47 — *Halomonas axialensis* Althf1^T (AF212206)

60 — *Halomonas meridiana* DSM 5425^T (AJ306891)

99 — *Halomonas aquamarina* DSM 30161^T (AJ306888)

Halomonas sp. H11 (in this research)

85

62 — *Halomonas johnsoniae* T68687^T (AM941399)

Halomonas magadiensis 21M1^T (X92150)

92

90 — *Halomonas hamiltonii* W1025^T (AM941396)

71 — *Halomonas stevensii* S18214^T (AM941388)

95

100 — *Halomonas venusta* DSM 4743^T (AJ306894)

Halomonas alkaliphila 18bAG^T (AJ640133)

100 — *Halomonas sulfidaeris* Esulfide1^T (AF212204)

99 — *Halomonas variabilis* DSM 3051^T (AJ306893)

71 — *Halomonas boliviensis* LC1^T (AY245449)

86 — *Halomonas neptunia* Eplume1^T (AF212202)

99 — *Halomonas gomseomensis* M12^T (AM229314)

Halomonas janggokensis M24^T (AM229315)

Halomonas elongata ATCC 33173^T (X67023)

Chromohalobacter marismortui ATCC 17056^T (X87219)

0.01

1

2   SUPPLEMENTAL FIG. 1. Phylogenetic analysis of *Halomonas* sp. H11 strain based on

3   16S rRNA sequence.

4   Indicator beneath the tree is scale bar representing 0.01 inferred substitutions per nucleotide

5   portion. The numbers shown in the branch mean bootstrap values. Type strain is indicated

6   as 'T' at the end of strain name. Accession number of 16S rRNA sequence is denoted by

7   parenthesis.