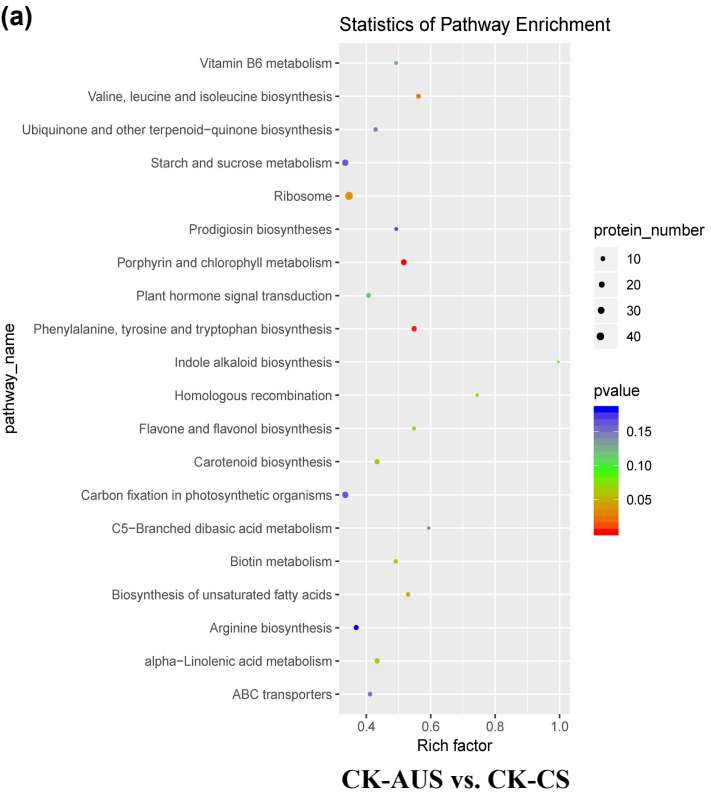
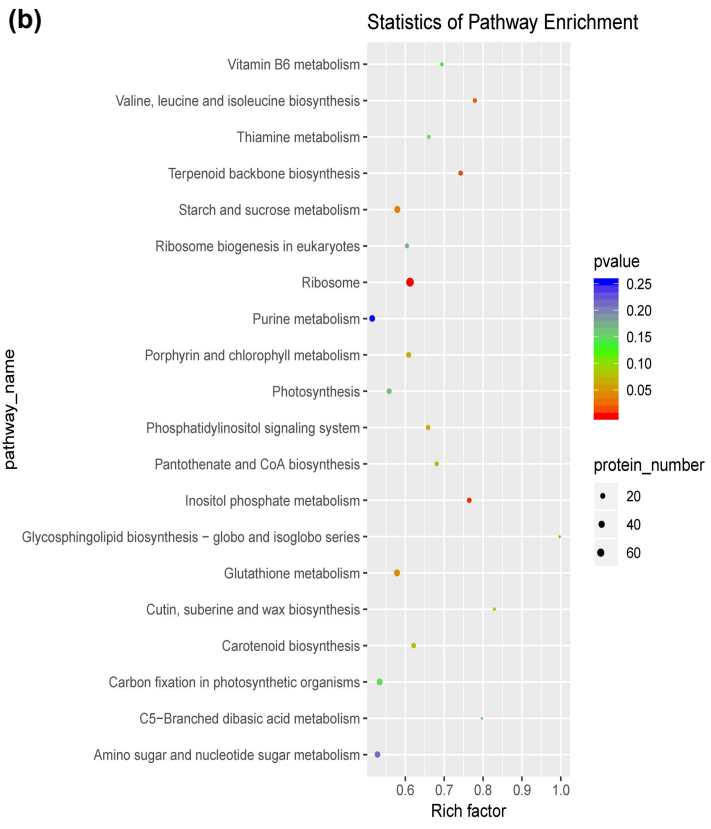
Effects of biological nitrogen metabolism on glufosinate-susceptible and resistant goosegrass (*Eleusine indica* L.)

