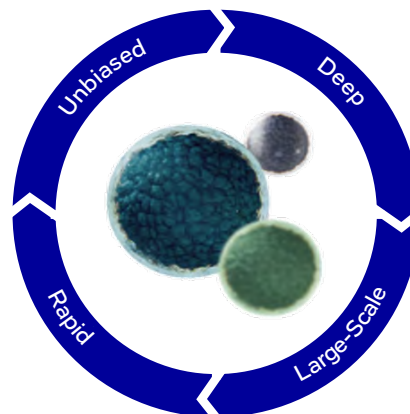


# Deep Proteomics at Scale to Drive Biomarker Discovery

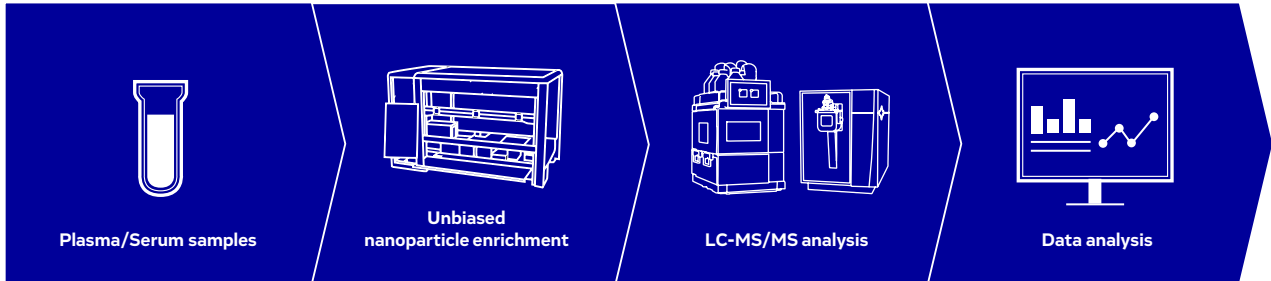
- ▶ Evotec's broad expertise in different target classes, modalities, technology and therapeutic areas enables Evotec to comprehensively address biomarker and translational research needs
- ▶ Evotec provides integrated solutions for translational biomarker discovery by combining its high-end proteomics platform with genomics, transcriptomics and metabolomics data
- ▶ These full translational capabilities are supported by multiple disciplines such as *in vitro/in vivo* pharmacology, imaging, and immunohistochemistry as well as privileged access to annotated clinical samples with clinical data
- ▶ To further boost Evotec's high-throughput proteomics platform Evotec has implemented the Proteograph™ platform from Seer, which enables automated and unbiased nanoparticle based protein enrichment for maximal proteomic insights
- ▶ This allows the robust and high-throughput analysis of large cohorts of challenging clinical samples, such as plasma, urine and cerebrospinal fluid, supporting biomarker discovery and identification of novel targets

- ▶ Proteomes are dynamic and far more diverse than genomes
- ▶ Full characterization of the proteome is essential to filling in the missing pieces of biology
- ▶ Unbiased nanoparticle based enrichment combined with highest mass spectrometry based proteomics performance delivers unprecedented proteome depth as NPs compress dynamic range of protein abundance enabling wide concentration range evaluation
- ▶ Proteograph assay automation drives scalability and speed
- ▶ Unlike targeted approaches peptide level quantitation allows for the distinction between proteoforms and identification of post-translational modifications
- ▶ Proprietary bioinformatics platform allows unprecedented data analysis and data integration





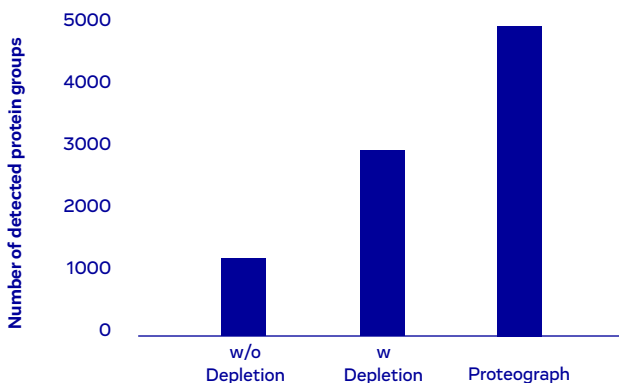
## High Throughput Proteomics Workflow



► The Proteograph technology<sup>1</sup> is fully integrated into Evotec's high performance proteomics platform to deliver highest throughput at unmet proteome depth

► Currently workflows are established for applications to plasma and serum and will be further extended to various sample types (e.g. CSE, Urine, Conditioned Media)

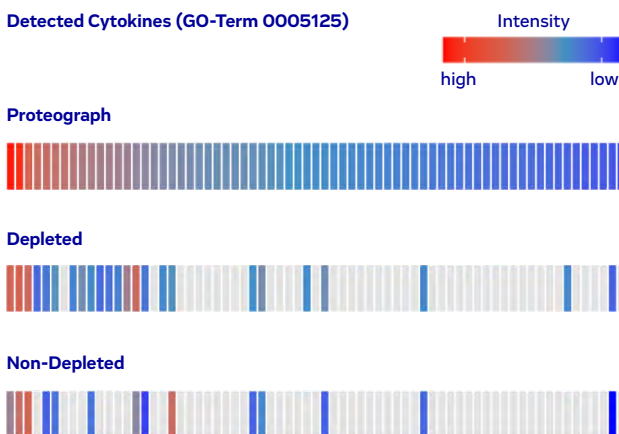
Proteome depth applying Evotec's plasma proteomics workflows



## Unparalleled Proteome Coverage

- Evotec's plasma proteomics workflows with or without antibody-based depletion of high abundant proteins already deliver outstanding proteome coverage (about 1,500 to 3,000 proteins, respectively)
- The Proteograph technology boosts proteome coverage to up to 5,000 proteins accessible in patient cohort studies (>3,000 proteins per individual sample)

Detected Cytokines (GO-Term 0005125)



## Unprecedented Proteome Depth

- Application of Proteograph technology significantly boosts sensitivity to detect low abundant proteins compared to workflows with and without antibody based depletion
- Identification of 30% more Cytokines when compared to large scale proteome studies which rely on extensive depletion and fractionation<sup>2</sup>

<sup>1</sup> Blume et al. 2020

<sup>2</sup> Keshishian et al. 2015