INOCRAS

Advancing Oncology Research and Minimal Residual Disease Detection with Inocras's Whole Genome Cancer Platform

AACR 2025 Spotlight Presentation

This Exhibitor Spotlight Theater is a promotional activity and is not approved for continuing education credit. The content of this Exhibitor Spotlight Theater and opinions expressed by presenters are those of the sponsor or presenter and are not of the American Association for Cancer Research; (AACR)."

Our speakers and agenda

Majd al Assaad, M.D.,
Senior Research Fellow
Weill Cornell Medicine

Ariel Jaimovich, Ph.D
VP of Applications
Ultima Genomics

Youngseok Ju, M.D., Ph.D
Genomics Co-Founder
Inocras Inc.

Erin Connolly-Strong, PhD
Chief Medical Officer
Inocras Inc.

Transforming Oncology with Whole Genome Precision

WGS Cancer Profiling Dx

- WGS: See more, detect more
- Real-world data: Head-to-head comparison of whole genome vs. panels

Ultra-Sensitive MRD Test, Redefined

- WGS x WGS approach
- Limit of detection as low as 1 ppm * powered by WGS x WGS approach

Data on file- *based on simulated analytical validation

Introducing Inocras

We focus on **whole genome sequencing** to identify 100% complete genomic makeup and mutations

Our IP protected technology and proprietary bioinformatics pipeline enable us to interpret massive WGS data into actionable insights

We are specialized in **cancer and rare disease**, with more than 13,000 patient cases

Our San Diego Lab is **CAP accredited + CLIA certified**; Seoul Lab is ISO certified

Locations

Our partners and customers

Applying whole genome to **cancer profiling Dx** and **MRD test**

CancerVision™

Whole genome cancer profiling

See more, see accurately

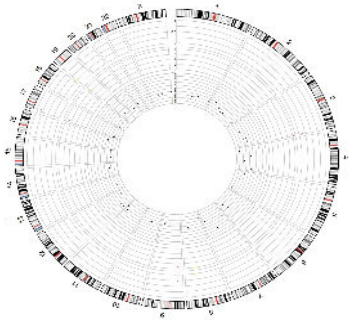
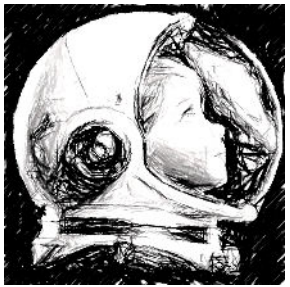
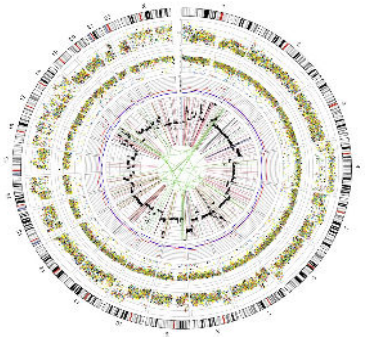
X

MRDVision™

Whole genome MRD monitoring

1 ppm level sensitivity (LOD50)

What do you see with whole genome?

For the same cancer patient		What you see…
Targeted panel (<0.03% of genome)		
Whole genome (>99% coverage)		

- Only select biomarkers covered
- Limited number of point mutation
- Limited copy number variation
- Limited structural variations
- Limited estimates of tumor purity and ploidy

- **Comprehensive** view of the genome
- **More** point mutations identified
- **More accurate**, genome-wide copy number variations
- **More accurate**, genome-wide structural variation
- **Non-coding** area also covered
- **More accurate genomic makers** (TMB, MSI, HRD)
- **More accurate** tumor purity and ploidy
- **Mutational signature**
- And more!

