

Table S1. Provenances of sampled trees in inland and coastal sites.

Provenance	Latitude (°N)	Longitude (°E)	District ¹	Habitat ²	No. of sampled trees ³										Total
					Inland site					Coastal site					
					<i>Qc</i> R	<i>Qc</i> N	<i>Qa</i>	<i>Qd</i> R	<i>Qd</i> N	<i>Qc</i> R	<i>Qc</i> N	<i>Qa</i>	<i>Qd</i> R	<i>Qd</i> N	
Meguma	45.41	141.83	NN	C			3					8			11
Bakkai	45.32	141.64	NWN	C			6					14			20
Hamayuchi	45.26	141.60	NWN	C			5								5
Onetomanai	45.20	141.57	NWN	C			3								3
Toyoushi	45.10	142.43	NE	C			1		4					7	12
Wakasakanai	45.08	141.64	NWN	C			22		1			16			39
Esashi	44.91	142.59	NE	C								10		6	16
Teshio	44.90	141.90	NWS	I		1									1
Saragishi	44.85	141.75	NWS	C					11					23	34
Nakagawa	44.80	142.10	NWS	I	1										1
Omu	44.60	142.80	O	I	3										3
Bifuka	44.50	142.40	O	I	3										3
Niupu	44.50	142.60	O	I	2										2
Okoppe	44.40	143.10	O	I	5										5
Yubetsu	44.21	143.67	O	C									2	6	8
Antaroma	43.85	142.69	O	I	2										2
Kitami	43.80	143.70	O	I	2	1				4	2				9
Asahikawa	43.70	142.30	O	I	3										3
Shintotsukawa	43.50	141.80	O	I	1										1
Takikawa	43.50	141.90	O	I	2										2
Bibai	43.30	141.90	O	I	1										1
Ishikari	43.20	141.30	O	C				3					8		11
Mikasa	43.20	141.90	O	I	2										2
Shihoro	43.20	143.20	O	I				6							6
Kanayama	43.10	142.40	O	I		1									1
Shintoku	43.10	142.80	O	I	1										1
Ikeda	42.90	143.50	O	I	2										2
Urahoro	42.80	143.70	O	I	2										2
Orikawa	42.70	140.10	O	I						3					3
Taiki	42.50	143.40	O	C									6		6
Donan	42.20	140.10	O	I	5					3					8
Ohnuma	42.00	140.60	O	I		1									1
Total					37	4	40	9	16	10	2	48	16	42	224

¹Northern provenances in southwestern (NWS), northwestern (NWN), northern (NN), eastern (NE) districts of the northernmost area of Hokkaido and provenances in the other areas of Hokkaido (O)

²Inland habitats (I) and coastal habitats (C)

³Trees with pubescent shoots are identified to *Quercus dentata* (*Qd*), trees with glabrous shoots in inland habitats are identified to *Q. mongolica* var. *crispula* (*Qc*), and trees with glabrous shoots in coastal habitats are identified to *Q. × angustilepidota* (*Qa*).

³R: reference samples, N: non-reference samples

(a)



(b)



Figure S1. Photographs of inland site (a) and coastal site (b) in 2017.

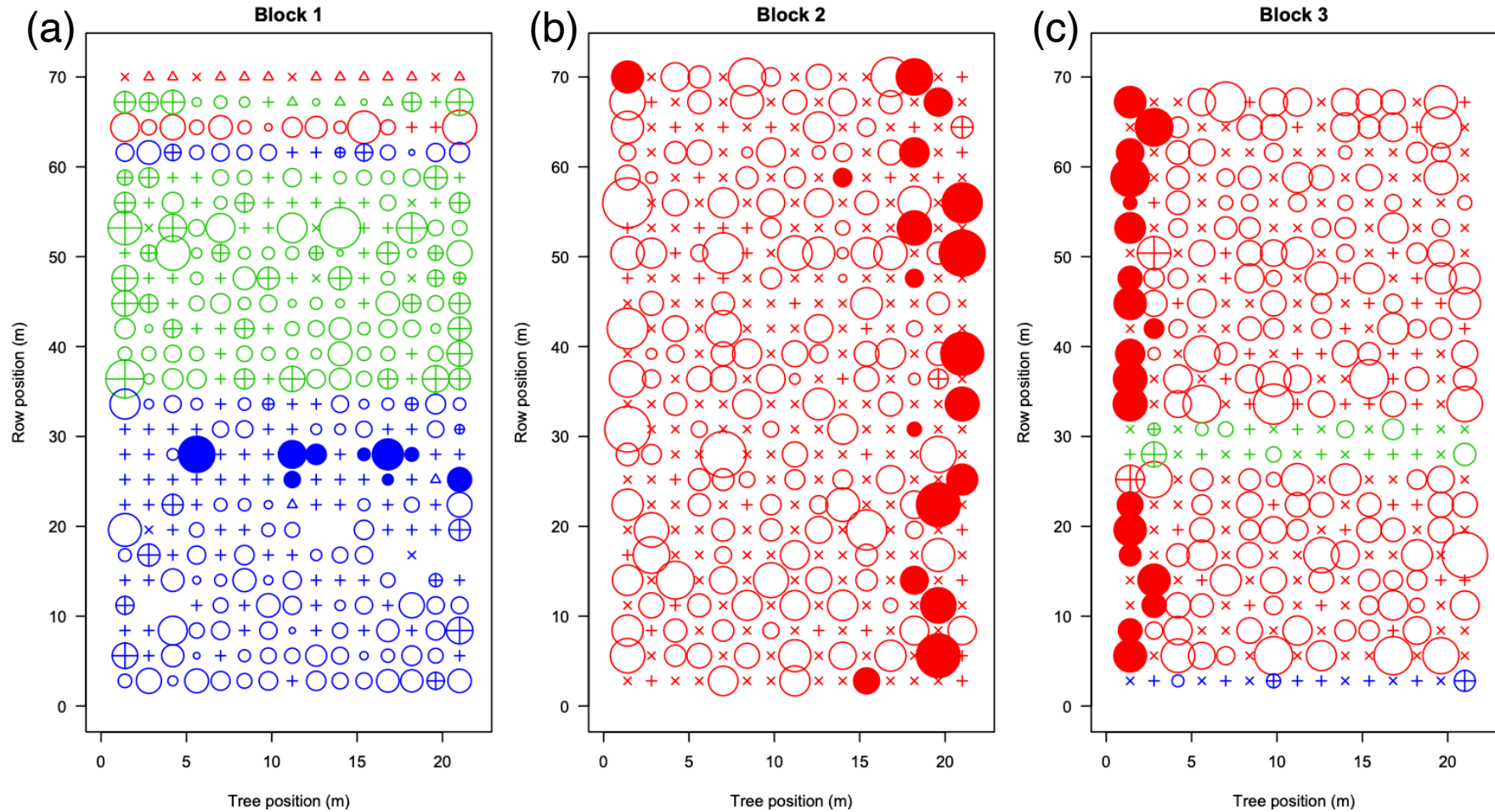


Figure S2. Locations and sizes of trees planted in three blocks (a–c) in inland site. Solid circles, circles with crosses, and open circles indicate sampled reference, sampled non-reference, and non-sampled living trees, respectively. Crosses, + and x, indicate dead and thinned trees, respectively. Triangles indicate non-experimental trees. Colors indicate taxa: *Quercus mongolica* var. *crispula* (red), *Q. × angustilepidota* (green), and *Q. dentata* (blue).

