

Supplementary Table 1: Elaborated relative abundances of the all taxa found in all three laminae (U1, U2, and U3) of the conical microbial mat from Lake Untersee, Antarctica

| 1. Phylum level | | | |
|---------------------------------|-----------|-----------|-----------|
| Taxa | U1 lamina | U2 lamina | U3 lamina |
| k__Bacteria;Other | 0.80% | 5.90% | 6.00% |
| k__Bacteria;p__Acidobacteria | 0.00% | 0.10% | 0.10% |
| k__Bacteria;p__Actinobacteria | 0.90% | 34.40% | 33.30% |
| k__Bacteria;p__Armatimonadetes | 0.00% | 0.00% | 0.00% |
| k__Bacteria;p__Bacteroidetes | 0.00% | 4.00% | 8.10% |
| k__Bacteria;p__Chlorobi | 0.00% | 0.00% | 0.00% |
| k__Bacteria;p__Chloroflexi | 0.00% | 0.00% | 0.00% |
| k__Bacteria;p__Cyanobacteria | 97.10% | 33.50% | 20.30% |
| k__Bacteria;p__Firmicutes | 0.00% | 0.80% | 0.00% |
| k__Bacteria;p__Gemmatimonadetes | 0.40% | 0.30% | 0.60% |
| k__Bacteria;p__Nitrospirae | 0.00% | 0.60% | 0.50% |
| k__Bacteria;p__OD1 | 0.00% | 0.00% | 0.00% |
| k__Bacteria;p__Planctomycetes | 0.00% | 0.00% | 0.10% |
| k__Bacteria;p__Proteobacteria | 0.00% | 3.20% | 8.30% |
| k__Bacteria;p__TM6 | 0.00% | 0.80% | 1.90% |
| k__Bacteria;p__TM7 | 0.00% | 0.40% | 0.20% |
| k__Bacteria;p__Verrucomicrobia | 0.80% | 16.00% | 20.40% |
| k__Bacteria;p__[Thermi] | 0.00% | 0.00% | 0.00% |
| | | | |
| 2. Genus level | | | |
| Taxa | U1 lamina | U2 lamina | U3 lamina |
| Leptolyngbya | 11.10% | 4.00% | 1.30% |
| Phormidium | 65.80% | 20.60% | 11.50% |
| Pseudanabaena | 1.80% | 0.50% | 0.80% |
| Cyanobacteria other | 18.40% | 8.40% | 6.60% |

| | | | |
|------------------------------|-------|--------|--------|
| family_C111 | 0.10% | 16.10% | 8.50% |
| family_Microbacteriaceae | 0.50% | 9.00% | 14.10% |
| Leifsonia | 0.20% | 2.30% | 3.70% |
| Yonghaparkia | 0.00% | 1.40% | 2.30% |
| Iamia | 0.00% | 1.80% | 1.30% |
| Salinibacterium | 0.00% | 0.00% | 0.50% |
| Actinobacteria other | 0.10% | 3.70% | 2.70% |
| family_Opitutaceae | 0.10% | 15.30% | 18.10% |
| Candidatus Xiphinematobacter | 0.20% | 0.00% | 0.30% |
| Haloferula | 0.20% | 0.10% | 0.10% |
| Luteolibacter | 0.20% | 0.00% | 0.10% |
| Verrucomicrobium | 0.00% | 0.10% | 0.20% |
| Opitutus | 0.00% | 0.10% | 0.60% |
| Verrucomicrobia other | 0.10% | 0.30% | 0.90% |
| family_Xanthomonadaceae | 0.00% | 0.40% | 3.40% |
| Anaerospira | 0.00% | 0.20% | 0.40% |
| Rhodobacter | 0.00% | 0.40% | 0.90% |
| Polaromonas | 0.00% | 0.00% | 0.30% |
| Mycoplana | 0.00% | 0.10% | 0.10% |
| Roseococcus | 0.00% | 0.10% | 0.20% |
| Roseomonas | 0.00% | 0.00% | 0.10% |
| Pseudoxanthomonas | 0.00% | 0.10% | 0.10% |
| Thermomonas | 0.00% | 0.00% | 0.20% |
| Proteobacteria other | 0.00% | 1.20% | 2.10% |
| family_Cytophagaceae | 0.00% | 3.00% | 6.40% |
| Sporocytophaga | 0.00% | 0.20% | 0.00% |
| Bacteroidetes other | 0.00% | 0.70% | 1.60% |
| Bryobacter | 0.00% | 0.00% | 0.10% |
| Paenisporosarcina | 0.00% | 0.60% | 0.00% |
| Gemmatimonas | 0.00% | 0.20% | 0.50% |

| | | | |
|----------------|-------|-------|-------|
| family_A1-B1 | 0.40% | 0.00% | 0.00% |
| Nitrospira | 0.00% | 0.60% | 0.50% |
| TM6 other | 0.00% | 0.80% | 1.90% |
| TM7 other | 0.00% | 0.30% | 0.20% |
| Bacteria other | 0.80% | 5.90% | 6.00% |

Supplementary Table 2: Oligotype ID, Oligotype Sequence, Representative Sequence, Abundance Oligotype, NCBI MEGABLAST results (including average E value and Identity), Taxonomical information (Phylum, Family, and Genus levels) of (a) *Phormidium*, (b) *Leptolyngbya*, (c) Cytophagaceae, (d) Opatutaceae, and (e) Xanthomonadaceae from all three laminae (U1, U2, and U3) of the conical microbial mat from Lake Untersee, Antarctica, used in this study.

Supplementary Table 2(a)

| Oligotype ID | Oligotype Sequence | Representative Sequence | Abundance Oligotype | NCBI MEGABLAST Results | Average E value | Average Identity (%) | Phylum | Family | Genus |
|--------------|--------------------|--|---------------------|---------------------------------|-----------------|----------------------|---------------|------------------|-------------------|
| Oligotype 1 | CTGATATGCAT | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCCGATGTA CCGCAAGGGCAAATATTTA TAGCCTGAAGAAGAGCTCG CGTCCGATTAGCTAGTTGG AGAGGTAAAAGCTCACCAA GGCGACGATCGGTAGCTGG TCTGAGAGGACGATCAGCC ACACTGGGACTGAGACACG GCCCAGACTCCTACGGGAG GCAGCAGTGGGGAATTTTC CGCAATGGGCGAAAGCCTG ACGGAGCAAGACCGCGTG GGGGAAGAAGGCTCTTGGG TTGTAAACCCCTTTTCTCTG GGAAGAAAGTTGTGAAAG CAGCCTGACGGTACCAGAG GAATCAGCAT | 1171 | Phormidium cf. uncinatum CYN108 | 9.00E-174 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium sp. Ant-Orange | 1.00E-171 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| Oligotype 2 | AGACACCATC | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACGAC TGCTAACCCCCGATGTACC | 652 | Phormidium cf. uncinatum CYN108 | 4.00E-172 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |

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|-------------|-----------------|--|-----|---------------------------------------|-----------|-----|-------------------|----------------------|-------------------|
| | | GCAAGGGCAAATATTTATA GCCTGAAGAAGAGCTCGCG TCCGATTAGCTAGTTGGAG AGGTAAAAGCTCACCAAGG CGACGATCGGTAGCTGGTC TGAGAGGACGATCAGCCAC ACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGC AGCAGTGGGGAATTTCCG CAATGGGCGAAAGCCTGAC GGAGCAAGACCGCGTGGG GGAAGAAGGCTCTTGGGTT GTAAACCCCTTTTCTCTGG GAAGAAAAGTTGTGAAAGC AGCCTGACGGTACCAGAGG AATCAGCATC | | | | | | | |
| Oligotype 3 | GCTGGTA AGCA | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCGACTGT ACCGCAAGGGCAAATATTT ATAGCCTGAAGAAGAGCTC GCGTCCGATTAGCTAGTTG GAGAGGTAAGCTCACCA AGGCGACGATCGGTAGCTG GTCTGAGAGGACGATCAGC CACACTGGGACTGAGACAC GGCCCAGACTCCTACGGGA GGCAGCAGTGGGGAATTTT CCGCAATGGGCGAAAGCCT GACGGAGCAAGACCGCGT GGGGGAAGAAGGCTCTTGG GTTGTAAACCCCTTTTCTCT GGGAAGAAAAGTTGTGAAA GCAGCCTGACGGTACCAGA GGAATCAGCA | 459 | Phormidium cf. uncinatum CYN108 | 1.00E-171 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 4 | TGAGTCT CTCC | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCGATGTA CCGCAAGGGCAAATATTTA TAGCCTGAAGAAGAGCTCG CGTCCGATTAGCTAGTTGG AGAGGTAAAAGCTCACCAA GGCGACGATCGGTAGCTGG TCTGAGAGGACGATCAGCC | 269 | Phormidium autumnale Ant- Ph68 | 2.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN79 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale SAG 35.90 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |

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|-------------|-----------------|--|-----|---|-----------|-----|-------------------|----------------------|-------------------|
| | | ACACTGGGACTGAGACACG GCCAGACTCCTACGGGAG GCAGCAGTGGGGAATTTTC CGCAATGGGCGAAAGCCTG ACGGAGCAAGACCGCGTG GGGGAAGAAGGCTCTTGGG TTGTAAACCCCTTTTCTCTG GGAAGAACGCAATGACGG TACCAGAGGAATCAGCATC GGCTAACTCC | | Phormidium cf. uncinatum CAWBG523 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 06363 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 07215 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 5 | ACCTGGA CAGC | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCGACTGT ACCGCAAGGGCAAATATTT ATAGCCTGAAGAAGAGCTC GCGTCCGATTAGCTAGTTG GAGAGGTAAGACTCACC AAGGCGACGATCGGTAGCT GGTCTGAGAGGACGATCAG CCACACTGGGACTGAGACA CGGCCAGACTCCTACGGG AGGCAGCAGTGGGGAATTT TCCGCAATGGGCGAAAGCC TGACGGAGCAAGACCGCGT GGGGGAAGAAGGCTCTTGG GTTGTAAACCCCTTTTCTCT GGGAAGAAAGTTGTGAAA GCAGCCTGACGGTACCAGA GGAATCAGC | 230 | Phormidium autumnale CYN79 | 7.00E-170 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. Ant-Orange | 1.00E-167 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 6 | GACGCCA ATCG | GAATCTACCTTCAGGACGG AGACAACAGTTGGAACGAC TGCTAACCCCGATGTACC GAAAGGGCAAATATTTATA GCCTGAAGAAGAGCTCGCG TCCGATTAGCTAGTTGGAG AGGTAAAGCTCACCAAGGC GACGATCGGTAGCTGGTCT GAGAGGACGATCAGCCAC ACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGC AGCAGTGGGGAATTTTCCG CAATGGGCGAAAGCCTGAC GGAGCAAGACCGCGTGGG GGAAGAAGGCTCTTGGGTT GTAAACCCCTTTTCTCTGG | 139 | Phormidium cf. uncinatum CYN108 | 1.00E-172 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. Ant-Orange | 2.00E-170 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |

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|-------------|-----------------|---|-----|---|-----------|-----|-------------------|----------------------|-------------------|
| | | GAAGAAAGTTGTGAAAGC AGCCTGACGGTACCAGAGG AATCAGCATCG | | | | | | | |
| Oligotype 7 | AAGGCAA TCCG | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACGAC TGCTAACCCCGATGTACC GCAAGGGCAAATATTTATA GCCTGAAGAAGAGCTCGCG TCCGATTAGCTAGTTGGAG AGGTAAGGCTACCAAGG CGACGATCGGTAGCTGGTC TGAGAGGACGATCAGCCAC ACTGGGACTGAGACCGGC CCAGACTCCTACGGGAGGC AGCAGTGGGGAATTTCCG CAATGGGCGAAAGCCTGAC GGAGCAAGACCGCTGGG GGAAGAAGGCTCTGGGTT GTAAACCCCTTTTCTCTGG GAAGAACGCAATGACGGT ACCAGAGGAATCAGCATCG GCTAACTCCG | 132 | Phormidium autumnale Arct- Ph5 | 2.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale Ant- Ph68 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN79 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale SAG 35.90 | 2.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CAWBG523 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 06363 | 2.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 07215 | 2.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 8 | AGCCCGG TCAG | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCGACTGT ACCGAAAGGGACAAATATT TATAGCCTGAAGAAGAGCT CGCGTCCGATTAGCTAGTT GGAGAGGTAAAAGACTCA CCAAGGGGACGATCGGTAG CTGGTCTGAGAGGACGATC AGCCCACTGGGACTGAGA CACGGCCAGACTCCTACG GGAGGCAGCAGTGGGGAA TTTTCCGCAATGGGCGAAA GCCTGACGGAGCAAGACCG CGTGGGGGAAGAAGGCTCT TGGGTTGTAAACCCCTTTTC TCTGGGAAGAAAGTTGTGA AAGCAGCCTGACGGTACCA GAGGAATCAG | 114 | Phormidium cf. uncinatum CYN108 | 5.00E-171 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 9 | GAGAATC ACTC | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCGACTGT | 100 | Phormidium autumnale Arct- Ph5 | 7.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |

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|-----------------|-----------------|---|----|---|-----------|-----|-------------------|----------------------|-------------------|
| | | ACCGCAAGGGCAAATATTT ATAGCCTGAAGAAGAGCTC GCGTCCGATTAGCTAGTTG GAGAGGTAAGCTCACCA AGGCGACGATCGGTAGCTG GTCTGAGAGGACGATCAGC CACACTGGGACTGAGACAC GGCCAGACTCCTACGGGA GGCAGCAGTGGGGAATTTT CCGCAATGGGCGAAAGCCT GACGGAGCAAGACCGCGT GGGGGAAGAAGGCTCTTGG GTTGTAAACCCCTTTTCTCT GGGAAGAACGCAATGACG GTACCAGAGGAATCAGCAT CGGCTAACTC | | Phormidium autumnale Ant- Ph68 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN79 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale SAG 35.90 | 7.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CAWBG523 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 06363 | 7.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 07215 | 7.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 10 | AAGCACG ATCA | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCGACTGT ACCGAAAGGGACAAATAA TTTATAGCCTGAAGAAGAG CTCGCTCCGATTAGCTAG TTGGAGAGGTAAGACTC ACCAAGGCGACGATCGGTA GCTGGTCTGAGAGGACGAT CAGCCACACTGGGACTGAG ACACGGCCCAGACTCCTAC GGGAGGCAGCAGTGGGGA ATTTCCGCAATGGGCGAA AGCCTGACGGAGCAAGACC GCGTGGGGGAAGAAGGCT CTTGGGTTGTAAACCCCTTT TCTCTGGGAAGAAAGTTGT GAAAGCAGCCTGACGGTAC CAGAGGAATCA | 65 | Phormidium cf. uncinatum CYN108 | 2.00E-169 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. Ant-Orange | 2.00E-165 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 11 | GCAGAAG AACT | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCGACTGT ACCGCAAGGGCAAATATTT ATAGCCTGAAGAAGAGCTC GCGTCCGATTAGCTAGTTG GAGAGGTAAGACTCACC AAGGCGACGATCGGTAGCT GGTCTGAGAGGACGATCAG | 46 | Phormidium autumnale Arct- Ph5 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale Ant- Ph68 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN79 | 7.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |

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|-----------------|-----------------|--|----|--|-----------|-----|-------------------|----------------------|-------------------|
| | | CCACACTGGGACTGAGACA CGGCCAGACTCCTACGGG AGGCAGCAGTGGGGAATTT TCCGCAATGGGCGAAAGCC TGACGGAGCAAGACCGCGT GGGGGAAGAAGGCTCTTGG GTTGTAAACCCCTTTTCTCT GGGAAGAACGCAATGACG GTACCAGAGGAATCAGCAT CGGCTAACT | | Phormidium autumnale SAG 35.90 | 3.00E-173 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CAWBG523 | 7.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 06363 | 3.00E-173 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 07215 | 3.00E-173 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 12 | GAATTAA AACA | TGGGGAATTTCCGCAATG GGCGAAAGCCTGACGGAG CAAGACCGCGTGGGGGAA GAAGGCTCTTGGGTTGTAA ACCCCTTTTCTCTGGGAAG AAAGTTGTGAAAGCAGCCT GACGGTACCAGAGGAATCA GCATCGGCTAACTCCGTGC CAGCAGCCGCGGTAAGACG GAGGATGCAAGCGTTATCC GGAATGATTGGGCGTAAAG CGTCCGCAGGTGGCAGTTC AAGTCTGCTGTCAAAGACC GGGGCTCAACCTCGGAAAG GCAGTGGAAACTGAACAGC TAGAGTATGGTAGGGCAA AGGGAATTCCTGGTGTAGC GGTAAAATGCGTAGAGATC AGGAAGAACA | 35 | Phormidium cf. uncinatum CYN108 | 2.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium uncinatum PACC 8693 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale JR8 | 2.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale CCALA 853 | 2.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. KU003 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 13 | GCAGGAA AATC | GAATCTACCTTCAGGACGG AGACAACAGTTGGAAACG ACTGCTAACCCCGACTGT ACCGAAAGGACGAAATA ATTTATAGCCTGAAGAAGA GCTCGCGTCCGATTAGCTA GTTGGAGAGGTAAGAACT CACCAAGGCGACGATCGGT AGCTGGTCTGAGAGGACGA TCAGCCACACTGGGACTGA GACACGGCCCAGACTCCTA CGGGAGGCAGCAGTGGGG AATTTTCCGCAATGGGCGA AAGCCTGACGGAGCAAGA CCGCGTGGGGGAAGAAGG | 34 | Phormidium cf. uncinatum CYN108 | 4.00E-167 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |

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|-----------------|-----------------|--|----|--|-----------|-----|-------------------|----------------------|-------------------|
| | | CTCTTGGGTTGTAAACCCC TTTTCTCTGGGAAGAAAGT TGTGAAAGCAGCCTGACGG TACCAGAGGAATC | | | | | | | |
| Oligotype 14 | CAAAGTG GAAC | TGGGGAATTTCCGCAATG GGCGAAAAGCCTGACGGA GCAAGACCGCTGGGGGA AGAAGGCTCTTGGGTTGTA AACCCCTTTTCTCTGGGAA GAAAGTTGTGAAAGCAGCC TGACGGTACCAGAGGAATC AGCATCGGCTAACTCCGTG CCAGCAGCCCGGTAAGAC GGAGGATGCAAGCGTTATC CGGAATGATTGGGCGTAAA GCGTCCGCAGGTGGCAGTT CAAGTCTGCTGTCAAAGAC CGGGGCTCAACCTCGGAAA GGCAGTGGAAACTGAACA GCTAGAGTATGGTAGGGGC AAAGGGAATTCCTGGTGTA GCGGTGAAATGCGTAGAGA TCAGGAAGAAC | 32 | Phormidium sp. Ant-Orange | 7.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. Ant-Lunch | 7.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CYN108 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale JR8 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale CCALA 853 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium uncinatum PACC 8693 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. KU003 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 15 | CGGAAGA CCGT | GAATCTACCTTCAGGACGG AGACAACAGTTGGAACGAC TGCTAACCCCGATGTACC GCAAGGGCAAATATTTATA GCCTGAAGAAGAGCTCGCG TCCGATTAGCTAGTTGGAG AGGTAAAGCTACCAAGGC GACGATCGGTAGCTGGTCT GAGAGGACGATCAGCCAC ACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGC AGCAGTGGGGAATTTCCG CAATGGGCGAAAAGCCTGAC GGAGCAAGACCGCGTGGG GGAAGAAGGCTCTTGGGTT GTAAACCCCTTTTCTCTGG GAAGAACGCAATGACGGT ACCAGAGGAATCAGCATCG GCTAACTCCGT | 31 | Phormidium autumnale Arct- Ph5 | 2.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale Ant- Ph68 | 1.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN79 | 5.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale SAG 35.90 | 2.00E-174 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CAWBG523 | 5.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 06363 | 2.00E-174 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 07215 | 2.00E-174 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 16 | CTGATAC CATC | GAATCTACCTTCAGGACGG AGACAACAGTTGGAACG | 19 | Phormidium cf. uncinatum | 9.00E-174 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |

