

Table S1. Primer sequences of differentially expressed genes.

| Gene ID | Forward Primer (5'3') | Reverse Primer (5'3') |
|------------------|--------------------------|-------------------------|
| Gohir.A11G156000 | AGCGTTGAAGGCTACAGAGGAGAG | TCAGTTCACACGAAGCAGCACAC |
| Gohir.A07G220600 | TCCTCTCCCCTTCCCCGAACATAG | CAGCACGCACTCCACCACAC |
| Gohir.D05G218300 | ATGTCCAACGCCTGTTCCCA | AGCCGCCCATGAATCGAGAA |
| Gohir.A11G141800 | TTCACCTTCTTCTTGCAGCG | GTGCAGGTTGGAGCTGTGGAT |
| Gohir.D02G166900 | TTTTCAGGCACTTGCTCGGC | ACCTTCAGTTCCTCTTCGGCA |
| Gohir.A05G304100 | AAAGGTTCCAGCAGACGCCA | AATGCAGCCTCCGCTAGGTC |
| Gohir.A09G158200 | ATATGGTGGATTGCGGGCCA | GGCGCGTGCTGTTTTTCGTAT |
| Gohir.A13G152200 | TCCTGACCAGCAAGTGGTGT | GCAATCAGGTGCCTCAACCC |
| Gohir.D05G218200 | TGGAGGTGTTGGACAAGCGA | TCTGCAAGGGTCAGCCTCAA |
| Actin | ATCCTCCGTCTTGACCTTG | TGTCCGTCAGGCAACTCAT |

Table S2. Experimental grouping.

| Sample Number | Organisation Site | Different Treatments | Experimental Grouping |
|---------------|-------------------|---|-----------------------|
| XJ0hR1 | blade | 0 h treatment of drought-resistant materials | control group |
| XJ0hR2 | blade | | control group |
| XJ0hR3 | blade | | control group |
| XJ0hS1 | blade | 0 h treatment of drought-sensitive materials | control group |
| XJ0hS2 | blade | | control group |
| XJ0hS3 | blade | | control group |
| XJ12hR1 | blade | 12 h treatment of drought-resistant materials | test group |
| XJ12hR2 | blade | | test group |
| XJ12hR3 | blade | | test group |
| XJ12hS1 | blade | 12 h treatment of drought-sensitive materials | test group |
| XJ12hS2 | blade | | test group |
| XJ12hS3 | blade | | test group |
| XJ24hR1 | blade | 24 h treatment of drought-resistant materials | test group |
| XJ24hR2 | blade | | test group |
| XJ24hR3 | blade | | test group |
| XJ24hS1 | blade | 24 h treatment of drought-sensitive materials | test group |
| XJ24hS2 | blade | | test group |
| XJ24hS3 | blade | | test group |

Note: A total of 18 materials were obtained; R, drought-resistant material Xinluzhong No. 82; S, drought-sensitive material Kexin No. 1; 0 h, 12 h, and 24 h represent different processing times; and R1, R2, R3, S1, S2, and S3 represent different biological repetitions.

Table S3. Gohir.A11G156000.v2.1. expression levels.

