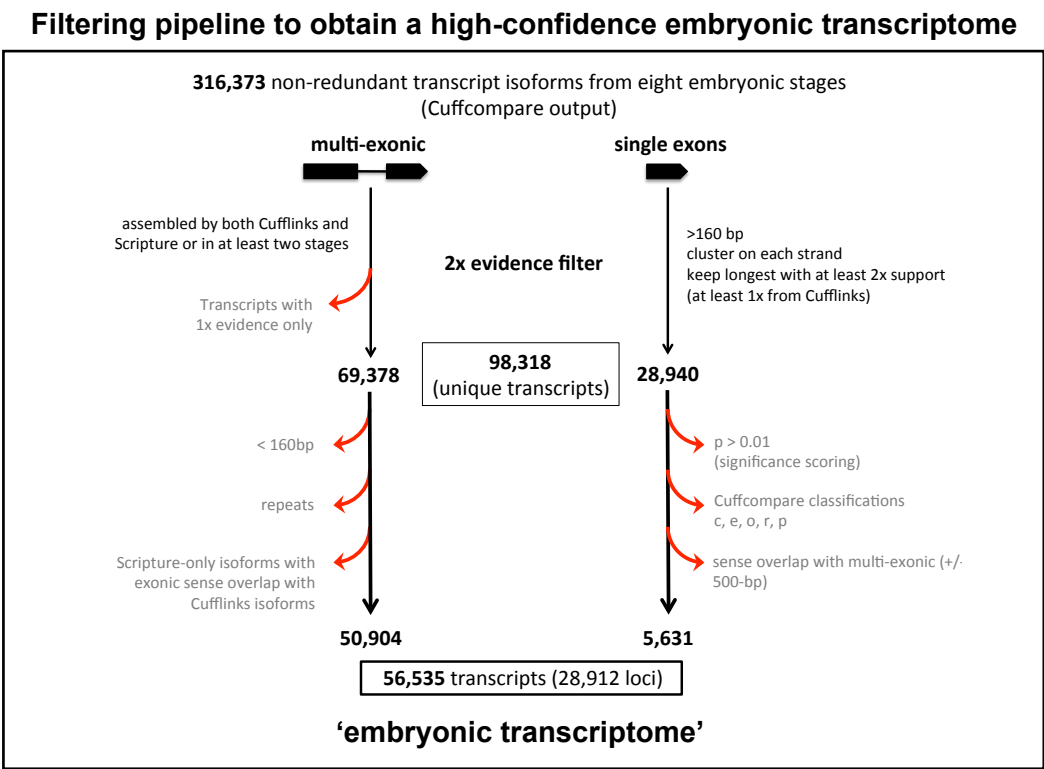
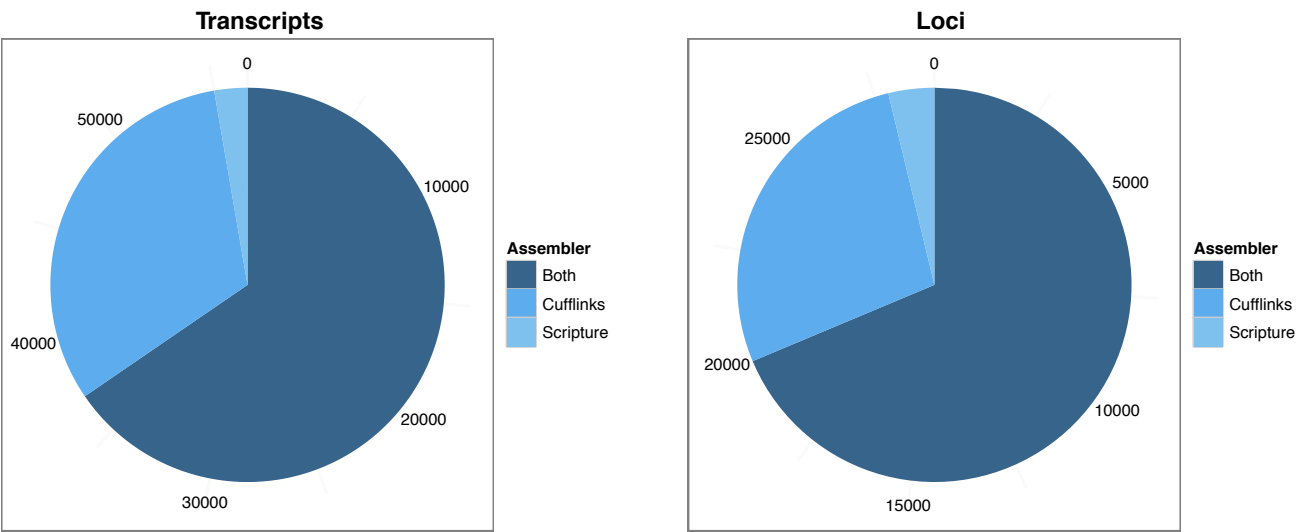


