

Table S8. Analysis of molecular variance (AMOVA) for populations of *Populus koreana* based on nSSR and cpDNA data.

Source of variation	<i>df</i>	<i>SS</i>	<i>VC</i>	<i>%V</i>	Φ -statistic
nSSR					
Individuals from the Greater Khingan					
Among populations	8	61.014	0.23129	6.71	$\Phi_{ST[nSSR]}$: 0.067***
Within populations	165	530.9	3.21758	93.29	
Total	173	591.914	3.44887		
Individuals from Southern Heilongjiang					
Among populations	10	55.151	0.12031	3.41	$\Phi_{ST[nSSR]}$: 0.034***
Within populations	185	630.94	3.41049	96.59	
Total	195	686.092	3.5308		
Individuals from the Changbai Mountains					
Among populations	12	104.078	0.24098	6.57	$\Phi_{ST[nSSR]}$: 0.066***
Within populations	271	928.439	3.42598	93.43	
Total	283	1032.518	3.66695		
Individuals from the Korean Peninsula					
Among populations	5	39.335	0.17501	5.3	$\Phi_{ST[nSSR]}$: 0.053***
Within populations	158	494.39	3.12905	94.7	
Total	163	533.726	3.30406		
All individuals (including Hebei)					
Among populations	39	452.242	0.39126	10.53	$\Phi_{ST[nSSR]}$: 0.105***
Within populations	808	2685.97	3.32422	89.47	
Total	847	3138.212	3.71548		
All individuals (excluding Hebei)					
Among regions	38	442.317	0.36850	9.92	$\Phi_{SC[nSSR]}$: 0.175***
Among populations	370	1455.17	0.58564	15.76	$\Phi_{ST[nSSR]}$: 0.257***
Within populations	409	1129.5	2.76161	74.32	$\Phi_{CT[nSSR]}$: 0.099***
Total	817	3026.988	3.71575		
cpDNA					
Individuals from the Greater Khingan					
Among populations	8	8.505	0.08352	15.87	$\Phi_{ST[cpDNA]}$: 0.159***
Within populations	59	26.113	0.44259	84.13	
Total	67	34.618	0.5261		
Individuals from Southern Heilongjiang					
Among populations	10	10.266	0.09458	25.28	$\Phi_{ST[cpDNA]}$: 0.253***
Within populations	78	21.802	0.27951	74.72	
Total	88	32.067	0.37409		
Individuals from the Changbai Mountains					
Among populations	12	11.622	0.08981	37.07	$\Phi_{ST[cpDNA]}$: 0.371***
Within populations	106	16.159	0.15244	62.93	
Total	118	27.782	0.24225		
Individuals from the Korean Peninsula					
Among populations	5	3.783	0.02034	3.46	$\Phi_{ST[cpDNA]}$: 0.035ns
Within populations	51	28.953	0.56771	96.54	

Total	56	32.737	0.58805		
All individuals (including Hebei)					
Among populations	39	49.262	0.10674	23.58	$\Phi_{ST[cpDNA]}$: 0.236***
Within populations	305	105.503	0.34591	76.42	
Total	344	154.765	0.45265		
All individuals (excluding Hebei)					
Among regions	3	7.678	0.01797	4.21	$\Phi_{SC[cpDNA]}$: 0.194***
Among populations	35	34.833	0.07922	18.55	$\Phi_{ST[cpDNA]}$: 0.228***
Within populations	294	97.003	0.32994	77.25	$\Phi_{CT[cpDNA]}$: 0.042*
Total	332	139.514	0.42713		

Abbreviations: *df*, degrees of freedom; *SS*, sum of squares; *VC*, variance components; *%V*, percent variation; Φ_{ST} , the ratio of the among-population variance component to the total genetic variance; Φ_{SC} , the ratio of the variance component of among-population within regions (σ_b^2) to σ_b^2 plus within-population variance component; Φ_{CT} , the ratio of the among-group (region) variance component to the total variance.

*, $P < 0.05$; ***, $P < 0.001$; ns, not significant.