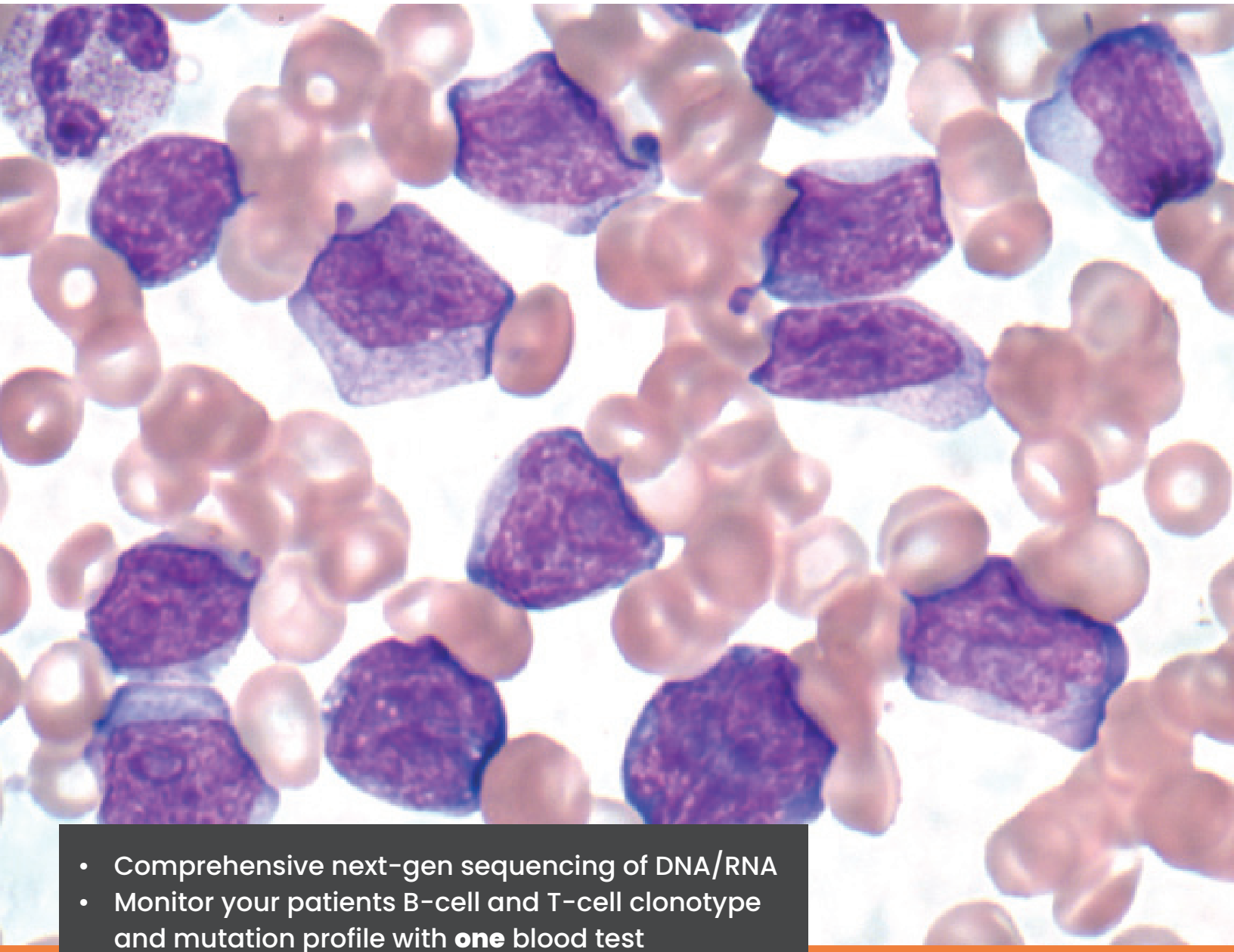
Hematologic Neoplasm Profiling

Precision Diagnosis, Classification, and Advanced Treatment



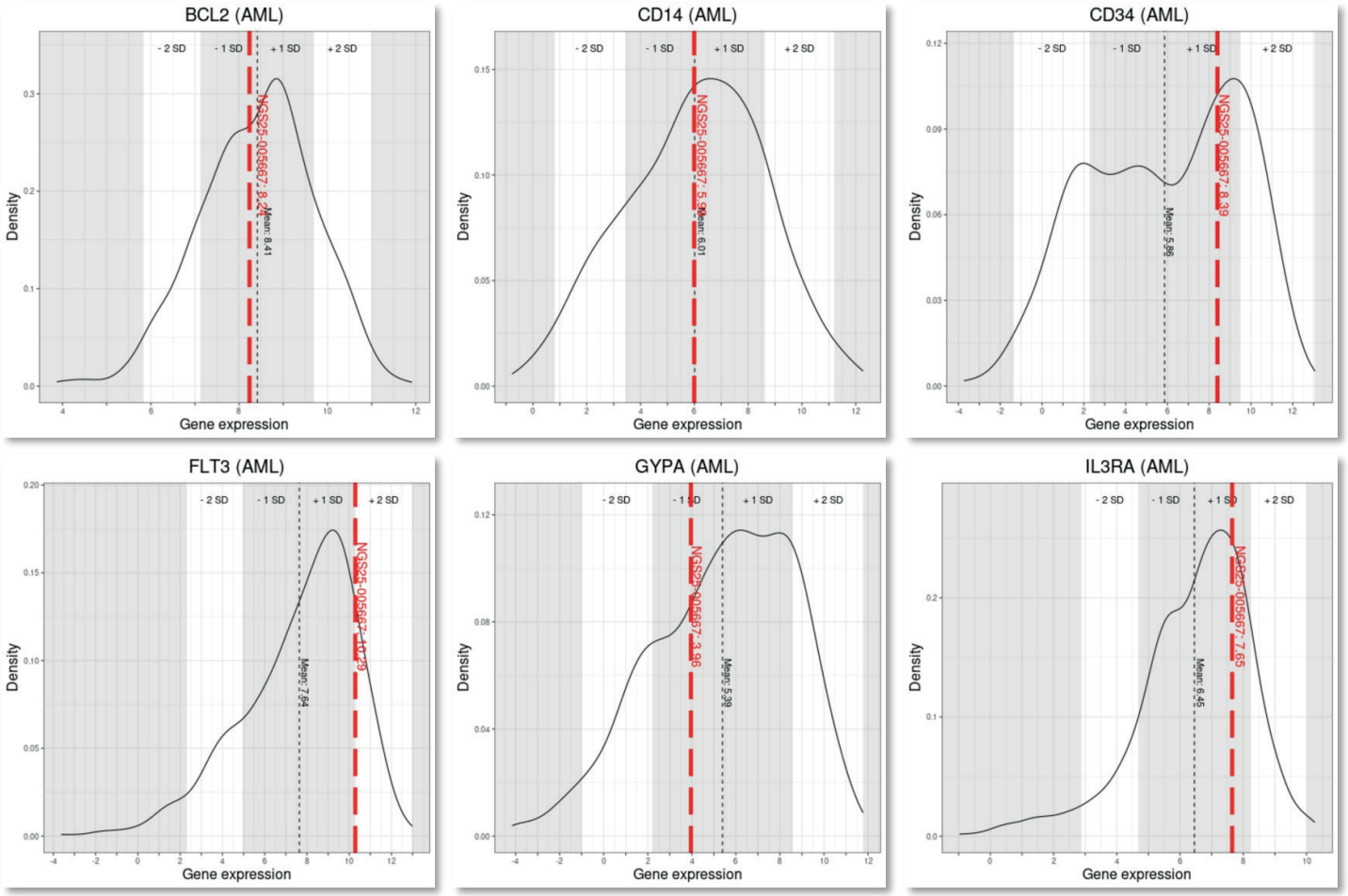
- Comprehensive next-gen sequencing of DNA/RNA
- Monitor your patients B-cell and T-cell clonotype and mutation profile with **one** blood test
- Liquid biopsy as a replacement for bone marrow biopsy
- Results in 5-10 days

GENOMIC® TESTING COOPERATIVE

GENOMIC TESTING COOPERATIVE®

DNA and RNA provide comprehensive answers.