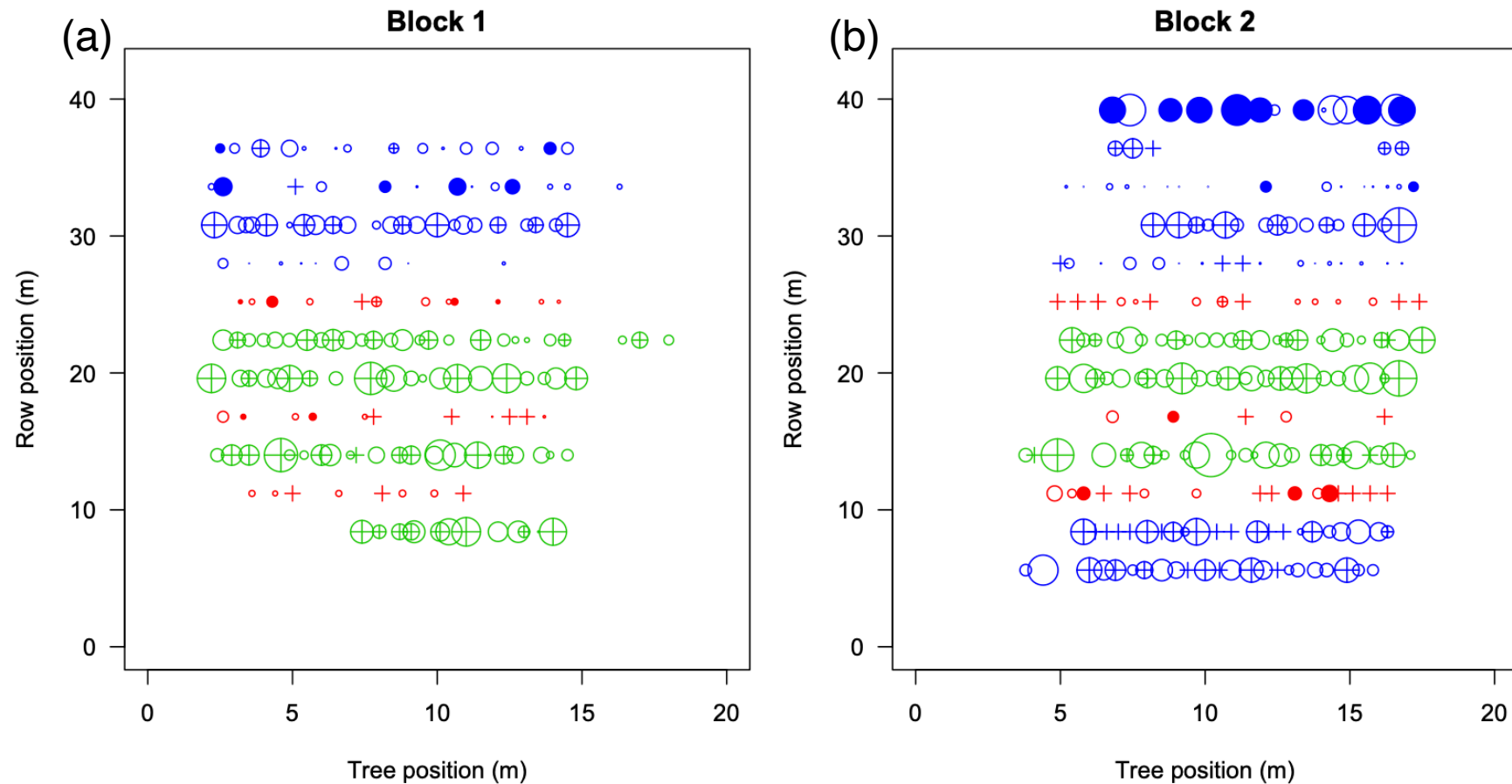


Figure S3. Locations and sizes of trees planted in two blocks (a, b) in coastal site. Solid circles, circles with crosses, and open circles indicate sampled reference, sampled non-reference, and non-sampled living trees, respectively. Crosses, + and x, indicate dead and thinned trees, respectively. Triangles indicate non-experimental trees. Colors indicate taxa: *Quercus mongolica* var. *crispula* (red), *Q. x angustilepidota* (green), and *Q. dentata* (blue).

