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JOB ID: c75ec994-28cf-45e2-94e6-5a4f6afce39a

RESULT PAGE: [https://tygs.dsmz.de/user\\_results/show?guid=c75ec994-28cf-45e2-94e6-5a4f6afce39a](https://tygs.dsmz.de/user_results/show?guid=c75ec994-28cf-45e2-94e6-5a4f6afce39a)

### 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
'CHUV2995'	belongs to known species	<i>Corynebacterium belfantii</i>	
'CMCNS703'	belongs to known species	<i>Corynebacterium belfantii</i>	
'FRC0043'	belongs to known species	<i>Corynebacterium belfantii</i>	
'631'	belongs to known species	<i>Corynebacterium diphtheriae</i>	
'1137'	belongs to known species	<i>Corynebacterium diphtheriae</i>	
'1556'	belongs to known species	<i>Corynebacterium diphtheriae</i>	
'1734'	belongs to known species	<i>Corynebacterium diphtheriae</i>	
'2937'	belongs to known species	<i>Corynebacterium diphtheriae</i>	
'4499'	belongs to known species	<i>Corynebacterium diphtheriae</i>	
'4663'	belongs to known species	<i>Corynebacterium diphtheriae</i>	
'4766'	belongs to known species	<i>Corynebacterium diphtheriae</i>	
'5130'	belongs to known species	<i>Corynebacterium diphtheriae</i>	

**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
'1137'	'1556'	99.6	[99.3 - 99.8]	100.0	[99.9 - 100.0]	99.9	[99.7 - 99.9]	0.01
'1556'	'4499'	99.6	[99.3 - 99.8]	100.0	[99.9 - 100.0]	99.9	[99.7 - 99.9]	0.01
'4499'	'4766'	99.7	[99.3 - 99.8]	100.0	[100.0 - 100.0]	99.9	[99.8 - 99.9]	0.09
'FRC0043'	<i>Corynebacterium belfantii</i> FRC0043	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	0.01
'4663'	'5130'	100.0	[100.0 - 100.0]	100.0	[99.9 - 100.0]	100.0	[100.0 - 100.0]	0.01
'1556'	'4766'	98.9	[98.1 - 99.4]	100.0	[99.9 - 100.0]	99.5	[99.2 - 99.7]	0.11
'631'	'1137'	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	0.0
'631'	'4499'	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	0.0
'4766'	'5130'	99.7	[99.3 - 99.9]	100.0	[99.9 - 100.0]	99.9	[99.8 - 99.9]	0.1
'1734'	'5130'	100.0	[100.0 - 100.0]	100.0	[99.9 - 100.0]	100.0	[100.0 - 100.0]	0.01
'1734'	'4663'	100.0	[100.0 - 100.0]	100.0	[99.9 - 100.0]	100.0	[100.0 - 100.0]	0.0
'CHUV2995'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	0.0
'631'	'1556'	99.6	[99.3 - 99.8]	100.0	[100.0 - 100.0]	99.9	[99.7 - 99.9]	0.01
'1137'	'4499'	100.0	[100.0 - 100.0]	100.0	[99.9 - 100.0]	100.0	[100.0 - 100.0]	0.0
'631'	'4766'	99.7	[99.3 - 99.8]	100.0	[99.9 - 100.0]	99.9	[99.7 - 99.9]	0.09
'4663'	'4766'	99.7	[99.3 - 99.8]	100.0	[100.0 - 100.0]	99.9	[99.7 - 99.9]	0.09
'1556'	'5130'	99.6	[99.2 - 99.8]	99.9	[99.9 - 100.0]	99.8	[99.7 - 99.9]	0.01
'1734'	'4766'	99.7	[99.3 - 99.8]	99.9	[99.9 - 100.0]	99.9	[99.7 - 99.9]	0.09
'1556'	'4663'	99.6	[99.2 - 99.8]	99.9	[99.8 - 99.9]	99.9	[99.7 - 99.9]	0.02
'1137'	'4766'	99.7	[99.3 - 99.8]	99.9	[99.9 - 100.0]	99.9	[99.7 - 99.9]	0.09
'1556'	'1734'	99.6	[99.2 - 99.8]	99.9	[99.9 - 100.0]	99.9	[99.7 - 99.9]	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
'631'	'4663'	100.0	[100.0 - 100.0]	99.8	[99.6 - 99.9]	100.0	[100.0 - 100.0]	0.0
'4499'	'4663'	100.0	[100.0 - 100.0]	99.8	[99.6 - 99.9]	100.0	[100.0 - 100.0]	0.0
'4499'	'5130'	100.0	[100.0 - 100.0]	99.8	[99.7 - 99.9]	100.0	[100.0 - 100.0]	0.01
'1734'	'4499'	100.0	[100.0 - 100.0]	99.8	[99.6 - 99.9]	100.0	[100.0 - 100.0]	0.0
'1137'	'5130'	100.0	[100.0 - 100.0]	99.8	[99.6 - 99.9]	100.0	[100.0 - 100.0]	0.01
'631'	'5130'	100.0	[100.0 - 100.0]	99.8	[99.7 - 99.9]	100.0	[100.0 - 100.0]	0.01
'631'	'1734'	100.0	[100.0 - 100.0]	99.8	[99.7 - 99.9]	100.0	[100.0 - 100.0]	0.0
'1137'	'1734'	100.0	[100.0 - 100.0]	99.7	[99.6 - 99.8]	100.0	[100.0 - 100.0]	0.0
'1137'	'4663'	100.0	[100.0 - 100.0]	99.6	[99.3 - 99.7]	100.0	[100.0 - 100.0]	0.0
'CHUV2995'	'CMCNS703'	95.6	[93.5 - 97.1]	94.1	[92.3 - 95.5]	97.1	[95.7 - 98.0]	0.21
'CMCNS703'	<i>Corynebacterium belfantii</i> FRC0043	94.4	[92.0 - 96.2]	94.1	[92.3 - 95.5]	96.2	[94.6 - 97.4]	0.11
'CMCNS703'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	95.6	[93.5 - 97.1]	94.1	[92.3 - 95.5]	97.1	[95.7 - 98.0]	0.21
'CMCNS703'	'FRC0043'	94.4	[92.0 - 96.2]	94.1	[92.3 - 95.5]	96.2	[94.6 - 97.4]	0.11
'CHUV2995'	<i>Corynebacterium belfantii</i> FRC0043	92.5	[89.7 - 94.6]	88.5	[86.1 - 90.6]	94.2	[92.1 - 95.8]	0.31
'FRC0043'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	92.5	[89.7 - 94.6]	88.5	[86.1 - 90.6]	94.2	[92.1 - 95.8]	0.32
'CHUV2995'	'FRC0043'	92.5	[89.7 - 94.6]	88.5	[86.1 - 90.6]	94.2	[92.1 - 95.8]	0.32
'4663'	<i>Corynebacterium diphtheriae</i> NCTC 11397	94.7	[92.3 - 96.4]	86.9	[84.4 - 89.2]	95.6	[93.8 - 96.9]	0.08
'5130'	<i>Corynebacterium diphtheriae</i> NCTC 11397	94.7	[92.3 - 96.4]	86.9	[84.3 - 89.1]	95.6	[93.8 - 96.9]	0.09
'4766'	<i>Corynebacterium diphtheriae</i> NCTC 11397	94.3	[91.8 - 96.0]	86.9	[84.3 - 89.1]	95.3	[93.4 - 96.6]	0.01
'1734'	<i>Corynebacterium diphtheriae</i> NCTC 11397	94.7	[92.4 - 96.4]	86.8	[84.2 - 89.0]	95.6	[93.8 - 96.9]	0.08
'631'	<i>Corynebacterium diphtheriae</i> NCTC 11397	94.8	[92.4 - 96.5]	86.8	[84.2 - 89.0]	95.7	[93.9 - 96.9]	0.08
'1137'	<i>Corynebacterium diphtheriae</i> NCTC 11397	94.8	[92.4 - 96.5]	86.8	[84.2 - 89.0]	95.7	[93.9 - 96.9]	0.08
'4499'	<i>Corynebacterium diphtheriae</i> NCTC 11397	94.8	[92.4 - 96.5]	86.7	[84.1 - 89.0]	95.7	[93.9 - 96.9]	0.08
'1556'	<i>Corynebacterium diphtheriae</i> NCTC 11397	93.8	[91.1 - 95.6]	86.6	[84.0 - 88.8]	94.9	[92.9 - 96.3]	0.1
'2937'	<i>Corynebacterium diphtheriae</i> NCTC 11397	92.1	[89.1 - 94.3]	85.3	[82.6 - 87.6]	93.5	[91.2 - 95.2]	0.04
'2937'	'5130'	94.8	[92.4 - 96.4]	85.1	[82.4 - 87.4]	95.4	[93.6 - 96.8]	0.05
'631'	'2937'	94.8	[92.5 - 96.5]	85.1	[82.3 - 87.4]	95.5	[93.7 - 96.8]	0.05