| XJ0hR1_ | XJ0hR2_ | CXJ0hR3_ | CXJ12hR1_ | XJ12hR2_ | XJ12hR3_ | XJ0hR1_F | XJ0hR2_F | XJ0hR3_F | XJ12hR1_ | XJ12hR2_ | XJ12hR3_ | p- | log2F | Regula |
|----------|----------|----------|-----------|----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|------------------------|--------|---------|
| Count | ount | ount | Count | Count | Count | PKM | PKM | PKM | FPKM | FPKM | FPKM | Value | C | ted |
| 4003 | 2474 | 3860 | 9632 | 7280 | 6983 | 16.35 | 13.45 | 16.82 | 46.05 | 40.35 | 37.97 | 1.22×10^{-7} | 0.922 | up |
| XJ0hS1_C | XJ0hS2_C | XJ0hS3_C | XJ12hS1_ | XJ12hS2_ | XJ12hS3_ | XJ0hS1_F | XJ0hS2_F | XJ0hS3_F | XJ12hS1_F | XJ12hS2_F | XJ12hS3_F | p- | log2F | regulat |
| ount | ount | ount | Count | Count | Count | PKM | PKM | PKM | PKM | PKM | PKM | value | C | ed |
| 3044 | 2876 | 2983 | 6772 | 7408 | 7241 | 16.60 | 14.66 | 15.43 | 35.89 | 40.32 | 38.38 | 1.12×10^{-12} | 0.784 | up |
| XJ12hR1_ | XJ12hR2_ | XJ12hR3_ | XJ24hR1_ | XJ24hR2_ | XJ24hR3_ | XJ12hR1_ | XJ12hR2_ | XJ12hR3_ | XJ24hR1_ | XJ24hR2_ | XJ24hR3_ | p- | log2F | regulat |
| Count | Count | Count | Count | Count | Count | FPKM | FPKM | FPKM | FPKM | FPKM | FPKM | value | C | ed |
| 9632 | 7280 | 6983 | 2018 | 2688 | 3567 | 46.05 | 40.35 | 37.97 | 10.84 | 14.24 | 17.42 | 6.38×10^{-13} | -1.239 | down |
| XJ12hS1_ | XJ12hS2_ | XJ12hS3_ | XJ24hS1_ | XJ24hS2_ | XJ24hS3_ | XJ12hS1_F | XJ12hS2_F | XJ12hS3_F | XJ24hS1_F | XJ24hS2_F | XJ24hS3_F | p- | log2F | regulat |
| Count | Count | Count | Count | Count | Count | PKM | PKM | PKM | PKM | PKM | PKM | value | C | ed |
| 6772 | 7408 | 7241 | 2537 | 3302 | 2516 | 35.89 | 40.32 | 38.38 | 13.28 | 17.41 | 12.90 | 1.74×10^{-12} | -1.101 | down |

