TYPE (STRAIN) GENOME SERVER

JOB SUMMARY

PRINT DATE:	2026-09-15 01:39:24 +0200
JOB ID:	588b9751-63ae-4a55-83b7-9ce39343dfee
RESULT PAGE:	https://tygs.dsmz.de/user_results/show?guid=588b9751-63ae-4a55-83b7-9ce39343dfee

Table 1: Phylogenies

Publication-ready versions of both the genome-scale GBDP tree and the 16S rRNA gene sequence tree can be customized and exported either in SVG (vector graphic) or PNG format from within the phylogeny viewers in your TYGS result page. For publications the **SVG format is recommended** because it is lossless, always keeps its high resolution and can also be easily converted to other popular formats such as PDF or EPS. Please follow the link provided above!

Table 2: Identification

The below list contains the result of the TYGS species identification routine.

Explanation of remarks that might occur in the below table:

remark [R1]: The TYGS type strain database is automatically updated on an almost daily basis. However, if a particular type strain genome is not available in the TYGS database, this can have several reasons which are detailed in the FAQ. You can request an extended 16S rRNA gene analysis via the 16S tree viewer found in your result page to detect **not yet genome-sequenced** type strains relevant for your study.

remark [R2]: > 70% dDDH value (formula d_4) and (almost) minimal dDDH values for gene-content formulae d_0 and d_6 indicate a potentially unreliable identification result and should thus be checked via the 16S rRNA gene sequence similarity. Such strong deviations can, in principle, be caused by sequence contamination.

remark [R3]: G+C content difference of > 1 % indicates a potentially unreliable identification result because within species G+C content varies no more than 1 %, if computed from genome sequences (PMID: 24505073).

Strain	Conclusion	Identification result	Remark
'Bacillus_cereus_AH187'	belongs to known species	*Bacillus paranthracis*	
'Bacillus_cereus_BAG5X2-1'	belongs to known species	*Bacillus wiedmannii*	
'Bacillus_cereus_AH1272'	belongs to known species	*Bacillus nitratireducens*	
'Bacillus_cereus_VD107'	belongs to known species	*Bacillus paramycoides*	
'Bacillus_cereus_172560W'	belongs to known species	*Bacillus cereus*	
'Bacillus_cereus_BAG1O-2'	belongs to known species	*Bacillus toyonensis*	
'Bacillus_cereus_AH603'	belongs to known species	*Bacillus mycoides*	
'Bacillus_cereus_ATCC_4342'	belongs to known species	*Bacillus tropicus*	
'Bacillus_anthracis_str_Ames_Ancestor'	potential new species		see [R1]
'Bacillus_anthracis_str_Kruger_B'	potential new species		see [R1]
'Bacillus_anthracis_str_Vollum'	potential new species		see [R1]
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1'	potential new species		see [R1]
'Bacillus_cereus_AH1271'	potential new species		see [R1]
'Bacillus_cereus_B5-2'	potential new species		see [R1]

Strain	Conclusion	Identification result	Remark
'Bacillus_cereus_BAG2X1-1'	potential new species		see [R1]
'Bacillus_cereus_BAG2X1-2'	potential new species		see [R1]
'Bacillus_cereus_HuA4-10'	potential new species		see [R1]
'Bacillus_cereus_R309803'	potential new species		see [R1]
'Bacillus_cereus_Rock3-44'	potential new species		see [R1]
'Bacillus_cereus_VD136'	potential new species		see [R1]

Table 3: Pairwise comparisons of user genomes vs. type-strain genomes

The following table contains the pairwise dDDH values between your user genomes and the selected type-strain genomes. The dDDH values are provided along with their confidence intervals (C.I.) for the three different GBDP formulas:

- formula d_0 (a.k.a. GGDC formula 1): length of all HSPs divided by total genome length
- formula d_4 (a.k.a. GGDC formula 2): sum of all identities found in HSPs divided by overall HSP length
- formula d_6 (a.k.a. GGDC formula 3): sum of all identities found in HSPs divided by total genome length

Note: Formula d_4 is independent of genome length and is thus robust against the use of incomplete draft genomes. For other reasons for preferring formula d_4, see the FAQ.

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_anthracis_str_Vollum.fna'**	100.0	[100.0 - 100.0]	99.8	[99.6 - 99.9]	100.0	[100.0 - 100.0]	0.03
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_anthracis_str_Vollum.fna'**	99.9	[99.8 - 100.0]	99.3	[98.8 - 99.5]	100.0	[99.9 - 100.0]	0.06
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus toyonensis* NCIMB 14858	89.9	[86.6 - 92.4]	99.3	[98.9 - 99.5]	93.8	[91.6 - 95.4]	0.42
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_anthracis_str_Kruger_B.fna'**	99.9	[99.8 - 100.0]	99.3	[98.9 - 99.6]	100.0	[99.9 - 100.0]	0.09
'Bacillus_cereus_AH1272.fna'	*Bacillus nitratireducens* 4049	84.0	[80.2 - 87.1]	94.4	[92.7 - 95.7]	88.5	[85.6 - 90.9]	0.08
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus wiedmannii* FSL W8-0169	89.2	[85.8 - 91.8]	88.0	[85.5 - 90.2]	91.6	[89.1 - 93.6]	0.01
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	80.7	[76.8 - 84.1]	84.6	[81.8 - 87.0]	84.3	[81.0 - 87.1]	0.12
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	80.5	[76.6 - 83.9]	84.5	[81.8 - 86.9]	84.1	[80.9 - 86.9]	0.09
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	80.1	[76.2 - 83.6]	84.3	[81.6 - 86.7]	83.8	[80.5 - 86.6]	0.03
'Bacillus_cereus_AH187.fna'	*Bacillus paranthracis* MCCC 1A00395	75.7	[71.7 - 79.3]	77.4	[74.4 - 80.2]	78.8	[75.3 - 81.8]	0.33
'Bacillus_cereus_VD107.fna'	*Bacillus paramycoides* NH24A2	78.2	[74.2 - 81.7]	77.1	[74.1 - 79.8]	80.9	[77.5 - 83.8]	0.06
'Bacillus_cereus_172560W.fna'	*Bacillus cereus* ATCC 14579	80.9	[77.0 - 84.3]	73.7	[70.7 - 76.6]	82.5	[79.2 - 85.4]	0.47
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus tropicus* N24	88.5	[85.1 - 91.2]	70.9	[67.9 - 73.7]	88.2	[85.3 - 90.6]	0.0
'Bacillus_cereus_AH603.fna'	*Bacillus mycoides* DSM 2048	73.4	[69.4 - 77.0]	70.5	[67.5 - 73.4]	75.4	[71.9 - 78.6]	0.09
'Bacillus_cereus_R309803.fna'	*Bacillus luti* MCCC 1A00359	78.9	[74.9 - 82.4]	69.9	[66.9 - 72.7]	80.0	[76.6 - 83.0]	0.09
'Bacillus_cereus_AH603.fna'	*Bacillus weihenstephanensis* NBRC 101238	71.1	[67.1 - 74.7]	69.8	[66.8 - 72.6]	73.2	[69.8 - 76.5]	0.09
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus wiedmannii* FSL W8-0169	83.8	[80.0 - 87.0]	69.3	[66.3 - 72.1]	84.1	[80.8 - 86.9]	0.02
'Bacillus_cereus_VD136.fna'	*Bacillus pseudomycoides* DSM 12442	67.9	[64.0 - 71.5]	68.5	[65.5 - 71.3]	70.2	[66.7 - 73.4]	0.2
'Bacillus_cereus_AH187.fna'	*Bacillus pacificus* MCCC 1A06182	78.1	[74.2 - 81.6]	67.5	[64.5 - 70.3]	78.9	[75.4 - 81.9]	0.31
'Bacillus_cereus_172560W.fna'	*Bacillus thuringiensis* ATCC 10792	74.6	[70.6 - 78.2]	67.5	[64.5 - 70.3]	75.8	[72.4 - 79.0]	0.01

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_BAG2X1-2.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	78.2	[74.2 - 81.7]	66.7	[63.7 - 69.5]	78.7	[75.3 - 81.8]	0.03
'Bacillus_cereus_AH1271.fna'	*Bacillus mobilis* MCCC 1A05942	77.2	[73.2 - 80.7]	66.4	[63.4 - 69.2]	77.8	[74.4 - 80.9]	0.01
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_ATCC_4342.fna'**	74.9	[70.9 - 78.5]	65.6	[62.7 - 68.4]	75.7	[72.2 - 78.8]	0.31
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus paranthracis* MCCC 1A00395	75.1	[71.1 - 78.7]	64.4	[61.5 - 67.2]	75.6	[72.1 - 78.7]	0.02
'Bacillus_cereus_AH187.fna'	*Bacillus tropicus* N24	74.4	[70.4 - 78.0]	63.1	[60.2 - 66.0]	74.7	[71.2 - 77.9]	0.31
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus paranthracis* MCCC 1A00395	72.4	[68.4 - 76.0]	62.4	[59.5 - 65.2]	72.8	[69.3 - 76.0]	0.06
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus paranthracis* MCCC 1A00395	73.1	[69.1 - 76.7]	61.6	[58.7 - 64.4]	73.2	[69.7 - 76.4]	0.03
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus paranthracis* MCCC 1A00395	73.3	[69.3 - 76.9]	61.6	[58.7 - 64.4]	73.4	[69.9 - 76.6]	0.06
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus paranthracis* MCCC 1A00395	72.8	[68.8 - 76.4]	61.4	[58.5 - 64.2]	72.9	[69.4 - 76.1]	0.04
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	74.7	[70.7 - 78.3]	60.9	[58.0 - 63.7]	74.4	[70.9 - 77.6]	0.09
'Bacillus_cereus_AH187.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	70.0	[66.1 - 73.6]	60.8	[58.0 - 63.6]	70.3	[66.9 - 73.6]	0.39
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	75.0	[71.0 - 78.6]	60.7	[57.8 - 63.5]	74.6	[71.1 - 77.8]	0.09
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_ATCC_4342.fna'**	80.2	[76.2 - 83.6]	60.7	[57.8 - 63.5]	79.0	[75.5 - 82.0]	0.01
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_ATCC_4342.fna'**	80.3	[76.4 - 83.8]	60.7	[57.9 - 63.5]	79.1	[75.7 - 82.2]	0.04
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_ATCC_4342.fna'**	79.9	[75.9 - 83.3]	60.6	[57.7 - 63.4]	78.7	[75.3 - 81.8]	0.05
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	78.5	[74.5 - 82.0]	60.4	[57.5 - 63.1]	77.5	[74.0 - 80.6]	0.08
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_HuA4-10.fna'**	71.5	[67.6 - 75.2]	60.4	[57.5 - 63.1]	71.5	[68.1 - 74.8]	0.12
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_AH187.fna'**	75.2	[71.2 - 78.8]	60.1	[57.2 - 62.9]	74.6	[71.2 - 77.8]	0.27
'Bacillus_cereus_B5-2.fna'	*Bacillus wiedmannii* FSL W8-0169	79.3	[75.4 - 82.8]	60.0	[57.1 - 62.8]	78.1	[74.6 - 81.2]	0.07
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_AH187.fna'**	75.0	[71.0 - 78.6]	60.0	[57.2 - 62.8]	74.4	[70.9 - 77.6]	0.3
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_AH187.fna'**	74.3	[70.3 - 77.9]	59.8	[57.0 - 62.6]	73.8	[70.3 - 77.0]	0.36
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus pacificus* MCCC 1A06182	74.0	[70.0 - 77.6]	59.7	[56.9 - 62.5]	73.5	[70.1 - 76.7]	0.0
'Bacillus_cereus_AH1271.fna'	*Bacillus wiedmannii* FSL W8-0169	74.9	[70.9 - 78.5]	59.5	[56.7 - 62.3]	74.2	[70.7 - 77.4]	0.07
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus mobilis* MCCC 1A05942	68.7	[64.8 - 72.3]	59.3	[56.5 - 62.0]	68.8	[65.4 - 72.0]	0.11
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	70.4	[66.5 - 74.1]	59.1	[56.3 - 61.8]	70.3	[66.8 - 73.5]	0.06
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus tropicus* N24	76.3	[72.3 - 79.9]	59.0	[56.2 - 61.7]	75.3	[71.8 - 78.5]	0.04

