

Appendix A

Table S1 Statistics of sequencing data output

Sample	Clean reads	Clean bases	GC content (%)	N (%)	Q20 (%)	Q30 (%)
BB-1	27220535.00	8144591130.00	43.14	0.02	96.33	91.40
BB-2	24324369.00	7274478118.00	43.11	0.02	96.26	91.31
BB-3	27398483.00	8199566706.00	43.01	0.02	96.19	91.15
RR-1	24138960.00	7225565490.00	42.93	0.02	96.30	91.36
RR-2	27356867.00	8187611288.00	42.59	0.02	95.99	90.79
RR-3	24665857.00	7383823862.00	42.91	0.02	96.17	91.10
RB-1	22558877.00	6732823606.00	43.22	0.02	96.27	91.33
RB-2	22226279.00	6641270222.00	43.06	0.02	96.13	91.08
RB-3	34683952.00	10376910660.00	43.19	0.02	95.81	90.48

BB-1, BB-2, BB-3: 100% blue LEDs treatment; RR-1, RR-2, RR-3: 100% red LEDs treatment;
RB-1, RB-2, RB-3: 75% red + 25% blue LEDs treatment

Appendix B

Table S2 Results of transcriptome sequencing data mapped to reference genes

Sample	Total reads	Mapped reads	Unique mapped reads	Multiple mapped reads	Only mapped to plus strand	Only mapped to minus strand
BB-1	54,441,070	45,443,265 (83.47%)	43,646,795 (80.17%)	1,796,470 (3.30%)	22,507,367 (41.34%)	22,651,418 (41.61%)
BB-2	48,648,738	40,138,389 (82.51%)	38,395,137 (78.92%)	1,743,252 (3.58%)	19,858,426 (40.82%)	20,007,465 (41.13%)
BB-3	54,796,966	45,780,518 (83.55%)	43,833,037 (79.99%)	1,947,481 (3.55%)	22,588,132 (41.22%)	22,783,650 (41.58%)
RR-1	48,277,920	39,636,984 (82.10%)	38,015,095 (78.74%)	1,621,889 (3.36%)	19,543,881 (40.48%)	19,719,371 (40.85%)
RR-2	54,713,734	40,147,180 (73.38%)	38,639,015 (70.62%)	1,508,165 (2.76%)	19,873,834 (36.32%)	20,005,213 (36.56%)
RR-3	49,331,714	40,572,242 (82.24%)	39,044,777 (79.15%)	1,527,465 (3.10%)	20,026,330 (40.60%)	20,197,160 (40.94%)
RB-1	45,117,754	37,962,442 (84.14%)	36,002,097 (79.80%)	1,960,345 (4.34%)	18,492,097 (40.99%)	18,803,008 (41.68%)
RB-2	44,452,558	37,335,379 (83.99%)	35,858,325 (80.67%)	1,477,054 (3.32%)	18,459,230 (41.53%)	18,589,494 (41.82%)
RB-3	69,367,904	57,964,181 (83.56%)	54,728,557 (78.90%)	3,235,624 (4.66%)	28,127,383 (40.55%)	28,664,947 (41.32%)

Total reads refers to coupled clean reads. BB-1, BB-2, BB-3: 100% blue LEDs treatment; RR-1, RR-2, RR-3: 100% red LEDs treatment; RB-1, RB-2, RB-3: 75% red + 25% blue LEDs treatment

