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                  |
|-------------------------|--------------------------------------|-----------------------------------|-------------------------|
| 'Cfalsenii_DSM44353'    | belongs to known species             | Corynebacterium falsenii         |                         |
| 'Cdoosanense_DSM45436'  | belongs to known species             | Corynebacterium doosanense        |                         |
| 'Ccasei_LMGS19264'      | belongs to known species             | Brevibacterium linens             | see [R2]                |
| 'Cbelfantii_FRC0043'    | belongs to known species             | Corynebacterium belfantii         | see [R3]                |
| 'Ccallunae_DSM20147'    | belongs to known species             | Corynebacterium callunae          |                         |
| 'Caurimucosum_ATCC700975' | belongs to known species           | Corynebacterium nigricans        |                         |
| 'Cefficiens_YS314'      | belongs to known species             | Corynebacterium efficiens         |                         |
| 'Ckroppenstedtii_DSM44385' | belongs to known species      | Corynebacterium kroppenstedtii    |                         |
| 'Cjeikeium_K41'         | belongs to known species             | Corynebacterium jeikeium          |                         |
| 'Ccamporealensis_DSM44610' | belongs to known species          | Corynebacterium camporealensis    |                         |
| 'Catypicum_R2070'       | belongs to known species             | Corynebacterium atypicum          |                         |
| 'Chumireducens_DSM45392' | belongs to known species             | Corynebacterium humireducens      |                         |
| 'Cimitans_DSM44264'     | belongs to known species             | Corynebacterium imitans           |                         |
| 'Cdeserti_GIMN1010'     | belongs to known species             | Corynebacterium deserti           |                         |
| Strain                  | Conclusion               | Identification result            | Remark               |
|------------------------|--------------------------|---------------------------------|----------------------|
| 'Cglycinophilum_AJ3170' | belongs to known species | Corynebacterium glycinophilum   |                      |
| 'Cepidermidicanis_DSM45586' | belongs to known species | Corynebacterium epidermidicanis |                      |
| 'Chalotolerans_YIM70093' | belongs to known species | Corynebacterium halotolerans    |                      |
| 'Cglutamicum_ATCC13032' | belongs to known species | Corynebacterium glutamicum      |                      |
| 'Cdiphtheriae_NCTC11397' | belongs to known species | Corynebacterium diphtheriae     |                      |
| 'Cargentoratense_DSM44202' | belongs to known species | Corynebacterium argentoratense |                      |
The overall number of pairwise comparisons was too large for a proper display and was thus reduced to only those comparisons having a digital DDH value ≥ 65% in at least one of the three formulae $d_0$, $d_4$, and $d_6$.

