

Figure S1. Mutations of the target site in *OsPDI* knock-out transgenic plants
(a) Sequencing results of the target sites, red bold letters indicated the PAM, the genotype of each lines were under the lines names in brackets. (b) The genotype of each mutation.

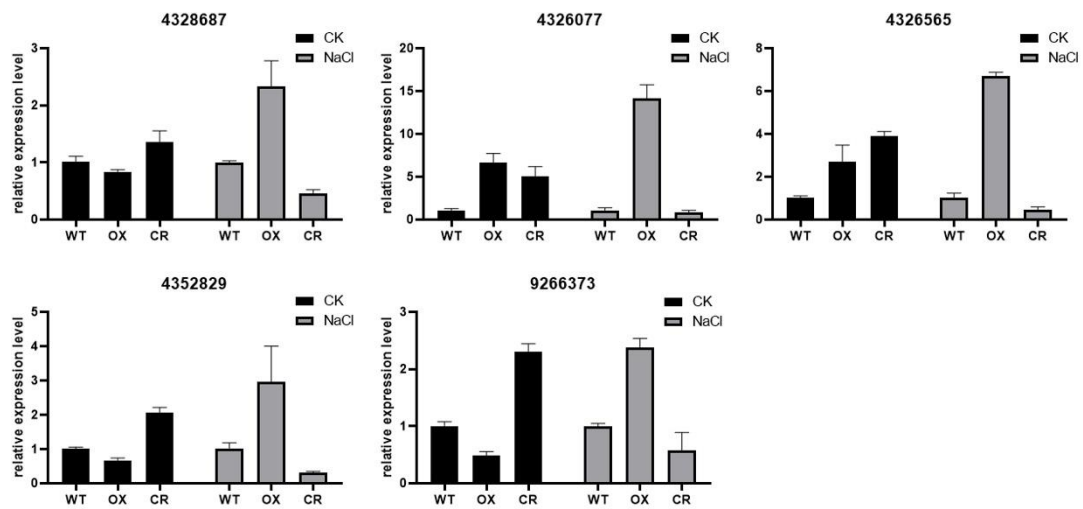
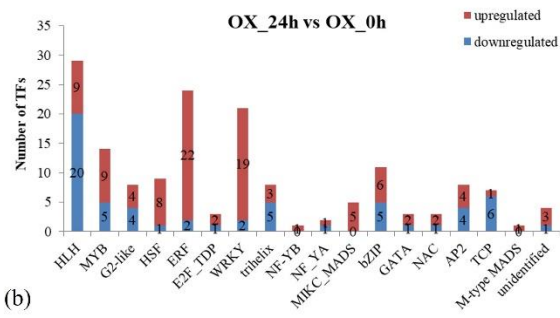
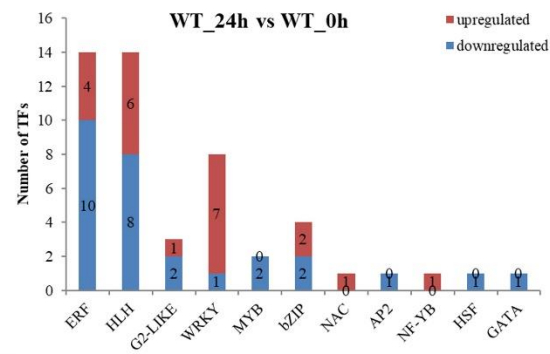


Figure S2. The relative expression levels of 5 randomly selected genes detected by qRT-PCR

(a)



(b)



(c)

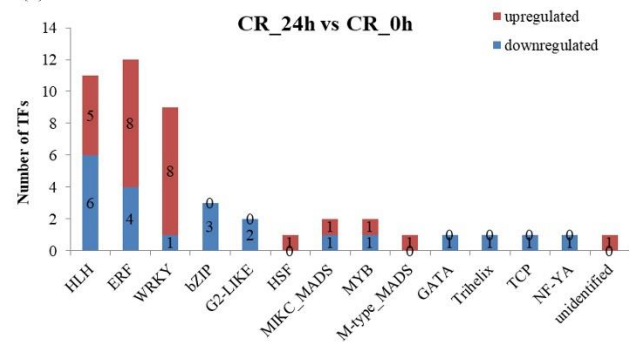


Figure S3. TFs of DEGs in OX_24h vs OX_0h (a), WT_24h vs WT_0h (b) and CR_24h vs CR_0h (c) comparison.

