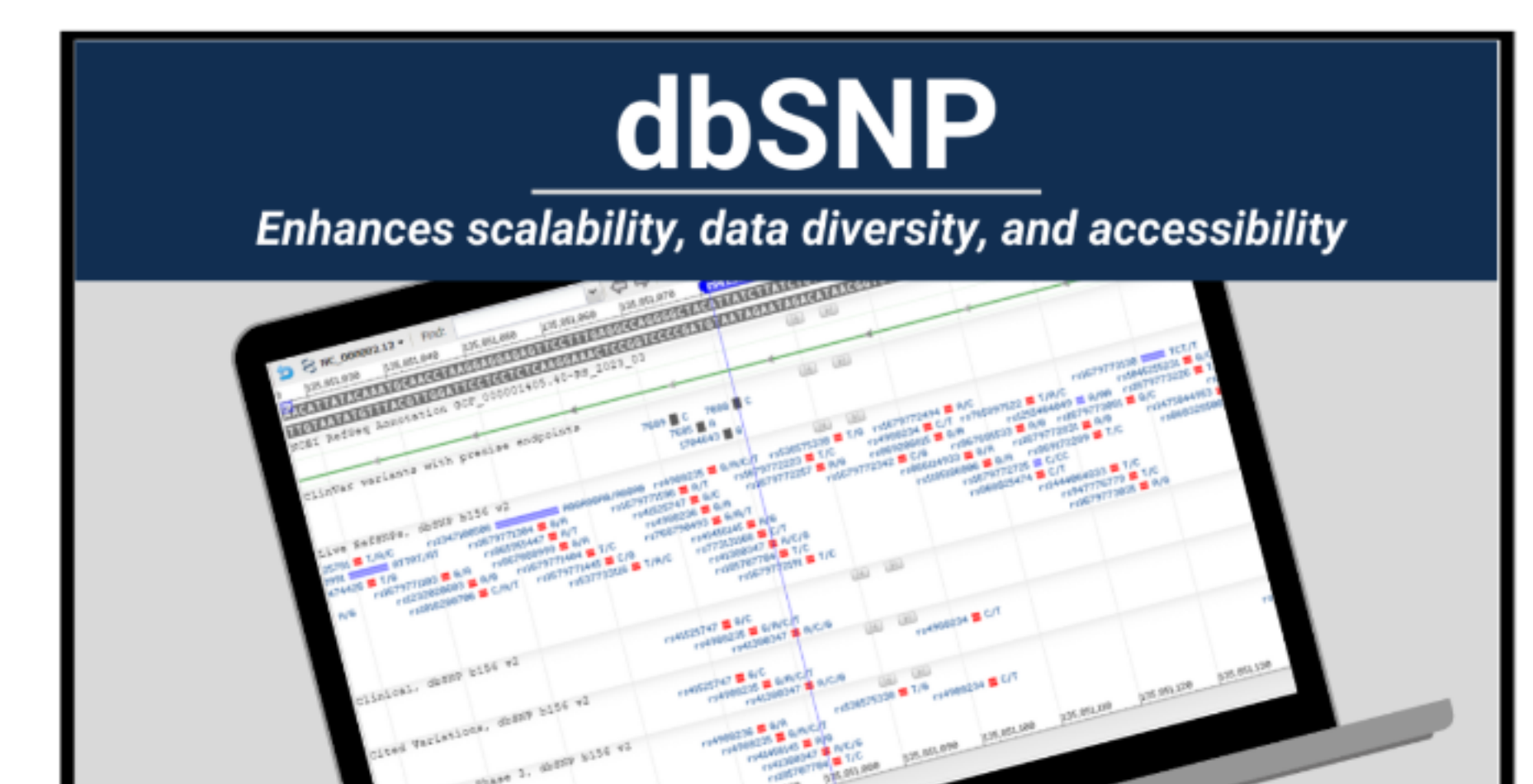
