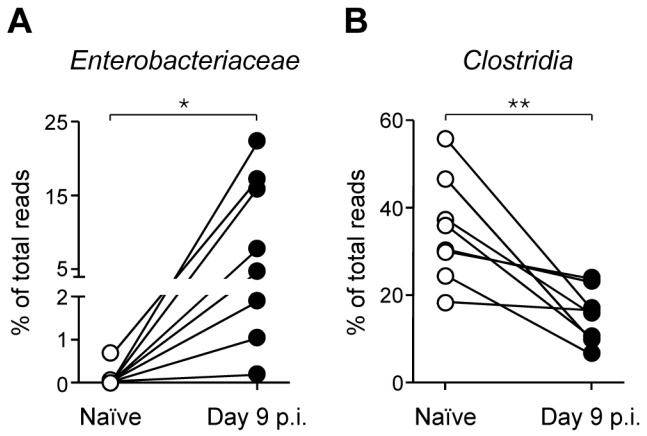



**Figure S1 (related to Figure 1). Statistical analysis of the genomic alterations observed between naïve and *T. gondii*-infected mice**. The 454 genomic analysis of fecal samples from naïve and acute *T. gondii* infected mice were found to have statistically significant increases in the proportion of *E. coli* (**A**) and reductions in Clostridia species (**B**). Each dot pair represents single mouse analyzed at the indicated time points (*$P<0.05$, **$P<0.01$). All data shown are representative of two independent experiments with similar results.

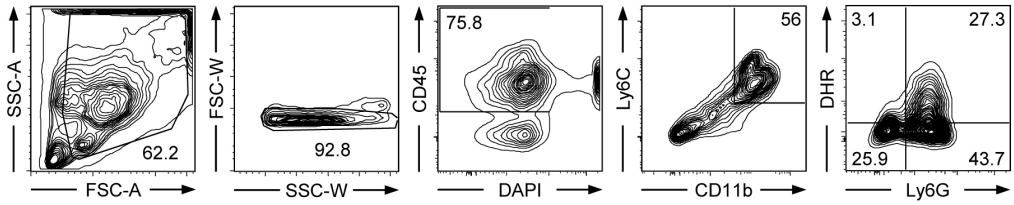



**Figure S2 (related to Figure 3). Gating strategy used to analyze the leukocytes from the lumen of *T. gondii*-infected mice by flow cytometry.**

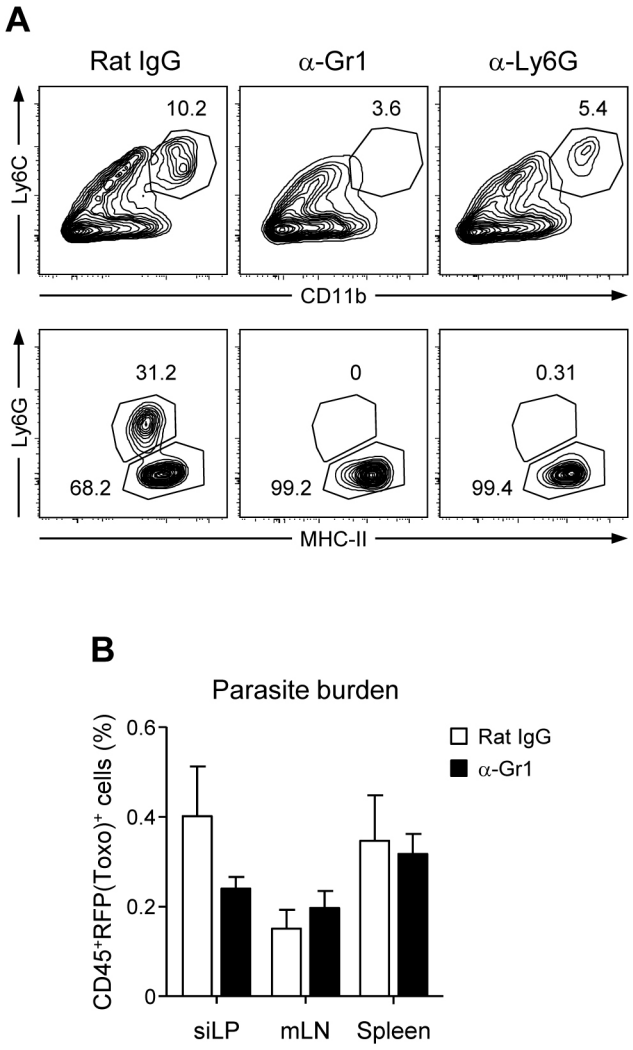



**Figure S3 (related to Figure 4). Depletion of neutrophils and inflammatory monocytes by α-Gr1 and α-Ly6G and effects on parasite burden.** (**A**) The percentage of inflammatory monocytes and neutrophils were determined in mice treated with either α-Gr1 or α-Ly6G. (**B**) The parasite burden of rat IgG and α-Gr1 treated *T. gondii*-infected mice was determined at day 9 p.i. by analyzing the percentage of infected $CD45^+$ cells. All data shown are representative of two independent experiments with similar results. Each bar represents the mean ± SEM of three to four mice analyzed. All data shown are representative of two independent experiments with similar results.

