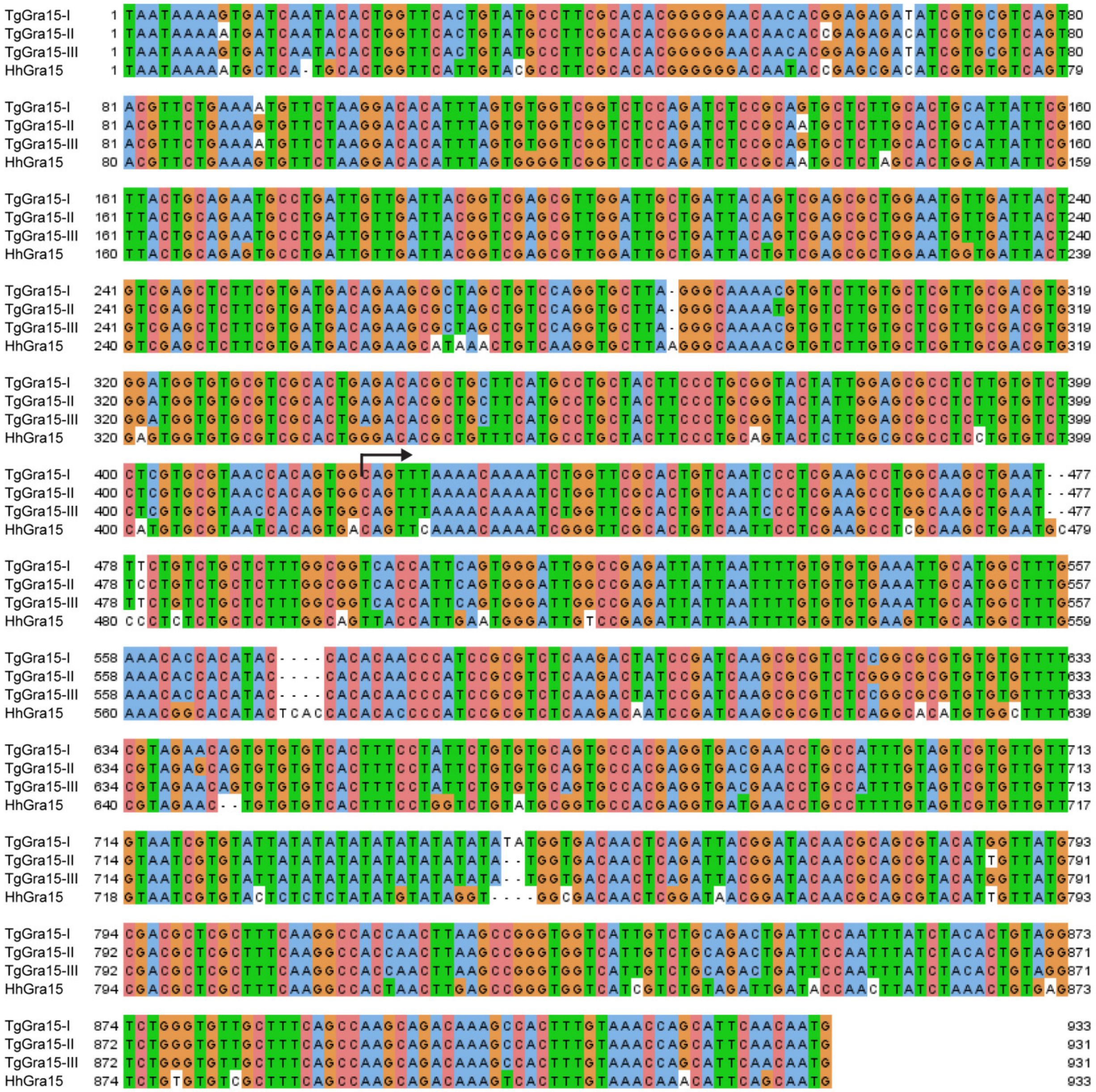
SUPPLEMENTARY FIGURES

S1.



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TgGra15-III   1 TAATAAAAGTGATCAATACACTGGTTCACTGTATGCCTTCGCACACGGGGGAACAACACGGAGAGATATCGTGCGTCAGT 80
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TgGra15-II   81 ACGTTCTGAAAGTGTTCTAAGGACACATTTAGTGTGGTCGGTCTCCAGATCTCCGCAATGCTCTTGCACTGCATTATTCG 160
TgGra15-III  81 ACGTTCTGAAAATGTTCTAAGGACACATTTAGTGTGGTCGGTCTCCAGATCTCCGCAGTGCTCTTGCACTGCATTATTCG 160
HhGra15      80 ACGTTCTGAAAGTGTTCTAAGGACACATTTAGTGGGGTCGGTCTCCAGATCTCCGCAATGCTCTAGCACTGGATTATTCG 159

TgGra15-I   161 TTACTGCAGAATGCCTGATTGTTGATTACGGTCGAGCGTTGGATTGCTGATTACAGTCGAGCGCTGGAATGTTGATTACT 240
TgGra15-II  161 TTACTGCAGAATGCCTGATTGTTGATTACGGTCGAGCGTTGGATTGCTGATTACAGTCGAGCGCTGGAATGTTGATTACT 240
TgGra15-III 161 TTACTGCAGAATGCCTGATTGTTGATTACGGTCGAGCGTTGGATTGCTGATTACAGTCGAGCGCTGGAATGTTGATTACT 240
HhGra15     160 TTACTGCAGAGTGCCTGATTGTTGATTACGGTCGAGCGTTGGATTGCTGATTACTGTCGAGCGCTGGAATGGTGATTACT 239

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TgGra15-II  241 GTCGAGCTCTTCGTGATGACAGAAGCGCTAGCTGTCCAGGTGCTTA-GGGCAAAATGTGTCTTGTGCTCGTTGCGACGTG 319
TgGra15-III 241 GTCGAGCTCTTCGTGATGACAGAAGCGCTAGCTGTCCAGGTGCTTA-GGGCAAAACGTGTCTTGTGCTCGTTGCGACGTG 319
HhGra15     240 GTCGAGCTCTTCGTGATGACAGAAGCATAAACTGTCAAGGTGCTTAAGGGCAAAACGTGTCTTGTGCTCGTTGCGACGTG 319

TgGra15-I   320 GGATGGTGTGCGTCGCACTGAGACACGCTGCTTCATGCCTGCTACTTCCCTGCGGTACTATTGGAGCGCCTCTTGTGTCT 399
TgGra15-II  320 GGATGGTGTGCGTCGCACTGAGACACGCTGCTTCATGCCTGCTACTTCCCTGCGGTACTATTGGAGCGCCTCTTGTGTCT 399
TgGra15-III 320 GGATGGTGTGCGTCGCACTGAGACACGCTGCTTCATGCCTGCTACTTCCCTGCGGTACTATTGGAGCGCCTCTTGTGTCT 399
HhGra15     320 GAGTGGTGTGCGTCGCACTGGGACACGCTGTTTCATGCCTGCTACTTCCCTGCAGTACTCTTGGCGCGCCTCCTGTGTCT 399

TgGra15-I   400 CTCGTGCGTAACCACAGTGGCAGTTTAAAACAAAATCTGGTTCGCACTGTCAATCCCTCGAAGCCTGGCAAGCTGAAT-- 477
TgGra15-II  400 CTCGTGCGTAACCACAGTGGCAGTTTAAAACAAAATCTGGTTCGCACTGTCAATCCCTCGAAGCCTGGCAAGCTGAAT-- 477
TgGra15-III 400 CTCGTGCGTAACCACAGTGGCAGTTTAAAACAAAATCTGGTTCGCACTGTCAATCCCTCGAAGCCTGGCAAGCTGAAT-- 477
HhGra15     400 CATGTGCGTAATCACAGTGACAGTTCAAAACAAAATCGGGTTCGCACTGTCAATTCCTCGAAGCCTCGCAAGCTGAATGC 479