Query	Subject	$d_0$	C.I. $d_0$	$d_4$	C.I. $d_4$	$d_6$	C.I. $d_6$	Diff. G+C Percent
'2937'	'4499'	94.8	[92.5 - 96.5]	85.1	[82.4 - 87.4]	95.5	[93.7 - 96.8]	0.05
'2937'	'4766'	94.1	[91.6 - 95.9]	85.1	[82.4 - 87.5]	95.0	[93.0 - 96.4]	0.05
'2937'	'4663'	94.8	[92.5 - 96.5]	85.1	[82.4 - 87.5]	95.5	[93.7 - 96.8]	0.04
'1137'	'2937'	94.8	[92.5 - 96.5]	85.1	[82.3 - 87.4]	95.5	[93.7 - 96.8]	0.05
'1734'	'2937'	94.8	[92.5 - 96.5]	85.0	[82.3 - 87.4]	95.5	[93.6 - 96.8]	0.05
'1556'	'2937'	93.4	[90.8 - 95.4]	84.9	[82.1 - 87.2]	94.4	[92.4 - 95.9]	0.06
'2937'	'CMCNS703'	74.5	[70.6 - 78.2]	63.4	[60.5 - 66.2]	74.9	[71.4 - 78.1]	0.17
'CMCNS703'	<i>Corynebacterium diphtheriae</i> NCTC 11397	76.1	[72.1 - 79.7]	63.1	[60.2 - 65.9]	76.1	[72.7 - 79.3]	0.21
'5130'	'CMCNS703'	75.6	[71.6 - 79.2]	62.9	[60.0 - 65.7]	75.6	[72.2 - 78.8]	0.12
'CHUV2995'	<i>Corynebacterium diphtheriae</i> NCTC 11397	71.1	[67.2 - 74.8]	62.9	[60.0 - 65.7]	71.8	[68.3 - 75.0]	0.42
'4663'	'CMCNS703'	75.5	[71.6 - 79.1]	62.9	[60.0 - 65.7]	75.6	[72.1 - 78.8]	0.13
'4499'	'CMCNS703'	75.6	[71.6 - 79.2]	62.8	[59.9 - 65.6]	75.7	[72.2 - 78.8]	0.12
'2937'	'CHUV2995'	69.0	[65.1 - 72.6]	62.8	[59.9 - 65.6]	69.9	[66.5 - 73.1]	0.38
'1734'	'CMCNS703'	75.5	[71.5 - 79.1]	62.8	[59.9 - 65.6]	75.6	[72.1 - 78.8]	0.12
'2937'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	69.0	[65.1 - 72.6]	62.8	[59.9 - 65.6]	69.9	[66.5 - 73.1]	0.38
'1137'	'CMCNS703'	75.6	[71.6 - 79.2]	62.8	[59.9 - 65.6]	75.7	[72.2 - 78.8]	0.12
'1556'	'CMCNS703'	75.4	[71.4 - 79.0]	62.8	[59.9 - 65.7]	75.5	[72.0 - 78.7]	0.11
'631'	'CMCNS703'	75.6	[71.6 - 79.2]	62.8	[59.9 - 65.7]	75.6	[72.2 - 78.8]	0.12
'4766'	'CMCNS703'	74.9	[70.9 - 78.5]	62.8	[59.9 - 65.6]	75.0	[71.6 - 78.2]	0.22
'1137'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	70.7	[66.8 - 74.3]	62.3	[59.4 - 65.1]	71.3	[67.8 - 74.5]	0.33
'4499'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	70.7	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.3	[67.8 - 74.5]	0.33
'631'	'CHUV2995'	70.7	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.3	[67.8 - 74.5]	0.33
'1734'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	70.6	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.2	[67.8 - 74.5]	0.33
'1137'	'CHUV2995'	70.7	[66.8 - 74.3]	62.3	[59.4 - 65.1]	71.3	[67.8 - 74.5]	0.33
'5130'	'CHUV2995'	70.6	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.3	[67.8 - 74.5]	0.33
'4663'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	70.6	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.2	[67.8 - 74.5]	0.34

