

Supplementary Materials

Digitaria sanguinalis

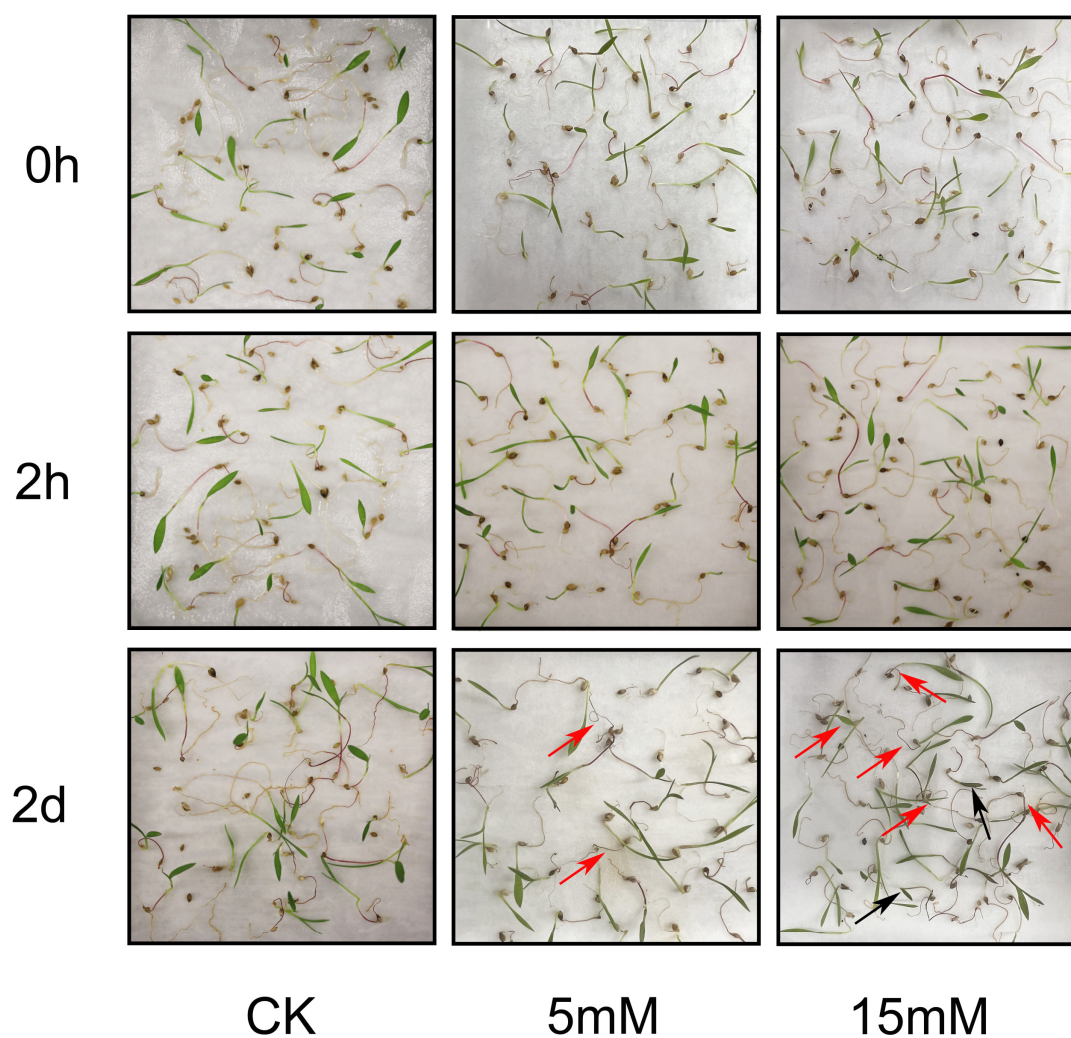


Figure S1. The phenotype of *Digitaria sanguinalis* after the treatment of 4,8-DHT. The 7-day old seedlings of *Digitaria sanguinalis* were treated with 0 mM, 5 mM and 15 mM 4,8-DHT solution for 0 h, 2 h and 2 d, respectively. Red arrows indicate severely browned plant roots and yellowing plant leaves and black arrows indicate dead plants.

