Supplementary Data

Supplementary Figure S1. HPAEC-PAD analysis of XyG derived from different tissues. XXXG heptasaccharide and XEG digest oligosaccharides from Arabidopsis are used as controls. XyG oligosaccharides are annotated using the one-letter code nomenclature described by Fry et al., 1993.

Supplementary Figure S2. Immunofluorescent labeling of rice 3-day-old root and shoot transverse sections with different antibodies. (A) to (C) Rice root cross-sections labeled with CCRC-M1 (A), CCRC-M48 (B), LM11 (C). (D) to (F) Rice shoot cross-sections labeled with CCRC-M1 (D), CCRC-M48 (E), LM11 (F). CCRC-M1 recognizes fucosylated xyloglucan; CCRC-M48 recognizes non-fucosylated xyloglucan; LM11 recognizes xylan. Bar=50 µm

Supplementary Figure S3. Phylogenic tree of MUR2 homologs in Arabidopsis, rice and Brachypodium. Genes shown in Table 1 are highlighted in yellow. Homologs were identified from Phytozome (http://www.phytozome.net). Bootstrap values are shown.

Supplementary Figure S4. Phylogenic tree of AXY4 homologs in Arabidopsis, rice and Brachypodium. Homologs were identified from Phytozome (http://www.phytozome.net) and only protein sequences from TBL17-TBL27 subclade were shown here. Genes listed in Table 1 are marked in yellow. Bootstrap values are shown.

Supplementary Figure S5. Phylogenic tree of MUR3 and XLT2 homologs in Arabidopsis, rice and Brachypodium. Homologs were identified from Phytozome (http://www.phytozome.net). Genes listed in Table 1 are marked in yellow. Bootstrap values are shown.

Supplementary Figure S6. XyG oligosaccharide mass profiling of 4-week-old leaves from Arabidopsis Col.0, *axy2.2/fut1* and *OsMUR2* transformants into *axy2.2* mutant. One representative line of *OsMUR2* transformants was shown here. OX, independent overexpression line.

Supplementary Figure S7. Xyloglucan HPAEC spectra derived from cell wall of 4-week-old leaves from Col.0, *axy2.2* and *OsMUR2* transformants into *axy2.2* mutant. One representative line of *OsMUR2* transformants was shown here. OX, independent overexpression line.

Supplementary Figure S8. RT-PCR analysis of total RNA extracted from 4-week-old leaves of Arabidopsis wild-type (Col.0), mutants and all transformants (*OsMUR2*-OX-*axy2.2*, *OsAXY4*-OX-*axy4-3*, *OsXLT2*-OX-*xlt2 mur3* and *OsMUR3*-OX-*xlt2 mur3*). The RT-PCR was performed using specific primers for each gene (See Supplementary Table S5). *AtPTB* transcript as a reference gene shown on lower panel. OX, overexpress. NCK, no template control.

Supplementary Figure S9. XyG oligosaccharide mass profiling of 4-week-old leaves from Arabidopsis Col.0, rice homologs of *AtMUR2* transformants into *axy2.2* mutant. One representative line of transformants was shown here. OX, independent overexpression line.

Supplementary Figure S10. XyG oligosaccharide mass profiling of 4-week-old leaves from Arabidopsis Col.0, *axy4-3* and *OsAXY4* transformants into *axy4-3* mutant. Two representative lines of *OsAXY4* transformants were shown here. OX, independent overexpression line.

Supplementary Figure S11. XyG oligosaccharide mass profiling of 4-week-old leaves from Arabidopsis Col.0, *xlt2 mur3.1*, *OsMUR3* and *OsXLT2* transformants into *xlt2 mur3* mutant. Two representative lines of *OsMUR3* and one *OsXLT2* transformants were shown here. OX, independent overexpression line.

Supplementary Figure S12. XyG HPAEC spectra derived from cell wall of 4-week-old leaves from Col.0, *xlt2 mur3.1*, *OsMUR3* and *OsXLT2* transformants into *xlt2 mur3* mutant. Xyloglucan oligosaccharides were identified based on their retention time and annotated as described in text. *mur3.1* and *xlt2* were used here as controls. Two representative lines of *OsMUR3* and one *OsXLT2* transformants were shown here. OX, independent overexpression line.

Supplementary Figure S13. Phenotype of 7-week-old plants of *Col.0, axy2.2* and *OsMUR2* transformants into *axy2.2* mutant. One representative plant from each line is shown here. OX, independent overexpression line. Bar=2 cm.

