Creative Proteomics

Why Creative Proteomics for Olink Explore HT

Audit-Ready QC, Bridging Expertise, Multi-Omics Integration, and Predictable Delivery

A pilot-to-scale decision package for biopharma translational biomarker teams (RUO).

Cross-batch comparability you can audit - so pilot results still hold at scale

Bridging-first comparability Designed bridge samples + plate discipline + diagnostics to prevent cohort drift.	**Audit-ready QC gates** Explicit pilot thresholds, pass/fail decisions, and corrective actions-documented.
Predictable milestone delivery 172 vs 600 planning with checkpoints, rerun buffers, and SLA-ready definitions.	**Multi-omics-ready outputs** NPX aligned to metadata + model-ready exports +optional integration deliverables.

Best-fit quick guide

- n > 5,000: HT at scale with bridging continuity and rolling releases
- n = 500-1,500: milestone batching + early QC gate to de-risk scale
- Pilot validation: replicate-forward design + go/no-go memo

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Why Olink Explore HT Projects Fail in Scale-Up (and How to Prevent It)

Most failures are not caused by "insufficient coverage" or "sequencing speed." They happen when unmodeled technical structure - plate effects, batch effects, and preanalytical drift - starts to dominate biology as sample counts and run counts grow. Pilot [1] scale: issues that look minor at n=80 can invalidate conclusions at n=800.

Common failure modes

- **Plate/batch effects accumulate:** false clusters emerge across runs and timepoints
- **Near-LOD targets destabilize:** CV increases and missingness rises in subsets of samples
- **Preanalytical drift amplifies:** processing window, freeze-thaw, storage and shipping affect detectability and call rate
- **Metadata inconsistency blocks interpretation:** stratification, covariate adjustment, and integration break downstream

Prevention summary

- Bridging by design (not after the fact)
- Audit-ready QC gates with explicit thresholds and corrective actions

Pilot vs Scale-up: Batch Effect Emergence(Illustrative)

