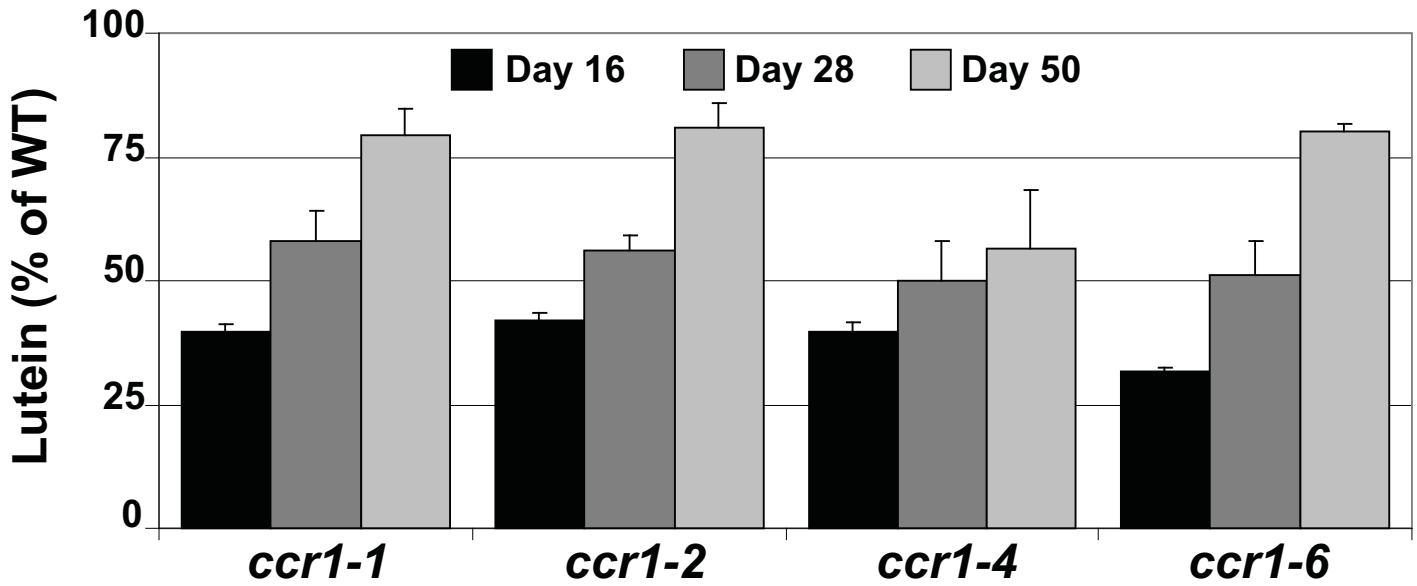
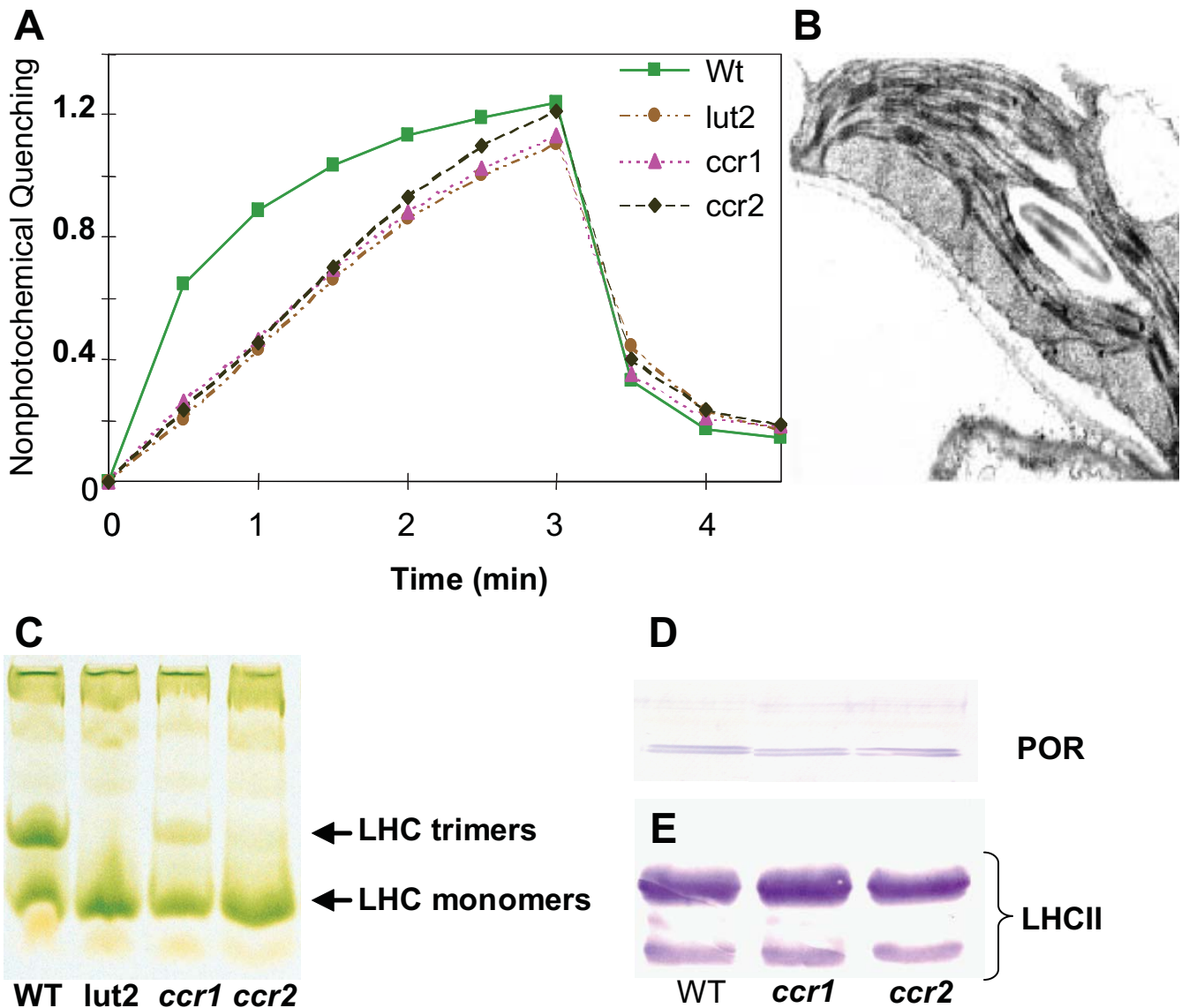


