

c2

c1

b2

b1

a2

a1

d2

d1

e

Supplementary Figure S1: Phylogenetic tree of CDF-like proteins from *Medicago*, other legumes, tomato, potato and Arabidopsis. The tree was constructed with full length amino acid sequences using the neighbour-joining algorithm implemented in PAUP* (version 4.0). Clades (a-c) of legume proteins have been named as described in Ridge et al. (2016). Additional nomenclature extended to clades d & e. Species included are; Ad - *Arachis duranensis*, Ai - *Arachis ipaensis*, At - *Arabidopsis thaliana*, Ca - *Cicer arietinum*, Cc - *Cajanus cajan*, Gm - *Glycine max*, La - *Lupinus augustifolius*, Mt - *Medicago truncatula*, Ps - *Pisum sativa*, Pv - *Phaseolus vulgaris*, Sl - *Solanum lycopersicum*, St - *Solanum tuberosum*, Va - *Vigna angularis* and Vr - *Vigna radiata*.

AtCDF1 1 4 4 24 30 29 30 39 31 49 59 69 79
M L E T K D P A K I L L E G R T M K P P P T V L E - - - - - V A D E E E E - - - - -
AtCDF2 1 4 4 29 30 39 31 49 59 69 79
M A D P A K I L L E G R T M L P L E L G V D V S S S Y T G - - - - - F L T E T Q I P V R L S D S C T G D D G G G E S I D T K K E E -
AtCDF3 1 4 4 28 29 31 43 53 63 73
M M M E T R D P A K I L L E G R T M P P S V F S A V T - - - - - V E D D E E D D W S G - - - - - G D D K S P E K - V T P E L S D K
AtCDF4 1 4 4 32 33 43 53 63 73
M A T O D S Q C K I L L E G R T M A F N - - - - - T R T I K N E E E - - - - -
AtCDF5 1 4 4 32 33 43 53 63 73
M S K S R D T E K I L L E G R T T S L L D V N C Y D P S S L S P - - - - - V H D V S D P S K E D S S S S S S C S P T I G P I R V P V K K S E Q E S N K F K
AtCOG1 1 4 4 32 33 43 53 63 73
M A T O D S Q C K I L L E G R T M T F N A N I - - - - - T O T I K K E E Q - - - - -
MtCDF1 12 22 32 41 51 61 71 79 86
M I N N S T I L L E G R T F I T H N I D V S T N D S S E S F - S P L P H E D L S H S L H S S M S S S P L E V N S T E H D A K R Y K E T S R K E L I - - - - - E - D E A S F Q T T
MtCDFc2_1 12 22 32 42 50 60 70 80 88
M I N N S T I L L E G R T F I T H N I D V S T N D S S E S F - S P L P H E D L S H S L H S S M S S S P L E V N S T E H D A K R Y K E T S R K E L I - - - - - E - D E A S F Q T T
MtCDFc2_4 12 22 32 42 50 60 70 80 88
M T N D S T I L L E G R T F Q T H N D V T T N D F S E L E F G S P L R P R D S S D H S P Y S - - S S C S P S E V N S T E H D A K R Y K E T S R K E L T S V O - - - - - E - D E A S F Q T T
MtCDFb2 1 4 4 32 33 43 53 63 73
M S E A K D P A K I L L E G R T M P V P E I P T G S G D S I G A P - - - - - S S S G D A V D D G I N Q N H G S F M D E H A I D E T M E D S T K C K E K D A L T Q S S
MtCDFd1_1 1 4 4 31 40 50 60 70 80 89
M N G E G D I C Y K N F S T M L E G R T M P V S D S Q I - - - - - Q A N S T T M I S C S N S K H K G M D P H T Q I I H E S K N S S
MtCDFb1 1 4 4 31 40 50 60 70 80 89
M L E T K D P A K I L L E G R T M P I L E V R V G - - D V V V E S - - - - - I D D D H H F S T N S S N E S R N K L E D Q D Q E I E K N T L G E K P S D E K N E - D G I P I Q S T
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M A E V R - - - - - K G E I N Q Q I K L F G T T I L K H G E E L K E G E K E S - - - - -
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- - - - - T H P - - - - - P E Q E A T I A V R S S S S D L T A E K R P D K I L P C P R C K S M E I T F C Y Y N N Y N V N O P R F E C K A G O R Y W T A G G T M R N V
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S K Q V N P Q E D A N A I N P M Y T G T L K P - - - - - V T K A V H R T N E H K T A K R D T D N Q E K V F R K P D K I L P C P R C N S L E I T F C Y Y N N Y N V N O P R F E C K A G O R Y W T A G G V I R N V
PsCDFc1 76 86 96 106 116 126 136 146 156 166 176 186 196
E D L K S L A A S S A I L E N S P T P S G - - - - - I E T N S L P K A S T N G E Q S E T S V S E D K T L L K P D K I L P C P R C N S M D I T F C Y Y N N Y N V N O P R F E C K A G O R Y W T A G G T M R N V

