

Supplemental Material

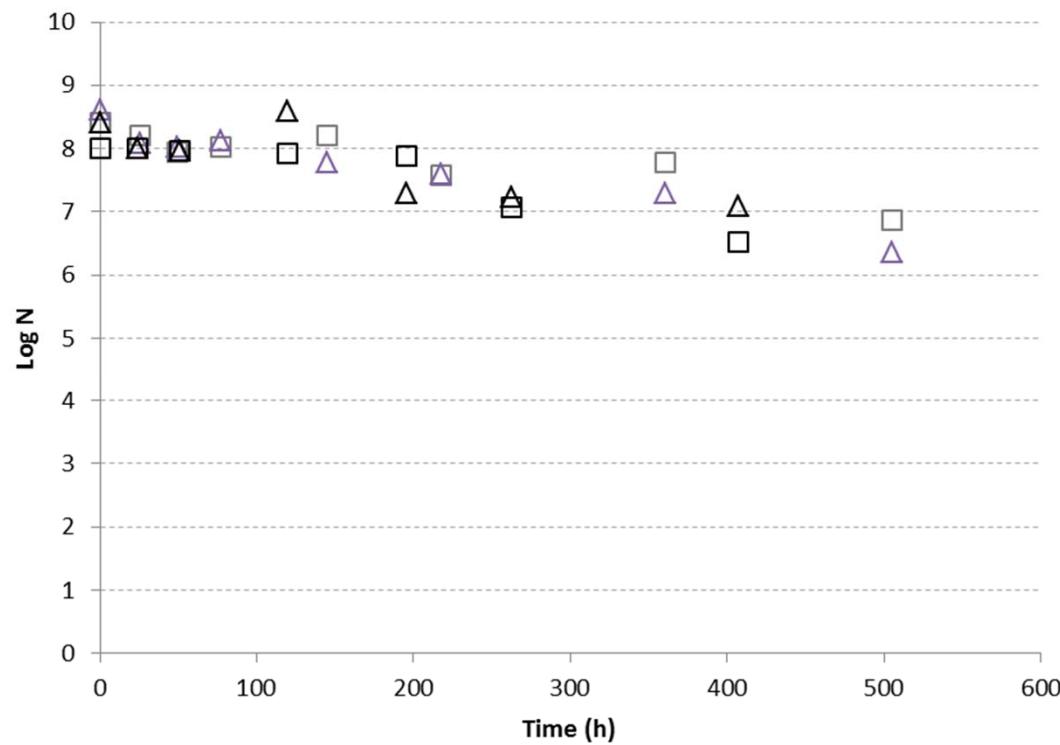
Table S1. Growth of WT and Δ BC_2216-17 mutant in various stressful conditions

Stress tested	Stress condition	Growth condition	Time to reach stationary phase for both strains	Conclusion for the 2 strains
high temperature	42°C	microplate	OD>1 in 3.5h	similar growth
	45°C	microplate	OD>1 in 4.5h	similar growth
	pH 5.5	microplate	OD>1 in 7h	similar growth
	pH 5.0	microplate	OD>1 in 12h	similar growth
acid (HCl supplementation)	pH 4.7	microplate	OD>1 in 32h	similar growth
	pH 8.5	microplate	OD>1 in 12h	similar growth
	pH 8.6	microplate	OD>1 in 13h	similar growth
Oxydative agent	100 μ M paraquat	microplate	OD>1.5 in 16h	similar growth
	150 μ M paraquat	microplate	OD>1.3 in 14h	similar growth
	AAPH 100mM	microplate	OD>1.2 in 12h	similar growth
	AAPH 150mM	microplate	OD>1.0 in 12h	similar growth
	0.020% H ₂ O ₂	microplate	OD>1 in 12h	similar growth
	0.025% H ₂ O ₂	microplate	OD>1 in 12h	similar growth
high osmolarity	4 % NaCl	microplate	OD>1 in 18h	similar growth
	6 % NaCl	microplate	OD>0.8 in 36h	similar growth
low osmolarity	0 % NaCl	flask	OD>1 in 4h	similar growth
	4%	flask	OD>1 in 3h	similar growth
Ethanol	6%	flask	OD>0.1 in 9h	similar growth
	EDTA 0.1mM	flask	OD>1 in 7h	similar growth
	EGTA 0.1mM	flask	OD>0.5 in 8h	similar growth
	2,2'-bipyridyl 100 μ M	flask	OD>0.2 in 5h	similar growth
Ions chelators	2,2'-bipyridyl 500 μ M	flask	OD>0.1 in 5h	similar growth

Growth in Erlenmeyer flasks was performed in 50ml LB at 37°C with shaking at 200rpm, after inoculation to an OD₆₀₀ of 0.01 by an overnight grown culture. OD₆₀₀ was measured in microcuvettes. Growth in microplates was performed in 250 μ l LB at 37°C with shaking, after inoculation by 10 μ l of an overnight grown culture in an automatic turbidimeter (see material & methods section). OD₆₀₀ was measured every 15 min.

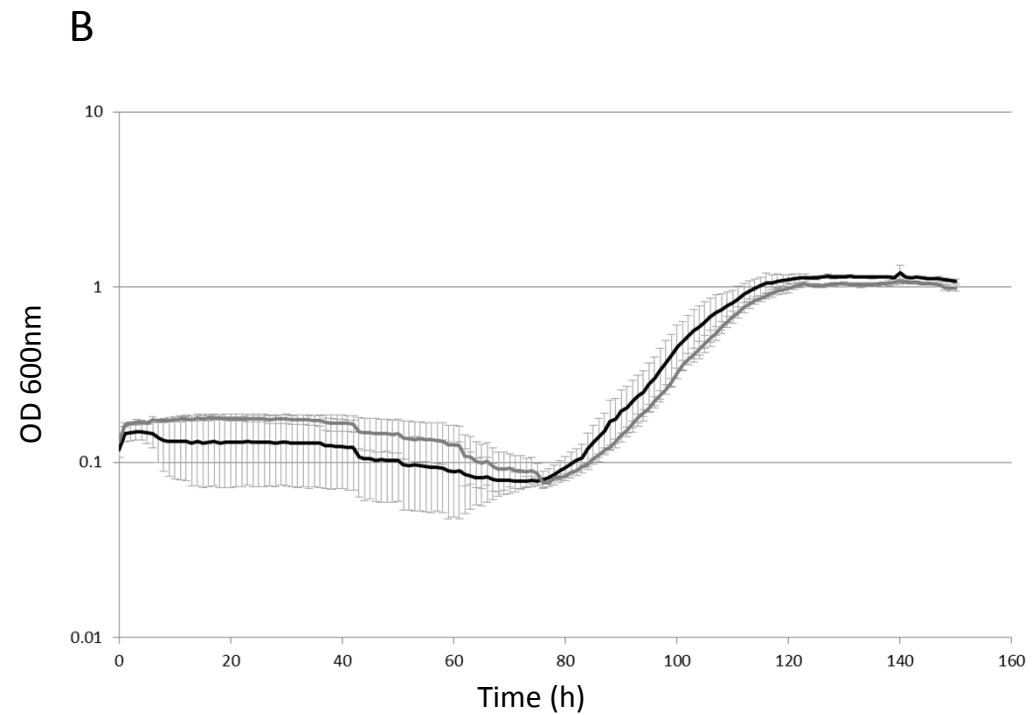
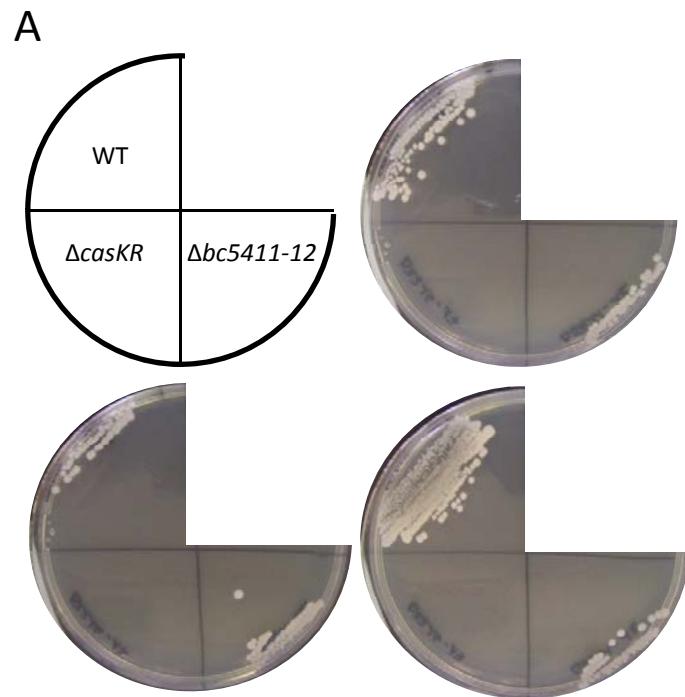
Temperature was set at 37°C, pH at 7.0, and NaCl concentration at 1%, unless stated differently.

Fig. S2 Survival of *B. cereus* WT and Δ *casKR* strains at 37°C



Bc WT (squares) and Δ *casKR* (triangles) bacterial suspension were incubated in LB at 37°C. Cfu numeration was performed regularly over time. Black and grey represent data from replicates 1 and 2, respectively.

Fig. S3. The Δ BC_5411-12 mutant can grow at low temperature

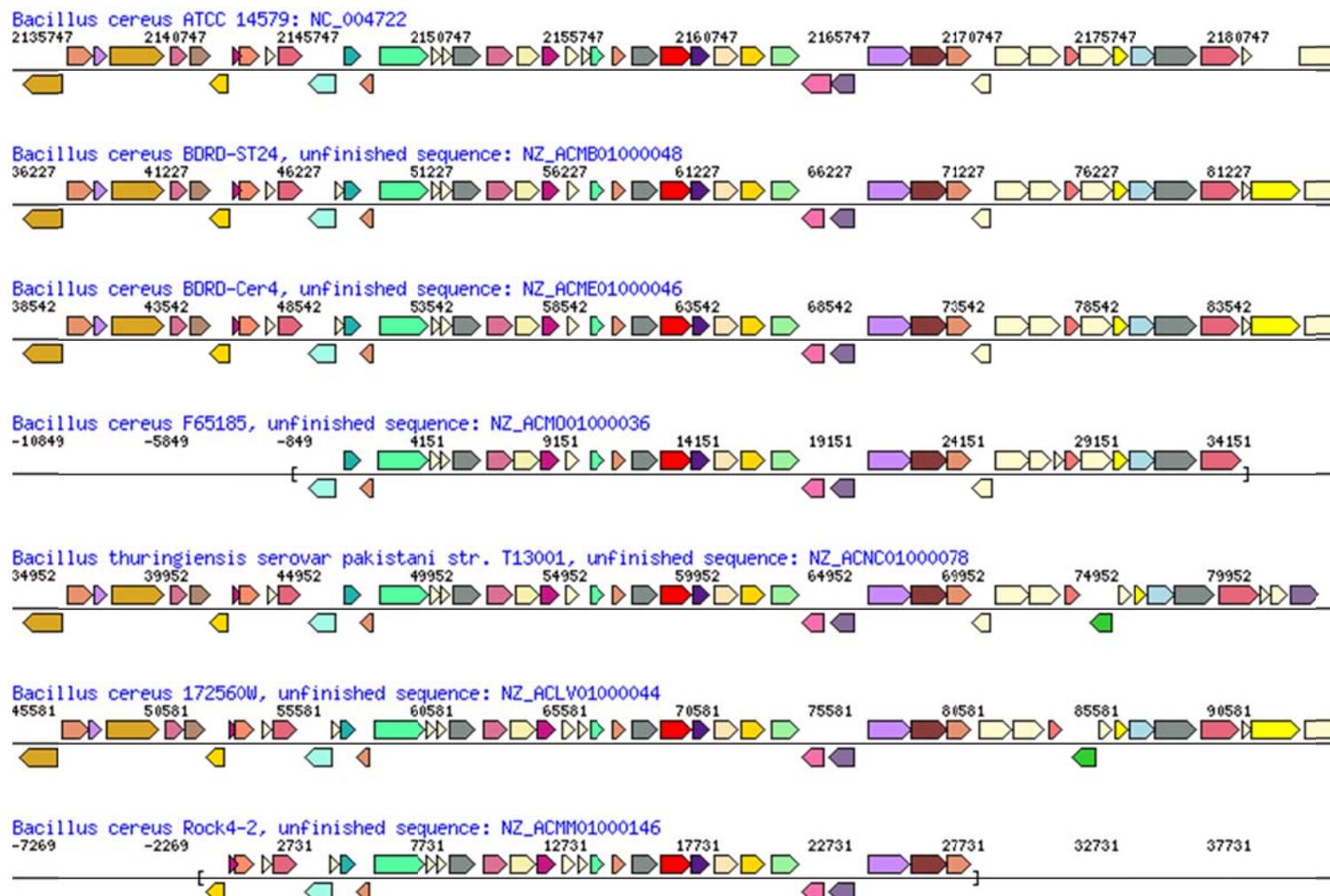


A. The Δ BC_5411-12 mutant can grow at T_{min} . One colony of overnight grown culture of *B. cereus* WT, Δ BC_5411-12 and Δ casKR was struck on LB agar and incubated at 10°C for 14 days. Three independent replicates are shown.

B. The Δ BC_5411-12 mutant can grow at 12°C, similarly as the WT strain. Growth of WT (black) and Δ BC_5411-12 (grey) strains was performed in an automated turbidimeter with shaking at 12°C. Mean values +/- SD of three biological replicates are shown.

Fig. S4. Graphic display of *casKR* Orthologs and Neighborhood genes in the *B. cereus* Group (*sensu lato*).

Orthologs of *casKR* genes (*bc2216-17*) and their neighborhoods in all available genomes are shown below, using Conserved Neighborhood Viewer of Integrated Microbial Genomes (Markowitz et al., 2012). Genes of the same color (except light yellow) are from the same cluster of orthologous gene (COG). Light yellow: no COG assignment; Red/Blue: *casKR* orthologs.

