

$K\text{-}\mathsf{TRACK^{TM}}:\mathsf{CONSENT}\;\mathsf{FORM}$

SECTION 1: PATIE		K-TRACK™ ID:										
Full name:				Date of birth: (dd/mm/yy) Gender: Male Female								
Phone:				Place of treatment:								
Referring physician:				Referring physician's email:								
<u> </u>		K-TRACK MET										
Blood sample (after radical surgery) Date of collection:												
Blood sample (before radical surgery) Date of collection:				Tissue sample Date of surgery/biopsy:								
Tissue sample Date of surgery/biopsy:												
K-Track N (Follow UP)		lection:		_)								
A. HISTORY AND TREATMENT PROCESS Cancer type*: Cancer stage at diagnosis:												
Lung Prostate Esophageal Colorect Endometrial Ovarian Others:		Negative	ceptor status:: PR HER									
B. PATHOLOGY (please ignore	if this is a follow-un tes	t and collect only bloods	sample)									
				llection: Place of collection:								
SECTION 2: TEST	AGREEMEN ⁻	Γ										
 l acknowledge that I have been fully provided with information and carefully went through all sections of this Consent form. I hereby acknowledge that I understand and agree that. l agree with all the terms and conditions in this Consent form. l agree to provide all details to perform the type of test mentioned in this Consent form and to sequence the gene on the sample at the Gene Solutions Lab Co. laboratory, I agree to allow Gene Solutions Lab Co. to perform data processing activities from genetic sequencing, including but not limited to collection, recording, analysis, validation, storage store, modify, disclose, combine, access, retrieve, revoke, encrypt, decrypt, copy, share, transmit, provide, transfer, delete, destroy personal data or other relevant action. l Consent to the processing of my personal data, including my health data, and residual material by Gene Solutions Lab Co. for research and scientific purposes as specified in this Consent form Providers may use customer residuals and de-identified information for scientific studies. These studies can be published in scientific journals or used to develop products and services. Customers will not be notified or paid for these research activities. I allow / do not allow my personal information and my genetic test result to be part of the research of Gene Solutions 												
I have fully explained the test, including the benefits, risks, and alternatives to clients based on the legal basis, and answered all of their questions. SECTION 3: SCOPE OF THE TEST Date:												
	Actiona		MRD			MSI			Germline			
Lung Cancer												
Liver Cancer												
Esophageal – Gastric Cance												
Pancreatic Cancer												
Colorectal Cancer												
Breast Cancer												
Ovarian Cancer												
Endometrial Cancer												
Prostate Cancer												
Panel 155 genes:												
ACVR2A ASXL2 CASP8 AFF3 ATM CDH1 AKT1 ATR CDK12 ALK AXIN1 CDKN2A AMER1 BCOR CHD4 APC BRAF CHEK2 AR BRCA1 CIC ARID1A BRCA2 CREBBP ARID1B BRIP1 CSDE1	CTNNB1 EPH/DICER1 EPH/DICER1 EPH/DINMT3B ERBE	A7 FGFR2 GRI 32 FGFR3 HR. 33 FH IDH 34 FHIT IDH C3 FLT1 IGF C4 FOXA1 IKZ 1 FOXP1 INF	N2A KIT AS KMT2A I1 KMT2B I2 KMT2C 2 KMT2D	MAP2K4 MAP3K1 MAX MDM2 MED12 MEN1 MET MGA MLH1	MSH6 MTOR MUTYH NCOR1 NCOR2 NF1 NFE2L2 NOTCH1 NOTCH2	NRG1 NSD1 NTRK1 NTRK2 NTRK3 PALB2 PARP1 PBRM1 PDE4DIP	PDPK1 PIK3C2G PIK3CA PIK3CD PIK3R1 PMS2 POLD1 POLE PRDM14	PRKD1 PTCH1 PTEN PTPN13 PTPRB PTPRD PTPRS PTPRT RAB35	RASA1 RB1 RBM10 RET RHOA RNF213 RNF43 ROS1 SETD2	SMAD4 SMARCA4 SOX9 STAT5A STK11 TBX3 TCF7L2 TERT promoter TP53	TSC1 TSC2 VHL ZFHX3 ZNF521	



A. PURPOSES AND BENEFITS OF TESTING

- 1. The test examines the genes related to targeted therapy and drug resistance.
- Lung Cancer: EGFR, KRAS, BRAF, NRAS, MET amplification/mutations, HER2 amplification/mutations, ALK fusion/mutations, ROS1 fusion, NTRK fusion, PIK3CA, RET fusion/mutations, TP53, SKT11, KEAP1
- Colorectal Cancer: KRAS, NRAS, BRAF, HER2 amplification/mutations, PIK3CA, NTRK fusion, RET fusion
- Breast Cancer: AKT1, PTEN, BRCA1, BRCA2, PALB2, PIK3CA, ESR1, HER2 amplification/mutations, NTRK fusion, RET fusion
- Esophageal Gastric Cancer: HER2 amplification/mutation, PIK3CA, NTRK fusion, BRAF, RET fusion
- Ovarian Cancer: BRCA1, BRCA2, BRAF, NTRK fusion, RET fusion
- Prostate Cancer: BRCA1, BRCA2, PALB2, AR, NTRK fusion, RET fusion
- Pancreatic Cancer: BRCA1, BRCA2, PALB2, KRAS, NRAS, BRAF, RET fusion, NTRK fusion
- Endometrial Cancer: POLE, POLD1, AKT1, BRAF, NTRK fusion, RET fusion/mutations
- Liver Cancer: BRAF, NTRK fusion
- 2. Microsatellite instability (MSI): is a marker that is associated with the ability to respond to adjuvant therapy or immunotherapy. For MSI, the percentage of microsatellite instability (MSI) regions is calculated using the MSIsensor-pro tool, comparing these regions between the tumor tissue samples and the corresponding leukocyte samples, and the threshold value for MSI-High classification is 20%.
- 3. Germline mutations associated with hereditary cancer: are identified from leukocyte samples, and the pathogenicity of these variants is classified according to the American College of Medical Genetics and Genomics (ACMG) criteria.

