

Table S1. Sequence of the oligonucleotides used for plasmid constructs.

LjCOPT1 Fw	5'	CATGGATCCATGGACATGCCCATGTCTAAC	3'
LjCOPT1 Rv	5'	CATAAGCTTTCAAATTTTGAGAGTAGCAGAGGAGGAC	3'
LjCOPT2 Fw	5'	CATGGATCCATGGAACCATCTTTATCAACAAG	3'
LjCOPT2 Rv	5'	CATAAGCTTCTACAGTTTTGAAGAATCCAATCCG	3'
LjCOPT3 Fw	5'	CATGGATCCATGATGCACATGACCTTTTACTGG	3'
LjCOPT3 Rv	5'	CATAAGCTTTCAAGCACAAGCGCAGG	3'
LjCOPT4 Fw	5'	CATGGATCCATGATGAAAATGACATTGCATTGGAG	3'
LjCOPT4 Rv	5'	CATAAGCTTCTAAGCGCATGCACAAGAATC	3'

Table S2. Sequence of the oligonucleotides used for qPCR.

qLjCOPT1 Fw	5'	GGAAAACATGCCACAGTGCT	3'
qLjCOPT1 Rv	5'	CGATAAATCTCAGTCGTAATGGC	3'
qLjCOPT2 Fw	5'	TGGGGCTACAAGGTGAACAT	3'
qLjCOPT2 Rv	5'	ACCAAGTAAGAAAGCCCGGA	3'
qLjCOPT3 Fw	5'	GCTGGAGATTGAAACCCCTC	3'
qLjCOPT3 Rv	5'	CACAAACACCCACCGTTAA	3'
qLjCOPT4 Fw	5'	GTTTTGTTCGGGGTGGACTC	3'
qLjCOPT4 Rv	5'	TCAACTTCAACTGCAGCACC	3'

Table S3. Effect of partial submergence on stomatal conductance (gs : $\text{mmol H}_2\text{O m}^{-2} \text{ s}^{-1}$), performance index (PIabs) and biomass production. Lt: *L. tenuis*; LtxLc: interspecific hybrid *L. tenuis* $\times$ *L. corniculatus* diploid; LcD: *L. corniculatus* diploid; LcT: *L. corniculatus* tetraploid and Lj: *L. japonicus*. *P*-value correspond to control vs. flooding treatment comparison (T-test).

Genotype	Stomatal conductance (<i>gs</i>)						<i>P</i> -value
	Control (mean ± SD)			Flooding (mean ± SD)			
LcD	457.89	±	72.88	400.30	±	186.30	0.4968
LtxLc	612.64	±	212.46	272.25	±	110.47	0.0059
Lt	611.05	±	292.10	253.23	±	124.79	0.0202
Lj	554.75	±	178.24	52.49	±	18.82	0.0010
LcT	499.66	±	287.23	27.56	±	20.49	0.0102

Genotype	Performance index (PIabs)						<i>P</i> -value
	Control (mean ± SD)			Flooding (mean ± SD)			
LcD	1.81	±	1.39	0.81	±	1.05	0.0957
LtxLc	3.34	±	1.70	1.05	±	0.58	0.0103
Lt	2.97	±	1.82	1.83	±	0.84	0.0973
Lj	1.33	±	1.29	0.17	±	0.17	0.0403
LcT	2.85	±	1.86	0.26	±	0.34	0.0102

Genotype	Biomass						<i>P</i> -value
	Control (mean ± SD)			Flooding (mean ± SD)			
LcD	3.38	±	0.70	0.95	±	0.31	<0.0001
LtxLc	6.16	±	1.78	2.12	±	0.47	0.0009
Lt	7.27	±	1.67	2.26	±	0.63	<0.0001
Lj	4.14	±	0.87	1.48	±	0.43	0.003
LcT	8.15	±	2.21	2.39	±	0.65	0.0001

Table S4. Matrix of identity between COPT proteins.

