

Distribution of Bacterial Phylum, Order, Family, and Genus Composition of Human Skin Microbiota Between Adult Males and Females

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1. Introduction

1.1. Goal

The goal of this analysis is to identify the potential statistical difference of taxonomic distributions of bacterial compositions of human skin microbiota between adult males and females at different taxonomic ranks. We are particularly interested in the potential overall difference at order/genus levels. If there are differences, we will identify the top microorganisms within each taxonomic level that have both statistical and practical differences between adult males and females in the study.

1.2. Analyses

We will conduct the following analyses will be performed.

Visual Analytics - Cluster Analysis

We will create heatmaps for visualizing the two-way taxonomic clusters of individual skin samples.

Statistical Significance Tests

The key research question is to assess whether the distributions of the compositions of micro-organisms at different taxonomic levels are different between males and females.

As we move to the lower level of the taxonomic hierarchy, the issue of sparse data arises due to more granular classification. To address the research questions, the following statistical testing will be performed;

- (1). Testing the compositional difference at each taxonomic level between males and females – Pearson chi-square and likelihood ratio tests were used to test the equality of two multivariate distributions. To ensure the statistical valid conclusions, we also perform a bootstrap test for each comparison.
- (2). We also testing the equality of the proportions of bacterial composition between males and females within each taxonomic level using the standard two-sample normal test.
- (3). The top 25 bacterial groups at each taxonomic level that have both statistical and practical differences are used to make the bar-chart for visualizing the discrepancy between males and females.

1.3. Results

The preliminary statistical results are presented in the following few sections. At each taxonomic level, the following three results are organized in the same way

- (1). Clustering heatmaps (not available at family and genus level);
- (2). P-values based on chi-square, likelihood ratio, and bootstrap version of the two tests for the difference between males and females.

- (3). Comparisons of individual compositional proportions within each taxonomic level.
- (4). Top 25 bacterial groups within each taxonomic level that are both statistical and practical significant were charted.

1.4. Conclusions

- (1). The overall compositional distributions of males and females at each taxonomic levels are statistically different;
- (2). Some bacterial groups within each taxonomic level are statistically significantly different between males and females but not practically significant (see the p-value tables).
- (3). Some of the bacterial groups do not appear in both females and males (see the p-value tables in each section)

2. Distribution of Bacterial Phyla Composition by Gender

22 skin samples taken from different human subjects. The data is

2.1. Pearson-Chi-square and Bootstrap Tests

```
## For improved execution time, we recommend calling
## Sys.setenv(LOCAL_CPPFLAGS = '-march=native')
## although this causes Stan to throw an error on a few processors.

## chi2  LRT
##    0    0

##    user  system elapsed
##    0.47    0.00    0.46

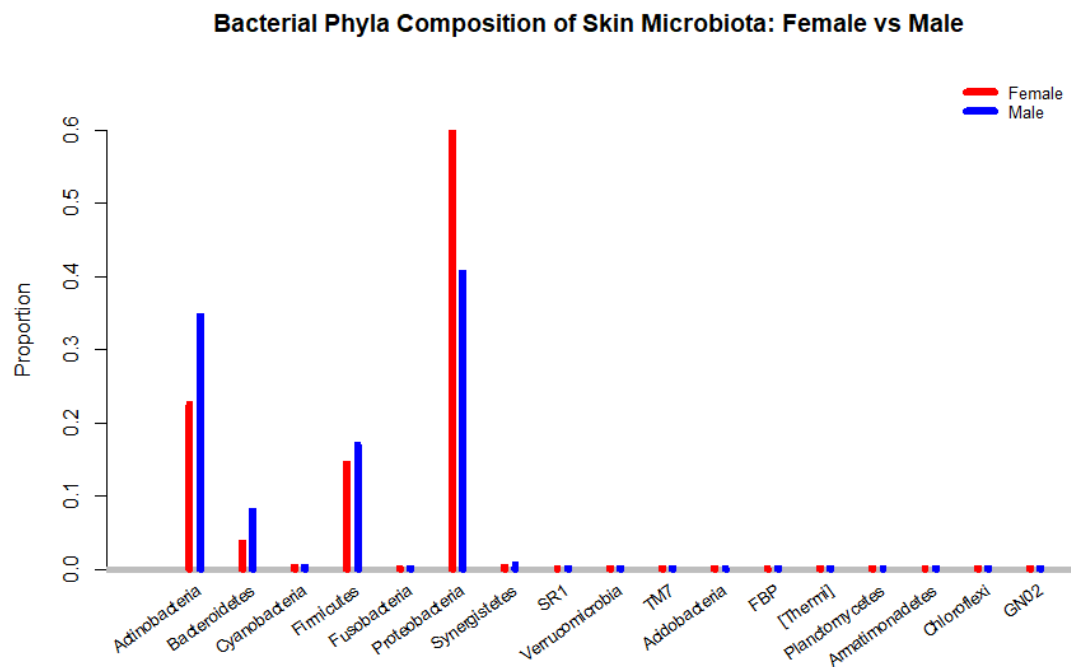
## chi2  LRT
##    0    0
```

2.2. P-values for Testing Individual Proportions

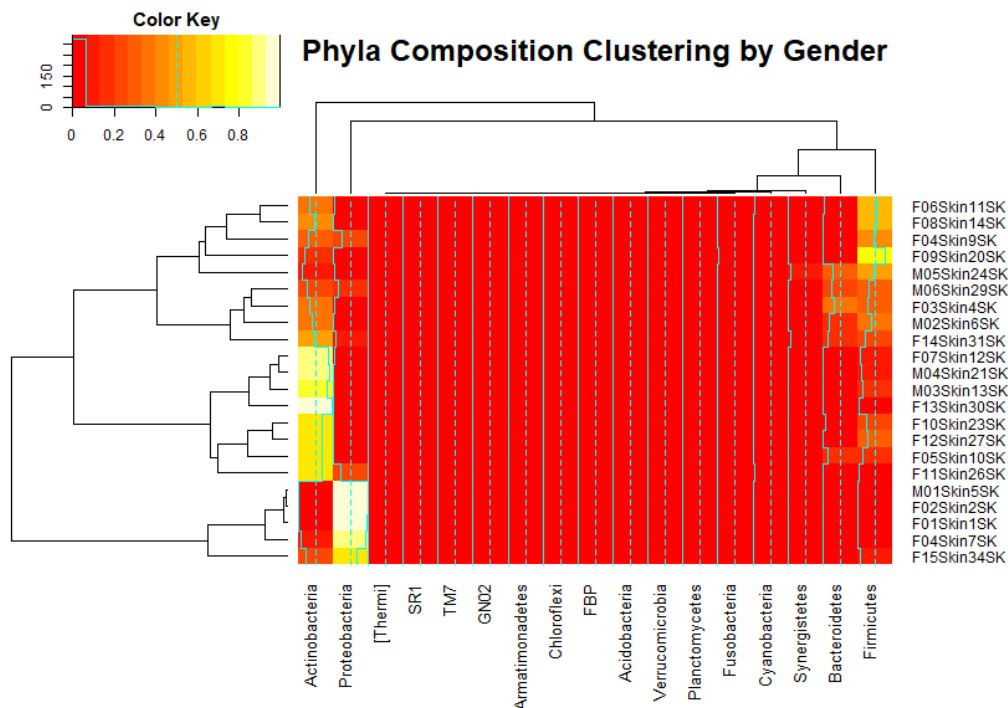
##	Actinobacteria	Bacteroidetes	Cyanobacteria	Firmicutes
##	0.0000	0.0000	0.0000	0.0000
##	Fusobacteria	Proteobacteria	Synergistetes	SR1
##	0.0000	0.0000	0.0000	0.0010

##	Verrucomicrobia	TM7	Acidobacteria	FBP
##	0.0042	0.0080	0.2788	0.4015
##	[Thermi]	Planctomycetes	Armatimonadetes	Chloroflexi
##	0.6560	0.8973	1.0000	1.0000
##	GN02			
##	1.0000			

