Supplementary materials

An NADPH oxidase regulates carbon metabolism and the cell cycle during root nodule symbiosis in common bean (*Phaseolus vulgaris*)

Citlali Fonseca-García, Noreide Nava, Miguel Lara, and Carmen Quinto*

Departamento de Biología Molecular de Plantas, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Avenida Universidad 2001, Colonia Chamilpa, Cuernavaca, Morelos 62210, Mexico.

Citlali Fonseca-García: citlali.fonseca@ibt.unam.mx;

Noreide Nava: noreide.nava@ibt.unam.mx

Miguel Lara: mlara@unam.mx

Carmen Quinto*: carmen.quinto@ibt.unam.mx; Tel.: +52-777-329-1642
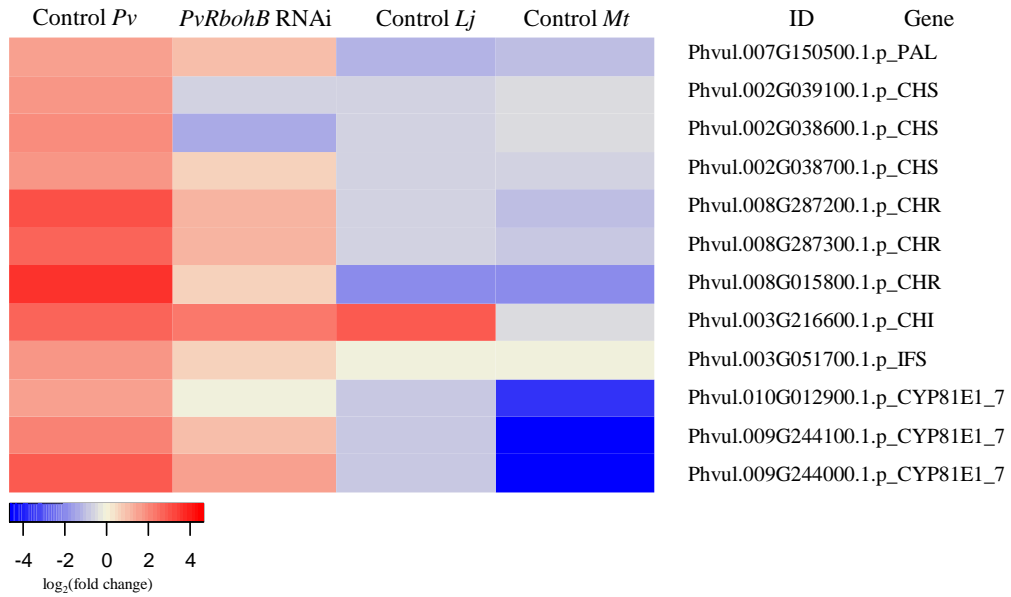
*Corresponding author

Figure S1. Expression profiles of genes related to the isoflavonoid biosynthesis pathway in legumes. DEGs encoding proteins related to isoflavonoid biosynthesis in control and *PvRbohB*-RNAi *P. vulgaris* roots at 7 dpi with *R. tropici*, together with their orthologous genes from wild-type *L. japonicus* roots inoculated with *M. loti* at 7 dpi, as well as *M. truncatula* nodules at 6 dpi with *S. meliloti*. The color bars represent the $\log_2$(fold change), with red representing upregulated genes and blue representing downregulated genes. A cut-off threshold of $\log_2$FC ≥ 1.5, Padj/FDR ≤ 0.05 was used.

