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SUPPLEMENTARY INFORMATION

Admixture mapping of quantitative traits in *Populus* hybrid zones: power and limitations

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Text S1 Details on simulations

Admixed populations were simulated using the software *quantiNemo* 1.0.4 (Neuenschwander *et al.* 2008), and were designed to match the real data as in Lindtke *et al.* (2012). Seventy-seven microsatellite markers on 19 chromosomes were generated by using the map positions and original allele frequencies from *P. alba* and *P. tremula* calculated from the Italian population, thus creating a realistic marker panel including loci with low information content. Four QTL (Q.3.1, Q.6.1, Q.6.2 and Q.7.1) were inserted into this marker panel as artificial loci that were differentially fixed for two alleles in the parental populations at chromosomes three, six (two loci), and seven, located between approximately one and five centimorgan (cM) away from its closest marker locus (Table S1). These QTL were subsequently used to generate phenotypes. The admixed population was induced in the first generation by migrating 50% of offspring from each parental patch, filled at carrying capacity of 1000 each, into an empty patch with carrying capacity of 500. From the second generation, migration of offspring from the parental patches into the hybrid patch was set to one per cent, in order to generate a distribution of *Q* similar to the observed data. Genotypes from the whole hybrid patch, consisting of different hybrid generations, backcrosses and immigrants, were sampled at generations seven, 12, and 22. After removing the QTL from the data set, the original parental and the simulated hybrid genotypes were combined, and LSA estimates were obtained by *structure*. For each of the data sets, 10 replicates were generated. Either all 500 individuals from the hybrid patch, or a reduced data set containing 100 randomly chosen individuals were subjected to further analyses.

Phenotypes were built for each of the hybrid data sets for eight different genetic architectures (no QTL; one QTL with additive, dominant, recessive, overdominant, or underdominant gene action; two or three additive QTL), each with one to six independent traits, and a proportion of phenotypic variation explained by genotype (total genetic effect) of 0.2 or 0.5 (Table S3). Although quantitative traits may involve a large number of genes, we simulated only QTL of major effect for simplicity, as QTL effect sizes are expected to follow an exponential distribution with only QTL of large effect size being generally detectable (Tanksley 1993; Orr 2001; Barton & Keightley 2002). Candidate QTL were identified and subjected to the stepwise model selection procedure as described in the main article; however, no exhaustive search was performed because of its high computational demand. Loci with a p-value ≤ 0.001 in the final multiple regression model were defined as final candidate QTL. Target loci were determined as the maximally three nearest loci within +/- 15cM from the

simulated QTL, and successful target detection occurred if a final candidate QTL matched a locus from this target loci list (only the nearest locus was tagged as successful target if several candidates referred to the same simulated QTL). False positives were defined as all final candidate QTL that were not present in the original target loci list. Power (proportion of successfully detected target loci) and false positive rate (FPR; number of false positives divided by the number of final candidate QTL) was determined for each generation, genetic architecture, genetic effect and replicate.

Table S1 General information about 77 microsatellite markers used in this study and positions of simulated QTL

Marker	Published name[a]	Chr	Position (bp)	bp/ 200 000[b]	Position obtained by[c]	Type	δ
O137	ORPM_137	1	9087453	45.44	BLAST	codom	0.98
G124	GCPM_124	1	9131303	45.66	BLAST	codom	0.78
O30_1	ORPM_30	1	12600000	63	cross	codom	0.05
ASP376	ASP112376	1	13305812	66.53	BLAST	codom	0.94
P2852	PMGC_2852	1	14548286	72.74	BLAST	codom	0.79
ASP302	ASP113302	1	30444558	152.22	BLAST	codom	0.58
G1719	GCPM_1719	1	35488312	177.44	BLAST	codom	0.56
G1274	GCPM_1274	1	45729682	228.65	BLAST	dom	0.49
G1158	GCPM_1158	2	2787112	13.94	BLAST	codom	1
G1376	GCPM_1376	2	23223025	116.12	BLAST	codom	1
G1133	GCPM_1133	3	4716293	23.58	BLAST	codom	0.81
O30_2	ORPM_30	3	10738184	53.69	BLAST	codom	0.88
G1887	GCPM_1887	3	11095921	55.48	BLAST	dom	0.24
G1629	GCPM_1629	3	11310185	56.55	BLAST	codom	0.81
O203	ORPM_203	3	12009782	60.05	BLAST	codom	0.43
Q.3.1	*Simulated*	*3*	*12400000*	*62*	-	*codom*	*1*
G1869	GCPM_1869	3	16805774	84.03	BLAST	codom	1
G1688	GCPM_1688	3	17574314	87.87	BLAST	codom	0.8
O127	ORPM_127	4	6447171	32.24	BLAST	codom	0.78
O220	ORPM_220	4	7778968	38.89	cross	codom	0.43
G1809	GCPM_1809	4	9110875	45.55	BLAST	codom	0.63
G1255	GCPM_1255	5	1728199	8.64	BLAST	codom	1
G1192	GCPM_1192	5	4083941	20.42	BLAST	codom	0.51
G1838	GCPM_1838	5	8802231	44.01	BLAST	codom	0.81
G20	GCPM_20	5	23171490	115.86	BLAST	codom	0.68
W15	WPMS_15	5	25424594	127.12	BLAST	codom	0.52
G139	GCPM_139	6	2281003	11.41	BLAST	codom	1
G1831	GCPM_1831	6	3671141	18.36	BLAST	codom	0.72
G1074	GCPM_1074	6	3989388	19.95	BLAST	codom	0.98
O26	ORPM_26	6	5786927	28.93	BLAST	codom	0.71
O167	ORPM_167	6	5821040	29.11	BLAST	codom	0.96
ASP933	ASP106933	6	13019647	65.1	BLAST	codom	1
O190	ORPM_190	6	13718036	68.59	BLAST	codom	0.95
Q.6.1	*Simulated*	*6*	*14400000*	*72*	-	*codom*	*1*
W12	WPMS_12	6	19471676	97.36	BLAST	codom	0.92
Q.6.2	*Simulated*	*6*	*20400000*	*102*	-	*codom*	*1*
G2034	GCPM_2034	6	22219025	111.1	BLAST	codom	0.96
O369	ORPM_369	6	22796697	113.98	BLAST	codom	0.33
O60	ORPM_60	6	23655126	118.28	BLAST	codom	0.65
G1065	GCPM_1065	6	24119014	120.6	BLAST	codom	0.82
ASP322	ASP112322	6	25184620	125.92	BLAST	codom	1
G1260	GCPM_1260	7	3438279	17.19	BLAST	codom	0.35
W17	WPMS_17	7	8696038	43.48	BLAST	codom	0.53
Q.7.1	*Simulated*	*7*	*9000000*	*45*	-	*codom*	*1*
G1416	GCPM_1416	7	9247522	46.24	BLAST	codom	0.06
G1295	GCPM_1295	7	11243952	56.22	BLAST	dom	0.65
O312	ORPM_312	7	11625195	58.13	BLAST	codom	0.89

