## Supplementary Tables and Figures

Supplementary Table S1. Primers used in this study.

| Name | Forward primer | Reverse primer | Purpose |
|---|---|---|---|
| *Ghd2*-OE | *ggggtacc*CTGGGAGATTTCTTCTGTTT | *cgggatcc*TCGAGTCCATGAGGCATA | Overexpression |
| Ghd2-flag | *ggggtacc*CTGGGAGATTTCTTCTGTTT | *cgggatcc*GGTGACGGCGCACGGGGC | Overexpression (3×flag) |
| Ghd2-sub | *cgcggatcc*CTGGGAGATTTCTTCTGTT | *cgcggatcc*CTTGACGAACCGGCCCTT | Subcellular localization |
| *Ghd2*-grna | *ggca*ATCCTCATCGTGCTTCAAGG | *aaac*CCTTGAAGCACGATGAGGAT | CRISPR |
| *Ghd2*-cas-PCR | TTTGTGCTGGGAGATTTCTT | GCCTCGTAGTTGAGCCTGA | PCR for sequencing |
| *Ghd2*-cas-seq | TCGGTGGAGGAGGAGGCG | | Sequencing |
| *CAS9*-PCR | GCATGAAGAGGATCGAGGAG | GATCTCTTGCTCGGACTTGG | *CAS9* detection |
| *HPT*-PCR | TACACAGCCATCGGTCCAGA | TAGGAGGGCGTGGATATGTC | *HPT* detection |
| *Ghd2*-probe | ATGGTCGAAGCGCAA | ACAACCCCGAGTAATGG | Northern |
| Ghd2-BiFC | *cgcggatcc*CTGGGAGATTTCTTCTGTT | *ggggtacc*GGTGACGGCGCACGGGGC | BiFC |
| GF14b-BiFC | *cgggatcc*GGCATTTGTAGAGTTTTTAGAT | *cgggatcc*CTGCCCCTCGCTGGAGT | BiFC |
| GF14c-BiFC | *cgggatcc*TAATCCCTTAATTGGTCAAA | *cgggatcc*CTGGCCCTCGCAGGCGT | BiFC |
| OsARID3-BiFC | *cgggatcc*GCATCTGGATTTGAGCCTA | *cgggatcc*CATTAACTTTGACTGCTCGAA | BiFC |
| Ghd2-Y2H | attB1TGAGCTGCAGCTCGGAGAA | *att*B2-TCGAGTCCATGAGGCATACG | Y2H |
| Ghd2-Y2H-N1 | *att*B1-TGAGCTGCAGCTCGGAGAA | *att*B2-*ccta**CTCCTCCACCGACGCC* | Y2H |
| Ghd2-Y2H-N2 | *att*B1-TGAGCTGCAGCTCGGAGAA | *att*B2-*ccta*TGCGGCCGCCGCGTCATC | Y2H |
| Ghd2-Y2H-N3 | *att*B1-TGAGCTGCAGCTCGGAGAA | *att*B2-*ccta*ATCCGGGAGCTGCTGCAC | Y2H |
| Ghd2-Y2H-N4 | *att*B1-TGAGCTGCAGCTCGGAGAA | *att*B2-*ccta*CAGCTCGTTGCTGTCGTC | Y2H |
| Ghd2-Y2H-N5 | *att*B1-TGAGCTGCAGCTCGGAGAA | *att*B2-*ccta*GCTGTTGGAGGCAACACC | Y2H |
| Ghd2-Y2H-N6 | *att*B1-TGAGCTGCAGCTCGGAGAA | *att*B2-*ccta*CACCGTCATCATCCCCAC | Y2H |
| Ghd2-Y2H-C1 | *att*B1-TGGGGATGATGACGGTGA | *att*B2-TCGAGTCCATGAGGCATACG | Y2H |

