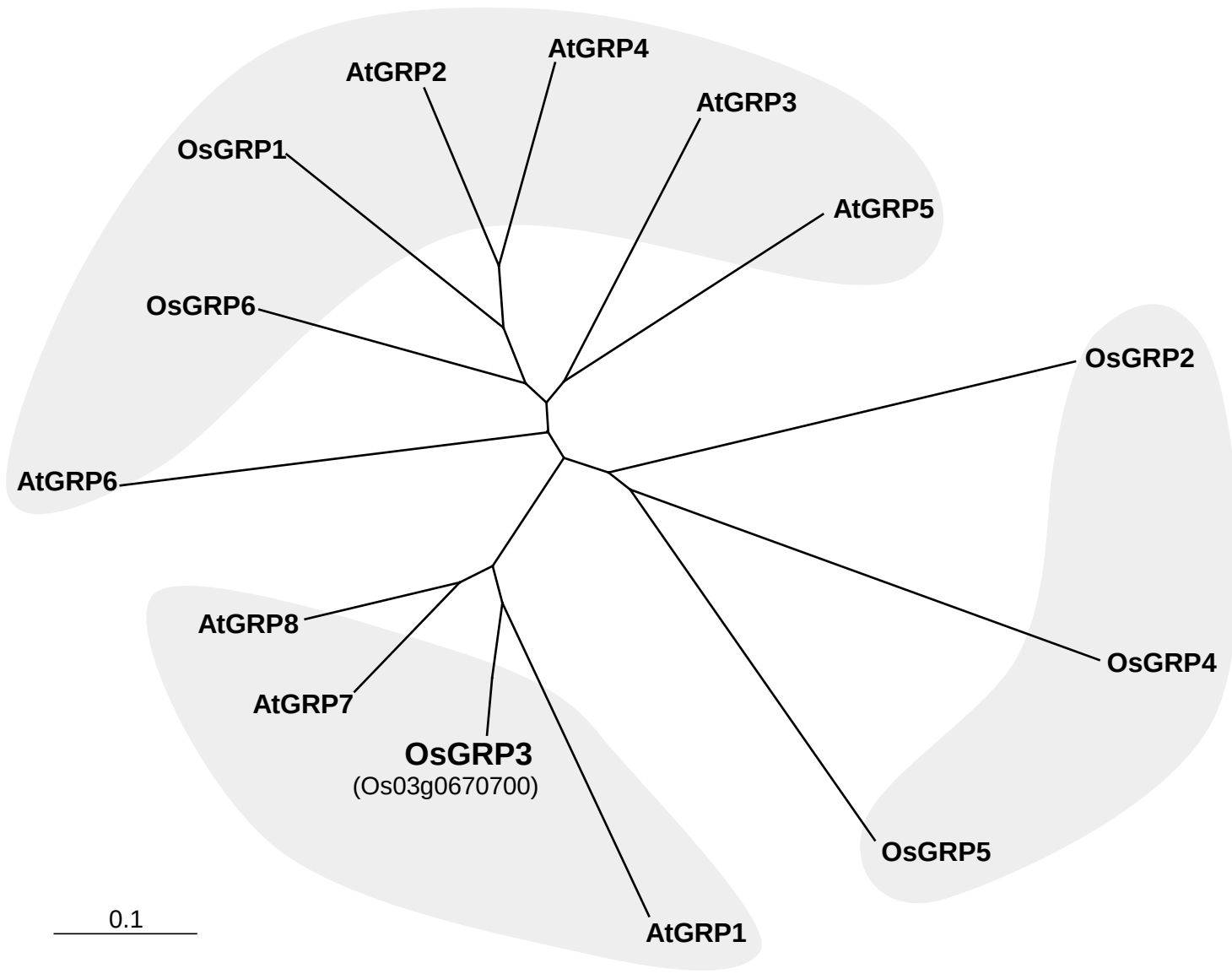
(a)



(b)

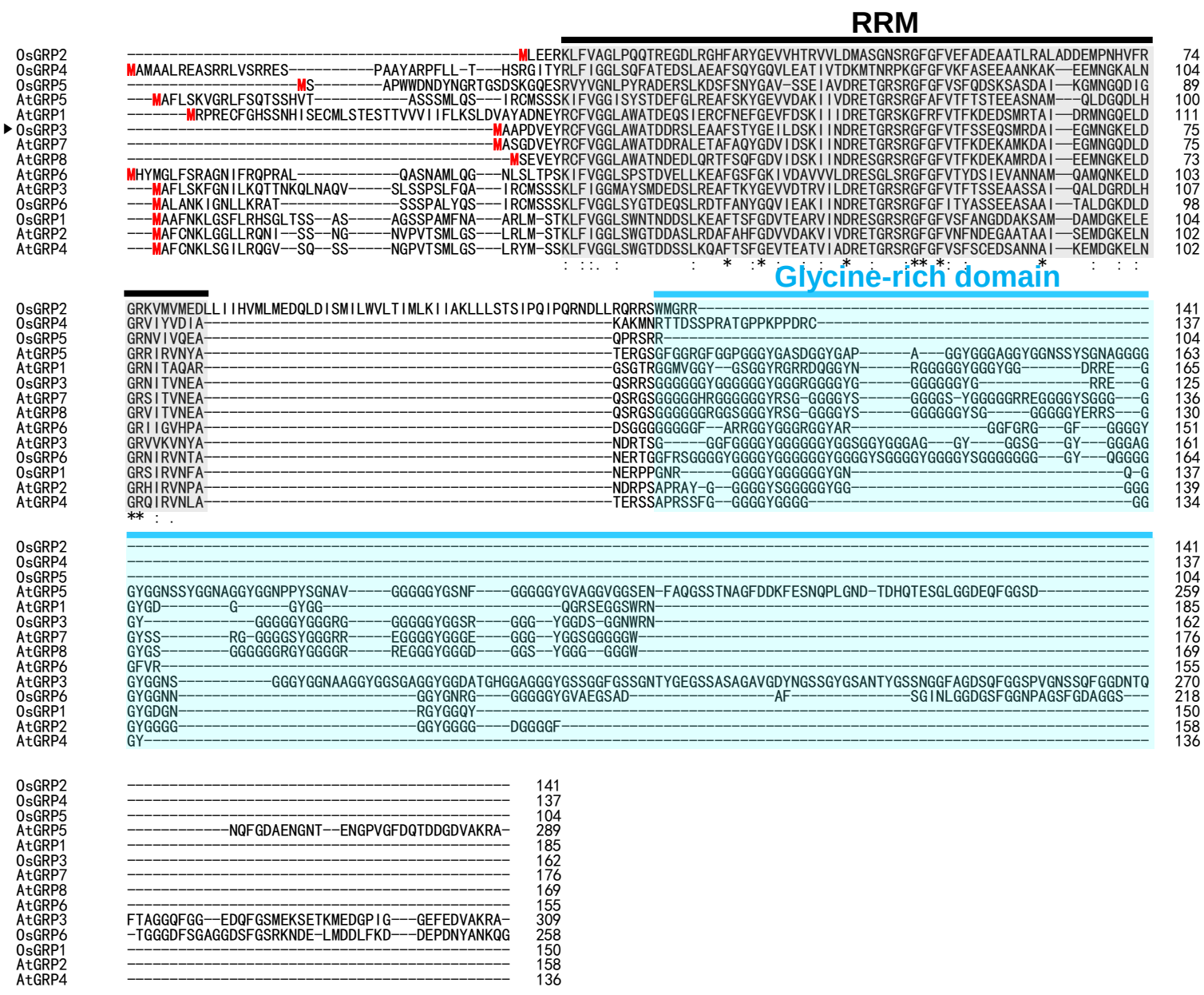


Figure S1. Phylogenetic analysis of *OsGRP* genes. (a) Phylogenetic tree was generated using the neighbor-joining method in ClustalW (http://www.clustal.org/clustal2/) using full-length amino acid sequences of Arabidopsis and rice GRP proteins. **(b)** Amino acid alignment of Arabidopsis and Rice GRP proteins. RRM; RNA-Recognition motif.

