# Techniques for validating the genomic drivers of nanoparticle interactions in cancer cells

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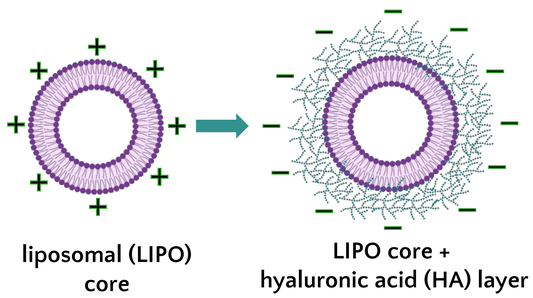
## Background

Current challenges of cancer therapies
Off-target effects, lack of specificity, and difficulty penetrating cancerous tissue[1]

Nanomedicine is an exciting way address these issues.
Nanomedicine = using nanotechnology for medical and biological applications
- Reduce early degradation & clearance
- Improve tissue specificity
- Lower toxicity[2]

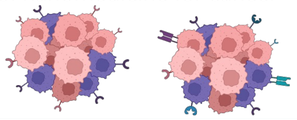
Layer-by-Layer nanoparticle (NP) assembly
- Tunable NP assembly platform allowing multiple therapeutic modalities and tissue targeting



liposomal (LIPO) core

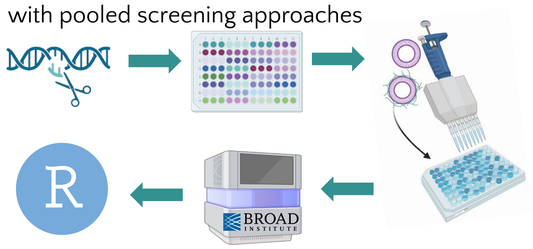
LIPO core + hyaluronic acid (HA) layer

Limitations of studying nano-bio interactions
- Tissue and cellular heterogeneity make it difficult to determine which chemical properties result in successful NP delivery in specific tissues[3]
- We hypothesize that an improved understanding of the biologic drivers of NP delivery will improve the utilization of nanomedicine for cancer

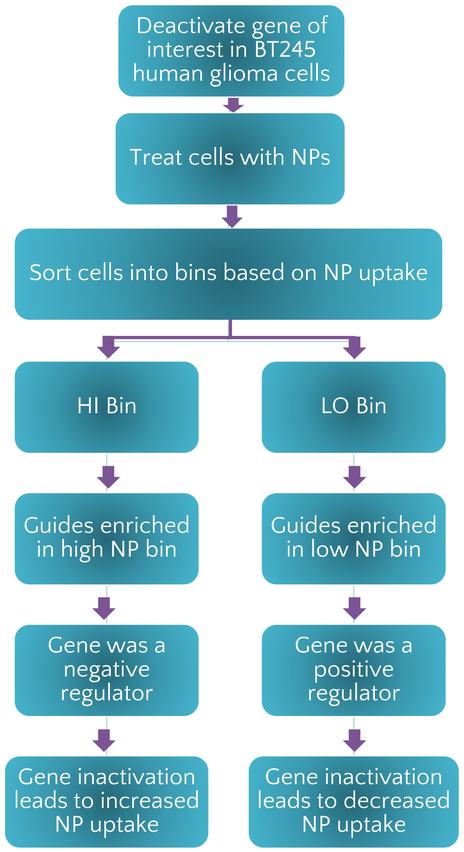


## High-throughput techniques

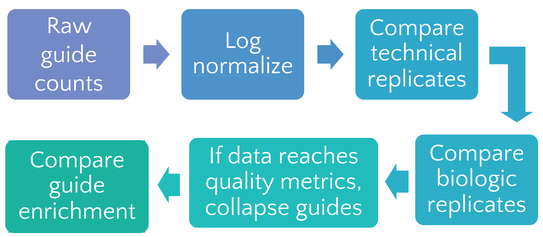
High throughput screening to validate the genomic drivers of NP-cell interactions
- We previously identified potential genes that regulate these interactions using previous methods[4]
- We seek to validate multiple genes simultaneously with pooled screening approaches




## Experimental Overview




**Data analysis pipeline**

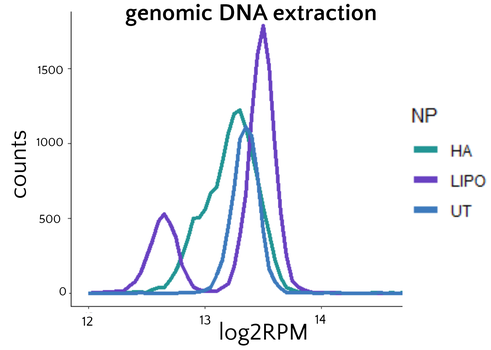



$$\text{Log}_2 \text{ normalized Reads (RPM)} = \text{Log}_2\left(\frac{\text{Reads for one guide in one sample}}{\text{Total reads for all guides in one sample}} \times 1e6 + 1\right)$$

