Predicted Toxoplasma FBPs

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FBP (putative)	RNA expression level	Cell cycle peak*	fold-change	Tag?	KO?	Overexpress?
TGME49_278815-H	high	S/M	3 logs			
TGME49_359350-H*	not reported	-	-			
TGME49_261370	high	M phase	3 logs^			
TGME49_299230+	very low	none	-			
TGME49_110910	medium	G1/S	<1 log			
TGME49_258900-H	high	S/M	3 logs			
TGME49_228380-H	high	C	2 logs			
TGME49_215620-H	medium	none				
TGME49_262530	medium	M/C	<1 log			
TGME49_243750+	low	none	-			
TGME49_305630	not reported	-	-			
TGME49_215210+	high	M/C	2 logs			
TGME49_275780	medium	none	-			
TGME49_225900+	high	M/C	3 logs			
TGME49_003040	high	M/C	2 logs			
TGME49_310930 •	high	none	-			

Data (Behnke et al 2010) reported at ToxoDB.org
+ reported also by Ponts et al 2008
* M= mitosis, C= cytokinesis
^ base 2

Fig. S4. Candidate F-box motif sequences from *Toxoplasma gondii* (type 1 strain ME49)

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Gene ID*            Length Start Sequence#                                                 domains

TGME49_278815-H   L=2186    84  LHLLPSSALSLLLRFL-HLDDVCRLALS-SKQLYLHPDLNTPFAVAHL
TGME49_359350-H*  L=1788   742  LRQLPPAILCAVLRFL-PCASVLAFGTT-CRYAHDLVQL--PAAWNLL
TGME49_261370     L=1618   941  WTSVPAEVLSTLCQFL-AVEDLVAFQRL-DRRAYAVGSH--ATVWRAL    WD40
TGME49_299230+    L= 636    16  PACLPTAIVFHVASFL-TPNDVCSMGAT-CRKWREVCCSDLQPLWREF    WD40
TGME49_110910^    L=3679   236  LESLSPCLLANLVSFL-LPLDIVSVSLC-SRSLLWLSRC--PFVWRRC    WD40
TGME49_258900-H   L=577      3  DLLQHPDIVGRILSCL-AWRERRQLAAV-CVSWREAAET--SPCWSDL
TGME49_228380-H   L=1726    42  PLCFDYPLCFDYLLSFL-DLRDFLTLSLV-SHSLRDILLSDLTRAARCV
TGME49_215620-H   L 1930    280 GAEAPEDARGCLLAFL-TWNDLARLRAV-SRQLKRLVEN-AALSARAV
TGME49_262530     L= 979   173  FAELPQEVLELIFSRL-GLADLSRCLCV-AKSWHPPLNA---VFAKTI    LRR
TGME49_243750+    L= 865   478  LCSLPQELLDVLPLYL-DAFALTRLSSC-CRLLHRLCGNRSDVCWRAK    TPR
TGME49_305630     L=2045    61  SPDGPCETIVFLLGFFLPVADLCSCSAV-CKAWWAVCTLQHQQLWRER
TGME49_215210+    L= 683   254  FNTCPAECLQAVFHFL-HVEDILRMQVV-SSAFFSTIRDEIGAFTHIR
TGME49_275780     L= 978   211  IDALPDDLLCEMLLFL-PFDEVGASIPLVSRRFCRLALL--PYIWTFF
TGME49_225900+    L=1461   160  LEALPAGCMYTLFAFF-DVSEVAELRLL-SRTVKAVVDS--PCSLRGC
TGME49_003040^    L=1894   311  FSDLPDVCVRICFSFL-SVEEILKYQFL-SRYIRRAIGL---DHVLPL
TGME49_310930•    L=808    444  FPFLDEPALSLLVPFL-FGRSLATCMTV-CPHWFMKINR---AMERMCG   AF-4
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*Sequence identifiers are from www.toxoDB.org/, version 8, except for ^=version 7.3 (see Table S2).
Acidic residues are in blue, basic in dark red, small in red, and hydrophobic in green. Positions matching the consensus motif (Fig. 1C) are highlighted in yellow (hydrophobic), gray (acidic), green (basic), or teal (small). Bolded residues correspond to the PxE motif, which is referred to as class 1; other s are referred to as class 2.
+= reported also by Le Roch [40]. * = Present only in GT1 strain, H= Identified by hidden markov model
H*= Identified at first in GT1 strain (since ToxoDB doesn't show the gene model for Me49 strain) and confirmed the presence in ME49 strain
• added by KR from MS data (2014)