SUPPLEMENTARY INFORMATION

Insights into transcriptional regulation by individual H3K4 methylation marks in *S. cerevisiae*

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Supplementary Table 1. Yeast Strains

Strain	Genotype	Reference
MBY1590	*MATa ura3-52 trp1Δ63 set1Δ::KANMX4 lys2-128δ*	This study
MBY2992	*MATa ura3-52::pRS406 trp1Δ63 set1Δ::KANMX4 lys2-128δ*	This study
MBY2994	*MATa ura3-52::pRS406-SET1 trp1Δ63 set1Δ::KANMX4 lys2-128δ*	This study
MBY2996	*MATa ura3-52::pRS406-set1-R1013H trp1Δ63 set1Δ::KANMX4 lys2-128δ*	This study
MBY2998	*MATa ura3-52::pRS406-set1-Y967A trp1Δ63 set1Δ::KANMX4 lys2-128δ*	This study
MBY3000	*MATa ura3-52::pRS406-set1-Y967F trp1Δ63 set1Δ::KANMX4 lys2-128δ*	This study
MBY3029	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52 set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 pHHT2-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3030	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52 set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 phht2-K4R-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3031	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52::pRS406-SET1 set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 pHHT2-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3032	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52::pRS406 set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 pHHT2-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3033	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52::pRS406-set1-Y967A set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 pHHT2-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3034	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52::pRS406-set1-Y967F set1Δ::KANMX4 (hht2-*	This study

	hhf2)Δ::KANMX4 pHHT2-HHF2-TRP1 CEN (leu2Δ1 or LEU2)	
MBY3035	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52::pRS406-set1-R1013H set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 pHHT2-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3037	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52 ::pRS406-SET1+ set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 phht2-K4R-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3038	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52 ::pRS406 set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 phht2-K4R-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3039	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52 ::pRS406-set1-Y967A set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 phht2-K4R-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3040	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52 ::pRS406-set1-Y967F set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 phht2-K4R-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3041	*MATa (hht1-hhf1)Δ::LEU2 lys2-128δ trp1Δ63 ura3-52 ::pRS406-set1-R1013H set1Δ::KANMX4 (hht2-hhf2)Δ::KANMX4 phht2-K4R-HHF2-TRP1 CEN (leu2Δ1 or LEU2)*	This study
MBY3148	*MAT alpha leu2Δ1 lys2-128δ ura3-52::pRS406-SET1 trp1Δ63 set1Δ::TRP1*	This study
MBY3149	*MAT alpha leu2Δ1 lys2-128δ ura3-52::pRS406 trp1Δ63 set1Δ::TRP1*	This study
MBY3151	*MAT alpha leu2Δ1 lys2-128δ ura3-52::pRS406-set1-Y967F trp1Δ63 set1Δ::TRP1*	This study
MBY3152	*MAT alpha leu2Δ1 lys2-128δ ura3-52::pRS406-set1-Y967A trp1Δ63 set1Δ::TRP1*	This study

MBY3154	*MAT alpha leu2Δ1 lys2-128δ ura3-52::pRS406-set1-G951A trp1Δ63 set1Δ::TRP1*	This study
MBY3181	*MAT alpha leu2Δ1 lys2-128δ ura3-52::set1-R1013H trp1Δ63 set1Δ::TRP1*	This study

Supplementary Table 2. Oligonucleotides

Oligo name (Collection number)	**Sequence**
HIS3 promoter FP (OM18)	TTG-GCC-TCC-TCT-AGT-ACA-CTC
HIS3 promoter RP (OM1212)	ACT-AGG-GCT-TTC-TGC-TCT-GTC
HIS3 5' ORF FP (OM1262)	GCA-GGC-AAG-ATA-AAC-GAA-GGC
HIS3 5' ORF RP (OM19)	GGT-CCA-GAA-ACC-CTA-TAC-CTG
HIS3 3' ORF FP (OM1101)	TGA-TCA-TCA-CCG-TAG-TGA-GAG
HIS3 3' ORF RP (OM1102)	GCA-TTA-CCT-TGT-CAT-CTT-CAG
ACT1 promoter FP (OM1260)	CTT-CCC-CTT-TCT-ACT-CAA-ACC
ACT1 promoter RP (OM1261)	CGC-TAG-AAC-ATA-CCA-GAA-TCC
IGR FP (OM482)	CAG-TCA-ATC-AGC-GTA-GTG-AC
IGR RP (OM483)	CAT-TCG-GGC-AGA-ACT-GTA-AAC