| | | | |
|---|---|---|---|
| Ghd2-Y2H-C2 | *att*B1-GGGTATCTCTCCCATCAT | *att*B2-TCGAGTCCATGAGGCATACG | |
| Ghd2-Y2H-C3 | *att*B1-TGCAGGACTCGTTCTACA | *att*B2-TCGAGTCCATGAGGCATACG | |
| Ghd2-Y2H-C4 | *att*B1-GCTTTGTCAACTTCGAAC | *att*B2-TCGAGTCCATGAGGCATACG | |
| Ghd2-Y2H-C5 | *att*B1-CCTCATCGTGCTTCAAGG | *att*B2-TCGAGTCCATGAGGCATACG | |
| Ghd2-Y2H-C6 | *att*B1-CGGCGGCGGCGGTGGGGA | *att*B2-TCGAGTCCATGAGGCATACG | |
| Ghd2-none | *cgggatcc*CTGGGAGATTTCTTCTGTTT | *ggggtacc*TCGAGTCCATGAGGCATA | |
| Ghd2-gal4BD | *cgggatcc*AGCTGCAGCTCGGAGAAG | *ggggtacc*TCGAGTCCATGAGGCATA | |
| *ICL*-190 | *cccaagctt*GAAACGAGAACTACGACGAGC | *gaagatct*CACGCACTGTCAACGATGAG | |
| *MS*-190 | *cccaagctt*TCTGTGAGACAGATAGGTGGA | *gaagatct*GTGTGAGTAGAAAATGGGAGT | |
| *OsPPDKB*-190 | *gaagatct*CCGTGTTTCACTGTTTCCCAATGTC | *gaagatct*CGATCTCCCCTCCAACTCCAAGC | LUC assay in protoplasts |
| *OsAS1*-190 | *cccaagctt*GACAAATACGCTGAATGCATA | *gaagatct*GCCGCGAGGATTACTACC | |
| *OsSGR*-190 | *cccaagctt*CGCTCTCGTTCATCCTGTT | *gaagatct*GCCTAACAACCAAAACGACTC | |
| *OsNYC3*-190 | *cgggatcc*AATCGTAGACCTCAAAACCC | *cgggatcc*CAGGAAGAAAAAAAGACATAGC | |
| *OsPAO*-190 | *cccaagctt*GCCTGCACCAGGGTAAAG | *gaagatct*GAAGAAGAGAGTAGGAAACGGA | |
| *Ghd2*-qRT | TTGCCTCCAACAGCAGGG | GCTTCGGATGAGCGCG | |
| *ICL*-qRT | GACAGGGCCTGGAAGTGAGA | CCTCTGAATAATCCTCATCACATCCT | |
| *MS*-qRT | ACTTCTCCGAGTACTTTGCTCATACTT | TCTAGTGCAAACAAACAGGAATTGT | |
| *OsAS1*-qRT | TGTGCCGTTCCTCGACAA | TTCCACTCAGGGTCCATGCT | |
| *OsSGR*-qRT | TTCGTTTGGTTGCCATGGTA | AGCACGCAGCGTCATTTG | qPCR |
| *OsNYC1*-qRT | GTCGTCTGCGCATTCATAATTC | GGGATCATGTGCCTGGAAGA | |
| *OsNYC3*-qRT | TGTGTGCTCCAAAGGGACAA | CCCTGCCTTTGGCACCTA | |
| *Ubi*-qRT | AACCAGCTGAGGCCCAAGA | ACGATTGATTTAACCAGTCCATGA | |

Supplementary Table S2. Public microarray results of *OsK*, *OsL*, and *OsJ* in response to drought stress treatment at 7-day-old seedling stage.

| Name | Normal growth | | | Drought stress | | |
|---|---|---|---|---|---|---|
| | Replicate 1 | Replicate 2 | Replicate 3 | Replicate 1 | Replicate 2 | Replicate 3 |
| *OsK* | 277.1 | 264.6 | 332.5 | 154.2 | 139.7 | 155.4 |
| *OsL* | 156.8 | 185.6 | 209.3 | 15.2 | 18.5 | 20.9 |
| *OsJ* | 828.5 | 780 | 1075 | 373 | 319.9 | 360 |

Supplementary Table S3. Public microarray results of *OsK* in response to drought stress treatment in three rice organs.