Appendix C

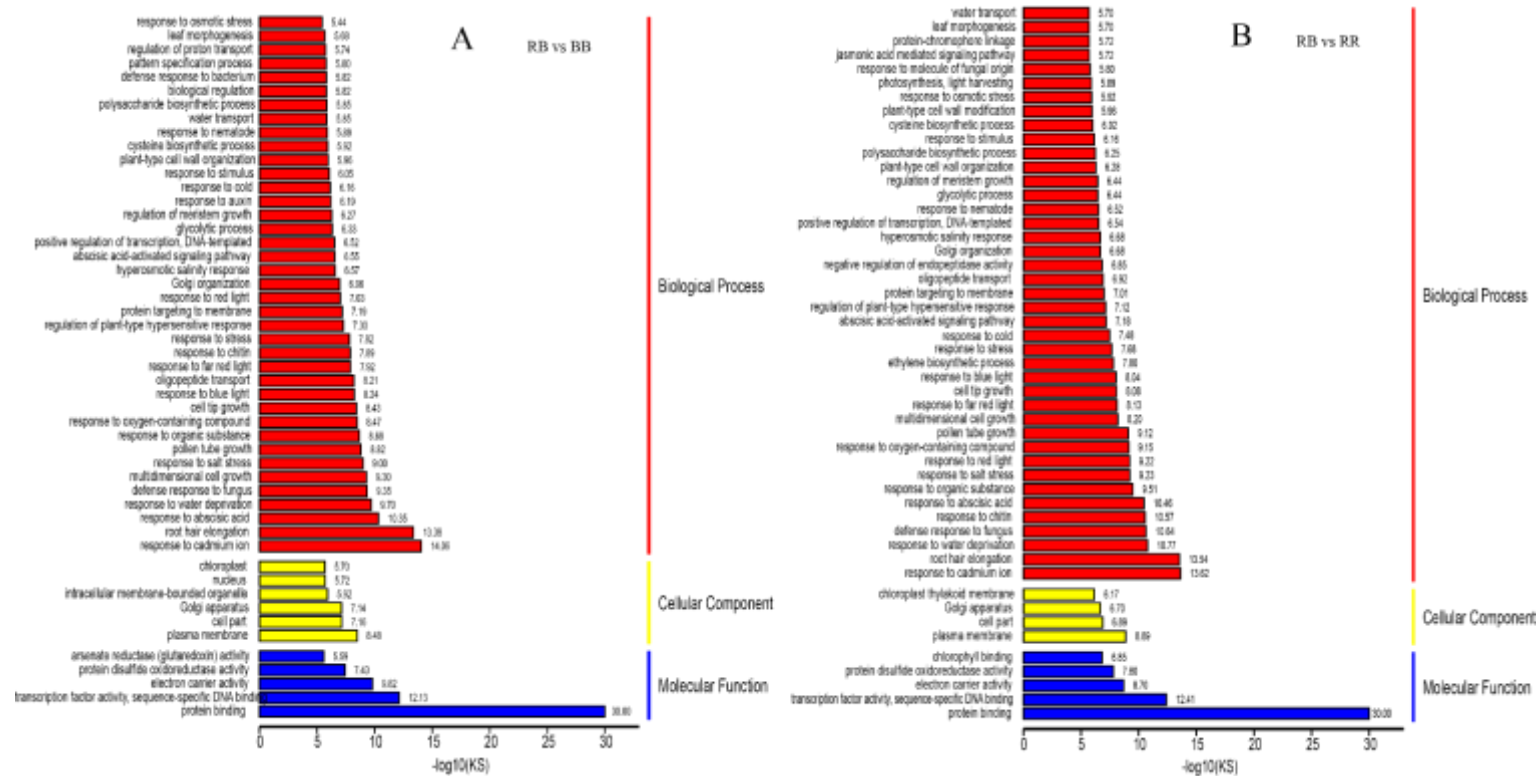


Fig S1. GO enrichment analysis of differentially expressed genes in RB vs BB and RB vs RR. RR: 100% red LEDs; BB: 100% blue LEDs; RB: 75% red + 25% blue LEDs

Appendix D

Table S3 Differentially expressed genes enriched in GO terms

Group	GO number	GO term	Total DEGs Number	Up-regualted DEGs number	Down-regulated DEGs number
RB vs BB	GO:0009535	chloroplast thylakoid membrane	0	0	0
	GO:0016168	chlorophyll binding	0	0	0
RB vs RR	GO:0009535	chloroplast thylakoid membrane	20	0	20
	GO:0016168	chlorophyll binding	5	0	5

BB: 100% blue LEDs treatment; RR: 100% red LEDs treatment; RB: 75% red + 25% blue LEDs treatment

