Thomas Kislinger Princess Margaret Cancer Centre Toronto, Canada

On behalf of the team (John Semmes, EVMS and Paul Boutros, OICR)

Systematic Development of Prostate Cancer Liquid Biopsies: Proteomics and Proteogenomics of Post-DRE Urines and Cancer Tissues

1. How did we get here? A. Proteomics of prostatic secretions and post-DRE urines

2. What will we do as part of the EDRN program? A. Preliminary data

A.CPC-GENE genomics and proteogenomics B.post-DRE urine (proteomics, lipidomics)

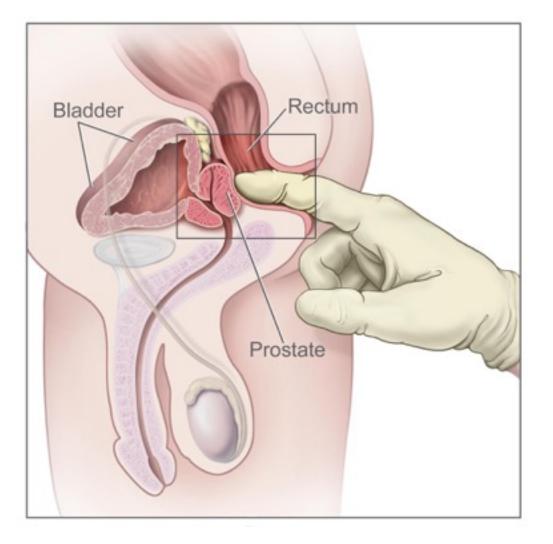
Overview

3. Additional prostate cancer proteomics data (PCC, OICR)



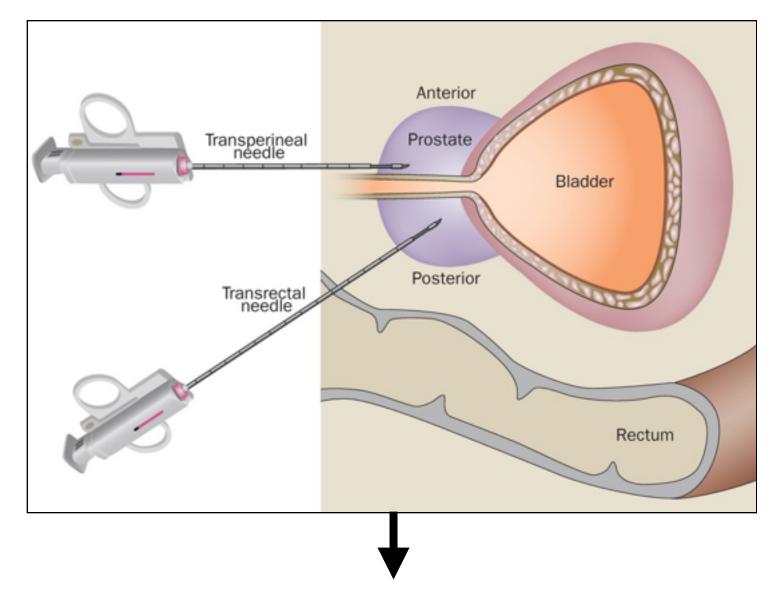
Prostate Cancer Prognosis

DRE



Imaging





TNM Stage

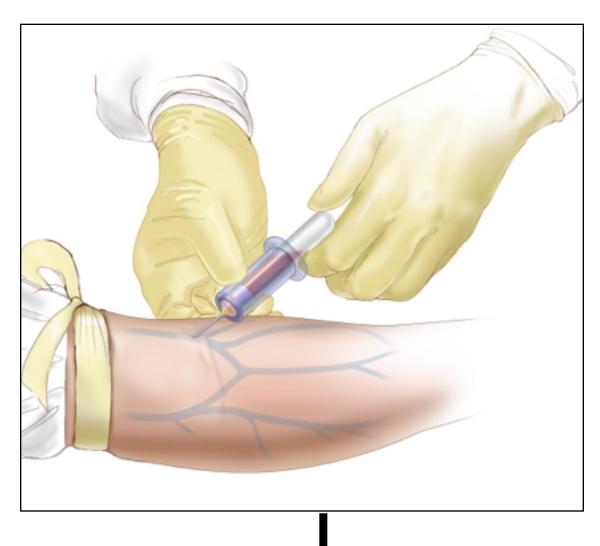
Low Risk

Intermediate Risk

Localized Cancers

Prostate biopsy

Blood test



Tumour Grade

PSA

High Risk

Metastatic



Expressed Prostatic Secretions

Direct-EPS	EPS-uri (post-DRE-
Proteins & cells shed by the gland	Prostatic secre urine (DF
Rich source of prostate biomarkers	Can be colle frequent longitudi
Collected prior to RP	Applicable to collection

>2,000 proteins & ~350 patients

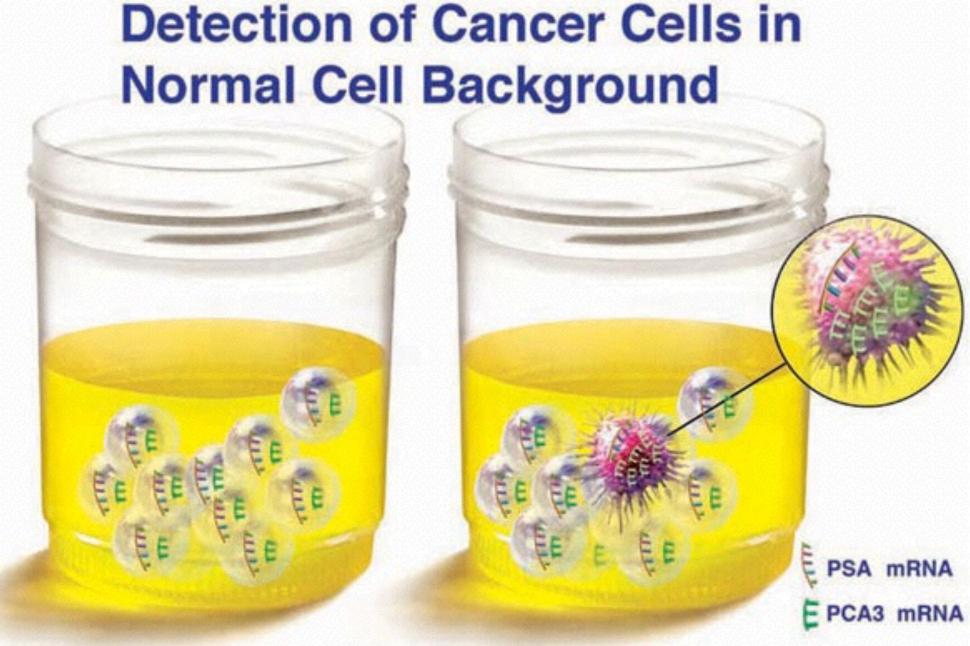
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Detection of Cancer Cells in Normal Cell Background

