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| **Supplementary Table S5:** Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment result of *A. vermiculophyllum* differentially expressed genes (DEGs) between the heat stress treatment (H) and control (C). | | | | | | |
| #Term | Database | ID | Input number | Background number | P-Value | Corrected P-Value |
| Protein processing in endoplasmic reticulum | KEGG PATHWAY | ko04141 | 203 | 1772 | 1.10E-07 | 1.02E-05 |
| Spliceosome | KEGG PATHWAY | ko03040 | 112 | 856 | 4.84E-07 | 2.25E-05 |
| Endocytosis | KEGG PATHWAY | ko04144 | 81 | 651 | 9.20E-05 | 0.002851 |
| Plant-pathogen interaction | KEGG PATHWAY | ko04626 | 63 | 621 | 0.030492 | 0.26407 |
| Oxidative phosphorylation | KEGG PATHWAY | ko00190 | 37 | 415 | 0.247381 | 0.830413 |
| RNA degradation | KEGG PATHWAY | ko03018 | 36 | 345 | 0.06372 | 0.423281 |
| Glycolysis / Gluconeogenesis | KEGG PATHWAY | ko00010 | 36 | 395 | 0.213688 | 0.794918 |
| Phagosome | KEGG PATHWAY | ko04145 | 31 | 428 | 0.692785 | 1 |
| Purine metabolism | KEGG PATHWAY | ko00230 | 29 | 259 | 0.046587 | 0.361046 |
| Ribosome biogenesis in eukaryotes | KEGG PATHWAY | ko03008 | 26 | 202 | 0.01496 | 0.19265 |
| Proteasome | KEGG PATHWAY | ko03050 | 26 | 204 | 0.016572 | 0.19265 |
| Carbon fixation in photosynthetic organisms | KEGG PATHWAY | ko00710 | 26 | 381 | 0.782127 | 1 |
| Ribosome | KEGG PATHWAY | ko03010 | 24 | 2014 | 1 | 1 |
| Citrate cycle (TCA cycle) | KEGG PATHWAY | ko00020 | 22 | 196 | 0.073728 | 0.457115 |
| RNA transport | KEGG PATHWAY | ko03013 | 20 | 428 | 0.994738 | 1 |
| Aminoacyl-tRNA biosynthesis | KEGG PATHWAY | ko00970 | 19 | 172 | 0.101468 | 0.528772 |
| Ubiquitin mediated proteolysis | KEGG PATHWAY | ko04120 | 19 | 218 | 0.362514 | 0.942759 |
| Nitrogen metabolism | KEGG PATHWAY | ko00910 | 18 | 146 | 0.052158 | 0.373133 |
| Pyrimidine metabolism | KEGG PATHWAY | ko00240 | 17 | 152 | 0.108029 | 0.528772 |
| Pyruvate metabolism | KEGG PATHWAY | ko00620 | 17 | 214 | 0.515452 | 1 |
| Nucleotide excision repair | KEGG PATHWAY | ko03420 | 15 | 96 | 0.014395 | 0.19265 |
| Glutathione metabolism | KEGG PATHWAY | ko00480 | 15 | 140 | 0.15694 | 0.663426 |
| Protein export | KEGG PATHWAY | ko03060 | 15 | 241 | 0.840818 | 1 |
| Alanine, aspartate and glutamate metabolism | KEGG PATHWAY | ko00250 | 14 | 173 | 0.494598 | 1 |
| Glyoxylate and dicarboxylate metabolism | KEGG PATHWAY | ko00630 | 14 | 261 | 0.941977 | 1 |
| Arginine biosynthesis | KEGG PATHWAY | ko00220 | 13 | 135 | 0.279377 | 0.871758 |
| Arginine and proline metabolism | KEGG PATHWAY | ko00330 | 12 | 111 | 0.182975 | 0.739854 |
| Peroxisome | KEGG PATHWAY | ko04146 | 12 | 198 | 0.843608 | 1 |