CancerVision™: Curating vast WG data to actionable insights

Our leading technology

- **Proprietary bioinformatics** tested with over 15,000 cancer and rare disease WGS cases
- **Target-Enhanced WGS**, merging benefits of targeted panel (500x depth) + WGS (40x depth for somatic, 20x germline)
- **FFPE correction technology (patent protected):** ML model based auto-correction for damaged specimen

More complete genomic test

- **2 in 1:** Somatic + germline paired test
- **Sensitivity/PPV:** >99%[1]
- **Accurate complex somatic variants** (SV, CNV, variants in non-coding areas)
- **Genome-wide mutational pattern** (TMB, MSI, HRD, mutational signatures)
- **Germline** variant detection

All these done within **14 days**

in our **CLIA/CAP lab** in San Diego

at **comparable price** (vs. targeted panel sequencing)

[1] Ferguson, S., Sriram, S., Wallace, J. K., Lee, J., Kim, J. A., Lee, Y., ... Connolly-Strong, E. (2024). Analytical and Clinical Validation of a Target-Enhanced Whole Genome Sequencing-Based Comprehensive Genomic Profiling Test. Cancer Investigation, 42(5), 390–399. https://doi.org/10.1080/07357907.2024.2352438

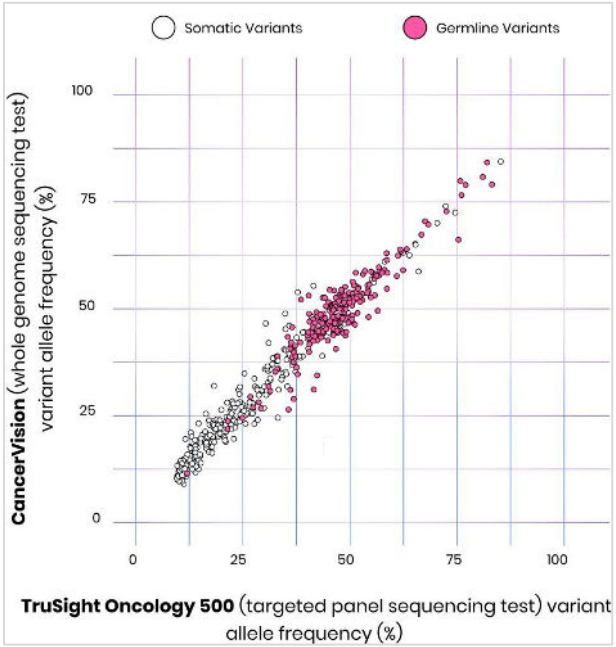
CancerVision: Head-to-head comparison with TSO500; TE-WGS presents additional insights not captured in standard panel sequencing

Objective: Head-to-head comparison between Illumina TSO500 (Standard Panel Sequencing) vs. Inocras CancerVision (TE-WGS)

Prospective observational study (N=49): Routine cancer molecular profiling (TSO 500) was performed on all patients. Then, patients provided peripheral blood samples for DNA extraction, for CancerVision

Results:

- **100% concordance** with TSO500 panel, detecting all 498 variants
- **High correlation in variant allele fraction (VAF)** with TSO500 (r=0.978), demonstrating unmatched accuracy
- **Unique germline vs. somatic detection:** TE-WGS identified 44.8% of shared variants as germline and 55.2% as somatic, offering a complete genomic profile
- **Additional actionable findings:** detected all actionable CNVs from TSO500, plus six additional key deletions missed by TSO500
- **Comprehensive insights into CNVs, gene fusions, MSI, and HRD,** enhancing clinical decision-making



Lee, S et al. Target-Enhanced Whole-Genome Sequencing (TE-WGS) Shows Clinical Validity Equivalent to Commercially Available Targeted Oncology Panel, Cancer Research and Treatment, Sep 2024

CancerVision: More accurate genome-wide markers, reducing false positive significantly

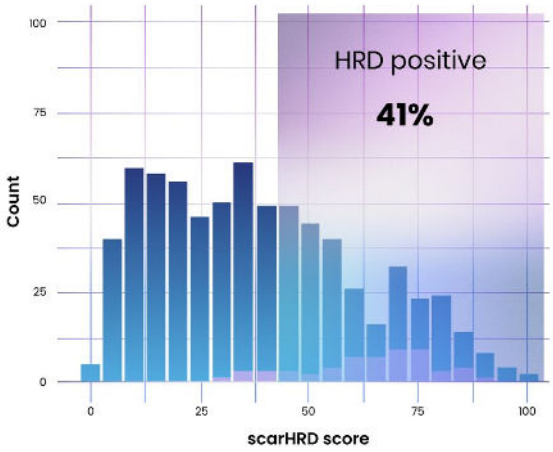
Objective: Assess Homologous Recombination Deficiency (HRD) status in **1,364 breast cancer patients** between standard targeted panel vs CancerVision approaches.

