The positions of TFIIF and TFIIE in the RNA Polymerase II transcription Preinitiation Complex Hung-Ta Chen, Linda Warfield and Steven Hahn

SUPPLEMENTARY MATERIAL

Supplementary Methods

Yeast plasmids. The original tRNA/Bpa-tRNA synthetase plasmid pESC-BPZ was a gift from P. Schultz. For more efficient suppression, plasmid pESC-BPZ was modified to replace the promoter of the tRNA_{CUA} gene by the 66 base S. cerevisiae tRNA promoter for the N(GTT)PR tRNA gene and this new plasmid is named pLH157. Plasmid pSH375 (SUA7, Cen, LEU2) was constructed by inserting the gene encoding SUA7 (TFIIB) into pRS315¹ vector at PstI/SacI sites. This plasmid was used as the wild-type TFIIB plasmid (Figure 1a). The TFIIB-Ser53 amber plasmid, pLH163, was generated through Quickchange mutagenesis (Stratagene) creating a TAG mutation at Ser53. Plasmid pHC2201 (RPB2, Cen, LEU2) was constructed by subcloning a 5.5kbp XbaI/SalI fragment containing RPB2 from pRP212² into pRS315. To create plasmid pHC2501 (RPB2-Myc, 2µ, LEU2), a 5.5-kbp NotI/SalI fragment from pHC2201 was first subcloned into pRS425³. Subsequently, the 414-bp of *S. cerevisiae* Adh1 promoter sequence was inserted in front of *RPB2* through PCR sewing and the 13-Myc epitope sequence was inserted at the C-terminus of RPB2 using Quickchange mutagenesis (Stratagene) with a DNA fragment that was generated by PCR amplification of the 13-Myc epitope sequence in plasmid pFA6a-13Myc-kanMX6⁴ with primer pairs carrying 5'- and 3'-sequences flanking RPB2 Cterminus. Rpb2 amber plasmids containing single TAG codon at the mutation sites were generated by using oligonucleotide-directed phagemid mutagenesis of pHC2501. Rpb1 amber plasmids were generated through phagemid mutagenesis of pHC1601 (*RPB1*-Myc, 2µ, *LEU2*) that contains Rpb1 gene sequence originally from pRP112⁵. Similar to the Rpb2 amber plasmid, Rpb1 is also driven by the Adh1 promoter and contains the 13-Myc epitope sequence at the Cterminus. Plasmid pHC2202 (RPB2-Flag, Cen, LEU2) was generated by inserting a triple Flag tag at the C-terminus of RPB2 in pHC2201 (Rpb2, Cen, LEU2) by using oligonucleotidedirected phagemid mutagenesis. Radical mutations of the Rpb2 lobe and protrusion domains were subsequently introduced to pHC2202 through phagemid mutagenesis.

1

Yeast Strains. The following strains were used for TFIIB study: LHy165 (MAT α ade 1 Δ leu 2 Δ his4A ura3A trp1::KanMX4 sua7::his4 [pSH375 and pLH157]); LHy167, isogenic to LHy165 except that plasmid pSH375 is replaced by pLH163 (TFIIB Ser53-amber). Each Rpb2 amber strain was generated from the shuffle strain HCy2501 through plasmid shuffling to contain both the Rpb2 amber plasmid and pLH157 plasmid. HCy2501 (MAT α ade2::hisG his3 Δ 200 $leu2\Delta lys2\Delta met15\Delta trp1\Delta 63 ura3\Delta \Delta rpb2::kanMX4 [pRPB2-URA3] was generated through$ transformation of a Rpb2-URA3 plasmid to the strain BY4705⁶, followed by one-step gene disruption of the chromosomal *RPB2* gene with a rpb2::KanMX4 DNA fragment that was generated by PCR amplification of the drug resistant cassette pFA6-kanMX4⁷ with primer pairs carrying RPB2 5'- and 3'-tails. Similarly, the Rpb1 amber strain containing both Rpb1 amber plasmid and pLH157 was generated from strain HCy1601 (MATα ade2::hisG his3Δ200 $leu2\Delta$ lys2 Δ met15 Δ trp1 Δ 63 ura3 Δ Δ rpb1::KanMX4 [pRPB1-URA3] through plasmid shuffling. The following are the strains containing triple Flag-tagged proteins: HCy1201 and HCy2201 contain a triple Flag epitope fused to the C-terminus of Rpb1 and Rpb2, respectively; HCv2202 containing Rpb2 triple Flag-tagged at the N-terminus; SHv384 and SHv564 containing a triple Flag epitope at the C-terminus of Tfg1 and Tfg2, respectively; SHy361 containing a triple Flag epitope at the C-terminus of Tfa1. The strain used for plasmid shuffling of Rpb2 lobe/protrusion mutant plasmids is HCy2501.