| Inositol phosphate metabolism | KEGG PATHWAY | ko00562 | 11 | 113 | 0.290586 | 0.871758 |
| Porphyrin and chlorophyll metabolism | KEGG PATHWAY | ko00860 | 11 | 196 | 0.89415 | 1 |
| Nicotinate and nicotinamide metabolism | KEGG PATHWAY | ko00760 | 10 | 54 | 0.016514 | 0.19265 |
| Steroid biosynthesis | KEGG PATHWAY | ko00100 | 10 | 78 | 0.105224 | 0.528772 |
| ABC transporters | KEGG PATHWAY | ko02010 | 10 | 97 | 0.250017 | 0.830413 |
| Basal transcription factors | KEGG PATHWAY | ko03022 | 9 | 92 | 0.312611 | 0.892836 |
| Glycerolipid metabolism | KEGG PATHWAY | ko00561 | 9 | 98 | 0.375076 | 0.942759 |
| RNA polymerase | KEGG PATHWAY | ko03020 | 8 | 40 | 0.021288 | 0.219978 |
| Selenocompound metabolism | KEGG PATHWAY | ko00450 | 8 | 81 | 0.319482 | 0.892836 |
| Pentose phosphate pathway | KEGG PATHWAY | ko00030 | 8 | 181 | 0.968986 | 1 |
| Cysteine and methionine metabolism | KEGG PATHWAY | ko00270 | 8 | 187 | 0.975954 | 1 |
| alpha-Linolenic acid metabolism | KEGG PATHWAY | ko00592 | 7 | 48 | 0.102165 | 0.528772 |
| Phenylalanine, tyrosine and tryptophan biosynthesis | KEGG PATHWAY | ko00400 | 7 | 84 | 0.495307 | 1 |
| Fatty acid degradation | KEGG PATHWAY | ko00071 | 7 | 108 | 0.739265 | 1 |
| Fructose and mannose metabolism | KEGG PATHWAY | ko00051 | 7 | 144 | 0.928839 | 1 |
| Photosynthesis - antenna proteins | KEGG PATHWAY | ko00196 | 7 | 269 | 0.999848 | 1 |
| Carotenoid biosynthesis | KEGG PATHWAY | ko00906 | 6 | 51 | 0.231994 | 0.829825 |
| beta-Alanine metabolism | KEGG PATHWAY | ko00410 | 6 | 55 | 0.281874 | 0.871758 |
| Biosynthesis of unsaturated fatty acids | KEGG PATHWAY | ko01040 | 6 | 90 | 0.706807 | 1 |
| Propanoate metabolism | KEGG PATHWAY | ko00640 | 6 | 93 | 0.734392 | 1 |
| Caffeine metabolism | KEGG PATHWAY | ko00232 | 5 | 13 | 0.007756 | 0.180338 |
| Base excision repair | KEGG PATHWAY | ko03410 | 5 | 33 | 0.138927 | 0.615246 |
| Homologous recombination | KEGG PATHWAY | ko03440 | 5 | 47 | 0.326413 | 0.892836 |
| DNA replication | KEGG PATHWAY | ko03030 | 5 | 50 | 0.370625 | 0.942759 |
| Valine, leucine and isoleucine biosynthesis | KEGG PATHWAY | ko00290 | 5 | 51 | 0.385394 | 0.943201 |
| Glycerophospholipid metabolism | KEGG PATHWAY | ko00564 | 5 | 55 | 0.444084 | 1 |
| Starch and sucrose metabolism | KEGG PATHWAY | ko00500 | 5 | 78 | 0.730156 | 1 |
| Valine, leucine and isoleucine degradation | KEGG PATHWAY | ko00280 | 5 | 102 | 0.896556 | 1 |
| Glycine, serine and threonine metabolism | KEGG PATHWAY | ko00260 | 5 | 159 | 0.993684 | 1 |
| Fatty acid elongation | KEGG PATHWAY | ko00062 | 4 | 23 | 0.128903 | 0.5994 |
| Vitamin B6 metabolism | KEGG PATHWAY | ko00750 | 4 | 28 | 0.200403 | 0.776561 |