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus tropicus* N24	76.1	[72.1 - 79.7]	58.9	[56.1 - 61.7]	75.1	[71.6 - 78.3]	0.01
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus tropicus* N24	75.9	[71.9 - 79.5]	58.8	[56.0 - 61.6]	74.9	[71.4 - 78.1]	0.05
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus tropicus* N24	74.6	[70.6 - 78.2]	58.7	[55.9 - 61.4]	73.7	[70.2 - 76.9]	0.08
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus mobilis* MCCC 1A05942	65.6	[61.8 - 69.3]	57.9	[55.1 - 60.6]	65.8	[62.4 - 69.0]	0.07
'Bacillus_cereus_AH1272.fna'	*Bacillus proteolyticus* MCCC 1A00365	65.5	[61.6 - 69.1]	57.8	[55.0 - 60.5]	65.6	[62.3 - 68.9]	0.07
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	77.5	[73.5 - 81.0]	57.7	[54.9 - 60.4]	75.9	[72.5 - 79.1]	0.05
'Bacillus_cereus_HuA4-10.fna'	*Bacillus mycoides* DSM 2048	67.6	[63.7 - 71.2]	57.0	[54.2 - 59.7]	67.3	[63.9 - 70.5]	0.03
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus pacificus* MCCC 1A06182	67.2	[63.3 - 70.8]	56.4	[53.7 - 59.2]	66.8	[63.4 - 70.0]	0.08
'Bacillus_cereus_HuA4-10.fna'	*Bacillus weihenstephanensis* NBRC 101238	69.8	[65.9 - 73.5]	56.2	[53.4 - 58.9]	69.0	[65.6 - 72.2]	0.03
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus pacificus* MCCC 1A06182	70.1	[66.2 - 73.7]	55.9	[53.1 - 58.6]	69.2	[65.7 - 72.4]	0.04
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus pacificus* MCCC 1A06182	69.5	[65.6 - 73.2]	55.8	[53.0 - 58.5]	68.7	[65.2 - 71.9]	0.05
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus pacificus* MCCC 1A06182	69.9	[65.9 - 73.5]	55.8	[53.1 - 58.6]	69.0	[65.5 - 72.2]	0.01
'Bacillus_cereus_AH1271.fna'	*Bacillus albus* N35-10-2	68.6	[64.7 - 72.2]	55.2	[52.4 - 57.9]	67.7	[64.3 - 70.9]	0.33
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus albus* N35-10-2	74.0	[70.0 - 77.6]	54.7	[52.0 - 57.4]	72.1	[68.7 - 75.4]	0.24
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_B5-2.fna'**	70.5	[66.5 - 74.1]	54.4	[51.7 - 57.1]	69.1	[65.6 - 72.3]	0.14
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus albus* N35-10-2	68.1	[64.3 - 71.8]	53.8	[51.1 - 56.5]	66.9	[63.5 - 70.2]	0.27
'Bacillus_cereus_B5-2.fna'	*Bacillus mobilis* MCCC 1A05942	66.6	[62.8 - 70.3]	53.7	[51.0 - 56.3]	65.6	[62.2 - 68.8]	0.16
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus albus* N35-10-2	73.6	[69.6 - 77.2]	53.2	[50.5 - 55.9]	71.4	[67.9 - 74.6]	0.27
'Bacillus_cereus_AH1272.fna'	*Bacillus mycoides* DSM 2048	65.9	[62.0 - 69.5]	52.9	[50.2 - 55.6]	64.7	[61.4 - 68.0]	0.01
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus albus* N35-10-2	69.3	[65.4 - 73.0]	52.8	[50.1 - 55.5]	67.7	[64.2 - 70.9]	0.18
'Bacillus_cereus_B5-2.fna'	*Bacillus tropicus* N24	70.7	[66.8 - 74.4]	52.8	[50.1 - 55.5]	68.8	[65.4 - 72.0]	0.08
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_B5-2.fna'**	71.8	[67.8 - 75.4]	52.6	[49.9 - 55.3]	69.7	[66.2 - 72.9]	0.08
'Bacillus_cereus_AH1272.fna'	*Bacillus weihenstephanensis* NBRC 101238	68.9	[65.0 - 72.6]	52.5	[49.8 - 55.2]	67.2	[63.8 - 70.5]	0.01
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus albus* N35-10-2	70.6	[66.7 - 74.2]	52.4	[49.7 - 55.1]	68.6	[65.2 - 71.8]	0.31
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus albus* N35-10-2	70.4	[66.5 - 74.1]	52.4	[49.7 - 55.0]	68.4	[65.0 - 71.7]	0.28
'Bacillus_cereus_B5-2.fna'	*Bacillus albus* N35-10-2	72.5	[68.5 - 76.1]	52.4	[49.8 - 55.1]	70.2	[66.7 - 73.4]	0.19

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_AH1271.fna'	*Bacillus pacificus* MCCC 1A06182	73.1	[69.1 - 76.7]	52.4	[49.7 - 55.0]	70.7	[67.2 - 73.9]	0.06
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus albus* N35-10-2	70.1	[66.1 - 73.7]	52.3	[49.6 - 54.9]	68.1	[64.7 - 71.3]	0.21
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_AH1271.fna'**	73.3	[69.3 - 76.9]	52.1	[49.5 - 54.8]	70.8	[67.3 - 74.0]	0.24
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus tropicus* N24	70.5	[66.5 - 74.1]	51.9	[49.2 - 54.5]	68.3	[64.9 - 71.6]	0.01
'Bacillus_cereus_AH187.fna'	*Bacillus albus* N35-10-2	64.1	[60.4 - 67.8]	51.8	[49.2 - 54.5]	63.0	[59.6 - 66.2]	0.57
'Bacillus_cereus_B5-2.fna'	*Bacillus paranthracis* MCCC 1A00395	64.8	[61.0 - 68.4]	51.7	[49.0 - 54.3]	63.5	[60.1 - 66.7]	0.06
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus wiedmannii* FSL W8-0169	77.0	[73.1 - 80.6]	51.7	[49.0 - 54.3]	73.7	[70.2 - 76.9]	0.01
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_B5-2.fna'**	66.4	[62.6 - 70.1]	51.6	[48.9 - 54.2]	64.8	[61.5 - 68.1]	0.12
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	71.9	[67.9 - 75.5]	51.6	[49.0 - 54.3]	69.4	[66.0 - 72.7]	0.0
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_ATCC_4342.fna'**	76.3	[72.3 - 79.9]	51.6	[48.9 - 54.3]	73.1	[69.6 - 76.3]	0.06
'Bacillus_cereus_B5-2.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	67.0	[63.1 - 70.6]	51.6	[48.9 - 54.2]	65.3	[62.0 - 68.5]	0.0
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus pacificus* MCCC 1A06182	63.8	[60.0 - 67.4]	51.5	[48.9 - 54.2]	62.6	[59.3 - 65.8]	0.0
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_B5-2.fna'**	66.2	[62.4 - 69.9]	51.5	[48.8 - 54.2]	64.7	[61.3 - 67.9]	0.09
'Bacillus_cereus_AH1271.fna'	*Bacillus tropicus* N24	74.4	[70.4 - 78.0]	51.5	[48.8 - 54.1]	71.5	[68.0 - 74.7]	0.06
'Bacillus_cereus_AH603.fna'	*Bacillus nitratireducens* 4049	66.3	[62.5 - 69.9]	51.4	[48.8 - 54.1]	64.7	[61.3 - 67.9]	0.19
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_B5-2.fna'**	63.1	[59.4 - 66.7]	51.4	[48.7 - 54.1]	62.0	[58.7 - 65.2]	0.39
'Bacillus_cereus_BAG5X2-1.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	69.4	[65.5 - 73.0]	51.4	[48.7 - 54.0]	67.2	[63.8 - 70.5]	0.09
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_B5-2.fna'**	66.1	[62.3 - 69.7]	51.4	[48.8 - 54.1]	64.5	[61.2 - 67.7]	0.03
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus tropicus* N24	74.6	[70.6 - 78.2]	51.3	[48.7 - 54.0]	71.6	[68.1 - 74.8]	0.03
'Bacillus_cereus_AH187.fna'	*Bacillus wiedmannii* FSL W8-0169	67.7	[63.9 - 71.4]	51.3	[48.7 - 54.0]	65.9	[62.5 - 69.1]	0.32
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	75.7	[71.7 - 79.3]	51.2	[48.6 - 53.9]	72.4	[69.0 - 75.6]	0.03
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_AH1272.fna'**	64.6	[60.8 - 68.2]	51.2	[48.6 - 53.9]	63.2	[59.8 - 66.4]	0.1
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus wiedmannii* FSL W8-0169	74.6	[70.6 - 78.2]	51.2	[48.6 - 53.9]	71.6	[68.1 - 74.8]	0.07
'Bacillus_cereus_AH187.fna'	*Bacillus mobilis* MCCC 1A05942	72.9	[69.0 - 76.6]	51.2	[48.5 - 53.8]	70.2	[66.7 - 73.4]	0.23
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	64.2	[60.5 - 67.9]	51.1	[48.5 - 53.8]	62.9	[59.5 - 66.1]	0.3
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus pacificus* MCCC 1A06182	65.9	[62.1 - 69.6]	51.1	[48.4 - 53.7]	64.3	[60.9 - 67.5]	0.03

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_B5-2.fna'	*Bacillus pacificus* MCCC 1A06182	65.6	[61.8 - 69.2]	50.9	[48.3 - 53.6]	63.9	[60.6 - 67.2]	0.08
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	65.9	[62.1 - 69.6]	50.9	[48.3 - 53.6]	64.2	[60.9 - 67.4]	0.03
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus paranthracis* MCCC 1A00395	65.5	[61.7 - 69.1]	50.9	[48.3 - 53.6]	63.8	[60.5 - 67.1]	0.02
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	65.7	[61.9 - 69.3]	50.9	[48.2 - 53.5]	64.0	[60.7 - 67.2]	0.0
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus wiedmannii* FSL W8-0169	70.7	[66.8 - 74.4]	50.8	[48.2 - 53.5]	68.2	[64.8 - 71.5]	0.02
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus paranthracis* MCCC 1A00395	70.2	[66.3 - 73.9]	50.8	[48.1 - 53.4]	67.8	[64.4 - 71.0]	0.01
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus wiedmannii* FSL W8-0169	71.0	[67.0 - 74.6]	50.8	[48.2 - 53.5]	68.4	[65.0 - 71.7]	0.05
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	65.2	[61.4 - 68.8]	50.8	[48.2 - 53.4]	63.6	[60.2 - 66.8]	0.06
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus wiedmannii* FSL W8-0169	70.4	[66.4 - 74.0]	50.7	[48.1 - 53.4]	67.9	[64.5 - 71.1]	0.04
'Bacillus_cereus_BAG2X1-2.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	70.8	[66.9 - 74.5]	50.7	[48.0 - 53.3]	68.3	[64.8 - 71.5]	0.05
'Bacillus_cereus_AH1271.fna'	*Bacillus paranthracis* MCCC 1A00395	67.0	[63.2 - 70.7]	50.6	[48.0 - 53.3]	65.1	[61.7 - 68.3]	0.08
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	70.6	[66.7 - 74.3]	50.5	[47.9 - 53.2]	68.0	[64.6 - 71.3]	0.07
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	70.4	[66.5 - 74.0]	50.5	[47.9 - 53.1]	67.8	[64.4 - 71.1]	0.04
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	66.5	[62.7 - 70.1]	50.5	[47.9 - 53.2]	64.6	[61.2 - 67.8]	0.34
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus mobilis* MCCC 1A05942	70.2	[66.3 - 73.8]	50.5	[47.9 - 53.2]	67.7	[64.3 - 70.9]	0.08
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	70.1	[66.2 - 73.8]	50.4	[47.7 - 53.0]	67.6	[64.2 - 70.8]	0.02
'Bacillus_cereus_AH1271.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	67.5	[63.7 - 71.2]	50.3	[47.7 - 52.9]	65.4	[62.0 - 68.6]	0.15
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_AH1271.fna'**	71.5	[67.6 - 75.2]	50.0	[47.3 - 52.6]	68.6	[65.2 - 71.8]	0.05
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_AH1271.fna'**	71.7	[67.7 - 75.3]	50.0	[47.4 - 52.6]	68.8	[65.3 - 72.0]	0.02
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_AH1271.fna'**	71.3	[67.3 - 74.9]	49.9	[47.2 - 52.5]	68.4	[64.9 - 71.6]	0.12
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus mobilis* MCCC 1A05942	65.0	[61.2 - 68.7]	49.5	[46.9 - 52.2]	63.1	[59.7 - 66.3]	0.16
'Bacillus_cereus_AH603.fna'	*Bacillus proteolyticus* MCCC 1A00365	62.1	[58.4 - 65.7]	49.4	[46.8 - 52.0]	60.5	[57.3 - 63.7]	0.03
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus mobilis* MCCC 1A05942	68.5	[64.6 - 72.2]	49.4	[46.7 - 52.0]	65.9	[62.5 - 69.2]	0.04
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus mobilis* MCCC 1A05942	68.4	[64.5 - 72.0]	49.3	[46.7 - 51.9]	65.8	[62.4 - 69.0]	0.07
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus mobilis* MCCC 1A05942	68.0	[64.1 - 71.7]	49.2	[46.6 - 51.8]	65.5	[62.1 - 68.7]	0.13
'Bacillus_cereus_HuA4-10.fna'	*Bacillus nitratireducens* 4049	66.2	[62.4 - 69.9]	49.0	[46.4 - 51.6]	63.9	[60.6 - 67.1]	0.06

