LEVITAS BIO®

Study conducted by DISCOVERY LIFE SCIENCES

Evercode WT assay by Parse BIOSCIENCES

10× the usable data. 1/10th the cost. One 40-minute run.

From 1 sequencing-ready cryopreserved tumor sample in 16 to 10, at a hard 70% viability cutoff. Study summary, September 2026.

52% → 75%
median viability after one 40-minute run, all 16 samples

10 of 16
samples cleared a 70% viability gate, up from 1 of 16

1/10 the cost
per sequencing-ready dataset, same 16 samples, below-gate samples written off

What was done

16 cryopreserved dissociated tumor samples from the Discovery Life Sciences biobank (8 colorectal, 4 lung, 4 bladder) were counted at the bench by AO/PI before and after a single LeviCell run with the LeviSelect Cell Debris Depletion Kit: about 40 minutes, label-free, no beads, columns or centrifugation shear. Ten samples were then prepared twice, as-is and levitated, with the Parse Evercode whole-transcriptome assay: 20 libraries, processed identically with split-pipe 1.9.0, compared pair by pair at matched depth across 21 quality metrics.

Bench results, 16 samples

- **Viability 52% → 75%** (median); +24 points per sample; colorectal median 47% → 81.5%; largest rescue 40% → 86%
- **89% of dead cells removed** (median, range 76–99%, 15 samples); optical debris roughly halved, 30.7% → 14.9% of objects
- **Samples clearing a viability gate:** 70% gate 1 → 10 of 16; 60% gate 2 → 13; 50% gate 9 → 16

Sequencing results, 20 libraries

- **21% less ambient RNA** (6.45% → 5.09%), 16–21% lower at every cutoff, 9 of 10 pairs, p = 0.004; the most contaminated sample fell 68% → 32%
- **6× fewer high-confidence doublets** (0.42% → 0.07%, p = 0.020), lower in all nine detected populations despite denser well loading
- **Biology unchanged:** 85 of 100 top marker genes carry over; pseudobulk agreement 0.852 against a 0.854 technical ceiling; dividing cells retained (35% → 40% in S or G2/M)
- **Kit protocol:** T/NK share 12.5% → 24.0%, B/plasma 7.4% → 12.6%; fibroblasts and endothelium depleted whole, not lysed. Run LeviCell without the kit to keep every population.

What it means for budgets

Illustrative model on US core and list-price benchmarks. A fully loaded sample costs about $5,700 to turn into data: $2,000 procurement, $300 thaw and QC, $2,250 library prep, $750 sequencing, $400 analysis, plus a $350 dead-cell kit or sort step that a $10 LeviCell consumable replaces. At a hard 70% viability cutoff, a below-gate sample is a write-off.

The same 16 samples, hard 70% cutoff	Without	With LeviCell
Samples bought, thawed, prepped, sequenced	16	**16**
Sequencing-ready datasets	1	**10**
Written off after QC	15	**6**
Total study cost	$96,800	**$91,360**
Cost per sequencing-ready dataset	$96,800	**$9,136**

Ten times the datasets from the same tissue, for about the same spend: one tenth the cost per dataset. If a lab salvages half of its below-gate samples instead, banking 16 good datasets takes 31 samples without levitation and 20 with it ($187,550 → $114,200; $11,720 → $7,140 per dataset, −38%). Downstream cost per usable cell: $0.65 → $0.45 (−31%).

Beyond the spreadsheet

- A consented patient sample that fails QC cannot be re-ordered; levitation puts it in the study instead of the freezer.
- Sourcing a replacement takes weeks to months. Here, four to five more of the same 16 samples became usable datasets.
- A 40-minute walkaway run replaces an hour or more of bead kits, spins and sorter time, with no core-facility queue.

> **What didn't improve.** Two of 16 samples did not gain viability: Lung 1 was flat (53% → 52%); Bladder 2, a 38,000-cell input with 97% debris, fell 80% → 50% and sat below what bench counts could measure reliably. A confirmatory same-run study is in progress, with a kit-free arm planned.

Request a quote or the full dataset: sales@levitasbio.com · levitasbio.com

Study conducted by Discovery Life Sciences on Discovery dissociated tumor cells; analysis by LevitasBio. Viability and removal data: AO/PI counts, n = 16. Sequencing: internal paired study, n = 10, Parse Evercode WT, depth-matched unfiltered matrices, 21 quality axes; confirmatory study in progress.

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