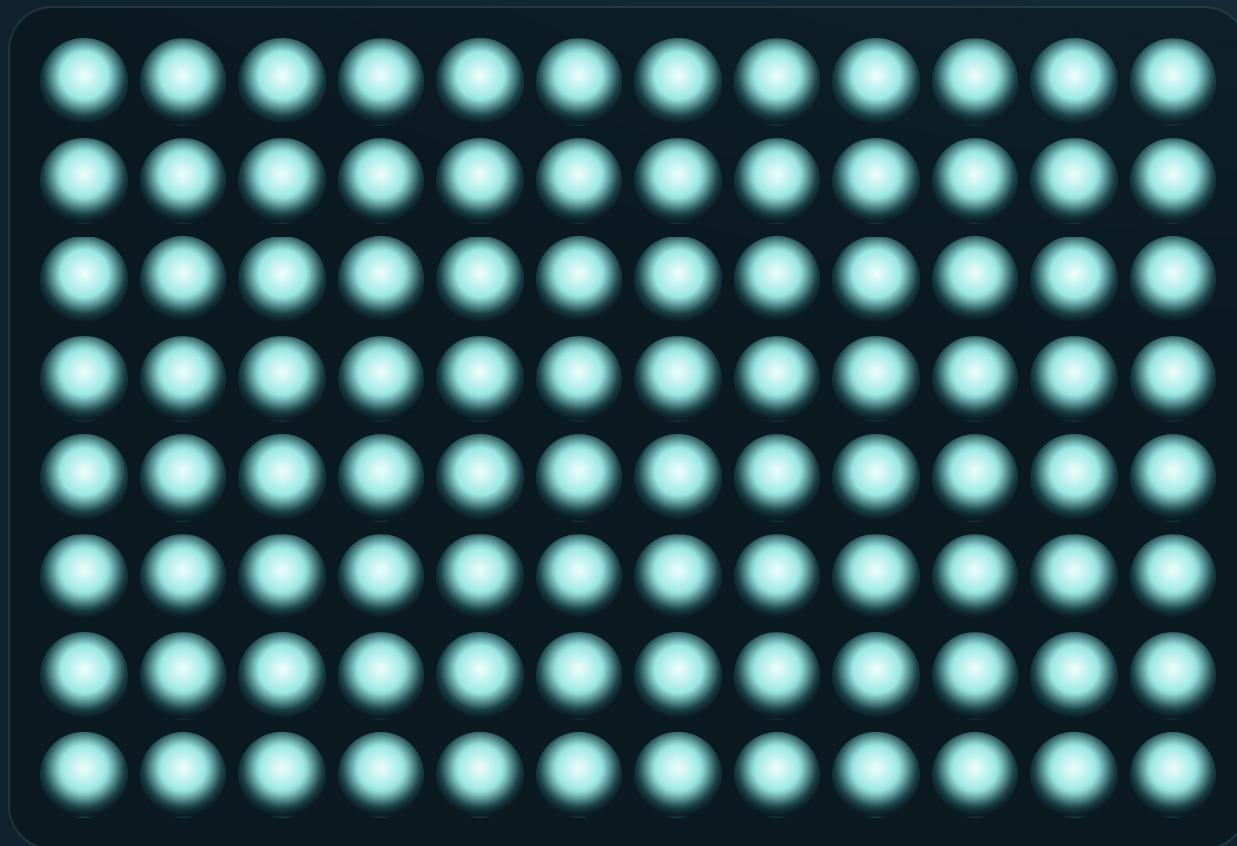


Single-cell data at scale

Where do batch effects actually come from?



Five minutes on the most manual step in the lab

Swipe

The steps nobody logs

Thaw. Spin. Strain. Bead kit. Repeat for 2,000 samples.

Every one of these is a hands-on step with hands-on variance. Across a hundred-million-cell program, that variance is in the training set, and the model will learn it as biology.

Dead cells and debris become noise

Thaw, transfection, editing, dissociation: they all leave dead cells behind.

Their RNA leaks into every cell's barcode as ambient RNA. Their fragments become doublets and debris. In the Discovery Life Sciences study, the most contaminated tumor sample spent 68% of its reads on soup, not cells.

The limit of software

You can regress out a batch effect you can measure.