Query	Subject	$d_0$	C.I. $d_0$	$d_4$	C.I. $d_4$	$d_6$	C.I. $d_6$	Diff. G+C Percent
'5130'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	70.6	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.3	[67.8 - 74.5]	0.33
'4766'	'CHUV2995'	70.0	[66.0 - 73.6]	62.3	[59.4 - 65.1]	70.7	[67.2 - 73.9]	0.43
'4663'	'CHUV2995'	70.6	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.2	[67.8 - 74.5]	0.34
'4766'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	70.0	[66.0 - 73.6]	62.3	[59.4 - 65.1]	70.7	[67.2 - 73.9]	0.43
'631'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	70.7	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.3	[67.8 - 74.5]	0.33
'4499'	'CHUV2995'	70.7	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.3	[67.8 - 74.5]	0.33
'1734'	'CHUV2995'	70.6	[66.7 - 74.3]	62.3	[59.4 - 65.1]	71.2	[67.8 - 74.5]	0.33
'1556'	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	70.3	[66.3 - 73.9]	62.2	[59.4 - 65.0]	70.9	[67.5 - 74.2]	0.32
'1556'	'CHUV2995'	70.3	[66.3 - 73.9]	62.2	[59.4 - 65.0]	70.9	[67.5 - 74.2]	0.32
'2937'	<i>Corynebacterium belfantii</i> FRC0043	76.7	[72.7 - 80.3]	62.0	[59.1 - 64.8]	76.4	[72.9 - 79.6]	0.07
'2937'	'FRC0043'	76.7	[72.7 - 80.3]	62.0	[59.1 - 64.8]	76.4	[72.9 - 79.6]	0.06
'FRC0043'	<i>Corynebacterium diphtheriae</i> NCTC 11397	77.0	[73.1 - 80.6]	61.9	[59.0 - 64.7]	76.6	[73.2 - 79.8]	0.1
'5130'	<i>Corynebacterium belfantii</i> FRC0043	77.3	[73.3 - 80.8]	61.6	[58.7 - 64.4]	76.8	[73.3 - 79.9]	0.01
'5130'	'FRC0043'	77.3	[73.3 - 80.8]	61.6	[58.7 - 64.4]	76.8	[73.3 - 79.9]	0.01
'4663'	'FRC0043'	77.3	[73.3 - 80.8]	61.6	[58.7 - 64.3]	76.7	[73.3 - 79.9]	0.02
'4663'	<i>Corynebacterium belfantii</i> FRC0043	77.3	[73.3 - 80.8]	61.6	[58.7 - 64.3]	76.7	[73.3 - 79.9]	0.02
'1556'	<i>Corynebacterium belfantii</i> FRC0043	76.0	[72.1 - 79.6]	61.5	[58.7 - 64.3]	75.7	[72.2 - 78.9]	0.0
'1137'	<i>Corynebacterium belfantii</i> FRC0043	77.3	[73.3 - 80.9]	61.5	[58.6 - 64.3]	76.8	[73.3 - 79.9]	0.02
'4499'	'FRC0043'	77.3	[73.3 - 80.8]	61.5	[58.7 - 64.3]	76.8	[73.3 - 79.9]	0.01
'631'	'FRC0043'	77.3	[73.3 - 80.8]	61.5	[58.7 - 64.3]	76.8	[73.3 - 79.9]	0.01
'4499'	<i>Corynebacterium belfantii</i> FRC0043	77.3	[73.3 - 80.8]	61.5	[58.7 - 64.3]	76.8	[73.3 - 79.9]	0.02
'1137'	'FRC0043'	77.3	[73.3 - 80.9]	61.5	[58.6 - 64.3]	76.8	[73.3 - 79.9]	0.01
'4766'	'FRC0043'	76.6	[72.6 - 80.1]	61.5	[58.6 - 64.3]	76.1	[72.7 - 79.3]	0.11
'631'	<i>Corynebacterium belfantii</i> FRC0043	77.3	[73.3 - 80.8]	61.5	[58.7 - 64.3]	76.8	[73.3 - 79.9]	0.02
'1734'	<i>Corynebacterium belfantii</i> FRC0043	77.3	[73.3 - 80.8]	61.5	[58.6 - 64.3]	76.7	[73.3 - 79.9]	0.02
'1556'	'FRC0043'	76.0	[72.1 - 79.6]	61.5	[58.7 - 64.3]	75.7	[72.2 - 78.9]	0.0

