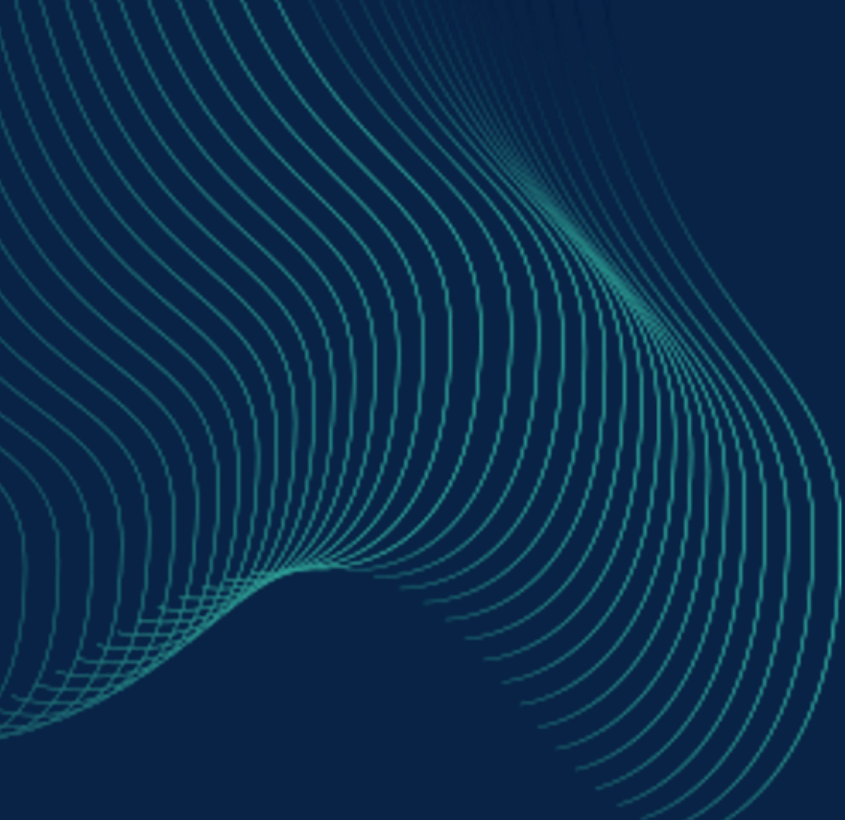




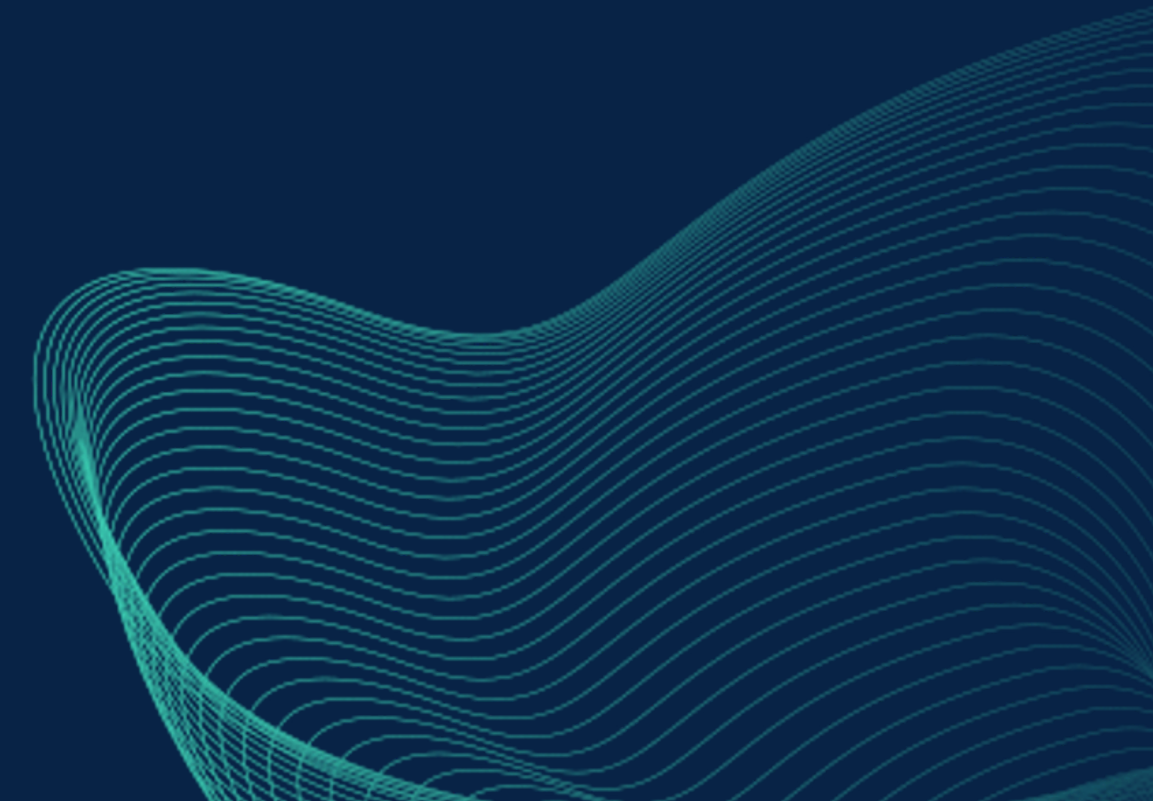
biostate.AI

RNA-seq Services

Contact : +1-7134899827

Email : rachan.raj@biostate.ai
contact@biostate.ai

Website : www.biostate.ai



RNA-SEQ SERVICES

Advanced • Affordable • Scalable Transcriptomics

Our Customers

Academia



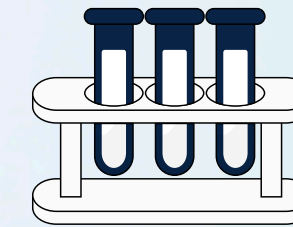
27,000 NIH-funded PIs

Biopharma



\$43B/yr Pre-clinical R&D budget

Biorepositories