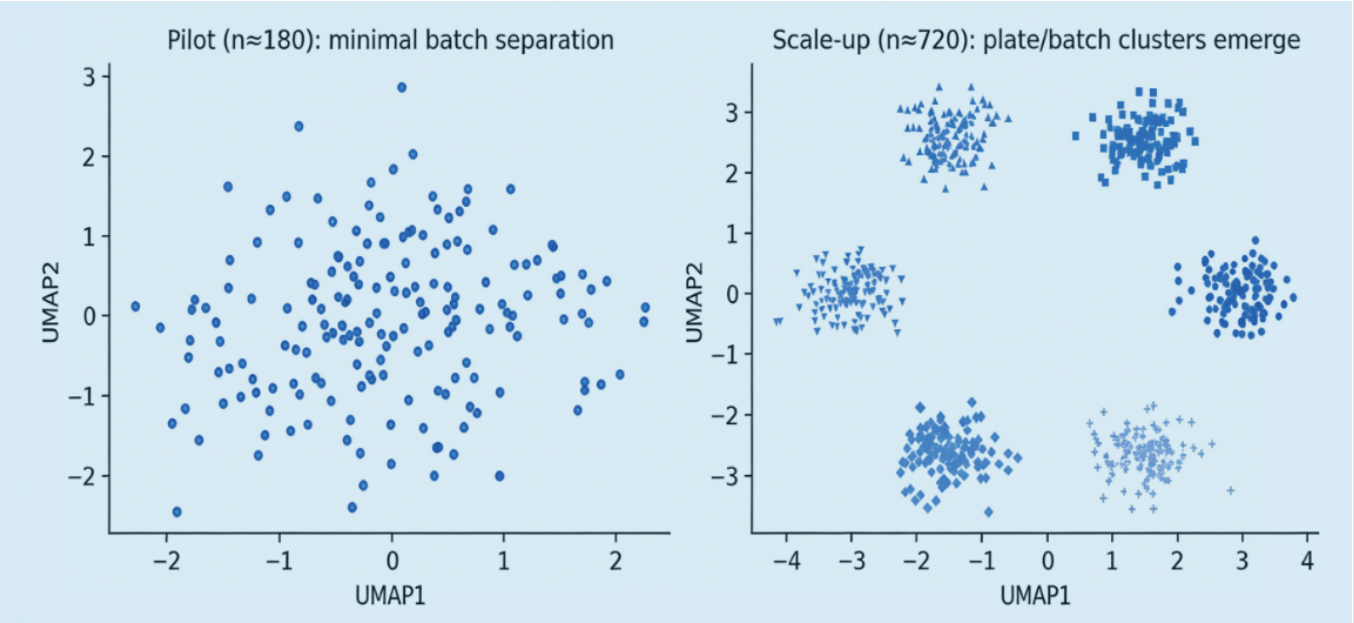

Figure 1. Pilot vs Scale-Up: Batch effect emergence (illustrative PCA/UMAP). Shows minimal clustering in a small pilot but clear plate/batch separation at scale when bridging is absent or underpowered.

Risk factor	Expected impact
Preanalytics variability	Call rate , missingness
Freeze-thaw burden	Near-LOD dropouts , CV
Weak plate randomization	PCA/UMAP plate separation
Near-LOD targets	Assay-level CV , replicate discordance

Learn more about our Olink proteomics services.

Bridging Expertise That Protects Cohort Integrity

Cross-batch comparability is not a promise - it's a designed control system. We implement bridging as an executable SOP with measurable diagnostics and documented decisions, so cohort-wide comparisons remain stable across plates and runs.

Bridging SOP (4-step mini workflow)

- **1) Bridge sample strategy:** Defined bridge samples per batch, placed in consistent positions across plates.
- **2) Plate layout discipline:** Controls + bridges positioned to support QC and harmonization diagnostics.
- **3) Locked randomization:** Randomization seed + script (or equivalent reproducibility artifact) locked before execution.
- **4) Centering/normalization loop:** Batch-aware processing paired with diagnostics to confirm residual structure is minimized.

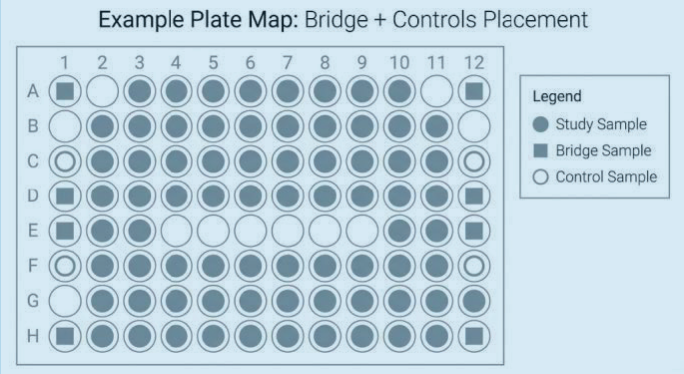

Figure 2. Example plate map schematic (bridge + controls placement).

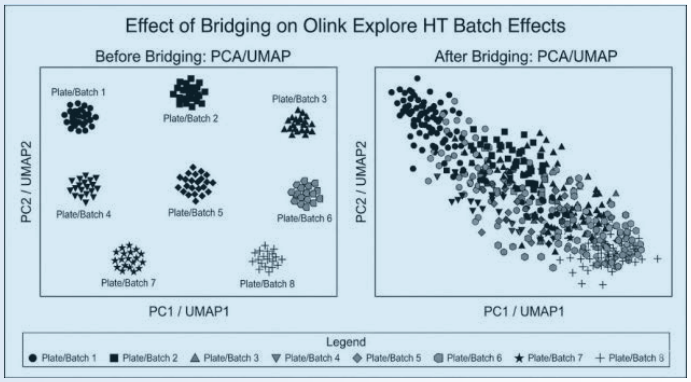

Figure 3. PCA/UMAP before vs after bridging (illustrative).

Evidence you will see

- Bridge-sample correlations reported as distributions (per batch and overall)
- Post-normalization PCA/UMAP shows no systematic plate-driven clustering
- Variance attribution confirms batch is not the dominant driver after harmonization

Audit-Ready QC Gates: Rubric, Thresholds, and Actions

We convert QC from a discussion into a decision. The rubric below defines pass thresholds for a pilot and the corrective actions used when a metric fails.