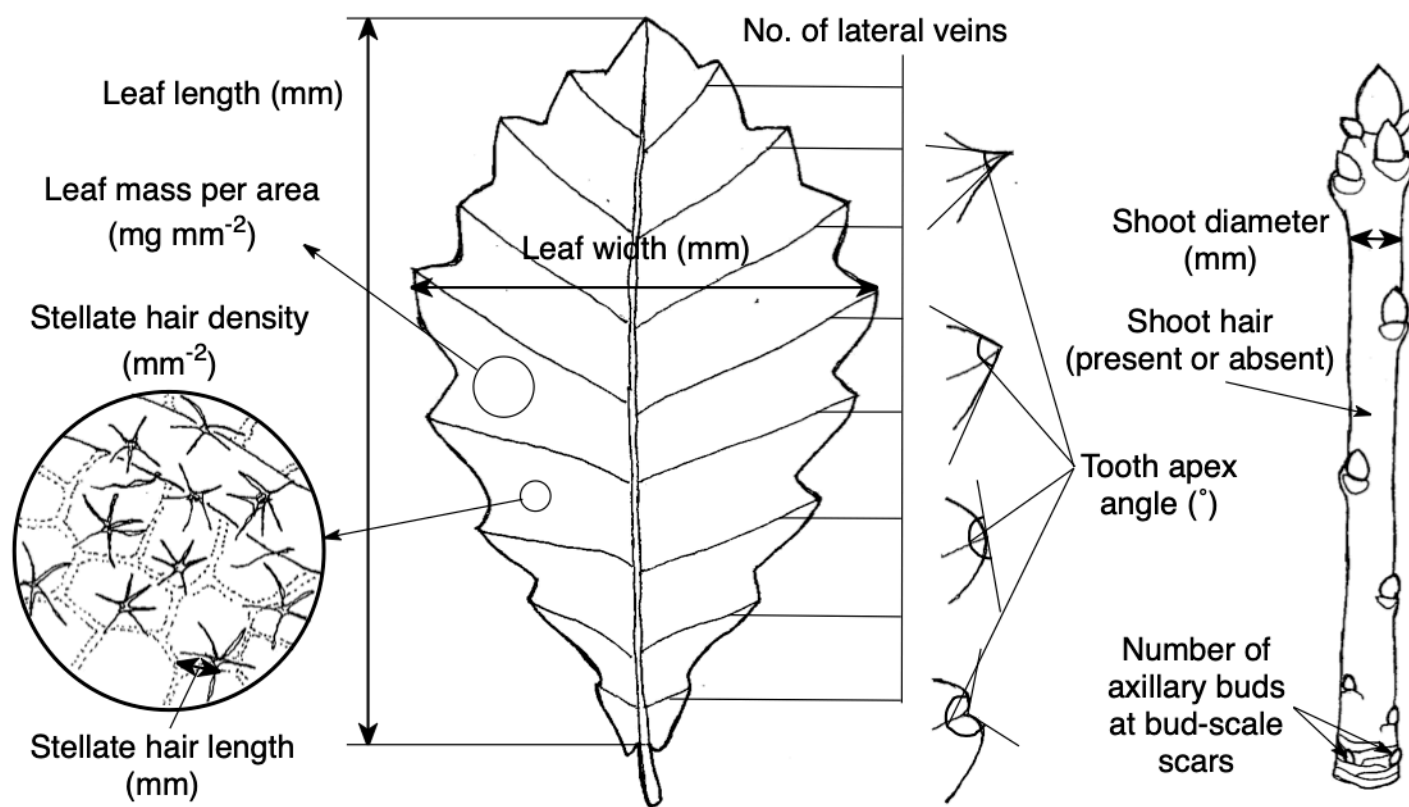


Figure S4. Measurements for morphological traits of leaves and shoots.

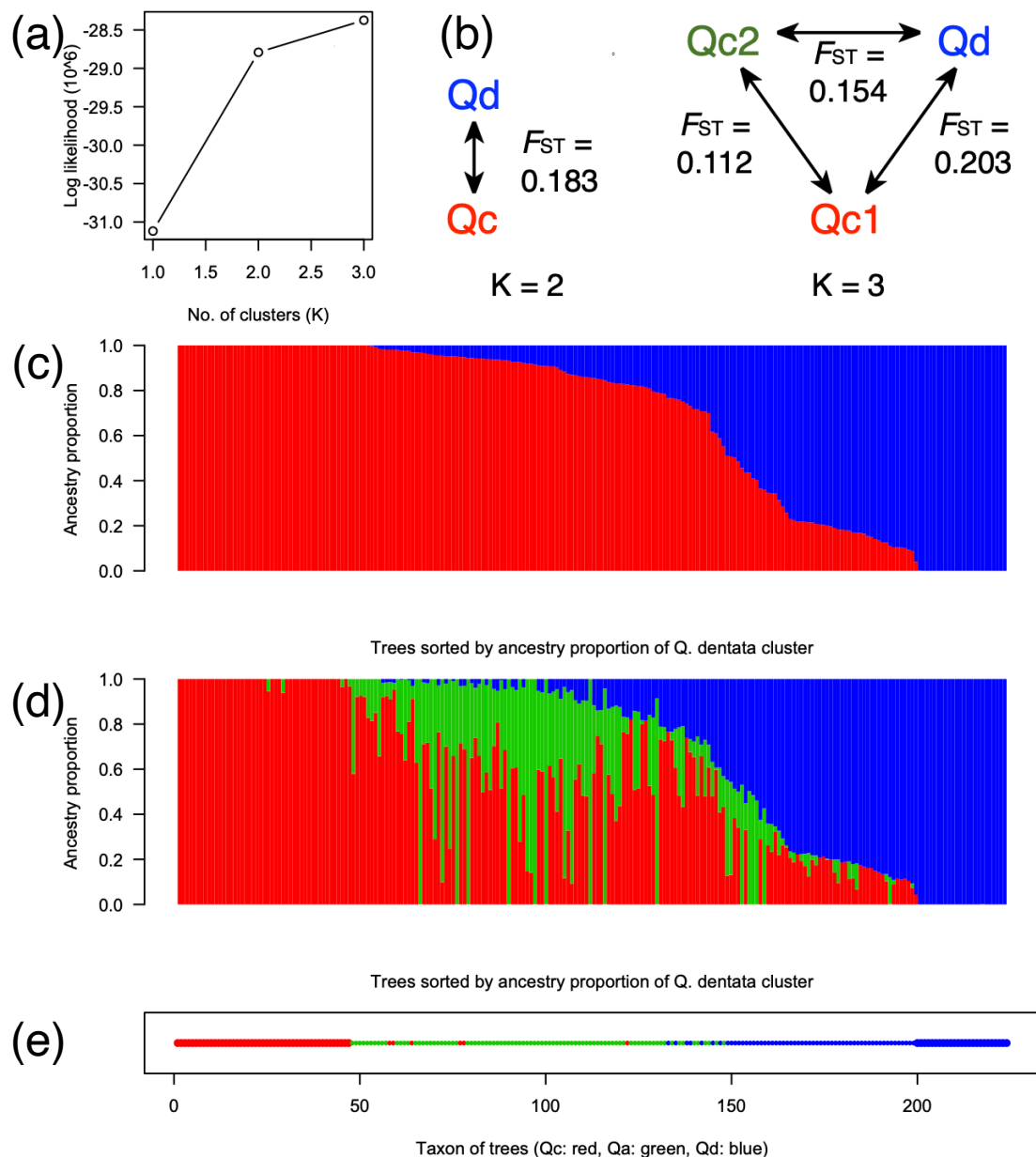


Figure S5. Bayesian clustering of SNP genotypes at ddRAD loci of sampled trees in both inland and coastal sites. Log likelihood when the number of clusters (K) are 1, 2, and 3 (a). Genetic differentiation (F_{ST}) between clusters when K = 2 and K = 3 (b). Bar plots of ancestry proportions of trees sorted by the ancestry proportion of clusters, when K = 2 (c) and K = 3 (d). Colors correspond to clusters (b, c, d). Colors of circles indicate taxa: *Quercus mongolica* var. *crispula* (red), *Q. × angustilepidota* (green), and *Q. dentata* (blue), and enlarged symbols indicate reference samples (e).

