

Figure S1. Biosynthetic pathway for cellulose in plants. SUCROSE PHOSPHATE SYNTHASE (SPS), SUCROSE PHOSPHATE PHOSPHATASE (SPP), FRUCTOKINASE (FK), PHOSPHOGLUCOMUTASE (PGM), GLUCOSE-6-PHOSPHATE ISOMERASE (GPI), SUCROSE SYNTHASE (SUS), HEXOKINASE (HXK), UDP-GLUCOSE PYROPHOSPHORYLASE (UGP) AND CELLULOSE SYNTHASE (CESA).

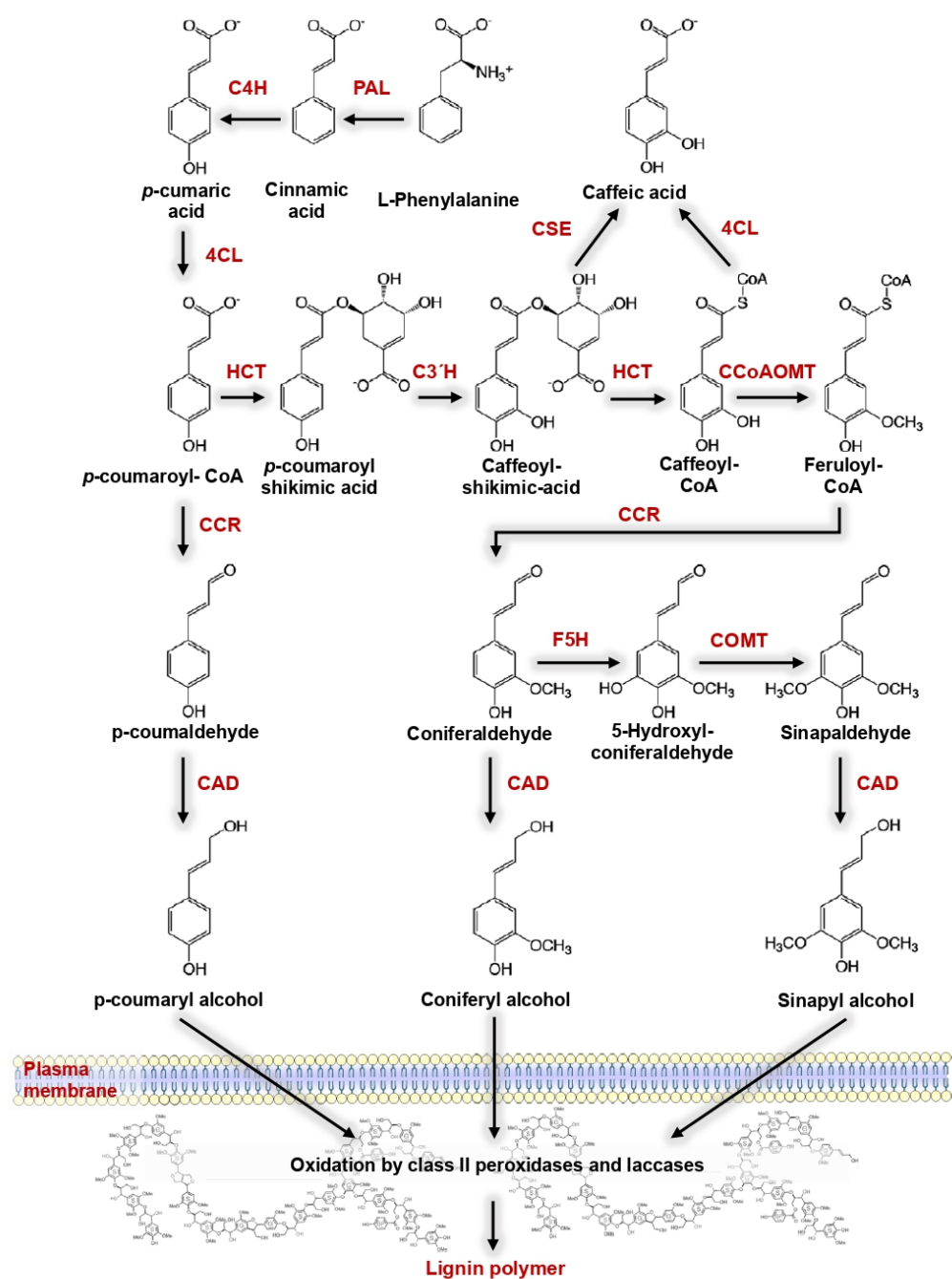


Figure S2. Biosynthetic pathway for lignin in plants. L-PHENYLALANINE AMMONIA-LYASE (PAL), CINNAMIC ACID 4-HYDROXYLASE (C4H), 4-HYDROXYCINNAMATE COA LIGASE (4CL), CAFFEYOYL SHIKIMATE ESTERASE (CSE), HYDROXYCINNAMOYL COA: SHIKIMATE HYDROXYCINNAMOYL TRANSFERASE (HCT), COUMARATE 3-HYDROXYLASE (C3H), CAFFEYOYL COA 3-O-METHYLTRANSFERASE (CCoAOMT), CINNAMOYL COA REDUCTASE (CRR), FERULIC ACID/CONIFERALDEHYDE 5-HYDROXYLASE (F5H), CAFFEIC ACID 3-O-METHYLTRANSFERASE (COMT) and CINNAMYL ALCOHOL DEHYDROGENASE (CAD).

