FLEXIBLE, CUSTOMIZABLE COMPREHENSIVE GENOMIC PROFILING SOLUTIONS

> Next generation sequencing panels that generate the solid tumor insights you need. Now available with modular HRD assessment.

Flexible CGP content means you can use resources on needed insights without wasting sequencing reads on unnecessary targets. Archer CGP solutions allow you to combine pre-designed panels, add on targets, or create panel content from scratch. Genomic signatures such as MSI, TMB, and HRD can be analyzed for every sample or on a by-sample basis, allowing for optimal use of sequencing resources. Complex key biomarkers like allele-specific copy number (ASCN), ITDs, and novels fusions can also be confidently detected in a variety of samples types like FFPE. As new gene targets are needed, Archer CGP solutions allow for the easy addition of content to in-use assays, without compromising performance and with minimal workflow disruption.

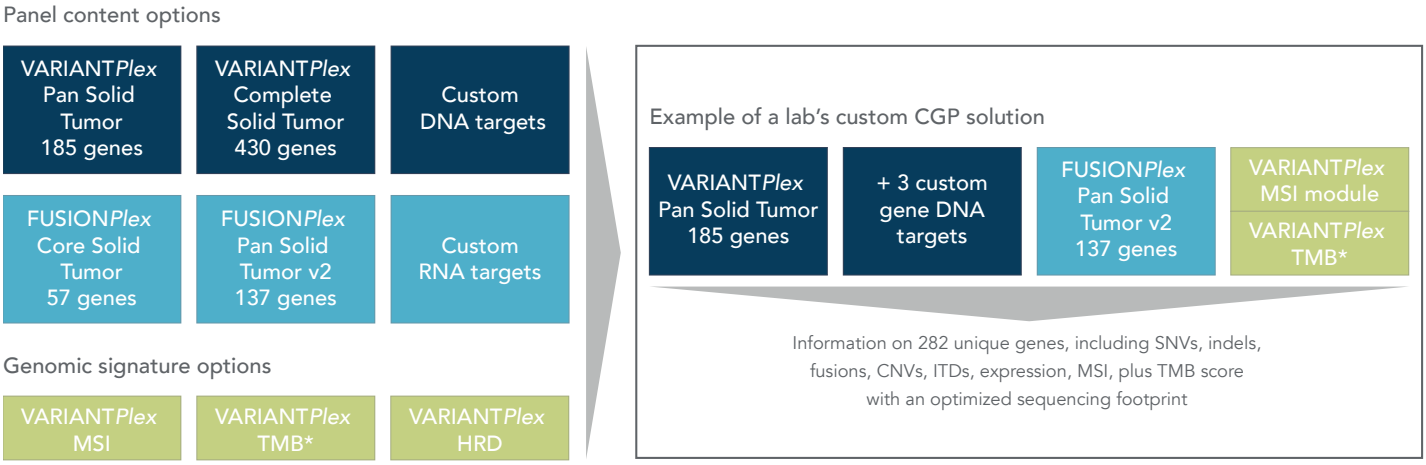
Insights you need, when you need them

Workflows that work for you

Confidence in calls with demonstrated performance

VARIANT*Plex*™ and FUSION*Plex*™ panels can be paired for resource-efficient solutions to provide a customized CGP solution providing information on SNVs, indels, CNVs, ITDs, fusions, and expression alterations, as well as relevant genomic signatures.

Archer flexible CGP solutions



* Microsatellite instability analysis available in all VARIANT*Plex* Solid Tumor pre-designed panels. Tumor mutational burden available with VARIANT*Plex* Pan Solid Tumor and VARIANT*Plex* Complete Solid Tumor.

IDTDNA.COM/ARCHER

INTEGRATED DNA TECHNOLOGIES ARCHER™

Efficiently generate a comprehensive genomic profile for solid tumor samples

Panels	Input	Total genes targeted	Reads	Genomic alterations detected	Samples† per NextSeq 500/550 high output kits v2.5
FUSION*Plex* Pan Solid Tumor v2 & VARIANT*Plex* Pan Solid Tumor v2	RNA & DNA	279	40.5 M*	Fusions, SNVs, indels, CNVs, ITDs, expression, MSI, TMB, HRD	10
FUSION*Plex* Pan Solid Tumor v2 & VARIANT*Plex* Complete Solid Tumor v2	RNA & DNA	511	60.5 M*	Fusions, SNVs, indels, CNVs, ITDs, expression, MSI, TMB, HRD	6

Data assumes Archer libraries are prepared using liquid adapters.

