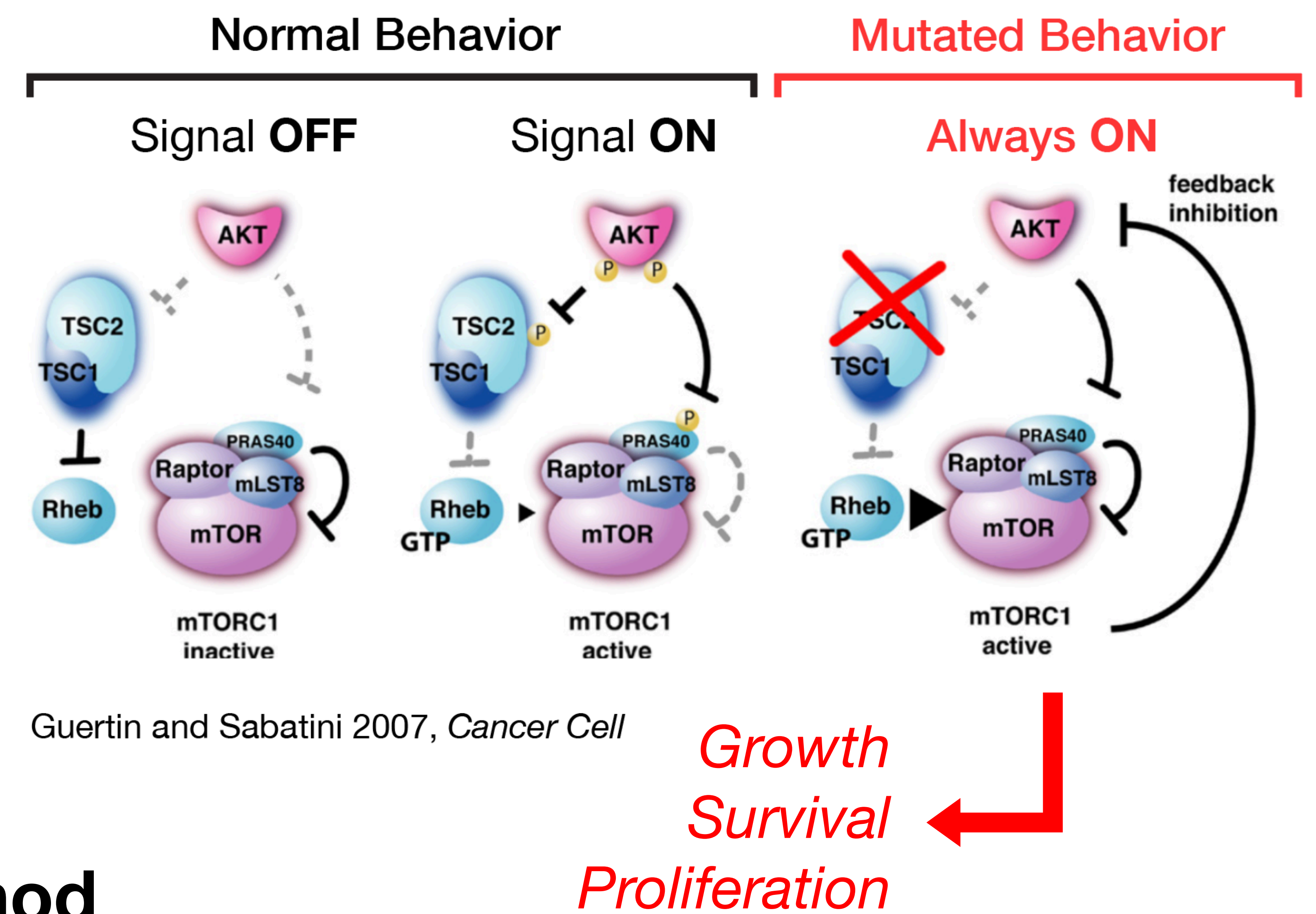




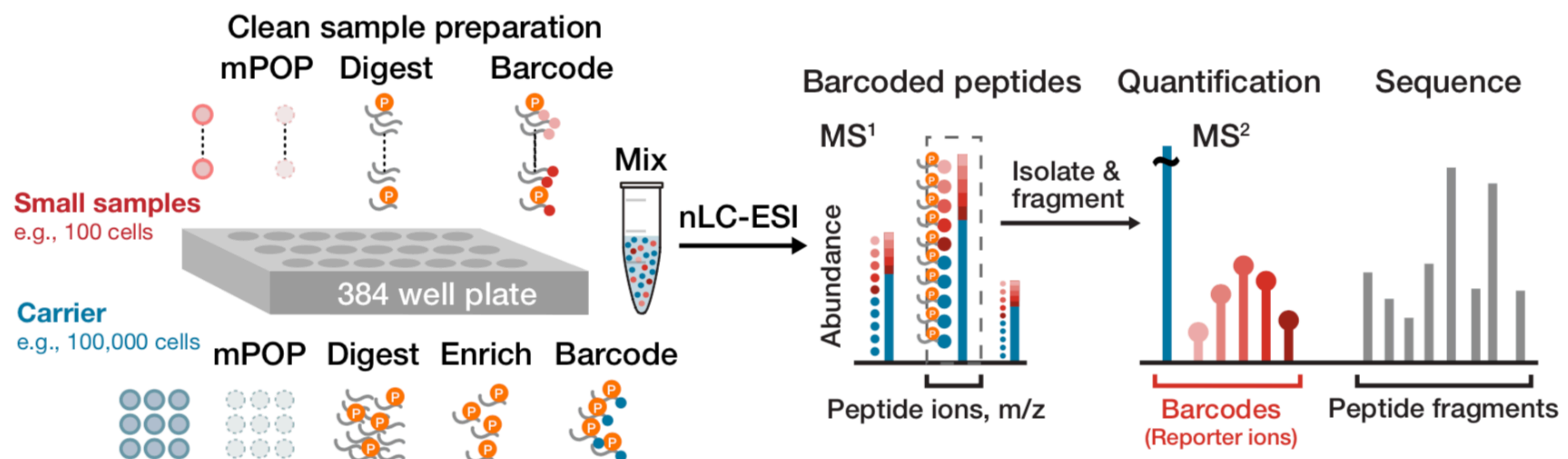
Summary

- 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

