

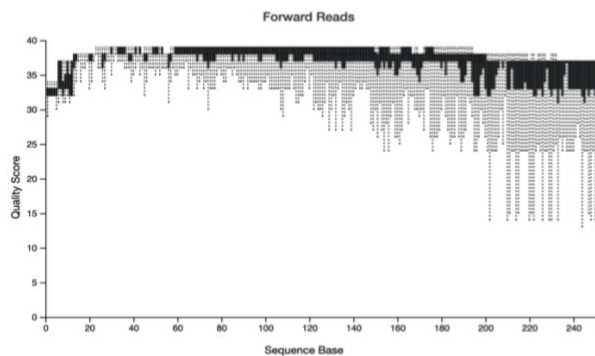
- 1.) I believe the population, sex, and flock columns will be useful for beta and alpha diversity. Population will help distinguish between migratory vs. resident. Sex can help if diversity differs between sex. Flock will help for diversity analysis as it groups sex and population together.
- 2.) Based on the plot, I would choose to trim --p-trunc-len-f 240, --p-trunc-len-r 180, --p-trim-left-f 0, & --p-trim-left-r 0. This is because for the forward reads you can see that the quality scores start to decrease after 240, similar with 180 on the reverse reads. For the start, I didn't trim anything because the quality scores were high. It also ensures that you don't accidentally cut off your primers.



Overview

Interactive Quality Plot

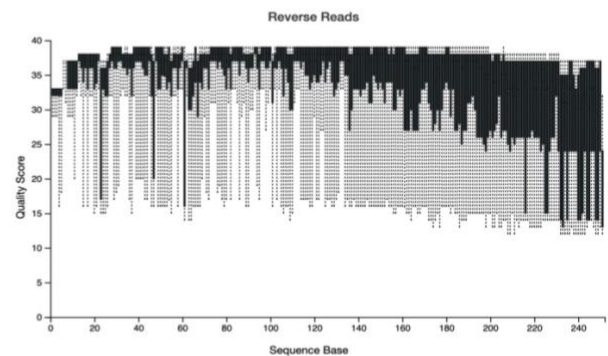
Click and drag on plot to zoom in. Double click to zoom back out to full size. Hover over a box to see the parametric seven-number summary of the quality scores at the corresponding position.



The plot at position 62 was generated using a random sampling of 10000 out of 332023 sequences without replacement. The minimum sequence length identified during subsampling was 247 bases. Outlier quality scores are not shown in box plots for clarity.

Parametric seven-number summary for position 62

| Box plot feature | Percentile | Quality score |
|------------------|------------|---------------|
| min              | 10         | 30            |
| Q1               | 25         | 35            |
| Median           | 50         | 38            |
| Q3               | 75         | 39            |
| max              | 90         | 40            |

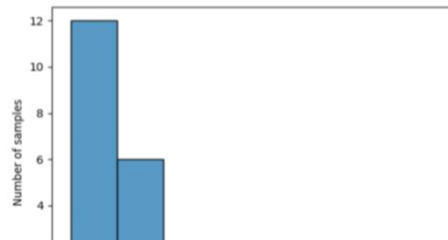


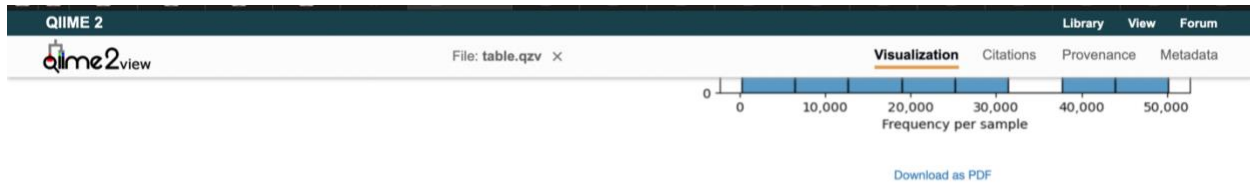
The plot at position 20 was generated using a random sampling of 10000 out of 332023 sequences without replacement. The minimum sequence length identified during subsampling was 246 bases. Outlier quality scores are not shown in box plots for clarity.

Parametric seven-number summary for position 20

| Box plot feature | Percentile | Quality score |
|------------------|------------|---------------|
| min              | 10         | 25            |
| Q1               | 25         | 30            |
| Median           | 50         | 35            |
| Q3               | 75         | 38            |
| max              | 90         | 40            |

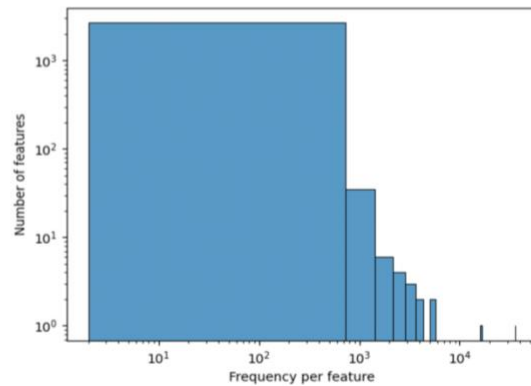
- 3.) Yes, there are 16 in total with less than 10,000 reads. There are 147\_S172\_L001, 80\_S123\_L001, 206\_S124\_L001, 386\_S173\_L001, 11\_S125\_L001, 375\_S99\_L001, 56\_S151\_L001, 273\_S101\_L001, 79\_S103\_L001, 267\_S150\_L001, 339\_S174\_L001, 179\_S127\_L001, 124\_S152\_L001, 270\_S126\_L001, 164\_S100\_L001, & 302\_S171\_L001.



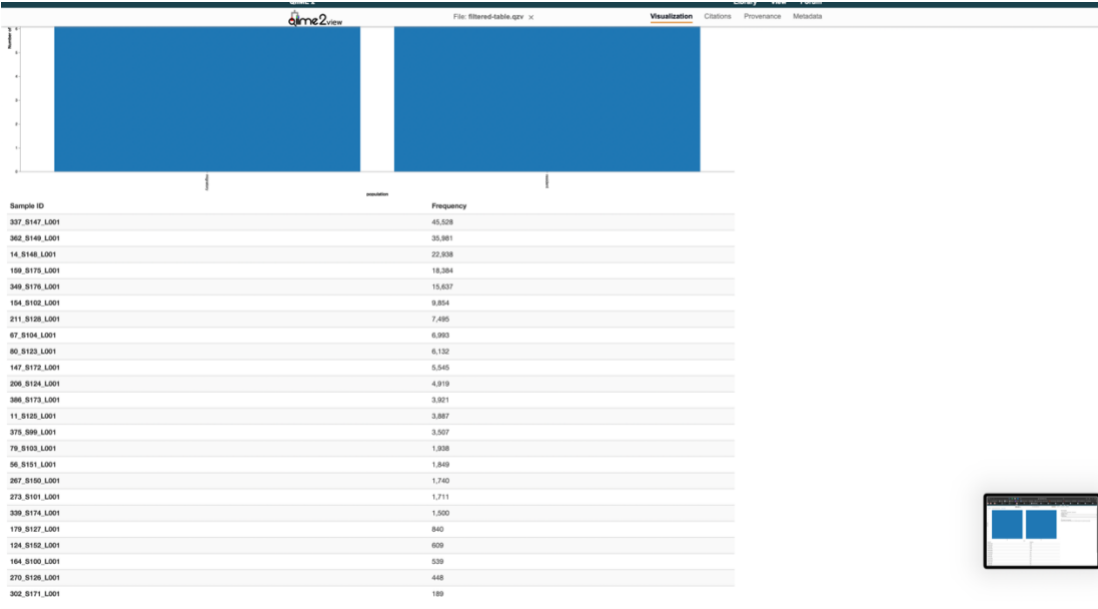
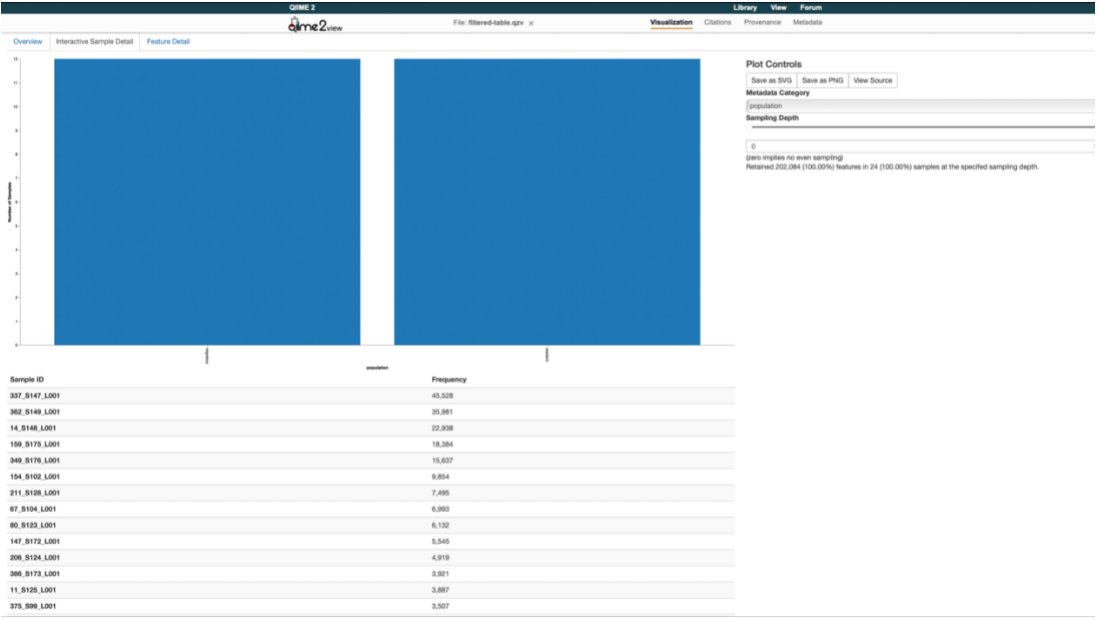