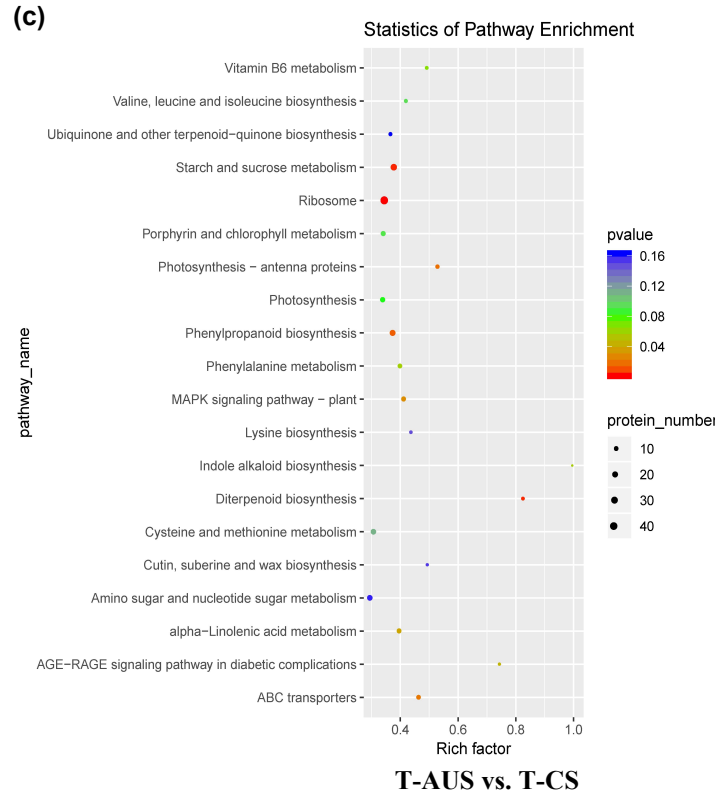
Figure S1. General analysis on characterizations of glufosinate-resistance goosegrass by proteomic sequencing. (a)-(h) Enrichment scatter plots of KEGG pathways in the eight comparative groups of the different goosegrass biotypes (NX, CS, and AUS) under glufosinate stress or under H_2O as the controls.



