A

NE4528 NF0595

Os01g0869200 (*OsMGT1*)

■ UTR   ▯ ORF   ▼ *TOS17*   — intron   → Primer

B

NH₂   COOH

G
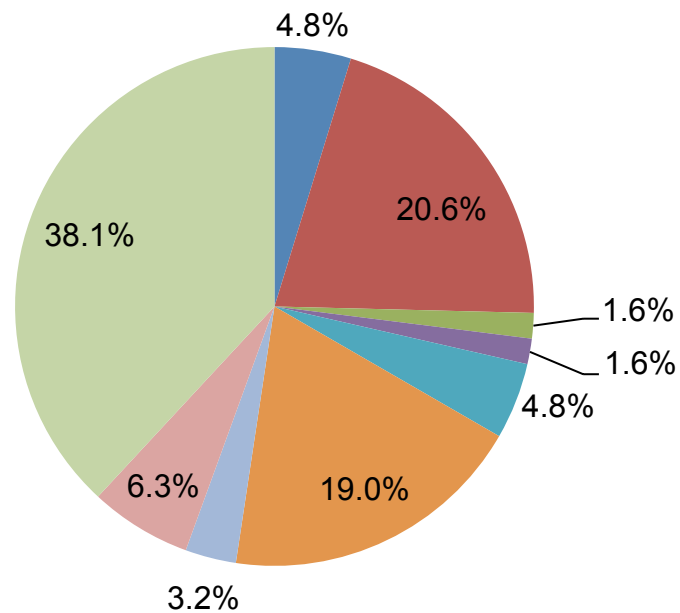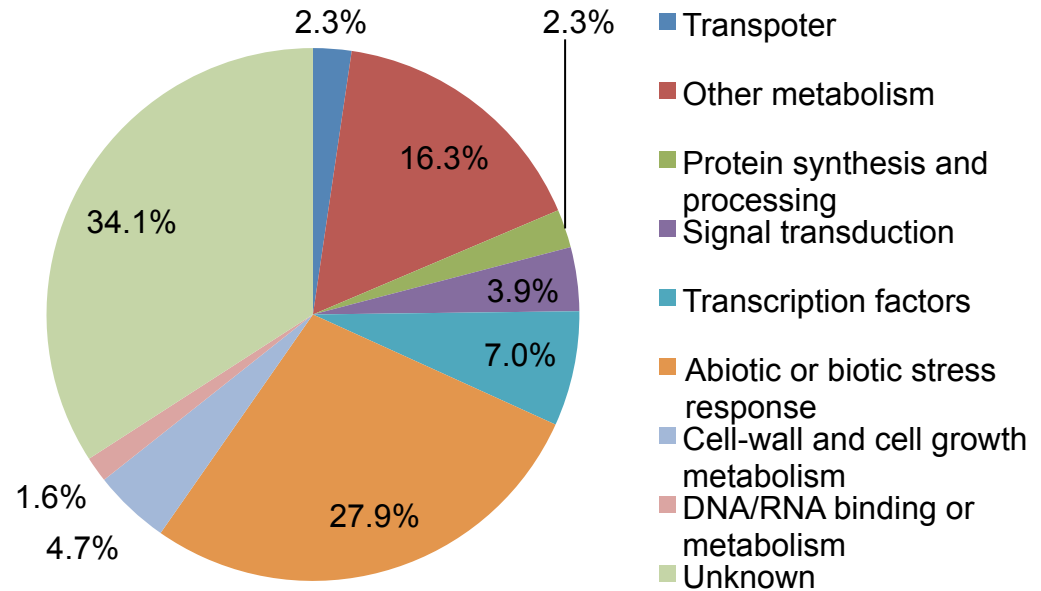M
N

C

WT   NF0595   NE4528

Histone H3

OsMGT1

Supplemental Figure S1. Gene structure (A), predicated membrane domains (B) and mRNA expression of Tos-17 lines of *OsMGT1* examined by RT-PCR. Insertion position of two Tos-17 insertion lines (NF0595 and NE4528) indicated by triangles.

Supplemental Figure S2. Phylogenetic tree of rice and Arabidopsis MGTs (A) and alignment of OsMGT1 with Arabidopsis homologs (B). Predicted C-terminal transmembrane domains (TM) and the conserved GMN motif are indicated. The alignment was performed by CLUSTAL W.

Down-regulated

4.8%	20.6%
38.1%	1.6%
	1.6%
	4.8%
6.3%	19.0%
3.2%	

Up-regulated

2.3%	2.3%
34.1%	16.3%
	3.9%
	7.0%
1.6%	27.9%
4.7%	

- Transpoter
- Other metabolism
- Protein synthesis and processing
- Signal transduction
- Transcription factors
- Abiotic or biotic stress response
- Cell-wall and cell growth metabolism
- DNA/RNA binding or metabolism
- Unknown

Supplemental Figure S3. Functional classification of down- or up-regulated genes in *OsMGT1* knockout line. Microarray analysis was conducted with roots of wild-type (WT) rice and a knockout line (NE4528) exposed to 50 μM (pH 4.5) Al for six hours. Genes significantly down-regulated or up-regulated more than 2 folds in the knockout line compared with WT were selected. Genes were categorized into 9 classes according to the OryzaExpress database (http://bioinf.mind.meiji.ac.jp/OryzaExpress/).