SUPPLEMENTAL TABLES AND FIGURE

Role of Bile Acids and GLP-1 in Mediating the Metabolic Improvements of Bariatric Surgery

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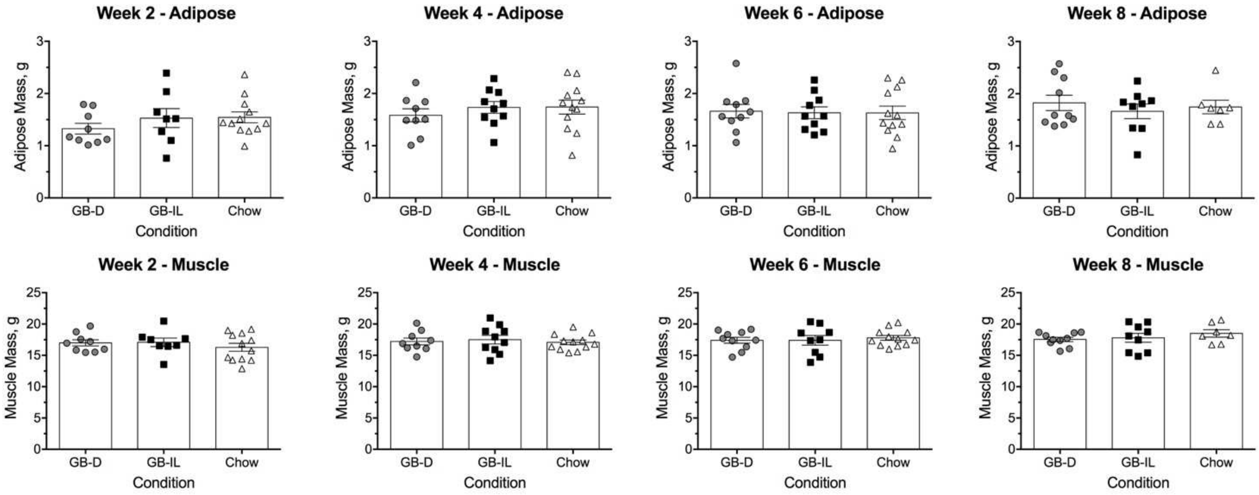
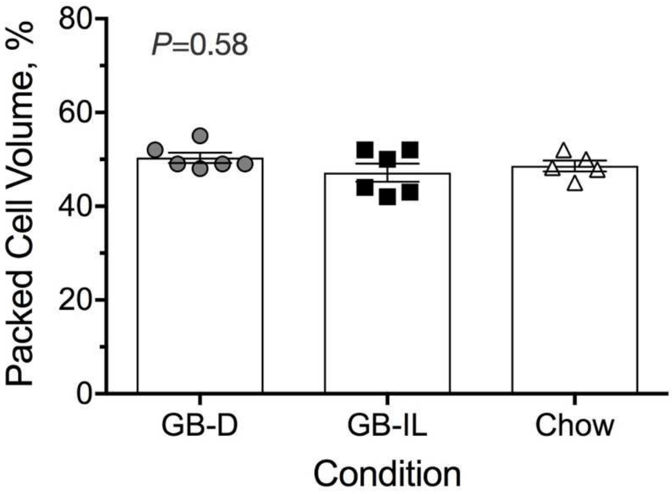
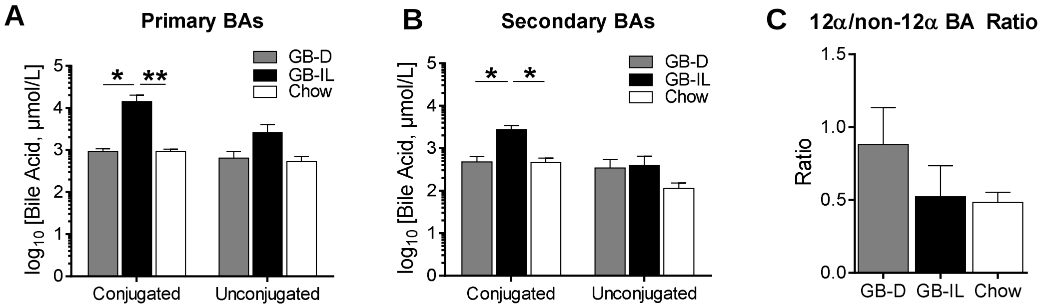
Supplemental Figures



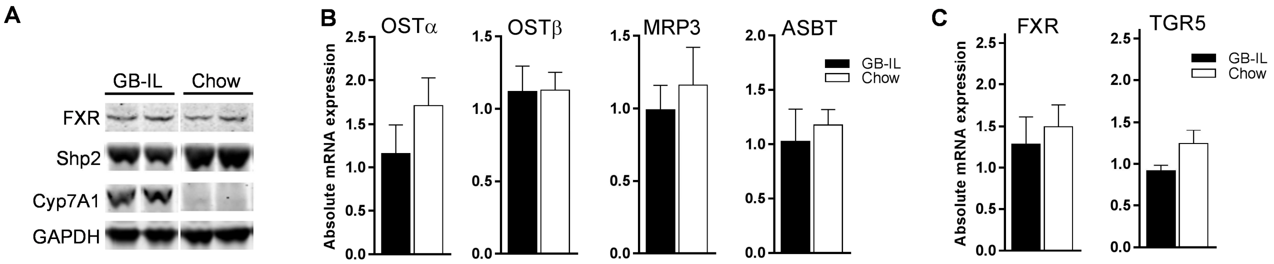
Supplemental Figure 1. Non-invasive measurement of body composition longitudinally in mouse cohorts. Chronically bile diverted animals or chow controls had body composition (adipose and muscle mass) measured at 2, 4, 6, and 8 weeks postoperative. Individual data are represented with underlying bar graphs representing the mean ± standard error. Data was analyzed using the Kruskal-Wallis test adjusted for multiplicity (n=9 GB-D, 8 GB-IL, 12 Chow).



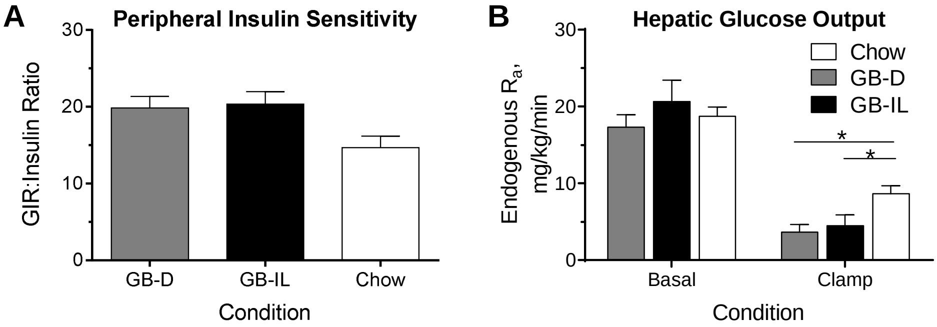
Supplemental Figure 2. Packed cell volumes in postoperative mice. Chronically bile diverted animals or chow controls had packed cell volumes (%) measured at four weeks. Individual data are represented with underlying bar graphs representing the mean ± standard error. Data was analyzed using the Kruskal-Wallis test adjusted for multiple comparisons (n = 6 GB-D, 6 GB-IL, 5 Chow).