10M+ banked samples



1 - Samples shipped



2 - Library Preparation



3 - Sequencing



4 - Data Analysis



5 - Data Delivery

WHY RNA-SEQ MATTERS ?

RNA-seq is foundational for modern biology — remains costly and difficult to scale. RNA sequencing enables



01 Gene expression profiling



02 Differential expression & pathway discovery



03 Biomarker identification



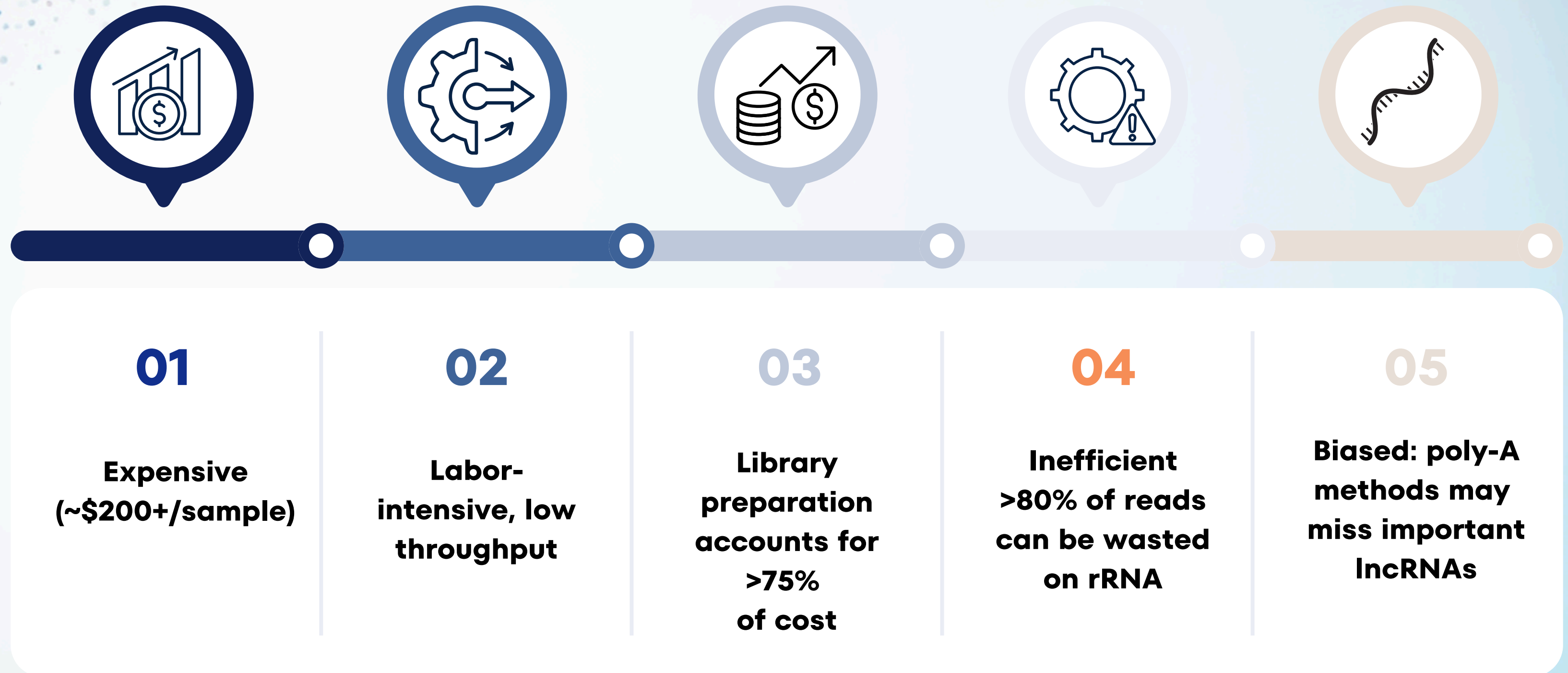
04 Translational & clinical research applications