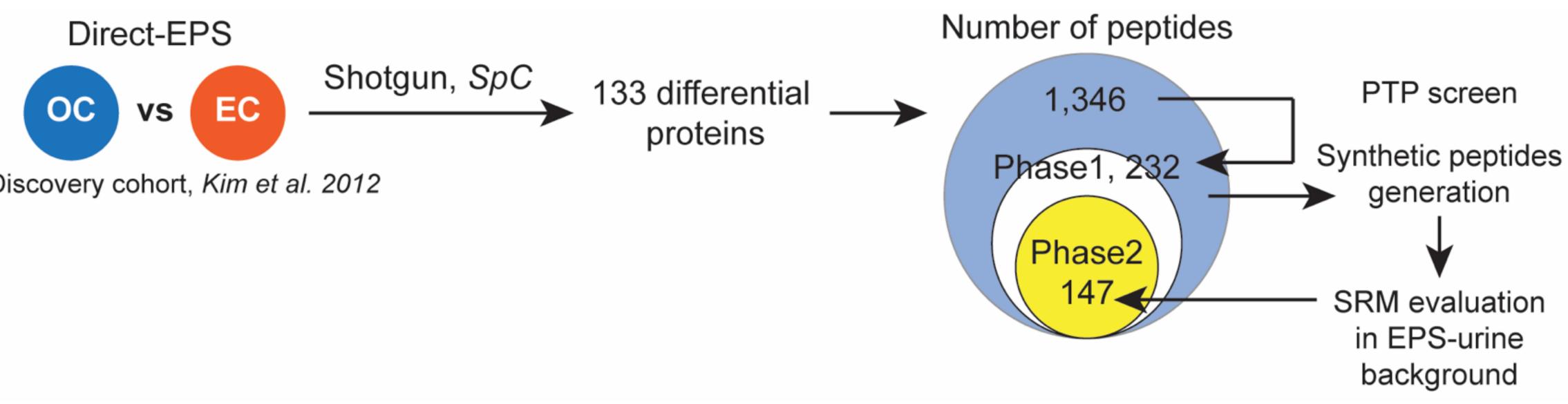


http://www.usrf.org/news/PCA3

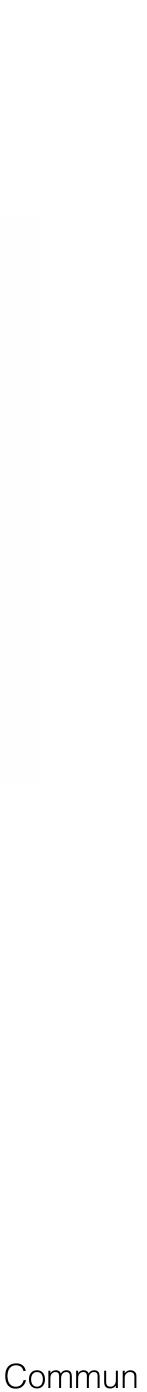
Kim Y, et al. Nat Commun. 2016 Yang L, et al. Oncotarget. 2015 Principe S, et al. Proteomics. 2013 Kim Y, et al. Mol Cell Proteomics. 2012 Principe S, et al. J Proteome Res. 2012 Drake RR, et al. J Proteome Res. 2010



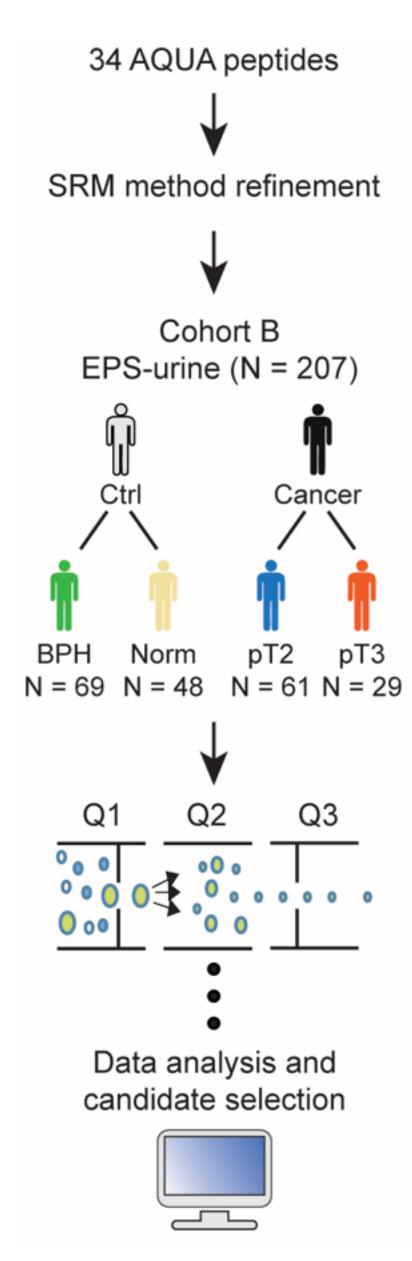
Development of Targeted Proteomics Assays