Control *Pv*	*PvRbohB* RNAi	Control *Lj*	Control *Mt*	ID	Gene

(heatmap)

ID	Gene
Phvul.008G237400.1.p	GS1a
Phvul.001G229500.1.p	GS1b
Phvul.001G123900.1.p	Fd-GOGAT
Phvul.001G076400.1.p	NADH-GOGAT
Phvul.004G080200.1.p	GDH
Phvul.007G231700.1.p	AMT1
Phvul.007G120200.1.p	AMT1
Phvul.008G094900.1.p	AMT2
Phvul.010G073700.1.p	AMT2
Phvul.006G198400.1.p	SAT1
Phvul.003G231200.1.p	SAT1

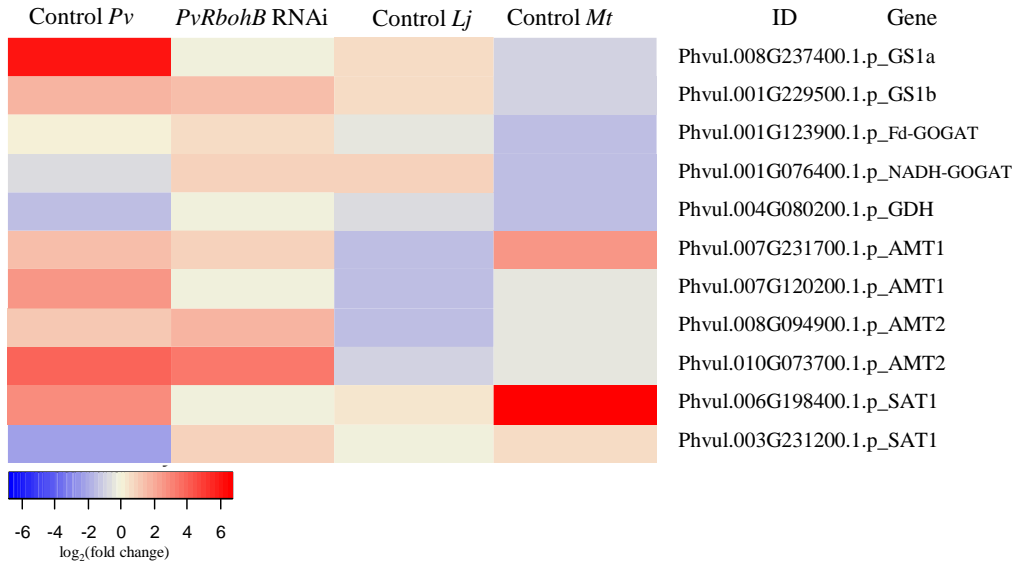-6 -4 -2 0 2 4 6
$\log_2$(fold change)

Figure S2. DEGs related to fixed ammonia assimilation and transmembrane transporters in nodules. The heatmap shows the DEGs from control and *PvRbohB*-RNAi *P. vulgaris* roots at 7 dpi with *R. tropici*, together with their orthologous genes from wild-type *L. japonicus* roots inoculated with *M. loti* at 7 dpi, as well as *M. truncatula* nodules at 6 dpi with *S. meliloti*. The color bars represent the $\log_2$(fold change), with red representing upregulated genes and blue representing downregulated genes. A cut-off threshold of $\log_2$FC ≥ 1.5, Padj/FDR ≤ 0.05 was used.

