

Tasting the differences: microbiota analysis of different insect-based novel food

Short title: Microbiota signature in insect-based food

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S1 Table. Insects used in the processed food analysed in this study.

Scientific name	<i>Acheta domesticus</i> (Linnaeus, 1758)	<i>Tenebrio molitor</i> (Linnaeus, 1758)	<i>Alphitobius diaperinus</i> (Panzer, 1797)
Taxonomy	Order: Orthoptera Family: Gryllidae	Order: Coleoptera Family: Tenebrionidae.	Order: Coleoptera Family: Tenebrionidae
Description	House cricket, native to Southwest Asia, widespread in tropical and temperate zones. Species is native to most of the European countries.	Known as mealworm. It has a cosmopolitan distribution, being common in Europe, as a pest of grain storages.	Known as lesser mealworm or litter beetle. It has a cosmopolitan distribution, being common in Europe, as a pest of grain storages and poultry farms.
Growth	Adults grow up to 20-22 mm, both sexes are fully winged. Adult females are slightly bigger with prominent ovipositor protruding from the abdomen. Crickets are greyish yellow in color.	The adult beetles are up to 15-18 mm long. It is shiny black or brown with reddish brown elytra. The eggs are oval, whitish, about 1.5 mm long. The larvae resemble larvae of other mealworms, at the final stage measuring up to 25 mm in length.	The adult beetles are 6 mm long, oval. It is shiny black or brown with reddish brown elytra. Color is variable among individuals and subpopulations and changing with age. The antennae are paler at the tips and are covered in tiny, yellowish hairs. The elytra have shallow longitudinal grooves. The eggs are narrow, whitish, about 1.5 mm long. The larvae resemble larvae of other mealworms, at the final stage measuring up to 11 mm in length.

Incubation period (days from egg-laying to hatch)	11	10-12	10-12
Time to maturity (days from hatch to max body weight)	32-49	280-400	280-400
Resistance	Species is resistant to environmental conditions, and is very productive in mass culture, tolerating high population densities. The species is however very susceptible to the Cricket Paralysis Virus.	Species is resistant to environmental conditions, and is very productive in mass culture, tolerating high population densities.	Species is resistant to environmental conditions and is very productive in mass culture.
Protein and fat content	Protein content in larvae and imagines varies from 60 to 70% (d.m.), with a fat content of 20-25 % (d.m.)	Protein content in larvae varies from 50 to 65% (d.m.), with a fat content of 30-40 % (d.m.) highly depending on the feed and rearing conditions.	Protein content in larvae varies from 50 to 65% (d.m.), with fat content of 30-40 % (d.m.) highly depending on the feed and rearing conditions.

Adapted from http://ipiff.org/wp-content/uploads/2019/03/IPIFF_Guide_A4_2019-v5-separate.pdf

S2 Table. List of primer pairs used for DNA barcoding and metabarcoding analyses.

Primer name	5'-3'	Barcode locus	Reference
LCO1490	GGTCAACAAATCATAAAGATATTGG	COI	[17]
HC02198	TAAACTTCAGGGTGACCAAAAAATCA		
340F	CTACGGGNGGCWGCAG	16S	[19]
806R	GACTACHVGGGTATCTAATCC		

S3 Table. Results of alpha microbial diversity.

Pairwise comparison of ASVs counts between samples among to the same insect (*A. domesticus* n=12; *A. diaperinus* n=9; *T. molitor* n=15)