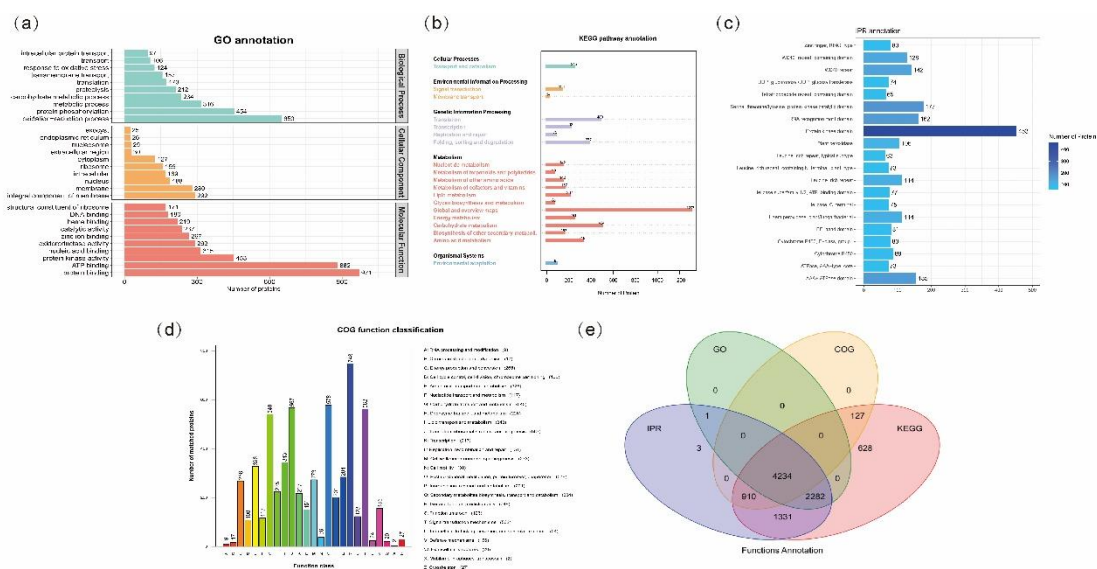


Figure S4. GO (a), KEGG (b), IRP (c) and COG (d) annotation of identified proteins, and venn diagram of them (e).

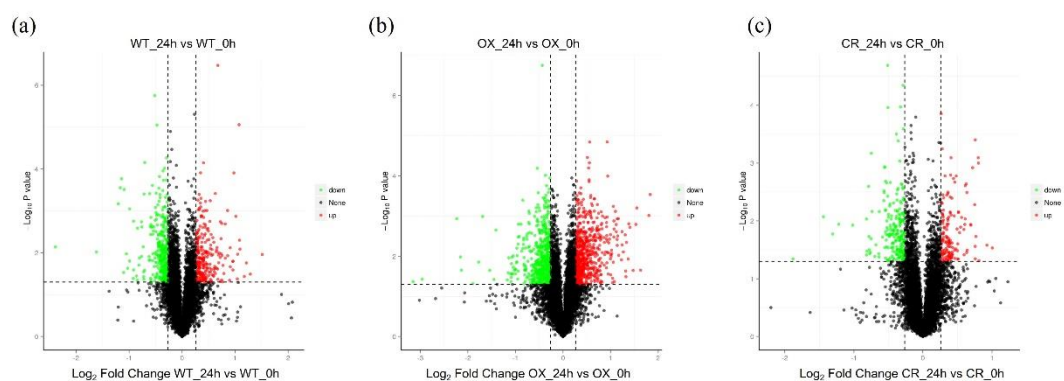


Figure S5. The volcano map of DEPs in WT_24h vs WT_0h (a), OX_24h vs OX_0h (b), and CR_24h vs CR_0h (c) comparison.

