

Scientific Reports

Supplementary information for

Sources and selection of snow-specific microbial communities in a Greenlandic sea ice snow cover

Lorrie Maccario^{1,2}, Shelly D. Carpenter³, Jody W. Deming³, Timothy M. Vogel¹, Catherine Larose¹

¹Environmental Microbial Genomics, Laboratoire Ampère, CNRS, École Centrale de Lyon, Écully, France.

²Microbiology Section, Department of Biology, University of Copenhagen, Copenhagen, Denmark

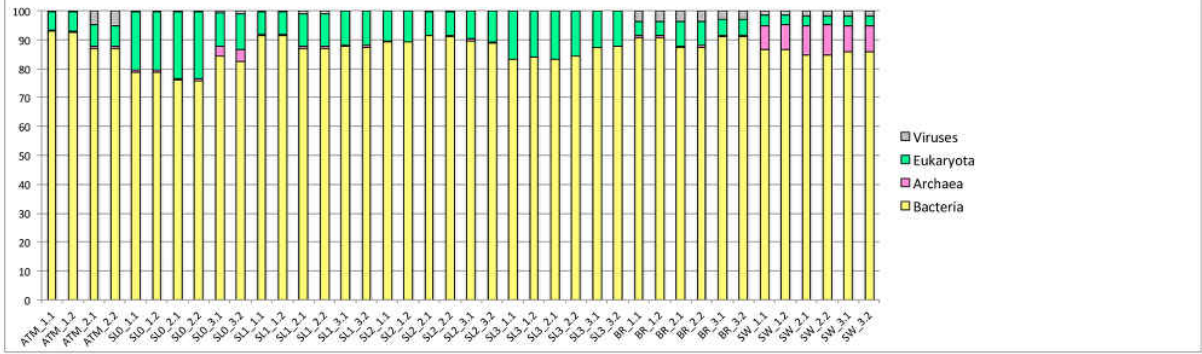
³School of Oceanography, University of Washington, Seattle, USA

Corresponding Author: Lorrie Maccario - lorrie.maccario@bio.ku.dk

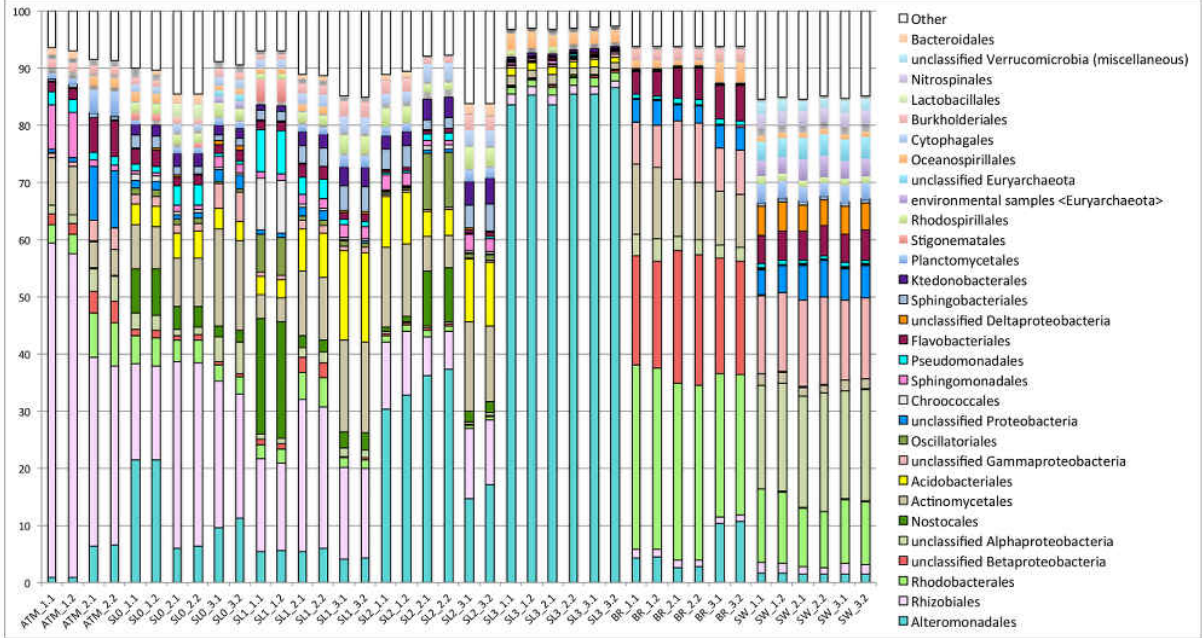
Figure S1: Taxonomic composition. Detailed taxonomic composition at kingdom level (A) and for prokaryotes (B), eukaryotes (C) and primary producers (D) (normalized to total abundance of annotated reads, as percentage).

