

Table S1 . The LACCASE family genes in *Brachypodium distachyon*

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Locus	Name
Bradi1g10570	BdLAC1
Bradi1g24880	BdLAC2
Bradi1g24910	BdLAC3
Bradi1g65100	BdLAC4
Bradi1g66720	BdLAC5
Bradi1g74320	BdLAC6
Bradi2g23350	BdLAC7
Bradi2g23370	BdLAC8
Bradi2g53800	BdLAC9
Bradi2g54680	BdLAC10
Bradi2g54690	BdLAC11
Bradi2g54740	BdLAC12
Bradi2g55050	BdLAC13
Bradi2g55060	BdLAC14
Bradi3g02290	BdLAC15
Bradi3g02300	BdLAC16
Bradi3g22320	BdLAC17
Bradi3g45190	BdLAC18
Bradi3g59180	BdLAC19
Bradi3g59190	BdLAC20
Bradi3g59210	BdLAC21
Bradi4g11830	BdLAC22
Bradi4g11840	BdLAC23
Bradi4g11850	BdLAC24
Bradi4g11860	BdLAC25
Bradi4g11770	BdLAC26
Bradi4g11780	BdLAC27
Bradi4g39330	BdLAC28
Bradi4g44810	BdLAC29

Supplemental Table S2. Amino acid sequences of laccases used in this study

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>GaLAC1

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SLITLPMNDTDAMINFLNQIRNTKVSQNPRINVPADKDIKRRVFMFLAVNNLPCNTCVVGSR  
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>ZmLAC3

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>SofLAC

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>BnTT10-1

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>Bradi3g02290

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>Bradi2g55060

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>Bradi2g55050

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>Bradi2g54740

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>Bradi2g54690

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>Bradi2g54680

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>Bradi2g53800

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>Bradi2g23350

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>Bradi1g65100

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>Bradi1g24910

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>Bradi1g24880

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>Bradi1g10570

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> AT1G18140 (Lac1)

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> AT2G29130 (Lac2)

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> AT2G30210 (Lac3)

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> AT2G38080 (Lac4)

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> AT2G40370 (Lac5)

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> AT2G46570 (Lac6)

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> AT3G09220 (Lac7)

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> AT5G01040 (Lac8)

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> AT5G01050 (Lac9)

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> AT5G01190 (Lac10)

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PPPQNATSVANTFVNSLRSLNSKTY PANVPITVDHDLFTVGLGINRCHSCKAGNFSRVAAIN  
NITFKMPKTALLQAHYFNLTGIYTTDFPAKPRRVDFDTGKPPSNLATMKATKLYKLPYNSTVQ  
VVLQDTGNVAPENHPIHLHG FNFFVVG LGTGNYSK KDSNKFNLVDPVERNTVGVPSGGWAA  
IRFRADNPGVWFMHCHLEVHTTWGLKMAFLVENGKGNQSIRPPPSDLPKC

> AT5G03260 (Lac11)

MKMGFLFLFCYLLAFLGYSPVDA AVKKYQFDVQVKNISRICNAKPIVTVNGMFPGP TVYAREG  
DRVIINVTNHVQYNMSIHW HGLKQYRNGWADGPAYITQCPIQTGQSYLYDFNVTGQRGTLW  
WHAHILWLRATVYGAIVILPAPGKPYFPQP YQESNIILGEWWNKDVETAVNQANQLGAPP  
MSDAHTINGKPGPLFPCSEKHTFVIEAEAGKTYLLRIINAALNDELFFGIAGHNMTVVEIDAVYT  
KPF TTKAILLPGQTTNVLVKTDRSPNRYFMAASPFMDAPVSVDNKTVTAILQYKGPNTVLP  
ILPKLPLPNDTSFALDYNGKLKSLNTPNFALVPLKVD RRLFYTIGLGINACPTCVNGTNLAASI  
NNITFIMPKTALLKAHYSNISGVFR TD FDRPPKAFNYTGVPLTANLGTSTGTRLSRVKFNTTI  
ELVLQDTNLLTVESH PFHLHGYNFFVVG TGVGNFDPK KDPKFNLDPPERNTVGVPTGGWA  
AIRFRADNPGVWFMHCHLEVHTMWGLKMAFVVENGETPELSVLPPP KDYPSC

> AT5G05390 (Lac12)