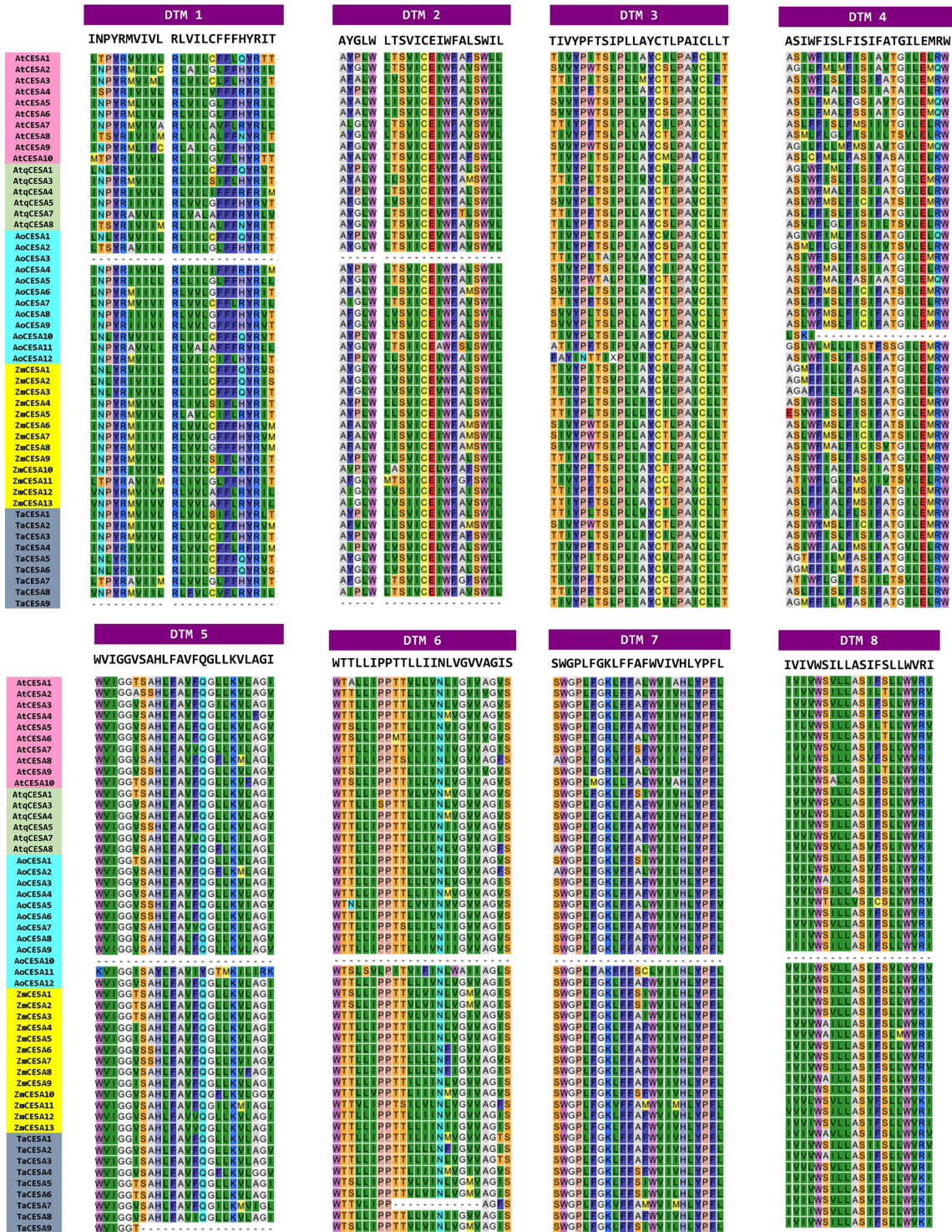


Figure S3. AtqCESA proteins have conserved transmembrane domains. Eight transmembrane domains (TMD) previously characterized in *A. thaliana* (AtCESA) were found to be conserved in *A. tequilana* (AtqCESA) respect to other species analyzed. *A. officinalis* (AoCESA), *Z. mays* (ZmCESA), *T. aestivum* (TaCESA). Consensus residues are indicated for each TMD.