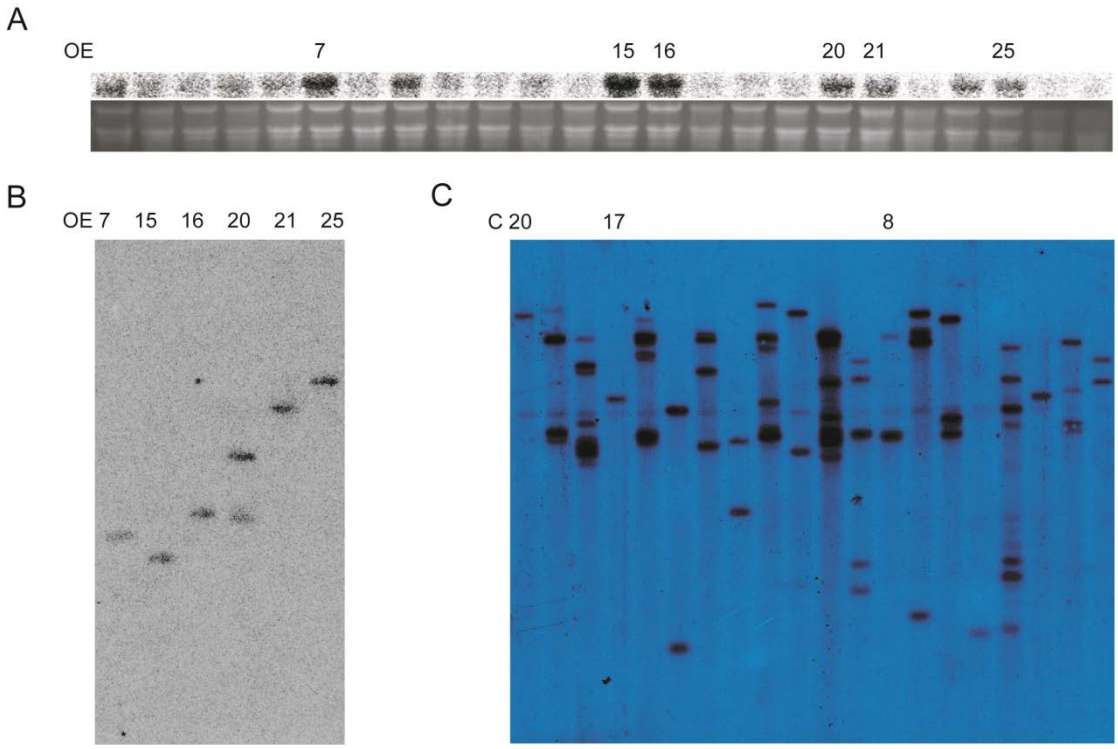
| Organ | Drought-1 | | Drought-2 | | Drought-3 | |
|---|---|---|---|---|---|---|
| | LogRatio | *P*-value | LogRatio | *P*-value | LogRatio | *P*-value |
| Flag leaf | -0.317 | 2.35E-02 | -0.233 | 1.58E-01 | -0.805 | 2.15E-02 |
| Shoot | -0.242 | 2.79E-01 | -0.016 | 8.49E-01 | -0.975 | 1.10E-04 |
| Panicle | N/A | N/A | N/A | N/A | -1.221 | 3.58E-02 |

Supplementary Table S4. GO analysis of up-regulated DEGs in the *Ghd2*-OE plants during drought stress treatment.

