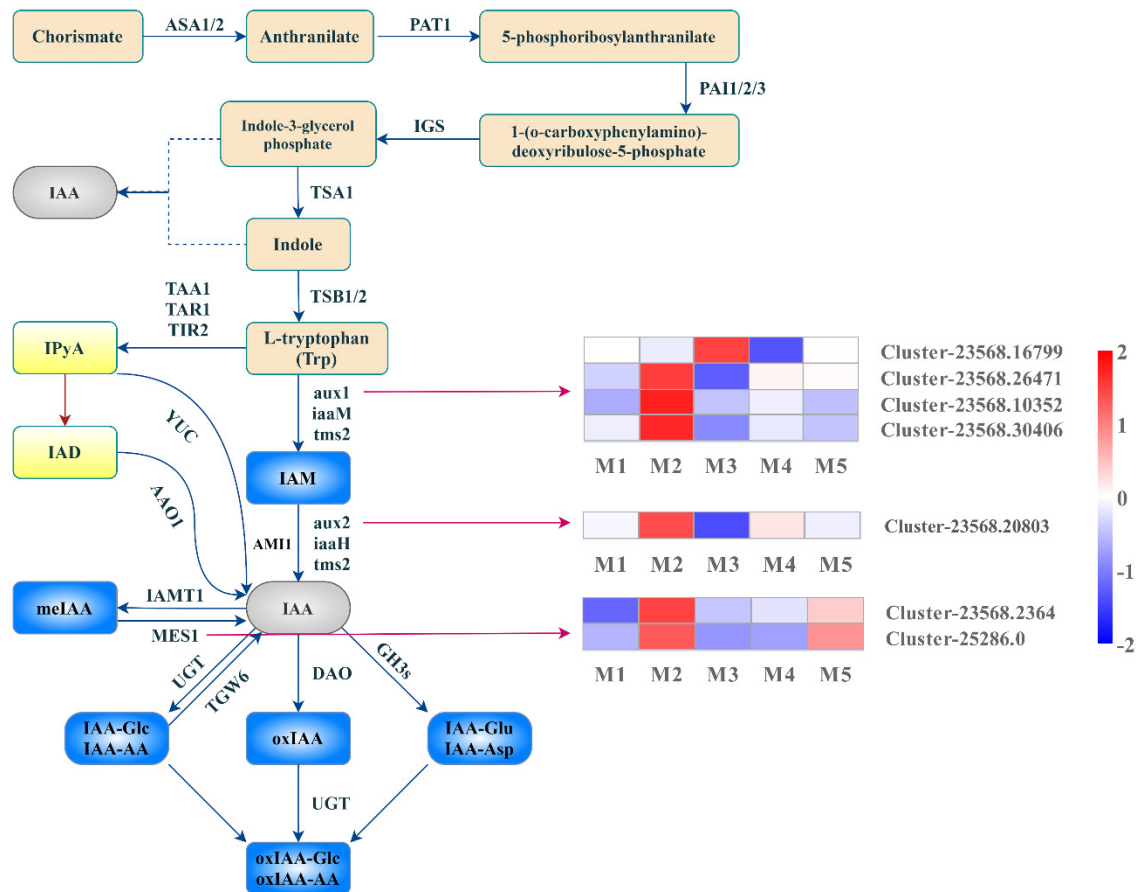


Supplementary Figure S6. Differentially expressed *Dacrydium pectinatum* unigenes identified in hormone metabolic pathways.

