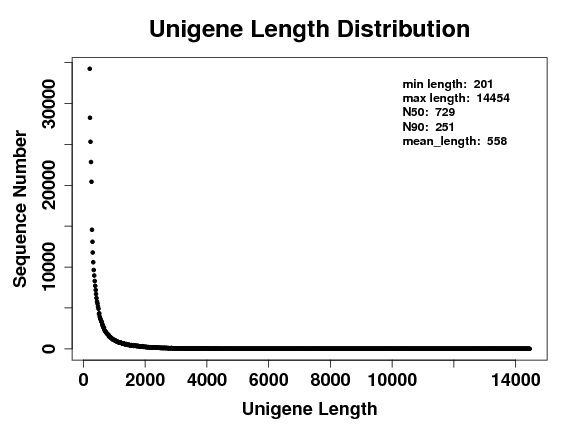
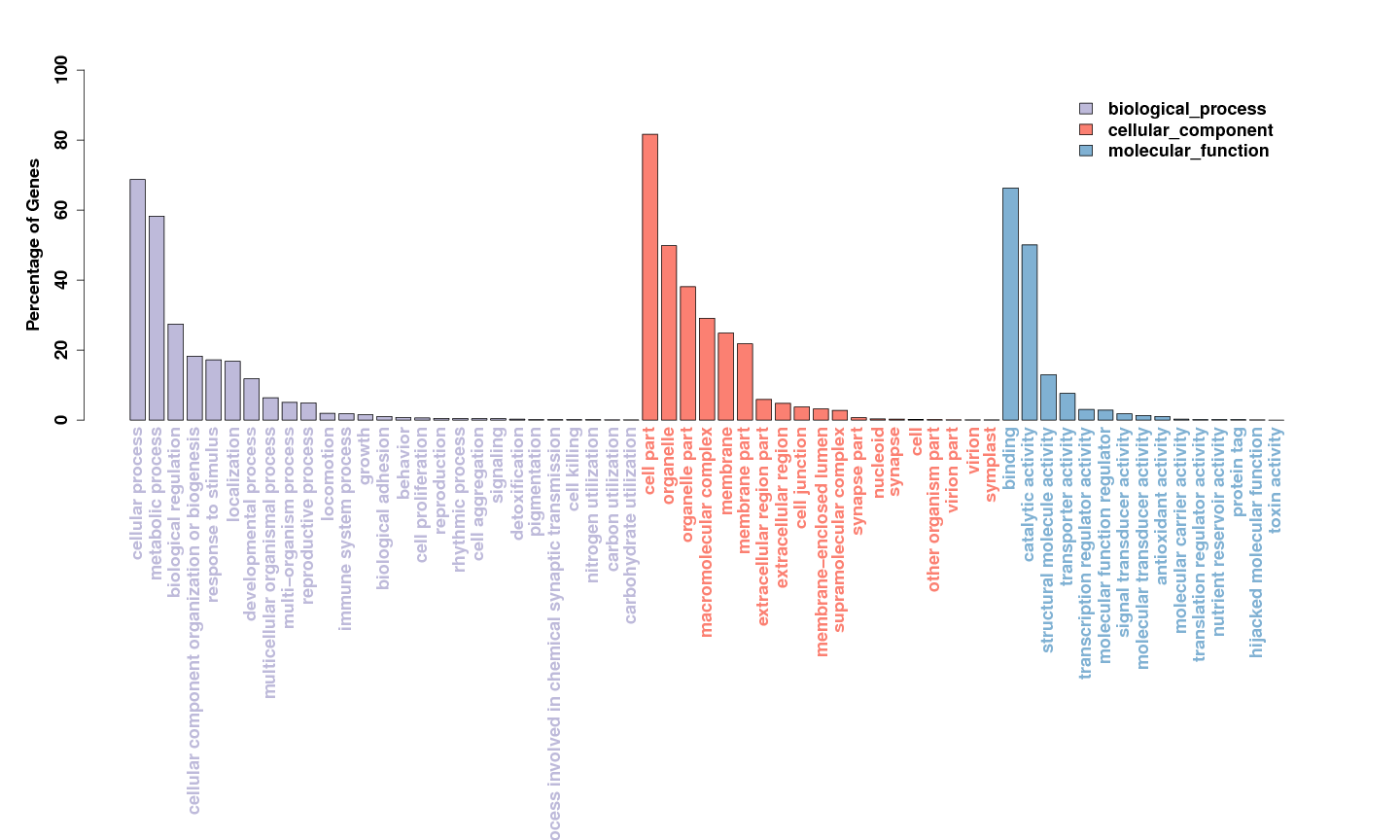
|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | **Total** | **Prot** | **GO** | **NR** | **NT** | **eggNOG** |
| Number of Unigenes | 378774 | 116187 | 137542 | 175517 | 68120 | 85285 |
| Percentage (%) | 100 | 30.674 | 36.312 | 46.338 | 17.984 | 22.516 |

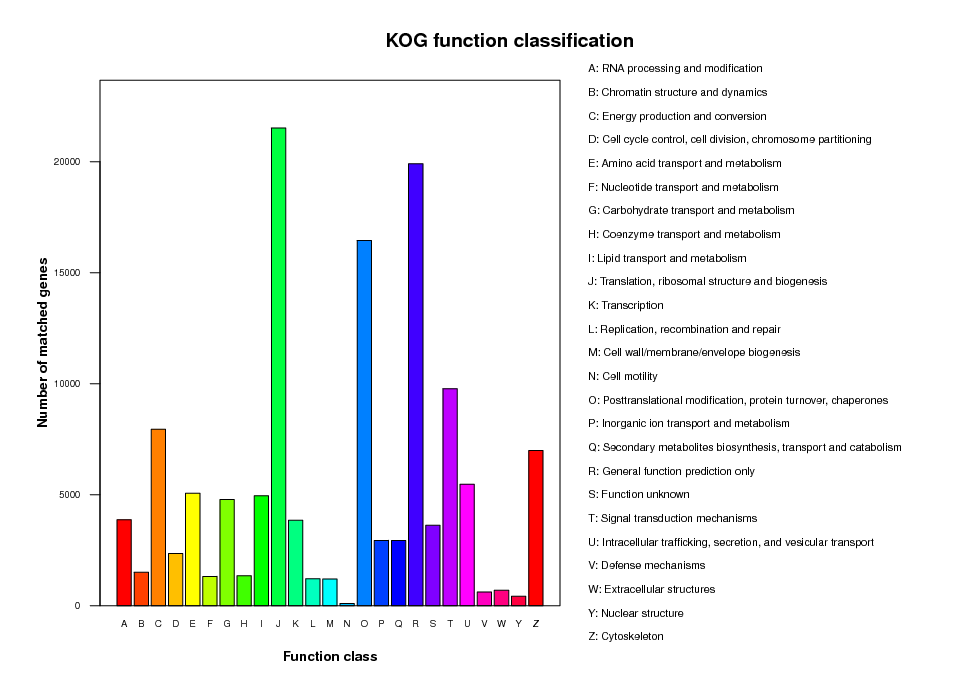
**Table S1.** Summary of annotations of the Iris pseudacorus variegate transcriptome.

