Supplementary Information for: High morphological differentiation in crown architecture contrasts with low population genetic structure of German Norway spruce stands

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Table S1: Concentration (c_i) of each forward and reverse primer in the multiplex reactions and single-plex.

Singleplex		Multiplex 1		Multiplex 2		Multiplex 3		Multiplex 4	
SSR	c_i (μM/μl)	SSR	c_i (μM/μl)	SSR	c_i (μM/μl)	SSR	c_i (μM/μl)	SSR	c_i (μM/μl)
PaGB8	3.57	*WS00111.K13*	3.57	*SpAGC1*	2.14	*EATC1E03*	1.25	*SpAGG2*	1.79
		EATC1D2	2.14	*EATC2G05*	2.14	*SpAG2*	1.79	*WS00016.O09*	3.57
				EATC1B2	1.07	*SpAC1F07*	3.57	*PaGB3*	1.07

Table S2: Relative frequencies of assessed morphological traits in each stand corresponding to the Figure 1 in the main paper. Stand abbreviation: LE: Low elevation type; HE: High elevation type; SBF: relict stand "Schlossbergfichte"; S: Ore Mountains (Saxony); Thy: Thuringia; H: Harz Mountains.

		HE_H	LE_H	HE_S	LE_S	SBF_Thy	HE_Thy	LE_Thy
crown shape	narrow	0.374	0.005	0.565	0.030	1.000	0.545	0.000
	intermediate	0.626	0.315	0.375	0.730	0.000	0.455	0.035
	broad	0.000	0.680	0.060	0.240	0.000	0.000	0.965
branching anle	downwards	0.865	0.025	0.655	0.065	1.000	0.555	0.000
	intermediate	0.135	0.430	0.345	0.660	0.000	0.445	0.175
	upwards	0.000	0.545	0.000	0.275	0.000	0.000	0.825
branching pattern	plate	0.730	0.000	0.365	0.025	1.000	0.545	0.000
	intermediate	0.207	0.400	0.625	0.485	0.000	0.455	0.355
	comb	0.063	0.600	0.010	0.490	0.000	0.000	0.645
crown damage	no	0.000	0.060	0.915	0.955	1.000	1.000	0.000
	yes	1.000	0.940	0.085	0.045	0.000	0.000	1.000
forking	no	0.000	0.665	0.960	0.970	1.000	1.000	0.460
	yes	1.000	0.335	0.040	0.030	0.000	0.000	0.540

All values are rounded to three decimals.

Table S3: Hierarchical AMOVA based on the regional and population membership of the individuals.

Source of variation	d.f.	Sum of squares	Variance component	Percentage variation	P-value
Among regions	2	30.1	0.00945	0.24	0.05833
Among populations within regions	4	26.5	0.00642	0.16	<0.0002
Among individuals within populations	1290	5618.7	0.37536	9.39	<0.0002
Within individuals	1297	4675.5	3.60486	90.21	<0.0002
Total	2593	10350.7	3.99608		

Significance of the (co-) variance components based on 5000 permutations, both calculated in Arlequin 3.5.2.2 [76].

Table S4: Paiwise F_{ST} values between population pairs (bolt) with corresponding p-values from 10000 permutations in GenAlEx 6.5 [77].

	HE_H	HE_S	HE_Thy	LE_H	LE_S	LE_Thy
HE_S	**0.004**					
	0.000					
HE_Thy	**0.004**	**0.003**				
	0.000	0.000				
LE_H	**0.002**	**0.004**	**0.004**			
	0.153	0.000	0.000			
LE_S	**0.003**	**0.002**	**0.003**	**0.004**		
	0.000	0.000	0.000	0.000		
LE_Thy	**0.003**	**0.002**	**0.003**	**0.004**	**0.002**	
	0.000	0.003	0.000	0.000	0.059	
SBF_Thy	**0.006**	**0.005**	**0.003**	**0.007**	**0.005**	**0.004**
	0.000	0.001	0.028	0.000	0.000	0.001

Table S5: Pairwise G''_{ST} values between population pairs in GenAlEx 6.5 [77].

	HE_H	HE_S	HE_Thy	LE_H	LE_S	LE_Thy
HE_S	0.024					
HE_Thy	0.021	0.009				
LE_H	0.002	0.022	0.022			
LE_S	0.011	0.008	0.010	0.016		
LE_Thy	0.016	0.007	0.009	0.022	0.003	
SBF_Thy	0.026	0.016	0.008	0.030	0.017	0.014

p-values are identical to Table S4 and therefore not given.

