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

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

Healthy cells make honest data

Every complex workflow stresses cells: thawing, dissociation, electroporation, editing, sorting, waiting. Stressed cells die, their RNA leaks into every barcode, and the survivors switch on stress programs that look like biology. Dead cells don't make data; they make noise. Only unperturbed cells report the biology you perturbed. Manual clean-up adds its own variance and leaves no record, and downstream correction can regress out a batch effect it can measure but cannot recover a sample that was never viable.

What the literature says

- **Ambient RNA is ubiquitous** and rises in necrotic or complex samples; uncorrected, it appears as false differentially expressed genes and pathways (Young & Behjati, GigaScience 2020; Arora et al., PLoS One 2025).
- **Handling induces a conserved stress program**: 512 immediate-early, heat-shock and stress genes across 155,165 cells (O'Flanagan et al., Genome Biology 2019; van den Brink et al., Nature Methods 2017).
- **Compromised cells "inevitably affect data interpretation"**; the reliable fix is not to load them (Ilicic et al., Genome Biology 2016). 10x Genomics recommends dead-cell clean-up below ~80% viability.
- **Models inherit the prep**: foundation-model embeddings were "primarily driven by batch effects" in zero-shot tests (Kedzierska et al., Genome Biology 2025).

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, debris included. Enrich live cells at thaw instead of 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 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, spins 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. Study figures are from cryopreserved dissociated tumor cells, the hardest common input (16 samples at bench scale, 10 at sequencing scale; confirmatory study in progress). The separation is physical and label-free, so the step applies to any suspension; the 96-sample run on side 2 measures it on your cells.

Book a workflow review: sales@levitasbio.com · levitasbio.com/data-at-scale · Full results and calculator: bettersinglecelldata.com

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

1
Enrich
Live cells levitate; dead cells and debris sink. No labels, beads or shear.

2
Wash
Buffer exchange in the well, no spins.

3
Collect, pool, concentrate
Fraction of interest, eluted in loading volumes.

Capabilities

Inputs	Cells, nuclei, organoids, spheroids, particles; fresh, thawed or fixed; 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, Tissue RBC Depletion, Immune Cell, Myelin Depletion.
Throughput	96 samples per SALT array; 5 min hands-on; 45 min from loading to enriched cells; walkaway.
Automation	SLAS/SBS 96-well footprint, one deck position, scripted on standard liquid handling; ships with the INTEGRA handler. No centrifuge, filters, beads or microfluidics; no moving parts in the consumable.
Prep records and imaging	A run log per plate. Add LeviCell Insight and every well is imaged at once before collection (about 5 min per array).
Scale path	Same chemistry from LeviCell 12 to 96; methods transfer without re-optimizing.
Economics and downstream	About $10 per sample in consumables, in place of a $350 dead-cell kit or sort step. 10x Genomics, Parse Evercode, flow cytometry, screening.

In customers' hands

- **Stress fingerprint absent:** 3.15% mitochondrial reads and no population co-expressing JUN and FOS after LeviCell clean-up before 10x (Remsik et al., Nature 2025).
- **After transfection:** iPSC-derived HSPCs 60–75% → 91–96% viability, 85% of live cells recovered; nucleofection made possible (UCSF).
- **After CRISPR and selection:** thawed leukemia samples 9% → 60–91% in 20 minutes; engraftment from 42,000 cells instead of 1–2 million (UCSF; Haematologica 2023).
- **Composition preserved, more cells:** nasal swabs that clogged the 10x ran after levitation with unchanged composition (Boston Children's); up to 5× more high-quality cells on gut tissue (Oxford; Nature 2026).

Evidence: Discovery Life Sciences study

The hardest common input: 16 cryopreserved dissociated tumor samples, one 40-minute step; ten sequenced with Parse Evercode WT, 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. In a separate DLS case study of 106 cryopreserved samples across 21 indications, samples above the 70% bar rose from 29 to 92 and 105 of 106 improved.

Three ways to start

- **Workflow review (15 min, free):** your handler, samples and throughput in; a one-page map of SALT on your robot with timing out.
- **96-sample standardization run (two weeks):** your samples, with us or at a partner lab; viability and debris counts before and after, side by side with your current prep.
- **Develop on 12, scale to 96:** same chemistry, flexible purchase options.

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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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