

Reduced expression of a gene encoding a Golgi localized monosaccharide transporter (*OsGMST1*) confers hypersensitivity to salt in rice (*Oryza sativa*).
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SUPPLEMENTARY DATA

Figure S1. Alignment of *OsGMST1* with other members in rice pGlcT (plastid glucose transporter) subfamily.

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Os09g23110 : -MQPPPPPPHFAALLPLPLPLFFCLPAAPRVGRGGTAVAALGAL-WPRLVAVESRPP- : 57
Os01g04190 : MAGTGASVKMIRCVMKCGGQQHVVAARGDRKSPALAAPPPATVRMGRVLCCGMRRSG : 60
OsGMST1 : -----MRWKLKSSAYKR-----VSRDAAMDLDVE- : 25

Os09g23110 : ---PPSSPPASASAPPLPEASAAAGLDAGIGGGGGGGGGG-----ADLGWLRVFP : 104
Os01g04190 : ADLAGVEMAAAGPQPGGVSGLFRGPRSSPRYSRV RATATVDPEDIPLEKVVQAKSSGSVLP : 120
OsGMST1 : ---TPAKMADGGAP-----SWRMSLP : 43

Os09g23110 : HVLTAWSMANFLFGYHIGVMNGPIEDIARELGFQGNPFLQGLVVSIFIVGAFPGSLGSSAL : 164
Os01g04190 : YVGVAWCLGAILFGYHIGVMNGALEYLAKDLGISENAVWLQGGVWVSTTLGATAGSFTGGAL : 180
OsGMST1 : HVCVATLTSFLFGYHSGVWNEPLESISTDLGFAGNTLAEGLVVSIWCLGGAFVGCCLFSGSI : 103

Os09g23110 : VDNFCCKRTLQIDSILLILGALLSAQADSLDEMLLGRFLVCIWICIGINTVLVPLVSEVAP : 224
Os01g04190 : ADKECRTRTFILDAIWBLAVGAFLSATAHDVRTMIIWGRLLAGTIGIGISSALVPLYISWISEISP : 240
OsGMST1 : ADGTCRRRAFQLSALWEMIIWCAAVSALTNWSLEGMLLGRFLVCIWCMGLGPPVASLYITEVSP : 163

Os09g23110 : TKYRCSLGTLCQIGTCLGIIAAFLSCLISESDPHWRTMLYAAWCVFGLVIVAGMQFAVES : 284
Os01g04190 : TEIRCALGSVNOLFICIGILAALVACLPLAGNPAWWRTMFGISIVPSILLALGMAVSEPS : 300
OsGMST1 : PSVRCWTYGSFVCIATCLGIVVSLLIWTEVKDIDRWRVCFWVAWAVWEATLQALGMEFCAES : 223

Os09g23110 : PRWLAKVGRIDDARNVVEHVWWCPSEVEKSMEEIQSVVANDDSQ-ASWSELLEPHNRVAL : 343
Os01g04190 : PRWLFQQGLSQAETAWIKKLYGREKVAEVWMYDLKAASQGSSEPDAGWLDLFSKRYWWKVVS : 360
OsGMST1 : PQWLYKCCRTTEAETQFEKLLWGPLHVKSAMAELSRWSERGDWGENVKYSELWFYGRNFWNVVF : 283

Os09g23110 : IGGSDWFLQCFAGINWGLYFSSLTFRDVWGITSGILASLYVWGITNFAGAIWVASILMDKQGR : 403
Os01g04190 : VGAAMFLFQQLAGINAVVYWSTSVFRSAGIASDVAASALVGAANVWCTMIASWSLMDKQGR : 420
OsGMST1 : ICTTLEALQQLSGINSVWFYFSSSTVWERSVGVPP-NLANICMWCIANLSWCSIVAMLLMDKLCR : 342

Os09g23110 : KKLLTGSYLGMALAMWELIVYAIWSFPLDEGVSHGLSITWCTLLYIFWFAICAGPVTGIIWIPE : 463
Os01g04190 : KSLWLITWSFSGMAASMLLLSWLFTWKALAPYSGPLAVAGTWVLYVLSWEALGAGPVPALLWLPE : 480
OsGMST1 : KVLLSGSFLGMWAFAMCLQAVGANRHHLGSASVYLSVCGMLWLFVLTEWSLGAGPVPGLLLWLPE : 402

