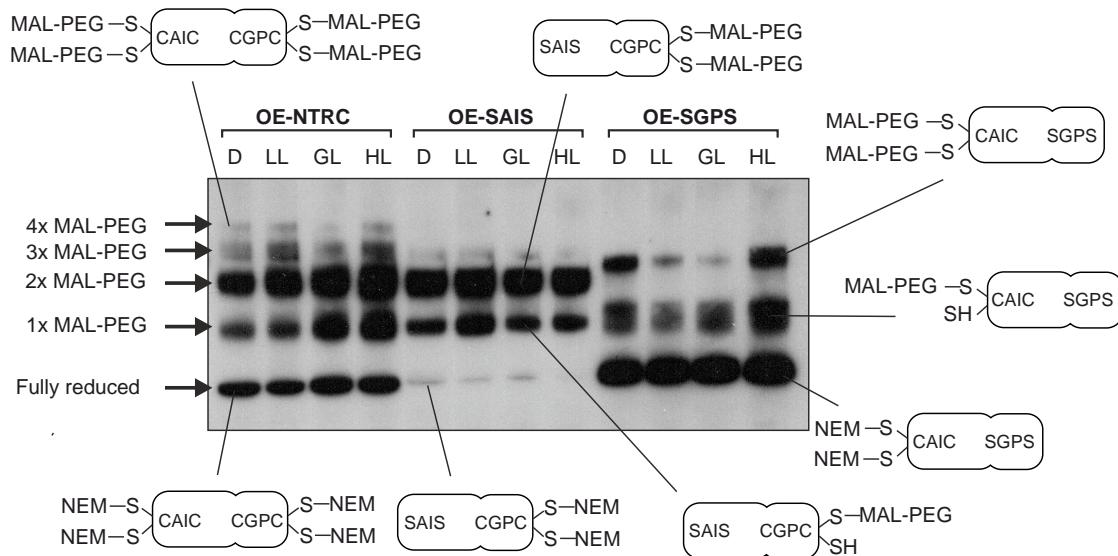
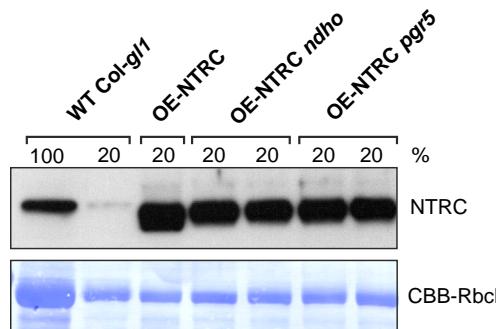
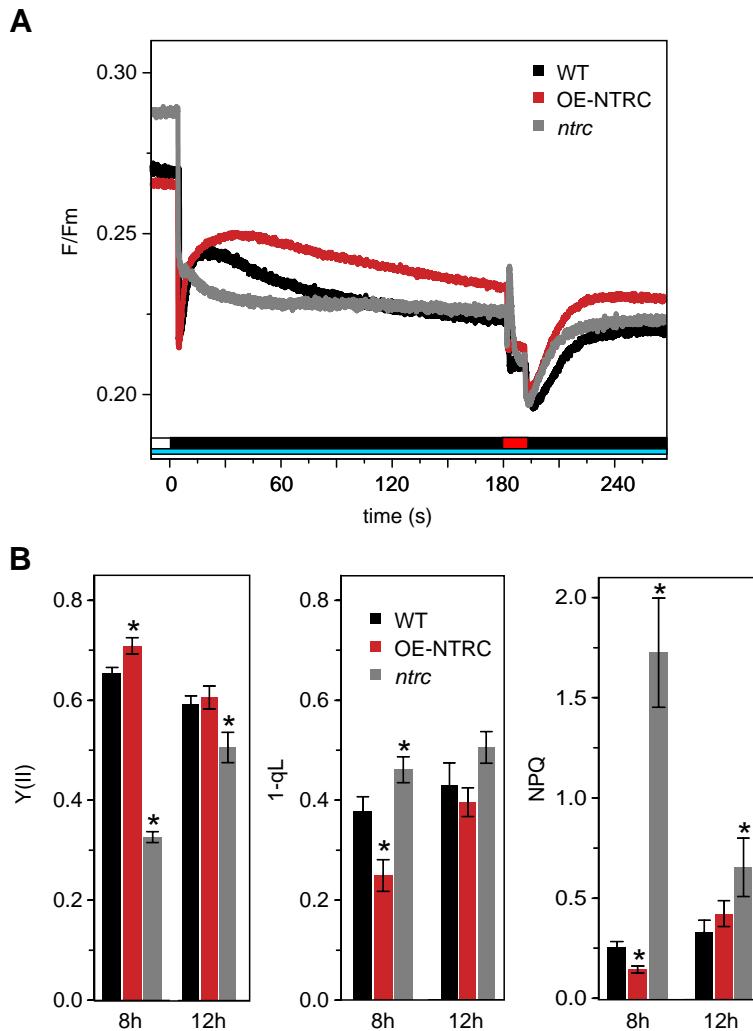


A**B****Supplemental Figure 1.** Redox state and expression of NTRC in transgenic lines.

(A) Redox-state pattern of NTRC in leaves overexpressing NTRC. Total leaf proteins were extracted from leaves overexpressing NTRC (OE-NTRC) and from lines overexpressing mutated forms of NTRC where the redox-active cysteines in either the reductase domain (OE-SAIS) or in the TRX domain (OE-SGPS) have been mutated to serines (Toivola et al. 2013). In the mutated forms only 2 cysteine residues are available for alkylation by MAL-PEG molecules. The schematic drawings depict possible locations of MAL-PEG binding in specific bands. Leaves were incubated in darkness (D), or illuminated for 2 h in low light (LL, 40 μmol photons $\text{m}^{-2} \text{s}^{-1}$), growth light (GL, 200 μmol photons $\text{m}^{-2} \text{s}^{-1}$) or high light (HL, 800 μmol photons $\text{m}^{-2} \text{s}^{-1}$).

