

Table S1 – Weight of cockroach gut sections with and without parasitic nematodes (La, *Leidynema appendiculatum*; Free, nematode-free; Hd, *Hammerschmidtella diesingi*; Tb, *Thelastoma bulhoesi*).

Host	Nematode	Gut section	Average (mg)	Standard dev.
<i>Periplaneta fuliginosa</i>	La	Foregut	18.93	17.00
		Midgut	12.33	0.80
		Hindgut	37.67	44.45
	Free	Foregut	13.17	5.86
		Midgut	32.47	21.97
		Hindgut	11.13	6.70
<i>Periplaneta americana</i>	Hd and Tb	Hindgut	16.07	6.26
	La		18.53	8.62
	Free		20.75	6.58

Table S2 – List of primers used in this study. Bold region highlighted in 16S V3–V4 region primers indicate the Illumina overhang adapter sequences.

Primers (5'-3')
<i>Leidynema appendiculatum</i> specific primer based in D2D3 region Forward GCTGGTTGCCAGGCTCTACTAC Reverse CCGCACCACCGCAGGCCAGCAT
<i>Hammerschmidtella diesingi</i> specific primer based in D2D3 region Forward TGGCTGGATGGCTGTACTACTG Reverse GCATCATCAGACGAGCCAACAC
<i>Thelastoma bulhoesi</i> specific primer based in D2D3 region Forward GTCATGTTGCTGACTGCTTCC Reverse GCACCACCAAACGGGCTAACGC
16S V3-V4 region Forward TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG CCTACGGGNGGCWGCAG Reverse GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG GACTACHVGGGTATCTAATCC

Table S3 – Characteristics of 16S rRNA gene amplicons from *Periplaneta fuliginosa* and *P. americana* with and without parasitic nematodes (La, *Leidynema appendiculatum*; Hd, *Hammerschmidtella diesingi*; Tb, *Thelastoma bulhoesi*)

Libraries	Accession	Gut Section	# Raw Pairs	% Trimmed Pairs	% Joined Pairs	% Cleaned Pairs	Mean Length	Pyrotags ¹
L1976	SRR3178367	Foregut	106,610	99.72	71.79	70.47	420	70819
L1977	SRR3180601	Midgut	114,524	99.70	67.72	66.75	421	73905
L1978	SRR3180617	Hindgut	113,967	99.67	68.89	65.83	416	67956
L1980	SRR3186995	Foregut	112,314	99.63	68.13	66.29	415	68331
L1981	SRR3186996	Midgut	110,814	99.61	68.07	66.44	418	69720
L1982	SRR3186998	Hindgut	109,556	99.57	69.03	65.06	411	65167
L1983	SRR3225595	Hindgut	111,834	99.61	63.97	60.28	406	56071
L1984	SRR3225596	Hindgut	115,686	99.67	69.74	66.07	414	59835
L1985	SRR3225597	Hindgut	113,802	99.64	68.86	64.80	413	69063

¹Number of pyrotags (sequences) per library after second quality-filtering

Table S4 – Genus abundance (%) for each library. The rarefaction level was 4528 sequences/library. The rarefaction level was 4,528 sequences in each library.

