

Figure S1. Similar composition and abundance of fecal bacterial species in ampicillin treated mice regardless of *C. albicans* intestinal colonization, Related to Figure 1

(A) Percent total reads for the most abundant bacterial species in the feces for each group of mice after drinking water ampicillin supplementation (12 days) with or without oral *C. albicans* inoculation (2 days after initiating ampicillin drinking water supplementation).

(B) Linear discriminant analysis comparing differential abundance of top 10 bacterial species with the most differences between specific pathogen-free control versus ampicillin treated (green), specific pathogen-free control versus *C. albicans* colonized (red), and ampicillin treated compared with *C. albicans* colonized (blue).



Figure S2. Protection against *C. albicans* invasive infection does not reflect enhanced immunogenicity of recombinant *C. albicans*, Related to Figure 2

Recoverable CFUs from the kidneys five days after intravenous infection (5 x 10^4 CFUs recombinant *C. albicans*) for mice colonized with either recombinant *C. albicans* (2W1S-*Candida*), non-recombinant parental WT *C. albicans* (strain SC5314), or no colonization control mice maintained on ampicillin supplemented drinking water.

****p<0.0001; n.s., not significant; Bar, mean ± SEM. L.o.D., limit of detection.



Figure S3. Systemic expansion of CD4⁺ T cells with surrogate *C. albicans* commensal specificity, Related to Figure 3

Total number of I-A^b:2W1S tetramer positive CD4⁺ T cells from spleen plus peripheral lymph nodes compared with the mesenteric lymph node of mice colonized with recombinant *C. albicans* compared with no colonization control mice.



Figure S4. Sustained expansion of *C. albicans* specific RORγt⁺ CD4⁺ T cells with antigen-restimulation after intravenous *C. albicans* challenge, Related to Figure 3

(A) Number and percent ROR γ t⁺ among I-A^b:2W1S positive CD4⁺ T cells amongst splenocyte and peripheral lymph node cells five days after intravenous infection (5 x 10⁴ CFUs recombinant *C. albicans*) for mice colonized with recombinant *C. albicans* or no colonization control mice.

(B) Total number and percent ROR γ t⁺ among I-A^b:2W1S positive CD4⁺ T cells recovered from the kidney for the mice described in (A).

**p*<0.05, ** *p*<0.01, Bar, mean ± SEM.





(A) Representative plots and composite data showing percent Tbet⁺ and FOXP3⁺ among CD4⁺ T cells with I-A^b:2W1S specificity (solid line) or compared with bulk CD4⁺ T cells (gray shaded) for cells from the spleen and peripheral lymph nodes 10 days after intestinal colonization with 2W1S-expressing recombinant *C. albicans* compared with no colonization controls. (B) Number of CD4⁺ T cells producing each cytokine after stimulation with non-recombinant heat killed *C. albicans* amongst spleen and peripheral lymph node cells for the mice described in (A). **p<0.01; n.s., not significant; Bar, mean ± SEM.



Figure S6. Fluconazole eradicates C. albicans intestinal colonization, Related to Figure 5

(A) Recoverable *C. albicans* from the feces of mice each day after initiating fluconazole to the ampicillin supplemented drinking water.

(B) Recoverable *C. albicans* 5 days after *C. albicans* intravenous infection (5 x 10^4 CFUs) at each time point after discontinuation of fluconazole, compared with mice with sustained fluconazole drinking water supplementation or no fluconazole treatment controls. Bar, mean ± SEM; L.o.D., limit of detection.



Figure S7. *C. albicans* fecal colonization absolute density in humans positively correlates with systemic levels of fungal-specific Th17 inflammation, Related to Figure 7 (A) Regression analysis comparing IL-17A or IL-17F production by CD4⁺ peripheral blood cells of after heat-killed *C. albicans* stimulation compared with the fecal absolute abundance of *C. albicans* or non-albicans *Candida spp.* for each individual determined by shotgun sequencing. (B) Regression analysis comparing intensity of IL-17RC staining by CD15⁺CD16⁺ neutrophils amongst peripheral blood cells compared with the fecal absolute abundance of *C. albicans* or non-albicans *Candida spp.* for each individual determined by shotgun sequencing. Levels below the limits of detection are shown as open circles on the y-axis.