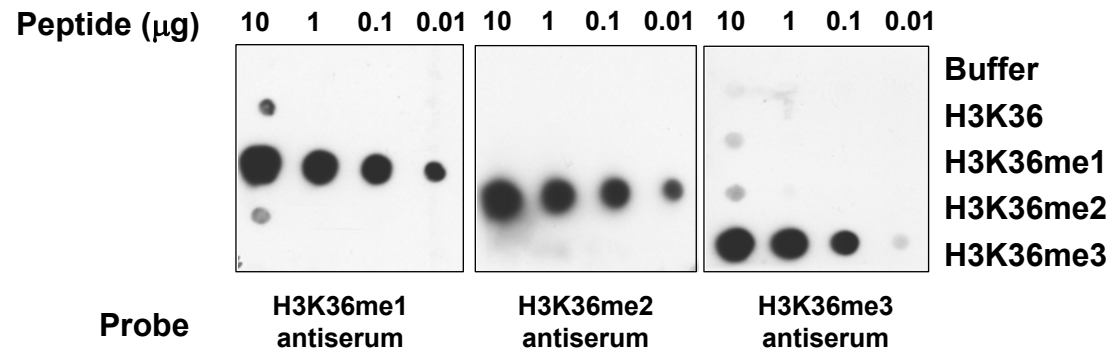


Supplemental Table 1. Experiments Performed. Array names in parentheses were technical replicates whose values were averaged and treated as a single biological replicate in data analysis. Log phase and heat shock t=0 experiments are identical, except that the t=0 experiments are paired with a corresponding heat shock sample.

Exp. Number	UNC Microarray Database Array Names	Strain	Cy5	Cy3	Growth Condition
1-8	br_g_002Q, br_PM_A214, br_PM_A106, br_PM_A160, br_PM_A120, (br_g_104Q and br_g_096Q), (br_g_103Q and br_g_095Q), (br_g_097Q and br_g_098Q)	AS4 (Wild-type)	H3K36me2 ChIP	AS4 input	Log phase
9,10	BR218C, BR115C	H4-myc	H3K36me2 ChIP	H4-myc input	Heat shock t=0
11, 12	BR125C, BR135C	AS4	H3K36me2 ChIP	AS4 input	Heat shock t=0
13	BR217C	H4-myc	H3K36me2 ChIP	H4-myc input	Heat shock t=15
14, 15	BR118C, BR129C	AS4	H3K36me2 ChIP	AS4 input	Heat shock t=15
16-23	br_g_100Q, br_g_107Q, br_PM_A117, br_PM_A154, br_g_003Q, br_PM_A135, br_PM_A125, br_PM_A54	set2Δ (AS4)	H3K36me2 ChIP	AS4 input	Log phase
24-26	BR136G, BR59G, BR207C	H4-myc	Myc ChIP	H4-myc input	Log phase
27, 28	BR172C, BR224C	H4-myc	Myc ChIP	H4-myc input	Heat shock t=0
29-31	BR181C, BR221C, BR223C	H4-myc	Myc ChIP	H4-myc input	Heat shock t=15
32, 33	BR117C, BR216C	H4-myc	H3K36me2 ChIP	Myc ChIP	Heat shock t=0
34, 35	BR77C, BR227C	AS4 (for H3K36me2) ; H4-myc	H3K36me2 ChIP	Myc ChIP	Heat shock t=0