2.3. Top 25 Significant Individual Bacterial Groups



2.4. Heatmap Clustering



3. Distribution of Bacterial Order Composition by Gender

3.1. Pearson-Chi-square and Bootstrap Tests

The Pearson-chi-square and likelihood ratio tests

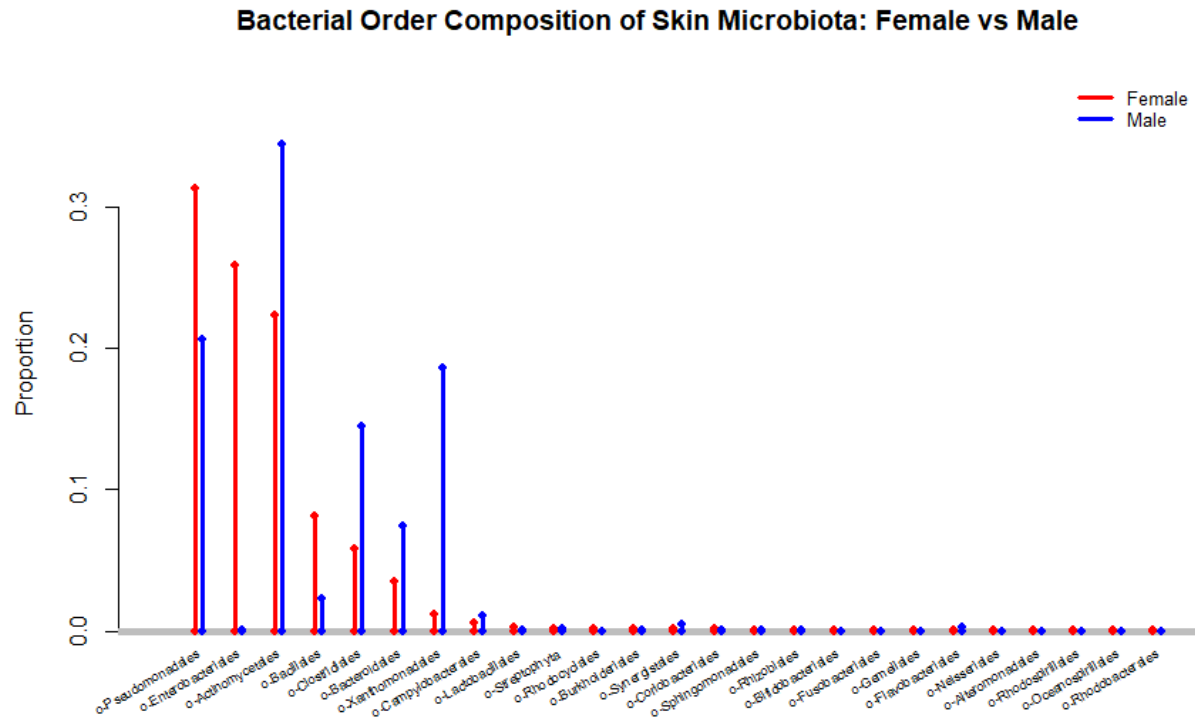
```
## chi2  LRT
##      0   0
```

Bootstrap tests

```
## chi2  LRT
##      0   0
```

3.2. Top 25 Significant Individual Bacterial Groups

Comparison of order proportions between Male and Female subjects.

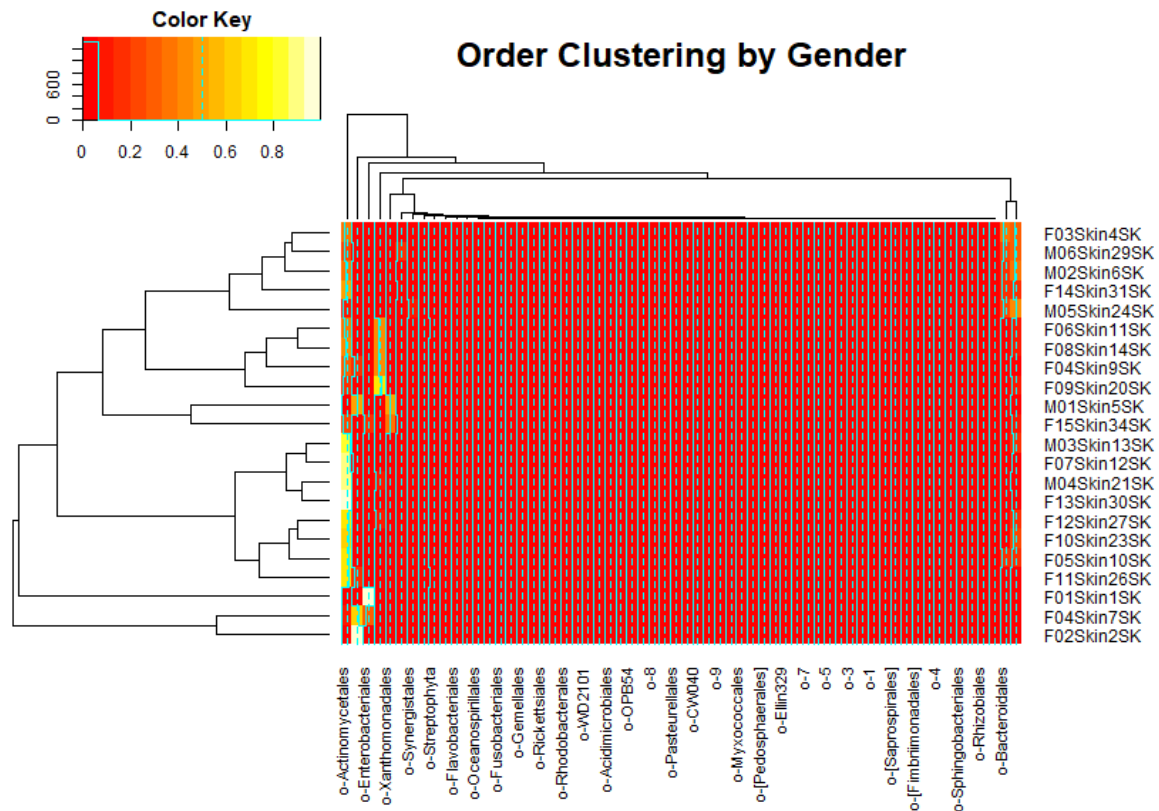


3.3. P-values for Testing Individual Proportions

##		fp	mp	pro.diff	pval
##	o-Pseudomonadales	3.133426e-01	2.066643e-01	1.066782e-01	0.0000
##	o-Enterobacteriales	2.586561e-01	1.786292e-04	2.584775e-01	0.0000
##	o-Actinomycetales	2.235429e-01	3.441388e-01	-1.205959e-01	0.0000
##	o-Bacillales	8.161370e-02	2.249279e-02	5.912090e-02	0.0000
##	o-Clostridiales	5.792117e-02	1.450252e-01	-8.710401e-02	0.0000
##	o-Bacteroidales	3.443081e-02	7.404663e-02	-3.961581e-02	0.0000
##	o-Xanthomonadales	1.158378e-02	1.858999e-01	-1.743161e-01	0.0000
##	o-Campylobacteriales	5.542999e-03	1.021566e-02	-4.672659e-03	0.0000
##	o-Lactobacillales	2.660504e-03	3.379471e-04	2.322557e-03	0.0000
##	o-Streptophyta	1.868242e-03	1.310752e-03	5.574902e-04	0.0000
##	o-Rhodocyclales	1.858049e-03	9.655632e-06	1.848393e-03	0.0000
##	o-Burkholderiales	1.383485e-03	2.389769e-04	1.144508e-03	0.0000
##	o-Synergistales	1.269091e-03	5.122313e-03	-3.853222e-03	0.0000
##	o-Coriobacteriales	1.074282e-03	8.014174e-04	2.728643e-04	0.0000
##	o-Sphingomonadales	5.549795e-04	1.013841e-04	4.535954e-04	0.0000
##	o-Rhizobiales	3.641345e-04	1.569040e-04	2.072305e-04	0.0000
##	o-Bifidobacteriales	3.409160e-04	9.655632e-06	3.312603e-04	0.0000
##	o-Fusobacteriales	3.035398e-04	9.655632e-06	2.938842e-04	0.0000

