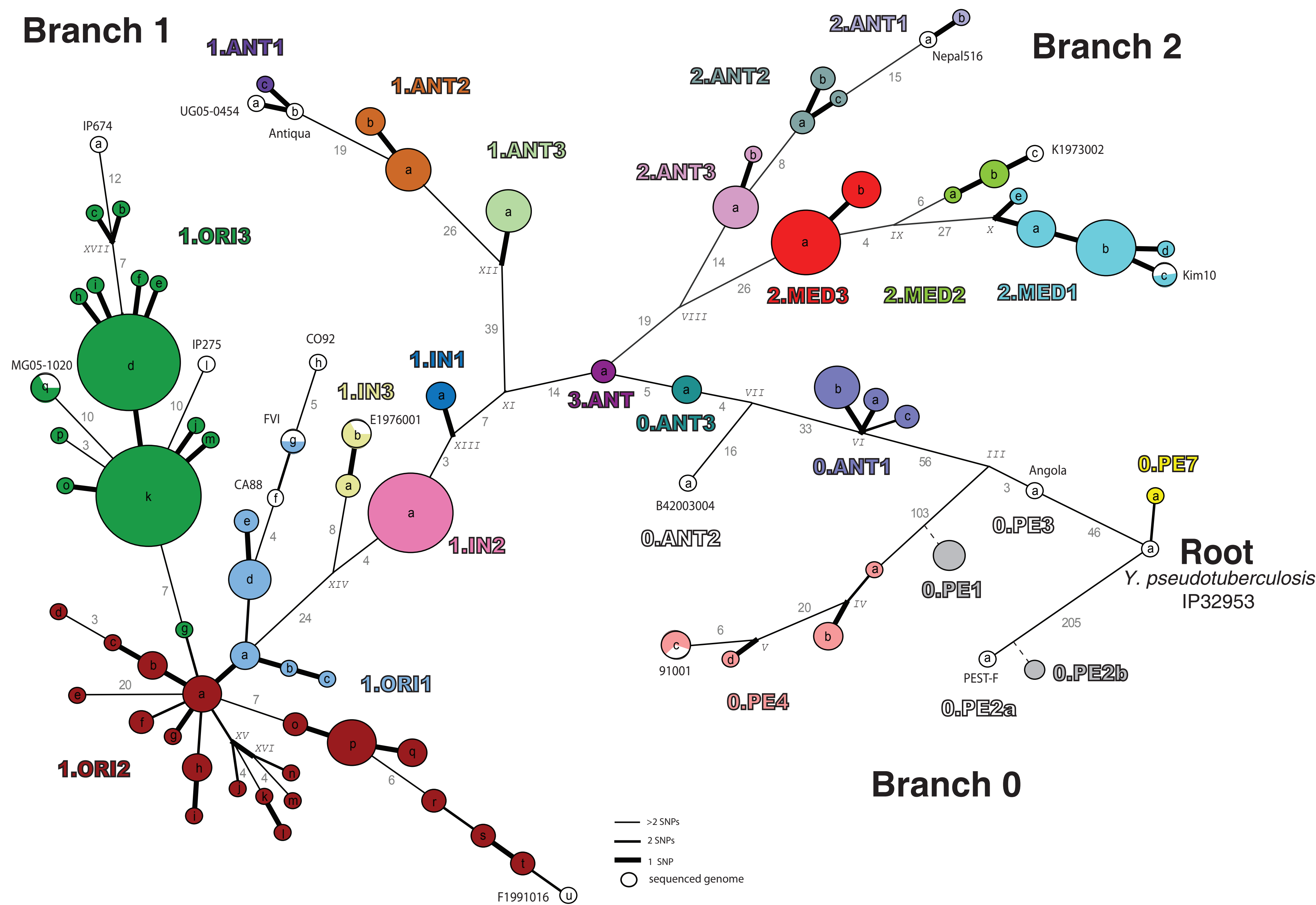


# Branch 1



Supplementary Fig. 7. Minimal spanning tree (MSTree) of genetic diversity of 289 isolates of *Y. pestis* coloured by population. The tree is fully parsimonious and is based on 933 SNPs (steps) (Supplementary Table 6). The regions corresponding to previously identified 0, 1 and 2 are indicated by large, bold text. Colours indicate populations (1.ORI3, 1.ANT1, etc.) and their corresponding nodes. Each node within a population is indicated by a letter (e.g. 1.ORI3.a). Strain designations near some terminal nodes indicate that they represent a genomic sequence whereas Roman numerals indicate hypothetical nodes. The lines between nodes indicate the numbers of intervening SNPs in grey, except where only one or two SNPs had accumulated, which are indicated by thick and thinner black lines, respectively. Nodes 0.PE1 and 0.PE2b were tested by a limited number of SNPs and are indicated in grey.