Fig. S1

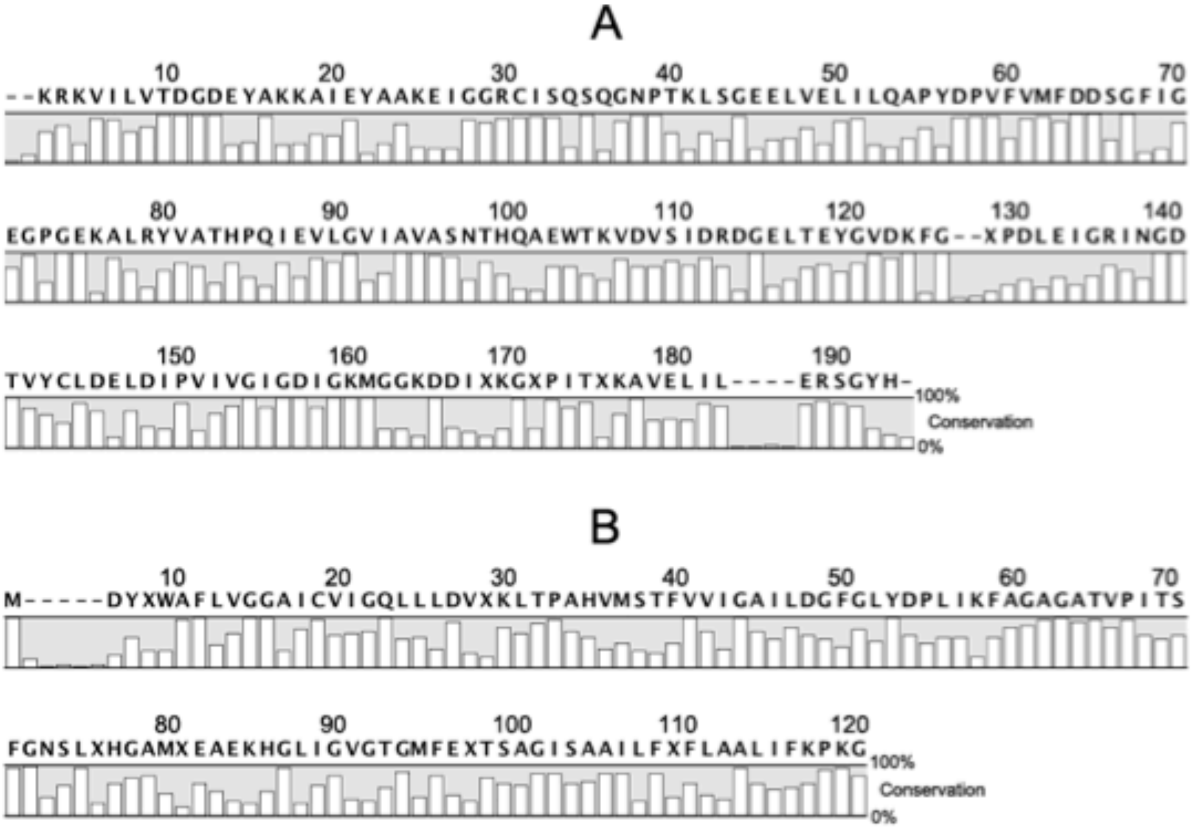

Fig. S1A,B. Conservation of the amino acid sequences of A) SpoVAEa and B) SpoVAEb in different species of the *Bacillales* and *Clostridiales* orders. Sequences of A) SpoVAEa and B) SpoVAEb in the genomes of species in the *Bacillales* and *Clostridiales* orders listed in Tables S1 and S2 were compared using the *B. subtilis* proteins' sequences shown in the figures as query sequences for an initial BLAST search on the NCBI genomic BLAST server; the translation initiating amino acid is shown for SpoVAEb but not shown for SpoVAEa, and is not taken into account in the numbering of residues. An alignment of the selected SpoVAEa and SpoVAEb homologs was performed using CLC

Main Workbench 6.9, and the conservation is shown in comparison to the *B. subtilis* sequences with relative levels of sequence conservation for each residue as shown.