Results:

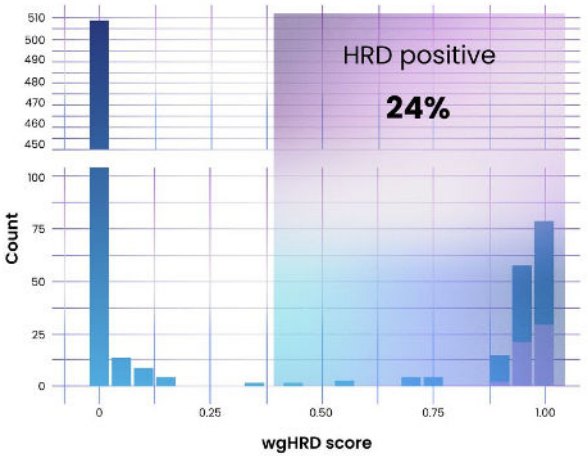
- Standard panel:
  - Contrived cut-off between HRD (+) vs. (-)
  - Elevated risk of false positives
- CancerVision:
  - Clear distinction between HRD (+) vs. (-)

HRD analysis is a part of CancerVision. NOT additional add-on test

Targeted panel (0.03% genome)



Whole-genome (>99% genome)



Ju, Y. S et al, (2024). Whole-Genome analyses of 1,364 breast cancers with clinical records. *Research Square* (Preprint). https://doi.org/10.21203/rs.3.rs-5094752/v1

CancerVision vs. Panel: Evaluating the Added Clinical Value of WGS in Prostate Cancer

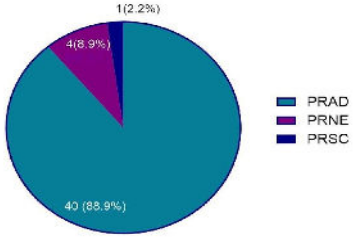
Study Population:

- Men with high-risk, advanced-stage prostate cancer
- Prior testing with common testing methods (*e.g.*, Oncomine, TruSight Oncology 500, Exome Cancer Test v1.0)

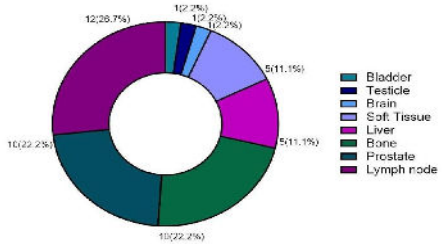
Primary Objective:

- To identify additional or missed clinically actionable variants by comparing targeted panel sequencing performed as part of routine clinical care with WGS performed using CancerVision.

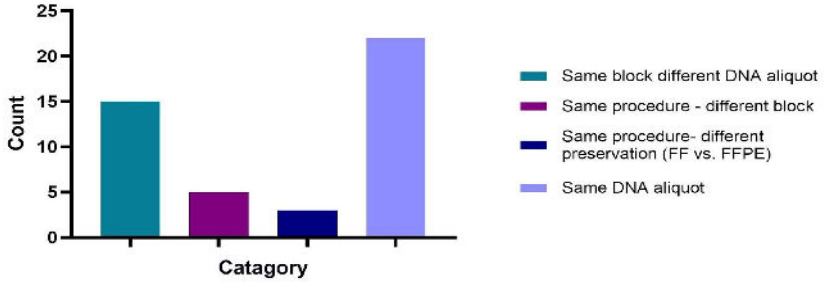
Distribution of Prostate Cancer Subtypes



