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## isomiRs as a feature for comparing microRNA regulatory networks in aggressive lymphomas

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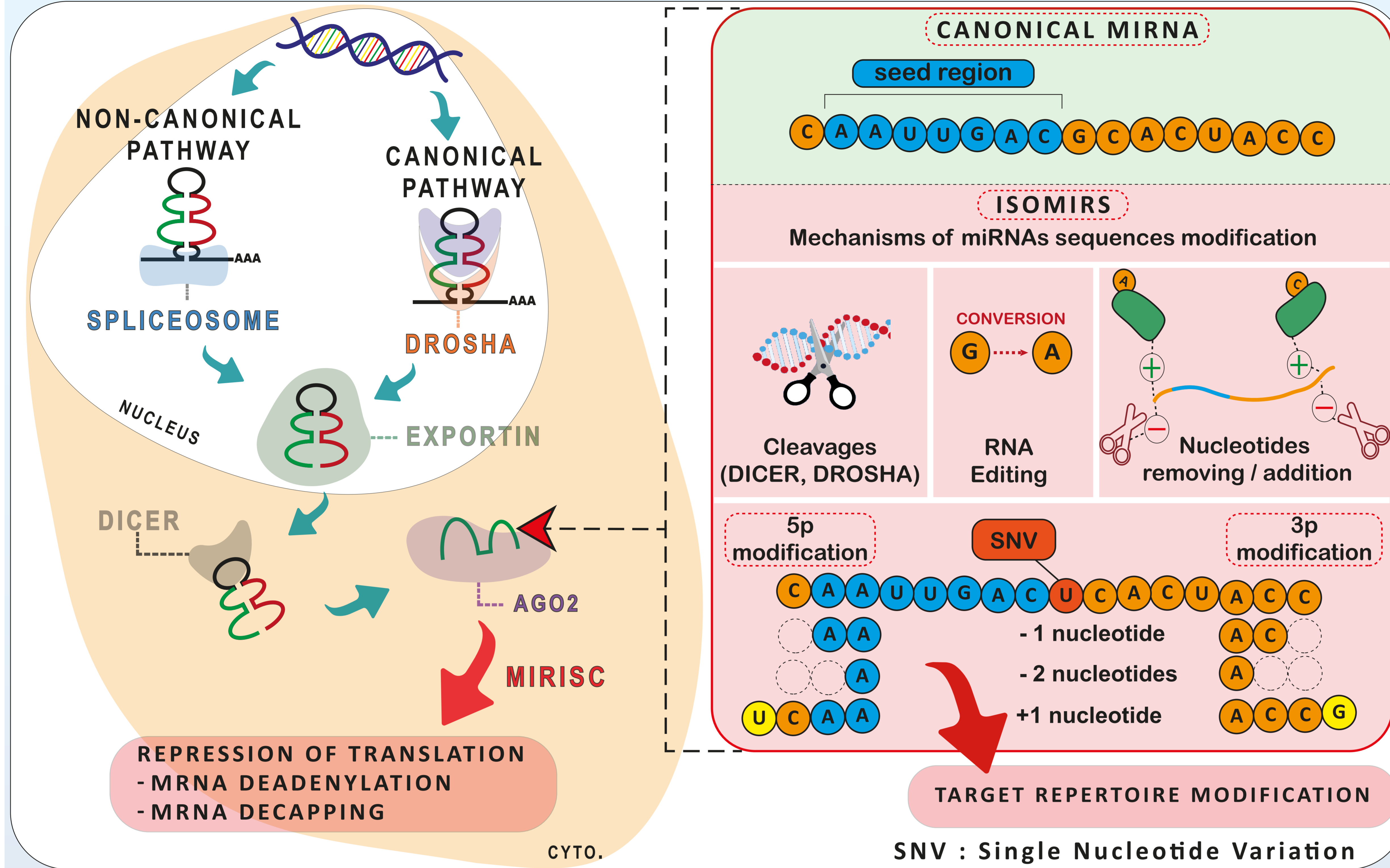
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### MIRNA & ISOMIRS

