

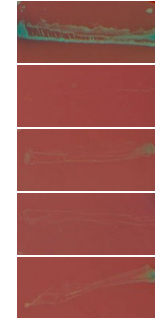
A

1. AD-HDA6 / BD-PIF3
2. AD-HDA9 / BD-PIF3
3. AD-HDA19 / BD-PIF3
4. AD-HDA2 / BD-PIF3
5. AD-HDA8 / BD-PIF3
6. AD-HDA14 / BD-PIF3
7. AD-HDA15 / BD-PIF3
8. AD-HDA18 / BD-PIF3
9. AD-HD2A / BD-PIF3
10. AD-HD2B / BD-PIF3
11. AD-HD2C / BD-PIF3
12. AD-HD2D / BD-PIF3
13. AD-SRT1 / BD-PIF3
14. AD-SRT2 / BD-PIF3

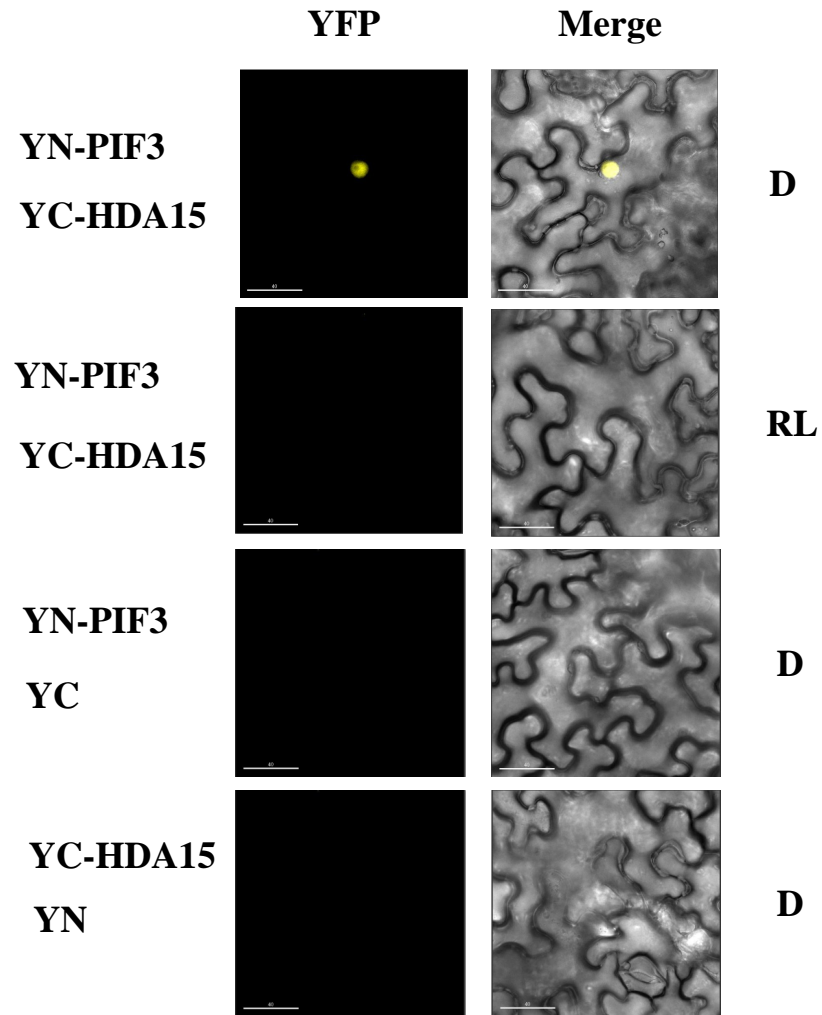


B

1. AD-HDA15 / BD-PIF3
2. AD-HDA15 / BD-PIF4
3. AD-HDA15 / BD-PIF5
4. AD-HDA15 / BD
5. AD / BD-PIF3

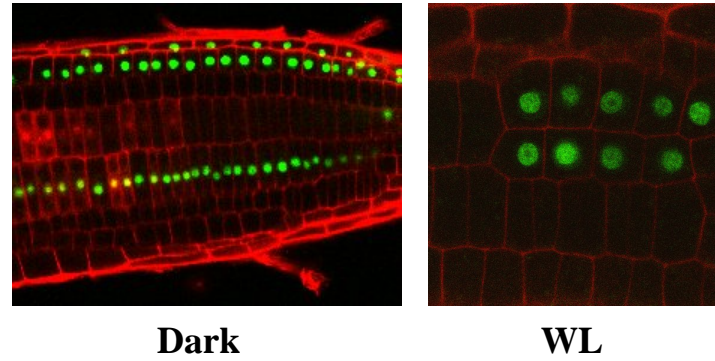


Supplemental Figure 1 HDA15 specifically interacts with PIF3 in yeast. (A) Protein-protein interaction between PIF3 and HDACs in yeast cells. Full length cDNAs of HDACs and PIF3 were fused with AD and BD vectors, respectively. (B) Protein-protein interaction between HDA15 and PIFs (PIF3, PIF4 and PIF5) in yeast cells. The constructs were cotransformed into the yeast strain AH109 and plated on SD/-Leu-Trp medium. The transformants were then plated on SD/-Leu-Trp-His plus x-a-gal medium to detect the interaction. 0.1 mM 3 AT was added to repress the auto-activation of PIF3 bait (BD-PIF3).