[illegible]

Table S5. Transcriptome comparative analysis from *Lotus japonicus* Gene Expression Atlas (LjGEA) database.

Tissue	Treat. type	<i>LjCOPT1</i>	<i>LjCOPT2</i>	<i>LjCOPT3</i>	<i>LjCOPT4</i>	Ecotype	Reference
Root (28 days-old plant)	Standard	1042.7	107.0	8486.3	30.1	MG20	Verdier et al. 2013
Stem (28 days-old plant)	Standard	29.6	158.1	4461.2	29.5	MG20	Verdier et al. 2013
Petiole (28 days-old plant)	Standard	23.9	150.1	3437.0	39.7	MG20	Verdier et al. 2013
Leaf (28 days-old plant)	Standard	31.6	28.5	3290.6	117.8	MG20	Verdier et al. 2013
Root 0h (uninoculated root)	Low N	1297.1	75.2	7638.6	26.4	MG20	Verdier et al. 2013
Nodule (Nod21 - 21 days post inoculation)	Low N	2483.3	27.4	8833.0	35.8	MG20	Verdier et al. 2013
WT Root Suseptible zone (3 week-old uninoculated plant)	Standard	800.1	71.6	3650.8	38.8	Gifu	Høgslund et al. 2009
WT Root tip (3 week-old uninoculated plant)	Standard	111.5	58.7	1997.3	33.9	Gifu	Høgslund et al. 2009
WT Root (3 week-old uninoculated plant)	Standard	622.1	81.2	3312.9	30.3	Gifu	Høgslund et al. 2009
WT Shoot (3 week-old uninoculated plant)	Standard	40.3	37.0	2647.9	58.1	Gifu	Høgslund et al. 2009
Pod10d (Pood+Seed)	Standard	27.6	59.3	3941.0	69.2	MG20	Verdier et al. 2013
Pod14d (Pood+Seed)	Standard	85.5	24.3	5178.6	71.7	MG20	Verdier et al. 2013
Pod20d (Pood+Seed)	Standard	509.1	24.7	4057.7	49.8	MG20	Verdier et al. 2013
Seed10d	Standard	40.8	29.5	3551.3	29.8	MG20	Verdier et al. 2013
Seed12d	Standard	42.9	28.0	3073.9	28.5	MG20	Verdier et al. 2013
Seed14d	Standard	43.5	28.2	4321.4	31.4	MG20	Verdier et al. 2013
Seed16d	Standard	77.0	24.5	3974.7	35.6	MG20	Verdier et al. 2013
Seed20d	Standard	406.9	30.9	3932.2	38.7	MG20	Verdier et al. 2013

LjCOPT1 (probeset: chr1.TM1284.2.1_at)

ATG**GACATGCC**ATGCTCTAACAGCAGCATGCCGATGGAGATGCAGAT**GAGTTTCTATTGGG**GAAAACATGCCACAGTGCTTTTTCTGGGTGGCCTAACCA
ACAGTGTTGGCATGTACATCTTAGCTCTCTTTTGTGTCTCTTTAGCCATTACGACTGAGATTATCGAAT

LjCOPT2 (probeset: chr1.TM1284.2_at)

ATGGAACCATCTTTATCAACAAGAATAATATCT**TCATGTTCTATCTTTCACGTC**CCCAACCTAACAGACAAGGTTCCATGCATATATATAATGTGCAAA
GTACAAACCATTTATCAATTTAT**CTACTCCATCACCTCAATATGTCGTA**CAACTCCACGGTGGCGACACGGCTGGGGCGACGGAGAATCCCCATACACAC
GACCCTCTACTGGGGCTACAAGGT**GAACATACGTTCATTTGCTGGCC**GGAAATAGCGCCGCATGT**ACGCGGTGGCGCTAATGCTCGTGTTCGCCATG**
GCG**GTATTGTTGGAGTGGCTTTCC**TTCACCAACATTGTGAAGCTCAAGCCCGGG**GTTCAAACACACGCTGTTGAGGCGCT**CCTTAAGACGGGGCTCTACG
GCGTGGCT**TCGGGCTTCTACTTGGTAATGCTGGCGTCATGCTGTAA**TGGCGGCGTTTCTCGCCGAATTGGC**GGCCACGTATGTTTCTT**
GATTTTCGGTACGCAGGCGCTTCCGGAAGAAGTCATTAGCGGATTGGATTCTTCAAACTGTAG