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 $d_6$ is independent of genome length and is thus robust against the use of incomplete draft genomes. For other reasons for preferring formula $d_6$, 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 |
|---------------------------|----------------------------------------------|-------|------------|-------|------------|-------|------------|------------------|
| 'Caurimucosum_ATCC700975.fna' | Corynebacterium nigricans ATCC 700975       | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Cimitans_DSM44264.fna'  | Corynebacterium imitans NCTC 13015          | 100.0 | [100.0 - 100.0] | 100.0 | [99.9 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Cepidermidicanis_DSM45586.fna' | Corynebacterium epidermidicanis DSM 45586 | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Chalotolerans_YIM70093.fna' | Corynebacterium halotolerans DSM 44683      | 100.0 | [99.9 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.06  |
| 'Kroppenstedtii_DSM44385.fna' | Corynebacterium kroppenstedtii DSM 44385    | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Glycinophilum_AJ3170000975.fna' | Corynebacterium glycinophilum ATCC 21341 | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Casei_LMG519246.fna'    | Corynebacterium casei DSM 44701              | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Chumireducens_DSM45392.fna' | Corynebacterium humireducens DSM 45392     | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Catypicum_R2070000975.fna' | Corynebacterium atypicum DSM 44849         | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Celfantii_FRC0043.fna' | Corynebacterium belfanti FRC0043            | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.01  |
| 'Cidptheriae_NCTC11397.fna' | Corynebacterium diphtheriae NCTC 11397     | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Cglutamicum_ATCC13032.fna' | Corynebacterium glutamicum ATCC 13032      | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Cfalsenii_DSM44353.fna' | Corynebacterium falsenii DSM 44353         | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Cimitans_DSM44264.fna' | Corynebacterium imitans DSM 44264         | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Ccallunae_DSM20147.fna' | Corynebacterium callunae DSM 20147        | 100.0 | [100.0 - 100.0] | 100.0 | [99.9 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Chalotolerans_YIM70093.fna' | Corynebacterium halotolerans YIM 70093     | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Cdesserti_GIMN1010000975.fna' | Corynebacterium deserti DSM 45689    | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Cargentoratense_DSM44202.fna' | Corynebacterium argenteratense DSM 44202 | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0   |
| 'Cdoosanense_DSM45436.fna' | Corynebacterium doosanense DSM 45436      | 99.9 | [99.8 - 100.0] | 100.0 | [99.9 - 100.0] | 100.0 | [99.9 - 100.0] | 0.13  |
| Query | Subject | \(d_0\) | C.I. \(d_0\) | \(d_s\) | C.I. \(d_s\) | \(d_s\) | C.I. \(d_s\) | Diff. G+C Percent |
|-------|---------|--------|-------------|--------|-------------|--------|-------------|------------------|
| 'Cdiphtheriae_NCTC1139 7.fna' | Corynebacterium diphtheriae DSM 44123 | 99.5 | [99.1 - 99.8] | 100.0 | [100.0 - 100.0] | 99.8 | [99.6 - 99.9] | 0.01 |
| 'Cefficiens_YS314.fna' | Corynebacterium efficiens YS-314 | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0 |
| 'Ccamporealensis_DSM4 4610.fna' | Corynebacterium camporealensis DSM 44610 | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.01 |
| 'Cchumireducens_DSM45 392.fna' | Corynebacterium humireducens NBRC 106098 | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0 |
| 'Ccelfantii_FRC0043.fna' | Corynebacterium diphtheriae subsp. lausannense CHUV2995 | 92.5 | [89.7 - 94.6] | 96.2 | [94.8 - 97.2] | 95.2 | [93.3 - 96.6] | 0.32 |
| 'Ccasei_LMGS19264.fna' | Brevibacterium linens ATCC 9172 | 13.1 | [10.4 - 16.4] | 77.1 | [74.1 - 79.9] | 13.6 | [11.2 - 16.4] | 9.08 |
| 'Cjeikeium_K41.fna' | Corynebacterium jeikeium NCTC 11913 | 91.7 | [88.7 - 94.0] | 70.6 | [67.6 - 73.4] | 90.8 | [88.2 - 92.9] | 0.08 |
| 'Cjeikeium_K41.fna' | Corynebacterium jeikeium ATCC 43734 | 88.7 | [85.3 - 91.4] | 70.2 | [67.2 - 73.0] | 88.2 | [85.3 - 90.7] | 0.28 |
| 'Cdiphtheriae_NCTC1139 7.fna' | Corynebacterium diphtheriae subsp. lausannense CHUV2995 | 71.1 | [67.2 - 74.8] | 62.9 | [60.0 - 65.7] | 71.8 | [68.3 - 75.0] | 0.42 |
| 'Cdiphtheriae_NCTC1139 7.fna' | Corynebacterium belfantii FRC0043 | 77.0 | [73.1 - 80.6] | 61.9 | [59.0 - 64.7] | 76.6 | [73.2 - 79.8] | 0.1 |
| 'Ccelfantii_FRC0043.fna' | 'Cdiphtheriae_NCTC1139 7.fna' | 77.0 | [73.1 - 80.6] | 61.9 | [59.0 - 64.7] | 76.6 | [73.2 - 79.8] | 0.1 |
| 'Ccelfantii_FRC0043.fna' | Corynebacterium diphtheriae subsp. NCTC 11397 | 77.0 | [73.1 - 80.6] | 61.9 | [59.0 - 64.7] | 76.6 | [73.2 - 79.8] | 0.1 |
| 'Ccelfantii_FRC0043.fna' | Corynebacterium diphtheriae DSM 44123 | 78.9 | [74.9 - 82.4] | 61.8 | [58.9 - 64.6] | 78.2 | [74.8 - 81.3] | 0.09 |
| 'Cbelfantii_FRC0043.fna' | Corynebacterium aurimucosum strain DSM 44532 | 84.5 | [80.7 - 87.6] | 50.4 | [47.8 - 53.0] | 79.4 | [76.0 - 82.4] | 0.26 |
| 'Ccaurimucosum_ATCC70 0975.fna' | Corynebacterium rouxii FRC0190 T | 75.7 | [71.7 - 79.3] | 49.3 | [46.7 - 51.9] | 71.8 | [68.4 - 75.1] | 0.3 |
| 'Cdiphtheriae_NCTC1139 7.fna' | Corynebacterium rouxii FRC0190 T | 73.0 | [69.0 - 76.6] | 45.4 | [42.8 - 47.9] | 68.2 | [64.8 - 71.4] | 0.39 |
| 'Cbelfantii_FRC0043.fna' | Corynebacterium pollutantsoli VDS | 66.3 | [62.5 - 69.9] | 29.4 | [27.0 - 31.9] | 55.2 | [52.1 - 58.3] | 0.06 |
| 'Cchumireducens_DSM45 392.fna' | Corynebacterium suranareae N24T | 65.9 | [62.1 - 69.5] | 27.5 | [25.1 - 30.0] | 53.6 | [50.5 - 56.7] | 2.02 |
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            |
|-------------------------------|-----------|----------------|--------------------------------------------------------------------------|------------|-------------|---------------|---------------|----------------------|----------------------|--------------------|--------------------|
| *Corynebacterium vitaeruminis* DSM 20294 | (Bechdel et al. 1928) Lanelle et al. 1980 | CCUG 28792; JCM 1323; ATCC 10234; IFO 12143; NBRC 12143; VKM B-1211; CIP 82.07; NCIB 9291; NCIMB 9291 | *Brevibacterium vitaeruminis; Corynebacterium vitaeruminis; Flavobacterium vitaerumen* | 2931/780  | 65.5        | 2577          | Gp0023683     | PRJNA172966          | SAMN03081455         | GCA_000550805      | 2558860221         |
| *Corynebacterium falsenii* DSM 44353 | Sjödén et al. 1998 emend. Nouioui et al. 2018 | CCUG 33651; JCM 11949; CIP 105466; Y13024 | *Corynebacterium falsenii*                                              | 2719/559  | 63.2        | 2306          | Gp0086746     | PRJNA235944          | SAMN02641485         | GCA_000525655      | 2571042744         |
| *Corynebacterium lubricantis* DSM 45231 | Kämpfer et al. 2009 emend. Nouioui et al. 2018 | CCUG 56567; JCM 16607; CCM 7546; KSS-3Se | *Corynebacterium lubricantis*                                           | 2945/292  | 58.6        | 2818          | Gp0013695     | PRJNA165249          | SAMN02256424         | GCA_000379245      | 2515154018         |
| *Corynebacterium doosanense* DSM 45436 | Lee et al. 2009 emend. Nouioui et al. 2018 | KCTC 19568; CCUG 57284; CAU 212 | *Corynebacterium doosanense*                                           | 2649/019  | 66.9        | 2590          | Gp0013691     | PRJNA165377          | SAMN02256506         | GCA_000372245      | 2515154029         |
| *Brevibacterium linens* ATCC 9172 | (Wolff 1910) Breed 1953 | NRRL B-4210; DSM 20425; JCM 1327; IFO 12142; NBRC 12142; VKM Ac-2112; CIP 101125; HAMBI 2038 | *Bacterium linens; Brevibacterium linens*                              | 3959/351  | 64.8        | 3518          | PRJE19834     | SAMEA103891064       | GCA_900169165        |                    |                    |
| Strain                      | Authority                                      | Other deposits                                      | Synonyms                                      | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID         |
|----------------------------|------------------------------------------------|-----------------------------------------------------|-----------------------------------------------|------------|-------------|--------------|-----------|----------------------|---------------------|-------------------|-----------------|
| *Corynebacterium mastitidis* DSM 44356 | Fernandez-Garayzabal et al. 1997 emend. Nououi et al. 2018 | LMG 19040; CCUG 38654; CECT 4843; JCM 12269; IFO 16160; NBRC 16160; CIP 105509; strain S-8 | *Corynebacterium mastitidis*                  | 2371       | 714         | 69.0         | Gp0013697 | PRJNA169809          | SAMN02441393       | GCA_000375365    | 2515154131     |
| *Corynebacterium pilosum* DSM 20521 | Yanagawa and Honda 1978                          | CCUG 27193; DSM 20521; JCM 3714; ATCC 29592; IFO 15265; NBRC 15285; NCTC 11862; CIP 103422 | *Corynebacterium pilosum*                     | 2532       | 067         | 60.7         | Gp0013698 | PRJNA169769          | SAMN02441706       | GCA_000373805    | 2515154153     |
| *Corynebacterium fournieri* Marseille-P2948 | Diop et al. 2018                                | DSM 103271; CSUR P2948                              | *Corynebacterium fournieri*                   | 2357       | 034         | 65.0         | Gp0370410 | PRJEB20393           | SAMEA10397581      | GCA_900176865    |                 |
| *Corynebacterium riegelii* DSM 44326 | Funke et al. 1998                               | CCUG 38180; JCM 10389; ATCC 700782; CIP 105310; DMMZ 2415 | *Corynebacterium riegelii*                    | 2519       | 232         | 60.4         | 2283      | PRJNA231221           | SAMN16357283       |                 |                 |
| *Corynebacterium anserum* 23H37-10 | Liu et al. 2021                                  | GD MCC 1.1737; KACC 21672                           | *Corynebacterium anserum*                     | 2208       | 656         | 55.2         | 1764      | PRJNA595090           | SAMN13546099       | GCA_014262665    |                 |
| *Corynebacterium godavarianum* LMG 29598 | Jani et al. 2018                                 | MCC 3388; KCTC 39803; PR007                         | *Corynebacterium godavarianum*                | 2521       | 298         | 65.6         | 2235      | PRJNA555895           | SAMN12335367       | GCA_007559235    |                 |
| *Corynebacterium endometrii* LMM-1653T | Ballas et al. 2020                               | LMG-31164; CCM 8952                                  | *Corynebacterium endometrii*                  | 2477       | 061         | 60.9         | 2189      | PRJNA224116           | SAMN11357123       | GCF_004795735    |                 |
| Strain | Authority | Other deposits | Synonyms | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID |
|--------|-----------|----------------|----------|------------|-------------|--------------|------------|----------------------|---------------------|------------------|---------|
| Corynebacterium aurimucosum strain DSM 44532 | Yassin et al. 2002 emend. Daneshvar et al. 2004 | NRRL B-24143; CCUG 47449; JCM 11766; IMMIB D-1488 | Corynebacterium aurimucosum | 2737 787 | 60.3 | 2417 | PRJNA231221 | SAMN16357278 | GCA_000626615 |
| Corynebacterium alimapuense CCUG 69366 | Claverias et al. 2019 | NCIMB 15118; VA37-3 | Corynebacterium alimapuense | 2281 535 | 57.1 | 2040 | Gp0385727 | PRJNA305687 | SAMN08535650 | GCA_003716585 |
| Corynebacterium phoceense MC1 | Cresci et al. 2016 | DSM 100570; CSUR P1905 | Corynebacterium phoceense | 2772 735 | 63.2 | 2701 | PRJNA224116 | SAMEA4059842 | GCF_900092335 |
| Corynebacterium diptheriae subsp. lausannense | Tagini et al. 2019 | CCUG 72509; DSM 107520 | Corynebacterium diptheriae subsp. lausannense | 3060 363 | 53.9 | 3145 | Gp0442955 | PRJEB24256 | SAMEA10467956 | GCA_900312965 |
| Corynebacterium bellanti FRC0043 | Dazas et al. 2018 | DSM 105776; CIP 111412 | Corynebacterium bellanti | 2598 827 | 53.6 | 2557 | Gp0364753 | PRJEB22103 | SAMEA104208677 | GCA_900205605 |
| Corynebacterium callunae DSM 20147 | (Lee and Good 1962) Yamada and Komagata 1972 emend. Nouioui et al. 2018 | CCUG 28793; JCM 9489; ATCC 15991; IF0 15359; NBRC 15359; CIP 104277; HAMBI 2053; NCFB 10338; NCIB 10338; NCIMB 10338 | Corynebacterium callunae | 2890 884 | 52.4 | 2679 | Gp0013686 | PRJNA185570 | SAMN02441249 | GCA_000420585 | 2522572159 |
| Corynebacterium urogenitale DSM 108747 | Ballas et al. 2020 | LMG 31163; LMM-1652 | Corynebacterium urogenitale | 2351 892 | 59.9 | 2058 | PRJNA224116 | SAMEA12924940 | GCF_009026825 |
| Corynebacterium choanae CCM 8831 | Busse et al. 2019 | 200CH; LMG 30628; CCUG 72166 | Corynebacterium choanae | 2986 773 | 57.0 | 2308 | Gp0443147 | PRJNA432431 | SAMN08448940 | GCA_003813965 |
| Strain                                      | Authority                             | Other deposits                                      | Synonyms                                 | Base pairs | Percent G+C | No. proteins | Goldstamp      | Bioproject accession | Biosample accession | Assembly accession | IMG OID         |
|--------------------------------------------|---------------------------------------|-----------------------------------------------------|------------------------------------------|------------|-------------|--------------|----------------|----------------------|---------------------|-------------------|------------------|
| Corynebacterium frankenforstense ST18      | Wiertz et al. 2013 emend. Nouioui et al. 2018 | CCUG 63371; DSM 45800                              | Corynebacterium frankenforstense         | 2604       | 71.5        | 1801         | Gp0118685      | PRJNA232093          | SAMN02991553       | GCA_001941485     |                  |
| Corynebacterium flavescens DSM 20296       | Barksdale et al. 1979 emend. Nouioui et al. 2018 | 8 of Orla-Jensen; LMG 4046; CCUG 28791; DSM 20296; JCM 1317; ATCC 10340; IFO 14136; NBRCC 14136; VKM Ac-1956; CIP 69.5; NCCB 42012; NCDO 1320; NCFB 1330; NCIB 8707; NCIB 8707 | Corynebacterium flavescens               | 2758       | 59.9        | 2202         | Gp0118684      | PRJNA242338          | SAMN02996497       | GCA_001941465     |                  |
| Corynebacterium sphenisci DSM 44792        | Goyache et al. 2003 emend. Nouioui et al. 2018 | CCUG 46309; CECT 9990; JCM 12270                    | Corynebacterium sphenisci               | 2594       | 74.7        | 1827         | Gp0118687      | PRJNA232092          | SAMN02996499       | GCA_001941505     |                  |
| Corynebacterium aquilae S-613              | Fernández-Garayzábal et al. 2003 emend. Nouioui et al. 2018 | CCUG 46511; CECT 5993; DSM 44791; JCM 12268        | Corynebacterium aquilae                 | 2926       | 60.9        | 2013         | Gp0118683      | PRJNA230273          | SAMN02996496       | GCA_001941445     |                  |
| Corynebacterium stationis DSM 20302        | (ZoBell and Upham 1944) Bernard et al. 2010 | CCUG 43497; JCM 11611; ATCC 14403; IFO 12144; NBRCC 12144; VKM B-1228; CIP 104228 | Achromobacter stationis; Brevibacterium stationis; Corynebacterium stationis | 2862       | 54.9        | 2380         | Gp0118688      | PRJNA242207          | SAMN02996501       | GCA_001941345     |                  |
| Strain                      | Authority                        | Other deposits                                                                 | Synonyms                                      | Base pairs | Percent G+C | No. proteins | Goldstamp       | Bioproject accession | Biosample accession | Assembly accession | IMG OID                |
|---------------------------|----------------------------------|--------------------------------------------------------------------------------|-----------------------------------------------|------------|-------------|--------------|------------------|----------------------|---------------------|---------------------|----------------------|
| *Corynebacterium appendicis* DSM 44531 | Yassin et al. 2002 emend. Nouioui et al. 2018 | NRRL B-24151; CCUG 48298; JCM 11765; IMMIB R-3491 | *Corynebacterium appendicis*                  | 2248 056   | 64.3        | 2155         | Gp0131803       | PRJEB18828                | SAMN05444817       | GCA_90015665       | 2681813517            |
| *Corynebacterium afermentans* DSM 44280 | Riegel et al. 1993 emend. Nouioui et al. 2018 | CCUG 32103; JCM 10390; ATCC 51403; CIP 103499; LCDC 88199 | *Corynebacterium afermentans; Corynebacterium afermentans subsp. afermentans* | 2326 687   | 64.9        | 2171         | Gp0131801       | PRJEB18848                | SAMN05421802       | GCA_900156035       | 2681813557            |
| *Corynebacterium mooreparkense* DSM 44702 | Brennan et al. 2001 emend. Nouioui et al. 2018 | LMG S-19265; JCM 12073; CIP 107183; DPC 5310; NCIMB 30131 | *Corynebacterium mooreparkense*               | 3433 007   | 67.1        | 3039         | Gp0008259       | PRJNA50001                | SAMN02603088       | GCA_900179395       | 2511231114            |
| *Corynebacterium nigricans* ATCC 700975 | Shukla et al. 2004 emend. Nouioui et al. 2018 | CCUG 48176; DSM 44827; JCM 12634; CIP 107346; CN-1 | *Corynebacterium nigricans*                   | 2819 226   | 60.6        | 2551         | Gp0004919       | PRJNA37279                | SAMN02603064       | GCA_0000022905     | 643692018             |
| *Corynebacterium tuberculosis* DSM 44922 | Feurer et al. 2004 | CCUG 45418; JCM 13389; ATCC 35692; CIP 107291; LDC-20; Medalle X | *Corynebacterium tuberculosis*                | 2453 172   | 59.7        | 2326         | Gp0126956       | PRJNA347115                | SAMN05878002       | GCA_013408445       | 2833975288            |
| Strain                                      | Authority                      | Other deposits                      | Synonyms                                      | Base pairs | Percent G+C | No. proteins | Goldstamp     | Bioproject accession | Biosample accession | Assembly accession | IMG OID      |
|--------------------------------------------|--------------------------------|-------------------------------------|-----------------------------------------------|------------|-------------|--------------|---------------|----------------------|--------------------|-------------------|--------------|
| *Corynebacterium efficiens* YS-314        | Fudou et al. 2002 emend.       |                                    | *Corynebacterium efficiens*                  | 3219       | 63.0        | 2998         | Gp0000636     | PRJNA305             | SAMD00061103       | GCA_000011305     | 644736345   |
|                                            | Fudou et al. 2018              |                                    |                                               | 505        |             |              |               |                      |                    |                   |              |
| *Corynebacterium kroppenstedtii* DSM 44385 | Collins et al. 1998 emend.     |                                    | *Corynebacterium kroppenstedtii*              | 2446       | 57.5        | 2018         | Gp0000013     | PRJNA38011           | SAMN02603033       | GCA_00023145      | 643692019   |
|                                            | Nouioui et al. 2018            |                                    |                                               | 804        |             |              |               |                      |                    |                   |              |
|                                            |                                |                                    |                                               |            |             |              |               |                      |                    |                   |              |
| *Corynebacterium urinapleomorphum* Marseille-P2799 | Niang et al. 2019            | DSM103272; CSURP279                 | *Corynebacterium urinapleomorphum*             | 2259       | 63.4        | 2097         | PRJEB18932    | SAMEA47264668       | GCA_900155535      |                   |              |
|                                            |                                |                                    |                                               | 535        |             |              |               |                      |                    |                   |              |
| *Corynebacterium maris* DSM 45190          | Ben-Dov et al. 2009            | LMG24561; JCM17018; Coryn-1         | *Corynebacterium maris*                       | 2833       | 66.6        | 2584         | Gp0023680     | PRJNA172964          | SAMN02603057       | GCA_000442645     | 2561511185  |
|                                            |                                |                                    |                                               | 547        |             |              |               |                      |                    |                   |              |
| *Corynebacterium silvaticum* KL0182        | Dangel et al. 2020            | LMG31313; DSM109166; CIP111672      | *Corynebacterium silvaticum*                  | 2548       | 54.4        | 2017         | PRJNA517029   | SAMN10039578         | GCA_004382825      |                   |              |
|                                            |                                |                                    |                                               | 487        |             |              |               |                      |                    |                   |              |
| *Corynebacterium resistens* DSM 45100      | Otsuka et al. 2005 emend.      | CCUG50093; JCM12819; GTC2026; SICGH158 | *Corynebacterium resistens*                   | 2601       | 57.1        | 2171         | Gp0003835     | PRJNA39683           | SAMN02603065       | GCA_000177535     | 650716029   |
|                                            | Ndiaye et al. 2018             | CSURP4329                          | *Corynebacterium senegalense*                 | 2310       | 68.7        | 2173         | Gp0359219     | PRJEB24601           | SAMEA4664250       | GCA_900411315     |              |
|                                            |                                |                                    |                                               | 902        |             |              |               |                      |                    |                   |              |
| *Corynebacterium senegalense* Marseille-P4329 | Ndiaye et al. 2019           | CSURP4329                          | *Corynebacterium senegalense*                 | 2310       | 68.7        | 2173         | Gp0359219     | PRJEB24601           | SAMEA4664250       | GCA_900411315     |              |
| Strain                                           | Authority                                                                 | Other deposits                                                                 | Synonyms                                     | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID          |