**Figure S1.** Length distribution of unigene

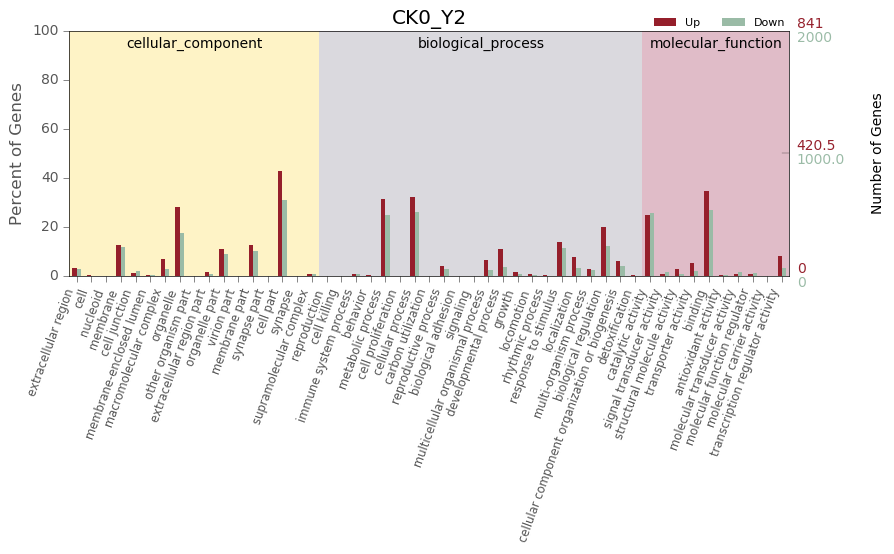
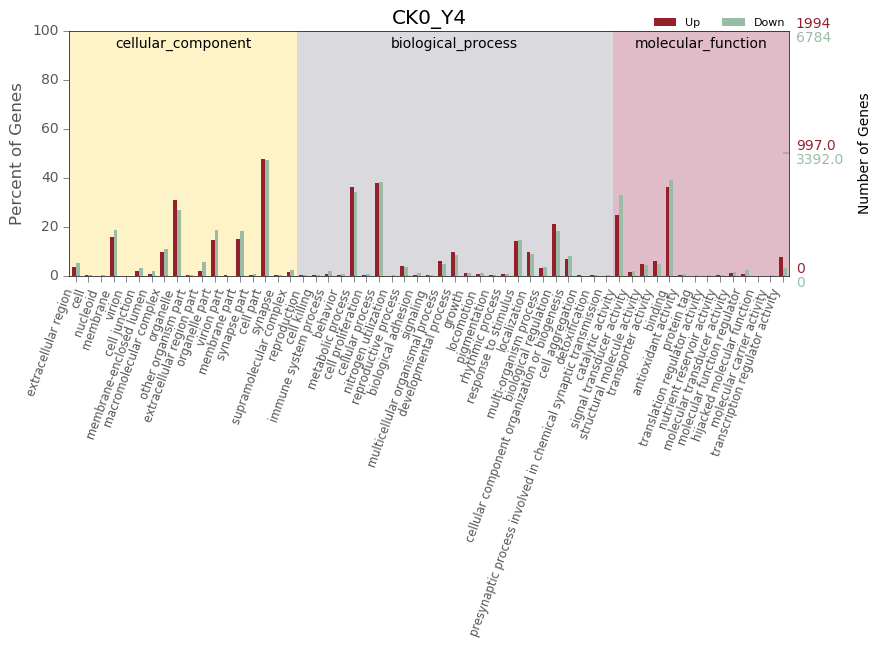


