

# Assessing the Cancer Risk of Lung Nodules by Proteomic or Gene Expression Panels

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# Outline

1. The problem
2. Potential Solutions
3. The Promise of Proteomics and Gene Expression
4. Deep learning?
5. How do we achieve broad implementation?

# 1. The Problem

- The mortality burden of lung cancer is high
- Early detection of cancerous lung nodules can save lives.
- However, most lung nodules are not cancer.

# We need better tools to:

- Improve the selection of individuals undergoing screening

- Assess the cancer risk of undetermined nodules that have been identified

## 2. Potential Solutions

**What options do we have to assess the cancer risk of nodules that have been identified?**

- Clinician Determination
- Clinical Models
- Proteomics or Genomics
- AI or deep learning

# 3. Proteomics and Gene Expression

- PANOPTIC Trial (Pulmonary Nodule Plasma Proteomic Classifier) - A prospective, multicenter trial (N= 685) with 8- to 30-mm lung nodules
- LG<sub>3</sub>BP + C<sub>16</sub><sub>3</sub>A
- Evaluated the accuracy of an integrated proteomic classifier in identifying benign nodules in patients with a pretest probability of cancer  $\leq 50\%$ .
- Results were integrated with a clinical risk prediction model to identify likely benign nodules.

# PANOPTIC: LG<sub>3</sub>BP + C16<sub>3</sub>A

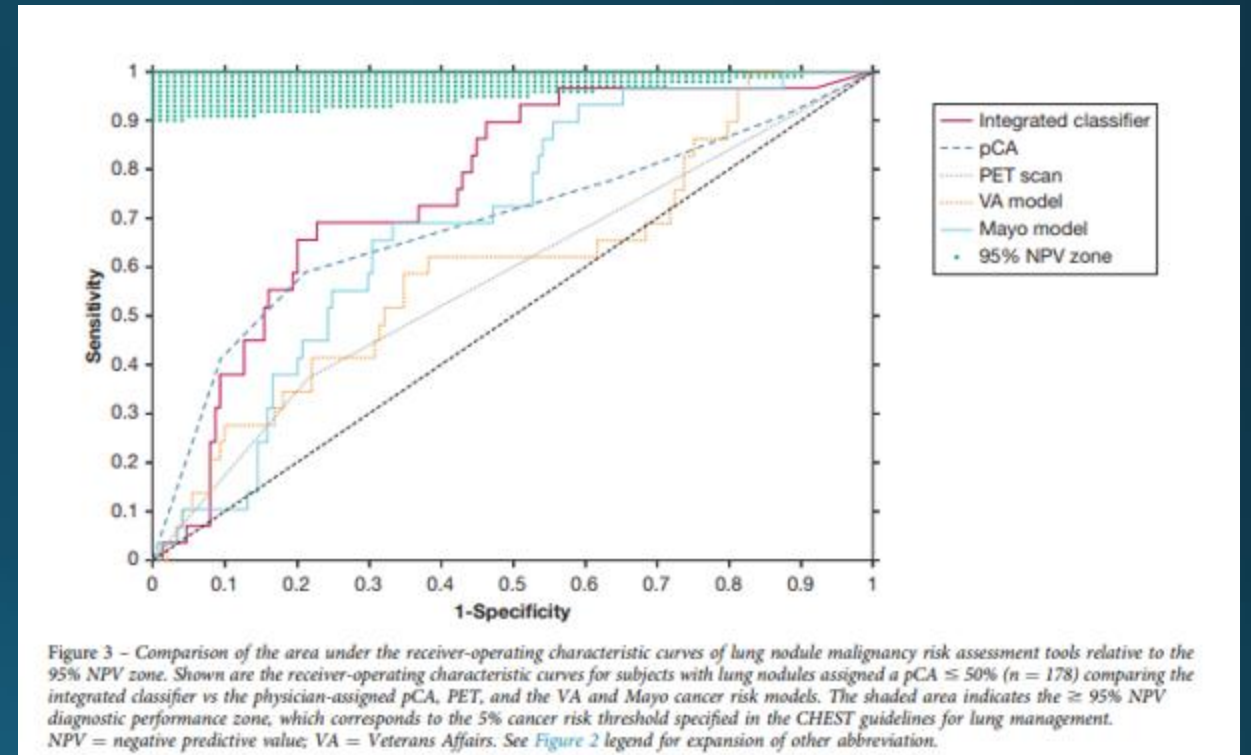
Two-protein biomarker ratio combined with a lung nodule clinical risk predictor had:

97% Sensitivity  
44% Specificity

40% relative reduction in invasive testing for patients with benign nodules

While potentially delaying the management of 3% of malignant nodules.

Approved for clinical use.



# 7 autoantibody Test (Murray 2010)

► [Ann Oncol. 2010 Aug;21\(8\):1687-1693. doi: 10.1093/annonc/mdp606.](#)

## Technical validation of an autoantibody test for the early detection of lung cancer

A Murray<sup>1</sup>, C J Chapman<sup>2</sup>, G Healey<sup>1</sup>, L J Peek<sup>3</sup>, G Parsons<sup>4</sup>, D Baldwin<sup>5</sup>, H F Sewell<sup>6</sup>, H A Fritsche<sup>7</sup>, J F R Robertson<sup>8</sup>

Affiliations + expand

PMID: 20124350 PMCID: [PMC2911202](#) DOI: [10.1093/annonc/mdp606](#)

► [Tumour Biol. 2012 Apr 11;33\(5\):1319-1326. doi: \[10.1007/s13277-012-0379-2\]\(#\)](#)

