

Table S1. Identification of genes that increase enzymatic saccharification efficiency

Gene ID	Overexpressed sequence <sup>a</sup>	Gene symbol	Function category <sup>b</sup>	Change in glucose yield <sup>c</sup> (seedlings)	Change in glucose yield <sup>c</sup> (stems)	Change in xylose yield <sup>c</sup> (stems)
AT1G64620	pda12524	DOF18	TF (Dof type)	160.47	106.23	113.37
AT5G15830	pda10857	BASIC LEUCINE-ZIPPER 3 (BZIP3)	TF (bZIP type)	128.41	92.29	92.39
AT5G20710	pda00366	BETA-GALACTOSIDASE 7 (BGAL7)	CAZyme (GH35)	125.00	103.70	98.38
AT1G22640	pda03176	MYB3	TF (MYB type)	123.66	92.32	106.57
AT1G02640	pda01641	BETA-XYLOSIDASE 2 (BXL2)	CAZyme (GH3)	123.52	131.78	117.09
AT2G26730	pda04099		LRR kinase	119.30	119.77	97.97
AT3G42950	pda04403		CAZyme (GH28)	117.80	105.98	102.51
AT5G44030	pda13285	CELLULOSE SYNTHASE 4 (CESA4)/IRREGULAR XYLEM 5 (IRX5)/NWS2	CAZyme (GT2)	113.87	85.43	106.24
AT3G16520	pda00717	UDP-GLUCOSYL TRANSFERASE 88A1	CAZyme (GT1)	113.73	110.31	104.94
AT3G18080	pda02043	B-S GLUCOSIDASE 44	CAZyme (GH1)	113.37	107.77	
AT3G62720	pda05997	XYLOSYLTRANSFERASE 1	CAZyme (GT34)	112.53	119.09	101.23
AT2G28110	pda08587	FRAGILE FIBER 8 (FRAS)/IRREGULAR XYLEM 7 (IRX7)	CAZyme (GT47)	111.84	106.74	95.99
AT5G20240	pda11065	PISTILLATA (PI)	TF (MADS-box type)	111.80	88.23	89.87
AT3G15350	pda03008		CAZyme (GT14)	110.49	115.65	114.03
AT3G18660	pda04027	GLUCURONIC ACID SUBSTITUTION OF XYLAN 1 (GXU1)	CAZyme (GT8)	109.51	95.80	104.55
AT5G13180	pda00727	VND-INTERACTING 2 (VNI2)	TF (NAC type)	108.59	107.89	109.62
AT4G24060	pda00786	DOF4.6	TF (Dof type)	107.98	113.85	120.99
AT2G30590	pda09817	WRKY21	TF (WRKY type)	107.96	103.95	101.85
AT1G19940	pda04559	GLYCOSYL HYDROLASE 9B5	CAZyme (GH9)	107.70	113.76	97.21
AT3G60140	pda01565	DARK INDUCIBLE 2 (DIN2)/BETA GLUCOSIDASE 30 (BGLU30)/SENESCENCE-RELATED GENE 2 (SRG2)	CAZyme (GH1)	107.62	98.58	97.85
AT3G16920	pda03591	CHITINASE-LIKE PROTEIN 2 (CTL2)	CAZyme (GH19)	109.97		
AT4G15550	pda05237	INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE (IAGLU)	CAZyme (GT1)	109.68		
AT4G23490	pda03723		Unknown function (DUF604)	108.44		
AT5G66460	pda09521	ENDO-BETA-MANNASE 7	CAZyme (GH5)	107.94		
AT4G18780	pda08626	CELLULOSE SYNTHASE 8 (CESA8)/IRREGULAR XYLEM 1 (IRX1)/LEAF WILTING 2 (LEW2)	CAZyme (GT2)	107.83		
AT1G45130	pda05881	BETA-GALACTOSIDASE 5 (BGAL5)	CAZyme (GH35)	107.68		
AT1G32170	pda05067	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 30 (XTH30)	CAZyme (GH16)	107.15		
