

Figure S1. Three hypotheses (a–b) explaining genetic divergence among populations of sub-alpine (A) and mountain (M) ecotypes in northern (1) and southern (2) mountain ranges.

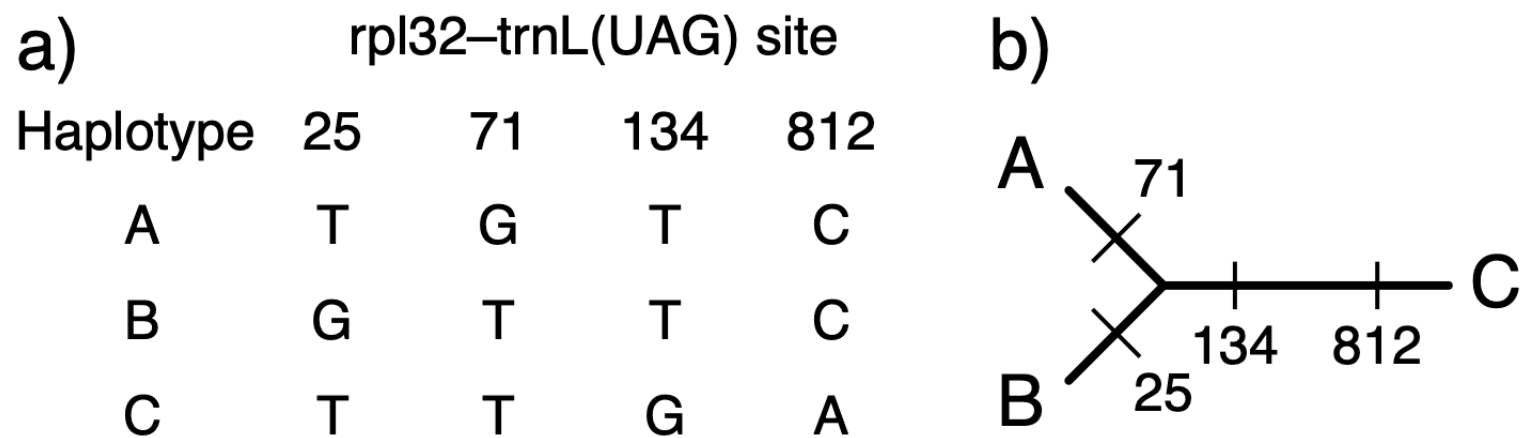


Figure S2. Chloroplast DNA haplotypes discriminated by substitutions at four nucleotide sites in rpl32–trnL(UAG) region. Nucleotide variation (a) and haplotype network (b) are shown.

