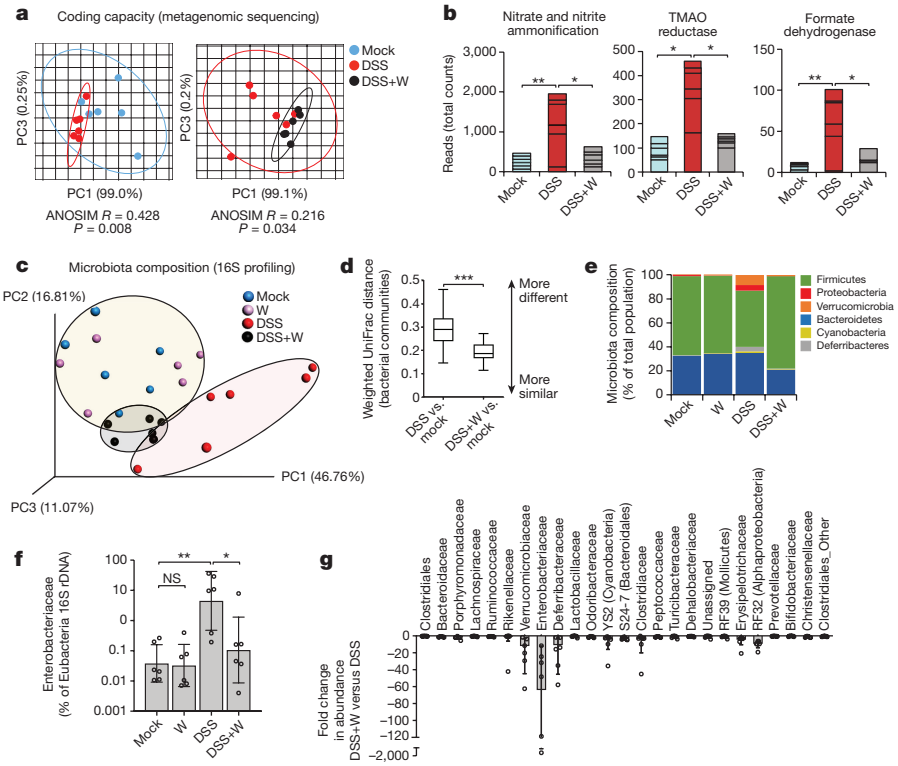

Figure 2 | Effect of tungstate treatment on composition of gut bacterial community and metabolic landscape. DNA extracted from the caecal contents of C57BL/6 mice ($n = 6$ per group) receiving the indicated treatments was analysed by metagenomic sequencing and 16S profiling. **a**, Principal coordinates analysis (PCoA) plots and analysis of similarity (ANOSIM) of the predicted coding capacity. Ellipses in **a** denote 95% confidence intervals. **b**, Tallied metagenomic reads mapped to anaerobic respiration and formate utilization pathways. **c**, PCoA of the microbiota composition (weighted UniFrac distances). **d**, Box-and-whisker plot (boxes show median, first and third quatiles, whisker denotes minimum to maximum range) of intercommunity β-diversity determined by weighted 16S UniFrac distances. **e**, Phylum-level microbiota composition. **f**, Abundance of Enterobacteriaceae quantified by qPCR. **g**, Changes in the population size of the 25 most abundant operational taxonomic units as the result of tungstate administration in the DSS-induced-colitis model. Unless otherwise noted, data are shown as geometric mean and geometric s.d.

tungsten-mediated manipulation of the gut microbiota could ameliorate gut inflammation. Alternatively, one could hypothesize that tungstate exerted anti-inflammatory effects directly on the host immune system. To test the latter hypothesis, we treated groups of germ-free C57BL/6 mice with DSS and tungstate or DSS alone for nine days and analysed the intestinal inflammatory responses. Treatment of germ-free mice with DSS resulted in moderate inflammation compared to germ-free control mice. Concomitant administration of tungstate did not

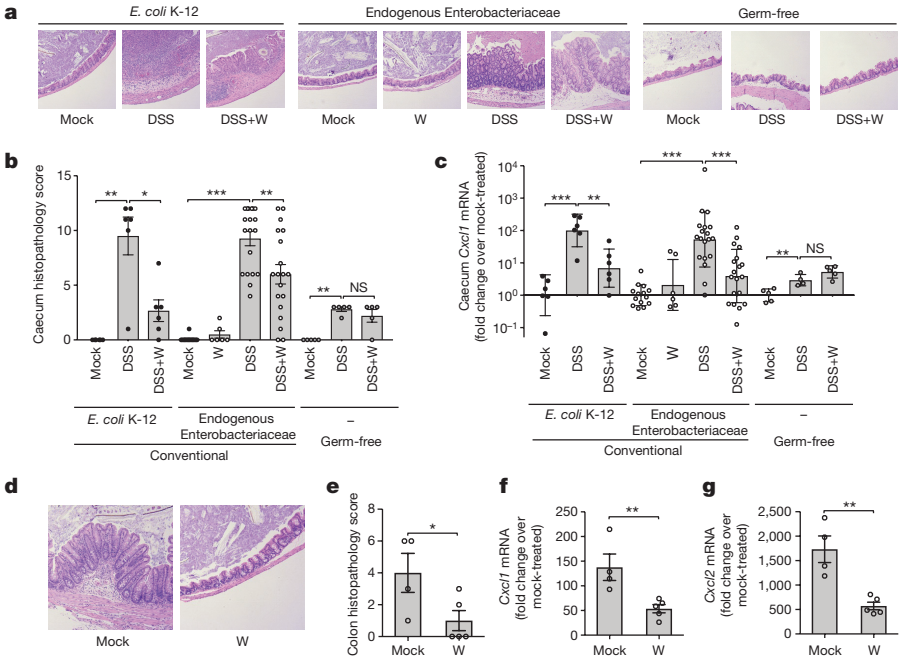

Figure 3 | Influence of tungstate treatment on mucosal inflammation. **a**–**c**, Conventionally raised C57BL/6 mice, treated with DSS or DSS and tungstate for four days, were inoculated with *E. coli* K-12 and samples were analysed after five days. C57BL/6 mice with a naive microbiota (including endogenous Enterobacteriaceae) or germ-free C57BL/6 mice were treated similarly with tungstate, DSS or DSS plus tungstate. *E. coli* K-12: $n = 6$ for all groups. Endogenous Enterobacteriaceae: mock, $n = 14$; W, $n = 6$; DSS, $n = 19$; DSS+W, $n = 19$. Germ-free: $n = 5$ for all groups (except in **c**; DSS, $n = 4$). **a**, Representative images of haematoxylin and eosin-stained caecal sections. **b**, Cumulative histopathology score for the caecum; data are shown as mean and s.e.m., and each dot represents one animal. **c**, Transcription of *Cxcl1* (also known as *KC*) in the caecal mucosa, determined by RT−qPCR. **d**–**g** Groups of *Il10*$^{-/-}$ mice were inoculated orally with *E. coli* NC101. Animals received piroxicam-fortified diet or piroxicam-fortified diet plus tungstate in drinking water for two weeks; mock, $n = 4$; W, $n = 5$. **d**, Representative images of haematoxylin and eosin-stained colonic sections. **e**, Cumulative histopathology score for the colon; data are shown as mean and s.e.m., and each dot represents one animal. **f**, **g**, Abundance of *Cxcl1* (**f**) and *Cxcl2* (**g**) mRNA in the colonic mucosa, determined by RT−qPCR. Unless otherwise noted, data are shown as geometric mean and geometric s.d.