Supporting Information for

SWAP1-SFPS-RRC1 splicing factor complex modulates pre-mRNA splicing to promote photomorphogenesis in Arabidopsis

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SI References

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Datasets S1 to S2

SI Materials and Methods

Vector construction and preparation of transgenic plants

To prepare *SWAP1*$_{pro}$*:SWAP1-GFP*, a genomic DNA fragment containing ~1.6kb promoter region and ~2.7kb gene body was amplified using primers listed in Table S2 and directionally cloned into *pENTR/D-TOPO* vector following the standard protocol (Life Technologies). *pENTR-SWAP1*$_{pro}$*:SWAP1* vector was recombined into *pGWB4* binary vector. To prepare *35Spro:SWAP1-4XFLAG*, full-length SWAP1 open reading frame (ORF) was amplified using primers listed in Table S2 and cloned into NheI/XmaI restriction sites of pEZS-NL. 4XFLAG DNA fragment was inserted in SmaI/XbaI site of pEZS-NL-SWAP1. SWAP1-4XFLAG was amplified using the primers listed in Table S2 and cloned into SacI/BamHI sites of pCHF1 binary vector. To prepare *35Spro:SWAP1-mCherry*, full-length ORF was amplified using primers listed in Table S2 and cloned into BamHI/XbaI restriction site of the binary vector. All the binary vectors were transformed to GV3101 *Agrobacterium* and then into plants using the floral dip method (1).

To prepare *pVP13-SWAP1* bacterial expression construct, the full-length SWAP1 ORF without the stop codon was amplified using primers listed in Table S2 and directionally cloned into *pENTR/D-TOPO* vector following standard protocol. pENTR-SWAP1 vector was recombined into pVP13 destination vector. The recombined vector was transformed to BL21 (DE3) strain of *E. coli*.

To construct pYES2-SWAP1-GFP, the full-length SWAP1 CDS was amplified using primers listed in Table S2 and cloned into pEZS-NL vector. SWAP1-GFP was digested from pEZS-NL and cloned into pYES2 vector (Life Technologies). pYES2-SWAP1-GFP construct was transformed into RKY1293 *Saccharomyces cerevisiae* yeast cells. To prepare pGAD424-SWAP1 and pGBT9-SWAP1 yeast 2-hybrid vectors, full-length SWAP1 ORF was amplified using primers listed in Table S2 and cloned into EcoRI/BamHI restriction site. These constructs along with their combinations were transformed into yeast strain *AH109*.

Bacterial and yeast protein induction and purification

To induce the expression of proteins in bacterial culture, ~3ml of well-grown culture at 37^0C was transferred to a 500mL flask containing 200mL of LB media and appropriate antibiotics. Flasks were transferred to 37^0C rotary shaker for bacterial growth. When the culture reached an

OD of ~0.5, isopropyl β-D-thiogalactoside (final concentration 0.1mM) was added and incubated in a rotary shaker for 16 hrs at 18^0C. After the incubation, bacteria were first pelleted and then resuspended in protein extraction buffer (100mM Tris-Cl, pH 8.0, 1mM EDTA, pH 8.0, 150mM NaCl, 1X protease inhibitor and 1mM PMSF). The bacterial suspension was sonicated, cell debris was pelleted, and the supernatant was used to purify tagged protein according to standard commercial protocols.

To induce the expression of proteins in yeast culture standard commercial protocol (Thermo Fischer Scientific Inc) was followed, albeit with a small modification. Phycocyanobilin (Frontier Scientific; Cat # P14137) was included in the media during the protein induction. Native protein extraction buffer (2) was supplemented with 1X protease inhibitor and 1mM PMSF. Crude protein extract was stored at -80^0C until the assay was performed.

***In Vitro* pull-down and *In Vivo* Co-IP assays**

To perform *in vitro* pull-down assays, GST and MBP tagged proteins were expressed in the bacterial system and purified following standard commercial protocols. An equal quantity of GST-tagged protein was added to the amylose resin-bound MBP or MBP-tagged protein. To investigate the *in vitro* interaction between MBP-SWAP1 and phyB-GFP, an equal quantity of crude extract of phyB-GFP was added to the tubes containing amylose resin-bound MBP or MBP-SWAP1. Dark treatment (phyB-Pr) tubes were constantly kept in the dark, while the red light treatment (phyB-Pfr) tubes were irradiated with the red light (7µmol m^{-2} s^{-1}). Sample tubes were incubated in a rotary mixer at 4^0C for 3 hrs. After the incubation, beads were pelleted and washed at least 5 times. Following the final wash, beads were immersed in 1X SDS loading buffer, boiled for ~5 minutes, and separated on 6-8% SDS gel. GST and GFP tagged proteins were detected using anti-GST (GE Health care Inc; Cat #RPN 1236) and anti-GFP (Abcam inc: Cat #ab290) antibodies, respectively.

To perform the *in vivo* co-IP assays, 4-day-old dark-grown seedlings were either kept in the dark or irradiated with the constant red light (7µmol m^{-2} s^{-1}) for 6 hrs. Sample tissues were frozen and ground thoroughly in native extraction buffer containing appropriate quantities of protease and proteasome inhibitors. Approximately ~1µg of appropriate antibody was added to the protein extract and incubated in a rotary mixer at 4^0C for 3 hrs to immunoprecipitate one of the two tagged-proteins. Following the final wash, beads were immersed in 1X SDS loading buffer, boiled at 65^0C

for ~5 minutes, and separated on 6-8% SDS gel. Interaction between bait and the prey protein was detected using appropriate combinations of primary and secondary antibodies.

Yeast two-hybrid assays

Different combinations of AD and BD vectors were transformed into yeast strains *AH109/Y187* and multiple positive double transformants were selected on yeast drop-out medium (SD-Ade-Leu-Trp/SD-Leu-Trp). To determine whether the two proteins are interacting within the yeast system, liquid β-galactosidase assay was performed following standard commercial protocol (Clonetech Lab; Matchmaker Two-Hybrid System).

RNA-seq data analyses

Wild-type, *swap1-1* single, three double (*swap1-1sfps-2, swap1-1rrc1-3, sfps-2rrc1-3*) and the triple (*swap1-1sfps-2rrc1-3*) mutant seedlings were grown under complete darkness for 4 days and then one batch of seedlings in triplicate biological repeats was exposed to continuous red light for 3 hrs (R: 7µmol m^{-2} s^{-1}), while the other batch was kept under darkness (D). Following treatment, seedlings were frozen immediately and ground to fine powder. Total RNA was isolated using a commercially available RNA isolation kit following manufacturer's instructions (Sigma inc: Cat #STRN250-1KT). Total RNA with RIN (RNA Integrity Number) > 6.5 and 28S/18S >1.0 was used for directional library preparation followed by sequencing using NovoSeq PE150 (Novogene, Inc). The sequencing yield is ~200 million reads per sample. For each library, > 90% of the reads were mapped to the unique loci of Arabidopsis TAIR10 genome with the STAR pipeline (3). Differential gene expression was analyzed using DEseq2 (4). Genes with FDR values lower than 0.05 and absolute log two-fold change greater than 0.58 (1.5-fold) were considered as differentially expressed.

AS was analyzed through ASpli (Version 2.4.0) as part of the Bioconductor R package (5), which quantifies the pre-mRNA splicing events through calculating PSI and PIR matrix. In the new version of ASpli, the AS events with an absolute FDR < 5% and Delta PSI_PIR > 20% were deemed differentially spliced. To generate heatmaps and scatterplots, the Z-scores of PSI_PIR values and square roots of PSI_PIR values were calculated as described (2). GO categories belonging to biological processes, molecular functions, and cellular components were analyzed

using GeneCodis4. GO terms with P value < 0.05 and FDR <0.05 were considered as significantly enriched.

RNA extraction and RT-qPCR analysis

To perform RT-qPCR analysis, seedlings were frozen immediately following different treatment conditions. Total RNA was isolated using a commercially available RNA isolation kit following manufacturer's instructions (Sigma Inc: Cat #STRN250-1KT). Contaminating DNA was removed using RNase-free DNase treatment and 1µg of total RNA was used to synthesize cDNA using reverse transcriptase enzyme following manufacturer's instructions (Invitrogen: Cat # 28025013). Gene-specific primer sequences used in this study are listed in Table S2. House-keeping gene *PP2A* was used as an internal control throughout the analyses and the relative expression level was calculated using the comparative C_T method.

RNA Immunoprecipitation assays

Ten-day-old *SWAP1*$_{pro}$*:SWAP1-GFP/swap1-1* transgenic seedlings grown under 12 hrs light/12 hrs dark conditions were harvested at ZT 12 and immediately cross-linked by vacuum infiltration with 0.5% formaldehyde for 10 mins and then quenched by vacuum infiltration with 0.125 M glycine for 5 mins. Samples were washed with large amounts of autoclaved de-ionized water and dried on filter paper. Samples were immediately frozen and then RNA-IP was conducted following the protocol described previously (2, 6). Primers used in this analysis are listed in Table S2.