### Frequency per feature

|                   | Frequency |
|-------------------|-----------|
| Minimum frequency | 2         |
| 1st quartile      | 11        |
| Median frequency  | 24        |
| 3rd quartile      | 50        |
| Maximum frequency | 36,041    |
| Mean frequency    | 93.8      |



- 4.) My top 3 hits sorted by confidence levels are 0.9999999339764707, 0.9999998136930262, and 0.9999997261496054. When sorted by taxon by top 3 hits were all unassigned.
- 5.) Level 3 of taxonomy would be Class. A trend I noticed was that most of the top hits based on confidence were from the class alphaproteobacteria, cytophagia, actinobacteria, and grammaproteobacteria.
- 6.) The cutoff value I would choose is 9,000 as it contains adequate amount of samples with high reads, while discarding the samples under 9,000 as it wouldn't be ideal for alpha and beta diversity.



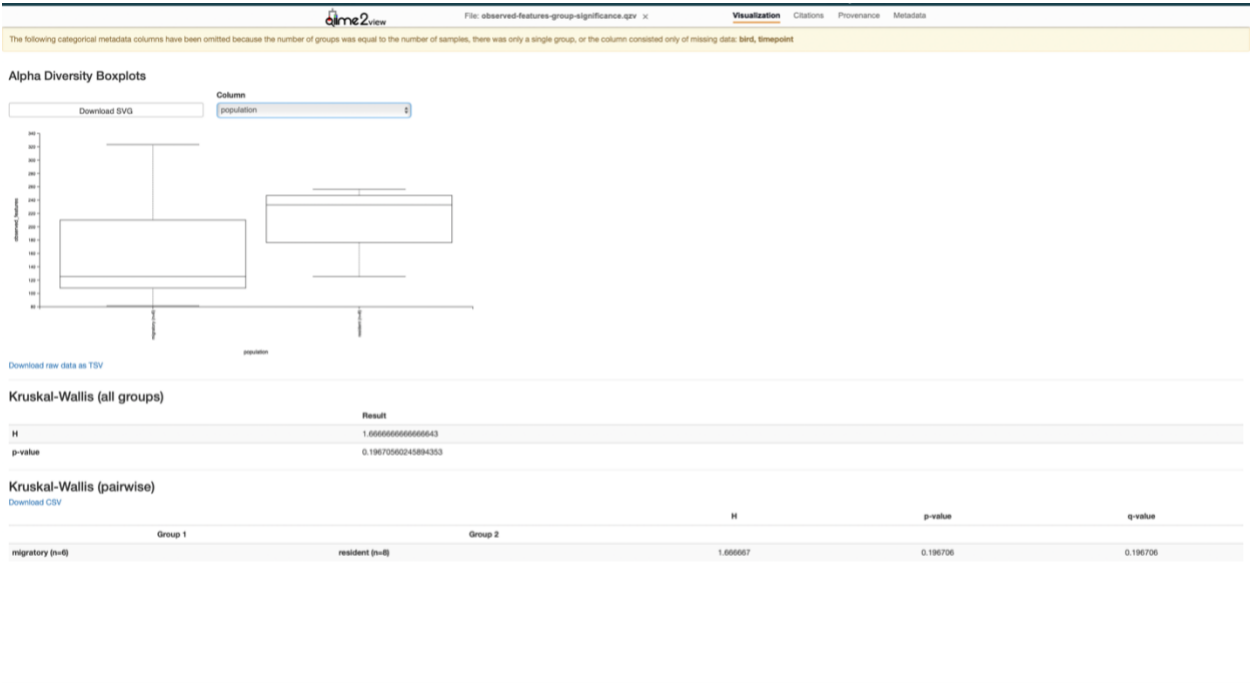
7.) Alpha diversity measures the richness and evenness of the samples provided. The differences between the two alpha diversities used is that for observed features it measures the numbers of unique taxa in the samples, which only focuses on the richness of the sample. While Shannon diversity measures the combination of richness and evenness, which focuses on the number of taxa present how are they are distributed.

8.)

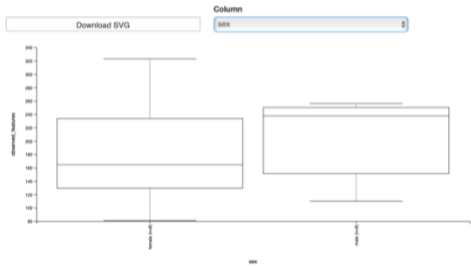
|          |                        |         |
|----------|------------------------|---------|
| Category | Alpha Diversity Metric | q-value |
|----------|------------------------|---------|

|            |                   |          |
|------------|-------------------|----------|
| Population | Shannon           | 0.698535 |
| Population | Observed Features | 0.196706 |
| Sex        | Shannon           | 0.366157 |
| Sex        | Observed Features | 0.438578 |
| Flock      | Shannon           | 0.514897 |
| Flock      | Observed Features | 0.428858 |

No, there aren't any significant comparisons between the metadata as all q-values are < 0.05.