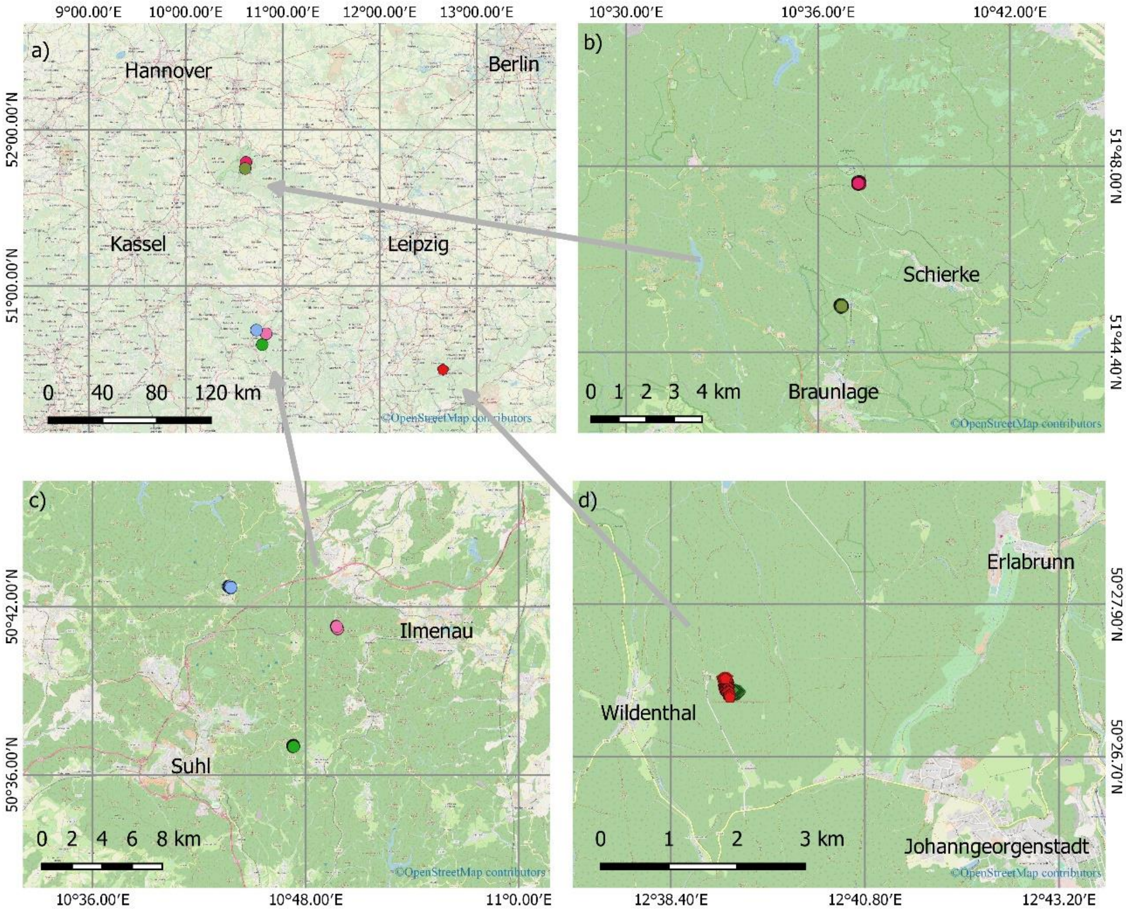

Figure S1 a-d: Overview map (a) and map sections of the stand locations. Harz region (b) with the northern high elevation (HE) and southern low elevation (LE) stand. Thuringian forest (c) with the northern relict stand “Schlossbergfichte”, the southern LE stand and the more eastern HE stands. Ore mountains in Saxony (d) with the western HE stand and eastern LE stand. Longitudinal and latitudinal coordinates are given on the corresponding sides of each map. Maps generated with QGIS 2.18.15 [132] using geodata from www.openstreetmaps.org[133].