A

Accession	Spectrum Number (Control)	Spectrum Number (SFPS)	Unique Peptides	Protein Coverage
At1g30480 (SFPS)	0	872	25	0.3979
At4g31200 (SWAP1)	0	31	12	0.2446

B

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  1 MDRRQHDYAA SSGLPYAQQQ QQQGPNFQQQ QQPQFGFHPQ HPQYPSPMNA
 51 SGFIPPHPSM QQFPYQHPMH QQQQPQHLPH PPHPQMFGQQ QPQAFLPHLP
101 PHHLPPPFPG PYDSAPPPPP PADPELQKRI DKLVEYSVKN GPEFEAMMRD
151 RQKDNPDYAF LFGGEGHGYY RYKHFLSMHP PGGPFDPPFP SSSMPMIHHP
201 PNPMMSPSMN NVPGALAVPP IRQPPFPPFH DHHQLQQHLP QPHPFAPHAR
251 PDFDQSTHAF RGLSGPLPAD VAMELNGVLG NLNGTKESIK SAKIWFMQRS
301 PFAPALAEAL RDRVFAMDDS DRQMHIVYLA NDILFDSLQR RTNLHEFDNE
351 ALAFRPILGS MLGRIYHFPQ NKEENQSRLE KILQFWASKE VFDQDTISSL
401 EKEMKSGPPA NTFSHSPIIA AHALQRPGML QQPPNSNVSS TMNLEHLTNP
451 VATQQFIPNV MPPGAFPGSI PLNASVPPPT QPPAGEKPPP YPLFPPGLIP
501 GMVRKMQIGS GVPYSPLSPL DIPTVIPPSD TPQSEVLERV SKFFKEIGEV
551 NPSEGPMGSE SQDDYDNYER DSPQRKGGAC IPPPPNLQVD PETGTYADGS
601 TDKKSGSGRL GLGATADPNE PTQYDDVYTS YRKHRSTNYH TSMSARATTR
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C

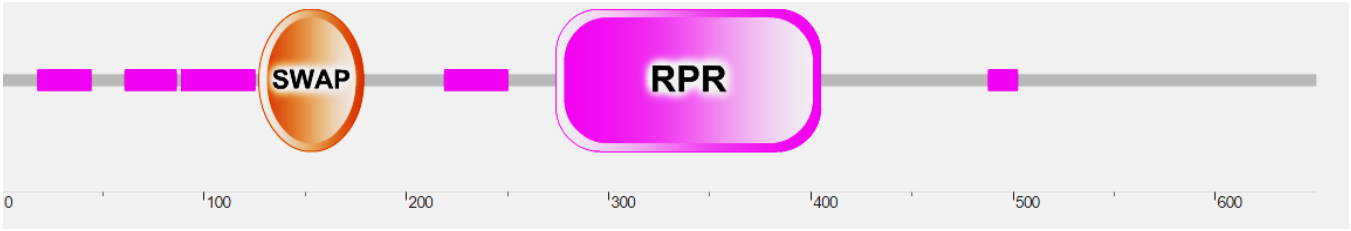

Fig. S1: Identification of SWAP1 as SFPS interactor in IP-MS (Immunoprecipitation followed by mass spectrometry) assay.

(A) SWAP1 co-immunoprecipitates with SFPS-GFP. Four-day-old dark-grown *$_{SFPSpro}$:SFPS-GFP/sfps-2* seedlings were either kept in the dark or irradiated with red light (7µmol m^{-2} s^{-1}) for 6 hrs. SFPS-GFP was immunoprecipitated using anti-GFP antibodies and interacting proteins were identified through MS-MS. (B) SWAP1 protein sequence showing peptides (colored) detected in MS-MS. (C) Predicted conserved domains of SWAP1 protein.

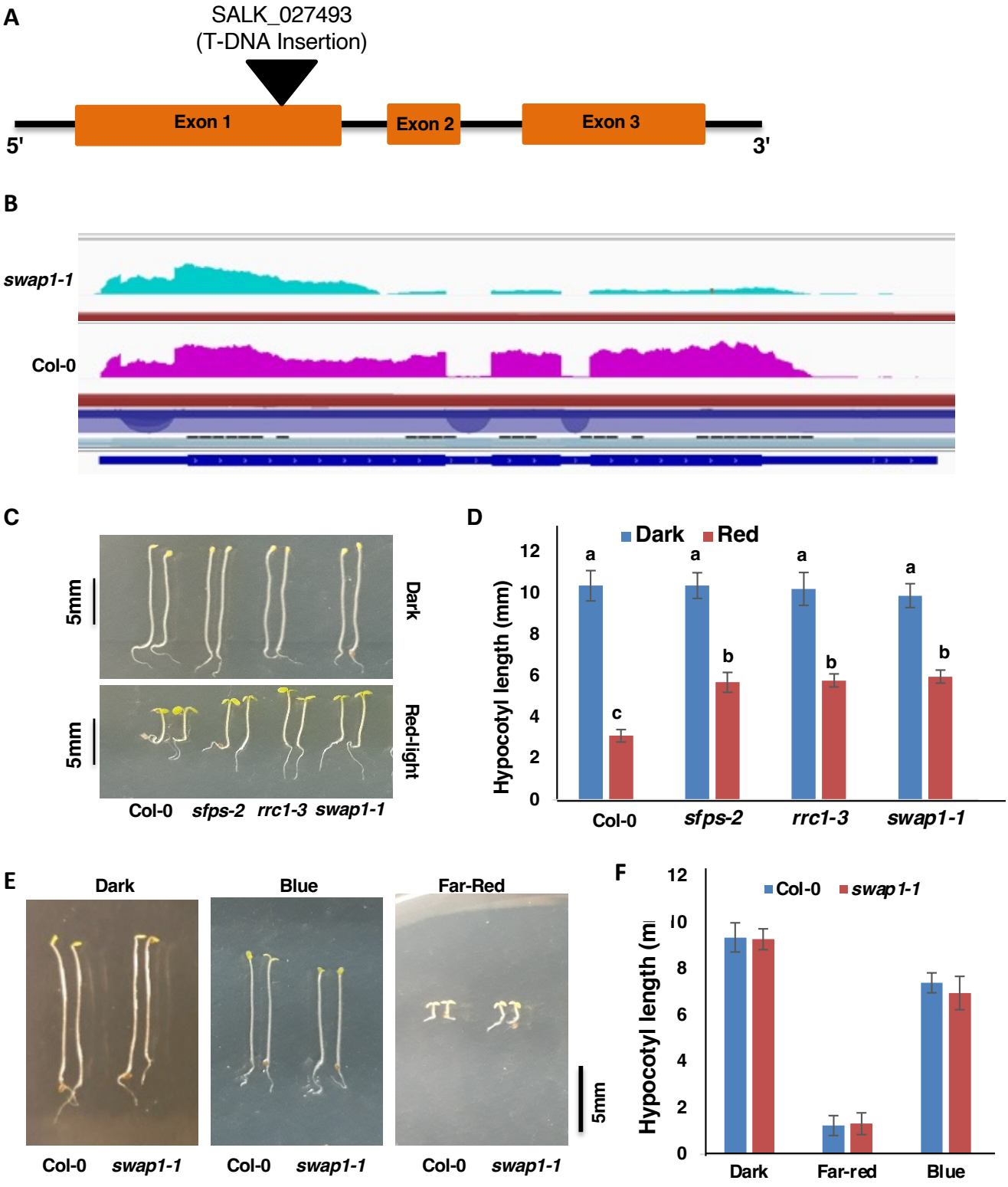

Fig. S2: *swap1-1* mutant seedlings display wild-type sensitivity on blue and far-red light

(A). Schematic diagram showing the gene structure of SWAP1 and the T-DNA insertion site of *swap1-1* (SALK_027493). Lines are not to the scale. (B) IGV visualization of *SWAP1* expression in Col-0 and *swap1-1* mutant. (C and D) Digital images of representative seedlings (C) and bar graph showing hypocotyl lengths (D) of different genotypes grown under either continuous dark or continuous red light (7µmolm^{-2}s^{-1}) for 4 days. Bars indicate mean length in mm and error bars indicate standard deviation. Statistical significance among different genotypes was determined using single factor ANOVA followed by Tukey's post hoc analysis and is indicated by different letters. (E) Digital images of representative seedlings of different genotypes grown under either continuous dark or continuous far-red-light or blue-light for 4 days. (F) Quantification of the hypocotyl length of 4-day-old seedlings grown under either continuous dark or continuous far-red light or blue light. Bars indicate mean length in mm and error bars indicate standard deviation. Statistical significance between Col-0 and *swap1-1* was determined by student's T-Test.

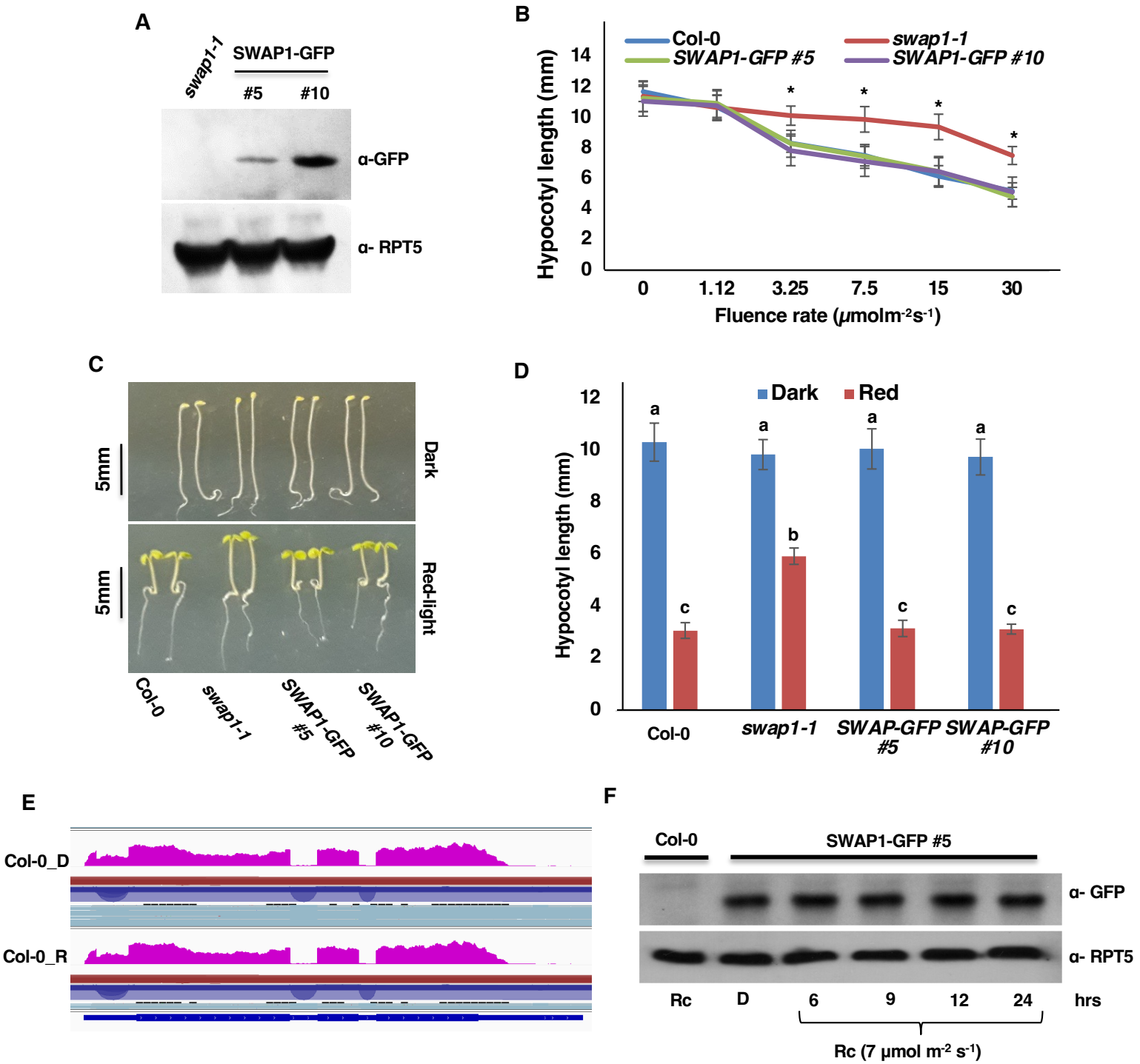

Fig. S3: *SWAP1*$_{pro}$*:SWAP1-GFP* complements the *swap1-1* mutant phenotype under red light