**Figure S2.** Gene ontology classifications of 137,542 orthologous unigenes

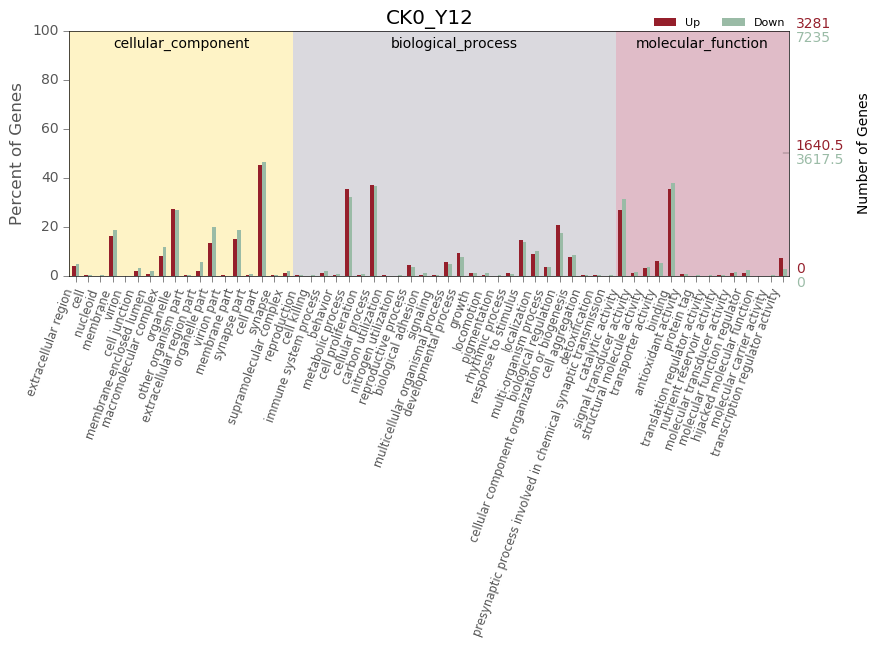


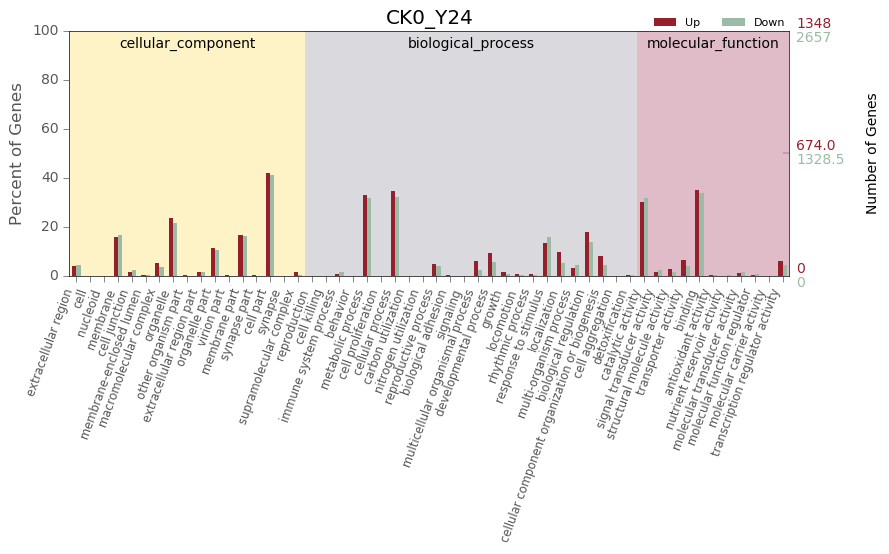
**Figure S3.** KOG function classification of the unigenes.****

**Figure S4.** GO classifications of the genes differentially expressed in different comparison groups(0h-2h)

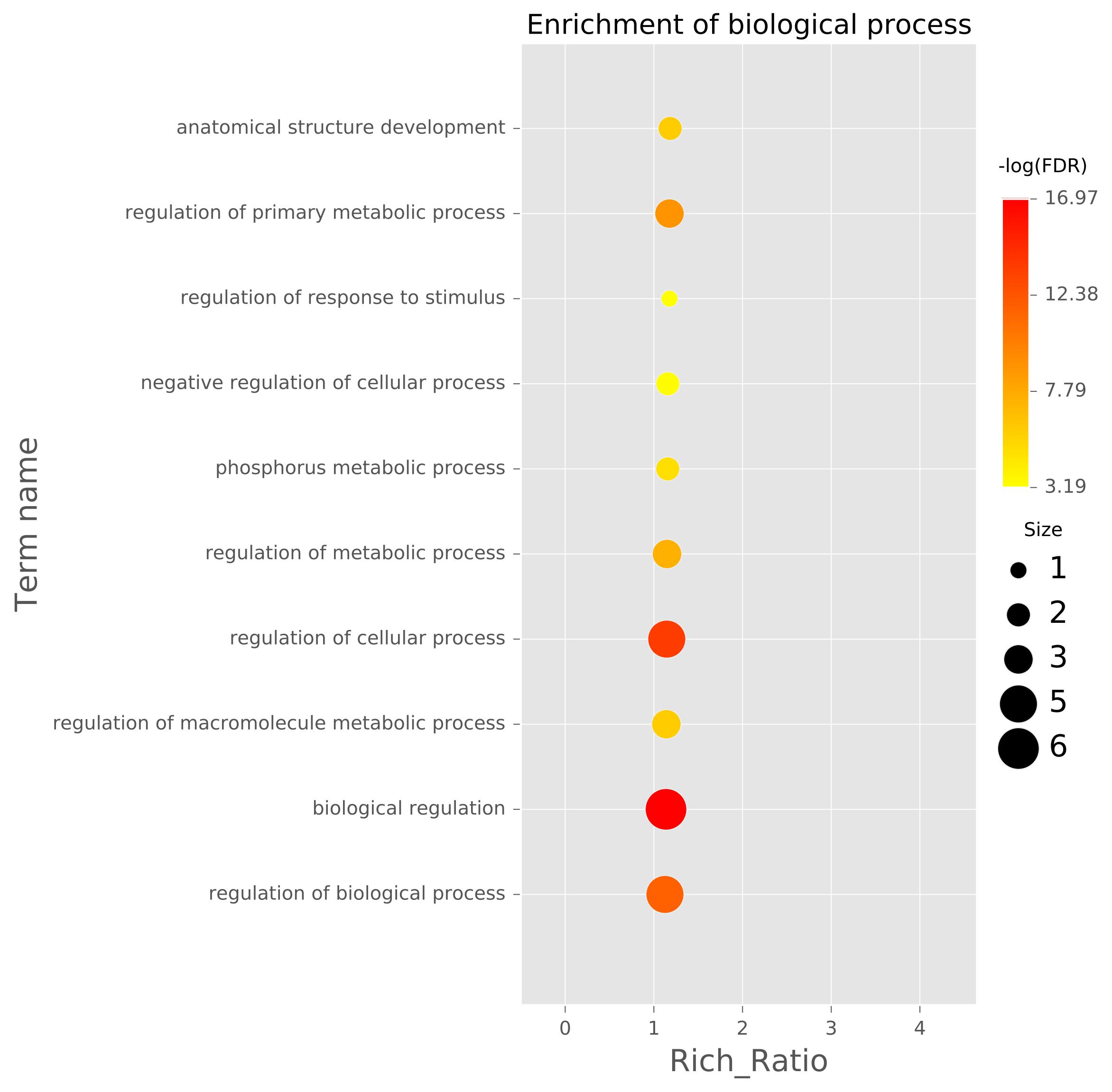
**Figure S5.** GO classifications of the genes differentially expressed in different comparison groups(0h-4h)