Protein Labeled Quantitative	Metric/Check	Pass threshold (pilot)	Typical action if fail
Platform performance	Intra-assay CV (Sample Control triplicates)	≤20%	Investigate outlier assays; check near-LOD effects; consider assay-level exclusions or re-run
Platform performance	Inter-plate CV (Sample Control across plates; cohort duplicates)	≤30%	Revisit normalization; confirm control-based centering; consider bridging; re-run suspect plate
Platform performance	Per-sample call rate	Median≥70% assays above LOD	Review LOD basis; exclude poor-quality samples; assess preanalytics and internal controls
Preanalytics & harmonization	Internal/external control checks	All within expected ranges; no failed plates	Re-run failing plates; audit pipetting/reagents
Preanalytics & harmonization	Post-normalization plate separation	No systematic plate clustering in PCA/UMAP	Re-check centering/bridging; adjust normalization strategy
Biological signal	Sentinel pathway directional-ity and effect sizes	Plausible directionality; consistent with prior	Revisit cohort balance; increase n for weak strata; reassess pathway targets

If fail, then...

Investigate → Isolate → Correct → Document

- identify outlier assays/samples/plates
- determine whether root cause is near-LOD, preanalytics, or
- technical artifact
- re-center / adjust harmonization / re-run where warranted

record decisions in an audit-ready memo

Variance Attribution After Harmonization (Example)

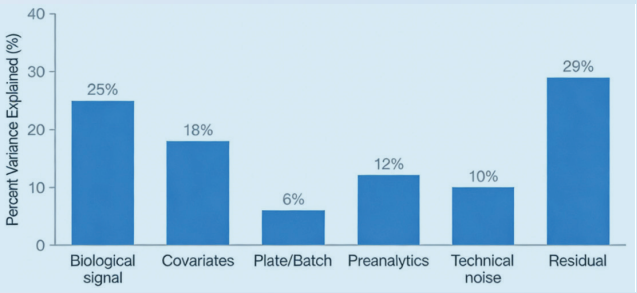

Figure 4. Variance attribution after harmonization (example).

Predictable Turnaround Without Guesswork: 172 vs 600 Samples

Timelines fail when providers plan as if reruns and batching do not exist. We plan execution as a milestone pipeline with checkpoints and buffers - so progress and risk are visible early.

Milestone pipeline: Intake QC → Plate map & randomization lock → Run execution (NGS) → Run completion → NPX + QC gate → Analysis & reporting → Final delivery

