



**Extended Data Figure 5 | Effect of tungstate on the naive gut microbiome.** Groups of C57BL/6 mice naturally harbouring Enterobacteriaceae were treated with 0.2% sodium tungstate, DSS, DSS plus tungstate or mock treatment for nine days (see also Extended Data Fig. 3b). **a**, Relative abundance of genes involved in formate and nitrate utilization in the caecal content shown by shotgun metagenomic sequencing (MEGAN5). Each section of the pie chart is representative of the number of mapped reads obtained for the individual animals ( $n = 6$

per group). **b**, Box-and-whisker plot (boxes show median, first and third quantiles, whisker denotes minimum to maximum range) of Chao1 alpha diversity of the caecal microbiota community based on 16S profiling ( $n = 6$  per group). **c**, Abundance of endogenous Enterobacteriaceae family members determined by plating on selective medium (MacConkey agar, **c**): mock,  $n = 14$ ; W,  $n = 6$ ; DSS,  $n = 19$ ; DSS+W,  $n = 19$ . Data are shown as geometric mean and geometric s.d.