## Supplementary Material

Effect of bacterial DNA enrichment on detection and quantification of bacteria in an infected tissue model by metagenomic next-generation sequencing

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Supplementary Figure 1. Taxonomic profiles generated using a metagenomic pipeline. Porcine sequences were removed by CLARK and BWA to generate the input data set. The relative abundances of sequence reads were determined by Kraken 2 using a k-mer database generated from bacterial, archaeal, fungal, protozoan, viral and phage genomic sequences. No correction for genome size was performed. M, direct microscopic examination; C, CFU (colony forming unit); Gro, glycerol; mNGS, metagenomic next-generation sequencing.