Arabidopsis thaliana

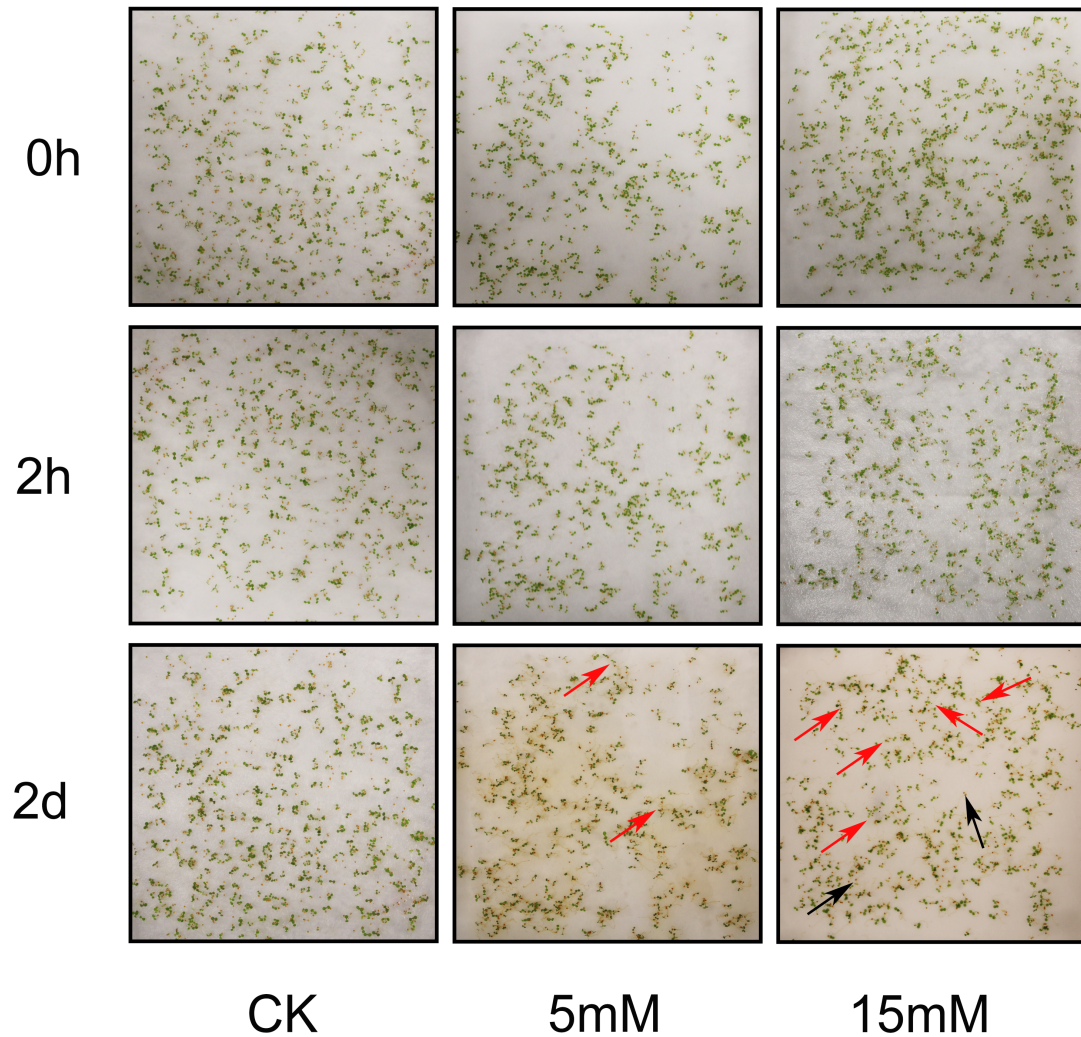


Figure S2. The phenotype of *Arabidopsis thaliana* after the treatment of 4,8-DHT. The 7-day old seedlings of *Arabidopsis thaliana* were treated with 0 mM, 5 mM and 15 mM 4,8-DHT solution for 0 h, 2 h and 2 d, respectively. Red arrows indicate severely browned plant roots and yellowing plant leaves and black arrows indicate dead plants.

Poa annua

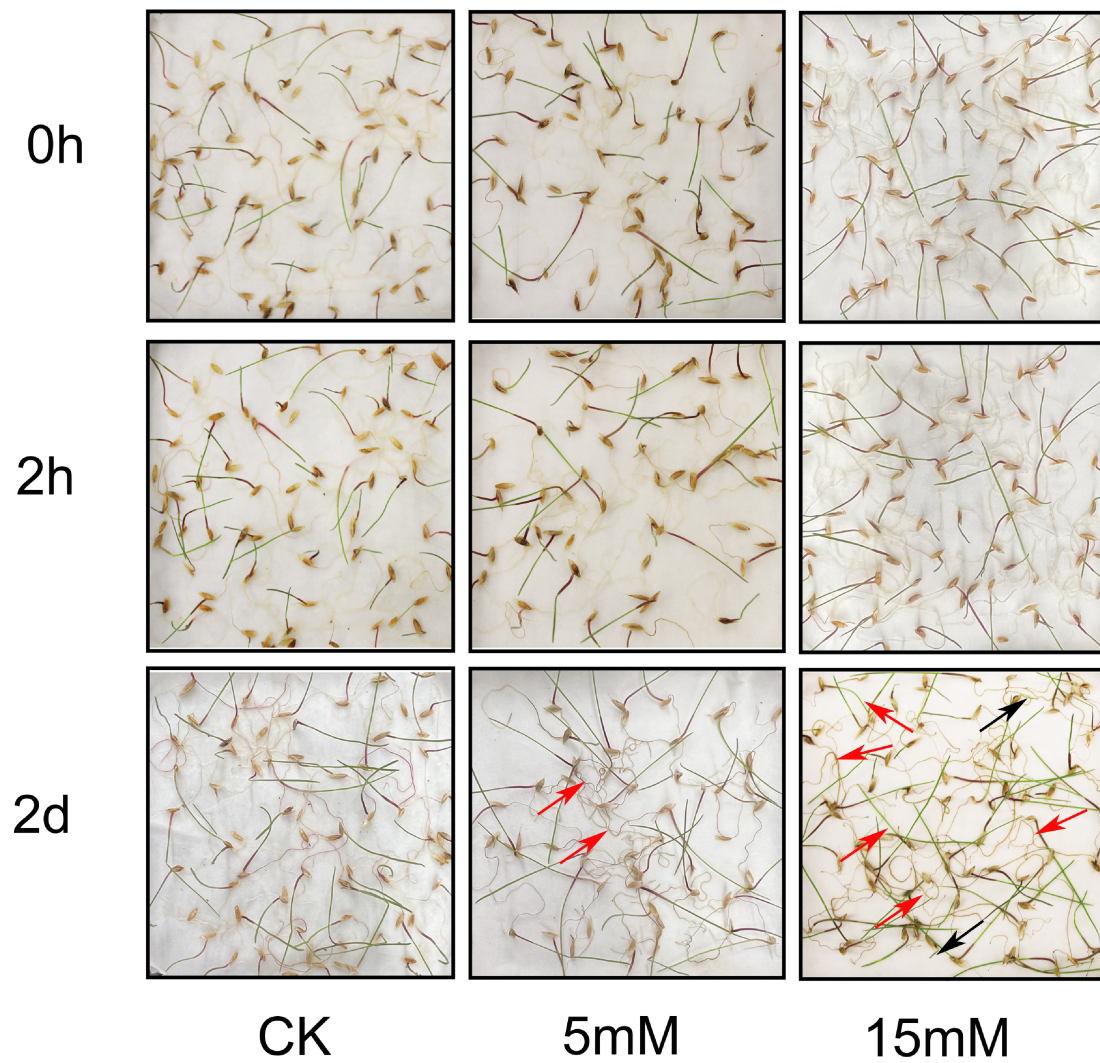


Figure S3. The phenotype of *Poa annua* after the treatment of 4,8-DHT. The 7-day old seedlings of *Poa annua* were treated with 0 mM, 5 mM and 15 mM 4,8-DHT solution for 0 h, 2 h and 2 d, respectively. Red arrows indicate severely browned plant roots and yellowing plant leaves and black arrows indicate dead plants.

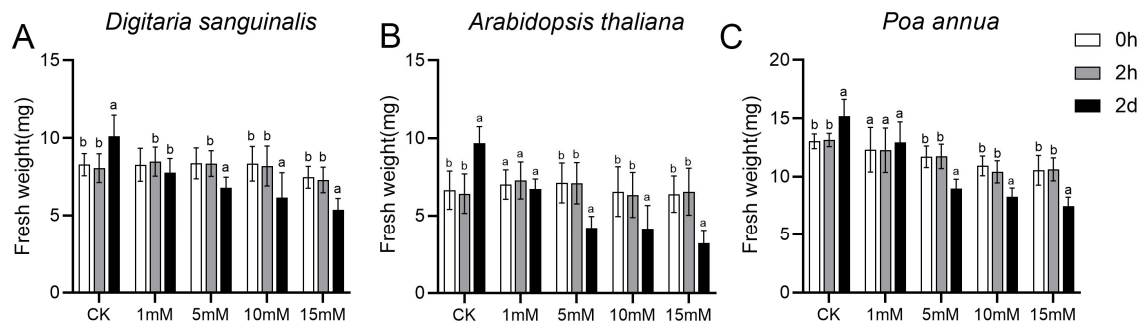


Figure S4. Effect of 4,8-DHT treatment on fresh weight of different species. Measurements of *Digitaria sanguinalis* (A), *Arabidopsis thaliana* (B) and *Poa annua* (C) fresh weights at 0 h, 2 h and 2 d with 0 mM, 5 mM and 15 mM 4,8-DHT treatment, respectively. Bars represent the mean \pm SD of at least three independent experiments. Different letters indicate a significant difference among the 4,8-DHT concentration or treatment time ($P < 0.05$) by Tukey's test.