Kingdom	Phylum	Class	Order	Family	Genus	<i>Periplaneta fuliginosa</i>										
						<i>Leidynea appendiculatum</i>		<i>Free-nematode</i>								
						L1976	L1977	L1978	L1980	L1981	L1982					
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	Methanosarcinaceae	Methanoniemicrococcus	0.00	0.00	0.07	0.00	0.00	0.00					
			Acidimicrobia	Acidimicrobiales	Other	0.00	0.00	0.02	0.20	0.00	0.00					
			Other	0.00	0.00	0.00	0.15	0.00	0.00							
			Actinobacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	4.37%	15.75%	0.75%	1.50%	1.46%	0.71%		
							Celulomonadaceae	0.29%	0.20%	0.00%	0.02%	0.02%	0.00%			
							Corynebacteriaceae	Corynebacterium	1.46%	1.48%	0.09%	1.63%	0.04%	0.00%		
							Dermabacteraceae	Brachybacterium	1.17%	5.10%	0.22%	0.91%	0.07%	0.00%		
							Dietziaceae	0.00%	0.00%	0.00%	0.44%	0.27%	0.00%			
							Glycomycetaceae	Glycomyces	0.07%	0.29%	0.04%	0.46%	0.09%	0.00%		
							Gordoniaceae	Gordonia	3.16%	2.58%	0.29%	13.94%	1.46%	0.04%		
							Intrasporangiaceae	0.04%	0.11%	0.02%	0.09%	0.00%	0.00%			
							Microbacteriaceae	Aeromyces	0.09%	0.11%	0.04%	0.18%	0.09%	0.00%		
								Leucobacter	0.00%	0.02%	0.00%	0.38%	0.02%	0.04%		
								Microbacterium	0.04%	0.09%	0.00%	0.09%	0.02%	0.00%		
								Arthrobracter	0.04%	0.09%	0.00%	0.07%	0.00%	0.00%		
								Micrococcaceae	0.04%	0.09%	0.00%	0.29%	0.00%	0.00%		
								Mycobacteriaceae	Mycobacterium	0.04%	0.04%	0.00%	5.08%	0.68%	0.07%	
								Norcardiaceae	Rhodococcus	0.02%	0.07%	0.00%	0.31%	0.04%	0.00%	
								Norcardioidaceae	0.07%	0.66%	0.02%	0.11%	0.02%	0.00%		
								Aeromicrobium	0.00%	0.00%	0.00%	0.22%	0.00%	0.00%		
								Promicromonosporaceae	Cellulosimicrobium	0.09%	0.07%	0.00%	1.19%	0.02%	0.02%	
								Xylanimicrobium	1.63%	5.98%	0.40%	0.42%	0.00%	0.02%		
									0.00%	0.15%	0.02%	0.02%	0.07%	0.00%		
								Pseudonocardaceae	Amycolatopsis	0.06%	0.00%	0.00%	0.09%	0.00%	0.00%	
									Pseudonocardia	0.02%	0.09%	0.00%	0.24%	0.00%	0.00%	
									Saccharopolyspora	0.00%	0.00%	0.00%	0.18%	0.29%	0.07%	
								Sanguibacteraceae	Sanguibacter	0.11%	0.51%	0.04%	0.09%	0.02%	0.00%	
								Streptomycetaceae	Streptomyces	0.18%	0.20%	0.00%	0.27%	0.02%	0.00%	
								Coriobacteriia	Coriobacteriales	Coriobacteriaceae	0.02%	0.13%	0.11%	0.00%	0.04%	0.02%
								Thermoleophiia	Solirubrobacterales	Other	0.00%	0.00%	0.00%	1.04%	0.13%	0.00%
									Patulibacteraceae	Patulibacter	0.00%	0.18%	0.02%	0.02%	0.07%	0.00%
							Bacteroidetes	Bacteroidetes	Bacteroidia	Bacteroidales	Other	0.04%	0.07%	3.00%	0.00%	0.00%
Bacteroidaceae	Bacteroides	0.64%									0.93%	4.39%	0.18%	0.07%	26.02%	
	Candidatus Azobacteroides	0.27%									0.29%	5.01%	0.00%	0.00%	0.00%	
	Dysgonomonas	0.57%									0.66%	7.64%	0.18%	0.00%	4.68%	
	Paludibacter	0.09%	0.18%	1.79%	0.00%	0.00%					0.00%					
	Parabacteroides	0.46%	0.33%	5.59%	0.00%	0.00%					0.00%					
	Tannerella	0.07%	0.00%	2.34%	0.00%	0.00%					0.00%					
	Rikenellaceae	Rikenella	0.42%	0.68%	6.49%	0.04%					0.00%	1.21%				
	Odoribacteraceae	Butyrivimonas	0.00%	0.00%	0.13%	0.00%					0.00%	0.00%				
		Odoribacter	0.04%	0.11%	1.24%	0.04%					0.00%	0.00%				
	Cytophagia	Cytophagaceae	0.40%	0.27%	0.09%	0.15%					0.07%	0.00%				
	Flavobacteriia	Flavobacteriales	Blattabacteriaceae	0.00%	0.00%	0.02%					1.19%	0.00%	0.00%			
	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	0.00%	0.00%	0.00%					0.35%	0.00%	0.00%			
	Flavobacteriia	Flavobacteriales	Weeksliaceae	0.13%	0.29%	0.00%					11.97%	0.02%	0.00%			
	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	0.53%	0.95%	0.15%					3.22%	0.00%	0.00%			
	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	0.15%	0.46%	0.09%					1.74%	0.07%	0.02%			
	Saprospirae	Saprospirales	Chitinophagaceae	1.13%	0.42%	0.07%					1.50%	0.00%	0.00%			
	Chloroflexi	Thermomicrobia	AKG1722	0.07%	0.00%	0.00%					0.62%	0.00%	0.00%			
	Chloroflexi	Thermomicrobia	UG30-KF-045	0.04%	0.33%	0.00%					2.15%	0.31%	0.02%			
	Cyanobacteria	Chloroplast	Streptophyta	0.00%	0.02%	0.00%					0.04%	0.02%	0.00%			
	Deferribacteres	Deferribacteres	Deferribacteriales	Deferribacteraceae	Mucispirillum	0.00%					0.00%	0.66%	0.00%	0.00%		
	Firmicutes	Bacilli	Bacillales	Bacillaceae	0.00%	0.11%					0.00%	1.10%	0.02%	0.00%		
	Firmicutes	Bacilli	Bacillales	Bacillaceae	0.93%	0.04%					0.02%	0.00%	0.00%	0.00%		
	Firmicutes	Bacilli	Bacillales	Paenibacillaceae	Paenibacillus	0.02%					0.00%	0.00%	0.18%	0.00%	0.04%	
	Firmicutes	Bacilli	Bacillales	Planococcaceae	0.17%	0.75%					0.04%	0.31%	0.44%	0.04%		
	Firmicutes	Bacilli	Bacillales	Planococcaceae	0.04%	0.04%					0.00%	0.11%	0.00%	0.00%		
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Jeotgaliococcus	0.18%					0.31%	0.00%	0.13%	0.00%	0.04%	
	Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	12.74%					11.97%	0.46%	2.34%	5.65%	0.97%	
	Firmicutes	Bacilli	Lactobacillales	Other	22.13%	12.72%					1.28%	6.65%	9.70%	0.99%		
	Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Enterococcus	1.02%					1.68%	0.84%	1.57%	10.40%	4.00%	
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	0.13%	5.98%					1.24%	0.00%	0.00%	0.00%		