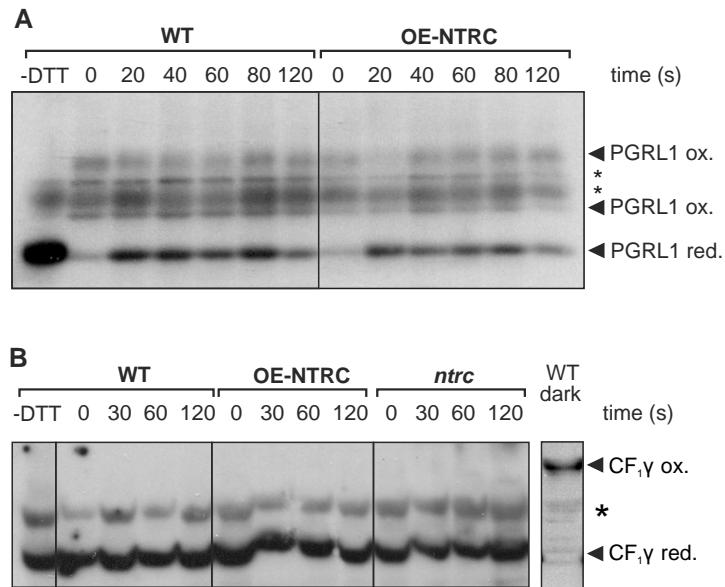
(B) Level of NTRC overexpression in OE-NTRC *ndho* and OE-NTRC *pgr5* plants detected by immunoblotting with an NTRC-specific antibody. 10 and 2 μg of soluble protein was loaded for WT and 2 μg for OE-NTRC, OE-NTRC *ndho* and OE-NTRC *pgr5*. Two individual plants were sampled for OE-NTRC *ndho* and OE-NTRC *pgr5*. Coomassie brilliant blue (CBB) staining was used as loading control.



Supplemental Figure 2. Post-illumination fluorescence rise (PIFR) in plants grown in a 12h/12h photoperiod.

(A) PIFR in dark-adapted WT, OE-NTRC and *ntrc* plants grown in a 12h/12h photoperiod under 120 μmol photons $\text{m}^{-2} \text{s}^{-1}$. The cyan bar indicates exposure to a 480 nm measuring light of 0.28 μmol photons $\text{m}^{-2} \text{s}^{-1}$, the white bar depicts illumination with 67 μmol photons $\text{m}^{-2} \text{s}^{-1}$ white light and the red bar shows the duration of a pulse of far red light. The curves are averages of 3–4 individual measurements.

(B) Quantum yield of PSII ($Y(\text{II})$), redox state of the PQ pool ($1-\text{qL}$) and non-photochemical quenching (NPQ) at $F_{\text{m}'}$ (after 7 min illumination) in plants grown either in an 8h or 12h photoperiod. The values are averages of 3–10 measurements $\pm \text{SE}$, and statistically significant differences to WT according to Student's T-tests ($P < 0.05$) are marked with *.



Supplemental Figure 3. *In vivo* redox states of PGRL1 and CF₁γ during changes in light conditions.

(A) MAL-PEG assay to determine the *in vivo* redox state of PGRL1 during dark to light transitions. Samples were collected 20, 40, 60, 80 and 120 seconds after moving dark-adapted WT and OE-NTRC leaves under growth light intensity illumination. –DTT is a control sample where free thiols were blocked with NEM but DTT was not added thereafter, preventing any alkylation by MAL-PEG.

(B) *In vivo* redox state of the ATP synthase γ subunit (CF₁γ) during transitions from low light (40 μmol photons m⁻² s⁻¹) to high light (600 μmol photons m⁻² s⁻¹) in WT, OE-NTRC and *ntrc* leaves. Samples were taken 0, 30, 60 and 120 seconds after the shift to high light. Prior to the light intensity shift plants grown under 200 μmol photons m⁻² s⁻¹ were kept 30 min under low irradiance. A dark-incubated control (WT dark) is seen in the right panel.* marks unspecific bands.

Supplemental Table 1. Parameters determined from OJIP transients of chlorophyll a fluorescence.

Apparent F_o values (F/F_m after 20 μ s of light), integrated area above O-J phase (0-3 ms) (A_{O-J}) and the initial slopes of the O-J transients ($m_{50-150 \mu s}$) in dark-adapted leaves of WT, OE-NTRC, *ntrc*, *pgr5* and *ndho* were calculated from the averaged curves in Figure 3.

line	$F_o (F_{20\mu s})$	A_{O-J}	$m_{50-150 \mu s}$
WT	0.18	1.62	0.58
OE-NTRC	0.21	1.46	0.74
<i>ntrc</i>	0.26	1.29	1.20
<i>pgr5</i>	0.21	1.84	0.47
<i>ndho</i>	0.17	1.76	0.57

Supplemental Table 2. Multiple alignment of NdhS amino acid sequences in embryophytes.

Sequences from *Physcomitrella patens* (PHYPADRAFT_188716), *Glycine max* (GLYMA03G01720), *Brachypodium distachyon* (BRADI3G21280), *Sorghum bicolor* (Sb07g028880), *Oryza sativa* (OS07G0196200), *Solanum lycopersicum* (Solyc08g082400.1), *Arabidopsis thaliana* (AT4G23890) and *Vitis vinifera* (VIT_02s0025g01470). Conserved cysteine residues are in bold and highlighted with red rectangles. * signifies full conservation of a residue in the current dataset, while ":" and ":" signify conservation of residues with strongly and weakly similar properties, respectively.