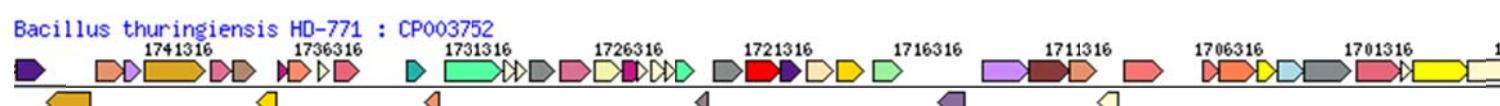
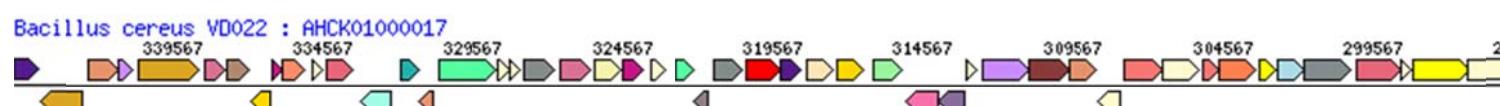
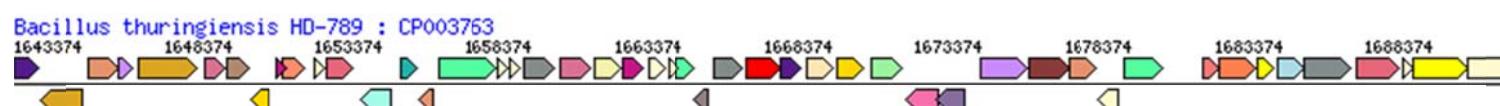
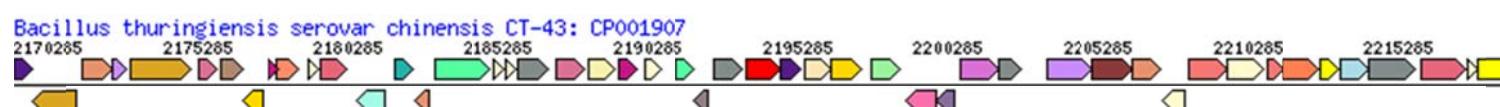
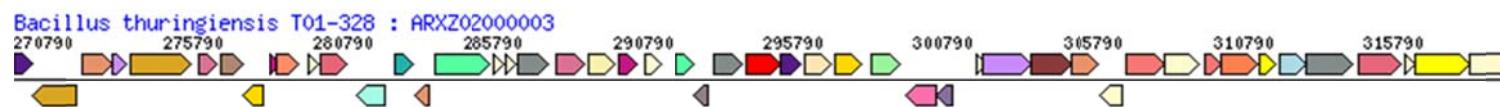
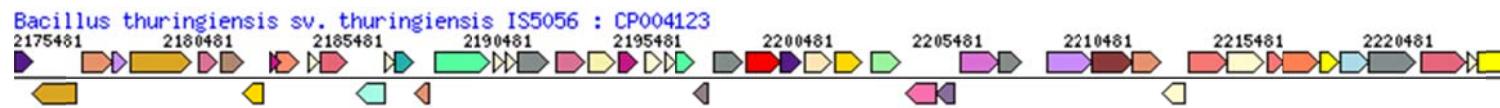
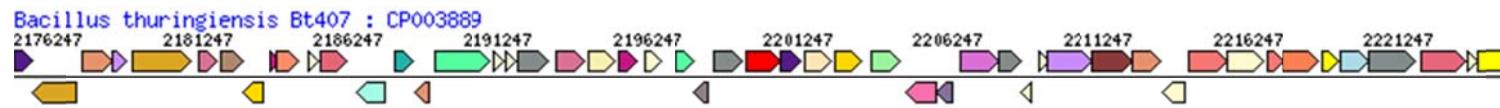


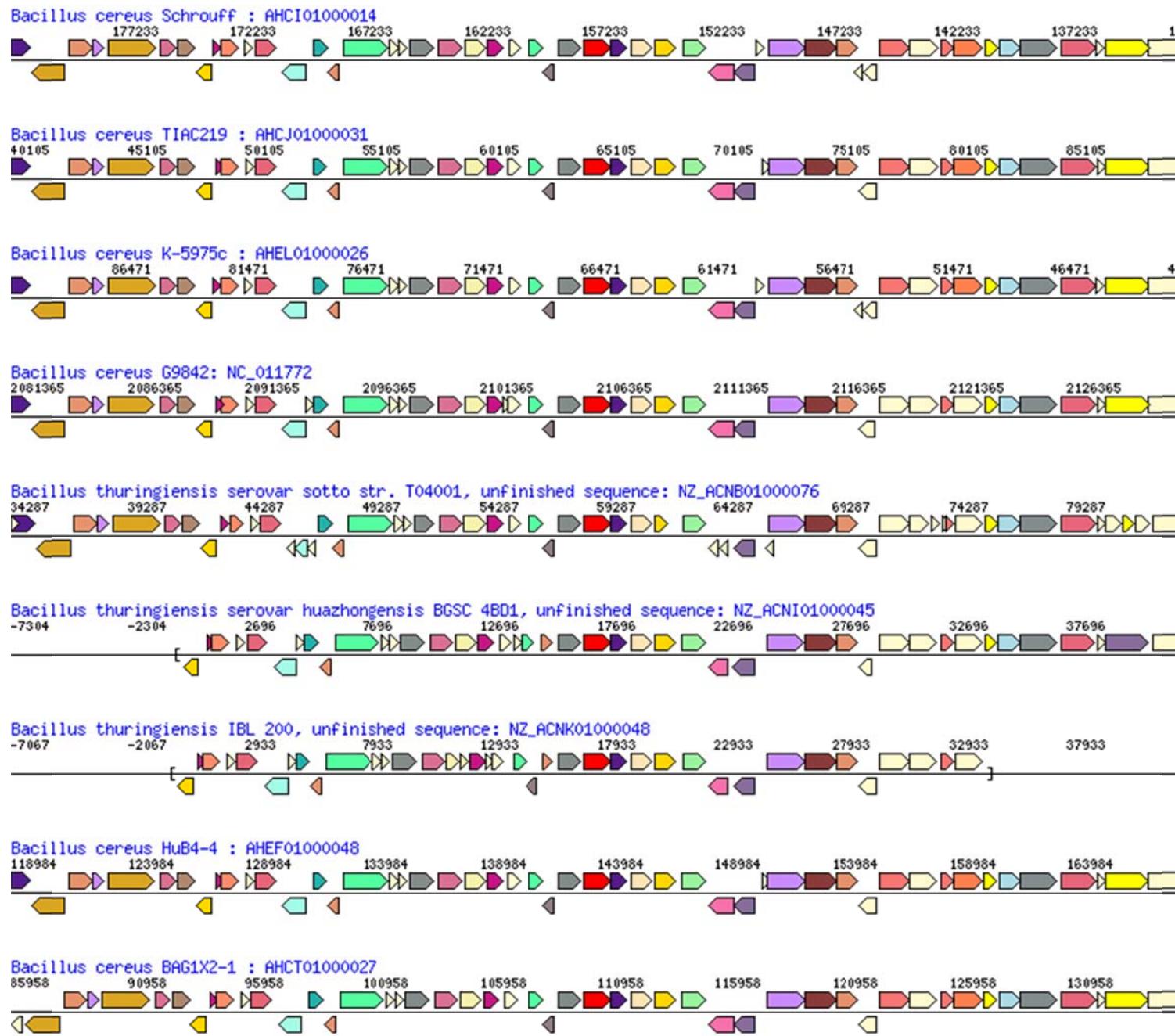


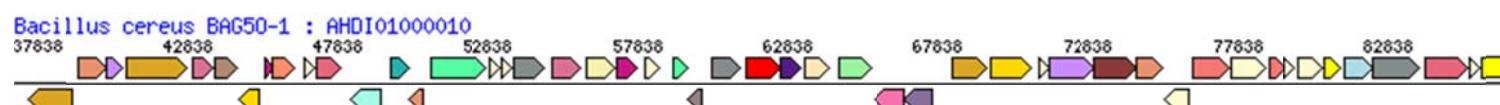
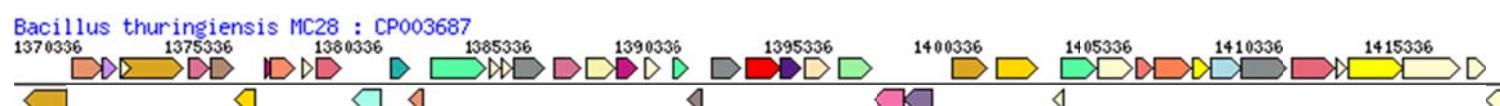
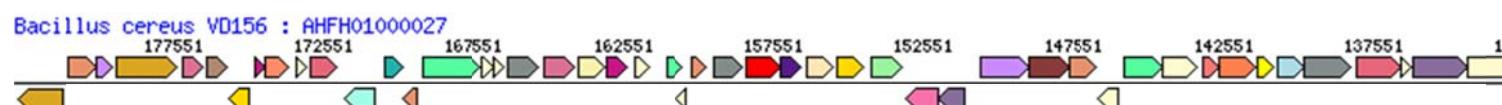
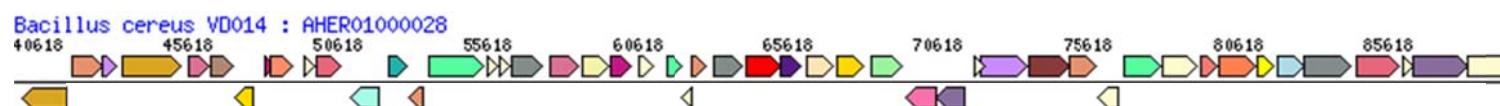
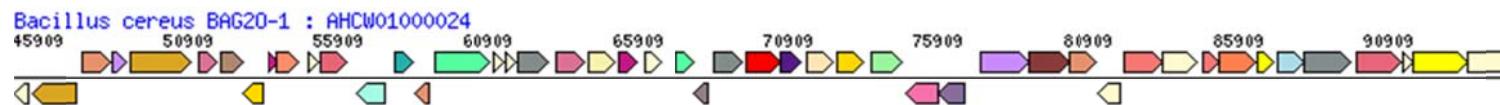
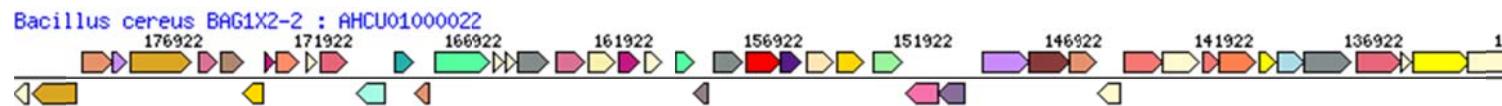
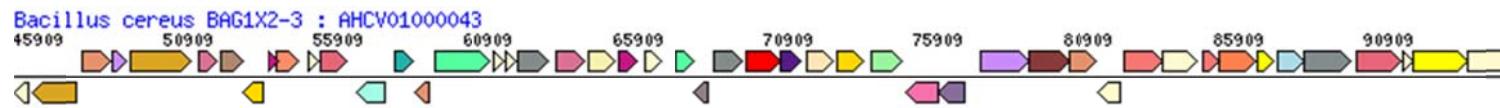