Table S4. Gohir.A07G220600.v2.1. expression levels.

| XJ0hR1_ Count | XJ0hR2_ Count | XJ0hR3_ Count | XJ12hR1_ Count | XJ12hR2_ Count | XJ12hR3_ Count | XJ0hR1_F PKM | XJ0hR2_F PKM | XJ0hR3_F PKM | XJ12hR1_ FPKM | XJ12hR2_ FPKM | XJ12hR3_ FPKM | <i>p</i> - Value | log2FC | Regulat ed |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------------|----------------------|---------------|
| 3279 | 2181 | 3912 | 164 | 287 | 156 | 8.600 | 7.616302 | 10.946612 | 0.503461 | 1.019193 | 0.542571 | 1.80×10^{-35} | - 4.078519 682 | down |
| XJ0hS1_ Count | XJ0hS2_ Count | XJ0hS3_ Count | XJ12hS1_ Count | XJ12hS2_ Count | XJ12hS3_ Count | XJ0hS1_F PKM | XJ0hS2_F PKM | XJ0hS3_F PKM | XJ12hS1_ FPKM | XJ12hS2_ FPKM | XJ12hS3_ FPKM | <i>p</i> - value | log2FC | regulat ed |
| 2364 | 3325 | 3246 | 370 | 281 | 154 | 8.282 | 10.884507 | 10.782553 | 1.259015 | 0.97912 | 0.52093 | 8.70×10^{-31} | - 3.832399 289 | down |
| XJ12hR1_ Count | XJ12hR2_ Count | XJ12hR3_ Count | XJ24hR1_ Count | XJ24hR2_ Count | XJ24hR3_ Count | XJ12hR1_ FPKM | XJ12hR2_ FPKM | XJ12hR3_ FPKM | XJ24hR1_ FPKM | XJ24hR2_ FPKM | XJ24hR3_ FPKM | <i>p</i> - value | log2FC | regulat ed |
| 164 | 287 | 156 | 4256 | 2021 | 2709 | 0.503 | 1.019193 | 0.542571 | 14.684347 | 6.871942 | 8.496771 | 3.55×10^{-19} | 4.003553 295 | up |
| XJ12hS1_ Count | XJ12hS2_ Count | XJ12hS3_ Count | XJ24hS1_ Count | XJ24hS2_ Count | XJ24hS3_ Count | XJ12hS1_ FPKM | XJ12hS2_ FPKM | XJ12hS3_ FPKM | XJ24hS1_ FPKM | XJ24hS2_ FPKM | XJ24hS3_ FPKM | <i>p</i> - value | log2FC | regulat ed |
| 370 | 281 | 154 | 2738 | 3093 | 2151 | 1.259 | 0.97912 | 0.52093 | 9.204302 | 10.476203 | 7.083376 | 3.89×10^{-23} | 3.435904 968 | up |