## EarlyCDT<sup>®</sup>-Lung test: improved clinical utility through additional autoantibody assays

[Caroline J Chapman](#)<sup>1,✉</sup>, [Graham F Healey](#)<sup>2</sup>, [Andrea Murray](#)<sup>2</sup>, [Peter Boyle](#)<sup>3</sup>, [Chris Robertson](#)<sup>4</sup>, [Laura J Peek](#)<sup>5</sup>, [Jared Allen](#)<sup>1,2</sup>, [Alison J Thorpe](#)<sup>1</sup>, [Geoffrey Hamilton-Fairley](#)<sup>2</sup>, [Celine B Parsy-Kowalska](#)<sup>2</sup>, [Isabel K MacDonald](#)<sup>2</sup>, [William Jewell](#)<sup>5</sup>, [Paul Maddison](#)<sup>6</sup>, [John F R Robertson](#)<sup>1,2</sup>

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PMCID: [PMC3460172](#) PMID: [22492236](#)

Cancer  
Prevention  
Research

Research Article

## EarlyCDT-Lung: An Immunobiomarker Test as an Aid to Early Detection of Lung Cancer

Stephen Lam<sup>1</sup>, Peter Boyle<sup>2</sup>, Graham F. Healey<sup>3</sup>, Paul Maddison<sup>4</sup>, Laura Peek<sup>7</sup>, Andrea Murray<sup>3</sup>, Caroline J. Chapman<sup>5</sup>, Jared Allen<sup>3</sup>, William C. Wood<sup>8</sup>, Herb F. Sewell<sup>6</sup>, and John F.R. Robertson<sup>5</sup>

Abstract

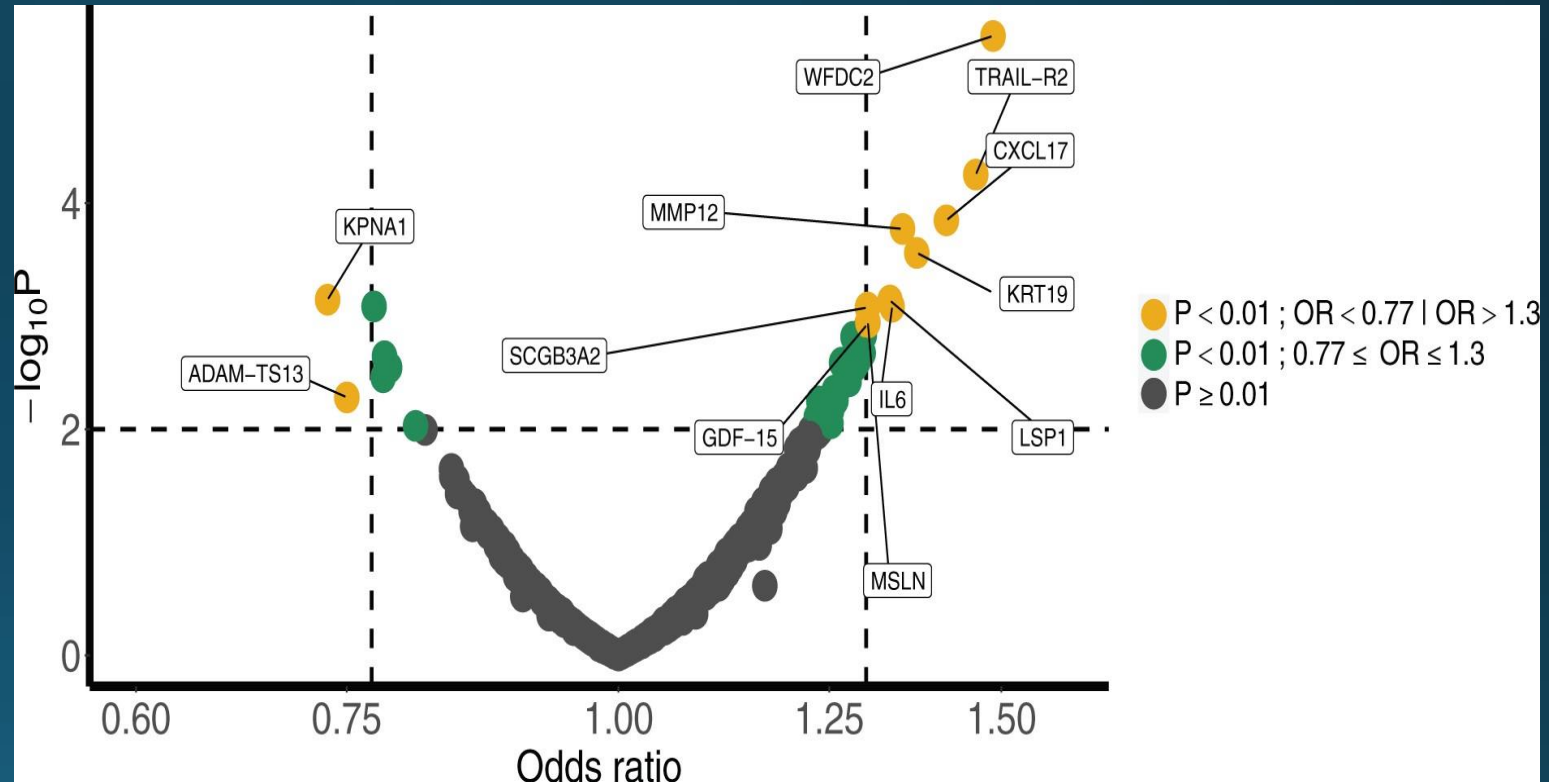
Recent publications have reported the technical and clinical validation of *EarlyCDT-Lung*, an autoantibody test which detected elevated autoantibodies in 40% of lung cancers at diagnosis. This manuscript reports the results of *EarlyCDT-Lung* run on four new (postvalidation) data sets. The following four cohorts of patients ( $n = 574$ ) with newly diagnosed lung cancer were identified: group 1 ( $n = 122$ ), 100% small cell lung cancer (SCLC); group 2 ( $n = 249$ ), 97% non-small cell lung cancer (NSCLC); group 3 ( $n = 122$ ), 100% NSCLC; group 4 ( $n = 81$ ), 62% NSCLC. Serum samples



# Moez et al. JNCI 2023

- 4 international LDCT screening studies
- Assayed 1078 protein markers using prediagnostic blood samples from 1253 participants based on a nested case-control design.
- 36 potentially informative circulating protein markers differentiating malignant from benign nodules

Single-marker analyses of nodule malignancy.

