P-SCOPE: Carrier-enabled low-input phosphoproteomics by mass spectrometry

Albert Tian Chen^{1,2}, David H. Perlman¹, Edward Emmott^{1,2}, R. Gray Huffman^{1,2}, Nikolai Slavov^{1,2,3}

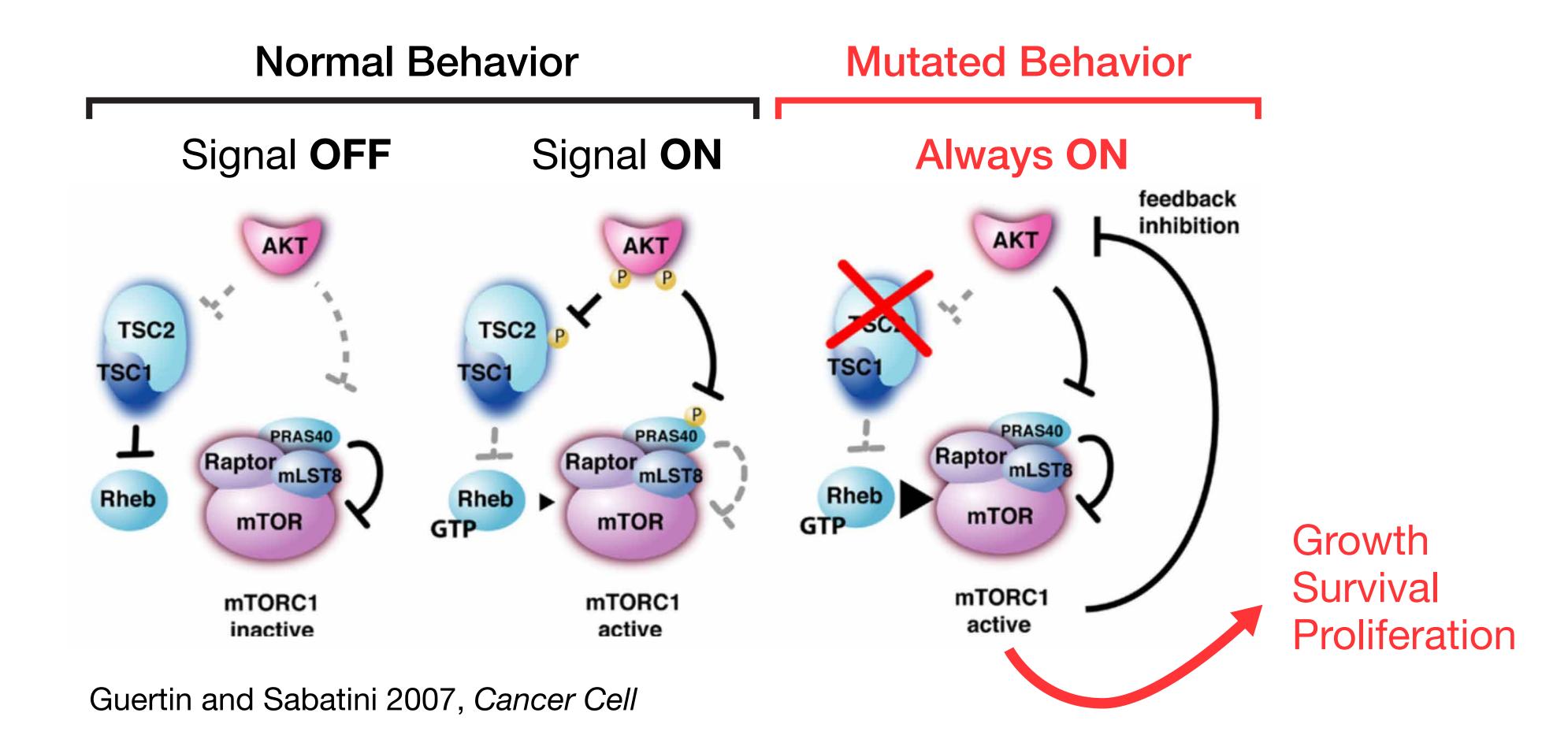
- 1 Department of Bioengineering, Northeastern University, Boston MA 02115, USA
- 2 Barnett Institute, Northeastern University, Boston MA 02115, USA
- 3 Department of Biology, Northeastern University, Boston MA 02115, USA



