



Additional Figure 1: Phylogenetic analysis of whole genome sequencing (WGS) and MLST data

Phylogenetic analysis of the *C. ulcerans* isolates. The evolutionary history was inferred using different algorithms with MEGA 6.0[1]. The percentage of replicate trees in which

the associated taxa clustered together in the bootstrap test (100 replicates) are shown next to the branches [2]. Shown are on the left panel trees which are based on the SNPs of the whole genome sequencing data (WGS), on the right side the data for the 7 MLST loci, similar to **Figure 2. (A)** Maximum likelihood phylogeny based on WGS data **(B)** Maximum likelihood phylogeny based on MLST data **(C)** Maximum Parsimony phylogeny based on WGS data **(D)** Maximum Parsimony phylogeny based on MLST data **(E)** Neighbor joining phylogeny based on WGS data **(F)** Neighbor joining phylogeny based on MLST data. The dendrograms for the WGS illustrate the higher resolution of WGS versus MLST data and also the higher accuracy and robustness as shown by much higher bootstrap values especially at the cluster of 08-1143, KL126, KL246, KL251, KL 252, KL387 and KL392. Note that MLST based methods completely fail to identify the matched pairs within this cluster and that the extremely low bootstrapping values indicate uncertainty in this cluster for MLST while WGS data provides almost perfect bootstrapping values.

1. Tamura K, Stecher G, Peterson D, Filipski A, Kumar S (2013) MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Mol Biol Evol* 30: 2725-2729.
2. Efron B, Halloran E, Holmes S (1996) Bootstrap confidence levels for phylogenetic trees. *Proc Natl Acad Sci U S A* 93: 7085-7090.