



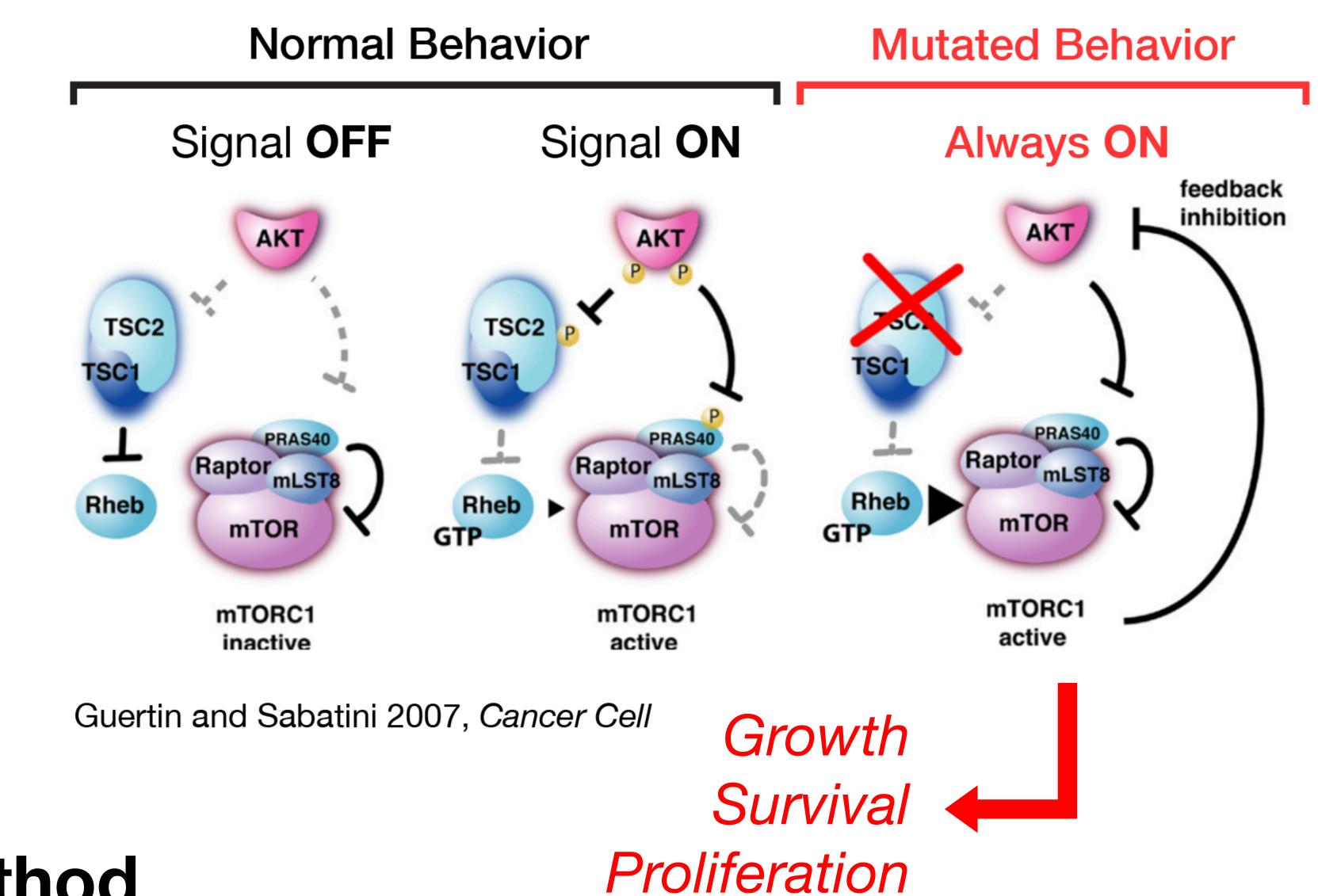
### P-SCOPE: Carrier-enabled low-input phosphoproteomics by mass spectrometry

