

Supplementary Tables

Supplementary Table S4: Primers, probes and gene targets for the detection of *Bacillus anthracis* from blood smear samples from Kruger National Park, South Africa by qPCR.

Primer/Probe (5'-3')	Chemistry	Target	Reference
Forward - GTACATCTTCTAGCTGTTGCAA Reverse – ACGTAGGAAGACCGTTGATTA Probe - VIC-CGTTGTTGTGTATTTG-MGB	TaqMan	<i>Ba-1</i>	Zincke et al., 2020
Forward – TAAGCCTGCGTTCTTCGTAAATG Reverse – GTTCCCAAATACGTAATGTTGATGAG Probe - NED-TTGCAGCGAATGAT-MGB	TaqMan	<i>capB</i>	
Forward – CACTATCAACACTGGAGCGATTCT Reverse – AATTATGTCATCTTTCTTTGGCTCAA Probe - Cy5-AGCTGCAGATTCC-MGB	TaqMan	<i>lef</i>	
Forward – CGGATCAAGTATATGGGAATATAGCAA Reverse - CCGGTTT AGTCGTTT CTAATGGAT BAPA-FL - TGCGGTAACACTT CACTCCAGTTCGA-X BAPA-LCRed 640 - CCTGTATCCACCCTCACTCTT CCATTTT C-P	FRET	<i>pagA</i>	Helgason et al., 200

Table extracted from the work of Ochai et al., 2024

Genomic features and identification

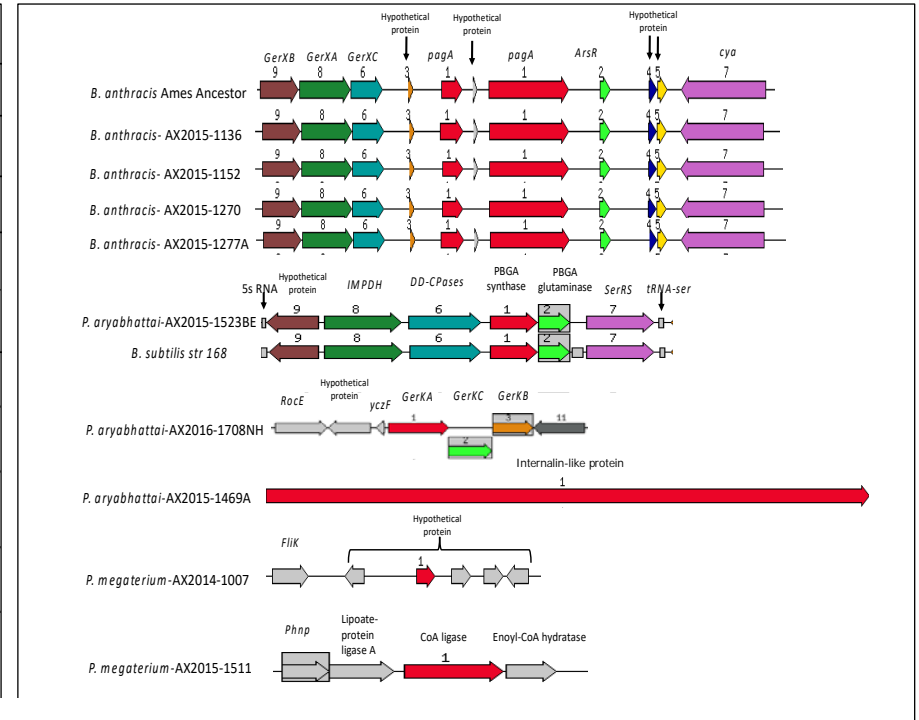
Genome metrics and features of the sequenced *Priestia* spp. isolates from this study are presented in Table S5. Quality assessment of the assembled genomes showed that the isolates (n = 9) have an average of 99,39 completeness. On average, 157.93 ± 108.45 contigs were determined which corresponds to an average N50 of $222,648.82 \pm 103,744.56$ for all the genomes. The average G+C content of the *Priestia* genomes was 37.50%, which was greater than that of the *B. anthracis* genomes averaging 35.12%. The G+C content for *P. aryabhatai* ranged from 37.30% to 37.85% which was lower than the reference *P. aryabhatai* K13 strain (38.20%). *P. endophytica* AX2014-729BE (37.31%) G+C content was greater than the reference *P. endophytica* KCTC13922 strain (36.51%), and RL201528 strain (37.31%) sequenced in this study. The G+C content of *B. anthracis* sequenced genomes (35.10%) were close to the reference genome of *B. anthracis* Ames Ancestor (35.20%). Furthermore, the G+C content of the *P. megaterium* strains that were sequenced ranged from 37.24% to 37.52%, which is in close proximity to the 37.83% reference genome of *P. megaterium* strain ATCC14581. The number of coding sequences (CDSs) on average were predicted to be $5,814.00 \pm 289.66$.

