

## Genetic environment of *cry1* genes indicates their common origin

Krzysztof Fiedoruk<sup>1</sup>, Tamara Daniluk<sup>1</sup>, Jacques Mahillon<sup>2</sup>, Katarzyna Leszczynska<sup>1</sup>, Izabela Swiecicka<sup>3,4</sup>

<sup>1</sup> Department of Microbiology, Medical University of Bialystok, Bialystok, Poland.

<sup>2</sup> Laboratory of Food and Environmental Microbiology, Earth and Life Institute, Université catholique de Louvain, Louvain-la-Neuve, Belgium.

<sup>3</sup> Department of Microbiology, University of Bialystok, Bialystok, Poland.

<sup>4</sup> Laboratory of Applied Microbiology, University of Bialystok, Bialystok, Poland.

## Supplementary Material online

<b>Table S1</b>	Plasmids screened for the presence of the <i>cry1</i> genes.
<b>Table S2</b>	Open reading frames (ORFs) in the ~120 kb plasmid region covering the insecticidal pathogenicity island (PAI) from <i>B. thuringiensis</i> IS5056 plasmid pIS56-285 (CP004136). ORFs were annotated using Blast2GO software.
<b>Figure S1</b>	The insecticidal pathogenicity island (PAI) in the <i>B. thuringiensis</i> plasmids.
<b>Figure S2</b>	The <i>cry1</i> gene cassette in the <i>B. thuringiensis</i> plasmids. The insecticidal pathogenicity island (PAI) was used as the reference.
<b>Figure S3</b>	(a) Alignment of the downstream region of <i>cry1</i> genes containing the positive retroregulator. (b) Comparison of sequence identity of the positive retroregulator between various <i>cry1</i> genes using UPGMA clustering method. (c) Prediction of the lowest free energy ( $\Delta G$ in kcal/mol) structure for mRNA of various variants of the <i>cry1</i> positive retroregulator. The analysis was done using RNA structure web server ( <a href="http://rna.urmc.rochester.edu/RNAstructureWeb/Servers/Predict1/Predict1.html">http://rna.urmc.rochester.edu/RNAstructureWeb/Servers/Predict1/Predict1.html</a> ).
<b>Figure S4</b>	Intergenic region between <i>cry1Aa</i> and <i>cry1la</i> from the insecticidal PAI (plasmid pBMB299, GenBank Acc. no. CP004876, was used as the reference sequence).
<b>Figure S5</b>	Comparison of plasmids with <i>ori44</i> and <i>repA</i> replication systems carrying <i>cry1A</i> or <i>cry1F</i> with related plasmids missing the <i>cry1</i> genes.
<b>Figure S6</b>	Comparison of plasmids with <i>ori60</i> replication type carrying <i>cry1A</i> or <i>cry1B</i> with similar plasmids missing the <i>cry1</i> genes.
<b>Figure S7</b>	Comparison of plasmid with <i>ori43</i> replication system carrying <i>cry1A</i> with related plasmids missing the <i>cry1</i> genes.
<b>Figure S8</b>	Putative gene cassette (~120 kb) covering the insecticidal PAI.
<b>Figure S9</b>	Inconsistencies in <i>cry1Ac</i> location in plasmids from the same <i>B. thuringiensis</i> strains deposited in GenBank by various sequencing projects; (a) <i>B. thuringiensis</i> sv. <i>kurstaki</i> HD-1 plasmids (CP009999-CP010000 vs. CP004875-CP004876), and (b) <i>B. thuringiensis</i> sv. <i>kurstaki</i> strain YBT-1520 plasmids (CP007613 vs. CP004862).
<b>Figure S10</b>	Genetic environment of <i>cry1l</i> , <i>cry1M</i> , <i>cry1N-like</i> and <i>cry3A</i> genes.
<b>Figure S11</b>	Comparison of <i>B. subtilis</i> $K^+(Na^+)/H^+$ antiporter encoded by the <i>yhaU-yhaT-yhaS</i> operon with $K^+(Na^+)/H^+$ antiporters from <i>B. thuringiensis</i> IS5056 chromosome and the <i>cry1</i> -carrying plasmids, using the tblastx algorithm.
<b>Figure S12</b>	Comparison of methyl-accepting chemotaxis protein (MCP) from the insecticidal PAI of <i>B. thuringiensis</i> IS5056 plasmid pIS56-285 (CP004136) with its chromosomal homolog (AGG02078.1).
<b>Figure S13</b>	Comparison of <i>B. subtilis</i> <i>xlyA</i> with N-acetylmuramoyl-L-alanine amidase genes from <i>B. thuringiensis</i> IS5056 chromosome and the <i>cry1</i> -carrying plasmids, using the tblastx algorithm.
<b>Figure S14</b>	Comparison (tblastx algorithm) of ADP-ribose 1-phosphate phosphatase gene locus from the insecticidal PAI ( <i>B. thuringiensis</i> IS5056 plasmid pIS56-285) with similar loci from the chromosomes of <i>Geobacillus subterraneus</i> , <i>Anoxybacillus amylolyticus</i> and <i>Paenibacillus</i> sp..

**Table S1.** Plasmids screened for the presence of the *cry1* genes.

<b>Strain and plasmid</b>	<b>Accession number</b>	<b>Length [bp]</b>
<i>B. bombysepticus</i> plasmid pBb	CP007513	577,809
<i>B. cereus</i> 03BB102 plasmid p03BB102_179	CP001406	179,680
<i>B. cereus</i> 03BB102 plasmid unnamed	CP009317	179,680
<i>B. cereus</i> 03BB108 plasmid pBFI_1	CP009639	281,957
<i>B. cereus</i> 03BB108 plasmid pBFI_2	CP009636	238,933
<i>B. cereus</i> 03BB108 plasmid pBFI_3	CP009640	85,879
<i>B. cereus</i> 03BB108 plasmid pBFI_4	CP009638	61,862
<i>B. cereus</i> 03BB108 plasmid pBFI_5	CP009637	42,470
<i>B. cereus</i> 03BB108 plasmid pBFI_6	CP009635	9,797
<i>B. cereus</i> 03BB108 plasmid pBFI_7	CP009634	4,898
<i>B. cereus</i> AH187 plasmid pAH187_12	CP001178	12,481
<i>B. cereus</i> AH187 plasmid pAH187_270	CP001179	270,082
<i>B. cereus</i> AH187 plasmid pAH187_3	CP001181	3,091
<i>B. cereus</i> AH187 plasmid pAH187_45	CP001180	45,173
<i>B. cereus</i> AH820 plasmid pAH820_10	CP001286	10,915
<i>B. cereus</i> AH820 plasmid pAH820_272	CP001285	272,145
<i>B. cereus</i> AH820 plasmid pAH820_3	CP001284	3,091
<i>B. cereus</i> ATCC 10987 plasmid pBc10987	AE017195	208,369
<i>B. cereus</i> ATCC 14579 plasmid pBClin15	AE016878	15,274
<i>B. cereus</i> ATCC 4342 plasmid pBGM	CP009627	36,802
<i>B. cereus</i> biovar <i>anthracis</i> strain Cl plasmid pBAstCI14	CP001749	14,219
<i>B. cereus</i> biovar <i>anthracis</i> strain Cl plasmid pCI-XO1	CP001747	181,907
<i>B. cereus</i> biovar <i>anthracis</i> strain Cl plasmid pCI-XO2	CP001748	94,469
<i>B. cereus</i> D17 plasmid unnamed	CP009299	210,673
<i>B. cereus</i> E33L plasmid pBCO_1	CP009967	465,970
<i>B. cereus</i> E33L plasmid pBCO_2	CP009966	53,501
<i>B. cereus</i> E33L plasmid pBCO_3	CP009969	9,146
<i>B. cereus</i> E33L plasmid pBCO_4	CP009970	7,863
<i>B. cereus</i> E33L plasmid pBCO_5	CP009965	4,983
<i>B. cereus</i> E33L plasmid pE33L466	CP000040	466,370
<i>B. cereus</i> E33L plasmid pE33L5	CP000041	5,108
<i>B. cereus</i> E33L plasmid pE33L54	CP000042	53,501
<i>B. cereus</i> E33L plasmid pE33L8	CP000043	8,191
<i>B. cereus</i> E33L plasmid pE33L9	CP000044	9,150
<i>B. cereus</i> F837/76 plasmid pF837_10	CP003189	10,288
<i>B. cereus</i> F837/76 plasmid pF837_55	CP003188	55,304
<i>B. cereus</i> FRI-35 plasmid p01	CP003748	218,786
<i>B. cereus</i> FRI-35 plasmid p02	CP003749	40,993
<i>B. cereus</i> FRI-35 plasmid p03	CP003750	36,273
<i>B. cereus</i> FRI-35 plasmid p04	CP003751	3,091
<i>B. cereus</i> G9241 plasmid pBC210	CP009591	209,255
<i>B. cereus</i> G9241 plasmid pBCX01	CP009592	190,860
<i>B. cereus</i> G9241 plasmid pBFH_1	CP009589	52,166
<i>B. cereus</i> G9842 plasmid pG9842_140	CP001188	140,001
<i>B. cereus</i> G9842 plasmid pG9842_209	CP001187	209,488
<i>B. cereus</i> H3081.97 plasmid pH308197_10	CP001168	10,077
<i>B. cereus</i> H3081.97 plasmid pH308197_11	CP001167	11,567
<i>B. cereus</i> H3081.97 plasmid pH308197_258	CP001166	258,484
<i>B. cereus</i> H3081.97 plasmid pH308197_29	CP001169	29,189
<i>B. cereus</i> H3081.97 plasmid pH308197_3	CP001171	3,424
<i>B. cereus</i> H3081.97 plasmid pH308197_73	CP001170	72,792
<i>B. cereus</i> NC7401 plasmid pNC1 DNA	AP007211	47,972
<i>B. cereus</i> NC7401 plasmid pNC2 DNA	AP007212	5,436
<i>B. cereus</i> NC7401 plasmid pNC3 DNA	AP007213	3,869
<i>B. cereus</i> NC7401 plasmid pNC4 DNA	AP007214	3,091
<i>B. cereus</i> NC7401 plasmid pNCclD DNA	AP007210	270,082