SI Fig 1. Lutein levels increase during plant development in *ccr1*.



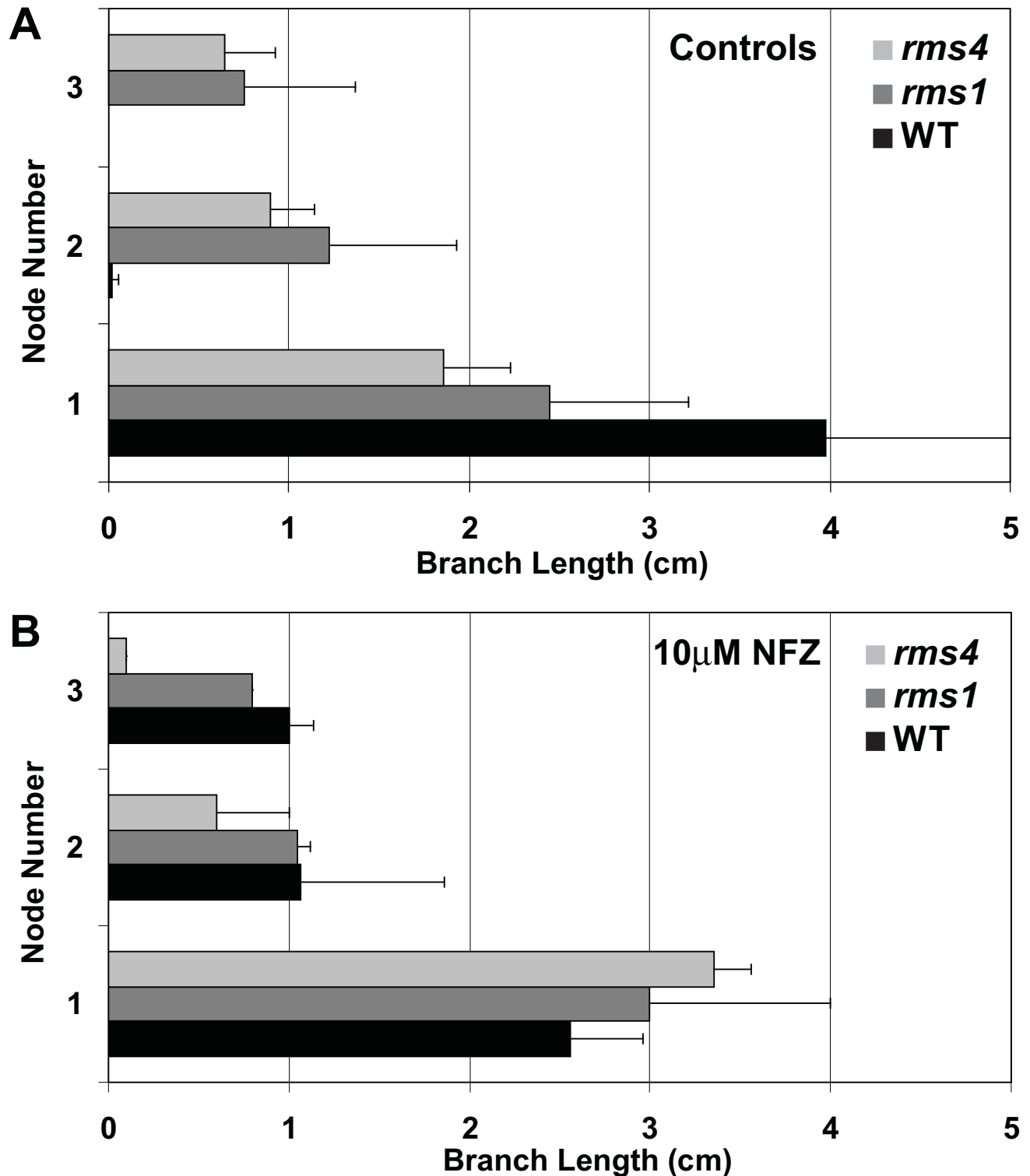
Lutein accumulation in aging leaf tissues from *ccr1* alleles. Lutein levels are expressed as a percentage of the total carotenoid pool relative to WT. Data are the average and standard errors (SE) of 2-5 biological replicates.