Query	Subject	$d_0$	C.I. $d_0$	$d_4$	C.I. $d_4$	$d_6$	C.I. $d_6$	Diff. G+C Percent
'1734'	'FRC0043'	77.3	[73.3 - 80.8]	61.5	[58.6 - 64.3]	76.7	[73.3 - 79.9]	0.01
'4766'	<i>Corynebacterium belfantii</i> FRC0043	76.6	[72.6 - 80.1]	61.5	[58.6 - 64.3]	76.1	[72.7 - 79.3]	0.11
'4663'	<i>Corynebacterium rouxii</i> FRC0190 T	78.0	[74.0 - 81.5]	49.1	[46.5 - 51.7]	73.6	[70.1 - 76.8]	0.38
'5130'	<i>Corynebacterium rouxii</i> FRC0190 T	77.9	[73.9 - 81.4]	49.1	[46.4 - 51.7]	73.5	[70.0 - 76.7]	0.38
'1734'	<i>Corynebacterium rouxii</i> FRC0190 T	78.0	[74.1 - 81.5]	49.0	[46.4 - 51.7]	73.6	[70.2 - 76.8]	0.38
'4766'	<i>Corynebacterium rouxii</i> FRC0190 T	77.6	[73.6 - 81.1]	49.0	[46.4 - 51.6]	73.2	[69.8 - 76.4]	0.29
'4499'	<i>Corynebacterium rouxii</i> FRC0190 T	78.1	[74.1 - 81.6]	49.0	[46.4 - 51.6]	73.7	[70.2 - 76.9]	0.38
'1137'	<i>Corynebacterium rouxii</i> FRC0190 T	78.1	[74.1 - 81.6]	49.0	[46.4 - 51.6]	73.6	[70.2 - 76.8]	0.38
'1556'	<i>Corynebacterium rouxii</i> FRC0190 T	76.5	[72.5 - 80.1]	49.0	[46.4 - 51.6]	72.4	[68.9 - 75.6]	0.39
'631'	<i>Corynebacterium rouxii</i> FRC0190 T	78.1	[74.1 - 81.6]	49.0	[46.4 - 51.6]	73.6	[70.2 - 76.9]	0.38
'2937'	<i>Corynebacterium rouxii</i> FRC0190 T	77.7	[73.7 - 81.2]	48.7	[46.1 - 51.3]	73.2	[69.8 - 76.4]	0.33
'CHUV2995'	<i>Corynebacterium rouxii</i> FRC0190 T	61.5	[57.8 - 65.1]	45.7	[43.1 - 48.2]	59.0	[55.7 - 62.1]	0.71
'CMCNS703'	<i>Corynebacterium rouxii</i> FRC0190 T	65.7	[61.9 - 69.3]	45.5	[43.0 - 48.1]	62.3	[59.0 - 65.5]	0.5
'FRC0043'	<i>Corynebacterium rouxii</i> FRC0190 T	73.0	[69.0 - 76.6]	45.4	[42.8 - 47.9]	68.2	[64.8 - 71.4]	0.39
'1734'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.5 - 16.6]	34.3	[31.9 - 36.8]	13.7	[11.3 - 16.5]	6.51
'5130'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.5 - 16.6]	34.3	[31.9 - 36.9]	13.7	[11.3 - 16.5]	6.51
'1556'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.5 - 16.6]	34.3	[31.9 - 36.8]	13.7	[11.3 - 16.5]	6.5
'4499'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.5 - 16.6]	34.3	[31.9 - 36.8]	13.7	[11.3 - 16.5]	6.51
'1137'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.5 - 16.6]	34.3	[31.9 - 36.8]	13.7	[11.3 - 16.5]	6.51
'631'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.5 - 16.6]	34.3	[31.9 - 36.8]	13.7	[11.3 - 16.5]	6.51
'4766'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.5 - 16.6]	34.3	[31.9 - 36.8]	13.7	[11.3 - 16.5]	6.6
'4663'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.5 - 16.6]	34.3	[31.9 - 36.9]	13.7	[11.3 - 16.5]	6.51
'2937'	<i>Corynebacterium singulare</i> DSM 44357	13.3	[10.6 - 16.6]	33.4	[31.0 - 35.9]	13.7	[11.3 - 16.5]	6.56
'CHUV2995'	<i>Corynebacterium striatum</i> ATCC 6940	13.4	[10.6 - 16.7]	31.8	[29.4 - 34.3]	13.8	[11.4 - 16.6]	5.48
'CMCNS703'	<i>Corynebacterium striatum</i> ATCC 6940	13.3	[10.6 - 16.7]	31.4	[29.0 - 33.9]	13.7	[11.4 - 16.5]	5.69
'4766'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.3]	30.2	[27.8 - 32.7]	13.4	[11.0 - 16.1]	11.66
'1137'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.2]	30.1	[27.7 - 32.6]	13.4	[11.0 - 16.1]	11.57

