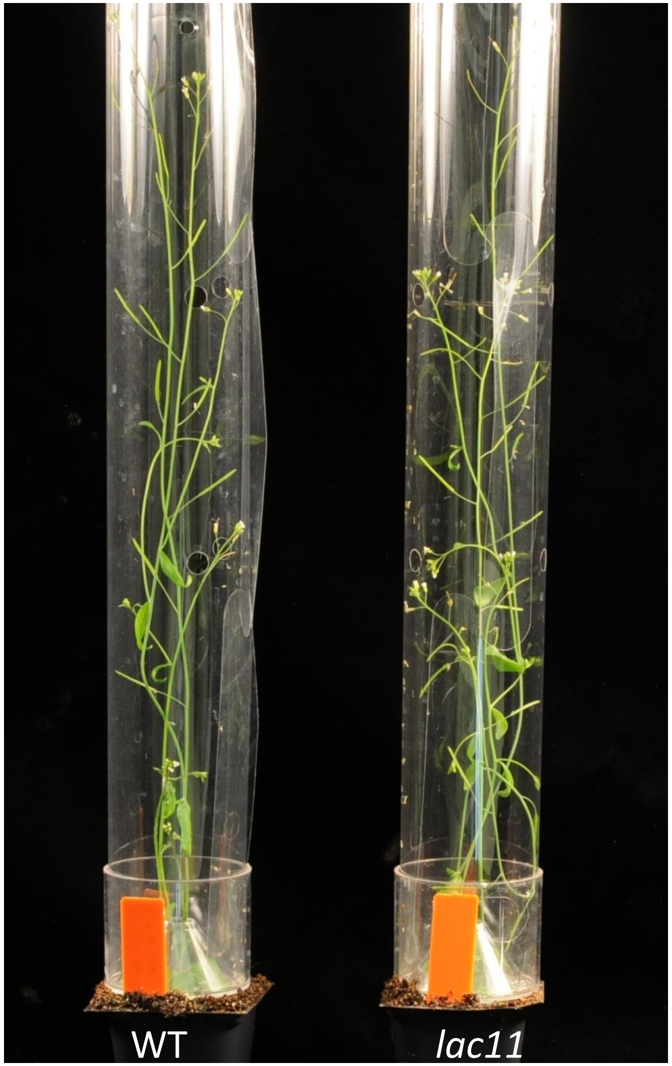

Figure S1. Seven-week-old wild-type and *lac11-1*mutant plants grown in the growth chamber. The single mutant appears to exhibit normal growth.

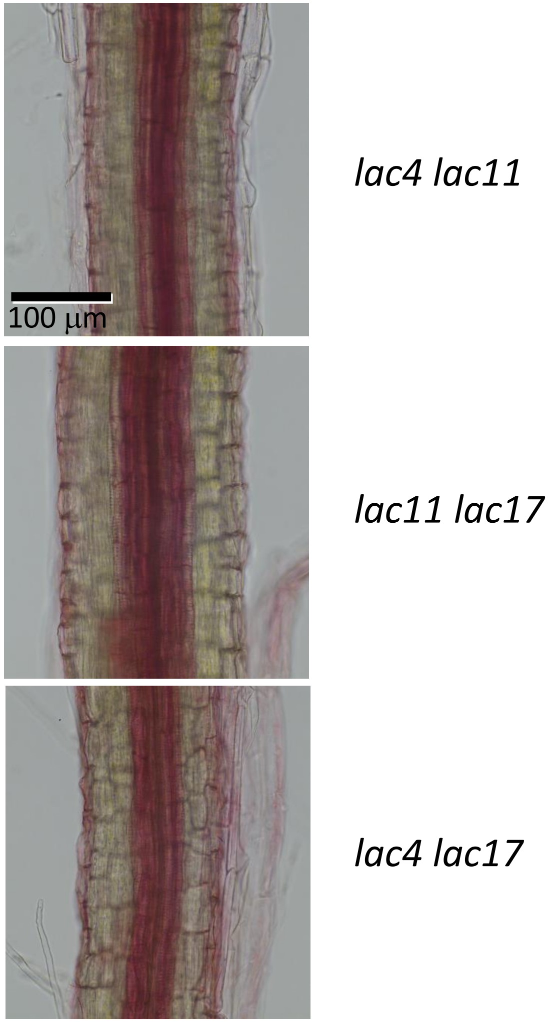

Figure S2. Phloroglucinol staining of roots of three-week-old plants. All three *lac* double mutants exhibit normal red lignin staining.

