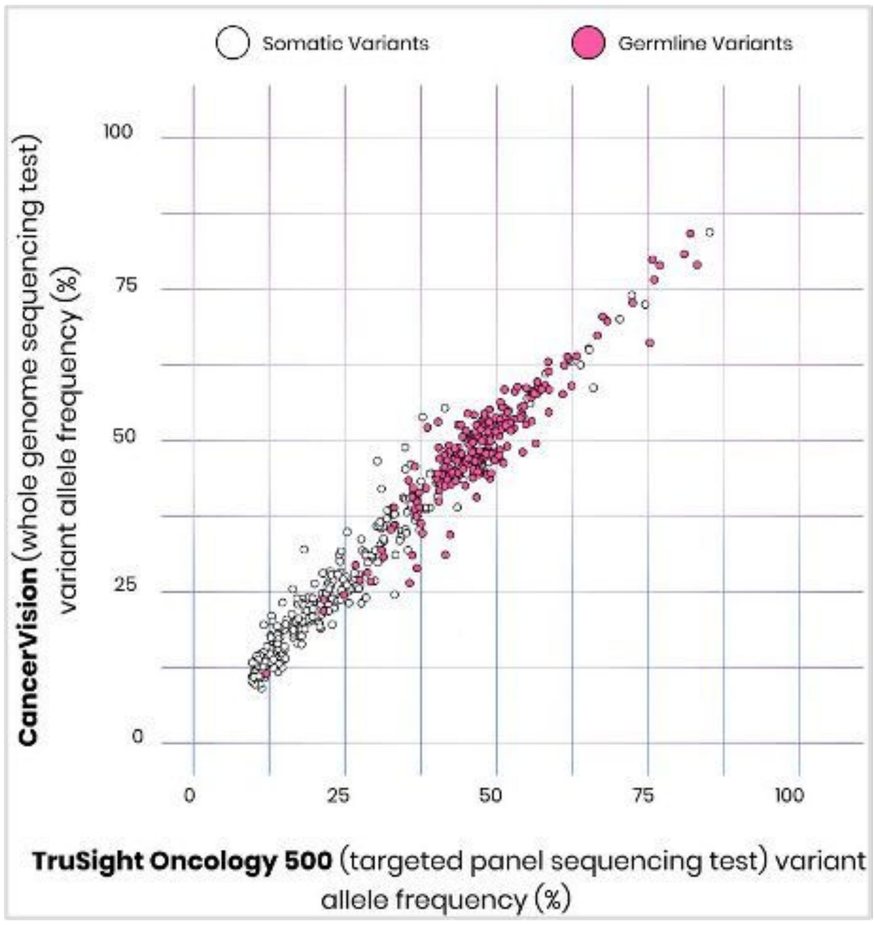
Expanding Genomic Insight Beyond Targeted Panels with Targeted-Enhanced Whole-Genome Sequencing

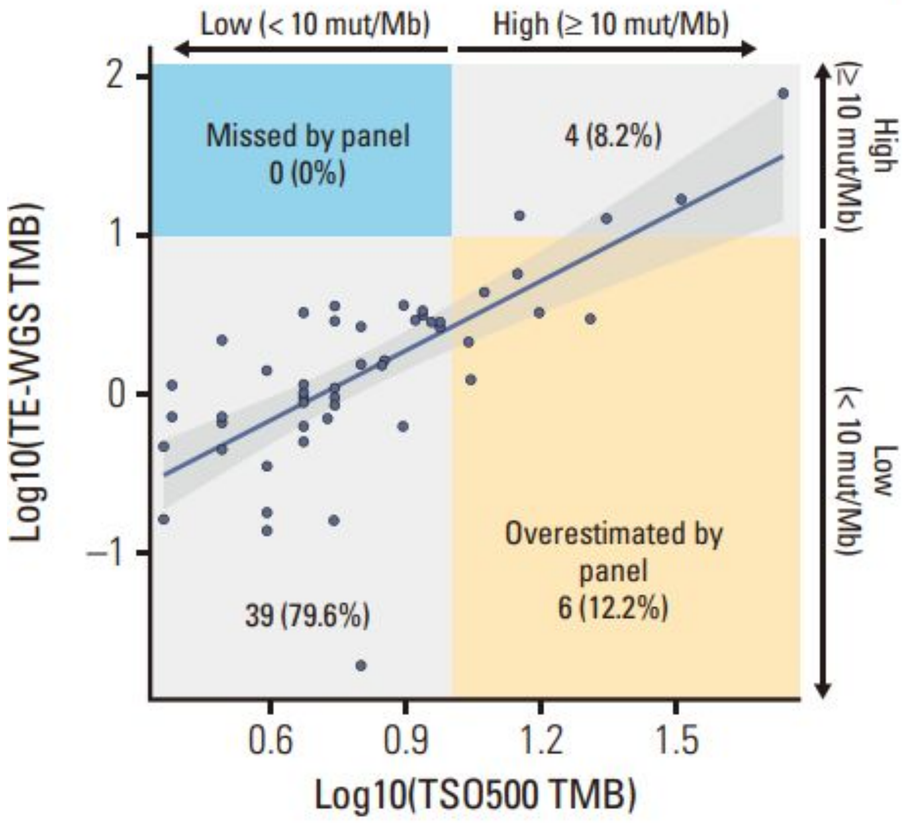
CancerVision reduces the likelihood of false positives by ruling out benign variants in the tumor sample