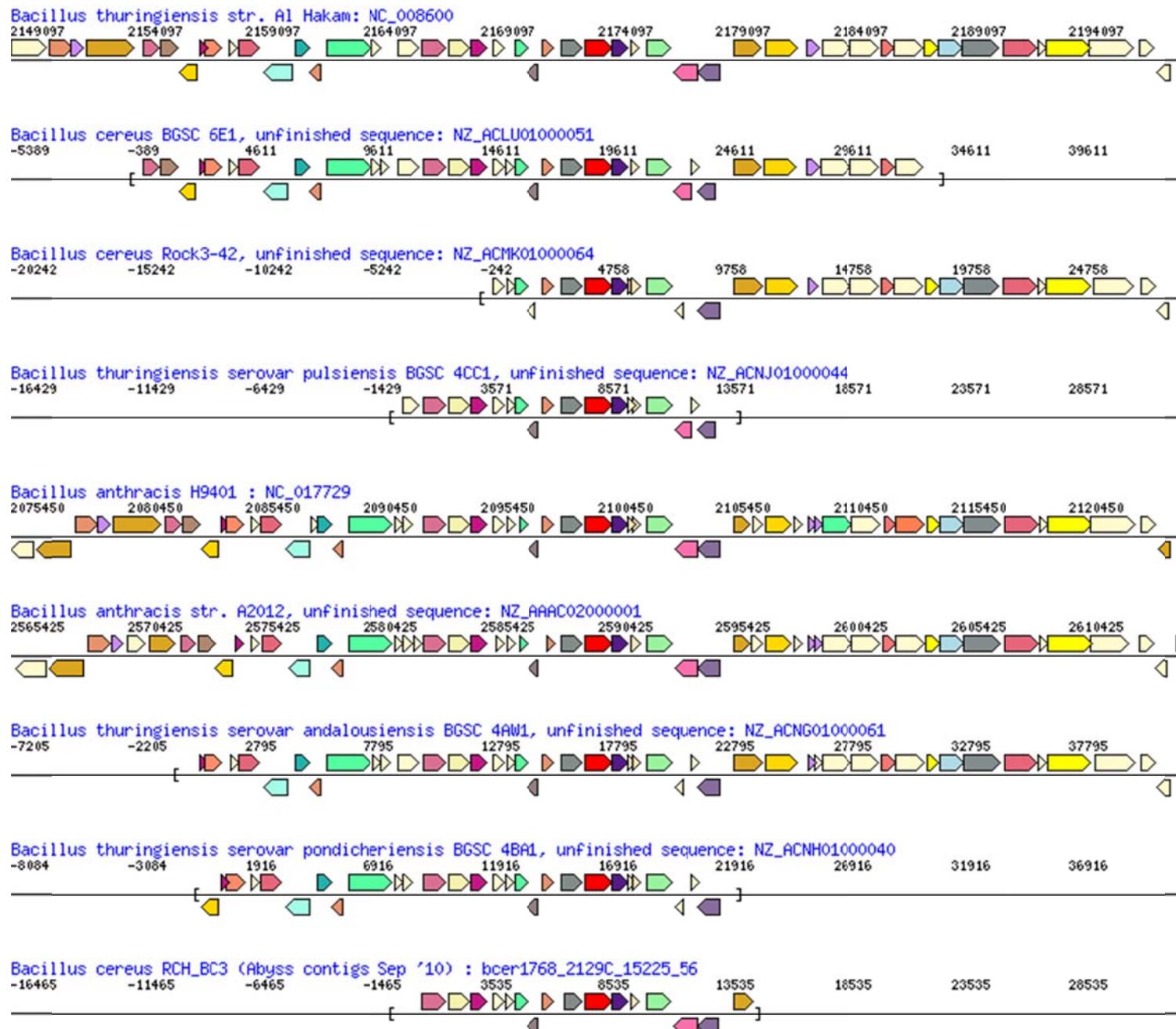




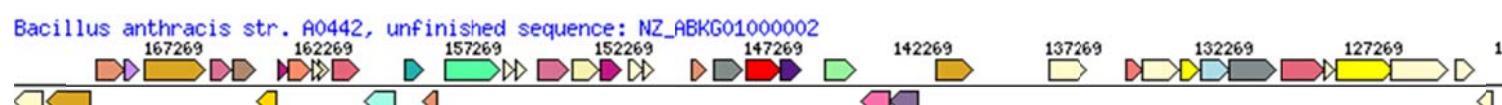
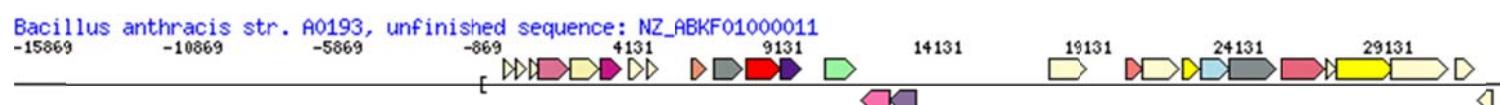
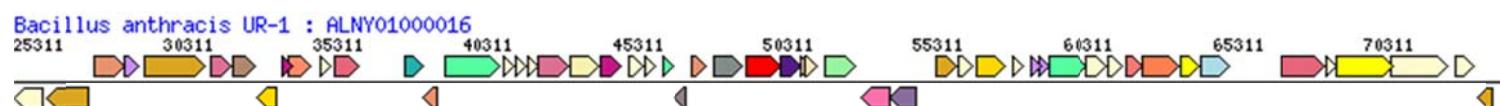
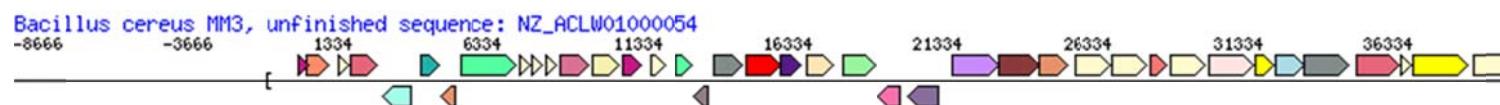
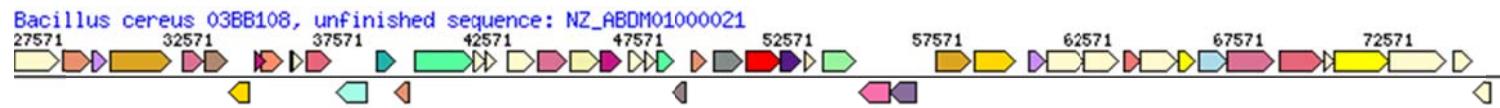


