

## Supplementary Figures

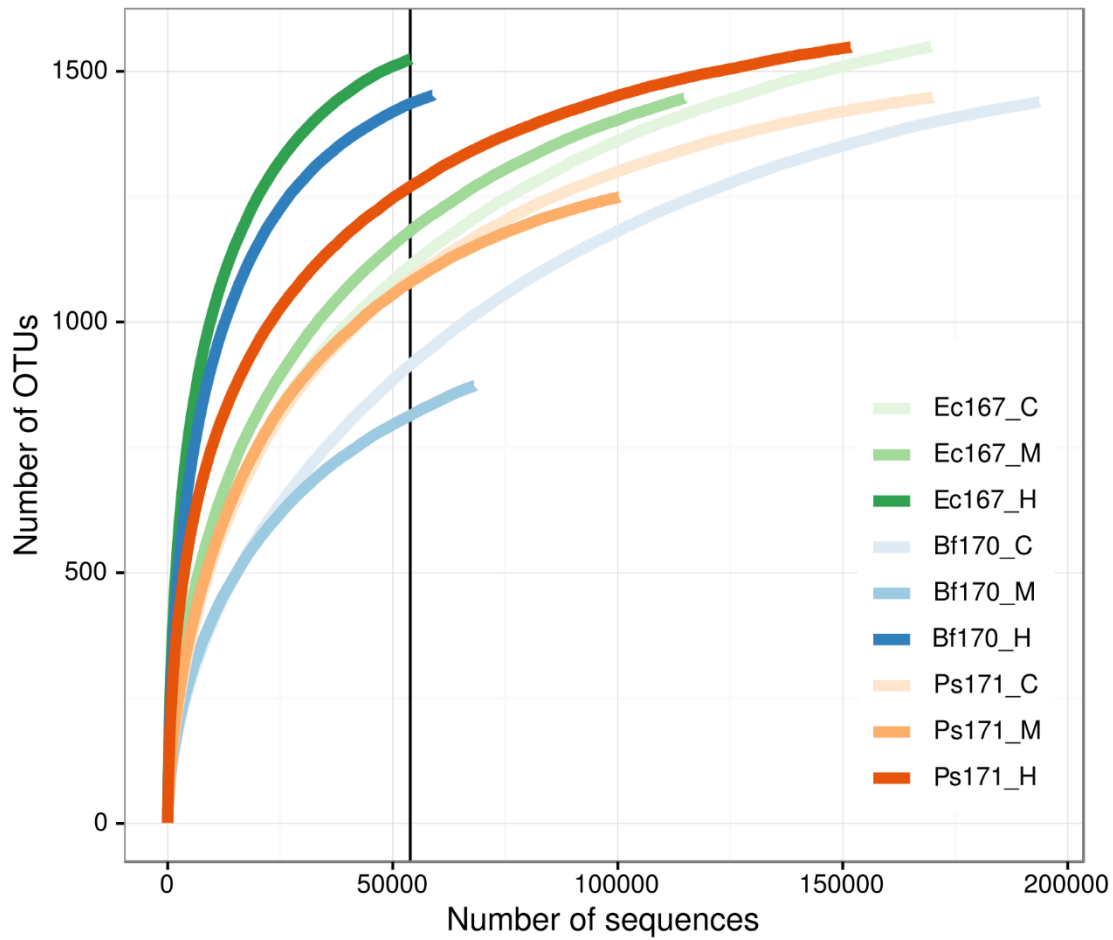


Figure S1 | Species richness as function of sequence depth for the nine gut samples. Each curve represents the number of identified OTUs (97% sequence similarity) as a function of the number of sequenced reads after quality filtering. The vertical line indicates the minimum number of reads to which all samples were subsampled.