Table S5: Genome features and assembly metrics of the *Bacillus anthracis* and *Priestia* spp. isolates in this study.

	Contigs	Largest contig	Genome size		G+C	Coding	RNAs	Prophage	Plasmid
			(bp)	N50	Content %	sequences		regions	replicons
<i>B. anthracis</i> Ames Ancestor*	3	5,227,419	5,503,926	181 677	35.20	5 855	128	4	2
AX2015-1136	72	548 990	5,359,201	157 399	35.10	5 943	77	5	1
AX2015-1152	76	641 194	5,459,155	186 582	35.10	5 861	58	6	2
AX2015-1270	72	450 267	5,545,411	221 866	35.10	5 851	49	5	2
AX2015-1277A	43	451 964	5,451,556	538 273	35.10	5 848	52	5	2
<i>P. aryabhatai</i> K13*	3	5,035,815	5,254,250	5,035,815	38.20	5 424	171	0	2
AX2014-950 A	218	274 182	5,780,111	85 682	37.57	5 945	58	0	1
AX2015-1469A	153	470 412	5,798,687	129 633	37.50	6 025	117	1	2
AX2015-1523BE	78	1,131,208	5,766,712	375 562	37.30	5 974	56	0	3
AX2016-1708NH	92	426 781	5,477,999	202 935	37.81	5 645	87	0	1
AX2016-1708NH2	89	454 837	5,477,829	203 035	37.85	5 660	58	0	0
<i>P. endophytica</i> KCTC13922*	40	857 582	5,121,484	355 847	36.51	5 303	76	0	0
RL201528	167	643 891	5,493,987	349 826	36.43	5 550	98	0	0
AX2014-729BE	124	337 171	5,360,059	127 231	37.31	5 466	66	1	2
<i>P. megaterium</i> ATCC14581*	7	5,343,114	5,746,640	5,343,114	37.83	5 971	166	0	6
AX2015-1511	175	688 778	5,787,931	123 204	37.52	6 023	87	1	4
AX2014-1007	401	253 841	6,295,826	59 052	37.24	6 566	98	0	5

