Expanded View Figures

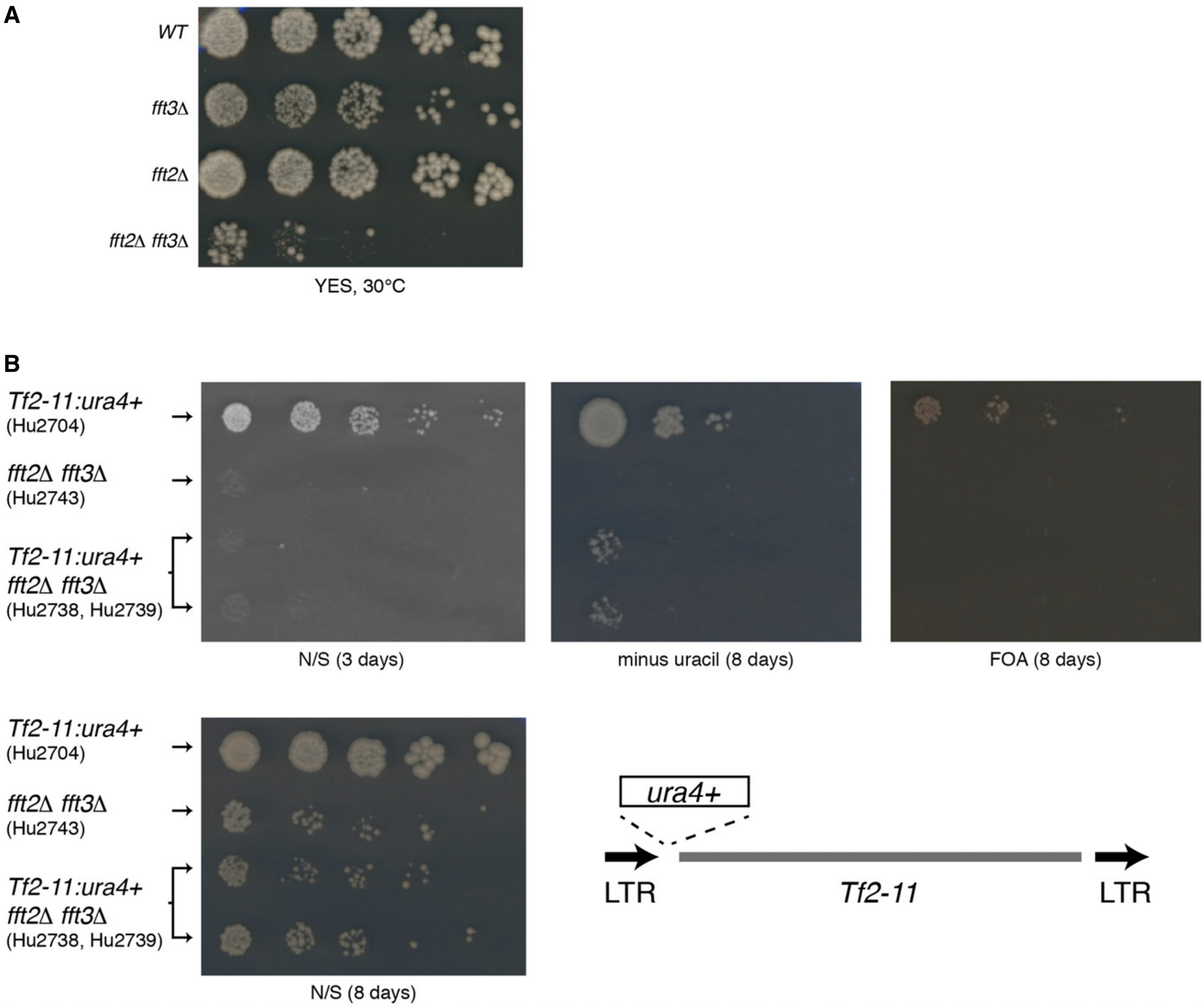

Figure EV1. Slow growth phenotype and *Tf2* element derepression in *fft2*Δ *fft3*Δ cells.

- A WT (Hu0029), *fft2*Δ (Hu1955), *fft3*Δ (Hu1867), and *fft2*Δ*fft3*Δ (Hu2000) cells were grown to log phase, spotted on YES media in fivefold serial dilutions, and grown at 30°C.
- B Fivefold dilutions of cells grown to log phase were spotted on nonselective (N/S), selective (minus uracil), or counterselective (FOA) media. Plates were incubated at 30°C for 3 days (N/S) or 8 days (minus uracil, FOA). Schematic shows the location of the *ura4+* insert, upstream of the *Tf2-11* translation start codon.