SI Fig 2. Photosynthetic parameters of *ccr1* are consistent with reduced lutein content.



(A) Nonphotochemical quenching. Mature leaves were exposed to actinic light for 3 minutes, after which it was switched off and NPQ was calculated as $(F_m - F_m')/F_m'$. (B) Electron micrograph of *ccr1* chloroplast exhibits normal morphology. A native green gel (C) shows fewer LHC trimers in, *lut2*, *ccr1* and *ccr2* compared to WT. Representative immunoblots of POR (D) and LHCII (E) shows that protein levels were identical in tissue from etiolated (POR) and light-grown leaf tissue (LHCII) in wild type, *ccr1*, and *ccr2*.

SI Fig 3. Inhibition of carotenoid biosynthesis affects shoot branching in pea.



Plants were grown on (A) MSO media alone or (B) 10 μ M norflurazon. The length of the branches developed at each shoot node, numbered from the shoot base, was determined after 12 days. The length of the shoot branch serves as an indication of bud outgrowth from the node. The average and SE of three to eight plants are given.

SI Table 1. Pigment Content and Photosynthetic Parameters

	Chloroplasts				Etioplasts
	F_v/F_m^a	Φ_{PSII}^a	Chl ^b	Chl <i>a/b</i> ^b	PChlde ^b
Wt	0.738±.004	0.425±.019	1210±70	3.30±0.1	1.15
<i>ccr1.1</i>	0.726±.002	0.433±.019	1040±90	3.26±0.1	0.77
<i>ccr2.1</i>	0.714±.006	0.448±.011	1150±60	3.27±0.2	0.88

Averages and standard deviations for 3 plants are given. ^aAbbreviations:

F_v/F_m , maximum photosynthetic efficiency Φ_{PSII} , photosynthetic efficiency of PSII. ^bChl, chlorophyll ($\mu\text{g/g}$ frsh wght) of six week old leaves, PChlde ratio, ratio of inactive and active forms of protochlorophyllide in etioplasts (Park et al. 2002).