**Figure S6.** GO classifications of the genes differentially expressed in different comparison groups(0h-12h)

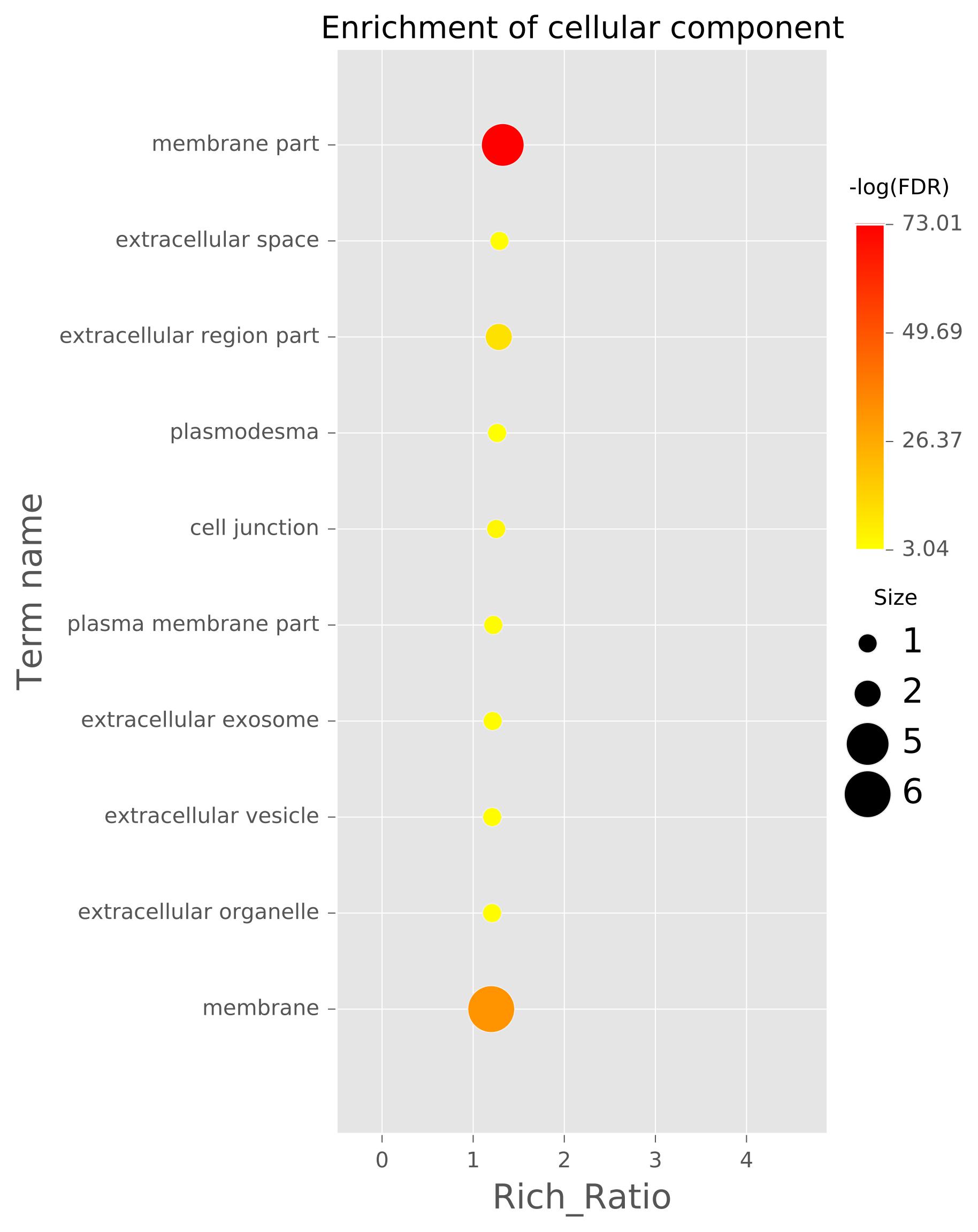


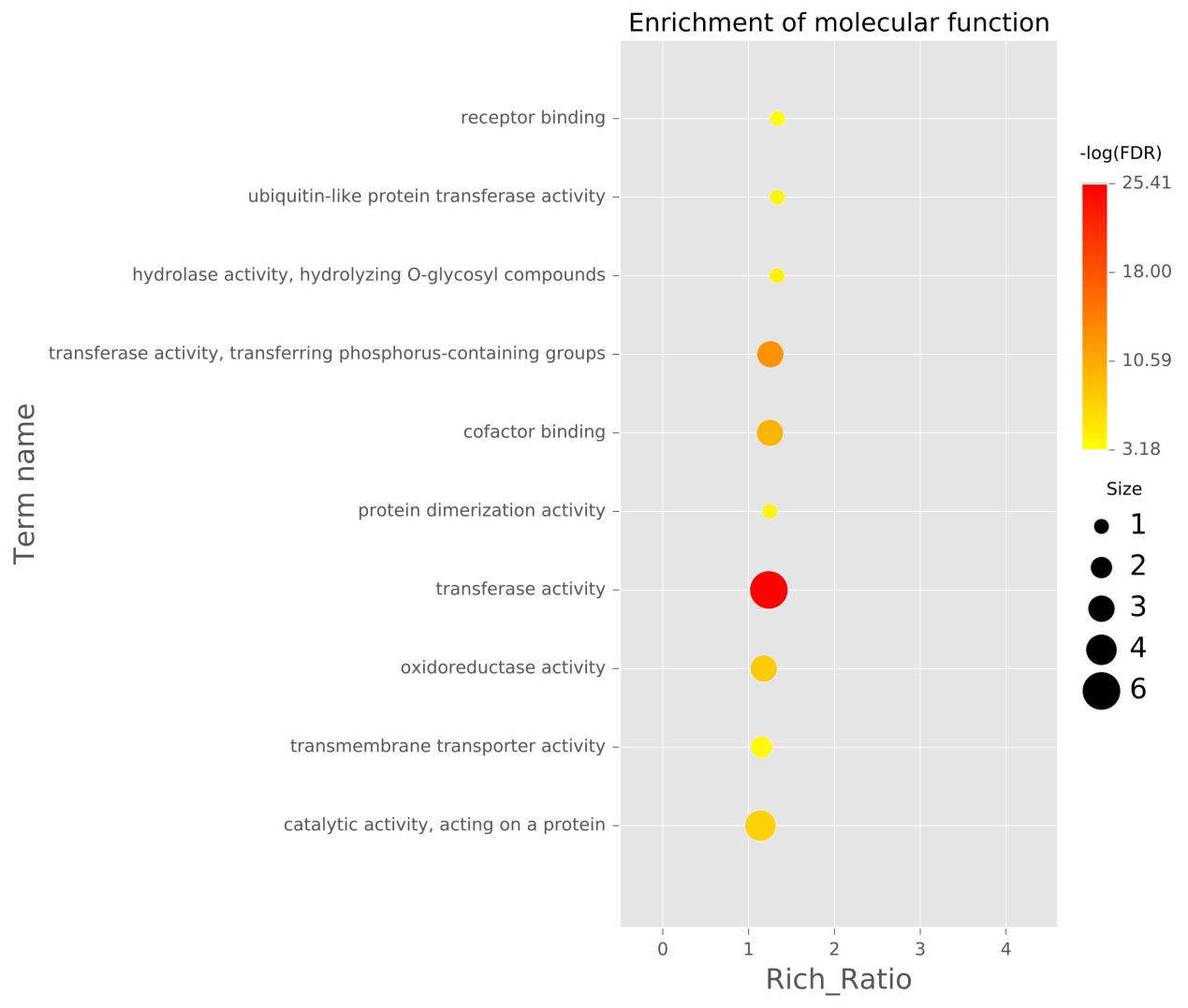
**Figure S7.** GO classifications of the genes differentially expressed in different comparison groups(0h-24h)