Table S1 Continued

Marker	Published name[a]	Chr	Position (bp)	bp/ 200 000[b]	Position obtained by[c]	Type	δ
G2062	GCPM_2062	8	5051212	25.26	BLAST	codom	0.86
O374	ORPM_374	8	6575467	32.88	BLAST	codom	0.97
O202	ORPM_202	8	13152189	65.76	BLAST	codom	0.51
O268	ORPM_268	8	13427006	67.14	BLAST	codom	0.83
G1949	GCPM_1949	9	1444490	7.22	BLAST	codom	0.34
O23	ORPM_23	9	4156696	20.78	BLAST	codom	0.98
O21	ORPM_21	9	5179553	25.9	BLAST	codom	0.24
G1250	GCPM_1250	10	1067244	5.34	BLAST[d]	dom	0.88
G2020	GCPM_2020	10	8741893	43.71	BLAST	codom	0.77
O344	ORPM_344	10	14738667	73.69	BLAST	codom	0.93
G1574	GCPM_1574	10	16527923	82.64	BLAST	codom	0.98
O149	ORPM_149	10	16581540	82.91	BLAST	codom	1
G114	GCPM_114	10	20637529	103.19	BLAST	codom	0.86
G1037	GCPM_1037	11	5503115	27.52	BLAST[d]	codom	0.25
G154	GCPM_154	12	8796449	43.98	BLAST	dom	0.68
W05	WPMS_5	12	9208533	46.04	BLAST	codom	1
G1186	GCPM_1186	12	13872383	69.36	BLAST	codom	0.95
O16	ORPM_16	13	282478	1.41	BLAST[d]	dom	0.29
G1353	GCPM_1353	13	817449	4.09	BLAST	codom	0.21
G1292	GCPM_1292	14	8054896	40.27	BLAST	dom	0.69
G1812	GCPM_1812	14	9862336	49.31	BLAST	codom	0.85
G2014	GCPM_2014	14	13260264	66.3	BLAST	dom	0.37
G1894	GCPM_1894	15	809326	4.05	BLAST	codom	0.97
G1454	GCPM_1454	15	913028	4.57	BLAST	codom	0.86
G1608	GCPM_1608	15	4979950	24.9	BLAST	codom	1
G430	ORPM_430	15	10362768	51.81	BLAST	dom	0.07
O14	ORPM_14	16	1290594	6.45	BLAST	codom	0.02
G1381	GCPM_1381	17	6100168	30.5	BLAST	dom	0.77
O214	ORPM_214	18	4583970	22.92	BLAST	codom	0.83
G1577	GCPM_1577	18	6074006	30.37	BLAST	codom	0.97
O28	ORPM_28	18	11993250	59.97	BLAST	codom	0.49
G162	GCPM_162	18	14881684	74.41	BLAST	codom	0.85
O276	ORPM_276	19	2850078	14.25	BLAST[d]	codom	0.17
O206	ORPM_206	19	3630075	18.15	BLAST	codom	0.09

Abbreviations: Chr, chromosome; bp, base pair; δ, allele frequency differential; dom, dominant marker; codom, co-dominant marker.

[a]Microsatellite markers were obtained from http://www.ornl.gov/sci/ipgc/ssr_resource.htm; van der Schoot *et al.* (2000), Smulders *et al.* (2001), Tuskan *et al.* (2004); and de Carvalho *et al.* (2010).

[b]The physical distance in bp was divided by 200 000 as a proxy for cM, assuming that 1cM corresponds roughly to 200kb (Tuskan *et al.* 2006, Supplementary information).

[c]Chromosomal positions were obtained by BLAST of the primer sequences against the *P. trichocarpa* genome assembly v2 (http://www.phytozome.net/poplar). In cases of no hits, positions were calculated using information from an interspecific cross *P. alba* x *P.* ×*canescens* (Macaya-Sanz, Alba, Gonzalez-Martinez, Lexer and coworkers, unpublished data). For O30_1, map position was estimated using additional information from Pakull *et al*., 2009; for O220, the simple midpoint between the two adjacent loci was computed.

[d]In some cases the BLAST search resulted in several hits; then the most likely position according to motive type or fragment length, or the average position over the most likely hits was used.

Table S2 Additional traits and measurements/calculations taken

Trait	Description	Calculation
LAML	Lamina length	Raw measurement [mm]
LAMW	Lamina width	Raw measurement [mm]
LOBW	Lobe width	Raw measurement [mm]
SINW	Sinus width	Raw measurement [mm]
PETXB.L	Petiole cross-section length[a] at petiole base	Raw measurement [mm]
PETXB.W	Petiole cross-section width[a] at petiole base	Raw measurement [mm]
PETXM.L	Petiole cross-section length[a] at petiole middle	Raw measurement [mm]
PETXM.W	Petiole cross-section width[a] at petiole middle	Raw measurement [mm]
PETXA.L	Petiole cross-section length[a] at petiole apex	Raw measurement [mm]
PETXA.W	Petiole cross-section width[a] at petiole apex	Raw measurement [mm]
LWRAT	Lobe width ratio	Lobe width/lamina length
PETXB.R	Petiole shape at petiole base	PETXB*PTRAT[b]
PETXM.R	Petiole shape at petiole middle	PETXM*PTRAT[b]
PETXA.R	Petiole shape at petiole apex	PETXA*PTRAT[b]

[a]The raw measurements of the petiole cross-sections were taken in a way that length is always the larger value of length and width.

[b]See Table 1, main article.

Table S3 Simulation scenarios

Scenario	Number of QTL per trait	Gene action	Number of traits	Architecture					
				Trait 1	Trait 2	Trait 3	Trait 4	Trait 5	Trait 6
null	0	none	1	None					
add	1	additive	4	Q.3.1	Q.6.1	Q.6.2	Q.7.1		
dom	1	dominant	4	Q.3.1	Q.6.1	Q.6.2	Q.7.1		
rec	1	recessive	4	Q.3.1	Q.6.1	Q.6.2	Q.7.1		
over	1	overdominant	4	Q.3.1	Q.6.1	Q.6.2	Q.7.1		
under	1	underdominant	4	Q.3.1	Q.6.1	Q.6.2	Q.7.1		
2loci	2	additive	6	Q.6.2 + 0.75*Q.3.1	Q.6.2 + 0.75*Q.6.1	Q.6.2 + 0.75*Q.7.1	Q.6.2 - 0.75*Q.3.1	Q.6.2 - 0.75*Q.6.1	Q.6.2 - 0.75*Q.7.1
3loci	3	additive	4	Q.6.2 + 0.9*Q.3.1 + 0.9*Q.7.1	Q.6.2 + 0.75*Q.3.1 + 0.75*Q.7.1	Q.6.2 - 0.9*Q.3.1 - 0.9*Q.7.1	Q.6.2 - 0.75*Q.3.1 - 0.75*Q.7.1		

Phenotypes were modeled as follows. The number of alleles with ancestry from the simulated *P. alba* population (0, 1 or 2 alleles) was recorded for each QTL (Q.3.1, Q.6.1, Q.6.2, and Q.7.1) and individual. The raw effect of a single locus on a quantitative trait was assigned as -1, 0 or 1 (additive gene action, add) if 0, 1 or 2 *P. alba* alleles were present at the simulated QTL. Similarly, the raw effects were assigned as -1, 1 or 1 for dominant (dom), -1, -1 or 1 for recessive (rec), -1, 1 or -1 for overdominant (over), and 1, -1 or 1 for underdominant (under) gene action if 0, 1 or 2 *P. alba* alleles were present. For complex architectures (2loci and 3loci), proportions of the raw effects (100, 90, or 75%) of several loci were totalized. Values were standardized, and a normally distributed stochastic term added to obtain 20 or 50 per cent of phenotypic variation explained by genotype ($y = \mathcal{N}(0,1)\sqrt{(1-g)} + \psi\sqrt{g}$, where y is the final quantitative trait value, $\mathcal{N}(0,1)$ is a random normal distribution with mean=0 and sd=1, ψ is the raw phenotype (100% under genetic control) standardized to mean=0 and sd=1, and g={0.2, 0.5} the genetic effect on final phenotype). For the null scenario, phenotype was modeled by a random normal distribution only.