Supplementary Figure S14. Phenotype of 7-week-old plants of *Col.0, axy4-3* and *OsAXY4* transformants into *axy4-3* mutant. One representative plant from each line was shown here. OX, independent overexpression line. Bar=2 cm.

Supplementary Figure S15. Sequence alignment of AtFUT1/MUR2 with Os02g52630/OsMUR2 and Os02g52640. Protein sequences are downloaded from TAIR (www.arabidopsis.org) and rice.plantbiology.msu.edu. Sequence alignment is done with the Multialign software at http://multalin.toulouse.inra.fr/multalin/cgi-bin/multalin.pl (Corpet, 1998).

Supplementary Figure S16. RNA-Seq FPKM expression values of rice genes in different tissues. RNA seq data were downloaded from rice.plantbiology.msu.edu. FPKM, fragments per kilobase of exon per million fragments mapped. EI, emergence inflorescence. DAP, day after pollination. *OsCESA4* and *OsUBI4* were used here as controls.

Supplementary Table S1. List of *m/z* with known or predicted XyG structures shown in this study.

m/z	Oligosaccharide composition	Known or predicted XyG structure
995	P2H4Ac1	XX$\underline{G}$G
1085	P3H4	XXXG
1157	P2H5Ac1	XX$\underline{G}$GG, XXG$\underline{G}$G, XL$\underline{G}$G, X$\underline{L}$GG
1199	P2H5Ac2	XX$\underline{GG}$G, X$\underline{LG}$G
1217	P4H4	XXSG, XXBG
1247	P3H5	XLXG, XXLG, XXXGG
1289	P3H5Ac1	XX$\underline{L}$G, XXX$\underline{G}$G
1361	P2H6Ac2	XX$\underline{GG}$GG, XL$\underline{GG}$G, L$\underline{LG}$G
1393	P3H5H$_{de}$1	XXFG
1403	P2H6Ac3	XX$\underline{GGG}$G, X$\underline{LGG}$G, $\underline{LLG}$G
1409	P3H6	XLLG, XLXGG, XXLGG, XXXGGG
1435	P3H5H$_{de}$1Ac1	XX$\underline{F}$G
1451	P3H6Ac1	XL$\underline{L}$G,XX$\underline{L}$GG,XXL$\underline{G}$G,XXX$\underline{G}$GG,XXXG$\underline{G}$G
1555	P3H6H$_{de}$1	XLFG, XXFGG
1597	P3H6H$_{de}$1Ac1	XL$\underline{F}$G,XX$\underline{F}$GG,XXF$\underline{G}$G

Note: P, pentose; H, hexose; H$_{de}$, deoxy hexose; Ac, acetate.

Supplementary Table S2. List of top 50 coexpressed genes with *OsCSLC3*.

R-value	Array	Gene Locus	Annotation
1	OsAffx.17009.1.S1_x_at	os08g15420	#UniProt: Probable xyloglucan glycosyltransferase 3 n #Rice: cDNA CSLC3 cellulose synthase like family C, expressed #Arabidopsis: ATCSLC5 (CELLULOSE SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups
0.92776	OsAffx.24868.1.S1_at	os02g54570	#UniProt: Putative uncharacterized protein n #Rice: cDNA SCP like extracellular protein, expressed #Arabidopsis: pathogenesis related protein, putative
0.92181	Os.53995.1.S1_at	os06g44970	#UniProt: Probable auxin efflux carrier component 2 n #Rice: cDNA auxin efflux carrier component, putative, expressed #Arabidopsis: EIR1 (ETHYLENE INSENSITIVE ROOT 1); auxin efflux transmembrane transporter/ auxin:hydrogen symporter/ transporter
0.92178	OsAffx.26451.1.S1_at	os04g44130	#UniProt: OSIGBa0131L05.12 protein n #Rice: cDNA DEF12 Defensin and Defensin like DEFL family, expressed #Arabidopsis: PDF2.1; peptidase inhibitor
0.92007	OsAffx.30244.1.S1_x_at	os10g02500	#UniProt: Putative uncharacterized protein n #Rice: cDNA serine/threonine protein kinase BRI1 like 2 precursor, putative, expressed #Arabidopsis: BRL2 (BRI1 LIKE 2); ATP binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase
0.91766	Os.54044.1.S1_at	os05g04690	#UniProt: Putative uncharacterized protein n #Rice: cDNA CHIT11 Chitinase family protein precursor, expressed #Arabidopsis: chitinase, putative
0.91346	OsAffx.15442.1.S1_at	os06g15600	#UniProt: Putative chemocyanin (Putative uncharacterized protein) n #Rice: cDNA plastocyanin like domain containing protein, putative, expressed #Arabidopsis:

			ARPN (PLANTACYANIN); copper ion binding / electron carrier
0.91281	OsAffx.30244.1.S1_at	os10g02500	#UniProt: Putative uncharacterized protein n #Rice: cDNA serine/threonine protein kinase BRI1 like 2 precursor, putative, expressed #Arabidopsis: BRL2 (BRI1 LIKE 2); ATP binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase
0.91281	OsAffx.14196.1.S1_at	os04g38860	#UniProt: OSJNBa0072F16.19 protein (Os04g0462400 protein) (B1358B12.11 protein) n #Rice: cDNA expressed protein #Arabidopsis: lysine and histidine specific transporter, putative
0.91014	OsAffx.18476.1.S1_at	os10g31540	#UniProt: Expressed protein (Putative uncharacterized protein) (Os10g0453000 protein) n #Rice: cDNA glycine rich cell wall structural protein 2 precursor, putative, expressed #Arabidopsis: glycine rich protein
0.90958	OsAffx.24060.1.S1_at	os02g02160	#UniProt: Putative uncharacterized protein n #Rice: cDNA expressed protein #Arabidopsis: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPR
0.90792	Os.18683.1.S1_at	os06g44280	#UniProt: Fibroin heavy chain like (Putative uncharacterized protein) (Os06g0652600 protein) n #Rice: cDNA retrotransposon protein, putative, Ty3 gypsy subclass, expressed #Arabidopsis: unknown protein
0.90607	Os.55806.1.S1_at	os05g20930	#UniProt: Os05g0286100 protein n #Rice: cDNA ZOS5 07 C2H2 zinc finger protein, expressed #Arabidopsis: nucleic acid binding / transcription factor/ zinc ion binding
0.90452	Os.7659.1.S1_s_at	os08g38560	#UniProt: Chromosome chr19 scaffold_66, whole genome shotgun sequence n #Rice: cDNA receptor like protein kinase 2 precursor, putative, expressed #Arabidopsis: leucine rich repeat protein kinase, putative
0.90392	OsAffx.24414.1.S1_at	os02g25020	#UniProt: Putative uncharacterized protein n #Rice: cDNA DNA binding protein, putative, expressed #Arabidopsis: DNA binding protein related
0.90351	OsAffx.4884.1.S1_at	os06g20570	#UniProt: Putative uncharacterized protein n #Rice: cDNA glycosyltransferase, putative, expressed #Arabidopsis: transferase, transferring glycosyl groups
0.90332	Os.18755.1.S1_at	os04g39230	#UniProt: OSJNBa0016O02.5 protein (OSIGBa0115M15.8 protein) n #Rice: cDNA expressed protein
0.90299	Os.55417.1.S1_at	os08g15420	#UniProt: Probable xyloglucan glycosyltransferase 3 n #Rice: cDNA CSLC3 cellulose synthase like family C, expressed #Arabidopsis: ATCSLC5 (CELLULOSE SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups
0.90171	Os.18711.1.S1_at	os10g31530	#UniProt: Expressed protein (Putative uncharacterized protein) (Os10g0452900 protein) n #Rice: cDNA glycine rich cell wall protein, putative, expressed #Arabidopsis: glycine rich protein
0.90098	OsAffx.27322.1.S1_s_at	os05g45480	#UniProt: Putative uncharacterized protein OJ1131_E09.17 n #Rice: cDNA POEI45 Pollen Ole e I allergen and extensin family protein precursor, expressed #Arabidopsis: pollen Ole e 1 allergen and extensin family protein
0.90005	Os.53691.1.S1_at	os03g05060[1]	#UniProt: Xyloglucan galactosyltransferase KATAMARI 1, putative, expressed (Os03g0144300 protein) n #Rice: cDNA exostosin family domain containing protein, expressed #Arabidopsis: MUR3 (MURUS 3); catalytic/ transferase, transferring glycosyl groups
0.89693	OsAffx.2887.1.S1_at	os02g37100	#UniProt: Putative uncharacterized protein n #Rice: cDNA expressed protein
0.89658	Os.55091.1.S1_at	os01g14010	#UniProt: Putative zinc finger protein ID1 (Os01g0242200 protein) n #Rice: cDNA ZOS1 05 C2H2 zinc finger protein, expressed #Arabidopsis: NUC (nutcracker); nucleic acid binding / transcription factor/ zinc ion binding
0.89489	Os.57396.1.S1_at	os03g60300	#UniProt: Putative uncharacterized protein n #Rice: cDNA expressed protein #Arabidopsis: unknown protein
0.89478	OsAffx.11944.1.S1_at	os02g09070	#UniProt: Putative uncharacterized protein n #Rice: cDNA zinc binding protein, putative, expressed #Arabidopsis: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAI
0.89285	OsAffx.19018.1.S1_x_at	os11g25920	#UniProt: Putative uncharacterized protein n #Rice: cDNA transcription factor related, putative, expressed #Arabidopsis: unknown protein
0.89282	Os.53625.1.S1_at	os06g42754	#UniProt: Putative uncharacterized protein P0505A04.40 (Os06g0634000 protein) n #Rice: cDNA expressed protein
0.89203	Os.53616.1.S1_at	os01g71060	#UniProt: Putative uncharacterized protein n #Rice: cDNA xylanase inhibitor, putative, expressed #Arabidopsis: aspartic type endopeptidase