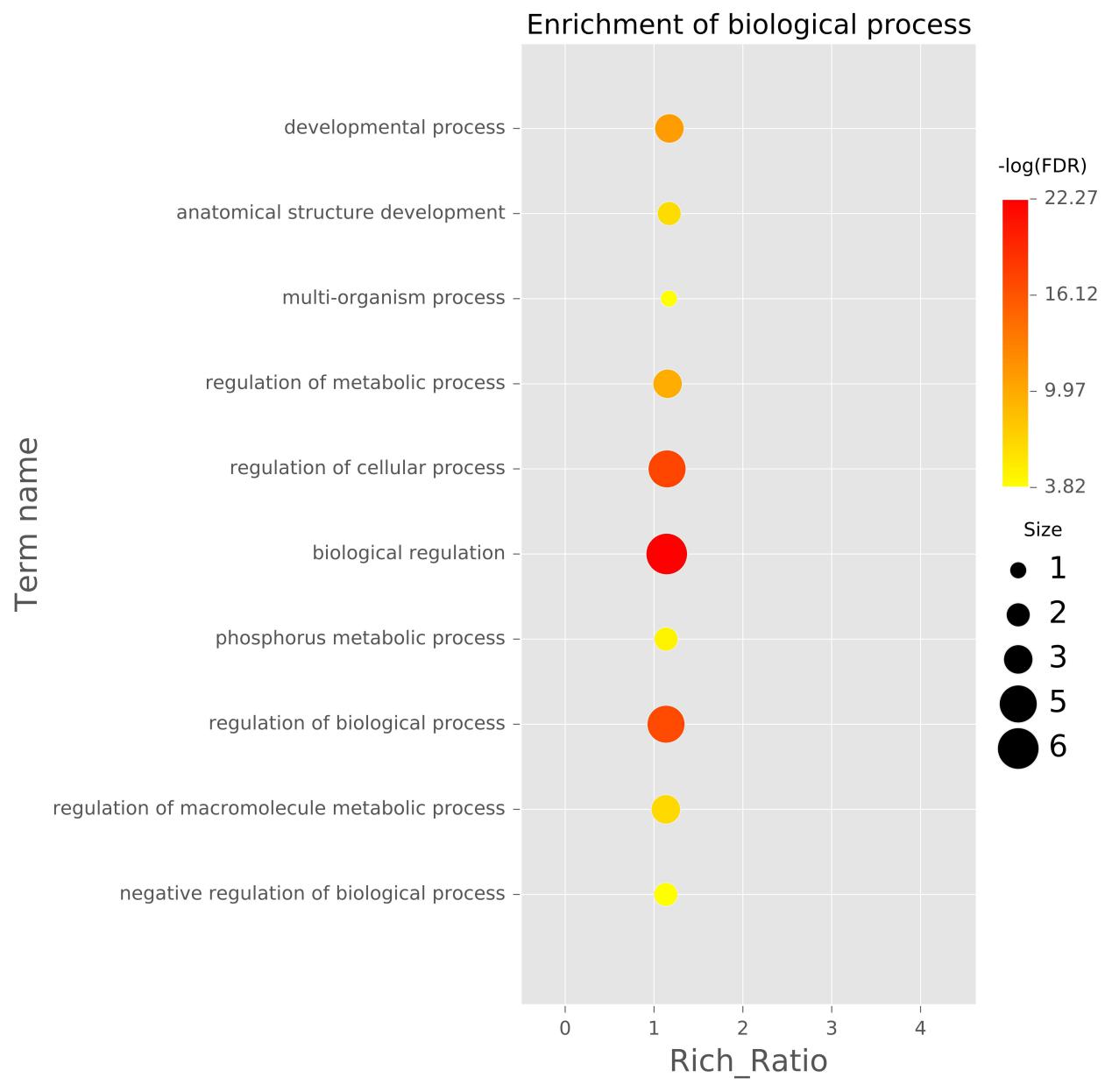
**Figure S8.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, biological process (BP) of DEGs enriched in roots waterlogged for 4 hours