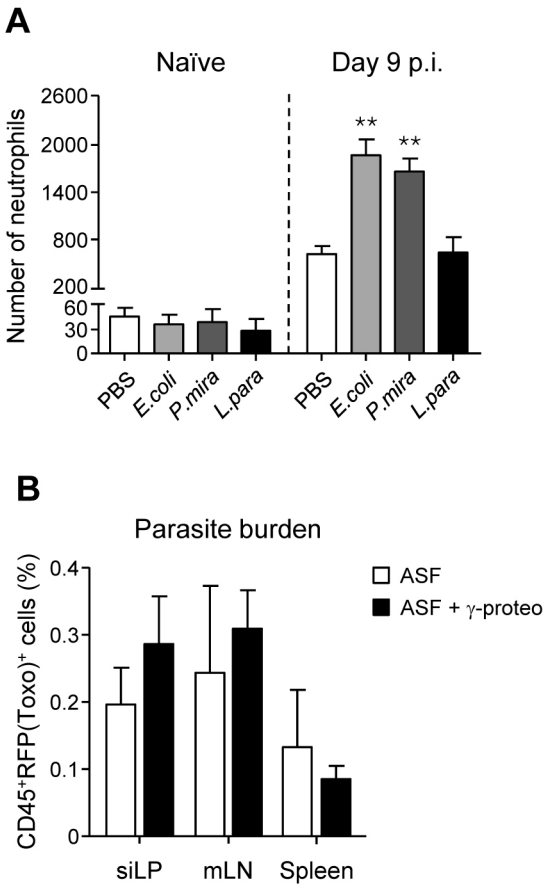
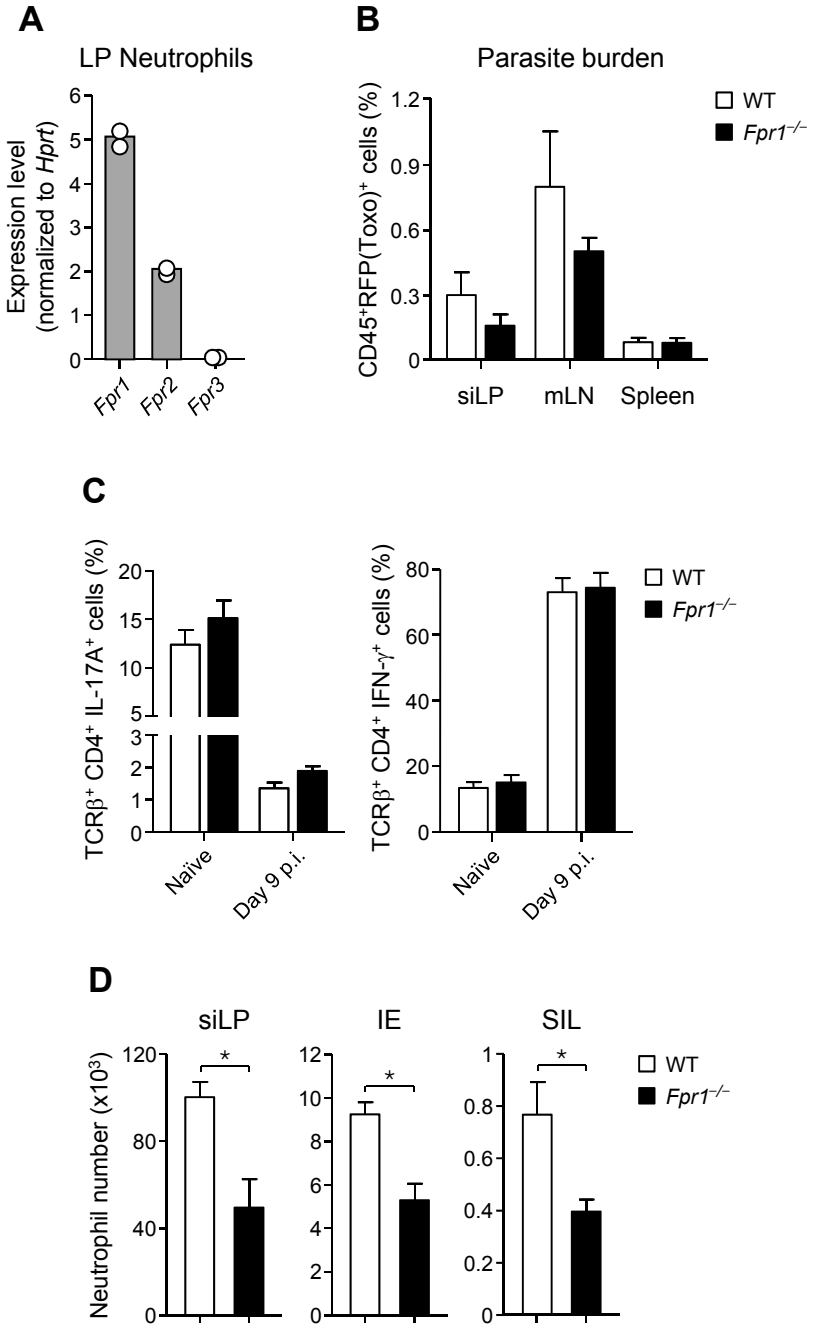



