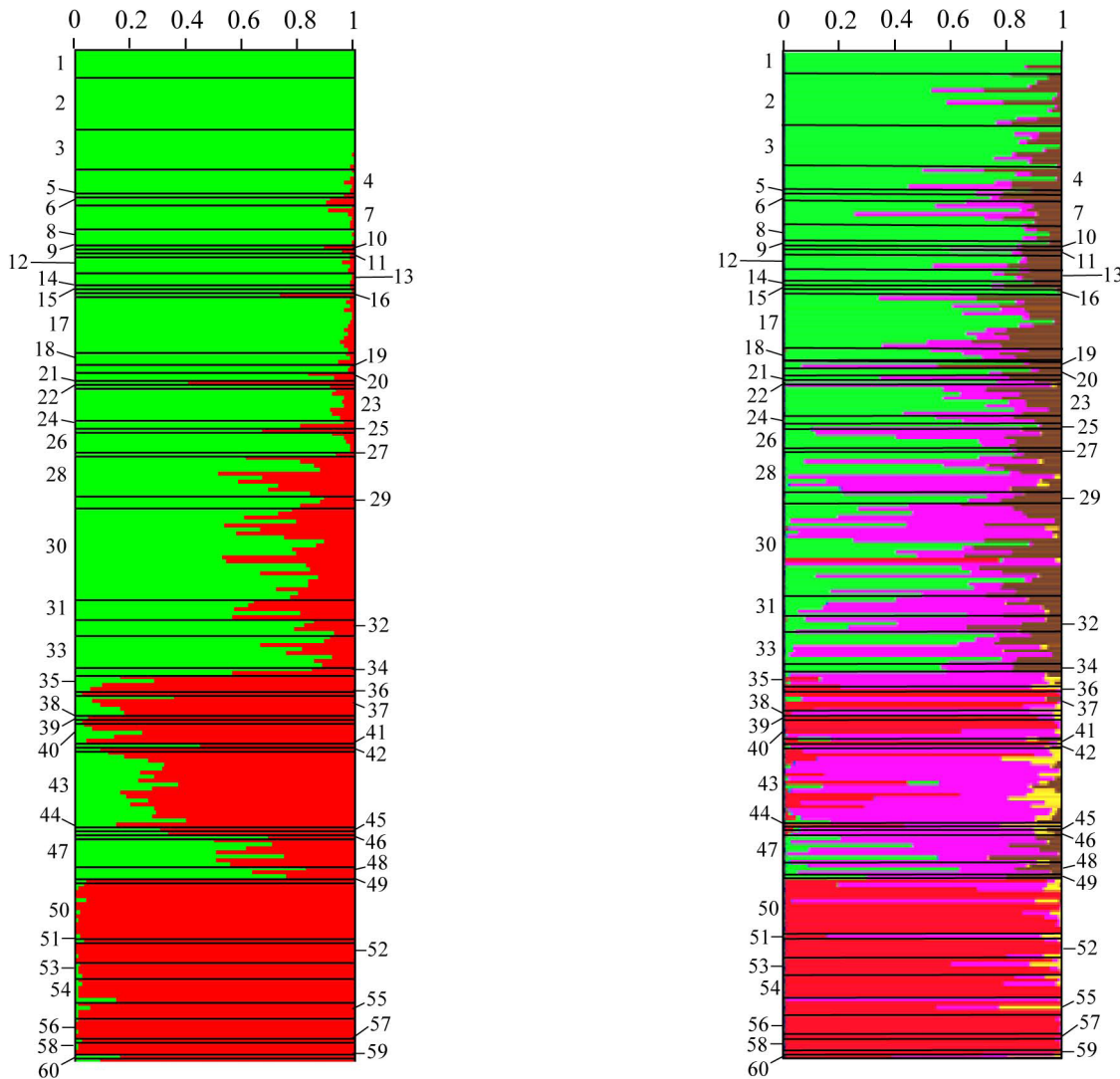**Figure S2: Bayesian-clustering assignment to parental, hybrid and backcrosses genotypic classes by the program NEWHYBRIDS.** Barplots from the analysis with STRUCTURE (K = 2) are also provided to allow direct comparison.

	1-17	23-35	37-48	50-56
parental *viridis*	0.82	0.38	0.06	0
backcrossed *viridis*	0.11	0.16	0.05	0
F1	0	0	0	0
F2	0.07	0.42	0.59	0.1
backcrossed *balearicus*	0	0	0.03	0.03
parental *balearicus*	0	0.04	0.27	0.87

STRUCTURE probability of assignment
- viridis
- balearicus

NEWHYBRIDS probability of assignment
- Parental - *viridis*
- Parental - *balearicus*
- F1 hybrid
- F2 hybrid
- Backcrossed *viridis*
- Backcrossed *balearicus*