

Multiplexing Clinical Protein Targets in Dried Blood Spots

Skyline Users Group – May 31st, 2015
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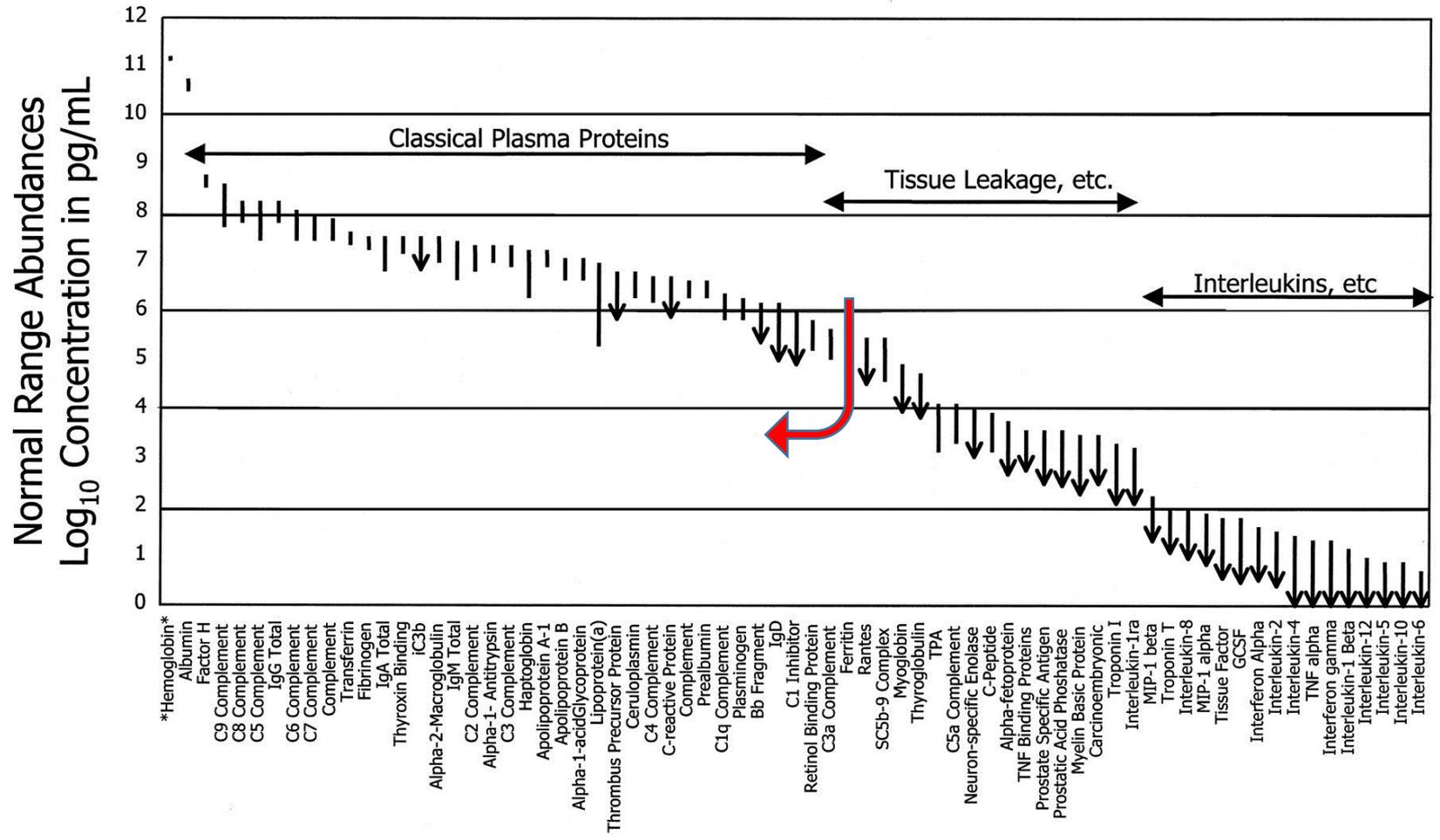
Outline

- Selection of candidate **proteins** for the multiplex analysis of DBS via targeted proteomics
- The currently employed strategies for the selection of candidate **peptides** for targeted proteomics
- An empirical refinement process for the selection of optimal **peptides** and their respective MS/MS transitions

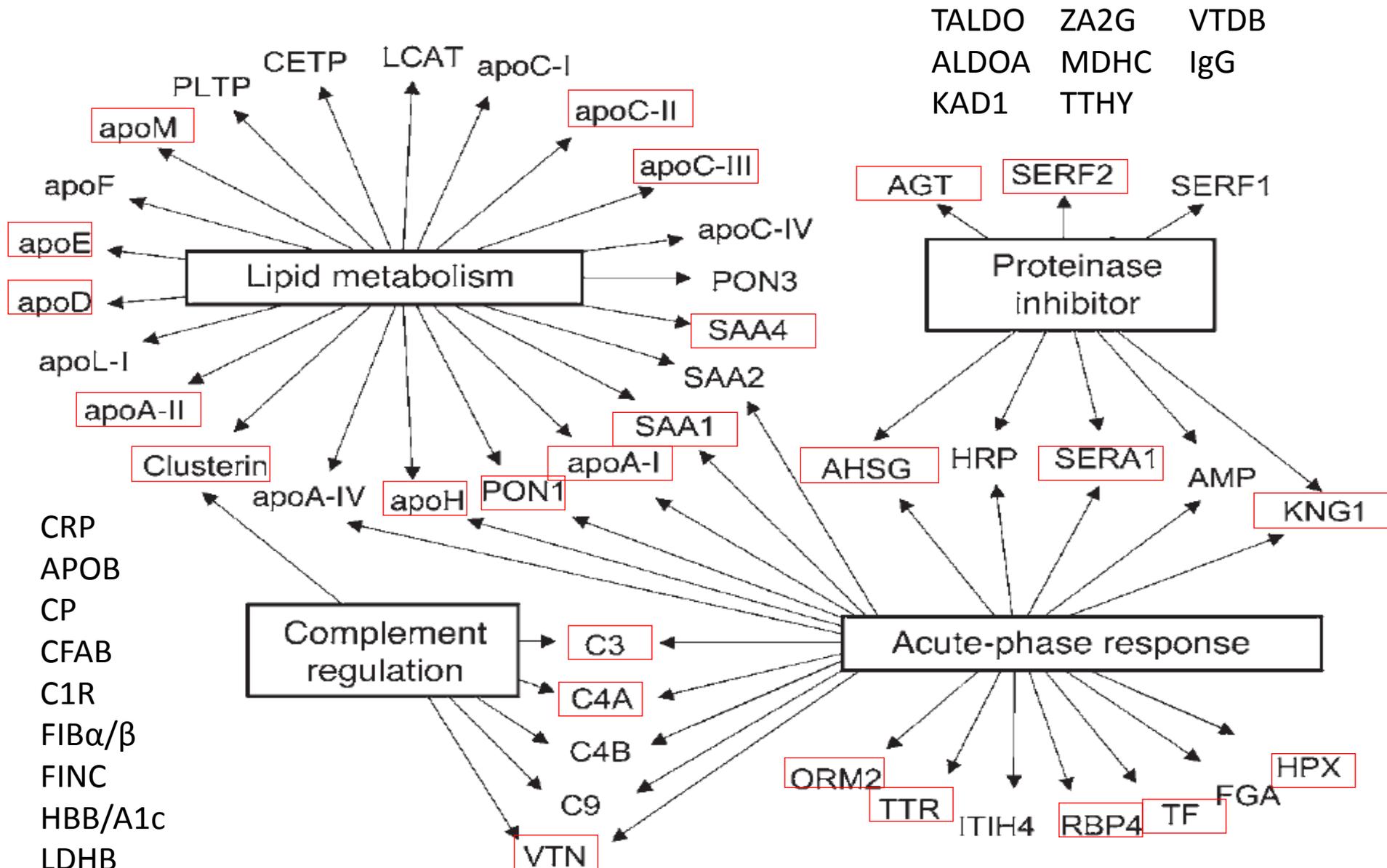
Selection of Protein Targets for DBS Wellness Assay