	20	40	60	80	100	
AtCAD1	-----	-----	-----	-----	-----	MSSSESVENECMCAARDPSGLLSPHTITRRSVTTDDVSLTITHCGVCYADVIISRN 57
AtCAD2	-----	-----	-----	-----	-----	MVDQNKAFGWAANDESGVLSPFHFSRRENGENDVTVKILFCGVCHSDLHTIKN 53
AtCAD3	-----	-----	-----	-----	-----	MVDQNRADFWAANDESGVLSPFHFSRRENGENDVTVKILFCGVCHSDLHTIKN 53
AtCAD4	-----	-----	-----	-----	-----	MGSVEAGEKKALGWAARDPSGVLSPYSYTLRSTGADDVYIKVICCGICHTDIHQIKN 57
AtCAD5	-----	-----	-----	-----	-----	MGIMEAERKTTGWAARDPSGILSPYTYTLRETGPENVRIRIICCGICHTDLHQTKN 56
AtCAD6	-----	-----	-----	-----	-----	MERLSGEKEQSVEAFGWAARDSSGHLSPFVFSRRKTGEEEVNRVKVLYCGICHSDLHCLKN 60
AtCAD7	-----	-----	-----	-----	-----	MGKVLKEAFGLAAKDESGILSPFSFRRATGEKDVRFKVLFCGICHTDLSMAKN 55
AtCAD8	-----	-----	-----	-----	-----	MGKVLQKEAFGLAAKDN SGVLSPFSTTRRETGEKDVRFKVLFCGICHSDLHMVKN 55
AtCAD9	-----	-----	-----	-----	-----	MAKSPETEHPNKFVWGARGDSGLSPFHFSSRRDNGENDVTVKILFCGVCHTDLHTIKN 59
AtqCAD1	-----	-----	-----	-----	-----	MDAESGNCLGWAARDTSGALSPYKFSRRSLGNEDISVRITHCGVCYADVIITRN 54
AtqCAD2	-----	-----	-----	-----	-----	MEAKENGKQAAPAAEQRRREAVGWAARDSSGILSPFSFSSRRNNGDDVTLKIMYCGICHSDLSIKN 66
AtqCAD3	-----	-----	-----	-----	-----	MAMEQEPQKAIGWAAKDSGVSPFSFTRRANGDHDVTIRILYCGICHTDLHYAKN 56
AtqCAD4	-----	-----	-----	-----	-----	MAELHTAFGWAARDATGILSPFNSTRAIGDNDVTLKILYCGICHTDLHTIKN 53
AtqCAD5	-----	-----	-----	-----	-----	MGSVASERTVTGWAAKDASGVLSPYTYSLRPTGAEDVVVKVLYCGVCHTDLHQTRN 56
AtqCAD6	-----	-----	-----	-----	-----	MVVAANGTKASSPETEHPKAFGWAARDSSGVLSPFTFSRRNNGDDVTLKILYCGICHSDLHTIKN 67
AtqCAD7	-----	-----	-----	-----	-----	MDTKSGNGDCLGWAARDVSGVLSPYKFSRRVVGSDVSLKITHCGVCYADVIITRN 56
ZmCAD1	-----	-----	-----	-----	-----	MAPVEAEQHRRRALALAHDASGAVSPIRISRRDTGDDVAIQILYCGICHSDLHTIKN 59
ZmCAD2	-----	-----	-----	-----	-----	MAAESENGNCCKAWAARDPSGVLSPHSFNRRRAVQSGDVSLLKIIYCGVCYADVAITRN 56
ZmCAD3	-----	-----	-----	-----	-----	MGSLASERKVVGWAARDATGHLSPYSYTLRNTGPEDVVVKVLYCGICHTDLHQAKN 56
ZmCAD4	MSYHCRVLPVPFHYPPGAGARVGAGAGSPFPSASRALRLPRPRASVEKREQVAAMEEQGGGAALGWAARDSSGVLSPYSFSSRRVPKDDVTIKVLYCGICHTDLHTIKN 110					
TaCAD1	-----	-----	-----	-----	-----	MGSVDASETTVTGWAARDATGHLSPYRYTLRKTGPEDVVLKVYCYGICHTDVHQVKN 57

