

## ***Supplementary Materials***

Table S1: List of the RIN (RNA integrity number) value of the samples.

<b>Samples</b>	<b>RIN value</b>
CK-NG-1	6.4
CK-NG-2	6.7
CK-NG-3	6.1
CK-OG-1	6.4
CK-OG-2	6.2
CK-OG-3	6.4
S-NG-1	7.1
S-NG-2	6.5
S-NG-3	6.6
S-OG-1	6.3
S-OG-2	6.8
S-OG-3	6.6

Table S2: List of primers used for qRT-PCR of gibberellin (GA) pathway associated genes.

Gene name	Primer sequence
<i>Actin</i>	f- ATTGTGCTCAGTGGTGGGTCA
	r- CCAATCCAAACACTGTACTTCCTC
<i>PHYC</i>	f- GGGATCAGCACCCCTCTGAAG
	r- GCTGTCCGTACTTAGCCCAG
<i>PIF4</i>	f- CCAATCTGCTGGGACGAACT
	r- TTCTTGTTTGCTGCTCACA
<i>DELLA</i>	f- CGCACCTGAAGCTGAATGTC
	r- TCGTCCATCTCTCTTCACGC
<i>SPY</i>	f- TAGAAGTGTTGGCGGACCAG
	r- AGCATTCGCTCTCTGTGCTT
<i>CPS4</i>	f- AACGGCGATTCTTACCGAGG
	r- GCCACACAGAACCTTGAGAGA
<i>GA3ox2-2</i>	f- GCCACAATGCACCTCAACTG
	r- CTGCATGGTGGAGTACGTGT
<i>KAOI</i>	f- GTTTGGTTGGCCCTGGAAAG
	r- GCGTCCCCAAAGCAGTTCAT
<i>GA2ox5</i>	f- ACGCCGACTCCTTCTTCATC
	r- AAGATCATGGACACCCTCGG

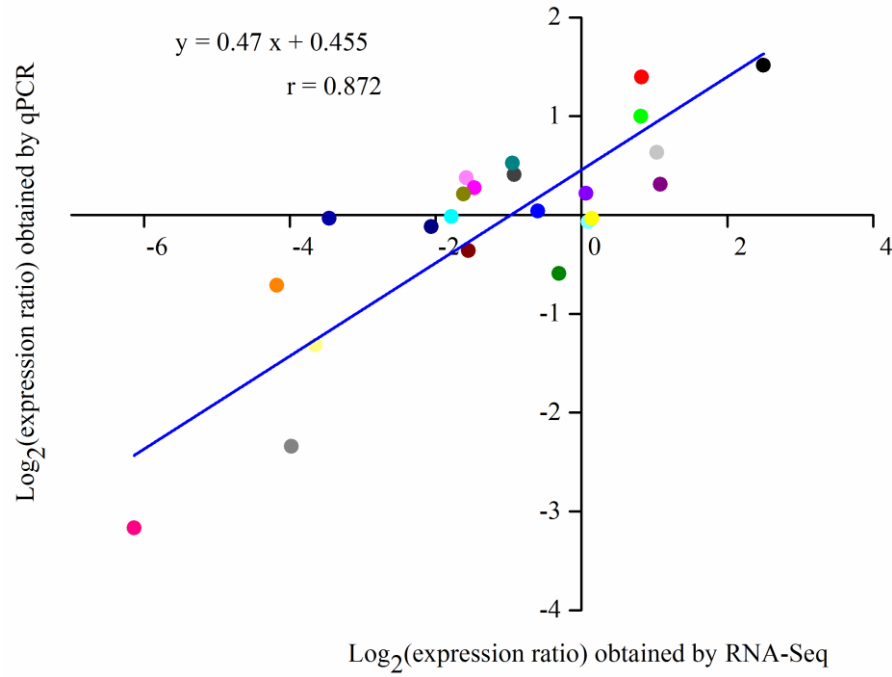


Figure S1: Correlations of the  $\text{log}_2$  values of gene expression ratios obtained from RNA-Seq platform and qRT-PCR methods.