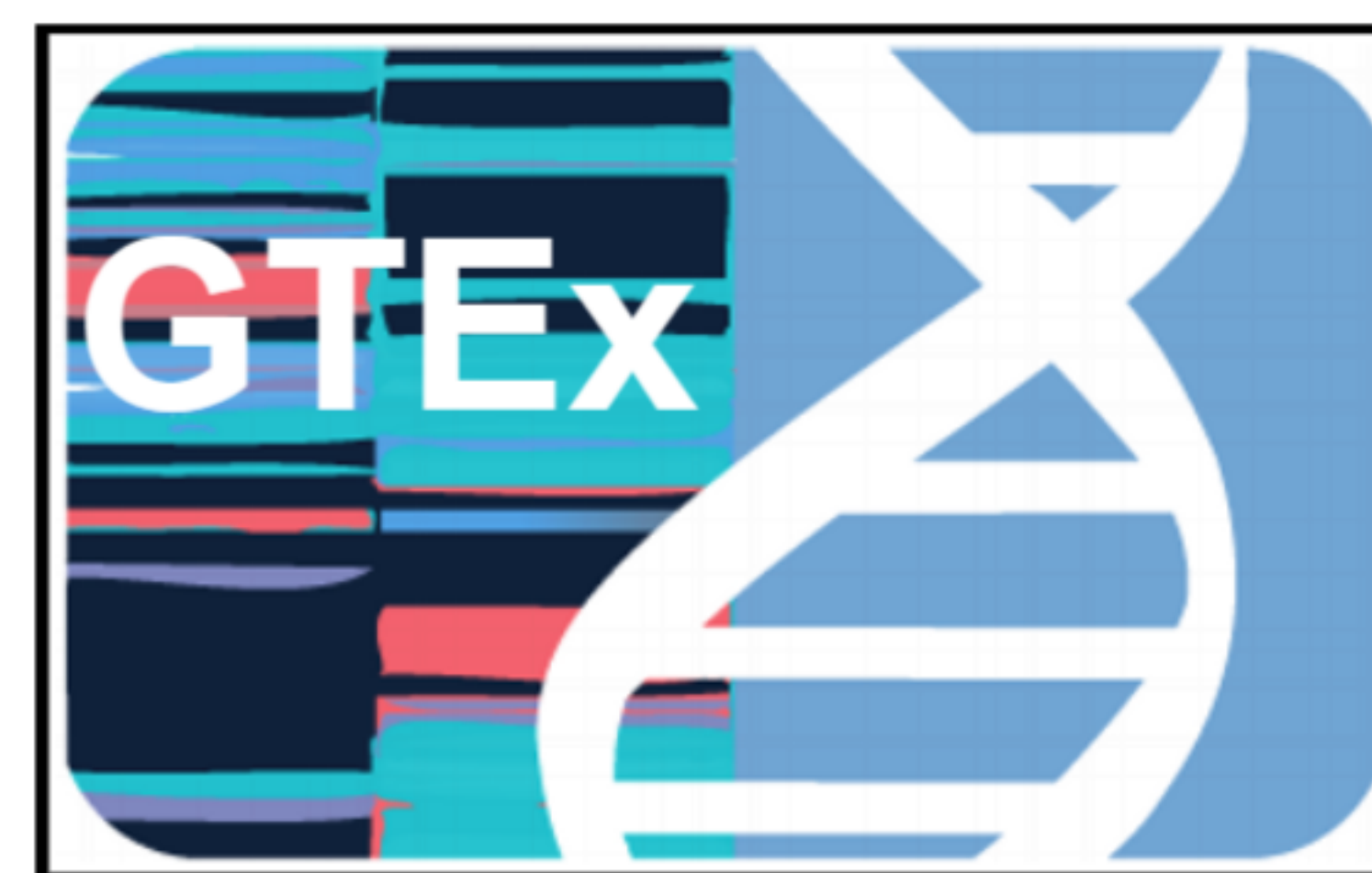
