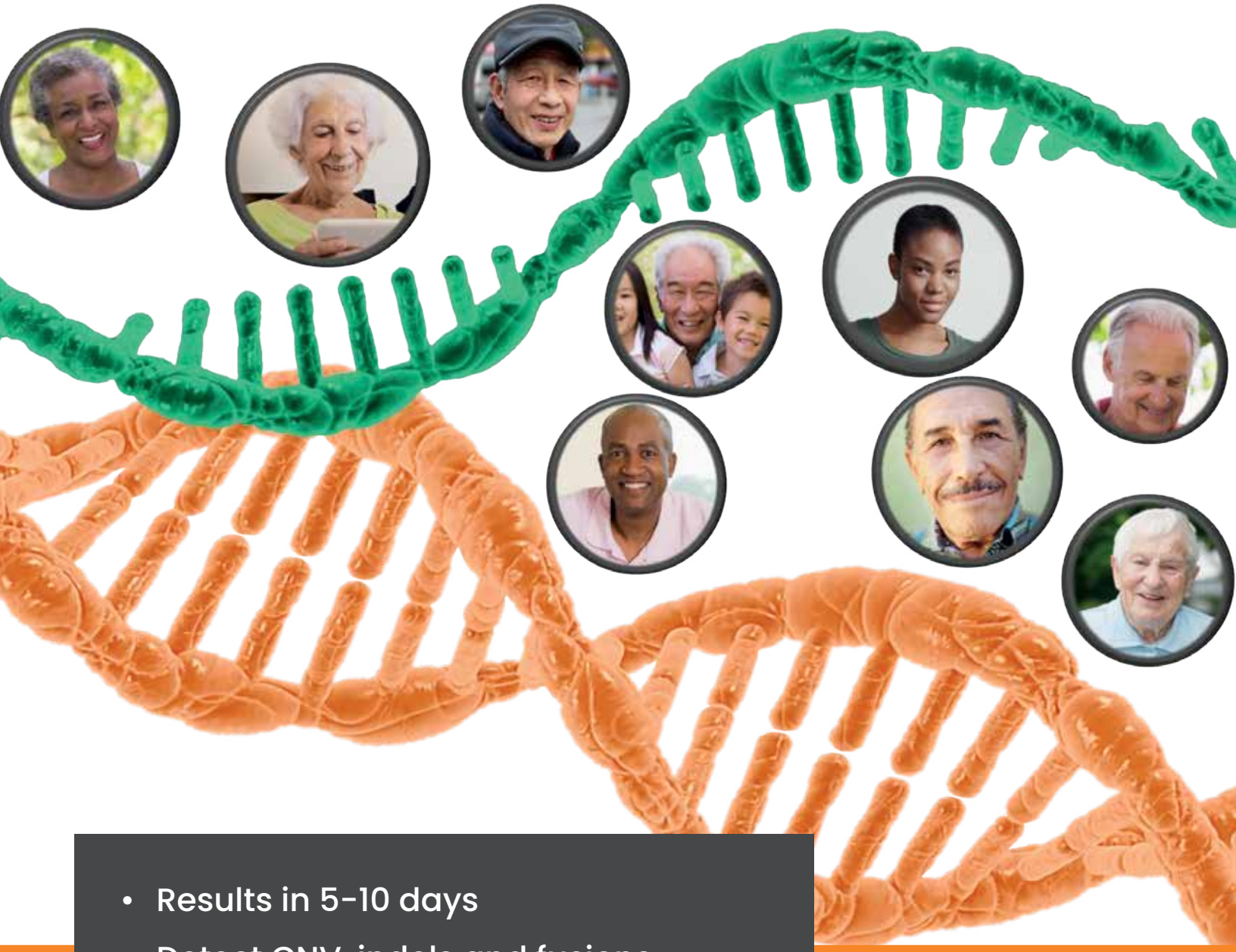
Solid Tumor DNA/RNA Profiling

Targeted and Immunotherapy Matching



- Results in 5-10 days
- Detect CNV, indels and fusions
- Low QNS rate of <1%

GENOMIC TESTING COOPERATIVE®

Cancer Hope
אונקולוגיה מותאמת אישית
לתיאום בדיקה: 03-919-57-57
וצאפ: 054-468-7377
מייל: info@CancerHope.co.il