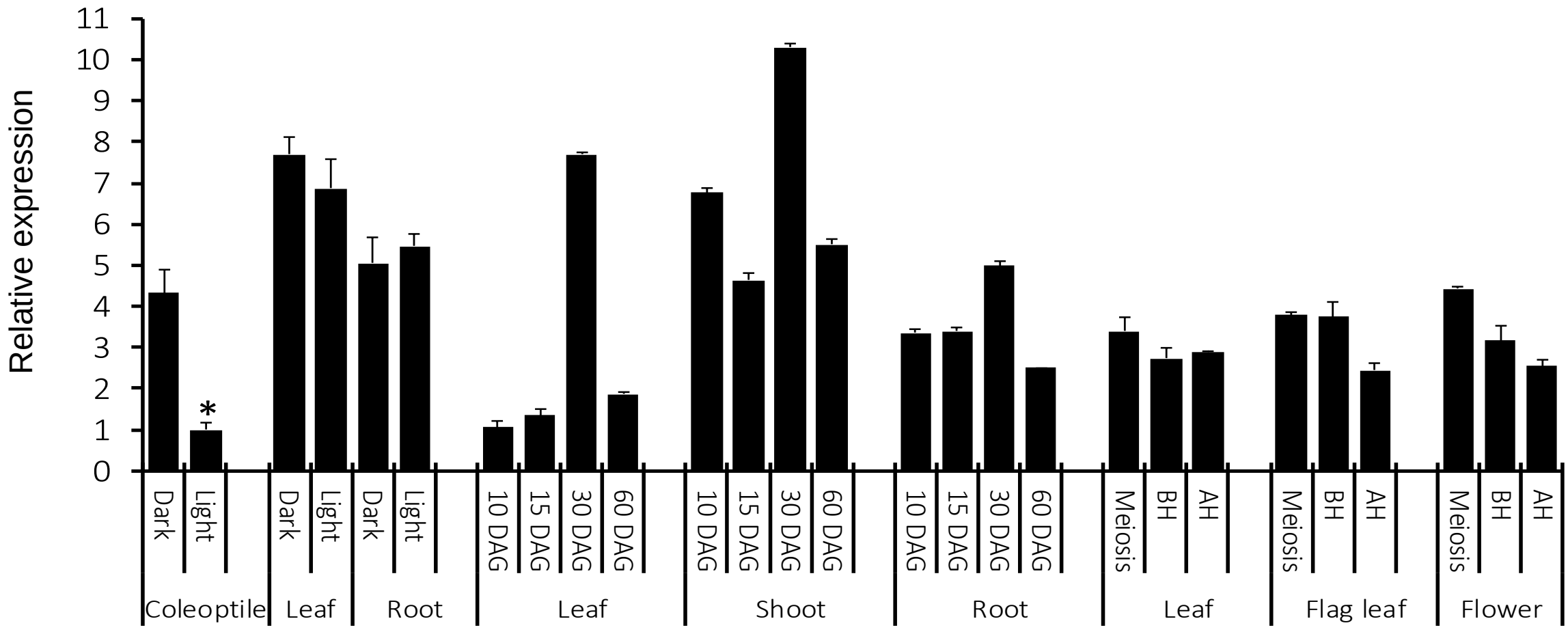


Figure S2. Expression levels of *OsGRP3* in various rice tissues at different developmental stages. qRT-PCR analysis was performed using RNA extracted from various rice tissues at different developmental stages (*Oryza sativa*. L. Japonica cv.Ilmi). DAG, day after germination; BH, Before heading; AH, after heading. Rice *UBIQUITIN* (*OsUbi*) was used as an internal control for normalization. Data represent mean value + standard deviation (SD) (n=3). Relative expression value was represented by expression level in Coleoptile (asterisk mark)

