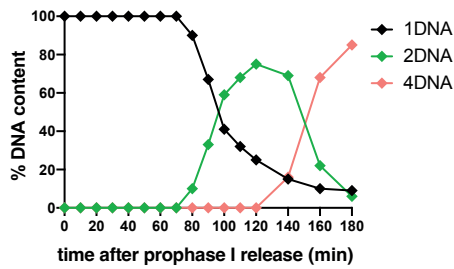


Appendix

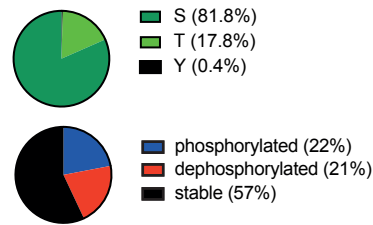
Appendix Figure S1: The phosphorylation landscape of the MI-MII transition in budding yeast
-repeat 2 (page 1)

Appendix Figure S1 legend (page 2)

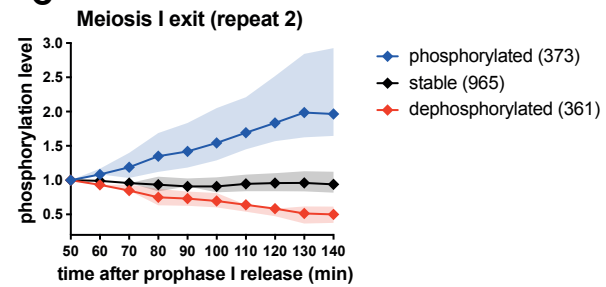
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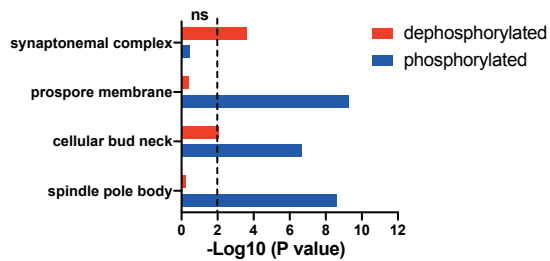
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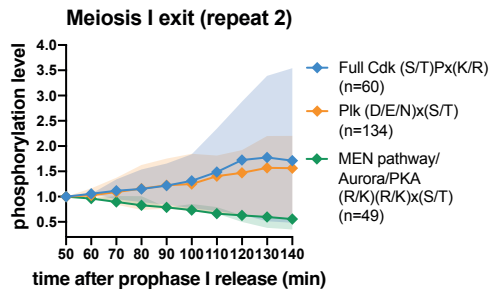
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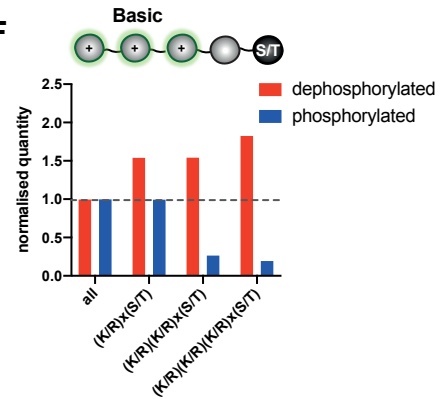
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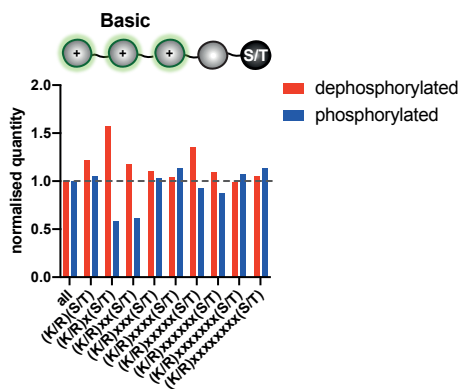
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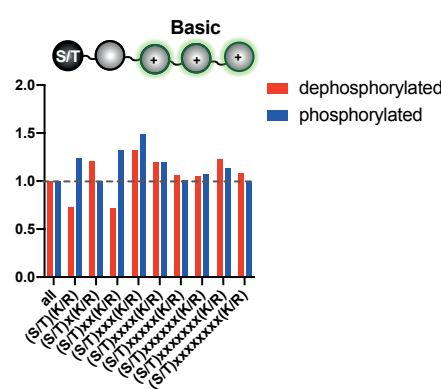
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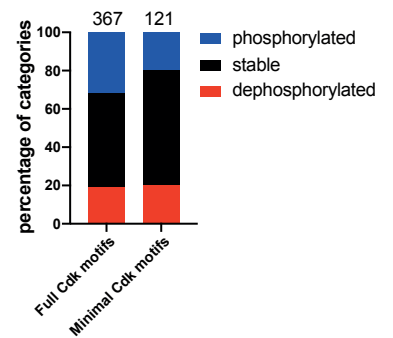
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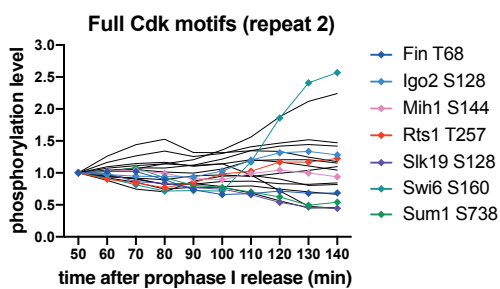
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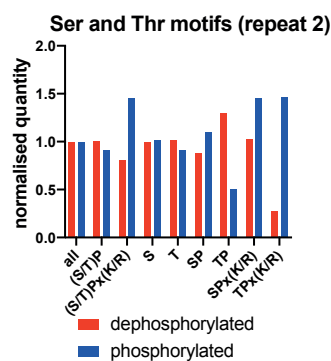
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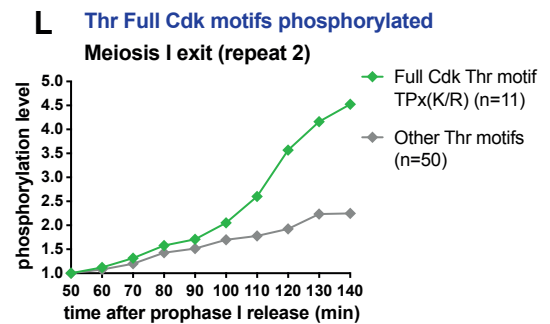
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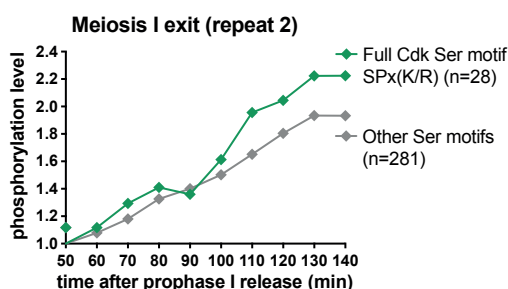


