

Melitaea britomartis

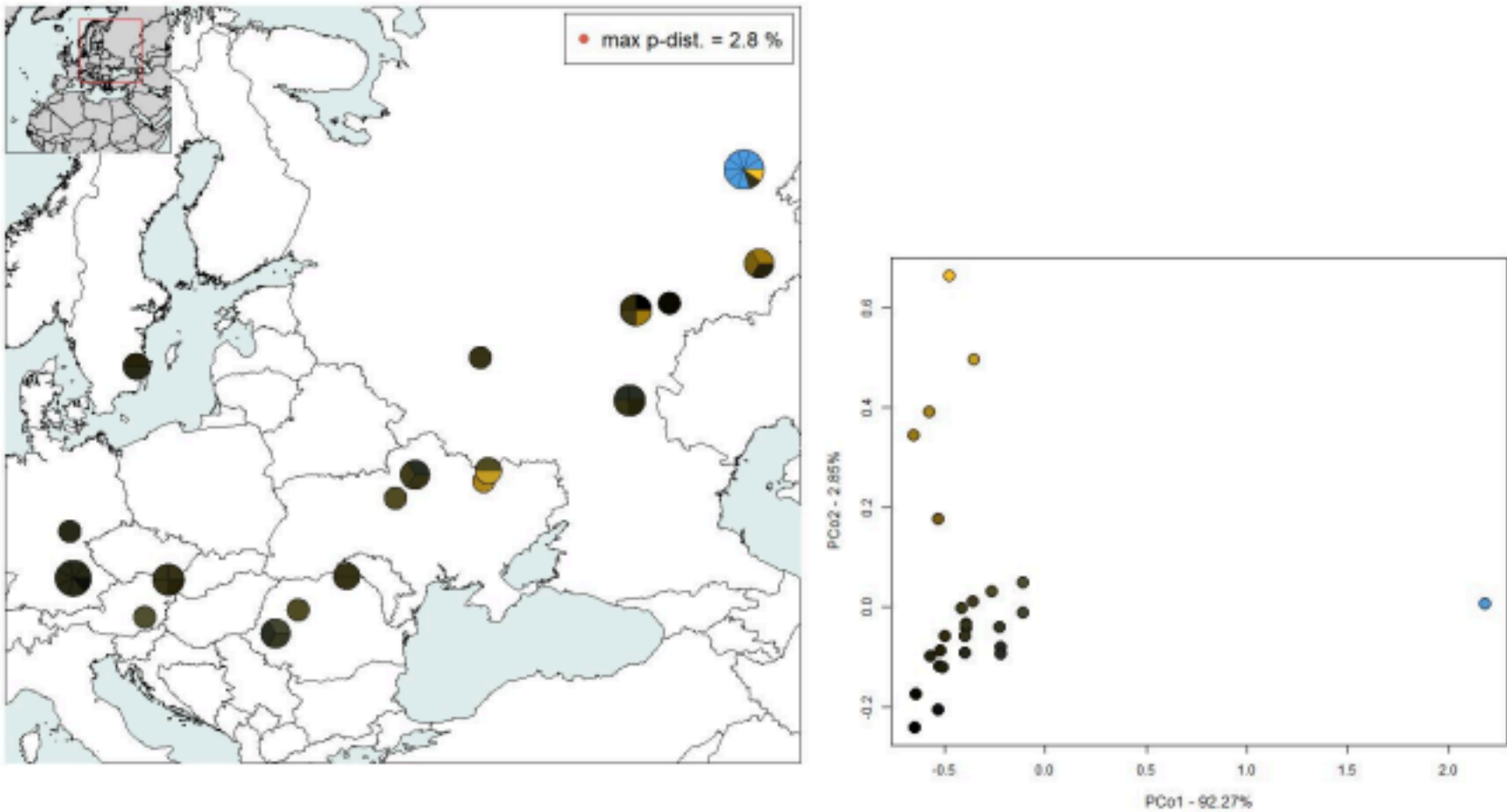


Figure 621 Map of *Melitaea britomartis* showing the localities of the sequenced specimens (left). Nearby localities are grouped in pies. Colours match the bidimensional colour space of the PCoA projection (right) of max p-dists among sequences (dots). Sequences= 51; Hap obs.= 22; Hap asympt.= 118.1; Hap % obs.= 18.6%; GST= 0.485; DST= 0.0056; HD= 0.929; ND= 0.0096; max p-dist= 2.8%.