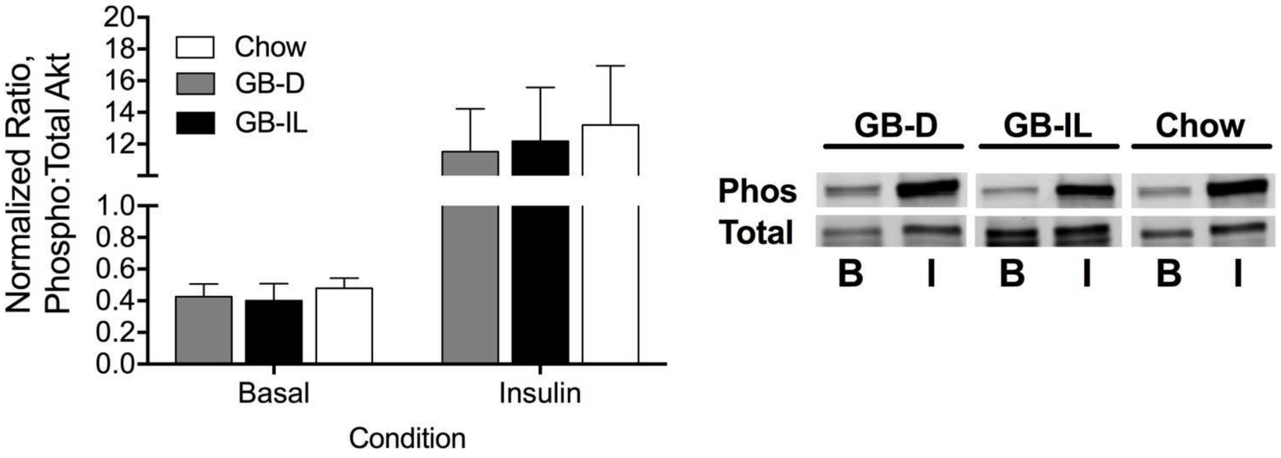
Supplemental Figure 3. Plasma bile acid responses after chronic bile diversion surgery. Mice underwent bile diversion (GB-IL), sham diversion (GB-D), or no operation (Chow) and subsequently euthanized at 8 weeks for biochemical and tissue analysis. (**A**) Total plasma bile acids (BAs), (**A**) primary conjugated and unconjugated BAs, (**B**) secondary conjugated and unconjugated BAs were measured and (**C**) the 12α-hydroxylated/non-12α-hydroxylated bile acid ratio was calculated. Data are represented as the mean ± SE. Statistical analysis using Kruskal-Wallis test adjusted for multiplicity was used on sample sizes. (n=6 GB-D, 6 GB-IL, and 7 Chow mice per group). *$P<0.05$, **$P< 0.01$.



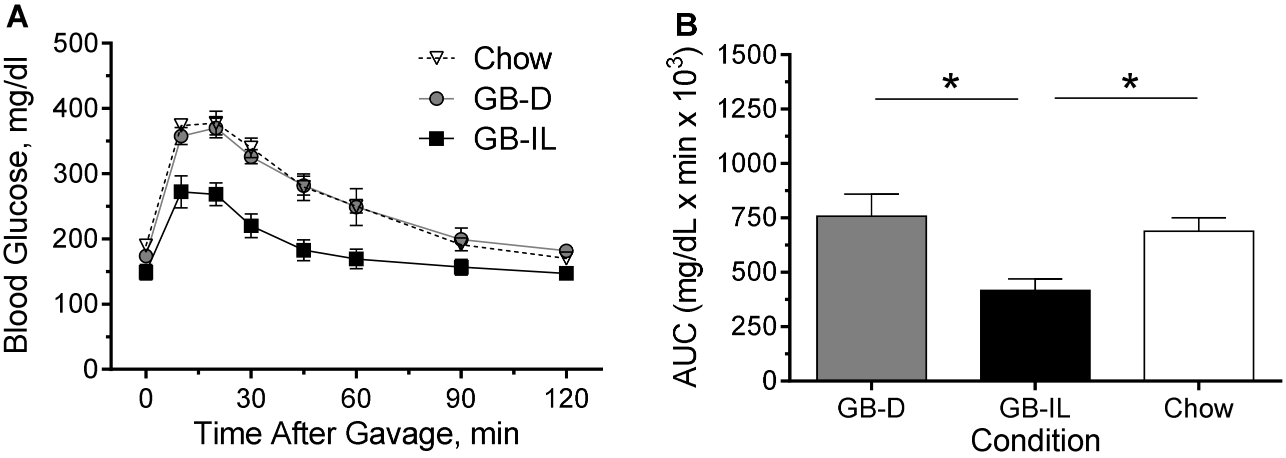
Supplemental Figure 4. Hepatic bile acid signaling and ileum gene expression profiles after bile diversion surgery. (**A**) Relative liver protein expression was measured for BA signaling (Fxr, Shp) and synthetic markers (Cyp7a1) at 8 weeks postoperative. Ileum mRNA levels of (**B**) basolateral (OSTα and OSTβ) and apical (ASBT, MRP3) bile acid transporters as well as (**C**) bile acid receptors (Fxr and Tgr5) were measured in the ileum of GB-IL and Chow mice. Data are represented as the mean ± SEM. (**A**-**C**) n=8 per group**.** Statistical analysis of Chow, GB-D and GB-IL groups using Student's *t*-test.



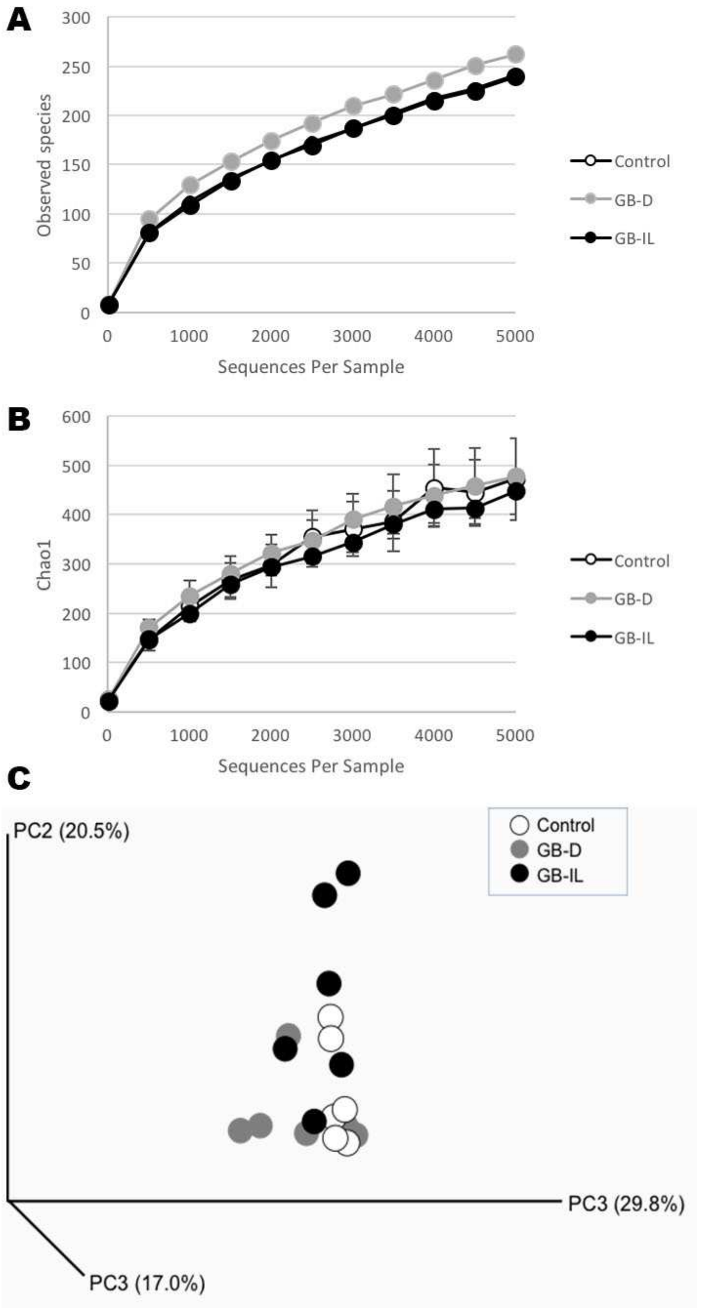
Supplemental Figure 5. Peripheral insulin sensitivity and hepatic glucose production in bile diverted animals. (**A**) The ratio of glucose infusion rate to average plasma insulin concentration at steady-state (M/I) is a surrogate of peripheral insulin sensitivity. (**B**) The endogenous rate of glucose appearance, R_a, which is equal to hepatic glucose output during clamp conditions was calculated from tracer-derived parameters. Data are represented as the mean ± SE. Statistical analysis using Kruskal-Wallis test adjusted for multiplicity was used on sample sizes (**A-B**) 8 GB-D, 6 GB-IL, 8 Chow. Asterisk (*) indicates $P<0.05$ of the comparison marked by a horizontal bar.



