsub_trnI2</i> -CAU1		GGACCUUUAGCUCAGUUGGUUAGAGCAGACGGCUC AUAACCGUCCGGUCGUAGGUUCGAGUCCUACAAGG UCCACCA
<i>Bsub_trnI</i> - GAU1		GGGCCUGUAGCUCAGCUGGUUAGAGCGCACGCCUG AUAAGCGUGAGGUCGAUGGUUCGAGUCCAUUCAGG CCCACCA
<i>Bsub_trnI2</i> -GAU1		GGGCCUGUAGCUCAGCUGGUUAGAGCGCACGCCUG AUAAGCGUGAGGUCGGUGGUUCGAGUCCACUCAGG CCCACCA
<i>Bsub_trnI2</i> -GAU2		GGGCCUGUAGCUCAGCUGGUUAGAGCGCACGCCUG AUAAGCGUGAGGUCGGUGGUUCGAGUCCACUCAGG CCCACCA
<i>Ecol_trnfM</i> -CAU1		CGCGGGGUGGAGCAGCCUGGUAGCUCGUCGGGCUC AUAACCCGAAGGUCGUCGGUUCAAAUCCGGCCCCC GCAACCA
<i>Ecol_trnfM</i> -CAU2		CGCGGGGUGGAGCAGCCUGGUAGCUCGUCGGGCUC AUAACCCGAAGGUCGUCGGUUCAAAUCCGGCCCCC GCAACCA
<i>Ecol_trnfM</i> -CAU3		CGCGGGGUGGAGCAGCCUGGUAGCUCGUCGGGCUC AUAACCCGAAGGUCGUCGGUUCAAAUCCGGCCCCC GCAACCAA

<i>Ecol_trnfM</i> -CAU4		CGCGGGGUGGAGCAGCCUGGUAGCUCGUCGGGCUC AUAACCCGAAGAUCGUCGGUUCAAAUCCGGCCCCC GCAACCA
<i>Ecol_trnM</i> -CAU1		GGCUACGUAGCUCAGUUGGUUAGAGCACAUCACUC AUA AUGAUGGGGUCACAGGUUCGAAUCCCGUCGUA GCCACCA
<i>Ecol_trnM</i> -CAU2		GGCUACGUAGCUCAGUUGGUUAGAGCACAUCACUC AUA AUGAUGGGGUCACAGGUUCGAAUCCCGUCGUA GCCACCA
<i>Ecol_trnI</i> -GAU1		AGGCUUGUAGCUCAGGUGGUUAGAGCGCACCCCUG AUAAGGGUGAGGUCGGUGGUUCAAGUCCACUCAGG CCUACCA
<i>Ecol_trnI</i> -GAU2		AGGCUUGUAGCUCAGGUGGUUAGAGCGCACCCCUG AUAAGGGUGAGGUCGGUGGUUCAAGUCCACUCAGG CCUACCA
<i>Ecol_trnI2</i> -CAU1		GGCCCCUAGCUCAGUGGUUAGAGCAGGCGACUCA UAAUCGCUUGGUCGCUGGUUCAAGUCCAGCAGGGG CCACCA
<i>Ecol_trnI2</i> -CAU2		GGCCCCUAGCUCAGUGGUUAGAGCAGGCGACUCA UAAUCGCUUGGUCGCUGGUUCAAGUCCAGCAAGGG CCACCA
<i>Ecol_trnI</i> -GAU3		AGGCUUGUAGCUCAGGUGGUUAGAGCGCACCCCUG AUAAGGGUGAGGUCGGUGGUUCAAGUCCACUCAGG CCUACCA
<i>Cpan_trnM</i> -CAU1		ACCUACUUAACUCAGUGGUUAGAGUAUCGCUUUA UACGGCGGGAGUCAUUGGUUCAAUCCAAUAGUAG GUA
<i>Cpan_trnM</i> -CAU2		UGCGGGGUAGAGCAGUUUGGUAGCUCGCAAGGCUC AUAACCUUGAGGUCACGGGUUCAAUCCCGUCUCC GCCA
<i>Cpan_trnI</i> -GAU1		UGGGCUAUCCUGGACUUGAACCAGAGACCUCGCCC GUAUCAGGGGCGCGCUCUACCACUGAGCUAAUAGC CC
<i>Cpan_trnI</i> -GAU2		GGGCUAUUAGCUCAGUGGUAGAGCGCGCCCCUGAU GGGCGAGGUCUCUGGUUCAAGUCCAGGAUAGCCCA
<i>Cpan_trnI</i> -AUA		GCAUCCAUGGCUGAACGGUUAAGCGCCCAACUCA UAAUUGGCGAAUUCGCAGGUUCAAUUCCUGCUGGA UGCA