GENOMIC TESTING COOPERATIVE®

Don't accept partial results. DNA and RNA provide a complete picture for 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.
- Detect Cancer of Unknown Primary (CUP)

The solid tumor profiles provide:

- Targeted and immunotherapy matching
- DNA and RNA profiling
- Tumor Mutation Burden (TMB)
- Microsatellite Instability (MSI)
- Fusion/translocations
- Copy number variation and deletion detection
- HRD/HRR
- Viral HPV testing
- IHC for PD-L1 and FOLR1
- T-cell & B-cell clonality analysis
- HLA genotyping
- Gene expression

Solid Tumor Tests

GTC-Solid Tumor Profile PLUS™
DNA/RNA

Liquid Trace® Hematology
First in class cfDNA/cfRNA

GTC-Solid Tumor Profile™
DNA

GTC-Solid Tumor Profile PLUS™

GTC-Solid Tumor Profile Plus™ tests for abnormalities in 434 DNA genes and >1600 RNA genes

- A pan-tumor assay that can detect all types of cancer
- Includes detection of single nucleotide variation, copy number variation, expression, known and novel fusions, exon skipping, alternative splicing, T-cell & B-cell clonality analysis
- HLA genotyping
- Immunohistochemistry (IHC) testing for PD-L1 and FOLR1 can be complemetary ordered.

Liquid Trace® Hematology

Liquid Trace® Solid Tumor is a pan-cancer highly sensitive test evaluating cfDNA and cfRNA

- Can be used for diagnoses, evaluating the host immune response, and identifying biomarkers for predicting response to various therapies.
- Can reduce the need for tissue biopsies for certain cancer patients, especially when obtaining tissue from the tumor is difficult.
- T-cell & B-cell clonality analysis
- HLA genotyping

GTC-Solid Tumor Profile™

GTC-Solid Tumor Profile™ detects the molecular abnormalities in various solid tumors by analyzing the DNA of 434 genes, covering all exons

- Detects microsatellite instability (MSI), tumor mutation burden (TMB) and homologous recombination deficiency (HRD)
- Chromosomal abnormalities
- Results provide prognosis, aid in therapeutic approach and predict response to therapy
- Useful for very small samples

Solid Tumor Tests Comparison Table

Available Tests	GTC-Solid Tumor Profile PLUS™	Liquid Trace® Solid Tumor	GTC-Solid Tumor Profile™
Genes	**434/>1600**	**302/>1600**	**434**
TAT	**5-10 Days**	**5-7 Days**	**5-7 Days**
Indications	All solid tumors: Detect known (ALK, RET, ROS1, NTRK, etc.) and novel fusions, Exon skipping (MET exon 14), PD-L1 levels, ERBB2 (low HER2) cut-offs and alternative splicing. Chromosomal translocations and amplifications. Viral EBV, HPV, and TTV testing. HLA genotyping. T- & B-cell clonality analysis	All solid tumors: Detect known (ALK, RET, ROS1, NTRK, etc.) and novel fusions, Exon skipping (MET exon 14), PD-L1 levels, ERBB2 (low HER2) cut-offs and alternative splicing. Chromosomal translocations and amplifications. Viral EBV, HPV, and TTV testing. HLA genotyping. T- & B-cell clonality analysis	All solid tumors: Full exon sequencing in 434 genes includes mutations, indels, copy number variation and chromosomal structural abnormalities, TMB, MSI, HRD, HRR
Sample Type	FFPE	Peripheral Blood, Plasma, CSF	FFPE
Sample Requirements	1 H&E slide and 6-8 unstained slides, 5-7 microns of tissue fixed with 10% NBF fixative	Peripheral blood: 8-10 mL. EDTA tube Plasma: 5 mL CSF: 7-10 mL Clear tube	1 H&E slide and 6-8 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.

