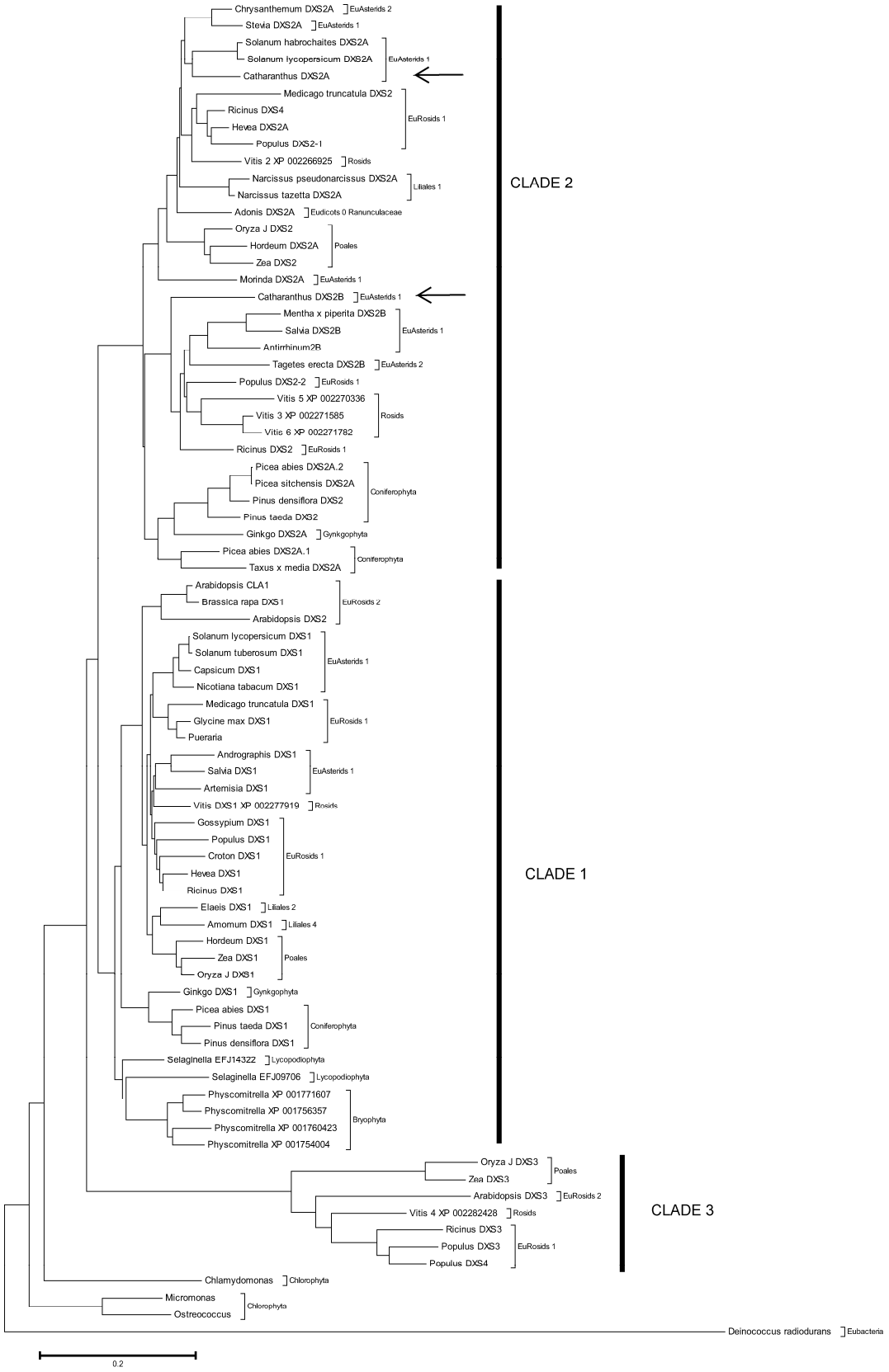
Chrysanthemum DXS2A
EuAsterids 2
Stevia DXS2A
EuAsterids 1
Solanum habrochaites DXS2A
Solanum lycopersicum DXS2A
EuAsterids 1
Catharanthus DXS2A
Medicago truncatula DXS2
Ricinus DXS4
Hevea DXS2A
Populus DXS2-1
EuRosids 1
Vitis 2 XP 002266925
Rosids
Narcissus pseudonarcissus DXS2A
Narcissus tazetta DXS2A
Liliales 1
Adonis DXS2A
Eudicots 0 Ranunculaceae
Oryza J DXS2
Hordeum DXS2A
Zea DXS2
Poales
Morinda DXS2A
EuAsterids 1
Catharanthus DXS2B
EuAsterids 1
Mentha x piperita DXS2B
Salvia DXS2B
EuAsterids 1
Antirrhinum2B
Tagetes erecta DXS2B
EuAsterids 2
Populus DXS2-2
EuRosids 1
Vitis 5 XP 002270336
Vitis 3 XP 002271585
Vitis 6 XP 002271782
Rosids
Ricinus DXS2
EuRosids 1
Picea abies DXS2A.2
Picea sitchensis DXS2A
Pinus densiflora DXS2
Pinus taeda DXS2
Coniferophyta
Ginkgo DXS2A
Gynkgophyta
Picea abies DXS2A.1
Taxus x media DXS2A
Coniferophyta
CLADE 2
Arabidopsis CLA1
Brassica rapa DXS1
Arabidopsis DXS2
EuRosids 2
Solanum lycopersicum DXS1
Solanum tuberosum DXS1
Capsicum DXS1
Nicotiana tabacum DXS1
EuAsterids 1
Medicago truncatula DXS1
Glycine max DXS1
Pueraria
EuRosids 1
Andrographis DXS1
Salvia DXS1
Artemisia DXS1
EuAsterids 1
Vitis DXS1 XP 002277919
Rosids
Gossypium DXS1
Populus DXS1
Croton DXS1
Hevea DXS1
Ricinus DXS1
EuRosids 1
Elaeis DXS1
Liliales 2
Amomum DXS1
Liliales 4
Hordeum DXS1
Zea DXS1
Oryza J DXS1
Poales
Ginkgo DXS1
Gynkgophyta
Picea abies DXS1
Pinus taeda DXS1
Pinus densiflora DXS1
Coniferophyta
Selaginella EFJ14322
Lycopodiophyta
Selaginella EFJ09706
Lycopodiophyta
Physcomitrella XP 001771607
Physcomitrella XP 001756357
Physcomitrella XP 001760423
Physcomitrella XP 001754004
Bryophyta
CLADE 1
Oryza J DXS3
Zea DXS3
Poales
Arabidopsis DXS3
EuRosids 2
Vitis 4 XP 002282428
Rosids
Ricinus DXS3
Populus DXS3
Populus DXS4
EuRosids 1
CLADE 3
Chlamydomonas
Chlorophyta
Micromonas
Ostreococcus
Chlorophyta
Deinococcus radiodurans
Eubacteria
0.2