A

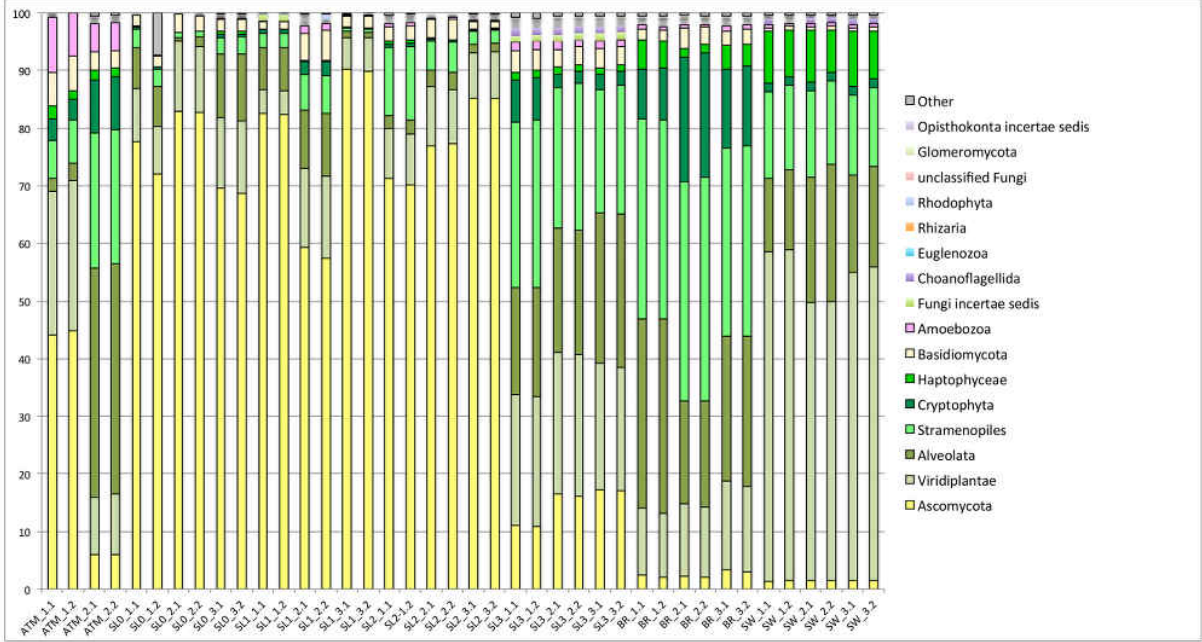
Relative abundance (%)

**B**

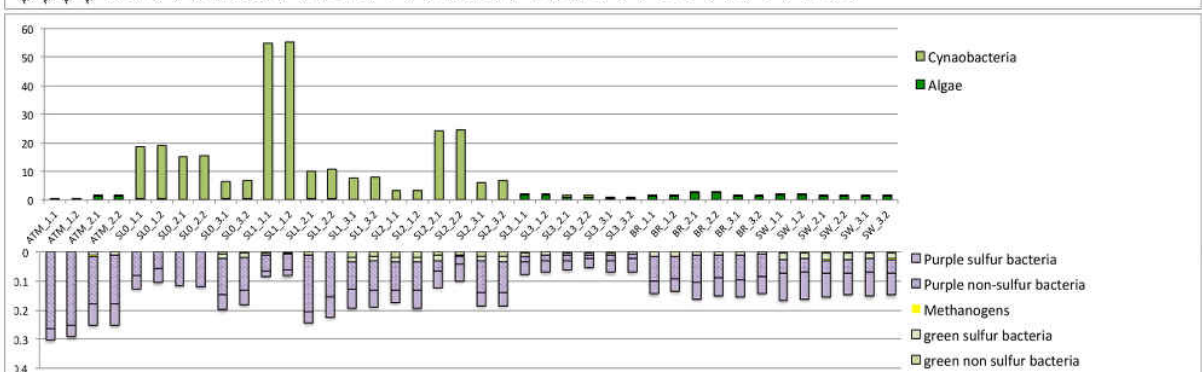
Relative abundance (%)