<i>B. cereus</i> plasmid pBC16	U32369	4,630
<i>B. cereus</i> plasmid pBC-Tim DNA	NC_025012	8,983
<i>B. cereus</i> plasmid pPRS3a	GQ404376	4,126
<i>B. cereus</i> Q1 plasmid pBc239	CP000228	239,246
<i>B. cereus</i> Q1 plasmid pBc53	CP000229	52,766
<i>B. cereus</i> strain 03BB87 plasmid pBCN	CP009939	52,166
<i>B. cereus</i> strain 03BB87 plasmid pBCX01	CP009940	209,381
<i>B. cereus</i> strain 3a plasmid pBFC_1	CP009593	7,300
<i>B. cereus</i> strain 3a plasmid pBFC_2	CP009594	51,531
<i>B. cereus</i> strain 3a plasmid pBFC_3	CP009595	312,478
<i>B. cereus</i> strain A1 plasmid pBCA1	CP015730	300,156
<i>B. cereus</i> strain A1 plasmid pBCA2	CP015728	70,374
<i>B. cereus</i> strain A1 plasmid pBCA3	CP015729	11,778
<i>B. cereus</i> strain AH187 plasmid pCER270	DQ889676	270,082
<i>B. cereus</i> strain AH818 plasmid pPER272	DQ889678	272,145
<i>B. cereus</i> strain AH820 plasmid pPER272	DQ889677	272,145
<i>B. cereus</i> strain AR156 plasmid pAR10	CP015590	10,789
<i>B. cereus</i> strain AR156 plasmid pAR41	CP015591	40,712
<i>B. cereus</i> strain AR156 plasmid pAR460	CP015592	459,971
<i>B. cereus</i> strain CMCC P0011 plasmid pRML05	CP011154	591,112
<i>B. cereus</i> strain CMCC P0021 plasmid pRML04	CP011152	591,110
<i>B. cereus</i> strain FM1 plasmid unnamed	CP009368	402,605
<i>B. cereus</i> strain FORC_013 plasmid pFORC13	CP011146	259,749
<i>B. cereus</i> strain G9241 plasmid pBC210	DQ889679	209,385
<i>B. cereus</i> strain G9241 plasmid pBCXO1	DQ889680	190,861
<i>B. cereus</i> strain HN001 plasmid pRML01	CP011156	435,420
<i>B. cereus</i> strain HN001 plasmid pRML02	CP011157	141,238
<i>B. cereus</i> strain NJ-W plasmid plasmid-32	CP012485	11,744
<i>B. cereus</i> strain NJ-W plasmid plasmid-35-36	CP012484	9,032
<i>B. cereus</i> strain NJ-W plasmid plasmid-37	CP012486	7,703
<i>B. cereus</i> strain S2-8 plasmid pBFR_1	CP009604	7,300
<i>B. cereus</i> strain S2-8 plasmid pBFR_2	CP009606	312,478
<i>B. cereus</i> strain S2-8 plasmid pBFR_3	CP009603	51,512
<i>B. cereus</i> subsp. <i>cytotoxins</i> NVH 391-98 plasmid pBC9801	CP000765	7,135
<i>B. cereus</i> VPC1401 plasmid pLVP1401	FR675941	56,149
<i>B. thuringiensis</i> 4Q2 plasmid pTX14-2	NC_004334	6,829
<i>B. thuringiensis</i> BMB171 plasmid pBMB171	NC_014172	312,963
<i>B. thuringiensis</i> Bt407 plasmid BTB_15p	CP003892	15,189
<i>B. thuringiensis</i> Bt407 plasmid BTB_2p	CP003897	2,062
<i>B. thuringiensis</i> Bt407 plasmid BTB_502p	CP003890	501,911
<i>B. thuringiensis</i> Bt407 plasmid BTB_5p	CP003896	5,518
<i>B. thuringiensis</i> Bt407 plasmid BTB_6p	CP003895	6,880
<i>B. thuringiensis</i> Bt407 plasmid BTB_78p	CP003891	77,895
<i>B. thuringiensis</i> Bt407 plasmid BTB_7p	CP003894	7,635
<i>B. thuringiensis</i> Bt407 plasmid BTB_8p	CP003893	8,240
<i>B. thuringiensis</i> Bt407 plasmid BTB_9p	CP003898	8,513
<i>B. thuringiensis</i> CT43 plasmid pBMB0558	NC_014937	109,464
<i>B. thuringiensis</i> H1.1 plasmid pGI3	NC_005567	11,365
<i>B. thuringiensis</i> HD1002 plasmid 1	CP009349	359,439
<i>B. thuringiensis</i> HD1002 plasmid 2	CP009348	349,602
<i>B. thuringiensis</i> HD1002 plasmid 3	CP009347	235,425
<i>B. thuringiensis</i> HD1002 plasmid 4	CP009350	107,443
<i>B. thuringiensis</i> HD1002 plasmid 5	CP009346	14,961
<i>B. thuringiensis</i> HD1002 plasmid 6	CP009345	7,697
<i>B. thuringiensis</i> HD1002 plasmid 7	CP009344	6,824
<i>B. thuringiensis</i> HD-771 plasmid p01	CP003753	171,030
<i>B. thuringiensis</i> HD-771 plasmid p02	CP003754	168,999
<i>B. thuringiensis</i> HD-771 plasmid p03	CP003755	69,876
<i>B. thuringiensis</i> HD-771 plasmid p04	CP003756	65,470

<i>B. thuringiensis</i> HD-771 plasmid p05	CP003757	45,262
<i>B. thuringiensis</i> HD-771 plasmid p06	CP003758	14,056
<i>B. thuringiensis</i> HD-771 plasmid p07	CP003759	9,070
<i>B. thuringiensis</i> HD-771 plasmid p08	CP003760	8,574
<i>B. thuringiensis</i> HD-789 plasmid pBTHD789-1	CP003764	349,599
<i>B. thuringiensis</i> HD-789 plasmid pBTHD789-2	CP003765	235,425
<i>B. thuringiensis</i> HD-789 plasmid pBTHD789-3	CP003766	224,872
<i>B. thuringiensis</i> HD-789 plasmid pBTHD789-4	CP003767	14,935
<i>B. thuringiensis</i> HD-789 plasmid pBTHD789-5	CP003768	7,697
<i>B. thuringiensis</i> HD-789 plasmid pBTHD789-6	CP003769	6,824
<i>B. thuringiensis</i> MC28 plasmid pMC183	CP003691	183,210
<i>B. thuringiensis</i> MC28 plasmid pMC189	CP003692	189,702
<i>B. thuringiensis</i> MC28 plasmid pMC319	CP003693	319,710
<i>B. thuringiensis</i> MC28 plasmid pMC429	CP003694	429,674
<i>B. thuringiensis</i> MC28 plasmid pMC54	CP003689	54,484
<i>B. thuringiensis</i> MC28 plasmid pMC8	CP003688	7,826
<i>B. thuringiensis</i> MC28 plasmid pMC95	CP003690	95,433
<i>B. thuringiensis</i> plasmid pBMB2062-2	NC_019228	2,062
<i>B. thuringiensis</i> plasmid pBMB67	NC_009841	67,159
<i>B. thuringiensis</i> plasmid pDAN-involved	NC_007203	6,909
<i>B. thuringiensis</i> plasmid pFR12	NC_010281	12,095
<i>B. thuringiensis</i> plasmid pFR12.5	NC_010282	12,459
<i>B. thuringiensis</i> plasmid pFR55	NC_010283	55,712
<i>B. thuringiensis</i> plasmid pK1S1	NC_009034	5,475
<i>B. thuringiensis</i> serovar <i>aizawai</i> strain 1-3 plasmid pBt1-3	NC_020884	11,363
<i>B. thuringiensis</i> serovar <i>alesti</i> strain BGSC 4C1 plasmid pBMB267	CP015177	267,609
<i>B. thuringiensis</i> serovar <i>alesti</i> strain BGSC 4C1 plasmid pBMB4227	CP015178	4,227
<i>B. thuringiensis</i> serovar <i>alesti</i> strain BGSC 4C1 plasmid pBMB57	CP015179	57,268
<i>B. thuringiensis</i> serovar <i>alesti</i> strain BGSC 4C1 plasmid pBMB71	CP015180	71,696
<i>B. thuringiensis</i> serovar <i>alesti</i> strain BGSC 4C1 plasmid pBMB8208	CP015181	8,208
<i>B. thuringiensis</i> serovar <i>alesti</i> strain BGSC 4C1 plasmid pBMB8291	CP015182	8,291
<i>B. thuringiensis</i> serovar <i>cameroun</i> plasmid pBMB2062-32	NC_017197	2,062
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT127	CP001908	127,885
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT14	CP001909	14,860
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT281	CP001910	281,231
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT51	CP001911	51,488
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT6880	CP001912	6,880
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT72	CP001913	72,074
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT8252	CP001914	8,252
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT83	CP001915	83,590
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT8513	CP001916	8,513
<i>B. thuringiensis</i> serovar <i>chinensis</i> CT-43 plasmid pCT9547	CP001917	9,547
<i>B. thuringiensis</i> serovar <i>coreanensis</i> strain ST7 plasmid pST7-1	CP016195	317,818
<i>B. thuringiensis</i> serovar <i>coreanensis</i> strain ST7 plasmid pST7-2	CP016196	149,450
<i>B. thuringiensis</i> serovar <i>coreanensis</i> strain ST7 plasmid pST7-3	CP016197	92,610
<i>B. thuringiensis</i> serovar <i>coreanensis</i> strain ST7 plasmid pST7-4	CP016198	60,883
<i>B. thuringiensis</i> serovar <i>finitimus</i> YBT-020 plasmid pBMB26	CP002509	187,880
<i>B. thuringiensis</i> serovar <i>finitimus</i> YBT-020 plasmid pBMB28	CP002510	139,013
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB12	CP010097	12,866
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB126	CP010092	126,898
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB267	CP010091	267,359
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB426	CP010090	426,282
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB47	CP010095	46,979
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB55	CP010094	55,460
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB7	CP010098	10,656
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB71	CP010093	71,373
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMB8	CP010099	8,423
<i>B. thuringiensis</i> serovar <i>galleriae</i> strain HD-29 plasmid pBMBLin15	NZ_CP010096	14,749
<i>B. thuringiensis</i> serovar <i>indiana</i> strain HD-521 plasmid pBTHD521-1	CP010107	7,042

<i>B. thuringiensis</i> serovar <i>indiana</i> strain HD-521 plasmid pBTHD521-2	CP010108	49,838
<i>B. thuringiensis</i> serovar <i>indiana</i> strain HD-521 plasmid pBTHD521-3	CP010109	71,771
<i>B. thuringiensis</i> serovar <i>indiana</i> strain HD-521 plasmid pBTHD521-4	CP010110	71,646
<i>B. thuringiensis</i> serovar <i>indiana</i> strain HD-521 plasmid pBTHD521-5	CP010111	253,580
<i>B. thuringiensis</i> serovar <i>indiana</i> strain HD-521 plasmid pBTHD521-6	CP010112	314,883
<i>B. thuringiensis</i> serovar <i>israelensis</i> strain HD-567 plasmid pBtoxis	NC_010076	127,923
<i>B. thuringiensis</i> serovar <i>israelensis</i> strain AM65-52 plasmid pAM65-52-5-100K	CP013280	99,993
<i>B. thuringiensis</i> serovar <i>konkukian</i> strain 97-27 plasmid pBT9727	CP000047	77,112
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB14	CP004883	14,721
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB2062	CP004878	2,062
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB299	CP004876	299,843
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB431	CP004877	431,546
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB46	CP004871	46,634
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB64	CP004872	64,522
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB65	CP004873	65,873
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB74	CP004874	74,480
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB7635	CP004879	7,635
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB8240	CP004880	8,240
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB8513	CP004881	8,513
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMB95	CP004875	95,983
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid pBMBLin15	CP004882	14,870
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-73 plasmid pAW63	CP004072	71,777
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-73 plasmid pHT11	CP004073	11,769
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-73 plasmid pHT7	CP004076	7,635
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-73 plasmid pHT73	CP004070	77,351
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-73 plasmid pHT77	CP004071	76,490
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-73 plasmid pHT8_1	CP004074	8,513
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-73 plasmid pHT8_2	CP004075	8,241
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB11	CP004863	11,769
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB11	CP007612	12,003
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB2062	CP004859	2,062
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB2062	CP007608	2,062
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB293	CP004861	293,574
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB293	CP007615	293,574
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB400	CP007616	416,210
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB422	CP004860	422,692
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB53	CP004862	53,838
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB67	CP004869	67,159
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB69	CP007613	69,416
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB7635	CP004867	7,635
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB7635	NC_011796	7,635
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB7921	CP004866	7,921
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB7921	CP007609	7,921
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB8240	CP004865	8,240
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB8240	CP007610	8,240
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB8513	CP004864	8,513
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB8513	CP007611	8,513
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB94	CP004868	94,568
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB95	CP007614	94,637
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain YBT-1520 plasmid pBMB9741	NC_001272	6,578
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed1	CP009998	412,022
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed10	CP010010	14,889
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed11	CP010009	8,279
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed12	CP010007	8,513
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed13	CP010011	7,635
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed14	CP010008	2,062
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed2	CP009999	317,336
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed3	CP010000	82,528
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed4	CP010001	82,303

