SUPPORTING INFORMATION

Differential effects of historical migration, glaciations and human impact on the genetic structure and diversity of the mountain pasture weed *Veratrum album* L.

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Appendix S1 Distribution map (Fig. S1.1) and pollen records (Fig. S1.2) of *Veratrum album*.

Figure S1.1 Map digitalized according to the *Atlas of the north European vascular plants* (Hultén & Fries, 1986). Grey shaded areas denote common or fairly common occurrences, outlined areas with incompletely or approximately stated occurrences, and dots for isolated but fairly exactly indicated occurrences. The red dots show the populations investigated in the present study. Projection: North Pole Lambert Azimuthal Equal Area.

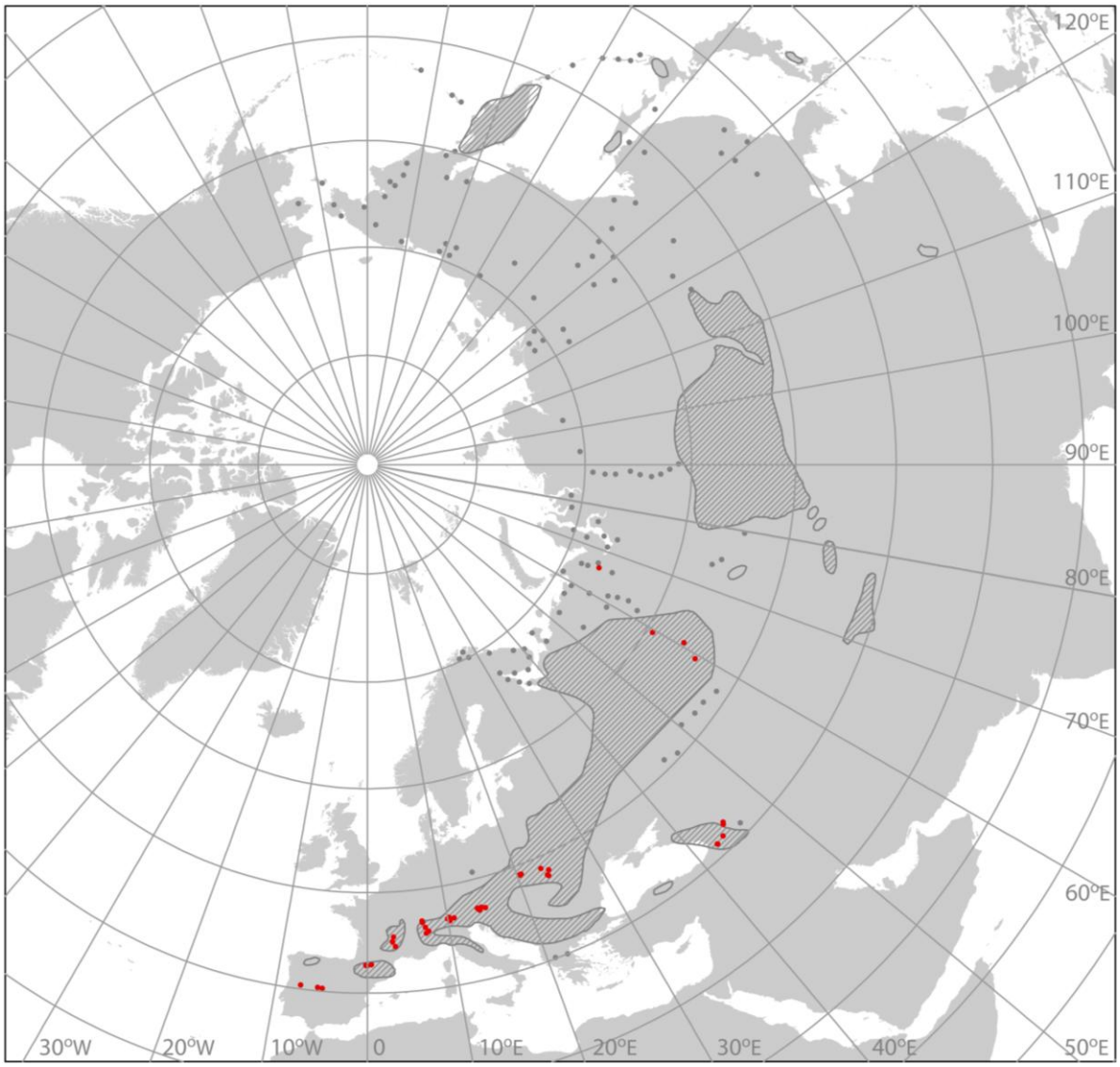
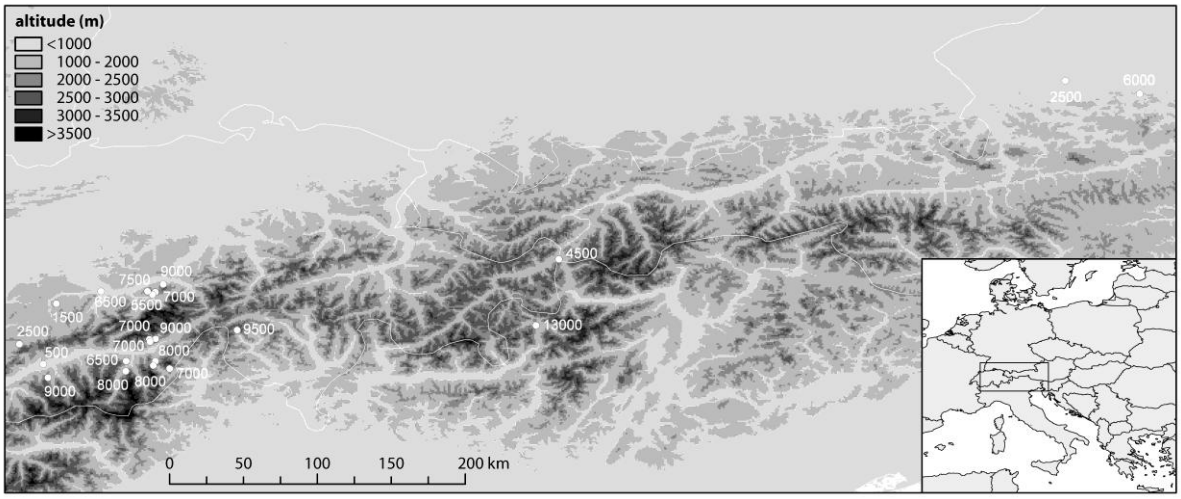


