Supplementary Materials

Genetic Structure and Geographical Differentiation of *Larix sibirica* Ledeb. in the Urals

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Supplementary Table S1. Studied populations of *L. sibirica.*

Populations	Geo referencing	Coordinates	Height above sea level, m
Kar	Karabash raion, 25 km north-west of the city of Karabash.	N 55.2909 E 60.1701	382
Irm	Mountain Big Iremel. 12 km north-west from the village Tyulyuk	N 54.5998 E 58.7900	595
Vsn	Plastovsky raion, village Verhnyaya Sanarka.	N 54.1304 E 60.2811	264
Kul	Abzelilovsky raion, 8 km south-west of the village Askarovo	N 53.1601 E 58.2603	613
Zil	Zilair raion, 15 km south-west of the village Zilair	N52.1202 E 57.2902	458
Kch	South-eastern slope of Kachkanar mountain. 34 km southeast from the town of Kachkanar	N 58.7824 E 59.4068	480-700
Bil	Urban district Pervouralsk. 1.5 km east of the town Bilimbay	N 56.9499 E 59.8483	290-350
Pol	Dobriansky raion. Protected areas "Polaznensky Bor". 500 m north-east from the village of Zaborie	N 58.2998 E 56.3664	196-207
Osa	Osinsky raion. 4.5 km north-west from the village of Monastyrka	N 57.3430 E 55.2568	210-230
Sks	Suksunsky raion. Protected areas "Larch Grove". 1 km from the village of Bor	N 57.0688 E 57.5653	240-250
Tul	Vishersky Nature Reserve, western slope of the Tulymsky Kamen ridge	N61.1130 E 58.8899	680-916
Ish	Vishersky Nature Reserve, southwestern slope of Mount Isherim	N61.1178 E 59.1537	730-810
Krv	Krasnovishersky raion. 10 km southeast from Krasnovishersk	N 60.3264 E 57.0931	190-200
Bnd	Cherdynsky raion. 5 km north of the village of Bondyug	N60.5147 E 55.9203	190-200
Gai	The upper reaches of the r. Kama. 50 km north-west of the village of Gainy	N60.1739 E 53.6213	192-207

N - north latitude, E - east longitude.

Supplementary Table S2. STRUCTURE startup options.

Running Length
Length of Burnin Period: 50000
Number of MCMC Reps after Burnin: 100000
Ancestry Model Info
Use Prior Population Information to Assist Clustering
* GENSBACK = 2
* MIGRPRIOR = 0.05
* For Individuals without population information data, use
Admixture Model
** Infer Alpha
** Initial Value of ALPHA (Dirichlet Parameter for Degree of Admixture): 1.0
** Use Same Alpha for all Populations
** Use a Uniform Prior for Alpha
*** Maximum Value for Alpha: 10.0
*** SD of Proposal for Updating Alpha: 0.025
Frequency Model Info
Infer Lambda (Allele Frequencies Parameter)
* Use a Uniform Lambda for All Population
* Initial Value of Lambda: 1.0
Advanced Options
Estimate the Probability of the Data Under the Model
Frequency of Metropolis update for Q: 10

Supplementary Table S3. MavericK startup options.

```
#### Data properties
headerRow_on    f
popCol_on       t

ploidyCol_on    f

ploidy  2
missingData     -9
dataFormat      2

#### Model parameters
Kmin    1
Kmax    10
admix_on        t
fixAlpha_on     f
alpha   1.0, 1.62, 1.24, 0.28, 0.14, 0.15, 0.14, 0.08, 0.04, 0.03
alphaPropSD     1.0, 0.30, 0.16, 0.07, 0.04, 0.04, 0.05, 0.02, 0.02, 0.01


#### Simulation parameters
exhaustive_on   f

mainRepeats     10
mainBurnin      10000
mainSamples     50000

thermodynamic_on        t
thermodynamicRungs      20
thermodynamicBurnin     10000
thermodynamicSamples    50000

EMalgorithm_on f
EMrepeats       100
EMiterations    100


#### Basic output properties
outputLog_on    t
outputLikelihood_on     t
outputQmatrix_ind_on    t
outputQmatrix_pop_on    t
outputQmatrixError_ind_on       t
outputQmatrixError_pop_on       t
outputEvidence_on       t
outputEvidenceNormalised_on     t
outputEvidenceDetails_ont
```

