Primer name	Primer sequence (5' to 3')	Primer sequence (5' to 3') Associated gene region Use		Expected amplified product size	
	5'-GAGGCTTACGTGGGATTTC-3'	Osfuct			
P1	(23265977–23265997)	genomic DNA	Genotyping	1,220 bp	
Do	5'-GCAGATTTTACACAACATTTCGAC-3'	Osfuct		1	
P2	(23266215–23266239)	genomic DNA	Genotyping		
 D2	5'-GCATAAAGCTTGAGGGCAAG-3'	Osfuct			
P3	(23267177–23267197)	genomic DNA	Genotyping	500 bp	
	5'-ACGTCCGCAATGTGTTATTAAGTTGT-3'			1	
P4	(8212–8237)	T-DNA	Genotyping		
P5	5'-ACGACCAGGTCGTCTAACGACTCCG-3'		RT-PCR/ cloning of genomic DNA	7,605 bp for gDNA & 1,542 bp for cDNA	
	(23265083–23266007)	Octuat			
	5'-	cDNA/geno			
P6	AACGATATIGCTGTGTGATATAATGTAATGTA CTATGTTATAACTG-3'	mic DNA			
	(23278263–23278307)				
	5'-GGTCCGCAGCATGCAAAGGC-3'				
P7	(23263321–23263341)	Osfuct	Cloning	2 852 hn	
Do	5'-GGGAGTTGGCAAGGCGACCTC-3'	promoter	8	_,	
P8	(23265061–23265082)				
Actin1	5'-CAACACCCCTGCTATGTACG-3'				
- F	(401–420)	Actin1 cDNA	RT-PCR	508 bp	
Actin1	5'-GTTGCCATATAGATCCTTCC-3'		_	ľ	
- R	(889–898)				

Table S1. Primers used in this study.

Table S2. Primers used in the qRT-PCR analysis.

Primer name	Primer sequence (5' to 3')	Gene name	Expected amplifie d product size
Os03g0629800_S1F	5'-GCTCGTGGTGCATGATGATA-3'	Hypothetical protein	98 hp
Os03g0629800_S1R	5′-GGGAAGAGAAATCCTGTGAATCT-3′		
Os07g0162450_S1F	5'-GAGCAATCTCTGCTCCTCATATC-3'		98 hp
Os07g0162450_S1R	5'-GTTTGTTGTCGAGCCGTAGA-3'	- Hypothetical protein	, , , , , , , , , , , , , , , , , , ,
Os01g0965300_S1F	5'-GTCGGAGATCGAGCGGTA-3'		02 hr
Os01g0965300_S1R	5'-TCGACGACGACCACCTC-3'	- Hypothetical protein	95 bp
Os03g0299700_S1F	5′-TGGTTACGTTCAAGCGAAGAG-3′		100 hrs
Os03g0299700_S1R	5'-CGGCACCAGCATAAGAAGAA-3'	- Hypothetical protein	100.00
Os03g0105500_S1F	5'-TGAATTCCTCGGTTGGATCTG-3'		106 hp
Os03g0105500_S1R	5'-TCCTTGTCACTATGTTGCTCTT-3'	 Hypothetical protein 	100 bp
Os07g0529000_S1F	5'-GGGCAAAGGAGTTACTGAAGAG-3'		80 hp
Os07g0529000_S1R	5'-TCCTGGATTTGGCAAGAACAT-3'	- Isocitrate lyase	ву рр
Os01g0872900_S2F	5'-CGTTGGGAGAAGTGTCCTTTAG-3'	Clutathiono S	00 hp
Os01g0872900_S2R	5'-CAAGTCCTGGGAAGCAACA-3'	transferase T3	99 bp
Os07g0511400_S1F	5'-GTTGGTGTCGGCGTTGG-3'		90 hp
Os07g0511400_S1R	5'-CGCCACGTCGATGTCTTAAC-3'	- Hypothetical protein	
Os01g0698800_S1F	5'-CACTTCTCTGGCCGTCTTATT-3'		93 hn
Os01g0698800_S1R	5'-GATCACCTAGAGAACGGGAAAC-3'	Hypothetical protein	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
Os10g0142700_S3F	5'-GCAGTATCCTCCGTCGTC-3'	Putative wall- associated protein	93 bp

