

Automating Transition Refinement for Parallel Reaction Monitoring

Lilian Heil

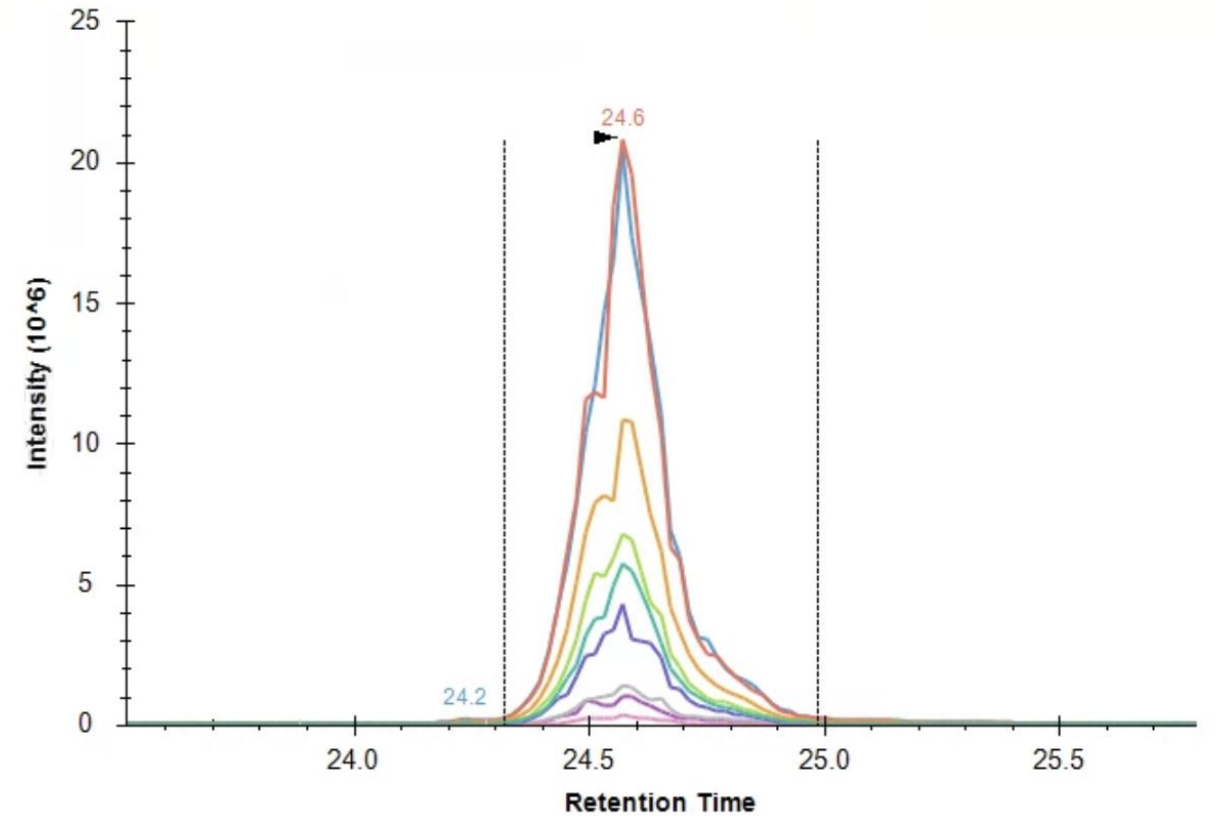
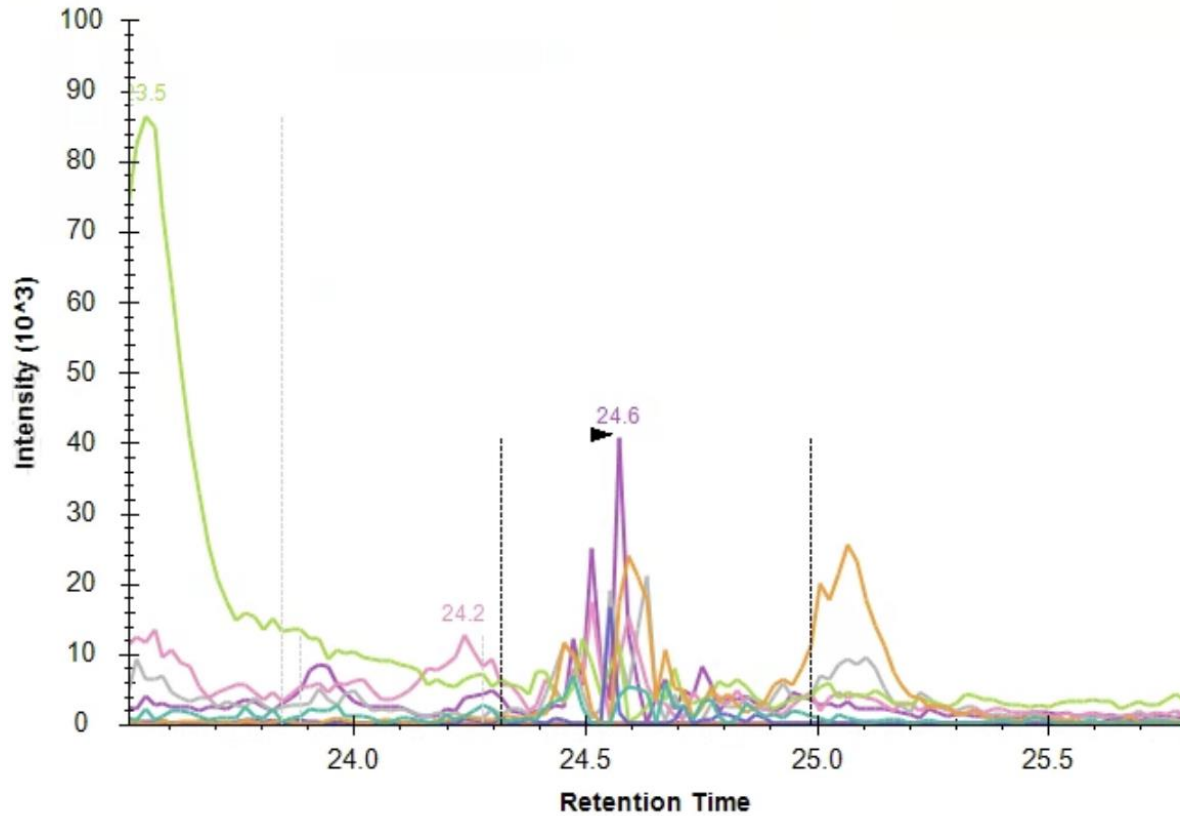
MacCoss Lab