- GTC's RNA goes beyond just fusion detection; it can also provide immunophenotype, molecular IHC and molecular karyotyping.
- Sophisticated AI systems that help with interpreting and reporting the data to make more accurate diagnoses and subclassifications
- Replacement for bone marrow aspirations and biopsy
- CSF Liquid Trace is useful for diagnosis of primary and secondary CNS lymphomas
- We analyze cutaneous lymphoid lesions to distinguish between benign and malignant entities



Gene expressions on AML

Plots showing the distribution of various markers expressed in the specific cancer shown in parenthesis using GTC expression database. The level of expression database. The level of expression of the indicated biomarker in the tested sample is indicated as a red line. The mean and plus and negative one and two standard deviations are shown for visual comparison

GTC-Hematology Profile PLUS™

GTC-Hematology Profile Plus™ combines expression and fusion with mutation analysis in DNA and RNA. This is a comprehensive evaluation of all hematologic neoplasms. However, it is especially recommended for:

- Fusions, Chromosomal Gain or Loss, and Translocations
- Cutaneous Lymphomas
- Multiple Myeloma Risk Stratification
- Viral RNA (EBV/TTV/HTLV-1)
- DPYD Genotyping
- Cell of Origin in Lymphoma
- All Types of Leukemias and MDS
- Classification of Subtypes of Lymphoma
- Other Hematologic Malignancies
- T-cell and B-cell Clonality
- IgHV Mutation Status
- HLA Genotyping
- Gene Expression

Liquid Trace® Hematology

Liquid Trace® Hematology is a pan-cancer, highly sensitive test evaluating cfDNA and cfRNA

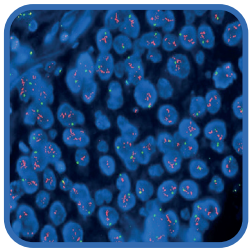
- Chromosomal Abnormalities
- Gene Amplification
- Exon Skipping
- T-cell & B-cell Clonality
- TMB
- DPYD Genotyping
- Viral RNA (EBV/TTV/HTLV-1)
- Therapeutic Monitoring and Detect Early Relapse
- Biomarker Discovery with AI for ADC's and Immunotherapy
- HLA Genotyping

GTC-Hematology Profile™

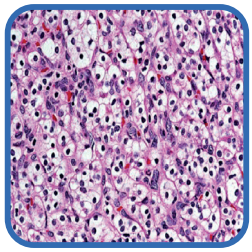
GTC-Hematology Profile™ is designed to profile the molecular abnormalities in various hematologic neoplasms including:

- Myelodysplastic Syndrome (MDS)
- Myeloproliferative Neoplasms (MPN)
- Distinguish Clonal Hematopoiesis of Indeterminate Potential (CHIP)
- VEXAS Disease

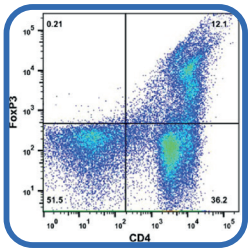
Get more from one test:



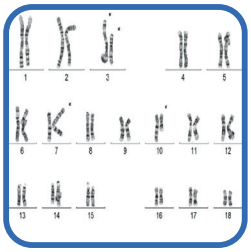
FISH



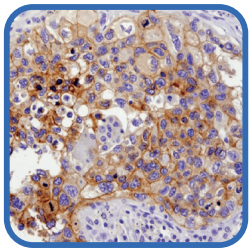
Morphology



Flow

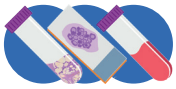
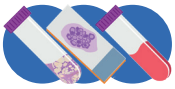