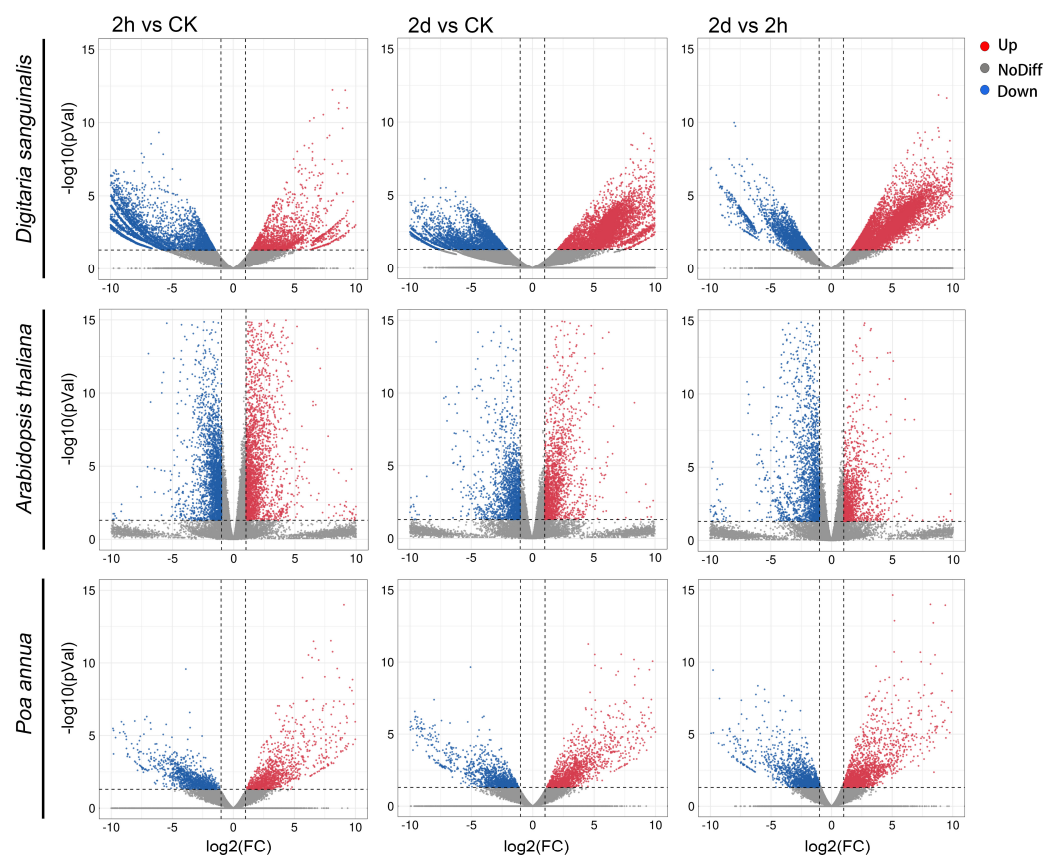


Figure S5. Volcano plots for *Digitaria sanguinalis* (Ds), *Arabidopsis thaliana* (At) and *Poa annua* (Pa) after the treatment of 5 mM 4,8-DHT at 2h vs CK, 2d vs CK and 2d vs 2h, respectively.

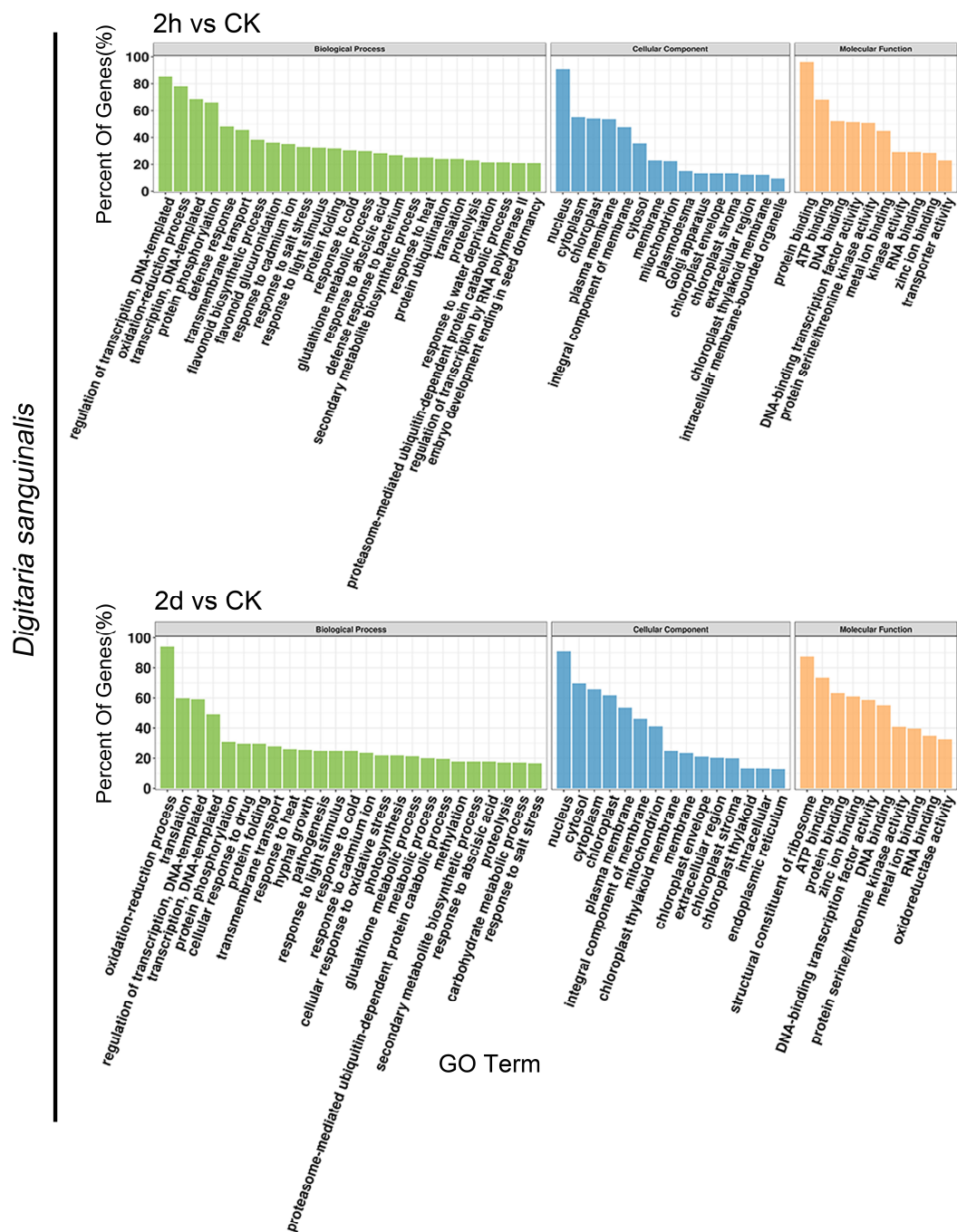


Figure S6. The top 50 GOs for *Digitaria sanguinalis* at the 2h vs CK and 2d vs CK. The x-axis indicates the number of genes per GO term as a percentage of the total number of genes, and the y-axis indicates the enriched GO terms. Different colors are used to distinguish between biological processes, cellular components and molecular functions.

