

## SUPPLEMENTAL FIGURE LEGEND

**Figure S1. The K-S statistic can distinguish between initiation and elongation-limitation for transcripts with low read coverage.** (A) Plot showing K-S statistic values for simulated ribosome footprints on initiation limited mRNAs using the inhomogenous I-TASEP model as a function of read density. (B,C) Plots showing K-S statistic values for simulated ribosome footprints with varying read densities which are derived from elongation-limited mRNAs with a (B) weak pause (minimal elongation rate is just rate-limiting) and (C) a strong pause (twice the strength of the weak pause).

**Figure S2. No enrichment for putative FMRP binding motifs among translationally downregulated proteins in the *Fmr1* KO mouse cortex.** (A) Plot showing the fold-enrichment of SFARI class I, class II and syndromic genes and genes encoding large proteins > 1,800 amino acids among the top 200 translationally downregulated genes in the *Fmr1* KO cortex. (B) Box plots showing that the raw number of putative FMRP binding sequences are similarly enriched among translationally downregulated genes in the *Fmr1* KO mouse cortex as a random 4-mer sequence. (C) Box plots showing that the density of putative FMRP binding sequences are statistically identical for downregulated genes and non-downregulated genes encoding large proteins in the *Fmr1* KO mouse cortex.

## TABLE LEGENDS

**Supplementary Table 1. Compiled RiboDiff output for *Fmr1* RNAi *Drosophila* oocyte and *Fmr1* KO mouse cortex analyses.**

**Supplementary Table 2. ClinGen haploinsufficiency scores for *Drosophila* orthologs of SFARI Class I, Class II, and syndromic autism genes translationally downregulated in**

**oocytes.**

**Supplementary Table 3. Compiled K-S statistic values for *Drosophila* and mouse *Fmr1* ribosome profiling analyses.**

**Supplementary Table 4. Compiled unprocessed gene expression data for *Drosophila* and mouse *Fmr1* ribosome profiling and RNA-seq experiments.**

**Supplementary Table 5. P-site offsets used for processing human, mouse, and *Drosophila* ribosome profiling data.**

These tables are provided separately as Excel files.

Figure S1

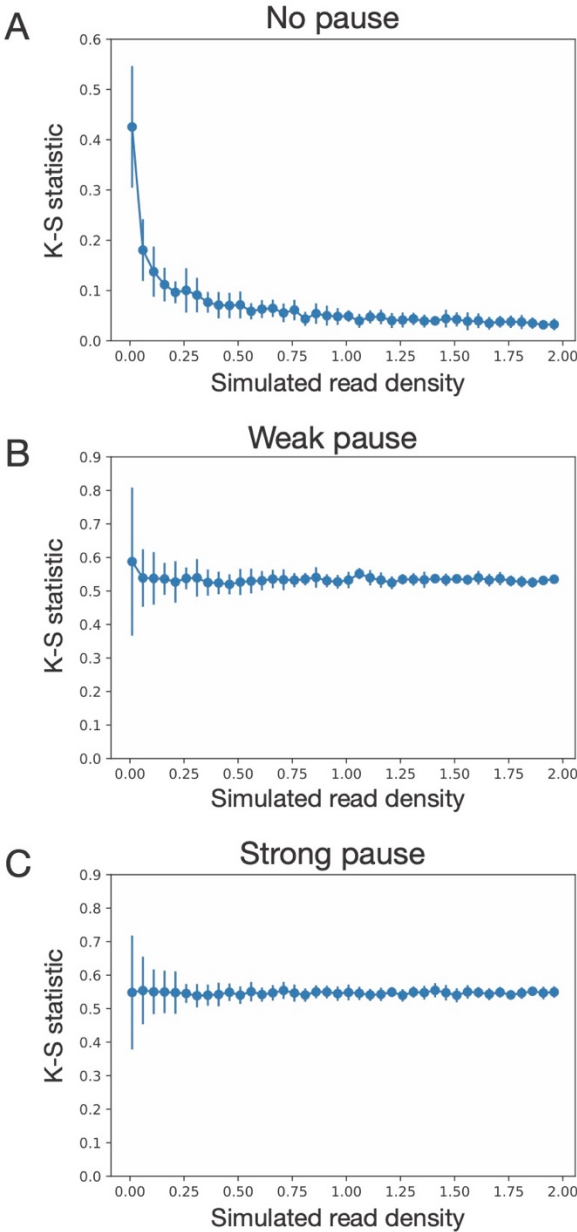


Figure S2

