

a)

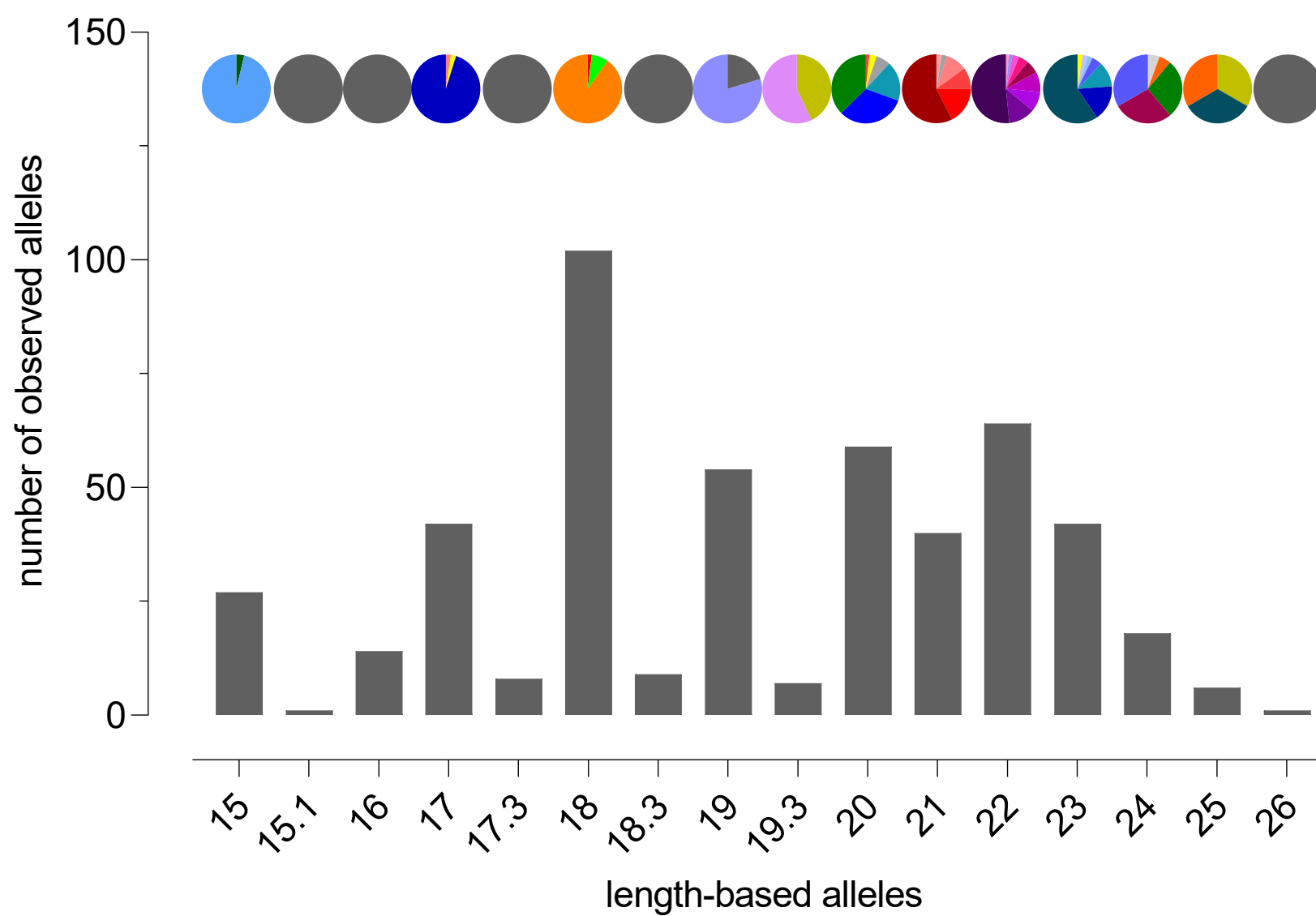
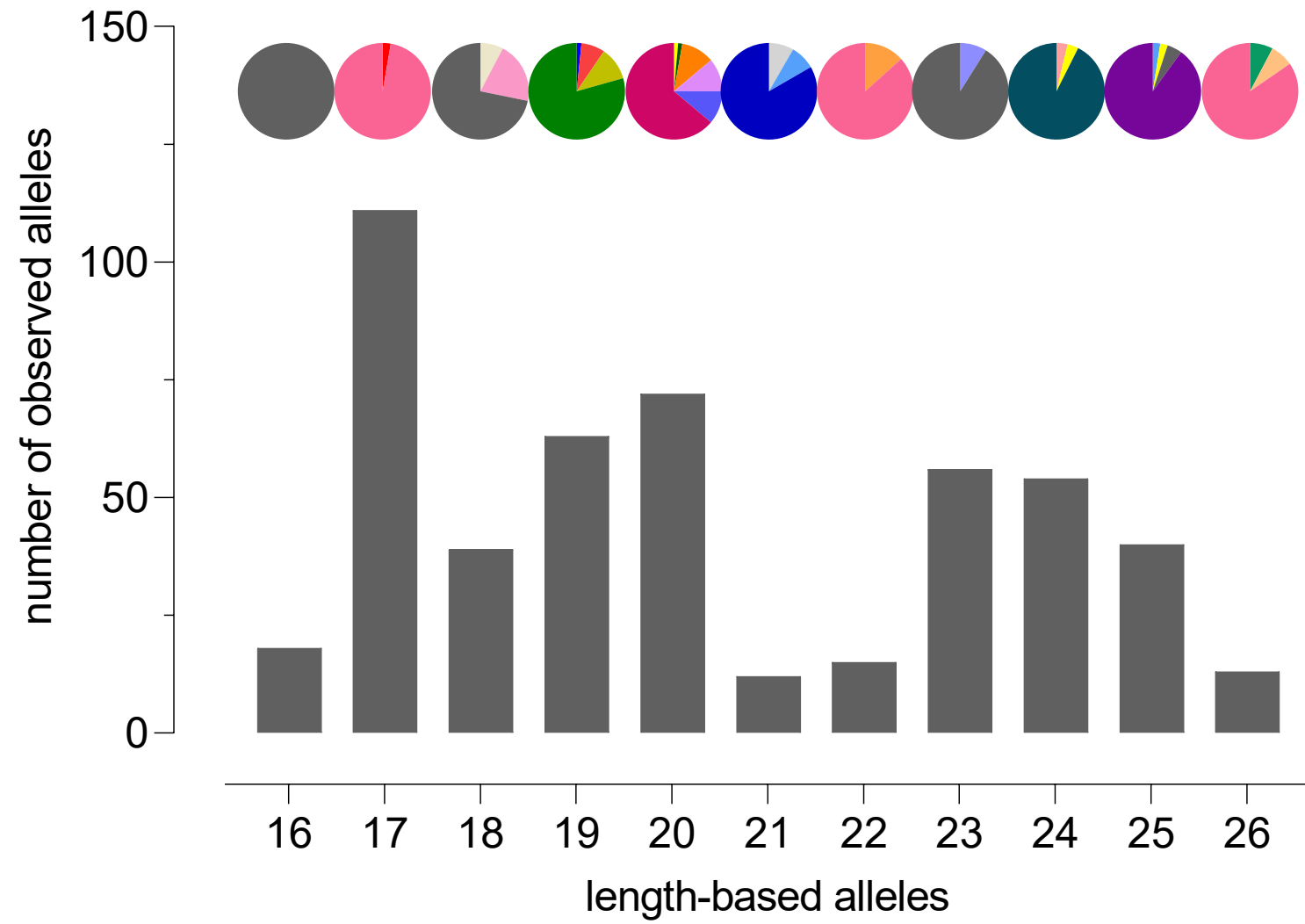


Fig. S7 Within the present dataset, including 22 autosomal STRs, particularly **a)** D12S391, **b)** D2S1338 and **c)** D21S11 were found to be highly variable. Compared to length-based STR analysis, MPS resulted in 3.3-fold, 3.0-fold and 2.6-fold increase in the number of distinguishable alleles, respectively. Pie charts on top of each bar represent the number (expressed in different colors) and relative distribution of observed sequence variants found in each length-based allele.

b)



c)

