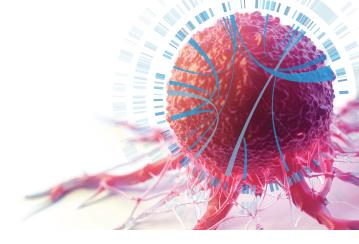


## Crack the Cancer Code

Comprehensive Somatic Variant Detection



#### The Cancer Genome Remains Unsolved

Despite extensive efforts, over 50% of late-stage cancers remain driver negative, underscoring serious gaps in somatic variant catalogs.

Current technologies struggle to detect large structural variants (SVs)—events too large for standard next generation sequencing (NGS) methods to reliably identify. To address this gap, researchers resort to using multiple platforms, increasing study complexity and cost—yet still miss key drivers of disease.

Despite their importance, accurate identification of somatic structural variants remains a significant bottleneck in cancer genomics.

Aydin et al. (2025) Nature Scientific Reports

~54%

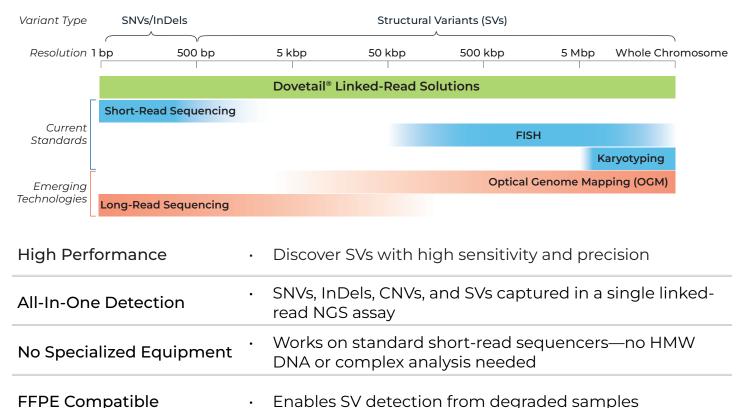
Of Late Stage Cancers

Are Driver Negative

Attalla et al. (2021) Clin. Cancer Res.



## One Assay. All Variants. Any Sample.



## The Solution—Dovetail® Linked-Reads + Dovetail® Analysis Portal

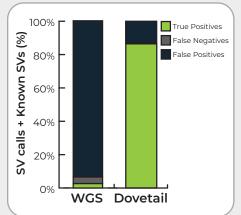
## **Linked-Read Assay**

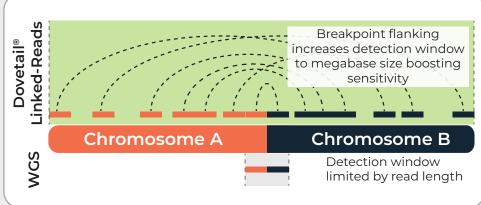
## **Dovetail® Analysis Portal**



#### Benefits of Dovetail® Linked-Reads

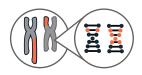
- 1. Sensitive SV discovery without sacrificing small variant calls.
- 2. Linked-reads improve read support and accuracy for SV calls.
- 3. Expands study possibilities through compatibility with many samples types, including FFPE.
- 4. Improved concordance with known SVs compared to standard WGS.





## **Better Profiling—Better Science**

#### Cancer Genomics



- Catalog genetic variants
- •NGS-based detection
- •Ultra-sensitive to SVs

### Molecular Oncology



- Identify oncogenic drivers
- Link SVs to oncogenes
- Unravel complex variants

# Therapeutic Advancement



- Develop Biomarkers
- Accelerated target ID
- Stratify cohorts

Unlock the full cancer genome with Dovetail® Genomics.

Contact us today to learn more.