<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed5	CP010002	80,285
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed6	CP010003	69,317
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed7	CP010006	46,634
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed8	CP010004	34,150
<i>B. thuringiensis</i> serovar <i>kurstaki</i> strain HD-1 plasmid unnamed9	CP010012	18,332
<i>B. thuringiensis</i> serovar <i>morrisoni</i> strain BGSC 4AA1 plasmid pBMB232	CP010578	232,994
<i>B. thuringiensis</i> serovar <i>morrisoni</i> strain BGSC 4AA1 plasmid pBMB48	CP010583	4,845
<i>B. thuringiensis</i> serovar <i>morrisoni</i> strain BGSC 4AA1 plasmid pBMB51	CP010582	51,723
<i>B. thuringiensis</i> serovar <i>morrisoni</i> strain BGSC 4AA1 plasmid pBMB68	CP010581	68,444
<i>B. thuringiensis</i> serovar <i>morrisoni</i> strain BGSC 4AA1 plasmid pBMB76	CP010580	76,979
<i>B. thuringiensis</i> serovar <i>morrisoni</i> strain BGSC 4AA1 plasmid pBMB92	CP010579	92,619
<i>B. thuringiensis</i> serovar <i>rongseni</i> plasmid pBMB2062-56	NC_019227	2,062
<i>B. thuringiensis</i> serovar <i>tenebrionis</i> plasmid pBMB175	NC_010895	14,841
<i>B. thuringiensis</i> serovar <i>tenebrionis</i> strain YBT-1765 plasmid pBMB165	NC_023074	77,627
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-107	CP004134	107,431
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-11	CP004127	11,331
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-15	CP004128	15,185
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-16	CP004129	16,206
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-233	CP004135	233,730
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-285	CP004136	285,459
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-328	CP004137	328,151
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-39	CP004130	39,749
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-6	CP004124	6,880
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-63	CP004131	63,864
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-68	CP004132	68,616
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-8	CP004125	8,251
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-85	CP004133	85,134
<i>B. thuringiensis</i> serovar <i>thuringiensis</i> strain IS5056 plasmid pIS56-9	CP004126	9,671
<i>B. thuringiensis</i> serovar <i>tolworthi</i> plasmid pKK1 DNA	NZ_AP014865	437,451
<i>B. thuringiensis</i> serovar <i>tolworthi</i> plasmid pKK2 DNA	NZ_AP014866	293,217
<i>B. thuringiensis</i> serovar <i>tolworthi</i> plasmid pKK3 DNA	NZ_AP014867	130,548
<i>B. thuringiensis</i> serovar <i>tolworthi</i> plasmid pKK4 DNA	NZ_AP014868	54,355
<i>B. thuringiensis</i> serovar <i>tolworthi</i> plasmid pKK5 DNA	NZ_AP014869	23,773
<i>B. thuringiensis</i> serovar <i>tolworthi</i> plasmid pKK6 DNA	NZ_AP014870	14,827
<i>B. thuringiensis</i> serovar <i>tolworthi</i> plasmid pKK7 DNA	NZ_AP014871	11,769
<i>B. thuringiensis</i> serovar <i>tolworthi</i> plasmid pKK8 DNA	NZ_AP014872	7,812
<i>B. thuringiensis</i> strain Al Hakam, plasmid pALH1	CP000486	55,939
<i>B. thuringiensis</i> strain 97-27 plasmid	CP010087	76,848
<i>B. thuringiensis</i> strain Al Hakam plasmid pBTZ_1	NZ_CP009650	273,588
<i>B. thuringiensis</i> strain Al Hakam plasmid pBTZ_2	NZ_CP009649	140,953
<i>B. thuringiensis</i> strain Al Hakam plasmid pBTZ_3	NZ_CP009648	11,903
<i>B. thuringiensis</i> strain Al Hakam plasmid pBTZ_4	NZ_CP009647	11,902
<i>B. thuringiensis</i> strain Al Hakam plasmid pBTZ_5	NZ_CP009645	4,920
<i>B. thuringiensis</i> strain Al Hakam plasmid pBTZ_6	NZ_CP009646	4,602
<i>B. thuringiensis</i> strain Bc601 plasmid pBTBC1	CP015151	14,888
<i>B. thuringiensis</i> strain Bc601 plasmid pBTBC2	CP015152	171,171
<i>B. thuringiensis</i> strain Bc601 plasmid pBTBC3	CP015153	42,357
<i>B. thuringiensis</i> strain Bc601 plasmid pBTBC4	CP015154	82,417
<i>B. thuringiensis</i> strain Bc601 plasmid pBTBC5	CP015155	83,987
<i>B. thuringiensis</i> strain Bc601 plasmid pBTBC6	CP015156	89,350
<i>B. thuringiensis</i> strain Bt185 plasmid pBT1850007	CP014290	7,486
<i>B. thuringiensis</i> strain Bt185 plasmid pBT1850012	CP014288	12,487
<i>B. thuringiensis</i> strain Bt185 plasmid pBT1850042	CP014287	41,937
<i>B. thuringiensis</i> strain Bt185 plasmid pBT1850046	CP014289	46,165
<i>B. thuringiensis</i> strain Bt185 plasmid pBT1850054	CP014286	54,205
<i>B. thuringiensis</i> strain Bt185 plasmid pBT1850055	CP014285	55,372
<i>B. thuringiensis</i> strain Bt185 plasmid pBT1850294	CP014284	293,705
<i>B. thuringiensis</i> strain Bt185 plasmid pBT1850636	CP014283	635,508
<i>B. thuringiensis</i> strain CTC plasmid	CP013273	25,529

<i>B. thuringiensis</i> strain HD-1011 plasmid 1	CP009336	358,965
<i>B. thuringiensis</i> strain HD-1011 plasmid 2	CP009334	349,601
<i>B. thuringiensis</i> strain HD-1011 plasmid 3	CP009332	82,340
<i>B. thuringiensis</i> strain HD-1011 plasmid 4	CP009333	69,773
<i>B. thuringiensis</i> strain HD-12 plasmid pHD120017	CP014848	17,228
<i>B. thuringiensis</i> strain HD-12 plasmid pHD120038	CP014849	38,333
<i>B. thuringiensis</i> strain HD-12 plasmid pHD120039	CP014850	39,023
<i>B. thuringiensis</i> strain HD-12 plasmid pHD120112	CP014851	112,429
<i>B. thuringiensis</i> strain HD-12 plasmid pHD120161	CP014852	161,353
<i>B. thuringiensis</i> strain HD-12 plasmid pHD120345	CP014853	345,196
<i>B. thuringiensis</i> strain HD-571 plasmid pBFQ	CP009599	55,939
<i>B. thuringiensis</i> strain HD-682 plasmid pBGN_1	CP009719	14,648
<i>B. thuringiensis</i> strain HD-682 plasmid pBGN_2	CP009718	56,203
<i>B. thuringiensis</i> strain HD-682 plasmid pBGN_3	CP009717	7,243
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-1	CP012100	509,170
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-2	CP012101	337,579
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-3	CP012102	92,085
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-4	CP012103	94,695
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-5	CP012104	42,726
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-6	CP012105	14,336
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-7	CP012106	4,669
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-8	CP012107	8,287
<i>B. thuringiensis</i> strain HS18-1 plasmid pHS18-9	CP012108	7,386
<i>B. thuringiensis</i> strain INTA-FR7-4 plasmid pFR12	EU362917	12,095
<i>B. thuringiensis</i> strain INTA-FR7-4 plasmid pFR12.5	EU362918	12,459
<i>B. thuringiensis</i> strain INTA-FR7-4 plasmid pFR55	EU362919	55,712
<i>B. thuringiensis</i> strain KNU-07 plasmid pBTKNU07-01	CP016589	514,994
<i>B. thuringiensis</i> strain KNU-07 plasmid pBTKNU07-02	CP016590	293,592
<i>B. thuringiensis</i> strain MYBT18246 plasmid p101287	CP015356	101,287
<i>B. thuringiensis</i> strain MYBT18246 plasmid p109822	CP015355	109,822
<i>B. thuringiensis</i> strain MYBT18246 plasmid p120416	CP015354	120,416
<i>B. thuringiensis</i> strain MYBT18246 plasmid p120510	CP015353	120,510
<i>B. thuringiensis</i> strain MYBT18246 plasmid p142098	CP015352	142,098
<i>B. thuringiensis</i> strain MYBT18246 plasmid p14456	NZ_CP015360	14,456
<i>B. thuringiensis</i> strain MYBT18246 plasmid p150790	CP015351	150,791
<i>B. thuringiensis</i> strain MYBT18246 plasmid p17175	NZ_CP015359	17,175
<i>B. thuringiensis</i> strain MYBT18246 plasmid p46701	CP015358	46,701
<i>B. thuringiensis</i> strain MYBT18246 plasmid p55166	NZ_CP015357	55,166
<i>B. thuringiensis</i> strain MYBT18246 plasmid p6330	CP015361	6,330
<i>B. thuringiensis</i> strain YC-10 plasmid pYC1	CP011350	761,374
<i>B. thuringiensis</i> strain YC-10 plasmid pYC10	CP011355	14,894
<i>B. thuringiensis</i> strain YC-10 plasmid pYC11	CP011356	7,129
<i>B. thuringiensis</i> strain YC-10 plasmid pYC20	CP011357	90,519
<i>B. thuringiensis</i> strain YC-10 plasmid pYC2226	CP011358	82,300
<i>B. thuringiensis</i> strain YC-10 plasmid pYC3	CP011351	80,704
<i>B. thuringiensis</i> strain YC-10 plasmid pYC4	CP011352	46,634
<i>B. thuringiensis</i> strain YC-10 plasmid pYC5	CP011353	17,063
<i>B. thuringiensis</i> strain YC-10 plasmid pYC6	CP011354	8,511
<i>B. thuringiensis</i> strain YWC2-8 plasmid pYWC2-8-1	CP013056	250,706
<i>B. thuringiensis</i> strain YWC2-8 plasmid pYWC2-8-2	CP013057	84,491
<i>B. thuringiensis</i> strain YWC2-8 plasmid pYWC2-8-3	CP013058	82,531
<i>B. thuringiensis</i> strain YWC2-8 plasmid pYWC2-8-4	CP013059	80,699
<i>B. thuringiensis</i> strain YWC2-8 plasmid pYWC2-8-5	CP013060	46,634
<i>B. thuringiensis</i> strain YWC2-8 plasmid pYWC2-8-6	CP013061	8,512
<i>B. thuringiensis</i> sv <i>darmstadiensis</i> INTA 14-4 plasmid pBMBt1	NC_006821	6,700
<i>B. thuringiensis</i> sv <i>entomocidus</i> LBIT-113 plasmid pUIBI-1	NC_004059	4,671
<i>B. thuringiensis</i> sv <i>israelensis</i> HI4 plasmid pTX14-3	NC_001446	7,649
<i>B. thuringiensis</i> sv <i>israelensis</i> plasmid pTX14-1	NC_002091	5,415
<i>B. thuringiensis</i> sv <i>thuringiensis</i> H1.1 plasmid pGI1	NC_004335	8,254