05 Drug target discovery and therapeutic development

The Problem with Traditional RNA-seq

Traditional RNA-seq workflows are:



BIRT + PERD vs Traditional Poly(A) RNA-seq

Workflow and Technical Differences

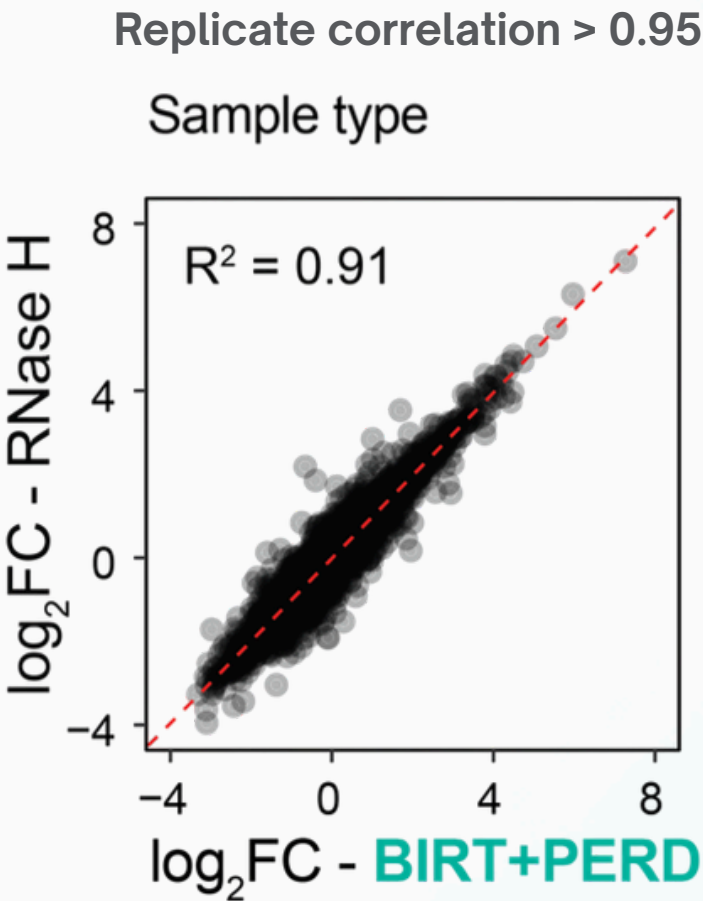
BIRT (Barcode-Integrated Reverse Transcription) + PERD (Probe-Enabled RNA Depletion)

CAPABILITY	POLYA SELECTION	BIRT + PERD
RNA Capture Method	Oligo(dT) — 3' end only	Random priming — full length
Non-coding RNA Detection	✗ Not captured	✓ Full coverage (lncRNA, etc.)
Ribosomal RNA Removal	Via poly-A enrichment	Probe-based depletion (99.8%)
Minimum RNA Input	100–500 ng	As low as 10 ng
FFPE / Degraded Samples	✗ Severe bias & data loss	✓ Optimized (accepts RIN > 2)
Transcript Coverage Uniformity	3' bias in degraded samples	✓ Even full-length coverage

