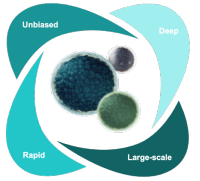


# Deep, Rapid and Unbiased Plasma Proteomics with the Proteograph™ Product Suite Enables Proteogenomic Studies with Differential Analysis of Proteoforms

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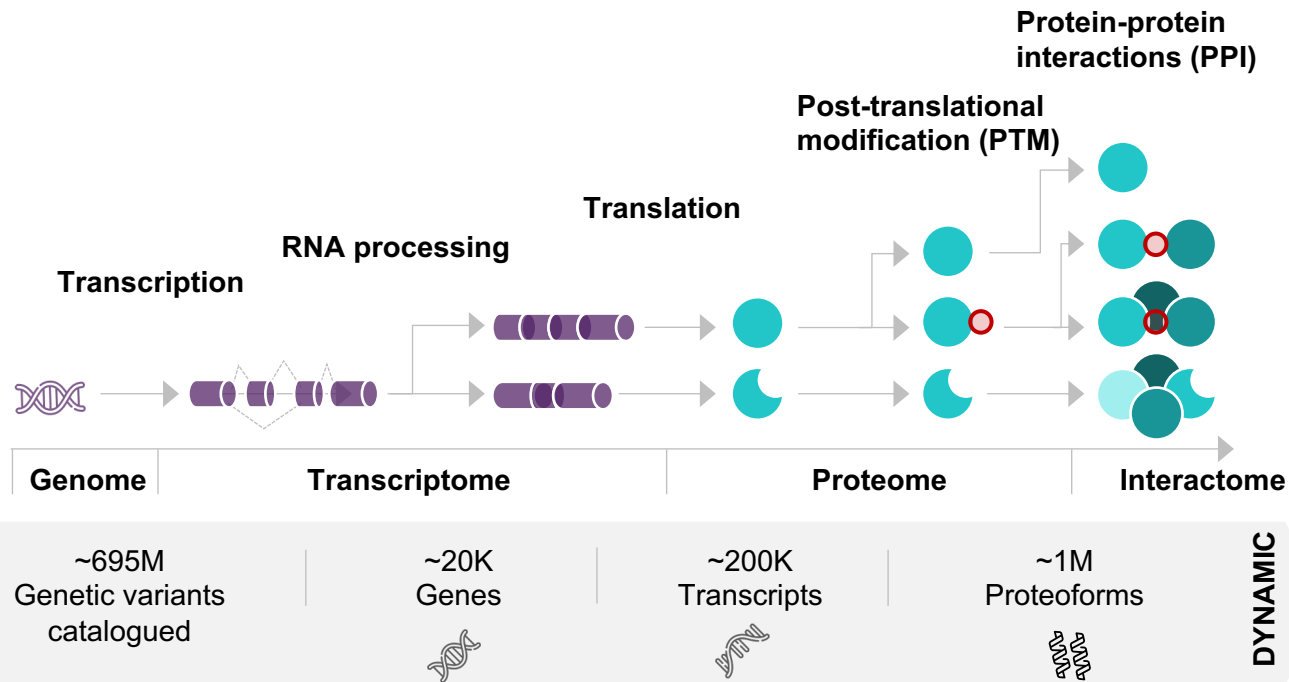


