

Table S3. Putative contaminant sequences identified via *decontam* from canine urine samples

Organism	P
<i>Escherichia-Shigella</i>	.17
<i>Ruminococcus gnavus group</i>	.06
<i>Paracoccus.1</i>	.18
<i>Anaerobacillus</i>	.19
<i>Paracoccus.2</i>	.17
<i>Cutibacterium</i>	.14
<i>Burkholderia-Caballeronia-Paraburkholderia</i>	.08
<i>Rhodobacteraceae.1</i>	.04

P is a composite score statistic that is assigned to each amplicon sequence variant (ASV). Using a threshold of 0.5 and the prevalence method, features are classified as contaminants if present in a higher fraction of negative controls than in biological samples [38]. Each ASV classified as a contaminant was removed from the dataset.