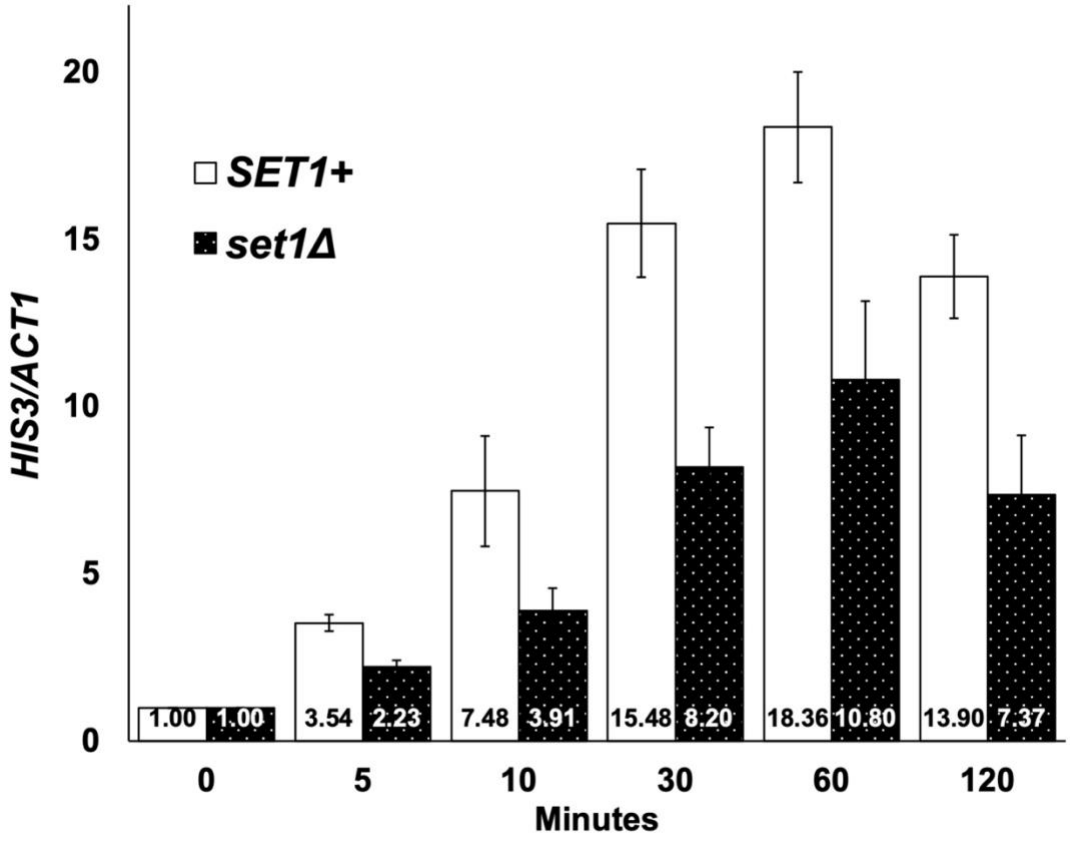

Figure S1. Time-course of induction of *HIS3* transcript with 10 mM 3AT. Cultures were grown to log phase in SC-His followed by addition of 10 mM 3AT to induce *HIS3* gene expression. *HIS3* mRNA levels over time after 3-AT induction were analyzed by Northern blot. Average *HIS3* mRNA levels were normalized to 18S ribosomal RNA. Each bar represents the ratio of (*HIS3/rRNA)* and the error bars (+/-SEM, n=3). The *HIS3* transcript level increased steadily, reaching a peak at 60 min after addition of 10 mM 3AT, and then decreased over the remainder of the time course. This pattern was also observed in the ***set1Δ*** culture, but the amount of *HIS3* mRNA was lower than in the corresponding *SET1*$^{+}$ samples.