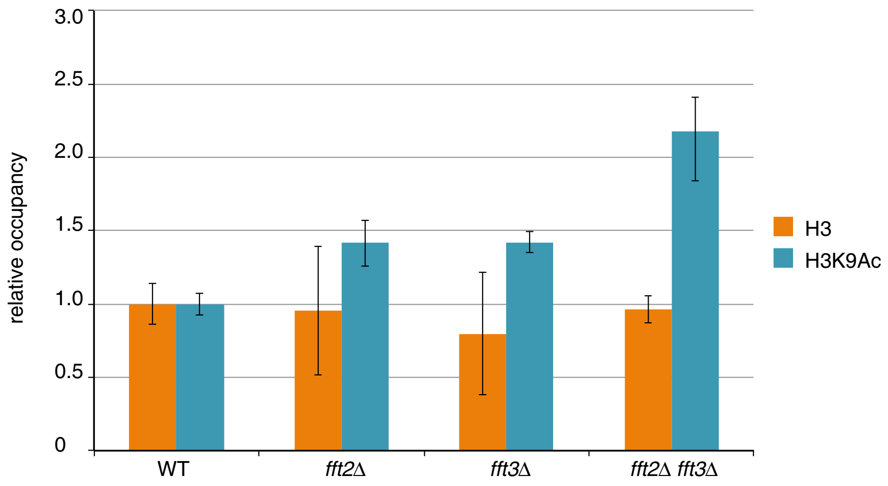

Figure EV2. Transcription-associated histone mark elevated in *fft2* and *fft3* mutants.
Acetylation of H3K9 is elevated at Tf2 elements in *fft2Δ*, *fft3Δ*, and *fft2Δ fft3Δ*. Error bars represent the standard deviation of biological triplicate samples. Occupancy is relative to a control gene (SPAC1F8.07c) promoter and to WT.

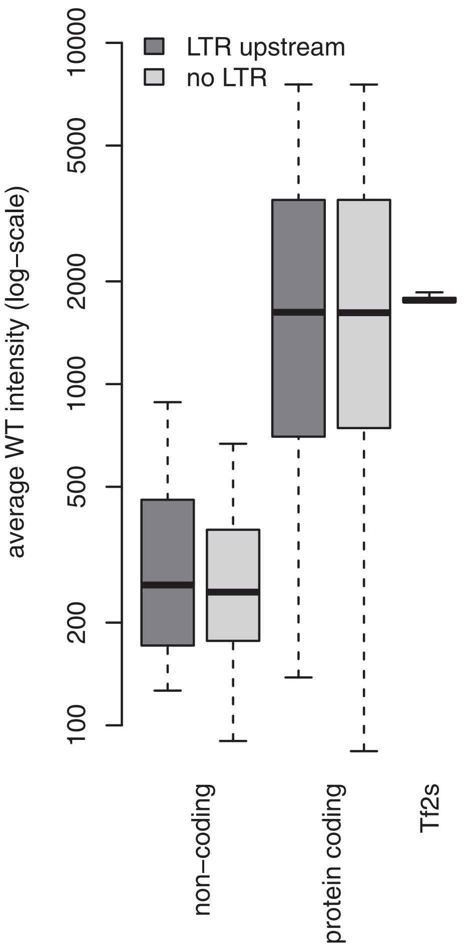

Figure EV3. Genes with an upstream LTR are not repressed in WT cells.
Transcripts with an upstream LTR are neither more nor less abundant than transcripts without an upstream LTR. Average signal intensity across genes of wild-type RNA hybridized to tiling array shown as box plot for each of the following categories: noncoding with LTR (n = 69)/without LTR (n = 1,665); protein coding with LTR (n = 246)/without LTR (n = 4,887); *Tf2*s (n = 13).

