**Supplementary material**

**Supplementary Table S1. Summary statistics for genome sequence assemblies.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Strain** | **Assembly accession number** | **Number of contigs** | **Total length (bp)** | **Number of genes** | **Contig N50 (bp)** |
| 782WT | GCA\_013325855.1 | 63 | 2,118,254 | 2,187 | 179,804 |
| 782R1 | GCA\_013328665.1 | 58 | 2,078,071 | 2,118 | 179,177 |
| 782R2 | GCA\_013373665.1 | 26 | 2,064,053 | 2,091 | 193,286 |
| 782R3 | GCA\_013325805.1 | 37 | 2,069,229 | 2,101 | 193,286 |
| B761 | GCA\_013328715.1 | 60 | 2,117,022 | 2,188 | 179,804 |
| BGNM1 | GCA\_013303115.1 | 127 | 5,354,843 | 5,565 | 934,258 |

Draft genome sequences of *S. agalactiae* B782WT, B782R1, B782R2, B782R3 and B761 have been deposited at the NCBI GenBank database under accession numbers: GCA\_013325855.1, GCA\_013328665.1, GCA\_013373665.1, GCA\_013325805.1 and GCA\_013328715.1, respectively. The genome of *B. cereus* BGNM1 was deposited under accession number GCA\_013303115.1 (Table 3). Genome sequences of *S. agalactiae* strains were approximately 2 Mb in size (2,118,254 bp -B782WT, 2,078,071 bp -B782R1, 2,064,053 bp-B782R2, 2,069,229 bp -B782R3 and 2,117,022 bp- B761), while the genome of *B. cereus* was around 5 Mb (5,354,843 bp). Comparative analyses of *S. agalactiae* B782WT with thusin resistant mutants (B782R1, B782R2 and B782R3) revealed that there are differences in both genome size and consequently in the numbers of predicted genes, where mutant strains had a lower number of contigs and coding genes (Supplementary Table S1).