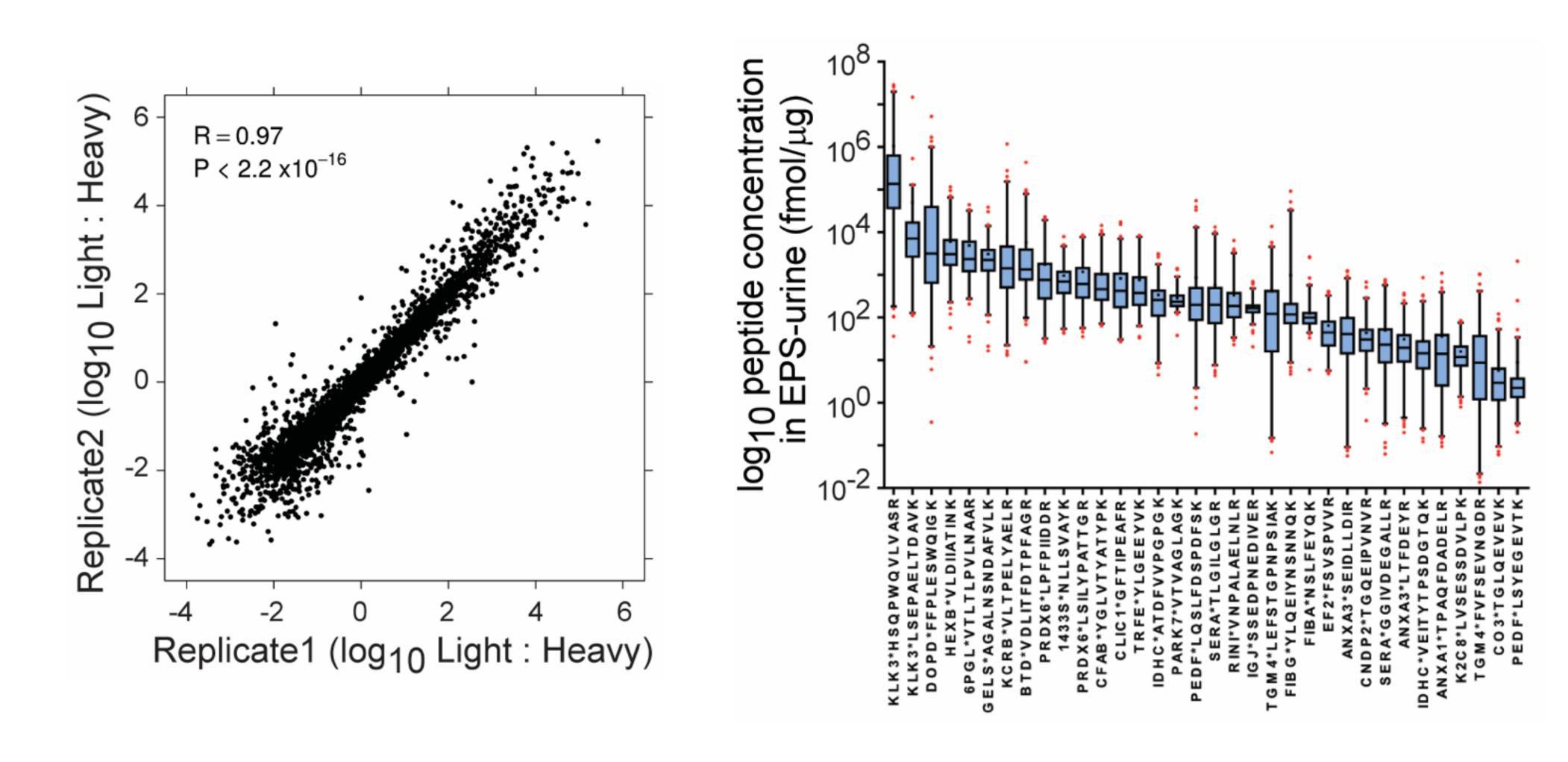


Discovery cohort, *Kim et al. 2012*

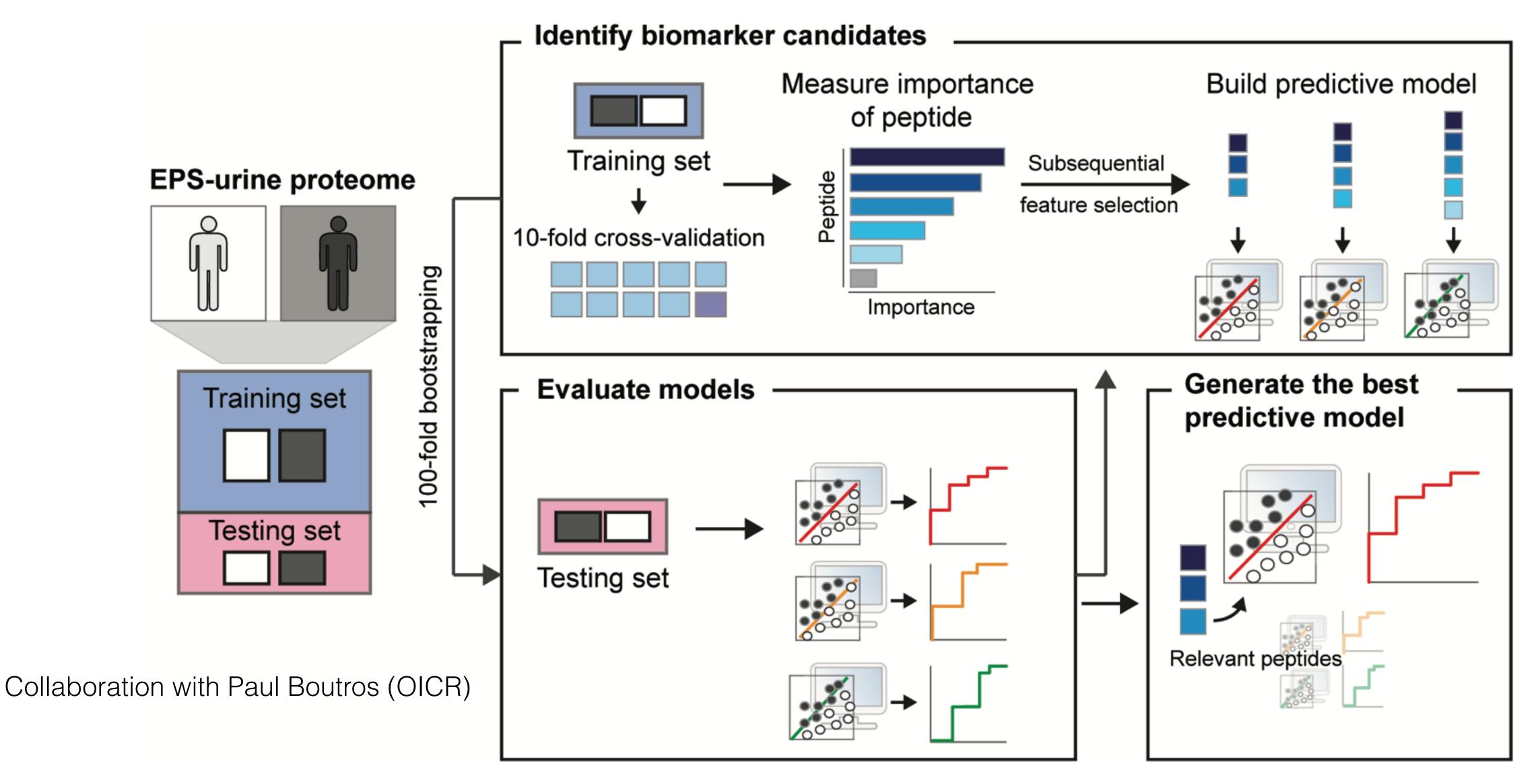


Tissue Proximal Fluids



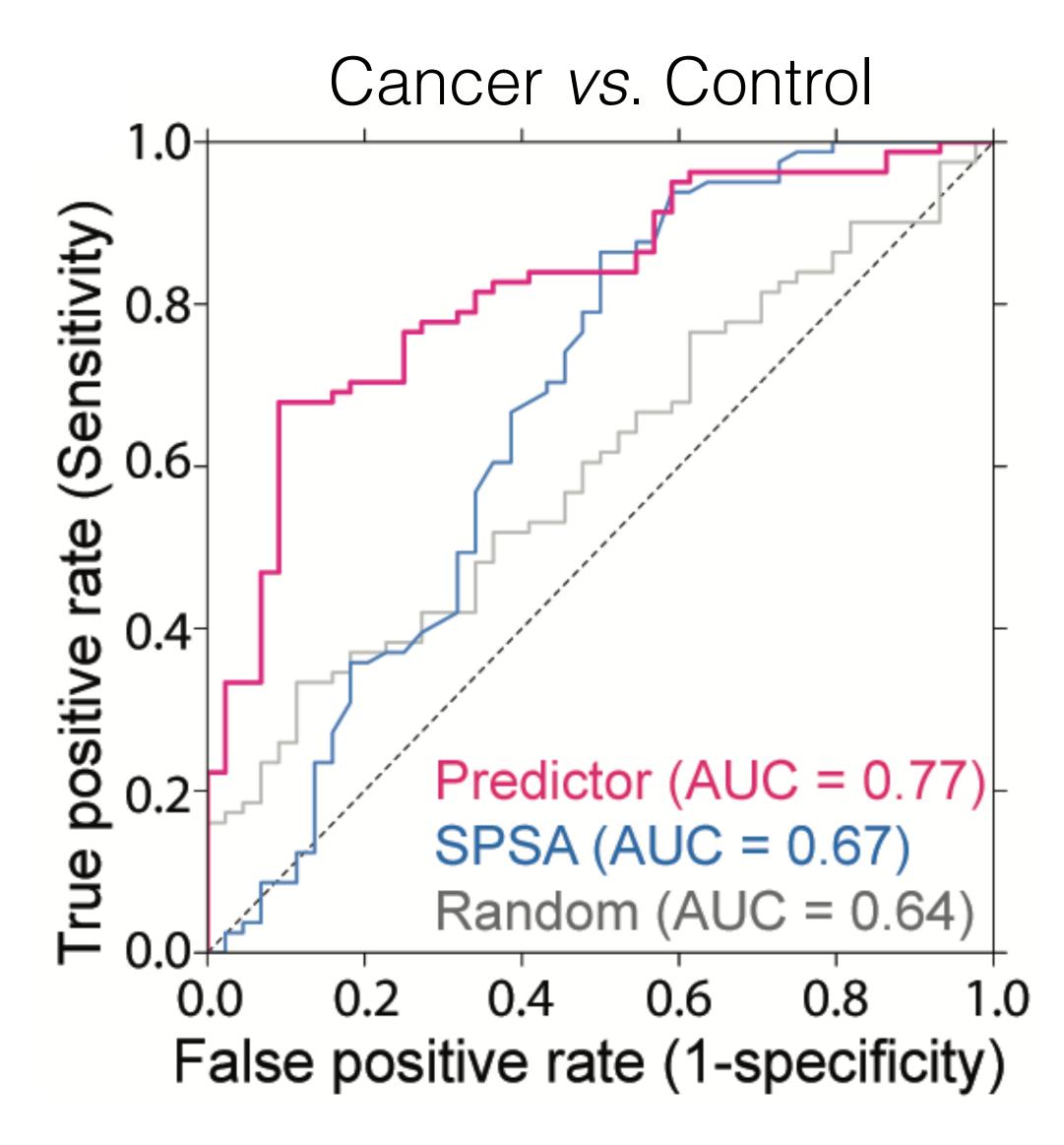


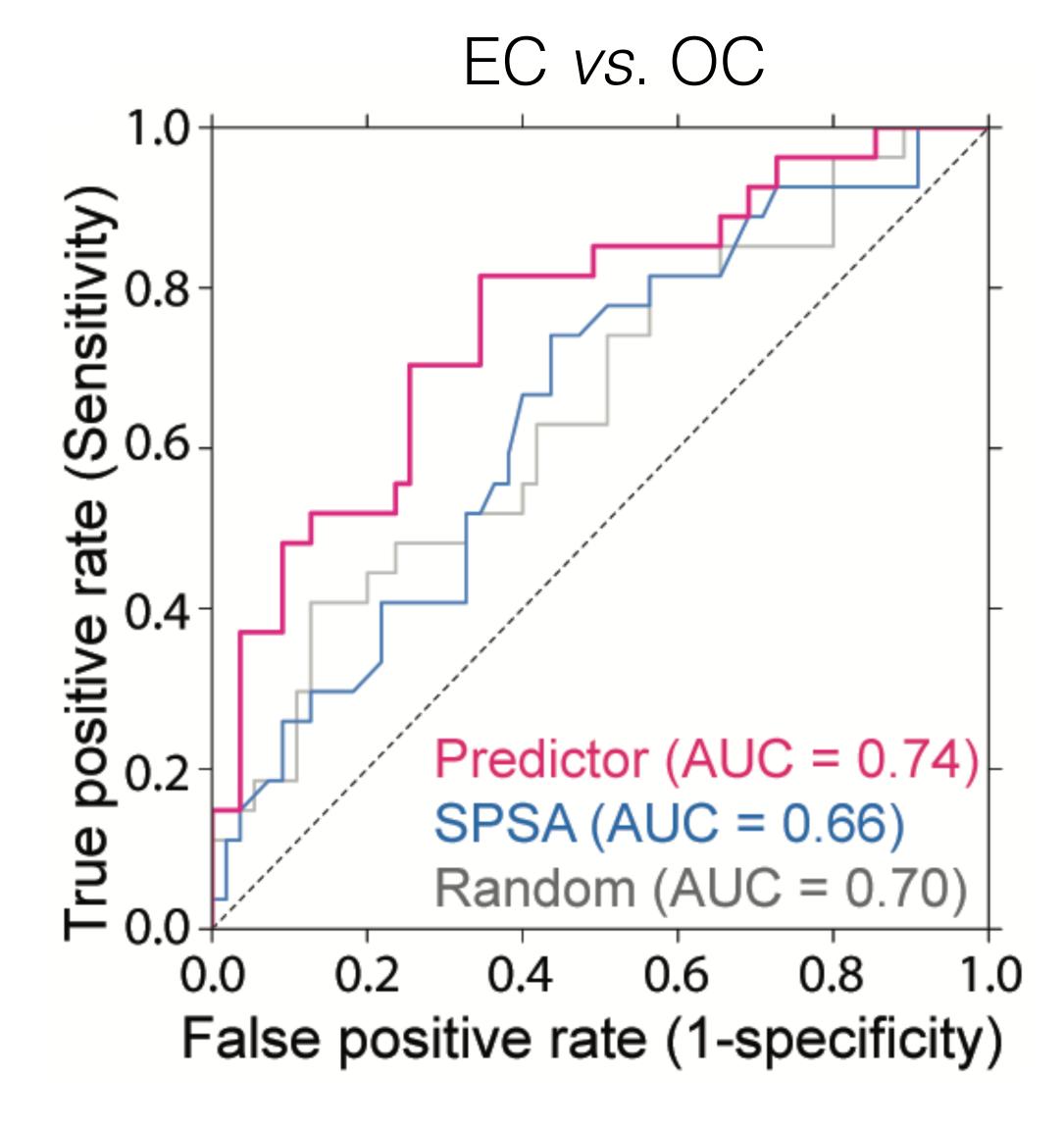
Tissue Proximal Fluids





Tissue Proximal Fluids







Aims of the EDRN Grant

Development of Protein Biomarkers in Post-DRE Urine for use in Liquid Biopsy of Prostate Cancer

Aim 1 **Development of Protein Biomarker Signature from Post-DRE Urine (Kislinger)** A) Validation and Assay Optimization of Liquid Biopsy Peptide Signature B) Discovery in