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|-----------------|-----------------|---|----|--|-----------|-----|-------------------|----------------------|-------------------|
| | | ACTGCTAACCCCGATGTA CCGAAAGGGCAAATATTTA TAGCCTGAAGAAGAGCTCG CGTCCGATTAGCTAGTTGG AGAGGTAAAAGCTCACCAA GGCGACGATCGGTAGCTGG TCTGAGAGGACGATCAGCC ACACTGGGACTGAGACACG GCCCAGACTCCTACGGGAG GCAGCAGTGGGGAATTTTC CGCAATGGGCGAAAGCCTG ACGGAGCAAGACCGCGTG GGGAAGAAGGCTTTGGG TTGTAAACCCCTTTTCTCTG GGAAGAAAGTTGTGAAAG CAGCCTGACGGTACCAGAG GATCAGCATC | | CYN108 | | | | | |
| Oligotype 17 | GGAACGG AGAA | TGGGGAATTTTCCGCAAT GGGCGAAAAGCCTGACGG AGCAAGACCGCTGGGGG AAGAAGGCTCTTGGGTTGT AAACCCCTTTTCTCTGGGA AGAAAGTTGTGAAAGCAGC CTGACGGTACCAGAGGAAT CAGCATCGGCTAACTCCGT GCCAGCAGCCGCGTAAGA CGGAGGATGCAAGCGTTAT CCGGAATGATTGGGCGTAA AGCGTCCGAGGTGGCAGT TCAAGTCTGCTGTCAAAGA CCGGGGCTCAACCTCGGAA AGGCAGTGGAACTGAAC AGCTAGAGTATGGTAGGGG CAAAGGGAATTCCTGGTGT AGCGGTGAAATGCGTAGAG ATCAGGAAGAA | 15 | Phormidium sp. Ant-Orange | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. Ant-Lunch | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CYN108 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium uncinatum PACC 8693 | 7.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale JR8 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale CCALA 853 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. KU003 | 7.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 18 | GATGAGA ACAT | TGGGGAATTTTCCGCAATG GGCGAAAAGCCTGACGGAG CAAGACCGCTGGGGGAA GAAGGCTCTTGGGTTGTAA ACCCCTTTTCTCTGGGAAG AAAGTTGTGAAAGCAGCCT GACGGTACCAGAGGAATCA GCATCGGCTAACTCCGTGC | 12 | Phormidium sp. Ant-Orange | 2.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. Ant-Lunch | 2.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CYN108 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium | 4.00E-177 | 99% | Cyanoba | Oscillatoriac | <i>Phormidium</i> |

| | | | | | | | | | |
|-----------------|-----------------|---|---|--|-----------|-----|--------------------|----------------------|-------------------|
| | | CAGCAGCCGCGGTAAGACG GAGGATGCAAGCGTTATCC GGAATGATTGGGCGTAAAG CGTCCGCAGGTGGCAGTTC AAGTCTGCTGTCAAAGACC GGGCTCAACCTCGGAAAGG CAGTGGAAACTGAACAGCT AGAGTATGGTAGGGGCAA AGGGAATTCCTGGTGTAGC GGTGAAATGCGTAGAGATC AGGAAGAACAT | | uncinatum PACC 8693 | | | acteria | eae | |
| | | | | Phormidium cf. autumnale JR8 | 9.00E-179 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale CCALA 853 | 9.00E-179 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. KU003 | 4.00E-177 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 19 | TATCAAT CGAA | TGGGGAATTTCCGCAATG GGCGAAAGCCTGACGGAG CAAGACCGCGTGGGGGAA GAAGGCTCTTGGGTTGTAA ACCCCTTTTCTCTGGGAAG AACGCAATGACGGTACCAG AGGAATCAGCATCGGCTAA CTCCGTGCCAGCAGCCGCG GTAAGACGGAGGATGCAA GCGTTATCCGGAATGATTG GGCGTAAAGCGTCCGCAGG TGGCAGTTCAAGTCTGCTG TCAAAGACCGGGGCTCAAC CTCGGAAAGGCAGTGGAA ACTGAACAGCTAGAGTATG GTAGGGGCAAAGGGAATTC CTGGTGTAGCGGTGAAATG CGTAGAGATCAGGAAGAA CATCGGTGGCGAA | 9 | Phormidium cf. uncinatum CAWBG523 | 2.00E-180 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale KNUA026 | 2.00E-180 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale CCALA 844 | 2.00E-180 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale CCALA 852 | 4.00E-177 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW20 | 2.00E-180 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW9 | 2.00E-180 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW11 | 2.00E-180 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW21 | 9.00E-179 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW24 | 9.00E-179 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW19 | 9.00E-179 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW16 | 9.00E-179 | 99% | Cyanoba acteria | Oscillatoriac eae | <i>Phormidium</i> |

| | | | | | | | | | |
|-----------------|-----------------|---|---|--|-----------|-----|-------------------|----------------------|-------------------|
| | | | | Phormidium autumnale VUW2 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN79 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN119 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN55 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale Ant- Ph68 | 1.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CAWBG527 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 06363 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium sp. CCALA 726 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. setchellianum CCALA 149 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. irriguum CCALA 815 | 4.00E-177 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Oligotype 20 | GGATGAG GCGA | TGGGGAATTTTCCGCAAT GGGCGAAAGCCTGACGGA GCAAGACCGCGTGGGGGA AGAAGGCTCTTGGGTTGTA AACCCCTTTTCTCTGGGAA GAACGCAATGACGGTACCA GAGGAATCAGCATCGGCTA ACTCCGTGCCAGCAGCCGC GGTAAGACGGAGGATGCA AGCGTTATCCGGAATGATT GGGCGTAAAGCGTCCGCAG GTGGCAGTTCAAGTCTGCT GTCAAAGACCGGGGCTCAA CCTCGGAAAGGCAGTGGAA ACTGAACAGCTAGAGTATG | 6 | Phormidium cf. autumnale CCALA 854 | 7.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale CCALA 852 | 7.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium cf. autumnale CCALA 844 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CCALA 697 | 7.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CCAP 1462/10 | 7.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |

| | | | | | | | | | |
|-------------------------|-----------|--|-------------------|--------------------------------------|-------------------|-----|-------------------|----------------------|-------------------|
| | | GTAGGGGCAAAGGGAATTC CTGGTGTAGCGGTGAAATG CGTAGAGATCAGGAAGAA CATCGGTGGCGA | | Phormidium autumnale Ant- Ph68 | 2.00E-175 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale Arct- Ph5 | 7.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale KNUA026 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW12 | 7.00E-180 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW20 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW9 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW11 | 3.00E-178 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW19 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW24 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW21 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW2 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale VUW16 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN79 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| | | | | Phormidium autumnale CYN119 | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> |
| Phormidium autumnale | 1.00E-176 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Phormidium</i> | | | | |

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|--|--|--|--|--|-----------|-----|---------------|------------------|-------------------|
| | | | | CYN55 | | | | | |
| | | | | Phormidium cf. uncinatum CCALA 849 | 7.00E-180 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CAWBG523 | 3.00E-178 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium cf. uncinatum CAWBG527 | 1.00E-176 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium sp. CCALA 845 | 7.00E-180 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium sp. CCALA 846 | 7.00E-180 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium sp. CCALA 726 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium sp. LEGE 06363 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium cf. setchellianum CCALA 149 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |
| | | | | Phormidium cf. irriguum CCALA 815 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Phormidium</i> |

Supplementary Table 2(b)

| Oligotype ID | Oligotype Sequence | Representative Sequence | Abundance Oligotype | NCBI MEGABLAST Results | Average E value | Average Identity (%) | Phylum | Family | Genus |
|--------------|--------------------|---|---------------------|-----------------------------------|-----------------|----------------------|---------------|------------------|---------------------|
| Oligotype 1 | ACCC | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAACGG CTGCTAATACCCGATGTGC CGAGAGGTGAAACTATTG GCCTGAGGATGAGCTCGCG TCTGATTAGCTAGTTGGAG TGGTAACGGCACACCAAGG CGACGATCAGTAGCTGGTC TGAGAGGATGATCAGCCAC ACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGC | 116 | Leptolyngbya antarctica ANT.L18.1 | 2.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 2.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 2.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica | 2.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |

| | | | | | | | | | |
|-------------|------|---|-----|---|-----------|-----|---------------|------------------|---------------------|
| | | AGCAGTGGGGAATTTCCG CAATGGGCGAAAGCCTGAC GGAGCAAGACCGCGTGCG GGAGGAAGGTCTATTGATT GTAAACCGCTTTTGATAGG GAAGAAGATCTGACGGTAC CTATCGAATCAGCATCGGC TAACTCCGTG | | ANT.LG2.5 | | | | | |
| | | | | Leptolyngbya antarctica ANT.L67.1 | 2.00E-175 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.3 | 1.00E-172 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya sp. CENA538 | 7.00E-160 | 96% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Uncultured Leptolyngbya sp. clone | 2.00E-156 | 96% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| Oligotype 2 | TTTT | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAAACG GCTGCTAATACCCGATGTG CCGAGAGGTGAAACTATTT GGCCTGAGGATGAGCTCGC GTCTGATTAGCTAGTTGGA GTGGTAACGGCACACCAAG GCGACGATCAGTAGCTGGT CTGAGAGGATGATCAGCCA CACTGGGACTGAGACACGG CCCAGACTCCTACGGGAGG CAGCAGTGGGGAATTTCC GCAATGGGCGAAAGCCTGA CGGAGCAAGACCGCGTGCG GGAGGAAGGTCTATTGATT GTAAACCGCTTTTGATAGG GAAGAAGATCTGACGGTAC CTATCGAATCAGCATCGGC TAACTCCGT | 109 | Leptolyngbya antarctica ANT.L18.1 | 4.00E-177 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 4.00E-177 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 4.00E-177 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.5 | 4.00E-177 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L67.1 | 4.00E-177 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.3 | 2.00E-174 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya sp. CENA538 | 5.00E-161 | 97% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Uncultured Leptolyngbya sp. clone | 3.00E-158 | 96% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| Oligotype 3 | GTGG | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAAACG GCTGCTAATACCCGATGTG CCGAGAGGTGAAACTATTT GGCCTGAGGATGAGCTCGC GTCTGATTAGCTAGTTGGA GTGGTAACGGCACACCAAG GCGACGATCAGTAGCTGGT CTGAGAGGATGATCAGCCA | 74 | Uncultured cyanobacterium clone | 6.00E-141 | 98% | Cyanobacteria | - | - |
| | | | | Oscillatoria amoena CCAP | 1.00E-142 | 93% | Cyanobacteria | Oscillatoriaceae | <i>Oscillatoria</i> |

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|-------------|------|---|----|-----------------------------------|-----------|-----|---------------|------------------|---------------------|
| | | CACTGGGACTGAGACACGG CCCAGACTCCTACGGGAGG CAGCAGTGGGGAATTTTCC GCAATGGGCGAAAGCCTGA CGGAGCAAGACCGCGTGG GGGAAGAAGGCTCTTGGGT TGTA AACCCCTTTTCTCTGG GAAGAAAGTTGTGAAAGC AGCCTGACGGTACCAGAGG AATCAGCATC | | | | | | | |
| Oligotype 4 | CGTA | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAACGG CTGCTAATACCCGATGTGC CGAGAGGTGAAACTATTTG GCCTGAGGATGAGCTCGCG TCTGATTAGCTAGTTGGAG TGGTAACGGCACACCAAGG CGACGATCAGTAGCTGGTC TGAGAGGATGATCAGCCAC ACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGC AGCAGTGGGGAATTTTCCG CAATGGGCGAAAGCCTGAC GGAGCAAGACCGCGTGGG GGAAGAAGGCTCTTGGGT GTAAACCCCTTTTCTCTGG GAAGAAAGTTGTGAAAGC AGCCTGACGGTACCAGAGG AATCAGCATCG | 69 | Uncultured cyanobacterium clone | 2.00E-140 | 96% | Cyanobacteria | - | - |
| | | | | Oscillatoria amoena CCAP | 2.00E-141 | 93% | Cyanobacteria | Oscillatoriaceae | <i>Oscillatoria</i> |
| | | | | Microcoleus vaginatus | 7.00E-140 | 93% | Cyanobacteria | Microcoleaceae | <i>Microcoleus</i> |
| Oligotype 5 | CGAG | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAACG GCTGCTAATACCCGATGTG CCGAGAGGTGAAACTATTT GGCCTGAGGATGAGCTCGC GTCTGATTAGCTAGTTGGA GTGGTAACGGCACACCAAG GCGACGATCAGTAGCTGGT CTGAGAGGATGATCAGCCA CACTGGGACTGAGACACGG CCCAGACTCCTACGGGAGG CAGCAGTGGGGAATTTCCGC AATGGGCGAAAGCCTGACG GAGCAAGACCGCGTGGCG GAGGAAGGTCTATTGATTG | 57 | Uncultured cyanobacterium clone | 2.00E-179 | 99% | Cyanobacteria | - | - |
| | | | | Leptolyngbya antarctica ANT.L18.1 | 2.00E-174 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 2.00E-174 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 2.00E-174 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.5 | 2.00E-174 | 99% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |

| | | | | | | | | | |
|-------------|------|--|----|-----------------------------------|-----------|-----|---------------|---------------|---------------------|
| | | TAAACCGCTTTTGATAGGG AAGAAGATCTGACGGTACC TATCGAATCAGCATCGGCT AACTCCGTGC | | Leptolyngbya antarctica ANT.L67.1 | 2.00E-174 | 99% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.3 | 2.00E-171 | 99% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya sp. CENA538 | 3.00E-158 | 96% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Uncultured cyanobacterium clone | 2.00E-155 | 95% | Cyanobacteria | - | - |
| Oligotype 6 | GAAA | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAAACG GCTGCTAATACCCGATGTG CCGAGAGGTGAAACTATTT GGCCTGAGGATGAGCTCGC GTCTGATTAGCTAGTTGGA GTGGTAACGGCACACCAAG GCGACGATCAGTAGCTGGT CTGAGAGGATGATCAGCCA CACTGGGACTGAGACACGG CCCAGACTCCTACGGGAGG CAGCAGTGGGGAATTTTCC GCAATGGGCGAAAGCCTGA CGGAGCAAGACCGCGTGCG GGAGGAAGGTCTATTGATT GTAAACCGCTTTTTGATAG GGAAGAAGATCTGACGGTA CCTATCGAATCAGCATCGG CTAACTCCG | 38 | Uncultured cyanobacterium clone | 7.00E-180 | 99% | Cyanobacteria | - | - |
| | | | | Leptolyngbya antarctica ANT.L18.1 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.5 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L67.1 | 7.00E-175 | 99% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.3 | 4.00E-172 | 99% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya sp. CENA538 | 3.00E-159 | 96% | Cyanobacteria | Oscillatoriae | <i>Leptolyngbya</i> |
| Oligotype 7 | AAAG | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAAACGG CTGCTAATACCCGATGTGC CGAGAGGTGAAACTATTTG GCCTGAGGATGAGCTCGCG TCTGATTAGCTAGTTGGAG TGGTAACGGCACACCAAGG CGACGATCAGTAGCTGGTC TGAGAGGATGATCAGCCAC ACTGGGACTGAGACACGGC | 30 | Uncultured cyanobacterium clone | 9.00E-139 | 96% | Cyanobacteria | - | - |
| | | | | Oscillatoria amoena CCAP | 7.00E-140 | 93% | Cyanobacteria | Oscillatoriae | <i>Oscillatoria</i> |

| | | | | | | | | | |
|-------------|------|---|----|-----------------------------------|-----------|-----|---------------|------------------|---------------------|
| | | CCAGACTCCTACGGGAGGC AGCAGTGGGGAATTTCCG CAATGGGCGAAAGCCTGAC GGAGCAAGACCGCGTGGG GGAAGAAGGCTCTTGGGTT GTAAACCCCTTCTCTGGG AAGAAAAGTTGTGAAAGCA GCCTGACGGTACCAGAGGA ATCAGCATCGG | | | | | | | |
| Oligotype 8 | CAGG | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAAACG GCTGCTAATACCCGATGTG CCGAGAGGTGAACTATTT GGCCTGAGGATGAGCTCGC GTCTGATTAGCTAGTTGGA GTGGTAACGGCACACCAAG GCGACGATCAGTAGCTGGT CTGAGAGGATGATCAGCCA CACTGGGACTGAGACACGG CCGAGACTCCTACGGGAGC AGCAGTGGGAAATTTCCGCA ATGGGCGAAAGCCTGACGG AGCAAGACCGCGTGC GGG AGGAAGGTCTATTGATTGT AAACCGCTTTTGATAGGGA AGAAGATCTGACGGTACCT ATCGAATCAGCATCGGCTA ACTCCGTGCC | 24 | Uncultured cyanobacterium clone | 1.00E-172 | 98% | Cyanobacteria | | - |
| | | | | Leptolyngbya antarctica ANT.L18.1 | 1.00E-172 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 1.00E-172 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 1.00E-172 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.5 | 1.00E-172 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L67.1 | 1.00E-172 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.3 | 7.00E-170 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya sp. CENA538 | 4.00E-157 | 96% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| Oligotype 9 | TACC | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAAACG GCTGCTAATACCCGATGTG CCGAGAGGTGAACTATTT GGCCTGAGGATGAGCTCGC GTCTGATTAGCTAGTTGGA GTGGTAACGGCACACCAAG GCGACGATCAGTAGCTGGT CTGAGAGGATGATCAGCCA CACTGGGACTGAGACACGG CCCAGACTCCTACGGGAGC AGCAGTGGGAAATTTCCGCA | 17 | Uncultured cyanobacterium clone | 1.00E-176 | 99% | Cyanobacteria | - | - |
| | | | | Leptolyngbya antarctica ANT.L18.1 | 2.00E-171 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 2.00E-171 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 2.00E-171 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |

| | | | | | | | | | |
|-----------------|------|--|----|---|-----------|-----|-------------------|----------------------|---------------------|
| | | ATGGCGAAAGCCTGACGGA GCAAGACCGCGTGCGGGA GGAAGGTCTATTGATTGTA AACCGCTTTTGATAGGGAA GAAGATCTGACGGTACCTA TCGAATCAGCATCGGCTAA CTCCGTGCCA | | Leptolyngbya antarctica ANT.LG2.5 | 2.00E-171 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L67.1 | 2.00E-171 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.3 | 9.00E-169 | 98% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya sp. CENA538 | 2.00E-155 | 95% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| Oligotype 10 | GCCG | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAACGG CTGCTAATACCCGATGTGC CGAGAGGTGAAACTATTTG GCCTGAGGATGAGCTCGCG TCTGATTAGCTAGTTGGAG TGGTAACGGCACACCAAGG CGACGATCAGTAGCTGGTC TGAGAGGATGATCAGCCAC ACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGGC AGCAGTGGGAATTTCCGCA ATGGGCGAAAGCCTGACGG AGCAAGACCGCGTGGGGG AAGAAGGCTCTTGGGTTGT AAACCCCTTTTCTCTGGGA AGAAAGTTGTGAAAGCAGC CTGACGGTACCAGAGGAAT CAGCATCGGC | 16 | Uncultured Antarctic cyanobacterium | 2.00E-145 | 94% | Cyanoba cteria | - | - |
| | | | | Oscillatoria amoena CCAP | 9.00E-139 | 93% | Cyanoba cteria | Oscillatoriac eae | <i>Oscillatoria</i> |
| | | | | Microcoleus vaginatus | 4.00E-137 | 92% | Cyanoba cteria | Microcoleac eae | <i>Microcoleus</i> |
| Oligotype 11 | CGCA | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAACGG CTGCTAATACCCGATGTGC CGAGAGGTGAAACTATTTG GCCTGAGGATGAGCTCGCG TCTGATTAGCTAGTTGGAG TGGTAACGGCACACCAAGG CGACGATCAGTAGCTGGTC TGAGAGGATGATCAGCCAC ACTGGGACTGAGACACGGC CCAGACTCCTACGGGAGCA GCAGTGGGAATTTCCGCAA TGGGCGAAAGCCTGACGGA GCAAGACCGCGTGGGGGA | 11 | Uncultured Antarctic cyanobacterium | 9.00E-144 | 93% | Cyanoba cteria | | - |
| | | | | Oscillatoria amoena CCAP | 4.00E-137 | 92% | Cyanoba cteria | Oscillatoriac eae | <i>Oscillatoria</i> |
| | | | | Microcoleus vaginatus | 2.00E-135 | 92% | Cyanoba cteria | Microcoleac eae | <i>Microcoleus</i> |

