

Supplementary Figure 1

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V15          VFKHSIFLR IYAGLVILVVLVAVFGYLLVQI I NYQRAQEYRESLTDGISYVISEGVARQP
17978       VFKHSIFLR IYAGLVILVVLVAVFGYLLVQI I NYQRAQEYRESLTDGISYVISEGVARQP
A118       VFKHSIFLR IYAGLVILVVLVAVFGYLLVQI I NYQRAQEYRESLTDGISYVISEGVARQP
*****
V15          GKQQKIDWISDASDLELPIYYTDASKVELSRTEKKRIEAQKSVVRYDASNSIAYVI IGL
17978       GKQQKIDWISDASDLELPIYYTDASKVELSRTEKKRIEAQKSVVRYDASNSIAYVI IGL
A118       GKQQKIDWISDASDLELPIYYTDASKVELSRTEKKRIEAQKSVVRYDASNSIAYVI IGL
*****

                                           166
V15          RDDPQHYSIKVDKITERQMKALPIFVLDYLMFYPGQEQEYLAKI QKHFSYPINIQNIQD
17978       RDDPQHYSIKVDKITERQMKALPIFVLDYLMFYPGQEQEYLAKI QKHFSYPINIQNIQD
A118       RDDPQHYSIKVDKITERQMKALPIFVLDYLMFYPGQEQEYLAKI EKHFSSYPINIQNIQD
*****

V15          VNLDSEQIGRLRQDQSVMLYKDSATVRGTTISIVS PIPNHPAQVLVLPVPMFNWMLQL
17978       VNLDSEQIGRLRQDQSVMLYKDSATVRGTTISIVS PIPNHPAQVLVLPVPMFNWMLQL
A118       VNLDSEQIGRLRQDQSVMLYKDSATVRGTTISIVS PIPNHPAQVLVLPVPMFNWMLQL
*****

V15          SAGITLFSLFLSLGVYGLILPLE RKIRQVRYALNRMKSGDLSLRVPIEGSDEMANLASS
17978       SAGITLFSLFLSLGVYGLILPLE RKIRQVRYALNRMKSGDLSLRVPIEGSDEMANLASS
A118       SAGITLFSLFLSLGVYGLILPLE RKIRQVRYALNRMKSGDLSLRVPIEGSDEMANLASS
*****

V15          YNNMSDHIQRLIEAQRELMRAVSHLRTFVARIRFGTEMLAEEDDYNHRMHQVDMIDKDI
17978       YNNMSDHIQRLIEAQRELMRAVSHLRTFVARIRFGTEMLAEEDDYNHRMHQVDMIDKDI
A118       YNNMSDHIQRLIEAQRELMRAVSHLRTFVARIRFGTEMLAEEDDYNHRMHQVDMIDKDI
*****

V15          EALNTLIDEIMTYAKLEQGTPSLDFAEIVLFEVLDQVAVETEALKTQKEIELIPPLYVK
17978       EALNTLIDEIMTYAKLEQGTPSLDFAEIVLFEVLDQVAVETEALKTQKEIELIPPLYVK
A118       EALNTLIDEIMTYAKLEQGTPSLDFAEIVLFEVLDQVAVETEALKTQKEIELIPPLYVK
*****

                                           455
V15          VDAERYLHRVVQNLVGNVRYCDNKVRIITGGIHS DGMFVVCVEDDGPPIPEQDRKRVFE
17978       VDAERYLHRVVQNLVGNVRYCDNKVRIITGGIHS DGMFVVCVEDDGPPIPEQDRKRVFE
A118       VDAERYLHRVVQNLVGNVRYCDNKVRIITGGIHS DGMFVVCVEDDGPPIPEQDRKRVFE
*****

                                           492
V15          AFARLDDSRTRASGGYGLGLSIVSRIAYWFGGEIKVDES PSLGGARFIMTWAHFRKQPP
17978       AFARLDDSRTRASGGYGLGLSIVSRIAYWFGGEIKVDES PSLGGARFIMTWAHFRKQPP
A118       AFARLDDSRTRVSGGYGLGLSIVSRIAYWFGGEIKVDES PSLGGARFIMTWAHFRKQPP
*****

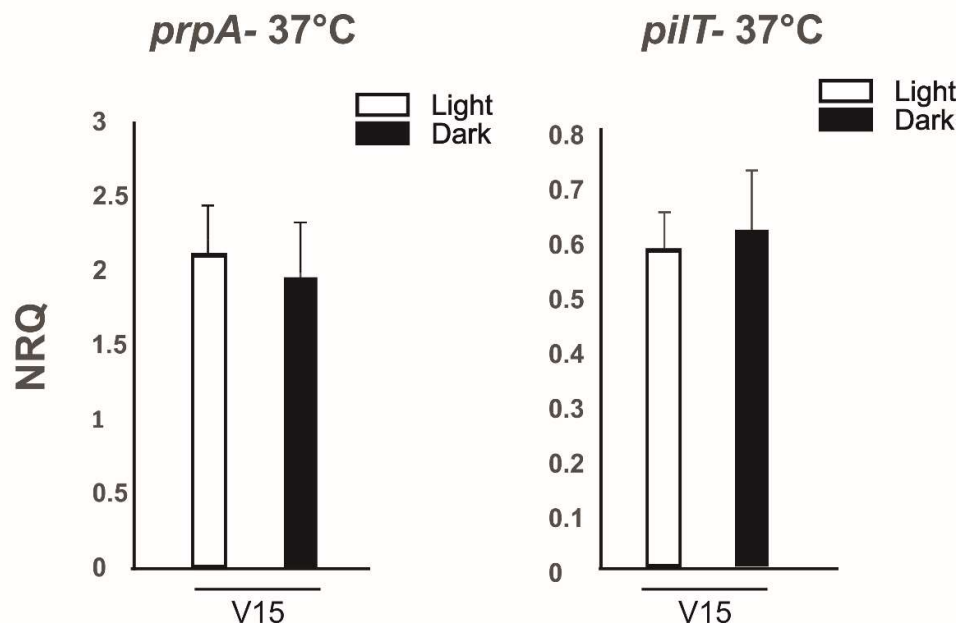
                                           543
V15          LKTNKKAPA
17978       LKTNKKAPA
A118       LKSNKKAPA
*****

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Supplementary Figure 1. Amino acid alignment of BfmS for the three *A. baumannii* strains V15, ATCC 17978 and V15. The numbers above the sequences indicate positions in the alignments where differences reside. In green are indicated differences between V15 and A118 respect to ATCC 17978, while

in blue are indicated differences between V15 and ATCC 17978 respect to A118. In pink boxes are indicated the predicted membrane spanning regions estimated by SOSUI (<https://harrier.nagahama-i-bio.ac.jp/sosui/>), which flank the extracellular sensor domain; and the C-terminal domain contains the histidine kinase domain. Identical (*) and conserved (:) amino acids at the given position are indicated below alignments.

Supplementary Figure 2



Supplementary Figure 2. Estimation by qRT-PCR of the expression levels of *prpA* and *pilT* in V15 cells recovered from motility plates incubated under blue light (L) or in the dark (D) at 37°C. The data shown are mean ± SD of normalized relative quantities (NRQs) calculated from transcript levels measured in at least

three biological replicates.