Supplementary Table S4. Assessment of genetic interregional and interpopulation variability of *L. sibirica* populations based on the results of molecular variance analysis (AMOVA)

Source	df	SS	MS	Dispersion	%	*p*
Among regions	2	58,107	29,053	0,053	2	<0,001
Among Populations	12	157,978	13,165	0,158	5	<0,001
Among Individuals	436	1600,308	3,670	0,966	33	<0,001
Within Individuals	451	784,000	1,738	1,738	60	<0,001
Total	901	2600,392		2,915	100	<0,001
F_{ST}	0,072					<0,001

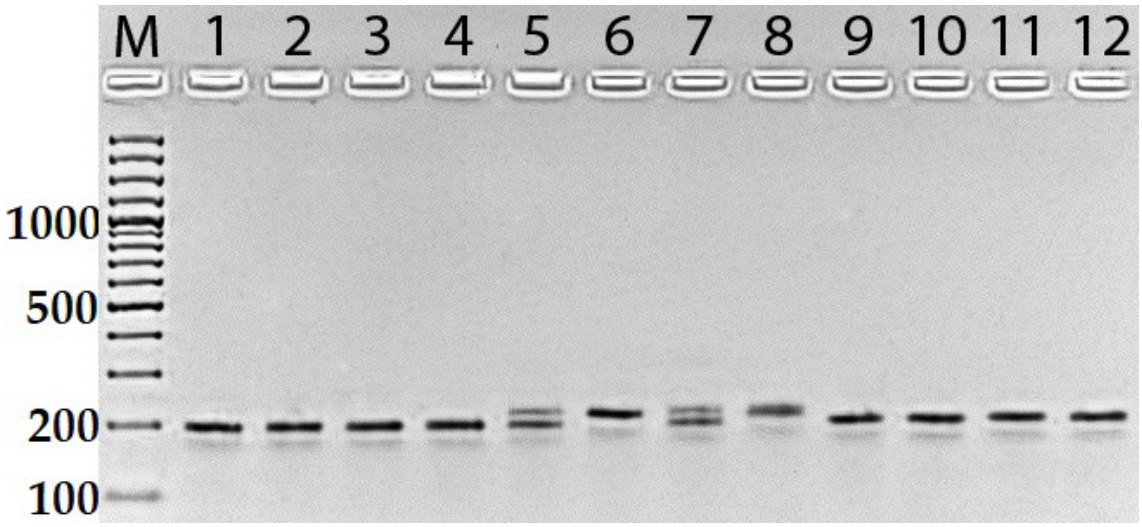
df - degrees of freedom, SS - sum of squares, MS - standard deviation, % - percentage of total genetic diversity, p - significance level using 999 rounds of permutations; F_{ST} - subdivision index.

Supplementary Table S5. Pairwise F_{ST} matrix for fifteen populations of Siberian larch in the Urals

