FILES S1-S3

Files S1-S3 are available for download as Excel files at http://www.genetics.org/cgi/content/full/genetics.110.118828/DC1.

File S1: Genotype data used for admixture analysis of the Danube hybrid zone of Populus alba and P. tremula, following structure 2.2 input format. Individual ID`s starting with alb refer to P. alba, ID`s starting with trem refer to P. tremula, ID`s starting with can refer to P. x canescens hybrids. See text for marker details and structure 2.2 manual for specifics of the input file format.

File S2: Genotype data used for admixture analysis of the Ticino hybrid zone of Populus alba and P. tremula, following structure 2.2 input format. Individual ID`s starting with alb refer to P. alba, ID`s starting with trem refer to P. tremula, ID`s starting with can refer to P. x canescens hybrids. See text for marker details and structure 2.2 manual for specifics of the input file format.

File S3: Genotype data used for admixture analysis of the Tisza hybrid zone of Populus alba and P. tremula, following structure 2.2 input format. Individual ID`s starting with alb refer to P. alba, ID`s starting with trem refer to P. tremula, ID`s starting with can refer to P. x canescens hybrids. See text for marker details and structure 2.2 manual for specifics of the input file format.

TABLE S1

Essential information for all 93 genetic marker loci typed in this study, including locus name, assignment to chromosomes, marker type, marker source, information about marker scoring, gene diversity (H_E) in *P. alba* and *P. tremula*, interspecific F_{ST} and G'_{ST} and probability for greater-than-neutral F_{ST}.

Locus[a]	Chrom	Type[b]	Source[c]	Scoring[d]	H_E alba	H_E trem	F_{ST}	G'_{ST}	P
G1274	1	mic	genomic	dom	0.402	0.032	0.052	0.041	0.463
G1719	1	mic	genomic	codom	0.867	0.628	0.182	0.694	0.701
A302	1	mic	EST	codom	0.852	0.778	0.070	0.358	0.338
P2852	1	mic	genomic	codom	0.807	0.868	0.042	0.245	0.082
O30_2	1	mic	genomic	codom	0.937	0.801	0.085	0.636	0.353
G1568	1	mic	genomic	codom	0.932	0.969	0.033	0.660	0.012
O137	1	mic	genomic	codom	0.512	0.489	0.488	0.968	0.994*
G124	1	mic	genomic	codom	0.560	0.708	0.350	0.947	0.905
G1376	2	mic	genomic	codom	0.024	0.619	0.669	0.979	1.000*
G1158	2	mic	genomic	codom	0.042	0.165	0.897	1.001	1.000*
G1133	3	mic	genomic	codom	0.646	0.697	0.306	0.920	0.866
A376	3	mic	EST	codom	0.477	0.788	0.366	0.994	0.916
G1629	3	mic	genomic	codom	0.820	0.826	0.124	0.681	0.545
O30_1	3	mic	genomic	codom	0.082	0.449	0.189	0.180	0.816
G1887	3	mic	genomic	dom	0.175	0.000	0.143	0.092	1.000*
G1416	3	mic	genomic	codom	0.452	0.379	0.000	0.000	0.192
AQ	3	seq	EST	codom	0.000	0.079	0.957	0.993	1.000*
O203	3	mic	genomic	codom	0.202	0.616	0.173	0.225	0.780
G1869	3	mic	genomic	codom	0.816	0.836	0.174	1.000	0.703
G1688	3	mic	genomic	codom	0.726	0.296	0.394	0.758	0.979
O220	4	mic	genomic	codom	0.000	0.515	0.740	0.996	1.000*

