Table S1 Microsatellite marker loci used in this study, including locus names, linkage groups (Lg), allele numbers (A), expected (HE) and observed (HO) heterozygosities, inbreeding coefficients FIS, and genetic divergence in the form of FST and Hedrick's (2005)

Table S3 Matrix of FST values for pairs of populations used in divergence- and diversity based neutrality tests at the European scale

Supporting Table 1. Microsatellite marker loci used in this study, including locus names, linkage groups (Lg), allele numbers (A), expected (H_E) and observed (H_O) heterozygosities, inbreeding coefficients F_{IS}, and genetic divergence in the form of F_{ST} and Hedrick's (2005) G'_{ST}.

Locus[1]	Lg[2]	Dist[2]	*A*	H_E	H_O	Var	F_{IS}	F_{ST}	[3]G'_{ST}
G1719	1	0.0	10	0.687	0.548	2.972	0.169	0.040	0.127
ASP302	1	6.8	12	0.776	0.829	10.973	-0.104	0.018	0.166
P2852	1	96.4	29	0.800	0.744	25.759	0.046	0.023	0.240
O30_2	1	26.9	10	0.815	0.790	7.703	-0.020	0.044	0.234
O137	1	31.2	6	0.428	0.140	4.002	0.630	0.079	0.160
G124	1	1.8	10	0.755	0.756	7.619	-0.071	0.057	0.274
G1376	2	0.0	18	0.708	0.446	6.324	0.303	0.099	0.256
G1158	2	144.9	7	0.322	0.192	2.582	0.305	0.093	0.165
G1133*	3	0.0	18	0.661	0.269	2.605	0.529*	0.061	0.267
ASP376	3	21.9	24	0.778	0.719	9.480	0.031	0.025	0.206
O30_1	3	0.0	4	0.372	0.381	0.180	-0.069	0.057	0.163
G1416	3	6.7	4	0.495	0.264	0.072	0.311	0.335	0.471
O203	3	1.7	7	0.663	0.641	0.429	-0.010	0.035	0.131
G1869	3	43.3	14	0.858	0.716	5.886	0.127	0.036	0.327
G1688	3	7.7	9	0.375	0.232	0.667	0.347	0.072	0.044
O220	4	0.0	4	0.583	0.575	3.438	-0.016	0.041	0.130
O127	4	55.5	8	0.683	0.342	4.789	NA	0.056	0.245
G1809	4	18.7	9	0.813	0.732	1.094	0.004	0.052	0.313

G1255	5	0.0	1	0.000	0.000	0.000	NA	NA	NA
G1838	5	35.3	17	0.800	0.672	7.986	0.125	0.034	0.228
G20	5	61.6	2	0.074	0.068	0.037	0.047	0.007	0.187
W15	5	29.9	9	0.711	0.594	9.738	0.156	0.034	0.123
G1065	6	0.0	8	0.748	0.700	2.714	0.031	0.017	0.163
O369	6	11.0	5	0.571	0.574	0.364	-0.012	0.047	0.031
G2034	6	12.6	6	0.358	0.288	0.380	0.153	0.024	0.024
ASP322	6	2.0	9	0.643	0.610	4.425	-0.024	0.140	0.215
O60	6	4.1	9	0.494	0.313	5.651	0.288	0.124	0.143
W12*	6	12.9	19	0.721	0.328	10.853	0.533*	0.034	0.146
O190	6	11.3	4	0.387	0.335	10.780	0.132	0.014	0.081
ASP933	6	2.1	11	0.711	0.370	0.600	0.355	0.149	0.493
G1485	6	26.5	3	0.035	0.034	0.799	-0.034	0.038	0.098
Asl-1	6	11.4	8	0.412	0.393	5.115	NA	0.003	0.000
O26	6	14.9	2	0.010	0.013	0.005	0.000	-0.005	0.089
O167	6	10.0	4	0.014	0.019	0.078	0.000	0.002	0.000
G1074	6	3.5	2	0.105	0.123	0.052	0.001	0.049	0.045
G1831	6	2.2	12	0.756	0.794	4.616	-0.099	0.040	0.169
G139	6	10.4	8	0.759	0.616	3.102	0.162	0.025	0.160
G1260	7	0.0	2	0.477	0.571	0.238	-0.213	0.086	0.226
W17	7	0.0	7	0.611	0.589	2.893	0.001	0.023	0.139
O312	7	2.5	10	0.728	0.671	9.760	0.015	0.049	0.179

