Sup Table 1 List of primers and vectors used in this study

primer	sequence	direction	site	use	plasmid	linearisation	strain
T. gondii							
ASH1ann-s	GGAAATCCTCCTCCCCCCCGAG	sense	-	annotation of TgASH1	-	-	-
ASH1ann-a	CCTCGCGTCTCCTTCCTCGCTCGCTCGG	antisense	-				
ASH1-s	GAATTCCCTGGAGGGAAATTCACACATGCCGC	sense	EcoRI	overexpression of Tub8 promoter controlled second copy with C-term Ty tag	pT8-ASH1Ty-HX	BamHI	ASH1-Ty
ASH1-a	ATGCATCGTTTGTTGTGAGGACGTTTTCGATGAATCGTCG	antisense	NsiI				
ASH1-KI-s	CCGGGTACCGCGGGGTGGGCCGACCTCG	sense	KpnI	C-term epitope tagging of endogenous gene	ASH1-3Ty-KI-HX	AvrII	ASH1-3Ty
ASH1-KI-a	CCATGCATGTTTGTTGTGAGGACGTTTTCGATG	antisense	NsiI				
ASH1-KO-s	CCGTTAATTAATCCATATTATGTCTAGATGGGAATCTGG	sense	PacI	Knock-out of endogenous gene -5'UTR fragment cloned into ASH1-3Ty-KI-HX	ASH1-KO-HX	PacI	ash1-ko
ASH1KO-a	CCGGTTAACGTGCGGTGCACAGCAGCCAGC	antisense	HpaI				
ASH1KO-c (P1)	CATATGCCGCCCTTGTCCTTGAAAGTTTC	sense	NdeI	confirmation of ASH1KO - WT locus	-	-	-
ASH1KO-c (P2)	AAGCTTTGCATCGTTTGTTGTGAGGACGTTTTC	antisense	HindIII				
ASH1KO-c (P3)	TAATACGACTCACTATAGGG	sense	-	confirmation of ASH1KO - 3' integration	-	-	-
ASH1KO-c (P4)	CCTCGCGTCTCCTTCCTCGCTCGCTCGG	antisense	-				
ASH1KO-c (P5)	GGAGCGGCCGCGCGGGGTGGGCCGACCTCG	sense	NotI	control	-	-	-
ASH2-KI-s	TACTTCCAATCCAATTTAATGCCCAATCTTTTTGCTCTGAGC	sense	KpnI	C-term epitope tagging of endogenous gene	ASH2-3Ty-KI-HX	SnaBI	ASH2-3Ty
ASH2-KI-a	TCCTCCACTTCCAATTTTAGCAAATGCATTTTCAGACCTTCTTTCGCAAGTCG	antisense	NsiI				
ASH2-KO-s	TACTTCCAATCCAATTTAATGCCCAATCTTTTTGCTCTGAGC	sense	KpnI	Endogenous gene truncation	ASH2-3Ty-KO-HX	EcoRI	ash2-ko
ASH2-KO-a	TCCTCCACTTCCAATTTTAGCAAATGCATTCTGGTGAGGTCTCTGCACCG	antisense	NsiI				
ASH2KO-c (P1)	TACTTCCAATCCAATTTAATGCCCAATCTTTTTGCTCTGAGC	sense	KpnI	control	-	-	-
ASH2KO-c (P2)	TCCTCCACTTCCAATTTTAGCAAATGCATTCTGGTGAGGTCTCTGCACCG	antisense	NsiI				
ASH2KO-c (P3)	GTGACACCTGCAAGCCACAGCGG	antisense	-	Integration 5'	-	-	-
ASH2KO-c (P4)	CCCAACGTTCAGAGCTATGCAGCTCTAGG	sense	-	WT locus/recombinant locus	-	-	-
