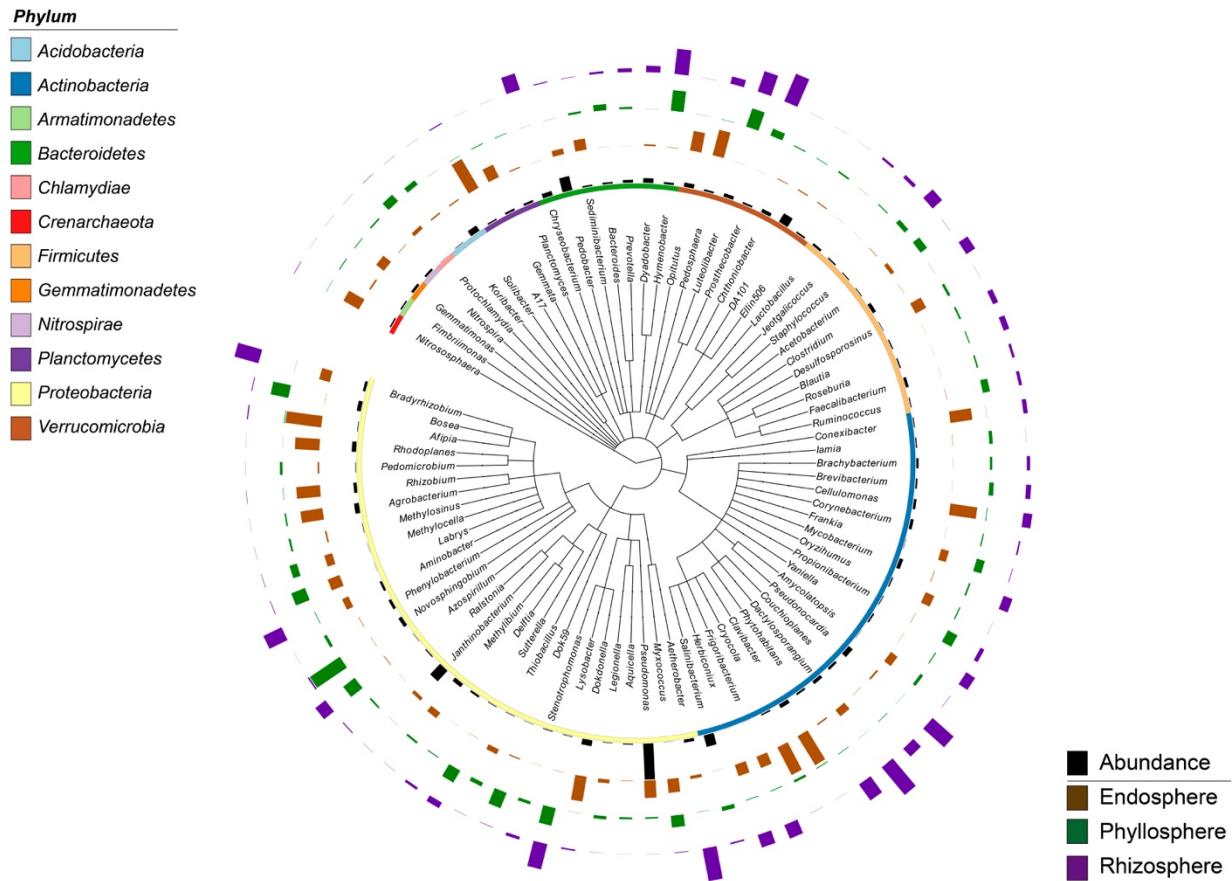


**Supplementary Table S1.** Distribution of shared and unique operational taxonomic units (OTUs) among bacterial communities in the endosphere (E), phyllosphere (P) and rhizosphere (R) of two Antarctic vascular plants, based on high-throughput DNA sequencing data in each plant species ( $n=4$ ).