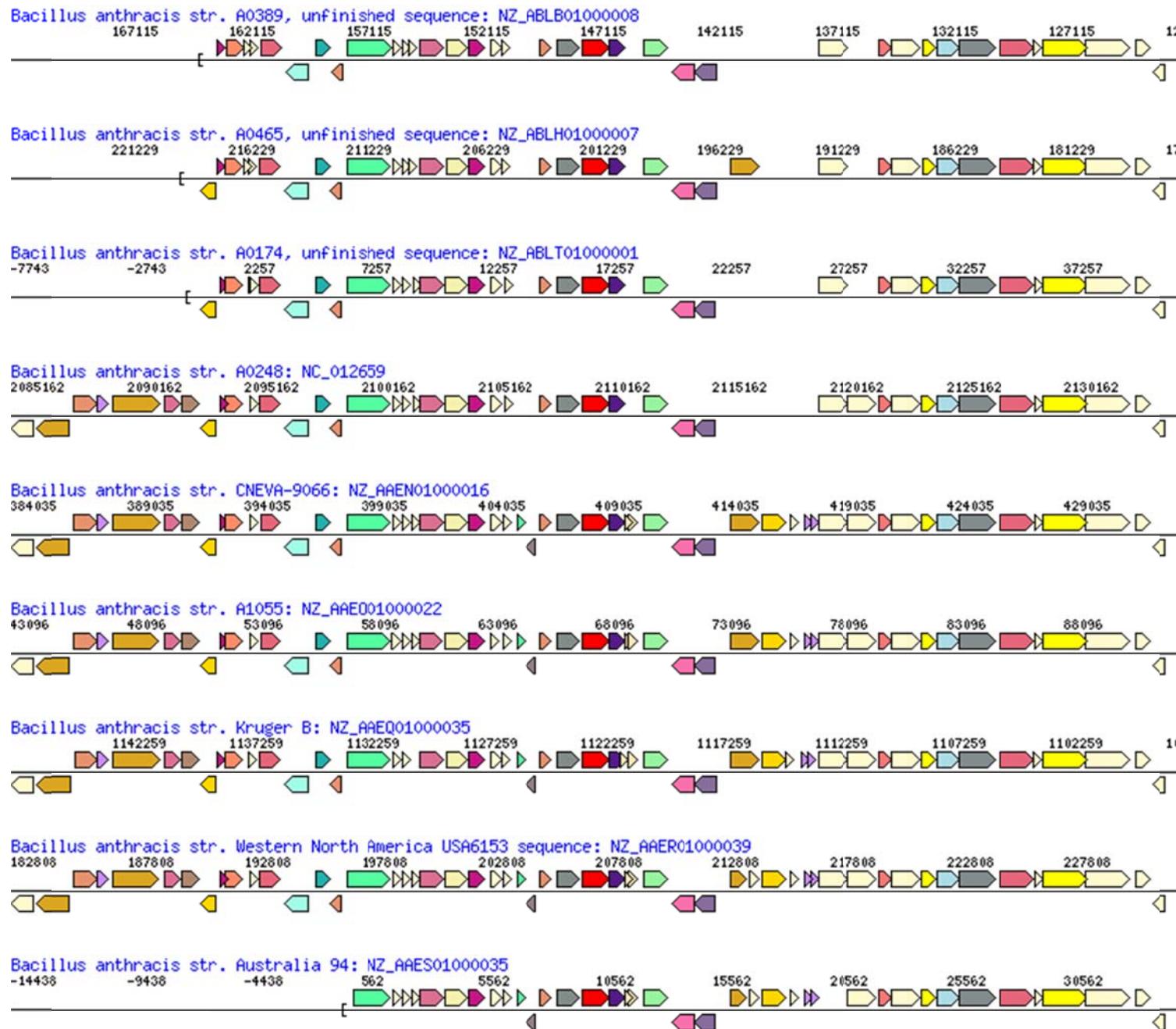




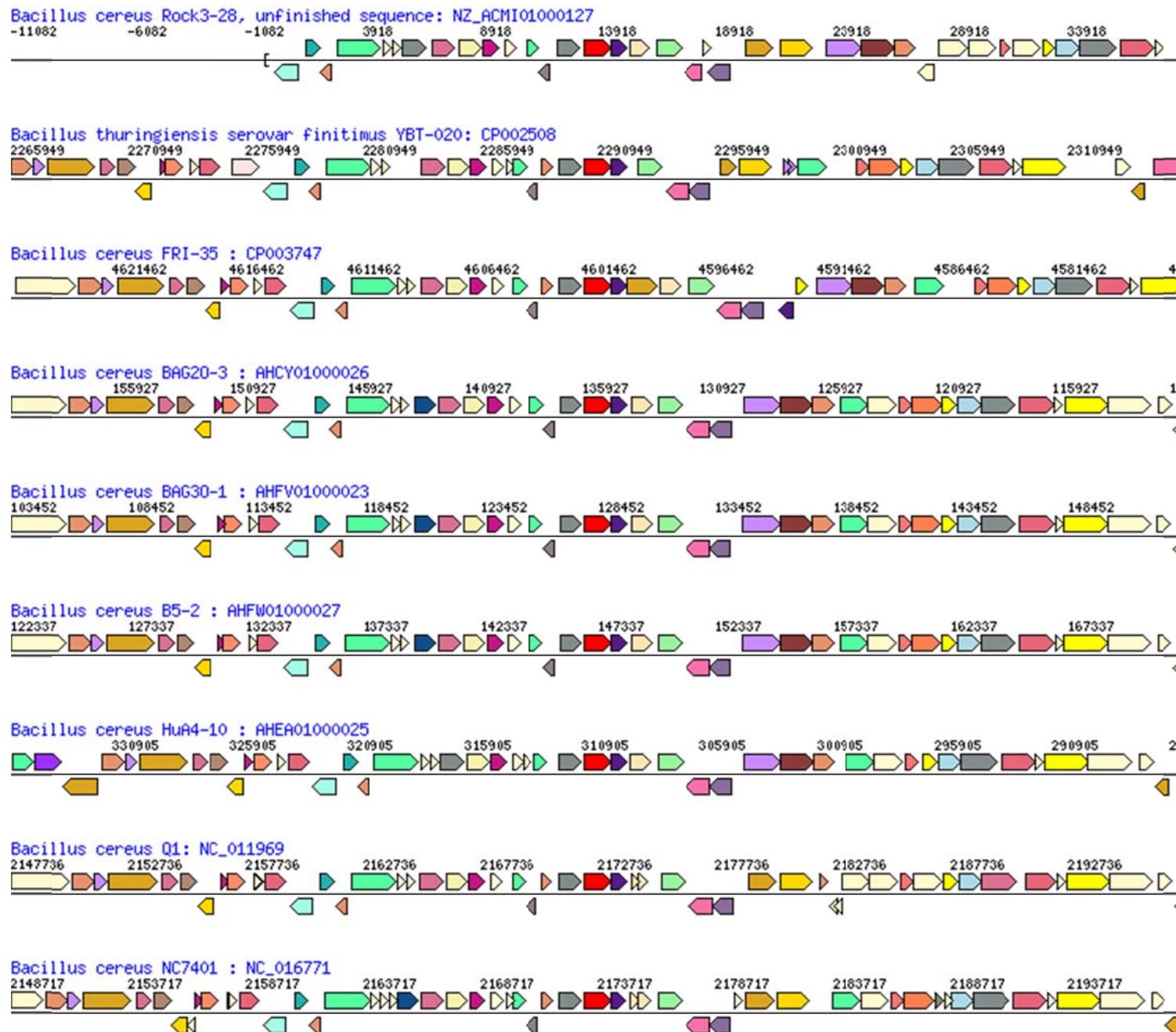




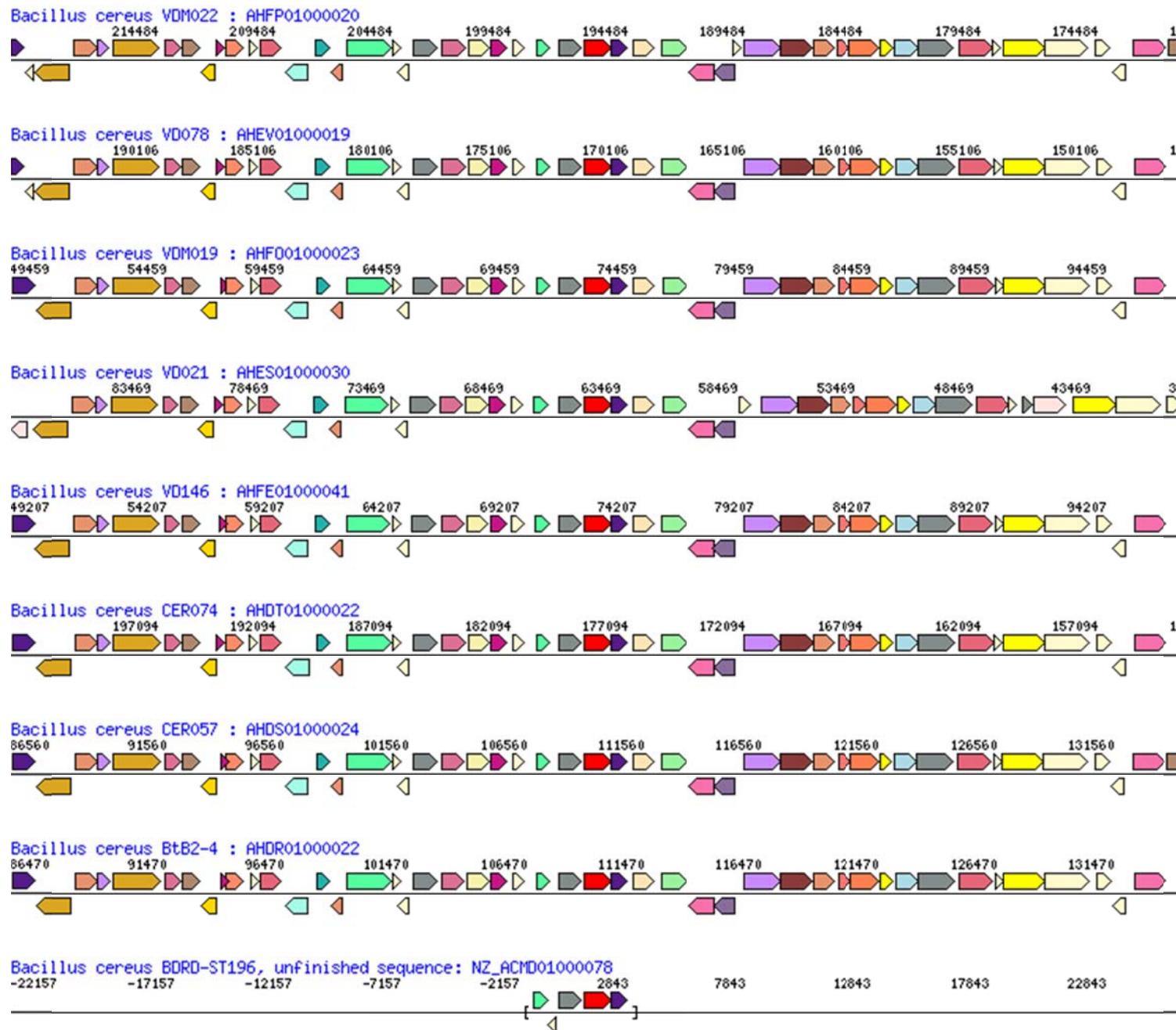












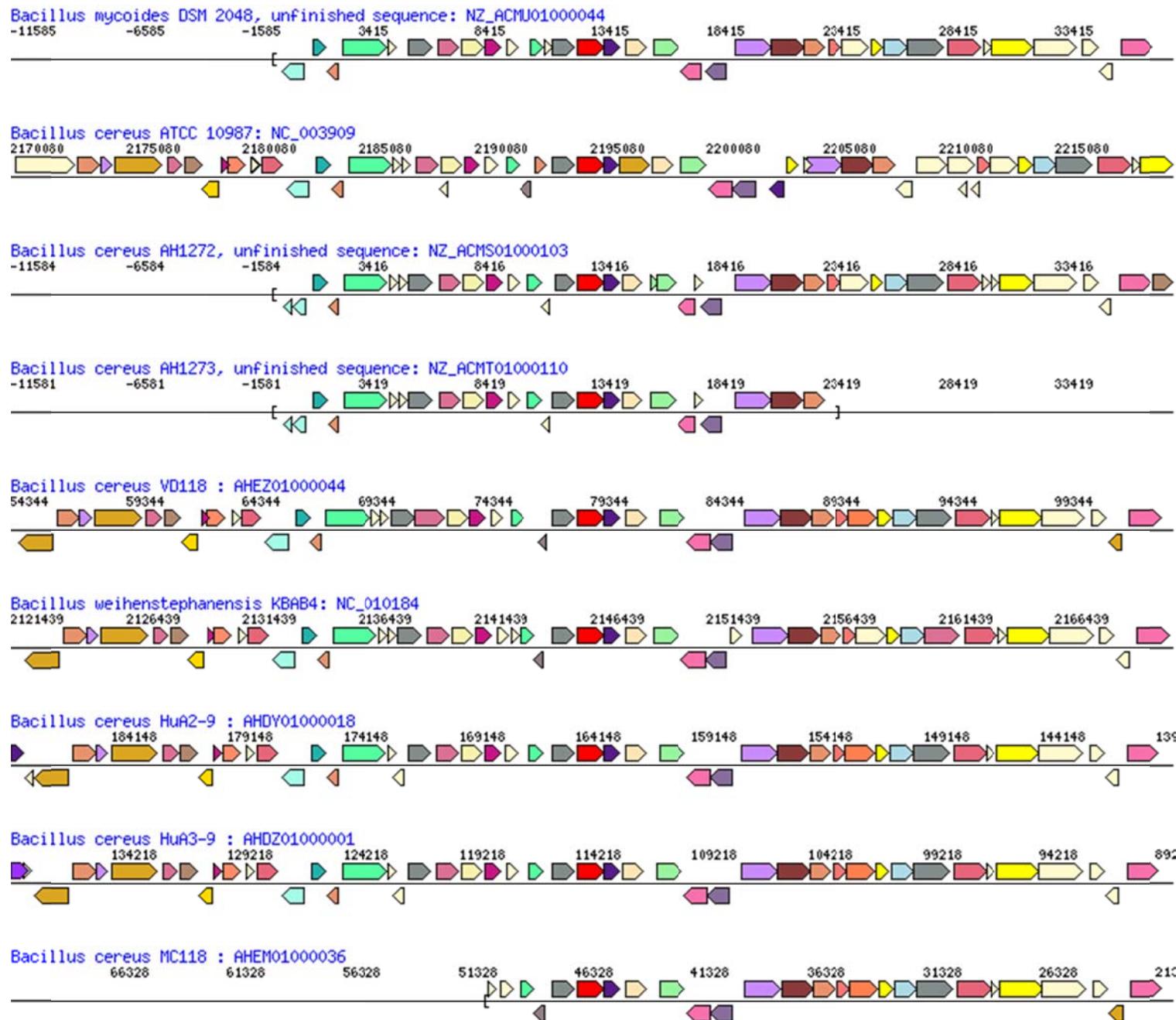








Table S5a. Genome affiliation to phylogenetic groups and identification of *bc2216* orthologs among *B. cereus* group (*sensu lato*)

Genome Name	Phylogenetic Group ⁽¹⁾	Scaffold ID	Scaffold Length	GC ⁽²⁾	Locus Tag	Product Name	Percent Identity ⁽³⁾	Length	E-value	Bit Score
<i>Bacillus cereus ATCC 14579_ (Reference genome)</i>	IV	NC_004722	5427083bp	F	BC2216	sensor histidine kinase	NA ⁽⁴⁾	374aa	NA	NA
<i>Bacillus cereus BDRD-ST24</i>	IV	NZ_ACMB01000048	151278bp	D	bcere0012_20160	Two-component sensor protein yhcY	100.00%	374aa	1.2e-211	741
<i>Bacillus cereus BDRD-Cer4</i>	IV	NZ_ACME01000046	194316bp	D	bcere0015_21090	Two-component sensor protein yhcY	100.00%	374aa	1.2e-211	741
<i>Bacillus cereus F65185</i>	IV	NZ_ACMO01000036	35373bp	D	bcere0025_19920	Two-component sensor protein yhcY	99.70%	374aa	6.0e-211	739
<i>Bacillus thuringiensis sv pakistani t13001</i>	IV	NZ_ACNC01000078	109636bp	D	bthur0005_20360	Two-component sensor protein yhcY	99.70%	374aa	6.0e-211	739
<i>Bacillus cereus 172560W</i>	IV	NZ_ACLV01000044	203905bp	D	bcere0005_19890	Two-component sensor protein yhcY	99.50%	374aa	1.3e-210	738
<i>Bacillus cereus Rock4-2</i>	IV	NZ_ACMM01000146	28838bp	D	bcere0023_20870	Two-component sensor protein yhcY	99.50%	374aa	1.3e-210	738
<i>Bacillus thuringiensis BMB171</i>	IV	NC_014171	5330088bp	F	BMB171_C1993	two-component sensor protein yhcY	100.00%	372aa	1.8e-210	737
<i>Bacillus cereus mm1550</i>	IV	NZ_ACMA01000043	126214bp	D	bcere0011_20370	Two-component sensor protein yhcY	99.50%	374aa	3.9e-210	736
<i>Bacillus thuringiensis sv kurstaki T03a001</i>	IV	NZ_ACND01000061	99414bp	D	bthur0006_20020	Two-component sensor protein yhcY	99.20%	374aa	3.9e-210	736
<i>Bacillus cereus RCH_B2C (Abyss contigs Sep '10)</i>	IV	bcer1769_4272G_16094_60	15995bp	D	bcer_00025110	Histidine kinase./Histidine kinase., DNA gyrase B-, and HSP90-like ATPase.	99.70%	372aa	8.7e-210	735
<i>Bacillus cereus VD196</i>	IV	AHFL01000006	907882bp	D	IKE_01195	two-component sensor protein yhcY	99.70%	372aa	8.0e-210	735
<i>Bacillus cereus VD154</i>	IV	AHFG01000004	113576bp	D	IK5_00160	hypothetical protein	99.70%	372aa	8.0e-210	735
<i>Bacillus cereus VD166</i>	IV	AHFI01000016	199438bp	D	IK9_02661	hypothetical protein	99.70%	372aa	8.0e-210	735
<i>Bacillus cereus B4264</i>	IV	NC_011725	5419036bp	F	BCB4264_A2244	sensor histidine kinase	99.70%	372aa	8.7e-210	735
<i>Bacillus cereus AH676</i>	IV	NZ_ACMQ01000078	51755bp	D	bcere0027_20460	Two-component sensor protein yhcY	99.70%	372aa	8.7e-210	735
<i>Bacillus cereus BAG4X12-1</i>	IV	AHDG01000022	138381bp	D	IE9_01903	hypothetical protein	99.50%	372aa	1.9e-209	734
<i>Bacillus cereus BAG5X12-1</i>	IV	AHDK01000019	138549bp	D	IEG_02652	two-component sensor protein yhcY	99.50%	372aa	1.8e-209	734
<i>Bacillus cereus ATCC 10876</i>	IV	NZ_ACLT01000051	124434bp	D	bcere0002_20140	Two-component sensor protein yhcY	98.70%	374aa	1.9e-209	734
<i>Bacillus cereus VD045</i>	IV	AHETO1000016	251981bp	D	II_E_02716	hypothetical protein	99.50%	372aa	2.5e-209	733
<i>Bacillus cereus VD133</i>	IV	AHFB01000032	75389bp	D	IIU_01732	two-component sensor protein yhcY	99.50%	372aa	2.3e-209	733
<i>Bacillus cereus RCH_B1C1 (Abyss contigs Sep '10)</i>	IV	bcer1767_2270L_16145_157	16047bp	D	bcer_00006760	Histidine kinase./Histidine kinase., DNA gyrase B-, and HSP90-like ATPase.	99.20%	372aa	4.3e-209	733
<i>Bacillus thuringiensis sv berliner ATCC 10792</i>	IV	NZ_ACNF01000056	23738bp	D	bthur0008_20550	Two-component sensor protein yhcY	98.40%	374aa	4.3e-209	733
<i>Bacillus cereus BAG3X2-2</i>	IV	AHDE01000025	131584bp	D	IE5_02002	hypothetical protein	99.20%	372aa	5.6e-209	732
<i>Bacillus cereus BAG4O-1</i>	IV	AHDF01000026	136920bp	D	IE7_01952	hypothetical protein	99.20%	372aa	5.6e-209	732
<i>Bacillus cereus BAG3O-2</i>	IV	AHDC01000029	204250bp	D	IE1_03383	hypothetical protein	99.20%	372aa	5.6e-209	732
<i>Bacillus cereus ISP2954</i>	IV	AHEJ01000042	196971bp	D	IGU_04172	two-component sensor protein yhcY	99.20%	372aa	5.2e-209	732
<i>Bacillus cereus VD169</i>	IV	AHFJ01000020	132507bp	D	IIKA_01948	hypothetical protein	99.50%	372aa	5.2e-209	732
<i>Bacillus cereus HD73</i>	IV	AHDU01000043	153296bp	D	IG1_03387	hypothetical protein	99.20%	372aa	5.2e-209	732
<i>Bacillus cereus BMG1.7</i>	IV	AHDQ01000057	245541bp	D	IES_04543	two-component sensor protein yhcY	99.20%	372aa	5.2e-209	732
<i>Bacillus thuringiensis sv. kurstaki HD73</i>	IV	CP004069	5646799bp	F	HD73_2503	Two-component sensor protein yhcY	99.20%	372aa	5.2e-209	732
<i>Bacillus cereus HuB13-1</i>	IV	AHEC01000057	147352bp	D	IGG_04651	two-component sensor protein yhcY	99.20%	372aa	5.2e-209	732
<i>Bacillus cereus Rock1-15</i>	IV	NZ_ACMH01000053	126604bp	D	bcere0018_19640	Two-component sensor protein yhcY	99.50%	372aa	5.6e-209	732
<i>Bacillus cereus VD184</i>	IV	AHFK01000037	145615bp	D	IKC_03223	two-component sensor protein yhcY	99.20%	372aa	2.0e-208	730
<i>Bacillus cereus VD200</i>	IV	AHFM01000030	215702bp	D	IKG_02034	hypothetical protein	99.20%	372aa	2.0e-208	730
<i>Bacillus cereus MSX-A1</i>	IV	AHEO01000031	220851bp	D	II5_02767	hypothetical protein	98.70%	372aa	2.8e-208	730
<i>Bacillus cereus HuB1-1</i>	IV	AHEB01000024	113213bp	D	IGE_03450	hypothetical protein	98.70%	372aa	2.8e-208	730
<i>Bacillus cereus VD140</i>	IV	AHFD01000030	151399bp	D	IIY_03177	two-component sensor protein yhcY	98.90%	372aa	2.6e-208	730
<i>Bacillus cereus BAG1X1-2</i>	IV	AHCRO1000018	110115bp	D	ICE_01401	hypothetical protein	98.70%	372aa	2.6e-208	730
<i>Bacillus cereus BAG1O-3</i>	IV	AHCP01000020	112813bp	D	ICA_02677	two-component sensor protein yhcY	98.70%	372aa	2.6e-208	730
<i>Bacillus thuringiensis sv israelensis ATCC 35646</i>	IV	NZ_AAJM01000131	11252bp	D	RBTH_04913	Two-component sensor protein yhcY	98.10%	376aa	4.8e-208	729
<i>Bacillus thuringiensis IBL4222</i>	IV	NZ_ACNL01000070	125086bp	D	bthur0014_20550	Two-component sensor protein yhcY	98.10%	374aa	4.8e-208	729
<i>Bacillus thuringiensis Bt407</i>	IV	CP003889	5500501bp	F	BTB_c2290	sensor histidine kinase YhcY	98.40%	372aa	6.2e-208	729
<i>Bacillus thuringiensis sv. thuringiensis IS5056</i>	IV	CP004123	5491935bp	F	H175_ch2214	Nitrate/nitrite sensor protein	98.40%	372aa	5.7e-208	729
<i>Bacillus thuringiensis T01-328</i>	IV	ARXZ02000003	577520bp	D	BTCBT_002054	Oxygen sensor histidine kinase nreB	98.40%	372aa	5.7e-208	729
<i>Bacillus thuringiensis Bt407</i>	IV	NZ_ACNM01000048	23795bp	D	bthur0002_20900	Two-component sensor protein yhcY	98.40%	372aa	6.2e-208	729
<i>Bacillus thuringiensis sv thuringiensis T01001</i>	IV	NZ_ACNA01000049	23795bp	D	bthur0003_20490	Two-component sensor protein yhcY	98.40%	372aa	6.2e-208	729
<i>Bacillus thuringiensis sv chinensis CT-43</i>	IV	CP001907	5486830bp	F	CT43_CH2180	two-component sensor protein yhcY	98.40%	372aa	6.2e-208	729
<i>Bacillus thuringiensis HD-789</i>	IV	CP003763	5495278bp	F	BTF_018590	sensor histidine kinase	98.10%	372aa	6.8e-207	725
<i>Bacillus cereus VD022</i>	IV	AHCK01000017	384667bp	D	IC1_02730	hypothetical protein	98.10%	372aa	6.8e-207	725
<i>Bacillus thuringiensis HD-771</i>	IV	CP003752	5886036bp	F	BTG_08795	sensor histidine kinase	98.10%	372aa	6.8e-207	725
<i>Bacillus cereus Schrouff</i>	IV	AHI01000014	233045bp	D	IAW_02772	two-component sensor protein yhcY	98.10%	372aa	6.3e-207	725
<i>Bacillus cereus TIAC219</i>	IV	AHCJ01000031	206847bp	D	IAY_03108	two-component sensor protein yhcY	98.10%	372aa	6.3e-207	725
<i>Bacillus cereus K-5975c</i>	IV	AHEL01000026	142331bp	D	IGY_03387	two-component sensor protein yhcY	98.10%	372aa	6.3e-207	725
<i>Bacillus cereus G9842</i>	IV	NC_011772	5387334bp	F	BCG9842_B3079	sensor histidine kinase	98.10%	372aa	6.9e-207	725
<i>Bacillus thuringiensis sv sotto T04001</i>	IV	NZ_ACN01000076	108111bp	D	bthur0004_20720	Two-component sensor protein yhcY	98.10%	372aa	6.9e-207	725
<i>Bacillus thuringiensis sv huazhongensis BGSC 4BD1</i>	IV	NZ_ACNI01000045	55583bp	D	bthur0011_19860	Two-component sensor protein yhcY	97.60%	374aa	6.9e-207	725
<i>Bacillus thuringiensis IBL200</i>	IV	NZ_ACNK01000048	34437bp	D	bthur0013_21900	Two-component sensor protein yhcY	97.60%	374aa	6.9e-207	725
<i>Bacillus cereus HuB4-4</i>	IV	AHEF01000048	212111bp	D	IGM_02642	two-component sensor protein yhcY	97.80%	372aa	1.4e-206	724
<i>Bacillus cereus BAG1X1-2</i>	IV	AHCT01000027	397641bp	D	IC1_02064	two-component sensor protein yhcY	97.60%	372aa	2.6e-206	723
<i>Bacillus cereus BAG1X2-3</i>	IV	AHCV01000043	227718bp	D	ICM_01502	two-component sensor protein yhcY	97.60%	372aa	2.6e-206	723
<i>Bacillus cereus BAG2O-1</i>	IV	AHCW01000022	346857bp	D	ICK_03288	two-component sensor protein yhcY	97.60%	372aa	2.6e-206	723
<i>Bacillus cereus BAG1X1-1</i>	IV	AHCQ01000035	321089bp	D	ICO_02064	two-component sensor protein yhcY	97.60%	372aa	2.6e-206	723
<i>Bacillus cereus VD014</i>	IV	AHER01000028	227718bp	D	ICC_03316	two-component sensor protein yhcY	97.60%	372aa	2.4e-206	723
<i>Bacillus cereus VD156</i>	IV	AHFR01000027	312533bp	D	IIA_02023	hypothetical protein	97.80%	372aa	4.4e-206	723
<i>Bacillus cereus ABD1134</i>	IV	NZ_ABDA01000020	381846bp	D	IK7_03413	hypothetical protein	97.80%	372aa	4.4e-206	723
<i>Bacillus thuringiensis MC28</i>	V	CP003687	5414494bp	F	MC28_1436	Two-component sensor protein yhcY	96.80%	374aa	6.4e-205	719
<i>Bacillus cereus Rock3-29</i>	V	NZ_ACMJ01000039	97142bp	D	bcere0020_20060	Two-component sensor protein yhcY	96.80%	374aa	6.4e-205	719
<i>Bacillus cereus BAG5O-1</i>	V	AHD10100010	130701bp	D	IEC_01440	hypothetical protein	96.80%	372aa	9.3e-204	715
<i>Bacillus cereus BAG4X2-1</i>	V	AHDH01000032	330562bp	D	IEA_03297	hypothetical protein	96.80%	372aa	9.3e-204	715
<i>Bacillus cereus Hub2-9</i>	V	AHED01000029	246371bp	D	IG1_03215	hypothetical protein	96.80%	372aa	9.3e-204	715
<i>Bacillus cereus BAG1O-2</i>	V	AHCO01000024	152083bp	D	IC9_03286	hypothetical protein	96.80%	372aa	9.3e-204	715
<i>Bacillus cereus VD214</i>	V	AHFN01000040	381629bp	D	IKI_01462	two-component sensor protein yhcY	96.80%	372aa	8.5e-204	715
<i>Bacillus cereus Hub4-10</i>	V	AHEEO1000007	439990bp	D	IGK_01461	hypothetical protein	96.80%	372aa	8.5e-204	715
<i>Bacillus cereus HuA2-3</i>	V	AHWD01000034	545065bp	D	IG5_01447	two-component sensor protein yhcY	96.80%	372aa	8.5e-204	715
<i>Bacillus cereus VD148</i>	V	AHFF01000025	190720bp	D	IK3_03300	hypothetical protein	96.80%	372aa	8.5e-204	715
<i>Bacillus cereus VD131</i>	V	AHFA01000025	142105bp	D	IIS_01432	two-component sensor protein yhcY	96.80%	372aa	8.5e-204	715
<i>Bacillus cereus BAG6O-1</i>	V	AHDM01000026	317235bp	D	IEK_03254	hypothetical protein	96.80%	372aa	8.5e-204	715
<i>Bacillus cereus Hub5-5</i>	V	AHEGO1000020	369993bp	D	IGO_02023	hypothetical protein	96.80%	372aa	8.5e-204	715
<i>Bacillus cereus BAG2O-2</i>	V	AHXC01000025	67731bp	D	ICQ_02027	hypothetical protein	96.80%	372aa	8.5e-204	715
<i>Bacillus cereus Rock1-3</i>	V	NZ_ACMG01000035	266699bp	D	bcere0017_20310	Two-component sensor protein yhcY	96.80%	372aa	9.3e-204	715
<i>Bacillus cereus VD115</i>	V	AHEY01000021	276254bp	D	IIO_02810	hypothetical protein	92.70%	372aa	3.4e-198	696
<i>Bacillus cereus Rock3-28</i>	V	NZ_ACMI01000127	59467bp	D	bcere0019_20120	Two-component sensor protein yhcY	93.00%	372aa	1.0e-197	695
<i>Bacillus cereus VD102</i>	III	AHEW01000010	609057bp	D	IIK_02552	hypothetical protein	94.40%	376aa	1.1e-201	708
<i>Bacillus cereus MSX-D12</i>	III	AHEQ01000022	1							

