

Deciphering the role of SPL12 and AGL6 from a genetic module that functions in nodulation and root regeneration in *Medicago sativa*

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Table S3. Validation of RNA-Seq data using qRT-PCR

Gene name	RNAi12-24/WT		RNAi12-29/WT	
	RNA-Seq	qRT-PCR	RNA-Seq	qRT-PCR
ABA/WDS induced protein	--	0.73	0.07	0.88
GRAS family transcription factor	0.53	0.53	0.41	0.28
WRKY family transcription factor 41	0.2	0.7	0.27	0.51
lateral organ boundaries (LOB) domain protein	0.57	0.89	0.47	0.23
Nod26 MIP family transporter	5.52	1.56	3.57	1.27
peptide/nitrate transporter	3.98	1.53	2.14	2.33
two-component response regulator ARR3-like protein	2.52	77.39	3.85	4.39
sulfate/bicarbonate/oxalate exchanger and transporter sat-1	4.53	2.22	2.54	1.81
high affinity sulfate transporter type 1	4.37	4.9	1.87	2.1
nitrate reductase [NADH]-like protein 1	8.15	1.24	2.50	1.09
nitrate reductase [NADH]-like protein 2	6.29	4.14	1.99	1.01
high affinity sulfate transporter type 1	1.95	2.36	1.74	2.78
component of high affinity nitrate transporter	2.02	0.43	1.52	0.77
caffeic acid O-methyltransferase	6.52	2.96	5.12	3.12

