GENE SOLUTIONS K-TRACK | TEST REQUISITION FORM

For Gene Solutions Use Only
K-TRACK ID: _____

PATIENT INFORMATION

Full Name: | Referring Physician:

Date of Birth: *(DD/MM/YY)* | Clinic/Hospital Name:

National ID/Passport: | Physician Email:

Gender: ☐ Male ☐ Female | Physician Phone:

Phone:

TEST SELECTION & SAMPLE INFORMATION

☐ **K-TRACK (Tumor + Blood)**
Genomic (DNA) Profiling
+ ctDNA-MRD Monitoring

☐ **K-TRACK (Tumor Only)**
Genomic (DNA) Profiling

☐ **K-TRACK (n)**
ctDNA Follow-up Test

Tissue Sample
Date of FFPE Collection: *(DD/MM/YY)*

Blood Sample: _____ mL; _____ tube(s)
Date of Collection: *(DD/MM/YY)*

For K-TRACK (Tumor Profiling Only), complete the "Tissue Sample" field only. For the K-TRACK (n) test, complete the "Blood Sample" field only.

HOSPITAL PATHOLOGY LAB *(The tumor cellularity of FFPE specimens must be ≥20%)*

Pathology Code: | Site of Biopsy:

Date of Surgery/Biopsy: *(DD/MM/YY)* | Tumor Cellularity (%):

Place of Collection:

See page 5 for "Sample Requirement" information.

CANCER HISTORY & TREATMENT PROCESS

Cancer type
(select one)

☐ Cervical	☐ Ampulla of Vater	☐ Esophageal	☐ Liver
☐ Endometrial	☐ Bladder	☐ Gallbladder	☐ Pancreatic
☐ Lung	☐ Fallopian Tube	☐ Cholangiocarcinoma	☐ Gastric	☐ Other:
☐ Mediastinal	☐ Ovarian	☐ Colorectal	☐ GIST	☐ Prostate*
☐ Mesothelioma	☐ Uterine	☐ Breast, receptor status: *ER:* ☐- ☐+ *PR:* ☐- ☐+ *HER2:* ☐- ☐+		

Cancer Stage at Diagnosis: ☐ I ☐ II ☐ III ☐ IV | Metastatic Organs:

Diagnosis Date: *(DD/MM/YY)* | Date of Treatment: *(DD/MM/YY)*

Regimen (radiotherapy/chemotherapy/immunotherapy/hormones, if any):

See page 4 for "Scope of the Test" information for each cancer.

INFORMED CONSENT FORM

I acknowledge that I have reviewed and fully understood the information presented in this Informed Consent Form. ▪ I consent with all the terms and conditions in this Informed Consent Form. ▪ I consent to provide all necessary information and to have genetic sequencing performed on my sample at Gene Solutions' laboratory for the purpose of conducting the test described. ▪ I authorize Gene Solutions to process the personal data I have provided, including conducting genetic sequencing and performing related processing activities such as collection, recording, analysis, validation, storage, modification, disclosure, combination, access, retrieval, revocation, encryption, decryption, copying, sharing, transmission, provision, transfer, deletion, and destruction of my personal data, as well as any other processing actions permitted under applicable personal data protection regulations. ▪ I understand that the data processed in this testing process includes sensitive personal data such as genetic information, health-related data, biological samples, financial identifiers, digital identity information, and images of identification documents. ▪ I consent to the processing of my personal data (including health-related data and residual material) by Gene Solutions for research and product development purposes as specified in this Consent Form, only in anonymized or de-identified form, unless I provide explicit additional consent. ☐ allow ☐ not allow ▪ I consent Gene Solutions to share my personal data to the parties as mentioned in this Consent Form, only to the extent necessary. Each receiving party is obligated to maintain confidentiality and implement security safeguards as required by the applicable regulations. ▪ I understand that all sharing will remain within the purposes stated in this Consent Form and fully comply with the current applicable regulations. ▪ I understand that I have the rights and obligations in accordance with the current applicable regulations. I may exercise these rights by contacting Gene Solutions via the contact information as provided herein. ▪ I understand that my personal data will be stored for the duration necessary to provide testing services, or for the legally required period for medical and regulatory compliance. ▪ I warrant that the information provided by me under this Informed Consent Form is truthful, complete and accurate. Gene Solutions shall not be liable for any loss or damages caused by untruthful, incomplete or inaccurate information provided by me. ▪ Where I am the patient's representative, I warrant that I am the valid representative by law or under a valid decision or judgment of the court or competent authority, and I have the full rights and obligations to represent the patient in all personal and legal matters, including the matters set forth in this Informed Consent Form.	Signature of **Patient / Patient's Representative** Full Name:…… Date: *(DD/MM/YY)*……
▪ I have fully explained the test, including its benefits, risks, and available alternatives, to the clients in accordance with applicable legal requirements, and have answered all their questions. ☐ I request not to receive germline mutation results as part of this test report.	**Physician Signature** Full Name:…… Date: *(DD/MM/YY)*……