<i>B. thuringiensis</i> YBT-1518 plasmid pBMB0228	NC_020124	17,706
<i>B. thuringiensis</i> YBT-1518 plasmid pBMB0229	CP005936	45,206
<i>B. thuringiensis</i> YBT-1518 plasmid pBMB0230	CP005937	49,195
<i>B. thuringiensis</i> YBT-1518 plasmid pBMB0231	CP005938	146,276
<i>B. thuringiensis</i> YBT-1518 plasmid pBMB0232	CP005939	171,593
<i>B. thuringiensis</i> YBT-1518 plasmid pBMB0233	CP005940	240,661
<i>B. thuringiensis, kurstaki</i> HD-3a3b	NC_007202	2,058
<i>B. toyonensis</i> BCT-7112 plasmid pBCT77	CP006864	76,974
<i>B. toyonensis</i> BCT-7112 plasmid pBCT8	CP006865	7,971
<i>B. weihenstephanensis</i> KBAB4 plasmid pBWB401	CP000904	417,054
<i>B. weihenstephanensis</i> KBAB4 plasmid pBWB402	CP000905	75,107
<i>B. weihenstephanensis</i> KBAB4 plasmid pBWB403	CP000906	64,977
<i>B. weihenstephanensis</i> KBAB4 plasmid pBWB404	CP000907	52,830
<i>B. thuringiensis</i> strain XL6 plasmid	CP013001	393,620
<i>B. cereus</i> strain FORC021 plasmid	CP014487	41,600
<i>B. cereus</i> strain M3 plasmid pBCM301	CP016317	229,356
<i>B. cereus</i> strain M13 plasmid pBCM1301	CP016361	87,088
<i>B. cereus</i> strain M13 plasmid pBCM1302	CP016362	11,745
<i>B. cereus</i> strain M13 plasmid pBCM1303	CP016363	3,088
<i>B. cereus</i> strain K8 plasmid pBCM301	CP016596	319,570
<i>B. cereus</i> strain K8 plasmid pBCK802	CP016597	71,854
<i>B. thuringiensis</i> strain SCG04-02 plasmid PSCG61	CP017573	61,350
<i>B. thuringiensis</i> strain SCG04-02 plasmid PSCG364	CP017574	364,037
<i>B. thuringiensis</i> strain SCG04-02 plasmid PSCG11	CP017575	11,179
<i>B. thuringiensis</i> strain SCG04-02 plasmid PSCG5	CP017576	5,650
<i>B. cereus</i> strain FORC_047 plasmid pFORC47_1	CP018741	257,708
<i>B. cereus</i> strain FORC_047 plasmid pFORC47_2	CP018742	213,830
<i>B. cereus</i> strain ISSFR-3F plasmid unnamed	CP018932	97,731
<i>B. cereus</i> strain ISSFR-9F plasmid unnamed1	CP018934	97,634
<i>B. cereus</i> strain JEM-2 plasmid unnamed1	CP018936	94,665
<i>B. thuringiensis</i> strain YGD22-03 plasmid pYGD30	CP019231	30,343
<i>B. thuringiensis</i> strain YGD22-03 plasmid pYGD36	CP019232	36,974
<i>B. thuringiensis</i> strain YGD22-03 plasmid pYGD5	CP019233	5,650
<i>B. thuringiensis</i> strain YGD22-03 plasmid pYGD83	CP019234	83,894
<i>B. thuringiensis</i> strain YGD22-03 plasmid pYGD98	CP019235	98,137
<i>B. thuringiensis</i> strain L-7601 plasmid unnamed1	CP020003	55,336
<i>B. thuringiensis</i> strain L-7601 plasmid unnamed2	CP020004	49,952
<i>B. thuringiensis</i> strain L-7601 plasmid unnamed3	CP020005	408,071
<i>B. mycoides</i> strain Gnyt1 plasmid unnamed1	CP020744	460,379
<i>B. mycoides</i> strain Gnyt1 plasmid unnamed2	CP020745	114,265
<i>B. mycoides</i> strain Gnyt1 plasmid unnamed3	CP020746	102,550
<i>B. mycoides</i> strain Gnyt1 plasmid unnamed4	CP020747	82,671
<i>B. mycoides</i> strain Gnyt1 plasmid unnamed5	CP020748	73,408
<i>B. mycoides</i> strain Gnyt1 plasmid unnamed6	CP020749	64,682
<i>B. mycoides</i> strain Gnyt1 plasmid unnamed7	CP020750	51,563
<i>B. mycoides</i> strain Gnyt1 plasmid unnamed8	CP020751	10,665
<i>B. cereus</i> strain BC-AK plasmid pBC244 sequence	CP020938	244,929
<i>B. cereus</i> strain BC-AK plasmid pBC52 sequence	CP020939	52,693
<i>B. cereus</i> strain BC-AK plasmid pBCXO1 sequence	CP020940	168,378
<i>B. cereus</i> strain BC-AK plasmid pBCXO2 sequence	CP020941	88,621
<i>B. thuringiensis</i> strain ATCC 10792 plasmid poh1	CP021062	584,623
<i>B. thuringiensis</i> strain ATCC 10792 plasmid poh2	CP021063	113,294
<i>B. thuringiensis</i> strain ATCC 10792 plasmid poh3	CP021064	92,949
<i>B. thuringiensis</i> strain ATCC 10792 plasmid poh4	CP021065	86,488
<i>B. thuringiensis</i> strain ATCC 10792 plasmid poh5	CP021066	11,332

**Table S2.** Open reading frames (ORFs) in the ~120 kb plasmid region covering the insecticidal pathogenicity island (PAI) from *B. thuringiensis* IS5056 plasmid pIS56-285 (CP004136). ORFs were annotated using Blast2GO software.

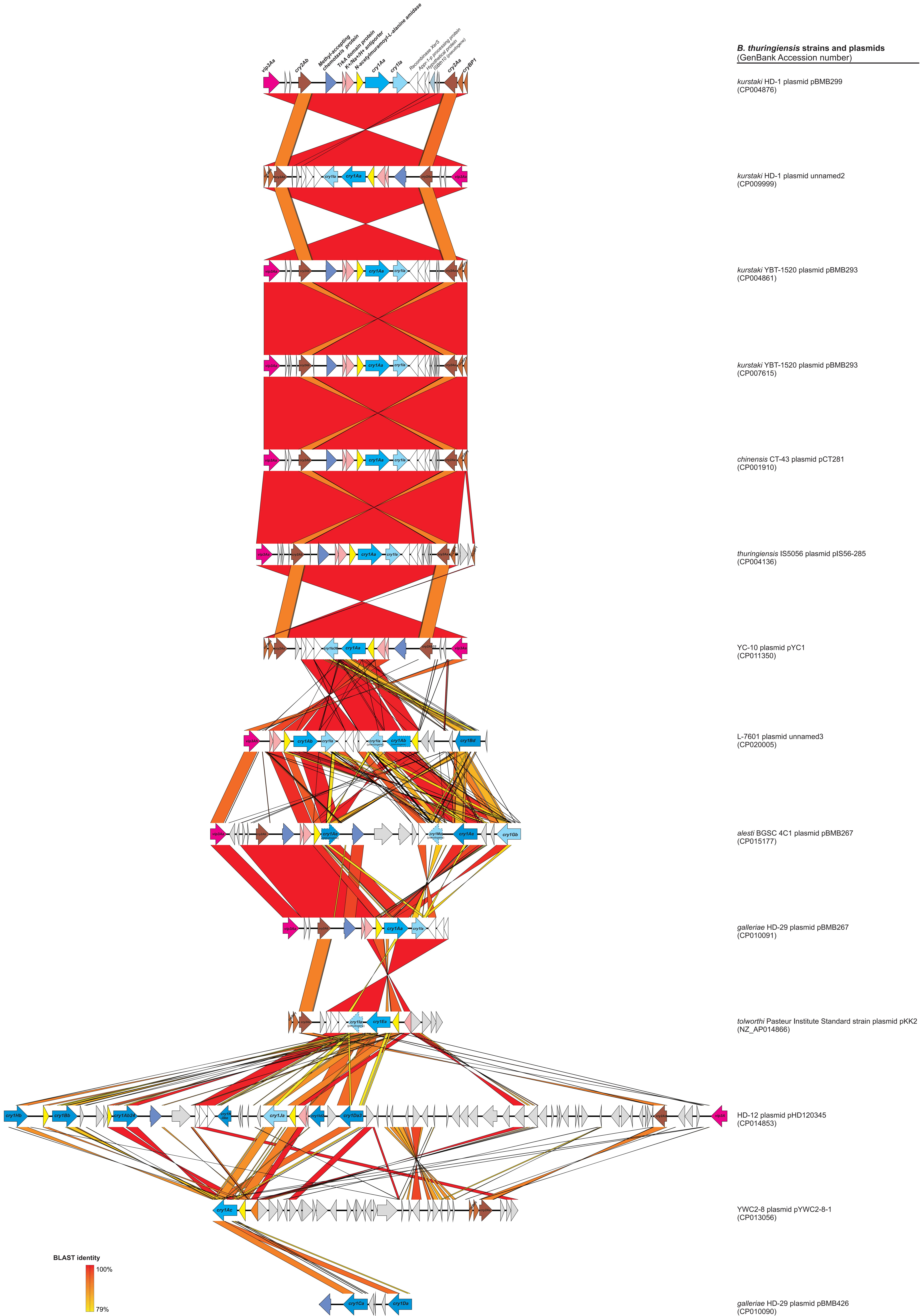
ORF	Length [aa]	GO category <sup>a</sup>	Enzyme Codes
20 kDa in cryBP1 5'-region (ORF1) (plasmid)	88		
Transposase	431	F: DNA binding P: transposition P: DNA recombination P: DNA integration F: ATP binding	
Transposase	250		
20 kDa in cryBP1 5'-region (ORF1) (plasmid)	123		
pBt10 (plasmid)	81		
Holin	140	C: integral component of membrane	
N-hydroxyarylamine O-acetyltransferase	104	P: acyl-carrier-protein biosynthetic process F: N-hydroxyarylamine O-acetyltransferase activity	EC:2.3.1.118
N-hydroxyarylamine O-acetyltransferase	72	P: acyl-carrier-protein biosynthetic process F: N-hydroxyarylamine O-acetyltransferase activity	EC:2.3.1.118
DUF3221 domain-containing	134		
1-phosphatidylinositol phosphodiesterase	41	F: phosphatidylinositol diacylglycerol-lyase activity P: lipid metabolic process C: membrane C: integral component of membrane F: lyase activity F: phosphoric diester hydrolase activity	
Cell filamentation Fic	349		
Membrane	42	C: integral component of membrane	
N-hydroxyarylamine O-acetyltransferase	51	P: acyl-carrier-protein biosynthetic process F: N-hydroxyarylamine O-acetyltransferase activity	EC:2.3.1.118
Uncharacterised	51		
IS605 family transposase	372		
transposase	132	F: DNA binding F: transposase activity P: transposition, DNA-mediated C: integral component of membrane	
Membrane	100		
N-hydroxyarylamine O-acetyltransferase	280	P: acyl-carrier-protein biosynthetic process F: N-hydroxyarylamine O-acetyltransferase activity	EC:2.3.1.118
Lumazine binding domain (plasmid)	48	C: nucleus C: cytosol	
IS4 family transposase	473	F: DNA binding F: transposase activity C: integral component of membrane	
Membrane (plasmid)	37	P: transposition, DNA-mediated C: integral component of membrane	
ADP-ribosyltransferase	178	C: extracellular region F: transferase activity P: pathogenesis	
ADP ribosyltransferase	94	F: transferase activity, transferring glycosyl groups C: extracellular region P: pathogenesis	
IS4 family transposase	476	F: DNA binding F: transposase activity C: integral component of membrane	
Family transporter	290	P: transposition, DNA-mediated C: integral component of membrane	
Hypothetical protein H175_285p028 (plasmid)	40		
Exosporium leader peptide	338		
Transcriptional regulator	99	F: DNA binding C: transcription factor complex F: transcription factor activity, sequence-specific DNA binding P: regulation of transcription, DNA-templated P: regulation of transcription, DNA-templated	
Transposase	237	C: integral component of membrane	
pXO1-04 (plasmid)	209		
Membrane (plasmid)	211	C: integral component of membrane	
pXO1-02 (plasmid)	204	F: RNA-directed DNA polymerase activity C: integral component of membrane P: RNA-dependent DNA biosynthetic process	EC:2.7.7.49

Hypothetical protein	194	
Hypothetical protein	127	C: integral component of membrane
pXO1-01 (plasmid)	212	
Membrane (plasmid)	37	C: integral component of membrane
NADH dehydrogenase	66	C: integral component of membrane
NADH dehydrogenase	57	C: integral component of membrane
DNA topoisomerase I	887	F: DNA binding F: metal ion binding F: DNA topoisomerase type I activity P: DNA topological change P: pathogenesis EC:5.99.1.2
Thermonuclease (plasmid)	214	F: nucleic acid binding P: nucleic acid phosphodiester bond hydrolysis F: nuclease activity
pXO1-140 (plasmid)	95	
Pyruvate decarboxylase	152	F: magnesium ion binding F: thiamine pyrophosphate binding F: DNA binding P: transcription, DNA-templated F: catalytic activity P: regulation of transcription, DNA-templated F: carboxy-lyase activity
Disulfide bond formation B	145	P: obsolete electron transport F: protein disulfide oxidoreductase activity C: integral component of membrane P: oxidation-reduction process
Family transcriptional regulator	97	C: plasma membrane F: DNA binding C: transcription factor complex F: transcription factor activity, sequence-specific DNA binding P: regulation of transcription, DNA-templated P: regulation of transcription, DNA-templated
Histidine kinase	363	P: phosphorylation F: kinase activity
(Plasmid)	44	
Transposase (plasmid)	93	
pXO1-134 (plasmid)	125	
Hypothetical protein	171	
Recombinase	332	F: DNA binding P: DNA recombination P: DNA integration
Hypothetical protein CT43_P281221 (plasmid)	109	
Cobalamin synthesis P47K (plasmid)	137	
N-hydroxyarylamine O-acetyltransferase	271	P: acyl-carrier-protein biosynthetic process F: N-hydroxyarylamine O-acetyltransferase activity EC:2.3.1.118
Transposase	273	F: nucleic acid binding P: DNA integration
Transposase	226	F: transposase activity F: sequence-specific DNA binding P: transposition, DNA-mediated
DNA topoisomerase I	46	F: isomerase activity
Transposase	134	F: DNA binding F: transposase activity P: transposition, DNA-mediated
Aldo keto reductase	98	F: DNA binding P: carbohydrate metabolic process C: membrane C: integral component of membrane F: hydrolase activity, hydrolyzing O-glycosyl compounds; F: hydrolase activity
Transposase (plasmid)	372	
4-oxalomesaconate tautomerase	357	F: methylitaconate delta-isomerase activity EC:5.3.3.6
EamA-like transporter family	303	C: integral component of membrane
IS605 family transposase	37	F: DNA binding
IS605 family transposase	372	
Hemolysin BL lytic component L2	439	C: membranę P: pathogenesis
Hemolysin BL lytic component L1	409	C: integral component of membrane P: pathogenesis
Hemolysin BL-binding component	377	C: membranę P: pathogenesis
DNA replication (plasmid)	55	F: ATP binding