Supplemental Figure 6. Basal and insulin-stimulated skeletal muscle Akt signaling. A separate cohort of mice was studied at four weeks postoperative for the response to a maximally-stimulating dose of intravenous insulin in an effort to unmask an alteration in skeletal muscle insulin signaling in response to chronically elevated bile acids. Following rapid induction of anesthesia (3% isoflurane), the right gastrocnemius was harvested and then the abdomen was opened on the midline and twenty units of regular insulin were injected into the inferior vena cava. The left gastrocnemius was harvested at three minutes post-injection. Both skeletal muscle samples were immediately freeze clamped upon harvesting and subsequently processed for investigation of Akt phosphorylation status. Statistical analysis using Kruskal-Wallis test adjusted for multiple comparisons was used on the following sample sizes (7 GB-D, 5 GB-IL, 5 Chow).



Supplemental Figure 7. Glucose tolerance following chronic bile diversion. C57/BL6 mice that received bile diversion to the duodenum (GB-D) or ileum (GB-IL) underwent an oral glucose tolerance test at 8 weeks postoperative (*n* =12 WT; *n* =7 GB-D; and *n* =7 GB-IL). (A) Blood glucose was measured after a gavage of 20% (w/w) glucose and plasma glucose was measured at baseline, 10, 20, 30, 45, 60, 90 and 120 min. (B) Data are represented as mean ± SEM. **P*<0.05.



Supplemental Figure 8. Fecal microbiome phenotypes of lean mice subjected to bile diversion. Cecal contents were obtained 8 weeks after surgery. Microbial diversity was analyzed by bacterial tag encoded FLX amplicon pyrosequencing (bTEFAP) using a Roche 454 pyrosequencer and titanium reagents, and 3-5k nominal sequences per sample of high quality extracted DNA. (**A**) Rarefaction curves (OTU at sequences dissimilarity cutoff < 3%). Rarefaction curves were calculated for OTUs and indicated that the analysis neared plateau but could benefit from additional sequencing. (**B**) Chao1 estimates of gut microbial diversity. (**C**) Principal component analysis indicating relative microbiome variance (n=6 per group).

Supplemental Table 1.

Supplemental Table 1. Bile Acid Species Concentrations in Postoperative Mice.

Bile Acid Species	Condition		
	GB-D	GB-IL	Chow
tauro-omega-muricholic acid	490 ± 70	3128 ± 1172**	483 ± 76††
alpha-muricholic acid	107 ± 25	310 ± 96	138 ± 38
tauro-alpha-muricholic acid	108 ± 49	1104 ± 349*	88 ± 25†
beta-muricholic acid	112 ± 50	436 ± 174	153 ± 54
tauro-beta-muricholic acid	225 ± 37	8569 ± 3997*	229 ± 49†
ursodeoxycholic acid	70 ± 31	133 ± 89	59 ± 24
tauro-ursodeoxycholic acid	25 ± 6	180 ± 86*	20 ± 4†
hyodeoxycholic acid	36 ± 14	135 ± 73	82 ± 30
tauro-hyodeoxycholic acid	48 ± 8	531 ± 197*	75 ± 16†
cholic acid	362 ± 202	1712 ± 1126	223 ± 69
tauro-cholic acid	74 ± 24	1097 ± 332*	67 ± 20†
chenodeoxycholic acid	59 ± 21	141 ± 92	76 ± 25
tauro-chenodeoxycholic acid	31 ± 10	312 ± 171**	36 ± 7†
deoxycholic acid	274 ± 207	259 ± 176	54 ± 21
tauro-deoxycholic acid	391 ± 164	1998 ± 620	354 ± 119
tauro-lithocholic acid	11 ± 0.2	15 ± 2	13 ± 0.7

Note: All concentrations are µM, data are represented as the mean ± standard error (n=6 GB-D, 6 GB-IL, 7 Chow). Significant differences between GB-IL and GB-D are indicated with asterisks (**P* <0.05, ***P* <0.001) and differences between GB-IL and Chow are indicated with crosses (†*P* <0.05, ††*P* <0.001). Bile acid concentrations were non-normally distributed and statistical analysis was completed with the Kruskal-Wallis test with adjustments for multiple comparisons.

Supplemental Table 2.

Supplementary Table 2. Tissue Glucose Uptake during Euglycemic Conditions in Bile Diversion

Tissue	**Condition**		
	Chow	**GB-D**	**GB-IL**
Gastrocnemius	7.1 ± 0.7	11.1 ± 1.9	13.2 ± 3.0
Soleus	47.8 ± 9.5	55.8 ± 10.1	76.3 ± 13.2
Vastus Lateralis	7.6 ± 0.6	9.6 ± 1.8	6.4 ± 0.7
Heart	354.3 ± 8.5	341.0 ± 26.2	394.7 ± 41.4
Perigonadal Adipose	3.9 ± 0.8	3.1 ± 0.4	4.8 ± 0.8
Subcutaneous Adipose	10.4 ± 2.2	11.7 ± 2.1	16.9 ± 3.2
Brown Adipose	192.6 ± 17.4	176.8 ± 32.4	181.6 ± 21.7
Duodenum	13.9 ± 3.0	10.7 ± 0.9	13.5 ± 1.5
Jejunum	13.3 ± 1.6	13.8 ± 1.2	16.5 ± 1.5
Ileum	16.0 ± 1.3	19.3 ± 1.3	19.0 ± 1.9
Brain	49.6 ± 2.8	55.0 ± 4.9	58.8 ± 3.7

Note: Units are µmol/min/100g tissue, data are represented as the mean ± standard error (n=8 GB-D, 6 GB-IL, 8 Chow). Rates of tissue glucose uptake were non-normally distributed and statistical analysis was completed with the Kruskal-Wallis test with adjustments for multiple comparisons. No significant differences in tissue glucose uptake were observed among any tissues.

Supplemental Table 3. OTU Table for Cecal Microbiome Analysis

	Control						GB-IL						GB-D					
	1	2	3	4	5	6	1	2	3	4	5	6	1	2	3	4	5	6
OTU Table																		
p_Crenarchaeota;c_MCG`;o_pGrfC26;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Crenarchaeota;c_Thaumarchaeota;o_Nitrososphaerales;f_Nitrososphaeraceae;g_Candidatus Nitrososphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.59E-05	0	0
p_Euryarchaeota;c_Methanobacteria;o_Methanobacteriales;f_Methanobacteriaceae;g_Methanobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Euryarchaeota;c_Methanomicrobia;o_Methanocellales;f_Methanocellaceae;g_Methanocella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Euryarchaeota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanomicrobiaceae;g_Methanoculleus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Euryarchaeota;c_Methanomicrobia;o_Methanosarcinales;f_Methanosaetaceae;g_Methanosaeta	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Euryarchaeota;c_Thermoplasmata;o_E2;f_[Methanomassiliicoccaceae];g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bacteria																		
p_Acidobacteria;c_Acidobacteria-6;o_iii1-15;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000135	0	0
p_Acidobacteria;c_Acidobacteria-6;o_iii1-15;f_mb2424;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Acidobacteria;c_BPC102;o_MVS-40;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Acidobacteria;c_Solibacteres;o_Solibacterales;Other;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Acidimicrobiia;o_Acidimicrobiales;f_Microthrixaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Trueperella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Beutenbergiaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Beutenbergiaceae;g_Salana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Actinotalea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Cellulomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Demequina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Corynebacteriaceae;g_Corynebacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Dermabacteraceae;g_Brachybacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Frankiaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Gordoniaceae;g_Gordonia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kineosporiaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kineosporiaceae;g_Kineococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Agromyces	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Cryocola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Curtobacterium	0	0	0	0	0	3.70E-05	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Frigoribacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Leucobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Microbacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Salinibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Arthrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Rothia	0	0	0	0	0	0	0	0	0	0	0	0	0	6.11E-06	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Mycobacteriaceae;g_Mycobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae;g_Rhodococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_Aeromicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_Nocardioides	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_Cellulosimicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_Promicromonospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Actinomycetospora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Pseudonocardia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Saccharopolyspora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;g_Thermobispora	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Streptomycetaceae;g_Streptomyces	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Streptosporangiaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Thermomonosporaceae;g_Actinomadura	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium	1.54E-05	0.002744	2.85E-05	3.18E-05	0.001142	0	0.002845	0.002984	0.002898	0	0.001887	0	7.76E-05	0.000128	0.000923	1.59E-05	9.91E-06	1.01E-05
p_Actinobacteria;c_Actinobacteria;o_Micrococcales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3.18E-05	0	0
p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_	0.000308	0.002082	0.000124	0.000414	8.92E-05	6.17E-05	0.000102	0.000246	0.000366	0.000468	0.003791	2.53E-05	0.000551	0.000525	0.000351	6.36E-05	8.92E-05	0.000252