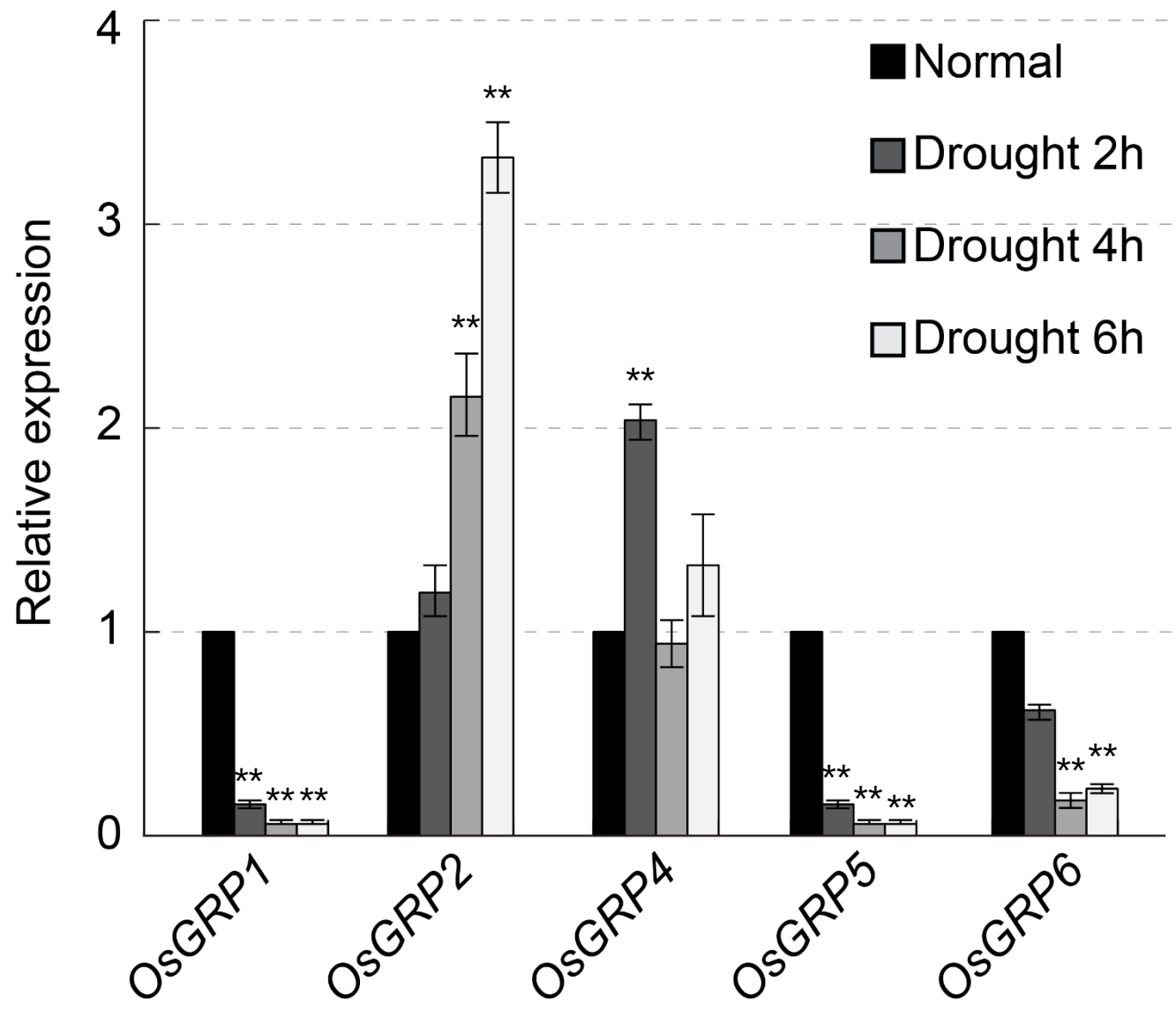


Figure S3. Expression patterns of *OsGRPs* under drought conditions. Expression patterns of *OsGRPs* were analyzed by qRT-PCR. Two-week-old rice seedlings were exposed to drought stress and leaves of the treated rice seedlings were harvested at indicated time point after the treatments. Rice *UBIQUITIN* (*OsUbi*) was used as an internal control for normalization. Data