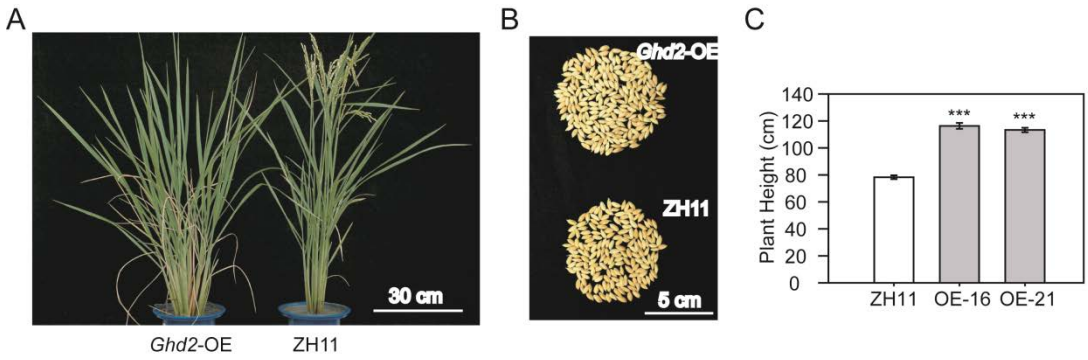
| GO Term | | Count[a] | *P*-value |
|---|---|---|---|
| Biological process | | | |
| GO:0003333 | amino acid transmembrane transport | 36 | 1.20E-06 |
| GO:0098656 | anion transmembrane transport | 65 | 3.10E-06 |
| GO:0006787 | porphyrin-containing compound catabolic process | 25 | 3.70E-06 |
| GO:0033015 | tetrapyrrole catabolic process | 25 | 3.70E-06 |
| GO:0051187 | cofactor catabolic process | 28 | 6.70E-06 |
| GO:0015849 | organic acid transport | 129 | 3.80E-05 |
| GO:0046942 | carboxylic acid transport | 129 | 3.80E-05 |
| GO:0015996 | chlorophyll catabolic process | 23 | 6.60E-05 |
| GO:0046149 | pigment catabolic process | 24 | 7.90E-05 |
| GO:0006865 | amino acid transport | 75 | 8.90E-05 |
| Molecular function | | | |
| GO:0015171 | amino acid transmembrane transporter activity | 71 | 6.60E-05 |
| GO:0005342 | organic acid transmembrane transporter activity | 105 | 7.50E-05 |
| GO:0046943 | carboxylic acid transmembrane transporter activity | 105 | 7.50E-05 |
| GO:0015293 | symporter activity | 126 | 0.00023 |
| GO:0008514 | organic anion transmembrane transporter activity | 131 | 0.0003 |
| GO:0015294 | solute:cation symporter activity | 37 | 0.00045 |
| GO:0016746 | transferase activity, transferring acyl groups | 344 | 0.00056 |
| GO:0008509 | anion transmembrane transporter activity | 200 | 0.00078 |
| GO:0016798 | hydrolase activity, acting on glycosyl bonds | 363 | 0.00087 |
| GO:0016747 | transferase activity, transferring acyl groups other than amino-acyl groups | 308 | 0.00089 |
| Cellular component | | | |
| GO:0000329 | fungal-type vacuole membrane | 14 | 0.00015 |
| GO:0000324 | fungal-type vacuole | 15 | 0.00019 |
| GO:0009570 | chloroplast stroma | 331 | 0.00024 |
| GO:0009532 | plastid stroma | 335 | 0.00026 |
| GO:0000322 | storage vacuole | 17 | 0.00028 |
| GO:0044434 | chloroplast part | 651 | 0.00151 |
| GO:0009536 | plastid | 1784 | 0.00202 |
| GO:0044435 | plastid part | 686 | 0.0024 |
| GO:0009507 | chloroplast | 1755 | 0.00349 |
| GO:0000323 | lytic vacuole | 88 | 0.00478 |

Note: The listed terms is top ten overrepresented GO terms according to the *P*-value.