0.8912	Os.54004.1.S1_at	os12g22800	#UniProt: Expressed protein (Os12g0416800 protein) n #Rice: cDNA expressed protein #Arabidopsis: unknown protein
0.89104	Os.10029.1.S1_at	os07g44550	#UniProt: Putative uncharacterized protein n #Rice: cDNA peroxidase precursor, putative, expressed #Arabidopsis: peroxidase, putative
0.891	Os.57354.1.S1_at	os04g56500	#UniProt: OSIGBa0132E09 OSIGBa0108L24.22 protein n #Rice: cDNA expressed protein #Arabidopsis: proline rich family protein
0.88908	Os.20535.1.S1_at	os03g06000	#UniProt: Expansin A12 n #Rice: cDNA expansin precursor, putative, expressed #Arabidopsis: ATEXPA11 (ARABIDOPSIS THALIANA EXPANSIN 11)
0.88715	OsAffx.4247.1.S1_at	os05g04240	#UniProt: Putative uncharacterized protein n #Rice: cDNA GDSL like lipase/acylhydrolase, putative, expressed #Arabidopsis: GDSL motif lipase/hydrolase family protein
0.88705	Os.53557.1.S1_at	os06g10910	#UniProt: Putative uncharacterized protein n #Rice: cDNA xyloglucan fucosyltransferase, putative, expressed #Arabidopsis: FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups
0.88494	Os.49612.1.S1_at	os02g52630	#UniProt: Putative uncharacterized protein n #Rice: cDNA xyloglucan fucosyltransferase, putative, expressed #Arabidopsis: FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups
0.88155	OsAffx.17505.1.S1_at	os08g43770	#UniProt: Putative uncharacterized protein n #Rice: cDNA carrier, putative #Arabidopsis: unknown protein
0.88111	Os.54057.1.S1_at	os06g23420	#UniProt: Putative xyloglucan galactosyltransferase (Os06g0342000 protein) n #Rice: cDNA exostosin family domain containing protein, expressed #Arabidopsis: exostosin family protein
0.88017	Os.36470.1.S1_at	os07g15320	#UniProt: Leaf senescence related protein like protein (Putative uncharacterized protein) (Os07g0256700 protein) n #Rice: cDNA leaf senescence related protein, putative, expressed #Arabidopsis: unknown protein
0.87973	Os.56849.1.S1_x_at	os03g22600	#UniProt: Transposon protein, putative, Mutator sub class, expressed (Os03g0347700 protein) n #Rice: cDNA BTBN6 Bric a Brac, Tramtrack, Broad Complex BTB domain with non phototropic hypocotyl 3 NPH3 and coiled coi #Arabidopsis: phototropic responsive NPH3 family protein
0.87926	Os.49859.1.S1_at	os02g40070	#UniProt: Putative uncharacterized protein n #Rice: cDNA AP2 like ethylene responsive transcription factor PLETHORA 2, putative, expressed #Arabidopsis: PLT2 (PLETHORA 2); transcription factor
0.87866	Os.50694.1.S1_at	os04g41710	#UniProt: OSIGBa0103O01.7 protein n #Rice: cDNA expressed protein #Arabidopsis: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall, plant type cell wall; E
0.8783	Os.33904.1.S1_at	os01g14540	#UniProt: Os01g0248000 protein (Fragment) n #Rice: cDNA STIGL1 Stigma specific Stig1 family protein precursor, expressed #Arabidopsis: Encodes a Stigma specific Stig1 family protein
0.87707	Os.49220.1.S1_at	os09g12970	#UniProt: Os09g0300800 protein n #Rice: cDNA plant protein of unknown function domain containing protein, expressed #Arabidopsis: unknown protein
0.87474	OsAffx.29094.1.S1_at	os08g08020	#UniProt: Putative uncharacterized protein n #Rice: cDNA expressed protein #Arabidopsis: unknown protein
0.87444	Os.29907.1.S1_at	os01g48800	#UniProt: Purine permease like protein (Os01g0680200 protein) n #Rice: cDNA purine permease, putative, expressed #Arabidopsis: ATPUP4; purine transmembrane transporter
0.87395	OsAffx.3069.1.S1_at	os02g54450	#UniProt: Putative uncharacterized protein OJ1715_H01.38 (Putative uncharacterized protein OJ1316_E06.1) n #Rice: cDNA hypro1, putative, expressed #Arabidopsis: transferase, transferring glycosyl groups
0.87371	OsAffx.27695.1.S1_at	os06g18880	#UniProt: Embryogenesis transmembrane protein like (Os06g0292100 protein) n #Rice: cDNA cadmium tolerance factor, putative #Arabidopsis: ankyrin repeat family protein
0.87267	OsAffx.25840.1.S1_at	os04g02560	#UniProt: Os04g0115900 protein n #Rice: cDNA expressed protein #Arabidopsis: SR33; RNA binding / protein binding

