### Table S2. Probes that hybridized differentially to B. bronchiseptica complex I and IV genomes as determined by SAM analysis

| Probe ID | Species | BB ORF | BP ORF | BPP ORF | Mean fold change | Gene name and product | Function | Gene name and product | Function |
|----------|---------|--------|--------|---------|-----------------|----------------------|----------|----------------------|----------|
| 6038     | BB      | 0488   | 0488   | 0.34    |                 | putative glutamine amidotransferase | Global regulatory functions |                  |          |
| 5022     | BB      | [0449] | [0448] | 0.07    |                 | intergenic region | Conserved in other organisms |                  |          |
| 5207     | BB      | 0216   | 0212   | 0.10    |                 | conserved hypothetical protein | Global regulatory functions |                  |          |
| 5209     | BB      | 0214   | 0210   | 0.36    |                 | AraC family transcriptional regulator | Global regulatory functions |                  |          |
| 5157     | BB      | 0142   |        | 0.48    |                 |                       |                      |                      |          |
| 5159     | BB      | 0141   |        | 0.44    |                 |                       |                      |                      |          |
| 5160     | BB      | 0140   |        | 0.33    |                 |                       |                      |                      |          |
| 7397     | BB      | 1028   |        | 0.38    |                 | putative exported protein | Transport/binding proteins |                  |          |
| 7393     | BB      | 1024   |        | 0.42    |                 | LysR-family transcriptional regulator | Global regulatory functions |                  |          |
| 7391     | BB      | 1021   |        | 0.14    |                 | putative membrane protein | Inner membrane |                  |          |
| 2266     | BP      | 0925   | 3455   | 0.46    |                 | putative taurine dioxygenase | Amines |                  |          |
| 5219     | BB      | 0909   |        | 0.09    |                 | conserved hypothetical protein | Conserved in other organisms |                  |          |
| 7330     | BB      | 0821   | 0735   | 0.25    |                 | autotransporter | Global regulatory functions |                  |          |
| 7247     | BB      | 0720   |        | 0.49    |                 | putative membrane protein | Inner membrane |                  |          |
| 7245     | BB      | 0718   |        | 0.36    |                 |                       |                      |                      |          |
| 7181     | BB      | 0653   |        | 0.11    |                 | 3-hydroxyisobutyrate dehydrogenase | Not classified (including putative assignments) |                  |          |
| 7124     | BB      | 0587   | 0581   | 0.12    |                 | conserved hypothetical protein | Global regulatory functions |                  |          |
| 7108     | BB      | 0571   | 0565   | 0.48    |                 | putative branched-chain amino acid transport ATP-binding protein | Global regulatory functions |                  |          |
| 7071     | BB      | 0534   | 0529   | 0.46    |                 | putative exported protein | Global regulatory functions |                  |          |
| 7065     | BB      | 0528   |        | 0.11    |                 | putative DNA-binding protein | Not classified (including putative assignments) |                  |          |
| 7058     | BB      | 0500   |        | 0.29    |                 | putative integrase | Phage-related functions and prophages |                  |          |
| 7057     | BB      | 0499   | 0494   | 0.12    |                 | hypothetical protein | Not classified (including putative assignments) |                  |          |
| 7055     | BB      | 0497   |        | 0.05    |                 | hypothetical protein | Unknown function, no known homologs |                  |          |
| 7778     | BB      | 2188   | 0.02   |         |                 | phage-related hypothetical protein | Phage-related functions and prophages |                  |          |
| 5019     | BB      | 2189   | 0.29   |         |                 | phage-related conserved hypothetical protein | Phage-related functions and prophages |                  |          |
| 7777     | BB      | 2188   | 0.04   |         |                 | phage-related conserved hypothetical protein | Phage-related functions and prophages |                  |          |
| 5566     | BB      | [1903] | [2455] | 0.45    |                 | intergenic region |                       |                      |          |
| 5500     | BB      | 1701   | 0.04   |         |                 | phage-related conserved hypothetical protein | Phage-related functions and prophages |                  |          |
| 7731     | BB      | 1691   | 0.09   |         |                 | phage-related hypothetical protein | Phage-related functions and prophages |                  |          |
| 5526     | BB      | 1671   | 0.07   |         |                 | phage-related hypothetical protein | Phage-related functions and prophages |                  |          |
| 5527     | BB      | 1670   | 0.19   |         |                 | phage-related hypothetical protein | Phage-related functions and prophages |                  |          |
| 5676     | BB      | 1665   | 0.08   |         |                 | phage-related putative exported protein | Phage-related functions and prophages |                  |          |
| 5444     | BB      | 1606   | 2209   | 0.46    |                 | Putative oxidoreductase | Phage-related functions and prophages |                  |          |
| 7662     | BB      | 1499   | 2103   | 0.14    |                 | Putative monoxygenase | Global regulatory functions |                  |          |
| 7660     | BB      | 1497   | 2101   | 0.19    |                 | putative exported protein | Global regulatory functions |                  |          |
| 7658     | BB      | 1495   | 2099   | 0.43    |                 | Putative transcriptional regulator | Global regulatory functions |                  |          |
| 7657     | BB      | 1494   | 2098   | 0.44    |                 | conserved hypothetical protein | Global regulatory functions |                  |          |
| 7637     | BB      | 1474   | 0.01   |         |                 | putative DNA-binding protein | Not classified (including putative assignments) |                  |          |
| 7633     | BB      | 1470   | 0.07   |         |                 | conserved hypothetical protein | Conserved in other organisms |                  |          |
| 6060     | BPP     | 1366   | 1054   | 1150   | 0.49            | pln; probable hydrolase | Phage-related functions and prophages |                  |          |
| 5429     | BB      | 1344   | 1128   | 0.50    |                 | probable hydrolase | Phage-related functions and prophages |                  |          |
| 7468     | BB      | 1101   |        | 0.49    |                 | two component sensor kinase | Global regulatory functions |                  |          |
| 7422     | BB      | 1054   | 0.50   |         |                 | LysR-family transcriptional regulator | Global regulatory functions |                  |          |

