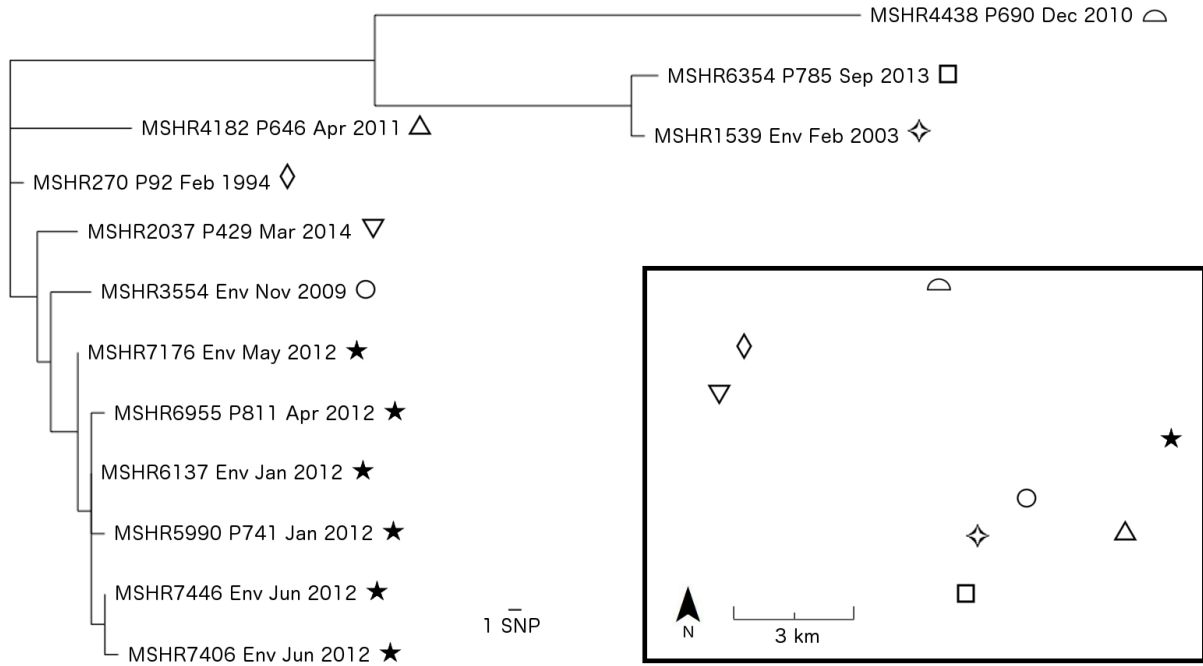


1 **Supplemental Figure Legends**



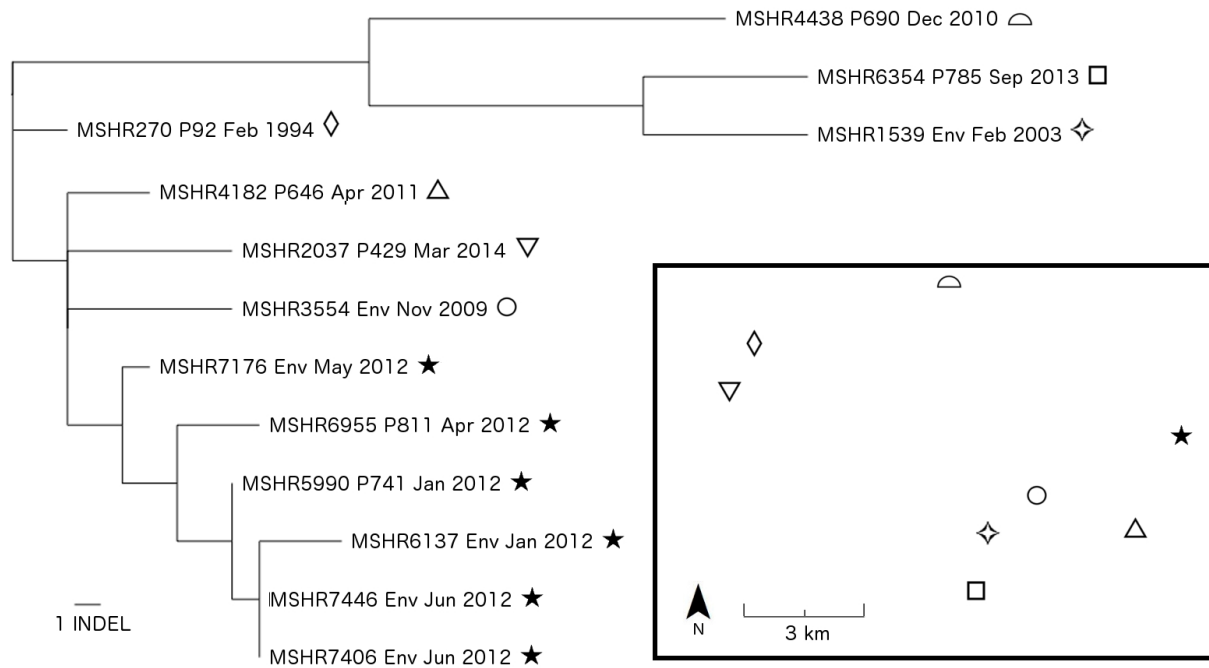
2

3 **Supplemental Figure 1:** Maximum parsimony whole genome core SNP phylogeny of  
4 environmental and clinical isolates from a melioidosis outbreak in the Darwin rural region,  
5 northern Australia. P, patient; Env, environmental. Consistency index=1. Inset: Sampling  
6 locations for this study. A solid star shows patient and environmental samples collected at the  
7 outbreak property. Hollow shapes show isolates used as outgroups.

8

9

10 **Supplemental Figure 2 legend:**



11

12 **Supplemental Figure 2:** Maximum parsimony whole genome indel phylogeny of environmental

13 and clinical isolates from a melioidosis outbreak in the Darwin rural region, northern Australia.

