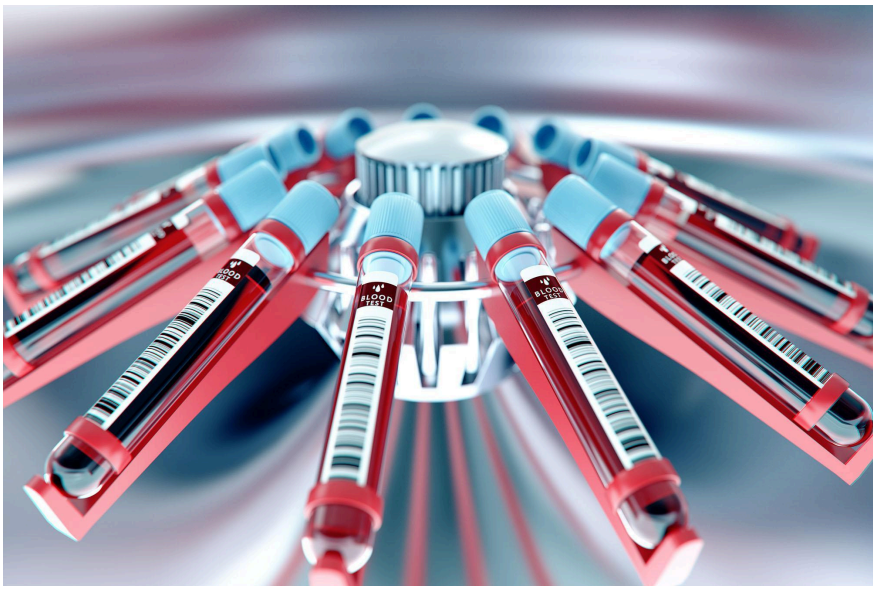
Liquid Biopsy Labs

Next-Generation Sequencing and Laboratory

Frequently Asked Questions



Accurate, Comprehensive, Fast.

***Always* Ahead of the Curve.**

Table of Contents

About Liquid Biopsy Labs

Precision oncology represents one of the most advanced approaches to understanding cancer biology today. By analyzing the molecular characteristics of tumor samples, Liquid Biopsy Labs aims to provide detailed molecular data that may assist physicians and researchers in understanding tumor biology.

Our mission is to provide high-quality molecular testing and comprehensive analysis that supports scientific understanding of cancer biology.

Liquid Biopsy Labs' early cancer detection and treatment monitoring tests were developed as a result of the experience of our co-founders, Alex Rolland and Michelle Morand, who worked for many years prior as personalized cancer researcher and patient advocate, respectively.

This is why our tests focus on covering as many cancer-related genes as possible and with the highest accuracy. Every test offered by Liquid Biopsy Labs was researched, designed, and developed in-house to meet the unique needs of each patient that Alex and Michelle have worked with over the years. And now these highly accurate and specialized oncogenomic tests are available to you.

Every element – from whole-transcriptome RNA sequencing to DNA sequencing to our analytical reporting – is designed to generate high-resolution molecular data that can support scientific understanding of tumor biology and be reviewed by licensed physicians and/or research scientists within the context of patient care, medical science, research, and/or other related oncogenomic endeavours.

We believe that every researcher and lab facility deserves to benefit from the same technologies and insights that drive global cancer breakthroughs.

As research evolves, so will our methods. Liquid Biopsy Labs continues to collaborate with leading laboratories, regulatory bodies, and oncologists worldwide to ensure that molecular testing technologies continue to advance responsibly.

We remain committed to transparency, accuracy, and compassion in everything we do – because every result, and every life, matters deeply to us.

Liquid Biopsy Labs provides molecular laboratory testing and technical genomic analysis. The laboratory generates molecular sequencing data and analytical reports based on the biological characteristics of the submitted specimen.

The laboratory does not diagnose disease, prescribe treatments, or provide medical advice. All clinical interpretation and treatment decisions remain the responsibility of the patient's licensed treating physician.

PART 1 – About Our Laboratory

Q: Where are the tests performed?