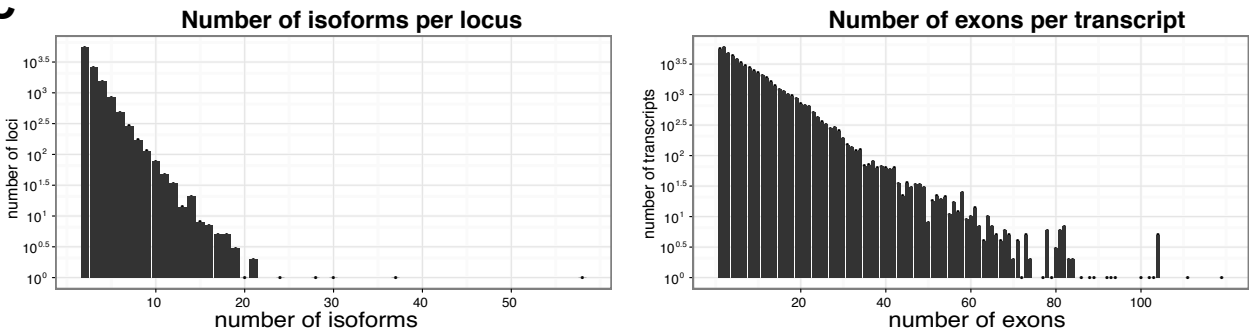
A



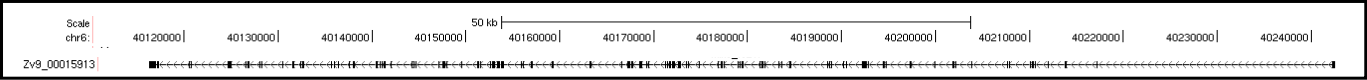
B



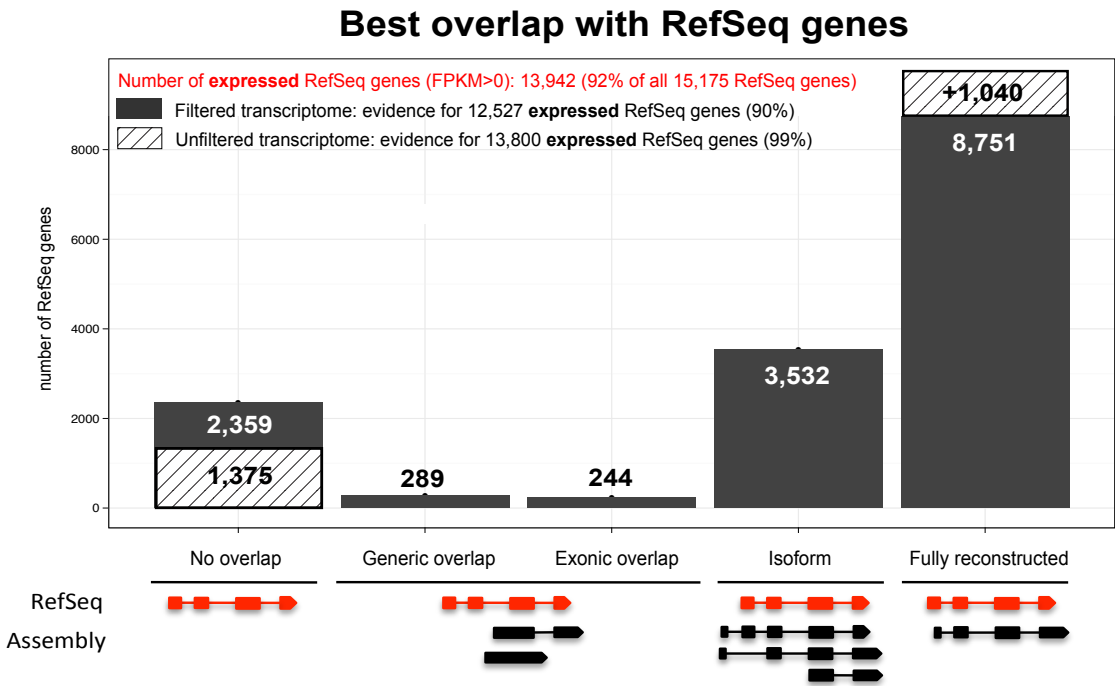
C