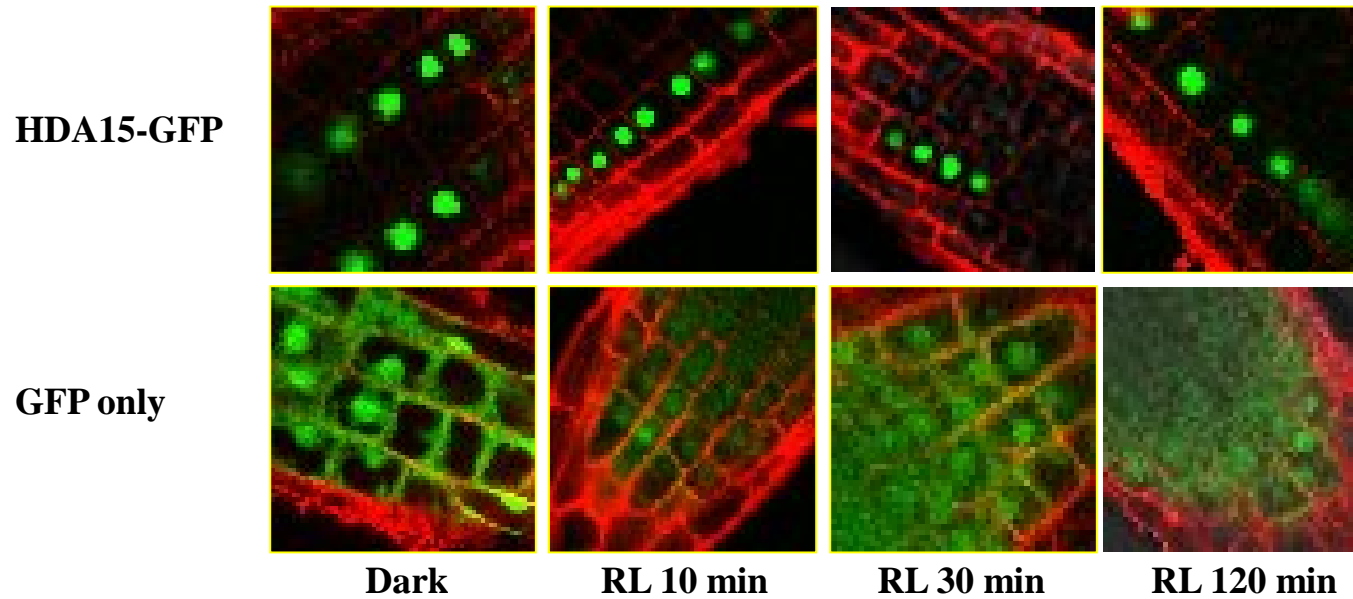


Supplemental Figure 2. HDA15 interacts with PIF3 in tobacco epidermal cells in dark. PIF3 and HDA15 fused with the N-terminus (YN) and the C-terminus (YC) of YFP were cotransfected into tobacco leaves with *Agrobacterium* strains (GV3101) and then incubated in dark (D) or red light (RL) at $10 \mu\text{mol m}^{-2}\text{s}^{-1}$ for 2 days.

