

Supplementary Information:
**Silencing of *OsGRXS17* in rice improves drought stress tolerance by
modulating ROS accumulation and promoting ABA-mediated
stomatal closure**

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Table S1 Primers used for qRT-PCR

Gene name	Accession #	Primer sequence
<i>OsGRXS17</i>	AK067982.1	Forward: TTCAGTACGGTTATATTGCCAGTT Reverse: AAGCACCCCTCTATTAATTGCGATA
<i>RAB16A</i>	NM_001074376	Forward: CCAGTTCCAGCCGATGAG Reverse: TCCTCCCTCCCATTCCAT
<i>LEA3</i>	NM_001062730	Forward: ACCAAGGACTCTGCCATC Reverse: GCTCTTCACCTGCTCACT
<i>DREB1A</i>	XM_015755426	Forward: GGCTGGGACCTGTACTAC Reverse: CTAGTAGCTCCAGAGTGG
<i>DREB1E</i>	XM_015779684.1	Forward: CACAGGGAATGCTCATCG Reverse: CAGTAGCTCCATAGATTGACC
<i>SalT</i>	XM_015766617.1	Forward: TGACAAGTGCTAATAATACATACG Reverse: GTTCCAGACCTTCCAAAGA
<i>LIP9</i>	XM_015771723.1	Forward: GAAGACGCAACTGCTGTG Reverse: CTGCTCACTTCCTCTGTAG
<i>AP59</i>	AY587109.1	Forward: CAACAAGCGGCCATATCC Reverse: GAAGACGACGACGAGGAG
<i>AP37</i>	KM262835.1	Forward: GCAGCAATAGCACGGTAG Reverse: AACAAATCCAAGTCCAGAGTC
<i>TFIIAγ5</i>	NM_001060961	Forward: GGGTTTGCCTGGTATTTGTAG Reverse: GTTGCTGCTGTGATATACTCTG



Fig. S1 Multiple amino acid sequence alignment of GRXS17 in *Arabidopsis*, tomato (*Solanum lycopersicum*), potato (*Solanum tuberosum*), maize (*Zea mays*) and rice (*Oryza sativa*, long isoform). Completely conserved residues are indicated by black boxes and residues conserved in the majority of sequences are indicated by gray boxes. The CGFS active domains are indicated by red border rectangles.

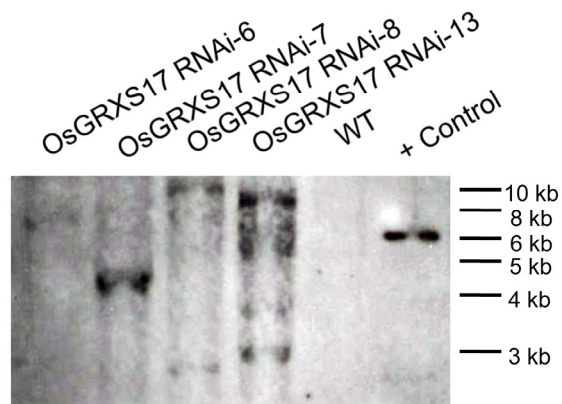


Fig. S2 Southern-blot analysis of T-DNA copy number of the *OsGRXS17* transgene. DNA probe of a *hygromycin phosphotransferase* gene was used for hybridization.

