SUPPLEMENTAL FIGURE LEGENDS

Figure S1. TgIF2K-B gene encodes a eIF2 kinase homologue. Schematic diagram depicting the TgIF2K-B genomic locus, is approximately 8.3 kb with two introns. Northern blot shows that the gene encodes an mRNA >9.0 kb containing an open reading frame of 7665 bp. The protein is predicted to be 2554 amino acid residues, with a large kinase domain (black) that is interrupted by two lengthy insertions (stippled boxes).

Figure S2. Alignment of the kinase domain from the *T. gondii* and human eIF2 kinase family members. Amino acid sequences from the kinase domain of the eIF2 kinases from *Homo sapiens* (Hs) [PKR, PEK, GCN2, and HRI] have been aligned with those in *T. gondii* (TgIF2K-A and –B). Letters in black boxes are residues identical in every kinase domain while shaded letters are residues that are chemically similar. Upper case letters in the consensus line represent identity and lower case letters denote conserved residues in at least 4 of the 6 species aligned. Kinase subdomains (I-XI) were represented using a black bar above the corresponding sequence. Dashes indicate gaps in the sequence that were removed to maximize the alignment. An insert of varying length is present in each eIF2 kinase domain between subdomains IV and V (represented by “///” in consensus line). A novel second insert is present in TgIF2K-A and -B between subdomains VII and VIII (represented by “\\\” in consensus line). The number of amino acid residues comprised by the insert is represented at its respective location. The threonine (T) residue underscored in subdomain VIII contributes to kinase activation via autophosphorylation during stress.

Figure S3. Predicted eIF2 kinase homologues in representative apicomplexan species. Schematic diagram depicting the predicted eIF2 kinase (eIF2K) protein structures in apicomplexans. Three classes of eIF2 kinases are represented in apicomplexans, including those containing transmembrane domains (TM), the TgIF2K-B present only in *T. gondii*, and the GCN2-like eIF2 kinases. Tg = *T. gondii*; Pf = *Plasmodium falciparum*; Cp = *Cryptosporidium parvum*; Ta = *Theileria annulata*. Accession numbers are listed on the figure. Stippled boxes represent transmembrane domains. Black boxes denote the catalytic (kinase) domain.

Figure S1

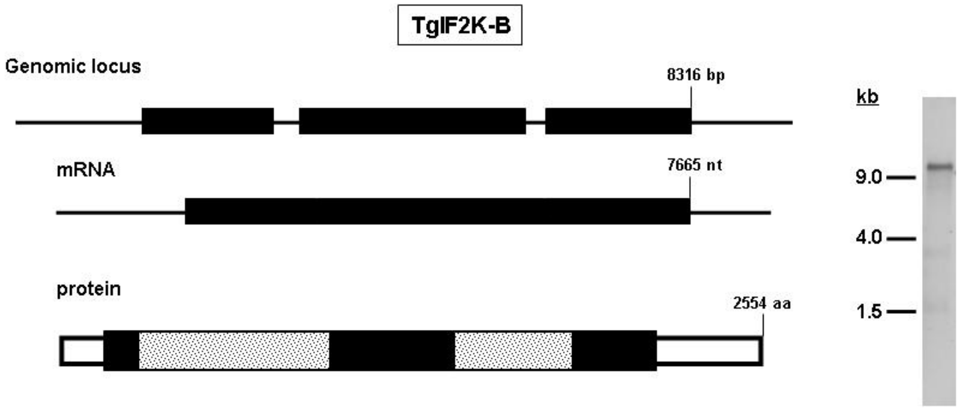
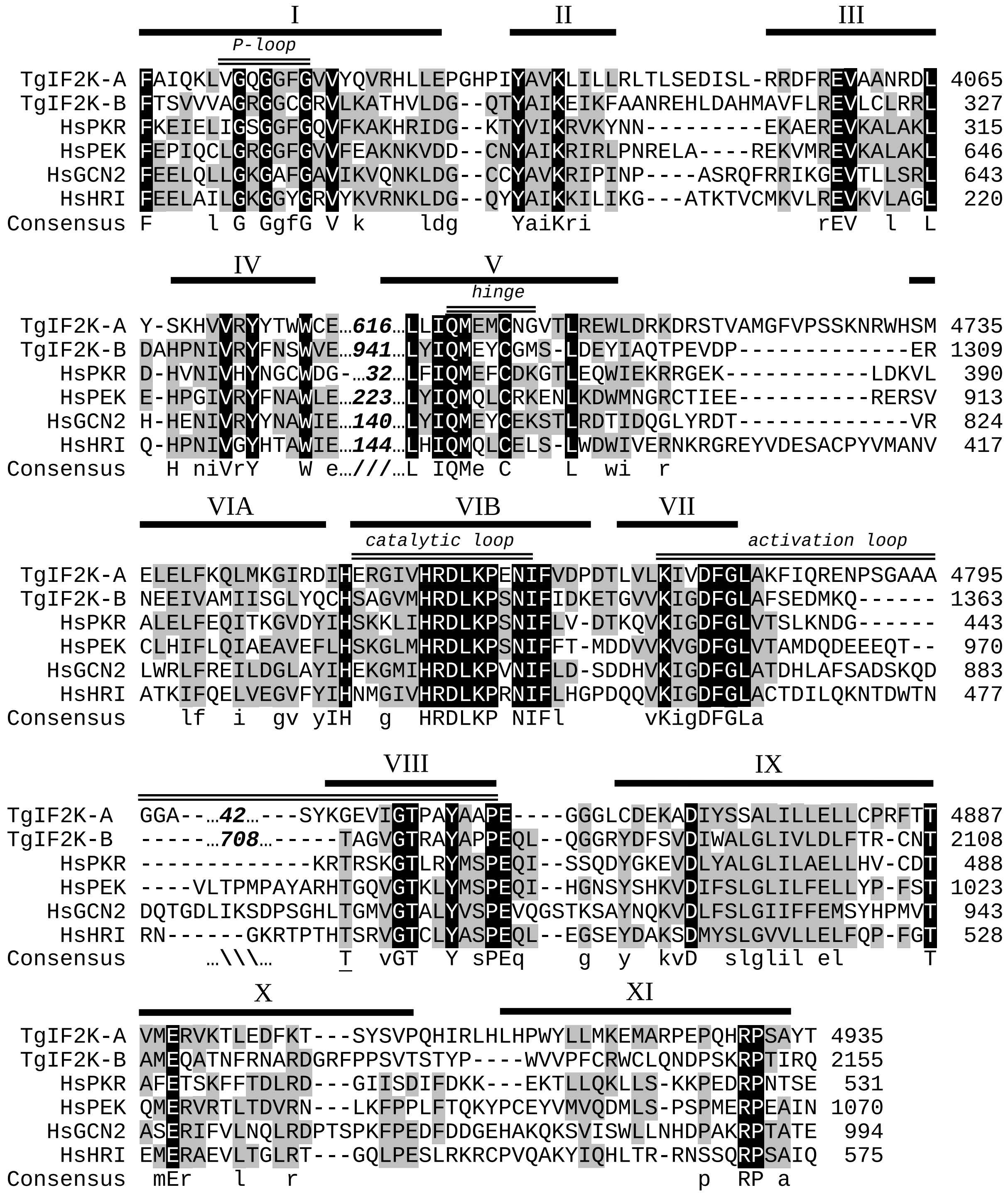