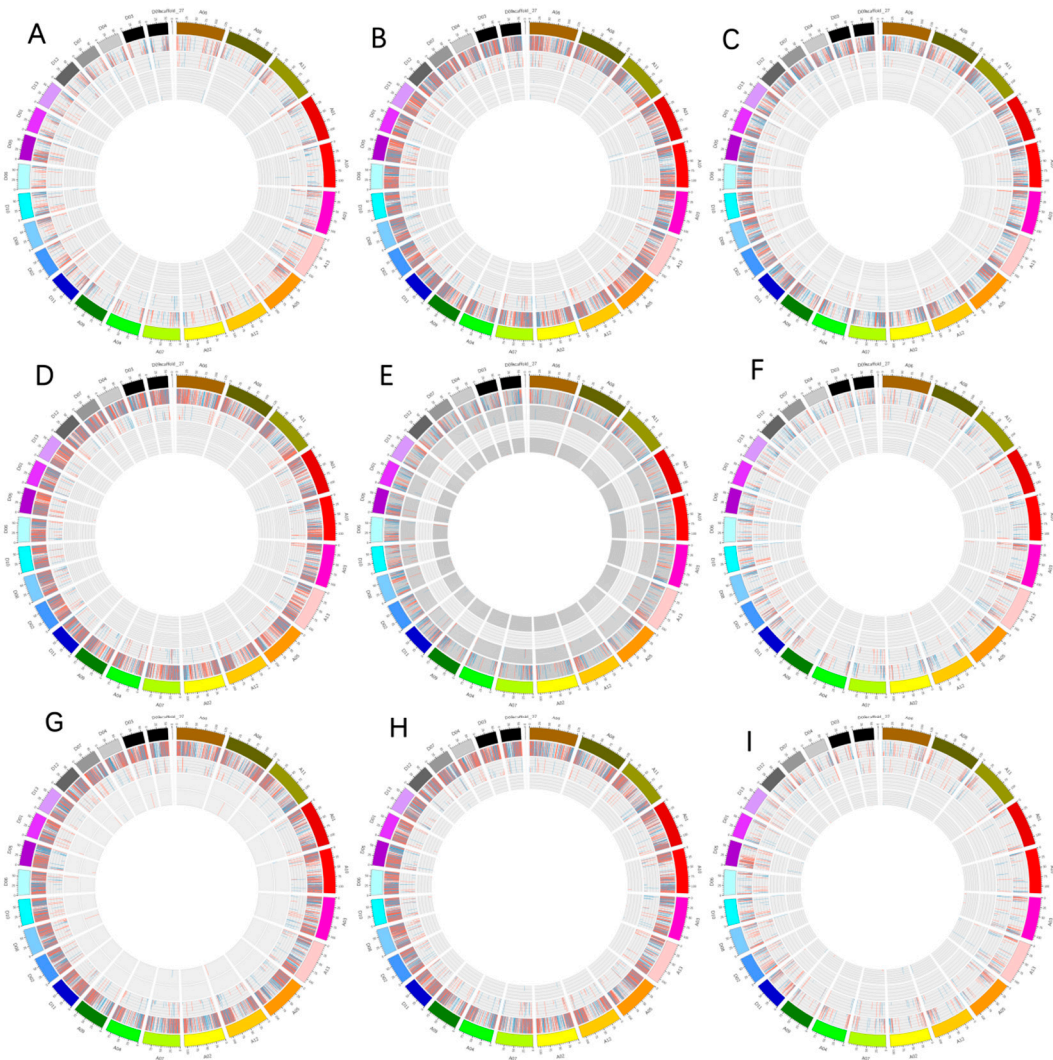


Figure S1. Circos diagrams for different levels of significance across RNA types. Note: The outermost circle shows chromosome information, followed by mRNA, lncRNA, circRNA, and miRNA. In the diagrams for each group, red represents upregulation, blue represents downregulation, and the height represents significance ($-\log_{10}(\text{FDR or } p\text{-value})$).