Group 1	Group 2	H	P-value	Q-value
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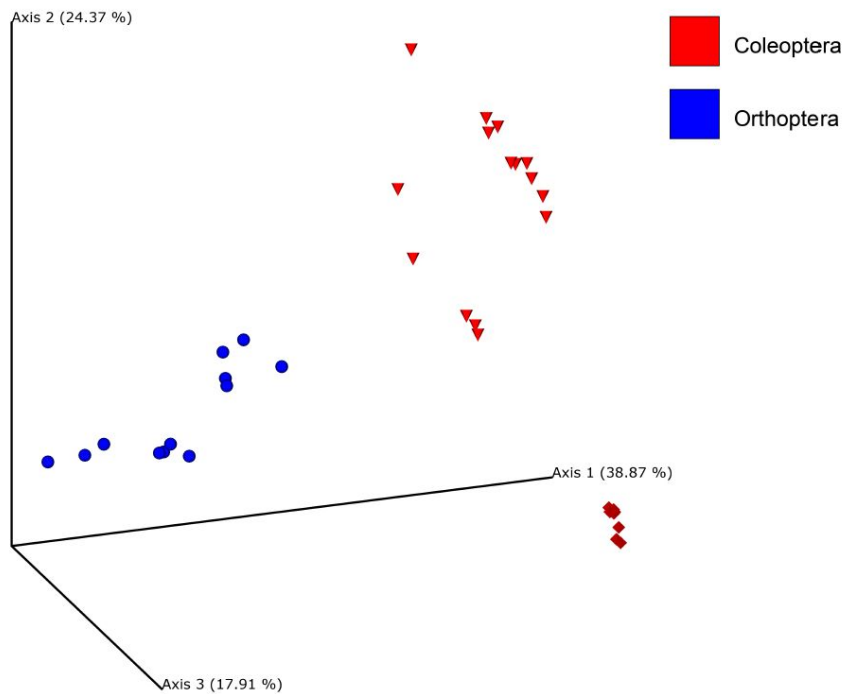
<i>A. domesticus</i>	<i>A. diaperinus</i>	14.78	< 0.01	< 0.01
<i>A. domesticus</i>	<i>T. molitor</i>	5.83	0.015	0.015
<i>A. diaperinus</i>	<i>T. molitor</i>	14.82	< 0.01	< 0.01

Pairwise comparison of Shannon index between samples among to the same insect (*A. domesticus* n=12; *A. diaperinus* n=9; *T. molitor* n=15)

Group 1	Group 2	H	P-value	Q-value
<i>A. domesticus</i>	<i>A. diaperinus</i>	14.72	< 0.01	< 0.01
<i>A. domesticus</i>	<i>T. molitor</i>	19.28	< 0.01	< 0.01
<i>A. diaperinus</i>	<i>T. molitor</i>	16.20	< 0.01	< 0.01

S4 Table. Results of beta microbial diversity.

PCoA Emperor plots based on the Bray-Curtis metric. Food samples were compared based on insect order (red: Coleoptera; blue: Orthoptera) and insect species (sphere: *A. domesticus*; triangle: *T. molitor*; square: *A. diaperinus*).



Raw materials (flour, n=12) vs food products (crackers, pasta, protein bars; n=24)	Pseudo-F	P-value
Jaccard	5.80	0.001
Unweighted UniFrac	5.40	0.001
Bray-Curtis	6.38	0.001
Weighted UniFrac	8.21	0.002

Differences among samples belong to different insects (<i>A. domesticus</i> n=12; <i>A. diaperinus</i> n=9; <i>T. molitor</i> n=15)	Pseudo-F	P-value
Jaccard	10.39	0.001
Unweighted UniFrac	11.37	0.001
Bray-Curtis	16.87	0.001
Weighted UniFrac	25.63	0.001

Pairwise comparisons to test differences among samples belong to different insects (*A. domesticus* n=12; *A. diaperinus* n=9; *T. molitor* n=15).

Insects	Group 1	Group 2	Pseudo-F	P-value	Q-value
Jaccard	<i>A. domesticus</i>	<i>A. diaperinus</i>	11.81	0.001	0.001
	<i>A. domesticus</i>	<i>T. molitor</i>	8.30	0.001	0.001
	<i>A. diaperinus</i>	<i>T. molitor</i>	12.35	0.001	0.001
Unweighted UniFrac	<i>A. domesticus</i>	<i>A. diaperinus</i>	14.51	0.001	0.001
	<i>A. domesticus</i>	<i>T. molitor</i>	12.27	0.001	0.001
	<i>A. diaperinus</i>	<i>T. molitor</i>	7.43	0.001	0.001
Bray-Curtis	<i>A. domesticus</i>	<i>A. diaperinus</i>	16.20	0.001	0.001
	<i>A. domesticus</i>	<i>T. molitor</i>	12.51	0.001	0.001
	<i>A. diaperinus</i>	<i>T. molitor</i>	25.95	0.001	0.001
Weighted UniFrac	<i>A. domesticus</i>	<i>A. diaperinus</i>	29.20	0.001	0.001
	<i>A. domesticus</i>	<i>T. molitor</i>	25.16	0.001	0.001

	<i>A. diaperinus</i>	<i>T. molitor</i>	21.19	0.001	0.001
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Supplementary S6