represent mean value ± standard deviation (SD) (n=3). Asterisks indicate statistically significant difference compared with normal sample (without drought treatment) as analyzed by one-way ANOVA followed by t -test: **, $P < 0.01$.

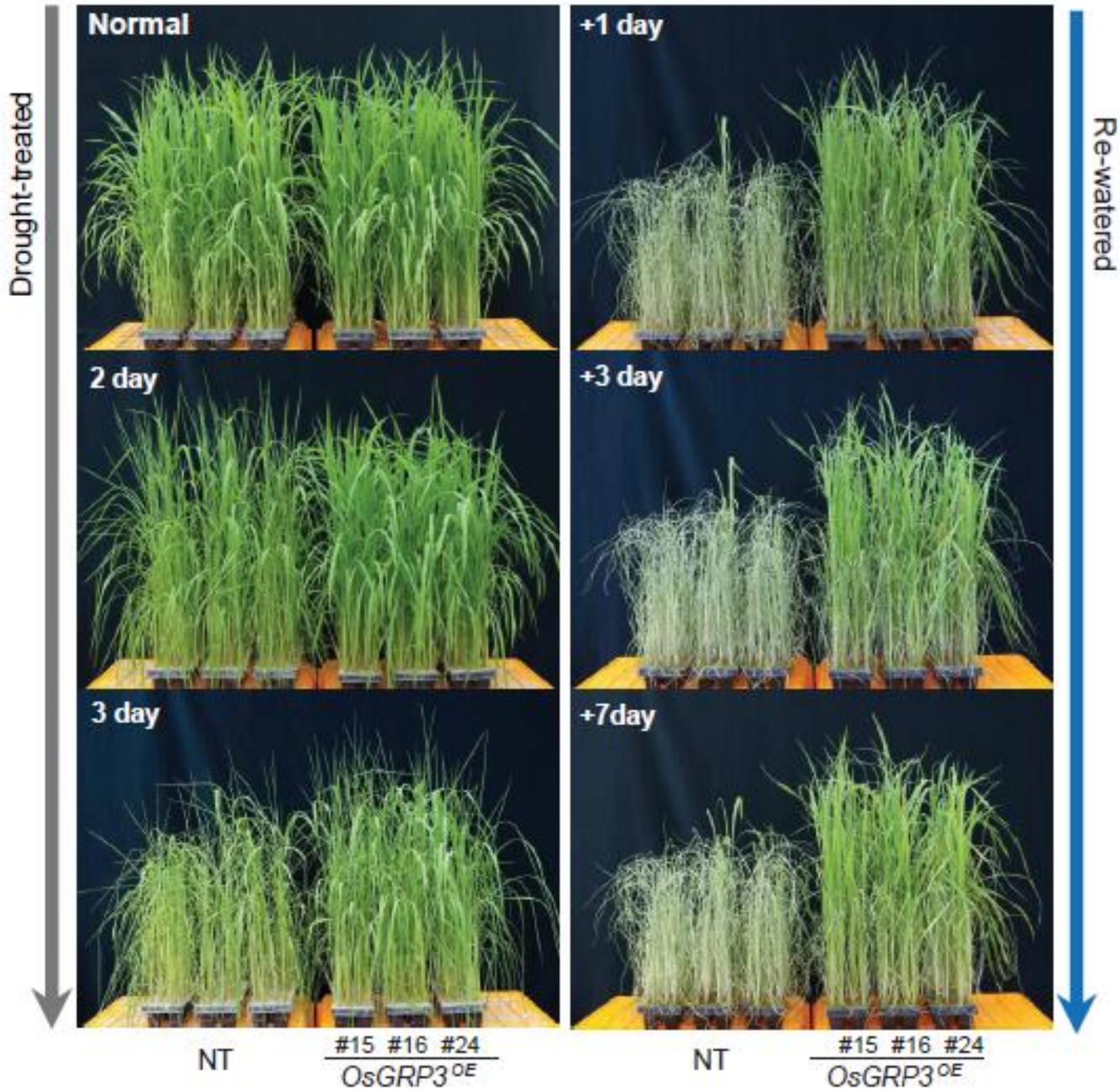
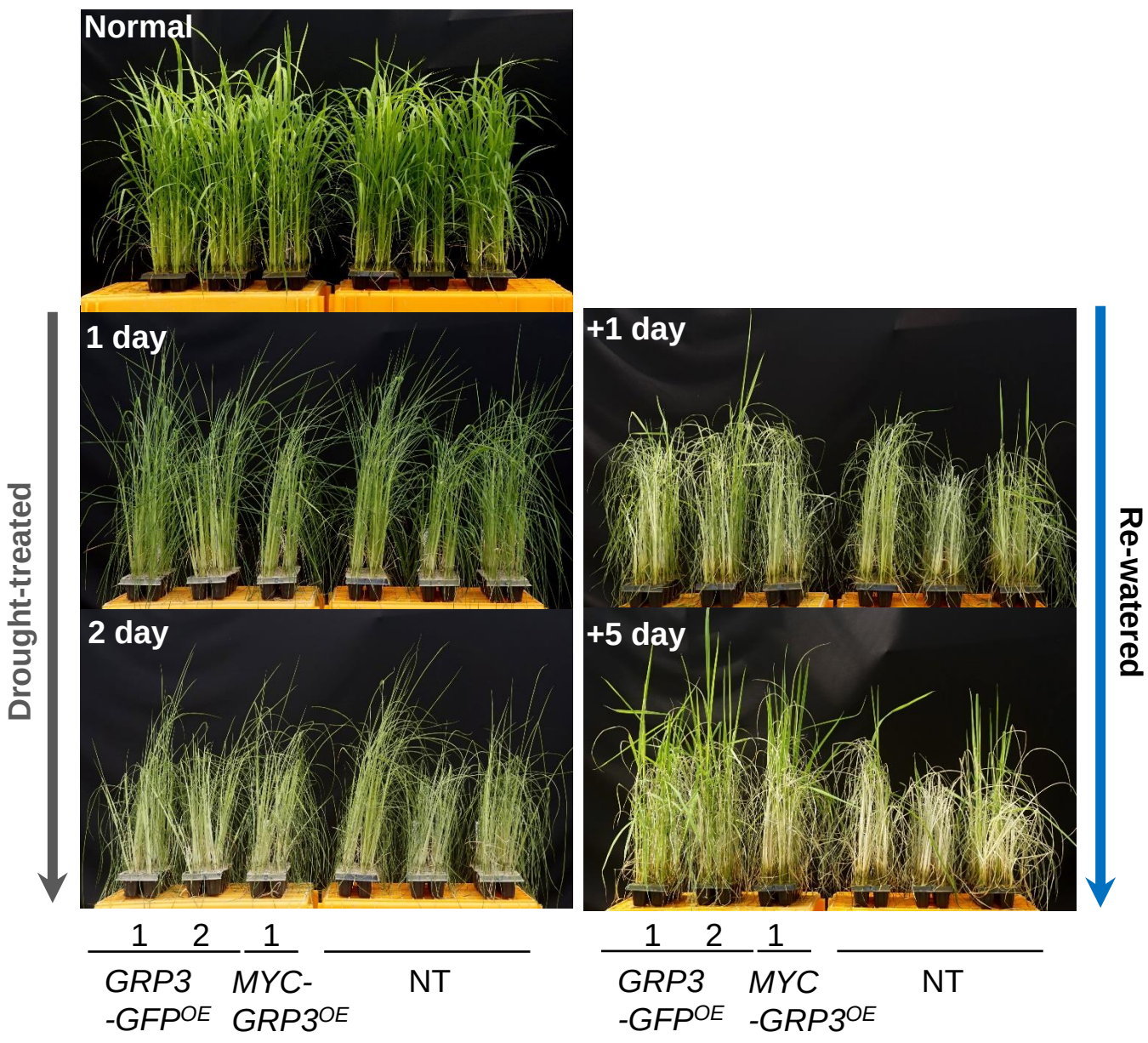
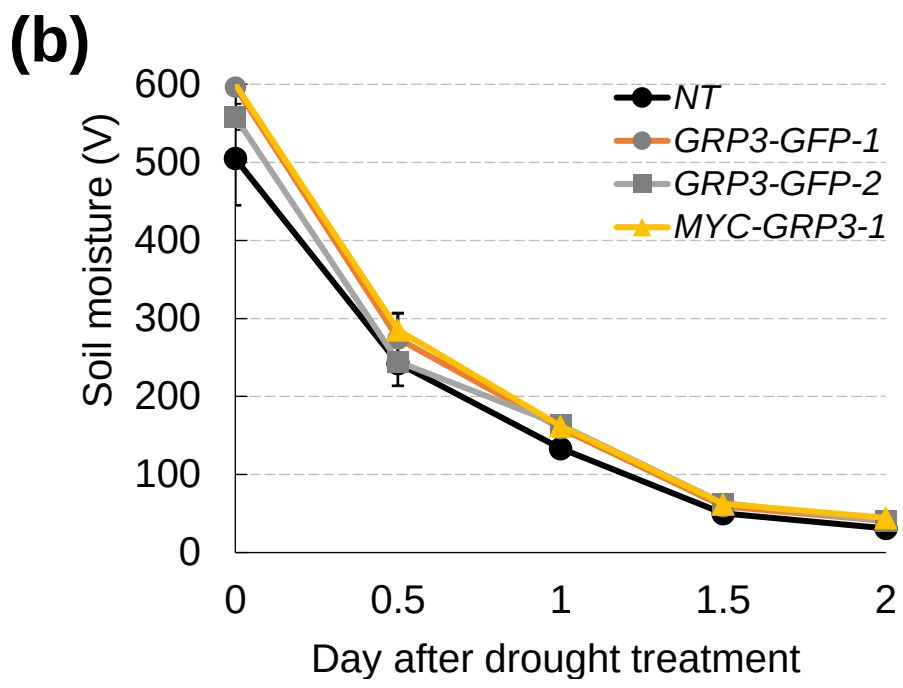
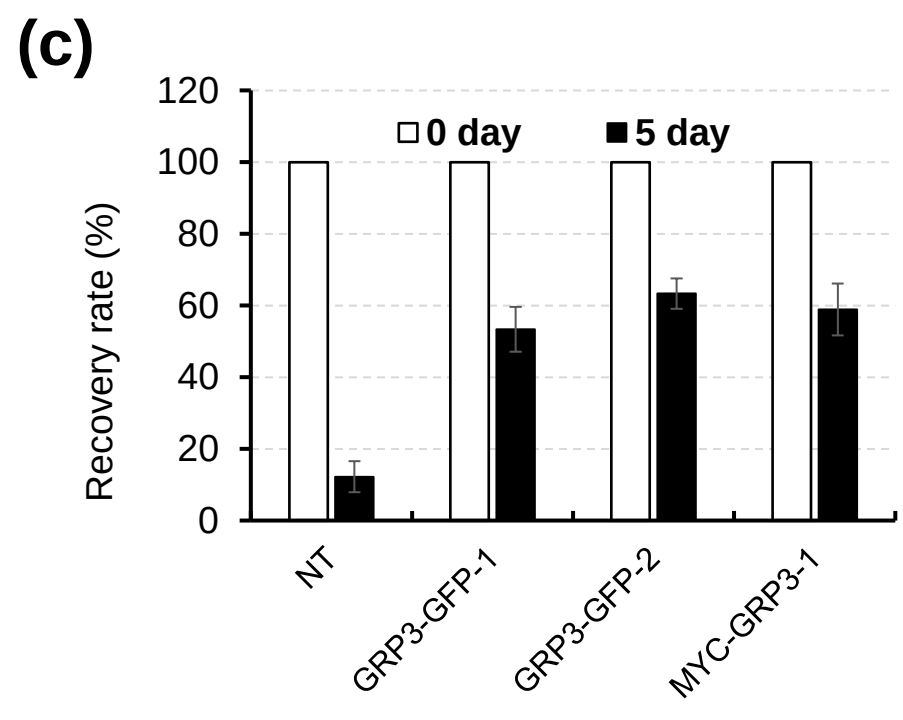