Alpha Diversity Boxplots



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Kruskal-Wallis (all groups)

|         | Result             |
|---------|--------------------|
| H       | 0.6000000000000014 |
| p-value | 0.4385780260809993 |

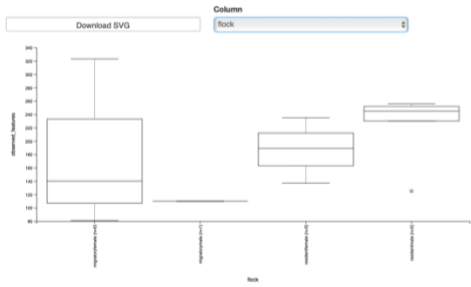
Kruskal-Wallis (pairwise)

[Download CSV](#)

|              | Group 1 | Group 2    | H   | p-value  | q-value  |
|--------------|---------|------------|-----|----------|----------|
| female (n=8) |         | male (n=6) | 0.6 | 0.438578 | 0.438578 |



Alpha Diversity Boxplots



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Kruskal-Wallis (all groups)

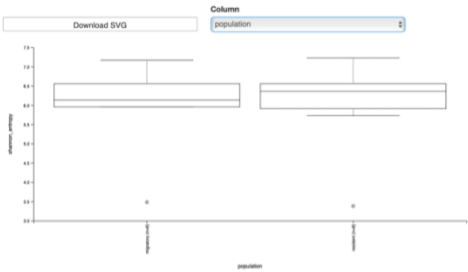
|         | Result             |
|---------|--------------------|
| H       | 2.76761904761905   |
| p-value | 0.4268581748939646 |

Kruskal-Wallis (pairwise)

[Download CSV](#)

|                       | Group 1 | Group 2              | H        | p-value  | q-value  |
|-----------------------|---------|----------------------|----------|----------|----------|
| migratoryfemale (n=5) |         | migratorymale (n=1)  | 0.085714 | 0.769698 | 0.769698 |
|                       |         | residentfemale (n=3) | 0.200000 | 0.654721 | 0.769698 |
|                       |         | residentmale (n=5)   | 0.883636 | 0.347208 | 0.520811 |
| migratorymale (n=1)   |         | residentfemale (n=3) | 1.800000 | 0.179712 | 0.520811 |
|                       |         | residentmale (n=5)   | 2.142857 | 0.143235 | 0.520811 |
| residentfemale (n=3)  |         | residentmale (n=5)   | 1.086889 | 0.296718 | 0.520811 |

Alpha Diversity Boxplots



[Download raw data as TSV](#)

Kruskal-Wallis (all groups)

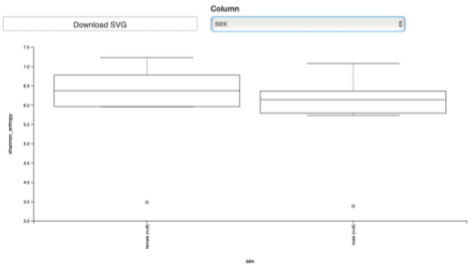
|         | Result              |
|---------|---------------------|
| H       | 0.14999999999999858 |
| p-value | 0.69853535830334    |

Kruskal-Wallis (pairwise)

[Download CSV](#)

|                 | Group 1        | Group 2 | H    | p-value  | q-value  |
|-----------------|----------------|---------|------|----------|----------|
| migratory (n=6) | resident (n=6) |         | 0.15 | 0.698535 | 0.698535 |

Alpha Diversity Boxplots



[Download raw data as TSV](#)

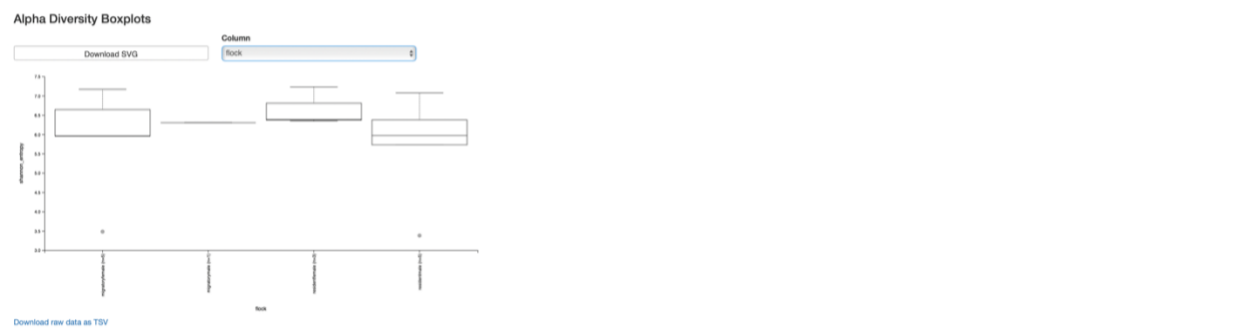
Kruskal-Wallis (all groups)

|         | Result             |
|---------|--------------------|
| H       | 0.8166666666666629 |
| p-value | 0.3661565601940615 |

Kruskal-Wallis (pairwise)

[Download CSV](#)

|              | Group 1    | Group 2 | H        | p-value  | q-value  |
|--------------|------------|---------|----------|----------|----------|
| female (n=6) | male (n=6) |         | 0.816667 | 0.366157 | 0.366157 |



Kruskal-Wallis (all groups)

|         |  | Result            |
|---------|--|-------------------|
| H       |  | 2.287619047619046 |
| p-value |  | 0.514896917405882 |

Kruskal-Wallis (pairwise)

Download CSV

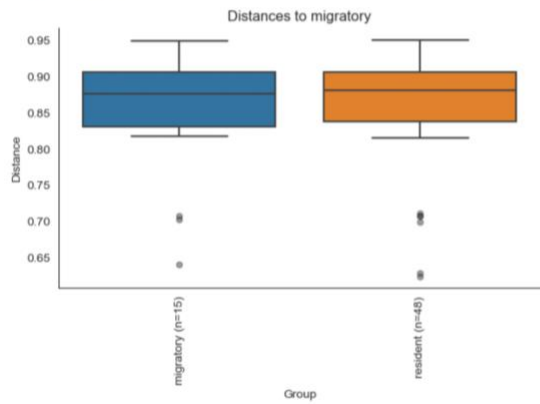
|                       |                      | H        | p-value  | q-value  |
|-----------------------|----------------------|----------|----------|----------|
| migratoryfemale (n=3) | migratorymale (n=1)  | 0.085714 | 0.769698 | 0.769698 |
|                       | residentfemale (n=3) | 1.088889 | 0.296718 | 0.593435 |
| migratorymale (n=1)   | residentfemale (n=3) | 0.098182 | 0.754023 | 0.769698 |
|                       | residentmale (n=3)   | 1.800000 | 0.179712 | 0.539137 |
| residentfemale (n=3)  | residentmale (n=3)   | 0.085714 | 0.769698 | 0.769698 |
|                       | residentmale (n=3)   | 1.800000 | 0.179712 | 0.539137 |

9.) Yes, there are significance in population (p-value 0.049) and flock (p-value 0.022). This shows that population, resident vs. migratory birds is different. While flock shows a difference between the different groups.

