

Supplementary data

Supplementary Figures and Tables Captions

Supplementary Table S1. Summary of reads quality control.

Sample	Raw Data Read	Valid Data Read	Q20%	Q30%
WFB1YE1	58067824	51827564	99.97	96.90
WFB1YE2	55856602	50440052	99.97	96.42
WFB1YE3	49093548	44323472	99.97	96.93
WFB10YE1	55154582	48373938	99.97	96.89
WFB10YE2	32577058	29566054	99.97	97.09
WFB10YE3	57707296	53939666	99.97	96.82
CH1YE1	47223226	43972676	99.97	96.90
CH1YE2	50148850	47276426	99.97	96.38
CH1YE3	59521130	56657380	99.97	96.43
CH10YE1	49924152	47693980	99.96	95.71
CH10YE2	56697348	53102578	99.96	96.23
CH10YE3	51910576	49064482	99.96	96.10
WFY1YE1	42521008	39987756	99.97	96.29
WFY1YE2	42407886	38573182	99.97	95.61
WFY1YE3	49399744	44670540	99.97	95.66
WFY10YE1	59642288	54054670	99.96	96.48
WFY10YE2	58586170	53489318	99.96	96.37
WFY10YE3	59388316	57894440	99.95	95.66
WFB1YM1	41877940	37466360	99.96	95.28
WFB1YM2	37675788	34596514	99.96	95.32
WFB1YM3	43931940	40412444	99.96	95.25
WFB10YM1	55179068	48185880	99.96	96.55
WFB10YM2	37529196	33435912	99.97	96.20
WFB10YM3	36929212	32208332	99.96	95.35
CH1YM1	37453408	31809752	99.96	95.95
CH1YM2	49902748	44269166	99.96	96.03
CH1YM3	39974474	34311360	99.96	95.72
CH10YM1	42010238	36958032	99.97	95.77
CH10YM2	48782678	43370946	99.96	96.03
CH10YM3	49215802	43682886	99.96	96.08
WFY1YM1	58915542	52942812	99.96	96.32
WFY1YM2	35801982	31728748	99.96	95.16
WFY1YM3	38811202	32672228	99.96	95.73
WFY10YM1	45758222	39934752	99.96	95.85
WFY10YM2	49112104	40312014	99.96	95.47
WFY10YM3	41302046	36012804	99.96	95.36

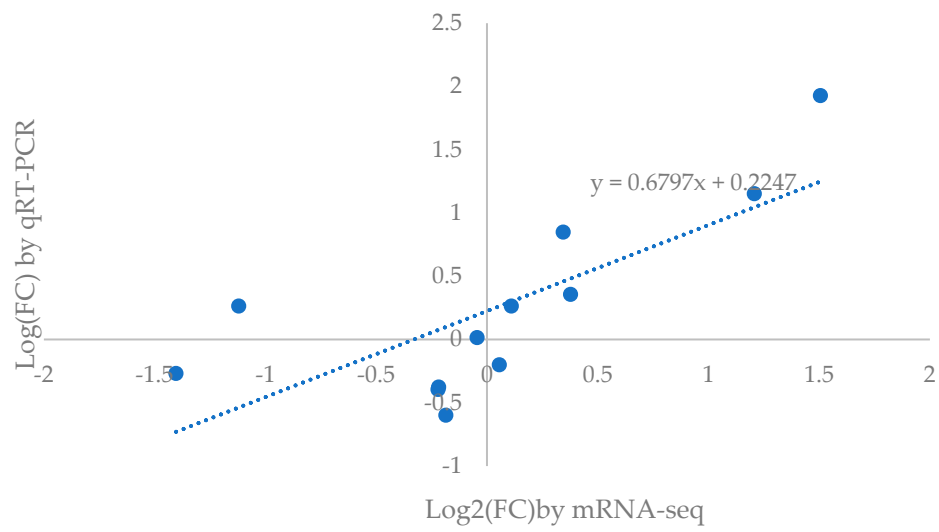
CH, WFY and WFB represent CHT025, WFYT025 and WFB, respectively. E and M represent early and middle. Y represent flag leaf. 1, 10 represent 1 DPA and 10 DPA. For example, WFB1YE1 represent in the early rice environment, the flag leaf of WFB at 1 DPA.