- Acid Phosphatase
- **Alanine Aminotransferase**
- **Albumin**
- **Aldolase**
- Alkaline Phosphatase
- **α-1-acid glycoprotein**
- **α-1-antitrypsin (SERPINA1)**
- **α-1-antichymotrypsin (SERPINA3)***
- **α-1-antiplasmin (SERPINF2)**
- **α-2-HS-glycoprotein (FetuinA)**
- α-fetoprotein (AFP)
- Amylase
- ACE
- **Antithrombin III (SERPINC1)**
- **Apolipoprotein A1**
- **Apolipoprotein B**
- **Apolipoprotein C2***
- **Apolipoprotein C3***
- **Apolipoprotein E***
- **Apolipoprotein H***
- **Apolipoprotein J***
- Aspartate Aminotransferase
- **β-2-microglobulin**
- β-Thromboglobulin
- Biotinidase
- Cancer antigen 125
- Cancer antigen 15-3
- Human epididymis protein 4
- Carcinoembryonic antigen (CEA)
- **Ceruloplasmin**
- Cholinesterase
- **Complement C1 (C1R/C1S)**
- **Complement C1 inhib.**
- **Complement C1Q**
- **Complement C3**
- **Complement C4**
- **Complement C5**
- **C-reactive Protein**
- Creatine Kinase-BB
- Creatine Kinase-MM
- Cystatin C
- Erythropoietin
- Factor IX antigen
- Factor X
- Factor XIII
- Ferritin
- **Fibrinogen**
- **Fibronectin**
- FSH
- γ glutamyl transferase (I/V)
- **Haptoglobin**
- β-hCG
- **Hemoglobin A1C (HBB)**
- **Hemopexin**
- Her-2/neu
- Human growth hormone
- Human placental lactogen
- IgA
- IgD
- IgE
- **IgG**
- IgM
- Inhibin-A
- Insulin
- IGF-1
- IGF-2
- IGFBP-1
- IGFBP-2
- Interleukin-2 receptor
- **Isocitric dehydrogenase**
- **κ light chains**
- **Kininogen 1***
- **Lactate Dehydrogenase (heart)**
- Lactoferrin
- **λ Light Chains**
- Lipase
- Lp(a)
- LP-PLA2
- Leutinizing hormone
- Lysozyme
- Myeloperoxidase
- Myoglobin
- Osteocalcin
- Parathyroid hormone
- Phosphohexose isomerase (GPI)
- **Plasminogen**
- Plasminogen activator inhib.
- **Prealbumin (transthyretin)**
- BNP
- Procalcitonin
- Prolactin
- **Properidin Factor B (CFB)**
- Prostatic acid phosphatase
- PSA
- Protein C
- Protein S
- Pseudocholinesterase
- Pyruvate kinase
- Renin
- **Retinol binding protein**
- Mesothelin-related peptide
- **Sorbital dehydrogenase**
- Thyroglobulin
- TSH
- Thyroxine binding globulin
- Tissue plasminogen activator
- **Transferrin**
- Troponin T (TnT)
- Troponin I (TnI)
- Trypsin
- Urokinase
- **Vitamin D binding protein***
- **Vitronectin**
- Von Willebrand factor
- **Zinc-α-2-glycoprotein**

