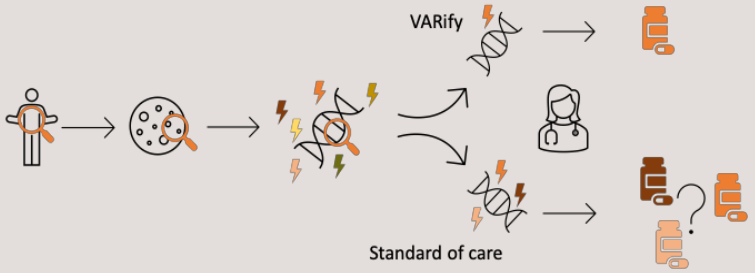
Application Note: VARify®

VARify® - Precision data analysis in solid cancer to guide accurate therapy selection

Precision cancer medicine relies on the identification of mutations in tumors that are not present in the patient's normal, healthy tissue. The unique molecular profile of the tumor is used as a basis for guiding treatment. Lack of precision in mutation detection may lead to consequences such as unnecessary side effects, suboptimal treatment outcome and inadequate prognosis for the patient along with substantial costs for drugs that do not work.

Oncodia have developed a robust and reliable software solution tailored for Next Generation Sequencing (NGS) data analysis for cancer diagnostics and precision oncology. By comparing the information from tumor and normal tissue from the same patient, the software uses proprietary algorithms to trim, align and organize sequencing data to identify actionable mutations, reduce false positive calls and excel in the identification of small insertions/deletions. VARify filters out sequencing artifacts and delivers a cleaner, clinically relevant VCF-file containing only statistically significant somatic mutations of the tumor.



The individual tumor profile, characterized by NGS sequencing, is used as a basis for selection of therapy. In contrast to standard-of-care analysis, VARify narrows the dataset and delivers only statistically significant somatic mutations, thereby simplifying selection of therapy.

Features and Benefits

- ☑ Fast and reliable analysis of NGS data in cancer diagnostics
- ☑ Proprietary algorithms filter out sequencing artifacts for higher signal-to-noise ratio
- ☑ High reproducibility of data reporting Single Nucleotide Polymorfisms (SNPs) and small Insertions/Deletions (InDels)
- ☑ Highly portable for easy deployment in an existing workflow
- ☑ CE marked for IVD

Conclusion

VARify is a CE-IVD medical device software for mutation analysis in precision oncology. Patented statistical methods are used to eliminate technical artifacts and to report clinically relevant tumor-specific mutations in a fast, robust and reproducible fashion.

By eliminating the impact of false positive mutations reported by many competing solutions, VARify offers you the tool you need for precision data analysis to guide the decision of accurate anti-cancer therapy in clinical routine.

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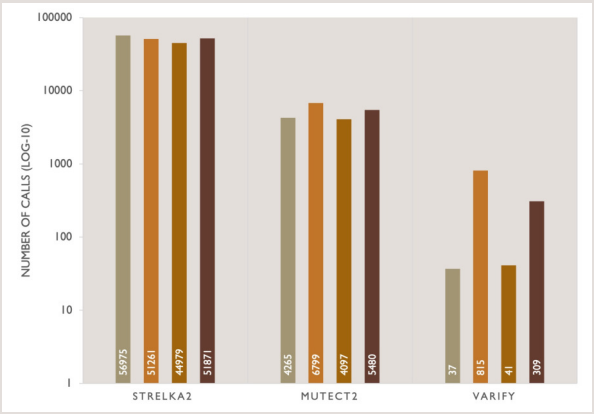
Results

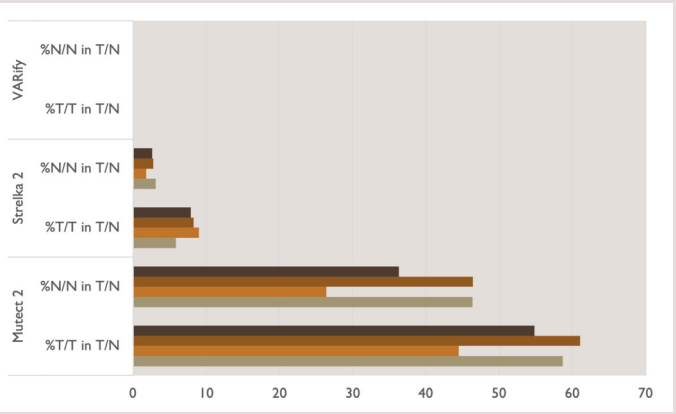
DNA extracted from tissue material of four colorectal cancer patients (tumor and patient-matched normal) was enriched by a TruSight Oncology 500 gene panel and sequenced on an Illumina NextSeq 500, following best clinical practice. Analysis of sequencing data was performed using reference software pipelines based on Strelka2, Mutect2 and Oncodia (VARify).

