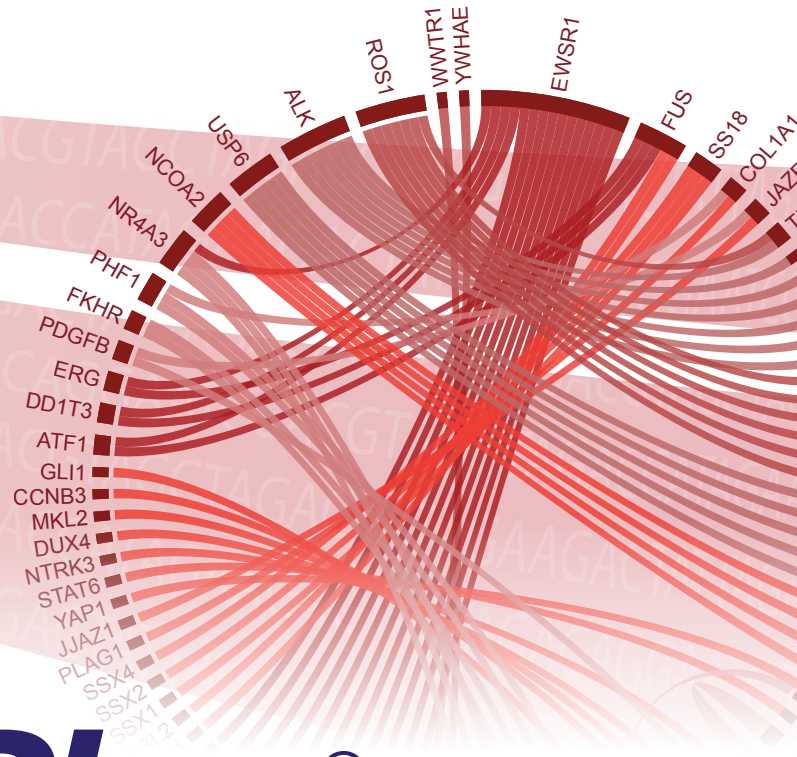
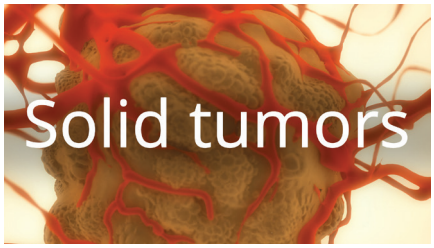
ARCHER®



FUSIONPlex®

Unleash the power of NGS for focused fusion detection



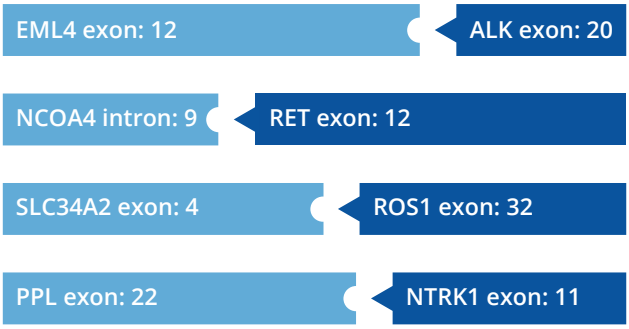
Archer® FusionPlex® NGS Assays and Bioinformatic Analysis

- Purpose-built to sequence FFPE samples
- Simple lyophilized workflow
- Known and novel fusion detection
- Molecular barcode (MBC)-driven sensitivity
- RNA-based SNV and expression profiling

Archer FusionPlex RNA Assays

Targeted RNA-seq to identify oncogenic driver mutations from low-quality RNA

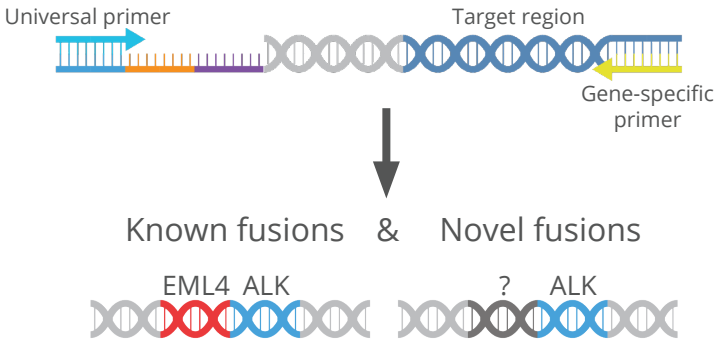
- ☑ Detect known and novel gene fusions
- ☑ Confirm key point mutations (SNVs/indels)
- ☑ Capture RNA abundance & expression imbalance