G2062	8	0.0	11	0.811	0.764	8.726	0.005	0.043	0.293
O374*	8	5.4	49	0.948	0.726	34.995	0.196*	0.056	0.638
O202	8	73.0	3	0.566	0.561	0.930	-0.050	0.036	0.101
O268	8	0.0	9	0.374	0.137	0.864	0.622	0.093	0.000
G1949	9	0.0	13	0.750	0.563	23.125	0.163	0.068	0.293
O23*	9	10.2	21	0.737	0.435	6.896	0.403*	0.015	0.148
G2020	10	0.0	18	0.695	0.633	7.845	0.012	0.058	0.260
O149	10	54.2	7	0.597	0.593	1.581	-0.004	0.028	0.066
O344	10	9.0	5	0.616	0.605	4.670	-0.021	0.068	0.196
G1574	10	14.7	17	0.777	0.660	5.371	0.099	0.052	0.183
G114*	10	25.2	16	0.696	0.281	25.401	0.590*	0.038	0.175
G1037	11	31.6	4	0.458	0.492	0.145	-0.116	0.071	0.116
G154*	12	0.0	29	0.872	0.644	10.562	0.230*	0.026	0.213
W05*	12	12.2	24	0.758	0.496	40.480	0.336*	0.047	0.186
G1186	12	46.5	4	0.439	0.327	0.261	0.231	0.049	0.159
G1353	13	0.0	8	0.663	0.565	8.460	0.037	0.125	0.255
G162	13	178.0	38	0.883	0.790	70.693	0.047	0.055	0.381
G1812	14	17.2	7	0.686	0.706	5.774	-0.046	0.017	0.139
G1894	15	0.0	5	0.113	0.082	0.258	0.154	0.012	0.000
1454	15	0.6	16	0.784	0.785	22.762	-0.052	0.031	0.178
G1608	15	36.3	7	0.281	0.121	7.207	0.521	0.074	0.199
O14	16	0.0	6	0.149	0.152	3.617	-0.009	0.013	0.000

O214	18	0.0	4	0.349	0.316	0.128	0.105	0.058	0.088
G1577	18	5.2	2	0.049	0.010	0.024	0.490	0.029	0.246
O28	18	18.9	10	0.278	0.261	1.782	0.023	0.005	0.036
O276	19	0.0	9	0.593	0.450	3.405	0.199	0.054	0.208
Yin1	19	0.0	6	0.605	0.652	2.021	-0.134	0.012	0.140
Con58.1	19	4.4	20	0.755	0.696	128.338	-0.029	0.069	0.267
Yin2	19	1.4	24	0.893	0.807	8.355	0.026	0.069	0.472
O206	19	6.9	11	0.561	0.475	1.439	0.155	0.018	0.029

Asterisks (*) indicate loci with significant HWE deficits at the 0.05 level. 'NA' refers to missing data due to monomorphy in particular populations; locus G1255 was included despite monomorphy in all populations of *P. tremula* to facilitate tests for range-wide selective sweeps.

[1]Loci with G refer to GCPM, loci with O refer to ORPM, loci with W to WPMS, loci with P to PMGC on the *Populus* genome project web page (http://www.ornl.gov/sci/ipgc). Primer information for these markers was also published by van der Schoot *et al*. (2000), Tuskan *et al*. (2004), and Smulders *et al*. (2001). Loci Yin1 and Yin2 refer to tri-repeats starting at positions 102637 and 112352 of chromosome 19 in Yin *et al*. (2009). Loci starting with ASP were newly identified within ESTs, their repeat type and primer sequences were, ASP302: repeat = $(GA)_n$, forward (F) = GGCAGCGTCTTCATTCCTAT, reverse (R) = AAAGCCATTGAAGTGGAGGA; ASP376: repeat = $(GT)_n$ AT $(GT)_n$, F = GCTCGAGATCTATCGGCAAC, R = TCCTCTCCAGGAAACTCCAA; ASP322: repeat = $(AG)_n$, F = CATTAACGCCCCATTTCAGT, R = GTGAGGCACCACCCTGATAG; ASP933: repeat = $(CT)_n$, F = AGCCAGTAGGCTTCTTCAACA, R = CATCCCTCCCTAATCCCATT.

Locus Asl-1 was identified within the transcribed sequence of Asymmetric leaves 1 as described by Joseph & Lexer (2008), repeat = $(CCCCAT)_n$, F = AATTGACGAGGGCAAGTACG, R = CTCCAGCTGCAACTCTACCC. Locus Con58.1 was identified on contig 58/position 706705 of *P. trichocarpa* scaffold 117, recently found to be homologous to chromosome 19 of *Populus*, repeat = $(TC)_nT(TC)_nTGCC(TC)_n$, F = TAGCTGTGTTCCTCGTCGTC, R = TACGGATGTCCTTGCTTGTG.

[2]Genomic locations of marker loci were used for graphical representation and Bayesian STRUCTURE analysis only. Linkage group (Lg) assignments and map distances are according to *Populus* genetic maps (e.g. Yin *et al*. 2004) and *P. trichocarpa* genome assembly v1.1. In cases where marker loci were mapped to more than one Lg in *P. trichocarpa*, chromosomal positions were confirmed by BLAST of the primer sequences against the *P. trichocarpa* genome assembly. In rare cases where no recombination distances in centi morgan (cM) were available from *P. trichocarpa*, mapping distances from an interspecific cross *P. alba* x *P. tremula* were used (Macaya-Sanz, Alba, Gonzalez-Martinez, Lexer and coworkers, unpublished data).

Supporting Table 3. Matrix of F_{ST} values for pairs of populations used in divergence- and diversity based neutrality tests at the European scale.

	Swe	Spain	Scot	Aus	Russ
Swe	0.000				
Spain	0.083	0.000			
Scot	0.034	0.074	0.000		
Aus	0.022	0.094	0.039	0.000	
Russ	0.030	0.110	0.061	0.036	0.000

All p-values < 0.01; Population Aus was composed of Aus/BM and Aus/Alps and population Russ consisted of Russ/C and Russ/SE, respectively, based on the results of STRUCTURE analysis. For population abbreviations and details see Table 1 and Methods of the main paper.