

Supplementary

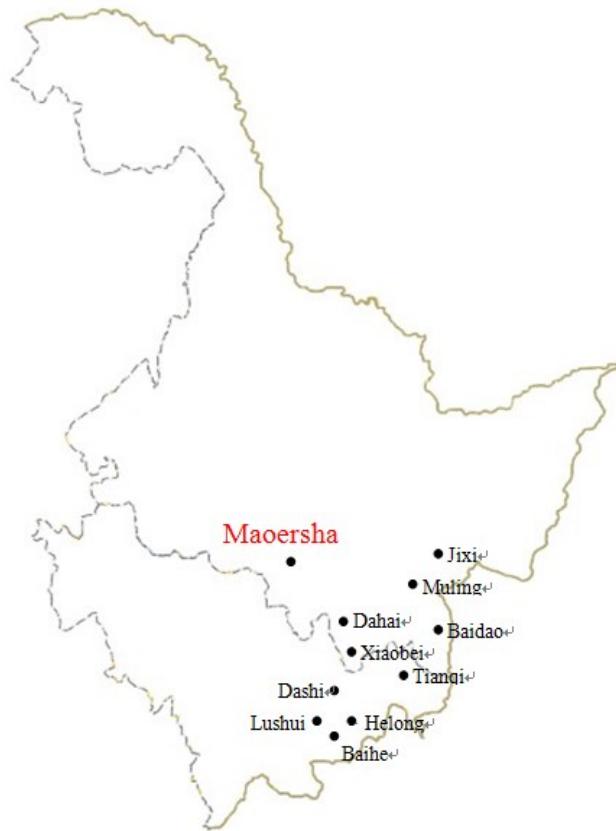


Figure S1. A map showing the populations sampled in the original distribution area of China.

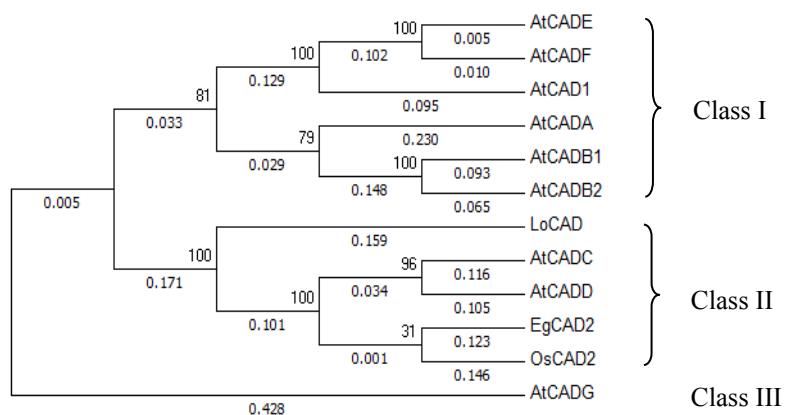


Figure S2. Phylogenetic analysis of the CAD protein family. Accession number of proteins used to build the tree are: *Arabidopsis thaliana* AtCAD1 (NP_195643); AtCAD-A (NP_195510); AtCAD-B1 (CAA48027); AtCAD-B2 (NP_195512); AtCAD-C (NP_188576); AtCAD-D (NP_195149); AtCAD-E (NP_179765); AtCAD-F (NP_179780); AtCAD-G (NP_177412); *Eucalyptus gunnii* EgCAD2(X65631.1); *Oryza sativa* OsCAD2 (DAA02237).