Control *Pv*   *PvRbohB* RNAi   Control *Lj*   ID   Gene

Phvul.006G186700.1.p_AllB
Phvul.004G176900.1.p_ENPP1_3
Phvul.005G018700.1.p_purH
Phvul.008G226900.1.p_purB
Phvul.006G186800.1.p_allB
Phvul.007G234300.1.p_UaZ
Phvul.007G125700.1.p_UAH
Phvul.004G045400.1.p_PAPSS
Phvul.003G225600.1.p_ylbA
Phvul.001G100100.1.p_ENTPD1_3_8
Phvul.007G150300.1.p_ADK
Phvul.011G103800.1.p_purF
Phvul.001G190100.1.p_RRM1
Phvul.002G290100.1.p_guaA
Phvul.007G260200.1.p_NUDT23
Phvul.009G002200.1.p_purF
Phvul.009G210300.1.p_NTPCR
Phvul.011G170200.1.p_purF
Phvul.011G003000.1.p_AK
Phvul.003G208500.1.p_ndk
Phvul.007G182100.1.p_purD
Phvul.007G224500.1.p_PK
Phvul.003G228800.1.p_PRPS
Phvul.009G004700.1.p_PFAS
Phvul.007G062900.1.p_PAPSS
Phvul.002G273500.1.p_purM
Phvul.005G048700.1.p_IMPDH
Phvul.009G092200.1.p_APRT
Phvul.006G082500.1.p_FHIT
Phvul.010G078200.1.p_AMPD
Phvul.008G178500.1.p_purC
Phvul.009G115100.1.p_RRM1
Phvul.001G135600.1.p_gmk
Phvul.007G253800.1.p_gmk
Phvul.006G155400.1.p_gmk
Phvul.007G106100.1.p_PK
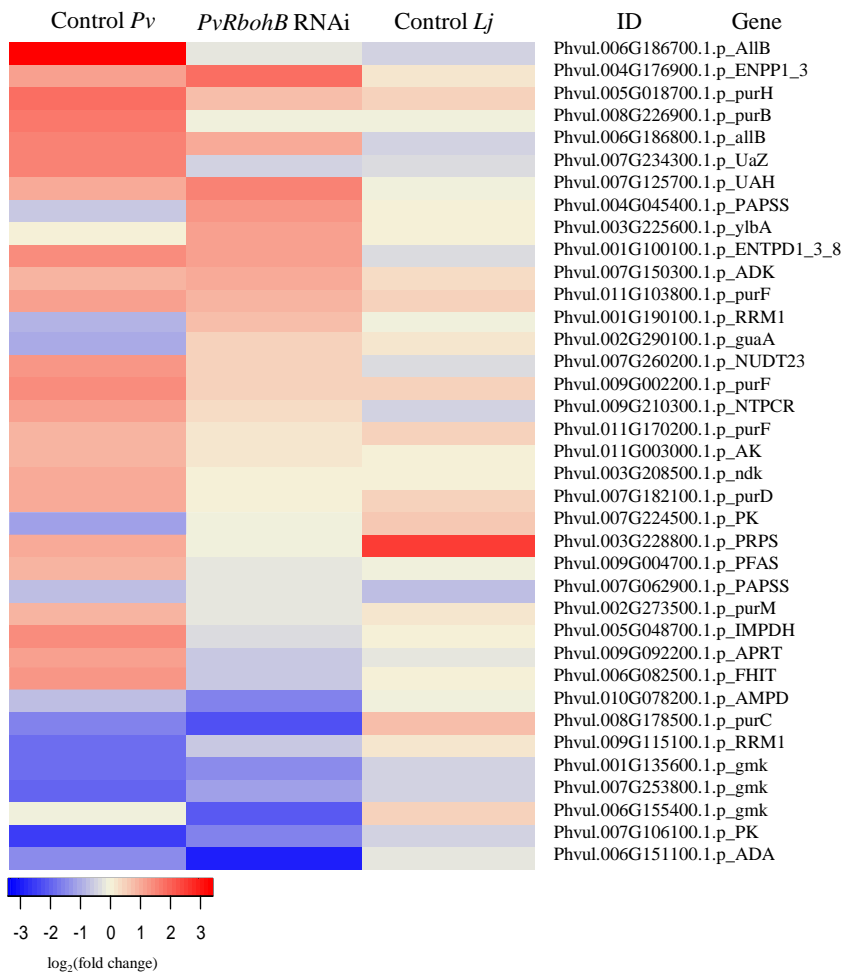Phvul.006G151100.1.p_ADA

-3 -2 -1 0 1 2 3
$\log_2$(fold change)

