

## SUPPLEMENTAL MATERIALS

**Table S1. ApiAP2 mRNA expression in Type II strains across *Toxoplasma* life cycle stages.**

**mRNA expression analysis.** Microarray data: ME49 strain tachyzoite and 2 day *in vitro* bradyzoite. RNA-seq data: M4 strain 21 day *in vivo* bradyzoite, 10 day oocyst (sporozoites), CZ-H3 strain tachyzoite and 3 day post-infection of cats (merozoites). All 67 *Toxoplasma* ApiAP2 factors were ranked from highest (rank 1) to lowest (rank 67) level of expression in each sample. The percentile expression indicated in parentheses is included to provide a reference for the relative expression of each ApiAP2 mRNA against all genes expressed in the RNA sample. **The highest levels of mRNA expression for developmental ApiAP2s are indicate by larger bold font.** Column color code: yellow=*in vitro* tachyzoites, green=bradyzoites, red=fully sporulated oocysts containing sporozoites, blue=merozoites, orange=tachyzoite cell cycle regulated ApiAP2s with the highest amplitude ApiAP2 mRNAs indicated as *dynamic cell cycle*. Note: ApiAP2 mRNAs that are transiently expressed are not fully captured particularly dynamic cell cycle factors (e.g. AP2IV-4 75th percentile only S phase-mitosis). For some ApiAP2 factors, mRNA expression has been confirmed at the protein level indicated by (P). Strain-specific differences in expression are evident in some data but were not highlighted.

AP2 name cell cycle orange	ME49 tachy	ME49 2d brady	M4 21d brady	M4-10d oocyst	CZ-H3 tachy	CZ-H3 3d mero	Developmental Expression *see additional evidence ToxoDB (P) confirmed at the protein level
AP2Ib-1	62 <sup>(11)</sup>	<b>28</b> <sup>(60)</sup>	57 <sup>(22)</sup>	37 <sup>(33)</sup>	63 <sup>(18)</sup>	<b>21</b> <sup>(53)</sup>	early bradyzoites (P) & feline cycle stages*
AP2III-1	56 <sup>(25)</sup>	64 <sup>(15)</sup>	65 <sup>(5)</sup>	52 <sup>(21)</sup>	65 <sup>(8)</sup>	62 <sup>(21)</sup>	no clear stage pattern
AP2III-2	<b>9</b> <sup>(72)</sup>	<b>22</b> <sup>(62)</sup>	<b>24</b> <sup>(66)</sup>	<b>16</b> <sup>(64)</sup>	<b>25</b> <sup>(62)</sup>	63 <sup>(20)</sup>	intermediate life cycle (P) & highest in unsporulated oocysts*
AP2III-3	67 <sup>(1)</sup>	67 <sup>(0)</sup>	66 <sup>(5)</sup>	<b>13</b> <sup>(70)</sup>	67 <sup>(6)</sup>	65 <sup>(15)</sup>	sporozoite specific
AP2III-4	66 <sup>(1)</sup>	65 <sup>(4)</sup>	63 <sup>(11)</sup>	31 <sup>(41)</sup>	64 <sup>(15)</sup>	<b>17</b> <sup>(58)</sup>	feline cycle specific
AP2IV-1	37 <sup>(47)</sup>	30 <sup>(53)</sup>	40 <sup>(38)</sup>	<b>11</b> <sup>(72)</sup>	28 <sup>(55)</sup>	<b>10</b> <sup>(68)</sup>	highest in feline cycle stages* & oocyst sporulation*
AP2IV-2 <sup>+</sup>	34 <sup>(48)</sup>	29 <sup>(54)</sup>	36 <sup>(42)</sup>	45 <sup>(27)</sup>	59 <sup>(20)</sup>	26 <sup>(52)</sup>	no clear stage pattern
AP2IV-3	64 <sup>(9)</sup>	<b>13</b> <sup>(72)</sup>	33 <sup>(48)</sup>	<b>6</b> <sup>(91)</sup>	58 <sup>(21)</sup>	<b>7</b> <sup>(71)</sup>	early bradyzoites (P), sporozoites & merozoites
AP2IV-4	33 <sup>(49)</sup>	52 <sup>(37)</sup>	27 <sup>(61)</sup>	28 <sup>(46)</sup>	31 <sup>(50)</sup>	29 <sup>(49)</sup>	likely tachyzoite-specific <i>dynamic cell cycle</i> (P)

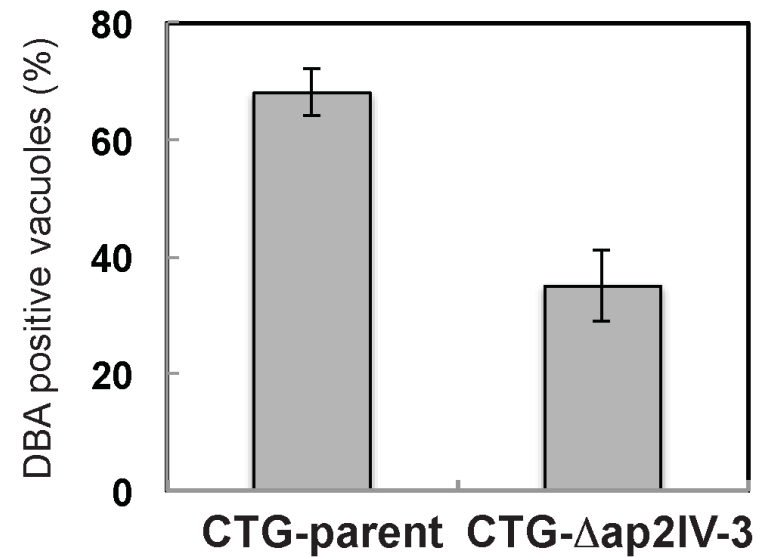
AP2IV-5	<b>21</b> <sup>(62)</sup>	49 <sup>(38)</sup>	58 <sup>(19)</sup>	<b>10</b> <sup>(73)</sup>	<b>15</b> <sup>(74)</sup>	44 <sup>(33)</sup>	tachyzoites & sporozoites
AP2V-1	<b>24</b> <sup>(59)</sup>	37 <sup>(47)</sup>	57 <sup>(22)</sup>	27 <sup>(48)</sup>	<b>13</b> <sup>(77)</sup>	59 <sup>(20)</sup>	highest in tachyzoites
AP2V-2	60 <sup>(21)</sup>	63 <sup>(16)</sup>	65 <sup>(5)</sup>	24 <sup>(49)</sup>	45 <sup>(37)</sup>	54 <sup>(24)</sup>	no clear stage pattern
AP2VI-1 <sup>+</sup>	<b>2</b> <sup>(89)</sup>	<b>3</b> <sup>(87)</sup>	<b>2</b> <sup>(95)</sup>	<b>4</b> <sup>(93)</sup>	<b>6</b> <sup>(86)</sup>	<b>2</b> <sup>(78)</sup>	high expression in all stages <i>dynamic cell cycle</i> (P)
AP2VI-2	54 <sup>(29)</sup>	32 <sup>(50)</sup>	34 <sup>(46)</sup>	<b>18</b> <sup>(59)</sup>	32 <sup>(50)</sup>	33 <sup>(44)</sup>	highest in unsporulated oocysts*
AP2VI-3	52 <sup>(30)</sup>	<b>35</b> <sup>(49)</sup>	55 <sup>(25)</sup>	44 <sup>(27)</sup>	49 <sup>(35)</sup>	<b>5</b> <sup>(72)</sup>	highly expressed in merozoites & possibly early bradyzoites
AP2VIIa-1	55 <sup>(29)</sup>	<b>24</b> <sup>(61)</sup>	<b>20</b> <sup>(73)</sup>	<b>3</b> <sup>(93)</sup>	52 <sup>(30)</sup>	32 <sup>(45)</sup>	bradyzoites & sporozoites <i>dynamic cell cycle</i> (P)
AP2VIIa-2	<b>1</b> <sup>(92)</sup>	<b>2</b> <sup>(89)</sup>	<b>1</b> <sup>(97)</sup>	39 <sup>(32)</sup>	<b>3</b> <sup>(90)</sup>	40 <sup>(38)</sup>	intermediate life cycle (P) & unsporulated oocysts*
AP2VIIa-3	<b>3</b> <sup>(88)</sup>	<b>5</b> <sup>(85)</sup>	<b>11</b> <sup>(85)</sup>	<b>2</b> <sup>(95)</sup>	<b>5</b> <sup>(86)</sup>	36 <sup>(40)</sup>	intermediate life cycle (P) & sporozoites
AP2VIIa-4	<b>19</b> <sup>(63)</sup>	<b>8</b> <sup>(83)</sup>	<b>21</b> <sup>(71)</sup>	33 <sup>(38)</sup>	<b>23</b> <sup>(64)</sup>	<b>16</b> <sup>(59)</sup>	intermediate life cycle (P) & merozoites
AP2VIIa-5	<b>11</b> <sup>(70)</sup>	<b>25</b> <sup>(61)</sup>	39 <sup>(39)</sup>	65 <sup>(06)</sup>	<b>29</b> <sup>(54)</sup>	34 <sup>(43)</sup>	highest in tachyzoites (P) & early bradyzoites
AP2VIIa-6	<b>14</b> <sup>(68)</sup>	<b>17</b> <sup>(67)</sup>	35 <sup>(45)</sup>	<b>8</b> <sup>(86)</sup>	47 <sup>(37)</sup>	64 <sup>(20)</sup>	highest in sporozoites also moderate in tachyzoites (P)/early bradyzoites
AP2VIIa-7	35 <sup>(48)</sup>	44 <sup>(44)</sup>	31 <sup>(49)</sup>	23 <sup>(51)</sup>	27 <sup>(58)</sup>	51 <sup>(28)</sup>	86th percentile in unsporulated oocysts*
AP2VIIa-8	<b>27</b> <sup>(54)</sup>	<b>18</b> <sup>(65)</sup>	<b>13</b> <sup>(81)</sup>	<b>5</b> <sup>(93)</sup>	<b>19</b> <sup>(67)</sup>	66 <sup>(12)</sup>	intermediate life cycle & sporozoites, <i>dynamic cell cycle</i> (P)
AP2VIIa-9	51 <sup>(30)</sup>	43 <sup>(45)</sup>	<b>18</b> <sup>(74)</sup>	66 <sup>(06)</sup>	37 <sup>(47)</sup>	<b>13</b> <sup>(62)</sup>	mature bradyzoites? & feline life cycle*
AP2VIIb-1	40 <sup>(43)</sup>	36 <sup>(48)</sup>	43 <sup>(37)</sup>	22 <sup>(52)</sup>	39 <sup>(42)</sup>	41 <sup>(30)</sup>	no clear stage pattern