**C**

Relative abundance (%)

**D**

Relative abundance (%)



| | | BACTERIA | | | | | | | | | | |
|---|---|----------|-----------|----------|----------|---------|-----------|----------|----------|---------|----------|---------|
| | | p-values | ATM: mean | ATM: std | SL: mean | SL: std | SL3: mean | SL3: std | BR: mean | BR: std | SW: mean | SW: std |
| Amino Acid Metabolism | Lysine degradation | 1.97E-13 | 0.842 | 0.071 | 0.769 | 0.032 | 0.988 | 0.024 | 0.951 | 0.028 | 1.021 | 0.019 |
| Amino Acid Metabolism | Glycine, serine and threonine metabolism | 1.19E-10 | 1.986 | 0.070 | 1.764 | 0.343 | 1.961 | 0.059 | 2.666 | 0.067 | 3.033 | 0.024 |
| Amino Acid Metabolism | Histidine metabolism | 1.20E-08 | 0.737 | 0.091 | 0.715 | 0.048 | 0.838 | 0.004 | 0.863 | 0.009 | 0.925 | 0.026 |
| Amino Acid Metabolism | Valine, leucine and isoleucine biosynthesis | 7.15E-08 | 0.887 | 0.076 | 0.943 | 0.114 | 1.066 | 0.036 | 1.131 | 0.029 | 1.273 | 0.023 |
| Amino Acid Metabolism | Valine, leucine and isoleucine degradation | 2.03E-07 | 1.948 | 0.305 | 1.456 | 0.183 | 2.158 | 0.010 | 1.856 | 0.061 | 1.754 | 0.047 |
| Amino Acid Metabolism | Arginine and proline metabolism | 1.19E-06 | 1.637 | 0.429 | 2.204 | 0.196 | 2.610 | 0.013 | 2.424 | 0.034 | 2.498 | 0.030 |
| Amino Acid Metabolism | Alanine, aspartate and glutamate metabolism | 1.57E-06 | 1.793 | 0.326 | 2.139 | 0.203 | 2.504 | 0.023 | 2.273 | 0.028 | 2.587 | 0.022 |
| Amino Acid Metabolism | Phenylalanine metabolism | 3.14E-05 | 1.113 | 0.138 | 0.859 | 0.111 | 0.776 | 0.015 | 1.018 | 0.015 | 0.867 | 0.022 |
| Biosynthesis of Other Secondary Metabolites | Biosynthesis of Other Secondary Metabolites | 6.52E-07 | 1.194 | 0.075 | 1.330 | 0.178 | 1.127 | 0.032 | 0.944 | 0.016 | 0.904 | 0.023 |
| Carbohydrate Metabolism | Starch and sucrose metabolism | 1.05E-12 | 1.124 | 0.058 | 1.879 | 0.317 | 1.325 | 0.020 | 0.694 | 0.076 | 0.484 | 0.018 |
| Carbohydrate Metabolism | Propanoate metabolism | 1.88E-10 | 1.965 | 0.127 | 1.696 | 0.103 | 1.989 | 0.057 | 2.003 | 0.020 | 2.176 | 0.024 |
| Carbohydrate Metabolism | Amino sugar and nucleotide sugar metabolism | 4.30E-08 | 1.330 | 0.227 | 1.778 | 0.126 | 1.483 | 0.031 | 1.389 | 0.020 | 1.339 | 0.038 |
| Carbohydrate Metabolism | Citrate cycle (TCA cycle) | 7.57E-08 | 1.879 | 0.031 | 1.676 | 0.217 | 2.159 | 0.021 | 1.974 | 0.010 | 2.261 | 0.032 |