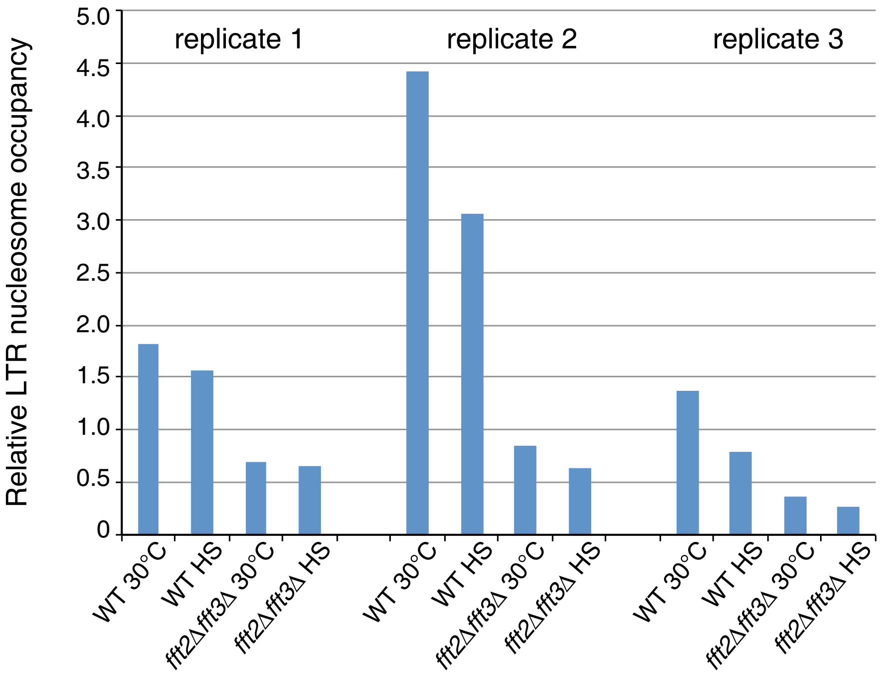

Figure EV4. LTR nucleosome occupancy is reduced upon heat shock.

This reduction is more pronounced in WT cells than in *fft2*Δ *fft3*Δ cells. LTR nucleosome occupancy shown relative to occupancy of the *Tf2* ORF + 1 nucleosome, measured by qPCR.

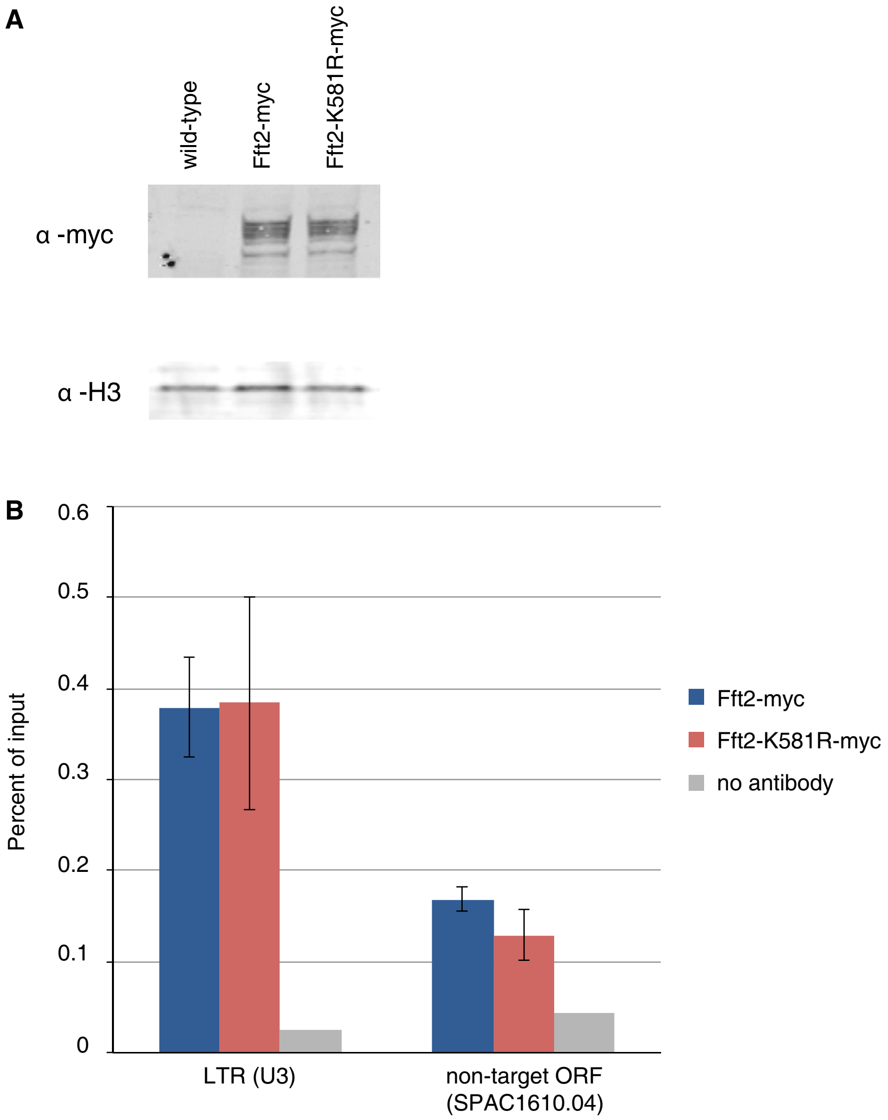

Figure EV5. Fft2-K581R-myc is expressed and binds to chromatin at WT levels.

- A Whole-cell lysates, including an epitope-free WT control, were immunoblotted with α-myc, to determine Fft2 expression level, and with α-H3, to confirm equal loading.
- B Chromatin immunoprecipitation indicates that Fft2-K581R-myc is recruited to LTR elements to the same degree as functional Fft2-myc. Results are shown as percent input, and a no-antibody control indicates the level of nonspecific protein A binding. Error bars reflect technical duplicates of biological duplicates.