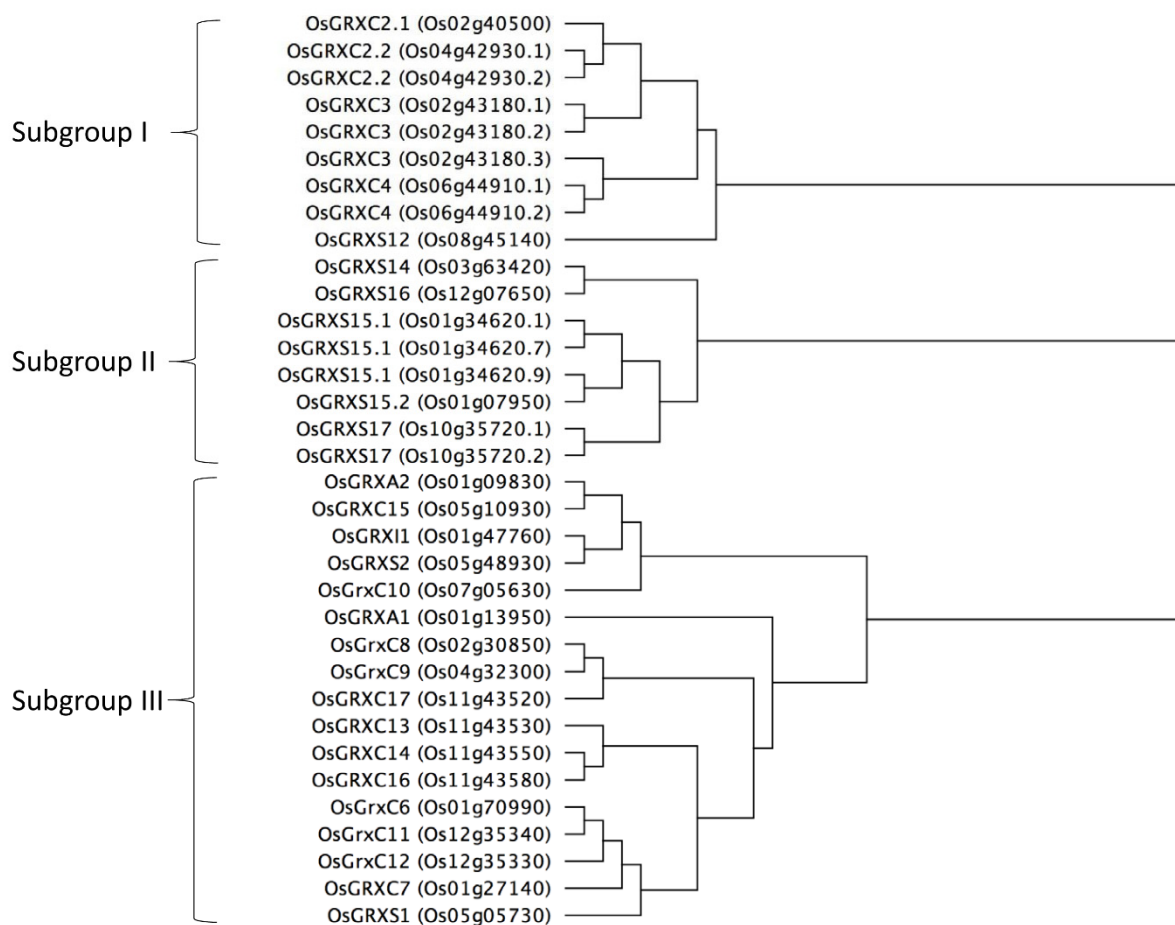
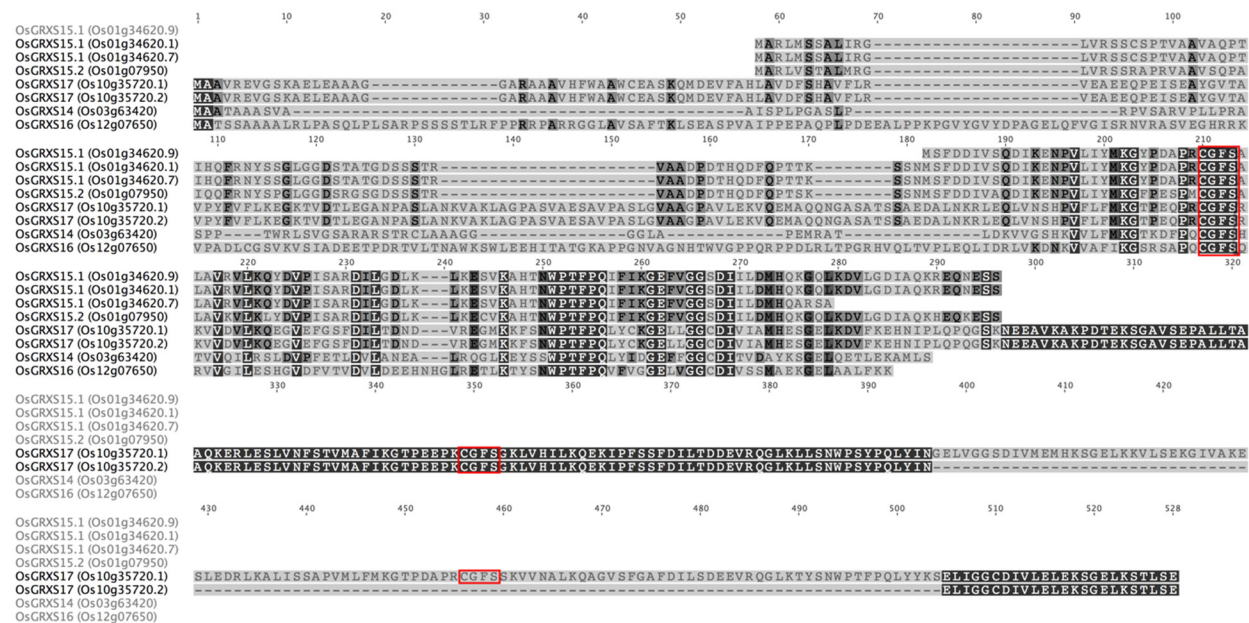