Skyline User Group Meeting

June 5, 2022

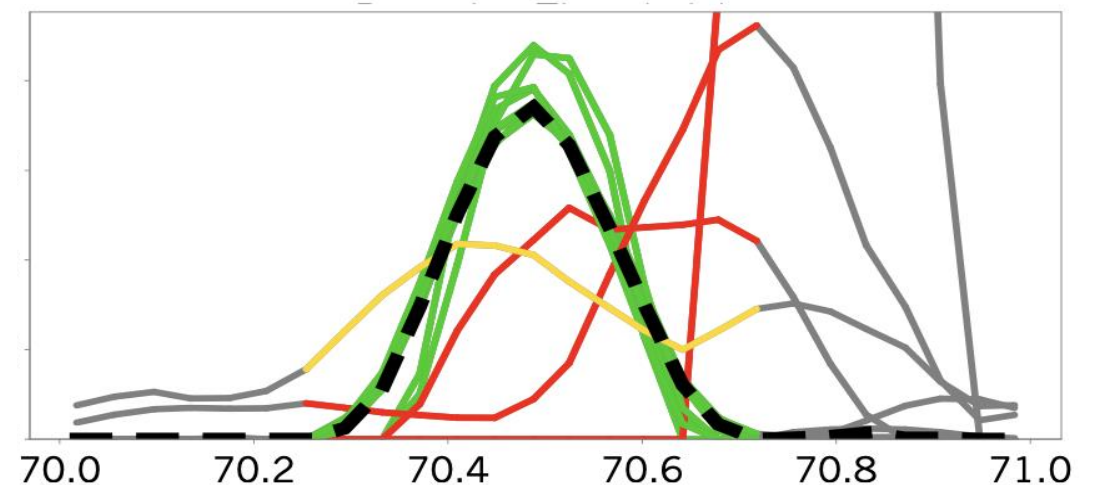
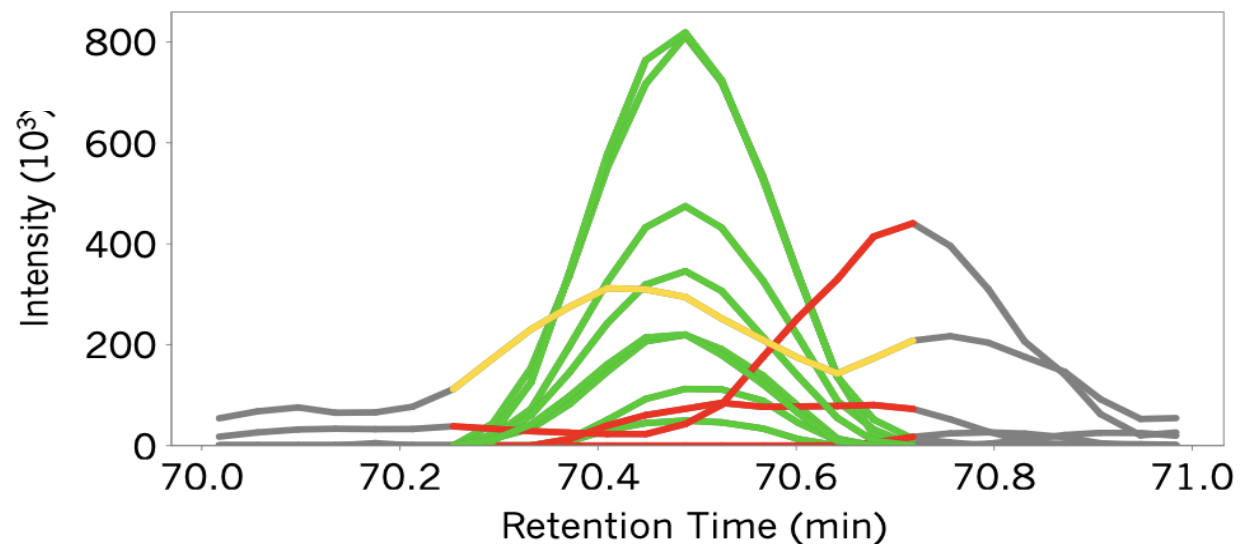
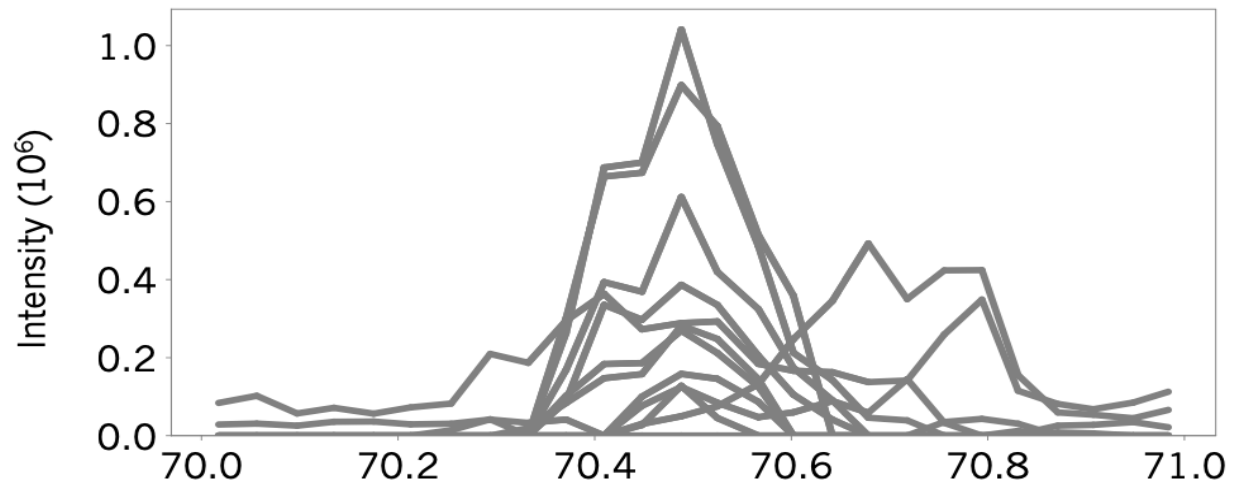