T. molitor

100%ofsamples							
Feature ID	2%	9%	25%	50%	75%	91%	98%
D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Entomoplasmatales;D_4_Spiroplasmataceae;D_5_Spiroplasma;D_6_uncultured Spiroplasma sp.	108.2	273.4	651	23608	38182	38720.24	38955.72
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae; ;_	373.44	420.48	528	13517	21499	22918.52	23539.56
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Enterococcaceae;D_5_Enterococcus;_	29.44	97.48	253	1607	2968	3427.52	3628.56
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Staphylococcaceae;D_5_Staphylococcus;_	42.44	117.48	289	1209	1811	2555.96	2881.88
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Enterobacter;_	9.92	30.64	78	565	621	626.76	629.28
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Streptococcaceae;D_5_Lactococcus;D_6_uncultured bacterium	2.24	3.08	5	443	465	565.48	609.44
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Pseudomonadaceae;D_5_Pseudomonas;_	73.28	112.76	203	330	339	395.32	419.96
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Bacillaceae;D_5_Bacillus;_	72.32	80.44	99	177	181	638.6	838.8
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Serratia;_	5.24	20.08	54	71	183	327	390
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Pantoea;_	11.08	11.36	12	43	70	89.2	97.6
70%ofsamples							
Feature ID	2%	9%	25%	50%	75%	91%	98%
D_0_Bacteria;D_1_Tenericutes;D_2_Mollicutes;D_3_Entomoplasmatales;D_4_Spiroplasmataceae;D_5_Spiroplasma;D_6_uncultured Spiroplasma sp.	108.2	273.4	651	23608	38182	38720.24	38955.72
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae; ;_	373.44	420.48	528	13517	21499	22918.52	23539.56
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Streptococcaceae;D_5_Lactococcus;_	0.4	1.8	5	1846	1974	2781.04	3134.12
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Enterococcaceae;D_5_Enterococcus;_	29.44	97.48	253	1607	2968	3427.52	3628.56
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Lactobacillaceae;D_5_Lactobacillus;D_6_uncultured bacterium	6.96	31.32	87	1268	1938	2294.48	2450.44
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Staphylococcaceae;D_5_Staphylococcus;_	42.44	117.48	289	1209	1811	2555.96	2881.88
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Leuconostocaceae;D_5_Weissella;D_6_Weissella confusa	0.24	1.08	3	661	1114	1327.12	1420.36
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Lactobacillaceae;D_5_Lactobacillus;_	0.56	2.52	7	626	766	1038	1157
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Enterobacter;_	9.92	30.64	78	565	621	626.76	629.28
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Staphylococcaceae;D_5_Staphylococcus;D_6_uncultured bacterium	12	54	150	464	751	1063.32	1199.96
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Streptococcaceae;D_5_Lactococcus;D_6_uncultured bacterium	2.24	3.08	5	443	465	565.48	609.44
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Lactobacillaceae;D_5_Pediococcus;D_6_Pediococcus pentosaceus	0.08	0.36	1	389	480	613.12	671.36
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Pseudomonadaceae;D_5_Pseudomonas;_	73.28	112.76	203	330	339	395.32	419.96
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Pseudomonadaceae;D_5_Pseudomonas;D_6_Pseudomonas aeruginosa	7.52	33.84	94	183	186	339.6	406.8
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Bacillaceae;D_5_Bacillus;_	72.32	80.44	99	177	181	638.6	838.8
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Pseudomonadaceae;D_5_Pseudomonas;D_6_uncultured bacterium	1.76	7.92	22	75	118	182.64	210.92
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Serratia;_	5.24	20.08	54	71	183	327	390
Unassigned; ; ; ; ; ; ;_	3.6	16.2	45	52	71	172.12	216.36
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Pantoea;_	11.08	11.36	12	43	70	89.2	97.6
D_0_Bacteria;D_1_Actinobacteria;D_2_Actinobacteria;D_3_Micrococcales;D_4_Micrococcaceae;D_5_Kocuria;_	0.56	2.52	7	41	71	90.84	99.52
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Leuconostocaceae;D_5_Leuconostoc;D_6_Leuconostoc pseudomesenteroides	0.24	1.08	3	28	33	39.4	42.2