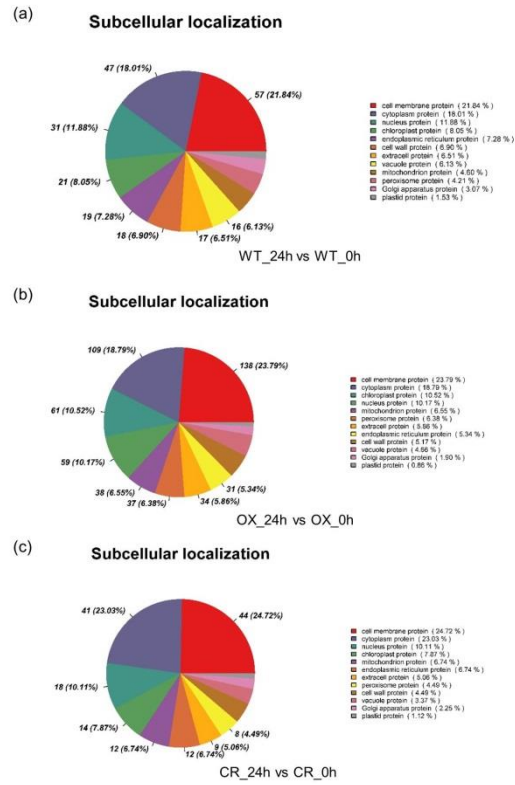


Figure S6. The subcellular location of DEPs in WT_24h vs WT_0h (a), OX_24h vs OX_0h (b), and CR_24h vs CR_0h (c) comparison.

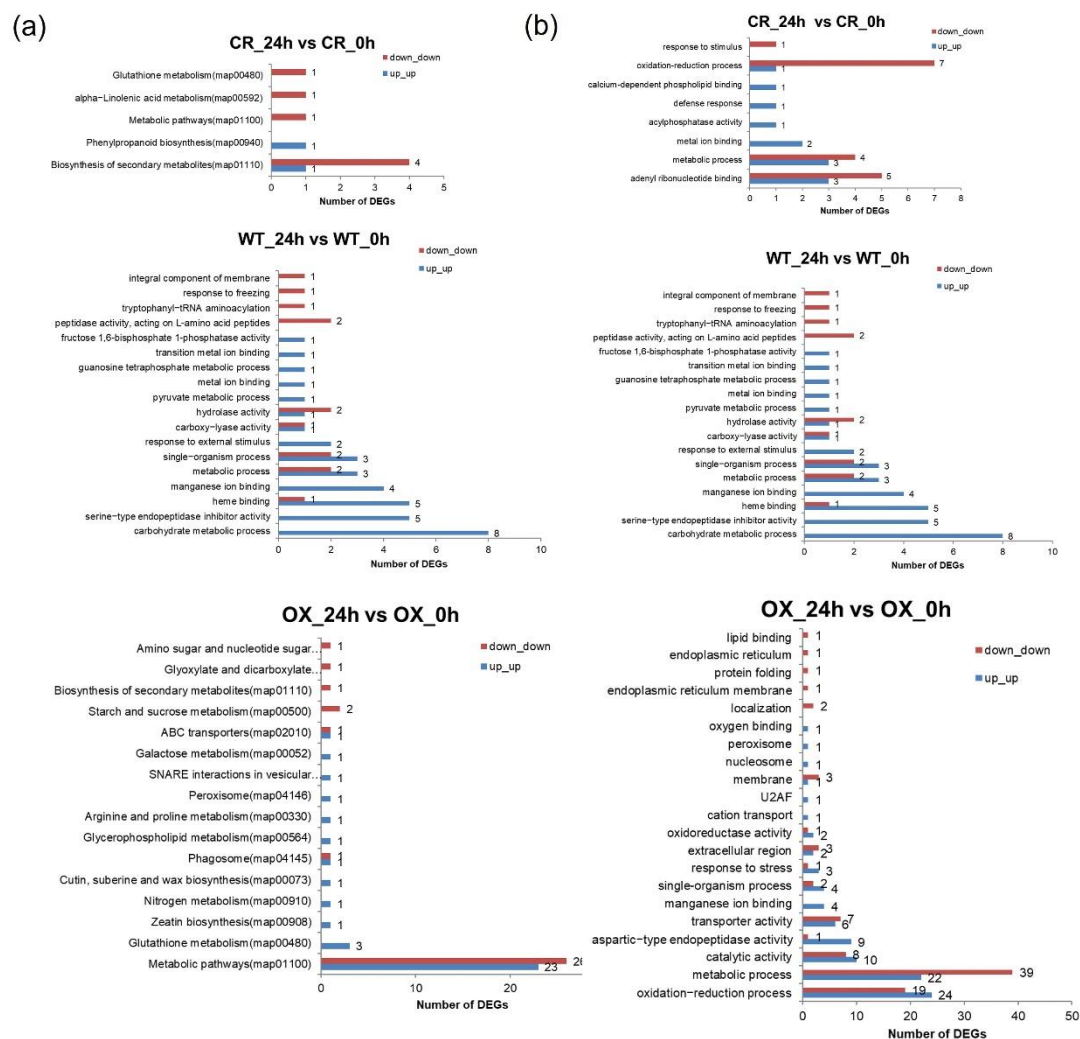


Figure S7. The GO terms (a) and KEGG pathways (b) of DEGs with consistent tendency at RNA and protein level in 3 comparisons.