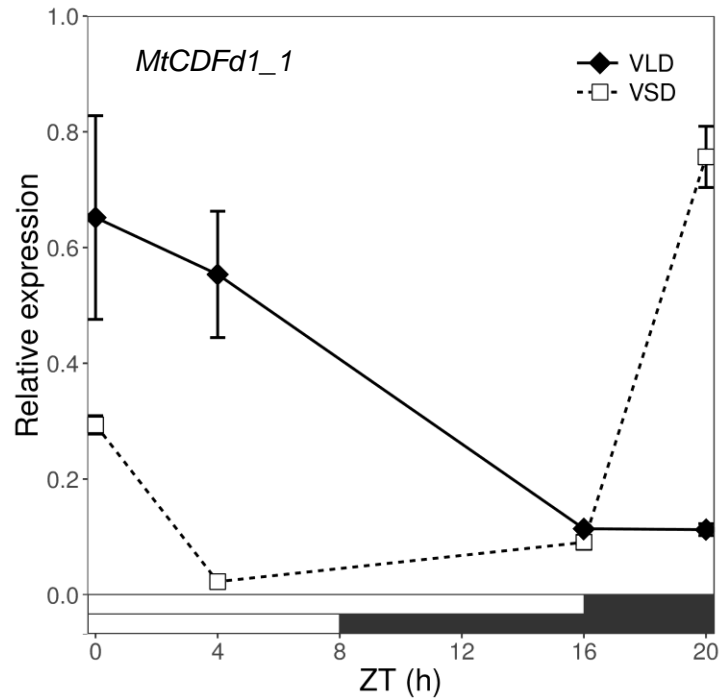
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P M G A G R R K N S P A S H Y N R H V S I T S A E A M Q K - - - - - V A R T D L Q H P N G A N I T F E G S D S V L C E S - - - - -
AtCDF3 112 113 124 124
P M G A G R R K N S S S S H Y R H I T I S E A L E A A R L D P - - - - - G L Q A N T R I G L E A Q Q Q H V A A P M T P V - - - - - M
AtCDF4 183 197 198 212 214
P M G A G R R K N P G R V - - - - - V V G M I G D G - - - - -
AtCDF5 183 197 198 212 214
P M G S G R R K N Q W P S S N H Y L Q V T - - - - - S E D C D N N S G T I S I E - - - - -
AtCOG1 87 117 124 212 214
P M G A G R R K N P G R V G G F A E I L G A A - - - - -
MtCDF1 87 195 196 207 217
P M G G S G R K N K S K S K - - - - - F N S D A S H Y H Q M S T M T F E G S D S P - - - - -
MtCDFc2_1 183 195 196 203 213 213
L I L G A G R R K N L N - - - - - A A N G L H S T I L L T F E G S D S P - - - - -
MtCDFb2 187 197 215 225 235 245 255 265
P M G A G R R K N S A S H F R Q I T V P E T A V Q N S L D S P N - - - - - G V H H P S L N C N G M F T E R T D T P L C E S M A L N A D Q G V N I S Q K N G F I R P E A L R I H
MtCDFd1_1 186 196 208 209 217 227 237 247 257
A M G A G R R K N H I A S Q Y R H I V A S D G I P T A S L E T N D S S R Y Q H G S N L E S A A V F R C S N D N G V L K F G R E N A S L D E S - - - - -
MtCDFb1 186 196 208 209 217 227 237 247 257
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MtCDFe 187 196 206 214 232
P M G A G R R K A K - - - - - P P G - - - - - H E D S - - - - -
MtCDFa2 187 196 206 214 232
P M G A G R R K N N - N S S S H Y R H I T I S E A L D A A R I I S P - - - - - N G T H L L Q N L K T N R N I F E G - - - - -
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MtCDFc2_3 183 184 195 205 215 222 232 243 244 248
L V G A G R R K N I S S - - - - - L S S D A S H N C O M S T V I T F E G S D S P - - - - -
MtCDFc2_2 140 150 160 170 183 196
P M G A G R R K N S S - - - - - F S S D A S H N R Q M S V I T F E G S D S P - - - - -
MtCDFd1_2 140 150 160 170 183 196
P I L G A G R R K N I A S Q Y R H I V A S G G I S T S N F S E N D S S - - - - - T E S A A V F R C S N N N G V L K F G P E N E S N D - - - - -
MtCDFd1_3 169 179 196 197 205 215 203 163
P I L G A G R R K N H L A S Q Y R Q I V T T N G I P T R L E S T N S S - - - - - D H H H T S T D N E V L K E G P D T P L C E S - - - - -
MtCDFd2 169 183 193 201 207 217 227 237 242 249
P I L G A G R R N N O S P L Q N C Q P V P T L D A V P V I H I D S K E - - - - - E V P L S E S V E V N L K G H R K - - - - -
PsCDFc1 173 183 193 201 207 217 227 237 242 249
P M G A G R R K N T S P A H Y R H L M I P E G V K V H S P N G L H - - - - - G S V L A F D S D S P L C N T M T S V L K I G E R V P N C V P N G F H Q A T G P N - - - - - T F V S Y S G E D D H

