Supplementary Material

RNAseq and Gene Ontology Analysis Reveal Differences Associated with Low R/FR induced Shade Responses in Cultivated Lentil and its Wild Relatives

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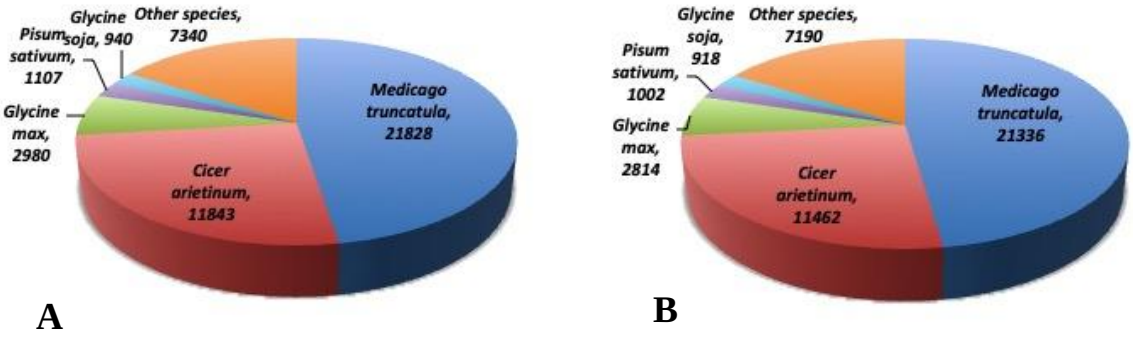
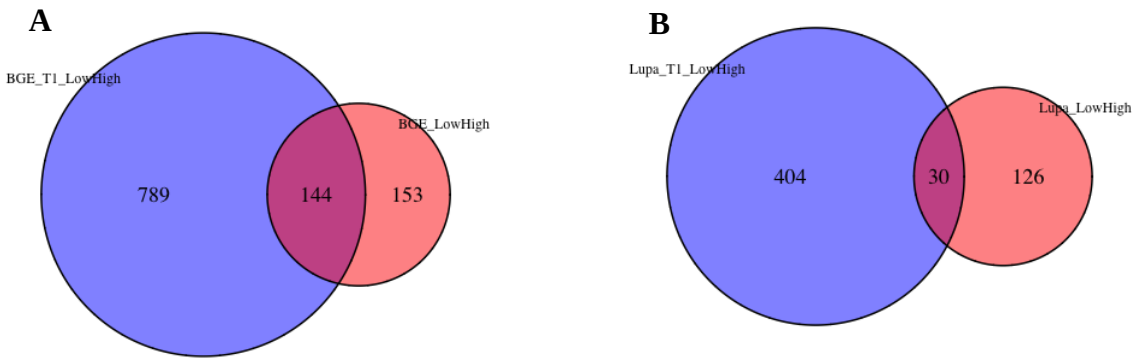
Supplementary Table S1. Summary statistics of differentially expressed transcription factor (TF) classes in both *L. orientalis* BGE 016880 and *L. culinaris* cv. Lupa. TFs were assigned using Mercator pipeline (Lohse *et al.*, 2014; Schwacke *et al.*, 2019) from *de novo* assembled transcriptomes of both genotypes and then used to identify differentially expressed TFs from DEG lists.

Differentially expressed TF class	*L. orientalis* BGE 016880		*L. culinaris* cv. Lupa	
	T1	LH	T1	LH
bHLH	13	11	6	4
MYB	13	6	2	2
WRKY	10	6	1	N/A
AP2/ERF	9	6	3	2
Homeobox	6	1	1	1
MADS/AGL	4	7	N/A	4
NAC	5	2	N/A	1
Other TFs	24	4	8	6
Total TF DEGs	84	43	21	20