SI Table 2. Quantitative PCR Primers

Target	Target Name	Mutant	Accession Number	Sequence (5'-->3')	Direction	Amplicon Size (bp)
Cyclo	Cyclophilin	-	At2g29960	TCTTCCTCTTCGGAGCCATA	Forward	250
PP2	Protein Phosphatase 2A	-	At1g13320	AAGCTGGGAATGATTCGATG CTTCGTGCAGTATCGCTTCTC ATTGGAGAGCTTGATTTGCG	Reverse Reverse Forward	249
Carotenoid Biosynthesis						
PSY	Phytoene synthase		At5g17230	TGGGAGTTTGATTCTTCTAACTGTA	Forward	251
PDS	Phytoene desaturase		At4g14210	GGTATCTGCTTCTTCTTACCTTTGT	Reverse	
ZDS	Carotene desaturase		At3g04870	GATCACCTACTCTTTAGCAGAAGTAA	Forward	334
CRTISO	Carotenoid isomerase	<i>ccr2</i>	At1g06820	GTACACAGATCTTGGAGTCTTAAC	Reverse	
εLCY	ε-lycopene cyclase	<i>lut2</i>	At5g57030	TTATGCTCTAGGTTTCATAGACTGC	Forward	248
βLCY	β-lycopene cyclase		At3g10230	CTAGTCCAGTGACATAAGTTTCTCC	Reverse	
εOH1	ε-hydroxylase I	<i>lut1</i>	At3g53130	GAAAAGGAAGGGATCCTTGG	Forward	256
βOH1	β-hydroxylase I		At4g25700	GCAAAGCATTGACTGTGCTC	Reverse	
βOH2	β-hydroxylase II		At5g52570	TCGGTTTGTGTAGTGTGAGAGC	Forward	253
				AAGGCTAAACCAGCAGGACC	Reverse	
				CTTGTTTCTAGTATGACAAACCTTAC	Forward	245
				GACCAGGTCTAGCAACTAAAGAAGT	Reverse	
				ATGCAGAAGACGGAAGTGCT	Forward	240
				CAGCCTTTTCAGCTTTTCACC	Reverse	
				TCTTCGATTTAAACGCTTTTCTG	Forward	115
				AGCGTCTATAGCGTTTGTGGA	Reverse	
				GCAAACCACCCTATATCCAC	Forward	178
				GCGACGTCATCAAGATCTCA	Reverse	
Novel Branching Hormone Perception and Biosynthesis						
CCD1	Carotenoid cleavage dioxygenases		At3g63520	GCTCCCATCCGTGATGAAAC	Forward	248
CCD4	Carotenoid cleavage dioxygenases		At4g19170	TTGGCAGCTCCGAAGAACTC	Reverse	
CCD7	Carotenoid cleavage dioxygenases	<i>max3</i>	At2g44990	TACGCGGCGATTGGAGATCC	Forward	250
CCD8	Carotenoid cleavage dioxygenases	<i>max4</i>	At4g32810	GCGATTTAGCGTCCATCACC	Reverse	
MAX1	More Auxillary 1	<i>max1</i>	At2g26170	ACTCAAACCTCGTCCGTAATTG	Reverse	258
				CCCATAAACCATGAAAACCC	Forward	
				TGCTCAACGACCTTGTAACCTC	Reverse	243
				TAGGGAAACTTGGCTCTTGC	Forward	
				TCGATCAGGTCATTAAGAGGC	Forward	249
				TACCGAATGGGATGAAAGCG	Reverse	

Histone Modification of Chromatin Surrounding CRTISO						
SAM	S-adenosyl methionine transferase		At4g01850	TGAAGTCCAAAAGCAAAAACC GACGGAGAAGAAGAGCGAAA	Forward Reverse	197
CH2	CRTiso promoter 2		AT1g06820	GATTGACCATAACAGTGGATCG CTCGACACTATCCTTGGATTG	Forward Reverse	209
CH1	CRTiso promoter 1		AT1g06820	ACAAAGATGCGGTCTCAACG CCCAACCAAGTTGGAATAGCT	Forward Reverse	216
CH3	CRTiso exon 1		AT1g06820	GTGTTTTCAAATCCCGTAAAG CCATCTCTTTCGTCCCTTG	Forward Reverse	210
CH4	CRTiso exon 2		AT1g06820	CTTAATTTGAAGGGAACAGGGG ATCCCTTCCTTTTCGTGAGG	Forward Reverse	198
Genes Neighbouring CRTISO						
SAM	S-adenosyl-methione		At4g01850	GACGGAGAAGAAGAGCGAAA TGAAGTCCAAAAGCAAAAACC	Forward Reverse	197
6800	Lipase III		At1g06800	GTTGAGAGTGGTGAACGAGCAC GTCCTTTCCCATGATACCCG	Forward Reverse	242
6810	Unknown		At1g06810	TAGGCTACAATGGTCCTGTCAC TTATCAACGCCTTGACCAGC	Forward Reverse	229
6830	Glutaredoxin		At1g06830	GCTCCTGTTGTTTGTCTATGC ATGGCTTCACTAGGGGAACG	Forward Reverse	234
6840	Kinase		At1g06840	CATGGCAAGAACATTGTGCG AGATCCGCTGTCTTGGCTAC	Forward Reverse	239
Auxin Transport						
PIN1	Auxin Transporter 1		At1g73590	CCAGTTTATTCGGCATCACC ACGGCATAAGAAGCAACGAG	Forward Reverse	244
PIN6	Auxin Transporter 6		At1g77110	TGGGCCGTTTTCTTCAAAGC GATTGATCCGGCTGCTTGAC	Forward Reverse	255

