**Supplementary Tables and Figures**

**Supplementary Table S1.** Primer sequences of genes used for quantitative RT-PCR verification.

|  |  |  |
| --- | --- | --- |
| Seq ID | Forward Primer (5’→3’) | Reverse Primer (5’→3’) |
| UBQ | CAGACCAGCAGCGCTTGA | TTACTGGCCACCACGGAGA |
| *EC\_V6.g007956* | CGTTCGACATGTTCAGCCAC | GGTAGTCGAAGCGGTAGACG |
| *EC\_V6.g089449* | ACCACGGCAAGTACTCGTTC | AAAGGTAGCGCATGAGGGTG |
| *EC\_V6.g033915* | TCGTGTGCTTCAGGATCGTC | TTCCCCGTCTTGTTCATCCG |
| *EC\_V6.g045995* | GTATGATTGCGGGCAAAGCC | TGTCCATGTGCCATCGTTGA |
| *EC\_V6.g043558* | GTCGGCACCTACTCCAAGAT | CGAGGAGGATAACGTCGAAGG |
| *EC\_V6.g059445* | ACAGCAACGTCCCTCAGTG | AAGCCAACAGAGTAGAGCCC |
| *EC\_V6.g005145* | CCCATCACCGAGTCCAACAT | CCTCGAGGTTCATATGCGGG |
| *EC\_V6.g100178* | TCATCGTAGGCAAGCTCGTG | AGATTGGGTGGAAGGCGATG |
| *EC\_V6.g071938* | GTGGTTCATCCTGGACGAGAT | AGGACGAGACCCAAGGTGA |
| *EC\_V6.g083936* | CGGTGTGGTTCATCCTGGAC | AGGAGGACGAGATCCAAGGT |
| *EC\_V6.g029186* | TCCATCCTCTTCACGCACTC | CAGAGGCGCTTGTTCTCGAT |
| *EC\_V6.g029187* | TCAAGGAGACGTTCAAGCCC | CTGAGGGGCTTGTTCTCGAT |
| *EC\_V6.g052409* | CGTCGTCAACTCCGACAGG | CTCGGCGTAAGTGTAGTCCC |
| *EC\_V6.g107400* | CGACCAGATCGAGGCAAGTG | TCTCCTTGTTCACCGTCGTG |
| *EC\_V6.g030555* | ACGGCGTGAAAACAAACCTG | CTTGCCGTACTCGACCATGT |
| *EC\_V6.g030557* | ATCGAGAAGACCTTTGGCGG | ATCGAGAAGACCTTTGGCGG |

**Supplementary Table S2.** Summary of the sequencing.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample | Clean reads | Cleans bases | Error Rate (%) | Q20 percentage (%) | Q30 percentage (%) | GC content |
| CK | 55,009,494.67 | 8,251,424,200 | 0.38 | 96.70 | 91.95 | 56.54 |
| LF | 55,992,401.33 | 8,398,860,200 | 0.41 | 96.44 | 91.38 | 58.17 |
| HF | 54,856,558.67 | 8,228,483,800 | 0.43 | 96.21 | 90.90 | 57.37 |

