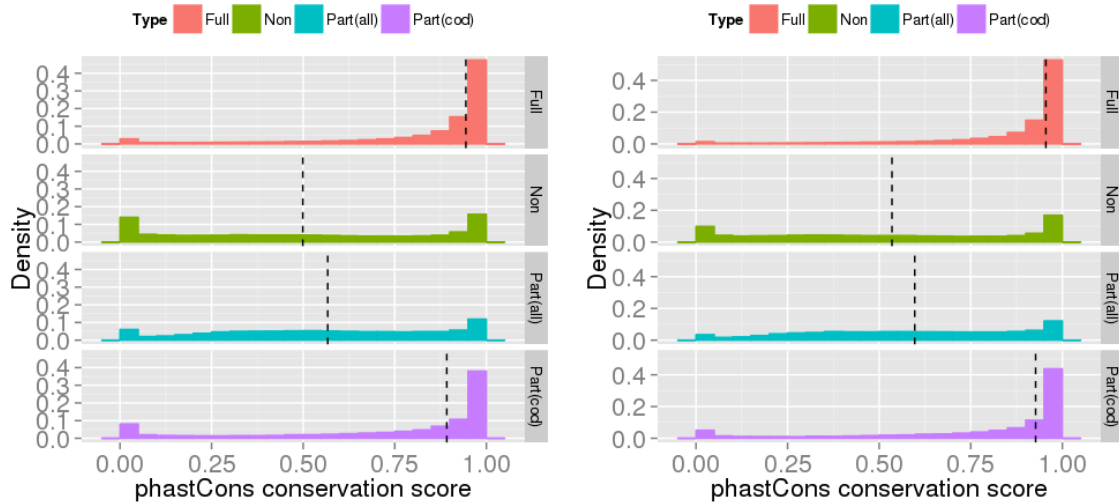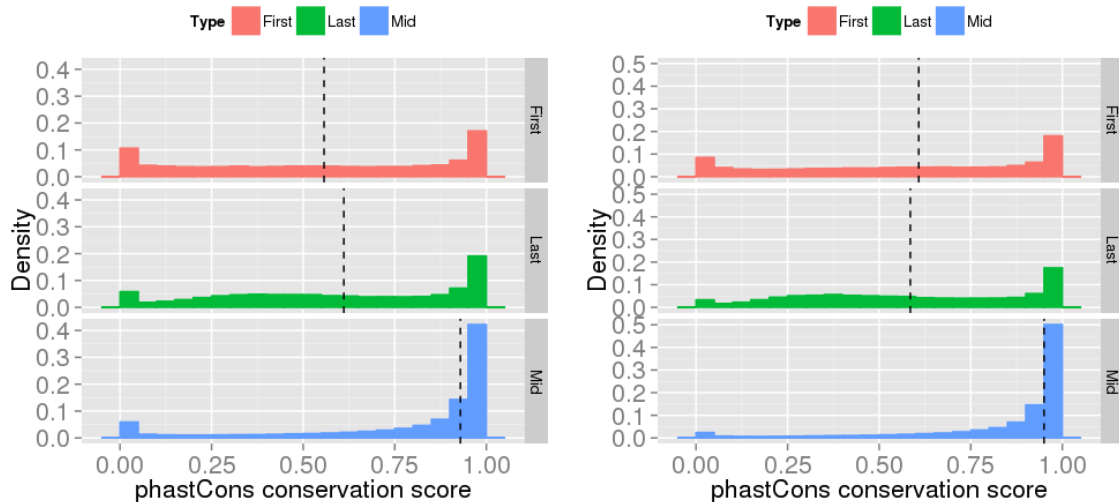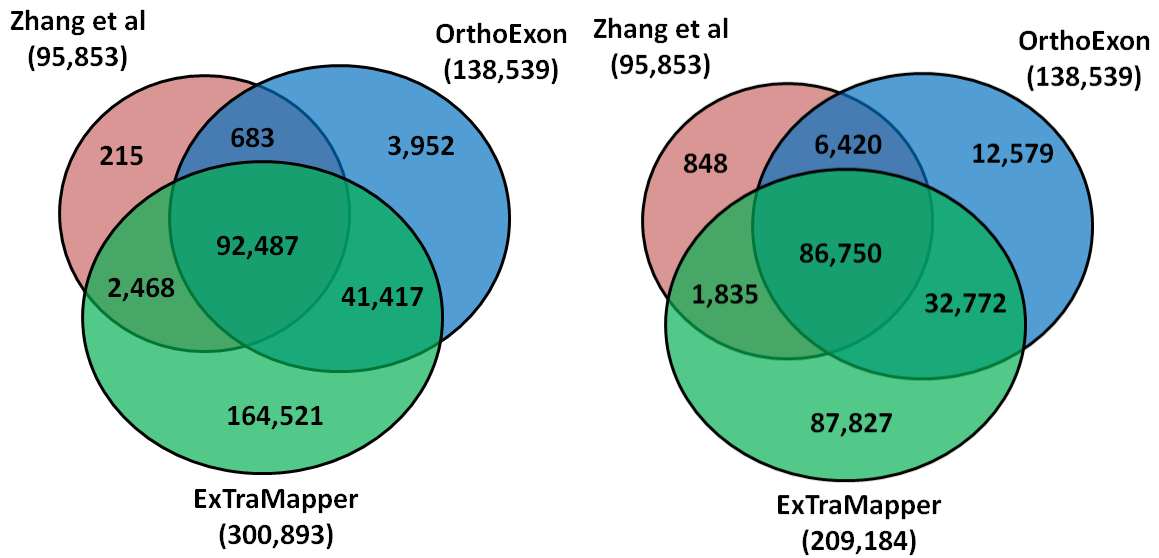# Supplementary Information