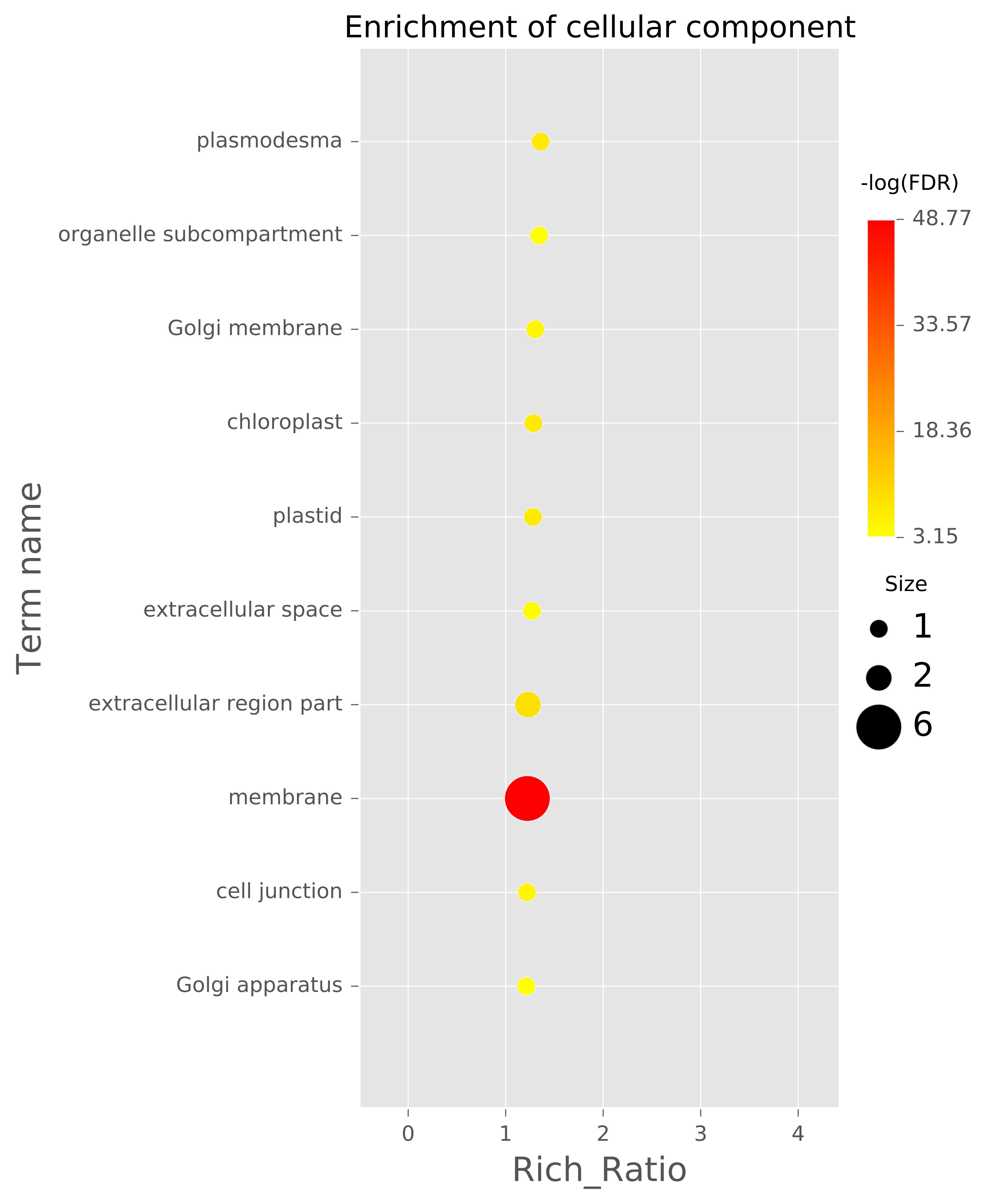


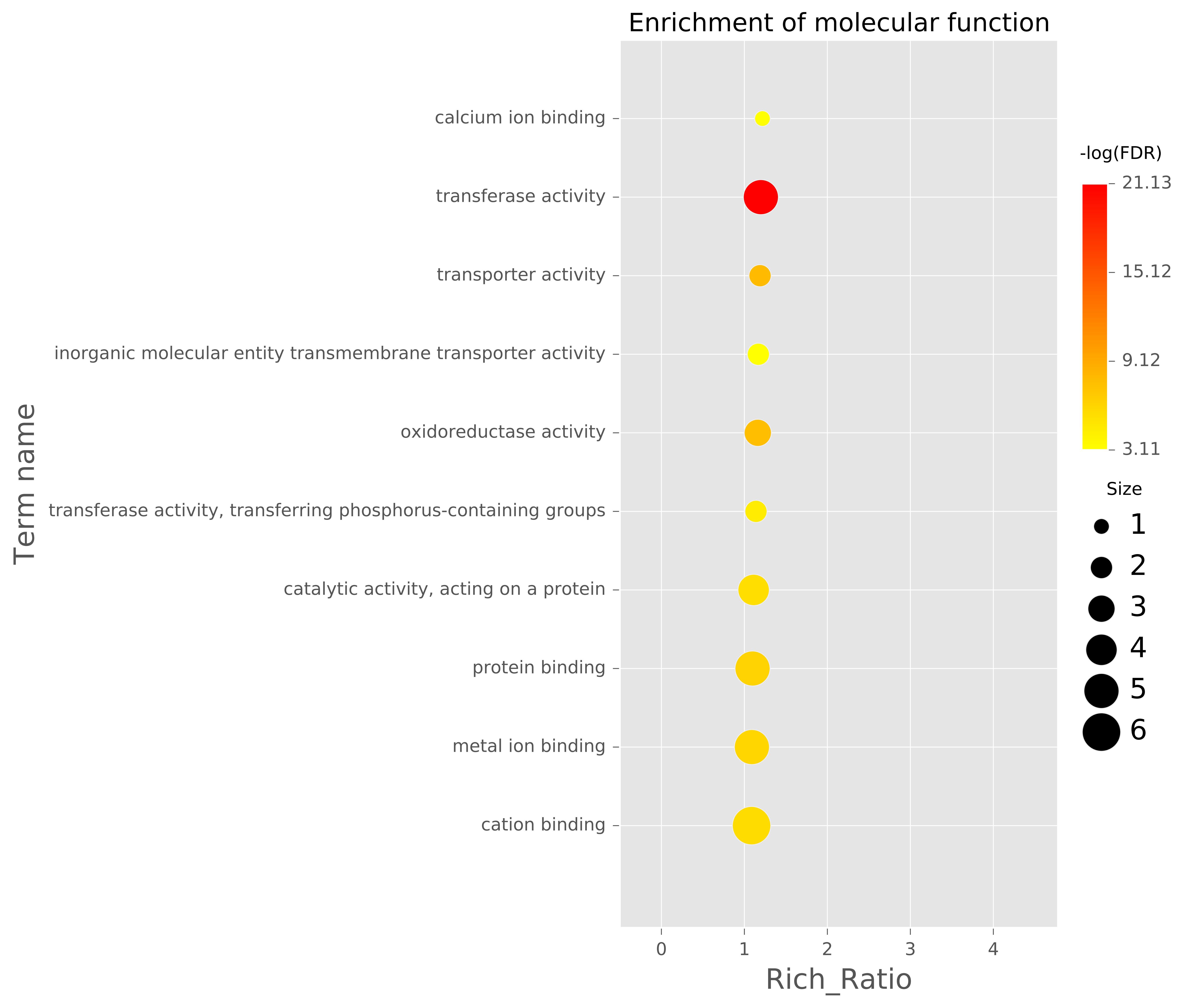
**Figure S9.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, cellular component (CC) of DEGs enriched in roots waterlogged for 4 hours