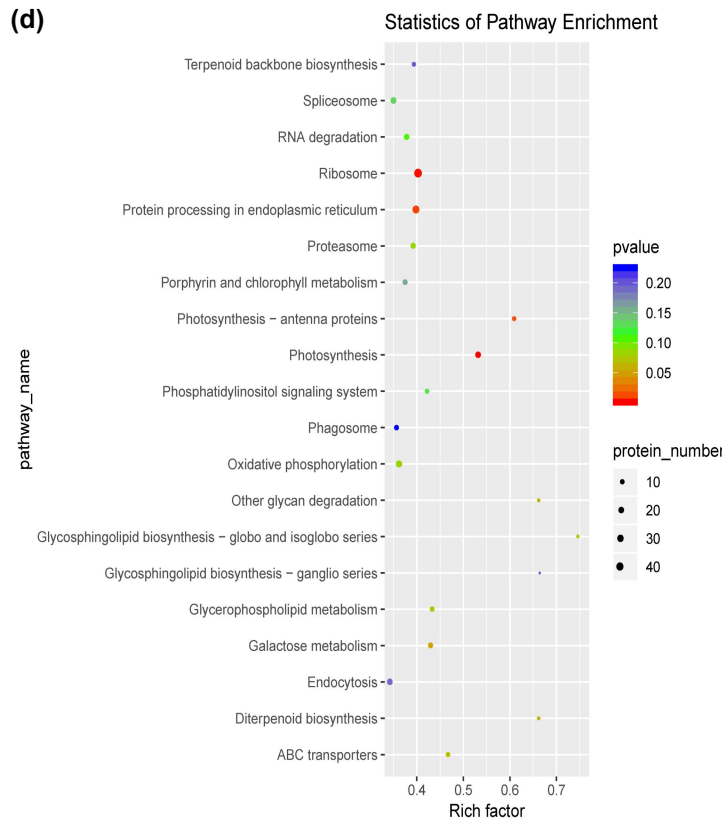
CK-AUS vs. CK-CS



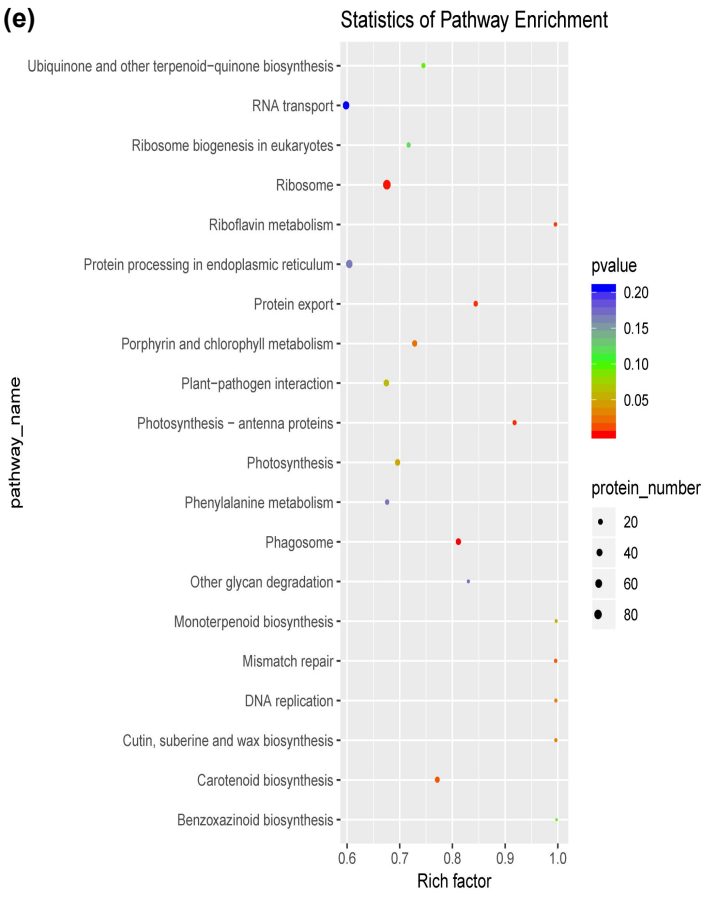
CK-AUS vs. CK-NX



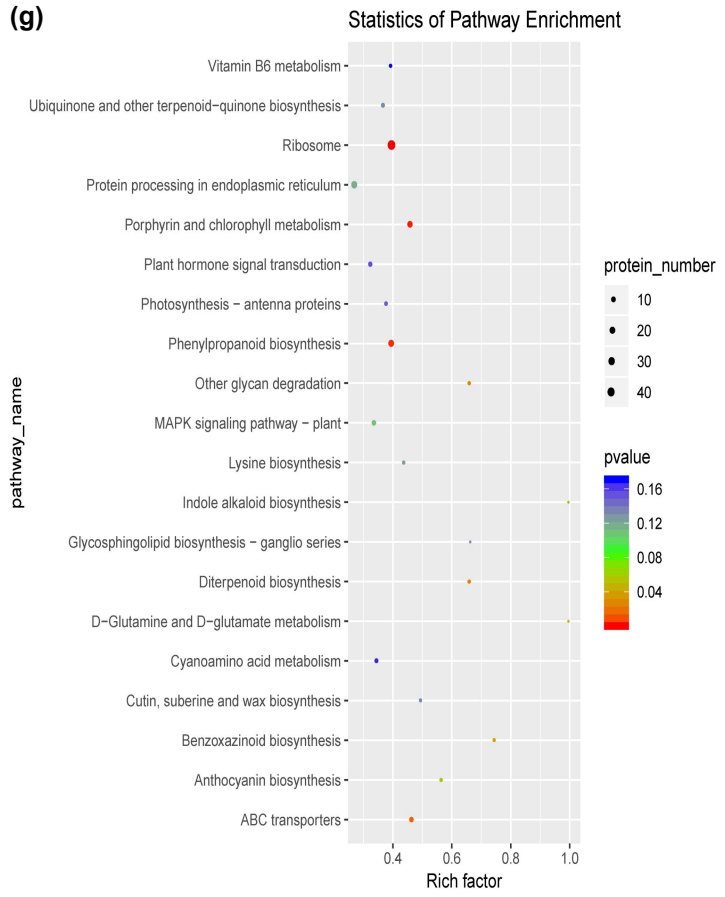
T-AUS vs. T-CS



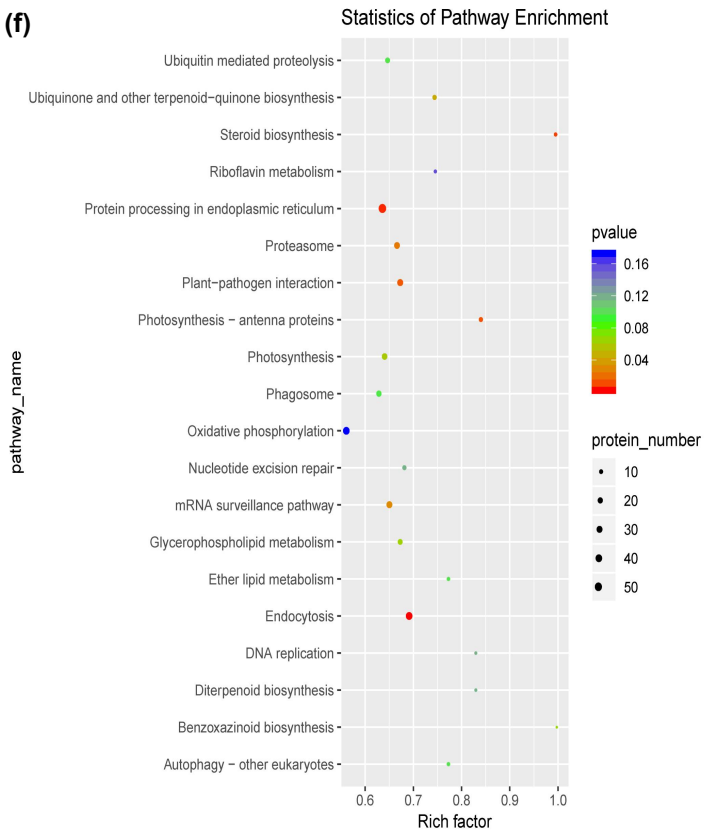