p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia	0.000879	0.001502	0.000893	0.000997	0.001464	0.001567	0.001034	0.000805	0.001403	0.007667	0.002743	0.000202	0.000715	0.00143	0.001816	0.001105	0.001705	0.002529
p_Actinobacteria;c_Thermoleophilia;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Thermoleophilia;o_Gaiellales;f_AK1AB1_02E;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Patulibacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Actinobacteria;c_Thermoleophilia;o_Solirubrobacterales;f_Solirubrobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Armatimonadetes;c_Armatimonadia;o_Armatimonadales;f_Armatimonadaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Armatimonadetes;c_SJA-176;o_RB046;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Armatimonadetes;c_[Fimbriimonadia];o_[Fimbriimonadales];f_[Fimbriimonadaceae];g_Fimbriimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	0.000216	9.32E-05	7.60E-05	0.000456	1.78E-05	0.000185	0	0.000715	0.000224	4.46E-05	0.000392	0.000447	8.62E-06	0.005169	0.000211	0.020708	0.000337	0.000121
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Parabacteroides	0	0	0	0	8.92E-06	0	3.07E-05	0	0	0	0	0	0	0.000214	0	0	0	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Porphyromonas	0	0	0	0	0	2.47E-05	0	0	0	0	0	0	0	6.11E-06	0	0	0	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella	0.000509	0.001874	0.000542	0.001867	0.006996	0.000111	0.000184	0.007532	0.011845	0.00039	0.00453	0.006693	0.000146	3.67E-05	0.000893	0.063831	0.001864	0.000443
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_	0	4.14E-05	0	9.55E-05	0.000143	0	0	0.000838	0.000478	2.23E-05	0	0.000253	8.62E-06	0.000415	0	0.003035	0.000119	3.02E-05
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_AF12	0	0	0	0	0	0	0	0.000168	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_	0.002144	0.002817	0.001967	0.002238	0.001892	0.000333	0.000972	0.002805	0.002481	0.000579	0.001394	0.004459	0.001887	0.047521	0.003551	0.047224	0.003837	0.000453
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteraceae];g_Butyricimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3.01E-05	0	0	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteraceae];g_Odoribacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.98E-05	0
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae];g_Paraprevotella	0	0	0	0	0	2.47E-05	0	0	0	0	0	0	0	1.83E-05	0	0.000175	0	1.01E-05
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae];g_[Prevotella]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000111	0	0

p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Dyadobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Flectobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Cytophagia;o_Cytophagales;f_Cytophagaceae;g_Hymenobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Cryomorphaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Cryomorphaceae;g_Fluviicola	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_Flavobacteriaceae;g_Flavobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Chryseobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Cloacibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.59E-05	0	0
p_Bacteroidetes;c_Flavobacteriia;o_Flavobacteriales;f_[Weeksellaceae];g_Elizabethkingia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Olivibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Pedobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_Sphingobacteriia;o_Sphingobacteriales;f_Sphingobacteriaceae;g_Sphingobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Chitinophaga	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Bacteroidetes;c_[Saprospirae];o_[Saprospirales];f_Chitinophagaceae;g_Sediminibacterium	0	1.04E-05	9.50E-06	2.12E-05	0	0	0	0	0	1.11E-05	0	0	0	0	0	3.18E-05	0	0
p_Chlamydiae;c_Chlamydiia;o_Chlamydiales;Other;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chlamydiae;c_Chlamydiia;o_Chlamydiales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chlamydiae;c_Chlamydiia;o_Chlamydiales;f_Parachlamydiaceae;Other	0	0	0	0	0	0	0	3.35E-05	0	0	0	0	0	0	0	0	0	0
p_Chlamydiae;c_Chlamydiia;o_Chlamydiales;f_Parachlamydiaceae;g_Candidatus Protochlamydia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chlamydiae;c_Chlamydiia;o_Chlamydiales;f_Parachlamydiaceae;g_Parachlamydi	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

a																		
p_Chlorobi;c_Ignavibacteria;o_Ignavibacteriales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.01E-05
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chloroflexi;c_Anaerolineae;o_Anaerolineales;f_Anaerolinaceae;g_Anaerolinea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chloroflexi;c_Anaerolineae;o_SBR1031;f_SHA-31;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chloroflexi;c_Anaerolineae;o_SBR1031;f_oc28;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chloroflexi;c_Ellin6529;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chloroflexi;c_Gitt-GS-136;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Chloroflexi;c_Thermomicrobia;o_JG30-KF-CM45;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8.74E-05	0	0
p_Cyanobacteria;Other;Other;Other;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Cyanobacteria;c_4C0d-2;o_SM1D11;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Cyanobacteria;c_4C0d-2;o_YS2;f_;g_	0.001527	0.008481	0.001473	0.016123	0.003739	0	0.00217	0.047883	0.01273	0.011534	0.006325	0.011177	0.012184	0.001271	0.00316	0.003504	0.002865	0.001582
p_Cyanobacteria;c_Chloroplast;o_Streptophyta;f_;g_	0	0	0	2.12E-05	0	0	0	0	0	1.11E-05	0	0	0	0	0	5.56E-05	1.98E-05	0
p_Cyanobacteria;c_ML635J-21;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Cyanobacteria;c_Oscillatoriophycideae;o_Chroococcales;f_Xenococcaceae;g_	0	0	0	0	0	0	0	5.59E-05	0	0	0	0	0	0	0	0	0	0
p_Cyanobacteria;c_Oscillatoriophycideae;o_Chroococcales;f_Xenococcaceae;g_Chroococcidiopsis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Deferribacteres;c_Deferribacteres;o_Deferribacterales;f_Deferribacteraceae;g_Mucispirillum	0	0	0	0	0	0	4.09E-05	0.000816	0	0	0	0	0	0	0	0	0	0
p_FBP;c_;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;Other;Other;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;Other;Other	0	1.04E-05	0	0	0	9.87E-05	0	0	0	0	0	3.37E-05	0	0	2.01E-05	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Anaerobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Anoxybacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Geobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.38E-05	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Brevibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Cohnella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Paenibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g_Lysinibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g_Rummeliibacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g_Sporosarcina	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Sporolactobacillaceae;g_Sporolactobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Bacillales;f_Thermoactinomycetaceae;g_Planifilum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	1.83E-05	0	0	0	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;Other;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;Other	0	0	0	0	0	1.23E-05	0	0	1.02E-05	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus	0	0	0	0	0	0.000271	0.000113	0	9.15E-05	0.000212	2.73E-05	0	0.000345	3.05E-05	0	0	0.000714	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	0.012384	0.076747	0.006872	0.029414	0.097279	0.119335	0.01439	0.053794	0.110371	0.080157	0.029821	0.010713	0.001146	0.007203	0.007001	0.000278	0.006623	0.067045
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Leuconostocaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Leuconostocaceae;g_Leuconostoc	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus	1.54E-05	1.04E-05	0	0	0	0	0	0	0	1.11E-05	0	8.43E-06	8.62E-06	0	0	7.95E-06	0	0
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	1.54E-05	3.11E-05	0	1.06E-05	0	3.70E-05	0.000143	0.000212	4.07E-05	0.000836	0.000128	6.74E-05	5.17E-05	0.000104	8.02E-05	7.95E-05	0.000139	0.000272
p_Firmicutes;c_Bacilli;o_Turicibacterales;f_Turicibacteraceae;g_Turicibacter	0	1.04E-05	0	0	2.68E-05	0	0	0	0	0.00029	0	0	0.000379	0	1.00E-05	0	0	0.000463
p_Firmicutes;c_Clostridia;o_Clostridiales;Other;Other	0	9.32E-05	0	0	7.14E-05	0.000148	2.05E-05	4.47E-05	0.000142	7.80E-05	8.20E-05	0.000101	2.59E-05	7.33E-05	6.02E-05	7.95E-06	3.97E-05	5.04E-05
p_Firmicutes;c_Clostridia;o_Clostridiales;f_;g_	0.468107	0.476316	0.507917	0.434968	0.431389	0.606185	0.582738	0.357038	0.379085	0.227712	0.340309	0.451778	0.535303	0.613328	0.671294	0.469244	0.581425	0.459133
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Christensenellaceae;g_	0	0	0	0	0	0	0	0.000715	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_	0.001326	0.001149	0.00096	0.00227	0.001874	0.001246	0.001054	0.003352	0.002888	0.007511	0.002224	0.000649	0.002585	0.001002	0.001073	0.00027	0.001487	0.001572
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Alkaliphilus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Candidatus Arthromitus	0	0.000217	0	0.001824	0.000794	0.000173	0	0.002146	0.000661	6.69E-05	9.11E-05	0.000834	8.62E-06	0.002132	0.000632	0.000747	0.003143	0.000564
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium	6.17E-05	0	0	0	1.78E-05	2.47E-05	3.07E-05	0	0	0.000189	9.11E-06	0	0	0	4.01E-05	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Oxobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Proteiniclasticum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_SMB53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae;g_Dehalobacterium	0.004411	0.006079	0.003013	0.009504	2.68E-05	0.001332	0.026048	0.000626	0.001708	0.00214	0.001704	0.016681	0.001258	0.003373	0.005426	0.008916	0.020096	0.002166
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Acetobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Eubacteriaceae;g_Anaerofustis	0	0	0	0	0	0	0	0	0	5.57E-05	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Gracilibacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Gracilibacteraceae;g_Gracilibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;Other	0.008806	0.053343	0.008953	0.002981	0.077718	0.003787	0.004401	0.002738	0.003599	0.034702	0.033312	0.002057	0.001215	0.007387	0.06944	0.004704	0.105258	0.068406
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_	0.32573	0.272244	0.317502	0.46262	0.323446	0.168061	0.115622	0.208651	0.176218	0.444069	0.221115	0.166268	0.212978	0.145055	0.139834	0.241015	0.227292	0.305226