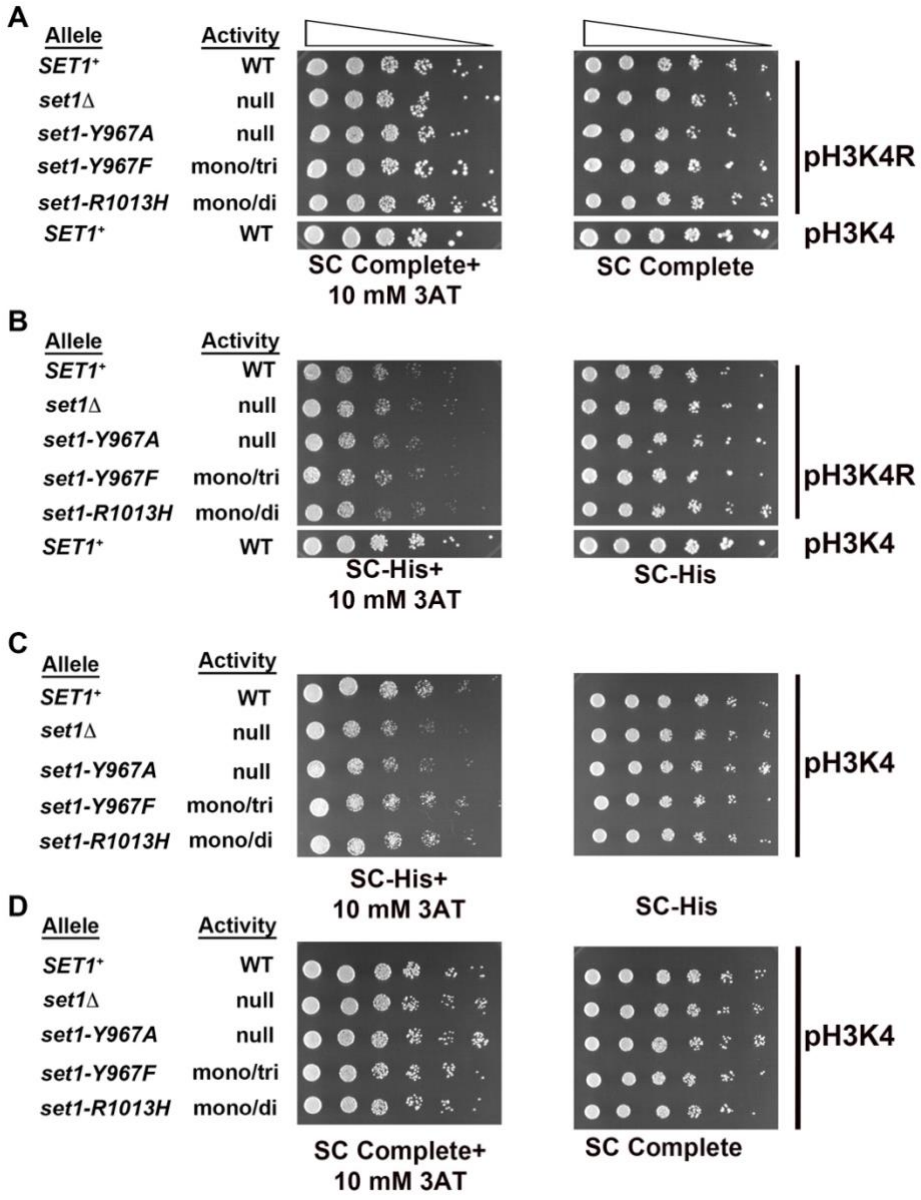

Figure S2. Set1 methylation of histone H3K4 is required for robust growth on SC-His with 3AT.