Supplemental Figure S1. A phylogenetic tree was constructed from the amino acid sequence of DXS from the following species : *Adonis aestivalis* (ABK35283.1) ; *Amomum villosum* (ACR02668.1) ; *Andrographis paniculata* (AAP14353.1) ; *Arabidopsis thaliana* (CLA1 At4g15560 ; DXS2 At3g21500; DXS3 AT5G11380); *Artemisia annua* (AAD56390.2) ; *Antirrhinum majus* (AAW28999.1) ; *Brassica rapa* (ABE60813.1) ; *Capsicum annuum* (CAA75778.1) ; *Catharanthus roseus* (DXS2.1 renamed DXS2A CAA09804.2, DXS2.2 renamed DXS2B ABI35993.1) ; Chlamydomonas reinhardtii (CAA07554.1) ; *Chrysanthemum x morifolium* (BAE79547.1) ; *Croton stellatopilosus* (BAF75640.1) ; *Deinococcus radiodurans* R1 (NP_295198.1) ; *Elaeis guineensis* (AAS99588.1) ; *Glycine max* (ACO72582.1) ; *Ginkgo biloba* (DXS1 AAS89341.1, DXS2 AAR95699.1) ; *Gossypium barbadense* (ABN13970.1) ; *Hordeum vulgare* (BAJ94232.1. BAJ98888.1) ; *Hevea brasiliensis* (DXS1 clade AAS94123.1, DXS2 clade ABF18929.1; BAF98288.1) ; *Medicago truncatula* (DXS1, CAD22530.1, DXS2, CAN89181.1); *Mentha piperita* (AAC33513) ; *Morinda citrifolia* (AAL32062.1) ; *Narcissus pseudonarcissus* (CAC08458.1) ; *Narcissus tazetta* (ADD82535.1); *Nicotiana tabacum* (CBA12009.1) ; *Oryza sativa* (DXS1 NP_001055524, DXS2 NP_001059086, DXS3 clade BAD67657.1) ; *Ostreococcus lucimarinus* (XP_001416190.1); *Physcomitrella patens* (XP 001771607, XP 001756357, XP 001760423, XP 001754004); *Picea abies* (ABS50519.1 ; ABS50518.1); *Picea sitchensis (ACN39837.1)* ; *Picrorhiza kurrooa LAMIALES (ACB55417.1)* ; *Pinus densiflora* (DXS1 ACC54557.1, DXS2 ACC54554.1) ; *Pinus taeda* (DXS1 ACJ67021.1, DXS2 ACJ67020.1) ; *Populus trichocarpa* (DXS1 XP_002312717.1, DXS2 XP_002303416.1, XP_002331678.1, DXS3 XP_002308644.1) ; *Pueraria montana* (AAQ84169.1) ; *Ricinus communis* (DXS1 XP_002516843.1, DXS2 XP_002533688.1, DXS3 XP_002514364.1 ; DXS4 XP_002532384.1) ; *Salvia miltiorrhiza* (DXS1 ACF21004.1, DXS2 ACQ66107.1) ; *Selaginella moellendorffii* (EFJ14322.1) ; *Sorghum bicolor* (XP_002441088) ; *Solanum lycopersicum* (CAZ66648 ; AF143812_1) ; Solanum tuberosum (DXS1 ADK73609.1) ; *Stevia rebaudiana* (ACI43010) ; Taxus x media (AAS89342.1) ; *Vitis vinifera* (DXS1, XP 002277919 ; DXS2, XP 002266925 ; DXS3, XP 002271585 ; DXS4, XP 002282428 ; DXS5, XP 002270336 ; DXS6, XP 002271782) ; *Zea mays* (DXS1 ABP88134.1, DXS2 : ABP88135.1, DXS3 ADN 22972). Note that *C. roseus* DXS2.1 and DXS2.2 have been renamed DXS2A and DXS2B in this tree.