Table S4 Factor Analysis scores used to pick representative phenotypic traits for mapping. Characteristic traits of the first seven factors that were chosen for further analysis and their respective factor loadings are indicated in bold.

Trait	F 1	F 2	F 3	F 4	F 5	F 6	F 7	F 8	F 9	F 10	F 11	F 12	F 13
LAML	0.94		-0.29								0.18		
LAMW	0.95										-0.15		
LOBW	0.91												
SINW	0.86		0.12				-0.2						
PETL	0.55	0.44									0.35		
PETXB.L	0.9			0.2					0.44			0.14	
PETXB.W	0.89			-0.19					0.53				
PETXM.L	0.98				0.3			0.4					
PETXM.W	1.17				-0.23			0.57					
PETXA.L	1.03					0.19				0.46			
PETXA.W	1.1					-0.15				0.51			
LFAREA	**1.04**											0.26	
LFSHAP			**-1.04**										0.14
LDRAT							**1**						
LWRAT			0.97										0.14
PTRAT		**1.06**		-0.11	-0.11	-0.12							
PETXB				**1.02**									
PETXM					**1**								
PETXA						**1.02**							
PETXB.R		0.75		0.47									
PETXM.R		0.74			0.44								
PETXA.R		1.04	-0.17	-0.11		0.22					-0.12		
Eigenvalues	*10.96*	*3.54*	*2.21*	*1.4*	*1.36*	*1.18*	*1.05*	*0.51*	*0.49*	*0.48*	*0.22*	*0.11*	*0.05*

Table S5 Summary of mapping results by using different mapping methods, including single-marker regression analysis, multivariate regression analysis (stepwise or exhaustive search), and *ADMIXMAP* software. Loci scored as dominant markers are indicated with an asterisk

					Single marker		Stepwise search		Exhaustive search				*ADMIXMAP*	
							add	dom/rec	add		dom/rec			
Trait	Marker	Chr	Position (bp)	δ	ΔAIC add	ΔAIC dom/ rec	-Log10 (p-val)	-Log10 (p-val)	Imp	Coef (β_1)	Imp	Coef (β_2)	-Log10 (p-val)	Score
PETL	ASP302	1	30444558	0.58	**8.55**	**12.36**	2.28		**0.91**	-1.24	0.47	-0.74	**4.45**	-12.03
	G1133	3	4716293	0.81	**10.22**	**9.89**	1.95	1.51	**0.93**	-1.24	**0.51**	-0.99	**3.94**	-19.17
	G1869	3	16805774	1.00	1.06	**4.95**		1.97	0.09	-0.09	**0.60**	-0.83	0.75	-3.07
	G2034	6	22219025	0.96	-2.00	**6.52**		**5.70**	0.01	-0.01	**1.00**	2.48	0.25	-1.57
	G1065	6	24119014	0.82	**4.66**	2.32					0.01	-0.01	**3.12**	-16.95
	Q								***0.52***	*0.96*	*0.04*	*-0.13*		
LFAREA	ASP302	1	30444558	0.58	**8.14**	**12.06**	**3.98**	1.70	**1.00**	-1.63	**0.88**	-1.69	**3.82**	-11.78
	G1133	3	4716293	0.81	3.86	2.65							**2.35**	-14.71
	G1869	3	16805774	1.00	1.15	**4.08**			0.25	-0.28	0.04	-0.05	0.81	-3.24
	G2034	6	22219025	0.96	-1.68	**5.17**					0.28	0.36	0.01	-0.08
	G1065	6	24119014	0.82	1.95	0.08							**1.81**	-12.65
	ASP322	6	25184620	1.00	**6.93**	**4.43**	**5.15**		**1.00**	2.37	0.03	0.01	**2.01**	5.63
	G2062	8	5051212	0.86	**6.09**	3.63	**3.83**		**0.93**	-1.28	0.07	-0.07	**3.28**	-10.55
	O344	10	14738667	0.93	3.94	**4.93**			0.13	0.11	0.17	0.18	**1.89**	10.14
	G1894	15	809326	0.97	-1.18	-0.93							**2.27**	3.87
	G1454	15	913028	0.86	-0.88	-2.72							**2.43**	3.63
	G1381*	17	6100168	0.77	**6.11**	**5.06**							NA	NA
	Q										*0.16*	*0.39*		
PTRAT	ASP302	1	30444558	0.58	**5.01**	**5.69**	**4.33**		**0.80**	-0.97	0.37	-0.56	2.35	-9.87
	G1719	1	35488312	0.56	-1.24	**4.48**					**0.79**	1.87	0.60	-3.05
	G1133	3	4716293	0.81	**4.06**	3.91			**0.56**	-0.58	0.40	-0.72	1.64	-12.74
	Q										*0.08*	*-0.19*		

Table S5 Continued

Trait	Marker	Chr	Position (bp)	δ	Single marker		Stepwise search		Exhaustive search				*ADMIXMAP*	
							add	dom/rec	add		dom/rec			
					ΔAIC add	ΔAIC dom/ rec	-Log10 (p-val)	-Log10 (p-val)	Imp	Coef (β_1)	Imp	Coef (β_2)	-Log10 (p-val)	Score
PETXM	O137	1	9087453	0.98	-1.71	**5.02**					**0.78**	0.95	0.24	-2.19
	G1838	5	8802231	0.81	3.69	**7.76**	1.62		0.28	-0.32	0.22	-0.29	**2.80**	-7.49
	W17	7	8696038	0.53	-0.63	**7.78**			0.05	-0.06	0.22	-0.47	0.52	-2.72
	G1295*	7	11243952	0.65	**4.56**	1.96			0.25	-0.28	0.25	-0.59	NA	NA
	O312	7	11625195	0.89	**4.84**	2.62	2.53		0.40	0.45			1.78	7.66
	O28	18	11993250	0.49	**10.29**	**9.21**	2.00		**0.91**	-1.43			**3.59**	-9.32
	Q								*0.31*	*0.67*	*0.05*	*-0.13*		
PETXB	O268	8	13427006	0.83	**4.24**	**5.26**			**0.51**	0.74	0.07	-0.07	1.53	9.32
	G1949	9	1444490	0.34	-1.88	**5.74**			0.10	-0.08	0.44	-1.54	0.31	-2.48
	Q								***0.62***	*-1.24*	*0.22*	*0.72*		
PETXA	G1838	5	8802231	0.81	0.31	**5.79**		1.52	0.04	-0.01	**0.53**	-0.74	0.82	-4.09
	G1831	6	3671141	0.72	2.11	**4.75**	**3.02**		**1.00**	1.38	0.31	-0.37	2.73	4.52
	Q										*0.13*	*0.30*		
LFSHAP	O220	4	7778968	0.43	**5.03**	3.38			**0.79**	1.03			**3.28**	7.79
	O23	9	4156696	0.98	1.13	-2.03							**2.74**	11.39
	O149	10	16581540	1.00	0.20	**6.21**		2.84			**0.89**	1.30	0.54	3.02
	G1381*	17	6100168	0.77	**8.29**	**5.95**	**3.21**		0.42	0.45	0.34	0.80	NA	NA
	Q								*0.05*	*-0.07*				
LDRAT	O167	6	5821040	0.96	0.81	**4.70**		2.00	0.24	-0.26	**0.64**	1.07	0.08	0.66
	W12	6	19471676	0.92	**6.21**	**6.12**		1.98	**0.81**	-0.98	0.33	0.63	2.56	-14.40
	G1894	15	809326	0.97	**5.08**	**6.87**			**0.95**	1.61	0.39	0.69	1.20	3.61
	Q							***3.78***	*0.11*	*-0.27*	***0.77***	*-4.00*		