Fig. S3 Phylogenetic tree of rice glutaredoxin genes in subgroup I, II and III.

a



b

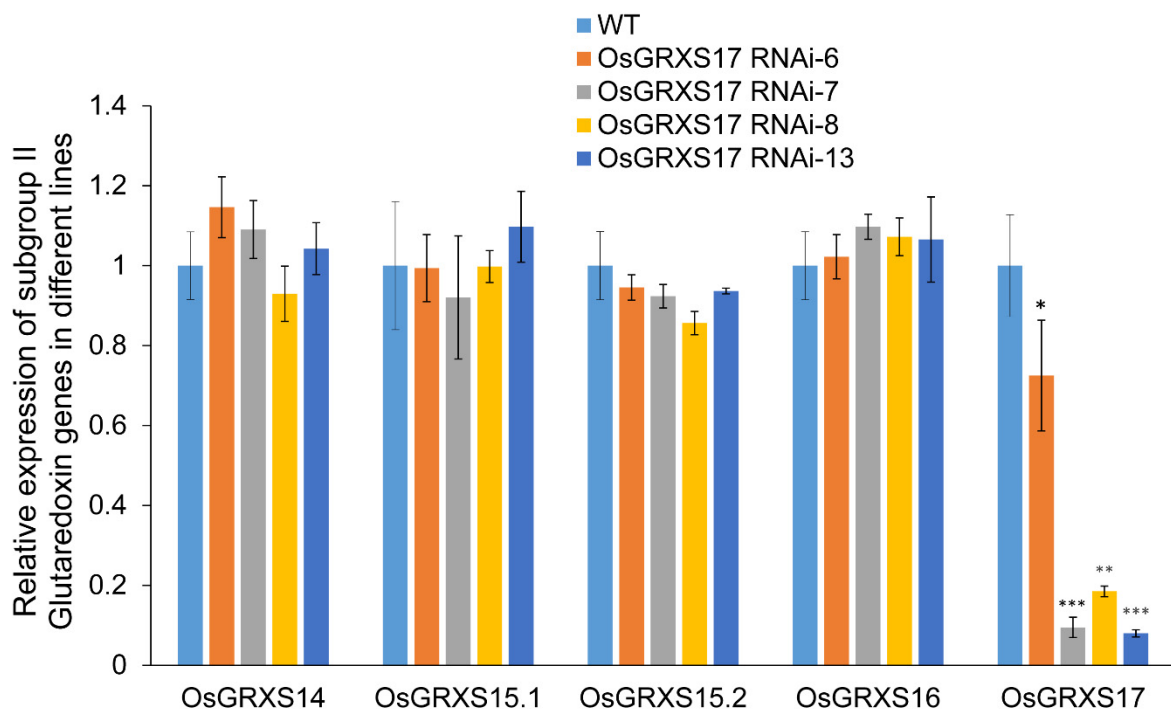


Fig. S4 (a) Multiple amino acid sequence alignment of rice glutaredoxin genes in subgroup II. Completely conserved residues are indicated by black boxes and residues conserved in the majority of sequences are indicated by gray boxes. The CGFS active domains are indicated by red border rectangles. (b) The relative expression levels of subgroup II glutaredoxin genes were measured by qRT-PCR in wild-type and four *OsGRXS17*-silenced rice plants.

