Table S1: Statistics for the sequenced *A. subglaciale*-related genomes.

|                              | I   | J   | K   | L   | M   | N   | O   |
|------------------------------|-----|-----|-----|-----|-----|-----|-----|
| Genome assembly size (Mb)    | 47.65 | 47.45 | 25.42 | 25.39 | 52.91 | 52.46 | 55.34 |
| GC content (%)               | 49.96 | 49.96 | 51.11 | 51.10 | 50.29 | 50.20 | 50.18 |
| CDS total length (Mb)        | 18.15 | 17.96 | 13.15 | 13.15 | 25.98 | 25.31 | 26.45 |
| CDS total length (% of genome)| 38.09 | 37.86 | 51.72 | 51.80 | 49.09 | 48.24 | 47.79 |
| Predicted genes (n)          | 15073 | 14923 | 8477 | 8451 | 16948 | 16484 | 17264 |
| Gene average length (bp)     | 1294 | 1295 | 1670 | 1677 | 1652 | 1653 | 1650 |
| Number of exons (n)          | 34285 | 34061 | 22220 | 22111 | 44194 | 42951 | 44981 |
| Exons per gene (average)     | 2.27 | 2.28 | 2.62 | 2.62 | 2.61 | 2.61 | 2.61 |
| Number of intron (n)         | 19212 | 19138 | 13743 | 13660 | 27246 | 26467 | 27717 |
| Intron average length (bp)   | 72   | 72   | 76   | 77   | 76   | 75   | 75   |

Figure S1: "The intergenomic distances have been calculated with Dashing as described by Gostinčar (2020) using a k-mer length 20."