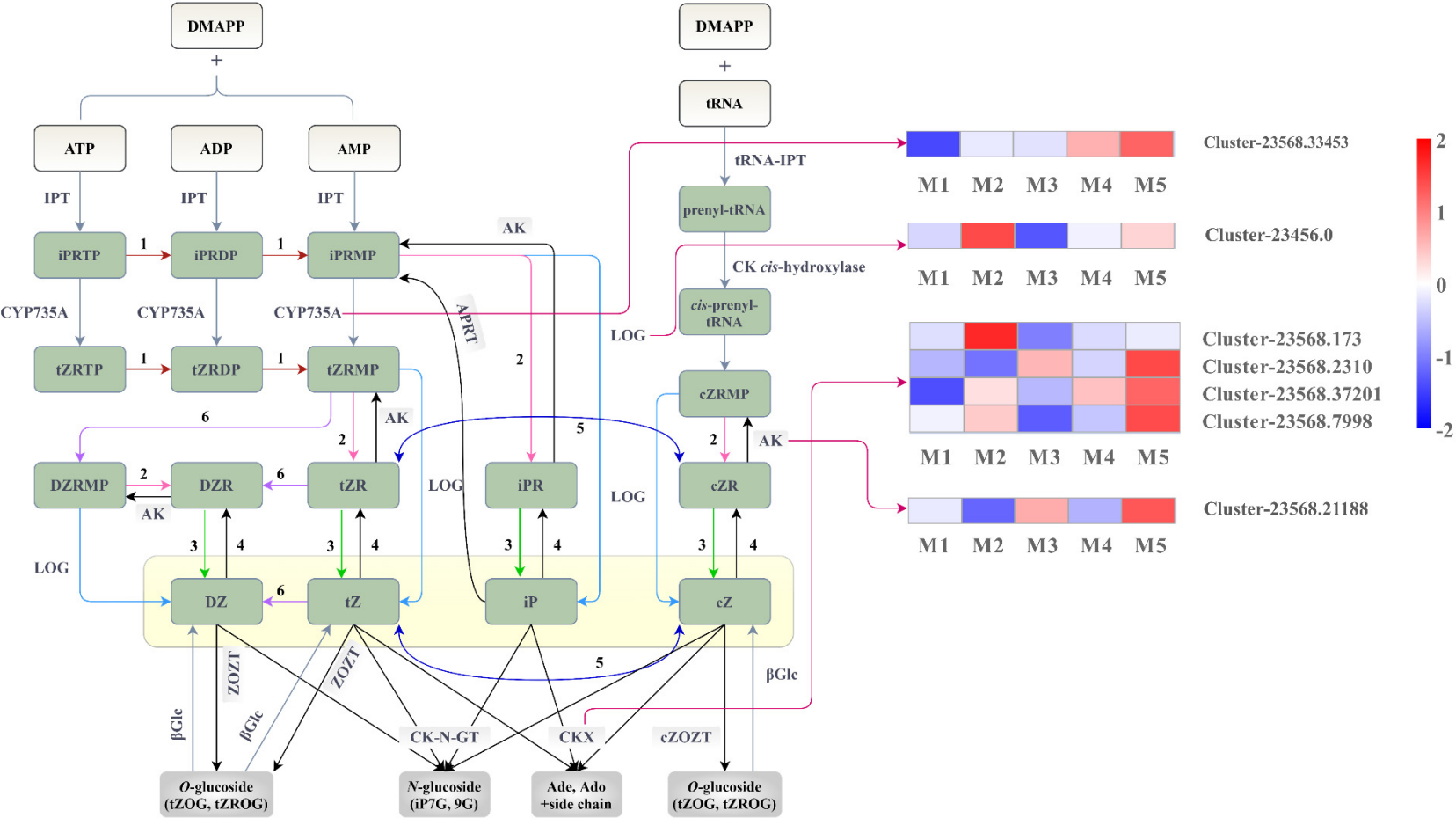
Cluster analysis of differentially expressed genes (DEGs) identified in *D. pectinatum* male cone of various development stages (M1~5: April, May, June, July and November 2019). The gradient-colored barcode at the top right indicates the $\log_2(\text{FC})$ value. Fold change is calculated based on the difference multiple of FPKM in different periods. **A:** Absciscic acid de novo biosynthesis occurs in the plastid and the cytosol. ABA is synthesized from the precursor isopentenyl diphosphate. The scheme shows the biosynthetic pathway from zeaxanthin to ABA. Enzymes are denoted next to the catalytic steps. ABA-GE: ABA-glucosyl ester; ZEP: Zeaxanthin epoxidase; VDE: Violaxanthin de-epoxidase; ABA4 is involved in the enzymatic step that catalyses the conversion of all-trans-violaxanthin into all-trans-neoxanthin; NCED: 9-*cis*-epoxycarotenoid dioxygenase; ABA2: Short-chain alcohol dehydrogenase/reductase; ABA3: Molybdenum cofactor sulfurase; AAO3: ABA-aldehyde oxidase 3; CYP707As: Cytochrome P450 707A family of proteins; UGT71B: ABA-uridine diphosphate glucosyltransferases 71B; BG1/2: β -glucosidase homologues 1/2. **B:** A current model of cytokinin biosynthesis and the two known activation pathways. DMAPP: Dimethylallyl diphosphate; iPRTP: iP riboside 5'-triphosphate; iPRDP: iP riboside 5'-diphosphate; iPRMP: iP riboside 5'-monophosphate; tZRTP: tZ riboside 5'-triphosphate; tZRDP: tZ riboside 5'-diphosphate; tZRMP: tZ riboside 5'-monophosphate; DZRMP: DZ riboside 5'-monophosphate; cZRMP: cZ riboside 5'-monophosphate; DZR, DZ riboside; tZR: tZ riboside; cZR: cZ riboside; iPR: iP riboside; tZ: Cytokinins trans-zeatin; iP: N⁶-(D2-isopentenyl)adenine; cZ: *cis*-zeatin; DZ: Dihydrozeatin; 1: tZRDP tZR 5'-diphosphate; 2: tZRTP tZR 5'-triphosphate; 3: 5-ribonucleotide phosphohydrolase; 4: Adenosine nucleosidase; 5: Purine nucleoside phosphorylase; 6: Zeatin reductase; 7: Cytokinin *cis*-hydroxylase; IPT: Adenosine phosphate-isopentenyltransferase; CYP735A: Cytochrome P450 735A mono-oxygenases; LOG: Cytokinin nucleoside 5'-monophosphate phosphoribohydrolase; APRT: Adenine ribosyltransferase; AK: Adenylate kinase; CKX: Cytokinin oxidase; ZOGT: Zeatin *O*-glucosyltransferase; CK-N-GT: Cytokinin *N*-glucosyltransferase; β Glc: β -glucosidase. **C:** Unified gibberellins biosynthetic pathway. Bioactive GAs are shown in a yellow box. GGDP: geranylgeranyl diphosphate; CPP: *ent*-copalyl diphosphate; CPS: *ent*-Copalyl diphosphate synthase; KS: *ent*-Kaurene synthase; KO: *ent*-Kaurene oxidase; KAO: *ent*-kaurenoic acid oxidase; 13ox: 13 oxidase; 20ox: 20-oxoglutarate-dependent dioxygenase; 3ox: 3 oxidase; 2ox: 2 oxidase. **D:** Presumptive pathways for indole-3-acetic acid biosynthesis and metabolic in plants. A dashed arrow denotes the tryptophan-independent IAA biosynthetic pathway. IAA: Indole-3-acetic acid; IAM: Indole-3-acetamide; IPyA: Indole-3-pyruvic acid; IAD: Indole-3-acetaldehyde; meIAA: Methylindole-3-acetic acid; oxIAA: 2-oxindole-3-acetic acid; IAA-Glc: IAA-glucose; IAA-AA: IAA-amino acid; IAA-Glu: IAA-glutamic acid; IAA-Asp: Aspartic acid; ASA: Anthranilate synthase α subunit; PAT: phosphoribosylanthranilate transferase; PAI: phosphoribosylanthranilate isomerase; IGS: Indole-3-glycerol phosphate synthase; ISA: Trp synthase α subunits; TSB: Trp synthase β subunits; TAA1/TAR1/TIR2: Tryptophan aminotransferase; YUC: YUCCA flavin-containing monooxygenases; AAO1: Aldehyde oxidase; aux1/2: Auxin transporter-like protein 1/2; AMI1: Amidase-like protein 1; IAMT1: Indole-3-acetate *O*-methyltransferase 1; MES1: Methyltransferase 1; DAO: Dioxygenase for auxin oxidation; UGT: Uridine-diphosphate glycosyltransferase; GH3: Gretchen hagen3; TGW6: IAA hydrolases. **E:** A current model of ethylene acid biosynthesis. Met: Methionine; SAM: S-adenosyl methionine; MTA: 5'-methylthioadenosine; MTR: Methylthioribose; ACC: 1-aminocyclopropane-1-carboxylic acid; SAM synthetase: L-methionine-S-adenosyltransferase; ACS: ACC synthase; ACO: ACC oxidase; AVG: Aminoethoxyvinylglycine; AOA: Aminoxyacetic acid. **F:** A current model of jasmonic acid biosynthesis and the two known activation pathways. Enzymes are denoted next to the catalytic steps. 13-HPOT: 13-hydroperoxy octadecatrienoic acid; 12,13-EOT: 12,13-epoxyoctadecatrienoic acid; 12-OPDA: 12-oxo-phytodienoic acid; OPC-8: 3-oxo-2-(2-pentenyl)-cyclopentane-1-octanoic acid; JA-Me: JA methyl ester; 12-OH-JA: 12-hydroxy-JA; 12-OH-JA-Ile: 12-hydroxy-JA-Ile; dnOPDA: dinor-OPDA; tnOPDA: tetranor-OPDA; 4,5-ddh-JA: 4,5-didehydro-JA; PLA1: Phospholipase A1; DAD1: Delayed anther dehiscence1; DGL and DALL: DAD1-LIKE lipase; LOX: Lipoyxygenase; AOS: Allene oxide synthase; AOC:

Allene oxide cyclase; OPR3: OPDA reductase3; JMT: Jasmonic acid carboxyl methyl transferase; OPR2: OPDA reductase2; JAR1: Jasmonic resistant 1 (a JA amino acid conjugate synthase); JOX1/2/3/4: Jasmonate-induced oxygenases 1 to 4; CYP94B1/B3: JA-Ile-12-hydroxylase; CYP94C1: 12-OH-JA-Ile carboxylase.