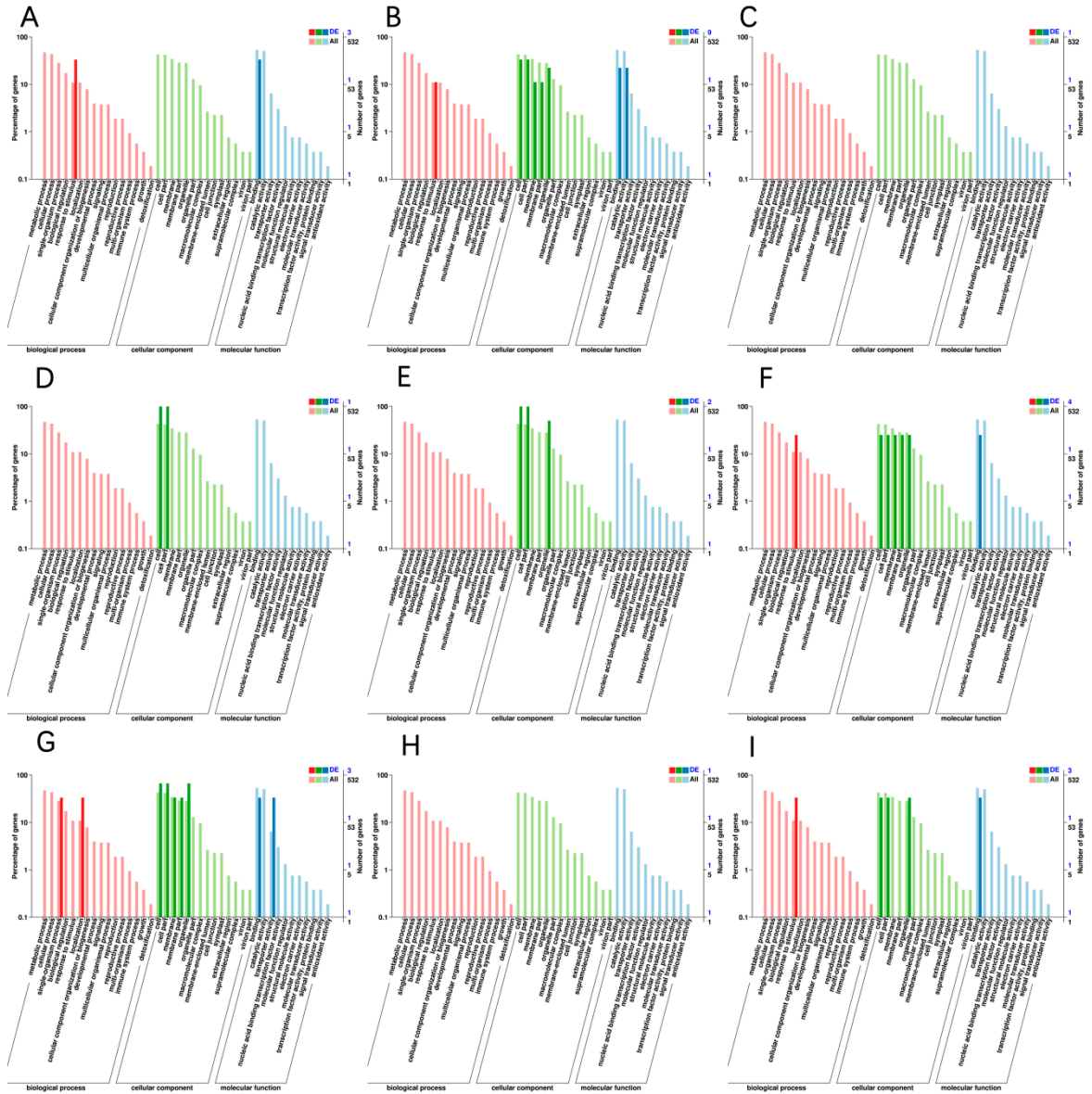


Figure S2. Annotation statistics diagrams of the GO secondary nodes of the different circRNA source genes in each comparison group. Note: The abscissa is the GO classification, the left ordinate is the percentage of the number of genes, and the right is the number of genes. This figure shows the gene annotation status of each secondary function of GO based on circRNA source genes and all genes. It reflects the status of each secondary function in the two backgrounds. The secondary functions with obvious proportional differences indicate that circRNA source genes are compared with all genes, indicating that if the enrichment trend of genes is different, this function is important. A:XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ0hS1_XJ0hS2_XJ0hS3;B:XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ12hR1_XJ12hR2_XJ12hR3;C:XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ24hR1_XJ24hR2_XJ24hR3;D:XJ0hS1_XJ0hS2_XJ0hS3_vs_XJ12hS1_XJ12hS2_XJ12hS3;E:XJ0hS1_XJ0hS2_XJ0hS3_vs_XJ24hS1_XJ24hS2_XJ24hS3;F:XJ12hR1_XJ12hR2_XJ12hR3_vs_XJ12hS1_XJ12hS2_XJ12hS3;G:XJ12hR1_XJ12hR2_XJ12hR3_vs_XJ24hR1_XJ24hR2_XJ24hR3;H:XJ12hS1_XJ12hS2_XJ12hS3_vs_XJ24hS1_XJ24hS2_XJ24hS3;I:XJ24hR1_XJ24hR2_XJ24hR3_vs_XJ12hS1_XJ12hS2_XJ12hS3.

