

SUPPORTING INFORMATION

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      *      20      *      40      *      60      *      80
AT5G63790.1 : -----MDFALFSSISIFEINHKDPPIRRFIKTQNRILSTRKQGGTFPKMAELNLPAGFRFHTDEELVKFYLCR : 70
AT5G63790.2 : MNLDPFVYKSSMDFALFSSISIFEINHKDPPIRRFIKTQNRILSTRKQGGTFPKMAELNLPAGFRFHTDEELVKFYLCR : 80
      *      100     *      120     *      140     *      160
AT5G63790.1 : RCASEPINVPVIAEIDLKFNWELPEMALYGEKEWYFFSHRDRKYPNGSRPNRAAGTGYWKATGADKPIGKPKTLGIKK : 150
AT5G63790.2 : RCASEPINVPVIAEIDLKFNWELPEMALYGEKEWYFFSHRDRKYPNGSRPNRAAGTGYWKATGADKPIGKPKTLGIKK : 160
      *      180     *      200     *      220     *      240
AT5G63790.1 : ALVFIYAGKAPKGIKTNWIMHEYRLANVDRSASTNKKNNLRLLDDWVLCRIYNNKGTMEKYLPAAAEKPTEKMSTSDSRCSS : 230
AT5G63790.2 : ALVFIYAGKAPKGIKTNWIMHEYRLANVDRSASTNKKNNLRLLDDWVLCRIYNNKGTMEKYLPAAAEKPTEKMSTSDSRCSS : 240
      *      260     *      280     *      300     *      320
AT5G63790.1 : HVISPDVTCSDNWEVESEPKWINLEDALEAFNDDTSMFSSIGLLQNDADFVPQFQYQSSDFVDSFQDPEQKPFLLNWNFAF : 310
AT5G63790.2 : HVISPDVTCSDNWEVESEPKWINLEDALEAFNDDTSMFSSIGLLQNDADFVPQFQYQSSDFVDSFQDPEQKPFLLNWNFAF : 320
      *      340     *      360     *      380     *      400
AT5G63790.1 : QG : 312
AT5G63790.2 : QG : 322
      *      420     *      440     *      460     *      480
AT5G63790.1 : QG : 312
AT5G63790.2 : QG : 322

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Figure S1. Alignment of two NAC102 isoforms

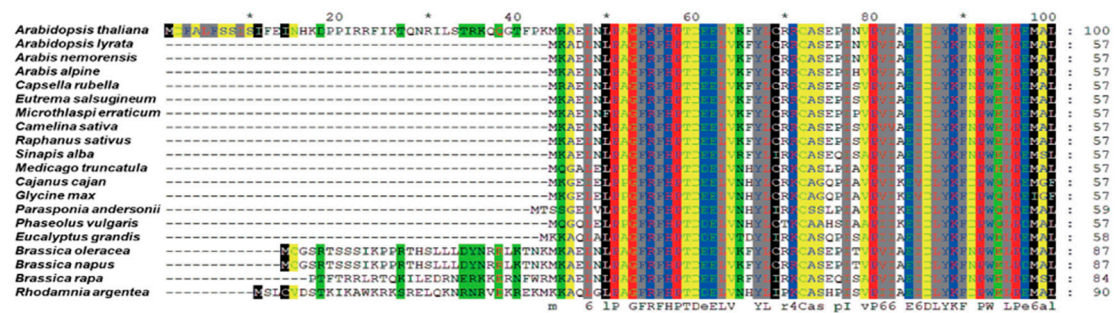


Figure S2. Alignment of NAC102 orthologs

The N-Terminal sequences of NAC102 orthologs from *Arabidopsis thaliana* (NP_201184.2), *Arabidopsis lyrata* (XP_002866576.1), *Arabis nemorensis* (VVB17923.1), *Arabis alpine* (KFK28073.1), *Capsella rubella* (XP_006280952.1), *Eutrema salsugineum* (XP_006394242.1), *Microthlaspi erraticum* (CAA7034898.1), *Camelina sativa* (XP_010460978.1), *Raphanus sativus* (XP_018439406.1), *Sinapis alba* (KAF8081687.1), *Medicago truncatula* (RHN43155.1), *Cajanus cajan* (KYP61874.1), *Glycine max* (NP_001341065.1), *Parasponia andersonii* (PON61827.1), *Phaseolus vulgaris* (XP_007159873.1), *Eucalyptus grandis* (KCW54084.1), *Brassica oleracea* (VDD27371.1), *Brassica napus* (CDY39846.1), *Brassica rapa* (VDC78532.1), and *Rhodamnia argentea* (XP_030551358.1) were aligned using ClustalW.