Panel genes: ALK, APC, ATM, BRCA1, BRCA2, BRIP1, CDH1, CDKN2A, CHEK2, DICER1, EGFR, EPCAM, ERCC3, ERCC4, FH, HRAS, KIT, MAX, MEN1, MET, MLH1, MSH2, MSH6, MUTYH, NF1, NF2, PALB2, PDGFRA, PMS2, POLD1, POLE, PTCH1, PTEN, RET, RNF43, SMAD4, SMARCA4, STK11, TP53, TSC1, TSC2, VHL

4. Minimal residual disease (MRD) testing: based on LIQUID BIOPSY technology, designed for each patient, and utilizes Next-generation Sequencing technology with deep coverage (10,000X). Therefore, it helps detect ctDNA at low levels (LOD: 0.05%) facilitating early detection of recurrence and evaluation of treatment effectiveness. In addition to personalized mutations for each patient, the K-TRACKTM MET also examines an additional panel of 300-500 hotspot mutations specifically designed for metastatic stage.

Panel genes (the entire gene length is not examined, but only some hotspot mutations. The location and quantity of mutations examined depends on each different type of cancer): ACVR2A, AKT1, ALK, AMER1, APC, ARID1A, AXIN1, BRAF, BRCA1, BRCA2, CDH1, CTNNB1, EGFR, ERBB2, ESR1, FBXW7, GATA3, GNAS, HRAS, IDH1, IDH2, KEAP1, KRAS, LRP1B, MET, NRAS, PIK3CA, POLE, PPP2R1A, PTEN, RB1, SMAD4, STK11, TCF7L2, TERT, TP53, ZFHX3.

PROCEDURE FOR CONDUCTING K-TRACKTM TEST TO MONITOR ctDNA



B. METHODS FOR RETURNING RESULTS

The K-TRACK™ test package includes 2 result tables:

- 1. The K-TRACK[™] result for Actionable mutations + Microsatellite Instability (MSI).
- 2. The K-TRACK™ result for detection of Minimal residual disease (MRD)/ctDNA dynamics + Germline mutations

The K-TRACKTM result for detection of Minimal residual disease (MRD)/ctDNA dynamics will manifest in 2 forms: POSITIVE or NEGATIVE, indicating the presence of ctDNA in the blood. This outcome will provide physicians with additional information and aid in determining the suitable treatment regimen for each individual.

- NEGATIVE: indicates that ctDNA is not detected in the blood. For patients diagnosed with early-stage cancer, this signifies the absence of residual disease or the presence of very low, undetectable levels within the body. In the case of metastatic (late-stage) cancer, a negative result suggests the effectiveness of the treatment. Recommendation: It is advisable to maintain ongoing ctDNA monitoring.
- POSITIVE: indicates the presence of ctDNA in the blood. This signifies an elevated risk of cancer recurrence or inadequate response to treatment. Your
 physician may recommend a repeated test to assess your tumor's response to treatment. Recommendation: Please consider undergoing imaging
 (PET/MRI) for further evaluation

C. LIMITATION

- The test results are TIME-DEPENDENT. Therefore, a K-TRACKTM analysis result indicating a negative residual tumor does not provide an absolute assurance against future cancer detection or progression. Consequently, it is of utmost importance to undergo repeated analyses as directed by your physician in order to facilitate early detection of recurrence and ensure ongoing monitoring of treatment effectiveness.
- The K-TRACKTM test CANNOT be performed on patients who meet any of the following criteria:
 - Pregnancy
 - · History of bone marrow transplant
 - History of whole blood transfusion within the past three months.
- The examined mutations encompass point mutations, deletions and short insertions (less than 20 nucleotides) in the coding region and in the vicinity of intron (-20/+10 nucleotides from exon) of the genes under examination.
- Additional mutations include variants outside the coding region, large deletions and insertions (greater than 100 nucleotides), short continuous repeats
 (nucleotide repeats), CG-rich region, high homologous regions (pseudogenes) and mosaicism. Detecting these mutations may not be reliable enough to be
 detected in this test.
- The test does not encompass the comprehensive examination of all genes implicated in cancer. Consequently, a negative result (indicating no detected
 mutations) does not definitively exclude the possibility that the participant may carry a mutation in another gene that is not included in this test.
- This test serves as a valuable adjunct to existing methodologies for monitoring recurrence and evaluating treatment efficacy, offering additional insights and assisting in the informed decision-making process for effective treatment strategies.
- The test may not yield results in the following scenarios:
 - No cancer-specific mutations were identified or
 - The tumor demonstrates challenges in releasing ctDNA, often attributable to factors such as tumor location and type or
 - The quality of the tissue sample (FFPE) does not meet the requirements for next-generation gene sequencing.

D. SUPPORT

Patients with a positive ctDNA result will receive free counseling on the test results as well as referrals to the best cancer specialists to optimize treatment and disease monitoring..

(*) We always comply with HIPAA law and Privacy Policy to protect customer's medical information, please check our website to learn more about privacy policy