Figure S3. **Percentage of non-uniquely mapping reads from ChIP-Seq experiments at all thirty-two telomeres.** Reads that mapped non-uniquely in the Sir4 input dataset from (THURTLE and RINE 2014) were determined by those reads with a MAPQ flag of 0. The number of reads that mapped non-uniquely at that base-pair position was determined and divided by the total number of reads that mapped at that position. This percentage of non-uniquely mapped reads was plotted for each telomere. 20 kbp for each telomere is shown. Salient features as annotated in SGD are indicated below the X-axis for each telomere as in Figure 2. The light gray rectangles indicate regions deleted in the sequenced W303 derived lab strain relative to the SGD sacCer2 reference genome.

Ellahi *et al.*