



Supplemental Figure S7. Comparisons of the allelic profiles for the 138 sequence types (isolates) available in the MLST database with the allelic profile for JCVI SC001. **a)** Trees were generated using PHYLIP suite of programs (web-based tools available for the MLST database) to create trees from allelic profile data. A graphical representation of the tree was generated with Phylodendron. Scale bar is 0.1. **b)** Minimum-spanning tree. A minimum-spanning tree was generated from MLST profile data. (www.pubmlst.org). BURST clustering is used to give meaningful results. The two STs with the greatest number of single locus and then double locus variants are linked first, preferably using intermediate STs. ST-68 is the nearest sequence type and this sequence type is shared with *P. gingivalis* strain TDC60.