Lab & Address
Liquid Biopsy Labs
118-8337 Eastlake Drive
Burnaby, BC, V5M 4W2

Accreditation Status
Liquid Biopsy Labs is in the process of accreditation through the Diagnostic Accreditation Program (DAP) administered by the College of Physicians and Surgeons of British Columbia and continues to develop laboratory quality systems aligned with recognized ISO-based frameworks.

In the meantime, all laboratory workflows are conducted under the strict oversight of our Regulatory Affairs Department and in full adherence to ISO-aligned quality and procedural requirements. All assays are performed by highly trained PhD-level molecular scientists to ensure the highest standards of scientific accuracy and compliance.

Q: Which tests are run at your facility vs. external partners?

Our Burnaby, BC facility performs a full spectrum of advanced liquid-biopsy and tissue-based molecular diagnostics, including exosomal RNA (Liquid RNA/LRNA) testing with differential exosomal RNA expression analysis, tumor RNA sequencing, and complete NGS workflows – library preparation, templating, and sequencing – on the Ion Chef™ and GeneStudio™ S5 Prime platforms.

We also conduct in-house tissue DNA sequencing using Ion Torrent technology and perform liquid-biopsy ctDNA mutation detection through our Absolute Q digital PCR workflow. All results undergo rigorous bioinformatics processing, including full-transcriptome evaluation, STAT-1/STAT-2 algorithms, CPS computation, and targeted RNA/DNA variant interpretation, enabling precision oncology insights across 20,813 transcripts.

While we complete ISO 15189, ISO 13485:2016, and ISO 9001:2015 accreditation, patients or physicians may elect to have certain analyses performed through external accredited laboratories depending on the specific testing requested.

Q: How deep is your sequencing (reads) and why does it matter?

Depth / Reads
In sequencing, “reads” and “depth” refer to how many times each gene is measured during analysis. The more times a gene is read, the clearer and more reliable the picture becomes – much like zooming in with a high-resolution camera rather than looking at a blurry image. Although our platform measures expression across the entire transcriptome, the core clinical interpretation relies on a defined set of cancer-related genes used in our statistical models.

Each sample must meet a strict minimum of 2 million total reads to be accepted, which already ensures an average of ≈5,700 reads per clinically relevant transcript. In daily practice, however, our lab consistently generates several million reads per sample – often far above the minimum threshold – resulting in effective per-transcript coverage that commonly reaches 10,000 to 15,000+ reads for these key cancer-associated transcripts.

This is deeper than many sequencing workflows used for broader screening applications, where assays may operate at lower read depths depending on the design and objectives of the test. By generating thousands of data points per transcript instead of a few dozen, we achieve far more accurate quantification of the transcriptomic behavior, allowing our system to detect molecular signals – such as early changes in exosomal RNA expression or subtle oncogenic activity – that would be invisible to low-depth tests.

Why it matters
High sequencing depth is not just a technical advantage – it has direct, life-changing clinical implications. Cancer often reveals itself through weak, early, or low-abundance molecular signals: a slightly overexpressed gene in exosomal RNA, a low-frequency mutation, or a subtle shift in tumor-related biology.

Sequencing workflows that use lower read depths may have reduced sensitivity for detecting very low-abundance molecular signals depending on the analytical design of the assay. With 5,000 to 15,000+ reads per cancer-relevant gene in our workflow, we dramatically reduce the chance of false negatives and ensure that true biological events are accurately detected.

This depth stabilizes the STAT-1 and STAT-2 fold-change calculations, strengthens CPS scoring, and provides a clearer and more reliable assessment of tumor activity, treatment response, or residual risk. For patients and physicians, deeper sequencing can provide more stable molecular measurements that may assist physicians when reviewing molecular findings alongside other clinical information.

In short, our deeper sequencing provides a level of clarity and accuracy that empowers both patients and clinicians to make earlier, smarter, and more personalized oncology decisions.

PART 2 – Testing Specifications: DNA, RNA, Platforms

Q: What is the full specification of your DNA panel?