Supplementary Table S2. Primers used in this study.

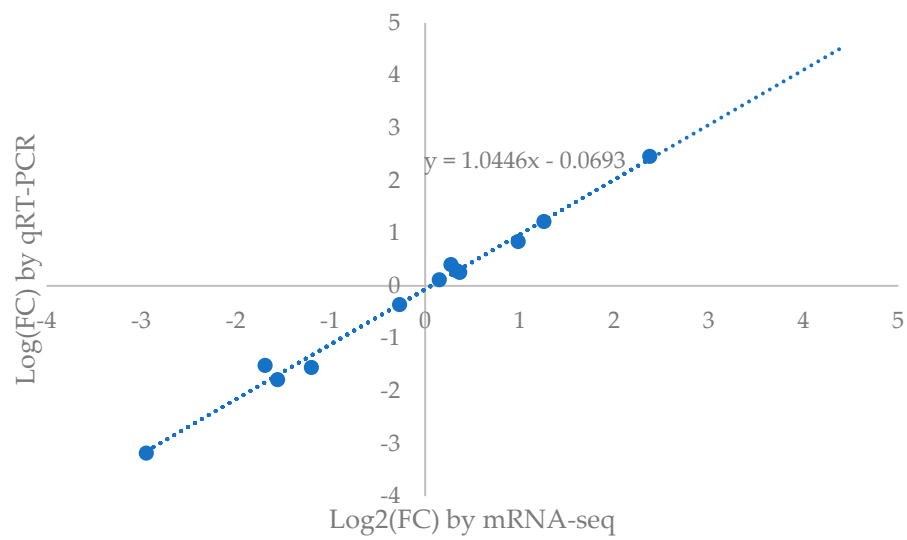
Gene ID	Forward primer	Reverse primer
<i>OS09G0555500</i>	GCAATCTGGGCGATATACGTGTG	TGTACCTCGACTTCGTTAGGTC
<i>OS04G0578400</i>	TGCCGATGACCGAGATGTTT	CATGCCGAACAGCGTAATCC
<i>OS03G0592500</i>	TATGGACCTGACCGTCCCAA	CTTCACCCCGTTCTTGGACA
<i>OS03G0856700</i>	CGGCTTCTTCCTGGTGGTTA	GTCGTTGCGCTGGAAGAATC
<i>OS04G0611800</i>	TACAAGAGGATTCGGCGTGG	CATCCCCATGGCAAGGCTAA
<i>OS01G0580500</i>	GGAGGTGAAGAGCTTCGTGT	AGTAGGTGGCCTCCCAGTC
<i>OS01G0656200</i>	CAGCAGGTGGCAGGGTTATC	GATACCACATCCCACAGCCC
<i>OS01G0841600</i>	CCTTCACTGGCGAGATCAGT	GGTCTCACCAATGCAAGCAA
<i>OS02G0171100</i>	TCGAGTGGCGAGAAGACAAA	CCCCAAGGAATATCTGCTGGA
<i>Os11g0171300</i>	TCCTTGCCATGGATGAGTCG	GAGACCTTGGCACCATGACT
<i>Os06g0133800</i>	GACGAGGTCATGCGGTACAA	GATGGCCTGGAGTCTTGCTT
<i>Os08g0434300</i>	AATTGCTGCCGAGGTTCTGA	CATGACCACCGACAACCTGGA

Supplementary Figure S1 Comparison of the log₂ (FC) of 12 randomly selected transcripts using RNA-Seq and qRT-PCR. **A-C:** In the early rice environment, compare 1 DPA and 10 DPA about CHT025, WFB and WFYT025, respectively. **D-E:** In the middle rice environment, compare 1 DPA and 10 DPA about CHT025, WFB and WFYT025, respectively.