Abbreviations: Chr, chromosome; bp, base pair; δ, allele frequency differential; add, additive; dom/rec, dominant/recessive; Imp, relative importance; Coef, full-model averaged parameter estimate; *Q*, genome-wide effects *G* and *G'*. For single marker regression, add or dom/rec denote additive or dominant/recessive models; for stepwise or exhaustive search, add or dom/rec denote additive or dominant/recessive model components.

Only loci with FDR=0.1 for *ADMIXMAP* or loci with ΔAIC ≥4 for single marker regression analysis are listed. Bold, loci with ΔAIC ≥4 (single marker regression), -Log10(p-val) ≥3 (stepwise search), relative importance >0.5 (exhaustive search), or loci with FDR=0.1 (*ADMIXMAP*).

Table S6 Simulation results for different numbers of admixed individuals (100 or 500), genetic effects (0.2 or 0.5), genetic architectures and gene action, and seven, 12, or 22 generations since admixture. Mean and standard deviation (sd; in parentheses) over 10 replicate simulations are given

Scenario	Simulated QTL per scenario[a]	True positives detected			False positives		
		Gen 7	Gen 12	Gen 22	Gen 7	Gen 12	Gen 22
a) n = 500; genetic effect = 0.5							
null	0	0 (0)	0 (0)	0 (0)	0.2 (0.42)	0.3 (0.48)	0.3 (0.67)
add	4	4 (0)	4 (0)	3.9 (0.32)	0.6 (0.97)	1.1 (1.1)	1 (0.94)
dom	4	4 (0)	4 (0)	3.9 (0.32)	0.6 (1.07)	1 (1.05)	1.5 (1.08)
rec	4	4 (0)	4 (0)	3.9 (0.32)	0.4 (0.7)	0.4 (0.52)	1.8 (1.23)
over	4	4 (0)	4 (0)	3.8 (0.42)	0.4 (0.52)	0.6 (0.7)	1 (0.94)
under	4	4 (0)	4 (0)	3.3 (0.82)	0.3 (0.67)	0.3 (0.67)	1.5 (1.65)
2loci	12	11.9 (0.32)	12 (0)	11.6 (0.52)	0.9 (1.29)	1.5 (2.46)	2.8 (2.53)
3loci	12	10.6 (0.7)	10.7 (0.67)	9.2 (1.75)	0.7 (1.34)	1.3 (1.83)	1.6 (1.58)
b) n = 100; genetic effect = 0.5							
null	0	0 (0)	0 (0)	0 (0)	0.2 (0.63)	0.3 (0.48)	0 (0)
add	4	3.9 (0.32)	3.9 (0.32)	2.7 (1.06)	0.6 (1.07)	0.5 (0.85)	1.6 (1.71)
dom	4	3.6 (0.52)	3.5 (0.53)	2.6 (0.97)	0.8 (0.63)	0.8 (1.03)	1.9 (1.97)
rec	4	4 (0)	3.6 (0.52)	2.2 (0.42)	0.6 (0.84)	0.8 (0.92)	1 (0.94)
over	4	3.8 (0.42)	3 (0.94)	1 (0.82)	0.7 (0.82)	1 (1.05)	1.1 (0.99)
under	4	3.6 (0.52)	3.1 (0.99)	1.5 (0.85)	0.7 (0.82)	0.4 (0.7)	0.3 (0.48)
2loci	12	8.7 (1.77)	6.7 (2.75)	4.7 (3.53)	1.2 (1.62)	1.2 (1.55)	2.1 (2.13)
3loci	12	5.9 (1.91)	3.5 (1.72)	2.8 (1.93)	1.5 (1.51)	1.3 (1.34)	1.2 (1.69)
c) n = 500; genetic effect = 0.2							
null	0	0 (0)	0 (0)	0 (0)	0.2 (0.42)	0.3 (0.48)	0.3 (0.67)
add	4	4 (0)	4 (0)	3.6 (0.52)	0.8 (1.62)	0.9 (1.2)	1.3 (1.16)
dom	4	3.9 (0.32)	3.9 (0.32)	3.5 (0.53)	0.6 (1.35)	1.4 (1.58)	1.3 (0.95)
rec	4	4 (0)	3.9 (0.32)	3.5 (0.71)	0.9 (1.37)	0.9 (0.99)	1.5 (1.43)
over	4	4 (0)	3.8 (0.42)	2.2 (1.14)	0.8 (1.48)	1.2 (1.4)	1 (1.83)
under	4	4 (0)	3.9 (0.32)	2.2 (1.14)	0.7 (1.25)	0.8 (1.14)	1.6 (2.01)
2loci	12	10.4 (1.51)	9.7 (1.89)	7.3 (2.87)	1.3 (2.31)	1.8 (3.74)	2.9 (2.73)
3loci	12	7.6 (1.65)	6.3 (2)	4.4 (2.5)	1.2 (1.81)	1.8 (2.04)	2.2 (1.93)
d) n = 100; genetic effect = 0.2							
null	0	0 (0)	0 (0)	0 (0)	0.2 (0.63)	0.3 (0.48)	0 (0)
add	4	2.8 (1.03)	2.4 (0.84)	1.5 (0.85)	1 (1.56)	1.3 (2.06)	1.2 (1.23)
dom	4	1.8 (0.92)	1.2 (0.63)	0.7 (0.67)	1 (1.49)	1 (1.25)	1.3 (1.49)
rec	4	2.6 (0.97)	1.6 (1.17)	0.8 (0.42)	1 (1.33)	1 (0.94)	0.7 (0.95)
over	4	1.7 (0.95)	0.8 (0.92)	0.2 (0.42)	0.8 (1.55)	0.9 (1.29)	0.9 (1.45)
under	4	2.4 (0.84)	0.5 (0.71)	0.7 (0.67)	0.5 (0.85)	0.7 (1.34)	0.3 (0.67)
2loci	12	4.7 (2.11)	2.1 (2.38)	1.6 (2.07)	1.1 (1.97)	2.1 (2.77)	2.1 (2.23)
3loci	12	1.8 (1.48)	0.8 (1.03)	0.8 (0.92)	1.3 (1.42)	1.1 (1.37)	1.5 (1.65)

Abbreviations: null, no QTL; add, additive; dom, dominant; rec, recessive; over, overdominant; under, underdominant; 2loci, two additive loci; 3loci, three additive loci; Gen, generation since admixture.