(*) Gene Solutions complies with all relevant data protection and privacy laws; please refer to genesolutions.com for details of the data privacy policy.

PERSONAL DATA COLLECTION NOTICE

A. PURPOSES

Purposes for the collection and processing of patients' personal data:

- Conducting testing activities, diagnostics, providing advice, consultation, relevant guidance, and other healthcare related activities in accordance with the laws on medical examination and treatment;
- Performing other health-related services and activities requested by the patient and provided by Gene Solutions;
- Conducting internal management, reporting, archiving, and fulfilling statutory obligations of Gene Solutions under the laws on personal data protection and requirements of competent authorities.

B. TYPES OF PERSONAL DATA PROCESSED

Depending on the test requested, the personal data collected and processed includes basic personal data and sensitive personal data as defined under the applicable regulations on personal data protection:

- Basic Personal Data includes: full legal name; date of birth; gender; place of birth; address; nationality; phone number; personal identification number; marital status; and other identifying information.
- Sensitive Personal Data includes: health status; medical conditions; genetic characteristics; genetic data from tests; biometric identifiers; images of ID cards; and login credentials linked to digital identity accounts.

C. DATA PROCESSING ACTIVITIES

Gene Solutions will carry out data processing activities arising from genetic sequencing, which may include but are not limited to: collection, recording, analysis, storage, modification, disclosure, access, retrieval, encryption, decryption, copying, sharing, transmission, provision, transfer, deletion, destruction, and other actions as permitted by the applicable regulations.

D. DATA CONTROLLER AND DATA PROCESSOR

Gene Solutions is the data controller and processor of the patient's personal data under the current law on Personal Data Protection .

For any questions or communications regarding personal data processing, please contact:

- Tel: +66 99-345-2242

Gene Solutions may share personal data, to the extent permitted by law, with:

- Healthcare personnel and healthcare institutions (hospitals/ clinics) providing medical examination and treatment to the patient;
- Administrative staffs of Gene Solutions or its affiliate companies;
- Third parties who are authorized to process personal data to ensure the most effective medical examination and treatment. However, these organizations and individuals are bound by strict data confidentiality obligations under the applicable laws and under contracts signed with Gene Solutions;
- The requesting physician/ clinics/ hospitals for research, scientific purposes.

E. RIGHTS AND OBLIGATIONS OF THE PATIENT

Unless otherwise provided by the applicable law, the patient has the following rights and obligations regarding their personal data:

Rights:

- to request access to and copies of my personal data;
- to obtain explanations regarding data processing activities;
- to request correction, update or deletion of their personal data;
- to withdraw consent at any time by contacting Gene Solutions, noting that Gene Solutions will be released from any obligations that cannot be performed without necessary personal data;
- to file complaints, denunciations, or initiate lawsuits with competent authorities concerning violations of personal data rights.

Obligations:

- to provide complete and accurate personal data when allowing Gene Solutions to process personal data;
- to self-protect their personal data;
- to comply with the applicable regulations on the protection of personal data.

F. DE-IDENTIFIED INFORMATION

Gene Solutions may use the patient's residual samples and de-identified information for research and scientific purposes. These studies may be published in scientific journals or used for product and service development. The patient will not be notified or compensated for these research activities.