GAD	4	indel	EST	dom	0.361	0.000	0.184	0.146	0.989
O127	4	mic	genomic	codom	0.064	0.695	0.375	0.513	0.994*
G1809	4	mic	genomic	codom	0.028	0.839	0.431	0.695	0.992*
DE	4	seq	EST	codom	0.103	0.191	0.571	0.537	1.000*
G1255	5	mic	genomic	codom	0.021	0.000	0.990	1.000	0.500
G1192	5	mic	genomic	codom	0.658	0.361	0.146	0.243	0.754
PER1	5	indel	EST	dom	0.000	0.411	0.671	0.766	1.000*
G1838	5	mic	genomic	codom	0.694	0.792	0.208	0.788	0.748
G20	5	mic	genomic	codom	0.565	0.000	0.558	0.691	1.000*
W15	5	mic	genomic	codom	0.799	0.656	0.141	0.479	0.619
G1065	6	mic	genomic	codom	0.000	0.749	0.628	1.006	1.000*
O369	6	mic	genomic	codom	0.446	0.545	0.026	0.039	0.463
G2034	6	mic	genomic	codom	0.922	0.307	0.388	1.007	0.913
A322	6	mic	EST	codom	0.779	0.805	0.188	0.892	0.719
O60	6	mic	genomic	codom	0.759	0.265	0.397	0.767	0.979
W12	6	mic	genomic	codom	0.767	0.823	0.163	0.775	0.659
O190	6	mic	genomic	codom	0.266	0.374	0.638	0.908	1.000*
A933	6	mic	EST	codom	0.387	0.534	0.538	0.995	1.000*
G1485	6	mic	genomic	codom	0.000	0.139	0.061	0.036	0.882
AS1	6	seq	EST	codom	0.000	0.229	0.829	0.891	1.000*
AS1MIC	6	mic	EST	codom	0.372	0.289	0.046	0.047	0.419
O26	6	mic	genomic	codom	0.863	0.000	0.548	0.950	1.000*
O167	6	mic	genomic	codom	0.061	0.021	0.959	1.000	1.000*
G1074	6	mic	genomic	codom	0.044	0.000	0.978	0.999	1.000*
G1831	6	mic	genomic	codom	0.696	0.737	0.247	0.853	0.811
G139	6	mic	genomic	codom	0.000	0.778	0.624	1.033	1.000*
G1260	7	mic	genomic	codom	0.614	0.494	0.208	0.404	0.727
W17	7	mic	genomic	codom	0.616	0.628	0.194	0.461	0.726
G1295	7	mic	genomic	dom	0.492	0.000	0.000	0.000	0.151

O312	7	mic	genomic	codom	0.782	0.756	0.159	0.663	0.670
G2062	8	mic	genomic	codom	0.862	0.847	0.077	0.511	0.331
PHYB	8	seq	EST	codom	0.113	0.352	0.234	0.213	1.000*
O374	8	mic	genomic	codom	0.778	0.889	0.160	0.961	0.663
O202	8	mic	genomic	codom	0.525	0.573	0.283	0.567	0.881
O268	8	mic	genomic	codom	0.650	0.401	0.254	0.468	0.906
THAU	9	mic	EST	codom	0.797	0.536	0.331	0.991	0.887
G1949	9	mic	genomic	codom	0.568	0.805	0.096	0.271	0.512
O23	9	mic	genomic	codom	0.858	0.724	0.209	1.001	0.762
O21	9	mic	genomic	codom	0.198	0.000	0.090	0.058	1.000*
G2020	10	mic	genomic	codom	0.857	0.666	0.205	0.844	0.770
O149	10	mic	genomic	codom	0.369	0.533	0.548	0.996	1.000*
O344	10	mic	genomic	codom	0.041	0.538	0.721	1.022	1.000*
G1574	10	mic	genomic	codom	0.250	0.781	0.458	0.930	0.991*
G114	10	mic	genomic	codom	0.087	0.745	0.572	0.970	1.000*
G1250	11	mic	genomic	dom	0.000	0.000	0.945	0.895	0.500
G1037	11	mic	genomic	codom	0.410	0.396	0.000	0.000	0.187
G154	12	mic	genomic	dom	0.000	0.000	0.495	0.329	0.500
W5	12	mic	genomic	codom	0.689	0.787	0.244	0.923	0.802
G1186	12	mic	genomic	codom	0.781	0.502	0.353	0.980	0.893
G1353	13	mic	genomic	codom	0.497	0.646	0.076	0.145	0.452
O16	13	mic	genomic	dom	0.408	0.082	0.009	0.008	0.210
PHYA	13	seq	EST	codom	0.029	0.110	0.895	0.931	1.000*
G162	13	mic	genomic	codom	0.821	0.854	0.148	0.902	0.664
ENDO	14	seq	EST	codom	0.045	0.172	0.798	0.825	1.000*
G1292	14	mic	genomic	dom	0.000	0.000	0.946	0.897	0.500
G1812	14	mic	genomic	codom	0.831	0.671	0.176	0.679	0.712
G2014	14	mic	genomic	dom	0.447	0.000	0.114	0.095	0.644
G1306	14	mic	genomic	dom	0.243	0.000	0.079	0.052	0.670