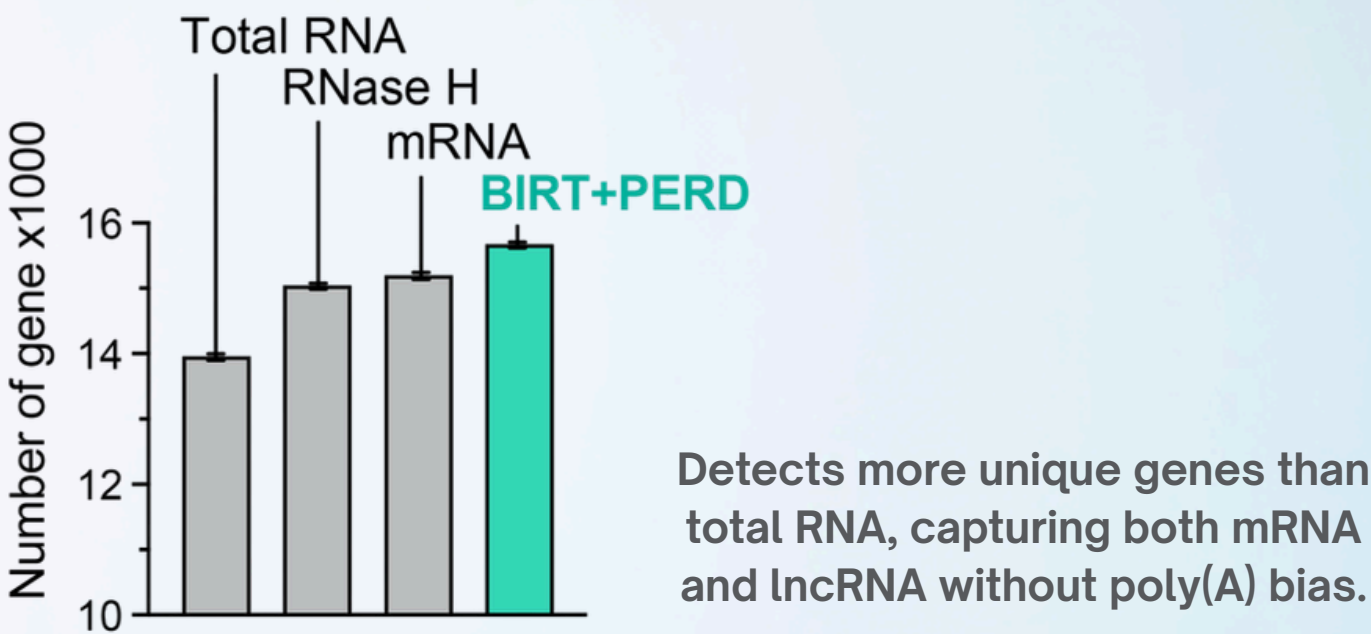
BIRT + PERD: Lower input · Broader capture · Even coverage · Faster workflow · From \$60/sample

Why Biostate AI is Better?