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	19.63%	13.01%					1.06%	15.44%	16.83%	1.90%		
	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Pediococcus	0.35%	0.13%	0.00%	0.02%	0.00%	0.00%					
	Firmicutes	Clostridia	Clostridiales	0.27%	0.31%	3.03%	0.11%	0.07%	4.42%							
	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	0.09%	0.29%	3.25%	0.15%	0.29%	5.30%						
	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	0.00%	0.02%	0.15%	0.00%	0.02%	1.26%						
	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	0.02%	0.15%	0.00%	0.02%	0.11%	0.00%						
	Firmicutes	Clostridia	Clostridiales	Dehalobacteriaceae	0.00%	0.00%	0.00%	0.00%	0.00%	0.11%						
	Firmicutes	Clostridia	Clostridiales	Dehalobacteriaceae	Dehalobacterium	0.00%	0.00%	0.04%	0.00%	0.00%						
	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Anaerofustis	0.02%	0.04%	0.00%	0.00%	0.00%						
	Firmicutes	Clostridia	Clostridiales	Eubacteriaceae	Eubacterium	0.02%	0.02%	0.00%	0.00%	0.00%						
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	0.02%	0.00%	0.20%	0.04%	0.00%	0.24%						
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	0.53%	0.38%	2.45%	0.33%	16.74%	10.27%						
	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Caprococcus	0.00%	0.00%	0.13%	0.00%	0.00%						
	Firmicutes	Clostridia	Clostridiales	Peptostreptococcaceae	0.07%	0.84%	0.04%	0.75%	1.97%	0.02%						
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	0.00%	0.00%	0.09%	0.00%	0.00%	0.04%						
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	0.42%	0.57%	6.12%	0.84%	3.58%	16.50%						
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	0.00%	0.00%	0.09%	0.00%	0.00%	0.15%						
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Oscillospira	0.02%	0.02%	0.57%	0.13%	0.24%	3.98%					
	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Ruminococcus	0.00%	0.04%	0.40%	0.00%	0.49%	2.12%					
	Firmicutes	Clostridia	Clostridiales	Veillonellaceae	0.02%	0.09%	0.64%	0.00%	0.00%	0.00%						
	Firmicutes	Clostridia	Clostridiales	Mogibacteriaceae	0.02%	0.00%	0.07%	0.00%	0.00%	0.00%						
	Firmicutes	Clostridia	Clostridiales	Mogibacteriaceae	0.04%	0.04%	0.20%	0.00%	0.02%	0.07%						
	Firmicutes	Clostridia	Clostridiales	Mogibacteriaceae	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%						
	Firmicutes	Clostridia	Clostridiales	SHA-98	0.00%	0.00%	0.04%	0.02%	0.00%	0.24%						
	Firmicutes	Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae	0.60%	0.40%	1.30%	0.04%	2.80%	3.25%						
	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	0.00%	0.00%	0.22%	0.00%	0.00%	0.00%						
	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium	0.42%	0.09%	2.98%	0.00%	0.00%	0.00%					
	GNO2	BDI-5	0.02%	0.02%	0.09%	0.00%	0.00%	0.00%	0.00%							
	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%						
	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae	0.00%	0.02%	0.02%	0.80%	0.04%	0.02%						
	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae	Planctomycetes	0.07%	0.09%	0.04%	2.39%	0.11%	0.00%					
	Planctomycetes	vadinHA49	PeH47	0.07%	0.09%	1.81%	0.00%	0.00%	0.00%							
	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	0.00%	0.00%	0.00%	0.31%	0.00%	0.00%						
	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	0.40%	0.53%	0.11%	0.33%	0.00%	0.00%					
	Proteobacteria	Alphaproteobacteria	Rhizobiales	0.18%	0.38%	0.00%	0.00%	0.00%	0.00%							
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae	0.00%	0.02%	0.00%	0.07%	0.00%	0.00%						
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Brucellaceae	0.04%	0.86%	0.02%	0.00%	0.00%	0.00%						
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bruceellaceae	0.22%	2.32%	0.07%	1.63%	0.57%	0.07%						
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae	0.51%	0.51%	0.13%	0.84%	0.09%	0.00%						
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%						
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae	0.09%	0.31%	0.02%	0.82%	0.15%	0.02%						
	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	0.00%	0.00%	0.00%	0.07%	0.13%	0.04%						
	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteraceae	0.00%	0.00%	0.00%	0.02%	0.00%	0.04%						
	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteraceae	Paracoccus	0.00%	0.00%	0.00%	0.51%	0.02%	0.00%					
	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%						
	Proteobacteria	Alphaproteobacteria	Rickettsiales	Rickettsiaceae	0.02%	0.00%	0.00%	0.11%	0.00%	0.00%						
	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	0.00%	0.00%	0.00%	0.11%	0.00%	0.00%						
	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	0.00%	0.00%	0.00%	0.11%	0.00%	0.00%						
	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Novosphingobium	0.09%	0.09%	0.02%	0.38%	0.00%	0.00%					
	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingopyxis	0.27%	0.18%	0.00%	0.15%	0.00%	0.00%					
	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	0.31%	0.33%	0.02%	2.05%	0.27%	0.02%						
	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	0.00%	0.04%	0.00%	0.07%	0.02%	0.00%						
	Proteobacteria	Betaproteobacteria	Burkholderiales	Alcaligenaceae	0.02%	0.60%										

Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfurificaceae	Desulfobulbus	0.02%	0.02%	0.97%	0.00%	0.00%	0.00%
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfovibrionaceae		0.38%	0.80%	19.79%	0.09%	2.05%	5.65%
Proteobacteria	Deltaproteobacteria	Desulfobacterales	Desulfovibrionaceae	Desulfovibrio	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Proteobacteria	Deltaproteobacteria	Myxococcales			0.00%	0.00%	0.00%	0.15%	0.00%	0.00%
Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae		0.00%	0.00%	0.00%	0.15%	0.00%	0.00%
Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae		0.02%	0.07%	0.07%	0.00%	0.00%	0.00%
Proteobacteria	Gammaaproteobacteria	Enterobacterales			0.00%	0.02%	0.00%	0.51%	20.91%	2.54%
Proteobacteria	Gammaaproteobacteria	Enterobacterales			0.15%	0.09%	0.02%	0.11%	0.00%	0.00%
Proteobacteria	Gammaaproteobacteria	Enterobacterales	Enterobacteriaceae	Enterobacter	0.00%	0.00%	0.00%	0.04%	0.00%	0.07%
Proteobacteria	Gammaaproteobacteria	Enterobacterales	Enterobacteriaceae	Serratia	2.58%	0.31%	0.00%	0.27%	0.02%	0.00%
Proteobacteria	Gammaaproteobacteria	Pseudomonadales	Moraxellaceae	Acinetobacter	1.57%	0.86%	0.07%	0.40%	0.07%	0.00%
Proteobacteria	Gammaaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	0.46%	0.20%	0.07%	0.62%	0.07%	0.07%
Proteobacteria	Gammaaproteobacteria	Xanthomonadales	Xanthomonadaceae		0.00%	0.00%	0.09%	0.00%	0.00%	0.00%
Proteobacteria	Gammaaproteobacteria	Xanthomonadales	Xanthomonadaceae	Luteimonas	0.18%	0.68%	0.09%	0.04%	0.00%	0.00%
Proteobacteria	Gammaaproteobacteria	Xanthomonadales	Xanthomonadaceae	Stenotrophomonas	0.02%	0.04%	0.04%	0.22%	0.11%	0.04%
SR1					0.00%	0.04%	0.02%	0.00%	0.00%	0.00%
Spirochaetes	Spirochaetes	Spirochaetales			0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Spirochaetes	Spirochaetes	Spirochaetales			0.00%	0.00%	0.02%	0.00%	0.00%	0.00%
Synergistetes	Synergistia	Synergistales			0.00%	0.02%	0.11%	0.00%	0.00%	0.00%
TM6	SJA-4				0.00%	0.04%	0.00%	1.02%	0.04%	0.02%
TM7	TM7-3	CWO40			0.04%	0.00%	0.07%	0.00%	0.00%	0.00%
TM7	TM7-3	CWO40			0.00%	0.11%	0.29%	0.00%	0.00%	0.00%
TM7	TM7-3	I025			0.00%	0.02%	0.00%	0.00%	0.00%	0.00%
Tenericutes	CK-104-19				0.02%	0.00%	0.00%	0.00%	0.00%	0.00%
Tenericutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae		0.02%	0.02%	0.35%	0.00%	0.00%	0.00%
Tenericutes	Mollicutes	Acholeplasmatales	Acholeplasmataceae	Acholeplasma	0.00%	0.00%	0.11%	0.00%	0.00%	0.00%
Tenericutes	Mollicutes	Anaeroplasmatales	Anaeroplasmataceae	Anaeroplasma	0.00%	0.00%	0.00%	0.00%	0.04%	1.94%
Tenericutes	Mollicutes	RsaHF231			0.07%	0.15%	0.00%	0.00%	0.00%	0.00%
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Akkermansia	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%
Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Luteibacter	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%
WP2					0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Thermi	Deinococci	Deinococcales	Trueperaceae		0.00%	0.00%	0.00%	0.24%	0.00%	0.00%
Unassigned					0.04%	0.02%	1.90%	0.02%	0.00%	0.15%