Os10g0142700_S3R	5'-TTTGGTTGGCACCTCTTTC-3'	kinase (Non protein coding RNA)	
Os04g0301500_S1F	5'-TCATCACCGCCAACATCAC-3'	Transcription factor	102 bp
Os04g0301500_S1R	5'-CCTCCACCATCTGCTTCATTT-3'	bHLH35	1
Os10g0142600_S1F	5'-GCTAACAAAGGGAGCCTCTAC-3'	Putative wall- associated protein	01.1
Os10g0142600_S1R	5'-CCGACCCAACAGCAATATCT-3'	kinase (protein kinase APK1A, chloroplastic)	91 bp
Os01g0204900_S1F	5'-CGACTTGAGCTGCAAACTTATC-3'		106 bp
Os01g0204900_S1R	5'-GTATTATCCATTGGGCCACATATTC-3'	- Hypothetical protein	1
Os02g0441000_S1F	5'-GGAGAAGAGAGTGGTGGTTTC-3'		102 bp
Os02g0441000_S1R	5'-CCACCTCCTAGCTGCAATAAT-3'	- Hypothetical protein	
Os11g0477400_S1F	5'-GAGAGGTGTCCGTGTGTTTAG-3'		96 bp
Os11g0477400_S1R	5'-CCAGACTTGTTGAGCGTAACT-3'	- Hypothetical protein	1
Os05g0211800_S1F	5'-TTAGCGAGGTTGCACCATATTA-3'		101 bp
Os05g0211800_S1R	5'-GGCAAACACGAAGAATCAATACA-3'	- Hypothetical protein	Ĩ
Os08g0193600_S3F	5'-GGGAATCAGGCGGAGATG-3'		97 bp
Os08g0193600_S3R	5'-GAGGGTTAGGGTTTGAGAGAG-3'	F-box protein-like	<i>57 bp</i>
Os09g0358000_S1F	5'-CACAGCTGAAGGAGAGTCTAAC-3'	Probable LRR receptor-like	
Os09g0358000_S1R	5'-CCATAGCCACCACTACATCATC-3'	serine/threonine- protein kinase At1g51810	90 bp
Os12g0140266_S1F	5'-CAGTTCTACTGTGTGTGGAGAG-3'	Transcription initiation factor IIE	91 bp
Os12g0140266_S1R	5'-GTCTTCCTGCCTCTTCTGTATG-3'	subunit alpha isoform X1	r
Os02g0146600_S4F	5'-GAGAACTACCTCCATCGCATTG-3'	Eukaryotic initiation	97 bp
Os02g0146600_S4R	5'-CGAACAGCATCCTCTCATCATC-3'	factor 4A-3	1
Os02g0252400_S4F	5'-TACTACGCGCCTCTCATCA-3'	Dof zinc finger protein	88 bp

Os02g0252400_S4R	5'-GCTGCATCAGAGAACCAGAA-3'		
Os01g0137150_S3F	5'-CCAACTGTACCTCTTGCTTCA-3'		101 bp
Os01g0137150_S3R	5'-GATGAGGACTTCTGCCCTAAAG-3'	- Hypothetical protein	1
Os04g0192200_S4F	5'-CCTCACCATGCTCTCCAAA-3'		77 hn
Os04g0192200_S4R	5'-AGAAGACGGTGGTCGATCT-3'	- Hypothetical protein	<i></i> p
Os02g0269650_S1F	5'-CGACCGGCCAACAAGAA-3'		75 hn
Os02g0269650_S1R	5'-GTTGGAAATGGAGGAGGAGAAA-3'	- Hypothetical protein	75 bp
Os10g0340100_S3F	5'-TCAGATCCAACATCAACCTTCTC-3'		89 hp
Os10g0340100_S3R	5'-TTTCCTCCCTCCACTCCAT-3'	- Hypothetical protein	89 bp
Os04g0397800_S1F	5'-CAGGCTAGGGTTTGGGATATTT-3'		90 hp
Os04g0397800_S1R	5'-TCGCATGCGGTTGCTTAT-3'	- Hypothetical protein	90 bp
Os12g0543800_S3F	5'-AAGAAGACCGCCAATGATTCT-3'	Hypothetical protein	99 hp
Os12g0543800_S3R	5'-TCTTCCCTCACCTACTGTATTCT-3'		<i>уу бр</i>
Os09g0356800_S4F	5'-GCTGGATCACCGAGAATAGTG-3'	Probable LRR receptor-like	
Os09g0356800_S4R	5'-TGATGTGACCATGACCTTGTAATA-3'	serine/threonine- protein kinase At1g51810	99 bp
Os04g0112100_S2F	5'-GGCTGGACAAGTCGATGAAT-3'	Putative disease	98 bp
Os04g0112100_S2R	5'-ATCTCCTCCTCCTTGTGATGA-3'	resistance protein RGA4	r I
Os12g0169300_S4F	5'-AAGAAGACCGCCAATGATTCT-3'	Disheveled-	99 bp
Os12g0169300_S4R	5'-TCTTCCCTCACCTACTGTATTCT-3'	- associated activator of morphogenesis 1	<i>уу бр</i>
Os12g0228500_S1F	5'-AAGAAGACCGCCAATGATTCT-3'		103 bp
Os12g0228500_S1R	5'-TCTTCCCTCACCTACTGTATTCT-3'	- Hypothetical protein	r
Os01g0605500_S1F	5'-TGTTGCTGCTGGTCTTACTC-3'	Kinesin-like protein	99 bn
Os01g0605500_S1R	5'-CGGGTTGGTTCTGTTGTTCTA-3'	KIF19	r

