

Supplement figure

Fig. S1 The distribution of reads along with mature miRNA length

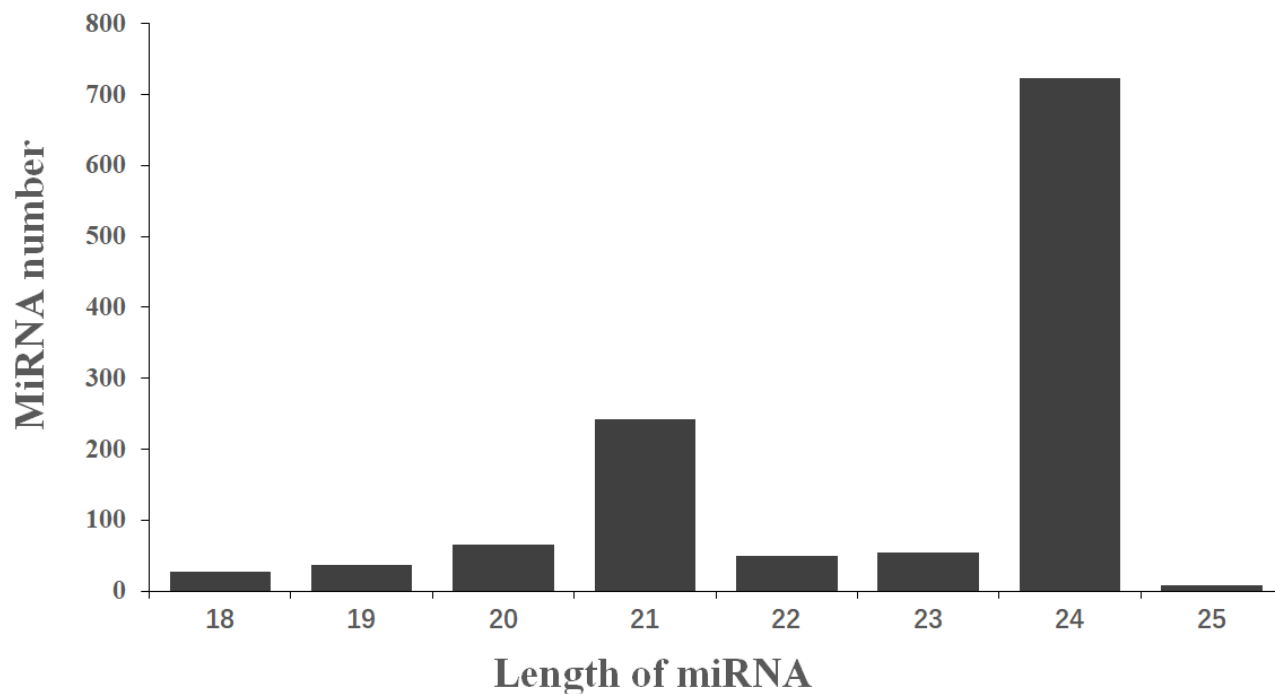


Fig. S2 The presence of the miRNAs nucleotide bias at each position along with the mature miRNAs length

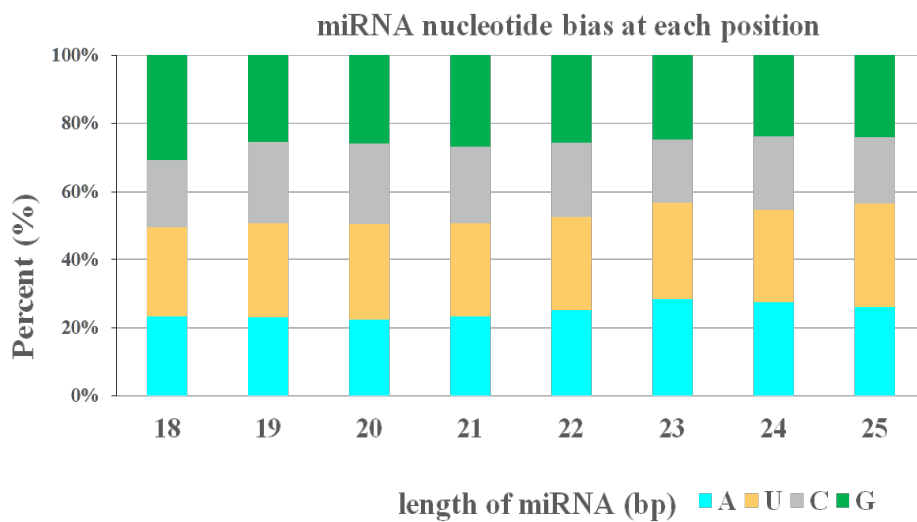


Fig. S3 The presence of the first nucleotide of miRNAs along with the mature miRNA length.

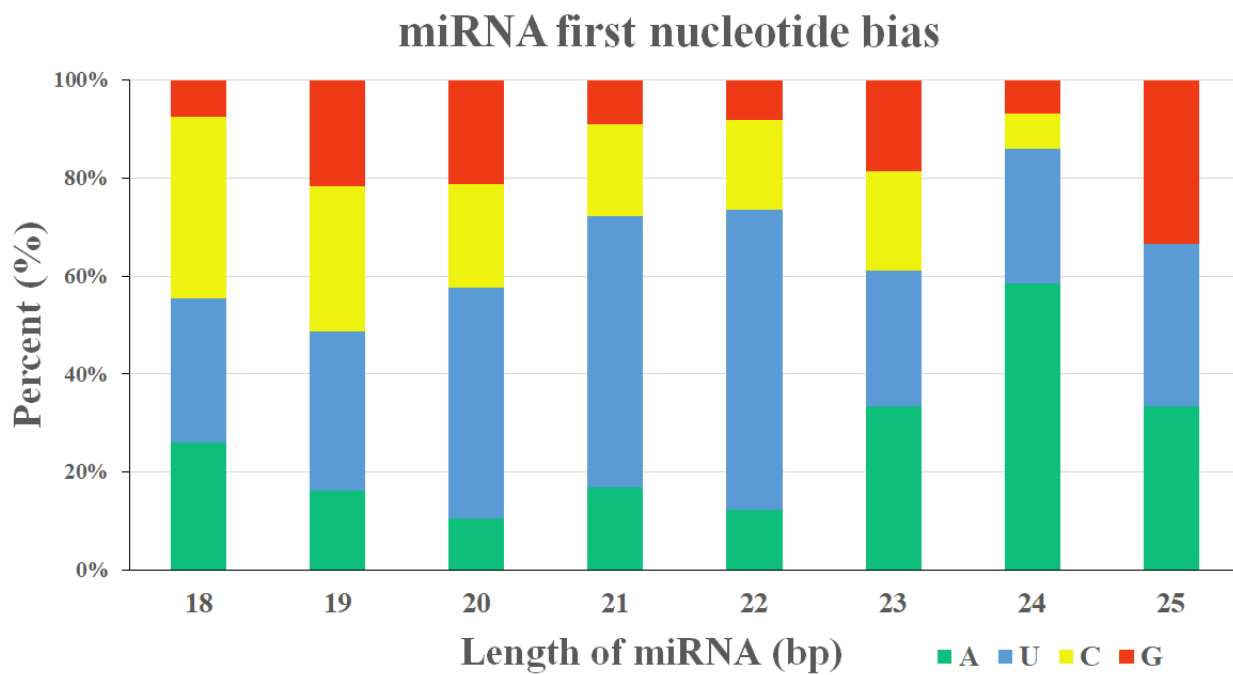


Fig. S4 Pearson correlation coefficients among gene expression profiles generated by RNA-seq analysis of biological replicates.

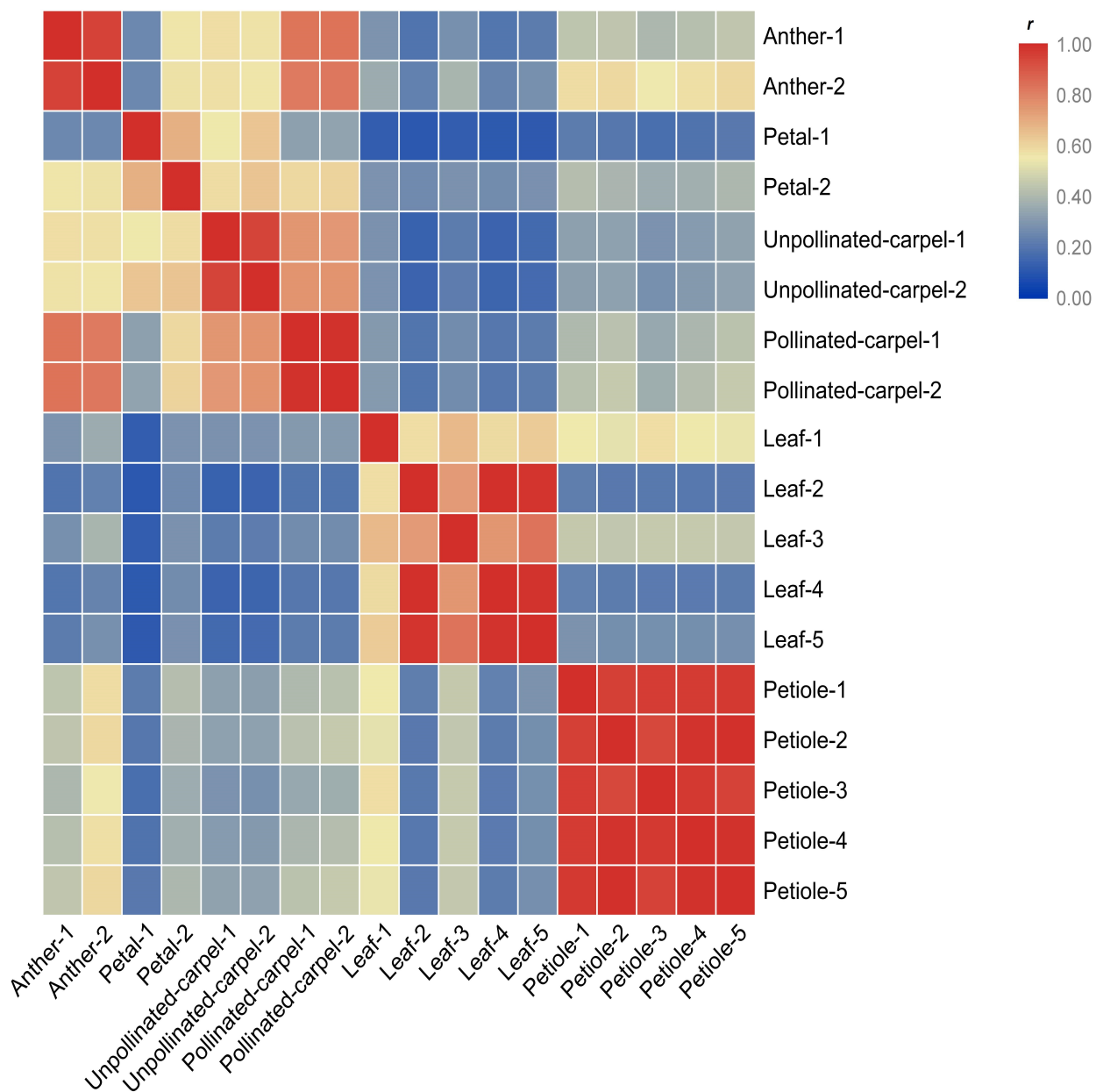


Fig. S5 Expression profile of selected miRNAs and targeted genes. The expression of miRNAs are showed in line graphs. The expression of targeted genes are showed in the bar graph. The correlation coefficient between miRNA and targeted gene is showed. Gray : RT-PCR result; red: RNA-seq result. (a-f) “*nnu-miR394*” and its corresponding targeted gene. (e-h) “*miR159-3p*” and its corresponding targeted gene.