Os09g23110 : LSGARTWRSKVMGFSFTVWHWICNWFLVGLYFLELAKKWLVGAVWAGFGGVSLLSALFAYNFI : 523
Os01g04190 : IFASRIRAKAVALSLGMWHWVSNWFEICLYFWLSVVKWFCISTVYWLGWASVCALAVVYIAGNV : 540
OsGMST1 : IFPNKIRAKAMALCMSVWHWVNFWFVSLWFLRLLEQLWCPQVWLTWMFSSACVVAWAIFVRRHV : 462

Os09g23110 : VETKGRSLEIEWMSLSPAAPGKRE : 547
Os01g04190 : VETKGRSLEIWTERALSWSAS----- : 559
OsGMST1 : VETKCKTWLEIEVSLWLQTQ----- : 481

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Figure S2. Growth of hexose transporter deficient yeast cells transformed with sense and antisense *OsGMST1* on plates supplemented with sugars. S1, S2 are two dependent transformant lines of EBY VW4000 expressing *OsGMST1* in sense orientation, AS1 is one transformant line expressing *OsGMST1* in antisense orientation, and Vector is one line transformed with the empty vector pEX-Tag. Transformant lines (S1, S2, AS1, Vector) were grown on maltose for 2 days, and on other monosaccharides (glucose, fructose, mannose, galactose, ribose, xylose) as the sole carbon source for 3 days.

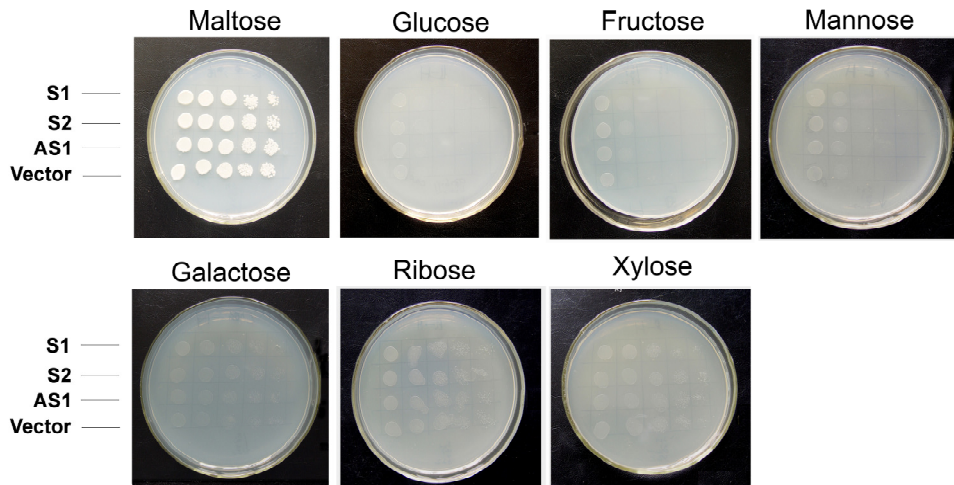


Figure S3 Distribution of stress related cis-elements in the *OsGMST1* promoter region.

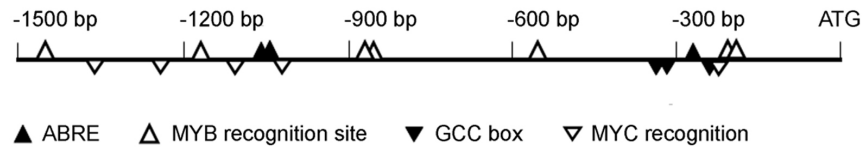


Figure S4. Molecular identification and phenotype observation of *OsGMST1* knockdown transgenic rice plants. **A)** Diagram of *OsGMST1* antisense construct for rice transformation. LB, left border; RB, right border; *Gus*, β -glucuronidase; *Ubi*, ubiquitin promoter; *NOS*, *NOS* terminator; *Hpt*, hygromycin phosphotransferase. **B)** Southern blot analysis of antisense independent transgenic rice lines. WT indicates the wild type, AS-L4, L12, L18 indicate the antisense transgenic lines. Rice genome DNA in the left 4 lanes are digested by *EcoRI* and the right 4 lanes are digested by *HindIII*. **C)** Real time PCR analysis of the *OsGMST1* relative expression in knockdown lines. WT indicates the wild type rice, and AS4, 5, 12, 18 indicate the antisense transgenic rice lines. Data are means \pm SD ($n = 3$). ** indicates $P < 0.01$ by student's T-test. **D)** Quantitative PCR analysis of the *Os01g04190* and *Os09g23110* relative expression in *OsGMST1* knockdown lines. WT indicates the wild type rice, and AS12, 18 indicate the knockdown transgenic rice lines. Data are means \pm SD. **E)** Phenotype observation of the *OsGMST1* antisense transgenic plants under normal growth conditions WT and AS-L12 indicate wild type and the *OsGMST1* knockdown rice respectively. a, Seeds. b, Seeds germinated for 2 days. c, 4-week-old seedlings. d, Rice at grain filling stage. a, b, Bars = 0.5 cm. c, Bar = 5 cm. d, Bar = 20 cm.

