

Figure S6: Detailed haplotype maps, networks and sequence alignment for all 4 primer combinations and replicates of selected taxa. **a)** Haplotype maps for both replicates for each of the four primer combinations. For *A. aquaticus* only the 10 most common haplotypes are shown in different colours (remaining ones in white). For each primer combination, the haplotypes in the map and network have the same corresponding colours. **b)** Haplotype networks for each primer pair. Each cross line represents one base pair difference between the respective haplotypes. Haplotypes present in just one replicate are indicated by A or B next to the network node. Dashed lines around a circle indicate novel haplotypes that were not available in the BOLD reference database. **c)** Quantification of similarity between both replicates, by plotting abundance of individual haplotypes of each sampling point against each other. The red line indicates the best fit (with significance and adjusted R² value given in each plot). **d)** Sequence alignment of all haplotypes, with mismatching nucleotides between sequences highlighted (green = T, red = A, yellow = G and blue = C).

See the following pages for example plots of:

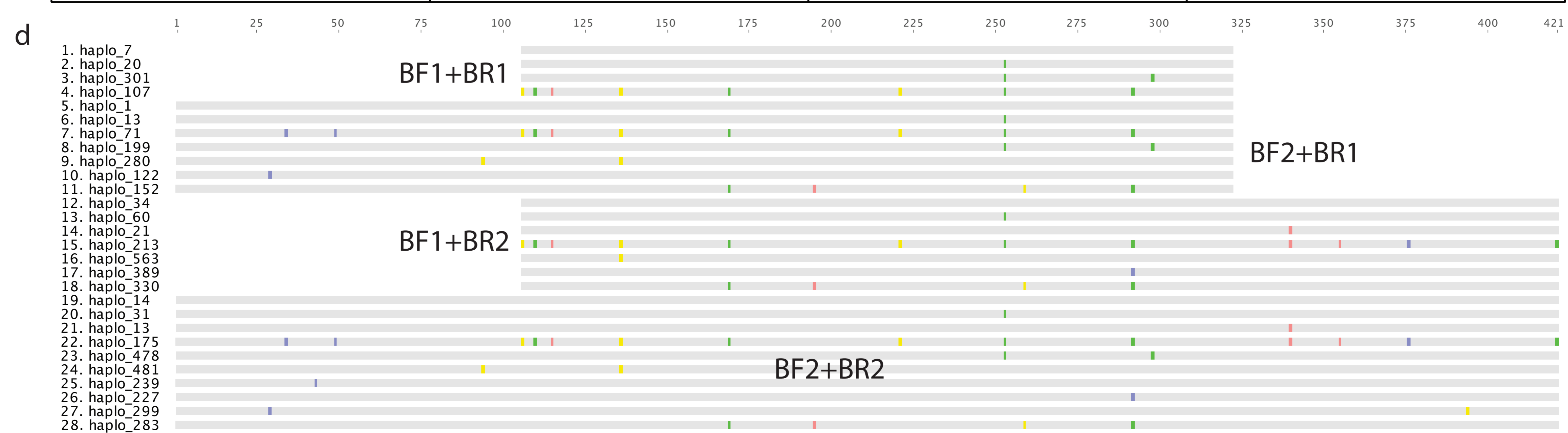
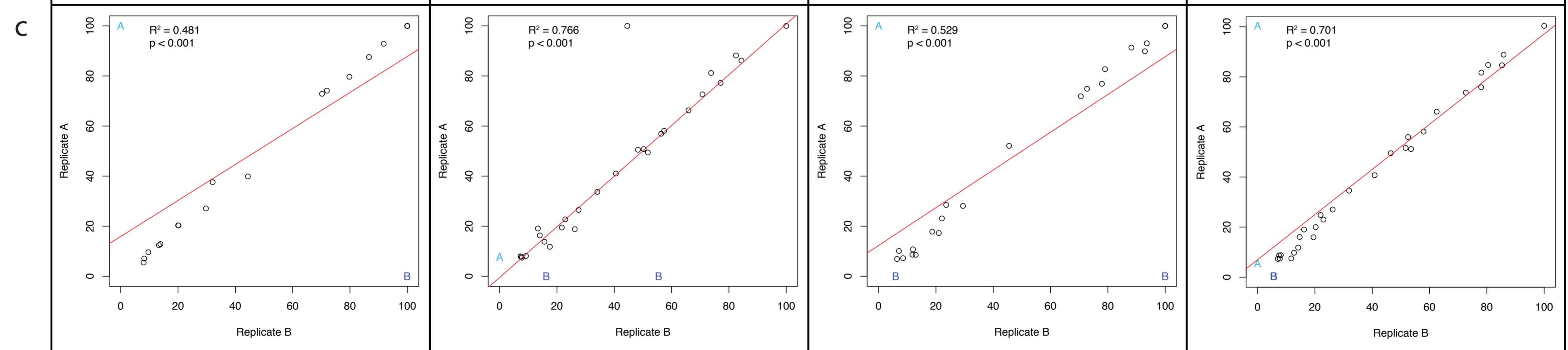
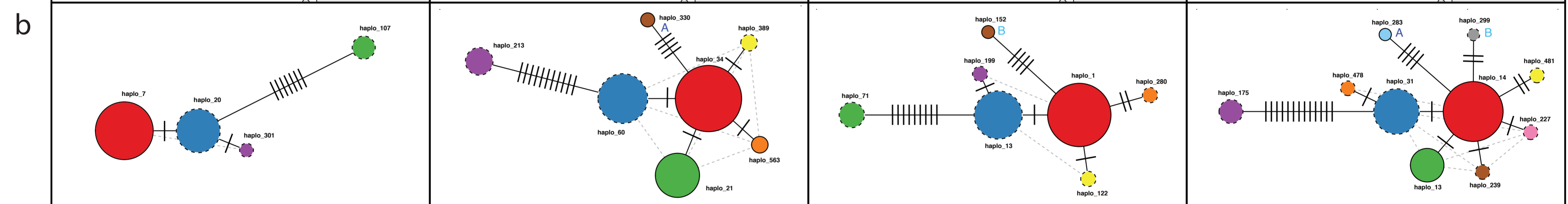
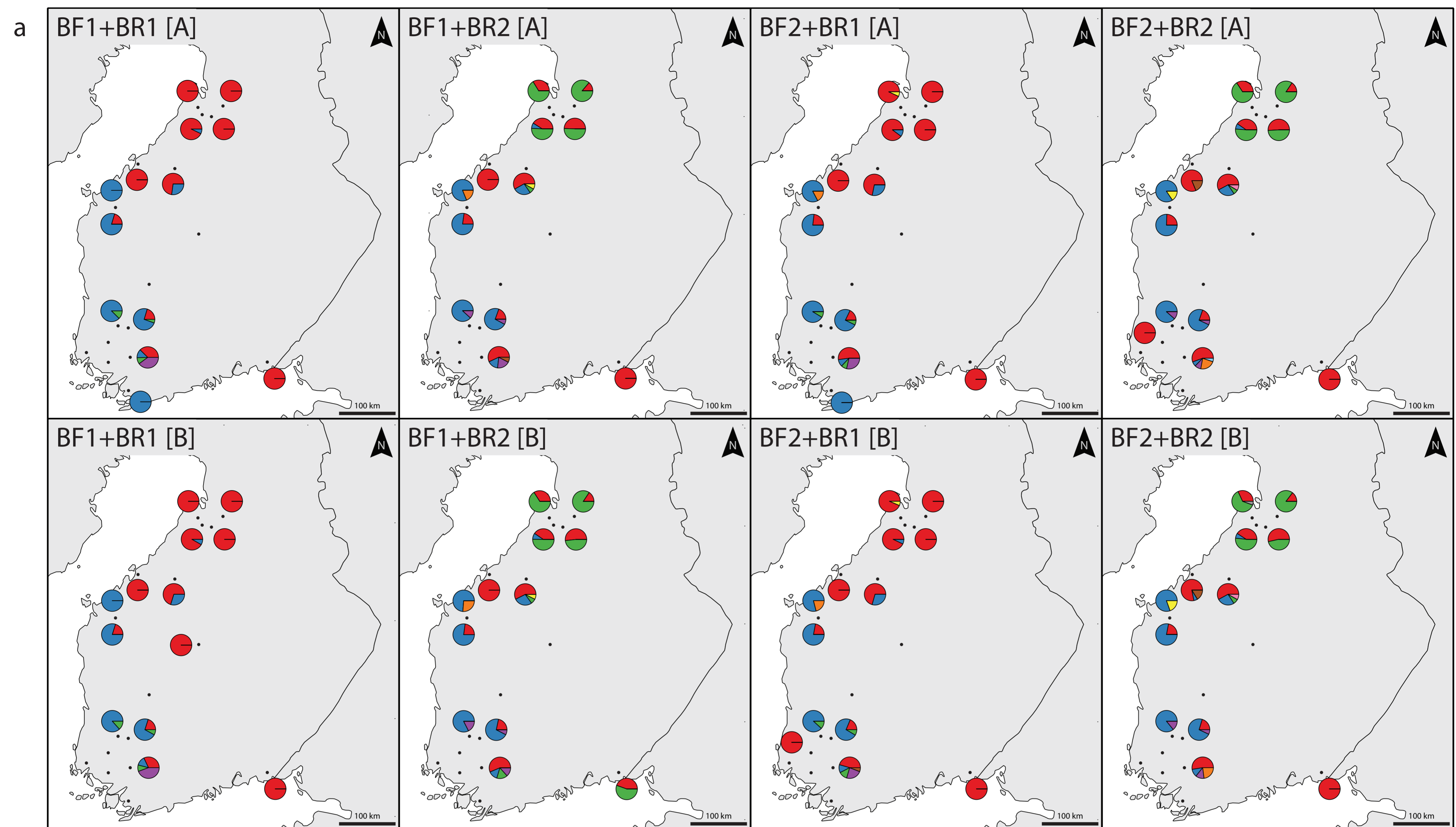
Page 2: *Taeniopteryx nebulosa*