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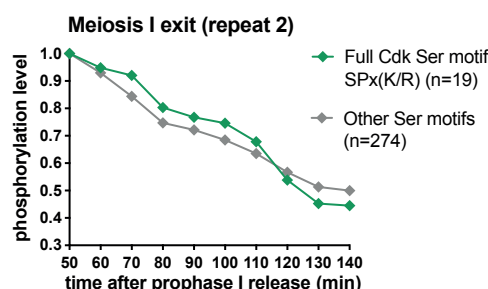
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Ser Full Cdk motifs phosphorylated



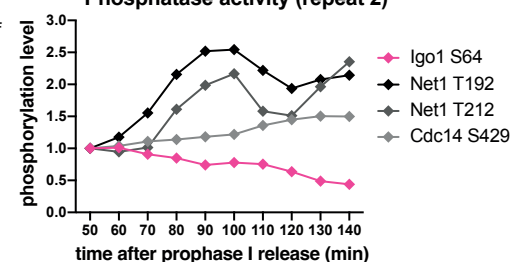
M

Ser Full Cdk motifs dephosphorylated



N

Phosphatase activity (repeat 2)



The phosphorylation landscape of the MI-MII transition in budding yeast - repeat 2

A) One hundred cells were scored for spindle length and DNA content at each timepoint (0 to 180min after β -estradiol addition) to determine the cell cycle phases. 1DNA, 2DNA and 4DNA indicate the number of DNA mass observed by DAPI staining.

B) Fractions of quantified serine (S), threonine (T), or tyrosine (Y) phosphosites (top).

Fractions of phosphosites phosphorylated (blue), dephosphorylated (red), or remaining stable (black) through meiosis I exit (bottom).

C) Normalized median intensity profiles and interquartile range of the phosphosites that undergo a 1.5-fold decrease (red) or a 1.5-fold increase (blue) in phosphorylation abundance through meiosis I exit. Normalized median intensity profiles and interquartile range of the phosphosites remaining stable are in black.

D) Enrichment analysis of gene ontology cellular compartment (GOCC). -Log10 raw p-value is represented for the dephosphorylated proteins (red) and the phosphorylated proteins (blue) in the meiosis I exit datasets. Non-significant (ns) enrichment is represented on the left of the dashed line and significant enrichment on the right ($P < 0.05$).

E) Normalized median intensity profiles and interquartile range of the phosphosites that adhere to the three indicated kinase consensus motifs. For better visualization of the data, stable phosphosites of each category were not included in the median intensity profile. Of note (D/E/N)x(S/T) and (R/K)(R/K)x(S/T) categories exclude Cdk sites (S/T)P.

F-H) Percentage of dephosphorylated and phosphorylated sites categorized by amino acid motif identity after normalization to the total amount of sites. Phosphosites with single, double, or triple basic upstream amino acids in F, with distinct basic upstream amino acids are presented in G and with distinct basic downstream amino acids in H.

I) Percentage of the full Cdk sites (S/T)Px(K/R) and minimal Cdk sites (S/T)P in each category.

J) Profile plot of the 20 full Cdk sites in common between the meiosis I exit dataset repeat 1 that are dephosphorylated during mitotic exit (Figure 3D). Profiles of essential cell cycle regulators are highlighted in colors.

K) Percentage of dephosphorylated (red) and phosphorylated (blue) sites categorized by amino acid motif identity after normalization to total amount of sites.

L) Normalized median intensity profiles of sites phosphorylated on the full Cdk threonine motifs TPx(K/R) (light green) or the other threonine sites (grey) during meiosis I exit.

M) Normalized median intensity profiles of sites phosphorylated on the full Cdk serine motifs SPx(K/R) (dark green) or the other serine sites (grey) during meiosis I exit.

N) Normalized median intensity profiles of the sites dephosphorylated on full Cdk serine motifs SPx(K/R) (dark green) or the other serine sites (grey) during meiosis I exit.

O) Profile plot of phosphosites implicated in phosphatase regulation during meiosis I exit.