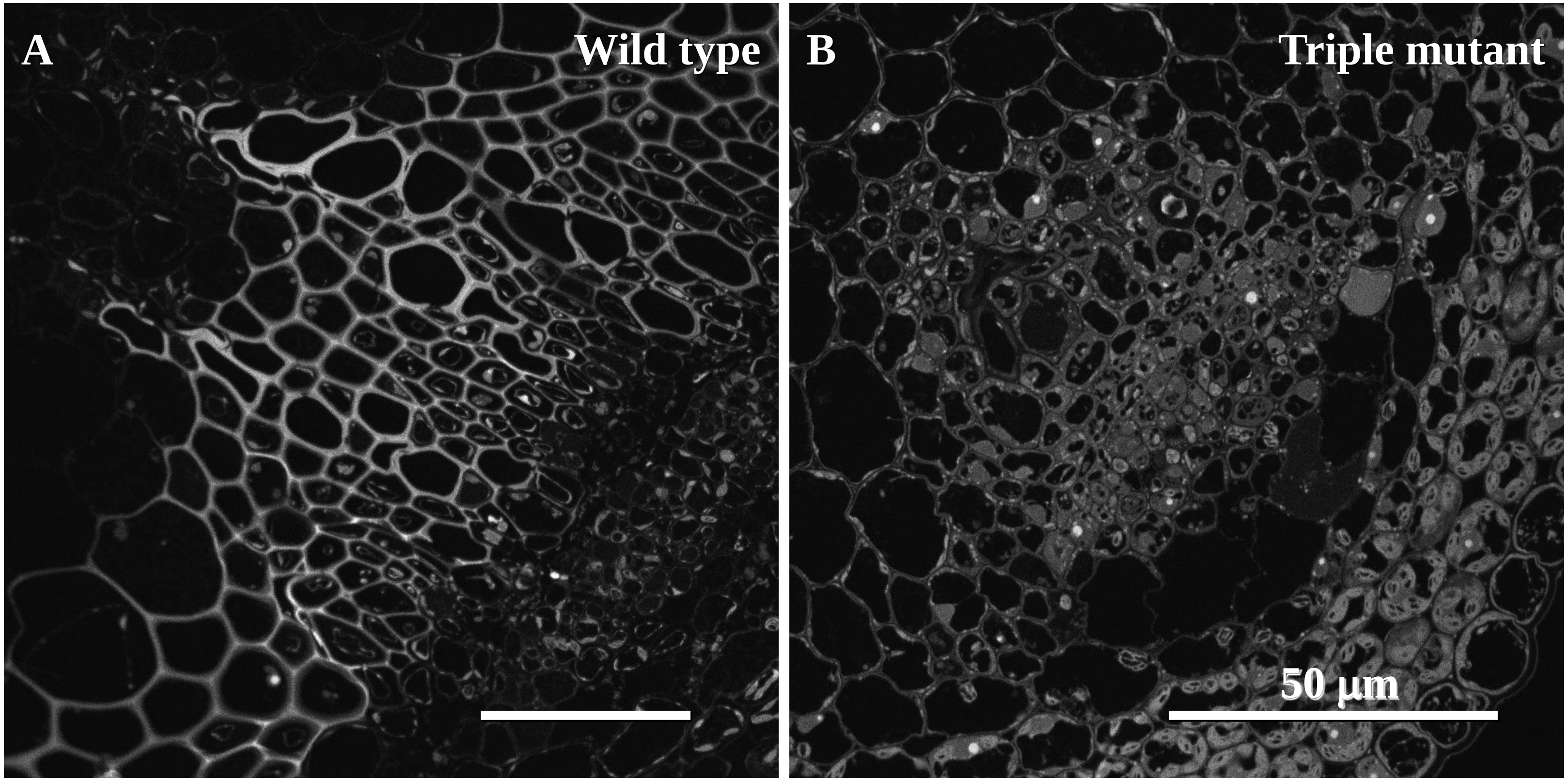

Figure S3. UV autofluorescence of stem cross sections. Serial semi-thin sections that were presented in Figure 3D were further examined under a 405 nm blue diode laser. There was little visible phenolic material accumulated in cell walls of the triple mutant, whereas lignin autofluorescence is clearly evident in xylem tissues of the wild type. Note the stem tissues from the triple mutant contain abundant cytoplasmic components and organelles (autofluorescence) especially chloroplasts in the cortex.