Page 3: *Hydropsyche pellucidula*

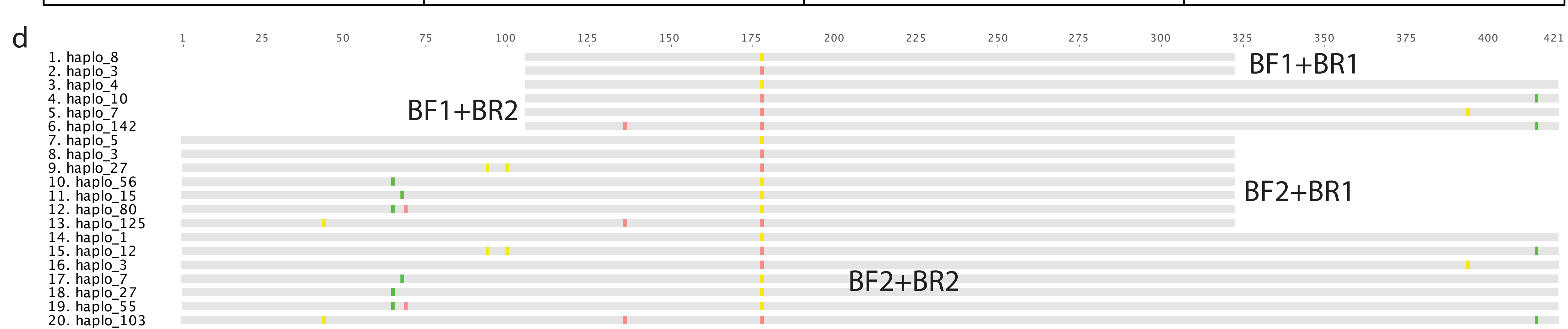
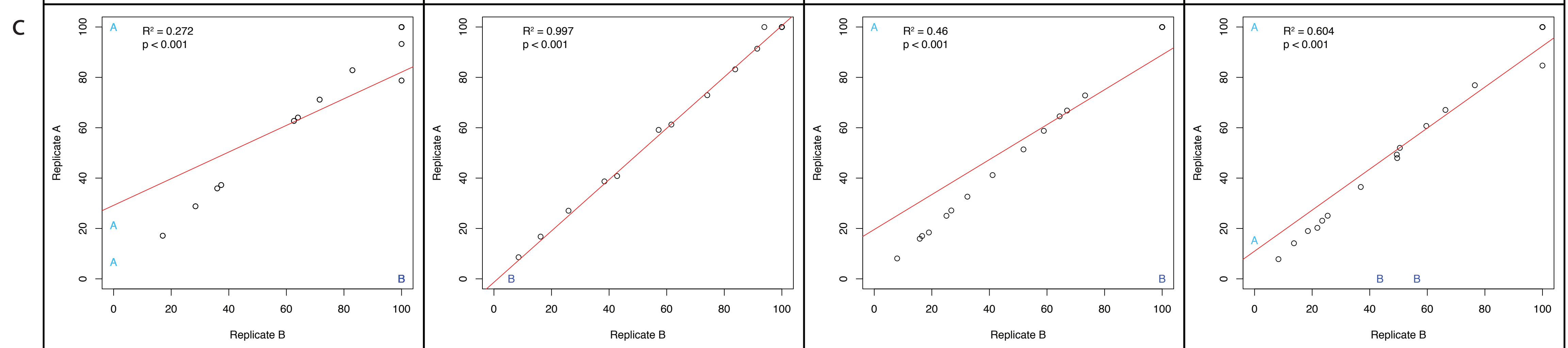