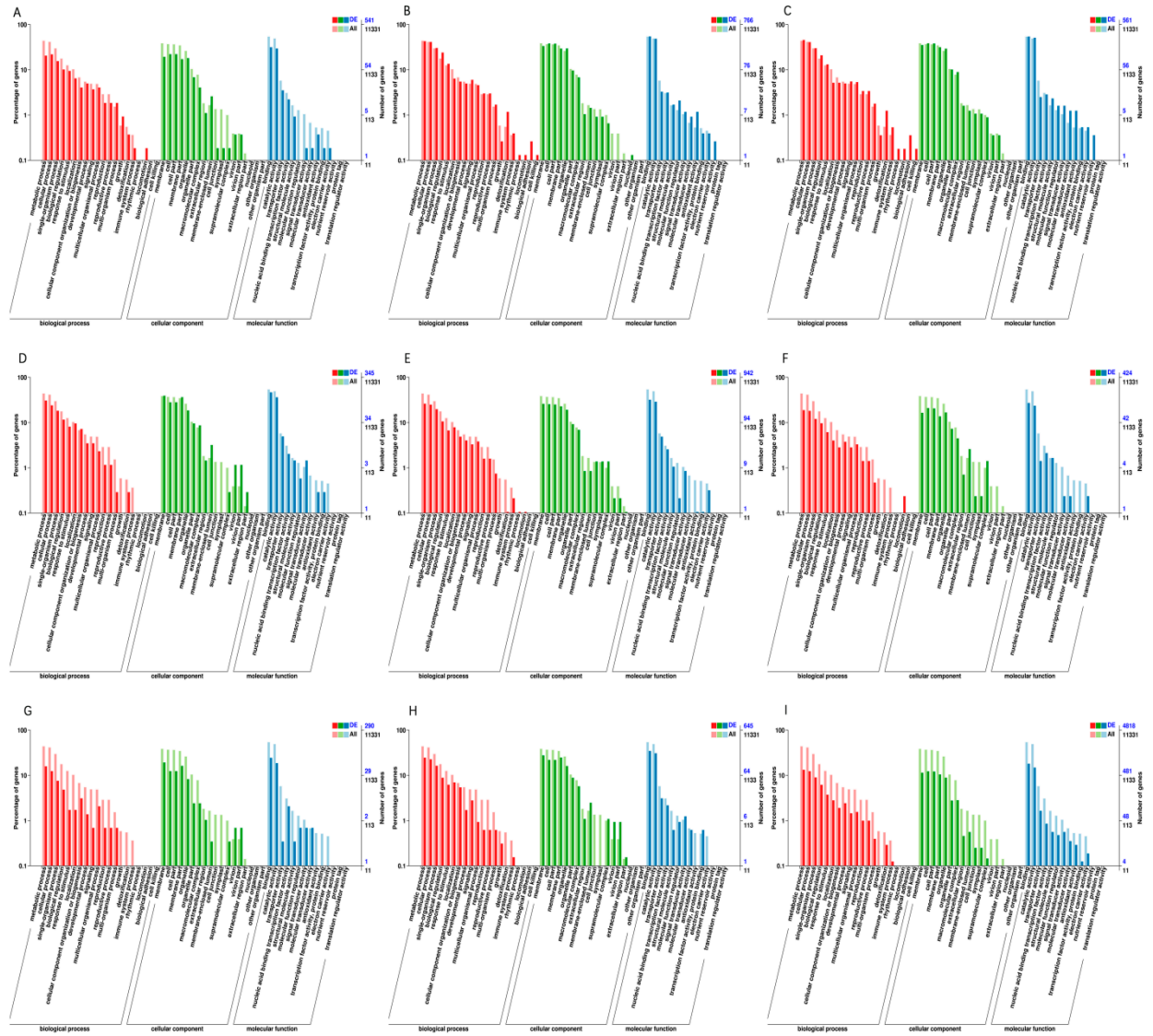


Figure S3. GO annotation classification statistics of differentially expressed miRNA target genes. Note: The abscissa is the GO classification, the left ordinate is the percentage of the number of genes, and the right is the number of genes. This figure shows the gene enrichment of each secondary function of GO based on the differentially expressed miRNA target genes and all the genes, reflecting the status of each secondary function in the two backgrounds. The secondary functions with obvious proportional differences indicate that circRNA source genes are compared with all genes, indicating that if the enrichment trend of genes is different, this function is important. (A) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ0hS1_XJ0hS2_XJ0hS3; (B) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ12hR1_XJ12hR2_XJ12hR3; (C) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ24hR1_XJ24hR2_XJ24hR3; (D) XJ0hS1_XJ0hS2_XJ0hS3_vs_XJ12hS1_XJ12hS2_XJ12hS3; (E) XJ0hS1_XJ0hS2_XJ0hS3_vs_XJ24hS1_XJ24hS2_XJ24hS3; (F) XJ12hR1_XJ12hR2_XJ12hR3_vs_XJ12hS1_XJ12hS2_XJ12hS3; (G) XJ12hR1_XJ12hR2_XJ12hR3_vs_XJ24hR1_XJ24hR2_XJ24hR3; (H) XJ12hS1_XJ12hS2_XJ12hS3_vs_XJ24hS1_XJ24hS2_XJ24hS3; (I) XJ24hR1_XJ24hR2_XJ24hR3_vs_XJ12hS1_XJ12hS2_XJ12hS3.