Enzyme	Primer	Sequence (5' – 3')	Amplification
DXS2.2	DXS2forA	GGAGATAGTGTATTCTGTGGCCA	3' end with T7
	DXS2-rev1	CTATCTCCTCCCTTAATTCGTCAGC	5' end with M13 reverse
	DXS2-full-for	CGACGAGTACTCTAGCATTCCTATCCTC	Full-length ORF
	DXS2-full-rev	CCTAATTCCACAATTGTATTCATCACCAAGTA	
CMS	CMS1	GGNCAGCCWATTGCHTTRTA	Internal cDNA fragment
	CMS3	TCATCRGGTGTHGTNACCTT	
	CMS7	AGCGGAGGATGTTGAGAAGGT	3' end with T7
	CMS5	TCAGGCATGCGGGAGAAAGTA	5' end with M13 reverse
	CMS11	AGAAGATGTCAATTCTTCGGC	Full-length ORF
	CMS12	GAATTACTATGCAGAGATGGG	
CMK	CMKfor	CATGAYYTRGCITCHYTITTTCAT	Internal cDNA fragment
	CMKrev	GTTGCWGCATTRCTRCTYCCWCC	
	3CMKfor1	GGTTCATCTCGATAAAAAGGTGCC	3' end with T7
	5CMKrev1	GTTATCAGTGCCAGTCTTCTTCCTAT	5' end with M13 reverse
	CMK-full-for	GGATAGACAAAAAGGCATATCTTGAATG	Full-length ORF
	CMK-full-rev	TGGTTTTGGCATTTATAACCATTTTC	
HDR	LytCR8	GAGCGTGCWGTYCARATTG	Internal cDNA fragment
	LytCR10	GAGCGTGCWGTYCARATTG	
	LytCR12	GATCCAGATGAGGATCTCAT	3' end with T7
	LytCR13	GATTGTGAATAATTTCATTCGTA	5' end with M13 reverse
	HDR1	ACAATGGCAATCTCTCTCCAA	Full-length ORF
	HDR2	AATCTATGCCAGTTGAAGGGC	

