



Figure S2. No tag ChIP-Seq control at all thirty-two yeast telomeres. The IP/Input enrichment values of the no tag ChIP-Seq dataset from (THURTLÉ and RINE 2014) was mapped at all thirty-two *S. cerevisiae* telomeres. 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.