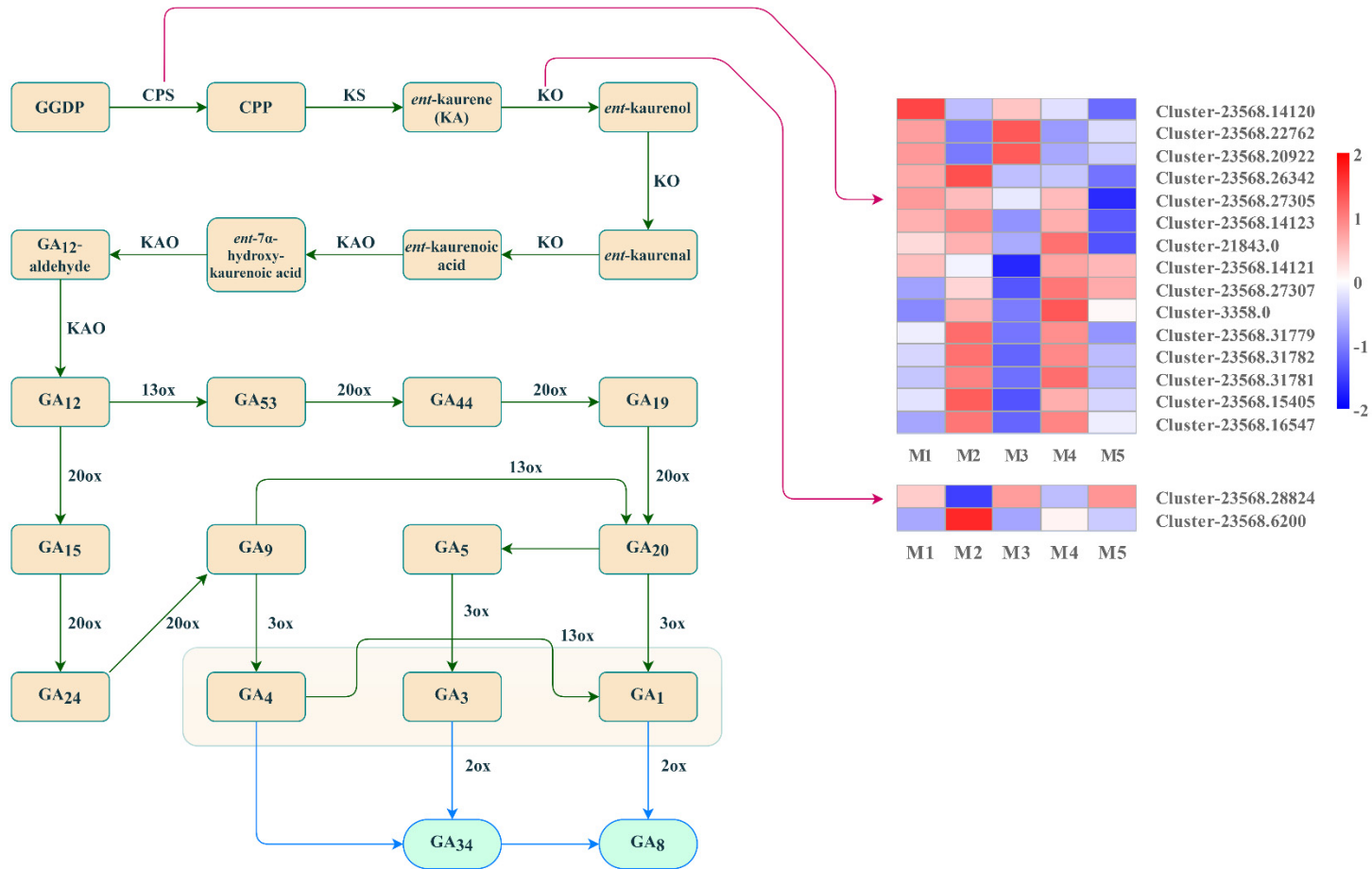
A. Indoleacetic acid (IAA)