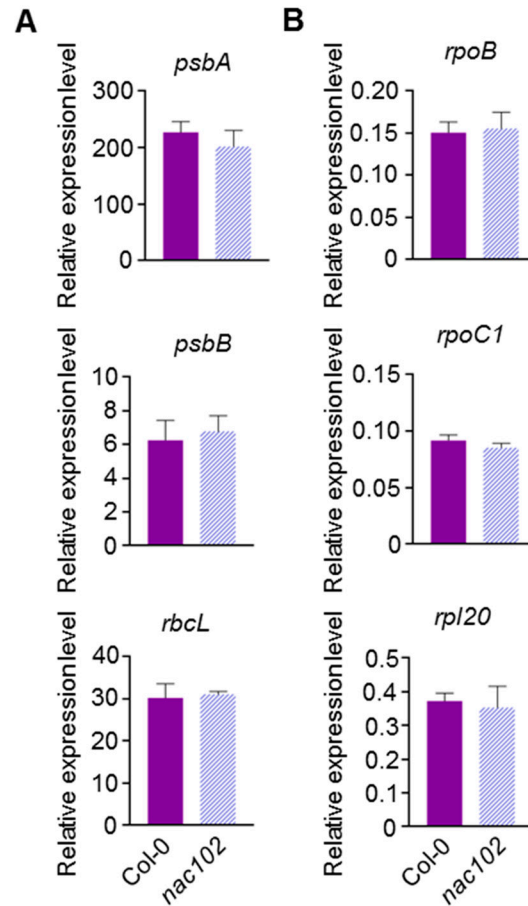


Figure S3. The chloroplast gene expression in the *nac102* mutant

The relative expression levels of the chloroplast genes were determined by qRT-PCR analysis using *EF1 α* as the normalizer. (A) The PEP-dependent genes. (B) The NEP-dependent genes. Data represent mean \pm SD ($n = 3$). The statistical significances were determined using Student's t-test (* $p < 0.05$, ** $p < 0.01$, and *** $p < 0.001$).

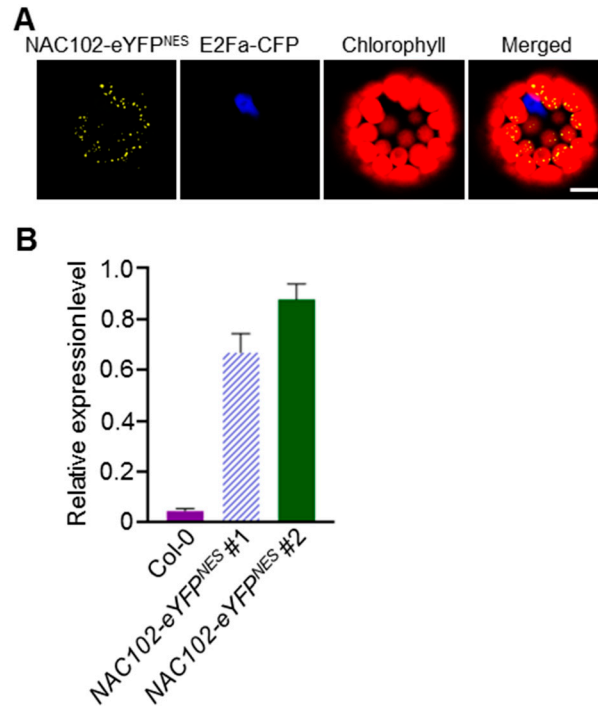


Figure S4. Construction of *NAC102-eYFP^{NES}* overexpression lines

(A) Subcellular localization of the *NAC102-eYFP^{NES}*. The fusion proteins were transiently expressed in *Arabidopsis* protoplasts. E2Fa-CFP was used as the nucleus marker and the chlorophyll fluorescence was used as the chloroplast marker. The pictures were captured using confocal microscopy. Bar = 10 μ m.

(B) The relative expression levels of *NAC102* in Col-0 and the *NAC102-eYFP^{NES}* transgenic lines were determined by qPCR using *EF1 α* as the normalizer. The data are represented as means \pm SD (n = 3).

