

Supplementary Information

TgDrpC, an atypical dynamin-related protein in *Toxoplasma gondii*, is associated with vesicular transport factors and parasite division

Running Title: Characterization of TgDrpC

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Figure S1. DrpC protein expression levels in presence and absence of Shld1. A) Immunoblot staining for TgDrpC-HA-DD protein in the presence and absence of 200 nM Shld1 at 36, 42 and 48 hours. Anti-SAG1 antibody used as loading control. B) Protein quantitation by densitometry analysis of three biological replicates of TgDrpC-HA-DD parasites growth with or without Shld1 (n=3). Densitometry values were normalized to SAG1 and the ratio DrpC –Shld1/DrpC +Shld1 was calculated.

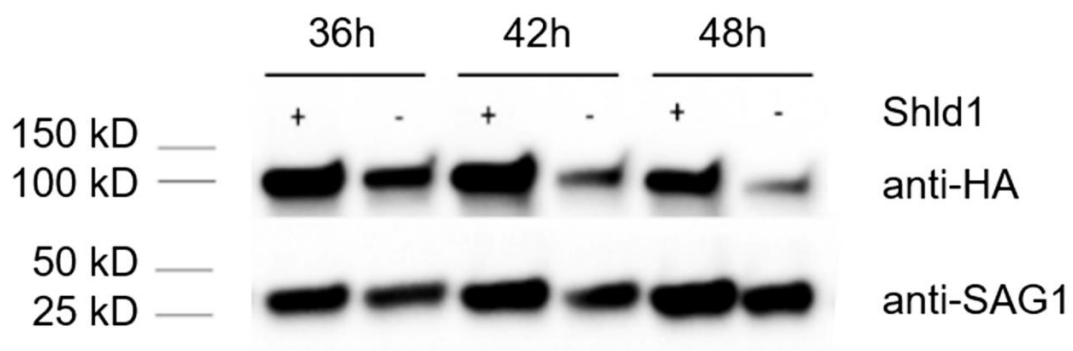
Figure S2. Immunoblot of interactor tagged strains. A) Immunoblot of parasite extract of strains expressing TgDrpC-HA, or both TgDrpC-HA and TGGT1_272600-myc, was probed with anti-myc antibodies. B) Immunoblot of parasite extract of strains expressing TgDrpC-HA, or both TgDrpC-HA and TGGT1_262150-myc, was probed with anti-myc antibodies.

Table S1. Data with number of peptides detected for all experimental (HA 1, HA 2, HA 3) and control (IgG 1, IgG 2, IgG3) immunoprecipitations from DrpC-HA expressing parasites. Also included are the number of peptides detected in immunoprecipitation from non-HA expressing control parasites using HA conjugated beads (Parental HA) or IgG control (Parental IgG). Column A shows the ID for the proteins detected, column B has the annotation based on ToxoDB.

Table S2. List of primers used in this study. *T. gondii* genomic sequence are shown in capital letters. Restriction enzymes are shown in italics.

Figure S1

A



B

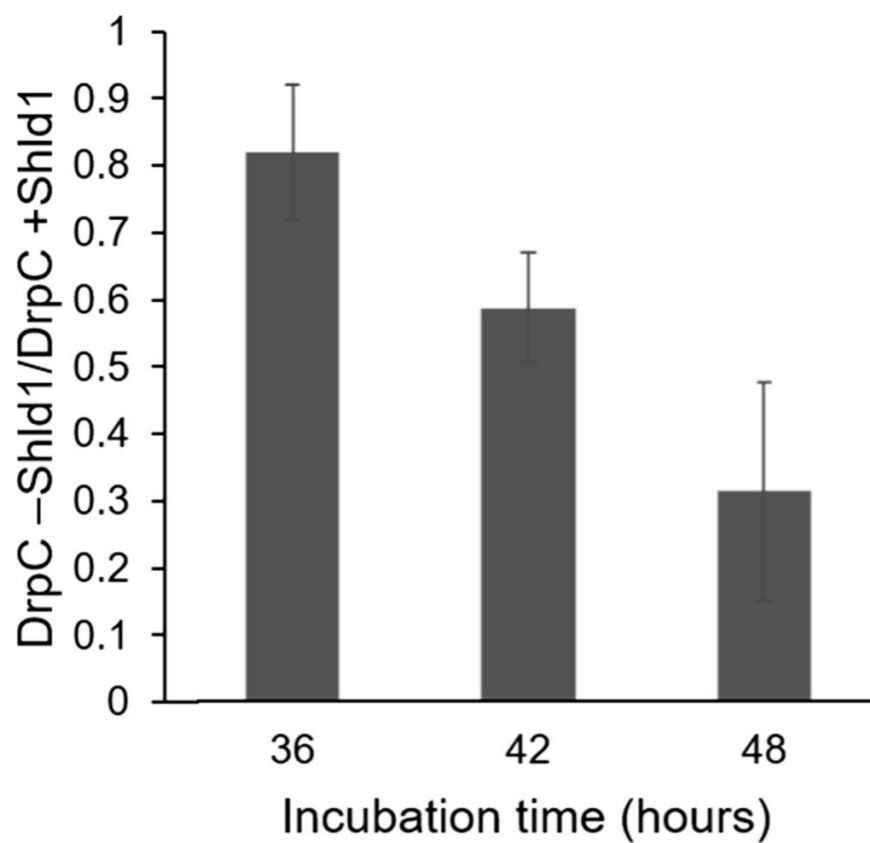
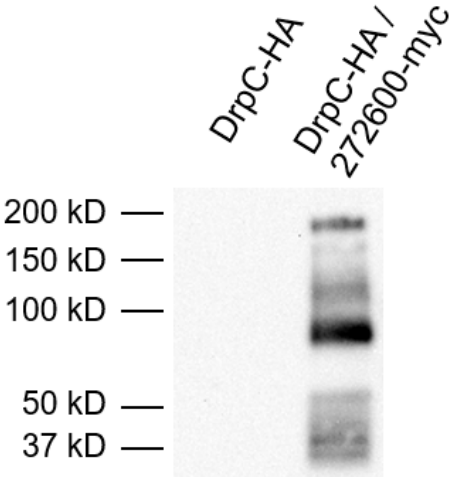