(A) SWAP1-GFP protein quantification in two independent homozygous *SWAP1*$_{pro}$*:SWAP1-GFP* transgenic seedlings. (B) Quantification of the hypocotyl length of 4-day-old seedlings of two independent transgenic lines expressing SWAP1-GFP under its own promoter along with *swap1-1* grown under either continuous dark or continuous red light of different fluence rate. Error bars indicate sem (n>30), and astericks indicate significant difference compared to Col-0 ($P < 0.05$) based on student's t-test. (C and D) Digital images of representative seedlings (B) and bar graph showing hypocotyl lengths (C) of different genotypes grown under either continuous dark or continuous red light (7μmolm^{-2}s^{-1}) for 4 days. Bars indicate mean length in mm and error bars indicate standard deviation. Statistical significance among different genotypes was determined using single factor ANOVA followed by Tukey's post hoc analysis and is indicated by different letters. (E)) IGV visualization of *SWAP1* expression in Col-0 under dark and red-light irradiated conditions. (F) SWAP1-GFP protein abundance in dark and red light treated seedlings. Total protein was extracted in denaturing buffer and protein was separated on 10% SDS-PAGE gel. Protein was transferred to a PVDF membrane and the presence of SWAP1-GFP was detected using α-GFP antibody. RPT5 protein was used as an internal control.

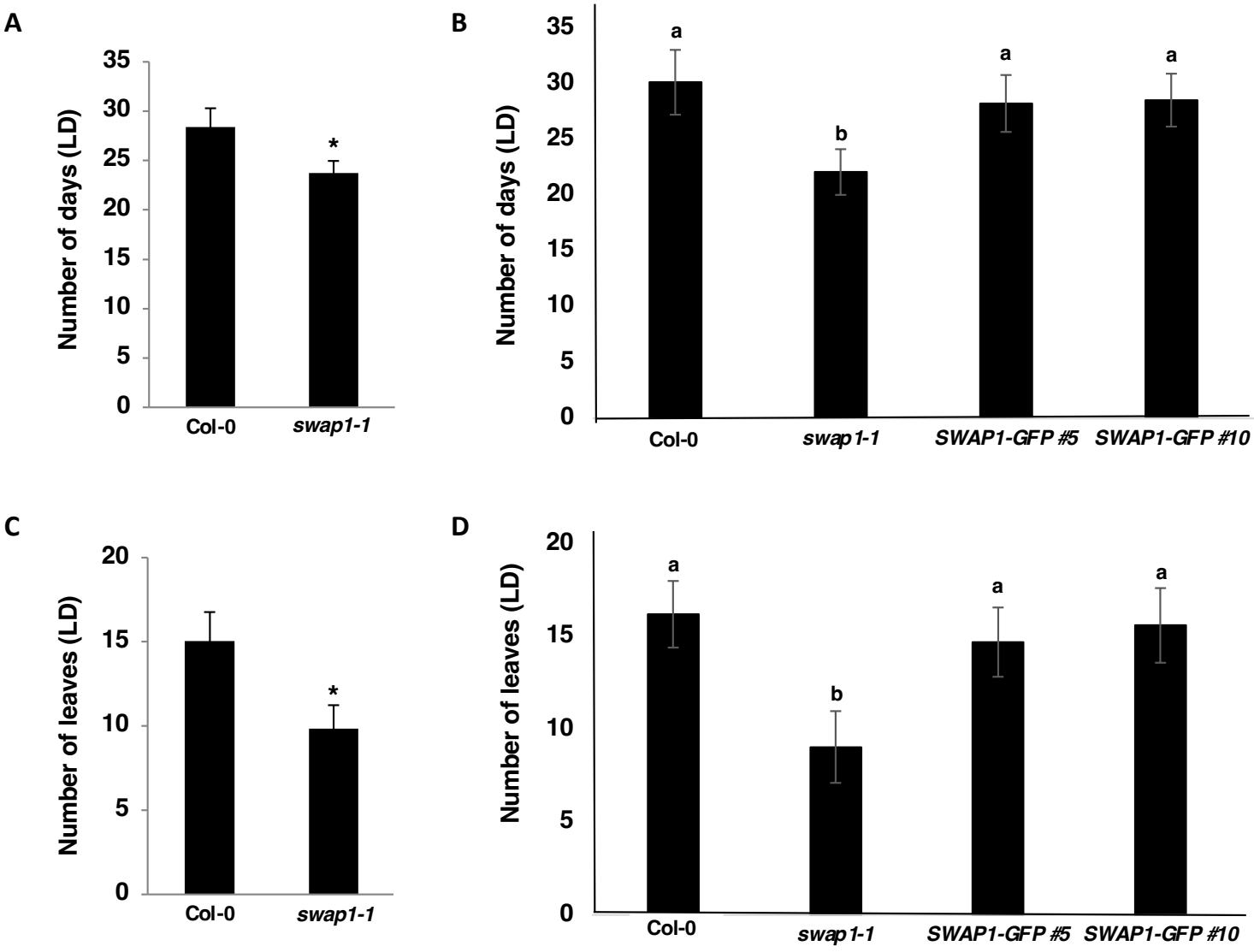

Fig. S4: *swap1-1* mutant plants flower early under long-day conditions.

(A) And (B) Number of days it takes plants show 1cm bolting under long-days (LD: 16hrs light/8hrs dark) condition. (C) and (D) Number of rosette leaves plants have when plants show 1cm bolting under LD condition. Each data point represents the mean average of at least 20 plants and the error bars show SD. Either Student's T-Test or one-way ANOVA followed by Tukey's post-hoc test was carried out to determine the statistical significance between or among samples, respectively.

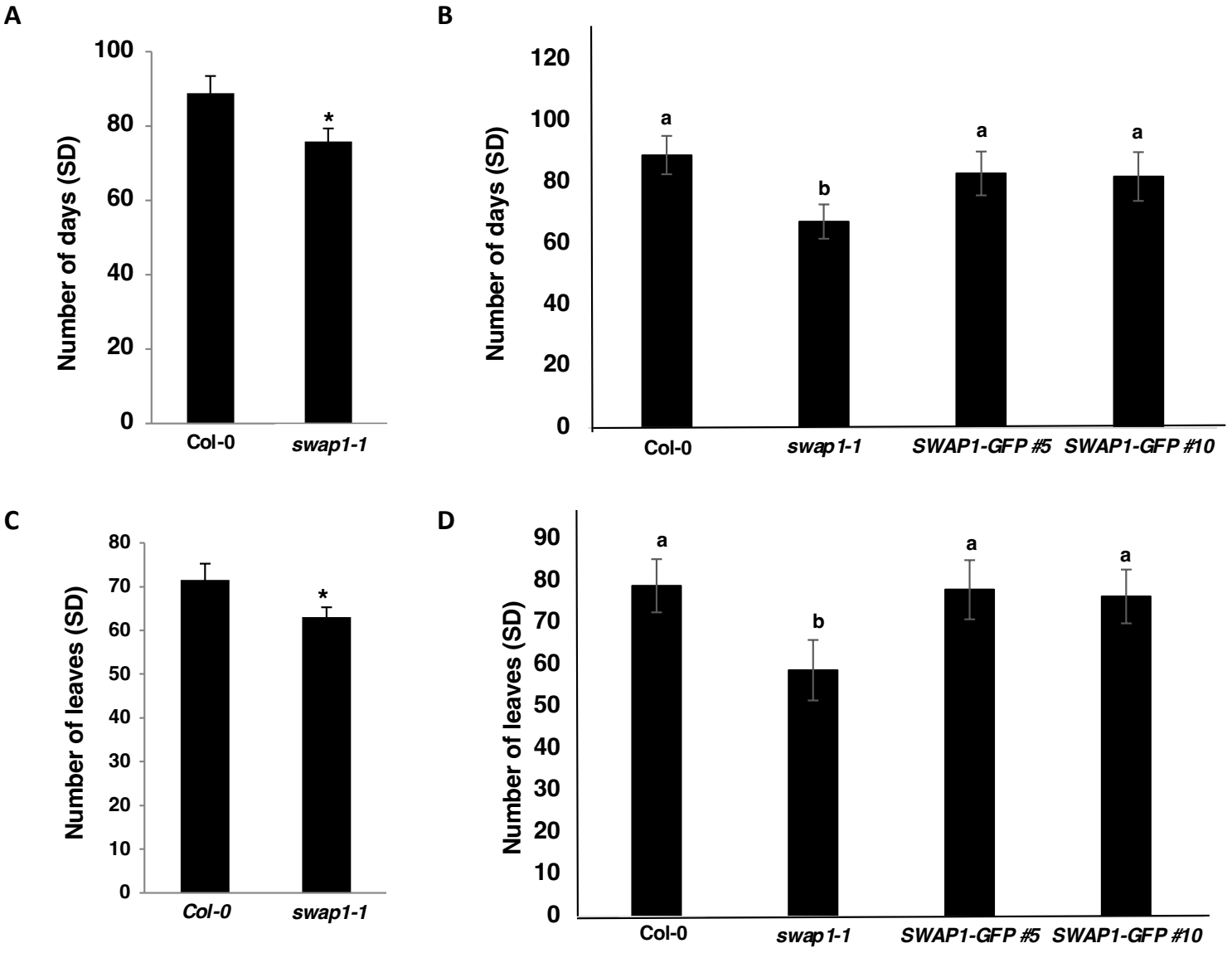

Fig. S5: *swap1-1* mutant plants flower early under short-day conditions.

