Elucidating the RNA Structure of Alu Elements

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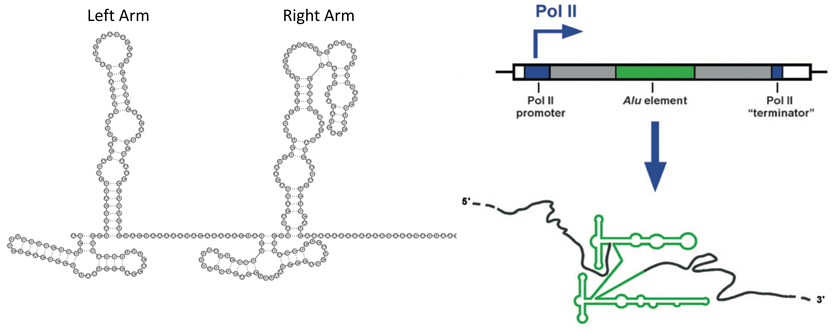
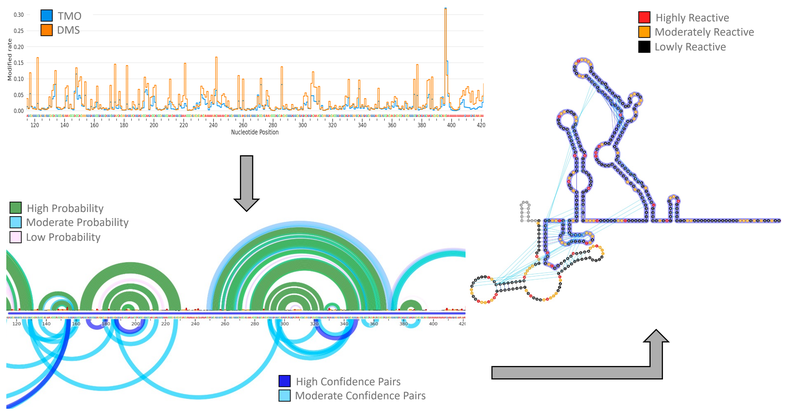
Significance

Alu elements are a family of largely inactive retrotransposons that comprise around 11% of the human genome, mostly encoded in intronic sequences. Over evolutionary time, Alu elements have evolved into three subfamilies, J, S, and Y.[1] Moreover, there is substantial evidence that suggests a role of Alu elements in both normal biology and disease states. Their abundance and disease relevance characterize Alu elements as an enticing therapeutic target. However, a lack of robust structural information exists beyond a widely reported, single general structure, despite the diversity in sequence and function.[2] By exploring the RNA structure space assumed by Alu elements and generating robust, chemical probing-informed structural data, we can open the doors to novel therapeutic targets.

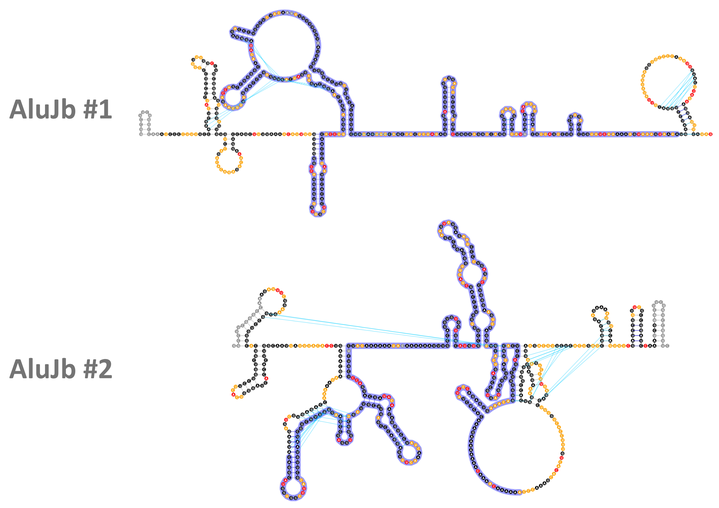
A single consensus secondary structure has historically been reported for Alu elements[3]



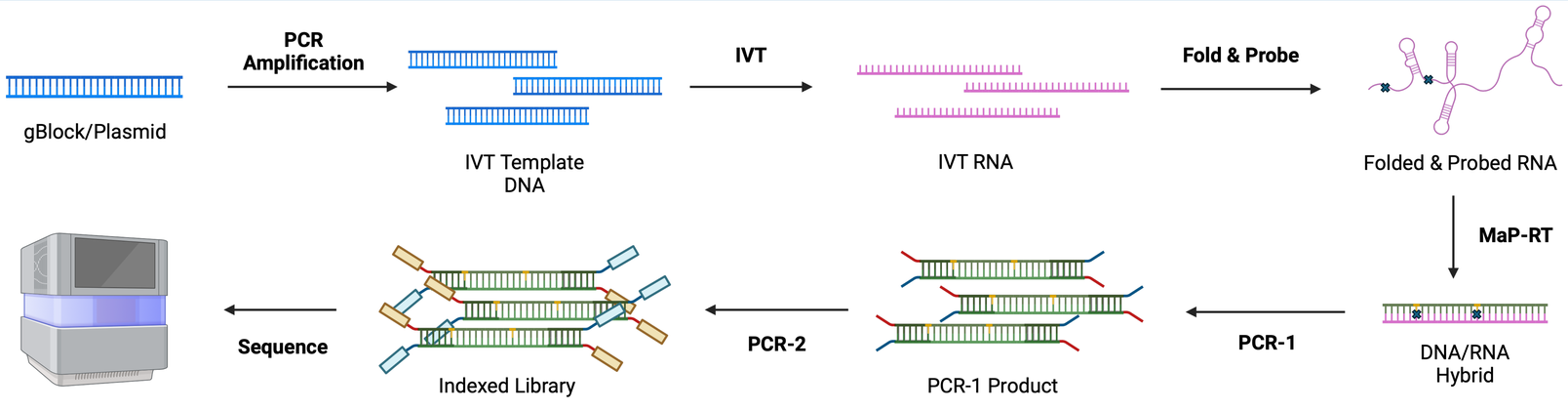
Chemical probing data is utilized bioinformatically to inform structural predictions