CancerVision vs. Illumina TruSight Oncology 500 (TSO500)

- CancerVision detected 100% (498/498) of the variants detected by TSO500 (n=49 pan cancer patients)
- High VAF correlation between TSO500 and CancerVision (r = 0.97)
- Germline accounted for a substantial number of the variants detected by TSO500
  - 223 variants (44.8%) identified as germline variants (red dots)
  - 275 variants (55.2%) identified as somatic variants (gray dots)



CancerVision offers broader insights that conventional genetic tests may have overlooked

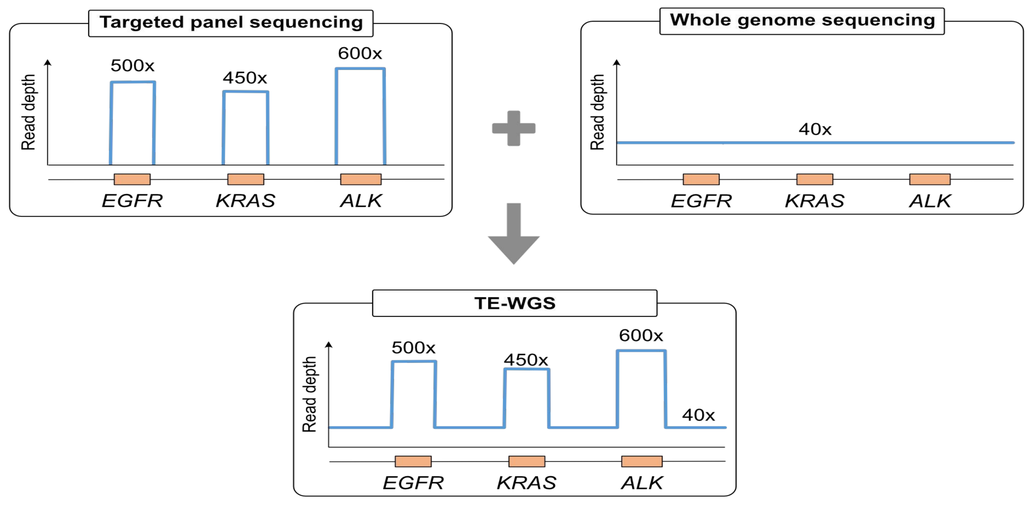


All the tier I and II CNVs from TSO500 were also detected by TE-WGS.

- **Cancer Vision identified six deletions that were not reported by TSO500: four CDKN2A, one TP53, and one BAP1 deletion.**
- TMB scores calculated by TE-WGS exhibited a good correlation with those derived from TSO500 (r=0.89)
- **Six TSO500-tested tumors classified as TMB-high (12.2%) were reclassified as TMB-low (≤ 10 mutations/Mb) by the TE-WGS approach, highlighting instances of discordance**

Technical Features of CancerVision: A Transformative Approach to Genomic Profiling

- **Target-enhanced whole-genome sequencing**: An average of 40x depth WGS backbone with focused exploration of an average of 500x depth for 500+ key biomarker genes.
- **A 2-in-1 test: Paired somatic-germline testing**
- All types of alterations: Single nucleotide variants (SNVs), small indel variants, large structural variants (SV), and copy number variants (CNV), including variants in non-coding regions.
- Genome-wide signatures: Our proprietary algorithms for Tumor Mutational Burden (TMB), Microsatellite instability (MSI), and Homologous recombination deficiency (HRD).
- **2-week turnaround time**
- Provides **valuable genomic information at a comparable price** to the average standard panel sequencing test



Parallel sequencing from a single library, with data integration performed during the bioinformatics stage.

INOCRAS

Lee S et al., Target-Enhanced Whole-Genome Sequencing (TE-WGS) Shows Clinical Validity Equivalent to Commercially Available Targeted Oncology Panel. Cancer Res Treat. 2024 Sep 19. doi: 10.4143/crt.2024.114. Epub ahead of print. PMID: 39300929.