

## **Supplementary Material**

### **SNP-ChIP: A versatile and tag-free method to quantify changes in protein binding across the genome**

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Supplementary Figures 1 – 4

Supplementary Table 1

Supplementary References

## Supplementary Figures

**Figure S1.** Distribution of distances between consecutive single-nucleotide polymorphisms (SNPs) found between the SK1 and S288c yeast genomes. Values above 500 bp are not displayed.

**Figure S2.** Spike-in normalization factors calculated using different input data types. (a) Red1 amount relative to wild type for a collection of available samples. Values are the ratio between test sample and wild type's spike-in normalization factors calculated using one of four different kinds of data: aligned read counts (read counts; standard procedure) or the mean value of the aligned read pileup score at all genomic positions (read pileups), at SNP positions only (read pileups on SNPs), or at SNP positions falling within called signal peaks (read pileups on SNPs in peaks). (b) Comparison of spike-in normalization factors calculated using total read counts with the three other methods for the same samples plotted in (a).

**Figure S3.** Same-species spike-in causes loss of information but does not affect the overall target distribution patterns. (a) Red1 occupancy obtained using a same-species spike-in compared to a non-spiked replicate. The bottom panel shows a zoom-in on a smaller region, with SNPs annotated as vertical red bars. The red arrow points to a region where signal is lost in the spiked sample due to the lack of SNPs. (b) Comparison of narrow and broad peaks produced using MACS2 to highlight the proportion of peaks that overlap (intersected) or are unique to each of the samples.

**Figure S4.** Red1 occupancy is mildly decreased in histone methyltransferase mutants relative to wild type. (a) Target protein Red1 levels relative to wild type produced by SNP-ChIP. Points represent individual replicate values and bars represent average value. (b) Spike-in-normalized average Red1 signal on individual chromosomes. (c) Spike-in-normalized fragment pileup produced using MACS2 with SPMR sequencing depth normalization (fragment pileup per million reads) plotted on two example chromosomes.

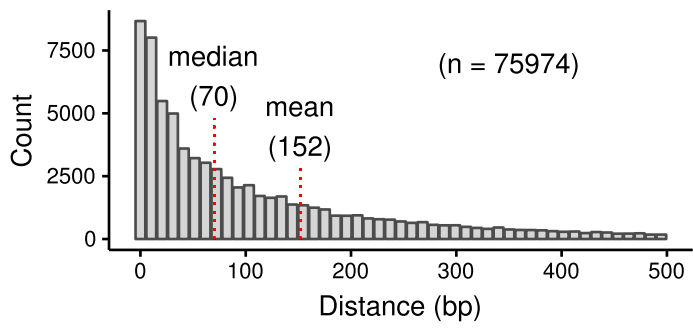
**Supplementary Table 1.** Strains used in this study

