

Figure S1. Cell cycle regulation of genes that change expression during or after invasion.

(A) Histogram representation of the maximum RNA abundance of genes that show cell cycle regulation in intracellular replicating parasites (2,833 genes total; based on {{2374 Behnke,M.S. 2010;}}). Note the modal pattern of gene expression peaks in late S phase, early G1 phase, and late G1 phase.

(B) Histogram of the maximum RNA abundance of genes with expression differences during invasion that are also cell cycle regulated (723 genes total). The overall pattern is similar to that of all cell cycle regulated genes (panel A). These genes are listed in Table S5.

(C) A randomly selected set of 723 genes from the *Toxoplasma* genome shows a more widely distributed pattern, supporting the validity of the pattern for genes that change in expression between extracellular and intracellular 2 h parasites.

(D) Genes up-regulated in extracellular parasites that are also cell cycle regulated (577 genes total) show peak expression in late S phase and M/C phase. These genes are listed in Table S5.

(E) Genes up-regulated in intracellular 2 h parasites that are also cell cycle regulated (36 genes total) show peak expression in late G1 phase. These genes are listed in Table S5.

(F) Genes down-regulated in newly invaded parasites that are also cell cycle regulated (104 genes total) show peak expression throughout the cell cycle. These genes are listed in Table S5.

Figure S2. Genes regulated exclusively in newly invaded parasites.

(A) Genes up- or down-regulated in newly invaded parasites compared to extracellular or intracellular 2 h parasites. (For a list of these genes see Table S3 and S4). Each line represents one gene. Genes that are elevated in extracellular parasites are colored red to orange whereas genes with increased expression in newly invaded parasites are colored blue.

(B) Genes up- or down-regulated in newly invaded parasites were classified into 9 categories based on known or implied function and graphed as stacked columns. Category assignments are listed in Table S3 and S4.

