

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

ESM_4 TESTS FOR HARDY-WEINBERG EQUILIBRIUM (HWE) ON THE 18UNIK AND 10UNIK DATA
SETS

In order to test the HWE per sampling region, we first separated the sampling regions with the function `seppop()` from package `adegenet`, focusing on the analytical p values by setting $B = 0$. We then created a matrix that only contains p values, with sampling regions in columns and loci in rows. From this matrix we created the figures below which are heatmap showing significant departure from HWE. Note, that all loci shown in pink are loci suspected of not being in HWE with $p \leq 0.05$.

ESM_4A TESTS FOR HWE OVER ALL SAMPLING REGIONS (18UNIK)

Locus	chi²	Df	Pr(chi²>)	Pr.exact
CsCAT14	36.14	10	0.000	0
CsCAT2	925.289	171	0.000	0
EMCS15	13.682	6	0.033	0.027
CsCAT16	110.958	45	0.000	0
CsCAT3	375.864	465	0.999	0.022
QpZAG36	28.894	10	0.001	0
CsCAT41B	717.913	55	0.000	0
QpZAG110	47.17	55	0.765	0.176
QrZAG4	0.554	1	0.457	0.597
QrZAG96	72.068	21	0.000	0
CsCAT1	125.739	55	0.000	0.102
CsCAT15	52.317	45	0.211	0.003
CsCAT6	467.523	120	0.000	0
CsCAT8	393.228	36	0.000	0
CsCAT17	97.665	45	0.000	0
RIC	3.585	6	0.733	0.653
OCI	24.222	10	0.007	0.007
OAL	59.518	36	0.008	0.011

ESM_4C TESTS FOR HWE OVER ALL SAMPLING REGIONS (10UNIK)

Locus	chi^2	df	Pr(chi^2>)	Pr.exact
CsCAT14	60.4	15	0.000	0.000
CsCAT2	1716.4	190	0.000	0.000
EMCS15	31.7	6	0.000	0.000
EMCS2	25.1	3	0.000	0.000
CsCAT16	183.4	45	0.000	0.000
CsCAT3	544.1	528	0.305	0.003
QpZAG36	47.4	10	0.000	0.000
CsCAT41B	2044.5	78	0.000	0.000
QpZAG110	67.2	55	0.125	0.009
QrZAG96	107.0	21	0.000	0.000

ESM_4D HEATMAP OF ANALYTICAL P VALUES FROM HWE TESTS PER SAMPLING REGION (10UNIK)