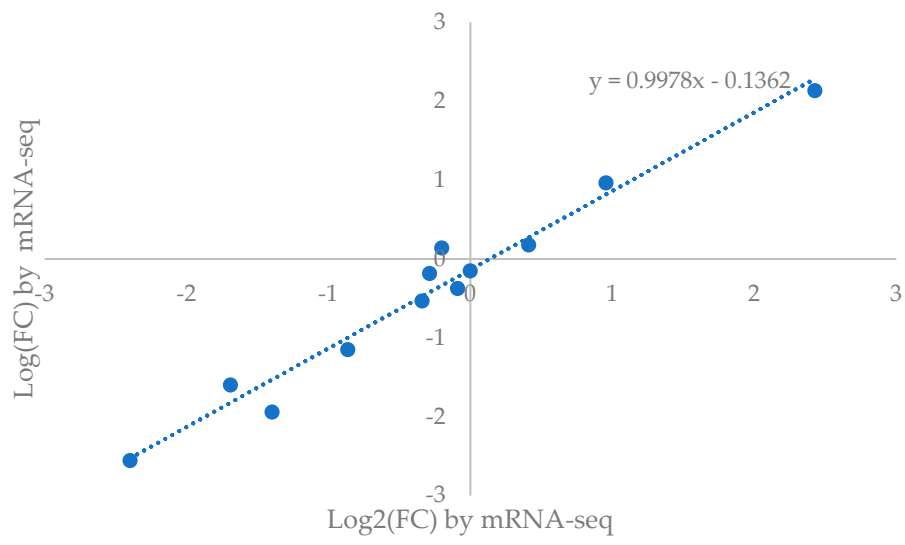
A.