	120	140	160	180	200	220							
AtCAD1	QHGD	SKYPLVP	GHEIAGIVTKVGNPVRQRFKVG	DHVGVTYVNSCRECEYCN	EGQEVNCAKGVFTFNGIDHDG--SVTKGGYSSHIVH	ERYCYKIPVDYPLESAAPLLC	164						
AtCAD2	HMGFS	RYPIIP	GHEIVGIATKVGKNVTKFKEGDRVGV	GIIGSCQSCESCNDLENYCPKVVFTYNSRSDG--TSR	QGGYSDVIVVDH	RFVLSIPDGLPSDSGAPLLC	161						
AtCAD3	HMGFS	RYPIIP	GHEIVGIATKVGKNVTKFKEGDRVGV	GIIGSCQSCESCNDLENYCPKVVFTYNSRSDG--TR	NQGGYSDVIVVDH	RFVLSIPDGLPSDSGAPLLC	160						
AtCAD4	DLGMS	NYPMVP	PGHEVVG	EVGSDVSKFTVGDVVG	VGVVGGCGSCKPCSSLEQYCNK--RINSYNDVYTDG--KPTQGGFADTMIVNQKFVVKI	PEGMAVEQAAPLLC	164						
AtCAD5	DLGMS	NYPMVP	PGHEVVG	EVGSDVSKFTVGDVVG	VGVVGGCGSCKPCERDLEQYCPK--KINSYNDVYING--QPTQGGFAKATVVHQFVVKI	PEGMAVEQAAPLLC	163						
AtCAD6	EWHS	SIYPLVP	GHEI	GEVSEIGNKVS	KNLGD	KVGVGCI	VDSCRTCESCREQENYCTK--AIATYNGVHHDG--TINYGGYSDHIVDERYAVKIPHTLPLVSAAPLLC	167					
AtCAD7	EWGL	TTYPLVP	GHEIVGV	TEVGA	KVKFNAGDKVGV	GMAGSC	RCSDCNDG	ENYCPK--MILTS	GAKNFDD--TMTGGYSDH	MVCAEDFIIRIPDNPLDGAAPLLC	162		
AtCAD8	EWGM	STYPLVP	GHEIVGV	TEVGA	KVKFKTGEK	VGVGLVSS	CGSCDSCTEGMENYCPK--SIQTYGFPYYDN--TITYGGYSDH	MVCEEGFVIRIPDNPLDAAAPLLC	162				
AtCAD9	DWGS	YYPVVP	PGHEIVGIATKVGKNVTKFKEGDRVGV	GISGSCQSCESCNDLENYCPQ--MSFTYNAIGSDG--TK--NYGGYSE	NIIVDQRFVLRFPENLPSDSGAPLLC		166						
AtqCAD1	KVGDS	NYPLVP	GHEIVGV	TFG	SNVRQRFKVG	DHVG	VGYAVNSCRDCQYCN	EQLEVYCSKGITFTFNAPDSG--TFTKGGYSSYIVVHNR	YCYKIPDGYPLAKAAPLLC	162			
AtqCAD2	DWGT	TRYPLV	AGHEIAGIVTEVGNVQKFKIGDKVGV	GVGIVGSCRCSCQSCQDLENYCPN--LI	FTYNSIDNDG--TVTYGGYSNMLVNEHF	AVKFPDNPLD	KGAPLLC	173					
AtqCAD3	DHGF	SLYPIVP	GHEIMGEVTRIGSKVKFKVGD	KVGVGCLVVRTCGECENC	RGDLECYCPK--PVYTYNSVDHDG--SVTYGGYSNQI	VDEHYAIRVPHNPLD	SAAPLLC	163					
AtqCAD4	DFGIS	MPVVP	PGHEIVGV	TEAGNR	VRKFRKRGDKIGV	GMVGS	SACDCAQGFENYCPK--IVPTNSGIRSDG--TITYGGFADKL	VVDEHF	AVRLPENL	DLDKAAPLLC	160		
AtqCAD5	HLGMS	NYPMVP	PGHEVVG	EVGSGV	GKCRVGDVVG	AGCIVGCC	RECGPC	KANIEQYCSK--KINSYNDVYTDG--KPTMGGFASAMVVDQKFVVKI	PAGLAPEQAAPLLC	163			
AtqCAD6	EWQNT	SYPVVP	PGHEIVGV	TEVGS	NVNVKFKVGD	KVIGICMVES	CRSCDSCNQHL	ENYCPK--IIFTYNSINKD--TKTYGGYS	DMIVNEHFVVKFENMPLD	KGAPLLC	174		
AtqCAD7	KFGDS	NYPLVP	GHEIVGV	IEGS	NVHKFKVGD	HVGVTYVNS	CRDCENCNE	YQETHCSK--ITSTYNSLDLDG--TFTKGGFSNYI	IVHD	RYCYKIPVGYPLAMAAPLLC	163		
ZmCAD1	EWKN	NANYPV	VPGHEIAGLITEVGNV	KFRFNVGD	KVGVGCMVNTCQSC	ESCEGGHENYCSK--IIFTYNSH	DRD--TVTYGGYS	DMVVNERFVIRF	PDGMPLDRGAPLLC	166			
ZmCAD2	KLND	SKYPLVP	GHEIAGVVTQVGADV	KGKFKVGD	HVGVTYVNS	CRDCENCNISLDNHCPK--AVYTFNGIDTDG--TVTKGGY	STHIVH	ERYCFKIPDGYPLAKAAPLLC	163				
ZmCAD3	HLGAS	KYPMVP	PGHEVVG	EVGPEVAKYGVGD	VVGVI	VGCCRE	CSPCANVEQYCNK--KINSYNDVYTDG--RPTQGGFASAMVVDQKFVVKI	PAGLAPEQAAPLLC	163				
ZmCAD4	DWRN	AMYPVVP	PGHEIVGV	TVGGGV	TRFKAGD	TVGVGVFVGS	CRSCDSCGK	GDDNYCAG--IVLTSNGVD	HAHGGAPTRGGFSDVL	VASEHYVVRP	DGLALDR	TAPLLC	219
TaCAD1	DLGAS	KYPMVP	PGHEVVG	EVGPEVSKFRAGD	VVGVI	VGCCRC	CRCPKANVEQYCNK--KINSYNDVYTDG--KPTQGGFASAMVVDQKFVVKI	PAGLAPEQAAPLLC	164				