Selection of Protein Targets for DBS Wellness Assay

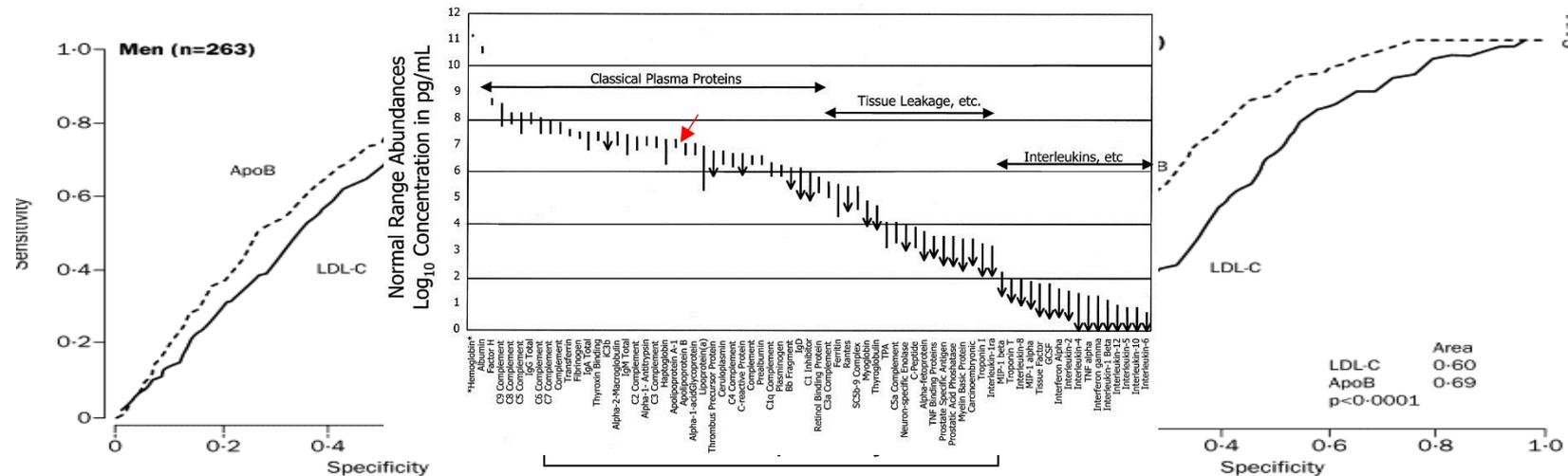


Selection of Protein Targets for DBS Wellness Assay

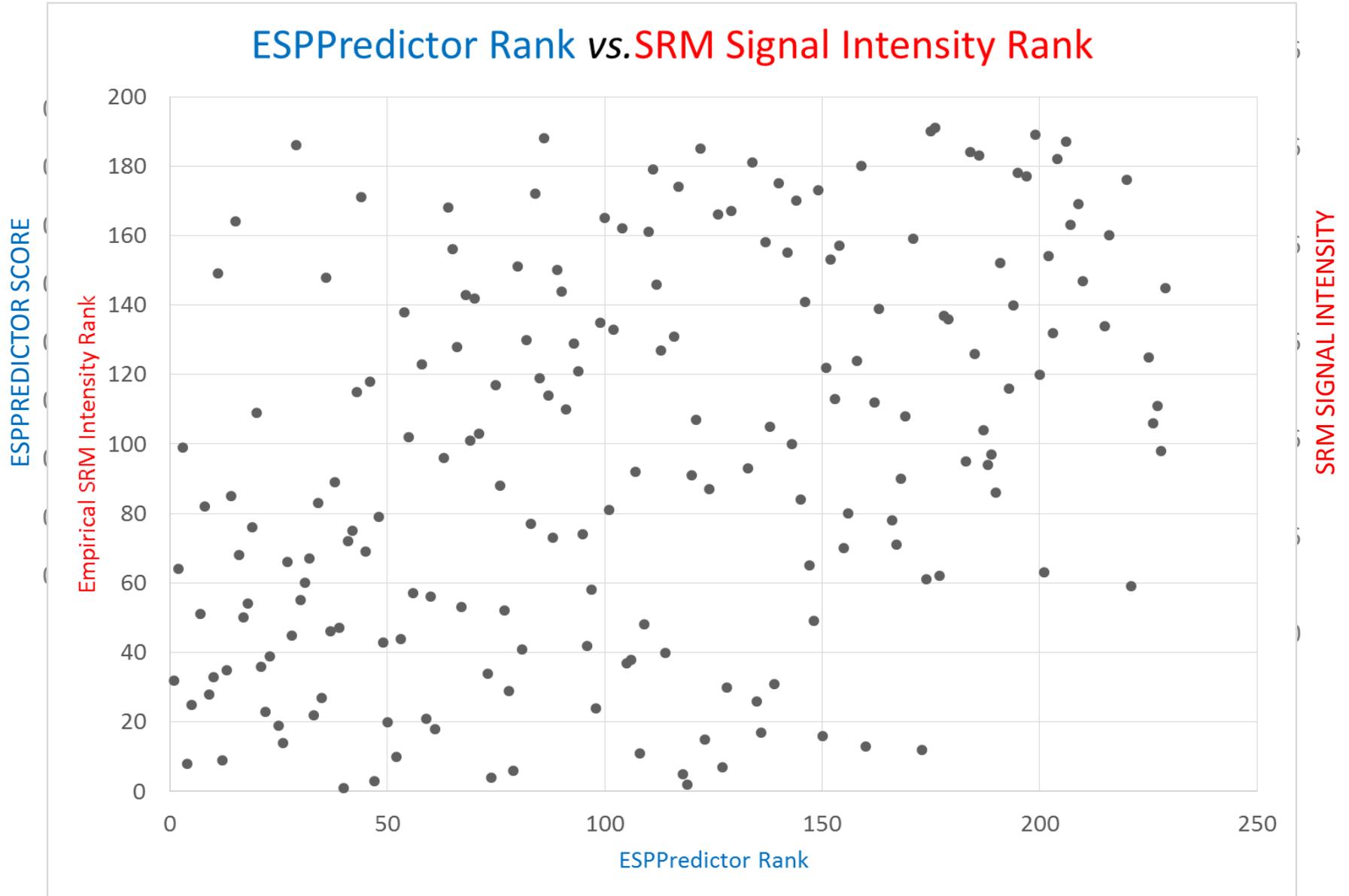


How Does One Select an Optimal Set of Peptides for a Targeted Proteomic Experiment?

Apolipoprotein B (P04114) – 516 kDa, Serum reference range (~0.5-2 g/L)



ESPPredictor Score vs. SRM Signal Intensity: Apolipoprotein B100

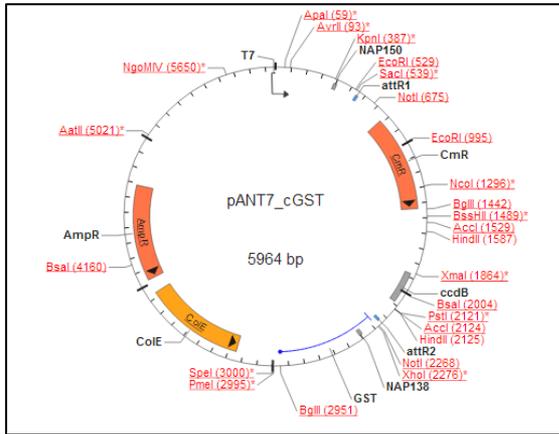


Mallick, P. & Aebersold, R. et al. *Nature Biotechnology*(2007) 25 (1): 125-131

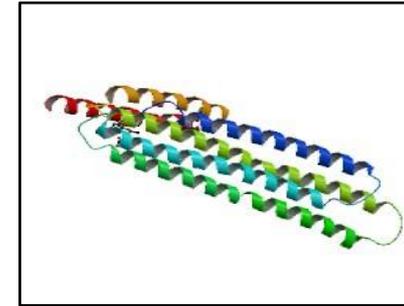
Fusaro, V.A. & Carr, S.A. et al. *Nature Biotechnology* (2009) 27:190-198.