Figure S1.2 Pollen records for the Alps. For each site the oldest dated pollen record is given (^{14}C cal. yr BP, rounded to 500 years; van der Knaap, 2007). *Veratrum* pollen data are scarcely available and, because of its wider distribution, mostly attributed to *V. album*. However, *V. nigrum*, cannot be excluded. For additionally published *Veratrum* pollen data see Burga & Perret (1998) and van der Knaap & van Leeuwen (1997).



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Appendix S2 Ecological and genetic parameters of the 40 investigated *Veratrum album* populations.

Population	managed[(a)]	area[(b)]	density[(c)]	N	P	pH	$rarity_1$	P_{pl}	$H_j \pm SE$
1	n	s	r	14.19	1.15	4.58	2.43	22.44%	0.1342 ± 0.0060
2	n	s	r	NA	NA	NA	2.40	†13.37%	†0.1675 ± 0.0064
3	n	s	r	14.28	1.35	4.75	3.42	†15.12%	†0.1875 ± 0.0066
4	y_p	m	1.76	6.56	0.62	5.21	2.92	60.81%	0.2186 ± 0.0059
5	n	l	1.23	3.08	0.58	5.76	2.05	40.81%	0.1699 ± 0.0059
6	y_p	l	5.72	2.77	0.42	5.56	2.78	56.28%	0.2125 ± 0.0060
7	n	l	1.11	5.63	0.61	4.89	2.16	47.79%	0.1886 ± 0.0060
8	y_p	l	4.99	12.13	1.56	5.05	2.23	45.58%	0.1824 ± 0.0061
9	y_p	m	1.17	8.81	2.29	5.06	2.26	46.40%	0.1877 ± 0.0061
10	y_h	l	11.22	10.65	1.73	5.46	2.35	48.60%	0.1918 ± 0.0061
11	y_p	l	2.36	3.88	0.67	5.78	2.07	47.91%	0.1876 ± 0.0060
12	y_p	l	1.28	2.49	0.62	6.32	2.09	49.88%	0.1955 ± 0.0060
13	y_p	l	8.20	3.40	0.80	5.06	2.24	48.37%	0.1958 ± 0.0061
14	y_p	l	3.31	3.31	0.54	5.06	2.15	45.35%	0.1903 ± 0.0062
15	y_p	l	0.67	5.78	1.35	5.67	2.01	44.77%	0.1862 ± 0.0062
16	y_p	l	0.59	3.99	1.15	5.99	2.06	48.37%	0.1916 ± 0.0062
17	y_h	l	3.83	4.50	0.85	6.33	2.14	50.23%	0.1974 ± 0.0061
18	y_p	m	5.60	4.58	1.02	4.93	2.28	46.86%	0.1859 ± 0.0060
19	y_h	l	8.94	4.25	1.27	4.74	2.25	46.86%	0.1890 ± 0.0061
20	y_p	l	1.73	2.74	1.04	5.52	2.18	45.81%	0.1799 ± 0.0059
21	y_p	l	1.47	6.30	0.81	4.60	2.10	44.07%	0.1803 ± 0.0059
22	y_p	l	1.74	3.24	1.05	4.64	1.88	43.02%	0.1756 ± 0.0061
23	n	l	2.43	8.53	1.51	4.38	2.27	49.77%	0.1920 ± 0.0061
24	n	l	5.53	5.51	0.84	4.29	2.12	46.51%	0.1789 ± 0.0059
25	n	l	3.37	7.90	1.04	4.49	2.17	47.91%	0.1845 ± 0.0059
26	n	m	2.91	7.79	1.18	3.96	2.11	46.40%	0.1768 ± 0.0058
27	n	m	3.66	15.81	1.64	4.06	2.44	53.95%	0.1981 ± 0.0059
28	y_h	l	3.55	5.36	0.83	4.74	2.90	57.67%	0.2162 ± 0.0059
29	$y_{p/h}$	l	2.13	5.02	0.96	4.37	1.95	43.72%	0.1787 ± 0.0061
30	n	m	1.65	3.01	0.51	4.22	2.31	49.07%	0.1931 ± 0.0061
31	$y_{p/h}$	m	3.33	5.31	1.08	4.27	2.19	47.21%	0.1859 ± 0.0060
32	y_p	l	1.41	7.49	1.74	5.40	2.20	41.05%	0.1750 ± 0.0061
33	n	m	1.05	6.30	0.90	5.41	2.39	48.60%	0.1896 ± 0.0061
34	y_p	l	0.30	5.12	1.14	5.51	1.65	36.63%	0.1528 ± 0.0059
35	y_p	l	1.28	6.61	1.48	5.06	1.71	35.93%	0.1492 ± 0.0059
36	y_p	m	4.61	7.94	1.25	5.26	2.55	47.56%	0.1822 ± 0.0061
37	n	m	0.35	2.41	1.04	5.78	2.93	43.37%	0.1748 ± 0.0060
38	n	l	0.22	9.96	1.09	4.36	2.55	38.95%	0.1619 ± 0.0060
39	n	m	0.33	4.21	1.36	6.87	2.41	37.44%	0.1676 ± 0.0062
40	n	l	0.88	9.61	1.68	4.01	2.08	38.84%	0.1655 ± 0.0062

[(a)]population site with ‘n’, no obvious management, or ‘y’, with management (subscripts: p, pasture; h, hayfield)

