

Supporting Information

Stroud et al. 10.1073/pnas.1203145109

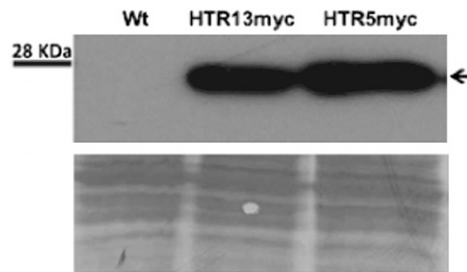


Fig. S1. Expression of Myc-tagged H3.1 and H3.3 proteins. Total protein extracts of 10-d-old plants were fractionated by 15% SDS/PAGE. Western blots were developed with anti-myc 4A6 antibody (1:3,000; Millipore).

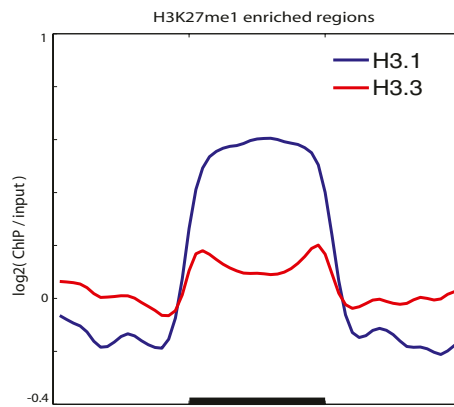


Fig. S2. Positive correlation between H3.1 and H3K27me1. Distribution of H3.1 and H3.3 over defined H3K27me1 sites in the arms of chromosomes.

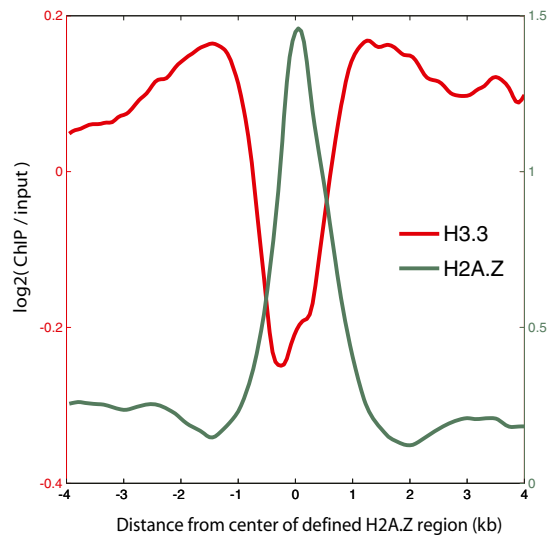


Fig. S3. Anticorrelation between H3.3 and H2A.Z. Distribution of H3.3 and H2A.Z over defined H2A.Z regions.

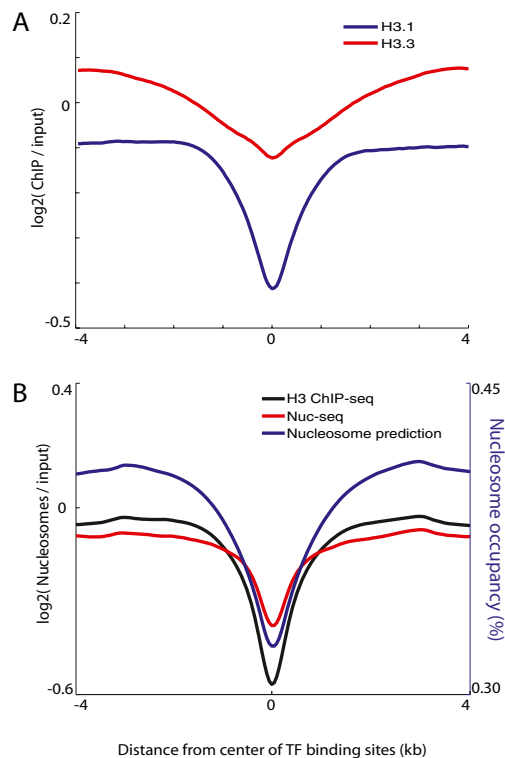


Fig. S4. H3.1 and H3.3 are depleted in transcription factor (TF)-binding sites. (A) Distribution of H3.1 and H3.3 over TF-binding sites. (B) Distribution of H3 ChIP-seq, Nuc-seq, and predicted nucleosomes occupancies over TF-binding sites.

Table S1. Primers used for generating epitope-tagged H3 plants

Primer name	Primer sequence
HTR13-GW-F	<i>attB1</i> -ATTCGTTCTGTCGATCCTCCAT
HTR13-GW-R	<i>attB2</i> -AGCTCTTCTCCTCTGATTCTCC
HTR5-GW-F	<i>attB1</i> -CATTGAGCTCAAGAACGAAGTA
HTR5-GW-R	<i>attB2</i> -AGCACGTTCTCCTCTGATCCT
<i>attB1</i>	GGGGACAAGTTTGTACAAAAAAGCAGGCT
<i>attB2</i>	GGGGACCACTTTGTACAAGAAAGCTGGGTC

Table S2. Sequencing reads obtained in this study

	Total sequenced reads	Total uniquely mapping reads to nuclear genome	Total uniquely mapping reads after collapsing reads that map to identical locations
Input DNA for myc-HTR5 ChIP	194,205,864	112,501,338	90,857,500
ChIP-seq myc-HTR5	244,370,063	130,932,886	87,054,216
Input DNA for myc-HTR13 ChIP	236,119,264	111,147,375	90,483,249
ChIP-seq myc-HTR13	245,103,638	105,735,670	75,847,226
mRNA-seq 10-d seedling	51,774,795	33,353,995	—