Os04g0116800_S4F	5'-GGACATCATCAGTGAGCTTCAG-3'	Hypothetical protein	101 bp
Os04g0116800_S4R	5'-CACTACCATCATTGTACTACTCCTATTT-3'		
Os04g0103800_S3F	5'-CTCACTCCTCTCCCACGTC-3'	WASH complex	97 bp
Os04g0103800_S3R	5'-TCGTCGTCGCTCGTCAT-3'	homolog	-
Os01g0974600_S4F	5'-GCTGGTGGACATTTATCCCATTA-3'	Glycine-rich RNA-	78 bp
Os01g0974600_S4R	5'-GAGGCAGAAGCAATCCAACT-3'	binding protein 2	
Os04g0125700_S2F	5'-CGTACTCTTGGACGACGATTT-3'	L-type lectin-domain	101 bp
Os04g0125700_S2R	5'-AGCCTATGGCAGTTGTCTTC-3'	kinase IX.1	1
Os01g0629000_S2F	5'-GCACTCTGCAGGCAAAGATA-3'		79 bp
Os01g0629000_S2R	5'-TGCAGAATCTGAAGACTGTTGT-3'	Hypothetical protein	I
Os03g0794000_S1F	5'-ACCACTCCAGCATCCACTA-3'	Non-specific lipid transfer protein GPI-	77 bp
Os03g0794000_S1R	5'-GCGACGAGGATGACCAATATC-3'	anchored 2 isoform X1	1
Os09g0286300_S2F	5'-CCATGATTGGAGGGAGGAAAG-3'	ENDOSPERM	89 bp
Os09g0286300_S2R	5'-GAACCTGTACTGGAGGTAGGA-3'	DEFECTIVE 1	0, 2p
Os10g0552600_S1F	5'-CTCTGCACCGCCATCAA-3'	Cortical cell-	83 bp
Os10g0552600_S1R	5'-CCGCAGTTGTTGAGGATGA-3'	delineating protein	ou up
Os08g0472600_S1F	5'-GTTCCTGTGTGGAAGGATGAA-3'	Glycoprotein 3-	89 bp
Os08g0472600_S1R	5'-TGTGTAAGGCCGATTGGATAAA-3'	alpha-L- fucosyltransferase A	
Hygromycin_S1F	5'- GCTTTCAGCTTCGATGTAGGA -3'	Hygromycin	96 bp
Hygromycin_S1R	5'- CGATGCAAAGTGCCGATAAAC -3'		
UBI_S1F	5'- GAAGTAAGGAAGGAGGAGGA -3'	Ubiquitin	99 hn
UBI_S1R	5'- AAGGTGTTCAGTTCCAAGG -3'		

7	
8	
9	
10	
11	
12	
13	
14	
15	
16	
17	
18	Table S3. Structures and corresponding calculated masses of the major N-glycans for
19	the wild-type (DJ), Osfuct mutant (HM, homozygote; HT, heterozygote) and restore
20	lines (R12) plants.

m/z	Structure	DJ	HM	HT	R12
1065.2	Man ₃ XylGlcNAc ₂	+	+	+	+
1081.2	Man ₃ FucGlcNAc ₂	+	+	+	+
1211.3	Man ₃ XylFucGlcNAc ₂	+	-	+	+
1268.7	GlcNAcMan ₃ XylGlcNAc ₂	-	+	+	+
1414.6	GlcNAcMan ₃ XylFucGlcNAc ₂	+	-	+	+
1617.4	GlcNAc2Man3XylFucGlcNAc2	+	-	+	+
1926.3	(FA)GnFXF/Gn(FA)XF	+	-	+	+
2235.6	(FA)(FA)XF ₃	+	_	+	+

