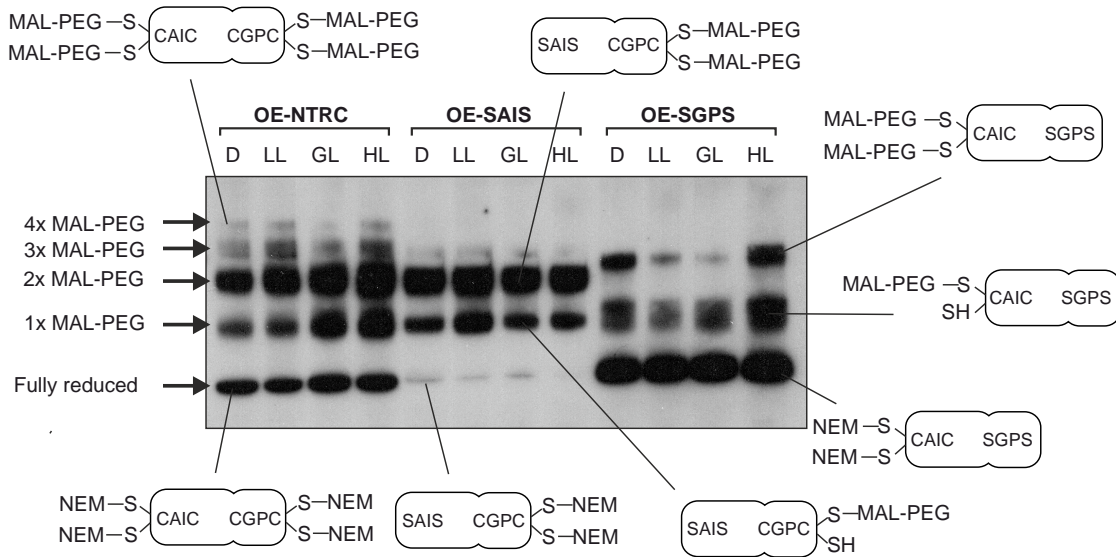
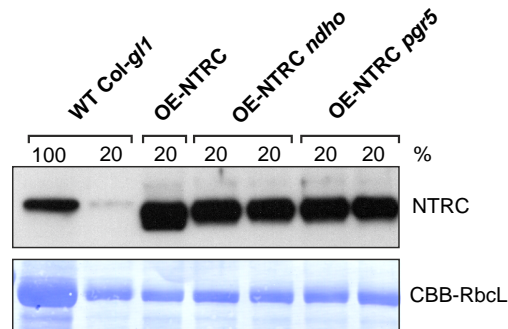


