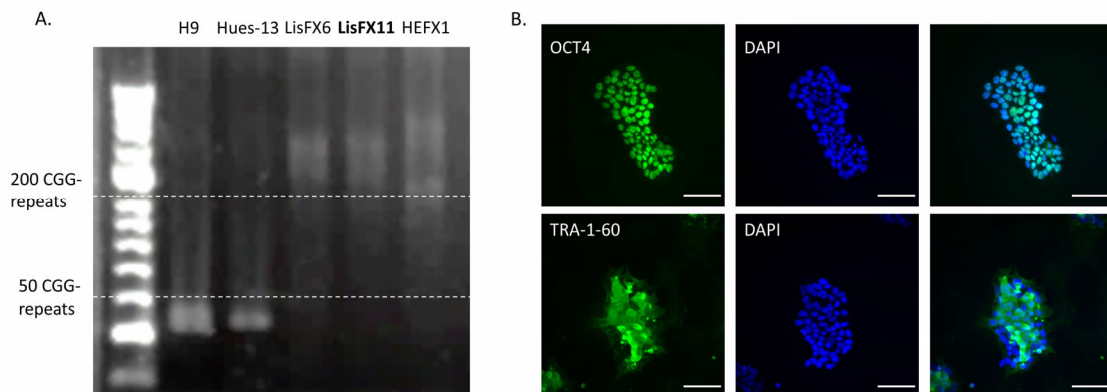


Supplementary Figure S1. Identification of non-human RNA in two of the samples. **(A)** PCA of 13 and 23 DIV samples. Samples suspected of including impure cell population are marked in red. **(B)** Breakdown of sequencing reads by quality and alignment metrics. **(C)** The taxonomic classification of reads that were not mapped to the reference genome. Including reads omitted due to non-unique alignment.



Supplementary Figure S2. Characterization of FX-hESC line **(A)** Analysis of the CGG repeat size by PCR-based repeat-number assay of three different FX-hESC lines used in Fig. 1A. **(B)** Expression of pluripotent genes (OCT4 and TRA-1-60; green) in Lis-FX11. Cell nuclei were stained blue by DAPI. Scale bar: 100 μ m.