| Carbohydrate Metabolism | Galactose metabolism | 1.26E-07 | 0.408 | 0.087 | 0.704 | 0.127 | 0.432 | 0.012 | 0.437 | 0.047 | 0.381 | 0.013 |
| Carbohydrate Metabolism | Ascorbate and aldarate metabolism | 8.77E-06 | 0.381 | 0.042 | 0.344 | 0.086 | 0.187 | 0.012 | 0.307 | 0.011 | 0.430 | 0.006 |
| Carbohydrate Metabolism | Pyruvate metabolism | 1.01E-05 | 2.202 | 0.096 | 2.148 | 0.335 | 2.740 | 0.018 | 2.626 | 0.041 | 2.752 | 0.030 |
| Carbohydrate Metabolism | Inositol phosphate metabolism | 1.67E-05 | 0.139 | 0.040 | 0.281 | 0.084 | 0.168 | 0.014 | 0.267 | 0.003 | 0.352 | 0.014 |
| Carbohydrate Metabolism | C5-Branched dibasic acid metabolism | 2.59E-05 | 0.403 | 0.062 | 0.445 | 0.097 | 0.460 | 0.021 | 0.549 | 0.016 | 0.640 | 0.016 |
| Carbohydrate Metabolism | Glycolysis / Gluconeogenesis | 8.67E-05 | 2.010 | 0.077 | 2.057 | 0.164 | 2.243 | 0.022 | 2.210 | 0.071 | 2.364 | 0.034 |
| Cell Growth and Death | Cell Growth and Death | 2.10E-06 | 1.532 | 0.298 | 1.025 | 0.151 | 0.805 | 0.025 | 0.932 | 0.019 | 0.976 | 0.024 |
| Cell Motility | Cell Motility | 2.84E-15 | 1.250 | 0.163 | 1.173 | 0.196 | 2.132 | 0.088 | 1.543 | 0.122 | 0.392 | 0.019 |
| Energy Metabolism | Carbon fixation pathways in prokaryotes | 9.79E-10 | 2.358 | 0.047 | 2.076 | 0.201 | 2.728 | 0.037 | 2.549 | 0.011 | 2.622 | 0.017 |
| Lipid Metabolism | Sphingolipid metabolism | 8.16E-14 | 0.258 | 0.045 | 0.296 | 0.041 | 0.070 | 0.005 | 0.082 | 0.012 | 0.176 | 0.010 |
| Lipid Metabolism | Arachidonic acid metabolism | 3.06E-10 | 0.189 | 0.015 | 0.192 | 0.025 | 0.237 | 0.005 | 0.114 | 0.011 | 0.146 | 0.006 |
| Lipid Metabolism | Fatty acid metabolism | 6.38E-08 | 1.679 | 0.253 | 1.341 | 0.127 | 1.823 | 0.010 | 1.296 | 0.024 | 1.266 | 0.032 |
| Lipid Metabolism | Fatty acid biosynthesis | 1.27E-06 | 0.960 | 0.210 | 0.768 | 0.099 | 0.535 | 0.011 | 0.643 | 0.020 | 0.929 | 0.020 |
| Lipid Metabolism | Synthesis and degradation of ketone bodies | 2.21E-05 | 0.403 | 0.041 | 0.293 | 0.065 | 0.419 | 0.021 | 0.356 | 0.013 | 0.277 | 0.008 |
| Lipid Metabolism | Biosynthesis of unsaturated fatty acids | 6.28E-05 | 0.466 | 0.118 | 0.421 | 0.060 | 0.373 | 0.011 | 0.297 | 0.008 | 0.286 | 0.009 |
| Membrane Transport | Membrane Transport | 1.81E-07 | 6.527 | 0.142 | 5.462 | 0.933 | 3.622 | 0.072 | 5.438 | 0.071 | 3.893 | 0.077 |
