Figure S1. PRO-seq and PRO-cap capture transcription elongation and initiation genome-wide in *S. cerevisiae*. A. Browser tracks of PRO-seq (plus strand: red; minus strand: blue) and PRO-cap data (plus strand: green; minus strand: yellow) derived from *S. cerevisiae*. Green gene models show the re-annotated, 'observed' transcription start-sites based on PRO-cap data. Blue gene models correspond to the longest major transcript isoform identified by (Pelechano et al. 2013). B. Heatmaps of *S. cerevisiae* PRO-cap signal for each base within +/- 250 bp around either the annotated TSS (left) or PRO-cap-observed TSS (right) for all active and filtered genes (N = 3403). Genes within heatmaps...
are sorted by increasing downstream distance of observed TSS relative to annotated TSS.  
C. Sequence logos of 10 bp sequence centered on annotated TSS (left) and observed TSS (right) were generated using WebLogo (Crooks et al. 2004).  
D. Median PRO-cap signal from samples prepared either with or without Tobacco Acid Pyrophosphatase (TAP) treatment centered on annotated TSS. The TAP-minus samples represent empirical levels of background for each genomic position.  
E. Median PRO-cap signal from samples prepared either with or without TAP treatment centered on observed TSS.  
F. Median MNase-seq coverage centered on annotated TSSs (blue) or observed TSSs (brown). For the meta-gene plots, the y-axis shows the median read counts for each base-pair (D & E), or median read coverage within 10 bp bins (F). In figures D, E and F, the 12.5% and 87.5% quantiles are shown in lightly shaded regions.