|------------------------------------------------|---------------------------------------------------------------------------|--------------------------------------------------------------------------------|---------------------------------------------|------------|-------------|--------------|-----------|----------------------|--------------------|-------------------|------------------|
| Corynebacterium striatum NBRC 15291             | (Chester 1901) Eberson 1918 emend. Nouioui et al. 2018                   | CCUG 27949; DSM 20668; JCM 9390; ATCC 6940; IFO 15291; NBRC 15291; NCTC 764; CIP 81.15 | Bacterium striatum; Corynebacterium striatum | 3106       | 742         | 59.1         | 2949      | PRJDB8042            | SAMD00169825        |                   | GCA_006538485    |
| Corynebacterium flavescens NBRC 14136           | Barksdale et al. 1979 emend. Nouioui et al. 2018                         | 8 of Orla-Jensen; LMG 4046; CCUG 28791; DSM 20296; JCM 1317; ATCC 10340; IFO 14136; NBRC 14136; VKM Ac-1956; CIP 69.5; NCCB 42012; NCDO 1320; NCBO 1320; NCIB 8707; NCIMB 8707 | Corynebacterium flavescens                   | 2633       | 833         | 60.0         | 2430      | PRJDB6000            | SAMD00097245        |                   | GCA_006539465    |
| Corynebacterium xerosis ATCC 373                 | (Lehmann and Neumann 1896) Lehmann and Neumann 1899 emend. Nouioui et al. 2018 | CCUG 27544; DSM 20743; JCM 1971; ATCC 373; IFO 16721; NBRC 16721; NCTC 11861; CIP 100653 | Bacillus xerosis; Corynebacterium xerosis    | 2661       | 590         | 69.5         | 1843      | PRJNA280206           | SAMN03458390        |                   | GCA_000988235    |
| Strain | Authority | Other deposits | Synonyms | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID |
|--------|-----------|----------------|----------|------------|-------------|--------------|------------|----------------------|-------------------|-------------------|---------|
| Corynebacterium diptheriae DSM 44123 | (Kruse 1886) Lehmann and Neumann 1896 emend. Nouioui et al. 2018 | DSM 44123; ATCC 27010; NCTC 11397; CIP 100721 | Bacillus diptheriae; Corynebacterium diptheriae; Corynebacterium diptheriae subsp. diptheriae | 2364 574 | 53.5 | 2116 | PRJNA296455 | SAMN04099181 | GCA_001913265 |
| Corynebacterium minutissimum NCTC10288 | (ex Sarkany et al. 1962) Collins and Jones 1983 emend. Nouioui et al. 2018 | CCUG 541; DSM 20651; JCM 9387; ATCC 23348; IFO 15361; NBRC 15361; NCTC 10288; CIP 100652 | Corynebacterium minutissimum | 2695 970 | 59.9 | 2463 | PRJEB6403 | SAMEA4030732 | GCA_900478045 |
| Corynebacterium renale NCTC7448 | (Migula 1900) Ernst 1906 emend. Nouioui et al. 2018 | CCUG 27542; DSM 20688; JCM 9391; ATCC 19412; IFO 15290; NBRC 15290; NCTC 7448; CIP 103421; HAMBI 2321 | Bacterium renale; Corynebacterium renale | 2335 089 | 59.1 | 2161 | PRJEB6403 | SAMEA4030736 | GCA_900478035 |
| Corynebacterium imitans NCTC 13015 | Funke et al. 1997 emend. Nouioui et al. 2018 | 2023; CCUG 36877; DSM 44264; JCM 10386; ATCC 700354; IFO 16163; NBRC 16163; NBRC 100416; NCTC 13015; CIP 105130 | Corynebacterium imitans | 2565 606 | 64.3 | 2347 | PRJEB6403 | SAMEA4535761 | GCA_900187215 |
| Strain                  | Authority               | Other deposits | Synonyms              | Base pairs | Percent G+C | No. proteins | Goldstamp      | Bioproject accession | Biosample accession | Assembly accession | IMG OID            |
|------------------------|-------------------------|----------------|-----------------------|------------|-------------|--------------|----------------|----------------------|---------------------|--------------------|--------------------|
| *Corynebacterium*       |                         |                |                       |            |             |              |                |                      |                     |                    |                   |
| *urealyticum* NCTC12011| Pitcher et al. 1992 emend. Nouioui et al. 2018 | LMG 19041; CCUG 18158; DSM 7109; JCM 10395; ATCC 43042; NCTC 12011; CIP 103524 | Corynebacterium urealyticum | 2377 532  | 64.2        | 2005         | PRJEB6403       | SAMEA4530651         | GCA_900187235      |                    |                   |
| *jeikeium* NCTC 11913   | Jackman et al. 1988 emend. Nouioui et al. 2018 | CCUG 27192; DSM 46361; DSM 7171; JCM 9384; ATCC 43734; NCTC 11913; CIP 103337 | Corynebacterium jeikeium | 2526 027  | 61.4        | 2220         | PRJEB6403       | SAMEA4017703         | GCA_900461185      |                    |                   |
| *minutissimum* NCTC 10289| (ex Sarkany et al. 1962) Collins and Jones 1983 emend. Nouioui et al. 2018 | CCUG 541; DSM 20651; JCM 9387; ATCC 23348; IFO 15361; NBRC 15361; NCTC 10288; CIP 100652 | Corynebacterium minutissimum | 2736 326  | 59.9        | 2571         | PRJEB6403       | SAMEA104016176       | GCA_900447475      |                    |                   |
| *pilosum* NCTC 11862    | Yanagawa and Honda 1978 | CCUG 27193; DSM 20521; JCM 3714; ATCC 29592; IFO 15285; NBRC 15285; NCTC 11862; CIP 103422 | Corynebacterium pilosum | 2593 653  | 60.7        | 2398         | PRJEB6403       | SAMEA4530650         | GCA_900447205      |                    |                   |
| Strain                                        | Authority                                      | Other deposits       | Synonyms                                      | Base pairs | Percent G+C | No. proteins | Goldstamp         | Bioproject accession | Biosample accession | Assembly accession | IMG OID               |
|----------------------------------------------|-----------------------------------------------|----------------------|-----------------------------------------------|------------|-------------|--------------|-------------------|----------------------|---------------------|---------------------|----------------------|
| Corynebacterium striatum NCTC 764            | (Chester 1901) Eberson 1918 emend. Nouioui et al. 2018 | CCUG 27949; DSM 20668; JCM 9390; ATCC 6940; IFO 15291; NBR 15291; NCTC 764; CIP 81.15 | Bacterium striatum; Corynebacterium striatum | 2924       | 59.1        | 2730         | PRJEB6403         | SAMEA4521472                 | GCA_900447675          |
| Corynebacterium spheniscorum CCUG 45512      | Goyache et al. 2003 emend. Nouioui et al. 2018 | CCUG 45512; CECT 5986; DSM 44757; JCM 12271; PG 39 | Corynebacterium spheniscorum | 2456       | 57.5        | 2059         | PRJNA563568        | SAMN12771121                 | GCA_008693095          |
| Corynebacterium flavescens CCUG 28791        | Barksdale et al. 1979 emend. Nouioui et al. 2018 | 8 of Orla-Jensen; LMG 4046; CCUG 28791; DSM 20296; JCM 1317; ATCC 10340; IFO 14136; NBR 14136; VKM Ac-1956; CIP 69.5; NCCB 42012; NCCD 1320; NCFB 1320; NCIB 8707; NCIMB 8707 | Corynebacterium flavescens | 2687       | 60.0        | 2369         | PRJNA563568        | SAMN12771119                 | GCA_008693105          |
| Corynebacterium humireducens NBRC 106098     | Wu et al. 2011 emend. Nouioui et al. 2018     | DSM 45392; NBR 106098; CGMCC 2452; MFC 5 | Corynebacterium humireducens | 2609       | 68.8        | 2525         | Gp0023682          | PRJDB440                     | SAMD00046477           | GCA_001571025          |
| Strain                                | Authority                          | Other deposits                                      | Synonyms                           | Base pairs | Percent G+C | No. proteins | Goldstamp               | Bioproject accession | Biosample accession  | Assembly accession  | IMG OID            |
|---------------------------------------|------------------------------------|-----------------------------------------------------|------------------------------------|------------|-------------|--------------|--------------------------|---------------------|----------------------|----------------------|--------------------|
| Corynebacterium camporealesensis CIP 105508 | Fernández-Garayzábal et al. 1998 emend. Nouioui et al. 2018 | CCUG 39412; CECT 4897; DSM 44610; JCM 11664; ATCC BAA-77; CIP 105508; strain CRS-51 | Corynebacterium camporealesensis | 2440 812   | 59.4        | 1684         | Gp0149906               | PRJNA262863         | SAMN03092874         | GCA_000766885        |                    |
| Corynebacterium heidelbergense DSM 104638T | Braun et al. 2018                  |                                                     | Corynebacterium heidelbergense    | 2287 330   | 65.1        | 2027         | Gp0393075               | PRJNA419723         | SAMN08095970         | GCA_003285565        |                    |
| Corynebacterium tuscaniense CCUG 51321 | Riegel et al. 2006                 | DSM 45101; JCM 15294; ATCC BAA-1141; ISS-5309        | Corynebacterium tuscaniense       | 2232 117   | 59.4        | 2073         | PRJNA224116              | SAMN12771122        | GCF_008693065        |                     |                    |
| Corynebacterium halotolerans DSM 44683 | Chen et al. 2004 emend. Nouioui et al. 2018 | DSM 44683; JCM 12676; CCTCC AA 001024; YIM 70093 | Corynebacterium halotolerans      | 3202 499   | 68.4        | 2914         | Gp0013694               | PRJNA215338         | SAMN02743911         | GCA_000688435        | 2556921045         |
| Corynebacterium variabile NBRC 15286  | (Müller 1961) Collins 1987         | NRRL B-4201; CCUG 45246; DSM 20132; JCM 2154; ATCC 15753; IFO 15286; VKM Ac-1122; CIP 102112; HAMBI 1872; NCIB 9455; NCIMB 9455 | Arthrobacter variabilis; Corynebacterium variabile | 3170 194   | 67.4        | 2983         | PRJDB6001                | SAMD00097555        | GCA_006539825        |                     |                    |
| Corynebacterium tapiri LMG 28165      | Baumgardt et al. 2015              | 2385/12; CCUG 65456                                 | Corynebacterium tapiri            | 2246 156   | 62.3        | 2045         | PRJNA545602              | SAMN11928016        | GCA_006334925        |                     |                    |
| Strain                              | Authority                                      | Other deposits                  | Synonyms                                | Base pairs | Percent G+C | No. proteins | Goldstamp     | Bioproject accession | Biosample accession | Assembly accession | IMG OID       |
|------------------------------------|-----------------------------------------------|---------------------------------|-----------------------------------------|------------|-------------|--------------|---------------|---------------------|--------------------|-------------------|---------------|
| *Corynebacterium rouxii*           | FRC0190 T Badell et al. 2020                  | DSM 110354; CIP 111752          | *Corynebacterium rouxii*               | 2451       | 019         | 53.2         | 2365          | PRJNA224116         | SAMEA5992727       | GCF_902702935    |               |
| *Corynebacterium mucificiens*      | ATCC 700355 Funke et al. 1997                 | CCUG 36878; DSM 44265; JCM 10384; CIP 105129; DMMZ 2278 | *Corynebacterium mucificiens*         | 2180       | 041         | 65.5         | 2028          | PRJNA622446         | SAMN14517857       | GCA_012396315    |               |
| *Corynebacterium suranareae*       | N24T Nantapong et al. 2020                    | TBRC 5845; CCUG 113465          | *Corynebacterium suranareae*           | 3537       | 057         | 51.8         | 3194          | PRJNA224116         | SAMD00000552       | GCF_002355155    |               |
| *Corynebacterium spheniscorum*     | DSM 44757 Goyache et al. 2003 emend. Nouioui et al. 2018 | CCUG 45512; CECT 5986; DSM 44757; JCM 12271; PG 39 | *Corynebacterium spheniscorum*         | 2451       | 087         | 57.5         | 2156          | Gp0102878           | SAMN05660282       | GCA_900113445    | 2599185219     |
| *Corynebacterium cystitidis*       | DSM 20524 Yanagawa and Honda 1978 emend. Nouioui et al. 2018 | CCUG 28794; DSM 20524; JCM 3715; ATCC 29593; IF0 15284; NBRC 15284; NCTC 11863; CIP 103424 | *Corynebacterium cystitidis*           | 2943       | 080         | 57.0         | 2789          | Gp0102855           | SAMN05661109       | GCA_900111265    | 2599185266     |
| *Corynebacterium crudilactis*      | DSM 100882 Zimmermann et al. 2016             | LMG 29813; CCUG 69192; JZ16     | *Corynebacterium crudilactis*          | 3217       | 086         | 51.7         | 2825          | Gp0203249           | SAMN04990137       | GCA_001643015    |               |
| *Corynebacterium hadale*           | NBT06-6 Wei et al. 2018                       | MCCC 1K03347; DSM 105365        | *Corynebacterium hadale*               | 2679       | 019         | 65.2         | 2362          | Gp0374689           | SAMN07460149       | GCA_002273005    |               |
| Strain                          | Authority                  | Other deposits                          | Synonyms                                      | Base pairs | Percent G+C | No. proteins | Goldstamp     | Bioproject accession | Biosample accession | Assembly accession | IMG OID        |
|--------------------------------|---------------------------|----------------------------------------|-----------------------------------------------|------------|-------------|--------------|---------------|----------------------|----------------------|-------------------|-----------------|
| Corynebacterium pollutisoli VDS | Negi et al. 2016          | MCC 2722; KCTC 39687; DSM 100104; VDS1 | Corynebacterium pollutisoli                  | 2535 040   | 68.5        | 2430         | Gp0156991     | PRJEB20263           | SAMN06295981       | GCA_900177745     |                 |
| Corynebacterium yudongzhengii 2183 | Zhu et al. 2020           | DSM 106264; CGMCC 1.16416             | Corynebacterium yudongzhengii               | 2511 302   | 64.9        | 2142         | PRJNA431327    |                       | SAMN08388720       | GCA_003065405     |                 |
| Corynebacterium provencense SN15 | Lo et al. 2019            | DSM 101074; CSURP2161                  | Corynebacterium provencense                 | 3075 769   | 66.9        | 2799         | PRJEB12691     |                       | SAMEA3869306       | GCA_900049755     |                 |
| Corynebacterium bouchesdurhone nse SN14 | Lo et al. 2019            | DSM 100846; CSURP2067                  | Corynebacterium bouchesdurhone nse          | 2255 535   | 68.0        | 2147         | PRJEB13138     |                       | SAMEA3905754       | GCA_900078305     |                 |
| Corynebacterium pseudotuberculosis ATCC 19410 | (Buchanan 1911) Eameron 1918 emend. Nouioui et al. 2018 | CCUG 2806; DSM 20689; JCM 9389; ATCC 19410; IFO 15363; NBRC 15363; NCTC 3450; CIP 102968 | Bacillus pseudotuberculosis; Corynebacterium pseudotuberculosis | 2337 763   | 52.2        | 2146         | Gp0223239     | PRJNA382169       | SAMN06701041       | GCA_002155265     |                 |
| Dermabacter jinjuensis 32      | Park et al. 2016          | DSM 101003; NCCP 1613                 | Dermabacter jinjuensis                       | 2398 786   | 62.9        | 1996         | Gp0266532     | PRJNA407870       | SAMN07665299       | GCA_002443115     |                 |
| Corynebacterium jeddahense JCB | Edouard et al. 2017       | DSM 45997; CSUR P778                   | Corynebacterium jeddahense                   | 2472 125   | 67.2        | 2341         | Gp0101187     | PRJEB4941           | SAMEA3138931       | GCA_000577555     |                 |
| Strain                          | Authority                     | Other deposits                                                                 | Synonyms                                                                 | Base pairs | Percent G+C | No. proteins | Goldstamp     | Bioproject accession | Biosample accession | Assembly accession | IMG OID        |
|--------------------------------|-------------------------------|--------------------------------------------------------------------------------|--------------------------------------------------------------------------|------------|-------------|--------------|---------------|----------------------|---------------------|---------------------|------------------|
| *Corynebacterium pseudotuberculosis* DSM 20689 | (Buchanan 1911) Eberon 1918 emend. Nouioui et al. 2018 | CCUG 2806; DSM 20689; JCM 9389; ATCC 19410; IFO 15363; NBRC 15363; NCTC 3450; CIP 102968 | *Bacillus pseudotuberculosis*; *Corynebacterium pseudotuberculosis* | 2338        | 52.2        | 2084         | Gp0220522     | PRJNA442833          | SAMN08778220        | GCA_003634885     | 2756170169     |
| *Corynebacterium ulcerans* NCTC 7910 | (ex Gilbert and Stewart 1927) Riegel et al. 1995 | CCUG 2708; DSM 46325; JCM 10387; ATCC 51799; CIP 106504 | *Corynebacterium ulcerans* | 2453        | 53.3        | 2178         | Gp0262745     | PRJEB6403            | SAMEA4504038        | GCA_900187135     | 2880529280     |
| *Corynebacterium aquatimans* DSM 45632 | Aravena-Román et al. 2012 | CCUG 61574; IMMIB L-2475 | *Corynebacterium aquatimans* | 2525        | 61.0        | 2230         | Gp0305023     | PRJNA303721          | SAMN04488535        | GCA_900103625     | 2634166344     |
| *Corynebacterium mycoides* DSM 20632 | (ex Castellani 1942) Collins 1983 emend. Nouioui et al. 2018 | CCUG 27538; JCM 9388; ATCC 43995; IFO 15269; NBRC 15289; NCTC 9864; CIP 55.51 | *Corynebacterium mycoides* | 2266        | 66.6        | 2129         | Gp0116506     | PRJNA303721          | SAMN04488535        | GCA_900103625     | 2634166344     |
| *Corynebacterium timonense* DSM 45434 | Merhej et al. 2009 emend. Nouioui et al. 2018 | CCUG 540174; CCUG 53856; DSM 45434; CIP 109424; CSUR P20 | *Corynebacterium timonense* | 2633        | 66.6        | 2470         | Gp0116508     | PRJNA303719          | SAMN04488539        | GCA_900105305     | 2636416018     |
| Strain | Authority | Other deposits | Synonyms | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID |
|--------|-----------|----------------|----------|------------|-------------|--------------|-----------|---------------------|-------------------|------------------|---------|
| Corynebacterium ammoniagenes DSM 20306 | (Cooke and Keith 1927) Collins 1987 emend. Nouioui et al. 2018 | CCUG 38796; JCM 1305; ATCC 6871; IFO 12612; NBRC 12612; VKM B-672; CIP 101283; NCCB 60030; NCIB 8143; NCIMB 8143 | Bacterium ammoniagenes; Brevisbacterium ammoniagenes; Corynebacterium ammoniagenes | 2759 010 | 55.6 | 2654 | Gp0003415 | PRJNA38319 | SAMN00189098 | GCA_000164115 | 647000230 |
| Corynebacterium pyruviciproducens ATCC BAA-1742 | Tong et al. 2010 | 06-17730; CCUG 57046; DSM 45565; WAL 19168 | Corynebacterium pyruviciproducens | 2703 797 | 61.2 | 2447 | Gp0012480 | PRJNA78965 | SAMN02596973 | GCA_000411375 | 2541047000 |
| Corynebacterium accolens ATCC 49725 | Neubauer et al. 1991 emend. Nouioui et al. 2018 | CNCTC Th 1/57; CCUG 28779; DSM 44278; JCM 8331; CIP 104783 | Corynebacterium accolens | 2406 629 | 59.7 | 2333 | Gp0003417 | PRJNA31443 | SAMN00002226 | GCA_000159115 | 643886058 |
| Corynebacterium lipophiloflavum DSM 44291 | Funke et al. 1997 | CCUG 37336; JCM 10383; ATCC 700352; CIP 105127; DMMZ 1944 | Corynebacterium lipophiloflavum | 2287 535 | 64.9 | 2371 | Gp0003463 | PRJNA31447 | SAMN00001476 | GCA_000159635 | 643886002 |
| Strain                    | Authority                                      | Other deposits                             | Synonyms                                      | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID          |
|--------------------------|-----------------------------------------------|--------------------------------------------|-----------------------------------------------|------------|-------------|--------------|-----------|---------------------|--------------------|-------------------|------------------|
| *Corynebacterium striatum* ATCC 6940 | (Chester 1901) Ebersen 1918 emend. Nouioui et al. 2018 | CCUG 27949; DSM 20668; JCM 9390; ATCC 6940; IFO 15291; NBRCC 15291; NCTC 764; CIP 81.15 | *Bacterium* striatum; *Corynebacterium striatum* | 2717 381   | 59.4        | 2677         | Gp0003467 | PRJNA31449          | SAMN00001507       | GCA_000159135     | 643886057        |
| *Rothia mucilaginosa* ATCC 25296 | (Bergan and Kocur 1982) Collins et al. 2000 emend. Nouioui et al. 2018 | CCUG 20962; DSM 20746; JCM 10910; IFO 15673; NBRCC 15673; NCTC 10663; CCM 2417; CIP 71.14 | *Rothia mucilaginosa*; *Stomatococcus mucilaginosus* | 2255 154   | 59.5        | 1737         | Gp0004126 | PRJNA31405          | SAMN00001919       | GCA_000175615     | 645058800        |
| *Corynebacterium amycolatum* ATCC 49368 | Collins et al. 1988 | CCUG 35685; DSM 6922; JCM 7447; IFO 15207; NBRCC 15207; CIP 103452; NCFB 2768; NCIMB 13130; S160 | *Corynebacterium amycolatum* | 2448 224   | 58.7        | 2128         | PRJNA224116 | SAMN07741515       | GCA_014335175      |                    |                  |
| *Corynebacterium atypicum* DSM 44849 | Hall et al. 2003 emend. Nouioui et al. 2018 | CCUG 45804; JCM 12348; CIP 107431; R2070 | *Corynebacterium atypicum* | 2359 433   | 65.4        | 1578         | Gp0099220 | PRJNA255205          | SAMN02911287       | GCA_000732945     |                  |
| *Corynebacterium auriscans* CIP 106629 | Collins et al. 2000 emend. Nouioui et al. 2018 | CCUG 39938; DSM 44609; JCM 12369; M598/96/1 | *Corynebacterium auriscans* | 2568 862   | 58.5        | 1537         | Gp0107708 | PRJNA262562          | SAMN03106126       | GCA_000767255     |                  |
| Strain                                      | Authority                                                | Other deposits                                                                 | Synonyms                                         | Base pairs | Percent G+C | No. proteins | Goldstamp       | Bioproject accession | Biosample accession | Assembly accession | IMG OID         |
|---------------------------------------------|----------------------------------------------------------|-------------------------------------------------------------------------------|-------------------------------------------------|------------|-------------|--------------|-----------------|----------------------|--------------------|-------------------|-----------------|
| Corynebacterium camporealesis DSM 44610    | Fernández-Garayzábal et al. 1998 emend. Nouioui et al. 2018 | CCUG 39412; CECT 4897; DSM 44610; JCM 11664; ATCC BAA-77; CIP 105508; strain CRS-51 | Corynebacterium camporealesis                    | 2451       | 59.4        | 2249         | Gp0110294       | PRJNA276036         | SAMN03365263       | GCA_000980815     |
| Corynebacterium casei DSM 44701            | Brennan et al. 2001 emend. Nouioui et al. 2018          | LMG S-19264; JCM 12072; CIP 107182; DPC 5298; NCIMB 30130                     | Corynebacterium casei                            | 3132       | 55.7        | 2809         | Gp0036841       | PRJNA186910         | SAMN03081454       | GCA_000550785     | 255860241       |
| Corynebacterium humireducens DSM 45392     | Wu et al. 2011 emend. Nouioui et al. 2018                | DSM 45392; NBRC 106098; CGMCC 2452; MFC-5                                    | Corynebacterium humireducens                     | 2681       | 68.6        | 2545         | Gp0023681       | PRJNA172965         | SAMN03283197       | GCA_000819445     |
| Corynebacterium imitans DSM 44264          | Funke et al. 1997 emend. Nouioui et al. 2018             | 2023; CCUG 38677; DSM 44264; JCM 10386; ATCC 700354; IFO 16163; NBRC 16163; NBRC 100416; NCTC 13015; CIP 105130 | Corynebacterium imitans                          | 2565       | 64.3        | 2013         | Gp0094474       | PRJNA246650         | SAMN02950575       | GCA_000739455     |