<i>Physcomitrella</i>	MA--AMTGCIRAPLSLALQRESSFWGSNVGVHQQQKSASSNSGGSTGGVRVGIRAE GFDF
<i>Glycine</i>	-----MSSFVALQQLHGSLLSQFLQDQTLTHFPRNKASSTIQ-NKPTTAQQPSAKFDM
<i>Brachypodium</i>	-----MAPAPTPSFLRPPPLPHR-----V-R--LPPPPPSASFR
<i>Sorghum</i>	-----MAPPPTSSFLRPPPLPHP-----H-PRLH-FRPPSASFRV
<i>Oryza</i>	-----MAPTPASFLRPPPLPHH-----H-PRIVRLPPPSATFRV
<i>Solanum</i>	MASASSFQLSSLQIQTTPPLKKSNFQSVNLNLS-SSVHTKSAM-KSSNSVTPIAKFNL
<i>Arabidopsis</i>	---MATSSITIPTIRTP-IHRSKFLGQTHQFSTVNRSVFPPPKQ-QSKLYQVKAMGFNL
<i>Vitis</i>	---MAYSFTVPSLQRPLPHKSHFLGQGHFPNNIQKASLSR---TRTPLPVKASAKFDL
	* .
<i>Physcomitrella</i>	WQVLGGRGLKGGEGLKQEKTARVLQEAKKNLVVE-KKKKGSVEGNVEAAEGLPGTFNKE
<i>Glycine</i>	LQIVGGRGLCNGEAGLKQELKKQVGVDKGQTSAT-SGKEQEEEESTSVVATEDGFEKE
<i>Brachypodium</i>	AEILGGRGLCNGEVGIRKELSSSTPTPSTPTADSS-P---GAAAAEADPPAVDPDAFEKE
<i>Sorghum</i>	SEILGGRGLCNGEVGVRKELTSGSSAST---TTSS-PAPSPSPSTESPPPAPVLDADFKE
<i>Oryza</i>	ADLLGGRGLCNGEVGIRKELASDSPAAPPSTTTSS-DEPAESPPPPPAASGVDPDAFDKE
<i>Solanum</i>	YEILGGRGLCNGEEGIEKELKKSISEEQKAVGSAAAASDDDNQENKETGEIPEDGFEKE
<i>Arabidopsis</i>	WEVMGGGRGLCNGEKGIEKELQRNIEDEQETSKAEN-NETERESDDSNLSFKVPEDGFEKE
<i>Vitis</i>	FGIMGGGRGLCNGEGLQQELKRNIEPAPSPDSVKD-E---EKPALAAVDDVPEDGFDKE
	*:*** . ** * : : * . : ***
<i>Physcomitrella</i>	LGGWTGGFPGEKGLRQFVQSNPPPAKASQMSNEIRKLQDSISRPLKPRAPSPLLMPGM
<i>Glycine</i>	LMGLTGGFPGEVHSG-----KPSSSKTKSSKN-LKLALSKKPKPELPLLPGM
<i>Brachypodium</i>	MMGLTGGFPGEVGLKDFVAKNPPPPPRTQPDGIAGS-AAVVAERPRRPELPLFLPGM
<i>Sorghum</i>	MMGLTGGFPGEVGLKDFVAKNPPPPRSKKSNSQLVAP-QATTLSAPPRTPELPLFLPGM
<i>Oryza</i>	MMGLTGGFPGEVGLKDFVAKNPPPPPAHRKGLA----AAATVERPRAPELPLFLPGM
<i>Solanum</i>	MMGFTGGFPGEKGLMKFIEKNPPPPPKTESSMVSG-FNQSLVKKPKPELPLLPGM
<i>Arabidopsis</i>	MMGLTGGFPGEKGLKTFIEKNPPPPPKQGSDA-SAVATDKKPKAPKLPLLMPGM
<i>Vitis</i>	LLGLTGGFPGEKGLQFLEKNPPPEKT-----SGNI-IENARLRKPKPELPLLMPGM
	: * ***** . * . : ***:***
<i>Physcomitrella</i>	TVKVVISPSNPYFEEFIGIVQRVTDGKVGVI FEGGNWDKLVSFKLQDLERTSQGPPMSNPKS
<i>Glycine</i>	IAIVKNPNPFPYMYC K IIVQRITDG-----PRMKNPKS
<i>Brachypodium</i>	IVLVKNPRNAYHMYCGIVQRVTDGKVGVLFEGGNWDRLITFGVDELEGREKGPPMVNPKS
<i>Sorghum</i>	VVLVKNPNNAAYMYCGIVQRVTDGKVALFEGGIWDRLLITFDLDELEGREKGPPMVNPKS
<i>Oryza</i>	VVLVKNPNNAAYHMYCGIVQRVTDGKVGVLFEGGIWDRLLITFDLDELEGREKGPPMVNPKS
<i>Solanum</i>	IAIVKNSNNPYMYCGIVQRITDGKAABL FEGGNWDRLISFRLEELERREKGPPMVNLKS
<i>Arabidopsis</i>	IAIVKNQNSPYHMYCGIVQRITDGKAGVL FEGGNWDRLITFRLEELERREKGPPGKNPKS
<i>Vitis</i>	IAIVKNPNPFPYMYCGIVQRITDGKAGVL FEGGNWDRLITFRLEELQRRDKGPPMKNPKS
	. * . . : * * : *** * * ***
<i>Physcomitrella</i>	AILERMIVPEGTSSPEGASS-----
<i>Glycine</i>	AVLKPFLKK-----
<i>Brachypodium</i>	VVLEALVADLADDTEAEE---TEKKEEEAGAAA AKA
<i>Sorghum</i>	VVLEDIVAQLEDDDDKE-DEAKKEKEPEGAAAAA-
<i>Oryza</i>	VLLESIAEEMDDVAKEEEGEEAKKKKEEEGTAAA-
<i>Solanum</i>	VILEKMVEKSSEA-----
<i>Arabidopsis</i>	CILEPLIEQMOKKEEAAP-----
<i>Vitis</i>	AILETLLEQEA-----

Supplemental Table 3. Multiple alignment of NdhH amino acid sequences in photosynthetic organisms.

Sequences from *Synechocystis PCC 6803* (slr0261), *Physcomitrella patens* (NDHH_PHYP), *Glycine max* (NDHH_SOYBN), *Brachypodium distachyon* (NDHH_BRADI), *Sorghum bicolor* (NDHH_SORBI), *Oryza sativa* (Osp1g00970), *Solanum lycopersicum* (NDHH_SOLLC), *Arabidopsis thaliana* (ATCG01110) and *Vitis vinifera* (NDHH_VITVI) were obtained aligned as described in the legend for Supplemental table 2.