CK-CS vs. CK-NX



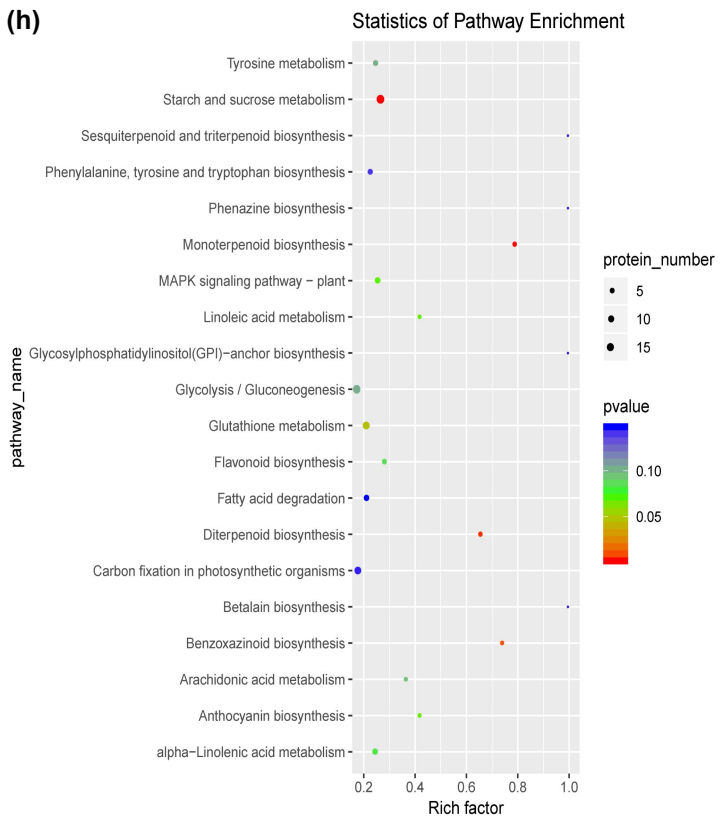
T-AUS vs._CK-AUS



T-AUS VS. T-NX



T-CS vs. CK-CS

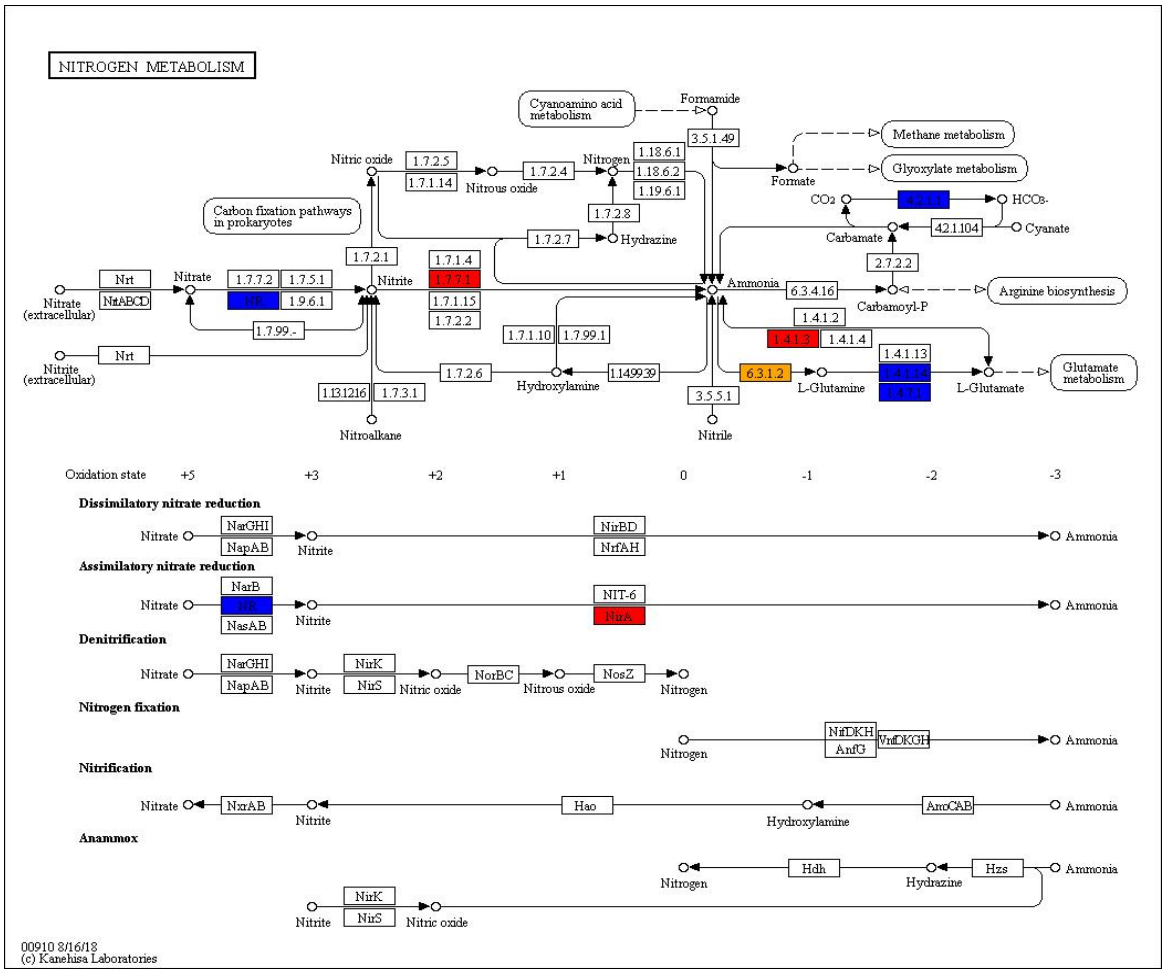


T-CS vs. T-NX

Figure S2. Differential expressions of genes and proteins in KEGG pathways of nitrogen metabolism. (a) and (b) Transcriptome and proteome analyses in the comparative group T-NX vs. CK-NX. (c) and (d) Transcriptome analyses in the comparative group T-AUS vs. CK-AUS and T-CS vs. CK-CS, respectively.

