Discover your assay solutions for solid tumor, blood cancer, immune profiling, and genetic disease research

Deliver answers confidently using Archer NGS assays, designed with patented Anchored Multiplex PCR (AMP™) chemistry, streamlined workflows, and user-friendly analysis.

- VARIANT*Plex*™ panels provide sensitive variant DNA detection, including in low-input or degraded samples such as FFPE tissue.
- FUSION*Plex*™ panels use RNA to identify both known and novel fusions, ensuring you receive comprehensive information.
- LIQUID*Plex*™ panels pinpoint low-frequency variants in ctDNA samples.
- IMMUNO Verse[™] panels provide immune profile insights to blood cancer and solid tumor research samples.

To keep up with the pace of discovery, you can customize Archer panel content. Easily add predesigned, functionally-tested primers to existing panels or create a panel from scratch that fits your exact requirements with the Archer's design tool, Assay Marketplace.



Workflows for VARIANTPlex, FUSIONPlex, LIQUIDPlex, and IMMUNO Verse research assays. Put Assay Marketplace to work for you with support for panel selection and/or design. Library preparation, sequencing, and analysis have similar workflows and bench-top protocols for all panels, allowing for lab efficiencies. Extraction and sequencing is not included with Archer NGS assays, but assays are compatible with common sample types and sequencing platforms.

Archer assay technology has been designed for flexibility with different sample types, nucleic acid inputs, genes targeted, and genomic alterations identified. This design allows for easier adoption, training, and continued research use in your lab with multiple Archer panels.



Solid Tumor Catalog Panels

Sensitive, targeted NGS assays for solid tumor tissue and plasma samples ensure that you receive reliable, comprehensive genomic information for your oncology research

		Genes Targeted	Genomic alterations detected	Recommended reads
,	VARIANT <i>Plex</i>			
	Complete Solid Tumor	430	SNVs, indels, CNVs, ITDs, MSI, TMB	45 M NEW!
lnpu	Pan Solid Tumor	185	SNVs, indels, CNVs, ITDs, MSI, TMB	25 M NEW!
DNA Input	Expanded Solid Tumor	76	SNVs, indels, CNVs, ITDs, MSI	6 M
_	Core Solid Tumor	60	SNVs, indels, CNVs, ITDs, MSI	4.5 M
	Solid Tumor Focus v2	20	SNVs, indels, CNVs, ITDs, MSI	1.5 M
	FUSION <i>Plex</i>			
put	Pan Solid Tumor v2	137	Fusions, SNVs, indels, expression	3.5 M
RNA Input	Core Solid Tumor	57	Fusions, SNVs, indels, expression	3 M NEW!
~	Sarcoma v2	63	Fusions, SNVs, indels, expression	2 M
	Lung v2	17	Fusions, SNVs, indels, expression	1 M
ctDNA Input	LIQUID <i>Plex</i>			
	Universal Solid Tumor	29	SNVs, indels	5 M

Customize panels or design from scratch. Get started at Assay-Marketplace.Archerdx.com.

Solid Tumor Complete Genomic Profiling Solutions

Pair reliable DNA- and RNA-based research assays to efficiently generate a complete biomarker profile

Paired Panels	Genes	Reads	Samples* per NextSeq 500/550 high output kits v2.5	
FUSION <i>Plex</i> Lung v2	17	1 M	160	
VARIANT <i>Plex</i> Solid Tumor Focus v2	20	1.5 M		
FUSION <i>Plex</i> Core Solid Tumor	57	3 M		
VARIANT <i>Plex</i> Core Solid Tumor	60	4.5 M	53	
FUSION <i>Plex</i> Pan Solid Tumor v2	137	3.5 M	14	
VARIANT <i>Plex</i> Pan Solid Tumor	185	25 M		
FUSION <i>Plex</i> Pan Solid Tumor v2	137	3.5 M	8	
VARIANT <i>Plex</i> Complete Solid Tumor	430	45 M		

Data assumes Archer libraries are prepared using liquid adapters. *Sample = 1 VARIANTPlex library + 1 FUSIONPlex library

VARIANT*Plex* and FUSION*Plex* panels can be paired for cost-effective solutions to provide SNVs, indels, CNVs, ITDs, fusions, expression, MSI, and TMB information from a single sample.

High-throughput workflows enabled with liquid reagents and scalable analysis



Compatible with all VARIANT*Plex* and FUSION*Plex* panels for Illumina[®] sequencers, liquid reagents enable automated liquid handling workflows for high volume research labs. To best suit your lab's needs, liquid reagents are available in 24- and 96-reaction kits and are color matched to protocol steps for easy use.

NEW: Liquid reagents



Handle hundreds of samples simultaneously with rapid analysis times, without expensive hardware or associated maintenance, when you use Archer's Analysis Unlimited, a private cloud-based solution.

