## **Supporting Information**

## Bel et al. 10.1073/pnas.1319114111

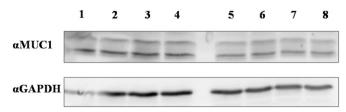


Fig. S1. Levels of Mucin 1 in colon of WT mice and mice lacking Tata Element Modulatory Factor (TMF<sup>-/-</sup>) mice colon. Western blot analysis of whole colon tissue from WT (lanes 1–4) and knockout (KO; lanes 5–8) mice. Samples were stained with anti-MUC1 antibody, as indicated, and with anti-GAPDH to ensure equal loading. Each lane represents a sample from a different mouse.

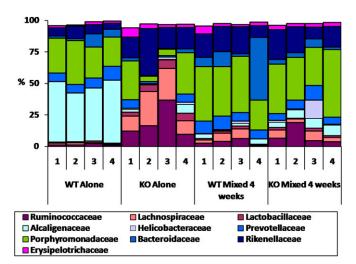


Fig. S2. Effects of cohousing on WT and  $TMF^{-/-}$  mice microbiota. KO and WT mice were either housed alone or cohoused for 4 wk. Fecal samples were then collected, and microbiota composition was analyzed via 16S rRNA analysis. Taxon-based analysis at familial level among the different groups. Data are shown as percent relative abundance. Families with >1% abundance are shown. Each bar represents one mouse. Each color represents one phylum or family, as indicated at the bottom of the histograms.

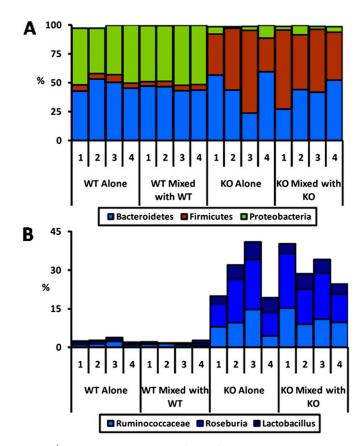


Fig. S3. Effects of cohousing on WT and TMF<sup>-/-</sup> mice microbiota. WT mice from different cages were cohoused in one cage, and TMF<sup>-/-</sup> (KO) mice from different cages were cohoused in another cage for a period of 4 wk before collecting fecal samples. Microbiota composition was determined via 16S rRNA analysis. (A) Taxon-based analysis at phylum level among the different groups. Data are shown as percent relative abundance. Phyla with >1% abundance are shown. Each bar represents one mouse. Each color represents one phylum or family, as indicated at the bottom of the histograms. (B) Relative abundance of an uncultured member of the Ruminococcaceae, Roseburia and Lactobacillus genus among the different groups. Each bar represents one mouse. Color index is shown at the bottom.

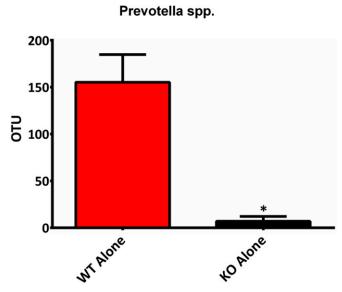


Fig. S4. Reduced colonization of TMF $^{-/-}$  mice by mucus degrading bacteria *Prevotella spp*. KO and WT mice were housed alone for 4 wk. Fecal samples were then collected and microbiota composition was determined via 16S rRNA analysis. Average number of *Prevotella spp*. Operational taxonomy units detected in fecal samples from WT and TMF $^{-/-}$  mice are shown ( $\pm$ SE). \* $^{+}$ P < 0.05 (Student  $^{+}$ t test;  $^{-}$ n = 5).