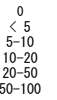


Table S5 – Statistical differences between all pairwise libraries comparisons.

sample 1	sample 2	p value	p value (Bonferroni corrected)
L1976	L1977	0.03	0.45
L1976	L1978	0.00	<=1.0e-02
L1976	L1980	0.00	<=1.0e-02
L1976	L1981	0.00	<=1.0e-02
L1976	L1982	0.00	<=1.0e-02
L1977	L1978	0.00	<=1.0e-02
L1977	L1980	0.00	<=1.0e-02
L1977	L1981	0.00	<=1.0e-02
L1977	L1982	0.00	<=1.0e-02
L1978	L1980	0.00	<=1.0e-02
L1978	L1981	0.00	<=1.0e-02
L1978	L1982	0.00	<=1.0e-02
L1980	L1981	0.00	<=1.0e-02
L1980	L1982	0.00	<=1.0e-02
L1981	L1982	0.00	<=1.0e-02

Unweighted UniFrac distance matrix was used as a significance test with 999 Monte Carlo permutations.

Table S6- Genus abundance (%) for each library. The rarefaction level was 5000 sequences/library. (La, *Leidynea appendiculatum*; Free, Free-nematode; Hd, *Hammer Schmidella diesingi*; Tb, *Thelastoma bulhoesi*).