Fig. S1

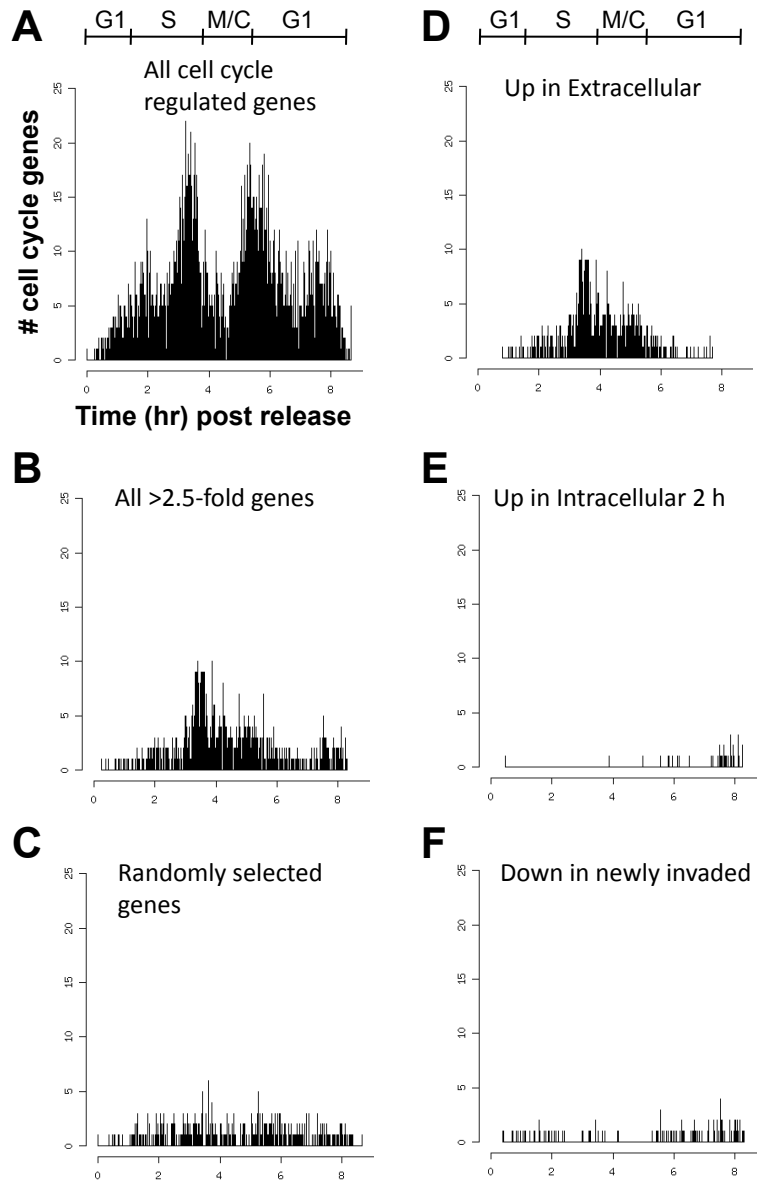


Fig. S2

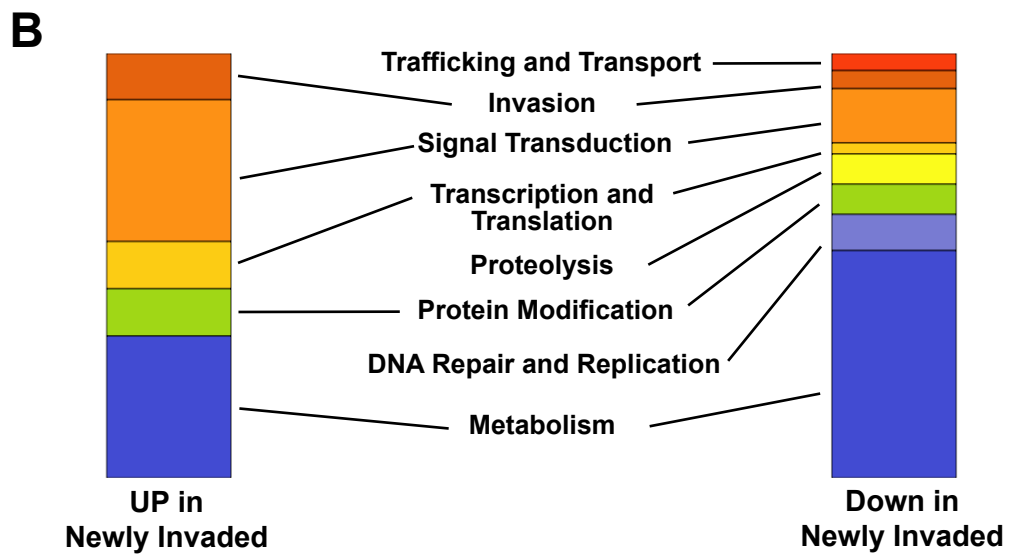
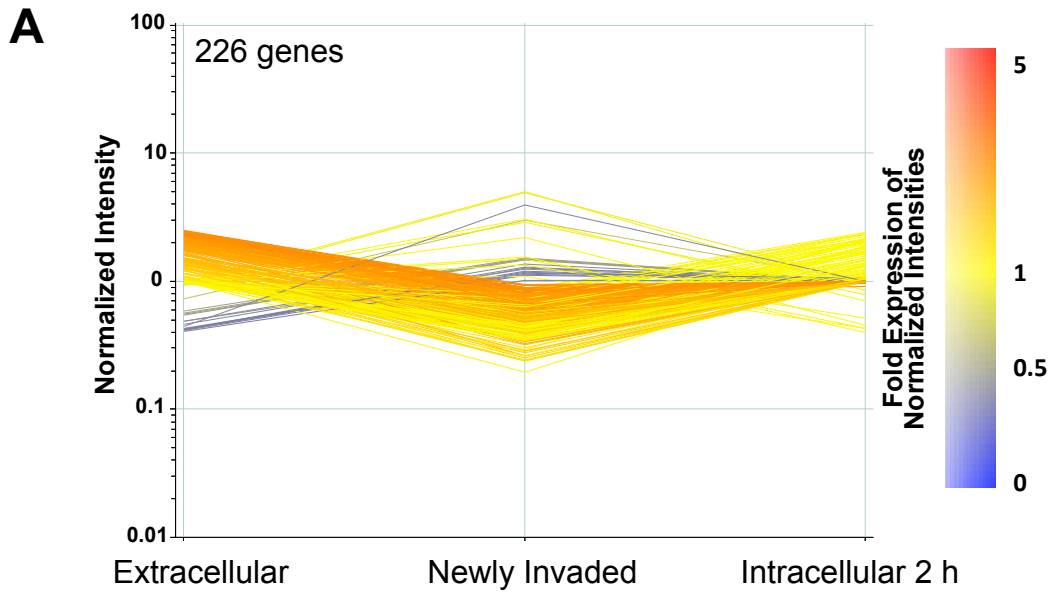


