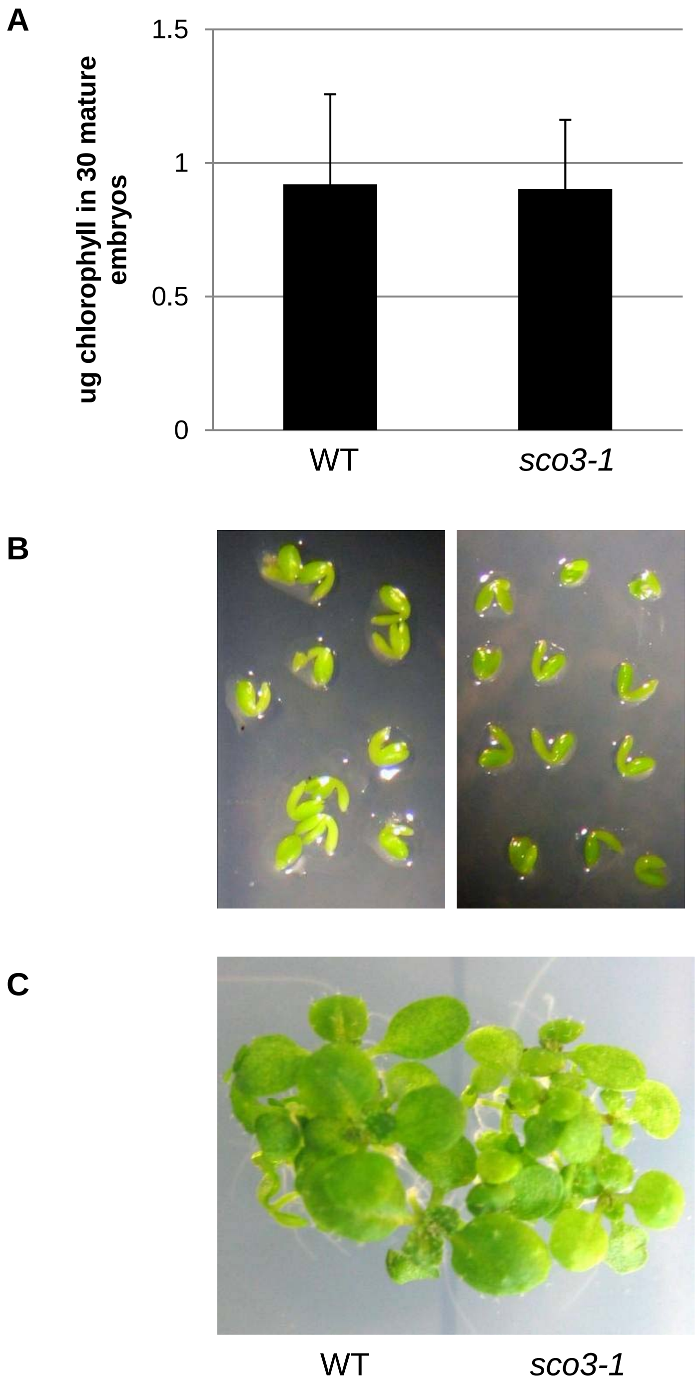
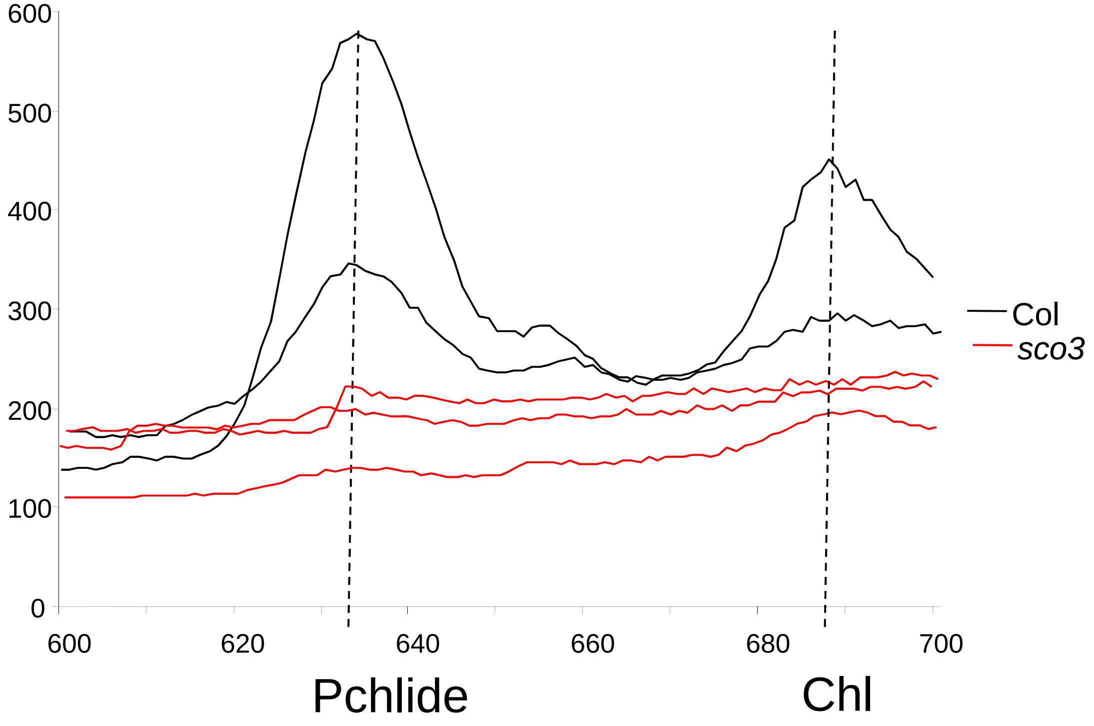
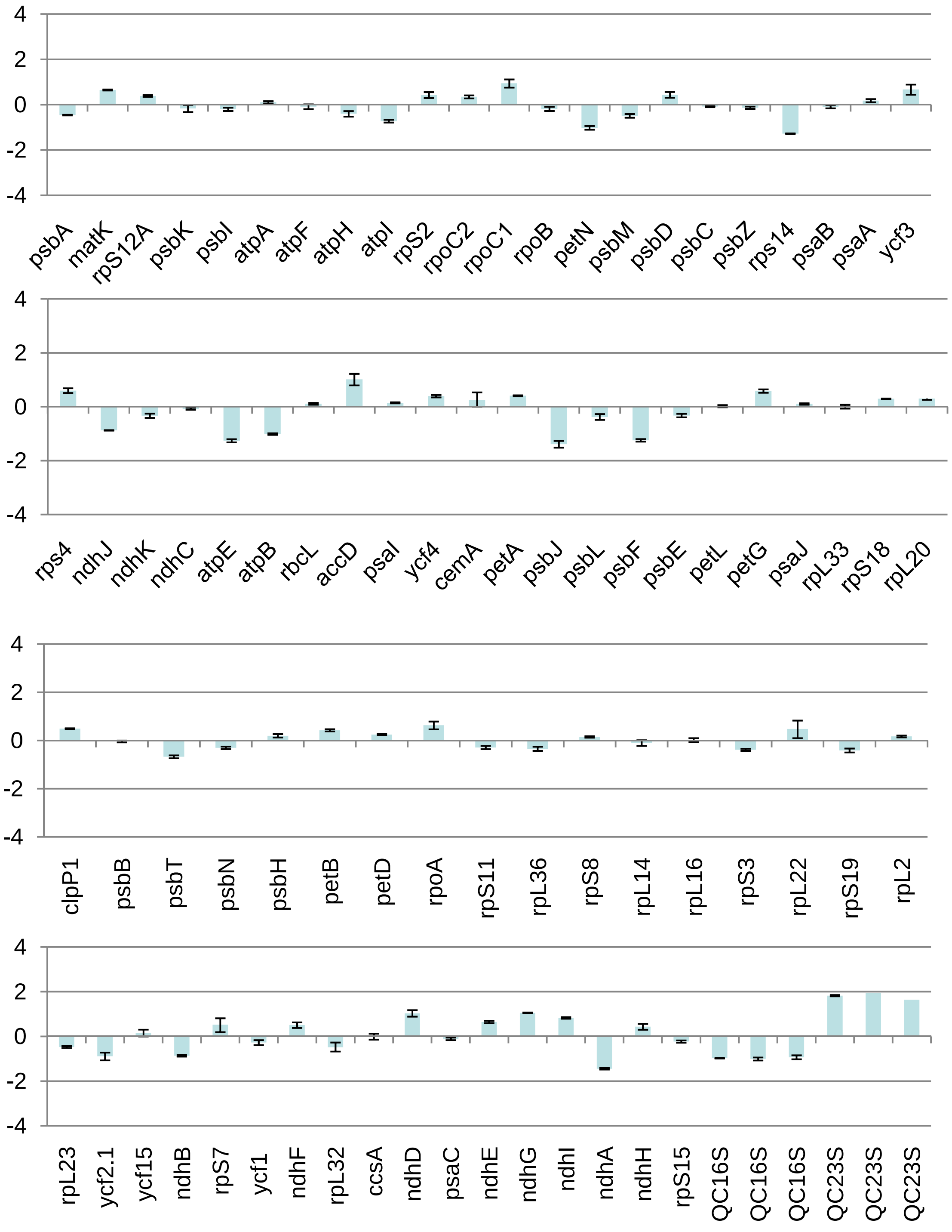


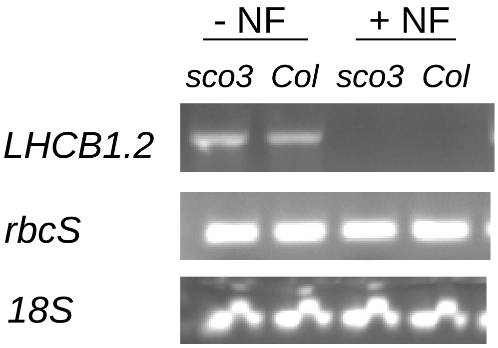
Supplemental Figure 1: Embryo development in the *sco3-1* mutant. (A) chlorophyll content in mature embryos of wildtype (WT) and *sco3-1* indicating the average and the standard deviation of three independent measurments. Phenotype of extracted mature embryos before (B) and after precocious germination (C).