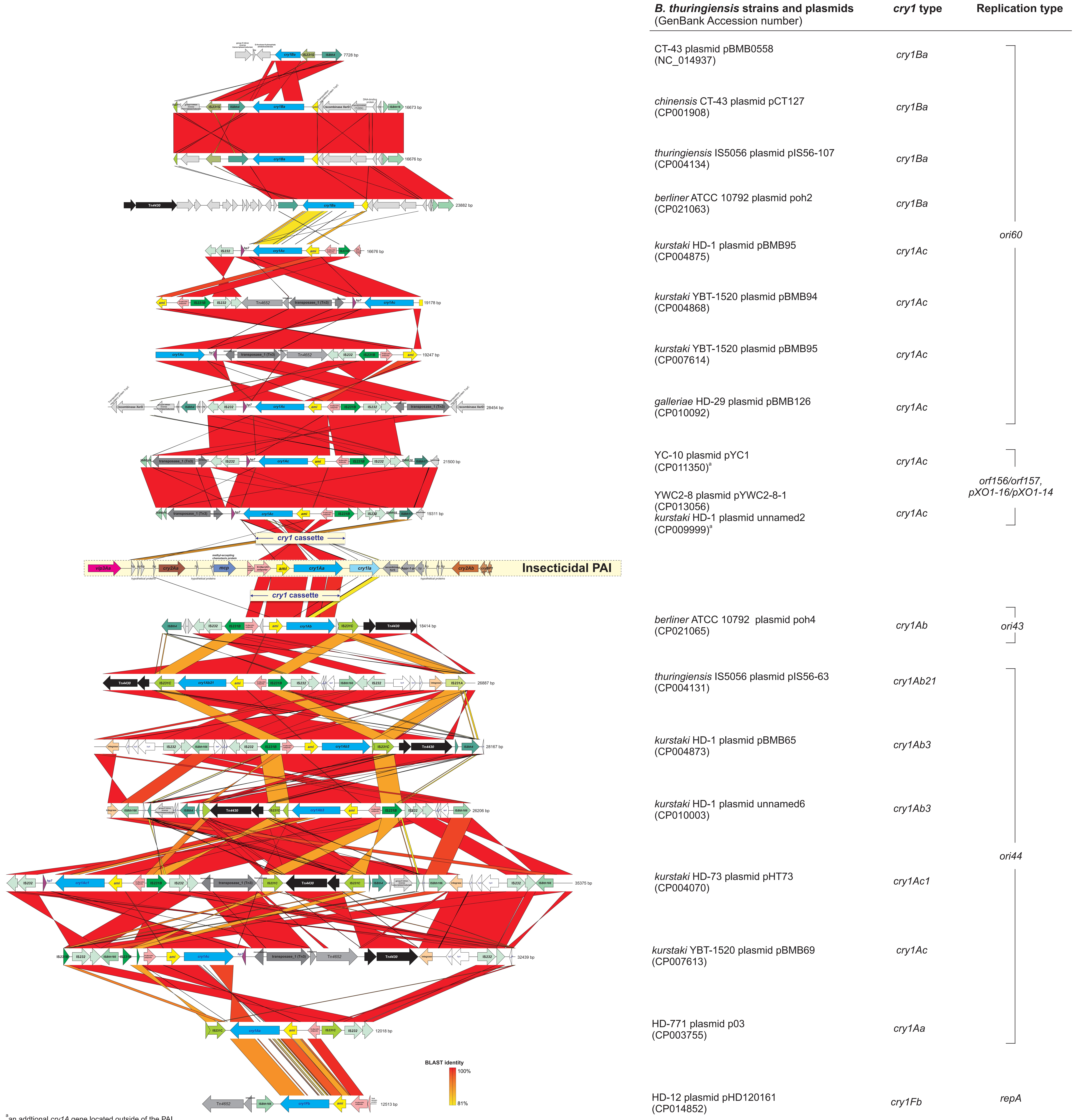
Spore coat (plasmid)	43	F: DNA binding F: transposase activity C: viral capsid P: transposition, DNA-mediated
Cobalt chelatase	67	C: membrane C: integral component of membrane P: cobalamin biosynthetic process F: cobaltochelatase activity F: ligase activity
IS6 family transposase	61	F: nucleic acid binding P: DNA integration
IS6 family transposase	37	F: nucleic acid binding C: integral component of membrane P: DNA integration
Hypothetical protein	331	
Hypothetical protein H175_285p252 (plasmid)	40	
Family transcriptional regulator	89	F: DNA binding C: transcription factor complex F: transcription factor activity, sequence-specific DNA binding P: regulation of transcription, DNA-templated P: regulation of transcription, DNA-templated
Immunity	200	C: integral component of membrane P: response to toxic substance
SdpA family antimicrobial peptide system	176	C: membrane
Sporulation-delaying protein SdpB	316	C: integral component of membrane
SdpC family antimicrobial peptide	206	C: membrane C: integral component of membrane P: phosphorylation F: kinase activity
Thiol-disulfide oxidoreductase	130	
Amidohydrolase	438	F: hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds P: nitrogen compound metabolic process
Membrane	177	C: integral component of membrane
Hypothetical protein H175_285p261 (plasmid)	37	
Family transcriptional regulator	296	F: DNA binding C: transcription factor complex F: transcription factor activity, sequence-specific DNA binding P: regulation of transcription, DNA-templated P: regulation of transcription, DNA-templated
Transposase (plasmid)	122	
IS605 family transposase	245	
Hypothetical protein H175_285p265 (plasmid)	41	
Hypothetical protein	150	
Transposase	120	
Transposase	47	
Transposase	120	
Transposase DDE domain (plasmid)	49	
Transposase for IS660 (plasmid)	44	C: membrane C: integral component of membrane
M trans-acting positive regulator (Mga) (plasmid)	471	P: regulation of transcription, DNA-templated
Transposase	47	
Transposase (plasmid)	64	
IS605 family transposase	47	
Vegetative insecticidal	789	F: hydrolase activity, acting on glycosyl bonds
Helix-turn-helix domain-containing partial	94	
IS605 family partial	38	
IS605 family transposase	77	
N-acetylmuramoyl-L-alanine amidase (plasmid)	39	P: peptidoglycan catabolic process F: N-acetylmuramoyl-L-alanine amidase activity F: hydrolase activity
Crystal protein cry2Ab	633	P: signal transduction P: defence response F: receptor binding P: pathogenesis P: sporulation resulting in formation of a cellular spore
Hypothetical protein H175_285p282 (plasmid)	40	
Hypothetical protein H175_285p283 (plasmid)	55	C: integral component of membrane

Methyl-accepting chemotaxis	532	P: chemotaxis P: signal transduction C: integral component of membrane F: signal transducer activity
Potassium transporter	164	P: potassium ion transport P: cation transmembrane transport F: cation transmembrane transporter activity
Potassium transporter	399	F: solute: proton antiporter activity C: integral component of membrane P: hydrogen ion transmembrane transport P: regulation of pH
N-acetylmuramoyl-L-alanine amidase (plasmid)	316	P: peptidoglycan catabolic process P: peptidoglycan biosynthetic process F: N-acetylmuramoyl-L-alanine amidase activity
Crystal protein cry1Aa (plasmid)	1176	EC:3.5.1.28 P: signal transduction P: defence response F: receptor binding P: pathogenesis P: sporulation resulting in formation of a cellular spore
Cry1Ia	719	P: signal transduction P: defence response F: receptor binding P: pathogenesis P: sporulation resulting in formation of a cellular spore
Tyrosine recombinase	368	F: DNA binding P: DNA recombination P: DNA integration
Appr-1-p processing	341	
Hypothetical protein	210	
Hypothetical protein H175_285p293 (plasmid)	39	
Transposase	44	F: DNA binding F: transposase activity P: transposition, DNA-mediated
Hypothetical protein	42	C: integral component of membrane
Cry2Aa (plasmid)	633	P: signal transduction P: defence response F: receptor binding P: pathogenesis P: sporulation resulting in formation of a cellular spore
CryBP1 5'-region	252	

<sup>a</sup>GO, Gene Ontology; P - biological process; F - molecular function; C - cellular component

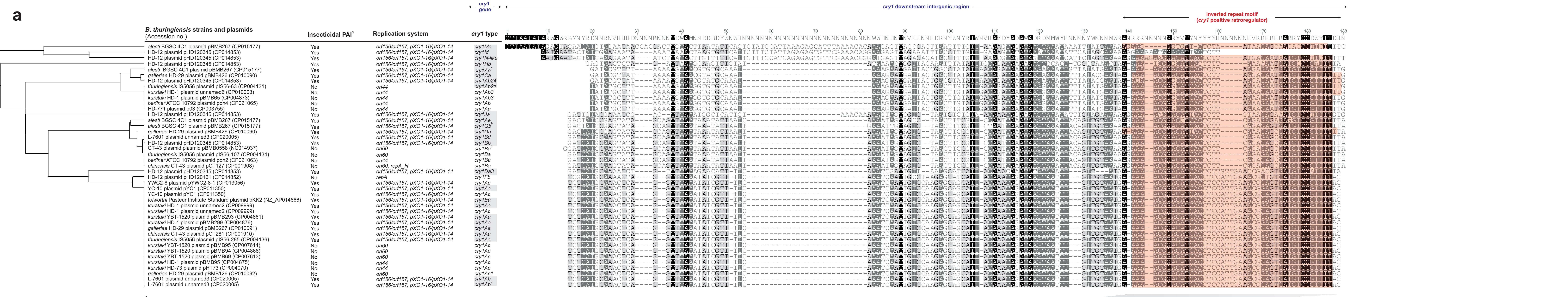


**Fig. S1.** The insecticidal pathogenicity island (PAI) in the *B. thuringiensis* plasmids.

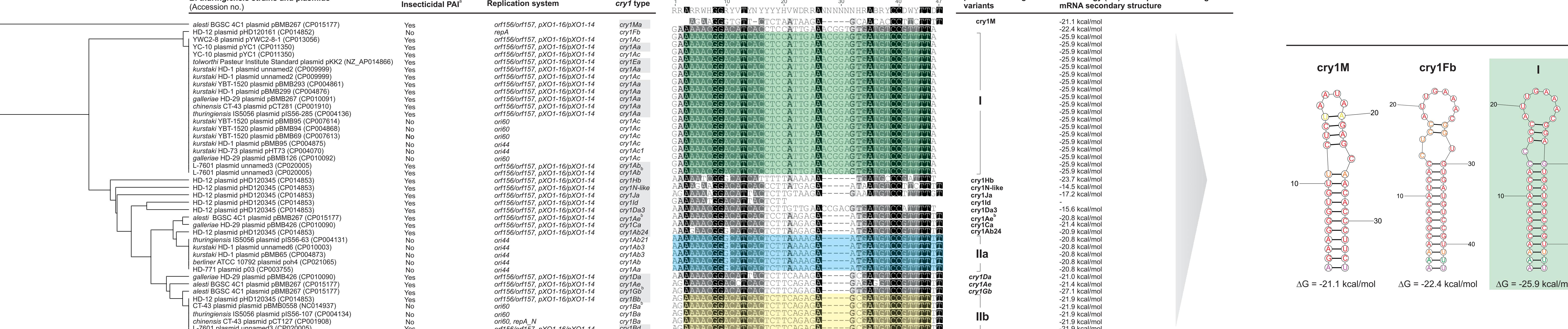


**Fig. S2.** The cry1 gene cassette in *B. thuringiensis* plasmids. The insecticidal pathogenicity island (PAI) was used as the reference.