Our Approach.....

Workup of Recombinant/Native Protein Standard

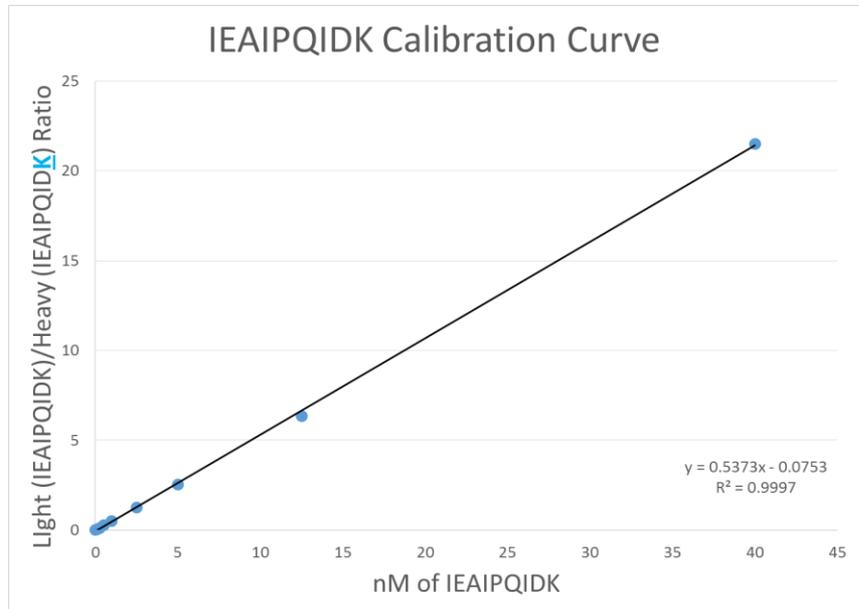


<http://dnasu.org>

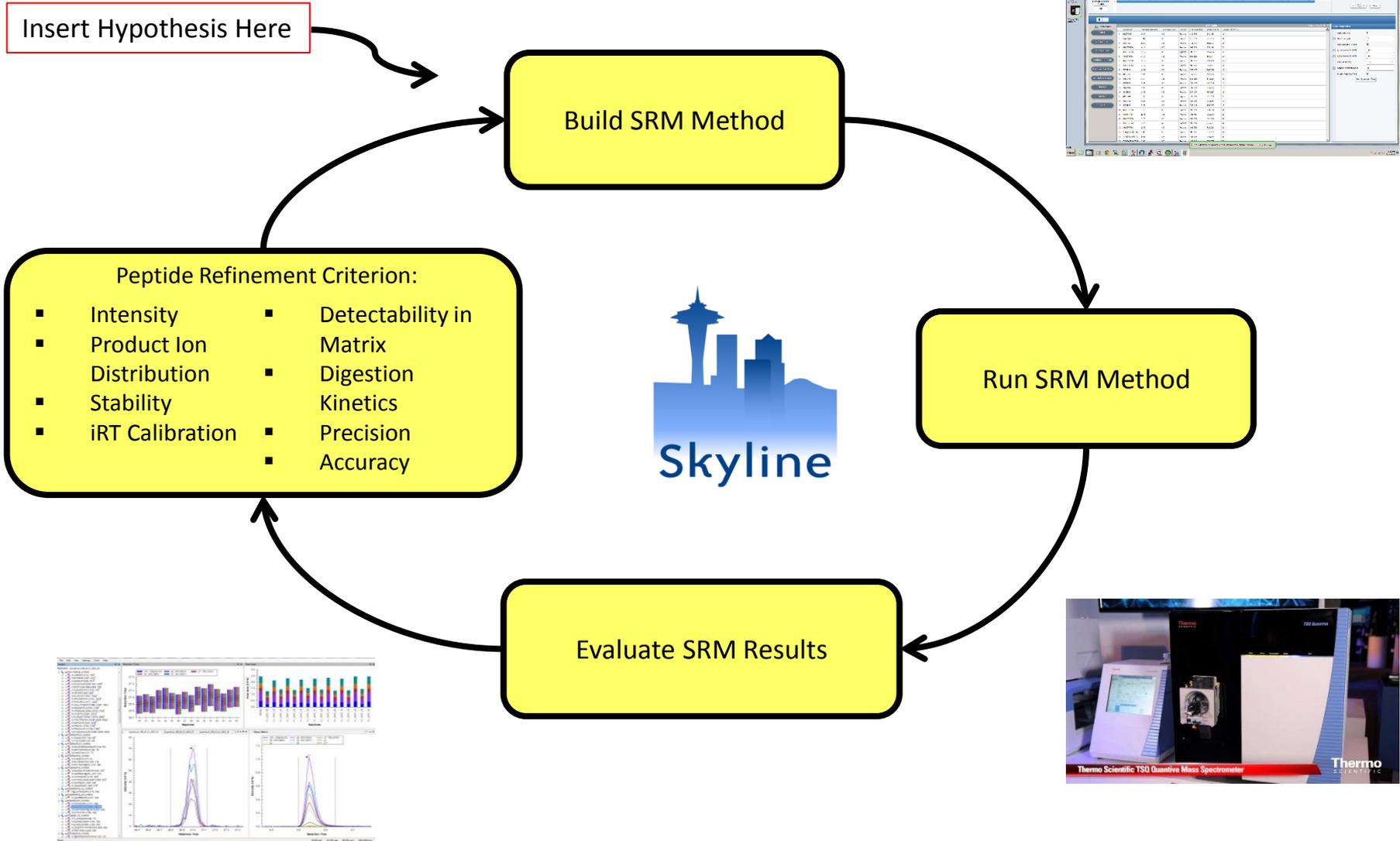


IEAIPQIDK
+
IEAIPQIDK

~25-500 femtomoles/25uL IVT
< \$20.00/Protein



SRM Method Refinement Cycle



Round 1 nanoLC MS/MS: SRM Signal Intensity Rank

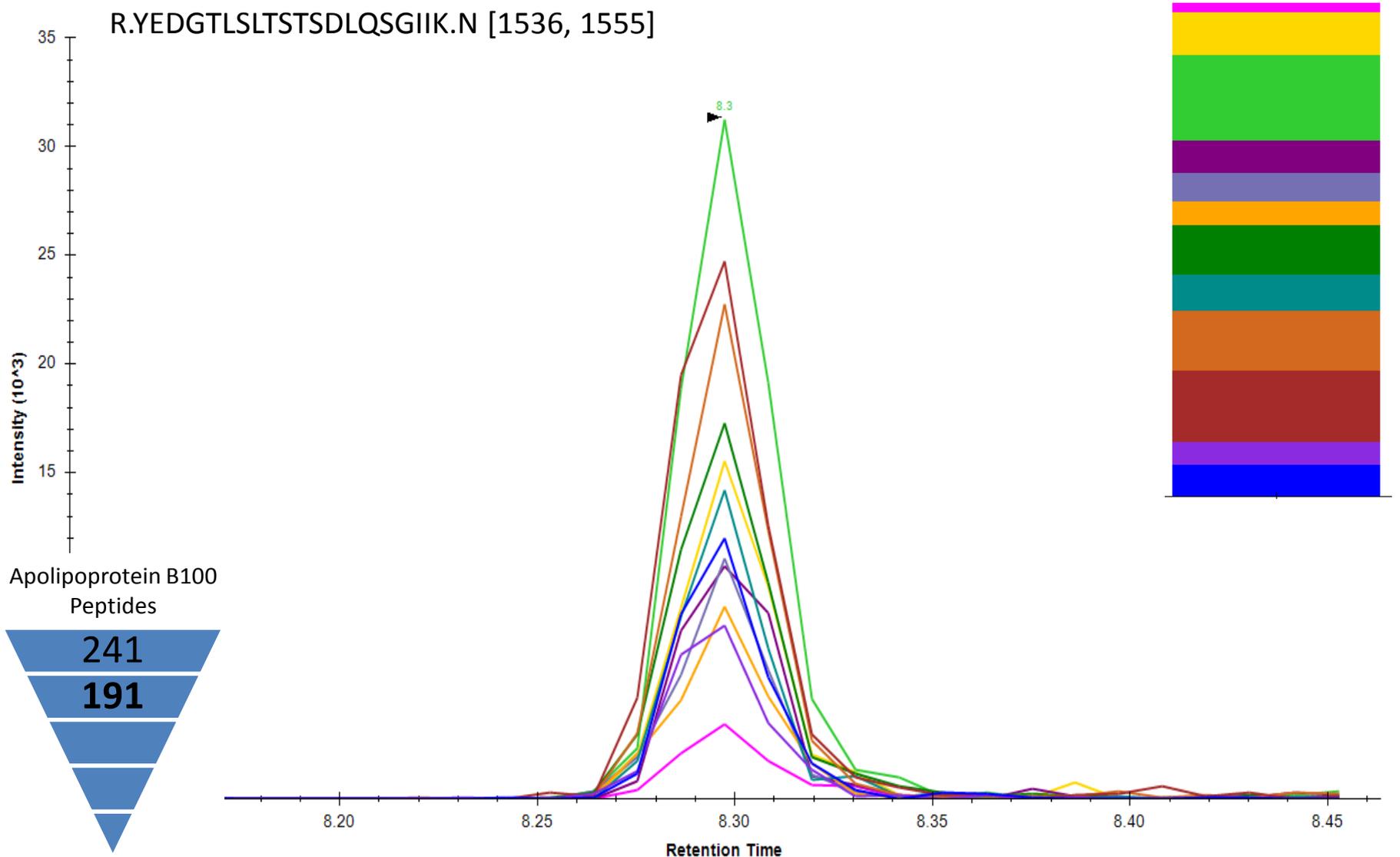
Apolipoprotein B100 - SRM Peak Area

SRM Peak Area

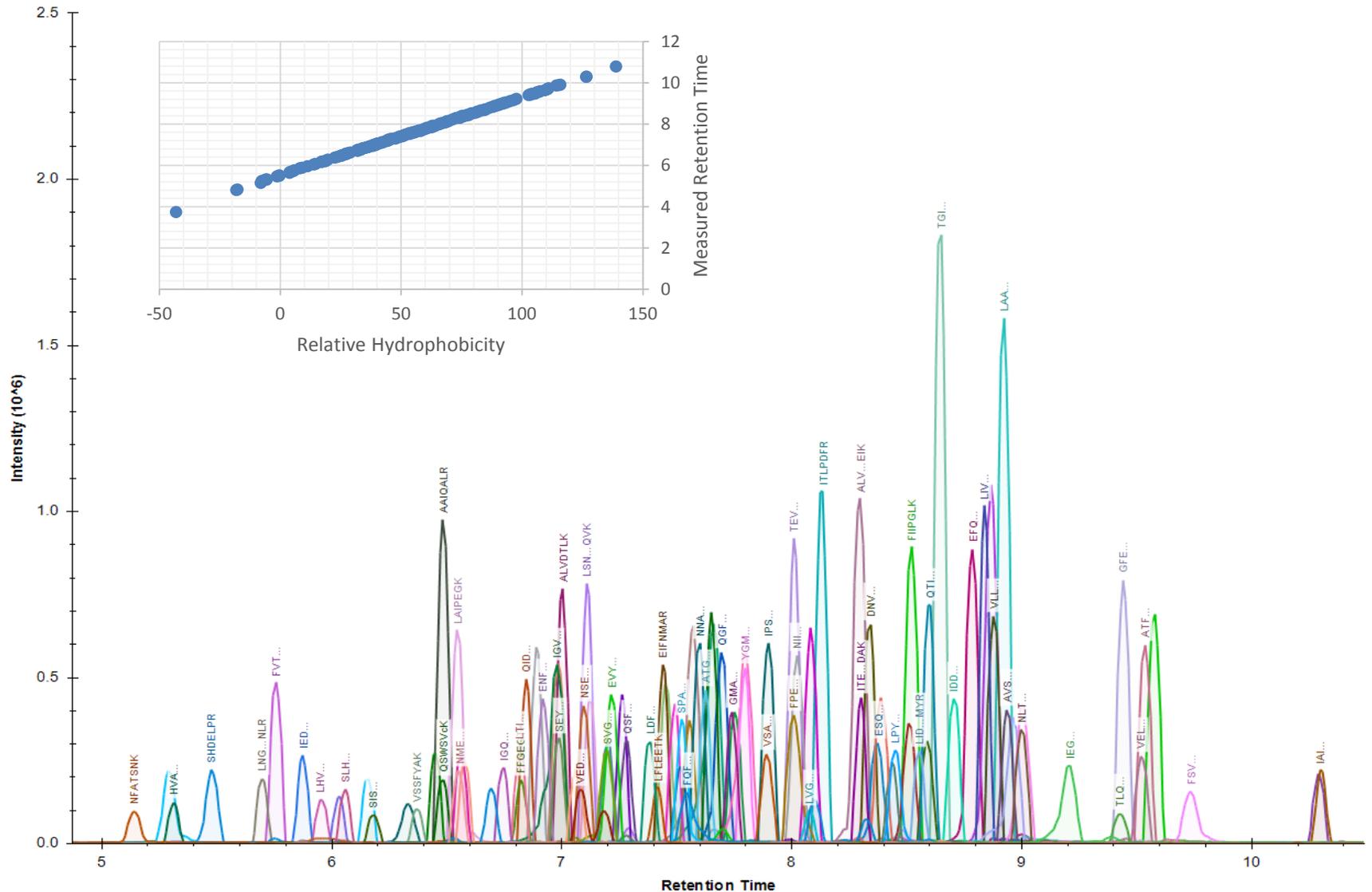
Peptide	SRM Peak Area (approx.)
TGISPLALIK	5.2E+06
FIIPSPK	4.2E+06
TEVIPPLIENR	3.0E+06
SLWDFLK	2.2E+06
LSLPDK	2.0E+06
NIILPVYDK	1.8E+06
LDVTTISGR	1.6E+06
QTIIVLENVQR	1.5E+06
TSSFALNLTPEVK	1.4E+06
LLLMGAR	1.3E+06