MTTVHTFSILLFFCSLFSASLI AKVQHHD FVIQETPVKRLCKTRNAITVNGMFPGP TLEVNNGD  
TLEVKVHNRARYNITIHWHGVRQIR TGWADGPEFVTQCPIRPGKSYTYRFTIQGQEGTLWWH  
AHSSWLRATVYGALIIHPTPGSSFPKPD RQTALMLGEWWNANPVDVINQATRTGAAPNIS  
DAYTINGQPGDLYNCSTKETV VVPINSGETSLLRVINAALNQLFFTVANHKLTVVGADASYLK  
PFTTKVLMLGPGQTTD VLLTADQPPKRYIIAARAYQSAQNAPFDNTTTT TAILQYKKT TTTTSKPI  
MPVLP AFNDTNTVTSFSRKF KSLRN VVPKTIDDNLFFTIGLGLDNC PKKFPKSR CQGLNGTRF  
TASMNNVSFVLP SNFSLQAHSNGIPGVFTTDFPSKPPVKFDYTGNNISRALFQPVKGTKLYKL

KYGSRVQVVLQDTNIVTSENHPIHLHGDFYIVGEGFGNFPKDKTSKFNLVDPPLRNTVAVP  
VNGWAVIRFVADNPGVWLMHCHLDVHIKWGLAMAFLVDNGVGELETLEAPPHDLPIC

> AT5G07130 (Lac13)

MEQLRPFLLLAIFVASLVNAEVHFHEFVIQETPVKRLCRVHNSITVNGQFPGPTLEVRNGDSL  
VITAINKARYNISLHWHGIRQMRNPWADGPEYITQCPIQPGGSYTYRFTMEDQEGTLWWHAH  
SRWLRATVYGALIIRPPLSSPHYFPFVIPKREITLLLGEWWDNRNPMVDLNLAQFTGAAPNISDA  
FTINGQPGDLYRCSSQETLRLFLVGSGEIVLLRVINSALNQELFFGVANHKLTVVAADASYTKPFS  
TNVIMLPGGQTTDVLTTADQPPAHYYMAAHAYNSANAAFDNTTTTAILKYKDASCVTLQAKS  
QARAIPAQLPGFNDTATAAAFTAQMKSPSKVKVPLEIDENLFFTVGLGLFNCPTPNTQRCQGP  
NGTRFTASINNVSFVFPKQNSIMQAYYQGTPTGVFTTDFPPTPPVTFDYTGNSRGLWQPTRG  
TKAYKLFNSQVQIILQDTSIVTTENHPMHLHGYEFYVVGTVGVGNFNPNTDTSSFNLDPPRRN  
TIGTPPGGWVAIRFVANNPGAWLMHCHIDSHIFWGLAMVFLVENGEHLQSVQSPPLDLPQC

> AT5G09360 (Lac14)

MEFKLNIPNTIHKTLQTIVFFLVLLAFQIAEAEIHHHTFKIKSKAYTRLCNTNKILTVNGEFPGP  
TLKAYRGDKLIVNVINNANYNITLHWHGARQIRNPWSDGPEYVTQCPIRPGESYVYRIDLKVEE  
GTIWWHAHSQWARATVHGAFIVYPKRGSSYPFKPHREIPLILGEWWKKNIMHIPGKANKT  
GGEPASDSYTINGQPGYLYPCSKPETFKITVVRGRRYLLRIINAVMDEELFFAIANHTLTVVAK  
DGFYLKHFKSDYLMITPGQSMVDLLHANQRPNHYFVAARAYSSAFGAGFDKTTTTAILQYKGD  
TLNRIKPILPYLPPYNRTEASTRFTNQFRSQRPVNVVKINTRLLYAISVNLMNCSDDRPCTGPF  
GKRFSSINNISFVNPSVDILRAYRHIGGVFQEDFPRNPPTKFNYTGENLPFPTRFGTKVVLD  
YNSSVELILQGTTVWASNIHPIHLHGYNFYVVGSGFGNFDRRKDPLRYNLVDPPEETTVGVPR  
NGWTAVRFVANNPGVWLLHCHIERHATWGMNTVFIVKDGPTKSSRMVKPPPDLPC

> AT5G48100 (Lac15)