G1894	15	mic	genomic	codom	0.837	0.084	0.516	0.941	1.000*
G1454	15	mic	genomic	codom	0.820	0.781	0.131	0.632	0.569
G1608	15	mic	genomic	codom	0.669	0.215	0.558	1.000	1.000*
O430	15	mic	genomic	dom	0.000	0.000	0.946	0.897	0.500
O14	16	mic	genomic	codom	0.000	0.100	0.041	0.023	0.864
G1381	17	mic	genomic	dom	0.000	0.000	0.512	0.345	0.500
SOS2	18	mic	EST	codom	0.485	0.083	0.280	0.292	0.972
O214	18	mic	genomic	codom	0.194	0.142	0.819	0.974	1.000*
G1577	18	mic	genomic	codom	0.831	0.042	0.564	1.000	1.000*
O28	18	mic	genomic	codom	0.468	0.233	0.161	0.183	0.725
O276	19	mic	genomic	dom	0.000	0.254	0.346	0.270	1.000*
O206	19	mic	genomic	codom	0.062	0.553	0.517	0.659	1.000*
AP2	scaffold 28	seq	EST	codom	0.214	0.096	0.726	0.779	1.000*
PAL	scaffold 28	seq	EST	codom	0.259	0.816	0.201	0.371	0.765

[a]Markers starting with G refer to GCPM, markers starting with O refer to ORPM, markers with W refer to WPMS, markers with P refer to PMGC microsatellite loci available at http://www.ornl.gov/sci/ipgc. For all other markers see JOSEPH and LEXER (2008) and DE CARVALHO *et al.* (2010). See text for details.

[b]Marker type: mic, microsatellite; seq: sequence polymorphism, indel: insertion-deletion polymorphism.

[c]Marker source: genomic, genomic library or shotgun genome sequence; EST, expressed sequence tag.

[d]Marker scoring: codom, codominant; dom, dominant (presence/absence information). Loci with greater-than-neutral F_{ST} at the 99% level are indicated by an asterisk.

TABLE S2

Eighty (80) microsatellite loci used for Bayesian admixture analysis with a linkage model, including

marker name, chromosome assignment, and assumed chromosomal distance in centimorgan (cM).

Locus	Chrom	cM[a]	Locus	Chrom	cM[b]
G1274	1	-1	G139	6	10.41
G1719	1	42.5	G1260	7	-1
ASP302	1	6.76	W17	7	0
P2852	1	96.44	G1295	7	12.5
O30_2	1	26.9	O312	7	2.5
G1568	1	9.3	G2062	8	-1
O137	1	31.23	O374	8	5.4
G124	1	1.77	O202	8	73
G1376	2	-1	O268	8	0
G1158	2	144.86	G1949	9	-1
G1133	3	-1	O23	9	10.22
ASP376	3	21.92	O21	9	13.2
G1629	3	9.48	G2020	10	-1
O30_1	3	9.48	O149	10	54.2
G1887	3	9.48	O344	10	9
G1416	3	6.7	G1574	10	14.68
O203	3	1.7	G114	10	25.2
G1869	3	43.34	G1250	11	-1
G1688	3	7.7	G1037	11	31.56
O220	4	-1	G154	12	-1
O127	4	55.52	W05	12	12.22
G1809	4	18.7	G1186	12	46.48
G1255	5	-1	G1353	13	-1
G1192	5	22.2	O16	13	13.8
G1838	5	35.26	G162	13	178
G20	5	61.56	G1292	14	-1
W15	5	29.92	G1812	14	17.19
G1065	6	-1	G2014	14	25.73
O369	6	11	G1306	14	2.08
G2034	6	12.6	G1894	15	-1
ASP322	6	1.96	G1454	15	0.59
O60	6	4.06	G1608	15	36.33
W12	6	12.88	G430	15	36
O190	6	11.3	O14	16	-1
ASP933	6	2.11	G1381	17	-1
G1485	6	26.49	O214	18	-1
O26	6	14.9	G1577	18	5.2
O167	6	10.02	O28	18	18.9