Anatomic Origin of Tumor Samples



Sample Source for TPS vs. CancerVision Comparison



Weill Cornell Medicine

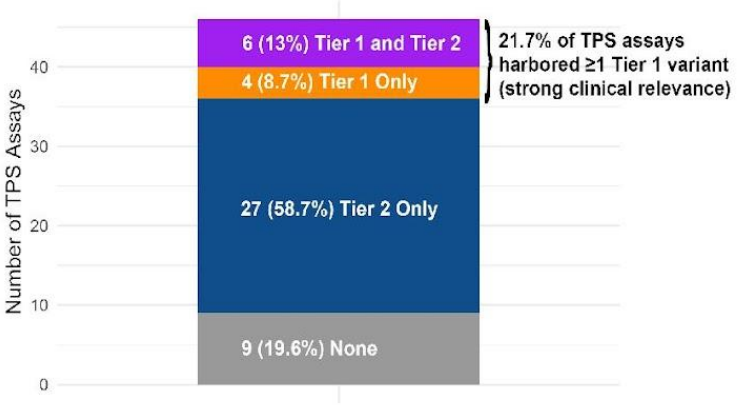
CancerVision Detected 96% of Clinically Reported Variants—With **Added Insights**

CancerVision successfully detected 79/82 variants reported by TPS, yielding an overall sensitivity of 96.3%.

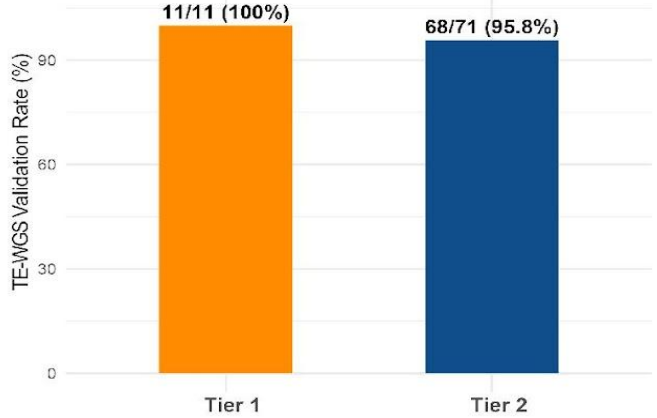
Detected variant types:

- 100% (11/11) of Tier 1 variants
- 95.8% (68/71) of Tier 2 variants
  - including all 13 gene fusions identified by TPS

Distribution of Clinically Reported Variants by TPS Assay



CancerVision Validation Rates for Tier 1 and Tier 2 Variants



Uncovering Clinically Actionable with **CancerVision**

Actional Variants

Targeted Panel Sequencing (TPS):

- 6 actionable variants detected in 11.1% of samples (5/45)
- Variants included SNVs in *PTEN* (n=3), *BRCA2* (n=1), and *ATM* (n=1)

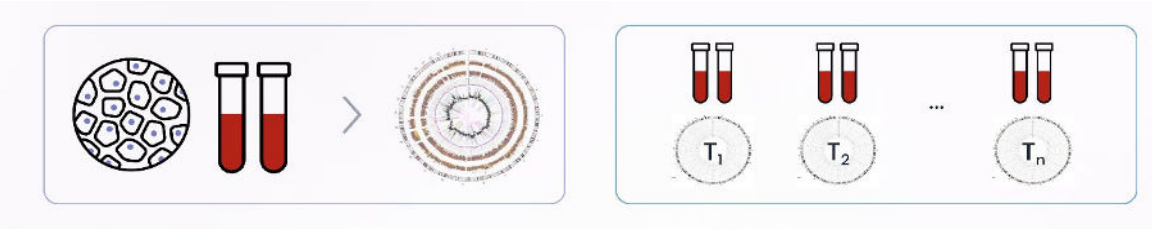
CancerVision (TE-WGS):

- Identified the same 6 actionable variants **plus additional treatment targets** in 40.0% of samples (18/45)
- Notably, **35.6%** of samples (16/45) had no actionable findings by TPS but harbored at least one actionable alteration identified by CancerVision (TE-WGS)

MRD**Vision**™: Whole genome x whole genome approach

WGS baseline
Create whole genome fingerprint

ctDNA monitoring
Comparing WGS baseline vs. WGS data in ctDNA



Cancer**Vision** delivers whole genome cancer profiling, creating individualized WGS tumor fingerprint as a baseline for each patient.

MRD**Vision** then utilizes this unique WGS baseline (fingerprint) to measure cancer DNA fraction levels (MRD) in the blood by analyzing WGS data from cfDNA.