A calculated mass of the major N-glycans was compared with earlier reports to
assign the corresponding structures ([15], [16], [40]). A, galactose; F, fucose; (FA),
Lewis A determinant; Gn, *N*-acetylglucosamine; M, mannose; X, xylose. For the

25	corresponding structures, refer to Figure S3 .
26	
27	
28	
29	
30	
31	
32	
33	

- **Table S4**. Microarrays genes significantly (log₂ fold change> 1.6and *p*-value < 0.1) up-
- 35 regulated in *Osfuct* mutant compared with wild-type (Dongjin).

SN	Gene ID	Gene location	DJ vs HM (log ₂ ratio)	Gene descriptions
1	Os07g0162450	33715363372781	21.91	Hypothetical protein
2	Os07g0529000	2069110320693734	10.46	Isocitrate lyase
3	Os12g0169300	35254593528156	4.53	Disheveled-associated activator of morphogenesis 1
4	Os12g0228500	69841946988897	4.47	Hypothetical protein
5	Os01g0872900	3786012937865917	3.74	Glutathione S- transferase T3

6	Os01g0698800	2891021128911075	3.04	Hypothetical protein
7	Os04g0301500	1346644513468863	2.95	Transcription factor bHLH35
8	Os05g0211800	69040226904580	2.67	Hypothetical protein
9	Os11g0477400	1670875616734818	2.54	Hypothetical protein
10	Os02g0441000	1494787114950082	2.49	Hypothetical protein
11	Os02g0252400	85902878594087	2.12	Dof zinc finger protein
12	Os12g0140266	19421631948013	1.98	Transcription initiation factor IIE subunit alpha isoform X1
13	Os09g0358000	1157602211588924	1.93	Probable LRR receptor- like serine/threonine- protein kinase At1g51810
14	Os02g0146600	25575642561015	1.83	Eukaryotic initiation factor 4A-3
15	Os01g0137150	19912441996867	1.69	Hypothetical protein
16	Os04g0192200	62658966271636	1.67	Hypothetical protein

Table S5. Microarrays genes significantly (\log_2 fold change> 1.6 and *p*-value < 0.1)

44 down-regulated in *Osfuct* mutant compared with wild-type (Dongjin).

SN	Gene ID	Gene location	DJ vs HM (log ₂ ratio)	Gene descriptions
----	---------	---------------	---	-------------------

1	Os10g055260	21600206 21607772	2.18	Cortical cell-
	0	2109030021097772	-2.10	delineating protein
2	Os09g028630	(2(9202 (271210	1.05	ENDOSPERM
2	0	03002920371219	-1.95	DEFECTIVE 1
2	Os01g097460	42070905 42071121	1 07	Glycine-rich RNA-
3	0	430/0805430/1131	-1.82	binding protein 2
	$\Omega_{c}04a012570$			L-type lectin-domain
4	0504g012570	15622561572689	-1.81	containing receptor
	0			kinase IX.1
5	Os01g062900	26781020 26784102	1 7/	Hypothetical protein
5	0	2070192920704102	-1./4	
				Non-specific lipid
6	Os03g079400	22027845 22020214	1.65	transfer protein GPI-
6	0	3302704333029314	-1.03	anchored 2 isoform
				X1

5.

	No.	Sample	Туре	Comment					
	1	Dongjin_1	Control	Cultivar to make Osfuct mutant					
	2	Dongjin_7	Control	Cultivar to make Osfuct mutant					
	3	Dongjin_8	Control	Cultivar to make Osfuct mutant					
	4	PMHMABFT5	Osfuct mutant	Homozygote of Osfuct mutant					
	5	PMHMABFT8	Osfuct mutant	Homozygote of Osfuct mutant					
	6	PMHMABFT9	Osfuct mutant	Homozygote of <i>Osfuct</i> mutant					
61 62 63									
64									
65									
66									
67									
68									
69									
70									
71									
72									
73									
74									
75									
76									
77									
78	Table S7. Experimental metrics report.								

Table S6. Experimental design of Roche Nimblegen Oryza sativa 135 K microarray.