| Corynebacterium marinum DSM 44953          | Du et al. 2010 emend. Nouioui et al. 2018                | 7015; NRRL B-24779; DSM 44953; CGMCC 1.6998; D7015                          | Corynebacterium marinum                          | 2729       | 67.8        | 2550         | Gp0023707       | PRJNA172963         | SAMN02800399       | GCA_000835165     |
| Strain                                | Authority                                      | Other deposits         | Synonyms                           | Base pairs | Percent G+C | No. proteins | Goldstamp      | Bioproject accession | Biosample accession | Assembly accession | IMG OID          |
|---------------------------------------|------------------------------------------------|------------------------|------------------------------------|------------|-------------|--------------|----------------|---------------------|---------------------|-------------------|-------------------|
| Corynebacterium singulare DSM 44557   | Riegel et al. 1997 emend. Nouioui et al. 2018 | CCUG 37330; JCM 10385; IFO 16162; NBR 16162; CIP 105491; IBS 52218 | Corynebacterium singulare          | 2830       | 60.1        | 2561         | Gp0109683      | PRJNA246651            | SAMN03177398         | GCA_000833575     |                   |
| Corynebacterium testudinoris DSM 44614| Collins et al. 2001 emend. Nouioui et al. 2018| CCUG 41823; JCM 12108; CIP 106763; M935/96/4 | Corynebacterium testudinoris       | 2721       | 63.1        | 2560         | Gp0114695      | PRJNA280910            | SAMN03480629         | GCA_001021045     |                   |
| Corynebacterium ureicelivorans DSM 45051| Yassin 2007 emend. Nouioui et al. 2018       | CCUG 53377; JCM 15295; IMMIB RIV-2301 | Corynebacterium ureicelivorans     | 2328       | 65.0        | 1922         | Gp0103378      | PRJNA257688            | SAMN02953970         | GCA_000747315     |                   |
| Corynebacterium deserti DSM 45689     | Zhou et al. 2012 emend. Nouioui et al. 2018  | NRRL B-59552; CCTCC AB 2010341; GIMN1.010 | Corynebacterium deserti            | 3033       | 55.3        | 2724         | Gp0109766      | PRJNA222609            | SAMN02950576         | GCA_001277995     |                   |
| Corynebacterium glyciniphilum ATCC 21341 | (ex Kubota et al. 1972 Al-Dilaimi et al. 2015) | AJ 3170; DSM 45795 | Corynebacterium glyciniphilum      | 3568       | 64.8        | 3270         | Gp0047724      | PRJNA221205            | SAMN03081498         | GCA_000626675     | 2576861442        |
| Corynebacterium epidemidicanis DSM 45586 | Frischmann et al. 2012 emend. Nouioui et al. 2018 | 410; LMG 26322; CCUG 60915 | Corynebacterium epidemidicanis     | 2692       | 58.1        | 2465         | Gp0114694      | PRJNA280479            | SAMN03462986         | GCA_001021025     |                   |
| Corynebacterium minutissimum ATCC 23348 | (ex Sarkany et al. 1962 Collins and Jones 1983 emend. Nouioui et al. 2018) | CCUG 541; DSM 20651; JCM 9387; ATCC 23348; IFO 15361; NBR 15361; NCTC 10288; CIP 100652 | Corynebacterium minutissimum        | 2663       | 60.0        | 2276         | Gp0122002      | PRJNA264738            | SAMN03140311         | GCA_000805675     |                   |
| Strain                          | Authority                                                                 | Other deposits                                                      | Synonyms                                                                 | Base pairs | Percent G+C | No. proteins | Goldstamp       | Bioproject accession | Biosample accession | Assembly accession | IMG OID         |
|--------------------------------|---------------------------------------------------------------------------|---------------------------------------------------------------------|--------------------------------------------------------------------------|------------|-------------|--------------|----------------|---------------------|---------------------|-------------------|------------------|
| Corynebacterium minutissimum   | (ex Sarkany et al. 1962) Collins and Jones 1983 emend. Nouioui et al. 2018 | CCUG 541; DSM 20651; JCM 9387; ATCC 23348; IFO 15361; NBRC 15361; NCTC 10288; CIP 100652 | Corynebacterium minutissimum                                           | 2663       | 60.0        | 2464         | Gp0024448       | PRJDB438            | SAMD00046517       | GCA_001552395     |
|                                |                                                                           |                                                                     |                                                                          | 455        |             |              |                |                     |                     |                  |                  |
| Corynebacterium halotolerans   | Chen et al. 2004 emend. Nouioui et al. 2018                              | DSM 44683; JCM 12676; CCTCC AA 001024; YIM 70093                    | Corynebacterium halotolerans                                           | 3222       | 68.3        | 2865         | Gp0023456       | PRJNA168616          | SAMN02603027       | GCA_000341345     | 2524023198       |
|                                |                                                                           |                                                                     |                                                                          | 002        |             |              |                |                     |                     |                  |                  |
| Corynebacterium xerosis        | (Lehmann and Neumann 1896) Lehmann and Neumann 1899 emend. Nouioui et al. 2018 | CCUG 27544; DSM 20743; JCM 1971; ATCC 373; IFO 16721; NBRC 16721; NCTC 11861; CIP 100653 | Bacillus xerosis; Corynebacterium xerosis                            | 2686       | 69.7        | 2351         | Gp0024449       | PRJDB439            | SAMD00046521       | GCA_001552415     |                  |
|                                |                                                                           |                                                                     |                                                                          | 219        |             |              |                |                     |                     |                  |                  |
| Corynebacterium nuruki         | Shin et al. 2011 emend. Nouioui et al. 2018                              | DSM 45695; JCM 17162; KACC 15032                                    | Corynebacterium nuruki                                                | 3106       | 69.5        | 2787         | Gp0011122       | PRJNA66913           | SAMN02470217       | GCA_000213935     | 2547132106       |
|                                |                                                                           |                                                                     |                                                                          | 595        |             |              |                |                     |                     |                  |                  |
| Corynebacterium glutamicum     | (Kinoshita et al. 1958) Abe et al. 1967 emend. Nouioui et al. 2018       | LMG 3730; NRRL B-2784; CCUG 27702; DSM 20300; JCM 1318; IFO 12168; NBRC 12168; CIP 82.08; HAMBI 2052 | Corynebacterium glutamicum; Micrococcus glutamicus                   | 3282       | 53.8        | 3057         | Gp0000615       | PRJNA13760           | SAMEA3138338       | GCA_000196355     | 639279306        |
| Strain                      | Authority          | Other deposits                                      | Synonyms                                         | Base pairs | Percent G+C | No. proteins | Goldstamp     | Bioproject accession | Biosample accession | Assembly accession | IMG OID         |
|-----------------------------|--------------------|-----------------------------------------------------|--------------------------------------------------|------------|-------------|--------------|---------------|----------------------|---------------------|------------------|-----------------|
| Corynebacterium urealyticum | Pitcher et al. 1992 emend. Nouioui et al. 2018 | LMG 19041; CCUG 18158; DSM 7109; JCM 10395; ATCC 43042; NCTC 12011; CIP 103524 | Corynebacterium urealyticum                     | 2369 219   | 64.2        | 2024         | Gp0001357     | PRJNA29211           | SAMEA3138282       | GCA_000069945   | 641522620       |
| Corynebacterium marinum     | Du et al. 2010 emend. Nouioui et al. 2018        | 7015; NRRL B-24779; DSM 44953; CGMCC 1.6998; D7015 | Corynebacterium marinum                         | 2680 020   | 67.9        | 2569         | PRJDB10509    | SAMD00245145        | GCA_014645275     |                  |                 |
| Propionibacterium cyclohexanicum | Kusano et al. 1997          | CCUG 48885; NRIC 247; JCM 21245; ATCC 700429; NBRC 103082; CIP 105414; IAM 14535; TA-12 | Propionibacterium cyclohexanicum                | 2808 867   | 66.9        | 2525         | Gp0131643    | PRJNA332060          | SAMN05443377       | GCA_900111365   | 2675903216       |
| Dermabacter vaginalis AD1-86 | Chang et al. 2016          | KCTC 39585; DSM 100050                                | Dermabacter vaginalis                           | 2392 314   | 62.6        | 2129         | Gp0203766     | PRJNA286956          | SAMN03777429       | GCA_001678905   |                 |
| Corynebacterium pacaense    | Bellali et al. 2019        | CSUR P2417                                            | Corynebacterium pacaense                        | 3027 822   | 63.7        | 2736         | PRJEB19973    | SAMEA103910525       | GCA_900169525     |                  |                 |
| Corynebacterium oculi       | Bernard et al. 2016        | LMG 28277; CCUG 65816; R-50187; TVRM83/2006F4/44     | Corynebacterium oculi                           | 2413 873   | 64.8        | 2327         | Gp0145072     | PRJNA295863          | SAMN04091236       | GCA_001412105   |                 |
| Strain                          | Authority                  | Other deposits                                                                 | Synonyms                      | Base pairs | Percent G+C | No. proteins | Goldstamp     | Bioproject accession | Biosample accession | Assembly accession  | IMG OID         |
|--------------------------------|---------------------------|-------------------------------------------------------------------------------|-------------------------------|------------|-------------|--------------|---------------|----------------------|---------------------|---------------------|------------------|
| Corynebacterium gottingense DSM 103494 | Atasayar et al. 2017; Bernard et al. 2020 | 22991/201 6; 9221/201 6; JCM 31931 | Corynebacterium gottingense   | 2616 814   | 65.5        | 2362         | Gp0377217     | PRJNA497573          | SAMN10261082       | GCA_003693265     |                  |
| Corynebacterium timonense 5401744 | Merhej et al. 2009; Nouioui et al. 2018 | 5401744; CCUG 53856; DSM 45434; CIP 109424; CSUR P20 | Corynebacterium timonense     | 2551 022   | 66.9        | 2376         | Gp0023376     | PRJEB67              | SameA2271986       | GCA_000312345     | 2551306128      |
| Corynebacterium pilosum CIP 103422 | Yanagawa and Honda 1978   | CCUG 27193; DSM 20521; JCM 3714; ATCC 29592; IF0 15285; NBRC 15285; NCTC 11862; CIP 103422 | Corynebacterium pilosum       | 2545 970   | 60.7        | 2772         | Gp0120674     | PRJNA284680          | SameA03731012      | GCA_001044155     |                  |
| Corynebacterium dentalis Marseille-P4122 | Ben Abdelkader et al. 2020 | CSURP412 2 | Corynebacterium dentalis | 2302 937   | 59.9        | 2080         | PRJNA224116   | SameA104348950       | GCF_900232865      |                    |                  |
| Corynebacterium lowii LMG 28276 | Bernard et al. 2016       | CCUG 65815; NML 130206; R-50085; TKD4 | Corynebacterium lowii         | 2354 433   | 62.9        | 2108         | PRJNA224116   | SameA04091594        | GCF_001412085      |                    |                  |
| Corynebacterium liangguodongii 2184 | Zhu et al. 2020           | DSM 106203; CGMCC 1.18417 | Corynebacterium liangguodongii | 2357 924   | 66.1        | 2115         | PRJNA431327   | SameA08388739        | GCA_003070865      |                    |                  |
| Corynebacterium jeikeium ATCC 43734 | Jackman et al. 1988; Nouioui et al. 2018 | CCUG 27192; DSM 46361; DSM 7171; JCM 9384; ATCC 43734; NCTC 11913; CIP 103337 | Corynebacterium jeikeium      | 2425 907   | 61.6        | 2224         | Gp0004510     | PRJNA31445           | SameA00001506      | GCA_000163435     | 647000231       |
| Strain                                      | Authority                        | Other deposits                          | Synonyms                                                                 | Base pairs | Percent G+C | No. proteins | Goldstamp      | Bioproject accession | Biosample accession | Assembly accession | IMG OID       |
|---------------------------------------------|----------------------------------|-----------------------------------------|--------------------------------------------------------------------------|------------|-------------|--------------|----------------|----------------------|---------------------|----------------------|---------------|
| Corynebacterium neomassiliense              | Boxberger et al. 2020            | CCUG7235; CSURP388                      | Corynebacterium neomassiliense                                           | 3139       | 66.9        | 2729         | PRJNA224116     | SAMEA5140071         | GCF_900626215     |                       |               |
| Corynebacterium diphtheriae                  | (Kruze 1886) Lehmann and Neumann 1896 emend. Nouioui et al. 2018 | DSM 44123; ATCC 27010; NCTC 11397; CIP 100721 | Bacillus diphtheriae; Corynebacterium diphtheriae; Corynebacterium diphtheriae subsp. diphtheriae | 2463       | 53.5        | 2337         | Gp0132011      | PRJEB6403            | SAMEA2517360         | GCA_001457455     |               |
| Corynebacterium argentoratense              | Riegel et al. 1995 emend. Nouioui et al. 2018 | CCUG 34893; JCM 10392; ATCC 51927; CIP 104296; IBS B10697 | Corynebacterium argentoratense                                           | 2031       | 58.9        | 1875         | Gp0044215      | PRJNA209048           | SAMN02603032         | GCA_000590555     | 2554235426     |
| Corynebacterium terpenotabidum              | Takeuchi et al. 1999             | DSM 44721; JCM 10555; IFO 14764; NBRC 14764; VKM Ac-2071; CIP 105927 | Corynebacterium terpenotabidum                                           | 2751       | 67.0        | 2369         | Gp0022753      | PRJNA168617           | SAMN02603028         | GCA_000418365     | 2554235357     |
| Cargentoratense_DSM44202.fna                |                                  |                                         |                                                                          | 2031       | 58.9        | 1896         |                |                      |                    |                     |               |
| Catypicum_R207_0.fna                        |                                  |                                         |                                                                          | 2359       | 65.4        | 2165         |                |                      |                    |                     |               |
| Caurimucosum_ATCC700975.fna                 |                                  |                                         |                                                                          | 2819       | 60.6        | 2662         |                |                      |                    |                     |               |
| Cbelfantii_FRC0043.fna                      |                                  |                                         |                                                                          | 2609       | 53.6        | 2663         |                |                      |                    |                     |               |
| Ccallunae_DSM20147.fna                      |                                  |                                         |                                                                          | 2928       | 52.5        | 2707         |                |                      |                    |                     |               |
| Ccamporealensis_DSM44610.fna                |                                  |                                         |                                                                          | 2451       | 59.4        | 2263         |                |                      |                    |                     |               |
| Strain                  | Authority       | Other deposits | Synonyms          | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID |
|------------------------|-----------------|----------------|-------------------|------------|-------------|--------------|-----------|----------------------|--------------------|------------------|--------|
| Ccasei_LMGS19          |                 |                |                   | 3132       | 55.7        | 2889         |           |                      |                    |                  |        |
| 264.fna                |                 |                |                   | 213        |             |              |           |                      |                    |                  |        |
| Cdeserti_GIMN1          |                 |                |                   | 3033       | 55.3        | 2818         |           |                      |                    |                  |        |
| 010.fna                |                 |                |                   | 893        |             |              |           |                      |                    |                  |        |
| Cdiphtheriae_NC        |                 |                |                   | 2463       | 53.5        | 2343         |           |                      |                    |                  |        |
| TC11397.fna            |                 |                |                   | 666        |             |              |           |                      |                    |                  |        |
| Cdoosanense_D          |                 |                |                   | 2698       | 66.8        | 2609         |           |                      |                    |                  |        |
| SM45436.fna            |                 |                |                   | 995        |             |              |           |                      |                    |                  |        |
| Cefficiens_YS31        |                 |                |                   | 3219       | 63.0        | 2877         |           |                      |                    |                  |        |
| 4.fna                  |                 |                |                   | 505        |             |              |           |                      |                    |                  |        |
| Cepidermidicani s_DSMDSM45586.fna |     |                |                   | 2692       | 58.1        | 2485         |           |                      |                    |                  |        |
|                        |                 |                |                   | 072        |             |              |           |                      |                    |                  |        |
| Cfalsenii_DSM44        |                 |                |                   | 2719       | 63.2        | 2371         |           |                      |                    |                  |        |
| 353.fna                |                 |                |                   | 616        |             |              |           |                      |                    |                  |        |
| Cglutamicum_A          |                 |                |                   | 3282       | 53.8        | 3031         |           |                      |                    |                  |        |
| TCC13032.fna           |                 |                |                   | 708        |             |              |           |                      |                    |                  |        |
| Cglycinophilum_ AJ3170.fna |             |                |                   | 3568       | 64.8        | 3325         |           |                      |                    |                  |        |
|                        |                 |                |                   | 218        |             |              |           |                      |                    |                  |        |
| Chalotolerans_YIM70093.fna |             |                |                   | 3222       | 68.3        | 2908         |           |                      |                    |                  |        |
|                        |                 |                |                   | 008        |             |              |           |                      |                    |                  |        |
| Chumireducens_D        |                 |                |                   | 2681       | 68.6        | 2586         |           |                      |                    |                  |        |
| SM45392.fna            |                 |                |                   | 312        |             |              |           |                      |                    |                  |        |
| Cimitans_DSM4          |                 |                |                   | 2565       | 64.3        | 2367         |           |                      |                    |                  |        |
| 4264.fna               |                 |                |                   | 321        |             |              |           |                      |                    |                  |        |
| Cjeikeium_K41.fna      |                 |                |                   | 2476       | 61.4        | 2137         |           |                      |                    |                  |        |
|                        |                 |                |                   | 822        |             |              |           |                      |                    |                  |        |
| Ckroppenstedtii_DSM44385.fna |         |                |                   | 2446       | 57.5        | 2127         |           |                      |                    |                  |        |
|                        |                 |                |                   | 804        |             |              |           |                      |                    |                  |        |
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 2021-02-09. 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 14130 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**

