**Supplementary materials**

Table S1. Results of one-way ANOVA and post-hoc Tukey’s HSD testing among-elevation variation in environmental and biotic variables. For the Tukey HSD column, elevation not sharing a letter are significantly different (p<0.05).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Variables** | **F** | ***df*** | ***p*** | **Tukey HSD (Mean)** |
| Respiration | 2.73 | 2 | 0.067 |  |
| Temperature | 127.60 | 2 | <0.001 | High (17.14)a > Middle (13.46)b > Low(10.23)c |
| Moisture | 108.20 | 2 | <0.001 | High (17.87)c < Middle (25.80)b < Low (58.79)a |
| Dry/Wet Weight Ratio | 103.0 | 2 | <0.001 | High (0.89)a > Middle (0.79)b > Low (0.60)c |
| C/N Ratio | 8.57 | 2 | <0.001 | High (12.88)b , Middle (12.42)b < Low (14.05)a |
| pH | 0.062 | 2 | 0.94 |  |
| *Coverage* |  |  |  |  |
| Rock | 22.63 | 2 | <0.001 | High (15.43)a > Middle (9.60)b > Low (4.72)c |
| Cryptogram | 12.69 | 2 | <0.001 | High (40.13)a > Middle (29.77)b , Low (24.95)b |
| Sediment | 30.59 | 2 | <0.001 | High (33.25)a > Middle (20.63)b > Low(8.24)c |
| Vascular Plant | 186.00 | 2 | <0.001 | High (18.32)c < Middle(45.80)b < Low (70.47)a |

Table S2. Environmental fitness of environmental parameters correlated with DCA ordinations of Generalists, Common taxa, and Specialists (Fig. 1).

|  |  |  |  |
| --- | --- | --- | --- |
|  | Generalists | Common taxa | Specialists |
|  | DCA1 | DCA2 | *r*2 | *P* | DCA1 | DCA2 | *r*2 | *P* | DCA1 | DCA2 | *r*2 | *P* |
| Respiration | 0.83 | -0.55 | 0.01 | 0.532 | 0.82 | 0.58 | 0 | 0.807 | -0.87 | 0.49 | 0 | 0.95 |
| Temperature | -0.94 | -0.35 | 0.11 | **0.001** | -1.00 | 0.01 | 0.10 | **0.001** | -0.87 | 0.49 | 0.14 | **0.001** |
| Moisture | 0.84 | 0.54 | 0.05 | 0.003 | 0.96 | -0.28 | 0.06 | **0.001** | 0.88 | -0.47 | 0.10 | **0.001** |
| C/N Ratio | -0.98 | -0.22 | 0.10 | **0.001** | -0.94 | 0.34 | 0.17 | **0.001** | -0.98 | 0.21 | 0.18 | **0.001** |
| pH | 0.94 | -0.34 | 0.05 | 0.003 | 0.89 | 0.46 | 0.07 | **0.001** | 0.84 | 0.54 | 0.11 | **0.001** |
| Ec | 0.98 | 0.20 | 0.06 | 0.002 | 0.98 | 0.18 | 0.07 | **0.001** | 0.98 | -0.20 | 0.09 | **0.001** |
| Elevation | -0.93 | -0.38 | 0.26 | **0.001** | -0.99 | 0.16 | 0.25 | **0.001** | -0.93 | 0.38 | 0.29 | **0.001** |
| *Coverage* |  |  |  |  |  |  |  |  |  |  |  |  |
| Rock | -0.97 | -0.23 | 0.03 | 0.036 | -0.97 | -0.23 | 0.03 | 0.064 | -0.90 | -0.43 | 0.02 | 0.164 |
| Cryptogram | 0.39 | -0.92 | 0.01 | 0.489 | 0.56 | 0.83 | 0 | 0.584 | 0.16 | -0.99 | 0.01 | 0.625 |
| Sediment | -0.71 | -0.71 | 0.02 | 0.148 | -0.78 | 0.62 | 0.01 | 0.303 | -0.57 | 0.82 | 0.03 | 0.042 |
| Vascular Plant | 0.74 | 0.67 | 0.09 | **0.001** | 0.80 | -0.60 | 0.07 | **0.001** | 0.88 | -0.47 | 0.08 | **0.001** |

Table S3. Module hubs and connectors in Total network and their topological characteristics and taxonomical features

