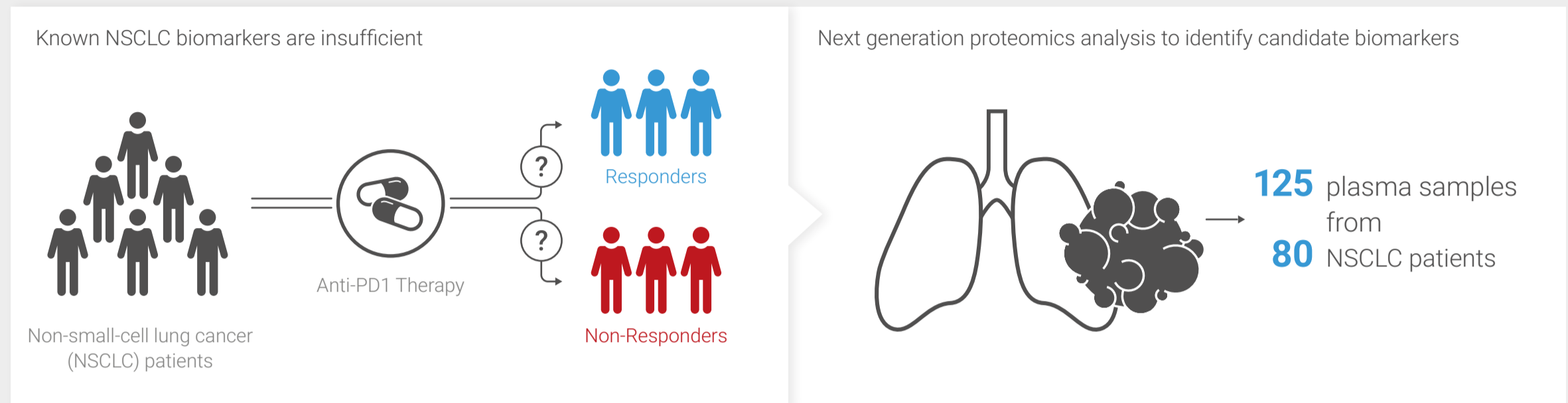


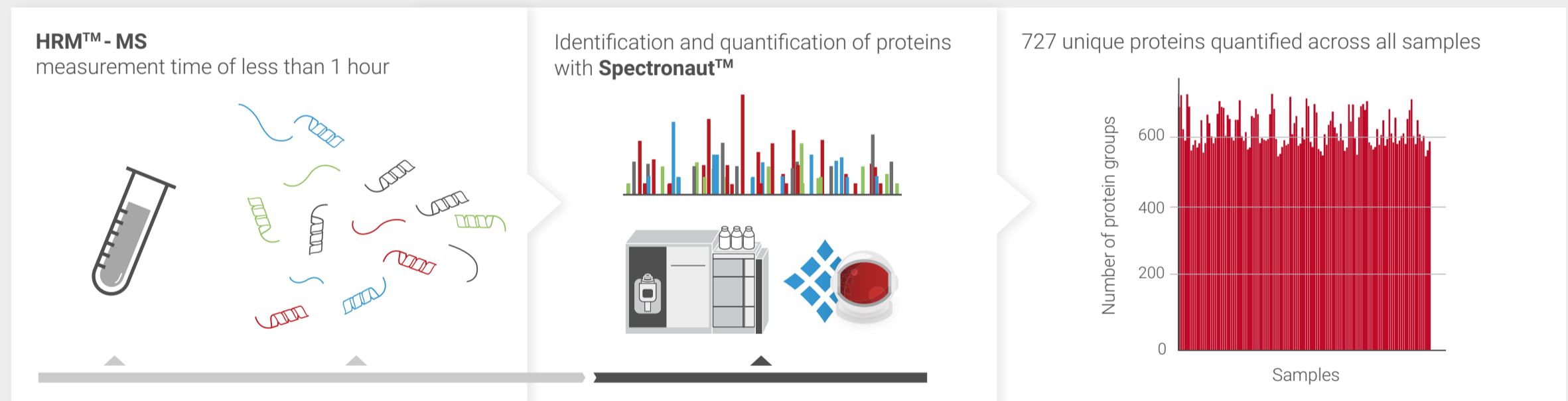
NEXT GENERATION PROTEOMICS IDENTIFIES CANDIDATE BIOMARKERS FOR IMMUNOTHERAPY

This study was conducted in collaboration with Institut Curie and has been presented as a poster at ESMO 2020

INTRODUCTION Differentiating Anti-PD1 therapy responders from non-responders through plasma proteome analysis in NSCLC



METHODOLOGY Hyper Reaction Monitoring™ - Mass Spectrometry (HRM™-MS) coupled with Spectronaut™ software analysis



CONCLUSION A holistic perspective on plasma proteome changes associated with response to anti-PD1 treatment in NSCLC patients

26 identified proteins associated to response and progression-free survival

Underlying mechanisms

- **Cell adhesion & actin remodeling**
e.g. VCL, MADCAM1
- **Inflammation and immune response**
e.g. ARPC4, Immunoglobulins
- **Metabolic processes & cell growth**
e.g. TIMP1, HPR

Unsupervised hierarchical clustering of all samples based on candidate biomarkers

Significant difference in progression-free survival between subjects from **cluster 1** and **cluster 2**

p = 0.0018