…TCGTTCCTCTAGATTTCAAGCTGTGCACGATTTCGTTCATTCTGGCTTCGATTGGTATGTCCTGTCTTGTAATTGTTG
TTTCCATCGGCCTGTTTATTTTTTTGCGTTTCAGCACTTTTTGAAAAGCTCCGATCATATCATAGACCGTGACAGAGAG
CTTTTGCTCAGACTGTTTTACTTCTTTTGCATATTCACTCAAATCACTCGGCGGTTTCGTGAACGATTTTTGTCTTTCT
TCTTCCCGTTCTTTTAAATCCTTCGCCGCATCTTTATATTTTTCGGTACTCAATCAGCTTTTCAATCAGTTCCTCCCGCG
GATCTTCTTCTTCAAGTAATTCATCTTCAAAAAGCTCCTCCTCTTGCTTCGGGAGCAGCATTCTGCTTTTAATGCTGAG
CAGCGTGGCAGCCATAACCAAATACTCGCTGGCAATGTCGAGCTCAAGCACGCGCATCGTATGTACATATAATAAATAT
TGTTCAGTGATCTTCGCCACAGGTATCATATATGTCAATTTCAAGACGATTGATTAAATGAAGCAGCAGGTCCAATG
GGCCCTCAAACGTATCAATTTTCACTTGATATTCTTCCATCATCTCACCATTTTCAAGTATCACTCTCATTGCCGGAAA
AACTGGCTACCCTATAGTATAAGCCACCAAAAAGCTCTCGTCCAATACTATTTCATATCCTGTTTTGAAGGAGTTTGTA
CAGAATATTCAAAACACAAGAGGTGTTTGCTCGGAGCGCAGAAGCGGGAGAAAAAGCCTTTGCTTCTGGTTTTCCTTTC
TAAGAAGCACTAGAGGCCGGGCGTTCTTTTTTTCCTTTTATCCCTTCTATGGTACACTAAAAGCACATTAAAGGAGGAAG
CACCTTGTATCCGAAAGCTTATATAGATTATCTCGTTGAGTTTCATGCGACACGGGATTATTTTGAATGCCATGAAATA
TTAGAAGAATATTGGAAGGAAGATCCGCCAAAGAAACGAAAACGCTATTGGGTGGGCTTTATTCAGCTTGCAGTGGCTT
TATATCATCACAGAAGGCAGAATACAGCCGGGGCAAAAGACTGATGGCGAACAGCATCC…

Supplementary figure 1: Sequence of *B. subtilis* subsp. *subtilis* str. 168 genome sequence [Genbank:CP010052.1] corresponding to the region containing part of Contig00019 and Contig00022

There is a gap of 37 basepairs (uncoloured region in the figure) between Contig00019 (pink region in figure) and Contig00022 (yellow region in figure), when aligning the obtained contigs to *B. subtilis* subsp. *subtilis* str. 168 genome sequence [Genbank:CP010052.1]. PCR and sequence analysis were used to confirm that the genomic regions present on both contigs are indeed adjacent in the GM-*Bacillus* genome. Hereto, primers Scaf-19-F3-seq (positioned on Contig00019, indicated in green) and Scaf-22-R-seq (positioned on Contig00022, indicated in blue) were used to amplify the flanking regions of the junction between Contig00019 and Contig00022. Subsequently, the obtained PCR fragment was sequenced.