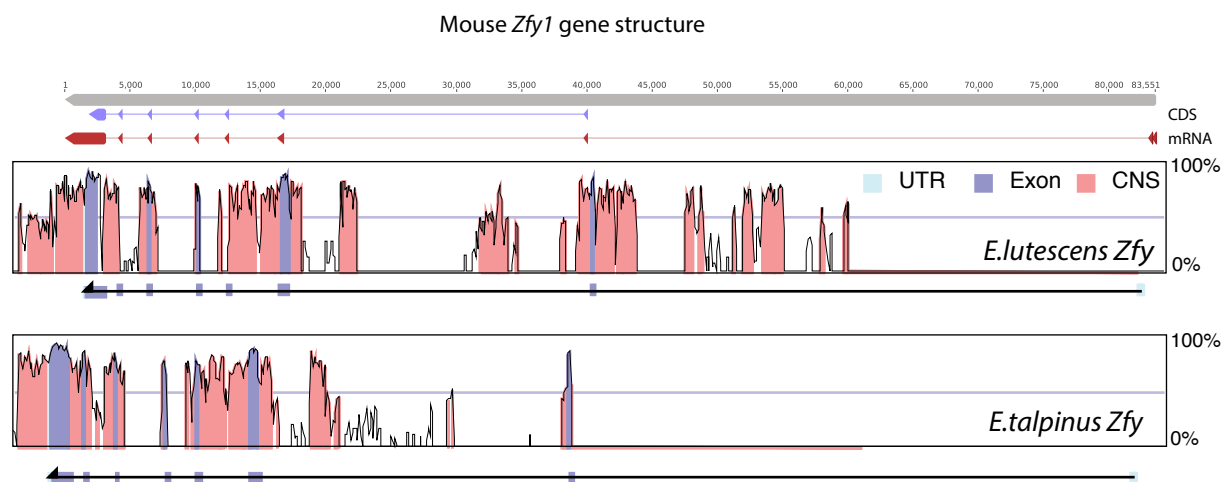
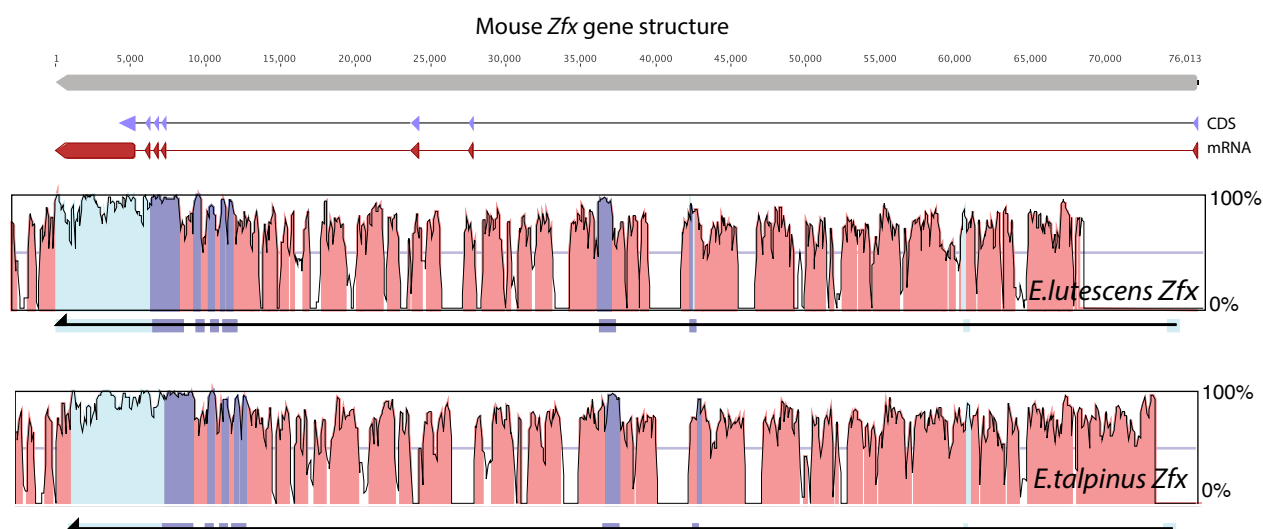


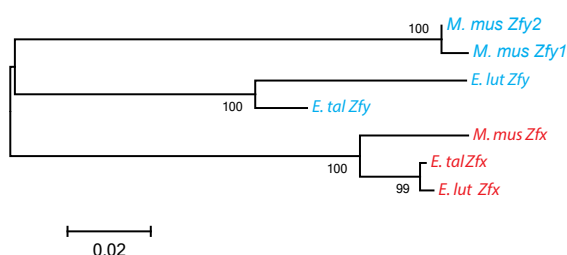
A



B



C



D

	<i>E. lut Zfy</i>	<i>E. tal Zfy</i>	<i>M. mus Zfy1</i>	<i>M. mus Zfy2</i>	<i>E. lut Zfx</i>	<i>E. tal Zfx</i>	<i>M. mus Zfx</i>
1	100	94.14	81.83	79.88	81.98	81.98	80.93
2		100	84.53	82.58	84.83	84.83	83.78
3			100	81.98	81.98	81.98	81.53
4				100	80.18	80.33	79.88
5					100	99.40	95.80
6						100	95.80
7							100

Supplemental Figure S2: Conservation of *E. lutescens* and *E. talpinus* *Zfy* and *Zfx* genes

A) *E. lutescens* and *E. talpinus* *Zfy* orthologous regions compared to mouse *Zfy*. The mouse *Zfy* gene structure, longest mRNA and coding sequences (CDS) are shown on top. The gVISTA (<http://genome.lbl.gov/>) software package was used to find the *E. lutescens* and *E. talpinus* *Zfy* orthologous regions in mouse. In gVISTA, query sequence contigs are anchored on the base genome by local alignment matches (Kent 2002) and then globally aligned to candidate regions using the AVID program (Bray et al. 2003; Couronne et al. 2003). The Y-axis shows the percentage of sequence identity of *E. lutescens* or *E. talpinus* *Zfy* to that of mouse *Zfy* sequences. UTR, exons and non coding regions are shown in different colors (exons: dark blue, UTRs: light blue: non-coding: pink). Gaps indicate genome assembly gaps or not conserved regions.

B) *E. lutescens* and *E. talpinus* *Zfx* orthologous regions compared to mouse *Zfx*. The mouse *Zfx* gene structure, longest mRNA and CDS are shown on top. Alignment was performed as described in a). The Y-axis shows the percentage of sequence identity of *E. lutescens* or *E. talpinus* *Zfx* to that of mouse *Zfx* sequences. UTR, exons and non coding regions are shown in different colors (exons: dark blue, UTRs: light blue: non-coding: pink). Gaps indicate genome assembly gaps or not conserved regions.

C) Phylogenetic relationship between *E. lutescens* and *E. talpinus* *Zfy* and *Zfx* and mouse *Zfy1*, *Zfy2*, and *Zfx* genes (based on a 10 kb genomic region). Bootstrap values are shown on four nodes.

D) Alignment percentage identity of *E. lutescens* and *E. talpinus* *Zfy* and *Zfx* with mouse *Zfy1* and *Zfy2* and *Zfx*.

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