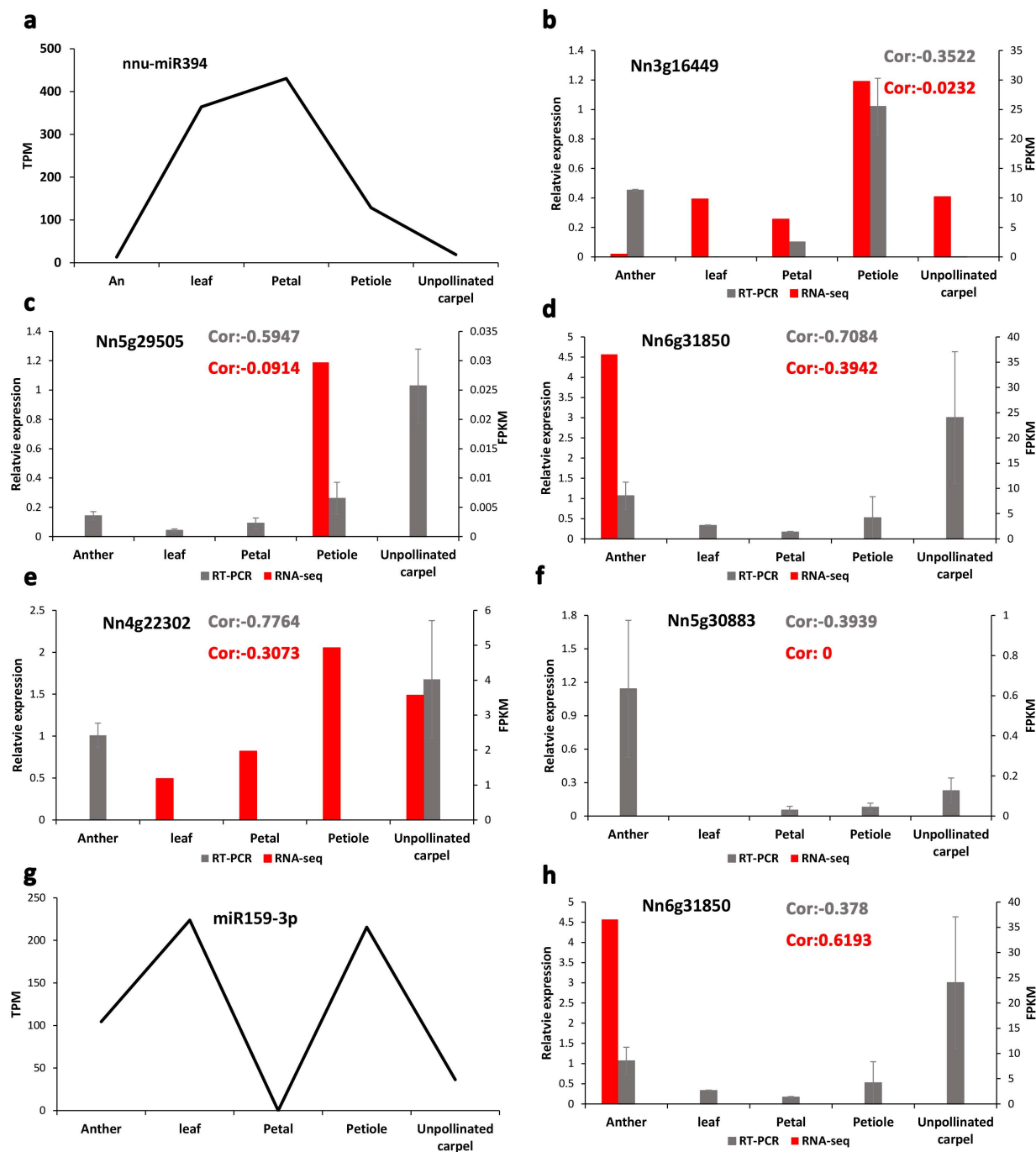
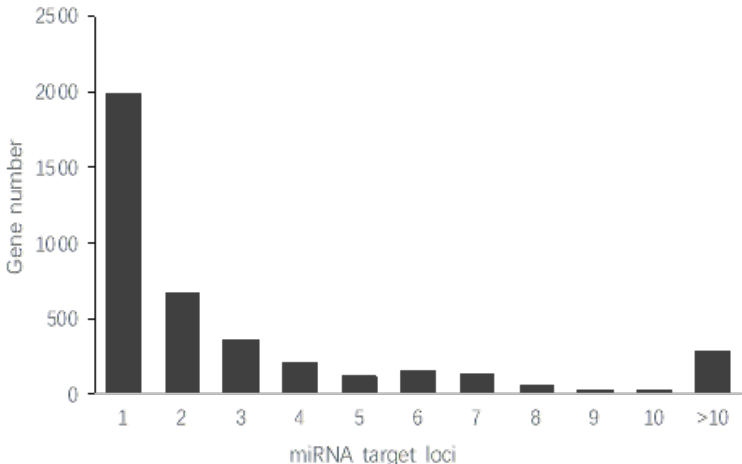


Fig. S6 Characterization of identified miRNAs target loci of lotus. a) The distribution of miRNAs target loci in genes. b) The distribution of miRNAs target loci in isoforms

a



b

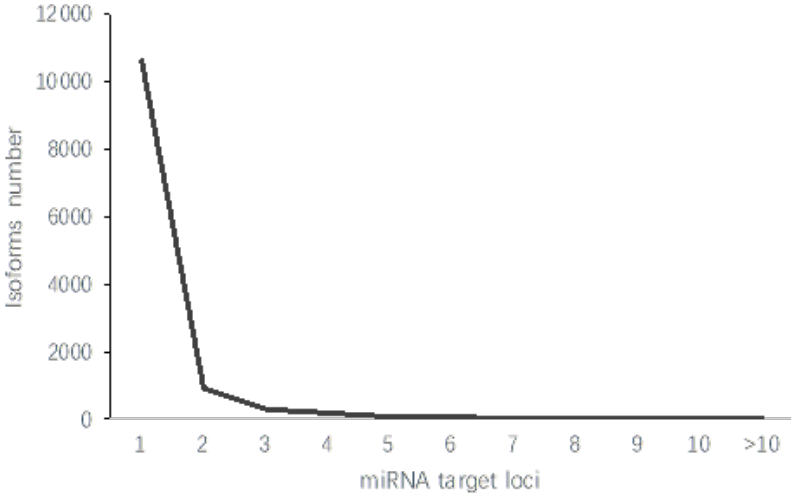


Fig. S 7 The target analysis of miRNA and isoforms. The upper part show that the blue box-line is the construct of isoforms and the down part was the target loci of gene's different isoforms.

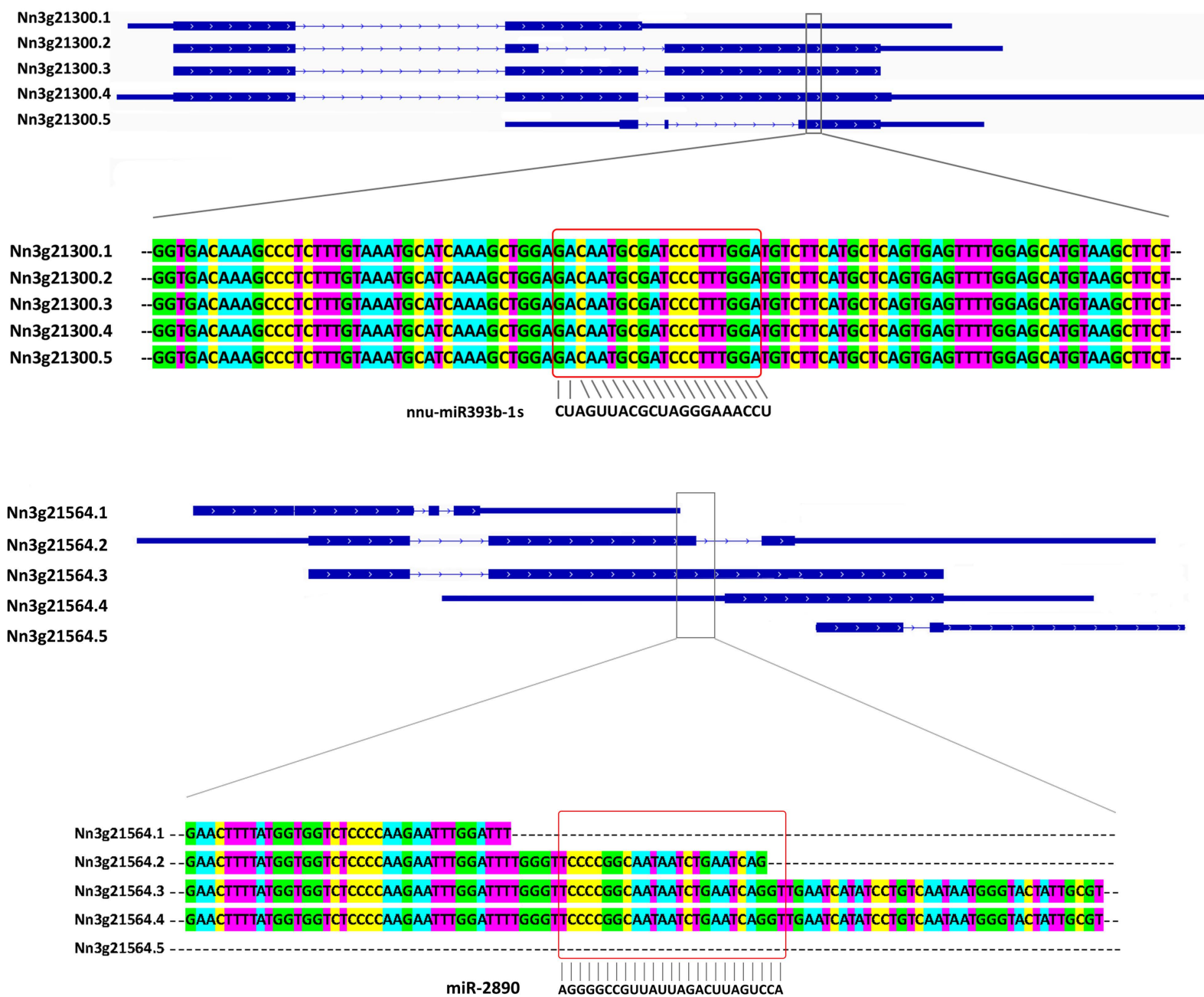


Fig. S8 The expression analysis of miRNA targeted isoforms and non-miRNA targeted isoforms from same genes in lotus six samples.

