Supplemental materials

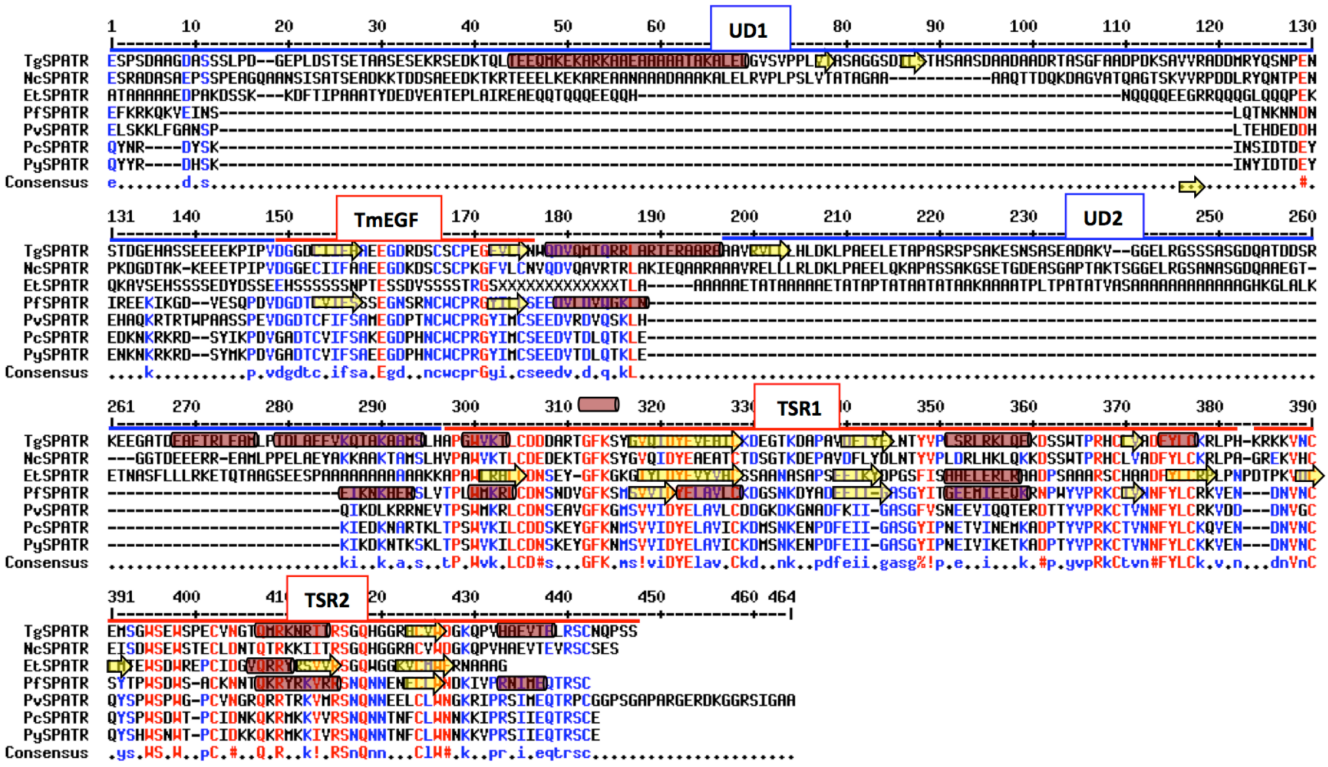

FIG. S1. Multiple sequence alignment of apicomplexan SPATRs. Sequences were obtained as indicated in Table S1. Alignment was created with multalin (http://multalin.toulouse.inra.fr/multalin/multalin.html) using sequences beginning at the determined (TgSPATR) or predicted (HhSPATR, NcSPATR) mature N-terminal sequence or immediately after the predicted (EtSPATR, PfSPATR, PvSPATR, PcSPATR, PySPATR) signal sequence cleavage site based on analysis by SignalP 4.1 (http://www.cbs.dtu.dk/services/SignalP/). Domain designations are indicated along with secondary structure elements shown as cylinders (helix) or arrows (sheets). Strands in TSR1 and TSR2 are labeled according to the corresponding structures in human thrombospondin (S1). Genus and species abbreviations are: Tg, *Toxoplasma gondii*; Hh, *Hammondia hammondi*; Nc, *Neospora caninum*; Et, *Eimeria tenella*; Pf, *Plasmodium falciparum*; Pv, *Plasmodium vivax*; Pc, *Plasmodium chabaudi*; Py, *Plasmodium yoelii*.