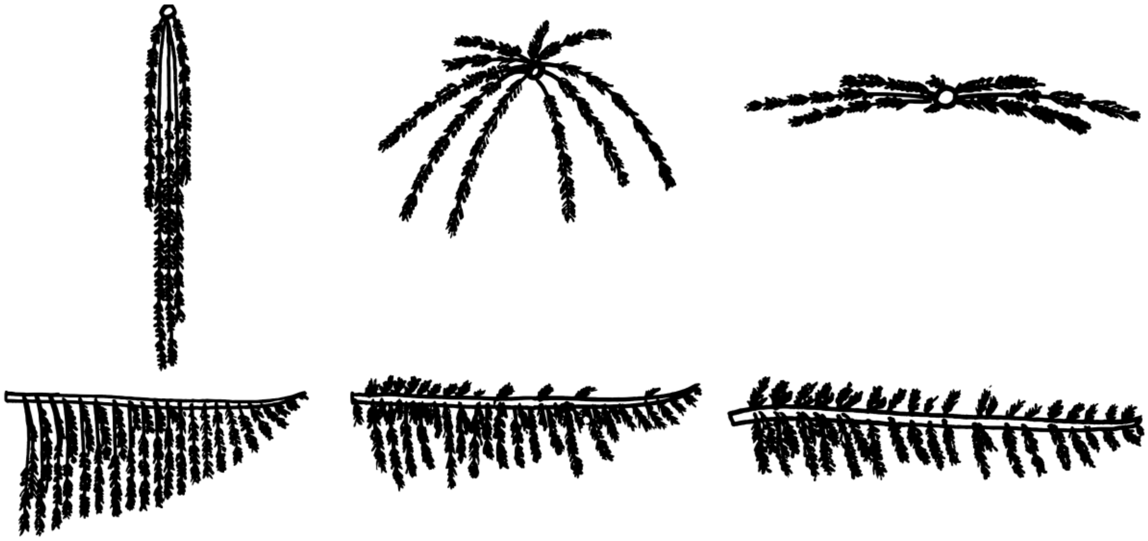

Figure S2: Schematic presentation of the three main crown architectural types. From left to right, lowland combe type, intermediate brush type and narrow high elevation plate type. Top secondary branching pattern as cross-sectional view and bottom in side view (Figures modified and reproduced with permission from J. D. Sauerländer's Verlag; Gruber, *Allg. Forst- u. J.-Ztg*,**160**, published by J. D. Sauerländer's Verlag, 1989 [5]).

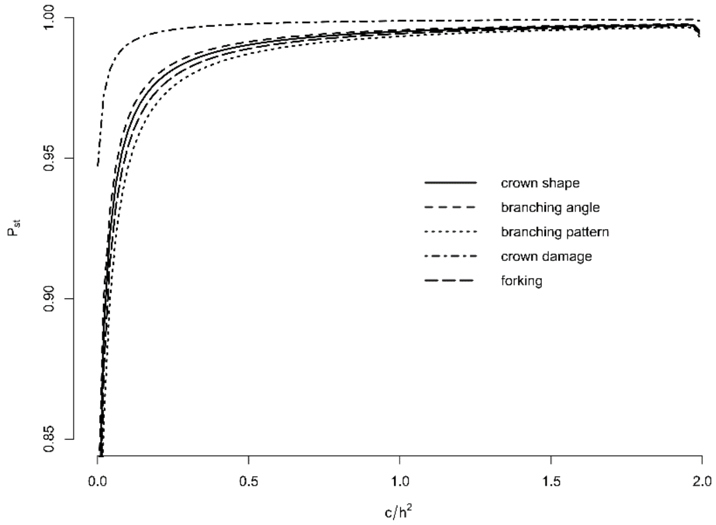

Figure S3: Relationship of phenotypic divergence in a trait across populations (P_{ST}) [60-62] over the ratio of the total variance explained by additive genetic effects across populations and the narrow sense heritability (c/h^2)