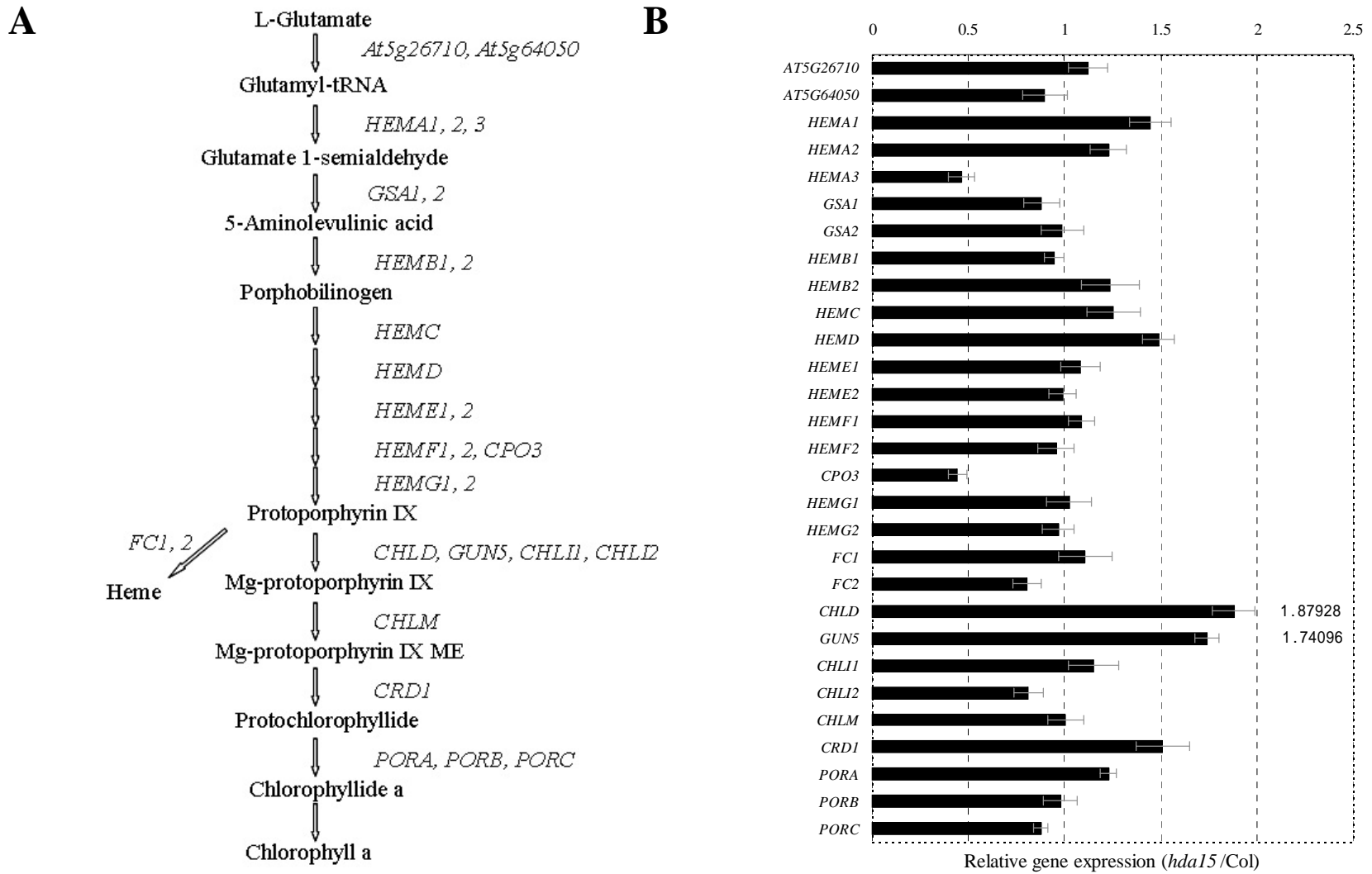
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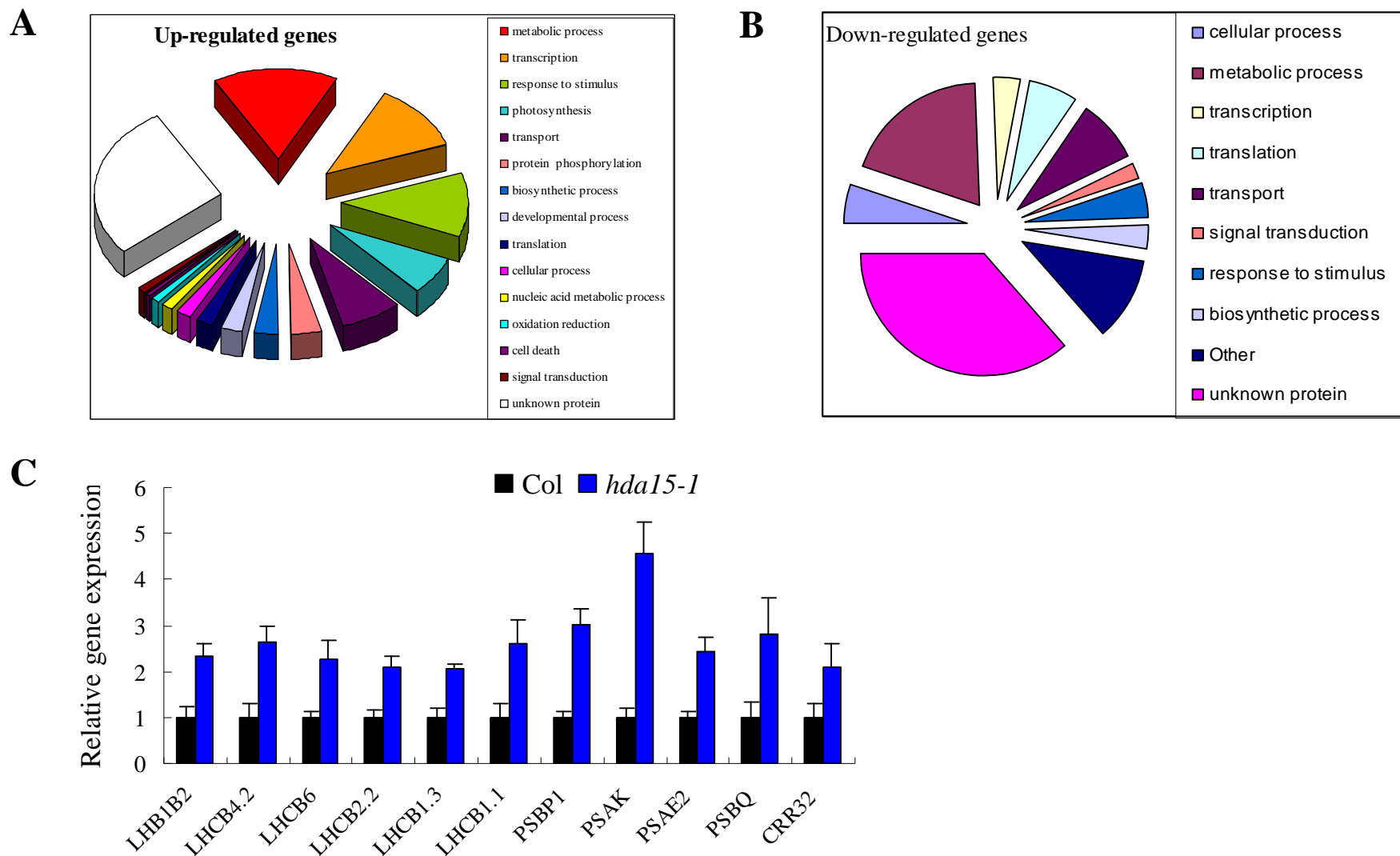
B