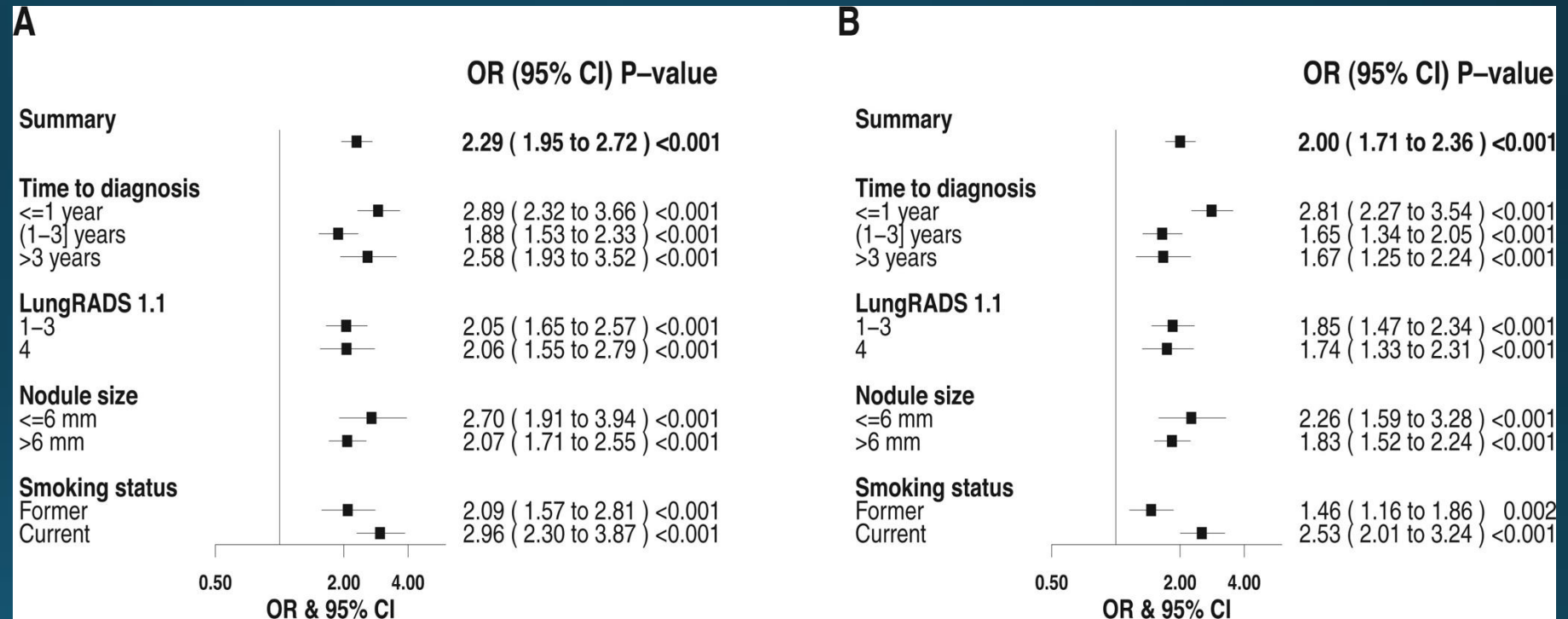


Khodayari Moez E, Warkentin MT, Brhane Y, Lam S, Field JK, Liu G, Zulueta JJ, Valencia K, Mesa-Guzman M, Nialet AP, Atkar-Khattra S, Davies MPA, Grant B, Murison K, Montuenga LM, Amos CI, Robbins HA, Johansson M, Hung RJ. Circulating proteome for pulmonary nodule malignancy. J Natl Cancer Inst. 2023 Sep 7;115(9):1060-1070.

# Moez et al. JNCI 2023

- Tightly connected biological network.
- Ten markers particularly relevant for imminent lung cancer diagnoses within 1 year

Protein burden scores illustrating the association with nodule malignancy.



Khodayari Moez E, Warkentin MT, Brhane Y, Lam S, Field JK, Liu G, Zulueta JJ, Valencia K, Mesa-Guzman M, Nialet AP, Atkar-Khattra S, Davies MPA, Grant B, Murison K, Montuenga LM, Amos CI, Robbins HA, Johansson M, Hung RJ. Circulating proteome for pulmonary nodule malignancy. J Natl Cancer Inst. 2023 Sep 7;115(9):1060-1070.

# Gene Expression Panels

> Eur Respir J. 2021 Jan 14;57(1):2002682. doi: 10.1183/13993003.02682-2020. Print 2021 Jan.

