

## Supplemental Information for:

### **An explicit test of Pleistocene survival in peripheral versus nunatak refugia in two high mountain plant species**

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Table S1 Summary statistics for each population of *Pedicularis asplenifolia* and *Carex fuliginosa* based on SNP data.

	pop <sup>1</sup>	Summary statistics <sup>2</sup>					
		$H_{obs}$	$H_{exp}$	$H$	$\pi$	$K$	$A_p$
<b><i>P. asplenifolia</i></b>	83	0.2368	0.1708	0.1951	0.1952	1.4622	52.4 / 15.6
	107	0.1965	0.1366	0.1561	0.1562	1.3725	29.5 / 13.7
	66	0.2223	0.1484	0.1696	0.1696	1.3986	8.2 / 2.1
	113	0.1833	0.1220	0.1394	0.1395	1.3308	2.6 / 0
	286	0.1536	0.0958	0.1094	0.1095	1.2485	11.6 / 3.3
	285	0.1658	0.1038	0.1186	0.1186	1.2901	7.6 / 1.5
	287	0.1844	0.1138	0.1301	0.1301	1.3103	6.8 / 5.5
<b><i>C. fuliginosa</i></b>	279	0.1577	0.1196	0.1328	0.1329	1.3660	15.7 / 6.3
	82	0.1550	0.1030	0.1145	0.1145	1.3105	22.1 / 20.9
	362	0.1372	0.0814	0.0930	0.0930	1.2071	12.3 / 12.3
	284	0.1432	0.0862	0.0984	0.0985	1.2506	75.9 / 66.0
	71	0.1624	0.1044	0.1160	0.1160	1.3181	3.7 / 3.7
	114	0.1536	0.0911	0.1041	0.1041	1.2469	9.6 / 6.8
	283	0.1513	0.1073	0.1191	0.1192	1.3193	1.2 / 1.2
	282	0.1596	0.1145	0.1271	0.1272	1.3439	1.1 / 1.1
	280	0.1536	0.0909	0.1038	0.1038	1.2578	5.5 / 4.1
	281	0.1418	0.0929	0.1031	0.1032	1.2642	11.1 / 8.3

<sup>1</sup> population (pop) numbers correspond to voucher numbers in Table 1

<sup>2</sup>  $H_{obs}$  = mean observed heterozygosity;  $H_{exp}$  = mean expected heterozygosity;  $H$  = mean heterozygosity over loci for each population;  $\pi$  = Nucleotide diversity.  $K$  = mean number of alleles over loci for each population;  $A_p$  = number of private alleles, given as nearly fixed (i.e., present in at least 75% of the individuals) / fixed (i.e., present in all individuals), corrected by nucleotide diversity as described in Westergaard *et al.* (2019).

Table S2 Pairwise  $F_{ST}$  values for *Pedicularis asplenifolia* and *Carex fuliginosa* based on SNP data.

***Pedicularis asplenifolia***

pop <sup>1</sup>	83	107	66	113	286	285
107	0.210					
66	0.166	0.200				
113	0.199	0.254	0.008			
286	0.286	0.332	0.106	0.099		
285	0.278	0.310	0.109	0.094	0.012	
287	0.246	0.301	0.080	0.061	0.116	0.104

***Carex fuliginosa***

pop <sup>1</sup>	279	82	362	284	71	114	283	282	280
82	0.207								
362	0.314	0.374							
284	0.234	0.231	0.405						
71	0.187	0.204	0.346	0.167					
114	0.213	0.212	0.389	0.205	0.148				
283	0.168	0.200	0.340	0.183	0.152	0.182			
282	0.146	0.206	0.324	0.179	0.134	0.152	0.136		
280	0.192	0.253	0.363	0.211	0.151	0.228	0.168	0.087	
281	0.250	0.268	0.422	0.254	0.197	0.187	0.230	0.109	0.211

<sup>1</sup> population (pop) numbers correspond to voucher numbers in Table 1

Table S3 Comparison of Pleistocene survival scenarios of the study species using two individuals per population and one population less for *Carex fuliginosa*.