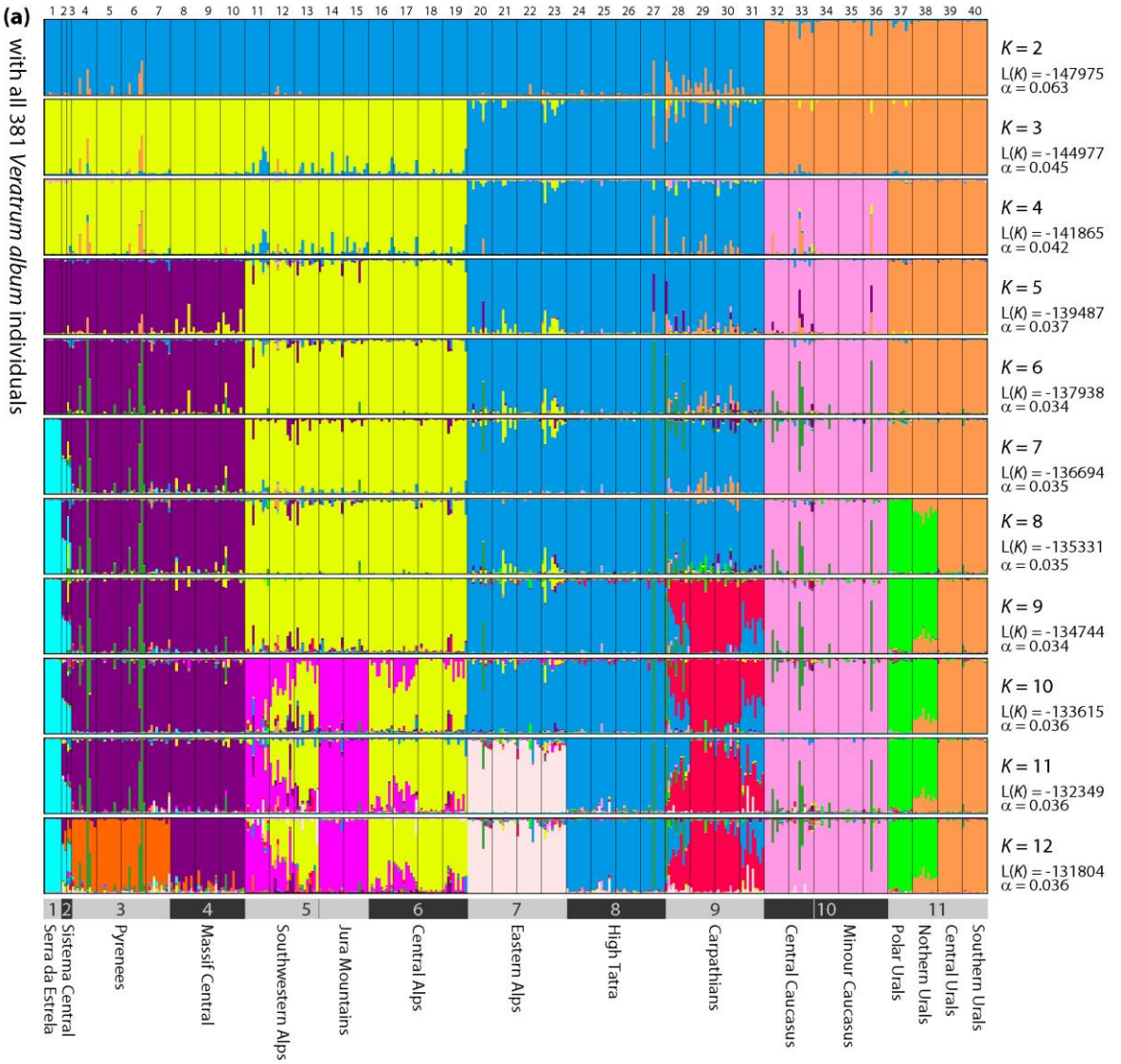
[(b)]estimate of the area covered by *V. album* shoots (s, only single patches; m, small to medium area; l, large and not delimitable area)