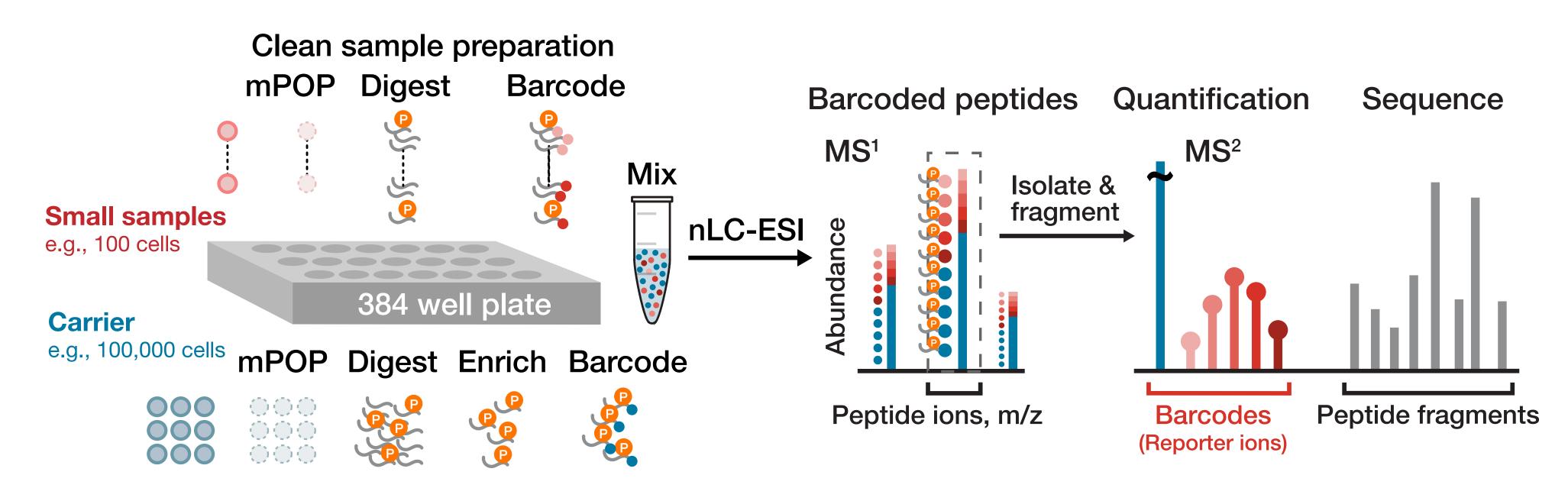
Summary

- Cellular signaling pathways are primarily mediated by phosphorylation, and dysregulation of these pathways is the cause of many diseases such as cancer
- Understanding signaling pathways and developing targeted clinical therapies would benefit from measuring every component of the pathway.
- Current measurements are limited to large samples or a handful of proteins
- P-SCOPE allows measuring hundreds-thousands of phosphoproteins for low-abundance samples
- P-SCOPE's carrier design can be extended to other post-translational modifications, such as glycosylation or ubiquitination