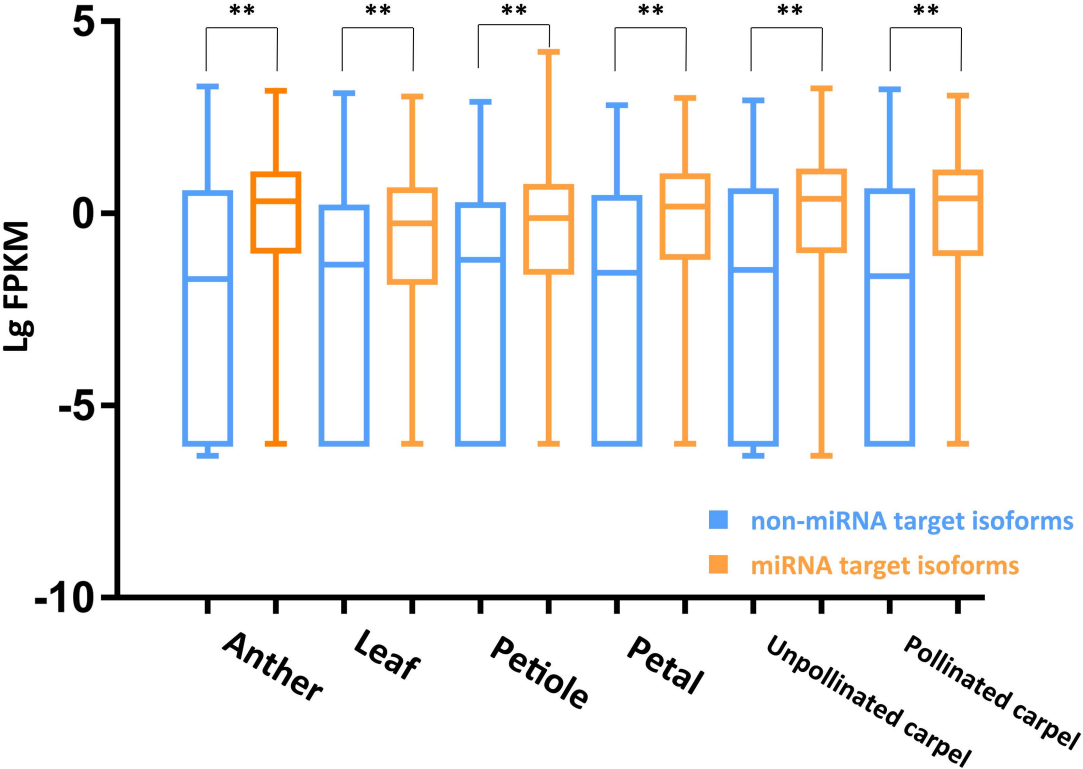


Fig. S9 The GO and its enrichment analysis of all miRNAs target genes

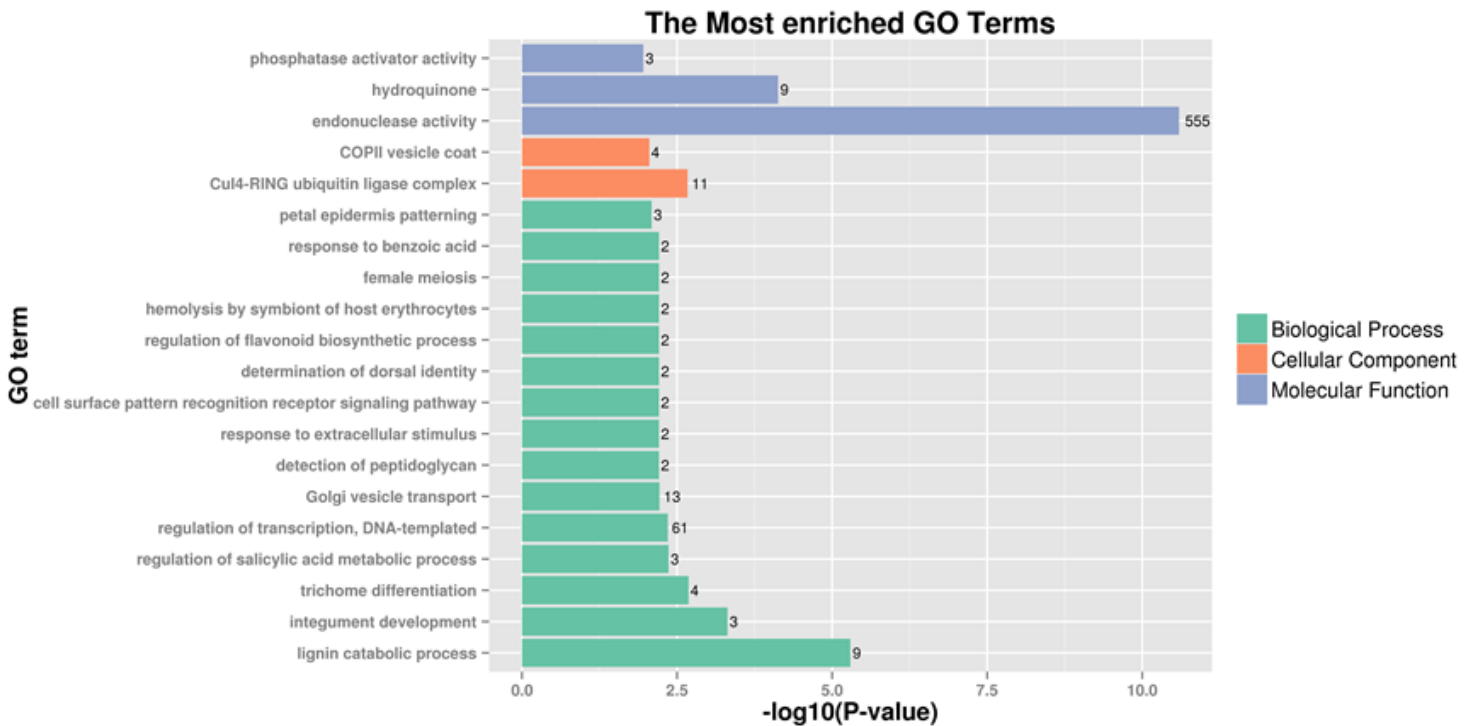
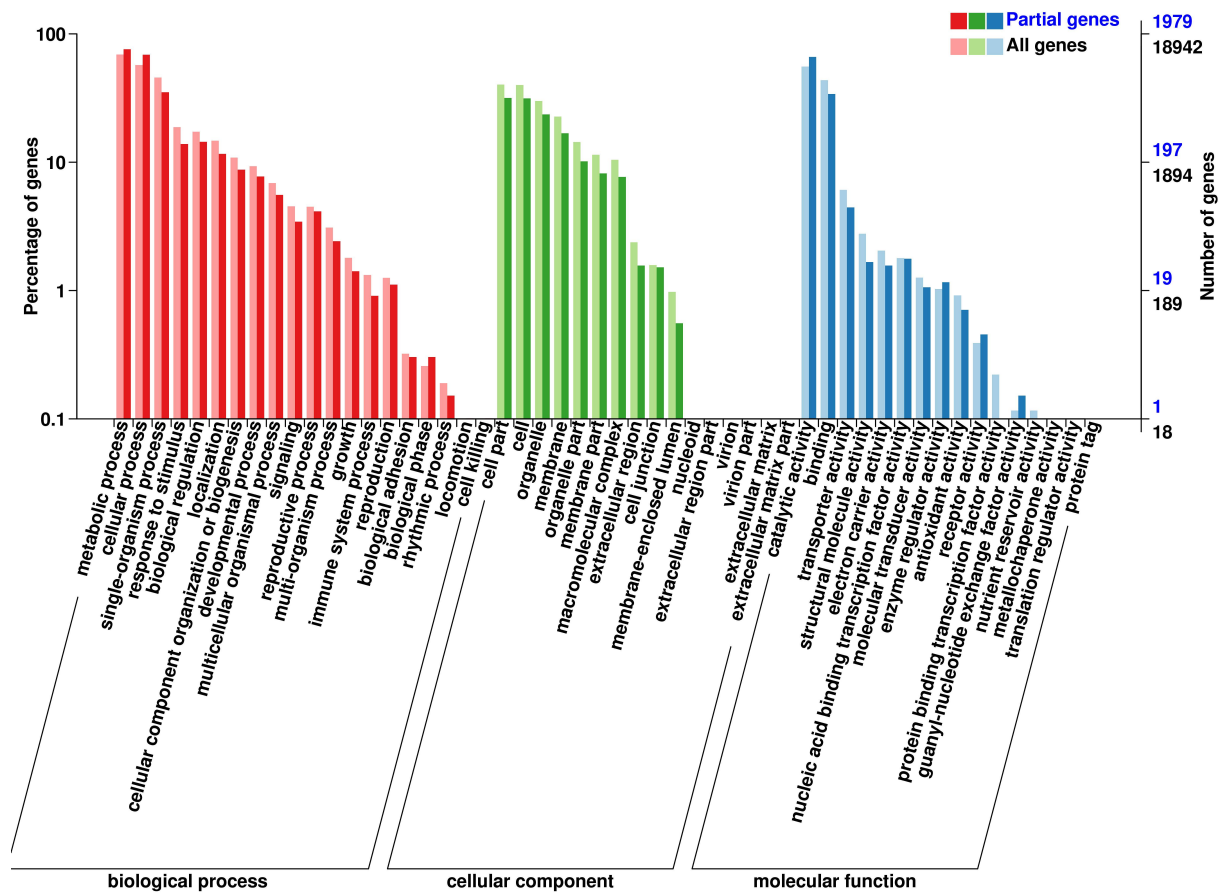
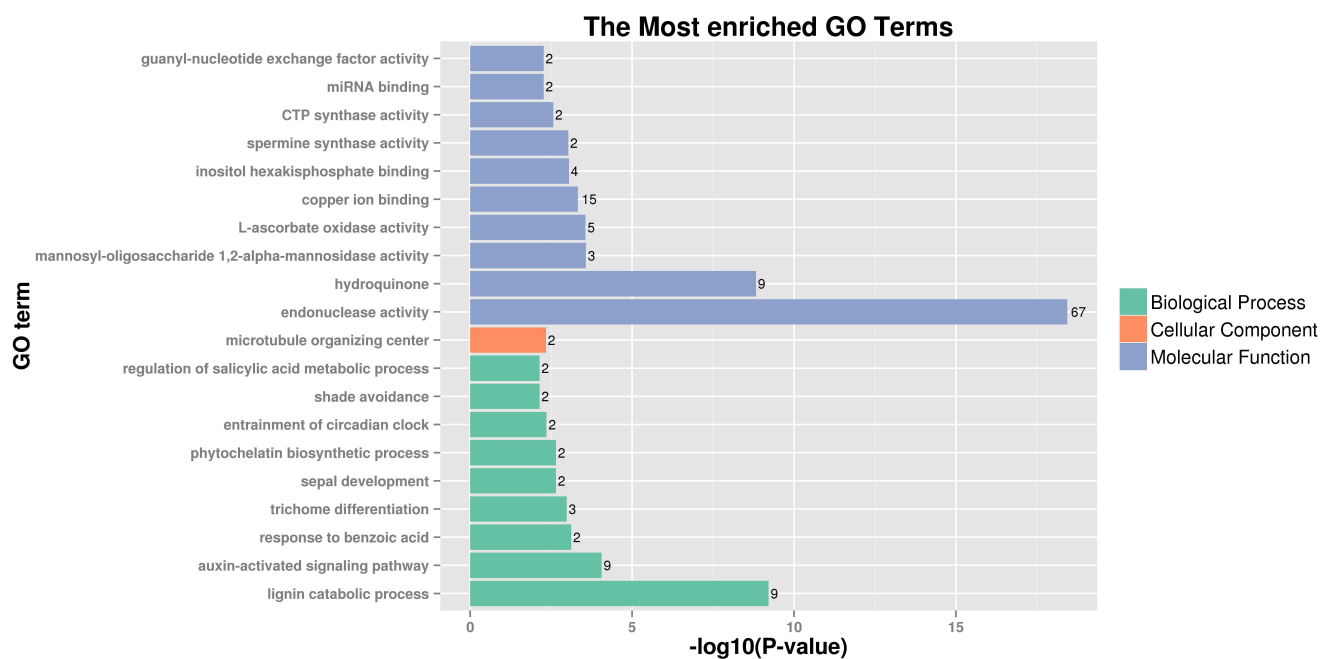
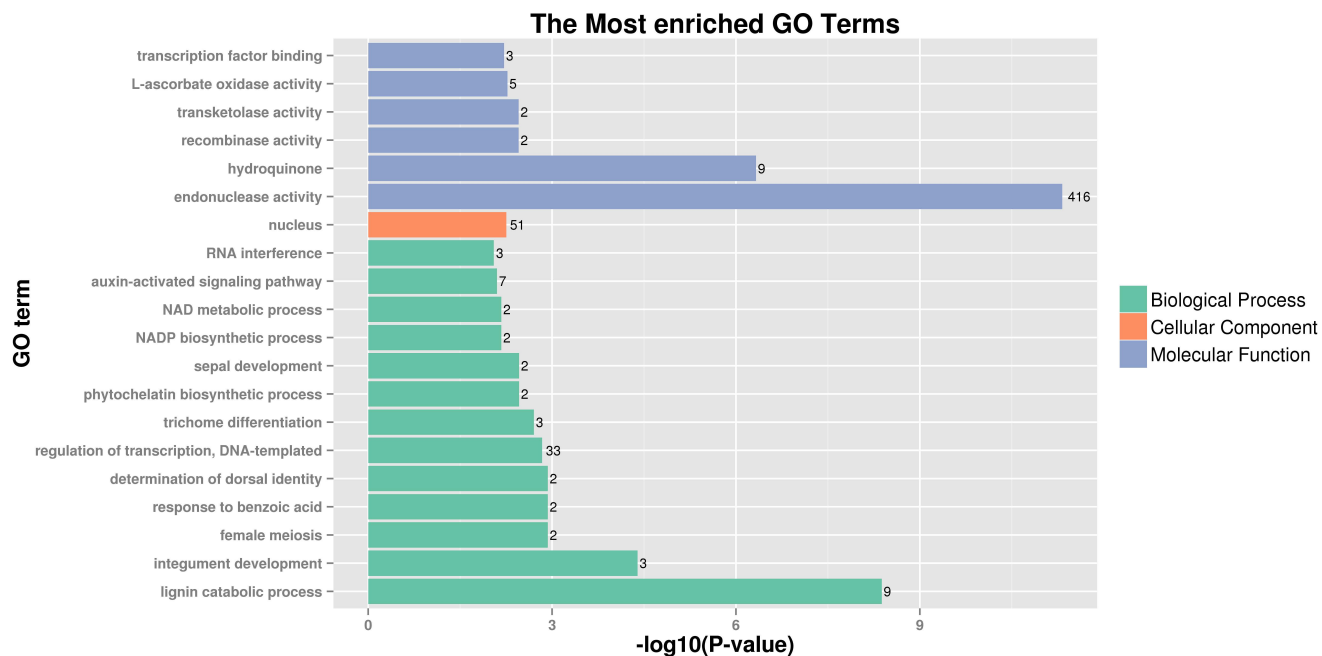


Fig. S10 The GO enrichment analysis in 6 samples. a) anther; b) leaf; c) petal; d) petiole; e) unpollinated carpel ; f) pollinated carpel.

