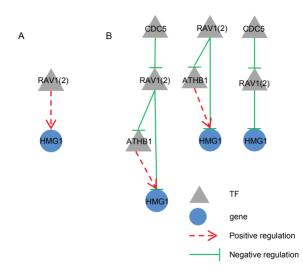
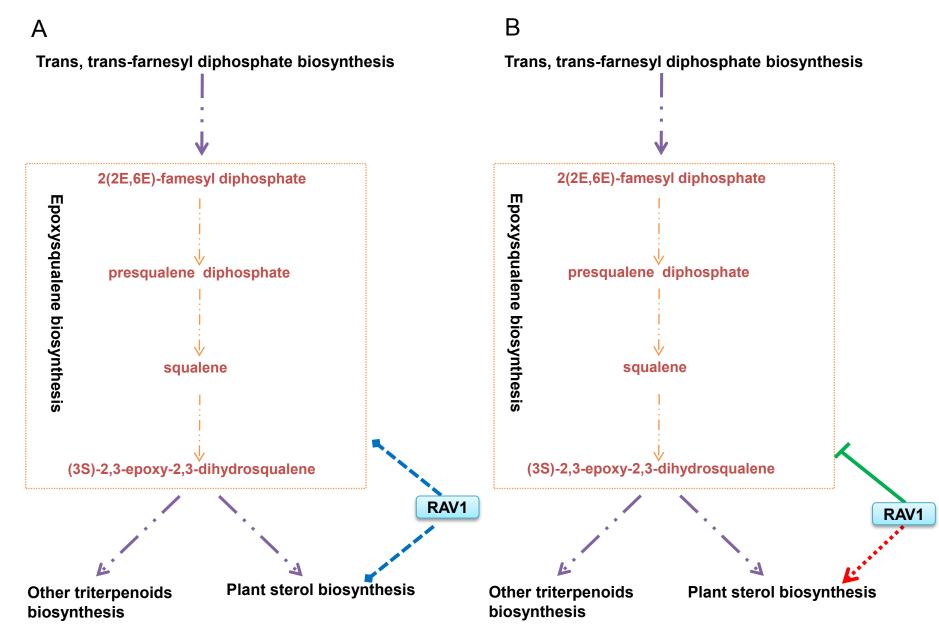


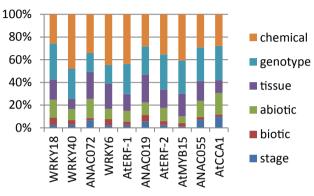
Supplementary Figure S1: Significant performance of processed regulatory interactions. (A) Numbers of target pathways in processed regulatory interactions and raw dataset compared with random generated dataset. (B) Numbers of target pathways in processed regulatory interactions and raw dataset compared with average number of random target pathways. For each pathway, random genes were generated with the same pathway gene number. And random genes' regulatory interactions were used to generate random target pathways of TFs. This procedure was repeated 1,000 times to draw the boxplot and to compute the average number of random target pathways.



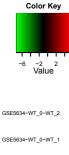
Supplementary Figure S2: The regulatoy influence of RAV1 on HMG1. (A) RAV1 positively regulates HMG1 independently. (B) RAV1 negatively regulates HMG1.



Supplementary Figure S3: Regulatory rewirings of RAV1 on epoxysqualene biosynthesis and sterol biosynthesis. (A) RAV1 regulated epoxysqualene biosynthesis and plant sterol biosynthesis in the same way. (B) RAV1 negative regulated epoxysqualene biosynthesis and positive regulated plant sterol biosynthesis.



Supplementary Figure S4: The contrasts of six experiment categories for differentially expressed TFs. (TFs were ranked by numbers of experiments when they were differentially expressed; and the top ten TFs were used to compute the percentages of six experiment categories: tissue, stage, genotype, chemical, biotic and abiotic.)