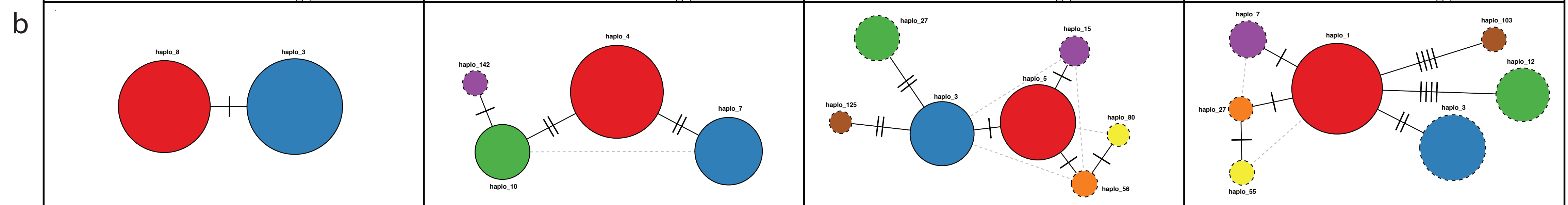
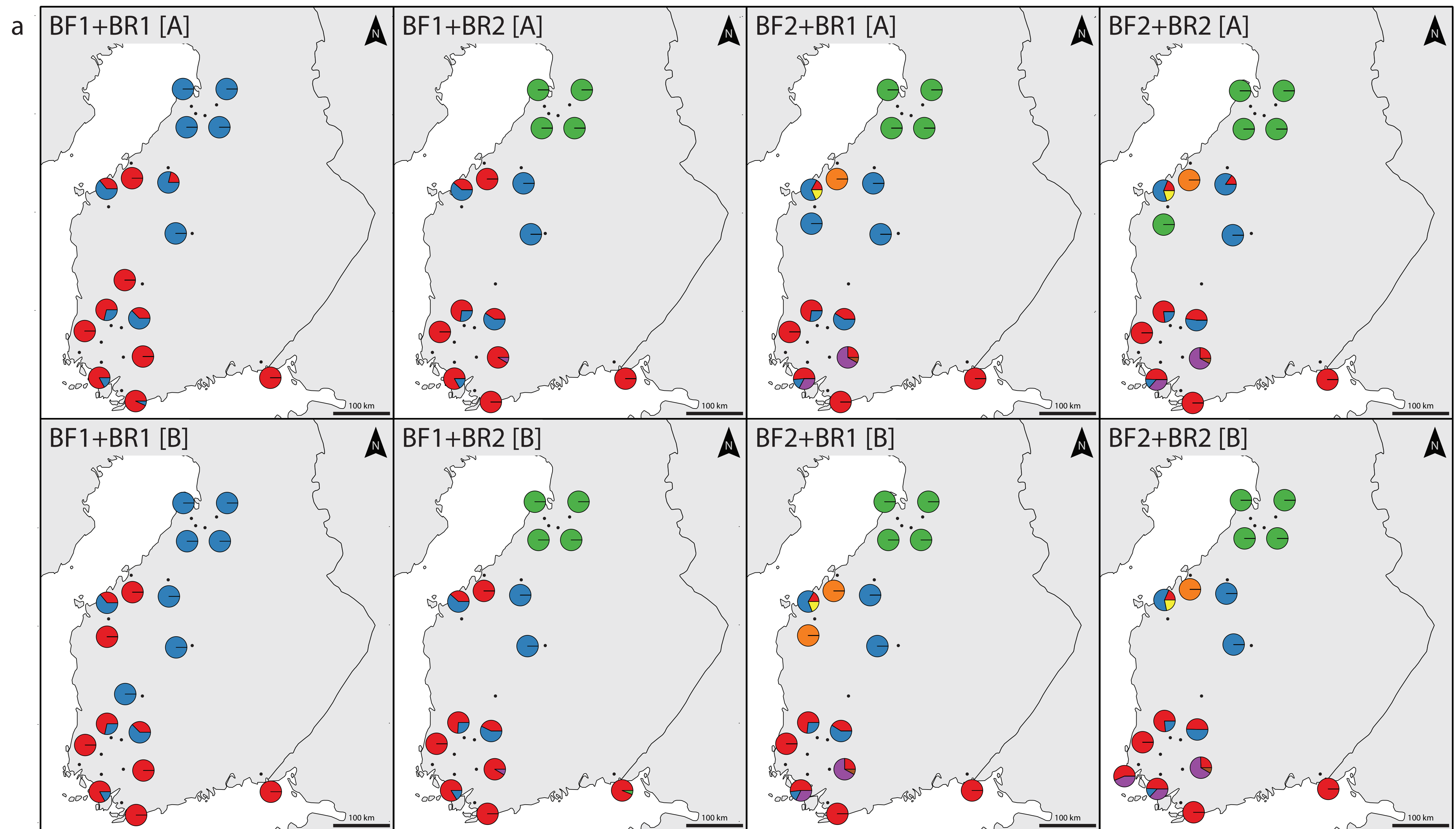
Page 4: *Oulimnius tuberculatus*