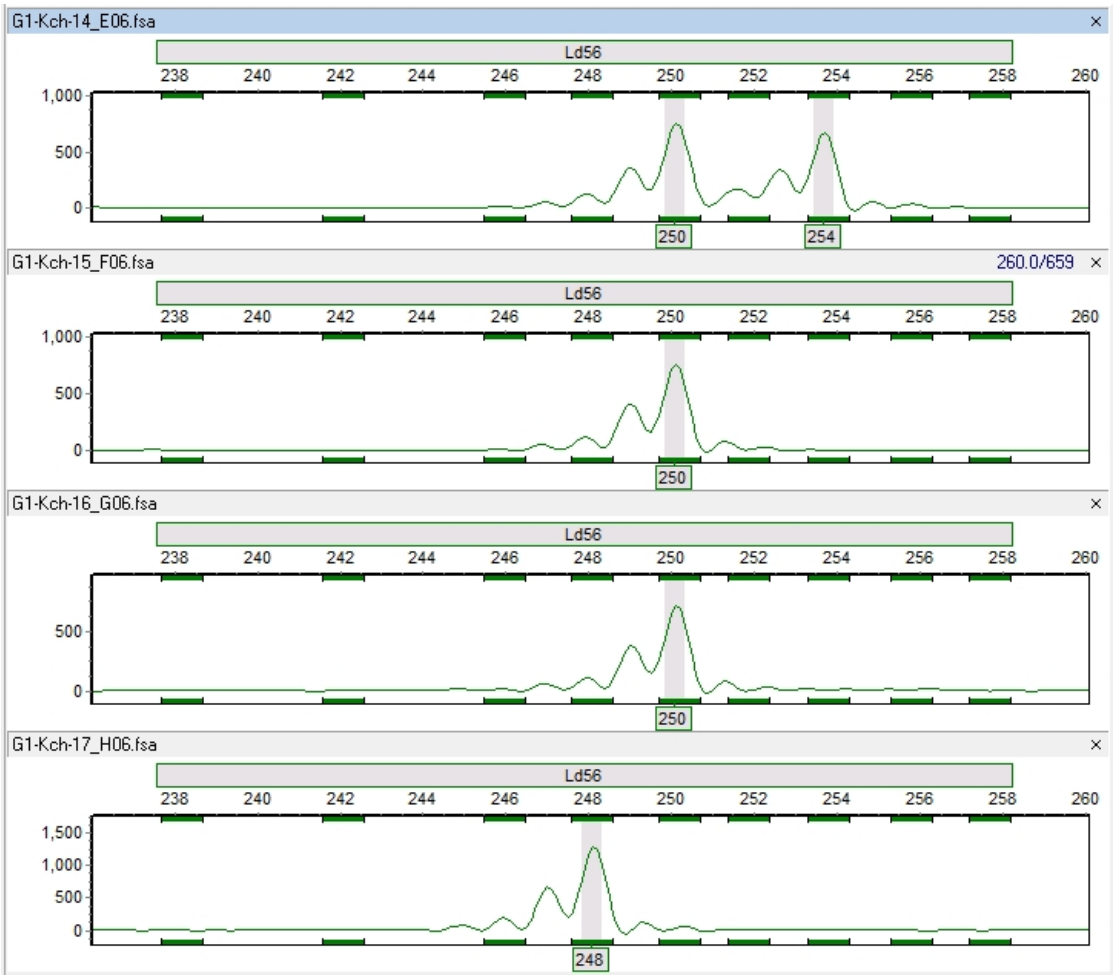
	Kar	Irm	Vsn	Kul	Zil	Tul	Ish	Krv	Bnd	Gai	Kch	Pol	Osa	Sks
Irm	0.041													
Vsn	0.009	0.016												
Kul	0.054	0.022	0.030											
Zil	0.046	0.036	0.026	0.023										
Tul	0.110	0.117	0.065	0.112	0.108									
Ish	0.114	0.095	0.068	0.058	0.076	0.078								
Krv	0.067	0.071	0.033	0.062	0.055	0.056	0.029							
Bnd	0.110	0.075	0.073	0.068	0.045	0.108	0.082	0.057						
Gai	0.022	0.014	-0.014	0.020	0.018	0.054	0.051	0.001	0.022					
Kch	0.075	0.061	0.038	0.045	0.043	0.050	0.037	0.018	0.021	0.002				
Pol	0.066	0.069	0.018	0.063	0.056	0.070	0.087	0.030	0.069	0.023	0.056			
Osa	0.023	0.013	0.001	0.014	0.034	0.059	0.070	0.022	0.058	0.008	0.010	0.036		
Sks	0.171	0.145	0.114	0.173	0.166	0.151	0.179	0.133	0.156	0.132	0.143	0.121	0.126	
Bil	0.088	0.080	0.044	0.065	0.053	0.060	0.069	0.013	0.027	0.022	-0.002	0.049	0.037	0.159