Figure S4. Drought tolerance of *OsGRP3*^{OE} plants. Four-week-old non-transgenic (NT) and *OsGRP3* overexpressing plants (*OsGRP3*^{OE}) were subjected to drought stress by withholding water for 3 days, followed by re-watering for 7 days. The phenotype of tested plants was visualized by taking pictures at indicated time point after drought treatment and re-watering.







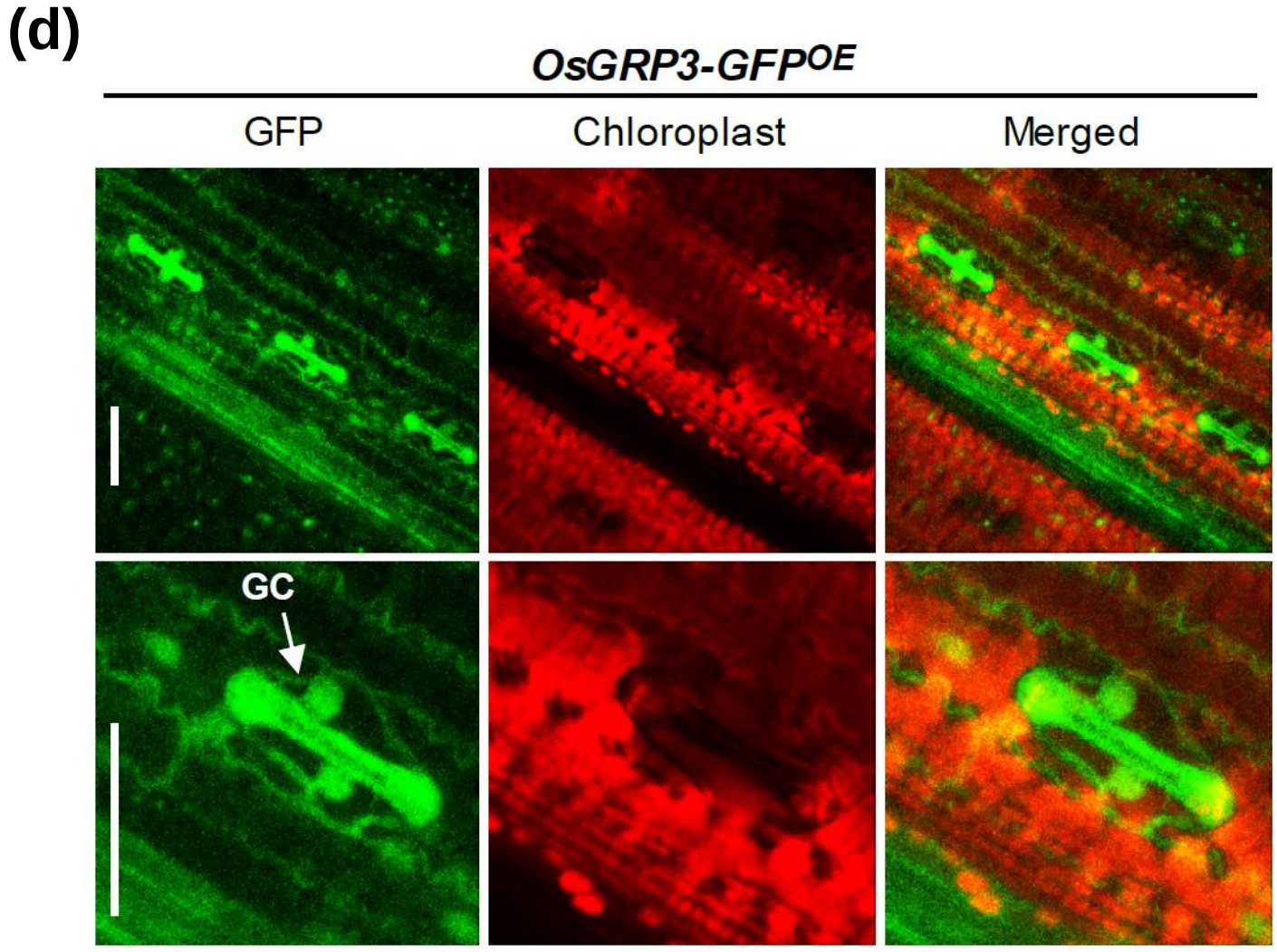
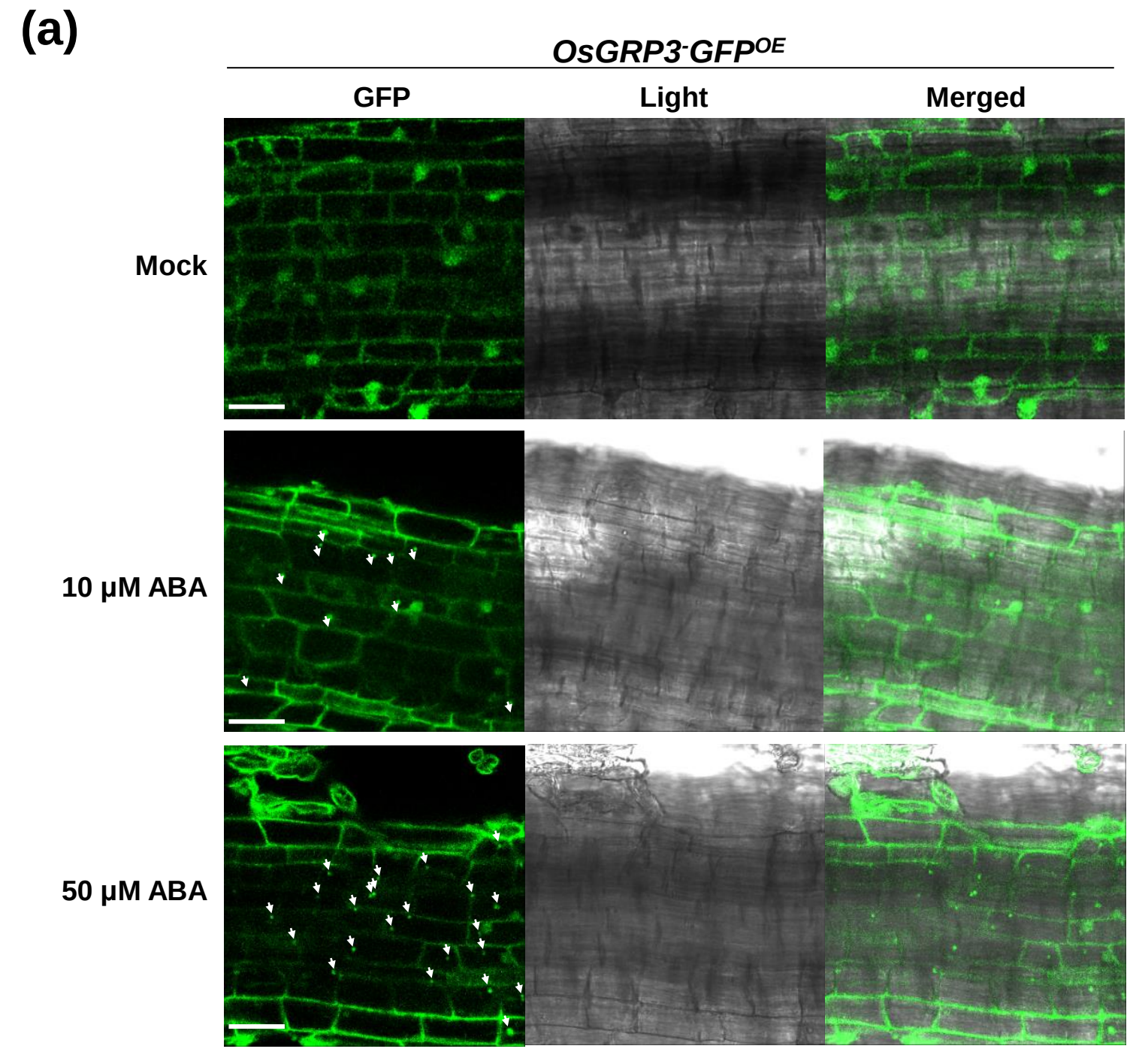


Figure S5. Drought phenotypes of *OsGRP3-GFP*^{OE} and *MYC-OsGRP3*^{OE} plants and subcellular localization of OsGRP3 in leaves of rice plants. (a) Four-week-old non-transgenic (NT), *OsGRP3-GFP* (*OsGRP3-GFP*^{OE}), or *MYC-OsGRP3* overexpressing plants (*MYC-OsGRP3*^{OE}) were subjected to drought stress by withholding water for 2 days, followed by re-watering for 5 days. The phenotype of tested plants was visualized by taking pictures at indicated time point after drought treatment and re-watering. **(b)** Soil moisture content was monitored during drought treatment. Data represent the mean value ± standard deviation (SD) of 30 independent measurements performed at different locations of pots. **(c)** The survival rate of NT and *OsGRP3-GFP*^{OE} transgenic plants was calculated by counting the number of plants recovered from drought stress after re-watering. **(d)** GFP fluorescence and auto-fluorescence of chloroplasts were detected in leaves of *OsCc1::OsGRP3-GFP* (*OsGRP3-GFP*^{OE}) using a confocal microscopy. GC: guard cell, Bar= 30 μm.