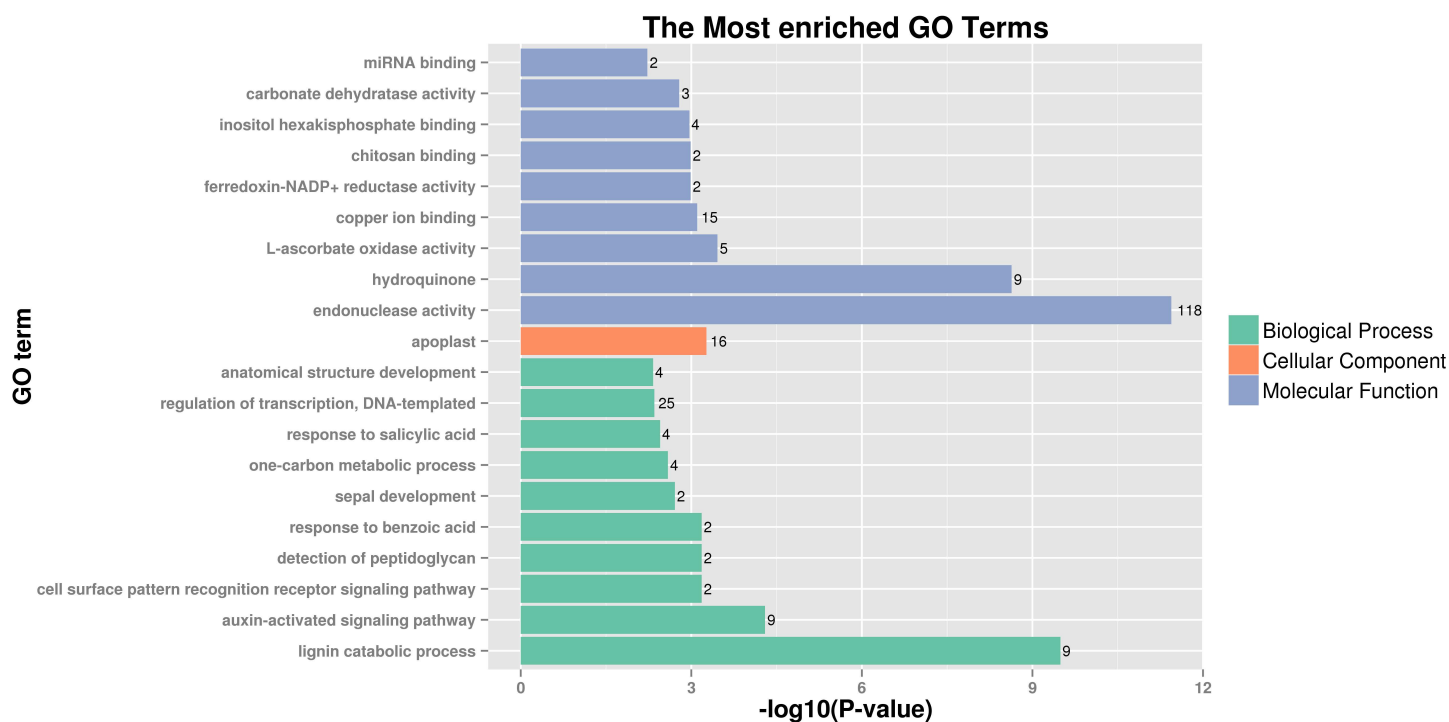
Anther



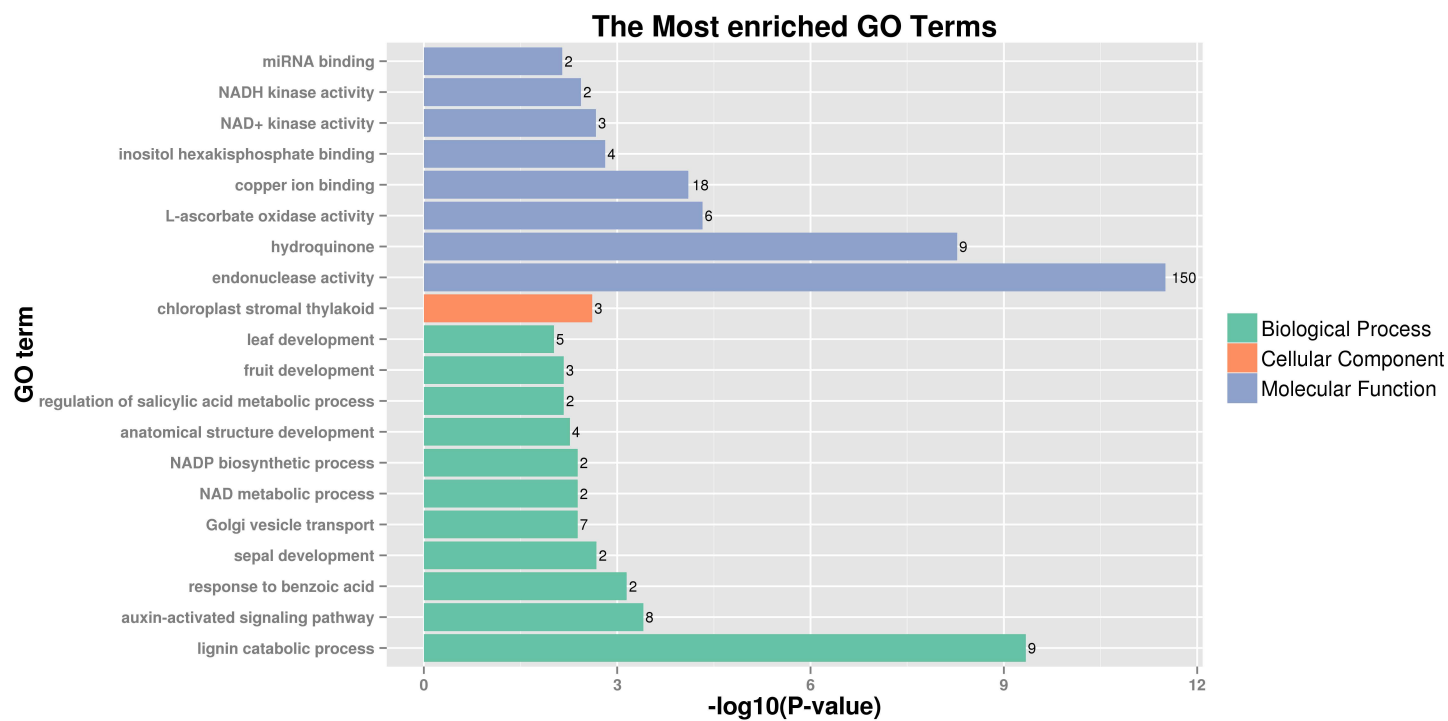
Leaf



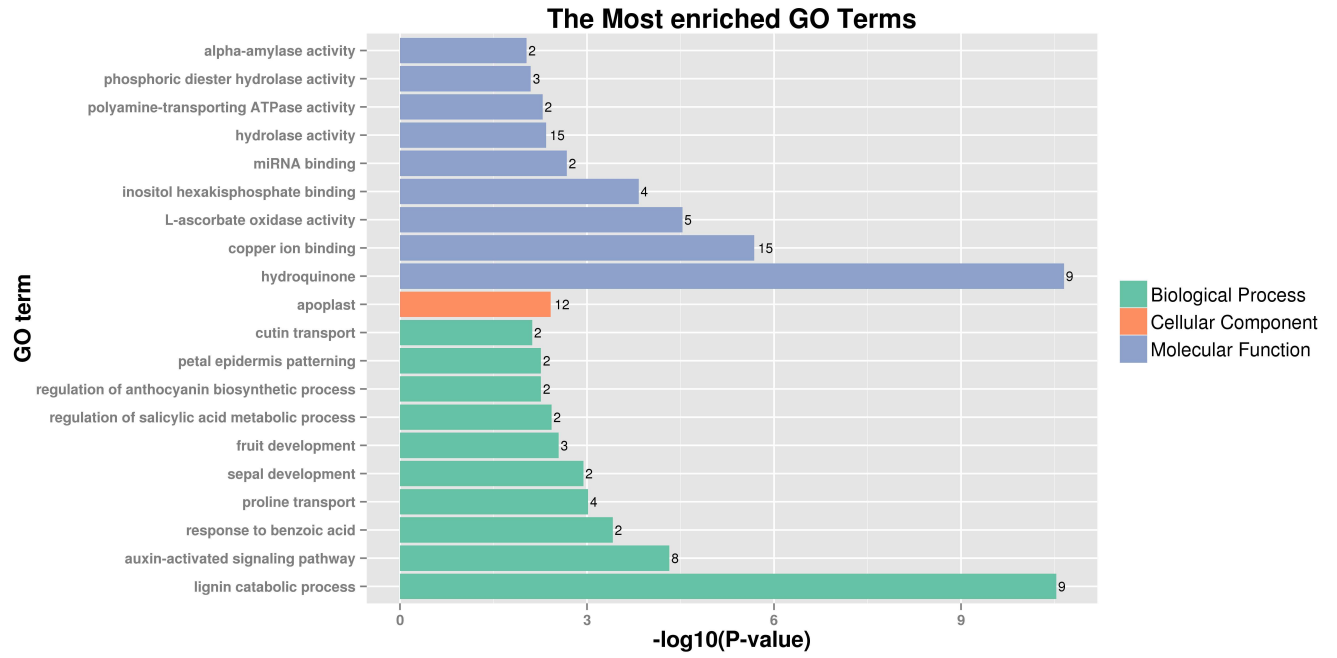
Petal



Petiole



Unpollinated carpel



Pollinated carpel

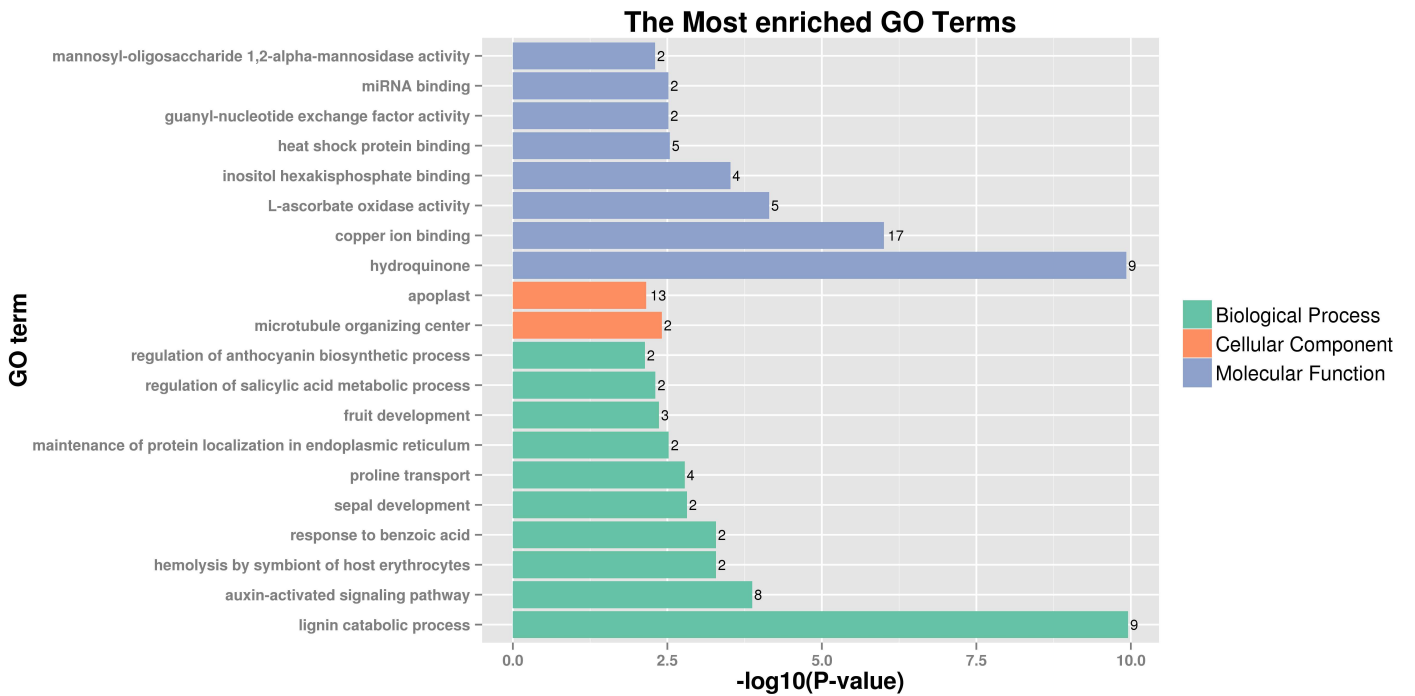


Fig. S11 Heatmap of filtered isoforms in 6 samples. The expression level is displayed with different color based on \log_2 (FPKM).