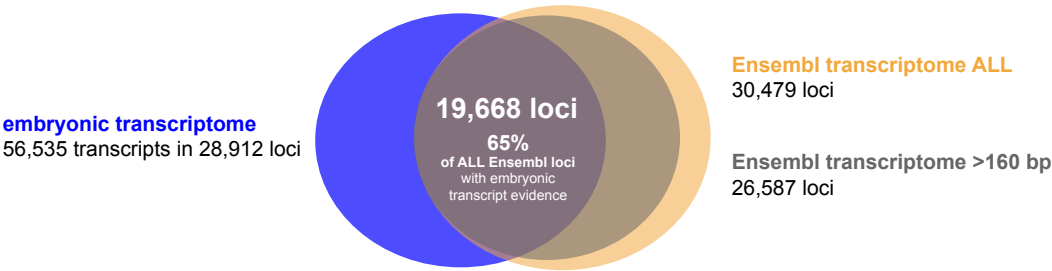
col7a homolog with 119 exons



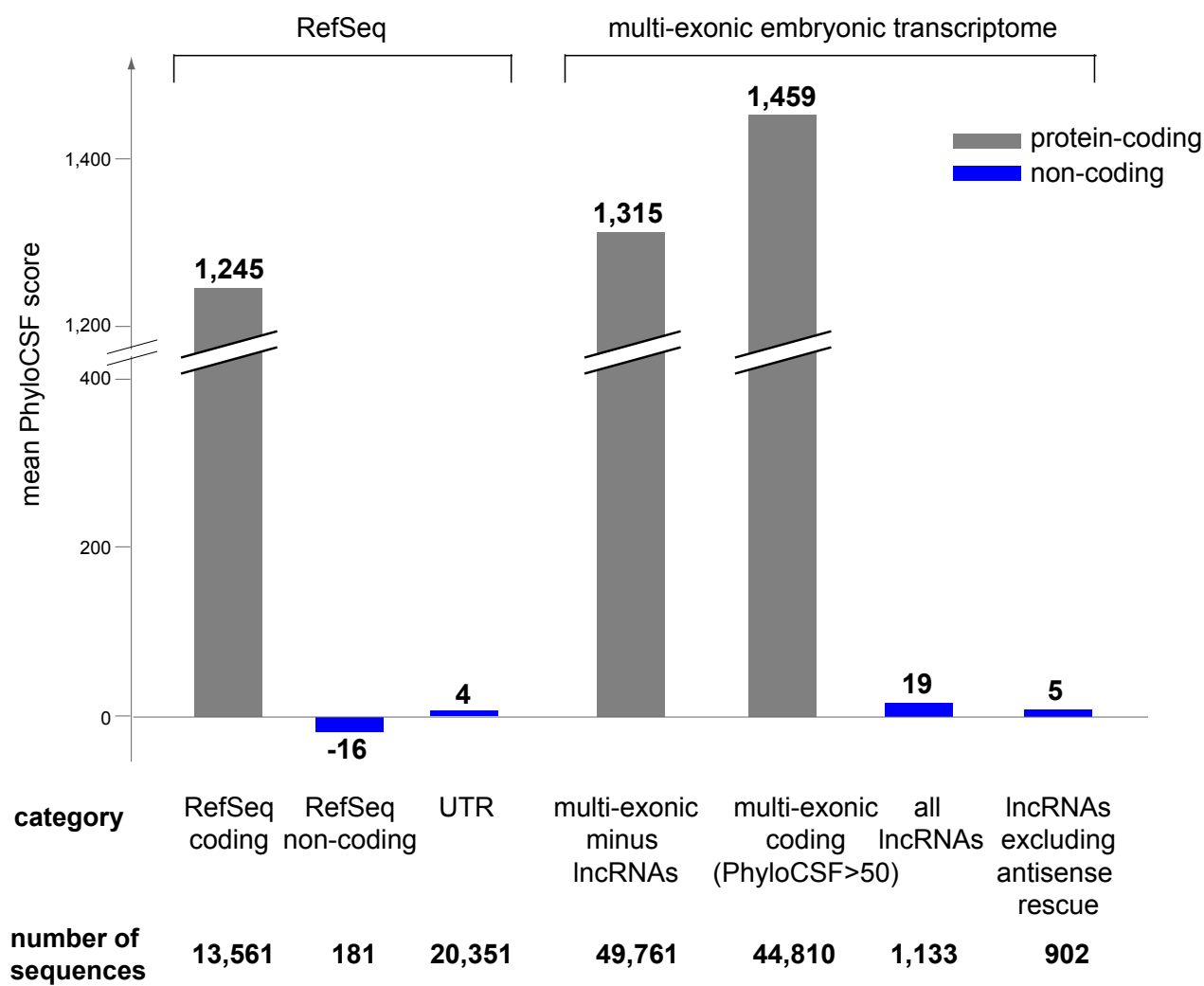
A



B

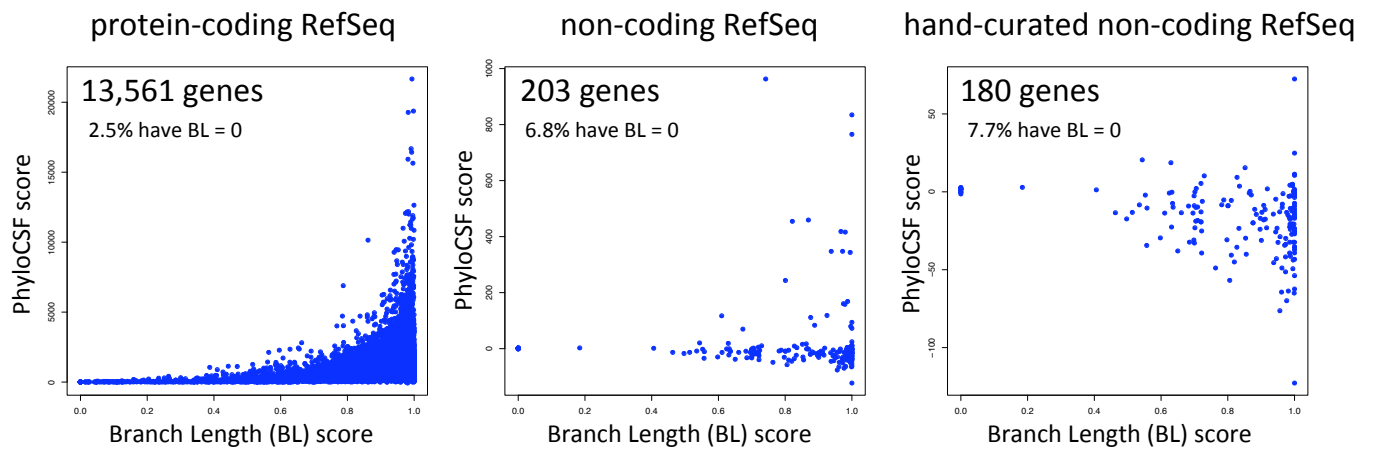