Arabidopsis thaliana

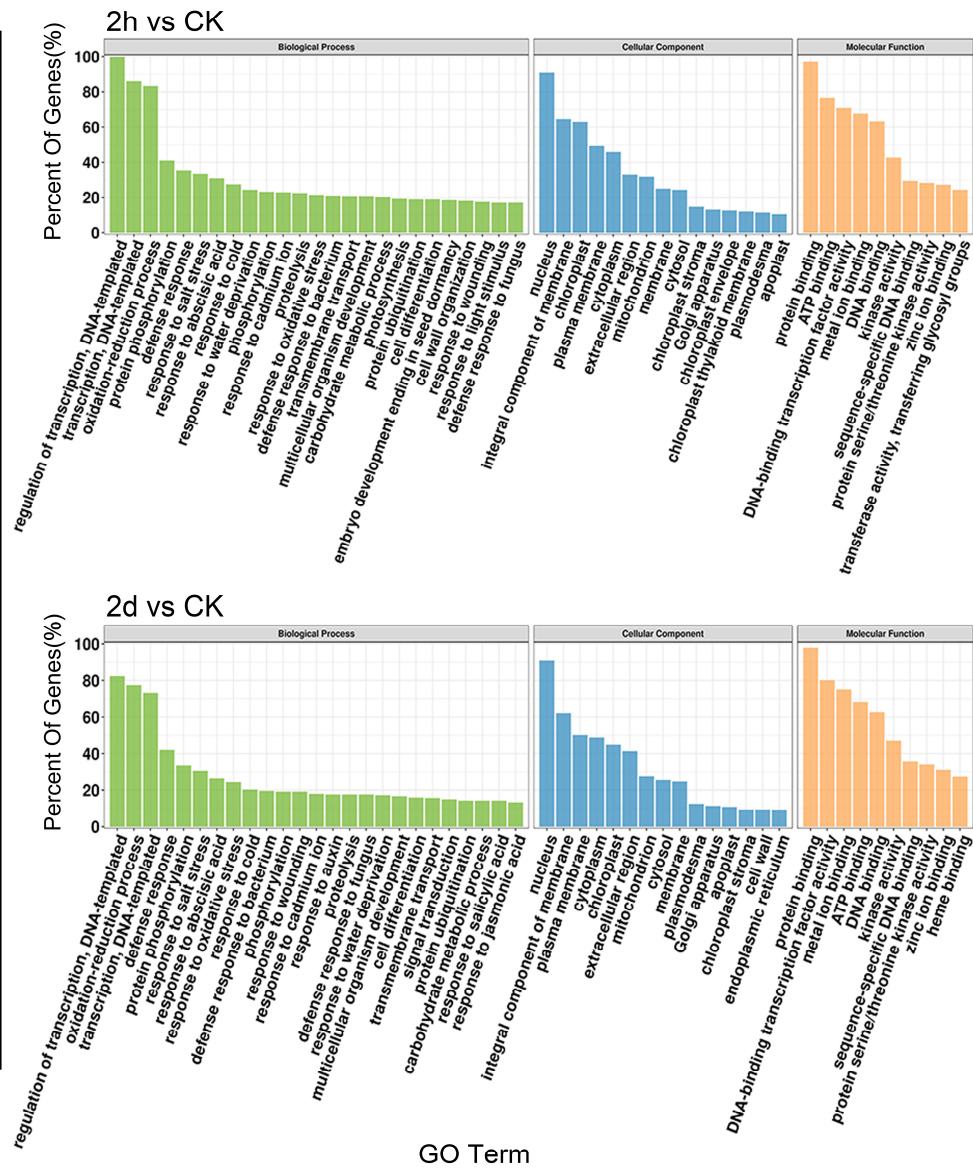


Figure S7. The top 50 GOs for *Arabidopsis thaliana* at the 2h vs CK and 2d vs CK. The x-axis indicates the number of genes per GO term as a percentage of the total number of genes, and the y-axis indicates the enriched GO terms. Different colors are used to distinguish between biological processes, cellular components and molecular functions.