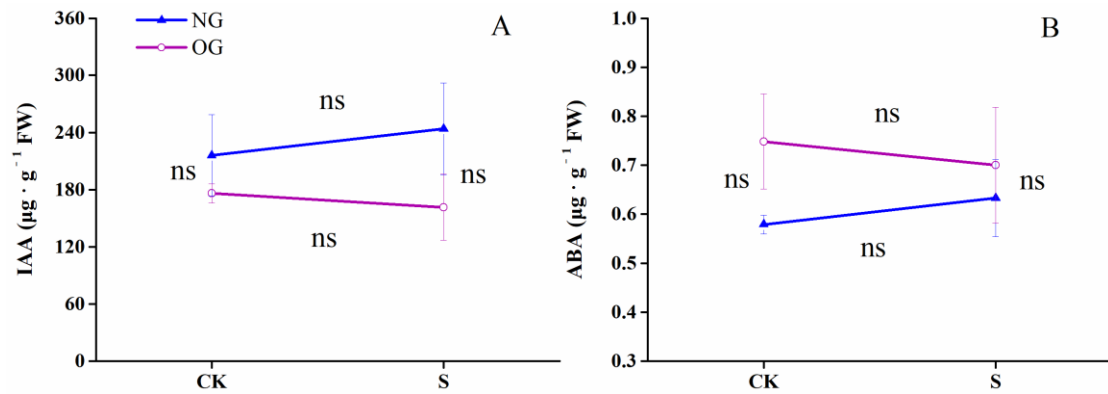


Figure S2: Effects of parental grazing environment on offspring IAA (A) and ABA (B) content in shade (S) and full light (CK). Blue and purple lines represent the responses of ungrazed and overgrazed offspring to shade treatment, respectively. "ns" indicates no significant difference. Each plot displays the mean  $\pm$  s.e.

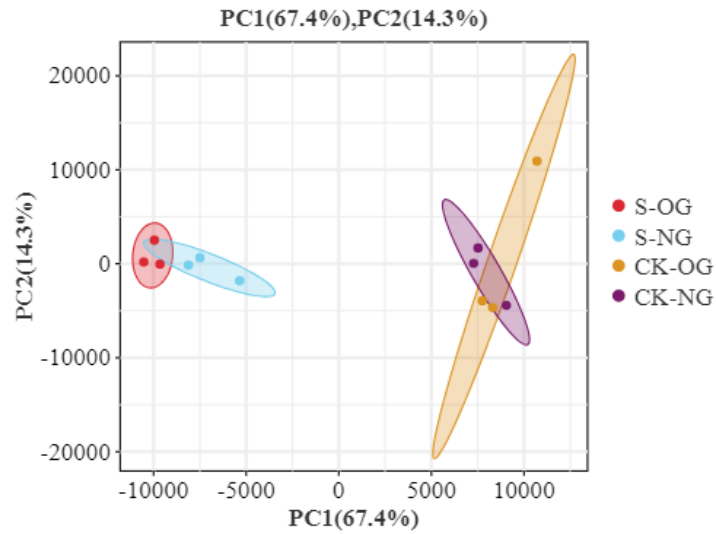


Figure S3: Principal component analysis (PCA) plots of transcriptomic data of offspring leaves. CK-NG, full light (no-grazing); CK-OG, full light (overgrazing); S-NG, shade (no-grazing); S-OG, shade (overgrazing).

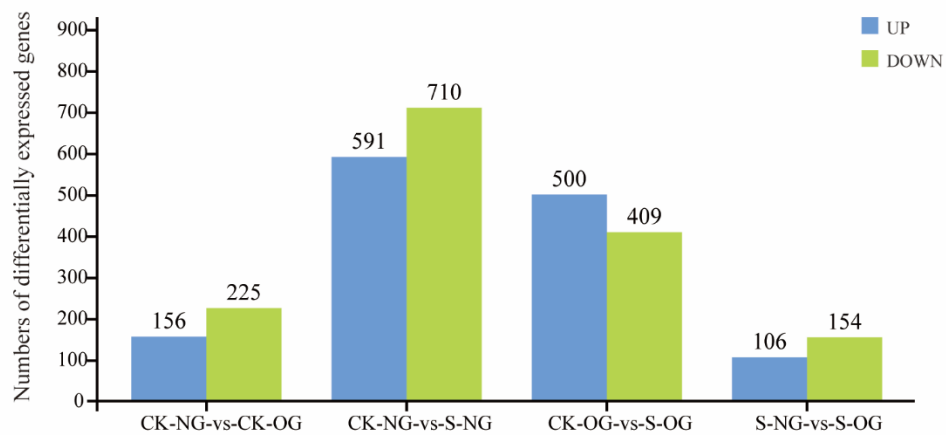


Figure S4: Column diagrams of the number of differentially expressed genes (FDR < 0.05 and Log<sub>2</sub>FC > 1) under different treatments. CK-NG, full light (no-grazing); CK-OG, full light (overgrazing); S-NG, shade (no-grazing); S-OG, shade (overgrazing).