VARIANTPlex™

ARCHER VARIANT*Plex*™ COMPLETE SOLID TUMOR AND PAN SOLID TUMOR

Easily identify key oncology biomarkers

The expansive landscape of genetic biomarkers relevant to oncology continues to grow due to diligent research efforts across the globe. Informed decisions not only rely on identifying oncology genes, but understanding the magnitude of genome-wide signatures such as:

- **Microsatellite instability** (MSI), which measures changes in the number of repeats found in microsatellites that could indicate defects in DNA mismatch repair (MMR) genes
- **Tumor mutational burden** (TMB), which represents the number of acquired mutations per megabase (mut/Mb) of sequenced DNA and functions as a predictive biomarker for neoantigen production by cancer cells.

Consequently, creating comprehensive genomic profiles (CGP) of cancers requires data across a broad genomic target space for all types of mutations. In addition, the data needs to flex with an ever-changing landscape of knowledge.

Archer VARIANT*Plex* panels for solid tumors provide comprehensive coverage, flexibility, and scalability using proven chemistry for fast answers to your questions.

VARIANT*Plex* panels for solid tumor research

Comprehensive

Identify relevant oncology genes and genomic signatures such as MSI and TMB

Flexible

Add custom content to your NGS panels for state-of-the-art assays*

Fast results

1.5-day library preparation with 3.5 hours hands-on-time

AMP™ chemistry

Proven chemistry for dependable NGS libraries

Archer™ Analysis

Powerful analysis platform for actionable insight

*Custom targets do not factor into TMB calculation due to algorithm constraints.

INTEGRATED DNA TECHNOLOGIES ARCHER™

Solid tumor analysis for comprehensive or focused targets

VARIANT*Plex* Pan Solid Tumor

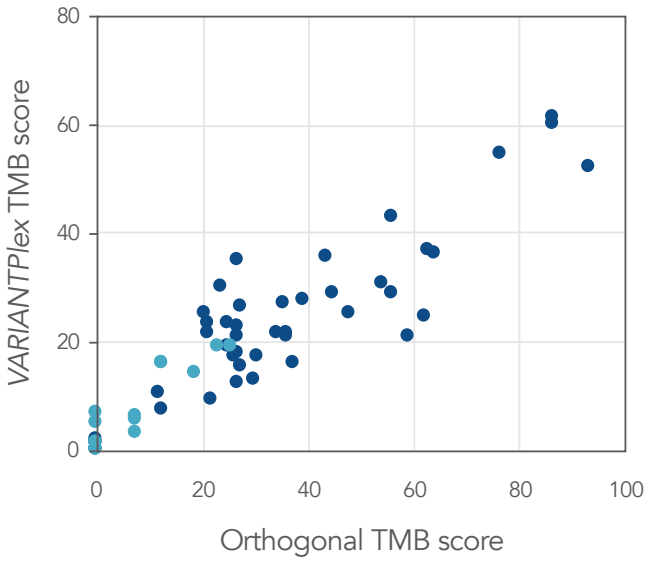
- CNVs
- SNVs
- Indels
- Microsatellite instability (MSI)
- Tumor Mutational Burden (TMB)†
- Covers coding region of 185 genes

VARIANT*Plex* Complete Solid Tumor

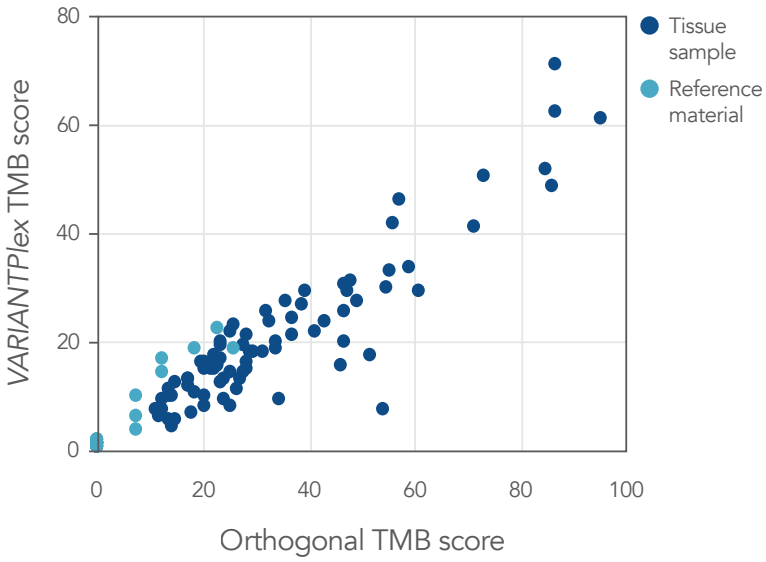
- CNVs
- SNVs
- Indels
- Microsatellite instability (MSI)
- Tumor Mutational Burden (TMB)†
- Covers coding region of 430 genes

†TMB analysis requires use of VARIANT*Plex* Pan Solid Tumor or VARIANT*Plex* Complete Solid Tumor. Custom TMB panels must contain all Pan or Complete Solid Tumor content.