SCOPE OF THE TEST

Panel	Cancer Type	Somatic Mutations (Actionable/Resistance)	ctDNA-MRD Monitoring*	MSI Status	Germline Mutations*	
					Hereditary Cancer Risk	Pharmaco genomics
Thoracic Cancers	Lung Cancer	✓	✓	✓	✓	
	Mediastinal Cancer	✓	✓	✓	✓	
	Mesothelioma Cancer	✓	✓	✓	✓	
Digestive Cancers	Ampulla of Vater	✓	✓	✓	✓	✓
	Bladder Cancer	✓	✓	✓	✓	
	Cholangiocarcinoma	✓	✓	✓	✓	
	Colorectal Cancer	✓	✓	✓	✓	✓
	Esophageal Cancer	✓	✓	✓	✓	✓
	Gallbladder Cancer	✓	✓	✓	✓	
	Gastric Cancer	✓	✓	✓	✓	✓
	GIST	✓	✓	✓	✓	
	Liver Cancer	✓	✓	✓	✓	
	Pancreatic Cancer	✓	✓	✓	✓	✓
Breast & Gynecological Cancers	Breast Cancer	✓	✓	✓	✓	✓
	Cervical Cancer	✓	✓	✓	✓	
	Endometrial Cancer	✓	✓	✓	✓	
	Fallopian Tube Cancer	✓	✓	✓	✓	
	Ovarian Cancer	✓	✓	✓	✓	
	Uterine Cancer	✓	✓	✓	✓	
Other	Prostate Cancer	✓		✓	✓	

✓ *Applicable to all cancer stages* ✓ *Applicable to metastatic stage*

** The K-TRACK (Tumor Profiling Only) test does not report results for ctDNA-MRD monitoring and germline mutations.*
See pages 6 and 7 for detailed gene panels.

A. INTENDED USE

K-TRACK

This comprehensive genomic profiling test, designed for 20 solid tumors, aligns with recommendations from the National Comprehensive Cancer Network (NCCN), European Society for Medical Oncology (ESMO), and U.S. Food and Drug Administration (FDA). By identifying patient-specific molecular alterations, the test enables clinicians to:

- **Provide personalized treatment:** Determine the most appropriate targeted therapy and/or immunotherapy for each individual.
- **Monitor treatment response:** Assess response to therapy and identify potential resistance mechanisms.
- **Detect early recurrence:** Monitor for molecular signs of disease recurrence, enabling proactive surveillance and intervention.

This approach provides a **comprehensive genomic landscape** of the tumor and liquid biopsy, facilitating **informed clinical decision-making** and potentially improving patient outcomes.

TEST RESULT

- **Actionable mutations and resistance mutations** for targeted therapy, including single nucleotide variants, small and large indels (**SNVs, INDELs**), **amplification, fusion,** detected by FFPE DNA-sequencing combined with Liquid biopsy profiling.
- **Microsatellite instability (MSI)** is an independent marker associated with response to immunotherapy and chemotherapy in advanced solid tumors.
- **Germline mutations (using white blood cell sample)** for the genetic mutations that run in families, including biallelic inactivation status.
- **Minimal residual disease (MRD)/Dynamics of ctDNA (using plasma sample)** to monitor early recurrence or assess response to therapy.

K-TRACK (n)

A **follow-up ctDNA-MRD test** leveraging the previously established personalized genomic profile for **longitudinal** monitoring.

B. METHODOLOGY

K-TRACK:

K-TRACK is a comprehensive tumor and liquid biopsy profiling assay. Genomic DNA (gDNA) was extracted from formalin-fixed paraffin-embedded (FFPE) tumor using AllPrep DNA/RNA FFPE Kit (Qiagen, Germany). gDNA was extracted from white blood cells (WBC) using GeneJET Genomic DNA Purification kit (Thermo Scientific, USA). For DNA analysis, DNA libraries from matching FFPE and WBC were prepared using the NEBNext Ultrashear FFPE DNA and NEBNext Ultra II FS DNA library preparation kits (New England Biolabs, USA) respectively, then pooled together and hybridized with probes targeting 164 genes (IDT, USA) to identify somatic and germline biomarkers. For ctDNA-MRD analysis, cell-free DNA (cfDNA) was extracted from plasma samples using the MagMAX cell-free DNA Isolation kit (Applied Biosystems, USA). cfDNA libraries barcoded with unique molecular identifiers (UMI) were prepared by the xGen™ cfDNA Library Prep v2 MC kit (IDT, USA), pooled and hybridized with custom probes (IDT, USA). All libraries were sequenced on the next-generation sequencing (NGS) platform in paired-read mode. Sequenced reads were aligned to human reference genome (GRCh38) for analysis.