AtCDF1 136 143 158 159 169 177 181
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AtCDF2 ---MAGSLNLVEKSLKTKTQVLQEPNEGLKITVPLNQTN---E EAGTVSPLKGNPCF288 290 298 308
AtCDF3 LKQEDQKLVNAGARRNFIQLADQRLVARFVENGDDCSSG5255VTTSSNNH5VDESRAQSGSVVEAQMNNNNNNNNNYACI290 298 307
AtCDF4 ---NGVRQVELINGLLVEEQHAAAHAAGSFRHDF244 245 255 265
AtCDF5 ---GSSSEISVTEITGKHGSDGATKISADSVSQENK162 163 171 171
AtCOG1 ---TGAVDQVELDALLVEEVR--AATASHGGRHDF119 120 135
MtcDF1 ---TASSSISIPSSAAATTPTLQPADKSDSHSN5D249 250 259 267
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MtcDFc2_4 ---SMSSTSLDKKVNVAHEETFDKSYQS-FPQP245 246 257 263
MtcDFb2 VPYVGEFKSDEHSIKSSDSTLTLEDAAASSVEQVMPNCSQFQPVYPPS-APWLLPWSQSQSVQVQPPAFFPQGF276 276 276 276
MtcDFb1_1 ---KGSMLNLMNRRRHVDASGNNCRENGEETSLSVCSVTNGHTRG---NELFSEONRSKPMOSYPASS344 344
MtcDFb1 VPHTSEQGEDQNSKSVSTSTKSTEGATTNVSQEQAMNDH5FFPQGGYFPHGTWHLWPNVQMS5PI-PPAFPCP276 276 276 276
MtcDFe ---GSPESICLYEAAASDDG---HNYLG277 277 282 292
MtcDFa2 ---LDHPHLYDSMNSDPAEAKKVLNDRNRGFRSASVTVSKSMF---ESGKNMTQESLPQKNNGFIQPCPT296 296 296 296
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MtcDFc2_3 ---VMSSTSLAKKKNVGSNDNETFD225NQCFPPQF238 239 250 256
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MtcDFd1_2 ---MESMLHLRDQKRNDANANSVQHR-EDPSLKGSSVTNTGNQ---NEVSS-EHNASNWKOCYQVSP264 264
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PsCDFc1 330 331 341 345 354 364 372 378 388 398
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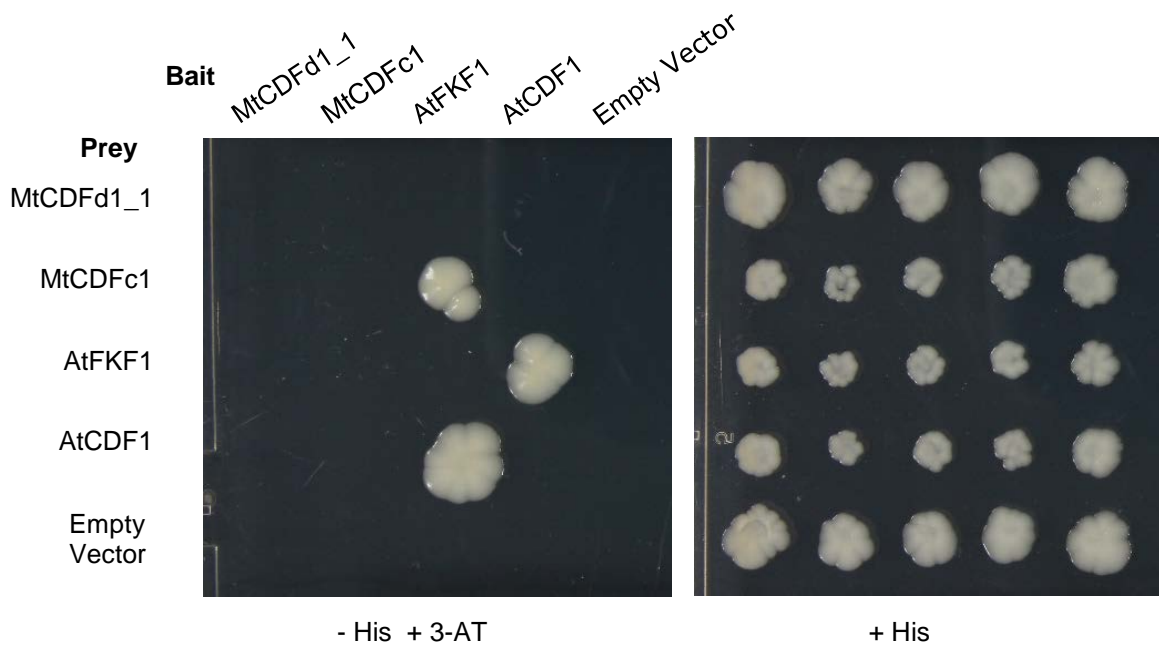
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AtCDF2 407 416 426 436 445 457
ETTLGKIKNE-NADTFGAFR5SSTKEKLS5EGRLPGR-RPELIQANPAALSRSLNFIHQ
AtCDF3 399 407 417 427 436 448
TTLGKIKNE--AMCKAGMEKEDHKTMYNNDKAEN-SPVLIKANPAALSRSLNFIHQ
AtCDF4 ---GSSC---170 200
AtCDF5 SKLPTKPE---KKTQGF5LENGEDTKGNSNRSS5LVS5ETSHTLIQANPAAMSRAMNREIR5SMQ
AtCOG1 ---GSSC---172 175
MtcDF1 157 167 177 187 197 206
VVQGD5V5MLNHQOFSNEEG5LDWIEGGANTVDQ5YWTQSHWSDIIVH5SS5L5HLP
MtcDFc2_1 ---RUSKGFAS351 361
MtcDFc2_4 338 341 351 361 369 377 385 395 405
STLGLKKN---GEL5EMGF5ASKGGVKNHVQTS---SVLIQANPAALSRSLVIEHRI
MtcDFb2 446 456 466 475 483 495
TTLGKIKNDKADAIRGGLEKAFAS5SNEK-DSVQN---SPAMQANPAAMSRSLI5FIHETS
MtcDFb1_1 355 358 368 466 474 486
PSSST5NSCISVNGTPI5LGKHT456 466 474 486
MtcDFb1 TTLGKIKNNAD5VPPRRL5QA5F5K5CDEKNHLVQV---SVLIQANPAALSRSLI5FIHETS
MtcDFe ---KSSGYS5LA---SS5L161
MtcDFa2 419 427 434 444 453 465
ETLGLKKN---GLSRG-GMTKAF---QSKKDGKNHVQT-SPMLIMANPAALARS5LNFIHNS
MtcDFc1 415 425 435 445 453 465
SKLGNNDKANS5LNGGEMNGE5QSKDMNHSVGT-SPMLIYANPAALSR5RTIHE
MtcDFc2_3 327 330 340 350 359 371
TTLGKIKN---GGLENGE5AS5VGDNRNHVEAD-5SVLIKANPAALSR5FVIRMI
MtcDFc2_2 319 322 332 342 351 363
LTLGLKKN---GGRF5NGE5ASTGGDKNHVVEAN-SLAIKANPAALSR5LVIHRI
MtcDFd1_2 P5SST5S
MtcDFd1_3 P5SST5S
MtcDFd2 399 409 419 429 439 449 459 469 479 489
SLTRTKSEONKPI5MKS5EKS5IEPK5NAS5RDLDDN---OILIRANPAALSR5G5K5SV
PsCDFc1 SKLGI5SNDK5TNS5LNG5M5NA5F5Q5K5GDK5TNH5A5EA---SP5LMI5ANPAAL5SR5RTI5H5GT