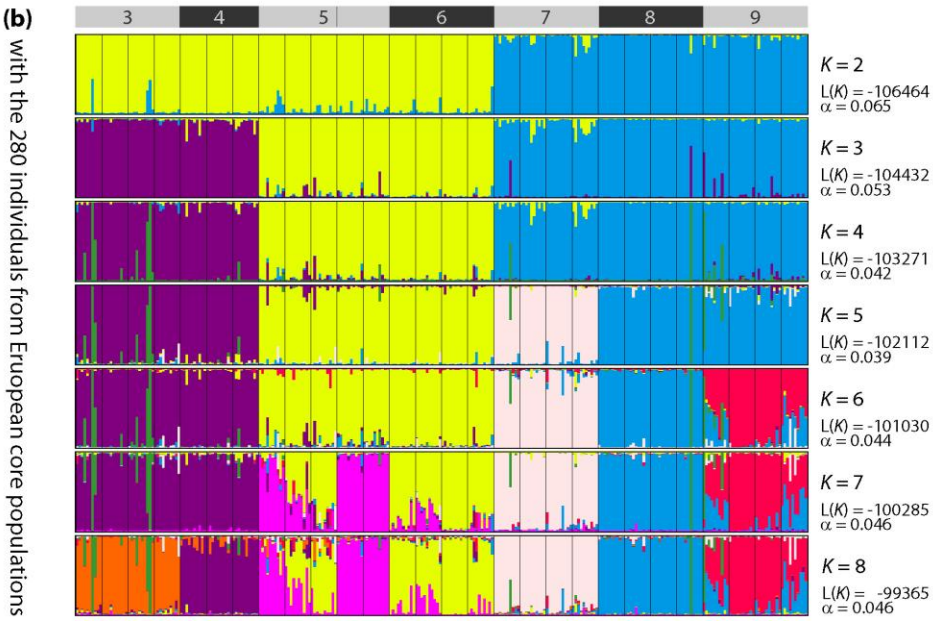
[(c)]number of *V. album* shoots within a 50 × 2 m transect given as shoots/m^2 or ‘r’ if plants were rare (here a value of 0.3 was set for calculations)

(N) soil nitrogen, (P) phosphorus, and pH–H_2O; $rarity_1$, a measure of the mean amount of rare fragments per plant within a population (calculations with AFLPdat 20.06.2010; Ehrich, 2006); proportion of polymorphic loci (P_{pl}) per population; H_j ± standard error (SE), mean gene diversity in the jth population according to Lynch & Milligan (1994), calculations with AFLPsurv 1.0 (Vekemans, 2002); †values have to be interpreted with caution since only two plants where available for population 2 and 3. Population 1 was completely sampled (31 shoots with 7 identified individuals) and for populations 4–40 ten plants were sampled; for numbering of populations see Table 1.

Appendix S3 Identification of genetic clusters with individual-based STRUCTURE (Fig. S3.1) and population based SAMOVA analyses (Fig. S3.2).

Figure S3.1 Rows of plots showing the proportion of cluster association for each individual for a given number of groups, *K*, inferred with STRUCTURE 2.3.3 (Pritchard *et al.*, 2000; Falush *et al.*, 2007). For each *K* the run with the highest posterior probability, $L(K) = \ln\Pr(X|K)$, is shown. Populations (labelled at the top, cf. Table 1) are delimitated with vertical lines. Panel (a) shows assignments for individuals from all predefined regions (given at the bottom) and panel (b) shows assignments for individuals from the European core populations. Emerging genetic clusters are supported by the consistency in genetic splits across different group numbers and between the full and reduced dataset [panels (a) & (b)]. We tested different iteration schemes (e.g. at least 10 runs with a burn-in of 5000 and sampling of 15,000 generations but also 10,000/50,000, $10^4/10^5$, $10^5/10^5$ and $10^5/10^6$ iterations with 5 runs for each *K*-value) and found that for up to $K = 8$ (all individuals) or $K = 6$ (reduced dataset) good and consistent results are obtained with relatively low iteration numbers (parameters of alpha, ln likelihood, and F_{ST} stabilized generally fast) while more iterations improved and stabilised $L(K)$ also for higher *K*-values. Similar, the ΔK statistics (results not shown) introduced by Evanno *et al.* (2005, Mol. Ecol, 14, 2611-2620) suggests a higher optimal group number when more iterations were run (e.g., $K = 7$, 9, and 12 for all individuals, panel a) or $K = 6$ and 8 for the European core individuals, panel b). We are thus confident, that the clusters identified for $K = 12$ [panel (a); cf. $K = 8$ panel (b)] represent well the genetic structure and levels of admixture in our sample. Levels of admixed origin of individuals are indicated with α: values much smaller than 1 imply that individuals mostly originate from a single population, i.e. no or very low levels of admixture. All STRUCTURE plots were created with the program DISTRUCT (Rosenberg 2004, Mol. Ecol. Notes, 4, 137–138).
Panel (c) shows a table with analysis of molecular variance (AMOVA) inferred fixation indices (cf. Fig. 5) for groups recovered by STRUCTURE on European core individuals. However, individuals were excluded from these analyses if they have been assigned to a different cluster than the majority of the other individuals of a given population (e.g. individuals of group 4). Additionally we provide below each fixation index (in brackets) values from analyses with the same set of individuals and group number (*K*) but for clusters identified by spatial analysis of molecular variance (SAMOVA) (Fig. 5). The table thus allows a direct comparison between STRUCTURE and SAMOVA and indicates that STRUCTURE prioritizes within-group homogeneity (lower F_{SC}-values) while SAMOVA rather optimises among-group differentiation (higher F_{CT}-values). The different priorities possibly cause the discrepancy between these analyses when comparing results for a series of increasing *K*-values (cf. Fig. S3.1a with Fig. S3.2 or Fig S3.1b with Fig. 5).