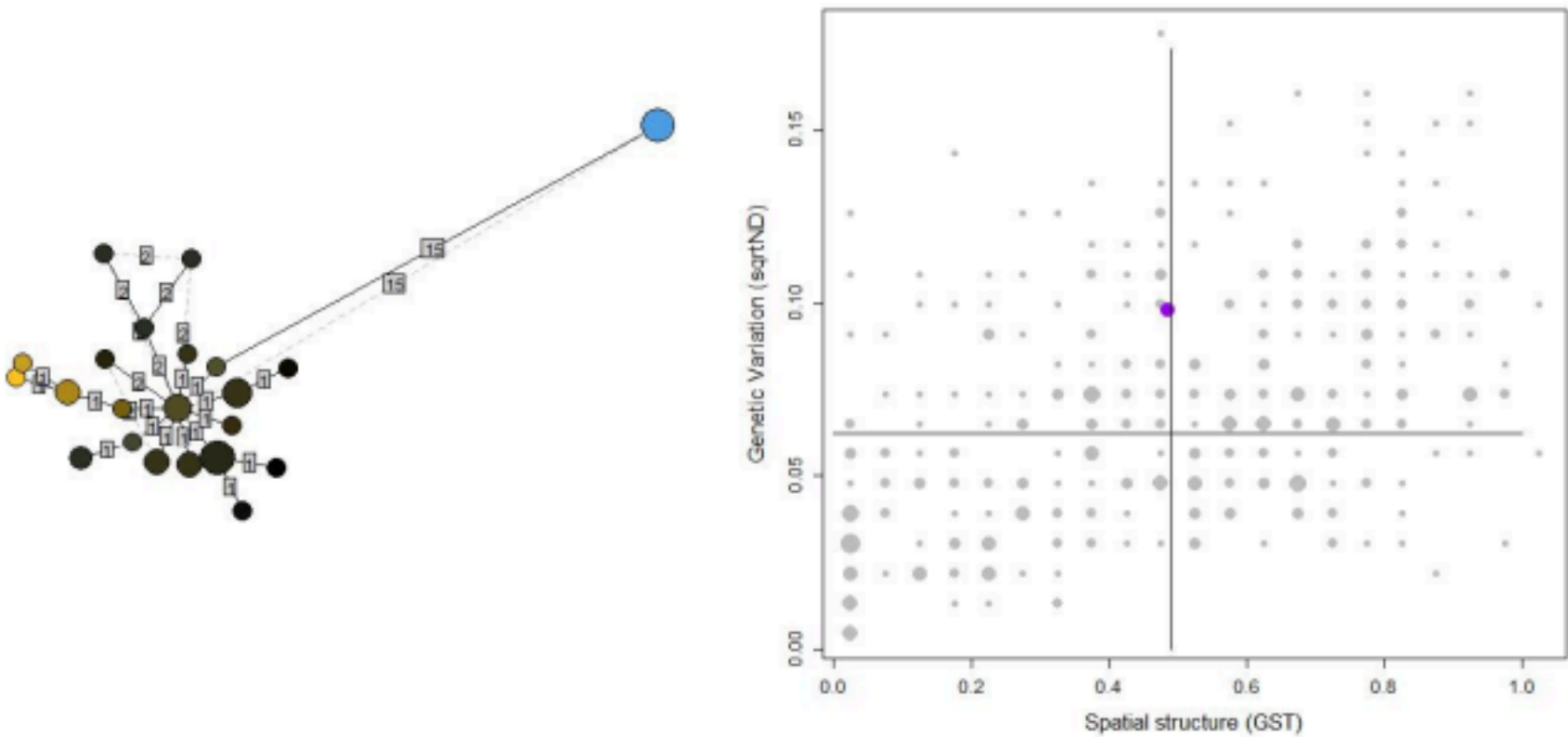