Supplementary Figure S2: Alignment of Medicago, Arabidopsis and pea CDF protein sequences showing the highly conserved DOF domain (green box) present in all the proteins and three other domains present in most of the CDF proteins, the N-terminal TOPLESS (TPL) interacting domain (red box) and two C-terminal domains, a putative GI-interacting domain (yellow box) and a FKF1-interacting region (blue).



Supplementary Figure S3. *MtCDFd1_1* gene transcript levels have a diurnal cycle. Gene expression of *MtCDFd1_1* in a Jester diurnal time course in VSD and VLD. Results are presented as averages \pm SE of three biological replicates at each time point and normalised to *Medicago PROTEIN PHOSPHATASE 2A (PP2A)*. Data are presented relative to the highest value observed overall. Bars underneath each graph show the length of light and dark conditions for LD (16 h light/8 h dark; upper) and SD (8 h light/16 dark; lower). ZT (zeitgeber time) indicates hours after dawn.

Each replicate consists of two fully-expanded trifoliolate leaves from vernalised (V) wild type Jester plants grown in SD or LD.



Supplementary Figure S4. *MtCDFd1_1* does not interact with AtFKF1 in yeast two hybrid assays. **(B)** Diploid yeast colonies containing prey and bait constructs from *MtCDFd1_1*, *MtCDFc1*, AtCDF1 and FKF1 or empty vector controls, were grown on medium selecting for protein-protein interactions, lacking His with 2mM 3-AT (left) or on medium with His (right). Colonies were allowed to develop over 11 days at 28°C. The vectors were pDEST22 (prey vector with the GAL4 activation domain) and pDEST32 (bait vector with GAL4 binding domain). Vectors containing inserts encoding full length CDF proteins were tested while the fragment encoding the KELCH-repeat region of AtFKF1 (amino acids 284 to 619) was used. The positive control interaction was between AtCDF1 and AtFKF1; AtCDF1, as either bait or prey, interacted with AtFKF1 (Imaizumi et al., 2005; Ridge et al., 2016). One of the Medicago CDFs, *MtCDFc1* interacted with AtFKF1 only in one direction, when it was the prey. However, as predicted from the lack of conservation of the C-terminal domains with predicted GI and FKF1 binding functions, there was no evidence of interaction between *MtCDFd1_1* and AtFKF1. Similar results were obtained with a second experiment using independent colonies.

Supplementary Table S1: Summary of the results of screening of *MtCDF Tnt1* insertion mutants.

Medicago gene ID ¹	Gene Names ²	Thomson et al. Nomenclature ⁴	<i>Tnt1</i> line	<i>Tnt1</i> position	Fl. time LD [*]		Fl. time VLD [*]		Fl. time VSD [*]		Gene expression KD/KO [*]	