GSE4847-MU1_0-MU1_1

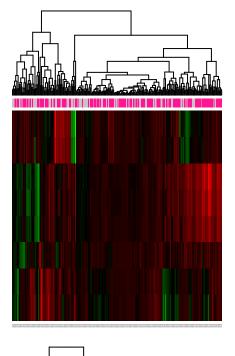
Color Key

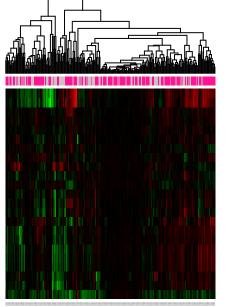
GSE17159-MU1 0-MU1 3 GSE17159-WT_0-WT_3 GSE9719-MU1_0-MU3_0 GSE9719-MU1 2-MU3 2 GSE9719-MU1_1-MU3_1 GSE9719-MU2 1-MU3 1 GSE17159-WT_0-WT_2 GSE9719-MU3 1-MU3 2 GSE5615-WT_0-WT_7 GSE9719-MU2_0-MU2_1 GSE9719-MU2_0-WT_0 GSE9719-MU3_0-MU3_2 GSE9719-MU1_0-MU1_1 GSE9719-MU3_0-MU3_1 GSE9728-WT 0-WT 1 GSE12856-MU1_0-MU1_1 GSE12856-WT 0-WT 1 GSE17500-WT_0-WT_1 GSE17500-MU2_0-MU2_1 GSE17500-MU1_0-MU1_1 GSE6583-WT_0-WT_1 GSE6583-MU1 0-MU1 1 GSE1512-WT_1-WT_2

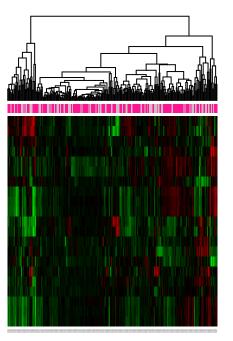
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Е

GSE10749-MU1_0-MU2_0 GSE10749-MU1_1-MU2_1 GSE5699-WT 0-WT 1 GSE8951-MU2_0-WT_0 GSE12551-MU1_1-MU2_1 GSE12551-MU1 0-MU2 0 GSE10646-MU1_0-MU3_0 GSE9728-MU3_1-WT_1 GSE9728-MU1 1-WT 1 GSE9728-MU2_1-WT_1 GSE10749-MU2_1-WT_1 GSE10749-MU2_0-WT_0 GSE6583-MU1 1-WT 1 GSE10646-MU3_0-WT_0 GSE8951-MU1_0-MU2_0 GSE6151-WT 8-WT 9 GSE5698-MU1_1-WT_1 GSE5698-MU1_0-WT_0 GSE9728-MU3 0-WT 0 GSE9728-MU2_0-WT_0 GSE9728-MU1_0-WT_0





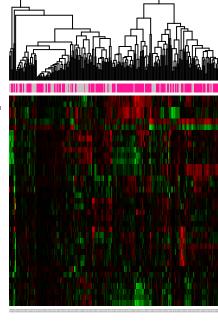


В



Color Key

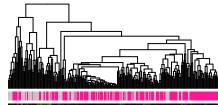


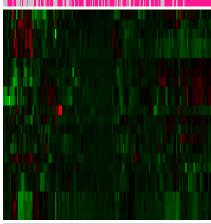




D

GSE11758-WT 1-WT 4 GSE5615-WT_2-WT_9 GSE5616-MU1 0-MU1 2 GSE5616-MU1_0-WT_0 GSE5615-WT_10-WT_7 GSE8925-WT_0-WT_1 GSE13739-WT 0-WT 5 GSE8912-WT_0-WT_1 GSE5751-MU1_0-MU1_1 GSE5751-MU1 0-MU1 2 GSE4733-MU1_4-WT_0 GSE17479-MU1 0-MU1 2 GSE6158-WT_1-WT_4 GSE12887-WT 0-WT 1 GSE12887-MU1_0-MU1_1 GSE18153-MU1_1-MU1_2 GSE6181-WT_0-WT_1 GSE6832-MU1 1-WT 1 GSE6832-MU1_0-WT_0 GSE5615-WT_12-WT_5 GSE5615-WT 11-WT 4 GSE5615-WT_10-WT_3