A. diaperinus

70%and100%ofsamples							
Feature ID	2%	9%	25%	50%	75%	91%	98%
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae;D_5__Enterobacter;__	3451.48	3547.66	3767.5	4111	50509	80203.72	93195.16
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae;__;_	799.08	1089.86	1754.5	2793	2841.5	2872.54	2886.12
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Enterococcaceae;D_5__Enterococcus;__	356.6	376.2	421	491	1392	1968.64	2220.92
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Staphylococcaceae;D_5__Staphylococcus;_	232.96	267.82	347.5	472	903.5	1179.66	1300.48
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Streptococcaceae;D_5__Lactococcus;D_6__uncultured bacterium	131.92	156.14	211.5	298	1386.5	2083.14	2387.92
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Streptococcaceae;D_5__Lactococcus;__	157.24	165.08	183	211	1049	1585.32	1819.96
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Enterococcaceae;D_5__Enterococcus;D_6__Enterococcus faecalis	15.56	17.52	22	29	335.5	531.66	617.48
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Listeriaceae;D_5__Listeria;__	15.24	16.08	18	21	244.5	387.54	450.12
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Brevibacteriaceae;D_5__Brevibacterium;__	13.08	13.36	14	15	140.5	220.82	255.96
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Corynebacteriales;D_4__Corynebacteriaceae;D_5__Corynebacterium 1;__	10.16	10.72	12	14	208	332.16	386.48
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Dermabacteraceae;D_5__Brachybacterium;__	6.32	7.44	10	14	100.5	155.86	180.08
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Bacillaceae;D_5__Bacillus;_	4.04	4.18	4.5	5	5	5	5
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Moraxellaceae;D_5__Acinetobacter;__	2.08	2.36	3	4	17.5	26.14	29.92
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Bacillaceae;D_5__Bacillus;D_6__Bacillus pumilus	3	3	3	3	4	4.64	4.92