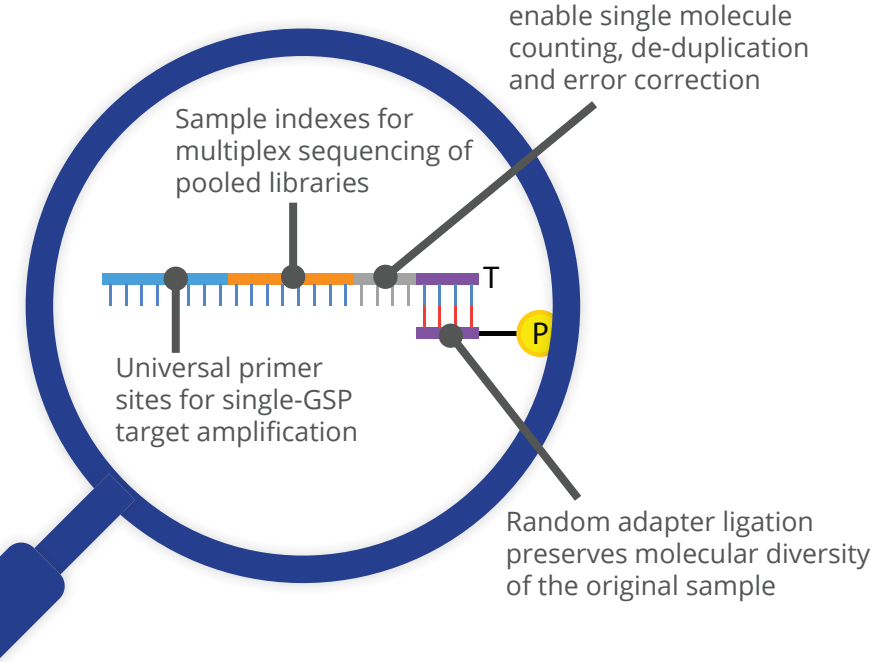


Known and Novel Fusions

Anchored Multiplex PCR (AMP™) chemistry relies on MBC adapters for target amplification. These partially-functional adapters are ligated to cDNA fragments and contain a universal primer binding site that permits amplification of both known and unknown genomic regions of interest.

This approach generates libraries with random start sites and varying lengths, increasing library complexity and retaining sample heterogeneity. AMP chemistry can capture both 5′ and 3′ fusions, including novel fusions that would be missed by opposing primer-based methodologies.





Adapter-driven Accuracy

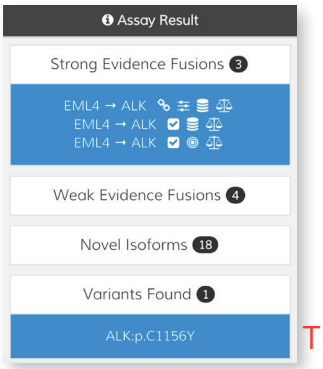
Archer Molecular Barcode (MBC) Adapters are at the heart of AMP chemistry. These half-functional adapters are ligated to nucleic acid fragments prior to amplification to capture unique fragments.

Each adapter molecular carries a unique molecular identifer (UMI) that, combined with random start sites, can be used to deduplicate reads. This approach eliminates amplification bias, corrects PCR and sequencing errors, identifies expression imbalance and strengthens statistical confidence.

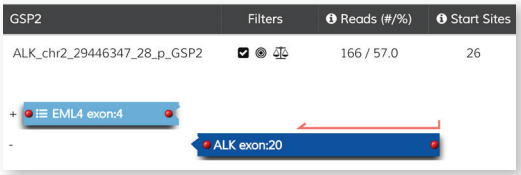
Comprehensive Analysis

Oncogenic driver mutations are diverse, and established methods of detection do not provide a complete picture of a tumor's unique mutation profile. Archer FusionPlex assays are complemented by Archer Analysis bioinformatics software to report fusions, relevant point mutations and expression imbalance. Now that's *real* comprehensive tumor profiling.