G1074	6	3.48	O276	19	-1
G1831	6	2.2	O206	19	21.5

[a]The first marker sampled on each chromosome is indicated by -1. [b]Approximate chromosomal distances were obtained from *P. trichocarpa* genome assembly v.1 and genetic maps; for markers that mapped to more than one chromosome in *P. trichocarpa*, map positions were clarified by using segregation data from a controlled cross between *P. alba* and *P. tremula* (Macaya-Sanz, Gonzalez-Martinez, Alba, unpublished data).

TABLE S3

Genetic diversity statistics and results of genomic clines for mapped codominant microsatellites studied in three hybrid zones of *P. alba* and *P. tremula*, including number of alleles (A), expected (H_E) and observed (H_O) heterozygosity in each parental population, allele frequency differential (delta) and the following genomic cline parameters: ln likelihood, probability for departure from neutrality, and indications for significant over- or underrepresentation (+ or -) of individual genotypic classes. A: Danube (Austria), 68 loci; B: Ticino (Italy), 18 loci; C: Tisza (Hungary), 18 loci.

A)   Danube/Austria

Locus	Ch	A alba	He alba	Ho alba	A trem	H_E trem	H_O trem	delta	lnL ratio	P	Selection[a]		
G1719	1	12	0.867	0.844	7	0.628	0.568	0.625	7.49	0.004	TT:+	TA:	AA:-
A302	1	9	0.852	0.841	9	0.778	0.773	0.448	1.24	0.648	TT:	TA:	AA:
P2852	1	15	0.807	0.563	19	0.868	0.813	0.490	2.11	0.341	TT:	TA:	AA:
O30_2	1	19	0.937	0.911	8	0.801	0.915	0.677	26.60	0.000	TT:+	TA:	AA:-
G1568	1	25	0.932	0.514	36	0.969	0.644	0.740	46.82	0.000	TT:+	TA:	AA:-
O137	1	3	0.512	0.313	7	0.489	0.229	0.969	20.55	0.000	TT:	TA:-	AA:+
G124	1	5	0.560	0.617	6	0.708	0.721	0.885	6.28	0.015	TT:	TA:	AA:
G1376	2	2	0.024	0.024	12	0.619	0.341	0.906	4.49	0.049	TT:+	TA:-	AA:
A376	2	3	0.477	0.362	12	0.788	0.475	0.948	6.70	0.008	TT:	TA:	AA:
G1158	2	3	0.042	0.043	4	0.165	0.174	0.979	10.20	0.000	TT:	TA:	AA:
G1133	3	10	0.646	0.196	9	0.697	0.109	0.802	49.75	0.000	TT:+	TA:-	AA:
G1629	3	18	0.820	0.705	17	0.826	0.457	0.729	7.10	0.007	TT:+	TA:	AA:
O30_1	3	2	0.082	0.043	3	0.449	0.340	0.292	3.76	0.060	TT:	TA:	AA:
G1416	3	5	0.452	0.283	2	0.379	0.125	0.083	15.48	0.000	TT:	TA:	AA:+
O203	3	4	0.202	0.087	6	0.616	0.533	0.406	6.81	0.009	TT:	TA:	AA:
G1869	3	10	0.816	0.614	13	0.836	0.745	0.979	5.36	0.031	TT:	TA:	AA:
G1688	3	11	0.726	0.565	6	0.296	0.222	0.698	5.86	0.013	TT:+	TA:	AA:-