Kingdom	Phylum	Class	Order	Family	Genus	<i>P. fuliginosa</i>			<i>P. americana</i>				
						La L1978	Free L1982	HdTb L1983	La L1984	Free L1985			
Archaea	Euryarchaeota	Methanomicrobia	Methanosarcinales	Methanosarcinaceae	Methanobrevibacter	0.12%	0.00%	0.10%	0.00%	0.50%			
		Thermoplasta	E2	Methanomassiliicoccaceae	Methanomicrococcus vandin11	0.00%	0.00%	0.10%	0.00%	0.00%			
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Brevibacteriaceae	Brevibacterium	0.72%	0.60%	0.90%	0.72%	0.06%			
				Cellulomonadales	Cellulomonas	0.00%	0.00%	0.00%	0.00%	0.68%			
				Corynebacteriaceae	Corynebacterium	0.14%	0.02%	0.00%	0.00%	0.08%			
				Dermabacteriaceae	Brachybacterium	0.26%	0.00%	0.00%	1.18%	0.04%			
				Dietziaceae	Other	0.00%	0.02%	0.00%	0.18%	0.00%			
				Glycomycetaceae	Glycomyces	0.02%	0.00%	0.02%	0.18%	0.00%			
				Gordoniaceae	Gordonia	0.24%	0.00%	0.02%	0.10%	0.02%			
				Intrasporangiaceae	Other	0.02%	0.00%	0.00%	0.02%	0.00%			
				Microbacteriaceae	Other	0.02%	0.00%	0.00%	0.10%	0.00%			
					Agromyces	0.00%	0.04%	0.00%	0.00%	0.00%			
					Other	0.02%	0.00%	0.00%	0.00%	0.04%			
					Arthrobacter	0.00%	0.00%	0.00%	0.00%	0.02%			
					Mycobacterium	0.02%	0.06%	0.00%	0.00%	0.00%			
					Nocardioideae	0.04%	0.00%	0.00%	0.02%	0.00%			
					Promicromonosporaceae	Cellulosimicrobium	0.04%	0.02%	0.00%	0.00%			
					Xylanimicrobium	0.40%	0.00%	0.02%	0.24%	0.00%			
					Pseudonocardiae	Pseudonocardia	0.06%	0.00%	0.00%	0.02%	0.00%		
					Sanguibacteraceae	Sanguibacter	0.00%	0.00%	0.00%	0.48%	0.00%		
					Streptomycetaceae	Streptomyces	0.02%	0.02%	0.00%	0.10%	0.00%		
					Coriobacteriaceae	Coriobacter	0.12%	0.04%	0.74%	0.54%	0.64%		
							3.22%	0.00%	5.36%	0.00%	7.74%		
				Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	5.46%	24.24%	12.06%	0.00%	4.90%
							GZKB19		0.00%	0.00%	0.14%	0.00%	0.00%
								Candidatus Azobacteroides	4.80%	0.00%	1.92%	0.00%	1.80%
								Dysgonomonas	7.46%	5.42%	0.36%	2.22%	1.78%
								Parabacteroides	2.46%	0.00%	0.00%	0.00%	0.00%
								Tannerella	5.22%	0.00%	12.98%	0.00%	4.60%
	Rikenellaceae	Rikenella	1.70%				0.00%	0.02%	0.00%	0.60%			
			5.78%				1.10%	1.80%	0.00%	8.18%			
			0.10%				0.00%	0.20%	0.00%	0.30%			
			0.06%				0.00%	1.16%	0.00%	1.58%			
			1.78%				0.00%	6.22%	0.00%	1.14%			
	Cytophagia	Cytophagales	Cytophagaceae					0.02%	0.00%	0.52%	0.00%		
							0.00%	0.00%	0.00%	0.34%	0.00%		
	Flavobacteriia	Flavobacteriales	Flavobacteriaceae					0.00%	0.04%	0.00%	0.08%		
							0.00%	0.00%	0.00%	0.00%	0.06%		
							0.04%	0.00%	0.12%	0.00%	0.00%		
							0.00%	0.00%	0.00%	0.14%	0.00%		
	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae				Sphingobacterium	0.06%	0.02%	0.02%	0.32%	0.00%	
							0.04%	0.02%	0.04%	0.28%	0.02%		
Chloroflexi	Saprosirae	Saprosirales	Chitinophagaceae		0.10%	0.00%	0.02%	1.32%	0.00%				
Deferribacteres	Thermomicrobia	JG30-KF-OM45			0.02%	0.02%	0.00%	0.06%	0.00%				
Firmicutes	Bacilli	Bacillales	Deferribacteres	Deferribacteraceae	Mucispirillum	0.64%	0.00%	0.22%	0.00%	1.02%			
			Bacillaceae		0.00%	0.00%	0.00%	0.10%	0.00%				
			Planococcaceae	Lysinibacillus	0.10%	0.02%	0.00%	0.00%	0.00%				
			Staphylococcaceae	Staphylococcus	0.40%	0.92%	0.00%	0.02%	1.84%				
			Lactobacillales	Enterococcaceae	Enterococcus	1.32%	1.38%	0.28%	2.08%	6.20%			
				Lactobacillaceae	Other	0.82%	4.08%	0.52%	5.32%	1.74%			
						1.32%	0.00%	0.00%	0.00%	0.00%			
						1.14%	2.04%	0.56%	1.16%	2.64%			
						2.70%	4.20%	6.56%	4.48%	3.76%			
						3.48%	5.52%	3.24%	5.12%	4.64%			
Bacteria	Firmicutes	Clostridia	Clostridiales	Christensenellaceae	Christensenella	0.00%	0.00%	0.10%	0.54%	0.04%			
					Other	0.28%	1.06%	0.10%	0.20%	0.00%			
				Clostridiaceae	Clostridium	0.00%	0.00%	0.04%	0.00%	0.04%			
				Dehalobacteriaceae	Dehalobacterium	0.00%	0.04%	0.04%	0.00%	0.00%			
				Dehalobacteriaceae	Dehalobacterium	0.10%	0.08%	0.16%	0.10%	0.10%			
				Eubacteriaceae	Anaerofustis	0.00%	0.00%	0.02%	0.00%	0.02%			
				Eubacteriaceae	Pseudoramibacter_Eubacterium	0.00%	0.00%	0.80%	0.00%	0.00%			
					Other	0.36%	0.20%	0.20%	0.54%	0.00%			
				Lachnospiraceae	Anaerostipes	2.30%	10.68%	4.20%	7.42%	2.54%			
					Coprococcus	0.22%	0.18%	0.38%	0.40%	0.32%			
					Other	0.06%	0.02%	1.06%	0.16%	0.04%			
						0.12%	0.02%	0.00%	0.12%	0.06%			
						6.14%	15.82%	8.32%	21.10%	10.04%			
						0.14%	0.36%	0.02%	0.00%	0.30%			
						0.72%	4.60%	1.28%	9.38%	1.14%			
						0.50%	2.16%	0.20%	3.14%	0.66%			
						0.88%	0.00%	0.32%	0.00%	0.36%			
					Veillonellaceae	Phascolarctobacterium	0.00%	0.00%	0.48%	0.00%	0.00%		
						Other	0.00%	0.00%	0.00%	0.00%	0.02%		
							0.16%	0.10%	0.94%	0.18%	0.16%		
							0.04%	0.06%	0.26%	0.10%	0.12%		
							0.04%	0.30%	1.16%	0.00%	0.02%		
					Erysipelotrichi	Erysipelotrichales	Erysipelotrichaceae		1.20%	3.42%	3.88%	1.56%	0.50%
				Fusobacteriia	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Other	0.22%	0.00%	0.06%	0.00%	0.00%
								Fusobacterium	3.14%	0.00%	0.32%	0.00%	0.96%
				GN02	BD-1				0.14%	0.00%	0.00%	0.00%	0.00%
				Planctomycetes	Planctomycetia	Planctomycetales	Pirellulales	Pirellulaceae		0.04%	0.00%	0.04%	0.00%
vadinHA49	Planctomycetaceae		0.00%				0.02%	0.00%	0.02%	0.00%			
					1.84%	0.00%	0.62%	0.00%	1.36%				
					0.00%	0.00%	0.00%	0.02%	0.00%				
					0.00%	0.00%	0.00%	1.52%	0.00%				
					0.10%	0.00%	0.00%	0.06%	0.00%				
					0.86%	0.00%	0.00%	0.00%	0.14%				
					0.00%	0.00%	0.00%	0.20%	0.02%				
					0.00%	0.04%	0.00%	0.40%	0.10%				
					0.04%	0.00%	0.00%	1.82%	0.00%				
					0.04%	0.02%	0.00%	0.10%	0.02%				
					0.00%	0.04%	0.00%	0.10%	0.00%				
					0.00%	0.06%	0.00%	0.00%	0.00%				
					0.02%	0.00%	0.00%	0.00%	0.00%				
					0.00%	0.00%	0.00%	0.06%	0.00%				
					0.02%	0.00%	0.32%	0.02%	0.00%				
					0.00%	0.00%	0.00%	0.00%	0.00%				
					0.02%	0.06%	0.00%	0.10%	0.06%				
					0.00%	0.00%	0.00%	0.04%	0.00%				
					0.04%	0.02%	0.00%	0.04%	0.00%				
					0.20%	0.00%	0.00%	0.00%	5.76%				
					0.08%	0.00%	0.08%	0.00%	0.20%				
					0.00%	0.00%	0.04%	0.00%	0.00%				
					0.14%	0.00%	0.00%	0.00%	0.00%				
					3.32%	0.00%	0.26%	0.00%	1.16%				
					0.00%	0.00%	0.04%	0.00%	0.04%				
					1.30%	0.00%	0.86%	0.00%	2.30%				
					0.00%	0.00%	0.80%	0.00%	0.00%				
					0.86%	0.00%	0.42%	0.00%	0.56%				
					19.14%	6.20%	7.74%	11.58%	6.84%				
					0.00%	0.00%	0.00%	0.00%	0.00%				
					0.16%	0.00%	0.54%	0.00%	0.00%				
					0.00%	0.00%	0.02%	0.00%	0.00%				
					0.00%	2.62%	0.00%	5.72%	0.26%				
					0.00%	0.00%	0.12%	0.22%	0.06%				
					0.00%	0.04%	0.00%	0.00%	0.00%				
					0.00%	0.00%	0.00%	0.20%	0.00%				
					0.10%	0.00%	0.00%	0.02%	0.00%				
					0.00%	0.00%	0.00%	0.00%	0.06%				
					0.10%	0.02%	0.00%	0.20%	0.00%				
					0.10%	0.00%	0.00%	0.00%	0.00%				
					0.14%	0.00%	0.02%	0.36%	0.00%				
					0.00%	0.00%	0.00%	0.84%	0.00%				
					0.02%	0.04%	0.00%	0.00%	0.00%				