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TgGra15-II  478 TCCTGTCTGCTCTTTGGCGGTCACCATTCAGTGGGATTGGCCGAGATTATTAATTTTGTGTGTGAAATTGCATGGCTTTG 557
TgGra15-III 478 TTCTGTCTGCTCTTTGGCGGTCACCATTCAGTGGGATTGGCCGAGATTATTAATTTTGTGTGTGAAATTGCATGGCTTTG 557
HhGra15     480 CCCTCTCTGCTCTTTGGCAGTTACCATTGAATGGGATTGTCCGAGATTATTAATTTTGTGTGTGAAGTTGCATGGCTTTG 559

TgGra15-I   558 AAACACCACATAC----CACACAACCCATCCGCGTCTCAAGACTATCCGATCAAGCGCGTCTCCGGCGCGTGTGTGTTTT 633
TgGra15-II  558 AAACACCACATAC----CACACAACCCATCCGCGTCTCAAGACTATCCGATCAAGCGCGTCTCGGGCGCGTGTGTGTTTT 633
TgGra15-III 558 AAACACCACATAC----CACACAACCCATCCGCGTCTCAAGACTATCCGATCAAGCGCGTCTCCGGCGCGTGTGTGTTTT 633
HhGra15     560 AAACGGCACATACTCACCACACACCCCATCCGCGTCTCAAGACAATCCGATCAAGCGCGTCTCAGGCACATGTGGCTTTT 639

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TgGra15-II  634 CGTAGAGCAGTGTGTGTCACTTTCCTATTCTGTGTGCAGTGCCACGAGGTGACGAACCTGCCATTTGTAGTCGTGTTGTT 713
TgGra15-III 634 CGTAGAACAGTGTGTGTCACTTTCCTATTCTGTGTGCAGTGCCACGAGGTGACGAACCTGCCATTTGTAGTCGTGTTGTT 713
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TgGra15-II  714 GTAATCGTGTATTATATATATATATATATATA--TGGTGACAACTCAGATTACGGATACAACGCAGCGTACATTGTTATG 791
TgGra15-III 714 GTAATCGTGTATTATATATATATATATATATA--TGGTGACAACTCAGATTACGGATACAACGCAGCGTACATGGTTATG 791
HhGra15     718 GTAATCGTGTACTCTCTCTATATGTATAGGT----GGCGACAACTCGGATAACGGATACAACGCAGCGTACATTGTTATG 793

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TgGra15-II  792 CGACGCTCGCTTTCAAGGCCACCAACTTAAGCCGGGTGGTCATTGTCTGCAGACTGATTCCAATTTATCTACACTGTAGG 871
TgGra15-III 792 CGACGCTCGCTTTCAAGGCCACCAACTTAAGCCGGGTGGTCATTGTCTGCAGACTGATTCCAATTTATCTACACTGTAGG 871
HhGra15     794 CGACGCTCGCTTTCAAGGCCACTAACTTGAGCCGGGTGGTCATCGTCTGTAGATTGATACCAACTTATCTAAACTGTGAG 873

TgGra15-I   874 TCTGGGTGTTGCTTTCAGCCAAGCAGACAAAGCCACTTTGTAAACCAGCATTCAACAATG                     933
TgGra15-II  872 TCTGGGTGTTGCTTTCAGCCAAGCAGACAAAGCCACTTTGTAAACCAGCATTCAACAATG                     931
TgGra15-III 872 TCTGGGTGTTGCTTTCAGCCAAGCAGACAAAGCCACTTTGTAAACCAGCATTCAACAATG                     931
HhGra15     874 TCTGTGTGTCGCTTTCAGCCAAGCAGACAAAGTCACTTTGTAAACAAACATTCAGCAATG                     933
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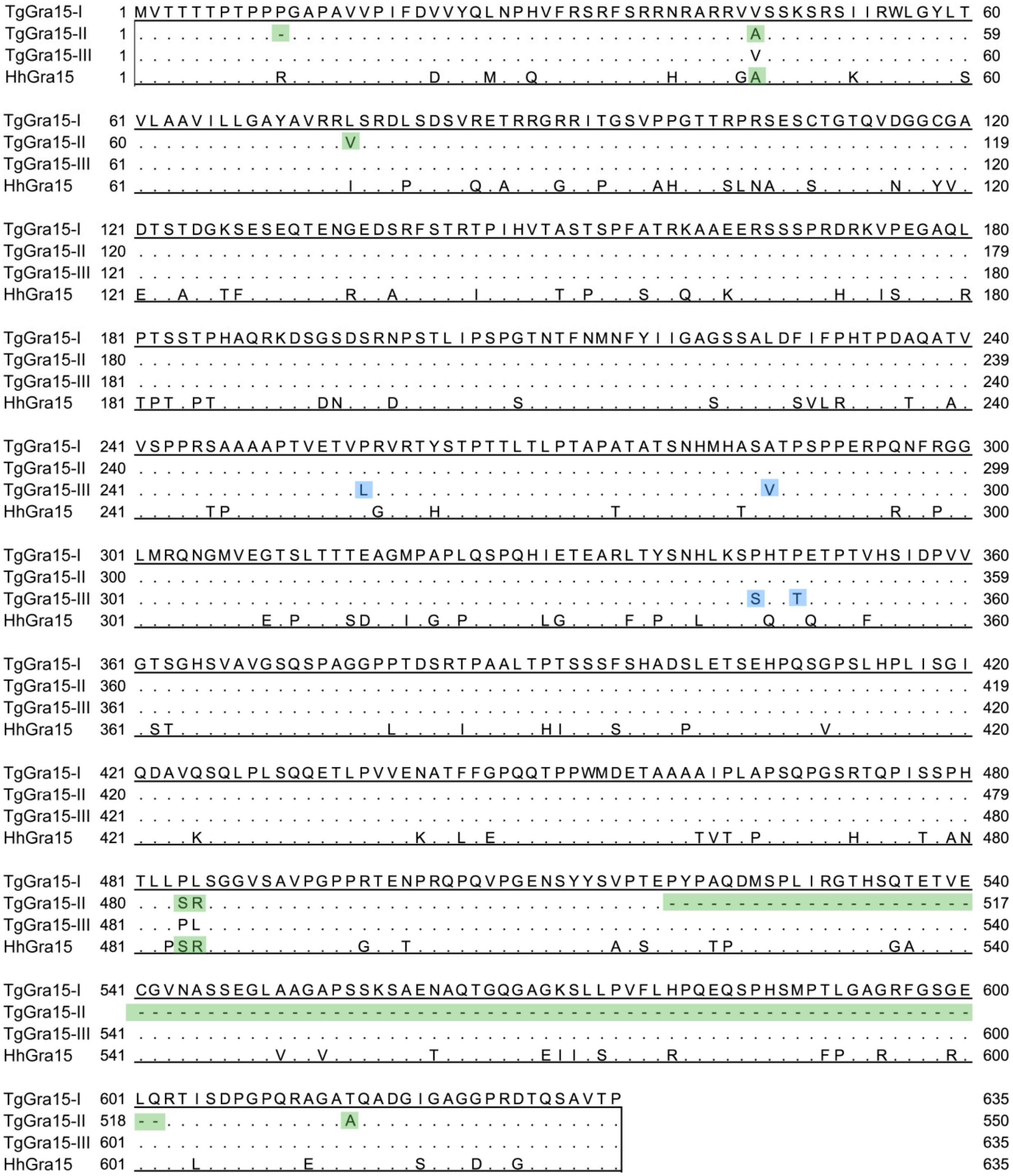
Figure S1: Alignment of the predicted promoters of *GRA15* in *T. gondii*-$_{\text{I,II,III}}$ and *H. hammondi*. These are the same upstream regions used in luciferase reporter assays. An arrowhead indicates the putative transcriptional start site.

S2.