AP2VIIb-2	53 <sup>(29)</sup>	50 <sup>(37)</sup>	41 <sup>(38)</sup>	17 <sup>(60)</sup>	44 <sup>(37)</sup>	22 <sup>(52)</sup>	no clear stage pattern
AP2VIIb-3	<b>12</b> <sup>(69)</sup>	<b>9</b> <sup>(81)</sup>	<b>8</b> <sup>(86)</sup>	42 <sup>(27)</sup>	<b>22</b> <sup>(64)</sup>	42 <sup>(37)</sup>	intermediate life cycle (P)
AP2VIII-1	39 <sup>(44)</sup>	48 <sup>(38)</sup>	50 <sup>(30)</sup>	58 <sup>(16)</sup>	36 <sup>(46)</sup>	48 <sup>(30)</sup>	no clear stage pattern
AP2VIII-2	41 <sup>(43)</sup>	54 <sup>(36)</sup>	38 <sup>(40)</sup>	49 <sup>(24)</sup>	46 <sup>(36)</sup>	47 <sup>(30)</sup>	no clear stage pattern
AP2VIII-3	<b>10</b> <sup>(71)</sup>	<b>14</b> <sup>(70)</sup>	<b>19</b> <sup>(73)</sup>	<b>12</b> <sup>(70)</sup>	<b>21</b> <sup>(64)</sup>	18 <sup>(56)</sup>	intermediate life cycle & sporozoites
AP2VIII-4	36 <sup>(48)</sup>	<b>26</b> <sup>(60)</sup>	<b>30</b> <sup>(52)</sup>	60 <sup>(16)</sup>	48 <sup>(36)</sup>	58 <sup>(23)</sup>	possible bradyzoite specific*
AP2VIII-5	<b>16</b> <sup>(66)</sup>	<b>15</b> <sup>(69)</sup>	32 <sup>(48)</sup>	21 <sup>(52)</sup>	<b>20</b> <sup>(66)</sup>	<b>1</b> <sup>(82)</sup>	tachyzoites, early bradyzoites & merozoites
AP2VIII-6	<b>8</b> <sup>(75)</sup>	<b>6</b> <sup>(85)</sup>	<b>7</b> <sup>(91)</sup>	63 <sup>(12)</sup>	<b>7</b> <sup>(85)</sup>	<b>14</b> <sup>(61)</sup>	intermediate life cycle & merozoites
AP2VIII-7	<b>4</b> <sup>(88)</sup>	<b>1</b> <sup>(91)</sup>	<b>4</b> <sup>(94)</sup>	34 <sup>(37)</sup>	<b>1</b> <sup>(92)</sup>	<b>15</b> <sup>(61)</sup>	intermediate cycle (P) & merozoites
AP2IX-1	63 <sup>(10)</sup>	60 <sup>(25)</sup>	52 <sup>(29)</sup>	<b>15</b> <sup>(66)</sup>	54 <sup>(25)</sup>	<b>6</b> <sup>(74)</sup>	feline cycle stages* & sporozoites
AP2IX-2 <sup>+</sup>	50 <sup>(32)</sup>	42 <sup>(46)</sup>	N/A	N/A	60 <sup>(19)</sup>	57 <sup>(23)</sup>	no clear stage pattern
AP2IX-3	44 <sup>(40)</sup>	46 <sup>(39)</sup>	62 <sup>(12)</sup>	19 <sup>(59)</sup>	61 <sup>(19)</sup>	62 <sup>(20)</sup>	no clear stage pattern
AP2IX-4	<b>7</b> <sup>(76)</sup>	<b>4</b> <sup>(87)</sup>	<b>3</b> <sup>(95)</sup>	38 <sup>(32)</sup>	<b>26</b> <sup>(59)</sup>	49 <sup>(29)</sup>	intermediate life cycle <i>dynamic cell cycle</i> (P)
AP2IX-5	28 <sup>(52)</sup>	41 <sup>(47)</sup>	48 <sup>(31)</sup>	43 <sup>(27)</sup>	18 <sup>(66)</sup>	43 <sup>(36)</sup>	no clear stage pattern
AP2IX-6	43 <sup>(42)</sup>	33 <sup>(49)</sup>	46 <sup>(32)</sup>	40 <sup>(30)</sup>	38 <sup>(44)</sup>	<b>8</b> <sup>(70)</sup>	feline cycle stages*
AP2IX-7	57 <sup>(25)</sup>	61 <sup>(23)</sup>	56 <sup>(25)</sup>	61 <sup>(15)</sup>	53 <sup>(28)</sup>	53 <sup>(25)</sup>	no clear stage pattern
AP2IX-8	<b>17</b> <sup>(66)</sup>	<b>23</b> <sup>(62)</sup>	<b>25</b> <sup>(66)</sup>	56 <sup>(19)</sup>	<b>16</b> <sup>(72)</sup>	<b>20</b> <sup>(52)</sup>	intermediate life cycle & possibly merozoites
AP2IX-9	58 <sup>(24)</sup>	<b>12</b> <sup>(72)</sup>	<b>5</b> <sup>(93)</sup>	41 <sup>(29)</sup>	50 <sup>(33)</sup>	25 <sup>(52)</sup>	early bradyzoite specific, protein was not detected <i>in vivo</i> cysts (P)
AP2X-1	47 <sup>(37)</sup>	58 <sup>(28)</sup>	45 <sup>(34)</sup>	59 <sup>(16)</sup>	40 <sup>(42)</sup>	38 <sup>(39)</sup>	no clear stage pattern