ASH2KO-c (P5)	ATGCATCTTCAGACCTTCTTTCGCAAGTCGCATC	antisense	NsiI	WT locus	-	-	-
ASH3-KI-s	TACTTCCAATCCAATTTAATGGTACCAAGAAAGGCGTGCAGGTGGG	sense	KpnI	C-term epitope tagging of endogenous gene	ASH3-3Ty-KI-HX	StuI	ASH3-3Ty
ASH3-KI-a	TCCTCCACTTCCAATTTTAGCAAATGCATGACCGCCATGGCAATTCGACG	antisense	NsiI				
ASH3-KO-s	TACTTCCAATCCAATTTAATGGTACCAAGAAAGGCGTGCAGGTGGG	sense	KpnI	Endogenous gene truncation	ASH3-3Ty-KO-HX	StuI	ash3-ko
ASH3-KO-a	TCCTCCACTTCCAATTTTAGCAAATGCATGGGCATTCAGCTGCGTCTCCTC	antisense	NsiI				
ASH3KO-c (P1)	TACTTCCAATCCAATTTAATGGTACCAAGAAAGGCGTGCAGGTGGG	sense	KpnI	control	-	-	-
ASH3KO-c (P2)	TCCTCCACTTCCAATTTTAGCAAATGCATGGGCATTCAGCTGCGTCTCCTC	antisense	NsiI				
ASH3KO-c (P3)	GTGACACCTGCAAGCCACAGCGG	antisense	-	Integration 5'	-	-	-
ASH3KO-c (P4)	CGTACGGGGTTGCCCGAGCGCTTG	sense	-	WT locus/recombinant locus	-	-	-
ASH3KO-c (P5)	CAATCGTATCTGTGCTTCCTCACC	antisense	-	WT locus	-	-	-
ASH4-KI-s	TACTTCCAATCCAATTTAATGCGGGAAGCCGTCAGAGCAGGGAGTGTATG	sense	KpnI	C-term epitope tagging of endogenous gene	ASH4-3Ty-KI-HX	NcoI	ASH4-3Ty
ASH4-KI-a	TCCTCCACTTCCAATTTTAGCAACTGCAGTTCTGACGAGACGCGCCGTGGAACTGAGG	antisense	PstI				
ASH4-KO-s	TACTTCCAATCCAATTTAATGCTCACCATCATCTTCAGTCACGGAAATG	sense	KpnI	Endogenous gene truncation	ASH4-3Ty-KO-HX	SnaBI	-
ASH4-KO-a	TCCTCCACTTCCAATTTTAGCAAATGCATTGTGCCCATATCCTGGAAAGATCAAACG	antisense	NsiI				
ASH4KO-c (P1)	TACTTCCAATCCAATTTAATGCTCACCATCATCTTCAGTCACGGAAATG	sense	KpnI	control	-	-	-
ASH4KO-c (P2)	TCCTCCACTTCCAATTTTAGCAAATGCATTGTGCCCATATCCTGGAAAGATCAAACG	antisense	NsiI				
ASH4KO-c (P3)	GTGACACCTGCAAGCCACAGCGG	antisense	-	Integration 5'	-	-	-
ASH4KO-c (P4)	GGATCCATGGGGAACGCTCTGAAGCGGATG	sense	BamHI	WT locus/recombinant locus	-	-	-
ASH4KO-c (P5)	GCGGCCGCTCATCTGACGAGACGCGCCG	antisense	NotI	WT locus	-	-	-
E. coli							
rASH1-His-s	GGATCCATGGCGTCTCTCCAGCCAGGCGACGGCTA	sense	BamHI	producing recombinant ASH1 with 8-His N-term tag	His-rASH1	-	-
rASH1-His-a	CTCGAGTCAGTTTGTTGTGAGGACGTTTTCGATGAATC	antisense	XhoI				

