

**Table S3** Distribution of SLH protein genes in genomes of *B. cereus* group strains

Strain	SH3_3	Transglut _core	LRR_RI	Peptidase	Peptidoglycan catabolism	Beta-lactam_ resistance	Adhesin	Ca++ binding	Big_5	NEAT	Rnases	T2SS-T3SS_pil_N	S-layer	other	unknown	total
<b>Ia</b>																
Bc_03BB108	0	1	0	0	8	2	0	1	0	2	0	0	2	1	9	26
Bt_4AJ1	0	1	0	0	8	1	0	1	0	2	1	0	2	0	10	26
Bt_4CC1	0	1	0	1	9	2	0	0	0	2	0	0	2	0	9	26
Ba_CNEVA-9066	1	1	1	0	8	1	1	1	0	1	0	0	2	0	8	25
Ba_Australia-94	1	1	1	0	7	1	1	1	0	1	0	0	2	0	8	24
Ba_Kruger-B	1	1	1	0	7	1	1	1	0	1	0	0	2	0	8	24
Ba_Vollum	1	1	1	0	7	1	1	1	0	1	0	0	2	0	8	24
Bc_03BB102	0	1	0	1	8	3	1	1	0	0	0	0	2	0	7	24
Bc_MSX-A12	0	1	0	0	6	1	0	1	1	2	1	0	2	0	9	24
Bt_4BA1	0	1	0	1	8	1	0	1	0	2	0	0	2	0	8	24
Ba_USA6153	1	1	1	0	7	1	1	1	0	0	0	0	2	0	8	23
Bc_6E1	0	1	0	1	8	2	0	1	0	1	0	0	2	0	7	23
Bc_AH820	0	1	0	0	7	1	0	1	0	2	1	0	2	0	8	23
Ba_Ames_Ancesor	0	1	0	0	7	1	1	1	0	1	0	0	2	0	8	22
Bc_CI	0	1	0	0	8	2	1	1	0	2	0	0	2	0	5	22
Bc_E33L	0	1	0	0	6	2	0	1	0	2	0	0	2	0	8	22
Ba_A1055	0	1	0	0	7	1	0	1	0	2	0	0	2	0	7	21
Ba_Ames	1	1	1	0	6	1	0	1	0	1	0	0	2	0	7	21
Ba_BF1	1	1	1	0	7	1	0	1	0	1	0	0	2	0	6	21
Ba_CDC-684	1	1	1	0	6	1	0	1	0	1	0	0	2	0	7	21
Ba_H9401	1	1	1	0	6	1	0	1	0	1	0	0	2	0	7	21
Ba_Sterne	1	1	1	0	6	1	0	1	0	1	0	0	2	0	7	21
Bc_ISP3191	0	1	0	0	7	1	0	1	0	2	0	0	2	0	7	21
Bt_Al_Hakam	0	1	0	0	7	2	0	1	0	2	0	0	2	0	6	21
Ba_A0442	0	1	0	0	6	1	1	1	0	1	0	0	2	0	7	20
Ba_A0465	0	1	0	0	6	1	1	1	0	1	0	0	2	0	7	20
Ba_UR-1	1	1	1	0	7	1	0	1	0	1	0	0	2	0	5	20
Bc_95_8201	0	1	0	0	7	1	0	0	0	2	0	1	2	0	6	20
Bc_Rock3_42	0	1	0	0	6	1	0	0	0	2	0	0	2	0	8	20