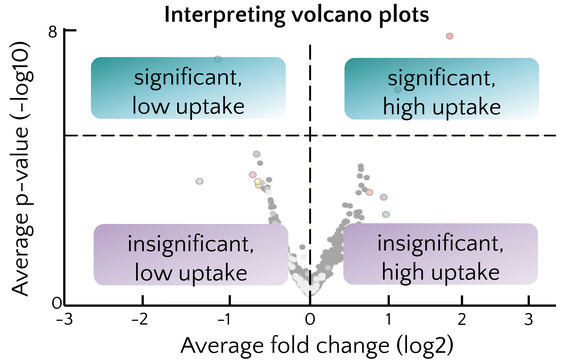
$$\text{Log}_2 \text{ fold change} = \text{Log}_2 \text{ normalized reads of HI} - \text{Log}_2 \text{ normalized reads of LO}$$

## Results

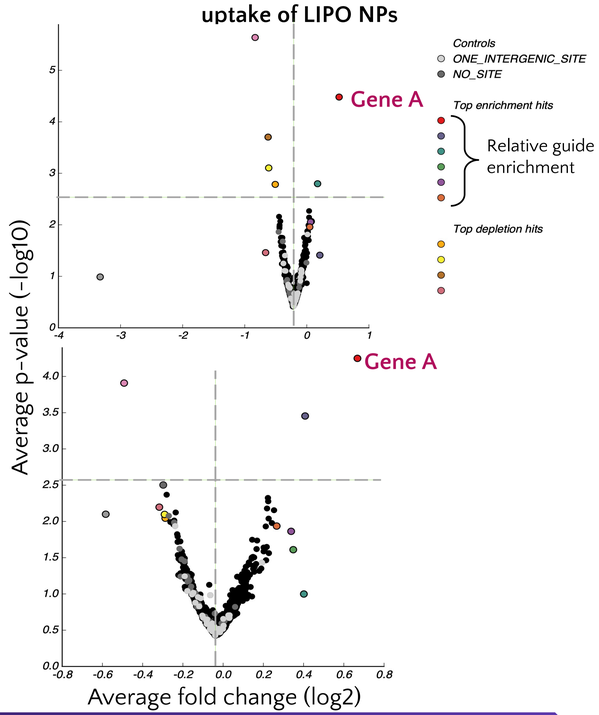
**$Log_2$RPM > 12 indicates adequate sample input and genomic DNA extraction**



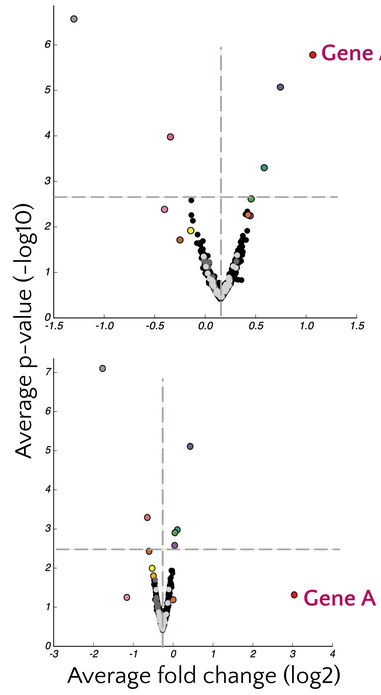

**Interpreting volcano plots**




**Volcano plot shows genes significantly involved in uptake of LIPO NPs**




**Similar results for HA NPs**




## Conclusion

- Developed a strategy to analyze results of CRISPR pooled screening with two different NP formulations
- Validated genes identified using computational methods
- Identified a previously less-explored gene that contributed to decreased uptake of LIPO and HA NPs

Next Steps
- Use the techniques developed here to study a larger library of NPs
- Perform screening on other cancer cell lines

## References

[1] Shi, J. J.; Kantoff, P. W.; Wooster, R.; Farokhzad, O. C.; Cancer nanomedicine: progress, challenges and opportunities. Nat. Rev. Cancer 2017, 17 (1), 20–37.
[2] Wilhelm, S.; Tavares, A. J.; Dai, Q.; Ohta, S.; Audet, J.; Dvorak, H. F.; Chan, W. C. W.; Analysis of nanoparticle delivery to tumours. Nat. Rev. Mater. 2016, 1 (5), 16014.
[3] Poon, W.; Kingston, B. R.; Ouyang, B.; Ngo, W.; Chan, W. C. W.; A framework for designing delivery systems. Nat. Nanotechnol. 2020, 15 (10), 819–829.
[4] Boehnke N, Straehla JP, Safford HC, Kocak M, Rees MG, Ronan M, et al. Massively parallel pooled screening reveals genomic determinants of nanoparticle delivery. Science 2022;377:eabm5551. https://doi.org/10.1126/science.abm5551.
Images created in part by BioRender.

## Acknowledgements

I would like to thank Dr. Joelle P. Straehla, Dr. Paula T. Hammond, the MIT MICRO leadership, and the MSRP leadership for their guidance and support this summer. Funding sources:

National Institutes of Health
T34 GM 136497