p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Anaerostipes	0.000478	0.001077	0.000352	0.000467	8.92E-05	0.000555	0	0	0.000397	0	0	0	0	0	0.000532	0	1.98E-05	0.000141
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Blautia	0	0	0	0	1.78E-05	0	0	0	3.05E-05	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Butyrivibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus	0.005938	0.005499	0.006767	0.004434	0.00381	0.015222	0.009037	0.003084	0.00184	0.00575	0.01481	0.002284	0.001861	0.003861	0.004875	0.004331	0.002528	0.002055
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea	0.000478	0.000828	0.00058	0.000509	0.000259	0.002788	0.001689	0.001743	0.000336	0.018844	0.000529	0.000379	0.003541	0.009659	0.001645	0.000532	0.000258	0.00142
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Epulopiscium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnospira	0	0	0	0	0	0	0	0	0	0	0	0	0	1.22E-05	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Roseburia	0	0.001647	1.90E-05	1.06E-05	0	0.003257	0	0	0.001047	0	0.000283	0	8.62E-06	1.83E-05	0.000451	0.000127	0	0.00682
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_[Ruminococcus]	0.001989	0.003883	0.002262	0.001432	0.003989	0.005169	0.003091	0.005543	0.000681	0.042982	0.049562	0.029577	0.002042	0.013588	0.007603	0.001208	0.005066	0.041769
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_	0	0	0	0	0	3.70E-05	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Dehalobacter_Syntrophobotulus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Desulfosporosinus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Pelotomaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_Sporotomaculum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_rc4-4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.00E-05	0	0	1.01E-05
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g_Peptostreptococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.01E-05
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;Other	0	3.11E-05	1.90E-05	9.55E-05	1.78E-05	0.000136	0.000225	0.000101	4.07E-05	3.34E-05	0	0.000523	4.31E-05	0.000293	6.02E-05	5.56E-05	1.98E-05	2.01E-05
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_	0.01223	0.020525	0.013192	0.013004	0.009531	0.029285	0.141199	0.020975	0.014865	0.016727	0.005605	0.117928	0.084917	0.071226	0.021144	0.023974	0.006781	0.009047
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Anaerotruncus	0.000154	0.000135	6.65E-05	0.000456	0.000268	9.87E-05	2.05E-05	0.001117	0.000173	0.000435	0.000182	0.000236	0.000198	6.72E-05	0.00015	0.000199	0.000268	0.000242

p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ethanoligenens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Faecalibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.00E-05	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira	0.002468	0.001905	0.002975	0.003012	0.00315	0.023475	0.01568	0.006191	0.005714	0.004045	0.001795	0.070314	0.010297	0.034972	0.018897	0.078492	0.017122	0.007616
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus	0.006292	0.007518	0.005912	0.004879	0.004426	0.007068	0.005895	0.007308	0.01878	0.016147	0.003709	0.001972	0.001947	0.008083	0.00316	0.008812	0.005453	0.009843
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Syntrophomonadaceae;g_Syntrophomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_BSV43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megasphaera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Sporomusa	0	0	0	0	0	0	1.02E-05	2.23E-05	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Veillonella	0	0	0	2.12E-05	0	0	0	0	0	0	0	0	0	4.28E-05	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_vadinHB04	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g_	0.00017	0.000331	0.000124	0.000562	0.000393	0.002048	0.000276	0.001117	0.000356	0.002351	0.000155	0.000228	0.000345	0.000214	0.000522	0.000103	0.000169	0.000343
p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g_Anaerovorax	0	0	0	0	0	0	0	0	0	5.57E-05	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Mogibacteriaceae];g_Mogibacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Helcococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Parvimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_Clostridiales;f_[Tissierellaceae];g_Sedimentibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_OPB54;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Clostridia;o_SHA-98;f_D2;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_	0.000108	0.002019	0.000333	0.000233	0.000643	7.40E-05	0.000113	0.001374	0.000142	0.000479	0.000237	0.000101	0.000663	0.000593	0.000562	0	0.000625	0.000232
p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum	0.007865	0.028406	0.005304	0.000297	0.003436	0.004564	0.016447	1.12E-05	0.006782	0.004948	0.014601	2.53E-05	0.00199	0.017144	0.030372	0.000326	0.001973	0.007324

p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Coprobacillus	4.63E-05	1.04E-05	9.50E-05	0.000233	1.78E-05	0	0	0.000201	1.02E-05	2.23E-05	0	0	4.31E-05	1.22E-05	0	5.56E-05	2.97E-05	1.01E-05
p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_[Eubacterium]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Fusobacteriaceae;g_Fusobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	1.83E-05	0	0	4.96E-05	0
p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales;f_Leptotrichiaceae;g_Leptotrichia	0	0	0	0	1.78E-05	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_NKB19;c_;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Nitrospirae;c_Nitrospira;o_Nitrospirales;f_0319-6A21;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.38E-05	0	0
p_OP11;c_;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Planctomycetes;c_Phycisphaerae;o_CPla-3;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Planctomycetes;c_Phycisphaerae;o_WD2101;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.59E-05	0	0
p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_Gemmata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Isosphaeraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_A17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Planctomycetes;c_Planctomycetia;o_Planctomycetales;f_Planctomycetaceae;g_Planctomyces	0	0	0	0	0	0	2.05E-05	0	0	0	0	0	0	0	0	0	0	3.02E-05
p_Proteobacteria;c_Alphaproteobacteria;Other;Other;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Brevundimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Mycoplana	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;Other;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Aurantimonadaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Aurantimonadaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bartonellaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_	0	0	0	0	0	0	0	0	0	3.34E-05	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Beijerinckiaceae;g_Chelatococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_Balneimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiaceae;g_Bradyrhizobium	0	0	0	0	0	2.47E-05	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Ochrobactrum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Devosia	0	0	0	0	0	0	0	0	2.03E-05	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Hyphomicrobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiaceae;g_Rhodoplanes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_Methylobacterium	0	0	0	0	0	2.47E-05	0	0	0	3.34E-05	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_	0	0	0	0	0	0	2.05E-05	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylocystaceae;g_Pleomorphomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Mes	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