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_HuA4-10.fna'	*Bacillus proteolyticus* MCCC 1A00365	65.7	[61.9 - 69.4]	48.9	[46.3 - 51.5]	63.5	[60.1 - 66.7]	0.09
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_HuA4-10.fna'**	61.5	[57.7 - 65.0]	48.9	[46.3 - 51.5]	59.9	[56.6 - 63.0]	0.02
'Bacillus_cereus_R309803.fna'	*Bacillus mobilis* MCCC 1A05942	71.8	[67.9 - 75.5]	47.7	[45.1 - 50.3]	68.1	[64.7 - 71.3]	0.08
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_R309803.fna'**	68.4	[64.5 - 72.1]	47.3	[44.7 - 49.9]	65.2	[61.8 - 68.4]	0.09
'Bacillus_cereus_HuA4-10.fna'	**'Bacillus_cereus_VD107.fna'**	61.5	[57.8 - 65.0]	46.5	[44.0 - 49.1]	59.2	[55.9 - 62.3]	0.02
'Bacillus_cereus_HuA4-10.fna'	*Bacillus paramycoides* NH24A2	63.1	[59.4 - 66.7]	46.3	[43.8 - 48.9]	60.5	[57.2 - 63.7]	0.04
'Bacillus_cereus_BAG2X1-2.fna'	**'Bacillus_cereus_R309803.fna'**	65.6	[61.8 - 69.2]	46.2	[43.6 - 48.8]	62.5	[59.1 - 65.7]	0.18
'Bacillus_cereus_VD107.fna'	*Bacillus mycoides* DSM 2048	59.0	[55.4 - 62.6]	46.2	[43.7 - 48.8]	57.0	[53.8 - 60.1]	0.05
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_VD107.fna'**	56.8	[53.3 - 60.3]	46.1	[43.6 - 48.7]	55.1	[52.0 - 58.3]	0.14
'Bacillus_cereus_R309803.fna'	*Bacillus wiedmannii* FSL W8-0169	65.9	[62.1 - 69.5]	46.1	[43.5 - 48.6]	62.7	[59.4 - 65.9]	0.16
'Bacillus_cereus_BAG5X2-1.fna'	**'Bacillus_cereus_R309803.fna'**	61.4	[57.7 - 65.0]	45.9	[43.4 - 48.5]	58.9	[55.7 - 62.1]	0.15
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_R309803.fna'**	63.9	[60.2 - 67.5]	45.9	[43.4 - 48.5]	61.0	[57.7 - 64.2]	0.24
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus cereus* ATCC 14579	76.3	[72.3 - 79.9]	45.9	[43.4 - 48.5]	71.1	[67.6 - 74.3]	0.08
'Bacillus_cereus_VD107.fna'	*Bacillus weihenstephanensis* NBRC 101238	59.7	[56.0 - 63.2]	45.9	[43.3 - 48.5]	57.5	[54.3 - 60.6]	0.05
'Bacillus_cereus_AH187.fna'	*Bacillus cereus* ATCC 14579	67.9	[64.0 - 71.5]	45.8	[43.3 - 48.4]	64.2	[60.9 - 67.4]	0.22
'Bacillus_cereus_B5-2.fna'	*Bacillus luti* MCCC 1A00359	68.5	[64.6 - 72.2]	45.8	[43.3 - 48.4]	64.7	[61.4 - 67.9]	0.32
'Bacillus_cereus_AH603.fna'	*Bacillus paramycoides* NH24A2	58.1	[54.5 - 61.6]	45.7	[43.1 - 48.3]	56.1	[52.9 - 59.2]	0.08
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_ATCC_4342.fna'**	70.5	[66.6 - 74.1]	45.6	[43.1 - 48.2]	66.3	[62.9 - 69.5]	0.39
'Bacillus_cereus_R309803.fna'	*Bacillus pacificus* MCCC 1A06182	63.4	[59.7 - 67.0]	45.5	[43.0 - 48.1]	60.5	[57.2 - 63.6]	0.15
'Bacillus_cereus_172560W.fna'	*Bacillus tropicus* N24	68.1	[64.3 - 71.8]	45.3	[42.8 - 47.9]	64.3	[60.9 - 67.5]	0.38
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_R309803.fna'**	66.2	[62.3 - 69.8]	45.3	[42.8 - 47.9]	62.6	[59.3 - 65.8]	0.15
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus cereus* ATCC 14579	71.6	[67.6 - 75.2]	45.2	[42.6 - 47.7]	67.0	[63.6 - 70.2]	0.17
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus luti* MCCC 1A00359	65.8	[62.0 - 69.5]	45.2	[42.7 - 47.8]	62.3	[59.0 - 65.5]	0.24
'Bacillus_cereus_R309803.fna'	*Bacillus tropicus* N24	63.8	[60.0 - 67.4]	45.0	[42.5 - 47.6]	60.6	[57.3 - 63.8]	0.15
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus luti* MCCC 1A00359	71.0	[67.0 - 74.6]	45.0	[42.5 - 47.6]	66.4	[63.0 - 69.6]	0.27
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus cereus* ATCC 14579	70.3	[66.4 - 74.0]	45.0	[42.5 - 47.6]	65.9	[62.5 - 69.1]	0.05
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_R309803.fna'**	63.6	[59.8 - 67.2]	45.0	[42.5 - 47.6]	60.4	[57.2 - 63.6]	0.15

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus thuringiensis* ATCC 10792	65.0	[61.2 - 68.6]	45.0	[42.5 - 47.6]	61.6	[58.3 - 64.8]	0.38
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus cereus* ATCC 14579	70.1	[66.1 - 73.7]	44.9	[42.3 - 47.4]	65.6	[62.3 - 68.9]	0.08
'Bacillus_cereus_R309803.fna'	*Bacillus albus* N35-10-2	62.3	[58.6 - 65.9]	44.9	[42.3 - 47.4]	59.3	[56.1 - 62.5]	0.42
'Bacillus_cereus_172560W.fna'	*Bacillus paranthracis* MCCC 1A00395	64.0	[60.3 - 67.6]	44.8	[42.2 - 47.3]	60.7	[57.4 - 63.9]	0.37
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus toyonensis* NCIMB 14858	58.9	[55.3 - 62.5]	44.8	[42.3 - 47.4]	56.5	[53.3 - 59.6]	0.25
'Bacillus_cereus_172560W.fna'	*Bacillus toyonensis* NCIMB 14858	68.4	[64.5 - 72.0]	44.8	[42.2 - 47.4]	64.3	[60.9 - 67.5]	0.74
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus luti* MCCC 1A00359	69.9	[66.0 - 73.6]	44.8	[42.3 - 47.4]	65.5	[62.1 - 68.7]	0.24
'Bacillus_cereus_172560W.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	65.6	[61.8 - 69.2]	44.7	[42.2 - 47.3]	61.9	[58.6 - 65.1]	0.3
'Bacillus_cereus_B5-2.fna'	*Bacillus cereus* ATCC 14579	65.7	[61.9 - 69.4]	44.7	[42.2 - 47.3]	62.1	[58.8 - 65.3]	0.17
'Bacillus_cereus_R309803.fna'	*Bacillus paranthracis* MCCC 1A00395	61.8	[58.1 - 65.4]	44.7	[42.2 - 47.3]	58.9	[55.7 - 62.0]	0.17
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus cereus* ATCC 14579	69.4	[65.5 - 73.1]	44.6	[42.1 - 47.2]	65.0	[61.7 - 68.2]	0.14
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus luti* MCCC 1A00359	61.2	[57.5 - 64.8]	44.6	[42.0 - 47.1]	58.3	[55.1 - 61.5]	0.14
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_AH187.fna'**	63.8	[60.0 - 67.4]	44.6	[42.1 - 47.2]	60.5	[57.2 - 63.6]	0.69
'Bacillus_cereus_AH187.fna'	*Bacillus luti* MCCC 1A00359	64.7	[60.9 - 68.3]	44.5	[42.0 - 47.1]	61.2	[57.9 - 64.4]	0.07
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus thuringiensis* ATCC 10792	63.8	[60.0 - 67.4]	44.5	[42.0 - 47.1]	60.4	[57.2 - 63.6]	0.31
'Bacillus_cereus_B5-2.fna'	*Bacillus toyonensis* NCIMB 14858	65.6	[61.7 - 69.2]	44.5	[41.9 - 47.0]	61.8	[58.5 - 65.0]	0.43
'Bacillus_cereus_B5-2.fna'	*Bacillus thuringiensis* ATCC 10792	60.6	[57.0 - 64.2]	44.4	[41.9 - 47.0]	57.8	[54.6 - 60.9]	0.3
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_172560W.fna'**	66.0	[62.1 - 69.6]	44.4	[41.8 - 46.9]	62.1	[58.8 - 65.3]	0.43
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_B5-2.fna'**	66.2	[62.4 - 69.8]	44.4	[41.9 - 47.0]	62.3	[59.0 - 65.5]	0.3
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	69.8	[65.9 - 73.5]	44.4	[41.8 - 46.9]	65.2	[61.9 - 68.5]	0.32
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus cereus* ATCC 14579	72.6	[68.6 - 76.2]	44.4	[41.9 - 47.0]	67.5	[64.1 - 70.7]	0.15
'Bacillus_cereus_AH1271.fna'	*Bacillus luti* MCCC 1A00359	66.7	[62.9 - 70.4]	44.4	[41.9 - 47.0]	62.8	[59.5 - 66.0]	0.18
'Bacillus_cereus_R309803.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	62.7	[59.0 - 66.3]	44.4	[41.9 - 47.0]	59.5	[56.3 - 62.7]	0.24
'Bacillus_cereus_AH187.fna'	*Bacillus thuringiensis* ATCC 10792	60.0	[56.3 - 63.5]	44.3	[41.8 - 46.9]	57.2	[54.0 - 60.4]	0.69
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_172560W.fna'**	65.8	[62.0 - 69.4]	44.3	[41.8 - 46.9]	62.0	[58.7 - 65.2]	0.39
'Bacillus_cereus_172560W.fna'	*Bacillus wiedmannii* FSL W8-0169	67.8	[63.9 - 71.5]	44.3	[41.8 - 46.9]	63.6	[60.3 - 66.8]	0.38
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	58.3	[54.7 - 61.8]	44.3	[41.7 - 46.8]	55.8	[52.7 - 58.9]	0.17

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	63.9	[60.1 - 67.5]	44.3	[41.8 - 46.9]	60.4	[57.2 - 63.6]	0.39
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus thuringiensis* ATCC 10792	60.4	[56.7 - 63.9]	44.2	[41.6 - 46.7]	57.5	[54.3 - 60.6]	0.3
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus cereus* ATCC 14579	66.8	[62.9 - 70.4]	44.2	[41.7 - 46.8]	62.7	[59.4 - 65.9]	0.08
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_R309803.fna'**	64.0	[60.2 - 67.6]	44.2	[41.7 - 46.8]	60.5	[57.2 - 63.6]	0.15
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus luti* MCCC 1A00359	67.8	[63.9 - 71.5]	44.2	[41.7 - 46.8]	63.6	[60.2 - 66.8]	0.32
'Bacillus_cereus_172560W.fna'	*Bacillus pacificus* MCCC 1A06182	64.6	[60.8 - 68.2]	44.2	[41.7 - 46.8]	60.9	[57.7 - 64.1]	0.39
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_172560W.fna'**	65.6	[61.8 - 69.2]	44.2	[41.7 - 46.8]	61.8	[58.5 - 65.0]	0.33
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_R309803.fna'**	64.1	[60.4 - 67.8]	44.2	[41.7 - 46.8]	60.6	[57.3 - 63.8]	0.11
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus luti* MCCC 1A00359	67.1	[63.3 - 70.8]	44.1	[41.6 - 46.7]	63.0	[59.7 - 66.2]	0.2
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus toyonensis* NCIMB 14858	67.7	[63.9 - 71.4]	44.1	[41.6 - 46.7]	63.5	[60.1 - 66.7]	0.35
'Bacillus_cereus_VD107.fna'	*Bacillus proteolyticus* MCCC 1A00365	58.5	[54.9 - 62.0]	44.1	[41.6 - 46.6]	55.9	[52.8 - 59.1]	0.11
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_R309803.fna'**	63.9	[60.2 - 67.5]	44.1	[41.6 - 46.7]	60.4	[57.1 - 63.6]	0.21
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus luti* MCCC 1A00359	66.9	[63.1 - 70.5]	44.1	[41.6 - 46.7]	62.8	[59.5 - 66.0]	0.23
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus luti* MCCC 1A00359	66.9	[63.0 - 70.5]	44.0	[41.5 - 46.6]	62.7	[59.4 - 65.9]	0.3
'Bacillus_cereus_VD107.fna'	*Bacillus nitratireducens* 4049	59.8	[56.1 - 63.4]	44.0	[41.5 - 46.6]	57.0	[53.8 - 60.1]	0.04
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus thuringiensis* ATCC 10792	59.4	[55.7 - 62.9]	44.0	[41.5 - 46.6]	56.6	[53.5 - 59.8]	0.38
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_VD107.fna'**	56.7	[53.1 - 60.2]	44.0	[41.5 - 46.6]	54.4	[51.3 - 57.5]	0.04
'Bacillus_cereus_172560W.fna'	*Bacillus albus* N35-10-2	68.1	[64.2 - 71.8]	44.0	[41.5 - 46.6]	63.7	[60.4 - 66.9]	0.12
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus toyonensis* NCIMB 14858	69.3	[65.4 - 72.9]	44.0	[41.5 - 46.6]	64.7	[61.3 - 67.9]	0.38
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus thuringiensis* ATCC 10792	61.9	[58.2 - 65.5]	43.9	[41.4 - 46.5]	58.7	[55.4 - 61.8]	0.39
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	68.6	[64.7 - 72.3]	43.9	[41.4 - 46.5]	64.1	[60.8 - 67.3]	0.36
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_AH1271.fna'**	64.7	[60.9 - 68.3]	43.9	[41.4 - 46.4]	60.9	[57.7 - 64.1]	0.45
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus thuringiensis* ATCC 10792	62.1	[58.4 - 65.7]	43.9	[41.4 - 46.5]	58.8	[55.6 - 62.0]	0.42
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	66.5	[62.6 - 70.1]	43.8	[41.2 - 46.3]	62.3	[59.0 - 65.5]	0.02
'Bacillus_cereus_BAG2X1-1.fna'	**'Bacillus_cereus_R309803.fna'**	55.9	[52.3 - 59.4]	43.8	[41.3 - 46.4]	53.7	[50.6 - 56.8]	0.05
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus thuringiensis* ATCC 10792	61.6	[57.9 - 65.2]	43.8	[41.3 - 46.4]	58.4	[55.2 - 61.6]	0.33
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus cereus* ATCC 14579	70.8	[66.8 - 74.4]	43.7	[41.2 - 46.3]	65.8	[62.4 - 69.0]	0.11