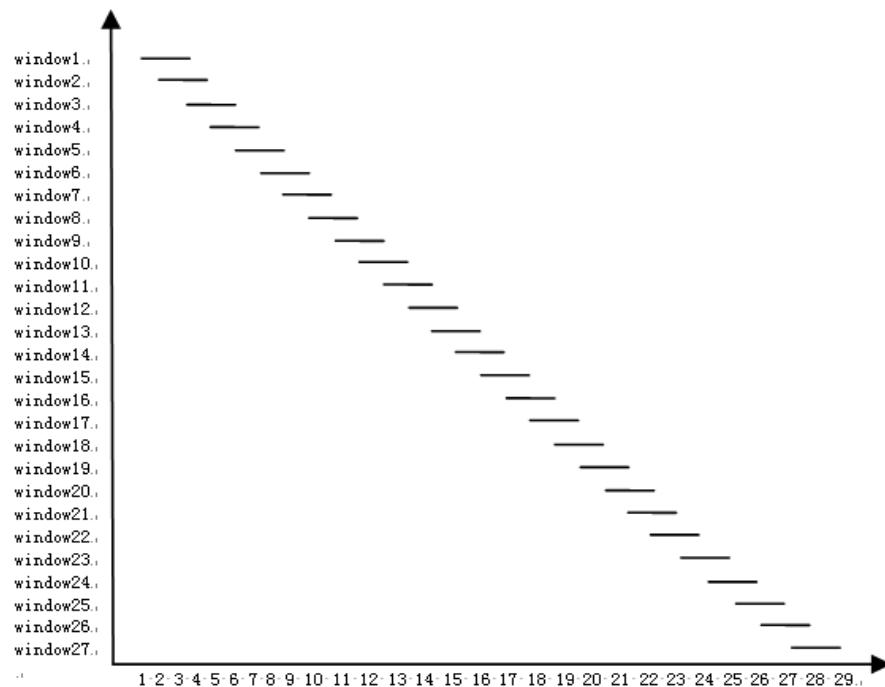


Figure S3. Haplotypes construction of CAD gene.

Table S1. The minimum, and maximum values, mean, standard error (SE) and coefficient of phenotypic variation [CV (%)] for each growth and wood property trait measured in *L. olgensis* provenance population.

Statistics	Lignin (%)	Holocellulose (%)	Height (m)	DBH (cm)	Volume (m ³)	Density (g/cm ³)	CB (kg)	CCR (%)
Min	0.155	0.494	3.900	10.90	0.039	0.281	39.99	0.489
Max	0.397	0.675	18.90	36.10	0.797	0.569	91.96	0.529
Mean	27.74	60.33	13.50	23.33	0.309	0.396	62.57	0.512
SE	0.0022	0.0017	0.1236	0.2556	0.0075	0.0018	0.6596	0.0006
CV (%)	15.15	5.382	17.17	20.55	45.66	8.621	19.78	2.128

H tree height; *D* the diameter at breast height; *V* stem volume; *MFA* microfiber angle; *N* number of trees sampled.

Table S2. The genotype combination in each window.

WINDOWS	SNP	Haplotype	Frequency ¹
WINDOW1	SNP1–3	A-T-T	0.07
		G-A-T	0.08
		G-T-A	0.39
		G-T-T	0.44
WINDOW2	SNP2–4	A-T-A	0.08
		T-A-A	0.39
		T-T-A	0.38
		T-T-T	0.13
WINDOW3	SNP3–5	A-A-C	0.41
		T-A-C	0.43
		T-T-C	0.13
WINDOW4	SNP4–6	A-C-C	0.25
		A-C-T	0.59
		T-C-T	0.13
WINDOW5	SNP5–7	C-C-C	0.25
		C-T-C	0.70
WINDOW6	SNP6–8	C-C-T	0.25
		T-C-C	0.05
		T-C-T	0.69
WINDOW7	SNP7–9	C-C-G	0.05
		C-T-A	0.16
		C-T-G	0.77
WINDOW8	SNP8–10	C-G-C	0.05
		T-A-C	0.18
		T-G-A	0.28
		T-G-C	0.49
WINDOW9	SNP9–11	A-C-A	0.18
		G-A-A	0.28
		G-C-A	0.41
		G-C-C	0.13
WINDOW10	SNP10–12	A-A-C	0.28
		C-A-C	0.52
		C-A-T	0.07
		C-C-C	0.13
WINDOW11	SNP11–13	A-C-T	0.80
		A-T-T	0.07
		C-C-A	0.08
		C-C-T	0.05
WINDOW12	SNP12–14	C-A-G	0.08
		C-T-G	0.51
		C-T-T	0.34
		T-T-G	0.07