orhizobium																		
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Phyllobacteriaceae;g_Phyllobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Agrobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Kaistia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Rhizobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Rhizobiaceae;g_Shinella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Labrys	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Xanthobacteraceae;g_Xanthobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Paracoccus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteraceae;g_Rhodobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Gluconobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Acetobacteraceae;g_Roseococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirillales;f_Rhodospirillaceae;g_Phaeospirillum	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiales;f_mitochondria;Other	0	0	0	0	0	0	2.05E-05	1.12E-05	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Erythrobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.01E-05
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Kaistobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Novosphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingobium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.38E-05	0	0
p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomonadales;f_Sphingomonadaceae;g_Sphingomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Achromobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.98E-05	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Sutterella	0	2.07E-05	0	0	0	0	0.000727	0	0	0	0	0	1.72E-05	0.001546	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Burkholderia	0	2.07E-05	0	8.49E-05	1.78E-05	0	1.02E-05	0	0	3.34E-05	3.65E-05	0	0	1.83E-05	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Burkholderiaceae;g_Pandoraea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_	0	2.07E-05	2.85E-05	0	2.68E-05	1.23E-05	0	0	0	0	1.82E-05	0	0	0	0	7.95E-06	0	3.02E-05
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Acidovorax	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_Comamonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.95E-06	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Cupriavidus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Janthinobacterium	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Ralstonia	0	5.18E-05	8.55E-05	3.18E-05	2.68E-05	0.000173	2.05E-05	0	0	0	0	0	0	1.22E-05	9.03E-05	0.000413	2.97E-05	3.02E-05
p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Neisseriales;f_Neisseriaceae;g_Neisseria	0	0	0	0	2.68E-05	0	0	0	0	0	0	0	0	2.44E-05	0	0.000262	0	0
p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoracaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bdellovibrionaceae;g_Bdellovibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_	6.17E-05	1.04E-05	0	0	0	0	0	1.12E-05	0	0	0	0	0	6.11E-06	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Bilophila	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio	0	2.07E-05	6.65E-05	2.12E-05	0	1.23E-05	0.028637	0.143258	2.03E-05	0	1.82E-05	0	1.72E-05	0	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_MIZ46;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.95E-05	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Myxococcaceae;g_Myxococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Spirobacillales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophorhabdaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Campylobacteraceae;g_Campylobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Helicobacteraceae;Other	1.54E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Helicobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Helicobacteraceae;g_Flexispira	1.54E-05	1.04E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Epsilonproteobacteria;o_Campylobacterales;f_Helicobacteraceae;g_Helicobacter	0	0	0	0	0	0	0	0.000425	0	0	0	0	0	0.000397	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;Other;Other;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Aeromonadales;f_Aeromonadaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_Cellvibrio	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Shewanellaceae;g_Shewanella	0	0	0	0	0	0	0	0	2.03E-05	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;Other	0	0	0	0	0	0	0	0	1.02E-05	0	9.11E-06	0	0	0	0	1.59E-05	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_	0.00037	0.000155	0.000836	0.000233	0.000125	0.000197	0.000409	0.000268	4.07E-05	0.000357	0.00062	0.000278	0.000233	0.000208	0.000181	0.009758	0.000357	0.000332
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Citrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7.95E-06	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Enterobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.59E-05	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Erwinia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Escherichia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Klebsiella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Pantoea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Proteus	0	0	0	0	0	0	0	0	0	0	9.11E-06	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Providencia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Trabulsiella	0	0	0	0	0	0	0	0	0	0	0	0	0	6.11E-06	0	0	0	0

p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_Aquicella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;g_Legionella	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;g_Tatlockia	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Actinobacillus	0	0	0	0	0	0	0	0	0	0	0	0	0	1.83E-05	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Aggregatibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	6.11E-06	0	0.000413	0	2.01E-05
p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales;f_Pasteurellaceae;g_Haemophilus	0	0	0	4.24E-05	0	0	0	0	0	0	0	0	0	3.67E-05	0	3.97E-05	0	3.02E-05
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Enhydrobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.59E-05	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	0	0	0	0	8.92E-06	0	0	0	0	0	0	0	0	1.22E-05	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae;g_Steroidobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_	1.54E-05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

e;g_Luteibacter																		
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Luteimonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Pseudoxanthomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Stenotrophomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Thermomonas	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_SR1;c_;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.00031	0	0
p_Spirochaetes;c_Spirochaetes;o_Spirochaetales;f_Spirochaetaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Spirochaetes;c_Spirochaetes;o_Spirochaetales;f_Spirochaetaceae;g_Treponema	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Spirochaetes;c_[Leptospirae];o_[Leptospirales];f_Sediment-4;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_TM6;c_SJA-4;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_TM7;c_TM7-3;o_;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_TM7;c_TM7-3;o_CW040;f_F16;g_	4.63E-05	0.000445	9.50E-06	0.000552	0.00075	6.17E-05	0.000328	0.00133	0.001678	0.000134	0.00021	8.43E-06	0	0	7.02E-05	4.77E-05	0.000466	0.000151
p_TM7;c_TM7-3;o_EW055;f_;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales;f_Anaeroplasmataceae;g_Anaeroplasma	0	0	0	0	0	0	0	0	2.03E-05	0	0	1.69E-05	6.89E-05	0	0	0.000135	0	0
p_Tenericutes;c_Mollicutes;o_RF39;f_;g_	0	0.000735	0	0.000318	0	6.17E-05	0.000256	0.000123	0.000305	0.000724	0.000264	8.43E-06	0.000457	7.33E-05	0.000421	0.000429	6.94E-05	2.01E-05
p_Verrucomicrobia;c_Opitutae;o_Opitutales;f_Opitutaceae;g_Opitutus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Akkermansia	0.134805	0.018796	0.110643	0.003214	0.020819	0.002603	0.023929	0.111556	0.239451	0.067086	0.257426	0.103675	0.120427	0.001375	0.0034	0.004132	0.001616	0.002075
p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Luteolibacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Prosthecobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Verrucomicrobia;c_[Methylacidiphilae];o_Methylacidiphilales;f_LD19;g_	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacterales];f_[Chthoniobacterace	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

ae];g_																		
p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacterales];f_[Chthoniobacteraceae];g_Candidatus Xiphinematobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.000135	0	0
p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacterales];f_[Chthoniobacteraceae];g_Chthoniobacter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacterales];f_[Chthoniobacteraceae];g_DA101	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3.18E-05	0	0
p_Verrucomicrobia;c_[Spartobacteria];o_[Chthoniobacterales];f_[Chthoniobacteraceae];g_heteroC45_4W	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_[Thermi];c_Deinococci;o_Deinococcales;f_Deinococcaceae;g_Deinococcus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_[Thermi];c_Deinococci;o_Deinococcales;f_Trueperaceae;g_Truepera	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_[Thermi];c_Deinococci;o_Thermales;f_Thermaceae;g_Meiothermus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p_[Thermi];c_Deinococci;o_Thermales;f_Thermaceae;g_Thermus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Supplemental Methods

Body Weight, Food Intake & Body Composition Analysis.

For measurement of body weight and food intake, daily measurements were made from singly housed animals to ensure accurate food intake. The difference in food weight was measured daily from the previous day's ration. Non-invasive measurements of body composition (i.e. fat mass, fat-free mass) were made weekly after a 2h period of food-restriction using a mq10 NMR analyzer (Bruker Optics Inc., Billerica, MA).