AP2X-2 <sup>+</sup>	30 <sup>(50)</sup>	27 <sup>(60)</sup>	49 <sup>(30)</sup>	7 <sup>(90)</sup>	41 <sup>(40)</sup>	24 <sup>(52)</sup>	sporozoite specific
AP2X-3 <sup>+</sup>	42 <sup>(42)</sup>	38 <sup>(47)</sup>	47 <sup>(31)</sup>	54 <sup>(20)</sup>	55 <sup>(24)</sup>	23 <sup>(52)</sup>	no clear stage pattern
AP2X-4	13 <sup>(69)</sup>	21 <sup>(64)</sup>	28 <sup>(60)</sup>	57 <sup>(20)</sup>	17 <sup>(69)</sup>	11 <sup>(67)</sup>	intermediate cycle & feline cycle stages
AP2X-5	23 <sup>(60)</sup>	56 <sup>(32)</sup>	9 <sup>(86)</sup>	14 <sup>(66)</sup>	10 <sup>(80)</sup>	35 <sup>(41)</sup>	tachyzoites (P), mature bradyzoites & sporozoites
AP2X-6	65 <sup>(4)</sup>	66 <sup>(4)</sup>	60 <sup>(17)</sup>	29 <sup>(44)</sup>	57 <sup>(22)</sup>	46 <sup>(31)</sup>	no clear stage pattern
AP2X-7	5 <sup>(86)</sup>	7 <sup>(84)</sup>	10 <sup>(86)</sup>	9 <sup>(90)</sup>	8 <sup>(85)</sup>	19 <sup>(55)</sup>	intermediate life cycle & sporozoites
AP2X-8	46 <sup>(39)</sup>	55 <sup>(34)</sup>	44 <sup>(36)</sup>	36 <sup>(34)</sup>	51 <sup>(32)</sup>	60 <sup>(23)</sup>	no clear stage pattern (P)
AP2X-9	6 <sup>(82)</sup>	11 <sup>(73)</sup>	22 <sup>(68)</sup>	32 <sup>(39)</sup>	2 <sup>(91)</sup>	12 <sup>(63)</sup>	intermediate life cycle (P) & merozoites*
AP2X-10	59 <sup>(24)</sup>	47 <sup>(38)</sup>	54 <sup>(25)</sup>	1 <sup>(96)</sup>	62 <sup>(18)</sup>	28 <sup>(49)</sup>	sporozoites & feline cycle*
AP2X-11	45 <sup>(39)</sup>	51 <sup>(37)</sup>	42 <sup>(37)</sup>	47 <sup>(25)</sup>	34 <sup>(48)</sup>	39 <sup>(39)</sup>	no clear stage pattern
AP2XI-1	20 <sup>(63)</sup>	10 <sup>(74)</sup>	61 <sup>(16)</sup>	26 <sup>(48)</sup>	56 <sup>(24)</sup>	56 <sup>(24)</sup>	no clear stage pattern <i>dynamic cell cycle</i> (P)
AP2XI-2	26 <sup>(56)</sup>	16 <sup>(67)</sup>	15 <sup>(77)</sup>	62 <sup>(14)</sup>	14 <sup>(74)</sup>	30 <sup>(47)</sup>	intermediate life cycle (P)
AP2XI-3	29 <sup>(50)</sup>	45 <sup>(43)</sup>	26 <sup>(62)</sup>	51 <sup>(22)</sup>	12 <sup>(77)</sup>	4 <sup>(76)</sup>	no clear stage pattern <i>important G1 regulator</i> (P)
AP2XI-4	18 <sup>(66)</sup>	20 <sup>(64)</sup>	29 <sup>(53)</sup>	46 <sup>(25)</sup>	43 <sup>(39)</sup>	52 <sup>(27)</sup>	likely intermediate cycle specific <i>dynamic cell cycle</i> (P)
AP2XI-5	25 <sup>(57)</sup>	31 <sup>(53)</sup>	14 <sup>(79)</sup>	30 <sup>(43)</sup>	9 <sup>(81)</sup>	3 <sup>(77)</sup>	no clear stage pattern (P)
AP2XII-1	31 <sup>(50)</sup>	39 <sup>(47)</sup>	6 <sup>(92)</sup>	50 <sup>(23)</sup>	4 <sup>(86)</sup>	55 <sup>(23)</sup>	no clear stage pattern
AP2XII-2	38 <sup>(44)</sup>	53 <sup>(37)</sup>	51 <sup>(30)</sup>	42 <sup>(28)</sup>	35 <sup>(47)</sup>	37 <sup>(40)</sup>	no clear stage pattern <i>dynamic cell cycle</i>
AP2XII-3	61 <sup>(20)</sup>	62 <sup>(18)</sup>	64 <sup>(11)</sup>	35 <sup>(36)</sup>	66 <sup>(6)</sup>	67 <sup>(4)</sup>	unsporulated oocyst specific*
AP2XII-4	15 <sup>(67)</sup>	34 <sup>(49)</sup>	23 <sup>(67)</sup>	25 <sup>(49)</sup>	33 <sup>(49)</sup>	31 <sup>(46)</sup>	no clear stage pattern (P)
AP2XII-5	48 <sup>(35)</sup>	57 <sup>(30)</sup>	17 <sup>(76)</sup>	20 <sup>(53)</sup>	42 <sup>(39)</sup>	45 <sup>(33)</sup>	no clear stage pattern (P)

<b>AP2XII-6</b>	<b>32<sup>(50)</sup></b>	<b>19<sup>(64)</sup></b>	<b>59<sup>(17)</sup></b>	<b>55<sup>(20)</sup></b>	<b>30<sup>(51)</sup></b>	<b>9<sup>(69)</sup></b>	tachyzoites and early bradyzoites & feline cycle
<b>AP2XII-8</b>	<b>22<sup>(61)</sup></b>	<b>40<sup>(47)</sup></b>	<b>16<sup>(76)</sup></b>	<b>48<sup>(25)</sup></b>	<b>11<sup>(78)</sup></b>	<b>27<sup>(50)</sup></b>	likely intermediate cycle specific*
<b>AP2XII-9</b>	<b>49<sup>(33)</sup></b>	<b>59<sup>(26)</sup></b>	<b>37<sup>(41)</sup></b>	<b>53<sup>(20)</sup></b>	<b>24<sup>(62)</sup></b>	<b>50<sup>(29)</sup></b>	no clear stage pattern <i>dynamic cell cycle (P)</i>
	11	15	21	13	16	8	# AP2s ≥ 70% per sample
	37	36	36	43	36	41	# AP2s ≤ 50% per sample
Other data comments	<ul style="list-style-type: none"> <li># of ApiAP2 factors expressed at &lt;60 percentile in all samples=18 ApiAP2 factors</li> <li>A single ApiAP2 factor is highly expressed in all samples, AP2VI-1</li> </ul>						
Data sources	<ul style="list-style-type: none"> <li>all normalized and percentile values were obtained from ToxoDB</li> <li>+ data for 5 ApiAP2 factors missing from ToxoDB was recovered from original data</li> <li>*Other ToxoDB data used in this analysis; acute vs 28 day CBA/J infected brain tissue (RNA-seq), 29 <i>Toxoplasma</i> strains (RNA-seq), RH synchronized tachyzoite cell cycle mRNAs (microarray)</li> </ul>						
Protein confirmation sources	<ul style="list-style-type: none"> <li>White, Sullivan, Kim, unpublished; AP2Ib-1, AP2III-2, AP2IV-3 (this paper), AP2IV-4, AP2VIIa-5, AP2VIIa-6, AP2VIIb-3, AP2VIII-7, AP2IX-4, AP2XII-4, AP2XII-5</li> <li>reference 6: AP2IX-9, AP2VI-1; reference 10: AP2X-5, AP2X-8, AP2X-9; reference 12: AP2VIIa-1, AP2VIIa-4, AP2VI-1, AP2XI-1, AP2XII-9; reference 26: AP2XI-4</li> </ul>						

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**Figure S1** Disruption of AP2IV-3 by genetic knockout in the Type III CTG strain also shows a decrease in the formation of tissue cysts. IFA quantification in triplicate of tissue cyst numbers (DBA-positive) formed by CTG parent versus CTG- $\Delta ap2IV-3$  clones grown in pH 8.2 media for 72 hrs.

**Dataset S1**

Analysis of 320 published alkaline-stress responsive genes (ref. 25, Behnke et al, 2008) in CTG parent and CTG transgenic strains (CTG- $\Delta ap2IV-3$  and CTG-<sup>DD</sup>AP2IV-3) grown in pH 7.0-pH 8.2 media as indicated. The complete microarray data for this experiment is deposited in GEO (GSE89469).

**Dataset S2**

Expression profiles of 42 mRNAs altered by AP2IV-3 Shield 1-overexpression in ME49 parasites grown in pH 7.0 and pH 8.2 media and M4 strain merozoites and sporozoites.

**Dataset S3**

Transgenic strains produced in this study and key primer sequences.

**Dataset S1 Analysis of 320 stress-induced bradyzoite genes from reference #25 Behnke et al 2008**

Strains: CTG (WT), CTG- <sup>DD</sup> AP2IV-3 (OE), CTG- $\Delta$ ap2IV-3(KO)							
	Conditions for microarray: Shield-1 (100nM)						Gray highlight are genes plotted in Fig4
Genbank	CTG (pH7.0) (RMA Value WT)	CTG (pH7.8) (RMA Value WT)	CTG (pH8.2) (RMA Value WT)	CTG- <sup>DD</sup> AP2IV-3 (pH7.0) (RMA Value OE)	CTG- <sup>DD</sup> AP2IV-3 (pH7.8) (RMA Value OE)	CTG- $\Delta$ ap2IV-3(pH8.2) (RMA Value KO)	Gene description
TGME49_200350	407.66	507.08	164.04	250.19	242.18	183.62	subtilase family serine protease
TGME49_201410	1942.56	1524.49	734.81	1672.66	1533.83	515.88	protein phosphatase 2C
TGME49_201760	651.16	516.88	160.50	585.72	499.34	168.75	hypothetical protein
TGME49_201840	758.06	684.13	205.72	618.50	585.17	116.63	eukaryotic aspartyl protease
TGME49_202010	205.67	215.52	38.05	238.24	219.06	37.95	hypothetical protein
TGME49_202020	312.26	762.66	496.70	630.88	663.65	121.12	DnaK-TPR
TGME49_202050	18.74	21.91	18.28	28.17	23.84	21.95	hypothetical protein
TGME49_202140	262.93	340.96	77.52	279.45	294.78	53.24	enoyl-CoA hydratase/isomerase family protein
TGME49_202200	4181.47	2898.67	1179.20	3033.07	2796.12	941.35	hypothetical protein
TGME49_203230	36.77	69.68	21.25	37.58	33.70	22.18	hypothetical protein
TGME49_203930	755.91	440.09	239.00	583.82	508.44	197.97	hypothetical protein
TGME49_204500	29.74	36.78	19.47	43.88	41.61	17.72	hypothetical protein
TGME49_205250	12.68	11.60	12.25	14.35	12.75	22.19	Rhoptry kinase family protein ROP18
TGME49_205360	295.19	162.69	68.44	212.43	223.03	65.65	hypothetical protein
TGME49_205490	345.41	405.67	62.32	356.99	288.90	61.55	integral membrane protein
TGME49_207130	366.64	324.80	103.78	422.31	384.85	93.33	SRS49A (= SAG2Y)
TGME49_207140	196.99	112.54	93.63	236.96	232.69	41.87	SRS49B (= SAG2X)
TGME49_207150	654.64	428.82	176.32	743.26	692.10	137.88	SRS49C (= SAG2D)
TGME49_207160	65.90	62.72	116.78	81.61	71.92	145.78	SRS49D (= SAG2C)
TGME49_207210	233.81	81.30	332.68	738.83	444.70	73.00	hypothetical protein (UNK)
TGME49_207590	315.62	231.04	54.75	236.26	229.09	67.02	T-cell activation protein phosphatase 2C
TGME49_207600	57.29	66.89	34.29	57.81	61.26	35.70	tubulin delta chain
TGME49_208020	19.76	24.11	13.28	28.69	20.52	14.14	hypothetical protein
TGME49_208320	509.27	392.93	204.54	420.18	448.94	202.67	polynucleotide kinase-3'-phosphatase



