

Figure S1. Spores harbor antisense transcripts to many “mating-type-specific” genes. RNA-seq reads from spores sorted by mating type were mapped onto the genome in a strand-specific manner. Biological replicates are numbered as “#1” and “#2”. For all but *DDR2*, the y axis scale is the same for both strands, as indicated by the numbers at top right of each plot.

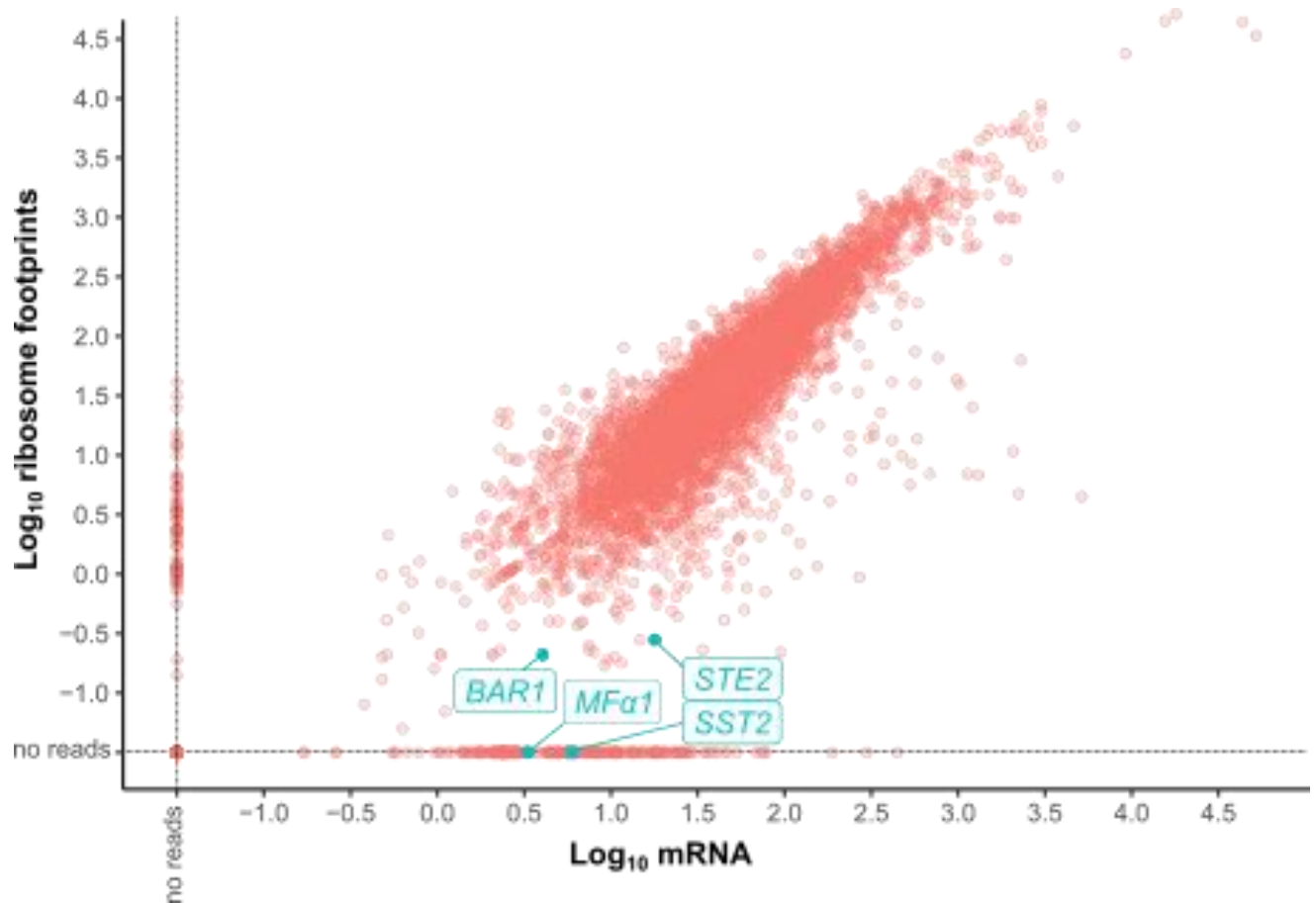


Figure S2. Limited translation in spores of mating-type-specific transcripts. Published transcriptome-wide RNA-seq and ribosome profiling data [6] from the final (18-hour) time point of synchronous sporulation using the traditional synchronization method were retrieved from the GEO database (GSM843742 and GSM843775) and plotted against each other after taking the \log_{10} value for each transcript. For values that were 0, the \log_{10} value is undefined, so these transcripts were assigned values of -1.5 for plotting purposes, and are marked here as “no reads”.

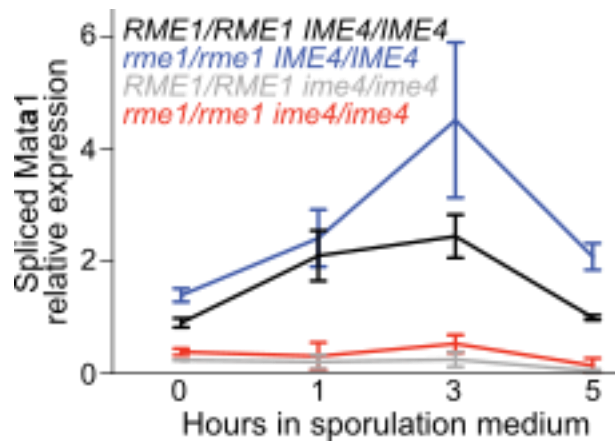


Figure S3. m⁶A methylation promotes Mata1 induction during sporulation.

Quantitative RT-PCR was used to quantify at each time point the amount of spliced Mata1 relative to Act1. Ratios were normalized to *RME1/RME1 IME4/IME4* at time point 0. “*RME1*” refers to the ins-308A insertion polymorphism in the *RME1* upstream region. “*rme1*” refers to the allele found in S288C-background strains that increases *RME1* expression [15]. “*RME1/RME1 IME4/IME4*” and “*RME1/RME1 ime4/ime4*” are the same strains as in Figure 3a. “*rme1/rme1 IME4/IME4*” and “*rme1/rme1 ime4/ime4*” are strains GBy222 and GBy225. Plot symbols show means and standard deviations from three biological replicates.