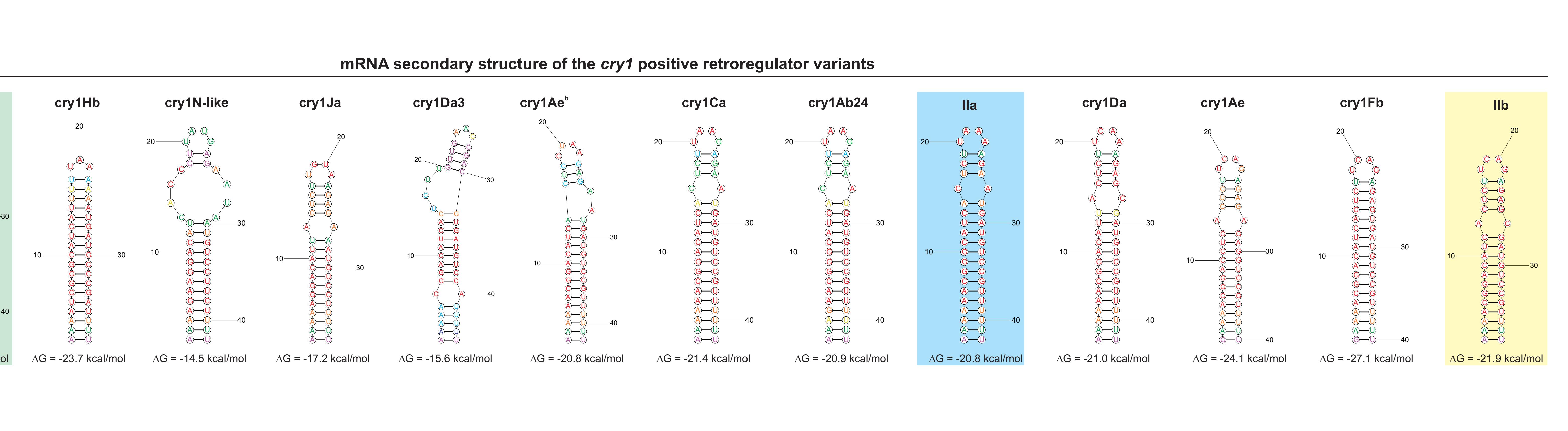
<sup>a</sup>an additional cry1A gene located outside of the PAI

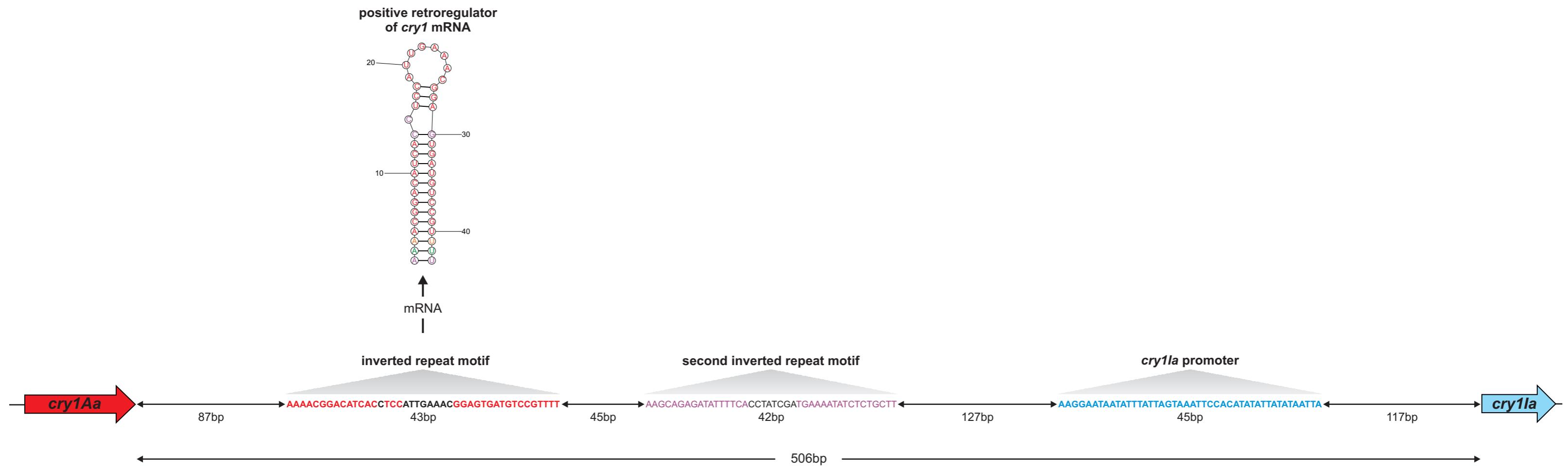
**a**<sup>a</sup> all PAI variants as showed in Additional file 2: Fig. S1<sup>b</sup> pseudogene

grey box, denotes location of cry1 inside the PAI


**b**<sup>a</sup> all PAI variants as showed in Additional file 2: Fig. S1<sup>b</sup> pseudogene

grey box, denotes location of cry1 inside the PAI

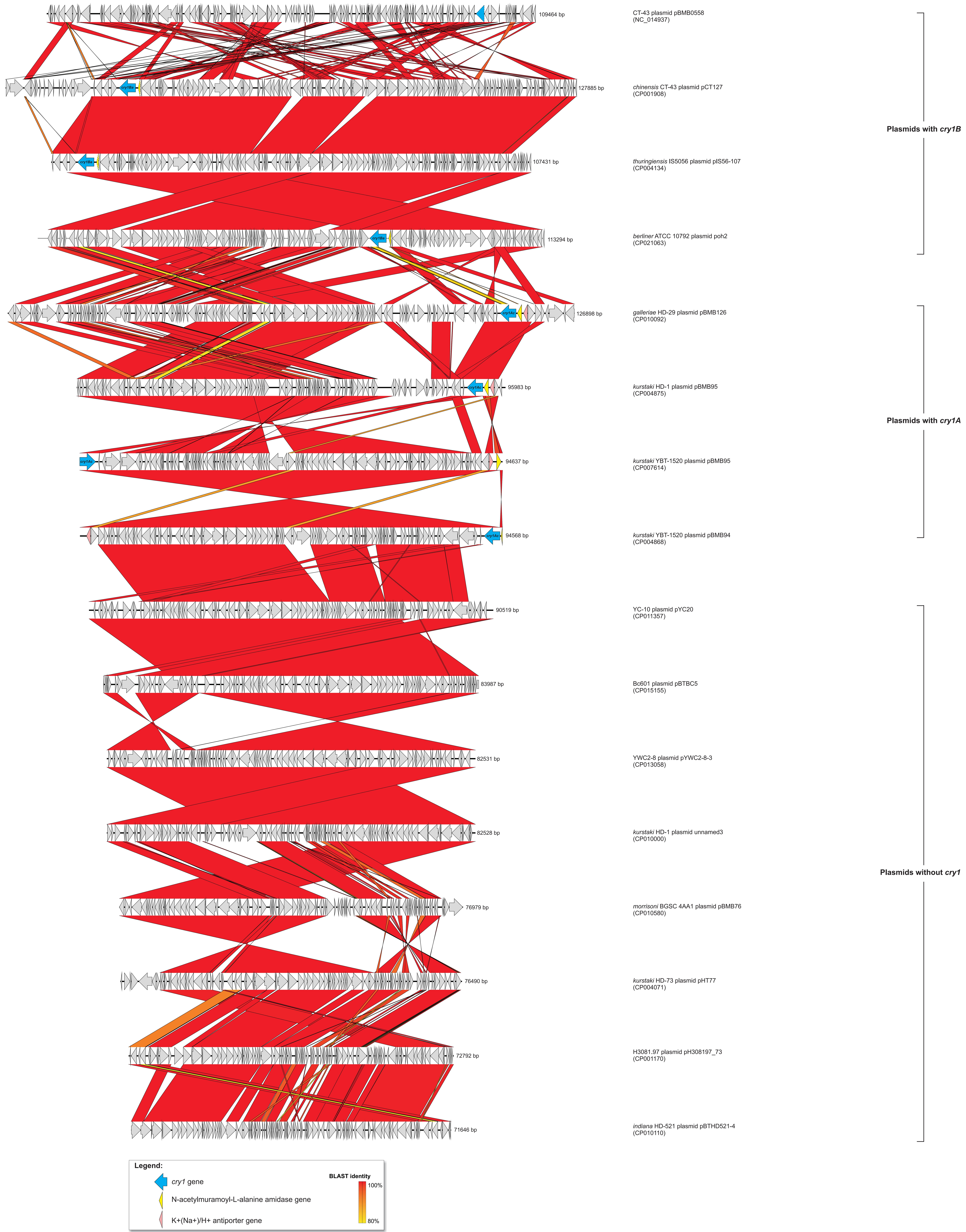
**c****Fig. S3.** (a) Alignment of the downstream region of cry1 genes containing the positive retroregulator. (b) Comparison of sequence identity of the positive retroregulator between various cry1 genes using UPGMA clustering method.The analysis was done using RNA structure web server (<http://rna.urmc.rochester.edu/RNAstructureWeb/Servers/Predict1.html>).




**Fig. S4.** Intergenic region between *cry1Aa* and *cry1la* from the insecticidal PAI (plasmid pBMB299, GenBank Acc. no. CP004876, was used as the reference sequence).



**Fig. S5.** Comparison of plasmids with *ori44* and *repA* replication systems carrying *cry1A* or *cry1F* with related plasmids missing *cry1* genes.



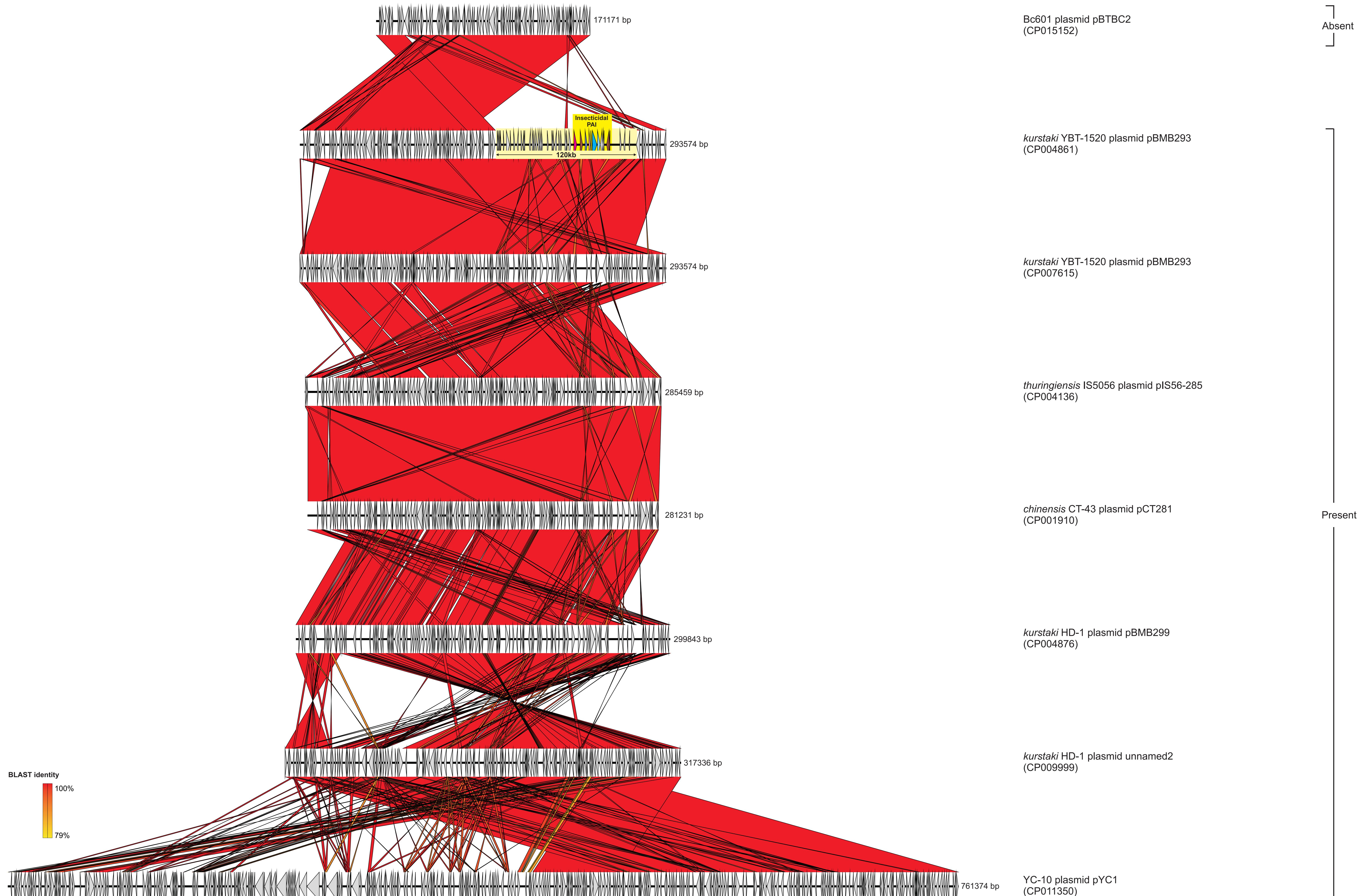
**Fig. S6.** Comparison of plasmids with *ori60* replication type carrying *cry1A* or *cry1B* with similar plasmids missing the *cry1* genes.