Tumor WG-informed whole-genome cfDNA monitoring

(CancerVision) (MRDVision)

Ultra-sensitive
With more markers, MRD testing gets more sensitive

Simple workflow - No panel creation step needed. Simple and more economical

Data on file

MRD**Vision**: Analytical validation methodology and results

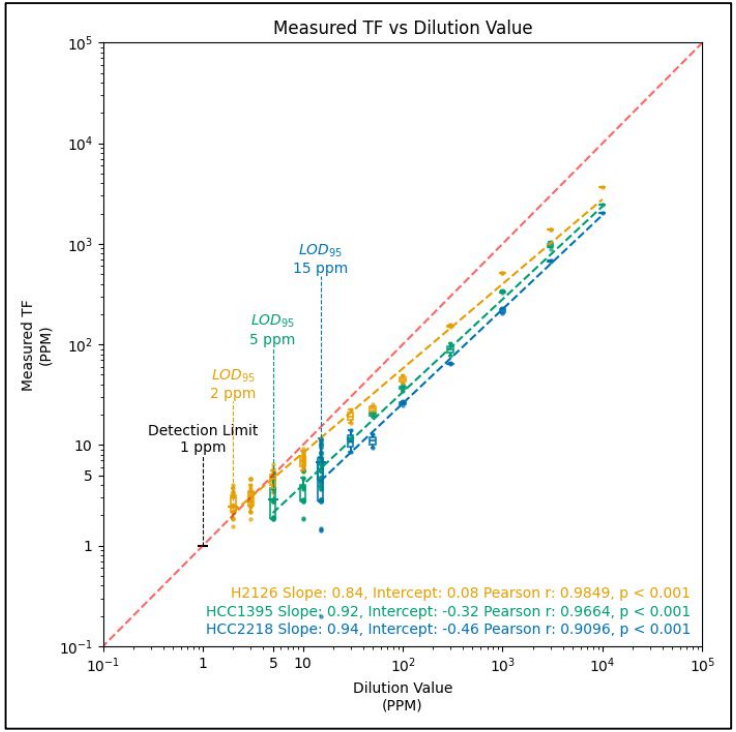
Methodology:

1. **Three tumor and matched-normal cell line pairs:**
   - HCC2218, HCC1395, and NCI-H2126 from American Type Culture Collection
   - Tumor DNAs were diluted into matched-normal DNAs at concentrations ranging from 10^{-2} to 10^{-7}, simulating various levels of circulating tumor DNA
   - Total of 84 ppmSeq experiments

2. **Samples were sequenced using Ultima Genomics ppmSeq**
   - 40x read-depth
   - A mixed (duplex) rate of 33%
   - Absolute error rate of $5.5x10^{-7}$

Limit of detection results:

- **Detection threshold (LOD50): 1 ppm**
  The minimum concentration at which a positive result can be reliably called at the defined specificity.
- **95% of Limit of detection (LOD95): as low as 2 ppm**
  At >10,000 mutations, 40x read-depth
  The concentration at which 95% of readings would be positively detected.



Data on file

MRD**Vision** Clinical validation - as low as 1 ppm sensitivity

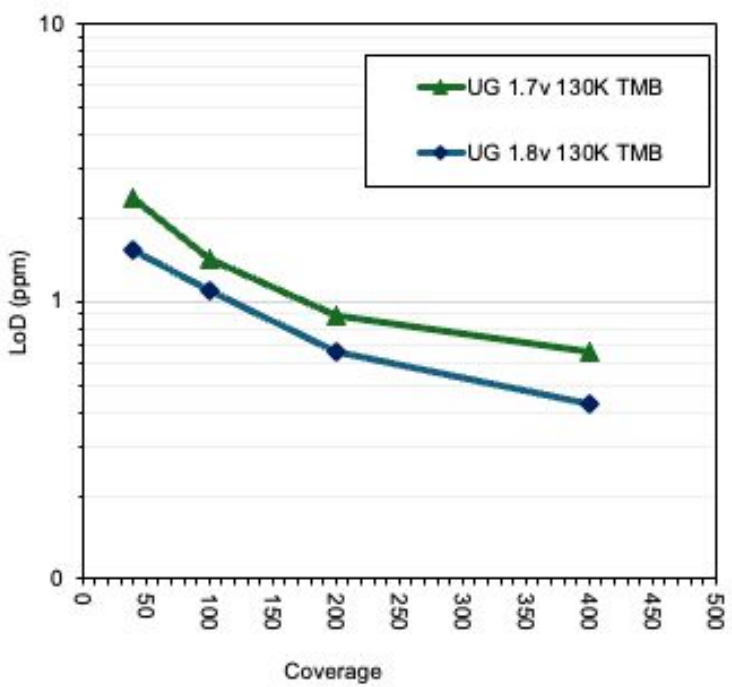
Methodology:

1. **Lung and Ovarian Cancer Patients**
   - Baseline tumor profile performed prior to surgical intervention
   - cfDNA sample collected pre and post surgery

2. **Samples were sequenced using Ultima Genomics ppmSeq**
   - Target 100x read-depth with 10ng DNA input
   - A mixed (duplex) rate of 36%
   - Absolute error rate of $3.76x10^{-7}$

Simulated Limit of Detection (LOD)results:

- **Detection threshold (LOD50): 0.56 ppm**
  The minimum concentration at which a positive result can be reliably called at the defined specificity.
- **95% of Limit of detection (LOD95): as low as 1 ppm**
  At >10,000 mutations, 100x read-depth
  The concentration at which 95% of readings would be positively detected.



Data on file

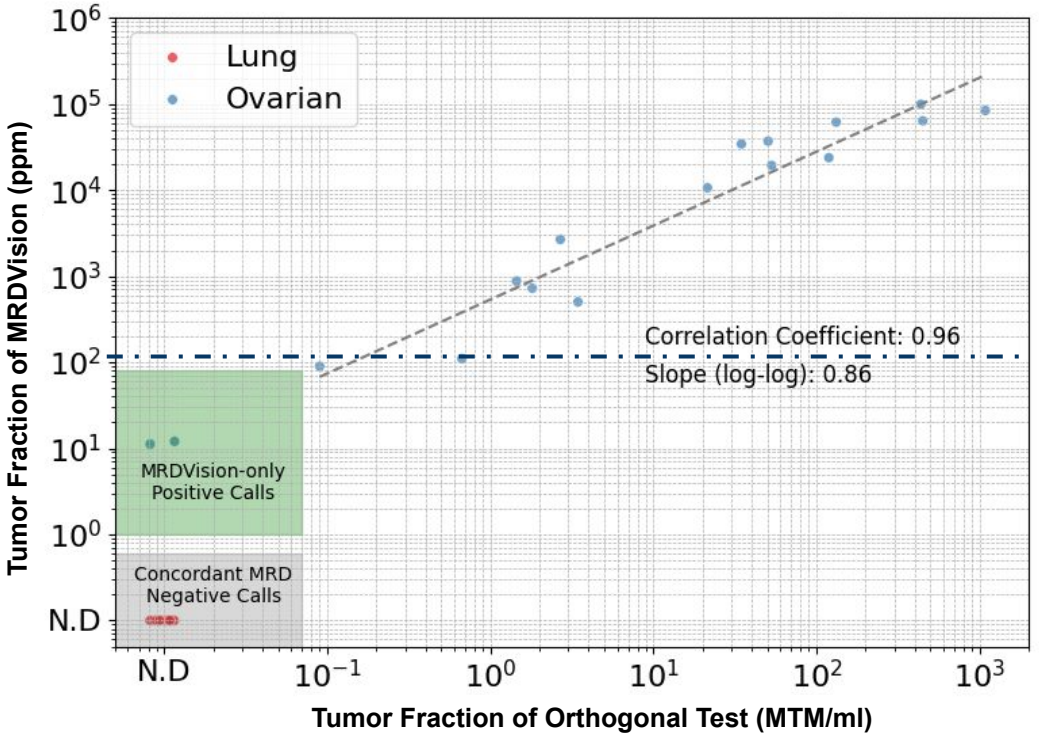
MRD**Vision** Clinical validation - Orthogonal study results

Methodology: Matched cfDNA samples were tested using both MRDVision and a widely used panel-based MRD assay (WES baseline × panel MRD).