Page 5: *Asellus aquaticus*

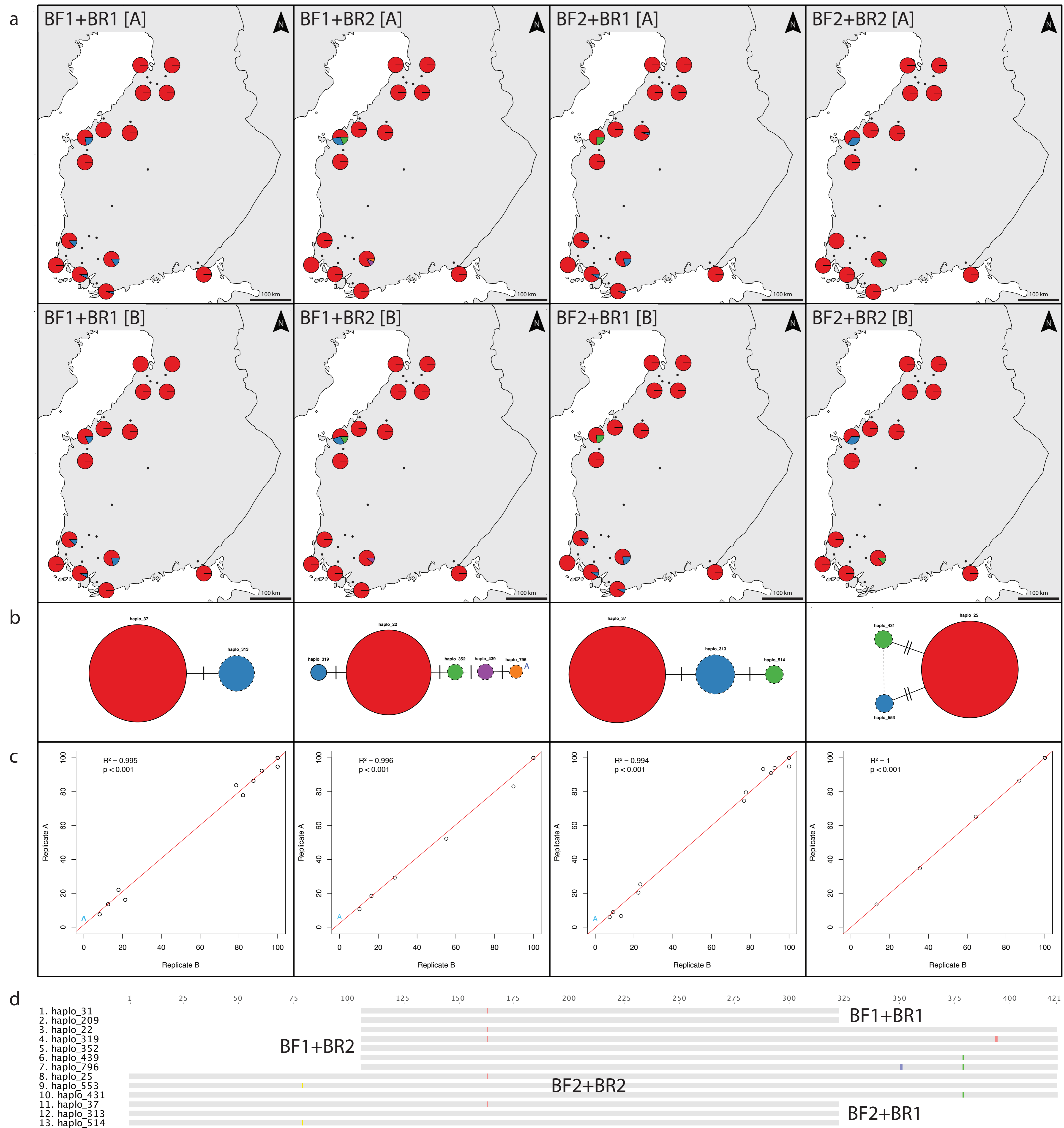
I) *Taeniopteryx nebulosa* (Plecoptera)



II) *Hydropsyche pellucidula* (Trichoptera)



III) *Oulimnius tuberculatus* (Coleoptera)



IV) *Asellus aquaticus* (Isopoda)