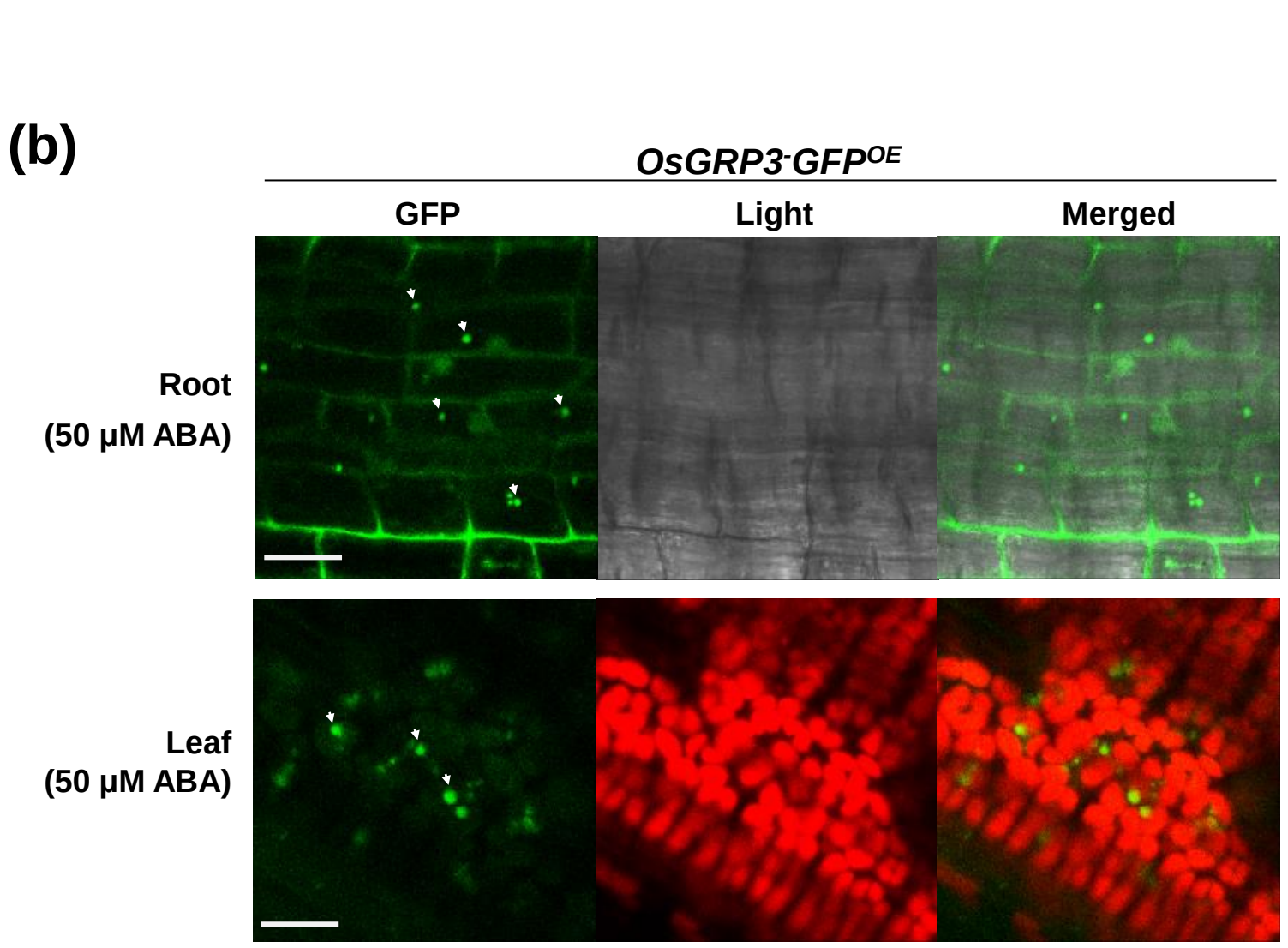


Figure S6. Effect of ABA treatments on subcellular localization of OsGRP3. (a) Two-week-old *OsCc1::OsGRP3-GFP* (*OsGRP3-GFP*^{OE}) transgenic plants were treated with two different concentrations of ABA (10 μM and 50 μM) for two hours. GFP fluorescence was detected in roots of *OsGRP3-GFP*^{OE} transgenic plants using a confocal microscopy. **(b)** Two-week-old *GOS2::OsGRP3-GFP* (*OsGRP3-GFP*^{OE}) transgenic plant were treated with 50 μM ABA for two hours. GFP fluorescence was detected in root or leaf **(c)** of *OsGRP3-GFP*^{OE} transgenic plants after drought treatments using a confocal microscopy. Arrow heads indicate cytoplasmic foci detected in ABA-treated plants. Bar= 30 μm.

