

Table 1 Suppl. Gene ID and primer sequences used in gene expression analysis (Liu *et al.* 2008, Ma *et al.* 2012).

Gene	Accession number	Forward primer 5'-3'	Reverse primer 5'-3'	Fragment size	Tm °C (F/R)
<i>MtPAP1</i>	AY804257	GGCAGAACTAGTACTTTTGT	CCACAACATCATGTTTCCCAT	1326 pb	64.15/66.2
<i>MtPT1</i>	AF000354	AAGAAGGATCATGAACATCACC	CCAAGAAGCATAGGACTGCAT C	156 pb	63.2/63.7
<i>MtPT3</i>	EF016358	TGGGCATTGCAACGTGATTAA	GCAGGCCACATCACACAACG	153 pb	64.6/64.2
<i>MtPT5</i>	EU670235	GAAAGCGTCGCTTGTGTTACCG	CTTTTGGTTTTGATTCTCAGC	241 pb	64.9/65.1
		GCT			
<i>Ubiquitin</i>	XM_003600493	GATCCAAATCCCGATGAC	CGGTGGCTTCATACTTGGTC	79 pb	65.8/64.6

Table 2 Suppl. The level of probability (Pr) and mean values for each measured parameters in *Medicago truncatula* genotypes under control and P deficiency conditions. D.F.: Degrees of freedom; *F* value: is used in analysis of variance (*ANOVA*). It is calculated as the ratio of two mean squares to determine the ratio of explained variance to unexplained variance.***, ** and *: the difference is statistically significant at 0.5%, 1%, and 5%, respectively; ns: non-significant according to Tukey HSD test.

		D.F.	Sum of squares	F-value	Pr (>F)
Shoot dry mass	genotype	3	0.0280667	120.2857	1.353e-14 ***
	treatment	2	0.0149389	96.0357	3.527e-12 ***
	genotype:treatment	6	0.00255	5.4643	0.001102 **
Root dry mass	genotype	2	0.0063920	53.8652	8.267e-11 ***
	treatment	2	0.0003669	4.6376	0.01982 *
	genotype:treatment	6	0.0040473	17.0534	1.369e-07 ***
Leaves P conc.	genotype	3	32460	167.432	3.189e-16 ***
	treatment	2	58775	454750	< 2.2e-16 ***
	genotype:treatment	6	16136	41.617	1.588e-11 ***
Roots P conc.	genotype	3	44750	75.3319	2.357e-12 ***
	treatment	2	74640	2188.47	2.116e-15 ***
	genotype:treatment	6	11555	9.7257	1.826e-05 ***
Acid phosphatase activity in roots	genotype	3	2572.92	830.401	< 2.2e-16 ***
	treatment	2	413.37	200.123	1.074e-15 ***
	genotype:treatment	6	181.30	29.257	6.592e-10 ***
Acid phosphatase activity released	genotype	3	423.60	306.023	< 2.2e-16 ***
	treatment	2	154.48	167.399	8.023e-15 ***
	genotype:treatment	6	50.65	18.297	7.042e-08 ***
SPAD	genotype	3	311.72	149.606	1.151e-15 ***
	treatment	2	1390.97	1001.374	< 2.2e-16 ***
	genotype:treatment	6	68.35	16.402	1.969e-07 ***
F_v/F_m	genotype	3	1.50550	2052.951	< 2.2e-16 ***
	treatment	2	0.10472	214.193	4.971e-16 ***
	genotype:treatment	6	0.01419	9.678	1.899e-05 ***
P_N	genotype	3	55.057	278.2297	< 2.2e-16 ***
	treatment	2	73.323	555.8014	< 2.2e-16 ***
	genotype:treatment	6	2.030	5.1281	0.001622 **
g_s	genotype	3	0.012700	19.0003	1.572e-06 ***
	treatment	2	0.086134	193.2930	1.591e-15 ***
	genotype:treatment	6	0.000860	0.6434	0.6948 ns
E	genotype	3	9.4128	104.383	6.594e-14 ***
	treatment	2	14.3170	238.153	< 2.2e-16 ***
	genotype:treatment	6	3.8435	21.311	1.611e-08 ***
C_i	genotype	3	35085	380.876	< 2e-16 ***
	treatment	2	30854	502.425	< 2e-16 ***
	genotype:treatment	6	557	3.024	0.02399 *

Fig. 1 Suppl. Schematic summary of potential mechanisms of phosphorus deficiency tolerance in *M. truncatula*.

