A

- MtCCD1
- PsCCD1
- AtCCD1
- SlCCD1b
- PhCCD1
- SlCCD1a
- OsCCD1
- ZmCCD1
- OsCCD4
- ZmCCD4
- SlCCD4
- AtCCD4
- PsCCD4
- MtCCD4a
- MtCCD4b
- PpCCD8
- AtCCD8
- OsCCD8a
- OsCCD8b
- ZmCCD8
- PsCCD8
- MtCCD8
- PhCCD8
- SlCCD8
- OsCCD7
- ZmCCD7
- PpCCD7
- AtCCD7
- PhCCD7
- SlCCD7
- LjCCD7
- PsCCD7
- MtCCD7

0.2

B

- MtD14-like 1b
- MtD14-like 1c
- MtD14-like 1a
- AtKAI2
- OsD14-like 1
- OsD14
- AtD14
- PhDAD2
- MtD14
- AtD14-like 2
- MtD14-like 2
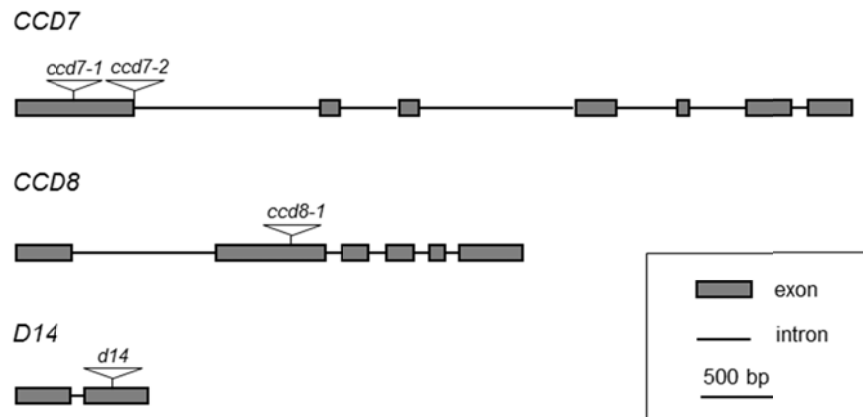- OsD14-like 2a
- OsD14-like 2b

0.1

Supplementary Figure S1

Phylogeny of strigolactone biosynthesis and response genes.

A. Maximum-likelihood tree of *CCD* genes. CCD7 and CCD8 isoforms are involved in strigolactone synthesis.

B. Maximum-likelihood tree of *D14* and *D14-like* genes. D14 proteins are involved in strigolactone perception.
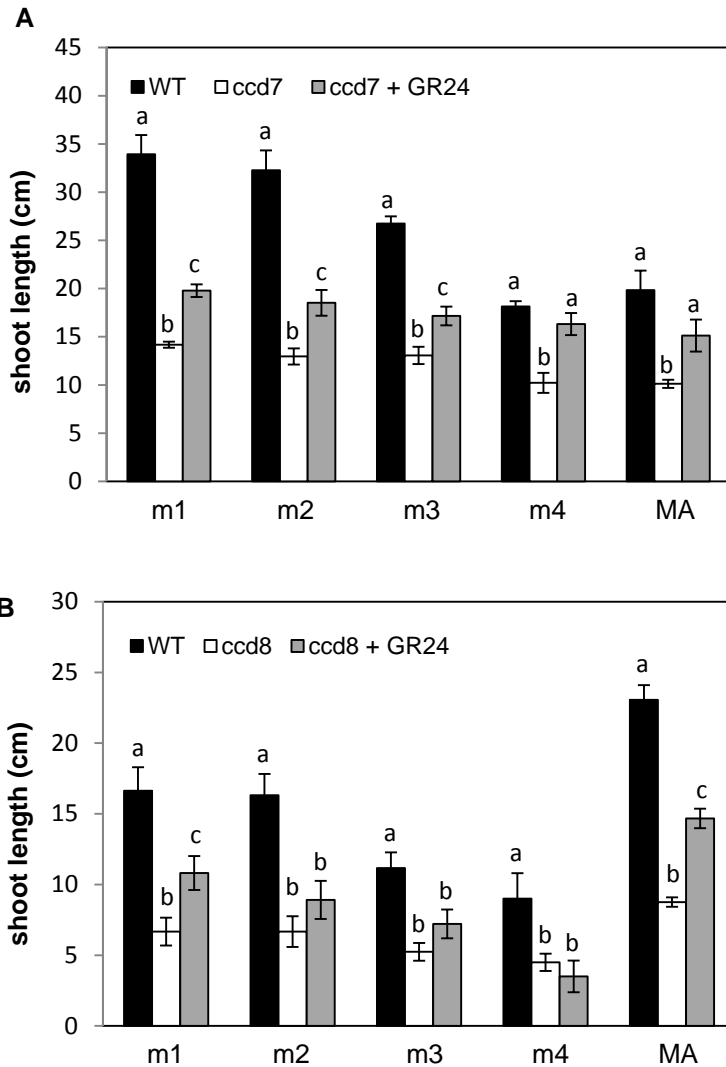
The *M. truncatula* (Mt) genes considered in this study are indicated by arrows. At: *Arabidopsis thaliana*; Lj: *Lotus japonicus*; Os: *Oryza sativa*; Ph: *Petunia hybrida*; Pp: *Physcomitrella patens*; Ps: *Pisum sativum*; Sl: *Solanum lycopersicum*; Zm: *Zea mays*. Accession numbers are listed in Supplementary Table 1.