LjCOPT3 (probeset: chr1.CM0133.59_at)

ATGATGCACATGACCTTTTACTGGGGGAAGAAG**GTAACAATCTCTTCGATTCATGGA**AAACC**GATTCTGGACGAGTTACATCTCTGA**GTCTACTCGCGT
CTTCATCATCGCTGTTTCTAC**CAAGTTCTCGAGA**ATCGCCGATTCGCCTCAAGCTCTTCGCCGCCGGAAGCCGTTCCGCT**GGAGATTGAAACCC**
TCATCTCGCCGGAAGATTGTCGGA**GATAAGGCGAAGGCTGGTGTGAAGGTTGGTGGATCGATTCTGTTCCG**GGGTGAGCTCG**GGATCGGGTATCTGCTC**
ATGCTGGCGGTTATGCTGTTAAACGGTGGGGTGTGTTGTGGCTATTGTGGTGGGGCTT**GCCTTTGGGTATTCTTCTCAGGA**GTGATGGGGAAGATTCTG
TTGTGGTTGATAGTCTCGCCTGTGCTTGA

LjCOPT4 (probeset: chr5.TM0455.6_at)

ATGATGAAATGACATTGCATTGGAGCAAAAGGG**TCACCCCTCTCATAGATTCATGGG**GAGACCGATTCTGGCTGAGTTACATTCTCAGTTTACTCGCGT
GCCTCATGGTTCCGCTTTCTACAGTATCTAGAGAGTCTCCGGTTTCGGCTGAAGAGAGGGGAGTCTCCGGGG**CGGAGATACGGACGCC**ACTTCTCG
GCGGAACAATGTTGCCGGGGTAAGGTTGCTGAAGCGGTTTTGTCGGG**TGGACTCTGCTGTTGGTATTGTTGATGTTGGCTATAATGTCATTCAAT**
GGAGGGGTGTTTT**GGCTATTGTTGGTGGTCTTATGCTA**GGTTACTTCTCTCAGGT**GTCAAGGGTGGAG**ACGGTGCTGCAGTTGAAGTTGACATTGATG
ATTCTTGTGCATGCGCTTAG

Here shows the full consensus sequence used during chip design (100 bp per line), in which the 11 25-mer probes are shown in **red** and **blue** alternatively. In case two probe sequences overlap, the overlapped portion is underlined. Also, the target sequence is shown in **bold** text. The target sequence normally starts from the first base of the first probe, and ends at the last base of the last probe

References

- J. Verdier, I. Torres-Jerez, M. Wang, A. Andriankaja, S.N. Allen, J. He, et al., Establishment of the *Lotus japonicus* Gene Expression Atlas (LjGEA) and its use to explore legume seed maturation, *Plant J.* 74 (2013) 351–362.
- N. Høgslund, S. Radutoiu, L. Krusell, V. Voroshilova, M.A. Hannah, N. Goffard, et al., Dissection of symbiosis and organ development by integrated transcriptome analysis of *Lotus japonicus* mutant and wild-type plants, *PLoS One.* 4 (2009) e6556.