					Days	Nodes	Days	Nodes	Days	Nodes		
<i>Medtr2g059540</i>	<i>CDF1</i> ³	<i>CDF1</i>	NF9016	exon 1	65.1±1.49	17.6±0.28	23.1±0.61	8.4±0.51	63.1±4.00	13.8±0.81	yes	
<i>Medtr5g041420</i>	<i>CDFc2_1</i>	<i>CDF2</i>	NF13527	exon 2	62.4±0.75	17.1±0.61	25.9±0.77	9.1±0.36	63.1±1.42	13.3±0.57	yes	
<i>Medtr5g041530</i>	<i>CDFc2_4</i>	<i>CDF3</i>	NF21008	exon 2	nd	nd	28.7±1.84	8.8±1.23	69.4±0.70	14.4±0.43	yes	
<i>Medtr6g012450</i>	<i>CDFb2</i>	<i>CDF4</i>	NF21606	exon 2	65.9±0.80	18.3±0.41	21.5±0.76	7.7±0.68	52.6±1.63	12.8±0.33	yes	
			NF0134	no <i>Tnt1</i>	na	na	na	na	na	na	na	na
			NF10121	no <i>Tnt1</i>	na	na	na	na	na	na	na	na
<i>Medtr6g027460</i>	<i>CDFd1_1</i> ³	<i>CDF5</i>	NF11690	intron 1	61.8±0.87	16.8±0.36	24.4±1.17	8.6±0.44	nd	nd	no	
			NF9161	no <i>Tnt1</i>	na	na	na	na	na	na	na	na
			NF9868	exon 2	nd	nd	19.0±1.15	6.0±0.00	nd	nd	yes	
<i>Medtr7g010950</i>	<i>CDFb1</i>	<i>CDF6</i>	NF20445	no <i>Tnt1</i>	na	na	na	na	na	na	na	
			NF6504	intron 1	nd	nd	20.5±6.35	7.0±0.00	nd	nd	no	
			NF14323	intron 1	63.5±2.76	17.2±0.81	22.3±1.22	8.1±0.42	nd	nd	no	
<i>Medtr2g016030</i>	<i>CDFe</i> ³	<i>CDFa</i>	NF13712	no <i>Tnt1</i>	na	na	na	na	na	na	na	
			NF7191	exon 1	58.7±2.63	16.4±0.54	28.3±1.59	9.9±0.43	69.5±0.77	14.4±0.63	yes	
<i>Medtr3g435480</i>	<i>CDFa2</i>	<i>CDFb</i>	NF16323	no <i>Tnt1</i>	na	na	na	na	na	na	na	
			NF9123	exon 2	66.1±2.14	18.2±0.56	27.9±0.83	10.5±0.34	68.0±0.99	13.6±0.46	yes	
<i>Medtr4g082060</i>	<i>CDFc1</i>	<i>CDFc</i>	NF11050	exon 2	nd	nd	30.2±2.50	11.1±0.83	nd	nd	yes	
			NF1963	no <i>Tnt1</i>	na	na	na	na	na	na	na	na
<i>Medtr5g041380</i>	<i>CDFc2_3</i>	<i>CDFd</i>	NF14291	exon 2	55.3±2.42	17.2±0.67	23.6±1.30	8.5±0.70	65.5±0.78	14.0±0.40	yes	
			NF2921	no <i>Tnt1</i>	na	na	na	na	na	na	na	na
<i>Medtr5g041400</i>	<i>CDFc2_2</i>	<i>CDFe</i>	NF4354	exon 1	64.1±2.31	16.4±0.80	27.7±0.89	10.4±0.39	59.5±0.98	12.9±0.38	yes	
			NF11400	exon 1	59.9±3.13	16.3±0.64	28.7±1.59	10.7±0.83	60.2±0.82	13.9±0.47	yes	
<i>Medtr6g027450</i>	<i>CDFd1_2</i> ³	<i>CDFf</i>	NF17470	exon 2	nd	nd	21.6±0.73	7.4±0.60	nd	nd	yes	
			NF1515	exon 2	nd	nd	20.1±0.98	7.2±0.64	nd	nd	nd	
<i>Medtr7g086780</i>	<i>CDFd1_3</i> ³	<i>CDFg</i>	NF19175	exon 2	63.4±4.66	17.5±1.61	22.3±1.07	7.8±0.30	61.1±5.08	13.6±0.73	yes	
			NF11642	exon 2	57.3±1.99	16.1±0.46	24.1±0.45	8.8±0.32	59.9±0.77	13.9±0.34	yes	
<i>Medtr8g044220</i>	<i>CDFd2</i> ³	<i>CDFh</i>	NF21417	exon 2	nd	nd	20.9±1.36	6.8±0.64	nd	nd	nd	
R108 WT					58.0±0.78 ^a	15.5±0.34 ^a	23.9±0.59 ^c	8.5±0.30 ^c	58.7±1.00 ^g	13.0±0.36 ^g		
					54.4±0.75 ^b	16.0±0.26 ^b	22.7±0.96 ^d	7.6±0.48 ^d	69.5±0.58 ^h	13.4±0.40 ^h		
							26.1±0.65 ^e	8.6±0.40 ^e	63.3±1.34 ⁱ	12.9±0.42 ⁱ		
							24.5±0.68 ^f	8.2±0.42 ^f				