Table S6. Primers used for q-RT PCR analysis

1. 76.m01659.RT.F	5' GATCGAGCTCCATGATGATG 3'
2. 76.m01659.RT.R	5' TTCGACAGGTGTGTTCCGGAC 3'
3. 80.m02181.RT.F	5' TCGTCCTCGACCGGAATGTC 3'
4. 80.m02181.RT.R	5' ATCTGCCGCATTCTTACACC 3'
5. 59.m07778.RT.F	5' ACATCTGGCGACGAATGTTC 3'
6. 59.m07778.RT.R	5' TGCCGGTCATTTCTTCCTGG 3'
7. 59.m03398.RT.F	5' AGGTACCATACCTAGTCAGC 3'
8. 59.m03398.RT.R	5' TAGCCGAGTTTAAACAACGCC 3'
9. TUB2.RT.F	5' GCGTCTTCTTGGATTTGGAG 3'
10. TUB2.RT.R	5' TGGAGACCAGTGCAGTTGTC 3'
11. EF1 α .RT.F	5' ATCAACTTGGTCGTCATCGG 3'
12. EF1 α .RT.R	5' TATCGATGGTGATAACCACGC 3'
13. 31.m00940 RT-F	5' ATGTCTCTATCCACCGCGC 3'
14. 31.m00940 RT-R	5' CTGCAACGTAGTTCGGCGTC 3'
15. 44.m02820 RT-F	5' ATGCCTTCGACGAGAGGAC 3'
16. 44.m02820 RT-R	5' CTCCTCGTGTGCGGGTCG 3'
17. 55.m10326 RT-F	5' ATGGAGGAATCGAAACGCTTG 3'
18. 55.m10326 RT-R	5' GGAAGTGAAGCATGATCAG 3'
19. 541.m01207 RT-F	5' TTTCGCCTTGTGTCTCGGC 3'
20. 541.m01207 RT-F	5' CTGAGTTGAGGCAGTCGAG 3'

Table S7. Primers used to make luciferase expression constructs

1. 583.m00018 (UPRT)-F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCAGCGAACGCTTCCACCGAAAC 3'
2. 583.m00018 9UPRT)-R	5' GGGGACCACTTTGTACAAGAAAGCTGGGTCCGCCATTTTAGAAGCCCTGTGGAAAGGTC 3'
3. 542.m00223 (TK)-F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCACTACCTCACCACGTGGAAC 3'
4. 542.m00223 (TK)-R	5' GGGGACCACTTTGTACAAGAAAGCTGGGTCCGCCATGCTGACAGCGCAG 3'
5. 80.m00003 (GAPDH)-F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTACACCTTCCGAGCATGCTGC 3'
6. 80.m00003 (GAPDH)-R	5' GGGGACCACTTTGTACAAGAAAGCTGGGTCCGCCATCTTGGCAAAGTGTCTGACAG 3'
7. 583.m00022 (α -tub)-F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTGCTAGAATGCAGCGACCAGATG 3'
8. 583.m00022 (α -tub)-R	5' GGGGACCACTTTGTACAAGAAAGCTGGGTCCGCCATTTGTGCAAAAAGGGAATTCAAG 3'

Table S8. Primers used in UPRT promoter analysis

1. -1301.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCAGCGAACGCTTCCACCGAAAC 3'
2. -868.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCATCTGTAACAGAGAGACTAGC 3'
3. -462.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTCCAGTCCAGCTGGTGTCATAG 3'
4. -430.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTCTAGAGTGCCACGAAAGAG 3'
5. -407.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCCCTCCTTTTATTCGTTGTTTCC 3'
6. -319.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGGTACGAGCTATCTTGTGGC 3'
7. -303.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGTCGACTCTTCGTTGCATGCAG 3'
8. -279.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGTTTCTGCGCAAGATACTC 3'
9. -255.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCACAGAGCCACAGAAAGTGGTAG 3'
10. -165.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTGATTTTCTGCACGTTGGCAGC 3'
11. +54.F	5' GGGGACAAGTTTGTACAAAAAAGCAGGCTTCTTTTCGTCGTCATCGGCTGTCC 3'