

Table S1. Analysis of molecular variance (AMOVA).

Source of variation	<i>df</i>	Variance components	% Total variation	<i>Fst</i>	<i>P</i>
Among populations	2	0.450	10.83	0.108	< 0.0001
Within populations	435	3.705	89.17		

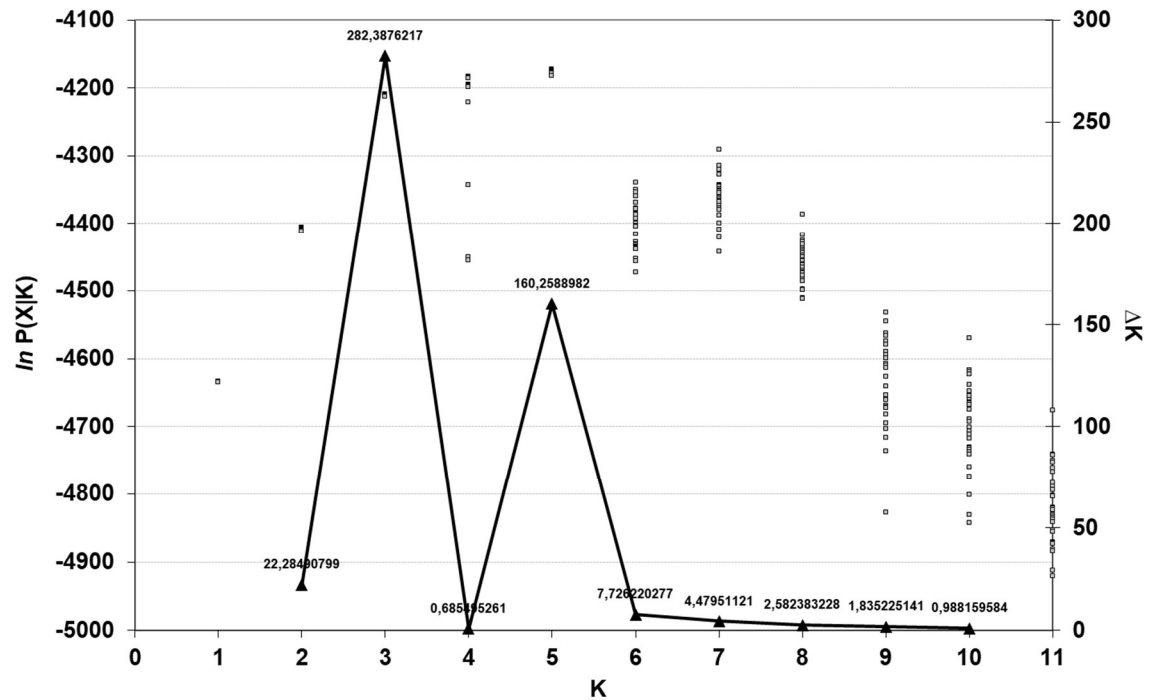


Figure S1. Inference of K, the most probable number of clusters, using STRUCTURE software, based on microsatellite analysis of 219 total samples of sweet chestnut.

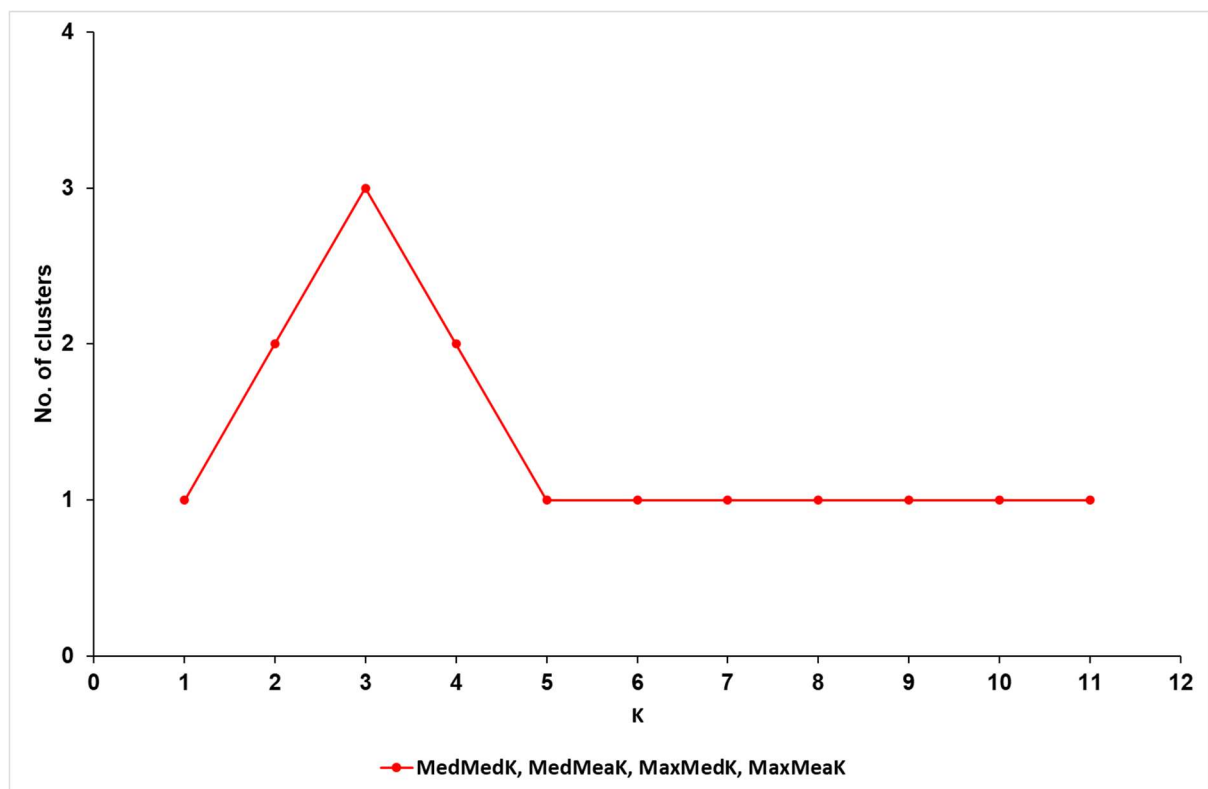


Figure S2. The optimal number of clusters calculated by MedMeaK, MaxMeaK, MedMedK and MaxMedK as implemented in StructureSelector.