Query	Subject	$d_0$	C.I. $d_0$	$d_4$	C.I. $d_4$	$d_6$	C.I. $d_6$	Diff. G+C Percent
'631'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.2]	30.1	[27.7 - 32.6]	13.4	[11.0 - 16.1]	11.57
'4663'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.2]	30.1	[27.7 - 32.6]	13.4	[11.0 - 16.1]	11.57
'1556'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.2 - 16.2]	30.1	[27.7 - 32.6]	13.4	[11.0 - 16.1]	11.55
'5130'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.2]	30.1	[27.7 - 32.6]	13.4	[11.0 - 16.1]	11.56
'1734'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.3]	30.1	[27.7 - 32.6]	13.4	[11.0 - 16.1]	11.57
'4499'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.2]	30.1	[27.7 - 32.6]	13.4	[11.0 - 16.1]	11.57
'CMCNS703'	<i>Corynebacterium singulare</i> DSM 44357	13.4	[10.6 - 16.7]	30.0	[27.6 - 32.5]	13.8	[11.4 - 16.6]	6.39
'CHUV2995'	<i>Corynebacterium singulare</i> DSM 44357	13.4	[10.6 - 16.7]	29.7	[27.4 - 32.2]	13.7	[11.4 - 16.5]	6.18
'CMCNS703'	<i>Corynebacterium phoceense</i> MC1	13.3	[10.6 - 16.6]	28.9	[26.5 - 31.4]	13.7	[11.3 - 16.5]	9.49
'5130'	<i>Corynebacterium phoceense</i> MC1	13.2	[10.5 - 16.6]	28.9	[26.5 - 31.4]	13.6	[11.3 - 16.4]	9.61
'2937'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.3]	28.9	[26.6 - 31.4]	13.4	[11.0 - 16.2]	11.61
'4766'	<i>Corynebacterium phoceense</i> MC1	13.3	[10.5 - 16.6]	28.8	[26.5 - 31.3]	13.6	[11.3 - 16.4]	9.71
'4499'	<i>Corynebacterium phoceense</i> MC1	13.2	[10.5 - 16.6]	28.8	[26.4 - 31.3]	13.6	[11.3 - 16.4]	9.62
'631'	<i>Corynebacterium phoceense</i> MC1	13.2	[10.5 - 16.6]	28.8	[26.5 - 31.3]	13.6	[11.3 - 16.4]	9.62
'4663'	<i>Corynebacterium phoceense</i> MC1	13.2	[10.5 - 16.6]	28.8	[26.5 - 31.3]	13.6	[11.3 - 16.4]	9.62
'1556'	<i>Corynebacterium phoceense</i> MC1	13.2	[10.5 - 16.6]	28.8	[26.4 - 31.3]	13.6	[11.3 - 16.4]	9.6
'1137'	<i>Corynebacterium phoceense</i> MC1	13.2	[10.5 - 16.6]	28.8	[26.5 - 31.3]	13.6	[11.3 - 16.4]	9.62
'CHUV2995'	<i>Corynebacterium phoceense</i> MC1	13.3	[10.5 - 16.6]	28.8	[26.5 - 31.3]	13.7	[11.3 - 16.5]	9.28
'2937'	<i>Corynebacterium phoceense</i> MC1	13.3	[10.5 - 16.6]	28.7	[26.3 - 31.2]	13.7	[11.3 - 16.4]	9.66
'CMCNS703'	<i>Corynebacterium hadale</i> NBT06-6	13.1	[10.4 - 16.4]	28.6	[26.2 - 31.1]	13.5	[11.1 - 16.3]	11.44
'1734'	<i>Corynebacterium phoceense</i> MC1	13.2	[10.5 - 16.6]	28.6	[26.3 - 31.1]	13.6	[11.3 - 16.4]	9.62
'CHUV2995'	<i>Corynebacterium hadale</i> NBT06-6	13.0	[10.3 - 16.3]	28.2	[25.9 - 30.7]	13.4	[11.1 - 16.2]	11.23
'5130'	<i>Corynebacterium striatum</i> ATCC 6940	13.2	[10.5 - 16.5]	27.6	[25.3 - 30.1]	13.6	[11.2 - 16.4]	5.81
'1734'	<i>Corynebacterium striatum</i> ATCC 6940	13.2	[10.5 - 16.5]	27.6	[25.3 - 30.1]	13.6	[11.2 - 16.4]	5.81
'4499'	<i>Corynebacterium striatum</i> ATCC 6940	13.2	[10.5 - 16.5]	27.6	[25.3 - 30.1]	13.6	[11.2 - 16.4]	5.81
'1556'	<i>Corynebacterium striatum</i> ATCC 6940	13.2	[10.5 - 16.5]	27.6	[25.2 - 30.1]	13.6	[11.2 - 16.4]	5.8
'631'	<i>Corynebacterium striatum</i> ATCC 6940	13.2	[10.5 - 16.5]	27.6	[25.3 - 30.1]	13.6	[11.2 - 16.4]	5.81

Query	Subject	$d_0$	C.I. $d_0$	$d_4$	C.I. $d_4$	$d_6$	C.I. $d_6$	Diff. G+C Percent
'1137'	<i>Corynebacterium striatum</i> ATCC 6940	13.2	[10.5 - 16.5]	27.6	[25.3 - 30.1]	13.6	[11.2 - 16.4]	5.81
'4663'	<i>Corynebacterium striatum</i> ATCC 6940	13.2	[10.5 - 16.5]	27.6	[25.3 - 30.1]	13.6	[11.2 - 16.4]	5.81
'4766'	<i>Corynebacterium striatum</i> ATCC 6940	13.2	[10.5 - 16.5]	26.6	[24.2 - 29.1]	13.6	[11.2 - 16.4]	5.9
'CHUV2995'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	26.6	[24.3 - 29.1]	13.5	[11.1 - 16.2]	7.48
'CMCNS703'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	26.2	[23.9 - 28.7]	13.5	[11.1 - 16.3]	7.27
'2937'	<i>Corynebacterium striatum</i> ATCC 6940	13.1	[10.4 - 16.4]	26.0	[23.7 - 28.5]	13.5	[11.2 - 16.3]	5.86
'FRC0043'	<i>Corynebacterium striatum</i> ATCC 6940	13.1	[10.4 - 16.4]	25.8	[23.5 - 28.3]	13.5	[11.2 - 16.3]	5.8
'CHUV2995'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.4	[10.7 - 16.8]	25.2	[22.9 - 27.7]	13.8	[11.4 - 16.6]	11.58
'2937'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	25.2	[22.8 - 27.7]	13.6	[11.2 - 16.4]	5.34
'4766'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.6]	25.1	[22.8 - 27.6]	13.6	[11.2 - 16.4]	5.39
'CMCNS703'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.4	[10.7 - 16.7]	25.1	[22.8 - 27.6]	13.8	[11.4 - 16.6]	11.79
'FRC0043'	<i>Corynebacterium phoceense</i> MC1	13.2	[10.5 - 16.5]	25.1	[22.8 - 27.6]	13.6	[11.2 - 16.4]	9.6
'1556'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	25.0	[22.7 - 27.5]	13.6	[11.2 - 16.4]	5.28
'5130'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	25.0	[22.7 - 27.5]	13.6	[11.2 - 16.4]	5.29
'4499'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	25.0	[22.7 - 27.5]	13.6	[11.2 - 16.4]	5.29
'2937'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	25.0	[22.7 - 27.5]	13.5	[11.1 - 16.3]	7.1
'1137'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	25.0	[22.7 - 27.5]	13.6	[11.2 - 16.4]	5.29
'4663'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	25.0	[22.7 - 27.5]	13.6	[11.2 - 16.4]	5.3
'631'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	25.0	[22.7 - 27.5]	13.6	[11.2 - 16.4]	5.29
'1734'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	25.0	[22.7 - 27.5]	13.6	[11.2 - 16.4]	5.29
'CMCNS703'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.3	[10.5 - 16.6]	24.9	[22.6 - 27.4]	13.6	[11.2 - 16.4]	5.69
'FRC0043'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.9	[22.6 - 27.4]	13.4	[11.1 - 16.2]	7.16
'FRC0043'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.4	[10.6 - 16.7]	24.9	[22.6 - 27.4]	13.8	[11.4 - 16.5]	11.9
'4663'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.8	[22.5 - 27.3]	13.5	[11.1 - 16.3]	7.14



