**Supplementary figure X. Proteome-wide analysis of intrinsic disorder among CDK substrates and dynamic phosphoproteins**

a. Venn diagram of observed ,*in vitro* (red) and *in vivo* (blue)*,* yeast CDK targets. *In vivo* targets showing CDK minimal consensus motif phosphorylations are highlighted in yellow.

b. Violin and box plots showing the distribution of the percentage of disordered residues per protein for CDK targets vs the rest of the phosphoproteome for human and yeast. Intrinsic disorder information of thirteen different predictors was obtained from MobiDB, except for SPOT (calculated).

c. Fraction of the Uniprot reviewed human, Xenopus and yeast proteomes predicted as disordered by the 12 methods compiled in MobiDB.

d. Differential amino acid composition, **calculated as** **(Disordered regions composition - Proteome composition)/ Porteome composition,** in disordered regions for Xenopus, human and yeast determined with three IDRs predictors. Amino acids were colored in a rainbow fashion based on their relative abundance in each proteome. **Disruptions in the rainbow pattern show specific compositional signatures for IDRs.**

e.Diagrams of IUPred scores over the length of humans and Xenopus proteins identified as primary components of MLOs. Regions with scores >0.5 (red) are considered to be disordered, and <0.5 (grey) structured. Blue vertical lines indicate Ser and Thr residues; yellow circles, phosphorylated sites; green circles, CDK1 subfamily phosphorylations and phosphorylations showing a dynamic behavior throughout the cell cycle, for human and Xenopus respectively.