TgIF2K-B
Genomic locus
8316 bp
mRNA
7665 nt
protein
2554 aa
kb
9.0
4.0
1.5

Figure S2



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 TgIF2K-A FAIQKLVGQGGFGVVYQVRHLLEPGHPIYAVKLILLRLTLSEDISL-RRDFREVAANRDL 4065
 TgIF2K-B FTSVVVAGRGGCGRVLKATHVLDG--QTYAIKEIKFAANREHLDAHMAVFLREVLCLRRL  327
    HsPKR FKEIELIGSGGFGQVFKAKHRIDG--KTYVIKRVKYNN---------EKAEREVKALAKL  315
    HsPEK FEPIQCLGRGGFGVVFEAKNKVDD--CNYAIKRIRLPNRELA----REKVMREVKALAKL  646
   HsGCN2 FEELQLLGKGAFGAVIKVQNKLDG--CCYAVKRIPINP----ASRQFRRIKGEVTLLSRL  643
    HsHRI FEELAILGKGGYGRVYKVRNKLDG--QYYAIKKILIKG---ATKTVCMKVLREVKVLAGL  220
Consensus F    l G GgfG V k    ldg    YaiKri                 rEV  l  L

 TgIF2K-A Y-SKHVVRYYTWWCE…616…LLIQMEMCNGVTLREWLDRKDRSTVAMGFVPSSKNRWHSM 4735
 TgIF2K-B DAHPNIVRYFNSWVE…941…LYIQMEYCGMS-LDEYIAQTPEVDP-------------ER 1309
    HsPKR D-HVNIVHYNGCWDG-…32…LFIQMEFCDKGTLEQWIEKRRGEK-----------LDKVL  390
    HsPEK E-HPGIVRYFNAWLE…223…LYIQMQLCRKENLKDWMNGRCTIEE----------RERSV  913
   HsGCN2 H-HENIVRYYNAWIE…140…LYIQMEYCEKSTLRDTIDQGLYRDT-------------VR  824
    HsHRI Q-HPNIVGYHTAWIE…144…LHIQMQLCELS-LWDWIVERNKRGREYVDESACPYVMANV  417
Consensus   H niVrY   W e…///…L IQMe C     L  wi  r