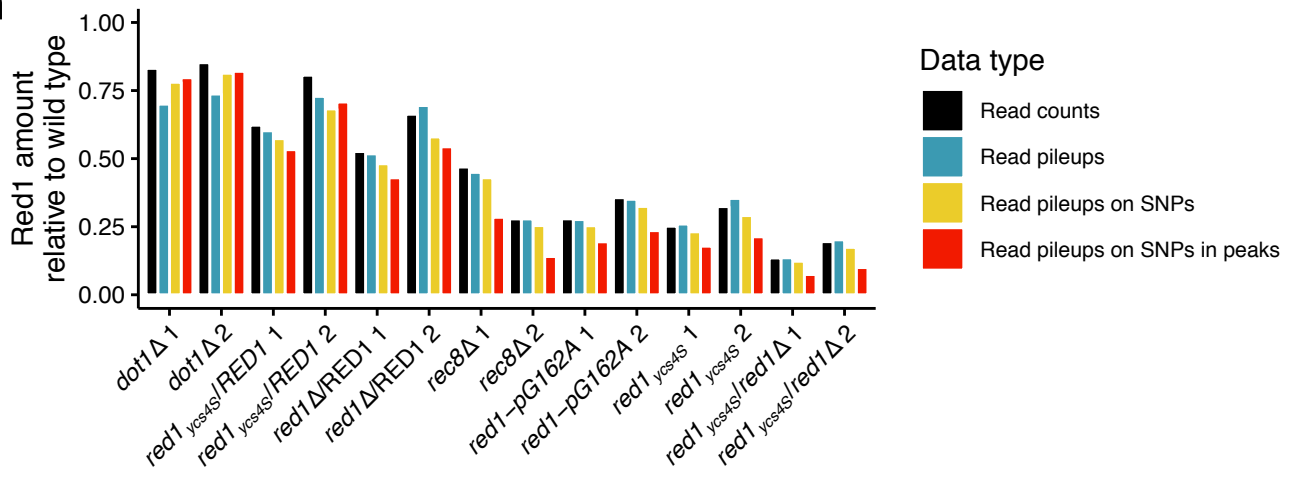
Strain name	Genotype	Back ground	Reference	Figures
NKY1551	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/”, leu2::hisG/”, his4B::LEU2/his4X::LEU2(Bam)-URA3, arg4-BglII/arg4-Nsp</i>	SK1	<sup>1</sup>	All figures
H7011	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/URA3, leu2::hisG/LEU2, his3::hisG/HIS3, trp1::hisG/TRP1, red1<sub>ycs4S</sub>/red1<sub>ycs4S</sub></i>	SK1	<sup>2</sup>	1, 4, S2
H8218	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/URA3, leu2::hisG/LEU2, his3::hisG/HIS3, trp1::hisG/TRP1, red1<sub>ycs4S</sub>/RED1</i>	SK1	<sup>2</sup>	1, 4, S2
H8219	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/URA3, leu2::hisG/LEU2, his3::hisG/HIS3, trp1::hisG/TRP1, red1<sub>ycs4S</sub>/red1Δ::KanMX4</i>	SK1	<sup>2</sup>	1, 4, S2
H8220	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/URA3, leu2::hisG/LEU2, his3::hisG/HIS3, trp1::hisG/TRP1, red1Δ::KanMX4/RED1</i>	SK1	<sup>2</sup>	1, 4, S2
H9048	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/URA3, leu2::hisG/LEU2, his3::hisG/HIS3, trp1::hisG/TRP1, HphMX4::red1-pG162A/HphMX4::red1-pG162A</i>	SK1	<sup>2</sup>	2, S2, S3
H4206	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/”, leu2::hisG/”, his4B::LEU2/his4X::LEU2(Bam)-URA3, arg4-BglII/arg4-Nsp spo11-Y135F-HA::URA3/spo11-Y135F-HA::URA3</i>	SK1	This study	4
H8104	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/URA3, leu2::hisG/LEU2, his3::hisG/HIS3, trp1::hisG/ trp1::hisG, dot1Δ::TRP1/dot1Δ::TRP1</i>	SK1	This study	S2, S4
H8151	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/”, leu2::hisG/”, his4B::LEU2/his4X::LEU2(Bam)-URA3, arg4-BglII/arg4-Nsp rec8::HIS3/rec8::HIS3</i>	SK1	This study	3, S2
H8583	<i>MATa/MATa, ho::LYS2/”, lys2/”, ura3/URA3, leu2::hisG/LEU2,</i>	SK1	This study	S4

	<i>trp1::hisG/'</i> , <i>dot1Δ::TRP1/dot1Δ::TRP1</i> <i>set1Δ::KanMX6/set1Δ::KanMX6</i>			
H8584	<i>MATa/MATα</i> , <i>ho::LYS2/'</i> , <i>lys2/'</i> , <i>ura3/URA3</i> , <i>leu2::hisG/LEU2</i> , <i>set1Δ::KanMX6/set1Δ::KanMX6</i>	SK1	This study	S4
H9120	<i>MATa/MATα</i> , <i>ho::LYS2/'</i> , <i>lys2/'</i> , <i>ura3/URA3</i> , <i>leu2::hisG/LEU2</i> , <i>his3::hisG/HIS3</i> , <i>trp1::hisG/'</i> , <i>hop1::LEU2/hop1::LEU2</i>	SK1	This study	3
H8644	<i>MATa/MATα</i> , <i>his3Δ1/his3Δ1::pRS303::HIS3</i> , <i>leu2Δ0/leu2Δ::pRS305::LEU2</i> , <i>lys2Δ0/lys2Δ::pRS307::LYS2</i> , <i>ura3Δ0/URA3(SK1)</i> , <i>RME1(ins-308a)/RME1(ins-308a)</i> , <i>TAO3(E1493Q)/TAO3(E1493Q)</i> , <i>MKT1(D30G)/MKT1(D30G)</i>	S288c	This study	All figures

## Supplementary References

- 1 Bishop, D. K., Park, D., Xu, L. & Kleckner, N. *DMC1*: a meiosis-specific yeast homolog of E. coli recA required for recombination, synaptonemal complex formation, and cell cycle progression. *Cell* **69**, 439-456 (1992).
- 2 Markowitz, T. E. *et al.* Reduced dosage of the chromosome axis factor Red1 selectively disrupts the meiotic recombination checkpoint in *Saccharomyces cerevisiae*. *PLoS Genet* **13**, e1006928, doi:10.1371/journal.pgen.1006928 (2017).



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