Transition selection can make or break an experiment



Same peptide, different transitions

Eliminating Transitions with Interference Using Correlation with the Median



Select transitions that
correlate with the median to
ensure quantitative accuracy

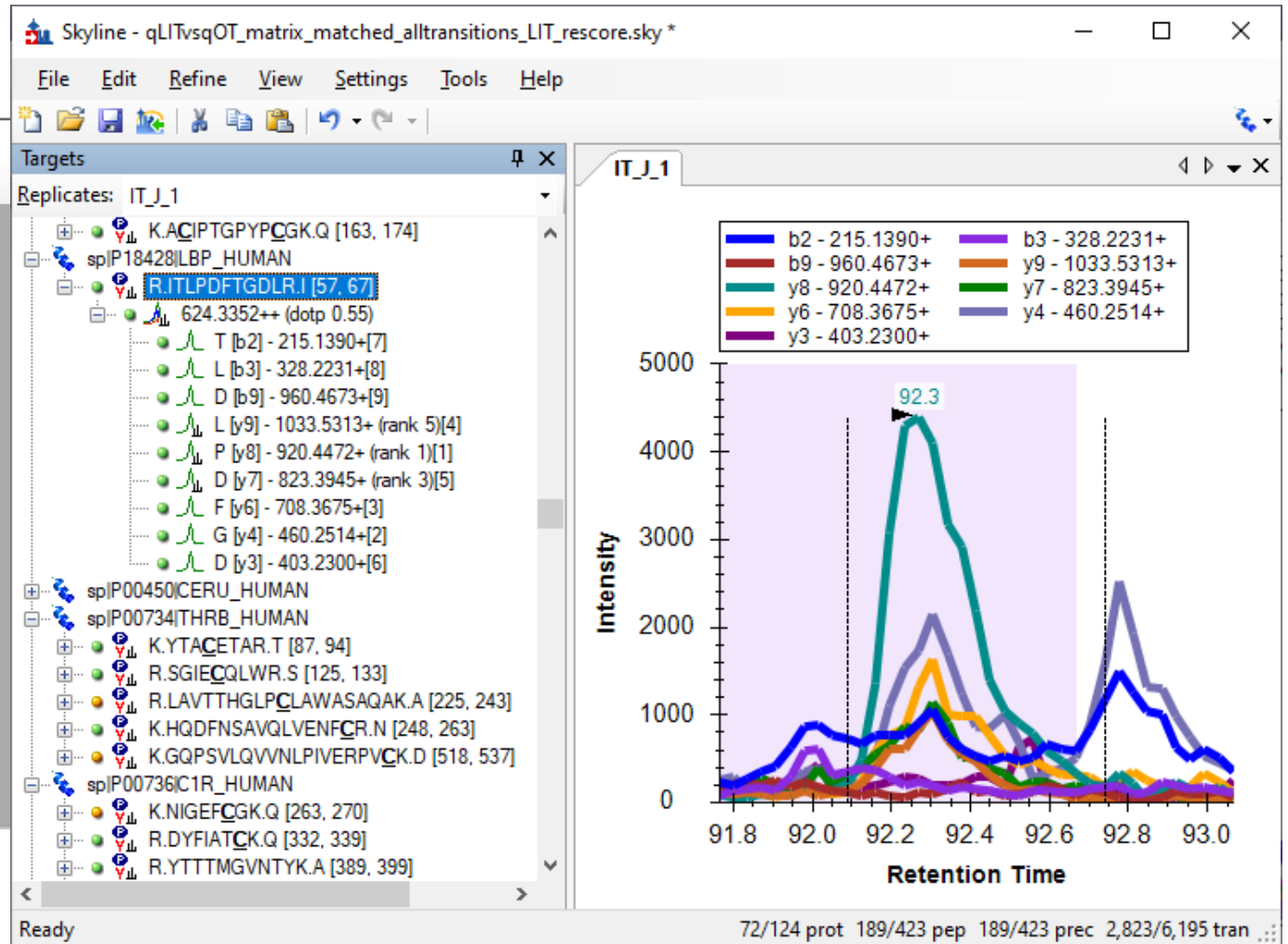
Automated transition refinement based on median correlation