	-	 r -	 	 - r

I	IMAGE_	INTER	SIGNAL	UNIFOR	UNIFOR	NUM_	MEAN_	NUM_EX	MEAN_	NUM_R	MEAN_R

NAME	QUART	_RANG	MITY_	MITY_	EMPTY	EMPTY	PERIME	EXPERIM	ANDO	ANDOM
	NSITY	E	WILAIN	CV			INTAL	ENTAL	IVI	
Dongjin1	2.81	0.239	3044.05	0.05	146232	826.06	137604	2779	11735	390.03
Dongjin7	2.90	0.38	3664.08	0.07	146232	910.46	137604	3335	11735	409.48
Dongjin8	2.99	0.33	3996.99	0.06	146232	933.00	137604	3558	11735	381.90
PM-HM-	2.02	0.52	2014 01	0.08	146222	020.00	127604	2406	11725	407.02
ABFT5	2.93	0.52	3914.91	0.08	140252	920.90	137004	3490	11755	407.02
PM-HM-	2.87	0.25	2/12 28	0.05	146222	010.88	127604	2100	11725	404.10
ABFT8	2.07	0.23	3413.30	0.05	140232	910.00	137004	5122	11755	404.10
PM-HM-	2.87	2.87 0.27	4105.82	0.04	146232	1036.66	137604	3725	11735	465.37
ABFT9_										

80

IMAGE_NAME (the name of the analyzed image file); INTERQUARTILE_DENSITY 81 (the interquartile range of the raw signal intensities); SIGNAL_RANGE (the signal 82 range represents the signal range on a per channel basis for both one- and two-color 83 84 microarray applications); UNIFORMITY_MEAN (the mean signal intensity of all the probes in each uniformity block); UNIFORMITY_CV (the coefficient of variation of 85 the block uniformity means); NUM_EMPTY (the number of empty features present 86 87 on the array); MEAN_EMPTY (the mean signal intensity of empty features present on the array); NUM_EXPERIMENTAL (the number of experimental features present 88 on the array); MEAN_EXPERIMENTAL (the mean signal intensity of the 89 experimental features present on the array); NUM_RANDOM (the number of 90 random control features present on the array); MEAN_RANDOM (the mean signal 91 92 intensity of the random control features present on the array). Reference: NimbleGen 93 Arrays User's Guide: CGH Analysis v6.0







Figure S1. Phenotype of *Osfuct* mutant. Morphological phenotype of mutant (HM
and HT) compared with Dongjin. (A) Phenotype of Dongjin (B) HM. (C) HT. Scale
bar is 17 cm.



106

Figure S2. Multiple sequence alignment of OsFucT with other glycosyltransferase proteins. Comparisons of the deduced amino sequence of OsFucT with glycosyl transferase proteins from *T. aestivum*, *H. vulgare*, *S. italica*, *Z. mays*, *S. bicolor*, *C. cajan*, *G. max*, *N. tabacum*, *S. lycopersicum*, *S. moekkendorffii* and *P. patens*. A number of the amino acid residue is shown in the upper of the sequence. Conserved glycosyl transferase domain shown in the black box, low complexity and transmembrane domain is underlined. Chemically similar residues are denoted with a color and

shade. Dashes indicate gaps introduced to maximize the alignment of homologousregion.

116



Figure S3. Glycans profiling of Dongjin (wild-type), *Osfuct* mutant (HM and HT) and rescued rice line using mass spectrometry (MALDI-TOF). (A) Dongjin; (B) HM, homozygote line; (C) HT, heterozygote line; (D) R12, rescued lines. Values in parentheses indicate numerical representation of the peak intensity. (E) Representative structures examples of *N*-linked glycans obtained from Dongjin,





Figure S4. Chip information of whole genome 135K oligo microarray. Sequence
source (RAP2), probe length (60 mer), probe per array (125,956), feature size (13 μm
x 13 μm), array dimensions (8.9 mm x 6.5 mm), overall slide dimensions (25 x 75
mm).







- 151

 152

 153

 154

 155

 156

 157

 158



Figure S6. Signal distribution in Dongjin and PH_HM_ABF microarrays. Signal
 comparison between Dongin (A-C) and PH_HM_ABF microarrays (D-F).



Figure S7. qRT-PCR results for the differentially expressed transcripts in wild-type
(DJ) and *Osfuct* mutant (HM) to verify transcriptome profile data produced by
microarray analysis. Error bars show standard deviation.