Supplemental Table S1. Details of primer sequences and cloning procedure used to amplify the *DX2.2*, *CMS*, *CMK* and *HDR* cDNAs.

Enzyme	Primer sequence (5'-3')	Restriction site added	Plasmids *cloning sites*	Complemented *E. coli* strain
DXS2.2	**pQE-DXS2-Hindfor** GCAAGCTTGCTGCTGCTCATGGGCATGCT	*Hind*III	pQE-30 *Hind*III	**EcAB4-2 (MG1655 *dxs::CAT MVA*+)**
	pQE-DXS2-Hindrev GCAAGCTTCTAAAACTGGAGAACTTGAAGAG TATTCTT	*Hind*III		
CMS	**pQE-CMSBam** TCGGATCCGAGAAAAGTGTCTCGGTAATTCT	*BamH*I	pQE-30 *BamH*I-*Hind*III	**EcAB4-7 (MG1655 *ygbP::CAT MVA*+)**
	pQE-CMSHind TCAAGCTTAGCAGAGATGGGATTCAAAATTC T	*Hind*III		
CMK	**pQE-CMKBam** ACGGATCCTGGAATAAGCTAGCTGATGAAGT A	*BamH*I	pQE-30 *BamH*I-*Kpn*I	**EcAB4-9 (MG1655 *ychB::CAT MVA*+)**
	pQE-CMKKpn TCGGTACCTTCAGAAGACTGGGAGAAGTCT	*Kpn*I		
HDR	**pQE-HDR-Bam2** GCGGATCCGAATTCGATGCTAAGAAATTCAG GCAC	*BamH*I	pQE-30 *BamH*I-*Hind*III	**MG1655 *ara<>ispH***
	pQE-HDR-Bam3 GCGGATCCGAACAGAGCACAGAGCTGATGAA C	*BamH*I		
	pQE-HDR-Hind GCAAGCTTCTATGCCAGTTGAAGGGCTTCTTCAC G	*Hind*III		

Supplemental Table S2. Details of primer sequences and cloning procedures used to express proteins for functional validation.

Enzyme	Primer	Séquence (5'-3')
DXS2.1	qDXS-up	TTGATGTAGGTATTGCCGAGCA
	qDXS-down	ACAATGAGTGGGTCCATCTGC
DXS2.2	qDXS2-up	GCTACAGTTGTTGATGCCCGA
	qDXS2-down	TTCAAAGCCAAGAACTGTGCC
DXR	qDXR-up	GCAGCAAATGAGAAGGCAGTT
	qDXR-down	GGGCTCAAACCAAGACTGTTC
CMS	qCMS-up	GCAACTTTGTCTCCTCAGCATT
	qCMS-down	GCAACTTTGTCTCCTCAGCATT
CMK	qCMK-up	AAAGATTGAAGCAGCGTGTGC
	qCMK-down	AGAGGCTTCAGACAAGGAAACG
MECS	qMECS-up	TAGAGGATGCGAGGCTCACT
	qMECS-down	TCATAACCTGCCTCGTCCATC
HDS	qHDS-up	GTCCCTTACTGAACCTCCAGAG
	qHDS-down	AATCACCTGTCCTGCGTTGG
HDR	qHDR-up	GATTGAGAGGACGATGATGCGT
	qHDR-down	AGTTCCACCCTCCAACGACT
RPS9 AJ749993	qRPS9-for	TTACAAGTCCCTTCGGTGGT
	qRPS9-rev	TTACAAGTCCCTTCGGTGGT

Supplemental Table S3. The sequence of primers used in the qRT-PCR analysis.