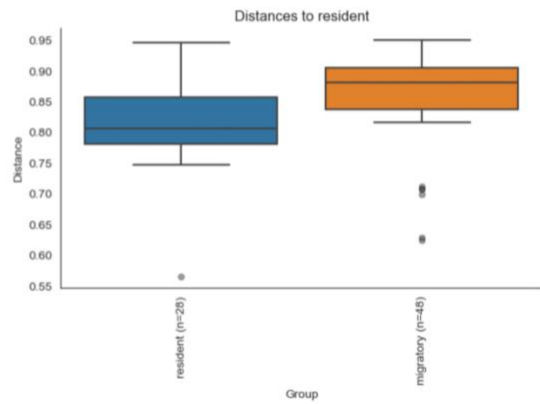


Group significance plots

Download raw data as TSV



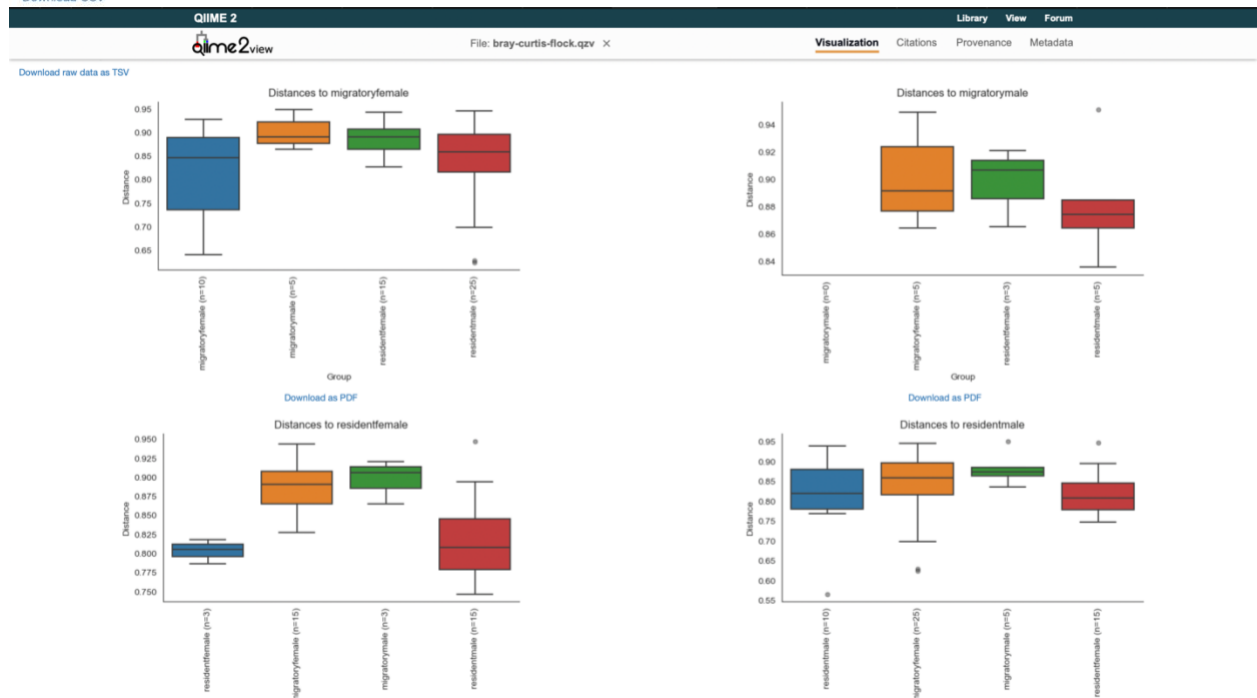
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Pairwise permanova results

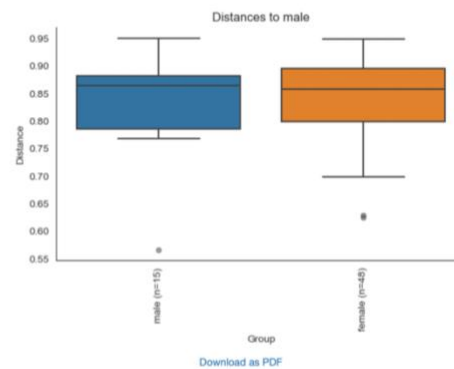
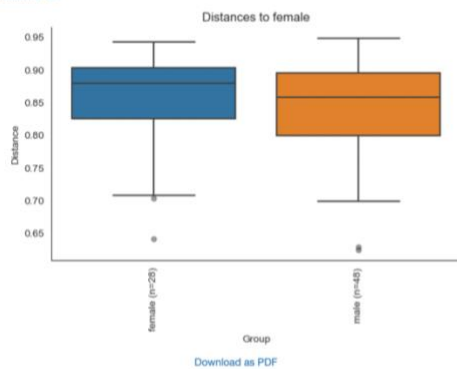
Download CSV



| QIIME 2   |  | Library                                | View          | Forum     |
|---|--|--|---------------|-----------|
|  |  | File: bray-curtis-sex-significance.qzv | Visualization | Citations |
| number of groups  |  | 2                                      |               |           |
| test statistic  |  | 0.91901                                |               |           |
| p-value   |  | 0.579                                  |               |           |
| number of permutations  |  | 999                                    |               |           |

## Group significance plots

[Download raw data as TSV](#)

