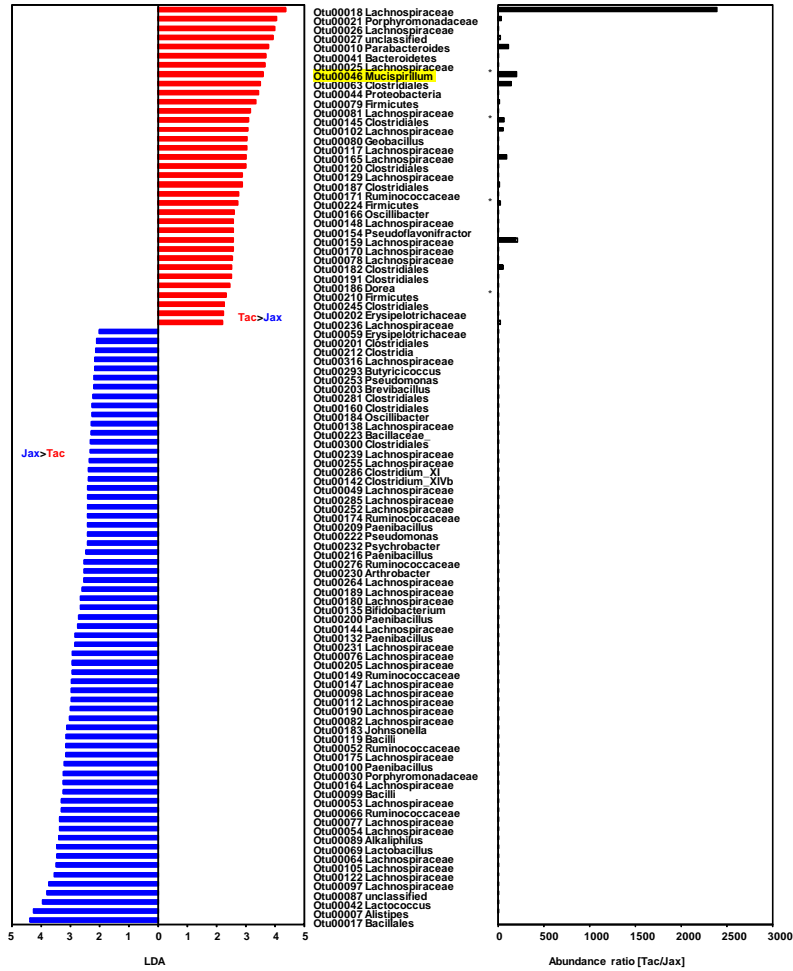
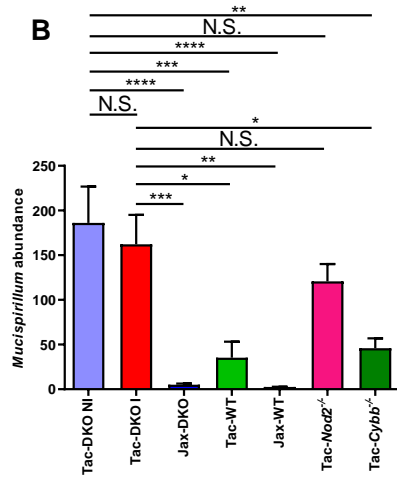


A

Tac-DKO-NI vs Jax-DKO



B



C

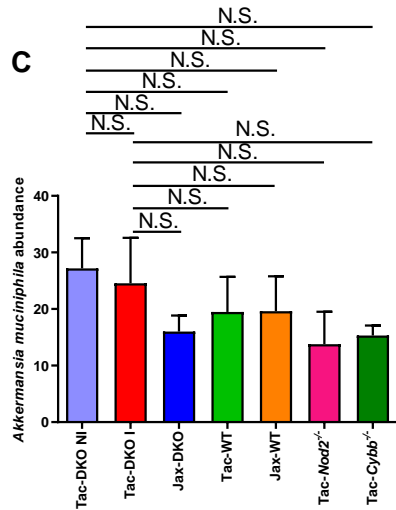


Fig. S6. Analysis of the gut microbiota in Tac- and Jax-fostered doubly deficient *Nod2/Cybb* mice and quantification of mucus-dwelling bacteria in fostered mice. (A) LEfSe analysis shows bacterial OTUs that were differentially abundant between age-matched Tac-DKO mice prior the development of intestinal inflammation (Tac-DKO NI, n=12) and Jax-DKO animals (n=10). The LDA score and the abundance ratio are shown. OTU that belongs to *Mucispirillum* is highlighted in yellow. Asterisks indicate bacteria under detection (zero read) in 16S rRNA gene Illumina MiSeq analysis in denominator groups. Two independent experiments (B and C) The presence of *Mucispirillum* (B) and *Akkermansia muciniphila* (C) was quantified in colonic mucus scrapings harvested from 4-6 week old fostered mice and normalized to the universal 16S rRNA gene. Mean \pm SEM of at least 6 individual mice. Data are pooled from three independent experiments. *P<0.05; **P<0.01; ***P<0.001; ****P<0.0001; N.S. not significant by Kruskal-Wallis test followed by Dunn's multiple comparisons test.