Figure S3. Heatmap of the expression patterns of genes related to ureide biosynthesis. DEGs encoding proteins related to ureide metabolism in control and *PvRbohB*-RNAi *P. vulgaris* roots at 7 dpi with rhizobia. Their respective orthologous genes from wild-type *L. japonicus* roots inoculated with *M. loti* at 7 dpi, were included in the analysis, along with *M. truncatula* nodules at 6 dpi with *S. meliloti*. The color bars represent the $\log_2$(fold change), with red representing upregulated genes and blue representing downregulated genes. A cut-off threshold of $\log_2$FC $\geq$ 1.5, Padj/FDR $\leq$ 0.05 was used.
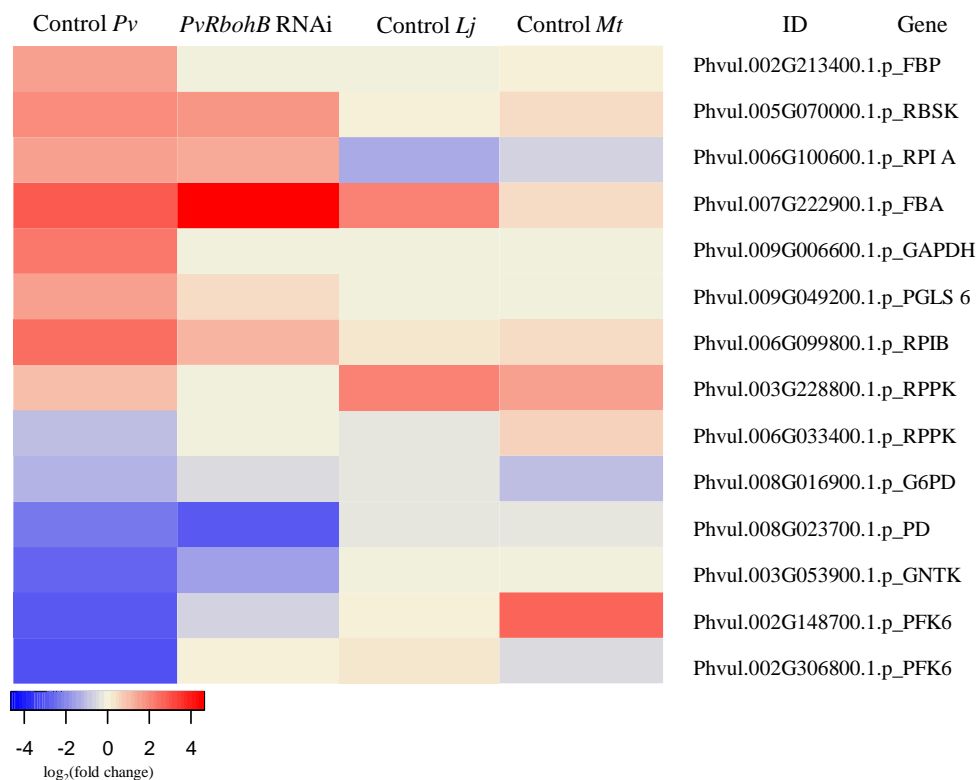
Figure S4. DEGs related to the oxidative and non-oxidative phases of the Pentose Phosphate Pathway (PPP). Data were analyzed in control and *PvRbohB*-RNAi *P. vulgaris* roots at 7 dpi with rhizobia. Their respective orthologous genes from wild-type *L. japonicus* roots inoculated with *M. loti* at 7 dpi were included in the analysis, along with *M. truncatula* nodules at 6 dpi with *S. meliloti*. The color bars represent the $\log_2$(fold change), with red representing upregulated genes and blue representing downregulated genes. A cut-off threshold of $\log_2 FC \geq 1.5$, Padj/FDR ≤ 0.05 was used.