A. domesticus

100%ofsamples							
Feature ID	2%	9%	25%	50%	75%	91%	98%
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Tannerellaceae;D_5_Parabacteroides;D_6_uncultured bacterium	327.68	407.06	588.5	725	1343.75	2451.11	2935.58
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Bacteroidaceae;D_5_Bacteroides;__	93.32	129.44	212	294	850.25	1843.37	2277.86
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;__;_	116.76	126.42	148.5	219	349.5	486.78	546.84
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;__;_	89.66	102.47	131.75	149.5	184.5	246.9	274.2
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Tannerellaceae;D_5_Parabacteroides;__	71.12	82.04	107	139	369	774.12	951.36
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Rikenellaceae;D_5_Alistipes;__	31.1	38.45	55.25	108.5	170.5	204.1	218.8
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Enterococcaceae;D_5_Enterococcus;__	64.2	68.4	78	90.5	463	1163.8	1470.4
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Dysgonomonadaceae;D_5_Dysgonomonas;__	25.12	36.04	61	79	96	119.04	129.12
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Enterobacter;__	19.82	29.69	52.25	71.5	103.75	151.27	172.06
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_uncultured;__	55.24	56.08	58	63.5	74.75	87.71	93.38
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_GCA-900066225;__	19.38	24.21	35.25	56	71.25	71.73	71.94
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Klebsiella;__	11.46	20.07	39.75	51.5	58.25	68.33	72.74
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Rikenellaceae;D_5_Alistipes;D_6_uncultured bacterium	23.42	24.89	28.25	50.5	72.75	76.11	77.58
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Pseudomonadaceae;D_5_Pseudomonas;__	43.36	44.62	47.5	49.5	75.25	123.73	144.94
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Citrobacter;__	11.98	18.91	34.75	47.5	59.5	73.9	80.2
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Candidatus Soleaferrea;__	25.12	25.54	26.5	35	44.5	47.38	48.64
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Streptococcaceae;D_5_Lactococcus;D_6_uncultured bacterium	14.6	16.7	21.5	34.5	289	757.48	962.44
D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfovibrionales;D_4_Desulfovibrionaceae;D_5_Desulfovibrio;__	12.3	13.35	15.75	24.5	41	58.28	65.84
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Candidatus Soleaferrea;D_6_uncultured bacterium	2.36	3.62	6.5	16	26	29.84	31.52
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_uncultured;D_6_uncultured bacterium	6.24	7.08	9	16	31.5	49.74	57.72
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_Anaerovorax;__	5.18	5.81	7.25	14	20	20	20
D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes;D_3_Selenomonadales;D_4_Acidaminococcaceae;D_5_uncultured;__	3.6	5.7	10.5	13	13.75	15.19	15.82
D_0_Bacteria;D_1_Verrucomicrobia;D_2_Verrucomicrobiae;D_3_Verrucomicrobiales;D_4_Akkermansia;D_5_Akkermansia;D_6_uncultured bacterium	5.3	6.35	8.75	13	28	51.04	61.12
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Paludibacteraceae;D_5_Paludibacter;__	8.06	8.27	8.75	11	15.75	21.03	23.34
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Erysipelatoclostridium;D_6_uncultured bacterium	5.18	5.81	7.25	10.5	13	13	13
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnoclostridium;__	5	5	5	8.5	13.25	15.65	16.7
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodospirillales;D_4_Magnetospirillaceae;__;_	2.3	3.35	5.75	7.5	8	8	8
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_GCA-900066575;D_6_uncultured bacterium	4.06	4.27	4.75	5	7.25	11.57	13.46
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Erysipelatoclostridium;__	1.12	1.54	2.5	3	7.25	15.41	18.98
70%ofsamples							
Feature ID	2%	9%	25%	50%	75%	91%	98%
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Tannerellaceae;D_5_Parabacteroides;D_6_uncultured bacterium	327.68	407.06	588.5	725	1343.75	2451.11	2935.58
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Bacillales;D_4_Bacillaceae;D_5_Bacillus;__	1.14	5.13	14.25	355	1693.75	3619.03	4461.34
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Bacteroidaceae;D_5_Bacteroides;__	93.32	129.44	212	294	850.25	1843.37	2277.86
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;__;_	116.76	126.42	148.5	219	349.5	486.78	546.84
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;__;_	89.66	102.47	131.75	149.5	184.5	246.9	274.2
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Tannerellaceae;D_5_Parabacteroides;__	71.12	82.04	107	139	369	774.12	951.36
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Rikenellaceae;D_5_Alistipes;__	31.1	38.45	55.25	108.5	170.5	204.1	218.8
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Enterococcaceae;D_5_Enterococcus;__	64.2	68.4	78	90.5	463	1163.8	1470.4
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Dysgonomonadaceae;D_5_Dysgonomonas;__	25.12	36.04	61	79	96	119.04	129.12
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Enterobacter;__	19.82	29.69	52.25	71.5	103.75	151.27	172.06
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_uncultured;__	55.24	56.08	58	63.5	74.75	87.71	93.38
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_GCA-900066225;__	19.38	24.21	35.25	56	71.25	71.73	71.94
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Klebsiella;__	11.46	20.07	39.75	51.5	58.25	68.33	72.74
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Rikenellaceae;D_5_Alistipes;D_6_uncultured bacterium	23.42	24.89	28.25	50.5	72.75	76.11	77.58
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Pseudomonadales;D_4_Pseudomonadaceae;D_5_Pseudomonas;__	43.36	44.62	47.5	49.5	75.25	123.73	144.94
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Citrobacter;__	11.98	18.91	34.75	47.5	59.5	73.9	80.2
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Candidatus Soleaferrea;__	25.12	25.54	26.5	35	44.5	47.38	48.64

