S6 Fig. MALDI-TOF MS analysis of CTD-only peptides confirms seven SRPK1 phosphorylation sites in the HBc CTD and a distinctly lower phosphorylation extent by the catalytic domain of PKA. (A) Scheme of CTD peptide origins. The synthetic CTD (sCTD) was obtained from a commercial supplier (Proteogenix, France). The other CTD peptides were derived by TEV protease cleavage from the indicated NHisGFP-TEV-CTD fusions expressed in E. coli as such, or coexpressed with SRPK1NS1 or the catalytic domain of cAMP-dependent protein kinase A (PKAcd). Details are provided in S1 Protocols. Final products were analyzed by SDS-PAGE / CB staining; the gel picture shows a section of the gel in Fig 4C. All CTD peptides routinely co-migrated with the 10 kDa marker; this aberrant mobility is likely due to their high content of charged amino acids. All samples were then subjected to MALDI-TOF mass spectrometry (B-E). (B) sCTD. (C) CTD ex fusion protein expressed without kinase. (D) CTD ex fusion protein expressed with SRPK1NS1. The data in (D) are the same as in Fig 4 and here shown for convenient comparison with the other samples. (E) CTD ex fusion protein expressed with PKAcd. In (D) and (E), the potential phosphorylation target residues are shown as outlined fonts.