Supporting Information

Modulation of JNK-1/ β-catenin signaling by *Lactobacillus casei,* inulin and their combination in 1,2 dimethylhydrazine- induced colon cancer in mice

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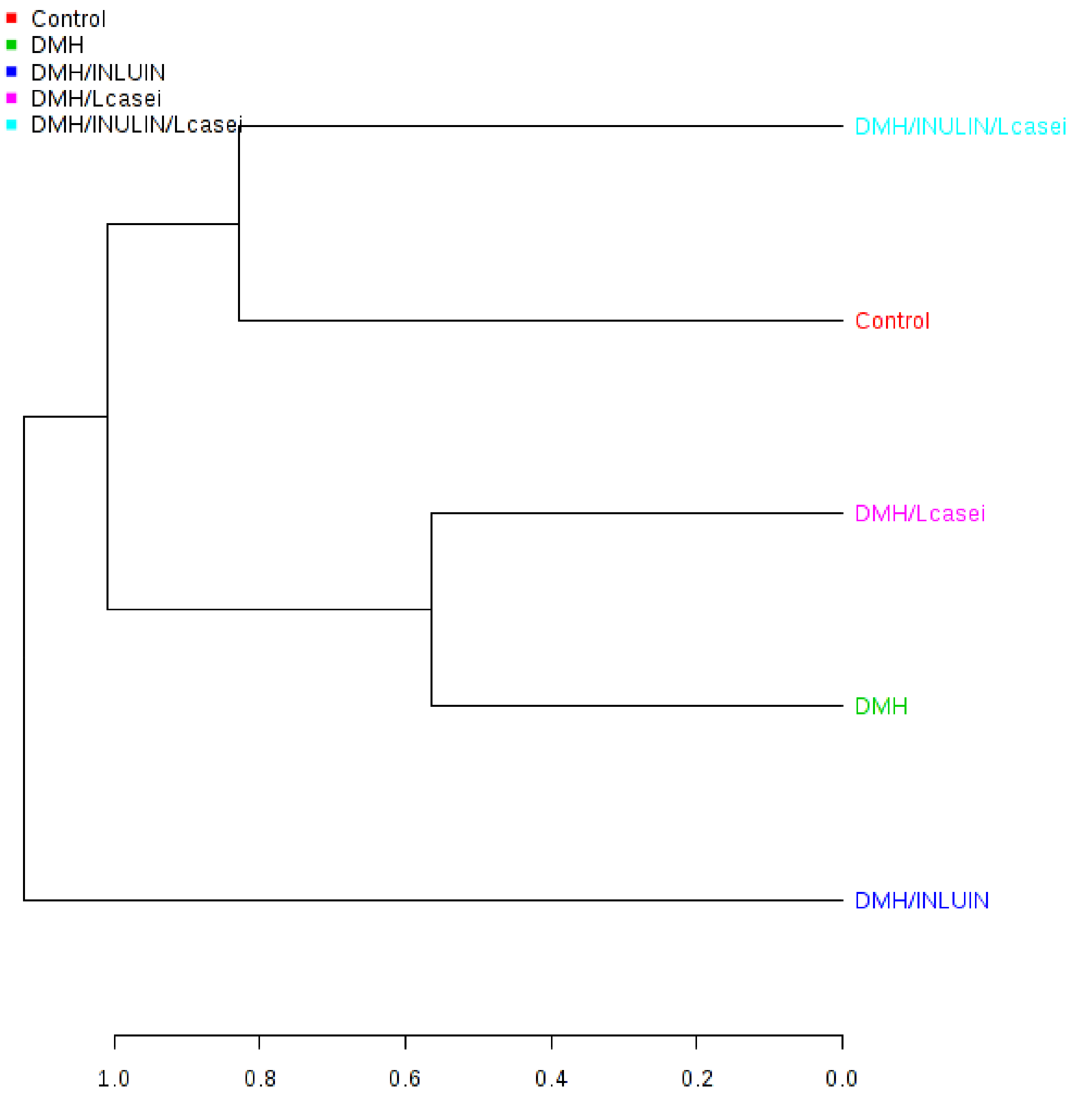
1. **Figure S1 , Phylogenetic relation of the animal groups based on the reads counts obtained from the microbiome results**

(Figure generated using MicrobiomeAnalyst https://www.microbiomeanalyst.ca)



2. Table S1, The distribution of reads along the quality check protocol and DADA2 routine.

	input	**filtered**	**denoised**	**merged**	**non-chimeric**
Control	73617	59262	59262	58527	57980
DMH	150362	119594	119594	117061	114847
DMH + Inulin	121299	96494	96494	95531	95251
DMH + L. casei	111737	88378	88378	86741	85662
DMH + L. casei + Inulin	128539	100553	100553	99112	97899
Sequencing control	834	291	291	227	227

3. Table S2 Kingdom-level taxon distribution of the reads count obtained

#OTU ID	Control	DMH	DMH + Inulin	DMH + L. casei	DMH + L. casei + Inulin	Sequencing control
k__Bacteria	57971	114842	95249	85656	97886	227
Unassigned	9	5	2	6	13	0

4. Table S3 Phylum-level taxon distribution of the reads count obtained

#OTU ID	Control	DMH	DMH + Inulin	DMH + L. casei	DMH + L. casei + Inulin	Sequencing control
k__Bacteria;p__Acidobacteria	21	0	0	0	13	0
k__Bacteria;p__Actinobacteria	971	2289	1471	943	1873	12
k__Bacteria;p__Bacteroidetes	10577	54531	7161	39453	25101	17
k__Bacteria;p__Chlamydiae	49	8	21	10	54	0
k__Bacteria;p__Chloroflexi	16	3	5	7	38	0
k__Bacteria;p__Coprothermobacteraeota	0	0	4	0	5	0
k__Bacteria;p__Cyanobacteria	2118	535	1673	492	1641	4
k__Bacteria;p__Dadabacteria	13	0	7	0	14	0
k__Bacteria;p__Deferribacteres	0	38	0	52	13	0
k__Bacteria;p__Deinococcus-Thermus	14	3	6	0	9	0
k__Bacteria;p__Epsilonbacteraeota	0	168	16	577	43	0
k__Bacteria;p__Firmicutes	7929	20721	59270	27539	14961	33
k__Bacteria;p__Fusobacteria	12	0	41	9	11	7
k__Bacteria;p__Gemmatimonadetes	0	0	0	0	6	0
k__Bacteria;p__Kiritimatiellaeota	0	0	2	0	0	0
k__Bacteria;p__Nitrospirae	0	0	6	0	3	0
k__Bacteria;p__Patescibacteria	1625	10373	939	2379	2372	0
k__Bacteria;p__Planctomycetes	92	10	81	51	121	0
k__Bacteria;p__Proteobacteria	34442	25882	24467	12017	37236	149
k__Bacteria;p__Spirochaetes	12	74	15	62	33	0
k__Bacteria;p__Synergistetes	8	0	0	0	0	0

k__Bacteria;p__Tenericutes	69	187	24	223	92	0
k__Bacteria;p__Verrucomicrobia	0	15	40	1840	14237	5
k__Bacteria;__	3	5	0	2	10	0
Unassigned;__	9	5	2	6	13	0