 TgIF2K-A ELELFKQLMKGIRDIHERGIVHRDLKPENIFVDPDTLVLKIVDFGLAKFIQRENPSGAAA 4795
 TgIF2K-B NEEIVAMIISGLYQCHSAGVMHRDLKPSNIFIDKETGVVKIGDFGLAFSEDMKQ------ 1363
    HsPKR ALELFEQITKGVDYIHSKKLIHRDLKPSNIFLV-DTKQVKIGDFGLVTSLKNDG------  443
    HsPEK CLHIFLQIAEAVEFLHSKGLMHRDLKPSNIFFT-MDDVVKVGDFGLVTAMDQDEEEQT--  970
   HsGCN2 LWRLFREILDGLAYIHEKGMIHRDLKPVNIFLD-SDDHVKIGDFGLATDHLAFSADSKQD  883
    HsHRI ATKIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTN  477
Consensus    lf  i  gv yIH  g  HRDLKP NIFl      vKigDFGLa

TgIF2K-A  GGA--…42…---SYKGEVIGTPAYAAPE----GGGLCDEKADIYSSALILLELLCPRFTT 4887
TgIF2K-B  -----…708…-----TAGVGTRAYAPPEQL--QGGRYDFSVDIWALGLIVLDLFTR-CNT 2108
    HsPKR -------------KRTRSKGTLRYMSPEQI--SSQDYGKEVDLYALGLILAELLHV-CDT  488
    HsPEK ----VLTPMPAYARHTGQVGTKLYMSPEQI--HGNSYSHKVDIFSLGLILFELLYP-FST 1023
   HsGCN2 DQTGDLIKSDPSGHLTGMVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVT  943
    HsHRI RN------GKRTPTHTSRVGTCLYASPEQL--EGSEYDAKSDMYSLGVVLLELFQP-FGT  528
Consensus      …\\\…      T  vGT  Y sPEq    g  y  kvD  slglil el      T

 TgIF2K-A VMERVKTLEDFKT---SYSVPQHIRLHLHPWYLLMKEMARPEPQHRPSAYT 4935
 TgIF2K-B AMEQATNFRNARDGRFPPSVTSTYP----WVVPFCRWCLQNDPSKRPTIRQ 2155
    HsPKR AFETSKFFTDLRD---GIISDIFDKK---EKTLLQKLLS-KKPEDRPNTSE  531
    HsPEK QMERVRTLTDVRN---LKFPPLFTQKYPCEYVMVQDMLS-PSPMERPEAIN 1070
   HsGCN2 ASERIFVLNQLRDPTSPKFPEDFDDGEHAKQKSVISWLLNHDPAKRPTATE  994
    HsHRI EMERAEVLTGLRT---GQLPESLRKRCPVQAKYIQHLTR-RNSSQRPSAIQ  575
Consensus  mEr   l   r                              p  RP a
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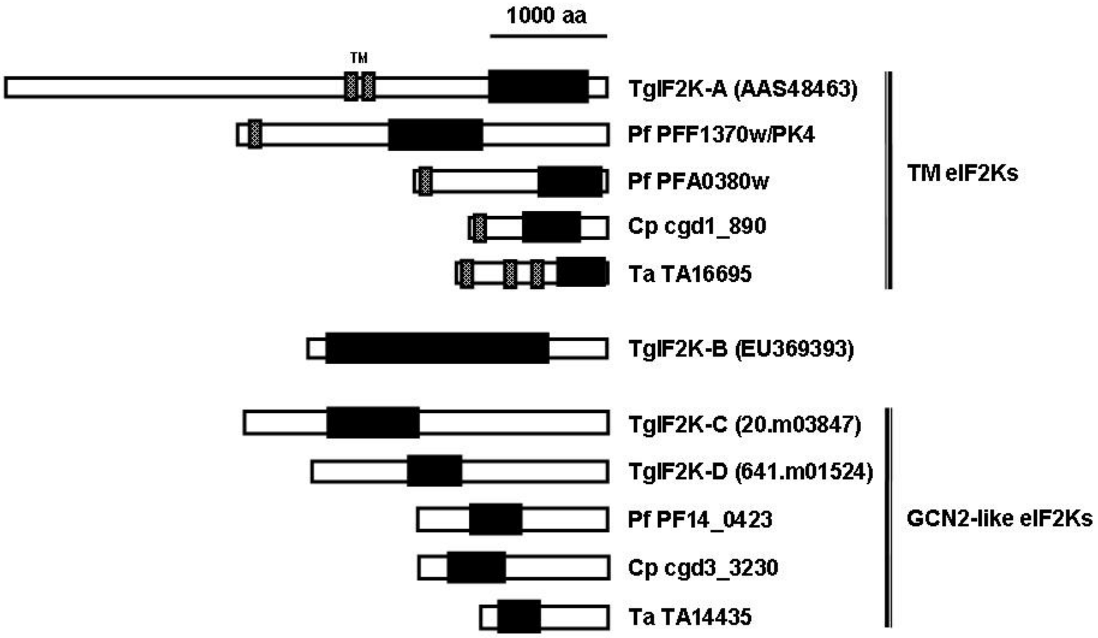
Figure S3


1000 aa
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Pf PFA0380w
Cp cgd1_890
Ta TA16695
TM eIF2Ks
TgIF2K-B (EU369393)
TgIF2K-C (20.m03847)
TgIF2K-D (641.m01524)
Pf PF14_0423
Cp cgd3_3230
Ta TA14435
GCN2-like eIF2Ks