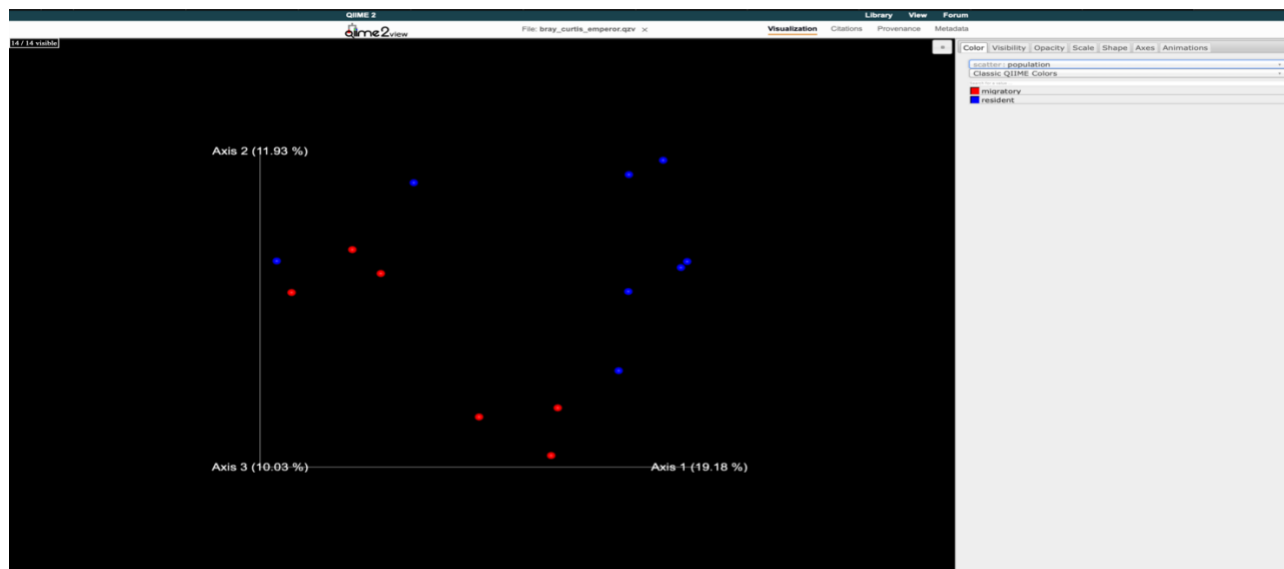


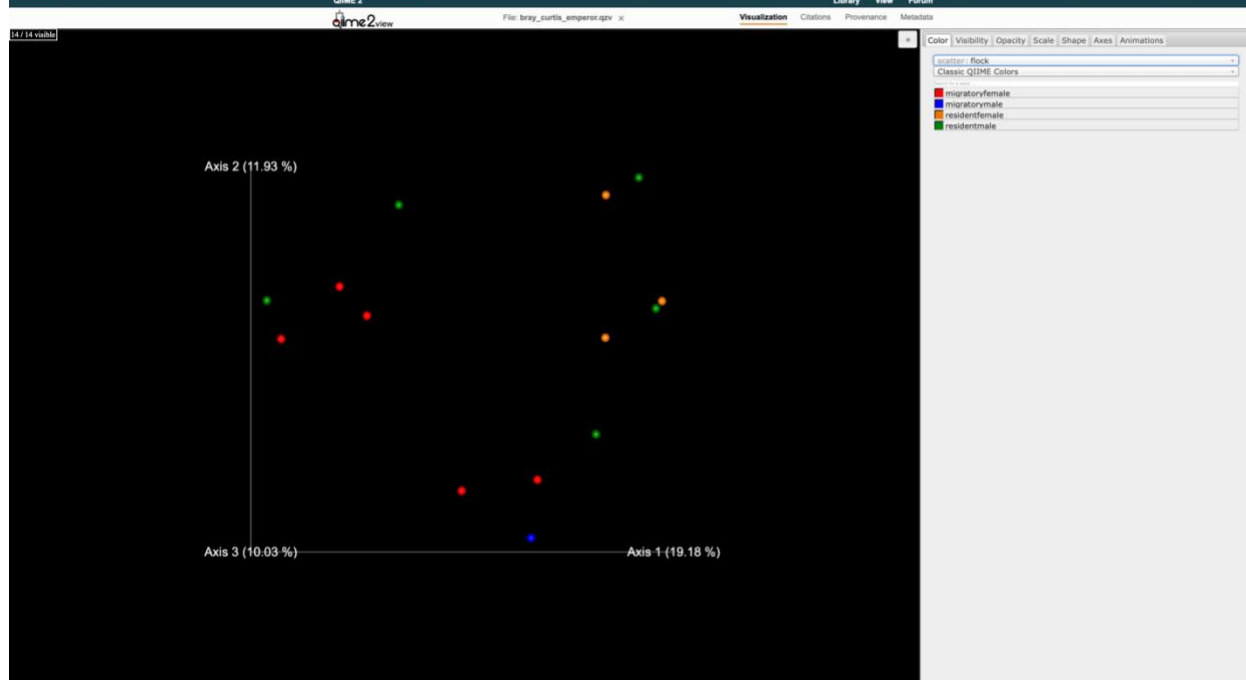
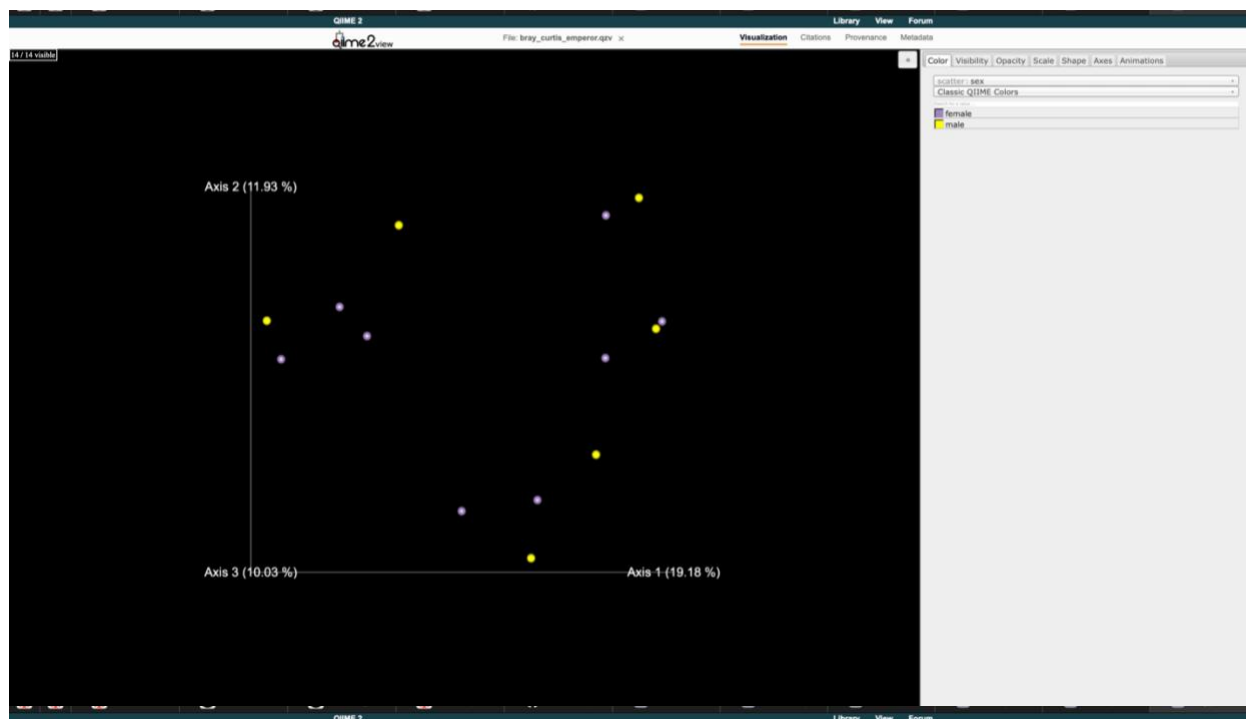
## Pairwise permanova results

[Download CSV](#)

| Sampld.stre | Permutations | permut.F | p-value | p-value |
|-------------|--------------|----------|---------|---------|
|-------------|--------------|----------|---------|---------|

- 10.) It helps visually confirm the patterns as all data is in one plot. Since population and flock showed significance there should be clusters of the similar groups together. For population you can see the migratory being lower on the axis compared to the residents.





## 11.) Lactobacillaceae,

view.qiime2.org

Microbiome Sect... Create assemble... Sampling Depth f... Transcriptomics... Fiona1777/Microb... ancombc-sex.qz... ancombc-popula... ancombc-flock.q... taxonomy.qzv - Q...

QIIME 2 Library View Forum

qiime2view File: ancombc-sex.qzv x Visualization Citations Provenance Metadata

### p-Values

Groups used to define the intercept:  
sex::female (and any numerical metadata columns)

|                                  | (Intercept)  | sexmale  |
|----------------------------------|--------------|----------|
| id                               |              |          |
| de4c8f59c9c37b7b6e73149398d53aea | 3.063119e-04 | 0.000011 |
| e7dd01d01c0203abc3708549d99e4e9c | 9.082477e-01 | 0.372048 |
| 65d43491988bfe557da4d86a5ba25dae | 1.809358e-02 | 0.940727 |
| b0a41da16f5aac6c22cf64661cc3666c | 5.654261e-01 | 0.550190 |
| dd8229814f2d127e61ac92c5d275db8b | 5.206764e-02 | 0.272054 |
| 77a920bd965da12d31f93c1adf2c5ea1 | 1.532956e-01 | 0.415061 |
| 6c33785c46c3fef68941d9addceaf948 | 7.651288e-01 | 0.445166 |
| c10442f1117bbfe857fcc8b57429324e | 7.735108e-01 | 0.548075 |
| 922d33a2963d3e87a3d4df6b82371235 | 1.589609e-01 | 0.765871 |
| 8059cc93ba42a3cc1bd6acfd8a84b0e1 | 3.677910e-01 | 0.549552 |
| 68c56896f754db932a51a88ebad5bc6a | 7.639644e-01 | 0.700638 |
| 98cea5793fe96443ce3fd0bee61c8257 | 1.197875e-01 | 0.631754 |
| ca6c2b3b469c08212142e8821c65882a | 3.619049e-03 | 0.883061 |
| ff9a93d7b7e4678756af2d241caanf3b | 8.541963e-01 | 0.774968 |

## Comamonadaceae

view.qiime2.org

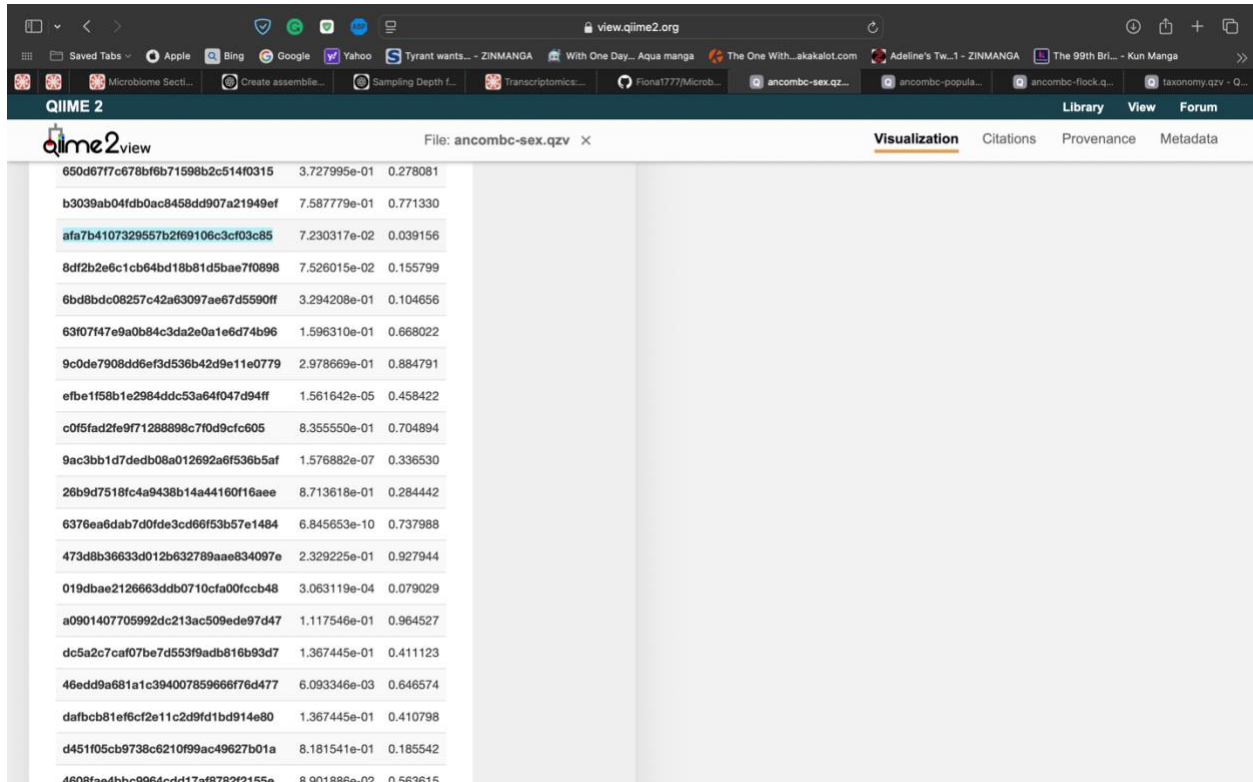
Microbiome Sect... Create assemble... Sampling Depth f... Transcriptomics... Fiona1777/Microb... ancombc-sex.qz... ancombc-popula... ancombc-flock.q... taxonomy.qzv - Q...