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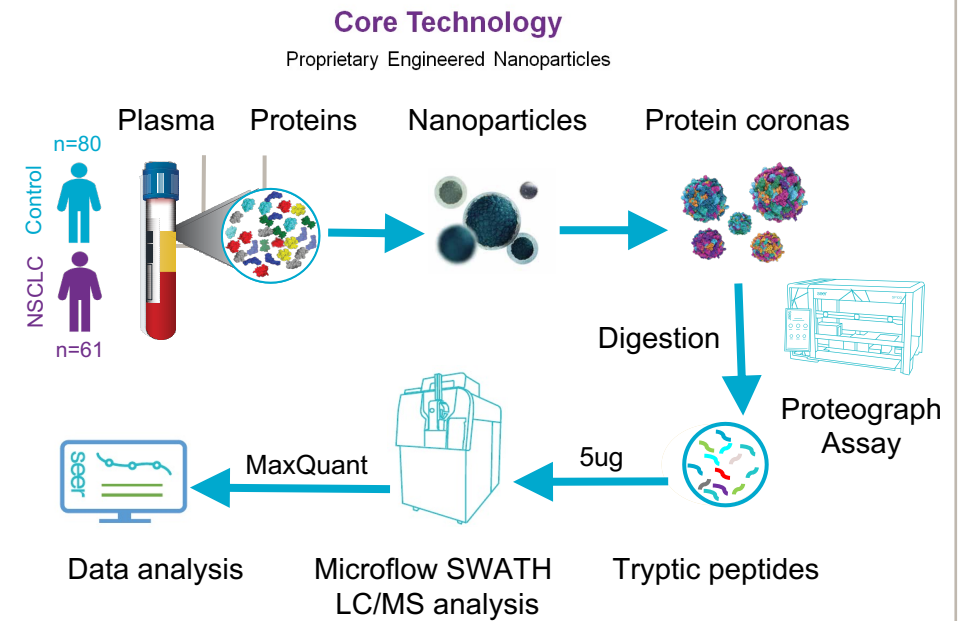
## Challenge

Comprehensive coverage of the proteome remains elusive, because of proteoforms arising from alternative splicing, allelic variation, and protein modifications.