* Includes 12 M reads for HRD assessment which can be used as a spike-in module, if needed.

† Sample = 1 VARIANT*Plex* library + 1 FUSION*Plex* library

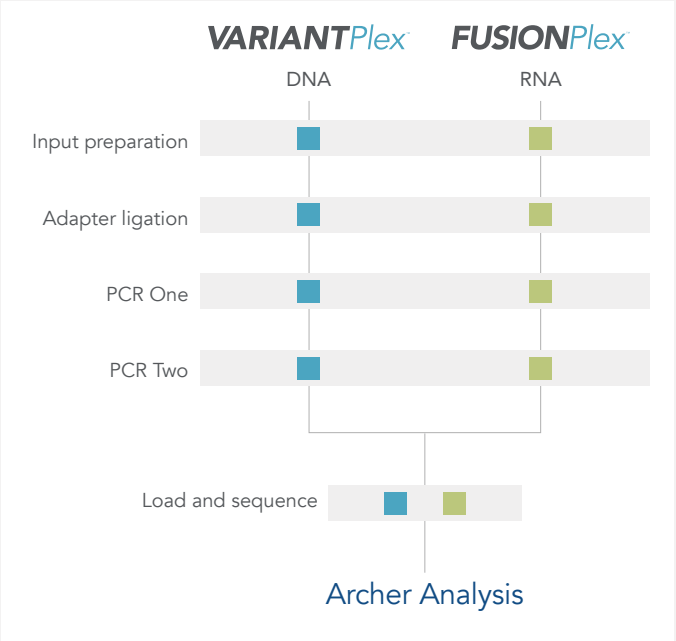
Workflows that work for you

Library preparation workflows can be run in parallel, and sample indexing allows for all Archer libraries to be sequenced together.

Flexible run sizes are available with choice of lyophilized reagents in 8-tube strips, allowing for runs as small as one sample, or 96-well breakaway plates for larger runs.

Scalable, high-throughput, liquid reagents are available in single-use, 24-, and 96-reaction kits. Regardless of format, Archer reagents are color-coded to match protocol steps for easier benchwork.

Automation support is available that can reduce hands-on time to as little as 20 minutes and enable nucleic acid to sequencer loading in under 12 hours.



Confidence in calls with demonstrated performance

Archer CGP solutions are powered by Anchored Multiplex PCR (AMP™) chemistry and Archer Analysis, which have advantages for :

- **Detection of novel and known fusions**: Key fusions detected with as little as 10% tumor content using 50 ng of FFPE input with FUSION*Plex* NGS assays
- **Variant identification**: VARIANT*Plex* NGS assays demonstrated high concordance (93.9–100%) with other profiling methods (IHC, qPCR, Sanger, targeted NGS, WES) in a multisite study
- **Allele frequency (AF) calls**: VARIANT*Plex* NGS assays have shown high concordance with AF calls from ddPCR, including low AFs, even with low input
- **High concordance when assessing key genomic signatures**: VARIANT*Plex* NGS assays demonstrated high concordance* with orthogonal methods when assessing TMB, MSI, and HRD status

* Data on file

VARIANT*Plex* HRD concordance with genomic instability score

The VARIANT*Plex* Complete Solid Tumor v2 panel and Archer Analysis 7.4 generated highly concordant results when compared to an orthogonal genomic instability score, with 92.3% concordance for HRD classification calls using the standard threshold of 42 (Figure 1).