Table S1. Species used in the alignment of SpoVAEa sequences.

Species	NCBI Reference Sequence
Alicyclobacillus acidocaldaruis	ZP_03493816.1
Anoxybacillus flavithermus	YP_002315371.1
Bacillus amyloliquefaciens	YP_003920831.1
Bacillus alcalophilus	EJS96865.1
Bacillus anthracis	PY_030226.1
Bacillus atrophaeus	YP_003973859.1
Bacillus azotoformans	ZP_11315037.1
Bacillus bataviensis	ZP_11307970.1
Bacillus cellulosilyticus	ADU30060.1
Bacillus cereus	EJV82262.1
Bacillus clausii	BAD64334.1
Bacillus coagulans	AEP02085.1
Bacillus coahuilensis	ZP_03226570.1
Bacillus cytotoxicus	ABS22997.1
Bacillus halodurans	BAB05261.1
Bacillus licheniformis	EID47371.1
Bacillus macauensis	EIT86505.1
Bacillus megaterium	YP_003564829.1
Bacillus mojavensis	ZP_10514755.1
Bacillus mycoides	EEL97907.1
Bacillus pseudofirmus	ADC51022.1
Bacillus pseudomycoides	EEM15492.1
Bacillus pumilus	ZP_03055607.1
Bacillus subtilis	ZP_03592104.1
Bacillus thuringiensis	ADY23232.1
Bacillus vallismortis	ZP_10507974.1
Brevibacillus laterosporus	EGP31866.1
Desmospora sp.	EGK14224.1
Geobacillus kaustophilus	YP_148156.1
Geobacillus thermodenitrificans	YP_001126327.1
Clostridium acetobutylicum	NP_348918.1
Clostridium clariflavum	YP_005045742.1
Clostridium arbusti	ZP_10773829.1
Clostridium thermocellum	EIC04841.1
Desulfotomaculum carboxydivorans	AEF94903.1
Acetonema longum	EGO63654.1

All species in this table contain both *spoVAEa* and *spoVAEb* genes.

Table S2. Species used in the alignment of SpoVAEb sequences

Species	NCBI Reference Sequence
*Alicyclobacillus hesperidum**	ZP_10953636.1
Amphibacillus xylanus	YP_006845536.1
*Anoxybacillus flavithermus **	YP_002315370.1
*Bacillus amyloliquefaciens **	YP_005130890.1
*Bacillus anthracis **	YP_002816854.1
*Bacillus cereus **	ZP_00236989.1
*Bacillus megaterium **	YP_003564830.1
*Bacillus thuringiensis **	YP_005567651.1
*Bacillus subtilis **	YP_003097759.1
*Geobacillus thermodenitrificans**	YP_001126328.1
*Clostridium acetobutylicum **	NP_348919.1
Clostridium botulinum	YP_001920241.1
Clostridium tetani	NP_782788.1
Clostridium perfringens	NP_562961.1
*Clostridium cellulovorans **	YP_003843610.1
Halobacillus halophilus	YP_006180964.1
*Geobacillus kaustophilus **	YP_146708.1
Kyrpidia tusciae	YP_003589673.1
*Geobacillus thermoleovorans **	YP_004983001.1
Lysinibacillus fusiformis	ZP_18168291.1
Oceanobacillus iheyensis	NP_692300.1
Ornithinibacillus scapharcae	ZP_08785617.1
Paenibacillus alvei	ZP_10865316.1
Paenibacillus curdlanolyticus	ZP_07385551.1
Solibacillus silvestris	YP_006463786.1
Thermobacillus composti	ZP_08919581.1

The asterisk indicates that these species contain both *spoVAEa* and *spoVAEb* genes, while species without an asterisk contain only *spoVAEb*.