SR1					0.04%	0.00%	0.00%	0.00%	1.42%	
Spirochaetes	Spirochaetes	Spirochaetales	Spirochaetaceae	Treponema	0.02%	0.00%	0.22%	0.00%	0.06%	
					0.06%	0.00%	0.02%	0.00%	0.08%	
Synergistetes	Synergistia	Synergistales	Dethiosulfovibrionaceae	TGS	0.10%	0.00%	0.12%	0.00%	0.20%	
			Synergistaceae	Candidatus Tammella	0.04%	0.00%	0.00%	0.00%	0.06%	
				vadinCA02	0.02%	0.00%	0.46%	0.00%	0.06%	
TM7	TM7-3	CW040	F16		0.02%	0.00%	0.12%	0.00%	2.68%	
		I025	Other		0.00%	0.00%	0.04%	0.00%	0.00%	
Tenericutes	CK-104-19				0.00%	0.00%	0.06%	0.00%	0.00%	
					0.36%	0.00%	0.06%	0.00%	0.00%	
	Mollicutes	Acholeplasmatales	Acholeplasmataceae	Acholeplasma	0.14%	0.00%	0.12%	0.00%	0.00%	
				Anaeroplasma	0.00%	1.74%	0.00%	0.64%	0.00%	
		RsaHF231			0.02%	0.00%	0.06%	0.00%	0.06%	
Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus	0.00%	0.00%	0.06%	0.00%	0.14%	
				Akkermansia	0.08%	0.00%	0.00%	0.26%	0.12%	
	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae	Luteolibacter	0.00%	0.00%	0.00%	0.18%	0.00%	
WPS-2					0.00%	0.00%	0.10%	0.56%	0.00%	
Unassigned					1.86%	0.12%	1.20%	1.54%	0.84%	