AT2G29730	pda08391	UDP-GLUCOSYL TRANSFERASE 71D1	CAZyme (GT1)	106.95		
AT1G12240	pda11488	VACUOLAR INVERTASE 2 (VI2)/FRUCTOSIDASE 4 (FRUCT4)	CAZyme (GH32)	106.90		
AT4G01070	pda02106	UDP-GLUCOSE-DEPENDENT GLUCOSYLTRANSFERASE 72 B1	CAZyme (GT1)	106.38		
AT5G59590	pda13180	UDP-GLUCOSYL TRANSFERASE 76E2	CAZyme (GT1)	106.16		
AT1G67510	pda11649		LRR kinase	105.82		
AT1G66140	pda01764	ZINC FINGER PROTEIN 4 (ZFP4)	TF (C2H2 type)	104.83		
AT2G34710	pda08908	ATHB14/PHABULOSA (PHB)	TF (HD-ZIP type)	104.79		
AT1G26800	pda01727		RING-U-box protein	104.59		
AT4G39000	pda10879	GLYCOSYL HYDROLASE 9B17	CAZyme (GH9)	104.57		
AT2G46400	pda07725	WRKY46	TF (WRKY type)	104.24		
AT1G72220	pda03693		RING-U-box protein	103.88		
AT1G32860	pda09327		CAZyme (GH17)	103.46		
AT1G62990	pda11355	KNOTTED-LIKE HOMEBOX OF ARABIDOPSIS THALIANA 7 (KNA17)/IRREGULAR XYLEM 11 (IRX11)	TF (Homeobox type)	103.23		
AT1G23870	pda06559	TREHALOSE-6-PHOSPHATASE SYNTHASE S9 (TPS9)	CAZyme (GT20)	103.00		
AT5G09460	pda09252	SAC51 LIKE 1 (SACL1)	TF (bHLH type)	102.69		
AT5G17420	pda09751	CELLULOSE SYNTHASE 7 (CESA7)/IRREGULAR XYLEM 3 (IRX3)/MUR10	CAZyme (GT2)	102.64		
AT5G49260	pda09629	BETA-XYLOSIDASE 1 (BXL1)	CAZyme (GH3)	102.52		
AT1G22370	pda00728	UDP-GLUCOSYL TRANSFERASE 85A5	CAZyme (GT1)	102.24		
AT4G28530	pda12409	ANAC074	TF (NAC type)	102.03		
AT1G19300	pda06025	GALACTURONOSYLTRANSFERASE-LIKE 1 (GTL1)/GAOLAOZHUANGREN 1 (GLZ1)/PARVUS	CAZyme (GT8)	101.89		
AT5G61600	pda05682	ERF104	TF (ERF/AP2 type)	101.84		
AT4G08160	pda10378		CAZyme (GH10)	101.65		
AT4G36540	pda00396	BR ENHANCED EXPRESSION 2 (BEE2)	TF (bHLH type)	101.57		
AT3G52840	pda01770	BETA-GALACTOSIDASE 2 (BGAL2)	CAZyme (GH35)	101.56		
AT5G56870	pda07078	BETA-GALACTOSIDASE 4 (BGAL4)	CAZyme (GH35)	101.33		
AT1G28470	pda11199	SECONDARY WALL-ASSOCIATED NAC DOMAIN PROTEIN 3 (SND3)	TF (NAC type)	101.12		
AT5G49690	pda10179		CAZyme (GT1)	101.07		
AT3G03690	pda01556	UNFERTILIZED EMBRYO SAC 7 (UNE7)	CAZyme (GT14)	100.72		
AT2G44480	pda10838	BETA GLUCOSIDASE 17 (BGLU17)	CAZyme (GH1)	100.69		
AT4G33330	pda11621	GLUCURONIC ACID SUBSTITUTION OF XYLAN 2 (GXU2)	CAZyme (GT8)	100.64		
AT5G49450	pda10097	BASIC LEUCINE-ZIPPER 1 (BZIP1)	TF (bZIP type)	99.95		
AT2G47180	pda04796	GALACTINOL SYNTHASE 1 (GOL1)	CAZyme (GT8)	99.88		
AT1G43640	pda06010	TUBBY LIKE PROTEIN 5 (TLP5)	TF (TLP type)	99.77		
AT5G20250	pda08032	DARK INDUCIBLE 10 (DIN10)/RAFFINOSE SYNTHASE 6 (RS6)	CAZyme (GH36)	99.68		
