NeXT Personal®

Tissue-based MRD Liquid biopsy

Ultrasensitive ctDNA test

designed to see very small traces of cancer recurrence, early[1,5]

Sensitivity matters for patients with lung cancer

Lung TRACERx is one of the most robust prospectively collected observational ctDNA studies for early-stage non-small cell lung cancer (NSCLC) with **170+ patients** in the NeXT Personal® Dx 2023 ESMO cohort collected with **median 5 years of follow-up**, analyzed retrospectively.[1]

Cancer types:
adenocarcinoma (LUAD),
non-adenocarcinoma (non-LIUAD)
Stages: IA - IIIA

Up to 4X higher sensitivity[1-4]

NeXT Personal® Dx showed up to 4X higher sensitivity for pre-operative ctDNA detection in LUAD patients compared to non-Personalis, previous generations assays.

6-month lead time over imaging[1]

NeXT Personal® Dx detected ctDNA recurrence with a median lead time of 6 months compared to radiographic imaging.

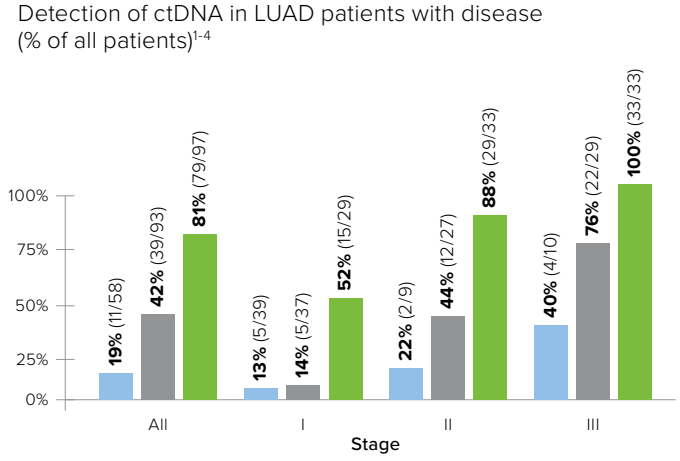
94% PPV of single timepoint detection at Landmark*[1]

NeXT Personal® Dx ctDNA detection in the Landmark window (10-120 days post-op) was strongly predictive of relapse with 94% PPV.

*Patients may be on adjuvant therapy at Landmark

NeXT Personal® Dx detected 100% of non-LUAD cases across all stages,and showed up to 4X higher sensitivity in LUAD compared to non-Personalis, previous generation assays.[1-4]

Detection of ctDNA in LUAD patients with disease (% of all patients)[1-4]



- LUAD is the most common subtype of NSCLC and has been challenging for MRD testing as a low-shedder of ctDNA
- **NeXT Personal® Dx showed 2 - 4x better sensitivity for LUAD** (across Stages I, II, and III)

For pre-surgical (baseline) comparisons across Abbosh '17, Abbosh '23, and this study, while the patients were drawn from the TRACERx cohort, the specific patients analyzed may be different.

1. Black, JRM, et al. (2023, November) An ultrasensitive and specific ctDNA assay provides novel pre-operative disease stratification in early stage lung cancer. ESMO annual meeting. **2.** Abbosh, C., et al. Phylogenetic ctDNA analysis depicts early-stage lung cancer evolution. Nature 545, 446–451 (2017) **3.** Abbosh, C. et al. Tracking early lung cancer metastatic dissemination in TRACERx using ctDNA. Nature 616, 553–562 (2023) **4.** For evaluations across Abbosh '17, Abbosh '23, and this study, while the patients were drawn from the TRACERx cohort, the specific patients analyzed may be different, which may lead to potential differences in study results.

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Sensitivity matters for patients with breast cancer

In a study with early-stage breast cancer patients (n=78) in collaboration with Professor Nicholas Turner at **The Royal Marsden Hospital** and the **Institute of Cancer Research, London:** NeXT Personal® detected recurrence, on median, about **~15 months ahead of scans.**[5]

Cancer types:
early-stage breast cancer (all subtypes)
Tumor grade:
II,III, no known

In this study:

- 100% (11/11) of patients that relapsed had detectable circulating tumor DNA (ctDNA) prior to relapse.[5]
- 100% (60/60) of patients that had undetectable ctDNA longitudinally after surgery did not relapse.[5]
- Patients who started with detectable ctDNA and subsequently reached undetectable ctDNA in multiple repeat serial testing did not relapse.[5]

89 patients included

10 Failed Panel Design
1 Successful panel design but plasma did not meet analysis threshold

78 patients Successful Panel Design and met analysis criteria

619 Plasma Samples successfully analyzed

Median: 8 samples/ patients (range 2-14)

Prior to any treatment, **98% (49/50) of baseline samples had ctDNA detected**[5]
- Median 1,225 PPM[5]

15 Relapse

4 Non Samples post Baseline

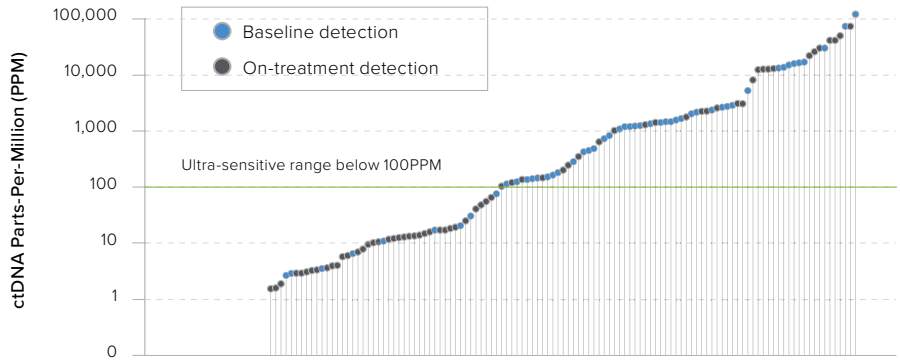
11 Relapse

63 Non-Relapse

* 4 patients that relapsed had Baseline sample available for analysis but had no samples post-surgery or during follow-up

54% of detections during disease monitoring may have been missed by a less sensitive assay[5]

Results: ctDNA detection levels



39% (44/114) of ctDNA detections were in the ultrasensitive range below 100 Parts per Million (PPM).[5]

Median detection 366 PPM (range 3.73-112,011).[5]

54% (35/65) of monitoring post-surgery detections were in the ultra-sensitive range.

5. Garcia-Murillas, I. et al. (2025, February 04). Whole genome sequencing-powered ctDNA sequencing for breast cancer detection. ESMO Annals of Oncology. https://www.annalsofoncology.org/article/S0923-7534(25)00053-5/

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