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 \( d_5 \) [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 120 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 94 species clusters and the provided query strains were assigned to 20 of these. Moreover, user strains were located in 20 of 98 subspecies clusters.

**Figure caption SSU tree**

**Figure 1.** 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 72.7 %. The tree was rooted at the midpoint [7].

**Figure caption genome tree**

**Figure 2.** 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 38.4 %. The tree was rooted at the midpoint [7].
References

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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!

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                          |
|-----------------------|-----------------------------|--------------------------------------|---------------------------------|
| 'Cvitaeruminis_DSM20294' | belongs to known species    | Corynebacterium vitaeruminis         |                                 |
| 'CriegeliiPUDD83A45'   | belongs to known species    | Corynebacterium riegelii             |                                 |
| 'Cmaris_DSM45190'      | belongs to known species    | Corynebacterium maris                |                                 |
| 'Csilvaticum_KL0182'   | belongs to known species    | Corynebacterium silvaticum           |                                 |
| 'Curealyticum_DSM7109' | belongs to known species    | Corynebacterium urealyticum          |                                 |
| 'Crouxii_FRC0190'      | belongs to known species    | Corynebacterium rouxii               |                                 |
| 'Cpseudotuberculosis_31' | belongs to known species  | Corynebacterium pseudotuberculosis  |                                 |
| 'Cpseudotuberculosis_ATCC19410' | belongs to known species | Corynebacterium pseudotuberculosis |                                 |
| 'Culcerans_NCTC7910'   | belongs to known species    | Corynebacterium ulcerans             |                                 |
| 'Ckutscheri_DSM20755'  | belongs to known species    | Corynebacterium kutscheri            |                                 |
| 'Cmarinum_DSM44953'    | belongs to known species    | Corynebacterium marinum              |                                 |
| 'Cmustelae_DSM45274'   | belongs to known species    | Corynebacterium mustelae             |                                 |
| 'Csingulare_IBSB52218' | belongs to known species    | Corynebacterium singulare            |                                 |
| 'Ctestudinoris_DSM44614' | belongs to known species  | Corynebacterium testudinoris         |                                 |
| 'Cureicelerivorans_IMMIBRIV2301' | belongs to known species | Corynebacterium ureicelerivorans     |                                 |
| Strain               | Conclusion               | Identification result                  | Remark     |
|---------------------|--------------------------|---------------------------------------|------------|
| 'Cuterequi DSM45634' | belongs to known species | Corynebacterium uterequi              |            |
| 'Clactis RW25'      | belongs to known species | Corynebacterium lactis                |            |
| 'Cterpenotabidum Y11' | belongs to known species | Corynebacterium terpenotabidum        |            |
| 'Csimulans PES1'    | potential new species    |                                       | see [R1]   |
| 'Culcerans NCTC12077' | potential new species   |                                       | see [R1]   |
Table 3: Pairwise comparisons of user genomes vs. type-strain genomes

The overall number of pairwise comparisons was too large for a proper display and was thus reduced to only those comparisons having a digital DDH value ≥ 65% in at least one of the three formulae $d_0$, $d_4$, and $d_6$.

