

Uncovering The Most Complex Genomic Alterations

SOLID TUMORS

BLOOD CANCERS

SARCOMAS

INHERITED DISEASES



FUSIONPlex®

























A single platform for reliable genomic profiling.

ANCHORED MULTIPLEX PCR (AMP™)

AMP is a robust technology for DNA and RNA sequencing that enables sensitive and specific detection of multiple mutation types.

BUILT FOR MAXIMUM GENE FUSION DETECTION TARGETS BOTH KNOWN AND EMERGING GENOMIC ALTERATIONS MOLECULAR BARCODES ENABLE ADVANCED ERROR CORRECTION

STANDARD NGS	ARCHER*
Liquid workflows can be complex and require master mixes	Simple, lyophilized reagents reduce the risk of contamination and save time
Can miss rare or unknown fusions	Detects fusions regardless of partner
Cannot discern starting molecule from PCR duplicates	Uniquely tracks starting molecules prior to amplification
PCR duplicates introduce errors, inflate true coverage and mask library complexity	PCR duplicates are utilized for error correction to increase sensitivity and specificity

ROBUST DETECTION CAPABILITIES FOR ALL MUTATION TYPES













FUSIONS

CNVs

SPLICING

InDELs







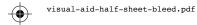














Simplified workflow for reliable and fast genomic profiling.



CONSISTENT AND FAST WORKFLOWS

- SIMILAR WORKFLOW ACROSS ALL PRODUCT LINES
- 2.5 HOURS HANDS-ON TIME
- SINGLE DAY LIBRARY PREPARATION*



Lyophilized reagents ensure consistent results

SINGLE-USE, LYOPHILIZED REAGENTS

- NO MASTER MIXES
- MINIMIZED USER ERROR AND CONTAMINATION
- LONGER HALF-LIFE VS. LIQUID REAGENTS



8-tube strip format for run size flexibility

FLEXIBLE

- VARIABLE INPUT AMOUNTS STARTING FROM 10ng
- FFPE OPTIMIZED
- COMPATIBLE WITH AUTOMATION
- 8-TUBE STRIP FORMAT

*RNA panels up to 1.5 days



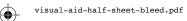








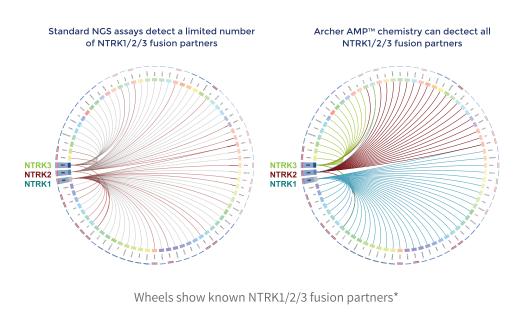




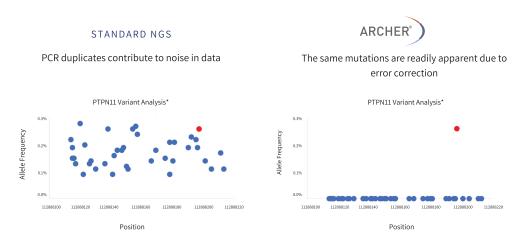




Sensitive fusion detection without prior knowledge of fusion partners.

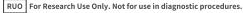


Better Detection of Low Allele Frequency Mutations vs. Standard NGS



*Data on file

















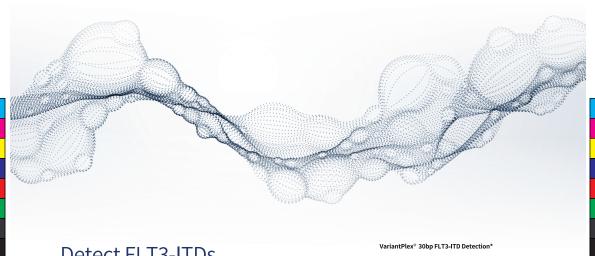
ARCHER®





Not all NGS assays detect FLT3-ITDs the same.

