Table S1. Average amino acid identity (AAI) matrices of *Bacillus subtilis* subsp. *subtilis* str. 168^T, *Bacillus indicus* LMG 22858^T and strain SJS^T compared to representatives of other genera within the *Bacillaceae.*

Species designations shown in bold correspond to the type species of the genus. When a type strain genome was not available for a particular taxon, the 16S rRNA pairwise similarity of the strain shown and the type strain of the taxon is indicated. Matrices are shown in groups of 11 strains due to limitations in the SEED Viewer sequence-based comparison tool used to calculate AAI. Colour shade of the AAI value cells is derived from the conditional formatting tool of Microsoft Excel to facilitate recognition of high vs. low values.

Organism (genome accession)		**Average Amino Acid Identity (AAI)**									
***Bacillus subtilis* subsp. *subtilis* str. 168^T (NC_000964)**	**1**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Bacillus indicus LMG 22858^T (WGS:JGVU)	**2**	62.3									
strain SJS^T (WGS:JAVQ)	**3**	61.6	65.1								
***Aeribacillus pallidus* 8m3 (99.80%) (WGS:LWBR)**	**4**	61.1	62.9	61.7							
***Anoxybacillus pushchinoensis* K1^T (IMG:2654588147)**	**5**	61.6	63.4	62.2	64.3						
***Geobacillus stearothermophilus* ATCC 12980^T (WGS:JYNW)**	**6**	60.4	61.8	61.0	63.1	70.3					
***Caldibacillus debilis* DSM 16016^T (WGS:ARVR)**	**7**	57.2	57.8	57.4	59.5	60.8	60.8				
***Domibacillus robiginosus* WS 4628^T (WGS:LAHL)**	**8**	58.5	58.2	57.6	58.8	59.2	58.9	56.3			
***Terribacillus saccharophilus* DSM 21619^T (IMG:2636416060)**	**9**	56.0	54.0	54.3	54.4	56.3	55.6	53.4	54.9		
***Calditerricola satsumensis* JCM 14719^T (WGS:BBCF)**	**10**	54.4	55.2	54.8	55.4	57.4	58.1	55.3	53.9	52.4	
***Caldalkalibacillus thermarum* TA2.A1 (99.87%) (WGS:AFCE)**	**11**	53.7	54.6	54.0	55.1	57.1	56.3	53.9	52.9	51.2	58.7
***Bacillus subtilis* subsp. *subtilis* str. 168^T (NC_000964)**	**1**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Bacillus indicus LMG 22858^T (WGS:JGVU)	**2**	62.3									
strain SJS^T (WGS:JAVQ)	**3**	61.6	65.1								
Halolactibacillus miurensis JCM 19043 (100%) (WGS:BAXD)	**4**	53.3	53.4	53.2							
***Amphibacillus xylanus* NBRC 15112^T (NC_018704)**	**5**	53.2	52.4	52.8	62.8						
Gracilibacillus boraciitolerans JCM 21714^T (WGS:BAVS)	**6**	55.8	55.8	55.4	59.2	59.8					
Paraliobacillus sp. PM-2 (97.2%) (WGS:CTEI)	**7**	54.3	54.5	54.3	61.2	60.9	62.3				
***Pontibacillus chungwhensis* BH030062^T (WGS:AVBG)**	**8**	55.4	57.1	56.5	55.5	55.7	58.7	59.2			
Salimicrobium jeotgali MJ3^T (WGS:AMPQ)	**9**	54.2	54.9	54.4	55.6	55.7	58.2	58.2	60.5		
Thalassobacillus devorans MSP14 (99.73%) (WGS:AWXW)	**10**	55.4	57.2	56.4	56.3	57.0	59.9	60.7	63.7	64.0	
***Halobacillus halophilus* DSM 2266^T (NC_017668)**	**11**	54.5	56.2	55.4	55.1	56.0	59.1	59.0	63.4	65.4	67.3
***Bacillus subtilis* subsp. *subtilis* str. 168^T (NC_000964)**	**1**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Bacillus indicus LMG 22858^T (WGS:JGVU)	**2**	62.3									
strain SJS^T (WGS:JAVQ)	**3**	61.6	65.1								
Ornithinibacillus scapharcae TW25^T (WGS:AEWH)	**4**	54.4	55.4	54.8							
***Paucisalibacillus globulus* DSM 18846^T (WGS:AXVK)**	**5**	54.1	54.9	54.1	77.2						
Lentibacillus juripiscarius JCM 12147^T (WGS:BBCA)	**6**	58.7	58.9	58.4	68.6	68.3					
***Virgibacillus pantothenticus* DSM 26^T (WGS:LGTO)**	**7**	54.0	54.1	53.8	64.3	63.6	67.6				
***Oceanobacillus iheyensis* HTE831^T (NC_004193)**	**8**	53.5	54.4	54.0	62.8	62.1	65.6	63.6			
Sediminibacillus halophilus NSP9.3 (99.3%) (WGS:AWXX)	**9**	55.7	56.2	55.4	61.4	60.9	64.9	61.0	60.3		
***Piscibacillus salipiscarius* JCM 13188^T (WGS:BBCD)**	**10**	56.8	57.5	57.2	60.6	60.5	62.6	60.1	60.3	61.3	
***Alkalibacillus haloalkaliphilus* C5 (99.65%) (WGS:AKIF)**	**11**	53.6	54.2	53.9	57.1	56.7	60.9	56.8	56.7	57.8	68.8
***Bacillus subtilis* subsp. *subtilis* str. 168^T (NC_000964)**	**1**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
Bacillus indicus LMG 22858^T (WGS:JGVU)	**2**	62.3									
strain SJS^T (WGS:JAVQ)	**3**	61.6	65.1								
***Lysinibacillus boronitolerans* JCM 21713^T (WGS:JPVR)**	**4**	54.1	54.7	54.3							
***Viridibacillus arvi* DSM 16317^T (WGS:LILB)**	**5**	54.5	54.8	54.4	65.1						
Marinococcus halotolerans DSM 16375^T (WGS:ATVM)	**6**	53.4	53.6	52.9	50.6	50.4					
***Natribacillus halophilus* DSM 21771^T (IMG:2634166325)**	**7**	52.1	52.5	52.4	49.6	49.7	55.2				
***Salsuginibacillus kocurii* DSM 18087^T (WGS:ARIV)**	**8**	53.5	54.0	53.3	50.3	50.7	57.7	58.0			
***Alteribacillus bidgolensis* IBRC-M10614^T (IMG:2654587895)**	**9**	55.0	55.5	54.8	51.4	51.8	61.0	57.5	61.1		
***Halalkalibacillus halophilus* DSM 18494^T (WGS:AUHI)**	**10**	52.9	53.8	53.6	50.7	51.3	51.6	51.2	52.6	53.0	
***Hydrogenibacillus schlegelii* DSM 2000^T (WGS:JYFD)**	**11**	47.5	48.0	47.7	46.3	46.7	47.2	47.2	47.3	47.5	46.1