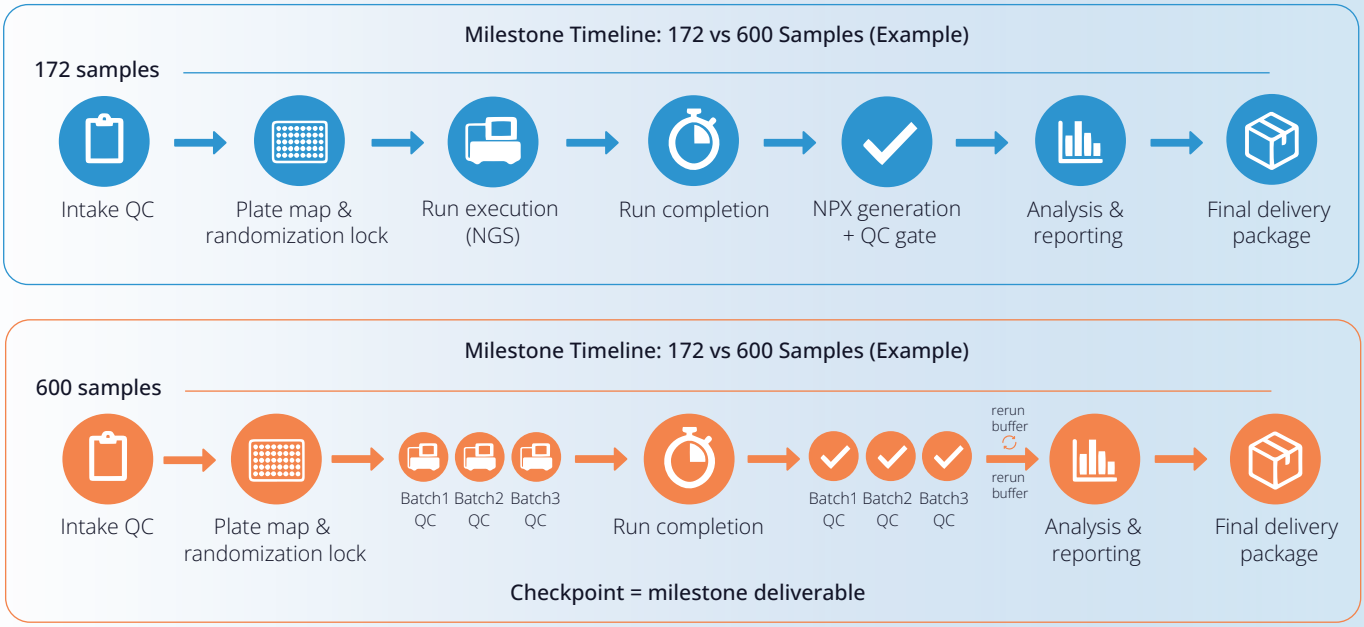

Figure 5. Milestone timeline (172 vs 600) with checkpoints and rerun buffers (illustrative).

Operational KPIs aligned at project start (example)

- **Intake QC completion:** % of samples passing intake verification (volume, matrix, condition, metadata completeness)
- **First-pass QC rate:** % of plates/batches meeting QC gates without rerun
- **Rerun triggers (pre-defined):** explicit conditions that initiate investigation and rerun (e.g., failed control ranges, abnormal plate-level metrics, residual plate clustering)
- **SLA-ready "on-time delivery":** delivery within the agreed milestone window, excluding client-driven delays, and including documented rerun buffer handling

Deliverables by Default: What Your Team Receives

High-quality Olink Explore HT support is measured by what your internal teams can do the same day the package arrives: QC review, modeling, and stakeholder-ready reporting - without chasing missing files.

Data

- Annotated NPX matrix (study-ready format)
- Read-level QC summaries and sequencing run metrics (and assay count summaries where applicable)

QC & Harmonization

- QC dashboards (CVs, call rates, missingness, control tracking, plate/batch diagnostics, PCA/UMAP)
- Bridging/harmonization documentation (plate maps, randomization artifacts, bridging report with decisions)

Reproducibility assets

- Version notes and parameters
- Signed pilot decision memo (when pilot gating is used)

Integration-ready outputs

- Metadata codebook / data dictionary (covariates, endpoints, batch fields, sample lineage)
- Export-ready, model-ready tables aligned to your analysis plan

Optional add-on modules

- Statistical discovery: differential proteins, covariate models, multiplicity control
- Mechanistic analytics: pathways, networks, module summaries
- Multi-omics integration: joint modeling deliverables and reproducible notebooks