Query	Subject	$d_0$	C.I. $d_0$	$d_4$	C.I. $d_4$	$d_6$	C.I. $d_6$	Diff. G+C Percent
'631'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.3	[10.6 - 16.7]	24.8	[22.5 - 27.3]	13.7	[11.3 - 16.5]	11.92
'1556'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.8	[22.5 - 27.3]	13.5	[11.1 - 16.3]	7.16
'4499'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.3	[10.6 - 16.7]	24.8	[22.5 - 27.3]	13.7	[11.3 - 16.5]	11.92
'1137'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.8	[22.5 - 27.3]	13.5	[11.1 - 16.3]	7.15
'4766'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.8	[22.5 - 27.3]	13.5	[11.1 - 16.3]	7.05
'5130'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.8	[22.5 - 27.3]	13.5	[11.1 - 16.3]	7.15
'4663'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.3	[10.6 - 16.7]	24.8	[22.5 - 27.3]	13.7	[11.3 - 16.5]	11.92
'1734'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.3	[10.6 - 16.7]	24.8	[22.5 - 27.3]	13.7	[11.3 - 16.5]	11.92
'5130'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.3	[10.6 - 16.7]	24.8	[22.5 - 27.3]	13.7	[11.3 - 16.5]	11.91
'4499'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.8	[22.5 - 27.3]	13.5	[11.1 - 16.3]	7.14
'1556'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.3	[10.6 - 16.7]	24.8	[22.5 - 27.3]	13.7	[11.3 - 16.5]	11.9
'631'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.8	[22.5 - 27.3]	13.5	[11.1 - 16.3]	7.15
'1137'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.3	[10.6 - 16.7]	24.8	[22.5 - 27.3]	13.7	[11.3 - 16.5]	11.92
'4766'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.4	[10.6 - 16.7]	24.8	[22.5 - 27.3]	13.7	[11.3 - 16.5]	12.01
'1734'	<i>Corynebacterium kutscheri</i> DSM 20755	13.1	[10.4 - 16.4]	24.7	[22.4 - 27.2]	13.5	[11.1 - 16.3]	7.14
'2937'	<i>Corynebacterium vitaeruminis</i> DSM 20294	13.3	[10.6 - 16.6]	24.7	[22.4 - 27.2]	13.7	[11.3 - 16.5]	11.97
'CMCNS703'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	24.7	[22.4 - 27.2]	13.6	[11.2 - 16.4]	5.17
'CHUV2995'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	24.7	[22.4 - 27.2]	13.6	[11.2 - 16.4]	4.96
'FRC0043'	<i>Corynebacterium singulare</i> DSM 44357	13.0	[10.3 - 16.3]	24.7	[22.4 - 27.2]	13.4	[11.0 - 16.2]	6.5
'CHUV2995'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.3	[10.6 - 16.6]	24.6	[22.3 - 27.1]	13.7	[11.3 - 16.5]	5.48
'2937'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	24.2	[21.9 - 26.6]	13.4	[11.0 - 16.1]	5.86
'CHUV2995'	<i>Corynebacterium silvaticum</i> KL0182	14.4	[11.5 - 17.7]	23.8	[21.5 - 26.3]	14.6	[12.2 - 17.5]	0.51
'FRC0043'	<i>Corynebacterium argentoratense</i> DSM 44202	13.2	[10.5 - 16.5]	23.7	[21.4 - 26.1]	13.5	[11.2 - 16.3]	5.28
'1137'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.4 - 17.5]	23.4	[21.1 - 25.9]	14.5	[12.0 - 17.3]	0.3
'631'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.4 - 17.5]	23.4	[21.1 - 25.9]	14.5	[12.0 - 17.3]	0.3
'4499'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.4 - 17.5]	23.4	[21.1 - 25.9]	14.5	[12.0 - 17.3]	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
'1556'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.3 - 17.5]	23.4	[21.1 - 25.8]	14.4	[12.0 - 17.3]	0.31
'5130'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.3 - 17.5]	23.3	[21.0 - 25.8]	14.4	[12.0 - 17.3]	0.3
'4663'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.3 - 17.5]	23.3	[21.0 - 25.8]	14.4	[12.0 - 17.3]	0.29
'5130'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	23.3	[21.0 - 25.7]	13.4	[11.0 - 16.1]	5.81
'4766'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.4 - 17.6]	23.3	[21.0 - 25.8]	14.5	[12.0 - 17.3]	0.2
'1734'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.3 - 17.5]	23.3	[21.1 - 25.8]	14.5	[12.0 - 17.3]	0.29
'1556'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	23.3	[21.0 - 25.7]	13.4	[11.0 - 16.1]	5.8
'631'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	23.3	[21.0 - 25.7]	13.4	[11.0 - 16.1]	5.81
'1137'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	23.3	[21.0 - 25.7]	13.4	[11.0 - 16.1]	5.81
'4663'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	23.3	[21.0 - 25.7]	13.4	[11.0 - 16.1]	5.82
'1734'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	23.3	[21.0 - 25.7]	13.4	[11.0 - 16.1]	5.82
'4499'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	23.3	[21.0 - 25.7]	13.4	[11.0 - 16.1]	5.81
'4766'	<i>Corynebacterium tuscaniense</i> CCUG 51321	13.0	[10.3 - 16.3]	23.2	[20.9 - 25.7]	13.4	[11.0 - 16.1]	5.91
'CHUV2995'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.3 - 17.5]	23.1	[20.8 - 25.6]	14.4	[12.0 - 17.3]	0.63
'CMCNS703'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	23.1	[20.8 - 25.6]	14.5	[12.0 - 17.3]	0.72
'CMCNS703'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.4 - 17.6]	23.0	[20.7 - 25.5]	14.5	[12.1 - 17.4]	0.42
'2937'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.4 - 17.6]	23.0	[20.7 - 25.4]	14.5	[12.1 - 17.3]	0.25
'FRC0043'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	22.7	[20.4 - 25.2]	14.5	[12.0 - 17.3]	0.83
'FRC0043'	<i>Corynebacterium ulcerans</i> NCTC 7910	14.2	[11.4 - 17.6]	22.6	[20.3 - 25.0]	14.5	[12.0 - 17.3]	0.31
'2937'	<i>Corynebacterium silvaticum</i> KL0182	14.3	[11.4 - 17.6]	22.5	[20.2 - 24.9]	14.5	[12.1 - 17.4]	0.89
'FRC0043'	<i>Corynebacterium hadale</i> NBT06-6	12.9	[10.2 - 16.2]	22.4	[20.2 - 24.9]	13.3	[10.9 - 16.1]	11.55
'631'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	22.2	[19.9 - 24.6]	14.5	[12.0 - 17.3]	0.84
'1556'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	22.2	[19.9 - 24.6]	14.5	[12.0 - 17.3]	0.83
'4766'	<i>Corynebacterium silvaticum</i> KL0182	14.3	[11.4 - 17.6]	22.2	[19.9 - 24.6]	14.5	[12.1 - 17.4]	0.93
'4663'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	22.1	[19.8 - 24.6]	14.5	[12.0 - 17.3]	0.84
'4499'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	22.1	[19.9 - 24.6]	14.5	[12.1 - 17.3]	0.84
'1734'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	22.1	[19.8 - 24.6]	14.5	[12.0 - 17.3]	0.84