Enzyme	Primer sequence (5'-3')	Restriction site added	Plasmids *cloning sites*	Fusion protein
DXS2.1	**DXS-GFP-S** ATAGATCTTATGGCGGTTTCCGGGGCT	*Bgl*II	pSCA-cassette-GFPi pSCA-cassette-YFPi *Bgl*II-*Spe*I	DXS-GFP DXS-YFP
	DXS-GFP-AS CGACTAGTTTGAAGTTTAAGGGTTCT	*Spe*I		
DXS2.2	**DXS2-GFP-S** AGGCTAGCATGGCGGTGGCATCGAAT	*Nhe*I	pSCA-cassette-GFPi pSCA-cassette-YFPi *Spe*I	DXS2-GFP DXS2-YFP
	DXS2-GFP-AS CGGCTAGCAAACTGGAGAACTTGAAGAG	*Nhe*I		
DXR	**DXR-GFP-S** GGAGATCTTATGGCTTTGAATTCGCTGTCC	*Bgl*II	pSCA-cassette-GFPi pSCA-cassette-YFPi *Bgl*II-*Spe*I	DXR-GFP DXR-YFP
	DXR-GFP-AS GGACTAGTGGCAGGGCTCAAACCAAGACT	*Spe*I		
CMS	**CMS-GFP-S** CGAGATCTTATGTCAATTCTTCGGCTC	*Bgl*II	pSCA-cassette-GFPi *Bgl*II-*Spe*I	CMS-GFP
	CMS-GFP-AS CGACTAGTAGCAGAGATGGGATTCAA	*Spe*I		
CMK	**CMK-GFP-S** GCACTAGTATGGCTTCCTCTCAGTCTCTATG TGGT	*Spe*I	pSCA-cassette-GFPi *Spe*I	CMK-GFP
	CMK-GFP-AS GCACTAGTCTATTCAGAAGACTGGGAGAAGT CTGT	*Spe*I		
MECS	**MECS-GFP-S** TCAGATCTTATGGCTATGGCGACTTCT	*Bgl*II	pSCA-cassette-GFPi *Spe*I	MECS-GFP
	MECS-GFP-AS GCACTAGTCTTCCTCATAAGAAGTAC	*Spe*I		
HDS	**HDS-GFP-S** GGAGATCTGATGGCGACCGGAACAGTTC	*Bgl*II	pSCA-cassette-GFPi pSCA-cassette-YFPi *Bgl*II-*Spe*I	HDS-GFP HDS-YFP
	HDS-GFP-AS GGACTAGTGTCTTCTGCAGGAGGATCAACC	*Spe*I		
HDR	**HDR-GFP-S** GCAGATCTTATGGCAATCTCTCTCCAA	*Bgl*II	pSCA-cassette-GFPi *Bgl*II-*Spe*I	HDR-GFP
	HDR-GFP-AS TAACTAGTTGCCAGTTGAAGGGCTTC	*Spe*I		

Supplemental Table S4. Details of primer sequences and cloning procedure used to express full-length MEP pathway enzyme fused to FP.

Enzyme	Primer sequence (5'-3')	Restriction site added	Plasmids *cloning sites*	Fusion protein
DXS2.1	**DXS-GFP-S** ATAGATCTTATGGCGGTTTCCGGGGCT	*Bgl*II	pSCA-cassette-GFPi *Bgl*II-*Spe*I	tpDXS-GFP
	peptideL-DXSrev GCACTAGTTGCTCTAAGTTCTGCAGCGAGCTG	*Spe*I		
DXS2.2	**DXS2-GFP-S** AGGCTAGCATGGCGGTGGCATCGAAT	*Nhe*I	pSCA-cassette-GFPi *Spe*I	tpDXS2-GFP
	peptideL-DXS2rev GCGCTAGCGATGGTATCCAAAATAGGAGTAAAAGGCTT	*Nhe*I		
DXR	**DXR-GFP-S** GGAGATCTTATGGCTTTGAATTCGCTGTCC	*Bgl*II	pSCA-cassette-GFPi pSCA-cassette-YFPi *Bgl*II-*Spe*I	tpDXR-GFP tpDXR-YFP
	peptideL-DXRrev GCACTAGTATTCTCAGCAACTATATCTAGTGTCTG	*Spe*I		
HDS	**HDS-GFP-S** GGAGATCTGATGGCGACCGGAACAGTTC	*Bgl*II	pSCA-cassette-GFPi pSCA-cassette-YFPi *Bgl*II-*Spe*I	tpHDS-GFP tpHDS-YFP
	peptideL-HDSrev GCACTAGTGTCACTACCAAGGGCTACATTCCC	*Spe*I		

