

Fig. S12. Specificity of *Mucispirillum*-induced intestinal inflammation in doubly deficient *Nod2/Cybb* mice. (A) The presence of *Mucispirillum* in fecal samples from SPF DKO, *Cybb*^{-/-}, *Nod2*^{-/-} and WT mice gavaged with *Mucispirillum* was quantified before bacterial administration (day 0) and 7 days after infection (day 7) and normalized to the universal 16S rRNA gene. Fecal DNA from Tac-DKO mice was included as positive control. Mean ± SEM of at least 4 mice; data

are pooled from four independent experiments. *P<0.05; ****P<0.0001; N.S. not significant by Kruskal-Wallis test followed by Dunn's post-test. (B) Fecal Lcn-2 concentration was measured before (day 0), on day 7 after oral infection with either *Mucispirillum* (n=4) or *B. uniformis* (n=4) in Jax-DKO mice. Bars show mean. One-way ANOVA followed by Tukey's multiple comparisons test (*P<0.05; N.S. not significant). (C) Colon length was measured in Mucispirillum-infected DKO (n=4) and in B. uniformis-infected DKO mice (n=4) on day 7 post infection. Bars show mean. Two-tailed Unpaired t-test (**P=0.0044). (**D**) Representative histology of H&E-stained sections from large intestines of Mucispirillum-infected and B. uniformis-infected DKO mice (on day 7 post infection). Arrows show inflammatory cell infiltrate. Scale bar, 500 µm. (E) Histopathological scores of cecal and colonic tissues from Mucispirilluminfected (n=4) and B. uniformis-infected DKO mice (n=4) (on day 7 post infection). Bars show median. *P=0.0286 by Two-tailed Mann Whitney test. (F) The presence of B. uniformis was quantified in fecal samples from B. uniformis-infected DKO mice before bacterial administration (day 0) and 7 days after infection (day 7) and normalized to the universal 16S rRNA gene. Data are mean ± SEM of 4 mice. *P=0.0133 by Two-tailed Unpaired t-test. (B to F) Pooled data from two independent experiments.