Dysregulated signaling pathways can lead to diseases such as cancer

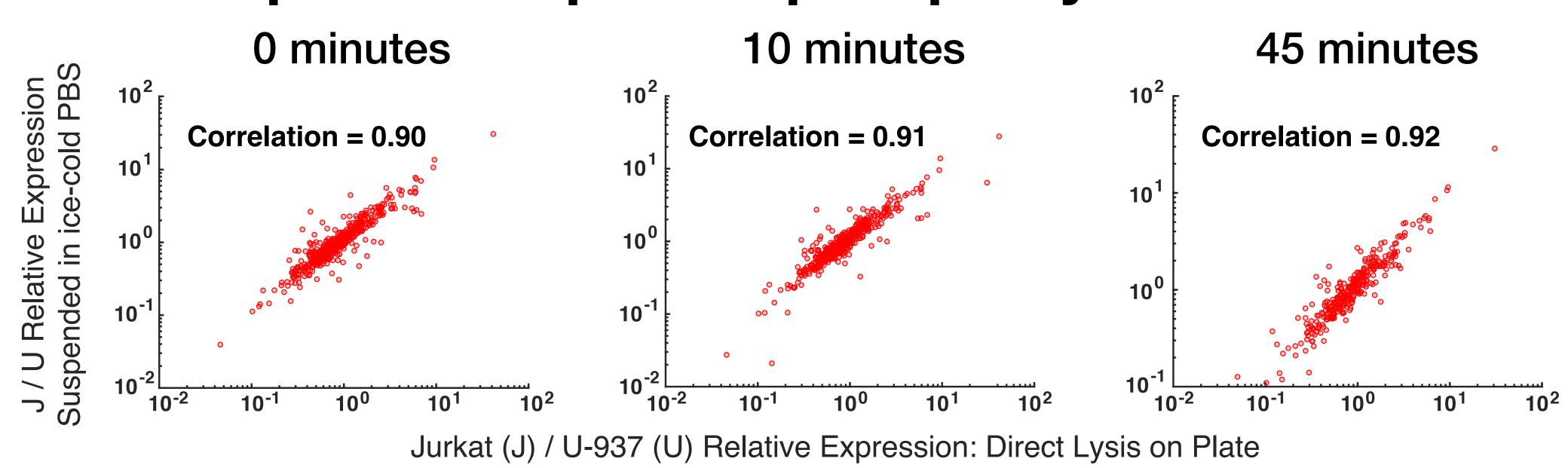


P-SCOPE Mass Spectrometry Method



Thanks to members of the Slavov Laboratory. This work was funded by startup funds from Northeastern University, a New Innovator Award from the NIGMS from the National Institutes of Health to N.S. under Project Number 1DP2GM123497-01, and by the Northeastern Office of Undergraduate Research and Fellowships to A.C.

P-SCOPE preserves protein phosphorylation

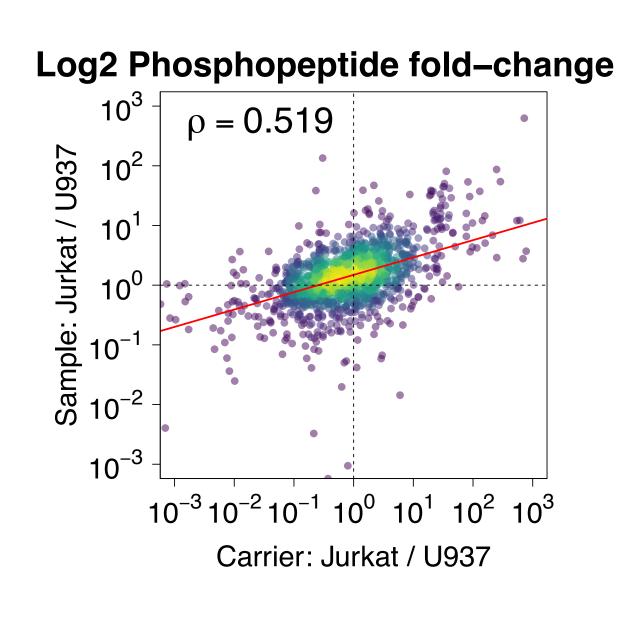


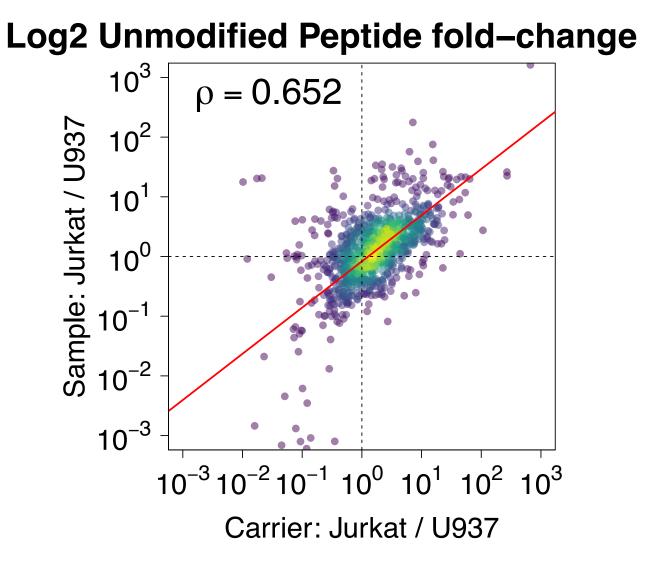
• Phosphorylation motifs in small samples are not lost during realistic cell sorting timelines (< 45 min, suspended in PBS, on ice), compared to cell lysis on plate

