Mutations associated with hematologic neoplasms can be distinguished from CHIP using cfRNA from 40 genes.

Conclusions:

- Analyzing cfRNA expression levels adds another level of confidence to the ability of interpreting mutations detected in liquid biopsy testing.

- Machine learning algorithms are needed for interpreting low level cfRNA biomarkers in circulation.

- cfRNA in machine learning when combined with cfDNA is particularly important in liquid biopsy testing for minimal residual disease (MRD) when a tissue baseline sample is not tested (tumor-agnostic).