Antisera. Anti-Flag M2 monoclonal antibody was from Sigma, anti-Myc monoclonal antibody (9E10) and anti-Rpb1CTD monoclonal antibody (8WG16) were from Covance. Other antisera have been described previously^{8,9}.

TFIIF purification. The 6xHis-SUMO-TFIIF expression plasmid from above was transformed into *E. coli* strain BL21 (DE3) RIL (Stratagene). The transformed cells were grown in 2 L YT medium containing ampicillin and chloramphenicol. Expression of SUMO-TFIIF fusion protein was induced by addition of IPTG to 0.1 mM when the O.D. of cell density was around 0.8. The cells were harvested by centrifugation 4 hours after induction and the cell paste was subsequently frozen in liquid nitrogen and stored at -70 °C. Cells were lysed by sonication in 25 ml lysis buffer of 250 mM KCl, 10% (v/v) glycerol, 20 mM imidazole, 5 mM β -mercaptoethanol (BME), 1 mM PMSF, 0.05% (v/v) NP-40, and 20 mM Tris (pH 7.8) and the lysate was clarified by

2

centrifugation. After centrifugation, the supernatant was incubated with 3 ml pre-equilibrated Nickel-Sepharose (GE Healthcare) at 4 °C. After 1.5-hour incubation, the supernatant was removed and the Nickel-Sepharose beads were washed twice with 25 ml wash buffer containing 1 M KCl, 10% (v/v) glycerol, 5 mM BME, 1 mM PMSF, 0.05% (v/v) NP-40 and 20 mM Tris (pH 7.8). The SUMO fusion protein was eluted with 24 ml elution buffer containing 250 mM imidazole, 250 mM KCl, 10% (v/v) glycerol, 5 mM BME, 1 mM PMSF, and 20 mM Tris (pH 7.8). The eluted protein sample was dialyzed against SUMO digestion buffer 150 mM KCl, 10% (v/v) glycerol, 1 mM PMSF, 1 mM DTT, 20 mM Tris pH 7.8. The resulting protein sample was subjected to SUMO protease digestion with 8 µg protease and 1 hr incubation at RT. The digested protein sample was loaded onto a 6 ml BioRex 70 (BioRad) column pre-equilibrated with the SUMO digestion buffer. The *Sm*Tfg1/*Sc*Tfg2 heterodimer was eluted from the column with a salt gradient of 150 to 600 mM KCl. The fractions containing TFIIF were pooled and concentrated with Centriprep YM-10 concentrator (Amicon) to ~0.8 mg ml⁻¹. The typical yield of a TFIIF variant is approximately from 0.5-1mg from 2-L induction. The protein solution was frozen with liquid nitrogen and stored at -70 °C.

References

- 1. Sikorski, R.S. & Hieter, P. A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae. *Genetics* **122**, 19-27 (1989).
- 2. Scafe, C., Nonet, M. & Young, R.A. RNA polymerase II mutants defective in transcription of a subset of genes. *Mol Cell Biol* **10**, 1010-6 (1990).
- 3. Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. & Hieter, P. Multifunctional yeast high-copy-number shuttle vectors. *Gene* **110**, 119-22 (1992).
- 4. Longtine, M.S. et al. Additional modules for versatile and economical PCR-based gene deletion and modification in Saccharomyces cerevisiae. *Yeast* **14**, 953-61 (1998).
- 5. Nonet, M.L. & Young, R.A. Intragenic and extragenic suppressors of mutations in the heptapeptide repeat domain of Saccharomyces cerevisiae RNA polymerase II. *Genetics* **123**, 715-24 (1989).
- 6. Brachmann, C.B. et al. Designer deletion strains derived from Saccharomyces cerevisiae S288C: a useful set of strains and plasmids for PCR-mediated gene disruption and other applications. *Yeast* **14**, 115-32 (1998).
- Wach, A., Brachat, A., Pohlmann, R. & Philippsen, P. New heterologous modules for classical or PCR-based gene disruptions in Saccharomyces cerevisiae. *Yeast* 10, 1793-808 (1994).

- 8. Chen, H.T. & Hahn, S. Mapping the location of TFIIB within the RNA polymerase II transcription preinitiation complex: a model for the structure of the PIC. *Cell* **119**, 169-80 (2004).
- 9. Ranish, J.A., Yudkovsky, N. & Hahn, S. Intermediates in formation and activity of the RNA polymerase II preinitiation complex: holoenzyme recruitment and a postrecruitment role for the TATA box and TFIIB. *Genes Dev* **13**, 49-63 (1999).