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TgGra15-II    1 ..........-.................................A...............  59
TgGra15-III   1 ............................................V...............  60
HhGra15       1 ..........R..........D...M..Q.........H....GA......K.......S  60

TgGra15-I    61 VLAAVILLGAYAVRRLSRDLSDSVRETRRGRRITGSVPPGTTRPRSESCTGTQVDGGCGA 120
TgGra15-II   60 ...............V............................................ 119
TgGra15-III  61 ............................................................ 120
HhGra15      61 ...............I...P....Q.A...G..P...AH...SLNA..S.....N..YV. 120

TgGra15-I   121 DTSTDGKSESEQTENGEDSRFSTRTPIHVTASTSPFATRKAAEERSSSPRDRKVPEGAQL 180
TgGra15-II  120 ............................................................ 179
TgGra15-III 121 ............................................................ 180
HhGra15     121 E..A..TF.......R..A.....I.....T.P...S..Q..K.......H..IS....R 180

TgGra15-I   181 PTSSTPHAQRKDSGSDSRNPSTLIPSPGTNTFNMNFYIIGAGSSALDFIFPHTPDAQATV 240
TgGra15-II  180 ............................................................ 239
TgGra15-III 181 ............................................................ 240
HhGra15     181 TPT.PT.......DN...D........S..............S.....SVLR....T..A. 240

TgGra15-I   241 VSPPRSAAAAPTVETVPRVRTYSTPTTLTLPTAPATATSNHMHASATPSPPERPQNFRGG 300
TgGra15-II  240 ............................................................ 299
TgGra15-III 241 ................L............................V.............. 300
HhGra15     241 .....TP..........G...H............T........T..........R..P.. 300

TgGra15-I   301 LMRQNGMVEGTSLTTTEAGMPAPLQSPQHIETEARLTYSNHLKSPHTPETPTVHSIDPVV 360
TgGra15-II  300 ............................................................ 359
TgGra15-III 301 ............................................S..T............ 360
HhGra15     301 .........E.P...SD..I.G.P.....LG....F.P..L....Q..Q...F....... 360

TgGra15-I   361 GTSGHSVAVGSQSPAGGPPTDSRTPAALTPTSSSFSHADSLETSEHPQSGPSLHPLISGI 420
TgGra15-II  360 ............................................................ 419
TgGra15-III 361 ............................................................ 420
HhGra15     361 .ST...............L....I.....HI...S....P.........V.......... 420

TgGra15-I   421 QDAVQSQLPLSQQETLPVVENATFFGPQQTPPWMDETAAAAIPLAPSQPGSRTQPISSPH 480
TgGra15-II  420 ............................................................ 479
TgGra15-III 421 ............................................................ 480
HhGra15     421 ....K...............K..L.E..............TVT.P......H....T.AN 480

TgGra15-I   481 TLLPLSGGVSAVPGPPRTENPRQPQVPGENSYYSVPTEPYPAQDMSPLIRGTHSQTETVE 540
TgGra15-II  480 ...SR.................................---------------------- 517
TgGra15-III 481 ...PL....................................................... 540
HhGra15     481 ..PSR...........G..T..............A.S....TP...........GA.... 540

TgGra15-I   541 CGVNASSEGLAAGAPSSKSAENAQTGQGAGKSLLPVFLHPQEQSPHSMPTLGAGRFGSGE 600
TgGra15-II      ------------------------------------------------------------
TgGra15-III 541 ............................................................ 600
HhGra15     541 ..........V..V.......T.......EII.S....R..........FP..R....R. 600

TgGra15-I   601 LQRTISDPGPQRAGATQADGIGAGGPRDTQSAVTP                          635
TgGra15-II  518 --.............A...................                          550
TgGra15-III 601 ...................................                          635
HhGra15     601 ....L.......E.......S...D..G.......                          635
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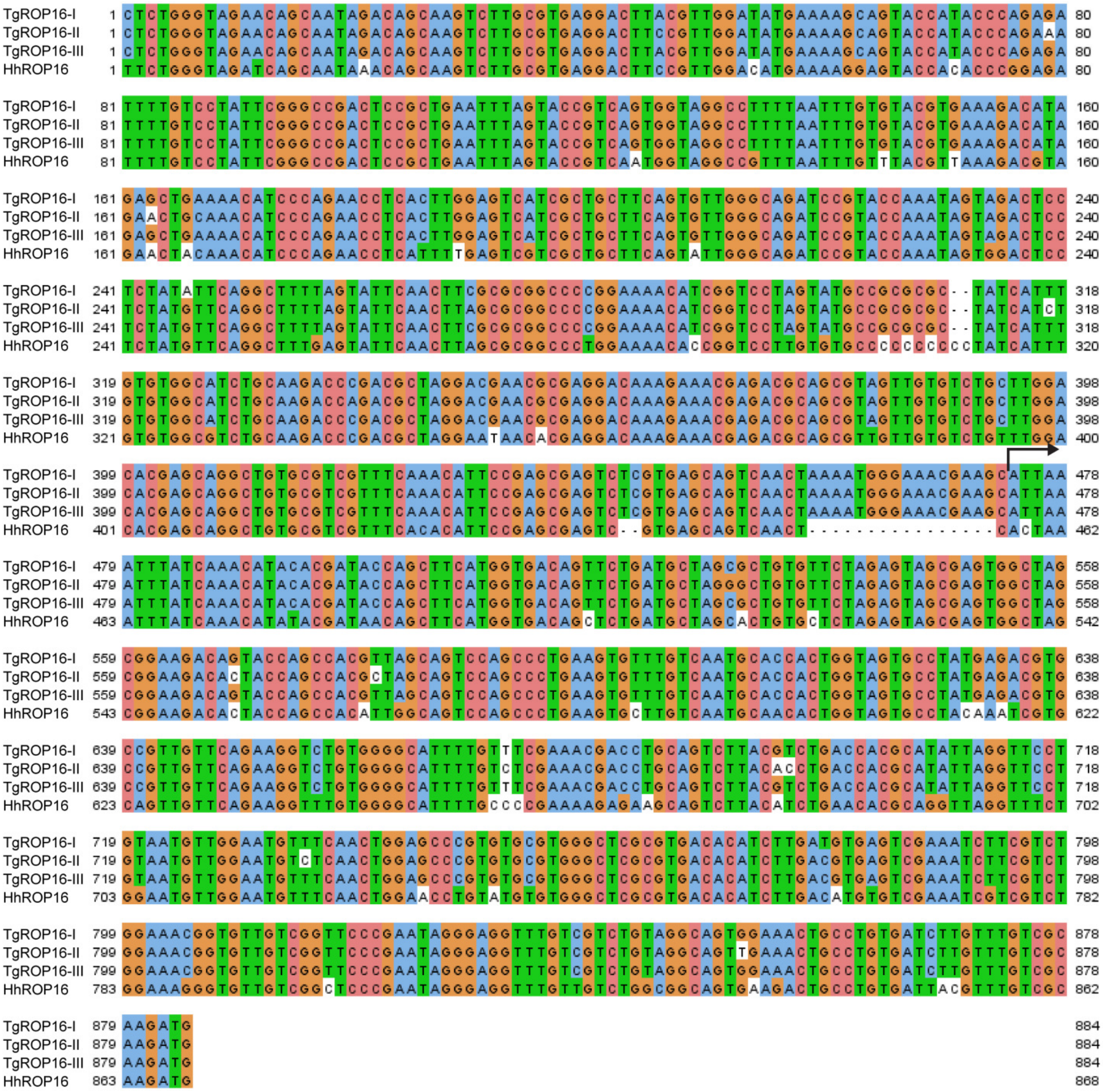
Figure S2. Alignment of the predicted protein sequence region of GRA15 in *T. gondii*-$_{\mathrm{I,II,III}}$ and *H. hammondi*. Polymorphisms unique to types II and III are indicated in green and blue, respectively. There are no GRA15 polymorphisms unique to *T. gondii* Type I. Sites in *H. hammondi* GRA15 that are the same as Type II at unique polymorphic sites are also colored green. There were no Type III-specific polymorphisms that were conserved in HhGRA15.

S3.