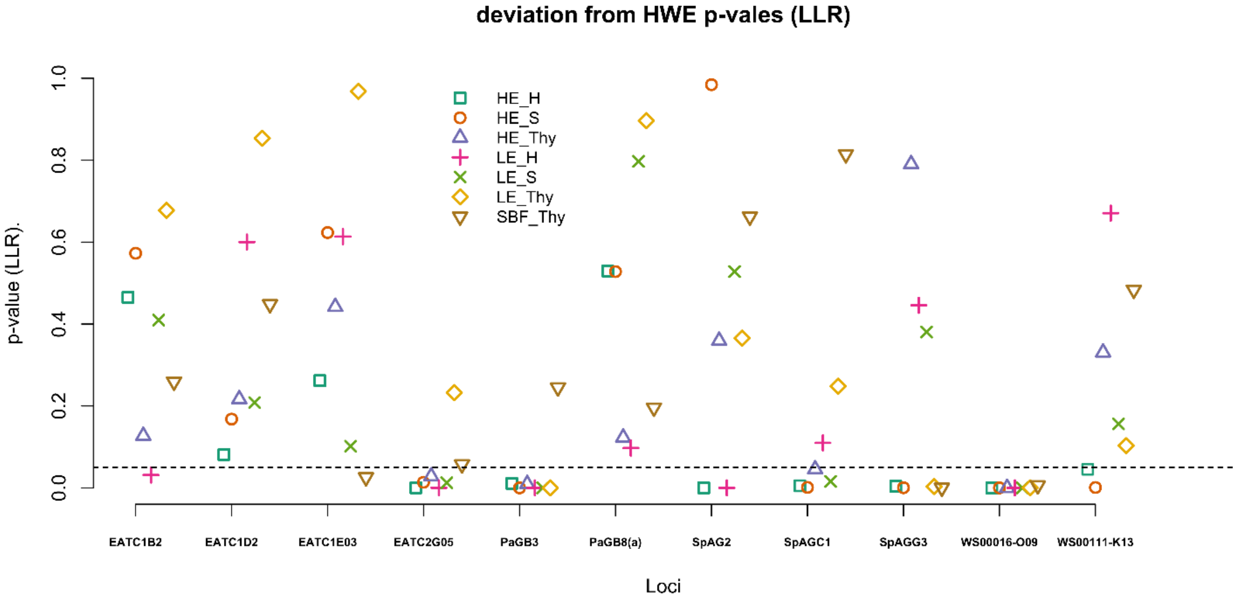

Figure S4: Corresponding p- value of the log likelihood ratio test on the deviation from HWE of each locus genotyped in each population sampled. Test statistic is based on either full enumeration or Monte Carlo sampling on the count tables depended on the number of tables to be observe (for details see [67,68]).

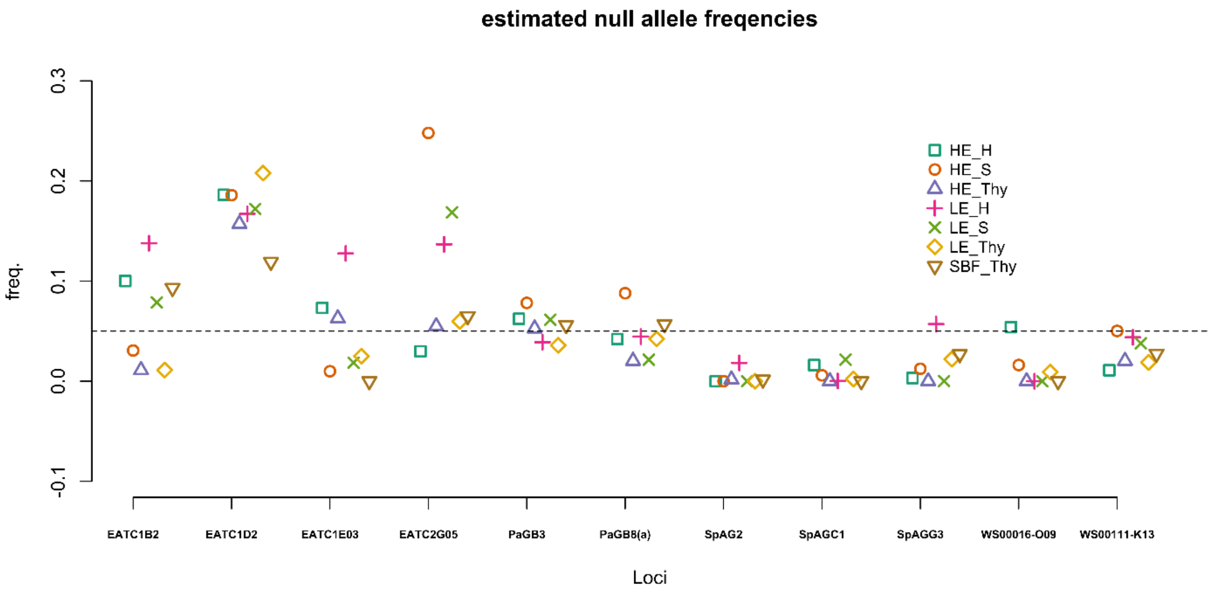

Figure S5: Estimation of the null allele frequency at each locus in each population separately. Average of maximum likelihood estimation expectation maximisation [71] in genepop [72] and ML estimation in ML-Nullfreq [73]. Dashed line indicating the estimated 5% frequency, as it can be seen as a threshold value for reporting null alleles [74].