Fl., flowering; WT, wild type; nd, not done; na, not applicable; KD/KO, knock-down/knock-out

¹ Medicago gene identifiers from JCVI Medicago genome Mt4.0, <http://www.jcvi.org/medicago/>

² Gene names based on nomenclature from Ridge et al. 2016; ³ Additional extended nomenclature based on clades seen in Supplementary Figure 1

⁴ Nomenclature from Thomson et al. 2019

* Based on qRT-PCR and/or full length cDNA amplification

+ Values expressed as means ± 95% confidence intervals

^a Same batch as NF9016, NF13527, NF21606, NF11690 and NF14323 in LD; ^b same batch as NF7191, NF9123, NF14291, NF4354, NF11400, NF19175 and NF11642 in LD; ^c same batch as NF9016, NF13527, NF21008, NF21606, NF11690 and NF14323 in VLD; ^d same batch as NF9868 and NF6504; ^e same batch as NF7191, NF9123, NF11050, NF14291, NF4354, NF11400, NF17470 and NF11642 in VLD; ^f same batch as NF1515, NF19175 and NF21417 in VLD; ^g same batch as NF9016, NF13527, NF21008 and NF21606 in VSD; ^h same batch as NF7191, NF9123 and NF14291 in VSD; ⁱ same batch as NF4354, NF11400, NF19175 and NF11642 in VSD