Fusion calls

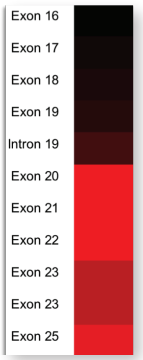


Breakpoint visualization

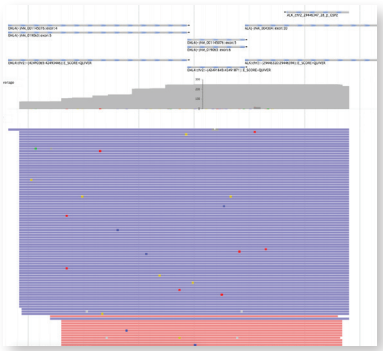


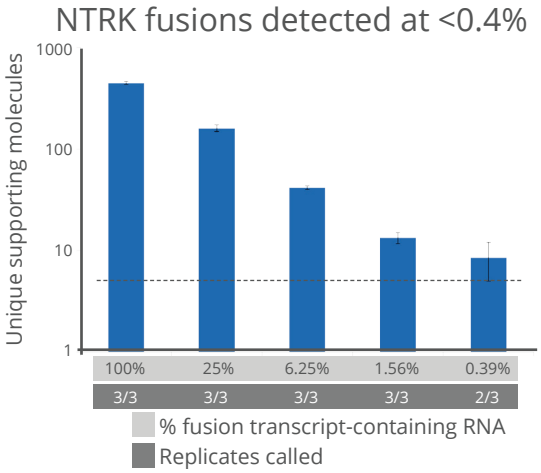
TKI resistance mutation

Expression imbalance



Read visualization





Sensitive Mutation Detection

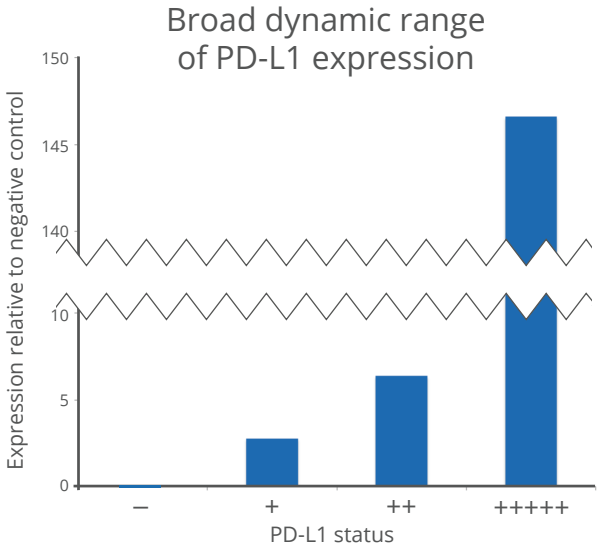
Archer FusionPlex NGS assays show sensitive detection of translocations and point mutations. In the figure at left, TPM3:NTRK1 fusion-containing RNA was serially diluted into fusion-negative background RNA and libraries were prepared using the Archer FusionPlex CTL Assay using 100ng total input. After sequencing, fusions were called based on sequencing reads spanning the fusion breakpoint down to 0.39% fusion-containing RNA. A minimum of 5 supporting unique start sites are required for fusion calls, as indicated by the dotted line.

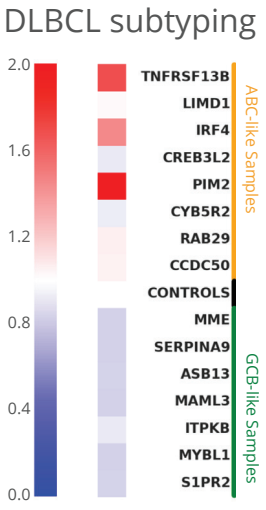
RNA Expression

Relative RNA abundance can be determined for select genes, because molecular barcodes are ligated to input material prior to amplification. Knowing RNA abundance helps with tissue of origin identification, expression signature-based differentiation of diffuse large B-cell lymphoma (DLBCL) subtypes and relative expression level detection in critical genes.

The figure to the right shows how relative RNA abundance can be used to measure CD274 (PD-L1) expression levels across 4 FFPE expression standards* of varying PD-L1 status (*left panel*) and across different DLBCL subtypes (*right*