Genomic Testing Cooperative, LCA, 175 Technology Drive, Suite 100, Irvine, CA 92618
Tel: 1-866-484-8870 www.genomictestingcooperative.com
CLIA #: 05D2111917 CAP #: 9441547

Solid Tumor Profile Plus

Sample Report Page

Patient Name:		Ordering Physician:	
Date of Birth:		Physician ID:	
Gender (M/F):		Accession #:	
Client:		Specimen Type:	
		Specimen ID:	
Case #:			
Body Site:			
MRN:		Reason for Referral:	
Collected Date:			
Received Date:			
Reported Date:			

Detected Genomic Alterations				
Level 1 (FDA-Approved)	Level 2 (Standard of Care)	Level 3 (Clinical Evidence)	Level 4 (Biological Evidence)	Other
-PIK3R1 mutation -Combined +7/-10 chromosomal changes -CDK4 and MDM2 amplification	-Tumor Mutation Burden Low: 5 Mut/Mb -No evidence of microsatellite instability -Homologous recombination deficiency (HRD): Negative -MGMT promoter methylation: Not detected	FANCA, IGF1R	FANCM, TERTp, DST, CNTRL	Chromosomal structural analysis shows +7, -10, -11, +12 (CDK4 and MDM2 amplification), 14q-, and 20p+

Results Summary

Genomic Testing Cooperative, LCA, 175 Technology Drive, Suite 100, Irvine, CA 92618
Tel: 1-866-484-8870 www.genomictestingcooperative.com
CLIA #: 05D2111917 CAP #: 9441547

Sample Report Page

-EBV viral RNA: Not detected
-HPV viral RNA : Not detected
-HLA Genotyping:
-HLA-A: A*02:844-A*02:05
-HLA-B: B*55:01-B*50:01
-HLA-C: C*06:02-C*01:02
-MGMT promoter methylation: Not detected
-MGMT mRNA expression: slightly above average.

-The findings are consistent with glioblastoma, IDH-wild type, CNS WHO grade 4.

-PIK3R1 mutation suggests possible response to mTOR inhibitors.

-Mutations in FANCA gene suggest possible response to PARP inhibitors.

-MDM2 amplification suggests targeting with nutlin-3a and its class of compounds.

-IGF1R mutation suggests possible response to IGF1R inhibitors (Mecasermin, Masoprocol, Linsitinib ...).

Tumor Heterogeneity
There is an abnormal clone with FANCM, PIK3R1, FANCA, TERT, IGF1R, DST, and CNTRL mutations.

Expression
Increased EGFR and VEGFA mRNA

Diagnostic Implications
The findings are consistent with glioblastoma, IDH-wild type, CNS WHO grade 4.

Levels 2, 3 & 4 (Standard of Care and Clinical/Biological Evidence)	
PIK3R1	PI3K, AKT, MTOR inhibitors
FANCA	DNA cross-linking agents such as diepoxybutane (DEB) and mitomycin C (MMC)
IGF1R	IFG1-R Inhibitor

Relevant Genes with NO Alteration		
-No evidence of mutation in KRAS, NRAS, EGFR, BRAF, TP53, or BRCA 1/2 -No specific mutation in DPYD gene, associated with enzymatic deficiency	No evidence of fusion mRNA involving ALK, RET, ROS1, or NTRK	-No evidence of MET14 deletion or EGFR Viii -No evidence of ERBB2 (HER2) amplification

Genomic Testing Cooperative, LCA, 175 Technology Drive, Suite 100, Irvine, CA 92618
Tel: 1-866-484-8870 www.genomictestingcooperative.com
CLIA #: 05D2111917 CAP #: 9441547

scription:

omprehensive molecular profile which uses next generation sequencing (NGS), fragment length d Sanger Sequencing testing to identify molecular abnormalities (including SNVs, INDELS, CNVs, MB, MSI, HRD, EBV, and HPV) in DNA of 434 genes and RNA in 1600 genes implicated in solid henever possible, clinical relevance and implications of detected abnormalities are described

al relevance of detected Alterations

The Fanconi anemia complementation group (FANC) currently includes FANCA, FANCB, FANCC, FANCD1 (also called BRCA2), FANCD2 ANCF, FANCG, FANCI, FANCJ (also called BRIP1), FANCL, FANCM and FANCN (also called PALB2). The previously defined group the same as FANCA. Fanconi anemia is a genetically heterogeneous recessive disorder characterized by cytogenetic instability, sitivity to DNA crosslinking agents, increased chromosomal breakage, and defective DNA repair. The members of the Fanconi anemia entation group do not share sequence similarity; they are related by their assembly into a common nuclear protein complex. This odes the protein for complementation group M. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr

Phosphatidylinositol 3-kinase phosphorylates the inositol ring of phosphatidylinositol at the 3-prime position. The enzyme comprises catalytic subunit and a regulatory subunit of either 85, 55, or 50 kD. This gene encodes the 85 kD regulatory subunit. tidylinositol 3-kinase plays an important role in the metabolic actions of insulin, and a mutation in this gene has been associated with sistance. Alternative splicing of this gene results in four transcript variants encoding different isoforms. [provided by RefSeq, Jun

The Fanconi anemia complementation group (FANC) currently includes FANCA, FANCB, FANCC, FANCD1 (also called BRCA2), FANCD2 ANCF, FANCG, FANCI, FANCJ (also called BRIP1), FANCL, FANCM and FANCN (also called PALB2). The previously defined group the same as FANCA. Fanconi anemia is a genetically heterogeneous recessive disorder characterized by cytogenetic instability, sitivity to DNA crosslinking agents, increased chromosomal breakage, and defective DNA repair. The members of the Fanconi anemia entation group do not share sequence similarity; they are related by their assembly into a common nuclear protein complex. This odes the protein for complementation group A. Alternative splicing results in multiple transcript variants encoding different isoforms. s in this gene are the most common cause of Fanconi anemia. [provided by RefSeq, Jul 2008]

lomerase is a ribonucleoprotein polymerase that maintains telomere ends by addition of the telomere repeat TTAGGG. The enzyme of a protein component with reverse transcriptase activity, encoded by this gene, and an RNA component which serves as a template lomere repeat. Telomerase expression plays a role in cellular senescence, as it is normally repressed in postnatal somatic cells in progressive shortening of telomeres. Deregulation of telomerase expression in somatic cells may be involved in oncogenesis. mouse suggest that telomerase also participates in chromosomal repair, since de novo synthesis of telomere repeats may occur at randed breaks. Alternatively spliced variants encoding different isoforms of telomerase reverse transcriptase have been identified; ngth sequence of some variants has not been determined. Alternative splicing at this locus is thought to be one mechanism of of telomerase activity. [provided by RefSeq, Jul 2008]