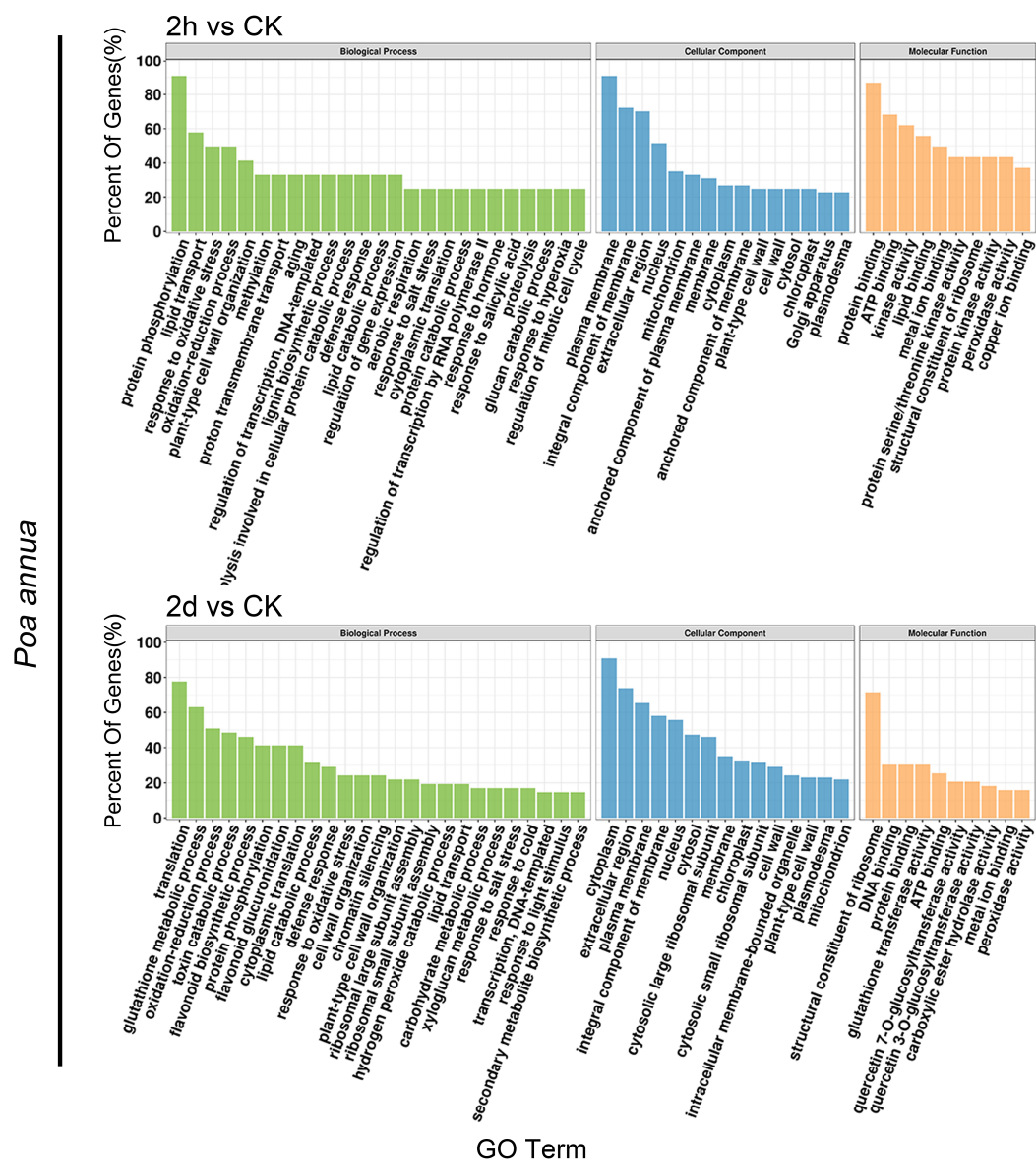


Figure S8. The top 50 GOs for *Poa annua* at the 2h vs CK and 2d vs CK. The x-axis indicates the number of genes per GO term as a percentage of the total number of genes, and the y-axis indicates the enriched GO terms. Different colors are used to distinguish between biological processes, cellular components and molecular functions.

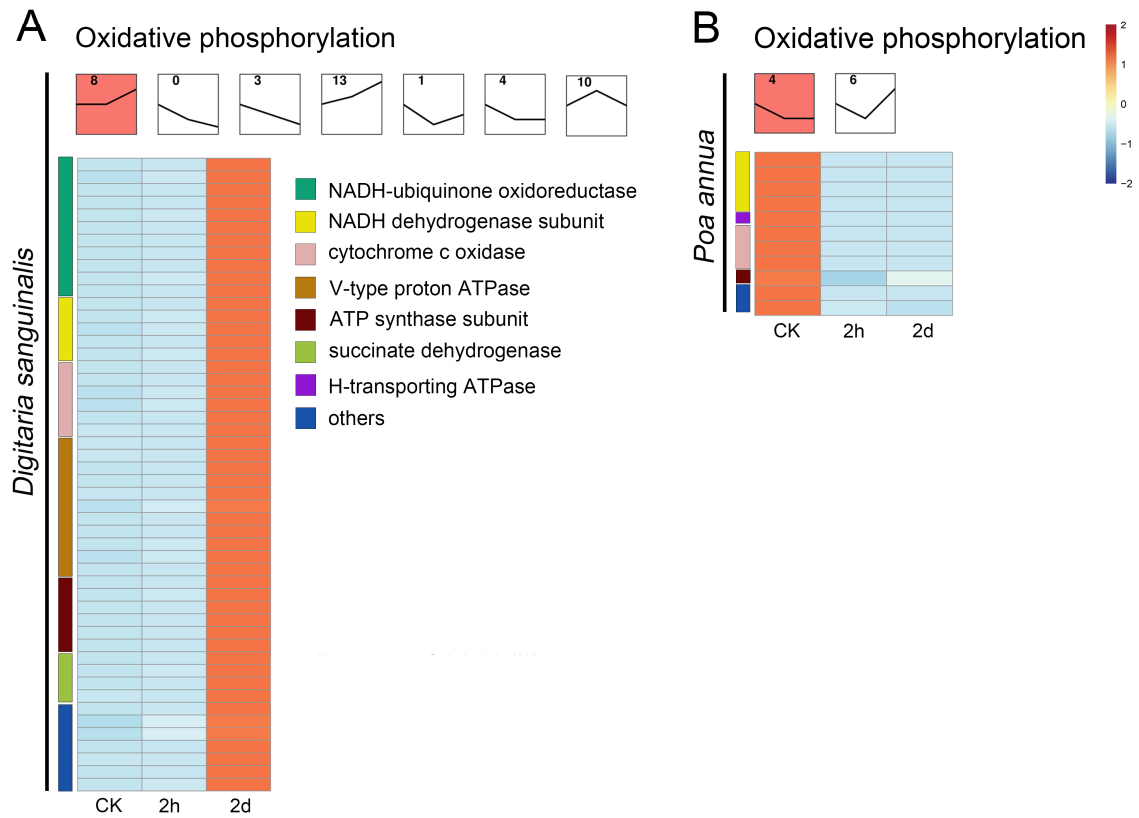


Figure S9. STEM plots and heatmaps of DEGs in oxidative phosphorylation of *Digitaria sanguinalis* (A) and *Arabidopsis thaliana* (B) after the 0h, 2h and 2d treatment of 5 mM 4,8-DHT. STEM has multiple temporal expression patterns, and the colored modules represent the most significant among these DEGs. The different-colored squares on the left of the heatmaps correspond to the genes of the same-colored squares on the right. The different number in the square only indicates the serial number of the expression patterns.