A - Reproducibility

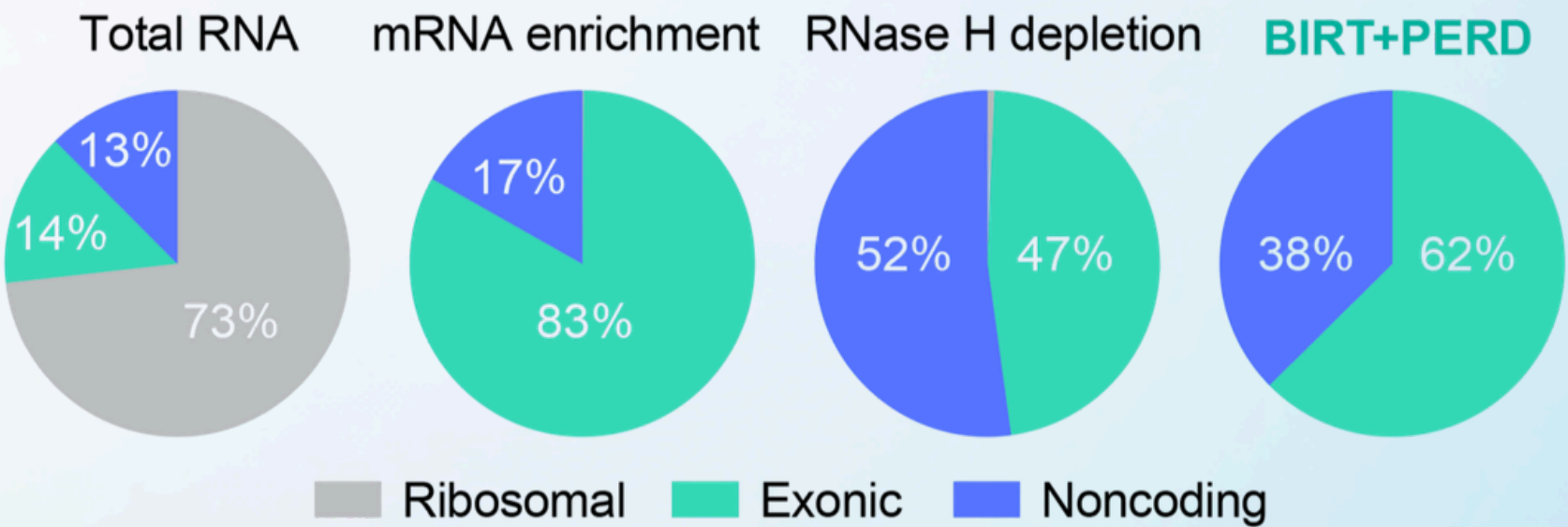


B - Broader Transcriptome Coverage



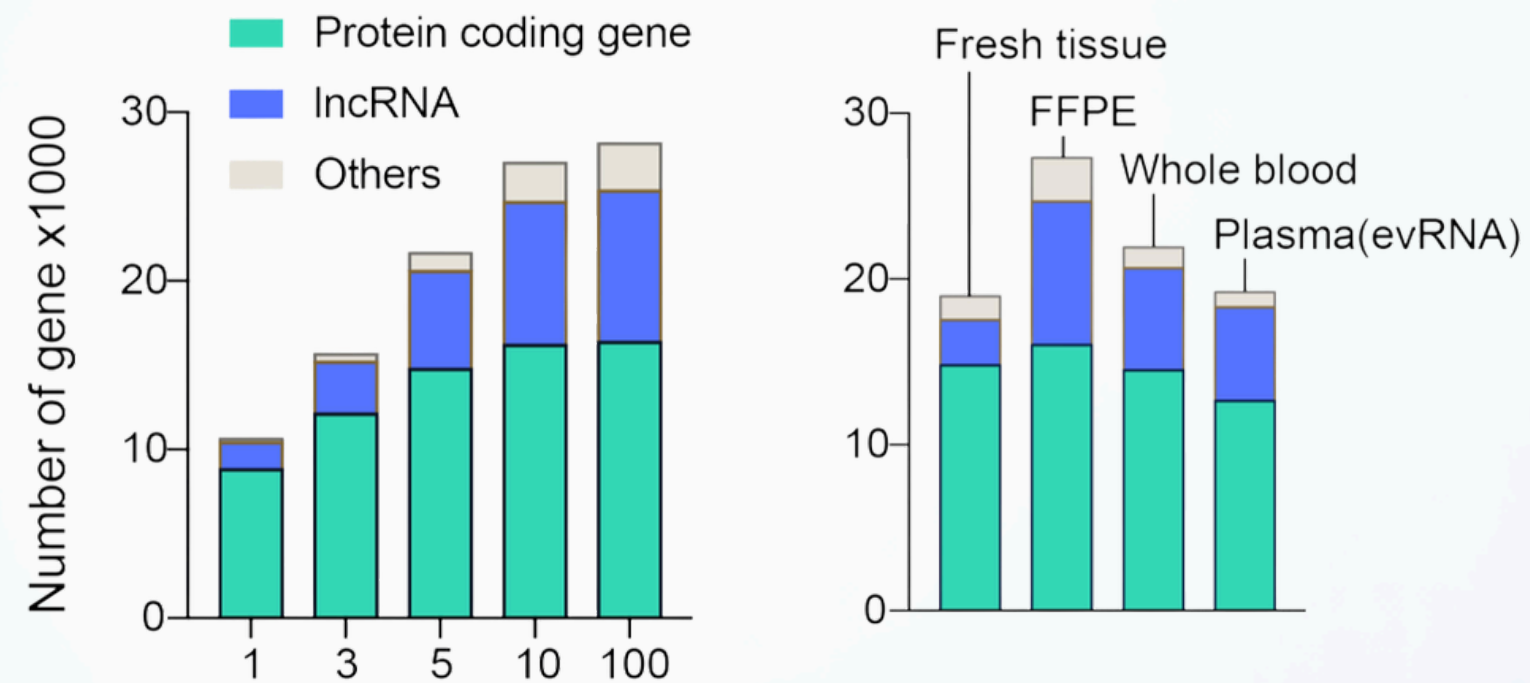
C- Efficient rRNA Depletion