Our next-generation sequencing (NGS) tissue DNA panel provides a comprehensive, clinically focused genomic profile across approximately 550 cancer-associated genes (excluding gene fusions).

The panel includes all major oncogenes, tumor-suppressor genes, DNA-repair genes, cell-cycle regulators, and treatment-response markers, offering a broad and actionable view of the tumor's molecular landscape. This enables identification of driver mutations, resistance mechanisms, and pathway-level alterations that may provide molecular information for physician review within the broader clinical context.

To ensure high analytical sensitivity, our internal LBL workflow uses deep sequencing, routinely delivering thousands of reads per gene across this 550-gene panel. In practice, this means ~5,000 to 10,000+ reads per gene, depending on the sample and tumor content – depth levels that substantially enhance the detection of low-frequency variants and reduce the likelihood of false-negative results.

This is the same high-resolution philosophy used in our RNA and exosomal RNA workflows, ensuring consistency and reliability across all molecular analyses.

For patients who prefer to use our CLIA-certified partner, Fulgent Genetics, their DNA panel covers approximately 500 genes at a sequencing depth of roughly ~100 reads per gene, which meets standard clinical laboratory requirements. Sequencing depth and analytical parameters may vary between laboratories depending on the design and intended use of the assay.

In summary, our LBL DNA panel delivers broad gene coverage and deep sequencing designed to support comprehensive molecular analysis.

Q: What is the full specification of your RNA test?

Our RNA test is a comprehensive next-generation sequencing (NGS) transcriptome assay that measures expression across all 20,813 human genes using the Thermo Fisher AmpliSeq full-transcriptome panel. This provides one of the most comprehensive RNA expression profiles available for transcriptome analysis.

Every sample is required to meet a strict minimum of 2 million total reads, ensuring a reliable baseline of expression coverage; however, in routine operation, our laboratory consistently generates several million reads per sample, providing high-resolution expression data across the entire transcriptome.

This depth translates into thousands of reads per gene, with particularly rich coverage across the focused cancer-associated transcripts that anchor our STAT-1, STAT-2, and Combined Positive Score (CPS) analysis. These high coverage levels allow us to detect subtle changes in differential exosomal RNA expression, early tumor-related signals, and nuanced molecular activity that may be more difficult to detect in sequencing workflows designed with lower read depth.

Our RNA test is engineered to provide a robust, clinically meaningful expression profile rather than a broad but low-resolution snapshot. Because we sequence deeply across all 20,813 genes, we can distinguish true biological signal from background variability, capture faint gene-expression shifts that often precede radiologic or symptomatic changes, and deliver more stable and accurate STAT and CPS scores.

This makes the assay uniquely powerful for identifying changes in gene-expression patterns and molecular activity within tumor-related pathways, and generating molecular data that may be reviewed by physicians within the broader clinical context.

This makes the assay useful for identifying changes in gene-expression patterns and molecular activity within tumor-related pathways, generating molecular data that **may be reviewed by physicians within the broader clinical context**.

In short, our RNA test provides broad coverage and high-depth sequencing, **generating detailed molecular information regarding gene-expression patterns and tumor biology.**

Q: Why is whole-transcriptome RNA expression essential?

Whole-transcriptome RNA expression testing is essential because it reveals which genes are actually active, overactive, or dysregulated inside the tumor, providing a real-time picture of the cancer's functional behavior. DNA shows what could happen; RNA shows what is happening right now.

By measuring expression across all 20,813 human genes, we can identify the exact molecular pathways driving the cancer, determine which targets are biologically relevant, and understand how the tumor is responding – or not responding – to treatment.

This allows clinicians to select therapies based on active biology, not assumptions or broad guidelines.

Most laboratories that offer RNA testing focus on gene fusions or a limited subset of transcripts. While these approaches can provide useful information, they examine only a portion of the transcriptome and therefore capture a narrower set of gene-expression signals related to cancer biology.

