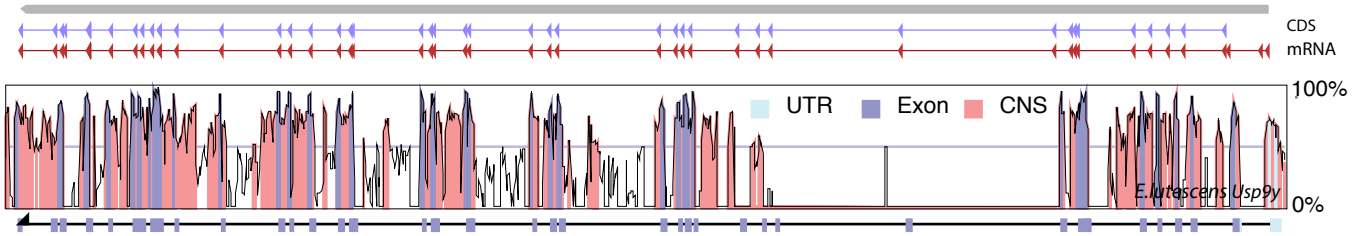
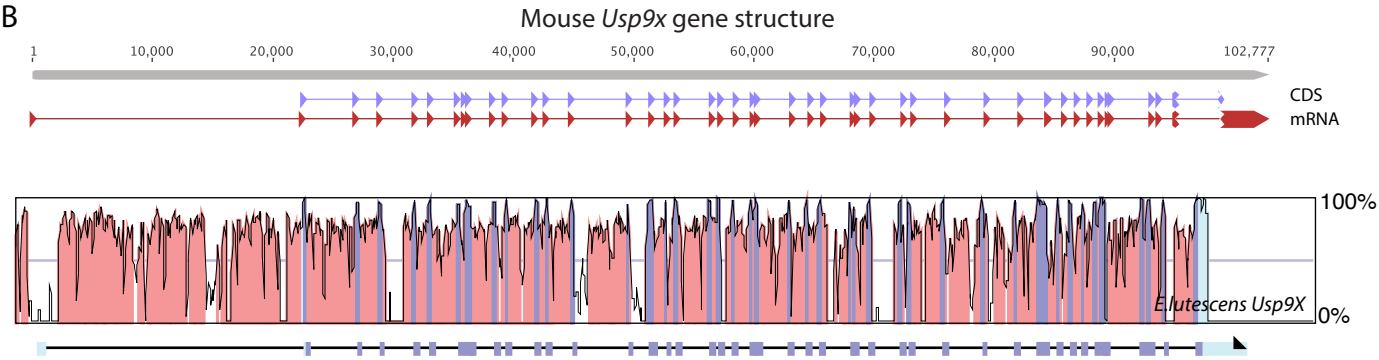
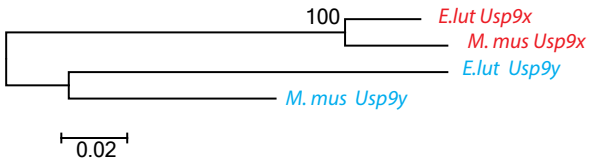
A



B



C



D

	1	2	3	4
E.lut Usp9y	1	100	85.65	80.58	80.41
M. mus Usp9y	2		100	83.99	83.41
E.lut Usp9x	3			100	94.92
M. mus Usp9x	4				100

Supplemental Figure S4: Conservation of *E. lutescens Usp9y*

A) *E.lutescens Usp9y* orthologous region compared to mouse *Usp9y*. The mouse *Usp9y* gene structure, longest mRNA and CDS are shown on top. The gVISTA (http://genome.lbl.gov/) software package was used to find the *E. lutescens* and *E. talpinus Usp9y* orthologous regions in mouse. In gVISTA, query sequence contigs are anchored on the base genome by local alignment matches(and then globally aligned to candidate regions using the AVID program. The Y-axis shows the percentage of sequence identity of *E.lutescens Usp9y* to that of mouse *Usp9y* 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 Usp9x* orthologous regions compared to mouse *Usp9x*. Data presentation and alignment were performed as described in A.

C) Phylogenetic relationship between *E. lutescens Usp9y* (3707 bp) and *Usp9x* (10017 bp) and the orthologous regions of the mouse *Usp9y* and *Usp9x* cDNAs (based on mRNA sequences). Bootstrap value is shown on one node.

D) Alignment percentage identity of *E. lutescens Usp9y* and *Usp9x* with mouse *Usp9y* and *Usp9x* cDNAs, using the sequences indicated in C.