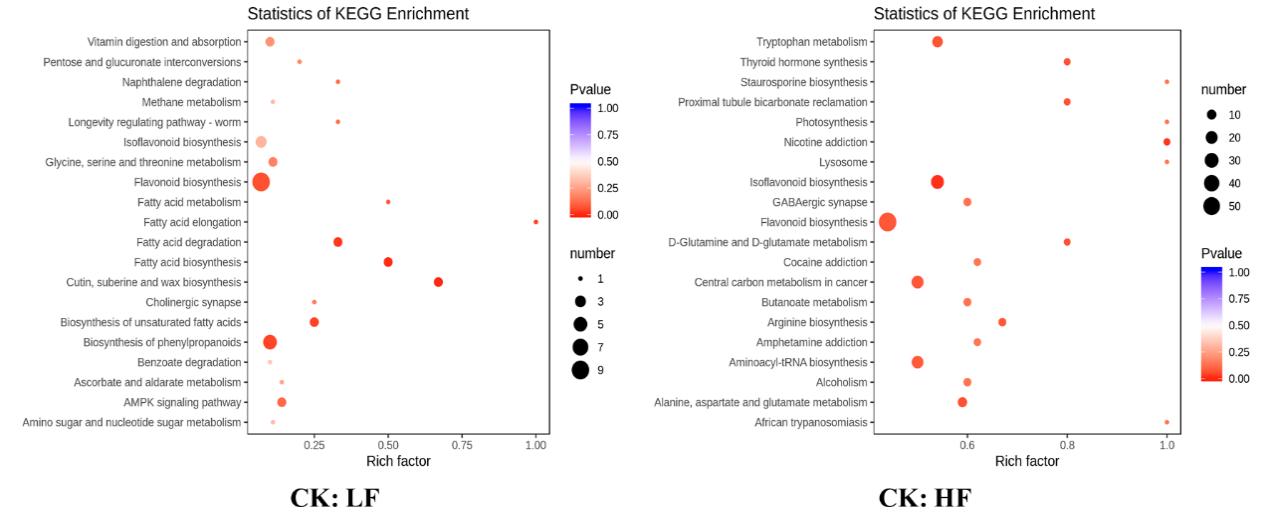
CK: the blank control group (0 g/L FA), LF: the low concentration group (0.02 g/L FA), HF: the high concentration group (0.8 g/L FA).

**Supplementary Table S3.** The DEGs of transcription of auxin responsive genes.

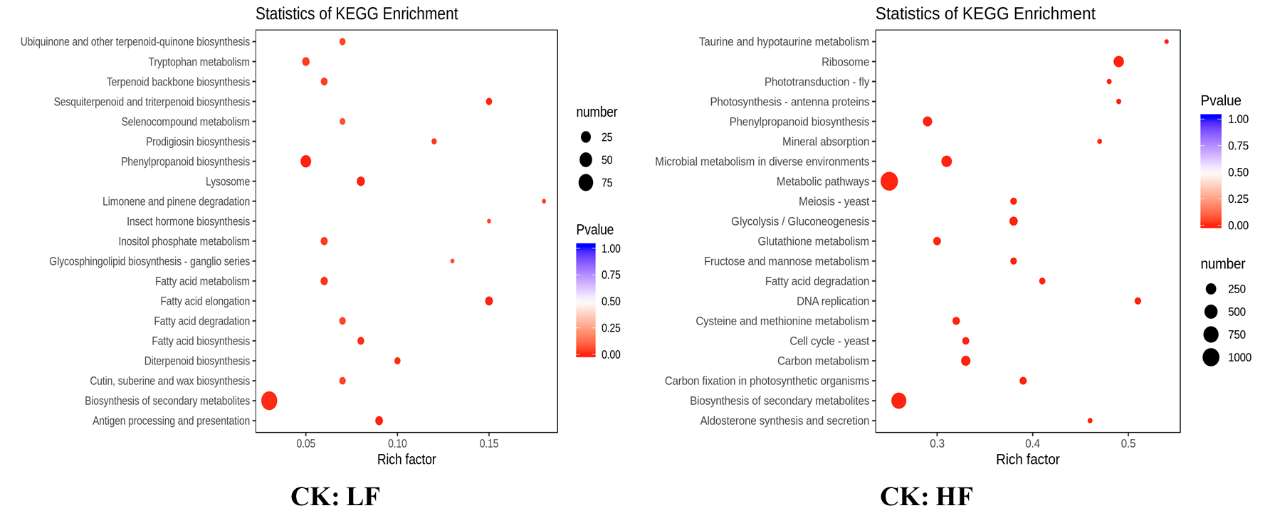
|  |  |  |
| --- | --- | --- |
| Gene name | LF: CK | HF: CK |
| *AUX/IAA* | 2 (Down-regulation) | 8 (Up-regulation)  11 (Down-regulation) |
| *GH3* | 0 | 4 (Up-regulation) |
| *SAUR* | 3 (Up-regulation) | 6 (Up-regulation)  8 (Down-regulation) |