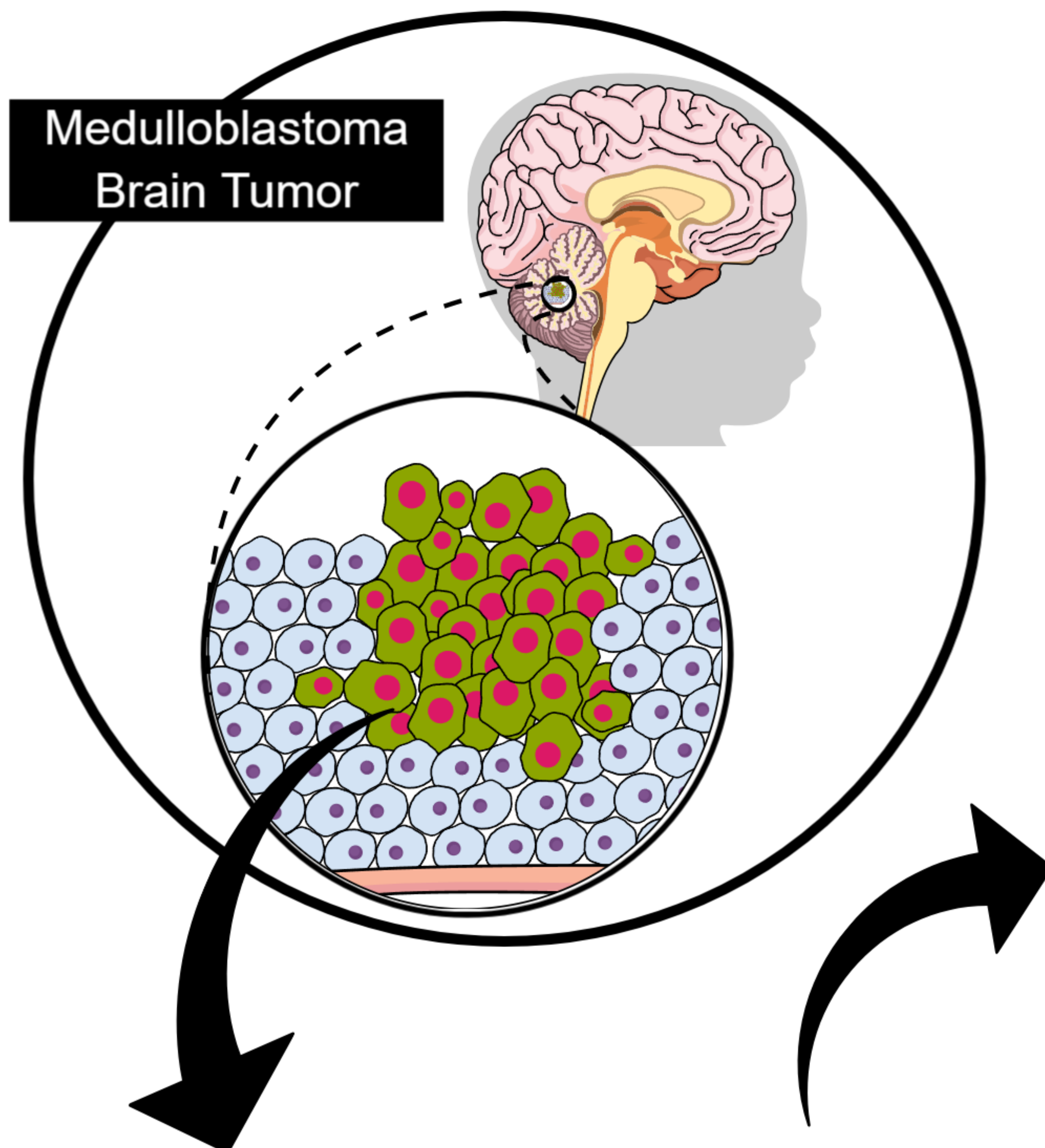


