Tissue-specific expression and post-translational modifications of plant- and bacterial-type phosphoenolpyruvate carboxylase isozymes of the castor oil plant, *Ricinus communis* L.

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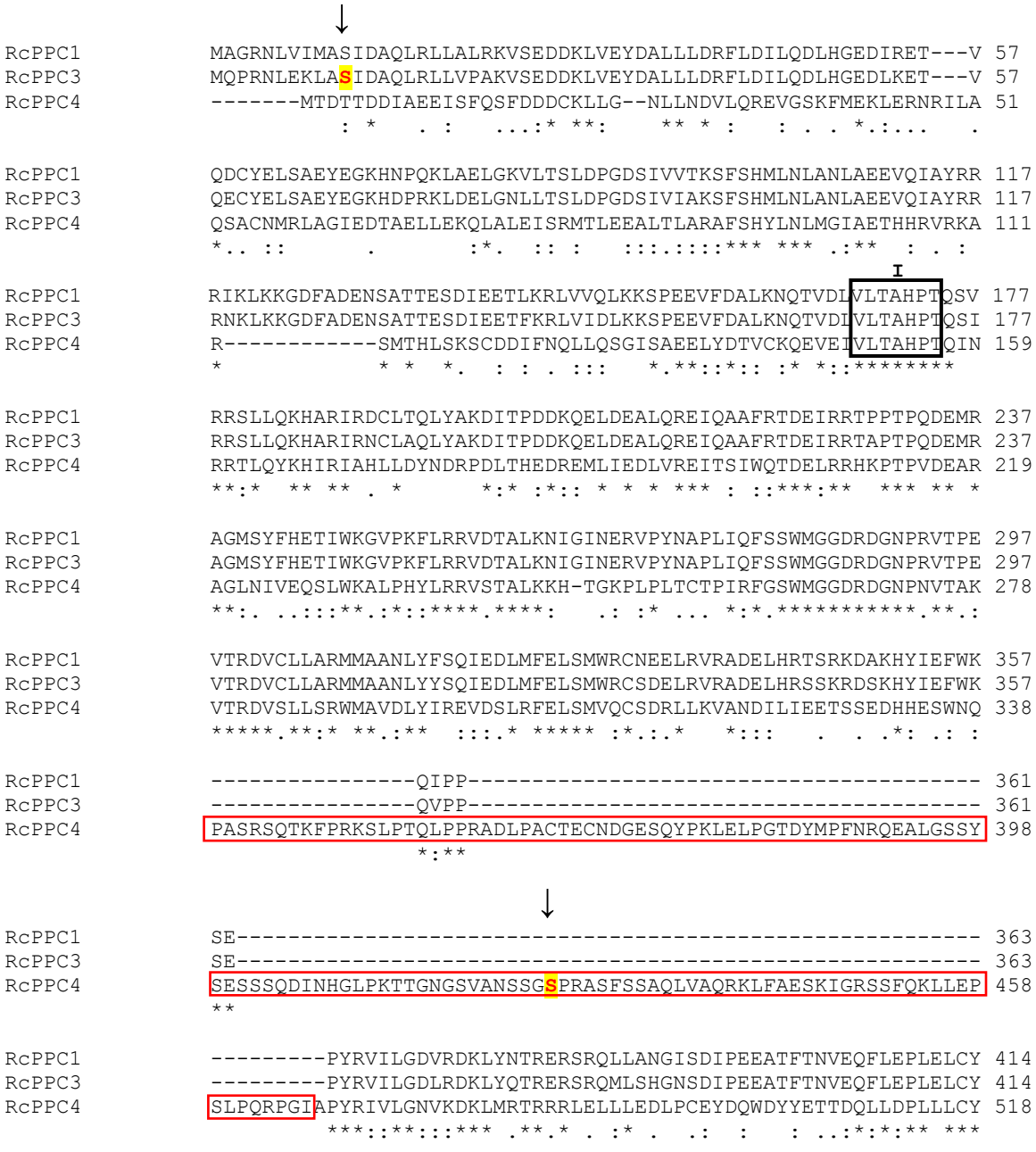
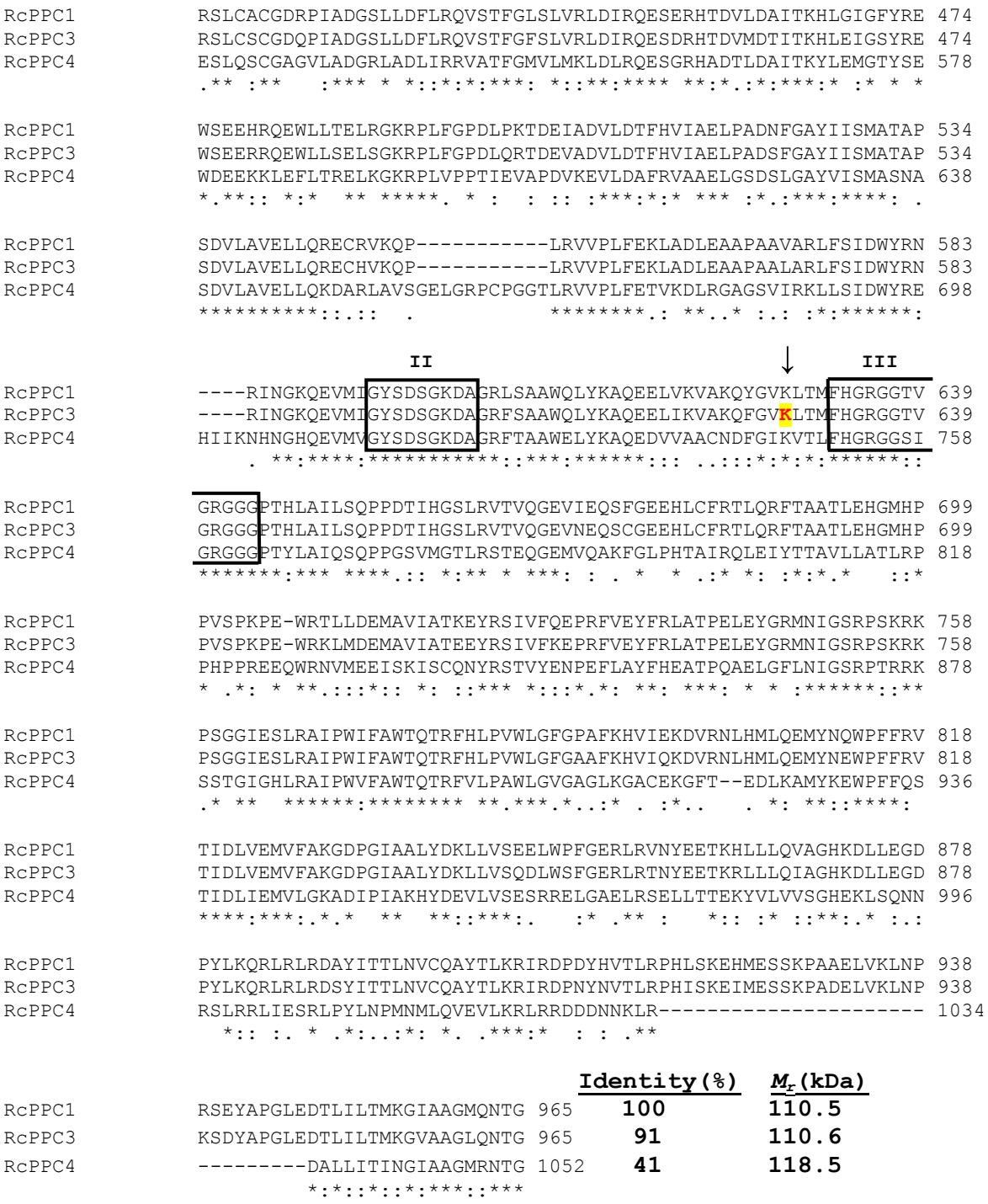
Supplemental Fig. S1. Sequence alignment of cDNA-deduced primary structures of castor PTPC (RcPPC1 and RcPPC3) and BTPC (RcPPC4) isozymes. Experimentally verified *in vivo* phosphorylation (Ser-11 and Ser-425 of RcPPC3 and RcPPC4, respectively) and monoubiquitination (Lys-628 of RcPPC3) sites are indicated with arrows and a bold/red font. RcPPC4's highly divergent ~10-kDa domain that was predicted to exist largely as an intrinsically disordered region (O'Leary et al., 2011) is enclosed in a red rectangle. Boxes I-III denote conserved subdomains essential for PEPC catalysis (Izui et al., 2004). The predicted M_r of each deduced polypeptide and their % sequence identity with RcPPC1 is also indicated. The corresponding NCBI protein accession numbers are as follows: RcPPC1 (PTPC), ABR29877.1; RcPPC3 (PTPC), ABR29876; RcPPC4 (BTPC) ABR29876.1. Semi-colons and asterisks indicate identical and conserved amino acids respectively. Sequences were aligned using the Clustal W software (http://www.ebi.ac.uk/Tools/msa/clustalw2/).





References

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