



Fig. S10. *Mucispirillum*-specific colonization and Ig production in $J_H^{-/-}$, $IgA^{-/-}$ and $FcRn^{-/-}$ mice. (A) Schematic representation of the experimental design for co-housing and fostering experiments. (B to D) The presence of *Mucispirillum* was quantified in fecal samples collected from Jax $J_H^{-/-}$, $IgA^{-/-}$ and $FcRn^{-/-}$ mice before (Jax $J_H^{-/-}$, $IgA^{-/-}$ and $FcRn^{-/-}$) and after 4-week co-housing with Tac mice (Tac $J_H^{-/-}$, $IgA^{-/-}$ and $FcRn^{-/-}$) by qPCR. Results were normalized to the universal 16S rRNA gene. Data are mean \pm SEM of at least 4 mice. Data are pooled from two independent experiments. * $P=0.0457$ (B); * $P=0.0304$ (C); * $P=0.0471$ (D) by Paired t-test. (E and

F) ELISA of *Mucispirillum*-specific and total IgA (E) and IgG (F) in the luminal content of Tac-co-housed $J_H^{-/-}$, $IgA^{-/-}$ and $FcRn^{-/-}$ mice. Fecal samples were collected after at least 4 weeks of co-housing. Results are mean \pm SEM of at least 8 individual mice. Data are pooled from two independent experiments. * $P < 0.05$; *** $P < 0.001$; **** $P < 0.0001$; N.S. not significant by Kruskal-Wallis test followed by Dunn's post-test.