Supplementary Figure S2

Strigolactone insertional mutant alleles used in this study.
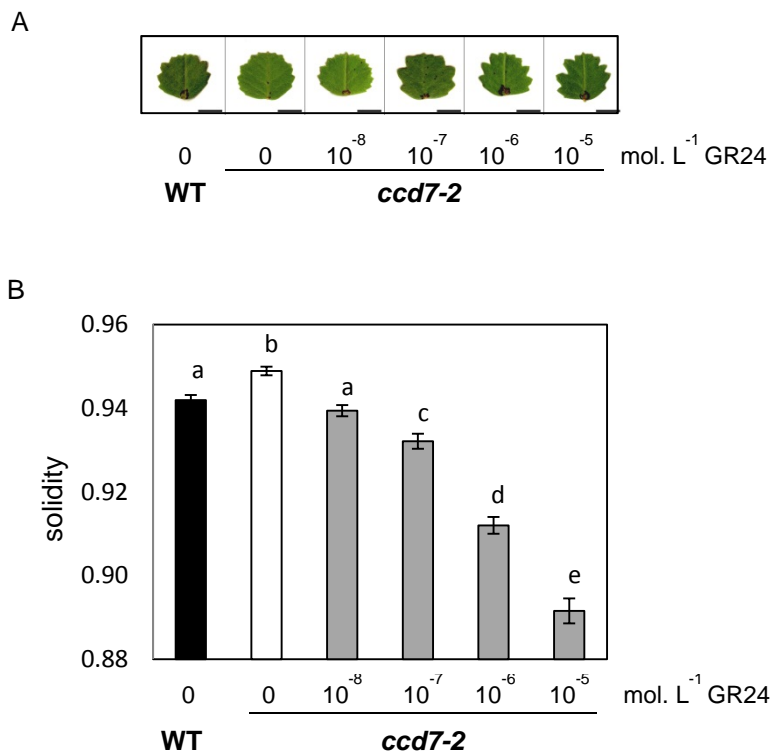
Position of *Tnt1* transposon insertion in *ccd7*, *ccd8* and *d14* mutant alleles. *Tnt1* presence and position were confirmed by PCR and sequencing.

Supplementary Figure S3

Exogenous strigolactone partly restores shoot elongation in *ccd7* and *ccd8* mutants.

Shoot lengths of the first axes (emerging from metamers m1 to m4) and of the main axis (MA) measured after 40 days of growth. Mutants (A: *ccd7-2*; B: *ccd8-1*) were treated or not with 10^{-5} M GR24 applied at the shoot apex. Values correspond to the mean +/- s.e.m. of 5-6 plants per genotype. Statistical analysis was performed independently for each axis. For a given axis, different letters indicate statistically significant differences according to one-way ANOVA followed by Fisher's LSD test.
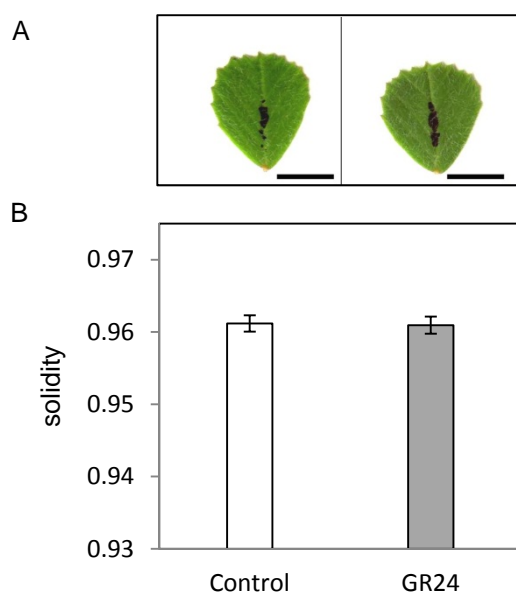
A

