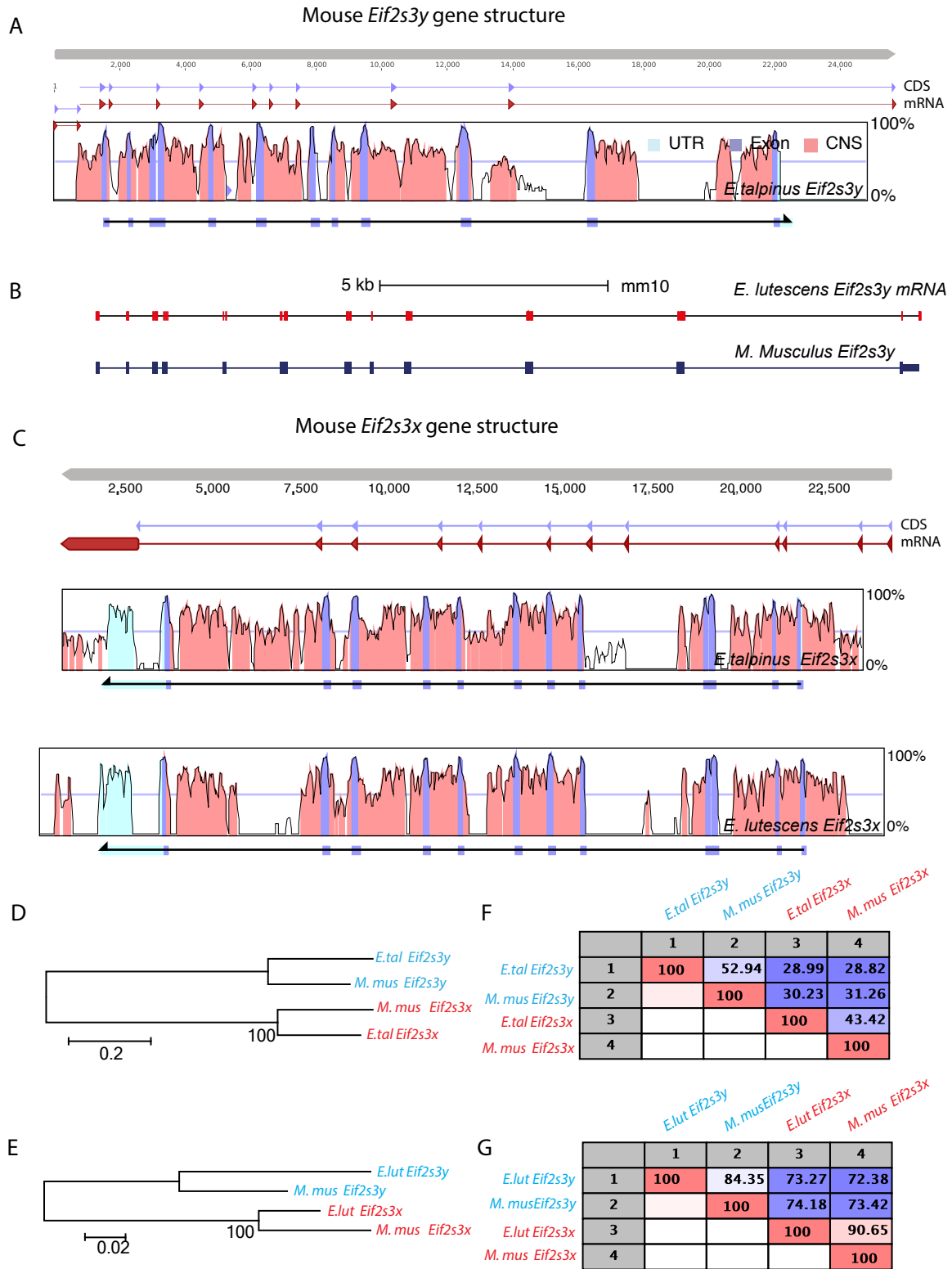




Supplemental Figure S3: Conservation of *E. lutescens* and *E. talpinus* *Eif2s3y* genes

A) *E. talpinus* *Eif2s3y* orthologous regions compared to mouse *Eif2s3y*. The mouse *Eif2s3y* 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* *Eif2s3y* 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* or *E. talpinus* *Eif2s3y* to that of mouse *Eif2s3y* 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) Alignment of *E. lutescens* *Eif2s3y* mRNA sequences to mouse *Eif2s3y* exons, using a BLAT search. The mouse *Eif2s3y* sequences were derived from *M. musculus* Genome assembly 10, at the UCSC genome browser. Although the complete *E. lutescens* *Eif2s3y* mRNA could not be assembled, all exons are represented in the RNA sequencing data. The red boxes indicate >90% identity between *E. lutescens* and *M. musculus* exonic sequences.

C) *E. lutescens* and *E. talpinus* *Eif2s3x* orthologous regions compared to mouse *Eif2s3x*. Data presentation and alignment were performed as described in A).

D) Phylogenetic relationship between *E. talpinus* *Eif2s3y* (8589 bp) and *Eif2s3x* (6544 bp), and the orthologous regions of the mouse *Eif2s3y* and *Eif2s3x* genes (based on genomic sequences). Bootstrap value is shown on one node.

E) Phylogenetic relationship between *E. lutescens* *Eif2s3y* (1370 bp) and *Eif2s3x* (2663bp) and the orthologous regions of the mouse *Eif2s3y* and *Eif2s3x* cDNAs (based on mRNA sequences) Bootstrap value is shown on one node.

F) Alignment percentage identity of *E. talpinus* *Eif2s3y* and *Eif2s3x*, and the orthologous regions of the mouse *Eif2s3y* and *Eif2s3x* genes (based on genomic sequences indicated in D)

G) Alignment percentage identity of *E. lutescens* *Eif2s3y* and *Eif2s3x*, and the orthologous regions of mouse *Eif2s3y* and *Eif2s3x* cDNAs (based on mRNA sequences indicated in E)