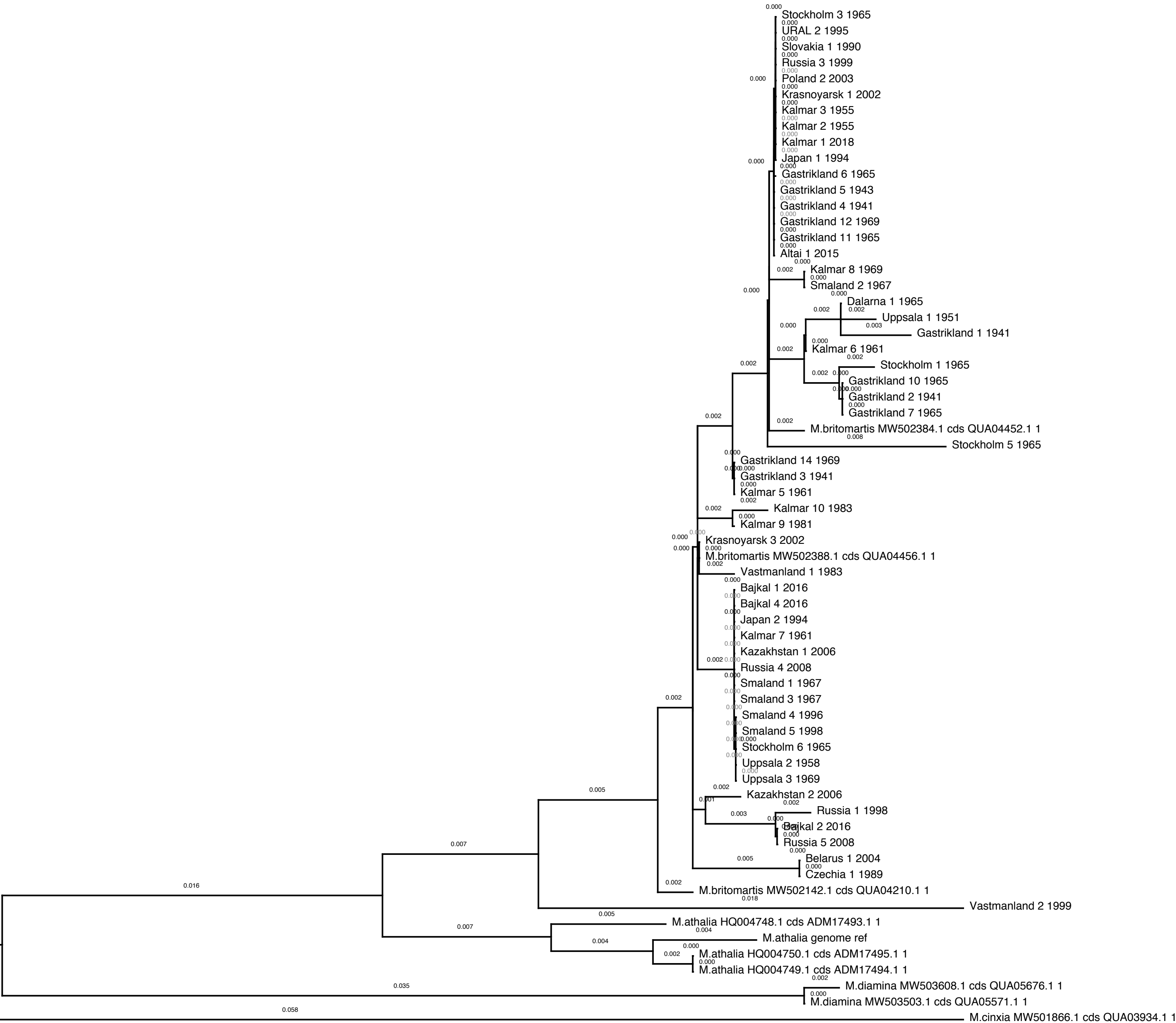


