

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

Label-free, scripted sample prep for million-cell datasets, on standard SBS robotics.

96

samples in parallel on one SALT array

>95%

viability into sequencing, cytometry or screening

3

hands-on steps; the rest runs on the robot

\$10

per sample
so million-cell studies fit the budget

The problem the model can't unlearn

Virtual cell models, perturbation atlases and foundation-scale datasets are built from thousands of samples over months: cell lines after transfection or editing, PBMCs and dissociated tissue out of the freezer, iPSC-derived cells, organoids, nuclei. Every one arrives with dead cells and debris; their RNA becomes ambient background and their fragments become doublets in every profile. Manual clean-up (spins, strainers, bead kits) adds operator and day-to-day variance before the first barcode and leaves no record.

The limit of software

Downstream correction can regress out a batch effect it can measure. It cannot recover a sample that was never viable, and it 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 processing in every well, with a QC record per sample stored alongside the data.

Every workflow that relies on cells needs the same step

Levitation separates cells by their physical properties, so it does not care how the damage happened. It belongs right before cells are fixed, barcoded or loaded.

Cryopreserved PBMCs and dissociated tissue

Half the cells can be dead at thaw, with the debris in the tube. Enrich live cells at thaw instead of waiting for a recovery culture that adds time and variance.

Measured on cryopreserved tumor DTCs: viability 52% → 75%; sequencing-ready samples from 1 in 16 → 10 in 16.

Cell lines after transfection or electroporation

Electroporation and lipofection kill a large share of cells in the first days; the dying cells and fragments are still there at harvest. Remove them label-free, right before fixation or barcoding, with no spins on fragile cells.

Timing: enrich at harvest, not after a recovery step that selects for the fittest clones.

CRISPR and Perturb-seq screens

Dead cells and debris inflate ambient RNA and doublets, and both corrupt guide assignment and perturbation calls. Clean input makes the perturbation the only variable that changed.

Measured: 21% less ambient RNA and six-fold fewer doublets, lower in every cell population.

Drug perturbation and dose response

Cytotoxic conditions produce apoptotic fractions by design. Enrich the survivors so their transcriptomes describe the response, or collect defined fractions when death is the readout.

Label-free: no antibody or dye decides which cells are kept.

iPSC-derived cells and organoids

Differentiated cells and dissociated organoids are fragile and carry dissociation debris. A passive magnetic field, with no shear, centrifugation or filtering, keeps them intact and their transient states unchanged.

Cells, nuclei, organoids and spheroids; fresh, thawed or fixed.

Nuclei from frozen tissue

Nuclei preps carry cytoplasmic debris and clumps that read as background in every barcode. Clean up the nuclei suspension on the same array: debris and aggregates removed, nuclei collected ready to load.

Label-free clean-up of nuclei preps; no spins, no filters.

What we don't claim. The study figures are from cryopreserved dissociated tumor cells, the hardest common input (16 samples at bench scale, 10 at sequencing scale; confirmatory same-run study in progress). The separation is physical and label-free, so the same step applies to any suspension; the 96-sample standardization run on side 2 measures it on your cell type.

Every prep step, scripted, on the robot you already run.

- 1**
Enrich
 Live cells levitate into one band; dead cells and debris sink. No labels, beads or shear.
- 2**
Wash
 Buffer exchange in the well, no centrifuge spins.
- 3**
Collect, pool, concentrate
 Fraction of interest, pooled to the study design, eluted in loading volumes.

Capabilities

Inputs	Cells, nuclei, organoids and spheroids, particles. Fresh, thawed and fixed-cell workflows. 15,000 to 500,000 cells per well.
Protocols	Viable-cell enrichment (keeps every population); wash and buffer exchange; nuclei clean-up (debris and aggregates removed).
LeviSelect kits	Targeted depletion in the same run: Cell Debris Depletion (deeper clean-up, immune and tumor focus), Tissue RBC Depletion, Immune Cell kits, Myelin Depletion.
Throughput	96 samples per SALT array; 5 minutes hands-on; 40-minute levitation; 45 minutes from loading to enriched cells; walkaway.
Automation	SLAS/SBS 96-well footprint, one standard deck position, scripted on standard liquid handling. LeviCell 96 System ships with the INTEGRA handler. No centrifuge, filters, beads or microfluidics; no moving parts in the consumable.
Prep records	Scripted protocols leave a run log for every plate; viability counted before and after (AO/PI) in the standardization run gives each sample a record of how it was prepared, stored with the dataset.
Scale path	Same chemistry from LeviCell 12 (benchtop) to the LeviCell 96 System; methods transfer without re-optimizing. Flexible purchase options.
Downstream	10x Genomics, Parse Evercode, flow cytometry, screening.
Economics	About \$10 per sample in consumables, in place of a \$350 dead-cell kit or sort step.

Evidence: Discovery Life Sciences study

The hardest common input: 16 cryopreserved dissociated tumor samples, one 40-minute levitation step; ten sequenced with the Parse Evercode WT assay, untouched and levitated.

Measured	Before	After
Samples sequencing-ready, hard 70% cutoff	1 of 16	10 of 16
Median viability	52%	75%
Dead cells removed, typical sample		89%
Ambient RNA, 9 of 10 pairs (p = 0.004)	6.45%	5.09%
High-confidence doublets (p = 0.020)	0.42%	0.07%
Top-100 marker genes retained		85
Cost per sequencing-ready dataset, same 16 samples	\$96,800	\$9,136

Ten times the datasets from the same tissue for about the same spend. Validated separately by Discovery on more than 100 cryopreserved samples across 20 indications (LeviCell 1.0): 80% dead-cell and debris removal, 100% of samples improved.

Three ways to start

15 minutes Liquid handler review

Your handler, sample types and throughput; we return a one-page map of SALT on your robot with timing. Free.

Two weeks 96-sample standardization run

Send 96 samples to us, or run them at a partner service lab. Viability and debris counts for every sample before and after, side by side with your current prep.

Scale path Develop on 12, scale to 96

Same chemistry; flexible purchase options; scaling up is a schedule decision.

Book a liquid handler review: sales@levitasbio.com · levitasbio.com/data-at-scale

Performance figures from LevitasBio specifications and the September 2026 Discovery Life Sciences study (AO/PI counts, n = 16; paired Parse Evercode WT libraries, n = 10 samples, 20 libraries). Cost figures from an illustrative model on US list-price benchmarks.

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