

**Additional file 4: Table S3 – Variant exoproteome of the strain C231 of *Corynebacterium pseudotuberculosis***

| Protein description                           | Protein ID <sup>a</sup> | M <sub>r</sub> / pI <sup>b</sup> | Ortholog <sup>c</sup>       |                    | Predicted localization by SurfG+ <sup>d</sup> | Number of peptides observed <sup>e</sup> | Sequence coverage (%) <sup>f</sup> |
|-----------------------------------------------|-------------------------|----------------------------------|-----------------------------|--------------------|-----------------------------------------------|------------------------------------------|------------------------------------|
|                                               |                         |                                  | Organism                    | E-value            |                                               |                                          |                                    |
| Phospholipase D (PLD)                         | ADL09524                | 32.45 / 8.77                     | <i>C.pseudotuberculosis</i> | 4e <sup>-173</sup> | E (S)                                         | 11                                       | 33.6                               |
| Serine proteinase precursor (CP40)            | ADL11339                | 43.00 / 6.48                     | <i>C.pseudotuberculosis</i> | 0                  | E (S)                                         | 25                                       | 48.4                               |
| Hypothetical protein                          | ADL10001                | 27.21 / 4.77                     | <i>C.diphtheriae</i>        | 2e <sup>-06</sup>  | E (S)                                         | 7                                        | 32.9                               |
| Putative secreted protein                     | ADL09871                | 16.80 / 8.30                     | <i>C. tropicalis</i>        | 0.87               | E (S)                                         | 6                                        | 34.6                               |
| Conserved hypothetical exported protein       | ADL10384                | 49.61 / 8.69                     | <i>C.diphtheriae</i>        | 7e <sup>-96</sup>  | E (S)                                         | 9                                        | 19.0                               |
| Hypothetical protein                          | ADL11213                | 33.55 / 4.48                     | <i>C.diphtheriae</i>        | 6e <sup>-08</sup>  | E (S)                                         | 12                                       | 32.7                               |
| Putative secreted protein                     | ADL21537                | 23.4 / 9.36                      | <i>C.litoralis</i>          | 1.2                | E (S)                                         | 7                                        | 43.7                               |
| Putative secreted protein                     | ADL10489                | 24.73 / 5.07                     | <i>C.diphtheriae</i>        | 9e <sup>-77</sup>  | E (S)                                         | 7                                        | 37.7                               |
| Secreted penicillin-binding protein           | ADL09532                | 50.75 / 5.67                     | <i>C.diphtheriae</i>        | 0                  | E (S)                                         | 12                                       | 29.7                               |
| Putative secreted protein                     | ADL21555                | 26.57 / 5.43                     | <i>C.diphtheriae</i>        | 1e <sup>-74</sup>  | E (S)                                         | 7                                        | 30.3                               |
| Putative surface-anchored protein             | ADL11344                | 27.85 / 9.24                     | <i>C. jeikeium</i>          | 9e <sup>-21</sup>  | E (S)                                         | 5                                        | 17.2                               |
| Putative penicillin-binding secreted protein  | ADL09697                | 83.00 / 5.38                     | <i>C.diphtheriae</i>        | 0                  | E (S)                                         | 14                                       | 22.2                               |
| Putative membrane anchored protein            | ADL11338                | 21.15 / 9.59                     | <i>C.diphtheriae</i>        | 6e <sup>-16</sup>  | E (S)                                         | 6                                        | 19.1                               |
| Hypothetical protein                          | ADL11326                | 34.65 / 5.85                     | <i>H.mukohataei</i>         | 8e <sup>-07</sup>  | E (PSE)                                       | 13                                       | 36.4                               |
| Transcriptional regulator                     | ADL09990                | 55.05 / 4.97                     | <i>C.diphtheriae</i>        | 0                  | E (PSE)                                       | 13                                       | 38.5                               |
| Putative serine threonine protein kinase      | ADL10880                | 80.10 / 4.80                     | <i>C.diphtheriae</i>        | 0                  | E (PSE)                                       | 10                                       | 16.2                               |
| Putative extracellular solute-binding protein | ADL09852                | 61.54 / 5.31                     | <i>C.glucuronolyticum</i>   | 0                  | E (PSE)                                       | 13                                       | 30.7                               |
| Maltotriose-binding protein                   | ADL09872                | 43.93 / 5.07                     | <i>C.diphtheriae</i>        | 5e <sup>-180</sup> | E (PSE) +                                     | 10                                       | 30.4                               |
| Putative zinc metallopeptidase                | ADL10626                | 35.38 / 5.29                     | <i>C.diphtheriae</i>        | 3e <sup>-110</sup> | E (PSE)                                       | 7                                        | 25.1                               |

|                                                           |          |              |                             |                    |           |    |      |
|-----------------------------------------------------------|----------|--------------|-----------------------------|--------------------|-----------|----|------|
| Putative iron transport system binding (secreted) protein | ADL10460 | 30.05 / 5.16 | <i>C.diphtheriae</i>        | 8e <sup>-119</sup> | E (PSE) + | 6  | 25.2 |
| Glycerophosphoryl diesterphosphodiesterase                | ADL11410 | 40.28 / 5.13 | <i>C. amycolatum</i>        | 2e <sup>-113</sup> | E (PSE) + | 10 | 32.2 |
| Putative metal-binding like protein                       | ADL10663 | 20.81 / 5.48 | <i>C.diphtheriae</i>        | 4e <sup>-65</sup>  | E (PSE) + | 10 | 51.2 |
| Iron siderophore binding protein – FagD                   | ADL09528 | 37.47 / 5.05 | <i>C.pseudotuberculosis</i> | 0                  | E (PSE) + | 5  | 16.3 |

<sup>a</sup> Accession numbers in Entrez Protein (NCBI Genome Projects 40687 and 40875).

<sup>b</sup> Theoretical molecular weights (Mr) and isoelectric points (pI), calculated by the Compute pI/MW tool (ExPASy tools).

<sup>c</sup> Major similarity found by Blast-p against the nr database: *Corynebacterium diphtheriae*; *Corynebacterium glutamicum*; *Corynebacterium amycolatum*; *Candida tropicalis*; *Congregibacter litoralis*; *Halomicrobium mukohataei*.

<sup>d</sup> E = extracytoplasmic; S = secreted; PSE = potentially surface exposed; C = cytoplasmic; M = membrane.

<sup>e, f</sup> Average values calculated from three experimental replicates.

§ Predicted Tat-associated signal peptide.

+ Predicted lipoprotein.

¥ Predicted LPXTG cell wall-anchoring motif.

\* SecretomeP prediction of non-classical secretion.

# Extensive literature evidence for exportation by non-classical pathways.