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TgROP16-III   1 CTCTGGGTAGAACAGCAATAGACAGCAAGTCTTGCGTGAGGACTTACGTTGGATATGAAAAGCAGTACCATACCCAGAGA  80
HhROP16       1 TTCTGGGTAGATCAGCAATAAACAGCAAGTCTTGCGTGAGGACTTCCGTTGGACATGAAAAGGAGTACCACACCCGGAGA  80

TgROP16-I    81 TTTTGTCCTATTCGGGCCGACTCCGCTGAATTTAGTACCGTCAGTGGTAGGCCTTTTAATTTGTGTACGTGAAAGACATA  160
TgROP16-II   81 TTTTGTCCTATTCGGGCCGACTCCGCTGAATTTAGTACCGTCAGTGGTAGGCCTTTTAATTTGTGTACGTGAAAGACATA  160
TgROP16-III  81 TTTTGTCCTATTCGGGCCGACTCCGCTGAATTTAGTACCGTCAGTGGTAGGCCTTTTAATTTGTGTACGTGAAAGACATA  160
HhROP16      81 TTTTGTCCTATTCGGGCCGACTCCGCTGAATTTAGTACCGTCAATGGTAGGCCGTTTAATTTGTTTACGTTAAAGACGTA  160

TgROP16-I   161 GAGCTGAAAACATCCCAGAACCTCACTTGGAGTCATCGCTGCTTCAGTGTTGGGCAGATCCGTACCAAATAGTAGACTCC  240
TgROP16-II  161 GAACTGCAAACATCCCAGAACCTCACTTGGAGTCATCGCTGCTTCAGTGTTGGGCAGATCCGTACCAAATAGTAGACTCC  240
TgROP16-III 161 GAGCTGAAAACATCCCAGAACCTCACTTGGAGTCATCGCTGCTTCAGTGTTGGGCAGATCCGTACCAAATAGTAGACTCC  240
HhROP16     161 GAACTACAAACATCCCAGAACCTCATTTTGAGTCGTCGCTGCTTCAGTATTGGGCAGATCCGTACCAAATAGTGGACTCC  240

TgROP16-I   241 TCTATATTCAGGCTTTTAGTATTCAACTTCGCGCGGCCCCGGAAAACATCGGTCCTAGTATGCCGCGCGC--TATCATTT  318
TgROP16-II  241 TCTATGTTCAGGCTTTTAGTATTCAACTTAGCGCGGCCCCGGAAAACATCGGTCCTAGTATGCCGCGCGC--TATCATCT  318
TgROP16-III 241 TCTATGTTCAGGCTTTTAGTATTCAACTTCGCGCGGCCCCGGAAAACATCGGTCCTAGTATGCCGCGCGC--TATCATTT  318
HhROP16     241 TCTATGTTCAGGCTTTGAGTATTCAACTTAGCGCGGCCCTGGAAAACACCGGTCCTTGTGTGCCCCCCCCCCTATCATTT  320

TgROP16-I   319 GTGTGGCATCTGCAAGACCCGACGCTAGGACGAACGCGAGGACAAAGAAACGAGACGCAGCGTAGTTGTGTCTGCTTGGA  398
TgROP16-II  319 GTGTGGCATCTGCAAGACCAGACGCTAGGACGAACGCGAGGACAAAGAAACGAGACGCAGCGTAGTTGTGTCTGCTTGGA  398
TgROP16-III 319 GTGTGGCATCTGCAAGACCCGACGCTAGGACGAACGCGAGGACAAAGAAACGAGACGCAGCGTAGTTGTGTCTGCTTGGA  398
HhROP16     321 GTGTGGCGTCTGCAAGACCCGACGCTAGGAATAACACGAGGACAAAGAAACGAGACGCAGCGTTGTTGTGTCTGTTTGGA  400

TgROP16-I   399 CACGAGCAGGCTGTGCGTCGTTTCAAACATTCCGAGCGAGTCTCGTGAGCAGTCAACTAAAATGGGAAACGAAGCATTAA  478
TgROP16-II  399 CACGAGCAGGCTGTGCGTCGTTTCAAACATTCCGAGCGAGTCTCGTGAGCAGTCAACTAAAATGGGAAACGAAGCATTAA  478
TgROP16-III 399 CACGAGCAGGCTGTGCGTCGTTTCAAACATTCCGAGCGAGTCTCGTGAGCAGTCAACTAAAATGGGAAACGAAGCATTAA  478
HhROP16     401 CACGAGCAGGCTGTGCGTCGTTTCACACATTCCGAGCGAGTC--GTGAGCAGTCAACT----------------CACTAA  462

TgROP16-I   479 ATTTATCAAACATACACGATACCAGCTTCATGGTGACAGTTCTGATGCTAGCGCTGTGTTCTAGAGTAGCGAGTGGCTAG  558
TgROP16-II  479 ATTTATCAAACATACACGATACCAGCTTCATGGTGACAGTTCTGATGCTAGGGCTGTGTTCTAGAGTAGCGAGTGGCTAG  558
TgROP16-III 479 ATTTATCAAACATACACGATACCAGCTTCATGGTGACAGTTCTGATGCTAGCGCTGTGTTCTAGAGTAGCGAGTGGCTAG  558
HhROP16     463 ATTTATCAAACATATACGATAACAGCTTCATGGTGACAGCTCTGATGCTAGCACTGTGCTCTAGAGTAGCGAGTGGCTAG  542

TgROP16-I   559 CGGAAGACAGTACCAGCCACGTTAGCAGTCCAGCCCTGAAGTGTTTGTCAATGCACCACTGGTAGTGCCTATGAGACGTG  638
TgROP16-II  559 CGGAAGACACTACCAGCCACGCTAGCAGTCCAGCCCTGAAGTGTTTGTCAATGCACCACTGGTAGTGCCTATGAGACGTG  638
TgROP16-III 559 CGGAAGACAGTACCAGCCACGTTAGCAGTCCAGCCCTGAAGTGTTTGTCAATGCACCACTGGTAGTGCCTATGAGACGTG  638
HhROP16     543 CGGAAGACACTACCAGCCACATTGGCAGTCCAGCCCTGAAGTGCTTGTCAATGCAACACTGGTAGTGCCTACAAATCGTG  622

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TgROP16-II  639 CCGTTGTTCAGAAGGTCTGTGGGGCATTTTGTCTCGAAACGACCTGCAGTCTTACACCTGACCACGCATATTAGGTTCCT  718
TgROP16-III 639 CCGTTGTTCAGAAGGTCTGTGGGGCATTTTGTTTCGAAACGACCTGCAGTCTTACGTCTGACCACGCATATTAGGTTCCT  718
HhROP16     623 CAGTTGTTCAGAAGGTTTGTGGGGCATTTTGCCCCGAAAAGAGAAGCAGTCTTACATCTGAACACGCAGGTTAGGTTTCT  702

TgROP16-I   719 GTAATGTTGGAATGTTTCAACTGGAGCCCGTGTGCGTGGGCTCGCGTGACACATCTTGATGTGAGTCGAAATCTTCGTCT  798
TgROP16-II  719 GTAATGTTGGAATGTCTCAACTGGAGCCCGTGTGCGTGGGCTCGCGTGACACATCTTGACGTGAGTCGAAATCTTCGTCT  798
TgROP16-III 719 GTAATGTTGGAATGTTTCAACTGGAGCCCGTGTGCGTGGGCTCGCGTGACACATCTTGACGTGAGTCGAAATCTTCGTCT  798
HhROP16     703 GGAATGTTGGAATGTTTCAACTGGAACCTGTATGTGTGGGCTCGCGTGACACATCTTGACATGTGTCGAAATCGTCGTCT  782

TgROP16-I   799 GGAAACGGTGTTGTCGGTTCCCGAATAGGGAGGTTTGTCGTCTGTAGGCAGTGGAAACTGCCTGTGATCTTGTTTGTCGC  878
TgROP16-II  799 GGAAACGGTGTTGTCGGTTCCCGAATAGGGAGGTTTGTCGTCTGTAGGCAGTTGAAACTGCCTGTGATCTTGTTTGTCGC  878
TgROP16-III 799 GGAAACGGTGTTGTCGGTTCCCGAATAGGGAGGTTTGTCGTCTGTAGGCAGTGGAAACTGCCTGTGATCTTGTTTGTCGC  878
HhROP16     783 GGAAAGGGTGTTGTCGGCTCCCGAATAGGGAGGTTTGTTGTCTGGCGGCAGTGAAGACTGCCTGTGATTACGTTTGTCGC  862