5. Table S4 Class-level taxon distribution of the reads count obtained

#OTU ID	Control	DMH	DMH + Inulin	DMH + L. casei	DMH + L. casei + Inulin	Sequencing control
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria	1474	16268	1657	699	1469	98
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria	32955	9245	22747	11053	35361	39
k__Bacteria;p__Firmicutes;c__Bacilli	6147	11581	56006	20778	7576	22
k__Bacteria;p__Firmicutes;c__Clostridia	1372	7890	1608	4445	4986	11
k__Bacteria;p__Bacteroidetes;c__Bacteroidia	10577	54531	7161	39453	25101	17
k__Bacteria;p__Firmicutes;c__Negativicutes	315	380	760	552	142	0
k__Bacteria;p__Coprothermobacteraeota;c__Coprothermobacteria	0	0	4	0	5	0
k__Bacteria;p__Acidobacteria;c__Acidobacteriia	21	0	0	0	0	0
k__Bacteria;p__Acidobacteria;c__Blastocatellia (Subgroup 4)	0	0	0	0	4	0
k__Bacteria;p__Acidobacteria;c__Subgroup 6	0	0	0	0	9	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia	14	0	7	2	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria	702	286	1219	186	1038	12
k__Bacteria;p__Actinobacteria;c__Coriobacteriia	250	2003	245	753	835	0
k__Bacteria;p__Actinobacteria;c__Nitriliruptoria	0	0	0	2	0	0
k__Bacteria;p__Actinobacteria;c__Thermoleophilia	5	0	0	0	0	0

k__Bacteria;p__Chlamydiae;c__Chlamydiae	49	8	21	10	54	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae	6	0	0	0	14	0
k__Bacteria;p__Chloroflexi;c__Chloroflexia	3	0	0	7	24	0
k__Bacteria;p__Chloroflexi;c__Gitt-GS-136	7	3	5	0	0	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria	207	98	68	68	327	0
k__Bacteria;p__Cyanobacteria;c__Oxyphotobacteria	1911	437	1605	424	1314	4
k__Bacteria;p__Dadabacteria;c__Dadabacteriia	13	0	7	0	14	0
k__Bacteria;p__Deferribacteres;c__Deferribacteres	0	38	0	52	13	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci	14	3	6	0	9	0
k__Bacteria;p__Epsilonbacteraeota;c__Campylobacteria	0	168	16	577	43	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia	95	870	896	1764	2257	0
k__Bacteria;p__Fusobacteria;c__Fusobacteriia	12	0	41	9	11	7
k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes	0	0	0	0	6	0
k__Bacteria;p__Kiritimatiellaeota;c__Kiritimatiellae	0	0	2	0	0	0
k__Bacteria;p__Nitrospirae;c__Nitrospira	0	0	6	0	3	0
k__Bacteria;p__Patescibacteria;c__Saccharimonadia	1625	10373	939	2379	2372	0
k__Bacteria;p__Planctomycetes;c__Phycisphaerae	59	0	37	14	46	0
k__Bacteria;p__Planctomycetes;c__Planctomycetacia	33	10	44	37	75	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria	13	369	63	265	406	12
k__Bacteria;p__Spirochaetes;c__Spirochaetia	12	74	15	62	33	0
k__Bacteria;p__Synergistetes;c__Synergistia	8	0	0	0	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes	69	187	24	223	92	0
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae	0	15	40	1840	14237	5
k__Bacteria;__;__	3	5	0	2	10	0
Unassigned;__;__	9	5	2	6	13	0

6. Table S5 Order-level taxon distribution of the reads count obtained

#OTU ID	Control	DMH	DMH + Inulin	DMH + L. casei	DMH + L. casei + Inulin	Sequencing control
k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Solibacterales	21	0	0	0	0	0
k__Bacteria;p__Acidobacteria;c__Blastocatellia (Subgroup 4);o__11-24	0	0	0	0	4	0
k__Bacteria;p__Acidobacteria;c__Subgroup 6;__	0	0	0	0	9	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales	14	0	7	2	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales	20	0	120	0	16	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales	14	2	26	11	6	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales	138	176	333	36	451	12
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales	14	2	0	0	4	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales	369	76	526	93	397	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micromonosporales	8	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales	135	30	214	46	161	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Pseudonocardiales	4	0	0	0	3	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales	250	2003	245	753	835	0
k__Bacteria;p__Actinobacteria;c__Nitriliruptoria;o__Nitriliruptorales	0	0	0	2	0	0
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales	5	0	0	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales	10027	54235	6928	39298	24533	11
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales	53	40	67	49	118	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales	308	62	30	59	277	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales	97	165	77	24	105	3
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales	92	29	59	23	68	3

k__Bacteria;p__Chlamydiae;c__Chlamydiae;o__Chlamydiales	49	8	21	10	54	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Caldilineales	0	0	0	0	11	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__RBG-13-54-9	0	0	0	0	3	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;__	6	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Chloroflexales	3	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Thermomicrobiales	0	0	0	7	24	0
k__Bacteria;p__Chloroflexi;c__Gitt-GS-136;o__uncultured bacterium	7	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Gitt-GS-136;__	0	3	5	0	0	0
k__Bacteria;p__Coprothermobacteraeota;c__Coprothermobacteria;o__Coprothermobacterales	0	0	4	0	5	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Gastranaerophilales	37	56	2	29	90	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Obscuribacterales	170	42	66	39	237	0
k__Bacteria;p__Cyanobacteria;c__Oxyphotobacteria;o__Chloroplast	1911	437	1605	424	1314	4
k__Bacteria;p__Dadabacteria;c__Dadabacteriia;o__Dadabacteriales	13	0	7	0	14	0
k__Bacteria;p__Deferribacteres;c__Deferribacteres;o__Deferribacterales	0	38	0	52	13	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Deinococcales	0	0	6	0	4	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Thermales	14	3	0	0	5	0
k__Bacteria;p__Epsilonbacteraeota;c__Campylobacteria;o__Campylobacterales	0	168	16	577	43	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales	510	1002	53327	12389	3457	9
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales	5637	10579	2679	8389	4119	13
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales	1372	7890	1608	4445	4975	11
k__Bacteria;p__Firmicutes;c__Clostridia;o__DTU014	0	0	0	0	11	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales	95	870	896	1764	2257	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales	315	380	760	552	142	0
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales	12	0	41	9	11	7
k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales	0	0	0	0	6	0
k__Bacteria;p__Kiritimatiellaeota;c__Kiritimatiellae;o__WCHB1-41	0	0	2	0	0	0
k__Bacteria;p__Nitrospirae;c__Nitrospira;o__Nitrospirales	0	0	6	0	3	0

k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales	1625	10373	939	2379	2372	0
k__Bacteria;p__Planctomycetes;c__Phycisphaerae;o__Phycisphaerales	59	0	37	14	46	0
k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Gemmatales	29	10	44	37	75	0
k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Planctomycetales	4	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Acetobacterales	3	0	5	0	8	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales	254	76	119	109	242	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Dongiales	7	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Elsterales	26	14	21	7	19	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Holosporales	318	147	272	96	239	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Paracaedibacterales	0	0	0	0	13	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Reyranellales	15	0	13	5	22	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales	1003	394	677	634	1056	25
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales	532	117	282	11	47	4
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales	48	117	13	150	91	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales	33	55	33	123	36	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sneathiellales	67	7	79	42	82	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales	30627	8318	21204	9876	33493	10
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Tistrellales	8	0	13	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__uncultured	14	0	16	0	13	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales	3	0	0	0	3	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfarculales	10	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales	0	0	0	0	8	3
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales	0	367	56	265	387	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales	0	0	0	0	8	9
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__MBNT15	0	0	7	0	0	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales	0	2	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales	49	184	36	4	0	0