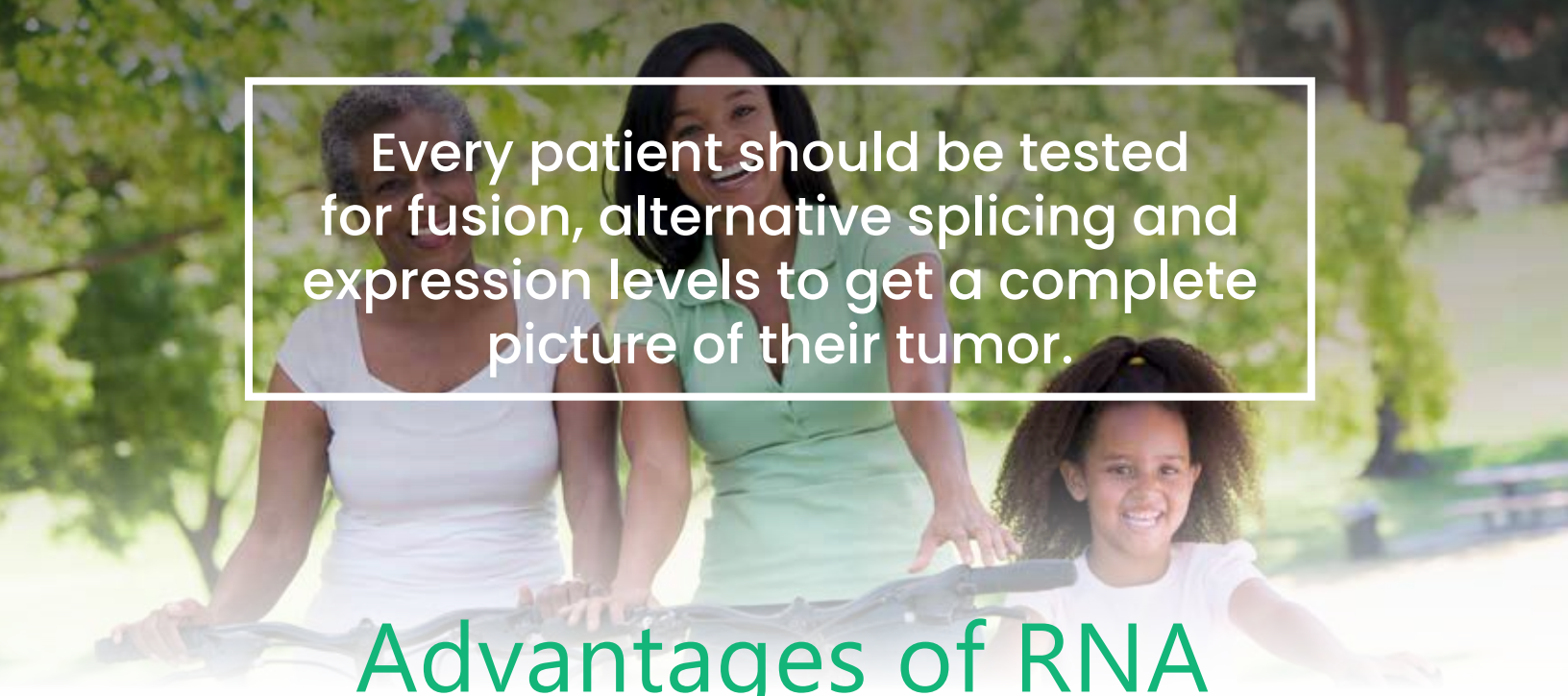
his receptor binds insulin-like growth factor with a high affinity. It has tyrosine kinase activity. The insulin-like growth factor I receptor ritical role in transformation events. Cleavage of the precursor generates alpha and beta subunits. It is highly overexpressed in most ting cell tissues where it functions as an anti-apoptotic agent by enhancing cell survival. Alternatively spliced transcript variants encoding distinct isoforms have been found for this gene. [provided by RefSeq, May 2014]

- DST. This gene encodes a member of the plakin protein family of adhesion junction plaque proteins. Multiple alternatively spliced transcript variants encoding distinct isoforms have been found for this gene, but the full-length nature of some variants has not been defined. It has been reported that some isoforms are expressed in neural and muscle tissue, anchoring neural intermediate filaments to the actin cytoskeleton, and some isoforms are expressed in epithelial tissue, anchoring keratin-containing intermediate filaments to hemidesmosomes. Consistent with the expression, mice defective for this gene show skin blistering and neurodegeneration. [provided by RefSeq, Mar 2010]
- CNTRL. This gene encodes a centrosomal protein required for the centrosome to function as a microtubule organizing center. The gene product is also associated with centrosome maturation. One version of stem cell myeloproliferative disorder is the result of a reciprocal translocation between chromosomes 8 and 9, with the breakpoint associated with fibroblast growth factor receptor 1 and centrosomal protein 1. [provided by RefSeq, Jul 2008]