FIGURE S1 - A - Mass spectrometry spectra of identified inhibitor targets. Parasite lysates treated first with the inhibitors, then with FP-Rh probe were run on a gel next to active serine hydrolases purified using biotinylated FP (FP-biotin). Bands were cut at appropriate positions for inhibitor targets (as identified by the disappearance of a band in the lysate lanes compared to the RH control) and analysed by mass spectrometry

A

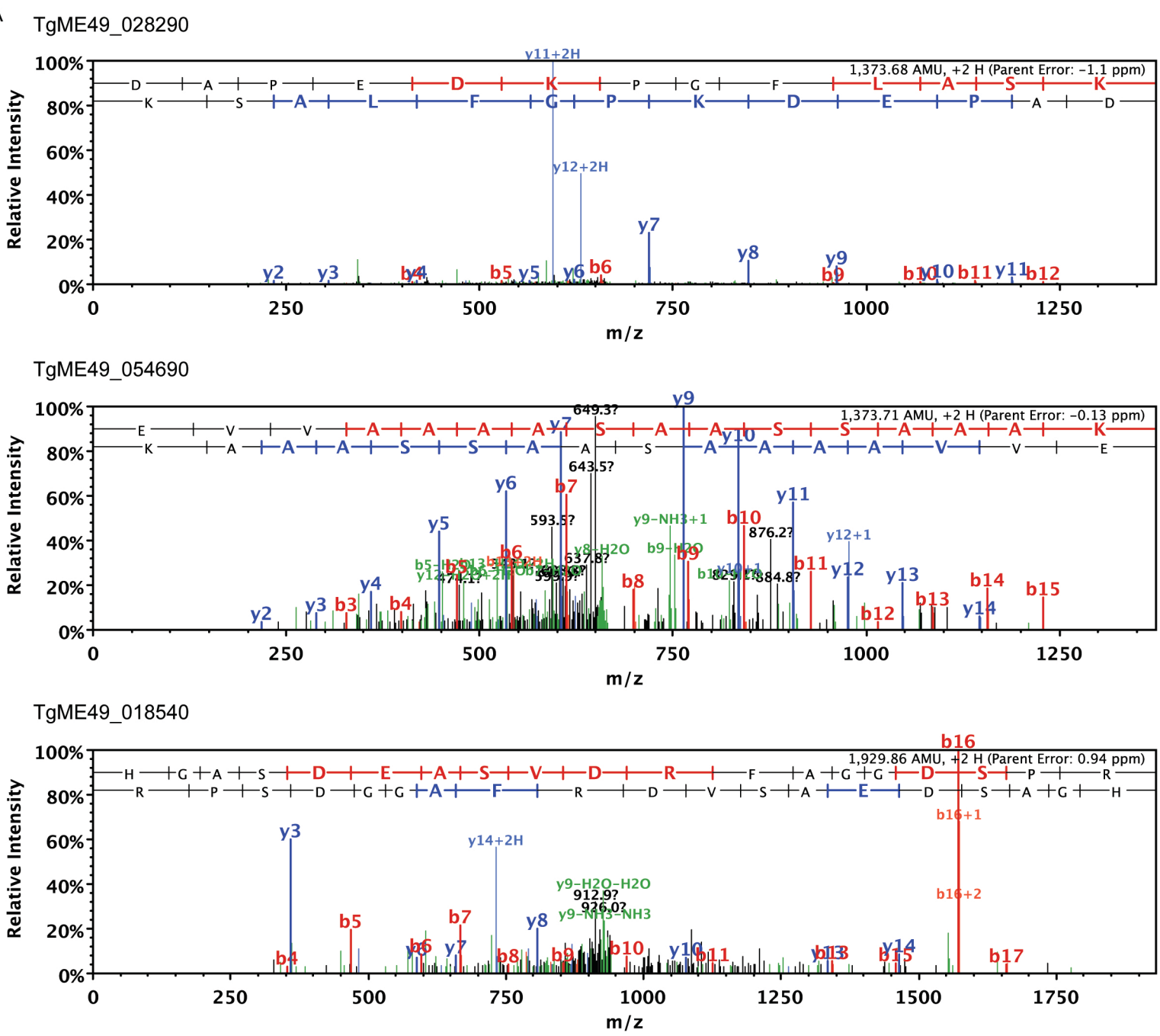

Figure S2- A- Alignment of APT1 homologues and alternative candidates across multiple species. B- Alignment of human APT1 with related coccidian proteins using ClustalOmega (EMBL-EBI). For the identity of the genes and organisms, see legend for Fig. 4.