A



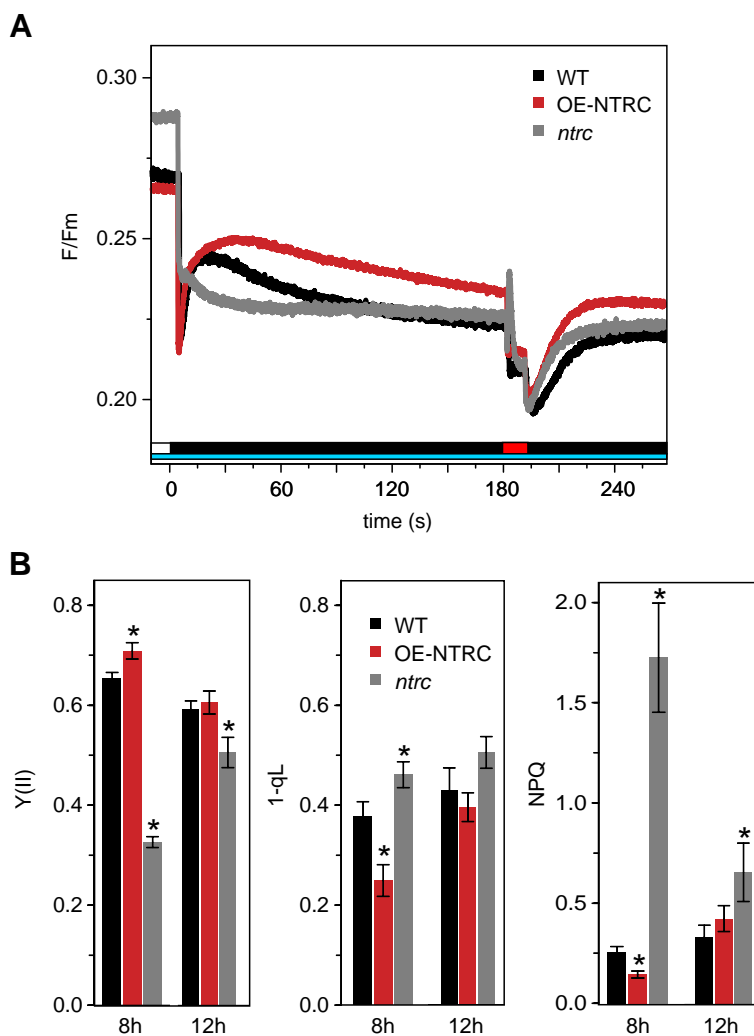
B



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, $40 \mu\text{mol photons m}^{-2} \text{s}^{-1}$), growth light (GL, $200 \mu\text{mol photons m}^{-2} \text{s}^{-1}$) or high light (HL, $800 \mu\text{mol photons m}^{-2} \text{s}^{-1}$).