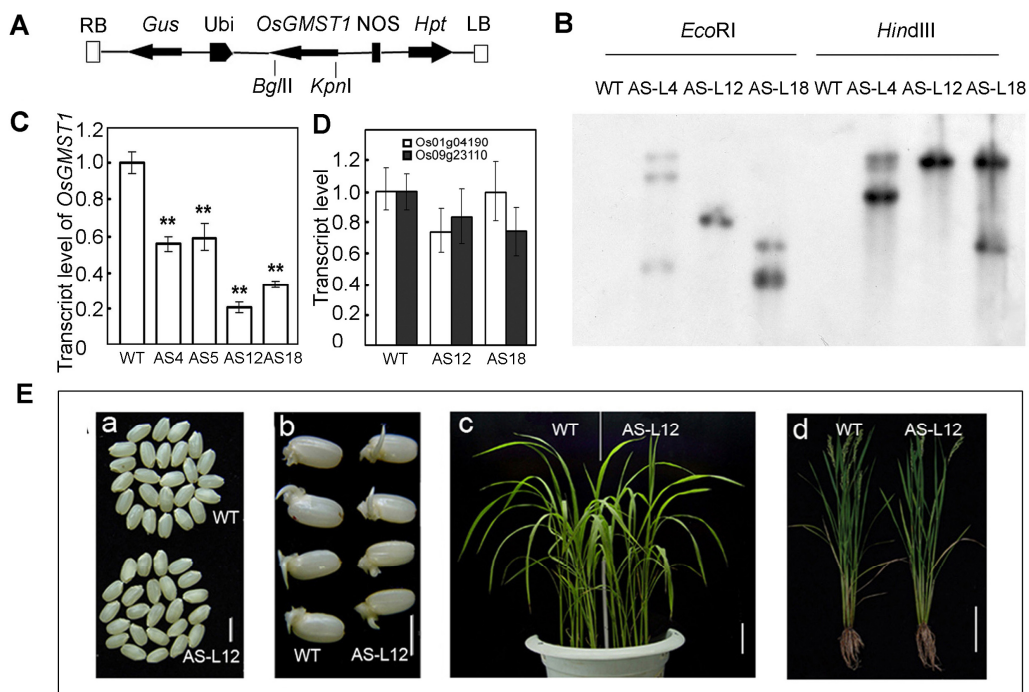


Figure S5. Molecular identification and phenotype observation of *OsGMST1* overexpressed transgenic rice plants. **A)** Southern blot analysis of independent transgenic rice lines. WT indicates the wild type, OE3, OE8, OE24 indicate the transgenic lines. Rice genome DNA in the left 4 lanes are digested by *EcoRI* and the right 4 lanes are digested by *HindIII*. **B)** Real time PCR analysis of the *OsGMST1* relative expression in overexpressor lines. WT indicates the wild type rice, and OE3, OE6, OE8, OE24 indicate the transgenic rice lines. Data are means \pm SD ($n = 3$). **C)** Growth of WT and *OsGMST1* overexpressed transgenic seedlings before (left) and after (right) NaCl treatment. 2-week-old seedlings were treated by 200 mM NaCl for 11 days, and then recovered for 7 days. **D)** Survival rate of WT and *OsGMST1* transgenic seedlings after treated with 150 mM and 200 mM NaCl. 24 seedlings of 3 weeks old were used in each repeat. Error bars are SE of three replicates. **E)** Phenotype observation of *OsGMST1* overexpressed rice plants under normal growth conditions. WT and OE3 indicate wild type and *OsGMST1* overexpressed rice respectively. a, Seeds. b, Seeds germinated for 2 days. c, 4-week-old seedlings. d, Rice at grain filling stage. a, b, Bars = 0.5 cm. c, Bar = 5 cm. d, Bar = 20 cm.