Supplemental Table 3. Microarray analysis of *ccr1-1*

This table can be downloaded as a separate file in spreadsheet format.

SI Table 4. SDG8 /CCR1 /EFS Sequencing Primers

Foward		Reverse		SIZE
Name	Sequence	Name	Sequence	
EFS_Amp1F	TTTTTGGGGTCTCTGTTTGG	EFS_Amp1R	CACTCCCTGCTCCTGAGTGT	511
EFS_Amp2F	GATTGAGCAGATGGGATACGG	EFS_Amp2R	GTGGCGCTACAGCCAAATAC	570
EFS_Amp3F	GGAAGAAATGGACCATCGAG	EFS_Amp3R	AATAGGGGAATTGGCTTCCA	489
EFS_Amp4F	TGGTATGGCTGCTGATCTGA	EFS_Amp4R	AATCCCCACTCAGATGAACG	447
EFS_Amp5F	GCTCGCCATCTGAGAAAATC	EFS_Amp5R	AAAGGTGTGGGTCATCATCTAAA	605
EFS_Amp6F	AGAATTGCCAGGATCAGCAC	EFS_Amp6R	GCAGATTCGGAAAACCTTGGA	534
EFS_Amp7F	GATGAATTGCGTGCTTCAAA	EFS_Amp7R	CCAGGCACTCTCTGTGGAAT	574
EFS_Amp8F	GGTGCCCTTCTAGATGCTGA	EFS_Amp8R	CGCAACACACTGGAAAACGT	517
EFS_Amp9F	GGCCACACACTGTTCTGGCTA	EFS_Amp9R	ACCTGTCAAACGCTTGCTCT	537
EFS_Amp10F	GAGTTGGGCATAGGACAGGA	EFS_Amp10R	TCGCTTGCAAACAAGACATT	578
EFS_Amp11F	CGTGTTCCTTCTATTTTGG	EFS_Amp11R	TCCACACAGCTTTAAACAGCA	671
EFS_Amp12F	TGCTTTCAAGGGTCAGAAACA	EFS_Amp12R	GGGGAAAATTTCAACCGAGT	598
EFS_Amp13F	AAAAGCTTATGAGGGTTTTGGACA	EFS_Amp13R	ACCCTGTGAACGAACCAGAC	618
EFS_Amp14F	TGCAGTGGATGGTGAATGG	EFS_Amp14R	GCTGAAGAAGAGGTGGAGGA	498
EFS_Amp15F	GAGCAAATGCCACAGAGCTT	EFS_Amp15R	CTGCAAAAATTGGTGGTGCTA	567
EFS_Amp16F	AACAGCAGCCCATCAAATCT	EFS_Amp16R	AGGAATTCAGGCACAGGATGC	583
EFS_Amp17F	CAAACAGGATTCAGCAAAAGG	EFS_Amp17R	GGAAGTGCCTATGGGTTTGA	577
EFS_Amp18F	CAGAACACACTTGGCATTGG	EFS_Amp18R	ATTTTTGGAGCCAGGTGACA	503
EFS_Amp19F	AGTTGTTGAAATTTGGCTGTCT	EFS_Amp19R	TTTCAGGAGTTGCAGCCTTT	573
EFS_Amp20F	TTAGAAAACCTTGGCGCATC	EFS_Amp20R	CATGAGACACTGGCGGTAGA	555
EFS_Amp21F	CCGCAACAAAAGTTCCTTTC	EFS_Amp20R	CCTATGGGCCAAATAAACCA	532