| Metabolism of Cofactors and Vitamins | One carbon pool by folate | 4.77E-07 | 0.909 | 0.041 | 0.688 | 0.162 | 0.860 | 0.026 | 0.958 | 0.022 | 1.116 | 0.009 |
| Metabolism of Cofactors and Vitamins | Folate biosynthesis | 9.13E-07 | 0.379 | 0.029 | 0.497 | 0.113 | 0.698 | 0.019 | 0.414 | 0.019 | 0.367 | 0.006 |
| Metabolism of Cofactors and Vitamins | Biotin metabolism | 3.06E-05 | 0.354 | 0.149 | 0.141 | 0.060 | 0.217 | 0.003 | 0.105 | 0.011 | 0.107 | 0.007 |
| Metabolism of Other Amino Acids | beta-Alanine metabolism | 9.95E-10 | 0.696 | 0.016 | 0.639 | 0.058 | 0.775 | 0.019 | 0.607 | 0.012 | 0.848 | 0.013 |
| Metabolism of Other Amino Acids | Cyanamino acid metabolism | 5.77E-07 | 0.444 | 0.108 | 0.451 | 0.079 | 0.574 | 0.025 | 0.267 | 0.013 | 0.324 | 0.009 |
| Metabolism of Other Amino Acids | Taurine and hypotaurine metabolism | 6.60E-07 | 0.315 | 0.113 | 0.431 | 0.032 | 0.560 | 0.005 | 0.378 | 0.031 | 0.469 | 0.009 |
| Nucleotide Metabolism | Pyrimidine metabolism | 5.12E-09 | 3.767 | 0.609 | 3.072 | 0.211 | 2.674 | 0.072 | 3.942 | 0.087 | 3.954 | 0.058 |
| Signal Transduction | Signal Transduction | 3.19E-12 | 4.085 | 0.351 | 4.065 | 0.432 | 4.085 | 0.045 | 2.984 | 0.088 | 2.073 | 0.024 |
| Translation | Translation | 5.27E-05 | 3.524 | 0.092 | 3.691 | 0.546 | 3.714 | 0.070 | 4.044 | 0.072 | 4.719 | 0.043 |
| Transport and Catabolism | Transport and Catabolism | 2.97E-05 | 0.850 | 0.045 | 0.744 | 0.132 | 0.641 | 0.007 | 0.535 | 0.020 | 0.573 | 0.011 |
| Xenobiotics Biodegradation and Metabolism | Xenobiotics Biodegradation and Metabolism | 1.88E-05 | 3.912 | 0.707 | 3.326 | 0.330 | 2.990 | 0.029 | 2.749 | 0.008 | 2.612 | 0.077 |
| | | EUKARYA | | | | | | | | | | |
| | | p-values | ATM: mean | ATM: std | SL: mean | SL: std | SL3: mean | SL3: std | BR: mean | BR: std | SW: mean | SW: std |
| Amino Acid Metabolism | Phenylalanine metabolism | 5.63E-10 | 0.213 | 0.007 | 0.601 | 0.116 | 0.331 | 0.115 | 0.168 | 0.032 | 0.276 | 0.089 |
| Biosynthesis of Other Secondary Metabolites | Biosynthesis of Other Secondary Metabolites | 3.45E-05 | 0.375 | 0.065 | 1.231 | 0.387 | 0.792 | 0.152 | 0.606 | 0.058 | 0.647 | 0.172 |
| Carbohydrate Metabolism | C5-Branched dibasic acid metabolism | 1.15E-11 | 0.753 | 0.236 | 0.094 | 0.058 | 0.140 | 0.071 | 0.449 | 0.104 | 0.098 | 0.059 |