terpniods genes

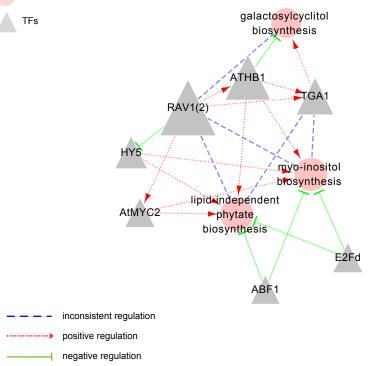
transcription factors

С

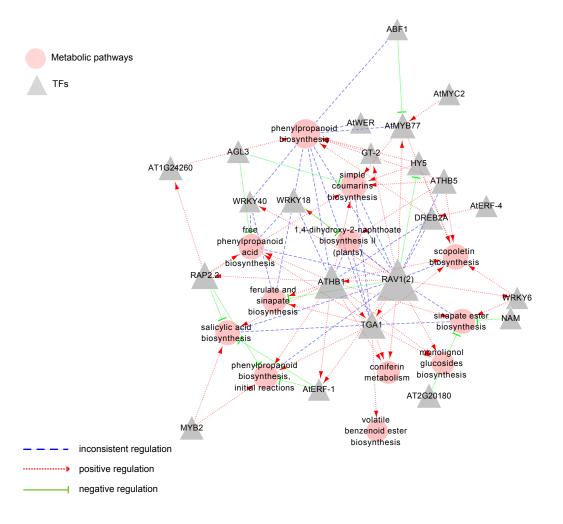
Supplementary Figure S5: The expression profiles of TF-encoding genes and TB genes under five

Supplementary Figure S5: The expression profiles of TF-encoding genes and TB genes under five categories of experimental conditions: (A) Grown and developmental stages; (B) Tissues; (C) Abiotic stresses; (D) Chemical treatments; (E) Genotypes.

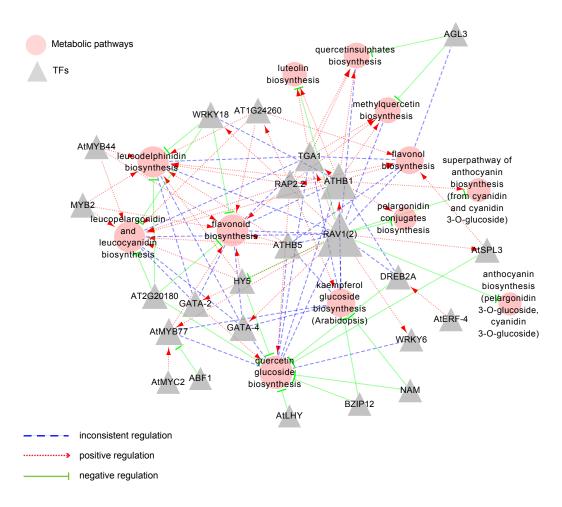




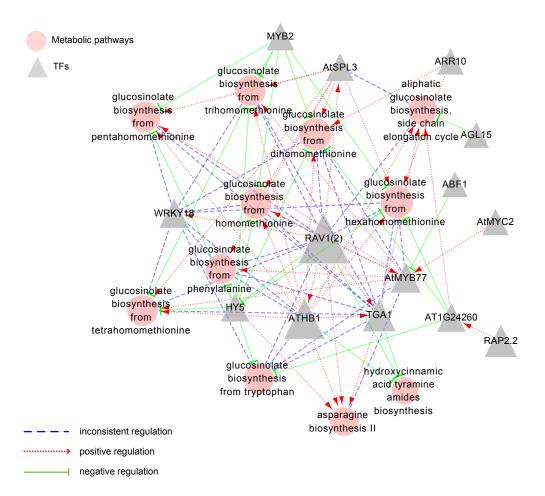
Supplementary Figure S6: Regulatory network of SDB metabolic pathways.