AT5G16600	pda08058	MYB43	TF (MYB type)	99.20		
AT3G13750	pda06012	BETA-GALACTOSIDASE 1 (BGAL1)	CAZyme (GH35)	98.95		
AT2G06850	pda02220	XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 4 (XTH4)	CAZyme (GH16)	98.89		
AT4G02010	pda09420		Protein kinase	98.87		
AT5G08370	pda08229	ALPHA-GALACTOSIDASE 2 (AGAL2)	CAZyme (GH27)	98.80		
AT4G32880	pda08603	ATHB8	TF (HD-ZIP type)	98.70		
AT1G30080	pda01029		CAZyme (GH17)	98.55		
AT3G10740	pda05444	ALPHA-L-ARABINOFURANOSIDASE 1	CAZyme (GH51)	98.42		
AT5G08750	pda11021	SHOOT APICAL MERISTEM ARREST 2 (SHA2)	RING-FYVE/PHD protein	97.83		
AT5G64570	pda08048	BETA-D-XYLOSIDASE 4 (XYL4)	CAZyme (GH3)	97.80		
AT3G04670	pda05451	WRKY39	TF (WRKY type)	97.57		
AT5G15470	pda11680	GALACTURONOSYLTRANSFERASE 14 (GAUT14)	CAZyme (GT8)	97.21		
AT5G39610	pda04657	ANAC092	TF (NAC type)	97.18		
AT2G29740	pda12967	UDP-GLUCOSYL TRANSFERASE 71C2	CAZyme (GT1)	97.13		
AT3G23060	pda09137	ARABIDOPSIS THALIANA BMI1C (AtBMI1C)	RING-U-box protein	97.12		
AT5G25190	pda01468	ETHYLENE AND SALT INDUCIBLE 3 (ESI3)	TF (ERF/AP2 type)	97.09		
AT5G66320	pda09868	GATA5	TF (GATA type)	97.08		
AT1G52150	pda06113	ATHB15/CORONA (CNA)/INCURVAIA 4 (ICU4)	TF (HD-ZIP type)	96.89		
AT5G05410	pda03329	DEHYDRATION-RESPONSIVE ELEMENT BINDING PROTEIN 2A (DREB2A)	TF (ERF/AP2 type)	96.70		
AT5G64340	pda04943	SUPPRESSOR OF ACAULIS 51 (SACS1)	TF (bHLH type)	96.63		
AT5G67230	pda06500	IRREGULAR XYLEM 14-LIKE (IRX14-L)	CAZyme (GT43)	96.26		
AT5G24010	pda07724		Protein kinase	95.78		
AT2G31070	pda02921	TCP DOMAIN PROTEIN 10 (TCP10)	TF (TCP type)	95.63		
AT1G61810	pda08218	BETA-GLUCOSIDASE 45 (BGLU45)	CAZyme (GH1)	95.28		
AT1G78060	pda06112		CAZyme (GH3)	93.99		
AT1G77450	pda12014	ANAC032	TF (NAC type)	93.90		
AT3G26744	pda08970	INDUCER OF CBP EXPRESSION 1 (ICE1)/SCREAM (SCRM)	TF (bHLH type)	92.39		
AT4G25000	pda06256	ALPHA-AMYLASE-LIKE/AMY1	CAZyme (GH13)	91.62		
AT5G15050	pda06054	GLCA TRANSFERASE 14B (GLCAT14B)	CAZyme (GT14)	91.56		
AT1G34190	pda09853	REGULATORS OF AOX1A 2 (RAO2)	TF (NAC type)	90.17		
AT4G33440	pda12581		CAZyme (GH28)	89.81		
AT1G35460	pda02680	ATCF1 ASSOCIATED PROTEIN 2 (CFAP2)/FLOWERING BHLH 1 (FBH1)	TF (bHLH type)	89.54		
AT1G68810	pda06930	ABNORMAL SHOOT 5 (ABS5)/TMO5-LIKE1 (TSL1)	TF (bHLH type)	83.52		
AT3G04420	pda06907	ANAC048	TF (NAC type)	81.23		
AT3G02310	pda12886	AGAMOUS-LIKE 4 (AGL4)/SEPALATA 2 (SEP2)	TF (MADS-box type)	76.44		