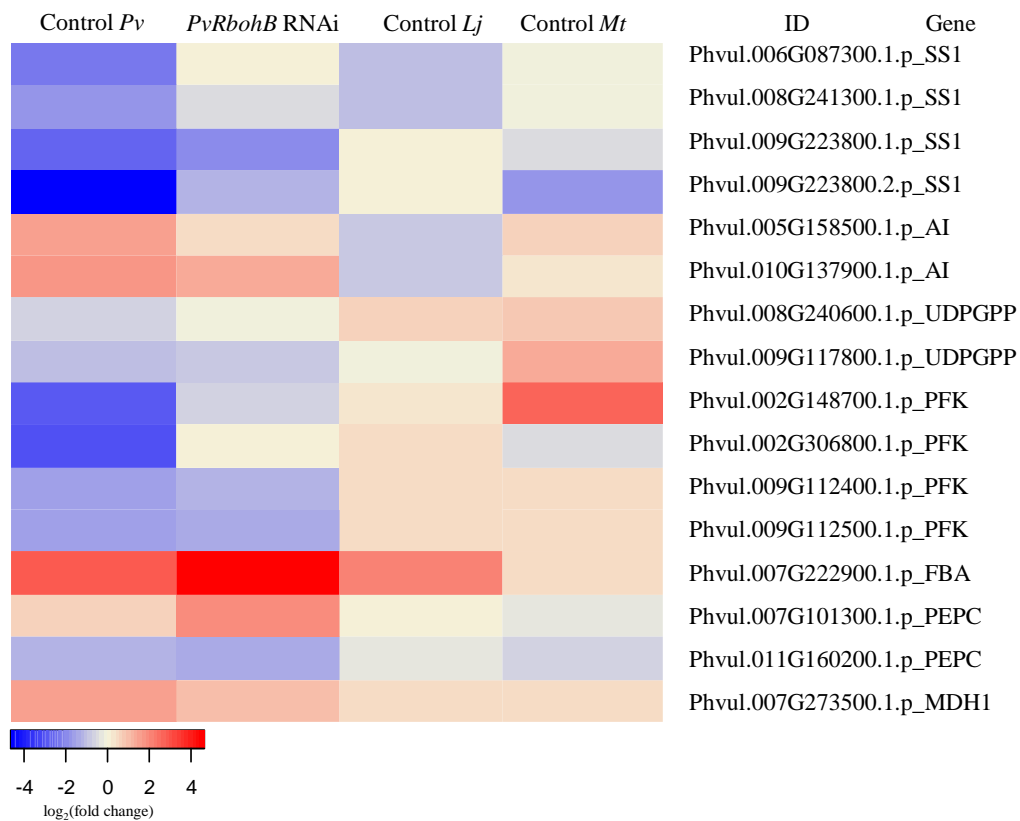|	Control *Pv*	*PvRbohB* RNAi	Control *Lj*	Control *Mt*	ID	Gene
					Phvul.006G087300.1.p_SS1	
					Phvul.008G241300.1.p_SS1	
					Phvul.009G223800.1.p_SS1	
					Phvul.009G223800.2.p_SS1	
					Phvul.005G158500.1.p_AI	
					Phvul.010G137900.1.p_AI	
					Phvul.008G240600.1.p_UDPGPP	
					Phvul.009G117800.1.p_UDPGPP	
					Phvul.002G148700.1.p_PFK	
					Phvul.002G306800.1.p_PFK	
					Phvul.009G112400.1.p_PFK	
					Phvul.009G112500.1.p_PFK	
					Phvul.007G222900.1.p_FBA	
					Phvul.007G101300.1.p_PEPC	
					Phvul.011G160200.1.p_PEPC	
					Phvul.007G273500.1.p_MDH1	

-4 -2 0 2 4
$\log_2$(fold change)

Figure S5. Expression profiles of genes related to sucrose catabolism to provide carbon skeletons to nodules. DEGs related to sucrose catabolism in control and *PvRbohB*-RNAi *P. vulgaris* roots at 7 dpi with rhizobia; their orthologous genes from wild-type *L. japonicus* roots inoculated with *M. loti* at 7 dpi were including in the analysis, along with *M. truncatula* nodules at 6 dpi with *S. meliloti*. The color bars represent the $\log_2$(fold change), with red representing upregulated genes and blue representing downregulated genes. A cut-off threshold of $\log_2$FC $\geq$ 1.5, Padj/FDR $\leq$ 0.05 was used.