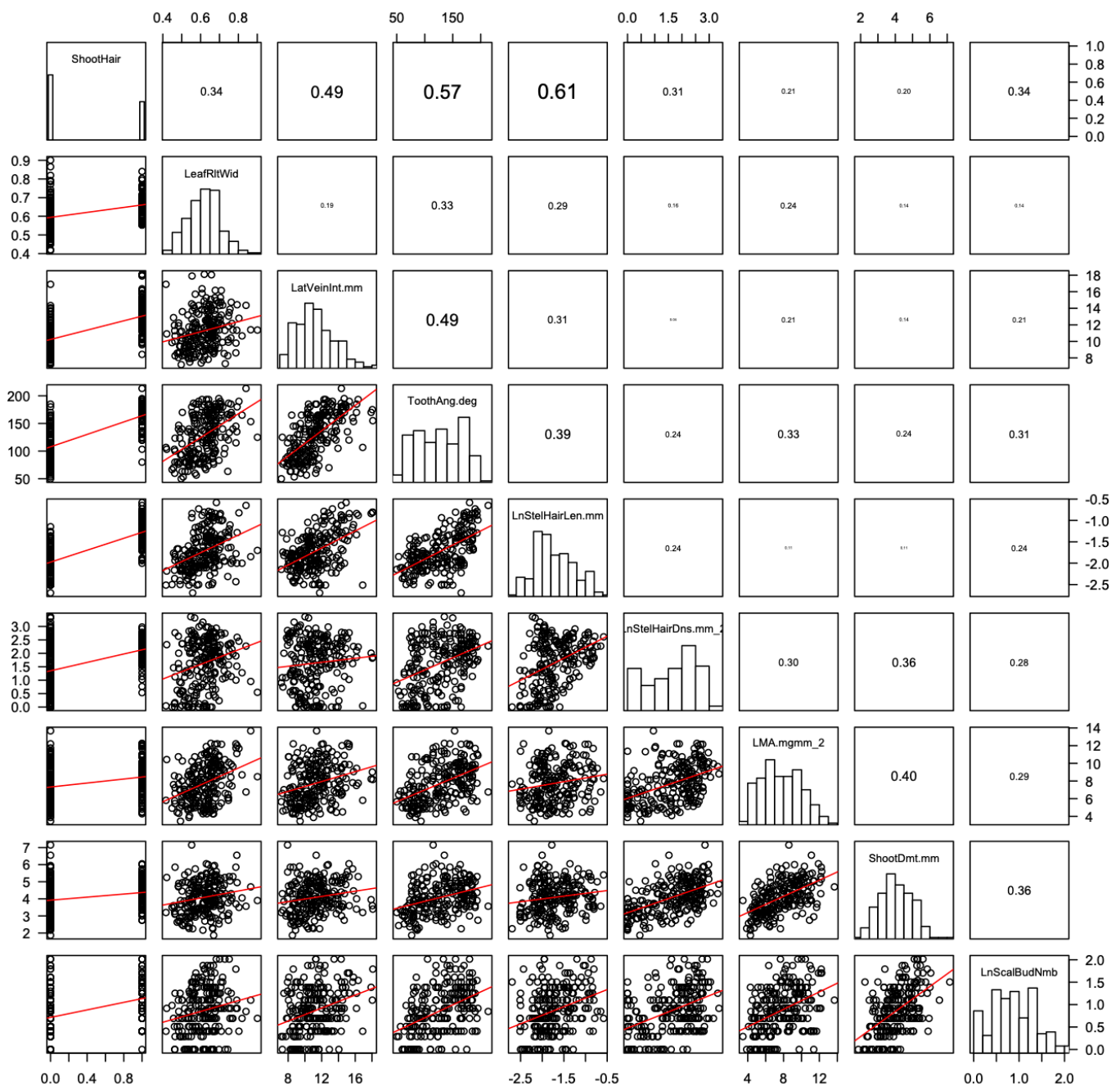


Figure S6. Frequency distributions (scatter plots) and correlations (histograms) for pairs of a taxon-diagnostic trait: shoot hair (0: absent and 1: present) and eight morphological traits: relative leaf width, lateral vein interval (mm), tooth angle ($^{\circ}$), loge length (mm) and loge density (mm^{-2}) of stellate hair on lower leaf surface, lead mass per area (mg mm^{-2}), shoot diameter (mm), and loge number of axillary buds at bud-scale scars. Numbers indicate Kendall's correlation coefficients, and red lines indicate linear regression lines.

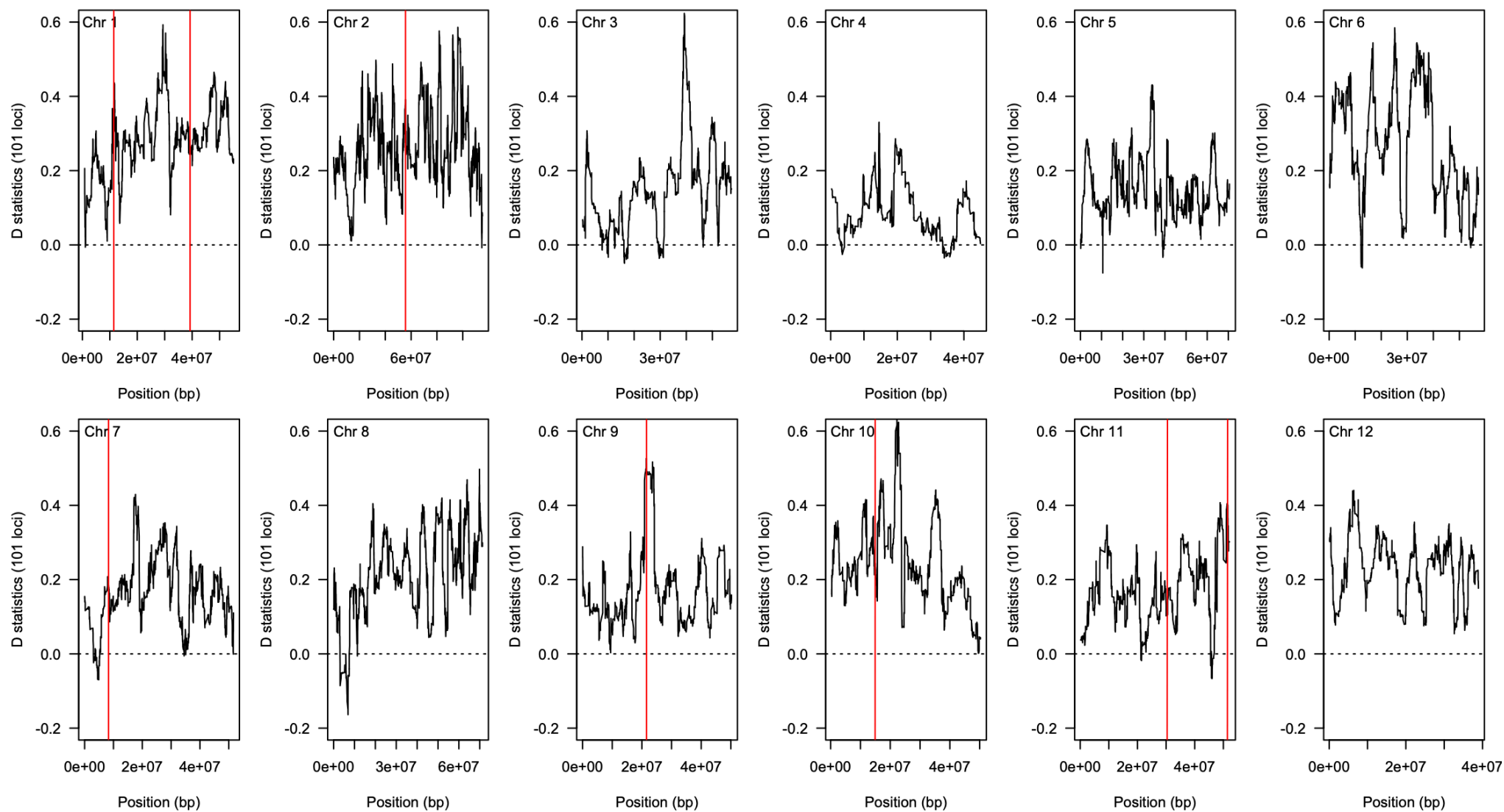


Figure S7. Patterson's D statistics at neighboring 101 ddRAD loci along chromosomes. Positive D values indicate introgression from *Quercus dentata* to *Q. mongolica* var. *crispula*. Red vertical lines indicate positions of trait-associated loci shown in Figure 7 and Table S2.