**Figure S4 (related to Figure 5). Gavage of γ-proteobacteria results in increased luminal recruitment of neutrophils into *T. gondii* infected mice but not in naïve mice. (**A**)** Mice were infected with 15 *T. gondii* cysts and gavaged at day 6 p.i. with either *E. coli*, *P. mirabilis* or *L. paracasei*. Bar graphs show the number (mean ± SEM) of luminal neutrophils isolated at day 9 p.i. (***P<0.01*). (**B**) The parasite burden of mice colonized with ASF or ASF + γ-proteobacteria was determined at day 9 p.i. by analyzing the percentage of infected CD45+ cells. Each bar represents the mean ± SEM of three to four mice analyzed. Data shown are representative of a single experiment.




Molloy et *al.* Figure S5

**Figure S5 (related to Figure 6). Analysis of WT and *Fpr1*$^{-/-}$ mice for alterations in immune function at steady state and during *T. gondii* infection. (A)** Small intestine *lamina propria* neutrophils express high levels of *Fpr1*. Neutrophils were FACS purified from the small intestine *lamina propria* of mice on day 8 after oral infection with 15 *T. gondii* cysts. Cells were resuspended in TRIzol and mRNA isolated. *Fpr1*, *Fpr2* and *Fpr3* expression levels were then analyzed by RT-PCR. Circles represent the relative expression for each sample after normalization to the housekeeping gene *Hprt* and bars the mean relative expression. (**B**) Parasite burden from WT and *Fpr1*$^{-/-}$ mice infected with *T. gondii* for 9 days. (**C**) Naïve and *T. gondii*-infected WT and *Fpr1*$^{-/-}$ mice were analyzed for differences in TCR$\beta^{+}$CD4$^{+}$ producing IFN-$\gamma$ and IL-17A. (**D**) Total neutrophils in the siLP, IE and lumen (SIL) of WT and *Fpr1*$^{-/-}$ mice on day 11 p.i. Each bar represents the mean $\pm$ SEM of three to four mice analyzed (*$P<0.05$). All data shown are representative of two independent experiments with similar results.

**Table S1: Bacterial 16S rRNA gene primers used in this study.**

| 16S rRNA gene | Forward Primer | Reverse Primer |
|---|---|---|
| Eubacteria (Universal) | ACTCCTACGGGAGGCAGCAGT | ATTACCGCGGCTGCTGGC |
| Enterobacteriacae | GTGCCAGCMGCCGCGGTAA | GCCTCAAGGGCACAACCTCCAAG |
| *Escherichia coli* | CATGCCGCGTGTATGAAGAA | CGGGTAACGTCAATGAGCAAA |
| Bacteroides | GGTTCTGAGAGGAGGTCCC | GCTGCCTCCCGTAGGAGT |
| *Eubacterium rectale/Clostridium coccoides* group (EREC) | ACTCCTACGGGAGGCAGC | GCTTCTTAGTCAGGTACCGTCAT |
| Segmented Filamentous Bacteria (SFB) | GACGCTGAGGCATGAGAGCAT | GACGGCACGGATTGTTATTCA |
| *Lactobacillus/Lactococcus* group | AGCAGTAGGGAATCTTCCA | CACCGCTACACATGGAC |