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_AH1272.fna'	*Bacillus paramycoides* NH24A2	57.5	[53.9 - 61.0]	43.7	[41.1 - 46.2]	55.0	[51.8 - 58.1]	0.02
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus thuringiensis* ATCC 10792	61.9	[58.1 - 65.4]	43.7	[41.2 - 46.3]	58.6	[55.4 - 61.7]	0.35
'Bacillus_cereus_AH1271.fna'	*Bacillus cereus* ATCC 14579	66.5	[62.7 - 70.2]	43.7	[41.2 - 46.3]	62.4	[59.1 - 65.6]	0.02
'Bacillus_cereus_AH1271.fna'	*Bacillus thuringiensis* ATCC 10792	60.6	[56.9 - 64.1]	43.5	[41.0 - 46.0]	57.4	[54.2 - 60.6]	0.44
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	69.9	[66.0 - 73.6]	43.4	[40.9 - 45.9]	64.9	[61.6 - 68.2]	0.03
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	67.8	[63.9 - 71.4]	43.4	[40.9 - 45.9]	63.2	[59.9 - 66.4]	0.07
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus wiedmannii* FSL W8-0169	71.2	[67.2 - 74.8]	43.4	[40.9 - 46.0]	66.0	[62.6 - 69.2]	0.05
'Bacillus_cereus_172560W.fna'	*Bacillus luti* MCCC 1A00359	63.7	[59.9 - 67.3]	43.3	[40.7 - 45.8]	59.9	[56.6 - 63.0]	0.63
'Bacillus_cereus_R309803.fna'	*Bacillus toyonensis* NCIMB 14858	63.2	[59.4 - 66.8]	43.3	[40.7 - 45.8]	59.5	[56.3 - 62.7]	0.2
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus toyonensis* NCIMB 14858	69.4	[65.4 - 73.0]	43.2	[40.6 - 45.7]	64.4	[61.1 - 67.6]	0.35
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_AH1272.fna'**	65.3	[61.4 - 68.9]	43.2	[40.6 - 45.7]	61.1	[57.8 - 64.3]	0.05
'Bacillus_cereus_AH187.fna'	*Bacillus toyonensis* NCIMB 14858	62.6	[58.9 - 66.2]	43.2	[40.7 - 45.8]	59.0	[55.8 - 62.2]	0.05
'Bacillus_cereus_172560W.fna'	*Bacillus mobilis* MCCC 1A05942	60.6	[56.9 - 64.1]	43.1	[40.6 - 45.7]	57.3	[54.1 - 60.5]	0.46
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus toyonensis* NCIMB 14858	64.7	[60.9 - 68.3]	43.1	[40.6 - 45.7]	60.7	[57.4 - 63.9]	0.31
'Bacillus_cereus_AH1271.fna'	*Bacillus toyonensis* NCIMB 14858	64.8	[61.0 - 68.4]	43.1	[40.6 - 45.6]	60.7	[57.4 - 63.9]	0.29
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus toyonensis* NCIMB 14858	64.5	[60.7 - 68.1]	43.0	[40.5 - 45.6]	60.5	[57.2 - 63.6]	0.34
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus luti* MCCC 1A00359	68.8	[64.9 - 72.4]	43.0	[40.5 - 45.6]	63.9	[60.6 - 67.1]	0.31
'Bacillus_cereus_R309803.fna'	*Bacillus cereus* ATCC 14579	63.2	[59.4 - 66.8]	42.9	[40.4 - 45.5]	59.3	[56.1 - 62.5]	0.07
'Bacillus_cereus_AH1272.fna'	*Bacillus mobilis* MCCC 1A05942	64.2	[60.5 - 67.9]	42.8	[40.3 - 45.3]	60.2	[56.9 - 63.3]	0.06
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus toyonensis* NCIMB 14858	64.0	[60.2 - 67.6]	42.8	[40.3 - 45.3]	60.0	[56.7 - 63.1]	0.41
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_R309803.fna'**	60.3	[56.7 - 63.9]	42.8	[40.3 - 45.4]	57.0	[53.8 - 60.2]	0.54
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus toyonensis* NCIMB 14858	66.7	[62.9 - 70.3]	42.8	[40.3 - 45.3]	62.1	[58.8 - 65.3]	0.44
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_cereus_R309803.fna'**	61.9	[58.2 - 65.5]	42.7	[40.2 - 45.2]	58.3	[55.1 - 61.4]	0.22
'Bacillus_cereus_R309803.fna'	*Bacillus thuringiensis* ATCC 10792	54.9	[51.3 - 58.3]	42.7	[40.2 - 45.2]	52.5	[49.4 - 55.6]	0.53
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	68.9	[65.0 - 72.6]	42.7	[40.2 - 45.2]	63.9	[60.5 - 67.1]	0.06
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus tropicus* N24	68.3	[64.4 - 71.9]	42.6	[40.1 - 45.2]	63.3	[60.0 - 66.5]	0.06
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	64.8	[61.0 - 68.4]	42.6	[40.1 - 45.1]	60.5	[57.3 - 63.7]	0.13

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus nitratireducens* 4049	66.8	[63.0 - 70.5]	42.5	[40.0 - 45.0]	62.1	[58.8 - 65.3]	0.13
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	61.1	[57.4 - 64.7]	42.5	[40.0 - 45.0]	57.5	[54.3 - 60.7]	0.37
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	55.4	[51.9 - 58.9]	42.5	[40.0 - 45.1]	52.9	[49.8 - 56.0]	0.19
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	60.9	[57.2 - 64.5]	42.4	[39.9 - 45.0]	57.4	[54.2 - 60.5]	0.05
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	63.8	[60.1 - 67.4]	42.4	[39.9 - 44.9]	59.7	[56.4 - 62.9]	0.07
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	64.1	[60.3 - 67.7]	42.4	[39.9 - 45.0]	59.9	[56.6 - 63.1]	0.1
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	66.0	[62.2 - 69.6]	42.3	[39.8 - 44.9]	61.4	[58.1 - 64.6]	0.02
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus wiedmannii* FSL W8-0169	57.2	[53.6 - 60.7]	42.3	[39.8 - 44.9]	54.3	[51.2 - 57.4]	0.11
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	63.6	[59.8 - 67.2]	42.3	[39.8 - 44.8]	59.5	[56.2 - 62.6]	0.01
'Bacillus_cereus_BAG2X1-1.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	55.7	[52.2 - 59.2]	42.3	[39.8 - 44.8]	53.1	[50.0 - 56.2]	0.1
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	58.6	[55.0 - 62.1]	42.2	[39.7 - 44.7]	55.4	[52.2 - 58.5]	0.01
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus nitratireducens* 4049	62.6	[58.8 - 66.2]	42.2	[39.7 - 44.8]	58.6	[55.4 - 61.8]	0.09
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus albus* N35-10-2	66.3	[62.4 - 69.9]	42.2	[39.7 - 44.7]	61.6	[58.3 - 64.8]	0.2
'Bacillus_cereus_AH1272.fna'	*Bacillus wiedmannii* FSL W8-0169	62.0	[58.3 - 65.6]	42.2	[39.7 - 44.8]	58.2	[55.0 - 61.3]	0.03
'Bacillus_cereus_BAG2X1-1.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	55.4	[51.8 - 58.9]	42.2	[39.7 - 44.8]	52.8	[49.7 - 55.9]	0.13
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus mobilis* MCCC 1A05942	61.8	[58.1 - 65.4]	42.1	[39.6 - 44.6]	58.0	[54.8 - 61.1]	0.14
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus paranthracis* MCCC 1A00395	62.9	[59.2 - 66.5]	42.1	[39.6 - 44.7]	58.9	[55.6 - 62.0]	0.05
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus cereus* ATCC 14579	55.9	[52.3 - 59.4]	42.1	[39.6 - 44.7]	53.1	[50.0 - 56.2]	0.02
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus proteolyticus* MCCC 1A00365	56.5	[52.9 - 60.0]	42.1	[39.6 - 44.7]	53.7	[50.5 - 56.8]	0.16
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus thuringiensis* ATCC 10792	49.1	[45.7 - 52.6]	42.0	[39.5 - 44.6]	47.5	[44.5 - 50.6]	0.48
'Bacillus_cereus_AH1272.fna'	*Bacillus toyonensis* NCIMB 14858	60.7	[57.0 - 64.3]	41.9	[39.4 - 44.5]	57.0	[53.8 - 60.2]	0.34
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus pacificus* MCCC 1A06182	61.5	[57.8 - 65.1]	41.9	[39.4 - 44.4]	57.6	[54.4 - 60.8]	0.07
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus proteolyticus* MCCC 1A00365	62.0	[58.3 - 65.6]	41.9	[39.4 - 44.4]	58.1	[54.9 - 61.2]	0.01
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	53.6	[50.1 - 57.0]	41.8	[39.3 - 44.4]	51.2	[48.1 - 54.2]	0.49
'Bacillus_cereus_AH1271.fna'	*Bacillus nitratireducens* 4049	63.0	[59.2 - 66.6]	41.7	[39.2 - 44.3]	58.8	[55.6 - 61.9]	0.04
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_B5-2.fna'**	60.1	[56.4 - 63.6]	41.7	[39.2 - 44.3]	56.5	[53.3 - 59.6]	0.1
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	54.4	[50.9 - 57.9]	41.6	[39.1 - 44.1]	51.8	[48.7 - 54.8]	0.04

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_B5-2.fna'	*Bacillus nitratireducens* 4049	64.3	[60.5 - 67.9]	41.6	[39.1 - 44.2]	59.8	[56.5 - 62.9]	0.18
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus mobilis* MCCC 1A05942	53.6	[50.1 - 57.0]	41.6	[39.1 - 44.1]	51.1	[48.0 - 54.2]	0.03
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_R309803.fna'**	63.6	[59.8 - 67.2]	41.6	[39.1 - 44.2]	59.2	[56.0 - 62.4]	0.14
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus nitratireducens* 4049	65.7	[61.8 - 69.3]	41.4	[38.9 - 44.0]	60.8	[57.5 - 64.0]	0.16
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	60.4	[56.7 - 64.0]	41.4	[38.9 - 43.9]	56.6	[53.4 - 59.7]	0.08
'Bacillus_cereus_HuA4-10.fna'	*Bacillus toyonensis* NCIMB 14858	61.2	[57.5 - 64.8]	41.3	[38.8 - 43.8]	57.2	[54.0 - 60.3]	0.32
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	53.1	[49.6 - 56.6]	41.2	[38.7 - 43.8]	50.6	[47.5 - 53.7]	0.06
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	52.9	[49.4 - 56.4]	41.2	[38.7 - 43.7]	50.4	[47.4 - 53.5]	0.1
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_AH1272.fna'**	60.5	[56.8 - 64.1]	41.2	[38.7 - 43.7]	56.6	[53.4 - 59.7]	0.29
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	52.9	[49.4 - 56.4]	41.1	[38.6 - 43.6]	50.4	[47.3 - 53.5]	0.16
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	53.9	[50.4 - 57.4]	41.1	[38.6 - 43.6]	51.3	[48.2 - 54.3]	0.09
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus tropicus* N24	58.0	[54.4 - 61.5]	41.1	[38.6 - 43.7]	54.5	[51.4 - 57.6]	0.11
'Bacillus_cereus_B5-2.fna'	*Bacillus proteolyticus* MCCC 1A00365	58.5	[54.9 - 62.0]	41.1	[38.6 - 43.6]	54.9	[51.8 - 58.0]	0.03
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus paranthracis* MCCC 1A00395	54.6	[51.1 - 58.1]	41.1	[38.6 - 43.6]	51.8	[48.7 - 54.9]	0.12
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	53.6	[50.1 - 57.1]	41.1	[38.6 - 43.7]	51.0	[47.9 - 54.1]	0.2
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	57.1	[53.6 - 60.6]	41.1	[38.6 - 43.6]	53.9	[50.7 - 57.0]	0.1
'Bacillus_cereus_AH1272.fna'	*Bacillus pacificus* MCCC 1A06182	62.5	[58.8 - 66.1]	41.0	[38.6 - 43.6]	58.2	[55.0 - 61.3]	0.02
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus nitratireducens* 4049	57.8	[54.2 - 61.3]	41.0	[38.5 - 43.5]	54.4	[51.2 - 57.5]	0.01
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_cereus_HuA4-10.fna'**	63.1	[59.3 - 66.7]	41.0	[38.5 - 43.5]	58.6	[55.4 - 61.7]	0.1
'Bacillus_cereus_AH603.fna'	*Bacillus toyonensis* NCIMB 14858	61.7	[58.0 - 65.3]	41.0	[38.5 - 43.5]	57.5	[54.3 - 60.6]	0.44
'Bacillus_cereus_BAG2X1-1.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	52.8	[49.3 - 56.2]	41.0	[38.5 - 43.6]	50.3	[47.2 - 53.3]	0.19
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus proteolyticus* MCCC 1A00365	58.1	[54.4 - 61.6]	41.0	[38.5 - 43.5]	54.5	[51.4 - 57.6]	0.06
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus pacificus* MCCC 1A06182	54.8	[51.3 - 58.3]	40.9	[38.4 - 43.4]	51.9	[48.8 - 55.0]	0.1
'Bacillus_cereus_BAG2X1-1.fna'	**'Bacillus_cereus_HuA4-10.fna'**	57.7	[54.1 - 61.2]	40.9	[38.4 - 43.5]	54.2	[51.1 - 57.3]	0.07
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus proteolyticus* MCCC 1A00365	59.5	[55.9 - 63.1]	40.8	[38.3 - 43.4]	55.7	[52.5 - 58.8]	0.03
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus albus* N35-10-2	51.9	[48.4 - 55.3]	40.8	[38.3 - 43.4]	49.5	[46.4 - 52.5]	0.37
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus mycoides* DSM 2048	67.0	[63.1 - 70.6]	40.7	[38.2 - 43.3]	61.5	[58.3 - 64.7]	0.07