[a]For each scenario, one to six traits were simulated, each built by zero to three QTL (Table S3), resulting in up to 12 detectable true QTL per tested scenario.

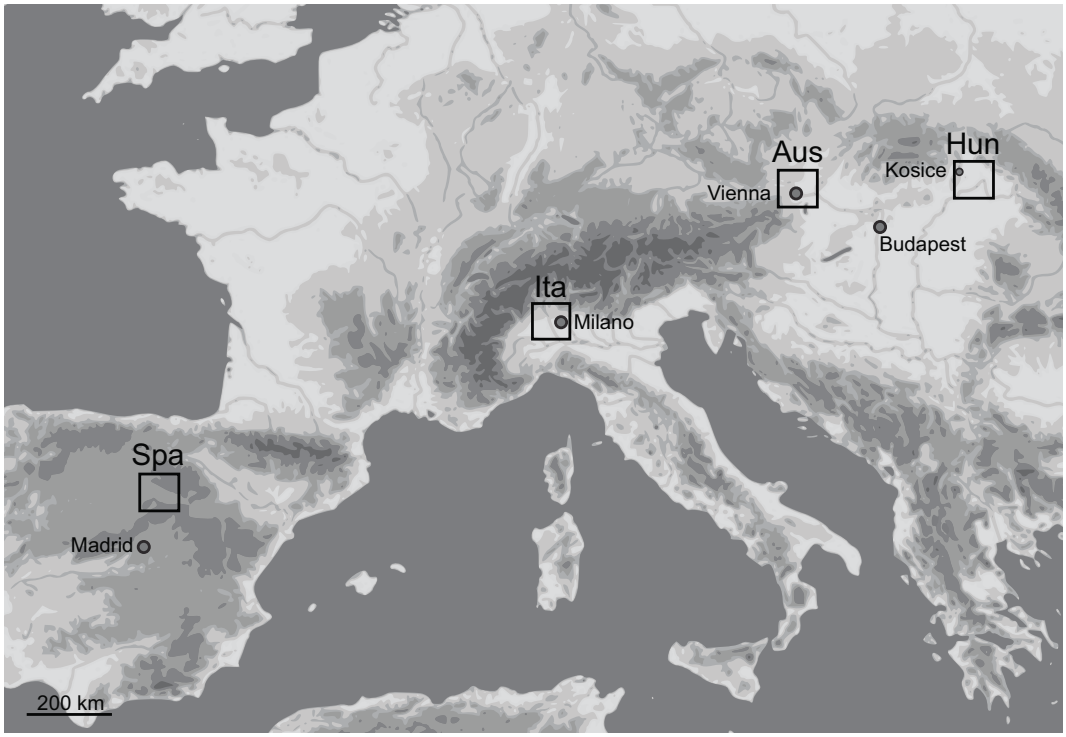

Figure S1 Map showing localities of sampled *Populus* hybrid zones in Spain (Spa), Italy (Ita), Austria (Aus), and Hungary (Hun). Physical map modified from www.euratlas.com.

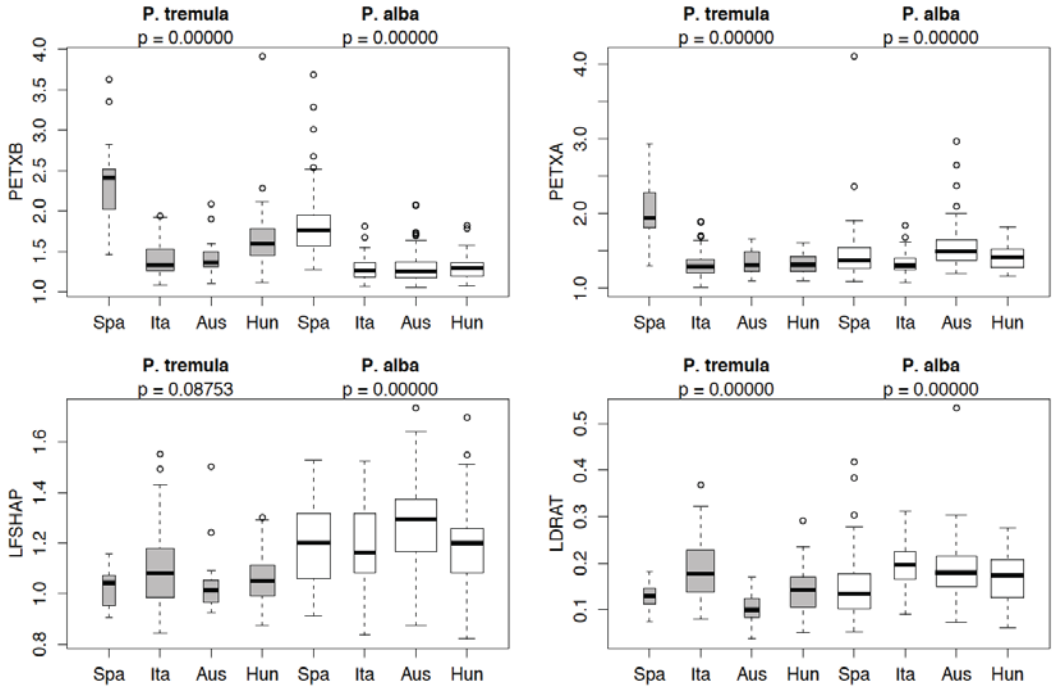

Figure S2 Boxplots of untransformed phenotypic measurements for *P. tremula* (gray) and *P. alba* (white) at all four localities (Spa, Spain; Ita, Italy; Aus, Austria; Hun, Hungary). Indicated are p-values of Kruskal-Wallis rank sum tests for the null-hypothesis that within a species, all four localities have the same median. Shown are all those traits not shown in Figure 1, main article).