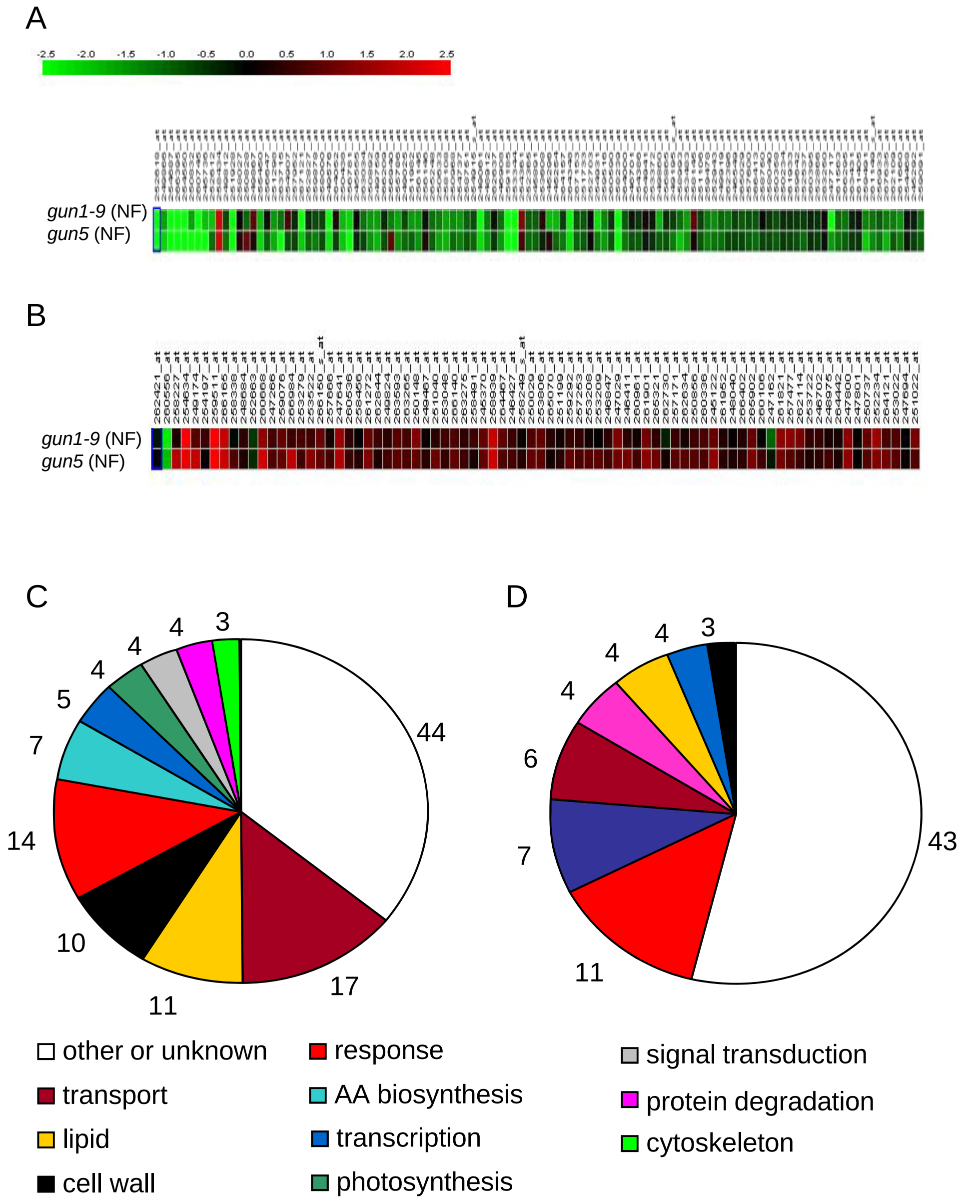
Supplemental Figure 2: Measurement of the protochlorophyllide (Pchlide) autofluorescence of 4d old etiolated seedlings of *sco3-1* (red line) and Col (black line) using the 77K low temperature fluorescence. Trace levels of chlorophyll (Chl) indicate brief exposure to light during the procedure. Note that for *sco3-1* no peak for the Pchlide could be detected.



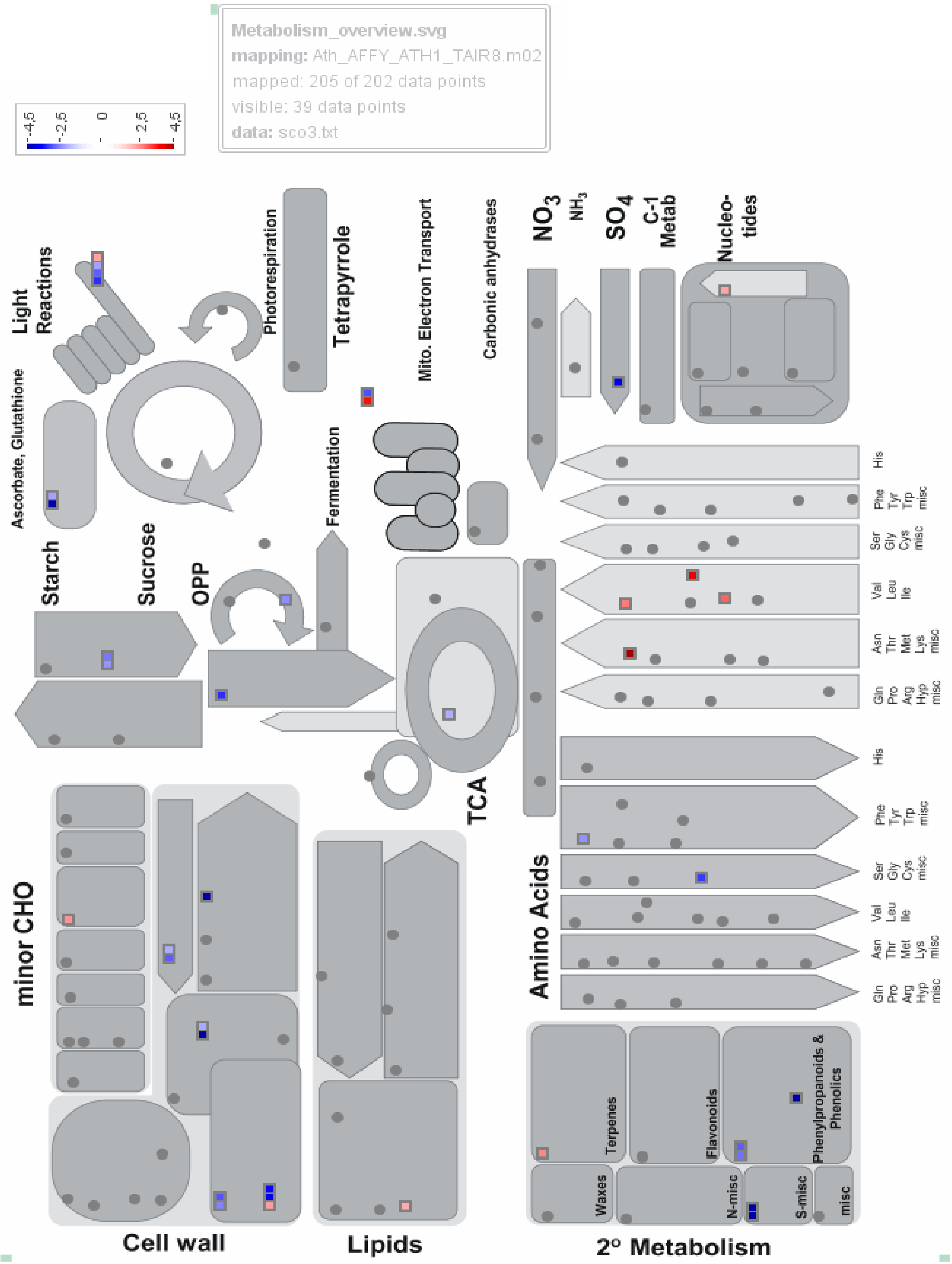