| | | | | | | | | | |
|-----------------|------|---|----|---|-----------|------|-------------------|----------------------|---------------------|
| | | AGAAGGCTCTTGGGTTGTA AACCCTTTTCTCTGGGAA GAAAGTTGTGAAAGCAGCC TGACGGTACCAGGAATC AGCATCGGCT | | | | | | | |
| Oligotype 12 | GAAC | TGGGGAATTTCCGCAATG GGCGAAAAGCCTGACGGAG CAAGACCGCGTGCGGGAG GAAGGTCTATTGATTGTAA ACCGCTTTTGATAGGGAAG AAGATCTGACGGTACCTAT CGAATCAGCATCGGCTAAC TCCGTGCCAGCAGCCGCGG TAATACGGGGGATGCAAGC GTTATCCGGAATTATTGGG CGTAAAGCGTCCGTAGGTG GTTTTAAAAGTCTGTTGTC AAATCGCGAGGCTTAACCT CGTACAGGCAGTGGAAACT ATAAGACTAGAGTGCGGTA GGGGTAGAGGGAATTTCCA GTGTAGCGGTGAAATGCGT AGATATTGAAAGAACACC GGTGGCGAAG | 10 | Uncultured cyanobacterium clone | 2.00E-170 | 100% | Cyanoba cteria | - | - |
| | | | | Uncultured Antarctic cyanobacterium | 4.00E-157 | 100% | Cyanoba cteria | - | - |
| | | | | Leptolyngbya antarctica ANT.L18.1 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.5 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L67.1 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.3 | 9.00E-179 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWAV6.1 | 6.00E-156 | 99% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| Oligotype 13 | GGAA | GGATCTGCCCTTAGGACGG GGACAACAGCTGGAAACG GCTGCTAATACCCGATGTG CCGAGAGGTGAAACTATTT GGCCTGAGGATGAGCTCGC GTCTGATTAGCTAGTTGGA GTGGTAACGGCACACCAAG GCGACGATCAGTAGCTGGT CTGAGAGGATGATCAGCCA CACTGGGACTGAGACACGG CCCAGACTCCTACGGGAGG CAGCAGTGGGGAATTTTCC | 8 | Uncultured cyanobacterium clone | 7.00E-155 | 95% | Cyanoba cteria | - | - |
| | | | | Leptolyngbya antarctica ANT.L18.1 | 7.00E-145 | 94% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 7.00E-145 | 94% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 7.00E-145 | 94% | Cyanoba cteria | Oscillatoriac eae | <i>Leptolyngbya</i> |

| | | | | | | | | | |
|--------------|------|---|---|-----------------------------------|-----------|-----|---------------|------------------|----------------------|
| | | GCAATGGGCGAAAGCCTGACGGAGCAAGACCGCTGGGGAAAGGGCTCTTGGGTGTAAACCCCTTTTCTCTGGGAAGAACGCAATGACGGTACCAGAGGAATCAGCATCGGCTAACTCCG | | Leptolyngbya antarctica ANT.LG2.5 | 7.00E-145 | 94% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L67.1 | 7.00E-145 | 94% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Synechococcus sp. NgrSCC7 | 9.00E-144 | 94% | Cyanobacteria | Synechococaceae | <i>Synechococcus</i> |
| Oligotype 14 | GATC | GGATCTGCCCTTAGGACGGGACGAACAGCTGGAAACGGACTGCTAATAACCCGACTGTGCCGAGAGGTGAAACTAATTTGGCCTGAGGATGAGCTCGCGTCTGATTAGCTAGTTGGAGTGGTAACGGCACACCAAGGCGACGATCAGTAGCTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGAGGCAGCAGTGGGGAAATTTCCGCAATGGGCGAAAGCCTGACGGAGCAAGACCGCGTGCGGGGAGGAAGGTCTATTGATTGTAAACCGCTTTTGTATAGGGAAGAAGATCTGACGGTACCTATCGAATCAGCATCGGCTAAC | 6 | Uncultured cyanobacterium clone | 4.00E-172 | 99% | Cyanobacteria | - | - |
| | | | | Leptolyngbya antarctica ANT.L18.1 | 9.00E-169 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L18.2 | 9.00E-169 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LWA.1 | 9.00E-169 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.5 | 9.00E-169 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.L67.1 | 9.00E-169 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica ANT.LG2.3 | 5.00E-166 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya sp. CENA538 | 3.00E-153 | 95% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya sp. O-77 | 7.00E-150 | 95% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya frigida ANT.L52.2 | 9.00E-149 | 95% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| Oligotype 15 | ACCA | GGATCTGCCCTTAGGACGGGACGAACAGCTGGAAACGGACTGCTAATAACCCGACTGTGCCGAGAGGTGAAACTAATTTGGCCTGAGGATGAGCTCGCGTCTGATTAGCTAGTTGGAGTGGTAACGGCACACCAAGGCGACGATCAGTAG | 4 | Uncultured cyanobacterium clone | 5.00E-171 | 98% | Cyanobacteria | - | - |
| | | | | Leptolyngbya antarctica ANT.L18.1 | 1.00E-167 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |
| | | | | Leptolyngbya antarctica | 1.00E-167 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> |

| | | | | | | | | |
|--|--------------------------------------|-----------|-----|---------------|------------------|---------------------|--|--|
| <p>CTGGTCTGAGAGGATGATC AGCCACACTGGGACTGAGA CACGGCCAGACTCTACG GGAGGCAGCAGTGGGAATT TTCCGCAATGGGCGAAAGC CTGACGGAGCAAGACCGCG TGCGGGAGGAAGGTCTATT GATTGTAAACCGCTTTTGA TAGGGAAGAAGATCTGACG GTACCTATCGAATCAGCAT CGGCTAACT</p> | ANT.L18.2 | | | | | | | |
| | Leptolyngbya antarctica ANT.LWA.1 | 1.00E-167 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> | | |
| | Leptolyngbya antarctica ANT.LG2.5 | 1.00E-167 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> | | |
| | Leptolyngbya antarctica ANT.L67.1 | 1.00E-167 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> | | |
| | Leptolyngbya antarctica ANT.LG2.3 | 7.00E-165 | 98% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> | | |
| | Leptolyngbya sp. CENA538 | 2.00E-151 | 95% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> | | |
| | Leptolyngbya sp. O-77 | 3.00E-148 | 95% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> | | |
| | Leptolyngbya frigida ANT.L52.2 | 1.00E-147 | 94% | Cyanobacteria | Oscillatoriaceae | <i>Leptolyngbya</i> | | |

Supplementary Table 2(c)

| Oligotype ID | Oligotype Sequence | Representative Sequence | Abundance Oligotype | NCBI MEGABLAST Results | Average E value | Average Identity (%) | Phylum | Family | Genus |
|--------------|--------------------|---|---------------------|--|-----------------|----------------------|---------------|--------|-------|
| Oligotype 1 | TTC | <p>TAGGGAATATTGGACAATG GGTGCAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTA CTGCTTTTACCAGGGGATA AAAAGACCATGCGTGGTCA ATTGAAGGTACCTGGTGAA TAAGCCACGGCTAACTACG TGCCAGCAGCCGCGGTAAT ACGTAGGTGGCAAGCGTTG TCCGGATTTATTGGGTTTA AAGGGTGCCTAGGCGGTTT TGTAAGTCAGTGGTGAAAT ACTCCAGCTCAACTGGAGA GGTGCCATTGATACTGCAG</p> | 99 | Uncultured bacterium clone | 2.00E-165 | 100% | - | - | - |
| | | | | Uncultured Bacteroidetes bacterium clone | 4.00E-142 | 96% | Bacteroidetes | - | - |

| | | | | | | | | | |
|-------------|-----|---|----|--|-----------|-----|-------------------|---|---|
| | | AACTTGAGTACAGACGAGG TAGGCGGAATTGACGG | | | | | | | |
| Oligotype 2 | CCA | TAGGGAATATTGGACAATG GGTGCGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTAAA CTGCTTTTACCAGGGGATA AAAGACCATGCGTGGTCAA TTGAAGGTACCTGGTGAAT AAGCCACGGCTAACTACGT GCCAGCAGCCGCGGTAATA CGTAGGTGGCAAGCGTTGT CCGGATTTATTGGGTTTAA AGGGTGCGTAGGCGTTTT GTAAGTCAGTGGTAAAATA CTCCAGCTCAACTGGAGAG GTGCCATTGATACTGCAGA ACTTGAGTACAGACGAGGT AGGCGGAATTGACGGT | 49 | Uncultured bacterium clone | 8.00E-164 | 99% | - | - | - |
| | | | | Uncultured Bacteroidetes bacterium clone | 4.00E-142 | 96% | Bacteroi detes | - | - |
| Oligotype 3 | ATC | TAGGGAATATTGGACAATG GGTGAGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA AGGCCTTCTGGGTTGTAAA CTGCTTTTGCCGGGGGATA AAAGATCCCTGCGGGGAGA ATTGAAGGTACCCGGTGAA TAAGCCACGGCTAACTACG TGCCAGCAGCCGCGTAAT ACGTAGGTGGCAAGCGTTG TCCGGATTTATTGGGTTTA AAGGGTGCGTAGGCGGCC TGTAAGTCAGTGGTAAAAT ACGGCAGCTCAACTGTGCGA GGTGCCATTGATACTGCGG GGCTTGAGTACAGTCGAGG TAGGCGGAATTGACGG | 40 | Uncultured bacterium clone | 8.00E-159 | 99% | - | - | - |
| Oligotype 4 | TGT | TAGGGAATATTGGACAATG GGTGCGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTAAA CTGCTTTTACCAGGGGATA AAAAGACCATGCGTGGTCA ATTGAAGGTACCTGGTGAA TAAGCCACGGCTAACTACG | 27 | Uncultured bacterium clone | 3.00E-163 | 99% | - | - | - |
| | | | | Uncultured Bacteroidetes bacterium clone | 7.00E-140 | 95% | Bacteroi detes | - | - |

| | | | | | | | | | |
|-------------|-----|---|----|--|-----------|-----|-------------------|---|---|
| | | TGCCAGCAGCCGCGTAAT ACGTAGGTGGCAAGCGTTG TCCGGATTTTATTGGGTTTA AAGGGTGCCTAGGCGGTTT TGTAAGTCAGTGGTGAAT ACTCCAGCTCAACTGGAGA GGTGCCATTGATACTGCAG AACTTGAGTACAGACGAGG TAGGCCGAATTGACG | | | | | | | |
| Oligotype 5 | AAG | TAGGGAATATTGGACAATG GGTGCAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTAAC TGCTTTTACCAGGGGATAA AAGACCATGCGTGGTCAAT TGAAGGTACCTGGTGAATA AGCCACGGCTAACTACGTG CCAGCAGCCGCGTAATAC GTAGGTGGCAAGCGTTGTC CGGATTTATTGGGTTTAAA GGGTGCGTAGGCGGTTTGT TAAGTCAGTGGTGAATAC TCCAGCTCAACTGGAGAGG TGCCATTGATACTGCAGAA CTTGAGTACAGACGAGGTA GGCGGAATTGACGGTG | 23 | Uncultured bacterium clone | 1.00E-162 | 99% | - | - | - |
| | | | | Uncultured Bacteroidetes bacterium clone | 5.00E-141 | 95% | Bacteroi detes | - | - |
| Oligotype 6 | GGT | TAGGGAATATTGGACAATG GGTGCAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTA CTGCTTTTACCAGGGGATA AAAAGAACCATGCGTGGTC AATTGAAGGTACCTGGTGA ATAAGCCACGGCTAACTAC GTGCCAGCAGCCGCGTAA TACGTAGGTGGCAAGCGTT GTCCGGATTTATTGGGTTT AAAGGGTGCCTAGGCGGTT TTGTAAGTCAGTGGTGA TACTCCAGCTCAACTGGAG AGGTGCCATTGATACTGCA GAACTTGAGTACAGACGAG GTAGGCCGAATTGACG | 21 | Uncultured bacterium clone | 3.00E-163 | 99% | - | - | - |
| | | | | Uncultured Bacteroidetes bacterium clone | 7.00E-140 | 95% | Bacteroi detes | - | - |
| Oligotype 7 | GAG | TAGGGAATATTGGACAATG | 16 | Uncultured | 3.00E-158 | 99% | - | - | - |

| | | | | | | | | | | |
|-------------|-----|--|----|--|-----------|-----|-------------------|---|---|---|
| | | GGTGCGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTA CTGCTTTTACCTAGGGGAG TAAAAGAACCATGCGTGGT CAATTGAAGGTACCTGGTG AATAAGCCACGGCTAACTA CGTGCCAGCAGCCGCGGTA ATACGTAGGTGGCAAGCGT TGCCGGATTTATTGGGTTT AAAGGGTGCCTAGGCGGTT TTGTAAGTCAGTGGTGAAA TACTCCAGCTCAACTGGAG AGGTGCCATTGATACTGCA GAACTTGAGTACAGACGAG GTAGGCGGAATTGAC | | bacterium clone | | | | | | |
| | | | | Uncultured Bacteroidetes bacterium clone | 1.00E-136 | 95% | Bacteroi detes | - | - | - |
| Oligotype 8 | CAG | TAGGGAATATTGGACAATG GGTGCGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTA CTGCTTTTACCAGGGGATA AAAGACCATGCGTGGTCAA TTGAAGGTACCTGGTGAAT AAGCCACGGCTAACTACGT GCCAGCAGCCGCGGTAATA CGTAGGTGGCAAGCGTTGT CCGGATTTATTGGGTTAAA GGGTGCGTAGGCGGTTTG TAAGTCAGTGGTGAAATAC TCCAGCTCAACTGGAGAGG TGCCATTGATACTGCAGAA CTTGAGTACAGACGAGTA GGCGGAATTGACGGTG | 15 | Uncultured bacterium clone | 1.00E-162 | 99% | - | - | - | - |
| | | | | Uncultured Bacteroidetes bacterium clone | 5.00E-141 | 95% | Bacteroi detes | - | - | - |
| Oligotype 9 | TCA | TAGGGAATATTGGACAATG GGTGCGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTA CTGCTTTTACCAGGGGATA AAAAGACCATGCGTGGTCA ATTGAAGGTACCTGGTGAA TAAGCCACGGCTAACTACG TGCCAGCAGCCGCGGTAAT ACGTAGGTGGCAAGCGTTG TCCGGATTTATTGGGTTA AAGGTGCGTAGGCGGTTTT | 11 | Uncultured bacterium clone | 8.00E-164 | 99% | - | - | - | - |
| | | | | Uncultured Bacteroidetes bacterium clone | 2.00E-140 | 95% | Bacteroi detes | - | - | - |

| | | | | | | | | | |
|-----------------|-----|---|---|--|-----------|-----|-------------------|----------------------|-------------|
| | | GTAAGTCAGTGGTGAAATA CTCCAGCTCAACTGGAGAG GTGCCATTGATACTGCAGA ACTTGAGTACAGACGAGGT AGGCGGAATTGACGGT | | | | | | | |
| Oligotype 10 | ACA | TAGGGAATATTGGACAATG GGTGAGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA AGGCCTTCTGGGTTGTAAA CTGCTTTTGCCGGGGATA AAAGATCCCTGCGGGGAGA ATTGAAGGTACCCGGTGAA TAAGCCACGGCTAACTACG TGCCAGCAGCCGCGTAAT ACGTAGGTGGCAAGCGTTG TCCGGATTTATTGGGTTTA AAGGTGCGTAGGCGGCCCT GTAAGTCAGTGGTGAAATA CGGCAGCTCAACTGTCGAG GTGCCATTGATACTGCGGG GCTTGAGTACAGTCGAGGT AGGCGGAATTGACGGT | 9 | Uncultured bacterium clone | 4.00E-157 | 98% | - | - | - |
| Oligotype 11 | CTC | TAGGGAATATTGGTCAATG GACGAGAGTCTGAACCAGC CATGCCGCGTGCAGGAAGA AGGCCTTCTGGGTTGTAAA CTGCTTTTGACAGGGAGCA AAATGGCTATGCGTAGCAA ATTGAGAGTACCTGTAGAA TAAGCACCGGCTAACTCCG TGCCAGCAGCCGCGTAAT ACGGAGGGTGCAAGCGTTG TCCGGATTTATTGGGTTTA AAGGGTGCCTAGGCGGCTA TATAAGTCAGTGGTGAAAT ACGACAGCTCAACTGTCGA ACTGCCATTGATACTGTAT GGCTTGAGTACAGACGAGG TAGGCGGAATTGATAG | 8 | Uncultured bacterium clone | 1.00E-142 | 96% | - | - | - |
| | | | | Uncultured Cytophaga sp. | 2.00E-130 | 93% | Bacteroi detes | Cytophagace ae | Cytophaga |
| | | | | Flexibacter aggregans | 1.00E-127 | 93% | Bacteroi detes | Flexibactera ceae | Flexibacter |
| Oligotype 12 | ATG | TAGGGAATATTGGACAATG GGTGCGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTAAC TGCTTTTACCAGGGATAAA | 2 | Uncultured bacterium clone | 6.00E-160 | 99% | - | - | - |
| | | | | Uncultured Bacteroidetes bacterium clone | 3.00E-138 | 95% | Bacteroi detes | - | - |

| | | | | | | | | | |
|--|--|---|--|--|--|--|--|--|--|
| | | AGACCATGCGTGGTCAATT GAGGTACCTGGTGAATAAG CCACGGCTAACTACGTGCC AGCAGCCGCGGTAATACGT AGGTGGCAAGCGTTGTCCG GATTTATTGGGTTTAAAGG GTGCGTAGGCGGTTTTGTA AGTCAGTGGTAAAATACTC CAGCTCAACTGGAGAGGTG CCATTGATACTGCAGAACT TGAGTACAGACGAGGTAGG CGGAATTGACGGTGTA | | | | | | | |
|--|--|---|--|--|--|--|--|--|--|

