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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 | |