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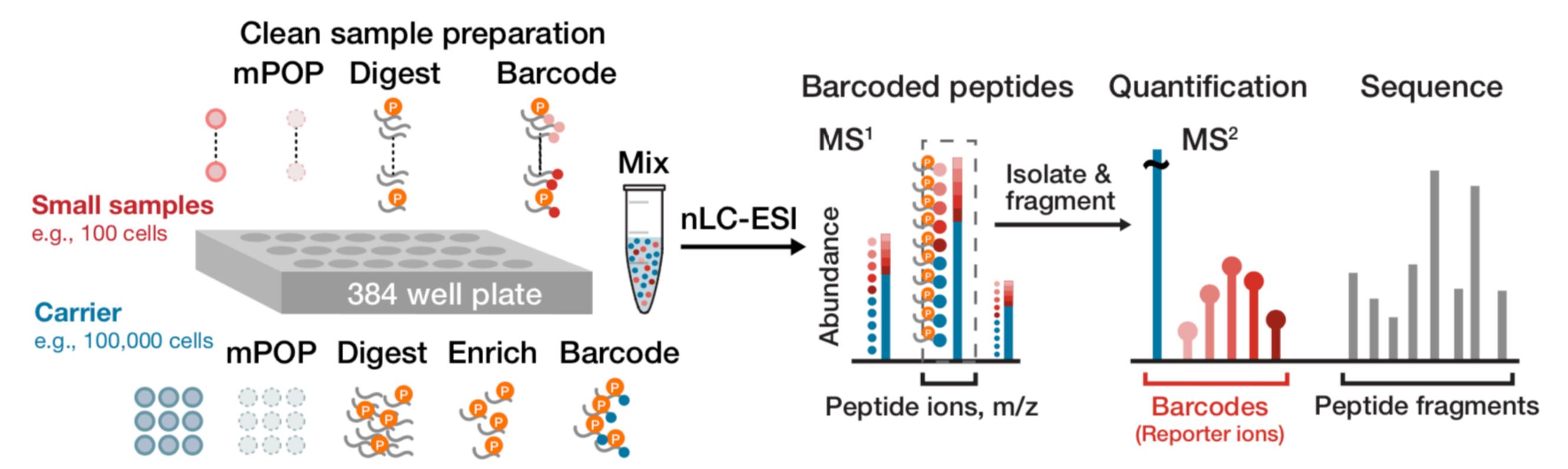
#### Summary

- 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

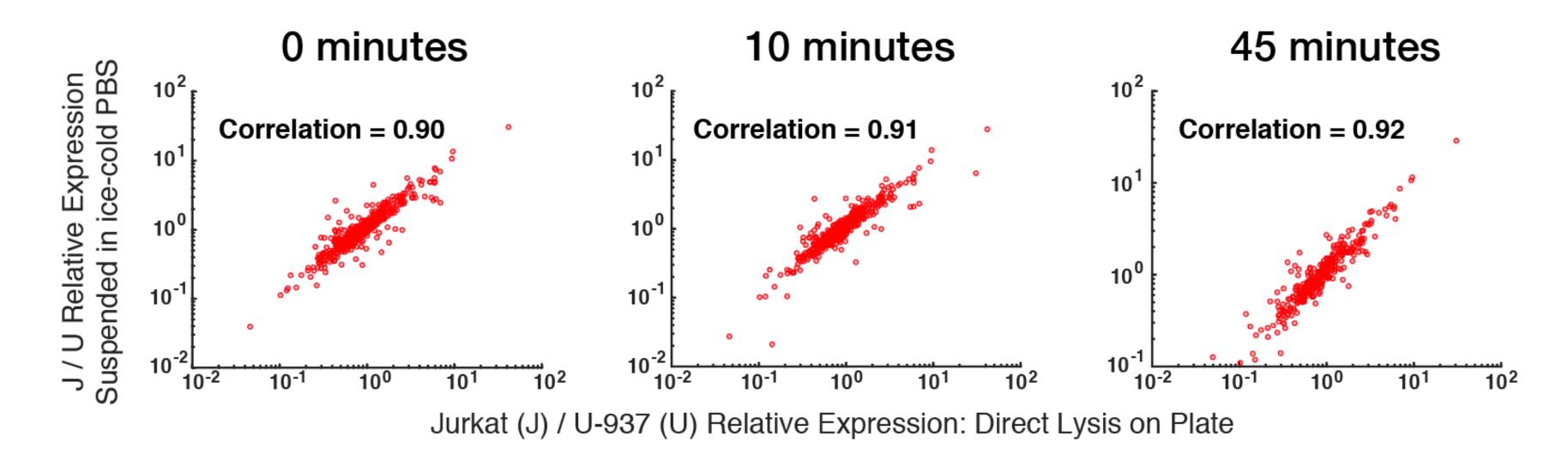
# Dysregulated signaling pathways can lead to diseases such as cancer