TgROP16-I   879 AAGATG                                                                            884
TgROP16-II  879 AAGATG                                                                            884
TgROP16-III 879 AAGATG                                                                            884
HhROP16     863 AAGATG                                                                            868
```

Figure S3. Alignment of the predicted *ROP16* promoters for *T. gondii*-$_{\text{I,II,III}}$ and *H. hammondi*. These are the same upstream regions used in luciferase reporter assays. Putative transcriptional start site is indicated by an arrowhead.

S4.

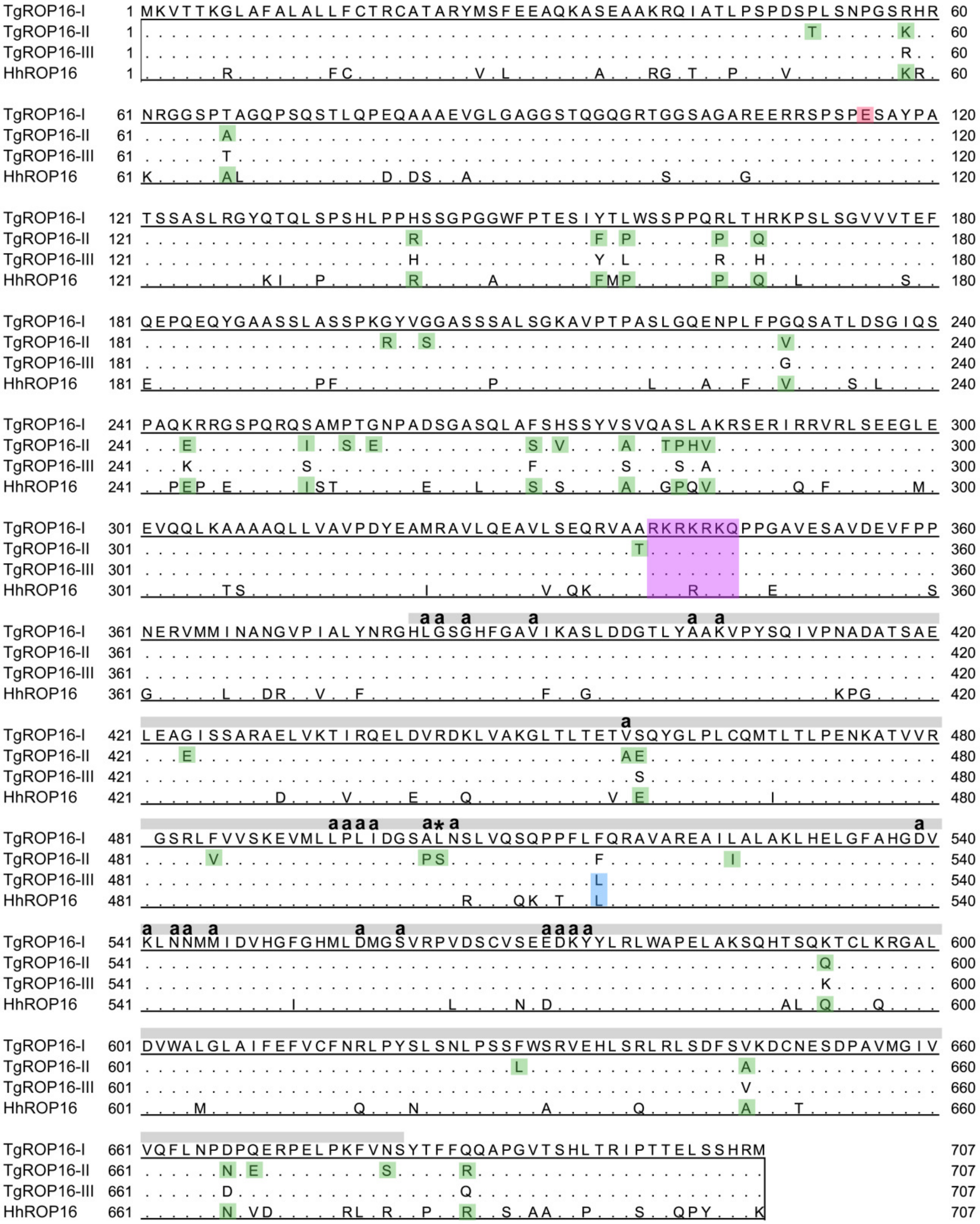


Figure S4. Alignment of the predicted protein sequence region of ROP16 in *T. gondii*-$_{I,II,III}$ and *H. hammondi*. Polymorphisms unique to types I, II and III are indicated in red, green and blue, respectively. At sites with unique polymorphisms in any of the 3 lineages, the *H. hammondi* sequence is also colored red, green or blue if it has the same amino acid at that site. The predicted class 4 NLS is highlighted in magenta. The kinase domain is indicated by the grey bar above the alignment, with active or ATP binding sites indicated by "**a**". The polymorphic leucine residue required for ROP16-driven STAT3 phosphorylation in TgROP16$_{I,III}$ is indicated by an asterisk.

S5.

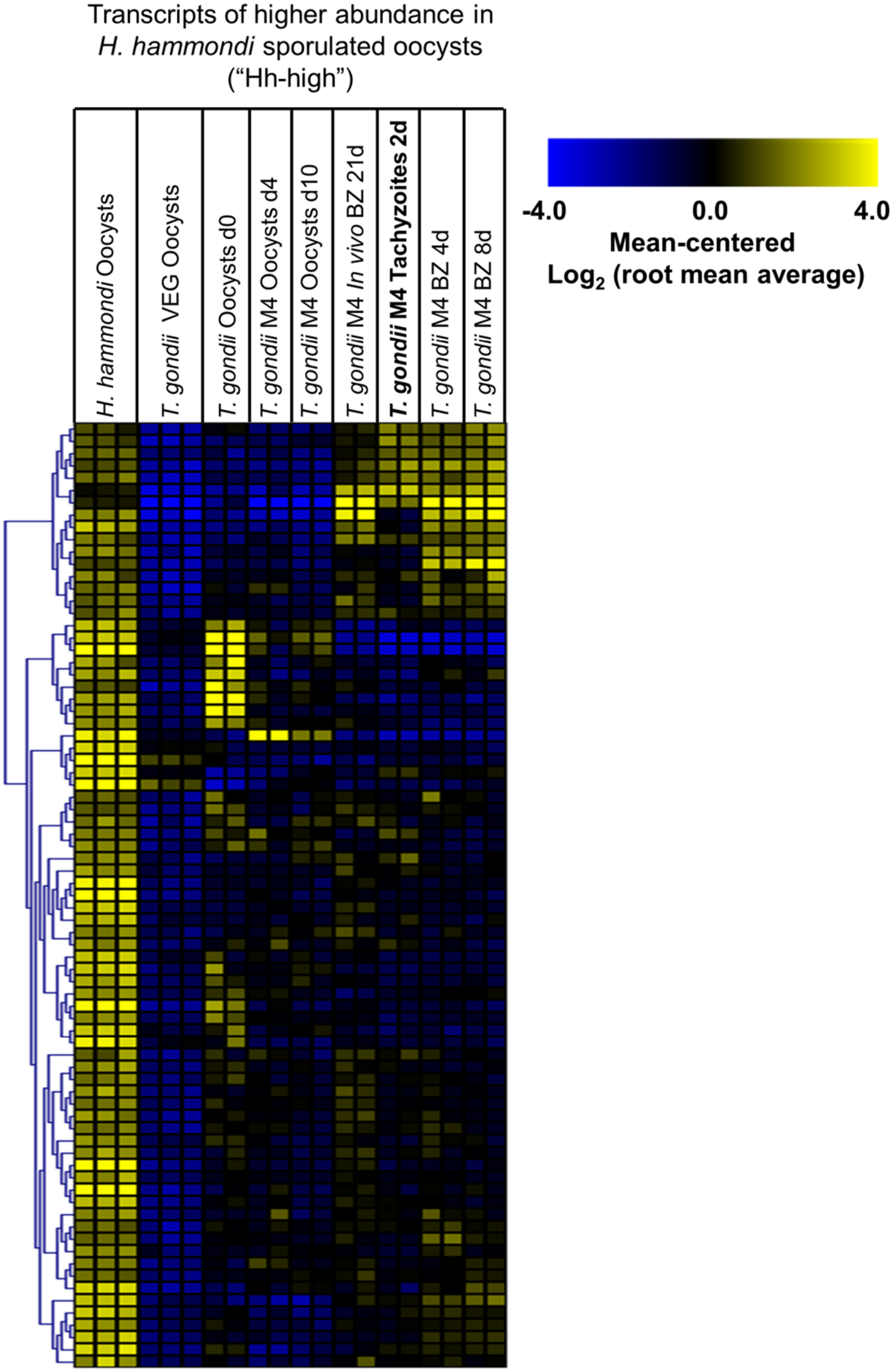


Figure S5. Heatmap of mean-centered, normalized data for *H. hammondi* HhGer041 and *T. gondii* VEG sporozoites showing genes with transcripts that were of higher abundance (FDR $P<0.01$) in *H. hammondi* compared to *T. gondii* VEG ("Hh-high"). Data from multiple life cycle stages of *T. gondii* strain M4 are shown for comparison. A subset of these genes (top cluster) are developmentally regulated during the tachyzoite to bradyzoite transition in *T. gondii* strain M4.