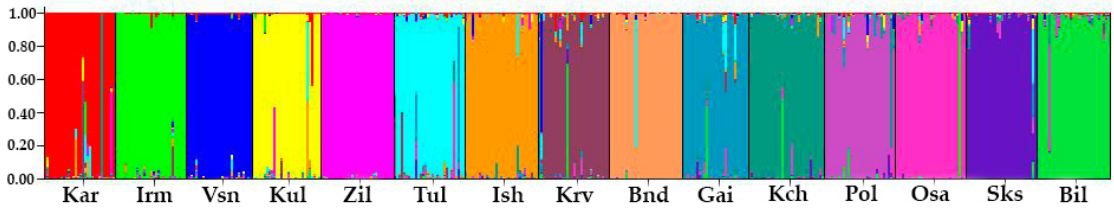
Supplementary Figure S1. Schematic map of the location of the studied populations of *L. sibirica*: Tul—Tulym; Ish—Isherim; Gai—Gainy, Krv—Krasnovishersk, Bnd—Bondyug, Kch—Kachkanar, Pol—Polazna, Osa—Osa, Sks—Syksyn, Bil—Bilimbai, Kar – Karabash, Irm – Iremel, Vsn - Verhnyaya Sanarka, Kul – Kulukasovo, Zil - Zilair.



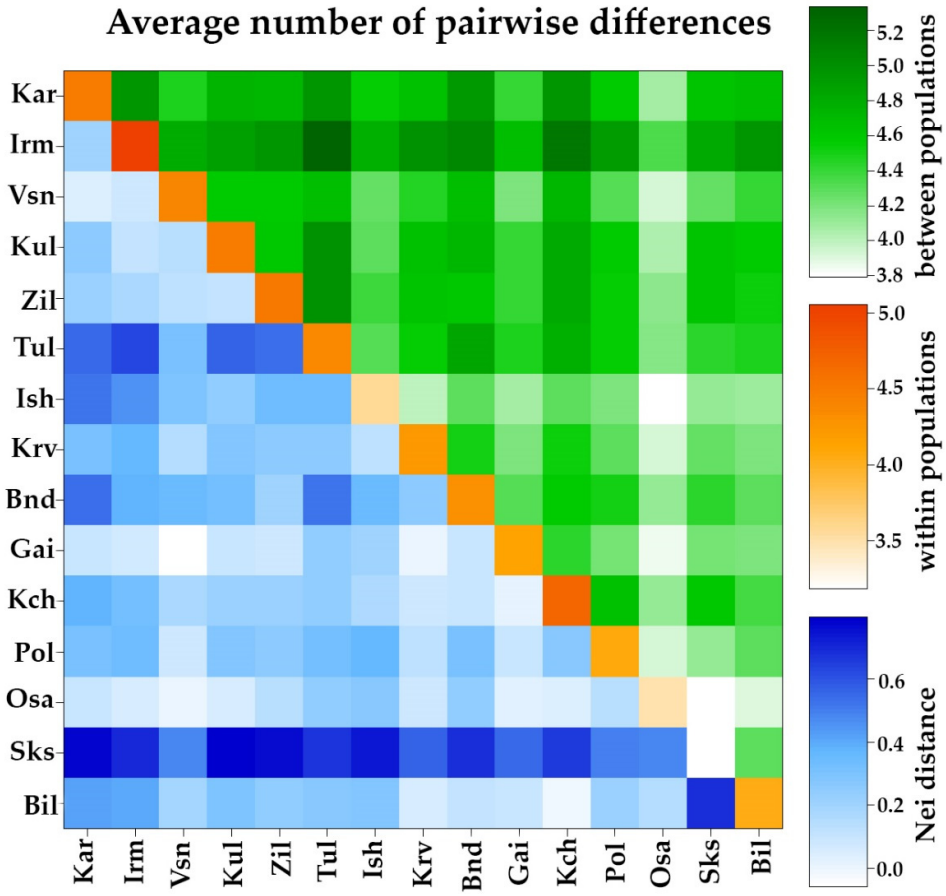
Supplementary Figure S2. Results of amplification of *L. sibirica* DNA with SSR amrker bcLK228. M - molecular weight marker - GeneRuler 100 bp Plus DNA Ladder (Thermo Fischer Scientific, Waltham, MA, USA); 1-12 - DNA samples.



