Supplementary Material

GENOME-ASSOCIATED RNA POLYMERASE II INCLUDES THE DISSOCIABLE RPB4/7 SUBCOMPLEX*

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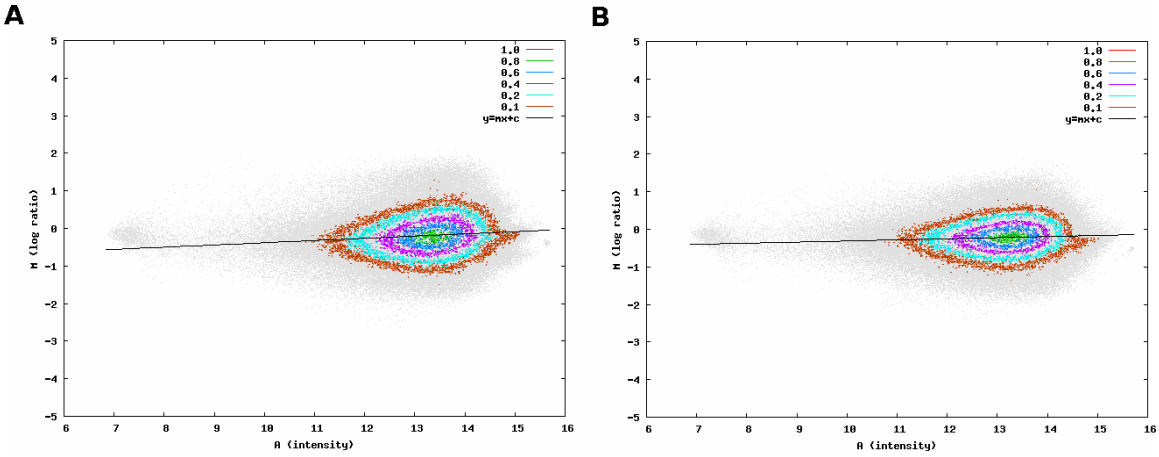
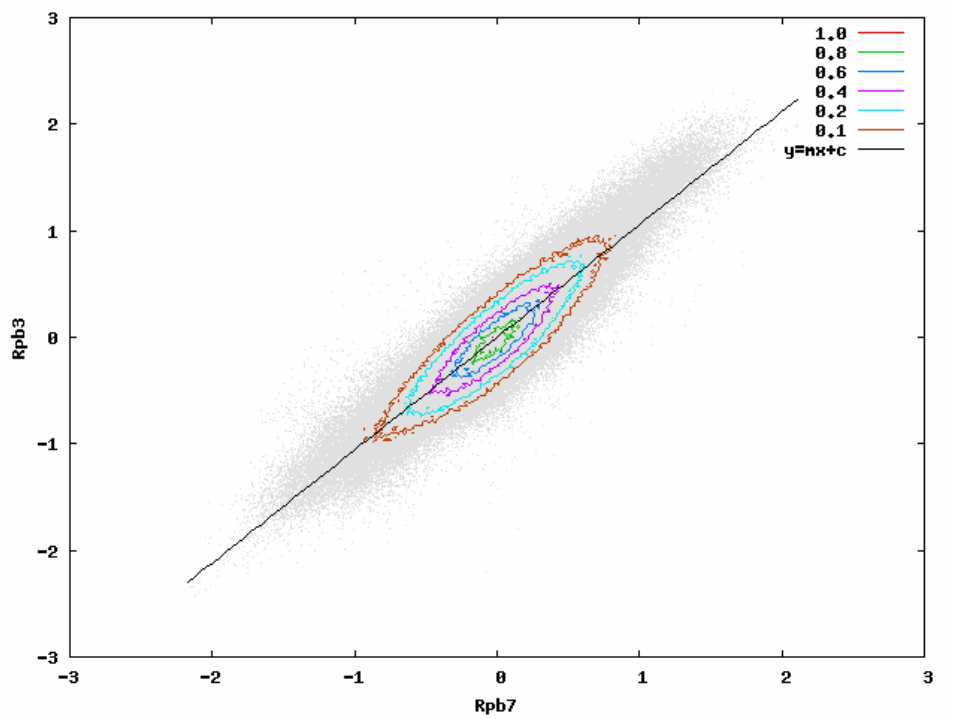


SUPPL. FIG. 1 Dye exchange averaging suppresses saturation effects in Rpb3 and Rpb7 signal

The classic MA plots chart the signal intensity (*M*) on the y-axis with respect to the average signal intensity (*I*) for Rpb3 (A) and Rpb7 (B). The signal *I* is the mean value of the logs (base 2) of the ChIP signals divided by the genomic background signals. Each tiling array probe contributes a grey dot. Contour lines indicate lines of constant density. The mean in (A) is taken over three measurements: the two measurements in which Cy5 is used to label the ChIP DNA get half the weight as the one using Cy3 to label ChIPed DNA (see main text). In (B), the mean is taken over two measurements with exchanged dyes using equal weights of 0.5. The average intensity *A* on the x-axes is the average of the logs (base 2) of the three ChIP and background signals in (A) and two ChIP and background signals in (B).



SUPPL. FIG. 2 Rpb3 and Rpb7 occupancies are highly correlated

The figure shows the Rpb3 versus Rpb7 signals (calculated as log base 2 of ChIP signal divided by genomic background signal). Each tiling array probe contributes a grey dot. Contour lines go from 0.8 to 0.1 of maximum density. Approximately 90% of probes are contained within the 0.1 contour. The correlation is very high (Pearson correlation coefficient 0.91), comparable to the correlation of Rpb7 signal between biological replicates and different strains. The slope of the regression line is 1.06. This factor is used to scale up the Rpb7 signal when calculating the difference signal (Rpb3 – Rpb7) in Figs. 1E and 2C.