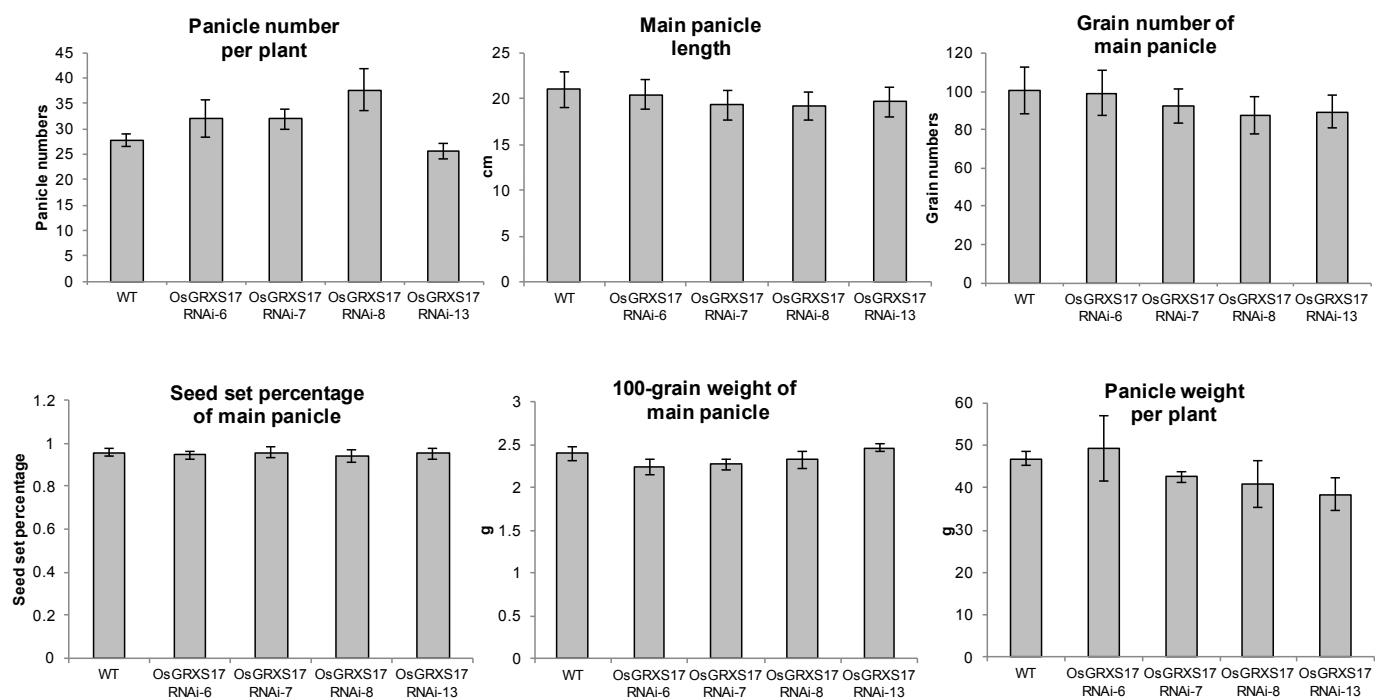


Fig. S5 Comparison of agronomic traits between wild-type and *OsGRXS17* silenced rice plants.

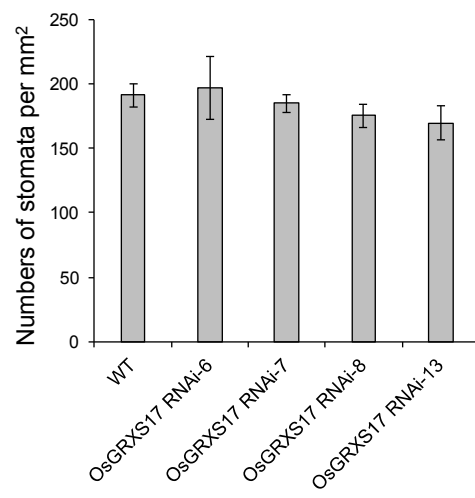


Fig. S6 Comparison of stomatal density between wild-type and *OsGRXS17* silenced rice plants.