Document Grid: ShapeCorrelations

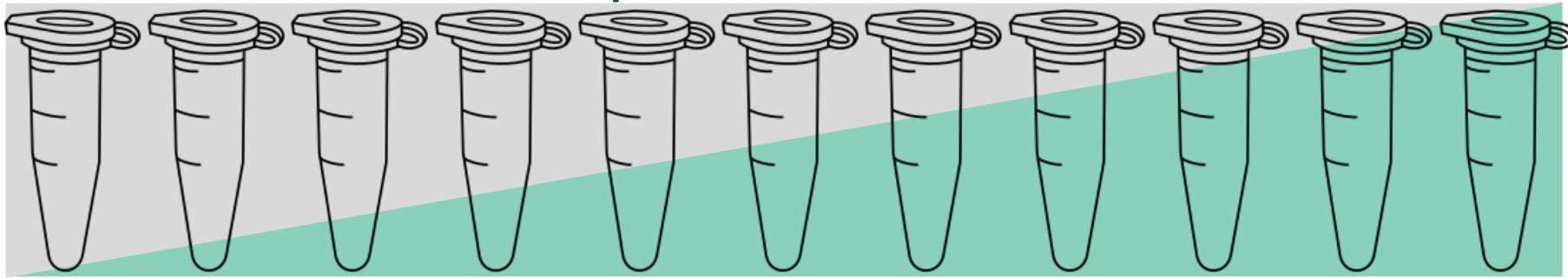
Reports 7 of 16 Export... Actions Find: ITLPDF

Peptide	Transition	Max Shape Correlation
ITLPDFTGDLR	P-b4+	0.437
ITLPDFTGDLR	T-b7+	0.583
ITLPDFTGDLR	G-b8+	0.65
ITLPDFTGDLR	D-b5+	0.703
ITLPDFTGDLR	F-b6+	0.83
ITLPDFTGDLR	T-y5+	0.843
ITLPDFTGDLR	L-y2-	0.89
ITLPDFTGDLR	L-b3+	0.921
ITLPDFTGDLR	D-y7+	0.951
ITLPDFTGDLR	L-y9+	0.962
ITLPDFTGDLR	T-b2+	0.964
ITLPDFTGDLR	G-y4+	0.977
ITLPDFTGDLR	D-b9+	0.979
ITLPDFTGDLR	P-y8+	0.979
ITLPDFTGDLR	F-y6+	0.985
ITLPDFTGDLR	D-y3+	0.991

Remove Peptide Peaks...
Remove Precursor Peaks...
Delete Proteins...
Delete Peptides...
Delete Precursors...
Delete Transitions...



