**Appendix C**

Correlation matrix showing the relationship between two samples. The color bar represents the Pearson’s correlation coefficient from -1 (red) to 1 (blue).
Appendix D

Appendix D. Validation of RNA-seq by real time RT-PCR. A, Expression levels of randomly selected genes determined by RNA-seq (FPKM) and real time RT-PCR. The genes included Zm00001d000107 (gene 1), Zm00001d002435 (gene 2), Zm00001d039118 (gene 3), Zm00001d005251 (gene 4), Zm00001d047210 (gene 5), Zm00001d009296 (gene 6), Zm00001d033455 (gene 7), Zm00001d026053 (gene 8). For the real time RT-PCR, the expression levels were normalized to the expression of ZmUBQ1. Data are presented as means ± SE (n=3). B, Correlation of differentially expressed genes between real time RT-PCR analysis and RNA-seq experiment.
Appendix G. The different N deficiency-responsive metabolic pathways between the roots of Qi319 or Ye478 determined by MapMan analysis.
Appendix H. Top 20 GO classification of special N deficiency responsive genes in Qi319 and Ye478. A, Top 20 GO classification of special N deficiency up-regulated genes in Qi319. B, Top 20 GO classification of special N deficiency down-regulated genes in Qi319. C, Top 20 GO classification of special N deficiency down-regulated genes in Ye478. The point size represented the number of genes in the pathway; the point color meant $-\log_{10}(P$-value). D, Net photosynthetic rates of Ye478 and Qi319 after 5 days of low N (LN) treatment. Error bars represent SE for nine independent experiments. **P < 0.01 (Student’s t-test) indicates significant difference between LN and NN.