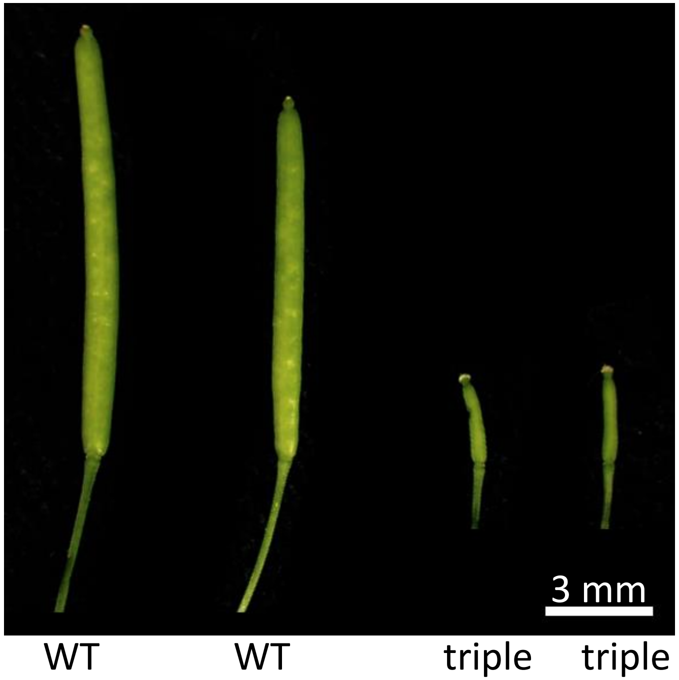

Figure S4. Siliques of wild type and laccase triple mutant. The triple mutant produces few siliques, and these are much smaller than the wild-type siliques

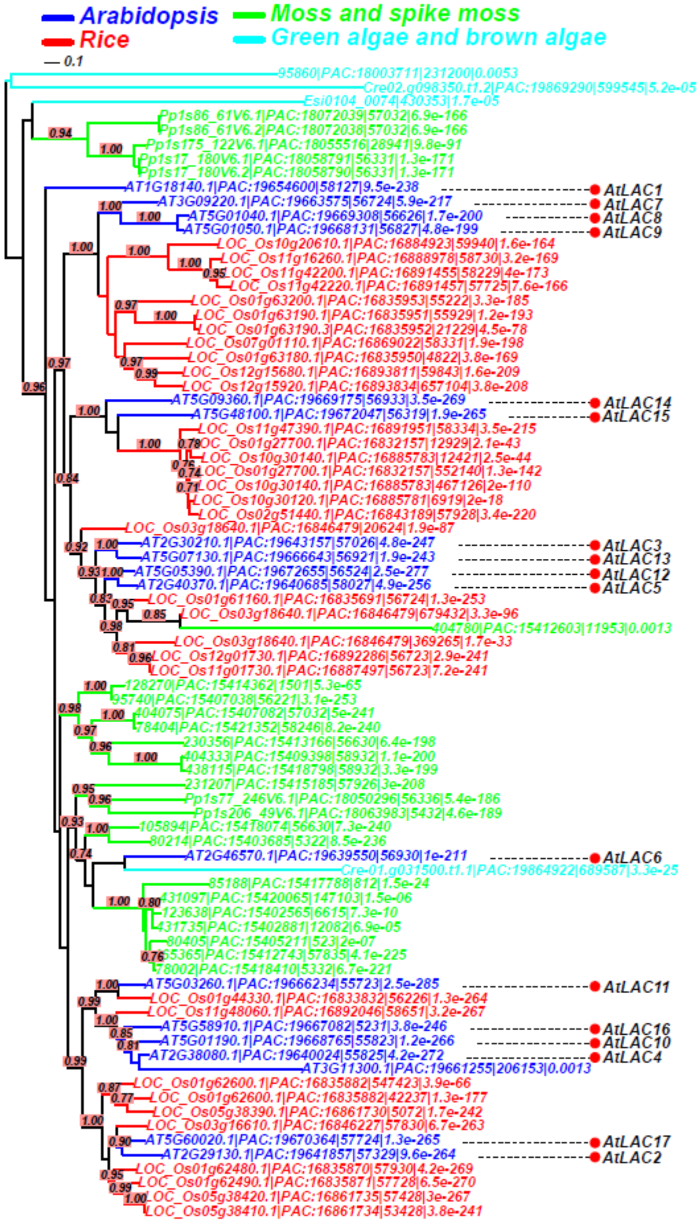

Figure S5. Phylogeny of higher and lower plant LACCASE proteins. This phylogeny includes eight different species and shows the evolutionary putative orthologs of *Arabidopsis* LACCASE in other species. The scale bar represents evolutionary distance of 0.1 amino acid substitutions per site. The numbers on each node are the bootstrap values, with 1.00 meaning a 100% support for the offspring nodes.

