**Supplementary Table 4. Haem uptake genetic loci of pathogenic *Burkholderia* species**

**Species Strain Locusa Old locusa**

*B. arborisb* ? ?

*B. ambifaria* AMMD BAMB\_RS23890-BAMB\_RS23910 Bamb\_4772-Bamb\_4776

*B. anthina* AZ-4-2-10-S1-D7 WS64\_27095-WS64\_27075 n/a

*B. cenocepacia* J2315 QU43\_RS67585-QU43\_RS67605 BCAM2626-BCAM2630

*B. cepacia* ATCC 25416 APZ15\_RS23630-APZ15\_RS23650 APZ15\_23630-APZ15\_23650

*B. contaminans* MS14 NL30\_RS16925-NL30\_RS16945 NL30\_16920-NL30\_16940

*B. diffusa*c MSMB866 WI71\_09210-WI71\_09190 n/a

*B. dolosa* AU0158 AK34\_RS00410-AK34\_RS00390 AK34\_3247-AK34\_3243

*B. lata* 383 BCEP18194\_RS23870-BCEP18194\_RS23850 Bcep18194\_B0221-Bcep18194\_B0217

*B. latens*d AU17928 WK25\_28740-WK25\_28760 n/a

*B. metallica* FL-6-5-30-S1-D7 WJ16\_RS31540-WJ16\_RS31560 WJ16\_31510-WJ16\_31530

Bcc

*B. multivorans*e ATCC 17616 BMUL\_RS16900-BMUL\_RS16880 Bmul\_3338-Bmul\_3334

 BMULJ\_RS25905-BMULJ\_RS25925 BMULJ\_05192-BMULJ\_05188

*B. paludis* MSh1 GQ56\_0128135-GQ56\_0128155 n/a

*B. pseudomultivorans* SUB-INT23-BP2 WS57\_RS01155-WS57\_RS01135 WS57\_01155-WS57\_01135

*B. pyrrocinia* 2327 (DSM10685) ABD05\_RS22580-ABD05\_RS22560 ABD05\_22580-ABD05\_22560

*B. seminalis* FL-5-4-10-S1-D7 WJ12\_33030-WJ12\_33050 n/a

*B. stabilis* ATCC BAA-67 BBJ41\_RS27015-BBJ41\_RS27035 BBJ41\_27015-BBJ41\_27035

*B. stagnalis*fMSMB735 WT74\_RS31830-WT74\_RS31855 WT74\_31785-WT74\_31810

*B. territorii* RF8-non-BP5 WS51\_RS09890-WS51\_RS09910 WS51\_09890-WS51\_09910

*B. ubonensis* MSMB22 BW23\_RS02620-BW23\_RS02640 BW23\_3819-BW23\_3823

*B. vietnamiensis*g G4 n/a n/a

*B. mallei* ATCC 23344 BMAA1826-BMAA1830 n/a

*B. pseudomallei* K96243 BPSS0244-BPSS0240 n/a

*B. gladioli*h BSR3 BGLA\_RS01200- BGLA\_RS01210 bgla\_1g02490-bgla\_1g02510

 BGLA\_RS33815-BGLA\_RS33820 bgla\_2g28390-bgla\_2g28400

aGene loci refer to the first and last genes (*bhuR* and *bhuV*, respectively) in the *bhuRSTUV* haem uptake gene cluster of representative

pathogenic *Burkholderia* species as shown in Figure 4.

bA *B. arboris* genome sequence is not currently available to interrogate.

cThe *bhu* gene cluster is inactivated in *B. diffusa* strain RF2-non-BP9.

dThe *bhuU* gene in *B. latens* contains multiple two codon repeats at the beginning of the ORF. It is annotated as a pseudogene but may be functional.

eTwo alternative annotations are shown for *B. multivorans* ATCC 17616.

fThe *B. stagnalis* haem uptake operon contains an additional gene encoding a VOC family metalloenzyme located between *bhuU* and *bhuV*.

g*B. vietnamiensis* does not contain the *bhu* gene cluster.

hThe *B. gladioli bhuRSTUV* genes are organised into two operons located on separate chromosomes (see text for details).

n/a, not applicable