

Efficient Target Capture for Cell-Free Mutation Detection



SNVs



InDEls



CNVs

RELEVANT FRAGMENT CAPTURE

AMP™-based target enrichment preferentially enriches for highly fragmented ctDNA over genomic cell-free DNA (cfDNA) to reduce background noise and increase detection sensitivity of low allelic frequency (AF) mutations.

SINGLE-DAY LIBRARY PREP

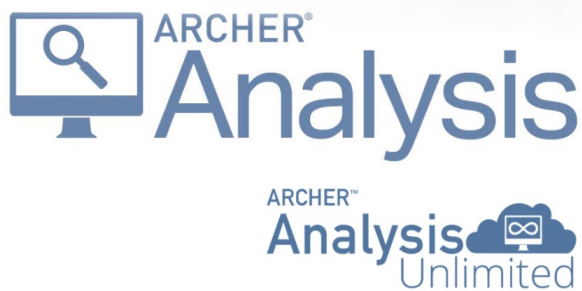
NGS-ready libraries can be prepared in under 8 hours with less than 1 hour of hands-on time, providing sequencing results in as little as 3 days.

ERROR CORRECTION & QUANTITATIVE ANALYSIS

Molecular barcode adapters ligated prior to amplification enable duplicate read binning and advanced error correction for confident variant calls.

SENSITIVE & ROBUST VARIANT DETECTION

Reliably detect high AF (5%) variants using as little as 5ng total ctDNA input and low AF (1%) variants from as little as 10ng.



Archer Analysis provides deep analytical metrics in an easy to interpret interface.



Powerful
Bioinformatics



Ultimate
Adaptability



User-Friendly
Analysis



Secure
Platform

Available for **local** or private **cloud-based** installation

ANALYZE

- Simple, Intuitive Web-Based Interface
- Integrate LIMS Data
- Automate Sample Processing
- Customize Outputs

INTERPRET

- Comprehensive Sample and Fusion QC Metrics
- Visualize Fusions, Variants, Expression
- Dynamic Post-Processing Filtering Sets
- Third-Party or Locally Curated Annotations

REPORT

- Assignment and Tracking
- Customize PDF Reports
- Automate With Third-Party Software
- Easy to Interpret Reporting