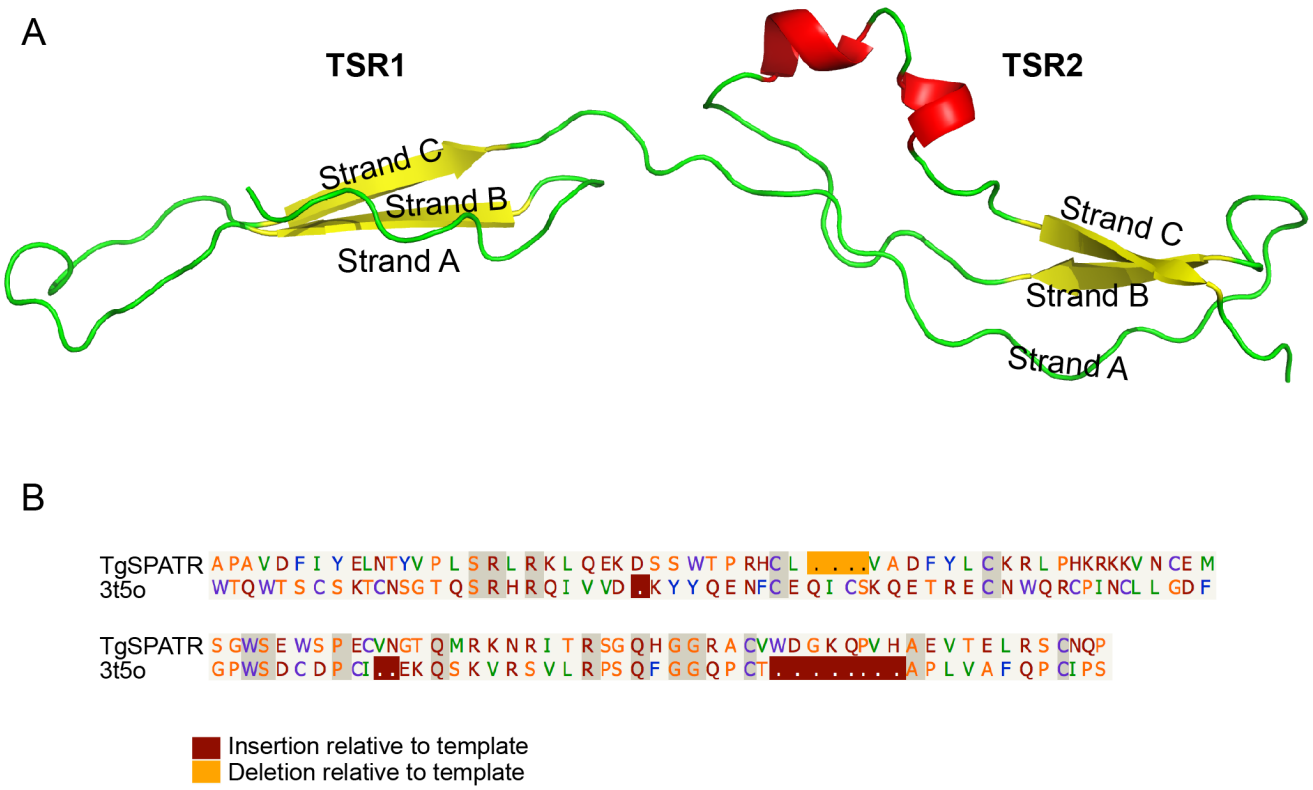

FIG. S2. Structural modeling of the TgSPATR thrombospondin type 1 repeats. (A) Shown is the top scoring model (99.6% confidence) from Phyre2 analysis of TgSPATR aa 385-534 encompassing TSR1 and TSR2. The model is based on protein database template 3t5o, human complement component C6. The modeling software was able to model the TgSPATR sequence beginning at residue 423. Strands in TSR1 and TSR2 are labeled according to the corresponding structures in human thrompospondin (S1). **(B)** Phyre2 sequence alignment of the TgSPATR TSR repeats and the template sequence of human complement component C6 (3t5o). The aligned sequences share 17% identity.