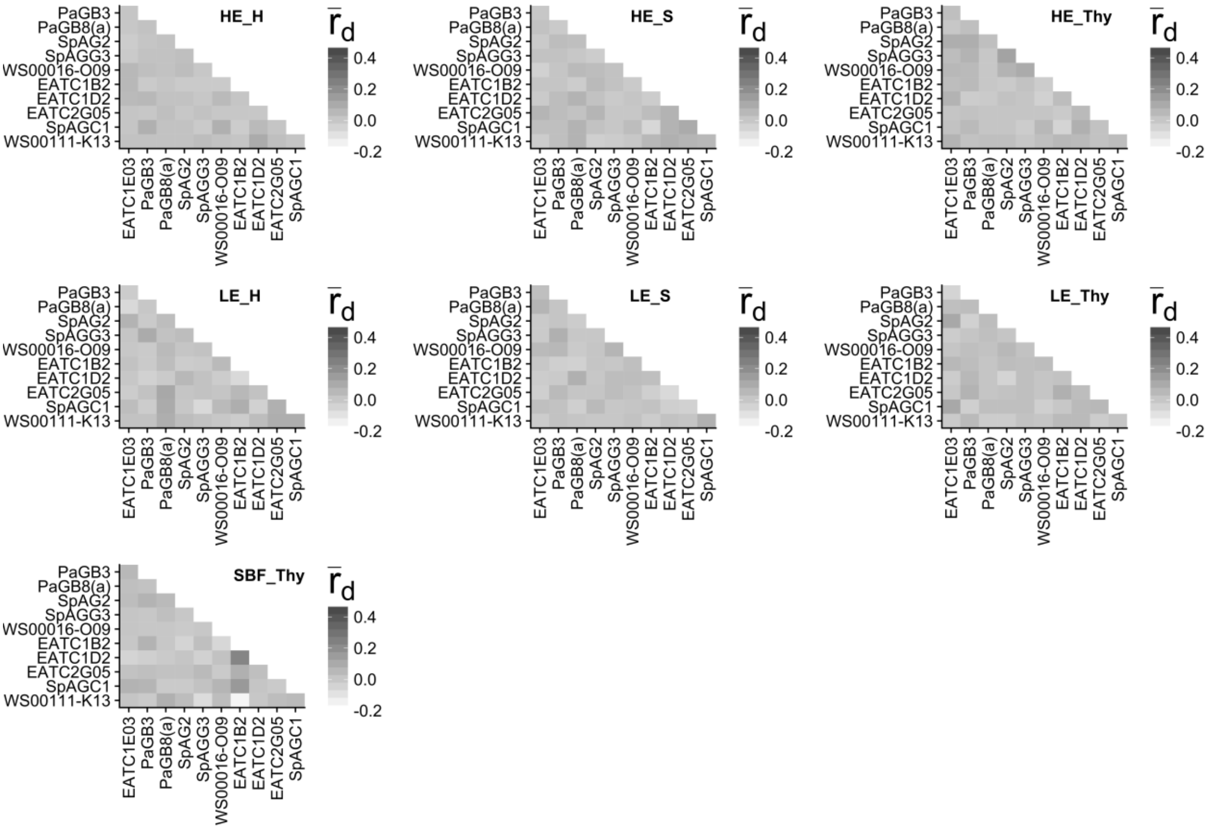

Figure S6: Heatmaps displaying the standardizes index of association $\bar{r}_d$ [69] for pairwise loci comparison for each stand separately. Low values are indicated in white, whereas higher values are indicated with increasing grey shades. Stand abbreviation: LE: Low elevation type; HE: High elevation type; SBF: relict stand “Schlossbergfichte”; S: Ore Mountains (Saxony); Thy: Thuringia; H: Harz Mountains.