				ID	Gene
Control *Pv*	*PvRbohB* RNAi	Control *Lj*	Control *Mt*		

Phvul.002G115100.1.p_CYCB2;3
Phvul.001G119700.1.p_CYCB1
Phvul.008G203300.1.p_ CYCB1
Phvul.001G000500.1 .p_CDKB2
Phvul.003G100900.1 .p_CDKL
Phvul.004G152000.1.p_ CDKD1
Phvul.004G165900.1 .p_CDKF
Phvul.005G103400.1.p_ CDKL
Phvul.002G298300.1.p_SKP1-21
Phvul.009G007400.1.p_APC
Phvul.010G020600.1.p_SKP1-21
Phvul.010G099600.1.p_SKP1-21
Phvul.001G197000.1.p_RING/U-box
Phvul.009G209800.1.p_RING/U-box
Phvul.001G232800.1.p_CDC20/FZR
Phvul.002G037700.1.p_CDC20
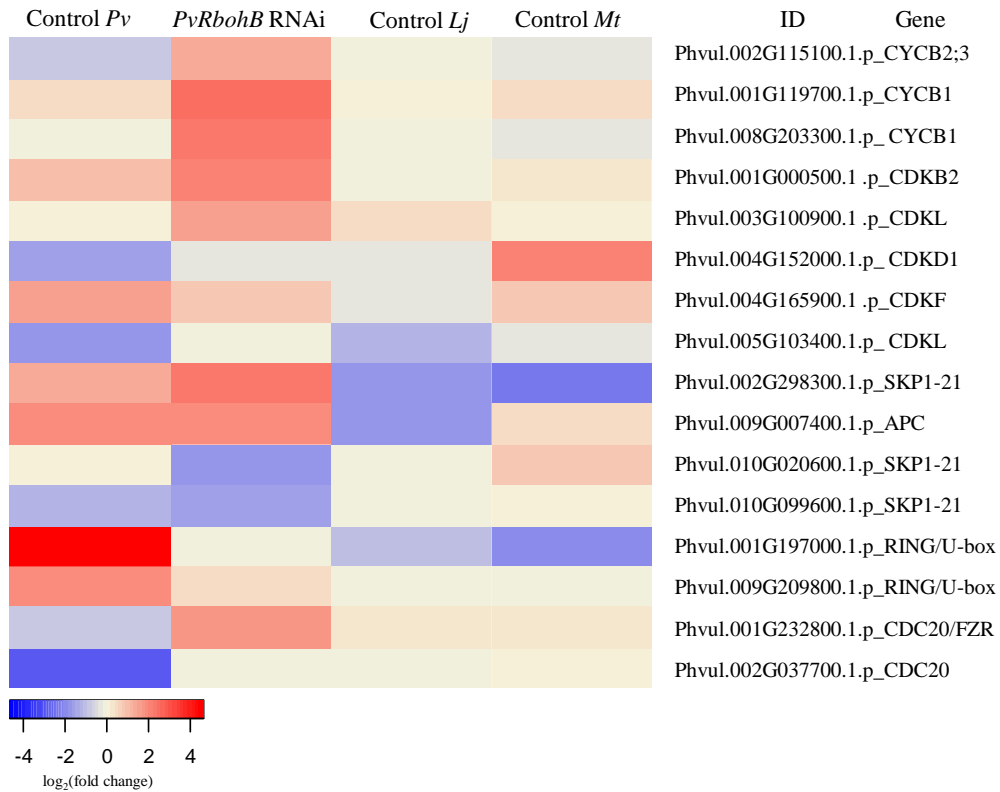
-4 -2 0 2 4
log$_2$(fold change)

Figure S6. DEGs involved in regulating the cell cycle in control and *PvRbohB*-RNAi *P. vulgaris* roots. Their respective orthologous genes from wild-type roots of *L. japonicus* inoculated with *M. loti* at 7 dpi were included in the analysis, along with *M. truncatula* nodules at 6 dpi with *S. meliloti* The color bars represent the log$_2$(fold change) of the DEG, with red and blue representing upregulated and downregulated genes, respectively. A cut-off threshold of log$_2$FC ≥ 1.5, Padj/FDR ≤ 0.05 was used.