Prostatic Secretions to Expand Utility of Existing Signature C) Discovery of Soluble/Secreted Glycoproteins in Prostatic Secretions

Aim 2

Exosomes as a Source of Liquid Biopsy Protein Biomarkers for Prostate Cancer (Semmes)

Aim 3

Integrating Biomarker Discovery through Bioinformatics (Boutros)



Aim 1

Development of Protein Biomarker Signature from Post-DRE Urine (Kislinger)

- A) Validation and Assay Optimization of Liquid Biopsy Peptide Signature
- B) Novel Discovery in Prostatic Secretions to Expand Utility of Existing Signature
- C) Targeted Discovery of Soluble/Secreted Glycoproteins in Prostatic Secretions

Current Protocol

- 4ml EPS-urine
- 3kDa filter concentration
- Methanol precipitation ullet
- TFE solubilization/digestion \bullet
- C18 purification
- Peptide quantification
- 1 ug peptides on column
- 15 cm n-HPLC-SRM-MS (TSQ Vantage)

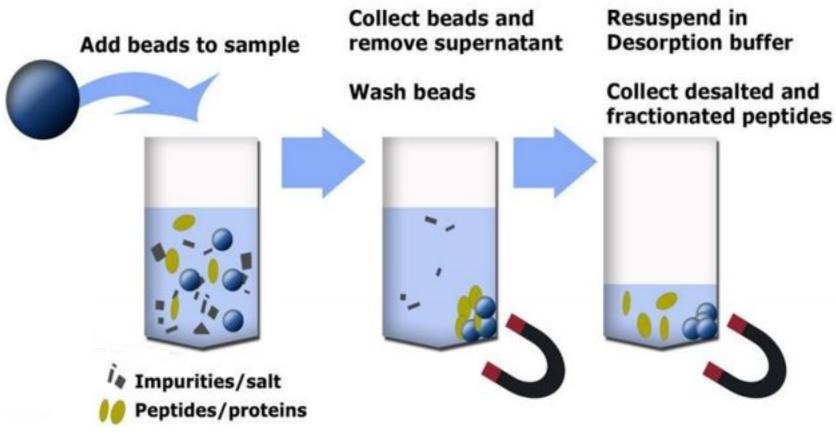
Work in Progress

Protocol Optimization

- PVDF membrane
- Magnetic C8 beads
- Compare to old protocol
- Use shotgun proteomics
- Coverage, time & automation
- Convert targeted assays •
- 50 cm nUPLC-PRM-MS (QE HF) \bullet
- Assay metrics (LOD, LOQ, linearity, scheduling)