Appendix E

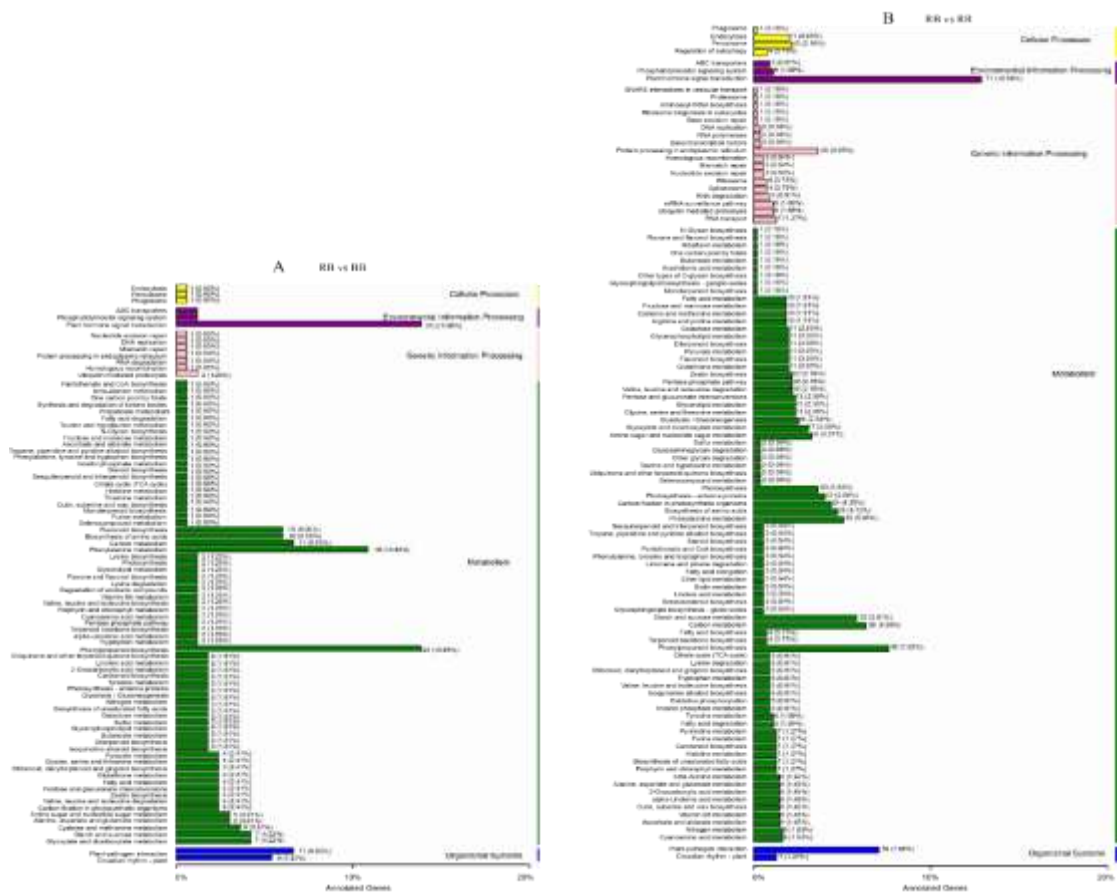


Fig S2. KEGG classification of differentially expressed genes in RB vs BB and RB vs RR. RR: 100% red LEDs; BB: 100% blue LEDs; RB: 75% red + 25% blue LEDs

Appendix F

Table S4 Differentially expressed genes enriched in KEGG pathways in RB vs BB and RB vs RR, respectively.

Group	KO ID	KEGG pathway	Total DEGs Number	Up-regulated DEGs number	Down-regulated DEGs number
	KO 04712	Circadian rhythm plant	9	9	0
	KO 04075	Plant hormone signal transduction	23	13	10
RB vs	KO 00360	Phenylalanine metabolism	18	10	8
BB	KO 00941	Flavonoid biosynthesis	10	9	1
	KO 00944	Flavone and flavonol biosynthesis	2	0	1
	KO 00940	Phenylpropanoid biosynthesis	23	18	5
	KO 01230	Biosynthesis of amino acids	10	10	0
	KO 04075	Plant hormone signal transduction	23	9	14
	KO 04626	Plant pathogen interaction	39	39	0
	KO 00630	Glyoxylate and dicarboxylate metabolism	17	0	17
	KO 00750	Vitamin B6 metabolism	8	0	8
	KO 00195	Photosynthesis	20	0	20
RB vs		Carbon fixation in photosynthetic			
RR	KO 00710	organisms	24	0	24
	KO 04075	Plant hormone signal transduction	71	64	7
	KO 00196	Photosynthesis - antenna proteins	22	0	22
	KO 01230	Biosynthesis of amino acids	26	0	26
	KO 04075	Plant hormone signal transduction	71	9	62

BB: 100% blue LEDs treatment; RR: 100% red LEDs treatment; RB: 75% red + 25% blue LEDs treatment

Appendix G

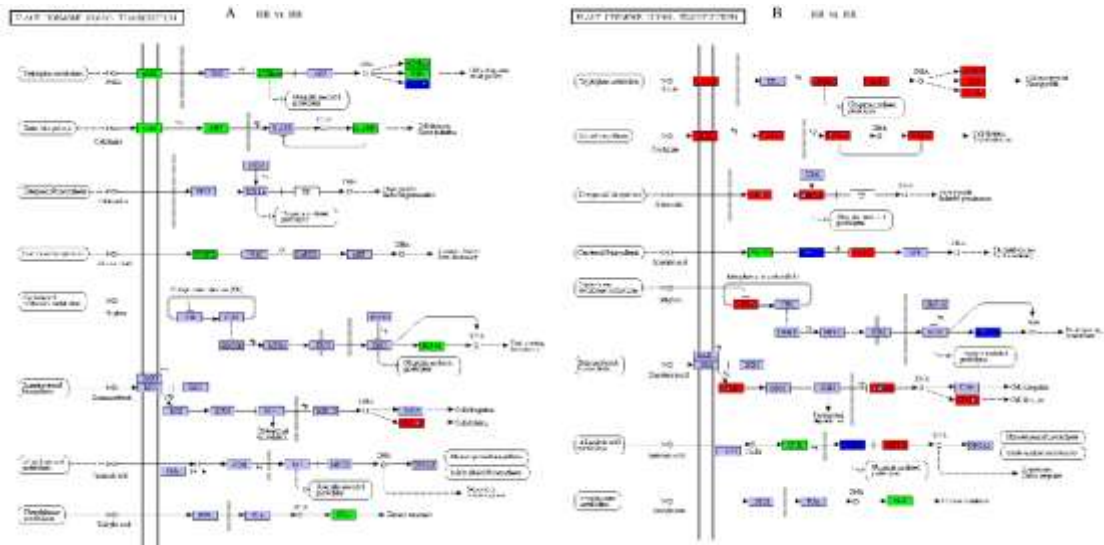


Fig S3. Differentially expressed genes enriched in “plant hormone signal transduction” KEGG pathway in RB vs BB and RB vs RR. RR: 100% red LEDs; BB: 100% blue LEDs; RB: 75% red + 25% blue LEDs