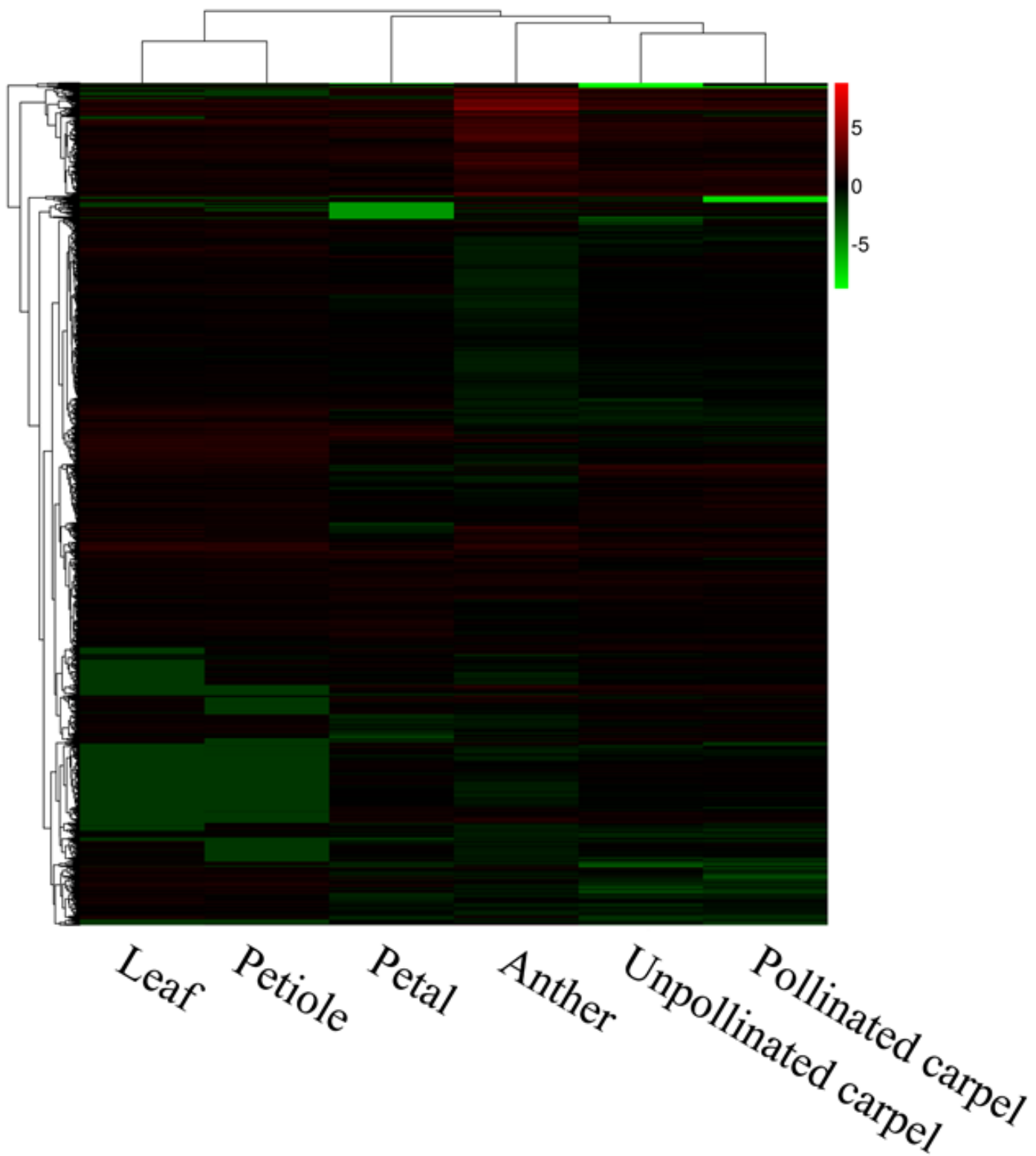
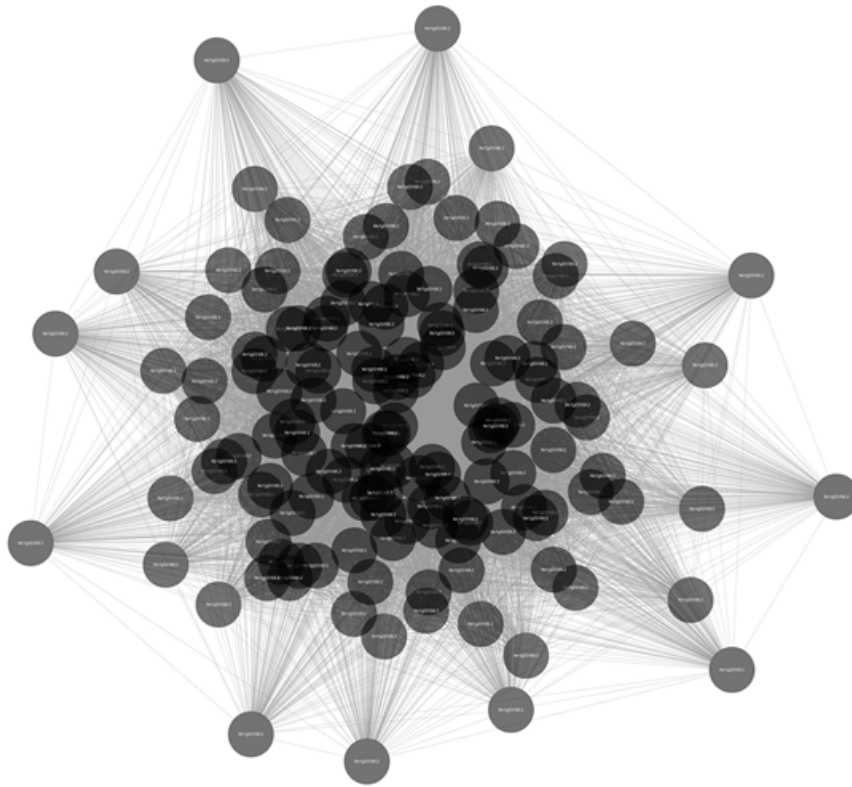
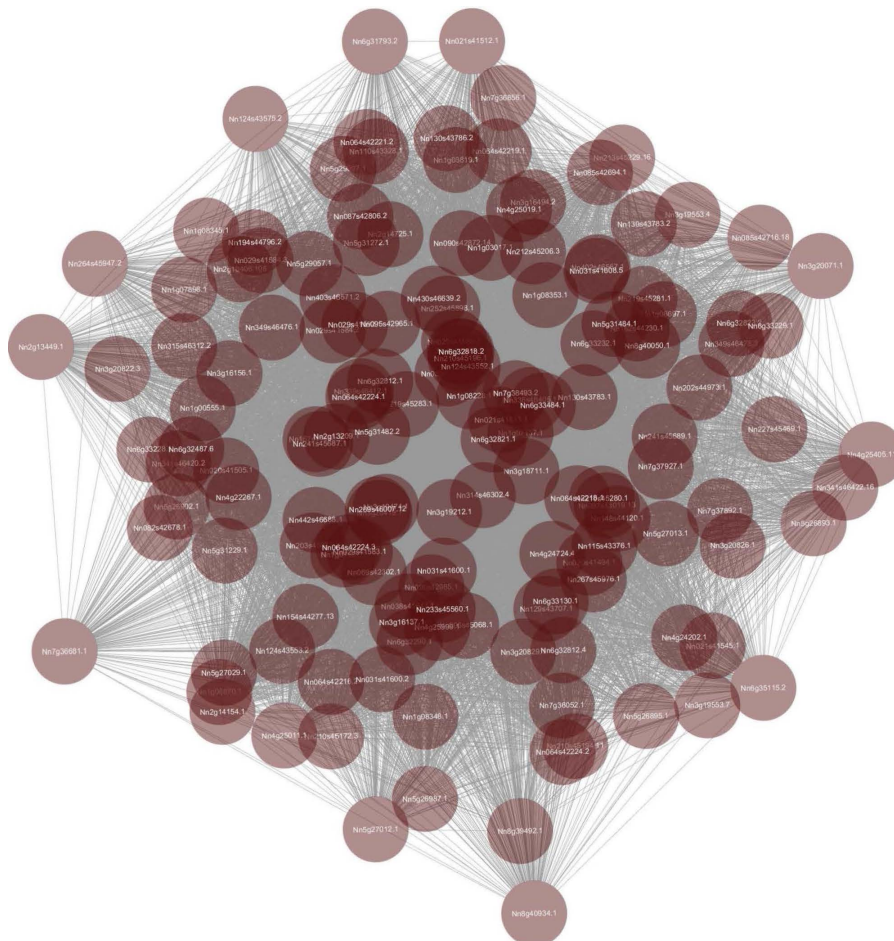


Fig. S12 The correlation network of hub isoforms in each module.