**Overrepresented in complex IV**

**Underrepresented in complex IV**
| Gene name and product as annotated by the Sanger Centre sequencing team | Fold difference between mean Cy5/Cy3 ratio in B. bronchiseptica complex IV versus complex I. | ORF numbers as annotated by the Sanger Centre sequencing team |
|---|---|---|
| 7941 BB 2720 2765 0.24 Conserved hypothetical protein | 5352 BB 2354 1289 0.47 putative exported protein | a Species from which the PCR product was amplified |
| 7941 BB 2720 2765 0.24 Conserved hypothetical protein | 5353 BB 2353 1288 0.36 conserved hypothetical protein | b ORF numbers as annotated by the Sanger Centre sequencing team |
| 7941 BB 2720 2765 0.24 Conserved hypothetical protein | 5355 BB 2352 1287 0.35 probable LysR-family transcription regulator (BPP pseudogene) | c Fold difference between mean Cy5/Cy3 ratio in B. bronchiseptica complex IV versus complex I. |
| 7941 BB 2720 2765 0.24 Conserved hypothetical protein | 5358 BB 2350 1285 0.34 conserved hypothetical protein | d Gene name and product as annotated by the Sanger Centre sequencing team |
| 7941 BB 2720 2765 0.24 Conserved hypothetical protein | 5361 BB 2349 1284 0.31 putative 2-pyrone-4,6-dicarboxylic acidhydrolase | e Species from which the PCR product was amplified |
| 7941 BB 2720 2765 0.24 Conserved hypothetical protein | 5365 BB 2345 1280 0.37 putative exported protein (BPP partial) | f Fold difference between mean Cy5/Cy3 ratio in B. bronchiseptica complex IV versus complex I. |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | g ORF numbers as annotated by the Sanger Centre sequencing team |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | h Gene name and product as annotated by the Sanger Centre sequencing team |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | i Fold difference between mean Cy5/Cy3 ratio in B. bronchiseptica complex IV versus complex I. |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | j ORF numbers as annotated by the Sanger Centre sequencing team |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | k Gene name and product as annotated by the Sanger Centre sequencing team |
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| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | m ORF numbers as annotated by the Sanger Centre sequencing team |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | n Gene name and product as annotated by the Sanger Centre sequencing team |
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| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | p ORF numbers as annotated by the Sanger Centre sequencing team |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | q Gene name and product as annotated by the Sanger Centre sequencing team |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | r Fold difference between mean Cy5/Cy3 ratio in B. bronchiseptica complex IV versus complex I. |
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| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | t Gene name and product as annotated by the Sanger Centre sequencing team |
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| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | w Gene name and product as annotated by the Sanger Centre sequencing team |
| 7806 BB 2330 2620 1269 0.40 probable membrane efflux protein Transport/binding proteins | 5377 BB 2322 1254 0.11 hypothetical protein | x Fold difference between mean Cy5/Cy3 ratio in B. bronchiseptica complex IV versus complex I. |
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Selected functional annotations
ORF numbers between brackets indicate intergenic regions.
Contiguous colors indicate that the probes are clustered on the genome.