GVISIPR	1.2E+06
MGLAFESTK	1.1E+06
HINIDQFVR	1.0E+06
SVGFLPSR	9.5E+05
QSFDSLVK	9.0E+05
VELEVPQLCSFILK	8.5E+05
LIDVISMYR	8.0E+05
YNALDLTNGK	7.5E+05
LPYTIITPPPK	7.0E+05
VSTAFVYTK	6.5E+05
SEYQADYESLR	6.0E+05
GNVATEISTER	5.5E+05
NMEVSVATTTK	5.0E+05
IAIANIDEIEK	4.5E+05
SPSQADINK	4.0E+05
LHVAGNLK	3.5E+05
HVAEAICK	3.0E+05
NIQEYLSILTPDGK	2.5E+05
VSSFYAK	2.0E+05
LVGFIDDAVK	1.8E+05
SISAALEHK	1.6E+05
VSQEGLK	1.4E+05
YEVDDQIQVLMDK	1.2E+05
SKPTVSSSMEFK	1.0E+05
GSTSHHLVSR	8.0E+04
LPQQANDYLNFSNWER	7.0E+04
AALTELSIGSAYQAMILGVDSK	6.0E+04
ATVAVVLESIQDTK	5.0E+04
HIQNIDIHLGK	4.0E+04
DSYDLHLK	3.0E+04
TQFNNEYSQDLDAYNTK	2.0E+04
LQSTTYMNPYMK	1.5E+04
VPLLLSEPINIDALEMR	1.0E+04
SFDYHQFVDETNDK	8.0E+03
