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| **Supplementary Table S4:** Top 20 most enriched functional groups of *A. vermiculophyllum* differentially expressed genes (DEGs) between the heat stress treatment (H) and control (C) in the gene ontology (GO) categories. |
| GO\_Term  | Name | Ontology | Percent | Number |
| GO:0044699  | single-organism process  | biological\_process  | 64.57 | 1296 |
| GO:0050896  | response to stimulus  | biological\_process  | 30.64 | 615 |
| GO:1901362  | organic cyclic compound biosynthetic process | biological\_process  | 30.64 | 615 |
| GO:0032774  | RNA biosynthetic process  | biological\_process  | 23.82 | 478 |
| GO:0006351  | transcription, DNA-templated  | biological\_process  | 23.62 | 474 |
| GO:0097659  | nucleic acid-templated transcription  | biological\_process  | 23.62 | 474 |
| GO:0006950  | response to stress  | biological\_process  | 17.09 | 343 |
| GO:0006396  | RNA processing  | biological\_process  | 12.71 | 255 |
| GO:0006457  | protein folding | biological\_process | 6.98 | 140 |
| GO:0005667  | transcription factor complex | cellular\_component  | 13.55 | 272 |
| GO:0005694  | chromosome  | cellular\_component  | 9.62 | 193 |
| GO:0044427  | chromosomal part  | cellular\_component  | 8.72 | 175 |
| GO:0005515  | protein binding  | molecular\_function  | 44.29 | 889 |
| GO:0016740  | transferase activity  | molecular\_function  | 33.93 | 681 |
| GO:0005524  | ATP binding  | molecular\_function  | 25.21 | 506 |
| GO:0032559  | adenyl ribonucleotide binding  | molecular\_function  | 25.21 | 506 |
| GO:0016772  | transferase activity, transferring phosphorus-containing groups  | molecular\_function  | 18.09 | 363 |
| GO:0003723 | RNA binding  | molecular\_function  | 15.15 | 304 |
| GO:0022891  | substrate-specific transmembrane transporter activity  | molecular\_function  | 14.6 | 293 |
| GO:0051082 | unfolded protein binding  | molecular\_function  | 7.08 | 142 |