RELIABLE REPORTING OF SOMATIC MUTATIONS



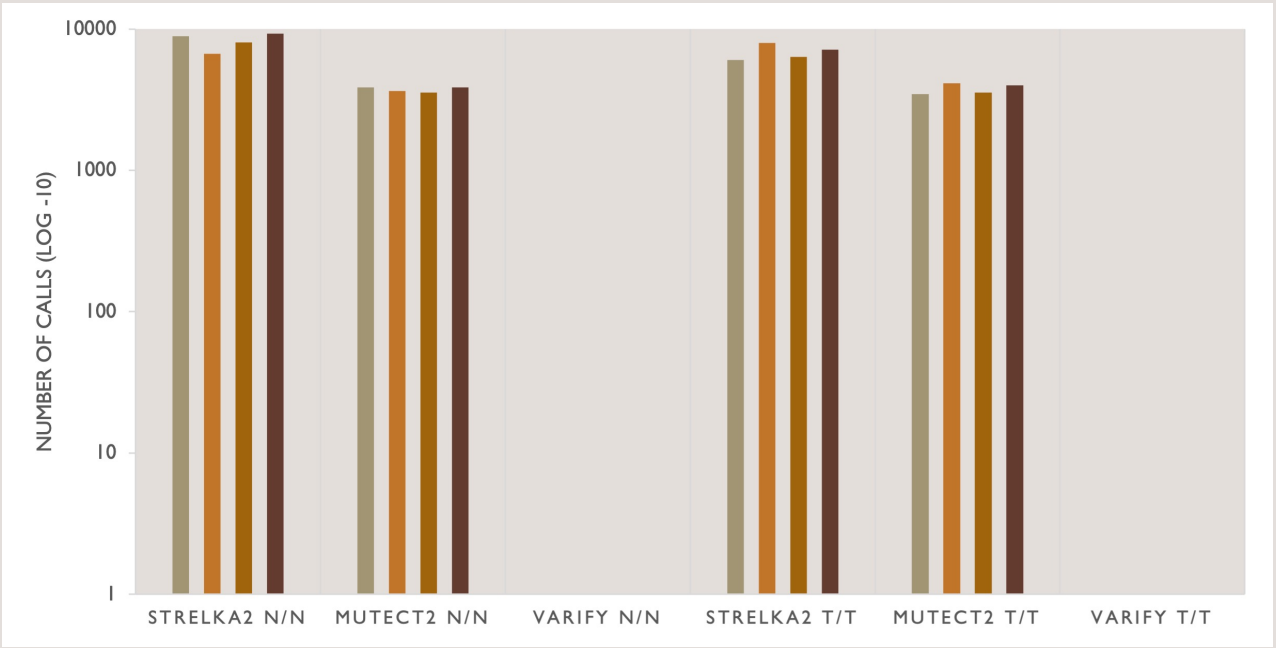
In contrast to the competitors, VARify narrows the reported mutations to include the clinically relevant calls and to eliminate the false positive events. The number of reported calls by VARify reflects the mutation status of the tumor sample (stable, low or high mutator type colorectal cancers, commonly referred to as MSS (Patient A and C), MSI-L (Patient D) and MSI-H (Patient B)).

FALSE POSITIVE MUTATIONS REPORTED IN REFERENCE OUTPUT



A substantial number of the false-positive mutations detected by the "Basic Oncodia Test" are present in the reference output of the competing pipelines. VARify shows superior consistency of somatic variant output by filtering out artifacts generated during sample preparation, sequencing or mapping errors. Both reference pipelines inflate the expected mutation counts with incorrect calls.

"BASIC ONCODIA TEST" ASSURES ACURATE AND CONSISTENT RESULTS IN A CLINICALLY RELEVANT MUTATION PROFILE



In what we call the "Basic Oncodia Test" of identical dataset comparisons (Normal/Normal or Tumor/Tumor), VARify does not report false positive mutations while the reference pipelines produce significant output. These false postive mutations are sometimes present in the golden standards for somatic analyses and even in manually curated datasets. In the "Basic Oncodia Test" false positive mutations are clear errors in the calling logic and can potentially mislead treatment desicions if they are left in the final report.

Ordering Information

Product	Description	Article no.
VARify	Software intended for the identification of somatic mutations in NGS data from person matched tumor and normal DNA samples	MS-101.01

For more information, see our website oncodia.com

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