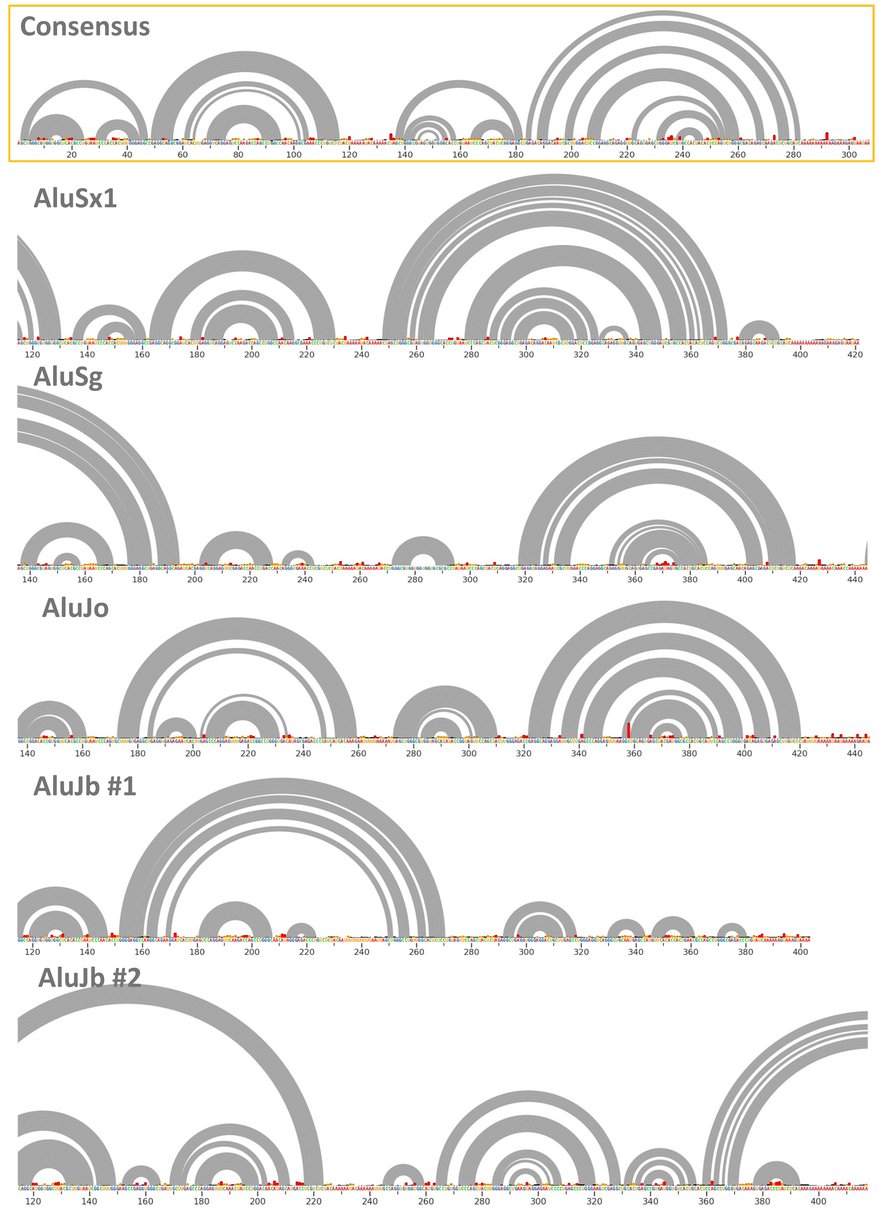
There appears to be great structural diversity within Alu element subfamilies



Chemical probing and mutational profiling enable robust RNA structure determination



Alu element secondary structures are unique and do not conform to the consensus structure



References

1. Deininger, P. Alu Elements: Know the SINEs. *Genome Biology* 2011, *12* (12), 236. https://doi.org/10.1186/gb-2011-12-12-236.
2. Sinnett, D.; Richer, C.; Deragon, J. M.; Labuda, D. Alu RNA Secondary Structure Consists of Two Independent 7 SL RNA-like Folding Units. *The Journal of Biological Chemistry* **1991**, *266* (14), 8675–8678.
3. Häsler, J.; Samuelsson, T.; Strub, K. Useful "Junk": Alu RNAs in the Human Transcriptome. *Cellular and Molecular Life Sciences* **2007**, *64* (14), 1793–1800. https://doi.org/10.1007/s00018-007-7084-0.