Supplementary Information

The RPB2 flap loop of human RNA polymerase II is dispensable for transcription initiation and elongation.

Murali Palangat,[1] Jeffrey A Grass,[1] Marie-France Langelier,[2,‡] Benoit Coulombe[2,3] and Robert Landick[1,4]

Department of Biochemistry, University of Wisconsin-Madison, Madison, WI-53706[1].
Institut de Recherches Cliniques de Montréal, 110, Montréal, Que., Canada H2W 1R7[2];
Départment de Biochimie, Université de Montréal, Montréal, Québec, Canada, H3C 3J7[3];
Department of Bacteriology, University of Wisconsin-Madison, Madison, WI-53706[4].

‡Present address: Department of Biochemistry and Molecular Biology, Kimmel Cancer Center, Thomas Jefferson University, Philadelphia, Pennsylvania 19107.

Supplementary Table 1, 2
Supplementary Figures 1

Supplementary Table 1.

Plasmid Stock #	Name	Description
5012	pJG012	hRpb2 wild-type expression plasmid. hRpb2 with N-terminal His_{10}, PPX, $Flag_{3x}$ & HA_{3x} epitope tags.
5019	pJG019	hRpb2 ΔFL expression plasmid. hRpb2 with N-terminal His_{10}, PPX, $Flag_{3x}$ & HA_{3x} epitope tags.

Oligonucleotide Stock #	Name	Sequence (5'-)
DNA		
6437	NT DNA	GGTCAGTACGTCCTAAGCGGCGGGTGGAAGAGATTCAGAGCCATC CCAATGGACACC
6438	T DNA	GGTGTCCATTGGGATGGCTCTGAATCTCTTCCACCCGCCGCTTAG GACGTACTGACC
RNA		
6359	RNA15	GAGUCUGGCGGCGGG

Supplementary Table 2.

Data set	Figure	CMARRT[a] regions	CMARRT regions with a Promoter near or within it	CMARRT regions with Promoters in it	CMARRT regions without a Promoter in it	CMARRT regions without a Promoter in it[b]	CMARRT regions not within an ENCODE region	CMARRT regions within an ENCODE region
WT Rpb2	6A	20159	18938	10919	8019	1221	19444	715
ΔFL Rpb2	6B	22216	20697	11771	8926	1519	21439	777
Rpb1	6C	18357	17093	11386	5707	1264	17871	486
WT/ΔFL	6D	850	789	49	740	61	783	67
ΔFL/RPB1	6E	966	843	76	767	123	849	117
WT/RPB1	6F	1988	1728	120	1608	255	1728	255
ΔFL/WT	-	19						
RPB1/ΔFL	-	0						
RPB1/WT	-	0						
WT/WT[c]	-	35						

[a] CMARRT: Correlation, Moving, Average, Robust and Rapid method on Tiling array. Extends the standard moving average approach by incorporating correlation structure to identify bound regions (1).
[b] Data not presented, outside of limits shown.
c Ratio of WT replicate 1 *vs* WT average.

1. Kuan, P. F., H. Chun, and S. Keles. 2008. CMARRT: A tool for the analysis of ChIP-Chip data from tiling arrays by incorporating the correlation structure. Pacific Symposium on Biocomputing 13:515-526.

Supplementary Figure 1. Amino acid sequence of the epitope tags.