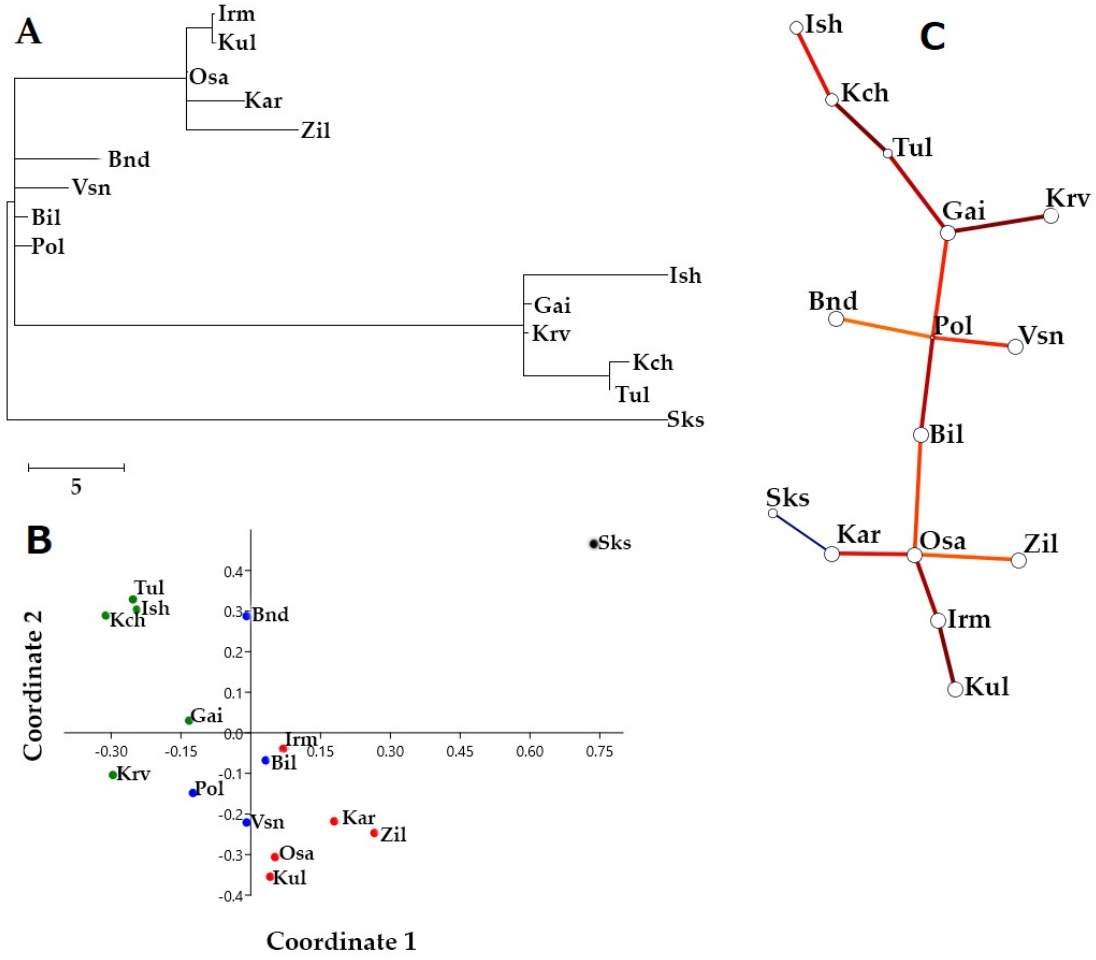
Supplementary Figure S3. Chromatograms of electrophoretic separation of amplification products of the Ld56 locus. There are no nonspecific products. Fragment length polymorphism is well represented.