TGME49_208380	12.62	13.52	12.81	15.72	16.54	11.90	hypothetical protein
TGME49_208430	372.02	339.84	155.07	418.65	440.22	192.02	serine proteinase inhibitor TgPI-2
TGME49_208550	267.16	446.35	37.81	150.57	169.27	53.06	hypothetical protein
TGME49_208730	141.50	154.92	109.37	219.50	207.60	71.77	hypothetical protein
TGME49_208740	226.48	356.23	165.78	574.02	467.48	48.69	microneme protein (MIC UNK)
TGME49_209750	7.17	8.12	8.51	7.27	7.46	8.96	hypothetical protein
TGME49_209760	12.78	10.18	19.84	21.67	19.04	12.34	hypothetical protein
TGME49_210370	1345.80	1071.99	363.34	1159.84	975.89	375.67	RNA helicase-1
TGME49_210420	671.29	487.25	187.30	542.90	453.72	168.53	hypothetical protein
TGME49_211290	3905.83	3513.55	1351.01	3340.56	3093.07	838.26	hypothetical protein
TGME49_212210	1024.03	1186.84	230.22	996.88	1124.95	259.04	hypothetical protein
TGME49_212920	539.33	683.57	241.04	680.50	678.54	223.84	hypothetical protein
TGME49_213450	993.01	1642.85	255.57	971.33	1153.29	341.28	hypothetical protein
TGME49_213460	20.86	25.22	14.82	17.90	17.30	12.25	hypothetical protein
TGME49_213470	582.03	869.70	197.15	568.88	635.41	141.01	hypothetical protein
TGME49_213480	86.83	88.52	30.84	87.50	92.06	20.78	hypothetical protein
TGME49_213880	27.63	33.33	16.74	29.27	28.13	16.87	hypothetical protein
TGME49_214400	150.80	117.77	39.16	146.07	162.65	54.11	hypothetical protein
TGME49_215770	177.27	183.70	88.23	406.88	376.16	49.51	Rhoptry kinase family protein ROP8 (incomplete catalytic triad)
TGME49_215910	389.57	507.41	203.62	403.70	341.77	166.75	hypothetical protein
TGME49_216140	1742.38	2005.07	95.75	16.20	19.39	94.80	ankyrin repeat-containing protein
TGME49_216460	556.25	389.31	143.34	472.26	444.74	108.51	hypothetical protein
TGME49_216490	253.29	310.58	158.61	288.60	272.06	103.98	hypothetical protein
TGME49_216620	470.80	293.46	77.09	302.12	322.07	66.61	EF hand domain-containing protein
TGME49_217410	246.63	251.54	114.39	294.10	288.15	63.81	hypothetical protein
TGME49_218270	1447.52	771.86	423.58	1098.65	938.89	487.04	hypothetical protein
TGME49_218520	5577.59	8411.51	2542.35	5994.98	6173.55	2558.61	microneme protein MIC6
TGME49_218740	996.61	1785.38	489.12	1132.85	1275.41	607.93	hypothetical protein
TGME49_220560	51.85	64.17	25.19	53.46	59.85	26.27	hypothetical protein
TGME49_221250	20.28	17.70	12.16	16.64	15.72	15.67	hypothetical protein
TGME49_221310	196.20	136.42	43.53	154.74	148.41	46.59	aminopeptidase N
TGME49_221540	330.24	277.63	62.45	263.31	207.36	60.35	hypothetical protein
TGME49_221840	334.69	402.38	143.73	445.43	420.88	72.36	hypothetical protein
TGME49_222100	1186.22	847.25	274.51	904.87	862.61	236.36	hypothetical protein

TGME49_222370	51.43	36.32	27.57	84.74	97.08	34.02	SRS13
TGME49_223060	362.53	418.19	172.24	382.39	364.87	69.47	MORN repeat-containing protein
TGME49_223550	83.32	172.41	77.45	184.07	181.59	46.37	hypothetical protein
TGME49_223850	226.42	277.40	72.99	326.18	275.76	52.03	hypothetical protein
TGME49_223920	2555.18	1585.89	874.54	1963.37	1701.44	621.62	hypothetical protein
TGME49_224170	93.33	103.61	57.05	101.48	104.62	46.11	SRS domain-containing protein
TGME49_224180	99.04	125.81	38.18	90.99	93.52	45.93	ankyrin repeat-containing protein
TGME49_224570	485.16	269.72	81.86	353.05	346.16	80.98	hypothetical protein
TGME49_224710	237.16	155.20	114.98	278.96	264.03	93.78	vacuolar sorting receptor protein
TGME49_224760	532.54	1091.80	163.94	453.90	459.18	76.75	SRS40E (= SRS4)
TGME49_225150	1402.05	962.96	273.14	1126.16	1048.57	266.91	hypothetical protein
TGME49_225290	428.63	294.28	128.82	310.32	320.21	65.60	nucleoside-triphosphatase
TGME49_225320	859.95	557.09	220.14	725.72	747.09	187.81	hypothetical protein
TGME49_225330	482.13	313.75	91.12	346.38	327.11	79.16	hypothetical protein
TGME49_225540	489.77	979.93	214.17	695.53	731.54	181.67	hypothetical protein
TGME49_225860	379.04	261.72	82.87	318.17	301.29	113.24	hypothetical protein
TGME49_226420	777.06	721.12	314.49	854.12	851.21	216.96	oligoendopeptidase F
TGME49_226690	222.96	166.86	66.51	182.32	174.23	76.67	hypothetical protein
TGME49_226710	1312.17	795.42	309.08	1025.46	872.00	215.15	hypothetical protein
TGME49_226770	223.17	137.65	28.55	150.00	123.26	35.67	cGMP-inhibited 3'
TGME49_227000	465.05	336.71	89.59	375.03	358.54	65.36	hypothetical protein
TGME49_227430	23.65	29.99	57.71	151.48	148.58	32.88	hypothetical protein
TGME49_227810	8472.18	5192.10	2798.61	6820.34	6123.81	1616.17	Rhoptry kinase family protein ROP11 (incomplete catalytic triad)
TGME49_228160	15.05	13.05	20.14	14.66	12.95	38.46	serine/threonine protein phosphatase
TGME49_229010	740.39	534.57	127.95	592.74	509.99	99.87	hypothetical protein
TGME49_229500	178.06	122.69	74.06	147.97	129.07	103.90	hypothetical protein
TGME49_229680	83.82	86.34	44.48	87.47	76.20	47.57	hypothetical protein
TGME49_229720	40.24	43.83	33.93	35.97	35.15	43.92	hypothetical protein
TGME49_230130	35.96	31.89	27.98	35.79	29.50	20.98	hypothetical protein
TGME49_230160	12618.33	15396.28	5903.58	11707.51	12050.84	5699.61	hypothetical protein
TGME49_230350	847.20	552.33	254.46	642.69	574.93	230.40	hypothetical protein
TGME49_230360	60.78	42.83	26.30	47.12	42.39	37.99	hypothetical protein
TGME49_230370	15.34	15.12	10.80	14.32	14.61	10.64	hypothetical protein

