

Table S1. Amplicon sequence variants classified as a contaminant via *decontam* in canine urine samples

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

P refers to a composite score statistic, which is assigned to each feature and classifies taxa as contaminants based on a predetermined threshold value. For the prevalence method with a threshold of $P = .5$, features are classified as contaminants if identified in a higher fraction of negative controls than in samples [35]. Each amplicon sequence variant identified as a putative contaminant was removed from the dataset prior to downstream analysis.