<sup>a</sup>Arabidopsis full-length cDNA clones developed by RIKEN Genomic Sciences Center were used to generate overexpressors.

<sup>b</sup>TF, transcription factor; CAZyme, carbohydrate active enzyme; GH, glycoside hydrolase; GT, glycosyltransferase.

<sup>c</sup>Three independent lines of overexpressors and control plants were subjected to enzymatic saccharification analysis, and the average yields of 3 lines were compared between overexpressors and control plants. Ratio of sugar yields of overexpressors to those of control plants were shown. Bold, statistically-significant different from the control (Student's t-test, p<0.05). Pink and blue shading indicate overexpression lines showing a statistically significant increase and decrease in glucose yields, respectively.

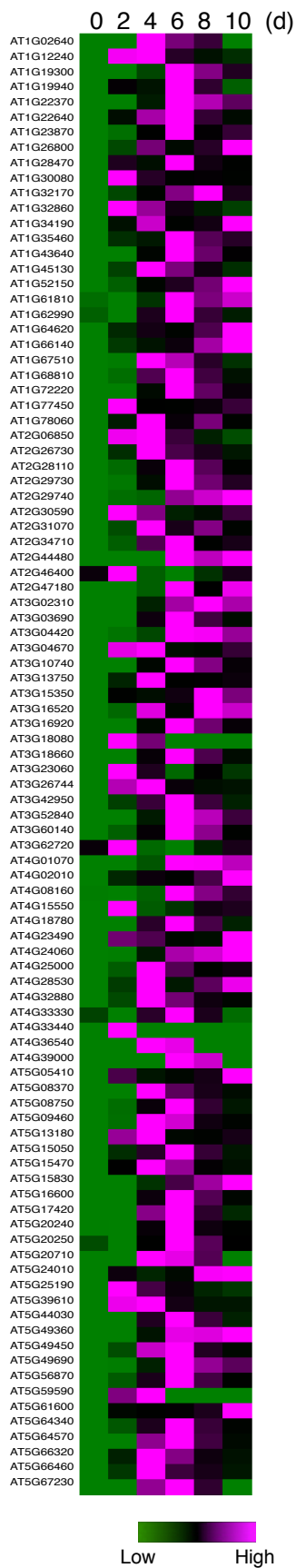


Figure S1. Expression patterns of the 96 selected genes during xylem vessel cell differentiation. The microarray data (the Arabidopsis full-genome GeneChip array ATH1, Affymetrix) for the 96 genes were extracted from the transcriptome data for the in vitro xylem vessel cell inducible system from Arabidopsis suspension cells (Kubo et al. 2005). The expression level of each gene was normalized within the time course (0, 2, 4, 6, 8, and 10 days after the induction of cell differentiation) data independently, and the data are displayed as heat maps. Note that all genes selected here were upregulated after the induction of xylem vessel cell differentiation. For details about the transcriptome data, please refer to Kubo et al. (2005).