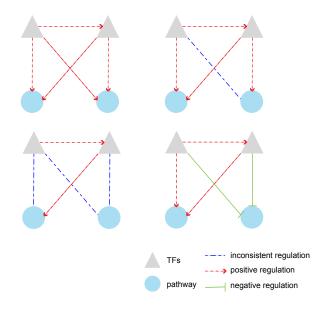
Supplementary Figure S7: Regulatory network of PDB metabolic pathways.



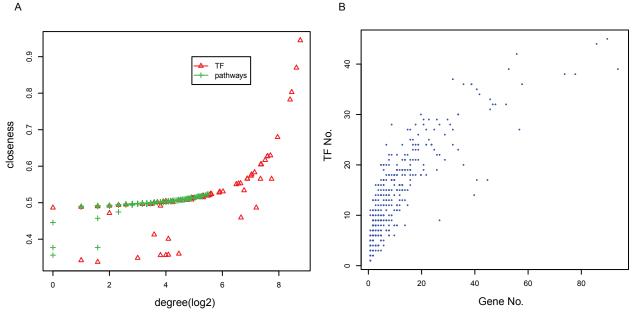
Supplementary Figure S8: Regulatory network of FB metabolic pathways.



Supplementary Figure S9: Regulatory network of NSCB metabolic pathways.

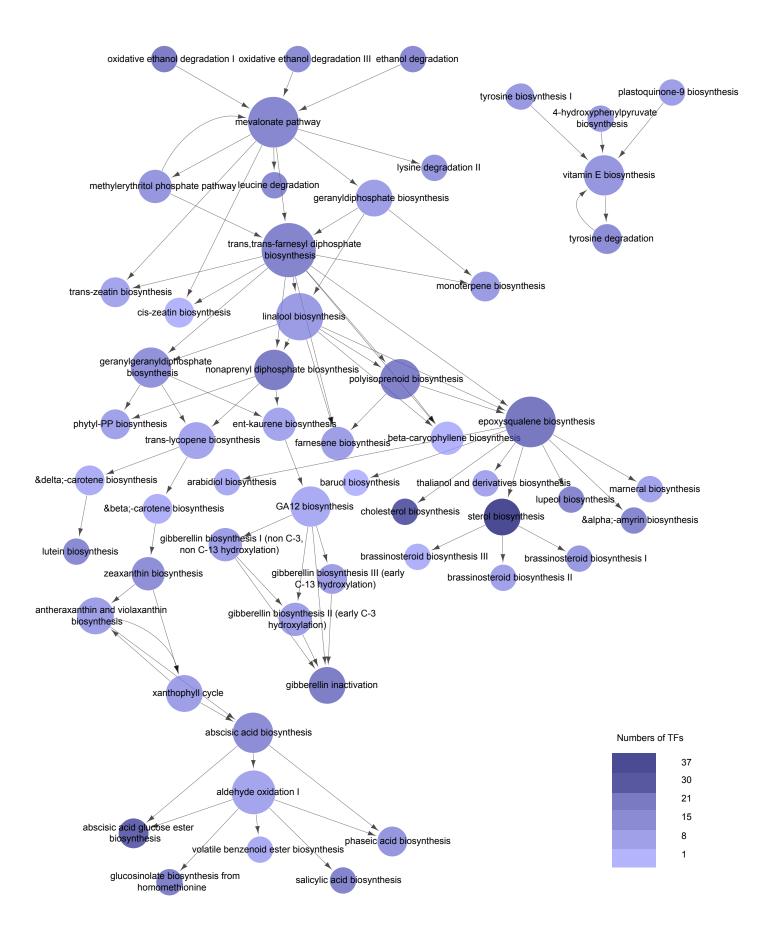


Supplementary Figure S10: Motifs with highest frequencies in secondary metabolic regulatory network.