Query	Subject	$d_0$	C.I. $d_0$	$d_4$	C.I. $d_4$	$d_6$	C.I. $d_6$	Diff. G+C Percent
'1137'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	22.1	[19.9 - 24.6]	14.5	[12.1 - 17.3]	0.84
'5130'	<i>Corynebacterium silvaticum</i> KL0182	14.2	[11.4 - 17.6]	22.1	[19.9 - 24.6]	14.5	[12.0 - 17.3]	0.83
'FRC0043'	<i>Corynebacterium tuscaniense</i> CCUG 51321	12.9	[10.2 - 16.2]	21.9	[19.6 - 24.3]	13.3	[11.0 - 16.1]	5.8
'CMCNS703'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.2	[11.3 - 17.5]	21.6	[19.4 - 24.1]	14.4	[12.0 - 17.2]	1.55
'CMCNS703'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.2	[11.3 - 17.5]	21.6	[19.4 - 24.1]	14.4	[12.0 - 17.2]	1.55
'CHUV2995'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.1	[11.3 - 17.5]	21.5	[19.3 - 23.9]	14.4	[11.9 - 17.2]	1.76
'CHUV2995'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.1	[11.3 - 17.5]	21.5	[19.3 - 23.9]	14.4	[11.9 - 17.2]	1.76
'2937'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.2	[11.4 - 17.5]	21.3	[19.0 - 23.7]	14.4	[12.0 - 17.3]	1.38
'2937'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.2	[11.4 - 17.5]	21.3	[19.0 - 23.7]	14.4	[12.0 - 17.3]	1.38
'FRC0043'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.2	[11.4 - 17.5]	21.1	[18.8 - 23.5]	14.4	[12.0 - 17.2]	1.44
'FRC0043'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.2	[11.4 - 17.5]	21.1	[18.8 - 23.5]	14.4	[12.0 - 17.2]	1.44
'631'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.3	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.42
'1556'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.3	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.5	[12.1 - 17.4]	1.44
'4766'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.4	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.33
'4766'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.4	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.33
'631'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.3	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.43
'4499'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.3	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.43
'1137'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.3	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.42
'4499'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.3	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.42
'1556'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.3	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.5	[12.1 - 17.4]	1.44
'1137'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.3	[11.5 - 17.7]	20.9	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.43

Query	Subject	$d_0$	C.I. $d_0$	$d_4$	C.I. $d_4$	$d_6$	C.I. $d_6$	Diff. G+C Percent
'4663'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.3	[11.5 - 17.7]	20.8	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.42
'4663'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.3	[11.5 - 17.7]	20.8	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.42
'1734'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.3	[11.5 - 17.7]	20.8	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.42
'1734'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.3	[11.5 - 17.7]	20.8	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.42
'5130'	<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	14.3	[11.5 - 17.7]	20.8	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.43
'5130'	<i>Corynebacterium pseudotuberculosis</i> DSM 20689	14.3	[11.5 - 17.7]	20.8	[18.6 - 23.3]	14.6	[12.1 - 17.4]	1.43