Five-fold serial dilutions of yeast cultures were spotted on to solid media with or without 10 mM 3AT, SC Complete (panels A and B) and SC-His (panels C and D). The strains express either wild-type histones H3 and H4 (pH3K4) or H3K4R mutant H3 and wild-type H4, (pH3K4R) from a plasmid. To simplify comparison of growth of cultures expressing mutant pH3K4R to a culture expressing wild type histone H3 from pH3K4, a dilution series of a *SET1*$^{+}$ pH3K4 culture is shown at the bottom of the pH3K4R panels. Plates were incubated at 30^{o}C for 72 hours prior to imaging. Other labels, as in Figure 2 (n=3).

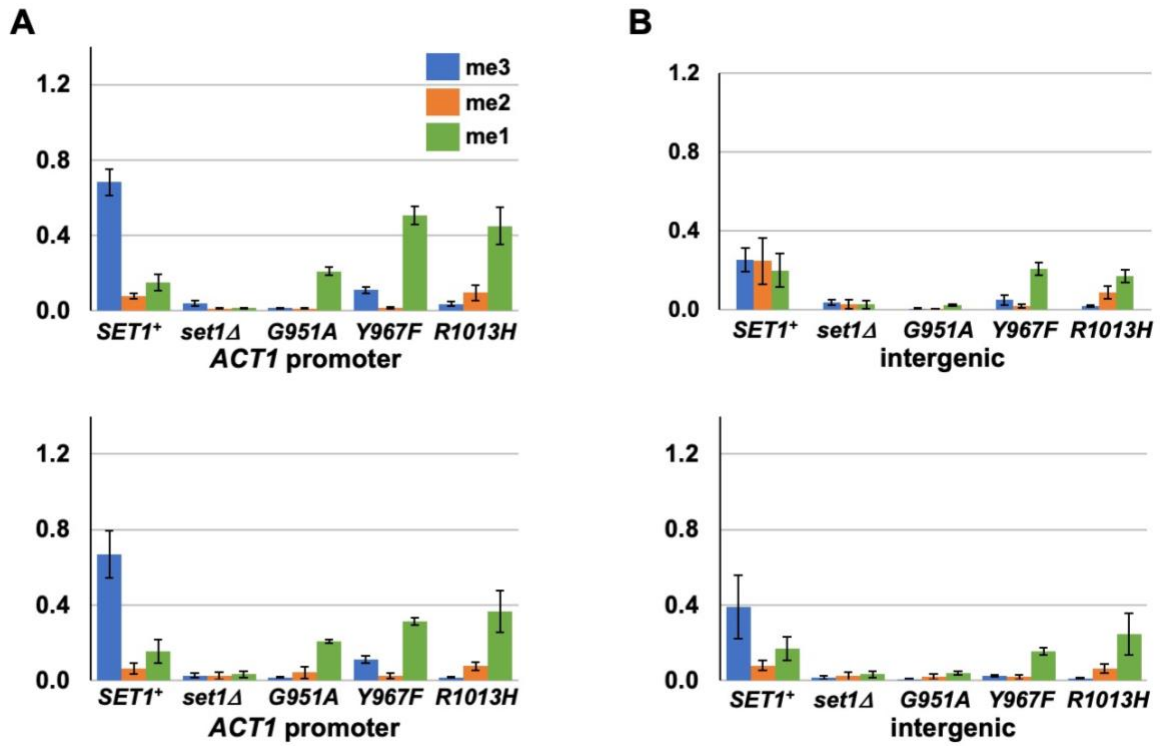

Figure S3. Distribution of H3K4me marks at the promoter of the *ACT1* gene and an intergenic region. A. H3K4me1, H3K4me2 and H3K4me3 measured at the *ACT1* promoter in yeast cultures grown in SC-HIS (upper) and SC-HIS+10 mM 3AT (lower). B. Levels of H3K4me1, H3K4me2 and H3K4me3 measured at an intergenic region on *S. cerevisiae* chromosome VIII from cultures grown in SC-HIS (upper) and SC-HIS+10 mM 3AT (lower). Percent IPs were normalized to total H3. Error bars (+/- SEM, n=4).