

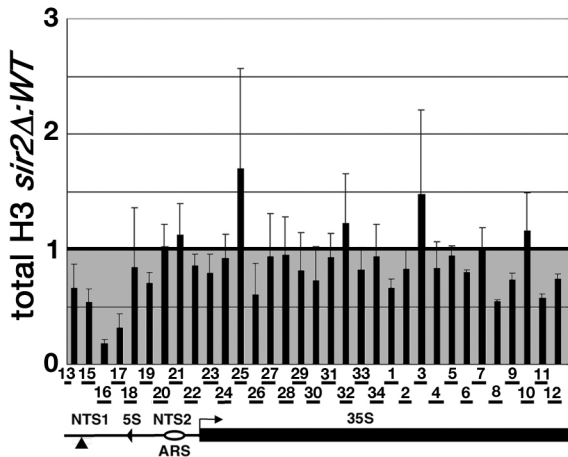
Supplemental Figure Legends

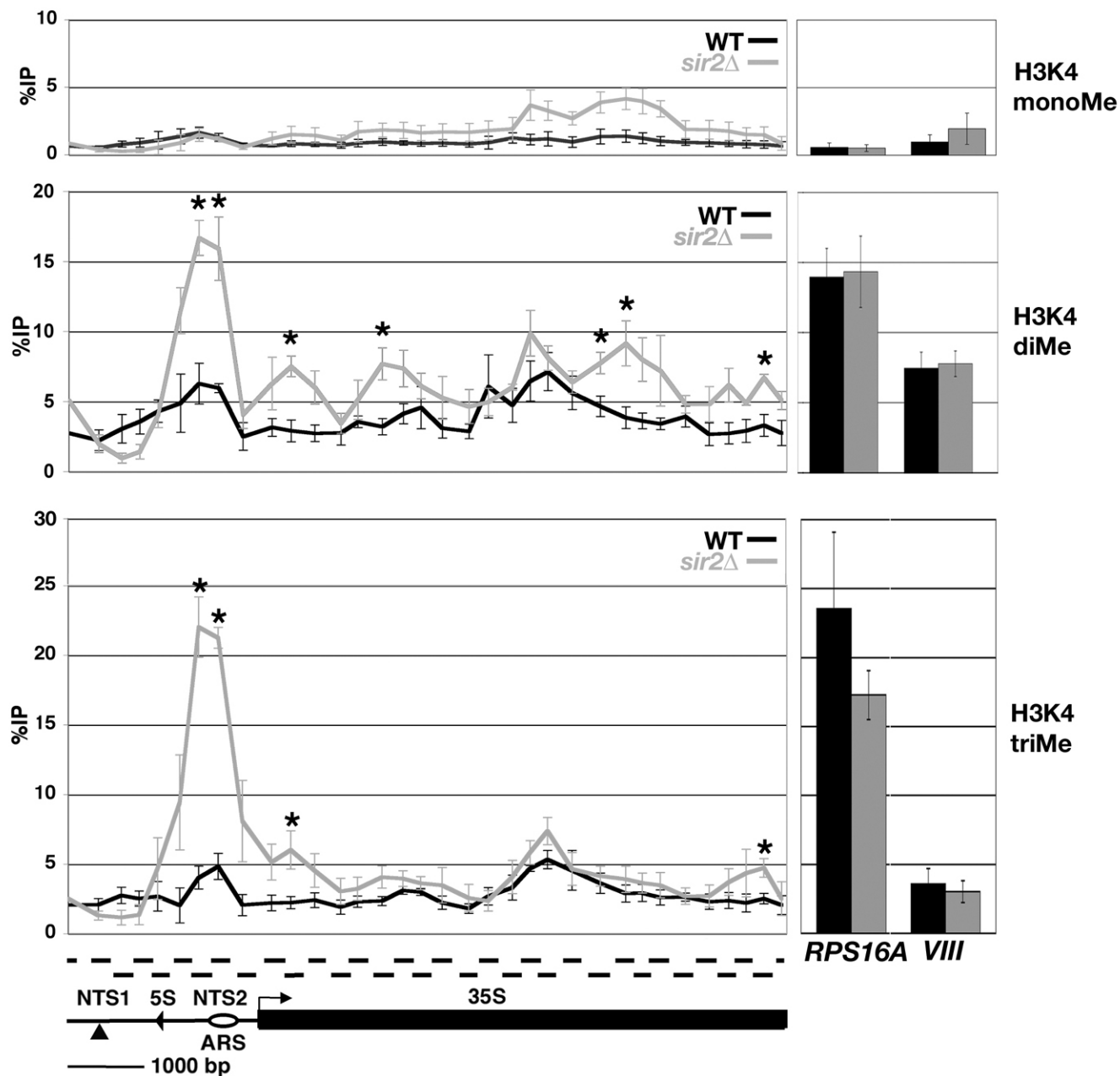
Figure S1. Cells lacking Sir2 have significantly lower levels of histone H3 at several positions in the rDNA repeat. Graphical representation of the average ratio of %IP of histone H3 in *sir2Δ* cells (MBY1238) relative to wild type cells (MBY1198) at the rDNA. The structure of an rDNA repeat unit is shown below the bottom panel with the Pol I-transcribed 35S ribosomal RNA (35S) gene and a non-transcribed spacer divided into NTS1 and NTS2 by the Pol III-transcribed 5S rRNA gene (5S). ARS, replication origin; bent line with arrow, transcription start site of the 35S rRNA gene; ▲, location of a silenced Ty1*his3AI* element present in one repeat. Horizontal numbered lines above the rDNA indicate PCR products generated during the analysis of ChIP experiments by quantitative real-time PCR. The average ratio of % IP +/-range from *sir2Δ* cells to wild-type cells from two independent experiments is plotted.

Figure S2. The levels of K4 di- and trimethylated histone H3 in the rDNA repeat are increased significantly in *sir2Δ* cells. Graphical representations of % IP of K4-monomethylated (top; +/- range; N = 2 or 3), K4-dimethylated (middle; +/- SE; N = 3), and K4-trimethylated (bottom ; +/- SE; N = 4) histone H3 with the rDNA, the *RPS16A* gene, and an intergenic region of chr *VIII* (*VIII*) in wild type (black line and bars) and *sir2Δ* cells (gray lines and bars). The plotted values have not been normalized to total histone H3 levels, which are reduced at the rDNA repeat in cells lacking Sir2 (See Figure S1). Asterisks, regions of the rDNA with significantly higher levels of K4-di- (middle panel) or trimethylated (bottom panel) H3 in *sir2Δ* cells compared to wild-type cells, as determined by Student's t-test ($P < 0.05$). Levels of K4-monomethylated H3 in wild type

and *sir2Δ* cells are not significantly different. The structure of a 9.1 kb rDNA unit is shown below the bottom panel (labels as in legend to Figure S1).

Figure S3. ChIP with anti-Sir2 antisera show that the levels of Sir2 protein are similar at the rDNA in cells containing p*SIR2* and *psir2H364Y*. Graph showing the average ratio of %IP of Sir2 (+/- SE; N = 3) across a region of the rDNA repeat in *psir2H364Y/pSIR2* cells. %IP values from *sir2Δ* cells containing an empty vector were subtracted from the %IP values to correct for background. The regions of the rDNA analyzed include the 2.5 kb NTS and 1.4 kb of the 35S rRNA gene. Labels for representation of rDNA repeat as in legend to Figure S1.





Li_Figure S3