Species	Model <sup>1</sup>	Marginal density	Bayes factor <sup>2</sup>	P-value
<i>P. asplenifolia</i>	Nun	$9.73 \times 10^{-20}$	>100	<0.001
	Peri <sub>East</sub> +Nun	$1.07 \times 10^{-4}$	0	0.987
	Peri <sub>South</sub> +Nun	$3.08 \times 10^{-8}$	>100	0.002
	Peri+Nun <sub>Central</sub>	$2.63 \times 10^{-13}$	>100	<0.001
	Peri <sub>East</sub>	$1.11 \times 10^{-6}$	96.39	0.031
	Peri <sub>South</sub>	$7.48 \times 10^{-6}$	14.30	0.065
<i>C. fuliginosa</i>	Nun	$4.28 \times 10^{-98}$	>100	<0.001
	Peri <sub>East</sub> +Nun	$2.78 \times 10^{-5}$	1.97	0.112
	Peri <sub>South</sub> +Nun	$5.79 \times 10^{-7}$	94.65	0.034
	Peri+Nun <sub>Central</sub>	$6.85 \times 10^{-115}$	>100	<0.001
	Peri <sub>East</sub>	$5.48 \times 10^{-5}$	0	0.486
	Peri <sub>South</sub>	$7.84 \times 10^{-7}$	69.89	0.023

<sup>1</sup> Nun, nunatak survival in interior refugia, the index indicating (where necessary) the location of the ancestral population (Central, central Alps); Peri, peripheral survival in peripheral refugia, the index indicating (where necessary) the location of the ancestral population (East, eastern Alps; South, southern Alps).

<sup>2</sup> the ratio between marginal densities of the best model (i.e., the one with the highest marginal density) and of the alternative model: the higher the value, the higher the support for the best model.

Fig. S1 Plots of (A, C) Delta  $K$  and of (B, D) mean  $\text{Log}_e(X|K)$  for each  $K$  value for (A, B) *P. asplenifolia* and for (C, D) *C. fuliginosa*.

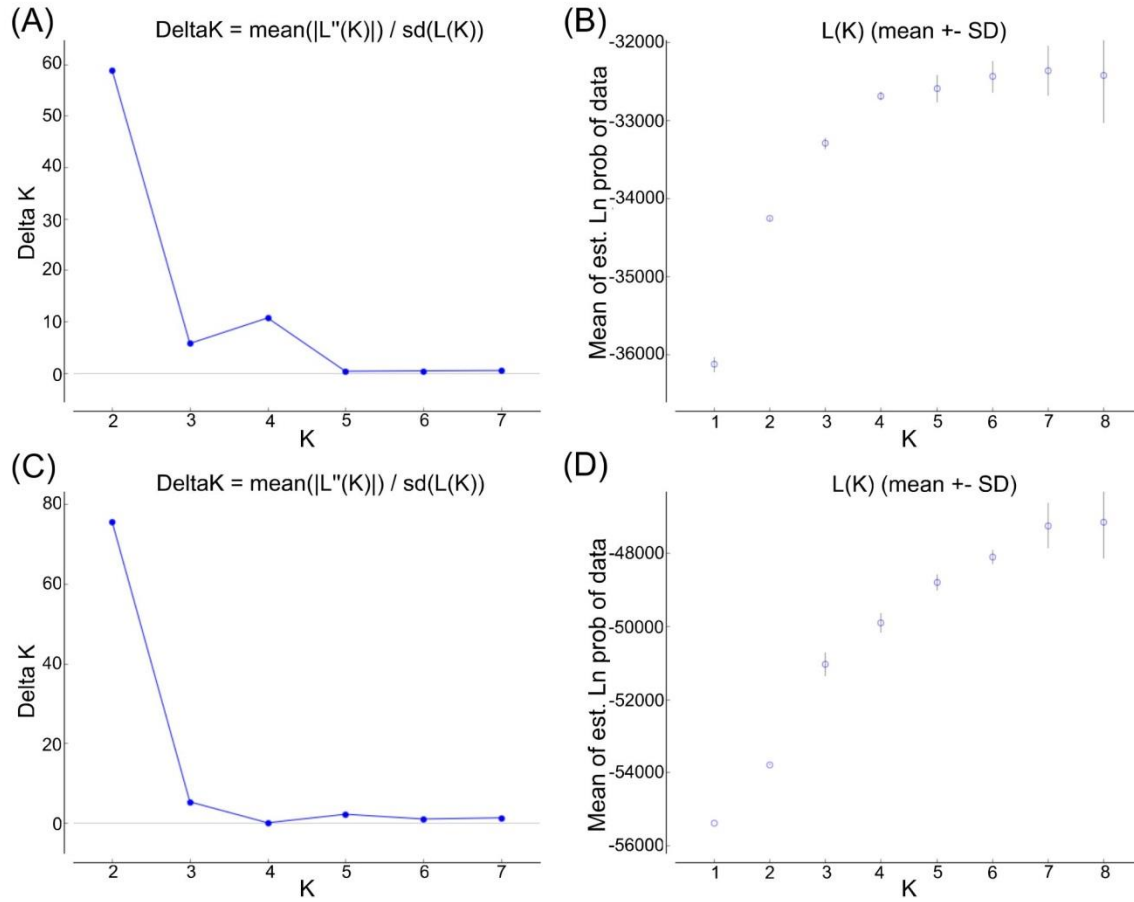
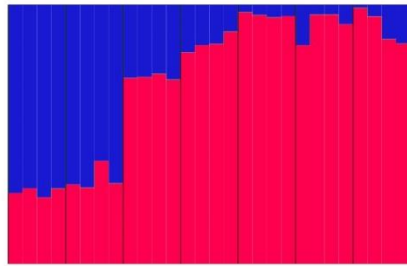