Supplemental Table S5. Details of primer sequences and cloning procedure used to fuse the first 100-residues of DXS2.1, DXS2.2, DXR and HDS to GFP.

Enzyme	Primer sequence (5'-3')	Restriction site added	Plasmids *cloning sites*	Fusion protein
DXR	**DXR-GFP-S** GGAGATCTTATGGCTTTGAATTCGCTGTCC	*Bgl*II	pSCA-cassette-YFPi *Bgl*II-*Spe*I	tpDXR(1-83)-YFP
	peptideL-DXRrev2 GCACTAGTAACTATTGAAATGGGCTTCTGACCTTC	*Spe*I		
	DXR-C-for2 GCACTAGTGGCTCTACAGGCTCAGTAGGAACTCAG	*Spe*I	pSCA-cassette-YFPi-tpDXR(1-83) *Nhe*I	Tp(1-83)-YFP-DXR(84-474)
	DXR-GFP-AS GGACTAGTGGCAGGGCTCAAACCAAGACT	*Spe*I		
HDS	**HDS-GFP-S** GGAGATCTGATGGCGACCGGAACAGTTC	*Bgl*II	pSCA-cassette-YFPi *Bgl*II-*Spe*I	tpHDS(1-100)-YFP
	peptideL-HDSrev GCACTAGTGTCACTACCAAGGGCTACATTCCC	*Spe*I		
	HDS-C-for2 GCACTAGTATGGTTGGGAATGTAGCCCTTGGTAGTGAC	*Spe*I	pSCA-cassette-YFPi-tpHDS(1-100) *Nhe*I	tp(1-100)-YFP-HDS(91-740)
	HDS-GFP-AS GGACTAGTGTCTTCTGCAGGAGGATCAACC	*Spe*I		

Supplemental Table S6. Details of primer sequences and cloning procedures used to create internal YFP fusion for DXR and HDS.

Enzyme	Primer sequence (5'-3')	Restriction site added	Plasmids *cloning sites*	Fusion protein
CAB1	**CAB1-for** GCACTAGTATGGCCGCCTCAACAATGGC	*Spe*I	pSCA-cassette-CFPi *Spe*I	CAB-CFP
	CAB1-rev GCACTAGTCTTTCCGGGAACAAAGTTGGTGGC	*Spe*I		
TIC40	**TIC40-for** GCACTAGTATGGAGAACCTTACCCTAGTTTCTTGCT	*Spe*I	pSCA-cassette-CFPi *Spe*I	TIC-CFP
	TIC40-rev GCACTAGTACCCGTCATTCCTGGGAAGAGC	*Spe*I		
CCD4	**CCD4-for** GCACTAGTATGGACTCTGTTTCTTCTTCTTCCTTCC	*Spe*I	pSCA-cassette-CFPi *Spe*I	CCD4-CFP
	CCD4-rev GCACTAGTAAGCTTATTAAGGTCACTTTCCTTGACAAATAAC	*Spe*I		

Supplemental Table S7. Details of primer sequences and cloning procedures used to create plastid subcompartment CFP-markers of. The CAB1 (chlorophyll a/b binding protein 1, At1g29930), TIC40 (translocon at the inner envelope of chloroplasts, At5g16620), CCD4 (carotenoid cleavage dioxygenase 4, At4g19170) proteins of *A. thaliana* were used as a marker of thylakoid, inner membrane of plastid and plastoglobuli, respectively. The coding sequence of these proteins was amplified using retro-transcribed RNA extracted from *A. thaliana* as a matrix.