

Fig. S1 Bar plot of the chloroplast haplotypes in each population. The upper rectangles indicate where populations sampled. The middle rectangles indicate *S. virgaurea* (red) and *S. yokusaiana* (blue). The colors of the lower bar plot correspond to the colors in Fig. 3a.

Mismatch distribution (demographic expansion)

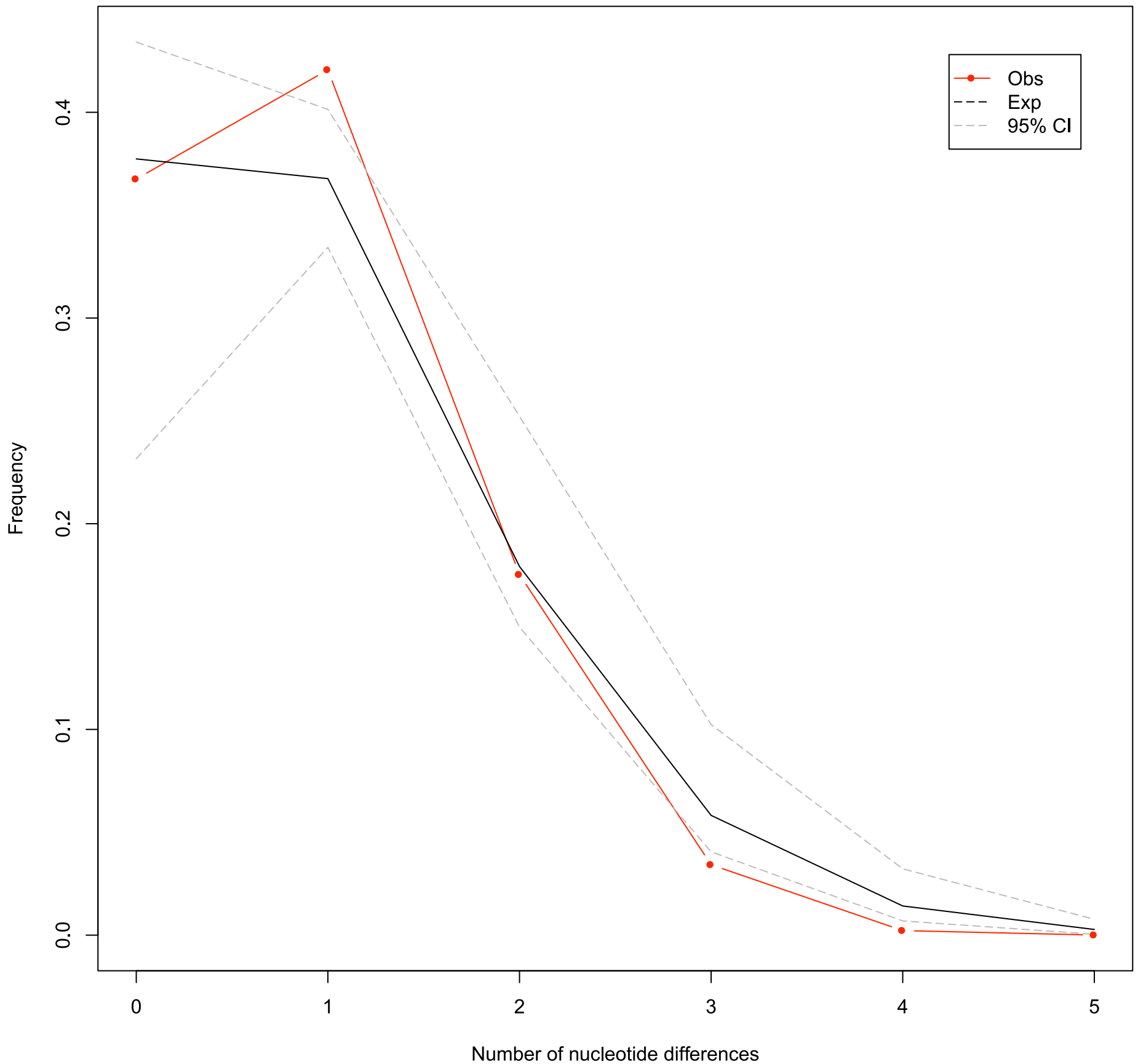