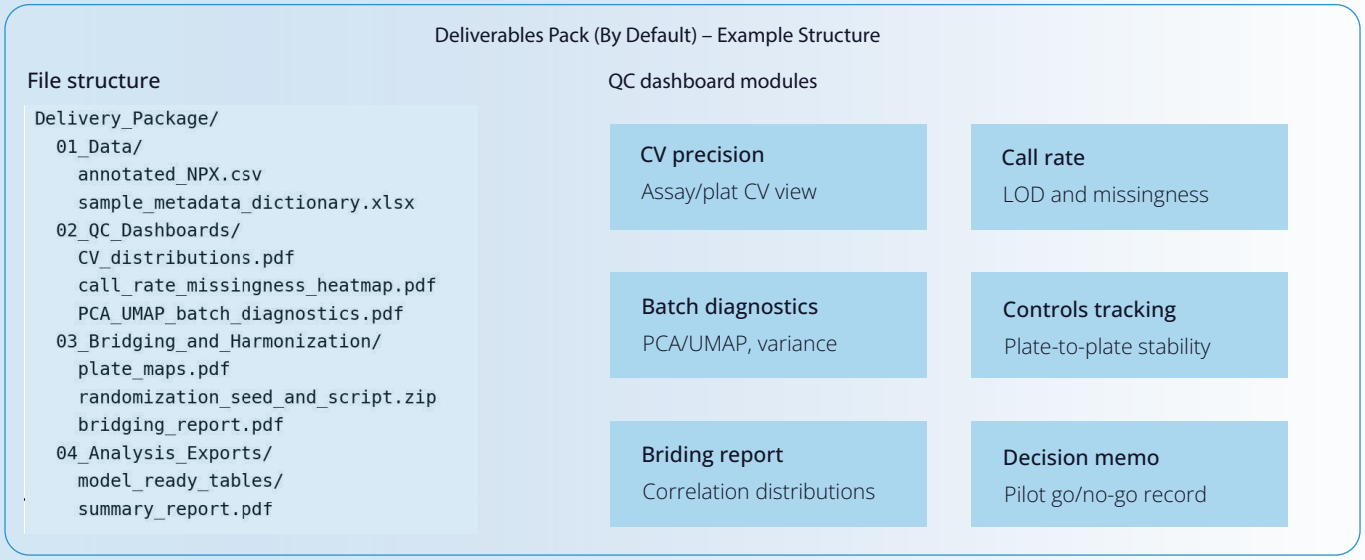

Figure 6. Deliverables pack schematic (dashboard modules + folder structure).

Multi-Omics Integration: Turning HT Signals into Mechanism and Action

Multi-omics is valuable when integration is planned, batch-aware, and reproducible. We align NPX with metadata and deliver model-ready exports so genomics and metabolomics can be incorporated without reformatting or rework.

The questions this supports

- arget prioritization: which proteins are plausible drivers vs correlated markers?
- MoA support: do pathways align with genetics, transcriptomics, or metabolic context?
- Patient stratification: which proteomic signatures define response subgroups?

What makes integration "real"

- Harmonized IDs + metadata schema designed for joint modeling
- Batch-aware exports (bridging diagnostics carried into integration tables)
- Reproducible notebooks + model-ready deliverables

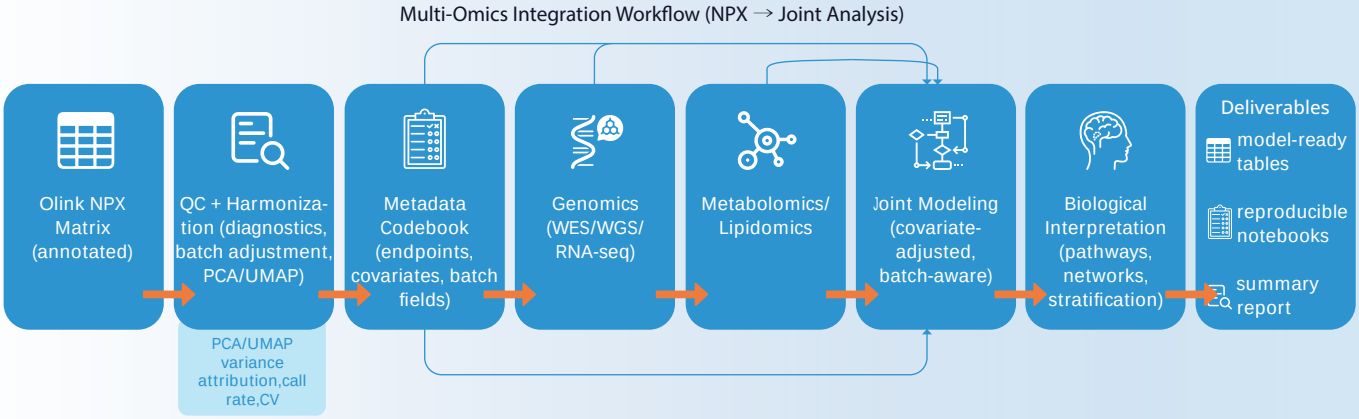

Figure 7. Multi-omics integration workflow (NPX ® harmonization ® joint analysis).