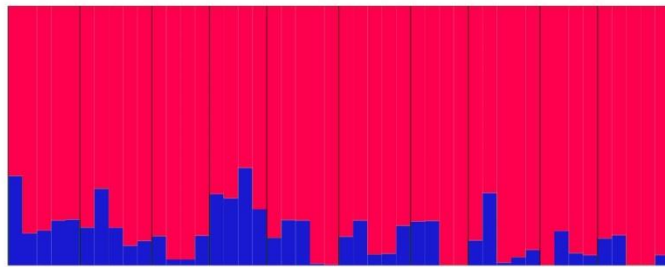
Fig. S2 Genetic structure ( $K=2$ ) of (A) *Pedicularis asplenifolia* and (B) *Carex fuliginosa* estimated using STRUCTURE. Each column corresponds to one individual. Population numbers correspond to voucher numbers in Table 1.

(A)



83 107 66 113 286 285 287

(B)



279 82 362 284 71 114 283 282 280 281

Fig. S3 Neighbor-Net for (A) *P. asplenifolia* and (B) *C. fuliginosa*. Population numbers correspond to voucher numbers in Table 1.

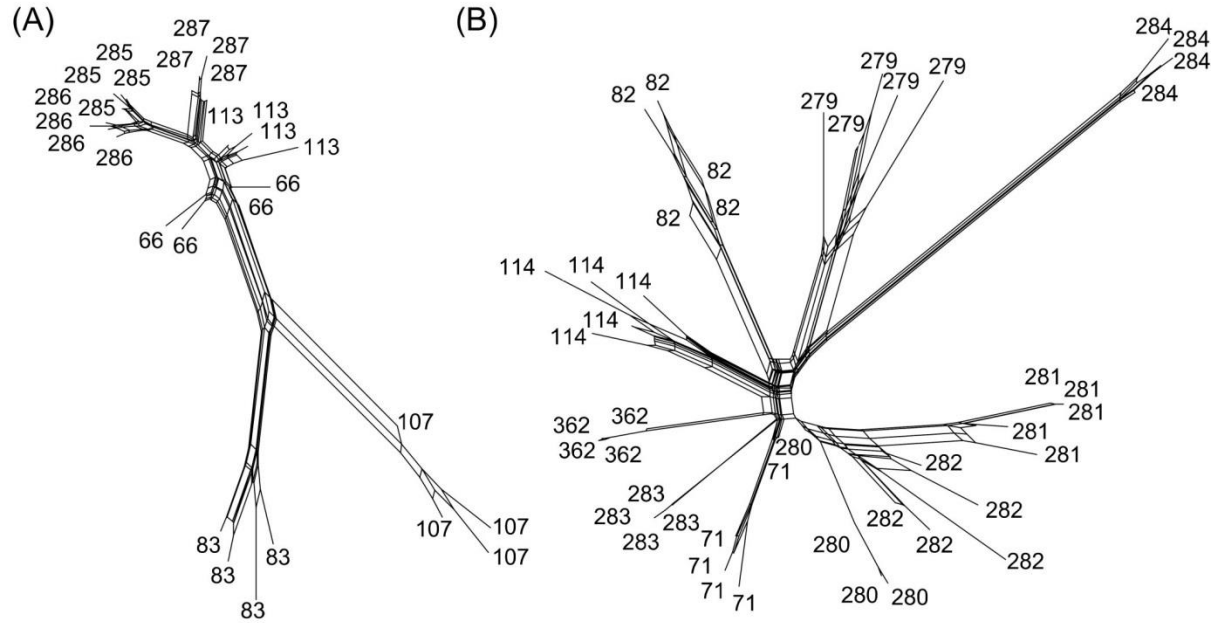


Fig. S4 Scatter-plots of the first two components of a principal component analysis (PCA) for (A) *P. asplenifolia* and (B) *C. fuliginosa* based on SNP data. Population numbers correspond to voucher numbers in Table 1.