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 formulae:

- 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 $d_6$ is independent of genome length and is thus robust against the use of incomplete draft genomes. For other reasons for preferring formula $d_6$, 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 |
|----------------------------|--------------------------------------------|-------|------------|-------|------------|-------|------------|-------------------|
| 'Cterpenabitidum_Y11.fna'  | Corynebacterium terpenabitidum Y-11        | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cmaris_DSM45190.fna'     | Corynebacterium maris DSM 45190            | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Culcerans_NCTC7910.fna'  | Corynebacterium ulcerans NCTC 7910        | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cmarinum_DSM44953.fna'   | Corynebacterium marinum DSM 44953          | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cureicelerivorans_IMMIBRIV2301.fna' | Corynebacterium ureicelerivorans DSM 45051 | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cmarinum_DSM44953.fna'   | Corynebacterium marinum CGMCC 1.6998       | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Csilvaticum_KL0182.fna'  | Corynebacterium silvaticum KL0182          | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Csinigulare_IBSB52218.fna' | Corynebacterium sinigulare DSM 44357       | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Ctestudinoris_DSM44614.fna' | Corynebacterium testudinoris DSM 44614    | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Curealyticum_DSM7109.fna' | Corynebacterium urealyticum DSM 7109       | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cpseudotuberculosis_ATCC19410.fna' | Corynebacterium pseudotuberculosis ATCC 19410 | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cactis_RW25.fna'         | Corynebacterium lactis DSM 45799           | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cmustelae_DSM45274.fna'  | Corynebacterium mustelae DSM 45274         | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cpseudotuberculosis_ATCC19410.fna' | Corynebacterium pseudotuberculosis DSM 20689  | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Citaeruminis_DSM20294.fna' | Corynebacterium viteruminis DSM 20294     | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Curealyticum_DSM7109.fna' | Corynebacterium urealyticum NCTC12011     | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.02              |
| 'Ckutscheri_DSM20755.fna' | Corynebacterium kutscheri NCTC 11138      | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Ckutscheri_DSM20755.fna' | Corynebacterium kutscheri DSM 20755       | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Crousii_FRC0190.fna'     | Corynebacterium rouxii FRC0190 T           | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| 'Cuterequi_DSM45634.fna'  | Corynebacterium cuterequi DSM 45634        | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 100.0 | [100.0 - 100.0] | 0.0               |
| Query                        | Subject                                      | $d_0$ | C.I. $d_0$ | $d_4$ | C.I. $d_4$ | $d_5$ | C.I. $d_5$ | Diff. G+C Percent |
|------------------------------|----------------------------------------------|-------|------------|-------|------------|-------|------------|------------------|
| 'Cpseudotuberculosis_31.fna' | Corynebacterium pseudotuberculosis ATCC 19410 | 99.1  | [98.3 - 99.5] | 89.4  | [87.0 - 91.4] | 99.0  | [98.3 - 99.4] | 0.02             |
| 'Cpseudotuberculosis_31.fna' | Corynebacterium pseudotuberculosis DSM 20689 | 99.1  | [98.3 - 99.5] | 89.4  | [87.0 - 91.4] | 99.0  | [98.3 - 99.4] | 0.02             |
| 'Cpseudotuberculosis_31.fna' | 'Cpseudotuberculosis_A TCC19410.fna'        | 99.1  | [98.3 - 99.5] | 89.4  | [87.0 - 91.4] | 99.0  | [98.3 - 99.4] | 0.02             |
| 'CriegeliiPUD083A45.fna'    | Corynebacterium riegelii DSM 44326           | 92.0  | [89.1 - 94.2] | 71.9  | [68.9 - 74.7] | 91.3  | [88.7 - 93.4] | 0.11             |
| 'Culcerans_NCTC12077.fna'   | Corynebacterium ulcerans NCTC 7910          | 94.4  | [92.0 - 96.2] | 66.8  | [63.8 - 69.6] | 92.3  | [89.9 - 94.2] | 0.07             |
| 'Culcerans_NCTC7910.fna'    | 'Culcerans_NCTC12077.fna'                   | 94.4  | [92.0 - 96.2] | 66.8  | [63.8 - 69.6] | 92.3  | [89.9 - 94.2] | 0.07             |
| 'Cureicerivorans_IMMI BRIV2301.fna' | Corynebacterium mucifaciens ATCC 700355 | 78.9  | [74.9 - 82.3] | 65.7  | [62.8 - 68.5] | 79.1  | [75.7 - 82.2] | 0.48             |
| 'Crouxii_FRC0190.fna'       | Corynebacterium diphtheriae NCTC 11397      | 75.7  | [71.7 - 79.3] | 49.3  | [46.7 - 51.9] | 71.8  | [68.4 - 75.1] | 0.3              |
| 'Crouxii_FRC0190.fna'       | Corynebacterium diphtheriae DSM 44123       | 77.9  | [73.9 - 81.4] | 49.1  | [46.5 - 51.7] | 73.6  | [70.1 - 76.8] | 0.31             |
| 'Crouxii_FRC0190.fna'       | Corynebacterium belfanti FRC0043           | 73.0  | [69.0 - 76.6] | 45.4  | [42.8 - 47.9] | 68.2  | [64.8 - 71.4] | 0.4              |
| 'Csilvaticum_KL0182.fna'    | 'Culcerans_NCTC12077.fna'                   | 87.1  | [83.5 - 90.0] | 41.0  | [38.5 - 43.6] | 77.6  | [74.1 - 80.7] | 1.06             |
| 'Csilvaticum_KL0182.fna'    | Corynebacterium silvaticum KL0182          | 87.1  | [83.5 - 89.9] | 41.0  | [38.5 - 43.6] | 77.6  | [74.1 - 80.7] | 1.06             |
| 'Csilvaticum_KL0182.fna'    | Corynebacterium silvaticum KL0182          | 91.7  | [88.7 - 94.0] | 40.9  | [38.4 - 43.5] | 81.5  | [78.1 - 84.4] | 1.14             |
| 'Csilvaticum_KL0182.fna'    | 'Culcerans_NCTC7910.fna'                    | 91.7  | [88.7 - 94.0] | 40.9  | [38.4 - 43.5] | 81.5  | [78.2 - 84.5] | 1.13             |
| 'Csilvaticum_KL0182.fna'    | Corynebacterium ulcerans NCTC 7910         | 91.7  | [88.7 - 94.0] | 40.9  | [38.4 - 43.5] | 81.5  | [78.2 - 84.5] | 1.13             |
| 'Csilvaticum_KL0182.fna'    | Corynebacterium pseudotuberculosis DSM 20689 | 82.9  | [79.1 - 86.2] | 28.6  | [26.2 - 31.0] | 65.9  | [62.6 - 69.2] | 2.26             |
| 'Cpseudotuberculosis_31.fna' | 'Csilvaticum_KL0182.fna'                   | 83.5  | [79.7 - 86.7] | 28.5  | [26.1 - 31.0] | 66.3  | [62.9 - 69.6] | 2.28             |
| 'Csilvaticum_KL0182.fna'    | Corynebacterium pseudotuberculosis ATCC 19410 | 82.8  | [78.9 - 86.1] | 28.5  | [26.2 - 31.0] | 65.9  | [62.5 - 69.1] | 2.26             |
| 'Cpseudotuberculosis_31.fna' | Corynebacterium silvaticum KL0182          | 83.5  | [79.7 - 86.7] | 28.5  | [26.1 - 31.0] | 66.3  | [62.9 - 69.5] | 2.28             |
| 'Cpseudotuberculosis_A TCC19410.fna' | 'Csilvaticum_KL0182.fna' | 82.8  | [78.9 - 86.1] | 28.5  | [26.2 - 31.0] | 65.9  | [62.5 - 69.1] | 2.26             |
| 'Cpseudotuberculosis_A TCC19410.fna' | Corynebacterium silvaticum KL0182 | 82.8  | [78.9 - 86.0] | 28.5  | [26.2 - 31.0] | 65.8  | [62.5 - 69.1] | 2.27             |
| 'Csingulare_IBSB52218.fna'  | Corynebacterium minutissimum NCTC 10289    | 67.3  | [63.4 - 71.0] | 27.8  | [25.4 - 30.2] | 54.8  | [51.6 - 57.9] | 0.17             |
| 'Cpseudotuberculosis_A TCC19410.fna' | 'Culcerans_NCTC7910.fna' | 88.1  | [84.6 - 90.8] | 27.7  | [25.3 - 30.2] | 68.9  | [65.5 - 72.2] | 1.13             |
| 'Cpseudotuberculosis_A TCC19410.fna' | 'Culcerans_NCTC7910.fna' | 87.2  | [83.7 - 90.1] | 27.7  | [25.3 - 30.2] | 68.3  | [64.8 - 71.5] | 1.15             |
| 'Cpseudotuberculosis_A TCC19410.fna' | Corynebacterium ulcerans NCTC 7910 | 88.1  | [84.6 - 90.8] | 27.7  | [25.3 - 30.2] | 68.9  | [65.5 - 72.2] | 1.13             |
| Query                      | Subject                                      | $d_0$ | C.I. $d_0$ | $d_4$ | C.I. $d_4$ | $d_s$ | C.I. $d_s$ | Diff. G+C Percent |
|----------------------------|----------------------------------------------|-------|------------|-------|------------|-------|------------|-------------------|
| 'Culcerans_NCTC7910.fna'  | Corynebacterium pseudotuberculosis DSM 20689 | 88.1  | [84.6 - 90.8] | 27.7  | [25.3 - 30.2] | 68.9  | [65.5 - 72.2] | 1.13              |
| 'Culcerans_NCTC7910.fna'  | Corynebacterium pseudotuberculosis ATCC 19410 | 88.1  | [84.6 - 90.8] | 27.7  | [25.3 - 30.2] | 68.9  | [65.5 - 72.2] | 1.13              |
| 'Cpseudotuberculosis_31.fna' | 'Culcerans_NCTC7910.fna'                      | 87.2  | [83.7 - 90.1] | 27.7  | [25.3 - 30.2] | 68.3  | [64.8 - 71.5] | 1.15              |
| 'Culcerans_NCTC12077.fna' | Corynebacterium pseudotuberculosis DSM 20689 | 82.5  | [78.6 - 85.0] | 27.6  | [25.2 - 30.1] | 64.8  | [61.4 - 68.0] | 1.2               |
| 'Cpseudotuberculosis_31.fna' | 'Culcerans_NCTC12077.fna'                     | 82.3  | [78.4 - 85.6] | 27.6  | [25.2 - 30.1] | 64.6  | [61.3 - 67.8] | 1.22              |
| 'Culcerans_NCTC12077.fna' | Corynebacterium pseudotuberculosis ATCC 19410 | 82.5  | [78.6 - 85.0] | 27.6  | [25.2 - 30.1] | 64.8  | [61.4 - 68.0] | 1.2               |
| 'Cpseudotuberculosis_ATCC19410.fna' | 'Culcerans_NCTC12077.fna'                 | 82.5  | [78.6 - 85.0] | 27.6  | [25.2 - 30.1] | 64.8  | [61.4 - 68.0] | 1.2               |
| 'Csingulare_IBSB52218.fna' | Corynebacterium minutissimum NCTC10288     | 67.7  | [63.9 - 71.4] | 27.4  | [25.0 - 29.8] | 54.7  | [51.6 - 57.8] | 0.22              |
| 'Csingulare_IBSB52218.fna' | Corynebacterium minutissimum ATCC 23348     | 67.8  | [63.9 - 71.5] | 27.2  | [24.8 - 29.7] | 54.7  | [51.5 - 57.8] | 0.16              |
| 'Csingulare_IBSB52218.fna' | Corynebacterium minutissimum NBRC 15361     | 67.9  | [64.0 - 71.5] | 27.2  | [24.9 - 29.7] | 54.7  | [51.6 - 57.8] | 0.17              |
### 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          |
|-----------------------------|-----------|----------------|--------------------------------------------------------------------------|------------|-------------|--------------|-------------|----------------------|--------------------|------------------|------------------|
| *Corynebacterium vitaeruminis* DSM 20294 | (Bechdel et al. 1928; Lanéelle et al. 1980) | CCUG 28792; JCM 1323; ATCC 10234; IFO 12143; NBRC 12143; VKM B-1211; CIP 82.07; NCIB 9291; NCIMB 9291 | Brevibacterium vitaeruminis; Corynebacterium vitaeruminis; Flavobacterium vitarumen | 2931 780   | 65.5         | 2577          | Gp0023683 | PRJNA172966          | SAMN03081455       | GCA_000550805 | 2558860221       |
| *Corynebacterium falsenii* DSM 44353 | Sjödén et al. 1998 | CCUG 33651; JCM 11949; CIP 105466; Y13024 | *Corynebacterium falsenii* | 2719 559   | 63.2         | 2306          | Gp0086746 | PRJNA235944          | SAMN02641485       | GCA_000525655 | 2571042744       |
| *Corynebacterium sanguinis* CCUG 58655T | Jaén-Luchoro et al. 2020 | CCM 8873 | *Corynebacterium sanguinis* | 2362 885   | 65.3         | 2243          | Gp0086746 | PRJNA224116          | SAMN10573883       | GCF_007641235 | 2515154018        |
| *Corynebacterium lubricantis* DSM 45231 | Kämpfer et al. 2009 | CCUG 56567; JCM 16607; CCM 7546; KSS-3Se | *Corynebacterium lubricantis* | 2945 292   | 58.6         | 2818          | Gp0013695 | PRJNA165249          | SAMN02256424       | GCA_000379425 | 2515154018        |
| *Corynebacterium doosanense* DSM 45436 | Lee et al. 2009 | KCTC 19568; CCUG 57284; CAU 212 | *Corynebacterium doosanense* | 2649 019   | 66.9         | 2590          | Gp0013691 | PRJNA165377          | SAMN02256506       | GCA_000372245 | 2515154029        |
| *Corynebacterium ulcerovis* DSM 45146 | Yassin 2009 | CCUG 55727; IMMIB L-1395 | *Corynebacterium ulcerovis* | 2300 430   | 59.2         | 2104          | Gp0013740 | PRJNA165381          | SAMN02256494       | GCA_000372445 | 2515154059        |
| *Corynebacterium fournieri* Marseille-P2948 | Diop et al. 2018 | DSM 103271; CSUR P2948 | *Corynebacterium fournieri* | 2357 034   | 65.0         | 2305          | Gp0370410 | PRJE20393            | SAMEA103975581     | GCA_900176865 | 2515154059        |
| Strain                                           | Authority                                      | Other deposits | Synonyms                  | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID       |
|--------------------------------------------------|-----------------------------------------------|----------------|---------------------------|------------|-------------|--------------|-----------|----------------------|--------------------|-------------------|---------------|
| Corynebacterium riegelii DSM 44526               | Funke et al. 1998                            | CCUG 38180; JCM 10389; ATCC 700782; CIP 105310; DMMZ 2415 | Corynebacterium riegelii | 2519 232  | 60.4        | 2283         | PRJNA231221 | SAMN16357283          |                    |                   |               |
| Corynebacterium anserum 23H37-10                 | Liu et al. 2021                              | GDMCC 1.1737; KACC 21672 | Corynebacterium anserum | 2208 656  | 55.2        | 1764         | PRJNA595090 | SAMN13546099          |                    |                   | GCA_014262665 |
| Corynebacterium godavaranum LMG 29598            | Jani et al. 2018                             | MCC 3388; KCTC 39803; PRD07 | Corynebacterium godavaranum | 2521 298  | 65.6        | 2235         | PRJNA555895 | SAMN12335367          |                    |                   | GCA_00759235  |
| Corynebacterium endometriti LMM-1653 T           | Ballas et al. 2020                           | LMG 31164; CCM 8952 | Corynebacterium endometriti | 2477 061  | 60.9        | 2189         | PRJNA224116 | SAMN11357123          |                    |                   | GCF_004795735 |
| Corynebacterium aurimucosum strain DSM 44532     | Yassin et al. 2002 emend. Daneshvar et al. 2004 | NRRL B-24143; CCUG 47449; JCM 11766; IMMIB D-1488 | Corynebacterium aurimucosum | 2737 787  | 60.3        | 2417         | PRJNA231221 | SAMN16357278          |                    |                   | GCA_00062615  |
| Corynebacterium alimapuense CCUG 69366           | Claverias et al. 2019                        | NCIMB 15118; VA37-3 | Corynebacterium alimapuense | 2281 535  | 57.1        | 2040         | Gp0385727  | PRJNA305687           | SAMN08535650       |                   | GCA_003716585 |
| Corynebacterium phoceense MC1                    | Cresci et al. 2016                           | DSM 100570; CSUR P1905 | Corynebacterium phoceense | 2772 735  | 63.2        | 2701         | PRJNA224116 | SAMEA4059842           |                    |                   | GCF_900092335 |
| Corynebacterium diphtheriae subsp. lausannense CHUV2995 | Tagini et al. 2019                        | CCUG 72509; DSM 107520 | Corynebacterium diphtheriae subsp. lausannense | 3060 363  | 53.9        | 3145         | Gp0442955  | PRJEB24256            | SAMEA104679569     |                   | GCA_900312965 |
| Corynebacterium belfantii FRC0043                 | Dazas et al. 2018                            | DSM 105776; CIP 111412 | Corynebacterium belfantii | 2598 827  | 53.6        | 2557         | Gp0364753  | PRJEB22103            | SAMEA104208677     |                   | GCA_900205605 |