Decoding the function of Long Non-Coding RNAs in Subgroup 3 Medulloblastoma: Integrative SNP and eQTL Analysis



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Through the integration of SNP and eQTL analysis using a bioinformatics approach, this study aims to decode the functional role of Long Non-Coding RNAs in Subgroup 3 Medulloblastoma, providing insights into their potential contributions to disease progression.



2 Online Database

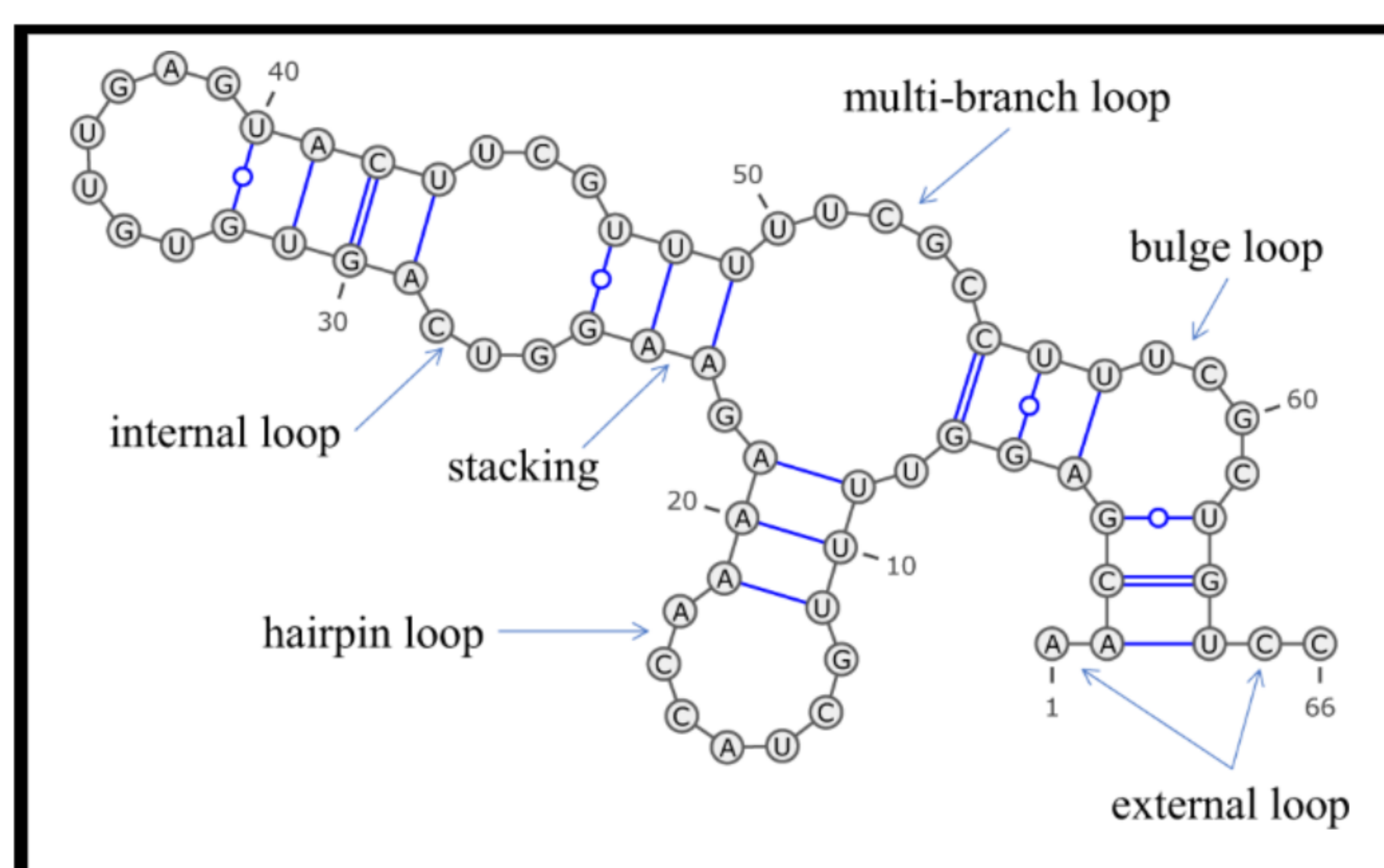