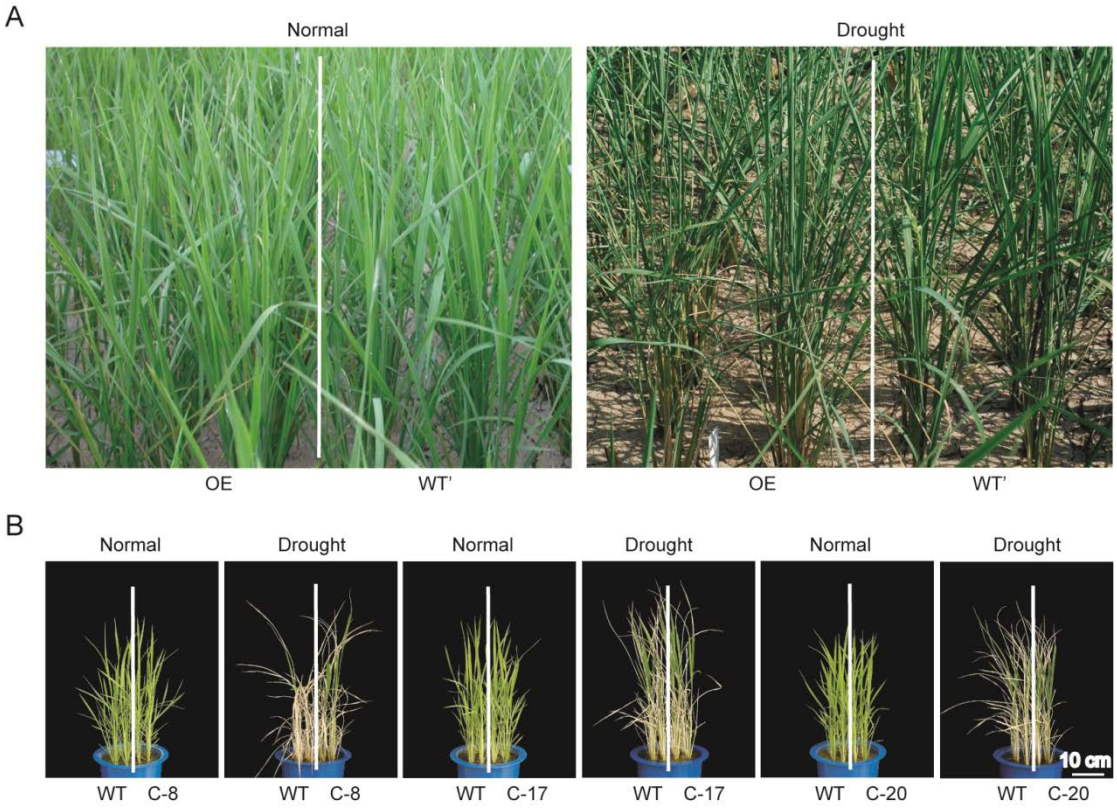
[a] The number of differential expressed genes fall in each GO in the *Ghd2*-overexpressing lines.