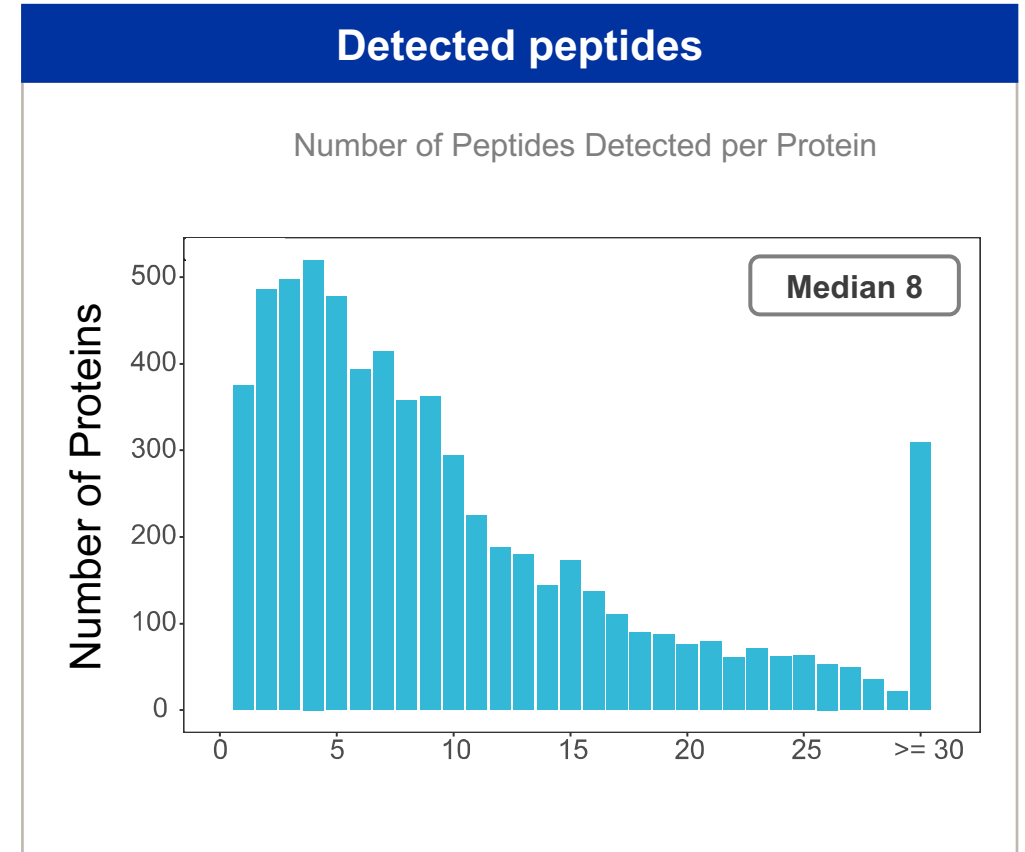
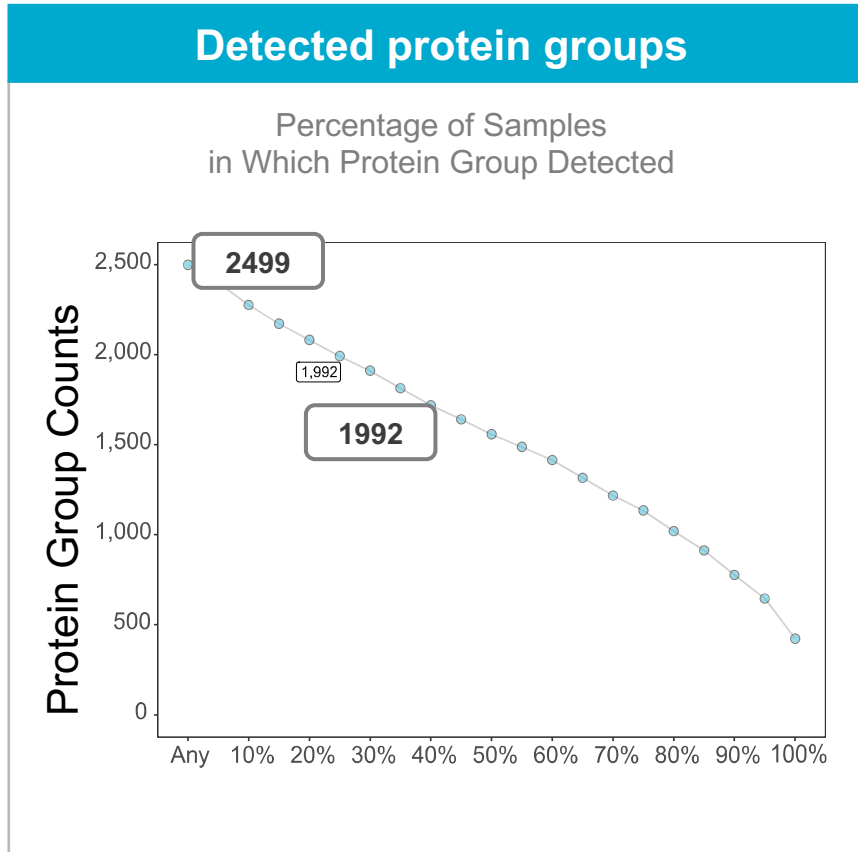
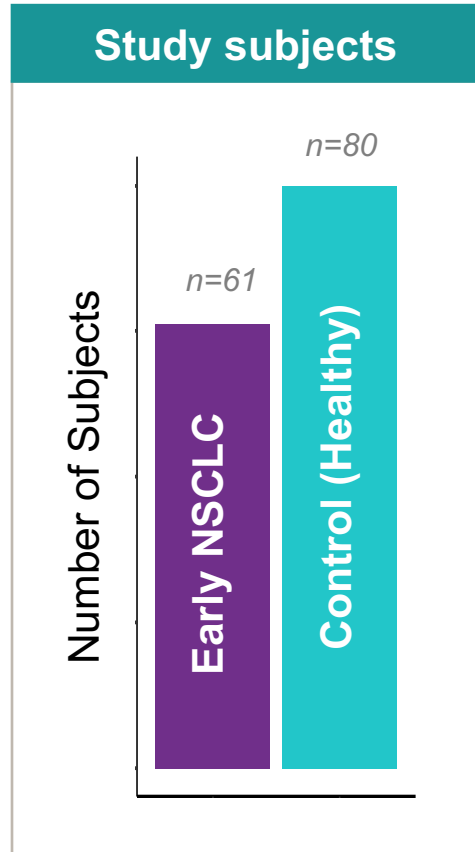
## Solution