* Denotes GenBank strains used as reference for comparative genome analysis

Isolate	Contig	Primer binding region
<i>B. anthracis</i> Ames Ancestor	NZ_AAEP01000051	Query: 1 tgcggtaacacttcactccagttcga 26 Sbjct: 28232 tgcggtaacacttcactccagttcga 28207
<i>B. anthracis</i> -AX2015-1136	k141_505	Query: 1 tgcggtaacacttcactccagttcga 26 Sbjct: 28232 tgcggtaacacttcactccagttcga 28207
<i>B. anthracis</i> -AX2015-1152	k141_87	Query: 1 tgcggtaacacttcactccagttcga 26 Sbjct: 16797 tgcggtaacacttcactccagttcga 16822
<i>B. anthracis</i> -AX2015-1270	k141_10	Query: 1 tgcggtaacacttcactccagttcga 26 Sbjct: 28184 tgcggtaacacttcactccagttcga 28159
<i>B. anthracis</i> -AX2015-1277A	Node_21	Query: 1 tgcggtaacacttcactccagttcga 26 Sbjct: 28083 tgcggtaacacttcactccagttcga 28058
<i>P. aryabhattai</i> -AX2015-1523BE	Node_34	Query: 7 aacacttcactc 18 Sbjct: 11088 aacacttcactc 11099
<i>P. aryabhattai</i> -AX2015-1469A	Node_10	Query: 3 cggtaacacttc 14 Sbjct: 41684 cggtaacacttc 41673
<i>P. aryabhattai</i> -AX2016-1708NH	k141_67	Query: 7 aacacttcactcca 20 Sbjct: 62675 aacacttcactcca 62688
<i>P. megaterium</i> -AX2014-1007	k141_195	Query: 3 cggtaacacttcactc 18 Sbjct: 9602 cggtaacacttcactc 9617
<i>P. megaterium</i> -AX2015-1511	NODE_7	Query: 5 gtaaacacttcac 16 Sbjct: 1456 gtaaacacttcac 1467