Pauli_Suppl. Figure 3

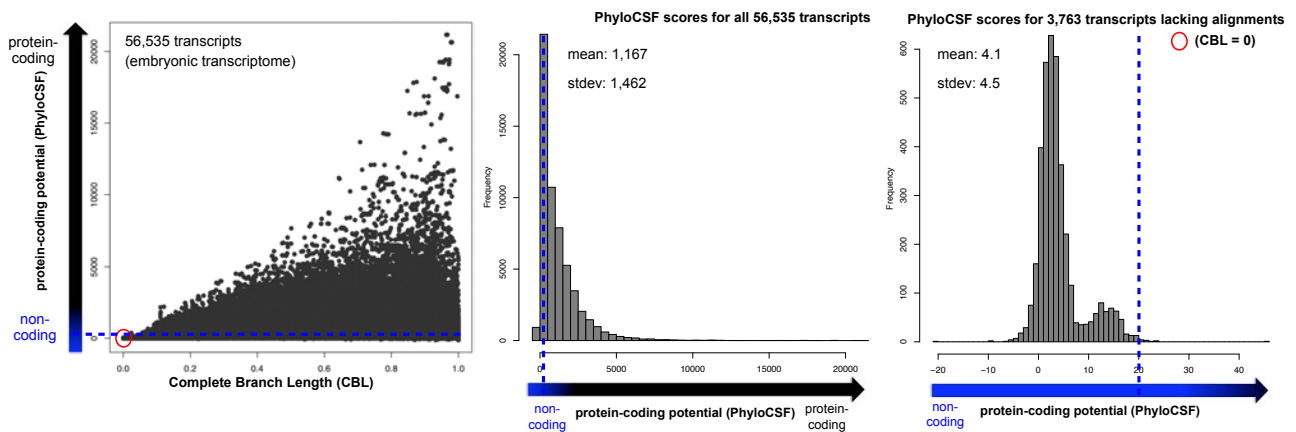


A

PhyloCSF score distribution of RefSeq genes as a function of Branch Lengths (BLs)