## o-Gemellales	2.888159e-04	0.000000e+00	2.888159e-04	0.0000
## o-Flavobacteriales	2.706941e-04	2.940140e-03	-2.669446e-03	0.0000
## o-Neisseriales	2.367157e-04	0.000000e+00	2.367157e-04	0.0000
## o-Alteromonadales	2.316190e-04	0.000000e+00	2.316190e-04	0.0000
## o-Rhodospirillales	1.863145e-04	0.000000e+00	1.863145e-04	0.0000
## o-Oceanospirillales	9.004259e-05	0.000000e+00	9.004259e-05	0.0000
## o-Rhodobacterales	8.890998e-05	0.000000e+00	8.890998e-05	0.0000
## o-Rickettsiales	4.983489e-05	8.931459e-05	-3.947970e-05	0.0025
## o-Cytophagales	4.926859e-05	2.172517e-05	2.754342e-05	0.0162
## o-Caulobacterales	3.964139e-05	0.000000e+00	3.964139e-05	0.0001
## o-8	2.605006e-05	0.000000e+00	2.605006e-05	0.0010
## o-[Chthoniobacterales]	1.982070e-05	0.000000e+00	1.982070e-05	0.0042
## o-Pasteurellales	1.868809e-05	0.000000e+00	1.868809e-05	0.0054
## o-WD2101	1.755547e-05	0.000000e+00	1.755547e-05	0.0070
## o-Planctomycetales	1.698917e-05	0.000000e+00	1.698917e-05	0.0080
## o-CW040	1.698917e-05	0.000000e+00	1.698917e-05	0.0080
## o-Acidimicrobiales	1.132611e-05	1.206954e-04	-1.093693e-04	0.0000
## o-Deinococcales	9.627195e-06	1.206954e-05	-2.442345e-06	0.6561
## o-9	8.494584e-06	0.000000e+00	8.494584e-06	0.0607
## o-Gaiellales	1.698917e-06	1.689736e-05	-1.519844e-05	0.0000
## o-RB41	1.698917e-06	0.000000e+00	1.698917e-06	0.4015
## o-Solirubrobacterales	1.698917e-06	0.000000e+00	1.698917e-06	0.4015
## o-Sphingobacteriales	1.698917e-06	0.000000e+00	1.698917e-06	0.4015
## o-4	1.698917e-06	0.000000e+00	1.698917e-06	0.4015
## o-iii1-15	1.132611e-06	0.000000e+00	1.132611e-06	0.4934
## o-OPB54	1.132611e-06	0.000000e+00	1.132611e-06	0.4934
## o-Pirellulales	5.663056e-07	3.379471e-05	-3.322841e-05	0.0000
## o-Chlorophyta	0.000000e+00	2.413908e-06	-2.413908e-06	0.0390
## o-Myxococcales	0.000000e+00	2.413908e-06	-2.413908e-06	0.0390
## o-0319-7L14	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-[Fimbriimonadales]	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-[Saprospirales]	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-Caldilineales	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-1	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-2	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-3	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-Halanaerobiales	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-5	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-6	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-7	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-Gemmatales	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-Ellin329	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-Aeromonadales	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-[Pedosphaerales]	0.000000e+00	0.000000e+00	0.000000e+00	1.0000

3.4. Heatmap Clustering



4. Comparison of Family Composition By Gender

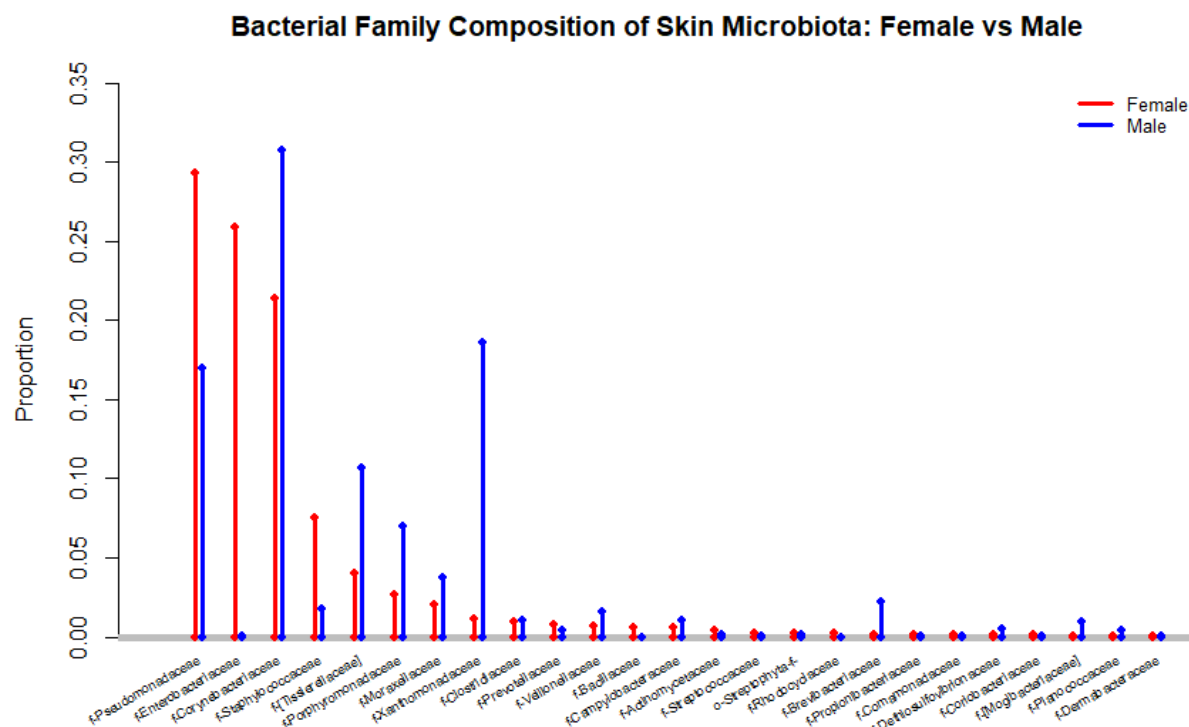
4.1. The Pearson-chi-square and likelihood ratio tests

```
## chi2 LRT
## 0 0
```

Bootstrap tests

Comparison of order proportions between Male and Female subjects.