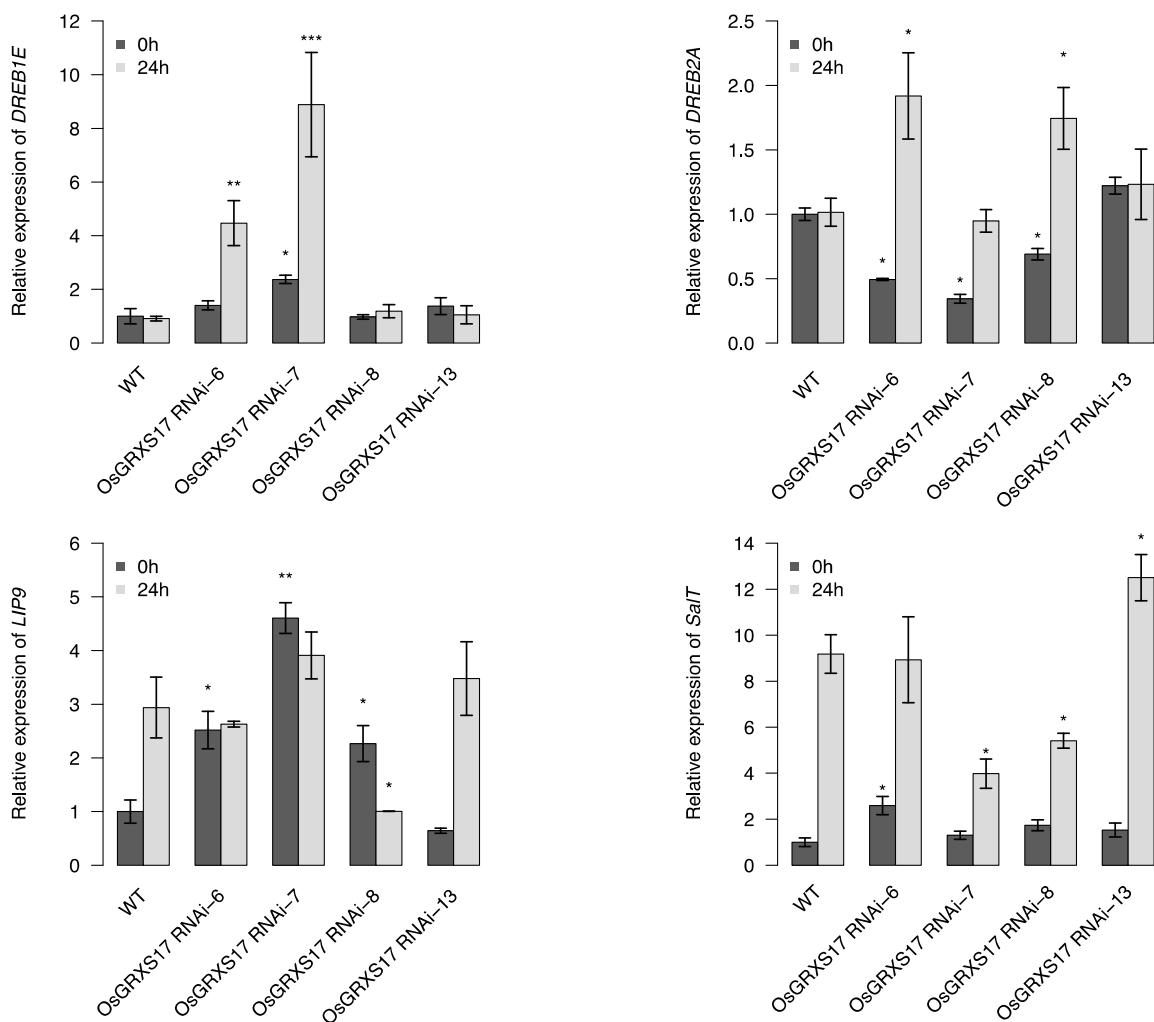


Fig. S7 Relative expression of four selected ABA-dependent and/or ABA-independent drought-responsive genes under ABA treatment.