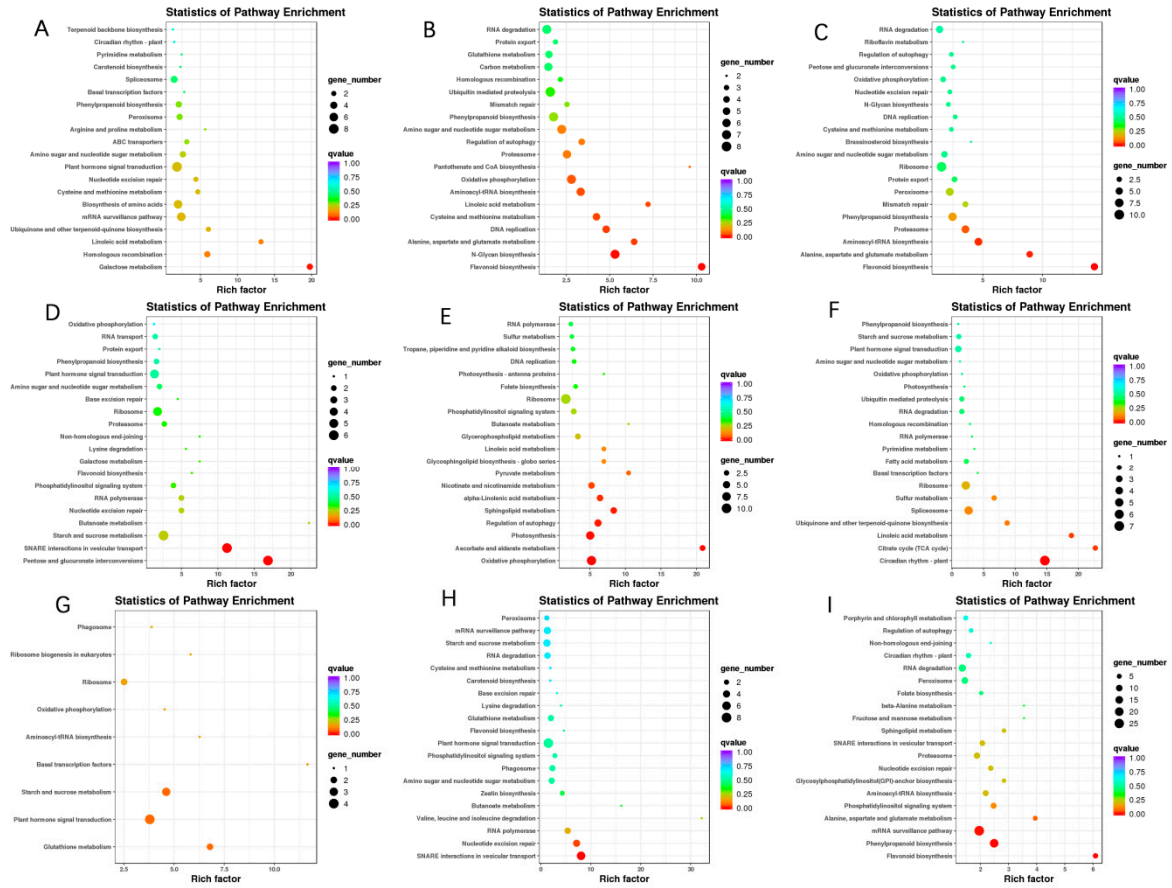


Figure S4. KEGG pathway enrichment scatter diagram of differentially expressed miRNA target genes. Note: Each graph in the figure represents a KEGG pathway; the abscissa is the enrichment factor, which represents the proportion of the number of differentially expressed miRNA target genes annotated to a pathway among the total number of genes annotated to the pathway. The larger the value is, the more significant the enrichment level of the differentially expressed miRNA target gene in the pathway. The ordinate is $-\log_{10}(Q \text{ value})$, where the $Q \text{ value}$ is the p -value after multiple hypothesis testing correction; therefore, the larger the ordinate is, the higher the enrichment significance of differentially expressed miRNA target genes in this pathway. (A) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ0hS1_XJ0hS2_XJ0hS3; (B) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ12hR1_XJ12hR2_XJ12hR3; (C) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ24hR1_XJ24hR2_XJ24hR3; (D) XJ0hS1_XJ0hS2_XJ0hS3_vs_XJ12hS1_XJ12hS2_XJ12hS3; (E) XJ0hS1_XJ0hS2_XJ0hS3_vs_XJ24hS1_XJ24hS2_XJ24hS3; (F) XJ12hR1_XJ12hR2_XJ12hR3_vs_XJ12hS1_XJ12hS2_XJ12hS3; (G) XJ12hR1_XJ12hR2_XJ12hR3_vs_XJ24hR1_XJ24hR2_XJ24hR3; (H) XJ12hS1_XJ12hS2_XJ12hS3_vs_XJ24hS1_XJ24hS2_XJ24hS3; (I) XJ24hR1_XJ24hR2_XJ24hR3_vs_XJ12hS1_XJ12hS2_XJ12hS3.

