RNA polymerase II termination involves CTD tyrosine dephosphorylation by CPF subunit Glc7

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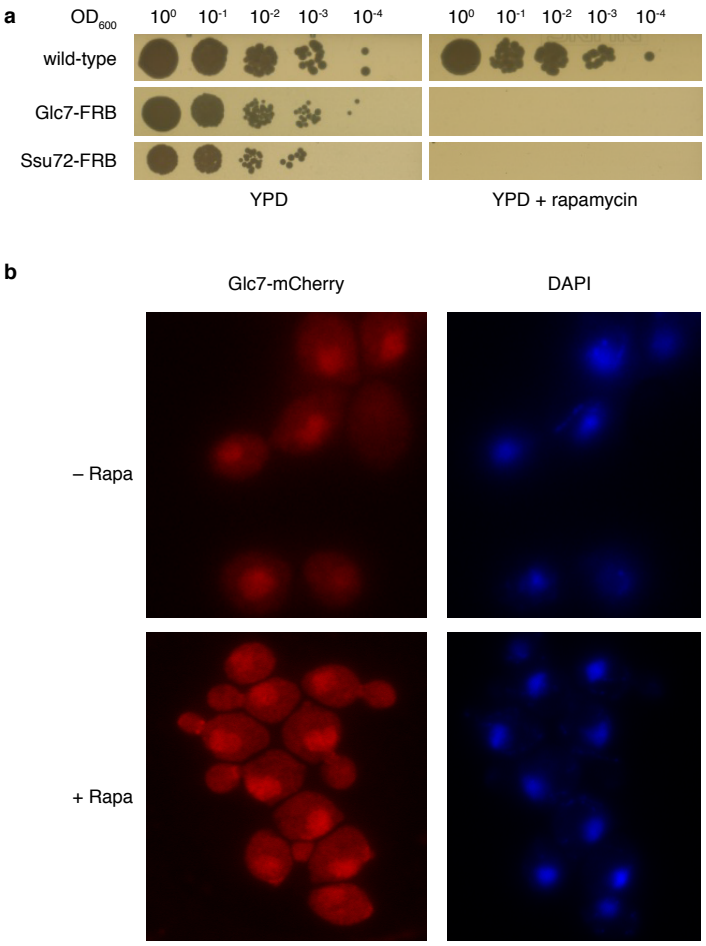
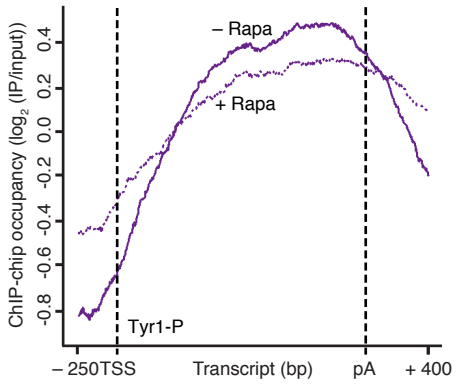


Supplementary Figure 1 Growth analysis and fluorescence microscopy of anchor-away yeast strains. (**a**) Serial dilutions of wild-type and Glc7 and Ssu72 anchor-away yeast strains plated on YPD (left panel) and YPD + rapamycin (right panel) show that rapamycin is lethal for the anchor-away strains but it has no effect on wild-type growth. FRB, FKBP12-rapamycin-binding. (**b**) Fluorescence microscopy of fixed cells of the Ssu72-FRB/Glc7-mCherry strain shows that Glc7 is located in both cytoplasm and nucleus (left panel). This distribution does not change when rapamycin is added to the cells (lower panel). DAPI stain is shown as a control (right panel).



Supplementary Figure 2 Depletion of Glc7 from the nucleus leads to a defect in Tyr1-P dephosphorylation.
ChIP-chip occupancy profile of Tyr1-phosphorylated Pol II over 619 genes without and with rapamycin (solid and dotted line, respectively; see Fig. 2a for normalized profiles). The profiles include the region from 250 nucleotides upstream of the transcription start site (TSS) to 400 nucleotides downstream of the polyadenylation site (pA).