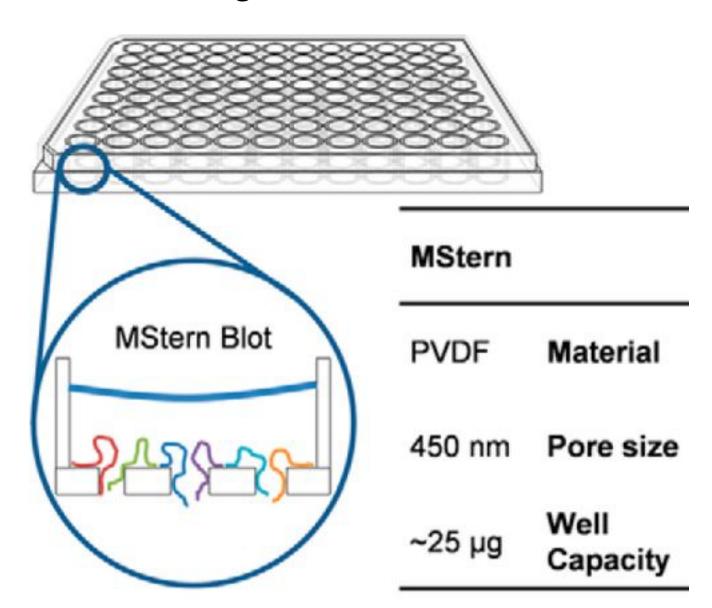
Sample Preparation Protocols **3KDa - TFE MStern** C8 beads