Supplementary Table 2(d)

| Oligotype ID | Oligotype Sequence | Representative Sequence | Abundance | NCBI MEGABLAST Results | Average E value | Average Identity (%) | Phylum | Family | Genus |
|--------------|--------------------|---|-----------|--|-----------------|----------------------|---------------------|-------------|----------|
| Oligotype 1 | CGT | ACAATTTACCTTCAAATGG GGAATAGCTCGGCGAAAGC CGGATTAATACCGCATGTG GTTGGCAGCTGCATGGTTG CCATACTAAAGTCGGGGAC CGCAAGGCCTGACGTTTGA AGAGGAGTTCGCGGCCTAT CAGCTAGTTGGCGGGGTAA CGGCCACCAAGGCTAAGA CGGGTAGCTGGTCTGAGAG GATGATCAGCCACACTGGA ACTGAGACACGGTCCAGAC ACCTACGGGTGGCAGCAGT TTCGAATCATTACAATGG GCGAAAAGCCTGATGGTGCG ACGCCGCGTGAGGGATGAA GGTCTTCGGATTGTAA | 275 | Uncultured bacterium clone | 2.00E-165 | 100% | - | - | - |
| | | | | Uncultured Opiritus sp. | 8.00E-164 | 99% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeGlc2 | 2.00E-140 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeCb1 | 9.00E-139 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus terrae | 4.00E-137 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Uncultured Verrucomicrobia bacterium clone | 2.00E-135 | 94% | Verruco microbia | - | - |
| Oligotype 2 | TAT | ACAATTTACCTTCAAATGG GGAATAGCTCGGCGAAAGC CGGATTAATACCGCATGTG GTTGGCAATCACATGATTG CCATACTAAAGTCGGGGAC CGCAAGGCCTGACGTTTGA AGAGGAGTTCGCGGCCTAT | 215 | Uncultured bacterium clone | 4.00E-157 | 98% | - | - | - |
| | | | | Uncultured Opiritus sp. | 2.00E-155 | 98% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Uncultured Verrucomicrobia bacterium clone | 9.00E-139 | 95% | Verruco microbia | - | - |

| | | | | | | | | | |
|-------------|-----|--|----|--|-----------|-----|---------------------|-------------|----------|
| | | CAGCTAGTTGGCGGGGTAA CGGCCACCAAGGCTAAGA CGGGTAGCTGGTCTGAGAG GATGATCAGCCACACTGGA ACTGAGACACGGTCCAGAC ACCTACGGGTGGCAGCAGT TTCGAATCATTACAATGG GCGAAAGCCTGATGGTGCG ACGCCGCGTGAGGGATGAA GGTCTTCGGATTGTAA | | Opiritus terrae | 4.00E-137 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Verrucomicrobia bacterium pACH90 | 2.00E-135 | 94% | Verruco microbia | - | - |
| | | | | Opiritus sp. VeCb1 | 2.00E-135 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| Oligotype 3 | ACG | ACAATTTACCTTCAAATAG GGGAAGTAGCTCGGCGAA AGCCGGATTAATACCGCAT GTGGTTGGCAGCTGCATGG TTGCCATACTAAAGTCGGG GACCGCAAGGCCTGACGTT TGAAGAGGAGTTTCGCGGCC TATCAGCTAGTTGGCGGGG TAACGGCCCCACCAAGGCTA AGACGGGTAGCTGGTCTGA GAGGATGATCAGCCACACT GGAAGTGAAGACACGGTCCA GACACCTACGGGTGGCAGC AGTTTCGAATCATTACAA TGGGCGAAAAGCCTGATGGT GCGACGCCGCGTGAGGGAT GAAGTCTTCGGATTGT | 97 | Uncultured bacterium clone | 1.00E-161 | 99% | - | - | - |
| | | | | Uncultured Opiritus sp. | 6.00E-160 | 99% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeGlc2 | 1.00E-136 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeCb1 | 7.00E-135 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus terrae | 3.00E-133 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| Oligotype 4 | GTC | ACAATTTACCTTCAAATGG GGAAGTAGCTCGGCGAAA GCCGGATTAATACCGCATG TGGTTGGCAGCTGCATGGT TGCCATACTAAAGTCGGGG ACCGCAAGGCCTGACGTTT GAAGAGGAGTTCGCGGCCT ATCAGCTAGTTGGCGGGGT AACGGCCCCACCAAGGCTAA GACGGGTAGCTGGTCTGAG AGGATGATCAGCCACACTG GAACTGAGACACGGTCCAG ACACCTACGGGTGGCAGCA GTTTCGAATCATTACAAT GGGCGAAAAGCCTGATGGTG CGACGCCGCGTGAGGGATG AAGTCTTCGGATTGTAA | 94 | Uncultured bacterium clone | 3.00E-163 | 99% | - | - | - |
| | | | | Uncultured Opiritus sp. | 1.00E-161 | 99% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeGlc2 | 3.00E-138 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeCb1 | 1.00E-136 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus terrae | 7.00E-135 | 94% | Verruco microbia | Opiritaceae | Opiritus |

| | | | | | | | | | |
|-------------|-----|--|----|--|-----------|-----|---------------------|-------------|----------|
| Oligotype 5 | TCA | ACAATTTACCTTCAAATGG GGAATAGCTCGGCGAAGCC GGATTAATACCGCATGTGG TTGGCAGCTGCATGGTTGC CATACTAAAGTCGGGGACC GCAAGGCCTGACGTTTGAA GAGGAGTTCGCGGCCTATC AGCTAGTTGGCGGGGTAAC GGCCACCAAGGCTAAGAC GGGTAGCTGGTCTGAGAGG ATGATCAGCCACACTGGAA CTGAGACACGGTCCAGACA CCTACGGGTGGCAGCAGTT TCGAATCATTACAATGGG CGAAAGCCTGATGGTGCGA CGCCGCGTGAGGGATGAAG GTCTTCGGATTGTAAA | 76 | Uncultured bacterium clone | 8.00E-164 | 99% | - | - | - |
| | | | | Uncultured Opitutus sp. | 4.00E-162 | 99% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus sp. VeGlc2 | 9.00E-139 | 95% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus sp. VeCb1 | 4.00E-137 | 95% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus terrae | 2.00E-135 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| Oligotype 6 | ACC | ACAATTTACCTTCAAATGG GGAAGTAGCTCGGCGAAA GCCGGATTAATACCGCATG TGGTTGGCAATCACATGAT TGCCATACTAAAGTCGGGG ACCGCAAGGCCTGACGTTT GAAGAGGAGTTCGCGGCCT ATCAGCTAGTTGGCGGGT AACGGCCACCAAGGCTAA GACGGGTAGCTGGTCTGAG AGGATGATCAGCCACACTG GAACTGAGACACGGTCCAG ACACCTACGGGTGGCAGCA GTTTCGAATCATTACAAT GGGCGAAAGCCTGATGGTG CGACGCCGCGTGAGGGATG AAGGTCTTCGGATTGTA | 71 | Uncultured bacterium clone | 6.00E-155 | 98% | - | - | - |
| | | | | Uncultured Opitutus sp. | 3.00E-153 | 98% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus terrae | 7.00E-135 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Verrucomicrobiae bacterium pACH90 | 3.00E-133 | 94% | Verruco microbia | - | - |
| | | | | Opitutus sp. VeCb1 | 3.00E-133 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| Oligotype 7 | GAA | ACAATTTTACCTTCAAATA GGGGAAGTAGCTCGGCGA AAGACCGGATTAATACCGC ATGTGGTTGGCAGCTGCAT GGTTGCCATACTAAAGTCG GGGACCGCAAGGCCTGACG TTTGAAGAGGAGTTTCGCGG CCTATCAGCTAGTTGGCGG GGTAACGGCCCAAGGC TAAGACGGGTAGCTGGTCT | 61 | Uncultured bacterium clone | 1.00E-157 | 99% | - | - | - |
| | | | | Uncultured Opitutus sp. | 6.00E-155 | 99% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Uncultured Verrucomicrobia bacterium clone | 2.00E-129 | 95% | Verruco microbia | - | - |
| | | | | Uncultured Opitutaceae bacterium clone | 1.00E-127 | 95% | Verruco microbia | Opitutaceae | - |

| | | | | | | | | | |
|--------------|-----|--|----|--|-----------|-----|---------------------|-------------|----------|
| | | GAGAGGATGATCAGCCACA CTGGAAGTACGACACGGTC CAGACACCTACGGGTGGCA GCAGTTTCGAATCATTAC AATGGGCGAAAGCCTGATG GTGCGACGCCGCGTGAGGG ATGAAGGTCTTCGGATT | | Opitutus sp. VeGlc2 | 1.00E-132 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus sp. VeCb1 | 5.00E-131 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus terrae | 2.00E-129 | 93% | Verruco microbia | Opitutaceae | Opitutus |
| Oligotype 8 | ATG | ACAATTTACCTTCAAATAG GGGAAGTAGCTCGGCGAA AGCCGGATTAATACCGCAT GTGGTTGGCAATCACATGA TTGCCATACTAAAGTCGGG GACCGCAAGGCCTGACGTT TGAAGAGGAGTTCGCGGCC TATCAGCTAGTTGGCGGGG TAACGGCCCACCAAGGCTA AGACGGGTAGCTGGTCTGA GAGGATGATCAGCCACACT GGAAGTACGACACGGTCCA GACACCTACGGGTGGCAGC AGTTTCGAATCATTACAA TGGGCGAAAGCCTGATGGT GCGACGCCGCGTGAGGGAT GAAGGTCTTCGGATTGT | 55 | Uncultured bacterium clone | 3.00E-153 | 98% | - | - | - |
| | | | | Uncultured Opitutus sp. | 1.00E-151 | 98% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Uncultured Verrucomicrobia bacterium clone | 7.00E-135 | 94% | Verruco microbia | - | - |
| | | | | Opitutus terrae | 3.00E-133 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Verrucomicrobiae bacterium pACH90 | 1.00E-131 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| Oligotype 9 | GAC | TTTCGAATCATTACAAATG GGCGAAAGCCTGATGGTGC GACGCCGCGTGAGGGATGA AGGTCTTCGGATTGTAAAC CTCTGTACCGGGGAAGAA ACGCTTTGAATTAACAGTC CAAAGCCTGACTTAACCCG GAGAGGAAGCAGTGGCTA ACTCTGTGCCAGCAGCCGC GGTAATACAGAGACTGCAA CGGTTATTTCGGATTCACTG GGCGTAAAGGGTGCGCAG GCGGCCGGATGTGTCAGGT GTGAAAGCCCGGGGCTTAA CCCCGGAATTGCGCCTGAA ACTGTCCGGCTAGAGTACT GGAGAGGGTAGCGGAATT | 47 | Uncultured bacterium clone | 4.00E-152 | 98% | - | - | - |
| | | | | Uncultured Opitutus sp. | 4.00E-152 | 98% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus sp. VeSm13 | 9.00E-139 | 95% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Verrucomicrobiae bacterium pACH90 | 4.00E-137 | 95% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus sp. NVT1 | 9.00E-134 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| Oligotype 10 | CGG | ACAATTTACCTTCAAATAG GGGAAGTAGCTCGGCGAA AGACCGGATTAATACCGCA | 38 | Uncultured bacterium clone | 2.00E-159 | 99% | - | - | - |
| | | | | Uncultured | 1.00E-157 | 99% | Verruco | Opitutaceae | Opitutus |

| | | | | | | | | | |
|-----------------|-----|--|----|--|-----------|-----|---------------------|-------------|----------|
| | | TGTGGTTGGCAGCTGCATG GTTGCCATACTAAAGTCGG GGACCGCAAGGCCTGACGT TTGAAGAGGAGTTTCGCGGC CTATCAGCTAGTTGGCGGG GTAACGCGCCACCAAGGCT AAGACGGGTAGCTGGTCTG AGAGGATGATCAGCCACAC TGGAAGTGGACACGGTCC AGACACCTACGGGTGGCAG CAGTTTCGAATCATTACA ATGGGCGAAAGCCTGATGG TGCGACGCCGCGTGAGGGA TGAAGTCTTCGGATTG | | Opiritus sp. | | | microbia | | |
| | | | | Opiritus sp. VeGlc2 | 2.00E-134 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeCb1 | 1.00E-132 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus terrae | 5.00E-131 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| Oligotype 11 | CCA | ACAATTTACCTTCAAATGG GGAATAGCTCGGCGAAGCC GGATTAATACCGCATGTGG TTGGCAATCACATGATTGC CATACTAAAGTCGGGGACC GCAAGGCCTGACGTTTGAA GAGGAGTTTCGCGCCTATC AGCTAGTTGGCGGGGTAAC GGCCACCAAGGCTAAGAC GGGTAGCTGGTCTGAGAGG ATGATCAGCCACACTGGAA CTGAGACACGGTCCAGACA CCTACGGGTGGCAGCAGTT TCGAATCATTACAATGGG CGAAAGCCTGATGGTGCGA CGCCGCGTGAGGGATGAAG GTCTTCGGATTGTAAA | 34 | Uncultured bacterium clone | 2.00E-155 | 98% | - | - | - |
| | | | | Uncultured Opiritus sp. | 8.00E-154 | 98% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Uncultured Verrucomicrobia bacterium clone | 4.00E-137 | 95% | Verruco microbia | - | - |
| | | | | Opiritus terrae | 2.00E-135 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Verrucomicrobiae bacterium pACH90 | 9.00E-134 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeCb1 | 9.00E-134 | 94% | Verruco microbia | Opiritaceae | Opiritus |
| Oligotype 12 | CGC | ACAATTTACCTTCAAATGG GGAATAGCTCGGCGAAAGC CGGATTAATACCGCATGTG GTTGGCAGCTGCATGGTTG CCATACTAAAAGTCGGGGA CCGCAAGGCCTGACGTTTG AAGAGGAGTTTCGCGCCTA TCAGCTAGTTGGCGGGGTA ACGGCCACCAAGGCTAAG ACGGGTAGCTGGTCTGAGA GGATGATCAGCCACACTGG AACTGAGACACGGTCCAGA CACCTACGGGTGGCAGCAG TTTCGAATCATTACAATG | 33 | Uncultured bacterium clone | 3.00E-163 | 99% | - | - | - |
| | | | | Uncultured Opiritus sp. | 1.00E-161 | 99% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeGlc2 | 3.00E-138 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus sp. VeCb1 | 1.00E-136 | 95% | Verruco microbia | Opiritaceae | Opiritus |
| | | | | Opiritus terrae | 7.00E-135 | 94% | Verruco microbia | Opiritaceae | Opiritus |

| | | | | | | | | | |
|-----------------|-----|--|----|--|-----------|-----|---------------------|-------------|----------|
| | | GGCGAAAGCCTGATGGTGC GACGCCGCGTGAGGGATGA AGGTCTTCGGATTGTA | | | | | | | |
| Oligotype 13 | TAC | ACAATTTACCTTCAAATGG GGAATAGCTCGGCGAAAGC CGGATTAATACCGCATGTG GTTGGCAATCACATGATTG CCATACTAAAAGTCGGGGA CCGCAAGGCCTGACGTTTG AAGAGGAGTTCGCGGCCTA TCAGCTAGTTGGCGGGGTA ACGGCCCACCAAGGCTAAG ACGGGTAGCTGGTCTGAGA GGATGATCAGCCACACTGG AACTGAGACACGGTCCAGA CACCTACGGGTGGCAGCAG TTTCGAATCATTACAATG GGCGAAAGCCTGATGGTGC GACGCCGCGTGAGGGATGA AGGTCTTCGGATTGTA | 24 | Uncultured bacterium clone | 6.00E-155 | 98% | - | - | - |
| | | | | Uncultured Opitutus sp. | 3.00E-153 | 98% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Uncultured Verrucomicrobia bacterium clone | 1.00E-136 | 95% | Verruco microbia | - | - |
| | | | | Opitutus terrae | 7.00E-135 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Verrucomicrobiae bacterium pACH90 | 3.00E-133 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Opitutus sp. VeCb1 | 3.00E-133 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| Oligotype 14 | TGT | ACAATTCACCGACAAGTGT GGAATAGCTCGTCGAAAGA CGAGATAATACCGCATATG GTCGTTTCATCGCATGATGG ACGAACTAAAGTTAGGGAC CGTAAGGCCTGACGCTAGT CGAGAAGTTCGCGGCCTAT CAGCTAGTTGGCGAGGTAA CGGCTACCAAGGCTAAGA CGGGTAGCTGATCTGAGAG GATGATCAGCCACACTGGA ACTGAGACACGGTCCAGAC ACCTACGGGTGGCAGCAGT TTTCGAATCATTACAATGG GCGAAAGCCTGATGGTGCG ACGCCGCGTGAGGGATGAA GGTCTTCGGATTGTAA | 12 | Uncultured bacterium clone | 2.00E-129 | 94% | - | - | - |
| | | | | Uncultured Opitutus sp. | 1.00E-127 | 94% | Verruco microbia | Opitutaceae | Opitutus |
| | | | | Uncultured Verrucomicrobia bacterium clone | 5.00E-126 | 94% | Verruco microbia | - | - |

Supplementary Table 2(e)

| Oligotype ID | Oligotype Sequence | Representative Sequence | Abundance OI | NCBI MEGABLAST Results | Average E value | Average Identity (%) | Phylum | Family | Genus |
|--------------|---------------------------------------|---|--------------|--------------------------------|-----------------|----------------------|----------------|------------------|-------------------|
| Oligotype 1 | TCAAACA CTCCTGC AGACTCA CTAG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | 31 | Uncultured bacterium clone | 5.00E-151 | 99% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 5.00E-151 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 5.00E-151 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Xanthomonas sp. | 5.00E-151 | 99% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Stenotrophomonas sp. | 1.00E-147 | 99% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 2 | TCAAACA CTCTCTGC ATACGGACTA | GGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAAC CTGGGAATTGCAGTGGATA CTGGGCGACTAGAG | 15 | Uncultured bacterium clone | 8.00E-149 | 99% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 3.00E-148 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 3.00E-148 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Xanthomonas sp. | 3.00E-148 | 99% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Pseudoxanthomonas ginsensisoli | 3.00E-148 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Stenotrophomonas sp. | 6.00E-145 | 98% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 3 | GAGGTTC TCTAGCA GTCTGGC TAGT | TGGGGGAATATTGGACAAT GGGCGCAAGCCTGATCCAG CCATACCGCGTGGGTGAAG AAGGCCTCGGGTTGTAAGC CCTTTTGTGGGTAAGAAA TCCTGCAGGTTAATAACCA | 11 | Uncultured bacterium clone | 1.00E-146 | 98% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 2.00E-145 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 2.00E-145 | 98% | Proteobacteria | Pseudomonadaceae | Pseudomonas |

| | | | | | | | | | |
|-------------|--|--|----|--------------------------------|-----------|------|----------------|------------------|-------------------|
| | | GTAGGGATGACGGTACCCA AAGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTACTCGGAATTACTGG CGTAAAGCGTGCCTAGGT GGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGTG | | Xanthomonas sp. | 2.00E-145 | 98% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Pseudoxanthomonas ginsengisoli | 2.00E-145 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Stenotrophomonas sp. | 4.00E-142 | 98% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 4 | GTTCCAA CTTCTGCA AACTTGC TAG | TGGGGAATATTGGACAATG GGGGCAACCCTGATCCAGC AATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTATTGGGAACGAA AAGCGATGGGTTAATACCT TATCGTGCTGACGGTACCC AAGGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTAATCGGAATTACTG GGCGTAAAGGGTGCCTAGG CGGTTATTTAAGTCTGTTGT GAAAGCCCTGGGCTCAACC TGGGAATGGCAATGGATAC TGGGTAGCTAGAGT | 10 | Uncultured bacterium clone | 4.00E-132 | 100% | - | - | - |
| | | | | Rhodanobacter sp. | 5.00E-126 | 94% | Proteobacteria | Xanthomonadaceae | Rhodanobacter |
| | | | | Rhodanobacter sp. | 2.00E-124 | 94% | Proteobacteria | Xanthomonadaceae | Rhodanobacter |
| | | | | Rhodanobacter ginsengisoli | 2.00E-124 | 94% | Proteobacteria | Xanthomonadaceae | Rhodanobacter |
| | | | | Dyella sp. | 1.00E-122 | 94% | Proteobacteria | Xanthomonadaceae | Dyella |
| | | | | Xanthomonadaceae bacterium | 1.00E-122 | 94% | Proteobacteria | Xanthomonadaceae | - |
| Oligotype 5 | CGCTGAT AGGTCTG CATAACGG ACTA | GTGGGGAATATTGGACAAT GGGCGCAAGCCTGATCCAG CCATACCGCGTGGGTGAAG AAGGCCTTCGGGTTGTAAA GCCCTTTTGTGGGAAAGA AATCCTGCAGGTTAATAAC CAGTAGGGATGACGGTACC CAAAGAATAAGCACCGGCT AACTTCGTGCCAGCAGCCG CGGTAATACGAAGGGTGCA AGCGTTACTCGGAATTACT GGGCGTAAAGCGTGCCTAG GTGGTTGTTTAAGTCTGCT GTGAAAGCCCCGGGCTCAA CCTGGGAATTGCAGTGGAT ACTGGGCGACTAGAG | 5 | Uncultured bacterium clone | 5.00E-151 | 99% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 5.00E-151 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 5.00E-151 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Xanthomonadaceae bacterium | 5.00E-151 | 99% | Proteobacteria | Xanthomonadaceae | - |
| | | | | Xanthomonas sp. | 5.00E-151 | 99% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Stenotrophomonas sp. | 1.00E-147 | 99% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 6 | GAGGTTCT TCTCTGCA | TGGGGAATATTGGACAATG GGGCGCAAGCCTGATCCAGC | 4 | Uncultured bacterium clone | 1.00E-147 | 99% | - | - | - |

