



Figure S5. Comparison of PRO-seq in yeast with other methods of mapping Pol II positions genome-wide. **A.** Composite profiles of *S. cerevisiae* PRO-seq (top) or NET-seq data (bottom) (GEO accession: GSM617027)(Churchman and Weissman 2011) relative to the observed TSS or CPS (N = 1614). **B.** Composite profiles of *S. pombe* PRO-seq (top) or Pol II ChIP-seq data (bottom) (GEO accession: GSM1202003)(DeGennaro et al. 2013) for not-paused (N = 2088), paused (N = 656), and all genes (N = 3214) relative to the observed TSS (left) or CPS (right).