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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.



R		I M1	IM2	
OsMGT1	TLYHIREYADDTEDYINIMLDEKQNQLLQMGVMLTT	ATVVVTAGIVVVSLFGMN	HIDLMKDPETPEMVRMSNMHFWETTFGTVAGCIAIYLLAIY	AGRKSKILQ-
AtMGT1	KLTSLKEYIDDTEDFINIQLDNVRNQLIQFELLLTT	ATFVVAIFGVVAGIFGMNF	EIDFFEKPGAFKWVLAITGVCGLVVFLAFLW	/FYKRRRLMPL
AtMGT2	KLTSLKEYIDDTEDFINIQLDNVRNQLIQFELLLTT	ATFVVAIFGVVAGIFGMNF	EIDFFNQPGAFRWVLIITGVCGFVIFSAFVW	/FFKYRRLMPL
AtMGT3	KLSSLKEYIDDTEDLINIKLGNVQNQLIQFQLLLTA/	ATFVAAIFAAVTAVF <mark>GMNI</mark> .	QDSVFQNPTTFQYVLLITGIGCGFLYFGFVL	YFKHKKVFPL
AtMGT4	KLSTLREYVDDTEDYINIMLDDKQNHLLQMGVMLTT	ATLVMSAFIAVAGVFGMN	TIELFTDNKHGPSRFIWTVIGGSIGSICLYVGAIG	WCKYKRLLE-
AtMGT5	KILLMKEHIDSTEAYVKILQNSRRNGLIHLMMLVNI(GNYAITAGTVVVNLFGMN	PIGLYSTPDIFGYVVWAVVALCIVLFIVTVG	YAKWKKLLD-
AtMGT6	KILTVREYIDDTEDYVNIQLDNQRNELIQLQLTLTI	ASFAIAAETLLASLFGMN	PCPLYSIHGVFGYFVWSVTALCIVLFMVTLG	YARWKKLLGS
AtMGT7	KLTELREYIDDTEDYINIQLDNHRNQLIQLELMLSAC	GTVCVSVYSMIAGIFGMNI	PNTWNHDHGYIFKWVVSLTGTFCIVLFVIILS	YARFRGLIGS
AtMGT8	KLTELREYVDETEDFLNIQLDSSRNQLIKFEIILTAG	GSICVSVYSVVVGILGMN	PFPWNIKKHMFKWVVSGTATVCAILFVTIMS	FARYKKLFGF
AtMGT9	RLTTLREYIDDTEDYINIQLDNHRNQLIQLELVLSS	GTVCLSMYSLVAGIFGMN	PYTWNDGHGYMFKYVVGLTGTLCVVVFVIIMS	YARYKGLVGS
AtMGT10	QAERLLDSAKEMEDSIAVNLSSRRLEVSRFELLLQV	GTFCVAVGALIAGIF <mark>GMNI</mark> .	RSYLEEQASAFWLTTGGIIIGAAVAFFLMYS	YLSRRKIF
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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.



Up-regulated

Down-regulated

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 μ M (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/).