Our whole-transcriptome approach captures the full expression landscape, enabling advanced differential exosomal RNA analysis, STAT-1 and STAT-2 algorithms, and CPS scoring that reflect real-time tumor activity with far greater precision. This depth of information is essential for modern precision oncology, where the most effective therapy is the one matched not only to a mutation – but to the actual biological drivers active in the patient's cancer at this moment.

Q: What platforms and instruments do you use?

We perform all of our sequencing on Thermo Fisher's Ion Chef™ automated system and the Ion GeneStudio™ S5 next-generation sequencer, a platform specifically selected for its ability to deliver high-depth, high-fidelity sequencing with exceptional consistency.

Our workflow is engineered to prioritize analytical sensitivity and depth, which is why we deliberately limit each run to a maximum of eight patient samples per batch. This controlled batching ensures that every sample receives the millions of reads required for deep coverage, allowing us to capture subtle gene-expression shifts, low-frequency variants, and early tumor-activity signals with far greater precision than high-throughput, low-depth workflows.

Different sequencing platforms are optimized for different analytical goals. Our laboratory utilizes the Thermo Fisher Ion Chef™ and GeneStudio™ S5 platform because it aligns with our sequencing workflow and analytical design.

Our platform choice reflects a strategic commitment: depth over volume, accuracy over throughput, and clinical precision over cost-cutting. By using Thermo Fisher's deep-sequencing architecture, we ensure that every patient receives the high-resolution molecular data required for truly personalized, evidence-driven cancer care – rather than the sequencing workflows designed for higher-throughput applications.

PART 3 – Testing Workflow: Validation, Reports, Timelines

Q: How do you ensure RNA accuracy (normal tissue comparison)?

While DNA analysis of tumor biopsy tissue, blood, or urine can identify whether a mutation is present, it does not indicate the degree to which that mutation is active or contributing to disease progression.

RNA analysis, in contrast, evaluates gene expression levels – providing insight into how actively specific mutations are being expressed. This allows clinicians to understand the relative significance of each mutation and its role among the primary drivers of a patient's cancer.

Because RNA-based testing focuses on expression levels, meaningful interpretation requires comparison against a reference. The quality and relevance of that comparison standard are critical to the accuracy and clinical value of the results.

There are several factors that distinguish the testing methodology used by Liquid Biopsy Labs and contribute to its precision and reliability.

One of those factors is that we ensure the highest possible accuracy in RNA expression analysis by using a unique, meticulously curated normal-tissue reference dataset that is unmatched in the sequencing industry. Unlike typical laboratories that rely on heterogeneous public databases or pooled reference sets, our baseline was created from carefully selected normal tissues, all prepared by the same expert pathologist using the same standardized protocols.

This level of uniformity eliminates the variability that commonly affects gene-expression baselines and provides a consistent, reliable comparator for evaluating differential expression in patient samples. It is this rigor in establishing a stable normal reference that allows our STAT-1, STAT-2, and CPS algorithms to detect even subtle deviations in exosomal or tissue RNA expression with exceptional precision.

Our analytical performance reflects this commitment to consistency and accuracy. Across our validated datasets, we achieve approximately 96% sensitivity and 92% accuracy, with many individual panels performing even higher. Although internal validation often demonstrates >98% analytical performance, we report conservatively to maintain full transparency and to ensure our results remain dependable and clinically trustworthy.

This conservative, evidence-driven approach – combined with a uniquely controlled normal-tissue dataset – positions our RNA test among the most accurate and reliable expression-based cancer tools available today.

Q: What reports will I receive and what do they include?

Depending on which services you hire our team to perform, you may receive:

- **Molecular Findings Report** (~10-20 pages): detailed breakdown of the genetics of your cancer, key molecular features, and summary of molecular findings and associated scientific literature.

- **Navigation Report** (~6-10 pages, delivered 2-3 days later): summarizing molecular pathways and relevant research findings, including comparative data on benefits, side effects, and access pathways.

    - Includes: Health Canada/FDA/EMA approval status, on/off-label indications, and relevant clinical trials (phase, eligibility, recruiting status).
    - We also identify private-pay access options and provide all raw sequencing data (your property).
    - Reports are shared with both the patient and their treating oncologist (at the patient's request).
    - Please note: Test results can be expedited for an additional fee.