Supplemental Figure 3: Quantitative Real time analysis of transcript levels of chloroplast-encoded genes. Analsyses have been performed on three independent replicates.



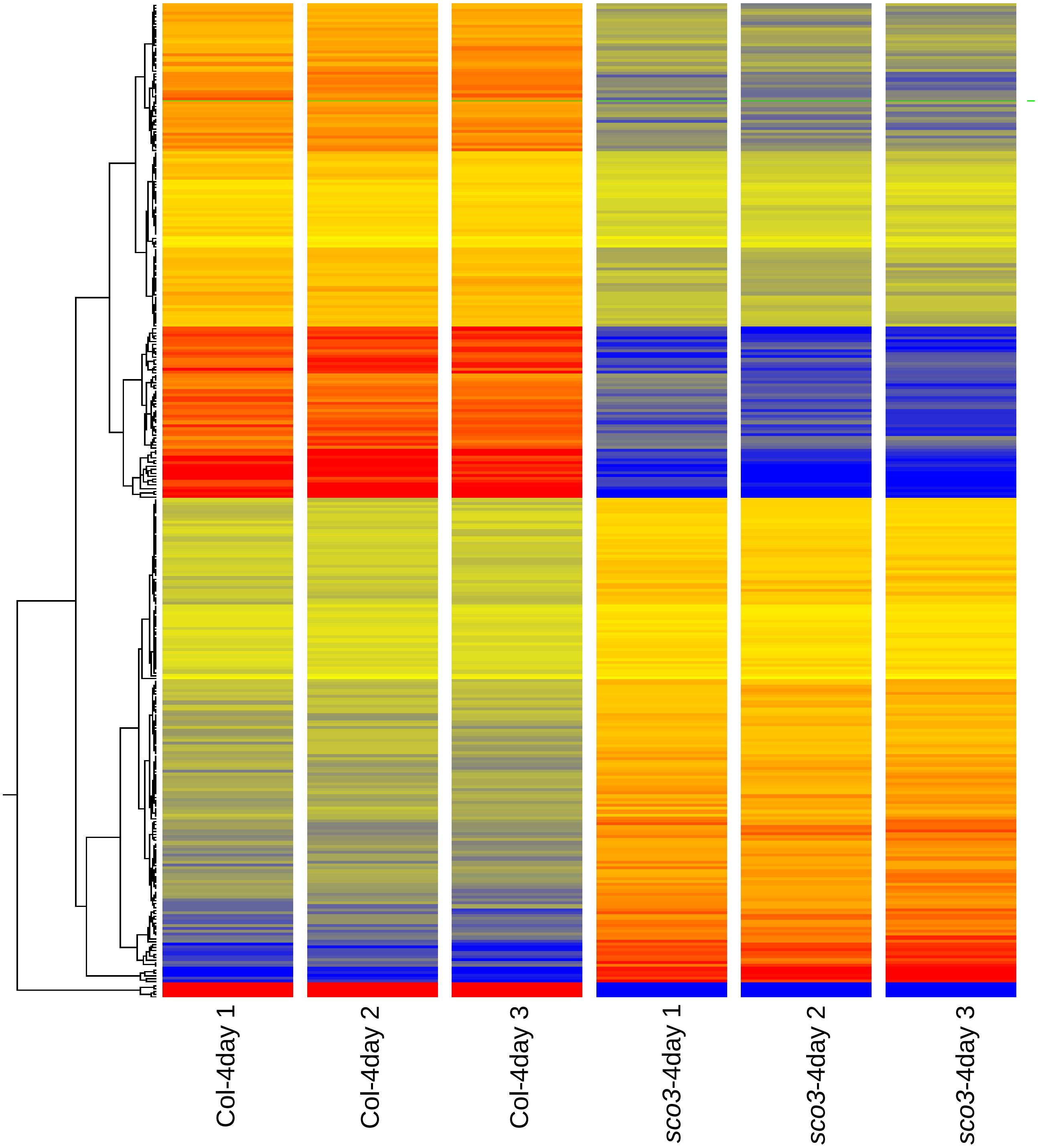
Supplemental Figure 4: RT-PCR analysis of transcript levels of retrograde signalling-controlled nuclear genes in *sco3-1* and Col on media either with or without the chloroplast biogenesis inhibitor Norflurazon (NF).