Supplementary Table S2: Primers used in this study

Primer name	Primer sequence	Primer used for	
GW_Medtr2g059540-F (MtCDF1)	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGGCAGATGGAAATCTTTTCTG	Gateway cloning	
GW_Medtr2g059540-R (MtCDF1)	GGGGACCACTTTGTACAAGAAAGCTGGGTTCATGGAAGATGAAAAAGAGAGGA		
GW_Medtr5g041420-F (MtCDFc2_1)	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGATTAATAATTCAACCATAACGCTT		
GW_Medtr5g041420-R (MtCDFc2_1)	GGGGACCACTTTGTACAAGAAAGCTGGGTGCCTTCAAACCAAGGTGTC		
GW_Medtr5g041530-F (MtCDFc2_4)	GGGGACAAGTTTGTACAAAAAAGCAGGCTAGCAAAAACCTACCTGAGATGACT		
GW_Medtr5g041530-R (MtCDFc2_4)	GGGGACCACTTTGTACAAGAAAGCTGGGTACACCGGACACACCTTCAAA		
GW_Medtr6g012450-F (MtCDFb2)	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGTCTGAAGCAAAAGACCCTG		
GW_Medtr6g012450-R (MtCDFb2)	GGGGACCACTTTGTACAAGAAAGCTGGGTTGCTGTGTCAATCGGCTCAT		
GW_Medtr6g027460-F (MtCDFd1_1)	GGGGACAAGTTTGTACAAAAAAGCAGGCTCACAAAAATGAATGGTGAAGGTGAC		
GW_Medtr6g027460-R (MtCDFd1_1)	GGGGACCACTTTGTACAAGAAAGCTGGGTACAGAATCTCATGTGTGTTTGCC		
GW_Medtr7g010950-F (MtCDFb1)	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTGTTTTAGCAACAAAAATGTTGGA		
GW_Medtr7g010950-R (MtCDFb1)	GGGGACCACTTTGTACAAGAAAGCTGGGTGGTTGAACACGGCCAAATCA		
GW_Medtr2g016030-F (MtCDFe)	GGGGACAAGTTTGTACAAAAAAGCAGGCTAATATGGCTGAAGTGAGAAAAGGTG		
GW_Medtr2g016030-R (MtCDFe)	GGGGACCACTTTGTACAAGAAAGCTGGGTACAAGAAATCACAAGGAGGATGCTA		
GW_Medtr3g435480-F (MtCDFa2)	GGGGACAAGTTTGTACAAAAAAGCAGGCTAAAAATGATTGAACTAAGGACCCT		
GW_Medtr3g435480-R (MtCDFa2)	GGGGACCACTTTGTACAAGAAAGCTGGGTTGACTAACCTCAATTCTCAAACACA		
GW_Medtr4g082060-F (MtCDFc1)	GGGGACAAGTTTGTACAAAAAAGCAGGCTTGAGTTGCACACAGATTTTCCT		
GW_Medtr4g082060-R (MtCDFc1)	GGGGACCACTTTGTACAAGAAAGCTGGGTTGCAATTCACAACCTAGGTTTCCT		
GW_Medtr6g027450-F (MtCDFc1_2)	GGGGACAAGTTTGTACAAAAAAGCAGGCTTGGTGTGTTTTGAGCTGTT		
GW_Medtr6g027450-R (MtCDFc1_2)	GGGGACCACTTTGTACAAGAAAGCTGGGTATTACCGGAGCGACAACCTAT		
GW_Medtr7g086780-F (MtCDFd1_3)	GGGGACAAGTTTGTACAAAAAAGCAGGCTATGTCTGAGACTCAGAAGGATC		
GW_Medtr7g086780-R (MtCDFd1_3)	GGGGACCACTTTGTACAAGAAAGCTGGGTTTATATGCTTTCCTGGATTGTATG		
Medtr2g059540-F (MtCDF1)	TGTGGTACAGCATGGGAGACTC		qRT-PCR
Medtr2g059540-R (MtCDF1)	AGACTGATCAACGGTGTAGCA		
Medtr5g041420-F (MtCDFc2_1)	ACCATCTTGGAGCGTGCAAT		
Medtr5g041420-R (MtCDFc2_1)	AGCTGCAGGGTTAGAAGCAA		
Medtr5g041530-F (MtCDFc2_4)	AAGCGCGTGTGATCCCTAA		
Medtr5g041530-R (MtCDFc2_4)	CCATGAAAAGCTCTCCCCCA		
R108_Medtr6g027460-F (MtCDFd1_1)	ATGGTGGCCGTTACAAACAT		
R108_Medtr6g027460-R (MtCDFd1_1)	TGGACACATTTCCATTCTG		
Medtr2g016030-F (MtCDFe)	TTCATTAGCATCCTCCTTGTGA		
Medtr2g016030-R (MtCDFe)	CACATGGGAGGAAAATGGTT		
Medtr3g435480-F (MtCDFa2)	TTGGTTTCCGCTCATACTC		
Medtr3g435480-R (MtCDFa2)	CATTTTCGTCGTTGGTGTG		