	240	260	280	300	320								
AtCAD1	AGITVYAPMMRHN	MN--QPGKSLG	VIGLGLGLGHMAV	KFGKAFGLSVTVF	STSISKKEEALNLLGAENF	VISSDHDQMKALEKSLDFLVD	TASGDHAFDPYMSLLK	IAGTYV 273					
AtCAD2	AGITVYSPMKYYG	MTKESGKRLGVN	GLGLGHI	IAVKIGKAFGLRVT	VISRSSEKERE	AIDRLGADSF	LVTTDSQKMK	EAVGTMDFIIDTVSAEHALLPLFSL	LKVNGKLV 271				
AtCAD3	AGITVYSPMKYYG	MTKESGKRLGVN	GLGLGHI	IAVKIGKAFGLRVT	VISRSSEKERE	AIDRLGADSF	LVTTDSQKMK	EAVGTMDFIIDTVSAEHALLPLFSL	LKVNGKLV 270				
AtCAD4	AGVTVYSPLSHF	GFLM--ASGLKGG	ILGLGGVGHMGVK	IAKAMGHVTVISS	SDKKKEEAIEHLGAD	DYVSSDPAEMQRLADS	LDYIIDTVPVF	HPLDPYLACL	KLDGKLI 273				
AtCAD5	AGVTVYSPLSHF	GFLK--QPGLRGG	ILGLGGVGHMGVK	IAKAMGHVTVISS	SNKKREALQDLGAD	DYVIGSDQAKMSELADS	LDYVIDTVPVH	HALEPYLL	LKLDGKLI 272				
AtCAD6	AGISMYSPMKYF	GFLT--GPDKHVG	IVGLGLGHI	GVRFKAFAGTKVT	VSSSTTGKSKDALD	TLGADGFLVSTDEDQ	MKAAMGTM	DGIIDTVSASH	SISPLIGLLK	SNGLKV 276			
AtCAD7	AGVTVYSPMKYH	GLD--KPGMHIG	VVLGLGLGHVAVK	FAKAMGKVT	VISTSERK	DEAVTRLGADAF	LVSRDPKQMKDAMG	TMDGIIDTVSATH	PLPLGLGL	KNKGKLV 271			
AtCAD8	AGITVYSPMKYH	GLD--KPGMHIG	VVLGLGLGHVAVK	FAKAMGKVT	VISTSEK	KEAEINRLGADAF	LVSRDPKQIKDAMG	TMDGIIDTVSATH	PLPLGLGL	KNKGKLV 271			
AtCAD9	AGITVYSPMKYYG	MT--EAGKHLG	VAGLGLGHVAVK	IGKAFGLKVT	VISSSTKAE	EAINHLAGDSF	LVTTDPQKMKAAIG	TMDYIIDTISAV	HALYPL	LGLLVN	GKLI 275		
AtqCAD1	AGITVYTPMIRH	RMN--QAGKSLG	VIGLGLGLGHMAV	KFGKFSGLRVT	VFTSASKD	EALKLLGADEFV	VSSDEKEMQSKANT	LDFILDTASGDH	PFDPYMSLLK	VGGVMS 271			
AtqCAD2	AGITVYSPMKNF	GFLN--EPGKHLG	VVLGLGLGHVAVK	FAKFGFMKVT	VISSSPSKEKEA	IERLGADSF	IVSSNPQIQAA	MGTM	DGIINTVSA	AAHITPLIF	LKPHGKMI 282		
AtqCAD3	AGITVYSPMKYF	GFLN--RPLGLH	VVLGLGLGHI	IAVKFGKAFGMKVT	VISTSPNKE	EAIERLGD	DAFLVSHNEEQMKA	AGISMDGIIDTVSAV	HPVAPFID	LKTHGKLI 272			
AtqCAD4	AGITVYSPMKYH	GLN--VPGKHLG	VVLGLGLGHVAVK	FAKAFGMKVT	VISSSPNKE	EAIEHFGADAF	LVSRNTEQMKAAIG	TMDGIIDTVSATH	PLPLGLGL	KNHGKMI 269			
AtqCAD5	AGVTVYSPLRH	FGLT--DPGLRGG	ILGLGGVGHMGVK	IAKAMGHVTVISS	SDKKRAEAMEHLGAD	AYLVSSDEAQMATT	LDSLDYIIDTVPVF	HPLPEPYLL	LKLVN	GKLI 272			
AtqCAD6	AGITVYSPMKQF	GFLN--EPGKHLG	VVLGLGLGHVAVK	FAKAFGMKVT	VISSSPSKEKEA	IERLGADAF	LSSNPEAMQAA	MGTM	DGIINTVSAV	HS	LVPLIF	LKLVH	GKMI 283
AtqCAD7	AGITVYSPMIQ	HKMN--QPGKSLG	VIGLGLGLGHMAV	KFGKAFGLKVT	VFTSASKKEEAL	KLLGAD	EFVSSDEKQMQSLKNS	LDFIIDTASGDH	PFDPYMSLLK	TRGVL 272			
ZmCAD1	AGITVYPMKHH	GLN--EAGKHIG	VVLGLGLGHVAVK	FAKAFGMKVT	VISTSPKKE	EAMETL	GADAFVSSGDANQ	MKAAGTMDG	IMNTAS	ASMSPYAL	LKPKQGKMI 275		
ZmCAD2	AGITVYTPMRRH	NMN--QPGKSLG	VIGLGLGLGHMAV	KFGKAFGLKVT	VFTSSEK	KEAEINRLGAD	NFVSSDTQ	QMESL	KNSLHF	IIDTASGDH	PFDPYMSLLK	VGGVMT 272	
ZmCAD3	AGVTVYSPLKH	FGLT--TPGLRGG	ILGLGGVGHMGVK	IAKAMGHVTVISS	SSKKRAEAM	DHLGAD	AYLVSSDAAAMG	PAADS	LDYIIDTVPV	HPLPEPYL	LKLDGKLV 272		
ZmCAD4	AGVTVYSPMRRH	GLN--EPGKHLG	VVLGLGLGHVAVK	FAKAFGMKVT	VISTSAS	KQEATENL	GADFEFLSR	DEDMQKAATG	TMDGIIDTVSA	WH	ITPL	LALLKPL	QGMV 328
TaCAD1	AGVTVYSPLKH	FGLM--TPGLRGG	ILGLGGVGHMGVK	IAKAMGHVTVISS	SNKKRAEAM	DDL	GADAYLVSSD	TQMAAA	ADSLDYIIDTV	PAKH	PLPEPYL	LALLKMDGKLV 273	