S6.

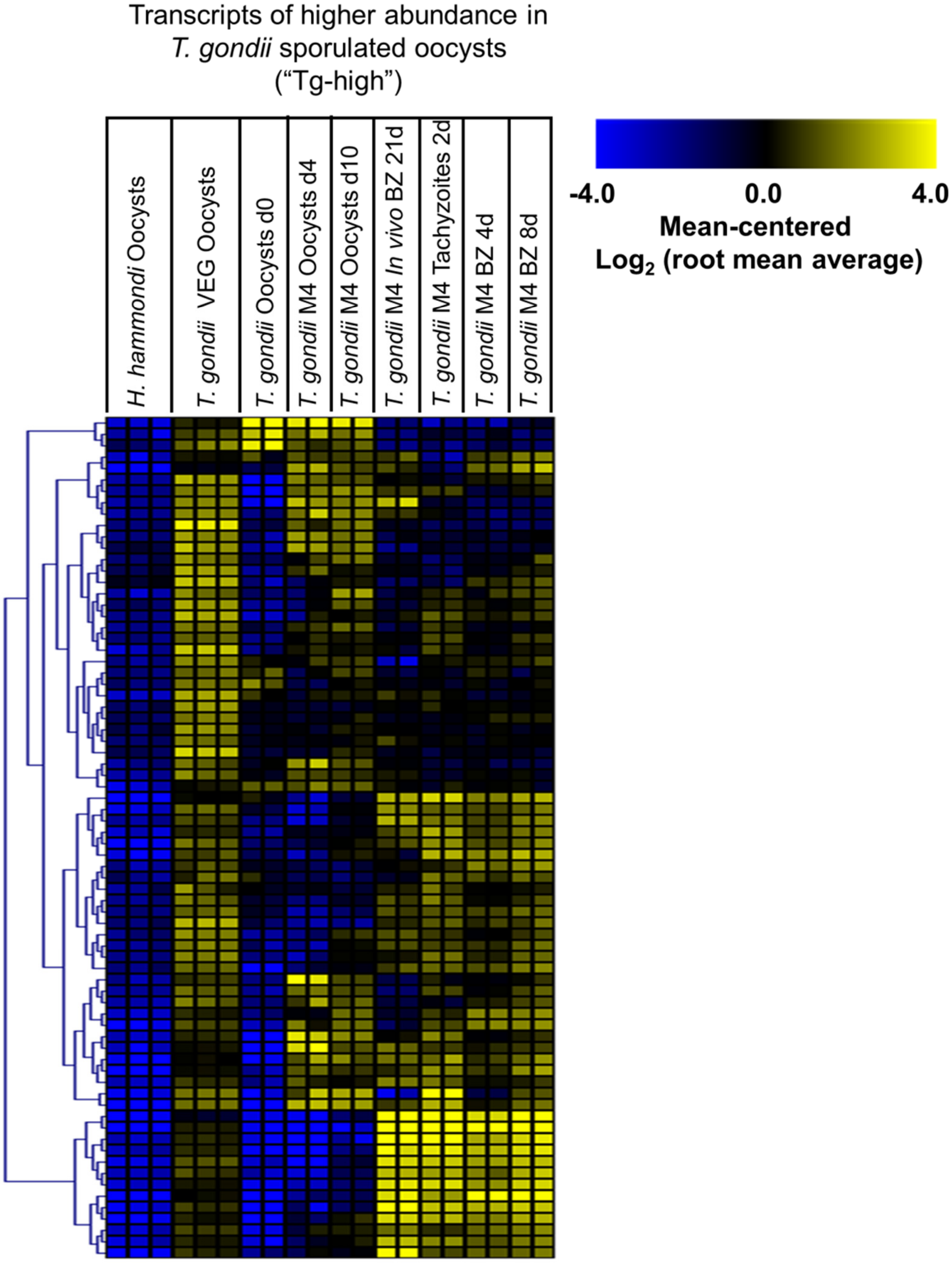


Figure S6. Heatmap of mean-centered, normalized data for *H. hammondi* HhCatGer041 and *T. gondii* VEG sporozoites showing genes with transcripts that were of higher abundance (FDR P<0.01) in *T. gondii* VEG compared to *H. hammondi* ("Tg-high"). Data from multiple life cycle stages of *T. gondii* strain M4 are shown for comparison.

S7.

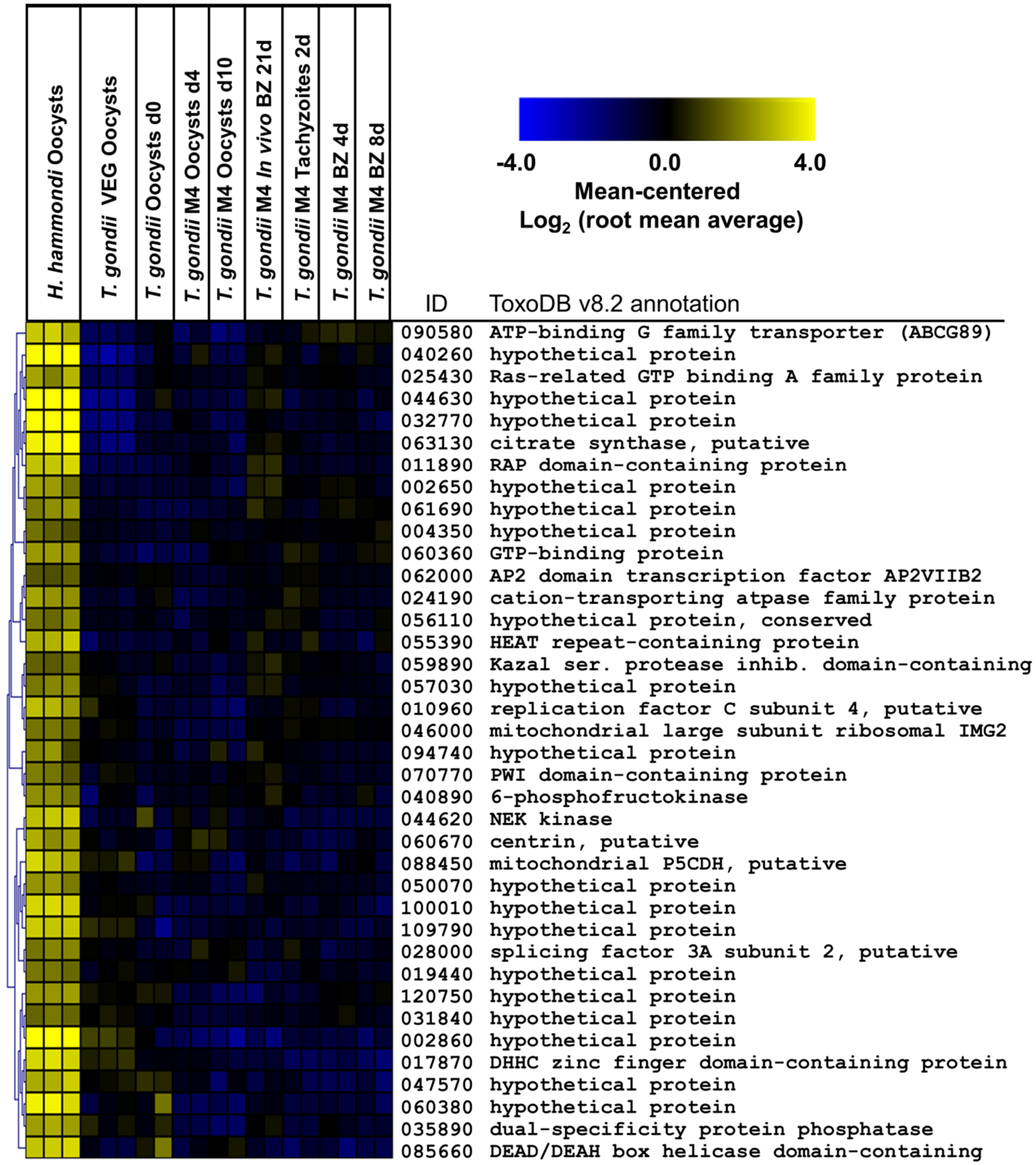


Figure S7. Heatmap of mean-centered, normalized data for *H. hammondi* HhGer041 and *T. gondii* VEG sporozoites showing genes with transcripts that were found to significantly (FDR $P<1x10^{-5}$) match the template (using Pavlidis Template Matching; see Materials and Methods) of high transcript level in *H. hammondi* sporozoites but lower in *T. gondii* VEG sporozoites and all life stages for *T. gondii* strain M4.

S8.

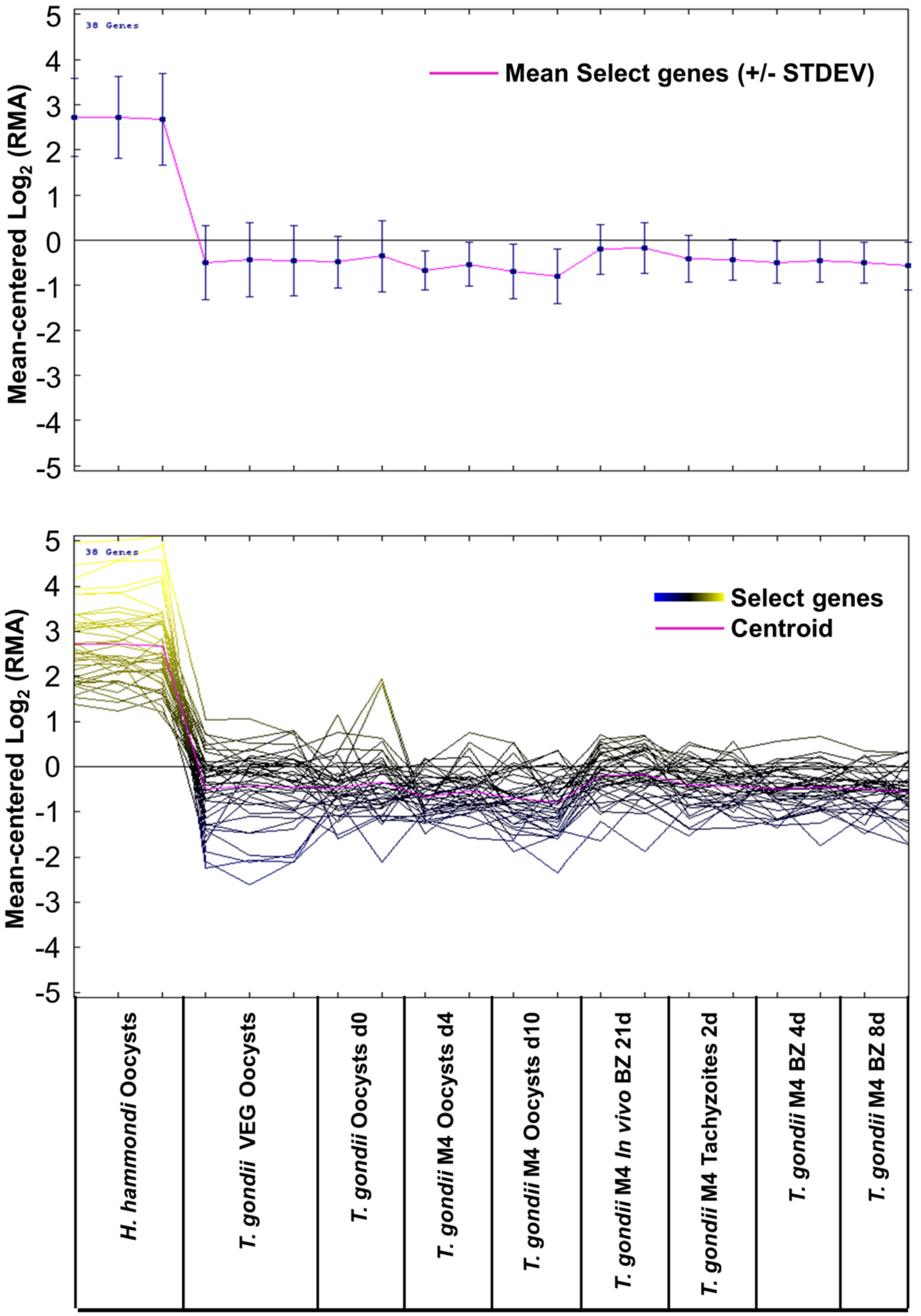
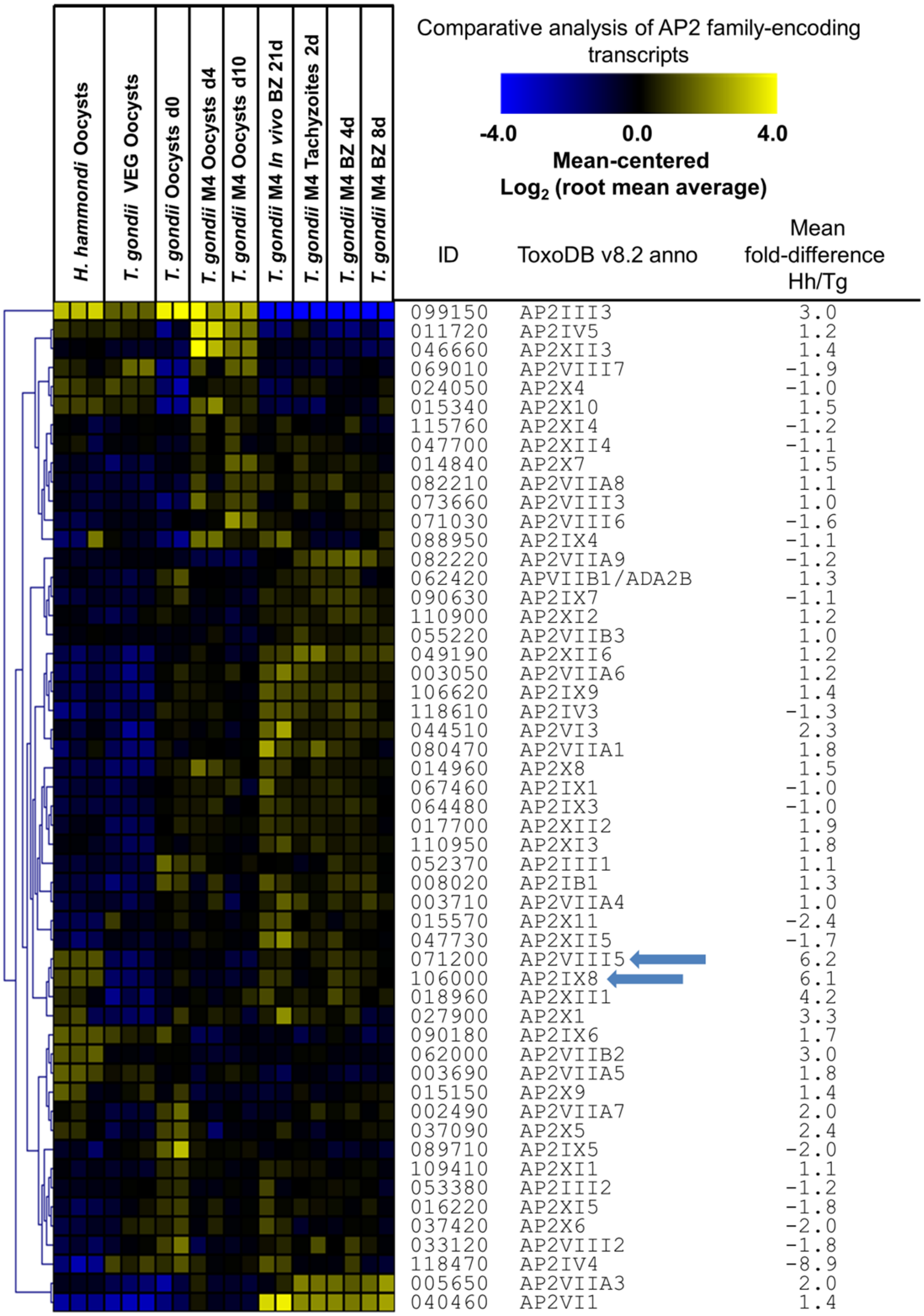


Figure S8. Mean +/- standard deviation (upper panel) or mean-centered hybridization intensity (lower panel) for all 38 genes shown in Fig. S7 in the *H. hammondi* and *T. gondii* sporozoite data obtained in the present study as well as that from the previously published dataset from *T. gondii* strain M4.

S9.



ID	ToxoDB v8.2 anno	Mean fold-difference Hh/Tg
099150	AP2III3	3.0
011720	AP2IV5	1.2
046660	AP2XII3	1.4
069010	AP2VIII7	-1.9
024050	AP2X4	-1.0
015340	AP2X10	1.5
115760	AP2XI4	-1.2
047700	AP2XII4	-1.1
014840	AP2X7	1.5
082210	AP2VIIA8	1.1
073660	AP2VIII3	1.0
071030	AP2VIII6	-1.6
088950	AP2IX4	-1.1
082220	AP2VIIA9	-1.2
062420	APVIIB1/ADA2B	1.3
090630	AP2IX7	-1.1
110900	AP2XI2	1.2
055220	AP2VIIB3	1.0
049190	AP2XII6	1.2
003050	AP2VIIA6	1.2
106620	AP2IX9	1.4
118610	AP2IV3	-1.3
044510	AP2VI3	2.3
080470	AP2VIIA1	1.8
014960	AP2X8	1.5
067460	AP2IX1	-1.0
064480	AP2IX3	-1.0