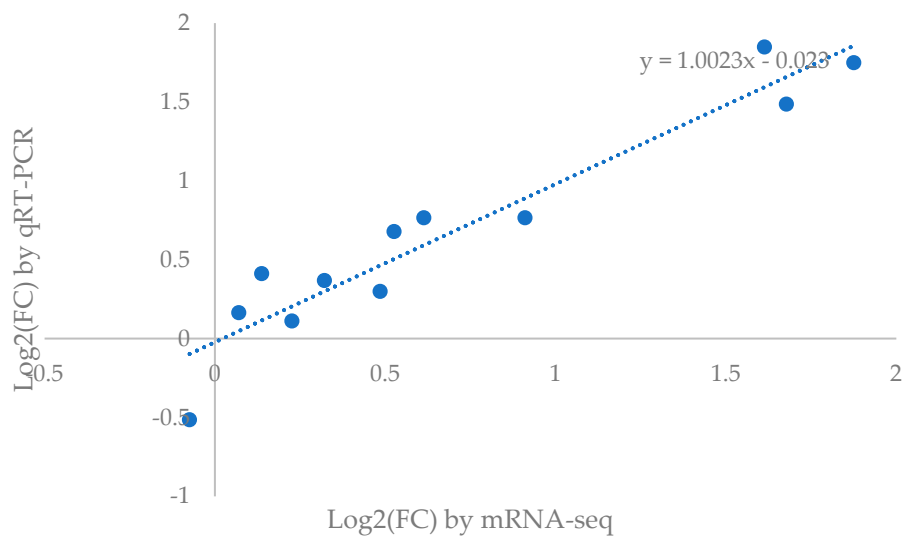
B



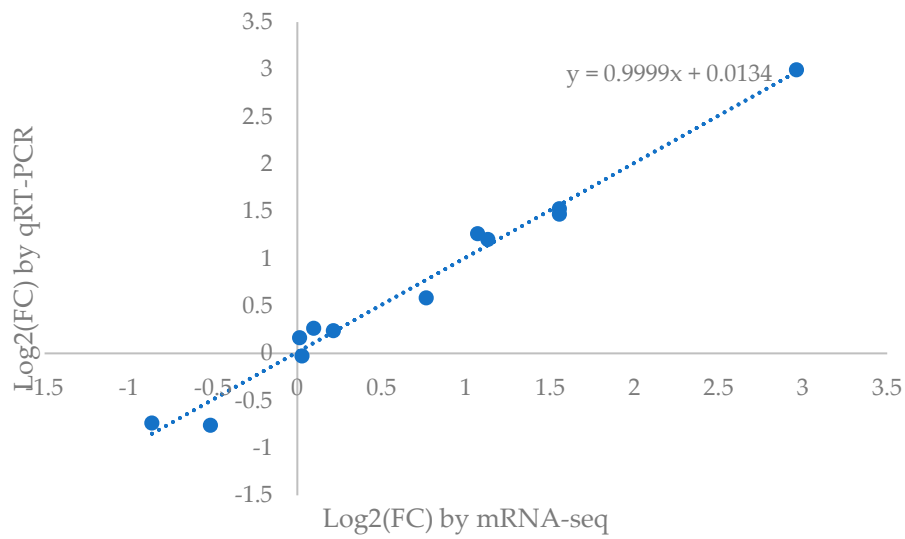
C



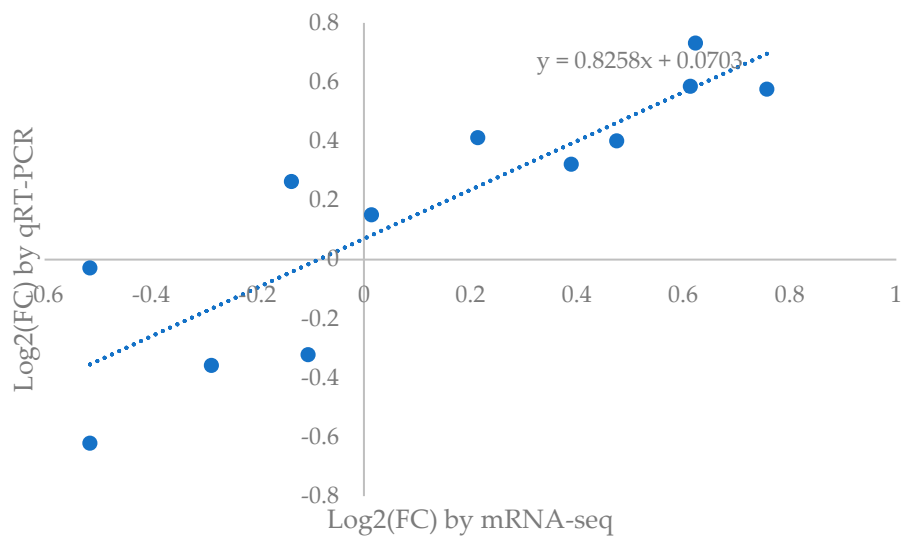
D



E



F

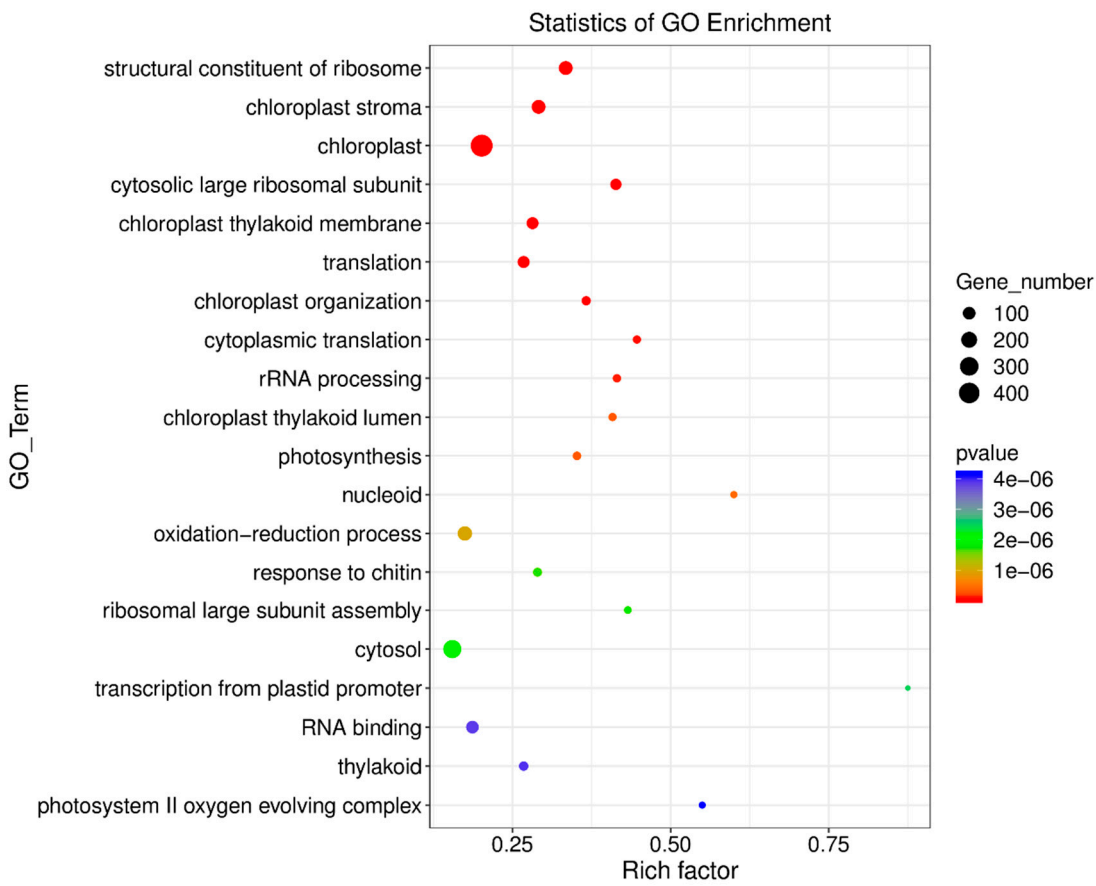


Supplementary Figure S2 Gene ontology (GO) enrichment analysis of DEGs(A)

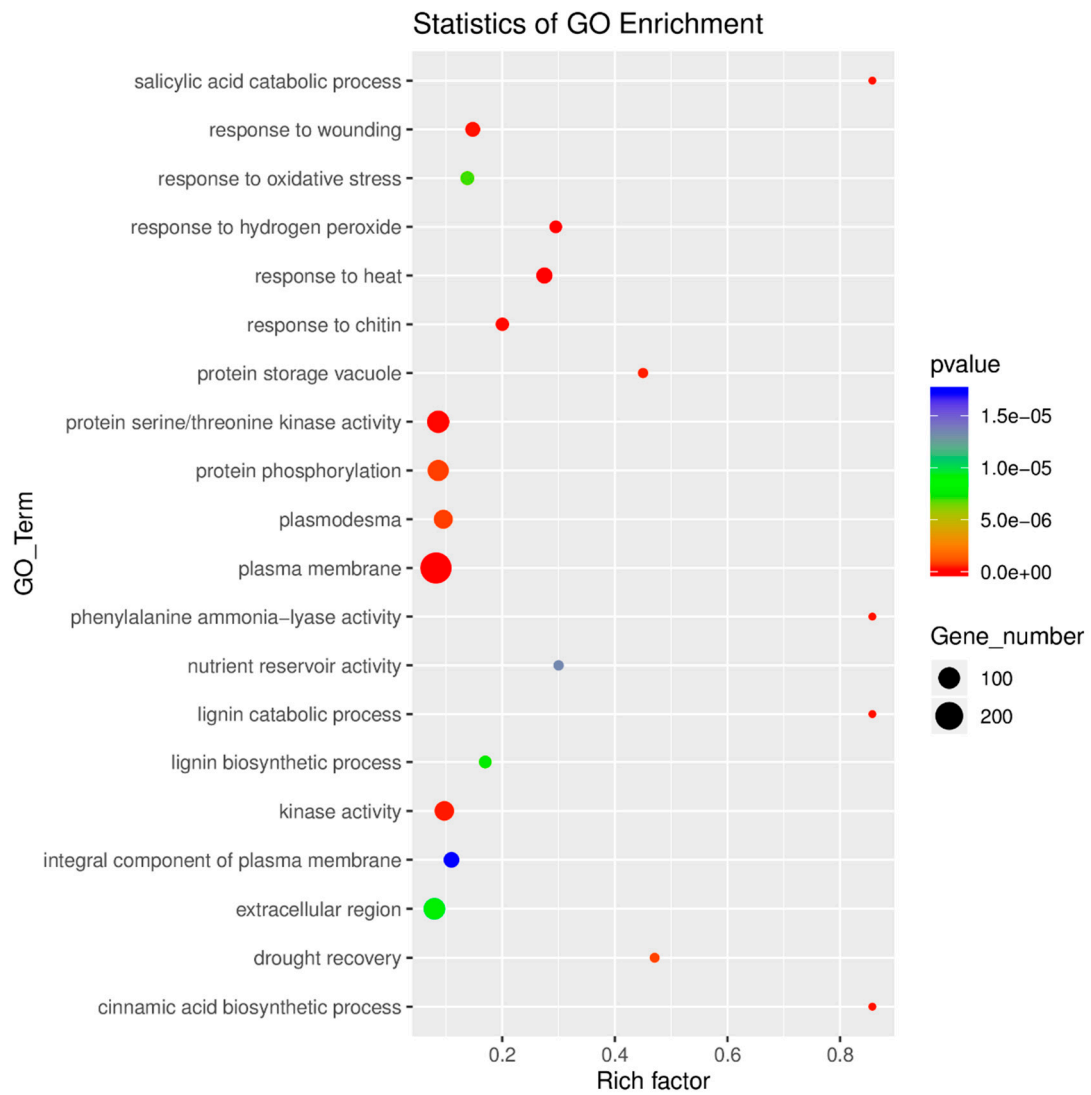
GO enrichment analysis of DEGs at 1 DPA and 10 DPA under the environment of early rice in WFYT025. **(B)** GO enrichment analysis of DEGs at 1 DPA and 10 DPA under the environment of middle rice in CHT025. **(C)** GO enrichment analysis of DEGs at 1 DPA and 10 DPA under the environment of middle rice in WFB. **(D)** GO enrichment analysis of DEGs at 1 DPA and 10 DPA under the