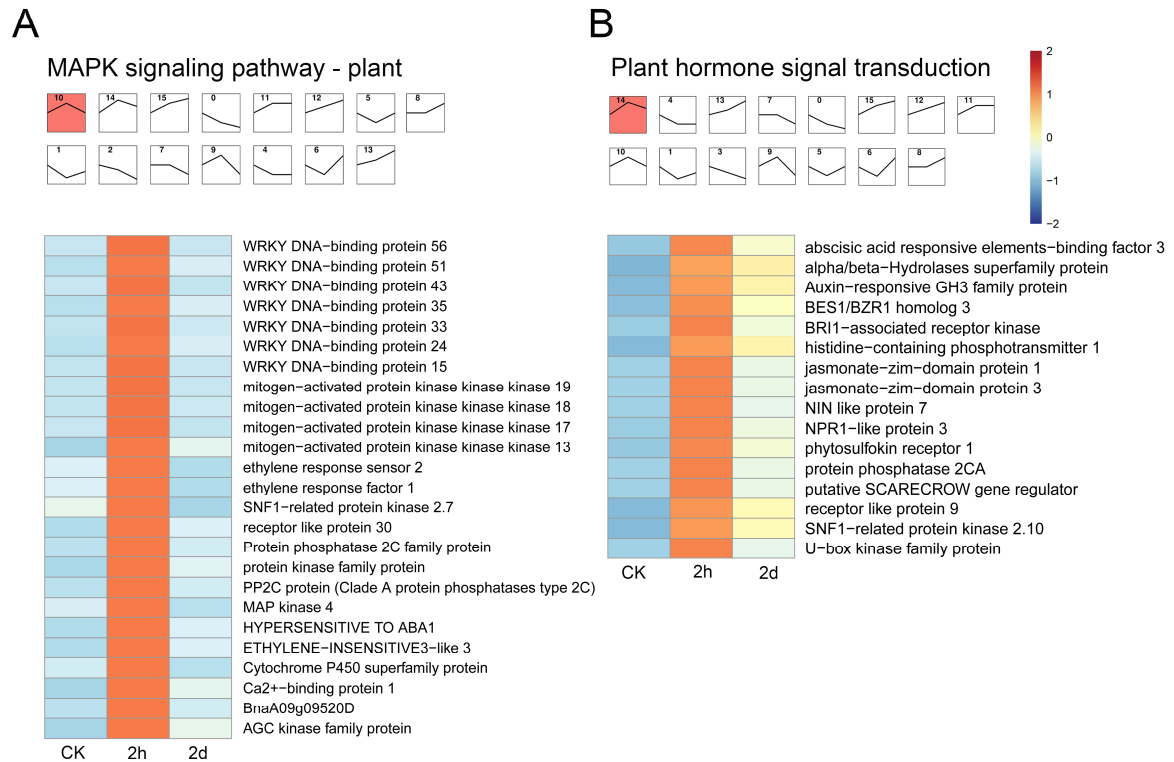
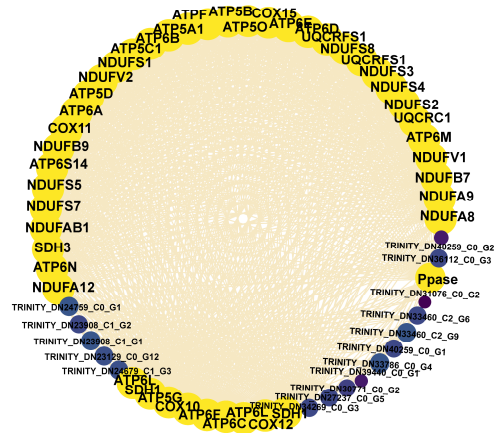
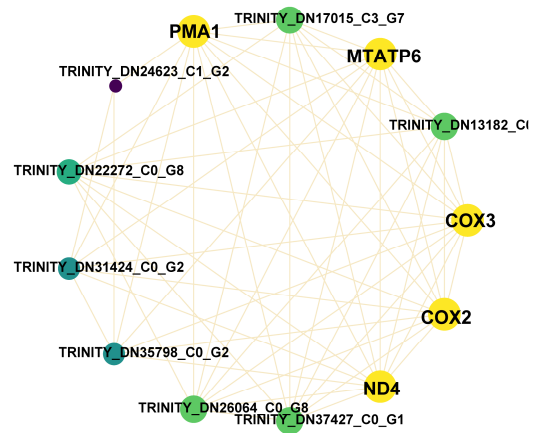


Figure S10. Changes in the DEGs associated with the resistance to oxidative stress in *Arabidopsis thaliana* (*At*) after the 0h, 2h and 2d treatment of 4,8-DHT. **(A)**. STEM plots and heatmaps of DEGs are involved in the plant hormone signal transduction; **(B)**. STEM plots and heatmaps of DEGs are involved in the MAPK signaling pathway. STEM has multiple temporal expression patterns, and the colored modules represent the most significant among these DEGs. The different number in the square only indicates the serial number of the expression patterns.

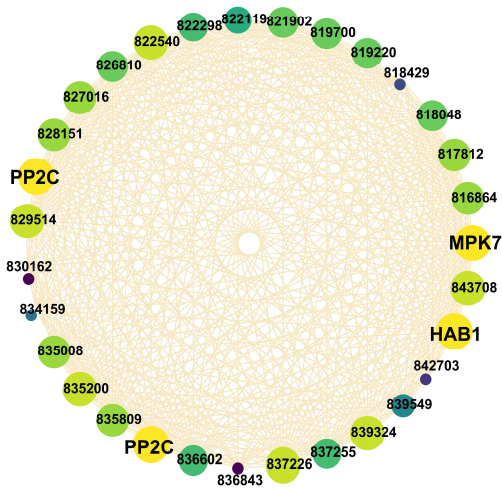
A Oxidative phosphorylation



B Oxidative phosphorylation



C MAPK signaling pathway



D Plant hormone signal transduction

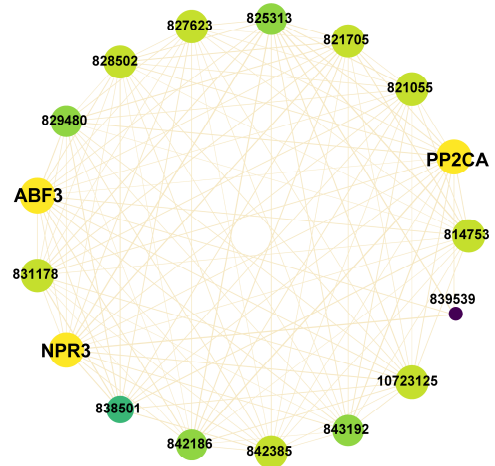


Figure S11. Correlation networks for oxidative phosphorylation, MAPK signaling pathway and plant hormone signal transduction in *Digitaria sanguinalis* (*Ds*), *Arabidopsis thaliana* (*At*) and *Poa annua* (*Pa*). (A). Correlation networks for *Ds* are involved in oxidative phosphorylation; (B). Correlation networks for *Pa* are involved in oxidative phosphorylation; (C). Correlation networks for *At* are involved in MAPK signaling pathway; (D). Correlation networks for *At* are involved in plant hormone signal transduction. Yellow represents key genes, and genes with higher linkage counts in the corresponding networks are shown in the larger circles.

Table S1. Key genetic information for correlation network analysis of photosynthetic pathways in *Digitaria sanguinalis* (*Ds*) and *Arabidopsis thaliana* (*At*).