**Strain**: Name of the bacterial strain.

**Authority**: Authors of the strain description.

**Other deposits**: Other available strain deposit numbers.

**Synonyms**: Synonyms for the bacterial strain.

**Base pairs**: Number of base pairs.

**Percent G+C**: Percentage of guanine and cytosine.

**No. proteins**: Number of proteins.

**Goldstamp**: The Goldstamp accession number.

**Bioproject accession**: The Bioproject accession number.

**Biosample accession**: The Biosample accession number.

**Assembly accession**: The Assembly accession number.

**IMG OID**: The IMG Object ID.
| Strain                                      | Authority                                      | Other deposits | Synonyms                          | Base pairs | Percent G+C | No. proteins | Goldstamp   | Bioproject accession | Biosample accession | Assembly accession | IMG OID           |
|--------------------------------------------|-----------------------------------------------|----------------|-----------------------------------|------------|-------------|--------------|-------------|----------------------|--------------------|---------------------|-------------------|
| Corynebacterium urogenitale DSM 108747     | Ballas et al. 2020                           |                | Corynebacterium urogenitale       | 2351       | 59.9        | 2058         | PRJNA224116  | SAMN12924940          |                    |                    | GCF_009026825      |
| Corynebacterium frankenforstense ST18      | Wiertz et al. 2013 emend. Nouioui et al. 2018 |                | Corynebacterium frankenforstense  | 2604       | 71.5        | 1801         | Gp0118685    | PRJNA232093          | SAMN02991553        |                    | GCA_001941485      |
| Corynebacterium sphenisci DSM 44792        | Goyache et al. 2003 emend. Nouioui et al. 2018 |                | Corynebacterium sphenisci         | 2594       | 74.7        | 1827         | Gp0118687    | PRJNA232092          | SAMN02996499        |                    | GCA_001941505      |
| Corynebacterium aquilae S-613              | Fernández-Garayzábal et al. 2003 emend. Nouioui et al. 2018 |                | Corynebacterium aquilae           | 2926       | 60.9        | 2013         | Gp0118683    | PRJNA230273          | SAMN02996496        |                    | GCA_001941445      |
| Corynebacterium afermentans DSM 44280      | Riegel et al. 1993 emend. Nouioui et al. 2018 |                | Corynebacterium afermentans; Corynebacterium afermentans subsp. afermentans | 2326       | 64.9        | 2171         | Gp0131801    | PRJEB18848           | SAMN05421802        |                    | GCA_900156035      | 2681813557        |
| Corynebacterium mooreparkense DSM 44702    | Brennan et al. 2001 emend. Nouioui et al. 2018 |                | Corynebacterium mooreparkense     | 3433       | 67.1        | 3039         | Gp0008259    | PRJNAS0001           | SAMN02603088        |                    | GCA_000179395      | 2511231114        |
| Corynebacterium nigricans ATCC 700975      | Shukla et al. 2004 emend. Nouioui et al. 2018 |                | Corynebacterium nigricans         | 2819       | 60.6        | 2551         | Gp0004919    | PRJNA37279           | SAMN02603064        |                    | GCA_000022905      | 643692018         |
| Corynebacterium urinapleomorphum Marseille-P2799 | Niang et al. 2019                            |                | Corynebacterium urinapleomorphum  | 2259       | 63.4        | 2097         | PRJEB18932   | SAMEA47264668        |                    |                    | GCA_900155535      |
| Strain                        | Authority                  | Other deposits                                                                 | Synonyms                     | Base pairs | Percent G+C | No. proteins | Goldstamp       | Bioproject accession | Biosample accession  | Assembly accession   | IMG OID       |
|------------------------------|----------------------------|--------------------------------------------------------------------------------|-------------------------------|------------|-------------|---------------|-----------------|-----------------------|-----------------------|----------------------|---------------|
| *Corynebacterium maris* DSM 45190 | Ben-Dov et al. 2009       | DSM 17018; LMG 24561; JCM 17018; Coryn-1                                       | *Corynebacterium maris*       | 2833       | 547         | 66.6          | 2584            | Gp0023680             | SAMN02603057          | GCA_000442645       | 2561511185   |
| *Corynebacterium silvaticum* KL0182 | Dangel et al. 2020        | DSM 109166; LMG 31313; DSM 11672; CIP 111672                                  | *Corynebacterium silvaticum*  | 2548       | 487         | 54.4          | 2017            | PRJNA517029           | SAMN10039578          | GCA_004382825       |               |
| *Corynebacterium resistens* DSM 45100 | Otsuka et al. 2005 emend. Nouioui et al. 2018 | CCUG 50093; JCM 12819; JTC 2026; GTC 1518; SICGH 185 | *Corynebacterium resistens*   | 2601       | 311         | 57.1          | 2171            | Gp0003835             | PRJNA39683            | SAMN02603065       | GCA_000177535     | 650716029    |
| *Kocuria soli* MSW7-7          | Tuo et al. 2019            | KCTC 49195; CGMCC 1.13744                                                   | *Kocuria soli*                | 2949       | 090         | 67.0          | 2529            | PRJNA501788           | SAMN10345596          | GCA_003797835       |               |
| *Corynebacterium senegalense* Marseille-P4329 | Ndiaye et al. 2019       | CSURP432 9; CCUG 1995; CGMCC 1.13744                                        | *Corynebacterium senegalense* | 2310       | 920         | 68.7          | 2173            | Gp0359219             | SAMEA4664250         | GCA_900411315       |               |
| *Corynebacterium haemomassilien se Marseille-Q3615* | Boxbberger et al. 2020 | CSUR Q3615                                                                     | *Corynebacterium haemomassilen se* | 2578       | 128         | 65.3          | 2331            | PRJNA646616           | SAMN15548222         | GCA_013978595       |               |
| *Corynebacterium striatum* NBRC 15291 | (Chester 1901) Eberon 1918; emend. Nouioui et al. 2018 | CCUG 27949; DSM 20668; JCM 9290; ATCC 6940; IFO 15291; NBRC 15291; NCTC 764; CIP 81.15 | *Bacterium striatum; Corynebacterium striatum* | 3106       | 742         | 59.1          | 2949            | PRJDB8042             | SAMD00169825         | GCA_006538485       |               |
| Strain                              | Authority                        | Other deposits                                                                 | Synonyms                                                                                   | Base pairs | Percent G+C | No. proteins | Goldstamp       | Bioproject accession | Biosample accession | Assembly accession | IMG OID               |
|------------------------------------|----------------------------------|--------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|------------|-------------|--------------|-----------------|----------------------|---------------------|---------------------|---------------------|
| Corynebacterium xerosis ATCC 373   | (Lehmann and Neumann 1896)       |                                                                                   | Bacillus xerosis; Corynebacterium xerosis                                                | 2661       | 69.5        | 1843         | PRJNA280206      | SAMN03458390         | GCA_000988235       |
|                                    | Lehmann and Neumann 1899 emend. |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | Nouioui et al. 2018              |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | CCUG 27544; DSM 20743; JCM 1971; |                                                                                   |                                                                                           | 590        |             |              |                 |                      |                     |                     |                     |
|                                    | ATCC 373; IFO 16721; NBRC 16721; |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | NCTC 11861; CIP 100653           |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | Bacillus diphtheriae; Corynebacterium diphtheriae; Corynebacterium diphtheriae subsp. diphtheriae |                                                                                   |                                                                                           | 2364       | 53.5        | 2116         | PRJNA296455      | SAMN04099181         | GCA_001913265       |
|                                    | (Kruse 1886) Lehmann and Neumann 1896 |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | emend. Nouioui et al. 2018       |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | DSM 44123; ATCC 27010; NCTC 11397; CIP 100721 |                                                                                   |                                                                                           | 574        |             |              |                 |                      |                     |                     |                     |
|                                    | Bacillus diphtheriae; Corynebacterium diphtheriae; Corynebacterium diphtheriae subsp. diphtheriae |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | (Migula 1900) Bergey et al. 1925 |                                                                                   |                                                                                           | 2354       | 46.5        | 2101         | PRJEB6403       | SAMEA4530649         | GCA_900637605       |
|                                    | emend. Nouioui et al. 2018       |                                                                                   |                                                                                           | 887        |             |              |                 |                      |                     |                     |                     |
|                                    | CCUG 27535; DSM 20755; JCM 9385; |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | ATCC 15677; IFO 15288; NBRC 15288; |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | NCTC 11138; CIP 103423           |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | Bacterium kutscheri; Corynebacterium kutscheri |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | (ex Sarkany et al. 1962) Collins and Jones 1983 |                                                                                   |                                                                                           | 2695       | 59.9        | 2463         | PRJEB6403       | SAMEA4030732         | GCA_900478045       |
|                                    | emend. Nouioui et al. 2018       |                                                                                   |                                                                                           | 970        |             |              |                 |                      |                     |                     |                     |
|                                    | CCUG 541; DSM 20651; JCM 9387;   |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | ATCC 23348; IFO 15361; NBRC 15361; |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
|                                    | NCTC 10288; CIP 100652           |                                                                                   |                                                                                           |            |             |              |                 |                      |                     |                     |                     |
| Strain                        | Authority                        | Other deposits               | Synonyms                  | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID         |
|------------------------------|----------------------------------|------------------------------|---------------------------|------------|-------------|--------------|-----------|----------------------|---------------------|-------------------|------------------|
| *Corynebacterium imitans* NCTC 13015 | Funke et al. 1997 emend. Nouioui et al. 2018 | 2023; CCUG 36877; DSM 44264; JCM 10386; ATCC 700354; IFO 16163; NBRC 16163; NBRC 100416; NCTC 13015; CIP 105130 | *Corynebacterium imitans* | 2565 606 | 64.3         | 2347         | PRJEB6403 | SAMEA4535761           | GCA_900187215     |
| *Corynebacterium urealyticum* NCTC12011 | Pitcher et al. 1992 emend. Nouioui et al. 2018 | LMG 19041; CCUG 18158; DSM 7109; JCM 10395; ATCC 43042; NCTC 12011; CIP 103524 | *Corynebacterium urealyticum* | 2377 532 | 64.2         | 2005         | PRJEB6403 | SAMEA4530651           | GCA_900187235     |
| *Corynebacterium jeikeium* NCTC 11913 | Jackman et al. 1988 emend. Nouioui et al. 2018 | CCUG 27192; DSM 46361; DSM 7171; JCM 9384; ATCC 43734; NCTC 11913; CIP 103337 | *Corynebacterium jeikeium* | 2526 027 | 61.4         | 2220         | PRJEB6403 | SAMEA4017703           | GCA_900461185     |
| *Corynebacterium minutissimum* NCTC 10289 | (ex Sarkany et al. 1962) Collins and Jones 1983 emend. Nouioui et al. 2018 | CCUG 541; DSM 20651; JCM 9387; ATCC 23348; IFO 15361; NBRC 15361; NCTC 10288; CIP 100652 | *Corynebacterium minutissimum* | 2736 326 | 59.9         | 2571         | PRJEB6403 | SAMEA104016176         | GCA_900447475     |
| Strain                          | Authority                          | Other deposits                                      | Synonyms                                | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID          |
|--------------------------------|------------------------------------|-----------------------------------------------------|-----------------------------------------|------------|-------------|--------------|------------|----------------------|---------------------|--------------------|-------------------|
| Corynebacterium pilosum NCTC 11862 | Yanagawa and Honda 1978            | CCUG 27193; DSM 20521; JCM 3714; ATCC 29592; IFO 15285; NBRCC 15285; NCTC 11862; CIP 103422 | Corynebacterium pilosum                  | 2593 653   | 60.7        | 2398         | PRJEB6403 | SAMEA4530650          | GCA_900447205      |                    |                  |
| Corynebacterium striatum NCTC 764 | (Chester 1901) Eberon 1918 emend. Nouioui et al. 2018 | CCUG 27949; DSM 20668; JCM 9390; ATCC 6940; IFO 15291; NBRCC 15291; NCTC 764; CIP 81.15 | Bacterium striatum; Corynebacterium striatum | 2924 414   | 59.1        | 2730         | PRJEB6403 | SAMEA4521472          | GCA_900447675      |                    |                  |
| Corynebacterium spheniscorum CCUG 45512 | Goyache et al. 2003 emend. Nouioui et al. 2018 | CCUG 45512; CECT 5986; DSM 44757; JCM 12271; PG 39 | Corynebacterium spheniscorum              | 2456 378   | 57.5        | 2059         | PRJNA563568 | SAMN12771121          | GCA_008693095      |                    |                  |
| Corynebacterium humireducens NBRC 106098 | Wu et al. 2011 emend. Nouioui et al. 2018 | DSM 45992; NBRCC 106098; CGMCC 2452; MFC-5 | Corynebacterium humireducens             | 2609 893   | 68.8        | 2525         | Gp0023682 | PRJDB440             | SAMD00046477        |                  | GCA_001571025      |
| Corynebacterium pseudopelargi CCM 8832 | Busse et al. 2019                  | 812CH; LMG 30627; CCUG 72167 | Corynebacterium pseudopelargi             | 2348 160   | 57.9        | 2199         | Gp0379416 | PRJNA224116           | SAMN08449372        |                  | GCF_003814005      |
| Corynebacterium tuscaniense CCUG 51321 | Riegel et al. 2006                 | DSM 45101; JCM 15294; ATCC BAA-1141; ISS-5309 | Corynebacterium tuscaniense              | 2232 117   | 59.4        | 2073         | PRJNA224116 | SAMN12771122          | GCF_008693065       |                  |                  |
| Strain                        | Authority                  | Other deposits | Synonyms                                                                 | Base pairs | Percent G+C | No. proteins | Goldstamp Accession | Bioproject Accession | Biosample Accession | Assembly Accession | IMG OID         |
|------------------------------|----------------------------|----------------|--------------------------------------------------------------------------|------------|-------------|--------------|---------------------|---------------------|--------------------|------------------|-----------------|
| *Corynebacterium halotolerans* DSM 44683 | Chen et al. 2004, Nouioui et al. 2018 | DSM 44683; JCM 12676; CCTCC AA 001024; YIM 70093 | *Corynebacterium halotolerans* | 3202 | 68.4 | 2914 | Gp0013694 | PRJNA215338 | SAMN02743911 | GCA_000688435 | 2556921045 |
| *Corynebacterium variabile* NBRC 15286 | (Müller 1961) Collins 1987 | NRRL B-4201; CCUG 45246; DSM 20132; JCM 2154; ATCC 15753; IFO 15286; VKM Ac-1122; CIP 102112; HAMBI 1872; NCIB 9455; NCIMB 9455 | *Arthrobacter variabilis, Corynebacterium variabile* | 3170 | 67.4 | 2983 | | PRJDB6001 | SAMD00097555 | GCA_006539825 |
| *Corynebacterium tapiri* LMG 28165 | Baumgardt et al. 2015 | 2385/12; CCUG 65466 | *Corynebacterium tapiri* | 2246 | 62.3 | 2045 | | PRJNA545602 | SAMN11928016 | GCA_006334925 |
| *Corynebacterium rouxii* FRC0190 T | Badell et al. 2020 | DSM 110354; CIP 111752 | *Corynebacterium rouxii* | 2451 | 53.2 | 2365 | | PRJNA224116 | SAMEA5992727 | GCF_902702935 |
| *Corynebacterium mucifaciens* ATCC 706555 | Funke et al. 1997 | CCUG 36878; DSM 44265; JCM 10384; CIP 105129; DMMZ 2278 | *Corynebacterium mucifaciens* | 2180 | 65.5 | 2028 | | PRJNA622446 | SAMN14517857 | GCA_012396315 |
| *Corynebacterium spheniscorum* DSM 44757 | Goyache et al. 2003, Nouioui et al. 2018 | CCUG 45512; CECT 5986; DSM 44757; JCM 12271; PG 39 | *Corynebacterium spheniscorum* | 2451 | 57.5 | 2156 | Gp0102878 | PRJNA262359 | SAMN05660282 | GCA_900113445 | 2599185219 |
| Strain                          | Authority | Other deposits | Synonyms                  | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID   |
|--------------------------------|-----------|----------------|---------------------------|------------|-------------|--------------|-----------|----------------------|---------------------|-------------------|-----------|
| *Corynebacterium pelargi* DSM 46737 | Kämpfer et al. 2015 | 136/3; DSM 28174; DSM 46737; CCM 8517; CIP 110778 | *Corynebacterium pelargi* | 2370/060 | 58.2 | 2169 | Gp0442046 | PRJNA224116 | SAMN06041739 | GCA_004114895 |
| *Corynebacterium hadale* NBT06-6 | Wei et al. 2018 | MCC 1K03347; DSM 105365 | *Corynebacterium hadale* | 2679/199 | 65.2 | 2362 | Gp0374689 | PRJNA396693 | SAMN07460149 | GCA_002273005 |
| *Corynebacterium pollutisoli* VDS | Negi et al. 2016 | MCC 2722; KCTC 39687; DSM 100104; VDS11 | *Corynebacterium pollutisoli* | 2535/040 | 68.5 | 2430 | Gp0156991 | PRJEB20263 | SAMN06295981 | GCA_900177745 |
| *Corynebacterium yudongzhengii* 2183 | Zhu et al. 2020 | DSM 106264; CGMCC 1.16416 | *Corynebacterium yudongzhengii* | 2511/302 | 64.9 | 2142 | PRJNA431327 | SAMN08388720 | GCA_003065405 |
| *Corynebacterium provencense* SN15 | Lo et al. 2019 | DSM 101074; CSURP216 1; Marseille-P2161 | *Corynebacterium provencense* | 3075/769 | 66.9 | 2799 | PRJEB12691 | SAMEA3869306 | GCA_900049755 |
| *Corynebacterium bouchesdurhone nse* SN14 | Lo et al. 2019 | DSM 100846; CSURP206 7; Marseille-P2067 | *Corynebacterium bouchesdurhone nse* | 2255/535 | 68.0 | 2147 | PRJEB13138 | SAMEA3905754 | GCA_900078305 |
| *Corynebacterium pseudotuberculosis* ATCC 19410 | (Buchanan 1911) Eberon 1918 emend. Nouioui et al. 2018 | CCUG 2806; DSM 20689; JCM 9389; ATCC 19410; IFO 15363; NBRC 15363; NCTC 3450; CIP 102968 | *Bacillus pseudotuberculosis*; *Corynebacterium pseudotuberculosis* | 2337/763 | 52.2 | 2146 | Gp0223239 | PRJNA382169 | SAMN06701041 | GCA_002155265 |
| Strain                          | Authority                  | Other deposits           | Synonyms                                | Base pairs | Percent G+C | No. proteins | Goldstamp        | Bioproject accession | Biosample accession | Assembly accession | IMG OID       |
|--------------------------------|----------------------------|--------------------------|-----------------------------------------|------------|-------------|--------------|------------------|----------------------|---------------------|---------------------|---------------|
| *Dermabacter jinjuensis* 32   | Park et al. 2016           | DSM 101003; NCCP 16133  | *Dermabacter jinjuensis*               | 2398       | 62.9        | 1996         | Gp0266532        | PRJNA407870          | SAMN07665299       | GCA_002443115    |               |
| *Corynebacterium jeddahense* JCB | Edouard et al. 2017       | DSM 45997; CSUR P778    | *Corynebacterium jeddahense*           | 2472       | 67.2        | 2341         | Gp0101187        | PRJEB4941            | SAMEA3138931       | GCA_000577555    |               |
| *Corynebacterium pseudotuberculosis* DSM 20689 | (Buchanan 1911) Eberson 1918 emend. Nouiou et al. 2018 | CCUG 2806; DSM 20689; JCM 9389; ATCC 19410; IFO 15363; NBRC 15363; NCTC 3450; CIP 102968 | Bacillus pseudotuberculosis; *Corynebacterium pseudotuberculosis* | 2338       | 52.2        | 2084         | Gp0220522        | PRJNA442833          | SAMN08778220       | GCA_003634885    | 2756170169    |
| *Corynebacterium ulcerans* NCTC 7910 | (ex Gilbert and Stewart 1927) Riegel et al. 1995 | CCUG 2708; DSM 46325; JCM 10387; ATCC 5179; CIP 106504 | *Corynebacterium ulcerans*           | 2453       | 53.3        | 2178         | Gp0262745        | PRJEB6403            | SAMEA4504038       | GCA_900187135    |               |
| *Corynebacterium aquatimens* DSM 45632 | Aravena-Román et al. 2012 | CCUG 61574; IMMIB L-2475 | *Corynebacterium aquatimens*           | 2525       | 61.0        | 2230         | Gp0305023        |                     |                     |               | 2880529280    |
| *Corynebacterium coyleae* DSM 44184 | Funke et al. 1997         | CCUG 38194; JCM 10381; ATCC 700219; CIP 104919; DMMZ 214 | *Corynebacterium coyleae*              | 2568       | 61.3        | 2419         | Gp0116505        | PRJNA303722          | SAMN04488531       | GCA_900105505    | 2634166170    |
| Strain                          | Authority                         | Other deposits | Synonyms                                                                 | Base pairs | Percent G+C | No. proteins | Goldstamp        | Bioproject accession | Biosample accession | Assembly accession | Assembly accessions | IMG OID            |
|--------------------------------|-----------------------------------|----------------|--------------------------------------------------------------------------|------------|-------------|--------------|-----------------|----------------------|---------------------|---------------------|---------------------|---------------------|
| *Corynebacterium mycetoides* DSM 20632 | (ex Castellani 1942) Collins 1983 emend. Nouioui et al. 2018 | CCUG 27538; JCM 9388; ATCC 43995; IFO 15289; NBRC 15289; NCTC 9864; CIP 55.51 | *Corynebacterium mycetoides* | 2266       | 66.6        | 2129         | Gp0116506       | PRJNA303721           | SAMN04488535         | GCA_900103625       | 2634166344         |
| *Corynebacterium accolens* ATCC 49725 | Neubauer et al. 1991 emend. Nouioui et al. 2018 | CNCTC Th 1/57; CCUG 28779; DSM 44278; JCM 8331; CIP 104783 | *Corynebacterium accolens* | 2406       | 59.7        | 2333         | Gp0003417       | PRJNA31443            | SAMN00002226         | GCA_000159115       | 643886058          |
| *Corynebacterium striatum* ATCC 6940 | (Chester 1901) Eberson 1918 emend. Nouioui et al. 2018 | CCUG 27949; DSM 20668; JCM 9390; ATCC 6940; IFO 15291; NBRC 15291; NCTC 764; CIP 81.15 | *Bacterium striatum; Corynebacterium striatum* | 2717       | 59.4        | 2677         | Gp0003467       | PRJNA31449            | SAMN00001507         | GCA_000159135       | 643886057          |
| *Corynebacterium amycolatum* ATCC 49368 | Collins et al. 1988 | CCUG 35685; DSM 6922; JCM 7447; IFO 15207; NBRC 15207; CIP 103452; NCFB 2768; NCIMB 13130; S160 | *Corynebacterium amycolatum* | 2448       | 58.7        | 2128         | PRJNA224116     | SAMN07741515           | GCA_014335175         |                       |                     |
| *Corynebacterium auriscanis* CIP 106629 | Collins et al. 2000 emend. Nouioui et al. 2018 | CCUG 39938; DSM 44609; JCM 12369; M598/96/1 | *Corynebacterium auriscanis* | 2568       | 58.5        | 1537         | Gp0107708       | PRJNA262562            | SAMN03106126         | GCA_000767255       |                     |
| Strain               | Authority                                  | Other deposits                                                                 | Synonyms                      | Base pairs | Percent G+C | No. proteins | Goldstamp         | Bioproject accession | Biosample accession | Assembly accession | IMG OID        |
|---------------------|--------------------------------------------|--------------------------------------------------------------------------------|--------------------------------|------------|-------------|--------------|-------------------|----------------------|--------------------|---------------------|------------------|
| *Corynebacterium*   |                                            |                                                                               |                                |            |             |              |                   |                      |                    |                    |                  |
| *humireducens*      |                                          |                                                                               |                                |            |             |              |                   |                      |                    |                    |                  |
| DSM 45392           | Wu et al. 2011 emend. Nouioui et al. 2018 | DSM 45392, NBRC 106098, CGMCC 2452, MFC-5                                      | *Corynebacterium humireducens* | 2681       | 68.6        | 2545         | Gp0023681        | PRJNA172965          | SAMN03283197       | GCA_000819445     |                  |
| *imitans* DSM 44264 | Funke et al. 1997 emend. Nouioui et al. 2018 | 2023; CCUG 36877, DSM 4264, JCM 10386, ATCC 700354, IFO 16163, NBRC 16163, NBRC 100416, NCTC 13015, CIP 105130 | *Corynebacterium imitans*    | 2565       | 64.3        | 2013         | Gp0094474        | PRJNA246650          | SAMN02950575       | GCA_000739455     |                  |
| *kutscheri* DSM 20755 | (Migula 1900) Bergey et al. 1925 emend. Nouioui et al. 2018 | CCUG 27535, DSM 20755, JCM 9385, ATCC 15677, IFO 15288, NBRC 15288, NCTC 11138, CIP 103423 | *Bacterium kutscheri*, *Corynebacterium kutscheri* | 2354       | 46.5        | 2047         | Gp0110293        | PRJNA276037          | SAMN03365283       | GCA_000980835     |                  |
| *marinum* DSM 44953 | Du et al. 2010 emend. Nouioui et al. 2018 | 7015; NRRL B-24779, DSM 44953, CGMCC 1.6998, D7015                              | *Corynebacterium marinum*     | 2729       | 67.8        | 2550         | Gp0023707        | PRJNA172963          | SAMN02800399       | GCA_000835165     |                  |
| *mustelae* DSM 45274 | Funke et al. 2010 emend. Nouioui et al. 2018 | 3105; CCUG 57279                                                             | *Corynebacterium mustelae*    | 3474       | 52.6        | 3110         | Gp0114696        | PRJNA282348          | SAMN03568800       | GCA_001020985     |                  |
| Strain                          | Authority                                      | Other deposits | Synonyms                  | Base pairs | Percent G+C | No. proteins | Goldstamp   | Bioproject accession | Biosample accession | Assembly accession | IMG OID          |
|--------------------------------|------------------------------------------------|----------------|---------------------------|------------|-------------|--------------|-------------|---------------------|---------------------|-------------------|-------------------|
| Corynebacterium singulare DSM 44557 | Riegel et al. 1997 emend. Nouioui et al. 2018 | CCUG 37330; JCM 10385; IFO 16162; NBRRC 16162; CIP 105491; IBS BS2218 | Corynebacterium singulare | 2830 499   | 60.1        | 2561         | Gp0109683   | PRJNA246651          | SAMN03177398       | GCA_000833575     |
| Corynebacterium testudinoris DSM 44614 | Collins et al. 2001 emend. Nouioui et al. 2018 | CCUG 41823; JCM 12108; CIP 106763; M935/96/4 | Corynebacterium testudinoris | 2721 226   | 63.1        | 2560         | Gp0114695   | PRJNA280910          | SAMN03480629       | GCA_001021045     |
| Corynebacterium ureicelerivorans DSM 45051 | Yassin 2007 emend. Nouioui et al. 2018 | CCUG 53377; JCM 15295; IMMIB RIV-2301 | Corynebacterium ureicelerivorans | 2328 188   | 65.0        | 1922         | Gp0103378   | PRJNA257688          | SAMN02953970       | GCA_000747315     |
| Corynebacterium uterequi DSM 45634 | Hoyles et al. 2013 emend. Nouioui et al. 2018 | CCUG 61235; VM 2298 | Corynebacterium uterequi | 2419 437   | 65.5        | 2163         | Gp0114697   | PRJNA280912          | SAMN03480647       | GCA_001021065     |
| Corynebacterium lactis DSM 45799 | Wiertz et al. 2013 emend. Nouioui et al. 2018 | CCUG 63372; RW2-5 | Corynebacterium lactis | 2769 745   | 60.5        | 2364         | Gp0067969   | PRJNA222474          | SAMN04012704       | GCA_001274895     |
| Corynebacterium glyciniphilum ATCC 21341 (ex Kubota et al. 1972) Al-Dilaimi et al. 2015 | | | Corynebacterium glyciniphilum | 3568 218   | 64.8        | 3270         | Gp0047724   | PRJNA221205          | SAMN03081498       | GCA_000626675     | 2576861442     |
| Corynebacterium epidermidicanis DSM 45586 | Frischmann et al. 2012 emend. Nouioui et al. 2018 | 410; LMG 26322; CCUG 60915 | Corynebacterium epidermidicanis | 2692 072   | 58.1        | 2465         | Gp0114694   | PRJNA280479          | SAMN03462986       | GCA_001021025     |
| Corynebacterium minutissimum ATCC 23348 (ex Sarkany et al. 1962) Collins and Jones 1983 emend. Nouioui et al. 2018 | | | Corynebacterium minutissimum | 2663 401   | 60.0        | 2276         | Gp0122002   | PRJNA264738          | SAMN03140311       | GCA_000805675     |
| Strain                        | Authority | Other deposits                  | Synonyms                                      | Base pairs | Percent G+C | No. proteins | Goldstamp   | Bioproject accession | Biosample accession | Assembly accession | IMG OID        |
|------------------------------|-----------|---------------------------------|-----------------------------------------------|------------|-------------|--------------|-------------|----------------------|---------------------|-------------------|---------------|
| *Corynebacterium minutissimum* NBRC 15361 | (ex Sarkany et al. 1962) Collins and Jones 1983; Nouioui et al. 2018 | CCUG 541; DSM 20651; JCM 9387; ATCC 23348; IFO 15361; NBRC 15361; NCTC 10288; CIP 100652 | *Corynebacterium minutissimum*              | 2663       | 60.0        | 2464         | Gp0024448   | PRJDB438               | SAMD00046517      | GCA_001552395    |
| *Corynebacterium halotolerans* YIM 70093 | Chen et al. 2004; Nouioui et al. 2018 | DSM 44683; JCM 12676; CCTCC AA 001024; YIM 70093 | *Corynebacterium halotolerans*               | 3222       | 68.3        | 2865         | Gp0023456   | PRJNA168616             | SAMN02603027      | GCA_000341345    | 2524023198     |
| *Corynebacterium xerosis* NBRC 16721 | (Lehmann and Neumann 1896); Lehmann and Neumann 1899; Nouioui et al. 2018 | CCUG 27544; DSM 20743; JCM 1971; ATCC 373; IFO 16721; NBRC 16721; NCTC 11861; CIP 100653 | *Bacillus xerosis*; *Corynebacterium xerosis* | 2686       | 69.7        | 2351         | Gp0024449   | PRJDB439               | SAMD00046521      | GCA_001552415    |
| *Corynebacterium nuruki* S6-4 | Shin et al. 2011; Nouioui et al. 2018 | DSM 45595; JCM 17162; KACC 15032 | *Corynebacterium nuruki*                     | 3106       | 69.5        | 2787         | Gp0011122   | PRJNA66913              | SAMN02470217      | GCA_000213935    | 2547132106     |
| *Corynebacterium glutamicum* ATCC 13032 | (Kinoshita et al. 1958); Abe et al. 1967; Nouioui et al. 2018 | LMG 3730; NRRL B-2784; CCUG 27702; DSM 20300; JCM 1318; IFD 12168; NBRC 12168; CIP 82.08; HAMBI 2052 | *Corynebacterium glutamicum*; *Micrococcus glutamicus* | 3282       | 53.8        | 3057         | Gp0000615   | PRJNA13760              | SAMEA3138338      | GCA_000196335    | 639279306      |
| Strain                        | Authority                      | Other deposits                  | Synonyms                      | Base pairs | Percent G+C | No. proteins | Goldstamp     | Bioproject accession | Biosample accession | Assembly accession | IMG OID     |
|------------------------------|--------------------------------|--------------------------------|-------------------------------|------------|-------------|--------------|---------------|---------------------|---------------------|-------------------|-------------|
| *Corynebacterium urealyticum* DSM 7109 | Pitcher et al. 1992 emend. Nouioui et al. 2018 | LMG 19041; CCUG 18158; DSM 7109; JCM 10395; ATCC 43042; NCTC 12011; CIP 103524 | *Corynebacterium urealyticum* | 2369 219  | 64.2        | 2024         | Gp0001357     | PRJNA29211         | SAMEA3138282       | GCA_000069945    | 641522620  |
| *Corynebacterium marinum* CGMCC 1.6998 | Du et al. 2010 emend. Nouioui et al. 2018 | 7015; NRRL B-24779; DSM 44953; CGMCC 1.6998; D7015 | *Corynebacterium marinum* | 2680 020  | 67.9        | 2569         | PRJDB10509     | SAMD00245145       | GCA_014645275     | 67044904601     | 67044904601  |
| *Dermabacter vaginalis* AD1-86 | Chang et al. 2016 | KCTC 39585; DSM 100050 | *Dermabacter vaginalis* | 2392 314  | 62.6        | 2129         | Gp0203766      | PRJNA286956        | SAMN03774729       | GCA_001678905    | 67044904601  |
| *Rhodococcus opacus* DSM 43205 | Klatte et al. 1995 | DSM 43205; JCM 9703; ATCC 51881; IFO 16217; NBRC 16217; NBRC 100624; CIP 104549 | *Rhodococcus opacus* | 8534 314  | 67.3        | 7425         | Gp0150346      | PRJNA224116        | SAMN04357312       | GCF_001646735    | 67044904601  |
| *Corynebacterium pacaense* Marseille-P2417 T | Bellali et al. 2019 | CSUR P2417 | *Corynebacterium pacaense* | 3027 822  | 63.7        | 2736         | PRJEB19973     | SAMEA103910525     | GCA_900169525     | 67044904601    | 67044904601  |
| Strain                          | Authority                        | Other deposits                                                                 | Synonyms                      | Base pairs | Percent G+C | No. proteins | Goldstamp      | Bioproject accession | Biosample accession | Assembly accession | IMG OID          |
|--------------------------------|----------------------------------|--------------------------------------------------------------------------------|-------------------------------|------------|-------------|--------------|----------------|----------------------|---------------------|--------------------|-------------------|
| Corynebacterium pilosum CIP 103422 | Yanagawa and Honda 1978         | CCUG 27193; DSM 20521; JCM 3714; ATCC 29592; IFO 15285; NBRC 15285; NCTC 11862; CIP 103422 | Corynebacterium pilosum       | 2545 970   | 60.7        | 2772         | Gp0120674      | PRJNA284680           | SAMN03731012       | GCA_001044155     |                  |
| Corynebacterium bovis DSM 20582   | Bergey et al. 1923               | CCUG 2705; JCM 11947; ATCC 7715; NCTC 3224; CIP 54.80                          | Corynebacterium bovis         | 2694 851   | 72.9        | 2169         | Gp0325157      | PRJNAS46935           | SAMN12024754       | GCA_014191555     | 2824244109       |
| Corynebacterium dentalis Marseille-P4122 | Benabdellaker et al. 2020     | CSURP4122                                                                     | Corynebacterium dentalis     | 2302 937   | 59.9        | 2080         | PRJNA224116     | SAMEA104348950       | GCF_900232865      |                   |                  |
| Corynebacterium lowii LMG 28276   | Bernard et al. 2016              | CCUG 65815; NML 130206; R-50085; TKD4                                         | Corynebacterium lowii        | 2354 433   | 62.9        | 2108         | PRJNA224116     | SAMN04091594           | GCF_001412085      |                   |                  |
| Corynebacterium durum DSM 45333   | Riegel et al. 1997              | CCUG 37331; DSM 44351; JCM 11948; CIP 105490; IBS G15036                      | Corynebacterium durum        | 2800 016   | 57.2        | 2613         | Gp0456002      | PRJNA431327           | SAMN08388739       | GCA_003070865     | 2856490523       |
| Corynebacterium liangguodongii 2184 | Zhu et al. 2020                | DSM 106202; CGMCC 1.16417                                                    | Corynebacterium liangguodongii | 2357 924   | 66.1        | 2115         | PRJNA431327     | SAMN08388739           | GCA_003070865     |                   |                  |
| Strain                          | Authority                  | Other deposits                                      | Synonyms                          | Base pairs | Percent G+C | No. proteins | Goldstamp     | Bioproject accession | Biosample accession | Assembly accession | IMG OID      |
|--------------------------------|----------------------------|-----------------------------------------------------|-----------------------------------|------------|-------------|--------------|---------------|----------------------|---------------------|-------------------|-------------|
| Corynebacterium jeikeium ATCC 43734 | Jackman et al. 1988 emend. Nouioui et al. 2018 | CCUG 27192; DSM 46361; DSM 7171; JCM 9384; ATCC 43734; NCTC 11913; CIP 103337 | Corynebacterium jeikeium          | 2425       | 61.6        | 2224         | Gp0004510     | PRJNA31445          | SAMN00001506      | GCA_000163435   | 647000231   |
| Corynebacterium neomassiliense Marseille-P3888 | Boxberger et al. 2020 | CCUG7235 2; CSURP388 8 | Corynebacterium neomassiliense | 3139       | 66.9        | 2729         | PRJNA224116    | SAMEA5140071      | GCF_900626215     |                   |             |
| Corynebacterium diphtheriae NCTC 11397 | (Kruse 1886) Lehmann and Neumann 1896 emend. Nouioui et al. 2018 | DSM 44123; ATCC 27010; NCTC 11397; CIP 100721 | Bacillus diphtheriae; Corynebacterium diphtheriae; Corynebacterium diphtheriae subsp. diphtheriae | 2463       | 53.5        | 2337         | Gp0132011      | PRJEB6403          | SAMEA2517360      | GCA_001457455   |             |
| Corynebacterium argentoratense DSM 44202 | Riegel et al. 1995 emend. Nouioui et al. 2018 | CCUG 34893; JCM 10392; ATCC 51927; CIP 104296; IBS B10697 | Corynebacterium argentoratense | 2031       | 58.9        | 1875         | Gp0044215      | PRJNA209048        | SAMN02603032      | GCA_000590555   | 2554235426   |
| Corynebacterium terpenotabidum Y-11 | Takeuchi et al. 1999 | DSM 44721; JCM 10555; IFO 14764; NRBC 14764; VKM Ac-2071; CIP 105927 | Corynebacterium terpenotabidum | 2751       | 67.0        | 2369         | Gp0022753      | PRJNA168617        | SAMN02603028      | GCA_000418365   | 2554235357   |
| Ckutscheri_DSM 20755.fna         |                            |                                                     |                                   | 2354       | 46.5        | 2113         |               |                     |                     |                  |             |
| Clactis_RW25.fna                 |                            |                                                     |                                   | 2769       | 60.5        | 2455         |               |                     |                     |                  |             |
| Cmarinum_DSM 44953.fna           |                            |                                                     |                                   | 2729       | 67.8        | 2543         |               |                     |                     |                  |             |
| Strain                        | Authority            | Other deposits | Synonyms                      | Base pairs | Percent G+C | No. proteins | Goldstamp | Bioproject accession | Biosample accession | Assembly accession | IMG OID |
|------------------------------|----------------------|----------------|-------------------------------|------------|-------------|--------------|-----------|----------------------|--------------------|-------------------|---------|
| Cmaris_DSM451 90.fna         |                      |                |                               | 2833       | 66.6        | 2608         |           |                      |                    |                   |         |
| Cmustelae_DSM 45274.fna      |                      |                |                               | 3474       | 52.6        | 3146         |           |                      |                    |                   |         |
| Cpseudotuberculosis ATCC1941 0.fna |            |                |                               | 2297       | 52.2        | 2123         |           |                      |                    |                   |         |
| CriegeliiPUDD83 A45.fna      |                      |                |                               | 2563       | 60.5        | 2402         |           |                      |                    |                   |         |
| Crouxii_FRC0190 .fna         |                      |                |                               | 2451       | 53.2        | 2366         |           |                      |                    |                   |         |
| Csilvaticum_KL0 182.fna      |                      |                |                               | 2553       | 54.4        | 2537         |           |                      |                    |                   |         |
| Csimulans_PES1 .fna          |                      |                |                               | 2737       | 59.0        | 2566         |           |                      |                    |                   |         |
| Csingulare_IBSB 5221B.fna    |                      |                |                               | 2830       | 60.1        | 2596         |           |                      |                    |                   |         |
| Cterpenotabidum m_Y11.fna    |                      |                |                               | 2751       | 67.0        | 2406         |           |                      |                    |                   |         |
| Ctestudinoris_DS M44614.fna  |                      |                |                               | 2721       | 63.1        | 2577         |           |                      |                    |                   |         |
| Culcerans_NCTC 7910.fna      |                      |                |                               | 2453       | 53.3        | 2207         |           |                      |                    |                   |         |
| Culcerans_NCTC 12077.fna     |                      |                |                               | 2616       | 53.4        | 2454         |           |                      |                    |                   |         |
| Curealyticum_DS M7109.fna    |                      |                |                               | 2369       | 64.2        | 2011         |           |                      |                    |                   |         |
| Cureicelevororan s_3MMIBRIV230 1.fna |          |                |                               | 2328       | 65.0        | 2298         |           |                      |                    |                   |         |
| Cuterequi_DSM4 5634.fna      |                      |                |                               | 2419       | 65.5        | 2184         |           |                      |                    |                   |         |
| Cvitaeruminis_D SM20294.fna  |                      |                |                               | 2931       | 65.5        | 2604         |           |                      |                    |                   |         |
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 2021-02-09. 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 14130 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