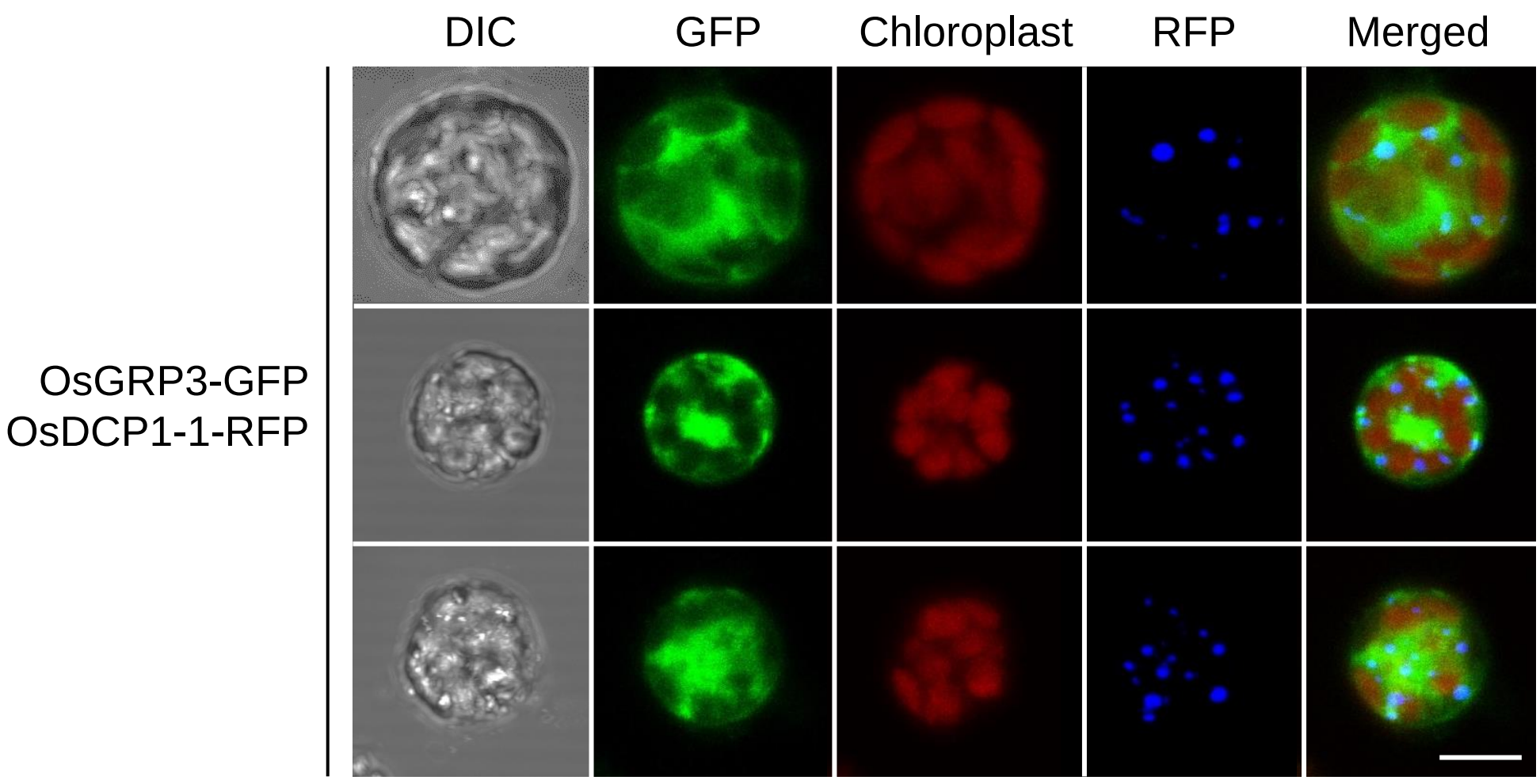


Figure S7. Effect of mannitol treatments on subcellular localization of OsGRP3 in rice protoplasts. Rice protoplasts were transformed with constructs expressing OsGRP3-GFP and OsDCP1-RFP. Fluorescence of GFP, RFP and chloroplast were analyzed in the transformed protoplasts 3 hours after 1.5 M mannitol treatments using a confocal microscope. Bar=10 μm.

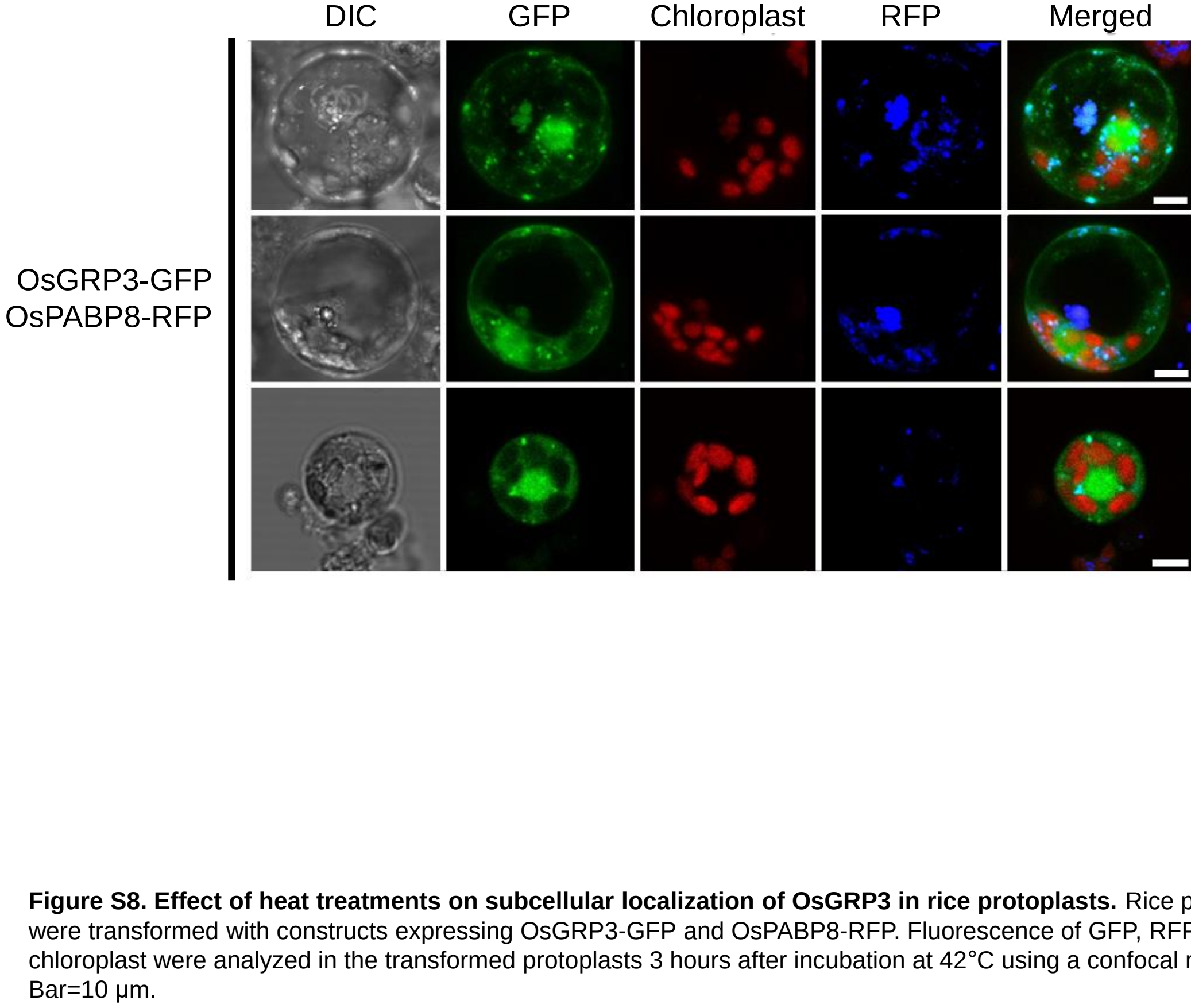


Figure S8. Effect of heat treatments on subcellular localization of OsGRP3 in rice protoplasts. Rice protoplasts were transformed with constructs expressing OsGRP3-GFP and OsPABP8-RFP. Fluorescence of GFP, RFP and chloroplast were analyzed in the transformed protoplasts 3 hours after incubation at 42°C using a confocal microscope. Bar=10 μm.

