

Appendix

Supporting Information

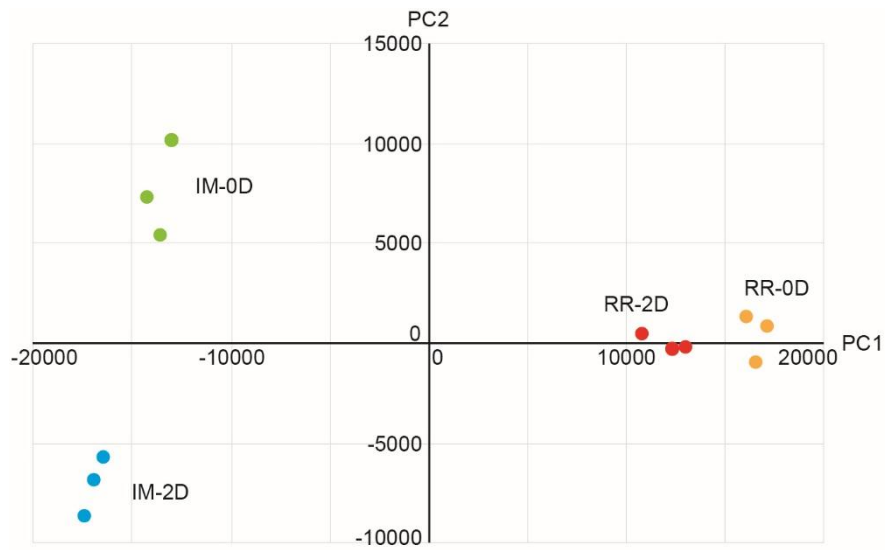


Figure S1 Principle component analysis (PCA) of the RNA-seq datasets

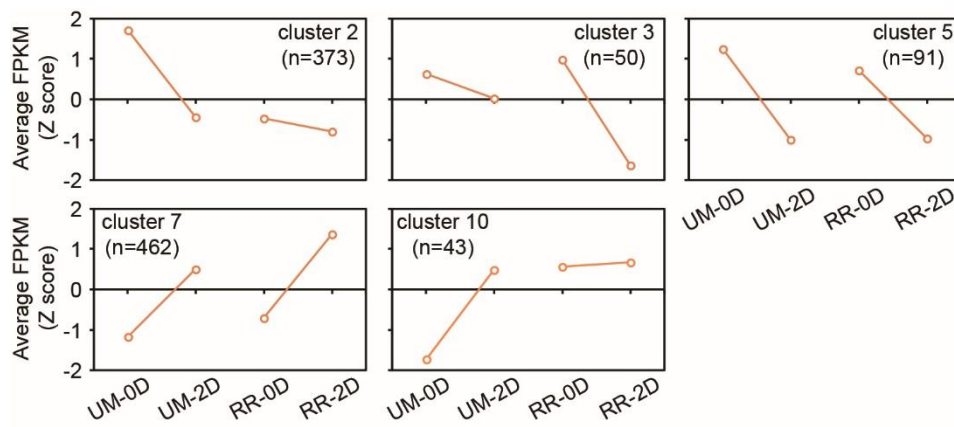


Figure S2 Co-expression patterns of the DEGs identified by pairwise comparison of the four RNA-seq treatments. The y axis indicates the normalized FPKM (Z score).

Table S1. Primer used for qRT-PCR analysis

Gene name	Gene ID	Primer sequence (5'-3')	
		Forward primer	Forward primer
<i>4CL</i>	<i>Solyc06g068650</i>	TTCACCTCAGGGATATCATGCTCATC	CATGTGAACAAGGTGAAGGATTATGC
<i>ANS</i>	<i>Solyc08g080040</i>	GAACTAGCACTTGGCGTCGAA	TTGCAAGCCAGGCACCATA
<i>CHI</i>	<i>Solyc05g010320</i>	CGGCGCAGGGAATAGAGGTTT	CCGTCAAGGGCAAGATCATAGTCAC
<i>DFR</i>	<i>Solyc02g085020</i>	AGTCCAAGGATCCAGAGAACGAAGTA	TGGACATCAAGAGTTCCAGCAGAT
<i>F3H</i>	<i>Solyc02g083860</i>	GTGAAAAGTTGATGGATTTGGC	GTAATGGTTCCTGGATCGGTGTGT
<i>F3'5'H</i>	<i>Solyc11g066580</i>	GGTACATGTGGGATGGTTGTTGC	ACTTCCAACGTGGTCCATAGGG
<i>SLACTIN</i>	<i>Solyc03g078400</i>	GGGATGGAGAAGTTTGGTGGTGG	CTTCGACCAAGGGATGGTGTAGC
<i>SLAN1</i>	<i>Solyc09g065100</i>	CTAAGAGTGCCCGCATACAGAC	ATCCGAAGTGGAGTGCTCAGATA
<i>SLAN2-like</i>	<i>Solyc10g086290</i>	CAAGCTTCTAGGCAATAGATGGTCACT	TTGGTCGTGGTCGTAGTATAGTGC
<i>SIHY5</i>	<i>Solyc08g061130</i>	TCTATTGCCGCTAGTTCCTACTAC	GGCACTCTTCTGATCTCATCAT

Primer sequences were taken from our previous study (Cao *et al.*, 2017).

Table S2. Summary of the transcriptome data.

Sample	Raw reads	Unique mapped reads
IM-2D-1	26,687,545	22,359,437
IM-2D-2	23,249,026	19,525,114
IM-2D-3	22,911,485	18,981,050
RR-2D-1	23,699,982	20,168,114
RR-2D-2	24,725,132	20,955,826
RR-2D-3	23,641,723	20,076,151
IM-0D-1	25,668,053	21,570,979
IM-0D-2	25,685,396	21,360,007
IM-0D-3	25,613,901	21,393,245
RR-0D-1	22,959,477	19,475,948
RR-0D-2	21,924,746	18,555,827
RR-0D-3	22,655,264	19,221,291