Erratum

Alternative transcript initiation and novel post-transcriptional processing of a leucine-rich repeat receptor-like protein kinase gene that responds to short-day photoperiodic floral induction in morning glory (*Ipomoea nil*)

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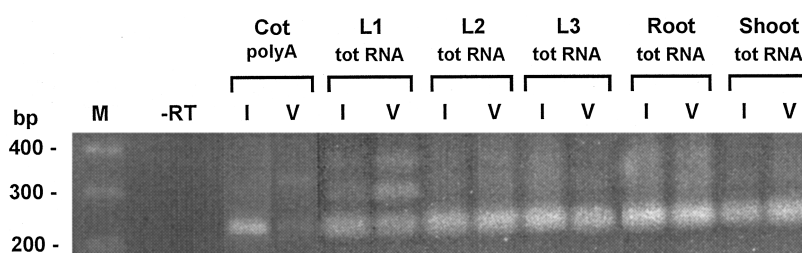Figures 4 and 6 of this article should appear as follows:

Figure 4. Processing of *inrpk1* small intron. Complementary DNA was synthesized from total and poly(A)$^+$ RNAs isolated from various tissues 5–6 days after SD induction or CL treatment. Primers on either side of the splice sites of the small intron were used in PCR to synthesize products from either processed (228 bp) or unprocessed (305 bp) mRNAs. PCR products were separated in gels and visualized with SYBR Gold. Sizes of molecular length markers are indicated to the left in bp. For all samples, total RNA was analyzed except for cotyledons where poly(A)$^+$ RNA was used, since only faint bands were obtained using cotyledon total RNA. M, molecular size markers; −RT, minus reverse transcriptase control; Cot; cotyledons; L1, leaf 1; L2, leaf 2; L3, leaf 3; I, SD florally induced plants; V, CL-treated vegetative controls.

A

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   1   MKVAVNTFLLSLCSTSSIYAAFALNSDGAALLSLTRHWTPIPSDITQSWNASDSTPCSWL
  61   GVECDRRQFVDTLNLSSYGISGEFGPEISHLKHLKKVVLSGNGFFGSIPSQLGNCSLLEH
 121   IDLSSNSFTARWKFTSWRYSTSGSFAGTEVIKFEQ
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B

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   1   MKVAVNTFLLSLCSTSSIYAAFALNSDGAALLSLTRHWTPIPSDITQSWNASDSTPCSWL
  61   GVECDRRQFVDTLNLSSYGISGEFGPEISHLKHLKKVVLSGNGFFGSIPSQLGNCSLLEH
 121   IDLSSNSFTGSLTELTKLSLGENSFSGGIPTSLFQSNKLLNLQLGGNLLAGCIPPVGALQ
 643   ALRSLNLSSNKLNGQLPIDLGKLKMLEELDVSHNNLSGTLRVLSTIQSLTFINISHNLFS
 703   GPVPPSLTKFLNSSPTSFSGNSDLCINCPADGLACPESSILRPCNMQSNTGKGGLSTLGI
 763   AMIVLGALLFIICLFLFSAFLFLHCKKSVQEIAISAQEGDGSLLNKVLEATENLNDKYVI
 823   GKGAHGTIYKATLSPDKVYAVKKLVFTGIKNGSVSMVREIETIGKVRHRNLIKLEEFWLR
 883   KEYGLILYTYMENGSLHDILHETNPPKPLDWSTRHNIAVGTAHGLAYLHFDCDPAIVHRD
 943   IKPMNILLDSDLEPHISDFGIAKLLDQSATSIPSNTVQGTIGYMAPENAFTTVKSRESDV
1003   YSYGVVLLELITRKKALDPSFNGETDIVGWVRSVWTQTGEIQKIVDPSLLDELIDSSVME
1063   QVTEALSLALRCAEKEVDKRPTMRDVVKQLTRWSIRSYSSSVRNKSK
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Figure 6. Polypeptides derived from alternative splicing or initiation of *inrpk1* transcripts. Translation of the alternatively spliced 2.6 and 2.7 kb transcripts are shown in A and B, respectively. LRRs are shadowed by gray boxes. A. INRPK1b predicted peptide. Dotted line indicates amino acids substituted by frame-shifting after the 3′ splice junction. B. 1-1109: INRPK1a. INRPK1c is shown boxed in from positions 667 to 1109. The predicted transmembrane region is underlined.