Measuring differential expression of phosphopeptides between T-cells and monocytes

Label (TMT tag)		P-SCOPE set: T-cells & monocytes
127N	10,000 U-937 cells (enriched)	
127C		empty
128N		empty
128C		1,000 Jurkat cells
129N		1,000 U-937 cells
129C		1,000 Jurkat cells
130N		1,000 U-937 cells
130C		empty
131N		empty
131C		empty

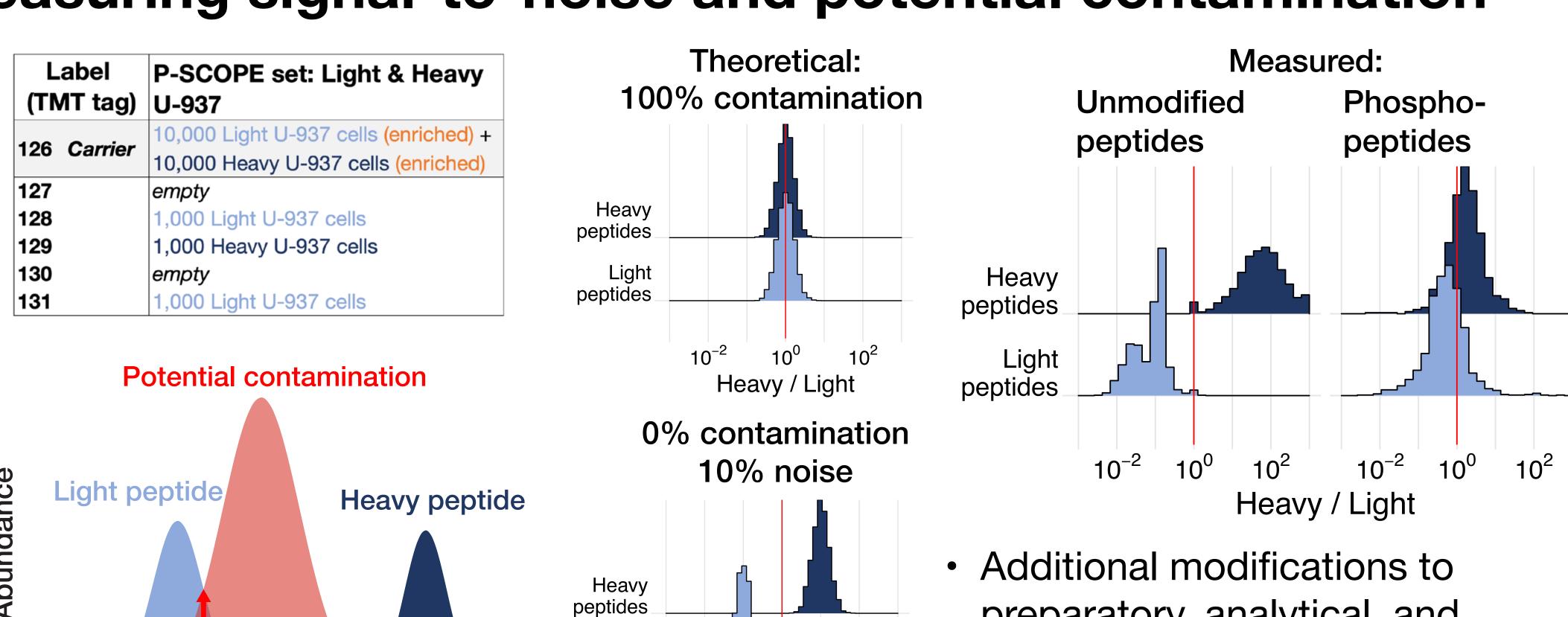
Barcoded peptides, m/z





Measuring signal-to-noise and potential contamination

Light peptides



 Additional modifications to preparatory, analytical, and computational methods needed to reduce noise and potential contamination