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus mycoides* DSM 2048	65.5	[61.7 - 69.1]	40.7	[38.2 - 43.2]	60.4	[57.1 - 63.5]	0.03
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus weihenstephanensis* NBRC 101238	67.7	[63.8 - 71.3]	40.7	[38.2 - 43.2]	62.1	[58.8 - 65.2]	0.07
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_BAG1O-2.fna'**	63.9	[60.1 - 67.5]	40.6	[38.1 - 43.2]	59.1	[55.9 - 62.2]	0.02
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus mycoides* DSM 2048	56.8	[53.2 - 60.3]	40.6	[38.1 - 43.1]	53.4	[50.3 - 56.5]	0.1
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus weihenstephanensis* NBRC 101238	67.0	[63.1 - 70.6]	40.6	[38.1 - 43.2]	61.5	[58.2 - 64.7]	0.03
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus weihenstephanensis* NBRC 101238	64.0	[60.2 - 67.6]	40.5	[38.0 - 43.0]	59.1	[55.9 - 62.3]	0.0
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus weihenstephanensis* NBRC 101238	57.5	[53.9 - 61.0]	40.5	[38.0 - 43.0]	53.9	[50.8 - 57.0]	0.1
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus mycoides* DSM 2048	62.6	[58.8 - 66.2]	40.5	[38.1 - 43.1]	58.0	[54.8 - 61.2]	0.0
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_BAG2X1-1.fna'**	55.2	[51.7 - 58.7]	40.5	[38.0 - 43.0]	52.1	[49.0 - 55.2]	0.19
'Bacillus_cereus_R309803.fna'	*Bacillus nitratireducens* 4049	61.5	[57.8 - 65.1]	40.4	[37.9 - 42.9]	57.1	[53.9 - 60.2]	0.06
'Bacillus_cereus_B5-2.fna'	*Bacillus mycoides* DSM 2048	62.7	[58.9 - 66.3]	40.2	[37.7 - 42.7]	57.9	[54.7 - 61.1]	0.09
'Bacillus_cereus_AH1271.fna'	*Bacillus proteolyticus* MCCC 1A00365	57.1	[53.5 - 60.6]	40.2	[37.7 - 42.8]	53.5	[50.4 - 56.6]	0.12
'Bacillus_cereus_AH1272.fna'	*Bacillus albus* N35-10-2	57.1	[53.5 - 60.6]	40.1	[37.6 - 42.6]	53.5	[50.4 - 56.6]	0.28
'Bacillus_cereus_AH1272.fna'	*Bacillus tropicus* N24	63.6	[59.8 - 67.2]	40.1	[37.6 - 42.6]	58.6	[55.4 - 61.7]	0.02
'Bacillus_cereus_B5-2.fna'	*Bacillus weihenstephanensis* NBRC 101238	63.6	[59.9 - 67.3]	40.1	[37.7 - 42.7]	58.7	[55.5 - 61.9]	0.08
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_ATCC_4342.fna'**	62.5	[58.8 - 66.1]	40.1	[37.6 - 42.6]	57.8	[54.6 - 60.9]	0.02
'Bacillus_cereus_AH1272.fna'	*Bacillus paranthracis* MCCC 1A00395	57.0	[53.4 - 60.5]	40.0	[37.5 - 42.5]	53.4	[50.3 - 56.5]	0.03
'Bacillus_cereus_R309803.fna'	*Bacillus proteolyticus* MCCC 1A00365	56.1	[52.6 - 59.6]	40.0	[37.5 - 42.5]	52.7	[49.6 - 55.8]	0.21
'Bacillus_cereus_BAG2X1-1.fna'	**'Bacillus_cereus_VD107.fna'**	55.9	[52.3 - 59.4]	40.0	[37.5 - 42.5]	52.5	[49.4 - 55.6]	0.05
'Bacillus_cereus_AH187.fna'	*Bacillus nitratireducens* 4049	59.6	[56.0 - 63.1]	40.0	[37.5 - 42.5]	55.5	[52.3 - 58.6]	0.21
'Bacillus_cereus_AH1272.fna'	*Bacillus luti* MCCC 1A00359	62.4	[58.6 - 66.0]	40.0	[37.5 - 42.6]	57.7	[54.5 - 60.8]	0.23
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus paramycoides* NH24A2	56.6	[53.0 - 60.1]	40.0	[37.5 - 42.6]	53.1	[50.0 - 56.2]	0.11
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus nitratireducens* 4049	66.6	[62.7 - 70.2]	40.0	[37.5 - 42.6]	61.0	[57.7 - 64.1]	0.1
'Bacillus_cereus_AH1272.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	56.2	[52.7 - 59.7]	39.9	[37.4 - 42.4]	52.7	[49.6 - 55.8]	0.1
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus nitratireducens* 4049	60.6	[56.9 - 64.2]	39.8	[37.3 - 42.3]	56.2	[53.0 - 59.3]	0.18

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus nitratireducens* 4049	62.2	[58.4 - 65.7]	39.7	[37.2 - 42.2]	57.3	[54.1 - 60.5]	0.09
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus nitratireducens* 4049	62.3	[58.6 - 65.9]	39.7	[37.2 - 42.3]	57.5	[54.3 - 60.6]	0.06
'Bacillus_cereus_AH1271.fna'	*Bacillus mycoides* DSM 2048	59.6	[56.0 - 63.2]	39.7	[37.2 - 42.2]	55.4	[52.2 - 58.5]	0.06
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_BAG5X2-1.fna'**	61.4	[57.7 - 65.0]	39.7	[37.2 - 42.2]	56.7	[53.6 - 59.9]	0.09
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus nitratireducens* 4049	61.9	[58.1 - 65.4]	39.6	[37.1 - 42.1]	57.1	[53.9 - 60.2]	0.15
'Bacillus_cereus_AH603.fna'	*Bacillus wiedmannii* FSL W8-0169	64.1	[60.3 - 67.7]	39.6	[37.1 - 42.1]	58.8	[55.6 - 62.0]	0.08
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_B5-2.fna'**	64.7	[60.9 - 68.3]	39.6	[37.1 - 42.1]	59.3	[56.1 - 62.5]	0.01
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_BAG2X1-2.fna'**	63.2	[59.4 - 66.8]	39.6	[37.2 - 42.2]	58.1	[54.9 - 61.3]	0.06
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus proteolyticus* MCCC 1A00365	61.0	[57.3 - 64.6]	39.6	[37.1 - 42.2]	56.4	[53.3 - 59.6]	0.06
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_AH1272.fna'**	60.4	[56.7 - 64.0]	39.6	[37.1 - 42.1]	55.9	[52.8 - 59.0]	0.01
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_AH1272.fna'**	60.6	[56.9 - 64.1]	39.6	[37.1 - 42.1]	56.1	[52.9 - 59.2]	0.02
'Bacillus_cereus_AH1271.fna'	*Bacillus weihenstephanensis* NBRC 101238	63.3	[59.5 - 66.9]	39.6	[37.1 - 42.1]	58.2	[55.0 - 61.3]	0.06
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_AH1272.fna'**	60.4	[56.7 - 64.0]	39.5	[37.0 - 42.0]	55.9	[52.7 - 59.0]	0.07
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus proteolyticus* MCCC 1A00365	56.0	[52.4 - 59.5]	39.5	[37.0 - 42.0]	52.4	[49.3 - 55.4]	0.03
'Bacillus_cereus_AH1272.fna'	*Bacillus thuringiensis* ATCC 10792	55.7	[52.2 - 59.2]	39.4	[36.9 - 41.9]	52.2	[49.1 - 55.2]	0.4
'Bacillus_cereus_BAG5X2-1.fna'	**'Bacillus_cereus_HuA4-10.fna'**	60.9	[57.2 - 64.5]	39.4	[36.9 - 41.9]	56.2	[53.1 - 59.4]	0.03
'Bacillus_cereus_172560W.fna'	*Bacillus proteolyticus* MCCC 1A00365	56.0	[52.4 - 59.5]	39.4	[36.9 - 41.9]	52.3	[49.3 - 55.4]	0.33
'Bacillus_cereus_AH1272.fna'	*Bacillus cereus* ATCC 14579	61.0	[57.3 - 64.6]	39.4	[36.9 - 41.9]	56.4	[53.2 - 59.5]	0.07
'Bacillus_cereus_AH187.fna'	*Bacillus proteolyticus* MCCC 1A00365	56.1	[52.6 - 59.6]	39.4	[36.9 - 41.9]	52.5	[49.4 - 55.6]	0.36
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_HuA4-10.fna'**	61.0	[57.4 - 64.6]	39.4	[37.0 - 42.0]	56.4	[53.2 - 59.5]	0.12
'Bacillus_cereus_VD107.fna'	*Bacillus toyonensis* NCIMB 14858	56.7	[53.1 - 60.2]	39.3	[36.8 - 41.8]	52.9	[49.8 - 55.9]	0.3
'Bacillus_cereus_172560W.fna'	*Bacillus nitratireducens* 4049	61.1	[57.4 - 64.6]	39.2	[36.7 - 41.7]	56.3	[53.1 - 59.4]	0.48
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus proteolyticus* MCCC 1A00365	58.1	[54.5 - 61.6]	39.2	[36.7 - 41.7]	54.0	[50.8 - 57.0]	0.1
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus proteolyticus* MCCC 1A00365	57.9	[54.3 - 61.4]	39.2	[36.7 - 41.7]	53.8	[50.7 - 56.9]	0.06
'Bacillus_cereus_BAG2X1-2.fna'	**'Bacillus_cereus_HuA4-10.fna'**	60.7	[57.1 - 64.3]	39.1	[36.7 - 41.7]	56.0	[52.9 - 59.1]	0.06
'Bacillus_cereus_HuA4-10.fna'	*Bacillus wiedmannii* FSL W8-0169	63.3	[59.5 - 66.9]	39.1	[36.7 - 41.7]	58.0	[54.8 - 61.1]	0.04
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_AH1272.fna'**	57.9	[54.3 - 61.4]	39.1	[36.7 - 41.7]	53.8	[50.6 - 56.8]	0.4

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus proteolyticus* MCCC 1A00365	57.9	[54.3 - 61.4]	39.1	[36.6 - 41.6]	53.7	[50.6 - 56.8]	0.0
'Bacillus_cereus_R309803.fna'	*Bacillus weihenstephanensis* NBRC 101238	58.9	[55.3 - 62.5]	39.0	[36.5 - 41.5]	54.5	[51.4 - 57.6]	0.15
'Bacillus_cereus_R309803.fna'	*Bacillus mycoides* DSM 2048	58.5	[54.9 - 62.0]	38.9	[36.4 - 41.4]	54.2	[51.1 - 57.3]	0.15
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_AH1271.fna'**	59.7	[56.0 - 63.2]	38.8	[36.3 - 41.3]	55.1	[51.9 - 58.2]	0.15
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus paramycoides* NH24A2	59.8	[56.2 - 63.4]	38.8	[36.4 - 41.4]	55.2	[52.0 - 58.3]	0.06
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_cereus_VD107.fna'**	56.5	[53.0 - 60.0]	38.7	[36.2 - 41.2]	52.5	[49.4 - 55.6]	0.12
'Bacillus_cereus_AH603.fna'	*Bacillus luti* MCCC 1A00359	62.4	[58.7 - 66.0]	38.7	[36.2 - 41.2]	57.2	[54.0 - 60.3]	0.33
'Bacillus_cereus_HuA4-10.fna'	*Bacillus luti* MCCC 1A00359	60.6	[56.9 - 64.1]	38.6	[36.2 - 41.2]	55.7	[52.5 - 58.8]	0.21
'Bacillus_cereus_AH603.fna'	*Bacillus mobilis* MCCC 1A05942	59.2	[55.6 - 62.7]	38.5	[36.0 - 41.0]	54.6	[51.4 - 57.7]	0.16
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_HuA4-10.fna'**	58.1	[54.5 - 61.6]	38.5	[36.0 - 41.0]	53.7	[50.6 - 56.8]	0.03
'Bacillus_cereus_HuA4-10.fna'	**'Bacillus_cereus_R309803.fna'**	54.9	[51.4 - 58.4]	38.4	[35.9 - 40.9]	51.2	[48.1 - 54.2]	0.12
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus mycoides* DSM 2048	62.3	[58.6 - 65.9]	38.3	[35.8 - 40.8]	56.9	[53.7 - 60.1]	0.0
'Bacillus_cereus_AH187.fna'	*Bacillus mycoides* DSM 2048	56.5	[52.9 - 60.0]	38.3	[35.9 - 40.9]	52.4	[49.3 - 55.5]	0.3
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_R309803.fna'**	60.0	[56.3 - 63.5]	38.3	[35.9 - 40.9]	55.1	[52.0 - 58.2]	0.24
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus weihenstephanensis* NBRC 101238	64.7	[60.9 - 68.3]	38.3	[35.8 - 40.8]	58.7	[55.5 - 61.9]	0.0
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus mycoides* DSM 2048	57.4	[53.8 - 60.9]	38.3	[35.8 - 40.8]	53.1	[50.0 - 56.2]	0.09
'Bacillus_cereus_HuA4-10.fna'	*Bacillus thuringiensis* ATCC 10792	55.5	[52.0 - 59.0]	38.3	[35.8 - 40.8]	51.6	[48.5 - 54.7]	0.41
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus mycoides* DSM 2048	58.0	[54.4 - 61.6]	38.2	[35.7 - 40.7]	53.5	[50.4 - 56.6]	0.04
'Bacillus_cereus_172560W.fna'	*Bacillus mycoides* DSM 2048	60.9	[57.3 - 64.5]	38.2	[35.7 - 40.7]	55.8	[52.6 - 58.9]	0.39
'Bacillus_cereus_172560W.fna'	*Bacillus weihenstephanensis* NBRC 101238	61.2	[57.5 - 64.7]	38.2	[35.8 - 40.7]	56.0	[52.8 - 59.1]	0.39
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus weihenstephanensis* NBRC 101238	59.1	[55.5 - 62.7]	38.2	[35.7 - 40.7]	54.4	[51.3 - 57.5]	0.09
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus weihenstephanensis* NBRC 101238	60.5	[56.9 - 64.1]	38.1	[35.6 - 40.6]	55.5	[52.3 - 58.6]	0.04
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_HuA4-10.fna'**	58.1	[54.5 - 61.6]	38.1	[35.6 - 40.6]	53.5	[50.4 - 56.6]	0.42
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus mycoides* DSM 2048	57.8	[54.2 - 61.4]	38.1	[35.7 - 40.7]	53.4	[50.3 - 56.5]	0.0
'Bacillus_cereus_AH187.fna'	*Bacillus weihenstephanensis* NBRC 101238	58.9	[55.2 - 62.4]	38.1	[35.7 - 40.7]	54.2	[51.0 - 57.3]	0.3