MSHSFFNLFLISLFLYNNCIAHHYFTVREVPYTKLCSTKAILTVNSQFPGPIIKVHKGDTIYVNV  
QNRASENITMHWHGVEQPRNPWSDGPEYITQCPIRPGSDFLYKVFISIEDTTVWWHAHSSWT  
RATVHGLIFVYPRPPQILPFPKADHEVPILGEWWKRDVREVVVEEFVRTGGAPNVSDALTINGH  
PGFLYPCSKSDTFHLTVEKGTKYRIRMVNAAMNLPFFAIANHSLTVVSADGHYIKPIKATYITI  
SPGETLDMLLHADQDPERTYYMAARAYQSGNIDFNNSTTIGILSYTSSCKAKTSSFSGYPTLPF  
YNDTSAAFGFFTKIKCLFSGQVPVQISRRIITTVSINLRMCPQNSCEGPNGSRLAASMNNISFVTP  
SHVDILKAYYYHIKGVYGRFPEFPPLIFNFTAENQPLFLETPLATEVKVIEFGQVVELVIQGT  
LVGGGLDHPMHLHGFSFYVVGFGNYNISEEDPSSRYNLYDPPYKNTMTVPRNGWIAIRFVA  
DNPGVWFMHCHLDRHQTWGMNVVFIVKNGREPQQILPPPDDLPCYE

> AT5G58910 (Lac16)

MTNTTKLCSSKPIVTVNGQFPGPTIVAREGDTILIKVVNHVKYNVSIHWTGWADGPAYITQCPI  
QPGQNYLHNFTLTGQRGTLWWHAHILWLRATVHGAIIVLPKLGVPYFPKPYKEKTIVLSEW  
WKSDVEELINEASRIGTAPSASDAHTINGHSGSISNCPSQSSYGLPVRAGKTYMLRIINAALNEE  
LFFKIAGHVLTVEVDVAVYTKPYKTDTVFIAPGQTTNVLLTANANAGSNYMVAATTTDAHIP  
YDNVTATATLHYIGHTSTVSTSKKTVLASLPPQNATWVATKFRSLRSLNSLEYPARVPTTVE  
HSLFFTVGLGANPCQSCNNGVRLVAGINNVFTMPKTALLQAHFFNISGVFTDDFPAKPSNPY  
DYTAPVKLGVNAATMKGTKLYRLPYNATVQIVLQNTAMILSDNHPFHLHGFFNFVGRGLGN  
FNPEKDPKAFNLVDPVERNTVGVVAGGWTAIRFIADNPGVWFMHCHLELHTTWGLKMAFVV  
DNGHGPDQSLPPPADLPKC

> AT5G60020 (Lac17)

MALQLLLAVFSCVLLLPQPAFGITRHYTLEIKMQNVTRLCHTKSLVSVNGQFPGPKLIAREGDQ  
VLIKVVNQVPNNISLHWHGIRQLRSGWADGPAYITQCPIQTGQSYVYNYTIVGQRGTLWYHAH  
ISWLRSTVYGPLIILPKRGVPYPFAKPHKEVPMIFGEWFNADTEAIRQATQTGGGPNVSDAYTI  
NGLPGPLYNCSAKDTFRLRVKPGKTYLLRLINAALNDELFFSIANHTVTVVEADAIYVKPFETE  
TILIAPGQTTNVLLKTKSSYPSASFFMTARPYVTGQGTFDNSTVAGILEYEPKQTKGAHSRTSI  
KNLQFKPILPALNDTNFATKFSNKLRLNSKNFPANVPLNVDRKFFFTVGLGTNPCNHKNNQ  
TCQGPTNTTMFAASISNISFTMPTKALLQSHYSGQSHGVYSPKFPWSPIVPFNYTGTPPNNTM  
VSNGTNLMVLPYNTSVELVMQDTSILGAESHPLHLHGFNFVVGQGFNFDPNKDPRNFNLV  
DPIERNTVGVPSGGWAAIRFLADNPGVWFMHCHLEVHTSWGLRMAWLVLVDG  
DKPDQKLLPPPADLPKC