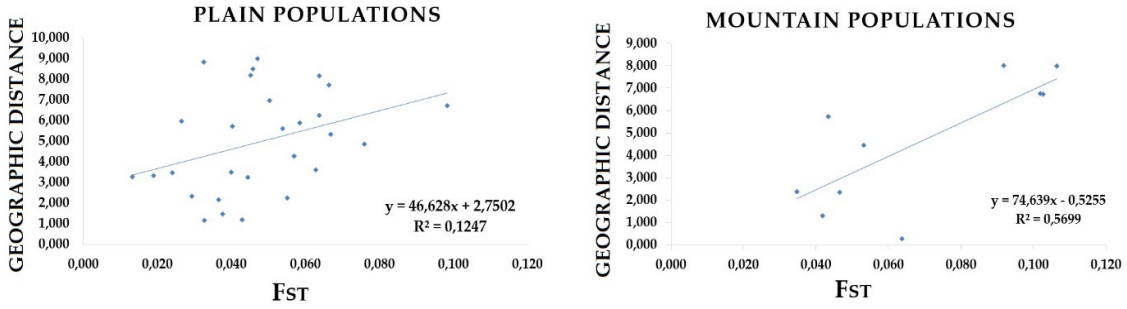
Supplementary Figure S4. STRUCTURE genetic migration test for *L. sibirica*. The sample names were given below the box plot with the individuals of different populations separated by vertical black lines. Each colour represents "one population".



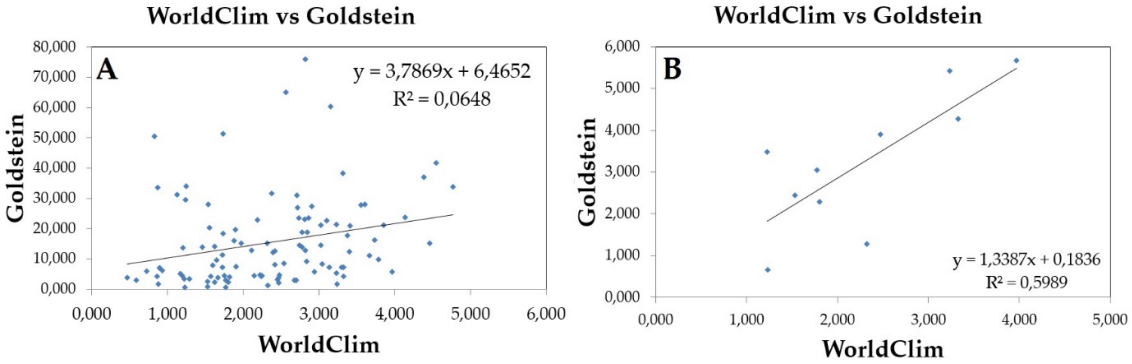
Supplementary Figure S5. Average number of pairwise differences.