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales	14	34	0	0	4	2
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales	482	1259	450	259	367	81
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cardiobacteriales	0	0	0	0	5	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cellvibrionales	0	0	0	7	3	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Diplorickettsiales	0	10	15	0	6	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__EPR3968-O8a-Bc78	0	0	0	0	7	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales	225	27	69	238	115	5
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Gammaproteobacteria Incertae Sedis	53	11	31	15	46	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales	0	0	0	0	13	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales	14	3188	14	3	7	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Orbales	0	2	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales	5	34	144	7	20	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales	527	11462	826	166	798	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Salinisphaerales	18	0	14	0	37	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales	0	0	17	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales	83	57	33	0	37	10
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__uncultured	4	0	4	0	4	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;__	0	0	4	0	0	0
k__Bacteria;p__Spirochaetes;c__Spirochaetia;o__Spirochaetales	12	74	15	62	33	0
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales	8	0	0	0	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales	37	47	11	137	29	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Izimaplasmatales	0	38	0	0	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mollicutes RF39	10	85	3	40	58	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mycoplasmatales	22	17	10	46	5	0
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Opitutales	0	15	0	14	6	0
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Pedosphaerales	0	0	0	5	0	0

k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales	0	0	40	1821	14231	5
k__Bacteria;__;__;__	3	5	0	2	10	0
Unassigned;__;__;__	9	5	2	6	13	0

7. Table S6 Family-level taxon distribution of the reads count obtained

#OTU ID	Control	DMH	DMH + Inulin	DMH + L. casei	DMH + L. casei + Inulin	Sequencing control
k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Solibacterales;f__Solibacteraceae (Subgroup 3)	21	0	0	0	0	0
k__Bacteria;p__Acidobacteria;c__Blastocatellia (Subgroup 4);o__11-24;__	0	0	0	0	4	0
k__Bacteria;p__Acidobacteria;c__Subgroup 6;__;__	0	0	0	0	9	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__Iamiaceae	9	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__Ilumatobacteraceae	0	0	0	2	0	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__Microtrichaceae	2	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__uncultured	3	0	7	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae	20	0	120	0	16	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae	14	2	26	11	6	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae	118	176	320	36	310	5
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Dietziaceae	9	0	13	0	120	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Mycobacteriaceae	0	0	0	0	13	0

k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Nocardiaceae	11	0	0	0	8	7
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales;f__Cryptosporangiaceae	0	0	0	0	4	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales;f__Geodermatophilaceae	14	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales;__	0	2	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Brevibacteriaceae	16	0	0	6	24	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Cellulomonadaceae	0	0	25	0	15	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermabacteraceae	49	14	23	14	57	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermatophilaceae	7	0	5	0	7	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Intrasporangiaceae	72	11	18	22	109	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae	37	20	16	0	25	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae	175	27	433	51	148	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Ruaniaceae	5	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;__	8	4	6	0	12	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micromonosporales;f__Micromonosporaceae	8	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae	17	0	6	8	7	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae	118	30	208	38	154	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Pseudonocardiales;f__Pseudonocardiaceae	4	0	0	0	3	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae	39	343	64	164	170	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriales Incertae Sedis	0	11	0	5	13	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae	206	1498	128	470	559	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__uncultured	5	151	53	114	93	0
k__Bacteria;p__Actinobacteria;c__Nitriliruptoria;o__Nitriliruptorales;f__Nitriliruptoraceae	0	0	0	2	0	0
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae	5	0	0	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae	4137	6281	507	8192	5143	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__F082	0	13	0	13	0	0

k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae	94	1060	150	877	334	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae	4396	24922	5052	20220	13182	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae	0	0	0	0	4	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae	0	0	12	0	10	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae	595	7687	525	4098	2937	11
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prolixibacteraceae	0	0	0	0	9	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae	629	4554	346	3474	1463	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rs-E47 termite group	7	84	29	428	94	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae	161	9634	278	1996	1357	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;__	8	0	29	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae	53	40	67	49	107	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae	0	0	0	0	11	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Hymenobacteraceae	39	0	12	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Spirosomaceae	269	62	18	59	277	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae	41	147	26	16	42	3
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae	56	18	51	8	63	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__CMW-169	0	0	0	0	0	3
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Lentimicrobiaceae	13	0	0	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae	46	22	31	9	29	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__env.OPS 17	33	7	28	14	39	0
k__Bacteria;p__Chlamydiae;c__Chlamydiae;o__Chlamydiales;f__Chlamydiaceae	0	0	0	0	14	0
k__Bacteria;p__Chlamydiae;c__Chlamydiae;o__Chlamydiales;f__Simkaniaceae	49	8	21	10	40	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae	0	0	0	0	11	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__RBG-13-54-9;f__uncultured bacterium	0	0	0	0	3	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;__;__	6	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Chloroflexales;f__Chloroflexaceae	3	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Thermomicrobiales;f__JG30-KF-CM45	0	0	0	7	24	0

k__Bacteria;p__Chloroflexi;c__Gitt-GS-136;o__uncultured bacterium;f__uncultured bacterium	7	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Gitt-GS-136;__;__	0	3	5	0	0	0
k__Bacteria;p__Coprothermobacteraeota;c__Coprothermobacteria;o__Coprothermobacterales;f__Coprothermobacteraceae	0	0	4	0	5	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Gastranaerophilales;f__uncultured bacterium	0	19	0	15	55	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Gastranaerophilales;f__uncultured rumen bacterium	9	20	0	0	0	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Gastranaerophilales;__	28	17	2	14	35	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Obscuribacterales;f__uncultured bacterium	29	9	38	3	57	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Obscuribacterales;__	141	33	28	36	180	0
k__Bacteria;p__Cyanobacteria;c__Oxyphotobacteria;o__Chloroplast;f__Aegypius monachus (black vulture)	0	0	20	0	0	0
k__Bacteria;p__Cyanobacteria;c__Oxyphotobacteria;o__Chloroplast;f__Poterioochromonas sp. DS	1118	273	1325	303	518	0
k__Bacteria;p__Cyanobacteria;c__Oxyphotobacteria;o__Chloroplast;__	793	164	260	121	796	4
k__Bacteria;p__Dadabacteria;c__Dadabacteriia;o__Dadabacteriales;f__uncultured candidate division SBR1093 bacterium	13	0	7	0	14	0
k__Bacteria;p__Deferribacteres;c__Deferribacteres;o__Deferribacterales;f__Deferribacteraceae	0	38	0	52	13	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Deinococcales;f__Deinococcaceae	0	0	6	0	0	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Deinococcales;f__Trueperaceae	0	0	0	0	4	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Thermales;f__Thermaceae	14	3	0	0	5	0
k__Bacteria;p__Epsilonbacteraeota;c__Campylobacteria;o__Campylobacterales;f__Arcobacteraceae	0	0	5	0	0	0
k__Bacteria;p__Epsilonbacteraeota;c__Campylobacteria;o__Campylobacterales;f__Campylobacteraceae	0	0	7	0	0	0
k__Bacteria;p__Epsilonbacteraeota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae	0	168	4	577	43	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Alicyclobacillaceae	0	5	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae	84	38	51317	35	74	0