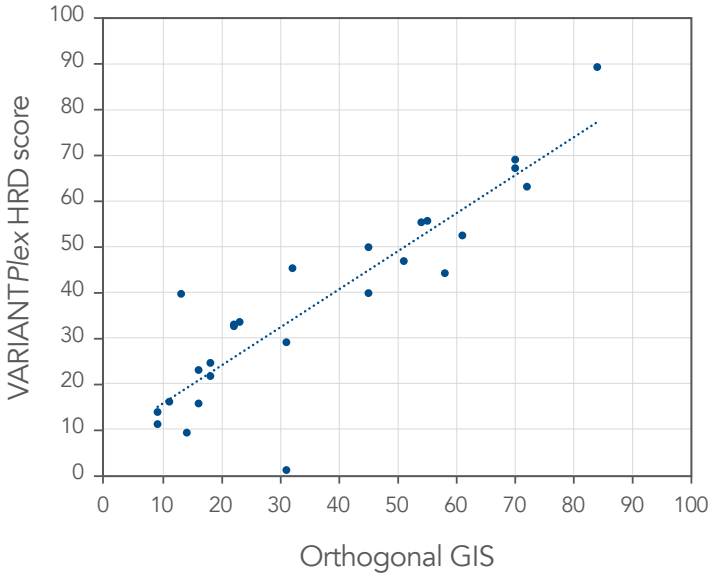
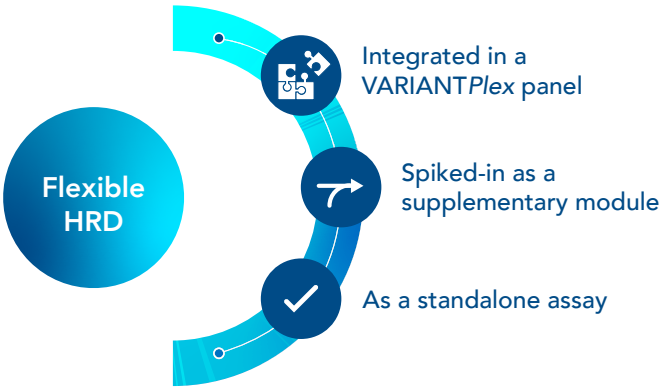


Figure 1. The VARIANT*Plex* HRD score is highly concordant with an orthogonal genomic instability score (GIS). Using the standard threshold of 42, 24/26 (92.3%) samples were concordant with the orthogonal genomic instability score method, which was based on hyb-cap and LOH + LST + TAI scoring approach. Samples were assessed with VARIANT*Plex* Complete Solid Tumor v2 and Archer Analysis 7.4. Samples analyzed included 22 FFPE samples from various solid tumor types as well as 1 blood sample and 3 FFPE reference materials. The reference materials included an HRD negative, an HRD low positive, and an HRD high positive sample—all of these were accurately classified by the assay.

Flexible options for HRD analysis

For solid tumor sample analysis, HRD assessment can be integrated into a VARIANT*Plex* panel, spiked-in as a supplementary module, or used as a standalone assay.



Custom panel content examples	Genes	Reads	Genomic alterations detected
BRCA1/2 + VARIANT*Plex* HRD Module	*BRCA1* & *BRCA2*	12.2 M	SNVs, indels, CNVs, large intragenic variants, HRD
5 HRR genes + VARIANT*Plex* HRD Module	*BRCA1, BRCA2, RAD51C, RAD51D, PALB2*	12.4 M	SNVs, indels, CNVs, large intragenic variants, HRD
32 HRR genes + VARIANT*Plex* HRD Module	*ARID1A, ATM, ATR, BARD1, BRAF, BRCA1, BRCA2, BRIP1, CDK12, CHEK2, CTNNB1, ERBB2, ESR1, FANCA, FANCC, FANCD2, FANCE, FANCF, KRAS, MRE11A, NBN, PALB2, PIK3CA, PPP2R1A, PTEN, RAD50, RAD51, RAD51B, RAD51C, RAD51D, RAD54L, TP53*	16.5 M	SNVs, indels, CNVs, large intragenic variants, HRD

Customize any Archer NGS assay by adding functionally-tested designs or create a new panel that fits your exact requirements with Assay Marketplace. Get started at www.idtdna.com/AssayMarketplace.

Learn more about Archer CGP solutions: IDTDNA.COM/CGP

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