| | | | | | | | | | |
|-------------|---------------------------------------|---|---|----------------------------|-----------|-----|----------------|------------------|-------------------|
| | GACTCAC TAG | CATACCGCGTGGGTGAAGA AGGCCTTCGGGTGTAAAG CCCTTTGTGGGAAGAAA TCCTGCAGGTTAATAACCA GTAGGGATGACGGTACCCA AAGAATAAGCACCGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTACTCGGAATTACTGG GCGTAAAGCGTGCGTAGGT GGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAAC CTGGGAATTGCAGTGGATA CTGGGCGACTAGAGT | | Pseudoxanthomonas sp. | 1.00E-147 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 1.00E-147 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Xanthomonadaceae bacterium | 1.00E-147 | 99% | Proteobacteria | Xanthomonadaceae | - |
| | | | | Xanthomonas sp. | 1.00E-147 | 99% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Stenotrophomonas sp. | 2.00E-144 | 98% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 7 | CGTGGCT GTGAGAG TGTGGAT AGAG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTGTAAAG CCCTTTGTGGGAAGAAAT CCTGCAGGTTAATAACCAG TAGGGATGACGGTACCCAA AGAATAAGCACCGGCTAAC TTCGTGCCAGCAGCCGCGG TAATACGAAGGGTGC AAGC GTTACTCGGAATTACTGGG CGTAAAGCGTGCGTAGGTG GTTGTTTAAGTCTGCTGTG AAAGCCCCGGGCTCAACCT GGGAATTGCAGTGGATACT GGGCGACTAGAGTGT | 4 | Uncultured bacterium clone | 3.00E-148 | 99% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 3.00E-148 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 3.00E-148 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Xanthomonadaceae bacterium | 3.00E-148 | 99% | Proteobacteria | Xanthomonadaceae | - |
| | | | | Xanthomonas sp. | 3.00E-148 | 99% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Xanthomonadaceae bacterium | 3.00E-148 | 99% | Proteobacteria | Xanthomonadaceae | - |
| | | | | Stenotrophomonas sp. | 6.00E-145 | 98% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 8 | GTTTCCAC TACTGCA CACTGGC TAG | TAGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC TATGCCGCGTGTGTGAAGA AGGCCTTCGGGTGTAAAG CACTTTGTCCGGAAGAA AAGCGCTGGGTTAACACCC TGGTGTCTGACGGTACCG GAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGC AA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTTGTTAAGTCTGATGT GAAAGCCCTGGGCTCAACC TGGGAATGGCACTGGATAC | 3 | Uncultured Thermomonas sp. | 2.00E-140 | 99% | Proteobacteria | Xanthomonadaceae | Thermomonas |
| | | | | Uncultured bacterium clone | 2.00E-149 | 99% | - | - | - |
| | | | | Thermomonas sp. | 1.00E-142 | 98% | Proteobacteria | Xanthomonadaceae | Thermomonas |
| | | | | Lysobacter sp. | 6.00E-140 | 97% | Proteobacteria | Xanthomonadaceae | Lysobacter |

| | | | | | | | | | |
|--------------|---------------------------------------|--|---|--|-----------|-----|----------------|------------------|-------------------|
| | | TGGCGAGCTAGAGT | | | | | | | |
| Oligotype 9 | AGGGCGG TCGGAGT GGGACGA ATTC | TGGGGAATATTGGACAACG GGCGCAAGCCTGATCCAGC AATGCCGCGTGGATGAAGA AGGTCTTCGGATTGTAAAG TCCTTTCGACGGGGACGAT GATGACGGTACCCGTAGAA GAAGCCCCGGCTAACTTCG TGCCAGCAGCCGCGTAAT ACGAAGGGTGCAAGCGTTA CTCGGAATTACTGGGCGTA AAGCGTGCGTAGGTGGTTG TTAAGTCTGCTGTGAAAG CCCCGGGCTCAACCTGGGA ATTGCAGTGGATACTGGGC GACTAGAGTGTGGTAGAGG ACAGTGGAATTTCC | 3 | Uncultured bacterium clone | 2.00E-125 | 95% | - | - | - |
| | | | | Uncultured Roseomonas sp. | 5.00E-101 | 94% | Proteobacteria | Acetobacteraceae | Roseomonas |
| | | | | Uncultured Acetobacteraceae bacterium | 1.00E-101 | 94% | Proteobacteria | Acetobacteraceae | - |
| | | | | Uncultured Gluconobacter sp. | 2.00E-100 | 91% | Proteobacteria | Acetobacteraceae | Gluconobacter |
| Oligotype 10 | TCTTTCAC TCCTGCA GACTCAC TAG | TAGGGAATCTTCCACAATG GACGAAGGTCTGATGGAGC AACGCCGCGTGAGTGAAGA AGGTTTTTCGGATCGTAAAA CTCTGTTGTAAGGGAAGAA CACGTACGAGAGTAACTGC TCGTACCTTGACGGTACCT TATTAGAAAGCCACGGCTA ACTACGTGCCGGCAGCCGC GGTAATACGAAGGGTGCAA GCGTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | 2 | Uncultured delta proteobacterium clone | 5.00E-111 | 91% | Proteobacteria | - | - |
| Oligotype 11 | TCGAACA CTCCTGC AGACTCA CTAG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTGTTGGGAAAGAA ATCCTGCGGATTAATACCC GGCAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA | 2 | Uncultured proteobacterium clone | 1.00E-152 | 99% | Proteobacteria | - | - |
| | | | | Pseudomonas sp. | 2.00E-144 | 98% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Stenotrophomonas sp. | 2.00E-144 | 98% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| | | | | Uncultured Pseudoxanthomonas sp. | 2.00E-144 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |

| | | | | | | | | | |
|--------------|---------------------------------------|--|---|--------------------------------|-----------|-----|----------------|------------------|-------------------|
| | | GCGTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTCGTTTAAAGTCTGCTGT GAAAGCCCCGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | | Xanthomonas sp. | 1.00E-142 | 98% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| Oligotype 12 | TCAAACC TCTAGCA GTCTGGC TAGT | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTACTCGGATTACTGG GCGTAAAGCGTGCGTAGGT GGTTGTTTAAAGTCTGCTGT GAAAGCCCCGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGTG | 2 | Uncultured bacterium clone | 2.00E-149 | 99% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 2.00E-149 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 2.00E-149 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Xanthomonas sp. | 2.00E-149 | 99% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Stenotrophomonas sp. | 5.00E-146 | 98% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| | | | | Pseudoxanthomonas ginsengisoli | 5.00E-146 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| Oligotype 13 | TCAAACA CTTCTGCA AACTTGC TAG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTACTCGGAATTACTG GGCGTAAAGGGTGCGTAGG CGGTTATTTAAGTCTGTTGT GAAAGCCCTGGGCTCAACC TGGGAATGGCAATGGATAC TGGGTAGCTAGAGT | 2 | Uncultured bacterium clone | 1.00E-136 | 98% | - | - | - |
| | | | | Pseudoxanthomonas yeongjuensis | 2.00E-139 | 97% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Stenotrophomonas sp. | 2.00E-139 | 97% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| | | | | Pseudoxanthomonas sp. | 1.00E-137 | 97% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 1.00E-137 | 97% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Xanthomonas sp. | 1.00E-137 | 97% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| Oligotype 14 | TCAAACA CGGTCTG CATACGG ACTA | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC | 2 | Uncultured bacterium clone | 8.00E-149 | 99% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 8.00E-149 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 8.00E-149 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |

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|-----------------|---------------------------------------|---|---|--|-----------|-----|--------------------|----------------------|-----------------------|
| | | AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAG GTGGTTGTTTAAGTCTGCT GTGAAAGCCCCGGGCTCAA CCTGGGAATTGCAGTGGAT ACTGGGCGACTAGAG | | Xanthomonadace ae bacterium | 8.00E-149 | 99% | Proteoba cteria | Xanthomona daceae | - |
| | | | | Xanthomonas sp. | 8.00E-149 | 99% | Proteoba cteria | Xanthomona daceae | Xanthomonas |
| | | | | Stenotrophomona s sp. | 2.00E-145 | 98% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |
| Oligotype 15 | GAGGTTC TTCCTGCA GACTCAC TAG | TGGGGGAATATTGGACAAT GGGCGCAAGCCTGATCCAG CCATACCGCGTGGGTGAAG AAGGCCTTCGGGTTGTAAG CCCTTTTGTGGGAAGAAA TCCTGCAGGTTAATAACCA GTAGGGATGACGGTACCCA AAGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTACTCGGAATTACTGG GCGTAAAGCGTGCGGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | 2 | Uncultured bacterium clone | 5.00E-146 | 98% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 6.00E-145 | 98% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 6.00E-145 | 98% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Xanthomonadace ae bacterium | 6.00E-145 | 98% | Proteoba cteria | Xanthomona daceae | - |
| | | | | Xanthomonas sp. | 6.00E-145 | 98% | Proteoba cteria | Xanthomona daceae | Xanthomonas |
| | | | | Stenotrophomona s sp. | 1.00E-141 | 98% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |
| Oligotype 16 | CGGGTTC TCTAGCA CTCTGACT AGT | TAGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATGCCGCGTGTGTGAAGA AGGCCTTCGGTTGTAAAGC ACTTTGTCCGAAAGAAAA GACGCTGGGTAAACACCTT GGTGTCTGACGGTACCGG AAGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTACTCGGAATTACTGG GCGTAAAGCGTGCGTAGGT GGTTTGTTAAGTCTGATGT GAAAGCCCTGGGCTCAACC TGGGAATGGCACTGGATAC TGGCGAGCTAGAGT | 2 | Uncultured gamma proteobacterium | 2.00E-149 | 99% | Proteoba cteria | - | - |
| | | | | Uncultured Thermomonas sp. | 1.00E-136 | 99% | Proteoba cteria | Xanthomona daceae | Thermomonas |
| | | | | Thermomonas sp. | 2.00E-139 | 97% | Proteoba cteria | Xanthomona daceae | Thermomonas |
| | | | | Lysobacter sp. | 1.00E-136 | 97% | Proteoba cteria | Xanthomona daceae | Lysobacter |
| Oligotype 17 | CCCGGTTT ATCCTTGC | TGGGGAATTTTTGGACAAT GGGCGCAAGCCTGATCCAG | 2 | Uncultured beta proteobacterium | 8.00E-114 | 94% | Proteoba cteria | - | - |

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|--------------|---------------------------------------|--|---|----------------------------------|-----------|-----|----------------|------------------|-------------------|
| | ATAGCGA CG | CCATGCCGCGTGTGTGAAA GAAGGCC TTCGGGTTGTAA AGCACTTTCGGCCGGAACG AAATCGCGCGGGCTATTAC CCC GCGTGGATGACGGTAC CGGAAGAAGAAGCACCGG CTAACTACGTGCCAGCAGC CGCGGTAATACGAAGGGTG CAAGCGTTACTCGGAATTA CTGGGCGTAAAGCGTGCGT AGGTGGTTGTTAAGTCTG CTGTGAAAGCCCCGGGCTC AACCTGGGAATTGCAGTGG ATACTGGGCGACTAGA | | clone | | | | | |
| | | | | Lysobacter sp. | 1.00E-136 | 97% | Proteobacteria | Xanthomonadaceae | Lysobacter |
| | | | | Xanthomonadaceae bacterium | 4.00E-112 | 92% | Proteobacteria | Xanthomonadaceae | - |
| | | | | Rehaibacterium terrae | 2.00E-110 | 92% | Proteobacteria | Xanthomonadaceae | Rehaibacterium |
| | | | | Arenimonas sp. | 4.00E-112 | 92% | Proteobacteria | Xanthomonadaceae | Arenimonas |
| | | | | Stenotrophomonas sp. | 4.00E-112 | 92% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| | | | | Pseudoxanthomonas sp. | 4.00E-112 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| Oligotype 18 | CCCGCAT AGGTCGG CATACCA GCTA | TAGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTGTTCGGAAAGA AAAGCGCTGGGTAAACACC CTGGTGCCTGACGGTACC GGAAGAATAAGCACCGGCT AACTTCGTGCCAGCAGCCG CGGTAATACGAAGGGTGCA AGCGTTACTCGGAATTACT GGGCGTAAAGCGTGCGTAG GTGGTTTGTAAAGTCTGAT GTGAAAGCCCTGGGCTCAA CCTGGGAATGGCACTGGAT ACTGGCGAGCTAGAG | 2 | Uncultured gamma proteobacterium | 4.00E-152 | 99% | Proteobacteria | - | - |
| | | | | Uncultured Thermomonas sp. | 2.00E-140 | 99% | Proteobacteria | Xanthomonadaceae | Thermomonas |
| | | | | Thermomonas sp. | 4.00E-142 | 98% | Proteobacteria | Xanthomonadaceae | Thermomonas |
| | | | | Lysobacter sp. | 2.00E-139 | 97% | Proteobacteria | Xanthomonadaceae | Lysobacter |
| Oligotype 19 | TAAACA CTCTCTGC ATACGGA CTA | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTGTGGGAAAGAA ATCCTGTAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTAAGTCTGCTGT GAAAGCCCCGGGCTCAAC CTGGGAATTGCAGTGGATA | 1 | Pseudoxanthomonas sp. | 8.00E-149 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 4.00E-147 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Xanthomonas sp. | 4.00E-147 | 99% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Stenotrophomonas sp. | 4.00E-147 | 99% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |

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|--------------|---------------------------------------|--|---|--|-----------|-----|--------------------|----------------------|-----------------------|
| | | CTGGGCGACTAGAG | | | | | | | |
| Oligotype 20 | TCTTTTAT TCCTGCA GACTCAC TAG | TAGGGAATCTTCCACAATG GACGAAGGTCTGATGGAGC AACGCCGCGTGAGTGAAGA AGGTTTTTCGGATCGTAAAA CTCTGTTGTAAGGGAAGAA CACGTACGAGAGTAACTGC TCGTACCTTGACGGTACCT TATTAGAAAAGCCACGGCTA ACTACGTGCCAGCAGCCGC GGTAATACGTAGGCGGCAA GCGTTGTCCGGAATCATTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | 1 | Uncultured bacterium clone | 2.00E-119 | 93% | - | - | - |
| Oligotype 21 | TCCAACA CTCCTGC GGACTGG CTAG | TGGGGGAATATTGGACAAT GGGCGCAAGCCTGATCCAG CCATACCGCGTGGGTGAAG AAGGCCTTCGGGTTGTAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC CGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTCGTTAAGTCTGCCG TGAAAGCCCCGGGCTCAAC CTGGGAATTGCGGTGGATA CTGGCGGGCTAGAGT | 1 | Uncultured gamma proteobacterium | 3.00E-143 | 98% | Proteoba cteria | - | - |
| | | | | Uncultured bacterium clone | 6.00E-140 | 97% | - | - | - |
| | | | | Luteimonas sp. | 1.00E-136 | 97% | | Xanthomona daceae | Luteimonas |
| | | | | Pseudoxanthomo nas sp. | 6.00E-135 | 96% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 6.00E-135 | 96% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| Oligotype 22 | TCAATTTG TGAGCAG TCTGGCT AGT | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGATGACGGTACCCA AAGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTACTCGGATTACTGGG | 1 | Uncultured bacterium clone | 5.00E-146 | 98% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 5.00E-146 | 98% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 5.00E-146 | 98% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Xanthomonas sp. | 5.00E-146 | 98% | Proteoba cteria | Xanthomona daceae | Xanthomonas |
| | | | | Stenotrophomona s sp. | 1.00E-142 | 98% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |

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|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|--------------------|----------------------|-----------------------|
| | | CGTAAAGCGTGCGTAGGTG GTTGTTTAAGTCTGCTGTG AAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGTG | | | | | | | |
| Oligotype 23 | TCAAACA TTCCTGCA GACTCAC TAG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTATTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | 1 | Uncultured bacterium clone | 2.00E-149 | 99% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 2.00E-149 | 99% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 2.00E-149 | 99% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Xanthomonas sp. | 2.00E-149 | 99% | Proteoba cteria | Xanthomona daceae | Xanthomonas |
| Oligotype 24 | TCAAACA CTCCTTGC ATACGGA CTA | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGGAATTGCAGTGGATA CTGGGCGACTAGAG | 1 | Uncultured bacterium clone | 8.00E-149 | 99% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 8.00E-149 | 99% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 8.00E-149 | 99% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Xanthomonas sp. | 8.00E-149 | 99% | Proteoba cteria | Xanthomona daceae | Xanthomonas |
| | | | | Stenotrophomona s sp. | 2.00E-145 | 98% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |
| Oligotype 25 | TCAAACA CTCCTGC AGACTAG CTAG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC | 1 | Uncultured bacterium clone | 2.00E-139 | 97% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 2.00E-139 | 97% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 2.00E-139 | 97% | Proteoba cteria | Pseudomona daceae | Pseudomonas |

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|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|--------------------|----------------------|-----------------------|
| | | AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGA CGGCTTGTTAAGTCTGCTG TGAAAGCCCTGGGCTCAAC CTGGGAACTGCAGTGGATA CTGGCAGGCTAGAGT | | | | | | | |
| Oligotype 26 | TCAAACA CTCCTAG CAATAGC GACG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTAGCAGTAGGAT ACTGGGCGACTAGA | 1 | Uncultured bacterium clone | 4.00E-147 | 99% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 4.00E-147 | 99% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 4.00E-147 | 99% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Stenotrophomona s sp. | 8.00E-144 | 98% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |
| Oligotype 27 | TCAAACA CTCCCTGC ATACGGA CTA | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC CTGGGAATTGCAGTGGATA CTGGGCGACTAGAG | 1 | Uncultured bacterium clone | 8.00E-149 | 99% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 8.00E-149 | 99% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 8.00E-149 | 99% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Stenotrophomona s sp. | 2.00E-145 | 98% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |
| Oligotype 28 | TCAAACA CGGGAAT TGGATGG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA | 1 | Uncultured bacterium clone | 6.00E-145 | 98% | - | - | - |
| | | | | Pseudoxanthomo | 6.00E-145 | 98% | Proteoba | Xanthomona | Pseudoxantho |

| | | | | | | | | | | |
|--------------|---------------------------------------|--|---|----------------------------|-----------|-----|---|----------------|------------------|-------------------|
| | CGAA | AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAAGCGTGCGTAG GTGGTTGTTAAGTCTGCT GTGAAAAGCCCCGGGCTC AACCTGGGAATTGCAGTGG ATACTGGGCGACTAG | | nas sp. | | | | cteria | daceae | monas |
| | | | | Pseudomonas sp. | 6.00E-145 | 98% | | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Stenotrophomonas sp. | 1.00E-141 | 98% | | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 29 | TCAAACA CGGCCTT GCATAGC GACG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAAGCGTGCGTAG GTGGTTGTTAAGTCTGCT GTGAAAAGCCCCGGGCTCA AACCTGGGAATTGCAGTGG TACTGGGCGACTAGA | 1 | Uncultured bacterium clone | 4.00E-147 | 99% | - | - | - | |
| | | | | Pseudoxanthomonas sp. | 4.00E-147 | 99% | | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 4.00E-147 | 99% | | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Stenotrophomonas sp. | 8.00E-144 | 98% | | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 30 | TCAAACA CGGCAAT TGGATGG CGAA | TAGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAAGCGTGCGTAGG TGGTTGTTAAGTCTGCT GTGAAAAGCCCCGGGCTCA AACCTGGGAATTGCAGTGG ATACTGGGCGACTAG | 1 | Uncultured bacterium clone | 8.00E-144 | 98% | - | - | - | |
| | | | | Pseudoxanthomonas sp. | 8.00E-144 | 98% | | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 8.00E-144 | 98% | | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Stenotrophomonas sp. | 2.00E-140 | 98% | | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |

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|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|----------------|------------------|-------------------|
| Oligotype 31 | TCAAACA CCTAGCA GTCTGGC TAGT | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGTG | 1 | Uncultured bacterium clone | 2.00E-149 | 99% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 2.00E-149 | 99% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 2.00E-149 | 99% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Stenotrophomonas sp. | 5.00E-146 | 98% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 32 | TCAAAAT TATCCTTG CATAGCG ACG | GTGGGGAATATTGGACAAT GGGCGCAAGCCTGATCCAG CCATACCGCGTGGGTGAAG AAGGCCTTCGGGTTGTAAAG GCCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCGA AGCGTTACTCGGAAATTAC TGGGCGTAAAGCGTGCGTA GGTGGTTGTTAAGTCTGC TGTGAAAGCCCCGGGCTCA ACCTGGGAATTGCAGTGGAT TACTGGGCGACTAGA | 1 | Uncultured bacterium clone | 2.00E-145 | 98% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 2.00E-145 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 2.00E-145 | 98% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Stenotrophomonas sp. | 4.00E-142 | 98% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 33 | TCAAAAT ATGCCTT GCATAGC GACG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTAACTCGGAATTACT GGGCGTAAAGCGTGCGTAG GTGGTTGTTAAGTCTGCT | 1 | Uncultured bacterium clone | 8.00E-144 | 98% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 8.00E-144 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Pseudomonas sp. | 8.00E-144 | 98% | Proteobacteria | Pseudomonadaceae | Pseudomonas |
| | | | | Stenotrophomonas sp. | 2.00E-140 | 97% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |