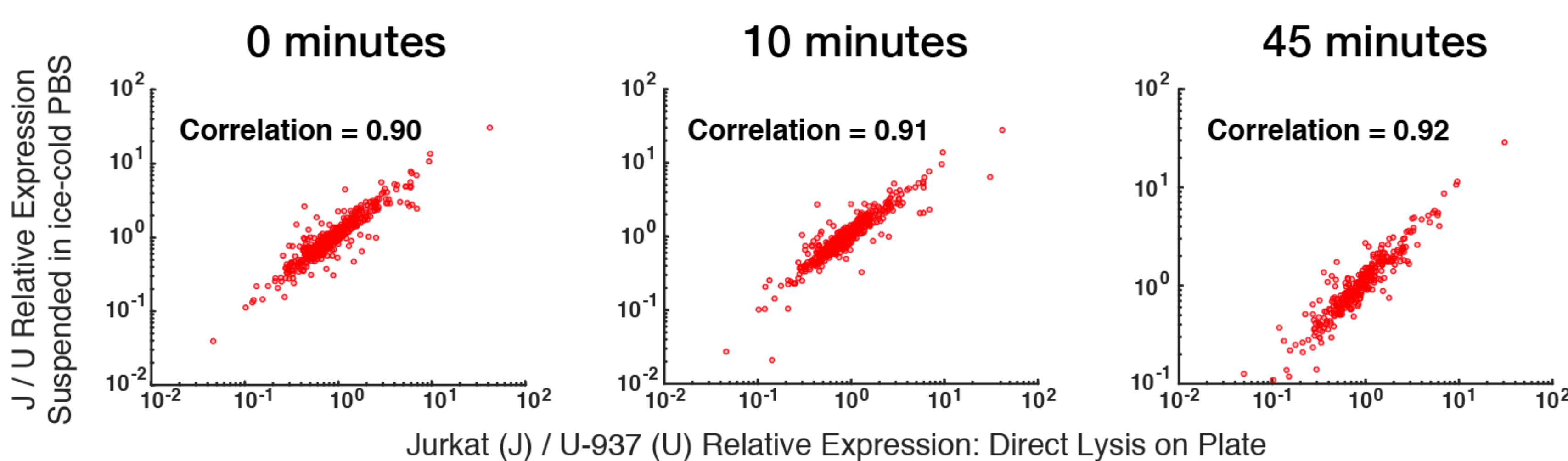
Dysregulated signaling pathways can lead to diseases such as cancer