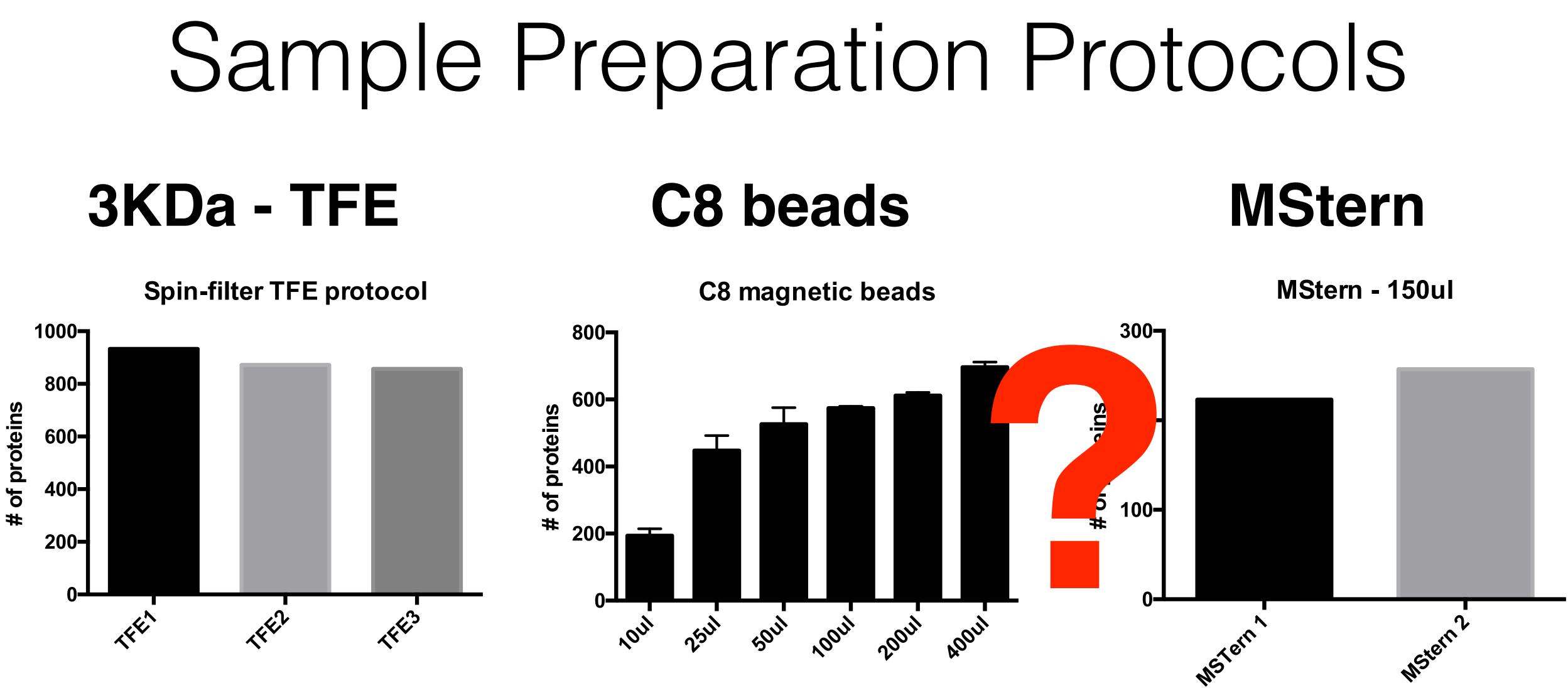


Collect desalted and

Berger et al. MCP 2015



150 µl of urine ~15 µg of protein



Prostate Cancer Proteomics

Prostate Proximal Fluids

Prostatic Secretions Post-DRE urines





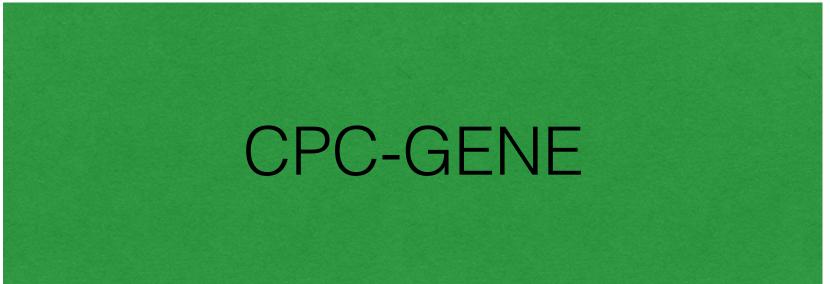








Prostate Cancer Tissues







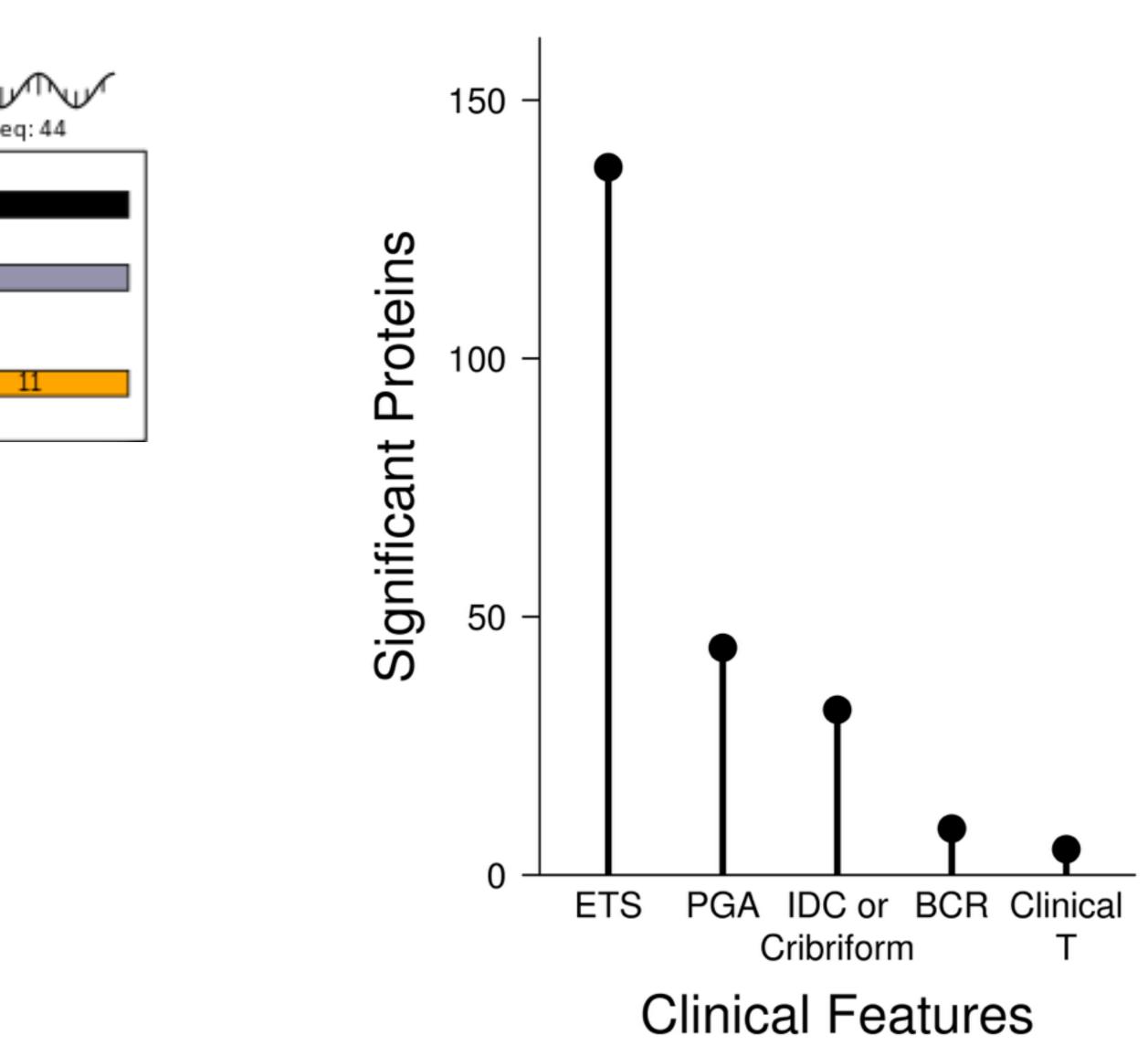




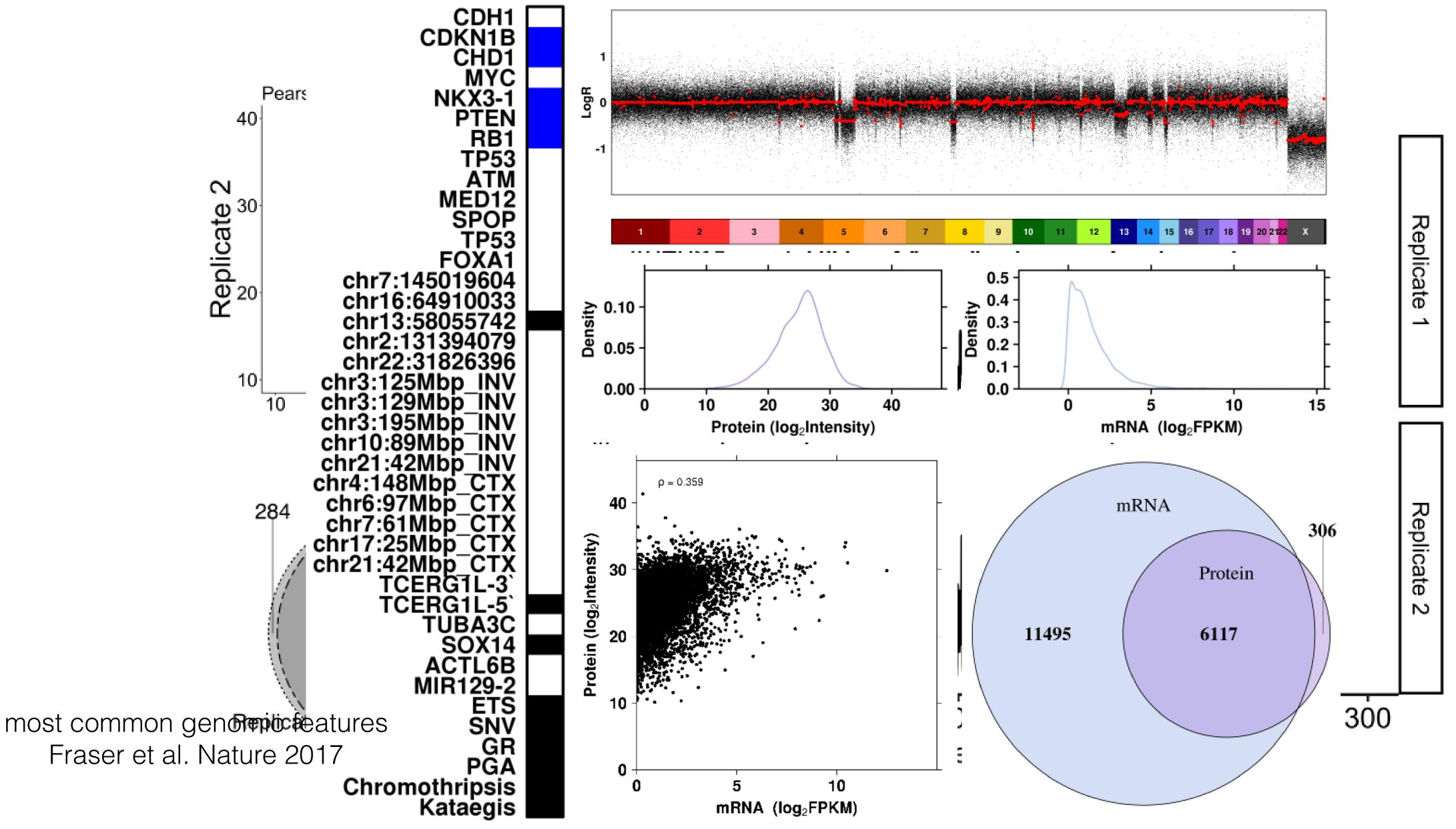
CPC-GENE Proteogenomics

55 Prostate Tumour Samples

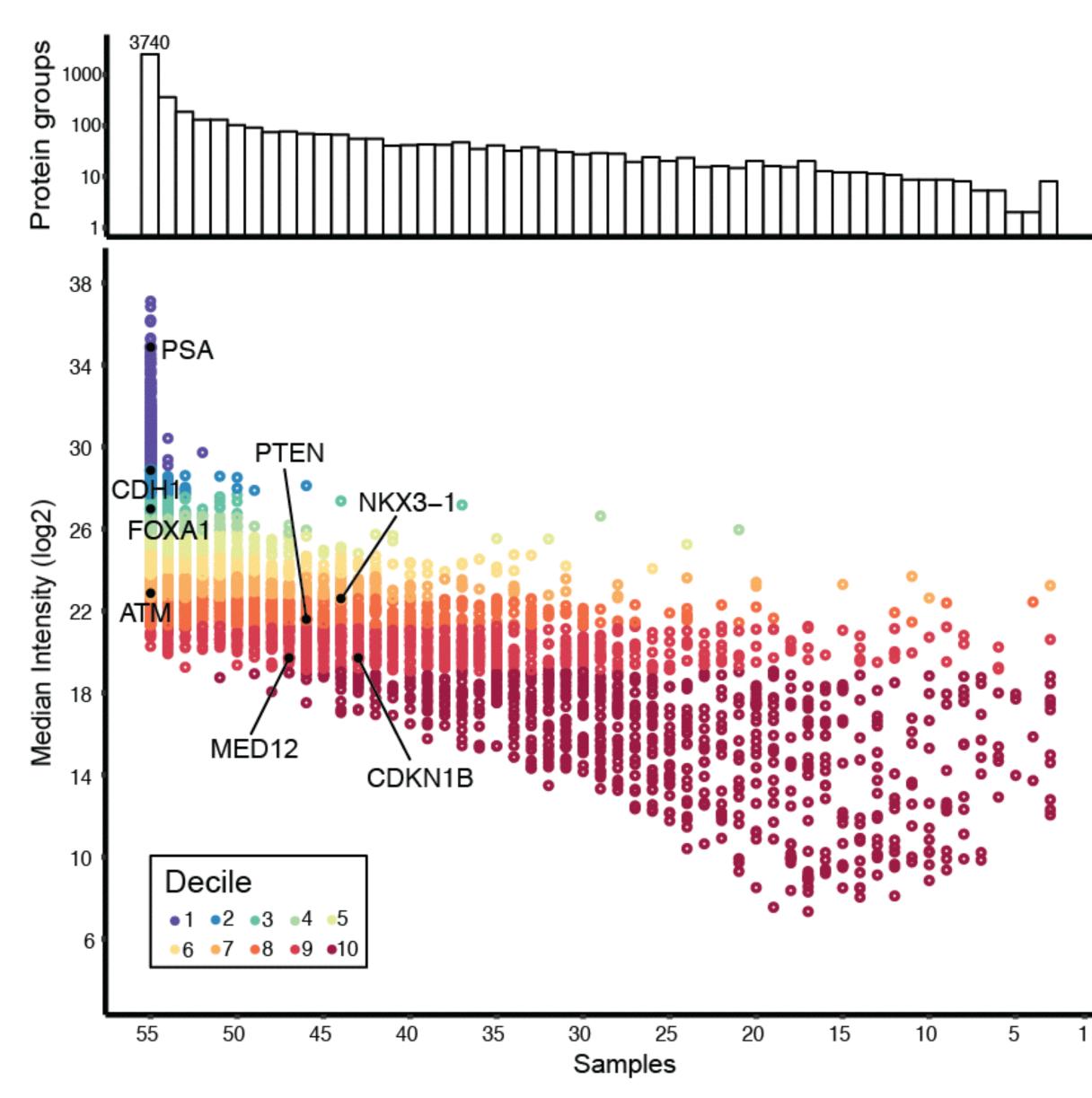
WGS: 51	Methylation: 54	
BCR:		
31		24
ETS consensus:		
23		32
False: 🗌 True: 📕		
Diagnostic Gleason Score:		
1	43	
3+3: 🔲 3+4: 🛄 4+3: 📕		



Patient-specific Proteogenomics



Prostate Cancer Proteogenomics



- 1. Proteins placed in abundance deciles
- 2. Span several orders of magnitude
- 3. 6050 proteins (85%) are in >40 tissues
- 4. Global correlation to mRNA abundance correlates with decile
- 5. Combination of protein and **mRNA best predict BCR** (preliminary!)

Summary

- identification of liquid biopsy signatures. A. Optimize, validate and extend
- (pre-vs. post-DRE urine)
- 3. Tissue-based proteogenomics (CPC-GENE) A. Multi-omic based signatures to predict BCR

1. Proteomics of prostatic secretions is useful for

2. Additional post-DRE urine proteomics & lipidomics

Acknowledgements

Generous donation by the **patients**

EDRN Team

John Semmes Julius O. Nyalwidhe Paul Boutros Vincent Huang Andrew Macklin Mukesh Kumar

CPC-GENE

Rob Bristow Theo van der Kwast Michael Fraser Stan Liu Ankit Sinha Vladimir Ignatchenko

Jacob Kagan

National Cancer Institute



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DCP Division of Cancer Prev Cancer Prevention