| Species | Gene ID | Gene Name | Gene Annotation |
|-----------------------------------|-----------------------|------------------------------|---|
| Photosynthesis | | | |
| <i>Digitaria sanguinalis</i> | TRINITY_DN34418_c0_g1 | <i>PetC</i> | cytochrome b6-f complex iron-sulfur subunit, chloroplastic isoform X2 |
| | TRINITY_DN27033_c1_g2 | <i>ATPF1G</i> | ATP synthase subunit gamma, chloroplastic |
| | TRINITY_DN27438_c0_g1 | <i>PsaH</i> | photosystem I reaction center subunit VI |
| | TRINITY_DN35842_c0_g1 | <i>Psb28</i> | photosystem II reaction center PSB28 protein, |
| | TRINITY_DN30137_c1_g1 | <i>PsbY</i> | photosystem II core complex proteins psbY |
| | TRINITY_DN33614_c0_g2 | <i>ATPG</i> | ATP synthase subunit b', chloroplastic |
| | TRINITY_DN30034_c0_g2 | <i>PsaG</i> | photosystem I reaction center subunit V, chloroplastic |
| | TRINITY_DN33317_c0_g5 | <i>PsaD</i> | photosystem I subunit II |
| <i>Arabidopsis thaliana</i> | 818532 | <i>PPL2</i> | PsbP-like protein 2 |
| | 821143 | <i>PsbQ</i> | PsbQ-like 1 |
| | 824699 | <i>PPL1</i> | PsbP-like protein 1 |
| | 825797 | <i>ATPC1</i> | ATPase, F1 complex, gamma subunit protein |
| | 825866 | <i>PsbQ</i> | photosystem II subunit Q-2 |
| | 827877 | <i>PsbQ</i> | photosystem II subunit QA |
| | 827996 | <i>PetC</i> | photosynthetic electron transfer C |
| | 828984 | <i>Psb28</i> | photosystem II reaction center PSB28 protein |
| | 829359 | <i>ATPF0B</i> | ATPase, F0 complex, subunit B/B', bacterial/chloroplast |
| | 836751 | <i>FNR1</i> | ferredoxin-NADP ⁺ reductase |
| | 837974 | <i>PsbQ</i> | PsbQ-like 2 |
| | 838591 | <i>FNR2</i> | ferredoxin-NADP [+-] oxidoreductase 2 |
| | 838622 | <i>PetE</i> | Cupredoxin superfamily protein |
| | 839449 | <i>Psb27</i> | photosystem II family protein |
| | 828183 | <i>PsaD</i> | photosystem I subunit D-1 |
| | 834534 | Trypsin family protein | Trypsin family protein |
| | 838876 | TPR-like superfamily protein | Tetratricopeptide repeat (TPR)-like superfamily protein |
| Photosynthesis - antenna proteins | | | |
| <i>Digitaria sanguinalis</i> | TRINITY_DN32282_c0_g1 | <i>LHCA1</i> | chlorophyll a-b binding protein 1B-21, chloroplastic |
| | TRINITY_DN35117_c0_g1 | <i>LHCB4</i> | chlorophyll a-b binding protein CP29.1, chloroplastic |
| | TRINITY_DN28327_c0_g2 | <i>LHCA4</i> | chlorophyll a-b binding protein P4, chloroplastic |
| | TRINITY_DN38985_c0_g1 | <i>LHCB7</i> | chlorophyll a-b binding protein 7, chloroplastic |
| <i>Arabidopsis thaliana</i> | 820043 | <i>LHCB4.2</i> | light harvesting complex photosystem II |
| | 835515 | <i>LHCB3</i> | chlorophyll a-b binding protein 3, chloroplastic |
| | 838151 | <i>LHCB6</i> | light harvesting complex photosystem II subunit 6 |

| | | | |
|--------------------|-----------------------|----------------|---|
| | 839869 | <i>LHCB3</i> | chlorophyll A/B binding protein 3 |
| Carbon fixation | | | |
| <i>Digitaria</i> | TRINITY_DN38874_C1_G1 | <i>Rubisco</i> | ribulose biphosphate carboxylase small chain A |
| <i>sanguinalis</i> | TRINITY_DN25725_C2_G1 | <i>GAPA</i> | glyceraldehyde-3-phosphate dehydrogenase A |
| | TRINITY_DN22992_C0_G1 | <i>PEPC</i> | C4 phosphoenolpyruvate carboxylase |
| <i>Arabidopsis</i> | 833829 | <i>Rubisco</i> | Ribulose biphosphate carboxylase (small chain) family protein |
| <i>thaliana</i> | 843565 | <i>ALT2</i> | alanine aminotransferase 2 |

Table S2. Key genetic information for correlation network analysis of phenylpropanoid biosynthesis and glutathione metabolism in *Digitaria sanguinalis* (*Ds*), *Arabidopsis thaliana* (*At*) and *Poa annua* (*Pa*).

| Species | Gene ID | Gene Name | Gene Annotation |
|------------------------------|-----------------------|---------------|---|
| Phenylpropanoid biosynthesis | | | |
| <i>Digitaria</i> | | | |
| <i>sanguinalis</i> | TRINITY_DN27015_c0_g3 | <i>POD A2</i> | peroxidase A2 |
| <i>Arabidopsis</i> | | | |
| <i>thaliana</i> | 829907 | <i>POD</i> | Peroxidase superfamily protein |
| <i>Poa annua</i> | TRINITY_DN21631_c0_g4 | <i>POD43</i> | Peroxidase 43 |
| Glutathione metabolism | | | |
| <i>Digitaria</i> | TRINITY_DN31220_c1_g1 | <i>GSTT1</i> | Glutathione S-transferase T1 |
| <i>sanguinalis</i> | TRINITY_DN28189_c0_g2 | <i>NDHL</i> | NAD(P)H-quinone oxidoreductase subunit L |
| | TRINITY_DN28158_c2_g6 | <i>GSTU6</i> | glutathione S-transferase 1 |
| | TRINITY_DN27465_c0_g4 | <i>GPX</i> | putative phospholipid hydroperoxide glutathione |
| | | | peroxidase 6, mitochondrial |
| <i>Arabidopsis</i> | 822003 | <i>GSR</i> | glutathione-disulfide reductase |
| <i>thaliana</i> | 826765 | <i>GPX6</i> | glutathione peroxidase 6 |
| <i>Poa annua</i> | TRINITY_DN35776_c0_g2 | <i>GSTU6</i> | probable glutathione S-transferase GSTU6 |
| | TRINITY_DN34256_c0_g2 | <i>GSTU6</i> | Probable glutathione S-transferase GSTU6 |
| | TRINITY_DN30998_c0_g1 | <i>GSTU6</i> | probable glutathione S-transferase GSTU6 |
| | TRINITY_DN29602_c0_g1 | <i>GSTU6</i> | putative glutathione S-transferase GSTU6 |
| | TRINITY_DN19080_c1_g3 | <i>GSTU6</i> | glutathione s-transferase U2 |

Table S3. Key genetic information for correlation network analysis of oxidative phosphorylation, MAPK signaling pathway and plant hormone signal transduction in *Digitaria sanguinalis* (Ds), *Arabidopsis thaliana* (At) and *Poa annua* (Pa).