Hyperinsulinemic-Euglycemic Clamp Studies

Insulin sensitivity was measured at 4 weeks postoperative by the Vanderbilt Mouse Metabolic Phenotyping Center (MMPC, Nashville, TN) similar to prior studies[1]. Briefly, one week prior to clamp, carotid artery and jugular vein catheters were placed for sampling and infusions, respectively. Washed erythrocytes were replaced to preclude any decrease in hematocrit that occurs with the repeated blood sampling. A primed (1.5µCi) continuous (0.075µCi/min) 3-[^{3}H]-glucose infusion was started at -20 min. The clamp was initiated at 0 min with a continuous insulin infusion (2.5 mU/kg/min) that was maintained for 145 min. This insulin dose was chosen to (a) achieve a steady-state, plasma insulin concentration similar to the peak insulin concentrations obtained during the OGTT and (b) to enable discernment of any potential effects on hepatic glucose production or peripheral glucose uptake. Arterial glucose was measured at 10 min intervals to provide feedback to adjust the glucose infusion rate (GIR) containing 3-[^{3}H]-glucose as needed to clamp glucose concentration and specific activity. Glucose kinetics were determined at -10 min and at 10 min intervals at steady state (*a priori* defined from t = 80-120 min). Plasma insulin was measured at -10, 100, and 120 min during the procedure to verify steady state insulin concentration and physiologic hyperinsulinemia. A 13µCi intravenous bolus of 2-[^{14}C]-deoxyglucose was administered at 120 min and used to determine the glucose metabolic index, an indication of tissue-specific glucose uptake. Blood samples were collected at 2, 5, 10 and 25 min after injection to measure decay of plasma 2-[^{14}C]-deoxyglucose. Tissues were collected to assess tissue specific rate of glucose uptake. All samples were deproteinized with $BaOH_2$ and $ZnSO_4$ prior to scintillation counting. Endogenous glucose production, a measure of hepatic glucose production, was calculated as described[1].

Hyperglycemic Clamp

Studies were performed as previously described[1]. Baseline blood sugar and insulin levels were drawn and infusions of insulin (Humulin Regular U100 at 4mU/kg/min) were started at t=0 and continued until t=120. Rate of glucose infusion was adjusted using measured glucose levels every 5 minutes throughout the experiment. 3-[^{3}H]-D-Glucose was infused continuously throughout the study and ^{14}C-2-deoxyglucose was infused at t=120 minutes to detect the rate of endogenous glucose production and the rate of glucose utilization in selected tissues. Mice were transfused with blood from age matched male mice to maintain hemoglobin levels during experiment.

Hepatic Glycogen Measurements

Pulverized liver tissue (100 mg) was added to a 5-fold volume of 0.6 N perchloric acid in pre-chilled tubes. After neutralization with potassium bicarbonate, samples were treated with an amyloglucosidase-sodium acetate solution and incubated in a 40℃ bath for 2 hours prior to the measurement of liberated glucose using the glucose oxidase assay (Infinity; Thermo Scientific) and oyster glycogen reference[2].

Glucose Tolerance Testing

At 4 or 8 weeks postoperative, mice were subjected to oral glucose tolerance (OGTT) testing after a 5h period of food restriction. Animal transport from the rodent housing facility to the laboratory was done early in the morning (0700-0800) following the beginning of the light cycle, and mice were acclimated to the laboratory environment. Blood was sampled from the tail vein before and at 10, 20, 30, 45, 60, 90 and 120 minutes after oral gavage of 20% dextrose (2 mg/g body weight). In additional experiments, 5 hr fasted mice at 4 weeks postoperative were dosed with the GLP-1R antagonist Ex9 (50 µg, i.p.; Tocris Biosciences) 120 min prior to OGTT[3]. Blood glucose concentration (mg/dl) was measured serially using a glucometer (Accu-Chek, Roche, Indianapolis, IN). Additional blood samples (~100µl) were collected (0, 20 min) for determination of insulin or GLP-1 concentration.

Intestinal Glucose Uptake

Determination of intestinal glucose uptake is well-described in rats as well as other larger animal models[4, 5] using the glucose analog, 3-O-methyl-glucose (3-OMG). 3-OMG is transported by SGLT1 and GLUT2[6], with an affinity similar to that of D-glucose, is non-metabolizable, and widely used to assess intestinal glucose absorption[7, 8]. The experiment was conducted on three separate groups of mice over a three-day period and fresh tracer was prepared no more than 30 minutes prior to gavage for each day. 3-[^{3}H]-OMG (~10 µCi/mouse) was spiked into a 20% dextrose solution and provided via oral gavage. Blood was collected for measurement of [^{3}H] at background and then at 2, 5, 10, 20, 30, 60, 90 and 120 min post-gavage. The rate of 3-OMG appearance (i.e. slope of the tracer appearance over time two to twenty minutes) in the blood was used as a surrogate for intestinal uptake. Small plasma samples for tracer appearance (disintegrations per minute, dpm), were measured using scintillation counting (LS 6500; Beckman Coulter) and expressed that as a percentage of total dpm administered to each animal via oral gavage.

Mesenteric Lymphatic Cannulation & Lymph Collection

Incretins and other intestinal-derived hormones are secreted by enteroendocrine cells into the lamina propria, the space drained by intestinal lacteals. These lacteals coalesce into the mesenteric lymphatics, and sampling from this space allows for a much more sensitive method to assess intestinal hormone secretion[9, 10]. In order to assess basal and nutrient-induced incretin responses after bile diversion, separate groups of mice underwent laparotomy and mesenteric lymph duct cannulation with polyvinylchloride (PVC) tubing (0.2 mm ID, 0.5 mm OD; Tyco Electronics). Cyanoacrylate tissue adhesive was used to secure the lymphatic catheter that drained to gravity. A second feeding PVC catheter (0.5 mm ID, 0.8 mm OD; Tyco Electronics) was inserted into the stomach and extended so that the tip of the catheter terminated within the first portion of the duodenum. The feeding catheter was held in place with a purse string suture and sealed with a drop of cyanoacrylate glue. Both catheters were exteriorized and mice were allowed to recover with a nutrient and electrolyte solution (5% dextrose in 0.9% saline) via the feeding catheter (500 µl/hr) to replace fluid losses. Mice were recovered overnight in Bollman mouse cages in a temperature- and humidity-controlled incubator at 25℃ and 45% relative humidity (Isolette Warmer Incubator, Hill-Rom Air-Shields). The following morning the dextrose/electrolyte solution is discontinued and 0.9% saline is begun and allowed to equilibrate for one hour prior to beginning lymph collection. Following equilibration, animals undergo a two-hour basal collection period and then a 300µl nutrient bolus (Ensure®, Abbott) is given in 50µl fractions over a three-minute period. Mesenteric lymph is collected hourly for the next 5h for analysis. To accurately measure the volume of lymph production, fractions are collected in pre-weighed tubes and the volume of lymph produced is calculated using an estimated density of 1.02 g/ml[11].

Bile Acid Controls, Chemicals, and Calibrators.

All bile acids were purchased from C.D.N. Isotopes Inc. (Pointe Claire, Montreal, PQ, CA). Tauro-β-muricholic-d4 acid (5β-cholanic acid-3α,6β,7β-triol-N-[2-sulphoethyl]-amide-2,2,4,4-d4, TβMCA-d4), was purchased from United States Biological Corp., Swampscott, MA). HPLC grade water, acetonitrile, ethanol, methanol, ammonium acetate and ammonia were purchased from Sigma Chemicals (St. Louis, MO). Formic acid was purchased from Thermo Scientific (Rockford, IL).

Stock solutions of 2.5 mM of all bile acids (THCA, HCA, TαMCA, TβMCA, TωMCA, HDCA, THDCA: 10 mM) were used to prepare calibrators with concentrations of 100 µM in methanol. For the preparation of calibrators, bile acids were mixed to achieve final concentrations of 20, 2.5, 0.75, 0.25, 0.05, 0.015, 0.005 µM. To prepare 20ml of a 2.0 nM internal standard, 250 µL each of d4-CDCA, d4-TCA, d4-GCDCA and 500 µL d4-CA, d4-TβMCA and d4-GCA were added to 20% (v/v) acetonitrile.

Sample preparation of bile acids for UPLC/ESI-MS.