| Carbohydrate Metabolism | Amino sugar and nucleotide sugar metabolism | 2.37E-07 | 0.478 | 0.038 | 1.499 | 0.325 | 0.827 | 0.187 | 0.724 | 0.154 | 1.203 | 0.200 |
| Cell Communication | Cell Communication | 1.10E-06 | 2.122 | 0.254 | 1.030 | 0.347 | 1.771 | 0.071 | 1.650 | 0.326 | 1.794 | 0.264 |
| Energy Metabolism | Carbon fixation in photosynthetic organisms | 3.66E-09 | 0.798 | 0.029 | 0.489 | 0.232 | 1.164 | 0.044 | 1.108 | 0.162 | 1.241 | 0.250 |
| Energy Metabolism | Oxidative phosphorylation | 1.19E-05 | 6.341 | 0.143 | 5.831 | 1.622 | 4.564 | 0.129 | 3.927 | 0.199 | 2.451 | 0.214 |
| Energy Metabolism | Nitrogen metabolism | 8.51E-05 | 1.657 | 0.211 | 0.755 | 0.384 | 1.461 | 0.291 | 1.337 | 0.243 | 1.132 | 0.164 |
| Glycan Biosynthesis and Metabolism | Glycan Biosynthesis and Metabolism | 8.41E-07 | 0.795 | 0.135 | 2.685 | 0.756 | 1.782 | 0.098 | 0.927 | 0.255 | 1.630 | 0.307 |
| Lipid Metabolism | Glycerophospholipid metabolism | 7.21E-06 | 0.959 | 0.030 | 1.541 | 0.545 | 0.639 | 0.115 | 0.378 | 0.088 | 0.999 | 0.255 |
| Membrane Transport | Membrane Transport | 1.74E-14 | 2.927 | 0.069 | 0.518 | 0.290 | 1.200 | 0.120 | 1.884 | 0.336 | 1.198 | 0.097 |
| Metabolism of Cofactors and Vitamins | Porphyrin and chlorophyll metabolism | 2.96E-06 | 1.166 | 0.177 | 0.439 | 0.309 | 0.732 | 0.100 | 0.819 | 0.162 | 1.202 | 0.172 |
| Metabolism of Other Amino Acids | Selenocompound metabolism | 2.71E-05 | 0.801 | 0.078 | 0.303 | 0.212 | 0.814 | 0.144 | 0.421 | 0.227 | 0.710 | 0.205 |
| Metabolism of Terpenoids and Polyketides | Metabolism of Terpenoids and Polyketides | 3.44E-07 | 0.375 | 0.065 | 1.009 | 0.208 | 1.036 | 0.083 | 0.630 | 0.136 | 1.225 | 0.091 |
| Nucleotide Metabolism | Pyrimidine metabolism | 1.36E-13 | 5.582 | 0.307 | 2.763 | 0.493 | 2.891 | 0.267 | 5.205 | 0.235 | 3.543 | 0.388 |
| Nucleotide Metabolism | Purine metabolism | 7.39E-08 | 5.375 | 0.100 | 3.763 | 0.765 | 3.665 | 0.285 | 5.917 | 0.153 | 4.395 | 0.352 |
| Replication and Repair | Replication and Repair | 8.53E-08 | 2.490 | 0.402 | 4.832 | 0.894 | 3.063 | 0.142 | 2.616 | 0.263 | 4.167 | 0.354 |
| Signal Transduction | Signal Transduction | 2.97E-05 | 6.379 | 0.335 | 4.658 | 0.838 | 6.293 | 0.321 | 5.975 | 0.847 | 6.030 | 0.199 |
| Transcription | Transcription | 1.35E-07 | 7.029 | 0.004 | 4.436 | 0.689 | 4.802 | 0.525 | 6.164 | 0.467 | 4.443 | 0.191 |