k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Family XI	16	0	114	12	13	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Family XII	18	0	13	4	17	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae	0	0	1173	12255	3	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae	52	15	69	32	2946	9
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae	340	944	636	49	404	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Thermoactinomycetaceae	0	0	5	2	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae	22	2575	94	16	62	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae	67	42	113	6	756	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae	8	20	0	23	9	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae	5179	5985	571	7530	2482	13
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae	13	5	18	5	10	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae	336	1952	1851	809	800	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;__	12	0	32	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae	20	3	4	3	6	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae 1	55	59	276	276	37	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae 4	0	0	6	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group	21	406	31	153	98	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Defluviitaleaceae	0	15	0	0	5	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XI	9	3	52	0	4	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XIII	3	3	13	13	30	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae	247	1145	169	786	879	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae	2	84	16	71	24	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae	22	209	65	68	287	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae	993	5963	976	3075	3605	11
k__Bacteria;p__Firmicutes;c__Clostridia;o__DTU014;f__uncultured bacterium	0	0	0	0	11	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae	95	870	896	1764	2257	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae	315	380	760	552	142	0

k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae	5	0	0	9	0	7
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae	7	0	41	0	11	0
k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae	0	0	0	0	6	0
k__Bacteria;p__Kiritimatiellaeota;c__Kiritimatiellae;o__WCHB1-41;f__uncultured bacterium	0	0	2	0	0	0
k__Bacteria;p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae	0	0	6	0	3	0
k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__Saccharimonadaceae	1625	10371	939	2377	2372	0
k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;__	0	2	0	2	0	0
k__Bacteria;p__Planctomycetes;c__Phycisphaerae;o__Phycisphaerales;f__Phycisphaeraceae	59	0	37	14	46	0
k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Gemmatales;f__Gemmataceae	29	10	44	37	75	0
k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Planctomycetales;f__uncultured	4	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Acetobacterales;f__Acetobacteraceae	3	0	5	0	8	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae	254	76	119	109	238	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Hyphomonadaceae	0	0	0	0	4	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Dongiales;f__Dongiaceae	7	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Elsterales;f__Elsteraceae	26	14	21	7	19	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Holosporales;f__Holosporaceae	318	147	272	96	239	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Paracaedibacterales;f__Paracaedibacteraceae	0	0	0	0	13	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Reyranellales;f__Reyranellaceae	15	0	13	5	22	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae	722	295	356	489	834	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Devosiaceae	3	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae	0	0	0	0	6	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Kaistiaceae	109	11	66	30	60	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Labraceae	7	5	0	4	10	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae	69	44	60	15	57	25

k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiales Incertae Sedis	0	0	0	5	2	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae	93	39	195	91	87	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae	532	117	282	11	47	4
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodopirillaceae	29	0	0	0	12	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae	0	0	6	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__uncultured	19	117	7	150	79	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__Mitochondria	17	19	16	30	18	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__uncultured	16	36	17	93	18	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sneathiellales;f__Sneathiellaceae	67	7	79	42	82	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae	30627	8318	21204	9876	33493	10
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Tistrellales;f__Geminicoccaceae	8	0	13	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__uncultured;__	14	0	16	0	13	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bacteriovoracaceae	0	0	0	0	3	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bdellovibrionaceae	3	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfarculales;f__Desulfarculaceae	10	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobulbaceae	0	0	0	0	8	3
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae	0	367	56	265	387	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Geobacteraceae	0	0	0	0	8	9
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__MBNT15;f__delta proteobacterium WX152	0	0	7	0	0	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Blfdi19	0	2	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae	49	184	36	4	0	0

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Alteromonadaceae	9	0	0	0	0	2
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Idiomarinaceae	0	34	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Marinobacteraceae	5	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae	0	0	0	0	4	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae	406	1233	261	239	346	72
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Hydrogenophilaceae	25	0	12	0	0	9
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Methylophilaceae	7	0	0	3	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Neisseriaceae	16	16	156	6	9	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Nitrosomonadaceae	28	5	21	11	8	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Rhodocyclaceae	0	0	0	0	4	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__TRA3-20	0	5	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cardiobacteriales;f__Cardiobacteriaceae	0	0	0	0	5	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cellvibrionales;f__Cellvibrionaceae	0	0	0	7	3	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Diplorickettsiales;f__Diplorickettsiaceae	0	10	15	0	6	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__EPR3968-O8a-Bc78;__	0	0	0	0	7	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae	225	27	69	238	115	5
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Gammaproteobacteria Incertae Sedis;f__Unknown Family	53	11	31	15	46	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae	0	0	0	0	13	0

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae	14	3188	14	3	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Pseudohongiellaceae	0	0	0	0	7	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Orbales;f__Orbaceae	0	2	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae	5	34	144	7	20	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae	220	10835	811	91	405	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae	307	627	15	75	393	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Salinisphaerales;f__Solimonadaceae	18	0	14	0	37	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Vibrionaceae	0	0	17	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae	18	0	0	0	0	4
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae	65	57	33	0	37	6
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__uncultured;f__metagenome	0	0	0	0	4	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__uncultured;__	4	0	4	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;__;__	0	0	4	0	0	0
k__Bacteria;p__Spirochaetes;c__Spirochaetia;o__Spirochaetales;f__Spirochaetaceae	12	74	15	62	33	0
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Synergistaceae	8	0	0	0	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales;f__Anaeroplasmataceae	37	47	11	137	29	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Izimaplasmatales;f__gut metagenome	0	38	0	0	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mollicutes RF39;f__metagenome	0	0	0	6	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mollicutes RF39;f__uncultured bacterium	0	59	0	21	25	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mollicutes RF39;__	10	26	3	13	33	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mycoplasmatales;f__Mycoplasmataceae	22	17	10	46	5	0
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Opitutales;f__Puniceicoccaceae	0	15	0	14	6	0
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Pedosphaerales;f__Pedosphaeraceae	0	0	0	5	0	0

k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae	0	0	40	1821	14231	5
k__Bacteria;__;__;__;__	3	5	0	2	10	0
Unassigned;__;__;__;__	9	5	2	6	13	0

8. Table S7 Genus-level taxon distribution of the reads count obtained

Taxa to genus level	Control	DMH	DMH + Inulin	DMH + L. casei	DMH + L. casei + Inulin	Sequencing control
k__Bacteria;p__Acidobacteria;c__Acidobacteriia;o__Solibacterales;f__Solibacteraceae (Subgroup 3);g__Bryobacter	21	0	0	0	0	0
k__Bacteria;p__Acidobacteria;c__Blastocatellia (Subgroup 4);o__11-24;__;__	0	0	0	0	4	0
k__Bacteria;p__Acidobacteria;c__Subgroup 6;__;__;__	0	0	0	0	9	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__Iamiaceae;g__Iamia	9	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__Ilumatobacteraceae;g__uncultured	0	0	0	2	0	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__Microtrichaceae;g__uncultured	2	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__uncultured;g__uncultured Acidimicrobidae bacterium	0	0	4	0	0	0