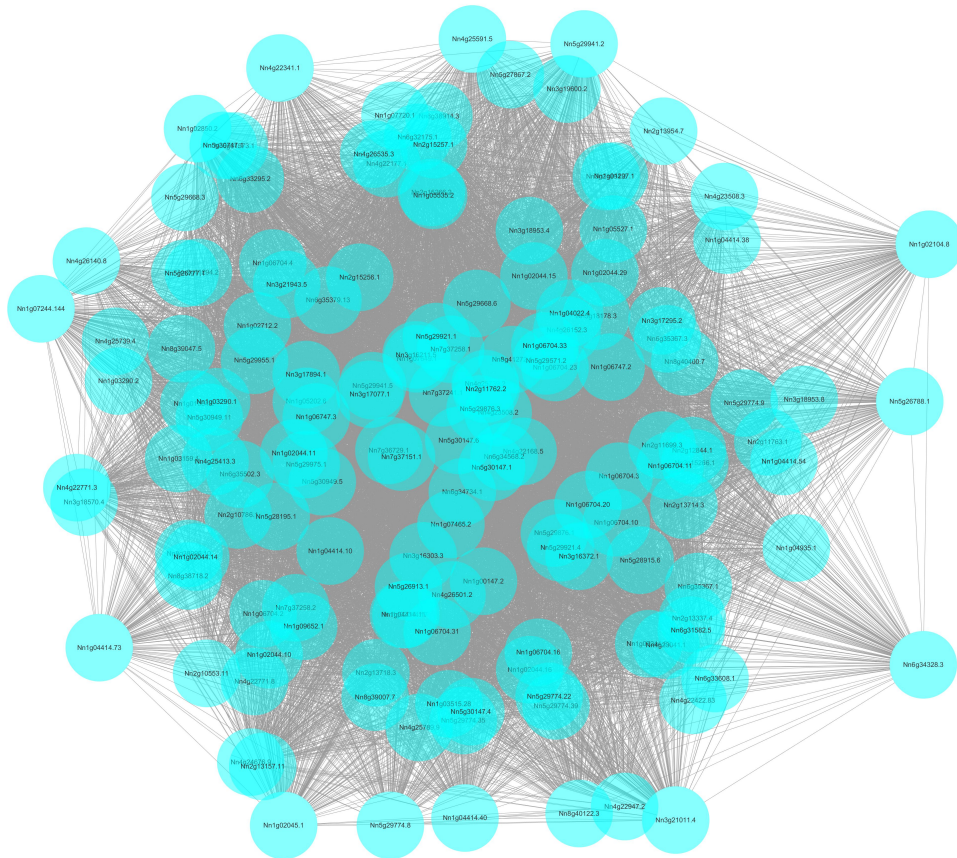
Black



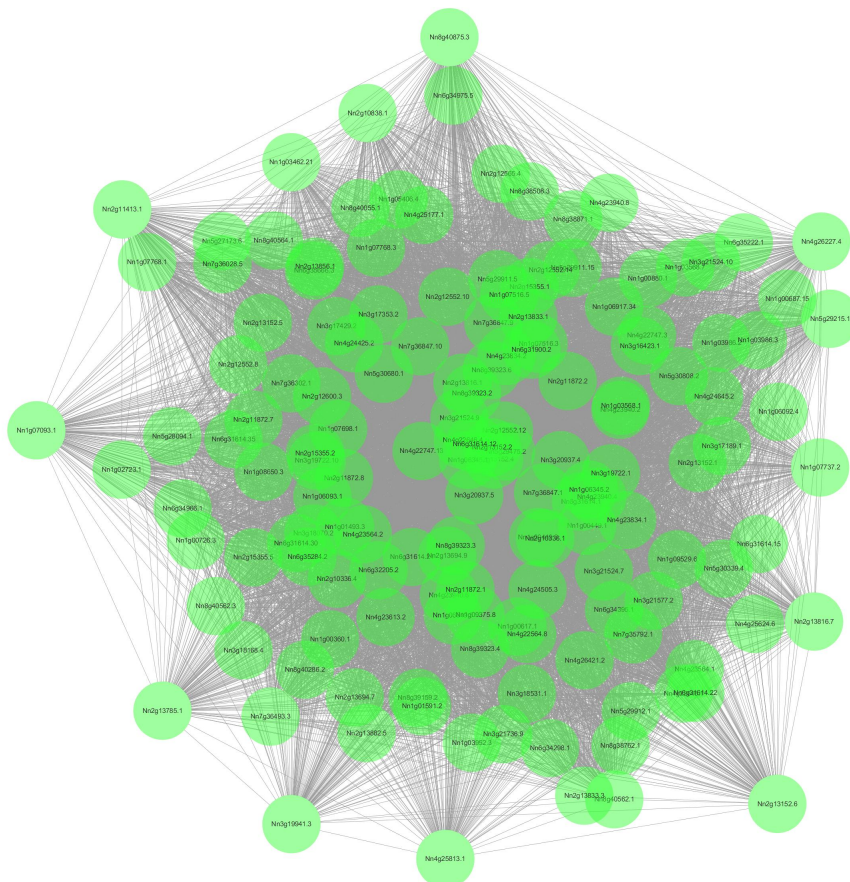
Brown



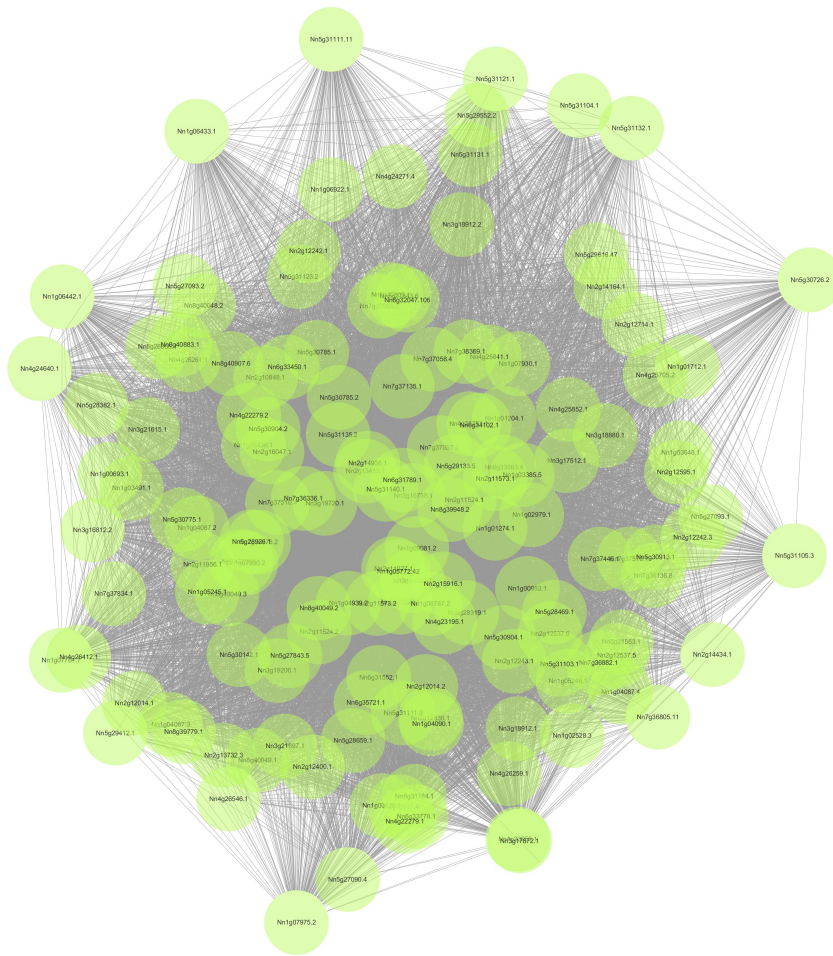
cyan



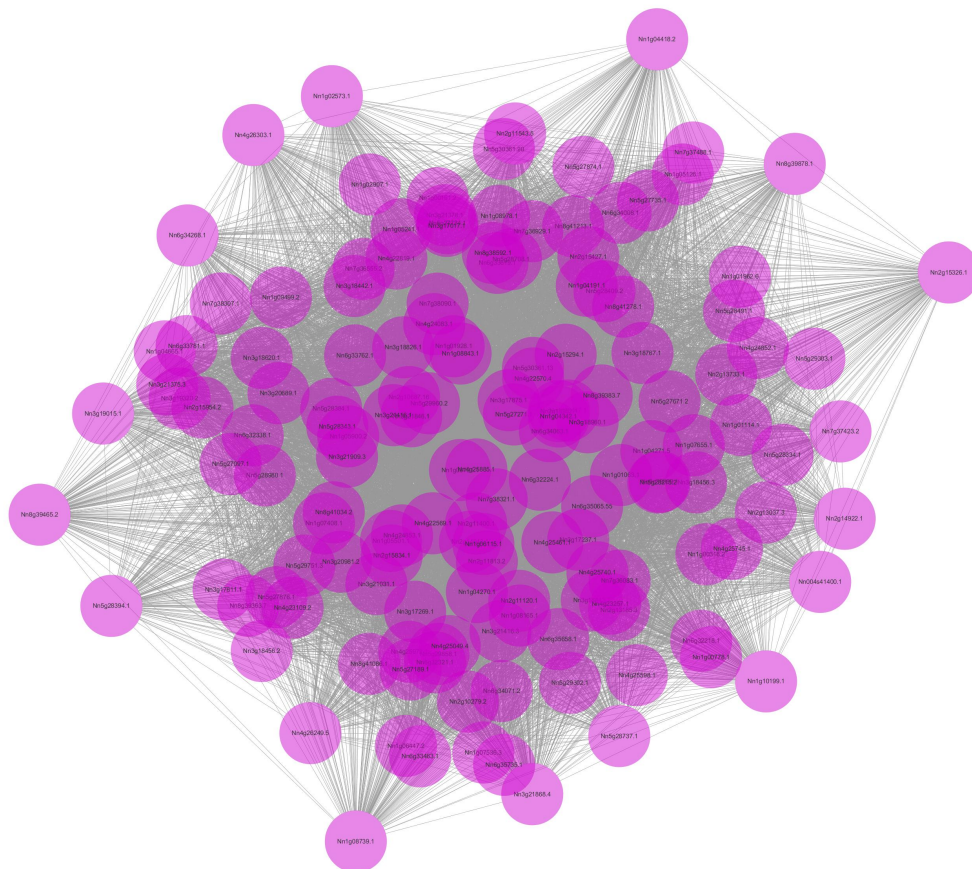
green



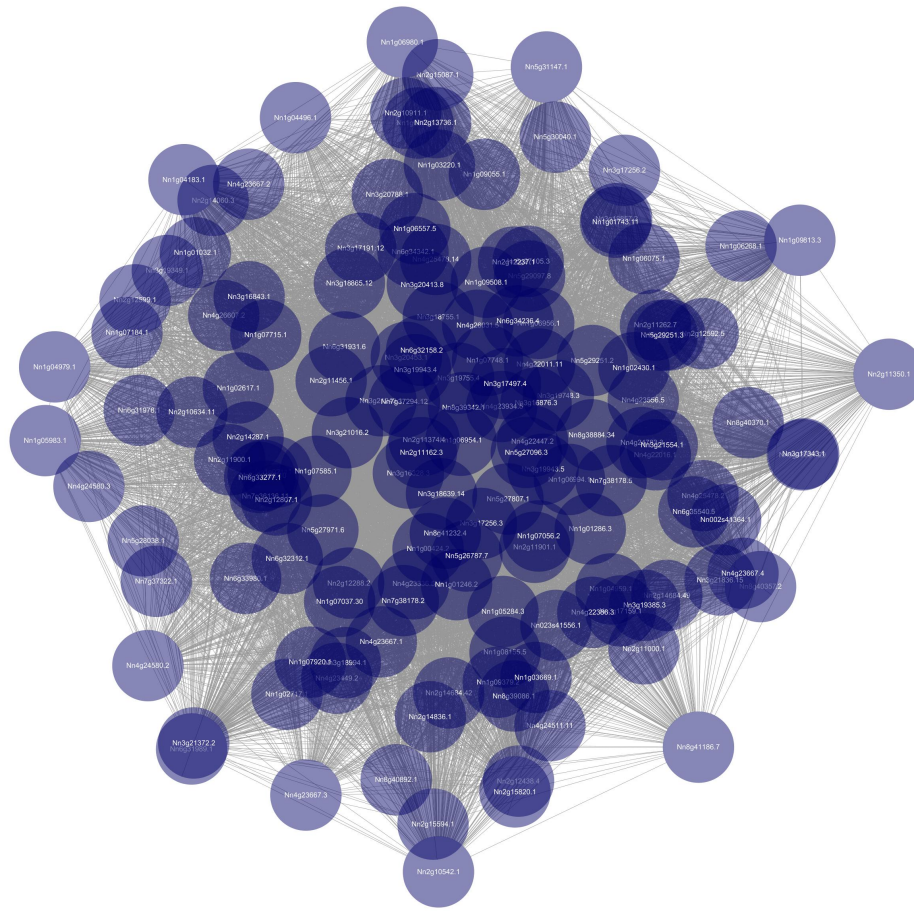
greenyellow



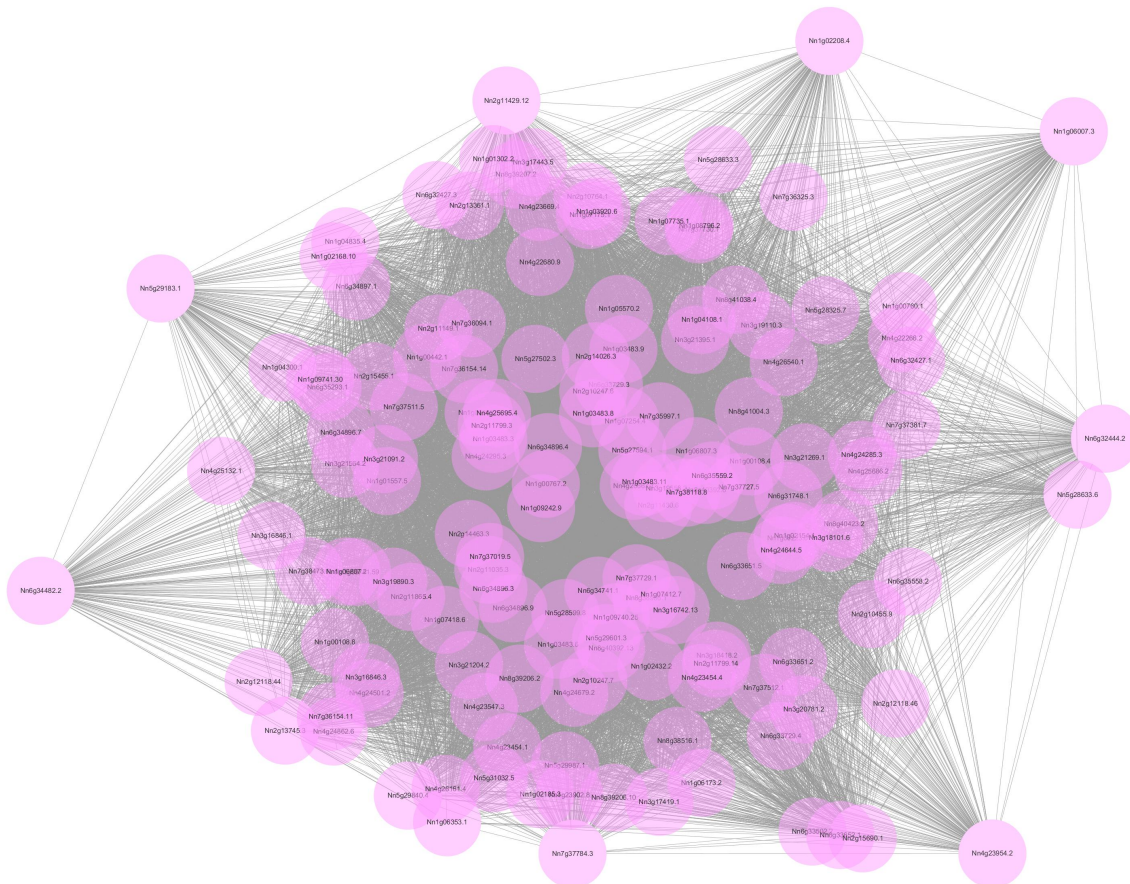
megenta



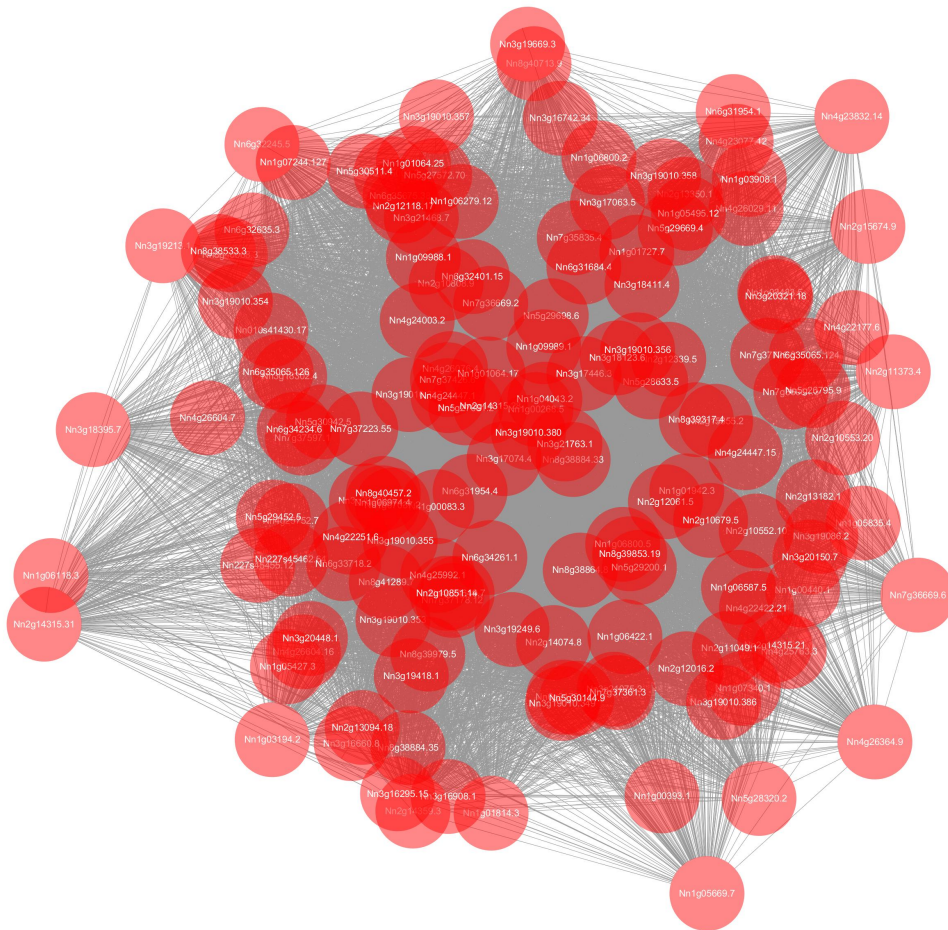
midnightblue



pink



red



yellow

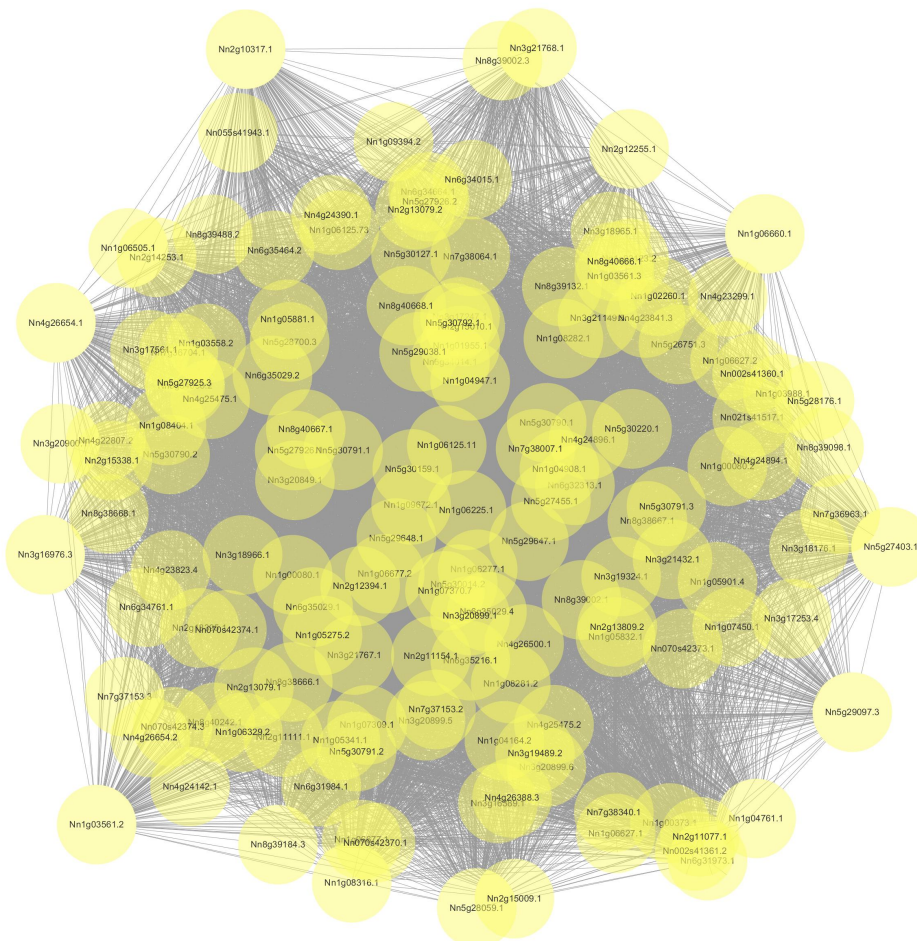


Fig. S13 The correlation analysis between different modules.