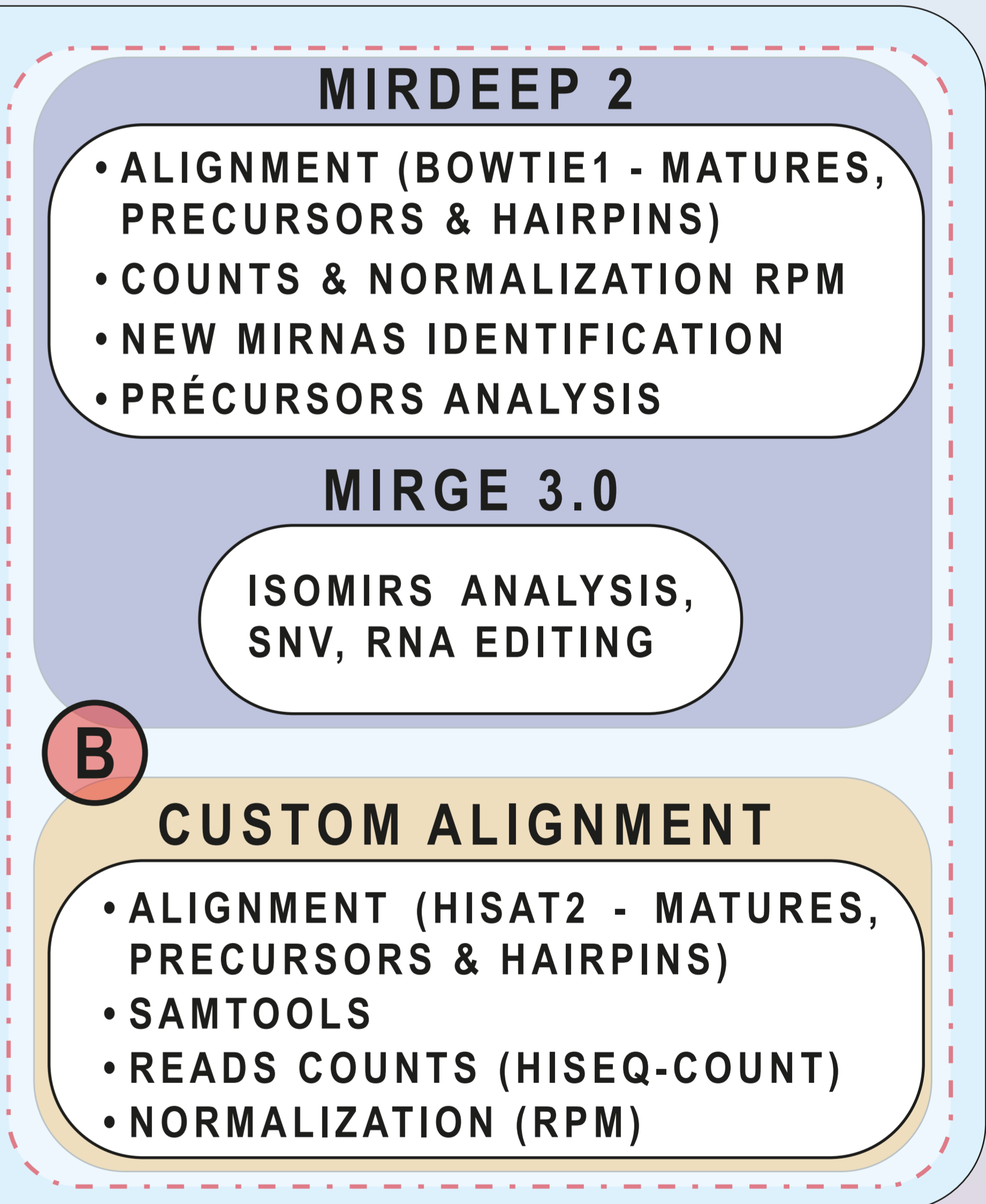
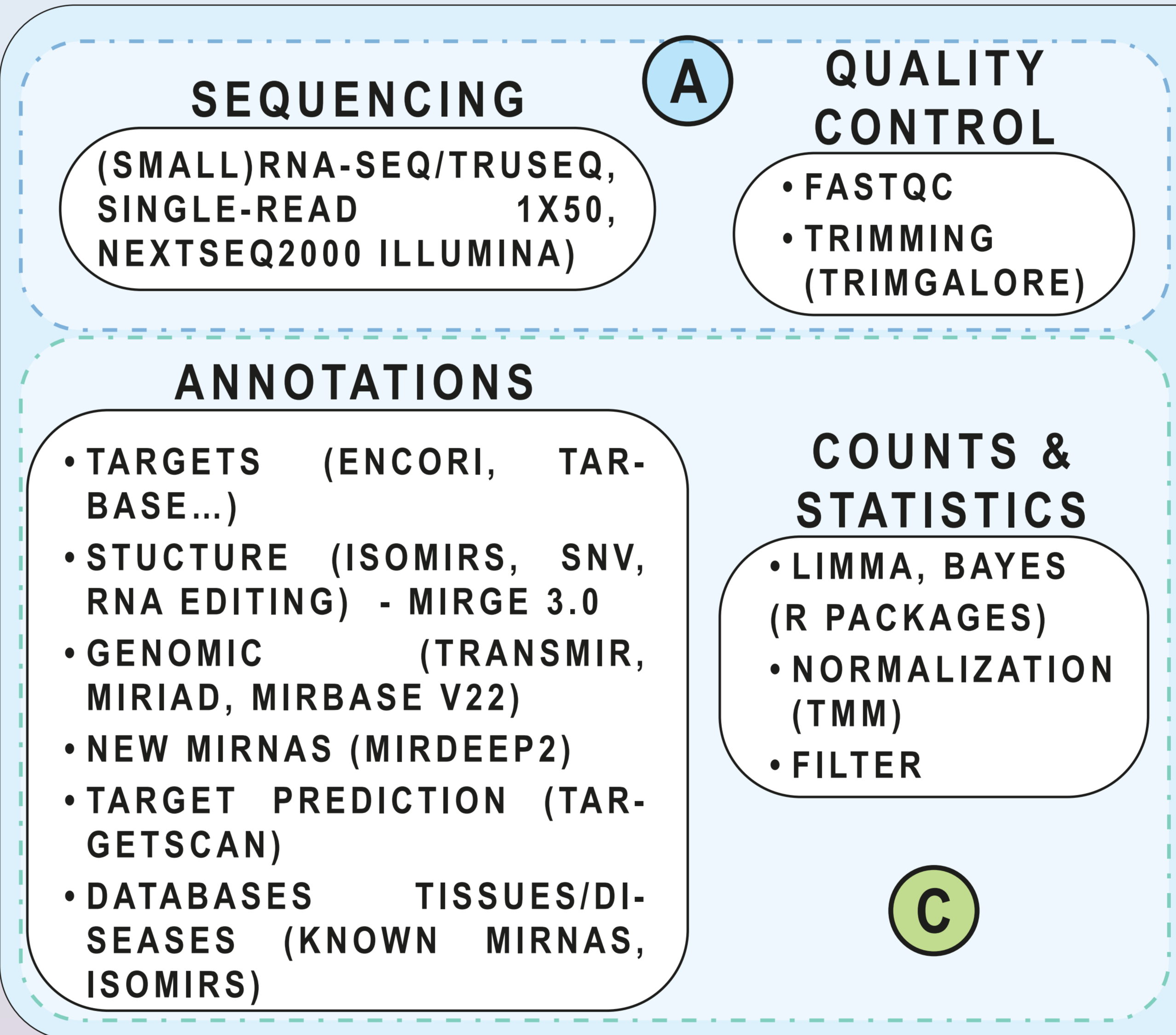
MicroRNAs (miRNAs) constitute a class of small non-coding RNAs that regulate protein translation by targeting messenger RNAs.