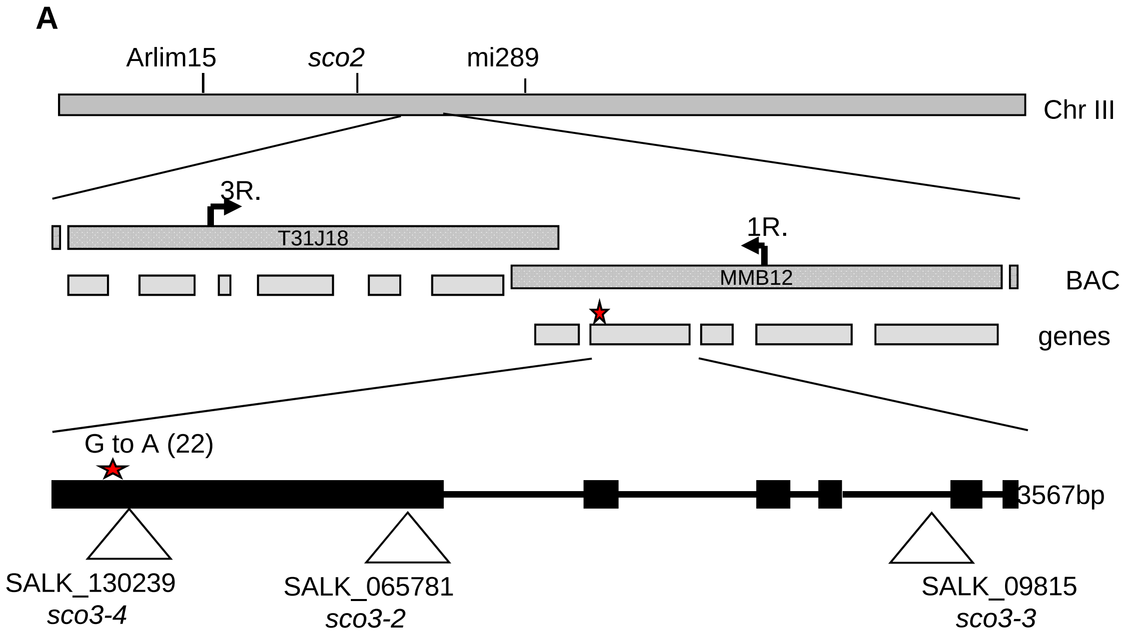
Supplemental Figure 5.: Microarray analysis. Heatmap of down- (A) and up-regulated genes (B) in *sco3-1* compared with their expression in Col, and the mutants *gun1-9,* and *gun5* treated with norflurazon. Summary of predicted function of (C) down-regulated and (D) up-regulated genes in *sco3-1.*



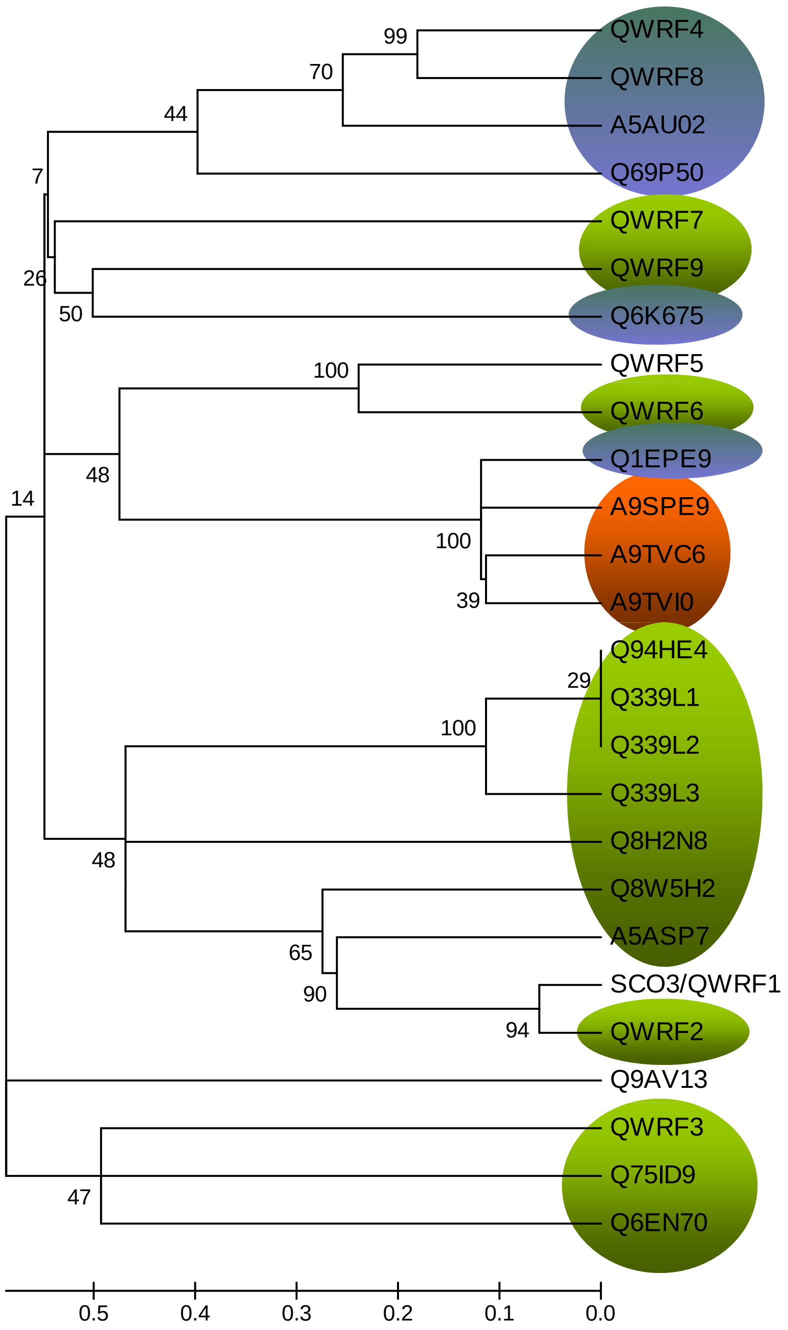
Supplemental Figure 6: Microarray analysis**.** MapMan analysis showing down- and up-regulated genes in *sco3-1.*



Supplemental Figure 7: Microarray analysis. Hierarchical graph of the expression data of differentially expressed genes in Col and *sco3-1*. Blue indicates no expression of the gene whereas red indicates high expression.



