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Human Melioidosis, Malawi, 2011

Technical Appendix

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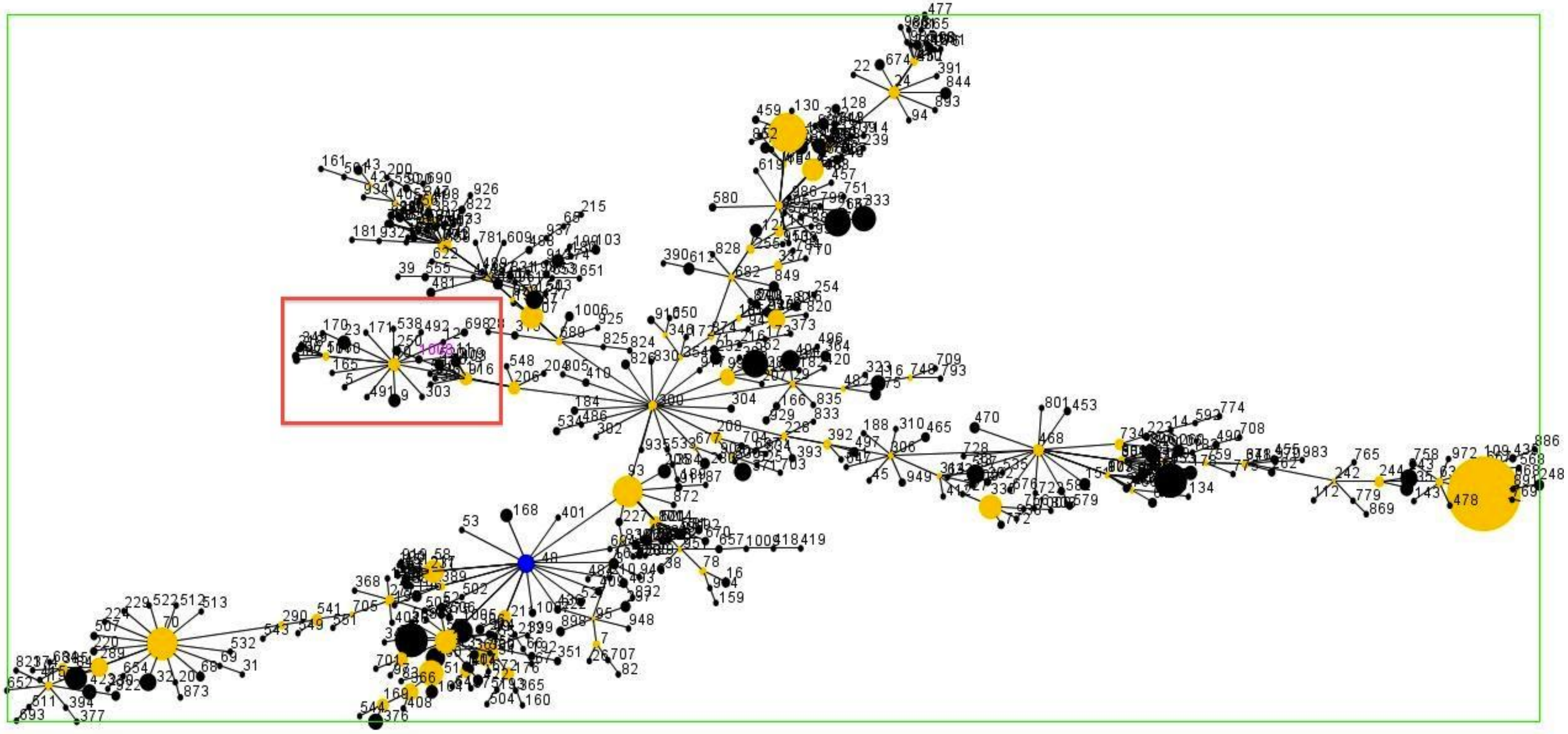
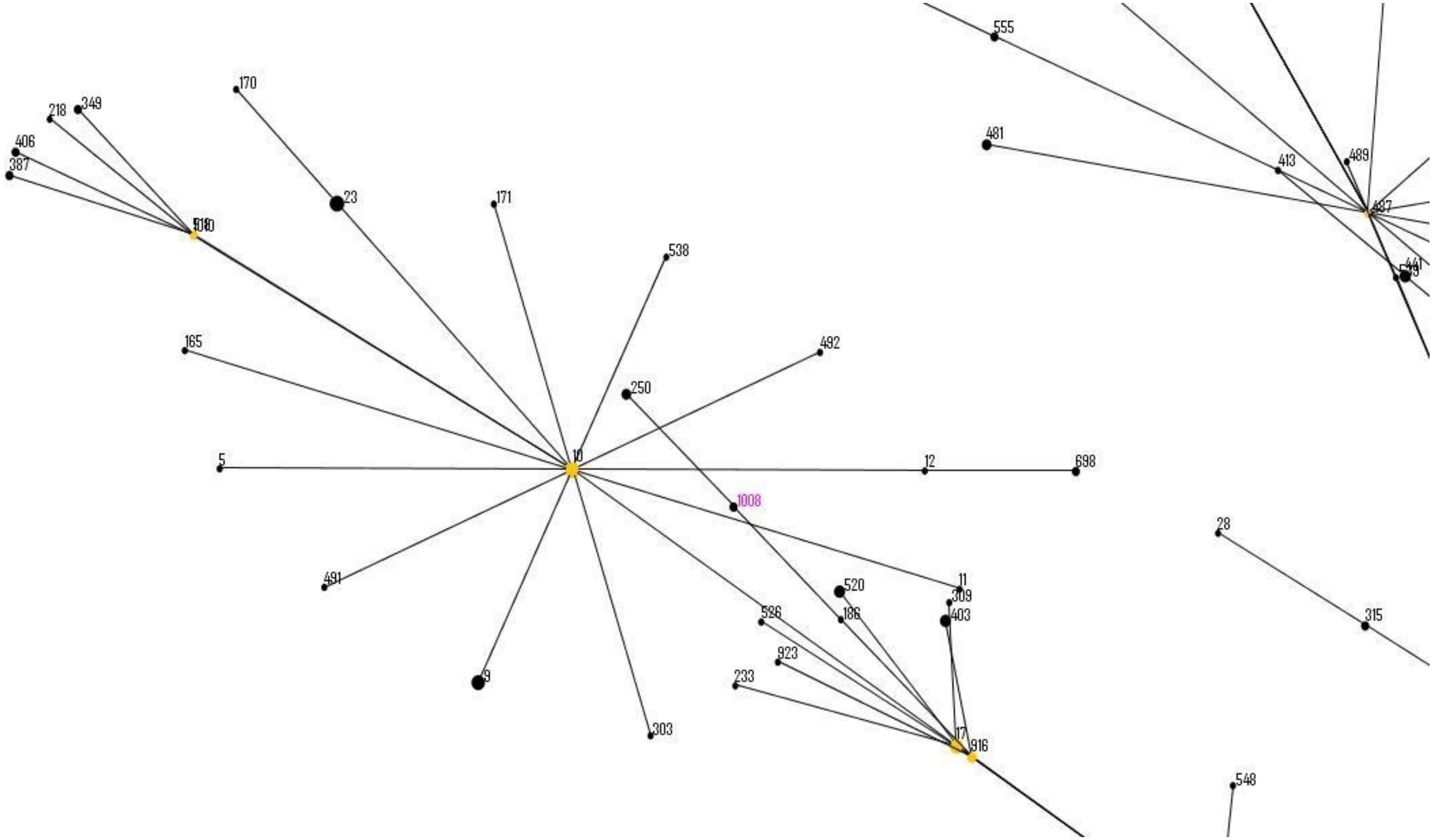


Technical Appendix Figure 1. eBURST diagram of clonal complex 1 *Burkholderia pseudomallei* sequence types (STs) submitted to the global multilocus sequence typing (MLST) database. Diagram shows predicted evolutionary relationship between strains by ST in 7 different alleles. Each circle indicates a particular ST, with the relative size of the circle indicating the number of isolations of that particular ST. Blue circle indicates the predicted founding genotype (ST48); yellow circles indicate predicted subgroup founders; and purple circle indicates ST1008 from the Malawi case described in this report. Lines between STs indicate STs that differ at a single allele. The red square is magnified in Technical

Appendix Figure 2 to illustrate more clearly STs closely related to ST1008. The complete database and the eBURST software can be accessed at http://bpseudomallei.mlst.net/



Technical Appendix Figure 2. Detail of eBURST clonal complex 1 subgroup for ST1008. ST1008 is labeled in magenta. The subgroup founder ST916 (bottom right) was isolated from samples in Cambodia. In the adjacent subgroup are STs (ST5 and ST-9) isolated from infections in humans in Kenya.