TWO MAIN GENETIC CLUSTERS WITH HIGH ADMIXTURE BETWEEN FOREST AND CULTIVATED CHESTNUT (*CASTANEA SATIVA* MILL.) IN FRANCE

ESM_9

Within-cluster genetic variability at 10 loci without MLGs, on strongly assigned individuals (ql≥ 80%)
N: number of unique individuals genotyped per cluster; Na: number of alleles; Ne: mean number of effective alleles; Ho: observed heterozygosity; He: expected heterozygosity; Fis: inbreeding coefficient with 95% confidence interval. The "total" row contains the sum of N, the total number of alleles (Na), and the mean for the other indices.

RPPs (ql≥ 80%)	N	Ne	Na	Ho	He	Fis
RPP1a | Cluster 3	42	2.23	46	0.592	0.545	-0.081 [-0.245;0.18]
RPP2a | Cluster 4	127	3.49	72	0.733	0.711	-0.029 [-0.06;0.011]
RPP2b| Cluster 5	119	2.6	53	0.627	0.613	-0.016 [-0.042;0.007]
RPP2d | Cluster 6	74	3.18	66	0.625	0.681	0.088 [0.026;0.153]
RPP2c | Cluster 2	96	3.11	63	0.676	0.675	0.003 [-0.03,0.032]
RPP1b | Cluster 1	106	3.39	70	0.686	0.702	0.024 [-0.067;0.141]
Total	564	3.96	112	0.657	0.654	-0.002