FDHTNSLNIAGLSLDFSSK	7.0E+03
LLLQMDSSATAYGSTVSK	6.0E+03
WNFYSPQSSPDK	5.0E+03
TIHDLHLFIENIDFNK	4.0E+03

TGISPLALIK
FIIPSPK
TEVIPPLIENR
SLWDFLK
LSLPDK
NIILPVYDK
LDVTTISGR
QTIIVLENVQR
TSSFALNLTPEVK
LLLMGAR
GVISIPR
MGLAFESTK
HINIDQFVR
SVGFLPSR
QSFDSLVK
VELEVPQLCSFILK
LIDVISMYR
YNALDLTNGK
LPYTIITPPPK
VSTAFVYTK
SEYQADYESLR
GNVATEISTER
NMEVSVATTTK
IAIANIDEIEK
SPSQADINK
LHVAGNLK
HVAEAICK
NIQEYLSILTPDGK
VSSFYAK
LVGFIDDAVK
SISAALEHK
VSQEGLK
YEVDDQIQVLMDK
SKPTVSSSMEFK
GSTSHHLVSR
LPQQANDYLNFSNWER
AALTELSIGSAYQAMILGVDSK
ATVAVVLESIQDTK
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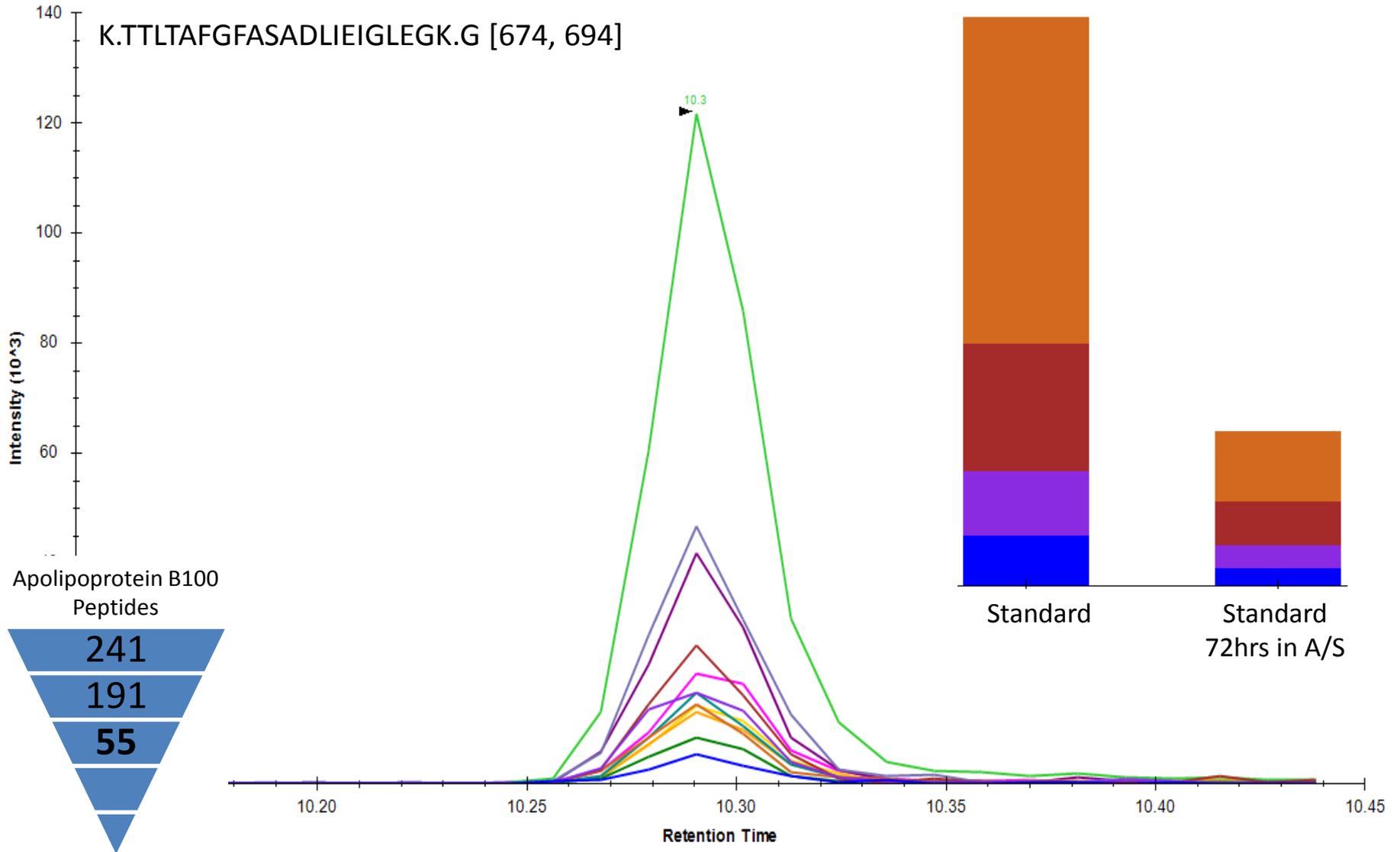
Round 1 nanoLC MS/MS: Relative Product Ion Distribution