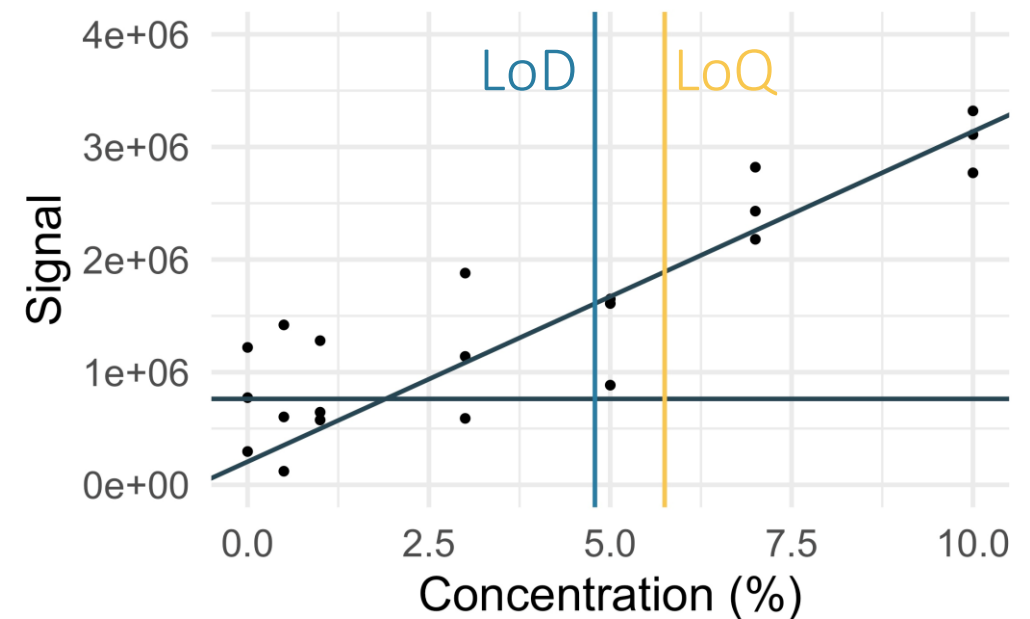
Automated transition selection that optimizes the lower limit of quantitation