DNA ANALYSIS

- For somatic mutations, variants were called using DRAGEN somatic pipeline from tumor sample and variant allele frequency (VAF) was computed using empirical read counts for each allele.
- For germline mutations, variants were called using DRAGEN germline pipeline from white blood cell sample, and pathogenicity was classified according to ACMG standards.
- For MSI, the percentage of unstable repeat loci was calculated using MSIsensor-pro, and the cut-off for MSI-High is 20%.
- For copy number variant at gene-level, DRAGEN somatic CNV pipeline was used, with copy ratio of the segment mean being ≥ 2.0.
- For fusion mutation, in-house algorithm was used with a cut-off of at least two breakpoint-spanning reads.

ctDNA-MRD ANALYSIS

Both tumor-derived and tumor-agnostic somatic mutations, including SNVs, indels, amplification and fusions, were examined in the liquid biopsy, using in-house ultra-sensitive read-based variant calling algorithm (variant-level LOD = 0.1%). Up to 20 tumor-derived mutations were selected from paired tumor-normal sequencing data and ranked based on in-house proprietary algorithm. A sample was considered positive for ctDNA if at least one mutation was found positive in liquid biopsy (sample-level ctDNA-MRD LOD = 0.01%).

K-TRACK (n)

K-TRACK (n) is a follow-up ctDNA-MRD blood test for patients who already have K-TRACK test and an established profile of ctDNA biomarkers. Cell-free DNA (cfDNA) was extracted from plasma samples using the MagMAX cell-free DNA Isolation kit (Applied Biosystems,USA). cfDNA libraries barcoded with unique molecular identifiers (UMI) were prepared by the xGen™ cfDNA Library Prep v2 MC kit (IDT, USA), pooled and hybridized with custom probes (IDT, USA). All libraries were then sequenced on the NGS platform in paired-read mode. Both tumor-derived and tumor-agnostic somatic mutations, together with ctDNA-MRD status were examined and reported similar to K-TRACK.

C. LIMITATIONS

- The K-TRACK 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 include point mutations, short insertions and deletions (less than 20 nucleotides) in the coding region and in the vicinity of intron (20/+10 nucleotides from exon) of all the genes in the panel. For large insertions and deletions (20–500 bp) or exon-level deletions (≥3 exons), the test only examines *BRCA1, BRCA2, MSH6, PMS2, MSH2, MLH1, APC* genes, with a minimum VAF threshold of ≥ 25%.
- Detection of variants outside the coding region, large insertions and deletions in other genes, short continuous repeats (nucleotide repeats), CG-rich region, high homologous regions (pseudogenes) and mosaicism may not be reliable in this test.
- The test does not examine 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 a gene not covered by this test.
- The ctDNA test result is TIME-DEPENDENT. Therefore, a K-TRACK result indicating negative ctDNA-MRD 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.
- This test serves as a valuable adjunct to existing methodologies for monitoring recurrence and evaluating treatment efficacy, offering additional insights and assisting the informed decision-making process for effective treatment strategies.
- The test may not provide accurate results in the following scenarios:
  For tumor profiling, a negative result could be false-negative due to
  - The quantity and quality of the tissue sample (FFPE) does not meet the requirements for next-generation sequencing, or
  - Tumor fraction is below 20%.

  For liquid biopsy profiling,
  - When ctDNA level is negative, a negative result for somatic mutations could be false-negative;
  - When ctDNA level is below 2%, a negative result for amplification status could be false-negative;

  For ctDNA-MRD detection, a negative result could be false-negative due to
  - No cancer-specific mutations are identified, or mutation is not covered by the gene panel, or
  - Poor quality of blood sample with extensive white blood cell lysis, or
  - Low cfDNA yield, resulting in cfDNA input below 15 ng, or
  - The tumor has low ctDNA-shedding rate, often attributable to factors such as tumor location and cancer type, or
  - ctDNA level is below LOD of the test.

D. SAMPLE REQUIREMENTS

FFPE TISSUE SAMPLE (choose 1 option)

- **BLOCKS:** Provide FFPE tissue blocks with a tissue size of approximately 4 mm × 4 mm and a minimum total block thickness of ≥50 µm..
- **SLIDES:** Provide 10–20 unstained slides from a single FFPE block. Slides must be unbaked and sectioned at a thickness of 7–10 µm.
- **RIBBONS:** Provide FFPE tissue sectioned into ribbon form. Submit 8–12 ribbons/tube sectioned at a thickness of 10 µm, with each ribbon measuring approximately 4 mm × 4 mm. Place ribbons into 1.5 mL or 2 mL microcentrifuge tubes, using multiple tubes as required (preferably 2 tubes).

BLOOD SAMPLE

- Provide 10–20 mL of whole blood collected in Streck tubes (preferably 20 mL).

