A) H3K56ac/H3 at RPS11B (+731)

B) H3K56ac/H3 at InterV (non-transcribed)

C) H3K56ac/H3 at PMA1 corrected on non-transcribed locus

D) H3K56ac/H3 in G1
**Supplemental Figure S7: Eaf7 suppresses histone exchange linked to transcription.**

(A-B) ChIP-qPCR analysis of histone exchange on the coding region of the transcriptionally active *RPS11B* gene and a non-transcribed intergenic region using the H3K56ac versus total H3 signal ratio after blocking the cells in G1 with alpha factor. (C) transcription-coupled histone exchange is similarly affected by the *eaf7* and *spt16* mutants. Since Spt16 is known to affect global histone exchange/nucleosome stability, relative replication-independent transcription-dependent new histone incorporation was measured by correcting H3K56ac/H3 signals at *PMA1* (from Fig. 7E) with the signals at the non-transcribed locus (from supFig. 7B) (H3K56ac/H3 at PMA1 divided by H3K56ac/H3 at InterV). (D) Combining *eaf7* and *spt16* mutants does not lead to higher histone exchange. H3K56ac/H3 signals were measured in G1-blocked cells of the indicated strains, after incubation for 1hr at 37°C.