Especially effective for challenging samples like blood, where high globin and rRNA content can otherwise reduce data quality



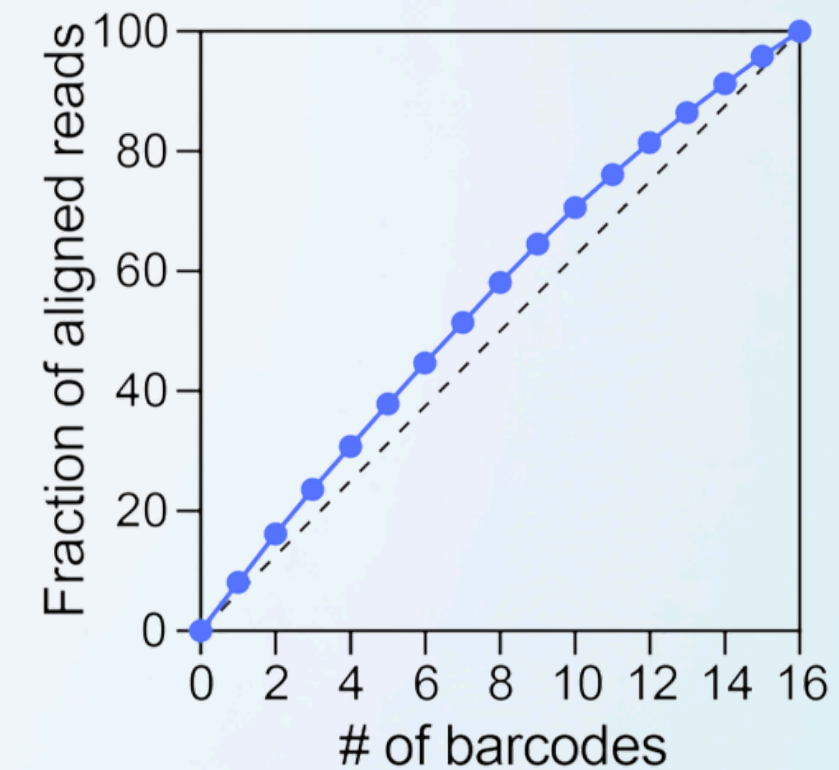
Why Biostate AI is Better?