017700	AP2XII2	1.9
110950	AP2XI3	1.8
052370	AP2III1	1.1
008020	AP2IB1	1.3
003710	AP2VIIA4	1.0
015570	AP2X11	-2.4
047730	AP2XII5	-1.7
071200	AP2VIII5	6.2
106000	AP2IX8	6.1
018960	AP2XII1	4.2
027900	AP2X1	3.3
090180	AP2IX6	1.7
062000	AP2VIIB2	3.0
003690	AP2VIIA5	1.8
015150	AP2X9	1.4
002490	AP2VIIA7	2.0
037090	AP2X5	2.4
089710	AP2IX5	-2.0
109410	AP2XI1	1.1
053380	AP2III2	-1.2
016220	AP2XI5	-1.8
037420	AP2X6	-2.0
033120	AP2VIII2	-1.8
118470	AP2IV4	-8.9
005650	AP2VIIA3	2.0
040460	AP2VI1	1.4

Figure S9. Heatmap of mean-centered, normalized data for *H. hammondi* HhCatGer041 and *T. gondii* VEG sporozoites showing hybridization data for 53 genes annotated as AP2 transcription factors. Data are shown from multiple life cycle stages of *T. gondii* strain M4 for comparison. Blue arrowheads indicate two genes for which transcript abundance was > 6-fold higher in *H. hammondi* compared to *T. gondii* VEG (discussed in the manuscript text).

Table S1: Raw luminescence values for *GRA15* and *ROP16* promoter assays

GRA15 Promoter Assays:

	Rep 1			**Rep 2**			**Rep 3**			**Rep 4**		
Firefly Construct	Firefly	*Renilla*	F/R*	Firefly	*Renilla*	F/R	Firefly	*Renilla*	F/R	Firefly	*Renilla*	F/R
None†	ND	ND	ND	ND	ND	ND	484	1887830	0.0003	722	1093746	0.0007
***T. gondii* Type II**	1547683	160438	9.7	1857258	161149	11.6	556312	44908	12.4	4206383	292684	10.23
H. hammondi	432109	129232	3.3	1402270	571176	2.5	1358314	576972	2.4	2071420	999741	1.9
Fold *Tg:Hh*			2.9			4.7			5.3			5.4
Fold *Hh*:None			ND			ND			9183.0			2697.0

***ROP16* Promoter Assays:**

	Rep 1			**Rep 2**		
Firefly Construct	Firefly	*Renilla*	F/R	Firefly	*Renilla*	F/R
None†	722	1025570	0.0007	564	2671755	0.0002
***T. gondii* Type II**	2394044	1669062	1.4	2540126	1340490	1.9
H. hammondi	68987	1229397	0.056	92930	1289598	0.072
Fold *Tg:Hh*			25.6			26.3
Fold *Hh*:None			79.7			341.6

