Additional file 4: Figure S2. Analysis of recombination in the population performed with ClonalFrameML. The input tree topology was that produced by BEAST (Fig. 2); branch length is corrected accounting the contribution of putative recombinant characters. The likelihood of recombination for each site along the concatenated core genomes (x-axis of the right panel) is shown on the heatmap, with colour codes as follows: light blue, low likelihood; yellow to orange, increasing likelihood; dark blue, highest likelihood.