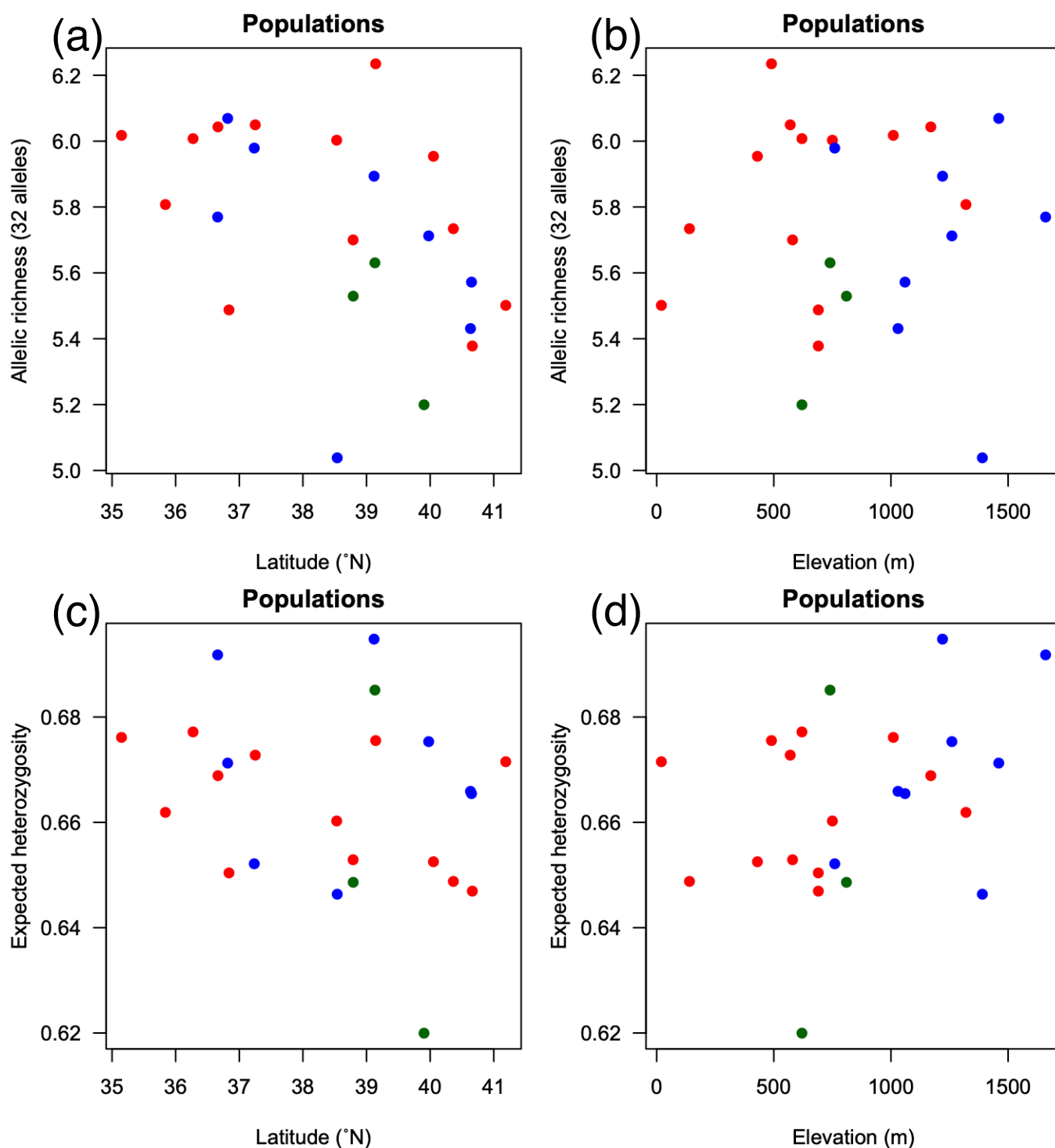


Figure S3. Allelic richness of 32 alleles (a, b) and expected heterozygosity (c, d) of populations along latitudinal (a, c) and elevational (b, d) gradients. Colors of circles indicate taxonomic and genetic categories (red: Qc, blue: Qch, and green: populations identified as Qch in the field observation but grouped to Qc in genetic analysis).

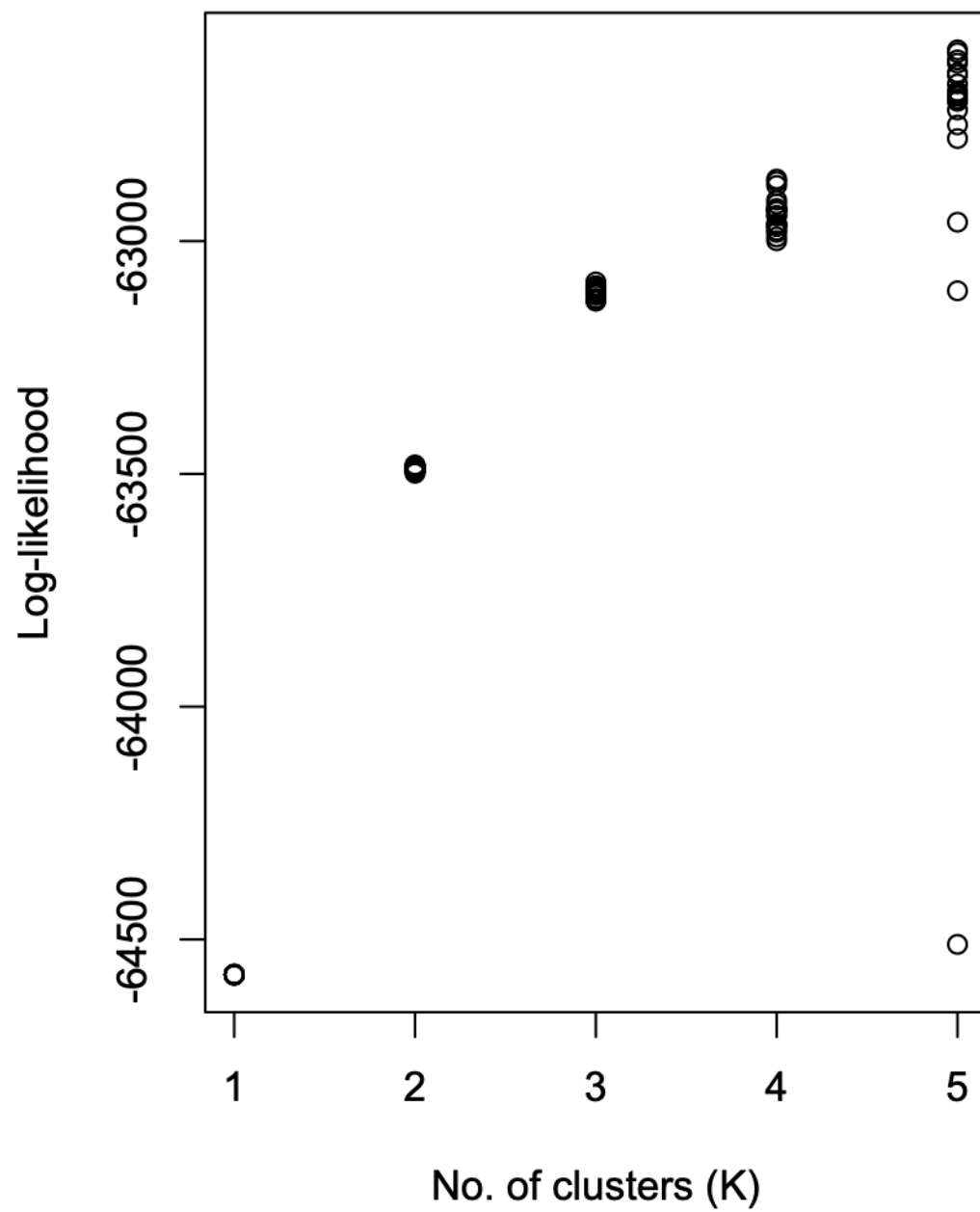


Figure S4. Log-likelihood of replications with 1–5 clusters in STRUCTURE analysis.