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 \( d_5 \) [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 103 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 85 species clusters and the provided query strains were assigned to 19 of these. Moreover, user strains were located in 19 of 87 subspecies clusters.

Figure caption SSU tree

**Figure 1.** 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 76.6 %. The tree was rooted at the midpoint [7].

Figure caption genome tree

**Figure 2.** 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 41.3 %. The tree was rooted at the midpoint [7].
References

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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 $d_6$ and $d_8$ 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                      |
|-----------------|-----------------------------|-------------------------------|-----------------------------|
| 'Mtuberculosis_H37Rv' | belongs to known species    | Mycobacterium tuberculosis   |                             |
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. | $d_4$    | C.I. | $d_6$    | C.I. | Diff. G+C Percent |
|----------------|--------------------------|----------|------|----------|------|----------|------|------------------|
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium tuberculosis H37Rv | 100.0    | [100.0 - 100.0] | 100.0    | [100.0 - 100.0] | 100.0    | [100.0 - 100.0] | 0.0  |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium microti ATCC 19422 | 98.6     | [97.6 - 99.2] | 98.7     | [98.0 - 99.1] | 99.3     | [98.8 - 99.6] | 0.27 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium caprae ATCC BAA-824 | 99.5     | [99.0 - 99.8] | 97.9     | [97.0 - 98.6] | 99.7     | [99.4 - 99.8] | 0.04 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium africanum ATCC 25420 | 99.6     | [99.3 - 99.8] | 97.8     | [96.9 - 98.5] | 99.8     | [99.6 - 99.9] | 0.07 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium bovis ATCC 19210 | 99.4     | [98.8 - 99.7] | 97.5     | [96.5 - 98.2] | 99.6     | [99.3 - 99.8] | 0.06 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium pinnipedii ATCC BAA-688 | 99.7     | [99.4 - 99.9] | 97.4     | [96.3 - 98.1] | 99.8     | [99.6 - 99.9] | 0.02 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium decipiens TBL 1200985 | 45.8     | [42.5 - 49.3] | 30.2     | [27.8 - 32.7] | 41.2     | [38.2 - 44.2] | 0.1  |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium shinjukuense CCUG 53584 | 39.3     | [36.0 - 42.8] | 25.8     | [23.5 - 28.3] | 34.9     | [31.9 - 38.0] | 2.14 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium shinjukuense JCM 14233 | 40.0     | [36.6 - 43.4] | 25.7     | [23.4 - 28.2] | 35.3     | [32.4 - 38.4] | 2.17 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium lacus JCM 15657 | 33.6     | [30.2 - 37.2] | 24.8     | [22.5 - 27.3] | 30.4     | [27.5 - 33.5] | 1.33 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium marinum DSM 44344 | 21.1     | [17.9 - 24.7] | 22.2     | [19.9 - 24.6] | 20.4     | [17.6 - 23.4] | 0.08 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium marinum NCTC 2275 | 21.0     | [17.8 - 24.6] | 22.1     | [19.9 - 24.6] | 20.2     | [17.5 - 23.3] | 0.05 |
| 'Mtuberculosis_H37Rv.fn a' | Mycobacterium marinum CCUG 20998 | 21.1     | [17.9 - 24.8] | 22.1     | [19.8 - 24.6] | 20.4     | [17.6 - 23.4] | 0.1  |
## 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          |
|-------------------------------|--------------------------------|-----------------------------------------|------------------------------------------------|------------|-------------|--------------|---------------|----------------------|---------------------|-------------------|-------------------|
| Mycobacterium bovis ATCC 19210 | Karlson and Lessel 1970       | NCTC 10772; CIP 105234                  | Mycobacterium bovis; Mycobacterium bovis subsp. bovis | 4303 498   | 65.6        | 4048         | PRJNA377261   | SAMN06462278        | GCA_002982285       |                   |                   |
| Mycobacterium africanum ATCC 25420 | Castets et al. 1969           | CIP 105147                              | Mycobacterium africanum                         | 4351 982   | 65.5        | 4043         | PRJNA224116   | SAMN06462277        | GCF_002982335       |                   |                   |
| Mycobacterium pinnipedi ATCC BAA-688 | Cousins et al. 2003       | 6482; NCTC 13288                         | Mycobacterium pinnipedi                         | 4324 277   | 65.6        | 4036         | PRJNA224116   | SAMN06462281        | GCF_002982275       |                   |                   |
| Mycobacterium marinum CCUG 20998 | Aronson 1926                  | CCUG 20998; CCUG 27843; DSM 43225; DSM 44344; JCM 12275; ATCC 927; NCTC 2275; CIP 104528 | Mycobacterium marinum                       | 6453 310   | 65.7        | 5434         | PRJNA414525   | SAMN07792364        | GCA_003391395       |                   |                   |
| Mycobacterium tuberculosis H37Rv | (Zopf 1883) Lehmann and Neumann 1896 emend. Riojas et al. 2018 | ATCC 27294                              | Bacterium tuberculosis; Mycobacterium tuberculosis; Mycobacterium tuberculosis subsp. tuberculosis | 4411 532   | 65.6        | 4018         | Gp00000774    | SAMEA3138326        | GCA_000195955       | 637000173        |                   |
| Mycobacterium shinjukuense JCM 14233 | Saito et al. 2011 emend. Nouiou et al. 2018 | CCUG 53584; DSM 45663; JCM 14233; GTC 2738 | Mycobacterium shinjukuense                   | 4504 020   | 67.8        | 4119         | PRJDB7717     | SAMD00153190        | GCA_010730055       |                   |                   |
| Strain                     | Authority                        | Other deposits                                                                 | Synonyms                                                                 | Base pairs | Percent G+C | No. proteins | Goldstamp accession | Bioproject accession | Biosample accession | Assembly accession | IMG OID         |
|----------------------------|----------------------------------|--------------------------------------------------------------------------------|--------------------------------------------------------------------------|------------|-------------|--------------|---------------------|----------------------|---------------------|-------------------|-----------------|
| **Mycobacterium lacus JCM 15657** | Turenne et al. 2002 emend. Nouioui et al. 2018 | DSM 44577; JCM 15657; ATCC BAA-323; NRCM 00-255 | Mycobacterium lacus                                                      | 5092       | 66.9        | 4794         | PRJDB7717            | SAMD00153198        | GCA_010731535     |                  |                 |
| **Mycobacterium marinum DSM 44344** | Aronson 1926                     | CCUG 20998; CCUG 27843; DSM 43225; DSM 44344; JCM 12275; ATCC 927; NCTC 2275; CIP 104528 | Mycobacterium marinum                                                      | 6269       | 65.7        | 5516         | PRJNA414948           | SAMN07811439        | GCA_003431645     |                  |                 |
| **Mycobacterium marinum NCTC 2275** | Aronson 1926                     | CCUG 20998; CCUG 27843; DSM 43225; DSM 44344; JCM 12275; ATCC 927; NCTC 2275; CIP 104528 | Mycobacterium marinum                                                      | 6318       | 65.7        | 5601         | PRJNA414948           | SAMN07811438        | GCA_003431655     |                  |                 |
| **Mycobacterium caprae ATCC BAA-824** | (Aranaz et al. 1999) Aranaz et al. 2003 | CIP 105776; gM-1; spc-1                                                              | Mycobacterium bovis subsp. caprae; Mycobacterium caprae; Mycobacterium tuberculosis subsp. caprae | 4304       | 65.6        | 4039         | PRJNA224116           | SAMN06462279        | GCF_002982225     |                  |                 |
| **Mycobacterium microti ATCC 19422** | Reed 1957                        | DSM 44155; NCTC 8710; CIP 104256                                                   | Mycobacterium microti                                                     | 4241       | 65.3        | 4102         | PRJNA224116           | SAMN06462280        | GCF_002982215     |                  |                 |
| Strain                  | Authority                      | Other deposits                  | Synonyms                        | Base pairs | Percent G+C | No. proteins | Goldstamp accession | Bioproject accession | Biosample accession | Assembly accession | IMG OID          |
|------------------------|--------------------------------|--------------------------------|---------------------------------|------------|-------------|--------------|---------------------|----------------------|--------------------|-------------------|------------------|
| **Mycobacterium shinjukuense CCUG 53584** | Saito et al. 2011 emend. Nouioui et al. 2018 | CCUG 53584; DSM 45663; JCM 14233; GTC 2738 | Mycobacterium shinjukuense | 4409 896 | 67.8         | 3701         | PRJNA224116          | SAMN06064260       |                    |                  | GCF_002086755    |
| **Mycobacterium decipiens TBL 1200985**   | Brown-Elliott et al. 2018     | DSM 105360; ATCC TSD-117        | Mycobacterium decipiens        | 5216 890  | 65.5         | 4492         | PRJNA354248          | SAMN06651657       |                    |                  | GCA_002104675    |
| **Mtuberculosis_H37Rv.fna**                |                                |                                |                                | 4411 709  | 65.6         | 4079         |                    |                      |                    |                  |                  |
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 2021-02-09. 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 14130 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

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 $d_5$ [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 13 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 5 species clusters and the provided query strains were assigned to 1 of these. Moreover, user strains were located in 1 of 5 subspecies clusters.

Figure caption SSU tree

**Figure 1.** 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 43.0 %. The tree was rooted at the midpoint [7].

Figure caption genome tree

**Figure 2.** 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 48.9 %. The tree was rooted at the midpoint [7].
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