Bacillus cereus AND1407	III	AHCM01000013	143725bp	D	IC5_01271	hypothetical protein	94.10%	376aa	4.0e-201	706
Bacillus cereus ATCC 4342	III	NZ_ACLZ01000032	174174bp	D	bcere0010_20400	Two-component sensor protein yhcY	93.90%	376aa	2.1e-200	704
Bacillus thuringiensis sv thochigenis BGSC 4Y1	III	NZ_ACMY01000057	79659bp	D	bthur0001_20510	Two-component sensor protein yhcY	93.90%	376aa	3.7e-200	703
Bacillus cereus MSX-A12	III	AHEP01000020	181700bp	D	II7_02030	hypothetical protein	93.30%	376aa	1.4e-199	701
Bacillus cereus IS845/00	III	AHEI01000047	256667bp	D	IGS_04100	two-component sensor protein yhcY	93.30%	376aa	1.3e-199	701
Bacillus cereus IS195	III	AHEH01000047	159830bp	D	IGQ_03857	two-component sensor protein yhcY	93.30%	376aa	1.3e-199	701
Bacillus cereus IS075	III	AHC02000004	262520bp	D	IAU_00161	two-component sensor protein yhcY	93.30%	376aa	1.3e-199	701
Bacillus thuringiensis sv konkukian 97-27	III	NC_005957	5237682bp	F	BT9727_2047	sensor histidine kinase	94.40%	372aa	1.4e-199	701
Bacillus cereus BDRD-ST26	III	NZ_ACMC01000050	24793bp	D	bcere0013_20810	Two-component sensor protein yhcY	93.30%	376aa	1.4e-199	701
Bacillus cereus 95/8201	III	NZ_ACMF01000045	63991bp	D	bcere0016_21180	Two-component sensor protein yhcY	93.90%	376aa	1.4e-199	701
Bacillus thuringiensis sv monterrey BGSC 4AJ1	III	NZ_ACNE01000046	68163bp	D	bthur0007_20370	Two-component sensor protein yhcY	93.90%	376aa	1.4e-199	701
Bacillus cereus ISP3191	III	AHEK01000015	169039bp	D	IGW_02590	hypothetical protein	93.60%	376aa	1.8e-199	701
Bacillus thuringiensis Al Hakam	III	NC_008600	5257091bp	F	BALH_2024	sensor histidine kinase	93.60%	376aa	1.8e-199	701
Bacillus cereus BGSC 6E1	III	NZ_ACLU01000051	33946bp	D	bcere0004_20540	Two-component sensor protein yhcY	93.60%	376aa	1.8e-199	701
Bacillus cereus Rock3-42	III	NZ_ACMK01000064	65761bp	D	bcere0021_20710	Two-component sensor protein yhcY	93.60%	376aa	1.8e-199	701
Bacillus thuringiensis sv pulsiniensis BGSC 4CC1	III	NZ_ACNJ01000044	14351bp	D	bthur0012_20940	Two-component sensor protein yhcY	93.60%	376aa	1.8e-199	701
Bacillus anthracis H9401	III	NC_017729	5218947bp	F	H9401_2149	Sensor histidine kinase	93.30%	376aa	4.0e-199	699
Bacillus anthracis A2012 (Florida isolate)	III	NZ_AAAC02000001	5093554bp	D	Bant_01002886	cog4585: Signal transduction histidine kinase	93.30%	376aa	4.0e-199	699
Bacillus thuringiensis sv andalusiensis BGSC 4AW1	III	NZ_ACNG01000061	98499bp	D	bthur0009_20350	Two-component sensor protein yhcY	93.30%	376aa	4.0e-199	699
Bacillus thuringiensis sv pondicheriensis BGSC 4BA1	III	NZ_ACNH01000040	22690bp	D	bthur0010_20430	Two-component sensor protein yhcY	93.30%	376aa	4.0e-199	699
Bacillus cereus RCH_B3 (Abyss contigs Sep '10)	III	bcer1768_2103G_42612_76	42513bp	D	bcer_00010160	Histidine kinase/Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	93.30%	376aa	5.3e-199	699
Bacillus cereus W	III	NZ_ABZC01000004	365325bp	D	BcerW_010100010597	sensor histidine kinase	94.10%	372aa	9.0e-199	698
Bacillus cereus AH187 [F4810/72]	III	NC_011658	5269030bp	F	BCAH187_A2374	sensor histidine kinase	93.50%	372aa	9.0e-199	698
Bacillus cereus AH820	III	NC_011773	5302683bp	F	BCAH820_2289	sensor histidine kinase	94.10%	372aa	9.0e-199	698
Bacillus cereus F837/76	III	NC_016779	5222906bp	F	bcf_11350	Nitrate/nitrite sensor protein	93.80%	372aa	1.2e-198	698
Bacillus cereus NVH0597-99	III	NZ_ABDK01000009	213404bp	D	BcerN_010100015353	sensor histidine kinase	93.80%	372aa	1.2e-198	698
Bacillus cereus 03BB108	III	NZ_ABDM01000021	89774bp	D	Bcer0_010100025924	sensor histidine kinase	93.80%	372aa	1.2e-198	698
Bacillus cereus 03BB102	III	NC_012472	5269628bp	F	BCA_2347	sensor histidine kinase	93.80%	372aa	1.2e-198	698
Bacillus anthracis CI	III	NC_014335	5196054bp	F	BACI_c22280	sensor histidine kinase	93.80%	372aa	1.2e-198	698
Bacillus anthracis UR-1	III	ALNY01000016	99008bp	D	B353_15448	Sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis Sterne	III	NC_005945	5228663bp	F	BAS2108	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis Tsiankovskii-I	III	NZ_ABDN01000002	584883bp	D	BantT_010100007320	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis A0193	III	NZ_ABKF01000011	156048bp	D	BAQ_2309	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis A0442	III	NZ_ABKG01000002	460661bp	D	BAH_2314	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis A0389	III	NZABL01000008	163817bp	D	BAK_2345	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis A0465	III	NZABLH01000007	218708bp	D	BAM_2308	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis A0174	III	NZ_ABLT01000001	672784bp	D	BAO_2258	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis A0248	III	NC_012659	5227419bp	F	BAA_2326	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis CNEVA-9066	III	NZ_AAEN01000016	1053408bp	D	BantC_010100013450	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis A1055	III	NZ_AAEQ01000022	1320955bp	D	BantA1_010100007279	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis Kruger B	III	NZ_AAEQ01000035	1294190bp	D	BantKB_010100021387	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis WesternNA USA6153	III	NZ_AAER01000039	367030bp	D	BantWNA_010100019234	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus anthracis Australia 94	III	NZ_AAE501000035	1143198bp	D	BantA9_010100017586	sensor histidine kinase	93.50%	372aa	2.6e-198	697
Bacillus cereus E33L (ZK)	III	NC_006274	5300915bp	F	BCZK2045	sensor histidine kinase	93.50%	372aa	7.6e-198	695
Bacillus anthracis A0488	III	NZ_ABCE01000007	164396bp	D	BAC_2283	sensor histidine kinase	93.30%	372aa	7.6e-198	695
Bacillus anthracis CDC 684	III	NC_012581	5230115bp	F	BAMEG_2332	sensor histidine kinase	93.30%	372aa	7.6e-198	695
Bacillus anthracis Vollum	III	NZ_AAEPO1000025	812727bp	D	BantV_010100004031	sensor histidine kinase	93.30%	372aa	7.6e-198	695
Bacillus thuringiensis sv. finitimus YBT-020	III	CP002508	5355490bp	F	VBT020_11600	sensor histidine kinase	93.30%	372aa	1.0e-197	695
Bacillus cereus FRI-35	III	CP003747	5083176bp	F	BCK_23520	sensor histidine kinase	93.30%	372aa	1.2e-197	694
Bacillus cereus Q1	III	NC_011969	5214195bp	F	BCQ_2199	sensor histidine kinase	94.00%	365aa	2.1e-195	687
Bacillus cereus NC7401	III	NC_016771	5221581bp	F	BCN_2192	sensor histidine kinase	93.40%	365aa	1.7e-194	684
Bacillus anthracis Ames	III	NC_003997	5227293bp	F	BA2264	sensor histidine kinase	93.40%	365aa	5.1e-194	682
Bacillus anthracis Ames Ancestor A2084	III	NC_007530	5227419bp	F	GBAA2264	sensor histidine kinase	93.40%	365aa	5.1e-194	682
Bacillus cereus G9241	III	NZ_AAEK01000006	163640bp	D	BCE_G9241_2226	sensor histidine kinase, putative	94.00%	365aa	1.9e-193	681
Bacillus cereus ATCC 10987	III	NC_003909	5224283bp	F	BCE_2292	sensor histidine kinase	92.90%	365aa	7.4e-193	679
Bacillus cereus H3081.97	III	NZ_ABLD01000001	619721bp	D	BcerH_010100003400	Absent	NA	NA	NA	NA
Bacillus cereus BAG5X2-1	II	AHDL01000023	238523bp	D	IEI_02861	hypothetical protein	93.80%	372aa	6.9e-199	699
Bacillus cereus MM3	II	NZ_ACLW01000054	76810bp	D	bcere0006_20650	Two-component sensor protein yhcY	93.30%	376aa	1.5e-198	698
Bacillus cereus AH1271	II	NZ_ACMR01000093	24635bp	D	bcere0028_20620	Two-component sensor protein yhcY	92.80%	374aa	3.4e-198	696
Bacillus cereus BAG2X1-2	II	AHDA01000026	141630bp	D	ICW_03516	hypothetical protein	93.30%	372aa	7.6e-198	695
Bacillus cereus BAG6X1-1	II	AHDO01000013	147985bp	D	IEO_01693	hypothetical protein	93.30%	372aa	7.0e-198	695
Bacillus cereus BAG2O-3	II	AHCY01000026	280303bp	D	ICS_03406	two-component sensor protein yhcY	92.70%	372aa	4.2e-196	689
Bacillus cereus BAG3O-1	II	AHFV01000023	196299bp	D	KQ1_02170	two-component sensor protein yhcY	92.70%	372aa	3.8e-196	689
Bacillus cereus B5-2	II	AHFV01000027	319887bp	D	KQ3_01488	two-component sensor protein yhcY	92.70%	372aa	3.8e-196	689
Bacillus cereus R309803	unclustered	NZ_ACYL01000040	178172bp	D	bcere0009_20280	Two-component sensor protein yhcY	92.00%	374aa	4.5e-198	696
Bacillus cereus BAG2X1-3	unclustered	AHDB01000024	344606bp	D	ICY_02622	hypothetical protein	91.40%	372aa	1.7e-194	684
Bacillus cereus BAG2X1-1	unclustered	AHZC01000025	240792bp	D	ICU_02793	hypothetical protein	91.40%	372aa	1.7e-194	684
Bacillus cereus AH1272	VI	NZ_ACMS01000103	52288bp	D	bcere0029_21250	Two-component sensor protein yhcY	90.40%	374aa	9.7e-193	678
Bacillus cereus AH1273	VI	NZ_ACMT01000110	23861bp	D	bcere0030_21270	Two-component sensor protein yhcY	90.40%	374aa	9.7e-193	678
Bacillus cereus VDM022	VI	AHP01000020	337261bp	D	IKM_03291	hypothetical protein	91.40%	372aa	4.0e-193	679
Bacillus cereus VD078	VI	AHEV01000019	252815bp	D	III_03207	hypothetical protein	91.10%	372aa	5.6e-193	679
Bacillus cereus VDM019	VI	AHF01000023	267709bp	D	IKK_01962	two-component sensor protein yhcY	91.10%	372aa	5.2e-193	679
Bacillus cereus VD021	VI	AHES01000030	145584bp	D	IIC_03351	two-component sensor protein yhcY	91.10%	372aa	5.2e-193	679
Bacillus cereus VD146	VI	AHFE01000041	267154bp	D	IK1_01448	two-component sensor protein yhcY	91.10%	372aa	5.2e-193	679
Bacillus cereus CER074	VI	AHDT01000022	288640bp	D	IEY_03320	hypothetical protein	91.10%	372aa	5.2e-193	679
Bacillus cereus CER057	VI	AHDS01000024	245438bp	D	IEW_02012	hypothetical protein	91.10%	372aa	5.2e-193	679
Bacillus cereus RTB2-4	VI	AHDR01000022	286458bp	D	IEU_02015	hypothetical protein	91.10%	372aa	5.2e-193	679
Bacillus cereus BDRD-ST196	VI	NZ_ACMD01000078	4187bp	D	bcere0014_20170	Two-component sensor protein yhcY	91.10%	372aa	5.7e-193	679
Bacillus mycoides DSM 2048	VI	NZ_ACMU01000044	68004bp	D	bmyco0001_19850	Two-component sensor protein yhcY	91.10%	372aa	5.7e-193	679
Bacillus weihenstephanensis KBAB4	VI	NC_010184	5262775bp	F	BcerKBAB4_2086	GAF sensor signal transduction histidine kinase	90.90%	372aa	1.3e-192	678
Bacillus cereus HuA2-9	VI	AHDY01000018	295569bp	D	IG9_02845	two-component sensor protein yhcY	90.90%	372aa	1.5e-192	677
Bacillus cereus HuA3-9	VI	AHDZ01000001	188645bp	D	IGA_00108	two-component sensor protein yhcY	90.90%	372aa	1.5e-192	677
Bacillus cereus WD048	VI	AHEU01000018	243114bp	D	IID_02690	hypothetical protein	90.90%	372aa	2.8e-192	677
Bacillus cereus HuA2-1	VI	AHDV01000009	199286bp	D	IG3_01726	hypothetical protein	90.60%	372aa	2.6e-192	677
Bacillus cereus AH621	VI	NZ_ACLX01000056	70672bp	D	bcere0007_20660	Two-component sensor protein yhcY	90.90%	372aa	2.8e-192	677
Bacillus cereus VD142	VI	AHCL02000009	142780bp	D	IC3_01100	two-component sensor protein yhcY	90.90%	372aa	4.4e-192	676
Bacillus cereus VDM062	VI	AHFS01000031	185835bp	D	IKS_03542	hypothetical protein	90.30%	372aa	9.8e-192	675
Bacillus cereus VDM034	VI	AHFQ01000013	137918bp	D	IKO_01630	hypothetical protein	90.30%	372aa	9.8e-192	675
Bacillus cereus HuA2-4	VI	AHDX01000025	223414bp	D	IG7_02075	hypothetical protein				

