ResolveSEQ MRD

BioSkryb GENOMICS

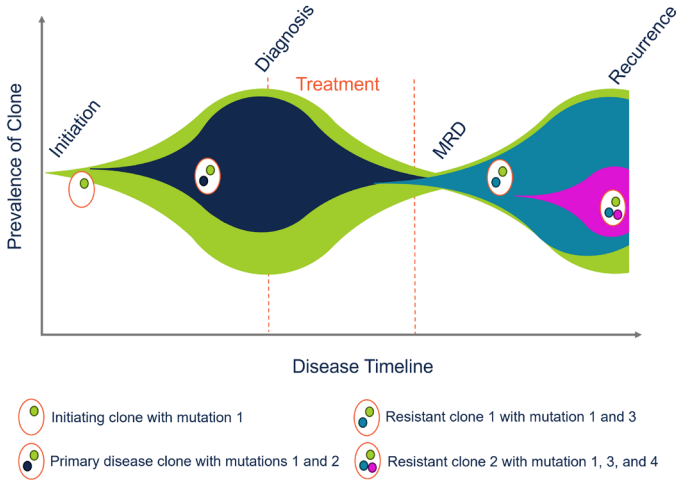
Defining resistance mechanisms of measurable residual disease (MRD) with single-cell multiomics

MRD monitoring of hematological malignancies like acute lymphoblastic leukemia, acute myeloid leukemia, chronic lymphocytic leukemia, and multiple myeloma has transformed patient care.

- MRD informs disease risk stratification and treatment.
- MRD monitoring improves patient outcomes while reducing toxicity from unnecessary treatment.

MRD monitoring can be achieved through flow cytometry.

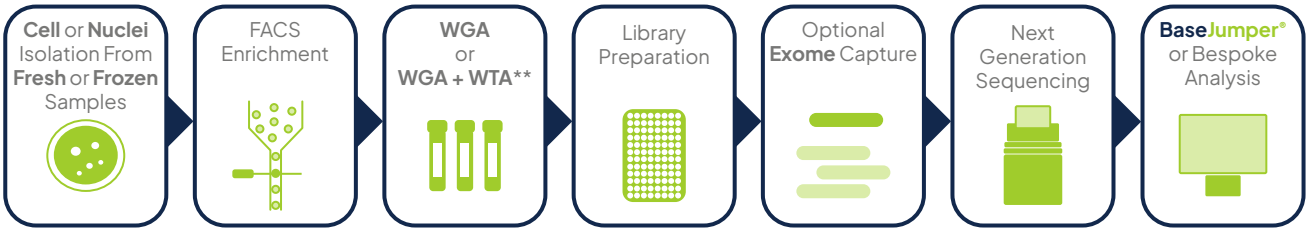
- Protein biomarkers are used to distinguish tumor from normal cells.
- Flow cytometry enumerates the number of tumor cells.



- MRD cells, enriched by flow cytometry, provide an excellent opportunity for genomic and transcriptomic characterization of persister cells.

Introducing ResolveSEQ MRD, a service offering from BioSkryb Genomics

ResolveServices℠ offers a comprehensive single-cell multiomic analysis of MRD cells (sample workflow below). This approach leverages enrichment of MRD cells through flow cytometry for cell plating into wells. Individual MRD cells then undergo whole genome amplification via primary template-directed amplification (PTA) and a reverse transcription and amplification step, providing unified genomic and transcriptomic data from individual MRD cells.



FACS: Fluorescence-Activated Cell Sorting, WGA: Whole Genome Amplification, WTA: Whole Transcriptome Amplification,
Optional **targeted protein detection available

Truly single-cell genomic and transcriptomic data for discovering novel prognostic and therapeutic signatures in MRD cells.

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