SUPPLEMENTARY MATERIALS

Quantitative Proteomics Demonstrates that the RNA Polymerase II Subunits Rpb4 and Rpb7 Dissociate During Transcription Elongation

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The tables described below are available as separate downloadable files.

Supplementary Tables 1-3: These tables provide the peptide spectrum matching information obtained from SEQUEST searches for all of the purifications used to create Figure 1. The tables are separated into the purifications for the core RNAPII subunits (Supplementary Table 1), purifications for associated proteins that interact with an RNAPII complex containing Rpb4/Rpb7 (Supplementary Table 2), and purifications for associated proteins that interact with an RNAPII complex that is depleted in Rpb4/Rpb7 (Supplementary Table 3). Each table contains the following columns: Sample set name, MS/MS sample name, Protein NCBI accession numbers, FASTA Database, Protein molecular weight (Da), Protein identification probability, Number of unique peptides, Number of total PSMs, Percentage sequence coverage, Spectrum name, Peptide sequence, SEQUEST XCorr score, SEQUEST DCn score, Fixed modifications identified, Variable modifications identified, Observed m/z, Actual peptide mass (AMU), Calculated +1H Peptide Mass (AMU), Spectrum charge, Other Proteins. The 'Other Proteins' column provides information about peptides that may be attributed to more than one protein.

Supplementary Table 4: This table provides the NSAF values for all proteins identified in RNAPII core, RNAPII associated protein, and MOCK purifications. Common lab contaminants including keratins and IgGs were removed prior to NSAF calculation.

Supplementary Table 5: This table provides the NSAF values for all proteins identified in RNAPII core and RNAPII associated protein purifications following contaminant extraction. These values were used for hierarchical clustering analysis that is shown in Figure 1.

Supplementary Table 6: This table provides the Complex NSAF (cNSAF) values for biological replicate purifications of Rpb3-TAP, Rpb11-TAP, Rpb7-TAP, and Rtr1-TAP that are described in Figure 2.

Yeast strains : The genotype and source of all strains used in this study are provided in Supplementary Table 7.

Name	Genotype	Source
Rpb11-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB11-TAP::HIS3MX6*	Open Biosystems
Rpb3-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB3-TAP::HIS3MX6*	Open Biosystems
Rpb7-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB7-TAP::HIS3MX6*	Open Biosystems
Cdc73-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 CDC73-TAP::HIS3MX6*	Open Biosystems
Spt4-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 SPT4-TAP::HIS3MX6*	Open Biosystems
Tfg1-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 TFG1-TAP::URA3*	This study
Npa3-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 NPA3-TAP::HIS3MX6*	Open Biosystems
Rtr1-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RTR1-TAP::HIS3MX6*	Open Biosystems
Asr1-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ASR1-TAP::HIS3MX6*	Open Biosystems
Set2-TAP	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 SET2-TAP::URA3*	This study
Rpb7-3X FLAG	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB7-3XFLAG::HPHMX4*	This study
Rpb3-TAP Rpb7-3X FLAG	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB7-3XFLAG::HPHMX4 RPB3-TAP::HIS3MX6*	This study
Spt4-TAP Rpb7-3X FLAG	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB7-3XFLAG::HPHMX4 SPT4-TAP::HIS3MX6*	This study
Tfg1-TAP Rpb7-3X FLAG	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB7-3XFLAG::HPHMX4 TFG1-TAP::HIS3MX6*	This study
Rtr1-TAP Rpb7-3X FLAG	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB7-3XFLAG::HPHMX4 RTR1-TAP::HIS3MX6*	This study
Asr1-TAP Rpb7-3X FLAG	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB7-3XFLAG::HPHMX4 ASR1-TAP::HIS3MX6*	This study
Set2-TAP Rpb7-3X FLAG	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 RPB7-3XFLAG::HPHMX4 SET2-TAP::URA3*	This study