SUPPLEMENTARY FIGURES

Supplementary Figure 1:

Distribution of evolutionary conservation scores for different coding types for human (left) and mouse (right) exons. The conservation scores are computed using PhastCons (Methods). From top to down the different types in each figure are: fully coding exons, non-coding exons, partially coding exons and only coding parts of partially coding exons.
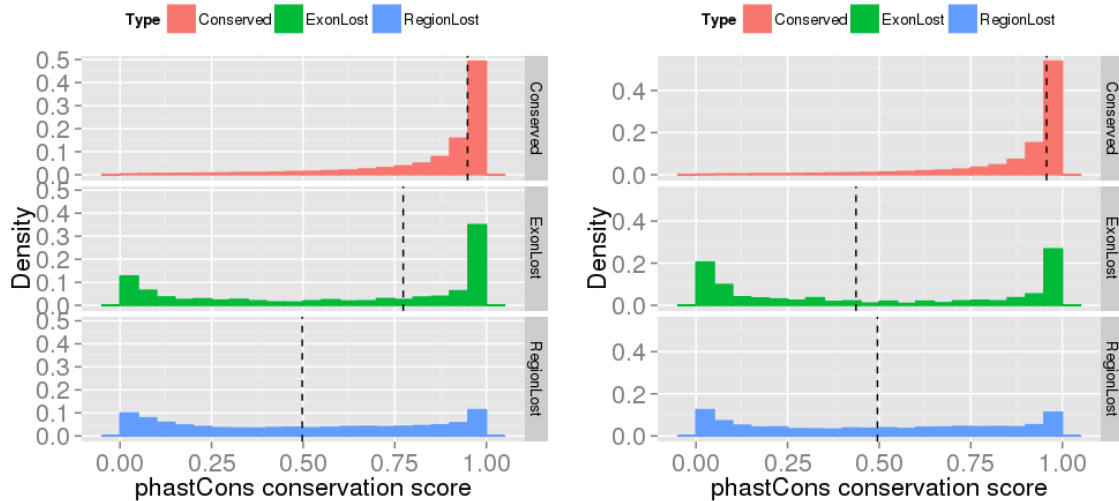

Supplementary Figure 2:

Distribution of evolutionary conservation scores for different exon position types for human (left) and mouse (right) exons. The conservation scores are computed using PhastCons (Methods). From top to down the different types in each figure are exons that are always: first, last and middle of each transcript.
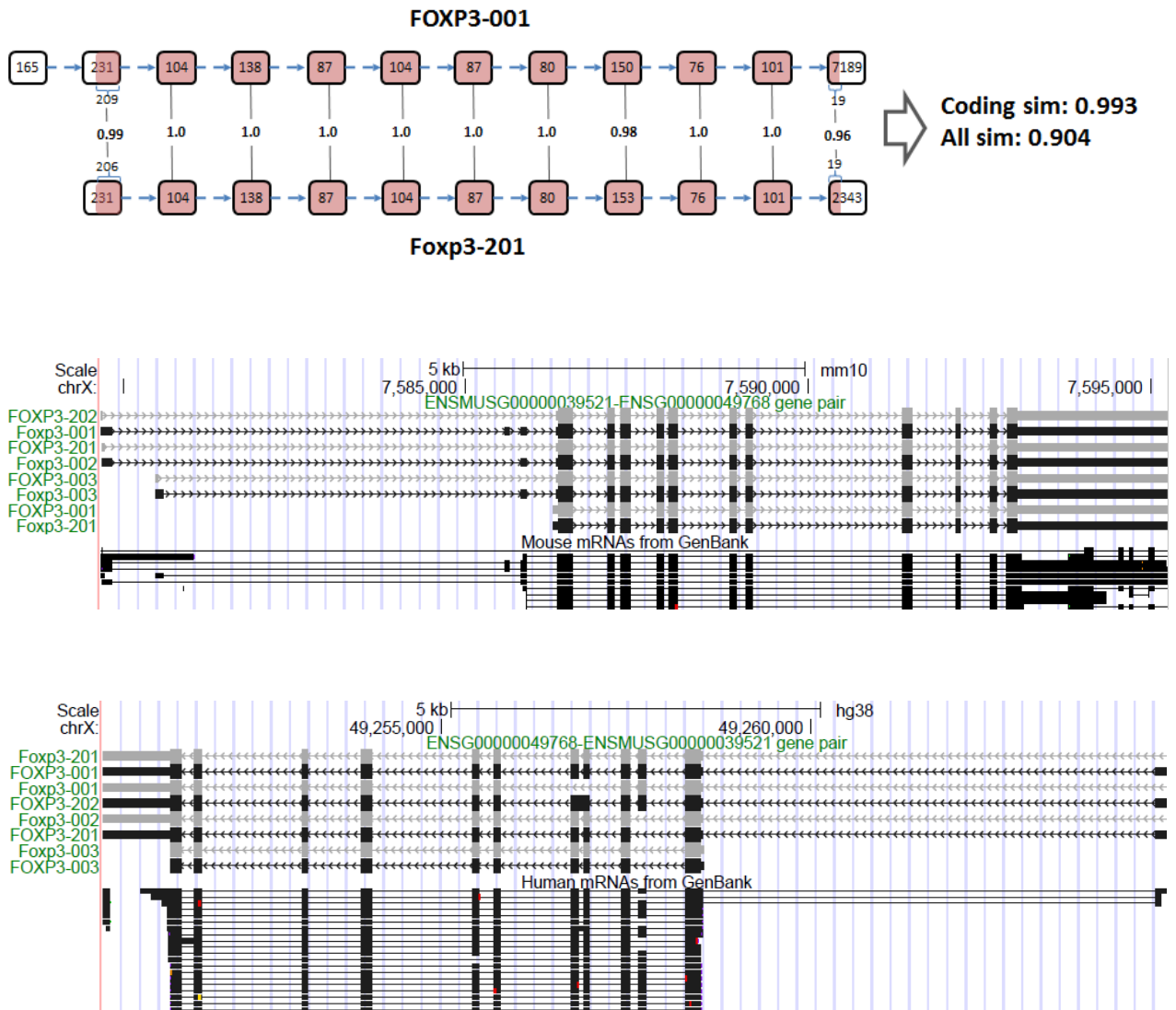
Supplementary Figure 3:

Venn diagrams showing intersections among human-mouse exon mappings reported by three different methods. We use an exon similarity score threshold of 0.9 (left) and 1.0 (right) ExTraMapper to determine the set of exon mappings. The numbers in parentheses indicate the number of total exon mappings found by the method.

Supplementary Figure 4:

Distribution of evolutionary conservation scores for different exon classes determined by ExTraMapper for human (left) and mouse (right) exons. The conservation scores are computed using PhastCons (Methods). From top to down the different types in each figure are exons that are classified as: conserved between human and mouse, region conserved but lost exon function in the other organism and exon regions that are lost in the other organism.

Supplementary Figure 5:

Transcript mappings for *FOXP3-Foxp3* gene pair. **Top row:** the most similar transcript pair for this gene pair visualized using squares with exon lengths in base pairs and filled squares for protein coding regions. Arrows indicate the direction of or transcription and vertical connectors report the coding similarity between the vertically aligned exons one from human (top) and one from mouse (bottom). **Middle row:** UCSC mouse genome browser (mm10) snapshot of four pairs of transcripts that are mapped by ExTraMapper. Each human transcript (*FOXP3*) is followed by the corresponding mouse transcript (*Foxp3*). All exons are shown for the mouse transcript whereas for human transcript only the exons that are mapped to a mouse exon are drawn. **Bottom row:** UCSC human genome browser (hg38) snapshot which shows the same transcript mappings but from the view of all human exons and only the mouse exons mapped to those human exons. Transcript pair coding similarities for these four pairs are: *FOXP3-001--Foxp3-201*→ 0.993, *FOXP3-201--Foxp3-002*→ 0.945, *FOXP3-003--Foxp3-003*→ 0.945 and *FOXP3-202--Foxp3-001*→ 0.904.