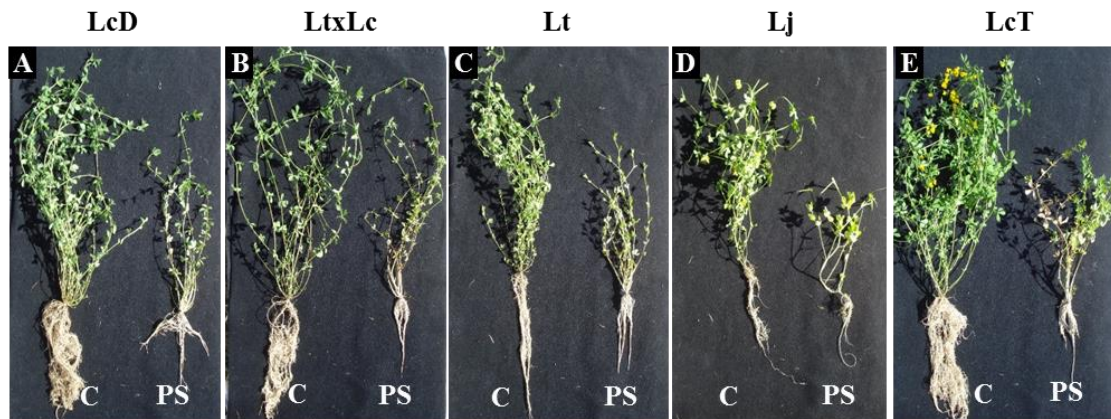


Figure S1. Effect of partial submergence in *Lotus* genus. Lt: *L. tenuis*; LtxLc: interspecific hybrid *L. tenuis* x *L. corniculatus* diploid; LcD: *L. corniculatus* diploid; LcT: *L. corniculatus* tetraploid and Lj: *L. japonicus*. Plants were grown as described in Figure 1; C: control. PS: partial submergence.

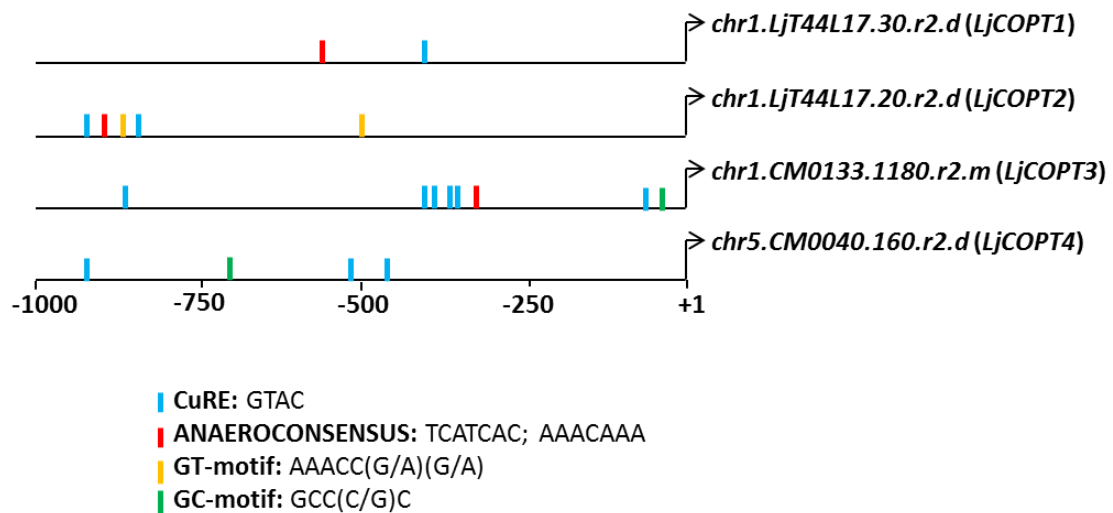


Figure S2. Sequence analysis of *LjCOPT1*, *LjCOPT2*, *LjCOPT3* and *LjCOPT4* promoters. Positions of putative *cis* regulatory elements are marked in different colors. Palindromic sequences are indicated only once. (References: Mohanty *et al.* 2005; Quinn and Merchant 1995; Hoeren 1998; Olive 1991).