Table S2. *Cont.*

WINDOWS	SNP	Haplotype	Frequency ¹
WINDOW13	SNP13–15	A-G-C	0.08
		T-G-C	0.54
		T-T-C	0.34
WINDOW14	SNP14–16	G-C-C	0.08
		G-C-T	0.54
		T-C-T	0.33
WINDOW15	SNP15–17	C-C-A	0.07
		C-C-C	0.85
WINDOW16	SNP16–18	C-C-C	0.05
		T-A-A	0.36
		T-A-C	0.52
WINDOW17	SNP17–19	A-A-T	0.34
		A-C-T	0.52
WINDOW18	SNP18–20	A-T-A	0.38
		C-C-G	0.05
		C-T-A	0.51
		C-T-G	0.05
WINDOW19	SNP19–21	C-G-C	0.07
		T-A-C	0.84
		T-A-G	0.05
		T-G-C	0.05
WINDOW20	SNP20–22	A-C-C	0.25
		A-C-T	0.59
		A-G-T	0.05
		G-C-T	0.11
WINDOW21	SNP21–23	C-C-C	0.25
		C-T-C	0.64
		C-T-T	0.07
		G-T-C	0.05
WINDOW22	SNP22–24	C-C-C	0.25
		T-C-C	0.43
		T-C-T	0.26
		T-T-C	0.07
WINDOW23	SNP23–25	C-C-A	0.59
		C-C-G	0.08
		C-T-A	0.26
		T-C-A	0.07
WINDOW24	SNP24–26	C-A-A	0.52
		C-A-G	0.13
		C-G-A	0.08
		T-A-A	0.26
WINDOW25	SNP25–27	A-A-A	0.16
		A-A-T	0.62
		A-G-T	0.13
		G-A-T	0.08

Table S2. *Cont.*

WINDOWS	SNP	Haplotype	Frequency¹
WINDOW26	SNP26–28	A-A-T	0.15
		A-T-A	0.13
		A-T-T	0.57
		G-T-T	0.11
WINDOW27	SNP27–29	A-T-A	0.15
		T-A-C	0.08
		T-A-G	0.07
		T-T-A	0.69

¹ The minor haplotype frequency is >5%.

Table S3. Effects of different genotypes SNP (g.590G > T) and SNP (g.1184A > T) on lignin content (least squares means).

Traits	SNP (g.590G > T)				SNP (g.1184A > T)			
	GG(108)	GT(23)	TT(68)	Phenotypic Variance ¹	AA(32)	AT(41)	TT(126)	Phenotypic Variance ¹
lignin	0.2405 ± 0.0076	0.2800 ± 0.0267	0.3052 ± 0.0076	0.1690	0.2425 ± 0.0149	0.2734 ± 0.0253	0.2836 ± 0.0068	0.1840
height	13.94 ± 0.36	14.31 ± 0.17	15.11 ± 0.52	0.0194	14.58 ± 0.69	13.21 ± 0.58	13.91 ± 0.32	0.0515
DBH	23.59 ± 0.30	23.41 ± 0.97	23.39 ± 0.42	0.0026	23.92 ± 0.57	23.23 ± 0.95	23.46 ± 0.26	0.0196
density	0.3979 ± 0.0028	0.3980 ± 0.0096	0.4062 ± 0.0041	0.0504	0.3957 ± 0.0056	0.3965 ± 0.0094	0.4014 ± 0.0026	0.0229
volume	0.3359 ± 0.0112	0.3332 ± 0.0226	0.3181 ± 0.0159	0.0126	0.3423 ± 0.0212	0.3252 ± 0.0353	0.3179 ± 0.0097	0.0242
CB	0.5117 ± 0.0019	0.5126 ± 0.0058	0.5154 ± 0.0026	0.0266	0.5105 ± 0.0036	0.5112 ± 0.0058	0.5133 ± 0.0016	0.0152
CCR	64.81 ± 2.43	65.32 ± 7.82	65.50 ± 3.43	0.0006	68.03 ± 4.61	65.97 ± 7.68	64.55 ± 2.11	0.0135

CB, carbon storage, CCR, carbon content rate; ¹ Percentage of phenotypic variance in the larch population.