14 P, patient; Env, environmental. Consistency index=0.95. Inset: Sampling locations for this study.

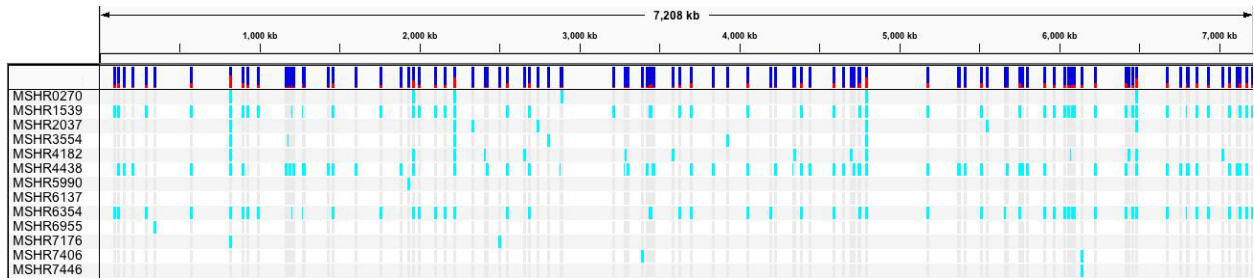
15 A solid star shows patient and environmental samples collected at the outbreak property. Hollow

16 shapes show isolates used as outgroups.

17

18 |

19



20 **Supplemental Figure 3:** Distribution of 111 SNP variants found among ST-325 *B. pseudomallei*  
21 isolates in comparison to MSHR6137. Dark blue/red bars indicate the proportion of isolates that  
22 have a particular SNP. Light blue bars indicate the presence of a particular SNP in a strain. SNP  
23 distribution was visualized using Integrative Genomics Viewer 2.3.4 (Robinson JT,  
24 Thorvaldsdóttir H, Winckler W, Guttman M, Lander ES, Getz G, Mesirov JP. 2011. Integrative  
25 genomics viewer. Nat Biotechnol **29**:24-26).