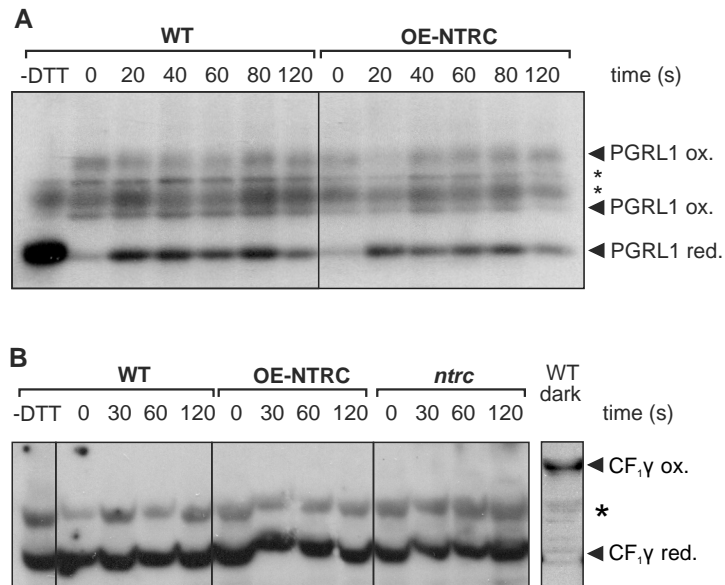
(B) Level of NTRC overexpression in OE-NTRC *ndho* and OE-NTRC *pgr5* plants detected by immunoblotting with an NTRC-specific antibody. 10 and 2 μg of soluble protein was loaded for WT and 2 μg for OE-NTRC, OE-NTRC *ndho* and OE-NTRC *pgr5*. Two individual plants were sampled for OE-NTRC *ndho* and OE-NTRC *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 $120 \mu\text{mol photons m}^{-2} \text{s}^{-1}$. The cyan bar indicates exposure to a 480 nm measuring light of $0.28 \mu\text{mol photons m}^{-2} \text{s}^{-1}$, the white bar depicts illumination with $67 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ 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(II)), redox state of the PQ pool (1-qL) and non-photochemical quenching (NPQ) at Fm' (after 7 min illumination) in plants grown either in an 8h or 12h photoperiod. The values are averages of 3–10 measurements \pm 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 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$) to high light (600 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$) 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 $\mu\text{mol photons l m}^{-2} \text{s}^{-1}$ 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_0 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_0 ($F_{20\mu s}$)	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 distachion* (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.

```

Physcomitrella MA--AMTGCICRAPLSLALQRESSFWGSNVGVHQQKSASSNSGGSTGGVRVGIARAEGFDF
Glycine -----MSSFVALQGLHGSLLSSQFLGQDTLTHFHPRNKASSTIQ-NKPTTAQQPSAKFDM
Brachypodium -----MAPAPTTPSFRLRPPPLPHHR-----V-R--LPPPPPSASFRL
Sorghum -----MAPPTSSSFLRPPPLPHHP-----H-PRLH-FRPPSASFRL
Oryza -----MAPTTPASFRLRPPPLPHHH-----H-PRIVRLPPPSATFRV
Solanum MASASSFQLSSLQIQTPPLKSNFLGQSVNLNLS-SSVHTKSAM-KSSSNSVTPIAKFNL
Arabidopsis ---MATSSITIPTIRTP-IHRSKFLGQTHQFSTVNRSVFPPPKQ-QSKLYQVKAMGKFNL
Vitis -----MAYSFTVPSLQRLPLPHKSHFLGQGHFPNNIQKASLSR-----TRTPLPVKASAKFDL
                                         *                                     *

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Physcomitrella WQVLGGRGLKGGEDGLKQEKARVLQEAKKNLVVE-KKKKGSVEGNVEAAEGLPGTFNKE
Glycine LQIVGGRGLCNGEAGLKQELKKQVGVDEKQTSAT-SGKEQEIEEEESTSVVATEDGFEKE
Brachypodium AEILGGRGLCNGEAGLIRKELSSPTTPTPTADSS-P---GGAAAEADPPAVDPDAFEKE
Sorghum SEILGGRGLCNGEAGLIRKELTSGSSAST---TTSS-PAPSPSPSTESPPAVDLDADFKE
Oryza ADLLGGRGLCNGEAGLIRKELASDSPAAPPSTTTSS-DEPAESPPPPPAASGVDPDAFDEKE
Solanum YEILGGRGLCNGEAGLIEKELKKSISEEQKAVGSAAAAASDDDNQENKETGEIPEDGFEKE
Arabidopsis WEVMGGRGLCNGEAGLIEKELQRNIEDEQETSKAEN-NETERESDDSNLSFKVPEDGFEKE
Vitis FGIMGGRGLCNGEAGLQQLKRNIEPAPSPDSVKD-E----EKPALAAVDDVPEDGFDEKE
          : : * * * * * . * * * * : : * * * * *

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```

Physcomitrella LGGWTGGFPGEKGLRQFVQSNPPPAKASQMSNEIRKLQDSISRPLKPRAPSPPLLMPGM
Glycine LMGLTGGFPGGEVHSG-----KPSSTKTKSSKN-LKLALSKKPKPELPLLLPGM
Brachypodium MMGLTGGFPGGEVGLKDFVAKNPPPPPKRTQPDGIAGS-AAVVAERPRRPELPLFLPGM
Sorghum MMGLTGGFPGGEVGLKDFVAKNPPPPRSKKSNSQLVAP-QATTLASAPRTPPELPLFLPGM
Oryza MMGLTGGFPGGEVGLKDFVAKNPPPPPKPAHRKGLA-----AAATVERPRAPELPLFLPGM
Solanum MMGFTGGFPGEKGLMKFIEKNPPPPPKKTESMVSF-FNQSLVKKPKPELPLLLPGM
Arabidopsis MMGLTGGFPGGEKGLKTFIEKNPPPPPPPPPAKQGSDA-SAVATDKKPKAPKLPLLLPGM
Vitis LLGLTGGFPGGEKGLKQFLEKNPPPEKT-----SGNI-IENARLRKPKPELPLLLPGM
          : * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