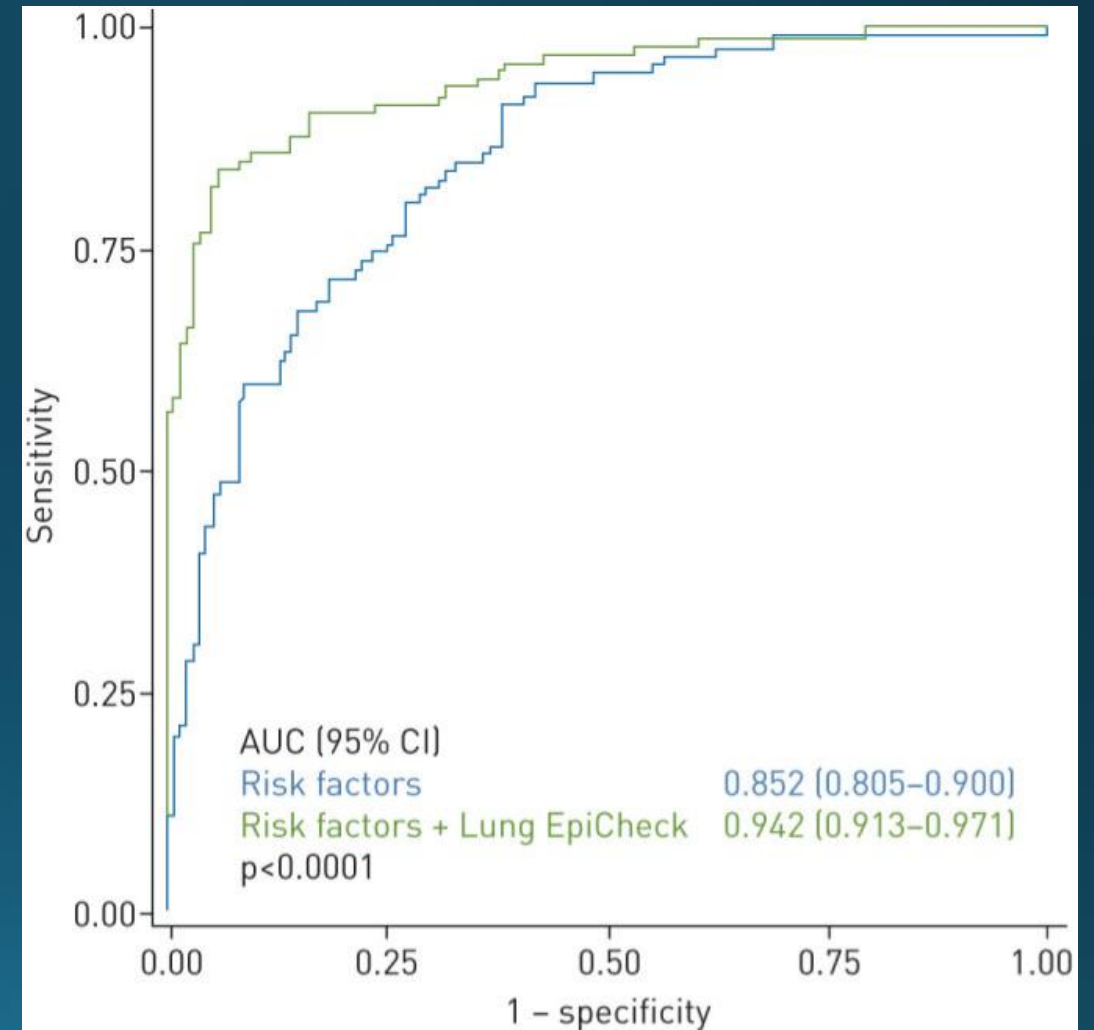
## Validation of Lung EpiCheck, a novel methylation-based blood assay, for the detection of lung cancer in European and Chinese high-risk individuals

Mina Gaga<sup>1</sup>, Joanna Chorostowska-Wynimko<sup>2</sup>, Ildikó Horváth<sup>3</sup>, Martin C Tammemagi<sup>4</sup>, David Shitrit<sup>5</sup>, Vered H Eisenberg<sup>6</sup>, Hao Liang<sup>7</sup>, David Stav<sup>8</sup>, Dan Levy Faber<sup>9, 10</sup>, Maarten Jansen<sup>11</sup>, Yael Raviv<sup>12</sup>, Vasileios Panagoulas<sup>13</sup>, Piotr Rudzinski<sup>2</sup>, Gabriel Izbicki<sup>14</sup>, Ohad Ronen<sup>15</sup>, Adiv Goldhaber<sup>16</sup>, Rawia Moalem<sup>17</sup>, Nadir Arber<sup>18</sup>, Ilana Haas<sup>19</sup>, Qinghua Zhou<sup>7</sup>

The risk factors of age, gender, smoking status, quit years, pack-years, and COPD together yielded an AUC of 0.852.

Adding six methylation biomarkers significantly increased the AUC to 0.942.

**This Technology is currently under clinical investigation.**



Gaga, M., Chorostowska-Wynimko, J., Horvath, I., Tammemagi, M.C., Shitrit, D., Eisenberg, V.H., Liang, H., Stav, D., Levy Faber, D., Jansen, M., et al. (2021). Validation of Lung EpiCheck, a novel methylation-based blood assay, for the detection of lung cancer in European and Chinese high-risk individuals. Eur. Respir. J. 57, 2002682.

