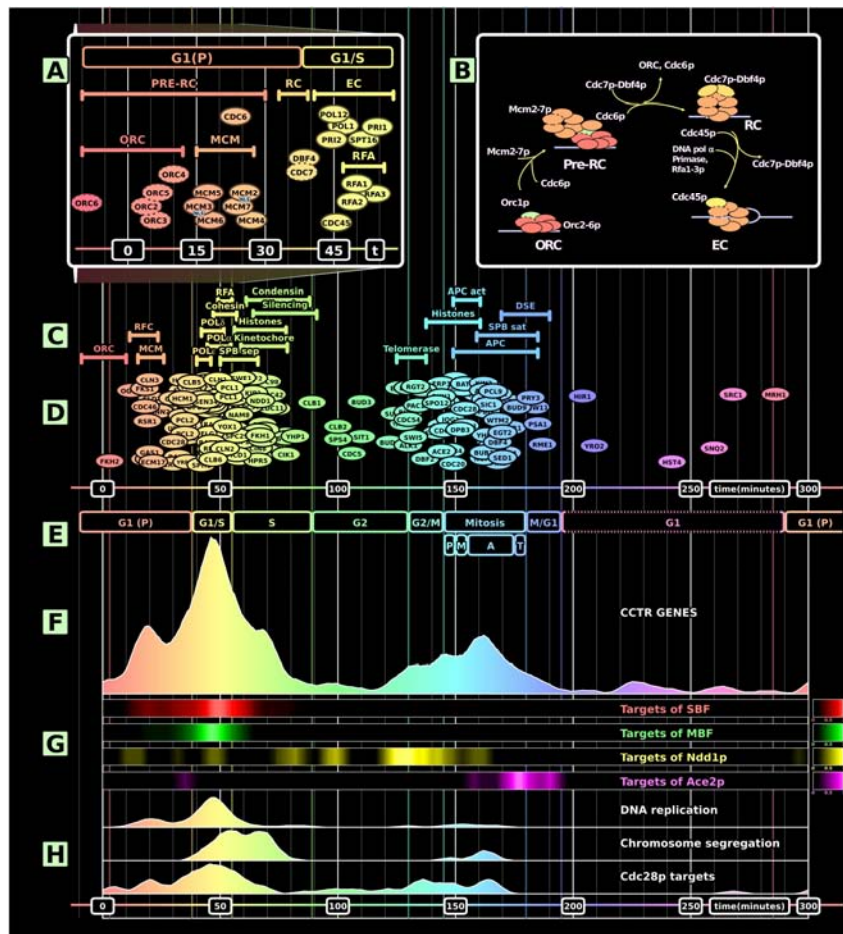


# Transcriptional program of the cell cycle: high-resolution timing

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The eukaryotic cell division cycle is dependent on an intricate sequence of transcriptional events. Using a novel algorithm based on Maximum Entropy deconvolution and expression data from a highly synchronized yeast culture, we have timed the peaks of expression of transcriptionally-regulated cell cycle genes to a previously unachievable accuracy of 1.9 minutes (ca. 1% of the cell cycle time). The set of 1,129 cell-cycle transcriptionally regulated (CCTR) genes were identified by a comprehensive analysis encompassing all available cell cycle yeast datasets. Our results reveal distinct subphases of the cell cycle undetectable by morphological observation as well as the precise timeline of macromolecular complex assembly during key cell cycle events.



**Transcriptional program of the yeast cell cycle.** (A, B) Proteins involved in DNA replication initiation, color-coded according to their expression time. The pre-Replication Complex (pre-RC) undergoes several changes before an elongation complex (EC), capable of initiation of DNA synthesis, is formed. The order of expression (A) agrees with the order gene products are needed (B). (C) Timing of CCTR complexes. Abbreviations: daughter-cell specific expression (DSE), APC activation (APC act), spindle pole body satellite formation (SPB sat) and SPB duplication and separation (SPB sep). (D) Peaks of selected CCTR genes. (E) Cell cycle phases. Note new pre-replicative G1(P) phase. (F, G, H) Histogram of expression peaks of all CCTR genes (F), targets of CCTR transcription factors (G) and genes of selected functions (H).