4.2. Top 25 Significant Individual Bacterial Groups



4.3. P-values for Testing Individual Proportions

##	fp	mp	pro.diff	pval
## f-Pseudomonadaceae	2.933429e-01	1.697355e-01	1.236074e-01	0.0000
## f-Enterobacteriaceae	2.587121e-01	1.786512e-04	2.585334e-01	0.0000
## f-Corynebacteriaceae	2.141376e-01	3.069638e-01	-9.282618e-02	0.0000
## f-Staphylococcaceae	7.511913e-02	1.801721e-02	5.710192e-02	0.0000
## f-[Tissierellaceae]	4.014050e-02	1.068310e-01	-6.669050e-02	0.0000
## f-Porphyromonadaceae	2.683227e-02	6.942771e-02	-4.259545e-02	0.0000
## f-Moraxellaceae	2.004816e-02	3.695424e-02	-1.690608e-02	0.0000
## f-Xanthomonadaceae	1.158629e-02	1.859228e-01	-1.743365e-01	0.0000
## f-Clostridiaceae	9.860381e-03	1.050662e-02	-6.462398e-04	0.0002
## f-Prevotellaceae	7.552186e-03	4.536292e-03	3.015895e-03	0.0000
## f-Veillonellaceae	6.924584e-03	1.580822e-02	-8.883631e-03	0.0000
## f-Bacillaceae	5.795693e-03	1.931364e-05	5.776379e-03	0.0000
## f-Campylobacteraceae	5.544199e-03	1.021692e-02	-4.672718e-03	0.0000
## f-Actinomycetaceae	4.241414e-03	1.460594e-03	2.780820e-03	0.0000
## f-Streptococcaceae	2.025547e-03	1.520949e-04	1.873452e-03	0.0000
## o-Streptophyta-f-	1.868646e-03	1.310913e-03	5.577330e-04	0.0000
## f-Rhodocyclaceae	1.858451e-03	9.656821e-06	1.848794e-03	0.0000
## f-Brevibacteriaceae	1.810304e-03	2.228794e-02	-2.047764e-02	0.0000

## f-Propionibacteriaceae	1.541817e-03	8.449718e-04	6.968456e-04	0.0000
## f-Comamonadaceae	1.259736e-03	2.172785e-04	1.042458e-03	0.0000
## f-Dethiosulfovibrionaceae	1.250107e-03	4.917736e-03	-3.667629e-03	0.0000
## f-Coriobacteriaceae	1.074514e-03	8.015161e-04	2.729981e-04	0.0000
## f-[Mogibacteriaceae]	8.694672e-04	9.581980e-03	-8.712513e-03	0.0000
## f-Planococcaceae	7.057695e-04	4.449380e-03	-3.743611e-03	0.0000
## f-Dermabacteraceae	6.683852e-04	4.273143e-04	2.410709e-04	0.0000
## f-Sphingomonadaceae	5.550996e-04	1.013966e-04	4.537030e-04	0.0000
## f-Lactobacillaceae	4.565411e-04	2.414205e-06	4.541269e-04	0.0000
## o-Actinomycetales-f-	4.202897e-04	7.435752e-04	-3.232855e-04	0.0000
## f-Microbacteriaceae	3.970661e-04	1.121640e-02	-1.081933e-02	0.0000
## f-Bifidobacteriaceae	3.409897e-04	9.656821e-06	3.313329e-04	0.0000
## f-Fusobacteriaceae	2.633891e-04	0.000000e+00	2.633891e-04	0.0000
## f-Gemellaceae	2.480955e-04	0.000000e+00	2.480955e-04	0.0000
## f-[Weeksellaceae]	2.429977e-04	2.940502e-03	-2.697504e-03	0.0000
## f-Neisseriaceae	2.367670e-04	0.000000e+00	2.367670e-04	0.0000
## f-[Chromatiaceae]	2.248720e-04	0.000000e+00	2.248720e-04	0.0000
## f-Micrococcaceae	1.784249e-04	1.931364e-05	1.591112e-04	0.0000
## f-Methylobacteriaceae	1.699284e-04	1.134676e-04	5.646080e-05	0.0095
## f-Acetobacteraceae	1.416070e-04	0.000000e+00	1.416070e-04	0.0000
## f-Aerococcaceae	1.053556e-04	1.520949e-04	-4.673929e-05	0.0113
## f-Halomonadaceae	9.006207e-05	0.000000e+00	9.006207e-05	0.0000
## f-Rhizobiaceae	8.949565e-05	0.000000e+00	8.949565e-05	0.0000
## f-Rhodobacteraceae	8.892922e-05	0.000000e+00	8.892922e-05	0.0000
## f-Burkholderiaceae	7.476851e-05	0.000000e+00	7.476851e-05	0.0000
## f-Carnobacteriaceae	7.136995e-05	0.000000e+00	7.136995e-05	0.0000
## f-Alcaligenaceae	5.550996e-05	2.414205e-06	5.309575e-05	0.0000
## f-Lachnospiraceae	5.211139e-05	2.655626e-05	2.555513e-05	0.0313
## f-Cytophagaceae	4.927925e-05	2.172785e-05	2.755140e-05	0.0162
## f-Rhodospirillaceae	4.474782e-05	0.000000e+00	4.474782e-05	0.0000
## f-mitochondria	4.418140e-05	8.932559e-05	-4.514420e-05	0.0003
## f-Streptomyetaceae	3.681783e-05	0.000000e+00	3.681783e-05	0.0001
## f-Caulobacteraceae	3.681783e-05	0.000000e+00	3.681783e-05	0.0001
## f-Leptotrichiaceae	3.455212e-05	9.656821e-06	2.489530e-05	0.0083
## o-Rhizobiales-f-	3.285283e-05	0.000000e+00	3.285283e-05	0.0002
## f-Flavobacteriaceae	2.775498e-05	0.000000e+00	2.775498e-05	0.0007
## f-Aurantimonadaceae	2.605569e-05	1.931364e-05	6.742053e-06	0.4327
## f-[Paraprevotellaceae]	2.605569e-05	0.000000e+00	2.605569e-05	0.0010
## p-SR1-c-o-f-	2.605569e-05	0.000000e+00	2.605569e-05	0.0010
## o-Gemellales-f-	2.435641e-05	0.000000e+00	2.435641e-05	0.0015
## f-Kineosporiaceae	2.378998e-05	1.931364e-05	4.476341e-06	0.5883
## f-Cellulomonadaceae	2.378998e-05	0.000000e+00	2.378998e-05	0.0017
## f-[Chthoniobacteraceae]	1.982499e-05	0.000000e+00	1.982499e-05	0.0042
## o-Synergistales-f-	1.925856e-05	2.076216e-04	-1.883631e-04	0.0000
## f-Xanthobacteraceae	1.869213e-05	0.000000e+00	1.869213e-05	0.0054
## f-Pasteurellaceae	1.869213e-05	0.000000e+00	1.869213e-05	0.0054
## o-WD2101-f-	1.755927e-05	0.000000e+00	1.755927e-05	0.0070
## f-S24-7	1.699284e-05	0.000000e+00	1.699284e-05	0.0080
## f-Planctomycetaceae	1.699284e-05	0.000000e+00	1.699284e-05	0.0080
## o-CW040-f-	1.699284e-05	0.000000e+00	1.699284e-05	0.0080