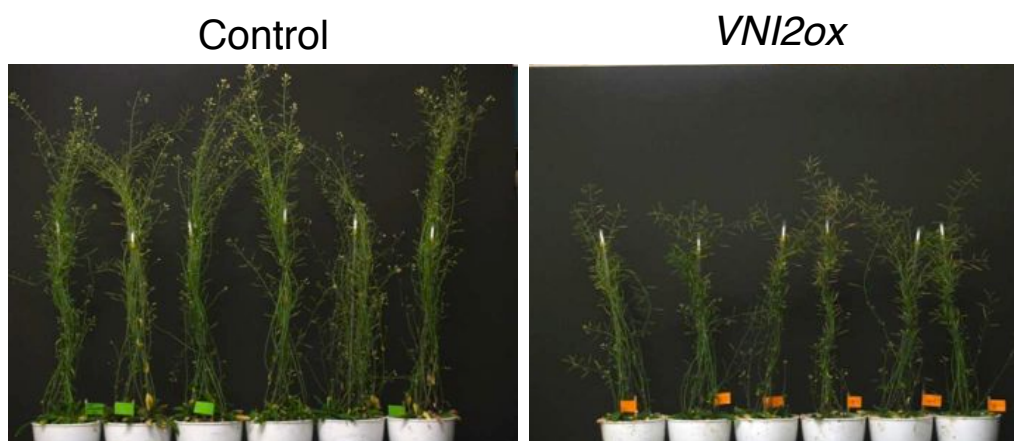


Figure S2. Effects of *VNI2* overexpression on plant growth. Forty-day-old plants of the control line (left) and the *VNI2* overexpressor (*VNI2ox*; right) are shown. The plant height of *VNI2ox* is clearly lower than that of the control lines, indicating that the overexpression of *VNI2* affects plant growth.

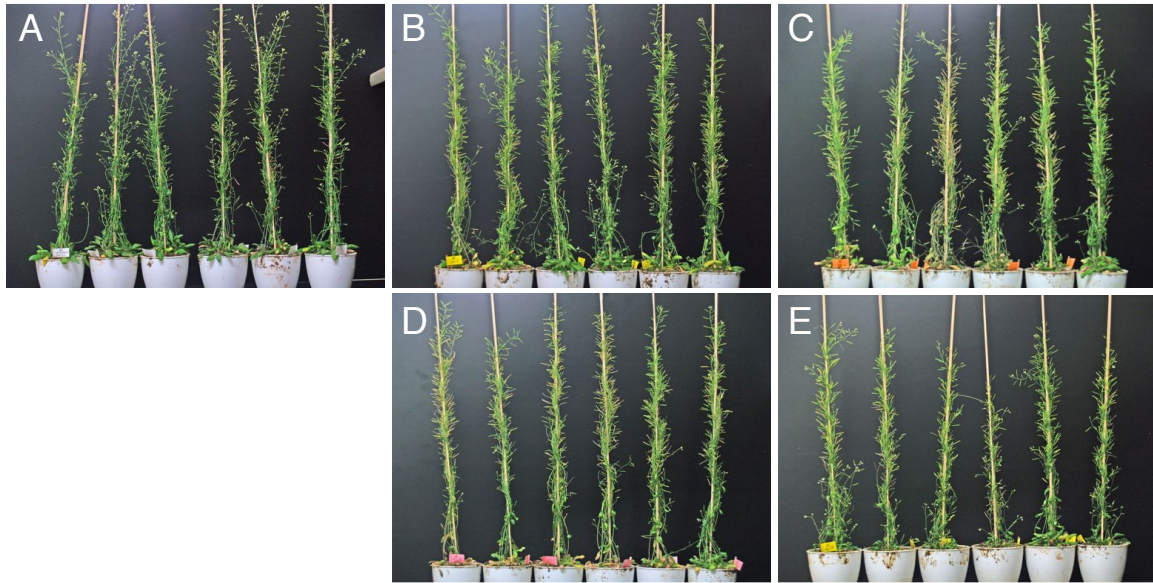


Figure S3. Images of 40-day-old plants of the control lines (A) and transgenic plants overexpressing *BXL2* (*BXL2ox*; B), *UGT88A1* (*UGT88A1ox*; C), *AT3G15350* (putatively encoding a class GT14 glycosyltransferase; *GT14ox*; D), and *Dof4.6* (*Dof4.6ox*; E). The plant sizes of the control and overexpressor lines were similar.