## Supplemental Table S3. List of genes co-expressed with *BdLAC5*

TranscriptID	Annotation
Bradi1g66720.1	<a href="#">laccase precursor protein, putative, expressed</a>
Bradi5g25090.1	IQ calmodulin_binding motif family protein, putative, expressed
Bradi5g04540.1	zinc finger, C3HC4 type domain containing protein, expressed
Bradi2g55340.1	transmembrane amino acid transporter protein, putative, expressed
Bradi2g46410.1	glycosyltransferase family 43 protein, putative, expressed
Bradi2g00880.1	No annotation
Bradi4g25540.1	BTB9 _ Bric_a_Brac, Tramtrack, Broad Complex BTB domain
Bradi2g54680.1	<a href="#">laccase precursor protein, putative, expressed</a>
Bradi2g17067.1	auxin_responsive protein, putative, expressed
Bradi1g67870.1	expressed protein
Bradi4g23910.1	KIP1, putative, expressed
Bradi4g29290.1	serine/threonine_protein kinase, putative, expressed
Bradi1g74320.1	<a href="#">laccase_22 precursor, putative, expressed</a>
Bradi5g20130.1	MYB family transcription factor, putative, expressed
Bradi1g28366.1	alpha_1,2_fucosidase, putative, expressed
Bradi1g21300.1	dehydrogenase, putative, expressed
Bradi3g59730.1	HEAT repeat family protein, putative, expressed
Bradi2g23300.1	expressed protein
Bradi3g16530.1	<a href="#">O_methyltransferase, putative, expressed</a>
Bradi1g67460.1	phospholipase A2, putative, expressed
Bradi4g37980.1	cell cycle control protein, putative, expressed
Bradi1g09460.1	endoglucanase, putative, expressed
Bradi1g25117.1	CSLF2 _ cellulose synthase_like family F
Bradi5g15490.1	ARPC2B, putative, expressed
Bradi2g46197.1	no apical meristem protein, putative, expressed
Bradi4g22250.1	dirigent, putative, expressed
Bradi2g54240.1	respiratory burst oxidase, putative, expressed
Bradi3g37530.1	ferric reductase, putative, expressed
Bradi3g47950.1	expressed protein
Bradi3g48730.1	DUF869 domain containing protein, expressed
Bradi3g32180.1	expressed protein
Bradi2g47330.1	MDR_like ABC transporter, putative, expressed
Bradi4g06680.1	expressed protein
Bradi4g31130.1	ferric reductase, putative, expressed
Bradi3g36887.1	<a href="#">cinnamoyl_CoA reductase, putative, expressed</a>
Bradi2g08790.1	Cupin domain containing protein, expressed
Bradi5g14720.1	transferase family protein, putative, expressed
Bradi5g23460.1	shikimate kinase, putative, expressed
Bradi5g12460.1	uncharacterized Cys_rich domain containing protein
Bradi2g49040.1	respiratory burst oxidase, putative, expressed
Bradi3g05750.1	AMP_binding domain containing protein, expressed
Bradi1g35477.1	STRUBBELIG_RECEPTOR FAMILY 7 precursor, putative
Bradi1g75350.1	RING finger and CHY zinc finger domain_containing protein 1
Bradi2g21300.1	<a href="#">cytochrome P450, putative, expressed</a>

Bradi1g54420.1	expressed protein
Bradi2g52060.2	membrane protein, putative, expressed
Bradi3g37230.1	GDU1, putative, expressed
Bradi1g06290.1	fasciclin domain containing protein, expressed
Bradi2g55730.1	cytochrome P450, putative, expressed
Bradi1g31820.1	vacuolar_sorting receptor precursor, putative, expressed
Bradi1g14050.1	uncharacterized protein At4g06744 precursor, putative
Bradi5g16060.1	expressed protein
Bradi5g09130.1	expressed protein
Bradi2g55720.1	hemerythrin family protein, expressed
Bradi4g21790.1	peptide transporter PTR2, putative, expressed
Bradi4g28260.1	hydroxyproline_rich glycoprotein family protein, putative
Bradi4g44860.1	PMR5, putative, expressed
Bradi2g26770.1	annexin, putative, expressed
Bradi5g02460.1	cytochrome P450 93A2, putative, expressed
Bradi3g09500.1	sulfotransferase domain containing protein, expressed
Bradi1g03940.1	leaf senescence related protein, putative, expressed
Bradi3g39800.1	citrate transporter, putative, expressed
Bradi1g68710.2	microtubule associated protein, putative, expressed
Bradi2g37970.1	glycosyltransferase family 43 protein, putative, expressed
Bradi2g23370.1	<b>laccase precursor protein, putative, expressed</b>
Bradi1g32850.1	RIC10, putative, expressed
Bradi1g57607.1	Homeobox domain containing protein, expressed
Bradi1g60750.1	phospho_2_dehydro_3_deoxyheptonate aldolase, expressed
Bradi2g12150.2	S_adenosylmethionine synthetase, putative, expressed
Bradi3g28350.1	CESA7 _ cellulose synthase, expressed
Bradi2g10302.1	flavin monooxygenase, putative, expressed
Bradi4g21240.1	plant_specific domain TIGR01627 family protein, expressed
Bradi4g21220.1	auxin_induced protein 5NG4, putative, expressed
Bradi2g59410.1	exostosin family domain containing protein, expressed
Bradi4g33490.1	fasciclin domain containing protein, expressed
Bradi5g15527.1	<a href="#">Os4bglu14 _ monolignol beta_glucoside homologue</a>
Bradi1g59880.2	COBRA_like protein precursor, putative, expressed
Bradi2g56970.1	amino acid transporter, putative, expressed
Bradi5g01737.1	peptide transporter PTR2, putative, expressed
Bradi2g16337.1	CGMC_MAPKCMGC_2.8 _ CGMC
Bradi1g17242.1	serine hydrolase domain containing protein, expressed
Bradi3g49260.1	<a href="#">phenylalanine ammonia_lyase, putative, expressed</a>
Bradi2g47600.1	zinc finger, C3HC4 type domain containing protein, expressed
Bradi2g19160.1	anthocyanidin 5,3_O_glycosyltransferase, putative, expressed
Bradi1g00710.1	expressed protein
Bradi1g07060.1	expressed protein
Bradi4g30437.1	methyladenine glycosylase, putative, expressed
Bradi1g10470.1	MYB family transcription factor, putative, expressed
Bradi1g34670.1	glycosyltransferase, putative, expressed
Bradi2g24010.1	protein kinase, putative, expressed
Bradi2g34790.1	GDSL_like lipase/acylhydrolase, putative, expressed
Bradi1g65530.1	expressed protein