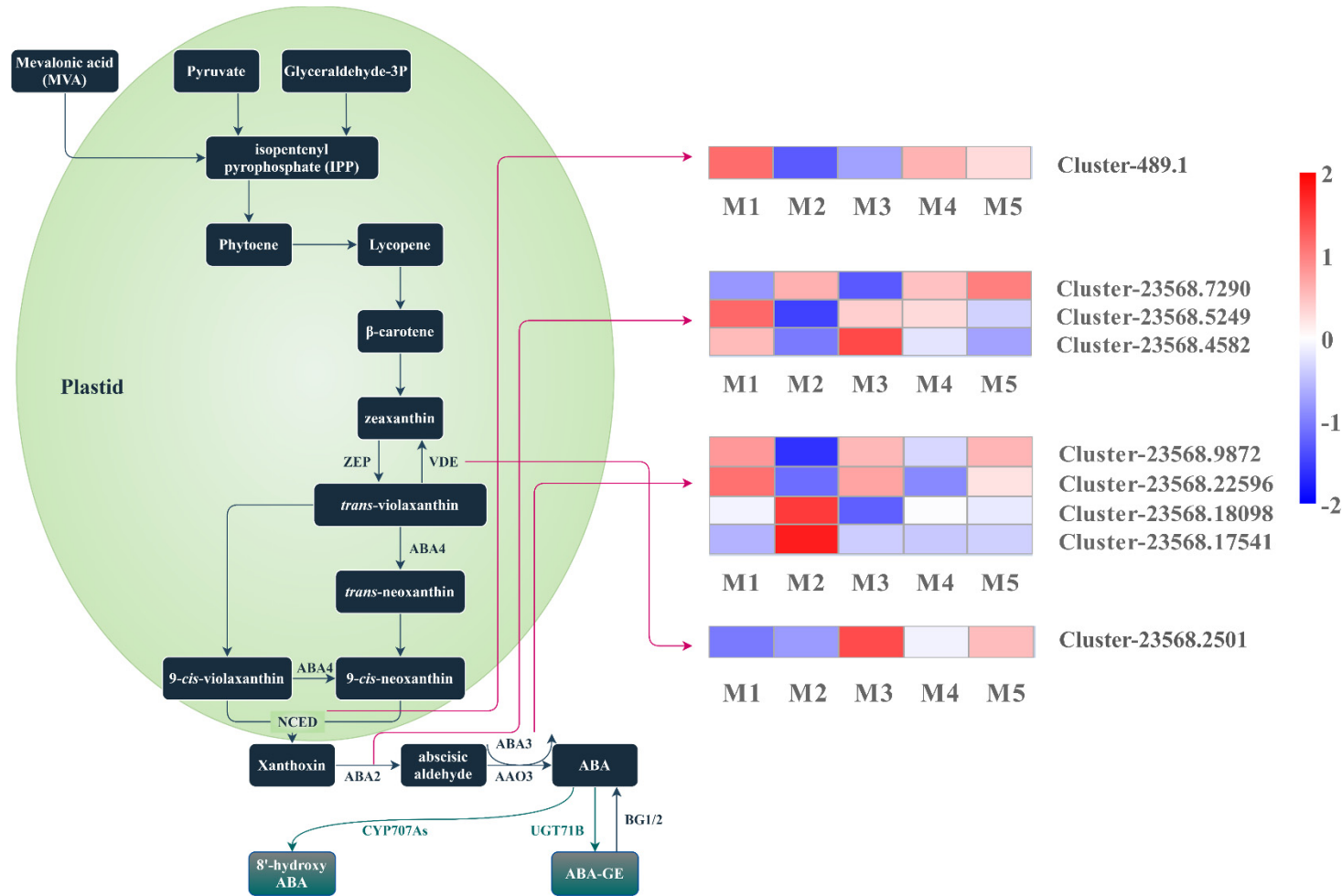
B. Cytokinin (CTK):



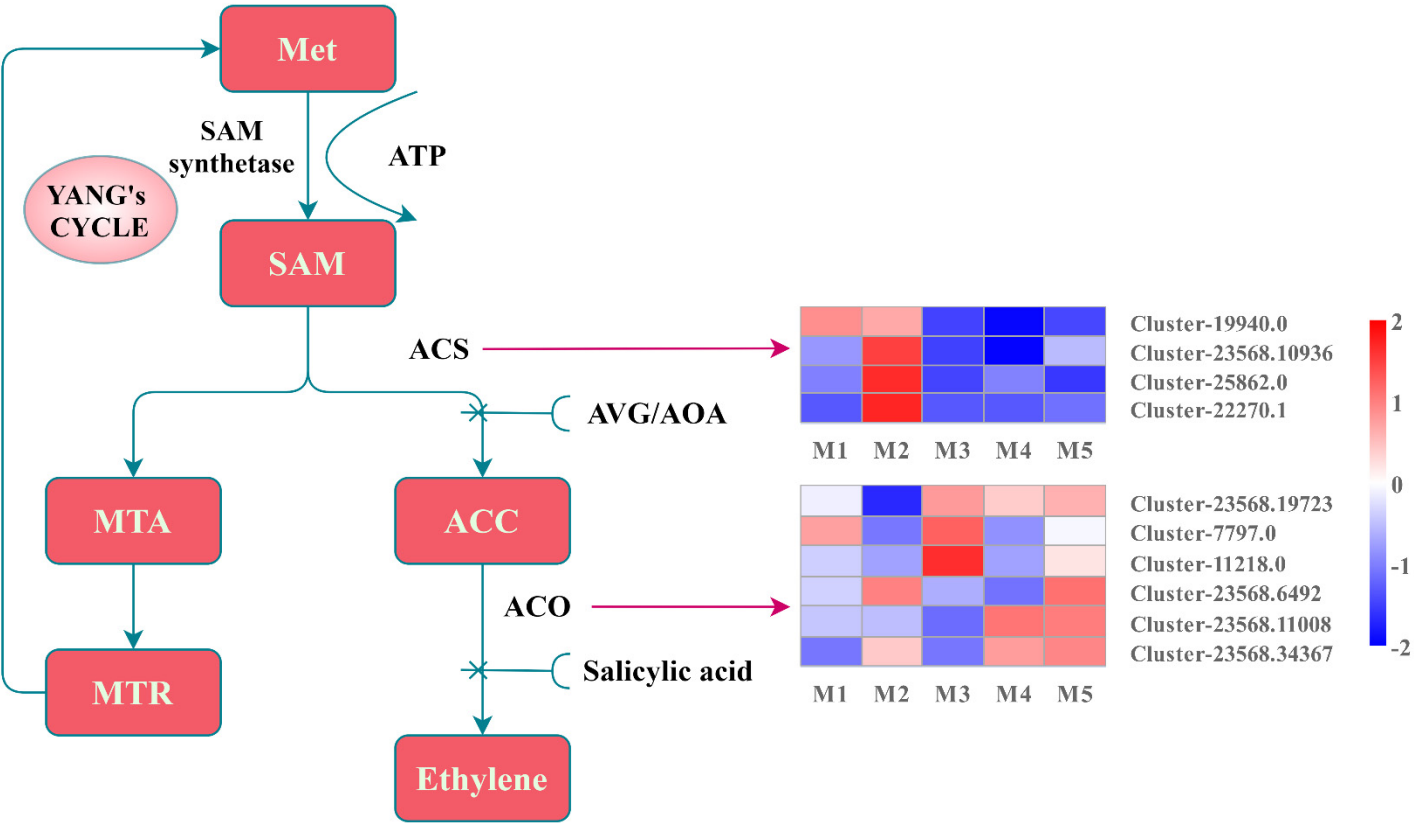
C. Gibberellin (GA)



D. Absciscic acid (ABA)



E. Ethylene:



F. Jasmonic acid (JA).