```

```

Physcomitrella TVKVISPSNPYFEFIGIVQRVTDGKVGVI FEGGNWDKLVSFKLQDLERTSQGPPMSNPKS
Glycine IAIVKNPNPNPFYMYCKIVQRITDG-----PRMKNPKS
Brachypodium IVLVKNPNRNAYHYMYCGIVQRVTDGKVGVL FEGGNWDRLITFGVDELEGREKGPPMVNPKS
Sorghum VVLVKNPNNAYYMYCGIVQRVTDGKVAVLFEGGIWDRDLITFDLDELEGREKGPPMVNPKS
Oryza VVLVKNPNNAYHYMYCGIVQRVTDGKVGVL FEGGIWDRDLITFDLDELEGREKGPPMVNPKS
Solanum IAIVKNSNPNPYMYCGIVQRITDGKAAVLFEGGNWDRLISFRLEELERREKGPPMVNPKS
Arabidopsis IAIVKNQNSPYHYMYCGIVQRITDGKAGVLFEGGNWDRLITFRLEELERREKGPPGKNPKS
Vitis IAIVKNPNPNPFYMYCGIVQRITDGKAGVLFEGGNWDRLITFRLEELQRDRKGPMPKNPKS
          . * . . : : * * * * * * * * * * * * * * * * * *

```

```

Physcomitrella AILERMIVPEGTSSPEGASS-----
Glycine AVLKPFLEKKS-----
Brachypodium VVLEALVADLADDTEAEE-----TEKKEEEEAGAAAAKA
Sorghum VVLEDIVAQLEDDDDDDKE-DEAAKKEKEPEGAAAAA-
Oryza VLLES�AAEMEDDVAKKEEKEEAKKKKEEETAAAAA-
Solanum VILEKMVEKSSEA-----
Arabidopsis CILEPLIEQMKEEAAP-----
Vitis AILETLLEQEA-----