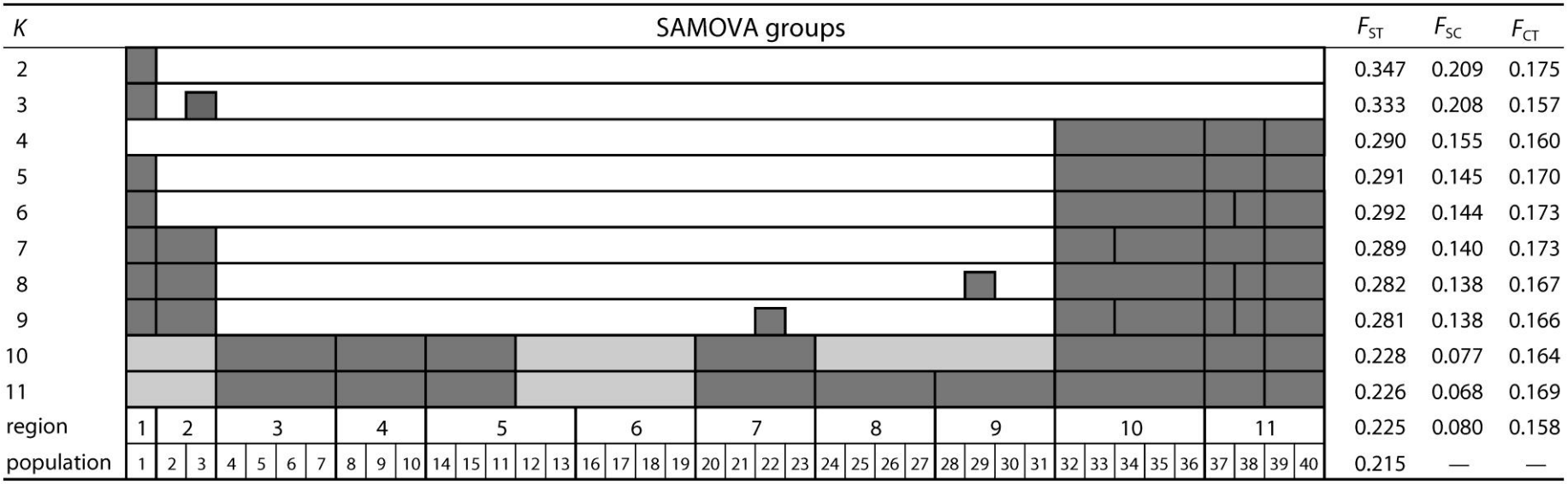




(c) AMOVA

K	F_{ST}	F_{SC}	F_{CT}
2	0.171 (0.188)	0.116 (0.129)	0.063 (0.067)
3	0.168 (0.186)	0.099 (0.115)	0.076 (0.081)
3	0.171 (0.191)	0.101 (0.118)	0.078 (0.083)
4	0.166 (0.172)	0.089 (0.090)	0.086 (0.090)
5	0.172 (0.170)	0.090 (0.080)	0.090 (0.098)
6	0.165 (0.165)	0.066 (0.065)	0.105 (0.108)
7	0.163 (0.163)	0.051 (0.051)	0.118 (0.118)

Figure S3.2 Spatial analysis of molecular variance (SAMOVA) for a given number of a priory defined groups, *K*. At the bottom, numbers for predefined regions and populations (see also Table 1). To the right, indices based on hierarchical analyses of molecular variance for the various population groups: F_{ST} = among-population differentiation, F_{SC} = differentiation among populations within groups, F_{CT} = differentiation among groups. Grey shading: groups that separated from the remaining populations, light grey shading: groups that did not agree with predefined mountain regions.



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