RNA polymerase II may interact with different transcription factors during elongation according to out-of-peak ChIP-seq signal analysis

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The general point of view (according to *in vitro* experiments) is that most transcription factors stay on promoter or dissociated from any complex when RNA polymerase II elongates. But the alternative version based upon ChIP-seq out-of-peak signal analysis is presented in this study.

Examined transcription factors (TFs) were: AP-2a, AP-2g, c-Fos, c-Jun, c-Myc, E2F1, E2F4, E2F6, HA-E2F1, junD, Max, Nrf1, TR4, BAF155, BAF170, Ini1, Brg1, BDP1, BRF1, BRF2, RPC155, TFIIIC. Functions of these TF are different. Proteins from AP-2a to TR4 are transcription factors, from BAF155 to Brg1 are subunits of Swi/Snf remodeling complex, from BDP1 to TFIIIC are transcription factors for RNA polymerase III. RNA polymerase II signal was also taken for several cell lines from Yale ChIP-seq.

ChIP-seq procedure is supposed to be intact for protein complexes on DNA (that they do not dissociate and free-associate to DNA). Swi/Snf complex subunits were used as a positive control because they travel with RNA polymerase II in elongation. TFs for RNA polymerase III were used as negative control because they are not with RNA polymerase II in elongation.

Average out-of-peak ChIP-seq signal for RNA polymerase II and all TFs inside genes and exons occurred to be higher than such signal outside them. Moreover out-of-peak ChIP-seq signal of RNA polymerase II occurred to be positively correlated with such signal of its TF to much more extend than with TFs for RNA polymerase III and to the same extend as with Swi/Snf complex.

Wide range of TFs was shown to be presumably colocalized with RNA polymerase II in genes so model was suggested where RNA polymerase II is connected with TFs in elongation and scheme where RNA polymerase II even stays connected with promoter through TFs that are

still connected to promoter is also discussed.

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