k__Bacteria;p__Actinobacteria;c__Acidimicrobiia;o__Microtrichales;f__uncultured;__	3	0	3	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Actinomyces	20	0	110	0	16	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Flaviflexus	0	0	7	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Actinomycetaceae;g__Varibaculum	0	0	3	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;g__Bifidobacterium	14	2	26	11	6	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium	0	0	0	0	48	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Corynebacterium 1	109	170	296	27	219	5
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Corynebacteriaceae;g__Lawsonella	9	6	24	9	43	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Dietziaceae;g__Dietzia	9	0	13	0	120	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Mycobacteriaceae;g__Mycobacterium	0	0	0	0	13	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Corynebacteriales;f__Nocardiaceae;g__Rhodococcus	11	0	0	0	8	7
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales;f__Cryptosporangiaceae;g__Fodinicola	0	0	0	0	4	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales;f__Geodermatophilaceae;g__Blastococcus	5	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales;f__Geodermatophilaceae;g__Geodermatophilus	9	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Frankiales;__;__	0	2	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Brevibacteriaceae;g__Brevibacterium	16	0	0	6	24	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Cellulomonadaceae;g__Actinotalea	0	0	13	0	15	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Cellulomonadaceae;g__Cellulomonas	0	0	12	0	0	0

k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermabacteraceae;g__Brachybacterium	49	14	23	14	53	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermabacteraceae;g__Dermabacter	0	0	0	0	4	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Dermatophilaceae;g__Piscicoccus	7	0	5	0	7	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Intrasporangiaceae;g__Aquipuribacter	0	0	5	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Intrasporangiaceae;g__Ornithinimicrobium	39	11	13	6	82	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Intrasporangiaceae;__	33	0	0	16	27	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Microbacteriaceae;g__Microbacterium	37	20	16	0	25	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Garicola	0	0	0	0	5	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Glutamicibacter	6	0	9	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Kocuria	106	18	36	34	92	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Micrococcus	50	0	143	17	24	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;g__Rothia	13	0	245	0	16	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Micrococcaceae;__	0	9	0	0	11	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;f__Ruaniaceae;g__Ruania	5	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micrococcales;__;__	8	4	6	0	12	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Micromonosporales;f__Micromonosporaceae;__	8	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae;g__Nocardioides	0	0	6	8	7	0

k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Nocardioidaceae;__	17	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Cutibacterium	118	30	208	38	136	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Propioniciclava	0	0	0	0	9	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Propionibacteriales;f__Propionibacteriaceae;g__Tessaracoccus	0	0	0	0	9	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Pseudonocardiales;f__Pseudonocardiaceae;g__Saccharomonospora	0	0	0	0	3	0
k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Pseudonocardiales;f__Pseudonocardiaceae;g__Saccharopolyspora	4	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae;g__Atopobium	0	0	7	3	0	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae;g__Coriobacteriaceae UCG-002	32	343	57	161	170	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Atopobiaceae;g__Olsenella	7	0	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriales Incertae Sedis;g__uncultured	0	11	0	5	13	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__DNF00809	0	10	15	14	0	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Enterorhabdus	193	1428	113	442	554	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;g__Parvibacter	0	26	0	0	0	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__Eggerthellaceae;__	13	34	0	14	5	0
k__Bacteria;p__Actinobacteria;c__Coriobacteriia;o__Coriobacteriales;f__uncultured;g__uncultured bacterium	5	151	53	114	93	0
k__Bacteria;p__Actinobacteria;c__Nitriliruptoria;o__Nitriliruptorales;f__Nitriliruptoraceae;g__uncultured Nitriliruptorales bacterium	0	0	0	2	0	0
k__Bacteria;p__Actinobacteria;c__Thermoleophilia;o__Solirubrobacterales;f__Solirubrobacteraceae;g__Parviterribacter	5	0	0	0	0	0

k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Bacteroides	4137	6281	507	8192	5143	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__F082;g__uncultured bacterium	0	13	0	13	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Butyricimonas	12	156	9	132	27	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinifilaceae;g__Odoribacter	82	904	141	745	307	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__Muribaculum	43	168	0	215	90	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__mouse gut metagenome	70	256	123	352	391	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__uncultured Bacteroidales bacterium	180	3810	405	748	548	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__uncultured Barnesiella sp.	0	0	14	38	57	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;g__uncultured bacterium	2313	15785	3579	13895	9306	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Muribaculaceae;__	1790	4903	931	4972	2790	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__Paludibacter	0	0	0	0	2	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Paludibacteraceae;g__uncultured	0	0	0	0	2	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas	0	0	12	0	10	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Alloprevotella	48	1927	228	172	39	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Paraprevotella	140	2025	19	555	516	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella	2	0	21	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella 1	0	0	2	0	0	0

k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella 2	0	0	6	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella 7	6	0	139	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella 9	0	0	0	0	0	11
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotellaceae UCG-001	370	2603	110	2609	1548	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotellaceae UCG-003	29	1132	0	762	834	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prolixibacteraceae;g__uncultured	0	0	0	0	9	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Alistipes	252	2604	143	1722	1022	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Rikenella	98	381	30	380	78	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;g__Rikenellaceae RC9 gut group	215	1398	155	1210	333	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae;__	64	171	18	162	30	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rs-E47 termite group;g__uncultured bacterium	7	84	29	428	94	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Tannerellaceae;g__Parabacteroides	161	9634	278	1996	1357	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;__;__	8	0	29	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Asinibacterium	14	15	28	24	59	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Sediminibacterium	39	25	34	25	46	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;g__Segetibacter	0	0	0	0	2	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Chitinophagaceae;__	0	0	5	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Chitinophagales;f__Saprospiraceae;g__uncultured	0	0	0	0	11	0

k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Hymenobacteraceae;g__Hymenobacter	28	0	10	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Hymenobacteraceae;g__Pontibacter	4	0	2	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Hymenobacteraceae;g__Rufibacter	7	0	0	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Cytophagales;f__Spirosomaceae;g__Arcicella	269	62	18	59	277	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Capnocytophaga	0	0	3	0	4	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Flavobacterium	0	0	12	0	0	3
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Gillisia	0	0	8	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Lutibacter	0	0	0	0	6	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Myroides	2	0	0	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Salegentibacter	24	0	0	0	6	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__Salinimicrobium	0	3	3	3	9	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;g__uncultured	15	144	0	13	9	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Flavobacteriaceae;__	0	0	0	0	8	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Bergeyella	0	0	0	0	16	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Chishuiella	27	0	5	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Chryseobacterium	16	13	19	8	27	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Cloacibacterium	13	0	15	0	3	0

k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Empedobacter	0	0	12	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Moheibacter	0	5	0	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;g__Ornithobacterium	0	0	0	0	14	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Flavobacteriales;f__Weeksellaceae;__	0	0	0	0	3	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__CMW-169;g__uncultured bacterium	0	0	0	0	0	3
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Lentimicrobiaceae;g__uncultured Owenweeksia sp.	13	0	0	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Mucilaginibacter	46	7	15	9	29	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__Sphingobacterium	0	0	16	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__Sphingobacteriaceae;g__uncultured	0	15	0	0	0	0
k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Sphingobacteriales;f__env.OPS 17;g__Tuber borchii symbiont b-17BO	33	7	28	14	39	0
k__Bacteria;p__Chlamydiae;c__Chlamydiae;o__Chlamydiales;f__Chlamydiaceae;g__Chlamydia	0	0	0	0	14	0
k__Bacteria;p__Chlamydiae;c__Chlamydiae;o__Chlamydiales;f__Simkaniaceae;g__uncultured	49	8	21	10	40	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__Caldilineales;f__Caldilineaceae;g__uncultured	0	0	0	0	11	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__RBG-13-54-9;f__uncultured bacterium;g__uncultured bacterium	0	0	0	0	3	0
k__Bacteria;p__Chloroflexi;c__Anaerolineae;__;__;__	6	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Chloroflexales;f__Chloroflexaceae;g__Candidatus Chloroploca	3	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Thermomicrobiales;f__JG30-KF-CM45;g__Paraburkholderia tropica	0	0	0	0	5	0
k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Thermomicrobiales;f__JG30-KF-CM45;g__uncultured bacterium	0	0	0	7	11	0