(A) And (B) Number of days it takes plants show 1cm bolting under short-days (SD: 8hrs light/16hrs dark) condition. (C) and (D) Number of rosette leaves plants have when plants show 1cm bolting under SD condition. Each data point represents the mean average of at least 20 plants and the error bars show SD. Either Student's T-Test or one-way ANOVA followed by Tukey's post-hoc test was carried out to determine the statistical significance between or among samples, respectively.

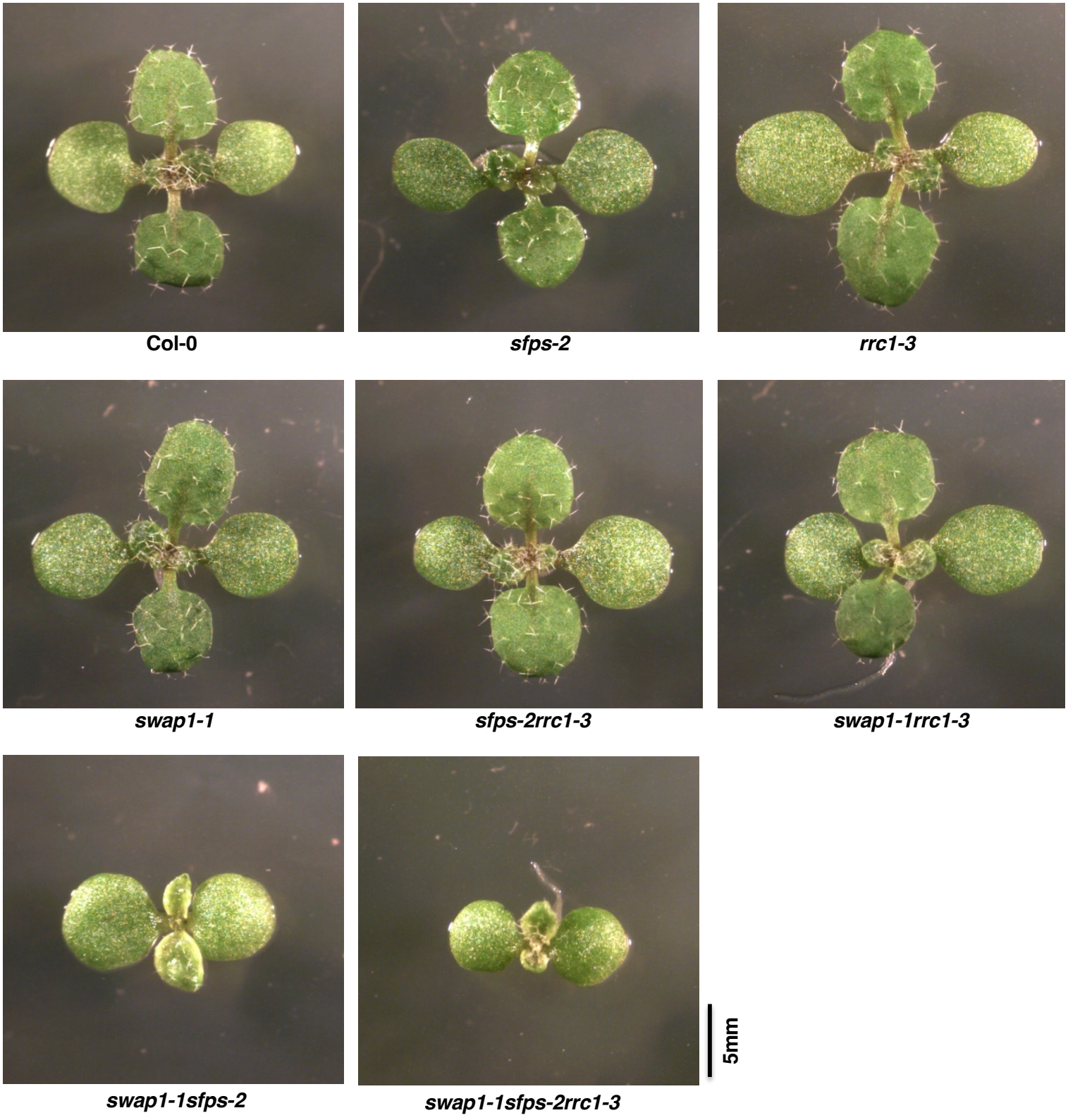

Figure S6: *swap1sfps-2* and *swap1sfps-2rrc1-3* display delayed onset of true-leaves at juvenile stage

Digital photographs showing the details of cotyledons and true leaves. Fourteen-day old light-grown seedlings were used for imaging.

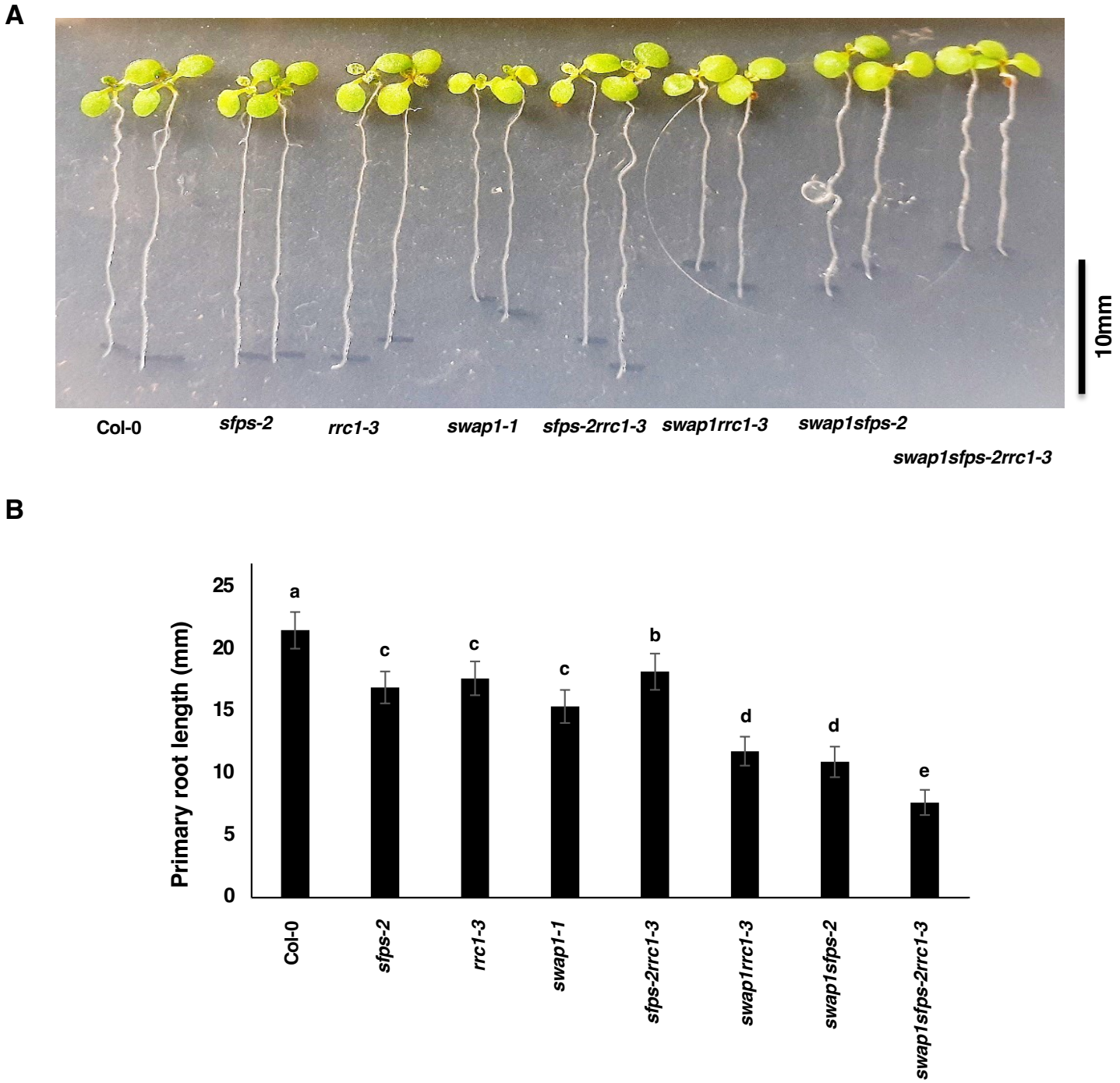

Figure S7: Single and higher order mutants display shorter primary roots under continuous light

(A) Digital photograph showing the representative image of length of primary root of 8-day old light-grown seedlings. (B) Quantification of primary root length. Each data point represents the mean of at least 20 seedlings and error bars represents SD. One-way ANOVA followed by Tukey's post-hoc test was carried out to determine the statistical significance among the samples.

Figure S8: *swap1* single, *swap1sfps*, *swap1rrc1* double and swap1sfpsrrc1 triple display shorter inflorescence and siliques compared to wild type at adult stage.

Digital photographs showing the inflorescence length of adult plants (A) and silique lengths (B). Seven-day old light-grown seedlings were transferred to the soil and then grown under continuous light for 5 weeks inside a growth chamber and then digital images were taken from representative plants and siliques.