Seer Core technology and Proteograph Product Suite provides unbiased, deep, and rapid proteomics at scale



# Utilizing Proteograph Platform to interrogate protein isoforms in a non-small cell lung cancer (NSCLC) plasma proteome study

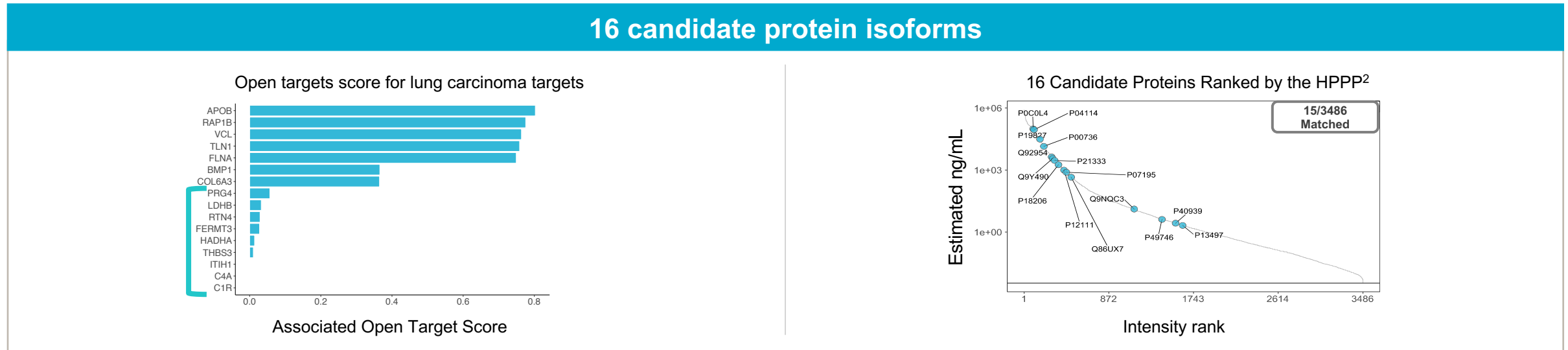
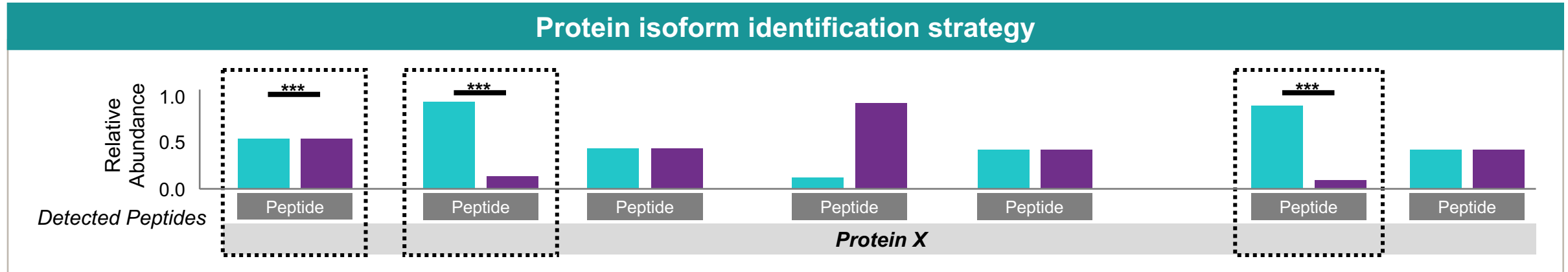
Median 8 peptides for each of the 1,992 proteins observed in at least 25% of the 141 subjects of NSCLC study<sup>1</sup>