Cytogenetics



IHC

Hematology Tests Comparison Table

Available Tests	GTC-Hematology Profile PLUS™	Liquid Trace™: Hematology	GTC-Hematology Profile™
Genes	>300/>1600	>300/>1600	>300
TAT	7-10 Days	5-7 Days	5-7 Days
Sample Type	 Bone Marrow, Peripheral Blood, Fresh Tissue.	 Peripheral Blood, CSF	 Bone Marrow, Peripheral Blood, Fresh Tissue.
Sample Requirements	Bone marrow: 2mL. Peripheral blood: 5 mL. EDTA tube preferred FFPE: 1 H&E slide and 6-10 unstained slides, 5-7 microns of tissue fixed with 10% NBF fixative	Peripheral blood: 8-10 mL. EDTA tube preferred* CSF: 7-10mL optimal (5 mL minimum)	Bone marrow: 2mL. Peripheral blood: 5 mL. EDTA tube preferred FFPE: 1 H&E slide and 6-10 unstained slides, 5-7 microns of tissue fixed with 10% NBF fixative
Results Reported	DNA + RNA	DNA + RNA	DNA

*Important: cfRNA stability is optimal 48-72 hours from blood draw. cfDNA stability is 7 days from blood draw. Samples received beyond 72 hours may include only cfDNA results.

For CSF, do not use collection devices with anticoagulants.

**See specimen requirements for details

Hematologic Malignancies Capabilities Overview

Features	PCR	Cytogenetics	FLOW	FISH	GTC Heme Plus	GTC Liquid Trace cfDNA & cfRNA
Differential diagnosis and classification	✗	✗	✓	✗	✓	✓
Enrichment of plasma cells	✗	✗	✓	✗	✓	✓
Chromosomal abnormalities including gain or loss, fusions and translocations (CNV's)	✗	✓	✗	✓	✓	✓
SNV's, Indels	✗	✗	✗	✗	✓	✓
Gene expression	✗	✗	✓	✗	✓	✓
T and B-cell clonality	✓	✗	✓	✗	✓	✓
Immunophenotyping	✗	✗	✓	✗	✓	✓
Identifies therapeutic targets	✗	✗	✓	✗	✓	✓
Risk stratification	✗	✓	✗	✓	✓	✓
Resistance markers	✗	✗	✗	✗	✓	✓
Viral RNA (EBV, TTV, HPV)	✗	✗	✗	✗	✓	✓
Monitoring of treatment response/MRD	✓	✗	✓	✗	✓	✓
Distinguishing CHIP from MDS	✗	✗	✗	✗	✓	✓
CAR-T Construct Detection	✗	✗	✗	✗	✓	✓
Pre and post transplant monitoring (recipient vs donor)	✗	✗	✗	✗	✓	✓

Sample Report Pages

GENOMIC TESTING COOPERATIVE
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CLIA #: 05D2111917 CAP #: 9441574

Liquid Trace Hematology

Patient Name:		Ordering Physician:	
Date of Birth:		Physician ID:	
Gender (M/F):		Accession #:	
Client:		Specimen Type:	CSF
Case #:		Specimen ID:	
Body Site:	CSF		

MRN:		Indication for Testing:	C82 Follicular lymphoma
Collected Date:	Time:		
Received Date:	Time:		
Reported Date:	05/09/2025 Time: 03:18 PM		

Detected Genomic Alterations

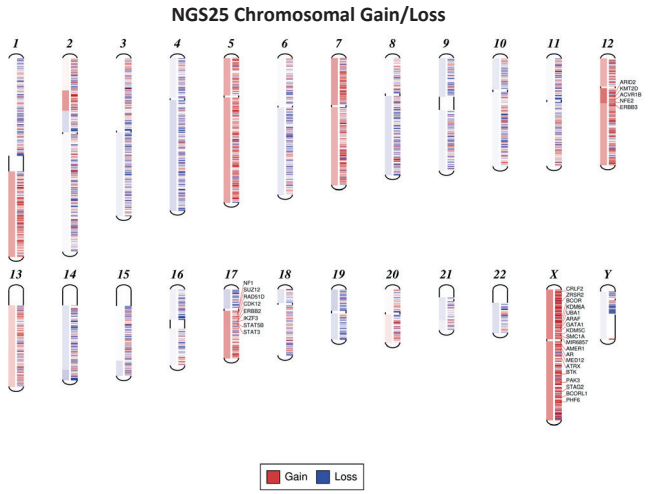
MED12	BCR (5 mutations)	MYC	BCL2 (2 mutations)	PIM1 (3 mutations)
PAX5	KMT2A	SOCS1 (2 mutations)	HSP90AA1	FAS
ARID1A	TP53 (4 mutations)	PTCH1	RAF1	HGF
KMT2C	DPYD (?Germline)	Autosomal chromosomal structural analysis shows: 1q+, partial 2p+, +5, +7, +12, +13, 17q+	t(14;18)(q32;q21) BCL2::IGH fusion mRNA	B cell clonality: Detected, biclonal [One heavy chain: IGHV4-34 and two light chains: IGKV4-1 (major), IGLV2-23 (minor)]
T cell clonality: Not detected	Increased MYC mRNA reflecting promoter hijacking			