Ba_A0174	0	1	0	0	5	1	1	1	0	1	0	0	2	0	7	19
Ba_A0193	0	1	0	0	6	1	1	1	0	0	0	0	2	0	7	19
Ba_A0389	0	1	0	0	5	1	1	1	0	1	0	0	2	0	7	19
Ba_A0488	0	1	0	0	6	1	1	1	0	1	0	0	2	0	6	19
Ba_Tsiankovskii-I	0	1	0	0	6	1	0	1	0	1	0	0	2	0	7	19
Ba_A0248	0	1	0	0	5	1	0	1	0	1	0	0	2	0	6	17
Bc_W	0	1	0	0	5	0	0	1	0	2	0	0	2	0	5	16
Bc_G9241	0	1	0	1	8	1	1	1	0	1	0	0	2	0	9	25
Bc_AH187	0	1	0	2	6	1	0	1	1	2	1	0	2	0	6	23
Bc_IS075	0	1	0	0	6	1	0	1	1	2	0	0	2	0	9	23
Bt_4Y1	0	1	0	0	7	2	0	1	0	2	0	0	2	0	8	23
Bc_BDRD_ST26	0	1	0	2	6	1	0	1	1	2	1	0	2	0	5	22
Bc_Q1	0	1	0	2	6	1	0	1	0	2	0	1	2	0	6	22
Bc_4342	0	1	0	0	7	2	0	0	0	2	0	0	1	0	8	21
Bc_AND1407	0	1	0	0	5	1	0	1	1	2	0	1	2	0	7	21
Bc_H3081.97	0	1	0	2	6	0	0	1	0	2	0	1	2	0	6	21
Bc_NC7401	0	1	0	0	6	1	0	1	1	2	0	0	2	0	7	21
Bt_YBT-020	0	1	0	1	7	2	0	1	0	2	0	0	2	0	5	21
Bc_MSX-D12	0	1	0	0	6	1	0	1	0	2	0	0	2	0	7	20
Bc_AH1271	0	1	0	0	7	1	0	1	0	2	0	1	2	0	4	19
Bc_m1293	0	1	0	1	6	1	0	1	0	2	0	0	2	0	5	19
Bc_VD045	0	1	0	0	10	0	0	0	0	1	0	0	0	1	5	19
Bc_FRI-35	0	1	0	0	6	1	0	1	0	2	0	0	2	0	5	18
Bc_VD102	0	1	0	0	6	1	0	1	0	2	0	0	2	0	5	18
Bc_10987	0	1	0	1	6	0	0	1	0	2	0	0	0	0	5	16
Bc_MSX-A1	0	1	0	0	6	0	0	0	0	2	0	0	0	1	3	13
<b>Ib</b>																
Bc_BAG1X1-3	0	2	0	0	8	1	0	0	0	2	0	0	1	1	6	21
Bc_BDRD_ST196	0	1	0	0	7	0	0	0	0	2	0	0	2	1	7	20
Bc_AH603	0	1	0	1	6	0	0	1	0	1	0	0	0	1	8	19
Bc_HuA2-4	0	1	0	0	7	0	0	1	0	2	0	0	2	0	6	19
Bc_AH1272	0	1	0	2	5	0	0	0	0	2	0	0	2	0	6	18
Bc_HuA2-1	1	1	0	0	6	0	0	1	0	2	0	0	1	0	5	18