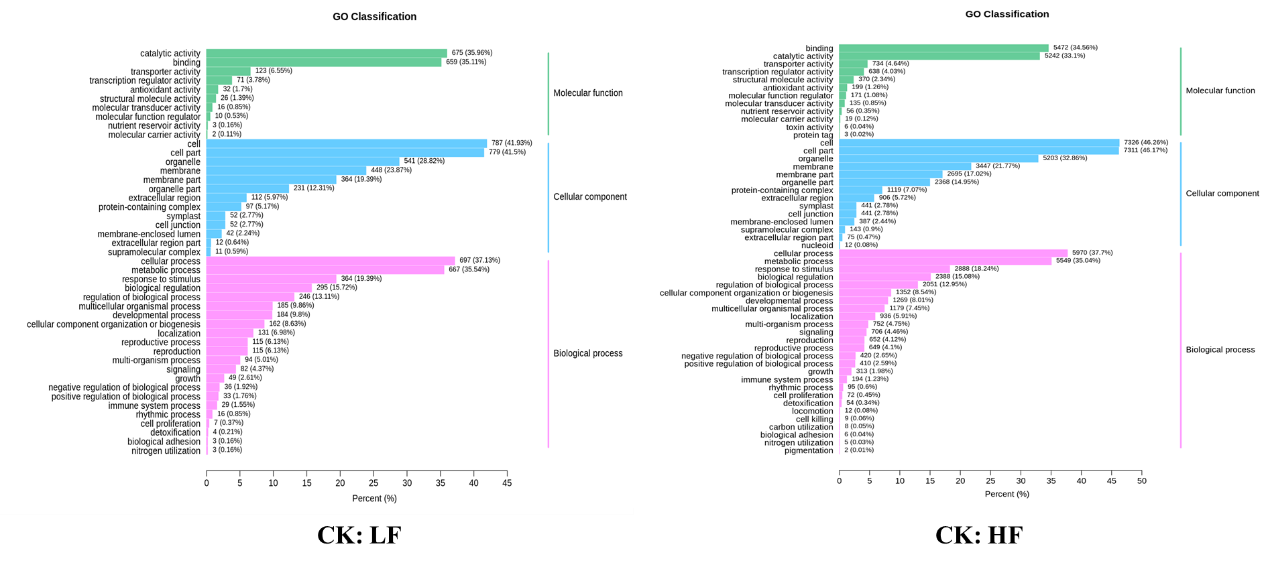
CK: the blank control group (0 g/L FA), LF: the low concentration group (0.02 g/L FA), HF: the high concentration group (0.8 g/L FA).

**Supplementary Figure Legends**

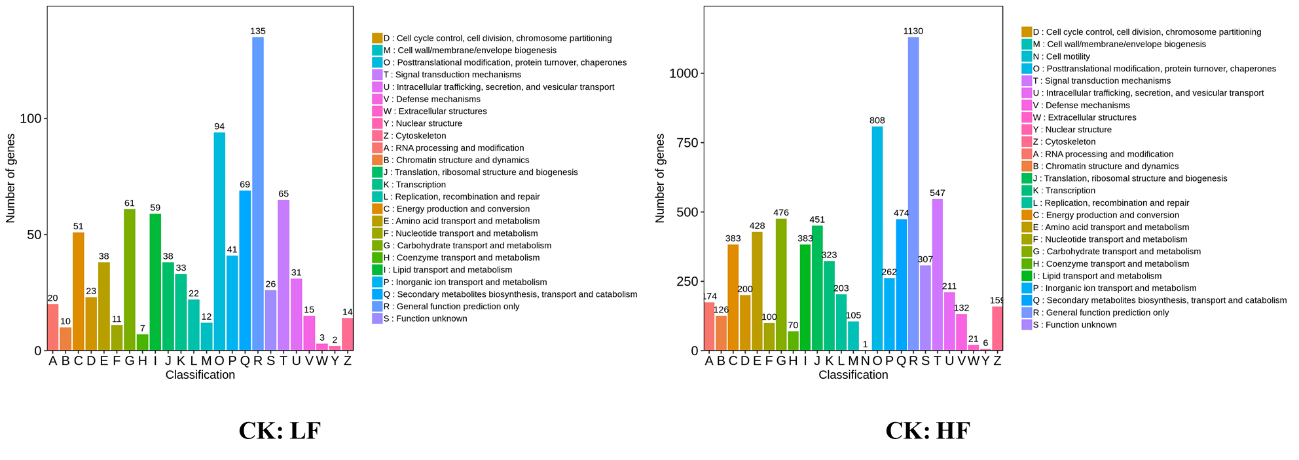


**Supplementary Figure S1.** Statistics of KEGG pathway enrichment for differential metabolites. CK: the blank control group (0 g/L FA), LF: the low concentration group (0.02 g/L FA), HF: the high concentration group (0.8 g/L FA).