QIIME 2 Library View Forum

qiime2view File: ancombc-sex.qzv x Visualization Citations Provenance Metadata

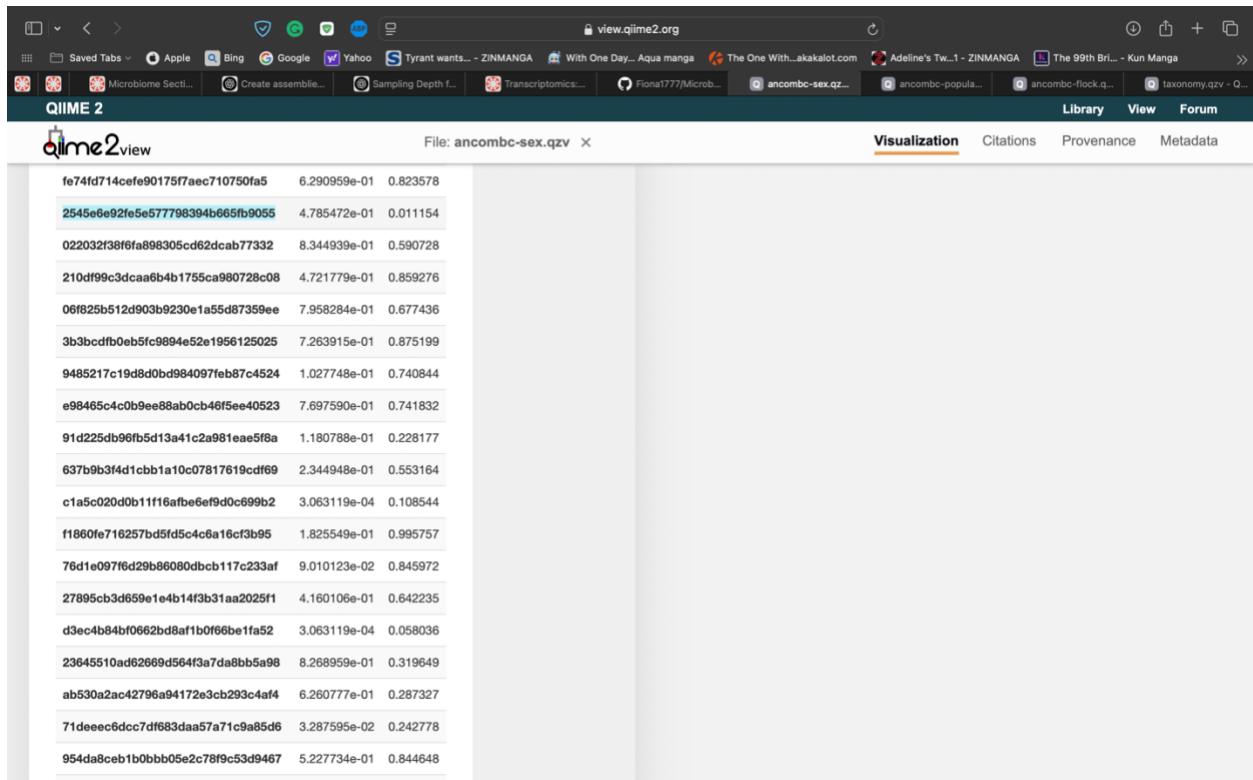
|                                  |              |          |
|----------------------------------|--------------|----------|
| d0f60e9c99ca8b06529c34a0e7ae244f | 8.314254e-01 | 0.438298 |
| 9980f5e5eb4480dc328ed75eee5c2efa | 6.481695e-01 | 0.565199 |
| 0f5f48d793a468de8ec2131049a25f1e | 4.707464e-01 | 0.006593 |
| c38cd0e9a18d9433b7f0cfa08da73f2  | 3.983406e-01 | 0.594355 |
| b5956402a24a9153484f4249effcec18 | 7.443259e-01 | 0.688029 |
| d2af52fc6f48ab4d05c96dad9527d8a2 | 8.714980e-01 | 0.325962 |
| bcc6da5f621cbdfc1f0c9becbac6cdf  | 1.859400e-02 | 0.093726 |
| ae04dca2a07ec1aa560e836bc399ea57 | 1.822817e-02 | 0.247451 |
| fd496fd32dc8c08ade2e8b6c9d8ee13d | 1.782881e-01 | 0.090504 |
| 4b6a9ae64400c8449303fe7088c1067  | 3.998598e-01 | 0.661979 |
| 5f0927bf984f286d11de39a8867c2ac7 | 5.607822e-01 | 0.127875 |
| 661ba07ab6853f514e2bca59bf8303af | 3.661958e-01 | 0.882342 |
| 68640b93e2968acf77f0bb3642bd546e | 2.898250e-02 | 0.495110 |
| 0e2e91fba1ca9ed7de2d11ea4786c914 | 5.625970e-01 | 0.182643 |
| 6f7fdad1419595b3bb1e5ceda289402b | 9.399623e-01 | 0.226139 |
| 49a250849d64ca63b354b4b3281030d0 | 1.256317e-01 | 0.950602 |
| 7de740fc99d1aac596beb5d090c5bc50 | 6.915769e-01 | 0.481014 |
| 2a39f0b75d31d00b3136b2edbe82962e | 7.202193e-06 | 0.856497 |
| d594219c7e58b9213a2cfe8f076d557f | 6.584828e-01 | 0.841884 |

## Rhizobiales



| Sequence ID                      | Relative Abundance | Visualization |
|----------------------------------|--------------------|---------------|
| 650d67f7c678bfb71598b2c514f0315  | 3.727995e-01       | 0.278081      |
| b3039ab04fdb0ac8458dd907a21949ef | 7.587779e-01       | 0.771330      |
| afa7b4107329557b2f69106c3cf03c85 | 7.230317e-02       | 0.039156      |
| 8df2b2e6c1cb64bd18b81d5bae7f0898 | 7.526015e-02       | 0.155799      |
| 6bd8bdc08257c42a63097ae67d5590ff | 3.294208e-01       | 0.104656      |
| 63f07f47e9a0b84c3da2e0a1e6d74b96 | 1.596310e-01       | 0.668022      |
| 9c0de7908dd6ef3d536b42d9e11e0779 | 2.978669e-01       | 0.884791      |
| efbe1f58b1e2984ddc53a64f047d94ff | 1.561642e-05       | 0.458422      |
| c0f5fad2fe9f71288898c7f0d9cfc605 | 8.355550e-01       | 0.704894      |
| 9ac3bb1d7dedb08a012692a6f536b5af | 1.576882e-07       | 0.336530      |
| 26b9d7518fc4a9438b14a44160f16aee | 8.713618e-01       | 0.284442      |
| 6376ea6dab7d0fde3cd66f53b57e1484 | 6.845653e-10       | 0.737988      |
| 473d8b36633d012b632789aae834097e | 2.329225e-01       | 0.927944      |
| 019dbae2126663ddb0710cfa00fccb48 | 3.063119e-04       | 0.079029      |
| a0901407705992dc213ac509ede97d47 | 1.117546e-01       | 0.964527      |
| dc5a2c7caf07be7d553f9adb816b93d7 | 1.367445e-01       | 0.411123      |
| 46edd9a681a1c39400785966f76d477  | 6.093346e-03       | 0.646574      |
| dafbc81ef6cf2e11c2d9fd1bd914e80  | 1.367445e-01       | 0.410798      |
| d451f05cb9738c6210f99ac49627b01a | 8.181541e-01       | 0.185542      |
| 4608fae4bbc9964cdd17af6782f2155e | 8.901886e-02       | 0.563615      |