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|-----------------|---------------------------------------|--|---|-------------------------------|-----------|-----|--------------------|----------------------|-----------------------|
| | | GTGAAAGCCCCGGGCTCA ACCTGGGAATTGCAGTGGA TACTGGGCGACTAGA | | | | | | | |
| Oligotype 34 | TCAAAAT AGGTCTG CATACGG ACTA | GGGGAATATTGGACAATGG GCGCAAGCCTGATCCAGCC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAAGAATAAGCACC GGCT AACTTCGTGCCAGCAGCCG CGGTAATACGAAGGGTGCA AGCGTTACTCGGAATTACT GGGCGTAAAGCGTGCGTAG GTGGTTGTTTAAGTCTGCT GTGAAAGCCCCGGGCTCAA CCTGGGAATTGCAGTGGAT ACTGGGCGACTAGAG | 1 | Uncultured bacterium clone | 4.00E-147 | 99% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 4.00E-147 | 99% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 4.00E-147 | 99% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Stenotrophomona s sp. | 8.00E-144 | 98% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |
| Oligotype 35 | TCAAAAT AGGCCTT GCATAGC GACG | TGGGGAATATTGGACAATG GGCGCAGGCCGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAAGCACC GGCT AACTTCGTGCCAGCAGCCG CGGTAATACGAAGGGTGCA AGCGTTACTCGGAATTACT GGGCGTAAAGCGTGCGTAG GTGGTTGTTTAAGTCTGCT GTGAAAGCCCCGGGCTCA ACCTGGGAATTGCAGTGGA TACTGGGCGACTAGA | 1 | Uncultured bacterium clone | 2.00E-145 | 98% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 2.00E-145 | 98% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 2.00E-145 | 98% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Stenotrophomona s sp. | 4.00E-142 | 98% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |
| Oligotype 36 | TCAAAAT AATGAAA TTGGATG GCGT | GGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAAGAA ATCCTGCAGGTTAATAACC AGTAGGGATGACGGTACCC AAAGAATAAAGCACC GGCT AACTTCGTGCCAGCAGCCG CGGTAATACGAAGGGTGCA AGCGTTACTCGGAATTACT GGGCGTAAAGCGTGCGTAG GTGGTTGTTTAAGTCTGCT GTGAAAGCCCCGGGCTCA ACCTGGGAATTGCAGTGGA TACTGGGCGACTAGA | 1 | Uncultured bacterium clone | 3.00E-143 | 98% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 1.00E-142 | 98% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 1.00E-142 | 98% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| | | | | Stenotrophomona s sp. | 2.00E-139 | 97% | Proteoba cteria | Xanthomona daceae | Stenotrophom onas |

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|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|--------------------|----------------------|-------------|
| | | GGTAATACGAAGGGTGCAA GCGTTAACTCGGAATFACT GGGCGTAAAAGCGTGCGTA GGTGGTTGTTTAAGTCTGC TGTGAAAGCCCCGGGCTC AACCTGGGGAATTGCAGTG GATACTGGGCGACTA | | | | | | | |
| Oligotype 37 | TAACAGT GATCCGT GTAGGGG GAAT | TGGGGAATTTCCGCAATG GGCGAAAGCCTGACGGAG CAAGACCGCGTGCGGGAG GAAGGTCTATTGATTGTAA ACCGCTTTTGATAGGGAAG AAGATCTGACGGTACCTAT CGAATCAGCATCGGCTAAC TCCGTGCCAGCAGCCGCGG TAATACGAAGGGTGCAAGC GTTACTCGGAATTACTGGG CGTAAAGCGTGCGTAGGTG GTTGTTTAAGTCTGCTGTG AAAGCCCCGGGCTCAACCT GGGAATTGCAGTGGATACT GGGCGACTAGAGTGTGGTA GAGGACAGTGGAAATTC | 1 | Uncultured bacterium clone | 1.00E-101 | 90% | - | - | - |
| Oligotype 38 | GTTTCCAC TCCTGCA GACTCAC TAG | TAGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTGTCCGAAAGAA AAGCGCTGGGTTAACACCC TGGTGTCTGACGGTACCG GAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | 1 | Uncultured bacterium clone | 1.00E-136 | 98% | - | - | - |
| | | | | Uncultured Thermomonas sp. | 1.00E-137 | 97% | Proteoba cteria | Xanthomona daceae | Thermomonas |
| Oligotype 39 | GTTTCCAC CTAGCAC TCTGACT AGT | TAGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATGCCGCGTGTGTGAAGA AGGCCCTTGGGTTGTAAGC ACTTTTGTCCGAAAGAAA | 1 | Uncultured bacterium clone | 1.00E-142 | 98% | - | - | - |
| | | | | Uncultured Thermomonas sp. | 5.00E-141 | 97% | Proteoba cteria | Xanthomona daceae | Thermomonas |

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|-----------------|---------------------------------------|---|---|---|-----------|-----|--------------------|----------------------|-------------|
| | | AGACGCTGGGTAAACACCC TGGTGCCTGACGGTACCG GAAGAATAAGCACC GGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTTGTTAAGCTGATGT GAAAGCCCTGGGCTCAACC TGGGAATGGCACTGGATAC TGGCGAGCTAGAGTG | | | | | | | |
| Oligotype 40 | GTTTCATA GGTCGGC ATACCAG CTA | TAGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC TATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTGTCCGAAAGAA AAGCGCTGGGTAAACACCC TGGTGCCTGACGGTACCG GAAGAATAAGCACC GGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACT GGGCGTAAAGCGTGCGTAG GTGGTTTGTTAAGTCTGAT GTGAAAGCCCTGGGCTCAA CCTGGGAATGGCACTGGAT ACTGGCGAGCTAGAG | 1 | Uncultured bacterium clone | 4.00E-147 | 99% | - | - | - |
| | | | | Uncultured beta proteobacterium clone | 8.00E-149 | 99% | Proteoba cteria | - | - |
| | | | | Thermomonas sp. | 2.00E-140 | 97% | Proteoba cteria | Xanthomona daceae | Thermomonas |
| | | | | Lysobacter sp. | 1.00E-137 | 97% | Proteoba cteria | Xanthomona daceae | Lysobacter |
| Oligotype 41 | GTTTCAA CTTCTGCA AACTTGC TAG | TAGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTGTCCGAAAGAA AAGCGCTGGGTAAACACCC TGGTGCCTGACGGTACCG GAAGAATAAGCACC GGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTAATCGGAATTACTG GGCGTAAAGGGTGCGTAGG CGGTTACTTAAGTCTGTTGT GAAAGCCCTGGGCTCAACC TGGGAATGGCAATGGATAC TGGGTAGCTAGAGT | 1 | Uncultured Thermomonas sp. | 4.00E-132 | 98% | Proteoba cteria | Xanthomona daceae | Thermomonas |
| | | | | Uncultured proteobacterium clone | 2.00E-139 | 97% | Proteoba cteria | - | - |
| | | | | Lysobacter sp. | 4.00E-132 | 97% | Proteoba cteria | Xanthomona daceae | Lysobacter |
| Oligotype | GTTCCAT | TGGGGAATATTGGACAATG | 1 | Uncultured | 6.00E-130 | 99% | - | - | - |

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|-----------------|---------------------------------------|--|---|------------------------------------|-----------|-----|----------------|------------------|------------------|
| 42 | AGGTCGG CATACGA GCTA | GGGGCAACCCTGATCCAGC AATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTATTGGGAACGAA AAGCGATGGGTTAATACCT TATCGTGCTGACGGTACCC AAGGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA AGCGTTAATCGGAATTACT GGGCGTAAAGGGTGCGTAG GCGGTTATTTAAGTCTGTT GTGAAAGCCCTGGGCTCAA CCTGGGAATGGCAATGGAT ACTGGGTAGCTAGAG | | bacterium clone | | | | | |
| | | | | Uncultured Rhodanobacter sp. | 8.00E-124 | 94% | Proteobacteria | Xanthomonadaceae | Rhodanobacter |
| | | | | Dyella sp. | 2.00E-120 | 93% | Proteobacteria | Xanthomonadaceae | Dyella |
| Oligotype 43 | GTTCCAA CTTCAAT GGGATGG TAGA | TGGGGAATATTGGACAATG GGGGCAACCCTGATCCAGC AATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTATTGGGAACGAA AAGCGATGGGTTAATACCT TATCGTGCTGACGGTACCC AAGGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTAATCGGAATTACTG GGCGTAAAGGGTGCGTAGG GCGTTATTTAAGTCTGTTGT CGAAAGCCCCTGGGCGTCA ACCTGGGAATGGCAATGGA TACTGGGTAGCTAG | 1 | Uncultured bacterium clone | 5.00E-126 | 99% | - | - | - |
| | | | | Uncultured Rhodanobacter sp. | 2.00E-120 | 94% | Proteobacteria | Xanthomonadaceae | Rhodanobacter |
| | | | | Dyella sp. | 3.00E-118 | 93% | Proteobacteria | Xanthomonadaceae | Dyella |
| Oligotype 44 | GTTCCAA CTCCTGC AGACTCA CTAG | TGGGGAATATTGGACAATG GGGGCAACCCTGATCCAGC AATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTATTGGGAACGAG AAGCGATGGGTTAATACCT TATCGTGCTGACGGTACCC AAGGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTAATCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC | 1 | Uncultured bacterium clone | 2.00E-120 | 94% | - | - | - |
| | | | | Acetobacter sp. | 2.00E-119 | 93% | Proteobacteria | Acetobacteraceae | Acetobacter |
| | | | | Stenotrophomonas sp. | 2.00E-119 | 93% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |

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|-----------------|---------------------------------------|--|---|-------------------------------|-----------|-----|--------------------|----------------------|-----------------------|
| | | TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | | | | | | | |
| Oligotype 45 | GTGACGG GCGCATG GAGGCTG AGTG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGTTGTAAGCC TTTTGTTGGGAAGAAATCC TGCAGGTTAATAACCAGTA GGGATGACGGTACCCAAAG AATAAGCACCGGCTAACTT CGTGCCAGCAGCCGCGGTA ATACGAAGGGTGCAAGCGT TACTCGGAATTACTGGGCG TAAAGCGTGCGTAGGTGGT TGTTTAAGTCTGCTGTGAA AGCCCCGGGCTCAACCTGG GAATTGCAGTGGATACTGG GCGACTAGAGTGTGG | 1 | Uncultured bacterium clone | 2.00E-145 | 98% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 2.00E-145 | 98% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 2.00E-145 | 98% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| Oligotype 46 | GGCTATA GACTTTG GCAGATG TAGG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGGGAAGA AGGCTCTTGGGTTGTAAAC CCCTTTTCTCTGGGAAGAA AGTTGTGAAAGCAGCCTGA CGGTACCAGAGGAATCAGC ATCGGCTAACTTCGTGCCA GCAGCCGCGGTAATACGAA GGGTGCAAGCGTACTCGG AATTACTGGGCGTAAAGCG TGCGTAGGCGGTTTGTTAA GTCTGATGTGAAAGCCCTG GGCTCAACCTGGGAATGGC ATTGGATACTGGCGATCTA GAATGTGGTAGAGGG | 1 | Lysobacter sp. | 2.00E-105 | 95% | Proteoba cteria | Xanthomona daceae | Lysobacter |
| | | | | Uncultured bacterium clone | 8.00E-104 | 90% | - | - | - |
| Oligotype 47 | GCAGGAC GGAGTGA TATAGGG TACT | TAGGGAATATTGGACAATG GGTGCAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTAAA CTGCTTTTACCAGGGGATA AAAAGACCATGCGTGGTCA ATTGAAGGTACCTGGTGAA TAAGCCACGGCTAACTACG TGCCAGCAGCCGCGTAAT ACGAAGGGTGCAAGCGTTA | 1 | Uncultured bacterium clone | 2.00E-99 | 94% | - | - | - |

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|-----------------|---------------------------------------|---|---|---------------------------------|-----------|-----|--------------------|----------------------|-------------------|
| | | ATCGGAATTACTGGGCGTA AAGGGTGCCTAGGCGGTTA TTTAAGCCTGTTGTGAAAG CCCTGGGCTCAACCTGGGA ATGGCAATGGATACTGGGT AGCTAGAGTACGGTA | | | | | | | |
| Oligotype 48 | GCAACTG GATCCGT GTAGGGG GAAT | TGGGGAATCTTGCGCAATG GGCGAAAGCCTGACGCAGC AACGCCGCGTGGGGGATGA AGGCTCTCGGGTTGTAAAC CCCTTTCAGCAGGGACGAA TCAAGACGGTACCTGCAGA ATAAGCGCCGGCTAACTTC GTGCCAGCAGCCGCGTAA TACGAAGGGTGCAAGCGTT ACTCGGAATTACTGGGCGT AAAGCGTGCGTAGGTGGTT GTTTAAGTCTGCTGTGAAA GCCCCGGGCTCAAACCTGG GAATTGCAGTGGATACTGG GCGACTAGAGTGTGGTAGA GGACAGTGGAAATTC | 1 | Uncultured bacterium clone | 3.00E-113 | 92% | - | - | - |
| Oligotype 49 | GCAACTG GAGTGTG TGGGATG AATC | TGGGGGAATCTTGACAAT GGGCGAAAGCCTGATGCAG CGACGCCGCGTGCGGGATG AAGGCCCTCGGGTCGTAAA CCGCTTTCAGCAGGGACGA TAGTGACGGTACCTGCAGA AGAAGCCCCGGCCAACTAC GTGCCAGCAGCCGCGTAA TACGAGGGGTGCAAGCGTT ATTCGGATTTACTGGGCGT AAAGCGTGCGTAGGTGGTT GTTTAAGTCTGCTGTGAAA GCCCCGGGCTCAAACCTGGG AATTGCAGTGGATACTGGG CGACTAGAGTGTGGTAGAG GACAGTGGAAATTC | 1 | Uncultured bacterium clone | 2.00E-114 | 92% | - | - | - |
| Oligotype 50 | GCAACTG GAGTATG CGGGGCG AATC | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC AATGCCGCGTGGATGAAGA AGGTCTTCGATTGTAAAA GTCCTTTCGACGGGGACGA TGATGACGGTACCCGTAGA | 1 | Uncultured bacterium clone | 2.00E-114 | 92% | - | - | - |
| | | | | Uncultured Gluconobacter sp. | 8.00E-109 | 91% | Proteoba cteria | Acetobactera ceae | Gluconobacte r |
| | | | | Roseomonas sp. | 8.00E-109 | 91% | Proteoba cteria | Acetobactera ceae | Roseomonas |

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|-----------------|---------------------------------------|---|---|--------------------------------|-----------|-----|--------------------|-----------------------|--------------|
| | | AGAAGCCCCGGCTAACTTC GTGCCAGCAGCCGCGGTAA TACGAAGGGGGCTAGCGTT ACTCGGAATTACTGGGCGT AAAGCGTGCGTAGGCGGTT TGTTAAGTCCGATGTGAAA GCCCTGGGCTCAACCTGGG AATGGCATGGGATACTGGC GAGCTAGAGTGCGGTAGAG GGGTGCGGAATTCCC | | | | | | | |
| Oligotype 51 | GCAACTG GAGTATA CGGGGTG AATC | TGGGGAATATTGGACAATG GGCGAAAGCCTGATCCAGC AATGCCGCGTGAGTGATGA AGGCCTTAGGGTCGTAAAG CTCTTTTTACCCGGGATGAT AATGACAGTACCGGGAGA ATAAGCTCCGGCTAACTTC GTGCCAGCAGCCGCGGTAA TACGAAGGGTGCAAGCGTT ACTCGGAATTACTGGGCGT AAAGCGTGCGTAGGCGGTT TGTTAAGTCTGATGTGAAA TCCCCGGGCTCAACCTGGG ACGTGCATTGGAACTGGC GATCTAGAGTACGGTAGAG GGTGGTGAATTCCC | 1 | Uncultured bacterium clone | 8.00E-124 | 94% | - | - | - |
| | | | | Uncultured Sphingobium sp. | 2.00E-119 | 93% | Proteoba cteria | Sphingomon adaceae | Sphingobium |
| | | | | Uncultured Burkholderia sp. | 1.00E-111 | 92% | Proteoba cteria | Burkholderia ceae | Burkholderia |
| Oligotype 52 | GAGGTTC TCTAGCA CTCTGACT AGT | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAGAAA TCCTGCAGGTTAATAACCA GTAGGGATGACGGTACCCA AAGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTACTCGGAATTACTGG GCGTAAAGCGTGCGTAGGT GGTTTGTTAAGTCTGATGT GAAAGCCCTGGGCTCAACC TGGGAATGGCACTGGATAC TGGCGAGCTAGAGTG | 1 | Uncultured bacterium clone | 1.00E-142 | 98% | - | - | - |
| | | | | Uncultured Luteimonas sp. | 1.00E-141 | 97% | Proteoba cteria | Xanthomona daceae | Luteimonas |
| | | | | Luteimonas sp. | 2.00E-139 | 97% | Proteoba cteria | Xanthomona daceae | Luteimonas |
| Oligotype 53 | GAGGTCA CTCCTGC | GGGGAATATTGGACAATGG GCGCAAGCCTGATCCAGCC | 1 | Uncultured bacterium clone | 8.00E-149 | 99% | - | - | - |

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|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|--------------------|----------------------|-----------------------|
| | AGACTCA CTAG | ATACCGCGTGGGTGAAGAA GGCCTTCGGGTTGTAAAGC CCTTTTGTTGGGAAGAAA TCCTGCAGGTTAATAACCA GTAGGGATGACGGTACCCA AAGAAAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGT | | Pseudoxanthomo nas sp. | 8.00E-149 | 99% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| Oligotype 54 | GAGGTAT TATCCTTG CATAGCG ACG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCTTTTGTTGGGAAGAAA TCCTGCAGGTTAATAACCA GTAGGGATGACGGTACCCA AAGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAA GTCGTTACTCGGAAATTAC TGGGCGTAAAGCGTGCGTA GGTGGTTGTTTAAGTCTGC TGTGAAAGCCCCGGGCTCA ACCTGGGAATTGCAGTGG TACTGGGCGACTAGA | 1 | Uncultured bacterium clone | 8.00E-144 | 98% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 8.00E-144 | 98% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Xanthomonas sp. | 8.00E-144 | 98% | Proteoba cteria | Xanthomona daceae | Xanthomonas |
| Oligotype 55 | GAGGGCA CTCCTGC AAACTTG CTAG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA GGGCCTTCGGGTTGTAAAG CCTTTTGTTGGGAAGAAA TCCTGCAGGTTAATAACCA GTAGGGAGTGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCTGGGCTCAACC TGGGAATGGCAATGGATAC | 1 | Uncultured bacterium clone | 3.00E-138 | 98% | - | - | - |
| | | | | Uncultured Xanthomonas sp. | 2.00E-140 | 97% | | | |