## f-Nocardioideaceae	1.642642e-05	1.931364e-05	-2.887225e-06	0.6848
## o-Clostridiales-f-	1.529356e-05	2.052074e-04	-1.899139e-04	0.0000
## f-Peptococcaceae	1.302785e-05	1.624760e-03	-1.611732e-03	0.0000
## f-Phyllobacteriaceae	1.189499e-05	3.379887e-05	-2.190388e-05	0.0015
## f-Deinococcaceae	9.629278e-06	1.207103e-05	-2.441747e-06	0.6562
## o-Acidimicrobiales-f-	8.496422e-06	1.207103e-04	-1.122138e-04	0.0000
## c-TM7-3-o-f-	8.496422e-06	0.000000e+00	8.496422e-06	0.0607
## f-Peptostreptococcaceae	5.664281e-06	8.449718e-05	-7.883290e-05	0.0000
## f-Oxalobacteraceae	3.398569e-06	5.552672e-05	-5.212815e-05	0.0000
## f-Mycobacteriaceae	3.398569e-06	0.000000e+00	3.398569e-06	0.2354
## f-Shewanellaceae	3.398569e-06	0.000000e+00	3.398569e-06	0.2354
## f-EB1017	2.832141e-06	0.000000e+00	2.832141e-06	0.2788
## o-Caulobacteriales-f-	2.265713e-06	0.000000e+00	2.265713e-06	0.3327
## f-Gaiellaceae	1.699284e-06	1.689944e-05	-1.520015e-05	0.0000
## f-Ellin6075	1.699284e-06	0.000000e+00	1.699284e-06	0.4015
## f-Jonesiaceae	1.699284e-06	0.000000e+00	1.699284e-06	0.4015
## o-Solirubrobacteriales-f-	1.699284e-06	0.000000e+00	1.699284e-06	0.4015
## f-Sphingobacteriaceae	1.699284e-06	0.000000e+00	1.699284e-06	0.4015
## p-FBP-c--o-f-	1.699284e-06	0.000000e+00	1.699284e-06	0.4015
## o-Bacillales-f-	1.699284e-06	0.000000e+00	1.699284e-06	0.4015
## f-Bradyrhizobiaceae	1.699284e-06	0.000000e+00	1.699284e-06	0.4015
## f-Hyphomicrobiaceae	1.699284e-06	0.000000e+00	1.699284e-06	0.4015
## f-RB40	1.132856e-06	0.000000e+00	1.132856e-06	0.4933
## o-OPB54-f-	1.132856e-06	0.000000e+00	1.132856e-06	0.4933
## f-Pirellulaceae	5.664281e-07	3.379887e-05	-3.323244e-05	0.0000
## f-Frankiaceae	5.664281e-07	0.000000e+00	5.664281e-07	0.6281
## f-[Exiguobacteraceae]	5.664281e-07	0.000000e+00	5.664281e-07	0.6281
## f-Thermoactinomycesaceae	5.664281e-07	0.000000e+00	5.664281e-07	0.6281
## f-Ruminococcaceae	0.000000e+00	3.186751e-04	-3.186751e-04	0.0000
## f-Bacteroidaceae	0.000000e+00	9.656821e-05	-9.656821e-05	0.0000
## f-Dermacoccaceae	0.000000e+00	7.001195e-05	-7.001195e-05	0.0000
## f-Williamsiaceae	0.000000e+00	1.689944e-05	-1.689944e-05	0.0000
## f-Dietziaceae	0.000000e+00	9.656821e-06	-9.656821e-06	0.0000
## f-Micromonosporaceae	0.000000e+00	2.414205e-06	-2.414205e-06	0.0390
## o-Chlorophyta-f-	0.000000e+00	2.414205e-06	-2.414205e-06	0.0390
## f-Cystobacteraceae	0.000000e+00	2.414205e-06	-2.414205e-06	0.0390
## f-Geodermatophilaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Intrasporangiaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Nocardiaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Thermomonosporaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-0319-7L14-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-[Fimbriimonadaceae]	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Chitinophagaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Caldilineaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## c-Ellin6529-o-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## c-Gitt-GS-136-o-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Trebouxioephyceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## c-ML635J-21-o-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Paenibacillaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Enterococcaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000

## f-Leuconostocaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Gracilibacteraceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Halanaerobiaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## c-OPB54-o-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## p-GN02-c--o-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## c-BD1-5-o-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Isosphaeraceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-Ellin329-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Beijerinckiaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Brucellaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Methylocystaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-Rhodospirillalesf-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Rickettsiaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Erythrobacteraceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## o-Myxococcales-f-	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Haliangiaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Polyangiaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Aeromonadaceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Sinobacteraceae	0.000000e+00	0.000000e+00	0.000000e+00	1.0000
## f-Ellin515	0.000000e+00	0.000000e+00	0.000000e+00	1.0000

5. Comparison of Genus Composition By Gender

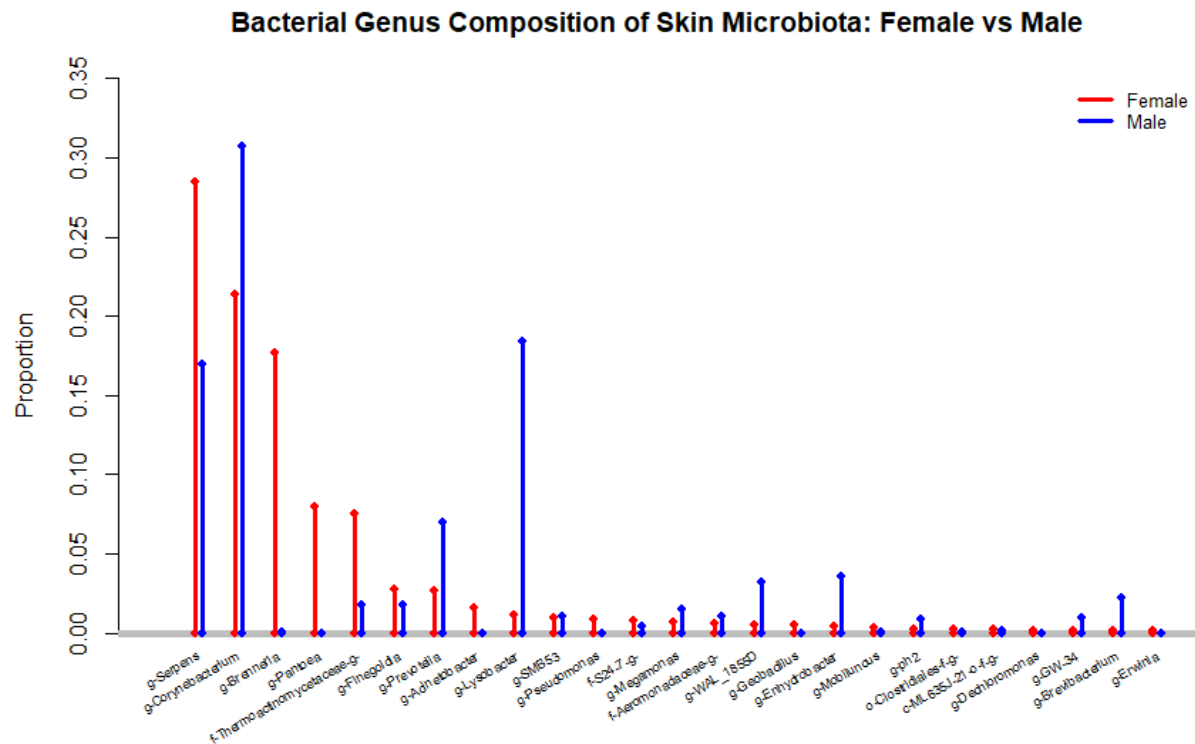
5.1. The Pearson-chisquare and likelihood ratio tests

```
## chi2  LRT
##      0    0
```

Bootstrap tests

Comparison of order proportions between Male and Female subjects.

5.2. Top 25 Significant Individual Bacterial Groups



5.3. P-values for Testing Individual Proportions

##	fp	mp	pro.diff	pval
## g-Serpens	2.850241e-01	1.696923e-01	1.153317e-01	0.0000
## g-Corynebacterium	2.140728e-01	3.069147e-01	-9.284189e-02	0.0000
## g-Brenneria	1.770684e-01	1.303432e-04	1.769380e-01	0.0000
## g-Pantoea	7.934891e-02	2.413762e-05	7.932477e-02	0.0000
## f-Thermoactinomycetaceae-g-	7.511978e-02	1.801632e-02	5.710346e-02	0.0000
## g-Finegoldia	2.735144e-02	1.749495e-02	9.856493e-03	0.0000
## g-Prevotella	2.683731e-02	6.938360e-02	-4.254629e-02	0.0000
## g-Acinetobacter	1.586050e-02	7.241287e-06	1.585325e-02	0.0000
## g-Lysobacter	1.086923e-02	1.840494e-01	-1.731801e-01	0.0000
## g-SMB53	9.861354e-03	1.052883e-02	-6.674768e-04	0.0001
## g-Pseudomonas	8.206282e-03	3.137891e-05	8.174903e-03	0.0000
## f-S24-7-g-	7.547764e-03	4.523391e-03	3.024373e-03	0.0000
## g-Megamonas	6.676912e-03	1.458637e-02	-7.909454e-03	0.0000
## f-Aeromonadaceae-g-	5.542765e-03	1.022470e-02	-4.681932e-03	0.0000
## g-WAL_1855D	5.344021e-03	3.170718e-02	-2.636316e-02	0.0000
## g-Geobacillus	5.110170e-03	1.689634e-05	5.093274e-03	0.0000
## g-Enhydrobacter	3.852021e-03	3.588058e-02	-3.202856e-02	0.0000
## g-Mobiluncus	3.113665e-03	2.220661e-04	2.891599e-03	0.0000