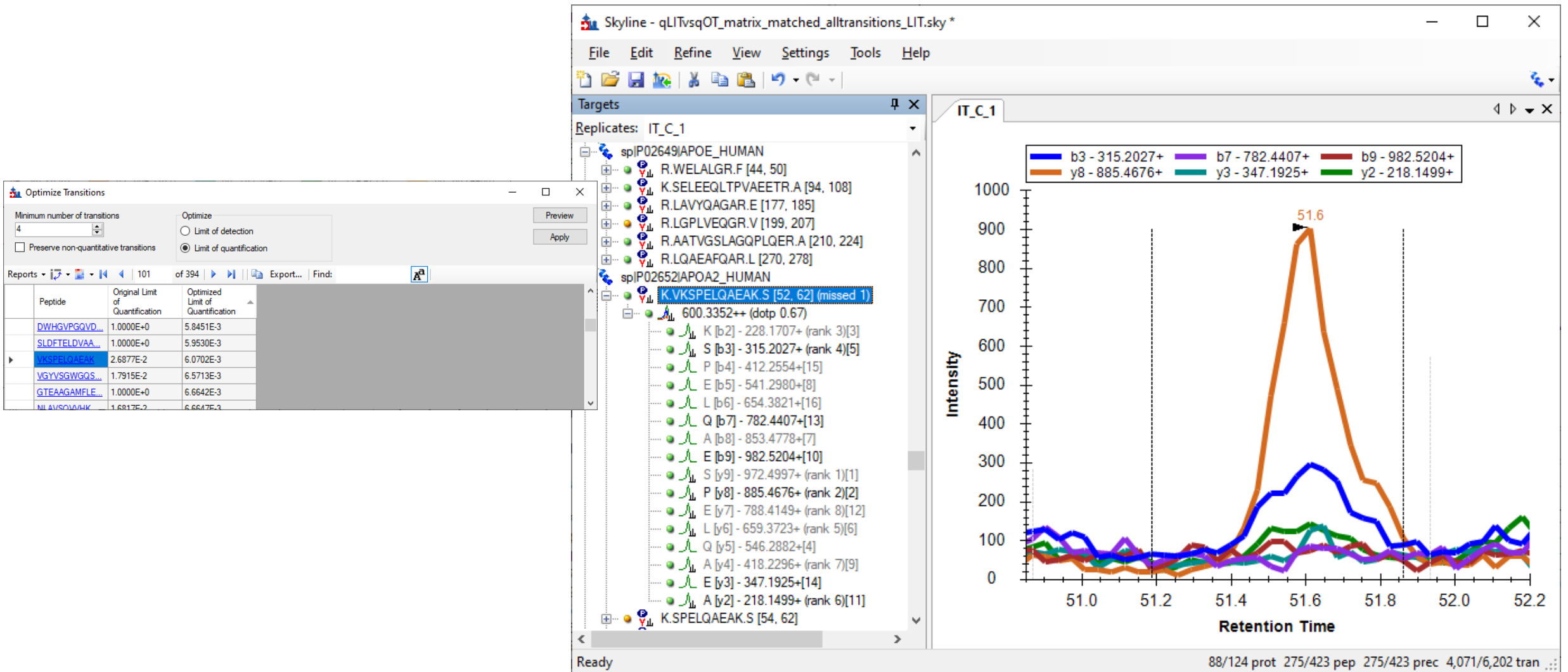
Matched matrix

1. Determine LoQ for every possible transition individually
2. Select top N transitions that give best LoQ
3. Calculate LoQ with new transition set
4. Re-calculate LoQ with the new transition set and every other possible transition
5. Keep all transitions that improve LoQ