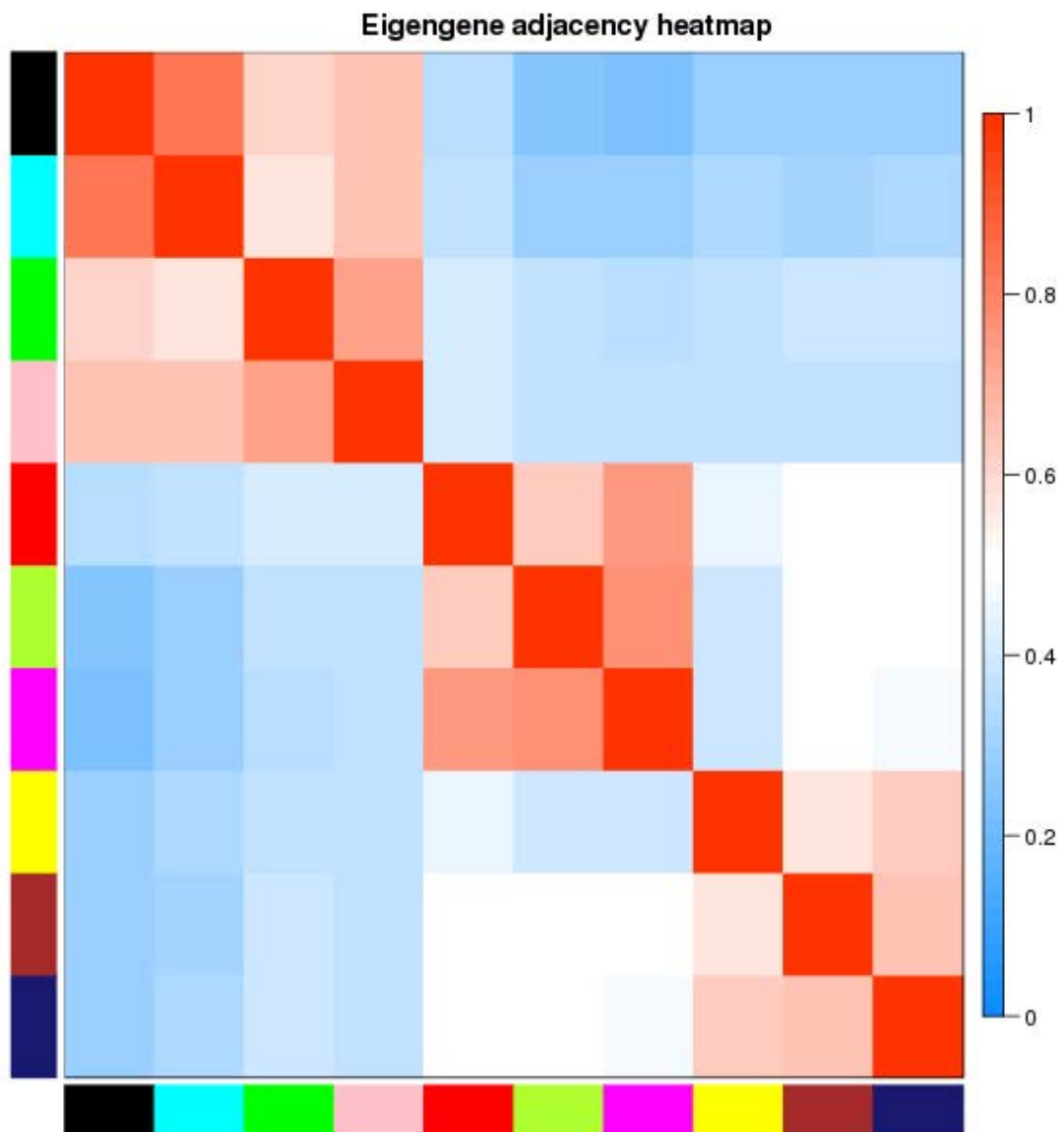
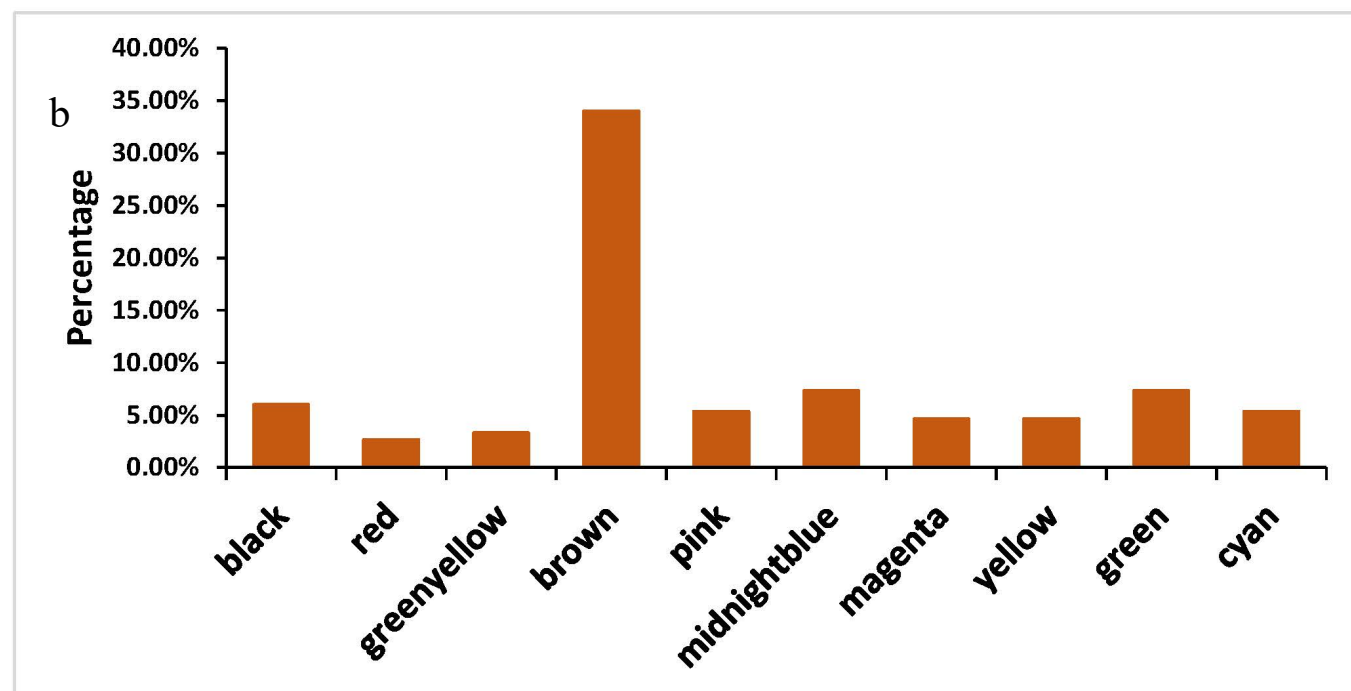
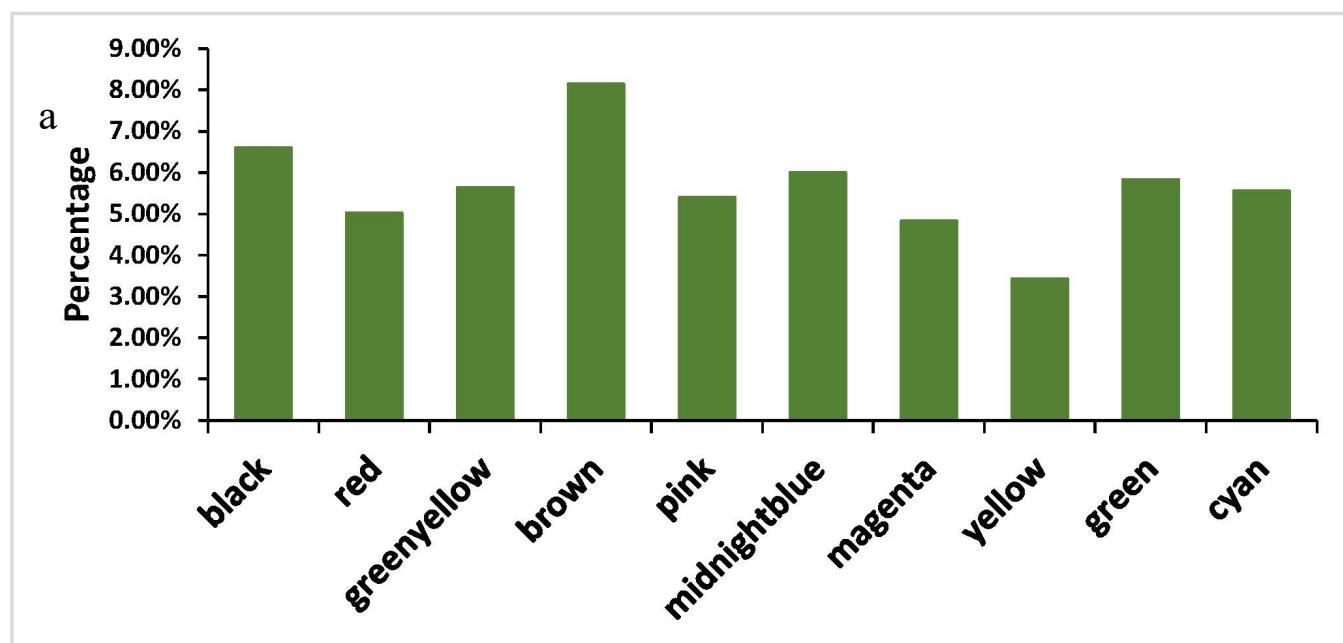


Fig. S14 The percentage of miRNA target isoforms in all isoforms. a) the percentage of miRNA targeted isoforms in each module isoforms. b) the percentage of miRNA targeted isoforms in hub isoforms of each module. c) the χ^2 test analysis between the the proportion of isoforms in all modules being targeted by miRNAs and the corresponding proportion of isoforms in hubs



c

module	black	red	greenyellow	brown	pink	midnightblue	magenta	yellow	green	cyan
p-value	0.781	0.213	0.259	1.26E-17	0.975	0.565	0.932	0.450	0.481	0.912

Fig. S15 The isoform module distribution of a IDDM gene “Nn5g29774”. The isoforms which are filtered out are transparent linked by imaginary line. The module isoforms are colored in the color of corresponding module. The isoforms targeted by miRNAs are linked by blue line.

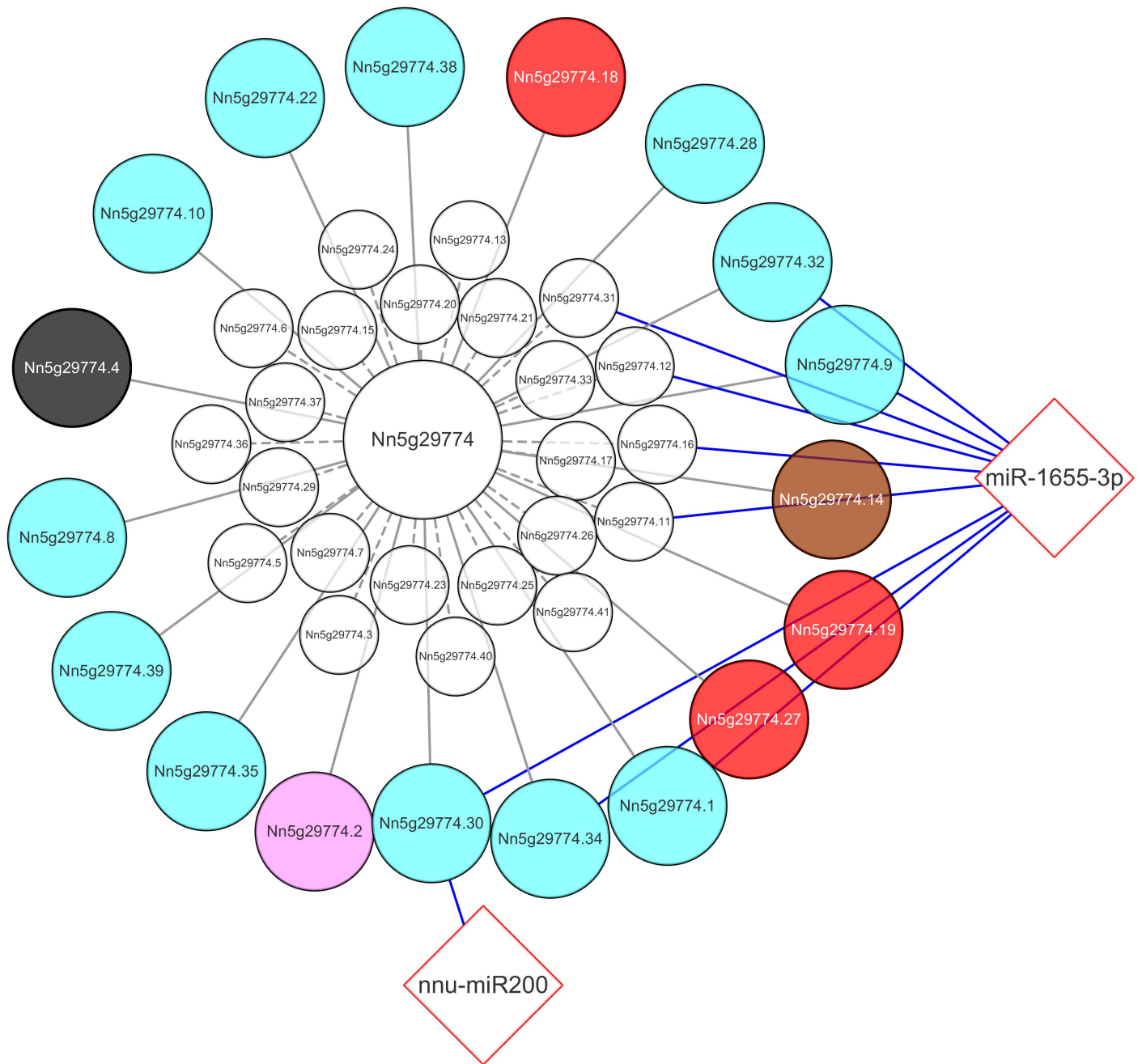


Fig. S16 The homology analyses of filtered isoforms between lotus and rice/Arabidopsis. The inside track is the result of genes which had at least two isoforms mapped to the rice/Arabidopsis. The out track is the result of genes whose isoforms divided into different modules. Gene can be divided into three categories: different isoforms from the same lotus gene with their closest homologs being different genes in rice or Arabidopsis (I); different isoforms from the same lotus gene with their closest homologs being the same one isoform from one gene in rice or Arabidopsis (II); different isoforms from the same lotus gene with their closest homologs being different isoforms from one gene in rice or Arabidopsis (III)

