Supplementary Figure 2. Incongruence of the 24-loci-MIRU-VNTR phylogeny of the strains belonging to the red lineage. Our multilocus sequence analysis identified 27 phylogenetically informative SNPs in the red lineage. When mapping each individual SNPs onto the 24-loci-MIRU-VNTR phylogeny, 13 of these 27 SNPs suggested convergent evolution (indicated in separate Figure panels below) which would lead to high degrees of homoplasy in the MLSA data. However, phylogenetic analyses of our MLSA data clearly demonstrate that these sequence data harbour negligible amounts of homoplasy (Figure 5).