| Species | Gene ID | Gene Name | Gene Annotation |
|------------------------------|-----------------------|-------------------|---|
| Oxidative phosphorylation | | | |
| <i>Digitaria sanguinalis</i> | TRINITY_DN33695_C0_G1 | <i>NDUFA9</i> | NADH-ubiquinone oxidoreductase 40 kDa subunit |
| | TRINITY_DN34085_C0_G1 | <i>Ppase</i> | inorganic pyrophosphatase-like |
| | TRINITY_DN25548_C0_G2 | <i>NDUFA8</i> | NADH-ubiquinone oxidoreductase 20.8 kDa subunit-like |
| | TRINITY_DN20554_C0_G1 | <i>ATP6M</i> | V-type proton ATPase subunit D-like |
| | TRINITY_DN22979_C0_G1 | <i>NDUFV1</i> | NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial-like |
| | TRINITY_DN32629_C0_G3 | <i>NDUFB7</i> | NADH-ubiquinone oxidoreductase B18 subunit |
| | TRINITY_DN27155_C0_G4 | <i>ATP6L</i> | V-type proton ATPase 16 kDa proteolipid subunit 2-like |
| | TRINITY_DN37634_C0_G3 | <i>NDUFS2</i> | NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial-like |
| | TRINITY_DN20671_C0_G1 | <i>NDUFV2</i> | NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial-like |
| | TRINITY_DN32506_C0_G3 | <i>ATP5D</i> | ATP synthase subunit delta, mitochondrial-like |
| | TRINITY_DN25108_C0_G1 | <i>ATP6A</i> | V-type proton ATPase catalytic subunit A-like |
| | TRINITY_DN21733_C0_G1 | <i>COX11</i> | cytochrome c oxidase assembly protein COX11, mitochondrial-like |
| | TRINITY_DN33762_C0_G1 | <i>COX10</i> | protoheme IX farnesyltransferase, mitochondrial-like |
| | TRINITY_DN39201_C1_G1 | <i>SDH1</i> | probable succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial |
| | TRINITY_DN27244_C0_G2 | <i>ATP6S14</i> | V-type proton ATPase subunit F-like |
| | TRINITY_DN34269_C0_G3 | <i>UQCRC1</i> | cytochrome c1, heme protein, mitochondrial-like |
| | TRINITY_DN36196_C0_G1 | <i>ATP6BATP6B</i> | V-type proton ATPase subunit B |
| | TRINITY_DN24551_C0_G2 | <i>ATP5C1</i> | ATP synthase subunit gamma, mitochondrial-like |
| | TRINITY_DN23012_C0_G2 | <i>ATP6F</i> | probable V-type proton ATPase 20 kDa proteolipid subunit |
| | TRINITY_DN20747_C0_G1 | <i>NDUFA2</i> | PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 |
| | TRINITY_DN30596_C0_G1 | <i>NDUFS8</i> | NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial-like |
| | TRINITY_DN31842_C0_G1 | <i>COX15</i> | cytochrome c oxidase assembly protein COX15-like |
| | TRINITY_DN40545_C0_G1 | <i>ATP5A1</i> | ATP synthase subunit alpha, mitochondrial |
| | TRINITY_DN36569_C0_G2 | <i>NDUFS1</i> | NADH-ubiquinone oxidoreductase 78 kDa subunit, mitochondrial-like |
| | TRINITY_DN25470_C0_G2 | <i>NDUFAB1</i> | vacuolar protein sorting-associated protein 74-like |
| | TRINITY_DN22757_C0_G1 | <i>NDUFS7</i> | NADH-ubiquinone oxidoreductase 19.3 kDa subunit |
| | TRINITY_DN30729_C1_G4 | <i>ATP6L</i> | V-type proton ATPase 16 kDa proteolipid subunit [Quercus suber] |
| | TRINITY_DN22557_C0_G1 | <i>NDUFS5</i> | NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B-like |
| | TRINITY_DN22393_C0_G2 | <i>COX12</i> | cytochrome c oxidase subunit 6B-like |
| | TRINITY_DN22308_C0_G1 | <i>NDUFB9</i> | NADH dehydrogenase (ubiquinone) 1 beta subcomplex subunit 9 |
| | TRINITY_DN27152_C0_G1 | <i>NDUFA12</i> | NADH: ubiquinone oxidoreductase 18 kDa subunit |
| | TRINITY_DN29967_C1_G2 | <i>ATP6C</i> | V-type proton ATPase subunit C 1-like |
| | TRINITY_DN33127_C0_G1 | <i>UQCRCFS1</i> | ubiquinol-cytochrome c reductase iron-sulfur subunit |
| | TRINITY_DN32704_C0_G1 | <i>ATP5O</i> | ATP synthase subunit 5, mitochondrial-like |
| | TRINITY_DN39508_C0_G1 | <i>ATP5B</i> | ATP synthase subunit beta, mitochondrial-like |

| | | | |
|-----------------------------------|-----------------------|---------------|---|
| <i>Poa annua</i> | TRINITY_DN24644_C0_G1 | <i>SDH3</i> | succinate dehydrogenase cytochrome B subunit, mitochondrial-like |
| | TRINITY_DN30954_C0_G3 | <i>ATP6N</i> | V-type proton ATPase subunit a-like |
| | TRINITY_DN27269_C0_G7 | <i>ATP5G</i> | ATP synthase subunit 9, mitochondrial-like |
| | TRINITY_DN40563_C1_G1 | <i>SDH1</i> | probable succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial |
| | TRINITY_DN25823_C0_G1 | <i>ATP6E</i> | V-type proton ATPase subunit E-like |
| | TRINITY_DN23908_C1_G3 | <i>ATPF</i> | ATP synthase protein YMF19 |
| | TRINITY_DN27129_C0_G3 | <i>NDUFS3</i> | NADH-ubiquinone oxidoreductase 30.4 kDa subunit, mitochondrial-like |
| | TRINITY_DN26189_C1_G5 | <i>ATP6D</i> | V-type proton ATPase subunit d-like |
| | TRINITY_DN35926_C0_G3 | <i>NDUFS4</i> | NADH-ubiquinone oxidoreductase 21 kDa subunit, mitochondrial-like |
| | TRINITY_DN10028_C0_G4 | <i>MTATP6</i> | H-transporting ATPase (mitochondrion) |
| | TRINITY_DN9456_C0_G1 | <i>COX2</i> | cytochrome c oxidase subunit 2 (mitochondrion) |
| | TRINITY_DN10028_C0_G1 | <i>COX3</i> | cytochrome c oxidase subunit 3 (mitochondrion) |
| | TRINITY_DN15424_C0_G3 | <i>PMA1</i> | Plasma membrane ATPase |
| | TRINITY_DN7227_C0_G1 | <i>ND4</i> | NADH dehydrogenase subunit 4 (mitochondrion) |
| MAPK signaling pathway | | | |
| <i>Arabidopsis</i> | 816330 | <i>MPK7</i> | mitogen-activated protein kinase 7 |
| <i>thaliana</i> | 828714 | <i>PP2C</i> | Protein phosphatase 2C family protein |
| | 836040 | <i>PP2C</i> | PP2C protein (Clade A protein phosphatases type 2C) |
| | 843609 | <i>HAB1</i> | hypersensitive to ABA1 |
| Plant hormone signal transduction | | | |
| <i>Arabidopsis</i> | 829547 | <i>ABF3</i> | abscisic acid responsive elements-binding factor 3 |
| <i>thaliana</i> | 834545 | <i>NPR3</i> | NPR1-like protein 3 |
| | 820314 | <i>PP2CA</i> | protein phosphatase 2CA |
