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Turn comprehensive tumor analyses into relevant insights

Get more from TruSight™ Oncology 500 with Clinical Genomics Workspace interpretation software from PierianDx

TruSight Oncology 500 enables comprehensive genomic profiling, assessing relevant DNA and RNA* biomarkers across 523 genes. In a single next-generation sequencing (NGS) cancer research assay, detection of small variants, tumor mutational burden (TMB), microsatellite instability (MSI), splice variants, and fusions is possible across multiple tumor types. Now, with PierianDx Clinical Genomics Workspace, you can do even more with results interpretation.

Harness the wealth of NGS information into a single report

PierianDx Clinical Genomics Workspace software offers:

- User-friendly, all-in-one informatics solution for labs that lack informatics expertise
- Comprehensive rule-based ranking, classification, and interpretation of each variant in final report
- Curated genomics data, practice guidelines, labels, clinical trials, and variant interpretations from other PierianDx customers comprise a best-in-class knowledgebase

PierianDx Clinical Genomics Workspace generates reports with evidence from millions of published articles and thousands of clinical trials

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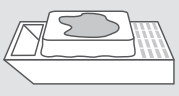
FFPE specimens	Sample	Library prep and enrichment	Sequence	Variant calling	Interpretation and reporting
					
Supports multiple tissue types	Commercial DNA/RNA* extraction kits	TruSight Oncology UMI kit DNA Probes (523 genes) RNA* Probes (55 genes) Automatable workflow	NextSeq™ System	TruSight Oncology 500 Local App	Powered by PierianDx Clinical Genomics Workspace

*The products to evaluate DNA and RNA variants (PN: 20028215, 20032626, 20028216, 20032627) consist of the TruSight Oncology 500 DNA panel and the TruSight Tumor 170 RNA panel.

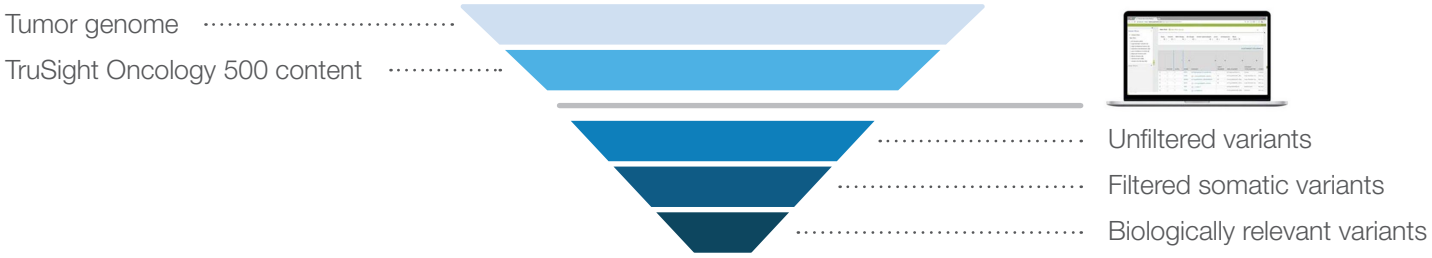
Take a deeper dive into sequencing data with PierianDx Clinical Genomics Workspace

Progress from DNA and RNA* samples to final report within 5 days in a comprehensive workflow

Integrating TruSight Oncology 500 assay with PierianDx Clinical Genomics Workspace interpretation and reporting allows you to:

- Reduce time between assay and report
- Simplify your informatics workflow
- Understand the significance of your sequencing results

Multiple levels of variant filtering



From thousands of variants in the genome, TruSight Oncology 500 and Clinical Genomics Workspace filter and prioritize biologically relevant variants for the final report.

Receive automated and customizable genomic reports

Sample Report

Variant Classification System

2 IA	0 IB	1 IIC	0 IID	High	Stable	13
GENOMIC FINDINGS BY TIER + LEVEL				TMB	MSI	TRIALS

Tier I - Strong Significance

VARIANT	INTERPRETATION
NCOA4-RET fusion A	RET encodes a receptor tyrosine kinase Involved in cell growth and differentiation which is known to undergo oncogenic activation in vivo and in vitro by cytogenetic rearrangement (provided by RefSeq, Jul 2008). NCOA4 encodes an androgen receptor coactivator which interacts with the androgen receptor in a ligand-dependent manner to enhance Its transcriptional activity. Chromosomal translocations between NCOA4 and RET, both located on chromosome 10, have been associated with papillary thyroid carcinoma (provided by RefSeq, Feb 2009). RET rearrangements resulting in fusion with partner genes including KIF5B, CCDC6 and NCOA4 have been reported in non-small cell lung cancer (NSCLC) patients(PMID- 29128428). A NCOA4-RET fusion is identified in this case. The N terminus of the NCOA4 gene fuses with the C terminus of the RET gene in this fusion (PMID-28011461). In PCCL3 cells, expression of NCOA4-RET fusion was reported to simultaneously activate DNA synthesis and apoptosis apart from interfering with thyroid differentiation at steps distal to the TSH-R (PMID-12690093, 2003). The NCOA4-RET fusion has been reported in patients with NSCLC specifically in lung adenocarcinoma patients (COSMIC, February 2019, PMID-23150706). RET rearrangements are one of the emerging biomarkers to identify novel therapies for patients with metastatic NSCLC (NCCN, NSCLC v.3.2019).

Evidence levels determined by expertly curated and up-to-date professional guidelines, clinical trials, cancer research databases, millions of publications, shared interpretations across thousands of specimens, and more.

Ready to combine comprehensive genomic profiling with variant interpretation?
Learn more.

TruSight Oncology 500
www.illumina.com/tso500

PierianDx Clinical Genomics Workspace
www.pieriandx.com/ClinicalGenomicsWorkspace

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For Research Use Only. Not for use in diagnostic procedures.

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