#### P-SCOPE Mass Spectrometry Method

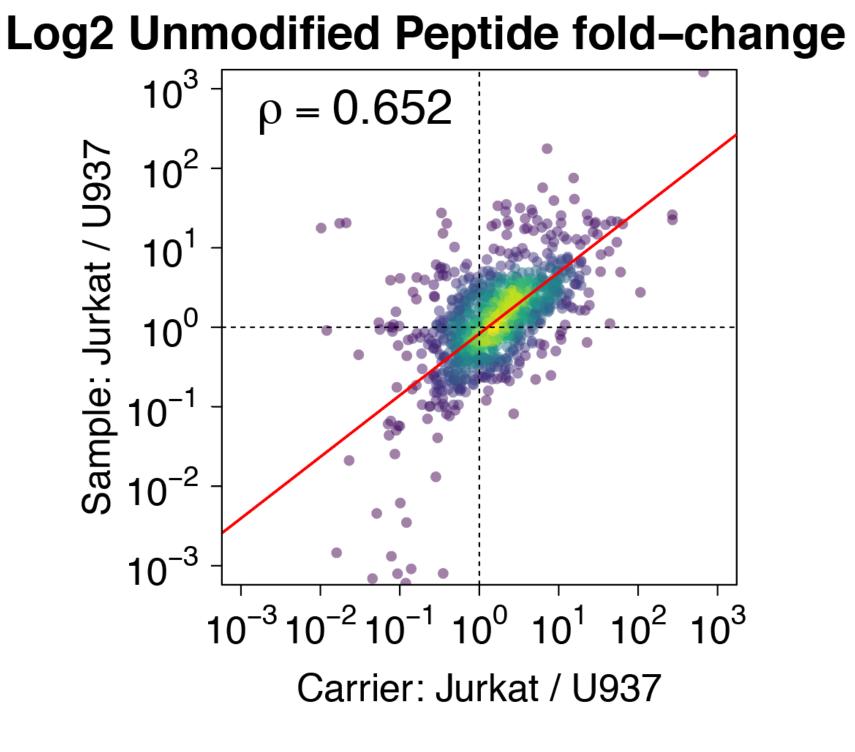


#### P-SCOPE preserves protein phosphorylation

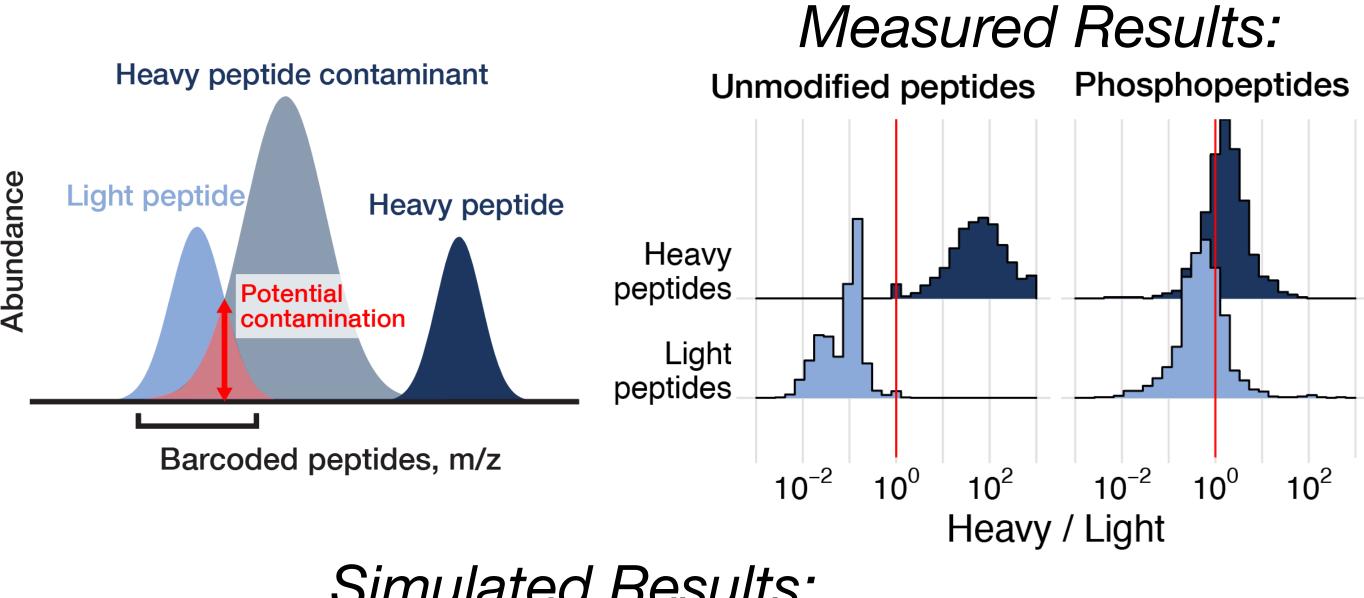


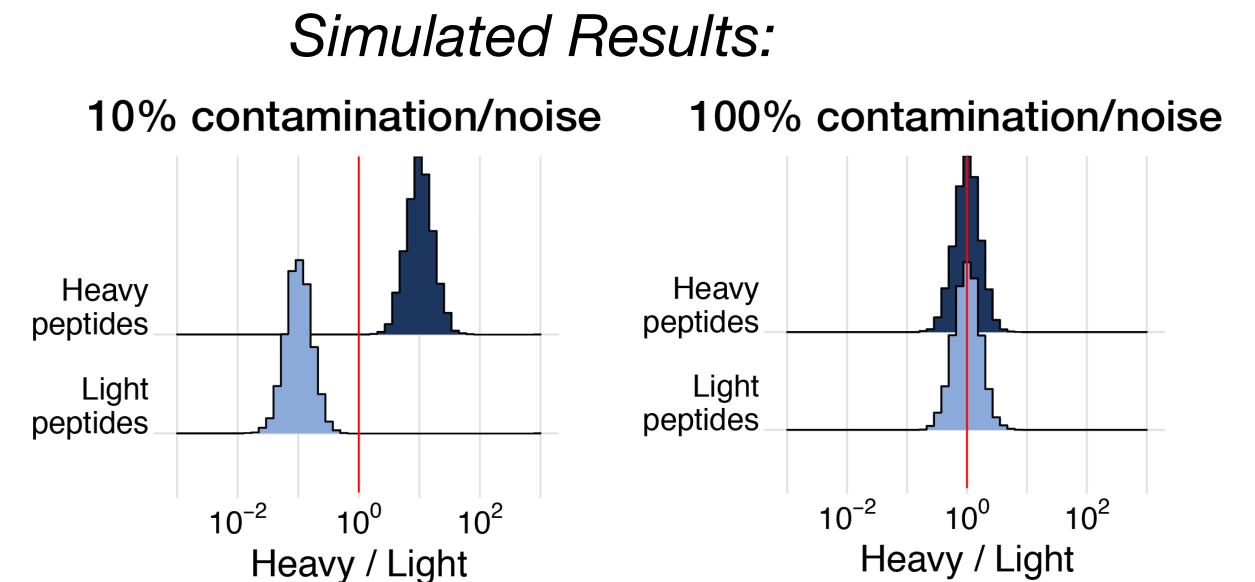
 Phosphorylation motifs in small samples are not lost during realistic cell sorting timelines (< 45 min, suspended in PBS, on ice), compared to cell lysis on plate

# 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

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