## g-ph2	2.047465e-03	8.798164e-03	-6.750698e-03	0.0000
## o-Clostridiales-f-g-	2.000469e-03	1.303432e-04	1.870126e-03	0.0000
## c-ML635J-21-o-f-g-	1.874767e-03	1.291363e-03	5.834043e-04	0.0000
## g-Dechloromonas	1.837963e-03	1.689634e-05	1.821066e-03	0.0000
## g-GW-34	1.812483e-03	9.382294e-03	-7.569812e-03	0.0000
## g-Brevibacterium	1.801724e-03	2.229592e-02	-2.049420e-02	0.0000
## g-Erwinia	1.657337e-03	2.413762e-06	1.654923e-03	0.0000
## f-Halanaerobiaceae-g-	1.598450e-03	3.765469e-03	-2.167019e-03	0.0000
## g-Anaerococcus	1.448967e-03	2.092732e-02	-1.947835e-02	0.0000
## g-Pyramidobacter	1.250222e-03	4.914420e-03	-3.664198e-03	0.0000
## g-Propionibacterium	1.023166e-03	5.406828e-04	4.824837e-04	0.0000
## g-Atopobium	9.472925e-04	7.530938e-04	1.941986e-04	0.0002
## g-Mogibacterium	8.680211e-04	9.551257e-03	-8.683236e-03	0.0000
## g-Xanthomonas	7.168394e-04	1.778943e-03	-1.062103e-03	0.0000
## g-Actinomyces	7.162732e-04	1.214122e-03	-4.978493e-04	0.0000
## g-Lysinibacillus	7.077798e-04	4.453391e-03	-3.745612e-03	0.0000
## g-Dermabacter	6.494587e-04	4.175809e-04	2.318779e-04	0.0000
## g-Diaphorobacter	5.945350e-04	1.882735e-04	4.062616e-04	0.0000
## g-Bacillus	5.934026e-04	7.241287e-06	5.861613e-04	0.0000
## g-Acidovorax	5.045054e-04	2.172386e-05	4.827816e-04	0.0000
## f-Propionibacteriaceae-g-	4.960121e-04	3.065478e-04	1.894643e-04	0.0000
## g-Gallicola	4.546777e-04	1.070262e-02	-1.024794e-02	0.0000
## g-Leuconostoc	4.546777e-04	7.241287e-06	4.474365e-04	0.0000
## g-Sphingosinicella	4.325950e-04	9.413673e-05	3.384583e-04	0.0000
## o_Actinomycetales-f-g-	4.235354e-04	7.506801e-04	-3.271446e-04	0.0000
## g-Trabulsiella	3.838998e-04	0.000000e+00	3.838998e-04	0.0000
## f-Coriobacteriaceae-g-	3.436979e-04	0.000000e+00	3.436979e-04	0.0000
## g-Pseudoclavibacter	3.204827e-04	3.162029e-04	4.279832e-06	0.8897
## g-Actinobaculum	3.034960e-04	0.000000e+00	3.034960e-04	0.0000
## g-Psychrobacter	2.848106e-04	1.030677e-03	-7.458659e-04	0.0000
## g-Leptotrichia	2.666914e-04	0.000000e+00	2.666914e-04	0.0000
## f-Enterobacteriaceae-g-	2.440425e-04	0.000000e+00	2.440425e-04	0.0000
## g-Elizabethkingia	2.281882e-04	0.000000e+00	2.281882e-04	0.0000
## f-[Mogibacteriaceae]-g-	2.044068e-04	9.655049e-06	1.947518e-04	0.0000
## g-Gemella	2.027081e-04	0.000000e+00	2.027081e-04	0.0000
## f_Rhodocyclaceae-g-	1.375924e-04	2.413762e-06	1.351786e-04	0.0000
## f-Rhodospirillaceae-g-	1.364599e-04	2.413762e-06	1.340462e-04	0.0000
## f-Methylocystaceae-g-	1.274004e-04	8.206792e-05	4.533245e-05	0.0160
## o-0319-7L14-f-g-	1.251355e-04	4.586148e-05	7.927399e-05	0.0000
## g-Rothia	1.115461e-04	0.000000e+00	1.115461e-04	0.0000
## g-Neisseria	9.739050e-05	2.413762e-06	9.497674e-05	0.0000
## g-Halomonas	9.739050e-05	0.000000e+00	9.739050e-05	0.0000
## g-Actinobacillus	8.946337e-05	0.000000e+00	8.946337e-05	0.0000
## g-Helcococcus	8.097001e-05	2.244799e-04	-1.435099e-04	0.0000
## g-Arcanobacterium	7.813889e-05	1.689634e-05	6.124255e-05	0.0000
## g-Rhodobacter	7.530777e-05	0.000000e+00	7.530777e-05	0.0000
## g-Enterococcus	7.134420e-05	2.413762e-06	6.893044e-05	0.0000
## g-Labrys	6.738064e-05	2.413762e-06	6.496687e-05	0.0000
## g-Ornithinibacillus	6.738064e-05	0.000000e+00	6.738064e-05	0.0000
## g-Lautropia	6.624819e-05	0.000000e+00	6.624819e-05	0.0000