Works with Challenging Samples



Compatible with degraded RNA (RIN > 2), requires as little as 10 ng input, and optimized for challenging samples including FFPE, blood, and plasma

Scalable Multiplexing Without Bias



Early pooling of 16–24 samples minimizes batch variability and drives significant cost efficiency

Biostate AI's Pricing Structure

STANDARD SAMPLES

Best for stable, cost-efficient workflows

\$60

per sample

INCLUDES:

- Cultured Animal Cells (>30k cells)
- Extracted RNA (Mammalian)

REQUIREMENTS:

- Conc. $\geq$ 16 ng/ μ L (min 10 μ l)
- RIN $\geq$ 7 (If QC available)

SPECIALTY SAMPLES

For complex inputs & clinical specimens

\$110

per sample

INCLUDES:

- Specialty and low-concentration RNA (evRNA, cfRNA)
- Biospecimens and clinical samples, (whole blood, plasma, serum, PBMC, tissues, FFPE)
- Unusual organisms (plants, octopus, axolotl, ...)

REQUIREMENTS:

- Minimum 3 ng input
- Accepts Degraded RNA (RIN 2-7)
- Bulk Discount: 100+ samples (Ask us)

Biostate AI – Additional Services

1. EXTRACTION SERVICES

Blood/PBMCs **\$20**

Tissue / FFPE / Other **\$60**

2. SEQUENCING ADD-ONS

+10 Million Reads **\$10**

Complementary Package (BioA) **\$15**

Paired-End 150bp available on request

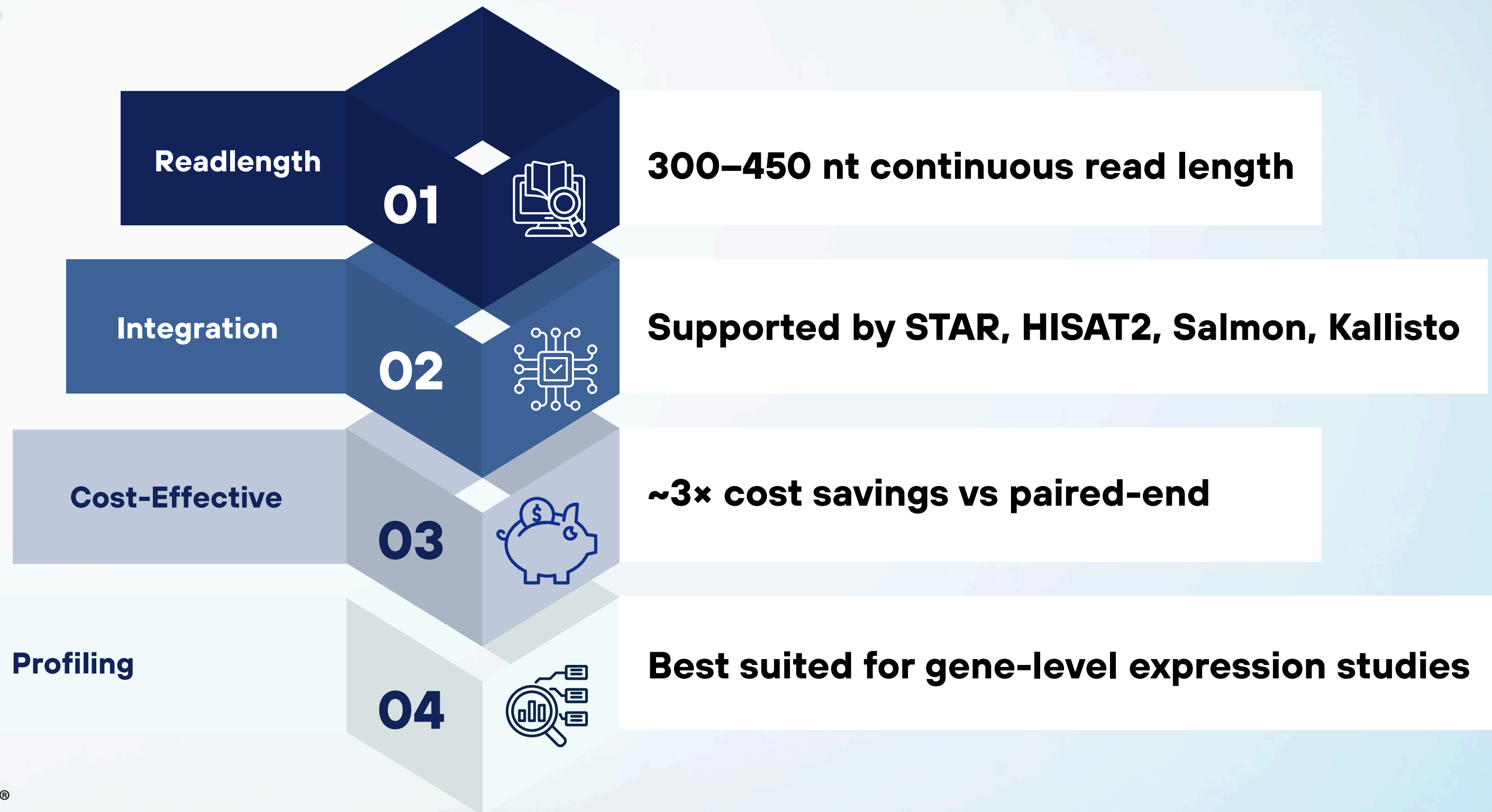
3.3. TURNAROUND AND SPECIFICATIONS

Standard turnaround **3-6 WEEKS** (SE: 5-6 weeks; PE: 3-4 weeks)

Rush service available on request

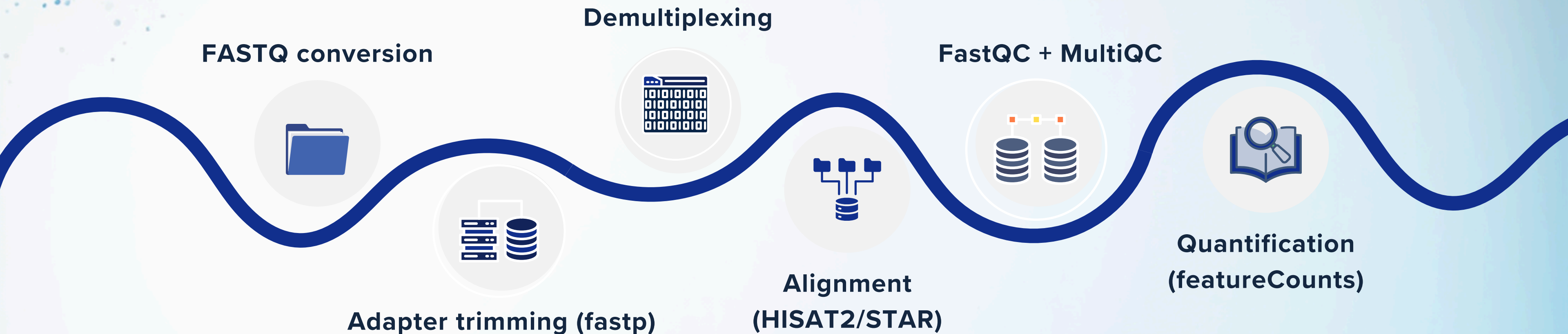
Why Single-End (SE) is Often Optimal

Use savings to increase biological replicates.