Q: What's the turnaround time and payment schedule? What if a test fails?

Timeline: Typically 6-8 weeks from initiation to delivery of the Treatment Options Report.

Payments: 50% deposit to begin; remaining balance split into two instalments (at 3 weeks and 6 weeks, before the delivery consult).

If the sample is inadequate: We do not proceed with testing and charge only a small administrative fee (pathology review, shipping, etc.). This occurs in <1% of cases. If necessary, we pivot to blood-based DNA/RNA testing as a strong alternative.

PART 4 – Access & Coordination with Public System

Q: How will you coordinate with my oncologist and integrate with public care?

We are highly experienced in collaborating with standard-of-care oncologists, including places like BC Cancer.

Each option is ranked by evidence, safety, and accessibility.

Top options may include off-label therapies in Canada but approved elsewhere; we provide the regulatory details (FDA, EMA, Health Canada).

We also identify clinical trial opportunities and, when appropriate, connect you with international oncologists.

Patients are encouraged to share laboratory reports with their treating physicians so results can be reviewed in the context of their clinical care.

Q: How does Liquid Biopsy Labs differ from standard testing?

Standard testing typically examines ~20 genes to guide chemotherapy or immunotherapy and assess prognosis. Different testing programs may evaluate different molecular markers depending on clinical scope and program design.

In contrast, Liquid Biopsy Labs uses large DNA panels (550+ genes) plus whole-transcriptome RNA (20,813 genes) to identify more actionable targets with far greater confidence.

Even with just a Precision Second Opinion alone, we identify treatment options not mentioned to patients through standard care.

Q: Why doesn't the government or other testing companies do this?

We are here for *you* – your care, your best outcome. This level of thoroughness takes time and costs money. We provide patients with resources that standard-of-care pathology labs are not able to offer.

PART 5 – Costs, Funding & Practicalities

Q: What happens if the sample is too small or degraded? Will I be out the full fee?

If the sample is not large enough or is degraded, we do not proceed with testing.

You pay only a small processing fee for review and handling.

This is rare (less than 1%). When it happens, we pivot to blood-based testing for DNA and RNA, which is an excellent second option.

Q: Do I receive my raw sequencing data?

Yes. Every piece of sequencing data generated belongs to you.

We provide full raw data files – hundreds of pages covering both DNA and RNA results – in addition to summary reports.

Q: Do you have validation data for the RNA/AI over-expression test?

We are recognized leaders in RNA testing.

Most commercial labs do not provide whole-transcriptome RNA analysis.

Our proprietary normal library ensures consistently accurate results – 96% Sensitivity & 92% Accuracy (some scoring 98.7%, but we conservatively report 92%).

The Thermo Fisher AmpliSeq 20,813-gene panel is used in all tests.

While Thermo Fisher does not pursue FDA approval for research panels, our proprietary methods are patent-pending, with regulatory submissions in progress through the FDA, EU, and Health Canada.

Liquid Biopsy Labs utilizes sequencing platforms manufactured by Thermo Fisher Scientific.

Additional Information

Please note: The information in this document is subject to change, as we are always iterating and improving our testing processes, as well as there being certain variables beyond our control. For the most current information, please contact our team directly. Our Lab Manager will be able to provide you with the latest information and answer any further questions directly.

Contact & Next Steps

If you've read this far, you're already taking one of the most important steps – learning what's possible through molecular testing and precision cancer medicine.

Every question, test, and report described in this document exists to empower patients and doctors with better information, faster answers, and the opportunity for better outcomes.

No matter what your specific goal is, Liquid Biopsy Labs is here to help support you and guide you through every stage – from accessing the newest diagnostics to ensuring your understanding and application of the results to optimize your unique mission.

You can reach us directly at:

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Our team typically responds within one business day to answer specific questions or arrange a free initial consultation.

Above all, know that we are here to support you in achieving your goals.

Science is advancing rapidly – and with the right testing, data, and support, there is always hope and a next step forward.