## Solirubrobacterales



| Sequence ID                       | Relative Abundance | Visualization |
|-----------------------------------|--------------------|---------------|
| fe74fd714cefe90175f7aec710750fa5  | 6.290959e-01       | 0.823578      |
| 2545e9e92fe5e577798394b665fb9055  | 4.785472e-01       | 0.011154      |
| 022032f38f6fa898305cd62dcab77332  | 8.344939e-01       | 0.590728      |
| 210df99c3dcaa6b4b1755ca980728c08  | 4.721779e-01       | 0.859276      |
| 06f825b512d903b9230e1a55d87359ee  | 7.958284e-01       | 0.677436      |
| 3b3bcdffb0eb5fc9894e52e1956125025 | 7.263915e-01       | 0.875199      |
| 9485217c19d8d0bd984097feb87c4524  | 1.027748e-01       | 0.740844      |
| e98465c4c0b9ee88ab0cb46f5ee40523  | 7.697590e-01       | 0.741832      |
| 91d225db96fb5d13a41c2a981eae5f8a  | 1.180788e-01       | 0.228177      |
| 637b9b3f4d1cbb1a10c07817619cdf69  | 2.344948e-01       | 0.553164      |
| c1a5c020d0b11f16afbe6ef9d0c699b2  | 3.063119e-04       | 0.108544      |
| f1860fe716257bd5fd5c4c6a16cf3b95  | 1.825549e-01       | 0.995757      |
| 76d1e097f6d29b86080dbcb117c233af  | 9.010123e-02       | 0.845972      |
| 27895cb3d659e1e4b14f3b31aa2025f1  | 4.160106e-01       | 0.642235      |
| d3ec4b84bf0662bd8af1b0f66be1fa52  | 3.063119e-04       | 0.058036      |
| 23645510ad62669d564f3a7da8bb5a98  | 8.268959e-01       | 0.319649      |
| ab530a2ac42796a94172e3cb293c4af4  | 6.260777e-01       | 0.287327      |
| 71deec6dcc7df683daa57a71c9a85d6   | 3.287595e-02       | 0.242778      |
| 954da8ceb1b0bbb05e2c78f9c53d9467  | 5.227734e-01       | 0.844648      |

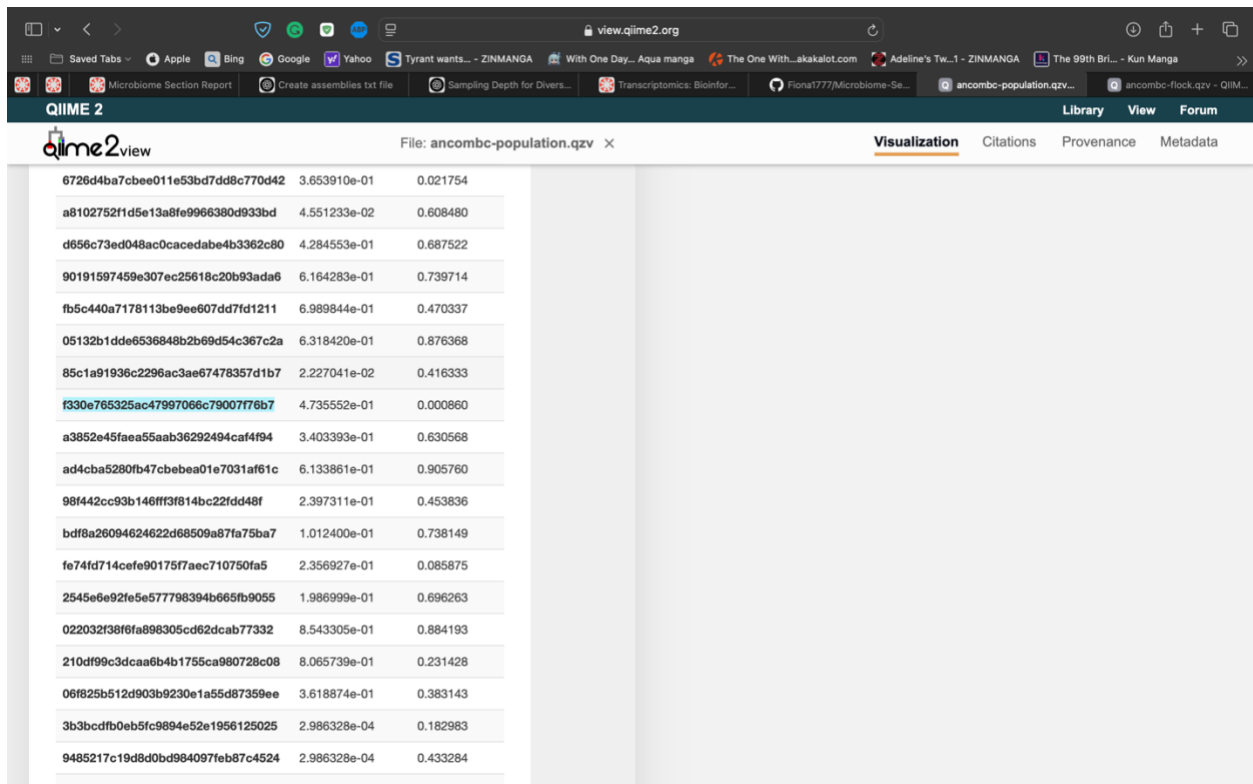
## cryoconitis

| ID                               | Value        | Classification |
|----------------------------------|--------------|----------------|
| 0e55339184fe9a032b6098595b39905f | 5.407973e-01 | 0.231656       |
| 287293951348f094a5abe9037c3175b2 | 2.914550e-01 | 0.768501       |
| 30dbf1c75521f969f69ff64101abcee2 | 4.830637e-01 | 0.564192       |
| bc94f796dba79cd0231cd42a8279697d | 1.357697e-01 | 0.379729       |
| 91b7e46fb9812c28c705795b1c6a3b48 | 2.986328e-04 | 0.495262       |
| fab36fed8422b57daf15bfeaa047aa5b | 1.155174e-01 | 0.597398       |
| bd65b53fc9871d4c791dcf42ad6816bb | 8.573074e-01 | 0.787920       |
| b5aa5682391aca4dd43353d2398acd61 | 2.872669e-01 | 0.854403       |
| 7c8e03cc2a602da71c0097f329151414 | 1.196723e-04 | 0.852436       |
| 892a0fc53b26d6a2c193d145b246da7  | 9.155162e-01 | 0.977942       |
| a9164d01308501b576afa06256a15b0f | 3.635931e-01 | 0.785730       |
| c2498206e5e32852e94d8a2586be9ac1 | 3.067134e-01 | 0.531418       |
| 1354d8eddb9222983aca5a2fd2c6c7a5 | 9.002827e-01 | 0.140926       |
| c36c1890ad28d3dd5f046772f4fd78f  | 8.851428e-02 | 0.466558       |
| c6d53155dc70f1d525e55de6061d4cea | 4.750311e-02 | 0.000464       |