(a)

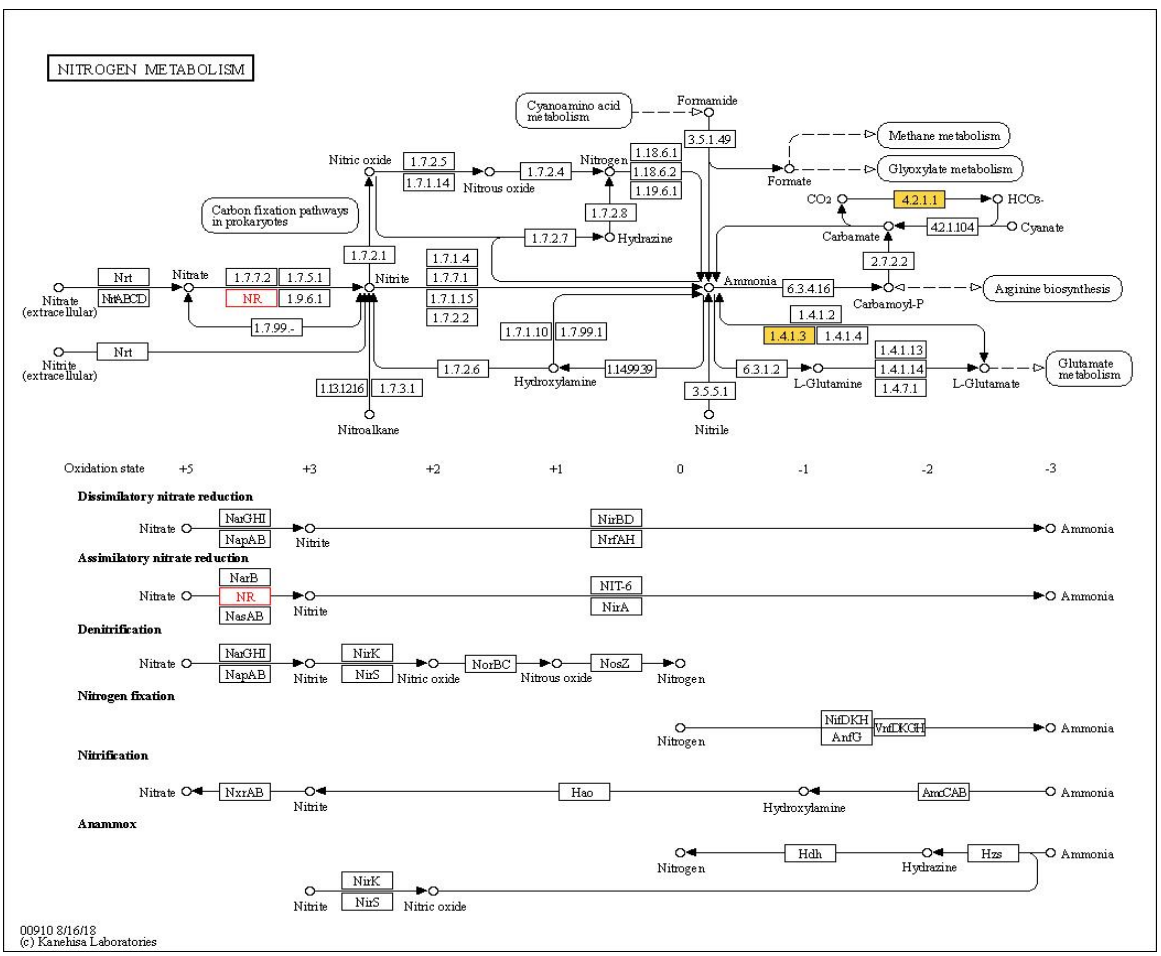
Transcriptome



T-NX vs. CK-NX

(b)