<i>Synechocystis</i>	MTKIEITRTEPMVLNMGPQHPSMHGVLRLIVTLDGEDVVD	C	EPVIGYLHRGMEKIAESRTN
<i>Physcomitrella</i>	--MLATKTKPMIVSMGPQHPSMHGVLRLIVTLDGENVID	C	EPILGYLHRGMEKIAENRTI
<i>Sorghum</i>	MSLSLRKDKLMIVNMGPKQHPSMHGVLRLIVTLDGEDVID	C	EPILGYLHRGMEKIAENRSI
<i>Brachypodium</i>	MSLPLTRKDKLMIVNMGPKQHPSMHGVLRLIVTLDGEDVID	C	EPILGYLHRGMEKIAENRTI
<i>Oryza</i>	MSLPLTRKDKLMIVNMGPKQHPSMHGVLRLIVTLDGEDVID	C	EPILGYLHRGMEKIAENRTI
<i>Glycine</i>	MNISTTRKDFMIVNMGPQHPSMHGVLRLIVTLDGEDVID	C	EPILGYLHRGMEKIAENRTI
Arabidopsis	MKRPVTGKDLMIVNMGPQHPSMHGVLRLIVTLDGEDVVD	C	EPILGYLHRGMEKIAENRAI
<i>Solanum</i>	MTAPTRKDKLMIVNMGPKQHPSMHGVLRLIVTLDGEDVVD	C	EPILGYLHRGMEKIAENRTI
<i>Vitis</i>	MNVPATREDLMIVNMGPKQHPSMHGVLRLIVTLDGEDVID	C	EPILGYLHRGMEKIAENRTI
	.	.	*
<i>Synechocystis</i>	IMYVPYVSRWDYAAGMFNEAITVNAPEKLADIEVPKRAQYIRVIMLELNRIANHLLWLGP		
<i>Physcomitrella</i>	VQYLPYVTRWDYLATMFTEAITVNAPEKLTNIQVPKRASYIRVMIMLELSRVASHLLWLGP		
<i>Sorghum</i>	IQYLPYVTRWDYLATMFTEAITVNAPEFLENIQIIPQRASYIRVIMLELSRIASHLLWLGP		
<i>Brachypodium</i>	IQYLPYVTRWDYLATMFTEAITVNAPEFLENIQIIPQRASYIRVIMLELSRIASHLLWLGP		
<i>Oryza</i>	IQYLPYVTRWDYLATMFTEAITVNAPEFLENIQIIPQRASYIRVIMLELSRIASHLLWLGP		
<i>Glycine</i>	IQYLPYVTRWDYLATMFTEAITVNGPEQLGNIQVPKRASYIRVIMLELSRIASHLLWLGP		
Arabidopsis	IQYLPYVTRWDYLATMFTEAITVNGPEQLGNIQVPKRASYIRVIMLELSRIASHLLWLGP	C	IQYLPYVTRWDYLATMFTEAITVNGPEQLGNIQVPKRASYIRVIMLELSRIASHLLWLGP
<i>Solanum</i>	IQYLPYVTRWDYLATMFTEAITINGPEQLGNIQVPKRASYIRVIMLELSRIASHLLWLGP		
<i>Vitis</i>	IQYLPYVTRWDYLATMFTEAITVNAPEQLGNIQVPKRASYIRVIMLELSRIASHLLWLGP		
	:	*	*
<i>Synechocystis</i>	FMADVGAQTPFFYIFREREMIYDLWEAASGMRLINNNYFRVGGVAVDLPYGWNDKCEDFC		
<i>Physcomitrella</i>	FMADIGAQTPFFYILREREMIYDLFEAATGMRRMH-NYFRIGGVAVDLPYGWIDKCLDFC		
<i>Sorghum</i>	FMADLGAQTPFFYIFRERELIYDLFEAATGMRRMH-NYFRIGGVADLPYGWMDKCLDFC		
<i>Brachypodium</i>	FMADLGAQTPFFYIFRERELIYDLFEAATGMRRMH-NYFRIGGVADLPYGWIEKCLDFC		
<i>Oryza</i>	FMADLGAQTPFFYIFRERELIYDLFEAATGMRRMH-NYFRIGGVADLPYGWIDKCLDFC		
<i>Glycine</i>	FMADIGAQTPFFYIFRERELIYDLFEAATGMRRMH-NFFRIGGVATDLPYGWVDKCYDFC		
Arabidopsis	FMADIGAQTPFFYIFREREFVYDLFEAATGMRRMH-NFFRIGGIAADLPYGWIDKCLDFC	C	FMADIGAQTPFFYIFREREFVYDLFEAATGMRRMH-NFFRIGGIAADLPYGWIDKCLDFC
<i>Solanum</i>	FMADIGAQTPFFYIFRERELIYDLFEAATGMRRMH-NYFRIGGVADLPYGWIDKCLDFC		
<i>Vitis</i>	FMADIGAQTPFFYIFRERELVYDLFEAATGMRRMH-NYFRIGGVADLPHGWIDKCLDFC		
	*****:	*****:	*****:
<i>Synechocystis</i>	DYFLPKVDEYEKLITNNP1FRRRVEVGTVTREEA1NWGLSGPMLRGSGVKWDLRKVDHY		
<i>Physcomitrella</i>	DYFLPKVNEYERLITNNP1FLKRVEGIGIIGKEEAINWGLSGPMLRASGVQWDLRKVDHY		
<i>Sorghum</i>	DYFLQGVVEYQQLITRNP1FLVERVEGVGFISGEEAVNWGLSGPMLRASGIQWDLRKIDPY		
<i>Brachypodium</i>	DYFLRGVVEYQQLITQNP1FLVERVERVGFISGEEAVNWGLSGPMLRASGIRWDLRKVDLY		
<i>Oryza</i>	DYFLRGVIEYQQLITQNP1FLVERVEGVGFISGEEAVNWGLSGPMLRASGIQWDLRKVDLY		
<i>Glycine</i>	DYFLTRIVEYQKLITRNP1FLVERVEGVVVDIKEVINWGLSGPMLRASGIQWDLRKVDNY		
Arabidopsis	DYFLTEVVEYQKLITRNP1FLVERVEGVIIGGEEAINWGLSGPMLRASGIPWDLRKIDRY	C	DYFLTEVVEYQKLITRNP1FLVERVEGVIIGGEEAINWGLSGPMLRASGIPWDLRKIDRY
<i>Solanum</i>	DYFLTGVAYQKLITRNP1FLVERVEGVGIIGRDEALNWGLSGPMLRASGIEWDLRKVDHY		
<i>Vitis</i>	DYFLTGVAYQKLITRNP1FLVERVEGVGIIGVEEAINWGLSGPMLRASGIQWDLRKVDHY		
	****:	****:	****:

<i>Synechocystis</i>	ECYDELDWEVQYETAGDCFARYLVRIREMRESVKIIRQALKAMPGGPYENLEAKRLQEGK
<i>Physcomitrella</i>	ECYDELDWQIQWQKEGDSLARYLVRIGEMKESIKIIQQALKSIPGGPYENLEARRLQRGK
<i>Sorghum</i>	ESYNQFDWKVQWQKEGDSLARYLVRVGEMRESIKIIQQAVEKIPGGPYENLEARRFKKAK
<i>Brachypodium</i>	ESYNQFGWKVQWQKEGDSLARYLVRIGEMRESIKIIQQAVEKIPGGPYENLEVRRFKKAK
<i>Oryza</i>	ESYNQFDWKVQWQKEGDSLARYLVRIGEMRESIKIIQQAVEKIPGGPYENLEVRRFKKAK
<i>Glycine</i>	ECYEEFDWEVQWQKEGDSLARYLVRIGEMMESIKIIQQALEGIPIGGPYENLEIRCFCREK
Arabidopsis	ESYDEFEWIQQWQKGDSLARYLVRLEMTESIKIIQQALEGLPIGGPYENLESRGFDRKR
<i>Solanum</i>	ESYDEFDWQVQWQREGDSLARYLVRIGEMTESIKIIQQALEGIPIGGPYENLEMRRFDRLK
<i>Vitis</i>	ECYDEFDWQVQWQKEGDSLRYLVRIGEMVASIKIIQQALEGIPIGGPYENLEIRCFCRDR
	.::: *::*: **.::*****: ** *:***:***: :*****: : : . :
 <i>Synechocystis</i>	 KSEWNDFQYQYIAKKVAPTFKIPAGEHYVRLESGKGELGIFIQGNDDVFPWRWKIRSADF
<i>Physcomitrella</i>	KSEWNNFEYQFISKKPSPTFKLPQEHYIRVEAPKGELGVFLIGDDSVFPWRWKIRPPGF
<i>Sorghum</i>	NPEWNDFEYRFLGKKPSPNFELSQQEYLVRVEAPKGELGIYLVGDDSLFPWRWKIRPPGF
<i>Brachypodium</i>	NSEWNDFEYRFLGKKPSPNFELSQQEYLVRIEAPKGELGIYLVGDDGLFPWRWKIRPPGF
<i>Oryza</i>	NSEWNDFEYRFLGKKPSPNFELSQQEYLARVEAPKGELGIYLVGDDSLFPWRWKIRPPGF
<i>Glycine</i>	EPEWNEFEYRFISKKPSPTFELPKQELYVRIEAPKGELGIFLIGDQNGFPWRWKIRPPGF
Arabidopsis	NPEWNDFEYRFISKKPSPTFELSQQEYLVRVEAPKGELGIFLIGDQSGFPWRWKIRPPGF
<i>Solanum</i>	DPEWNDFEYRFISKKPSPTFELSQQEYLVRVEAPKGELGIFLIGDQSVPWRWKIRPPGF
<i>Vitis</i>	DPELNDFEYRFISKKPSPTFELSQQEYLVRVEAPKGELGIFLIGDQNVPWRWKIRPPGF
	. * *:***:..** :*.**: * * *: * ****: : *:. ***** ..*
 <i>Synechocystis</i>	 NNLQILPHILKGVKVADIMAILGSIDIIMGSVDR
<i>Physcomitrella</i>	INLQILPQLVKGMKLADIMTILGSIDIIMGEVDR
<i>Sorghum</i>	INLQILPQLVKMKLADIMTILGSIDIIMGEVDR
<i>Brachypodium</i>	INLQILPQLVKMKLADIMTILGSIDIIMGEVDR
<i>Oryza</i>	INLQILPQLVKRMKLADIMTILGSIDIIMGEVDR
<i>Glycine</i>	INLQILPELVKRMKLADIMTILGSIDIIMGEVDR
Arabidopsis	INLQILPELVKRMKLADIMTILGSIDIIMGEVDR
<i>Solanum</i>	INLQILPQLVKRMKLADIMTILGSIDIIMGEVDR
<i>Vitis</i>	INLQILPQLVKRMKLADIMTILGSIDIIMGEVDR
	*****.::* :*:****:*****.***

Supplemental Table 4. Multiple alignment of Ndh48 (PNSB1) amino acid sequences in embryophytes.

Sequences from *Physcomitrella patens* (PHYPADRAFT_106212), *Oryza sativa* (Os08g0276100), *Brachypodium distachyon* (BRADI_3g19630), *Populus trichocarpa* (POPTR_0001s03600g), *Arabidopsis thaliana* (AT1G15980) and *Glycine max* (GLYMA_08G218800) were obtained and aligned as described in the legend for Supplemental table 2.