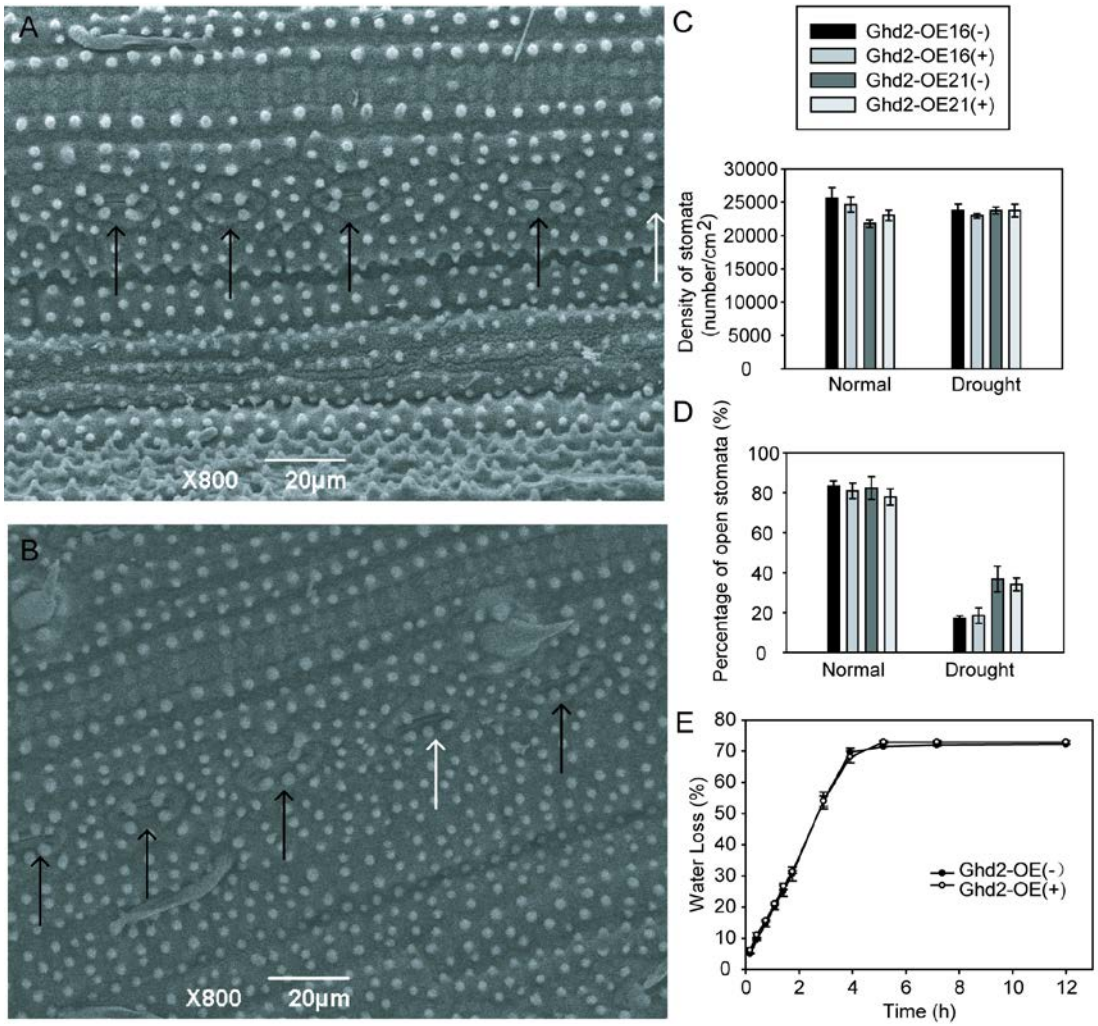

Supplementary Figure S1. Expression level and copy number detection by Northern and Southern blot respectively. Southern blot analysis used hygromycin resistance gene as a probe. (A) The *Ghd2*-OE lines were identified by Northern blot analysis. (B) Copy number of the *Ghd2*-OE lines detected by Southern blot analysis. (C) Copy number detection of the *Ghd2*-CRISPR lines by Southern blot analysis. Probes of (A) and (B) were radio-labeled, and probe for (C) was digoxigenin-labeled.




Supplementary Figure S2. Phenotypes of the *Ghd2*-OE plants with respect to grain number, plant height, and heading date. (A) Phenotypes of the *Ghd2*-OE and ZH11 plants on heading date. (B) Phenotypes of the *Ghd2*-OE and ZH11 plants on grain number per main panicle. (C) Plant height of the *Ghd2*-OE and ZH11 plants. Data represent the mean ± SE (n=9). ***$P$<0.005, *t*-test.




Supplementary Figure S3. Phenotypes of the *Ghd2*-OE plants at 60 DAG and the *Ghd2*-CRISPR plants at the seedling stage under drought stress treatment. (A) Phenotypes of the *Ghd2*-OE21 plants at 60 DAG under drought stress treatment in the field. (B) Phenotypes of the *Ghd2*-CRISPR plants at the seedling stage under drought stress treatment.




Supplementary Figure S4. Stomata and water loss rate in the *Ghd2*-OE and WT' plants. (A-B), SEM images of the *Ghd2*-OE (A) and WT' (B) plant leaves under drought stress. The open and closed stomata are indicated by white and black arrows respectively. (C-D), Stomata density (C) and percentage of open stomata (D) in the overexpression (Ghd2-OE (+)) and WT' control (Ghd2-OE (-)) plant leaves under drought stress. (E) Water loss rate in detached rice leaves of the *Ghd2*-OE and WT' control plants (n=3).