## Campylobacter

| ID                               | Value        | Classification |
|----------------------------------|--------------|----------------|
| 67560da40e74ce9425541888438ee095 | 2.900567e-01 | 0.904189       |
| 312f85fff91f5153e724b94b594e7ccb | 9.920845e-01 | 0.894185       |
| f1b5950264bdaa3d7c95febe8a4df3c7 | 2.986328e-04 | 0.006044       |
| 72f9e9afcc03ad4daa440ceae7b26211 | 5.861404e-01 | 0.595637       |
| c73b4232e9fb1412b245213a34d936a5 | 2.201180e-01 | 0.222432       |
| 820f6693f569e339f183638cd73a7fe6 | 7.888266e-01 | 0.465958       |
| a535da8ab82c27ac010261efbf184b1b | 7.287571e-01 | 0.210387       |
| 71832de33e8472eb96b673875f7a10ca | 5.923308e-03 | 0.001925       |
| 0e55339184fe9a032b6098595b39905f | 5.407973e-01 | 0.231656       |
| 287293951348f094a5abe9037c3175b2 | 2.914550e-01 | 0.768501       |
| 30dbf1c75521f969f69ff64101abcee2 | 4.830637e-01 | 0.564192       |
| bc94f796dba79cd0231cd42a8279697d | 1.357697e-01 | 0.379729       |
| 91b7e46fb9812c28c705795b1c6a3b48 | 2.986328e-04 | 0.495262       |
| fab36fed8422b57daf15bfeaa047aa5b | 1.155174e-01 | 0.597398       |
| bd65b53fc9871d4c791dcf42ad6816bb | 8.573074e-01 | 0.787920       |
| b5aa5682391aca4dd43353d2398acd61 | 2.872669e-01 | 0.854403       |
| 7c8e03cc2a602da71c0097f329151414 | 1.196723e-04 | 0.852436       |
| 892a0fc53b26d6a2c193d145b246da7  | 9.155162e-01 | 0.977942       |
| a9164d01308501b576afa06256a15b0f | 3.635931e-01 | 0.785730       |

## Brachybacterium



| OTU ID                            | Count        | Relative Abundance |
|-----------------------------------|--------------|--------------------|
| 6726d4ba7cbee011e53bd7dd8c770d42  | 3.653910e-01 | 0.021754           |
| a8102752f1d5e13a8fe9966380d933bd  | 4.551233e-02 | 0.608480           |
| d656c73ed048ac0cacedabe4b3362c80  | 4.284553e-01 | 0.687522           |
| 90191597459e307ec25618c20b93ada6  | 6.164283e-01 | 0.739714           |
| fb5c440a7178113be9ee607dd7fd1211  | 6.989844e-01 | 0.470337           |
| 05132b1dde6536848b2b69d54c367c2a  | 6.318420e-01 | 0.876368           |
| 85c1a91936c2296ac3ae67478357d1b7  | 2.227041e-02 | 0.416333           |
| f330e765325ac47997066c79007f76b7  | 4.735552e-01 | 0.000860           |
| a3852e45faea55aab3629249caf4f94   | 3.403393e-01 | 0.630568           |
| ad4cba5280fb47cbebea01e7031af61c  | 6.133861e-01 | 0.905760           |
| 98f442cc93b146fff3f814bc22fdd48f  | 2.397311e-01 | 0.453836           |
| bdf8a26094624622d68509a87fa75ba7  | 1.012400e-01 | 0.738149           |
| fe74fd714cefe90175f7aec710750fa5  | 2.356927e-01 | 0.085875           |
| 2545e6e92fe5e77798394b665fb9055   | 1.986999e-01 | 0.696263           |
| 022032f38f6fa898305cd62dcab77332  | 8.543305e-01 | 0.884193           |
| 210df99c3dcaa6b4b1755ca980728c08  | 8.065739e-01 | 0.231428           |
| 06f825b512d903b9230e1a55d87359ee  | 3.618874e-01 | 0.383143           |
| 3b3bcdffb0eb5fc9894e52e1956125025 | 2.986328e-04 | 0.182983           |
| 9485217c19d8d0bd984097feb87c4524  | 2.986328e-04 | 0.433284           |

## cryoconitis



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|                                   |              |              |          |              |
|-----------------------------------|--------------|--------------|----------|--------------|
|                                   | U1           |              |          |              |
| 3c17288efe19dbc5465439f6ee0084b4  | 5.124431e-01 | 4.469605e-01 | 0.755209 | 7.264610e-02 |
| 394962b765d3f25a4f20ed14bfa76817  | 6.889042e-01 | 5.932786e-01 | 0.972681 | 5.377483e-01 |
| 62c42ad76b49094286cfc4314bdf03de  | 3.684048e-01 | 2.995667e-01 | 0.269180 | 8.332337e-01 |
| 67560da40e74ce9425541888438ee095  | 1.205205e-01 | 5.061858e-01 | 0.094858 | 6.189429e-01 |
| 312f85fff9f1f5153e724b94b594e7ccb | 4.173733e-01 | 9.476198e-01 | 0.306611 | 4.247830e-01 |
| f1b5950264bdaa3d7c95febe8a4df3c7  | 3.496297e-01 | 5.563783e-01 | 0.000178 | 2.514051e-01 |
| 72f9e9afcc03ad4daa440ceae7b26211  | 3.357536e-01 | 9.196995e-01 | 0.258714 | 7.597645e-01 |
| c73b4232e9fbf412b245213a34d936a5  | 1.023215e-01 | 4.285950e-01 | 0.270368 | 2.828448e-01 |
| 820f6693f569e39f183638cd73a7fe6   | 1.112938e-01 | 9.125879e-02 | 0.083246 | 5.876987e-01 |
| a535da8ab82c27ac010261efbf184b1b  | 1.068633e-01 | 8.826674e-02 | 0.080560 | 2.760955e-01 |
| 71832de33e8472eb96b673875f7a10ca  | 6.478039e-04 | 5.329082e-02 | 0.378564 | 5.568163e-02 |
| 0e55339184fe9a032b6098595b39905f  | 1.109353e-01 | 9.569631e-02 | 0.358969 | 6.312744e-02 |

E.coli

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|                                   |              |              |          |              |
|-----------------------------------|--------------|--------------|----------|--------------|
|                                   | O2           |              |          |              |
| 02a021a4a33ccd51f4b020422088397b  | 5.787362e-01 | 4.964855e-01 | 0.449131 | 2.158327e-01 |
| 77057844175f36fb4482ebf9f357e75c  | 5.922202e-01 | 7.217351e-01 | 0.753329 | 5.331554e-01 |
| f74c5673e42a4cee36abe6aff088a9bb  | 3.496297e-01 | 5.563783e-01 | 0.762599 | 1.005890e-01 |
| bcba47620c299fd34809f143e3d26dff  | 5.175542e-01 | 4.507608e-01 | 0.411340 | 7.822181e-01 |
| 43fdff1528d4a98928fdd8c3a8ac23bfd | 6.202343e-04 | 7.231555e-02 | 0.029741 | 5.549912e-01 |
| 79c9235ff041fe7f6fdc89a18c5a222a  | 3.496297e-01 | 5.563783e-01 | 0.088968 | 7.838095e-01 |
| f617f0ce888fe9b6b91cb9069b7a11f5  | 3.496297e-01 | 5.563783e-01 | 0.039330 | 7.517087e-02 |
| 702af9e944edfd5a1a7f0dce0d566376  | 3.496297e-01 | 5.663842e-02 | 0.303464 | 3.541762e-01 |
| b68b9f9ea5a54a87e3dfdde8397e545b  | 3.496297e-01 | 5.563783e-01 | 0.362222 | 1.692720e-01 |
| 1390be990b3eede8ecc6bc9d45d2f008  | 3.567432e-01 | 2.940219e-01 | 0.928247 | 5.485149e-01 |
| a7c17d45d26c3be47bfd54ca7e5e9de   | 4.573386e-01 | 8.382381e-01 | 0.374256 | 3.281773e-01 |
| 3c17288efe19dbc5465439f6ee0084b4  | 5.124431e-01 | 4.469605e-01 | 0.755209 | 7.264610e-02 |