<i>Physcomitrella</i>	MSAMAAQVVL----GAGLANCPQCSICVTRATSSLHSNPSKLQLRAFGTRNVRLA
<i>Oryza</i>	MQTPTMSTSMAKLP---SPPS--LPIARQ-----CCCHL---LQLGRRG--G
<i>Brachypodium</i>	MQTPTMYTSMAARATSA--AANLP--APPPRQ-----CYYHL---LPPAGRR--S
<i>Populus</i>	---MASTSLLPKTISPFLTNPPP--LPSTHFTSKPSFFNPSADHH---LPCTRKP---
<i>Arabidopsis</i>	---MASSLPLLPKPISPFFKTPF--STSKPLV----FL---NFQ----TRLTSRSSDV
<i>Glycine</i>	MAATYYLLPTSPKTFSPFLRNPPS--IPSGHHVSSLGSLL---DYP---FHCSSRRGNN
:	
<i>Physcomitrella</i>	SS--VVSAKKGWFDDPFDYGADDEEDTMGELMSQGPQGAEDPRPARDPDSESGYLDFA
<i>Oryza</i>	AGVARASAKKKNPWLDPFDDGPDEFDY-RGAFSGG-KQEDPRPPEDPANPYGFLRFPA
<i>Brachypodium</i>	VWALSASPDKKKNPWLDPFDDGPDEFDY-TGVYSGG-KQDEDPRPPEDPNSPYGFLRFPM
<i>Populus</i>	-SILTPYAKKKNPWIDIFDDGEDLDMEY-GSLFVDG-KQDEDTRPVDPNNPYGFLKFHKP
<i>Arabidopsis</i>	S---VNLKKKNNPWLDPFDSEGDPDNEY-GSLFADG-KQDEDPRPPDPNPDNPYGFLKFHKP
<i>Glycine</i>	SVEANCNAKKKNPWLDPFDDGEDPEMEY-GSLFADG-KQEDPRPPDPDNPYGFLKFHKP
*: . : * ** * * : : * : ** * * : * . * : * **	
<i>Physcomitrella</i>	GFMPEVASLGILIRNDVRRCLCMISGGVYENLLFPVIQLLNRYPGVRIDVMATPRGKQ
<i>Oryza</i>	GYNPELDSLASKVRRDVRRACCVVSGGVYENVLFPPVQLLRDRYGPVVDVVASARGKQ
<i>Brachypodium</i>	GYNPELDSLASKVRGDVRRACCVVSGGVYENVLFPPVQLLKDRYGPVLIDVVASARGKQ
<i>Populus</i>	GYNVEVAQLGLKIRGDVRRCCCOMISGGVYENLLFPVIQMLKDRYGPILVDVLASDRGKQ
<i>Arabidopsis</i>	GYTVELASLPLKIRGDVRRCCCVISGGVYENLLFPTIQLIKDRYGPVQVDILTERGKQ
<i>Glycine</i>	GYSVETASLALKVRGDVRRCCCVISGGVYENLLFPATQLIKDRYGPVQIDVVVASERGKQ
*: *: . * : * **** . * :*****:*****. :* :*****: :*****: ****	
<i>Physcomitrella</i>	AYEMNKNRKAWVHPVDDQFLRPVDFTEVGKIKGEYYDLLVSTKLAGLGQSIFFWLAV
<i>Oryza</i>	VYEMCKNVRYADVYDPDDDWPEPAEYTHQLGVLKRNYYDLIISTKLAGIGHALFLFMSSA
<i>Brachypodium</i>	VYEMCKNVRYANVYDPDDDWPEPAEYTHQLGVLKRNYYDMILSTKLAGTGHALFLFMSSA
<i>Populus</i>	CYELNKNVRWANVYDPDG-DPEPAIYTDMIGVLKNRYYDLVLSKLAGLGHASFMFMSSA
<i>Arabidopsis</i>	TYELENKNVRWANVYDPDDHWPEPAEYTDMIGLLKGRRYDMVLSTKLAGLGHAALFMTTA
<i>Glycine</i>	TYELENKNVRWANAYDPDDEFPEPAEYTDMVGVLKRNYYDMVLSTKLAGLGHAALFMTTA
: * * . : * . . * :*. : * : * . ***: :***** * : * : : : ****	
<i>Physcomitrella</i>	RNKVSYTYPDVNAAGAAKFLDIAIKAPOLELAESGFNMYAEMIEELSQMGKNVPKTEVPP
<i>Oryza</i>	RDKVGVYVNVNSAGAGLFLTEMFRPPTTNLADSGYNMYQDMLEWIGRPAKGVPHEPVPP
<i>Brachypodium</i>	REKVGVYVNVNGAGAGLFLTEMFKPPTTNLSDGGYNMYQEMLEWLGRPGKGVPQQPIP
<i>Populus</i>	RDKVSYIYPNVNAAGAGLLLSETFTPDSANLSEGGYHMYHQMLDWLGRPIYNVPRQPVPP
<i>Arabidopsis</i>	RDRVSYIYPNVNSAGAGLMLSETFTAENTNLSELGYSMYTQMEDWLGRPFRSVPRTPLL
<i>Glycine</i>	RDRVSYIYPNVNAAGAGLLLSETFVPDFSQNLSDGGYNMYHQMDWLGKPFREVPRQPVPP
* :*.* **:***.***. :* : : * : * : * : * : : : * . : * :	
<i>Physcomitrella</i>	LEVIGIGSKVKAYVEAKYREAGVREGEFLVFHGIECDSSASMTSKGDKDCLLPLSMWAEIA
<i>Oryza</i>	LRVSISKRLRAFVEDKYSRAGVEKGKFVVGHIASDSFANMRSGDDDCLLPLEHWAEIA
<i>Brachypodium</i>	LRVSISKRLRGIVEDKYSRAGVEKGKFVVGHIASDSVANMTSRGDDDCLLPLEQWAEIA
<i>Populus</i>	LRVSLSRKLKQYVEAKYRAAGAEKGKYIVIHGIESDSKASMQRSGDTDSLLPLEWDQIA
<i>Arabidopsis</i>	LRVSISRKVKEVVAAKYRNAGAVTGKFIVIHGIESDSKASMQRSGDADSLLSLEWKAKII
<i>Glycine</i>	LRVSISKKLKEVVEAKYEKAGAKKGKYVVIHGIKSDFSKASMQRSGDPDSLLPIEVWAEIA
* . : * : * ** * * :* :* :*** * * * :* :* :* :* :* :* :* :* :* :* :*	

<i>Physcomitrella</i>	KSTS-----DKVVFVIPNEKRRKVKEI-CGENAHIVFITTPGQLGALINASKGVTTNT
<i>Oryza</i>	KEISSEDNGLKPLFVIPHQKHREEVEET-VGKDTNILFITTPGQLTCLINDSVGVVATNT
<i>Brachypodium</i>	KAISSQGNGLRPLFVMPHQKHREEIEDI-VGRETSYLFITTPGQLTCLINDSAGVVATNT
<i>Populus</i>	DAIS----GFKPVFVIPHEKERENVEEI IYNEDIGILFITTPGQ-ATLINDSAGVIATNT
Arabidopsis	KGVR----GFKPVFVIPHEKERENVEDF-VGDDTSIVFITTPGQLAALINDSAGVIATNT
<i>Glycine</i>	DVIR----DVTPLFVIPHEKERENVEEI-FSEDASIVFITTPGQLAALINDSAGVIATNT
	.
	:***:***: * .::: : . : :***** * * * * :***:***
<i>Physcomitrella</i>	AALQIAIALKKSTVALFASQEKA NLFIPDYAK-DACAMVASKTGKLCGLDLKAATMAVST
<i>Oryza</i>	AAVQLANARDKPCVALFSSKE KARLFLPYLEEKKGCTVVASETGKLIDIDVEAVKKAVKE
<i>Brachypodium</i>	AAVQLANARDRPCVALFSSKE KAKLFLPYAEDKKSC CTVVASATGKLADIDIEAVKN AVKE
<i>Populus</i>	AAIQLANAREKPSIALFGSE EKGKVFPNAEE-KKCII VSSKTGKL DIDVGAVKQAMQI
Arabidopsis	AAIQLANARDKPCIGLFSSEE KGKLFV PYAE EKSNC VIIASKTGKL ADIDIGTV KNAMQV
<i>Glycine</i>	TAVQLANAREKPCIALFCSEE GNKFV PRAEE-KKCII ISSKTGKL DIDVEAVKN AVQT
	:***:***: * .: :** * :***.. * :* . . * :***: *** . :*: :.. *:.
<i>Physcomitrella</i>	IAKEALVAA---
<i>Oryza</i>	FKAAPSVALAQT
<i>Brachypodium</i>	FEPAPS FALA AQK
<i>Populus</i>	FDM SLALV
Arabidopsis	FEGL SLALV
<i>Glycine</i>	FNLSPALV
	:
	..

Supplemental Table 5. Multiple alignment of NdhJ Amino acid sequences in photosynthetic organisms.

Sequences from *Arabidopsis thaliana* (ATCG00420), *Glycine max* (NDHJ_SOYBN), *Populus trichocarpa* (NDHJ_POPTR), *Oryza sativa Japonica* (NDHJ_ORYSJ), *Brachypodium distachyon* (NDHJ_BRADI), *Physcomitrella patens* (NDHJ_PHYPA), *Selaginella moellendorffii* (C7B2F7_SELML) and *Synechocystis PCC 6803* (NDHJ_SYNY3). Sequences were obtained and aligned as explained in the legend of Suppl. Table 2.