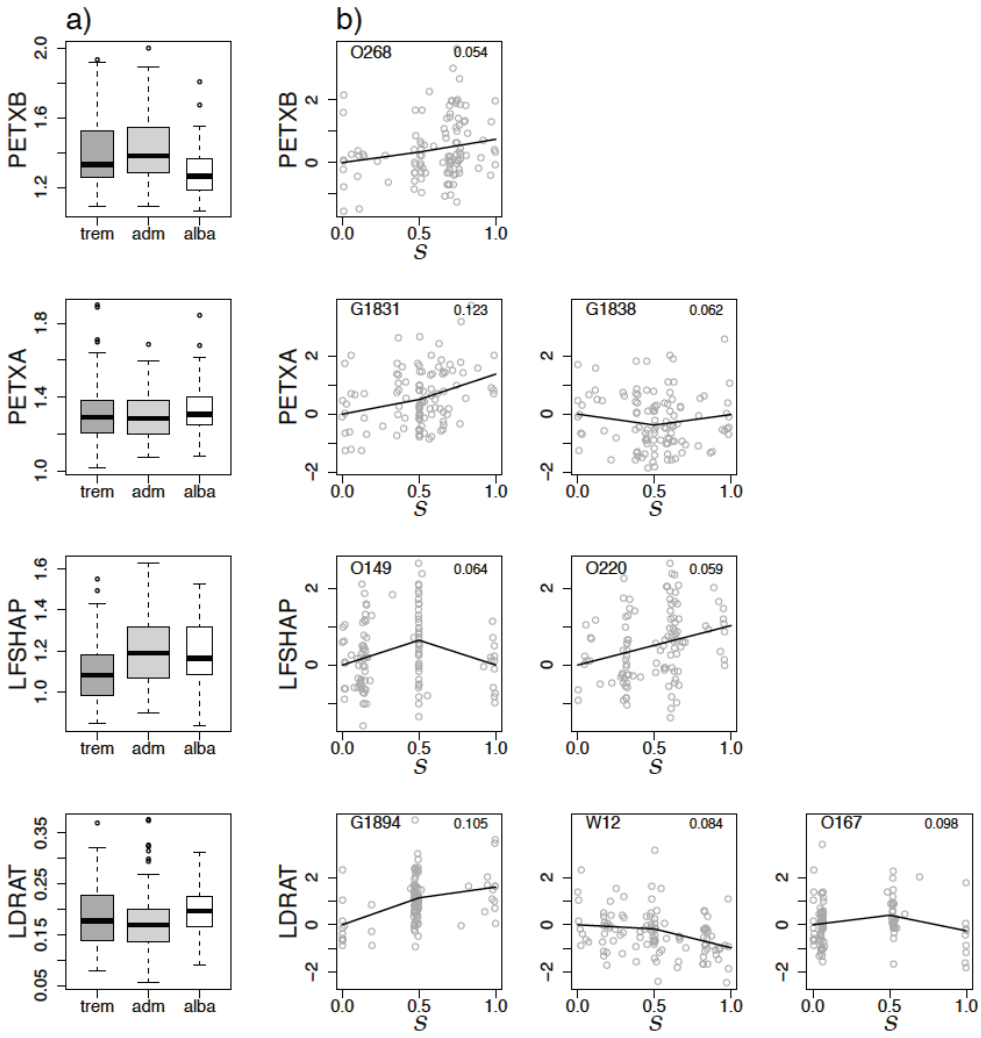

Figure S3 Raw phenotypes and locus-specific associations for traits not shown in Figure 2, main article, for the Italian hybrid zone. a) Boxplots of untransformed measurements for *P. tremula* (trem), admixed individuals (adm), and *P. alba* (alba), boxplot widths being proportional to sample size. b) Genotype-phenotype associations of admixed individuals for each candidate locus with relative importance >0.5. Residual phenotypes (y-axes) were calculated by using full-model averaged parameter estimates (Coef; Table 3) including all variables except the focal marker in the model, and are plotted against locus-specific admixture proportions *S* of the focal marker (x-axes, with 0.0 representing *P. tremula* and 1.0 representing *P.alba* ancestry; marker names indicated at top left of each scatterplot). Regression lines were computed from Coef (additive and dominant/recessive components) of the focal marker. R^2 for focal marker are indicated at top right of each scatterplot.

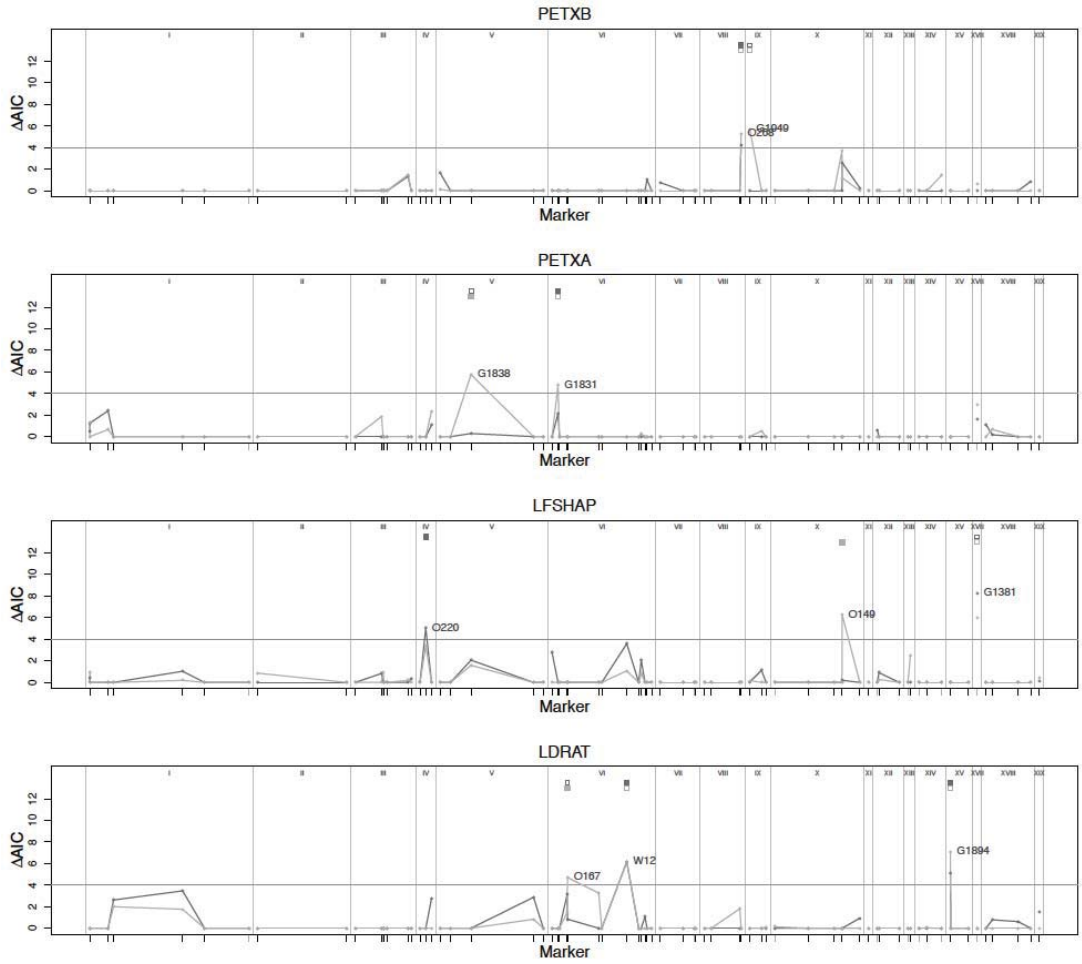

Figure S4 Genotype-phenotype associations, Italian hybrid zone. Depicted are ΔAIC from single-marker regression analyses, with values <0 truncated to zero. Dark gray lines, additive model; light gray lines, dominant/recessive model. Marker loci with ΔAIC values ≥4 (marked by horizontal line) are labeled. Squares indicate markers that were included in final multivariate regression model (Table 3); dark gray, additive component; light gray, dominant/recessive component; filled squares, relative importance >0.5. Tick marks on x-axes indicate markers in their relative map position on chromosomes I to XIX (separated by gray vertical lines); black tick marks, co-dominant markers; gray tick marks, dominant markers. Shown are all those traits not shown in Figure 3, main article).