NEW: Up to 70% faster variant calling



Blood Cancer Catalog Panels

Sensitive, purpose-built NGS assays ensure that you generate reliable, comprehensive genomic information for your hematological malignancy research

		Genes Targeted	Genomic alterations detected	Recommended Reads
	VARIANT <i>Plex</i>			
Ħ	Myeloid	75	SNVs, indels, ITDs	4 M
DNA Input	Core Myeloid	37	SNVs, indels, ITDs	3 M
O	MPN Focus	12	SNVs, indels, ITDs	800 K
	AML Focus	11	SNVs, indels, ITDs	800 K
	FUSION <i>Plex</i>			
	Pan-Heme	199	Fusions, SNVs, indels, expression levels	4.5 M
RNA Input	Heme v2	87	Fusions, SNVs, indels, expression levels	1.5 M
	Myeloid	84	Fusions, SNVs, indels, expression levels	1.5 M
	Lymphoma	125	Fusions, SNVs, indels, expression levels	2 M
	Acute Lymphoblastic Leukemia (ALL)	81	Fusions, SNVs, indels, expression levels	1.5 M

Customize panels or design from scratch. Get started at Assay-Marketplace.Archerdx.com.

Blood Cancer Complete Genomic Profiling Solutions

Pair reliable DNA- and RNA-based research assays to efficiently generate a complete biomarker profile

Paired Panels	Genes	Reads	Samples* per NextSeq 500/550 high output kits v2.5
FUSION <i>Plex</i> Pan Heme	199	4.5 M	47
VARIANT <i>Plex</i> Myeloid	75	4 M	47
FUSION <i>Plex</i> Myeloid	84	1.5 M	00
VARIANT <i>Plex</i> Core Myeloid	37	3 M	88

Data assumes Archer libraries are prepared using liquid adapters. *Sample = 1 VARIANTPlex library + 1 FUSIONPlex library

VARIANT*Plex* and FUSION*Plex* panels can be paired for cost-effective solutions to provide SNVs, indels, ITDs, fusions, and expression alterations from a single sample.

Scale easily with liquid reagents and analysis built for high-throughput



Liquid reagents enable high-throughput automated liquid handling workflows and are compatible with all VARIANT*Plex* and FUSION*Plex* panels for Illumina sequencers. Two different size kits (24- and 96- reactions) are available to suit your lab's needs, and protocol steps are color matched to reagents for easy use.





Built for high-throughput workflows, Archer Analysis Unlimited is a private, cloud-based bioinformatics solution that allows you to quickly analyze hundreds of samples simultaneously without expensive hardware or the associated maintenance.

NEW: Up to 70% faster variant calling



Immune Profiling Catalog Panels

Assess B- and T-cell clonalities, somatic hypermutations, tumor-infiltrating lymphocytes, and MRD with assays for your solid tumor and blood cancer research

		Target regions	Applications	Recommended Reads		
RNA Input	IMMUNO Verse					
	T-cell Receptor (TCR)	TCR beta, gamma, alpha, and delta chains	Clonality, MRD, TILs, profiling	250 K to 10 M*		
	B-cell Receptor (BCR)	BCR heavy (IGH) and light (kappa/lambda) chains	Clonality, MRD, profiling, somatic hypermutation	250 K to 10 M*		

^{*}Recommended reads vary depending on input type, quality, B- or T-cell content, and application.

Genetic Disease Catalog Panels

Discover genetic alterations for inherited disease research, including variants important for assessing diverse populations

Recommended
Genes Targeted Genomic alterations detected Reads

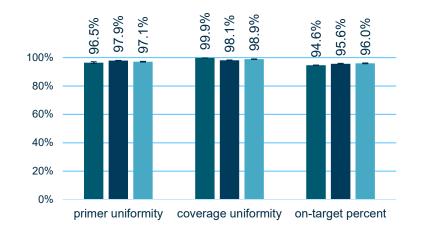
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VARIANT <i>Plex</i>					
Expanded Carrier	111	SNVs, indels, CNVs, ITDs	1.5 M		
CFTR v2	27 exons, select intronic regions	SNVs, structural variants, ITDs	100 K		

Custom Panel Design

Customizable panel content ensures that new designs don't derail your research

Since Archer assays use AMP primers that function independently, gene content can easily be customized without compromising assay performance. To get started, take your target list to Assay-Marketplace.Archerdx.com.





Visit Assay Marketplace

Small panel, 228 primers Medium panel, 554 primers Large panel, 2058 primers

High primer uniformity, coverage uniformity, and percent on-target with AMP primers, regardless of primer pool size, means assay performance remains high even when adding new content.

^{*}Read depth must be scaled appropriately.