# Gene Expression Panels

Cell Reports Medicine

CellPress  
OPEN ACCESS

## Article

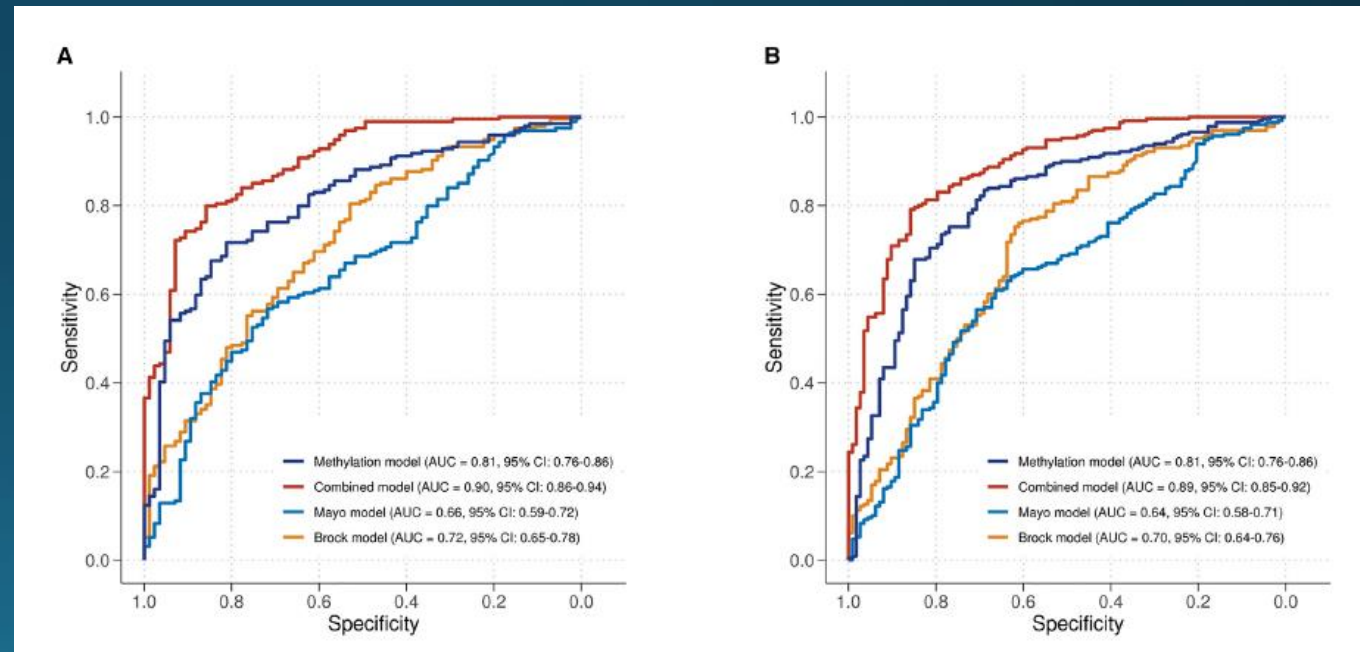
### A clinically effective model based on cell-free DNA methylation and low-dose CT for risk stratification of pulmonary nodules

Wenhua Liang,<sup>1,12,\*</sup> Jinsheng Tao,<sup>2,12</sup> Chao Cheng,<sup>3,12</sup> Haitao Sun,<sup>4,12</sup> Zhujia Ye,<sup>2,12</sup> Shuangxiu Wu,<sup>2</sup> Yubiao Guo,<sup>5</sup> Jiaqing Zhang,<sup>6</sup> Qunqing Chen,<sup>6</sup> Dan Liu,<sup>7</sup> Lunxu Liu,<sup>8</sup> Hui Tian,<sup>9</sup> Lin Teng,<sup>2</sup> Nanshan Zhong,<sup>10</sup> Jian-Bing Fan,<sup>2,11,\*</sup> and Jianxing He<sup>1,13,\*</sup>

An Oct 2024 study developed a blood-based risk prediction model by integrating 40 cfDNA methylation markers with six risk factors for distinguishing malignant from benign nodules.

Combining 6 common risk factors with cfDNA methylation markers significantly improved the performance.

36.9% and 25.4% increase in AUC vs. the Mayo Clinic and Brock models ( $p < 0.0001$ ).



This Technology is currently under clinical investigation.

Liang W, Tao J, Cheng C, Sun H, Ye Z, Wu S, Guo Y, Zhang J, Chen Q, Liu D, Liu L, Tian H, Teng L, Zhong N, Fan JB, He J. A clinically effective model based on cell-free DNA methylation and low-dose CT for risk stratification of pulmonary nodules. Cell Rep Med. 2024 Oct 15;5(10):101750. doi: 10.1016/j.xcrm.2024.101750. Epub 2024 Sep 27. PMID: 39341207; PMCID: PMC11513810.

# 4. Promise of Deep Learning and AI?

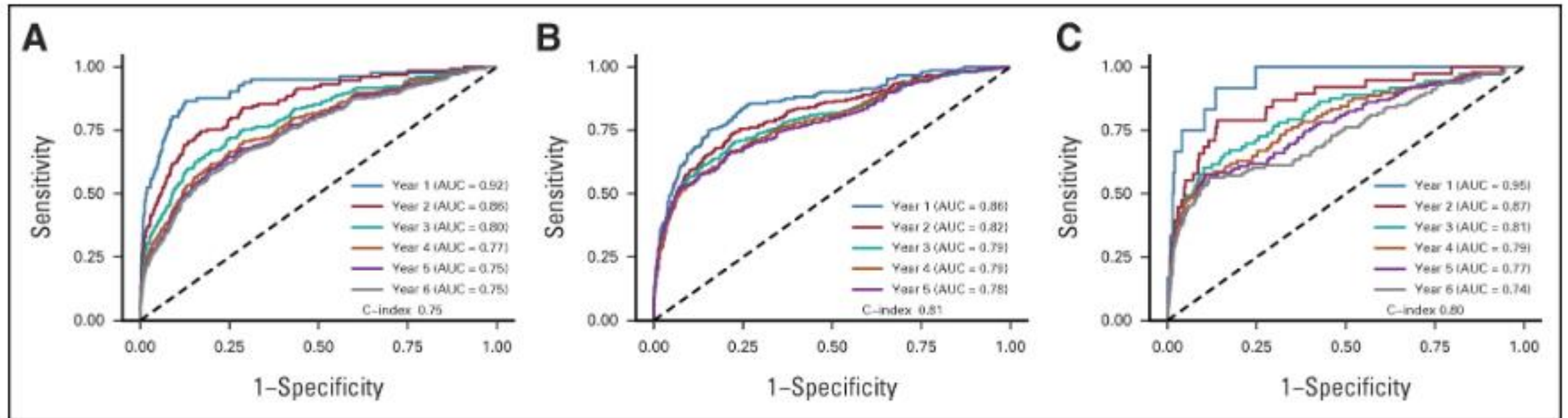
- Deep learning cancer risk model, Sybil, uses a single low-dose chest CT scan to predict lung cancers occurring 1-6 years after a screen



Mikhael PG, Wohlwend J, Yala A, Karstens L, Xiang J, Takigami AK, Bourgooin PP, Chan P, Mrah S, Amayri W, Juan YH, Yang CT, Wan YL, Lin G, Sequist LV, Fintelmann FJ, Barzilay R. Sybil: A Validated Deep Learning Model to Predict Future Lung Cancer Risk From a Single Low-Dose Chest Computed Tomography. *J Clin Oncol.* 2023 Apr 20;41(12):2191-2200.

