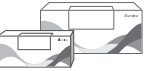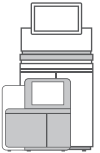illumına®

Simplifying the process to identify applicable variants in oncology samples

The TruSight™ Oncology 500 portfolio, the Illumina variant calling pipeline, and PierianDx Clinical Genomics Workspace™ software enable molecular pathology labs to implement comprehensive genomic profiling (CGP) for quick, easy identification of significant biomarkers.

	TruSight Oncology 500	TruSight Oncology 500 High-Throughput	TruSight Oncology 500 ctDNA
1. Prepare Analyze 523 cancer-related genes, including biomarkers in key guidelines and clinical trials Assess CNVs, SNVs, indels, fusions, splice variants, and complex genomic signatures, such as MSI and TMB*	• Solid tumor samples • DNA and RNA analyzed • Automation-friendly kits and method	• Solid tumor samples • DNA and RNA analyzed • Automation-friendly kits and method†	• Liquid biopsy samples • DNA analyzed
2. Sequence Exceptional data quality Flexible and scalable	NextSeq™ 550 and NextSeq 550Dx‡ Systems • Up to 8 samples per run	NextSeq 550 and NextSeq 550Dx‡ Systems • Up to 8 samples per run **NovaSeq™ 6000 System** • 16-192 samples per run	NovaSeq 6000 System • Up to 24 samples per run
3. Call variants Sophisticated, proprietary algorithms remove errors, artifacts, and germline variants High-sensitivity variant calling from raw sequencing data	**DRAGEN™ TruSight Oncology 500 Analysis Software†** • On-premise analysis deployed on the DRAGEN Bio-IT Platform **TruSight Oncology 500 Local App** • On-premise analysis requiring an external server **Local Run Manager** • On-instrument analysis (NextSeq platform only) **PierianDx Clinical Genomics Workspace** • Cloud-based analysis of BAM and FASTQ files	**DRAGEN TruSight Oncology 500 Analysis Software†** • On-premise analysis deployed on the DRAGEN Bio-IT Platform **TruSight Oncology 500 Local App** • On-premise analysis requiring an external server	**DRAGEN TruSight Oncology 500 ctDNA Analysis Software†** • On-premise analysis deployed on the DRAGEN Bio-IT Platform

4. Interpret results and produce actionable reports with PierianDx Clincal Genomics Workspace

pieriandx

Easy
Upload raw data files (BAM, FASTQ, VCF) and let PierianDx CGW do the interpretation and reporting work

Secure and compliant
Follow privacy best practices, including HIPAA, HITRUST, GDPR, CLIA, and CAP§

Scalable
Run data sets from multiple samples in parallel for fast turnaround of results

Relevant
Identify significant variants using the constantly curated, IVD-ready PierianDx Clinical Genomics Knowledgebase

Comprehensive
Learn from a partner sharing network comprised of world-leading cancer centers and health institutions aggregating real-world knowledge

Applicable
Output an evidence-based final interpretation report with clear, visual results in accordance with commonly accepted nomenclature and reporting guidelines

* CNV = copy number variations, SNV = small nucleotide variants, indel = insertions/deletions, MSI = microsatellite instability, TMB = tumor mutational burden
‡ NextSeq 550Dx System in Research Mode
§ HIPAA = Health Insurance Portability and Accountability Act, HITRUST = Health Information Trust Alliance, GDPR = General Data Protection Regulation, CLIA = Clinical Laboratory Improvement Amendments, CAP = College of American Pathologists

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

† **TruSight Oncology 500 High-Throughput automation kits available Q1 2021; on-premise and cloud-based DRAGEN TruSight Oncology 500 Analysis Software and cloud-based DRAGEN TruSight Oncology 500 ctDNA Analysis Software coming soon**

From sequence to applicable results

Illumina and PierianDx offer an easy, seamless workflow for turning raw sequence data into an easy-to-understand report.