```


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

Sequences from *Physcomitrella patens* (PHYPADRAFT_106212), *Oryza sativa* (Os08g0276100), *Brachypodium distachion* (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-----GAGLANCPQCSICVTRATSSLSHSNPSKQLQRAFGTRTNVRLENA
<i>Oryza</i>	MQTPTMSTSMATPAKLP---SPPS--LPIARQ-----CCCHL----LQLGRRG--G
<i>Brachypodium</i>	MQTPTMYTSMAARATSA--AANLP--APPPRQ-----CYHYL----LPPAGRR--S
<i>Populus</i>	---MASTSLLPKTIISPFLLTNPPP--LPSHFHTSKPSFFNPSADHH----LPCTRKP---
<i>Arabidopsis</i>	---MASSLPLLPKPIISPFKTPPF--STSKPLV-----FL---NFQ----TRLTSRSSDV
<i>Glycine</i>	MAATYYLLPTSPKTFSPFLRNPPS--IPSGHHVSLLGSL---DYP----FHCSSRRGNN
	:
<i>Physcomitrella</i>	SS--VVVSAKKGWFDDPFDDYGDDEEDTMGELMSQGPQGAEDPRPARDPDSESGYLDFFPA
<i>Oryza</i>	AGVARASAKKKNPWLDPFDDGPDDEFDY-RGAFSGG-KQEEDPRPPEDPANPYGFLRFPA
<i>Brachypodium</i>	VWALSASPKKKNPWLDPFDDGPDDEFDY-TGVYSGG-KQEDPRPPEDPANPYGFLRFPM
<i>Populus</i>	-SILTPYAKKKNPWLDPFDDGEDLDMEY-GSLFVDG-KQEDTRPVDPNPNPYGFLKFPK
<i>Arabidopsis</i>	S---VNLKKNPWLDPFDDGEDPDNEY-GSLFADG-KQEDPRPPDNDPNPYGFLKFPK
<i>Glycine</i>	SVEANCNAKKNPWLDPFDDGEDPEMEY-GSLFADG-KQEEDPRPPDNDPNPYGFLKFPK
	* : . : * * * * : : * : * * * * : * . * : * * *
<i>Physcomitrella</i>	GFMPEVASLGILIRNDVRRCCVMSISGGVYENLLFFPVIQLLKNRYPGVRIDVMATPRGKQ
<i>Oryza</i>	GYNPELDSLASKVRRDVRRAACVWSGGVYENLVFFPVVQLLRDRYPGVVDVVASARGKQ
<i>Brachypodium</i>	GYNPELDSLASKVRGDVRRACVWSGGVYENLVFFPVVQLLDRYPGVLIDVVASARGKQ
<i>Populus</i>	GYNVEVAQLGLKIRGDVRRCCVMSISGGVYENLLFFPVIQMLKDRYPGILVDVLASDRGKQ
<i>Arabidopsis</i>	GYTVELASLPLKIRGDVRRCCVMSISGGVYENLLFFPTIQLIKDRYPGVQVDILTTERGKQ
<i>Glycine</i>	GYSVEIASLALKVRGDVRRCCVMSISGGVYENLLFFPAIQMLIKDRYPGVQIDVVASERGKQ
	* : * : . * : * * * * . * : * * * * * : * * * * : * : : : * * * * : * : : : * * *
<i>Physcomitrella</i>	AYEMNKNVRKAWVHPVDDQFLRPVDFTEVTVGKIKGEYYDLLVSTKLAGLGQSIFFWLASV
<i>Oryza</i>	VYEMCKNVRADVYDPDDDDWPEPAEYTHQLGVLKNRYDLDLIISTKLAGIGHALFLFMSSA
<i>Brachypodium</i>	VYEMCKNVRANVYDPDDDDWPEPAEYTHQLGVLKNRYDMLILSTKLAGTGHALFLFMSSA
<i>Populus</i>	CYELNKNVRWANVYDPDG-DPEPAIYTDMIGVLKNRYDLDVLSTKLAGLGHASFMFMSSA
<i>Arabidopsis</i>	TYELNKNVRWANVYDPDDHWPEPAEYTDMIGLLKGRYDMLVSTKLAGLGHAAFLFMTTA
<i>Glycine</i>	TYELNKNVRWANVYDPDDDEFPEPAEYTDMVGVLKNRYDMLVSTKLAGLGHAAFLFMTTA
	** : * * * * * . : * . . * . : * : * . * * * * : * * * * * : * * * * * : *
<i>Physcomitrella</i>	RNKVSYTYPDVNAAGAAKFLDIAIKAPQLELAESGFNMYAEMIEELSQMGNVPKTEVPP
<i>Oryza</i>	RDKVGYVYPNVNSAGAGLFLTEMFRPPTTNLADSGYNMYQDMLEWIGRPAKGVPEHPVPP
<i>Brachypodium</i>	REKVGYYVYPNVNGAGAGLFLTEMFKPPTTNLSDGGYNMYQEMLEWLGKPGKGVPPQPIPP
<i>Populus</i>	RDKVSYIYPNVNAAGAGLLLTETFTPDSANLSEGGYHMYHQMLDWLGRPIYNVPRQPVP
<i>Arabidopsis</i>	RDRVSYIYPNVNSAGAGLMLSETFTAENTNLSELGYSMYTQMEDWLGKPFVPRQPVP
<i>Glycine</i>	RDRVSYIYPNVNAAGAGLLLTETFPDSONLSDGGYNMYHQMDWLKPFREVPRQPVP
	* : * . * * * : * * * * . * : * : * : * * * * : * : * : * * : * : *
<i>Physcomitrella</i>	LEVIGISKVKAYVEAKYREAGVREGEFLVFHGIIECDSSASMTSGDKDCLLPLSMWAEIA
<i>Oryza</i>	LRVSIKKLRAFVEDKYSRAGVEKGFVVVHGIASDSFANMRSRGDDCCLLPLEHWAEIA
<i>Brachypodium</i>	LRVSIKKLRGIVEDKYSRAGVEKGFVVVHGIASDSVANMTRSGDDCCLLPLEQWAEIA
<i>Populus</i>	LRVLSRKLKQYVEAKYRAGAEKGYIVIHGIESDSKASMQSRGDTDSLPLEVWDQIA
<i>Arabidopsis</i>	LRVSIKRKVEVAAKYRNAGAVTGKFIIVIHGIESDSKASMQSGDADSLLSLEKWAKII
<i>Glycine</i>	LRVSIKKLKEVVEAKYKAGAKKGYVVIHGIKSDSKASMQSRGDPDSLPLEVWAEIA
	* . * . : * : * * * * . * : * * * * . * * * * * : * * * * : * : *