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus mycoides* DSM 2048	57.7	[54.1 - 61.3]	38.1	[35.6 - 40.6]	53.3	[50.1 - 56.3]	0.06
'Bacillus_cereus_HuA4-10.fna'	*Bacillus mobilis* MCCC 1A05942	56.0	[52.4 - 59.5]	38.1	[35.7 - 40.7]	51.9	[48.8 - 55.0]	0.04
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus weihenstephanensis* NBRC 101238	59.9	[56.3 - 63.5]	38.0	[35.5 - 40.5]	54.9	[51.8 - 58.0]	0.06
'Bacillus_cereus_HuA4-10.fna'	*Bacillus cereus* ATCC 14579	60.9	[57.2 - 64.5]	38.0	[35.5 - 40.5]	55.7	[52.5 - 58.8]	0.05
'Bacillus_cereus_AH603.fna'	*Bacillus tropicus* N24	60.1	[56.5 - 63.7]	38.0	[35.5 - 40.5]	55.1	[51.9 - 58.2]	0.09
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus weihenstephanensis* NBRC 101238	60.3	[56.7 - 63.9]	38.0	[35.6 - 40.6]	55.3	[52.1 - 58.4]	0.01
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_ATCC_4342.fna'**	60.3	[56.6 - 63.9]	37.9	[35.4 - 40.4]	55.2	[52.0 - 58.3]	0.09
'Bacillus_cereus_B5-2.fna'	*Bacillus paramycoides* NH24A2	54.3	[50.8 - 57.7]	37.9	[35.4 - 40.4]	50.5	[47.4 - 53.5]	0.07
'Bacillus_cereus_VD107.fna'	*Bacillus luti* MCCC 1A00359	54.7	[51.2 - 58.2]	37.9	[35.5 - 40.4]	50.8	[47.7 - 53.9]	0.19
'Bacillus_cereus_AH603.fna'	*Bacillus cereus* ATCC 14579	61.4	[57.7 - 64.9]	37.9	[35.4 - 40.4]	56.0	[52.8 - 59.1]	0.17
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_VD107.fna'**	53.5	[50.0 - 57.0]	37.8	[35.4 - 40.4]	49.9	[46.8 - 52.9]	0.14
'Bacillus_cereus_HuA4-10.fna'	*Bacillus albus* N35-10-2	55.0	[51.5 - 58.5]	37.8	[35.4 - 40.3]	51.0	[48.0 - 54.1]	0.3
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_HuA4-10.fna'**	55.2	[51.7 - 58.7]	37.8	[35.3 - 40.3]	51.2	[48.1 - 54.2]	0.27
'Bacillus_cereus_R309803.fna'	**'Bacillus_cereus_VD107.fna'**	50.0	[46.5 - 53.4]	37.8	[35.4 - 40.3]	47.0	[44.0 - 50.0]	0.1
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus paramycoides* NH24A2	54.9	[51.4 - 58.4]	37.8	[35.3 - 40.3]	50.9	[47.9 - 54.0]	0.01
'Bacillus_cereus_HuA4-10.fna'	*Bacillus tropicus* N24	60.4	[56.7 - 63.9]	37.8	[35.4 - 40.3]	55.2	[52.1 - 58.3]	0.03
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_AH603.fna'**	61.7	[58.0 - 65.3]	37.8	[35.4 - 40.4]	56.3	[53.1 - 59.4]	0.3
'Bacillus_cereus_BAG5X2-1.fna'	**'Bacillus_cereus_VD107.fna'**	52.4	[49.0 - 55.9]	37.8	[35.3 - 40.3]	49.0	[45.9 - 52.0]	0.05
'Bacillus_cereus_AH603.fna'	*Bacillus thuringiensis* ATCC 10792	57.3	[53.7 - 60.8]	37.8	[35.3 - 40.3]	52.8	[49.7 - 55.9]	0.29
'Bacillus_cereus_VD107.fna'	*Bacillus wiedmannii* FSL W8-0169	54.6	[51.1 - 58.1]	37.8	[35.3 - 40.3]	50.7	[47.6 - 53.8]	0.07
'Bacillus_cereus_AH603.fna'	*Bacillus albus* N35-10-2	60.1	[56.4 - 63.6]	37.8	[35.4 - 40.3]	55.0	[51.8 - 58.1]	0.18
'Bacillus_cereus_BAG2X1-2.fna'	**'Bacillus_cereus_VD107.fna'**	53.4	[49.9 - 56.9]	37.7	[35.2 - 40.2]	49.7	[46.7 - 52.8]	0.09
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_HuA4-10.fna'**	56.1	[52.6 - 59.6]	37.7	[35.2 - 40.2]	51.8	[48.8 - 54.9]	0.01
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus paramycoides* NH24A2	55.2	[51.6 - 58.6]	37.7	[35.2 - 40.2]	51.1	[48.0 - 54.2]	0.02
'Bacillus_cereus_AH603.fna'	*Bacillus paranthracis* MCCC 1A00395	56.1	[52.5 - 59.6]	37.7	[35.2 - 40.2]	51.8	[48.7 - 54.9]	0.07
'Bacillus_cereus_R309803.fna'	*Bacillus paramycoides* NH24A2	51.2	[47.7 - 54.6]	37.7	[35.3 - 40.3]	48.0	[44.9 - 51.0]	0.16

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_AH603.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	57.3	[53.7 - 60.8]	37.7	[35.3 - 40.3]	52.8	[49.7 - 55.9]	0.0
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_HuA4-10.fna'**	60.7	[57.0 - 64.2]	37.7	[35.2 - 40.2]	55.4	[52.2 - 58.5]	0.03
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_HuA4-10.fna'**	55.9	[52.3 - 59.4]	37.6	[35.1 - 40.1]	51.6	[48.6 - 54.7]	0.03
'Bacillus_cereus_HuA4-10.fna'	*Bacillus paranthracis* MCCC 1A00395	55.7	[52.1 - 59.2]	37.6	[35.2 - 40.2]	51.5	[48.4 - 54.6]	0.05
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_AH603.fna'**	58.1	[54.5 - 61.6]	37.6	[35.2 - 40.1]	53.4	[50.3 - 56.5]	0.39
'Bacillus_cereus_HuA4-10.fna'	*Bacillus pacificus* MCCC 1A06182	59.0	[55.3 - 62.5]	37.6	[35.2 - 40.2]	54.1	[50.9 - 57.2]	0.03
'Bacillus_cereus_HuA4-10.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	55.2	[51.6 - 58.7]	37.6	[35.1 - 40.1]	51.1	[48.0 - 54.1]	0.12
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_AH603.fna'**	59.9	[56.2 - 63.4]	37.5	[35.0 - 40.0]	54.7	[51.5 - 57.8]	0.13
'Bacillus_cereus_Rock3-44.fna'	**'Bacillus_cereus_VD136.fna'**	49.6	[46.2 - 53.0]	37.5	[35.0 - 40.0]	46.6	[43.6 - 49.6]	1.17
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_HuA4-10.fna'**	55.8	[52.2 - 59.2]	37.5	[35.0 - 40.0]	51.5	[48.4 - 54.6]	0.09
'Bacillus_cereus_AH603.fna'	*Bacillus pacificus* MCCC 1A06182	59.9	[56.3 - 63.5]	37.5	[35.0 - 40.0]	54.7	[51.6 - 57.8]	0.09
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_AH603.fna'**	59.6	[56.0 - 63.2]	37.4	[35.0 - 40.0]	54.5	[51.4 - 57.6]	0.1
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_AH603.fna'**	59.5	[55.9 - 63.1]	37.4	[34.9 - 39.9]	54.4	[51.2 - 57.5]	0.03
'Bacillus_cereus_VD107.fna'	*Bacillus mobilis* MCCC 1A05942	50.3	[46.8 - 53.7]	37.4	[35.0 - 39.9]	47.1	[44.1 - 50.2]	0.02
'Bacillus_cereus_Rock3-44.fna'	*Bacillus pseudomycoides* DSM 12442	46.4	[43.0 - 49.9]	37.3	[34.8 - 39.8]	44.0	[41.0 - 47.0]	1.36
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_VD107.fna'**	53.0	[49.5 - 56.5]	37.3	[34.9 - 39.9]	49.3	[46.2 - 52.3]	0.01
'Bacillus_cereus_AH1271.fna'	*Bacillus paramycoides* NH24A2	53.5	[50.0 - 56.9]	37.3	[34.8 - 39.8]	49.6	[46.6 - 52.7]	0.07
'Bacillus_cereus_VD107.fna'	*Bacillus cereus* ATCC 14579	53.0	[49.5 - 56.4]	37.3	[34.8 - 39.8]	49.2	[46.2 - 52.3]	0.03
'Bacillus_cereus_VD107.fna'	*Bacillus thuringiensis* ATCC 10792	48.8	[45.4 - 52.2]	37.1	[34.6 - 39.6]	45.8	[42.8 - 48.9]	0.44
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_VD107.fna'**	50.9	[47.5 - 54.4]	37.1	[34.6 - 39.6]	47.5	[44.5 - 50.6]	0.25
'Bacillus_cereus_172560W.fna'	*Bacillus paramycoides* NH24A2	53.3	[49.9 - 56.8]	37.0	[34.6 - 39.5]	49.4	[46.4 - 52.5]	0.38
'Bacillus_cereus_AH187.fna'	*Bacillus paramycoides* NH24A2	52.4	[48.9 - 55.9]	37.0	[34.5 - 39.5]	48.7	[45.7 - 51.7]	0.31
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_VD107.fna'**	52.1	[48.6 - 55.6]	37.0	[34.5 - 39.5]	48.4	[45.4 - 51.5]	0.44
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_VD107.fna'**	51.8	[48.4 - 55.3]	36.9	[34.5 - 39.4]	48.2	[45.2 - 51.2]	0.02
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus paramycoides* NH24A2	53.8	[50.3 - 57.3]	36.9	[34.4 - 39.4]	49.7	[46.7 - 52.8]	0.05
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_VD107.fna'**	56.1	[52.5 - 59.6]	36.9	[34.4 - 39.4]	51.5	[48.4 - 54.6]	0.06