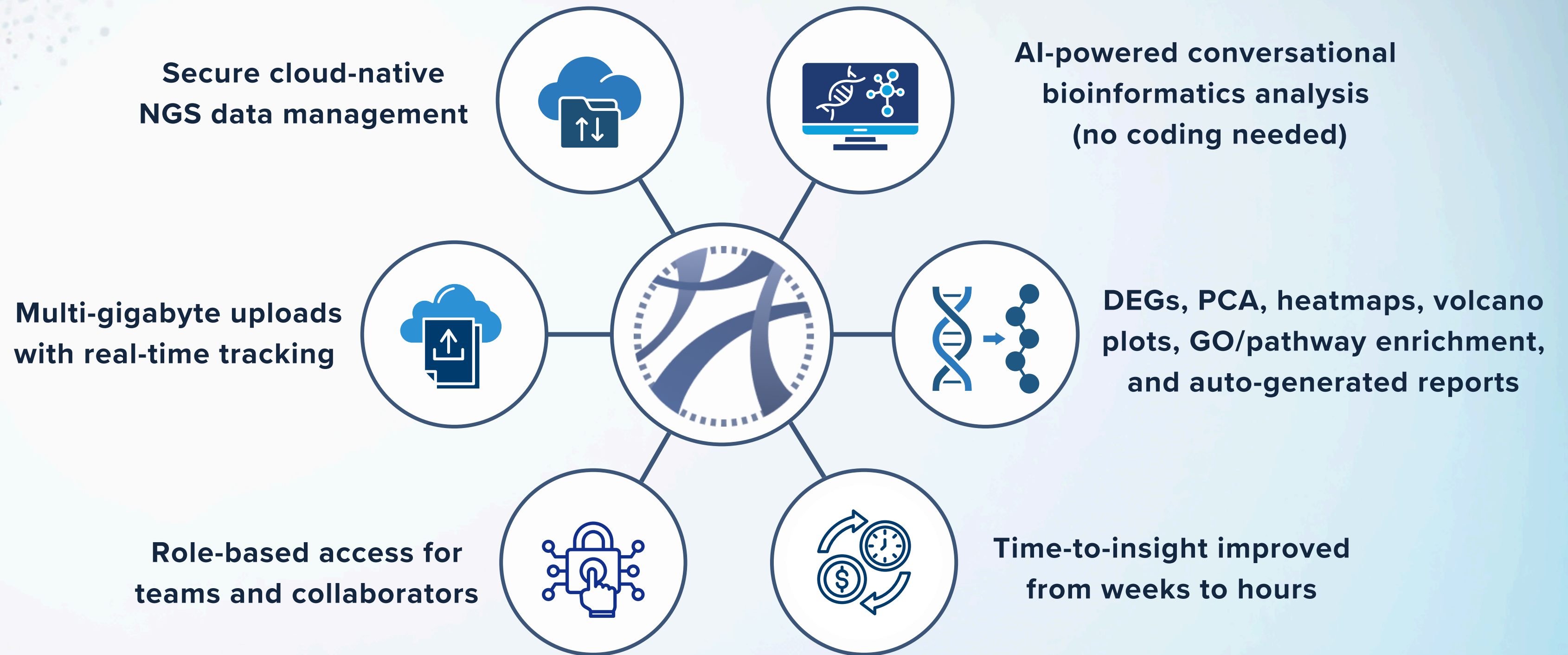
End-to-End Bioinformatics Pipeline

Biostate AI provides a complete standardized workflow



Delivered via OmicsWeb: raw FASTQ files, aligned gene count matrices, filtered protein-coding matrices
with free access to Omicsweb - Our AI bioinfo platform to support bioinformatics analysis

OMICSWEB + COPILOT PLATFORM



Ready to start your RNA-seq project?

We handle everything from sample receipt → sequencing → analysis → delivery.

Get the Quote! 



contact@biostate.ai



+1-7134899827



www.biostate.ai

www.biostate.ai/get-quote

Appendix

Biostate AI - Solution

BIRT + PERD: A New RNA-seq Paradigm with Robust performance across sample types.

BIRT - Barcode-Integrated Reverse Transcription

01

Barcodes added during first-strand synthesis

02

Samples pooled immediately after RT

03

Up to 16× throughput increase, Ideal for FFPE, Degraded RNA. Large cohort studies

04

Reduces labor and reagent consumption

05

Enables processing of low-input samples (~10 ng)

PERD - Probe-enabled RNA Depletion

01

Enzyme-free depletion of excess RNA

02

Up to 99.8% rRNA reduction

03

Compatible with pooled workflows

04

Captures noncoding RNA more effectively than mRNA enrichment

05

Enables broader transcriptome coverage - mRNA, lncRNA, other long RNA species

BIRT + PERD vs Traditional Poly(A) RNA-seq

Performance and Data Quality Comparison

Dry-lab metrics	NEB-mRNA	NEB-rRNA	BIRT-PERD-v3
Q30	94.3%	91.9%	92.4%
Adapter rate	5.4%	8.6%	9.1%
Mapping rate	97.5%	95.1%	93.2%
Exonic Percentage	86.3%	50.5%	46.8%
Intronic Percentage	11.2%	46.8%	46.0%
Replicates Correlation	> 0.95	> 0.95	> 0.95
Duplication rate	10.5%	16.4%	15.9%

Why Single-End Reads Are a Better Choice

For RNA profiling, single-end (SE) sequencing offers key technical advantages over paired-end (PE)- not just cost savings. Here's why SE is the optimal choice for most applications.

Advantage 1 : Superior Read Length

SE sequencing delivers **300-450 nt reads** from a single direction, providing ample coverage for gene expression profiling.



Advantage 2 : More Reliable Mutation Coverage

When detecting mutations, **SE provides consistent coverage from a fixed starting point.** PE reads start from both ends with variable insert sizes, meaning the middle region coverage is unpredictable.



Advantage 3 : Proven & Widely Adopted

Thousands of published RNA-seq studies use SE data. All major bioinformatics pipelines (STAR, HISAT2, Salmon, Kallisto) handle SE reads seamlessly. SE is the industry standard for expression profiling.

Advantage 4 : Its More Cost Effective

Our sequencing technology has been optimized for single-end reads, allowing us to offer SE at a significantly lower cost.

SINGLE-END (Included) \$1 / 1M molecules Extra depth: +\$10 / 10M reads	3x savings	PAIRED-END \$3 / 1M molecules Extra depth: +\$30 / 10M read pairs
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