Bacillus cereus VD107	VI	AHEX01000014	145386bp	D	IIM_01397	hypothetical protein	90.30%	372aa	1.9e-193	681
Bacillus cereus BAG5X1-1	VI	AHDJ01000028	167843bp	D	IEE_03023	hypothetical protein	91.10%	372aa	2.5e-193	680
Bacillus cereus VD118	VI	AHEZ01000044	257274bp	D	IIQ_01180	two-component sensor protein yhcY	90.90%	372aa	1.2e-192	678
Bacillus cereus MC118	VI	AHEM01000036	50635bp	D	II1_03385	two-component sensor protein yhcY	90.60%	372aa	2.0e-192	677
Bacillus cereus BAG60-2	VI	AHDN01000033	230347bp	D	IEM_03141	hypothetical protein	90.90%	372aa	2.0e-192	677
Bacillus cereus MC67	VI	AHEN01000003	229617bp	D	II3_00196	hypothetical protein	90.60%	372aa	2.0e-192	677
Bacillus cereus BAG1X1-3	VI	AHCS01000023	1262248bp	D	ICG_03309	hypothetical protein	90.60%	372aa	2.8e-192	677
Bacillus cereus VDM053	VI	AHFRO1000039	621715bp	D	IKQ_01731	two-component sensor protein yhcY	90.60%	372aa	2.6e-192	677
Bacillus cereus BAG1O-1	VI	AHCN01000021	162560bp	D	IC7_01508	two-component sensor protein yhcY	90.60%	372aa	2.6e-192	677
Bacillus cereus BAG3X2-1	VI	AHDD01000023	113935bp	D	IE3_03212	hypothetical protein	90.10%	372aa	1.4e-191	674
Bacillus mycoides Rock3-17	I	NZ_ACMW01000051	87918bp	D	bmyco0003_19320	Two-component sensor protein yhcY	84.80%	374aa	6.3e-184	649
Bacillus cereus VDM006	I	AHF01000037	802420bp	D	KOW_00626	two-component sensor protein yhcY	84.70%	372aa	2.9e-183	647
Bacillus cereus VDM021	I	AHFU01000038	209010bp	D	KOY_03298	two-component sensor protein yhcY	84.70%	372aa	2.9e-183	647
Bacillus cereus VD136	I	AHFC01000047	594013bp	D	IIW_01264	two-component sensor protein yhcY	84.40%	372aa	8.3e-183	645
Bacillus pseudomycoides DSM 12442	I	NZ_ACMX01000036	125315bp	D	bpmxy0001_20100	Two-component sensor protein yhcY	84.40%	372aa	2.0e-182	644
Bacillus cereus Rock3-44	I	NZ_ACML01000120	22469bp	D	bcere0022_18280	Two-component sensor protein yhcY	83.60%	372aa	6.5e-181	639
Bacillus mycoides Rock1-4	I	NZ_ACMV01000133	85498bp	D	bmyco0002_19200	Two-component sensor protein yhcY	84.30%	313aa	4.8e-152	543

All data, except data from the second column, came from Integrated Microbial Genomes data base (Markowitz et al., 2012) ; homologs for *casKR* genes were first determined through BLASTp hits between *casKR* genes from ATCC14579 genome (*bc2216-17*) and genes in all other genomes, and orthologs were computed as bidirectional best hits between genomes; percent identity, length of sequence, E-value and bit score are displayed for each ortholog. The C2S was absent on NVH391-98 genome (phylogenetic group VII)

(⁽¹⁾) affiliation to phylogenetic groups using *panC* gene sequence, as previously described (Guinebretiere et al., 2010) ; (⁽²⁾) Genome completion, D : draft, F : finished ; (⁽³⁾) percent identity for translated proteins ; (⁽⁴⁾) NA : not applicable

Table S5b. Genome affiliation to phylogenetic groups and identification of *bc2217* orthologs among *B. cereus* group (*sensu lato*).