Results Summary

- **-Somatic mutations in MED12, BCR (5 mutations), MYC, BCL2 (2 mutations), PIM1 (3 mutations), PAX5, KMT2A, SOCS1 (2 mutations), HSP90AA1, FAS, ARID1A, TP53 (4 mutations), PTCH1, RAF1, HGF, and KMT2C genes**
  -Possible germline mutation in DPYD gene, heterozygous
  -t(14;18)(q32;q21) BCL2::IGH fusion mRNA
  -Autosomal chromosomal structural analysis shows: 1q+, partial 2p+, +5, +7, +12, +13, 17q+
  -B cell clonality: Detected, biclonal [One heavy chain: IGHV4-34 and two light chains: IGKV4-1 (major), IGLV2-23 (minor)]
  -T cell clonality: Not detected
  -B cell markers: Increased with normal pattern
  -BCL2 mRNA: Marked increase, reflecting promoter hijacking
  -Increased MYC mRNA reflecting promoter hijacking

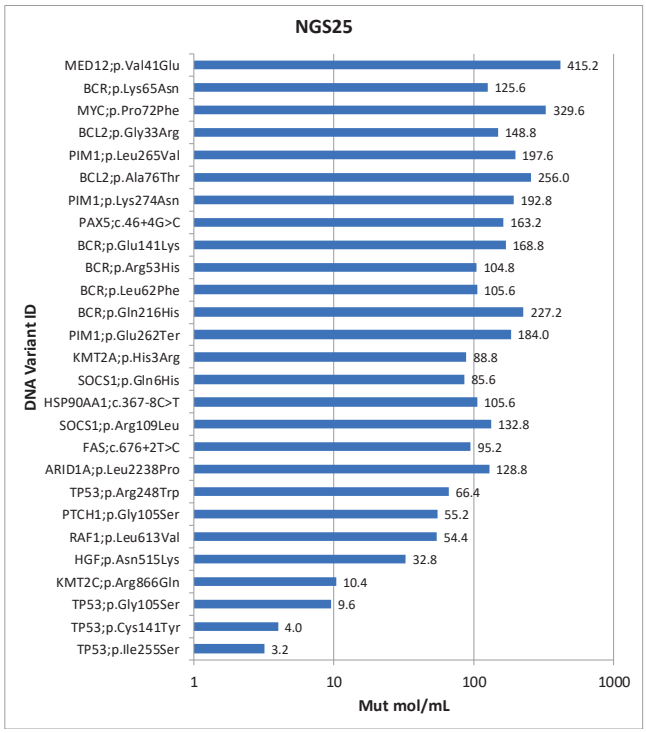
Additional Report Information

Chromosomal Abnormality Graph



Additional Report Information

Mutations Load (mol/mL)



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Diagnostic Implications	
MED12, BCR (5 mutations), MYC, BCL2 (2 mutations), PIM1 (3 mutations), PAX5, KMT2A, SOCS1 (2 mutations), HSP90AA1, FAS, ARID1A, TP53 (4 mutations), PTCH1, RAF1, HGF, KMT2C, DPYD	-These findings are consistent with high grade B-cell lymphoma. -The DPYD mutation is likely a germline variant.