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|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|---------------------|----------------------|------------------------|
| | | TGGGTAGCTAGAGT | | | | | | | |
| Oligotype 56 | GAGGACA CTCCTTGC AATAGCG ACG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAGAAA TCCTGCAGGTTAATAACCA GTAGGGGATGACGGTACCC AAAGAATAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAAATTGCAGTAGGAT ACTGGGCGACTAGA | 1 | Uncultured bacterium clone | 8.00E-144 | 98% | - | - | - |
| | | | | Pseudoxantho- nas sp. | 8.00E-144 | 98% | Proteoba- cteria | Xanthomona daceae | Pseudoxantho- monas |
| Oligotype 57 | CTCGGTTT GGTCTGC ATACGGA CTA | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGTAAAGA AATACCTGCAGGTTAATAA CCAGTAGGGATGACGGTAC CCAAAGAATAAGCACCGGC TAACTTCGTGCCAGCAGCC GCGGTAATACGAAGGGTGC AAGCGTTACTCGGAATTAC TGGGCGTAAAGCGTGCGTA GGTGGTTTTTAAGTCTGCT GTGAAAGCCCCGGGCTCAA CCTGGGAATTGCAGTGGAT ACTGGGCGACTAGAG | 1 | Uncultured bacterium clone | 2.00E-145 | 98% | - | - | - |
| | | | | Pseudoxantho- nas sp. | 2.00E-145 | 98% | Proteoba- cteria | Xanthomona daceae | Pseudoxantho- monas |
| Oligotype 58 | CTCGGTA TACGAAT TGGATGG CGAA | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTCGTTGGGTAAGA AATACCTGCAGGTTAATAA CCAGTAGGGAGTGACGGTA CCCAAAGAATAAGCACCGG CTAACTTCGTGCCAGCAGC CGCGGTAATACGAAGGGTG CAAGCGTTACTCGGAATTA | 1 | Uncultured bacterium clone | 3.00E-143 | 98% | - | - | - |
| | | | | Pseudoxantho- nas sp. | 3.00E-143 | 98% | Proteoba- cteria | Xanthomona daceae | Pseudoxantho- monas |

| | | | | | | | | | |
|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|---------------------|-----------------------|------------------------|
| | | CTGGGCGTAAAGCGTGCGT AGGTGGTTGTTAAGTCTG CTGTGAAAGCCCCGGGCTC AACCTGGGAATTGCAGTGG ATACTGGGCGACTAG | | | | | | | |
| Oligotype 59 | CTCGGTA TACGAAG GCGATGT ATGT | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATAACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCCTTTTGTTGGGAAAGA AATACCTGCAGGTTAATAA CCAGTAGGGAGTGACGGTA CCCAAAGAATAAGCACCGG CTAACTTCGTGCCAGCAGC CGCGGTAATACGAAGGGTG CAAGCGTTACTCGGAATTA CTGGGCGTAAAGCGTGCGT AGGTGGTTGTTAAGTCTG CTGTGAAAGCCCCGGGCTC AACCCAGAGAGGCCACTCG ATACTGCTATGACTA | 1 | Uncultured bacterium clone | 3.00E-128 | 98% | - | - | - |
| | | | | Pseudoxantho- nas sp. | 3.00E-128 | 98% | Proteoba- cteria | Xanthomona- daceae | Pseudoxantho- monas |
| Oligotype 60 | CGTGGTC TCTCTTGC ATACGGA CTA | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATAACCGCGTGGGTGAAGA AGGCCTTCGGTTGTAAAGCC CTTTTGTGGGAAAGAAAT CCTGCAGGTTAATAACCAG TAGGGATGACGGTACCCAA AGAATAAGCACCGGCTAAC TTCGTGCCAGCAGCCGCGG TAATACGAAGGGTGCAAGC GTTAACTCGGAATTAAGTGG GCGTAAAGCGTGCGTAGGT GGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAAC CTGGGGAATTGCAGTGGAT ACTGGGCGACTAGAG | 1 | Uncultured bacterium clone | 4.00E-142 | 98% | - | - | - |
| | | | | Pseudoxantho- nas sp. | 4.00E-142 | 98% | Proteoba- cteria | Xanthomona- daceae | Pseudoxantho- monas |
| Oligotype 61 | CGTGGGG GGTCGGT GGGGGCA GAGT | GGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATAACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAGC CCTTTTGTGGGAAAGAAAT CCTGCAGGTTAATAACCAG TAGGGATGACGGTACCCAA | 1 | Uncultured bacterium clone | 1.00E-146 | 98% | - | - | - |
| | | | | Pseudoxantho- nas sp. | 5.00E-146 | 98% | Proteoba- cteria | Xanthomona- daceae | Pseudoxantho- monas |
| | | | | Pseudomonas sp. | 5.00E-146 | 98% | Proteoba- cteria | Pseudomona- daceae | Pseudomonas |
| | | | | Xanthomonas sp. | 5.00E-146 | 98% | Proteoba | Xanthomona | Xanthomonas |

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|-----------------|---------------------------------------|--|---|-------------------------------|-----------|-----|----------------|------------------|-------------------|
| | | GAATAAGCACCGGCTAACT TCGTGCCAGCAGCCGCGGT AATACGAAGGGTGCAAGC GTTACTCGGAATTACTGGG CGTAAAGCGTGCGTAGGTG GTTGTTTAAGTCTGCTGTG AAAGCCCCGGGCTCAACCT GGGAATTGCAGTGGATACT GGGCGACTAGAGTGTG | | | | | acteria | daceae | |
| Oligotype 62 | CGTGGCT GTTATCA CGCTGGC TCGG | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG CCCTTTTGTGGGAAGAAT CCTGCAGGTTAATAACCAG TAGGGATGACGGTACCCAA AGAATAAGCACCGGCTAAC TTCGTGCCAGCAGCCGCGG TAATACGAAGGGTGCAAGC GTTACTCGGAATTACTGGG CTTAAAGGGTGCGTAGGCT GGCCATAAAGTGTCCGTGT GAAAGCCCACTGCTCAACG GTGGAACAGCACGGCAA CTGTGGGTCTCGAGGA | 1 | Uncultured Xanthomonas sp. | 4.00E-107 | 98% | Proteobacteria | Xanthomonadaceae | Xanthomonas |
| | | | | Pseudoxanthomonas sp. | 2.00E-105 | 97% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |
| | | | | Stenotrophomonas sp. | 2.00E-105 | 97% | Proteobacteria | Xanthomonadaceae | Stenotrophomonas |
| Oligotype 63 | CGGGTTC TCTAGCA TTCTGACT AGT | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATGCCGCGTGTGTGAAGA AGGCCTTCGGTGTAAAGC ACTTTTGTCCGGGAAGAAA GACACCGGTCAATACCCT GGTGTGATGACGGTACCGG AAGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTACTCGGAATTACTGG GCGTAAAGCGTGCGTAGGC GGTTTGTTAAGTCTGATGT GAAAGCCCTGGGCTCAACC TGGGAATGGCATTGGATAC TGGCGATCTAGAATG | 1 | Uncultured bacterium clone | 6.00E-140 | 98% | - | - | - |
| | | | | Lysobacter sp. | 1.00E-142 | 98% | Proteobacteria | Xanthomonadaceae | Lysobacter |
| Oligotype 64 | CGCTGAT AGGCCTT GCATAGG | TGGGGAATTTTGGACAAT GGGCGCAAGCCTGATCCAG CCATGCCGCGTGGGTGAAG | 1 | Uncultured bacterium clone | 4.00E-137 | 98% | - | - | - |
| | | | | Pseudoxanthomonas sp. | 4.00E-137 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas |

| | | | | | | | | | | |
|-----------------|---------------------------------------|--|---|-------------------------------|-----------|-----------|-----|---------------------------|----------------------------|----------------------|
| | GGCG | AAGGCCTTCGGGTTGTAAA GCCCTTTTGTGGGAAAGA AATCCTGCAGGTTAATAAC CAGTAGGGATGACGGTACC CAAAGAATAAGCACCGGCT AACTTCGTGCCAGCAGCCG CGGTAATACGAAGGGTGCA AGCGTTACTCGGAATTACT GGGCGTAAAGCGTGCCTAG GTGGTTGTTAAGTCTGCT GTGAAAGCCCCGGGCTCA ACCTGGGAATTGCGGTGGA TACTGGCGGGCTAGA | | nas sp. Pseudomonas sp. | | 4.00E-137 | 98% | acteria Proteobacteria | daceae Pseudomonadaceae | monas Pseudomonas |
| Oligotype 65 | CGAGGCT TTAGTGG TACAGAT TTCG | GGGGAATCTTGACAATGG GCGAAACGCCTGATGCAGC AACGCCGCGTGCGGAAGA AGGCCCTAGGGTTGTAAAC CGCTTTCAGTAGGGGAAGAA AATGACGGTACCTACAGAA GAAGGTGCGGCCAACTACG TGCCAGCAGCCGCGGTGAC ACGTAGGCACCAAGCGTTA TCCGGATTTATTGGGCGTA AAGCGTGCCTAGGTGGTTG TTAAGTCTGCTGTGAAAG CCCCGGCTCAACCTGGGAA TTGCAGTGGATACTGGGCG ACTAGAGTGTGGTAGAGGA CAGTGAATTTCCGGT | 1 | Uncultured bacterium clone | 1.00E-97 | 94% | - | - | - | |
| Oligotype 66 | CGACGGG TCGGAGT GGGACGA ATTC | TGGGGAATCTTGACAATG GGGGCAACCCTGATCCAGC CATGCCGCGTGGTGATGAA GGTCTTCGGATTGTAAAAC CCTTTTGGCGGGGACGATA ATGACGGTACCCGCAGAAAT AAGCACCGGCTAACTTCGT GCCAGCAGCCGCGGTAATA CGAAGGGTGCAAGCGTTAC TCGGAATTACGTGGGCGTA AAGCGTGCCTAGGTGGTTG TTAAGTCTGCTGTGAAAG CCCCGGCTCAACCTGGGA ATTGCAGTGGATACTGGGC GACTAGAGTGTGGTAGAGG ACAGTGAATTTCCG | 1 | Uncultured bacterium clone | 2.00E-124 | 94% | - | - | - | |

| | | | | | | | | | |
|-----------------|---------------------------------------|--|---|---------------------------------------|-----------|-----|----------------|------------------|---------------|
| Oligotype 67 | CCGTTTCT CTAGCAG TCTGGCT AGT | TGGGGAATTTTGGACAATG GGCGCAAGCCTGATCCAGC CATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTCGGCCGGAACGAA ATCGCGCGGGCTATTACCC GCGTGGATGACGGTACCGG AAGAAGAAGCACCGGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTACTCGGAATTACTG GGCGTAAAGCGTGCGTAGG TGGTTGTTTAAGTCTGCTGT GAAAGCCCCGGGCTCAACC TGGGAATTGCAGTGGATAC TGGGCGACTAGAGTG | 1 | Lysobacter sp. | 1.00E-117 | 94% | Proteobacteria | Xanthomonadaceae | Lysobacter |
| | | | | Uncultured bacterium clone | 1.00E-122 | 94% | - | - | - |
| Oligotype 68 | CCCGAAT AGGTCTG CATACGG CGAA | TGGGGAATTTTGGACAATG GGCGCAAGCCTGATCCAGC CATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTCGGCCGGAACGAA ATCGCGCGGGCTATTACCC CGCGTGGATGACGGTACCG GAAGAAGAAGCACCGGCT AACTTCGTGCCAGCAGCCG CGGTAATACGAAGGGTGCA AGCGTTTACTCGGAATTAC TGGGCGTAAAGCGTGCGTA GGTGGTTGTTTAAGTCTGC TGTGAAAGCCCCGGGCTCA ACCTGGGAATTGCAGTGG TACCTGGGGCGACTAG | 1 | Uncultured beta proteobacterium clone | 3.00E-113 | 94% | Proteobacteria | - | - |
| | | | | Lysobacter sp. | 2.00E-115 | 93% | Proteobacteria | Xanthomonadaceae | Lysobacter |
| | | | | Arenimonas sp. | 3.00E-113 | 92% | Proteobacteria | Xanthomonadaceae | Arenimonas |
| Oligotype 69 | CATTGAT AGGCTGC AAACTTG CTAG | TGGGGAATATTGGACAATG GGGGCAACCCTGATCCAGC AATGCCGCGTGTGTGAAG AAGGCCTTCGGGTTGTAAA GCACTTTTATTGGGAACGA AAAGCGATGGGTTAATACC TTATCGTGCTGACGGTACC CAAGGAATAAGCACCGGCT AACTTCGTGCCAGCAGCCG CGGTAATACGAAGGGTGCA AGCGTTAATCGGAATTACT GGGCGTAAAGGGTGCGTAG GCGTTACTTAAGTCTGTT | 1 | Uncultured bacterium clone | 4.00E-127 | 99% | - | - | - |
| | | | | Uncultured Rhodanobacter sp. | 1.00E-122 | 94% | Proteobacteria | Xanthomonadaceae | Rhodanobacter |

| | | | | | | | | | |
|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|--------------------|----------------------|-----------------------|
| | | GTGAAGCCCTGGGCTCAAC CTGGGAATGGCAATGGATA CTGGGTAGCTAGAGT | | | | | | | |
| Oligotype 70 | ATTTCAAT CTAGCAG GCTGGCT AGT | TGGGGAATATTGGACAATG GGGGCAACCCTGATCCAGC AATGCCGCGTGTGTGAAGA AGGCCTGCGGGTTGTAAAG CACTTTTATTCGGAACGAA AAGCAATGGATTAACACTC TGTTGTGCTGACGGTACCG GAAGAATAAGCACC GGCTA ACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAA GCGTTAATCGGAATTATTG GGCGTAAAGCGTGCGTAGG TGGTTTTTAAGTCTTTTGTG AAAGCCCTGGGCTCAACCT GGGAACTGCAGGAGAAAC TGGAAGGCTAGAGTC | 1 | Uncultured bacterium clone | 2.00E-130 | 95% | - | - | - |
| | | | | Uncultured Xanthomonas sp. | 2.00E-110 | 94% | Proteoba cteria | Xanthomona daceae | Xanthomonas |
| | | | | Lysobacter sp. | 4.00E-112 | 92% | Proteoba cteria | Xanthomona daceae | Lysobacter |
| Oligotype 71 | AGTGCGG TCGTGTGT GGGATGA ATC | TGGGGAATCTTGCACAATG GGCGAAAAGCCTGATGCAGC AACGCCGCGTGCGGGAAG AAGGCCCTAGGGTTGTAAA CCGCTTTCAGTAGGGAAGA AAATGACGGTACCCAAAGA ATAAGCACCGGCTAACTTC GTGCCAGCAGCCGCGGTAA TACGAAGGGTGCAAGCGTT ACTCGGAATTACTGGGCGT AAAGCGTGCGTAGGTGGTT GTTTAAGTCTGCTGTGAAA GCCCGGGCTCAACCTGGG GAATTGCAGTGGATACTGG GCGACTAGAGTGTGGTAGA GGACAGTGGAATTTC | 1 | Uncultured bacterium clone | 4.00E-97 | 99% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 4.00E-97 | 99% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |
| | | | | Pseudomonas sp. | 2.00E-95 | 99% | Proteoba cteria | Pseudomona daceae | Pseudomonas |
| Oligotype 72 | AGTGCGG TCGGAGT GGGACGA ATTC | TGGGGAATTTCCGCAATG GGCGAAAAGCCTGACGGAG CAATACCGCGTGAGGGACG AAGGTCTGTGGATTGTAAA CCTCTTTTGTGGGGAAGA TAATGACGGTACCCAACGA ATAAGCATCGGCTAACTCC GTGCCAGCAGCCGCGGTAA GACGGAGGATGCAAGCGTT | 1 | Uncultured bacterium clone | 4.00E-107 | 91% | - | - | - |

| | | | | | | | | | |
|-----------------|---------------------------------------|--|---|---------------------------------|-----------|-----|--------------------|----------------------|-------------------|
| | | ATCCGGAATTACTGGGCGT AAAGCGTGCGTAGGTGGTT GTTTAAGTCTGCTGTGAAA GCCCCGGGCTCAACCTGGG AATTGCAGTGGATACTGGG CGACTAGAGTGTGGTAGAG GACAGTGGGAATTTCCG | | | | | | | |
| Oligotype 73 | AGGGCGG TCGTGTGT GGGATGA ATC | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC AATTCCGCGTGGGTGAAGA AGGTCTTCGGATTGTAAAG CCCTTTCGTTGGGGACGAT GATGACGGTACCCAAAGAA GAAGCCCCGGCTAACTTCG TGCCAGCAGCCGCGTAAT ACGAAGGGTGCAAGCGTTA CTCGGAATTACTGGGCGTA AAGCGTGCGTAGGTGGTTG TTTAAGTCTGCTGTGAAAG CCCCGGGCTCAACCTGGGG AATTGCAGTGGATACTGGG CGACTAGAGTGTGGTAGAG GACAGTGGGAATTTCC | 1 | Uncultured bacterium clone | 8.00E-124 | 94% | - | - | - |
| | | | | Uncultured Thiothrix sp. | 1.00E-102 | 90% | Proteoba cteria | Thiotrichace ae | Thiothrix |
| Oligotype 74 | AGGGCGG TCGGGGC GGGGGGA ATTC | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC AATGCCGCGTGGATGAAGA AGGTCTTCGGATTGTAAAG TCCTTTCGACGGGGACGAT GATGACGGTACCCGTAGAA GAAGCCCCGGCTAACTTCG TGCCAGCAGCCGCGTAAT ACGAAGGGGGCTAGCGTTA CTCGGAATTACTGGGCGTA AAGCGTGCGTAGGCGGTTT GTTAAGTCCGATGTGAAAG CCCTGGGCTCAACCTGGGA ATGGCATGGGATACTGGCG AGCTAGAGTGCGGTAGAGG GGTGCGGAATTTCCCG | 1 | Uncultured bacterium clone | 2.00E-124 | 94% | - | - | - |
| | | | | Uncultured Gluconobacter sp. | 2.00E-110 | 91% | Proteoba cteria | Acetobactera ceae | Gluconobacte r |
| | | | | Roseomonas sp. | 2.00E-110 | 91% | Proteoba cteria | Acetobactera ceae | Roseomonas |
| Oligotype 75 | AGGACGG TCGGAGT GGGACGA ATTC | TGGGGAATCTTAGACAATG GGCGCAAGCCTGATCTAGC CATGCCGCGTGAGTGATGA AGGCCTTAGGGTCGTAAAG CTCTTTCGCTGGGGAAGAT | 1 | Uncultured bacterium clone | 1.00E-117 | 93% | - | - | - |

| | | | | | | | | | |
|-----------------|---------------------------------------|--|---|------------------------------------|-----------|-----|--------------------|----------------------|-------------------|
| | | AATGACGGTACCCAGTAAA GAAACCCCGGCTAACTTCG TGCCAGCAGCCGCGTAAT ACGAAGGGTGCAAGCGTTA CTCGGAATTACTGGGCGTA AAGCGTGCGTAGGTGGTTG TTAAGTCTGCTGTGAAAG CCCCGGGCTCAACCTGGGA ATTGCAGTGGATACTGGGC GACTAGAGTGTGGTAGAGG ACAGTGGAATTTCCG | | | | | | | |
| Oligotype 76 | AGAGTTC TCTAGCA ATCTGAC TAGT | TGGGGAATATTGGACAATG GGGGCAACCCTGATCCAGC AATGCCGCGTGTGTGAAGA AGGCCTTCGGGTTGTAAAG CACTTTTATTGGGAACGAA AGCGATGGGTAAATACCTT ATCGTGCTGACGGTACCCA AGGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTAATCGGAATTACTGG GCGTAAAGGGTGCGTAGGC GGTACTTAAGTCTGTTGT GAAAGCCCTGGGCTCAACC TGGGAATGGCAATGGATAC TGGTAGCTAGAGTA | 1 | Uncultured bacterium clone | 8.00E-129 | 99% | - | - | - |
| | | | | Uncultured Rhodanobacter sp. | 2.00E-125 | 94% | Proteoba cteria | Xanthomona daceae | Rhodanobacte r |
| | | | | Dyella sp. | 4.00E-122 | 94% | Proteoba cteria | Xanthomona daceae | Dyella |
| Oligotype 77 | AGAGTTC TCTAGAA TGTGGGT AGAA | GGGGAATATTGGACAATG GGGGCAACCCTGATCCAGC AATGCCGCGTGTGTGAAGA AGGCCTTCTGGTTGTAAAGC ACTTTTATTGGGAACGAAA AGCGATGGGTAAATATCTT ATCGTGCTGACGGTACCCA AGGAATAAGCACCGGCTAA CTTCGTGCCAGCAGCCGCG GTAATACGAAGGGTGCAAG CGTTAATCGGAATTACTGG GCGTAAAGGGTGCGTAGGC GGTACTTAAGTCTGTTGT GAAAGCCCTGGGCTCAACCT GGGAATGGCAATGGATACT GGGTAGCTAGAGTAC | 1 | Uncultured bacterium clone | 2.00E-124 | 98% | - | - | - |
| | | | | Uncultured Rhodanobacter sp. | 3.00E-118 | 93% | Proteoba cteria | Xanthomona daceae | Rhodanobacte r |
| Oligotype | AGAGGGG | TGGGGAATATTGGACAATG | 1 | Uncultured | 6.00E-140 | 97% | - | - | - |