Analyte matrix

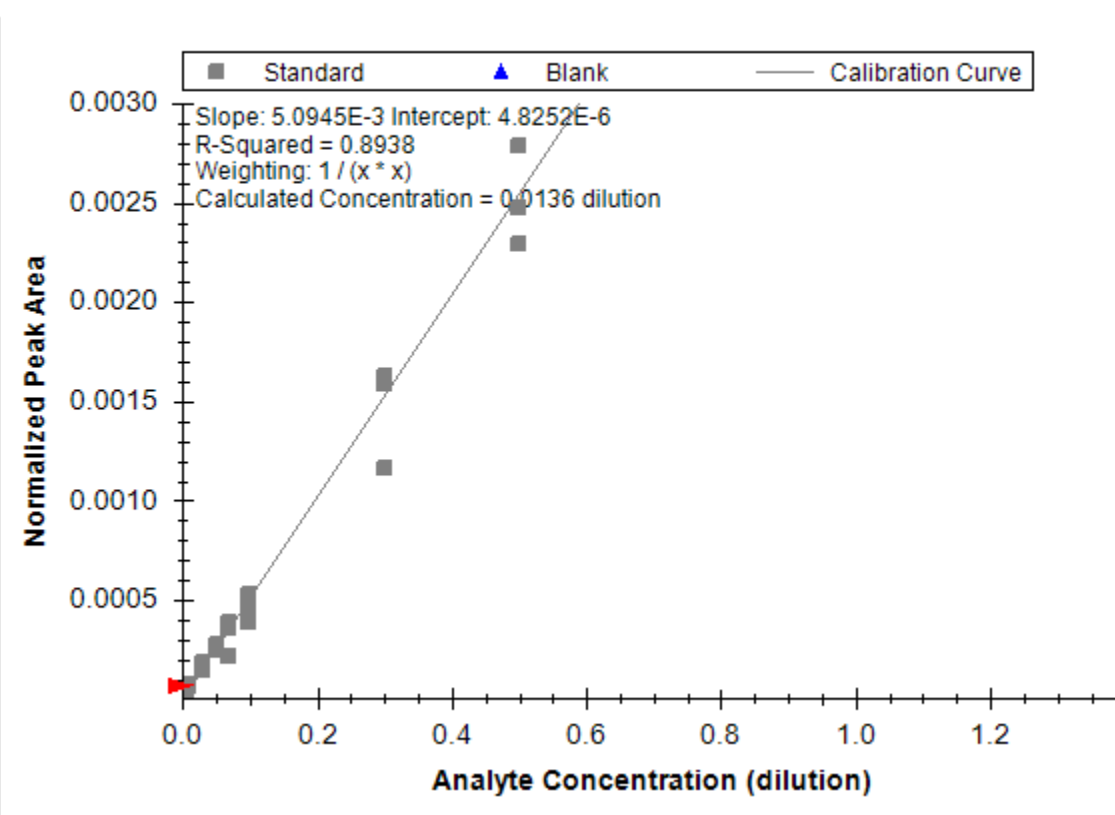


Automated transition selection that optimizes the lower limit of quantitation

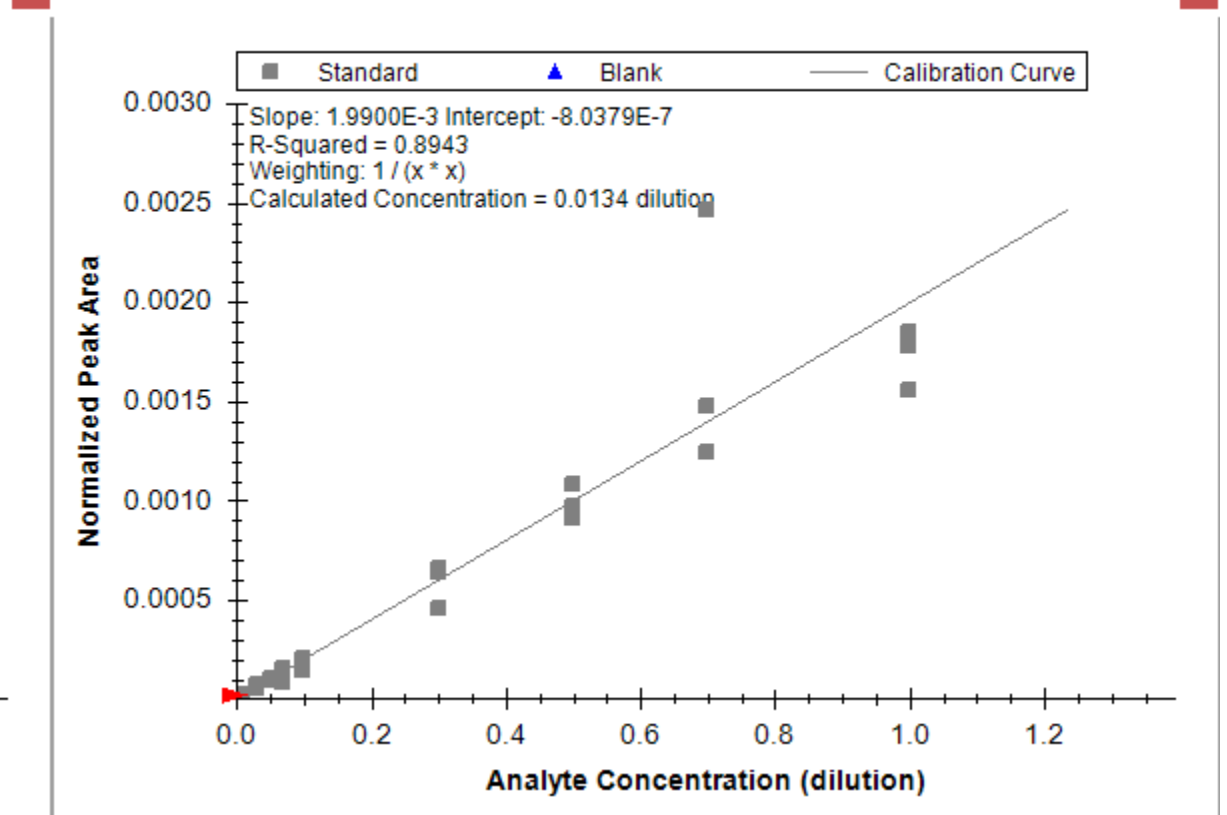


Automated transition selection that optimizes the lower limit of quantitation

Calibration Curve: VKSPELQAEAK



Calibration Curve: VKSPELQAEAK



Acknowledgements



Mike MacCoss

Nick Shulman

Brian Searle

Lindsay Pino

Christine Wu

Brook Nunn

Gennifer Merrihew

Rich Johnson

Eric Huang

Julia Robbins

Jea Park

Aaron Maurais

Kristine Tsantilas

Emma Timmins-Schiffman

Dani Faivre

Deanna Plubell

Miranda Mudge

Chris Hsu

Brendan Maclean

Brian Connolly

Brian Pratt

Kaipo Tamura

Nat Brace

Mark Belanger

Rita Chupalov

Vagisha Sharma

ThermoFisher
S C I E N T I F I C

Philip Remes

Jesse Canterbury



Genome Sciences
UNIVERSITY OF WASHINGTON