TGME49_230470	1438.40	1322.47	626.25	1385.48	1154.74	227.02	Rhoptry kinase family protein ROP46
TGME49_230980	130.71	104.72	54.77	132.62	94.93	58.88	myosin head motor domain-containing protein TgMyo I
TGME49_231840	350.79	261.79	120.34	256.10	256.48	111.53	tola protein.
TGME49_231880	13.95	12.07	18.05	14.07	12.45	17.68	glutamine/glutamic acid rich protein
TGME49_232020	143.54	111.32	33.71	120.97	126.51	45.35	hypothetical protein
TGME49_232350	6387.91	7498.43	2059.96	5975.51	6009.48	1336.90	lactate dehydrogenase
TGME49_232590	272.54	288.84	119.46	252.22	248.60	94.16	gamma-glutamylcysteine synthetase
TGME49_233030	906.84	773.83	161.02	788.20	668.12	159.63	myosin-A docking protein
TGME49_233450	3910.18	5294.72	1285.04	3618.72	3501.13	741.08	SRS29A (= SRS1)
TGME49_234540	622.62	427.09	146.97	540.05	505.52	121.56	hypothetical protein
TGME49_235500	507.46	844.90	197.75	538.31	576.75	94.80	hypothetical protein
TGME49_235860	246.15	155.60	88.73	183.20	165.84	35.79	subtilisin-like protease
TGME49_236010	1239.23	1431.79	505.88	1127.61	1121.95	384.49	prenylcysteine oxidase
TGME49_236070	1343.85	1782.84	586.62	1755.30	1703.00	438.86	pyrroline-5-carboxylate reductase
TGME49_237090	16.44	19.67	16.36	18.37	18.10	19.13	hypothetical protein
TGME49_237180	1365.29	1215.41	478.31	1162.17	1025.98	383.86	hypothetical protein
TGME49_237190	88.02	57.49	25.74	89.33	75.09	36.70	hypothetical protein
TGME49_237820	106.89	83.06	34.62	125.57	87.34	29.91	hypothetical protein
TGME49_238200	525.82	445.60	296.56	462.18	461.19	320.22	alpha/beta hydrolase fold domain containing protein
TGME49_238210	146.28	255.00	82.80	299.30	218.25	76.75	microneme protein
TGME49_238440	17.66	18.44	27.15	67.63	41.29	19.47	SRS22A
TGME49_239020	339.75	351.72	97.30	367.23	342.55	91.59	ATP-binding cassette protein subfamily B member 2
TGME49_240090	159.75	277.72	45.01	197.78	177.55	41.02	Rhoptry kinase family protein ROP34
TGME49_240470	57.83	90.77	61.54	120.14	148.89	32.50	hypothetical protein
TGME49_240930	67.58	63.83	47.09	99.17	90.38	44.91	molybdenum cofactor biosynthesis protein c
TGME49_240950	321.22	204.94	139.40	231.23	243.95	189.20	hypothetical protein
TGME49_241150	816.27	592.91	372.54	620.82	672.14	325.15	hypothetical protein
TGME49_242230	3389.20	2231.08	1201.88	2239.11	2394.41	481.09	Rhoptry kinase family protein ROP29
TGME49_243200	1029.96	515.13	112.40	647.92	628.30	139.15	hypothetical protein
TGME49_243470	205.93	306.91	108.55	62.92	65.51	71.99	hypothetical protein
TGME49_243690	4008.01	2827.73	1220.95	3094.05	2774.72	769.72	hypothetical protein

TGME49_243720	34.86	38.61	23.66	44.70	45.17	20.67	peroxisomal biogenesis factor 11 domain-containing protein
TGME49_243940	289.53	291.66	109.62	299.73	313.72	85.44	hypothetical protein
TGME49_244330	28.80	33.36	28.81	42.93	53.00	33.31	hypothetical protein
TGME49_244500	881.43	490.35	119.07	678.42	666.75	123.79	tubulin-tyrosine ligase family protein
TGME49_246070	32.47	29.22	22.67	45.61	39.77	23.14	SRS56A
TGME49_247400	1209.66	2381.92	741.89	1759.60	1722.29	511.71	hypothetical protein
TGME49_247530	3962.98	5697.82	1720.34	4806.37	4619.73	1053.26	hypothetical protein
TGME49_247740	133.18	152.99	69.72	147.06	164.92	45.88	RNA methyltransferase
TGME49_249150	191.45	288.75	40.57	105.42	85.42	39.82	PAN domain-containing protein
TGME49_249300	916.35	1154.03	284.57	904.75	970.60	261.49	hypothetical protein
TGME49_249540	46.89	72.62	24.11	69.92	53.61	24.27	hypothetical protein
TGME49_249570	2512.36	1305.76	649.04	2508.05	1482.50	612.83	hypothetical protein
TGME49_249770	142.26	147.32	51.77	154.29	145.64	73.29	hypothetical protein
TGME49_250120	212.10	517.18	100.37	237.20	218.54	159.73	hypothetical protein
TGME49_250360	168.12	346.21	147.39	234.18	215.07	159.43	esterase
TGME49_250760	21.45	24.04	14.16	22.44	22.11	18.00	PPR repeat-containing protein
TGME49_251490	195.84	201.76	43.03	207.57	196.64	53.40	hypothetical protein
TGME49_251540	1769.40	2058.79	632.25	1603.40	1528.34	369.63	GRA9 protein
TGME49_252200	279.22	199.78	71.84	284.28	239.32	61.00	zinc finger DHHC domain-containing protein
TGME49_252360	1863.29	1321.29	356.82	1438.22	1304.34	419.97	Rhoptry kinase family protein ROP24 (incomplete catalytic triad)
TGME49_252640	29.62	34.92	32.60	73.63	60.03	21.63	TgPMA1
TGME49_253330	1018.14	591.42	263.88	707.78	569.07	56.50	Rhoptry kinase family protein
TGME49_253340	14.89	19.82	14.68	15.85	15.28	10.97	hypothetical protein
TGME49_254040	193.15	130.84	130.08	146.00	146.97	128.81	hypothetical protein
TGME49_254060	20.02	22.67	24.21	29.19	40.49	22.18	SRS14
TGME49_254470	1125.64	1765.30	497.95	1176.97	1317.98	355.54	hypothetical protein
TGME49_254660	1371.62	1306.21	312.56	1310.11	1436.95	326.56	ankyrin repeat-containing protein
TGME49_254670	1108.18	1034.84	255.51	1139.76	1152.03	271.49	hypothetical protein
TGME49_254880	1472.31	881.74	426.30	1156.03	1141.52	327.18	alpha-galactosidase A
TGME49_254890	59.95	47.41	38.15	115.46	138.47	38.42	hypothetical protein
TGME49_256030	935.66	695.87	280.41	835.89	747.95	283.96	hypothetical protein
TGME49_257550	544.12	341.11	91.90	453.01	446.75	83.18	hypothetical protein
TGME49_257570	25.93	25.13	21.45	30.42	26.67	24.46	hypothetical protein

TGME49_257760	267.77	349.36	61.02	282.97	284.51	36.03	hypothetical protein
TGME49_258360	1684.18	1163.38	386.39	1578.67	1352.57	307.68	hypothetical protein
TGME49_258560	101.71	104.63	34.97	93.37	103.35	29.47	hypothetical protein
TGME49_258590	117.04	89.10	20.14	90.11	98.16	22.83	hypothetical protein
TGME49_258660	6523.33	4838.44	2088.77	5712.02	5348.17	1442.98	rhoptry protein 6
TGME49_258700	300.86	229.61	98.71	249.95	232.63	109.40	hypothetical protein
TGME49_258800	45.37	31.31	23.08	46.24	39.14	23.24	Rhoptry kinase family protein ROP31
TGME49_259020	58.81	58.84	184.78	737.09	512.01	40.73	bradyzoite antigen (BAG1)
TGME49_259700	1404.22	1290.87	407.54	1219.48	1138.32	303.58	hypothetical protein
TGME49_260190	151.27	153.10	41.91	163.25	190.00	22.33	microneme protein
TGME49_260440	2250.45	3104.06	1514.99	2806.44	3197.75	1019.77	46 kDa FK506-binding nuclear protein
TGME49_260580	248.85	150.99	50.95	233.12	191.83	44.65	hypothetical protein
TGME49_261650	261.85	261.48	152.40	315.51	304.80	103.74	hypothetical protein
TGME49_261740	18627.26	16857.48	7472.67	17332.77	16313.97	7670.01	hypothetical protein
TGME49_262050	5704.09	4572.61	2122.73	4938.21	4513.41	840.92	Rhoptry kinase family protein ROP39
TGME49_262730	807.37	654.50	241.30	761.71	703.55	190.91	Rhoptry kinase family protein ROP16
TGME49_262950	107.04	72.96	41.70	95.64	91.79	43.34	enterophilin-2L
TGME49_262970	124.35	137.11	32.85	181.29	143.58	36.43	zinc finger (CCCH type) protein
TGME49_263270	473.78	461.81	209.91	492.73	463.43	168.28	glycerophosphoryl diester phosphodiesterase family domain containing protein
TGME49_264150	24.16	28.52	15.72	49.19	40.97	17.21	hypothetical protein
TGME49_264590	44.95	70.86	26.61	55.33	51.91	22.36	hypothetical protein
TGME49_264600	2198.33	1454.31	647.23	2040.44	1829.65	480.22	hypothetical protein
TGME49_264630	23.29	21.60	23.44	58.08	41.59	29.00	hypothetical protein
TGME49_265070	312.38	192.56	73.25	250.72	237.07	72.57	hypothetical protein
TGME49_265420	600.67	482.17	133.33	561.29	491.33	117.79	hypothetical protein
TGME49_265650	368.79	229.22	80.47	251.26	246.74	75.82	hypothetical protein
TGME49_266270	28.51	30.91	19.70	35.82	36.21	14.14	2-methylbutyryl-CoA dehydrogenase
TGME49_266320	506.30	297.49	146.28	364.44	376.86	131.73	hypothetical protein
TGME49_266680	362.97	429.44	160.55	390.55	421.01	134.23	hypothetical protein
TGME49_266970	1181.58	1203.08	386.91	1186.58	1193.60	330.42	hypothetical protein
TGME49_267130	73.74	127.56	72.50	121.70	124.79	50.58	SRS38A
TGME49_267460	15.71	15.35	12.74	14.39	14.15	9.61	hypothetical protein
TGME49_267470	74.98	117.83	38.98	138.74	139.91	63.65	hypothetical protein