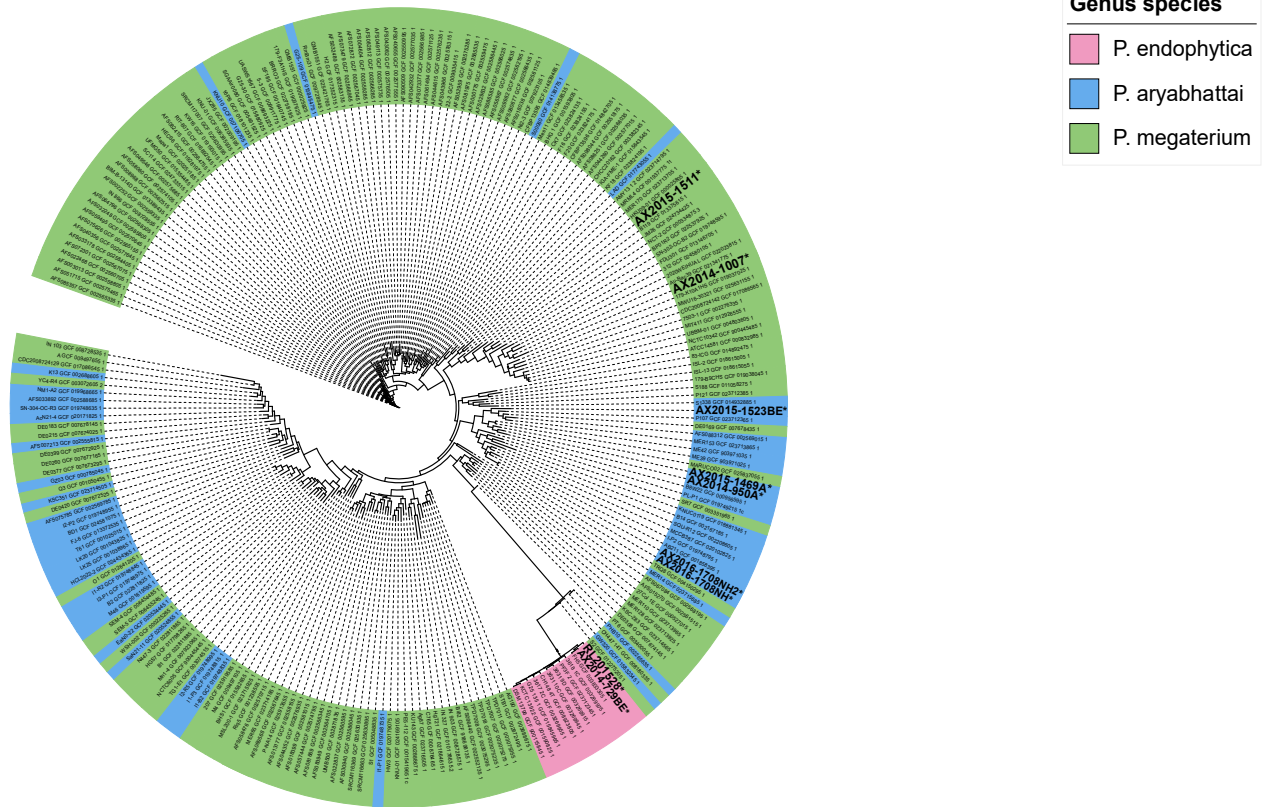


A

B

Supplementary Figure S1: The RAST BLASTn alignment and gene cluster using the protective antigen (*pagA*) forward Taqman probe sequence (5'-TGCGGTAACACTT CACTCCAGTTCGA-3'). A) BLASTn alignment results of the forward Taqman probe *pagA* sequence on *B. anthracis* and *Priestia* genome sequences. (B) Graphic depiction showing the gene cluster orientation of the *pagA* on *B. anthracis* and *Priestia* genome sequences. The reference strain of *B. anthracis* Ames Ancestor was included for comparative analysis. *B. subtilis* str 168 was the closest hit related to the *P. aryabhattai* AX2015-1523BE BLASTn sequence in this test. The graphic is centred on the focus gene (labelled 1 in red).

Tree scale: 1



Supplementary Figure S2: A pan-genomic analysis of 243 *Priestia* (*aryabhatai* [blue], *endophytica* [pink], and *megaterium* [green]) species. The genomes highlighted (bold and with asterisk*) were sequenced in this study (n = 9) and 234 strains were used for comparative genome analysis retrieved from GenBank,

Supplementary Table S6: BLASTn alignment of the *pagA* Taqman probe assay to the *Bacillus anthracis* and *Priestia* genomes.

Probe reverse sequence for <i>pagA</i>		BAPA-LCRed 640 - CCTGTATCCACCCTCACTCTCCATTTTC-P (29 bases)		
Isolate	Contig	Primer binding region		Annotation