Supplemental Figure 8: The identification of the *SCO3* gene. (A) The mapping of *SCO3* on the upper arm of chromosome III and BAC clones covering this region with predicted genes. The gene mutated in *SCO3* is marked with an asterisk. The positions of both T-DNA insertion lines from SALK are indicated.



Supplemental Figure 9: Phylogenetic tree (Mega4.0.2, neighbour joining, bootstrap consensus tree) of the identified QWRF proteins in *Arabidopsis thaliana, Vitis vitifera, Oriza sativa, Musa accuminata* and *Physcomitrella patens.* Proteins predicted for chloroplast localization are shaded green, for unknown localization with blue and proteins identified in *Physcomitrella* are highlighted in red.

```
SCO3/QWRF1 SAPARTSSSPSRVRNGVSEQMNAYNR-TLPSILCFSADIRRGKIGEDRVMDAHLLRLLYN 459
QWRF2      SSPARALSSPSRARNGVSDQMNAYNRNNTPSILSFSADIRRGKIGEDRVMDAHLLRLLYN 464
QWRF3      LVRSSTPPSRGVSPSRIRQTAQS--SSTNTSVLSFIADVKKGKK-ATYIEDVHQLRLLYN 394
QWRF4      ---------------------------------KSSPFTSPLKPKTCDTESAHQLKLMNN 225
QWRF5      ---------------------------PVAPNSKIQADTKKQKKALGQQADVHSLKLLHN 279
QWRF6      ---------------------------PMAP--KVPADTKKQRKVTEQLEDVHSLKLLHN 260
QWRF7      ---------------------------------VLKYFMAQKKVSPVQEEDYHRFRIFQN 207
QWRF8      FARPSTPPSRGISPSRIRQTTTSTQSSTTTSVLSFITDVKKGKK-ASYIEDVHQLRLLHN 439
QWRF9      ---------------------------------NVVKARVSQDRLEPSSHGLRKISVDSS 250

SCO3/QWRF1 RDLQWRFANARADSTLMVQRLSAEKILWNAWVSISELRHSVTLKRIKLLLMRQKLKLASI 519
QWRF2      RDLQWRFVNARADSTVMVQRLNAEKNLWNAWVSISELRHSVTLKRIKLLLLRQKLKLASI 524
QWRF3      RLLQWRFVNARACDVNKNVASQEKNQLLCAWDTLIKLNNLVLQERIKLQKKNLEMKLNYV 285
QWRF4      RYSQWRFANARAEGVSYVQSLI-------------------------------------- 416
QWRF5      RYLQWRFANANAEVKTQSQKAQAERMFYSLGLKMSELSDSVQRKRIELQHLQRVKAVTEI 339
QWRF6      RYLQWRFANANAQVKTQTHKTQTETMIHSFGSKISELHDSVQRKRIELQRLLKTKALLAI 320
QWRF7      RLLQWRFVNARTEATMANLKINVEDQLFWVWLRIYKMRNYVVENLIEIQRLRQDIKVREV 267
QWRF8      RYLQWRFAIARAESVMYIQRLTSEETLFNVWHAISELQDHVTRQRIGLQQLKLEIKLNSL 499
QWRF9      VLSPKEANCFQKVSRFDLLHLVNLRRLYNAWRSISNLYNSVSMKRIEMQHLKQNLKLISI 310

SCO3/QWRF1 LKEQMCYLEEWSLLDRNHSNSLSGATEALKASTLRLPVSG--------KAVVDIQDLKHA 571
QWRF2      LRGQMGFLEEWSLLDRDHSSSLSGATESLKASTLRLPIVG--------KTVVDIQDLKHA 576
QWRF3      FLSQVKHLEAWEDMEIQHLSSLSIIRDSLHSVLSRLPLKE--------GAKVNLESAVSI 337
QWRF4      --AKMVCLEDWAMVEREHISSLAGAIGDLEANTLRLPLAG--------GTKADLGSLKLA 466
QWRF5      VESQTPSLEQWAVLEDEFSTSLLETTEALLNASLRLPLDS--------KIKVETKELAEA 391
QWRF6      TESQTPCLEQWSAIEEEYSTSVSQTIQAFSNASLRLPLDG--------DIMVDSKQLGDG 372