P-SCOPE Mass Spectrometry Method

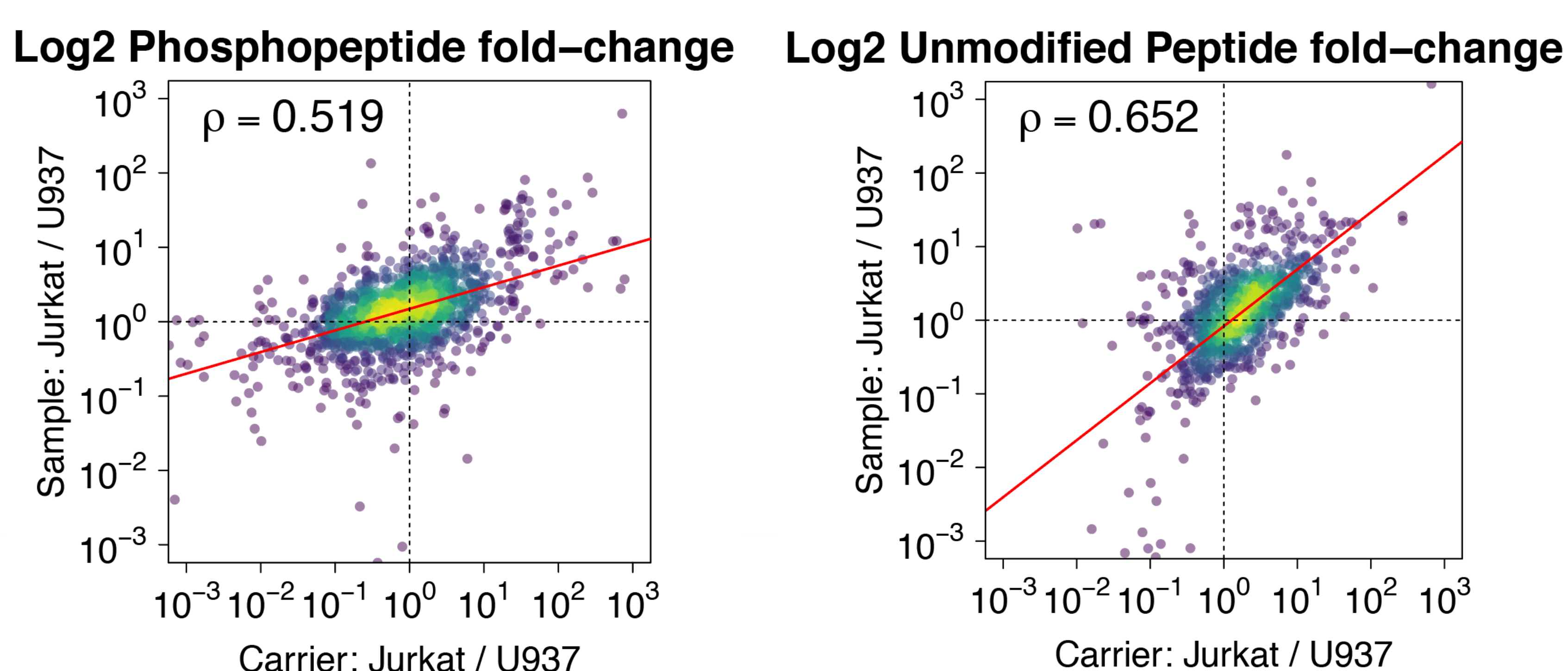


P-SCOPE preserves protein phosphorylation

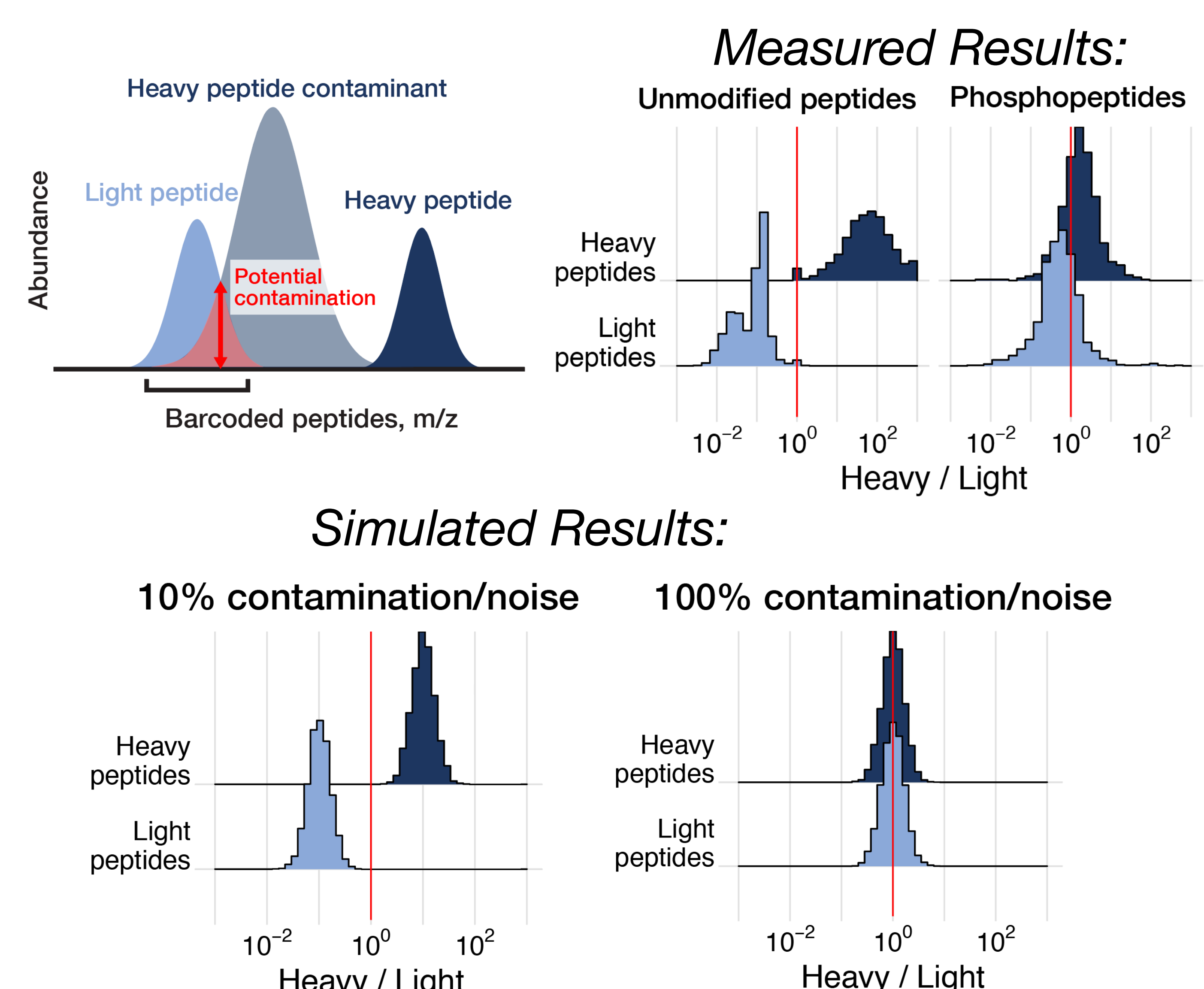


- Phosphorylation motifs in small samples are not lost during realistic cell sorting timelines (< 45 min, suspended in PBS, on ice), compared to cell lysis on plate

Measuring differential expression between T-cells and monocytes



Measuring signal-to-noise and potential contamination



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

Acknowledgements

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.