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Nucleus Developer Notes

Build a Base Cell Validation

DevStudio 2026 Capstone

Base Cell Validation Participants[1]

[1]Nucleus Labs, San Francisco, CA

Abstract

1. Overview

This DevNote validates the Build a Base Cell protocol at the DevStudio Capstone event. Documentation was accessed on 2026-10-13

- Process protocol: https://docs.nucleus.engineering/docs/processes/build-base-cell/main/
- Base cytosol specification: https://docs.nucleus.engineering/docs/modules/base-cytosol/spec/

2. Results

The plate held 11 wells, one or two per guest, imaged over 9 timepoints (t0-t8). Every well carries the same reporter construct, pOpen-T7-deGFP, 2812 bp, circular, from nucleus-eng/DNA.

seqviz

This block will be replaced with **./dna/pOpen-deGFP.gbk** when deployed to Curvenote.

Options:

Full notebook: Liposome Timeseries Analysis (2026-10-13).

Full resolution of participant dataset is available here: https://data.nucleus.engineering.

2.1. Population summaries

The population summary below comes from segmented liposome images taken at the Capstone.

3. Discussion

3.1. Did the protocol work as written?

- **Claudia Contini:** Everything worked as expected.
- **Michael Booth:** Instead of the 5 µL of water at the end, added 1 µL extra of ribosomes and 4 µL of water. Otherwise, the protocol worked very well and was clear, with Surendra Yadav also showing the steps.
- **Michael Clear:** Too much of the aqueous phase was still present before resuspending the pellet, roughly 100 µL of solution left at the time of resuspension.

Published Oct 13, 2026

Correspondence to
Base Cell Validation Participants
build@bnext.bio

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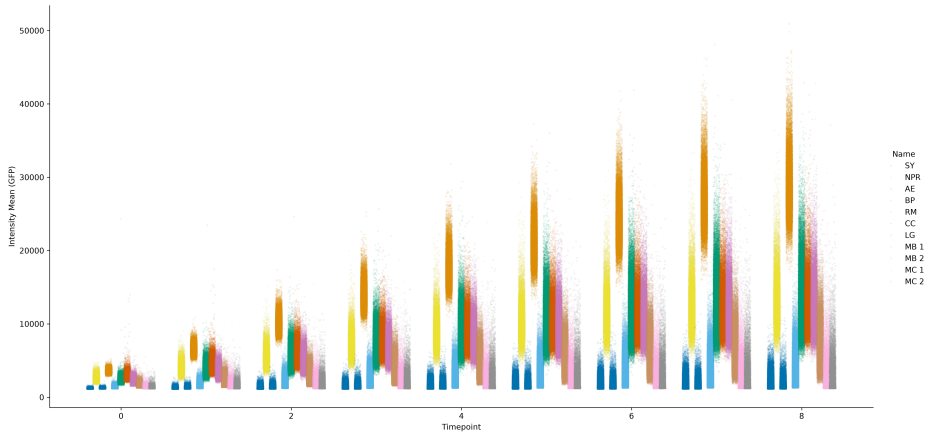

Figure 1. *Per-well GFP distributions compared directly against each other. Segmented data is available here: https://data.nucleus.engineering. Produced by fogplot-compare.ipynb, a trimmed extract of the full notebook linked above, keeping only the cells behind this figure.*

3.2. What was unclear or missing?

- **Claudia Contini:** Adding 20 µL of lipid-oil solution on top of glucose.
- **Michael Clear:** Some lack of clarity around the lipid removal step after centrifugation. The general approach was clear, but it was not optimized for concentration.

3.3. Base Cell Validation Participants

Surendra Yadav (b.next, well D5), Neha Kamat (Northwestern University, well D6), Andrew Ellington (University of Texas at Austin, well D7), Becky Pferdehirt (Astera Institute, well D8), Richard Murray (Schmidt Sciences, well D9), Leopold Green (Purdue University, well E5), Michael Booth (University College London, wells E6 and E7), Michael Clear (Schmidt Sciences, wells E8 and E9), and Claudia Contini (Imperial College London, well E10).

3.4. Acknowledgments

Thank you to Yen-Yu Hsu (b.next) and Surendra Yadav (b.next) for serving as TAs at this session.