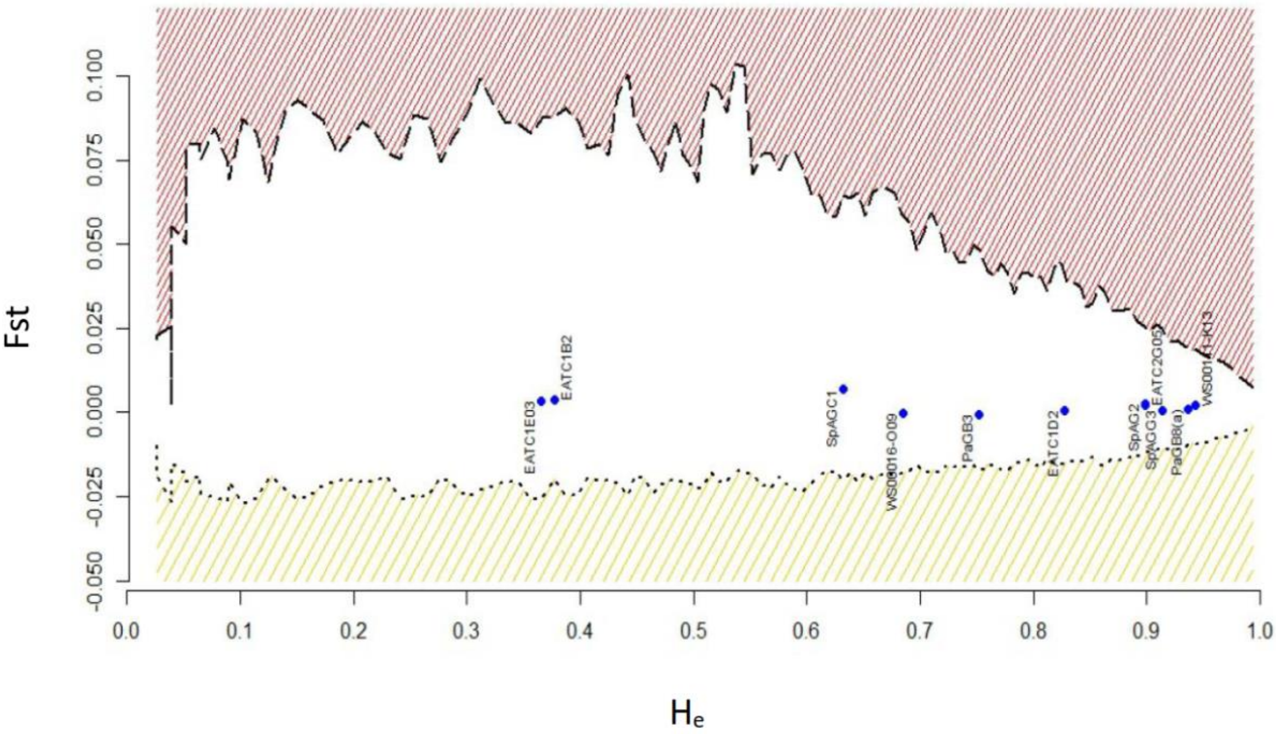

Figure S7: Detection of outlier loci in LOSITAN [82] exploring the relationship between F_{ST} and H_e among populations by permutations. Black dashed lines indicate the upper 95% confidence limit, also highlighted by fine red hatching. Black dotted lines indicate the lower 95% confidence limit, highlighted by rougher yellow hatching.

