

**Fig. S1** Measurement of soluble proteins under different N supplies in NH511 and MH23 respectively. The statistical analysis of comparing HN with LN was performed by t-tests in NH511 and MH23 respectively.



**Fig. S2** Nitrogen uptake efficiency analysis of NH511 and MH23 under HN supplies. The statistical analysis of between NH511 and MH23 was performed by t-tests. \*, *P*<0.05.



**Fig. S3** Volcano plot of DEGs identified under HN supplies. A, DEGs of NH511. The red pots represent 1576 significantly up-regulated unigenes. The green pots represent significantly down-regulated 880 unigenes. The black pots mean no significantly differential expression. B, DEGs of MH23 under HN and LN conditions. 113 significantly up-regulated unigenes and 153 down-regulated unigenes.

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**Fig. S4** Histogram description of Gene Ontology enrichment of DEGs. A, GO analysis of DEGs in NH511. B, GO analysis of DEGs in MH23. The DEGs were fell into three categories: biological process (BP), cellular component (CC) and molecular function (MF). The X-axis represents various gene function, the Y-axis corresponds to the number of DEGs.

Table S1 qRT-PCR primers used in this study.

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| **Primer name Sequence(5’-3’)** |
| ACTIN1-F ACCATTGGTGCTGAGCGTTT |
| ACTIN1-R CGCAGCTTCCATTCCTATGAA |
| OsNIA1-F TCAAGGTGTGGTACGTGGTG |
| OsNIA1-R CGAGGTCATAGCCCATCTTC |
| OsNIA2-F TGTACCAGGTCATCCAGTCGOsNIA2-R CGATGACGTACCACACCTTGOsNRT2.1-F CTTCACGTCGTCGAGGTACTOsNRT2.1-R CACTCGGAGCCGTAGTAGTGOsPHI1-F TCGACGGCTTCTGCATGAGOsPHI1-R GATCATCGAGGCGAGGGATATCOsLSI1-F CCATAGCGATACAGTACAGGAGOsLSI1-R GACGAACATCATGTTGAACGTCOsLSI2-F CTGGAGATGTCGGAGAACATAAOsLSI2-R GAAGCTCTTGAGGAACAGCTTCOsDREB1A-F GAACTGGACGTCCTGAGTGOsDREB1A-R CTAGTAGCTCCAGAGTGGGAOsNAC19-F GAAGAACGAGTGGGAGAAGATGOsNAC19-R TCGTCCATCGATTCTTTCTTGG |