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus paramycoides* NH24A2	53.0	[49.5 - 56.4]	36.9	[34.5 - 39.4]	49.1	[46.0 - 52.1]	0.08
'Bacillus_cereus_VD107.fna'	*Bacillus tropicus* N24	56.2	[52.6 - 59.7]	36.9	[34.4 - 39.4]	51.6	[48.5 - 54.7]	0.06
'Bacillus_cereus_VD107.fna'	*Bacillus albus* N35-10-2	49.5	[46.1 - 53.0]	36.8	[34.4 - 39.3]	46.3	[43.3 - 49.4]	0.32
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_VD107.fna'**	51.7	[48.2 - 55.1]	36.8	[34.4 - 39.3]	48.1	[45.0 - 51.1]	0.05
'Bacillus_cereus_VD107.fna'	*Bacillus paranthracis* MCCC 1A00395	51.1	[47.7 - 54.6]	36.8	[34.3 - 39.3]	47.6	[44.6 - 50.7]	0.07
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus paramycoides* NH24A2	53.7	[50.2 - 57.2]	36.8	[34.4 - 39.3]	49.6	[46.6 - 52.7]	0.02
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus paramycoides* NH24A2	58.4	[54.8 - 61.9]	36.8	[34.4 - 39.4]	53.3	[50.2 - 56.4]	0.01
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus paramycoides* NH24A2	53.6	[50.1 - 57.1]	36.7	[34.3 - 39.2]	49.5	[46.5 - 52.6]	0.05
'Bacillus_cereus_VD107.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	50.9	[47.5 - 54.4]	36.7	[34.3 - 39.2]	47.4	[44.4 - 50.5]	0.14
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_VD107.fna'**	51.5	[48.0 - 54.9]	36.7	[34.3 - 39.2]	47.9	[44.8 - 50.9]	0.11
'Bacillus_cereus_VD107.fna'	*Bacillus pacificus* MCCC 1A06182	53.2	[49.7 - 56.7]	36.7	[34.3 - 39.3]	49.2	[46.2 - 52.3]	0.06
'Bacillus_cereus_VD107.fna'	**'Bacillus_cereus_VD136.fna'**	32.0	[28.7 - 35.6]	28.4	[26.0 - 30.9]	30.1	[27.2 - 33.2]	0.31
'Bacillus_cereus_Rock3-44.fna'	**'Bacillus_cereus_VD107.fna'**	30.8	[27.4 - 34.4]	28.4	[26.0 - 30.9]	29.1	[26.2 - 32.2]	1.47
'Bacillus_cereus_VD136.fna'	*Bacillus proteolyticus* MCCC 1A00365	31.5	[28.1 - 35.0]	28.4	[26.1 - 30.9]	29.7	[26.7 - 32.8]	0.42
'Bacillus_cereus_Rock3-44.fna'	*Bacillus paramycoides* NH24A2	30.7	[27.4 - 34.3]	28.3	[25.9 - 30.8]	29.1	[26.1 - 32.2]	1.54
'Bacillus_cereus_VD136.fna'	*Bacillus mycoides* DSM 2048	31.1	[27.7 - 34.7]	28.2	[25.8 - 30.7]	29.3	[26.4 - 32.4]	0.36
'Bacillus_cereus_VD107.fna'	*Bacillus pseudomycoides* DSM 12442	30.7	[27.3 - 34.3]	28.2	[25.9 - 30.7]	29.0	[26.1 - 32.1]	0.11
'Bacillus_cereus_HuA4-10.fna'	*Bacillus pseudomycoides* DSM 12442	28.3	[24.9 - 31.9]	28.1	[25.8 - 30.6]	27.0	[24.1 - 30.1]	0.13
'Bacillus_cereus_HuA4-10.fna'	**'Bacillus_cereus_VD136.fna'**	29.8	[26.5 - 33.4]	28.1	[25.7 - 30.6]	28.3	[25.4 - 31.4]	0.33
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_VD136.fna'**	29.0	[25.7 - 32.6]	28.0	[25.6 - 30.4]	27.6	[24.7 - 30.7]	0.45
'Bacillus_cereus_VD136.fna'	*Bacillus paramycoides* NH24A2	32.6	[29.2 - 36.1]	28.0	[25.7 - 30.5]	30.5	[27.5 - 33.6]	0.37
'Bacillus_cereus_VD136.fna'	*Bacillus weihenstephanensis* NBRC 101238	30.7	[27.3 - 34.3]	28.0	[25.6 - 30.5]	28.9	[26.0 - 32.0]	0.36
'Bacillus_cereus_BAG2X1-1.fna'	**'Bacillus_cereus_Rock3-44.fna'**	30.6	[27.2 - 34.2]	28.0	[25.6 - 30.5]	28.9	[26.0 - 32.0]	1.42
'Bacillus_cereus_VD136.fna'	*Bacillus nitratireducens* 4049	31.5	[28.1 - 35.1]	27.9	[25.6 - 30.4]	29.6	[26.7 - 32.7]	0.27
'Bacillus_cereus_HuA4-10.fna'	**'Bacillus_cereus_Rock3-44.fna'**	29.3	[25.9 - 32.9]	27.9	[25.5 - 30.4]	27.8	[24.9 - 30.9]	1.5
'Bacillus_cereus_AH603.fna'	**'Bacillus_cereus_Rock3-44.fna'**	27.9	[24.5 - 31.5]	27.8	[25.5 - 30.3]	26.7	[23.8 - 29.8]	1.62

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_AH603.fna'	*Bacillus pseudomycoides* DSM 12442	28.2	[24.8 - 31.8]	27.8	[25.5 - 30.3]	26.9	[24.0 - 30.0]	0.25
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.5	[25.2 - 32.2]	27.7	[25.3 - 30.1]	27.2	[24.3 - 30.3]	1.51
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_Rock3-44.fna'**	27.8	[24.5 - 31.5]	27.7	[25.4 - 30.2]	26.6	[23.7 - 29.7]	1.22
'Bacillus_cereus_BAG2X1-1.fna'	*Bacillus pseudomycoides* DSM 12442	28.5	[25.2 - 32.2]	27.7	[25.3 - 30.2]	27.2	[24.3 - 30.3]	0.06
'Bacillus_cereus_Rock3-44.fna'	*Bacillus proteolyticus* MCCC 1A00365	29.6	[26.2 - 33.2]	27.7	[25.4 - 30.2]	28.0	[25.1 - 31.1]	1.59
'Bacillus_cereus_Rock3-44.fna'	*Bacillus mycoides* DSM 2048	28.8	[25.5 - 32.5]	27.7	[25.4 - 30.2]	27.4	[24.5 - 30.5]	1.52
'Bacillus_cereus_BAG2X1-1.fna'	**'Bacillus_cereus_VD136.fna'**	30.5	[27.1 - 34.1]	27.7	[25.3 - 30.2]	28.7	[25.8 - 31.8]	0.26
'Bacillus_cereus_AH1272.fna'	**'Bacillus_cereus_VD136.fna'**	28.7	[25.4 - 32.4]	27.6	[25.3 - 30.1]	27.3	[24.4 - 30.4]	0.35
'Bacillus_cereus_Rock3-44.fna'	*Bacillus nitratireducens* 4049	30.1	[26.7 - 33.7]	27.6	[25.2 - 30.1]	28.4	[25.5 - 31.5]	1.43
'Bacillus_cereus_Rock3-44.fna'	*Bacillus toyonensis* NCIMB 14858	29.7	[26.3 - 33.3]	27.6	[25.3 - 30.1]	28.1	[25.2 - 31.2]	1.18
'Bacillus_cereus_Rock3-44.fna'	*Bacillus weihenstephanensis* NBRC 101238	29.5	[26.1 - 33.1]	27.6	[25.3 - 30.1]	27.9	[25.0 - 31.0]	1.53
'Bacillus_cereus_VD136.fna'	*Bacillus toyonensis* NCIMB 14858	30.6	[27.3 - 34.2]	27.5	[25.2 - 30.0]	28.8	[25.9 - 31.9]	0.01
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.8	[25.4 - 32.4]	27.5	[25.1 - 30.0]	27.3	[24.4 - 30.5]	1.49
'Bacillus_cereus_AH1272.fna'	*Bacillus pseudomycoides* DSM 12442	28.0	[24.7 - 31.7]	27.5	[25.1 - 30.0]	26.7	[23.8 - 29.8]	0.15
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.6	[25.3 - 32.3]	27.4	[25.1 - 29.9]	27.2	[24.3 - 30.3]	1.52
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.6	[25.3 - 32.3]	27.4	[25.1 - 29.9]	27.2	[24.3 - 30.3]	1.59
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.2	[24.9 - 31.8]	27.4	[25.0 - 29.8]	26.8	[24.0 - 30.0]	1.61
'Bacillus_cereus_AH187.fna'	**'Bacillus_cereus_VD136.fna'**	28.5	[25.2 - 32.2]	27.4	[25.0 - 29.9]	27.1	[24.2 - 30.2]	0.06
'Bacillus_cereus_Rock3-44.fna'	*Bacillus luti* MCCC 1A00359	29.8	[26.4 - 33.4]	27.3	[25.0 - 29.8]	28.1	[25.2 - 31.2]	1.29
'Bacillus_anthracis_str_Ames_Ancestor.fna'	**'Bacillus_cereus_VD136.fna'**	28.5	[25.1 - 32.1]	27.3	[24.9 - 29.8]	27.0	[24.1 - 30.1]	0.32
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.6	[25.2 - 32.2]	27.3	[25.0 - 29.8]	27.1	[24.2 - 30.2]	1.58
'Bacillus_cereus_Rock3-44.fna'	*Bacillus cereus* ATCC 14579	29.4	[26.0 - 33.0]	27.3	[24.9 - 29.8]	27.8	[24.9 - 30.9]	1.44
'Bacillus_cereus_BAG1O-2.fna'	*Bacillus pseudomycoides* DSM 12442	29.6	[26.2 - 33.2]	27.3	[25.0 - 29.8]	27.9	[25.0 - 31.0]	0.23
'Bacillus_cereus_Rock3-44.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	28.4	[25.1 - 32.1]	27.3	[24.9 - 29.8]	27.0	[24.1 - 30.1]	1.61
'Bacillus_cereus_VD136.fna'	*Bacillus cereus* ATCC 14579	29.2	[25.8 - 32.8]	27.3	[25.0 - 29.8]	27.6	[24.7 - 30.8]	0.28
'Bacillus_cereus_BAG5X2-1.fna'	*Bacillus pseudomycoides* DSM 12442	27.9	[24.5 - 31.5]	27.3	[24.9 - 29.8]	26.6	[23.7 - 29.7]	0.16
'Bacillus_cereus_BAG1O-2.fna'	**'Bacillus_cereus_VD136.fna'**	30.0	[26.6 - 33.6]	27.3	[24.9 - 29.8]	28.3	[25.3 - 31.4]	0.43

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_B5-2.fna'	*Bacillus pseudomycoides* DSM 12442	28.5	[25.1 - 32.1]	27.2	[24.8 - 29.7]	27.0	[24.1 - 30.1]	0.25
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.0	[24.6 - 31.6]	27.2	[24.8 - 29.7]	26.6	[23.7 - 29.7]	1.92
'Bacillus_cereus_Rock3-44.fna'	*Bacillus thuringiensis* ATCC 10792	26.8	[23.5 - 30.5]	27.2	[24.8 - 29.7]	25.7	[22.8 - 28.8]	1.91
'Bacillus_cereus_B5-2.fna'	**'Bacillus_cereus_VD136.fna'**	29.3	[26.0 - 33.0]	27.2	[24.9 - 29.7]	27.7	[24.8 - 30.8]	0.45
'Bacillus_cereus_R309803.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.7	[25.3 - 32.3]	27.2	[24.8 - 29.6]	27.2	[24.3 - 30.3]	1.38
'Bacillus_anthracis_str_Vollum.fna'	**'Bacillus_cereus_VD136.fna'**	28.3	[24.9 - 31.9]	27.2	[24.9 - 29.7]	26.9	[24.0 - 30.0]	0.36
'Bacillus_cereus_Rock3-44.fna'	*Bacillus albus* N35-10-2	28.3	[24.9 - 31.9]	27.2	[24.8 - 29.7]	26.9	[24.0 - 30.0]	1.8
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_Rock3-44.fna'**	29.4	[26.0 - 33.0]	27.2	[24.9 - 29.7]	27.8	[24.8 - 30.9]	1.53
'Bacillus_anthracis_str_Ames_Ancestor.fna'	*Bacillus pseudomycoides* DSM 12442	27.0	[23.6 - 30.6]	27.2	[24.8 - 29.7]	25.8	[22.9 - 28.9]	0.13
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.4	[25.0 - 32.0]	27.2	[24.8 - 29.7]	26.9	[24.0 - 30.0]	1.47
'Bacillus_cereus_BAG5X2-1.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.4	[25.1 - 32.0]	27.2	[24.8 - 29.7]	27.0	[24.1 - 30.1]	1.52
'Bacillus_anthracis_str_Kruger_B.fna'	**'Bacillus_cereus_VD136.fna'**	28.3	[24.9 - 31.9]	27.1	[24.7 - 29.6]	26.8	[23.9 - 29.9]	0.42
'Bacillus_cereus_VD136.fna'	**'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'**	28.3	[24.9 - 31.9]	27.1	[24.8 - 29.6]	26.9	[24.0 - 30.0]	0.45
'Bacillus_cereus_VD136.fna'	*Bacillus thuringiensis* ATCC 10792	27.5	[24.2 - 31.2]	27.1	[24.7 - 29.6]	26.2	[23.4 - 29.4]	0.74
'Bacillus_cereus_BAG5X2-1.fna'	**'Bacillus_cereus_VD136.fna'**	29.4	[26.1 - 33.1]	27.1	[24.8 - 29.6]	27.8	[24.9 - 30.9]	0.36
'Bacillus_cereus_Rock3-44.fna'	*Bacillus paranthracis* MCCC 1A00395	28.1	[24.8 - 31.7]	27.1	[24.8 - 29.6]	26.7	[23.8 - 29.8]	1.55
'Bacillus_cereus_Rock3-44.fna'	*Bacillus tropicus* N24	29.3	[26.0 - 33.0]	27.1	[24.7 - 29.5]	27.7	[24.8 - 30.8]	1.53
'Bacillus_anthracis_str_Vollum.fna'	*Bacillus pseudomycoides* DSM 12442	26.9	[23.5 - 30.5]	27.1	[24.7 - 29.6]	25.7	[22.8 - 28.8]	0.16
'Bacillus_cereus_Rock3-44.fna'	*Bacillus mobilis* MCCC 1A05942	27.8	[24.4 - 31.4]	27.1	[24.7 - 29.6]	26.4	[23.5 - 29.5]	1.45
'Bacillus_cereus_172560W.fna'	**'Bacillus_cereus_VD136.fna'**	28.6	[25.3 - 32.2]	27.1	[24.8 - 29.6]	27.1	[24.2 - 30.2]	0.75
'Bacillus_cereus_BAG2X1-2.fna'	*Bacillus pseudomycoides* DSM 12442	27.3	[23.9 - 30.9]	27.1	[24.8 - 29.6]	26.1	[23.2 - 29.2]	0.2
'Bacillus_cereus_Rock3-44.fna'	*Bacillus pacificus* MCCC 1A06182	28.2	[24.8 - 31.8]	27.1	[24.8 - 29.6]	26.8	[23.9 - 29.9]	1.53
'Bacillus_cereus_BAG2X1-2.fna'	**'Bacillus_cereus_Rock3-44.fna'**	28.5	[25.1 - 32.1]	27.1	[24.7 - 29.6]	27.0	[24.1 - 30.1]	1.56
'Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna'	*Bacillus pseudomycoides* DSM 12442	26.8	[23.4 - 30.4]	27.0	[24.7 - 29.5]	25.6	[22.7 - 28.7]	0.25
'Bacillus_cereus_VD136.fna'	*Bacillus paranthracis* MCCC 1A00395	28.5	[25.2 - 32.2]	27.0	[24.6 - 29.4]	27.0	[24.1 - 30.2]	0.38
'Bacillus_cereus_AH1271.fna'	**'Bacillus_cereus_VD136.fna'**	28.2	[24.9 - 31.9]	27.0	[24.7 - 29.5]	26.8	[23.9 - 29.9]	0.3
'Bacillus_cereus_R309803.fna'	**'Bacillus_cereus_VD136.fna'**	28.1	[24.8 - 31.8]	27.0	[24.6 - 29.5]	26.7	[23.8 - 29.8]	0.21