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 distachion* (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 -----MGPVSTWLT'TNGFEHQSLTADHLGVEMVQVEADLLLPLCTALYAYG
Selaginella  TLDISATSASDGKVGQLPARPAEHESAHRLPLGFDHQGIETPQIQSEDRPSIAVALYVYG
Physcomitrella -----MQGRLSVWLANHKLPHRPLGFDYQGV EILQIRSEDWLSIAVALYVYG
Oryza        -----MQQGWL SNWLVKHEVVHRSLGFDHRGIETLQIKAEDWDSIAVILYVYG
Brachypodium -----MQQGWL SNWLVKHKVVHRSLGFDHRGIETLQIKAGDWD SIAVILYVYG
Arabidopsis -----MQGTL SVWLAKRGLVHRSLGFDYQGIETLQIKPEDWHSIAVILYVYG
Glycine      -----MQGRLSSWLVKHLIHRSLGFDYQGIETLQIKPEDWHSIAVILYVYG
Populus      -----MRGPLSAWLVKHLVHRSLGFDYQGIETLQIKPEDWHSIAVILYVYG
                * : . . * : * : * : * : . : . . * : * :
    
```

```

Synechocystis FNYLQCQ GAYDEGPGKSLVSFYHLVKLTED--TRNPEEVRLKVF LPRENPVVP SVYWIWK
Selaginella  SNHPRAQCARDVAPGGLLASVYHLAKVQDDEEADQPEELCIKVS SVSKKHPRIP SVFRVRK
Physcomitrella FNYLRSQCAYDVAPGGLLASVYHF TKIEDN-V-DQPEEICIKIFVSRQKPKIP SVFVIWK
Oryza        YNYLRSQCAYDVAPGGLSLASVYHLTRIQYG-I-DNPEEVCIKVFAQKDNPRIP SVFVIWR
Brachypodium YNYLRSQCAYDVAPGGLSLASVYHLTRIQYG-I-DNPEEVCIKVFAQKDNPRIP SVFVIWR
Arabidopsis YNYLRSQCAYDVAPGGLLASVYHLTRIEYG-V-NQAE EVCIKVFTHRSNPRIP SVFVWVK
Glycine      YNYLRSQCAYDVAPGGLLASVYHLTRIEYG-I-DQPEEVCIKIFVARKNPRIP SIFVWVK
Populus      YNYLRSQCAYDVAPGGLLASIYHLTRIEYG-ILDQPEEVCIKVFAPRKNPRIP SVFVWVK
                * : . * * * . * * * . * : * : * : * : . : . : * : * : * : * :
    
```

```

Synechocystis AADWQERECYDMFGIVYEGHPNLKRILMPEDWVGWPLRKDYISPDFYELQDAY-
Selaginella  SADLQERESYDMLGIFHESHPR LKRISMPDTWIGRPLRKDHTVPDFYEPQDSL R
Physcomitrella SADFQERESYDMLGISYENHPRLKRILMPDTWIGWPLRKDYIVPDFYELQDAY-
Oryza        SSDLFQERESFDMVGISYDNHPRLKRILMPESWIGWPLRKDYITPNFY EIQDAH-
Brachypodium SADFQERESYDMVGISYDNHPRLKRILMPESWVGWPLRKDYITPNFY EIQDAH-
Arabidopsis STDFQERESYDMLGITYD SHPR LKRILMPESWIGWPLRKDYIAPNFY EIQDAY-
Glycine      SADFQEKESYDMLGISYDNHPRLRRILMPESWIGWPLRKDYIAPNFY EIQDAH-
Populus      SADFQERESYDMLGISYDNHPRLKRILMPESWIGWPLRKDYIAPNFY EIQDAH-
                : * * : * : * : * : * : * : * : * : * : * : * : * : * :
    