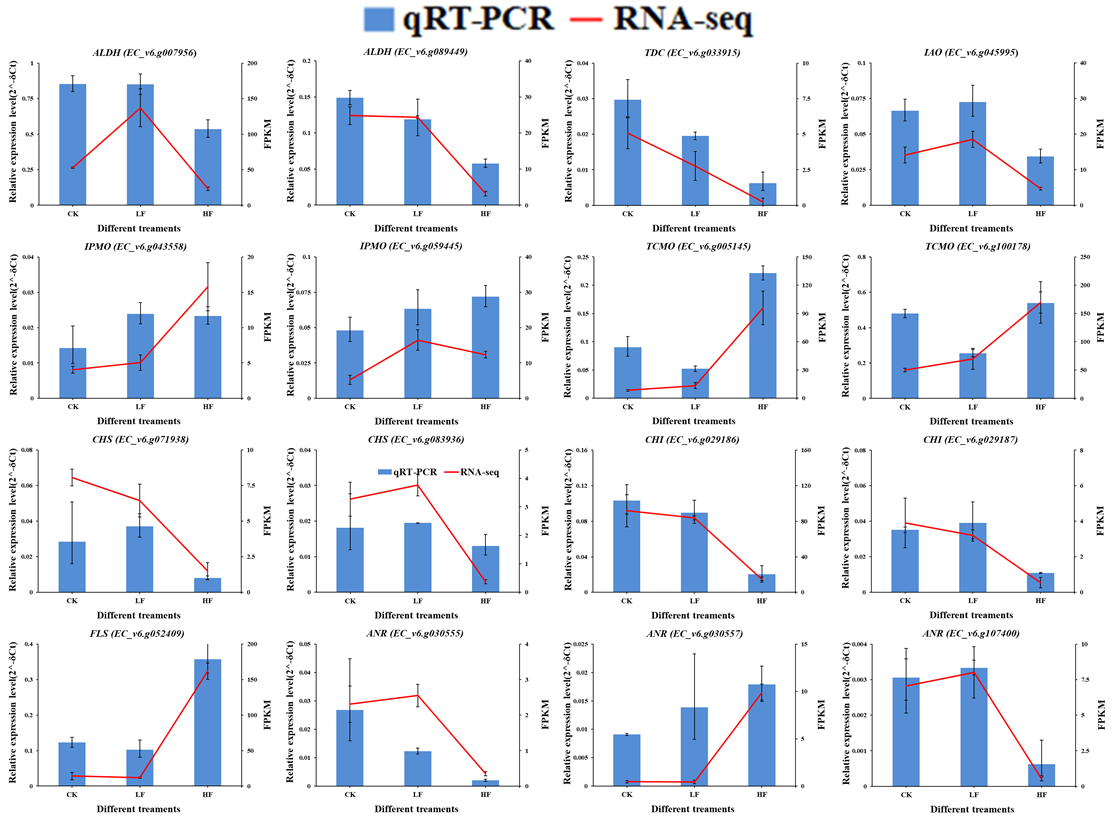
**Supplementary Figure S2.** Statistics of KEGG pathway enrichment for differentially expressed genes. CK: the blank control group (0 g/L FA), LF: the low concentration group (0.02 g/L FA), HF: the high concentration group (0.8 g/L FA).



**Supplementary Figure S3.** GO classification of differentially expressed genes. CK: the blank control group (0 g/L FA), LF: the low concentration group (0.02 g/L FA), HF: the high concentration group (0.8 g/L FA).



**Supplementary Figure S4.** COG functional classification of differentially expressed genes. CK: the blank control group (0 g/L FA), LF: the low concentration group (0.02 g/L FA), HF: the high concentration group (0.8 g/L FA).



**Supplementary Figure S5.** Expression of representative genes validated by qRT-PCR in barnyard grass stems and leaves of CK, LF and HF. CK: the blank control group (0 g/L FA), LF: the low concentration group (0.02 g/L FA), HF: the high concentration group (0.8 g/L FA).