TGME49_267670	75.43	100.21	47.49	148.01	138.36	51.62	hypothetical protein
TGME49_267980	10.15	11.09	11.26	10.71	11.46	10.71	hypothetical protein
TGME49_268360	139.89	106.63	79.35	236.21	233.29	25.65	hypothetical protein
TGME49_268760	1930.45	1952.45	601.91	1701.81	1580.90	442.33	hypothetical protein
TGME49_268860	12.17	12.60	17.21	34.54	28.35	11.29	enolase 1
TGME49_269300	18.01	15.20	13.48	15.96	15.14	10.14	lipase domain-containing protein
TGME49_269310	13.37	13.87	13.89	13.39	11.97	14.25	D13
TGME49_269340	2312.74	1521.53	614.18	1651.42	1572.95	416.30	hypothetical protein
TGME49_269600	1000.58	908.22	360.65	917.35	1001.55	126.42	biotin carboxyl carrier protein
TGME49_269610	123.36	121.14	28.51	130.09	143.55	30.17	hypothetical protein
TGME49_269870	2392.80	1414.12	635.44	1616.61	1501.67	468.74	hypothetical protein
TGME49_270160	192.98	167.41	54.15	174.20	166.74	41.10	hypothetical protein
TGME49_270260	21.93	44.30	19.75	37.28	35.12	18.99	hypothetical protein
TGME49_270700	272.93	633.46	101.29	422.63	514.15	117.34	hypothetical protein
TGME49_271070	51.09	40.48	21.31	46.43	55.80	22.03	cysteine protease domain containing protein
TGME49_271270	1409.43	1125.74	698.26	1221.76	1068.29	576.53	hypothetical protein
TGME49_271320	208.03	172.99	58.21	216.53	202.50	66.62	hypothetical protein
TGME49_271770	74.31	68.64	29.78	65.30	67.48	25.58	hypothetical protein
TGME49_272440	68.61	48.17	23.52	46.27	44.49	22.67	hypothetical protein
TGME49_273130	1094.69	799.25	488.72	873.29	848.75	392.54	SRS30A
TGME49_273980	320.41	352.18	219.70	960.00	837.27	107.94	hypothetical protein
TGME49_274140	69.27	93.75	26.07	67.07	79.36	28.82	RNA recognition motif-containing protein
TGME49_274170	60.64	82.58	56.56	137.45	107.94	40.71	protein kinase (incomplete catalytic triad)
TGME49_275980	225.24	241.07	66.06	179.12	197.59	47.11	ubiquinone biosynthesis protein COQ4
TGME49_276130	402.61	360.47	102.90	360.32	309.48	125.56	cathepsin C2 (TgCPC2)
TGME49_276930	2427.98	3077.19	1088.33	2839.60	3128.62	606.98	hypothetical protein
TGME49_277730	38.83	48.65	49.97	55.51	44.77	52.02	hypothetical protein
TGME49_278080	253.90	315.96	249.17	385.85	403.18	129.23	hypothetical protein
TGME49_278370	27.62	26.98	17.33	31.38	32.38	33.89	hypothetical protein
TGME49_278390	15.19	11.80	24.03	16.98	20.33	48.95	hypothetical protein
TGME49_278980	24.89	27.26	18.04	39.29	36.51	16.30	hypothetical protein
TGME49_280480	567.87	395.55	149.50	464.72	493.30	151.14	calmodulin

TGME49_280570	4292.89	3524.08	3175.13	5796.80	5319.56	679.60	bradyzoite surface antigen
TGME49_280580	4454.94	2986.60	1075.82	3099.33	3278.92	273.70	p18 surface antigen
TGME49_280670	1065.76	715.63	419.23	910.75	773.93	241.30	hypothetical protein
TGME49_281790	122.81	129.20	37.13	151.84	101.36	59.43	Rhoptry kinase family protein ROP45 (incomplete catalytic triad)
TGME49_284310	18.71	17.86	11.59	22.07	19.36	14.95	hypothetical protein
TGME49_284420	41.59	47.39	14.08	49.18	48.13	13.56	hypothetical protein
TGME49_285290	752.36	495.13	171.20	556.39	550.19	147.26	hypothetical protein
TGME49_285650	64.20	48.57	39.26	53.82	54.47	61.86	hypothetical protein
TGME49_285860	175.38	91.87	39.38	262.52	298.97	103.46	SRS20C
TGME49_285870	5719.36	4336.39	1620.79	6194.42	6130.06	946.50	SRS20A
TGME49_286000	60.63	131.89	40.30	132.16	141.28	34.76	hypothetical protein
TGME49_286150	25.72	28.72	23.88	32.76	37.36	13.57	PAN domain-containing protein
TGME49_286500	691.04	322.69	191.76	454.61	430.92	149.36	hypothetical protein
TGME49_286580	1237.05	1103.71	403.48	1206.86	994.48	467.06	lysophospholipase
TGME49_286670	260.93	274.62	77.10	229.36	260.76	61.01	hypothetical protein
TGME49_286740	108.61	163.23	29.94	130.72	112.17	27.84	microneme protein
TGME49_287970	583.14	341.70	153.85	413.14	384.85	198.68	hypothetical protein
TGME49_288000	256.72	328.16	63.82	258.57	259.45	58.76	hypothetical protein
TGME49_288690	85.95	127.40	29.17	134.09	99.47	26.52	DnaJ domain-containing protein
TGME49_289620	2088.23	3341.61	903.87	2345.14	2531.27	718.73	cathepsin C
TGME49_290970	475.31	227.55	267.78	811.61	563.46	93.34	serine palmitoyltransferase
TGME49_290980	312.92	322.76	64.56	235.64	250.70	80.90	aminotransferase domain-containing protein
TGME49_291040	29.88	17.60	34.37	117.68	68.28	18.21	lactate dehydrogenase (LDH2)
TGME49_291910	12.69	15.94	9.76	17.85	15.77	10.53	hypothetical protein
TGME49_291960	6411.67	4380.21	1864.22	5333.37	4821.65	1423.17	Rhoptry kinase family protein ROP40 (incomplete catalytic triad)
TGME49_293280	16.24	19.39	27.49	21.13	18.07	22.95	hypothetical protein
TGME49_293430	4002.27	3083.82	1144.27	3020.92	2660.13	984.49	hypothetical protein
TGME49_293540	551.81	407.90	127.80	478.03	388.88	107.88	hypothetical protein
TGME49_293780	820.92	656.91	232.06	594.33	505.99	89.23	hypothetical protein
TGME49_293790	61.54	50.06	37.70	82.85	62.84	28.15	hypothetical protein
TGME49_293810	96.59	120.30	34.17	87.15	80.87	31.55	2-methylisocitrate lyase
TGME49_294410	21.76	28.70	19.59	23.99	19.26	21.34	hypothetical protein

TGME49_294570	45.85	43.33	42.82	49.39	43.23	27.94	rhodanese-like domain containing protein
TGME49_294610	568.12	407.10	144.27	474.13	379.94	190.26	hypothetical protein
TGME49_294790	4783.75	4342.67	2273.79	5131.58	4643.21	1738.86	hypothetical protein
TGME49_295390	11.97	9.96	11.84	11.62	11.47	13.11	hypothetical protein
TGME49_295950	10.33	10.33	11.10	9.84	10.27	10.91	hypothetical protein
TGME49_295960	22.70	30.69	21.38	19.51	18.28	40.42	hypothetical protein
TGME49_297070	2350.88	1572.03	379.39	1706.85	1595.73	322.84	duplicated carbonic anhydrase
TGME49_297120	1166.86	693.59	304.83	855.71	913.12	238.49	hypothetical protein
TGME49_297860	488.85	319.07	155.38	440.47	403.16	150.37	hypothetical protein
TGME49_297960	1168.64	804.09	252.76	967.18	829.10	276.06	hypothetical protein
TGME49_299060	600.21	400.78	207.71	500.85	444.84	169.24	sodium/hydrogen exchanger
TGME49_300100	274.39	234.40	46.37	229.40	184.44	43.33	rhoptry neck protein 2
TGME49_300130	33.12	37.19	21.12	62.51	60.82	39.76	apical membrane antigen
TGME49_300290	131.23	105.06	50.74	96.72	113.03	82.73	SNARE domain-containing protein
TGME49_301160	532.76	416.96	194.55	631.68	661.31	83.17	SRS19C (= SRS7)
TGME49_301240	12.59	12.62	10.66	15.82	13.18	12.41	hypothetical protein
TGME49_301350	30.92	20.05	35.51	35.56	26.70	19.22	hypothetical protein
TGME49_301420	2050.74	1200.05	624.00	1634.16	1334.03	516.49	hypothetical protein
TGME49_304670	330.49	241.61	70.16	307.41	251.17	59.74	internalin
TGME49_304930	548.61	539.87	187.26	582.84	573.39	120.90	hypothetical protein
TGME49_304940	1504.86	1401.26	825.05	1495.75	1539.22	250.22	hypothetical protein
TGME49_305050	4173.08	4122.19	1133.81	4815.43	4628.56	1193.15	calmodulin
TGME49_305100	14.12	17.17	11.87	13.22	13.11	13.76	hypothetical protein
TGME49_305270	678.29	366.47	129.52	517.17	448.47	112.71	hypothetical protein
TGME49_305460	968.46	954.01	493.13	1290.07	1337.73	131.83	methionine aminopeptidase
TGME49_305510	2006.35	1436.53	521.36	1382.98	1338.06	328.84	hypothetical protein
TGME49_305590	524.56	324.53	75.50	420.58	393.91	68.96	ABC transporter
TGME49_306060	4946.44	3573.39	1359.38	3330.06	2916.54	945.05	hypothetical protein
TGME49_306230	99.87	116.00	46.34	101.55	96.60	54.02	hypothetical protein
TGME49_306340	219.88	219.85	141.66	192.60	162.64	62.36	dynein gamma chain
TGME49_306450	55.03	76.52	26.88	100.64	130.12	24.01	short chain dehydrogenase family protein
TGME49_306510	21.73	31.15	25.35	45.44	38.17	23.28	hypothetical protein
TGME49_306620	22.16	17.22	19.97	20.14	19.57	21.70	AP2IX-9