OsI_04426	-----MAKHFLVLTGAKIPSVGLGTWQSDPGVVGDVYAAVKAGYRHIDCARM	48
AKR4C14	-----MAKHFLVLTGAKIPSVGLGTWQSDPGVVGNVYAAVKAGYRHIDCASA	48
OsI_04429	-----MATHFTLTNGARIPSVGLGTWKAGTGVVADVSAAVKAGYRHIDCAPL	48
AKR4C10	MAGRAGRRRQCRLRRRQGDVALSEFNDKLIFFHVSFVLSEFSRRLIFHVLCCINCMLLQAGYRHIDCAQA	70
OsI_04426	YKNEKEVGLALKKLFEEGVVKREDLFITSKLWCDHAPEDVPESLDKTLSDLQLEBYLDLYLIHWPFRRVKK	118
AKR4C14	YKNEKEVGLALKKLFEEGVVKREDLFITSKLWCDHAPEDVPEALDATLNDLQLEBYLDLYLIHWPFRTKK	118
OsI_04429	YKNEKEIGGALKKLFDDGVVKREDLFITSKLWCDLAPEDVPLAMDSTLKDLQLDYVDLYLIHWPFQIKK	118
AKR4C10	YFNEKEIGVALKKVFDEGVVKREDLFITSKLWCTNHAPEDVPVALDSTLQDLQTDYVDLYLIHWPFVRMKK	140
OsI_04426	GSGISNTEDYIPDPDIPSTWGAMEKLYDSGKSRAIGVSNFSSKKLGDLLAVACVPPAVDQVECHPGWQQTK	188
AKR4C14	GSSI GKPSYLPDPDIPSTWAAMEKLYDSGKSRAIGVSNFSSKKLGDLAAARVPPAVDQVECHPGWQQMK	188
OsI_04429	GTELSPENFVKPDIPSTWRAMEQLYDSGKARAIGVSNFSSKKLGDLCCVARVPPAVDQVECHPGWQQAK	187
AKR4C10	GAGFGGQNVLETDIPATWAAMEKLYDSGKARAIGVSNFSSKKLEDLLAVARVPPAVDQVECHPVWQQTK	209
OsI_04426	LHNFCQSTGVHLSAYSPLGSP--GSTWMNSNVLKESVITISIAEKLGKTPAQVALHWNTQMCHSVLPKSVT	256
AKR4C14	LHNFCQSTGIHLSAYSPLGSP--GSTFMNGNVLKEPITISIAEKLGKTPAQVALRWNTQMCHSVLPKSVS	256
OsI_04429	LRAFCHTSGVHLSAYAPLG-----RMKGIAVDSVLPVAEMLGRTPAQVALRWGLQQGQSVLPKSVS	249
AKR4C10	LRKFCTSKGIHLSAYSPLGSPGTASVKAVGNVLAHPVVVSTAEKLGKTPAQVALRWGTQMCHSVLPKSTH	279
OsI_04426	EERIKQNTDVYDWSIPEDLLVKEFSEIKQVRLLRGDIVNPHSVYKTHEELWDGEI	311
AKR4C14	EERIKQNTDVYDWSIPEDLLAKFSEIKQVRLLRGNFIVNPQSVYKTHEELWDREI	311
OsI_04429	EARKENMDLFCWSIPEELCAKLSEIEQVQIRGDFGAHPESVYKTYEELFDGEI	304
AKR4C10	EERIKENTDVYDWSIPEDLFIKLEIEQMKLIRGEFWTHPEGVYKSTIEELWDGEI	334

Figure S8. The alignments of AKR4C10 and several known AKR4C members in rice.

The protein sequences were downloaded from Rice Genome Annotation Project (<http://rice.uga.edu/index.shtml>): AKR4C14 (locus identifier: LOC_Os01g62870), OsI_04426 (locus identifier: LOC_Os01g62860), OsI_04429 (locus identifier: LOC_Os01g62880), and AKR4C10 (locus identifier: LOC_Os05g38230).