Example Multi-Omics(Illustrative)

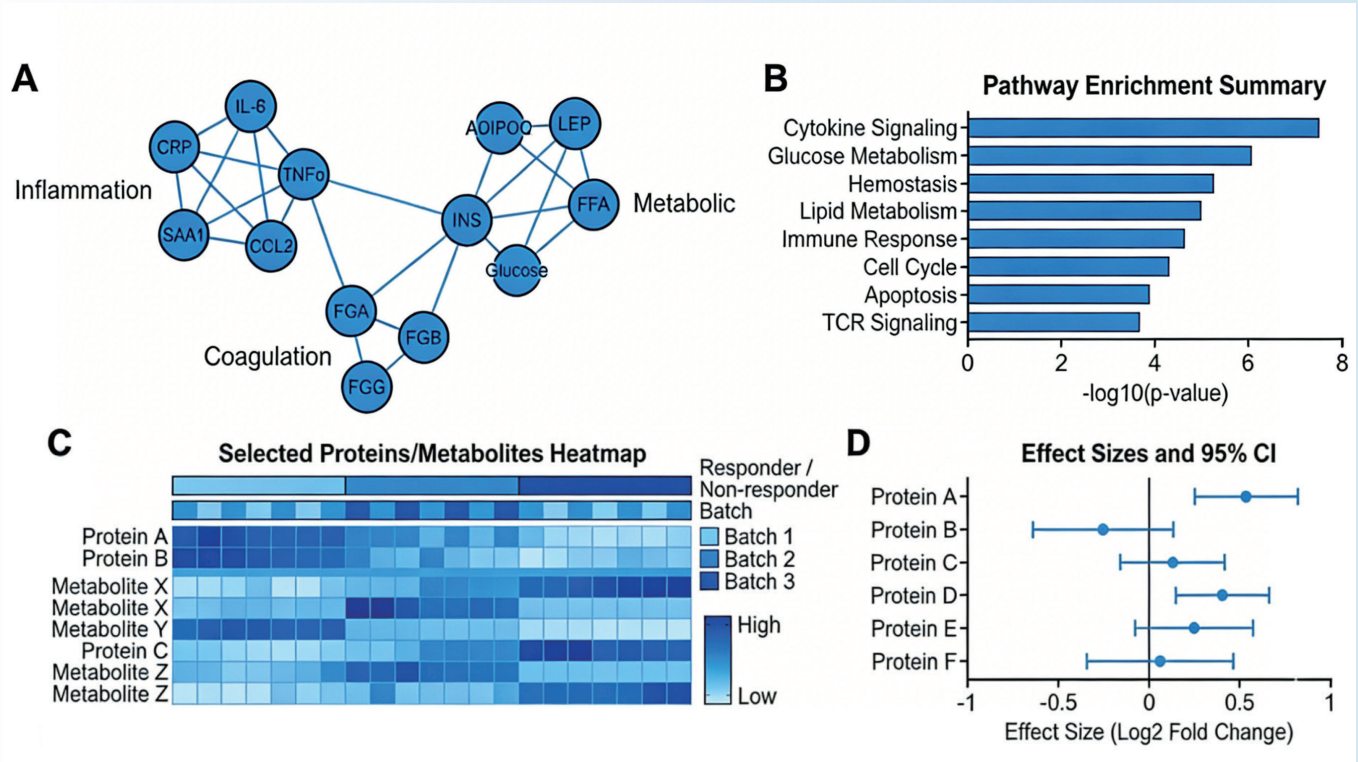

Figure 8. Example outputs panel (network, pathway enrichment, multi-omics heatmap, forest plot).

Choose the Right Engagement Path (Pilot → Scale-Up)

Path	Typical cohort size	Batch strategy	QC gates (examples)	Default deliverables	Best fit when...
A. Large discovery scale-up	n > 5,000	Rolling batches; scheduled releases	Stable CVs; no plate clustering; acceptable call-rate; bridging within band	NPX + QC dashboards + bridging report + randomization artifacts + run QC + data dictionary + model-ready exports	Population-scale discovery requiring cohort-wide comparability
B. Mid-size cohort	500–1,500	Planned batches with milestones/buffers	Pilot QC gate before full scale; clean plate/batch diagnostics; sentinel sanity checks	Same default package; optional discovery module	Predictable execution and audit-ready QC documentation
C. Pilot / iterative validation	≤500	Small batches, fast feedback loops	Priority proteins above LOD; acceptable precision; no plate separation; go/no-go memo	Default package + signed decision memo	Rapid learning before committing to scale

