

Table S1: Coverage data from the nine UK *C. burnetii* isolates sequenced in this study after remapping of sequence reads onto the NM-I reference genome. Remapping and coverage analysis was performed as described in the Methods section. Deletion events in MST33 isolates (right panel) that have previously been described for related Dutch outbreak strains by Kuley *et al.* (Front Microbiol 8, 2017. doi: 10.3389/fmicb.2017.01526) are highlighted in bold.