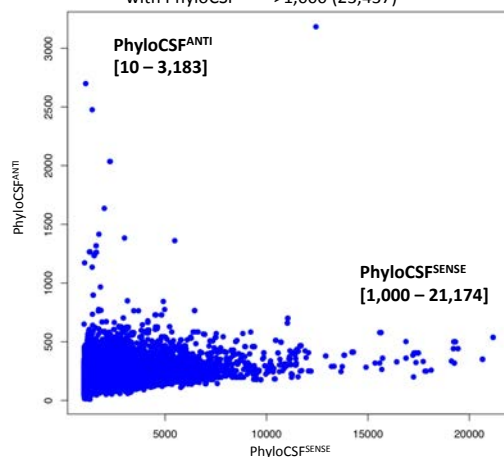


B



C

Relationship of the PhyloCSF^{SENSE} versus PhyloCSF^{ANTI} scores, Assessed on the sample set of embryonic protein-coding transcripts with PhyloCSF^{SENSE} > 1,000 (23,437)



D

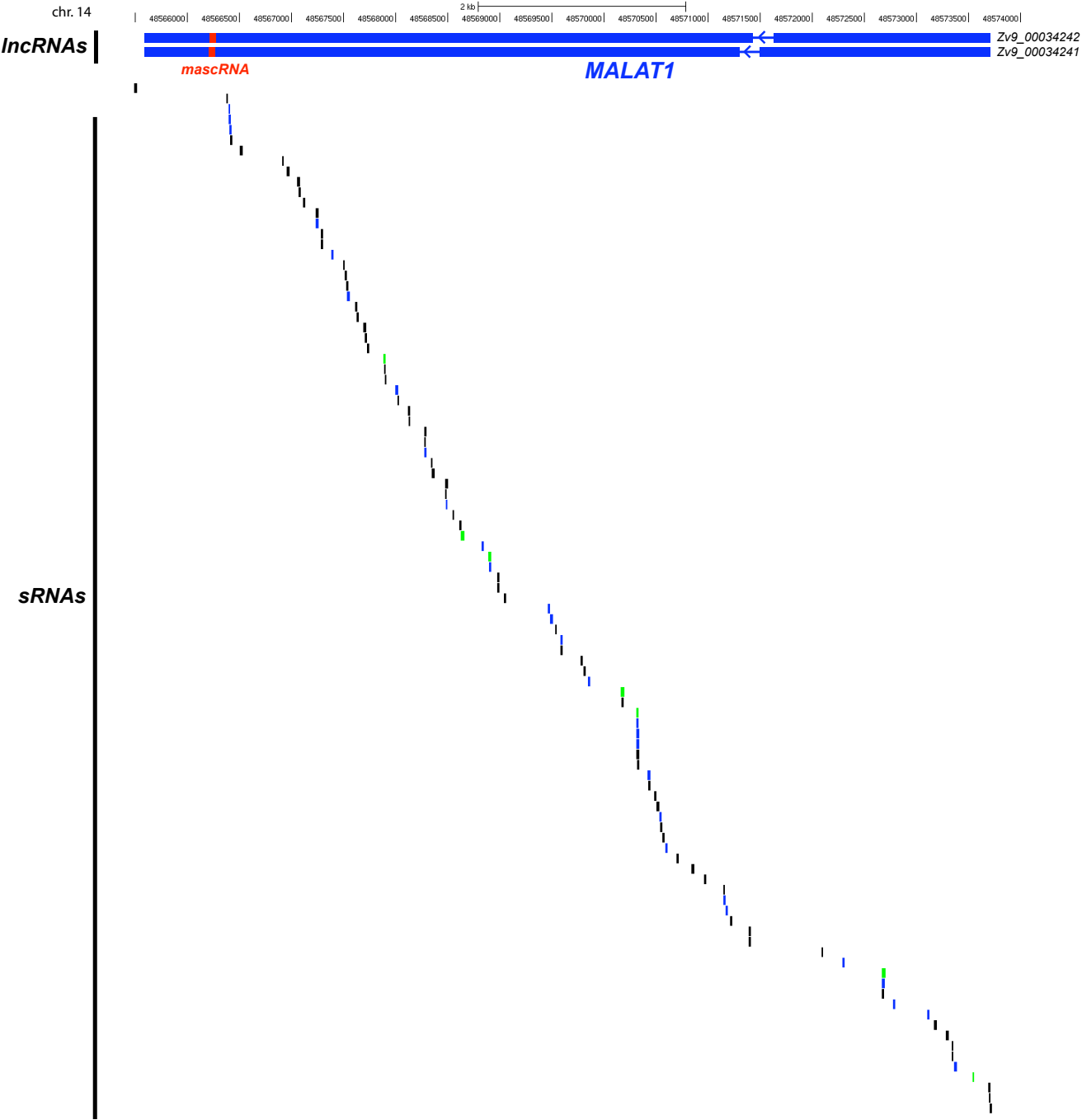
PhyloCSF^{SENSE} = 1,200
PhyloCSF^{ANTI} = 310