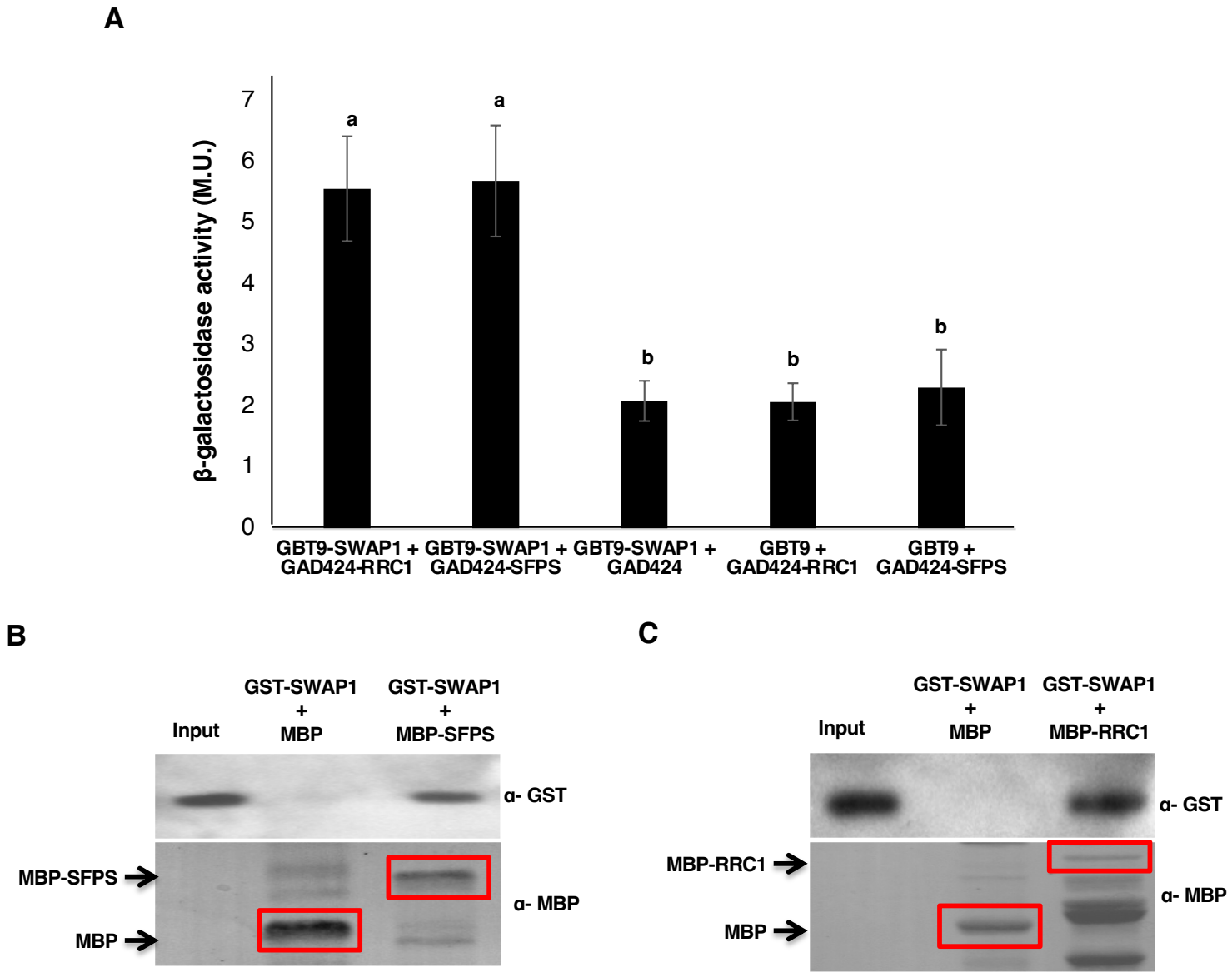

Fig. S9: SWAP1 interacts with SFPS and RRC1

(A) SWAP1 interacts with both SFPS and RRC1 in a yeast 2-hybrid system. Full-length SWAP1 CDS was inserted in pGBT9 vector, while full-length CDS of SFPS and RRC1 were inserted in pGAD424 vector. Liquid β- Galactosidase activity assay was carried out to quantify the strength of interaction between SWAP1 and SFPS/RRC1. Each data point reflects the average of three values and the error bars represents the SD. One-way ANOVA with Tukey's post-hoc test ($P<0.01$) was carried out to determine the statistical significance among the samples.

(B) GST-SWAP interacts with MBP-SFPS and MBP-RRC1 (C) *in vitro*. Bacterially expressed and amylose resin-bound MBP, MBP-SFPS and MBP-RRC1 were used as bait proteins to pull-down GST-SWAP1 prey protein. The pull-down reaction was incubated for 60mins at 4^0C on a rotating shaker. After the incubation, beads were washed at least 5 times. Proteins were separated on 10%SDS-PAGE gel, transferred to PVDF membrane and first immunoblotted with α- GST, followed by α- MBP.

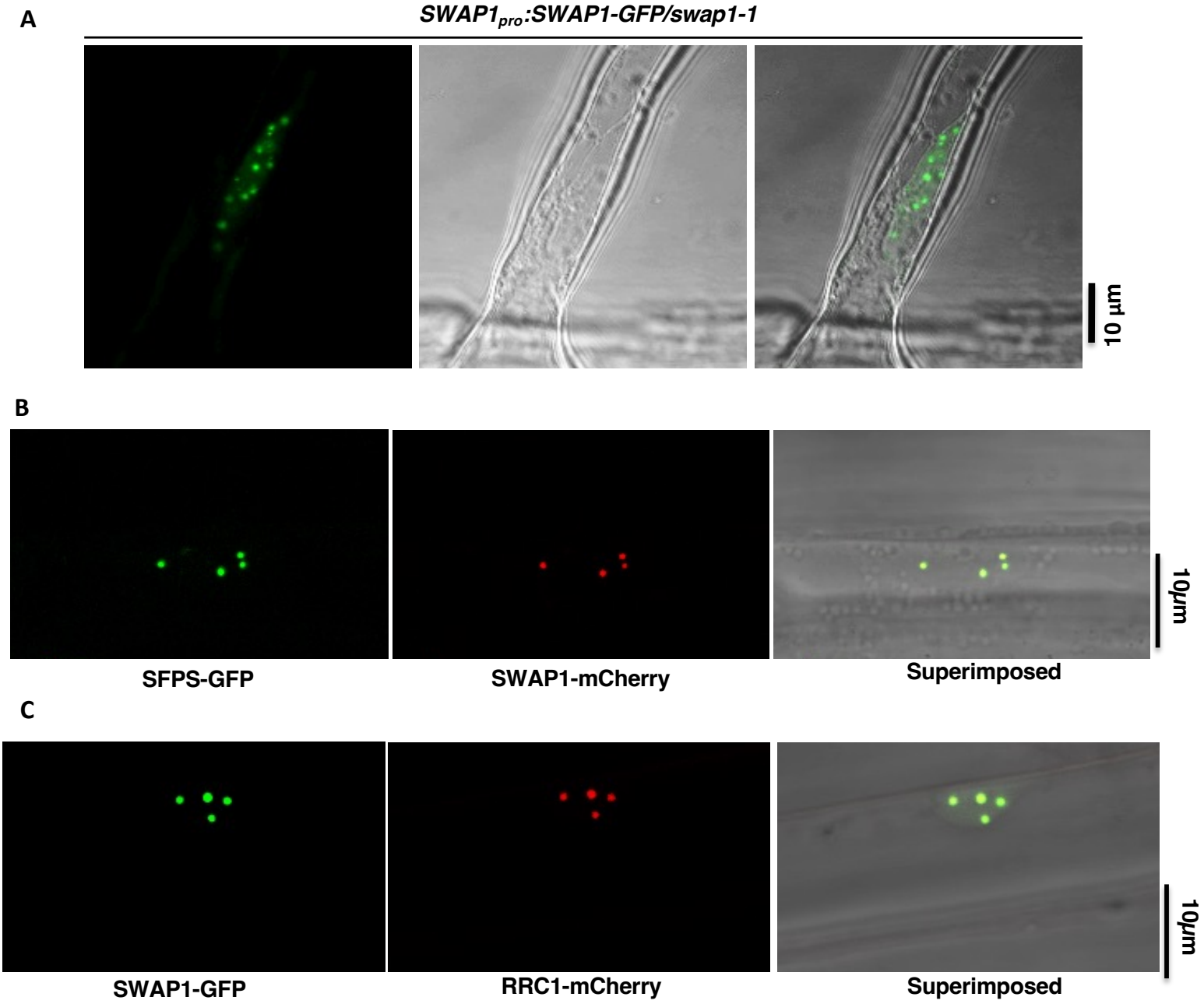

Fig. S10: SWAP1 nuclear speckles co-localize with SFPS and RRC1
(A) SWAP1-GFP forms nuclear speckles. (B) SFPS-GFP and SWAP1-mCherry nuclear speckles co-localize with each other. (C) SWAP1-GFP and RRC1-mCherry nuclear speckles co-localize with each other.