| Taxa (phylum)          | <i>Deschampsia antarctica</i> |    |             | <i>Colobanthus quitensis</i> |             |    |             |     |
|------------------------|-------------------------------|----|-------------|------------------------------|-------------|----|-------------|-----|
|                        | Shared OTUs                   |    | Unique OTUs |                              | Shared OTUs |    | Unique OTUs |     |
|                        | E                             | P  | R           | E                            | R           | R  |             |     |
| p_unclassified         |                               |    | 3           |                              |             |    | 1           |     |
| <i>Acidobacteria</i>   | 64                            | 2  | 9           | 374                          | 23          | 2  | 37          | 359 |
| <i>Actinobacteria</i>  | 196                           | 88 | 82          | 211                          | 157         | 48 | 138         | 197 |
| AD3                    |                               |    |             | 5                            |             |    |             | 7   |
| <i>Armatimonadetes</i> | 3                             | 1  | 2           | 40                           | 3           | 3  | 49          |     |
| <i>Bacteroidetes</i>   | 198                           | 15 | 87          | 294                          | 97          | 66 | 147         | 223 |
| BHI80-139              |                               |    |             | 2                            |             |    |             | 1   |
| BR1C1                  |                               |    |             | 3                            |             |    | 1           | 2   |
| <i>Chlamydiae</i>      |                               |    |             | 2                            |             |    | 1           | 5   |
| <i>Chlorobi</i>        | 2                             |    |             | 7                            | 15          | 1  | 1           | 4   |
| <i>Chloroflexi</i>     | 28                            | 2  | 3           | 48                           |             | 12 | 55          |     |
| <i>Crenarchaeota</i>   | 2                             |    |             | 1                            |             | 1  |             | 4   |
| <i>Cyanobacteria</i>   | 4                             | 3  | 2           | 16                           | 5           | 6  | 19          |     |
| <i>Elusimicrobia</i>   |                               |    | 1           | 15                           |             |    |             | 17  |

|                         |     |     |     |     |     |     |     |
|-------------------------|-----|-----|-----|-----|-----|-----|-----|
| <i>Euryarchaeota</i>    |     |     | 7   |     |     |     | 1   |
| FBP                     | 4   |     | 3   | 1   | 2   | 5   | 9   |
| <i>Fibrobacteres</i>    | 1   |     | 2   | 73  | 1   |     | 2   |
| <i>Firmicutes</i>       | 14  | 268 | 28  | 2   | 11  | 227 | 84  |
| <i>Fusobacteria</i>     |     |     |     | 45  |     |     | 7   |
| <i>Gemmatimonadetes</i> | 11  | 1   | 2   | 2   | 9   |     | 7   |
| <i>Lentisphaerae</i>    |     |     | 1   |     |     |     |     |
| <i>Nitrospirae</i>      | 3   |     |     | 7   |     |     | 2   |
| NKB19                   |     |     | 1   |     |     |     |     |
| OD1                     | 1   |     |     | 15  |     |     | 19  |
| OP11                    |     |     |     | 4   |     |     | 5   |
| OP3                     |     |     |     | 4   |     |     | 8   |
| <i>Planctomycetes</i>   | 25  | 9   | 6   | 181 | 13  | 3   | 10  |
| <i>Proteobacteria</i>   | 482 | 123 | 213 | 952 | 309 | 94  | 275 |
| <i>Spirochaetes</i>     |     |     |     |     |     |     | 1   |
| SR1                     |     |     |     | 1   |     |     | 1   |
| <i>Tenericutes</i>      |     | 1   | 1   |     |     |     |     |
| <i>Thermi</i>           | 3   |     | 1   | 2   |     | 1   | 2   |
| TM6                     |     |     |     | 11  |     |     | 11  |
| TM7                     | 16  | 2   | 11  | 29  | 7   | 1   | 7   |
| <i>Verrucomicrobia</i>  | 51  | 2   | 17  | 117 | 26  |     | 19  |
| WPS-2                   | 1   |     |     | 9   |     | 4   | 21  |

|           |       |       |       |               |
|-----------|-------|-------|-------|---------------|
| WS2       |       | 3     |       | 1             |
| WS3       |       | 3     |       | 4             |
| Sub-total | 517   | 472   | 2,489 |               |
|           |       |       |       | 447 764 2,292 |
| Total     | 1,109 | 3,478 | 678   | 3,503         |



**Figure S1.** Indicator tree showing the taxonomy and taxon-treatment-association strength of 84 microbial genera significantly ( $q < 0.1$ ) associated with different compartments within Antarctic plants. Colors within the inner circle identify phyla. Heights of black bars in the innermost ring represent the square-root transformed abundances of the corresponding genera in the overall community. Heights of the colored bars on the remaining rings represent the relative, significant, association-strength ( $q < 0.1$ ) between the corresponding genera and the different compartments in Antarctic plants.