Figure 622: Haplotype network (left) of *Melitaea britomartis* sequences > 599 bp with colours matching the PCoA colour space (above). The bubble plot for mt-DNA polymorphism (square root transformed nucleotide diversity) and spatial structure (GST) among all species in the atlas and values for *Melitaea britomartis* (purple dot). The horizontal and vertical lines represent median values of nucleotide diversity and GST, respectively. Sequences > 599 bp= 51.



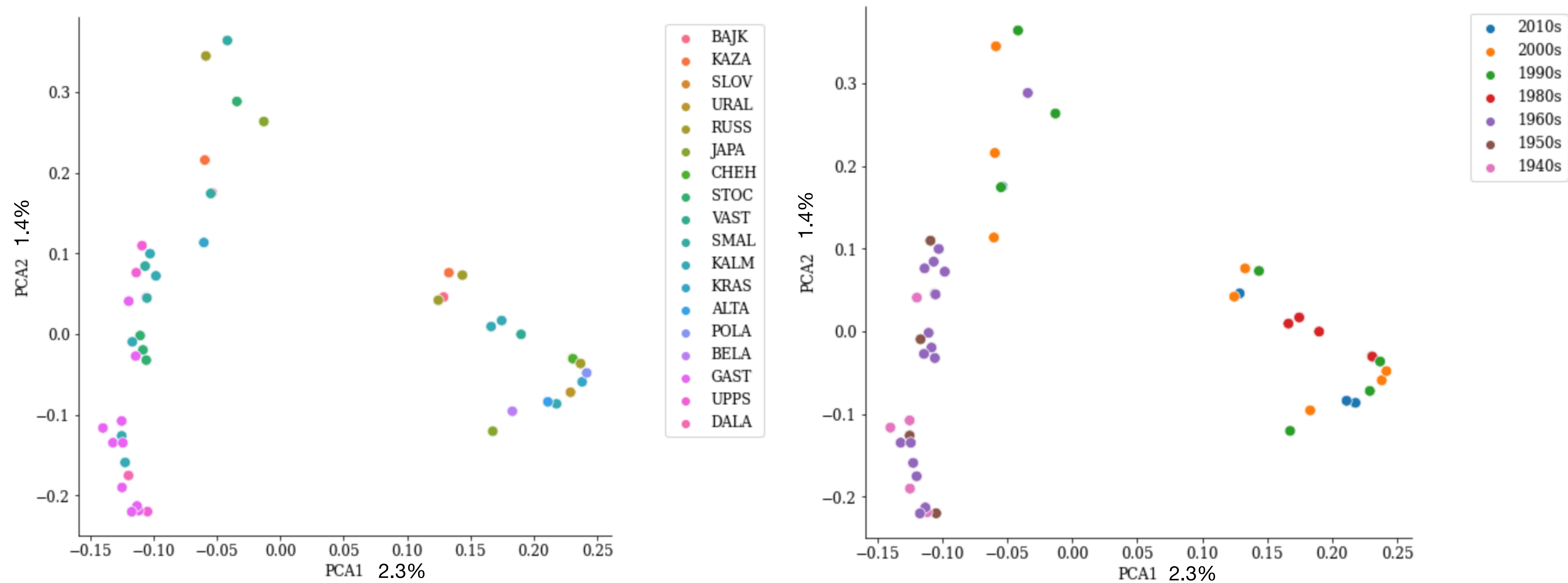
Samples after filtering and quality control

Total number of samples: 73 (3 excluded due to quality issues)



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Results after new set of filters



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Results after new set of filters

