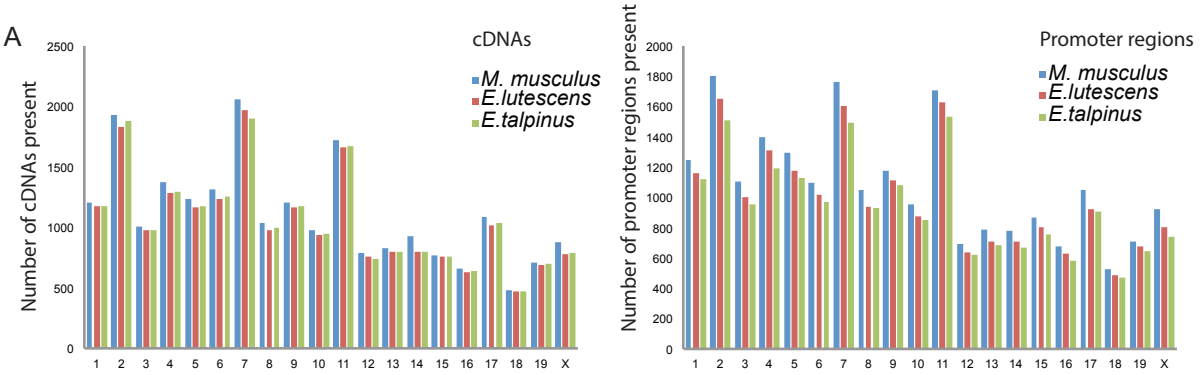

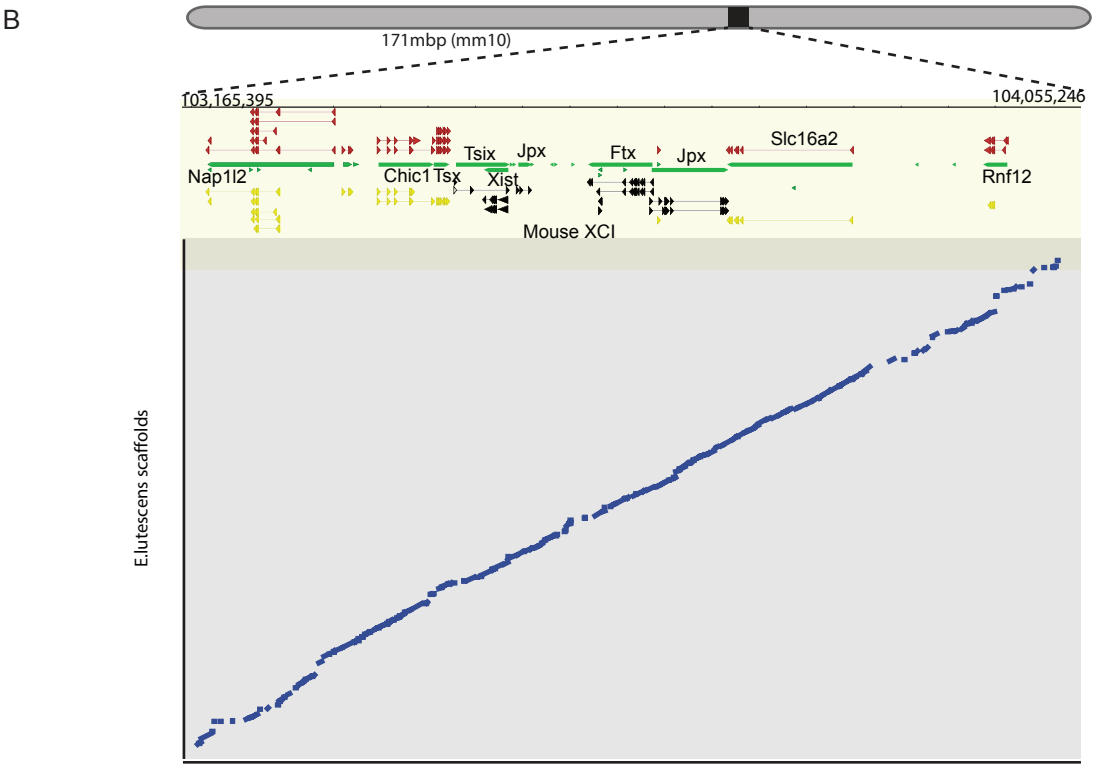

C

		E. lut Xist	E. tal Xist	M. mus Xist	R. nor Xist
		1	2	3	4
E. lut Xist	1	100	93.40	55.73	56.30
E. tal Xist	2		100	56.03	56.62
M. mus Xist	3			100	72.90
R. nor Xist	4				100

Supplemental Figure S7: Comparable conservation of *E. lutescens* and *E. talpinus* X Chromosome structure and gene content

A) Comparison of coding sequences (CDS, left) and promoter regions (right) of *E. lutescens* and *E. talpinus* to the mouse genome. For the CDS comparison, 88,366 mouse CDS sequences were obtained from Ensembl and blasted against *E. lutescens* and *E. talpinus* genomes, resulting in 22,658 genes that could be compared. We then scored for presence or absence (or extreme divergence) by setting an e-value threshold (>10^{-5} was considered absent), and counted the number of genes for each mouse chromosome. For the promoter comparison, 26,849 mouse sequences that are 1000 bp upstream of coding regions were obtained from Ensembl. After removing sequences that are at the same position and predicted genes, 19,761 sequences were blasted against the genomes of *E. lutescens* and *E. talpinus*. We then scored for presence or absence (or extreme divergence) by setting an e-value threshold as described for the CDS comparison and counted the numbers per mouse chromosome.

B) Conservation of the X-inactivation center. Scaffolds carrying the XCI region were merged and aligned to mouse XCI region using LASTZ. Blue line is alignment from forward strand (~900kb region).

C) Percentage identity of *Xist* genomic DNA compared between *E. lutescens*, *E.talpinus*, mouse and rat.