	340	360	380	400	420			
AtCAD1	LVGFPS-EIKISPA	NLNLGMRMLAGS	VTGGTKITQQMLDFCA	AHKIYPNIEVPIQK	INEALERVVKDIKYRF	VIDIKNSLK-----355		
AtCAD2	ALGLEKPLDLPTIFSLV	LGRKMVGGSQ	IGGMKETQEMLEFCA	HKIVSDIELIKMSD	INSAMDRLAKSDVRYR	RFVIDVANSLPESSAE	ILTEQVDHGVSITSRF376	
AtCAD3	ALGLEKPLDLPTIFPLV	LGRKMVGGSQ	IGGMKETQEMLEFCA	HKIVSDIELIKMSD	INSAMDRLVKS	SDVRYR	RFVIDVANSLPESSAE	ILTEHVDHGVSITSRF375
AtCAD4	LMGVINTPLQFVTPLV	LGRKVISGS	FISIKETE	EVLAFC	KEKGLTSTIETVKID	ELNIAFERLRKNDVRYR	RFVVDVAGSNLVEEA	ATTTN-----365
AtCAD5	LMGVINNPLQFLTPLL	MLGRKVITGS	FISGMKETE	EMLEFCKEGLSSI	IEVVKMDYVNTAFER	LEKNDVRYRFVVDVEG	SNLDA-----357	
AtCAD6	LLGATEKPFDISA	FSLILGRKSIAGS	GIGGMKETQEMIDF	AAEHGKAEIEIIS	MDYVNTAMDRLAKG	DVRYRFVIDISNTLA	ATRS-----363	
AtCAD7	MVGAPAEPLPVFLIF	LGRKMVGSMVGG	IKETQEMVDLAGKHNITADIEL	ISADYVNTAMERLAK	ADVRYRFVIDVANTM	KPTP-----357		
AtCAD8	MVGAPAEKPLEPVM	PLIFERKMVMGSM	IGGIKETQEMIDMAGKHNITADIEL	ISADYVNTAMERLEK	ADVRYRFVIDVANTL	KPNPNL-----359		
AtCAD9	ALGLEKPLEPMPFLV	LGRKMVGSDVGG	MKETQEMLDFCAKHNITADIELIK	MDEINTAMERLAKS	DVRYRFVIDVANSL	SPP-----360		
AtqCAD1	LVGFPS-EIKMHPG	SLIYGARTISGS	MTGGTKDTQEMLDFCA	ANKIYPDIEVPIQY	INEALERLIKDKVRYR	VIDIENSLK-----353		
AtqCAD2	LVGLPDKPFELPAYS	LLGGKILAGS	VMGGLKDTQEMIDFAGKHNITADIELI	CMDDVNKAMERLAKG	DVRYRFVIDVASS-----363			
AtqCAD3	VVGGIAEPLSVPTIPL	LLGRKLVAGSA	IGGIKETQEMIEFAAKHNIMADIEV	IPIDYISTAMERLAKG	DVRYRFVIDVANTL-----354			
AtqCAD4	NVGLPTKPM	EVPAFSLIQGGRT	LAGSVVGGMRDTQEMIDFAGKHNITAE	VEVVSMDYVNTAFERLAKG	DVRYRFVIDVANSLTPA-----354			
AtqCAD5	MMGVINQPMQFITP	MVLMGRKKTITGS	FISGMDTEQ	EVLEFCEKGLTSMIEMVKMDQVNEA	LERLERN	DVRYRFVVDVAGSNLD-----356		
AtqCAD6	MVGAPAEKPFELPV	FLIMAGKVL	AGSCTGGMKDTQEMIDFAGKHNVTADIEL	INMDYVNKAMERLAK	ADVRYRFVIDVANSLIAADQ-----370			
AtqCAD7	LVGAPS-EVKVEPR	SLIHGARTISGS	ATGGTKDTQEMLDFCA	AKKIYPEIEVPIQY	INEALERMIKRDVRYR	VIDIENSLK-----354		
ZmCAD1	LLGLEKPLQISAFSL	VTGGKTL	AGSCMGSIRDTQEMMDFAAKHGLAADIEL	IGTEEVNEAMERLAKG	EVRYRFVIDIGNTLNAAS	LGSSPVPAL-----370		
ZmCAD2	LVGFPS-EIKMHP	ASLILGARTLSGS	VVGGIKDIQEMVNFCAANNIYPEIEI	IKIDYINEALARLVN	RDVKYRFVIDIENS	FK-----354		
ZmCAD3	LLGVIGEPLSFVSP	MVLGRKAITGS	FIGSIDETA	EVLFQ	CDKGLTSQIEVVKMGYVNEA	LERLERN	DVRYRFVVDVAGSNVEAEAAAADAASN-----367	
ZmCAD4	VVGAPSKPLEPAY	IVPGGKGVAGNNVGS	VRDCQAMLEFAGKHGIGAEVEIKMDYVNTAMERLAK	NDVRYRFVIDVAGSLGSAA-----414				
TaCAD1	LMGVIAEPLSFVSP	MVLGRKKTITGS	FISGMDETE	EVLFQ	CDKGLTSQIEVVKMDYVNTAFER	LERLERN	DVRYRFVVDVGGSNIEDAA-----360	

Figure S4. Protein alignment for AtqCAD. Residues that compose the substrate-binding pocket of CAD proteins are highlight in color.

Table S1. Expression levels of genes involved in cellulose biosynthesis in *Agave tequilana* in several organs and tissues sampled. Values shown are transcripts per million (TPM).