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ASV.no | Role | Niche breadth | C.score | Z.score | Node degree | Betweenness | Assigned module ID | Phylum | Class | Order |
| ASV00009 | Connector | Generalist | 0.7 | -0.8 | 3 | 807.029 | T\_Module IV | Acidobacteriota | Acidobacteriae | Acidobacteriae Subgroup 2 |
| ASV00072 | Connector | Generalist | 0.7 | -0.7 | 6 | 1108.236 | T\_Module IV | Actinobacteriota | Thermoleophilia | Gaiellales |
| ASV00225 | Connector | Generalist | 0.6 | 0.7 | 22 | 10581.9 | T\_Module IV | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00383 | Connector | Common taxa | 0.7 | -0.7 | 6 | 9569.996 | T\_Module V | Chloroflexi | Ktedonobacteria | Ktedonobacterales |
| ASV00800 | Connector | Common taxa | 0.7 | -0.5 | 7 | 1271.356 | T\_Module III | Chloroflexi | Ktedonobacteria | Ktedonobacterales |
| ASV00559 | Connector | Common taxa | 0.6 | -0.6 | 4 | 1437.69 | T\_Module III | Acidobacteriota | Vicinamibacteria | Vicinamibacterales |
| ASV00147 | Module hub | Generalist | 0.1 | 2.6 | 109 | 11690.94 | T\_Module I | Acidobacteriota | Holophagae | Holophagae Subgroup 7 |
| ASV00038 | Module hub | Generalist | 0.5 | 3.7 | 62 | 25285.63 | T\_Module IV | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00008 | Module hub | Generalist | 0.1 | 3.0 | 38 | 45877.65 | T\_Module V | Proteobacteria | Gammaproteobacteria | WD260 |
| ASV00110 | Module hub | Common taxa | 0.2 | 4.1 | 52 | 28366.95 | T\_Module V | Proteobacteria | Alphaproteobacteria | Acetobacterales |
| ASV00130 | Module hub | Common taxa | 0.4 | 3.4 | 54 | 7421.026 | T\_Module V | Acidobacteriota | Acidobacteriae | Acidobacteriae Subgroup 2 |
| ASV00142 | Module hub | Common taxa | 0.1 | 2.5 | 109 | 8929.401 | T\_Module II | Acidobacteriota | Acidobacteriae | Acidobacteriales |
| ASV00255 | Module hub | Common taxa | 0.4 | 3.4 | 59 | 8637.462 | T\_Module VI | Acidobacteriota | Acidobacteriae | Bryobacterales |
| ASV00344 | Module hub | Common taxa | 0.1 | 3.0 | 121 | 14192.44 | T\_Module I | Acidobacteriota | Acidobacteriae | Bryobacterales |
| ASV00191 | Module hub | Common taxa | 0.1 | 2.6 | 107 | 14569.8 | T\_Module I | Proteobacteria | Gammaproteobacteria | Burkholderiales |
| ASV00928 | Module hub | Common taxa | 0.1 | 2.9 | 114 | 7761.666 | T\_Module I | Proteobacteria | Alphaproteobacteria | Caulobacterales |
| ASV00259 | Module hub | Common taxa | 0.0 | 2.8 | 37 | 9506.318 | T\_Module III | Bacteroidota | Bacteroidia | Chitinophagales |
| ASV00751 | Module hub | Common taxa | 0.0 | 2.8 | 37 | 3640.511 | T\_Module III | Bacteroidota | Bacteroidia | Chitinophagales |
| ASV00213 | Module hub | Common taxa | 0.5 | 3.0 | 80 | 13643.65 | T\_Module VI | Verrucomicrobiota | Verrucomicrobiae | Chthoniobacterales |
| ASV00240 | Module hub | Common taxa | 0.5 | 4.6 | 54 | 35495.63 | T\_Module IV | Verrucomicrobiota | Verrucomicrobiae | Chthoniobacterales |
| ASV00551 | Module hub | Common taxa | 0.0 | 2.8 | 37 | 13788.13 | T\_Module III | Verrucomicrobiota | Verrucomicrobiae | Chthoniobacterales |
| ASV00115 | Module hub | Common taxa | 0.4 | 4.4 | 63 | 18667.25 | T\_Module V | Actinobacteriota | Actinobacteria | Frankiales |
| ASV00153 | Module hub | Common taxa | 0.0 | 3.0 | 118 | 7856.094 | T\_Module II | Actinobacteriota | Actinobacteria | Frankiales |
| ASV00465 | Module hub | Common taxa | 0.1 | 3.9 | 50 | 11495.19 | T\_Module III | Proteobacteria | Gammaproteobacteria | Gammaproteobacteria Incertae Sedis |
| ASV00601 | Module hub | Common taxa | 0.0 | 3.3 | 124 | 14771.11 | T\_Module I | Gemmatimonadota | Gemmatimonadetes | Gemmatimonadales |
| ASV00632 | Module hub | Common taxa | 0.4 | 4.5 | 74 | 40610.88 | T\_Module III | Proteobacteria | Gammaproteobacteria | JG36-TzT-191 |