**Fig. S7.** Comparison of plasmid with *ori43* replication system carrying *cry1A* with related plasmids missing the *cry1* genes.

***B. thuringiensis* strains and plasmids  
(GenBank Accession number)**

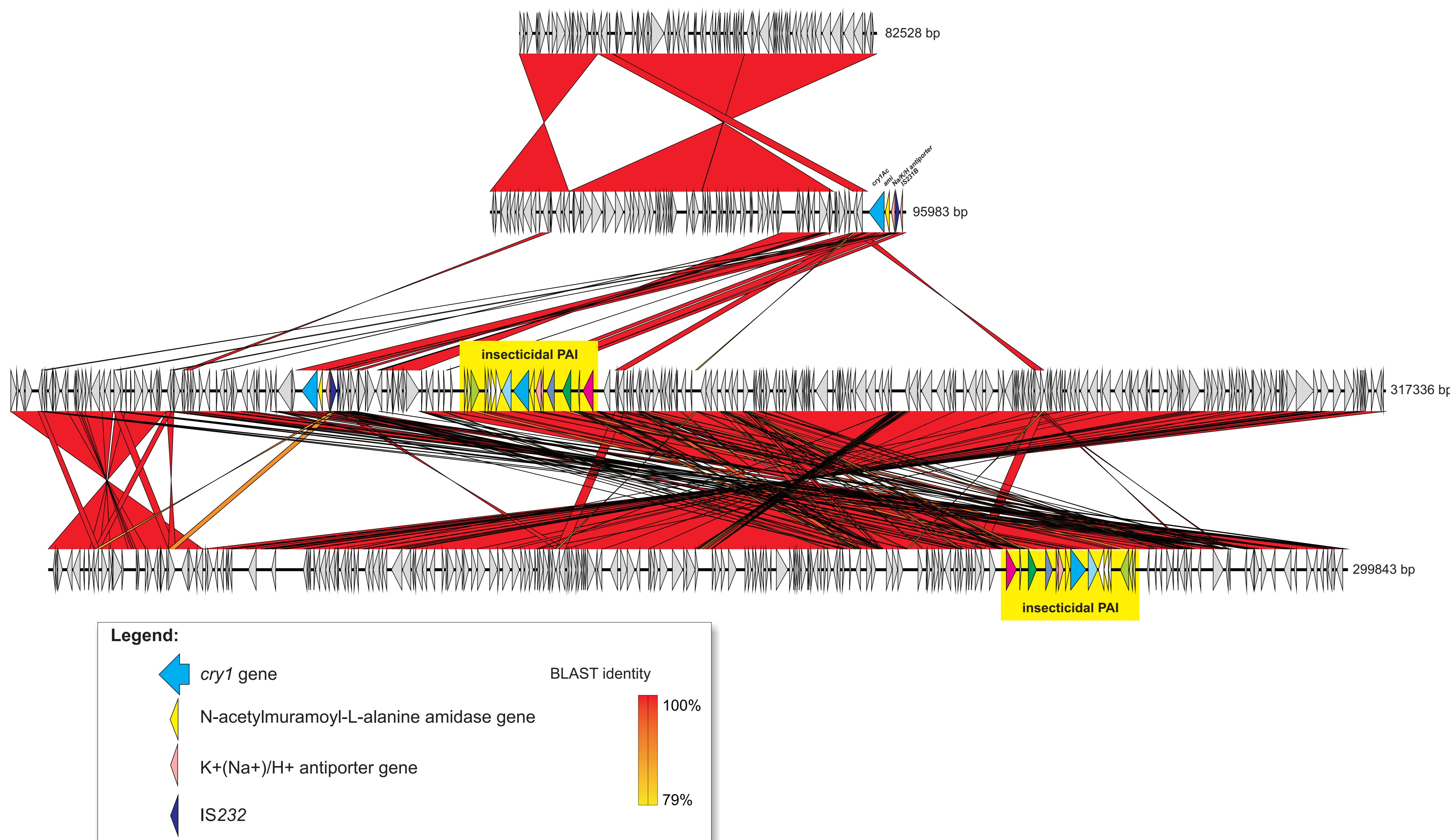
**Insecticidal PAI**



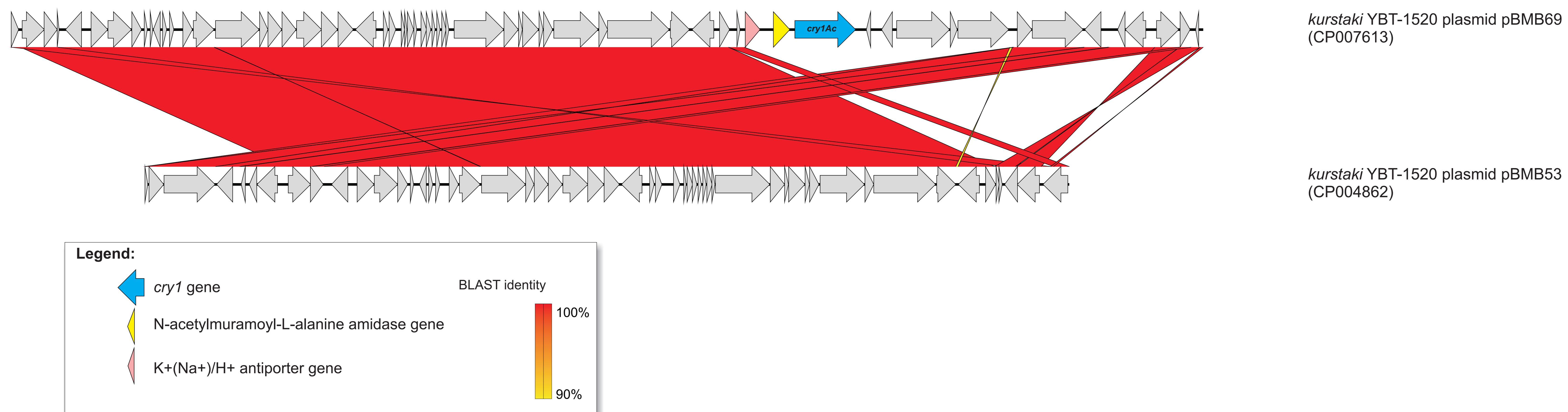
**Fig. S8.** Putative gene cassette (~120 kb) covering the insecticidal PAI.

**B. thuringiensis strains and plasmids**  
(GenBank Accession number)

a




b

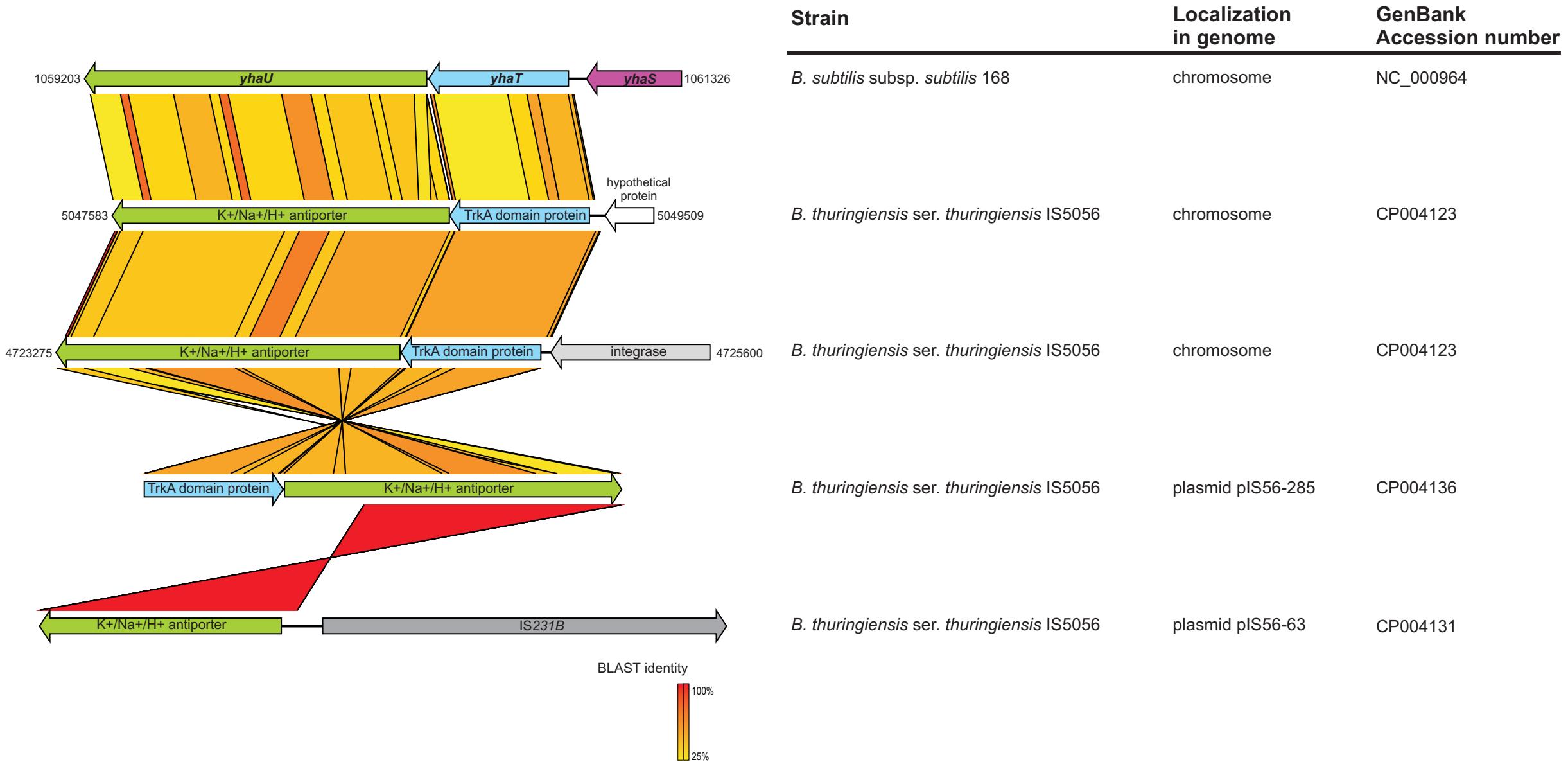


**Fig. S9.** Inconsistencies in cry1Ac location in plasmids from the same *B. thuringiensis* strains deposited in GenBank by various sequencing projects; (a) *B. thuringiensis* sv. *kurstaki* HD-1 plasmids (CP009999-CP010000 vs. CP004875-CP004876), and (b) *B. thuringiensis* sv. *kurstaki* strain YBT-1520 plasmids (CP007613 vs. CP004862).