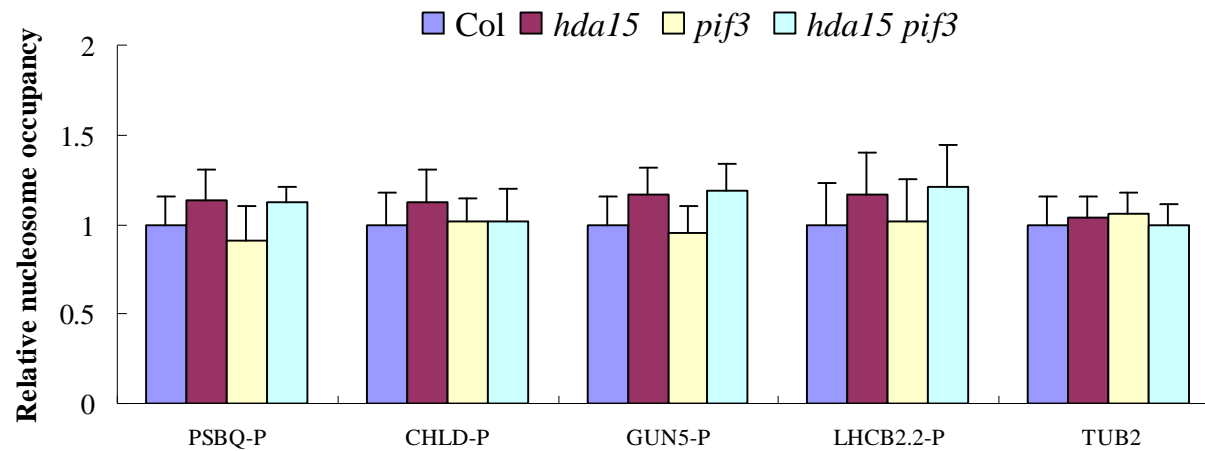
Supplemental Figure 3. HDA15 is constitutively localized in the nucleus under dark or light conditions. (A) Subcellular localization of HDA15 in 4-day-old transgenic plants (*35S:HDA15-GFP*). WL, white light, $100 \mu\text{mol m}^{-2}\text{s}^{-1}$, (B) Subcellular localization of HDA15-GFP when etiolated seedlings transferred to the RL ($10 \mu\text{mol m}^{-2}\text{s}^{-1}$). Cell walls are stained by propidium iodide.



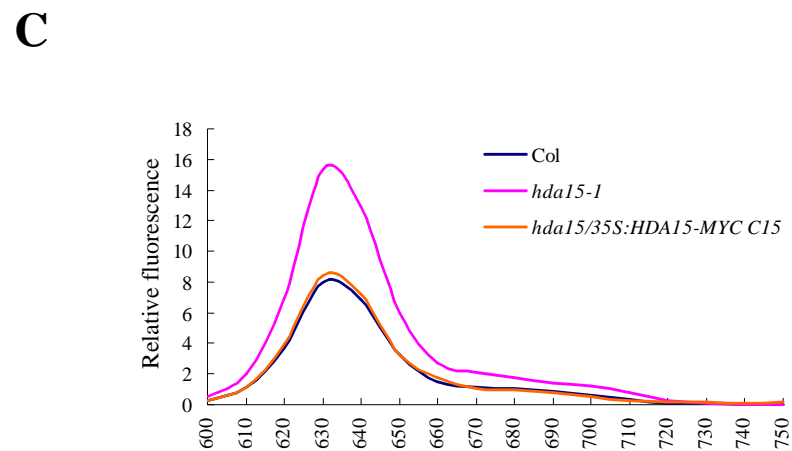
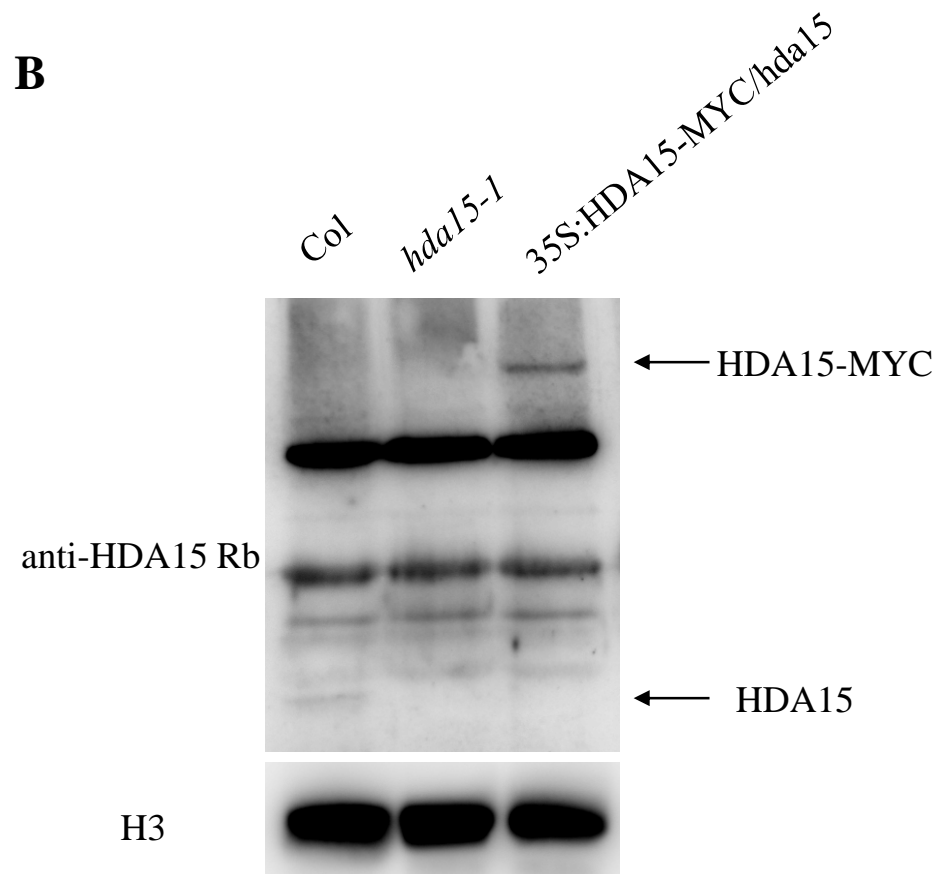
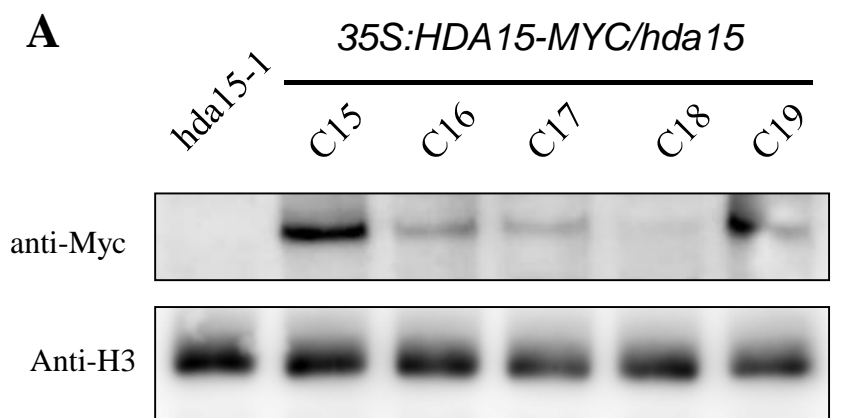
Supplemental Figure 4. Expression profiles of genes involved in the chlorophyll biosynthetic pathway in *hda15-1*. (A) A diagram of chlorophyll biosynthesis pathway. (B) Relative expression levels of genes involved in chlorophyll biosynthesis in *hda15-1* seedlings compared with Col seedlings grown in darkness for 2 days. The values are shown as means \pm SD.