Bradi3g38950.1	methyladenine glycosylase, putative, expressed
Bradi5g18150.1	expressed protein
Bradi2g12370.1	GDSL_like lipase/acylhydrolase, putative, expressed
Bradi2g47590.1	MYB family transcription factor, putative, expressed
Bradi3g56787.1	polygalacturonase, putative, expressed
Bradi3g00377.1	rhodanese_like domain containing protein, putative, expressed
Bradi3g42430.1	MYB family transcription factor, putative, expressed
Bradi4g27720.1	expressed protein
Bradi3g41210.1	microtubule associated protein, putative, expressed
Bradi1g22980.1	formin, putative, expressed
Bradi2g17680.3	CPuORF26 _ conserved peptide uORF_ containing transcript
Bradi3g40820.1	membrane protein, putative, expressed
Bradi3g04080.1	endoglucanase, putative, expressed
Bradi2g49912.1	CESA4 _ cellulose synthase, expressed
Bradi4g34300.1	membrane protein, putative, expressed
Bradi4g30540.1	CESA9 _ cellulose synthase, expressed
Bradi3g06480.1	dehydrogenase, putative, expressed
Bradi1g59160.1	flavin_ containing monooxygenase family protein, putative
Bradi2g11500.1	kelch motif family protein, putative, expressed
Bradi1g23620.1	expressed protein
Bradi2g18447.1	sulfotransferase domain containing protein, expressed
Bradi1g72350.1	glycosyl transferase, putative, expressed
Bradi1g17830.1	potassium transporter, putative, expressed
Bradi1g10660.1	histidine kinase, putative, expressed
Bradi3g49250.2	<a href="#">phenylalanine ammonia_lyase, putative, expressed</a>
Bradi3g05860.1	flavin_ containing monooxygenase family protein, putative
Bradi2g23530.1	homeodomain protein, putative, expressed
Bradi1g17680.1	B3 DNA binding domain containing protein, putative
Bradi1g69870.1	ATMAP70 protein, putative, expressed
Bradi1g65430.1	chloroplast unusual positioning protein, putative
Bradi4g16560.1	cytochrome P450, putative, expressed
Bradi2g45090.1	zinc finger C_x8_C_x5_C_x3_H type family protein
Bradi2g11010.1	TsetseEP precursor, putative, expressed
Bradi1g64560.1	glycosyltransferase, putative, expressed
Bradi2g58490.1	rho GDP_dissociation inhibitor 1, putative, expressed
Bradi4g36240.1	endoglucanase, putative, expressed
Bradi5g15850.1	transporter_related, putative, expressed
Bradi4g42400.1	RCN1 Centroradialis_like1 homologous to TFL1 gene
Bradi1g04750.1	expressed protein
Bradi2g16560.1	fasciclin domain containing protein, expressed
Bradi1g51960.1	RGH2B, putative, expressed
Bradi5g08907.1	heparan_alpha_glucosaminide N_acetyltransferase, putative
Bradi4g40400.1	plant_specific domain TIGR01627 family protein, expressed
Bradi3g56290.1	bZIP transcription factor domain containing protein, expressed
Bradi3g33070.1	expressed protein
Bradi4g05450.1	isoflavone reductase homolog

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This list was generated by PlaNet platform using BdLAC5 as bait with default parameters. Laccases were labeled in red , some other lignin related genes were in blue.

