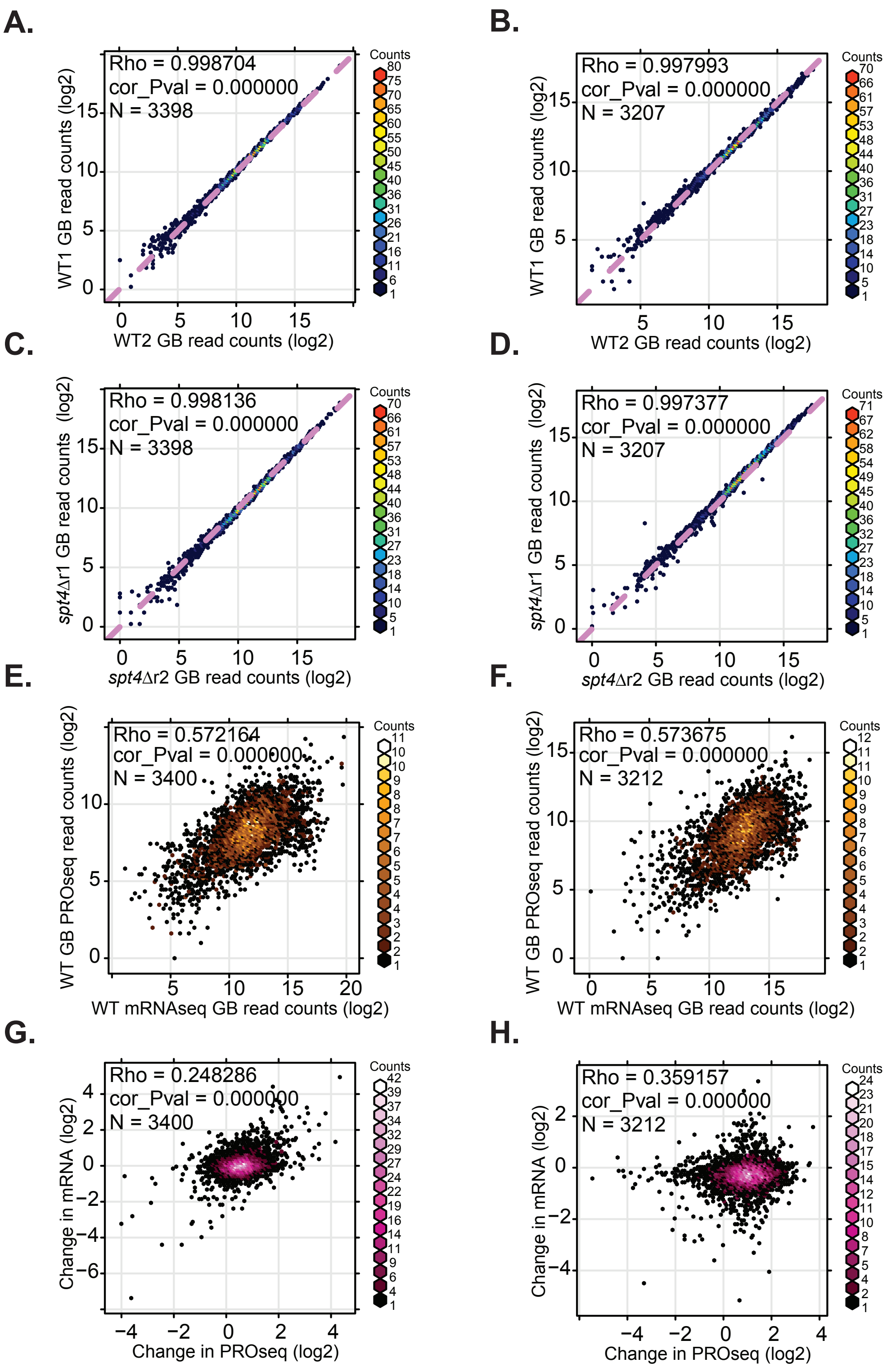

Figure S9: mRNA abundance is not as affected by deletion of Spt4 as nascent transcription in *S. cerevisiae* and *S. pombe*. A-D. Scatter plots of mRNA-seq gene-body read counts between biological replicates. Read counts were normalized based on the relative amount of reads that align uniquely to the spiked-in genome for each library.

E, F. Correlations between nascent RNA production (PRO-seq) and mRNA abundance (mRNA-seq), assayed as normalized read counts within the gene bodies of *S. cerevisiae* (E.) and *S. pombe* genes (F.). **G, H.** Scatter plots comparing $\log_2$ fold change *spt4Δ* vs. wild type in gene body read density as assayed by mRNA-seq and PRO-seq for *S. cerevisaie* (G.) and *S. pombe* (H.). All correlation values reflect Spearman's ρ.