# 4. Promise of Deep Learning and AI?

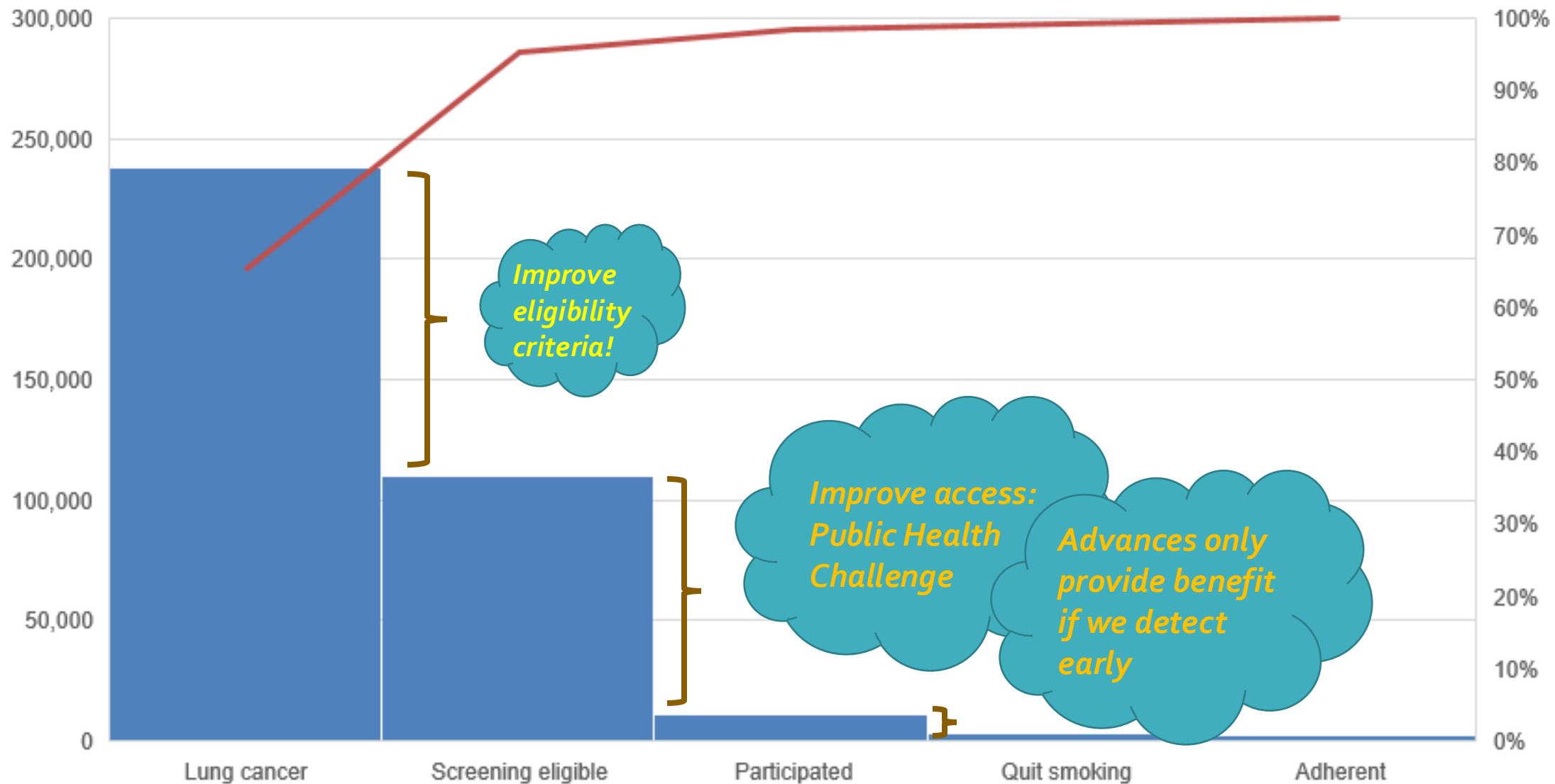
- Sybil can accurately predict an individual's future lung cancer risk from a single LDCT scan to further enable personalized screening, future study is required to understand Sybil's clinical applications.



- Proteomic panels provide promising opportunity.