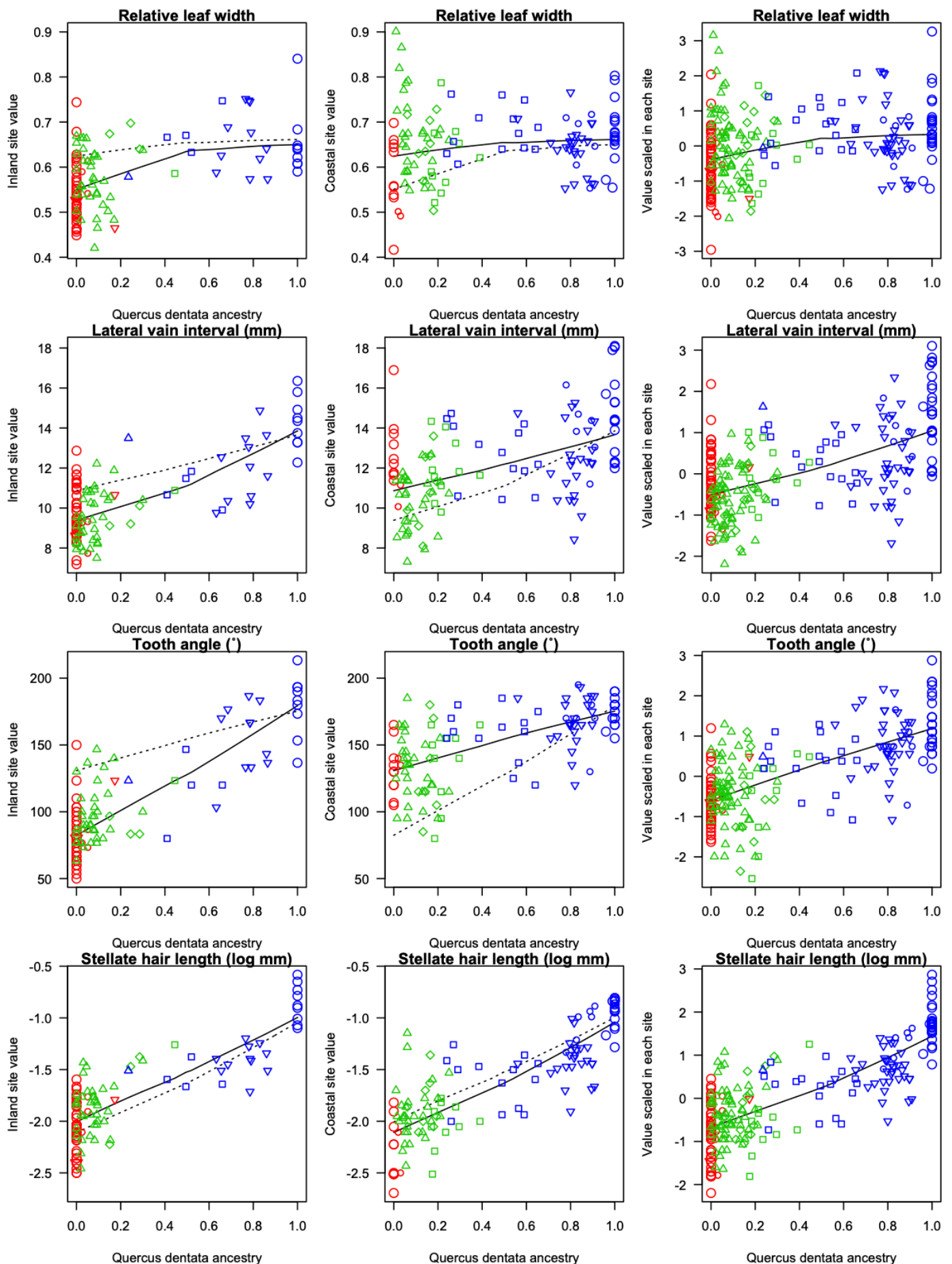


Figure S8. Phenotypic values of four taxon-specific traits in inland (left) and coastal (middle) sites and those values scaled in each site and pooled together (right) in relation to *Quercus dentata* ancestry. Solid and dotted lines are fitted to observations in the focal site and the other site, respectively, using the lowest method. Symbols are shown in the same way as Figure 1.

