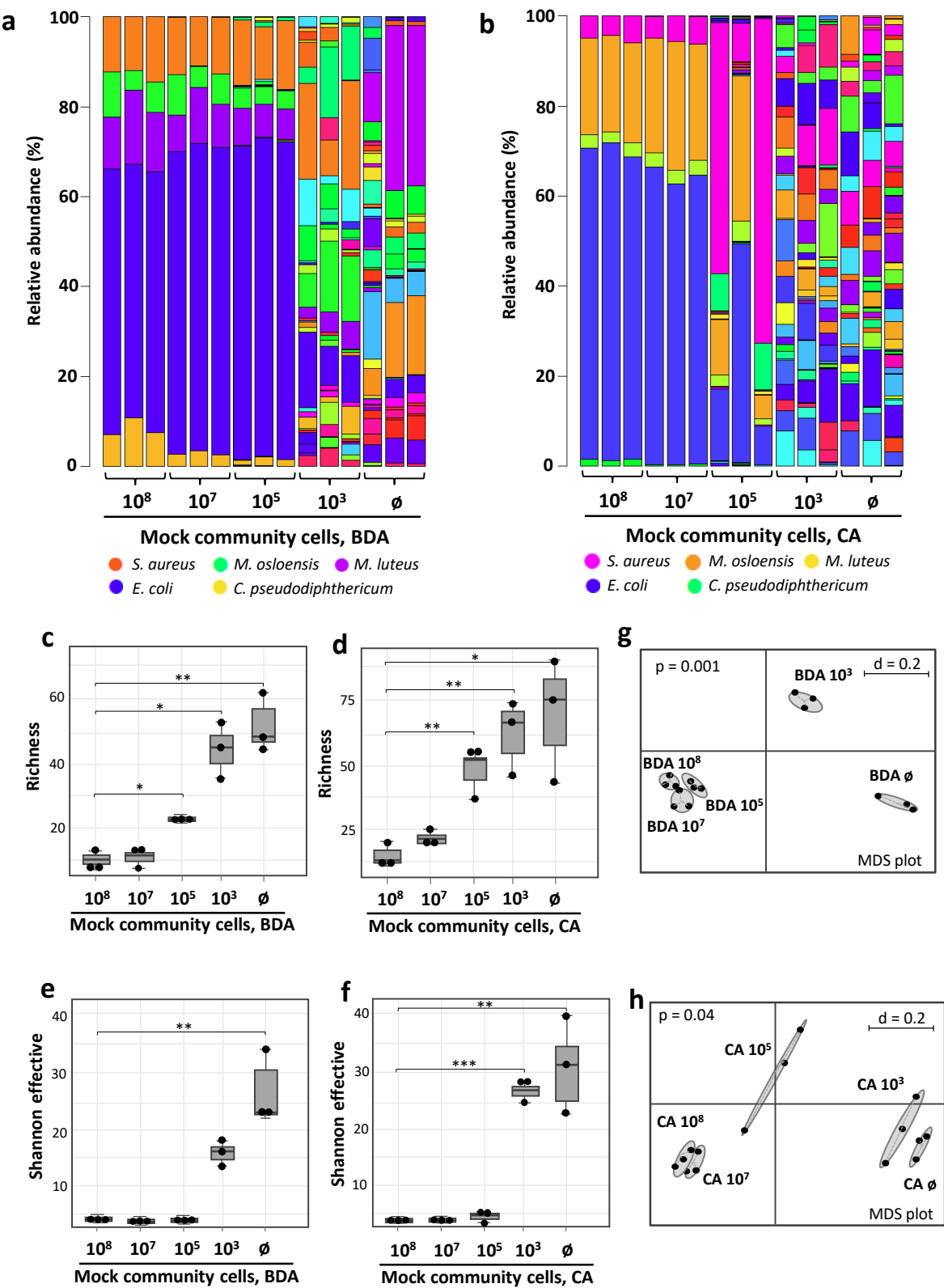


Supplementary Figure 4



The benzonase approach generates less diversity bias compared to CA in low bacterial DNA input samples. The mock community of living bacteria (10^8 CFU/sample) was diluted to 10^7 , 10^5 and 10^3 CFU/sample and then DNA extracted by the CA or the BDA. Taxonomic binning of bacterial taxa in samples processed by **a)** BDA or **b)** CA. **c, d)** Richness **e, f)** Shannon effective and **g, h)** β -diversity analysis of the mock community after dilution and extraction using BDA or CA. BDA (Benzonase digest approach), CA (conventional approach). * p $\leq$ 0.05, ** p $\leq$ 0.01, *** p $\leq$ 0.001.