0   0 10^{-8} 10^{-7} 10^{-6} 10^{-5} mol. L^{-1} GR24

WT   ***ccd7-2***

B

0   0 10^{-8} 10^{-7} 10^{-6} 10^{-5} mol. L^{-1} GR24

WT   ***ccd7-2***

Supplementary Figure S4

Leaflet serration phenotype of *ccd7-2* mutants.

GR24 was applied to the shoot tip at the indicated concentrations.

A. Scanned images of one representative leaflet in each condition. Representative leaflets with a solidity value equal to the average solidity of all leaflets in this condition were selected. Bar = 5 mm.

B. Solidity values for WT and *ccd7-2* mutant plants, treated or not with GR24. Values correspond to the mean +/- s.e.m. (n= 74 to 114 leaflets for each condition). Different letters indicate statistically significant differences according to Mann-Whitney's test (P<0.05 after Bonferroni adjustment).

Supplementary Figure S5

Effect of GR24 on leaflet serrations in *M. truncatula* ecotype Jemalong A17.

Plants were treated with 10^{-5} mol.L^{-1} GR24 or the solvent alone (control).

A. Scanned images of one representative leaflet in each condition. Bar = 5 mm.

B. Solidity values. Values correspond to the mean +/- s.e.m. (n= 56 to 75 leaflets per condition). No statistically significant difference between control and treated plants was found according to unequal variance t test.

Species	Accession number	Gene name
Medicago truncatula	XM_003622507	MtCCD7
Medicago truncatula	XM_003603562	MtCCD8
Medicago truncatula	FM204879	MtCCD1
Medicago truncatula	AES95418	MtCCD4a
Medicago truncatula	AES95417	MtCCD4b
Medicago truncatula	XM_003589038	MtD14
Medicago truncatula	AES90654	MtD14-like 1a
Medicago truncatula	AES94592	MtD14-like 1b
Medicago truncatula	AES67371	MtD14-like 1c
Medicago truncatula	AES76757	MtD14-like 2
Arabidopsis thaliana	Q7XJM2	AtCCD7
Arabidopsis thaliana	Q8VY26	AtCCD8
Arabidopsis thaliana	O65572	AtCCD1
Arabidopsis thaliana	O49675	AtCCD4
Arabidopsis thaliana	NP_566220	AtD14
Arabidopsis thaliana	Q9SZU7	AtKAI2
Arabidopsis thaliana	NP_189085	AtD14-like 2
Pisum sativum	ABD67496	PsCCD7
Pisum sativum	AAS66907	PsCCD8
Pisum sativum	BAC10552	PsCCD4
Pisum sativum	AB080191	PsCCD1
Oryza sativa	Q7XU29	OsCCD7
Oryza sativa	Q93VD5	OsCCD8a
Oryza sativa	Q8LIY8	OsCCD8b
Oryza sativa	BAF30414	OsCCD1
Oryza sativa	NP_001047858	OsCCD4
Oryza sativa	Q10QA5	OsD14
Oryza sativa	NP_001050445	OsD14-like 1
Oryza sativa	NP_001056487	OsD14-like 2a
Oryza sativa	NP_001043470	OsD14-like 2b
Petunia hybrida	ACY01408	PhCCD7
Petunia hybrida	AAW59435	PhCCD8
Petunia hybrida	AAT68189	PhCCD1
Petunia hybrida	J9U5U9	PhDAD2
Solanum lycopersicum	ACY39883	SlCCD7
Solanum lycopersicum	AEH96363	SlCCD8
Solanum lycopersicum	AAT68187	SlCCD1a
Solanum lycopersicum	AAT68188	SlCCD1b
Solanum lycopersicum	XP_004246004	SlCCD4
Zea mays	DAA36538	ZmCCD7
Zea mays	NP_001183929	ZmCCD8
Zea mays	AFW89638	ZmCCD1
Zea mays	AFW63527	ZmCCD4
Physcomitrella patens	XP_001754597	PpCCD7
Physcomitrella patens	XP_00175472	PpCCD8
Lotus japonicus	ADM88552	LjCCD7

Supplementary Table S1

Accession numbers of genes used in the phylogenetic analysis.