PhyloCSF^{SENSE} = 250
PhyloCSF^{ANTI} = 650

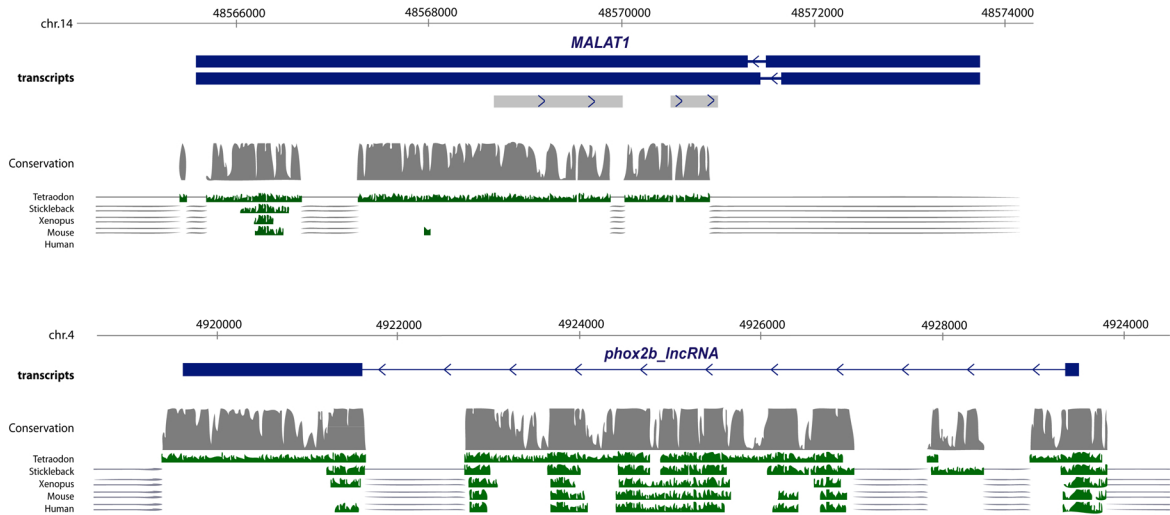
PhyloCSF = phylogenetic Codon Substitution Frequency score
HSR = Highest Scoring Region in PhyloCSF

A = protein-coding
B = non-coding (antisense exonic overlapping)