<i>B. anthracis</i> Ames Ancestor	NC_007322	Query: 1	cctgtatccaccctcaactcttccatttc 29 Sbjct: 145286 cctgtatccaccctcaactcttccatttc 145258	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>B. anthracis</i> - AX2015-1136	k141_505	Query: 1	cctgtatccaccctcaactcttccatttc 29 Sbjct: 28205 cctgtatccaccctcaactcttccatttc 28177	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>B. anthracis</i> -AX2015-1152	k141_87	Query: 1	cctgtatccaccctcaactcttccatttc 29 Sbjct: 16824 cctgtatccaccctcaactcttccatttc 16852	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>B. anthracis</i> - AX2015-1270	k141_10	Query: 1	cctgtatccaccctcaactcttccatttc 29 Sbjct: 28157 cctgtatccaccctcaactcttccatttc 28129	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>B. anthracis</i> - AX2015-1277A	NODE_21	Query: 1	cctgtatccaccctcaactcttccatttc 29 Sbjct: 28056 cctgtatccaccctcaactcttccatttc 28028	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>P. aryabhattai</i> -AX2015-1523BE	NODE_11	Query: 16	actcttccatttc 29 Sbjct: 142466 actcttccatttc 142453	Lipid A export ATP-binding/permease protein
<i>P. aryabhattai</i> -AX2015-1469A	NODE_4	Query: 16	actcttccatttc 29 Sbjct: 9222 actcttccatttc 9235	Lipid A export ATP-binding/permease protein
<i>P. aryabhattai</i> -AX2016-1708NH	k141_84	Query: 16	actcttccatttc 28 Sbjct: 67006 actcttccatttc 67018	DNA sulfur modification protein DndD
<i>P. megaterium</i> -AX2014-1007	k141_515	Query: 16	actcttccatttc 29 Sbjct: 58049 actcttccatttc 58062	DNA-binding response regulator
<i>P. megaterium</i> -AX2015-1511	NODE_17	Query: 16	actcttccatttc 29 Sbjct: 38747 actcttccatttc 38734	Lipid A export ATP-binding/permease protein

Supplementary Table S7: BLASTn alignment of the lethal factor (*lef*) primer sequences to the *Bacillus anthracis* and *Priestia* genomes.