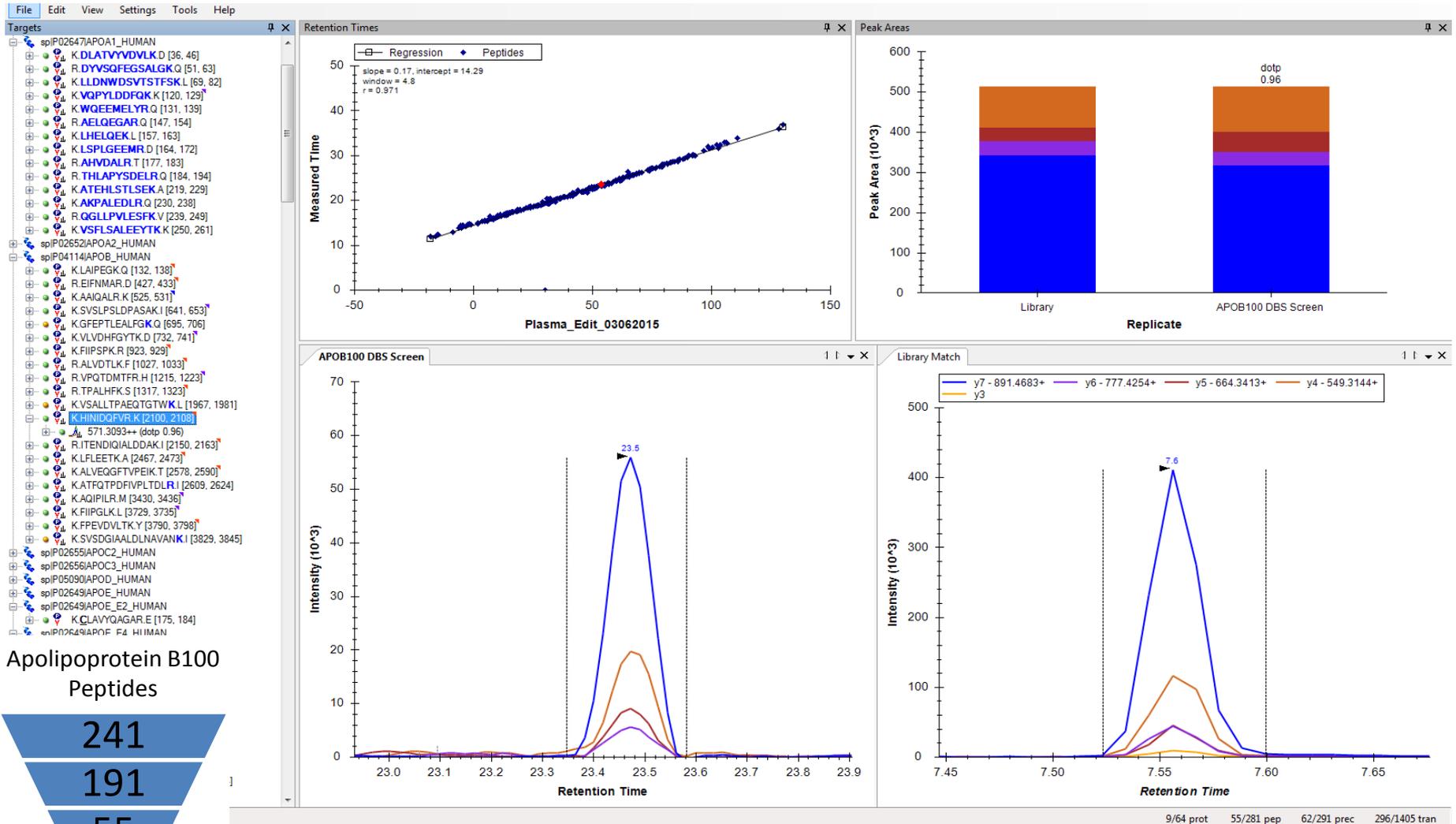
Round 2 nanoLC MS/MS: iRT Calibration with ^{15}N -APOA1



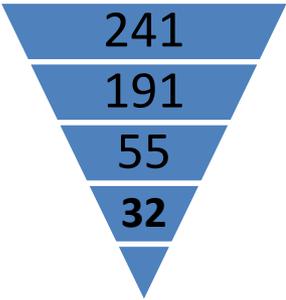
Round 2 nanoLC MS/MS: Peptide Stability Analysis



Round 3 nanoLC MS/MS: Validation of Peptides/Transitions in Matrix



Apolipoprotein B100 Peptides

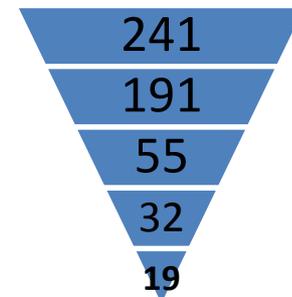


Method Refinement Considerations

Empirical Peptide Refinement:

- Round 1 -> peptides with non-existent or ambiguous chromatograms
- Round 2 -> peptides that fail to meet minimum stability requirements
- Round 3 -> peptides that were not observed in matrix
- Round 4 -> peptides that gave a sub-optimal digestion characteristics

Apolipoprotein B100 Peptides



Normalization?