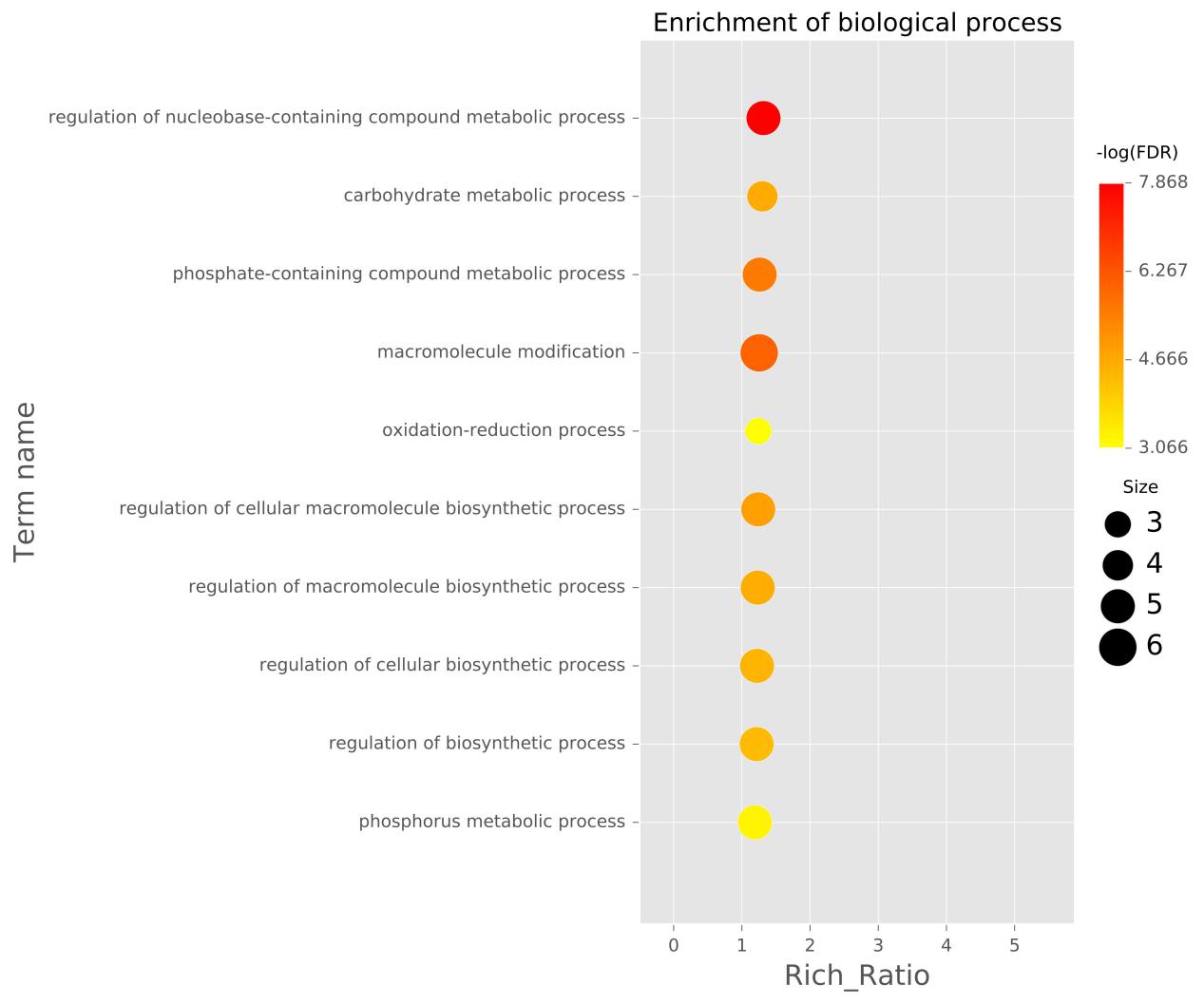
**Figure S10.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, molecular function (MF) of DEGs enriched in roots waterlogged for 4 hours

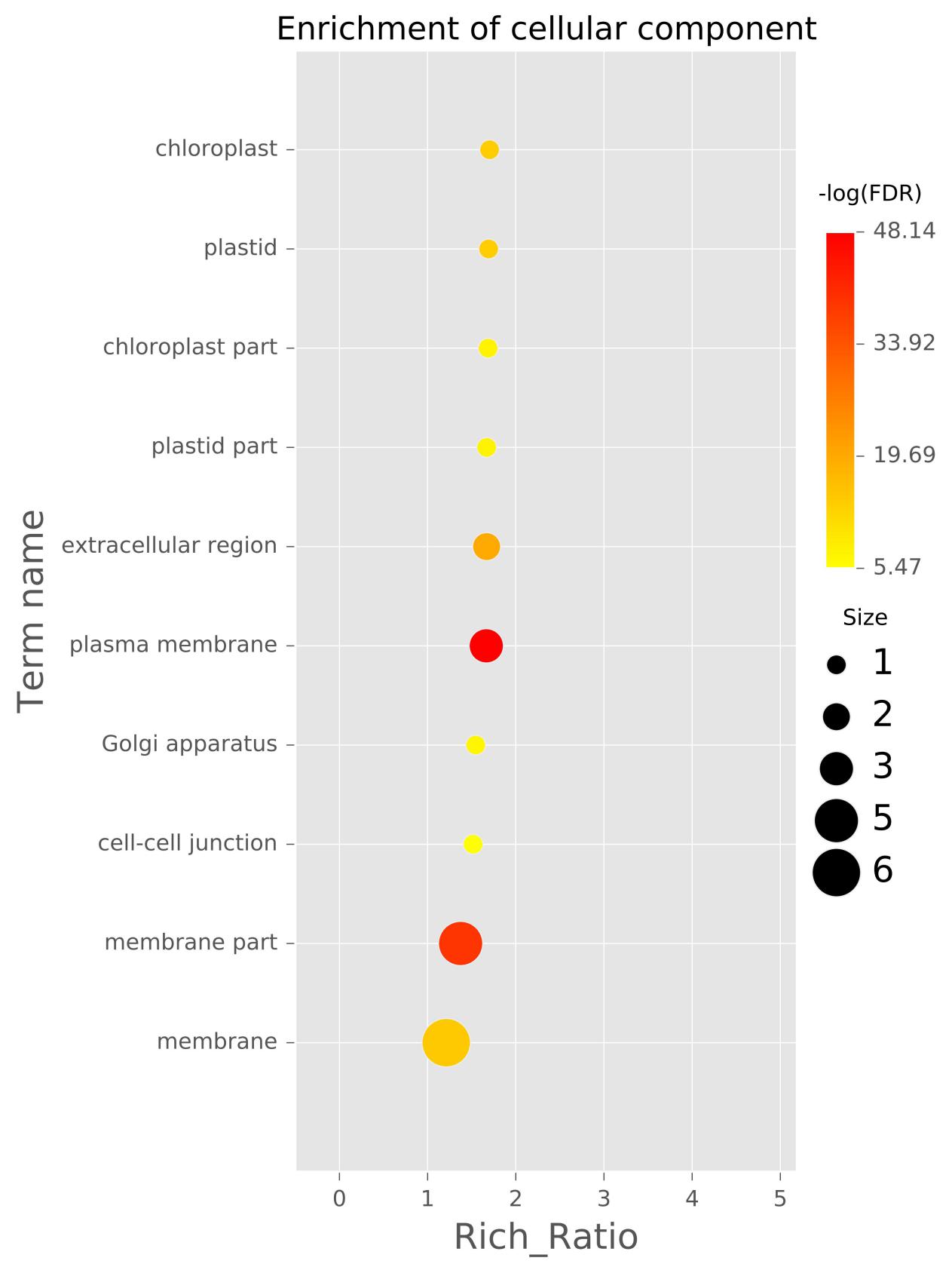
**Figure S11.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, biological process (BP) of DEGs enriched in roots waterlogged for 12 hours

