

Figure S1

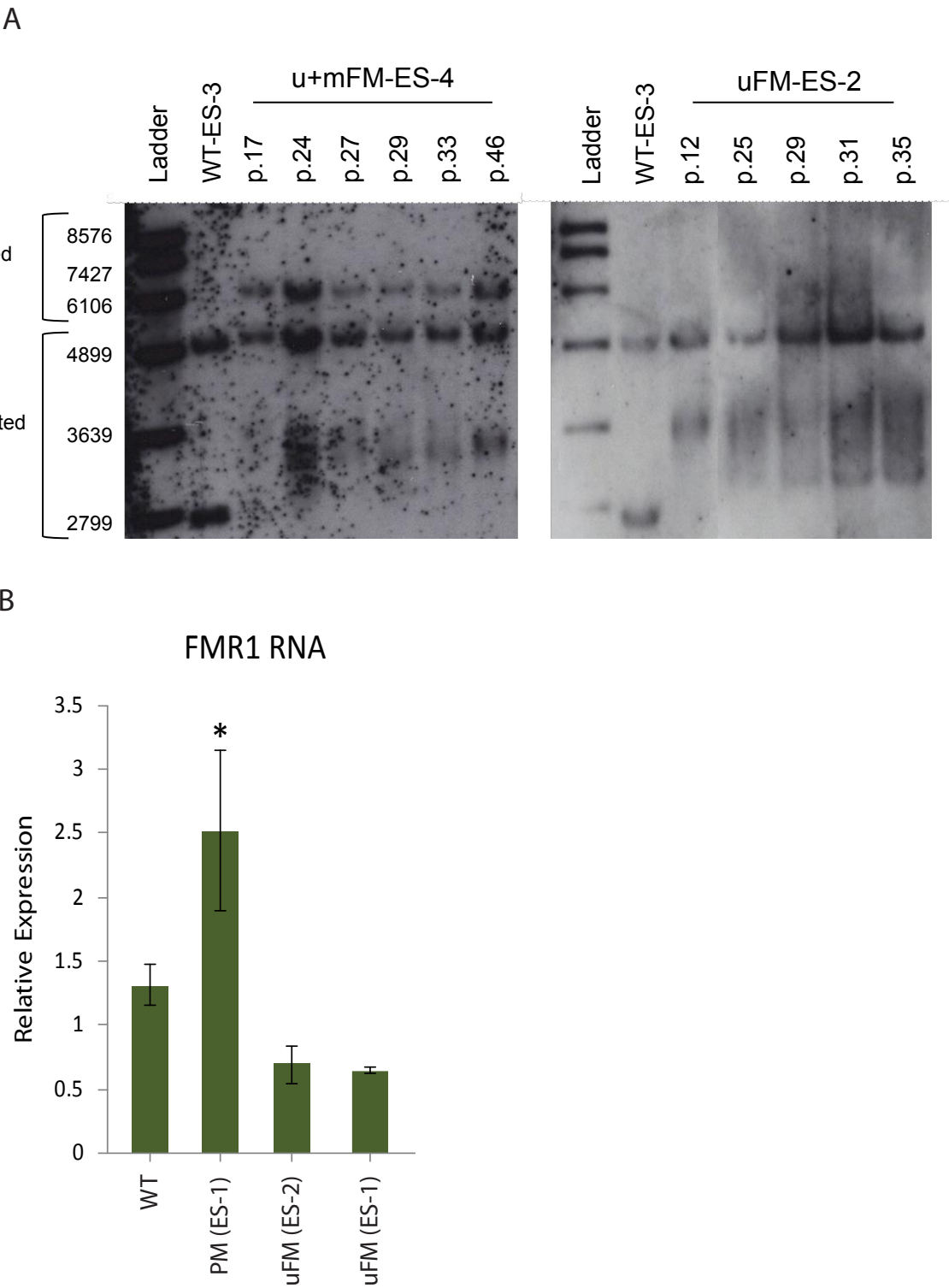


Figure S1. (A) Southern blot analysis of unmethylated FX hESC lines. Methylation-sensitive Southern blot analysis of two XX FX hESC lines (u+mFM-ES-4 and uFM-ES-2) during continuous growth in culture. This served to differentiate between unmethylated normal (2.8 kb), premutation (2.9–3.4 kb), and full-mutation alleles (3.4–5.8 kb) and their methylated counterparts, as indicated by 5.2 kb, 5.3–5.8 kb, and fragments larger than 5.8 kb, respectively. Note the tight inverse correlation between methylation and repeat instability in the full mutation range. (B) Relative expression levels of *FMR1* RNA in the hESCs by Taqman qRT-PCR. The expression level in each cell line represents an average of 3–4 independent experiments. Cycle threshold (Ct) values were normalized to the corresponding Ct value of *GUS*. Error bars represent SE (t test for equal variances, * $p < 0.05$). For cell lines specifications and expansion size see Table S1.