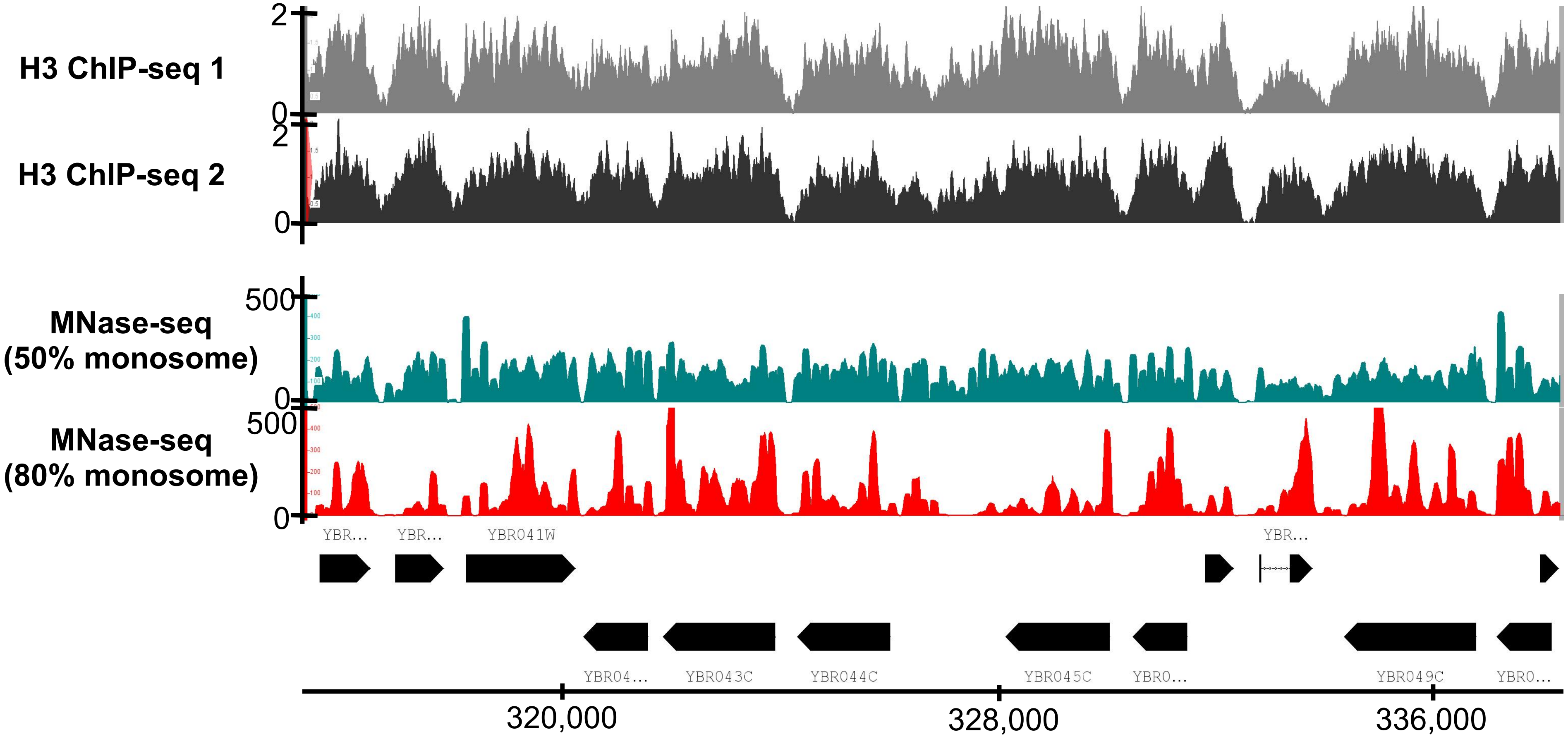
H3 ChIP-seq 1
2
0
H3 ChIP-seq 2
2
0
MNase-seq (50% monosome)
500
0
MNase-seq (80% monosome)
500
0
YBR...
YBR...
YBR041W
YBR...
YBR04...
YBR043C
YBR044C
YBR045C
YBR0...
YBR049C
YBR0...
320,000
328,000
336,000

Figure S1

Supplemental Figure S1. The nucleosome signals in MNase-seq data are highly sensitive to the strength of MNase digestion. Top 2 panels show two independent histone H3 ChIP-seq data, demonstrating the reproducibility. The two MNase-seq data are from the same strain but with two different strengths of MNase digestion. Note that the nucleosome positions are reproducible between the two conditions, but the heights of nucleosome signals, especially around NDRs, are highly variable between the two conditions. All data are from (McKnight et al. 2015).