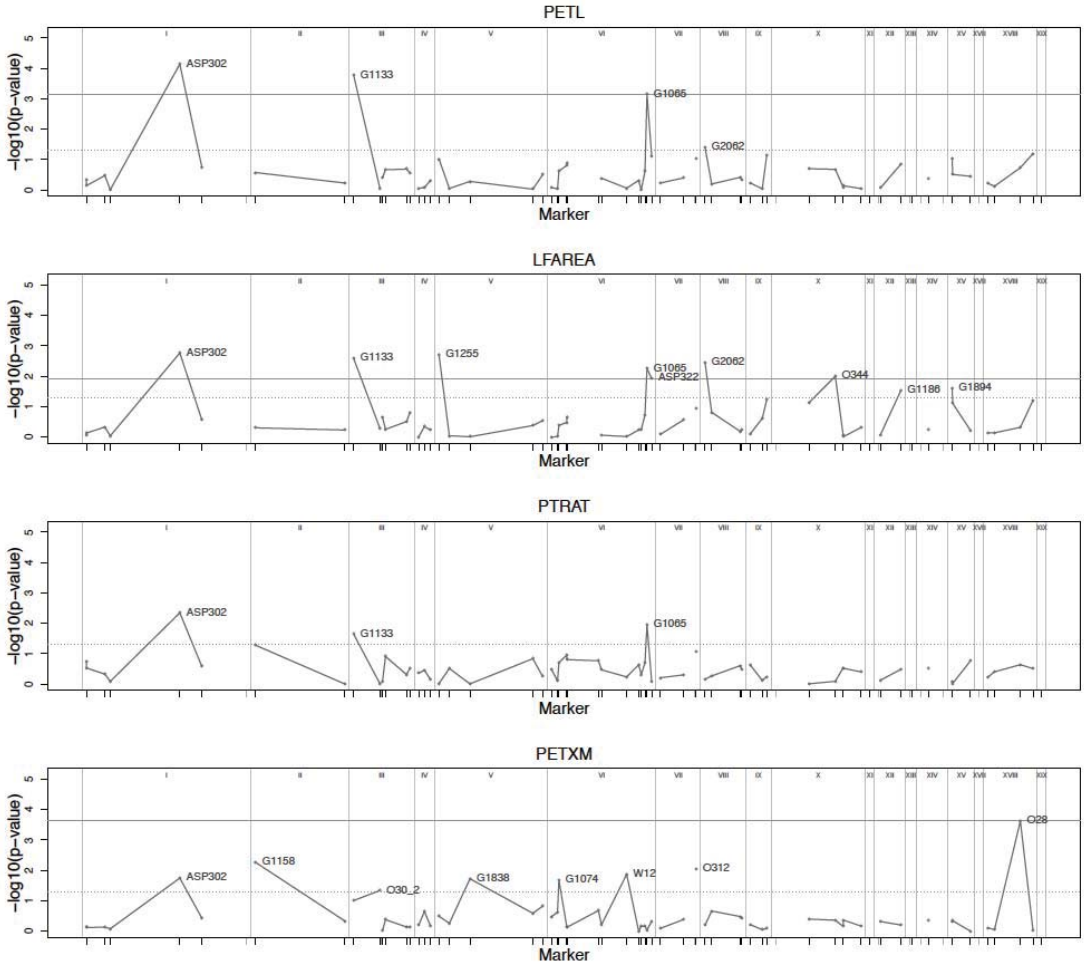

Figure S5 Genotype-phenotype associations, Italian hybrid zone. Depicted are -log10(p-values) from single-marker analyses, computed by *ADMIXMAP* software. Dotted horizontal line, -log10(0.05); horizontal line, -log10(p*), p* being the adjusted threshold computed for FDR=0.1 (line only plotted if any marker above threshold); markers with p-values ≥ -log10(0.05) are labeled. Tick marks on x-axes indicate markers in their relative map position on chromosomes I to XIX (separated by gray vertical lines); black tick marks, co-dominant markers; gray tick marks, dominant markers.