0.87243	Os.56930.1.S1_at	os03g17220	#UniProt: Os03g0280700 protein n #Rice: cDNA dirigent, putative, expressed #Arabidopsis: disease resistance responsive family protein / fibroin related
0.87144	OsAffx.14236.1.S1_at	os04g42040	#UniProt: Putative uncharacterized protein n #Rice: cDNA expressed protein #Arabidopsis: FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPR
0.87018	OsAffx.17916.1.S1_at	os09g26910	#UniProt: Putative uncharacterized protein OJ1344_B01.32 n #Rice: cDNA hypothetical protein #Arabidopsis: unknown protein

[1] Putative xyloglucan biosynthesis genes are marked in red.

Supplementary Table S3. Relative quantification of XyG oligosaccharide profile of *Col.0*, *axy2.2* and *OsMUR2* transformed into the Arabidopsis *axy2.2*.

			OsMUR2-OX-*axy2.2*			
	Col.0	*axy2.2*	1	2	3	4
XXXG	34.14 ± 2.28*	29.57 ± 0.71	41.05 ± 3.18*	44.12 ± 8.01*	40.40 ± 2.49*	39.21 ± 1.40*
XXLG/XLXG	9.67 ± 0.60*	41.84 ± 1.48	7.76 ± 1.33*	8.05 ± 0.73*	7.64 ± 0.54*	7.92 ± 1.09*
XXLG/XLXG-Ac	1.93 ± 0.28*	0.15 ± 0.10	1.85 ± 0.34*	2.12 ± 0.44*	1.78 ± 0.38*	2.08 ± 0.13*
XXFG	7.68 ± 0.68*	0.08 ± 0.06	9.48 ± 0.98*	9.30 ± 0.74*	9.99 ± 0.17*	11.14 ± 0.81*
XXFG-Ac	12.84 ± 1.62*	0.38 ± 0.07	11.66 ± 0.82*	10.61 ± 2.32*	12.94 ± 1.51*	13.67 ± 1.50*
XLLG	2.76 ± 0.70*	27.11 ± 0.48	1.79 ± 0.95*	1.82 ± 0.54*	1.45 ± 0.37*	2.45 ± 0.55*
XLLG-Ac	2.35 ± 0.18*	0.44 ± 0.10	2.07 ± 0.21*	2.28 ± 0.49*	2.01 ± 0.09*	1.72 ± 0.08*
XLFG	9.55 ± 1.84*	0.11 ± 0.09	11.10 ± 1.47*	9.94 ± 1.39*	10.47 ± 1.03*	10.54 ± 0.73*
XLFG-Ac	19.08 ± 2.16*	0.32 ± 0.13	13.24 ± 1.64*	11.77 ± 3.92*	13.33 ± 1.72*	11.26 ± 2.07*

Asterisk indicates statistically significant difference from the mutant (*axy2.2*; $P < 0.05$), $n \geq 3$.