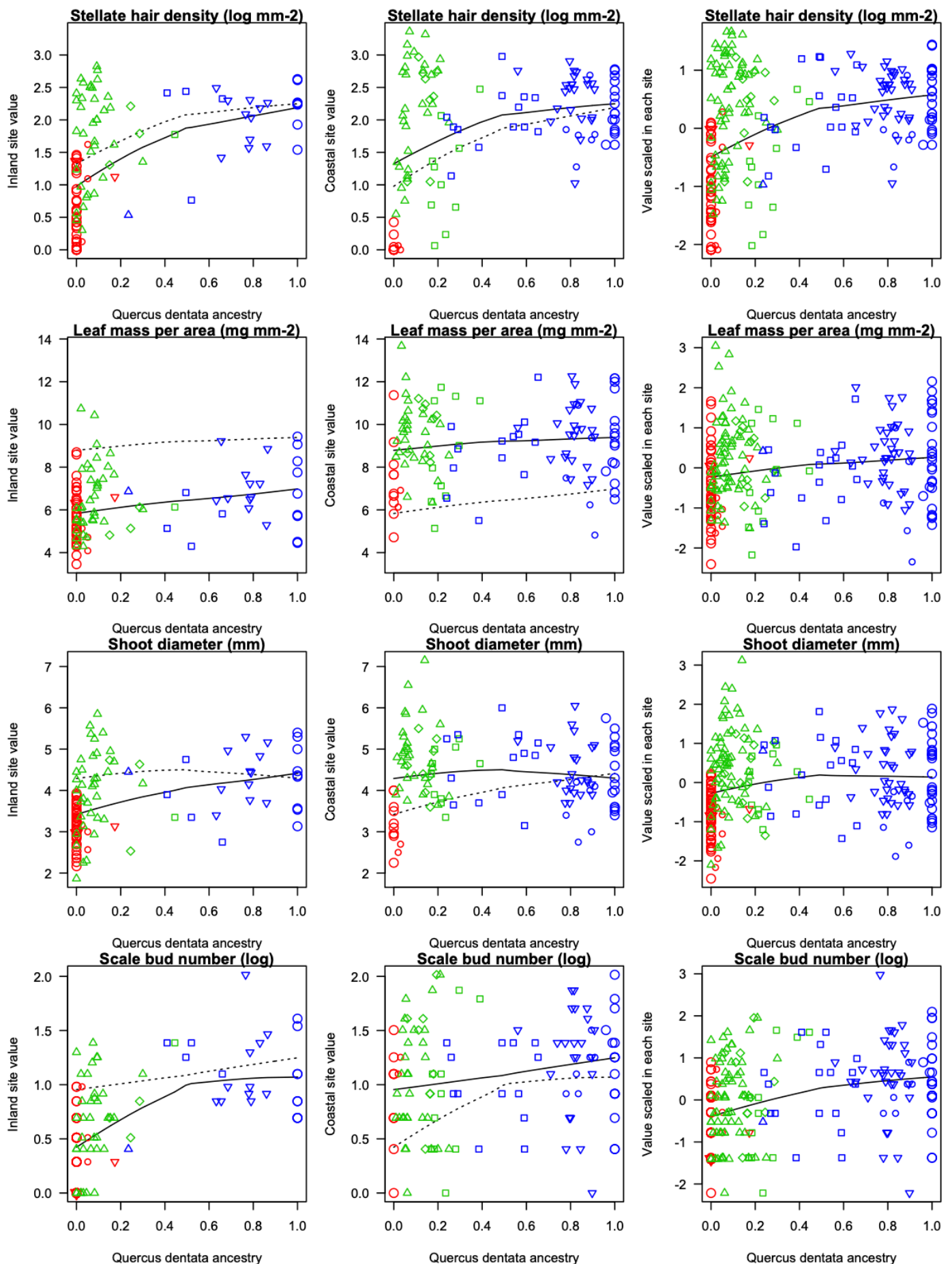


Figure S9. Phenotypic values of four habitat-specific traits in inland (left) and coastal (middle) sites and those values scaled in each site and pooled together (right) in relation to *Quercus dentata* ancestry. Solid and dotted lines are fitted to observations in the focal site and the other site, respectively, using the lowess method. Symbols are shown in the same way as Figure 1.

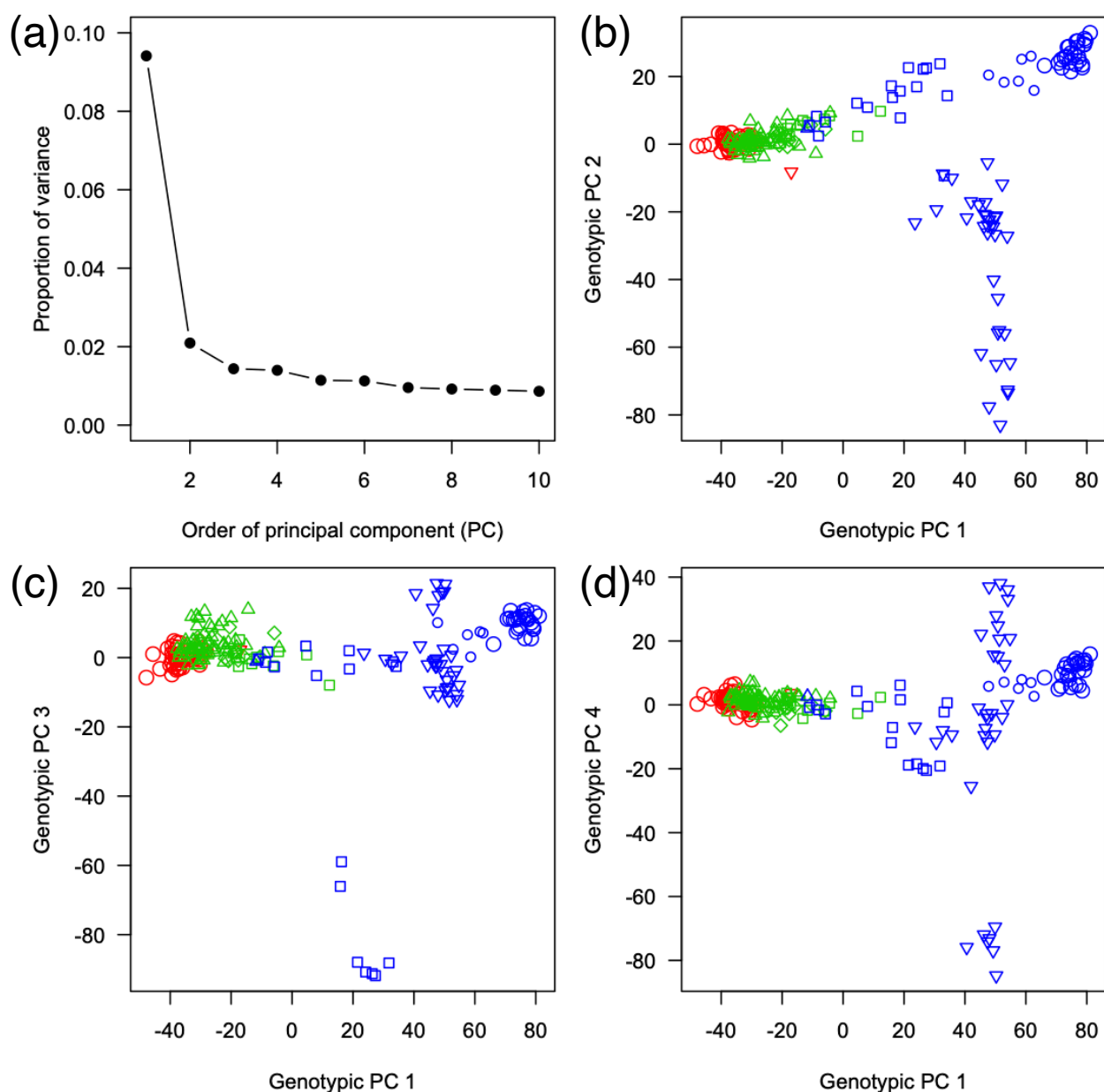


Figure S10. Principal component analysis for SNP genotypes at ddRAD loci of sampled trees in both inland and coastal sites. Proportion (%) of variances for the first 10 principal components (PCs) are shown (a). Coordination of sampled trees on the first and second PCs (b), the first and third PCs (c), and the first and fourth PCs (d) are shown. Symbols are shown in the same way as Figure 1.