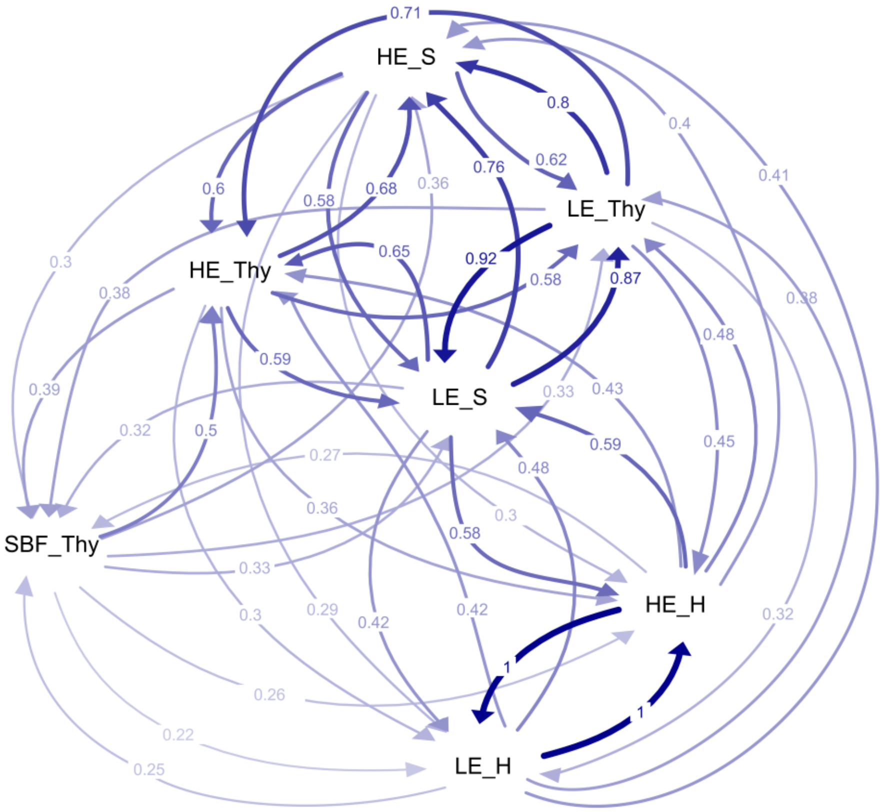

Figure S8: Directional relative migration network [85] based on G_{ST} [86] of potential allochthones and autochthones populations. The relative positions of the populations indicate relatedness from the perspective of hypothetical gene flow. Numbers and arrows indicate the direction and extent of gene flow (also underlined by arrow shading/thickness). Stand abbreviations: LE: Low elevation type; HE: High elevation type; SBF: relict stand “Schlossbergfichte”; S: Ore Mountains (Saxony); Thy: Thuringia; H: Harz Mountains.

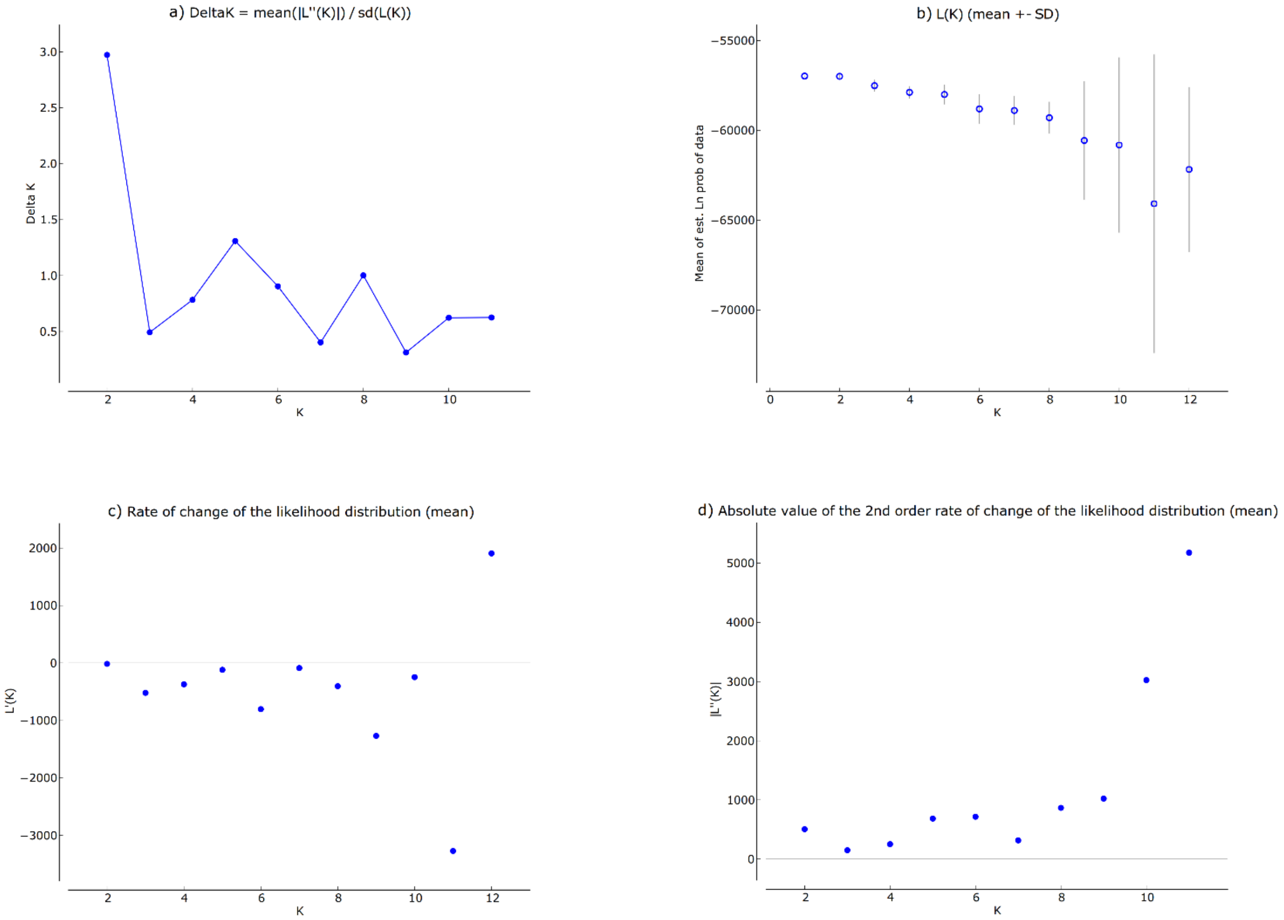

Figure S9 (a-d): Detection of the number of clusters K according to a) Delta*K* [101], the b) log-likelihood probability of *K* (*L(K)*) and the corresponding c) first and d) second order change of *L(K)* [96] calculated in STRUCTURE HARVESTER [102].