Gene name	Root	Pine	Leaves	Shoot apical meristem	Anther	Ovary	Tepal	Pistil
<i>SPS1</i>	0	45.2085807	0	33.3521462	42.7731031	33.9497662	53.4816066	65.6248299
<i>SPS2</i>	19.9594525	62.7254275	468.275016	29.4269683	185.443037	290.997996	356.030153	426.843449
<i>SPP1</i>	230.695629	100.550917	151.241681	122.924041	76.4881824	146.36058	113.69358	142.560071
<i>SPP2</i>	13.1874954	17.3677454	7.38183532	22.1081965	18.0150436	14.8979562	26.4107889	22.9780923
<i>FK1</i>	23.5236405	8.74042843	13.0076393	2.84777113	3.63613798	0.57058431	30.6841143	18.8036762
<i>FK2</i>	4.72611322	1.39332712	1.39367564	11.215472	4.4562891	0	0.48177287	4.70091905
<i>FK3</i>	126.885091	26.7354281	456.661052	68.3465071	50.097901	11.4116861	32.2787825	20.6840438
<i>FK4</i>	39.2060674	34.9617137	97.5572949	34.647882	48.0778243	49.0702503	69.3752936	78.5053481
<i>FK5</i>	81.0781475	53.275482	1.99760175	21.7712103	13.3890681	6.52748446	2.69311036	9.87663091
<i>GPI1</i>	146.131706	106.42757	83.6205385	140.015414	49.2898703	79.8818028	76.1201139	105.770679
<i>PGM1</i>	4.27702554	10.8175655	71.5373707	19.3885751	23.5056119	25.1456503	33.5843869	38.035136
<i>PGM2</i>	253.770182	251.929996	757.230432	234.466489	331.292571	297.845007	616.187504	688.214548
<i>SUS1</i>	17.3504669	9.56305699	1.20320664	35.9009013	7.13895089	42.2403561	9.51501423	25.0417958
<i>SUS2</i>	328.354379	235.17408	484.441653	30.1294185	1185.68399	2065.28695	2812.84055	4266.17805
<i>SUS3</i>	90.5303739	179.949997	15.3304321	179.409581	5.65621463	18.8292821	5.2995016	8.93174619
<i>HXK1</i>	4.27702554	5.85094562	2.81987038	6.9960244	109.544717	5.34637494	8.4695671	4.05689314
<i>HXK2</i>	7.16401778	12.1337712	0.95234502	11.732817	0.92115495	4.10250116	6.8604457	8.07617892
<i>UGP1</i>	335.033667	344.475709	957.919725	264.368086	270.286256	516.949381	660.028835	841.464509
<i>UGP2</i>	7.49192307	11.5219412	3.25190983	18.1450484	52.1179776	7.29777327	7.22659309	24.0310982
<i>UGP3</i>	0	0	6.77326362	2.8240397	0	0	0	1.11881873
<i>CESA1</i>	550.039741	265.667893	369.630654	286.699358	243.811132	190.854744	244.114315	732.788663
<i>CESA3</i>	424.159751	230.09949	232.990048	339.065123	116.126126	53.4922786	130.179848	442.041521
<i>CESA4</i>	223.118166	173.26614	229.491922	164.696097	1030.23909	87.8699831	187.89142	286.756062
<i>CESA5</i>	125.26695	2.00001568	65.7303889	1.42863185	2.02007665	0	0	1.88036762
<i>CESA7</i>	88.2920639	3.3573528	69.9857452	0	0	0	0	0.75684797
<i>CESA8</i>	201.597599	169.404927	111.865698	91.1998703	59.9558751	104.610927	76.1586557	125.664968

Table S2. Expression levels of genes involved in lignin biosynthesis in *Agave tequilana* in several organs and tissues sampled. Values shown are transcripts per million (TPM).

Gene name	Root	Pine	Leave	Shoot apical meristem	Anther	Ovary	Tepal	Pistil
<i>PAL1</i>	203.728983	15.0746683	28.2358685	9.00844933	4.18155867	9.60863971	17.7003353	30.3444324
<i>PAL2</i>	67.9761926	12.8175812	1.8535886	7.22859238	204.302472	78.6493407	185.72826	306.546931
<i>C4H</i>	353.595958	18.1698083	54.4787808	7.07196497	35.2260967	27.8102791	67.2362221	133.181737
<i>4CL</i>	58.4526824	34.9617137	5.57470257	18.0358838	90.9034494	13.6940233	66.9664293	157.010696
<i>CSE</i>	44.6236331	18.0721211	10.9821641	3.9156853	12.2901464	12.9237345	25.697765	11.1834864
<i>HCT1</i>	88.5486854	25.7688396	16.3663976	0.8353462	2.25036539	12.3873853	35.8439017	6.13469935
<i>HCT2</i>	3.11510027	0	0	0	0	0	0	0
<i>C3H</i>	164.665483	24.6788567	19.0469004	14.7134842	23.4328892	7.98818028	30.8334638	29.1456981
<i>CcoAOMT</i>	368.216257	15.851024	40.8579242	6.78718785	0	6.1623105	7.72281915	14.7843904
<i>CCR1</i>	9.3453008	0	0.24621603	0	0	0	0	0
<i>CCR2</i>	110.489826	56.5557134	27.4089543	21.3582835	11.3124293	7.41759597	31.7970096	13.6326652
<i>F5H</i>	112.628339	20.5657139	106.383907	0.94925704	37.3835385	2.85292153	25.4906027	10.6804881
<i>COMT1</i>	409.468168	152.278829	227.917069	52.270839	42.0781967	54.6905057	76.0671188	98.31032
<i>COMT2</i>	0	0.51414285	449.228115	34.647882	122.820661	82.16414	178.255963	314.961576
<i>CAD1</i>	45.2794437	32.0362409	33.5550639	31.235303	48.2232699	20.5125058	60.4817664	39.0035253
<i>CAD2</i>	0.71283759	2.57071424	6.96837821	36.0717676	0.80803066	18.2586978	1.44531862	8.93174619
<i>CAD3</i>	57.7398448	11.7070327	4.64558547	17.5517627	30.0587406	26.5207585	264.878725	75.1676955
<i>CAD4</i>	3.56418795	3.74810137	42.8694628	5.22091373	0.80803066	1.71175292	6.8267216	2.35045952
<i>CAD5</i>	137.313905	74.9825931	58.1906036	27.0016166	0	15.9478313	12.9596903	5.83854145
<i>CAD6</i>	0	1.6606814	0	9.97669152	4.2825625	48.2257855	3.46876468	2.86756062
<i>CAD7</i>	34.9290419	0.51414285	18.5823419	0.47462852	12.9284906	5.13525875	24.0886436	21.6242276