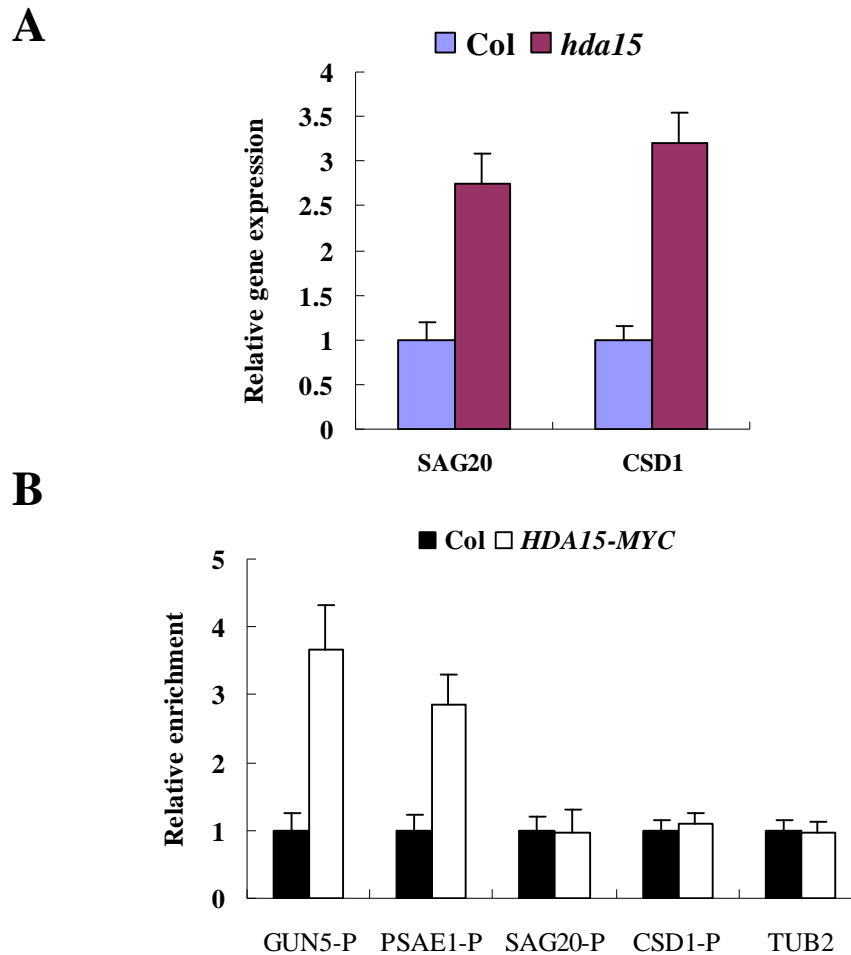
Supplemental Figure 5. Microarray analysis of HDA15 regulated genes in 2 day etiolated seedlings. (A, B) Up- and down-regulated genes in *hda15-1* seedlings. (C) qRT-PCR validation of genes expression detected by microarray analysis. *UBQ10* was used as a internal control. The values are shown as means + SD.



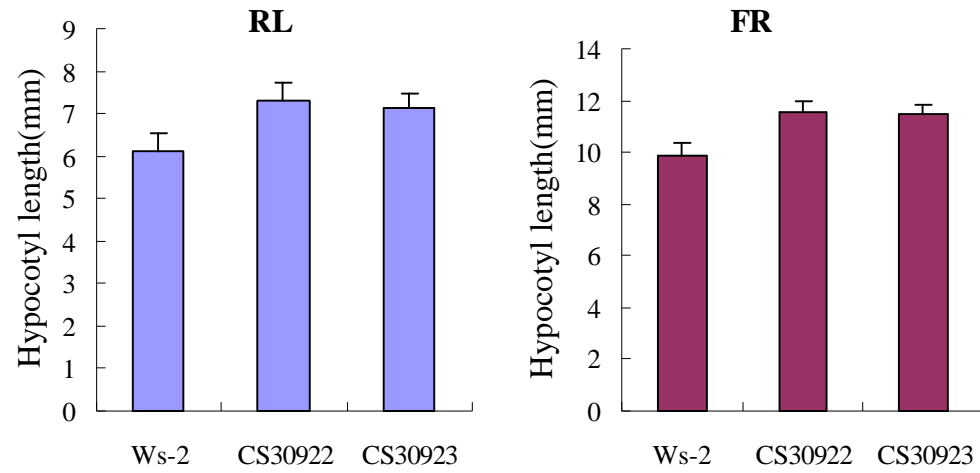
Supplemental Figure 6. Nucleosome occupancy analysis of the chlorophyll biosynthetic and photosynthetic genes in etiolated Col, *hda15*, *pif3* and *hda15pif3* seedlings. ChIP-qPCR analysis of DNA fragments co-immunoprecipitated with the anti-H4 antibody relative to Col. *TUB2* was used as a control. P indicated the promoter regions of the genes. The amounts of DNA after ChIP were quantified and normalized to *ACTIN2*. The values are shown as means + SD.