k__Bacteria;p__Chloroflexi;c__Chloroflexia;o__Thermomicrobiales;f__JG30-KF-CM45;__	0	0	0	0	8	0
k__Bacteria;p__Chloroflexi;c__Gitt-GS-136;o__uncultured bacterium;f__uncultured bacterium;g__uncultured bacterium	7	0	0	0	0	0
k__Bacteria;p__Chloroflexi;c__Gitt-GS-136;__;__;__	0	3	5	0	0	0
k__Bacteria;p__Coprothermobacteraeota;c__Coprothermobacteria;o__Coprothermobacterales;f__Coprothermobacteraceae;g__Coprothermobacter	0	0	4	0	5	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Gastranaerophilales;f__uncultured bacterium;g__uncultured bacterium	0	19	0	15	55	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Gastranaerophilales;f__uncultured rumen bacterium;g__uncultured rumen bacterium	9	20	0	0	0	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Gastranaerophilales;__;__	28	17	2	14	35	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Obscuribacterales;f__uncultured bacterium;g__uncultured bacterium	29	9	38	3	57	0
k__Bacteria;p__Cyanobacteria;c__Melainabacteria;o__Obscuribacterales;__;__	141	33	28	36	180	0
k__Bacteria;p__Cyanobacteria;c__Oxyphotobacteria;o__Chloroplast;f__Aegypius monachus (black vulture);g__Aegypius monachus (black vulture)	0	0	20	0	0	0
k__Bacteria;p__Cyanobacteria;c__Oxyphotobacteria;o__Chloroplast;f__Poterioochromonas sp. DS;g__Poterioochromonas sp. DS	1118	273	1325	303	518	0
k__Bacteria;p__Cyanobacteria;c__Oxyphotobacteria;o__Chloroplast;__;__	793	164	260	121	796	4
k__Bacteria;p__Dadabacteria;c__Dadabacteriia;o__Dadabacteriales;f__uncultured candidate division SBR1093 bacterium;g__uncultured	13	0	7	0	14	0
k__Bacteria;p__Deferribacteres;c__Deferribacteres;o__Deferribacterales;f__Deferribacteraceae;g__Mucispirillum	0	38	0	52	13	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus	0	0	6	0	0	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Deinococcales;f__Trueperaceae;g__Truepera	0	0	0	0	4	0
k__Bacteria;p__Deinococcus-Thermus;c__Deinococci;o__Thermales;f__Thermaceae;g__Meiothermus	14	3	0	0	5	0
k__Bacteria;p__Epsilonbacteraeota;c__Campylobacteria;o__Campylobacterales;f__Arcobacteraceae;g__Arcobacter	0	0	5	0	0	0

k__Bacteria;p__Epsilonbacteraeota;c__Campylobacteria;o__Campylobacterales;f__Campylobacteraceae;g__Campylobacter	0	0	7	0	0	0
k__Bacteria;p__Epsilonbacteraeota;c__Campylobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter	0	168	4	577	43	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Alicyclobacillaceae;g__Tumebacillus	0	5	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Aeribacillus	8	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Anaerobacillus	0	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Bacillus	58	9	51299	25	58	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Hydrogenibacillus	0	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Oceanobacillus	0	13	9	4	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Pseudogracilibacillus	15	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Ureibacillus	3	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__Virgibacillus	0	16	9	5	3	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;g__uncultured	0	0	0	0	6	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Bacillaceae;__	0	0	0	1	7	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Family XI;g__Gemella	16	0	114	12	13	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Family XII;g__Exiguobacterium	18	0	13	4	17	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae;g__Paenibacillus	0	0	1173	12255	3	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Chryseomicrobium	9	0	9	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Domibacillus	6	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Kurthia	19	12	8	14	35	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Lysinibacillus	9	3	4	0	0	9
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Planococcus	0	0	16	0	1700	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;g__Planomicrobium	0	0	0	0	33	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Planococcaceae;__	9	0	32	18	1178	0

k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Aliicoccus	0	0	0	0	27	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Jeotgalicoccus	20	101	11	5	14	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__S31	6	0	0	0	26	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Salinicoccus	62	8	14	10	131	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Staphylococcaceae;g__Staphylococcus	252	835	611	34	206	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Thermoactinomycetaceae;g__Novibacillus	0	0	0	2	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Thermoactinomycetaceae;g__uncultured	0	0	5	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Abiotrophia	0	0	0	0	2	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Aerococcus	0	699	27	16	38	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Eremococcus	9	0	10	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Facklamia	7	1832	55	0	22	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Aerococcaceae;g__Ignavigranum	6	44	2	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Alkalibacterium	34	12	16	6	71	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopococcus	0	0	0	0	8	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Atopostipes	2	30	3	0	9	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Desemzia	20	0	0	0	656	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Dolosigranulum	0	0	0	0	6	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Granulicatella	5	0	84	0	6	0

k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Marinilactibacillus	6	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Carnobacteriaceae;g__Trichococcus	0	0	10	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus	8	20	0	23	9	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus	5171	5985	568	7527	2482	13
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Pediococcus	8	0	3	3	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Leuconostoc	6	3	10	5	10	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Leuconostocaceae;g__Weissella	7	2	8	0	0	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus	87	1517	94	683	583	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus	249	435	1757	126	217	0
k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;__;__	12	0	32	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__Catabacter	5	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__Christensenellaceae R-7 group	9	0	4	3	6	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Christensenellaceae;g__uncultured	6	3	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae 1;g__Candidatus Arthromitus	0	5	0	2	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae 1;g__Clostridium sensu stricto 1	55	54	276	274	32	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae 1;g__Clostridium sensu stricto 12	0	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae 1;g__Proteiniclasticum	0	0	0	0	5	0

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae 4;g__Caminicella	0	0	6	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured Clostridia bacterium	0	24	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured Clostridiales bacterium	0	56	0	22	9	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;g__uncultured bacterium	18	306	26	102	78	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiales vadinBB60 group;__	3	20	5	29	11	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Defluviitaleaceae;g__Defluviitaleaceae UCG-011	0	15	0	0	5	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XI;g__Anaerococcus	2	3	32	0	4	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XI;g__Ezakiella	0	0	10	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XI;g__Finegoldia	0	0	8	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XI;g__Peptoniphilus	0	0	2	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XI;g__Tepidimicrobium	7	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XIII;g__Family XIII AD3011 group	3	3	0	6	5	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XIII;g__[Eubacterium] brachy group	0	0	13	7	9	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Family XIII;__	0	0	0	0	16	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Butyrivibrio 2	5	0	0	2	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Coprococcus 1	0	0	3	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Dorea	8	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Epulopiscium	3	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Hungatella	0	14	0	0	22	0

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoanaerobaculum	0	0	3	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnoclostridium	0	5	0	5	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospiraceae NK4A136 group	91	436	107	437	149	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Lachnospiraceae XPB1014 group	0	0	6	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Tyzzerella	0	0	0	22	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Bacteroides] pectinophilus group	0	4	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Eubacterium] hallii group	0	0	0	0	4	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Eubacterium] ruminantium group	0	0	6	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Eubacterium] xylanophilum group	16	65	8	54	51	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__[Ruminococcus] torques group	7	94	4	8	258	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;__	117	527	32	258	395	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__uncultured	2	84	16	71	24	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Paeniclostridium	6	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptoclostridium	6	2	0	0	16	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Peptostreptococcus	3	0	4	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Proteocatella	0	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptostreptococcaceae;g__Romboutsia	7	207	61	68	271	0