| ASV00148 | Module hub | Common taxa | 0.1 | 2.6 | 25 | 17313.46 | T\_Module IV | Chloroflexi | Ktedonobacteria | Ktedonobacterales |
| ASV00216 | Module hub | Common taxa | 0.0 | 2.6 | 23 | 3420.31 | T\_Module IV | Chloroflexi | Ktedonobacteria | Ktedonobacterales |
| ASV00234 | Module hub | Common taxa | 0.0 | 3.1 | 120 | 6411.158 | T\_Module II | Chloroflexi | Ktedonobacteria | Ktedonobacterales |
| ASV00256 | Module hub | Common taxa | 0.0 | 2.7 | 108 | 3552.733 | T\_Module II | Chloroflexi | Ktedonobacteria | Ktedonobacterales |
| ASV00070 | Module hub | Common taxa | 0.0 | 4.5 | 159 | 29082.51 | T\_Module I | Actinobacteriota | Acidimicrobiia | Microtrichales |
| ASV00041 | Module hub | Common taxa | 0.5 | 2.9 | 62 | 64912.5 | T\_Module V | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00251 | Module hub | Common taxa | 0.2 | 3.7 | 47 | 14075.61 | T\_Module V | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00287 | Module hub | Common taxa | 0.5 | 2.7 | 41 | 13295.99 | T\_Module IV | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00292 | Module hub | Common taxa | 0.0 | 3.9 | 141 | 17162.91 | T\_Module I | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00326 | Module hub | Common taxa | 0.1 | 2.7 | 39 | 26386.5 | T\_Module III | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00367 | Module hub | Common taxa | 0.0 | 2.6 | 107 | 5554.266 | T\_Module II | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00626 | Module hub | Common taxa | 0.1 | 2.5 | 103 | 9771.259 | T\_Module I | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00829 | Module hub | Common taxa | 0.4 | 2.6 | 30 | 7938.818 | T\_Module IV | Proteobacteria | Alphaproteobacteria | Rhizobiales |
| ASV00166 | Module hub | Common taxa | 0.2 | 3.5 | 48 | 132101.8 | T\_Module III | Planctomycetota | Phycisphaerae | Tepidisphaerales |
| ASV01652 | Module hub | Common taxa | 0.0 | 3.9 | 48 | 29742.9 | T\_Module III | Planctomycetota | Phycisphaerae | Tepidisphaerales |
| ASV01918 | Module hub | Common taxa | 0.1 | 3.0 | 42 | 6017.626 | T\_Module III | Planctomycetota | Phycisphaerae | Tepidisphaerales |
| ASV00616 | Module hub | Common taxa | 0.3 | 2.9 | 31 | 8710.969 | T\_Module IV | Chloroflexi | Gitt-GS-136 | unclassified Gitt-GS-136 |
| ASV00218 | Module hub | Common taxa | 0.5 | 4.0 | 76 | 24719.29 | T\_Module VI | Chloroflexi | TK10 | unclassified TK10 |
| ASV00446 | Module hub | Common taxa | 0.2 | 5.4 | 72 | 26855.36 | T\_Module III | Acidobacteriota | Vicinamibacteria | Vicinamibacterales |
| ASV00138 | Module hub | Specialist | 0.5 | 2.6 | 60 | 8631.699 | T\_Module VI | Chloroflexi | Ktedonobacteria | Ktedonobacterales |
| ASV00922 | Module hub | Specialist | 0.1 | 2.6 | 24 | 2422.926 | T\_Module IV | Chloroflexi | Ktedonobacteria | Ktedonobacterales |
| ASV00903 | Module hub | Specialist | 0.1 | 3.2 | 29 | 5285.609 | T\_Module IV | Chloroflexi | AD3 | unclassified AD3 |



**Figure S1** The distribution of the niche breadth (B) values of the ASVs. A B-value of >78 was chosen as a criterion for generalists as this value lies within the outlier area of the B-value distribution, while ASVs with B-values of <22 were regarded as specialists (lower quartile).



**Figure S2** Shannon diversity index of the nine different sampling sites in Salluit, Nunavik.



**Figure S3** (A) The relative abundance of Generalist, Common taxa, and Specialist modules in the total network module. (B) Composition of major modules.



**Figure S4.** Spearman's rank correlation matrix between the variables including the distribution patterns of individual modules and environmental parameters. The colors of the scale bar represent Spearman's correlation coefficient (*ρ*).