**Supplementary Figure 1.** Weighted gene co-expression network heatmap of all DEGs (A) and correlation heatmap of eight modules (B).
Supplementary Figure 2. Function enrichment analysis of DEGs in green module. A: GO enrichment analysis. B: KEGG enrichment analysis.
Supplementary Figure 3. qRT-PCR validation of 18 synthetic genes in amino acid biosynthesis pathway. The column chart shows the FPKM values in RNA-seq data. The line diagram represents the relative expression level in qRT-PCR.