Fig. S2 Mismatch distribution of the chloroplast haplotypes. The solid red line with points is the observed mismatch distribution, the solid black line is the simulated mismatch distribution of the demographic expansion model, and the dashed grey lines indicate the 95% CI of the simulated mismatch distribution.

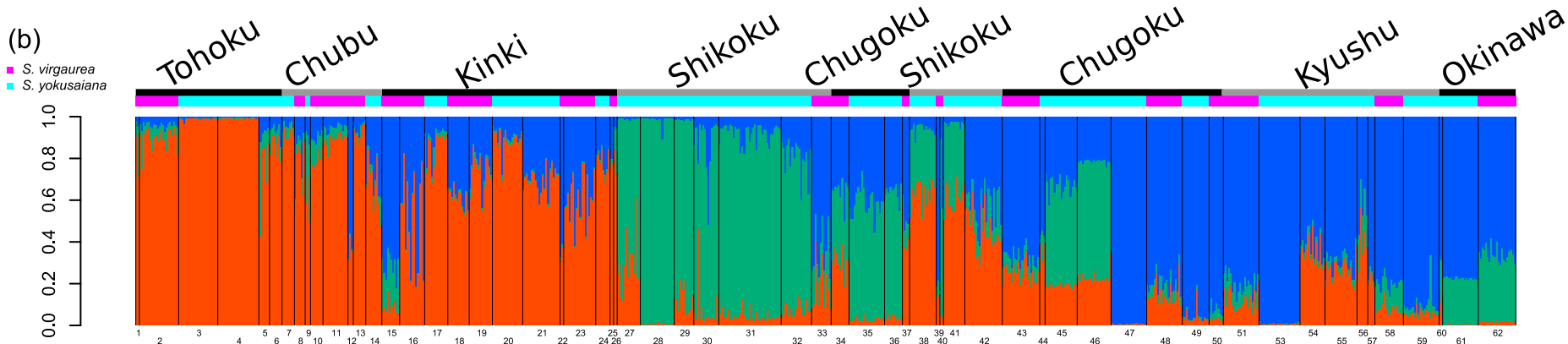
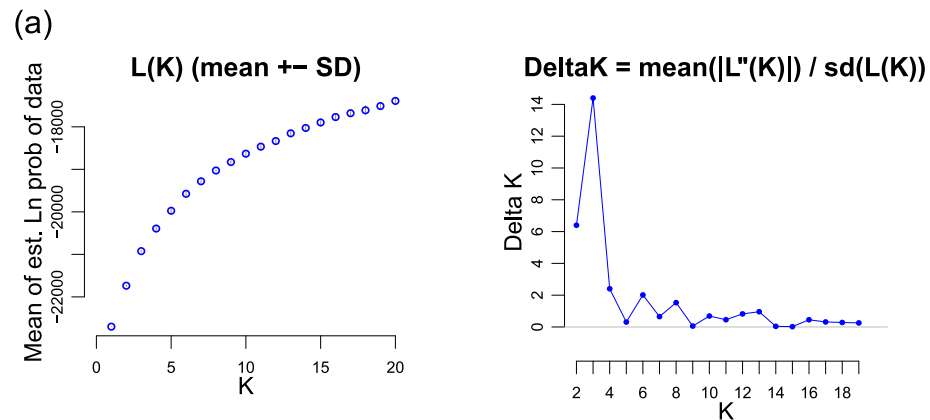
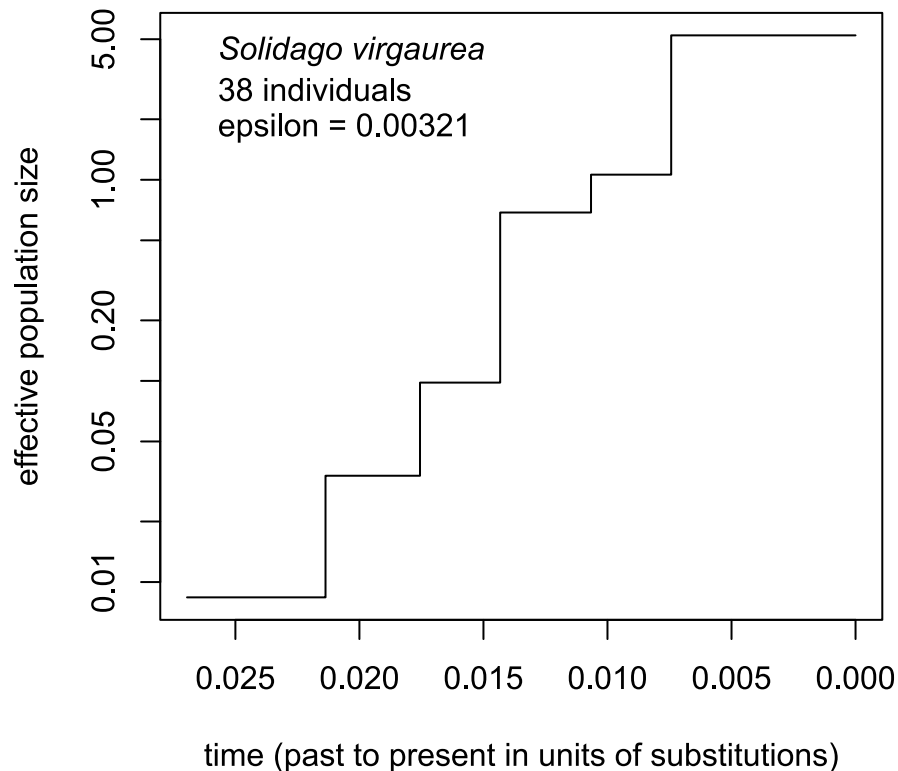