TGME49_307830	343.87	470.84	124.99	384.64	493.22	157.70	hypothetical protein
TGME49_309860	116.84	52.17	49.33	77.51	74.82	55.63	hypothetical protein
TGME49_309930	237.61	188.12	77.51	229.97	198.61	43.01	alpha-N-acetylgalactosaminidase
TGME49_310010	1391.70	997.40	435.07	1116.54	1090.45	352.89	sushi domain-containing protein / SCR repeat-containing protein
TGME49_310100	95.94	70.98	45.94	83.33	91.29	30.45	GPI mannosyltransferase 1
TGME49_310240	357.89	258.69	127.90	287.34	243.44	126.90	hypothetical protein
TGME49_311100	1484.48	2194.86	519.27	1324.64	1298.61	297.51	zinc finger (CCCH type) protein
TGME49_311370	161.31	248.82	104.95	252.83	340.65	46.91	methylmalonate-semialdehyde dehydrogenase
TGME49_311470	2676.60	1740.74	734.34	2002.86	1841.29	595.66	hypothetical protein
TGME49_312150	2927.58	2105.47	1063.03	2369.09	2292.26	750.52	hypothetical protein
TGME49_312320	333.72	153.88	254.61	606.67	445.44	93.76	hypothetical protein
TGME49_312950	1022.19	598.47	201.27	746.71	796.70	211.17	hypothetical protein
TGME49_313050	83.10	132.45	51.82	121.98	86.92	32.15	short-chain dehydrogenase/reductase family protein
TGME49_313780	680.38	419.36	116.64	560.27	506.47	105.78	hypothetical protein
TGME49_313840	15.80	13.90	15.02	15.04	15.62	15.52	hypothetical protein
TGME49_314250	85.22	144.46	252.85	1197.51	1395.85	122.48	bradyzoite rhoptry protein BRP1
TGME49_315210	1524.76	892.99	257.59	1069.73	924.51	261.64	rhoptry protein
TGME49_315220	1660.10	1150.73	511.66	1263.41	1127.84	445.50	rhoptry protein
TGME49_315470	257.63	160.50	37.30	194.13	183.45	41.09	hypothetical protein
TGME49_315490	603.36	507.94	138.13	534.46	498.71	143.42	hypothetical protein
TGME49_315500	955.90	528.81	344.25	739.91	680.24	329.22	hypothetical protein
TGME49_315510	610.21	407.14	226.06	479.02	431.28	201.32	hypothetical protein
TGME49_316260	1871.70	1203.34	648.30	1672.84	1392.71	504.37	hypothetical protein
TGME49_316280	2566.93	1734.14	954.12	2028.30	1936.76	706.68	hypothetical protein
TGME49_316580	8.73	10.67	9.49	9.49	9.66	9.19	hypothetical protein
TGME49_318610	12.47	13.46	152.16	5568.23	5063.30	16.11	AP2IV-3
TGME49_318660	1769.91	1833.42	641.02	1839.57	1737.06	415.37	protein phosphatase 2C
TGME49_318680	20.24	23.59	14.46	25.28	21.20	15.50	3',5'-cyclic-nucleotide phosphodiesterase, putative
TGME49_319350	1540.19	1222.50	507.47	1117.83	1130.46	428.25	SRS domain containing protein
TGME49_319360	54.62	181.53	62.29	189.81	193.86	62.74	SRS17
TGME49_320180	10.39	11.32	16.44	13.32	13.55	33.97	SRS16C (= BSR4, P36)

TGME49_320620	184.50	97.10	92.48	143.14	180.29	61.72	queuine tRNA-ribosyltransferase
TGME49_320630	1400.16	1248.34	301.11	1056.01	1066.56	274.39	choline kinase
TGME49_321470	14.71	14.44	28.51	16.84	16.76	32.04	SRS12D
TGME49_321480	221.15	316.92	87.11	198.89	159.70	81.01	SRS12B

**Dataset S2 Many of the 42 mRNAs altered by the overexpression of DDHA-AP2IV-3 are highly expressed in merozoites and/or sporozoites.** Data in columns B-G are percentile values, which provides a relative comparison to all mRNAs expressed in each sample. Percentile values for columns B and C were determined in the current analysis, whereas percentiles for columns D-G were obtained from each Gene Record in ToxoDB. **ToxoDB Data sources:** column D and E are White lab microarray data from Type II ME49 tachyzoite and 48 h pH8.2 samples; column F is a RNA-seq data of CZ-H3 strain (Hehl Lab) from 3 day post-cat infection merozoites samples; column G is a RNA-seq data of a Type II M4 (Boothroyd Lab) from 10 day oocysts (sporozoites) samples. The fold change in column I was determined by comparing the RMA values from the CTG-DDHA-AP2IV-3 transgenic grown in normal pH7.0 media plus 100 nM Shield 1 divided by the CTG parent also grown in normal media plus Shield 1. All values are sorted by the highest to lowest fold increases in column I. Columns J and K indicate genes whose mRNA levels are qualitatively increased in DD-AP2IV-3 parasites and either merozoites and/or sporozoites.

Genbank	CTG parent pH7.0	DDHA-AP2IV-3 plus Shield 1 pH7.0	ME49 tachyzoite pH7.0	ME49 bradyzoite pH8.2	M4 merozoite pH7.0	M4 sporozoite pH7.0	Gene description	Fold change CTG parent vs DDHA-AP2IV-3	elevated in DDHA-AP2IV-3 and merozoites	elevated in DDHA-AP2IV-3 and sporozoites
TGME49_318610	10.3	97.5	9.1	71.5	71.4	91.2	AP2IV-3	446.5	X	X
TGME49_314250	47.0	91.4	67.6	96.5	97.8	76.9	bradyzoite rhoptyr protein BRP1	14.1	X	X
TGME49_259020	41.3	87.0	58.1	99.8	13.1	70.0	bradyzoite antigen (BAG1)	12.5		X
TGME49_227430	28.0	58.8	46.0	86.7	14.8	29.1	hypothetical protein	6.4		
TGME49_291040	32.1	53.2	55.4	99.7	9.0	38.9	lactate dehydrogenase (LDH2)	3.9		
TGME49_238440	21.2	43.1	7.4	80.9	90.7	70.8	SRS22A	3.8	X	X
TGME49_319360	40.2	63.7	23.2	83.7	64.3	36.8	SRS17	3.5	X	
TGME49_207210	67.2	87.0	70.1	99.9	18.8	5.8	hypothetical protein (UNK)	3.2		
TGME49_273980	73.5	89.5	33.7	90.4	99.9	5.8	hypothetical protein	3.0	X	
TGME49_208740	66.6	83.9	72.6	99.7	15.5	99.7	microneme protein (MIC UNK)	2.5		X
TGME49_264630	27.7	40.7	27.1	88.8	52.4	72.9	hypothetical protein	2.5	X	X
TGME49_252640	32.0	44.7	24.9	95.5	4.4	77.4	TgPMA1	2.5		X
TGME49_220560	39.7	54.6	17.5	29.2	9.8	74.1	hypothetical protein	2.4		X
TGME49_215775	60.9	78.7	99.6	97.2	94.6	87.2	Rhoptry kinase family protein ROP8	2.3	X	X
TGME49_274170	41.8	56.5	15.0	78.9	90.1	44.6	protein kinase	2.3	X	
TGME49_286000	41.8	55.7	26.8	67.2	76.2	23.0	hypothetical protein	2.2	X	
TGME49_306510	26.4	37.2	22.2	73.5	57.7	81.1	hypothetical protein	2.1	X	X
TGME49_240470	41.0	53.7	19.3	83.1	13.6	66.1	hypothetical protein	2.1		X
TGME49_238210	56.9	73.2	53.4	85.0	64.3	41.7	microneme protein	2.0	X	
TGME49_264150	28.4	38.3	17.0	49.5	10.8	5.8	hypothetical protein	2.0		
TGME49_202020	72.9	85.3	60.0	94.3	8.8	49.1	DnaK-TPR	2.0		
TGME49_267670	45.0	58.3	38.8	84.7	73.7	72.9	hypothetical protein	2.0	X	X
TGME49_254890	41.5	52.9	22.0	72.2	76.0	5.8	hypothetical protein	1.9	X	
TGME49_300130	33.5	41.7	18.4	69.5	78.2	57.4	apical membrane antigen	1.9	X	X
TGME49_267470	44.9	56.7	34.2	90.6	94.3	33.0	hypothetical protein	1.9	X	
TGME49_312320	74.4	84.8	77.2	99.2	N/A	N/A	hypothetical protein	1.8		
TGME49_268360	56.0	68.4	74.4	47.0	12.7	31.3	hypothetical protein	1.7	X	
TGME49_267130	44.6	54.0	50.7	93.8	46.3	83.9	SRS38A	1.7		X
TGME49_222370	39.3	47.2	17.1	94.0	35.5	12.1	SRS13	1.6		
TGME49_278975	29.0	35.0	26.0	92.6	47.3	59.7	hypothetical protein	1.6	X	X
TGME49_311370	59.0	69.8	14.8	93.1	60.4	74.5	methylmalonate-semialdehyde dehydrogenase	1.6	X	X
TGME49_288690	47.2	56.0	16.4	26.3	N/A	N/A	DnaJ domain-containing protein	1.6		