**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
<i>Corynebacterium vitaeruminis</i> DSM 20294	(Bechdel et al. 1928) Lanéelle et al. 1980	CCUG 28792; ATCC 10234; JCM 1323; IFO 12143; NBRC 12143; VKM B-1211; CIP 82.07; NCIB 9291; NCIMB 9291	<i>Brevibacterium vitaeruminis</i> ; <i>Corynebacterium vitaeruminis</i> ; <i>Flavobacterium vitarumen</i>	2931780	65.5	2577	Gp0023683	PRJNA172966	SAMN03081455	GCA_000550805	2558860221
<i>Corynebacterium phoceense</i> MC1	Cresci et al. 2016	DSM 100570; CSUR P1905	<i>Corynebacterium phoceense</i>	2772735	63.2	2701		PRJNA224116	SAMEA4059842	GCF_900092335	
<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i> CHUV2995	Tagini et al. 2019	CCUG 72509; DSM 107520	<i>Corynebacterium diphtheriae</i> subsp. <i>lausannense</i>	3060363	53.9	3145	Gp0442955	PRJEB24256	SAMEA104679569	GCA_900312965	
<i>Corynebacterium belfantii</i> FRC0043	Dazas et al. 2018	DSM 105776; CIP 111412	<i>Corynebacterium belfantii</i>	2598827	53.6	2557	Gp0364753	PRJEB22103	SAMEA104208677	GCA_900205605	
<i>Corynebacterium silvaticum</i> KL0182	Dangel et al. 2020	LMG 31313; DSM 109166; CIP 111672	<i>Corynebacterium silvaticum</i>	2548487	54.4	2017		PRJNA517029	SAMN10039578	GCA_004382825	
<i>Corynebacterium tuscaniense</i> CCUG 51321	Riegel et al. 2006	DSM 45101; ATCC BAA-1141; JCM 15294; ISS-5309	<i>Corynebacterium tuscaniense</i>	2232117	59.4	2073		PRJNA224116	SAMN12771122	GCF_008693065	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Corynebacterium rouxii</i> FRC0190 T	Badell et al. 2020	DSM 110354; CIP 111752	<i>Corynebacterium rouxii</i>	2451 019	53.2	2365		PRJNA224116	SAMEA5992727	GCF_902702935	
<i>Corynebacterium hadale</i> NBT06-6	Wei et al. 2018	MCCC 1K03347; DSM 105365	<i>Corynebacterium hadale</i>	2679 199	65.2	2362	Gp0374689	PRJNA396693	SAMN07460149	GCA_002273005	
<i>Corynebacterium pseudotuberculosis</i> ATCC 19410	(Buchanan 1911) Ebersson 1918 emend. Nouioui et al. 2018	CCUG 2806; DSM 20689; ATCC 19410; NCTC 3450; JCM 9389; IFO 15363; NBRC 15363; CIP 102968	<i>Bacillus pseudotuberculosis</i> ; <i>Corynebacterium pseudotuberculosis</i>	2337 763	52.2	2146	Gp0223239	PRJNA382169	SAMN06701041	GCA_002155265	
<i>Corynebacterium pseudotuberculosis</i> DSM 20689	(Buchanan 1911) Ebersson 1918 emend. Nouioui et al. 2018	CCUG 2806; DSM 20689; ATCC 19410; NCTC 3450; JCM 9389; IFO 15363; NBRC 15363; CIP 102968	<i>Bacillus pseudotuberculosis</i> ; <i>Corynebacterium pseudotuberculosis</i>	2338 546	52.2	2084	Gp0220522	PRJNA442833	SAMN08778220	GCA_003634885	2756170169
<i>Corynebacterium ulcerans</i> NCTC 7910	(ex Gilbert and Stewart 1927) Riegel et al. 1995	CCUG 2708; DSM 46325; ATCC 51799; JCM 10387; CIP 106504	<i>Corynebacterium ulcerans</i>	2453 761	53.3	2178	Gp0262745	PRJEB6403	SAMEA4504038	GCA_900187135	
<i>Corynebacterium striatum</i> ATCC 6940	(Chester 1901) Ebersson 1918 emend. Nouioui et al. 2018	CCUG 27949; DSM 20668; NCTC 764; JCM 9390; IFO 15291; NBRC 15291; CIP 81.15	<i>Bacterium striatum</i> ; <i>Corynebacterium striatum</i>	2717 381	59.4	2677	Gp0003467	PRJNA31449	SAMN00001507	GCA_000159135	643886057

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
<i>Corynebacterium kutscheri</i> DSM 20755	(Migula 1900) Bergey et al. 1925 emend. Nouioui et al. 2018	CCUG 27535; ATCC 15677; NCTC 11138; JCM 9385; IFO 15288; NBRC 15288; CIP 103423	<i>Bacterium kutscheri</i> ; <i>Corynebacterium kutscheri</i>	2354 065	46.5	2047	Gp0110293	PRJNA276037	SAMN03365283	GCA_000980835	
<i>Corynebacterium singulare</i> DSM 44357	Riegel et al. 1997 emend. Nouioui et al. 2018	CCUG 37330; JCM 10385; IFO 16162; NBRC 16162; CIP 105491; IBS B52218	<i>Corynebacterium singulare</i>	2830 499	60.1	2561	Gp0109683	PRJNA246651	SAMN03177398	GCA_000833575	
<i>Corynebacterium diphtheriae</i> NCTC 11397	(Kruse 1886) Lehmann and Neumann 1896 emend. Nouioui et al. 2018	DSM 44123; ATCC 27010; CIP 100721	<i>Bacillus diphtheriae</i> ; <i>Corynebacterium diphtheriae</i> ; <i>Corynebacterium diphtheriae</i> subsp. <i>diphtheriae</i>	2463 666	53.5	2337	Gp0132011	PRJEB6403	SAMEA2517360	GCA_001457455	
<i>Corynebacterium argentoratense</i> DSM 44202	Riegel et al. 1995 emend. Nouioui et al. 2018	CCUG 34893; ATCC 51927; JCM 10392; CIP 104296; IBS B10697	<i>Corynebacterium argentoratense</i>	2031 862	58.9	1875	Gp0044215	PRJNA209048	SAMN02603032	GCA_000590555	2554235426
631				2397 667	53.6	2275					
1137				2398 650	53.6	2276					
1556				2445 187	53.6	2351					
1734				2394 567	53.6	2263					
2937				2466 271	53.6	2377					

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
4499				2397 617	53.6	2273					
4663				2393 381	53.6	2268					
4766				2352 296	53.5	2221					
5130				2392 741	53.6	2267					
CHUV2995				3060 363	53.9	3176					
CMCNS703				2892 379	53.7	3007					
FRC0043				2609 417	53.6	2663					



## 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 results were provided by the TYGS on 2020-06-19. In brief, 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 [2], 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 [3] and each sequence was subsequently BLASTed [4] against the 16S rDNA gene sequence of each of the currently 11861 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  $d_5$  [5]. These distances were finally used to determine the 10 closest type strain genomes for each of the user genomes.

### Pairwise comparison of genome sequences

All pairwise comparisons among the set of genomes were conducted using GBDP and accurate intergenomic distances inferred under the algorithm 'trimming' and distance formula  $d_5$  [5]. 100 distance replicates were calculated each. Digital DDH values and confidence intervals were calculated using the recommended settings of the GGDC 2.1 [5].

### Phylogenetic inference

The resulting intergenomic distances were used to infer a balanced minimum evolution tree with branch support via FASTME 2.1.4 including SPR postprocessing [6]. Branch support was inferred from 100 pseudo-bootstrap replicates each. The trees were rooted at the midpoint [7] and visualized with PhyD3 [8].

### 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 [9].

## 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 14 species clusters and the provided query strains were assigned to 2 of these. Moreover, user strains were located in 2 of 14 subspecies clusters.

### Figure caption genome tree

**Figure 1.** Tree inferred with FastME 2.1.6.1 [6] 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 37.1 %. The tree was rooted at the midpoint [7].

### Figure caption SSU tree

**Figure 2.** Tree inferred with FastME 2.1.6.1 [6] 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 51.6 %. The tree was rooted at the midpoint [7].

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