QWRF7      LSLQMPLLNEWSKIDAKNSEALSKLTRKLHALSVRLPLVHGATKLIIWKLQIDMVSIHEE 327
QWRF8      LNDQMVSLEDWATLERDHVSSLVGAISDLEANTLRLPATG--------GTKADTESLKAA 551
QWRF9      LNMQMGHLEEWLVIDRNYMGSLVGAAEALKGSTLCLPVDC--------GAMVNVQSVKDA 362

SCO3/QWRF1 VSSAVDVMHAMVSSIFSLTS------------------KVEEMNSVMAEMVNITGKEEVL 613
QWRF2      VSSAVDVMQAMSSSIFSLTS------------------KVDEMNSVMVETVNVTAKEKVL 618
QWRF3      IKNAEAVTDAIISTVDDYAP------------------TMEGIVPLASQLAEVVVQEKLM 379
QWRF4      MSSALDVMQSMGSSIWSLHS------------------QMEEMNKLVSDLAVIAKTENFL 508
QWRF5      LVVASKSMEGIVQNIGNLVP------------------KTQEMETLMSELARVSGIEKAS 433
QWRF6      LVAASKIVDGITQNVGNYMP------------------KAKEMESLLSELTRVARSERSL 414
QWRF7      MVIAIEVMDEIEDVIIKFLPRIHVKEINLRMSWVIKYQQVEIILYELTELIGMFNQELLY 387
QWRF8      MSSALDVMQAMGSSIWSLLS------------------KVEEMNIMVTELAVVVTKESSM 593
QWRF9      ICSAVDVMQAMASSICLLLP------------------KVGKISSLAAELGRVNAKDEGM 404

SCO3/QWRF1 LEQCQGFLTRVAAMQVTDCSMKTHIIQLSRL---------------------------- 644
QWRF2      LERCQGCLSRVAAMQVTDCSMKTHIIQLSRIPITSSLTPQL------------------ 659
QWRF3      LEKCHDLLRMISELEDCVFPCQSFATQFFKSKNYSILRLNKCCDSRKSLRFSVSDGTRW 438
QWRF4      LDKCENLLASTAVMEIEERSLKTHLIQKKQEEEVRDDAESSP-LLPLSKFQWP------ 560
QWRF5      VEDCRVALLKTHSSQMEECYLRSQLIQHQKKCHQQECTTSV------------------ 474
QWRF6      TENCVVALLKTQASQIEECSMRSQLIQQTTK---EESSSK------------------- 451
QWRF7      FEEMDESLLSIPLFTVIHYLLISLYICDRSGSFIYNLNGLFFIGSIWMWKLHRLKW--- 443
QWRF8      QGKCEDLLASTAIMQIEECSLRTHLIQTRREE--GEDAETPPPLLPLSKFPWP------ 644
QWRF9      LDVCRDLLNTISALQVQYLKFIIDLSALYLQCWGLISKLCR------------------ 445
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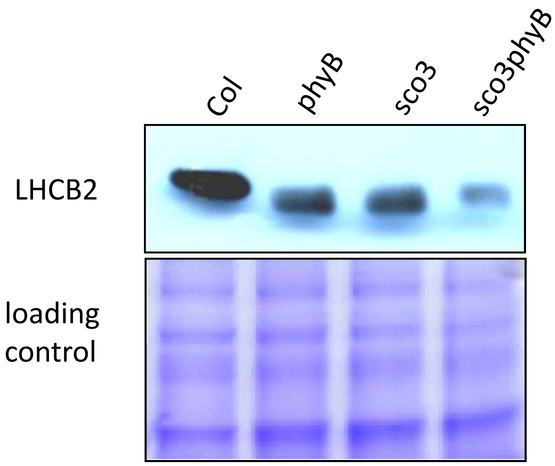
Supplemental Figure 10: ClustalW alignment of the QWRF domain of the different QWRF proteins in *Arabidopsis thaliana*. Amino acids conserved in eight of the nine proteins are highlighted in dark grey boxes. Light grey boxes indicate amino acids conserved in at least half of the QWRF proteins in *A. thaliana*.



Supplemental Figure 11: Immunoblot analysis on total protein extract of 4days old seedlings of Col, *sco3-1, phyB and sco3-1phyB* using monoclonal LHCB2 antibody (Agrisera). NO size differences between Col and the mutants could be detected. A coomassie-stained loading control is shown on the bottom.

Supplemental Table 1: List of the identified QWRF proteins in different plant species, their accession number, size of the proteins and the predicted localization of the different QWRF proteins.