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Bacillus_cereus_VD136.fna'	*Bacillus pacificus* MCCC 1A06182	28.1	[24.8 - 31.8]	27.0	[24.7 - 29.5]	26.7	[23.8 - 29.8]	0.36
'Bacillus_cereus_BAG2X1-2.fna'	**'Bacillus_cereus_VD136.fna'**	29.0	[25.6 - 32.6]	27.0	[24.7 - 29.5]	27.4	[24.5 - 30.5]	0.39
'Bacillus_cereus_AH187.fna'	*Bacillus pseudomycoides* DSM 12442	27.2	[23.8 - 30.8]	27.0	[24.7 - 29.5]	26.0	[23.1 - 29.1]	0.14
'Bacillus_cereus_Rock3-44.fna'	*Bacillus wiedmannii* FSL W8-0169	29.2	[25.8 - 32.8]	27.0	[24.7 - 29.5]	27.6	[24.7 - 30.7]	1.54
'Bacillus_anthracis_str_Kruger_B.fna'	*Bacillus pseudomycoides* DSM 12442	26.9	[23.5 - 30.5]	27.0	[24.6 - 29.5]	25.7	[22.8 - 28.8]	0.22
'Bacillus_cereus_ATCC_4342.fna'	*Bacillus pseudomycoides* DSM 12442	27.7	[24.4 - 31.4]	26.9	[24.5 - 29.4]	26.4	[23.5 - 29.5]	0.17
'Bacillus_cereus_VD136.fna'	*Bacillus tropicus* N24	29.2	[25.9 - 32.8]	26.9	[24.5 - 29.4]	27.6	[24.7 - 30.7]	0.37
'Bacillus_cereus_AH1271.fna'	*Bacillus pseudomycoides* DSM 12442	27.1	[23.8 - 30.8]	26.9	[24.5 - 29.4]	25.9	[23.0 - 29.0]	0.1
'Bacillus_cereus_VD136.fna'	*Bacillus luti* MCCC 1A00359	29.7	[26.4 - 33.3]	26.9	[24.6 - 29.4]	28.0	[25.1 - 31.1]	0.12
'Bacillus_cereus_172560W.fna'	*Bacillus pseudomycoides* DSM 12442	27.6	[24.3 - 31.2]	26.9	[24.6 - 29.4]	26.3	[23.4 - 29.4]	0.55
'Bacillus_cereus_ATCC_4342.fna'	**'Bacillus_cereus_VD136.fna'**	29.6	[26.3 - 33.3]	26.9	[24.6 - 29.4]	27.9	[25.0 - 31.0]	0.36
'Bacillus_cereus_VD136.fna'	*Bacillus albus* N35-10-2	29.0	[25.6 - 32.6]	26.9	[24.6 - 29.4]	27.4	[24.5 - 30.5]	0.63
'Bacillus_cereus_VD136.fna'	*Bacillus wiedmannii* FSL W8-0169	29.7	[26.4 - 33.3]	26.9	[24.5 - 29.4]	28.0	[25.1 - 31.1]	0.37
'Bacillus_cereus_VD136.fna'	*Bacillus mobilis* MCCC 1A05942	28.3	[24.9 - 31.9]	26.8	[24.4 - 29.3]	26.8	[23.9 - 29.9]	0.29
'Bacillus_cereus_R309803.fna'	*Bacillus pseudomycoides* DSM 12442	27.3	[23.9 - 30.9]	26.8	[24.4 - 29.3]	26.0	[23.1 - 29.1]	0.01

Table 4: Strains in your dataset

Joint dataset of automatically determined closest type strains (if this mode was chosen), manually selected type strains (if selected accordingly) and the provided user strains, if provided (marked in yellow).

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Bacillus paranthracis MCCC 1A00395	Liu et al. 2017	KCTC 33714; LMG 28873; Mn5	*Bacillus paranthracis*	5506804	35.2	5598		PRJNA224116	SAMN05231549	GCF_001883995	
Bacillus luti MCCC 1A00359	Liu et al. 2017	KCTC 33716; LMG 28872; TD41	*Bacillus luti*	5086523	35.4	5160		PRJNA224116	SAMN05231662	GCF_001884105	
Bacillus wiedmannii FSL W8-0169	Miller et al. 2016	DSM 102050; LMG 29269	*Bacillus wiedmannii*	5337981	35.2	5255	Gp0145452	PRJNA224116	SAMN03800026	GCF_001583695	
Bacillus pacificus MCCC 1A06182	Liu et al. 2017	KCTC 33858; EB422	*Bacillus pacificus*	5402566	35.2	5494		PRJNA224116	SAMN05231547	GCF_001884025	
Bacillus mobilis MCCC 1A05942	Liu et al. 2017	0711P9-1; KCTC 33717; LMG 28877	*Bacillus mobilis*	5629975	35.3	5644		PRJNA224116	SAMN05231544	GCF_001884045	
Bacillus albus N35-10-2	Liu et al. 2017	KCTC 33710; MCCC 1A02146; LMG 28875	*Bacillus albus*	5788872	34.9	5583		PRJNA326285	SAMN05231551	GCA_001884185	
Bacillus nitratireducens 4049	Liu et al. 2017	KCTC 33713; MCCC 1A00732; LMG 28871	*Bacillus nitratireducens*	5474975	35.3	5536		PRJNA224116	SAMN05231546	GCF_001884135	
Bacillus paramycoides NH24A2	Liu et al. 2017	KCTC 33709; MCCC 1A04098; LMG 28876	*Bacillus paramycoides*	5430522	35.2	5482		PRJNA224116	SAMN05231634	GCF_001884235	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Bacillus proteolyticus MCCC 1A00365	Liu et al. 2017	KCTC 33715; LMG 28870; TD42	*Bacillus proteolyticus*	5838763	35.1	5934		PRJNA224116	SAMN05231663	GCF_001884065	
Bacillus cereus ATCC 14579	Frankland and Frankland 1887	BCRC 10603; CCRC 10603; CIP 66.24; NRRL B-3711; NCIMB 9373; NCCB 75008; CCUG 7414; DSM 31; JCM 2152; IFO 15305; NBRC 15305; NCTC 2599; CCM 2010; VKM B-504; HAMBI 1887; IAM 12605; LMG 6923; NCDO 1771; NCFB 1771; NCIB 9373	*Bacillus cereus*	5427083	35.3	5255	Gp0000641	PRJNA384	SAMN02603340	GCA_000007825	637000017
Bacillus toyonensis NCIMB 14858	Jiménez et al. 2014	CECT 876; BCT-7112	*Bacillus toyonensis*	5025419	35.6	4942	Gp0067894	PRJNA225857	SAMN02389599	GCA_000496285	2558309069

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Bacillus mycoides DSM 2048	Flügge 1886 emend. Liu et al. 2018	CIP 103472; NRRL B-14799; NRRL B-14811; NRRL NRS-273; ATCC 6462; CCUG 26678; NBIMCC 3484; NBRC 101228; NCTC 12974; HAMBI 1827; LMG 7128	*Bacillus cereus* subsp. *mycoides*; *Bacillus mycoides*	5541876	35.2	5658	Gp0003829	PRJNA29701	SAMN00727646	GCA_000003925	643886175
Bacillus pseudomycoides DSM 12442	Nakamura 1998	CIP 105700; NRRL B-617; JCM 12231; NBRC 101232; LMG 18993	*Bacillus pseudomycoides*	5751974	35.4	5851	Gp0003852	PRJNA29707	SAMN00727631	GCA_000161455	643886172
Bacillus weihenstephanensis NBRC 101238	Lechner et al. 1998	CIP 105772; NRRL B-23307; DSM 11821; LMG 18989; WSBC 10204	*Bacillus weihenstephanensis*	5571630	35.2	5640	Gp0024087	PRJDB404	SAMD00041791	GCA_000513155	2563367135

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Bacillus thuringiensis ATCC 10792	Berliner 1915	CIP 53.137; NRRL HD-735; NCIMB 9134; NCCB 70008; CCUG 7429; DSM 2046; JCM 20386; NBRC 101235; VKM B-1544; HAMBI 478; IAM 12077; LMG 7138; NCAIM B.01292; NCIB 9134	*Bacillus thuringiensis*	6234842	34.8	6243	Gp0003758	PRJNA29723	SAMN00738287	GCA_000161615	643886085
Bacillus tropicus N24	Liu et al. 2017	KCTC 33711; MCCC 1A01406; LMG 28874	*Bacillus tropicus*	5203012	35.2	5218		PRJNA325891	SAMN05231550	GCA_001884035	
Bacillus_anthracis_str_Ames_Ancestor.fna				5503926	35.2	5756					
Bacillus_anthracis_str_Kruger_B.fna				5470007	35.1	5782					
Bacillus_anthracis_str_Vollum.fna				5488459	35.2	5765					
Bacillus_cereus_172560W.fna				5684325	34.8	5732					
Bacillus_cereus_AH187.fna				5599857	35.5	5660					
Bacillus_cereus_AH603.fna				5774274	35.1	5915					
Bacillus_cereus_AH1271.fna				5619907	35.3	5879					
Bacillus_cereus_AH1272.fna				5747878	35.2	6034					

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Bacillus_cereus_ATCC_4342.fna				5224275	35.2	5330					
Bacillus_cereus_B5-2.fna				5798705	35.1	5950					
Bacillus_cereus_BAG1O-2.fna				5568148	35.1	5582					
Bacillus_cereus_BAG2X1-1.fna				5109238	35.3	5272					
Bacillus_cereus_BAG2X1-2.fna				5524604	35.2	5691					
Bacillus_cereus_BAG5X2-1.fna				5777536	35.2	5930					
Bacillus_cereus_HuA4-10.fna				5761566	35.2	5808					
Bacillus_cereus_R309803.fna				5563546	35.4	5726					
Bacillus_cereus_Rock3-44.fna				4893949	36.7	5427					
Bacillus_cereus_VD107.fna				5319054	35.3	5366					
Bacillus_cereus_VD136.fna				5210989	35.6	5242					
Bacillus_thuringiensis_serovar_andalousiensis_BGSC_4AW1.fna				5463063	35.1	5701					

Methods, Results and References

The genome sequence data were uploaded to the Type (Strain) Genome Server (TYGS), a free bioinformatics platform available under https://tygs.dsmz.de, for a whole genome-based taxonomic analysis [1]. The analysis also made use of recently introduced methodological updates and features [2,3]. Information on nomenclature, synonymy and associated taxonomic literature was provided by TYGS's sister database, the List of Prokaryotic names with Standing in Nomenclature (LPSN, available at https://lpsn.dsmz.de) [2,3]. The results were provided by the TYGS on 2019-10-02. The TYGS analysis was subdivided into the following steps:

Determination of closely related type strains

Determination of closest type strain genomes was done in two complementary ways: First, all user genomes were compared against all type strain genomes available in the TYGS database via the MASH algorithm, a fast approximation of intergenomic relatedness [4], and, the ten type strains with the smallest MASH distances chosen per user genome. Second, an additional set of ten closely related type strains was determined via the 16S rDNA gene sequences. These were extracted from the user genomes using RNAmmer [5] and each sequence was subsequently BLASTed [6] against the 16S rDNA gene sequence of each of the currently 25346 type strains available in the TYGS database. This was used as a proxy to find the best 50 matching type strains (according to the bitscore) for each user genome and to subsequently calculate precise distances using the Genome BLAST Distance Phylogeny approach (GBDP) under the algorithm 'coverage' and distance formula d_5 [7]. These distances were finally used to determine the 10 closest type strain genomes for each of the user genomes.

Pairwise comparison of genome sequences

For the phylogenomic inference, all pairwise comparisons among the set of genomes were conducted using GBDP and accurate intergenomic distances inferred under the algorithm 'trimming' and distance formula d_5 [7]. 100 distance replicates were calculated each. Digital DDH values and confidence intervals were calculated using the recommended settings of the GGDC 4.0 [2,7].

Phylogenetic inference

The resulting intergenomic distances were used to infer a balanced minimum evolution tree with branch support via FASTME 2.1.6.1 including SPR postprocessing [8]. Branch support was inferred from 100 pseudo-bootstrap replicates each. The trees were rooted at the midpoint [9] and visualized with PhyD3 [10].

Type-based species and subspecies clustering

The type-based species clustering using a 70% dDDH radius around each of the 16 type strains was done as previously described [1]. The resulting groups are shown in Table 1 and 4. Subspecies clustering was done using a 79% dDDH threshold as previously introduced [11].

Results

Type-based species and subspecies clustering

The resulting species and subspecies clusters are listed in Table 4, whereas the taxonomic identification of the query strains is found in Table 1. Briefly, the clustering yielded 23 species clusters and the provided query strains were assigned to 17 of these. Moreover, user strains were located in 17 of 30 subspecies clusters.

Figure caption SSU tree

Figure 1. Tree inferred with FastME 2.1.6.1 [8] from GBDP distances calculated from 16S rDNA gene sequences. The branch lengths are scaled in terms of GBDP distance formula d_5. The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 28.3 %. The tree was rooted at the midpoint [9].

Figure caption genome tree

Figure 2. Tree inferred with FastME 2.1.6.1 [8] from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d_5. The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 88.9 %. The tree was rooted at the midpoint [9].

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