Table S3. Percentages of identity/similarity between amino acid sequences of orthologous CESA genes of *A. tequilana* (AtqCESA), *A. officinalis* (AoCESA), and *A. thaliana* (AtCESA)

	AtqCESA1	AtqCESA3	AtqCESA4	AtqCESA5	AtqCESA7	AtqCESA8
AoCESA1	93/96	66/74	61/71	65/75	61/72	56/67
AoCESA2	58/67	58/68	62/72	58/68	56/67	85/89
AoCESA3	50/55	58/60	49/54	48/54	48/53	47/54
AoCESA4	60/71	61/71	91/94	64/74	62/73	61/72
AoCESA5	60/71	58/68	60/71	70/80	59/72	53/66
AoCESA6	67/75	63/72	63/73	90/93	68/78	56/67
AoCESA7	63/72	65/72	63/72	68/77	77/85	57/67
AoCESA8	67/76	62/71	64/73	92/95	68/78	56/67
AoCESA9	65/74	61/70	63/72	90/93	67/77	55/66
AoCESA10	78/80	52/59	47/56	53/61	48/57	45/53
AoCESA11	47/60	48/60	45/59	46/58	53/63	44/57
AoCESA12	69/77	81/86	61/70	63/74	61/71	57/68
AtCESA1	82/89	64/74	60/71	64/74	60/72	56/66
AtCESA2	61/73	60/70	61/73	71/82	61/74	54/67
AtCESA3	69/78	77/84	61/69	63/72	61/72	57/68
AtCESA4	58/70	61/71	77/84	60/71	58/70	60/71
AtCESA5	62/72	60/70	62/73	70/81	60/75	55/68
AtCESA6	61/72	59/69	62/73	71/82	60/74	54/67
AtCESA7	62/71	63/72	64/73	66/76	73/83	56/67
AtCESA8	57/67	57/67	62/71	57/67	56/67	84/90
AtCESA9	61/72	59/69	60/71	71/80	60/73	55/66
AtCESA10	76/84	63/73	57/69	61/72	57/69	54/66

Table S4. Percentages of identity/similarity between amino acid sequences of orthologous CAD genes of *A. tequilana* (AtqCAD), *O. sativa* (OsCAD), and *A. thaliana* (AtCAD)

	AtqCAD1	AtqCAD2	AtqCAD3	AtqCAD4	AtqCAD5	AtqCAD6	AtqCAD7
OsCAD1	72/84	51/64	52/66	49/65	45/63	49/64	72/82
OsCAD2	41/60	45/62	48/65	48/65	80/88	45/62	42/59
OsCAD3	51/64	65/77	58/73	61/75	45/62	67/78	50/65
OsCAD4	69/79	47/62	48/63	45/62	41/58	47/62	70/80
OsCAD5	46/59	62/72	54/67	60/71	43/57	65/75	46/60
OsCAD6	49/64	54/69	54/70	56/69	48/64	56/69	50/64
OsCAD7	44/59	61/75	54/69	54/69	42/59	62/76	42/60
OsCAD8A	46/61	55/70	56/71	61/73	48/62	59/71	47/64
OsCAD8B	40/52	50/61	47/59	53/63	40/52	51/63	39/52
OsCAD8C	40/52	49/60	47/59	52/64	40/52	50/62	39/52
OsCAD8D	45/60	55/70	55/70	61/73	48/61	58/71	45/62
OsCAD9	45/61	54/72	56/71	59/75	46/66	58/73	45/62
AtCAD1	71/81	48/64	50/66	45/63	41/59	46/63	71/81
AtCAD2	47/60	56/70	55/69	53/70	45/62	57/70	45/59
AtCAD3	46/60	55/69	55/69	52/69	45/62	56/70	45/58
AtCAD4	43/61	45/63	48/66	46/63	73/82	46/63	45/59
AtCAD5	44/62	45/63	51/67	48/65	75/83	47/64	46/62
AtCAD6	46/61	59/75	60/76	58/76	47/65	60/76	48/64
AtCAD7	47/62	59/72	60/74	63/77	47/62	62/74	48/64
AtCAD8	46/60	60/73	61/74	60/75	48/63	64/74	47/61
AtCAD9	49/64	62/77	60/75	60/74	48/65	65/77	47/62

Table S5. cDNA libraries used in this study, previously reported by Gross et al., 2013 and deposited in Genbank (SRP019885)

cDNA library name	Read length (pb)	Tissue or organ sequenced
SRX253025	500	Juvenil leaf
SRX253024	250	Juvenil leaf
SRX253023	500	Roots
SRX253022	250	Roots
SRX253021	500	Stem apical meristem
SRX253020	250	Stem apical meristem
SRX253019	500	Adult leaf
SRX253018	250	Adult leaf

Table S6. Gene-specific oligonucleotides used for qPCR analysis

Gene name	Sequence (5'-3')
AtqSUS2	F: GAATGCTGCAACGCCATCAA R: CTTAGAGCTGCCATCTGCGA
AtqCESA1	F: GTGCCAGATCTGTGGTGACA R: CTGGTCAGACGTGGGATACG
AtqCESA7	F: GGCCCCGAGGATGTTGATAG R: GGGACGACGAAGAGAAGTCG
AtqCCR2	F: GCCCATTTGGTGGTCTACGA R: GTACGCCCAGGTCTCTTAGC
AtqCD5	F: TGTGTTCCATCCCTTGGAGC R: CGAGATTGCTTCCAGCAACG
AtqGAPDH	F: ACACTGTCCACGGTTCATGG R: TCCACAACGTACTCAGCACC

F= Forward; R= Reverse