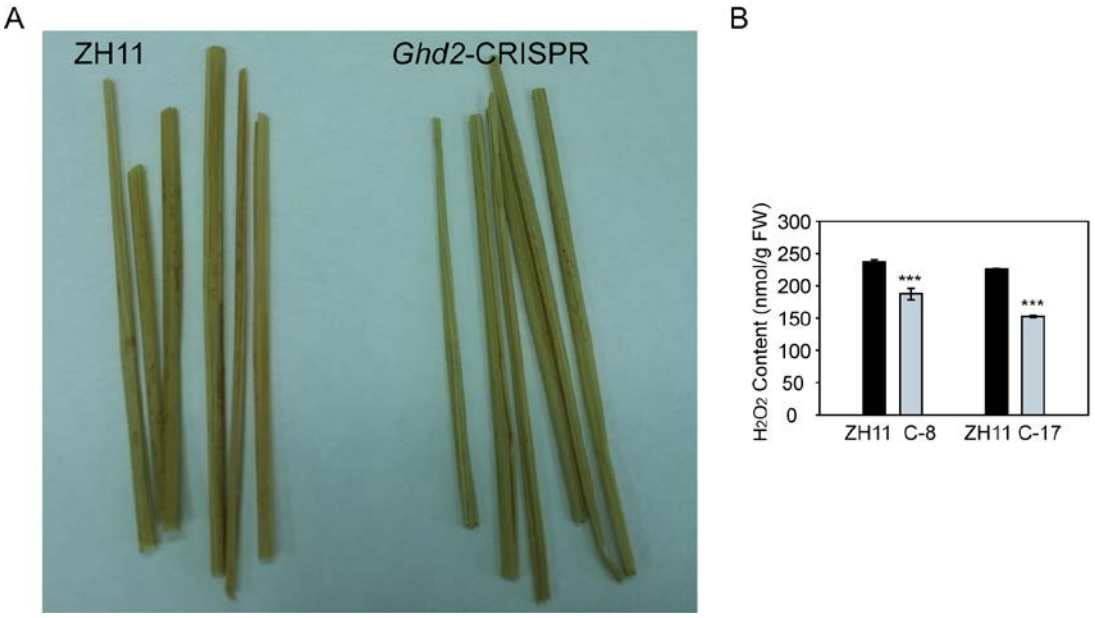
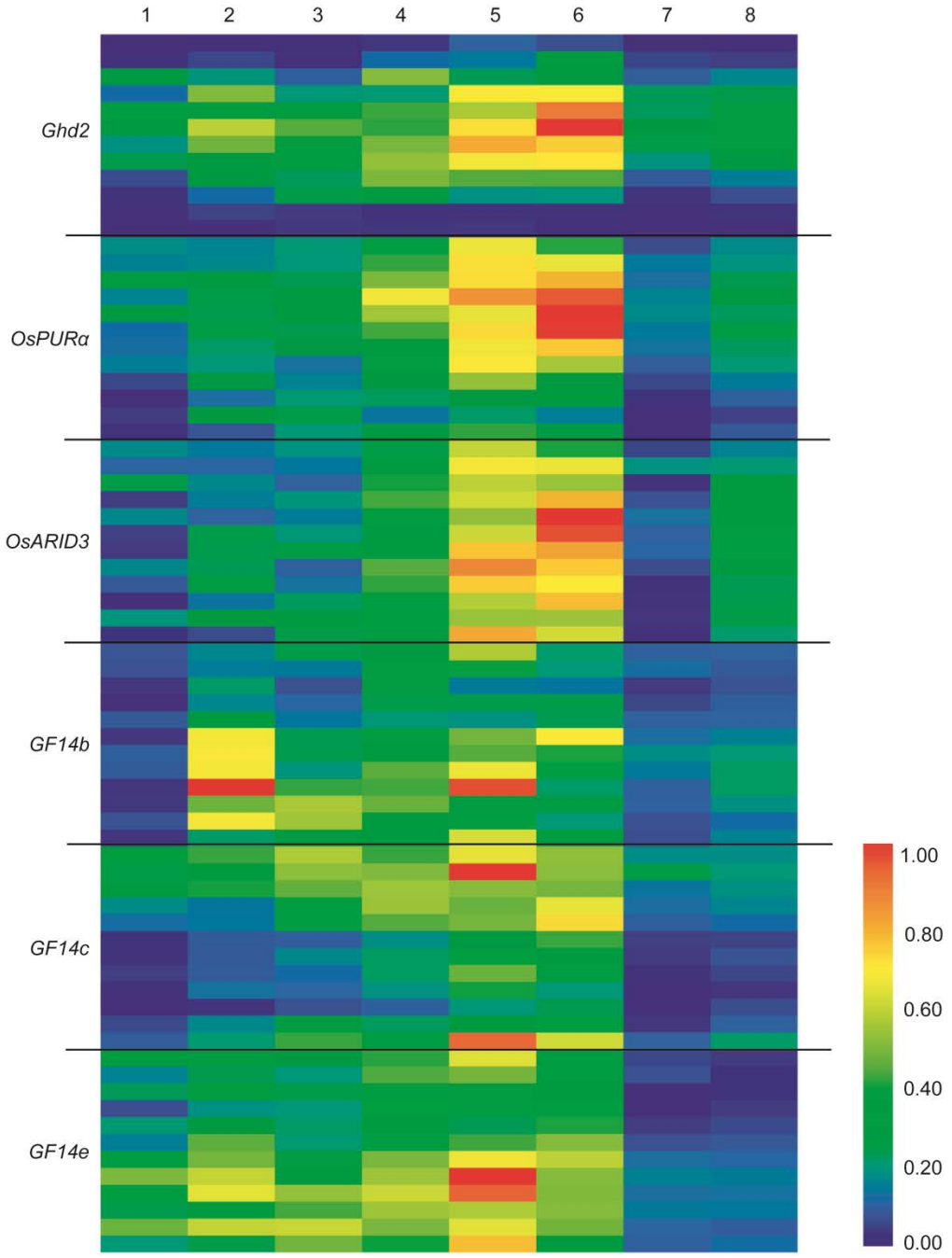
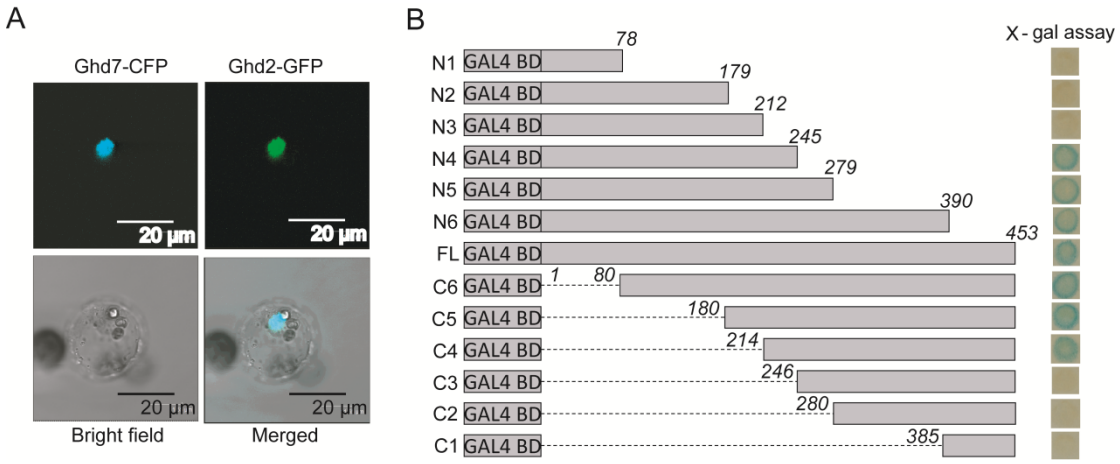