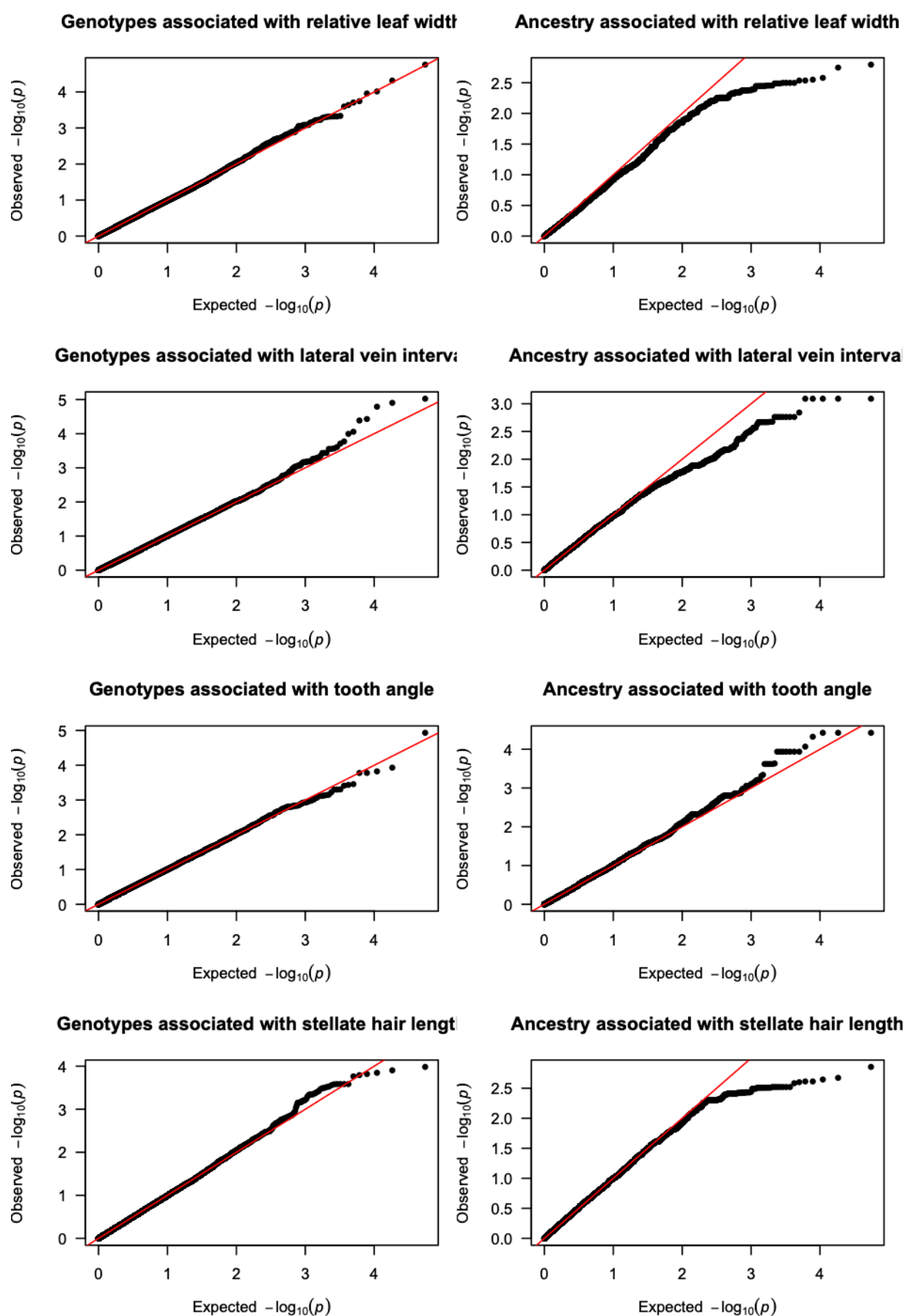


Figure S11. Q-Q plots of expected and observed $-\log_{10} p$ values for four taxon-specific traits. Red lines indicate identical expected and observed $-\log_{10} p$ values.

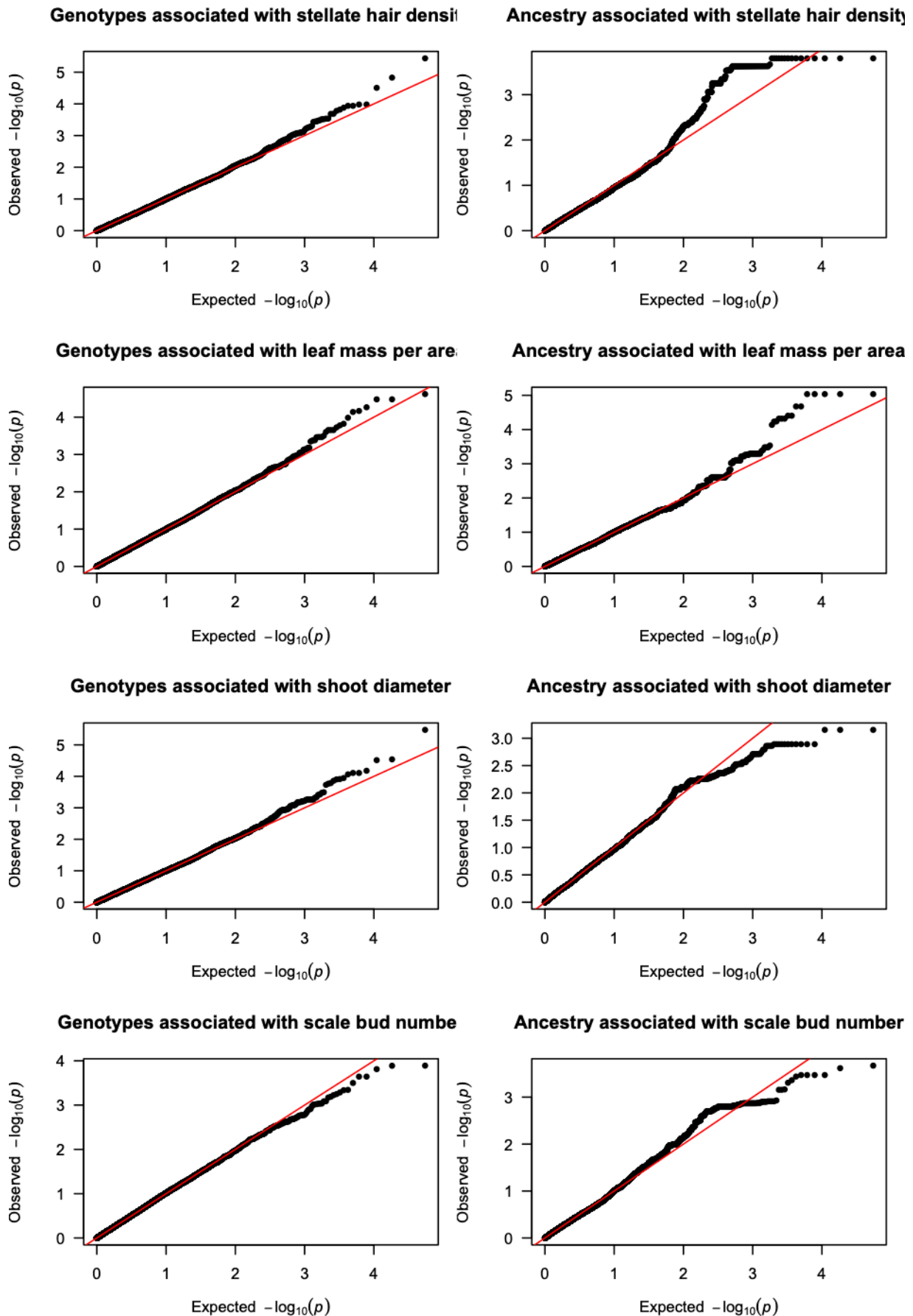


Figure S12. Q-Q plots of expected and observed $-\log_{10} p$ values for four habitat-specific traits. Red lines indicate identical expected and observed $-\log_{10} p$ values.

Table S2. ddRAD loci of SNP genotypes (G) and local ancestry (A) associated with traits (FDR < 0.15) and proteins nearest to or between trait-associated loci obtained from PM1N v2.3 Quercus robur annotation database.