Supplementary Table S4. Relative quantification of XyG oligosaccharides profiles of *Col.0*, *axy4-3,* and *OsAXY4* transformed into the Arabidopsis *axy4-3* mutant.

			OsAXY4-OX-*axy4-3*				
	Col.0	*axy4-3*	1	2	3	4	5
XXXG	29.11 ± 1.60	26.48 ± 1.58	24.36 ± 0.69*	29.16 ± 2.76	27.13 ± 1.82	29.03 ± 2.96	29.19 ± 1.91
XXLG/XLXG	9.07 ± 0.28*	10.96 ± 0.63	9.76 ± 0.49*	11.58 ± 1.28	10.34 ± 0.11	11.24 ± 1.32	11.17 ± 0.66
XXLG/XLXG-Ac	2.20 ± 0.28*	0.08 ± 0.01	0.15 ± 0.15	0.32 ± 0.18*	0.87 ± 0.34*	0.46 ± 0.18*	0.32 ± 0.03*
XXFG	7.47 ± 1.00*	25.79 ± 1.14	26.71 ± 2.93	25.73 ± 1.07	23.44 ± 1.12*	23.18 ± 1.19*	26.61 ± 1.89
XXFG-Ac	16.19 ± 1.18*	-0.30 ± 0.08	0.61 ± 0.07*	0.35 ± 0.70	2.01 ± 0.35*	0.80 ± 0.22*	0.44 ± 0.46*
XLLG	2.68 ± 0.47*	4.24 ± 0.18	3.89 ± 0.36	4.21 ± 0.37	4.05 ± 0.25	4.44 ± 0.37	3.76 ± 0.45
XLLG-Ac	2.75 ± 0.06*	0.12 ± 0.03	0.19 ± 0.15	0.22 ± 0.15	0.61 ± 0.23*	0.37 ± 0.07*	0.35 ± 0.09*
XLFG	7.30 ± 1.09*	32.76 ± 1.82	33.77 ± 3.79	27.75 ± 4.19	27.94 ± 3.09*	29.31 ± 4.29	27.42 ± 3.43*
XLFG-Ac	23.22 ± 1.30*	-0.13 ± 0.23	0.55 ± 0.26*	0.68 ± 0.12*	3.60 ± 0.60*	1.16 ± 0.23*	0.73± 0.33*

Asterisk indicates statistically significant difference from the mutant (*axy4-3*; $P < 0.05$), n =4.

Supplementary Table S5. Relative quantification of XyG oligosaccharides profiles of *Col.0*, *xlt2 mur3.1*, *OsMUR3,* and *OsXLT2* transformed into the Arabidopsis *xlt2 mur3.1*mutant.