Figure S2

A



B

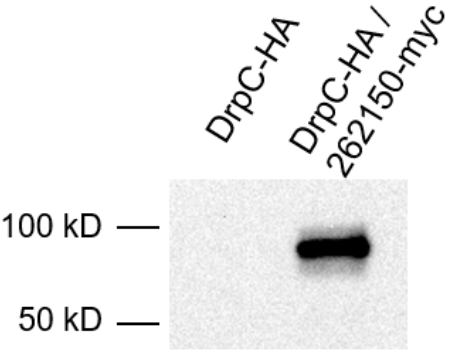


Table S1

Accession Number		SAINT Score (SP)	T-Test (p-value): (p < 0.05)	HA 1 Total Peptides	HA 2 Total Peptides	HA 3 Total Peptides	Total Peptides in Experimental IP	IgG1 Total Peptides	IgG2 Total Peptides	IgG3 Total Peptides	Parental HA IP Total Peptides	Parental IgG Total Peptides	Total Peptides in control IP
TGGT1_270690	DrpC	1	0,00024	146	191	195	532	0	1	2	0	0	3
TGGT1_294560	rhoptry kinase family protein ROP37 (incomplete catalytic triad)	1	0,0064	37	25	39	101	0	0	0	0	0	0
TGGT1_262150	kelch repeat and K+ channel tetramerisation domain containing protein	1	0,0031	19	31	24	74	0	0	0	0	0	0
TGGT1_227800	EF hand domain-containing protein	1	0,0008	19	25	23	67	0	0	0	0	0	0
TGGT1_227850	peptidyl-prolyl cis-trans isomerase, cyclophilin-type domain-containing protein	1	0,086	24	8	13	45	0	0	0	0	0	0
TGGT1_272600	adaptin c-terminal domain-containing protein	1	0,013	5	15	17	37	0	0	0	0	0	0
TGGT1_305940	peptidyl-prolyl cis-trans isomerase, cyclophilin-type domain-containing protein	1	0,0047	13	10	13	36	0	0	0	0	0	0
TGGT1_226240	putative bud site selection protein	1	0,001	10	11	11	32	0	0	0	0	0	0
TGGT1_257070	hypothetical protein	1	0,0053	4	7	5	16	0	0	0	0	0	0
TGGT1_239330	ribosomal protein RPL37	1	0,00039	4	5	5	14	0	0	0	0	0	0
TGGT1_312960	hypothetical protein	1	0,0095	3	6	4	13	0	0	0	0	0	0
TGGT1_261450	hypothetical protein	1	0,022	5	4	3	12	0	0	0	0	0	0
TGGT1_308890	transcription elongation factor SPT6	0,97	0,017	2	2	6	10	0	0	0	0	0	0
TGGT1_216435	hypothetical protein	0,98	0,032	4	2	3	9	0	0	0	0	0	0
TGGT1_221940	adaptin n terminal region domain-containing protein	0,7	0,023	2	3	5	10	0	0	0	0	0	0
TGGT1_313450	putative AP-2 complex subunit sigma-1	0,97	< 0,00010	2	2	3	7	0	0	0	0	0	0

Table S2

Set	Name	Sequence
A	DrpC_ <i>EcoRV</i> .F	5'- TTCCAATCCAATTTAATTAATGTCTGGCGCGGAGAAAC -3'
A	DrpC_ <i>EcoRV</i> .R	5'- CCACTTCCAATTTTAATTAAGCCCCATTCAACGGTGAC -3'
B	TGGT1_262150. <i>NcoI</i> .F	5'- ttcaatccaatttaattaaTCTTTTTCCTTTTCCTGCTCTGG -3'
B	TGGT1_262150. <i>NcoI</i> .R	5'- ccactccaattttaattaaCAAATTTGCCAAGAGAATGCCG -3'
C	TGGT1_272600. <i>NcoI</i> .F	5'- ttcaatccaatttaattaaCAACTGCCGGGCAGTCA -3'
C	TGGT1_272600. <i>NcoI</i> .R	5'- ccactccaattttaattaaGCTCGAAGAGAGCGGC -3'