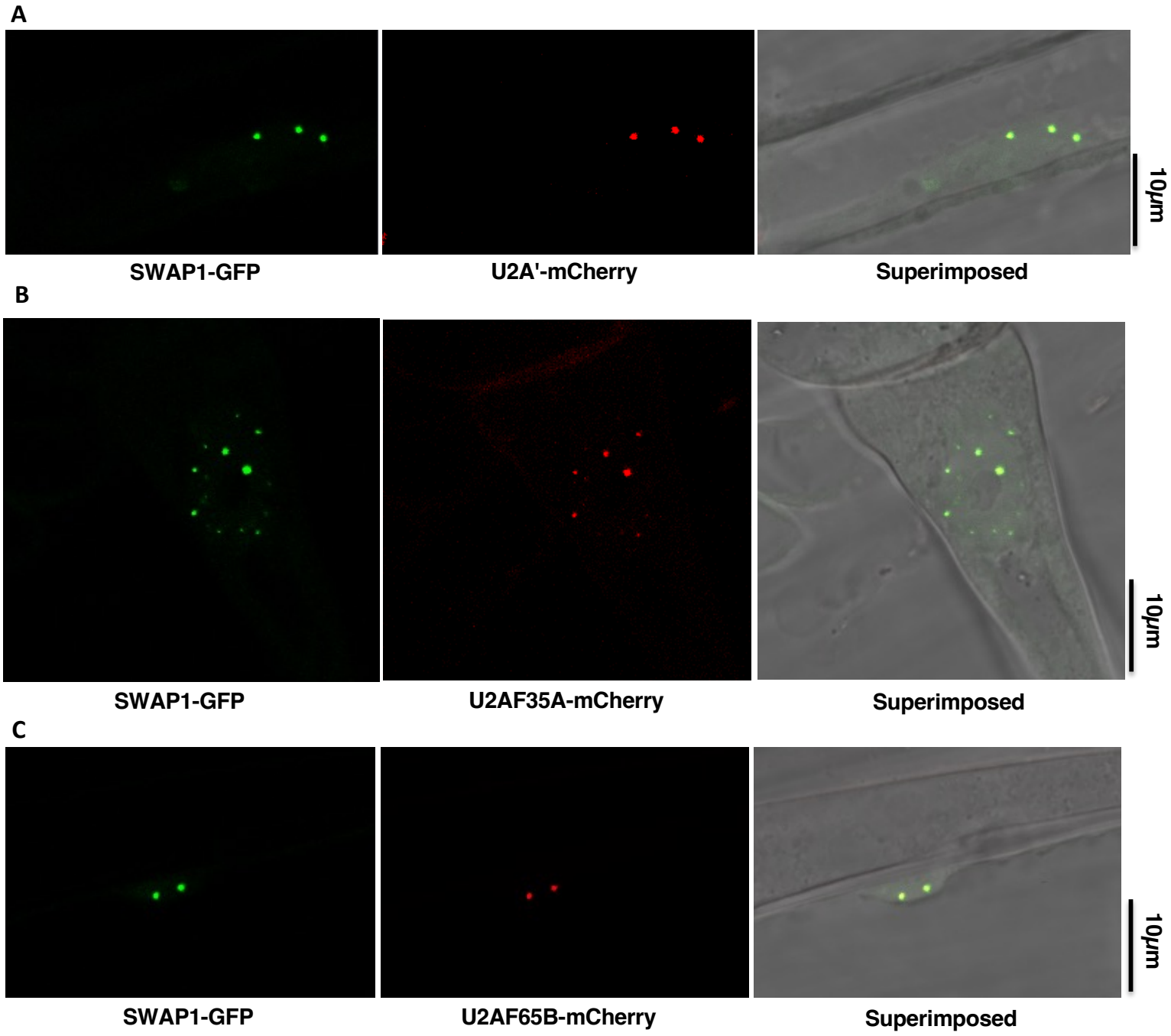

Fig. S11: SWAP1 nuclear speckles co-localize with U2- snRNPs associated components
(A) SWAP1-GFP nuclear speckles co-localize with nuclear speckles of U2A'-mCherry. (B) SWAP1-GFP nuclear speckles co-localize with nuclear speckles of U2AF35A-mCherry. (C) SWAP1-GFP nuclear speckles co-localize with nuclear speckles of U2AF65B-mCherry.

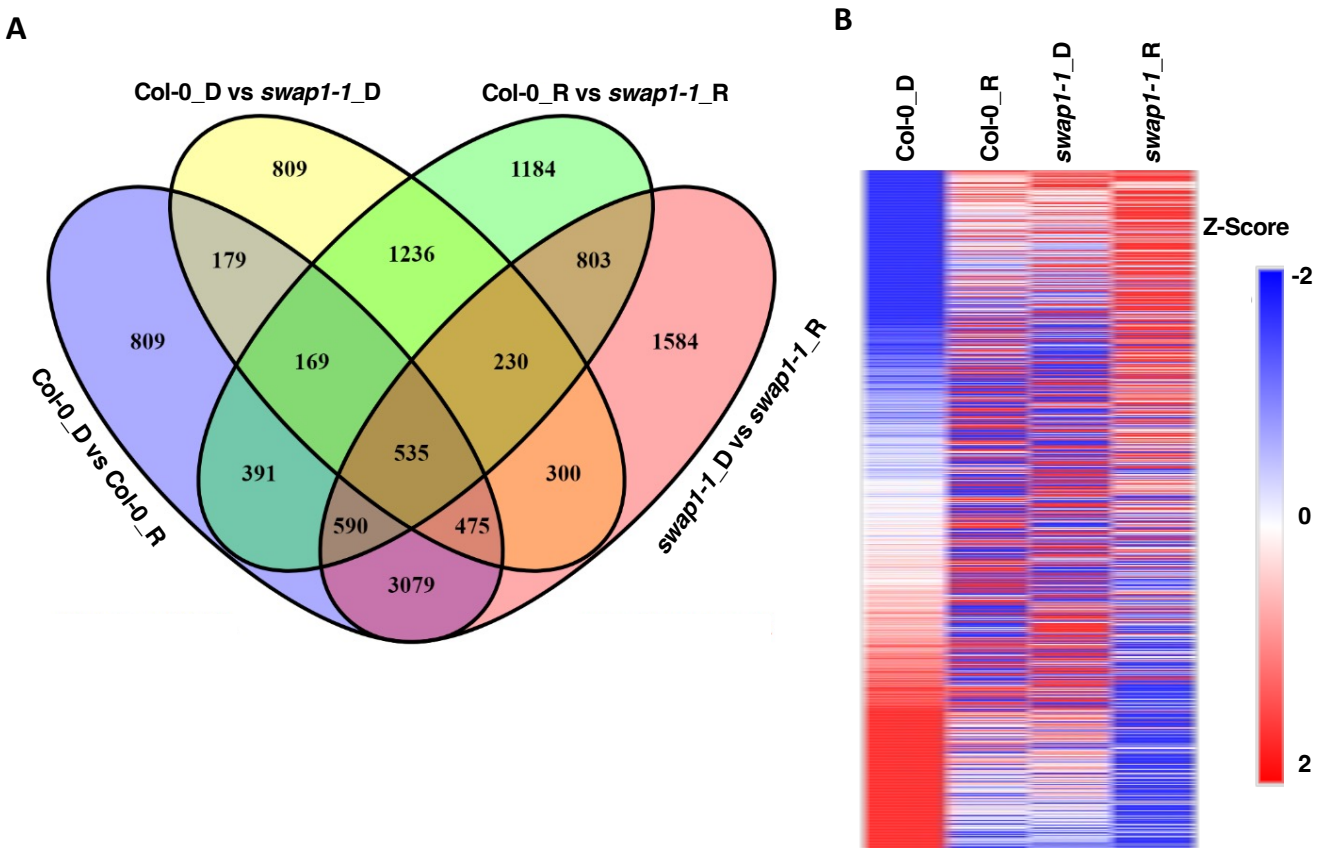

Fig. S12: SWAP1 regulates expression of a large number of genes both in dark and light conditions
(A) Venn diagram indicating both number and overlapping differentially expressed genes (DEGs) events in wild type and *swap1-1* mutant seedlings under D (Dark) and R (Red light) treated conditions.
(B) Heatmap of top 1000 DEGs events plotted based on their Z- scores. Z- scores are calculated based on the basis of their corresponding individual expression values under dark and red light treated conditions of wild type and *swap1-1* mutant samples.

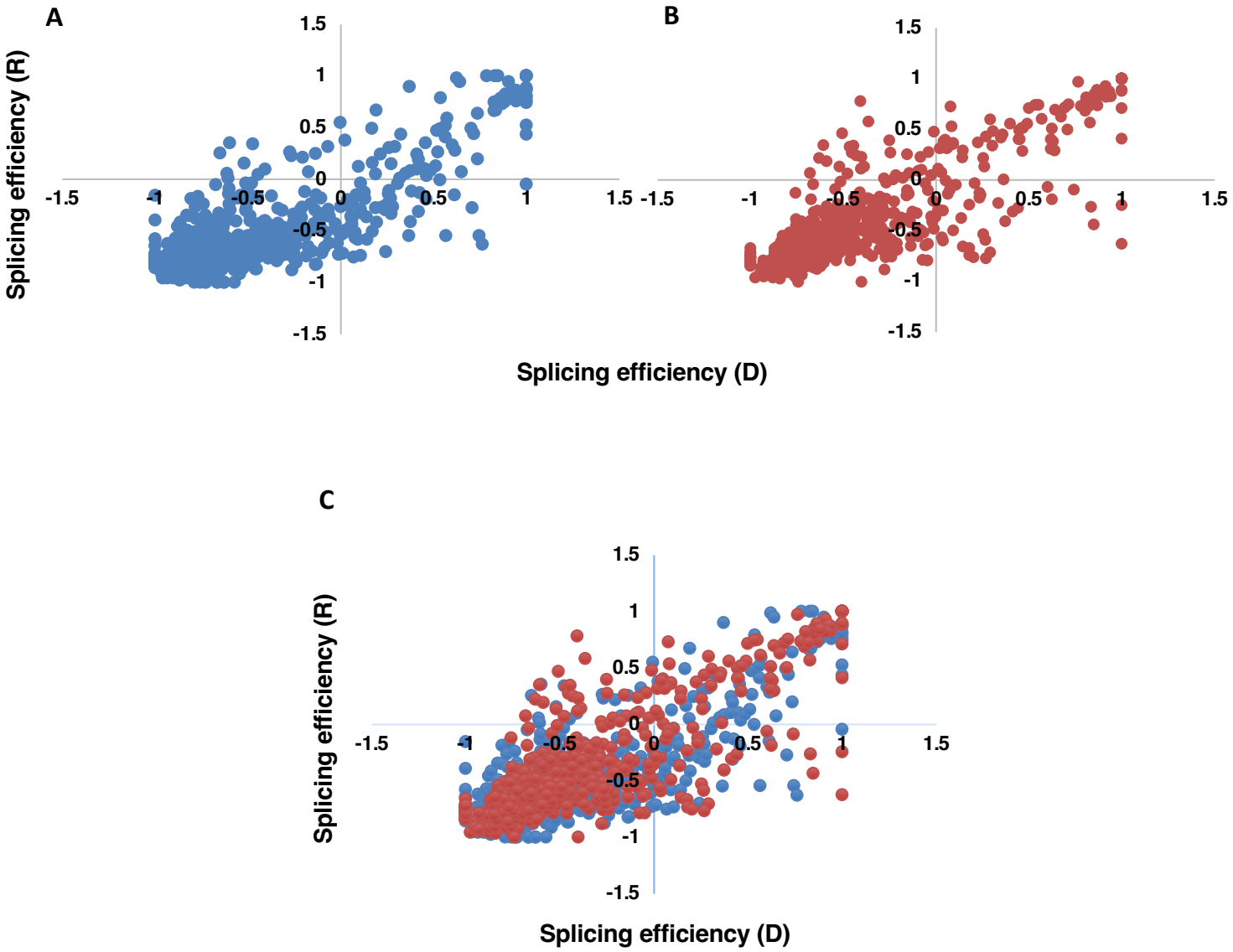

Fig. S13: *swap1-1* exhibits altered splicing efficiency compared to wild-type
Scatter plots exhibiting the splicing efficiency changes in wild-type (A) and *swap1-1* (B) mutant samples. (C) Overlapping of splicing efficiency observed in (A) and (B). The X-axis represents the splicing efficiency of samples in the dark, while Y-axis represents the splicing efficiency of samples under red light.