Fig. S3 Bayesian clustering analysis of nSSR data. (a) Plot of $L(K)$ and ΔK values based on structure harvester. (b) Bar plot of the Q-matrix ($K = 3$). The upper rectangles indicate where populations sampled. The middle rectangles indicate *S. virgaurea* (red) and *S. yokusaiana* (blue). The colors of the lower bar plot correspond to the colors in Fig. 3b.

(a)



(b)

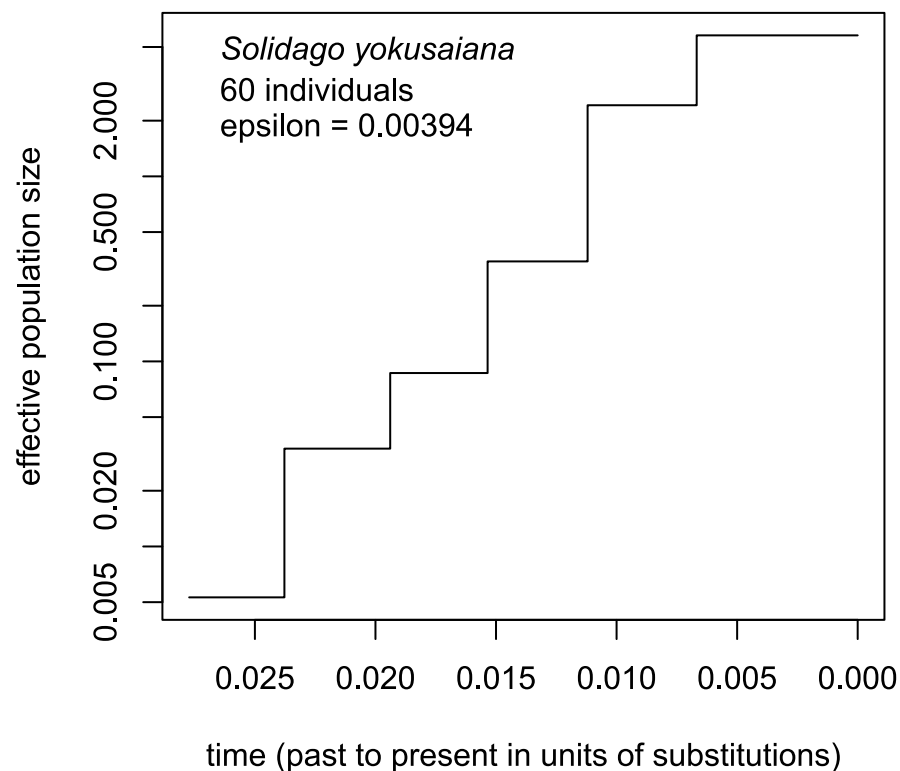


Fig. S4 Generalized skyline plots for the UPGMA trees with the Hamming distance for (a) *S. virgaurea* ($\epsilon = 0.00702$) and (b) *S. yokusaiana* ($\epsilon = 0.00572$).

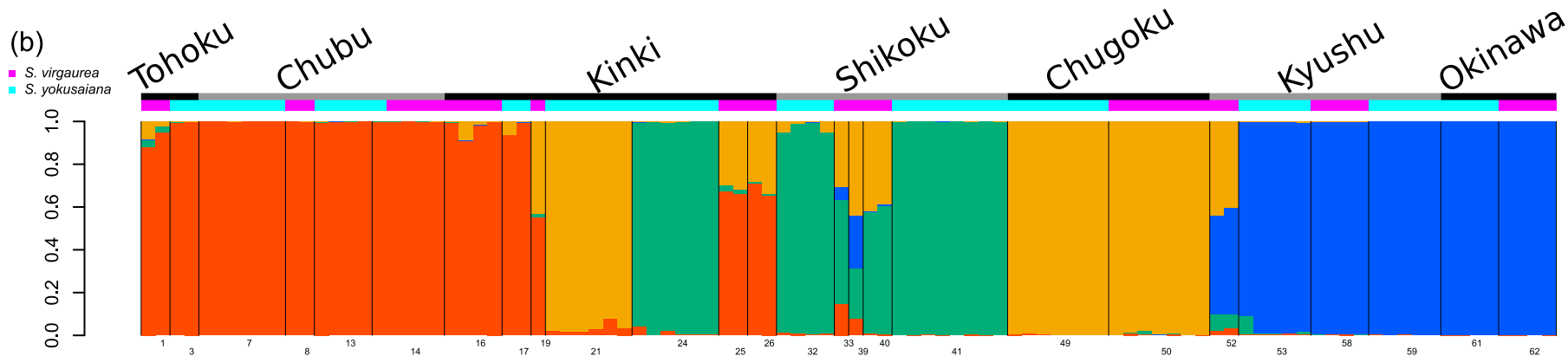
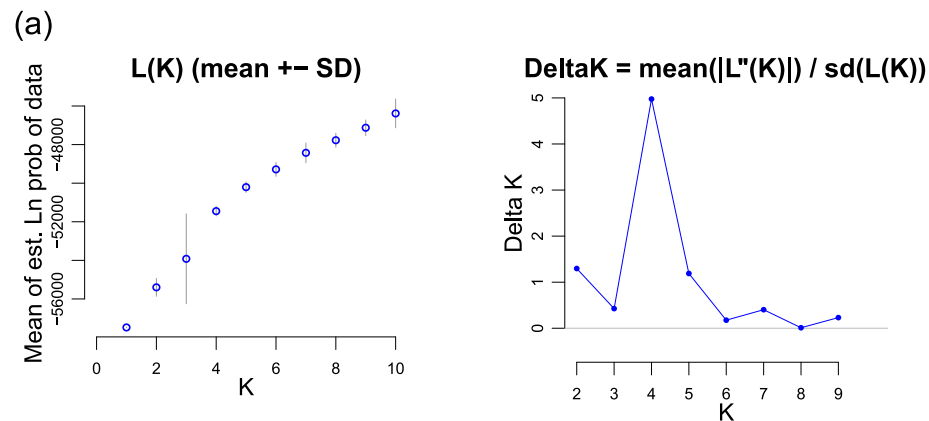