Bc_VD078	0	1	0	0	5	0	0	1	0	2	0	0	2	0	7	18
Bc_AH621	0	1	0	0	5	1	0	0	0	2	0	0	1	1	5	16
Bc_AH1273	0	1	1	1	3	0	0	0	0	1	0	0	2	0	6	15
Bc_CER057	0	1	0	0	5	0	0	1	0	1	0	1	2	0	5	15
Bc_CER074	0	1	0	0	5	0	0	1	0	1	0	1	2	0	5	15
Bc_VD048	0	1	0	0	5	1	0	0	0	2	0	0	1	0	5	15
Bc_391_98	0	1	0	1	6	0	0	1	0	0	0	1	2	0	2	14
Bc_BAG3X2-1	0	1	0	1	5	0	0	0	0	2	0	0	0	0	5	14
Bc_VD107	0	1	0	1	3	0	0	0	0	0	0	0	0	0	4	9
<b>IIa</b>																
Bt_9727	0	1	0	0	5	1	0	1	0	2	0	0	0	0	9	19
Bc_BAG6X1-1	0	1	0	0	6	0	0	1	0	1	0	0	0	0	6	17
Bc_BAG2X1-2	0	1	0	0	6	0	0	1	0	1	0	0	0	0	7	16
Bc_MM3	0	1	0	0	5	0	0	1	0	1	0	0	0	0	7	15
Bc_R309803	0	1	0	1	4	0	0	1	0	1	0	0	0	0	6	14
<b>IIb</b>																
Bc_VD156	0	1	0	0	7	0	0	0	0	1	0	0	0	2	6	17
Bc_VD166	0	1	0	0	8	0	0	0	0	1	0	0	0	0	6	16
Bc_VD169	0	1	0	0	8	0	0	0	0	1	0	0	0	0	6	16
Bc_AH1134	0	1	0	0	8	0	0	0	0	1	0	0	0	0	5	15
Bc_BAG6X1-2	0	1	0	0	4	0	0	0	1	2	0	0	1	0	6	15
Bc_VD022	0	1	0	0	8	0	0	0	0	1	0	0	0	0	5	15
Bc_BAG4X12-1	0	1	0	0	7	2	0	0	0	1	0	0	0	0	3	14
Bc_VD014	0	1	0	0	6	0	0	0	0	1	0	0	0	0	5	14
Bt_IBL_200	0	1	0	0	8	0	0	0	0	1	0	0	0	0	4	14
Bt_10792	0	1	0	0	5	0	0	0	0	1	0	0	0	0	6	13
Bt_4BD1	0	1	0	0	6	1	0	0	0	1	0	0	0	0	4	13
Bt_CT-43	0	1	0	0	5	0	0	0	0	1	0	0	0	0	5	13
Bc_10876	0	1	0	0	6	0	0	0	0	1	0	0	0	1	3	12
Bc_BAG3O-2	0	1	0	0	7	0	0	0	0	1	0	0	0	0	3	12
Bc_BAG4O-1	0	1	0	0	7	0	0	0	0	1	0	0	0	0	3	12
Bc_F65185	0	1	0	0	5	0	0	0	0	1	1	0	0	0	4	12
Bc_HuB1-1	0	1	0	0	7	0	0	0	0	1	1	0	0	0	2	12

Bc_VD142	0	1	0	0	6	0	0	1	0	2	0	0	0	0	2	12
Bt_HD-771	0	1	0	0	7	0	0	0	0	1	0	0	0	0	3	12
Bt_IBL_4222	0	1	0	0	8	0	0	0	0	1	0	0	0	0	2	12
Bt_T01001	0	1	0	0	5	0	0	0	0	1	0	0	0	0	5	12
Bc_BAG1X1-2	0	1	0	0	6	0	0	0	0	1	1	0	0	0	2	11
Bc_BAG3X2-2	0	1	0	0	6	0	0	0	0	1	0	0	0	0	3	11
Bc_G9842	0	1	0	0	6	0	0	0	0	1	0	0	0	0	3	11
Bc_HD73	0	1	0	0	5	0	0	0	0	1	0	0	0	0	4	11
Bc_Rock1_15	0	1	0	0	6	0	0	0	0	1	0	0	0	0	3	11
Bt_T03a001	0	1	0	0	5	0	0	0	0	1	0	0	0	0	4	11
Bc_14579	0	1	0	0	6	0	0	0	0	1	0	0	0	0	2	10
Bc_172560W	0	1	0	0	6	0	0	0	0	1	0	0	0	0	2	10
Bc_AH676	1	1	0	0	4	0	0	0	0	1	0	0	0	0	3	10
Bc_B4264	0	1	0	0	6	0	0	0	0	1	0	0	0	0	2	10
Bc_BDRD_ST24	0	1	0	0	5	1	0	0	0	1	0	0	0	0	2	10
Bc_BDRD-Cer4	0	1	0	0	6	0	0	0	0	1	0	0	0	0	2	10
Bc_VD200	0	1	0	0	6	0	0	0	0	1	0	0	0	0	2	10
Bt_BMB171	0	1	0	0	5	1	0	0	0	1	0	0	0	0	2	10
Bt_Bt407	0	1	0	0	5	0	0	0	0	1	0	0	0	0	3	10
Bt_HD-789	0	1	0	0	6	0	0	0	0	1	0	0	0	0	2	10
Bc_m1550	0	1	0	0	5	0	0	0	0	1	0	0	0	0	2	9
Bc_VD154	0	1	0	0	5	0	0	0	0	1	0	0	0	0	2	9
Bt_35646	0	1	0	0	6	0	0	0	0	1	0	0	0	0	1	9
Bt_4AW1	0	0	0	0	3	0	0	1	0	2	0	0	0	0	3	9
Bt_T13001	0	1	0	0	5	1	0	0	0	0	0	0	0	0	2	9
Bc_BAG5X1-1	0	1	0	0	4	0	0	0	0	1	0	0	0	0	2	8
Bc_HuA4-10	0	1	0	0	4	0	0	0	0	1	0	0	0	0	2	8
Bc_NVH0597_99	0	0	0	1	2	0	0	1	0	1	0	0	0	0	3	8
Bt_T04001	0	1	0	0	4	0	0	0	0	0	0	0	0	0	3	8