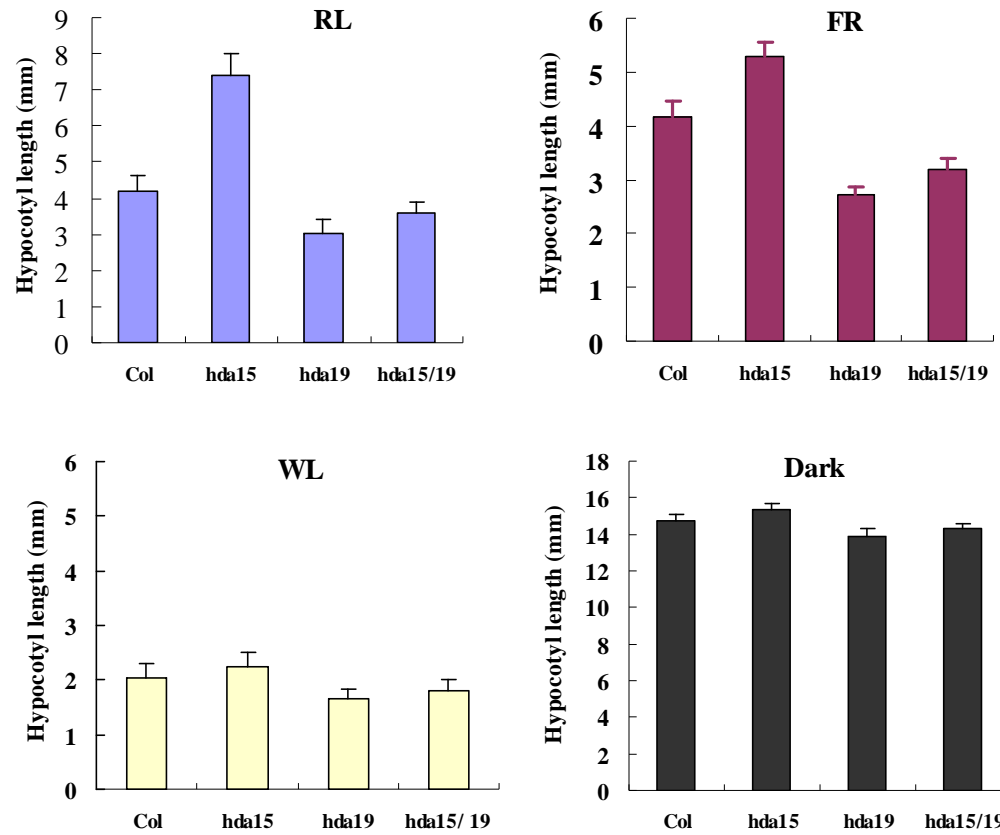
Supplemental Figure 7. Identification and analysis of *35S:HDA15-MYC* transgenic plants. (A) Western blot analysis of HDA15-MYC in *35S:HDA15-MYC/hda15* seedlings with anti-myc antibody. *hda15-1* was used as a negative control. C15 to C19 are individual transgenic lines in *hda15-1* background. (B) Western blot analysis of MYC-tagged HDA15 and endogenous HDA15 protein levels of Col and *35S:HDA15-MYC/hda15* transgenic plants with anti-HDA15 antibody. The arrows indicate HDA15-MYC and endogenous HDA15 proteins, respectively. (C) Measurement of protochlorophyllide content of 4-day-old etiolated *35S:HDA15-MYC/hda15* line C15.



Supplemental Figure 8. Detection and validation of HDA15 target genes. (A) qRT-PCR analysis of genes expression detected by microarray analysis. *UBQ10* was used as a internal control. The values are shown as means + SD. (B) ChIP-qPCR analysis of DNA fragments co-immunoprecipitated with the anti-myc antibody relative to Col. *TUB2* was used as a control. P indicated the promoter regions of the genes. The amounts of DNA after ChIP were quantified and normalized to *ACTIN2*. The values are shown as means + SD.



Supplemental Figure 9. Phenotypic analysis *HDA15* RNAi seedlings (CS30922 and CS30923) grown in RL and FR for 4 days. RL, $2.5 \mu\text{mol m}^{-2}\text{s}^{-1}$, FR, $2 \mu\text{mol m}^{-2}\text{s}^{-1}$. The values are shown as means + SD.



Supplemental Figure 10. HDA15 and HDA19 antagonistically regulate hypocotyl elongation. Quantification of hypocotyl lengths of 4-day-old Col, *hda15*, *hda19* and *hda15/19* seedlings under various light conditions. RL, 10 $\mu\text{mol m}^{-2}\text{s}^{-1}$, FR, 3.5 $\mu\text{mol m}^{-2}\text{s}^{-1}$, WL, 100 $\mu\text{mol m}^{-2}\text{s}^{-1}$. The values are shown as means + SD.

Supplemental Table 1. List of the genes that are induced in 2-day-old etiolated *hda15-1* and *pifq* (Leivar et al., 2009) seedlings relative to the wild-type.

