## Supplementary File 2

For the calculation of Average Nucleotide Identity (ANI) values, the program, JSpecies (Richter and RossellóMóra, 2009), was employed. Pair-wise comparisons between genomes were made by artificially sectioning each query genome into fragments consisting of 1020 nucleotides and then comparing these sections to the reference genome (Goris et al., 2007, Richter and Rosselló-Móra, 2009) using BLAST. Fragments with more than 30\% identity, as calculated across the entire segment, that aligned over more than $70 \%$ of the length of the fragments were considered homologous and used for further analysis (Goris et al., 2007). The percentage identity values obtained for the fragments were then averaged across all the fragments to obtain the ANI values between the two genomes (Goris et al., 2007). For the Pantoea dataset four isolates of Pan. ananatis, including the type strain, was compared to the genome of the type strain of Pan. allii. The ANI values for the Paraburkholderia isolates were obtained from published data (Steenkamp et al., 2015). For the Escherichia dataset two representatives for each of the Clades III, IV and V were compared to the type strain of E. coli.

## References

GORIS, J., KONSTANTINIDIS, K. T., KLAPPENBACH, J. A., COENYE, T., VANDAMME, P. \& TIEDJE,
J. M. 2007. DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. International Journal of Systematic and Evolutionary Microbiology, 57, 81-91.
RICHTER, M. \& ROSSELLÓ-MÓRA, R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. Proceedings of the National Academy of Sciences, 106, 19126-19131.
STEENKAMP, E. T., VAN ZYL, E., BEUKES, C. W., AVONTUUR, J. R., CHAN, W. Y., PALMER, M., MTHOMBENI, L. S., PHALANE, F. L., SEREME, T. K. \& VENTER, S. N. 2015. Burkholderia kirstenboschensis sp. nov. nodulates papilionoid legumes indigenous to South Africa. Systematic and Applied Microbiology, 38, 545-554.

Genomes used

| Isolate | Accession |
| :--- | :--- |
| Pantoea ananatis LMG 2665 T | JMJJ00000000 |
| Pantoea ananatis LMG5342 | HE617160.1 <br> HE617161.1 |
| Pantoea ananatis AJ13355 | AP012032.2 <br> AP012033.1 |
| Pantoea ananatis B1-9 | CAEI00000000 |
| Pantoea allii LMG 24248 T | MLFE00000000 |
| Paraburkholderia kirstenboschensis KB 15 T | JRZC00000000 |
| Paraburkholderia kirstenboschensis Rau2d2 | JRTU00000000 |
| Paraburkholderia caledonica NBRC 102488 | BAYE00000000 |
| Escherichia coli DSM 30083 T | AGSE000000000 |
| Escherichia Clade III TW09231 | AEJW000000000 |
| Escherichia Clade III TW09276 | AEJV00000000 |
| Escherichia Clade IV TW14182 | AEJZ00000000 |
| Escherichia Clade IV H605 | Broad Institute |
| Escherichia Clade V E1118 | Broad Institute |
| Escherichia Clade V TW09308 | AEME00000000 |

Average Nucleotide Identity (ANI) values calculated with JSpecies between four Pan. ananatis

|  | Pan. ananatis <br> AJ13355 | Pan. ananatis <br> LMG 5342 | Pan. ananatis <br> B1-9 | Pan. ananatis <br> LMG 2665 | Pan. allii <br> LMG 24248 |
| :--- | :---: | :---: | :---: | :---: | :---: |
| Pan. ananatis <br> AJ13355 | --- | 99 | 99.19 | 99.23 | 87.75 |
| Pan. ananatis <br> LMG 5342 | 99.07 | --- | 99.12 | 99.04 | 87.74 |
| Pan. ananatis <br> B1-9 | 99.22 | 99.1 | --- | 99.21 | 87.79 |
| Pan. ananatis <br> LMG 2665 | 99.22 | 98.97 | 99.18 | --- | 87.69 |
| Pan. allii LMG <br> 24248 | 88.12 | 88.1 | 88.11 | 88.21 | --- |

isolates and the type strain of Pan. allii

Average Nucleotide Identity (ANI) values calculated with JSpecies between two Par.
kirstenboschensis isolates and Par. caledonica

|  | Par. kirstenboschensis <br> KB15 | Par. kirstenboschensis <br> Rau2D2 | Par. caledonica <br> NBRC102488 |
| :--- | :--- | :--- | :--- |
| Par. kirstenboschensis <br> KB15 | --- | 96.37 | 92.11 |
| Par. kirstenboschensis <br> Rau2D2 | 97.18 | --- | 91.98 |
| Par. caledonica <br> NBRC102488 | 92.65 | 91.76 | --- |

Average Nucleotide Identity (ANI) values calculated with JSpecies between the E. coli type strain and representatives of each of the Escherichia clades

|  | E. coli <br> DSM30038 | Clade III <br> TW09231 | Clade III <br> TW09276 | Clade IV <br> H605 | Clade IV <br> TW14182 | Clade V <br> E1118 | Clade V <br> TW09308 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| E. coli <br> DSM30038 | --- | 91.71 | 91.77 | 92.13 | 91.95 | 90.68 | 90.87 |
| Clade III <br> TW09231 | 91.82 | --- | 98.39 | 96.4 | 96.3 | 92.08 | 92.15 |
| Clade III <br> TW09276 | 91.92 | 98.31 | --- | 96.45 | 96.31 | 92 | 92.01 |
| Clade IV <br> H605 | 92.27 | 96.3 | 96.37 | --- | 98.96 | 91.96 | 91.95 |
| Clade IV <br> TW14182 | 92.24 | 96.29 | 96.32 | 99.06 | --- | 91.95 | 91.97 |
| Clade V <br> E1118 | 90.83 | 92.06 | 92.04 | 92.04 | 91.89 | --- | 99.37 |
| Clade V <br> TW09308 | 90.89 | 92.09 | 92.02 | 91.95 | 91.88 | 99.3 | --- |