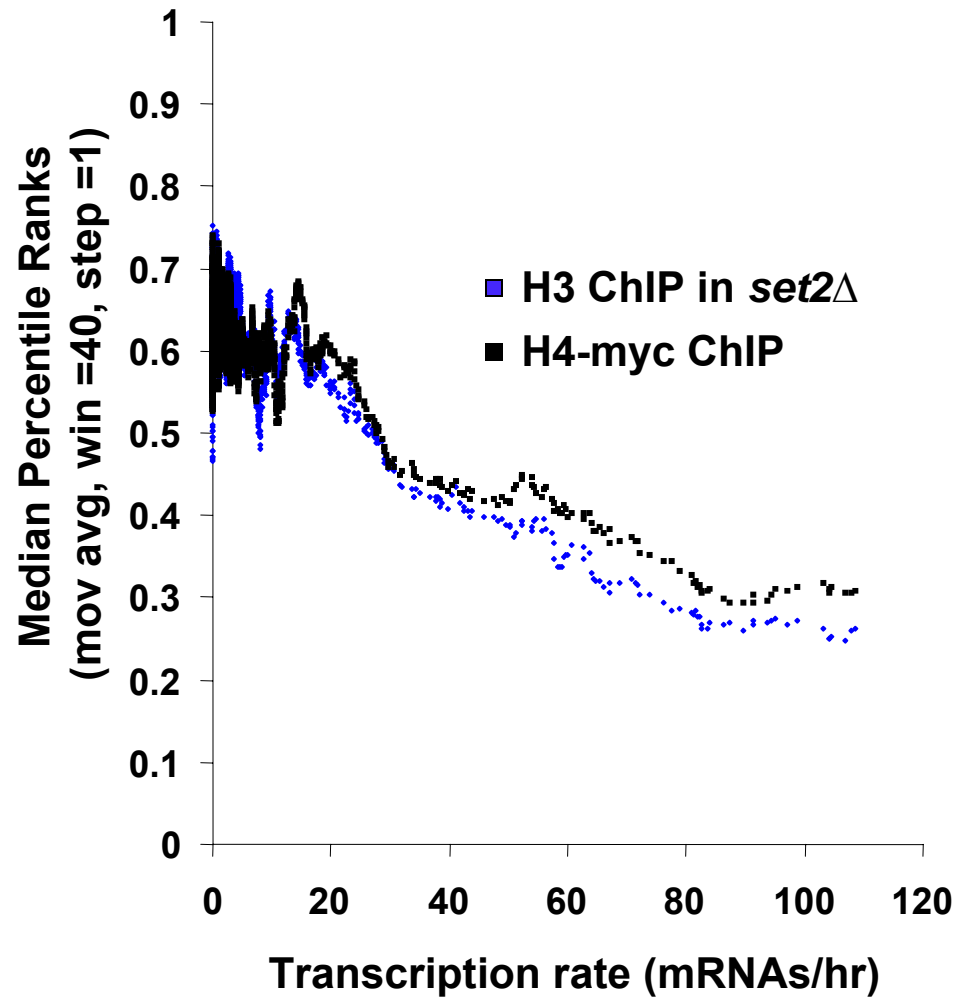
Rao *et al* Supplemental Figure 1

Specificity of H3K36me2 Antibodies

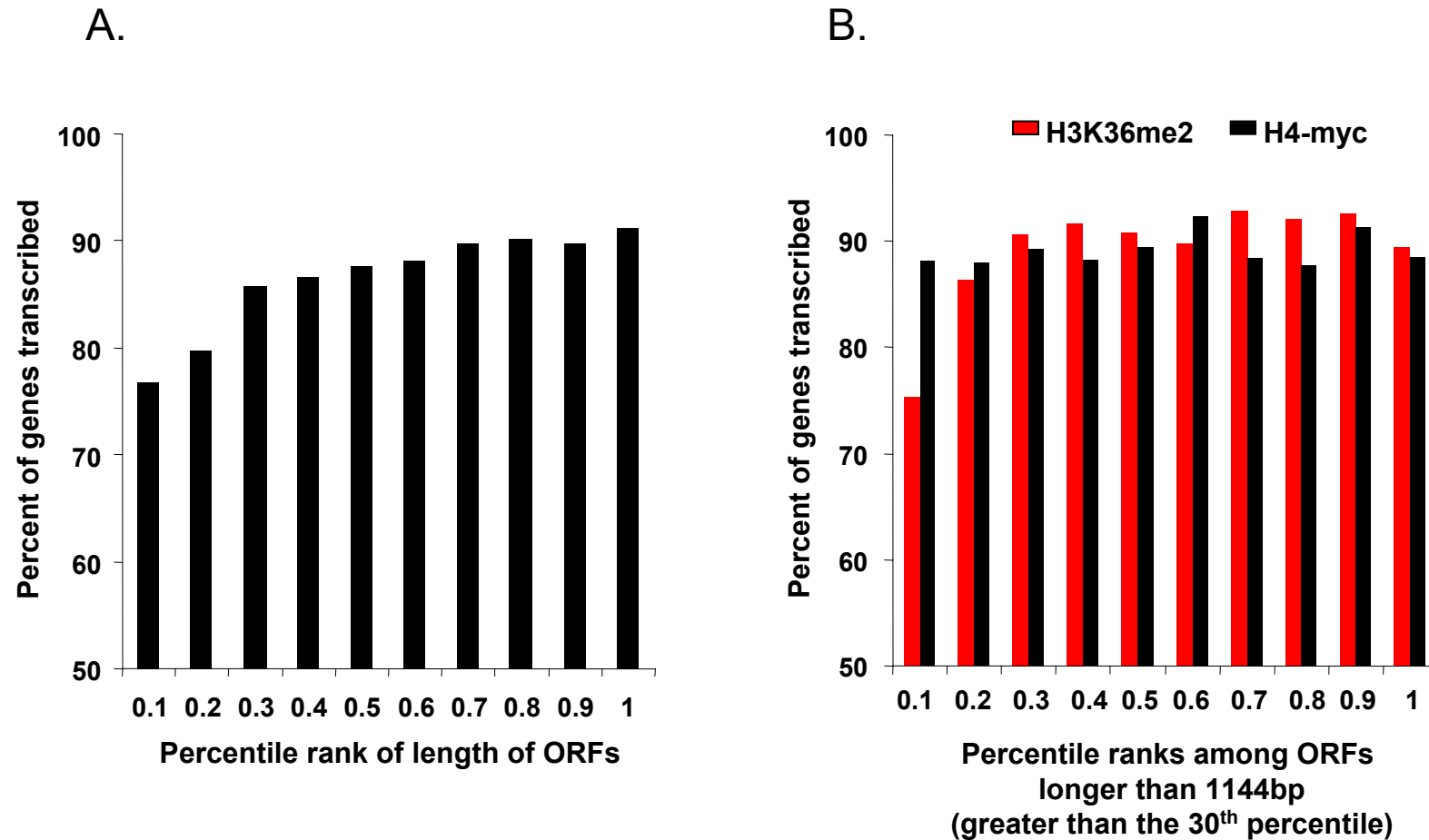


Supplemental Figure 1. Serial dilutions of unmodified K36 peptide, and the same peptide mono-, di-, or tri-methylated at lysine 36 were dot blotted onto PVDF membrane and subsequently subjected to Western blot analysis with the indicated antibody. The peptide sequence is as follows, with the position corresponding to lysine 36 underlined: CPSTGGVKKP.

**Loss of H3K36me2 does not affect Nucleosome Dynamics
in Heavily Transcribed ORFs**



Supplemental Figure 2. Moving average of median percentile ranks (win size=40, step size=1) of ChIP enrichment values for ORFs, plotted as a function of transcription rate (mRNAs/hr). H4-myc ChIPs (black) in a wild-type strain; H3 ChIPs in a *set2Δ* strain (blue)



Supplemental Figure 3. A. ORFs were equally divided into 10 bins according to their lengths (with longer ORFs having higher percentile ranks). The ORFs in each bin were then classified as either “ON” (> 0 mRNAs/hr) or “OFF” (0 mRNAs/hr). The percentage of genes in each bin that was classified as “ON” is shown. **B.** Same as Figure 4A except only ORFs above the 30th percentile for length (length greater than 1144bp) were used.