```

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 distachion* (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      --MASLISFLLPKPKAVR-----SSISAPQTQTINTEKLEDKFGRKGIFSES--N
Oryza            MATSSLLPLHLPTRPASVAVKASAA-----ATAAAAPTQSLEESFGRKGLRFAADPAT
Brachypodium     ---MAFLPLHLPASSPTLLTARASSTAVSVSPPAQTSLSLQVLEETFGRKGIRFGAD-AT
Populus          --MASLLSFSLRKPSI-I---KATSLSPT----TTSPSTPEVLEEKFGRKGIFLES--N
Glycine          --MASFLSLSLPKLNL-I---KASSAANTTTTTTTTTLPTAETLNEKFGRKGIFLES--D
                  :                               *:: ** * :.* .
```

```
Selaginella      GIVEARLKLACGSAATIALPQGVVTSYRPIM-WHESQEEVLHSKRFPLQGG-----CAYK
Arabidopsis      NIPMVELKVRNGSSSLKLSLSDAHVLSYKPKVYWKD---EGFEEVLYTVDGD-----ESR
Oryza            GAPTAELSVRNGSSSLQLRLADGLVTSYRPKVYWKD---DGCREVLHTVAGAG--AGGEVK
Brachypodium     GAPTAELSVRNGSSSLRLNDGLVTSYRPKVSWKEDKDGCREILHTVSDS-----KTLK
Populus          NVPTVELKVRNGSSVRVQIPNAYVSSYKPKVYWKD---DGFEEVLYTLPGEKEDSSGIK
Glycine          NTPIVDLTVRNGSSSLRLRIPDAHVTSYKPKVNWKD---DGFQEVLYTIPATETGP-YKAK
                  . . *.: **: : : . * **:* : **:* .. . :
```

```
Selaginella      GGIRASVARIPEVEDGEETKRANPPLSWIVNGVSRAPNKWVKITLGSS--LPNLKLNKNS
Arabidopsis      GGVGVVIVNGEEP----KGGSSVISGCDWSVKDSDAIDALQIELSCT--AGVLDITYI
Oryza            GVGGLALSEVSSS----GAAESLLVGESESVVDADSDSYDAVQVELGCTKSGTLEVTYV
Brachypodium     GVGGLVNLHAS-S----GSPSAAAVQPEWSVSAVSDSDSYDAMQVELGRGMSGPQLEVAIV
Populus          GGIGLVINDASEG----GSKGSLISSSEWTVKDVSDSIDAVQVELSCS--SGPLEISYV
Glycine          GVGGLVMNEVLQP----GAKGLLPSTLEWTVNDVSDSIDALQVELSCT--SRFFDITYI
                  **:* : . * * .. . ::: * . :::
```

```
Selaginella      VTLSKRQLQSTLSIENTGKAPCCFHASIATAVEVGDLAGAYAMGLLGTNFLSLGDESIAE
Arabidopsis      VSLYPVSMTALVVKNNGRKPVTLKPGIMSYLRFKKRSGAGIQGLKGCYCPNPLSSP-
Oryza            VTLYPLSMATAVMVKNNGKKPVSLTSAMLSHIKFDKRRGTAVEGLRGCYPCSHPPPAAG-
Brachypodium     VTLYATSMATAVIVKNAGKKPVALTGAVLSHIKFDKRRGTAVEGLMGCYCAHPPPPASG-
Populus          VSLYPLSMASAVIVKNNGRKDVTLTSAILSHLKFKKRAKAGIQGLRGCYCYCTQPPPLSSP-
Glycine          VTLYPVSMTAVVAKNIGPKPATLTNAILSHFRFKNRRGTAIKGLRSCYIIPHAPLSSP-
                  **.* : ::: :* * : . : : . . . : ** : :
```

```
Selaginella      NTTAGEEQGPRIFEKLAVALLSGGSYKRPERESQOGDESFGKDGRLWHRHCSEMAPLAPG
Arabidopsis      -----FELLSPSEAMKAESSGWFGESE---EGEKPGIWAVEDSVITLLEKK
Oryza            -----FALLTPAEAMKREDGGWFGGG-GGEEPRQGVVTVEDNLYTILKKK
Brachypodium     -----FALLTPAEAMKREESGWFGGGGGEEPRPGEWAVEENRYTILKKK
Populus          -----FEVLSPSEALKPESPLLDLDFD-FEPEEKPGSWKVQEEPIIILKDR
Glycine          -----FQILTPSEATISEPPRWLSFG-NETEAKPGTWGQQALSITLLENK
                  : :* . : * . *
```

```
Selaginella      MNRLY-----FMSSMPWTLDDRVRKASLVHLPEIGTEVSEPLQSG-ARVAGGR
Arabidopsis      MSRIYGAPPAERLKAVYNTPPSKFETIDQKKKVLDAKN-----KIKIPKGISNSFRE
Oryza            VSRVYAAPPEERKKRIYSTAPSKFTTIDQNSGLGFR-VVRMGYEDMYLCSPGEMYRKFYK
Brachypodium     VSRVYAAPPEERKKRVYNSAPSNFMTIDQSSGLGFR-VVKMGFEDMYLSSPGGMYDKFGN
Populus          LSRVYAAPPQERLKAFYNTSPTKYETLDQKELFFR-VIRIGFEDIYIGSPGSFAEKYK
Glycine          MSRVAAPPKERLKAFYNTPPSKYETIDQGRGLCFR-VIRMGFEDIYLSPPGSLSEKYK
                  :.*:* : :*: : . .
```