Genome Name	Phylogenetic Group ⁽¹⁾	Scaffold ID	Scaffold Length	GC ⁽²⁾	Locus Tag	Product Name	Percent Identity ⁽³⁾	Length	E-value	Bit Score
Bacillus cereus ATCC 14579_ (Reference genome)	IV	NC_004722	5427083bp	F	BC2217	two-component system response regulator yhcZ	NA⁽⁴⁾	213aa	NA	NA
Bacillus cereus BDRD-ST24	IV	NZ_ACMB01000048	151278bp	D	bcere0012_20170	DNA-binding response regulator	100.00%	213aa	1.5e-113	414
Bacillus cereus BDRD-Cer4	IV	NZ_ACME01000046	194316bp	D	bcere0015_21100	DNA-binding response regulator	99.50%	192aa	4.9e-101	373
Bacillus cereus F65185	IV	NZ_ACMO01000036	35373bp	D	bcere0025_19930	DNA-binding response regulator	99.50%	213aa	4.3e-113	413
Bacillus thuringiensis sv pakistani t13001	IV	NZ_ACNC01000078	109636bp	D	bthur0005_20370	DNA-binding response regulator	99.50%	192aa	4.9e-101	373
Bacillus cereus 172560W	IV	NZ_ACLV01000044	203905bp	D	bcere0005_19900	DNA-binding response regulator	99.00%	192aa	1.4e-100	371
Bacillus cereus Rock4-2	IV	NZ_ACMM01000146	28838bp	D	bcere0023_20880	DNA-binding response regulator	99.50%	213aa	4.3e-113	413
Bacillus thuringiensis BMB171	IV	NC_014171	5330088bp	F	BMB171_C1994	two-component response regulator yhcZ	99.50%	192aa	4.9e-101	373
Bacillus cereus mm1550	IV	NZ_ACMA01000043	126214bp	D	bcere0011_20380	DNA-binding response regulator	99.50%	213aa	4.3e-113	413
Bacillus thuringiensis sv kurstaki T03a001	IV	NZ_ACND01000061	99414bp	D	bthur0006_20030	DNA-binding response regulator	99.50%	213aa	4.3e-113	413
Bacillus cereus RCH_B2C (Abyss contigs Sep '10)	IV	bcer1769_4272G_16094_60	15995bp	D	bcer_00025120	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	99.10%	213aa	9.6e-113	412
Bacillus cereus VD196	IV	AHF01000006	907882bp	D	IKE_01196	two-component system response regulator yhcZ	100.00%	213aa	1.4e-113	414
Bacillus cereus VD154	IV	AHFG01000004	113576bp	D	IK5_00161	hypothetical protein	100.00%	213aa	1.4e-113	414
Bacillus cereus VD166	IV	AHFI01000016	199438bp	D	IK9_02660	hypothetical protein	100.00%	213aa	1.4e-113	414
Bacillus cereus B4264	IV	NC_011725	5419036bp	F	BCB4264_A2245	DNA-binding response regulator, LuxR family	99.50%	213aa	4.3e-113	413
Bacillus cereus AH676	IV	NZ_ACMQ01000078	51755bp	D	bcere0027_20470	DNA-binding response regulator	99.50%	192aa	4.9e-101	373
Bacillus cereus BAG4X12-1	IV	AHDG01000022	138381bp	D	IE9_01904	hypothetical protein	99.50%	213aa	4.3e-113	413
Bacillus cereus BAG5X12-1	IV	AHDK01000019	138549bp	D	IEG_02651	two-component system response regulator yhcZ	99.50%	213aa	3.9e-113	413
Bacillus cereus ATCC 10876	IV	NZ_ACLT01000051	124434bp	D	bcere0002_20150	DNA-binding response regulator	98.10%	209aa	1.3e-109	401
Bacillus cereus VD045	IV	AHETO1000016	251981bp	D	II_E_02715	hypothetical protein	100.00%	213aa	1.5e-113	414
Bacillus cereus VD133	IV	AHFB01000032	75389bp	D	IIU_01733	two-component system response regulator yhcZ	99.10%	213aa	1.5e-112	411
Bacillus cereus RCH_B1C (Abyss contigs Sep '10)	IV	bcer1767_2270L_16145_157	16047bp	D	bcer_00006750	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	99.10%	213aa	9.6e-113	412
Bacillus thuringiensis sv berliner ATCC 10792	IV	NZ_ACNF01000056	23738bp	D	bthur0008_20560	DNA-binding response regulator	97.60%	209aa	1.3e-109	401
Bacillus cereus BAG3X2-2	IV	AHDE01000025	131584bp	D	IE5_02003	hypothetical protein	99.50%	213aa	4.3e-113	413
Bacillus cereus BAG4O-1	IV	AHDF01000026	136920bp	D	IE7_01953	hypothetical protein	99.10%	213aa	9.5e-113	412
Bacillus cereus BAG3O-2	IV	AHDC01000029	204250bp	D	IE1_03382	hypothetical protein	99.10%	213aa	9.5e-113	412
Bacillus cereus ISP2954	IV	AHEJ01000042	196971bp	D	IGU_04173	two-component system response regulator yhcZ	99.50%	213aa	3.9e-113	413
Bacillus cereus VD169	IV	AHFJ01000020	132507bp	D	IIKA_01949	hypothetical protein	100.00%	213aa	1.4e-113	414
Bacillus cereus HD73	IV	AHDU01000043	153296bp	D	IG1_03388	hypothetical protein	99.50%	213aa	3.9e-113	413
Bacillus cereus BMG1.7	IV	AHDQ01000057	245541bp	D	IES_04542	two-component system response regulator yhcZ	99.50%	213aa	3.9e-113	413
Bacillus thuringiensis sv. kurstaki HD73	IV	CP004069	5646799bp	F	HD73_2504	LuxR family transcriptional regulator	99.50%	213aa	3.9e-113	413
Bacillus cereus HuB13-1	IV	AHEC01000057	147352bp	D	IGG_04652	two-component system response regulator yhcZ	99.50%	213aa	3.9e-113	413
Bacillus cereus Rock1-15	IV	NZ_ACMH01000053	126604bp	D	bcere0018_19650	DNA-binding response regulator	100.00%	213aa	1.5e-113	414
Bacillus cereus VD184	IV	AHFK01000037	145615bp	D	IKC_03224	two-component system response regulator yhcZ	99.50%	213aa	3.9e-113	413
Bacillus cereus VD200	IV	AHFM01000030	215702bp	D	IKG_02035	hypothetical protein	100.00%	213aa	1.4e-113	414
Bacillus cereus MSX-A1	IV	AHEO01000031	220851bp	D	II5_02766	hypothetical protein	97.70%	213aa	4.0e-111	406
Bacillus cereus HuB1-1	IV	AHEB01000024	113213bp	D	IGE_03449	hypothetical protein	98.10%	213aa	4.7e-112	409
Bacillus cereus VD140	IV	AHFD01000030	151399bp	D	IIY_03178	two-component system response regulator yhcZ	98.60%	213aa	4.4e-112	409
Bacillus cereus BAG1X1-2	IV	AHCRO1000018	110115bp	D	ICE_01402	hypothetical protein	98.10%	213aa	4.4e-112	409
Bacillus cereus BAG1O-3	IV	AHCPO1000020	112813bp	D	ICA_02676	two-component system response regulator yhcZ	98.10%	213aa	4.4e-112	409
Bacillus thuringiensis sv israelensis ATCC 35646	IV	NZ_AAJM01000131	11252bp	D	RBTH_04912	Two-component response regulator yhcZ	97.70%	219aa	1.8e-111	407
Bacillus thuringiensis IBL4222	IV	NZ_ACNL01000070	125086bp	D	bthur0014_20560	DNA-binding response regulator	97.60%	209aa	2.2e-109	401
Bacillus thuringiensis BT407	IV	CP003889	5500501bp	F	BTB_c22930	Two-component response regulator yhcZ	98.10%	213aa	4.7e-112	409
Bacillus thuringiensis sv. thuringiensis IS5056	IV	CP004123	5491935bp	F	H175_ch215	DNA-binding response regulator, LuxR family	98.10%	213aa	4.4e-112	409
Bacillus thuringiensis T01-328	IV	ARXZ02000003	577520bp	D	BTCBT_002055	Response regulator protein vraR	98.10%	213aa	4.4e-112	409
Bacillus thuringiensis BT407	IV	NZ_ACMZ01000048	23795bp	D	bthur0002_20910	DNA-binding response regulator	97.60%	209aa	1.3e-109	401
Bacillus thuringiensis sv thuringiensis T01001	IV	NZ_ACNA01000049	23795bp	D	bthur0003_20500	DNA-binding response regulator	97.60%	209aa	1.3e-109	401
Bacillus thuringiensis sv chinensis CT-43	IV	CP001907	5486830bp	F	CT43_CH2181	two-component response regulator yhcZ	98.10%	213aa	4.8e-112	409
Bacillus thuringiensis HD-789	IV	CP003763	5495278bp	F	BTF1_08595	LuxR family DNA-binding response regulator	98.10%	213aa	8.1e-112	409
Bacillus cereus VD022	IV	AHCK01000017	384667bp	D	IC1_02729	hypothetical protein	98.10%	213aa	8.1e-112	409
Bacillus thuringiensis HD-771	IV	CP003752	5886036bp	F	BTG_08790	LuxR family DNA-binding response regulator	98.10%	213aa	8.1e-112	409
Bacillus cereus Schrouff	IV	AHCJ01000014	233045bp	D	IAW_02771	two-component system response regulator yhcZ	97.70%	213aa	6.3e-111	406
Bacillus cereus TIAC219	IV	AHCJ01000031	206847bp	D	IAY_03109	two-component system response regulator yhcZ	98.10%	213aa	7.4e-112	409
Bacillus cereus K-5975c	IV	AHELO1000026	142331bp	D	IGY_03386	two-component system response regulator yhcZ	97.70%	213aa	6.3e-111	406
Bacillus cereus G9842	IV	NC_011772	5387334bp	F	BCG9842_B3078	DNA-binding response regulator, LuxR family	98.10%	213aa	8.1e-112	409
Bacillus thuringiensis sv sotto T04001	IV	NZ_ACN01000076	108111bp	D	bthur0004_20730	DNA-binding response regulator	97.60%	209aa	2.2e-109	401
Bacillus thuringiensis sv huazhongensis BGSC 4BD1	IV	NZ_ACNI01000045	55583bp	D	bthur0011_19870	DNA-binding response regulator	97.20%	213aa	9.0e-111	405
Bacillus thuringiensis IBL200	IV	NZ_ACNK01000048	34437bp	D	bthur0013_21910	DNA-binding response regulator	97.10%	209aa	1.3e-109	401
Bacillus cereus Hub4-4	IV	AHET01000048	212111bp	D	IGM_02643	two-component system response regulator yhcZ	98.10%	213aa	7.4e-112	409
Bacillus cereus BAG1X1-2	IV	AHCT01000027	397641bp	D	ICI_02065	two-component system response regulator yhcZ	99.10%	213aa	5.6e-113	412
Bacillus cereus BAG1X2-3	IV	AHCVO1000043	227718bp	D	ICM_01503	two-component system response regulator yhcZ	99.10%	213aa	5.6e-113	412
Bacillus cereus BAG1X2-2	IV	AHCVO1000022	346857bp	D	ICK_03287	two-component system response regulator yhcZ	99.10%	213aa	5.6e-113	412
Bacillus cereus BAG2O-1	IV	AHCW01000024	321089bp	D	ICO_02065	two-component system response regulator yhcZ	99.10%	213aa	5.6e-113	412
Bacillus cereus BAG1X1-1	IV	AHCQ01000035	227718bp	D	ICC_03315	two-component system response regulator yhcZ	99.10%	213aa	5.2e-113	412
Bacillus cereus VD014	IV	AHER01000028	222533bp	D	IIA_02024	hypothetical protein	97.20%	213aa	8.9e-111	405
Bacillus cereus VD156	IV	AHFH01000027	318846bp	D	IK7_03412	hypothetical protein	97.20%	213aa	8.9e-111	405
Bacillus cereus AH1134	IV	NZ_ABDA01000020	86615bp	D	BcerAH1_010100015478	Two-component response regulator yhcZ	98.60%	213aa	4.8e-112	409
Bacillus thuringiensis MC28	V	CP003687	5414494bp	F	MC28_1437	DNA-binding response regulator	96.70%	211aa	3.8e-109	400
Bacillus cereus Rock3-29	V	NZ_ACMJ01000039	97142bp	D	bcere0020_20070	DNA-binding response regulator	97.60%	211aa	7.6e-110	402
Bacillus cereus BAG5O-1	V	AHDIO1000010	130701bp	D	IEC_01441	hypothetical protein	97.60%	211aa	7.6e-110	402
Bacillus cereus BAG4X2-1	V	AHDHO1000032	330562bp	D	IEA_03296	hypothetical protein	97.60%	211aa	7.6e-110	402
Bacillus cereus Hub2-9	V	AHED01000029	246371bp	D	IG1_03214	hypothetical protein	97.60%	211aa	7.6e-110	402
Bacillus cereus BAG1O-2	V	AHC01000024	152083bp	D	IC9_03285	hypothetical protein	96.70%	211aa	3.8e-109	400
Bacillus cereus VD214	V	AHFN01000040	381629bp	D	IKI_01463	two-component system response regulator yhcZ	97.60%	211aa	7.0e-110	402
Bacillus cereus Hub4-10	V	AHEEO1000007	439990bp	D	IGK_01462	hypothetical protein	97.60%	211aa	7.0e-110	402
Bacillus cereus VD1A-2	V	AHDW01000034	545065bp	D	IGS_01448	two-component system response regulator yhcZ	97.60%	211aa	7.0e-110	402
Bacillus cereus VD148	V	AHFF01000025	190720bp	D	IK3_03299	hypothetical protein	97.60%	211aa	7.0e-110	402
Bacillus cereus VD131	V	AHFA01000025	142105bp	D	IIS_01433	two-component system response regulator yhcZ	97.60%	211aa	7.0e-110	402
Bacillus cereus BAG6O-1	V	AHDM01000026	317235bp	D	IEK_03253	hypothetical protein	97.60%	211aa	7.0e-110	402
Bacillus cereus Hub5-5	V	AHEG01000020	369993bp	D	IGO_02024	hypothetical protein	96.70%	211aa	3.5e-109	400
Bacillus cereus BAG2O-2	V	AHXC01000025	67731bp	D	ICQ_02028	hypothetical protein	96.70%	211aa	3.5e-109	400
Bacillus cereus Rock1-3	V	NZ_ACMG01000035	26669bp	D	bcere0017_20320	DNA-binding response regulator	96.70%	211aa	3.8e-109	400
Bacillus cereus VD115	V	AHEY01000021	276254bp	D	IIQ_02809	hypothetical protein	92.40%	211aa	2.8e-104	384
Bacillus cereus Rock3-28	V	NZ_ACMI01000127	59467bp	D	bcere0019_20130	DNA-binding response regulator	94.80%	211aa	2.1e-107	394
Bacillus cereus VD102	III	AHEW01000010	609057bp	D	IIK_02551	hypothetical protein	91.50%	214aa	6.9e-103	379
Bacillus cereus MSX-D12	III	AHEQ01000022	113765bp	D	II9_03245	hypothetical protein	91.50%	214aa	6.9e-103	379
Bacillus cereus m1293	III	NZ_ACLS01000062	182414bp	D	bcere0001_20480	DNA-binding response regulator	91.50%	214aa	9.0e-103	379