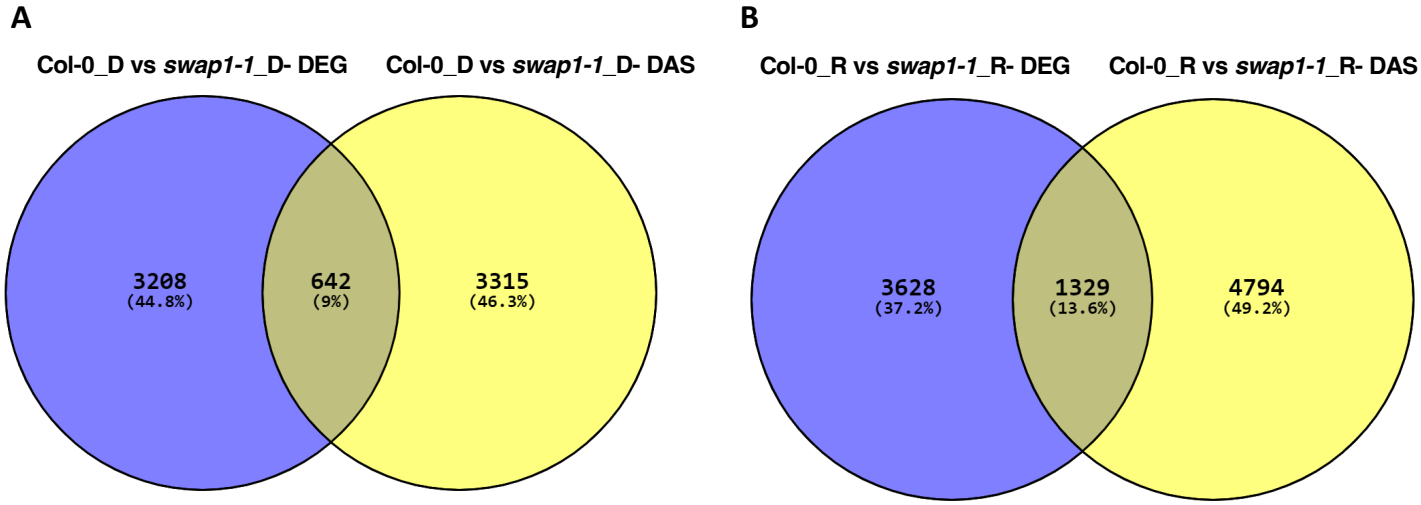

Fig. S14: Overlap of DEGs and DAS genes modulated by SWAP1

Venn diagram indicating both number and overlapping of DEGs and DAS genes in comparison of wild type vs *swap1-1* in the dark (A) and red light (B) illuminated conditions.

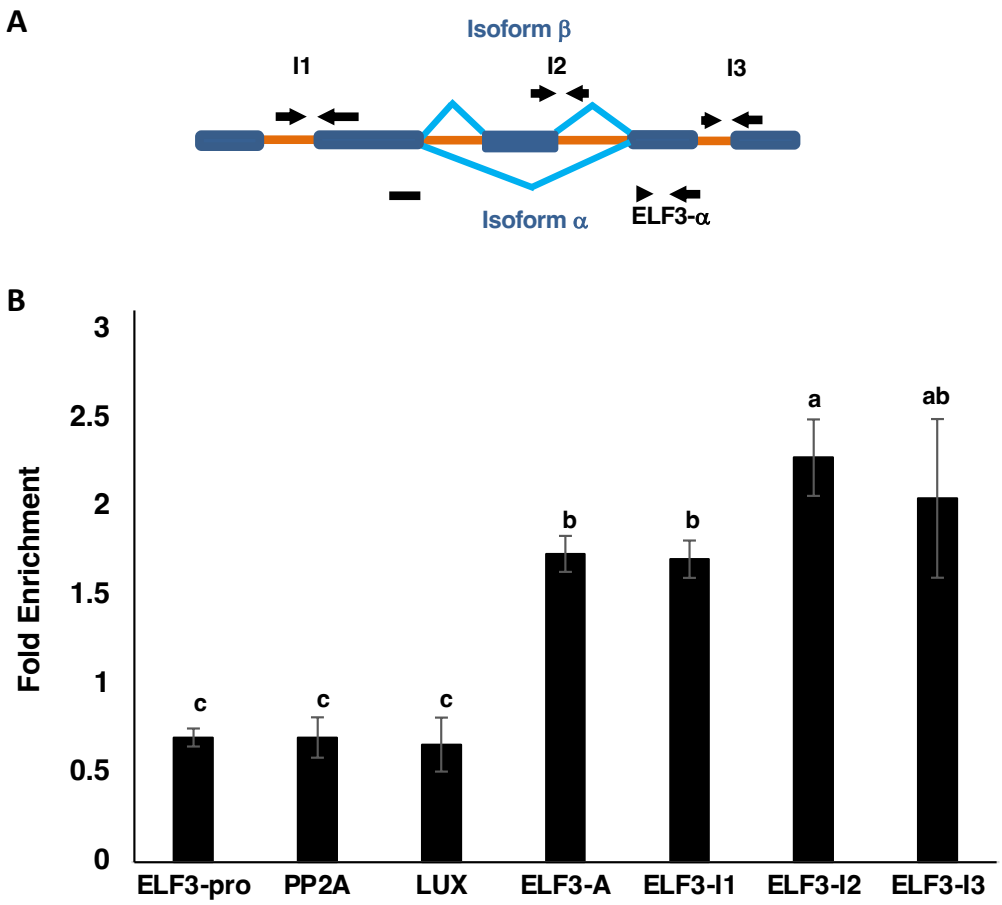

Fig. S15: SWAP1 associates with *ELF3* pre-mRNA under *in vivo* condition
(A) Schematic diagram showing gene structure, introns and exons, different isoforms as well as primer positions used in the RNA Immunoprecipitation-qRT-PCR assay. (B) Fold enrichment of different parts of ELF3 pre-mRNA following immunoprecipitation of SWAP1-GFP indicates that SWAP1 associates with ELF3 pre-mRNA under *in vivo* conditions. RNA/SWAP1-GFP complex was immunoprecipitated (IP) and extracted using anti-GFP antibodies. RNA was carefully purified from IP samples and reverse transcribed into cDNA following standard protocol. The abundance of each region in the transcript was quantified by qRT-PCR method. Each bar is the mean ± SEM (n= 3 biological repeats). Statistical difference was calculated based on One-way ANOVA followed by Tukey's post hoc analysis. Different letters indicate statistical significance among the gene parts.

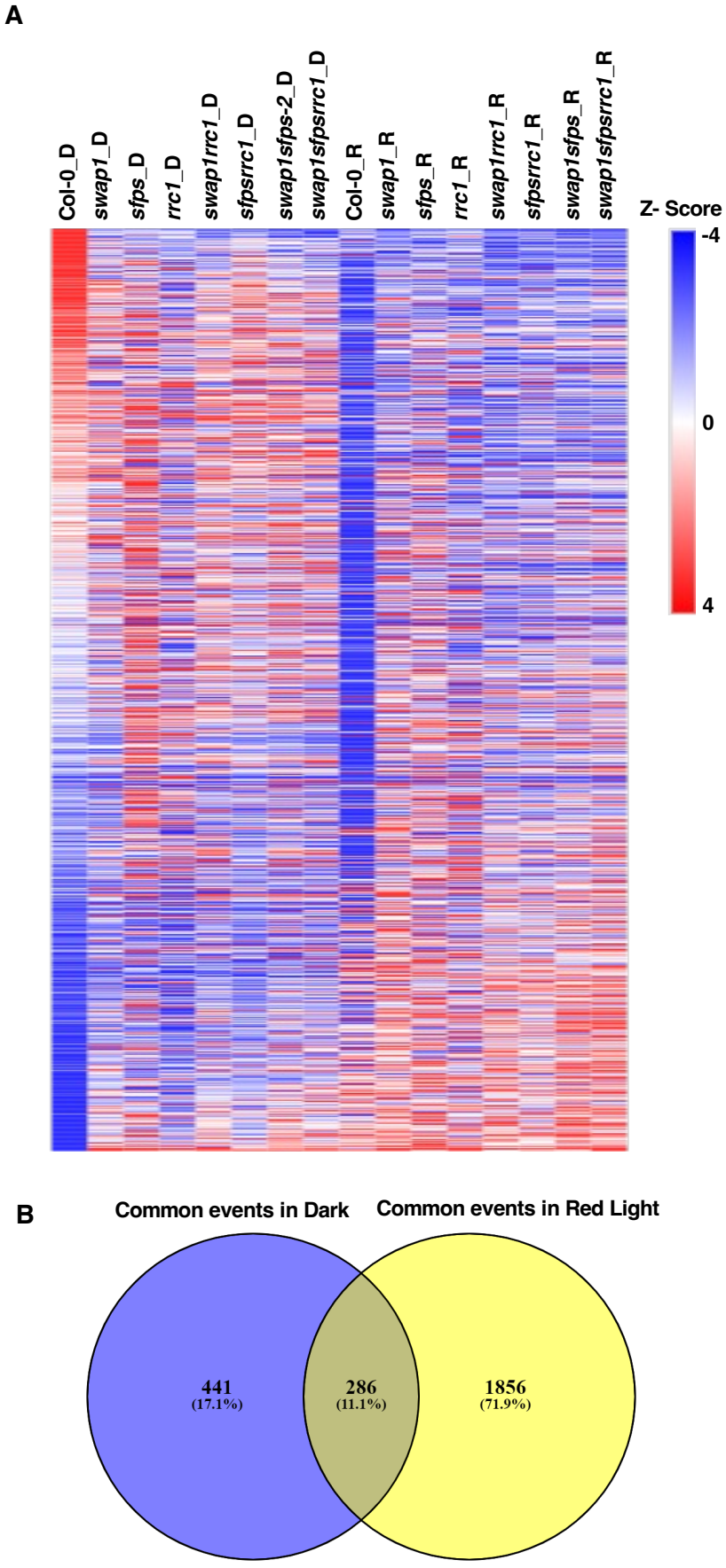

Fig. S16: SWAP1, SFPS and RRC1 coordinately regulate pre-mRNA splicing of a subset of genes
(A) Heatmap of top 1000 DAS events plotted based on their Z- scores calculated on the basis of their corresponding individual PSI/PIR values under dark and red light-treated conditions of wild type and different mutant samples.
(B) Venn diagram indicating both the number and overlapping DAS events regulated by all three splicing factors under dark and red light conditions.