<sup>1</sup>Blume et al. Nat. Comm. (2020)

# Identification of putative protein isoforms using peptide abundance

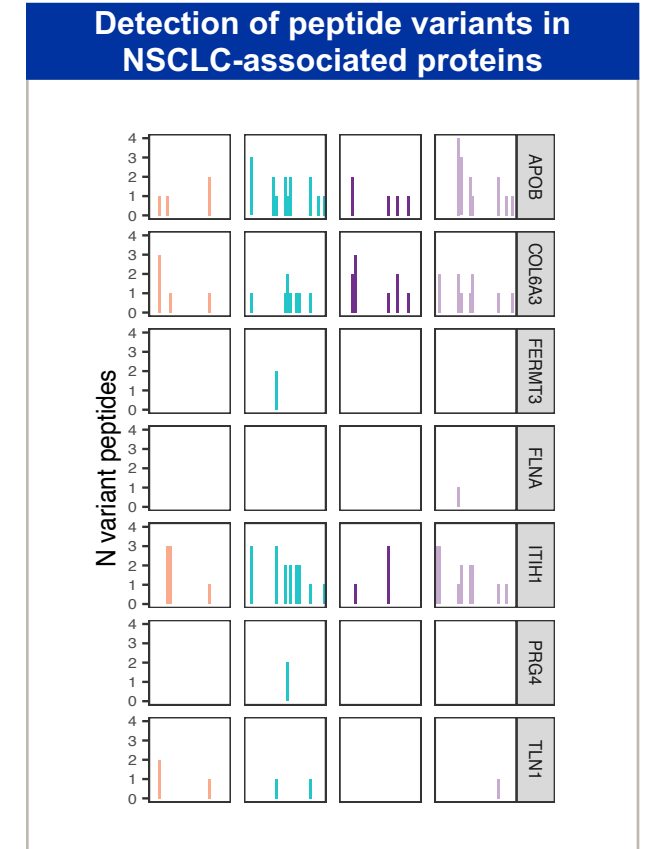
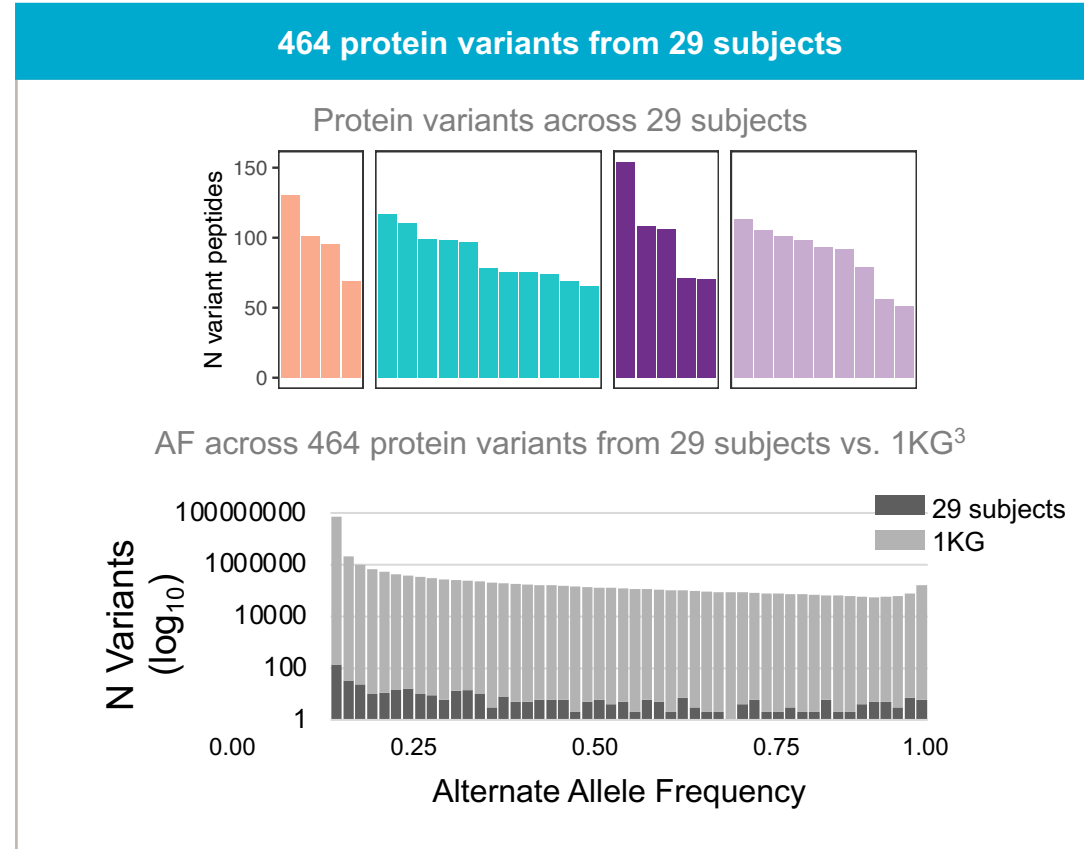
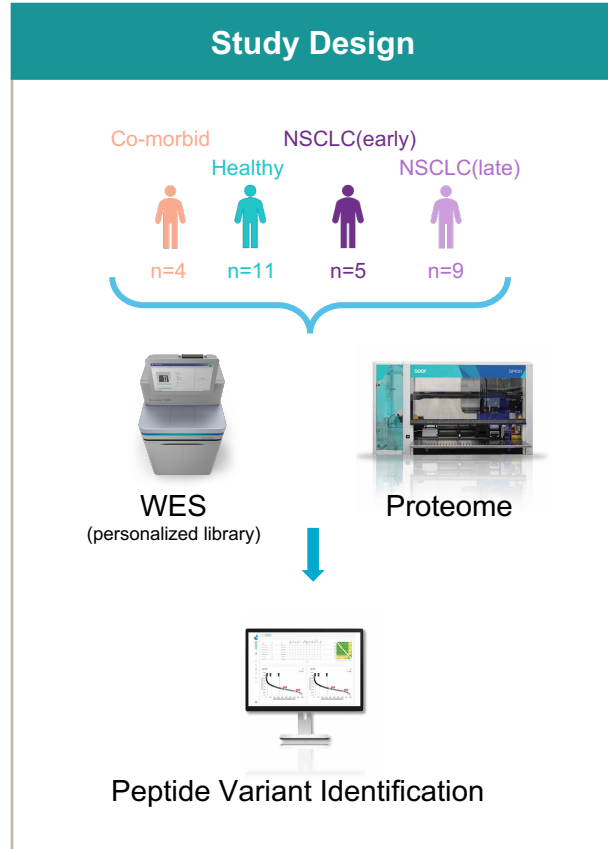
16 putative protein isoforms show known and novel associations with lung carcinoma targets and span the dynamic range



<sup>2</sup>Deutsch et al. J. Proteome Res.(2018)

# Proteogenomic Studies at Scale with an unbiased, deep and rapid method

## Peptide variant identification using personalized libraries



<sup>3</sup>1000 Genomes (2015)



# Conclusions

## *Proteograph Product Suite for Proteogenomic Analyses*



Using the Proteograph Product Suite, we detected 2499 protein groups, with 1,992 in 25% of the subjects, and 21,959 peptides in total with median 8 peptides per protein across all 141 subjects (control vs. early NSCLC plasma samples)



We identified 16 candidate protein isoforms associated with lung cancer (both known and novel targets) that span across the dynamic range, including one not reported in the Human Plasma Proteome Project



Proteogenomic analysis of a subset of the NSCLC subjects identified 464 peptide variants, of which map to 7 out of the 16 lung cancer-associated candidate protein isoforms

Proteograph can generate unbiased and deep plasma proteome profiles that enable identification of protein variants and peptides present in plasma at a scale sufficient to enable population-scale proteomic studies.