			OsMUR3-OX-*xlt2 mur3.1*				*OsXLT2*-OX-*xlt2 mur3.1*				
	Col.0	*xlt2 mur3.1*	1	2	3	4	1	2	3	4	5
XXG	34.51± 2.20*	89.78±4.62	20.62±14.09*	1.76±0.64*	1.96±0.94*	1.43±0.35*	65.28±1.97*	70.42±2.08*	64.83±5.30*	69.79±0.45*	82.99±3.
XLG/XLXG	7.66 ± 0.61*	1.04±0.69	6.32±1.53*	6.72±3.33*	6.43±1.76*	6.78±1.76*	28.54±2.50*	23.12±1.19*	26.79±3.58*	21.94±0.63*	10.05±2.9
XLG/XLXG-Ac	1.42 ± 0.18*	-0.05±0.16	4.20±0.91*	4.92±0.61*	5.00±1.69*	4.98±0.43*	0.04±0.11	-0.02±0.09	0.23±0.43	-0.08±0.05	-0.06±0.
XFG	4.14 ± 1.55*	0.80±0.90	21.35±11.81*	26.43±9.20*	36.23±14.64*	37.54±6.59*	0.45±0.23	0.46±0.06	0.68±0.31	0.73±0.15	0.62±0.
XFG-Ac	17.39 ± 1.55*	5.85±0.50	44.39±5.97*	54.15±11.86*	45.21±13.54*	45.25±7.14*	3.21±0.61*	3.91±0.57*	4.21±1.32	4.44±0.78*	6.22±1.
LLG	1.16 ± 0.48	0.11±0.92	0.84±0.79	1.61±0.74*	1.59±0.85*	1.45±0.50*	0.07±0.15	0.12±0.12	0.15±0.20	0.20±0.10	-0.30±0.
LLG-Ac	1.67 ± 0.12*	0.42±0.73	1.07±0.34	1.80±0.77*	1.06±0.35	0.83±0.57	0.04±0.09	0.02±0.03	0.06±0.40	-0.07±0.19	-0.32±0.
LFG	4.88 ± 2.60*	1.03±1.07	0.69±0.49	1.28±1.04	1.21±0.65	0.77±0.64	0.24±0.10	0.06±0.10	0.15±0.25	0.13±0.08	-0.17±0.
LFG-Ac	27.18 ± 2.86*	1.02±0.75	0.51±0.26	1.32±0.46	1.29±0.68	0.97±0.65	2.14±0.16*	1.91±0.51	2.90±1.31*	2.92±0.46*	0.97±0.

Asterisk indicates statistically significant difference from the mutant (*xlt2mur3*; $P < 0.05$), n =4.

Supplementary Table S6. Primers used in this study.

Primer	Sequence (5’->3’)
Os04g48480-CDS-GW-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGGCCGCGATGTATCGTCCC
Os04g48480-CDS-GW-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTACACTTTCCTCCAACTCCGTCGT
Os03g05110-CDS-GW-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGTCTGCTATGAGACGACGACC
Os03g05110-CDS-GW-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTTAGTTCTGACCTCTTTGTTCGTTT
Os02g52630-CDS-GW-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGCAGGTGCAGCAACGCAAG
Os02g52630-CDS-GW-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCTAGTTCGGACTTCCATTCGGATC
Os06g12870-CDS-GW-F	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGGTGACCACAAATTTCGTGCAGA
Os06g12870-CDS-GW-R	GGGGACCACTTTGTACAAGAAAGCTGGGTTCATCTGGTGATGGTCTGGAGCAGA
axy2.2-del-F	CACTAGATACTACGAAGCTTACTTATC
axy2.2-del-R	TTCGCTTTACAATCATAGAATGGAG
mur3.1-geno-F	CGAAGATCGGCATTTGACTC
mur3.1-geno-R	CATCCTCGGGGATGAATATC
Gabi-LB	CCCATTTGGACGTGAATGTAG
AtXLT2 –LP	GGAAACCGCTCTTCCTACATC
AtXLT2-RP	TCCGGTTTATCCGGTAAAAAC
Salk_044972-LP	TTATGCGATTATACGCAAGGG
Salk_044972-RP	TCATTTAAACCTTCCATCGCC

SALK_LBa1	TGGTTCACGTAGTGGGCCATCG
pOREE4GW-Seq-F	GGGAGAATTCGTCGACTTTG
Os4g48480-Genotype-R	CCATTAGACCGCTTGTAGTACG
Os3g05110-Genotype-R	CACATATTGGTCCAGAGGCTGAG
Os2g52630-Genotype-R	GTCTCTGGAGCTCCTCGTGCATC
PGWB511GW-seq-F	TGATATCTCCACTGACGTAAG
Os6g12870-Genotype-R	CGCAGCTCGTCCCGTTGTAGAG
AtPTB-RT-F	GCGAATGTCTTATTCAGCTCATACTGA
AtPTB-RT-R	CATTGCTGCTGTTGGTATATCAGAGTA
OsMUR3-qRT-F	ACAGTTGAGAAGAGATA
OsMUR3-qRT-R	ATTAGTAGATGGATTAGTAG
OsXLT2-RT-4F	GTGTACGTCTACGACCTCCC
OsXLT2-RT-4R	GAGTACCACGACCCAACCAG
OsMUR2-RT-2F	ACGAGAAATCATGTCGCAGC
OsMUR2-RT-2R	GACCACGTACTTGCACTGCT
OsAXY4-RT-3F	CCTCTACGCTCTCATCCCTCT
OsAXY4-RT-3R	TTCTCCGGCTATCGCATTCTTCTT

Reference:

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