Proteome

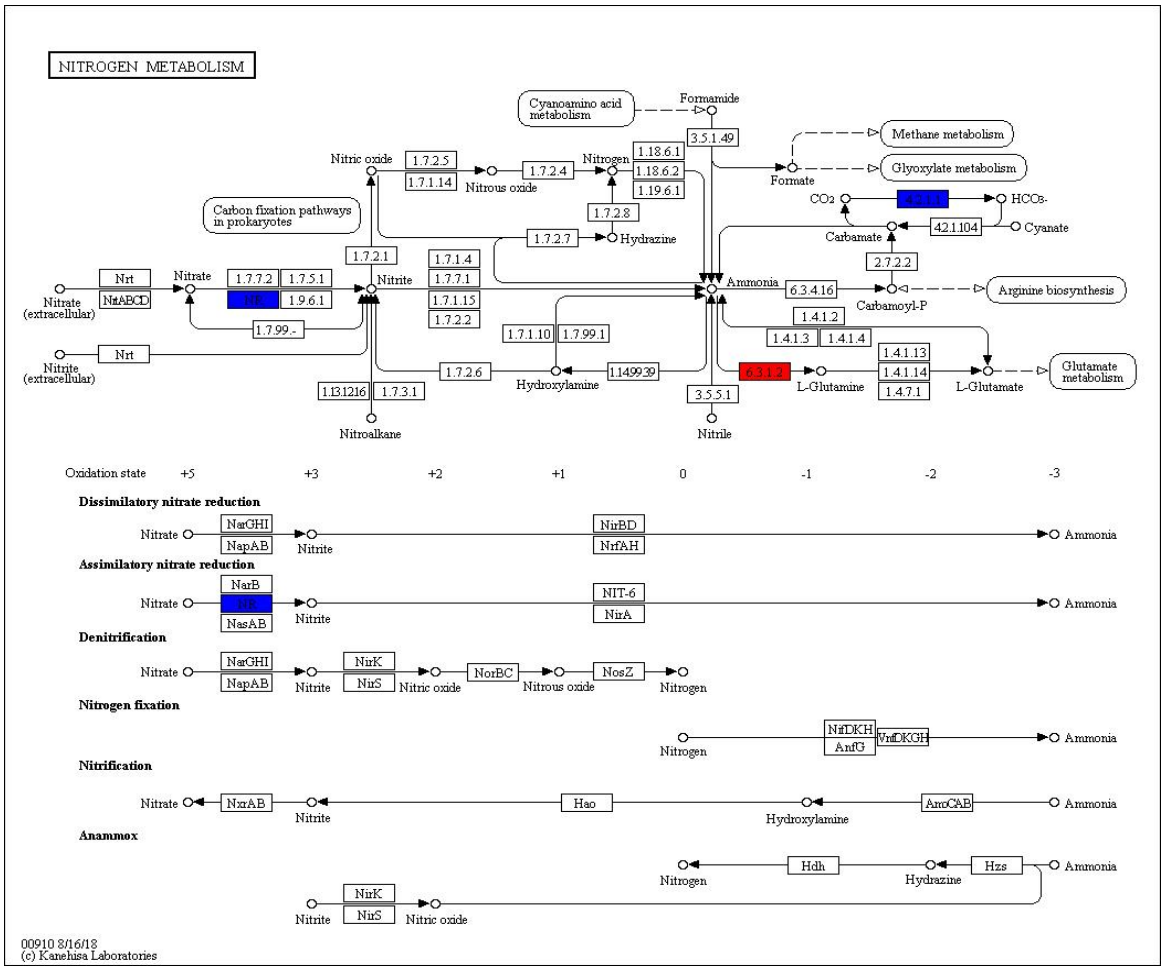


T-NX vs. CK-NX

(c)

Transcriptome

T-AUS vs. CK-AUS



(d)