5. What are the broader challenges and implementation barriers?

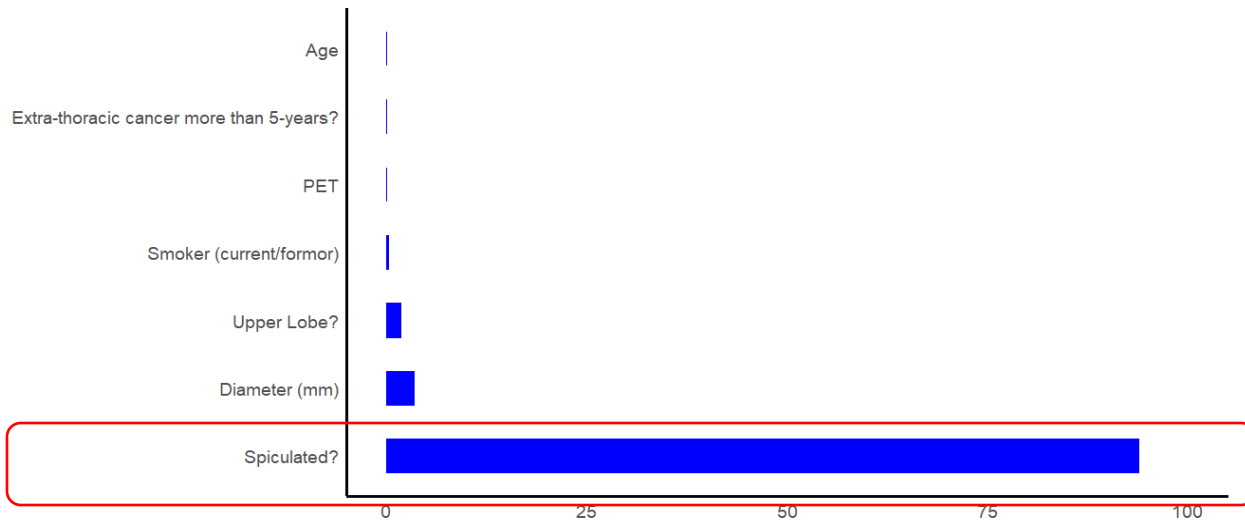
# Lung Cancer Screening USA 2023: Population-Level Access and Effectiveness Challenges!



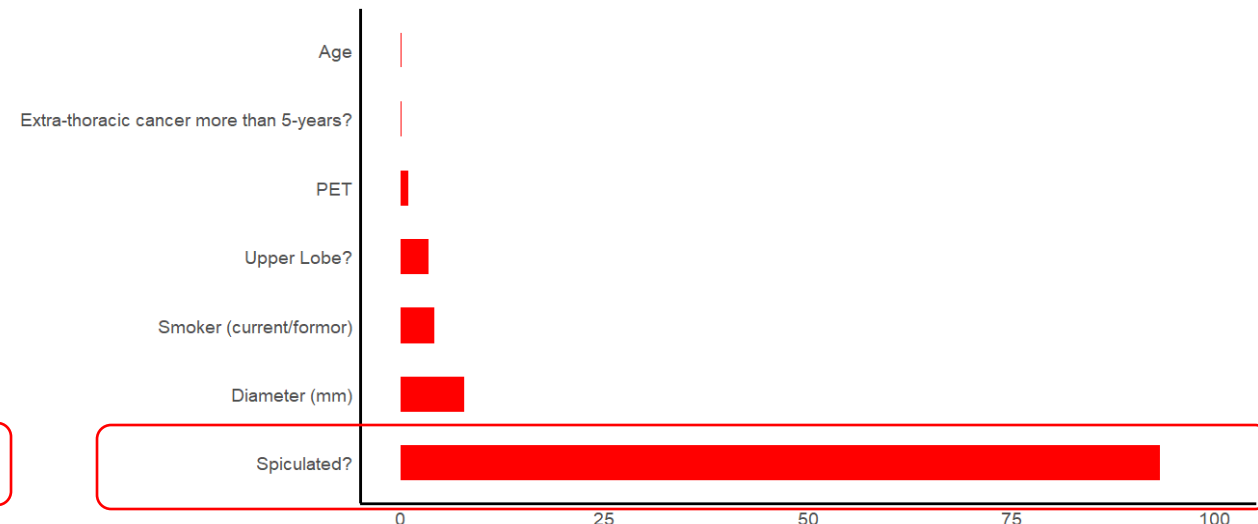


# Missing Variables and the Utility of Lung Cancer and Lung Nodule Risk Calculators in the DELUGE Cohort

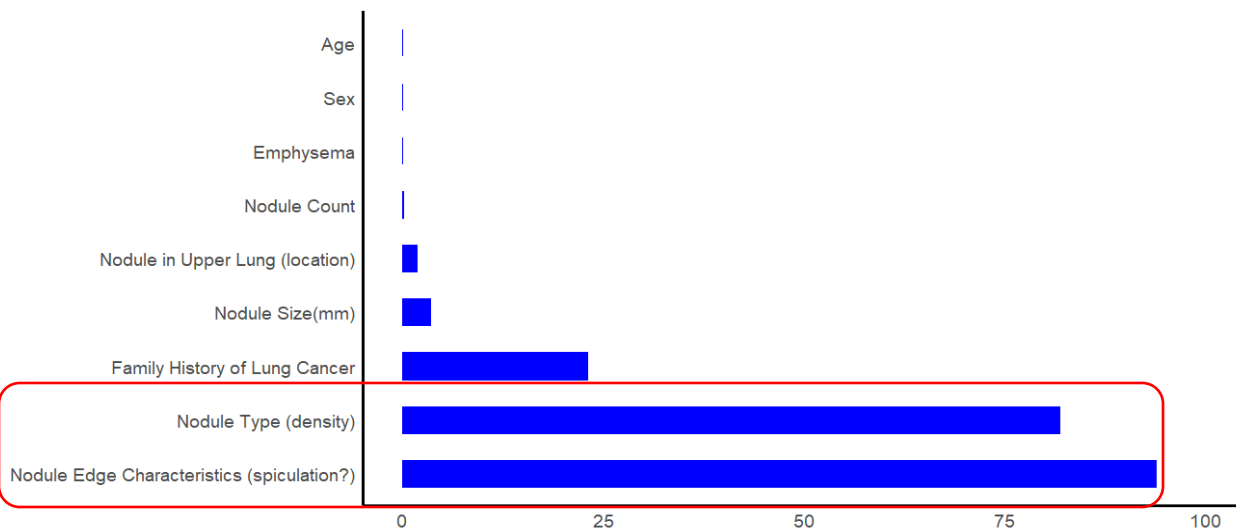
Percentage of missing variables in Lung Cancer Screening (LCS) cohort at initial enrollment for Herder Model