Calibration?

APOA1 Global Internal Standard (¹⁵N Protein)¹

Table 1. Performance characteristics of a multiplexed LC-MRM/MS assay.

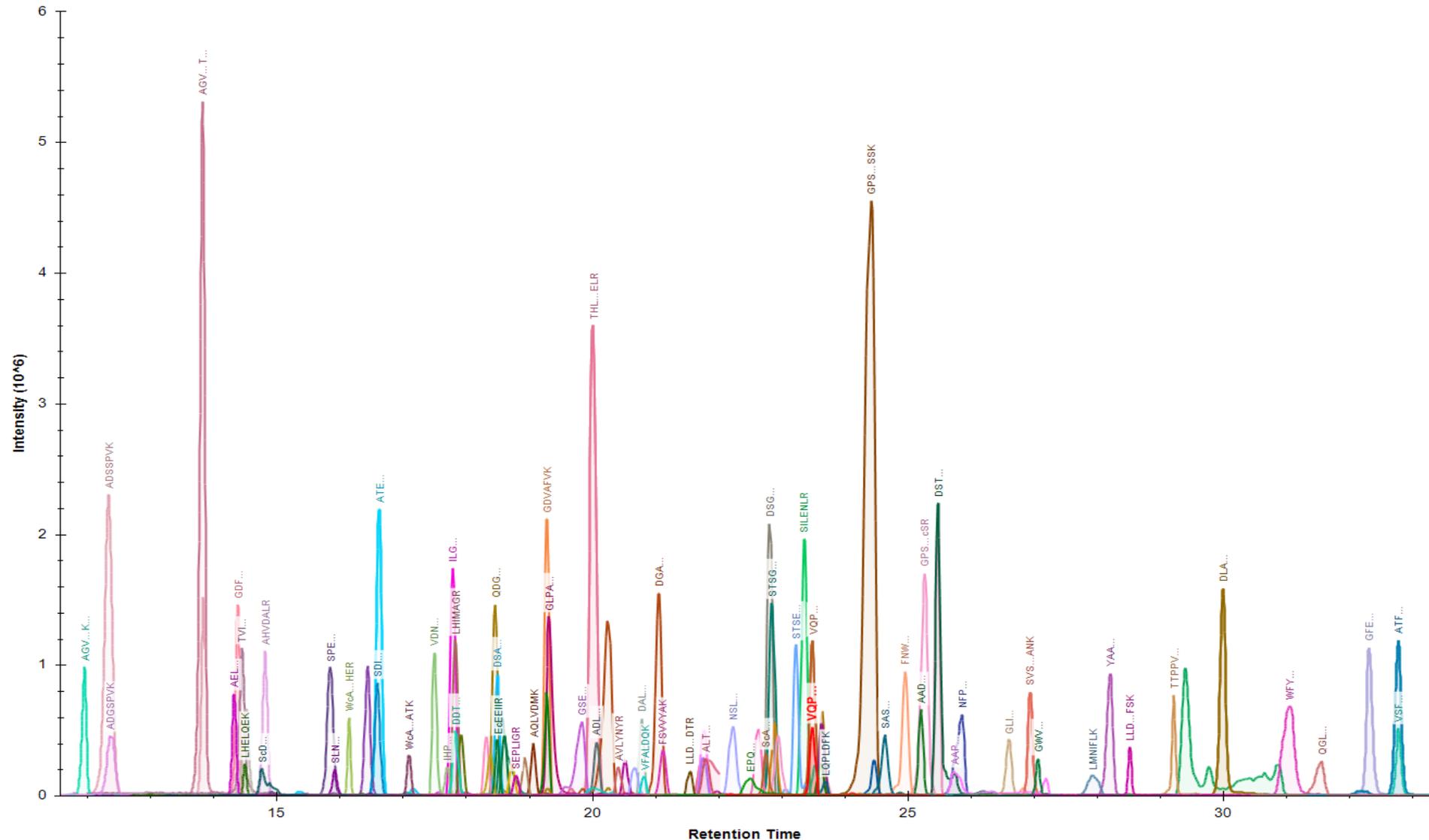
	IS _{prep} ^a					IS _{prot} ^b				
	r ^c	Imprecision, % CV				r	Imprecision, % CV			
		Linearity ^d	LC-MS ^e	Digest ^f	Total ^g		Linearity	LC-MS	Digest	Total
A-I	0.79	0.9982	2.6	9.4	9.8	0.96	0.9994	5.6	2.3	6.1
B	0.67	0.9983	6.4	2.6	6.9	0.61	0.9975	8.9	3.5	9.6
C-II	0.90	0.9948	4.1	4.6	6.1	0.92	0.9937	6.1	4.1	7.4
C-III	0.89	0.9962	9.5	5.0	10.7	0.88	0.9992	11.8	4.8	12.8
E	0.96	0.9984	2.2	3.3	4.0	0.92	0.9984	2.2	2.1	3.1
J	0.81	0.9994	9.3	6.8	11.5	0.79	0.9991	12.4	3.3	12.8

Single Point Calibrator² - Assign concentration with clinical immunoassay & measure in triplicate in each batch

2) Cox, B. et al. *Clin. Chem.* **2014**, 60(3); 541-8.

1) Hoofnagle, A.N. et al. *Clin. Chem.* **2012**, 58(4); 777-781.

Scheduled SRM Method for Analysis of DBS



Interested in developing a similar targeted assay?

- Let the MacCoss lab help!
- Services and consulting offered for development and application of targeted proteomics assays:
 - DIA
 - PRM
 - SRM
- Website: **<http://services.maccosslab.org>**
- Email: services@maccosslab.org
- In Person: Jarrett Egertson or Mike MacCoss