**SH3\_3 domains:** are protein interaction domains that bind proline-rich ligands with moderate affinity and selectivity, preferentially to PxxP motifs.

**Transglut\_core:** Transglutaminase-like superfamily. This family includes animal transglutaminases and other bacterial proteins of unknown function

**LRR\_RI:** Leucine-rich repeats (LRRs), ribonuclease inhibitor (RI)-like subfamily.

**Peptidase:** including C39\_like , M60-like and M23-like Peptidases

**Peptidoglycan catabolism:** including PGRP, Peptidoglycan recognition proteins (PGRPs) are pattern recognition receptors that bind, and in certain cases, hydrolyze peptidoglycans (PGNs) of bacterial cell walls. MurNAc-LAA, N-acetylmuramoyl-L-alanine amidase or MurNAc-LAA (also known as peptidoglycan aminohydrolase, NAMLA amidase, NAMLAA, Amidase 3, and peptidoglycan amidase; EC 3.5.1.28) is an autolysin that hydrolyzes the amide bond between N-acetylmuramoyl and L-amino acids in certain cell wall glycopeptides. Glucosaminidase: This family includes Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase EC:3.2.1.96, as well as the flageller protein J, which has been shown to hydrolyse peptidoglycan.

**Beta-lactam\_resistance:** including Beta-lactamase, This family appears to be distantly related to pfam00905 and PF00768 D-alanyl-D-alanine carboxypeptidase. Lactamase\_B: Metal-dependent hydrolases of the beta-lactamase superfamily III

**Adhesin:** BslA,

**Ca<sup>++</sup> binding:** Excalibur calcium-binding domain, Extracellular Ca<sup>2+</sup>-dependent nuclease YokF from *Bacillus subtilis* and several other surface-exposed proteins from diverse bacteria are encoded in the genomes in two paralogous forms that differ by a ~45 amino acid fragment, which comprises a novel conserved domain.

**Big\_5:** Bacterial Ig-like domain. Uncharacterized protein, homolog of Cu resistance protein CopC

**NEAT:** NEAr Transport domain, a component of cell surface proteins. NEAr Transporter (NEAT) domain; used by pathogenic bacteria to to scavenge heme-iron from host hemoproteins. The NEAT domain is a component of cell surface proteins (iron regulated surface determinants, or Isd, such as IsdA and IsdC) in various gram-positive bacteria, and may be arranged in tandem repeats.

**RNases:** microbial\_RNases. Ribonucleases (RNAses) cleave phosphodiester bonds in RNA and are essential for both non-specific RNA degradation and for numerous forms of RNA processing. The alignment contains fungal RNases (U2, T1, F1, Th, Pb, N1, and Ms) and bacterial RNases (barnase, binase, RNase Sa) , the majority of which are guanyl specific and fungal ribotoxins.

**T2SS-T3SS\_pil\_N:** Pilus formation protein N terminal region

**S-layer protein:** Sap and EA1 proteins

**Other:** existing in less than 5 strains