**B. thuringiensis strains and plasmids (or contigs)**  
(GenBank Accession number)



**Fig. S10.** Genetic environment of *cry1I*, *cry1M*, *cry1N-like* and *cry3A* genes.



**Fig. S11.** Comparison of *B. subtilis* K<sup>+</sup>(Na<sup>+</sup>)/H<sup>+</sup> antiporter encoded by the *yhaU*-*yhaT*-*yhaS* operon with K<sup>+</sup>(Na<sup>+</sup>)/H<sup>+</sup> antiporters from *B. thuringiensis* IS5056 chromosome and the *cry1*-carrying plasmids, using the tblastx algorithm.

```

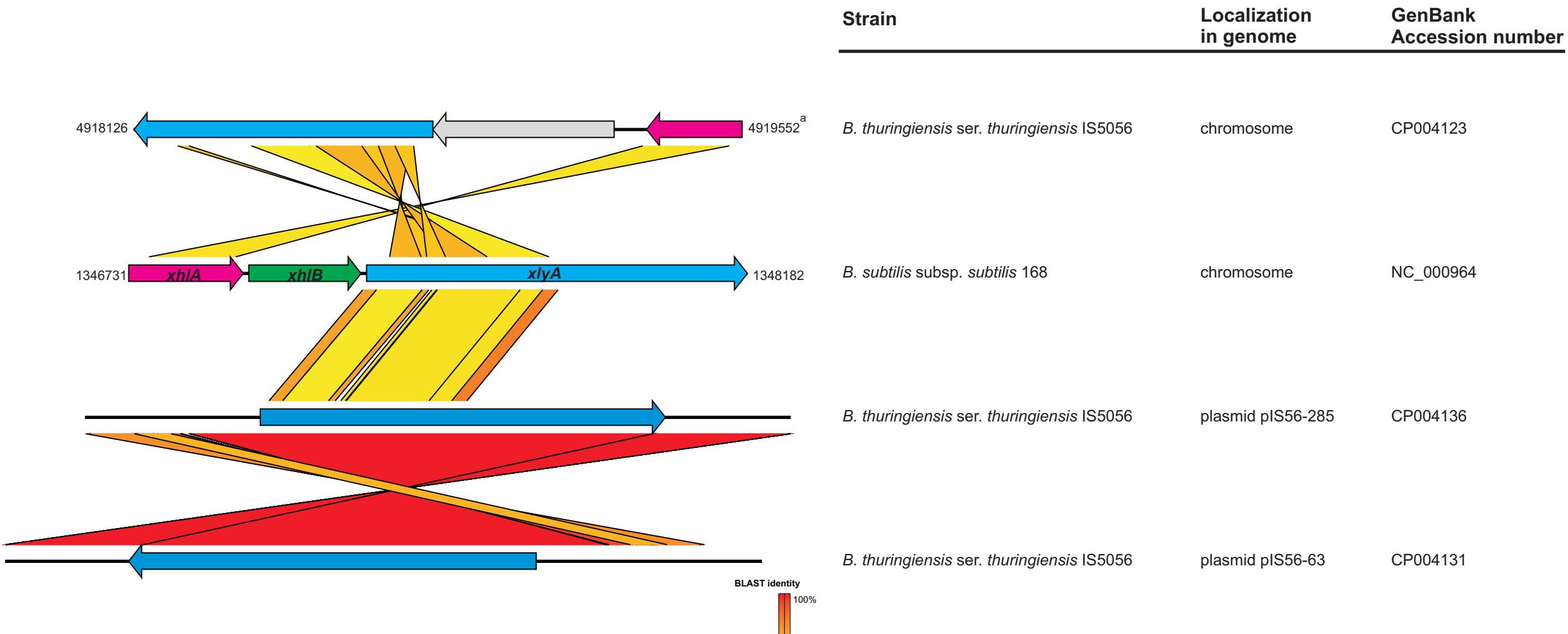
*   20      *   40      *   60      *   80      *   100     *   120     *   140     *   160     *   180     *   200     *   220
MCP_pIS56-285 : - M Y E N N I L I S C H I G V E P N I F F V N M I M E M M I S K D E R R S P L I P I D R E P E N D P I L K Q P E R K S I S N R E L K I Y K F Y G I F D E L R Q I K I D I N S N N E D I T Y I L K E I E P N M I K S I C E L I D Y N P N N A C L C E N I S I D N T M I F I S I S V L A I I I I I L I G Y H I R P K P F I I L I Q C M E K : 183
MCP_chromosome_Bt_IS5056 (AGG02078.1) : M E L L R N S P V G T K I N I I I T I S S I A C I V L S I L I G W G L E R G K S T S S I M Y E N N I L I P I G V E N I Y E V N M N M E I V S K D E R R S P L I P M G I D R E P E N D H I L K Q P E R P V I T E K E M E L V I N F E I N E R R Q M K I P E I G S N N E D I T Y I L K E I E P N M I K S I C E L I D Y N P N N A C L C E N I S I D N T M I F I S I S V L A I I I I I L I G Y H I R P K P F I I L I Q C M E K : 227
M Y E 1 N L I I 2 I G V E N 5 S E V N N N M E 6 M 6 S K D E R R E L 6 E 6 1 R E N D I L R Q F E W 6 S K E I Y F Y F I E R Q 6 M K Q 6 S N N E 5 Y Y L K E I E P N 6 K I S I E L I Y N N N A 2 I Q K N S N T M 6 F I S I S 6 L A I 6 I 6 I L I G Y I K I 4 P 6 6 I I Q C M E K

*   240     *   260     *   280     *   300     *   320     *   340     *   360     *   380     *   400     *   420     *   440     *
MCP_pIS56-285 : V A G N I L I D P I H N N E L G H I V S E N M I L N I Q Q I I E N V S I A N E V I S S T E G M I E N T R A S I L S N E V V C I S F V N I K I E Q Q I S I Q D S S S I E I P I G V Q I I A E S S I V I E M V E I T E V N G S E D I N S I L Q M N S V E V V E E T S V I I V I R I T Q Q I E A I D A I T N I A Q C I N I L A L N A A I E A A R A G E N G K G F A V V A E V R D L A E S K E P I A E N H L I K I D C M I K A : 410
MCP_chromosome_Bt_IS5056 (AGG02078.1) : V P A G L I D P I H P H N N E L G H I V S F N S M I L N I Q Q I I E N V S I A I V I S S T E G M I E N T R A S I L S N E V V C I S F V N I K I E Q Q I S I Q D S S S I E I P I G V Q I I A E S S I V V E E T S V I I V I R I T Q Q I E A I D A I T N I A Q C I N I L A L N A A I E A A R A G E N G K G F A V V A E V R D L A E S K E P I A E N H L I K I D C M I K A : 454
V A G I L I P T Y H N N E L G H I V S F N S M I L N I Q Q I I E N V S I A I V I S S T E G M I E N T R A S I L S N E V V C I S F V N I K I E Q Q I S I Q D S S S I E I P I G V Q I I A E S S I V V E E T S V I I V I R I T Q Q I E A I D A I T N I A Q C I N I L A L N A A I E A A R A G E N G K G F A V V A E V R D L A E S K E P I A E N H L I K I D C M I K A : 454

*   460     *   480     *   500     *   520     *   540     *   560     *   580     *   600
MCP_pIS56-285 : I V I V M Q R G Q R A I E G K E A A R A N Q F P S V V R D I I K I S C M C E W P A T T E E M S A G T E V N S I S V S V E T I A V A N G I S H A R A S T O P C A I S T E D I N S N M V C P V E E I I C V S C P T I I P S G K R D : 532
MCP_chromosome_Bt_IS5056 (AGG02078.1) : I V I V M Q R G Q R A I E G K E A A R A N Q F P S V V R D I I K I S C M C E W P A T T E E M S A G T E V N S I S V S I T I I P K E E Q T V S I C Q Q V S I D I S Q S N K M K P V E E I I P L V S C P T I I P S G K R D : 574
I V I V M Q 4 G Q R A 6 E G K E A A R A N Q F S 6 6 4 D I D K I 3 S Q 6 Q E V A A T T E E M S A G T E V N S I S V S I A V I S I Q Q A 6 S I E I Q S N K 6 K P V E E I I 2 I V S F I E G

```

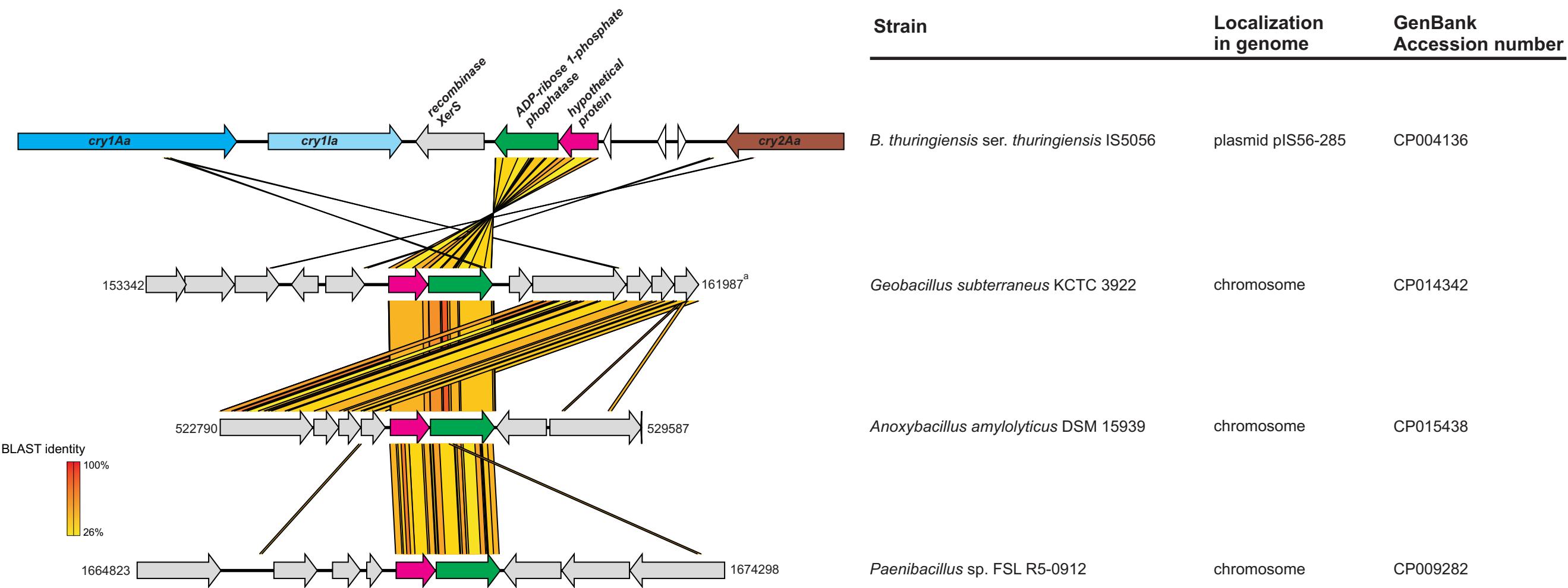
**Fig. S12.** Comparison of methyl-accepting chemotaxis protein (MCP) from the insecticidal PAI of *B. thuringiensis* IS5056 plasmid pIS56-285 (CP004136) with its chromosomal homolog (AGG02078.1).



<sup>a</sup>region inside a putative prophage according to PHASTER results for prophages screening:

Region Length	Completeness	Score	# Total Proteins	Region Position	Most Common Phage	GC %
41.1 kb	questionable	80	53	4909665-4950821	PHAGE_Bacill_phBC6A52(19)	35.21

**Fig. S13.** Comparison of *B. subtilis* *xlyA* with N-acetylmuramoyl-L-alanine amidase genes from *B. thuringiensis* IS5056 chromosome and the *cry1*-carrying plasmids, using the tblastx algorithm.



<sup>a</sup> region inside a putative prophage according to PHASTER results for prophages screening:

Region Length	Completeness	Score	# Total Proteins	Region Position	Most Common Phage	GC %
15.5 kb	incomplete	30	9	150734-166241	PHAGE_Enterophi92_NC_023693(4)	45.72

**Fig. S14.** Comparison (tblastx algorithm) of ADP-ribose 1-phosphate phosphatase gene locus from the insecticidal PAI (*B. thuringiensis* ser. *thuringiensis* IS5056 plasmid pIS56-285) with similar loci from chromosomes of *Geobacillus subterraneus*, *Anoxybacillus amyloolyticus* and *Paenibacillus* sp..