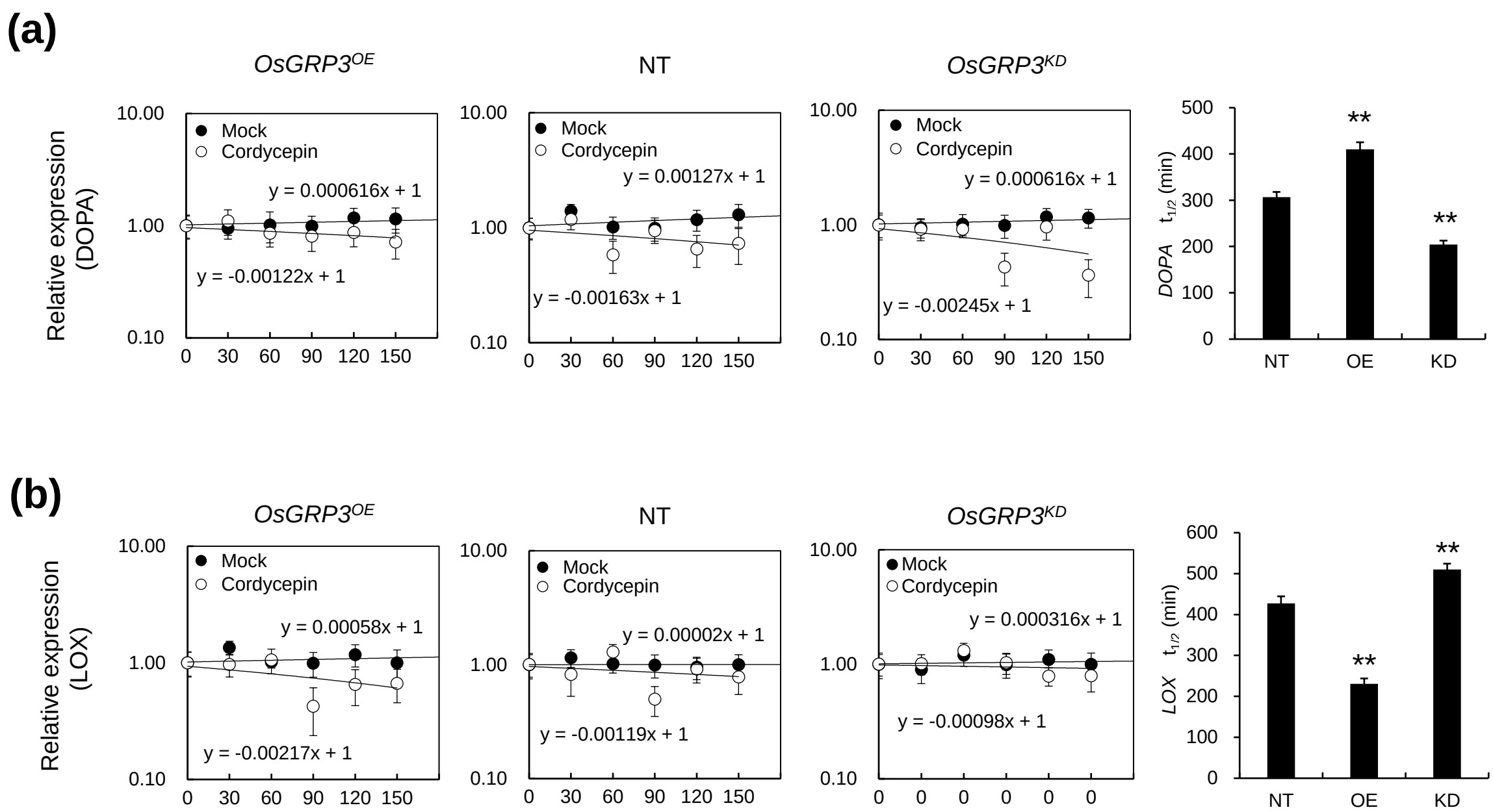


Figure S9. Effects of *OsGRP3* on stability of *DOPA* and *LOX* transcripts. (a *and* b) Stability of *DOPA* **(a)** and *Mt1d* **(b)** transcripts was analyzed under drought conditions. Two-week-old non-transgenic (NT), *OsGRP3* overexpression (*OsGRP3*^{OE}) and RNAi-mediated *OsGRP3* suppressing (*OsGRP3*^{KD}) transgenic plants were pre-treated with distilled water (closed circle) or 1 mM cordycepin for 30 minutes (open circle). Plants were then exposed to drought stress by air-drying and harvested every 30 minutes after the treatments. Total RNAs extracted from the harvested samples were applied for qRT-PCR analysis. Data represent mean value of three replicates. Regression curves and were plotted using sigma plot software (https://systatsoftware.com/). Half-life of transcripts were calculated based on regression curve. Asterisks indicate statistically significant difference compared with NT as analyzed by one-way ANOVA followed by t -test, **P < 0.01.

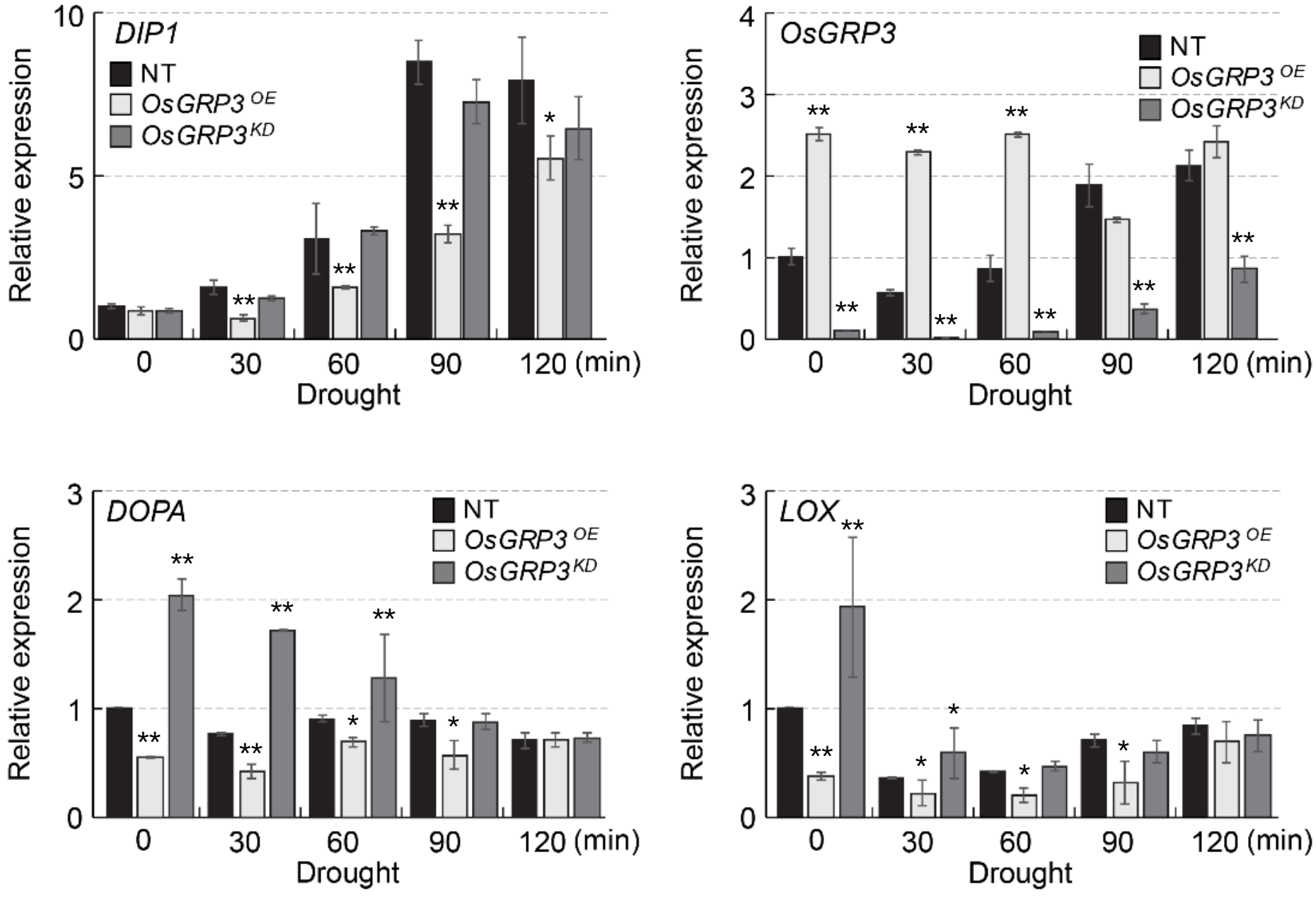


Figure S10. Expression patterns of *OsGRP3*, *DOPA* and *LOX* under drought conditions. Two-week-old non-transgenic (NT), *OsGRP3* overexpressing (*OsGRP3*^{OE}) and RNAi-mediated *OsGRP3* suppressing (*OsGRP3*^{KD}) transgenic plants were exposed to drought stress by air-drying and harvested at indicated time points. Total RNAs isolated from harvested leaves were analyzed by qRP-PCR. Rice *DIP1* was used as a positive control for drought treatments. Rice *UBIQUITIN* (*OsUbi*) was used as internal control for normalization. Data represent mean value ± standard deviation (SD) (n=3). Asterisks indicate statistically significant difference compared with NT as analyzed by one-way ANOVA followed by t -test: *P < 0.05, **P < 0.01.