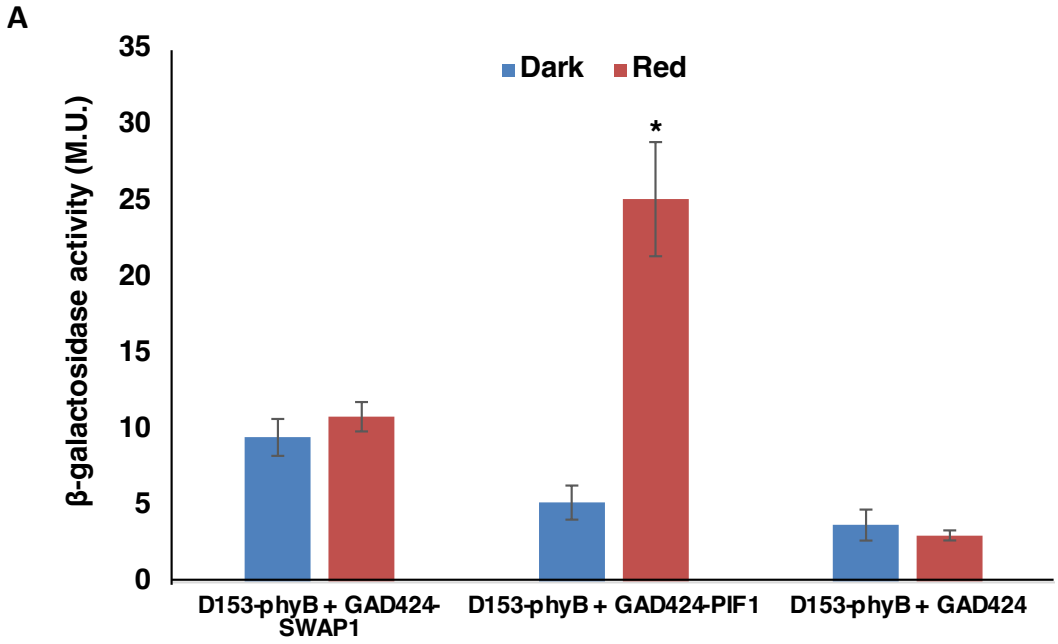

Fig. S17: SWAP1 interacts with phyB in yeast 2-hybrid system

Full-length *SWAP1* CDS was inserted in vector containing the GAL4 activation domain (AD), while the full-length *phyB* CDS was fused to the GAL4 DNA binding domain (BD). Liquid β- Galactosidase activity assay was carried out to quantify the strength of interaction between SWAP1 and phyB. Each data point reflects the average of three values and bars represent the SD. Student's T-Test was carried out to determine the statistical significance among the samples.

Table S1: Table shows the total number and types of DAS events and the corresponding gene loci numbers detected among different pairwise comparison.

Genotype	# of Events	# of Loci	IR	ES	Alt3SS	Alt5SS	ASCE	Novel ASP
Col-0_D vs Col-0_R	2007	1458	1417	24	8	13	138	289
Col-0_D vs *swap1-1*_D	7770	3957	3398	46	53	21	174	3327
Col-0_R vs *swap1-1*_R	12488	6123	7927	114	81	65	357	3190
*swap1-1*_D vs *swap1-1*_R	3098	2089	2261	27	5	34	229	355
Col-0_D vs *sfps-2*_D	9728	5438	7024	85	58	76	507	1467
Col-0_R vs *sfps-2*_R	13058	7047	10309	123	71	107	447	1460
Col-0_D vs *rrc1-3*_D	13510	6178	7248	59	140	127	1245	3159
Col-0_R vs *rrc1-3*_R	21297	8544	8391	92	163	156	1237	8900
Col-0_D vs *swap1sfpsrrc1*_D	11390	5235	5313	53	82	28	235	4618
Col-0_R vs *swap1sfpsrrc1*_R	14869	6683	8804	119	97	64	374	4265
*swap1sfps*_D vs *swap1sfpsrrc1*_D	188	160	20	0	0	0	14	121
*swap1sfps*_R vs *swap1sfpsrrc1*_R	223	197	24	0	0	0	16	141
*swap1rrc1*_D vs *swap1sfpsrrc1*_D	288	247	77	3	0	0	21	147
*swap1rrc1*_R vs *swap1sfpsrrc1*_R	215	187	26	1	0	0	16	132
*sfpsrrc1*_D vs *swap1sfpsrrc1*_D	2181	1506	511	10	7	2	47	1398
*sfpsrrc1*_R vs *swap1sfpsrrc1*_R	1690	1242	490	7	7	3	62	939

Table S2: Primer sequences used in this study

Primer	Sequence
SWAP1-Pro-F	CACC GGG TGA TTT TTT GCC ACC TCC T
SWAP1-Entry-F	CACC ATG GAT CGA AGA CAG CAC GA
SWAP1-R	TCT GGT TGT AGC TCT TGC ACT CA
SWAP1-Nhe1-F	AGA GCT AGC ATG GAT CGA AGA CAG CAC GAT TAT
SWAP1-FLAG1-R	ATC GTC TTT GTA GTC TCT GGT TGT A
SWAP1-FLAG2-R	GTC TTT GTA GTC CTT GTC GTC ATC GTC
SWAP1-FLAG3-R	TTT GTA GTC CTT GTC GTC ATC GTC TTT GTA
SWAP1-FLAG4-SmaI-R	ATA CCC GGG TCA CTT GTC GTC ATC GTC TTT GTA
SWAP1-BamH1-F	GCTGGATCCATGGATCGAAGACAGCACGA
SWAP1-Xba1-R	CCATCTAGATCTGGTTGTAGCTCTTGCACTC
SWAP1-EcoR1-F	AGA GAA TTC ATG GAT CGA AGA CAG CAC GAT TAT
SWAP1-Xma1-R	AGT CCC GGG C TCT GGT TGT AGC TCT TGC ACT CA
SWAP1-BamH1-R	GCTGGATCCTCATCTGGTTGTAGCTCTTGCA
SWAP1-qPCR-F	AAGTGGACCACCTGCAAATACC
SWAP1-qPCR-R	GTTGCAGCATTCCTGGACGTTG
ELF3-Intron1 3'-F	TTCTTGTGATTGCCCTGAGCAT
ELF3-Intron1 3'-R	TCCATGAAGGACATTTGGGAGACAA
ELF3-Intron2-F	CTGTCTCGGTTTGGTATTGCT
ELF3-Intron2-R	TTTAGATCCTGGGGTCCTCG
ELF3-Intron3-F	CAAACCTCTTCAACTGTGTAATAATCA
ELF3a-F1	CCATTGCCAATCAACAAAGAG
ELF3a-R1	TGGTCAGTCTTCTCCGAGTCAC
PP2A-Pro-F	TTA GCT GCT GCG AAA GAC GAG
PP2A-Pro-R	TTCCAAGTTCCGAGCGATCTATC
ELF3-Pro-F	AGC GAG TAT AAC CGT ATG ACC A
ELF3-Pro-R	GAGTGGTCGGATAGTGAGAAATC
BUD13-T-F	GGCAAAGGTTTAGCTCAGAAGCG
BUD13-T-R	TCAAGCTCCGGATCATCCCTTG
BUD13-IJ-F	ATT CAT AAA GAG ACC AGT CTT CA
BUD13-IJ-R	GAA TCC ATA TTT TTA AAC CTG TAG
RS31-T-F	AGGTCCAGCAGCTTATGAAAGACG
RS31-T-R	CTCTTGGGACTGGAGAACGACTTC
RS31-IJ-F	CTT CCT GCA AAA TCA TTT CTA CA
RS31-IJ-R	CGA TGA TTG GTA ATA GAC AGA C
BIM3-T-F	ATCTGTGCAGTTAAGCCTTCGG
BIM3-T-R	ACCATTATCCTCAGAAGCAAACGC
BIM3-IJ-F	TGG ATA CTA AGA GAG AAT GAT AT
BIM3-IJ-R	CAT TTA TCT CAT ACT CTA TCC TA
COP1-T-F	GTT GTA AAT GAA CCA GCA GAT AT
COP1-T-R	TTC ATG CTT ATT CCA ACT CAA GC
COP1-IJ-F	CAA TTA TTA CTA TGG GAT TCG TT

COP1-IJ-R	TCT CCT CAA GTG GCC TGC T
ELF3-T-F	CAA GTT TAT CTA AGT GTG GTT TA
ELF3-T-R	AGA AAC TTT CAT CGA ACT TCA GA
ELF3-IJ-F	GAG GGA CAT TCT CTG TTG ACC
ELF3-IJ-R	AAG CAA TAC CAA ACC GAG ACA G

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