environment of middle rice in WFYT025.

A.



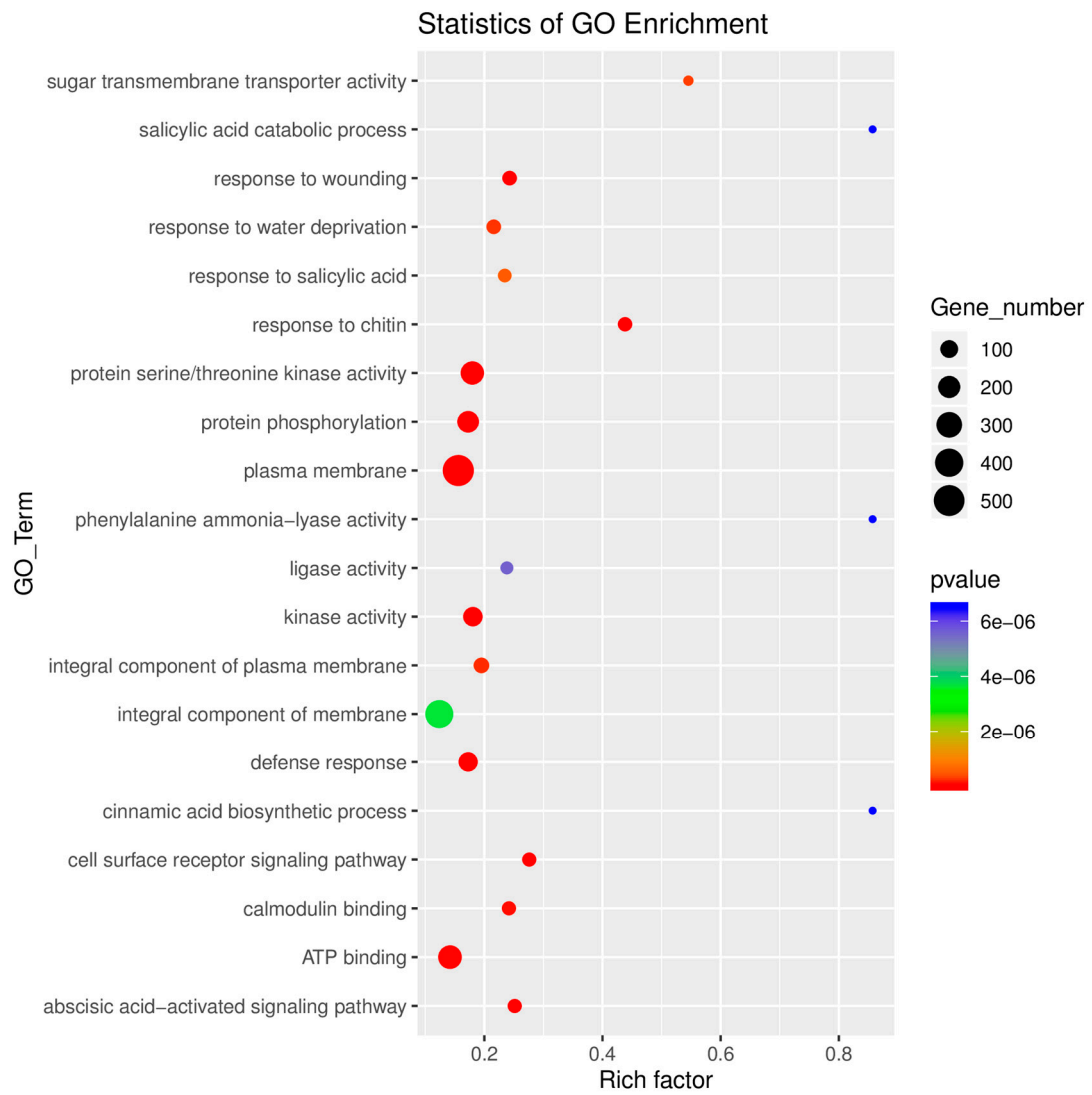
B



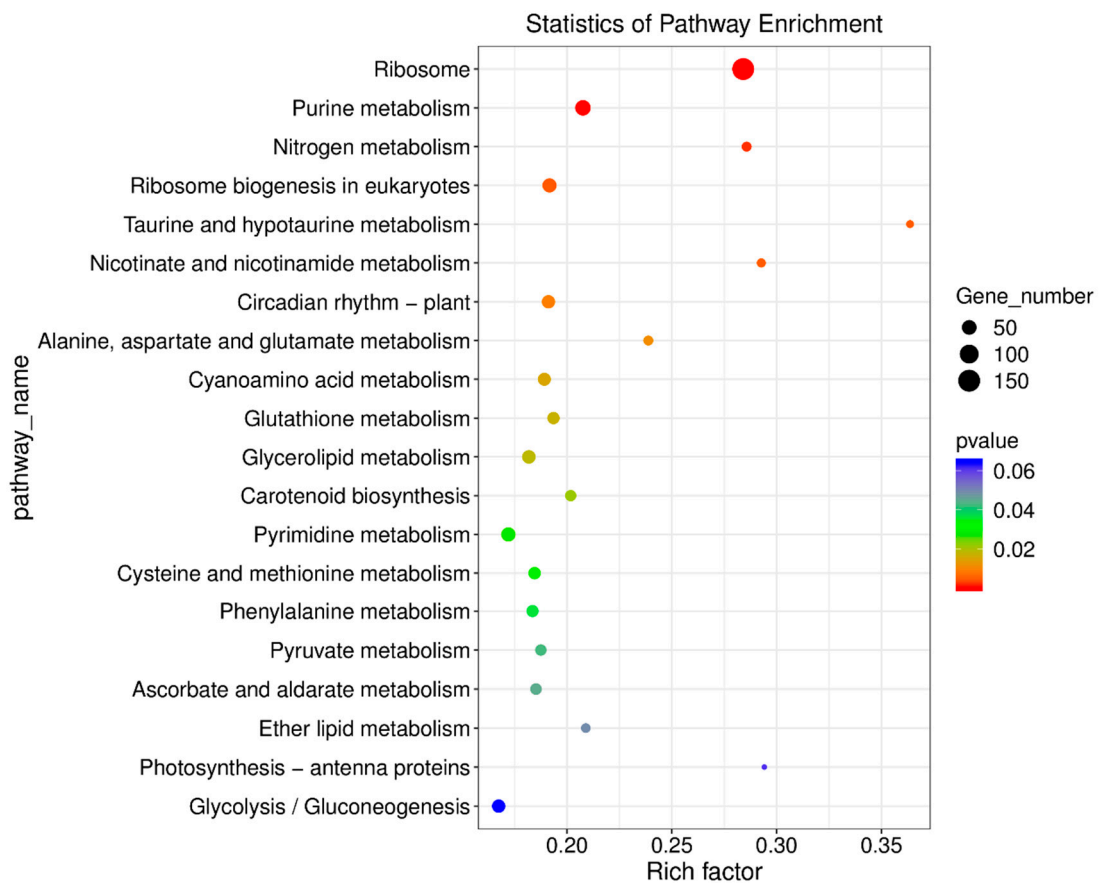
C



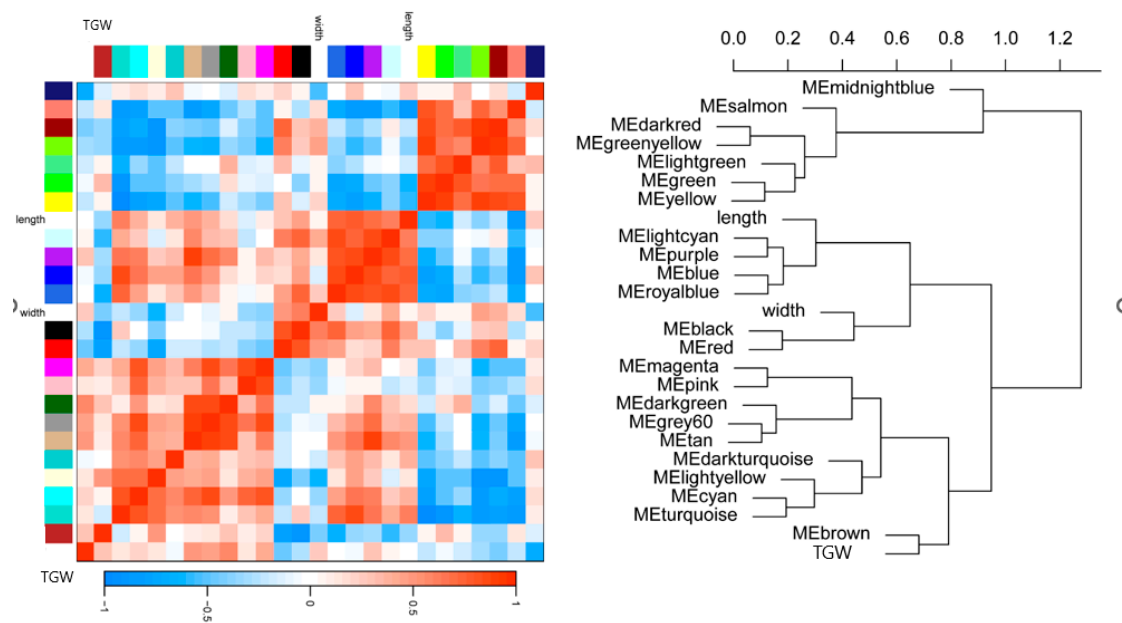
D



Supplementary Figure S3 KEGG analysis of DEGs between WFYT025 in the environment of early rice. That showed the top 20 most represented categories and the number of transcripts predicted to belong to each category.



Supplementary Figure S4 Correlation between gene expression profile of co-expression module and three phenotypic data (TGW; Length; Width). The legend on the right shows the correlation coefficients, with positive correlation in red and negative correlation in blue. Since the aim is to find genes related to seed development, the focus is on the co-expression module with high correlation with TGW (module color is midnightblue, the gene expression profile in this module is moderately negatively correlated with the TGW phenotype)



Supplementary Figure S5 Is the overall gene expression profile of the co-expression module MidnightBlue, which has the highest correlation with TGW.

There are 106 genes in this co-expression module. The graph is divided into three parts, the upper part is the expression heat map of the genes in the co-expression module. The middle part shows the relative expression of the eigengene in the module. The lower part shows the TGW phenotype values of the samples.