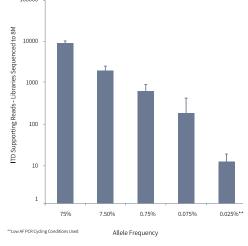
- Internal tandem duplications (ITDs) in FLT3 are actionable mutations but challenging to identify
- Archer® Blood Cancer NGS panels combine AMP™ chemistry with powerful bioinformatics to detect FLT3-ITDs
- Detect ITDs across a wide range of sizes and insertion points with Archer assays



Detect FLT3-ITDs with AMP Technology

- Archer assays can detect ITDs ranging in size from 3bp to 300bp+ at low allele frequencies
- Can readily customize to meet your needs without sacrificing performance
- Compatible with blood, bone marrow, PBL and FFPE sample types





*Data on file





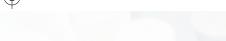














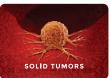




RNA-BASED FUSION, EXPRESSION AND VARIANT DETECTION



Comprehensive coverage of recurrent, rare and novel fusions









FUSIONS



SNVs & InDELs



SPLICING



NOVEL FUSIONS

AMP™ chemistry utilizes open-ended targeted amplification to identify gene fusions whether or not the partner is known.

LOW INPUT

AMP chemistry was purpose-built for library prep from low-input and degraded samples such as FFPE tissue.

EXPRESSION

Molecular barcoded fragments enable accurate RNA abundance calculations.

SPLICE VARIANTS & ISOFORMS OF INTEREST

Detect cancer-associated events such as METex14 skipping, EGFRvIII or kinase domain duplications.

QUIVER® FUSION DATABASE

Powerful fusion analysis combined with a curated database of relevant known translocations.

CUSTOMIZATION

Create from scratch or modify any panel to keep up with the pace of discovery.













DNA-BASED VARIANT AND CNV DETECTION

Confident variant detection powered by error-corrected sequencing







AMP™ chemistry was purpose-built for library prep from low-input and degraded samples such as FFPE tissue. Compatible with blood and bone marrow input types.



Error correction features within Archer Analysis reduce sequencer noise to reveal mutations below standard NGS-based detection thresholds.



SNVs



CNVs



InDELs

QUANTITATIVE CNV DETECTION

Molecular barcoded fragment counting provides robust copy number analysis.

COMPREHENSIVE COVERAGE

AMP chemistry provides complete, strand-specific and bi-directional coverage of target exons to maximize variant detection.

COMPLEX MUTATION DETECTION

Coverage combined with powerful bioinformatics enables mutation detection in traditionally difficult regions like CEBPA & FLT3.

CUSTOMIZATION

Create from scratch or modify any panel to keep up with the pace of discovery.













Efficient Target Capture for Cell-Free Mutation Detection





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.



InDELs

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.



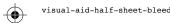


















T- and B-Cell Receptor Panels for Clone Tracking



IMMUNE REPERTOIRE CHARACTERIZATION

Unbiased amplification for a true and reproducible measure of diversity.

SENSITIVE CLONOTYPE IDENTIFICATION

AMP™-powered error correction provides a true measure of sample complexity and enables rare clone identification.

COMPREHENSIVE COVERAGE

Archer molecular barcode adapters contain universal primer binding sites allowing for open-ended amplification and sequencing throughout the entire V(D)J region, resulting in increased coverage of CDR3.

FLEXIBLE INPUT

Input amounts range from 25ng to 2µg of RNA from PBMC, FFPE or fresh frozen tissue sample types.

MULTIPLE APPLICATIONS

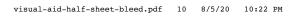
Archer Immunoverse™ can be used for disease tracking, repertoire profiling and immune reconstitution.





















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









Adaptability

User-Friendly

Secure

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

ANALYZE

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

NTERPRET

- 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







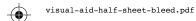


















- CREATE A CUSTOM ASSAY OR MODIFY AN EXISTING PANEL
- ENABLES FUTURE CONTENT ADDITIONS
- COMPATIBLE FOR ALL INPUT TYPES
- SCALABLE FOR HIGH-THROUGHPUT LABS



- EXPANDABLE WITHOUT COMPROMISING ASSAY PERFORMANCE
- LEVERAGE A SIMPLE WORKFLOW
- REPRODUCIBLE IN ALL SAMPLE TYPES

EFFICIENT FOCUSED

- DELIVERED IN AS FEW AS 4 5 WEEKS
- INTERNAL TEAM OF EXPERTS SUPPORTING INDIVIDUAL LABORATORY NEEDS







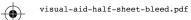




















ArcherDX is Your Comprehensive Genomic Sequencing Partner



ONE SOURCE

Comprehensive suite of assays across a broad range of disease states



SIMPLIFIED WORKFLOW

Simplified workflow using lyophilized reagents, ensuring minimal errors



USER-FRIENDLY

Integrated analytics in an easy to interpret, actionable report



Proven accuracy in detecting existing and novel fusions through enhanced technology



Fast turn-around time (~1 week)



FLEXIBLE

Easily create custom assays from scratch or modify an existing panel