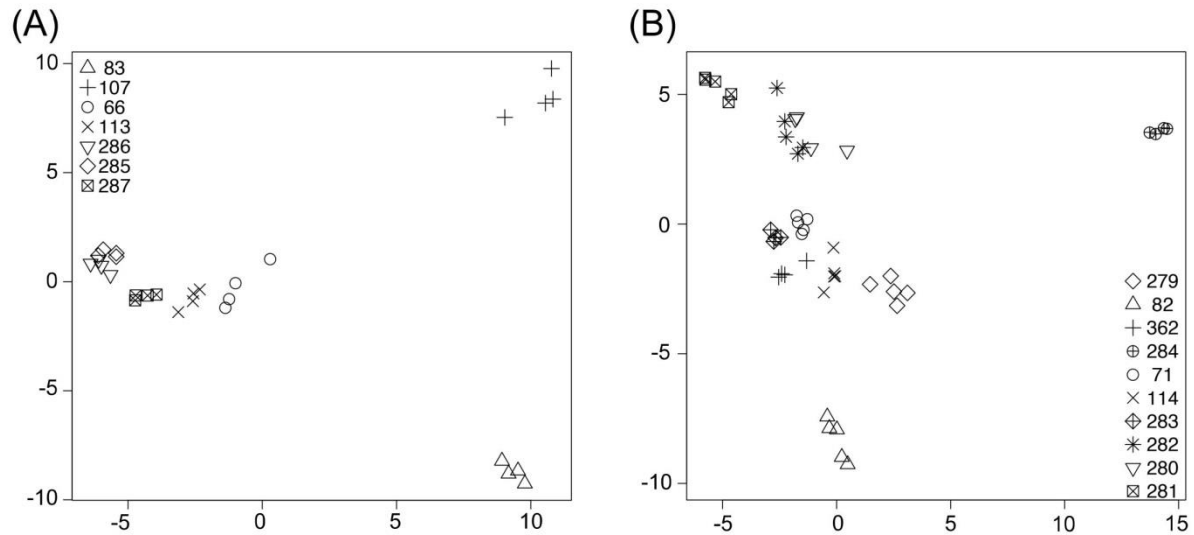




Fig. S5 Change in Root Mean Square Error (RMSE) with increasing number of Partial Least Squares (PLS) components for the most supported model in (A) *Pedicularis asplenifolia* (peripheral plus nunatak survival model with the ancestral population located in the eastern Alps) and (B) *Carex fuliginosa* (peripheral survival only model with the ancestral population located in the eastern Alps).  $N_{anc}$  = population size of the ancestral population;  $k$  = maximum carrying capacity;  $m$  = migration rate.

