



Fig. S1. Worldwide distribution pattern of MAH population groups.

Upper panel: Distribution of population groups inferred for 692 MAH global strains (based on 14-loci MLVA data). The BAPS mixture analysis result ($k=6$) is shown. Brackets denote equivalent population groups as inferred by core genome SNP-based analysis for the sequenced strains. Pie chart diameters are proportional to sample size. Lower panel: Results of the admixture analysis.