<i>Slyc</i> _trnfM-CAU		CGCGGGGUAGAGCAGUUUGGUAGCUCGCAAGGCUC AUAACCUUGAGGUCACGGGUUCAAUCCUGUCUCC GCAA
<i>Slyc</i> _trnM-CAU		ACCUACUUAACUCAGUGGUUAGAGUACUGCUUUCA UACGGCGGGAGUCAUUGGUUCAAUCCAAUAGUAG GUA
<i>Slyc</i> _trnI-CAU		GCAUCCAUGGCUGAAUGGUUAAAGCGCCCAACUCA UAAUUGGCGAAUUCGUAGGUUCAAUUCCUACUGGA UGCA
<i>Slyc</i> _trnI-GAU		GGGCUAUUAGCUCAGUGGUAGAGCGCGCCCCUGAU AAUUGCGGGGCGAGGUCUCUGGUUCAAGUCCAGGA UGGCCCA
<i>Scer</i> _trnIM-CAU1		AGCGCCGUGGCGCAGUGGAAGCGCGCAGGGCUCAU AACCUGAUGUCCUCGGAUCGAAACCGAGCGGCGC UA
<i>Scer</i> _trnIM-CAU2		AGCGCCGUGGCGCAGUGGAAGCGCGCAGGGCUCAU AACCUGAUGUCCUCGGAUCGAAACCGAGCGGCGC UA
<i>Scer</i> _trnIM-CAU3		AGCGCCGUGGCGCAGUGGAAGCGCGCAGGGCUCAU AACCUGAUGUCCUCGGAUCGAAACCGAGCGGCGC UA
<i>Scer</i> _trnIM-CAU4		AGCGCCGUGGCGCAGUGGAAGCGCGCAGGGCUCAU AACCUGAUGUCCUCGGAUCGAAACCGAGCGGCGC UA
<i>Scer</i> _trnIM-CAU5		AGCGCCGUGGCGCAGUGGAAGCGCGCAGGGCUCAU AACCUGAUGUCCUCGGAUCGAAACCGAGCGGCGC UA
<i>Scer</i> _trnM-CAU1		GCUUCAGUAGCUCAGUAGGAAGAGCGUCAGUCUCA UAAUCUGAAGGUCGAGAGUUCGAACCUCUCCUGGA GCA
<i>Scer</i> _trnM-CAU2		GCUUCAGUAGCUCAGUAGGAAGAGCGUCAGUCUCA UAAUCUGAAGGUCGAGAGUUCGAACCUCUCCUGGA GCA
<i>Scer</i> _trnM-CAU3		GCUUCAGUAGCUCAGUAGGAAGAGCGUCAGUCUCA UAAUCUGAAGGUCGAGAGUUCGAACCUCUCCUGGA GCA
<i>Scer</i> _trnM-CAU4		GCUUCAGUAGCUCAGUAGGAAGAGCGUCAGUCUCA UAAUCUGAAGGUCGAGAGUUCGAACCUCUCCUGGA GCA

Scer_trnM-CAU5		GCUUCAGUAGCUCAGUAGGAAGAGCGUCAGUCUCA UAAUCUGAAGGUCGAGAGUUCGAACCUCUCCUGGA GCA
Scer_trnM-CAU6		UGCAAUAUGAUGUAAUUGGUUAAACAUUUUAGGGUC AUGACCUAUUUAUACGUUCAAAUCGUUUUAUUG CUA
Scer_trnM-CAU7		GCUUGUAUAGUUUAAUUGGUUAAAACAUUUGUCUC AUAAAUAAAUAAUGUAAGGUUCAAUUCCUUCUACA AGUA
Scer_trnI-AAU1		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU2		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU4		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU3		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU5		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU6		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU7		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU9		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU8		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnI-AAU10		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA

Scer_trnl-AAU11		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnl-AAU12		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnl-AAU13		GGUCUCUUGGCCCAGUUGGUUAAGGCACCGUGCUA AUAACGCGGGGAUCAGCGGUUCGAUCCCGCUAGAG ACCA
Scer_trnl-GAU		GAAACUAUAAUUCAAUUGGUUAGAAUAGUAUUUUG AUAAGGUACAAAUUAGGUUCAUCCCGUUAGUU UCA
Scer_trnl-UAU1		GCUCGUGUAGCUCAGUGGUUAGAGCUUCGUGCUUA UAGCAACAUUCGGUUUCCGAAGUUUCUGUGCCAAA GACCUUUCAAACAGGCCUUUAAAAGCAACGCGACC GUCGUGGGUUCAAACCCCACCUCGAGCA
Scer_trnl-UAU2		GCUCGUGUAGCUCAGUGGUUAGAGCUUCGUGCUUA UAGCAACAUUCGGUUUCCGAAGUUUCUGUGCCAAA GACCUUUCAAACAGGCCUUUAAAAGCAACGCGACC GUCGUGGGUUCAAUCCCCCACCUCGAGCA