O220	4	1	0.000	0.000	4	0.515	0.583	1.000	8.68	0.001	TT:-	TA:+	AA:
O127	4	3	0.064	0.065	6	0.695	0.325	0.594	18.49	0.000	TT:+	TA:-	AA:
G1809	4	2	0.028	0.028	7	0.839	0.714	0.677	13.22	0.000	TT:+	TA:	AA:
G1255	5	2	0.021	0.021	1	0.000	0.000	1.000	11.09	0.001	TT:	TA:+	AA:
G1192	5	5	0.658	0.660	9	0.361	0.152	0.458	5.42	0.018	TT:	TA:	AA:
G1838	5	9	0.694	0.600	8	0.792	0.696	0.781	12.46	0.000	TT:-	TA:+	AA:-
G20	5	8	0.565	0.444	1	0.000	0.000	0.615	8.60	0.001	TT:+	TA:	AA:-
W15	5	7	0.799	0.688	6	0.656	0.646	0.542	5.94	0.010	TT:-	TA:	AA:
G1065	6	1	0.000	0.000	9	0.749	0.636	0.938	31.03	0.000	TT:+	TA:-	AA:
O369	6	5	0.446	0.417	6	0.545	0.521	0.219	9.43	0.000	TT:	TA:+	AA:-
G2034	6	16	0.922	0.756	4	0.307	0.277	0.958	6.72	0.012	TT:-	TA:	AA:
A322	6	11	0.779	0.787	8	0.805	0.783	0.813	10.78	0.000	TT:	TA:	AA:+
O60	6	9	0.759	0.646	6	0.265	0.167	0.813	59.90	0.000	TT:-	TA:	AA:+
W12	6	13	0.767	0.444	14	0.823	0.386	0.719	16.14	0.000	TT:+	TA:-	AA:+
O190	6	2	0.266	0.311	2	0.374	0.400	0.792	4.72	0.025	TT:-	TA:	AA:+
A933	6	6	0.387	0.364	8	0.534	0.511	0.969	8.35	0.001	TT:-	TA:	AA:
G1485	6	1	0.000	0.000	2	0.139	0.149	0.083	27.08	0.000	TT:+	TA:-	AA:
O26	6	9	0.863	0.909	1	0.000	0.000	0.875	13.14	0.000	TT:+	TA:-	AA:
O167	6	2	0.061	0.063	2	0.021	0.021	0.990	13.54	0.002	TT:	TA:+	AA:-
G1831	6	8	0.696	0.732	7	0.737	0.732	0.667	1.52	0.462	TT:	TA:	AA:
G1074	6	2	0.044	0.044	1	0.000	0.000	0.938	7.47	0.004	TT:-	TA:	AA:
G139	6	1	0.000	0.000	7	0.778	0.372	1.000	0.25	0.940	TT:	TA:	AA:
G1260	7	5	0.614	0.542	2	0.494	0.468	0.469	9.75	0.000	TT:+	TA:	AA:-
W17	7	9	0.616	0.489	8	0.628	0.556	0.521	15.86	0.000	TT:+	TA:	AA:-
O312	7	7	0.782	0.804	7	0.756	0.708	0.677	2.66	0.231	TT:	TA:	AA:
G2062	8	15	0.862	0.809	11	0.847	0.851	0.573	7.92	0.002	TT:-	TA:+	AA:
O374	8	15	0.778	0.575	17	0.889	0.625	0.760	24.97	0.000	TT:+	TA:	AA:-
O202	8	3	0.525	0.447	4	0.573	0.565	0.594	1.52	0.487	TT:	TA:	AA:
O268	8	4	0.650	0.591	5	0.401	0.214	0.531	3.75	0.092	TT:	TA:	AA:

Locus	Ch	A alba	He alba	Ho alba	A trem	H_E trem	H_O trem	lnL ratio	P	delta	Selection[1]		
G1949	9	7	0.568	0.351	9	0.805	0.457	0.479	7.08	0.010	TT:	TA:	AA:
O23	9	20	0.858	0.660	12	0.724	0.396	1.000	12.46	0.000	TT:-	TA:	AA:+
O21	9	3	0.198	0.196	1	0.000	0.000	0.125	8.39	0.001	TT:	TA:	AA:
G2020	10	14	0.857	0.850	13	0.666	0.667	0.740	6.38	0.014	TT:	TA:+	AA:
O149	10	3	0.369	0.333	4	0.533	0.543	0.958	11.45	0.000	TT:+	TA:	AA:-
O344	10	2	0.041	0.042	3	0.538	0.442	1.000	5.12	0.039	TT:	TA:+	AA:-
G1574	10	2	0.250	0.289	11	0.781	0.659	0.792	26.17	0.000	TT:+	TA:-	AA:
G114	10	3	0.087	0.089	8	0.745	0.341	0.885	2.52	0.290	TT:	TA:	AA:
G1037	11	5	0.410	0.478	3	0.396	0.395	0.073	10.92	0.000	TT:	TA:+	AA:-
W05	12	9	0.689	0.708	12	0.787	0.489	0.917	6.37	0.015	TT:	TA:	AA:
G1186	12	7	0.781	0.636	3	0.502	0.500	0.865	3.50	0.132	TT:	TA:-	AA:+
G1353	13	2	0.497	0.522	6	0.646	0.435	0.271	9.18	0.001	TT:	TA:	AA:
G162	13	9	0.821	0.786	14	0.854	0.773	0.823	0.63	0.741	TT:	TA:	AA:
G1812	14	11	0.831	0.432	6	0.671	0.700	0.656	5.97	0.010	TT:	TA:-	AA:+
G1894	15	11	0.837	0.830	4	0.084	0.085	0.906	3.77	0.101	TT:	TA:	AA:
G1454	15	11	0.820	0.667	12	0.781	0.667	0.708	7.27	0.008	TT:	TA:-	AA:+
G1608	15	10	0.669	0.488	3	0.215	0.116	0.896	46.01	0.000	TT:	TA:-	AA:+
O14	16	1	0.000	0.000	2	0.100	0.104	0.052	6.24	0.001	TT:+	TA:+	AA:-
O214	18	4	0.194	0.167	2	0.142	0.152	0.927	13.74	0.000	TT:	TA:+	AA:-
G1577	18	10	0.831	0.766	2	0.042	0.043	0.979	4.12	0.086	TT:	TA:	AA:
O28	18	3	0.468	0.542	4	0.233	0.255	0.333	3.38	0.119	TT:	TA:	AA:
O206	19	4	0.062	0.063	5	0.553	0.422	0.635	2.03	0.341	TT:	TA:	AA:

B) Ticino/Italy

Locus	Ch	A alba	He alba	Ho alba	A trem	H_E trem	H_O trem	lnL ratio	P	delta	Selection[1]		
P2852	1	10	0.577	0.350	15	0.870	0.590	8.90	0.001	0.825	TT:-	TA:	AA:
O30_2	1	20	0.933	0.909	8	0.686	0.750	10.01	0.001	0.900	TT:-	TA:+	AA:
O137	1	3	0.235	0.184	6	0.256	0.139	11.95	0.000	0.938	TT:-	TA:+	AA:

Locus	Ch	A alba	He alba	Ho alba	A trem	H_E trem	H_O trem	lnL ratio	P	Delta	Selection[1]		
O30_1	3	2	0.075	0.077	2	0.119	0.125	23.91	0.000	0.063	TT:+	TA:-	AA:+
O220	4	1	0.000	0.000	6	0.632	0.600	7.66	0.001	0.500	TT:-	TA:	AA:+
O127	4	1	0.000	0.000	6	0.702	0.282	9.19	0.000	0.875	TT:	TA:	AA:
W15	5	8	0.835	0.872	7	0.771	0.632	3.66	0.095	0.563	TT:	TA:	AA:
O60	6	7	0.818	0.763	5	0.659	0.256	23.58	0.000	0.738	TT:+	TA:-	AA:+
O167	6	2	0.099	0.103	3	0.120	0.125	44.91	0.000	0.950	TT:+	TA:-	AA:-
O312	7	5	0.714	0.825	4	0.619	0.538	14.35	0.000	0.913	TT:	TA:+	AA:-
O202	8	3	0.607	0.550	2	0.501	0.450	8.69	0.001	0.550	TT:-	TA:	AA:+
O21	9	2	0.315	0.179	1	0.000	0.000	30.78	0.000	0.213	TT:	TA:-	AA:+
O149	10	3	0.515	0.150	3	0.229	0.200	39.54	0.000	1.000	TT:+	TA:-	AA:-
O344	10	2	0.025	0.025	7	0.820	0.526	15.75	0.000	0.950	TT:-	TA:	AA:+
W05	12	4	0.649	0.487	8	0.723	0.300	8.99	0.001	1.000	TT:-	TA:+	AA:
O214	18	3	0.164	0.125	2	0.073	0.075	32.13	0.000	0.950	TT:-	TA:+	AA:-
O28	18	3	0.560	0.400	3	0.228	0.250	5.92	0.021	0.488	TT:	TA:	AA:-
O206	19	6	0.580	0.385	5	0.618	0.487	17.86	0.000	0.163	TT:	TA:-	AA:+

C) Tisza/Hungary

Locus	Ch	A alba	He alba	Ho alba	A trem	H_E trem	H_O trem	lnL ratio	P	Delta	Selection[1]		
P2852	1	9	0.768	0.725	14	0.836	0.850	2.77	0.208	0.625	TT:	TA:	AA:
O30_2	1	20	0.880	0.850	9	0.830	0.750	7.30	0.006	0.625	TT:	TA:+	AA:-
O137	1	5	0.534	0.475	7	0.690	0.258	7.93	0.003	0.975	TT:	TA:	AA:-
O30_1	3	2	0.141	0.150	4	0.397	0.300	2.41	0.266	0.238	TT:	TA:	AA:
O220	4	3	0.249	0.026	3	0.563	0.667	29.94	0.000	0.838	TT:+	TA:	AA:-
O127	4	1	0.000	0.000	7	0.737	0.343	5.39	0.040	0.663	TT:	TA:	AA:
W15	5	4	0.715	0.667	7	0.786	0.769	5.26	0.026	0.588	TT:	TA:	AA:-
O60	6	8	0.771	0.675	4	0.291	0.200	12.30	0.000	0.825	TT:	TA:	AA:
O167	6	4	0.310	0.282	1	0.000	0.000	18.20	0.000	1.000	TT:+	TA:-	AA:
O312	7	7	0.761	0.775	7	0.753	0.625	5.65	0.013	0.575	TT:+	TA:	AA:

O202	8	4	0.567	0.538	3	0.574	0.650	11.27	0.000	0.775	TT:+	TA:	AA:-
O21	9	2	0.240	0.075	1	0.000	0.000	10.94	0.000	0.138	TT:	TA:	AA:+
O149	10	5	0.658	0.368	4	0.636	0.425	7.31	0.007	0.888	TT:+	TA:	AA:
O344	10	3	0.143	0.150	5	0.687	0.575	4.03	0.078	0.975	TT:-	TA:	AA:
W05	12	12	0.834	0.769	15	0.876	0.575	14.88	0.000	0.800	TT:	TA:-	AA:+
O214	18	3	0.227	0.200	3	0.297	0.300	9.02	0.000	0.838	TT:	TA:	AA:
O28	18	3	0.492	0.475	4	0.317	0.256	4.99	0.020	0.375	TT:+	TA:	AA:
O206	19	2	0.025	0.025	6	0.581	0.550	2.30	0.273	0.675	TT:-	TA:	AA:

[a]AA, interclass homozygotes for *P.alba*; AT, interclass heterozygotes for *P. alba* and *P. tremula*; TT, interclass homozygotes for *P. tremula*.