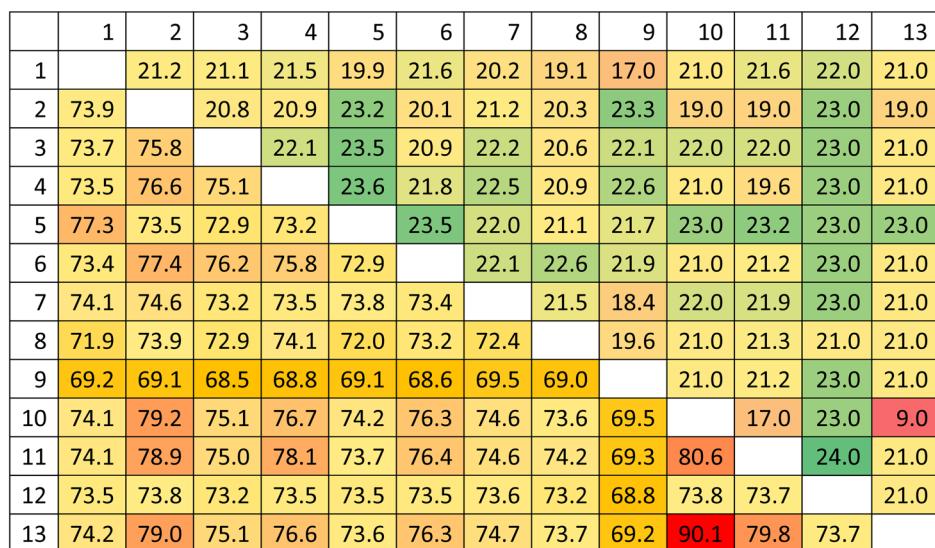**Supplementary Fig. 1.** Phylogenetic relationship based on the whole genome sequence of strain BRMEA1T and other *Neobacillus* strains using TYGS platform. The tree was inferred with FastMe 2.1.4 from GBDP distances calculated from genome sequences using formula d5. Leaf labels are annotated by affiliation to species (1) and subspecies clusters (2), genomic G+C content (3), δ values (4), overall genome sequence length (5), and numbers of proteins (6) (Meier-Kolthoff and Goker, 2019).

	1	2	3	4	5	6	7	8	9	10	11	12	13
1		21.2	21.1	21.5	19.9	21.6	20.2	19.1	17.0	21.0	21.6	22.0	21.0
2	73.9		20.8	20.9	23.2	20.1	21.2	20.3	23.3	19.0	19.0	23.0	19.0
3	73.7	75.8		22.1	23.5	20.9	22.2	20.6	22.1	22.0	22.0	23.0	21.0
4	73.5	76.6	75.1		23.6	21.8	22.5	20.9	22.6	21.0	19.6	23.0	21.0
5	77.3	73.5	72.9	73.2		23.5	22.0	21.1	21.7	23.0	23.2	23.0	23.0
6	73.4	77.4	76.2	75.8	72.9		22.1	22.6	21.9	21.0	21.2	23.0	21.0
7	74.1	74.6	73.2	73.5	73.8	73.4		21.5	18.4	22.0	21.9	23.0	21.0
8	71.9	73.9	72.9	74.1	72.0	73.2	72.4		19.6	21.0	21.3	21.0	21.0
9	69.2	69.1	68.5	68.8	69.1	68.6	69.5	69.0		21.0	21.2	23.0	21.0
10	74.1	79.2	75.1	76.7	74.2	76.3	74.6	73.6	69.5		17.0	23.0	9.0
11	74.1	78.9	75.0	78.1	73.7	76.4	74.6	74.2	69.3	80.6		24.0	21.0
12	73.5	73.8	73.2	73.5	73.5	73.5	73.6	73.2	68.8	73.8	73.7		21.0
13	74.2	79.0	75.1	76.6	73.6	76.3	74.7	73.7	69.2	90.1	79.8	73.7	

68.5 � 90.1

Supplementary Fig. 2. Pairwise heat map of ANI values (%, lower triangle) and dDDH (%, upper triangle) based on the whole genome of 13 type strains in the genus *Neobacillus*. Both ANI and dDDH are represented as percentage values. 1, *Neobacillus endophyticus* BRMEA1[T]; 2, *N. bataviensis* LMG 21833[T]; 3, *N. cucumis* DSM 101566[T]; 4, *N. drentensis* DSM 15600[T]; 5, *N. fumarioli* NBRC 102428[T]; 6, *N. jeddahensis* JCE[T]; 7, *N. mesonae* FJAT-13985[T]; 8, *N. niacin* DSM 2923[T]; 9, *N. notoginsengisoli* JCM 30743[T]; 10, *N. novalis* NBRC 102450[T]; 11, *N. soli* DSM 15604[T]; 12, *N. thermocopriae* SgZ-7[T]; 13, *N. vireti* DSM 15602[T]. The color-code heatmap displays the closest species in red and the farthest in green.