Figure S2

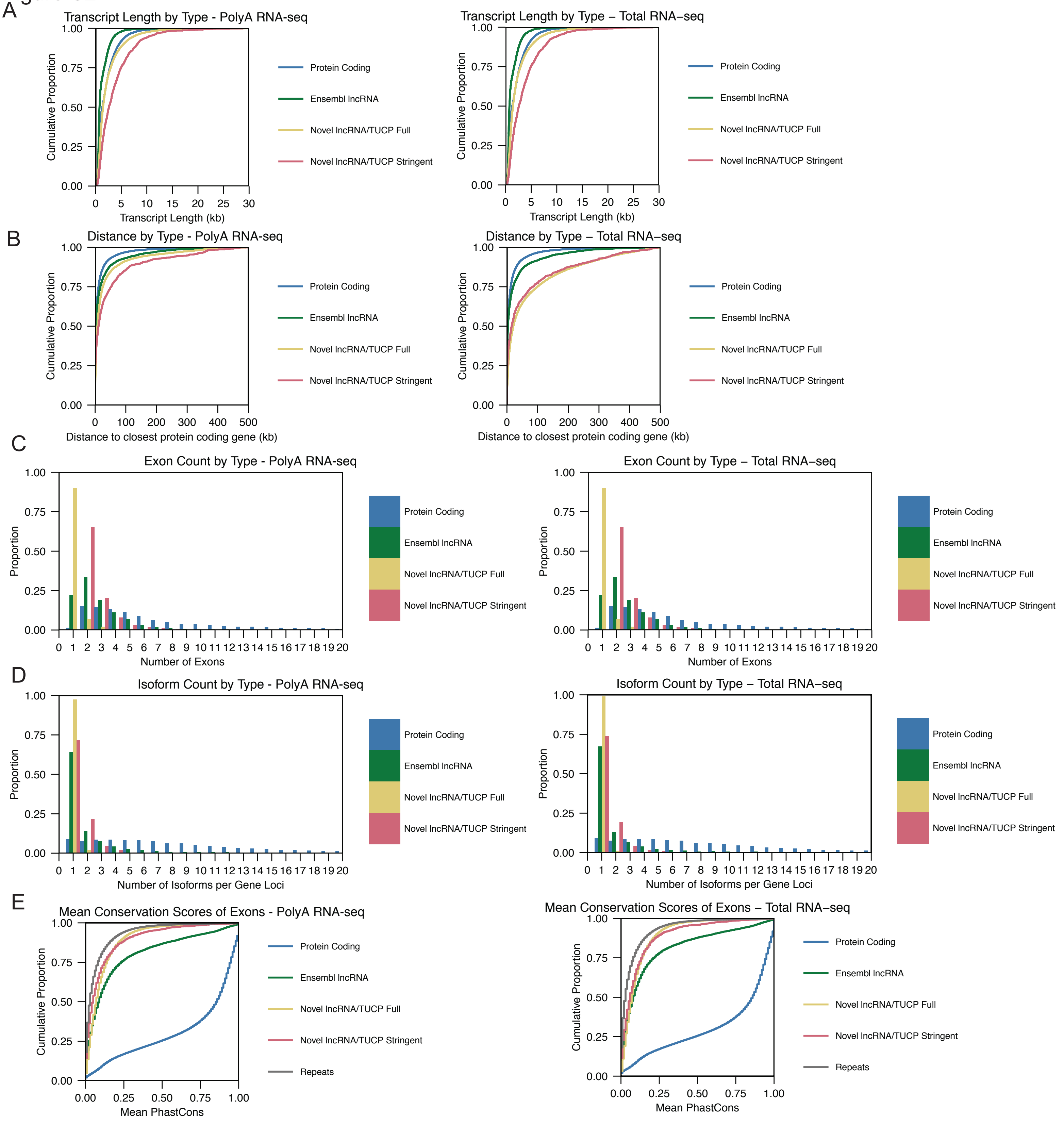

Figure S2. Genomic characteristics of lncRNAs expressed in human neocortex development

A) Cumulative distributions transcript length of mRNAs, Ensembl lncRNAs, and lncRNAs/TUCPs in the Full and Stringent references not annotated in Ensembl (novel). B) Cumulative distributions of distances between mRNAs or lncRNAs/TUCPs to their closest mRNA neighbors. Novel lncRNAs/TUCPs were farther from mRNAs than mRNAs were to their neighboring mRNAs. C) Histograms of exon counts for mRNA or lncRNA/TUCP transcripts. D) Histograms of number of unique isoforms for each mRNA or lncRNA/TUCP gene. E) Cumulative distributions of mean exonic PhastCons conservation scores for mRNAs or lncRNAs/TUCPs. All lncRNAs/TUCPs were less conserved than mRNAs, but were more conserved than repeat regions. Left panels represent results using polyA RNA data, right panels represent results using total RNA data.