## g-Delftia	6.398329e-05	0.000000e+00	6.398329e-05	0.0000
## g-Klebsiella	6.285085e-05	0.000000e+00	6.285085e-05	0.0000
## g-Kaistobacter	6.228462e-05	1.206881e-05	5.021581e-05	0.0001
## g-Victoria	6.001973e-05	8.689544e-05	-2.687572e-05	0.0537
## g-Abiotrophia	5.718861e-05	0.000000e+00	5.718861e-05	0.0000
## f-Aerococcaceae-g-	5.322504e-05	0.000000e+00	5.322504e-05	0.0000
## g-Oribacterium	5.152637e-05	2.172386e-05	2.980251e-05	0.0108
## g-Facklamia	5.152637e-05	4.827525e-06	4.669884e-05	0.0000
## g-Spirosoma	4.699658e-05	3.620643e-05	1.079014e-05	0.3512
## g-Aurantimonas	4.699658e-05	1.689634e-05	3.010024e-05	0.0066
## f-Micrococcaceae-g-	4.643036e-05	2.413762e-06	4.401659e-05	0.0000
## g-Variovorax	4.529791e-05	0.000000e+00	4.529791e-05	0.0000
## g-Skermanella	3.963567e-05	0.000000e+00	3.963567e-05	0.0001
## f-Microbacteriaceae-g-	3.906945e-05	8.986437e-03	-8.947368e-03	0.0000
## p-GN02-c-o-f-g-	3.737077e-05	4.827525e-06	3.254325e-05	0.0007
## g-Brevundimonas	3.623833e-05	2.413762e-06	3.382456e-05	0.0003
## o-Rhizobiales-f-g-	3.567210e-05	2.413762e-06	3.325834e-05	0.0004
## g-Propionimicrobium	3.510588e-05	0.000000e+00	3.510588e-05	0.0001
## g-Rathayibacter	3.397343e-05	9.655049e-06	2.431838e-05	0.0093
## f-Pseudomonadaceae-g-	3.397343e-05	2.413762e-06	3.155967e-05	0.0005
## g-Selenomonas	3.340721e-05	0.000000e+00	3.340721e-05	0.0002
## f-Gemellaceae-g-	3.284098e-05	4.827525e-06	2.801346e-05	0.0020
## f-Oxalobacteraceae-g-	3.227476e-05	2.413762e-06	2.986100e-05	0.0008
## g-Sutterella	3.057609e-05	0.000000e+00	3.057609e-05	0.0004
## g-Dyadobacter	3.000986e-05	0.000000e+00	3.000986e-05	0.0004
## f-Streptomycetaceae-g-	2.831119e-05	0.000000e+00	2.831119e-05	0.0006
## g-Methylobacterium	2.774497e-05	2.413762e-05	3.607345e-06	0.6879
## g-Kineococcus	2.717874e-05	1.931010e-05	7.868646e-06	0.3684
## o-Synergistales-f-g-	2.717874e-05	0.000000e+00	2.717874e-05	0.0008
## g-Streptococcus	2.661252e-05	7.241287e-06	1.937123e-05	0.0191
## g-Agrobacterium	2.548007e-05	2.413762e-06	2.306631e-05	0.0036
## g-Demequina	2.378140e-05	0.000000e+00	2.378140e-05	0.0017
## g-Novosphingobium	2.264895e-05	2.413762e-06	2.023519e-05	0.0069
## g-Jonquetella	2.208273e-05	2.196524e-04	-1.975696e-04	0.0000
## g-[Prevotella]	2.208273e-05	0.000000e+00	2.208273e-05	0.0025
## g-Flavobacterium	2.208273e-05	0.000000e+00	2.208273e-05	0.0025
## g-Deinobacterium	2.038406e-05	0.000000e+00	2.038406e-05	0.0037
## f-Rhodobacteraceae-g-	1.868539e-05	0.000000e+00	1.868539e-05	0.0054
## g-Azospira	1.811916e-05	0.000000e+00	1.811916e-05	0.0061
## f-Clostridiaceae-g-	1.755294e-05	2.051698e-04	-1.876169e-04	0.0000
## g-Varibaculum	1.755294e-05	1.206881e-05	5.484128e-06	0.4343
## f-Isosphaeraceae-g-	1.755294e-05	0.000000e+00	1.755294e-05	0.0070
## g-Quadrisphaera	1.698672e-05	9.655049e-06	7.331666e-06	0.2821
## g-Polaromonas	1.698672e-05	0.000000e+00	1.698672e-05	0.0080
## g-Microbacterium	1.642049e-05	3.137891e-05	-1.495842e-05	0.0483
## f-Peptostreptococcaceae-g-	1.585427e-05	1.631703e-03	-1.615849e-03	0.0000
## g-Trueperella	1.585427e-05	0.000000e+00	1.585427e-05	0.0104
## g-Capnocytophaga	1.585427e-05	0.000000e+00	1.585427e-05	0.0104
## f-Rhizobiaceae-g-	1.528804e-05	2.896515e-05	-1.367710e-05	0.0610
## g-Devriesea	1.415560e-05	0.000000e+00	1.415560e-05	0.0154

## g-Sphingomonas	1.415560e-05	0.000000e+00	1.415560e-05	0.0154
## g-Shewanella	1.415560e-05	0.000000e+00	1.415560e-05	0.0154
## o-Caulobacteriales-f-g-	1.358937e-05	0.000000e+00	1.358937e-05	0.0177
## f-Ellin515-g-	1.302315e-05	0.000000e+00	1.302315e-05	0.0202
## g-Aggregatibacter	1.245692e-05	7.241287e-06	5.215638e-06	0.3722
## g-Amaricoccus	1.189070e-05	0.000000e+00	1.189070e-05	0.0265
## f-Comamonadaceae-g-	1.189070e-05	0.000000e+00	1.189070e-05	0.0265
## o-Acidimicrobiales-f-g-	1.132448e-05	1.303432e-04	-1.190187e-04	0.0000
## TotalCounts	1.132448e-05	1.206881e-05	-7.443347e-07	0.8987
## g-Mycetocola	1.019203e-05	1.708944e-03	-1.698752e-03	0.0000
## g-Roseomonas	1.019203e-05	2.413762e-06	7.778267e-06	0.1269
## g-Oligella	1.019203e-05	0.000000e+00	1.019203e-05	0.0399
## f-Neisseriaceae-g-	9.059581e-06	0.000000e+00	9.059581e-06	0.0527
## g-Friedmanniella	8.493358e-06	0.000000e+00	8.493358e-06	0.0607
## f-Paenibacillaceae-g-	8.493358e-06	0.000000e+00	8.493358e-06	0.0607
## g-	7.927134e-06	1.931010e-05	-1.138296e-05	0.0379
## g-Kocuria	7.927134e-06	7.241287e-06	6.858469e-07	0.8869
## g-Streptomyces	7.927134e-06	0.000000e+00	7.927134e-06	0.0700
## o-CW040-f-g-	7.927134e-06	0.000000e+00	7.927134e-06	0.0700
## g-Veillonella	7.360910e-06	0.000000e+00	7.360910e-06	0.0808
## f-Sinobacteraceae-g-	7.360910e-06	0.000000e+00	7.360910e-06	0.0808
## g-Deinococcus	6.228462e-06	0.000000e+00	6.228462e-06	0.1082
## g-Chryseobacterium	5.662238e-06	2.939962e-03	-2.934300e-03	0.0000
## f-Trebouxioephyceae-g-	5.662238e-06	7.241287e-06	-1.579049e-06	0.7079
## g-Rhizobium	5.662238e-06	0.000000e+00	5.662238e-06	0.1256
## g-Granulicatella	5.096015e-06	1.593083e-04	-1.542123e-04	0.0000
## g-Micrococcus	5.096015e-06	1.206881e-05	-6.972797e-06	0.1109
## g-Zea	5.096015e-06	2.413762e-06	2.682252e-06	0.4681
## g-Mycobacterium	5.096015e-06	0.000000e+00	5.096015e-06	0.1462
## g-Fimbriimonas	5.096015e-06	0.000000e+00	5.096015e-06	0.1462
## g-Terribacillus	5.096015e-06	0.000000e+00	5.096015e-06	0.1462
## g-Ureibacillus	5.096015e-06	0.000000e+00	5.096015e-06	0.1462
## f-[Chromatiaceae]-g-	5.096015e-06	0.000000e+00	5.096015e-06	0.1462
## f-Ruminococcaceae-g-	4.529791e-06	8.689544e-05	-8.236565e-05	0.0000
## g-Brooklawnia	4.529791e-06	2.413762e-06	2.116028e-06	0.5463
## g-Pasteurella	4.529791e-06	2.413762e-06	2.116028e-06	0.5463
## g-Pedobacter	4.529791e-06	0.000000e+00	4.529791e-06	0.1707
## g-Didymeles	4.529791e-06	0.000000e+00	4.529791e-06	0.1707
## g-Citrobacter	4.529791e-06	0.000000e+00	4.529791e-06	0.1707
## g-Nesterenkonia	3.963567e-06	0.000000e+00	3.963567e-06	0.2000
## o-Bacillales-f-g-	3.963567e-06	0.000000e+00	3.963567e-06	0.2000
## f-Bacillaceae-g-	3.963567e-06	0.000000e+00	3.963567e-06	0.2000
## f-Phyllobacteriaceae-g-	3.963567e-06	0.000000e+00	3.963567e-06	0.2000
## g-Serratia	3.963567e-06	0.000000e+00	3.963567e-06	0.2000
## g-Cupriavidus	3.397343e-06	4.103396e-05	-3.763662e-05	0.0000
## g-Staphylococcus	3.397343e-06	0.000000e+00	3.397343e-06	0.2355
## g-Hydrogenophaga	3.397343e-06	0.000000e+00	3.397343e-06	0.2355
## g-Rubrivivax	3.397343e-06	0.000000e+00	3.397343e-06	0.2355
## o-Solirubrobacteriales-f-g-	2.831119e-06	1.931010e-05	-1.647898e-05	0.0001
## f-EB1017-g-	2.831119e-06	0.000000e+00	2.831119e-06	0.2788