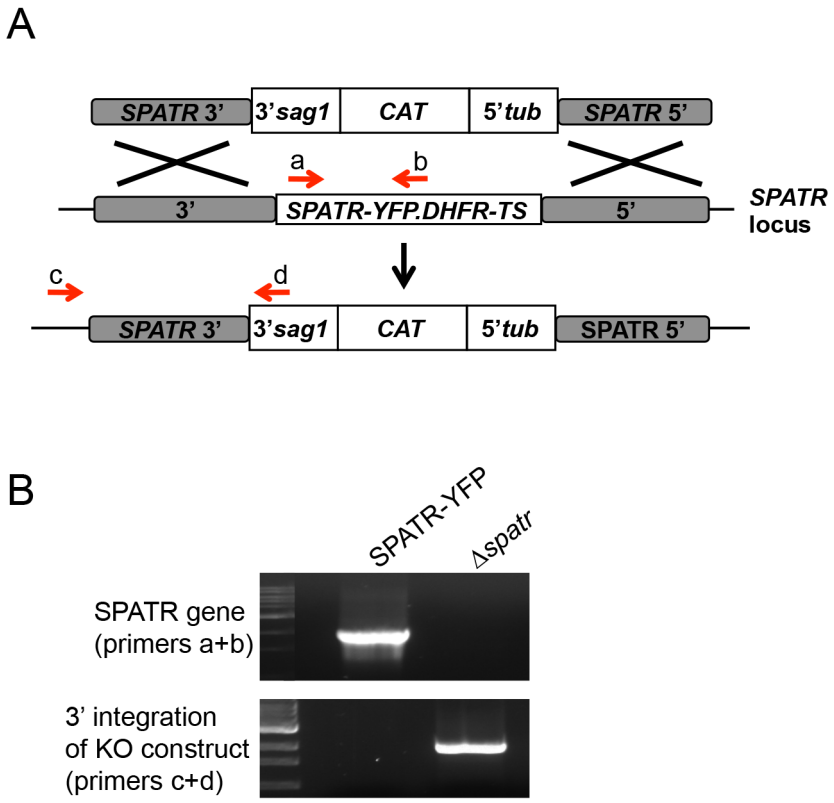

FIG. S3. **Targeted deletion of *SPATR*. (A)** Schematic illustration of the *spatr-yfp* locus and replacement by the chloramphenicol acetyl transferase selectable marker. **(B)** PCR confirming the absence of the *spatr* gene and integration of the knockout construct at the 3' end. Primer positions for the PCR reactions are indicated in A.

Table S1. Primers used in the study.

Primer name	Sequence[1]
TgSPATR.629358.F	CAAGGGACTCTGAATCTACGCCTACCAGTC
5'Tub.TgSPATR.5'.632256.R	ATGCATATCAAGCTTATCGATACCGCGGAAATTTGGAAGAGATACAAAAGAGACG
3'Sag1.TgSPATR.3'.638674.F	GTCGAACCGGTTAACACAATTCTTGCCAGTAGTGAGGGAAAGAGAGAAGAGCCCC
TgSPATR.640219.R	GTTCGGTGCTCCTCTCAGTGTTTTCATTTG
TgSPATR.3'.638674.3'Sag1.R	GGGGCTCTTCTCTCTTTCCCTCACTACTGGCAAGAATTGTGTTAACCGGTTCGAC
TgSPATR.5'.632256.5'Tub.F	CGTCTCTTTTGTATCTCTTCCAAATTTCCGCGGTATCGATAAGCTTGATATGCAT
TgSPATR.1605myc.PacI.R	GATCTTAATTAATTACAAATCTTCTTCAGAAATCAACTTTTGTTCAGACGAAGGCTGATTGCA
TgSPATR.1.NsiI.F	GATCATGCATATGGAGGTTTCAAGAAGTCACC
TgSPATR.35.F	GCTCTTCACCACACTCTTCATCT
TgSPATR.1185.R	GTCGTCACACAAAGTTTTTACCC
TgSPATR.629641.F	CATTGCTCAGAACACATATTAAACGGTACC
PfSPATR.NsiI.1.F	GATCATGCATGCCAAAATGAAGAA
PfSPATR.PacI.R	GATCTTAATTAATTACAAATCTTC

[1]Sequences are shown 5' to 3'.