Figure S5. $H_2O_2$ content in the *Ghd2*-CRISPR and WT plants under the drought stress treatment. (A) DAB staining of leaves in the *Ghd2*-CRISPR and ZH11 plants during the drought stress. (B) $H_2O_2$ content measurement in the leaves of the *Ghd2*-CRISPR lines (C-8 and C-17) and ZH11 plants during the drought stress. ***$P$<0.005, *t*-test. FW, Fresh Weight.




Supplementary Figure S6. Diurnal expression levels of *Ghd2*, *OsPURα*, *OsARID3*, and *14-3-3s* in rice leaves at different developmental stages. Numbers from 1 to 8 in the *x*-axis refer to “vegetative 1”, “vegetative 2”, “vegetative 3”, “vegetative reproductive”, “reproductive 1”, “reproductive ripening”, “ripening 1”, “ripening 2”, respectively (as named in the website), and the *y*-axis indicates time points of each gene from am10:00 to am 8:00. Original data was obtained from rice expression database (http://ricexpro.dna.affrc.go.jp/) and analyzed using Heatmap Illustrator.




Supplementary Figure S7. Ghd2 is located in the nucleus and functions as a transcriptional activator. (A) Nuclear localization of Ghd2 in rice protoplast. Nuclear localized CCT domain containing protein Ghd7 was used as a maker to show the nucleus. (B) The activation assay of a series of deletion mutants of Ghd2 in yeast to show the transactivation activity.