SYBR green primers for <i>pagA</i>		Forward – CCGATCAAGTATATGGGAATATAGCAA (27 bases)	
		Reverse - CCGGTTTAGTCGTTCTAATGGAT (24 bases)	
Isolate	Contig	Primer binding region	Annotation
<i>B. anthracis</i> Ames Ancestor	NC_007322	Query: 1 cggatcaagtatatgggaatatagcaa 27 Sbjct: 145220 cggatcaagtatatgggaatatagcaa 145246 Query: 1 ccggtttagtcgtttctaattggat 24 Sbjct: 145423 ccggtttagtcgtttctaattggat 145400	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>B. anthracis</i> - AX2015-1136	k141_505	Query: 1 cggatcaagtatatgggaatatagcaa 27 Sbjct: 28139 cggatcaagtatatgggaatatagcaa 28165 Query: 1 ccggtttagtcgtttctaattggat 24 Sbjct: 28342 ccggtttagtcgtttctaattggat 28319	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>B. anthracis</i> - AX2015-1270	k141_10	Query: 1 cggatcaagtatatgggaatatagcaa 27 Sbjct: 28091 cggatcaagtatatgggaatatagcaa 28117 Query: 1 ccggtttagtcgtttctaattggat 24 Sbjct: 28294 ccggtttagtcgtttctaattggat 28271	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>B. anthracis</i> - AX2015-1277A	NODE_21	Query: 1 cggatcaagtatatgggaatatagcaa 27 Sbjct: 27990 cggatcaagtatatgggaatatagcaa 28016 Query: 1 ccggtttagtcgtttctaattggat 24 Sbjct: 28193 ccggtttagtcgtttctaattggat 28170	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>B. anthracis</i> -AX2015-1152	k141_87	Query: 1 cggatcaagtatatgggaatatagcaa 27 Sbjct: 16890 cggatcaagtatatgggaatatagcaa 16864 Query: 1 ccggtttagtcgtttctaattggat 24 Sbjct: 16687 ccggtttagtcgtttctaattggat 16710	Anthrax toxin moiety, protective antigen, <i>pagA</i>
<i>P. aryabhattai</i> -AX2015-1523BE	NODE_16	Query: 10 tatatgggaatatag 24 Sbjct: 33458 tatatgggaatatag 33444 Query: 4 gtttagtcgttt 15 Sbjct: 5957 gtttagtcgttt 5968	Hydrolase proteins
<i>P. aryabhattai</i> -AX2016-1708NH	k141_78 k141_73	Query: 7 aagtatatggaaa 19 Sbjct: 47624 aagtatatggaaa 47636 Query: 4 gtttagtcgttt 15 Sbjct: 108858 gtttagtcgttt 108869	NADH peroxidase Npx Uronate isomerase
<i>P. aryabhattai</i> -AX2015-1469A	NODE_1	Query: 6 caagtatatggaaat 20 Sbjct: 2867716 caagtatatggaaat 2867702 Query: 12 gtttctaattgga 23 Sbjct: 2262982 gtttctaattgga 2262993	Membrane protein involved in the export of O-antigen NADP-specific glutamate dehydrogenase (EC 1.4.1.4)
<i>P. megaterium</i> -AX2014-1007	k141_432 k141_243	Query: 3 gatcaagtatatg 15 Sbjct: 99047 gatcaagtatatg 99035 Query: 8 agtcgtttctaatt 20 Sbjct: 74258 agtcgtttctaatt 74270	Recombination inhibitory protein MutS2 Fatty Acid Biosynthesis FASII
<i>P. megaterium</i> -AX2015-1511	NODE_3 NODE_2	Query: 3 gatcaagtatatg 15 Sbjct: 167360 gatcaagtatatg 167372 Query: 8 agtcgtttctaatt 20 Sbjct: 420607 agtcgtttctaatt 420595	Recombination inhibitory protein MutS2 Glucose dehydrogenase [pyrroloquinoline-quinone]