Table S1. List of primers used in this study

Primer name	Sequence (5'-3')	Applications
NAC102-eYFP F1	CAATTACATTTACAATTACCATGGACTTTGCTC TCTTCTC	Fusion proteins
NAC102-eYFP F2	CAATTACATTTACAATTACCATGAACCTCCCCT TCGTTTA	
NAC102-eYFP R1	TGGGCCGCGCCGGAGCCGCGCCGCGCCTG GCCCTTGAGGAGCAAAATTCC	
eYFP F1	CCAGGCGGCGGCGGCTCCGGCGGCGGCCC AGTGAGCAAGGGCGAGGAGCT	Fusion proteins
eYFP R	CCGGGTCTTAATTAAGTCTCTAGATTACTTGTA CAGCTCGTCCA	
NAC102-eYFP ^{NES} R1	TTAGTCTAAAGTGAGGCGCTCAAGTGGAGGG AGACACTTGACAGCTCGTCCATGC	Fusion proteins
NAC102-eYFP ^{NES} R2	CCGGGTCTTAATTAAGTCTCTAGATTAGTCTAA AGTGAGGCGCT	
NAC102 ^{ΔN43} -eYFP F	CAATTACATTTACAATTACCATGAAGGCGGAG TTGAATTT	Fusion proteins
NAC102 ^{N43} -eYFP R	AGCTCCTCGCCCTTGCTCACTTTTGGAAG TACCTTGTT	Fusion proteins
NAC102 ^{N60} -eYFP R	AGCTCCTCGCCCTTGCTCACGTCCGTCGGAT GAAATCGGA	Fusion proteins
NAC102 ^{N80} -eYFP R	AGCTCCTCGCCCTTGCTCACCGGAACGTTAA TCGGTTCTG	Fusion proteins
eYFP F2	GTGAGCAAGGGCGAGGAGCT	Fusion proteins
EF1α-qPCR F	AAATACTCCAAGGCTAGGTACG	qPCR
EF1α-qPCR R	AAATGGGATTTTGTGAGGGTTG	
NAC102-qPCR F	GAGATGTGCGTCAGAACCGA	qPCR
NAC102-qPCR R	TTTCTCACCGTACAACGCCA	
psbA-qPCR F	TGAGCACAACATTCTTATGCAC	qPCR
psbA-qPCR R	AGTTACCAAGGAACCATGCATA	
psbB-qPCR F	GTTTTGGCGCATTTCATGTAAC	qPCR
psbB-qPCR R	TGGAATAGGCCCGCTAATATAC	
rbcL-qPCR F	TCTGGTGGAGATCATATTCACG	qPCR
rbcL-qPCR R	ATCATCTCCAAAGATCTCGGTC	
rpoB-qPCR F	GCGAATCGAGCTTTAATGAGTT	qPCR
rpoB-qPCR R	AAACGATCTTCTCAGTGTGAGT	
rpoC1-qPCR F	GTGCTATCCGAGAACAATTAGC	qPCR
rpoC1-qPCR R	GACATAAAACCATCCATTCGGG	
rpl20-qPCR F	TATTTGCATCAAGCTTTCGAGG	qPCR
rpl20-qPCR R	TGATCCATAAACGGCGAAAATC	
NAC102 BD F	CTCAGAGGAGGACCTGCATATGGACTTTGCT CTCTTCTC	Y2H
NAC102 BD R	CTAGTTATGCGGCCGCTGCAGCCCTTGAGGA	

	GCAAAATTCC	
rpoA AD F	ACGTACCAGATTACGCTCATATGGTTTCGAGAG AAAGTCAA	Y2H
rpoA AD R	CAGTATCTACGATTCATCTGCAGTTTTTTTTCT AGAATGTCTA	
rpoB AD F	ACGTACCAGATTACGCTCATATGCTTGGGGAT GAAAAAGA	Y2H
rpoB AD R	CAGTATCTACGATTCATCTGCAGAACTTCCTT CCTATTAATCT	
rpoC1 AD F	ACGTACCAGATTACGCTCATATGATCGATCGG TATAAACA	Y2H
rpoC1 AD R	CAGTATCTACGATTCATCTGCAGGGTATCATAT GAACAGGCTT	
rpoC2 AD F	ACGTACCAGATTACGCTCATATGGCGGAACG GGCCAATCT	Y2H
rpoC2 AD R	CAGTATCTACGATTCATCTGCAGAATCCTAGA AAAGTCAGATT	
rpoTp AD F	ACGTACCAGATTACGCTCATATGGCTTCCGCT GCGGCGGC	Y2H
rpoTp AD R	CAGTATCTACGATTCATCTGCAGGTTGAAGAA GTACTGTGATT	
rpoTmp AD F	ACGTACCAGATTACGCTCATATGTCCAGTGCT CAAACCCC	Y2H
rpoTmp AD R	CAGTATCTACGATTCATCTGCAGGTTGAAGAA ATAAGGTGAAT	