A. Pan Solid Tumor



B. Complete Solid Tumor



	10 Mut/Mbp	(-) TMB-Intermediate 5–20 Mut/Mbp
Concordance	95.0%	100%
Positive % agreement (PPA)	93.2%	100%
Negative % agreement (NPA)	100%	100%

	10 Mut/Mbp	(-) TMB-Intermediate 6–17.5 Mut/Mbp
Concordance	83.8%	100%
Positive % agreement (PPA)	81.5%	100%
Negative % agreement (NPA)	100%	100%

Figure 1. VARIANT*Plex* TMB identification is highly concordant with orthogonal methods. 50–100 ng of DNA from samples with orthogonal TMB characterizations was converted into libraries using VARIANT*Plex* chemistry, sequenced on Illumina® NextSeq™ 500/550, NextSeq 2000, or NovaSeq® instruments, then processed through Archer Analysis. (**A**) Reference: 11 SeraCare® TMB standards and WES-characterized reference cell lines (ATCC or GIAB); tissue samples: 39 de-identified FFPE tumor tissue samples characterized with a 500+ gene hybrid capture NGS assay, 2 de-identified FFPE normal adjacent tissue samples, 4 de-identified peripheral blood samples. (**B**) Reference: 11 SeraCare TMB standards and 5 WES-characterized reference cell lines; tissue samples: 87 de-identified FFPE tumor tissue samples characterized with a 500+ gene hybrid capture NGS assay, 2 de-identified FFPE normal adjacent tissue samples, 10 de-identified peripheral blood samples. Normal cell lines and peripheral blood samples were assumed to have a TMB of 0. (-) TMB-Intermediate results exclude samples within the indicated default range for Archer Analysis across all assays evaluated.

Detect MSI with reliability

MSI is reliably identified with high concordance to orthogonal methods and is enabled for both VARIANT*Plex* Pan Solid Tumor and VARIANT*Plex* Complete Solid Tumor.

Panel coverage:

- 114 microsatellite loci targeted across the genome

Analytical Performance:

- 98.3% PPA (95% CI = 95.6–99.5%)
- 98.4% NPA (95% CI = 94.4–99.8%)

Analysis outputs:

- % unstable loci + MSS, intermediate, and MSI-H classifications

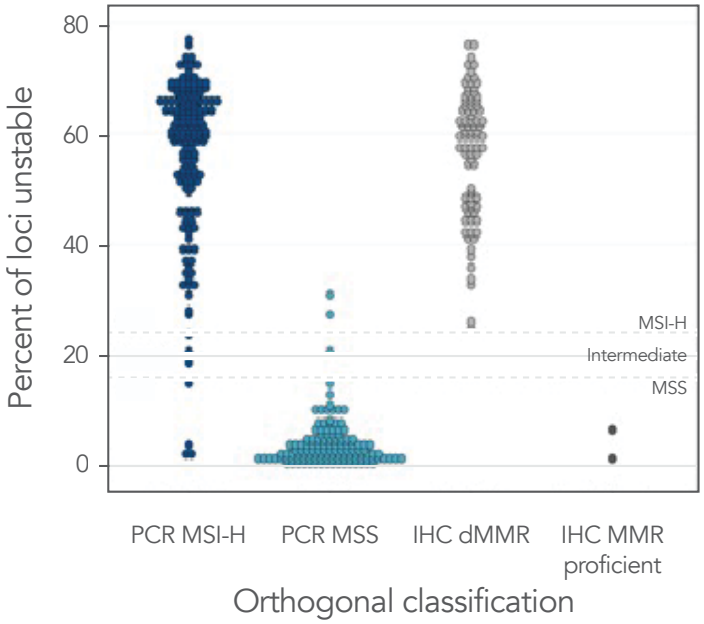


Figure 2. VARIANT*Plex* MSI identification is highly concordant with orthogonal methods. 50–250 ng of DNA from de-identified FFPE samples (*n* = 362) with orthogonal MSI characterizations was converted into libraries using VARIANT*Plex* chemistry and sequenced on Illumina NextSeq 500/550. Archer Analysis identified the percentage of unstable loci which is plotted on the y-axis; >30% = MSI-H (microsatellite instability-high); 20–30% = intermediate; <20% = MSS (microsatellite stable). Orthogonal classification was determined by PCR fragment analysis or immunohistochemistry (IHC) to identify whether the sample was deficient in mismatch repair (dMMR) or MMR proficient.

Archer Analysis 7.2

Sensitive and accurate data analysis is essential for informed decisions. Archer Analysis has been updated to identify TMB and MSI signatures in addition to other variants in key genes associated with solid tumors.

More data in less time

MSI and TMB analysis

Faster analysis for all panels

Support for CGP

Comprehensive analysis

DNA and RNA in one platform

Architecture update

Improved analysis performance

Infrastructure updates provide more security and reliability

For a full list of gene targets, see archerdx.com/research-products/solid-tumor-research/

New expanded panels	Size	Recommended reads	Product #
VARIANT*Plex* Pan Solid Tumor	~669 kb	25 M	AB0142
VARIANT*Plex* Complete Solid Tumor	~1.42 Mb	45 M	AB0144

Don't see your desired targets? You can design your own panel or add to an existing one at the Archer Assay Marketplace, just go to https://assay-marketplace.archerdx.com/

VARIANT*Plex* panels are customizable

Assay Marketplace™

Easily identify key oncology biomarkers

The powerful combination of Archer VARIANT*Plex* panels and purpose-built Archer Analysis software unlocks new capabilities without compromising performance on established biomarkers.

INTEGRATED DNA TECHNOLOGIES ARCHER™