| Cell cycle - Caulobacter | KEGG PATHWAY | ko04112 | 4 | 42 | 0.432192 | 1 |
| Ubiquinone and other terpenoid-quinone biosynthesis | KEGG PATHWAY | ko00130 | 4 | 45 | 0.481314 | 1 |
| Biotin metabolism | KEGG PATHWAY | ko00780 | 4 | 45 | 0.481314 | 1 |
| Zeatin biosynthesis | KEGG PATHWAY | ko00908 | 3 | 7 | 0.031234 | 0.26407 |
| SNARE interactions in vesicular transport | KEGG PATHWAY | ko04130 | 3 | 40 | 0.613781 | 1 |
| Tyrosine metabolism | KEGG PATHWAY | ko00350 | 3 | 40 | 0.613781 | 1 |
| Butanoate metabolism | KEGG PATHWAY | ko00650 | 3 | 43 | 0.659634 | 1 |
| Histidine metabolism | KEGG PATHWAY | ko00340 | 3 | 44 | 0.674014 | 1 |
| Lysine degradation | KEGG PATHWAY | ko00310 | 3 | 51 | 0.762168 | 1 |
| Tryptophan metabolism | KEGG PATHWAY | ko00380 | 3 | 64 | 0.874139 | 1 |
| Ascorbate and aldarate metabolism | KEGG PATHWAY | ko00053 | 3 | 74 | 0.925533 | 1 |
| Fatty acid biosynthesis | KEGG PATHWAY | ko00061 | 3 | 85 | 0.959333 | 1 |
| Amino sugar and nucleotide sugar metabolism | KEGG PATHWAY | ko00520 | 3 | 115 | 0.992988 | 1 |
| mRNA surveillance pathway | KEGG PATHWAY | ko03015 | 3 | 125 | 0.996199 | 1 |
| Pantothenate and CoA biosynthesis | KEGG PATHWAY | ko00770 | 2 | 26 | 0.614065 | 1 |
| N-Glycan biosynthesis | KEGG PATHWAY | ko00510 | 2 | 27 | 0.633364 | 1 |
| Lysine biosynthesis | KEGG PATHWAY | ko00300 | 2 | 27 | 0.633364 | 1 |
| Mismatch repair | KEGG PATHWAY | ko03430 | 2 | 29 | 0.669679 | 1 |
| Phenylalanine metabolism | KEGG PATHWAY | ko00360 | 2 | 34 | 0.747738 | 1 |
| Arachidonic acid metabolism | KEGG PATHWAY | ko00590 | 2 | 34 | 0.747738 | 1 |
| One carbon pool by folate | KEGG PATHWAY | ko00670 | 2 | 51 | 0.905909 | 1 |
| Sulfur metabolism | KEGG PATHWAY | ko00920 | 2 | 58 | 0.938699 | 1 |
| Photosynthesis | KEGG PATHWAY | ko00195 | 2 | 207 | 0.999998 | 1 |
| Non-homologous end-joining | KEGG PATHWAY | ko03450 | 1 | 9 | 0.529929 | 1 |
| Linoleic acid metabolism | KEGG PATHWAY | ko00591 | 1 | 9 | 0.529929 | 1 |
| Ether lipid metabolism | KEGG PATHWAY | ko00565 | 1 | 10 | 0.564118 | 1 |
| Sulfur relay system | KEGG PATHWAY | ko04122 | 1 | 10 | 0.564118 | 1 |
| Other glycan degradation | KEGG PATHWAY | ko00511 | 1 | 11 | 0.595822 | 1 |
| Thiamine metabolism | KEGG PATHWAY | ko00730 | 1 | 13 | 0.652485 | 1 |
| Carbapenem biosynthesis | KEGG PATHWAY | ko00332 | 1 | 13 | 0.652485 | 1 |
| Tropane, piperidine and pyridine alkaloid biosynthesis | KEGG PATHWAY | ko00960 | 1 | 16 | 0.722948 | 1 |
| Folate biosynthesis | KEGG PATHWAY | ko00790 | 1 | 18 | 0.7618 | 1 |
| C5-Branched dibasic acid metabolism | KEGG PATHWAY | ko00660 | 1 | 19 | 0.779133 | 1 |
| Terpenoid backbone biosynthesis | KEGG PATHWAY | ko00900 | 1 | 77 | 0.997261 | 1 |