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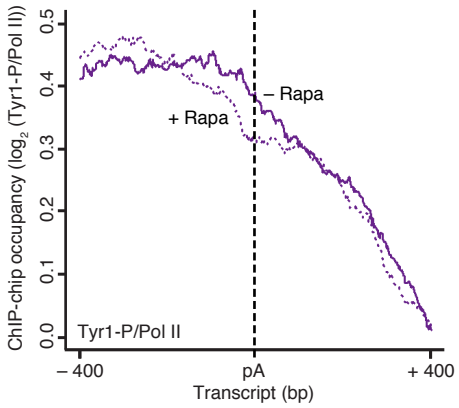
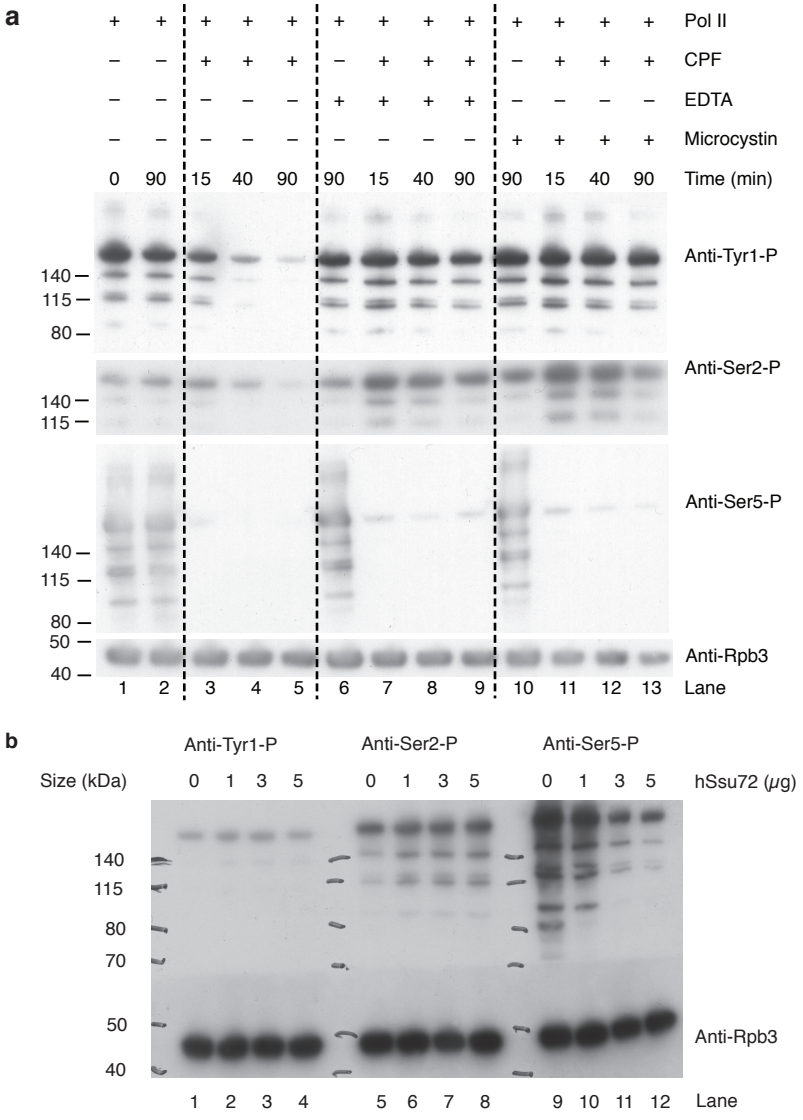


Supplementary Figure 3 Genome-wide ChIP occupancy of Tyr1-phosphorylated Pol II around the pA site is not influenced by rapamycin in wild-type yeast.
ChIP-chip occupancy profiling of Tyr1-phosphorylated Pol II over 619 genes aligned at the pA site (dashed line) and normalized against the corresponding Rpb3 profile without and with rapamycin (violet line and violet dotted line, respectively). The profile in a region from 400 nucleotides upstream to 400 nucleotides downstream of the polyA site is shown.



Supplementary Figure 4 Uncropped western blots of Pol II CTD *in vitro* assays.
(**a**) Uncropped blots of Figure 1b in the main text. (**b**) Uncropped blots of Figure 3a in the main text. See main text for details.