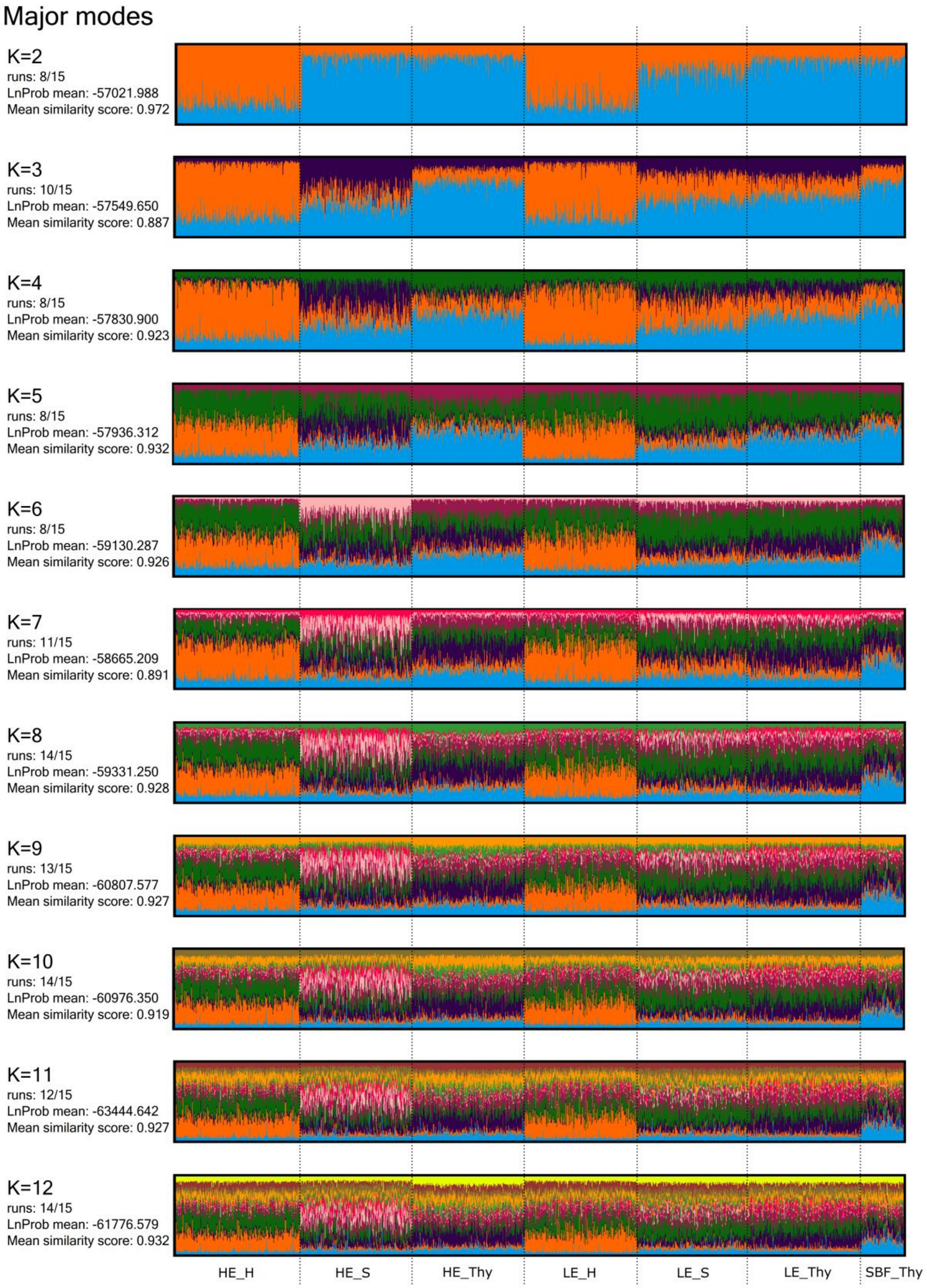

Figure S10: Major modes of cluster results from K 2 to 12 of STRUCTURE [96] analysis summarised in CLUMPAK [100]. For each K the major mode is given indication the number of runs and der mean similarity of the summarisation output as well as the mean ln probability of the mode. Individuals ordered by population membership as indicated at the bottom.