Mature miRNAs sequences are subject to variations, creating a panel of isomiRs with unique target repertoires and turnover rates. Recent studies increasingly underscore the involvement of isomiRs in cancer development.

### (SMALL)RNA-SEQ DATA ANALYSIS WORKFLOW

We have devised an original workflow integrating the functionalities of miRDeep2 and miRge3.0 with in-house approaches, which aims to fully characterize miRNA isotypes and their single nucleotide variations (SNVs).

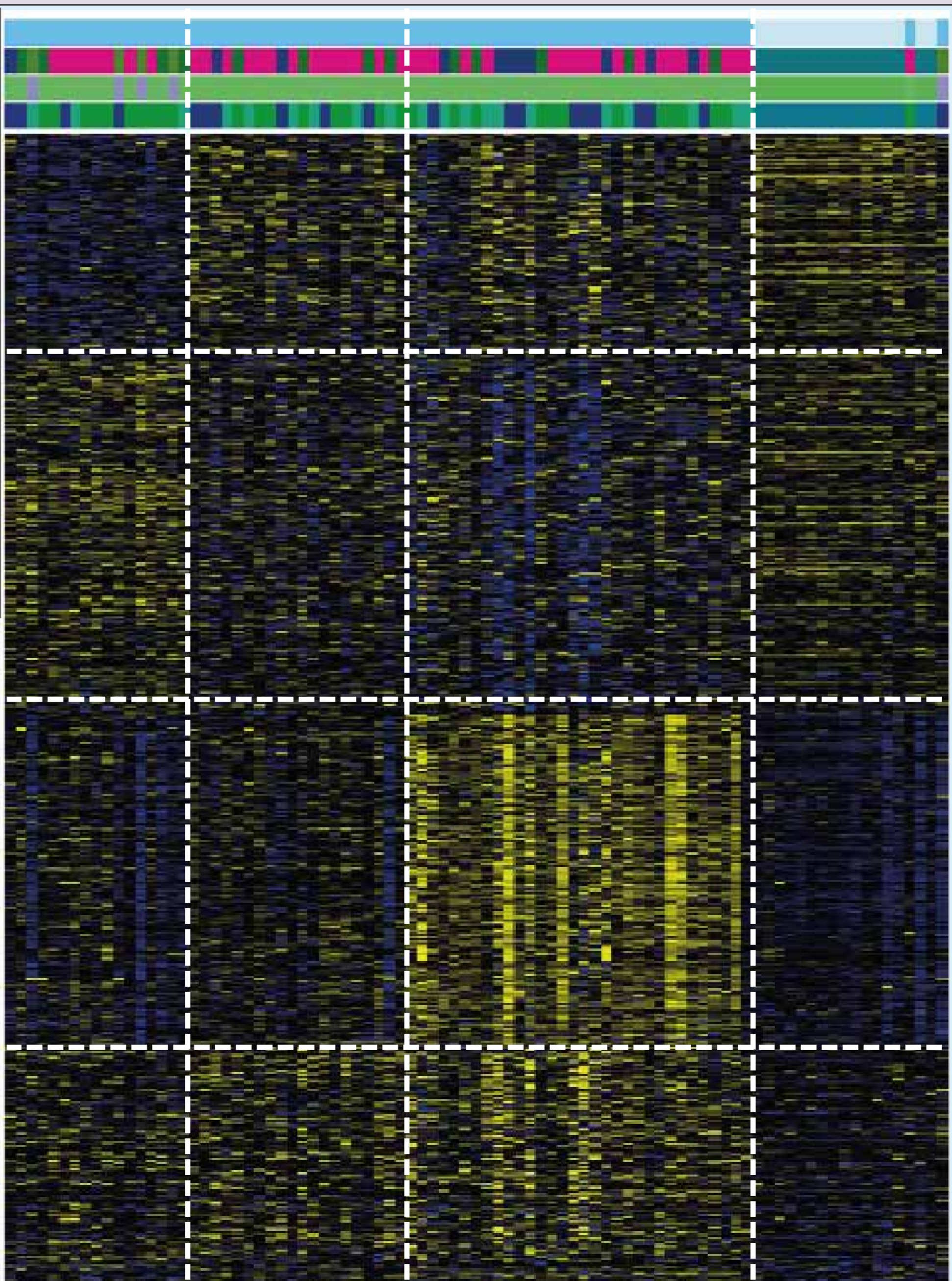
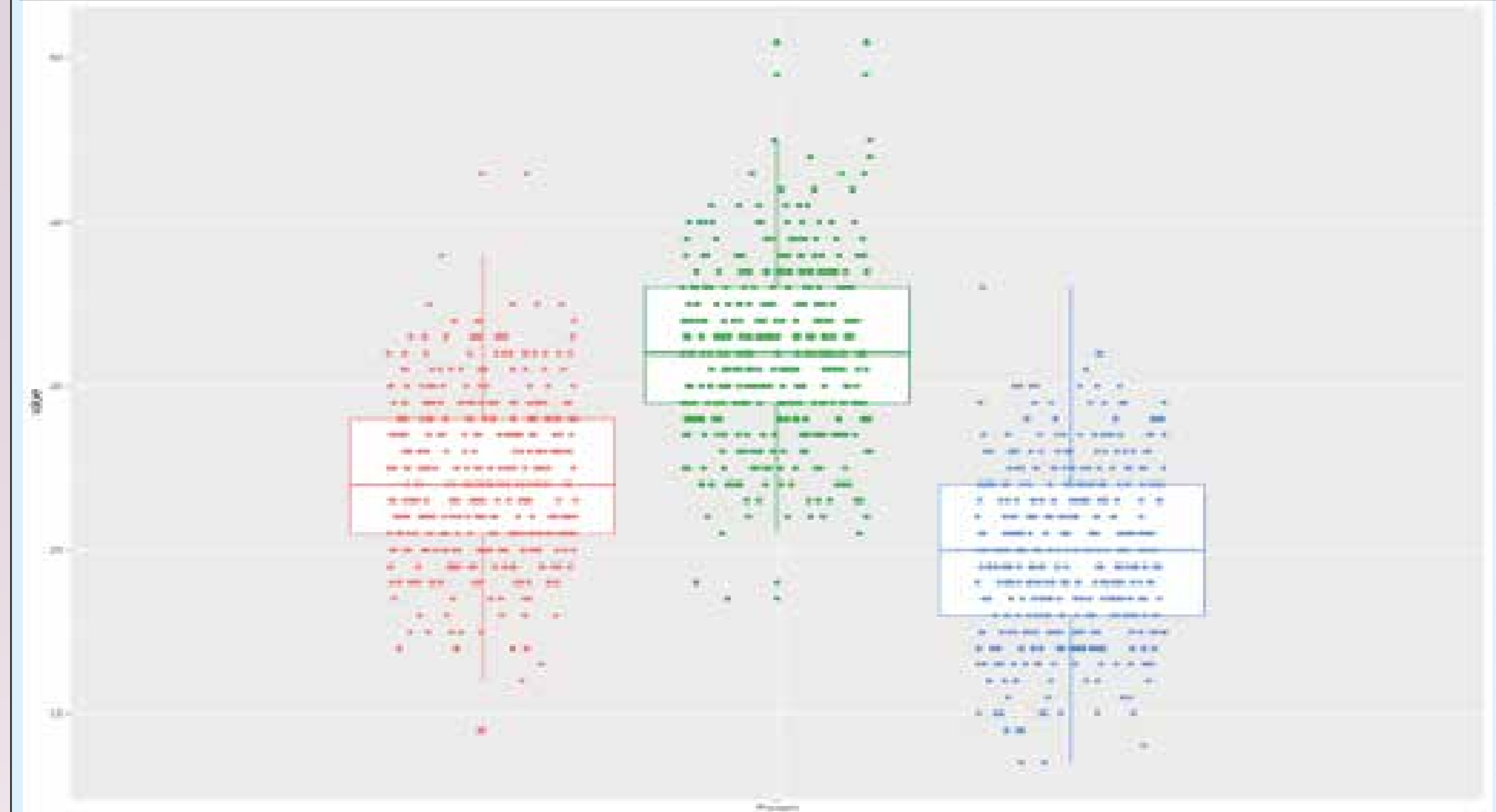
The pipeline computes metrics, abundances, descriptive and differential statistics related to each isomiRs, generating an isomiRnome for integration with other omics and reporting the regulatory network linked to miRNAs.



### ISOMIRS IN AGGRESSIVE LYMPHOMAS

We applied our methodology to a publicly available small-RNA-seq dataset of 102 diffuse large B-cell lymphoma (DLBCL) and healthy samples<sup>1</sup>.

Comparative analysis between relapsed DLBCL and non-relapsed DLBCL cases revealed variations in the average count of unique isotypes per miRNA, as well as differential isomiR proportions and SNVs.



### CONCLUSION

These findings suggest a global loss in the isotype repertoire diversity and a disruption of regulatory mechanisms controlling expression of miRNAs in relapsed DLBCLs.

This approach redefines isomiRs as intricate networks shaping the expression of miRNAs. It opens novel opportunities for investigating miRNA-seq data and for their use in multi-omics analyses.