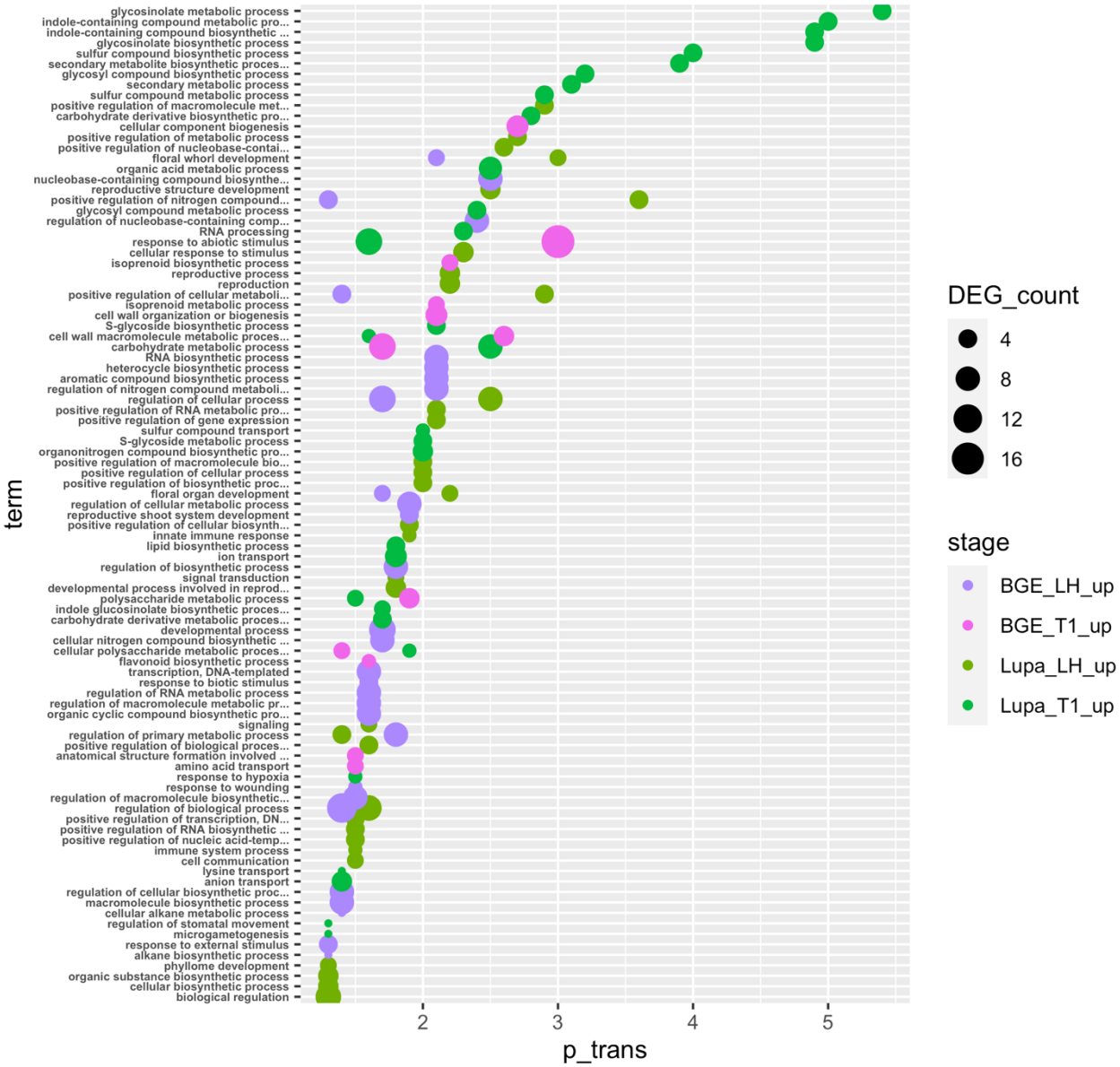


A **B**

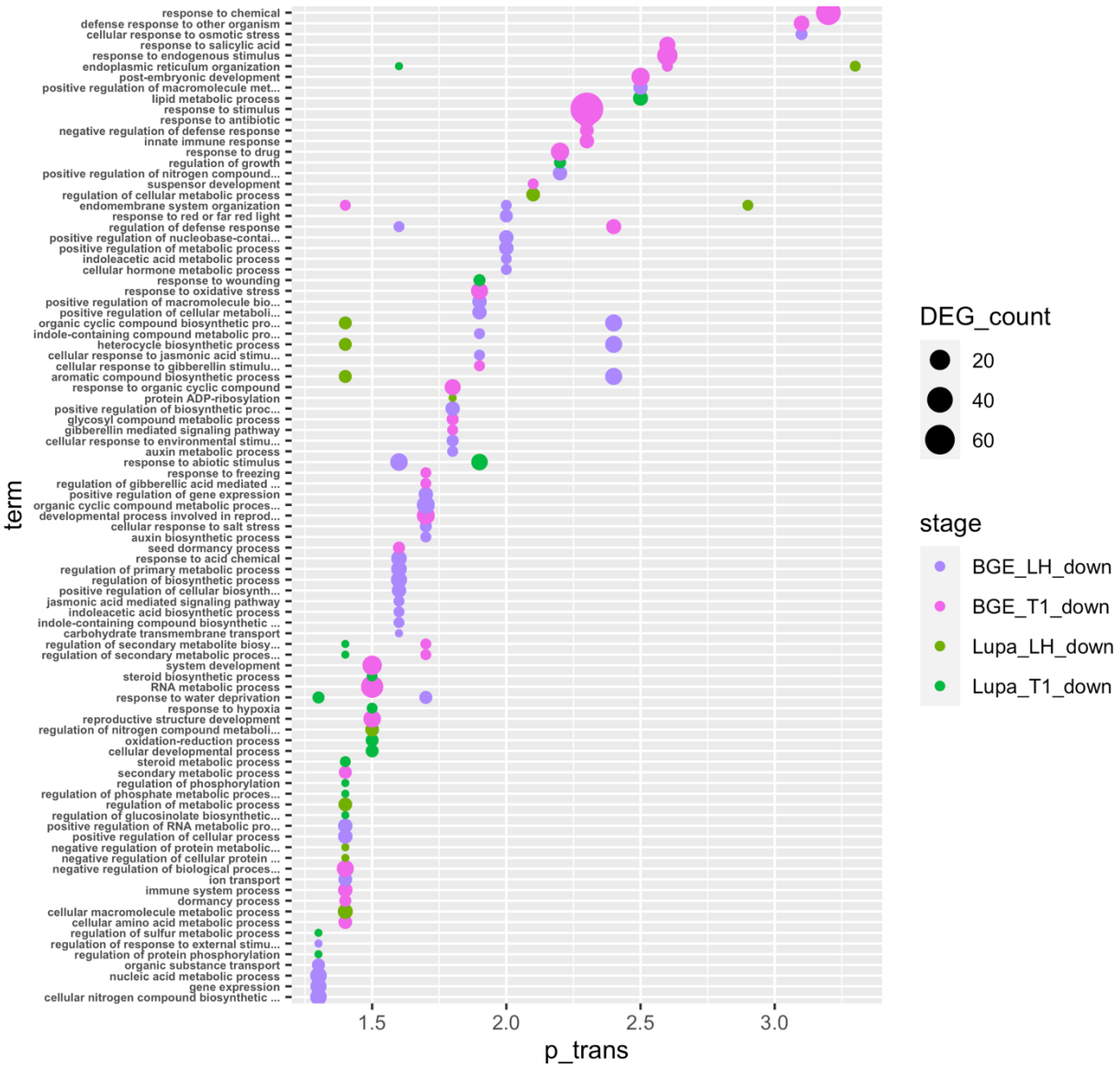
Supplementary Fig. S1 Taxonomy distribution of top BLAST hits for individual genes and the respective gene counts from *de novo* assembled transcriptomes of *L. orientalis* BGE 016880 (A) and *L. culinaris* cv. Lupa (B).



Supplementary Fig. S2 Venn Diagrams shown numbers of unique and common differentially expressed genes (DEGs) between T1 stage (T1_LowHigh) and all five growth stages (LowHigh) under low R/FR induced shade condition for both *L. orientalis* BGE 016880 (A) and *L. culinaris* cv. Lupa (B)



Supplementary Fig. S3 Significant enriched GO: BP terms in up-regulated DEGs from T1 stage and all five stages of *L. orientalis* BGE 016880 and *L. culinaris* cv Lupa under low R/FR induced shade condition. TopGO (version2.22) is employed and Fisher's exact tests were performed to find the significant enriched GO terms for the input gene set. P-value ≤ 0.05 was considered as significant. X-axis (p_trans) shows –log (P-value), while Y-axis shows significant enriched GO terms in Biological Process. DEG-count means the number of up-regulated DEGs within each enriched GO-BP term.



Supplementary Fig. S4 Significant enriched GO-BP terms in down-regulated DEGs from T1 stage and all five stages of *L. orientalis* BGE 016880 and *L. culinaris* cv Lupa under low R/FR induced shade condition. TopGO (version2.22) is employed and Fisher's exact tests were performed to find the significant enriched GO terms for the input gene set. P-value ≤ 0.05 was considered as significant. X-axis (p_trans) shows –log (P-value), while Y-axis shows significant enriched GO terms in Biological Process. DEG-count means the number of down-regulated DEGs within each enriched GO-BP term.