TGME49_208730	56.3	66.8	92.0	99.6	9.9	60.1	hypothetical protein	1.6		X
TGME49_244335	31.4	36.3	15.7	48.5	16.8	45.3	hypothetical protein	1.5		
TGME49_277730	35.7	40.1	26.4	55.8	16.4	69.9	hypothetical protein	1.5		X
TGME49_250360	59.8	68.2	65.5	91.4	73.3	55.8	esterase	1.5	X	X
TGME49_309860	52.5	45.5	39.8	86.1	63.0	86.7	hypothetical protein	0.7		
TGME49_216620	80.5	73.5	69.8	47.2	28.4	17.7	EF hand domain-containing protein	0.6		
TGME49_243200	89.9	85.6	90.0	79.6	69.2	34.5	hypothetical protein	0.6		
TGME49_249150	62.6	51.1	12.4	23.7	77.4	19.5	PAN domain-containing protein	0.6		
TGME49_243470	64.3	41.9	37.0	95.7	42.3	24.5	hypothetical protein	0.3		
TGME49_216140	93.5	17.8	22.1	96.8	27.3	54.5	ankyrin repeat-containing protein	0.0		

## Dataset S3 Primer sequences

Oligonucleotide function	Gene/locus	Orientation	Oligonucleotides (5'->3')
<b>Tagging of endogenous gene loci with 3xHA or myc epitope tags</b>			
LIC 5' primer for AP2IX-9	AP2IX-9	Forward	TACTTCCAATCCAATTTAATGCAGTGCTTGCGGCTCTCTGATGA
LIC 3' primer for AP2IX-9	AP2IX-9	Reverse	TCCTCCACTTCCAATTTTAGCGGCTGACGTTGTTTCGCGC
LIC 5' primer for AP2IV-3	AP2IV-3	Forward	TACTTCCAATCCAATTTAATGCACTGTCGATTGGTACCGGATCTGG
LIC 3' primer for AP2IV-3	AP2IV-3	Reverse	TCCTCCACTTCCAATTTTAGCCGCTGCGTTGTCCCCTGATGAAG
<b>Overexpression construct</b>			
AP2IV-3 CDS cloning into pCTDDHA3	AP2IV-3 CDS	Forward	ATTCCCGGGGCGGATGGCTCTCTAGTGAGG
AP2IV-3 CDS cloning into pCTDDHA3	AP2IV-3 CDS	Reverse	ATTCCTGCAGGTTACGCTGCGTTGTCCCCTG
<b>AP2IX-9 knockout constructs</b>			
AP2IX-9B4UTR5F	5' UTR of AP2IX-9	Forward	GGGGACAACCTTTGTATAGAAAAGTTGCATTTTTTAGGTTGAAGA ACCGAGCAGC
AP2IX-9B1rUTR5R	5' UTR of AP2IX-9	Reverse	GGGGACTGCTTTTTGTACAACTTGAACGGCATGGCCGAAC TACG
AP2IX-9B2rUTR3F	3' UTR of AP2IX-9	Forward	GGGGACAGCTTTCTTGTACAAAGTGGTTAACGTGAGTTGCGC AGTCTTGC
AP2IX-9B3UTR3R	3' UTR of AP2IX-9	Reverse	GGGGACAACCTTTGTATAATAAAGTTGCCCGCTGGAAAAAGAAA GCGAC
Verify AP2IX-9KO-F	AP2IX-9	Forward	TATGGTACCATATGGGCCACACGCTTTGGGTTCTTAG
Verify AP2IX-9KO-R	AP2IX-9	Reverse	ATAAAGCTTGGTGAGGATGTCTGTTTCATG
<b>AP2IV-3 knockout constructs</b>			
AP2IV-3B4UTR5F	5' UTR of AP2IV-3	Forward	GGGGACAACCTTTGTATAGAAAAGTTGGGCTTCTTTGCAAAAAGA CTGACCTC
AP2IV-3B1rUTR5R	5' UTR of AP2IV-3	Reverse	GGGGACTGCTTTTTGTACAACTTGGACAGTAGCAGACGGCG AAAGTT
AP2IV-3B2rUTR3F	3' UTR of AP2IV-3	Forward	GGGGACAGCTTTCTTGTACAAAGTGGATTTTTGTTAACCGGCAT CTTCGTTTCG
AP2IV-3B3UTR3R	3' UTR of AP2IV-3	Reverse	GGGGACAACCTTTGTATAATAAAGTGGACACGAAACATAAGACA GTCAGGATCAG
Verify AP2IV-3KO-F	AP2IV-3	Forward	CGTCTTTTAGTTCTAACTCCCGCACG
Verify AP2IV-3KO-R	AP2IV-3	Reverse	GGCTCCTTCATGGACAAAACCCTT
<b>Guide RNA constructs</b>			

AP2IX-9gRNA1	AP2IX-9	Forward	CGGCGGAGCGGCATTCGCTTTGGgtttagagctagaaatagc
AP2IX-9gRNA2	AP2IX-9	Forward	CGGTTGGTTCGTCAAACGCGGGGgtttagagctagaaatagc
AP2IX-9gRNA3	AP2IX-9	Forward	CGACGTCACCAATCAAGCGTgtttagagctagaaatagc
AP2IX-9gRNA4	AP2IX-9	Forward	CCTGGCGGGAAAGAAAACCTCGGgtttagagctagaaatagc
AP2IV-3gRNA1	AP2IV-3	Forward	CTCGCCGTGGTAATTTGTCTgtttagagctagaaatagc
AP2IV-3gRNA2	AP2IV-3	Forward	CCACGAACGCTCTAACGTTGgtttagagctagaaatagc

#### Target regions for ChIP-qPCR

ChIP-qPCR	BAG1 region 1	Forward	GCCAGTCGAAAGCCATTAA
ChIP-qPCR	BAG1 region 1	Reverse	TCACGCGTTCCTGCTACTC
ChIP-qPCR	BAG1 region 2	Forward	CGTCTCTCTGTCCACGAAC
ChIP-qPCR	BAG1 region 2	Reverse	ATGGGGAACTGGAGGAAGAT
ChIP-qPCR	BAG1 region 3	Forward	AGGTCGCCCCGTCTTATTCTT
ChIP-qPCR	BAG1 region 3	Reverse	ACCCAAACATGGAGTTCAGG
ChIP-qPCR	BAG1 region 4	Forward	GACGAGTTCCCGTTTTTCCT
ChIP-qPCR	BAG1 region 4	Reverse	ACAGAGGTCGCTGCGTAGAC
ChIP-qPCR	BAG1 region 5	Forward	CTTTTGCCAAAGGAGACCTG
ChIP-qPCR	BAG1 region 5	Reverse	ATGCCACTGAGCTACACACG
ChIP-qPCR	BAG1 region 6	Forward	GTCGTCTGTGAGAGCGTCAA
ChIP-qPCR	BAG1 region 6	Reverse	GACCTGGGCTTTGCAGATAA

### Dataset S3 Transgenic strains

Published parent and transgenic strains used in this study		
Designated name in this study	Genotype	Reference
Prugniaud (Pru)	Type II strain with $\Delta h x g p r t$	Martrou, 1965
Prugniaud- $\Delta ku80$ (PruQ)	Type II strain with $\Delta h x g p r t, \Delta ku80$	Fox, 2011
CTG	Type III strain	ATCC#: 50842

Transgenic strains produced for this study					
Name in this study	experimental use	Parent strain source for producing the transgenic	Transgene/selectable marker	Drug Selection	Clone #
PruQ-AP2IV-3HA	endogenous expression of AP2IV-3	PruQ	endogenous promoter::AP2IV-3(3xHA)/DHFR-TS	pyrimethamine	D8
PruQ-AP2IX-9myc-AP2VI-3HA	endogenous expression of AP2IX-9	PruQ-AP2IV-3HA	endogenous promoter::AP2VI-1(3xHA)/DHFR-TS	pyrimethamine	A2, A3
CTG- <sup>DD</sup> AP2IV-3	conditional expression of AP2IV-3	CTG	tub::(DD-3xHA)-AP2IV-3/sagCAT	chloramphenicol	C4, D4
CTG-BAG1-Luc	expressing BAG1::firefly luciferase transgene	CTG	PC3	pyrimethamine	A4, B2
CTG- <sup>DD</sup> AP2IV-3-BAG1-Luc	expressing BAG1::firefly luciferase transgene	CTG-DDAP2IV-3	PC3	pyrimethamine	A3, C5
Pru- $\Delta ap2IV-3$	knockout of AP2IV-3	Pru	3Frag-AP2IV-3KO/DHFR-TS	pyrimethamine	A9, A10
Pru- $\Delta ap2IX-9$	knockout of AP2IX-9	Pru	3Frag-AP2IX-9KO/DHFR-TS	pyrimethamine	
CTG- $\Delta ap2IV-3$	knockout of AP2IV-3	CTG	3Frag-AP2IV-3KO/DHFR-TS	pyrimethamine	A3, A6