Figure S7  Number of SNV positions that could be genotyped in X strains. For all detected variable sites, we tested in how many strains these sites could be genotyped reliably (coverage ≥ 2, samtools quality score ≥ 20, no signal of heterozygosity in any of the strains). Around 1.4 million positions could reliably be genotyped in all 104 strains. For most population genetic analysis was done using only those 1.4 mio SNV positions.