Comparison of phylum total abundances (counts) from metataxonomics vs. metagenomics

### Spring 2015 in southern station Selvogsbanki 5 (SB5)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 396 | 41327 |
| Bacteroidota | 6443 | 1099959 |
| Cyanobacteria | 1953 | 36181 |
| Firmicutes | 0 | 68633 |
| Others | 980 | 127304 |
| Proteobacteria | 12481 | 3010208 |
| Thermoplasmatota | 0 | 3897 |
| Verrucomicrobiota | 19 | 1851 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2016 in northern station Siglunes 8 (SI8)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 35 | 27446 |
| Bacteroidota | 1104 | 451913 |
| Cyanobacteria | 11 | 9366 |
| Firmicutes | 0 | 77851 |
| Others | 79 | 47237 |
| Proteobacteria | 1842 | 927102 |
| Thermoplasmatota | 0 | 19682 |
| Verrucomicrobiota | 59 | 34461 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2016 in southern station Selvogsbanki 5 (SB5)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 234 | 24624 |
| Bacteroidota | 1096 | 1051110 |
| Cyanobacteria | 508 | 96961 |
| Firmicutes | 0 | 99542 |
| Others | 152 | 54650 |
| Proteobacteria | 3464 | 2700306 |
| Thermoplasmatota | 0 | 27755 |
| Verrucomicrobiota | 6477 | 3944 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2017 in northern station Siglunes 8 (SI8)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 205 | 56687 |
| Bacteroidota | 4558 | 1158006 |
| Cyanobacteria | 50 | 22116 |
| Firmicutes | 0 | 173542 |
| Others | 1623 | 212065 |
| Proteobacteria | 16616 | 3387770 |
| Thermoplasmatota | 0 | 62722 |
| Verrucomicrobiota | 301 | 114758 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2017 in northern station Síglunes 3 (SI3)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 112 | 56057 |
| Bacteroidota | 4208 | 1783335 |
| Cyanobacteria | 20 | 20820 |
| Firmicutes | 0 | 98937 |
| Others | 189 | 63250 |
| Proteobacteria | 12390 | 2302223 |
| Thermoplasmatota | 0 | 45400 |
| Verrucomicrobiota | 176 | 31409 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2017 in southern station Selvogsbanki 5 (SB5)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 324 | 17017 |
| Bacteroidota | 5054 | 286097 |
| Cyanobacteria | 3027 | 26610 |
| Firmicutes | 0 | 185642 |
| Others | 221 | 43280 |
| Proteobacteria | 7750 | 874463 |
| Thermoplasmatota | 0 | 6421 |
| Verrucomicrobiota | 189 | 1399 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Summer 2017 in northern station Síglunes 3 (SI3)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 551 | 405618 |
| Bacteroidota | 1660 | 736426 |
| Cyanobacteria | 258 | 121661 |
| Firmicutes | 0 | 109174 |
| Others | 133 | 144803 |
| Proteobacteria | 2406 | 2806797 |
| Thermoplasmatota | 0 | 57865 |
| Verrucomicrobiota | 118 | 88264 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Summer 2017 in southern station Selvogsbanki 2 (SB2)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 129 | 154831 |
| Bacteroidota | 1225 | 625805 |
| Cyanobacteria | 420 | 114651 |
| Firmicutes | 0 | 100990 |
| Others | 174 | 128123 |
| Proteobacteria | 4036 | 3640737 |
| Thermoplasmatota | 0 | 69859 |
| Verrucomicrobiota | 284 | 187106 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2018 in northern station Síglunes 8 (SI8)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 337 | 18005 |
| Bacteroidota | 10688 | 685644 |
| Cyanobacteria | 114 | 2830 |
| Firmicutes | 0 | 53878 |
| Others | 900 | 51510 |
| Proteobacteria | 11665 | 1285502 |
| Thermoplasmatota | 0 | 14713 |
| Verrucomicrobiota | 872 | 152044 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2018 in northern station Síglunes 3 (SI3)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 91 | 27110 |
| Bacteroidota | 3901 | 541385 |
| Cyanobacteria | 32 | 14408 |
| Firmicutes | 0 | 50857 |
| Others | 348 | 42337 |
| Proteobacteria | 7000 | 1053586 |
| Thermoplasmatota | 0 | 35242 |
| Verrucomicrobiota | 159 | 13878 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2018 in southern station Selvogsbanki 2 (SB2)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 347 | 38079 |
| Bacteroidota | 5649 | 825440 |
| Cyanobacteria | 1313 | 22620 |
| Firmicutes | 0 | 41384 |
| Others | 728 | 143028 |
| Proteobacteria | 10743 | 2891246 |
| Thermoplasmatota | 0 | 45583 |
| Verrucomicrobiota | 629 | 53055 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1

### Spring 2018 in southern station Selvogsbanki 5 (SB5)

| Phylum | Metataxonomic counts | Metagenomics counts |
| --- | --- | --- |
| Actinobacteriota | 426 | 10006 |
| Bacteroidota | 6193 | 271713 |
| Cyanobacteria | 1607 | 25877 |
| Firmicutes | 0 | 23191 |
| Others | 418 | 38307 |
| Proteobacteria | 7837 | 918504 |
| Thermoplasmatota | 0 | 605 |
| Verrucomicrobiota | 35 | 1241 |

Pearson's Chi-squared test with simulated p-value (based on 2000 replicates)

X-squared = 48, df = NA, p-value = 1