0
< 5
5-10
10-20
20-50
50-100

The rarefaction level was 5,000 sequences in each library. (La. *Leidynema appendiculatum*; Free, nematode-free; Hd, *Hammerschmidtella diesingi*; Tb, *Thelastoma bulhoesi*).

Table S7 – Statistical differences between all pairwise libraries comparisons.

sample 1	sample 2	p value	p value (Bonferroni corrected)
L1978	L1982	0.00	<=1.0e-02
L1978	L1983	0.00	<=1.0e-02
L1978	L1984	0.00	<=1.0e-02
L1978	L1985	0.02	0.2
L1982	L1983	0.00	<=1.0e-02
L1982	L1984	0.00	<=1.0e-02
L1982	L1985	0.00	<=1.0e-02
L1983	L1984	0.00	<=1.0e-02
L1983	L1985	0.05	0.5
L1984	L1985	0.00	<=1.0e-02

Unweighted UniFrac distance matrix was used as a significance test with 999 Monte Carlo permutations.

Supplemental Figures legends

Fig. S1. Rarefaction curves based on observed OTUs in each sequence and sample. (A)

The rarefaction level was 4,528 sequences in each library, filtering the genus

Blattabacterium; (B) The rarefaction level was 5,000 sequences in each library, filtering

the genus *Blattabacterium*.

S1 Figure

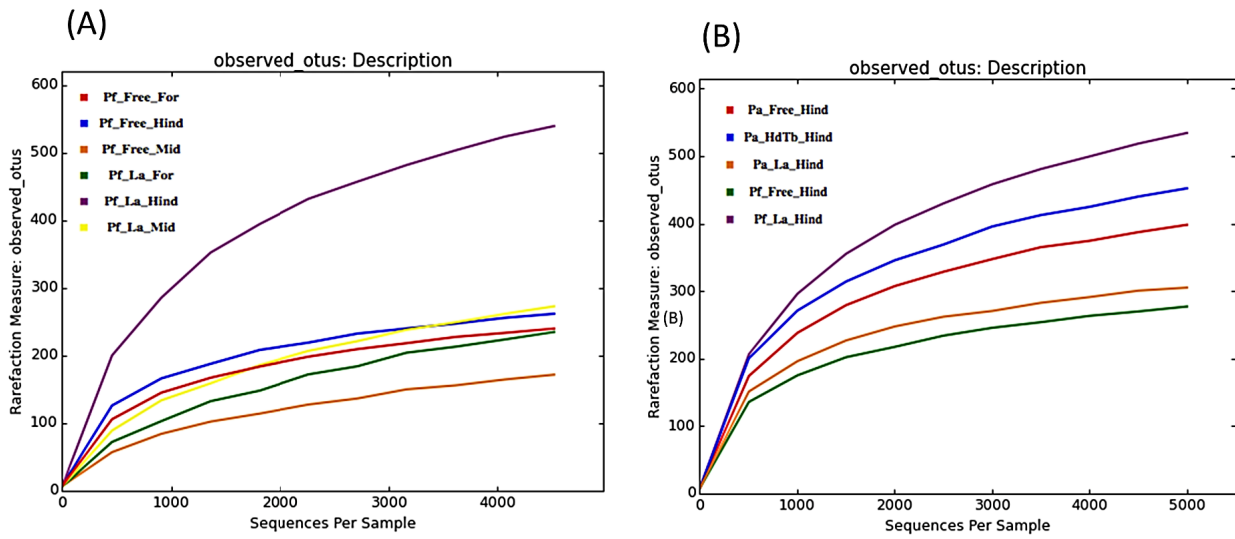


Fig. S1, Vicente