Therapeutic Implications	
MYC	MYC inhibitors
BCL2	BCL2 inhibitors
KMT2A	HDAC Inhibitors
ARID1A	sensitivity to radiation therapy and PARP inhibitors
TP53	Aurora kinase A inhibitors, Wee1 inhibitors, Chk1 inhibitors, kevetrin, APR-246, nutlins, gene therapy
PTCH1	Hedgehog inhibitors
RAF1	RAF inhibitors
HGF	Anti-HGF antibodies and MET inhibitors

Prognostic Implications	
MED12, MYC, BCL2 (2 mutations), KMT2A, TP53 (4 mutations), PTCH1, RAF1	Poor
BCR (5 mutations), PIM1 (3 mutations), PAX5, SOCS1 (2 mutations), HSP90AA1, FAS, ARID1A, HGF, KMT2C	Unknown

Relevant Genes with NO Alteration
No evidence of mutation in NOTCH, SF3B1, or MYD88

Every patient should be tested for fusions, alternative splicing and expression levels to get a complete picture of their tumor.

Advantages of RNA

GTC RNA results are compared with thousands of cases with expression levels, then run through our sophisticated AI systems that provide a summary of the findings for each patient.

- RNA Expression/Fusion profiling provides data on alternative splicing and levels of expression which helps in classification of genes
- RNA sequencing offers a superior method to identify gene fusion variants known to have prognostic and predictive significance in treatment.
- Measuring of cytokines, chemokines and interleukins
- Complete immunophenotyping
- Prediction of clinical behavior
- Alternative splicing
- Detect the presence or absence of EBV, HPV, TTV, and HTVL-1
- Evaluate cutaneous lymphoid lesions (CTCL)

GTC provides a 5-10 day turnaround time for all our tests

GTC is committed to helping physicians and patients get answers fast.
GTC consistently delivers results in 5-10 days.

Low QNS/TNP

Using innovative chemistry helps reduce QNS and TNP rates.

GTC's QNS rate is currently below 0.5%

Assay Sensitivity

Hematology Profile Plus

- >1% On Everything in This Assay
- For Hotspots it's 0.1%
- On Cases With Prior History, it's 0.001%

Read Depth 2,000-3,000X

Liquid Trace Hematology

- >1% On Everything
- 0.001% On Cases With a Tissue/Cell History (Tumor Informed)

Read Depth 25,000-30,000X

The Co-Op model

- Enables local labs to offer a comprehensive molecular testing menu to support their own communities.
- Provides economies of scale that benefit large labs with sophisticated technology at a local level.
- Reduces overhead costs (staffing, capital equipment, billing, etc.).

About GTC

GTC offers advanced genomic testing to communities everywhere at an affordable price.

Genomic Testing Cooperative (GTC) is a different kind of cancer diagnostic laboratory.

Our cooperative model allows us to partner with laboratories, hospitals, oncology practices and medical professionals to share resources which create efficiencies in cost, turnaround time and quality. In creating a network of Co-Op partners, we help get results to physicians faster, share knowledge and generate better outcomes for patients.

Our testing is focused on comprehensive profiling of DNA and RNA in hematologic neoplasms and solid tumors, embracing the latest sequencing technology and informatics tools, thereby providing better insights into the patient's tumor signature. Our RNA sequencing capabilities go beyond just the detection of fusions and include alternative splicing, gene expression and prediction. Our RNA profiling can be used to complement flow cytometry and immunohistochemistry (IHC) testing. GTC's capabilities include liquid biopsy testing that gives physicians testing options when tissue or bone marrow specimens are not available. Our informatics tools use artificial intelligence with sophisticated algorithms to interpret complex data sets; these informatics tools are unmatched anywhere on the market today.

GTC was founded in 2018 by Maher Albitar, MD, who has held senior roles at numerous diagnostic laboratories and was a tenured professor at MD Anderson Cancer Center. He has committed his life to helping cancer patients by advancing cancer diagnostics and democratizing testing. Dr. Albitar founded GTC because he had a vision to revolutionize diagnostics and scientific discovery by improving access to comprehensive genomic profiling with next generation sequencing to all patients. He believes every cancer patient should have access to comprehensive genomic profiling. Dr. Albitar is regularly published in the top medical journals in oncology with over 300 publications to date, and has authored over 50 patents.

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GENOMIC® TESTING COOPERATIVE

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