Bacillus cereus AND1407	III	AHCM01000013	143725bp	D	IC5_01272	hypothetical protein	91.50%	213aa	6.3e-103	379
Bacillus cereus ATCC 4342	III	NZ_ACLZ01000032	174174bp	D	bcere0010_20410	DNA-binding response regulator	91.40%	211aa	2.1e-104	384
Bacillus thuringiensis sv togigiensis BGSC 4Y1	III	NZ_ACMY01000057	79659bp	D	bthur0001_20520	DNA-binding response regulator	91.40%	211aa	2.8e-104	384
Bacillus cereus MSX-A12	III	AHEP01000020	181700bp	D	II7_02029	hypothetical protein	92.40%	209aa	1.8e-103	381
Bacillus cereus IS845/00	III	AHEI01000047	256667bp	D	IGS_04099	two-component system response regulator yhcZ	92.40%	209aa	1.7e-103	381
Bacillus cereus IS195	III	AHEH01000047	159830bp	D	IGO_03856	two-component system response regulator yhcZ	92.40%	209aa	1.7e-103	381
Bacillus cereus IS075	III	AHC02000004	262520bp	D	IAU_00162	two-component system response regulator yhcZ	92.40%	209aa	1.7e-103	381
Bacillus thuringiensis sv konkukian 97-27	III	NC_005957	5237682bp	F	BT9727_2048	response regulator	90.50%	209aa	1.7e-101	374
Bacillus cereus BDRD-ST26	III	NZ_ACMC01000050	24793bp	D	bcere0013_20820	DNA-binding response regulator	92.40%	209aa	1.8e-103	381
Bacillus cereus 95/8201	III	NZ_ACMF01000045	63991bp	D	bcere0016_21190	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus thuringiensis sv monterrey BGSC 4AJ1	III	NZ_ACNE01000046	68163bp	D	bthur0007_20380	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus cereus ISP3191	III	AHEK01000015	169039bp	D	IGW_02589	hypothetical protein	90.50%	209aa	4.4e-102	376
Bacillus thuringiensis Al Hakam	III	NC_008600	5257091bp	F	BALH_2025	DNA-binding response regulator	90.00%	221aa	3.8e-101	373
Bacillus cereus BGSC 6E1	III	NZ_ACLU01000051	33946bp	D	bcere0004_20550	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus cereus Rock3-42	III	NZ_ACMK01000064	65761bp	D	bcere0021_20720	DNA-binding response regulator	90.50%	209aa	2.2e-101	374
Bacillus thuringiensis sv pulsiniensis BGSC 4CC1	III	NZ_ACNJ01000044	14351bp	D	bthur0012_20950	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis H9401	III	NC_017729	5218947bp	F	H9401_2150	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis A2012 (Florida isolate)	III	NZ_AAAC02000001	5093554bp	D	Bant_010002887	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	90.50%	209aa	1.7e-101	374
Bacillus thuringiensis sv andalousiensis BGSC 4AW1	III	NZ_ACNG01000061	98499bp	D	bthur0009_20360	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus thuringiensis sv pondicheriensis BGSC 4BA1	III	NZ_ACNH01000040	22690bp	D	bthur0010_20440	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus cereus RCH_BC3 (Abyss contigs Sep '10)	III	bcer1768_2103G_42612_76	42513bp	D	bcer_00047010	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	90.00%	209aa	3.8e-101	373
Bacillus cereus W	III	NZ_ABZC01000004	365325bp	D	BcerW_010100010592	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus cereus AH187 [F4810/72]	III	NC_011658	5269030bp	F	BCAH187_A2375	DNA-binding response regulator, LuxR family	92.40%	209aa	1.8e-103	381
Bacillus cereus AH820	III	NC_011773	5302683bp	F	BCAH820_2290	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus cereus F837/76	III	NC_016779	5222906bp	F	bcf_11355	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus cereus NVH0597-99	III	NZ_ABDK01000009	213404bp	D	BcerN_010100015348	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus cereus 03BB108	III	NZ_ABDM01000021	89774bp	D	Bcer0_010100025929	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus cereus 03BB102	III	NC_012472	5269628bp	F	BCA_2348	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis CI	III	NC_014335	5196054bp	F	BACI_c2290	response regulator	90.50%	209aa	4.5e-102	376
Bacillus anthracis UR-1	III	ALNY01000016	99008bp	D	B353_15453	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis Sterne	III	NC_005945	5228663bp	F	BAS2109	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis Tsiankovskii-I	III	NZ_ABDN01000002	584883bp	D	BantT_010100007315	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis A0193	III	NZ_ABKF01000011	156048bp	D	BAQ_2310	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis A0442	III	NZ_ABKG01000002	460661bp	D	BAH_2315	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis A0389	III	NZABL01000008	163817bp	D	BAK_2346	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis A0465	III	NZABLH01000007	218708bp	D	BAM_2309	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis A0174	III	NZ_ABLT01000001	672784bp	D	BAO_2259	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis A0248	III	NC_012659	5227419bp	F	BAA_2327	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis CNEVA-9066	III	NZ_AAEN01000016	1053408bp	D	BantC_010100013455	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis A1055	III	NZ_AAEO01000022	1320955bp	D	BantA1_010100007284	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis Kruger B	III	NZ_AAEQ01000035	1294190bp	D	BantKB_010100021382	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis WesternNA USA6153	III	NZ_AAER01000039	367030bp	D	BantWNA_010100019239	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis Australia 94	III	NZ_AAES01000035	1143198bp	D	BantA9_010100017591	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus cereus E33L (ZK)	III	NC_006274	5300915bp	F	BCZK2046	response regulator	90.50%	209aa	1.7e-101	374
Bacillus anthracis A0488	III	NZ_ABJC01000007	164396bp	D	BAC_2284	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis CDC 684	III	NC_012581	5230115bp	F	BAMEG_2331	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis Vollum	III	NZ_AAEP01000025	812727bp	D	BantV_01010004036	DNA-binding response regulator	90.50%	209aa	1.7e-101	374
Bacillus thuringiensis sv. finitimus YBT-020	III	CP002508	5355490bp	F	VBT020_11605	response regulator	91.50%	216aa	9.6e-105	385
Bacillus cereus FRI-35	III	CP003747	5083176bp	F	BCK_23515	LuxR family transcriptional regulator	90.90%	211aa	9.1e-102	375
Bacillus cereus Q1	III	NC_011969	5214195bp	F	BCQ_2200	response regulator	91.50%	213aa	6.9e-103	379
Bacillus cereus NC7401	III	NC_016771	5221581bp	F	BCN_2193	DNA-binding response regulator, LuxR family	92.40%	209aa	1.8e-103	381
Bacillus anthracis Ames	III	NC_003997	5227293bp	F	BA2265	DNA-binding response regulator, LuxR family	90.50%	209aa	1.7e-101	374
Bacillus anthracis Ames Ancestor A2084	III	NC_007530	5227419bp	F	GBAA2265	dna-binding response regulator, luxr family	90.50%	209aa	1.7e-101	374
Bacillus cereus G9241	III	NZ_AAEK01000006	163640bp	D	BCE_G9241_2227	MW1789	92.40%	211aa	3.3e-105	387
Bacillus cereus ATCC 10987	III	NC_003909	5224283bp	F	BCE_2293	DNA-binding response regulator, LuxR family	91.40%	211aa	1.5e-102	378
Bacillus cereus H3081.97	III	NZ_ABLD01000001	619721bp	D	BcerH_010100003400	DNA-binding response regulator	91.50%	213aa	6.9e-103	379
Bacillus cereus BAG5X2-1	II	AHDLO1000023	238523bp	D	IEI_02860	hypothetical protein	92.60%	219aa	5.6e-105	386
Bacillus cereus MM3	II	NZ_ACLW01000054	76810bp	D	bcere0006_20660	DNA-binding response regulator	94.30%	215aa	1.8e-106	391
Bacillus cereus AH1271	II	NZ_ACMR01000093	24635bp	D	bcere0028_20630	DNA-binding response regulator	92.40%	215aa	2.5e-105	387
Bacillus cereus BAG2X1-2	II	AHDAO1000026	141630bp	D	ICW_03515	hypothetical protein	93.40%	215aa	8.6e-106	389
Bacillus cereus BAG6X1-1	II	AHDO01000013	147985bp	D	IEO_01694	hypothetical protein	93.40%	215aa	8.0e-106	389
Bacillus cereus BAG2O-3	II	AHYC01000026	280303bp	D	ICS_03405	two-component system response regulator yhcZ	93.80%	211aa	1.5e-105	388
Bacillus cereus BAG3O-1	II	AHFV01000023	196299bp	D	KQ1_02171	two-component system response regulator yhcZ	94.30%	211aa	4.7e-106	389
Bacillus cereus B5-2	II	AHFV01000027	319887bp	D	KQ3_01489	two-component system response regulator yhcZ	94.30%	211aa	4.7e-106	389
Bacillus cereus R309803	unclustered	NZ_ACYL01000040	178172bp	D	bcere0009_20290	DNA-binding response regulator	89.60%	211aa	3.4e-102	377
Bacillus cereus BAG2X1-3	unclustered	AHDB01000024	344606bp	D	ICY_02621	hypothetical protein	92.80%	211aa	6.2e-104	382
Bacillus cereus BAG2X1-1	unclustered	AHZC01000025	240792bp	D	ICU_02792	hypothetical protein	92.80%	211aa	6.2e-104	382
Bacillus cereus AH1272	VI	NZ_ACMS01000103	52288bp	D	bcere0029_21260	DNA-binding response regulator	91.90%	211aa	9.6e-105	385
Bacillus cereus AH1273	VI	NZ_ACMT01000110	23861bp	D	bcere0030_21280	DNA-binding response regulator	91.90%	211aa	9.6e-105	385
Bacillus cereus VDM022	VI	AHP01000020	337261bp	D	IKM_03290	hypothetical protein	93.40%	211aa	8.0e-106	389
Bacillus cereus VD078	VI	AHEV01000019	252815bp	D	III_03206	hypothetical protein	93.40%	211aa	1.1e-105	388
Bacillus cereus VDM019	VI	AHF01000023	267709bp	D	IKK_01963	two-component system response regulator yhcZ	93.40%	211aa	8.0e-106	389
Bacillus cereus VD021	VI	AHES01000030	145584bp	D	IIC_03350	two-component system response regulator yhcZ	93.40%	211aa	8.0e-106	389
Bacillus cereus VD146	VI	AHFE01000041	267154bp	D	IK1_01449	two-component system response regulator yhcZ	93.40%	211aa	8.0e-106	389
Bacillus cereus CER074	VI	AHDT01000022	288640bp	D	IEY_03319	hypothetical protein	93.40%	211aa	8.0e-106	389
Bacillus cereus CER057	VI	AHDS01000024	245438bp	D	IEW_02013	hypothetical protein	93.40%	211aa	8.0e-106	389
Bacillus cereus RTB2-4	VI	AHDR01000022	286458bp	D	IEU_02016	hypothetical protein	93.40%	211aa	8.0e-106	389
Bacillus cereus BDRD-ST196	VI	NZ_ACMD01000078	4187bp	D	bcere0014_20180	DNA-binding response regulator	93.40%	211aa	8.7e-106	389
Bacillus myoides DSM 2048	VI	NZ_ACMU01000044	68004bp	D	bmyco0001_19860	DNA-binding response regulator	93.40%	211aa	8.7e-106	389
Bacillus weihenstephanensis KBAB4	VI	NC_010184	5262775bp	F	BcerKBAB4_2087	two component transcriptional regulator, LuxR family	93.40%	213aa	8.7e-106	389
Bacillus cereus HuA2-9	VI	AHDY01000018	295569bp	D	IG9_02844	two-component system response regulator yhcZ	93.40%	211aa	8.0e-106	389
Bacillus cereus HuA3-9	VI	AHDZ01000001	188645bp	D	IGA_00107	two-component system response regulator yhcZ	92.90%	211aa	4.0e-105	386
Bacillus cereus WD048	VI	AHEU01000018	243114bp	D	IIG_02689	hypothetical protein	92.90%	211aa	5.6e-105	386
Bacillus cereus HuA2-1	VI	AHDV01000009	199286bp	D	IG3_01727	hypothetical protein	93.40%	211aa	8.0e-106	389
Bacillus cereus AH621	VI	NZ_ACLX01000056	70672bp	D	bcere0007_20670	DNA-binding response regulator	92.90%	211aa	5.6e-105	386
Bacillus cereus VD142	VI	AHCL02000009	142780bp	D	IC3_01099	two-component system response regulator yhcZ	93.40%	211aa	8.0e-106	389
Bacillus cereus VDM062	VI	AHFS01000031	185835bp	D	IKS_03541	hypothetical protein	93.40%	211aa	1.0e-105	388
Bacillus cereus VDM034	VI	AHFQ01000013	137918bp	D	IKO_01631	hypothetical protein	93.40%	211aa	1.0e-105	388
Bacillus cereus HuA2-4	VI	AHDX01000025	22341							

Bacillus cereus VD107	VI	AHEX01000014	145386bp	D	IIM_01398	hypothetical protein	91.90%	211aa	3.1e-103	380
Bacillus cereus BAG5X1-1	VI	AHDJ01000028	167843bp	D	IEE_03022	hypothetical protein	92.40%	211aa	1.6e-104	384
Bacillus cereus VD118	VI	AHEZ01000044	257274bp	D	IIQ_01181	two-component system response regulator yhcZ	91.90%	211aa	1.5e-104	384
Bacillus cereus MC118	VI	AHEM01000036	50635bp	D	II1_03384	two-component system response regulator yhcZ	93.40%	211aa	8.0e-106	389
Bacillus cereus BAG60-2	VI	AHDN01000033	230347bp	D	IEM_03140	hypothetical protein	91.90%	211aa	1.5e-104	384
Bacillus cereus MC67	VI	AHEN01000003	229617bp	D	II3_00195	hypothetical protein	93.40%	211aa	8.0e-106	389
Bacillus cereus BAG1X1-3	VI	AHCS01000023	1262248bp	D	ICG_03308	hypothetical protein	92.90%	211aa	8.6e-106	389
Bacillus cereus VDM053	VI	AHFRO1000039	621715bp	D	IKQ_01732	two-component system response regulator yhcZ	91.90%	211aa	8.8e-105	385
Bacillus cereus BAG1O-1	VI	AHCN01000021	162560bp	D	IC7_01509	two-component system response regulator yhcZ	92.90%	211aa	8.0e-106	389
Bacillus cereus BAG3X2-1	VI	AHDD01000023	113935bp	D	IE3_03211	hypothetical protein	92.90%	211aa	6.6e-106	389
Bacillus mycoides Rock3-17	I	NZ_ACMW01000051	87918bp	D	bmyco0003_19330	DNA-binding response regulator	90.40%	211aa	6.5e-101	372
Bacillus cereus VDM006	I	AHF01000037	802420bp	D	KOW_00627	two-component system response regulator yhcZ	89.90%	211aa	4.2e-99	366
Bacillus cereus VDM021	I	AHFU01000038	209010bp	D	KOY_03299	two-component system response regulator yhcZ	89.90%	211aa	4.2e-99	366
Bacillus cereus VD136	I	AHFC01000047	594013bp	D	IIW_01265	two-component system response regulator yhcZ	89.90%	211aa	4.2e-99	366
Bacillus pseudomycoides DSM 12442	I	NZ_ACMX01000036	125315bp	D	bpmxy0001_20110	DNA-binding response regulator	90.40%	211aa	6.5e-101	372
Bacillus cereus Rock3-44	I	NZ_ACML01000120	22469bp	D	bcere0022_18290	DNA-binding response regulator	89.50%	211aa	1.3e-98	365
Bacillus mycoides Rock1-4	I	NZ_ACMV01000133	85498bp	D	bmyco0002_19210	DNA-binding response regulator	90.40%	211aa	6.5e-101	372

All data, except data from the second column, came from Integrated Microbial Genomes data base (Markowitz et al., 2012) ; homologs for *casKR* genes were first determined through BLASTp hits between *casKR* genes from ATCC14579 genome (*bc2216-17*) and genes in all other genomes, and orthologs were computed as bidirectional best hits between genomes; percent identity, length of sequence, E-value and bit score are displayed for each ortholog. The C2S was absent on NVH391-98 genome (phylogenetic group VII)

(¹) affiliation to phylogenetic groups using *panC* gene sequence, as previously described (Guinebretiere et al., 2010) ; (²) Genome completion, D : draft, F : finished ; (³) percent identity for translated proteins ; (⁴) NA : not applicable