Drug Information

Alpelisib

Sample Report Page



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

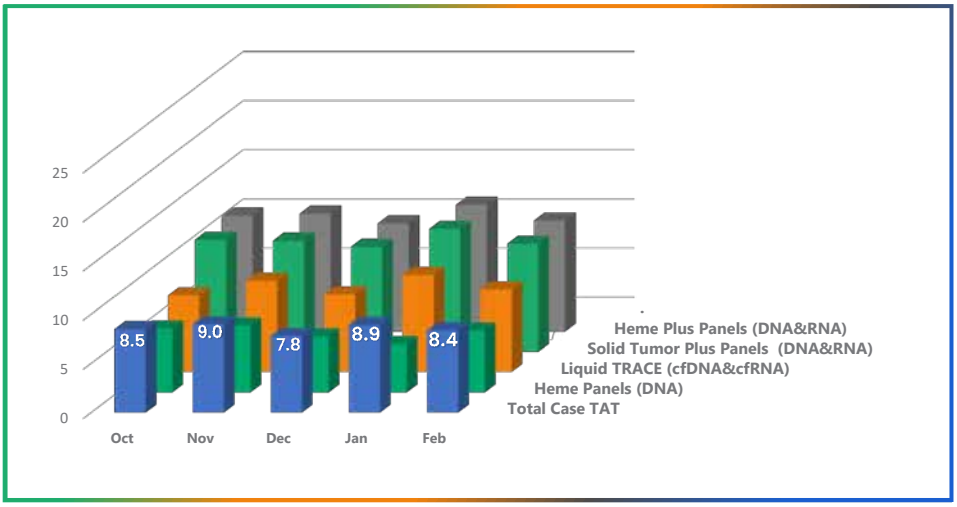
Advantages of RNA

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

- RNA can detect all possible translocations that may involve ALK, ROS1, RET, NTRK and FGFR.
- Our NGS assay will detect MET exon 14 skipping, which is also currently in NCCN guidelines and responds very well to capmatinib (TABRECTA™).
- With RNA testing we can evaluate the microenvironment, immune response, PD-L1, PD-L2, PD-1, CD8, etc., and determine the MET exon 14 skipping and various alternative splicing, expression and amplification of ERBB2 (HER2), MET and EGFR.
- Our NGS can detect all NTRK (1,2,3) fusions, which are also in current NCCN guidelines and patients will be eligible for NTRK inhibitors such as entrectinib (ROZLYTREK®) and larotrectinib (VITRAKVI®).
- Our assay can detect the ALK, ROS1, and RET fusions at significantly higher sensitivity than FISH and will require no additional tissue.
- Our NGS can detect the presence of ERBB2 (HER2) amplification/ overexpression, which is present in 5% of lung cancer and is within NCCN guidelines.
- Viral HPV testing is useful for screening head and neck cancer, plus staging/screening for cervical lesions.

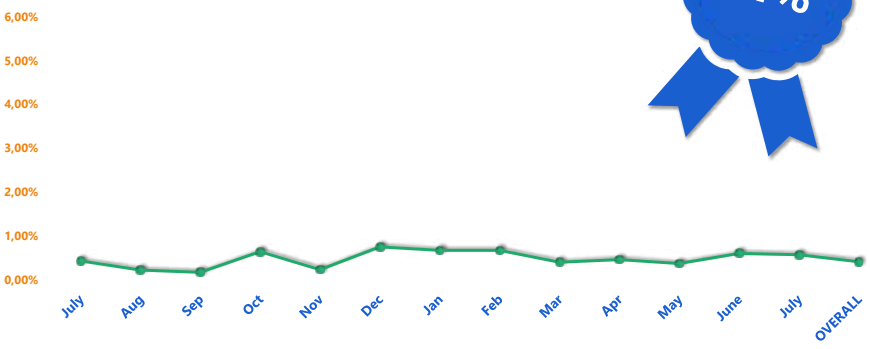
GTC provides a 5-10 day turnaround time for all our tests

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



Extremely Low QNS/TNP Rate

Overall QNS rate: 0.41%



Don't let QNS/TNP fears stop you from ordering comprehensive genomic profiling.

Using innovative chemistry helps reduce QNS and TNP rates.

GTC's QNS rate is currently less than 1%.

The Co-Op model

- Enables local labs to offer a comprehensive molecular testing menu to support their own communities.
- Provides economies of scale that large labs benefit from 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 give physicians testing options when tissue or bone marrow specimens are not available. The informatics tools we use utilize 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.

GENOMIC® TESTING COOPERATIVE

Cancer Hope
אונקולוגיה מותאמת אישית
לתיאום בדיקה: 03-919-57-57
וצאפ: 054-468-7377
מייל: info@CancerHope.co.il