Supplemental Table S4. Anatomical comparison in different genotypes.

Genotype	Stem Height (cm)	Internode Diameter ( $\mu\text{m}$ )	Vascular Bundles Area ( $\mu\text{m}^2$ )	Cell Wall Thickness ( $\mu\text{m}$ )
Bd21-3 WT	37.7 $\pm$ 3.7 a	946 $\pm$ 56 a	5134 $\pm$ 474 a	2.53 $\pm$ 0.19 a
Bd4442 HO	31.3 $\pm$ 1.4 b	811 $\pm$ 79 b	4634 $\pm$ 337 b	2.41 $\pm$ 0.33 a
Bd4442 CP3	37.4 $\pm$ 1.6 a	923 $\pm$ 31 a	5214 $\pm$ 162 ab	2.47 $\pm$ 0.15 a
Bd5024 HO	39.7 $\pm$ 2.3 a	973 $\pm$ 64 a	5536 $\pm$ 441 a	2.53 $\pm$ 0.17 a

The data represent means  $\pm$  standard deviation from biological replicates (n = 6). Letters indicate significant differences analyzed by one-way ANOVA (Tukey's HSD,  $P < 0.05$ ).

Supplemental Table S5. Quantification of thioglycolic acid lignin.

Genotype	Relative TGA Lignin Content (%)
Bd21-3 WT	100.0±2.5
Bd4442 HO	86.0±3.5
Bd4442 CP3	93.3±2.8
Bd5024 HO	97.5±3.7

TGA lignin content are shown in percentages of control plants (*Bd21-3*). The data represent means ± standard deviation from biological replicates (n = 3).

## Supplemental Table S6. Primers

Name	Primer (5' --- 3')	Anotation
QBdUbi4-R	GAGGGTGGACTCCTTCTGGA	qRT-PCR of BdUBI4
QBdUbi4-F	TGACACCATCGACAACGTGA	
QBdLAC5-3F	ACACCTTCAATGTGACGATGAAG	qRT-PCR of BdLAC5
QBdLAC5-3R	CTCACGCCGTGCCAGTGGATGGT	
QBdLAC6-3R	CTTACCCCATGCCAGTGGATGGTA	qRT-PCR of BdLAC6
QBdLAC6-3F	TACAAGTTCAATGTGGTTATGAGG	
BdLAC5probe-3F	GATAACCCCGGTGTGTGGTTCATG	synthesis of BdLAC6 anti-sense probe for in situ hybridization
BdLAC5probe-3R	TGTAATACGACTCACTATAGGGCTTGA ACAGAACTTCGATCGA	
BdLAC5probeCK-3F	TGTAATACGACTCACTATAGGGCGATAA CCCCGGTGTGTGGTTCATG	synthesis of BdLAC5 sense probe for in situ hybridization
BdLAC5probeCK-3R	TTCGAACAGAACTTCGATCGA	
BdLAC6probe-3F	TACAAGTTCAATGTGGTTATGAGG	synthesis of BdLAC6 anti-sense probe for in situ hybridization
BdLAC6probe-3R	TGTAATACGACTCACTATAGGGCCTTGA ACCCATCTTGTGAGGAAGC	
BdLAC6probeCK-3F	TGTAATACGACTCACTATAGGGCTACAA GTTCAATGTGGTTATGAGG	synthesis of BdLAC6 sense probe for in situ hybridization
BdLAC6probeCK-3R	CTTGAACCCATCTTGTGAGGAAGC GGGGACAAGTTTGTACAAAAAAGCAGGC	
GWBdLAC5cdnaF	TTCCACGAGCGCACGCTGTGGCTC GGGGACCACTTTGTACAAGAAAGCTGG	clone of BdLAC5 full length cDNA
GWBdLAC5cdnaR	GTCGCTTCGAACAGAACTTCGATCG	
HPT-F	CGCACAAATCCCACTATCCTTCGCAA	verification of BdLAC5 complementation lines
HPT-R	GGCAGTTCGGTTTCAGGCAGGTCTT	
proZmUBI-F	GGCACCTCCGCTTCAAGGT	verification of BdLAC5 complementation lines
4442cp-R	CTCACGCCGTGCCAGTGGATGGT	