Fig. S5 Bayesian clustering analysis of the ddRADseq data. (a) Plot of $L(K)$ and ΔK values based on structure harvester. (b) Bar plot of the Q-matrix ($K = 4$). The upper rectangles indicate where populations sampled. The middle rectangles indicate *S. virgaurea* (red) and *S. yokusaiana* (blue). The colors of the lower bar plot correspond to the colors in Fig. 3c.

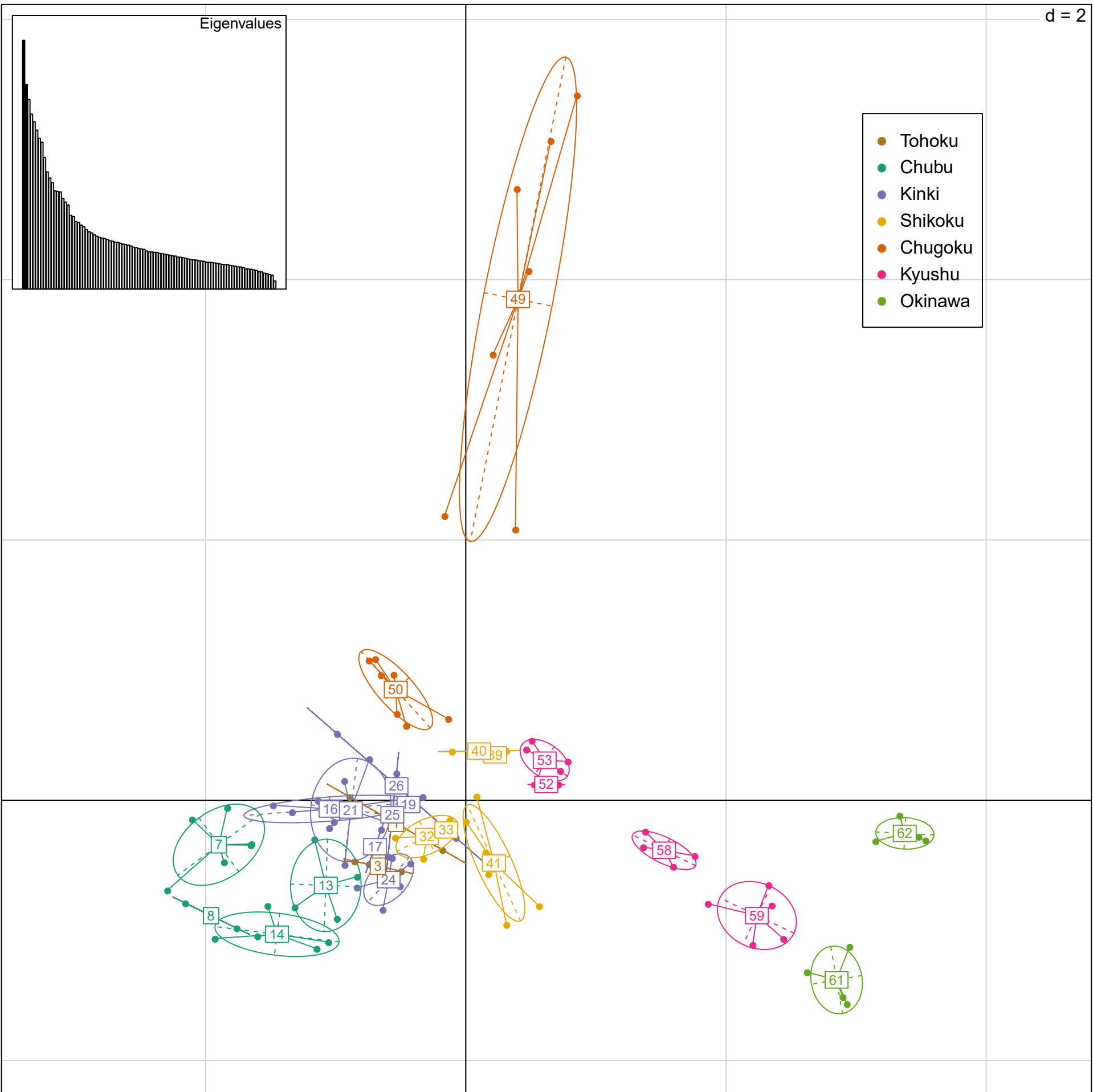


Fig. S6 Principal components analysis of the ddRADseq data. The ellipses correspond to populations, and colors indicate districts where populations sampled. Top-left bar plot indicates eigenvalues.

Table S2 Summary of nSSR loci and its primer sequence.

Locus	Repeat motif	Primer sequence (5'-3')	Reference
Sol_2001876	(ATC) ₈	F: AAGCTCATGGGTCCTCTGC R: ATCAAGCCAAAGCAGCTCG	Sakaguchi and Ito 2014
Sol_2003053	(GAT) ₉	F: TGAACCGACGGATGGAACC R: TGGGAGCTGGACATGTTGG	Sakaguchi and Ito 2014
Sol_2003631	(GAT) ₁₀	F: CACCAGGCATGATCTGAAGC R: CACCCTATCCACAATGCCAC	Sakaguchi and Ito 2014