Pauli_Suppl. Figure 5



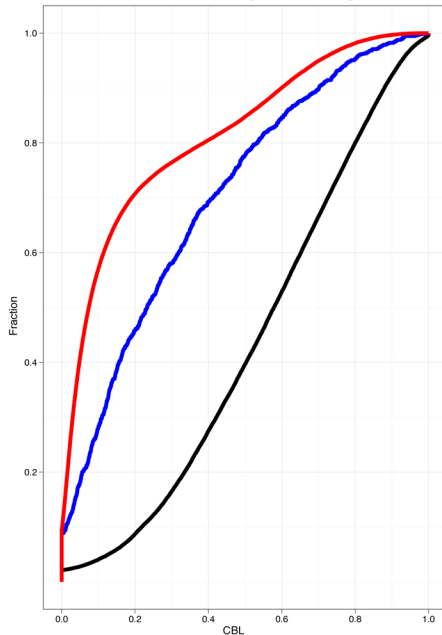
A



B

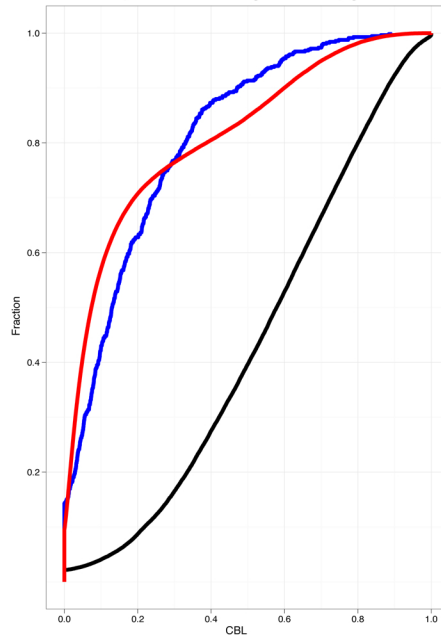
Complete Branch Length (CBL) scores for
ALL 1,133 lncRNAs
versus