Synechocystis	-----MGPVSTWLTTNGFEHQSLTADHLGVEMVQEADLLLPLCTALYAYG
Selaginella	TLDISATSASDGKVQGQLPARPAEHESAHRPLGFHDHQGIETPQIQSEDRPSIAVALYVYG
Physcomitrella	-----MQGRLSVWLANHKLPHRPLGFDYQGVEILQIRSEDWLSIAVALYVYG
Oryza	-----MQQGWLSNWLVKHEVVHRSLGFDHRCIETLQIKADEWDSIAVILYVYG
Brachypodium	-----MQQGWLSNWLVKHKKVVHRSLGFDHRCIETLQIKAGDWDSIAVILYVYG
Arabidopsis	-----MQGTLSVWLA KRG LVHRSLGFDYQGIE T LQIKPEDWHSIAVILYVYG
Glycine	-----MQGRLSSWLVKHGLIHRSLGFDYQGIE T LQIKPEDWHSIAVILYVYG
Populus	-----MRGPLSAWLVKHGLVHRSLGFDYQGIE T LQIKPEDWHSIAVILYVYG
	*: . . . * : * : * : * : . . . * . *
Synechocystis	FNYLQCQGAYDEGPGKSLVSFYHLVKLTED--TRNPEEVRLKVFLPRENPVVPSPVYWIWK
Selaginella	SNHPRAQC A DVAPGGLLASVYHLAKVQDDEADQPEE I CKVSVSKHPRIPSPVFRVRK
Physcomitrella	FNYLRSQC A DVAPGGLLASVYHFTKIEDN-V-DQPEE I CK I FVSRQPKP I SPSVFWIWK
Oryza	YNYLRSQC A DVAPGGLLASVYHLTRI Q YG-I-DNPEEV C IKVFA Q KDNPRIPSPVFWIWR
Brachypodium	YNYLRSQC A DVAPGGLLASVYHLTRI Q YG-I-DNPEEV C IKVFA Q KDNPRIPSPVFWIWR
Arabidopsis	Y NYLRSQC A DVAPGGLLASVYHLTRIEYG-V-NQAEEV C IKVFTHRSNPRIPSPVFWWK
Glycine	YNYLRSQC A DVAPGGLLASVYHLTRLEYG-I-DQPEEV C IKIFVARKNPRIPSIFWVWK
Populus	YNYLRSQC A DVAPGGLLASIYHLTRIEYG-ILDQPEEV C IKVFAPRKNPRI R IPSPVFWWK
	*: . . * * * . * * . * . . . : . . . : * : * : . . : * : * : * : * : :
Synechocystis	AADWQERECYDMFGIVYEGHPNLKRILMPEDWVGWPLRKDYIAPDFYEIQDAY-
Selaginella	SADLQERESYDMLGIFHESHPRLKRI S MPTWIGPRLKDHTVPDFYE P QDSL R
Physcomitrella	SADFQERESYDMLG I SYENHPRLKRI L MPDTWIGWPLRKDYI V PDFYE E IQDAH-
Oryza	SSDFQERESFD M VG I SYDNHPRLKRI L MPESWIGWPLRKDY I TPNFYE E IQDAH-
Brachypodium	SADFQERESYD M VG I SYDNHPRLKRI L MPESWVGWPLRKDY I TPNFYE E IQDAH-
Arabidopsis	STDF QERESYDMLG I TYD S HPRLKRI L MPESWIGWPLRKDY I APNFYE E IQDAY-
Glycine	SADFQEKE S YDMLG I SYDNHPRLRRI L MPESWIGWPLRKDY I APNFYE E IQDAH-
Populus	SADFQERESYDMLG I SYDNHPRLKRI L MPESWIGWPLRKDY I APNFYE E IQDAH-
	: * : * : . : * . * : . : * . : * : * : * : * : * : * : * : * : * : * : :

Supplemental Table 6. Multiple alignment of Ndh45 amino acid sequences embryophytes.

Sequences from *Arabidopsis thaliana* (AT1G64770), *Populus trichocarpa* (B9IPP5_POPTR), *Glycine max* (A0A0R0FL97_SOYBN), *Oryza sativa Japonica* (Q10RI6_ORYSJ), *Brachypodium distachyon* (I1H9J0_BRADI) and *Selaginella moellendorffii* (D8SKY5_SELML). Sequences were obtained and aligned as explained in the legend of Suppl. Table 2.