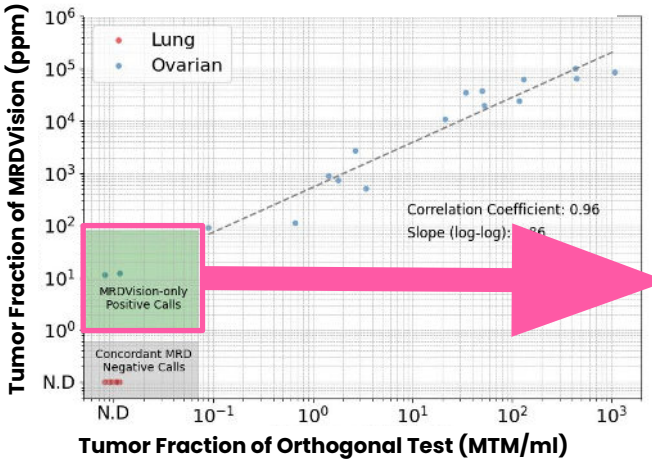
Results:

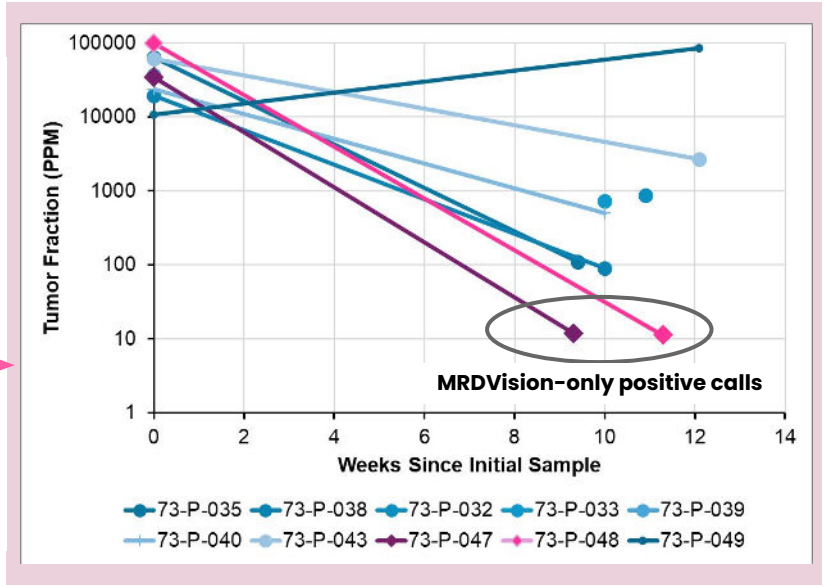
Strong quantitative concordance (r = 0.96; slope = 0.86, $\log_{10}$ scale)

Detection at low tumor fractions, consistent with validated and stimulated LOD



MRD**Vision** Clinical validation - Orthogonal study results





MRDVision identified low-level tumor DNA in cases missed by the orthogonal test

MRDVision-only positive samples show similar pattern in changes of MRD signals over time

50 out of 50 blank samples all confirmed

MRD**Vision** delivers accuracy, affordability, and more WGS data

Signal maximized
using **CancerVision™**
INOCRAS

Workflow streamed
using **Ultima ppmSeq™**
ULTIMA GENOMICS

Key features	Inocras - MRDVision	Widely adopted MRD products
Product concept	Tumor-informed	Tumor-infomed
Genome coverage	**Baseline:** WGS (CancerVision) **ctDNA:** WGS	**Baseline:** WES or WGS **ctDNA:** Panel
LOD	**0.0001%** LOD95: as low as **1 ppm***	Mostly 0.01% - 0.001% A very few has a single digit ppm for LOD95
Deliverable	**WGS ctDNA** monitoring report + **TE-WGS cancer profiling report** (CancerVision)	**ctDNA** monitoring report
Price	**Affordable** due to streamlined workflow	High cost due to personalized panel creation
TAT	First order: 4 weeks or less Follow-ups: 2 weeks or less	First order: 4-5 weeks Follow-ups: 7-14 days

Data on file- *based on simulated analytical validation

Fireside chat + Q&A

Youngseok Ju, MD, PhD – Inocras co-founder
Ariel Jaimovich, PhD – Ultima Genomics VP of Applications
Majd al Assaad, MD – Weill Cornell Medicine Senior Research Fellow

Hosted by Erin Connolly-Strong, PhD - Inocras Chief Medical Officer

Learn more about MRDVision