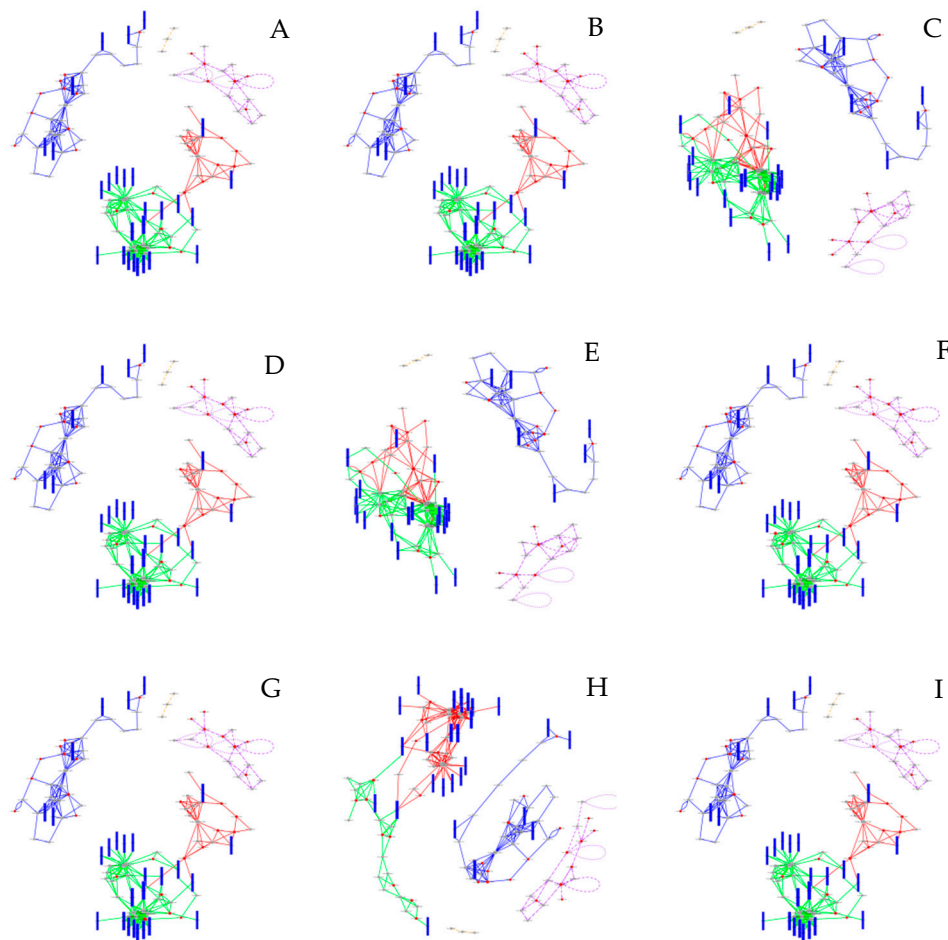


Figure S5. The top five most enriched pathways in each comparison group. Note: Each dot represents a gene, each rectangle represents a pathway, and the line represents the relationship between genes, and between genes and other pathways. The colours of different lines indicate that the relationship comes from different pathways. The red dots are the key genes. (A) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ0hS1_XJ0hS2_XJ0hS3; (B) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ12hR1_XJ12hR2_XJ12hR3; (C) XJ0hR1_XJ0hR2_XJ0hR3_vs_XJ24hR1_XJ24hR2_XJ24hR3; (D) XJ0hS1_XJ0hS2_XJ0hS3_vs_XJ12hS1_XJ12hS2_XJ12hS3; (E) XJ0hS1_XJ0hS2_XJ0hS3_vs_XJ24hS1_XJ24hS2_XJ24hS3; (F) XJ12hR1_XJ12hR2_XJ12hR3_vs_XJ12hS1_XJ12hS2_XJ12hS3; (G) XJ12hR1_XJ12hR2_XJ12hR3_vs_XJ24hR1_XJ24hR2_XJ24hR3; (H) XJ12hS1_XJ12hS2_XJ12hS3_vs_XJ24hS1_XJ24hS2_XJ24hS3; (I) XJ24hR1_XJ24hR2_XJ24hR3_vs_XJ12hS1_XJ12hS2_XJ12hS3.