Supplementary Table S8: BLASTn alignment of the *pagA* SYBR green assay to the *Bacillus anthracis* and *Priestia* genome

SYBR primers targeting the lethal factor <i>lef</i> Probe sequence targeting the lethal factor (<i>lef</i>)		Forward – CACTATCAACACTGGAGCGATTCT Reverse – AATTATGTCATCTTTCTTTGGCTCAA Probe - AGCTGCAGATTCC	(24 bases) (26 bases) (13 bases)
Isolate	Contig	Primer binding region	Annotation
<i>B. anthracis</i> Ames Ancestor	NC_007322	Query: 1 cactatcaaacactggagcgattct 24 Sbjct: 150859 cactatcaaacactggagcgattct 150836 Query: 1 aattatgctcatcttttttggctcaa 26 Sbjct: 150764 aattatgctcatcttttttggctcaa 150789 Query: 1 agctgcagattcc 13 Sbjct: 150804 agctgcagattcc 150792	calmodulin sensitive adenylate cyclase: lethal factor, <i>lef</i> , edema factor, <i>cya</i> , plasmid pXO1
<i>B. anthracis</i> - AX2015-1136	k141_505	Query: 1 cactatcaaacactggagcgattct 24 Sbjct: 33775 cactatcaaacactggagcgattct 33752 Query: 1 aattatgctcatcttttttggctcaa 26 Sbjct: 33680 aattatgctcatcttttttggctcaa 33705 Query: 1 agctgcagattcc 13 Sbjct: 33720 agctgcagattcc 33708	calmodulin sensitive adenylate cyclase: lethal factor, <i>lef</i> , edema factor, <i>cya</i> , plasmid pXO1
<i>B. anthracis</i> - AX2015-1270	k141_10	Query: 1 cactatcaaacactggagcgattct 24 Sbjct: 33739 cactatcaaacactggagcgattct 33716 Query: 1 aattatgctcatcttttttggctcaa 26 Sbjct: 33644 aattatgctcatcttttttggctcaa 33669 Query: 1 agctgcagattcc 13 Sbjct: 33684 agctgcagattcc 33672	calmodulin sensitive adenylate cyclase: lethal factor, <i>lef</i> , edema factor, <i>cya</i> , plasmid pXO1
<i>B. anthracis</i> - AX2015-1277A	NODE_21	Query: 1 cactatcaaacactggagcgattct 24 Sbjct: 33626 cactatcaaacactggagcgattct 33603 Query: 1 cactatcaaacactggagcgattct 24 Sbjct: 33626 cactatcaaacactggagcgattct 33603 Query: 1 agctgcagattcc 13 Sbjct: 33571 agctgcagattcc 33559	calmodulin sensitive adenylate cyclase: lethal factor, <i>lef</i> , edema factor, <i>cya</i> , plasmid pXO1
<i>B. anthracis</i> -AX2015-1152	k141_87	Query: 1 cactatcaaacactggagcgattct 24 Sbjct: 11254 cactatcaaacactggagcgattct 11277 Query: 1 aattatgctcatcttttttggctcaa 26 Sbjct: 11349 aattatgctcatcttttttggctcaa 11324 Query: 1 agctgcagattcc 13 Sbjct: 12545 agctgcagattcc 12533	calmodulin sensitive adenylate cyclase: lethal factor, <i>lef</i> , edema factor, <i>cya</i> , plasmid pXO1
<i>P. endophytica</i> -AX2014-729BE	k141_92	Query: 1 cactatcaaacactg 14 Sbjct: 18793 cactatcaaacactg 18806	FIG013452: putative tellurium resistance protein
	k141_424	Query: 10 atcttttttggct 23 Sbjct: 22529 atcttttttggct 22542	Chromosome (plasmid) partitioning protein ParB
	k141_247	Query: 1 agctgcagattcc 13 Sbjct: 12545 agctgcagattcc 12533	Histone acetyltransferase HPA2
<i>P. aryabhattai</i> -AX2014-950A	NODE_1	Query: 1 cactatcaaacact 13 Sbjct: 1178285 cactatcaaacact 1178297	Hypothetical protein
	NODE_2	Query: 5 atgctcatctttct 18 Sbjct: 203728 atgctcatctttct 203715	Dihydropteroate synthase
	NODE_13	Query: 1 agctgcagattcc 12 Sbjct: 7543 agctgcagattcc 7554	Hypothetical Spanning protein
<i>P. megaterium</i> -AX2014-1007	k141_489	Query: 4 tatcaaacactgg 15 Sbjct: 122856 tatcaaacactgg 122845	Gas vesicle structural protein (GVP)
	k141_432	Query: 11 tcttttttggct 23 Sbjct: 9309 tcttttttggct 9321	Gamma-aminobutyrate: alpha-ketoglutarate aminotransferase (EC 2.6.1.19)
	k141_531	Query: 1 agctgcagattcc 12 Sbjct: 5026 agctgcagattcc 5015	Betaine operon transcriptional regulator
<i>P. megaterium</i> -AX2015-1511	NODE_16	Query: 2 gctgcagattcc 13 Sbjct: 113534 gctgcagattcc 113523	5-deoxy-glucuronate isomerase

