

# 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.

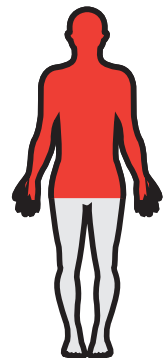
Current technologies struggle to detect large structural variants (SVs)—events too large for standard next generation sequencing (NGS) methods to reliably identify. To address this gap, researchers resort to using multiple platforms, increasing complexity and cost—yet still miss key drivers of disease.

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

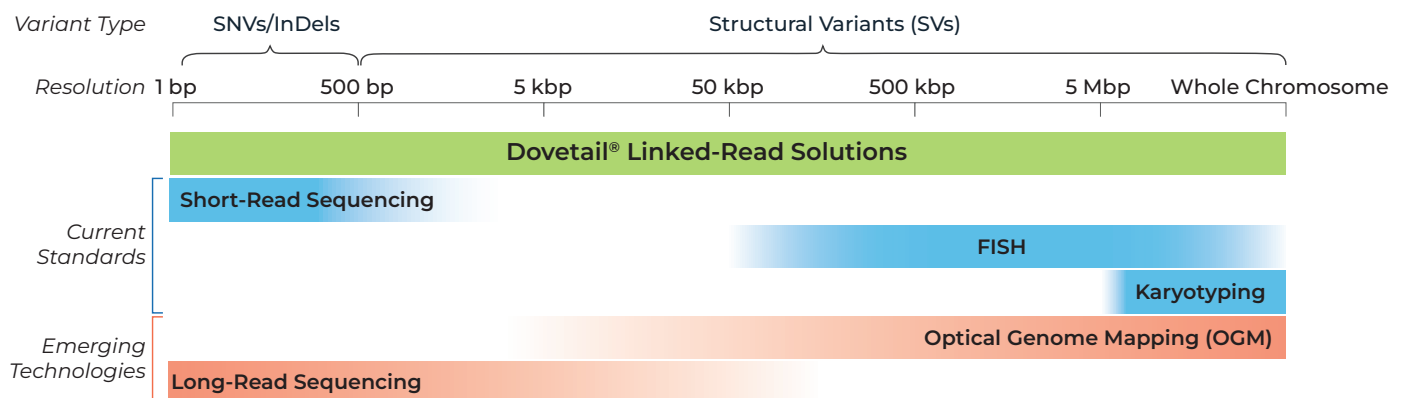
*Aydin et al. (2025) Nature Scientific Reports*

**~54%**  
**Of Late Stage Cancers  
Are Driver Negative**

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



### One Assay. All Variants. Any Sample.

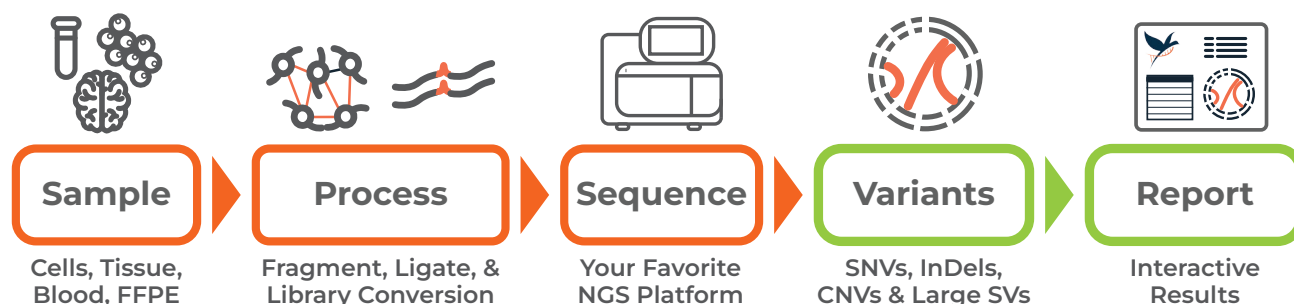


High Performance	<ul style="list-style-type: none"> <li>Discover SVs with high sensitivity and precision</li> </ul>
All-In-One Detection	<ul style="list-style-type: none"> <li>SNVs, InDels, CNVs, and SVs captured in a single linked-read NGS assay</li> </ul>
No Specialized Equipment	<ul style="list-style-type: none"> <li>Works on standard short-read sequencers—no HMW DNA or complex analysis needed</li> </ul>
FFPE Compatible	<ul style="list-style-type: none"> <li>Enables SV detection from degraded samples</li> </ul>

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

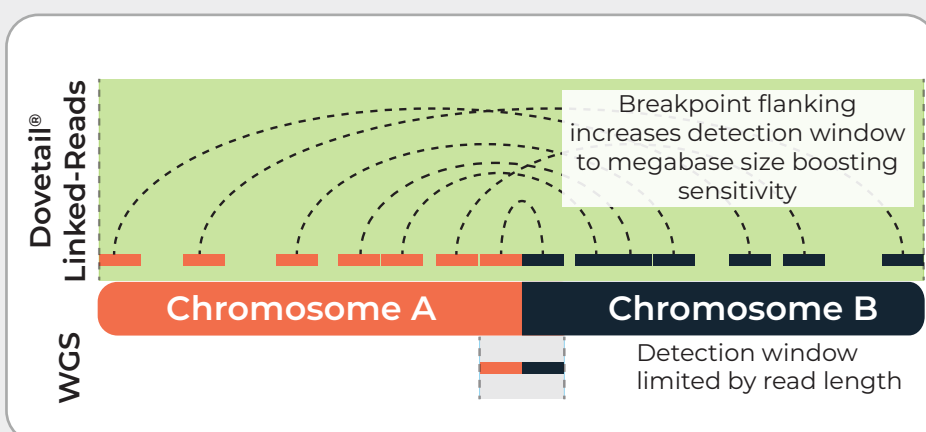
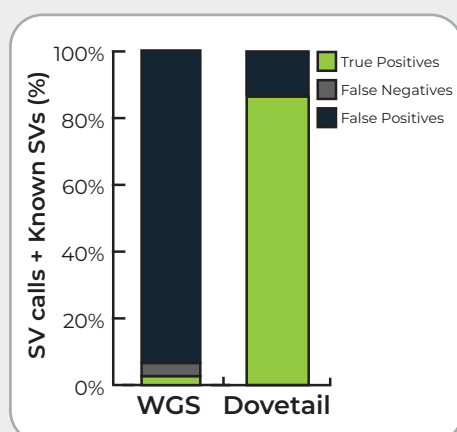
### Linked-Read Assay

### Dovetail® Analysis Portal



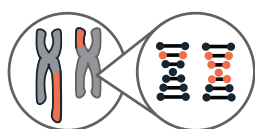
### The Benefit of Linked-Reads

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.