Table S1. Total lignin content of Arabidopsis *lac 11* single and double mutants as determined by the acetyl bromide method.

Line	Lignin content (mg/g CWR)
Wild type	157±3.1
lac4-2	150±2.1
lac11-1	155±1.8
lac17-1	152±3.6
lac4-2 lac11-1	141±2.8*
lac11-1 lac17-1	145±2.8*

All data are means ± SE (n = 6). Asterisks indicate values that were determined by Student's *t*-test to be significantly different from the wild-type control ($P < 0.05$).

Table S2. Additional lignin-associated genes with altered expression in the laccase triple mutant

Putative gene	***At Number***	***Gene Description***	***Mu/WT***	***Ave WT***	***SD WT***	***Ave Mu***	***SD Mu***
Pinoresinol reductase1 (PrR1)	At1g32100	Lignan biosynthetic gene	1.68	405	28	680	80
Pinoresinol reductase2 (PrR2)	At4g13660	Lignan biosynthetic gene	4.0	365	43	1469	87
Peroxidase	At5g19890	Peroxidase	9.8	79	21	766	393
Peroxidase	At3g21770	Peroxidase	9.4	342	141	3206	234
Peroxidase	At1g49570	Peroxidase	8.8	41	1.1	362	80
Peroxidase	At2g38390	Peroxidase	7.3	378	155	2751	605
Peroxidase	At2g18140	Peroxidase	7.2	158	0.9	1131	129
Peroxidase	At5g64120	Peroxidase	6.7	650	35	4378	576
Peroxidase	At4g30170	Peroxidase	5.9	475	188	2818	396
Peroxidase	At4g36430	Peroxidase	5.4	313	54	1699	21
Peroxidase	At5g06730	Peroxidase	5.3	30	6	160	22
Peroxidase	At4g08770	Peroxidase	5.3	140	90	742	309
Peroxidase	At5g64110	Peroxidase	5.3	59	2.5	314	95
Peroxidase	At2g18980	Peroxidase	4.3	227	91	977	158
Peroxidase	At5g64100	Peroxidase	3.8	1256	24	4842	451
Peroxidase	At4g11290	Peroxidase	3.7	150	39	560	232
Peroxidase	At4g08780	Peroxidase	3.7	37	5.5	139	35
Peroxidase	At2g39040	Peroxidase	3.5	56	18	194	85
Peroxidase	At3g01190	Peroxidase	3.0	378	118	1117	213
Peroxidase	At5g14130	Peroxidase	2.4	48	0.2	116	31
Peroxidase	At5g06720	Peroxidase	2.3	57	10	132	16
Peroxidase	At4g37530	Peroxidase	2.3	603	188	1037	47
Peroxidase	At2g37130	Peroxidase	2.2	846	24	1830	182
Laccase3	At2g30210	Putative laccase	4.0	181	20	720	254
Laccase7	At3g09220	Putative laccase	3.9	481	78	1855	210
Laccase5	At2g40370	Putative laccase	2.5	49	10	124	26

SGT	At3g21560	Sinapic acid:UDP-glucose glucosyltransferase	2.6	164	31	433	84
SMT	At2g22990	Sinapoylglucose:malate sinapoyltransferase	0.33	3820	365	1266	454
At-LIGB	At4g15093	Catalytic LigB subunit of aromatic ring-opening dioxygenase family	2.5	590	87	1470	111

Mu, laccase triple mutant; WT, wild type; SD, standard deviation (n = 3).

Table S3. Plant species used in the phylogenetic analysis.

Species	clade	# of UniGenes/proteins
Cyanidioschyzon merolae 10D	unicellular red algae	5014
Chlamydomonas reinhardtii	chlorophytic green algae	14598
Ectocarpus siliculosus	multicellular brown algae	16533
Volvox carteri	multicellular green algae	14542
Mesostigma_viride	multicellular green algae	7371
Marchantia polymorpha	liverwort	10959
Physcomitrella patens ssp patens	moss	35938
Selaginella moellendorffii	spike moss	34697
Adiantum capillus veneris	fern	16944
Pinus taeda	gymnosperms	77540
Arabidopsis thaliana	dicot	33410
Oryza sativa	monocot	51258

Species shaded in grey represent eight sequenced plant genomes from Phytozome v7.0; the remaining are EST assemblies taken from plantGDB in 2013. The species are ordered from lower plants to higher plants.