**Supplemental Table.**

**Table S1: Identification of OTUs with significantly different representations.** We listed OTUs for which Metastats analysis indicated significant differences in relative abundance (p<0.05, > 1% of all sequences in at least one treatment). Data is presented only for comparisons between extraction methods, preservation methods, or sequencing runs, which AMOVA showed a statistically significant difference between.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **OTU** | **DL-Enz** | **DL-APO-RL** | **p-value** | **Taxonomy** |
| Otu00005 | 0.081 | 0.061 | 0.046 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Burkholderiaceae\_Polynucleobacter |
| Otu00006 | 0.021 | 0.030 | 0.040 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Chitinophagaceae\_Sediminibacterium |
| Otu00007 | 0.017 | 0.044 | 0.000 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Cryomorphaceae\_Fluviicola |
| Otu00016 | 0.015 | 0.018 | 0.049 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Flavobacteriaceae\_Flavobacterium |
| Otu00017 | 0.005 | 0.010 | 0.003 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Flavobacteriaceae\_Flavobacterium |
| Otu00019 | 0.001 | 0.016 | 0.002 | Cyanobacteria |
| Otu00020 | 0.029 | 0.045 | 0.012 | Proteobacteria\_Betaproteobacteria\_Methylophilales\_Methylophilaceae\_LD28 |
| Otu00026 | 0.011 | 0.024 | 0.003 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Cyclobacteriaceae\_uncultured |
| Otu00043 | 0.002 | 0.015 | 0.000 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales |
| Otu00055 | 0.003 | 0.024 | 0.002 | Verrucomicrobia |
| Otu00057 | 0.002 | 0.028 | 0.000 | Verrucomicrobia\_Acidimethylosilex |
| Otu00059 | 0.086 | 0.008 | 0.008 | Planctomycetes\_Planctomycetacia\_Planctomycetales\_Planctomycetaceae |
| Otu00066 | 0.016 | 0.009 | 0.001 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales |
| Otu00068 | 0.059 | 0.021 | 0.011 | Cyanobacteria\_SubsectionI\_Synechococcus |
| Otu00079 | 0.006 | 0.012 | 0.000 | Bacteroidetes |
|  |  |  |  |  |
| **OTU** | **DL-Enz** | **DL-APS** | **p-value** |  |
| Otu00001 | 0.102 | 0.074 | 0.008 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Comamonadaceae\_Rhodoferax |
| Otu00002 | 0.120 | 0.082 | 0.001 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00004 | 0.097 | 0.066 | 0.009 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00005 | 0.081 | 0.031 | 0.001 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Burkholderiaceae\_Polynucleobacter |
| Otu00007 | 0.017 | 0.042 | 0.001 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Cryomorphaceae\_Fluviicola |
| Otu00019 | 0.001 | 0.026 | 0.001 | Cyanobacteria |
| Otu00021 | 0.011 | 0.008 | 0.006 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Comamonadaceae |
| Otu00022 | 0.001 | 0.013 | 0.001 | Planctomycetes\_Phycisphaerae\_Phycisphaerales\_Phycisphaeraceae\_CL500-3 |
| Otu00026 | 0.011 | 0.027 | 0.001 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Cyclobacteriaceae\_uncultured |
| Otu00028 | 0.004 | 0.010 | 0.001 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Flavobacteriaceae\_Flavobacterium |
| Otu00041 | 0.006 | 0.014 | 0.001 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Chitinophagaceae\_uncultured |
| Otu00043 | 0.002 | 0.018 | 0.001 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales |
| Otu00049 | 0.012 | 0.008 | 0.005 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00055 | 0.003 | 0.049 | 0.001 | Verrucomicrobia |
| Otu00059 | 0.086 | 0.004 | 0.001 | Planctomycetes\_Planctomycetacia\_Planctomycetales\_Planctomycetaceae |
| Otu00066 | 0.016 | 0.005 | 0.001 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales |
| Otu00073 | 0.001 | 0.011 | 0.001 | Verrucomicrobia\_Opitutae\_vadinHA64 |
| Otu00074 | 0.015 | 0.011 | 0.044 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00079 | 0.006 | 0.015 | 0.001 | Bacteroidetes |
| Otu00094 | 0.003 | 0.016 | 0.001 | Verrucomicrobia\_Verrucomicrobiae\_Verrucomicrobiales\_Verrucomicrobiaceae |
| Otu00115 | 0.003 | 0.010 | 0.001 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Saprospiraceae |
| Otu00126 | 0.007 | 0.016 | 0.002 | Verrucomicrobia\_Verrucomicrobiae\_Verrucomicrobiales\_Verrucomicrobiaceae\_Prosthecobacter |
|  |  |  |  |  |
| **OTU** | **DL-APS** | **DL-APO-RL** | **p-value** |  |
| Otu00001 | 0.074 | 0.099 | 0.005 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Comamonadaceae\_Rhodoferax |
| Otu00002 | 0.082 | 0.103 | 0.038 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00005 | 0.031 | 0.061 | 0.002 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Burkholderiaceae\_Polynucleobacter |
| Otu00022 | 0.013 | 0.008 | 0.021 | Planctomycetes\_Phycisphaerae\_Phycisphaerales\_Phycisphaeraceae\_CL500-3 |
| Otu00028 | 0.010 | 0.007 | 0.014 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Flavobacteriaceae\_Flavobacterium |
| Otu00030 | 0.003 | 0.012 | 0.000 | unclassified |
| Otu00032 | 0.021 | 0.010 | 0.001 | Candidate\_division\_OP10 |
| Otu00041 | 0.014 | 0.004 | 0.001 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Chitinophagaceae\_uncultured |
| Otu00049 | 0.008 | 0.014 | 0.001 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00055 | 0.049 | 0.024 | 0.025 | Verrucomicrobia |
| Otu00057 | 0.005 | 0.028 | 0.000 | Verrucomicrobia\_Acidimethylosilex |
| Otu00068 | 0.044 | 0.021 | 0.004 | Cyanobacteria\_SubsectionI\_Synechococcus |
| Otu00076 | 0.018 | 0.009 | 0.040 | Actinobacteria\_Actinobacteria\_Acidimicrobidae\_Acidimicrobiales\_Acidimicrobineae\_Acidimicrobiaceae\_marine\_group |
| Otu00079 | 0.015 | 0.012 | 0.021 | Bacteroidetes |
| Otu00094 | 0.016 | 0.007 | 0.001 | Verrucomicrobia\_Verrucomicrobiae\_Verrucomicrobiales\_Verrucomicrobiaceae |
| Otu00115 | 0.010 | 0.003 | 0.000 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Saprospiraceae |
| Otu00126 | 0.016 | 0.006 | 0.004 | Verrucomicrobia\_Verrucomicrobiae\_Verrucomicrobiales\_Verrucomicrobiaceae\_Prosthecobacter |
|  |  |  |  |  |
| **OTU** | **HR-APO-RP** | **HR-APO-NT** | **p-value** |  |
| Otu00001 | 0.085 | 0.143 | 0.043 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Comamonadaceae\_Rhodoferax |
| Otu00004 | 0.010 | 0.024 | 0.018 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00006 | 0.010 | 0.018 | 0.038 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Chitinophagaceae\_Sediminibacterium |
| Otu00011 | 0.010 | 0.022 | 0.007 | Proteobacteria\_Betaproteobacteria\_Methylophilales\_Methylophilaceae\_Methylophilus |
| Otu00019 | 0.060 | 0.004 | 0.006 | Cyanobacteria |
| Otu00069 | 0.013 | 0.007 | 0.034 | Bacteroidetes |
| Otu00164 | 0.005 | 0.012 | 0.007 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_env.OPS\_17 |
|  |  |  |  |  |