*Horizon® CD274 (PD-L1) Reference Standard



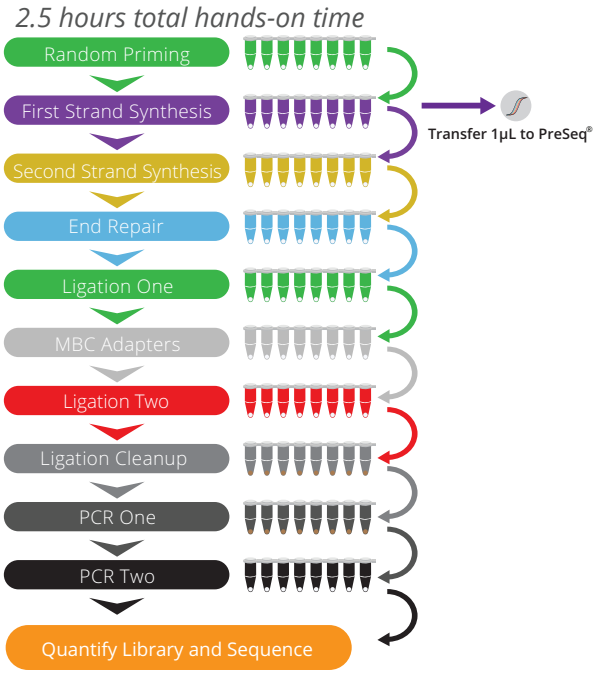


The Archer Advantage

Simple Workflow

Tech-friendly workflow simplifies library preparation, minimizes the potential for user error and ends wasted reagents

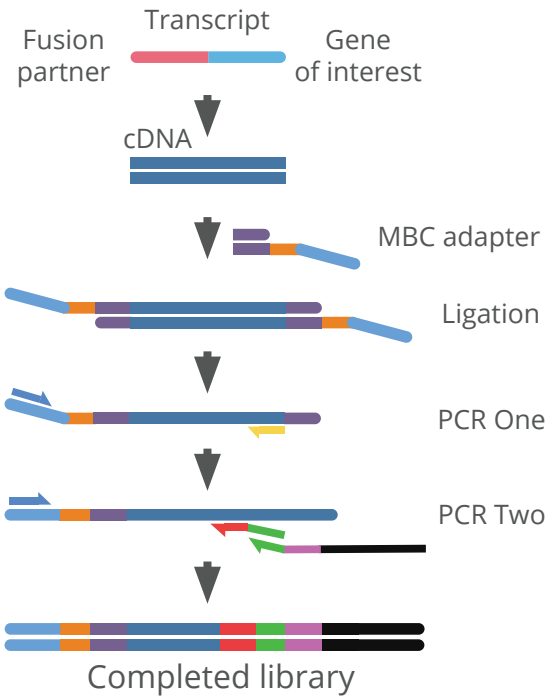
- Lyophilized reagents ensure consistent results
- Single-use reactions reduce contamination
- 8-tube strip format enables run size flexibility
- <2 days from extraction to sequencing



AMP Chemistry

Patented Anchored Multiplex PCR (AMP) target enrichment chemistry provides maximum resolution of oncogenic driver mutations

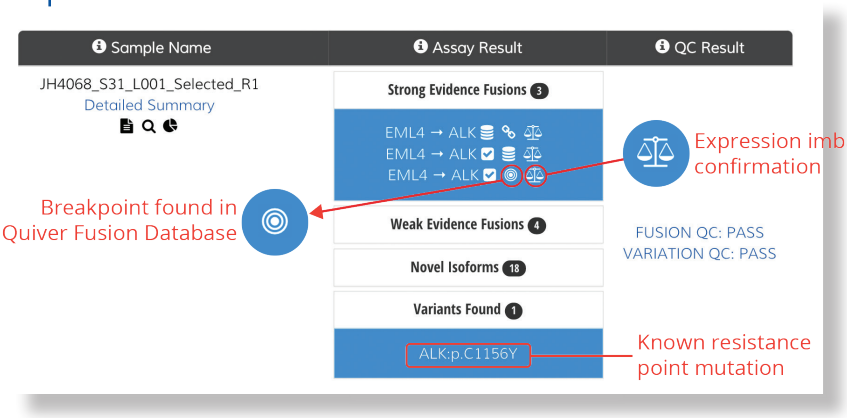
- Purpose-built for FFPE
- Unidirectional priming for novel fusion detection
- Molecular barcodes enable quantitative analysis
- Random start sites ensure high target coverage



Integrated Bioinformatic Pipeline

The Archer Analysis bioinformatics suite reports gene fusions and other relevant mutations in your sample at nucleotide-level resolution. The software cross-references the Archer Quiver® Fusion Database to report fusions that are in the literature to help you identify any novel fusions.

Archer Analysis also reports relevant point mutations and provides QC indicators to deliver confidence in your NGS data. Analysis is available as a virtual machine for local installation and as a cloud-based service.



ARCHER®

Learn more at archerdx.com/fusionplex

RUO For research use only. Not for use in diagnostic procedures.