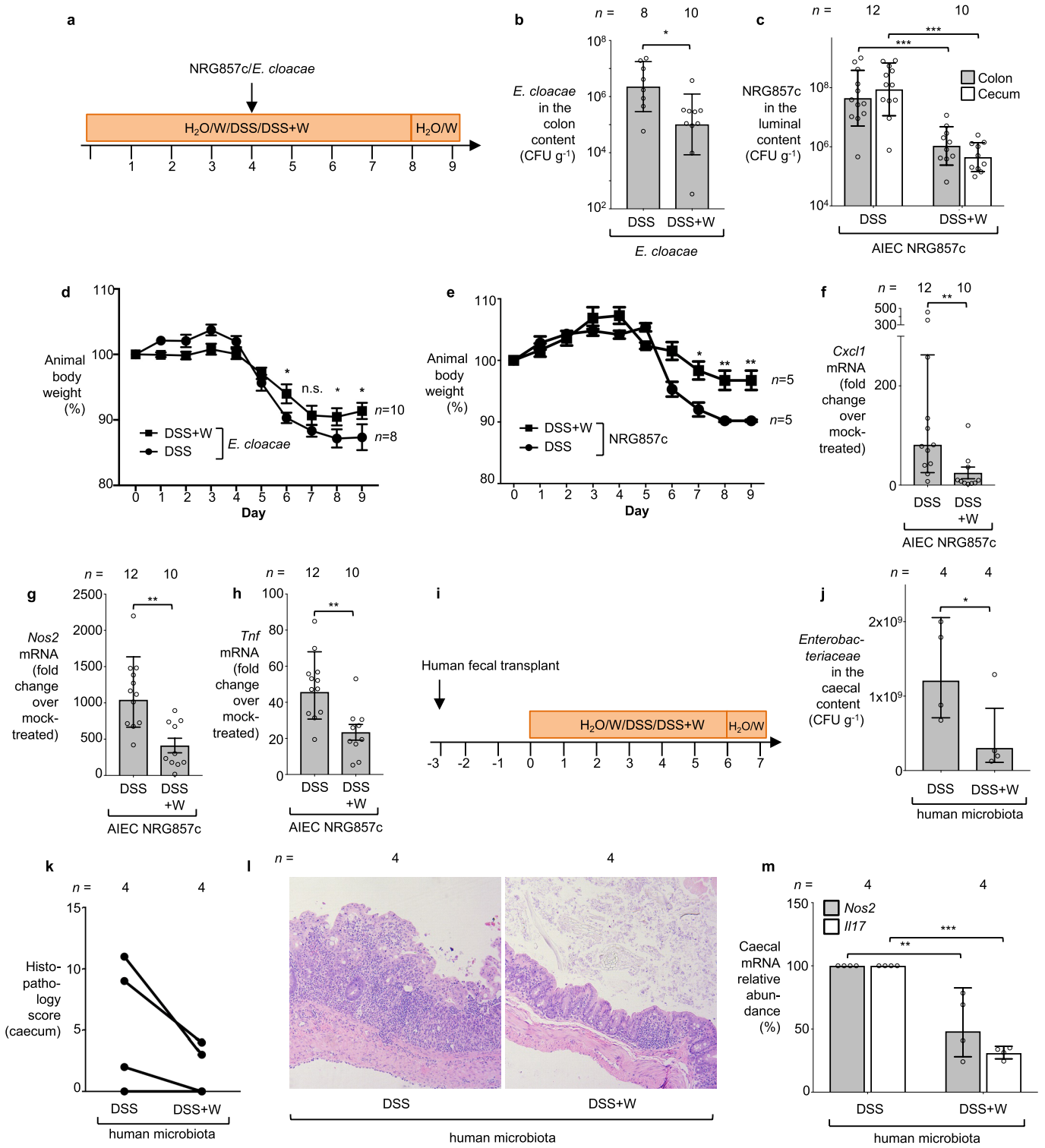

Extended Data Figure 4 | Effect of tungstate treatment on mice experimentally colonized with *Enterobacter cloacae* and adherent invasive *E. coli*. **a**–**h**, Conventionally raised C57BL/6 mice were treated with DSS or DSS plus tungstate. After four days, animals were inoculated intragastrically with the indicated bacterial strains. Samples were collected five days after inoculation. **a**, Schematic representation of the experiments. **b**, **c**, The total population of *E. cloacae* (**b**) and NRG857c (**c**; DSS, $n = 12$; DSS+W, $n = 10$) in the large intestinal content was determined by plating on selective medium. **d**, **e**, Animal body weight. In **b** and **d**: DSS, $n = 8$; DSS+W, $n = 10$. In **e**, $n = 5$ per group. **f**–**h**, Transcription levels of the inflammatory marker genes *Cxcl1* (**f**), *Nos2* (**g**) and *Tnf* (**h**) in the caecal mucosa were determined by RT–qPCR; DSS, $n = 12$; DSS+W, $n = 10$. **i**–**m**, Paired germ-free Swiss–Webster mice received human faecal transplants and were treated with DSS or DSS plus 0.2% sodium tungstate for seven days; DSS, $n = 4$; DSS+W, $n = 4$. **i**, Schematic representation of the experiments. **j**, The abundance of Enterobacteriaceae in the caecal content was determined by plating on selective medium (MacConkey agar). **k**, Formalin-fixed, haematoxylin and eosin-stained sections of the mouse caecum were scored for the presence of inflammatory lesions; **l**, representative images. **m**, Transcription levels of the inflammatory marker genes *Nos2* and *Il17* in the mouse caecal mucosa. Data are shown as geometric mean and geometric s.d.