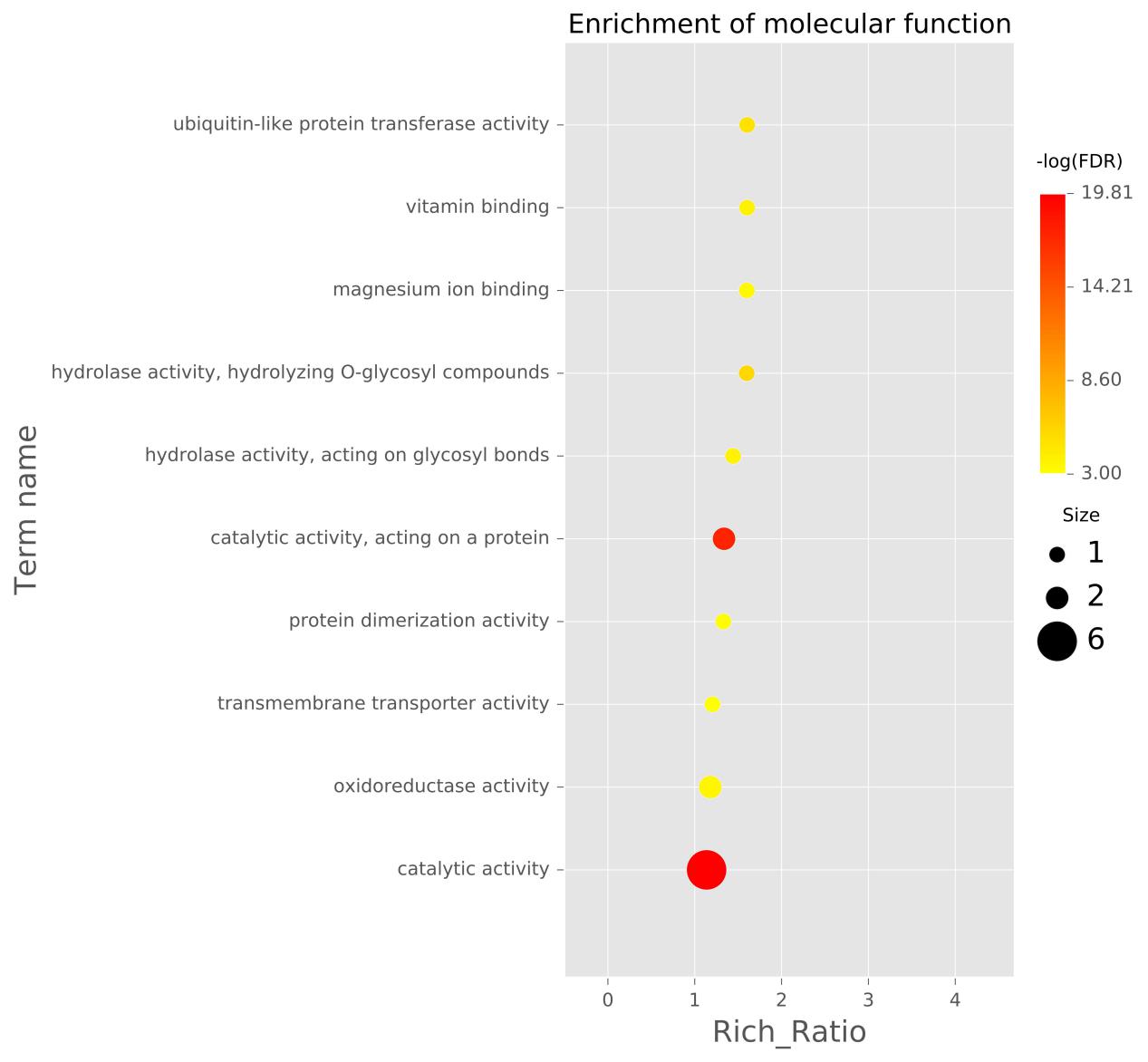
**Figure S12.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, cellular component (CC) of DEGs enriched in roots waterlogged for 12 hours

**Figure S13.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, molecular function (MF) of DEGs enriched in roots waterlogged for 12 hours

**Figure S14.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, biological process (BP) of DEGs enriched in roots waterlogged for 24 hours



**Figure S15.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, cellular component (CC) of DEGs enriched in roots waterlogged for 24 hours

**Figure S16.** The ten GO entries with the highest enrichment significance for different genes in each comparison group, molecular function (MF) of DEGs enriched in roots waterlogged for 24 hours

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene name** | **Forward primer 5'**→3' | **Reverse primer 5'**→3' | **Description** |
| UBQ | AAATATTCGACGATGTGTCTGC | CCAGTAAAATTGTTCTTOCGGTA | polyubiquitin |
| SUS4 | TTAGCTTGACCAAAGTGCCCAT | ACTTCAAGCTCCTGATCCCTCT | sucrose synthase (sus4) |
| SUS3 | AGATACTCCTCGGCCTTCGAC | CGCACAAGTACCAAGGGCAT | sucrose synthase (sus3) |
| ETR2 | GGATATCTCTACCATAAACAACGAGCAA | CAGCCTCCTTTATCATAGAATGCAA | ethylene receptor 2 |
| ADH | TCCACAATCCCTCCTGCTTCGT | ATTAAGATCCTCTACACTTCGCTATGCC | alcohol dehydrogenase |
| ENO | TAGCTTGTTTCCAGCATGTGA | TCTATACCAGCATATCGCCAA | enolase |
| PDC | GTCTCGGCAATCACAGCACTACTCCC | AACGAGCCTTTACGTGTTAATGTGCTCT | pyruvate decarboxylase |
| PK | TCCACCGGGAGTTTCTTGTAGCTCA | CCTTAAAGATGCAAAGCCAGTCCAAC | pyruvate kinase |
| PFK | ATCACTTTTCAAGCAAGCGGAGGA | TATGAGCCAACAGAGTGCAGTACACGTT | 6-phosphofructokinase 1 |
| PGK | AGTGTCACTCTTATTGCCTACCG | CAATGTCAAGCCCCATCCAACC | phosphoglycerate kinase |

**Table S5.** Nucleotide sequences of primers used for qRT-PCR.