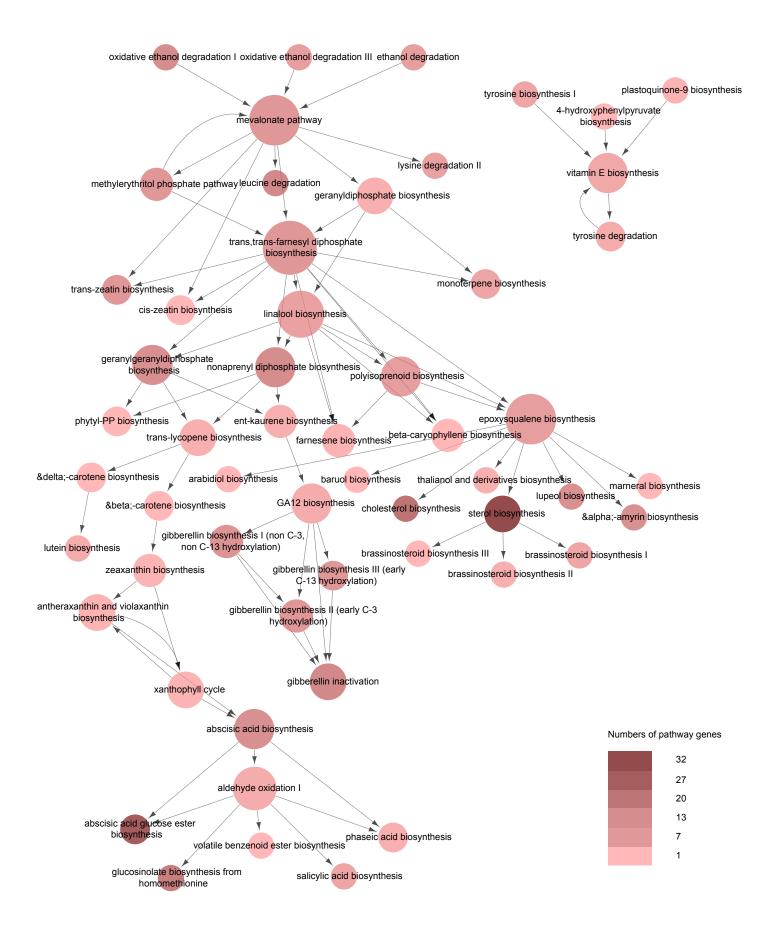


Supplementary Figure S11: Relationship of TF-encoding genes and pathways in the network. (A) The relationship of closeness and degree in both pathways and transcription factors. (B) The influence of pathway genes' number on TFs' number per pathway. (Each node represents a pathway.)

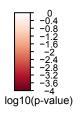
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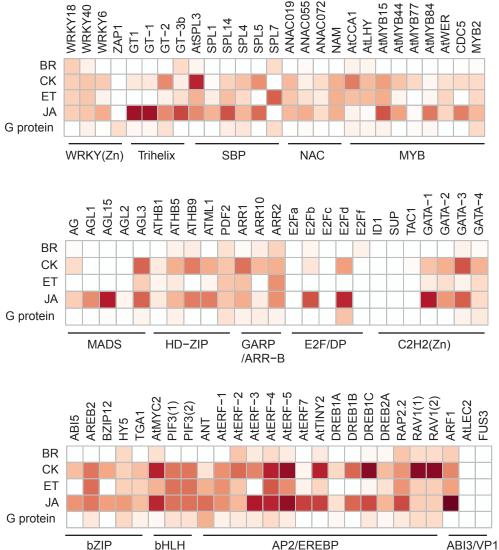


Supplementary Figure S12: Distribution of TFs' numbers in TB metabolic pathway network. (Node size: pathways' degree in metabolic network; Node color: TFs' numbers of pathways)



Supplementary Figure S13: Distribution of pathway genes' numbers in TB metabolic pathway network. (Node size: pathways' degree in metabolic network; Node color: pathway genes' numbers of pathways)





Supplementary Figure S14: Significance of co-expression relatonship between signal pathways and TFs. (BR, Brassinosteroid Signaling Pathway; CK, Cytokinin Signaling Pathway; ET, Ethylene Signaling Pathway; JA, Jasmonate Signaling Pathway; G protein, G Protein Signaling in the Regulation of Arabidopsis Seed Germination.)