Sol_2005991	(GAT) ₁₁	F: TGC GGCTGACAATAATACACC R: CCCAATTC CATCTGGGTTTC	Sakaguchi and Ito 2014
Sol_2006931	(AC) ₁₀	F: CTCTGCACCTCTTATCTGGAC R: AGCCACGTTTCGTCGTTTG	Sakaguchi and Ito 2014
Sol_2007258	(GAT) ₁₂	F: CGGAAGTGGGTTTGGATCG R: CATGCACGCTATGACTCGG	Sakaguchi and Ito 2014
Sol_2007556	(AAG) ₉	F: GCGTCGGCGCTTCATATC R: TTCCAACGCCTGAATCCC	Sakaguchi and Ito 2014
Sol_2012220	(AC) ₁₂	F: GGCCCGGATGGTTGATTTTC R: GCCGAAACACCAAGGCTC	Sakaguchi and Ito 2014
Sol_2013075	(CT) ₁₀	F: TCATGTGAAGACACGATCCG R: CAAGATAAGGCAAGCTCCCAC	Sakaguchi and Ito 2014
Sol_2013411	(GAT) ₁₀	F: TGTTGTGAAGAAAGTGGATACTC R: CCTTGCCAACAAAGCTTGC	Sakaguchi and Ito 2014
Sol_2071098	(CT) ₁₁	F: TCTTGGAGGTGAGGAAAGCC R: TGGTGTGCGTTCAAGGTTTC	Sakaguchi and Ito 2014
Salt1	(ATT) ₁₅	F: ACTACTGGCGGCGTAACAG R: CCGCCGGTTTCAATGTTGG	Sakata et al. 2013
Salt3	(ATT) ₁₄	F: GAAGAAGAGCTTCGGATGTTGT R: CGCCTAAATTGACTTGACACAG	Sakata et al. 2013
Salt17	(ACC) ₈	F: GCACCTTCTCCAAATGCCG R: TGTCCGCTGATACCAGTCC	Sakata et al. 2013