Supplementary Table S9: BLASTn alignment of the chromosomal marker Ba-1 primer sequences to the *Bacillus anthracis* and *Priestia* genomes

Primers targeting the chromosomal marker Ba-1		Forward - GTACATCTTCTAGCTGTGCAA Reverse - ACGTAGGAAGACCGTTGATTA Probe - VIC-GTTGTTGTATTG-MGB	(22 bases) (21 bases) (16 bases)
Isolate	Contig	Primer binding region	Annotation
<i>B. anthracis</i> -Ames Ancestor	NC_007530	Query: 1 gtacatcttctagctgttgcaa 22 Sbjct: 4857257 gtacatcttctagctgttgcaa 4857278	FIG01230969: hypothetical protein
		Query: 1 acgttaggaagaccggttgatta 21 Sbjct: 4857321 acgttaggaagaccggttgatta 4857301	
		Query: 1 cgttgttgatttg 16 Sbjct: 4857281 cgttgttgatttg 4857296	
<i>B. anthracis</i> -AX2015-1136	k141_385	Query: 1 gtacatcttctagctgttgcaa 22 Sbjct: 44775 gtacatcttctagctgttgcaa 44796	FIG01230969: hypothetical protein
		Query: 1 acgttaggaagaccggttgatta 21 Sbjct: 44839 acgttaggaagaccggttgatta 44819	
		Query: 1 cgttgttgatttg 16 Sbjct: 44799 cgttgttgatttg 44814	
<i>B. anthracis</i> -AX2015-1152	k141_52	Query: 1 gtacatcttctagctgttgcaa 22 Sbjct: 36985 gtacatcttctagctgttgcaa 36964	FIG01230969: hypothetical protein
		Query: 1 acgttaggaagaccggttgatta 21 Sbjct: 36921 acgttaggaagaccggttgatta 36941	
		Query: 1 cgttgttgatttg 16 Sbjct: 36961 cgttgttgatttg 36946	
<i>B. anthracis</i> -AX2015-1270	k141_33	Query: 1 gtacatcttctagctgttgcaa 22 Sbjct: 62492 gtacatcttctagctgttgcaa 62471	FIG01230969: hypothetical protein
		Query: 1 acgttaggaagaccggttgatta 21 Sbjct: 62428 acgttaggaagaccggttgatta 62448	
		Query: 1 cgttgttgatttg 16 Sbjct: 62468 cgttgttgatttg 62453	
<i>B. anthracis</i> -AX2015-1277A	k141_33	Query: 1 gtacatcttctagctgttgcaa 22 Sbjct: 62492 gtacatcttctagctgttgcaa 62471	FIG01230969: hypothetical protein
		Query: 1 acgttaggaagaccggttgatta 21 Sbjct: 62428 acgttaggaagaccggttgatta 62448	
		Query: 1 cgttgttgatttg 16 Sbjct: 62468 cgttgttgatttg 62453	
<i>P. aryabhattai</i> -AX2014-950A	NODE_2	Query: 7 cttctagctgttgca 21 Sbjct: 230426 cttctagctgttgca 230440	Hypothetical protein
	NODE_2	Query: 4 taggaagaccgt 15 Sbjct: 671994 taggaagaccgt 671983	Lysine Biosynthesis
	NODE_3	Query: 3 ttgttgattt 14 Sbjct: 473207 ttgttgattt 473218	Beta-ketoadipate enol-lactone hydrolase
<i>P. aryabhattai</i> -AX2015-1469A	k141_158	Query: 7 cttctagctgttgca 21 Sbjct: 84720 cttctagctgttgca 84734	Hypothetical protein
	k141_42	Query: 5 aggaagaccgtt 16 Sbjct: 63373 aggaagaccgtt 63384	Gas vesicle structural protein (GVP)
	k141_151	Query: 3 ttgttgattt 14 Sbjct: 234169 ttgttgattt 234180	beta-ketoadipate
<i>P. aryabhattai</i> -AX2016-1708NH	k141_65	Query: 5 atcttctagctgtt 18 Sbjct: 103442 atcttctagctgtt 103429	signaling protein
	k141_24	Query: 4 taggaagaccgt 15 Sbjct: 4890 taggaagaccgt 4901	Lysine Biosynthesis
	k141_72	Query: 3 ttgttgattt 16 Sbjct: 25822 ttgttgattt 25809	Spore germination protein GerKC
<i>P. endophytica</i> -AX2014-729BE	k141_359	Query: 4 catcttctagctgtt 19 Sbjct: 60153 catcttctagctgtt 60138	Protease precursor
	k141_179	Query: 7 gaagaccggtgatt 20 Sbjct: 13060 gaagaccggtgatt 13073	Transcription-repair coupling factor
	k141_386	Query: 3 ttgttgattt 13 Sbjct: 12320 ttgttgattt 12330	Hypothetical protein
<i>P. megaterium</i> -AX2014-1007	k141_174	Query: 7 cttctagctgttgca 21 Sbjct: 14455 cttctagctgttgca 14441	Hypothetical protein
	k141_489	Query: 5 aggaagaccgtt 16 Sbjct: 122921 aggaagaccgtt 122910	Gas vesicle structural protein (GVP)
	k141_526	Query: 2 gttgttgattt 13 Sbjct: 2015 gttgttgattt 2026	Hypothetical protein
<i>P. megaterium</i> -AX2015-1511	NODE_4	Query: 7 cttctagctgttgca 21 Sbjct: 66892 cttctagctgttgca 66878	Cardiolipin synthetase
	NODE_7	Query: 8 aagaccggtgat 19 Sbjct: 97373 aagaccggtgat 97384	Putative deoxyribonuclease, YcfH
	NODE_4	Query: 3 ttgttgattt 14 Sbjct: 108277 ttgttgattt 108266	Beta-ketoadipate enol-lactone hydrolase