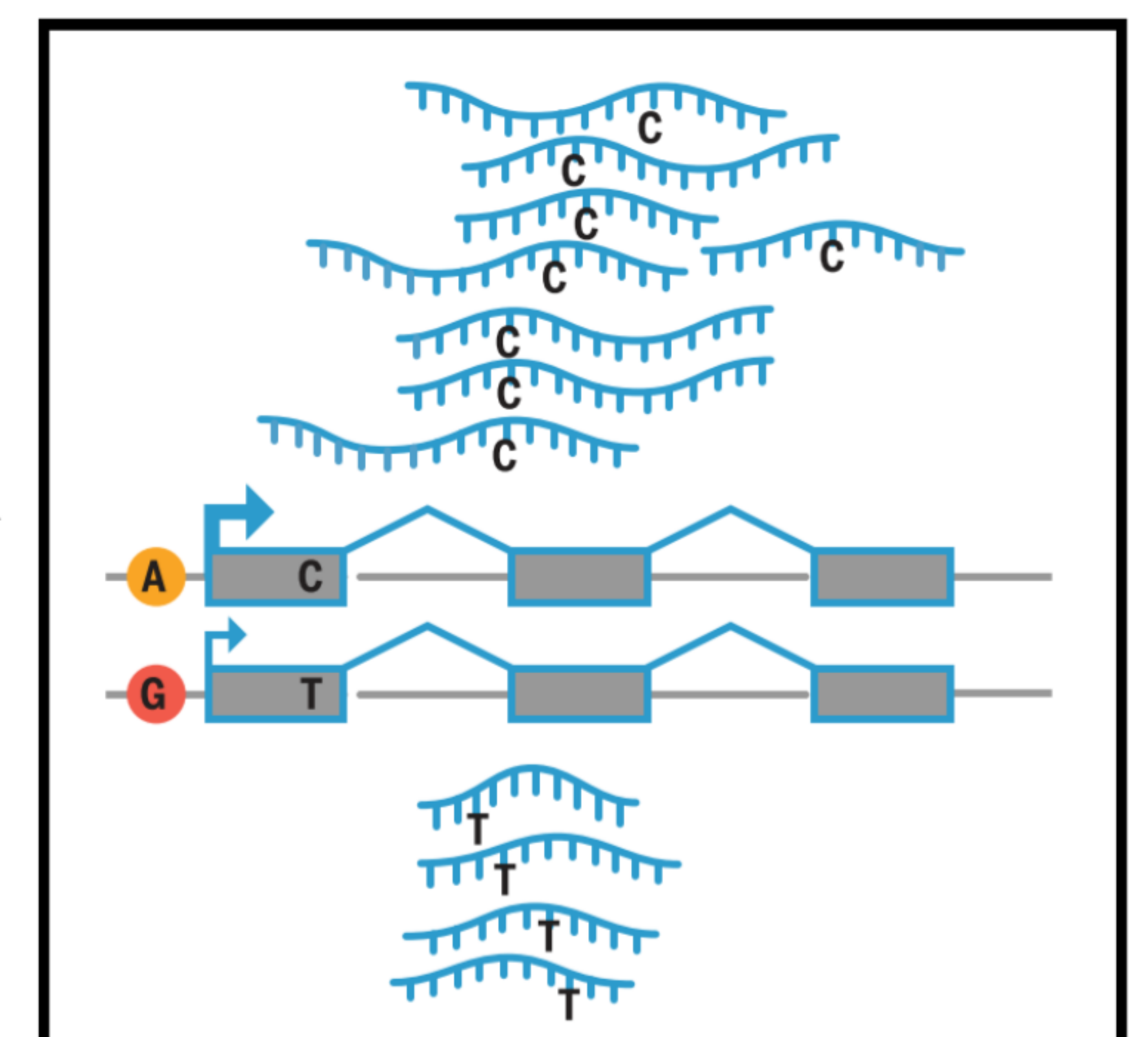
Databases used to identify expression quantitative trait loci (eQTLs) within the genomic loci of lncRNAs.

1 lncMBs

Three MYC-dependent lncRNAs identified in MB, experimentally showed to promote oncogenesis

3 eQTLs Analysis

Gene-variant association linking lncMBs loci with change in expression of nearby PCGs.



4 Structure prediction

RNAFold structure prediction of lncMB1 to study SNPs effect on its structure.