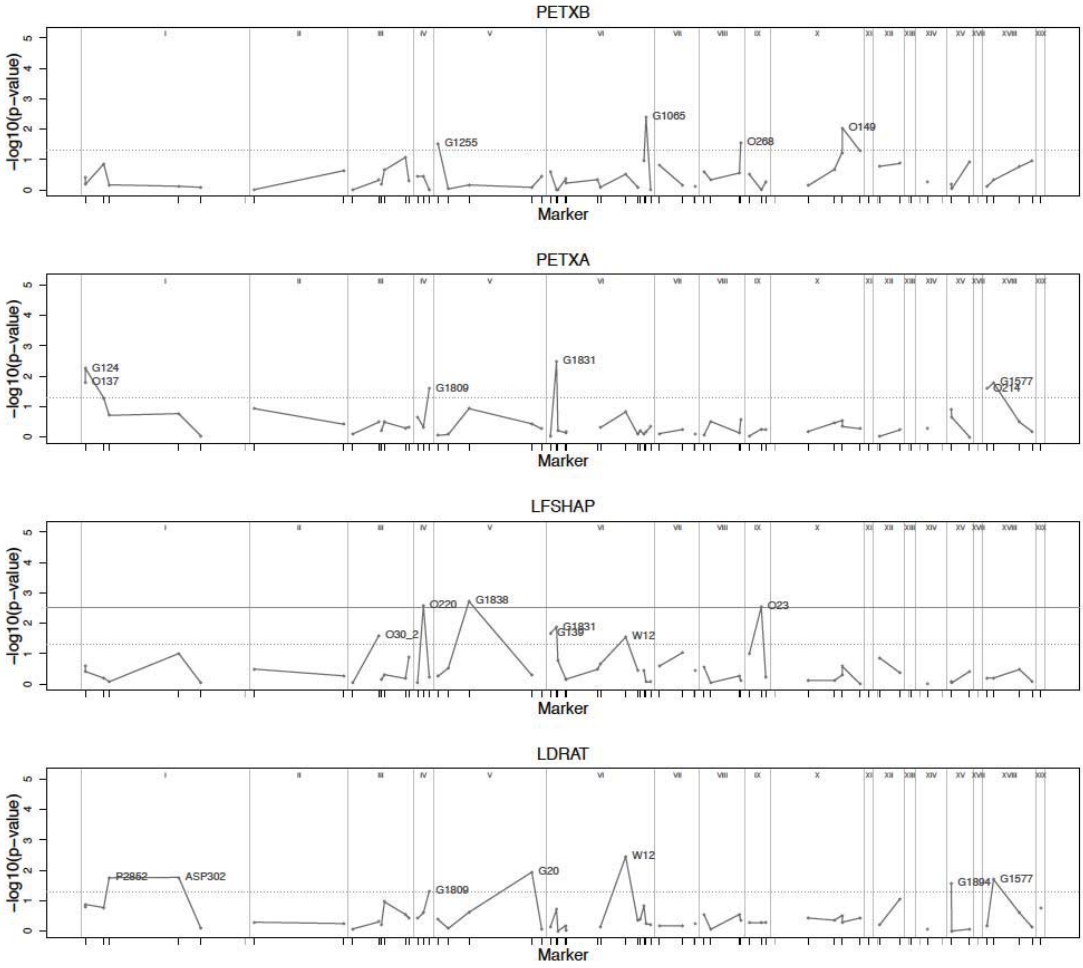

Figure S5 Continued

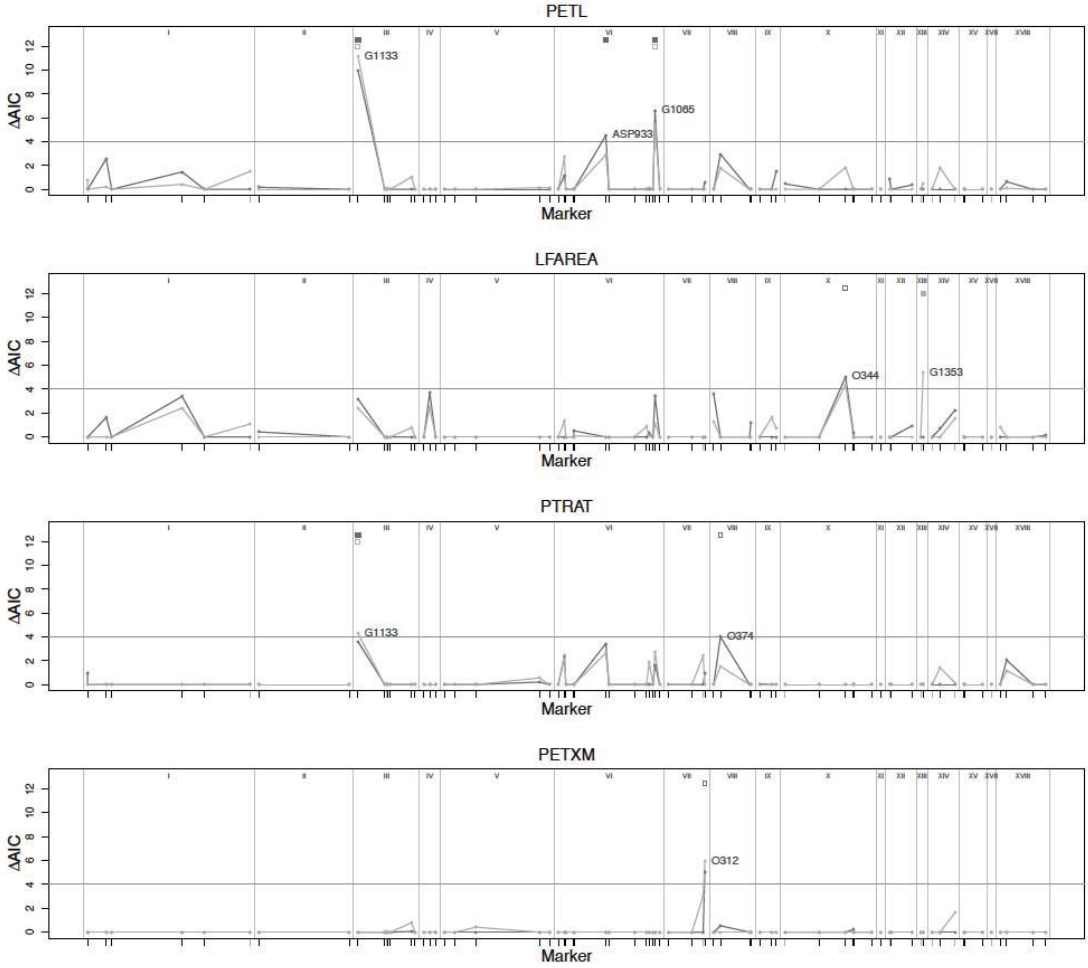

Figure S6 Genotype-phenotype associations, pooled data set including admixed individuals from four localities. Depicted are ΔAIC from single-marker regression analyses, with values <0 truncated to zero. Dark gray lines, additive model; light gray lines, dominant/recessive model. Marker loci with ΔAIC values ≥4 (marked by horizontal line) are labeled. Squares indicate markers that were included in final multivariate regression model; dark gray, additive component; light gray, dominant/recessive component; filled squares, relative importance >0.5. Tick marks on x-axes indicate markers in their relative map position on chromosomes I to XIX (separated by vertical lines); black tick marks, co-dominant markers; gray tick marks, dominant markers.

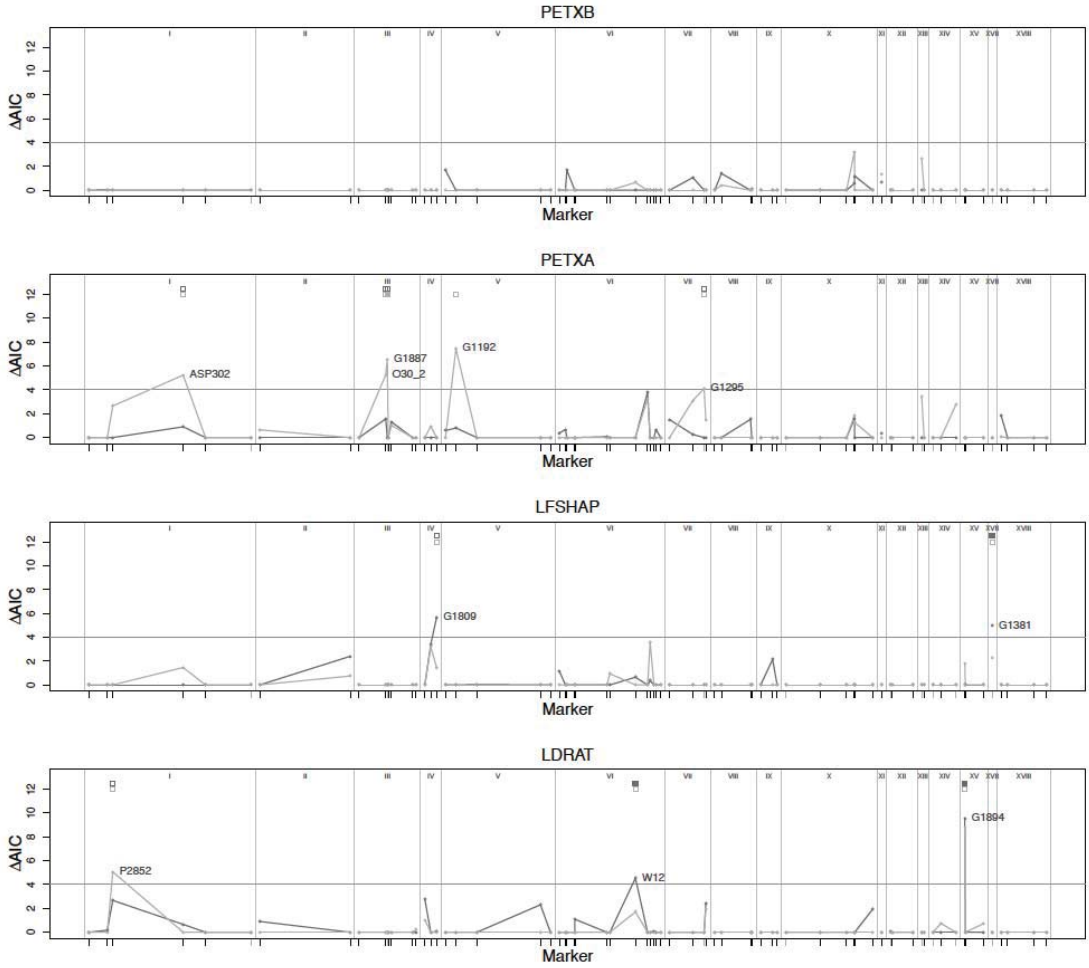

Figure S6 Continued

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