Medtr4g082060-F (MtCDFc1)	ATCCTCCACTTTGCAACACC		
Medtr4g082060-R (MtCDFc1)	TTTGAAGCCGTAACCGAAAC		
R108_Medtr5g041380-F (MtCDFc2_3)	ATCAAGAATGGTGGAGGACT		
R108_Medtr5g041380-R (MtCDFc2_3)	AGCACGCCTTCAACATATTC		
Medtr5g041400-F (MtCDFc2_2)	TTGGGAATATGTAGCACCGATA		
Medtr5g041400-R (MtCDFc2_2)	GGACGTTGAATCGACAGGAC		
Medtr6g027450-F (MtCDFc1_2)	GCCGAACATTGGCTTGCAAT		
Medtr6g027450-R (MtCDFc1_2)	TCTCTGGTGTGTTTTCCAAGG		
Medtr7g086780-F (MtCDFd1_3)	AGATTTTGGAAAGCCAGCTCA		
Medtr7g086780-R (MtCDFd1_3)	AGAGAAACAAAGGCCAGCAA		
MtFTa1-F	GTAGCAGTAGGAATCCACTAGC		
MtFTa1-R	ACACTCACTCTCGGTTGATTTCC		
MtFTb1-F	ATGAACCCTCTTGTGGTCTG		
MtFTb1-R	TGGATTGACTATTTGGGAAG		
MtFTb2-F	ACAAATCCTCTTGTTGTTGG		
MtFTb2-R	TGAGTTGATTATTTGAGAGG		
MtFTa2-F	AAGTGGTAGCAGACCGAATC		
MtFTa2-R	CACCACCATTGGTAACAGTC		
MtSOC1a-F	GCGTTGTTTCGAGCAAGAAAGAATCAGGC		
MtSOC1a-R	GGGGCTGCTTAGAGAGCCTGGCATT		
MtCOLa-F	GGTTGTGAGGTGGAGGAAGA		
MtCOLa-R	CAACAAAAGCCATGAAGCTG		
MtCOLb-F	CCGAACACGAACATGAACAC		
MtCOLb-R	CATCCATCGACGGTGAAGA		
MtCOLc-F	ATCTTCCTCGATGGACGTTG		
MtCOLc-R	GTCCCGTAACCACAGTTTGA		
MtCOLd-F	GCCGATGATGAATCACAACCTCAG		
MtCOLd-R	GTGAAGATGACGAAACGCTATG		
MtCOLh-F	GAATAGAGGGGATGCCATGTT		
MtCOLh-R	CAAATCGCCCTCTCACTCTC		
Medtr2g059540_genotyping-F (MtCDF1)	TCGCTACTGGACCAAAGGTG		Genotyping
Medtr2g059540_genotyping-R (MtCDF1)	ATCACCGAGTCTCCATGCTG		
Medtr5g041420_genotyping-F (MtCDFc2_1)	AACGCTTTTTGGGAGAACGA		
Medtr5g041420_genotyping-R (MtCDFc2_1)	TGGAACAACCTGGTCTGGTTTC		
Medtr5g041530_genotyping-F (MtCDFc2_4)	ACCCAAAATCTCCCTCGTCG		
Medtr5g041530_genotyping-R (MtCDFc2_4)	CCATGAAAAGCTCTCCCCCA		
Medtr6g012450_genotyping-F (MtCDFb2)	CCGTGTCCCCGTTGTTATAG		
Medtr6g012450_genotyping-R (MtCDFb2)	GGCGGTGGTTGACTTGAGA		
Medtr6g012450_genotyping-R2 (MtCDFb2)	AATCGCATCTGCCTTATCGT		
Medtr6g027460_genotyping-F (MtCDFd1_1)	CAATGTCAATCAACCTCGGCA		

Medtr6g027460_genotyping-R (MtCDFd1_1)	TGGACACATTTCCATTCTG
Medtr6g027460-F (MtCDFd1_1)	GCTACCCTGCATCTTCATGGA
Medtr6g027460-R (MtCDFd1_1)	GCATTGCAGTAGGATCAATGCC
Medtr7g010950_genotyping-F (MtCDFb1)	TCGTGTTGGAGATGTTGTTGT
Medtr7g010950_genotyping-F1 (MtCDFb1)	GGAGGTTTCATGTTGGAGATG
Medtr7g010950_genotyping-F2 (MtCDFb1)	AGTGAAGAACAAGGCGAGGA
Medtr7g010950_genotyping-R (MtCDFb1)	CCGATGGTTTTTCTCCCAATGT
Medtr7g010950_genotyping-R1 (MtCDFb1)	CGGAATCACGTTGAGTTTCA
Medtr7g010950_genotyping-R2 (MtCDFb1)	TGAAGCGACCTAGACAAATGC
Medtr2g016030_genotyping-F (MtCDFe)	CGGAAAGTTGTCTCTACGAAGC
Medtr2g016030_genotyping-R (MtCDFe)	TGAATAACCACCTGAGGTCTTCC
Medtr3g435480_genotyping-F (MtCDFa2)	TGGTAGAGTTCTCAACTTTGGGT
Medtr3g435480_genotyping-R (MtCDFa2)	ATTGCGCCAGAACTCCAAGT
Medtr4g082060_genotyping-F (MtCDFc1)	ACTGATCATCCCTGCCAACG
Medtr4g082060_genotyping-R (MtCDFc1)	ACGAGGCTGGTTGACATTGT
Medtr5g041380_genotyping-F (MtCDFc2_3)	ACAACACCGATGTTCTTACCA
Medtr5g041380_genotyping-R (MtCDFc2_3)	CCTCTGTGTTTTGTTTGGAGGC
Medtr5g041400_genotyping-F (MtCDFc2_2)	ACACGCAACACCGACGATTA
Medtr5g041400_genotyping-R (MtCDFc2_2)	GAGATTTTGTCTTGC GGCG
Medtr6g027450_genotyping-F (MtCDFc1_2)	CCCGACAAAATTGTTCAATGTCC
Medtr6g027450_genotyping-R (MtCDFc1_2)	GGTTGAAATCCACCGGAAGC
Medtr7g086780_genotyping-F (MtCDFd1_3)	CGATGCAACAGTTGGGACAC
Medtr7g086780_genotyping-R (MtCDFd1_3)	TCGAACCGGAACACACTTGT
Medtr8g044220_genotyping-F (MtCDFd2)	GATGCAGTACCTGTCATACACAT
Medtr8g044220_genotyping-R (MtCDFd2)	AGAAGAGCTGGAAGAGTTCTCA
Tnt1-F	ACAGTGCTACCTCCTCTGGATG
Tnt1-R	CAGTGAACGAGCAGAACCTGTG

Supplementary References

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