Table S1 – List of external populations per oak species, with sample size (n) and basic genetic statistics averaged across 10 microsatellite loci

Species	Population	Latitude N	Longi- tude E	n	N_a	H_e	F
Q. robur	Podul Iloaiei	47°03'	27°13'	41	15.2	0.807	0.014
	Prejmer	45°44'	25°44'	48	12.7	0.773	0.011
Q. pubescens	Macin	45°13'	28°14'	43	13.4	0.841	0.027
	Sacalaia	46°57'	23°56'	42	13.1	0.842	0.024
Q. petraea	Cristian	45°38'	25°33'	48	15.0	0.789	0.003
	Ronisoara	47°51'	24°07'	36	13.6	0.784	-0.009
Q. frainetto	Slatina	44°43'	24°28'	38	10.3	0.693	0.034
	Lugoj	45°43'	21°59'	50	10.2	0.672	0.008
Total				346			

N_a – mean number of alleles per locus, H_e – gene diversity, F – fixation index

Fig. S1 Number of clusters (*K*) derived from the Bayesian analysis implemented in STRUCTURE software. Mean and standard deviation of log probability of data over 10 runs are plotted. Calculations were done with STRUCTURE HARVESTER.
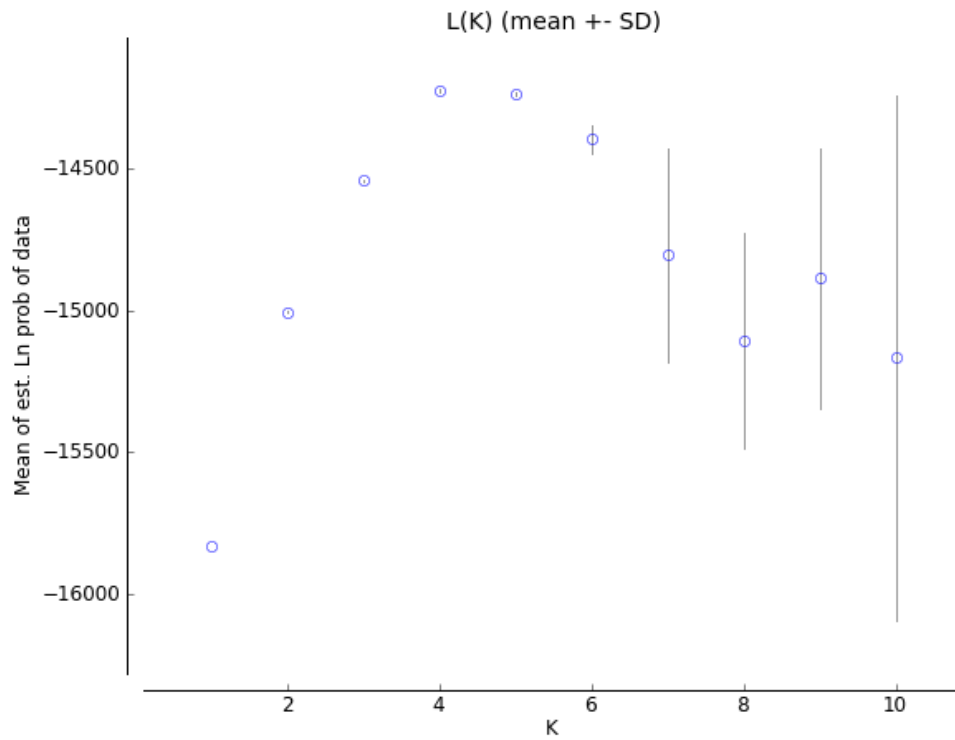
Fig. S2 Estimation of number of clusters (K) from the rate of change in the log probability of data L(K) between successive K values, as measured by ΔK. Calculations were done with STRUCTURE HARVESTER.