Chromosome	Position (bp)		Trait	Genetic data	-log ₁₀ P	FDR	Protein ID	Position (bp)		GO term	Protein name [EC] reference
	Start	End						Start	End		
1	11432817	11432817	Stellate hair density	G	5.44	0.100	Qrob_P0619080.2	11451267	11456090	5524 ATP binding, 3678 DNA helicase activity, 43141 ATP-dependent 5'-3' DNA helicase activity	OTU domain-containing protein 5 [EC:3.1.2.15]
1	39247601	39247601	Shoot diameter	G	5.48	0.091	Qrob_P0559890.2	39249048	39249986	3677 DNA binding	
2	55663257	55663257	Lateral vein interval	G	4.90	0.148	Qrob_P0202950.2	55665275	55671305	8152 metabolic process, 16491 oxidoreductase activity	
7	8293934	8293934	Lateral vein interval	G	4.79	0.148	Qrob_P0218810.2	8292719	8297719	16491 oxidoreductase activity, 55114 oxidation-reduction process	2-hydroxyglutarate dehydrogenase [EC:1.1.99.2] Engqvist et al. (2011) https://doi.org/10.1074/jbc.M110.194175
9	21549823	21549823	Lateral vein interval	G	5.02	0.148	Qrob_P0026840.2	21547671	21559909	5515 protein binding, 8270 zinc ion binding	
10	14717056	14754019	Stellate hair density	A	3.35	0.146	Qrob_P0142700.2	14746075	14746713	5509 calcium ion binding	
10	14926293	15132475	Stellate hair density	A	3.25	0.146	Qrob_P0555320.2	14929357	14930715	6355 regulation of transcription, DNA-templated, 3677 DNA binding	
10	14926293	15132475	Stellate hair density	A	3.25	0.146	Qrob_P0555330.2	14962180	14966852	3677 DNA binding	
10	14926293	15132475	Stellate hair density	A	3.25	0.146	Qrob_P0555340.2	14980666	14983249	3677 DNA binding	
10	14926293	15132475	Stellate hair density	A	3.25	0.146	Qrob_P0555360.2	15020596	15022009	16853 isomerase activity	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 [EC:5.2.1.8] Mokyakova et al. (2014) https://doi.org/10.1134/S1022795414020100
10	14926293	15132475	Stellate hair density	A	3.25	0.146	Qrob_P0555400.2	15050562	15054572	8152 metabolic process, 3824 catalytic activity, 5975 carbohydrate metabolic process, 16857 racemase and epimerase activity, acting on carbohydrates and derivatives	Ribulose-phosphate 3-epimerase [EC:5.1.3.1]
10	14926293	15132475	Stellate hair density	A	3.25	0.146	Qrob_P0555430.2	15096706	15098385	5515 protein binding	
10	14926293	15132475	Stellate hair density	A	3.25	0.146	Qrob_P0555450.2	15111177	15114808	3676 nucleic acid binding	
10	14926293	15132475	Stellate hair density	A	3.25	0.146	Qrob_P0555460.2	15120648	15124265	3676 nucleic acid binding, 4527 exonuclease activity	
11	29866211	30015191	Leaf mass per area	A	5.04	0.051	Qrob_P0171070.2	29865528	29873614	16020 membrane	
11	30838908	30926957	Leaf mass per area	A	4.40	0.110	Qrob_P0170630.2	30885776	30889097	3824 catalytic activity, 5975 carbohydrate metabolic process, 5509 calcium ion binding, 43169 cation binding, 4556 alpha-amylase activity	Alpha-amylase [EC:3.2.1.1]
11	30838908	30926957	Leaf mass per area	A	4.40	0.110	Qrob_P0170620.2	30892546	30902560	16021 integral component of membrane, 5783 endoplasmic reticulum	Acyl-CoA-dependent ceramide synthase [EC:2.3.1.24]
11	30838908	30926957	Leaf mass per area	A	4.40	0.110	Qrob_P0170610.2	30925800	30928502	5506 iron ion binding, 16705 oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 20037 heme binding, 55114 oxidation-reduction process	(+)-Abscisic acid 8'-hydroxylase [EC:1.14.13.93] Kushihiro et al. (2004) https://www.embopress.org/doi/full/10.1038/sj.emboj.7600121
11	51043879	51318001	Stellate hair density	A	3.34	0.146	Qrob_P0251550.2	51042013	51044917	3824 catalytic activity, 4722 protein serine/threonine phosphatase activity, 6470 protein dephosphorylation, 43169 cation binding	Protein phosphatase 2C homolog 2/3 [EC:3.1.3.16] Lorenzo et al. (2002) https://doi.org/10.1034/j.1399-3054.2002.1140318.x
11	51043879	51318001	Stellate hair density	A	3.34	0.146	Qrob_P0251510.2	51065798	51066091	5524 ATP binding	Homoserine kinase [EC:2.7.1.39] van Damme et al. (2009) https://doi.org/10.1105/tpc.109.066811
11	51043879	51318001	Stellate hair density	A	3.34	0.146	Qrob_P0251500.2	51079451	51086871	16020 membrane, 55085 transmembrane transport, 16021 integral component of membrane, 22857 transmembrane transporter activity, 22891 substrate-specific transmembrane transporter activity, 5215 transporter activity	
11	51043879	51318001	Stellate hair density	A	3.34	0.146	Qrob_P0251490.2	51094139	51094775	5515 protein binding	
11	51043879	51318001	Stellate hair density	A	3.34	0.146	Qrob_P0251430.2	51170728	51174833	5515 protein binding	
11	51043879	51318001	Stellate hair density	A	3.34	0.146	Qrob_P0251410.2	51224590	51227672	5524 ATP binding, 5634 nucleus, 3682 chromatin binding, 6270 DNA replication initiation, 3678 DNA helicase activity, 42555 MCM complex, 3688 DNA replication origin binding	
11	51043879	51318001	Stellate hair density	A	3.34	0.146	Qrob_P0251330.2	51315446	51319182	5515 protein binding	
11	51524292	51549907	Stellate hair density	A	3.80	0.120	Qrob_P0099790.2	51526994	51528343	8152 metabolic process, 3824 catalytic activity	Isopenicillin-N epimerase [EC:5.1.1.17]
11	51524292	51549907	Stellate hair density	A	3.80	0.120	Qrob_P0099750.2	51547955	51550308	5488 binding	
11	51549912	51811638	Stellate hair density	A	3.63	0.120	Qrob_P0099690.2	51599131	51604962	3677 DNA binding	
11	51549912	51811638	Stellate hair density	A	3.63	0.120	Qrob_P0099650.2	51626315	51627609	6355 regulation of transcription, DNA-templated	
11	51549912	51811638	Stellate hair density	A	3.63	0.120	Qrob_P0099630.2	51663338	51665116	3677 DNA binding	
11	51549912	51811638	Stellate hair density	A	3.63	0.120	Qrob_P0099550.2	51716545	51717543	6355 regulation of transcription, DNA-templated, 3690 double-stranded DNA binding, 5739 mitochondrion	