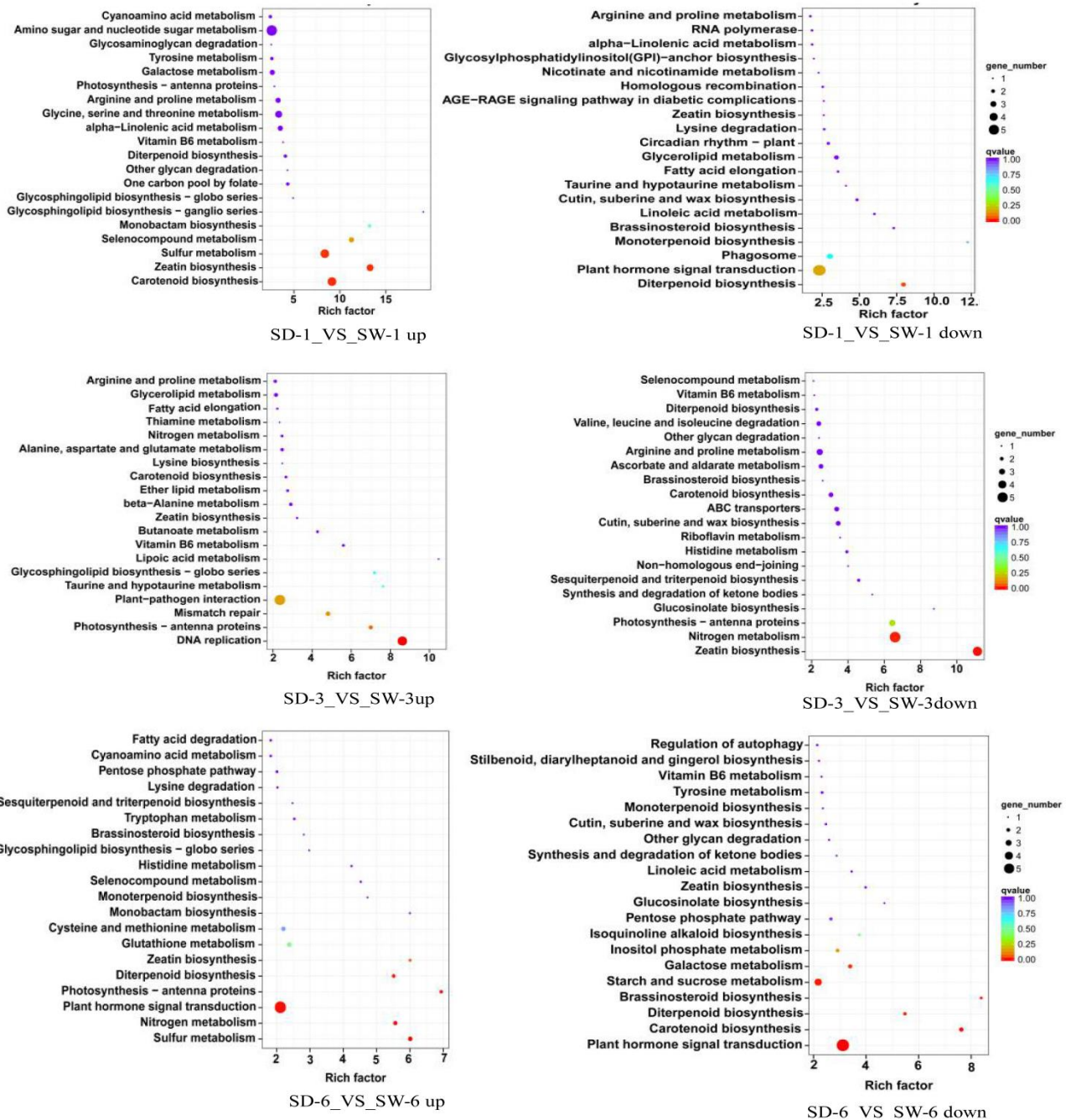
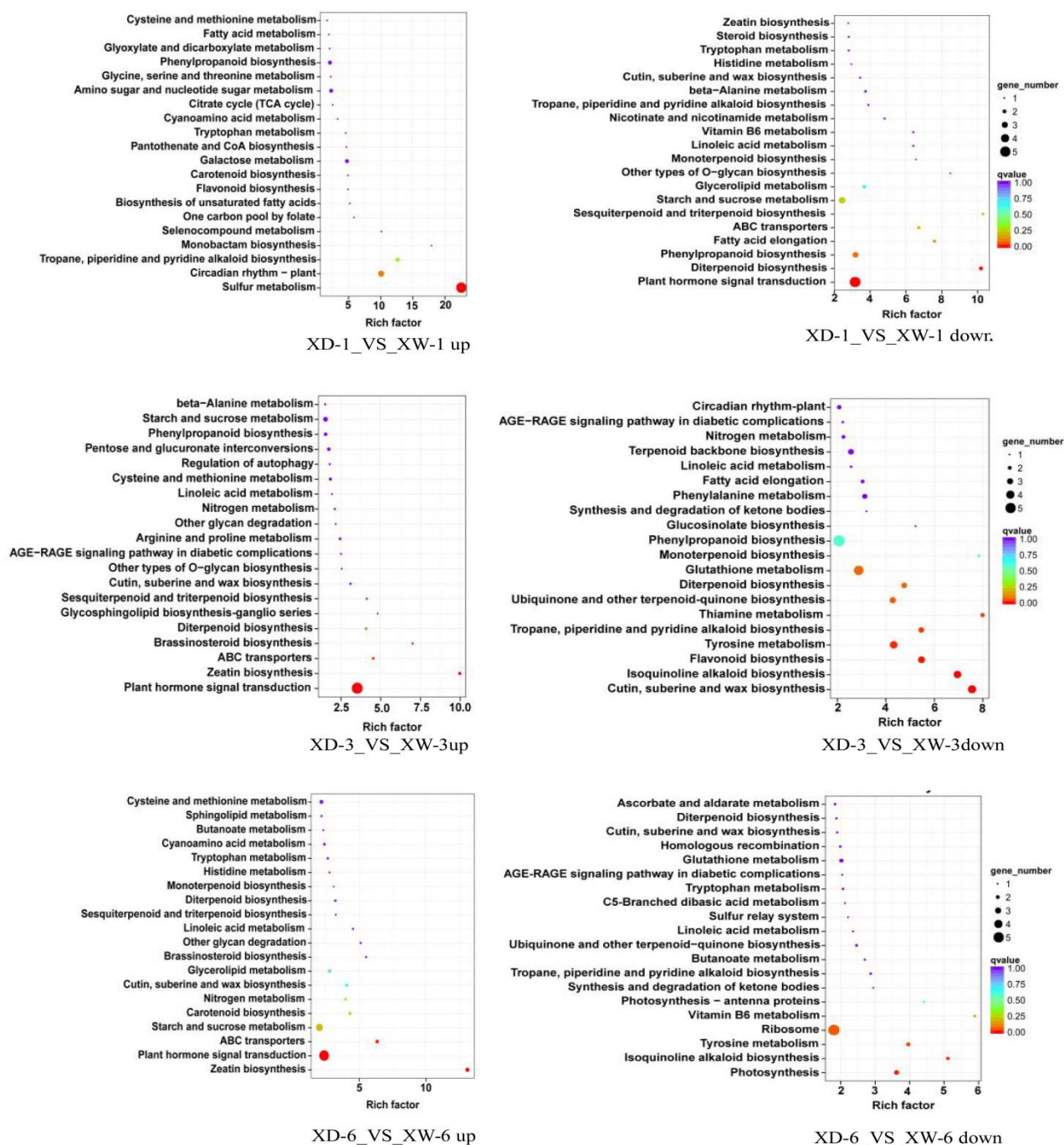


**Figure S1.** Pearson correlation between 36 samples



**Figure S2.** KEGG pathway enrichment analysis of up and down-regulated DEGs between MC and Water treatment at 3 time point in SD1068. Y-axis shows the KEGG pathways, and X-axis shows the Rich factor. The size and color of each circle represent the number of enriched genes in the corresponding pathway and the  $-\log_{10}(q\text{ value})$  value, respectively. SD-1, SD-3 and SD-6 represent samples at 1, 3 and 6 dps with MC treatment, respectively. SW-1, SW-3 and SW-6 represent samples at 1, 3 and 6 dps with water treatment, respectively.



**Figure S3.** KEGG pathway enrichment analysis of up and down-regulated DEGs between MC and Water treatment at 3 time point in XLZ74. Y-axis shows the KEGG pathways, and X-axis shows the Rich factor. The size and color of each circle represent the number of enriched genes in the corresponding pathway and the  $-\log_{10}(q \text{ value})$  value, respectively. XD-1, XD-3 and XD-6 represent samples at 1, 3 and 6 dps with MC treatment, respectively. XW-1, XW-3 and XW-6 represent samples at 1, 3 and 6 dps with Water treatment, respectively.