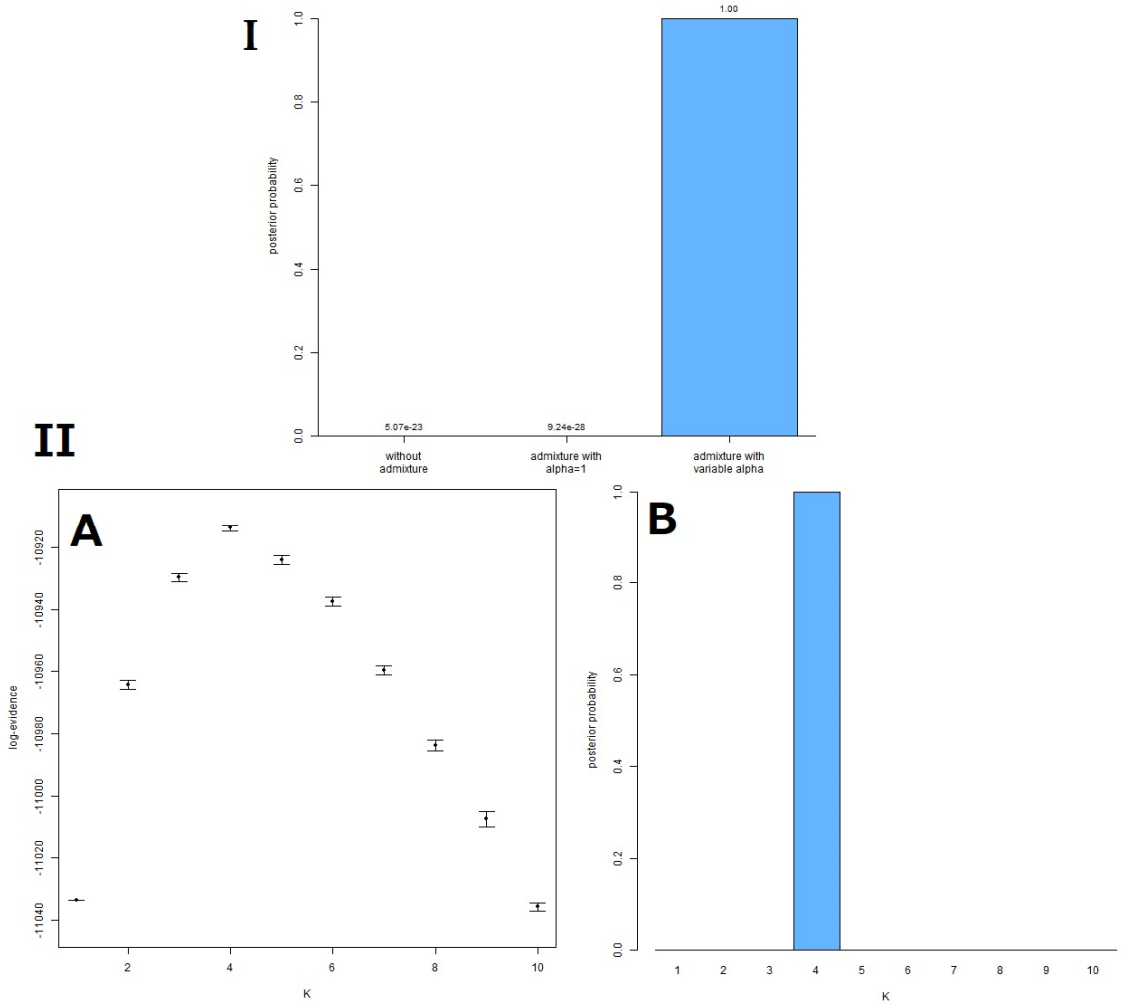
Supplementary Figure S6. Genetic structure of *L. sibirica* populations. **A**: Genetic similarity dendrogram constructed by UPGMA and least squares analysis based on Goldstein genetic distances for fifteen populations of larch; the scale is indicated below; **B**: Principal coordinate analysis (PCoA) for the Goldstein distance carried out with the genotypes of *L. sibirica*. individuals with 8 SSR markers. Red dots – south group; blue dots – middle group; green dots – north group; **C**: Minimum spanning tree based on Goldstein distances. The ribs color indicates the genetic distance (the lighter, the shorter the distance is). The nodes diameter is proportional to the clonal diversity of the populations.



Supplementary Figure S7. Graph of dependence of genetic (F_{ST}) and geographical distances in groups of mountain and lowland populations of *L. sibirica*.



Supplementary Figure S8. Mantel test for the WorldClim data and Goldstein distance; A: all populations; B: south group.



Supplementary Figure S9. I: Probabilistic models for the MavericK program. Posterior probability for different genetic structure models; **II**: Log-evidence (A) and posterior probability (B) for number of genetic clusters K.