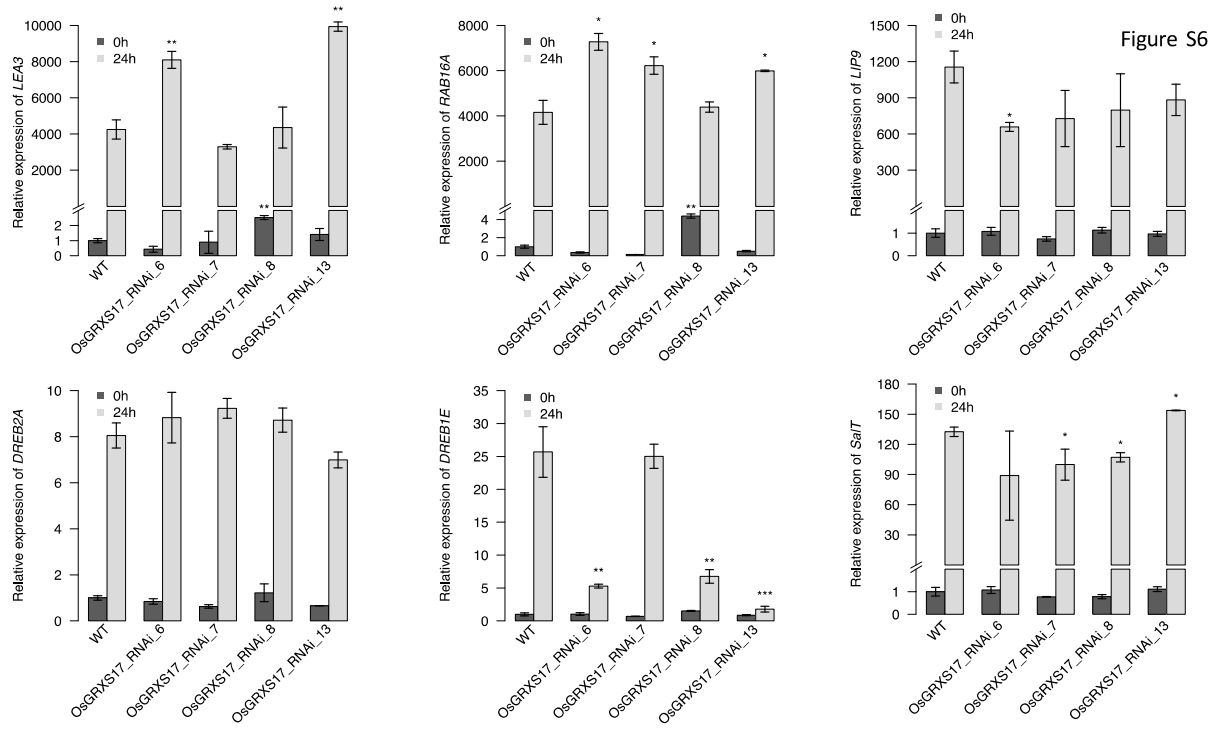


Fig. S8 Relative expression of six selected ABA-dependent and/or ABA-independent drought-responsive genes under drought treatment.

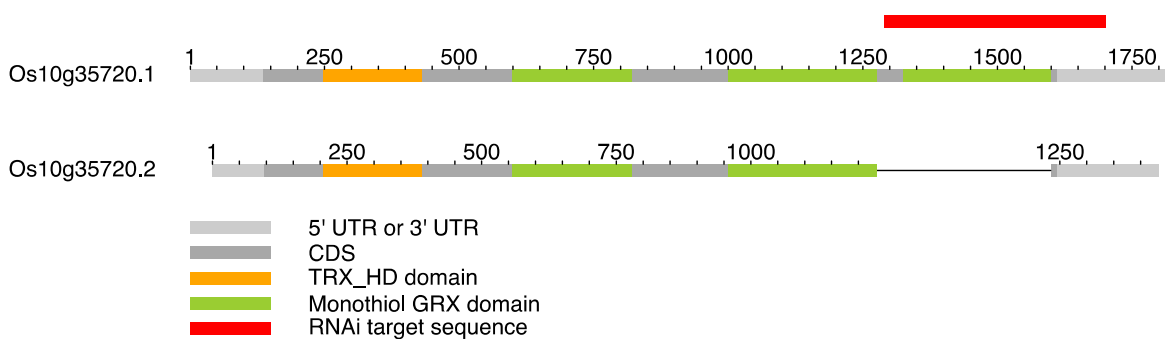


Fig. S9 Domain structure of two alternatively spliced *OsGRXS17* mRNAs. Red boxes indicate Thioredoxins_like homology domains; purple boxes indicate monothiol glutaredoxin domains; Orange boxes indicate RNAi target sequence.

(Full-length gels)



Fig. S10 Molecular characterization of *OsGRXS17*-silenced transgenic rice plants (progeny lines). The expression of a *hygromycin phosphotransferase* (*hpt*) gene was confirmed by RT-PCR in wild-type (NB) and nineteen *OsGRXS17*-silenced rice plants. The *TFIIAγ5* gene was included as control for uniform RT-PCR conditions (bottom).