You cannot recover a sample that was never viable, and you cannot see the variance that entered before the first barcode. The fix has to be physical, and it has to be the same every time.

Identical, scripted, on the robot

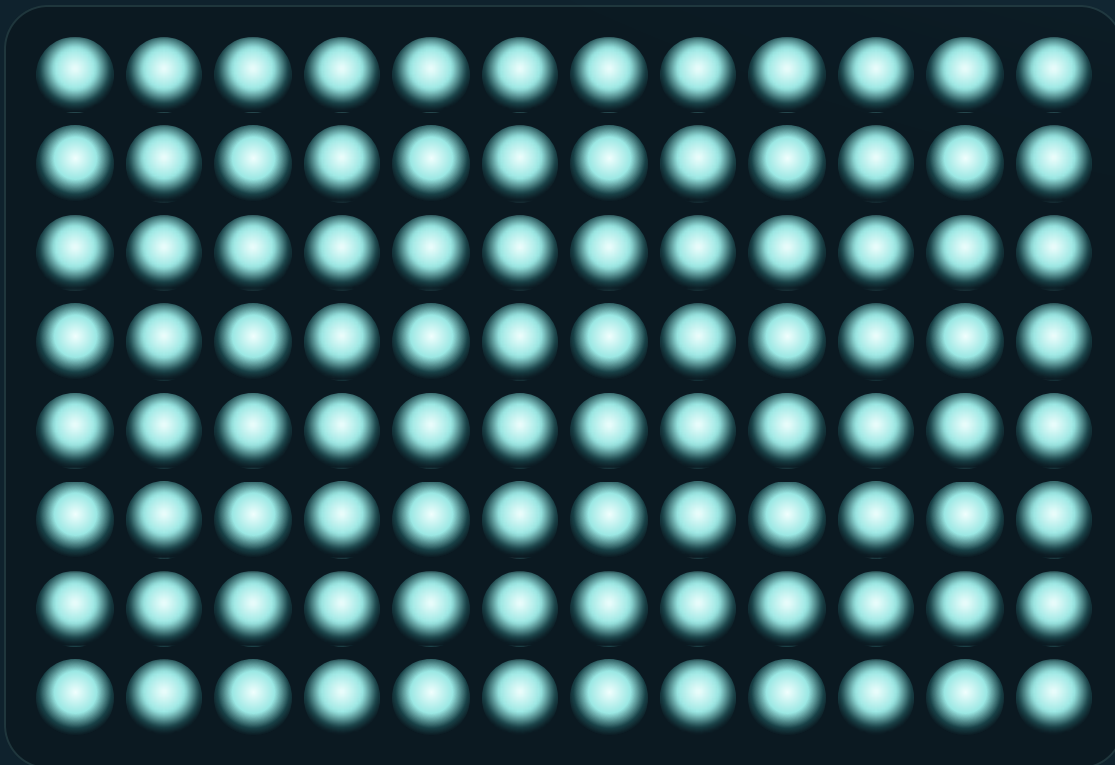
96 samples. One array. Every step scripted.

- 1 Enrich: live cells levitate, dead cells and debris sink label-free
- 2 Wash: buffer exchange in the well no spins
- 3 Collect, pool, concentrate: ready to load 45 min total
- 4 Repeat, identically, plate after plate scripted

A record for every plate

Same script, every well, logged.

A scripted protocol does the same thing to every well and leaves a run log behind. Pair it with viability counts before and after, and every sample in the dataset comes with a record of how it was prepared, and an answer when a cluster looks odd eighteen months later.



A prep record is part of the dataset, not a nice-to-have

levitasbio.com

What it did on 16 real samples

1 → **10**

of 16 sequencing-ready at a hard
70% viability cutoff

52% → **75%**

median viability after one 40-
minute run

6×

fewer high-confidence doublets;
21% less ambient RNA

85/₁₀₀

marker genes carry over: same
biology, cleaner input

Study conducted by



Evercode WT assay by



Train your model on biology, not on your sample prep.

Building a perturbation atlas, a virtual cell training set or a screening program in the thousands of samples? We'll map the LeviCell 96 onto your robot: your handler, your samples, your throughput. One page back, fifteen minutes, free.

Book a liquid handler review: sales@levitasbio.com