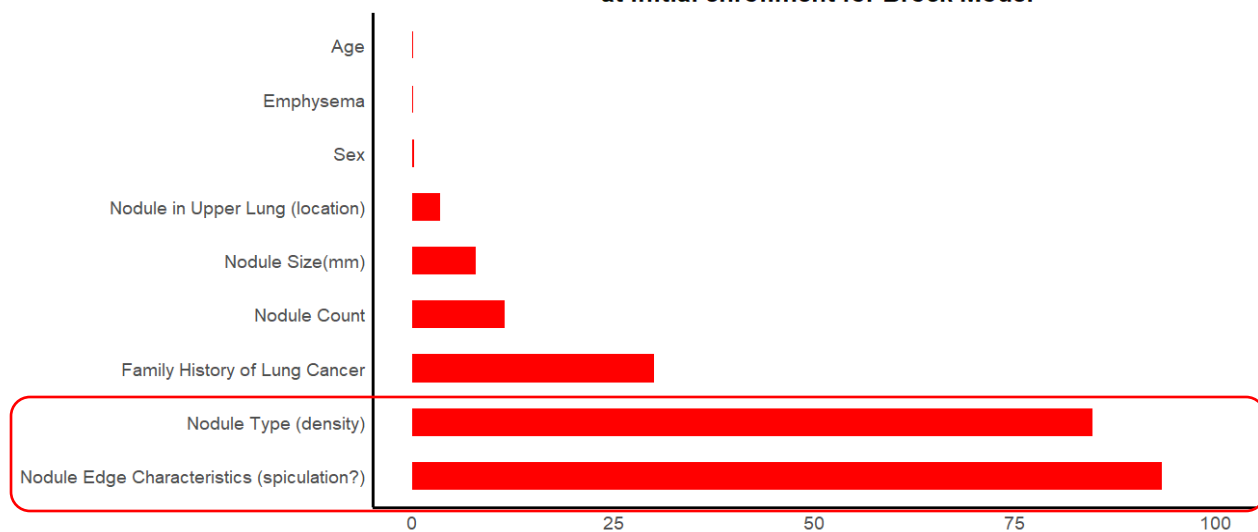
Percentage of missing variables in Lung Nodule Program (LNP) cohort at initial enrollment for Herder Model



Percentage of missing variables in Lung Cancer Screening (LCS) cohort at initial enrollment for Brock Model

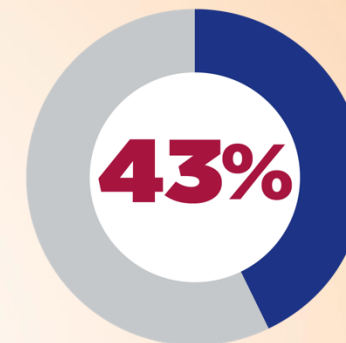
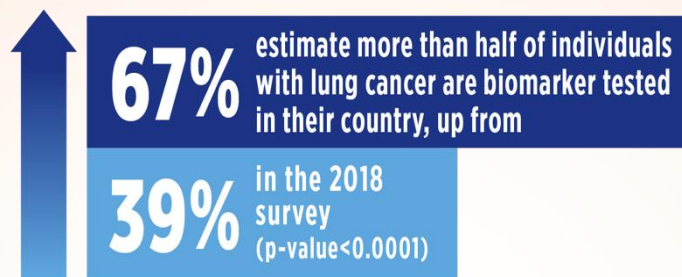


Percentage of missing variables in Lung Nodule Program (LNP) cohort at initial enrollment for Brock Model



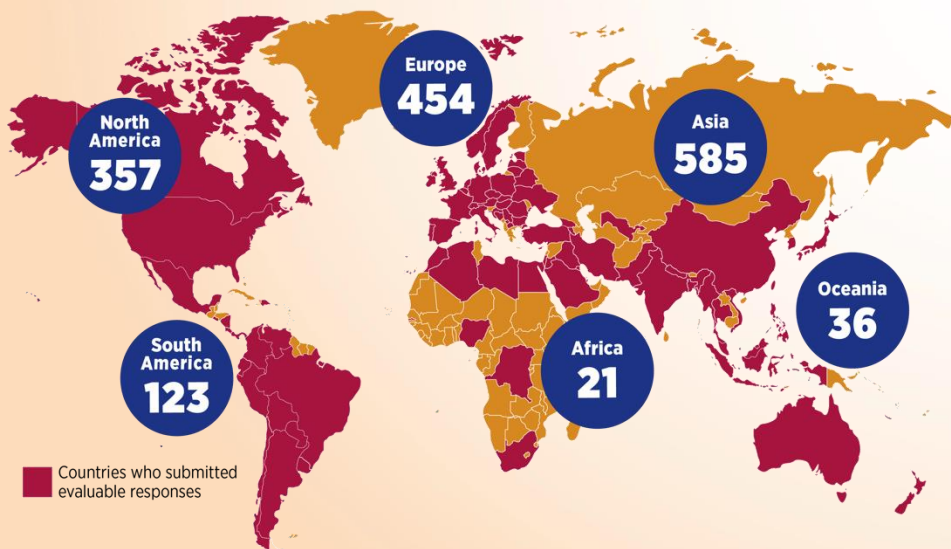
# The 2024 IASLC Global Survey on Biomarker Testing

Respondents report that testing rates have improved but continued, substantial barriers exist.



Sometimes or often treat patients prior to receiving biomarker results

**1,677** responses across **90** countries and **14** disciplines.



## The Highest Ranked Barriers

**COST**

**TIME**

**SAMPLE QUALITY**

**ACCESS**

**AWARENESS**

IASLC PARTNERS  
FOR THORACIC CANCER CARE



This survey is in partnership with the IASLC Partners for Thoracic Cancer Care.

# Take Home Message:

Proteomic and gene expression panels can improve lung cancer risk assessment, show promise for future refinement.

It is important that we optimize implementation and ensure broad access.

# Thank you!

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