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Anaerotruncus	0	0	0	0	3	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Butyricicoccus	6	0	0	0	8	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Candidatus Soleaferrea	4	0	0	4	6	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Faecalibacterium	0	0	10	0	8	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Fournierella	6	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__GCA-900066225	0	5	3	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Intestinimonas	0	75	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Oscillibacter	32	99	9	36	18	7
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Papillibacter	0	11	5	34	18	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium	0	15	0	0	18	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 1	0	33	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 5	18	304	6	76	34	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 6	0	55	3	5	9	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminiclostridium 9	15	185	0	96	16	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae NK4A214 group	6	22	3	17	25	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae UCG-002	5	0	0	0	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae UCG-004	11	19	88	6	0	0

k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae UCG-005	7	19	2	0	10	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae UCG-007	0	0	0	15	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae UCG-009	0	18	3	11	0	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae UCG-010	32	286	42	112	136	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae UCG-013	56	193	27	179	85	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcaceae UCG-014	308	2555	557	1361	2029	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcus 1	6	114	9	75	51	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcus 2	0	0	0	0	7	4
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__[Eubacterium] coprostanoligenes group	29	246	51	80	217	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__uncultured	39	607	2	156	44	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;__	413	1102	156	812	863	0
k__Bacteria;p__Firmicutes;c__Clostridia;o__DTU014;f__uncultured bacterium;g__uncultured bacterium	0	0	0	0	11	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Candidatus Stoquefichus	11	0	0	21	50	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Dubosiella	0	0	414	165	0	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Erysipelatoclostridium	13	74	0	45	49	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Erysipelotrichaceae UCG-002	0	0	4	0	0	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Faecalibaculum	0	6	0	0	4	0

k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Faecalitalea	0	0	0	0	6	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Solobacterium	0	0	9	0	0	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Turicibacter	0	681	465	1094	1841	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__[Clostridium] innocuum group	0	2	0	0	0	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;g__uncultured	24	31	4	27	55	0
k__Bacteria;p__Firmicutes;c__Erysipelotrichia;o__Erysipelotrichales;f__Erysipelotrichaceae;__	47	76	0	412	252	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Dialister	0	0	13	0	0	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Megasphaera	3	0	21	0	0	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Quinella	262	330	9	488	96	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Selenomonas 3	0	0	7	0	0	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Selenomonas 4	0	0	4	0	0	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__Veillonella	50	50	699	64	46	0
k__Bacteria;p__Firmicutes;c__Negativicutes;o__Selenomonadales;f__Veillonellaceae;g__uncultured	0	0	7	0	0	0
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Fusobacteriaceae;g__Fusobacterium	5	0	0	9	0	7
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__Leptotrichia	0	0	41	0	11	0
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;f__Leptotrichiaceae;g__Streptobacillus	7	0	0	0	0	0
k__Bacteria;p__Gemmatimonadetes;c__Gemmatimonadetes;o__Gemmatimonadales;f__Gemmatimonadaceae;__	0	0	0	0	6	0

k__Bacteria;p__Kiritimatiellaeota;c__Kiritimatiellae;o__WCHB1-41;f__uncultured bacterium;g__uncultured bacterium	0	0	2	0	0	0
k__Bacteria;p__Nitrospirae;c__Nitrospira;o__Nitrospirales;f__Nitrospiraceae;g__Nitrospira	0	0	6	0	3	0
k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__Saccharimonadaceae;g__Candidatus Saccharimonas	1620	10369	933	2371	2347	0
k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__Saccharimonadaceae;g__uncultured Candidatus Saccharibacteria bacterium	0	0	3	0	0	0
k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__Saccharimonadaceae;g__uncultured bacterium	0	0	0	6	18	0
k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;f__Saccharimonadaceae;__	5	2	3	0	7	0
k__Bacteria;p__Patescibacteria;c__Saccharimonadia;o__Saccharimonadales;__;__	0	2	0	2	0	0
k__Bacteria;p__Planctomycetes;c__Phycisphaerae;o__Phycisphaerales;f__Phycisphaeraceae;g__SM1A02	59	0	37	14	46	0
k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Gemmatales;f__Gemmataceae;g__Gemmata	29	3	36	37	69	0
k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Gemmatales;f__Gemmataceae;g__uncultured	0	7	8	0	6	0
k__Bacteria;p__Planctomycetes;c__Planctomycetacia;o__Planctomycetales;f__uncultured;g__uncultured bacterium	4	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Acetobacterales;f__Acetobacteraceae;g__Gluconobacter	3	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Acetobacterales;f__Acetobacteraceae;g__uncultured	0	0	5	0	8	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Brevundimonas	128	40	29	50	85	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;g__Caulobacter	126	36	90	59	153	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Hyphomonadaceae;g__Hyphomonas	0	0	0	0	4	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Dongiales;f__Dongiaceae;g__Dongia	7	0	0	0	0	0

k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Elsterales;f__Elsteraceae;g__Elstera	0	2	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Elsterales;f__Elsteraceae;g__uncultured	26	12	21	7	19	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Holosporales;f__Holosporaceae;g__uncultured	318	147	272	96	239	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Paracaedibacterales;f__Paracaedibacteraceae;g__uncultured	0	0	0	0	13	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Reyranellales;f__Reyranellaceae;g__Reyranella	15	0	13	5	22	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Bosea	6	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Methylobacterium	712	289	339	489	834	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Methylocystis	0	0	10	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__Microvirga	4	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Beijerinckiaceae;g__alphaI cluster	0	6	7	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Devosiaceae;g__Devosia	3	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Hyphomicrobiaceae;g__Pedomicrobium	0	0	0	0	6	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Kaistiaceae;g__Kaistia	109	11	66	30	60	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Labraceae;g__Labrys	7	5	0	4	10	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	18	14	15	0	14	14
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Aminobacter	0	5	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Mesorhizobium	8	13	17	13	30	0

k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Ochrobactrum	43	0	28	0	13	11
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Paenochrobactrum	0	12	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__uncultured	0	0	0	2	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiales Incertae Sedis;g__Nordella	0	0	0	0	2	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiales Incertae Sedis;g__uncultured	0	0	0	5	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Bradyrhizobium	82	39	195	91	80	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__Xanthobacter	11	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Xanthobacteraceae;g__uncultured	0	0	0	0	7	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Amaricoccus	0	0	8	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Palleronia	0	0	0	0	7	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus	532	117	274	11	20	4
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Rubellimicrobium	0	0	0	0	10	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__uncultured	0	0	0	0	5	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;__	0	0	0	0	5	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodopirillaceae;g__Defluviicoccus	29	0	0	0	12	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__Rhodospirillaceae;g__Candidatus Riegeria	0	0	6	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__uncultured;g__gut metagenome	7	28	0	0	0	0