- protein-coding genes
- introns of protein-coding RefSeq genes >160 bp

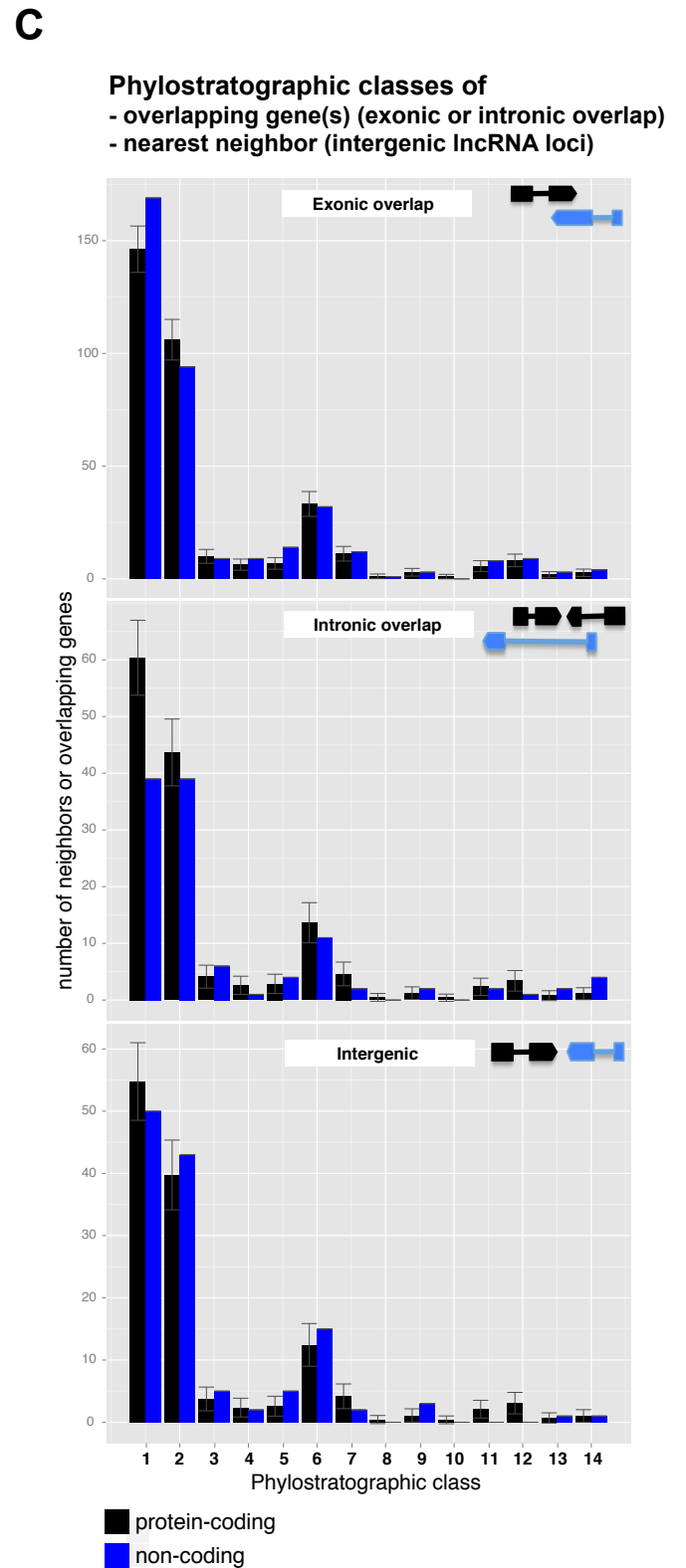
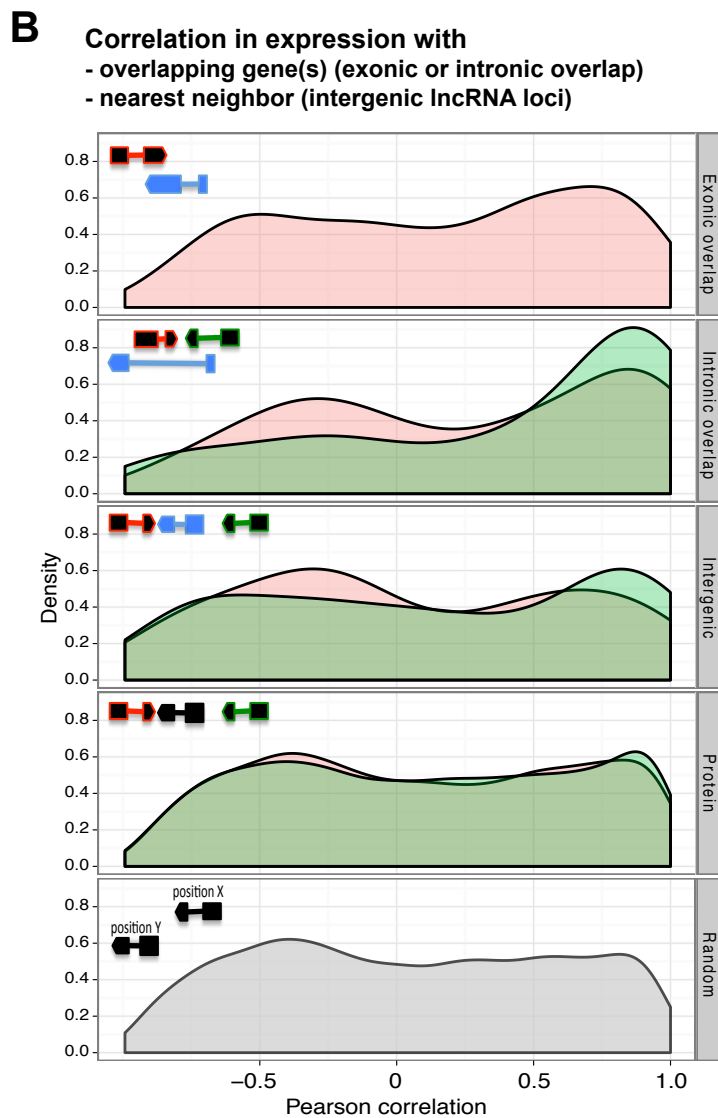
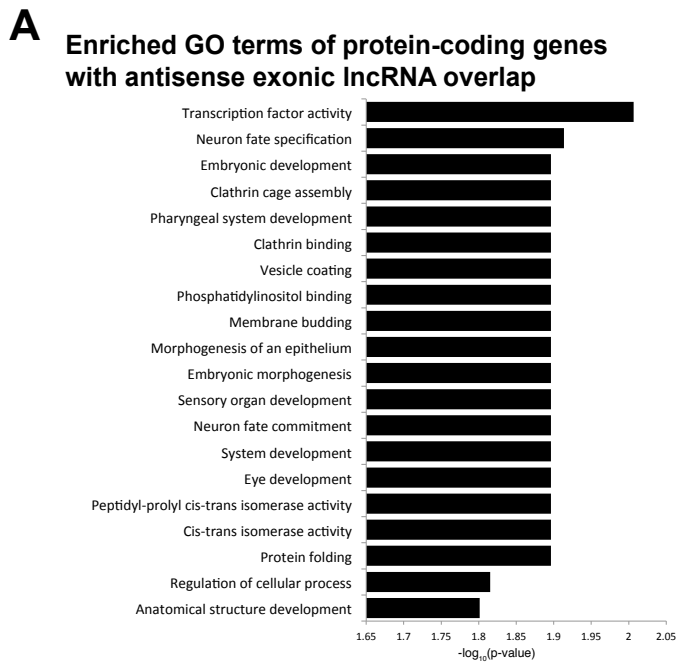


Complete Branch Length (CBL) scores for
581 lncRNAs without exonic overlap with proteins
versus

- protein-coding genes
- introns of protein-coding RefSeq genes >160 bp



— non-coding
— protein-coding
— introns >160 bp



Pauli_Suppl. Figure 8