Decision Tree: Choose Your Pilot → Scale-Up Path

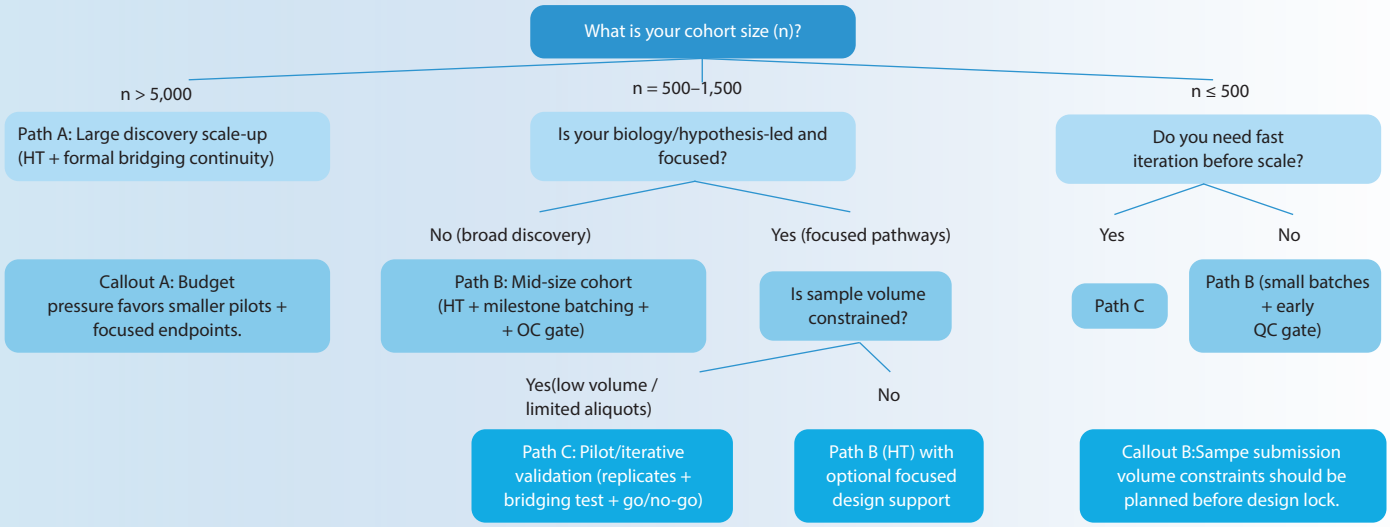

Figure 9. Decision tree: choose a pilot-to-scale pathway based on cohort size and constraints.

Getting started: intake checklist (what we need from you)

Item	Provide
Sample matrix & tube type	Plasma/serum/CSF; anticoagulant; processing window
Submission volume & aliquots	Available volume per sample; aliquot plan and reserves
Freeze-thaw & storage history	Freeze-thaw count; storage temperature; shipping constraints
Endpoints & covariates	Primary endpoints; key covariates; batch fields; timeline milestones

Pilot Design Template: Replicates + Bridge Samples + Randomization

Pilot cohort selection → Randomization & plate map lock → Bridging + QC gate → Scale-up decision

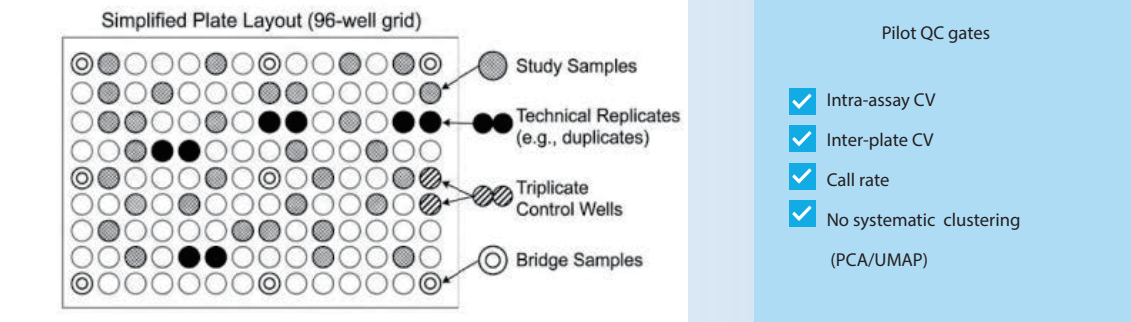

Figure 10. Pilot design template: replicates + bridge samples + randomization (illustrative).

Request a Study Plan & Analysis Quote

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