Selaginella	LEKVCAA-----RPNFG-----
Arabidopsis	RIVFQDDKDWRRDVCGIPRIDVGQVWEATLLRVHRSNVNARSCRCSLRRDMERSNGNRA
Oryza	DYFLCTGTAS----MLVPVVVNPGE EWRAAQVIEHDNL-----
Brachypodium	DYFLCTGPAS----LLVPVVVNPGE EWRAAQVIEHDNL-----
Populus	DYFICTGPAA----MLVPVVVKPGE EWKGAQMIEHDNL-----
Glycine	DYFICTGPAS----ILVPVTVNPGE EW RGAQVIEHDNLT-----

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'- CTGCAGAGGATCC <i>ATGG</i> CGACTTCTTCGATCAC -3'	BamHI
		Rev	5'- CTGCAGACCCGGGTGGTGCCTCTTCCTTTT -3'	XmaI
pSPYNE.NDH-S	AT4G23890.1	Frw	5'- CTGCAGAGGATCC <i>ATGG</i> CGACTTCTTCGATCAC -3'	BamHI
		Rev	5'- CTGCAGACCCGGGTGGTGCCTCTTCCTTTT -3'	XmaI
pSPYCE.PGR5	At2g05620.1	Frw	5'- CTGCAGAGGATCC <i>ATGG</i> GCTGCTGCTTCGATTTT -3'	BamHI
		Rev	5'- CTGCAGACCCGGGAGCAAGGAAACCAAGCCTCT -3'	XmaI
pSPYNE.PGR5	At2g05620.1	Frw	5'- CTGCAGAGGATCC <i>ATGG</i> GCTGCTGCTTCGATTTT -3'	BamHI
		Rev	5'- CTGCAGACCCGGGAGCAAGGAAACCAAGCCTCT -3'	XmaI
pSPYCE.PGRL1A	At4g22890	Frw	5'- CTGCAGAGGATCC <i>ATGG</i> GTAGCAAGATGTTGTTTA -3'	BamHI
		Rev	5'- CTGCAGACCCGGGAGCTTGGCTTCCTTCTGGC -3'	XmaI
pSPYNE.PGRL1A	At4g22890	Frw	5'- CTGCAGAGGATCC <i>ATGG</i> GTAGCAAGATGTTGTTTA -3'	BamHI
		Rev	5'- CTGCAGACCCGGGAGCTTGGCTTCCTTCTGGC -3'	XmaI