name	**species**	**gene/prot No**	**pred. localization**	**protein size**
SCO3/QWRF1	*A. thaliana*	At3g19570	unknown	644AA
QWRF2	*A. thaliana*	At1g49890	plastid	659AA
QWRF3	*A. thaliana*	At2g20815	plastid	438AA
QWRF4	*A. thaliana*	At2g24070	plastid	560AA
QWRF5/EDE1	*A. thaliana*	At2g44190	Nucl.microtubules	474AA
QWRF6	*A. thaliana*	At3g60000	plastid	451AA
QWRF7	*A. thaliana*	At4g25190	plastid	443AA
QWRF8	*A. thaliana*	At4g30710	unknown	644AA
QWRF9	*A. thaliana*	At5g43160	plastid	445AA
A7NU78	*Vitis vinifera*	A7NU78	plastid	555AA
A7QL53	*Vitis vinifera*	A7QL53	plastid	522AA
A7PFN8	*Vitis vinifera*	A7PFN8	unknown	638AA
A5AUO2	*Vitis vinifera*	A5AUO2	unknown	610AA
H5ASP7	*Vitis vinifera*	H5ASP7	plastid	600AA
A7QAR3	*Vitis vinifera*	A7QAR3	plastid	618AA
Q6K675	*Oryza sativa*	Q6K675	unknown	1369AA
Q69P50	*Oryza sativa*	Q69P50	unknown	579AA
Q9AV13	*Oryza sativa*	Q9AV13	mitochondria	369AA
Q75ID9	*Oryza sativa*	Q75ID9	plastid	529AA
Q94HE4	*Oryza sativa*	Q94HE4	plastid	461AA
Q339L2	*Oryza sativa*	Q339L2	plastid	431AA
Q6EN70	*Oryza sativa*	Q6EN70	plastid	497AA
Q339L1	*Oryza sativa*	Q339L1	plastid	322AA
Q8H2N8	*Oryza sativa*	Q8H2N8	plastid	520AA
Q8W5H2	*Oryza sativa*	Q8W5H2	plastid	653AA
Q339L3	*Oryza sativa*	Q339L3	plastid	462AA
Q1EPE9	*M. accuminata*	Q1EPE9	unknown	643AA
A9SPE9	*P.patens*	A9SPE9	unknown	859AA
A9TVI0	*P.patens*	A9TVI0	unknown	965AA
A9U2E5	*P.patens*	A9U2E5	unknown	784AA
A9TVC6	*P.patens*	A9TVC6	unknown	856AA

Supplemental Table 2: Primers used for the different analyses.

Primer	**Used for**	**sequence**
SCO3-pENTR-F	Cloning	TTT TgtcgacttATGGTGGCTGCGATTCCT
SCO3-pENTR-R	Cloning	TTT gcggccgc ttTAGCCGGCTAAGTTGTATTATGTGC
Sco3-sv1-RT-R:	Cloning	GCAGTCCGTAACCTGCATTGCT
SCO3-sv2-RT-R	Cloning	GCAAGAGGCATGTCTTGTTAAG
SCO3-F1	Sequencing and genotyping	cttcgctctg aagcaaaga
SCO3-R1	Sequencing and genotyping	Ctt ggg cta gaa cat tga ggt ga
SCO3-F2	Sequencing and genotyping	CGTGTGACTT TACTGCATCT
SCO3-R2	Sequencing and genotyping	CTCATCAAGAGCAACTTGATCCG
SCO3-F3	Sequencing and genotyping	gcctgat gctgatgtga tgaca
SCO3-R3	Sequencing and genotyping/RT-PCR	Ggt tgtg aag tgg cgt gag t
SCO3-RT-F	RT-PCR	GCCGTGGTTGATATTCAAG
Sco3-NcoI-F	Cloning	TTT TCC ATG GGG ATGGTGGCTGCGATTCCT
SCO3-oSRL-pENTR-R	Cloning	TTT Tgcggccgc ttAAGTTGTATTATGTGCGTCTT
SSU-NcoI-F	Cloning	TTT TCC ATG GGG ATGGCTTCCTCTATGCTCTC
SSU-SalI-R	Cloning	TTT Tgtcgac cttcttctttccaatcggt
psaA-F	RT-PCR	GGTAGATAGGGATCCCGTAA
psaA-R	RT-PCR	CATCTTGAAACCAAGCCAA
psbA-F	RT-PCR	tgccattattcctacttctgc
psbA-R	RT-PCR	cgtgagcagctacaatgttg
clpP-F	RT-PCR	CCA AGAGGTTGAT ACCGA
clpP-R	RT-PCR	cga act agc ggg ttg a
16S-F	RT-PCR	TAAGCATCGGCTAACTCTGTGCC
16S-R	RT-PCR	TACAGCACTGCACGGGTCGATAC
23S-F	RT-PCR	TGTGGTTAGGGGTGAAATGCCAC
23S-R	RT-PCR	ATCGCTTAGCCCCGTTCATCTTC
accD-F	RT-PCR	CCAAGGACATTCGCAA
accD-R	RT-PCR	ggatcatagtgcagatcgtt
rpoA-F	RT-PCR	GGCCAAGCCGACACA
rpoA-R	RT-PCR	ccgcgattcctctca
rpoB-F	RT-PCR	aCCAGTCAGAATTGGATCA
rpoB-R	RT-PCR	ggatccccacctacaca
CAB3-F (LHCB1.2)	RT-PCR	gtgtgacaatgaggaagact
CAB3-R (LHCB1.2)	RT-PCR	CTTCAACGGCTCCCATCA
POR B-F	RT-PCR	GATCCATTACCGGGAACA
POR B-R	RT-PCR	Ggatcactcaccacctgag
RBCS_F	RT-PCR	GTTCTTCCCGTCAGAGTAAGT
RBCS_R	RT-PCR	cttactcgcaacctcacg
18SrRNA-F	RT-PCR	gaattcctagtaagcgcgagtcatca
18SrRNA-R	RT-PCR	cacctacggaaaccttgttacgacttct
LHCB1.5-F	RT-PCR	ttatggcttcctcaacca
LHCB1.5-R	RT-PCR	ctttccggggacga
LHCB2.4-F	RT-PCR	atggccacttcagcaat
LHCB2.4-R	RT-PCR	ttttccggggacga