Selaginella	ME-----I---AGKSAIGLSPLKWERMERAELLQERFGCKELEFERS--D
Arabidopsis	--MASLISFSLLPKPKAVR-----SSISAPQTQTINTEKLEDKGFRKGKIKFSES--N
Oryza	MATSSLLPLHLPLPTRPSAVKASAA-----ATAAAAPTPQSLEESFGRKGLRFAADPAT
Brachypodium	---MAFLPLHLPLASSPTLLTARASSTAVSVSPPAQTSSSLQVQLEETFGRKGIRFGAD-AT
Populus	--MASLLSFSLRKPSI-I---KATSLSP----TTSPSTPEVLEEKFGRKGKIKFLES--N
Glycine	--MASFLSLSLPKLNLI---KASSAANTTTTTTLPTAETLNEKFGRKGKIKFLES--D
	: * : * * : . * .
Selaginella	GIVEARLKACGSAATIALPQGVVTSYRPIM-WHESQEEVLHSKRFPLQGG----CAYK
Arabidopsis	NIPMVELKVRNGSSLKLSLSDAHVLSYKPKVYWKD---EGFEEVLYTVDGD-----ESR
Oryza	GAPTAELSVRNGSSLQLRLADGLVTSYRPKVYWKD---DGCREVLHTVAGAG--AGGEVK
Brachypodium	GAPTAELSVRNGSSLRLNDGLVTSYRPKVSWKEDKDGCGREILHTVSDS----KTLK
Populus	NVPTVELKVRNGSSVRVQIPNAYVSSYKPKVYWKD---DGFEEVLYTLPGKEKDSSGIAK
Glycine	NTPIVDLTVRNGSSLRLRIPDAHVTSYKPKVNWKD---DGFQEVLYTIPATETGP-YKAK
	. . * . : * * : : : . * * : * : : .. . : :
Selaginella	GGIRASVARIPEVEDGEETKRANDPPLSWIVNGVSRAPNKWVKITLGSS--LPNLKLNS
Arabidopsis	GGVGVVIVNGEEP---KGGSSVISGCDWSVKDTSDAIDALQIELSCT--AGVLDITYI
Oryza	GGVGLALSEVSSS---GAAESLLVGSEWSVVDADSDSYDAVQVELGCTKGSGTLEVTVY
Brachypodium	GGVGLVLNHAS-S---GSPSAAAVQPEWSVSAVSDSDSYDAMQVELGRGMSGPQLEVAYV
Populus	GGIGLVINDASEG---GSKGSLISSSEWTVKDVSDDSIDAVQVELSCS--SGPLEISYV
Glycine	GGVGLVMNEVLQP---GAKGLLPSTLEWTVNDVSDSDSIDALQVELSCT--SRFFDITYI
	* : * : . . : : : * . : ..
Selaginella	VTLSKRQLQSTLSIENTGKAPCCFHASIATAVEVGDLAGAYAMGLGTNFISLGDEIAE
Arabidopsis	VSLYPVSMATALVVKNNNGRKPVTLKGIMSYLRFKKRSGAGIQGLKGCSYCPNPPLSSP-
Oryza	VTLYPLSMATAVMVKNNNGKKPVSLTSAMLSHIKFDKRRGTAVEGLRGCPYCSHPPPAAAG-
Brachypodium	VTLYATSMATAVIVKNAGKKPVALTGAVLSHIKFDKRRGTAVEGLMGCPYCAHPPPASG-
Populus	VSLYPLSMASAVIVKNNGRKDVTLTSAILSHLKFKKRAKAGIQGLRKCYCTQPPPLSSP-
Glycine	VTLYPVSMMATAVVAKINIGPKPATLTNAILSHFRFKNRRGTAIKGLRS CSYIIPHAPLSSP-
	* : * . : : : * * : . : : . : * * : : :
Selaginella	NTTAGEEQGPRIFEKLAVLLSGGSYKRPERESQQGDEFVGKDGLRLWHRHCSEMAPLAGP
Arabidopsis	-FELLSPSEAMKAESSGWFGE---EGEKGPGIWAVEDSVITLLEKK
Oryza	-FALLTPAAMKREDGGWFGGG-GGEEPRQGVWTVEDNLYTILKKK
Brachypodium	-FALLTPAAMKREESGWFGGGGGEPRPGEWAVEENRYTILKKK
Populus	-FEVLSPSEALKPESPGLLDFD-FEPEEKPGSWKVQEELYIILKDR
Glycine	-FQILTPSEATISEPPRWLDSFG-NETEAKPGTWGQQALSITLLENK
	: * . : * . : * .
Selaginella	MNRLY-----FMSSMPWTLLDRVORKASLVHLPEIGTEVSEPLQSG-ARVAGGR
Arabidopsis	MSRIYGAPPAPERLKAVYNTPPSKFETIDQKKKKVLD-AKN-----KIKIPKGISNSFRE
Oryza	VSRVYAAPPEERKKRIYSTAPSKFTTIDQNSGLGFR-VVRMGYEDMYLCSPGEMYRKFGK
Brachypodium	VSRVYAAPPEERKKRVYNAPSNSFMTIDQSSGLGFR-VVKMGFEDMYLSSPGGMYDKFGN
Populus	LSRVYAAPQERLKAFYNTSPKYETLDQGKELFFR-VIRIGFEDIYIGSPGSFAEKYGK
Glycine	MSRVYAAPKERLKAFYNTPPSKYETIDQGRGLCFR-VIRMGFEDIYLSSPGSLSEKYGK
	: * : * : * : . .

Selaginella	LEKVCAA-----RPNFG-----
Arabidopsis	RIVFQDDKDWRDVGIPRIDVGQVWEATLLRVHRSNVNARSRCRCSLRRDMERSNGNRA
Oryza	DYFLCTGTAS---MLVPVVNPGEERAAQVIEHDNL-----
Brachypodium	DYFLCTGPAS---LLVPVVNPGEERAAQVIEHDNL-----
Populus	DYFICTGPAA---MLVPVVVKPGEEWKGAQMIEHDNL-----
Glycine	DYFICTGPAS---ILVPVTVPNPGEERGAAQVIEHDNL-----

Supplemental Table 7. Forward and reverse primers used for cloning of bimolecular fluorescence complementation (BiFC) constructs.

Restriction enzyme sites are underlined and translational start codon is marked by bold italic. Frw = forward primer, rev = reverse primer. In order to get proper fusion to C-terminal YFP half, reverse primer lacks a stop codon. RE = restriction enzyme. The cDNA clones were obtained from the Arabidopsis Biological Resource Center (ABRC). All primers were purchased from Sigma Aldrich.

Construct(s)	AGI-code	Primer sequences	RE-sites
pSPYCE.NDH-S	AT4G23890.1	Frw 5'- CTGCAGAGGA <u>TCC</u> <i>ATGGCGACTTCTTCGATCAC</i> -3' Rev 5'- CTGCAGACC <u>CGGGTGGT</u> GCTGC <u>CTCTT</u> -3'	BamHI XmaI
pSPYNE.NDH-S	AT4G23890.1	Frw 5'- CTGCAGAG <u>GA<u>ATCC</u><i>ATGGCGACTTCTTCGATCAC</i></u> -3' Rev 5'- CTGCAGACC <u>CGGGTGGT</u> GCTGC <u>CTCTT</u> -3'	BamHI XmaI
pSPYCE.PGR5	At2g05620.1	Frw 5'- CTGCAGAG <u>GA<u>ATCC</u><i>ATGGCTGCTGCTTCGATTTC</i></u> -3' Rev 5'- CTGCAGACC <u>CGGGAGCAAGGAAACCAAGCCTCT</u> -3'	BamHI XmaI
pSPYNE.PGR5	At2g05620.1	Frw 5'- CTGCAGAG <u>GA<u>ATCC</u><i>ATGGCTGCTGCTTCGATTTC</i></u> -3' Rev 5'- CTGCAGACC <u>CGGGAGCAAGGAAACCAAGCCTCT</u> -3'	BamHI XmaI
pSPYCE.PGRL1A	At4g22890	Frw 5'- CTGCAGAG <u>GA<u>ATCC</u><i>ATGGTAGCAAGATGTTTTA</i></u> -3' Rev 5'- CTGCAGACC <u>CGGGAGCTGGCTCTCTGGC</u> -3'	BamHI XmaI
pSPYNE.PGRL1A	At4g22890	Frw 5'- CTGCAGAG <u>GA<u>ATCC</u><i>ATGGTAGCAAGATGTTTTA</i></u> -3' Rev 5'- CTGCAGACC <u>CGGGAGCTGGCTCTCTGGC</u> -3'	BamHI XmaI