Table S4. Association analysis of different haplotypes for SNP (g.590G > T) and SNP (g.1184A > T) lignin content.

Traits	p-value	G-A(21)	G-T(105)	T-A(12)	T-T(61)	Phenotypic Variance ¹
Lignin (%)	0.0042	0.2299 ± 0.0151	0.2718 ± 0.0078	0.2885 ± 0.0289	0.3061 ± 0.0107	0.2534
Height	0.1130	14.69 ± 0.77	13.78 ± 0.40	14.05 ± 1.49	14.45 ± 0.55	0.0297
DBH	0.0033	23.99 ± 0.63	23.52 ± 0.33	23.67 ± 1.22	23.36 ± 0.45	0.0091
density	0.0122	0.3965 ± 0.0060	0.3978 ± 0.0031	0.3899 ± 0.0116	0.4082 ± 0.0043	0.0987
volume	0.0012	0.3449 ± 0.0237	0.3184 ± 0.0123	0.3316 ± 0.0454	0.3172 ± 0.0168	0.0143
CB	0.1238	0.5082 ± 0.0039	0.5126 ± 0.0020	0.5196 ± 0.0074	0.5148 ± 0.0028	0.0568
CCR	0.1135	68.52 ± 5.14	63.97 ± 2.66	65.62 ± 9.86	65.61 ± 3.65	0.0108

CB, carbon storage, CCR, carbon content rate; ¹ Percentage of phenotypic variance in the larch population.

Table S5. Association analysis of lignin content-related different combination CAD genotypes for SNP (g.590G > T) and SNP (g.1184A > T).

Traits	<i>p</i> -value	GGAA	GTAA	GTAT	GTTC	TTAA	TTAT	TTTT	Phenotypic Variance ¹
lignin	0.0039	0.2299 ± 0.0151	0.2439 ± 0.0143	0.2399 ± 0.0231	0.2991 ± 0.0132	0.2885 ± 0.0289	0.2731 ± 0.0113	0.3061 ± 0.0107	0.2407
height	0.0131	14.69 ± 0.77	14.31 ± 0.21	14.71 ± 0.79	14.44 ± 0.43	14.05 ± 1.49	14.21 ± 0.89	14.45 ± 0.55	0.0314
DBH	0.0063	23.99 ± 0.63	23.74 ± 0.34	23.68 ± 1.01	23.41 ± 0.23	23.67 ± 1.22	23.45 ± 0.99	23.36 ± 0.45	0.0045
density	0.0092	0.3965 ± 0.0060	0.3891 ± 0.0014	0.3975 ± 0.0044	0.3943 ± 0.0088	0.3899 ± 0.0116	0.3901 ± 0.072	0.4082 ± 0.0043	0.0781
volume	0.0021	0.3449 ± 0.0237	0.3389 ± 0.0417	0.3469 ± 0.0237	0.3277 ± 0.0315	0.3316 ± 0.0454	0.3304 ± 0.0113	0.3172 ± 0.0168	0.0247
CB	0.0938	0.5082 ± 0.0039	0.5142 ± 0.0051	0.5099 ± 0.0044	0.5101 ± 0.0041	0.5196 ± 0.0074	0.5123 ± 0.0065	0.5148 ± 0.0028	0.0418
CCR	0.1025	68.52 ± 5.14	68.57 ± 2.01	66.42 ± 7.31	67.43 ± 3.04	65.62 ± 9.86	65.49 ± 4.67	65.61 ± 3.65	0.0263

CB, carbon storage, CCR, carbon content rate; ¹ Percentage of phenotypic variance in the larch population.