

SUPPLEMENTARY INFORMATION: Long-range RNA structures in the human transcriptome beyond evolutionarily conserved regions

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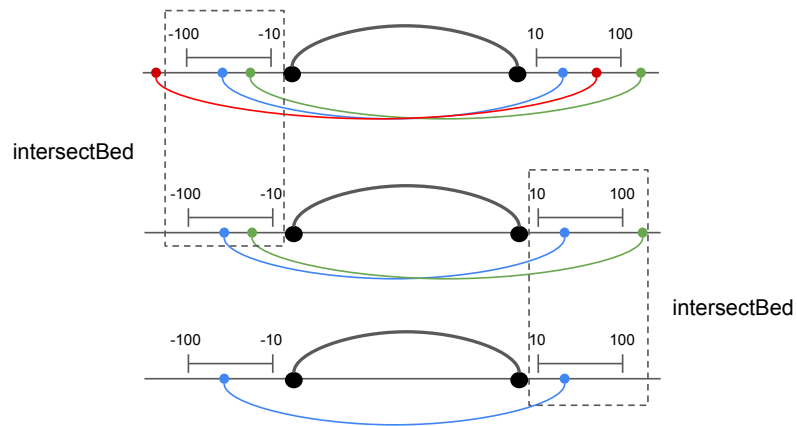


Figure S1: A schematic representation of the procedure to identify PNCC (see Methods).

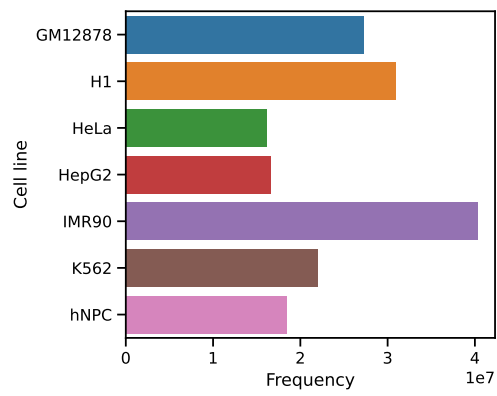


Figure S2: The number of split reads supporting RNA contacts from all RIC-seq experiments.

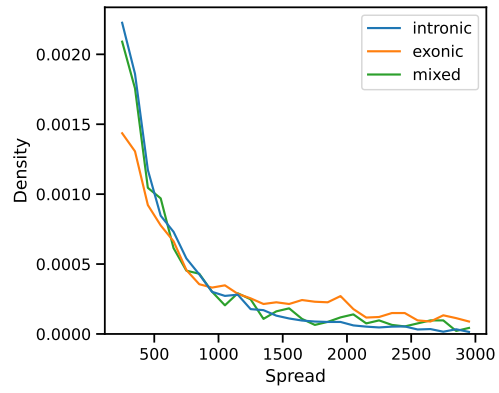


Figure S3: The distance between complementary sequences in intronic, exonic, and mixed regions.

HeLa	ENCSR000CPR
HepG2	ENCSR000CPE
GM12878	ENCSR000AED
H1	ENCSR000COU
IMR90	ENCSR000CTQ
hNPC	ENCSR244ISQ
neuron	ENCSR292TAP
K562	ENCSR000CPH

Table S1: Accession numbers of RNA-seq experiments used as a matched set control.