| **OTU** | **HR-APO-NT** | **HR-APO-RL** | **p-value** |  |
| Otu00004 | 0.024 | 0.011 | 0.030 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00007 | 0.008 | 0.014 | 0.037 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Cryomorphaceae\_Fluviicola |
| Otu00019 | 0.004 | 0.029 | 0.005 | Cyanobacteria |
| Otu00043 | 0.005 | 0.011 | 0.013 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales |
| Otu00136 | 0.007 | 0.012 | 0.040 | Planctomycetes\_Planctomycetacia\_Planctomycetales\_Planctomycetaceae |
| Otu00164 | 0.012 | 0.007 | 0.014 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_env.OPS\_17 |
|  |  |  |  |  |
| **OTU** | **HR-APO-NT** | **HR-APO-BU** | **p-value** |  |
| Otu00001 | 0.143 | 0.066 | 0.031 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Comamonadaceae\_Rhodoferax |
| Otu00006 | 0.018 | 0.010 | 0.039 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Chitinophagaceae\_Sediminibacterium |
| Otu00014 | 0.026 | 0.015 | 0.009 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_Cytophagaceae\_Arcicella |
| Otu00019 | 0.004 | 0.094 | 0.005 | Cyanobacteria |
| Otu00136 | 0.007 | 0.019 | 0.015 | Planctomycetes\_Planctomycetacia\_Planctomycetales\_Planctomycetaceae |
| Otu00164 | 0.012 | 0.003 | 0.006 | Bacteroidetes\_Sphingobacteria\_Sphingobacteriales\_env.OPS\_17 |
| Otu00184 | 0.006 | 0.017 | 0.014 | Planctomycetes\_Planctomycetacia\_Planctomycetales\_Planctomycetaceae\_uncultured |
|  |  |  |  |  |
| **OTU** | **LH-APO-NT** | **LH-APO-RL/RL-LYS** | **p-value** |  |
| Otu00003 | 0.015 | 0.022 | 0.035 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Flavobacteriaceae\_Flavobacterium |
| Otu00004 | 0.184 | 0.118 | 0.001 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00008 | 0.062 | 0.054 | 0.035 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
| Otu00009 | 0.003 | 0.014 | 0.003 | Verrucomicrobia\_Opitutae\_vadinHA64 |
| Otu00012 | 0.017 | 0.024 | 0.038 | Bacteroidetes\_Flavobacteria\_Flavobacteriales\_Flavobacteriaceae\_Flavobacterium |
| Otu00020 | 0.026 | 0.041 | 0.002 | Proteobacteria\_Betaproteobacteria\_Methylophilales\_Methylophilaceae\_LD28 |
| Otu00049 | 0.019 | 0.013 | 0.004 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales\_Frankineae\_Sporichthyaceae\_hgcI\_clade |
|  |  |  |  |  |
| **OTU** | **DL-Enz(2)** | **DL-Enz(1)** | **p-value** |  |
| Otu00001 | 0.125 | 0.069 | 0.002 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Comamonadaceae\_Rhodoferax |
| Otu00005 | 0.086 | 0.064 | 0.016 | Proteobacteria\_Betaproteobacteria\_Burkholderiales\_Burkholderiaceae\_Polynucleobacter |
| Otu00020 | 0.029 | 0.022 | 0.010 | Proteobacteria\_Betaproteobacteria\_Methylophilales\_Methylophilaceae\_LD28 |
| Otu00060 | 0.004 | 0.014 | 0.004 | Actinobacteria\_Actinobacteria\_Acidimicrobidae\_Acidimicrobiales\_Acidimicrobineae\_Acidimicrobiaceae |
| Otu00076 | 0.007 | 0.025 | 0.006 | Actinobacteria\_Actinobacteria\_Acidimicrobidae\_Acidimicrobiales\_Acidimicrobineae\_Acidimicrobiaceae\_marine\_group\_marine\_group |
| Otu00132 | 0.005 | 0.014 | 0.003 | Actinobacteria\_Actinobacteria\_Acidimicrobidae\_Acidimicrobiales\_Acidimicrobineae |
| Otu00136 | 0.005 | 0.011 | 0.036 | Planctomycetes\_Planctomycetacia\_Planctomycetales\_Planctomycetaceae |
| Otu00227 | 0.006 | 0.013 | 0.010 | Actinobacteria\_Actinobacteria\_Actinobacteridae\_Actinomycetales |