Transcriptome

T-CS vs. CK-CS

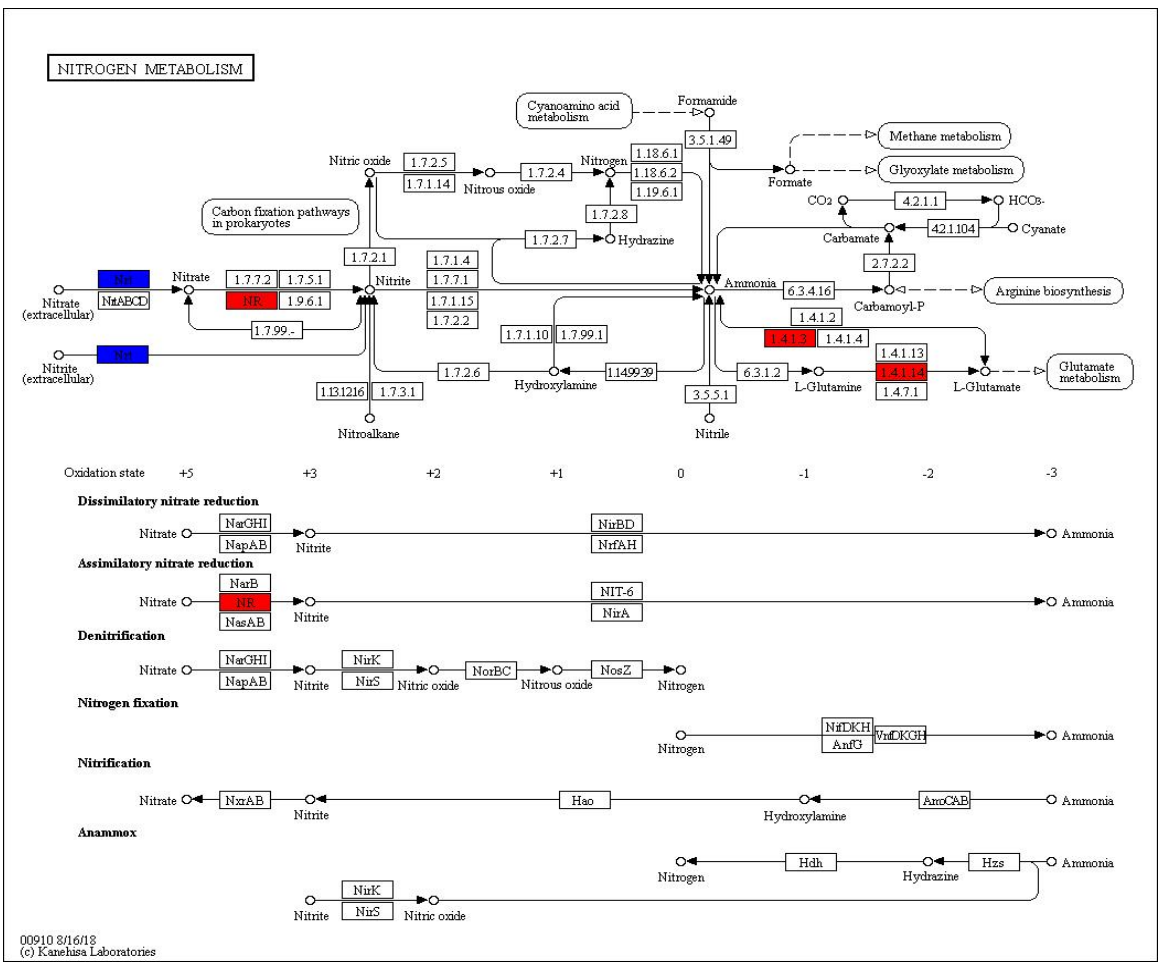


Figure S3. The CDS sequences of *GLN1-1*(a), *GDH2*(b), *GLSF*(c), *NIA1*(d), *Os01g0357100*(e) and *CA1*(f).

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(f) TRINITY_DN22941_c0_g1 Trans_ID=TRINITY_DN22941_c0_g1_i5 932bp (***CA1***)

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