| | | | | | | | | | | |
|-----------------|---------------------------------------|--|---|-------------------------------|-----------|-----|----------------|------------------|-------------------|--|
| 78 | GGTCGGT GGGGCA GAGT | GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAGC CCTTTGTTGGGAAGAATAC CTGCAGGTTAATAACCAGT AGGGAGTGACGGTACCCAA GAATAAGCACCGGCTAACT TCGTGCCAGCAGCCGCGGT AATACGAAGGGTGCAAGC GTTACTCGGAATTACTGGG CGTAAAGCGTGCGTAGGTG GTTGTTTAAGTCTGCTGTG AAAGCCCCGGGCTCAACCT GGGAATTGCAGTGGATACT GGGCGACTAGAGTGTG | | bacterium clone | | | | | | |
| | | | | Pseudoxanthomonas sp. | 6.00E-140 | 97% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas | |
| Oligotype 79 | AGAGAGG GGTTAGA TACGAGG TGTT | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAGC CCTTTGTTGGGAAGAAATC CTGCAGGTTAATAACCAGT AGGGATGACGGTACCCAAA GAATAAGCACCGGCTAACT TCGTGCCAGCAGCCGCGGT AATACGAAGGGTGCAAGC GTTACTCGGAATTACTGGG CGTAAAGCGTGCGTAGGTG GTTGTTTAAGTCTGCTGTG AAAGCCCCGGGCTCAACCTGG GAATGCAGTGGATACTGGG CGACTAGAGTGTGGTA | 1 | Uncultured bacterium clone | 2.00E-144 | 98% | - | - | - | |
| | | | | Pseudoxanthomonas sp. | 2.00E-144 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas | |
| Oligotype 80 | AGAGAGG GGTCGGT GGGGCA GAGT | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CATACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAGC CCTTTGTTGGGAAGAAATC CTGCAGGTTAATAACCAGT AGGGATGACGGTACCCAAA GAATAAGCACCGGCTAACT TCGTGCCAGCAGCCGCGGT AATACGAAGGGTGCAAGC GTTACTCGGAATTACTGGG CGTAAAGCGTGCGTAGGTG GTTGTTTAAGTCTGCTGTG AAAGCCCCGGGCTCAACCT | 1 | Uncultured bacterium clone | 1.00E-146 | 98% | - | - | - | |
| | | | | Pseudoxanthomonas sp. | 1.00E-146 | 98% | Proteobacteria | Xanthomonadaceae | Pseudoxanthomonas | |

| | | | | | | | | | |
|-----------------|---------------------------------------|--|---|------------------------------------|-----------|-----|--------------------|----------------------|-----------------------|
| | | GGGAATTGCAGTGGATACT GGGCGACTAGAGTGTG | | | | | | | |
| Oligotype 81 | ACTTGTAT ACGAATG GGATGGT AGA | TGGGGAATATTGGACAAAT GGGGGCAACCTGATCCAG CAATGCCCCGCGTGTGTGAA AGAAGGCCCTTCGGGTGTGTA AAGCACTTTTATTGGGAAC GAAAAGCGATGGGTAAATA TCTTATCGTGCTGACGGTA CCCAAGGAATAAGCACCGG CTAACTTCGTGCCAGCAGC CGCGGTAATACGAAGGGTG CAAGCGTTAATCGGAATTA CTGGGCGTAAAGGGTGCGT AGGCGGTTATTTAAGTCTG TTGTGAAAGCCCTGGGCTC AACCTGGGAATGGCAATGG ATACTGGGTAGCTAG | 1 | Uncultured bacterium clone | 5.00E-126 | 99% | - | - | - |
| | | | | Uncultured Rhodanobacter sp. | 8.00E-119 | 94% | Proteoba cteria | Xanthomona daceae | Rhodanobacte r |
| Oligotype 82 | ACTCTTTT GGGGTAC TACTGGT GGG | TAGGGAATATTGGACAAATG GGTGCGAGCCTGATCCAGC CATGCCGCGTGCAGGAAGA CGGCCTTCTGGGTTGTAAA CTGCTTTTACCAGGGGATA AAAGACCATGCGTGGGACA TTGCCGGTACCAGATGAAT AAGCACCGGCTAACTCCGT GCCAGCAGCCGCGGTAATA CGGAGGGTGCAAGCGTTGT CCGGATTTATTGGGTTTAA AGGTGCGTAGGTGGTTGTT TAAGTCTGCTGTGAAAGCC CCGGGCTCAACCTGGGAAT TGCAGTGGATACTGGGCGA CTAGAGTGTGGTAGA | 1 | Uncultured bacterium clone | 4.00E-97 | 93% | - | - | - |
| Oligotype 83 | ACAAGTA TACGAAA TTGGATG GCGT | TGGGGAATATTGGACAAATG GGCGCAAGCCTGATCCAGC CATAACCGCGTGGGTGAAGA AGGCCTTCGGGTTGTAAAG ACCCTTTTGTGGGAAAG AAATACCTGCAGGTTAATA ACCAGTAGGGATGACGGTA CCCAAAGAATAAGCACCGG CTAACTTCGTGCCAGCAGC CGCGGTAATACGAAGGGTG | 1 | Uncultured bacterium clone | 3.00E-143 | 98% | - | - | - |
| | | | | Pseudoxanthomo nas sp. | 3.00E-143 | 98% | Proteoba cteria | Xanthomona daceae | Pseudoxantho monas |

| | | | | | | | | | |
|-----------------|---------------------------------------|---|---|-------------------------------|-----------|-----|--------------------|----------------------|------------|
| | | CAAGCGT TACTCGGAATTA CTGGGCGTAAAGCGTGCGT AGGTGGTTGTTAAGTCTG CTGTGAAAGCCCCGGGCT CAACCTGGGAATTGCAGTG GATACTGGGCGACTA | | | | | | | |
| Oligotype 84 | AAACGGG GTACCGG GAAGTAT GGCC | TGGGGAATATTGGACAATG GGCGCAAGCCTGATCCAGC CAATGCCGCGTAGTGTGAA GAAGGCCTTCGGGTTGTAA AGACACTTTTGTCCGGGAA GAAAAGACACCGGGTCAAT ACCCTCGGTGTCATGACGG TACCGGAAGAATAAGCACC GGCTAACTTCGTGCCAGCA GCCGCGGTAATACGAAGGG TGCAAAGCGT TACTCGGAA T TACTGGGCGTAAAGCGTG CGTAGGTGGTTGTTAAGT CTGCTGTAGAAAAGCCCCGG GCTCAACCTGGGAATTGCA GTGATACTGGGCGACT | 1 | Uncultured bacterium clone | 3.00E-143 | 98% | - | - | - |
| | | | | Lysobacter sp. | 4.00E-122 | 94% | Proteoba cteria | Xanthomona daceae | Lysobacter |

Supplementary Table 3: Elaborated PICRUSt results at KEGG level 2 found in all three laminae (U1, U2, and U3) of the conical microbial mat from Lake Untersee, Antarctica.

| Level2 | Relative frequency (%) | | |
|-----------------------------------|------------------------|----------|----------|
| | U1 | U2 | U3 |
| Energy metabolism | 11.89138 | 8.199587 | 7.1746 |
| Carbohydrate Metabolism | 9.296634 | 11.36183 | 11.68234 |
| Genetic Information Processing | 3.322108 | 2.549536 | 2.481704 |
| Amino Acid Metabolism | 10.52104 | 11.58771 | 11.72825 |
| Cellular Processes and Signaling | 3.481018 | 3.335685 | 3.58969 |
| Folding, Sorting, and Degradation | 3.469229 | 2.876053 | 2.736253 |
| Replication and Repair | 7.203122 | 7.66769 | 7.8705 |

| | | | |
|---|----------|----------|----------|
| Transport and Catabolism | 0.126109 | 0.276976 | 0.321507 |
| Translation | 5.153554 | 4.897501 | 4.854273 |
| Transcription | 1.369528 | 2.283908 | 2.481662 |
| Metabolism of Cofactors and Vitamins | 6.569245 | 5.511531 | 5.072587 |
| Signal Transduction | 2.012908 | 2.060833 | 2.124958 |
| Glycan Biosynthesis and Metabolism | 2.099122 | 1.867456 | 2.004959 |
| Signaling Molecules and Interaction | 0.12071 | 0.176034 | 0.188935 |
| Cell Motility | 1.666703 | 1.750925 | 1.995287 |
| Enzyme Families | 3.223916 | 2.437874 | 2.282523 |
| Membrane Transport | 9.913693 | 12.15913 | 12.56327 |
| Metabolism of Other Amino Acids | 2.131889 | 1.999419 | 1.932856 |
| Cell Growth and Death | 0.787679 | 0.572525 | 0.531145 |
| Poorly Characterized | 5.090673 | 5.179542 | 5.303082 |
| Nucleotide Metabolism | 3.874769 | 3.714677 | 3.732172 |
| Biosynthesis of Other Secondary Metabolites | 1.340206 | 1.297615 | 1.306199 |
| Lipid Metabolism | 2.965564 | 3.669127 | 3.66454 |
| Metabolism of Terpenoids and Polyketides | 2.369206 | 2.566839 | 2.376703 |

Supplementary Table 4: Summarized PICRUSt results in (a) cyanobacteria and (b) heterotrophs at KEGG level 3 found in all three laminae (U1, U2, and U3) of the conical microbial mat from Lake Untersee, Antarctica. The results also have been presented in a bar graph format in Supplementary Figure 3.

Supplementary Table 4(a)

| KEGG LEVEL 3 | U1-Cyanobacteria | U2C-Cyanobacteria | U3C-Cyanobacteria |
|---|-------------------------|--------------------------|--------------------------|
| Amino Acid Metabolism | | | |
| Alanine, aspartate and glutamate metabolism | 84082 | 27076 | 15129 |
| Amino acid related enzymes | 107383 | 34548 | 19305 |
| Arginine and proline metabolism | 145654 | 46000 | 25708 |
| Cysteine and methionine metabolism | 109531 | 33430 | 18805 |

| | | | |
|---|--------|--------|--------|
| Glycine, serine and threonine metabolism | 69197 | 21786 | 12190 |
| Histidine metabolism | 58891 | 18356 | 10245 |
| Lysine biosynthesis | 50210 | 16110 | 9055 |
| Lysine degradation | 16310 | 5112 | 2839 |
| Phenylalanine metabolism | 35273 | 10682 | 5870 |
| Phenylalanine, tyrosine and tryptophan biosynthesis | 78877 | 24780 | 13937 |
| Tryptophan metabolism | 29273 | 9066 | 5014 |
| Tyrosine metabolism | 54930 | 16872 | 9373 |
| Valine, leucine and isoleucine biosynthesis | 69863 | 22302 | 12520 |
| Valine, leucine and isoleucine degradation | 20608 | 6904 | 3852 |
| Total | 930082 | 293024 | 163842 |
| Carbohydrate Metabolism | | | |
| Amino sugar and nucleotide sugar metabolism | 140750 | 43886 | 24563 |
| Butanoate metabolism | 33912 | 11142 | 6206 |
| C5-Branched dibasic acid metabolism | 32303 | 9928 | 5603 |
| Citrate cycle (TCA cycle) | 45611 | 14206 | 7995 |
| Fructose and mannose metabolism | 64469 | 20986 | 11796 |
| Galactose metabolism | 32648 | 10226 | 5820 |
| Glycolysis / Gluconeogenesis | 101692 | 33090 | 18572 |
| Glyoxylate and dicarboxylate metabolism | 46586 | 14908 | 8448 |
| Inositol phosphate metabolism | 9985 | 3204 | 1832 |
| Pentose and glucuronate interconversions | 25994 | 8102 | 4624 |
| Pentose phosphate pathway | 86747 | 27630 | 15311 |
| Propanoate metabolism | 36601 | 11746 | 6616 |
| Pyruvate metabolism | 91137 | 29640 | 16826 |
| Starch and sucrose metabolism | 61880 | 20640 | 11840 |
| Ascorbate and aldarate metabolism | 9680 | 3020 | 1747 |
| Total | 819995 | 262354 | 147799 |
| Cell Motility | | | |
| Bacterial chemotaxis | 22009 | 6528 | 3772 |

| | | | |
|---|---------|--------|--------|
| Bacterial motility proteins | 101720 | 33084 | 18838 |
| Total | 123729 | 39612 | 22610 |
| Energy Metabolism | | | |
| Carbon fixation in photosynthetic organisms | 70196 | 22526 | 12747 |
| Carbon fixation pathways in prokaryotes | 69851 | 22272 | 12530 |
| Methane metabolism | 88412 | 28914 | 16322 |
| Nitrogen metabolism | 76116 | 23922 | 13463 |
| Oxidative phosphorylation | 146994 | 47042 | 26568 |
| Photosynthesis | 201875 | 65224 | 36747 |
| Photosynthesis proteins | 286070 | 91070 | 51058 |
| Photosynthesis - antenna proteins | 80868 | 24786 | 13713 |
| Sulfur metabolism | 39579 | 12448 | 6959 |
| Total | 1059961 | 338204 | 190107 |
| Lipid Metabolism | | | |
| Biosynthesis of unsaturated fatty acids | 23871 | 7718 | 4214 |
| Fatty acid biosynthesis | 46562 | 14820 | 8344 |
| Lipid biosynthesis proteins | 64425 | 20884 | 11626 |
| Fatty acid metabolism | 27599 | 9294 | 5189 |
| Total | 162457 | 52716 | 29373 |
| Membrane Transport | | | |
| ABC transporters | 278664 | 91388 | 51630 |
| Bacterial secretion system | 37544 | 12316 | 6889 |
| Transporters | 445880 | 146472 | 82467 |
| Phosphotransferase system (PTS) | 0 | 2 | 0 |
| Total | 762088 | 250178 | 140986 |
| Metabolism of Cofactors and Vitamins | | | |
| Pantothenate and CoA biosynthesis | 50579 | 16468 | 9376 |
| Porphyrin and chlorophyll metabolism | 197208 | 63166 | 35413 |
| Riboflavin metabolism | 33262 | 10608 | 5904 |
| Thiamine metabolism | 45936 | 14410 | 8146 |

| | | | |
|--|--------|--------|-------|
| Total | 326985 | 104652 | 58839 |
| Nucleotide Metabolism | | | |
| Purine metabolism | 213109 | 67762 | 37923 |
| Pyrimidine metabolism | 130323 | 41650 | 23360 |
| Total | 343432 | 109412 | 61283 |
| Enzyme Families | | | |
| Peptidases | 206892 | 66188 | 37198 |
| Protein kinases | 79824 | 25344 | 14496 |
| Cyanophycin | 3335 | 1077 | 656 |
| Total | 286716 | 91532 | 51694 |
| Signal Transduction | | | |
| Two-component system | 161549 | 53536 | 30704 |
| Total | 161549 | 53536 | 30704 |
| Replication and Repair | | | |
| DNA repair and recombination proteins | 202304 | 66702 | 37337 |
| Total | 202304 | 66702 | 37337 |
| Signaling Molecules and Interaction | | | |
| Bacterial toxins | 3652 | 1300 | 749 |
| Total | 3652 | 1300 | 749 |
| Translation | | | |
| Ribosome | 182981 | 58400 | 32852 |
| Total | 182981 | 58400 | 32852 |

Supplementary Table 4(b)

| KEGG LEVEL 3 | U1-Heterotrophs | U2H-Heterotrophs | U3H-Heterotrophs |
|---|------------------------|-------------------------|-------------------------|
| Amino Acid Metabolism | | | |
| Alanine, aspartate and glutamate metabolism | 1129 | 52453 | 59666 |
| Amino acid related enzymes | 1255 | 63686 | 74792 |

| | | | |
|---|-------|--------|--------|
| Arginine and proline metabolism | 1511 | 68456 | 82019 |
| Cysteine and methionine metabolism | 1017 | 42172 | 52336 |
| Glycine, serine and threonine metabolism | 992 | 48594 | 56556 |
| Histidine metabolism | 657 | 32087 | 36575 |
| Lysine biosynthesis | 596 | 30637 | 35626 |
| Lysine degradation | 537 | 28369 | 27445 |
| Phenylalanine metabolism | 523 | 21176 | 25329 |
| Phenylalanine, tyrosine and tryptophan biosynthesis | 726 | 37009 | 44482 |
| Tryptophan metabolism | 787 | 37148 | 39417 |
| Tyrosine metabolism | 627 | 26674 | 31087 |
| Valine, leucine and isoleucine biosynthesis | 878 | 42724 | 48680 |
| Valine, leucine and isoleucine degradation | 928 | 51730 | 49952 |
| Total | 12163 | 582915 | 663962 |
| Carbohydrate Metabolism | | | |
| Amino sugar and nucleotide sugar metabolism | 1230 | 56891 | 68524 |
| Butanoate metabolism | 1172 | 58429 | 58924 |
| C5-Branched dibasic acid metabolism | 324 | 16491 | 18871 |
| Citrate cycle (TCA cycle) | 1095 | 49547 | 56033 |
| Fructose and mannose metabolism | 778 | 33836 | 40410 |
| Galactose metabolism | 594 | 25776 | 31202 |
| Glycolysis / Gluconeogenesis | 1473 | 63919 | 72464 |
| Glyoxylate and dicarboxylate metabolism | 843 | 43440 | 46540 |
| Inositol phosphate metabolism | 243 | 13036 | 13062 |
| Pentose and glucuronate interconversions | 722 | 30185 | 39706 |
| Pentose phosphate pathway | 956 | 41705 | 50490 |
| Propanoate metabolism | 925 | 52898 | 51928 |
| Pyruvate metabolism | 1226 | 63260 | 70535 |
| Starch and sucrose metabolism | 786 | 37930 | 47247 |
| Ascorbate and aldarate metabolism | 188 | 9056 | 10649 |
| Total | 12555 | 596399 | 676585 |

| | | | |
|---|-------|--------|--------|
| Cell Motility | | | |
| Bacterial chemotaxis | 173 | 19357 | 24553 |
| Bacterial motility proteins | 296 | 40943 | 56238 |
| Total | 469 | 60300 | 80791 |
| Energy Metabolism | | | |
| Carbon fixation in photosynthetic organisms | 464 | 23765 | 27292 |
| Carbon fixation pathways in prokaryotes | 875 | 51652 | 56604 |
| Methane metabolism | 988 | 52560 | 56797 |
| Nitrogen metabolism | 719 | 37422 | 44790 |
| Oxidative phosphorylation | 1123 | 71165 | 79321 |
| Photosynthesis | 269 | 14563 | 16752 |
| Photosynthesis proteins | 270 | 14843 | 17155 |
| Photosynthesis - antenna proteins | 0 | 0 | 0 |
| Sulfur metabolism | 236 | 16269 | 18119 |
| Total | 4944 | 282239 | 316830 |
| Lipid Metabolism | | | |
| Biosynthesis of unsaturated fatty acids | 289 | 14090 | 16571 |
| Fatty acid biosynthesis | 449 | 28080 | 31664 |
| Lipid biosynthesis proteins | 727 | 40781 | 44637 |
| Fatty acid metabolism | 764 | 41580 | 38507 |
| Total | 2229 | 124531 | 131379 |
| Membrane Transport | | | |
| ABC transporters | 4895 | 206211 | 225819 |
| Zinc transport system | 14 | 224 | 298 |
| Bacterial secretion system | 552 | 27719 | 37043 |
| Transporters | 8488 | 342786 | 388935 |
| Phosphotransferase system (PTS) | 192 | 5319 | 7113 |
| Arsenical resistance protein | 0 | 30 | 120 |
| Arsenical pump membrane protein | 0 | 80 | 134 |
| Total | 14127 | 582035 | 658910 |

| | | | |
|---|------|--------|--------|
| Metabolism of Cofactors and Vitamins | | | |
| Pantothenate and CoA biosynthesis | 609 | 31682 | 35625 |
| Porphyrin and chlorophyll metabolism | 610 | 46988 | 45947 |
| Riboflavin metabolism | 298 | 15390 | 16610 |
| Thiamine metabolism | 367 | 18921 | 19857 |
| Total | 1884 | 112981 | 118039 |
| Nucleotide Metabolism | | | |
| Purine metabolism | 2048 | 97858 | 115534 |
| Pyrimidine metabolism | 1517 | 73630 | 86846 |
| Total | 3565 | 171488 | 202380 |
| Enzyme Families | | | |
| Peptidases | 1528 | 72947 | 87331 |
| Protein kinases | 467 | 20028 | 22347 |
| Total | 1995 | 92975 | 109678 |
| Signal Transduction | | | |
| Two-component system | 1598 | 88468 | 106623 |
| Total | 1598 | 88468 | 106623 |
| Replication and Repair | | | |
| DNA repair and recombination proteins | 2738 | 126356 | 149637 |
| Total | 2738 | 126356 | 149637 |
| Signaling Molecules and Interaction | | | |
| Bacterial toxins | 77 | 4389 | 4759 |
| Total | 77 | 4389 | 4759 |
| Translation | | | |
| Ribosome | 1896 | 95642 | 109506 |
| Total | 1896 | 95642 | 109506 |