Table S1: Variability of the distribution of metabolic functions within sample groups. Comparisons by ANOVA were performed in order to identify functions (based on KEGG database annotation) with significant difference between samples groups: atmosphere (ATM), surface snow (SL0, SL1 and SL2), sea ice brine (BR) and seawater (SW). Mean and standard deviation of relative abundance of each function in each group as well as p-values of the test are indicated. Only functions with relative abundance > 0.1 % and with p-values < 0.0001 are listed.

| Genomic features associated with trophic strategies as defined by Lauro <i>et al.</i> (2009) | | | Comparison of relative abundance in our samples | | | | |
|---|---------------|---------------|---|-----------|--------|----------|----------|
| Markers | Copiotroph | Oligotroph | Surface snow | Deep snow | Brine | Seawater | p-values |
| COG3386 (gluconolactonase) | Low (0%) | High (0.065%) | 0.0349 | 0.0387 | 0 | 0 | 0.7705 |
| COG1804 (predicted acyl-CoA transferases/carnitine dehydratase) | Low (0%) | High (0.072%) | 0.0162 | 0 | 0.0188 | 0.0152 | 0.042 |
| COG3293 (transposase and inactivated derivatives) | Low (0%) | High (0.073%) | 0 | 0 | 0 | 0.0056 | 0.227 |
| COG2124 (cytochrome P450) | Low (0%) | High (0.078%) | 0.4501 | 0.1962 | 0.0286 | 0.1598 | 0.0164 |
| COG1228 (imidazolonepropionase and related amidohydrolases) | Low (0.064%) | High (0.089%) | 0 | 0.0043 | 0 | 0 | 0.227 |
| COG0483 (archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family) | Low (0.033%) | High (0.115%) | 0.021 | 0.0145 | 0 | 0.069 | 0.004 |
| COG1680 (β -lactamase class C and other penicillin binding proteins) | Low (0.059%) | High (0.115%) | 0.0144 | 0.0197 | 0 | 0.0282 | 0.3453 |
| COG0318 (Acyl-CoA synthetases [AMP-forming/AMP-acid ligases II]) | Low (0.149%) | High (0.235%) | 0.7389 | 0.1132 | 0.1695 | 0.2257 | 0.3634 |
| COG1024 (enoyl-CoA hydratase/carnitine racemase) | Low (0.149%) | High (0.308%) | 0.1245 | 0.0187 | 0 | 0.0503 | 0.4735 |
| COG0625 (GST) | Low (0.298%) | High (0.342%) | 0.0433 | 0.0334 | 0.0515 | 0.0424 | 0.5324 |
| COG1960 (acyl-CoA dehydrogenases) | Low (0.186%) | High (0.417%) | 0.131 | 0.1445 | 0.2902 | 0.4398 | 0.0002 |
| COG0596 (predicted hydrolases or acyltransferases: α / β hydrolase superfamily) | Low (0.327%) | High (0.514%) | 0.1585 | 0.0898 | 0.1687 | 0.1657 | 0.1694 |
| COG1028 (dehydrogenases with different specificities: related to short-chain alcohol dehydrogenases) | Low (0.476%) | High (1.135%) | 1.0019 | 0.1708 | 0.2788 | 0.7821 | 0.4607 |
| COG0183 (acetyl-CoA acetyltransferase) | Low (0.114%) | High (1.171%) | 0.1323 | 0.0282 | 0.1992 | 0.3869 | 0.0428 |
| COG category Q (secondary metabolites biosynthesis, transport, and catabolism) | Low (2.173%) | High (3.544%) | 2.5371 | 0.8922 | 1.0205 | 2.3367 | 0.0092 |
| COG category I (Lipid transport and metabolism) | Low (2.958%) | High (4.408%) | 3.6829 | 1.4936 | 2.0434 | 3.4013 | 2.00E-06 |
| COG0814 (amino acid permeases) | High (0.114%) | Low (0%) | 0.2164 | 0.1468 | 0.1012 | 0.007 | 0.597 |
| COG3325 (chitinase) | High (0.06%) | Low (0%) | 0.038 | 0.01 | 0 | 0 | 0.2611 |
| COG0737 (5'-nucleotidase/2',3'-cyclic phosphodiesterase and related esterases) | High (0.098%) | Low (0.035%) | 0.2849 | 0.019 | 0 | 0.0056 | 0.5606 |
| COG2200 (FOG:EAL domain) | High (0.372%) | Low (0.048%) | 0 | 0.0332 | 0 | 0 | 2.00E-06 |
| COG0243 (anaerobic dehydrogenases, typically selenocysteine-containing) | High (0.179%) | Low (0.0675%) | 0.0026 | 0 | 0 | 0 | 0.6693 |
| COG0110 (acetyltransferase: isoleucine patch superfamily) | High (0.166%) | Low (0.068%) | 0.0431 | 0 | 0 | 0 | 0.5158 |
| COG0583 (transcriptional regulator) | High (1.489%) | Low (0.371%) | 0 | 0 | 0 | 0.0158 | 0.0129 |
| COG category N (cell motility) | High (3.311%) | Low (1.006%) | 0.0324 | 0.1559 | 0.0518 | 0.0292 | 0.002 |
| COG category V (defense mechanisms) | High (1.474%) | Low (1.236%) | 0.8221 | 0.9221 | 0.7071 | 0.8415 | 0.2746 |
| COG category T (signal transduction mechanisms) | High (7.071%) | Low (3.632%) | 1.9456 | 4.7023 | 2.7709 | 1.4747 | 6.00E-08 |
| COG category K (transcription) | High (7.527%) | Low (6.621%) | 2.7798 | 2.2183 | 4.7613 | 2.2745 | 1.00E-10 |

Table S2: Genomic features associated with trophic strategies. Genes (as indexed in the COG database) associated with a specific trophic lifestyle, oligotrophy or copiotrophy, as determined in the study by Lauro and colleagues (Lauro *et al.*, 2009) from genomic and metagenomic comparisons in various marine environments that were retrieved in our datasets.