k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__uncultured;g__uncultured bacterium	12	89	7	150	15	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;f__uncultured;__	0	0	0	0	64	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__Mitochondria;g__uncultured alpha proteobacterium	0	9	0	11	6	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__Mitochondria;__	17	10	16	19	12	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__uncultured;g__uncultured alpha proteobacterium	0	0	0	67	18	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__uncultured;g__uncultured bacterium	3	10	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;f__uncultured;__	13	26	17	26	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sneathiellales;f__Sneathiellaceae;g__Taonella	67	7	79	42	82	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Blastomonas	26	10	0	0	33	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Novosphingobium	30170	8210	20920	9750	33073	2
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingobium	82	44	135	57	98	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Sphingomonas	349	54	145	69	289	8
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;__	0	0	4	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Tistrellales;f__Geminicoccaceae;g__Geminicoccus	8	0	13	0	0	0
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__uncultured;__;__	14	0	16	0	13	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bacteriovoracaceae;g__Peredibacter	0	0	0	0	3	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bdellovibrionaceae;g__OM27 clade	3	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfarculales;f__Desulfarculaceae;g__uncultured	10	0	0	0	0	0

k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobulbaceae;g__Desulfobulbus	0	0	0	0	5	3
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfobacterales;f__Desulfobulbaceae;g__Desulfofustis	0	0	0	0	3	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Bilophila	0	6	6	6	0	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Desulfovibrio	0	238	40	96	61	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__Lawsonia	0	0	10	61	315	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__uncultured	0	123	0	102	11	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfuromonadales;f__Geobacteraceae;g__Geobacter	0	0	0	0	8	9
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__MBNT15;f__delta proteobacterium WX152;g__delta proteobacterium WX152	0	0	7	0	0	0
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Blfdi19;__	0	2	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Aeromonas	49	0	36	4	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Aeromonadales;f__Aeromonadaceae;g__Oceanimonas	0	184	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Alteromonadaceae;g__Rheinheimera	6	0	0	0	0	2
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Alteromonadaceae;__	3	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Idiomarinaceae;g__Aliidiomarina	0	22	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Idiomarinaceae;g__Idiomarina	0	12	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Marinobacteraceae;g__Marinobacter	5	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__Shewanellaceae;g__Shewanella	0	0	0	0	4	0

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__AAP99	0	2	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Achromobacter	77	17	16	12	34	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Aquabacterium	14	0	22	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Burkholderia-Caballeronia-Paraburkholderia	117	33	77	34	87	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Candidatus Tremblaya	0	0	0	0	5	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Comamonas	0	0	0	0	10	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Cupriavidus	0	0	0	5	8	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Delftia	58	10	17	10	51	43
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Duganella	0	0	0	0	7	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Herbaspirillum	52	0	14	0	19	26
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Janthinobacterium	23	0	0	0	25	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Lautropia	0	0	4	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Massilia	0	0	9	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Oligella	4	810	28	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Paenalcaligenes	0	125	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Parasutterella	0	202	68	156	31	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Pelistega	0	0	0	0	5	0

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Pelomonas	44	0	0	11	27	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Pseudacidovorax	0	0	6	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Pusillimonas	0	16	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__Ralstonia	0	0	0	0	0	3
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;g__uncultured	0	7	0	11	6	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Burkholderiaceae;__	17	11	0	0	31	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Hydrogenophilaceae;g__Tepidiphilus	25	0	12	0	0	9
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Methylophilaceae;g__Methylophilus	0	0	0	3	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Methylophilaceae;__	7	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Neisseriaceae;g__Eikenella	0	7	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Neisseriaceae;g__Neisseria	16	9	149	6	9	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Neisseriaceae;g__uncultured	0	0	7	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Nitrosomonadaceae;g__DSSD61	28	5	21	11	8	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__Rhodocyclaceae;g__Thauera	0	0	0	0	4	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Betaproteobacteriales;f__TRA3-20;__	0	5	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cardiobacteriales;f__Cardiobacteriaceae;g__uncultured	0	0	0	0	5	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cellvibrionales;f__Cellvibrionaceae;g__Cellvibrio	0	0	0	7	0	0

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Cellvibrionales;f__Cellvibrionaceae;g__uncultured	0	0	0	0	3	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Diplorickettsiales;f__Diplorickettsiaceae;g__Rickettsiella	0	10	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Diplorickettsiales;f__Diplorickettsiaceae;g__uncultured	0	0	15	0	6	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__EPR3968-O8a-Bc78;__;__	0	0	0	0	7	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Enterobacter	28	15	0	2	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Escherichia-Shigella	44	12	18	12	34	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Klebsiella	25	0	0	6	11	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Pantoea	8	0	0	0	13	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Pectobacterium	0	0	7	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Proteus	5	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;g__Serratia	7	0	3	0	5	5
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae;__	108	0	41	218	52	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Gammaproteobacteria Incertae Sedis;f__Unknown Family;g__Acidibacter	53	11	31	15	46	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae;g__Legionella	0	0	0	0	13	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Chromohalobacter	0	0	0	3	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Halomonadaceae;g__Halomonas	14	3188	14	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Pseudohongiellaceae;g__Pseudohongiella	0	0	0	0	7	0

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Orbales;f__Orbaceae;g__Gilliamella	0	2	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Aggregatibacter	0	0	43	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Haemophilus	5	0	92	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae;g__Rodentibacter	0	34	9	7	20	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Acinetobacter	176	46	250	34	200	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Enhydrobacter	16	0	19	0	11	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Psychrobacter	28	10789	535	57	194	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;__	0	0	7	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae;g__Pseudomonas	307	627	15	75	393	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Salinisphaerales;f__Solimonadaceae;g__Hydrocarboniphaga	18	0	14	0	37	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Vibrionales;f__Vibrionaceae;g__Vibrio	0	0	17	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__Rhodanobacter	12	0	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Rhodanobacteraceae;g__uncultured	6	0	0	0	0	4
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Luteimonas	0	0	0	0	11	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Lysobacter	0	44	3	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Pseudoxanthomonas	0	0	0	0	9	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__Stenotrophomonas	65	0	30	0	17	6

k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae;g__uncultured	0	13	0	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__uncultured;f__metagenome;g__metagenome	0	0	0	0	4	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__uncultured;__;__	4	0	4	0	0	0
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;__;__;__	0	0	4	0	0	0
k__Bacteria;p__Spirochaetes;c__Spirochaetia;o__Spirochaetales;f__Spirochaetaceae;g__Treponema 2	8	0	10	33	24	0
k__Bacteria;p__Spirochaetes;c__Spirochaetia;o__Spirochaetales;f__Spirochaetaceae;__	4	74	5	29	9	0
k__Bacteria;p__Synergistetes;c__Synergistia;o__Synergistales;f__Synergistaceae;g__JGI-0000079-D21	8	0	0	0	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales;f__Anaeroplasmataceae;g__Anaeroplasma	37	47	11	137	29	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Izimaplasmatales;f__gut metagenome;g__gut metagenome	0	38	0	0	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mollicutes RF39;f__metagenome;g__metagenome	0	0	0	6	0	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mollicutes RF39;f__uncultured bacterium;g__uncultured bacterium	0	59	0	21	25	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mollicutes RF39;__;__	10	26	3	13	33	0
k__Bacteria;p__Tenericutes;c__Mollicutes;o__Mycoplasmatales;f__Mycoplasmataceae;g__Mycoplasma	22	17	10	46	5	0
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Opitutales;f__Puniceicoccaceae;g__uncultured	0	15	0	14	6	0
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Pedosphaerales;f__Pedosphaeraceae;__	0	0	0	5	0	0
k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia	0	0	40	1821	14231	5
k__Bacteria;__;__;__;__;__	3	5	0	2	10	0
Unassigned;__;__;__;__;__	9	5	2	6	13	0

9. References

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