***ROP16* Promoter deletion assays:**

	Rep 1			**Rep 2**			**Rep 3**		
Firefly Construct	Firefly	*Renilla*	F/R	Firefly	*Renilla*	F/R	Firefly	*Renilla*	F/R
None	ND	ND	ND	203	45993.5	0.004	ND	ND	ND
***T. gondii* Type II**	7350.5	70438	0.099	5416	24946.5	0.217	33167.5	145277	0.228
***T. gondii* Type IIΔ16 bp**	488	20520	0.023	454	16493.5	0.028	6781	137115	0.049
H. hammondi	586.5	57163	0.011	323	12740	0.025	2457	90171.5	0.027
***H. hammondi* + 16 bp**	1438.5	30591	0.047	3160.5	40279.5	0.078	9066.5	78437.5	0.116

******Firefly/Renilla signal ratio;* †*Parasites transfected with only the Renilla construct.*

Table S2. Ten transcripts with the Gene Ontology term GO:0003735, "Structural Constituent of Ribosome" that are of greater abundance in *T. gondii* Sporulated Oocysts compared to *H. hammondi* Sporulated Oocysts

v8* ID	v7[†] ID	Genomic Location	Product Description	Mean RMA[‡] *H. hammondi*	Mean RMA *T. gondii*	Fold-difference *Hh/Tg*
238010	038010	ME49 chrVI	ribosomal protein RPL23A	6.02	9.79	-13.66
242330	042330	ME49 chrVI	ribosomal protein RPS5	5.20	10.62	-42.95
239760	039760	ME49 chrVI	ribosomal protein RPL22	8.73	13.04	-19.77
238250	038250	ME49 chrVI	ribosomal protein RPL36	5.93	9.49	-11.84
203630	003630	ME49 chrVIIa	ribosomal protein RPL44	7.44	10.87	-10.72
262690	062690	ME49 chrVIIb	ribosomal protein RPL27	6.94	11.85	-29.98
232300	032300	ME49 chrVIII	ribosomal protein RPS3	8.64	13.44	-27.84
266060	066060	ME49 chrIX	ribosomal protein RPSA	9.30	13.41	-17.32
267060	067060	ME49 chrIX	ribosomal protein RPL14	8.24	12.50	-19.08
309120	109120	ME49 chrXI	ribosomal protein RPL4	6.76	11.52	-27.02

*Current gene name based on version 8.2 of the *T. gondii* ME49 genome annotation; [†]Gene name based on version 7.3 of the *T. gondii* ME49 genome annotation; [‡]Root mean average, determined as described in Materials and Methods. N=3 microarrays per species.