Probe Set ID	AGI	Fold change (<i>hda15-1</i> /Col)	Fold change (<i>pifq</i> /Col)	Gene
249941_at	AT5G22270	1.896	2.230	
251759_at	AT3G55630	1.519	2.005	ATDFD
257641_s_at	AT3G25760	2.132	2.941	AOC1
265481_at	AT2G15960	2.453	3.027	
267523_at	AT2G30600	1.896	2.208	
257832_at	AT3G26740	1.996	2.229	CCL
265894_at	AT2G15050	1.694	2.313	LTP
265387_at	AT2G20670	2.364	2.496	
251221_at	AT3G62550	2.472	2.283	
248186_at	AT5G53880	2.129	2.414	
246880_s_at	AT5G26000	2.072	2.129	TGG1
252415_at	AT3G47340	4.174	2.099	ASN1
259015_at	AT3G07350	2.270	2.111	
255008_at	AT4G10060	2.132	3.300	
260287_at	AT1G80440	2.037	2.585	
245264_at	AT4G17245	2.313	4.568	
260037_at	AT1G68840	1.893	2.364	RAV2
250972_at	AT5G02840	1.691	2.017	LCL1
249010_at	AT5G44580	1.721	2.894	
249694_at	AT5G35790	1.661	3.653	G6PD1
266672_at	AT2G29650	1.581	4.565	
252441_at	AT3G46780	4.668	7.706	PTAC16
266319_s_at	AT3G10280	1.959	2.949	HIC
248684_at	AT5G48485	1.856	3.571	DIR1
258929_at	AT3G10060	1.776	2.571	
247131_at	AT5G66190	1.504	2.294	ATLFNR1
259161_at	AT3G01500	5.192	7.014	CA1
255365_at	AT4G04040	2.243	2.215	MEE51
261118_at	AT1G75460	1.756	4.594	
265051_at	AT1G52100	1.719	2.085	
249927_at	AT5G19220	1.657	3.673	ADG2
255886_at	AT1G20340	1.903	2.287	DRT112
262986_at	AT1G23390	1.649	3.031	
259625_at	AT1G42970	1.644	3.162	GAPB
249645_at	AT5G36910	2.209	2.831	THI2.2
245592_at	AT4G14540	2.045	3.152	HAP3
257745_at	AT3G29240	1.568	3.164	

248224_at	AT5G53490	1.727	2.158	JR1
259383_at	AT3G16470	2.275	3.069	
260266_at	AT1G68520	1.824	5.993	
251017_at	AT5G02760	1.519	7.788	
261218_at	AT1G20020	1.504	2.444	ATLFNR2
251036_at	AT5G02160	1.901	4.283	
258897_at	AT3G05730	2.426	9.246	
253040_at	AT4G37800	2.174	27.653	
250243_at	AT5G13630	1.712	5.572	GUN5
257008_at	AT3G14210	7.332	31.751	ESM1
256015_at	AT1G19150	1.624	2.892	LHCA6
262632_at	AT1G06680	1.841	3.014	PSBP-1
247073_at	AT5G66570	2.155	3.666	PSBO1
251082_at	AT5G01530	1.791	3.677	LHCB4.1
262557_at	AT1G31330	1.687	4.088	PSAF
258993_at	AT3G08940	2.093	6.215	LHCB4.2
266979_at	AT2G39470	1.596	2.980	PPL2
256309_at	AT1G30380	3.618	3.395	PSAK
259491_at	AT1G15820	2.353	7.126	LHCB6
254970_at	AT4G10340	1.813	2.774	LHCB5
262288_at	AT1G70760	1.535	4.401	CRR23
265287_at	AT2G20260	2.419	4.505	PSAE-2
255248_at	AT4G05180	3.804	8.085	PSBQ
251814_at	AT3G54890	2.890	15.637	LHCA1
261746_at	AT1G08380	2.299	5.434	PSAO

Supplemental Table 2. List of primers used in this study

Primer	Sequence 5'~3'
Primer pairs for quantitative RT-PCR	
UBQ10 RT pr1	GATCTTTGCCGGAAAACAATTGGAGGATGGT
UBQ10 RT pr2	CGACTTGTCATTAGAAAGAAAGAGATAACAGG
LHCB2.2 RT pr1	ATGGCGTCGAACTCGC
LHCB2.2 RT pr2	GTTGAAAGGGATAACAATATCGCC
LHCB4.2 RT pr1	TTAGTGATCGGCTACATTGAG
LHCB4.2 RT pr2	GAGCATGTTTGATCTCAGCTA
LHCB6 RT pr1	GGCTTTTCTGAAATGGTACAG
LHCB6 RT pr2	CTCTCCAGCTTCTCAAAGTC
PSBQ RT pr1	GAACGTGTCAGTACCAGAAAG
PSBQ RT pr2	TTGCTTGGTCTGAGTTATCTG
PSAE1 RT pr1	ACCACCGATTGGTCCTAAGAG
PSAE1 RT pr2	GCGTAATTGACTTTTGCGAAC
PSAK RT pr1	TGATGACTACATTGCCTCAGT
PSAK RT pr2	TACACCGATGATATGACCAAC
LHB1B1 RT pr1	ATGGCCGCCTCGACAATG
LHB1B1 RT pr2	CTTTCCGGGGACGAAGTTG
CHLD RT pr1	TGCAATCTCCTCCCTGATCT
CHLD RT pr2	TCCGTCTCCGTATCCGTATC
GUN5 RT pr1	CAACCAAACCAGCCAAATCT
GUN5 RT pr2	AGAGATTGCACGGCTTCACT
LHB1B2 RT pr1	ACCGTGAGCTAGAAGTTATCC
LHB1B2 RT pr2	TCCAAACATAGAGAACATAGCC
LHCB1.3 RT pr1	AGAGGCATTCGCTGAGTTGA
LHCB1.3 RT pr2	TCCCTTACCAGTGACGATGG
LHCB1.1 RT pr1	CTGCGTCTTCCCTGAGCTTT
LHCB1.1 RT pr2	ATGCTCTGAGCGTGAACCAA
PSBP1 RT pr1	TCCTTAGGTTCTGAAGACAAC
PSBP1 RT pr2	TGAGATGATGACTCCAGAATG
PSAE2 RT pr1	AGCTACCGGATTTATTCTCAC
PSAE2 RT pr2	TCCTTAGAATCTTGACCTTGG
CRR23 RT pr1	AGCAAAGGCCTGTGATATACT
CRR23 RT pr2	AGGAAGTACCAAACGGATATG
AT5G26710 RT pr1	TCCACCACTTTCAGTCATCG
AT5G26710 RT pr2	TCGCTGATCGACCAACATAG
AT5G64050 RT pr1	GCTCCAGCTTTTCTCAGACG
AT5G64050 RT pr2	AGCAGTCCTTGCTCCACCTA
HEMA1 RT pr1	TCAAGTGCTTTCGTTGGTTG
HEMA1 RT pr2	CGAGCTTTTTGGATCAAACC

