**Supplementary information**

Table S1. Information about the *T. gondii* strains used in this study.

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| **Common name** | **Strain Genotype** | **Strain Description** |
| CEP | CEPΔhxgprt::Luciferase::GFP | Parental type III CEP *T.gondii* strain used for mutant construction, expresses GFP and Luciferace. |
| CEP+EV | CEPΔhxgprt::Luciferase::GFP | The CEP transfection control strain where pGRA-HA-HPT empty vector (EV) was transfected. |
| CEP+*Tg*ROP18I-HA | CEPΔhxgprt::Luciferase::GFP/*Tg*ROP18I-HA::HXGPRT | The CEP strain with insertion of HA-tagged wild type *Tg*ROP18I and HXGPRT drug selection marker. |
| CEP+*Tg*ROP18II-HA | CEPΔhxgprt::Luciferase::GFP/*Tg*ROP18II-HA::HXGPRT | The CEP strain with insertion of HA-tagged wild type *Tg*ROP18II and HXGPRT drug selection marker. |
| CEP+*Tg*ROP18-domain swap 1-HA | CEPΔhxgprt::Luciferase::GFP/*Tg*ROP18II N-terminus-*Tg*ROP18I kinase domain-HA::HXGPRT | The CEP strain with insertion of *Tg*ROP18II N-terminus-*Tg*ROP18I kinase domain-HA chimera and HXGPRT drug selection marker. |
| CEP+*Tg*ROP18-domain swap 2-HA | CEPΔhxgprt::Luciferase::GFP/*Tg*ROP18I N-terminus-*Tg*ROP18II kinase domain-HA::HXGPRT | The CEP strain with insertion of *Tg*ROP18I N-terminus-*Tg*ROP18II kinase domain-HA chimera and HXGPRT drug selection marker. |
| CEP+*Tg*ROP18I-KD-HA | CEPΔhxgprt::Luciferase::GFP/*Tg*ROP18I-D394A-HA::HXGPRT | The CEP strain with insertion of HA-tagged *Tg*ROP18I-D394A chimera and HXGPRT drug selection marker. |



Figure S1. Gel electrophoresis of the unsonicated and sonicated chromatin samples.

1: unsonicated chromatin from HFFs; 2: sonicated chromatin from HFFs; 3: unsonicated chromatin from HFFs stimulated with 500U/ml IFN-γ; 4: sonicated chromatin from HFFs stimulated with 500U/ml IFN-γ; 5: unsonicated chromatin from HFFs infected with CEP+EV; 6: unsonicated chromatin from HFFs infected with CEP+EV; 7: unsonicated chromatin from HFFs infected with CEP+*Tg*ROP18I; 8: sonicated chromatin from HFFs infected with CEP+*Tg*ROP18I; 9: unsonicated chromatin from HFFs infected with CEP+*Tg*ROP18II; 10: sonicated chromatin from HFFs infected with CEP+*Tg*ROP18II; M: GeneRuler 1kb Plus DNA Ladder (ThermoFisher Scientific). The sheared DNA fragment size of 100-1000bp (lanes 2, 4, 6, 8, and 10) indicate good quality of the input samples for immunoprecipitation.

Figure S2. *Tg*ROP18I is not sufficient to inhibit IFNγ-induced increases in IRF1 transcript and protein abundance. (A) HEK293T cells were transfected with the indicated plasmid or not and stimulated 24 h later with IFN-γ for 24h. IRF1 mRNA was quantified by qRT-PCR, normalized to β-Actin. UT, untransfected HEK293T cells. (B) HFFs were infected with the indicated strains at an MOI of 0.5, or left uninfected, for 18h, and subsequently stimulated, or not, with IFN-γ for 24h. Double immunofluorescence was performed with rabbit monoclonal anti-IRF1 (red). UI/US, uninfected and unstimulated HFFs (scale bar=10μm). (C) Normalized fluorescence intensity of nuclear IRF1 in infected HFFs, determined by immunofluorescence assay using ImageJ software. Mean ± SD indicates the fluorescence intensity of nuclear IRF1 in infected HFFs normalized to the fluorescence intensity of nuclear IRF1 in the neighboring uninfected cells, combined from a minimum of 5 and a maximum of 10 fields of view. (D) HEK293T cells were transfected with the indicated plasmid or not, for 24h, and subsequently stimulated with IFN-γ for 24h. Double immunofluorescence was performed with mouse monoclonal anti-FLAG (green) and rabbit monoclonal anti-IRF1 (red). UT/US, untransfected and unstimulated HEK293T cells (scale bar=10μm). (E) Normalized fluorescence intensity of nuclear IRF1 in transfected HEK293T cells, determined by immunofluorescence assay using ImageJ software. Mean ± SD indicates the fluorescence intensity of nuclear IRF1 in transfected cells normalized to the fluorescence intensity of nuclear IRF1 in the neighboring untransfected cells, combined from a minimum of 10 and a maximum of 18 fields of view. Experiments were repeated twice.



Figure S3. HEK293T cells were transfected with the indicated plasmid or not, for 24h, and subsequently stimulated with IFN-γ for 24h. IFP35 mRNA were assessed by qRT-PCR, normalized to β-Actin. UT, untransfected HEK293T cells. \*\*\*, one-way ANOVA followed by Dunnett’s Post-hoc test; p<0.001, compared to the IFN-γ group.



Figure S4. (A) Alignment of kinase domain region of *Tg*ROP18. (B) Maximum Likelihood tree of 11 *T. gondii* ROP18 alleles downloaded from [www.toxodb.org](http://www.toxodb.org). Bootstrap values are shown for each node based on 1000 permutations. Clades are color-coded to indicate type I, II and III-like alleles (red, green and blue, respectively). (C) Fisher’s Exact Test P-values for pairwise neutral evolution estimates as implemented in MEGA (version 6.0). Highlighted cells indicate comparisons with p<0.05.