For bile acid measurements, the following were added to 50µl of homogenate: 200µl of 100 mM aqueous sodium hydroxide and 50µl of a 2 nM internal standard mix. The sample was then heated at 64°C for 30 min, centrifuged for 10 min at 14,400 x *g*, and the supernatant acidified to pH 7.0 with 50µl of 0.1M hydrochloric acid. The sample was brought to a final volume of 1 ml with water and applied to a 1 ml (30 mg) Oasis HLB cartridge (Waters, Milford, MA) previously equilibrated first with 1 ml of methanol, then 1 ml of water (Rodrigues, 1996). The column bound bile acids were washed with 1 ml of 5% (v/v) aqueous methanol then 1 ml of 2% (v/v) aqueous formic acid. Bile acids were eluted from the column with 1 ml of 2% (v/v) ammonia in methanol and the eluent evaporated to dryness using a rotary evaporator at 30°C for 2 hr. Samples were re-suspended in 100µl of 25% (v/v) acetonitrile in water.

Bile acid analysis by HPLC-MS

MS analysis was performed using a TSQ Quantum mass spectrometer (ThermoFinnigan, Sunnydale, CA) equipped with an ESI probe in negative-ion mode. The following (optimized) parameters were used for the detection of the analytes and the internal standard; N2 sheath gas, 49 p.s.i.; N2 auxiliary gas, 25 p.s.i.; spray voltage, 3.0 kV; source CID, 25 V; capillary temperature, 300℃; capillary offset, -35 V; tube lens voltage, 160 V; Q2 gas pressure, 1.5 mtor; Q3 scan width 1 m/z; Q1/Q3 peak widths at half-maximum, 0.7 m/z. Calibration curves and concentration of individual bile acids were calculated by LCQuan 2.5.5 software (ThermoFinnigan). Concentrations of individual bile acids were calculated from peak area in the chromatogram detected with SRM relative to the appropriate internal standard.

An Acquity ultra performance liquid chromatography system (UPLC; Waters, Milford, MA) was used with an ACQUITY UPLC BEH C18 1.7 µm, 2.1 x 100 mm column, from Waters (Milford, MA), was heated to 50℃, and a binary solvent system of 20% (v/v) acetonitrile in water (mobile phase A) and 80% (v/v) acetonitrile in water (mobile phase B) both containing 1 mM ammonium acetate were used to resolve plasma bile acids as previously described[1] MS analysis was performed using a TSQ Quantum mass spectrometer (ThermoFinnigan, Sunnydale, CA) equipped with an ESI probe in negative-ion mode. The following (optimized) parameters were used for the detection of the analytes and the internal standard; N2 sheath gas, 49 p.s.i.; N2 auxiliary gas, 25 p.s.i.; spray voltage, 3.0 kV; source CID, 25 V; capillary temperature, 300℃; capillary offset, -35 V; tube lens voltage, 160 V; Q2 gas pressure, 1.5 mtor; Q3 scan width 1 m/z; Q1/Q3 peak widths at half-maximum, 0.7 m/z. Calibration curves and concentration of individual bile acids were calculated by LCQuan 2.5.5 software (ThermoFinnigan). Concentrations of individual bile acids were calculated from peak area in the chromatogram detected with SRM relative to the appropriate internal standard.

Immunoblot analyses.

Liver and skeletal muscle tissues were collected at four or eight weeks postoperatively and snap frozen in liquid nitrogen. Tissues were pulverized, powdered, and then homogenized in lysis buffer and pelleted. Protein concentrations of the supernatant were analyzed, and equivalent amounts of protein were loaded onto a polyacrylamide gel. Primary antibodies raised against CYP7A1 (ab65596, 1:1000) were purchased from Abcam (Cambridge, MA). Goat anti-FXR (sc-1204; 1:1000). Rabbit anti-SHP2 was a gift from Dr. Gen-Sheng Feng, University of California San Diego, CA. The primary antibodies were diluted in Li-Cor blocking buffer and incubated at room temperature for 1h. Goat anti-rabbit, donkey anti-goat, goat anti-mouse or donkey anti-sheep fluorescently-labeled secondary antibodies (Li-Cor Inc., Lincoln, NE) were diluted 1:10,000 and incubated in blocking buffer at room temperature for one hour with shaking. After three rinses with PBS solution, the membrane was scanned with the Odyssey Infrared Imaging System (Li-Cor, Inc.). Akt phosphorylation status in skeletal muscle as a surrogate for insulin signaling was examined in gastrocnemius harvested before or after intravenous insulin injection. Those tissues were pulverized, powdered and homogenized in total lysate buffer. Total protein concentration was assessed by Lowry Assay and 30µg of protein (equal volume and concentration) was added to a Mini-Protean Precast Gel TGX (*Bio-Rad*) 4-20% Acrylamide used with Tris/Glycine Buffer (Cat. # 456-1094). Volume of protein per well was 16 µL containing a 1:1 volume ratio of Laemmli Sample Buffer (*Bio-Rad,* Cat. # 161-0737) with β-Mercapto-ethanol denatured at 95℃ for 5min. Transfer efficiency was assessed using Ponceau S solution (0.1 % PonceauS (w/v) in 5% (v/v) acetic acid (*Sigma*, Cat#. P7170). Phospho-Akt (Ser473) Rabbit antibody was diluted 1:1000 in TBST containing 1% polyvinylpyrrolidone (PVP) (#9271S Cell Signaling), and total Akt (Cell Signaling #2920S) was diluted 1:1000 in TBST containing 1% PVP.

Cecal Content Sampling & Microbiota Analysis

Cecal content samples were collected 8 weeks postoperatively and stored at -80℃. DNA extraction, amplification, library prep, and sequencing were done by at Vanderbilt University as previously described[1]. Briefly, 16S universal Eubacteria primers (PCR primers 515/806) were used to amplify the V4 variable region. A single-step 30 cycle PCR using HotStarTaq Plus

Master Mix Kit (Qiagen, Valencia, CA) were used. Following PCR, all amplicon products from different samples were mixed in equal concentrations and purified using Agencourt Ampure beads (Agencourt Bioscience Corporation, MA, USA). Microbial sequencing was analyzed by bacterial tag encoded FLX amplicon pyrosequencing (bTEFAP) using a Roche 454 pyrosequencer and titanium reagents and 3-5K nominal sequences per sample of high quality extracted DNA. Sequences were depleted of barcodes and primers then short sequences < 200bp are removed, sequences with >1 ambiguous base calls removed, and sequences with homopolymer runs exceeding 6bp removed using the statistical software package Quantitative Insights Into Microbial Ecology (QIIME). Microbiome differences were calculated using the nonparametric Adonis method[12]. OTUs were then taxonomically classified using BLASTn against a curated GreenGenes database.

Clinical Chemistry

Plasma was collected from mice after 5h food-restricted and stored at -80^{o}C unless stated otherwise. Packed cell volume was measured on microvolume samples in pilot studies to rule out anemia. Plasma insulin was measured using an ultra-sensitive ELISA for mouse insulin (both exogenous and endogenous insulin; Mercodia, Uppsala, Sweden), while incretin concentrations (GLP-1, GIP) were measured using Luminex Bead-based Multiplex Assay (R&D Systems, Minneapolis, MN).

Fecal Fat Analysis

Total feces were collected over a 6h period and (100 mg) were extracted 3:1 with chloroform and methanol, respectively, with the resulting lipid extract weighed as described[13]. FFAs were analyzed using the non-esterified fatty acid analysis kit (Wako Life Sciences, Richmond, VA).

Statistical Analysis & Data Visualization

Sample size and power calculation estimates were based on previous weight loss and food intake observations in high-fat fed mice after bariatric procedures[1]. Data are expressed as means ± standard error unless otherwise stated. Error bars are included on all data, but may not be visible when the error bar is smaller than the symbol representing the mean. Nonparametric methods (Kruskal-Wallis with multiplicity adjustment) were used instead of parametric equivalents to decrease error likelihood and increase statistical power, as data distributions were not reliably normally distributed and nonparametric methods have 96% efficiency of parametric methods and are much more robust to violations in method assumptions[14]. Student's t-test (unpaired, two tailed) was used for binary comparisons. All analyses were two-tailed with alpha = 0.05. Statistical analyses and data visualization were performed using Prism version 6.0 (GraphPad, La Jolla, CA) or R version 3.2.1 (The R Foundation for Statistical Computing).

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