D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Streptococcaceae;D_5_Lactococcus;D_6_uncultured bacterium	14.6	16.7	21.5	34.5	289	757.48	962.44
D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfovibrionales;D_4_Desulfovibrionaceae;D_5_Desulfovibrio;__	12.3	13.35	15.75	24.5	41	58.28	65.84
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Tyzzera 3;__	0.84	3.78	10.5	20	26.75	28.19	28.82
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Candidatus Soleaferrea;D_6_uncultured bacterium	2.36	3.62	6.5	16	26	29.84	31.52
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_uncultured;D_6_uncultured bacterium	6.24	7.08	9	16	31.5	49.74	57.72
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Family XIII;D_5_Anaerovorax;__	5.18	5.81	7.25	14	20	20	20
D_0_Bacteria;D_1_Verrucomicrobia;D_2_Verrucomicrobiae;D_3_Verrucomicrobiales;D_4_Akkermansia;D_5_Akkermansia;D_6_uncultured bacterium	5.3	6.35	8.75	13	28	51.04	61.12
D_0_Bacteria;D_1_Firmicutes;D_2_Negativicutes;D_3_Selenomonadales;D_4_Acidaminococcaceae;D_5_uncultured;__	3.6	5.7	10.5	13	13.75	15.19	15.82
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Flavobacteriales;D_4_Weeksellaceae;D_5_Apibacter;__	0.54	2.43	6.75	12	20	29.6	33.8
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Paludibacteraceae;D_5_Paludibacter;__	8.06	8.27	8.75	11	15.75	21.03	23.34
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Erysipelatoclostridium;D_6_uncultured bacterium	5.18	5.81	7.25	10.5	13	13	13
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Lachnoclostridium;__	5	5	5	8.5	13.25	15.65	16.7
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Ruminococcaceae;D_5_Butyricoccus;__	0.48	2.16	6	8	14.5	26.98	32.44
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Blautia;__	0.36	1.62	4.5	8	13.25	19.49	22.22
D_0_Bacteria;D_1_Bacteroidetes;D_2_Bacteroidia;D_3_Bacteroidales;D_4_Dysgonomadaeaceae;D_5_uncultured;__	0.3	1.35	3.75	7.5	11.25	13.65	14.7
D_0_Bacteria;D_1_Proteobacteria;D_2_Alphaproteobacteria;D_3_Rhodospirillales;D_4_Magnetospirillaceae;__	2.3	3.35	5.75	7.5	8	8	8
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Enterobacteriales;D_4_Enterobacteriaceae;D_5_Dickeya;__	0.18	0.81	2.25	6	86.75	236.03	301.34
D_0_Bacteria;D_1_Proteobacteria;D_2_Gammaproteobacteria;D_3_Betaproteobacteriales;D_4_Neisseriaceae;__	0.06	0.27	0.75	5.5	10.5	11.46	11.88
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_GCA-900066575;D_6_uncultured bacterium	4.06	4.27	4.75	5	7.25	11.57	13.46
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Tyzzera;__	0.12	0.54	1.5	5	8.5	9.46	9.88
D_0_Bacteria;D_1_Fusobacteria;D_2_Fusobacteriia;D_3_Fusobacteriales;D_4_Fusobacteriaceae;D_5_Fusobacterium;__	0.12	0.54	1.5	4	9.75	16.95	20.1
D_0_Bacteria;D_1_Proteobacteria;D_2_Deltaproteobacteria;D_3_Desulfovibrionales;D_4_Desulfovibrionaceae;D_5_uncultured;D_6_uncultured bacterium	0.18	0.81	2.25	4	8.75	15.95	19.1
D_0_Bacteria;D_1_Firmicutes;D_2_Bacilli;D_3_Lactobacillales;D_4_Leuconostocaceae;D_5_Weissella;D_6_Weissella confusa	0.12	0.54	1.5	3.5	50.25	137.13	175.14
D_0_Bacteria;D_1_Firmicutes;D_2_Erysipelotrichia;D_3_Erysipelotrichales;D_4_Erysipelotrichaceae;D_5_Erysipelatoclostridium;__	1.12	1.54	2.5	3	7.25	15.41	18.98
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Lachnospiraceae;D_5_Blautia;D_6_uncultured bacterium	0.18	0.81	2.25	3	5.75	11.03	13.34
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Christensenellaceae;D_5_Christensenellaceae R-7 group;D_6_uncultured bacterium	0.12	0.54	1.5	2.5	4.75	8.11	9.58
D_0_Bacteria;D_1_Firmicutes;D_2_Clostridia;D_3_Clostridiales;D_4_Clostridiales vadinBB60 group;D_5_uncultured bacterium;D_6_uncultured bacterium	0.06	0.27	0.75	2	33.75	92.79	118.62

Venn results

Names	total	genera
Acheta ∩ Alphitobius ∩ Tenebrio	4	Enterobacteriaceae_genus
		Lactococcus
		Enterobacter
		Enterococcus
Alphitobius ∩ Tenebrio	2	Staphylococcus
		Bacillus
Acheta ∩ Tenebrio	1	Pseudomonas
Tenebrio	3	Spiroplasma
		Pantoea
		Serratia
Alphitobius	5	Brevibacterium
		Acinetobacter
		Brachybacterium
		Listeria
		Corynebacterium 1
Acheta	20	Paludibacter
		Candidatus_Soleaferrea
		Magnetospirillaceae_genus
		Bacteroides
		Parabacteroides
		Dysgonomonas
		Akkermansia
		Alistipes
		Acidaminococcaceae_uncultured
		Erysipelatoclostridium
		Lachnoclostridium
		Klebsiella
		Lachnospiraceae_GCA-900066575
		Ruminococcaceae_uncultured
		Ruminococcaceae_GCA-900066225
		Lachnospiraceae_uncultured
		Citrobacter
Lachnospiraceae_genus		
Desulfovibrio		
Anaerovorax		