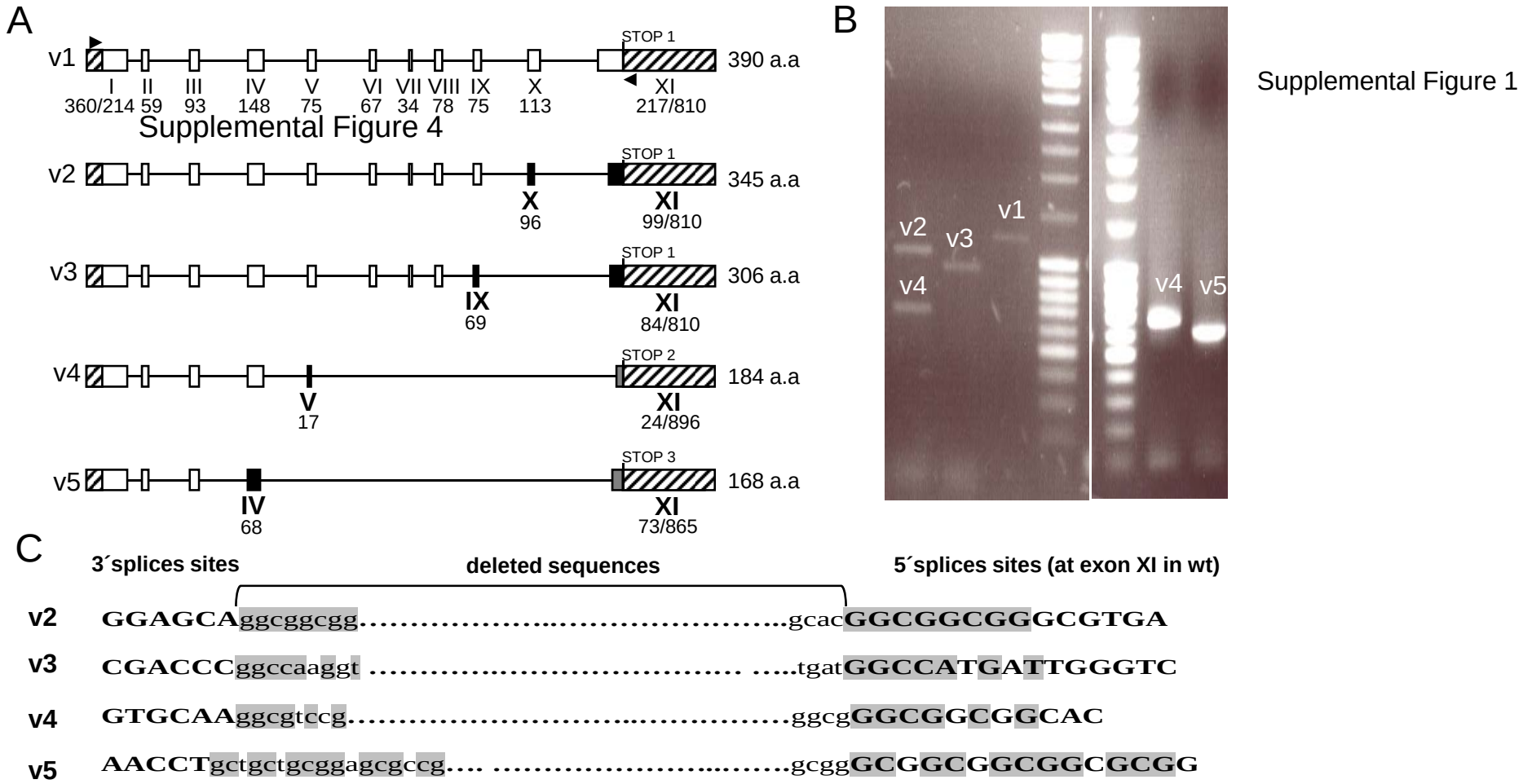

Supplemental Figure 4. A) Putative cDNA splice variants of *SNRK2.1*. RT-PCR was performed with specific primers for the *SNRK2.1* transcript; the positions of the primers are represented by horizontal arrows in the v1 variant. These primers amplified the entire CDS. Five different splice variants were generated using these primers (v1 to v5). v1 represent the longest variant, with white blocks representing full-length exons (sizes are indicated in v1) and lines representing introns. For v2, v3, v4 and v5, potential alternative 3´ splice sites occur within exons X, IX, V and IV, respectively; the potential splice events would produce smaller exons (represented by black boxes with the corresponding sizes in bp below the box). In all cases the alternative 3´ splice sites occur at different positions inside exon XI. v2 and v3 retain the same coding frame and stop codon (denoted by STOP 1) as in exon XI in v1. In v4 and v5 the coding frame for exon XI is changed (grey blocks) together with the stop codon (denoted by STOP 2 and STOP 3, respectively). The coding frames of v4 and v5 are also different from each other. 5´and 3´UTR were not analyzed in the splice variants. 3´UTR hypothetical sizes are given using data obtained from the v1 cDNA. **B) Two independent RT-PCR experiments reveal different splice variants of *SNRK2.1*.** Splice variants are denoted as v1, v2, v3, v4 and v5. In the left gel the different lanes correspond to different Taq-polymerase buffer conditions, although additional analyses have shown no apparent correlation between the specific buffer used and the splice variants observed (data not shown). The right gel shows re-amplification of weak bands that represent splice variant v4 and v5; splice variant v5 is not shown in the left gel and was re-amplified from a RT-PCR reaction that is not shown. **C) Proposed mechanism that could lead to artifactual splice variants generated by PCR**. The grey shaded nucleotides sequences are present in the proximity of the 3´ and 5´ putative splice sites of v2 to v5. Lower case letters indicate putative introns sequences. Partially elongated products generated during PCR could anneal to the complementary full length strands and serve as primers for a subsequent elongation that will generate deleted products.