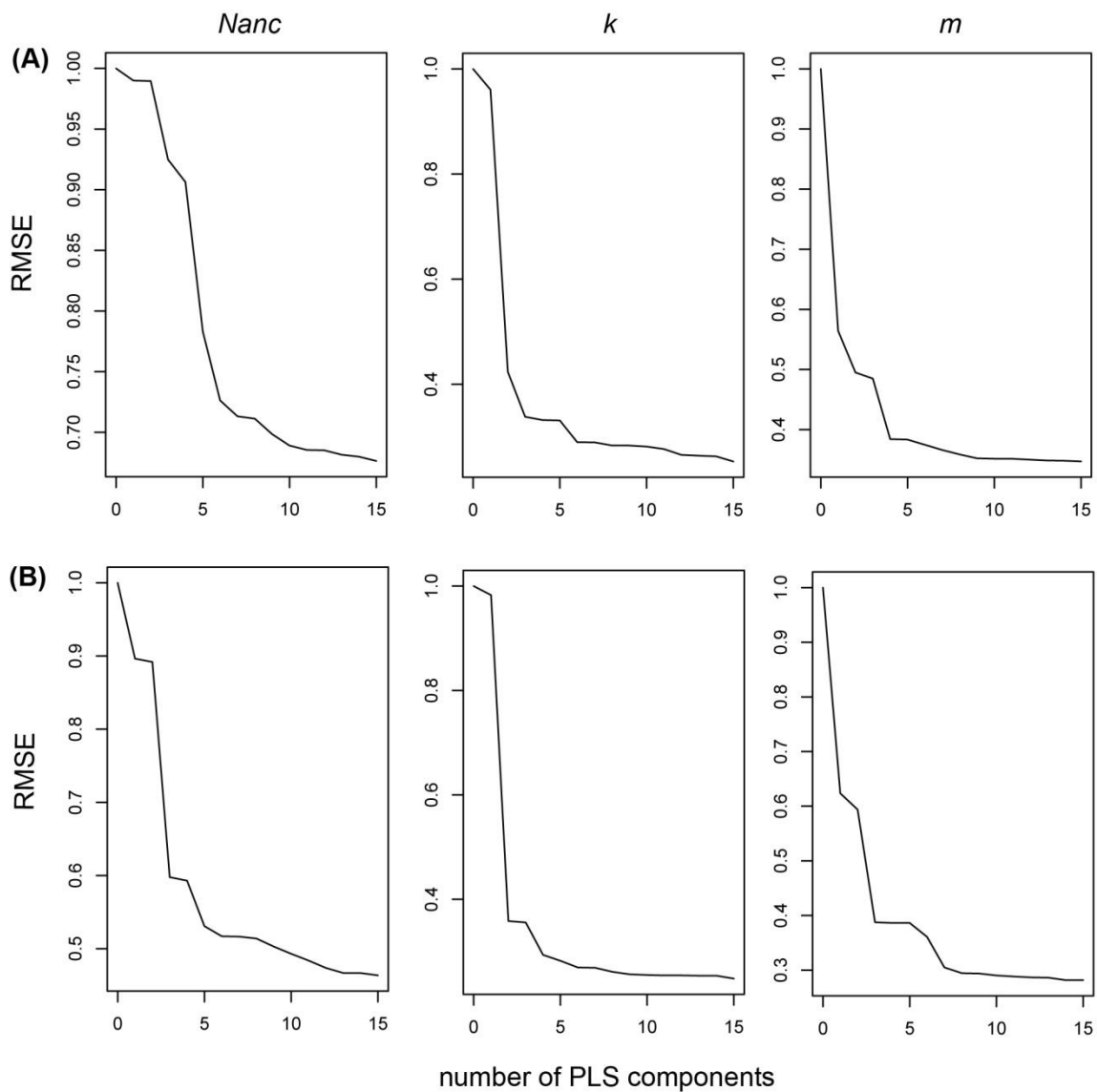


Fig. S6 Prior distributions (black line) and posterior distributions (grey line) of parameter estimates in (A) *Pedicularis asplenifolia* (peripheral plus nunatak survival model with the ancestral population located in the eastern Alps: Peri<sub>East+Nun</sub>) and (B) *Carex fuliginosa* (peripheral survival only model with the ancestral population located in the eastern Alps: Peri<sub>East</sub>).  $N_{anc}$  = population size of the ancestral population;  $k$  = maximum carrying capacity;  $m$  = migration rate.

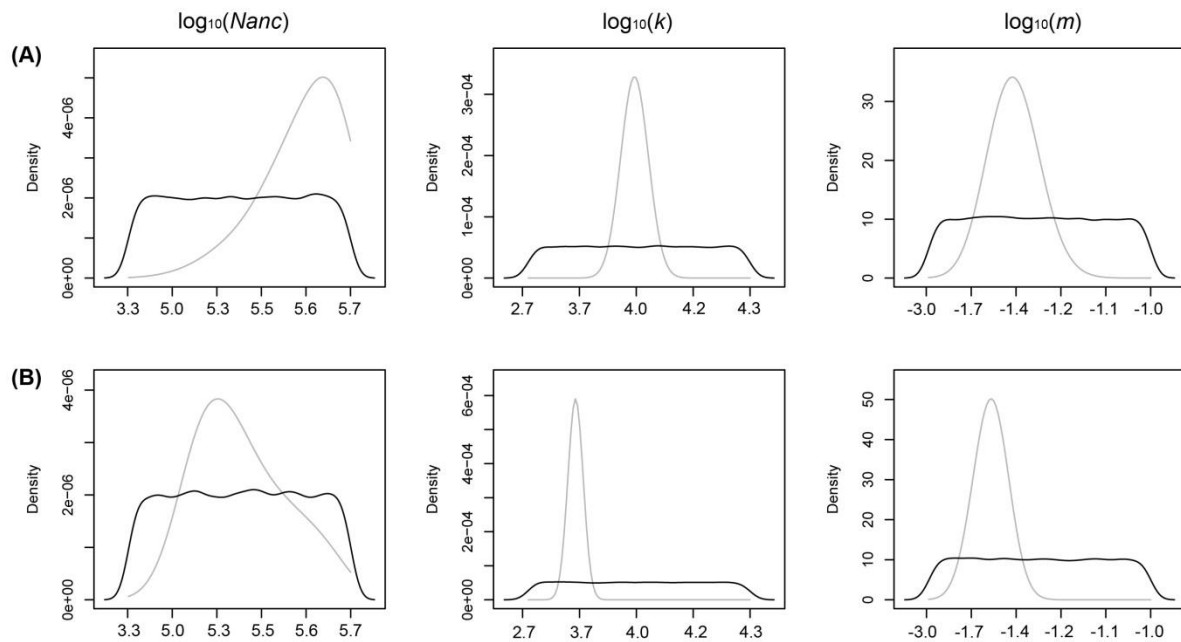


Fig. S7 Distribution of posterior quantiles of parameters for (A) *Pedicularis asplenifolia* (peripheral plus nunatak survival model with the ancestral population located in the eastern Alps: Peri<sub>East+Nun</sub>) and (B) *Carex fuliginosa* (peripheral survival only model with the ancestral population located in the eastern Alps: Peri<sub>East</sub>). Departures from a uniform distribution were tested with a Kolmogorov-Smirnov test ( $p$ -values  $<0.001$  in all six tests).  $N_{anc}$  = population size of the ancestral population;  $k$  = maximum carrying capacity;  $m$  = migration rate.