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HEMA2 RT pr2
HEMA3 RT pr1
HEMA3 RT pr2
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GSA1 RT pr2
GSA2 RT pr1
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CHLM RT pr2
CRD1 RT pr1
CRD2 RT pr2
PORA RT pr1

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CTCTACAACGGGTTCAAGCA
CTTCTCAATGAGGTCAGCCA
TTGCATATGTGGAAGAAGCC
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GGAATCCAAATAAGGCCAAA
AAATGGATAAACCGGTCTCG
CATCCTGCTCGGTTTATCCT
GCGTCTCTAACCGTCCCTAC
GCTATGGTTGCTGAAGCTGA
GCGGGTAATGTATCAACACG
AGAGTTCGAGGCTCTGCTTC
CAACGAAGATCTGTGCGGAGA
CCTTCAAGCTGCTTCTTTGG

PORA RT pr2	AGTTGAAGTCGCGATTGCTT
PORB RT pr1	TCCGAACATGGATCTTCCTC
PORB RT pr2	CACGTTCCATTTCCCTGTCT
PORC RT pr1	ACAGGGTTGTTTCAGAGAACACAT
PORC RT pr2	CAATACACTCCTGACTTCCCAAG
SAG20 RT pr1	TTCGTACCTCTCTCCGTCGT
SAG20 RT pr2	AGCAACAACGTTACCGATCC
CSD1 RT pr1	GGAACTGCCACCTTCACAAAT
CSD1 RT pr2	TCCAGTAGCCAGGCTGAGTT

Primer pairs used for ChIP-qPCR analysis

ACTIN2 pr1	CGTTTCGCTTTTCCTTAGTGTTAGCT
ACTIN2 pr2	AGCGAACGGATCTAGAGACTCACCTTG
TUB2 pr1	ACAAACACAGAGAGGAGTGAGCA
TUB2 pr2	ACGCATCTTCGGTTGGATGAGTGA
PSBQ-P pr1	ATCGCATTCTGGGAACACTC
PSBQ-P pr2	TTGGTGTGTTGGTTATGTGACAA
GUN5-P pr1	CACTCCCAAACCATGAAAATATG
GUN5-P pr2	GTTGGTTTTGAAGGTAAGTGGTG
LHCB2.2-P pr1	GCTCTCTGTTATCCTGTGACCTC
LHCB2.2-P pr2	GACCAACCAATACTCACGTGTTTCTT
PSAE1-P pr1	TACACGTGGCAGATCTCAAGT
PSAE1-P pr2	ATATGTTTCGTAAGGCTAAGAAAAGAGGA
GUN5-S pr1	CACCACTTACCTTCAAACCAAC
GUN5-S pr2	CGAAGAGGAGAGGATAGGAGAAG
LHCB2.2-S pr1	GAATCAGAACCCTCTGACGTG
LHCB2.2-S pr2	GGAGGATTGTTGGATAGCTGA
PSBQ-S pr1	TCCGAGTAATCTAAGTAACAACGTG
PSBQ-S pr2	CTTCAAGGACAGCCTGAGATG
PSAE1-S pr1	TCCTCTTTTCTTAGCCTTACGAAC
PSAE1-S pr2	CATTGGCCGGTAGAACAAATA
GUN5-E pr1	CAACCAAACCAGCCAAATCT
GUN5-E pr2	AGAGATTGCACGGCTTCACT
LHCB2.2-E pr1	ATGGCGTCGAACTCGC
LHCB2.2-E pr2	GTTGAAAGGGATAACAATATCGCC
PSBQ-E pr1	GAACGTGTCAGTACCAGAAAG
PSBQ-E pr2	TTGCTTGGTCTGAGTTATCTG
PSAE1-E pr1	TATTTGTTCTACCGCCAATG
PSAE1-E pr2	ACCCTCTCTTAGGACCAATCG
GUN5-A pr1	AAAAAGAGAATGAAGCGGTACTC
GUN5-A pr2	AAATGGAGCAATACATGTAGCC
LHCB2.2-A pr1	GCCGGAGTGTAACAGGTTTG
LHCB2.2-A pr2	ACATGGAGCGAGAGAGAGGA
PSBQ-A pr1	CAGTTGTGAACGCCAAAATG

PSBQ-A pr2	TTATCTACTGGCGGGTCAGG
PSAE1-A pr1	GCACAGAAACGTTTAGGGAAA
PSAE1-A pr2	TTGATGTAGCGCCAACACTT
LHB1B1-P pr1	AAATCTGATGCCAGCTCGAC
LHB1B1-P pr2	GTGAGAGTGTGGCGCAAGTA
LHCB6-P pr1	GCCACATAATGCAGCCATTT
LHCB6-P pr2	CACCCACACTCACCACTGTC
SAG20-P pr1	ACGGTGGGGTCAAACATTAG
SAG20-P pr2	GGGGTTGGGATCTGATTCTC
CSD1-P pr1	TCTTGTCTCGTCTGTGCTG
CSD1-P pr2	CGCCGATCATAAATCGAAAA