523	**1000s**	**<10**	**1**
Genes sequenced	Variants potentially called	Relevant variants typically identified	Meaningful report

File format: BAM, FASTQ | VCF | PDF
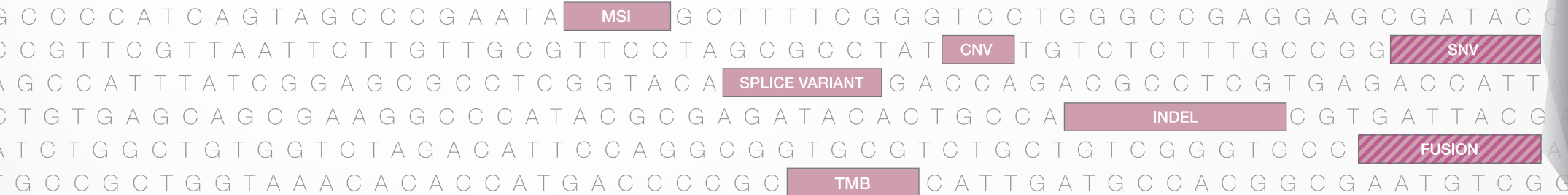
MSI · CNV · SPLICE VARIANT · INDEL · TMB · SNV · FUSION

Comprehensive Genomic Report

Powered by pierianDx

PATIENT	DOB	DISEASE	MEDICAL RECORD #	REPORT DATE	REPORT STATUS
John Doe	02/04/1951	Non-small cell Lung Cancer	6563465346	09/19/2019	Final

REPORT SUMMARY

Executive Summary
The patient tumor specimen harbors an **NCOA4-RET** fusion, **KRAS** G12D and **PDGFRA** D842V mutations and an amplification in the **MDM2** gene. RET fusions/rearrangements are an emerging biomarker and NSCLC patients harboring these are recommended targeted therapies involving cabozantinib or vandetinib by NCCN. Presence of KRAS mutations in NSCLC patients indicates poor prognosis independent of therapy, reduced responsiveness to EGFR TKI therapy and no impact on chemotherapeutic efficacy, as per recent NCCN guidelines. Targeted therapies against RET fusions, KRAS mutations, PDGFRA mutation or MDM2 amplification are available in clinical trials for patients with NSCLC.

Other Biomarkers

BIOMARKER	LEVEL
TMB	High
MSI	Stable

Genomic Findings

IA	IB	IIC	IID
NCOA4, RET — NCOA4-RET fusion	No variants reported.	PDGFRA — D.D842V c.2525A>T	No variants reported.
KRAS — p.G12D c.35G>A		MDM2 — MDM2 amplification	
10 Clinical Trials		5 Clinical Trials	

RELEVANT RESULTS

Tier I - Strong Significance

VARIANT	POTENTIAL IMPACT
NCOA4, RET NCOA4-RET fusion	May benefit from
A	- Cabozantinib or Vandatinib in non-small cell lung cancer

INTERPRETATION
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 (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 (RefSeq, Feb 2009).

NCOA4-RET fusions have been reported in lung adenocarcinoma (COSMIC, September 2019). NCCN recommends cabozantinib (FDA approved for treatment of advanced renal cell carcinoma (RCC) and patients with hepatocellular carcinoma (HCC) who have been previously treated with sorafenib) and vandetinib (FDA approved symptomatic or progressive medullary thyroid cancer in patients with unresectable locally advanced or metastatic disease, category 2A) as targeted agents for NSCLC patients harbouring RET rearrangements (NCCN, NSCLC v.7.2019).

Legend:
- Variants and signatures identified by variant calling tools
- Pathogenic variants identified by PierianDx Clinical Genomics Workspace

Trusight Oncology 500 Portfolio

- Sequence 523 genes in key cancer guidelines and clinical trials

Secondary analysis

- Identify genomic alterations present in sample data
- Call variants with 99.9998% analytical specificity and > 95% analytical sensitivity[1]
- Determine multiple variant types, including genomic signatures such as MSI and TMB
- Run Illumina secondary analysis pipeline in the PierianDx cloud, reducing risk, cost, and time

PierianDx Clinical Genomics Workspace

- Determine variant significance using literature, guidelines, drug labels, and trials information
- Filter out variants of uncertain significance or that are benign/likely benign
- Classify variants in tiers by clinical significance
- Map variants to guidelines and clinical trials
- Annotate and interpret relevant variants

Customizable genomic report

- Consolidate relevant information in one, easy-to-read report
- Adhere to AMP, CAP, ASCO, and ACMG guidelines*
- Generate meaningful information for oncologists

Learn more

Enable CGP with the TruSight Oncology 500 Portfolio at www.illumina.com/products/by-brand/trusight-oncology-500.html
Request a demo of PierianDx Clinical Genomics Workspace at www.pieriandx.com/request-a-demo

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