

D_2__Alphaproteobacteria; D_5__Rickettsia -	38.6	1
D_2__Actinobacteria; D_5__Corynebacterium 1 -	12.9	35.9
D_2__Bacteroidia; D_5__Porphyromonas -	3.5	14.4
D_2__Gammaproteobacteria; D_5__Escherichia-Shigella -	7	0
D_2__Clostridia; D_5__Anaerococcus -	2	11.1
D_2__Actinobacteria; D_5__Arthrobacter -	3.6	0.3
D_2__Actinobacteria; D_4__Corynebacteriaceae -	2.9	2.7
D_2__Actinobacteria; D_5__Trueperella -	1.5	3.7
D_2__Gammaproteobacteria; D_5__Coxiella -	2.2	0.9
D_2__Bacilli; D_5__Lactobacillus -	2	0.4
D_2__Clostridia; D_5__Helcococcus -	0.9	4.7
D_2__Gammaproteobacteria; D_5__Acinetobacter -	1.7	1.1
D_2__Clostridia; D_5__Peptoniphilus -	0.8	1.5
D_2__Clostridia; D_5__uncultured -	0.7	1.4
D_2__Actinobacteria; D_5__Pseudarthrobacter -	0.9	0.1
D_2__Gammaproteobacteria; D_5__Enhydrobacter -	0.8	0.3
D_2__Actinobacteria; D_5__Corynebacterium -	0.7	0.5
D_2__Actinobacteria; D_5__Brachybacterium -	0.6	0.4
D_2__Actinobacteria; D_5__Propionibacterium -	0.6	0.5
D_2__Actinobacteria; D_5__Knoellia -	0.6	0.2
	Amblyomma -	Hyalomma -

Figure S1. Comparative heatmap showing percentage grouped abundance of bacterial community at genus level