## g-Cystobacter	2.831119e-06	0.000000e+00	2.831119e-06	0.2788
## g-Enterobacter	2.831119e-06	0.000000e+00	2.831119e-06	0.2788
## g-Yonghaparkia	2.264895e-06	2.655139e-05	-2.428649e-05	0.0000
## f-Ellin6075-g-	2.264895e-06	2.413762e-06	-1.488669e-07	0.9546
## g-Arthrobacter	2.264895e-06	0.000000e+00	2.264895e-06	0.3327
## g-Blautia	2.264895e-06	0.000000e+00	2.264895e-06	0.3327
## f-Caulobacteraceae-g-	2.264895e-06	0.000000e+00	2.264895e-06	0.3327
## o-Rhodospirillales-f-g-	2.264895e-06	0.000000e+00	2.264895e-06	0.3327
## g-Comamonas	2.264895e-06	0.000000e+00	2.264895e-06	0.3327
## g-Candidatus Hamiltonella	2.264895e-06	0.000000e+00	2.264895e-06	0.3327
## g-Faecalibacterium	1.698672e-06	1.906872e-04	-1.889886e-04	0.0000
## f-[Tissierellaceae]-g-	1.698672e-06	2.413762e-05	-2.243895e-05	0.0000
## g-Brachybacterium	1.698672e-06	4.827525e-06	-3.128853e-06	0.2313
## f-Geodermatophilaceae-g-	1.698672e-06	4.827525e-06	-3.128853e-06	0.2313
## f-[Weeksellaceae]-g-	1.698672e-06	2.413762e-06	-7.150908e-07	0.7597
## f-RB40-g-	1.698672e-06	0.000000e+00	1.698672e-06	0.4015
## g-Virgibacillus	1.698672e-06	0.000000e+00	1.698672e-06	0.4015
## g-Coproccoccus	1.698672e-06	0.000000e+00	1.698672e-06	0.4015
## g-Bradyrhizobium	1.698672e-06	0.000000e+00	1.698672e-06	0.4015
## g-Rhodoplanes	1.698672e-06	0.000000e+00	1.698672e-06	0.4015
## g-Buchnera	1.698672e-06	0.000000e+00	1.698672e-06	0.4015
## g-Dickeya	1.698672e-06	0.000000e+00	1.698672e-06	0.4015
## c-TM7-3-o-f-g-	1.698672e-06	0.000000e+00	1.698672e-06	0.4015
## g-1-68	1.132448e-06	2.831343e-03	-2.830211e-03	0.0000
## g-Marinibacillus	1.132448e-06	2.413762e-06	-1.281315e-06	0.5269
## f-Planococcaceae-g-	1.132448e-06	2.413762e-06	-1.281315e-06	0.5269
## g-Burkholderia	1.132448e-06	2.413762e-06	-1.281315e-06	0.5269
## g-Janibacter	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Jonesia	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Agromyces	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Microbispora	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Rhodococcus	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Hymenobacter	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Sphingobacterium	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## f-Chitinophagaceae-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## c-Ellin6529-o-f-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Macroccoccus	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Exiguobacterium	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-[Ruminococcus]	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Peptococcus	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Peptostreptococcus	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## o-OPB54-f-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## c-OPB54-o-;f-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## o-Ellin329-f-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## f-Beijerinckiaceae-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Ochrobactrum	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Hyphomicrobium	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## f-Methylobacteriaceae-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Rickettsia	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## f-Erythrobacteraceae-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934

## g-Ralstonia	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## o-Myxococcales-f-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Haemophilus	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## p-SR1c-f-g-	1.132448e-06	0.000000e+00	1.132448e-06	0.4934
## g-Peptoniphilus	5.662238e-07	9.751600e-04	-9.745937e-04	0.0000
## g-Curtobacterium	5.662238e-07	6.999911e-05	-6.943288e-05	0.0000
## g-Leucobacter	5.662238e-07	5.068901e-05	-5.012278e-05	0.0000
## g-Bifidobacterium	5.662238e-07	2.172386e-05	-2.115764e-05	0.0000
## f-Kineosporiaceae-g-	5.662238e-07	2.413762e-06	-1.847538e-06	0.2638
## g-Frigoribacterium	5.662238e-07	2.413762e-06	-1.847538e-06	0.2638
## f-Streptococcaceae-g-	5.662238e-07	2.413762e-06	-1.847538e-06	0.2638
## g-Balneimonas	5.662238e-07	2.413762e-06	-1.847538e-06	0.2638
## f-Xanthomonadaceae-g-	5.662238e-07	2.413762e-06	-1.847538e-06	0.2638
## f-Dermabacteraceae-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## f-Frankiaceae-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Candidatus Aquiluna	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Cryocola	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Actinomadura	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## f-Gaiellaceae-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Bacteroides	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Cloacibacterium	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## f-Caldilineaceae-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## c-Gitt-GS-136-o-f-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## o-Chlorophyta-f-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## o-Streptophyta-f-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Solibacillus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## o-Gemellales-f-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Aerococcus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Lactobacillus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Lactococcus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Alkaliphilus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Caloramator	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Lutispora	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## f-Lachnospiraceae-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Ruminococcus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## c-BD1-5-o-fg-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## o-WD2101-f-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## f-Pirellulaceae-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Pirellula	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Mycoplana	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## o-Rhizobiales-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Aminobacter	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Mesorhizobium	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Paracoccus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## f-Acetobacteraceae-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Wolbachia	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## f-mitochondria-g-	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Citrullus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Geranium	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Nelumbo	5.662238e-07	0.000000e+00	5.662238e-07	0.6281

## g-Sphingobium	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Achromobacter	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Alicyclophilus	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Janthinobacterium	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Byssovorax	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Campylobacter	5.662238e-07	0.000000e+00	5.662238e-07	0.6281
## g-Dialister	0.000000e+00	1.209295e-03	-1.209295e-03	0.0000
## g-Acidaminococcus	0.000000e+00	1.110331e-04	-1.110331e-04	0.0000
## g-Parabacteroides	0.000000e+00	9.655049e-05	-9.655049e-05	0.0000
## g-Dermacoccus	0.000000e+00	7.241287e-05	-7.241287e-05	0.0000
## g-Pseudoxanthomonas	0.000000e+00	6.275782e-05	-6.275782e-05	0.0000
## g-Porphyromonas	0.000000e+00	3.620643e-05	-3.620643e-05	0.0000
## g-Planctomyces	0.000000e+00	2.896515e-05	-2.896515e-05	0.0000
## g-Desulfotomaculum	0.000000e+00	2.172386e-05	-2.172386e-05	0.0000
## g-Agrococcus	0.000000e+00	1.689634e-05	-1.689634e-05	0.0000
## g-Megasphaera	0.000000e+00	1.448257e-05	-1.448257e-05	0.0000
## f-Moraxellaceae-g-	0.000000e+00	9.655049e-06	-9.655049e-06	0.0000
## f-Dietziaceae-g-	0.000000e+00	7.241287e-06	-7.241287e-06	0.0003
## p-FBP-c-o-f-g-	0.000000e+00	7.241287e-06	-7.241287e-06	0.0003
## g-Moryella	0.000000e+00	7.241287e-06	-7.241287e-06	0.0003
## g-Gardnerella	0.000000e+00	4.827525e-06	-4.827525e-06	0.0035
## g-Oscillospira	0.000000e+00	4.827525e-06	-4.827525e-06	0.0035
## f-Intrasporangiaceae-g-	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-Clavibacter	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-Glaciibacter	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-Couchioplanes	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-Staphylococcus	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-Clostridium	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-Catonella	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-Fusobacterium	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## f-Sphingomonadaceae-g-	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## f-Haliangiaceae-g-	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-Stenotrophomonas	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390
## g-DA101	0.000000e+00	2.413762e-06	-2.413762e-06	0.0390