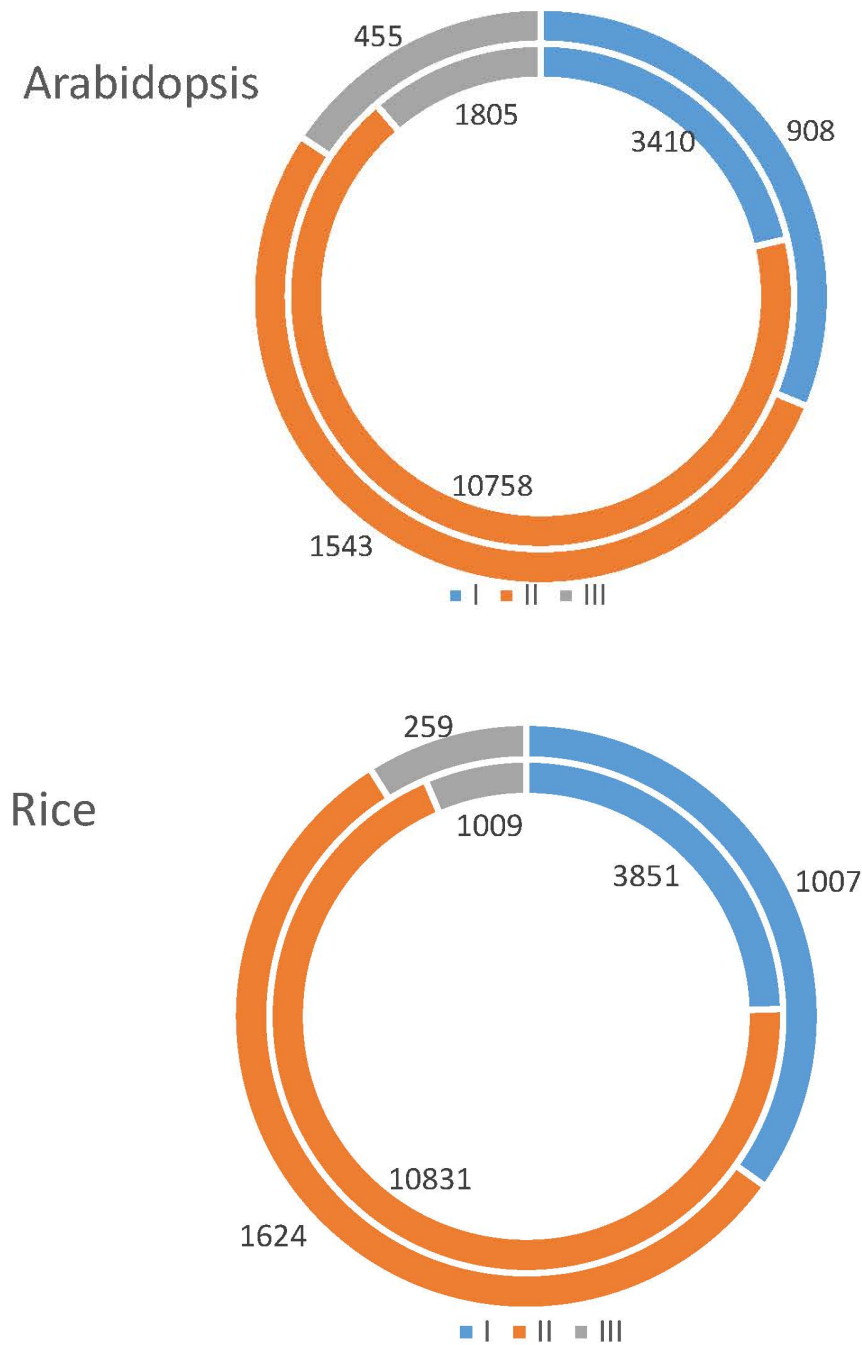


Fig. S17 Plant hormone signal transduction pathway and related miRNAs

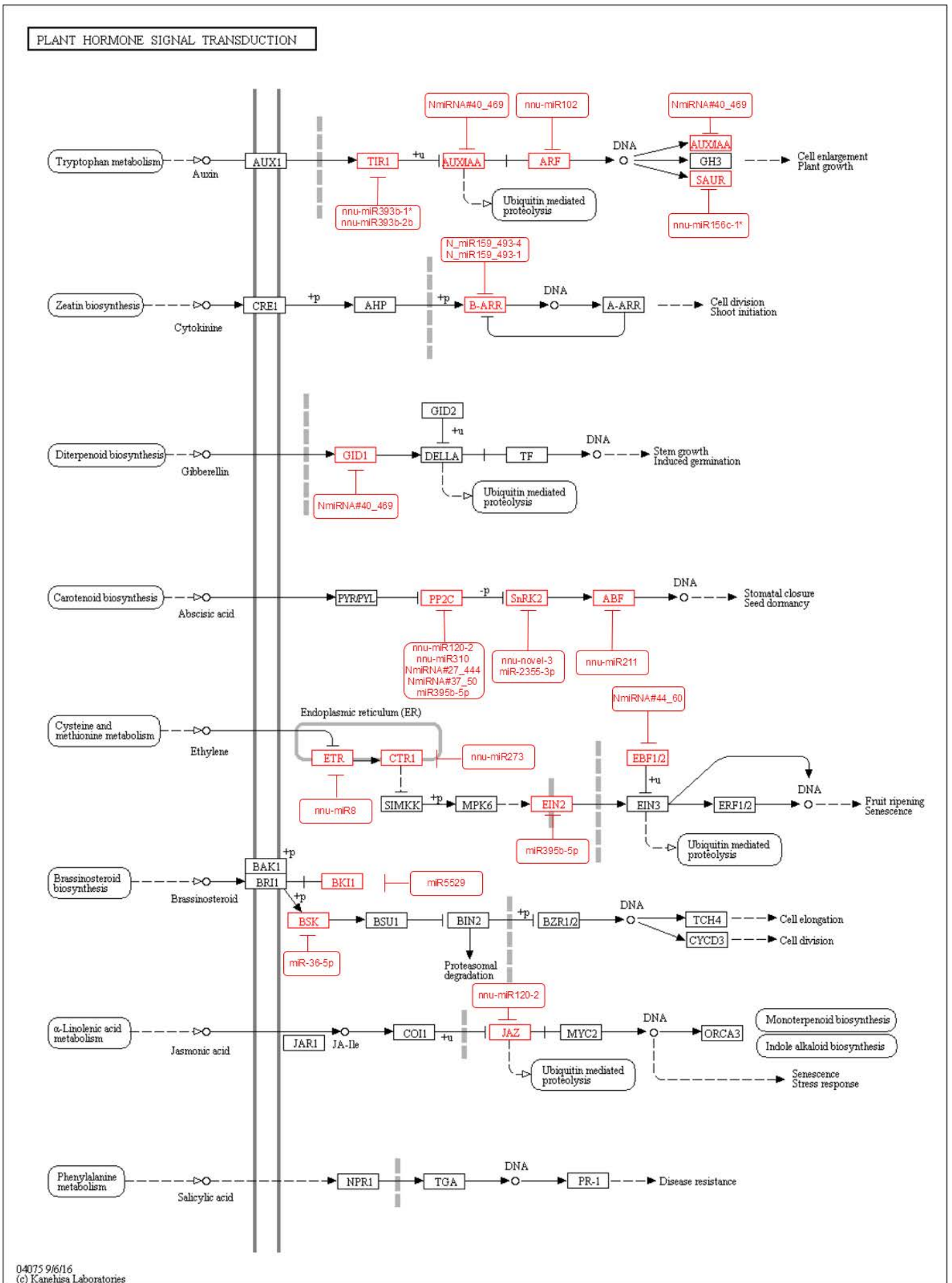


Fig. S18 Plant hormone signal transduction pathway gene and its ortholog genes' isoforms

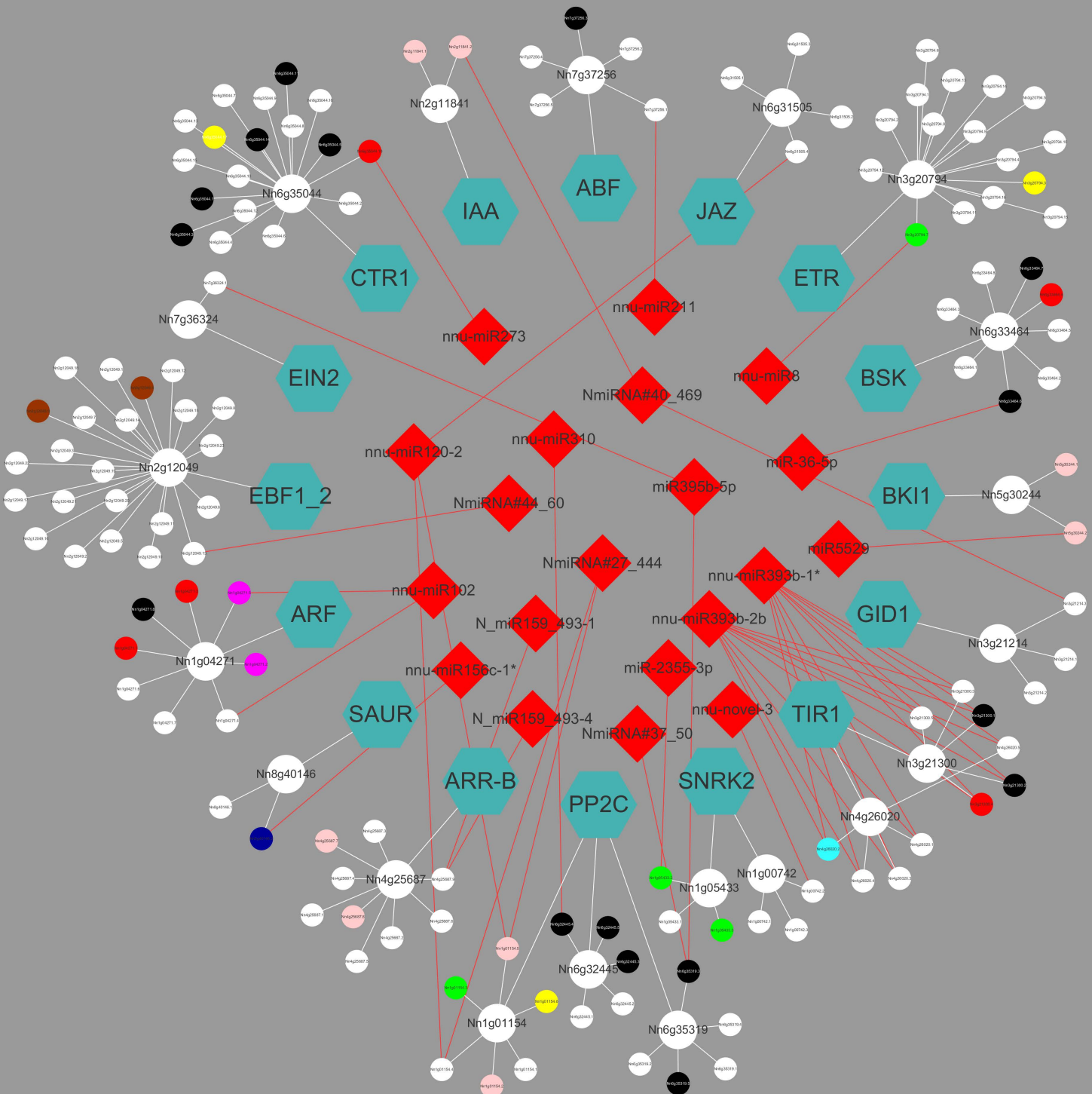


Fig. S19 The expression analysis of abscisic acid-associated genes and related miRNAs expression.