F. RESEARCH

We may use residual samples and de-identified patient information for research purposes. These studies may be published in scientific journals or used for the development of our products and services. Patients will not be notified or compensated for these research activities.

TUMOR PROFILING

164-GENE PANEL

All gene - full exon ● Amplification ● Fusion

1	*ACVR2A*	29	*CIC*	57	*FGFR2* ●	85	*LRP1B*	113	*PARP1*	141	*RHOA*
2	*AFF3*	30	*CREBBP*	58	*FGFR3* ●	86	*MAP2K1*	114	*PBRM1*	142	*RNF213*
3	*AKT1*	31	*CSDE1*	59	*FH*	87	*MAP2K4*	115	*PDE4DIP*	143	*RNF43*
4	*ALK* ●	32	*CTCF*	60	*FHIT*	88	*MAP3K1*	116	*PDGFRA*	144	*ROS1* ●
5	*AMER1*	33	*CTNNB1*	61	*FLT1*	89	*MAX*	117	*PDPK1*	145	*SETD2*
6	*APC*	34	*DICER1*	62	*FOXA1*	90	*MDM2*	118	*PIK3C2G*	146	*SF3B1*
7	*AR*	35	*DPYD*	63	*FOXP1*	91	*MED12*	119	*PIK3CA*	147	*SLC34A2*
8	*ARID1A*	36	*DNMT3B*	64	*GATA3*	92	*MEN1*	120	*PIK3CD*	148	*SLC3A2*
9	*ARID1B*	37	*DOT1L*	65	*GNA11*	93	*MET* ●	121	*PIK3R1*	149	*SMAD4*
10	*ARID2*	38	*EGFR*	66	*GNAS*	94	*MGA*	122	*PMS2*	150	*SMARCA4*
11	*ASXL2*	39	*EIF1AX*	67	*GRIN2A*	95	*MLH1*	123	*POLD1*	151	*SOX9*
12	*ATP1B1*	40	*ELF3*	68	*HRAS*	96	*MSH2*	124	*POLE*	152	*STAT5A*
13	*ATM*	41	*EP300*	69	*IDH1*	97	*MSH6*	125	*PRDM14*	153	*STK11*
14	*ATR*	42	*EPCAM*	70	*IDH2*	98	*MTOR*	126	*PREX2*	154	*TBX3*
15	*AXIN1*	43	*EPHA3*	71	*IGF2*	99	*MUTYH*	127	*PRKD1*	155	*TCF7L2*
16	*BCOR*	44	*EPHA5*	72	*IKZF1*	100	*NCOR1*	128	*PTCH1*	156	*TERT promoter*
17	*BRAF*	45	*EPHA7*	73	*INPP4B*	101	*NCOR2*	129	*PTEN*	157	*TP53*
18	*BRCA1*	46	*EML4*	74	*KDM6A*	102	*NF1*	130	*PTPN13*	158	*TPM3*
19	*BRCA2*	47	*ERBB2* ●	75	*KDR*	103	*NFE2L2*	131	*PTPRB*	159	*TRRAP*
20	*BRIP1*	48	*ERBB3*	76	*KEAP1*	104	*NOTCH1*	132	*PTPRD*	160	*TSC1*
21	*CAMTA1*	49	*ERBB4*	77	*KIF5B*	105	*NOTCH2*	133	*PTPRS*	161	*TSC2*
22	*CASP8*	50	*ERCC3*	78	*KIT*	106	*NRAS*	134	*PTPRT*	162	*VHL*
23	*CD74*	51	*ERCC4*	79	*KMT2A*	107	*NRG1* ●	135	*RAB35*	163	*ZFHX3*
24	*CDH1*	52	*ESR1*	80	*KMT2B*	108	*NSD1*	136	*RARA*	164	*ZNF521*
25	*CDK12*	53	*EZR*	81	*KMT2C*	109	*NTRK1* ●	137	*RASA1*		
26	*CDKN2A*	54	*FAT1*	82	*KMT2D*	110	*NTRK2* ●	138	*RB1*		
27	*CHD4*	55	*FAT4*	83	*KNSTRN*	111	*NTRK3* ●	139	*RBM10*		
28	*CHEK2*	56	*FBXW7*	84	*KRAS*	112	*PALB2*	140	*RET* ●		

43-GENE GERMLINE PANEL

1	*ALK*	9	*CHEK2*	17	*HRAS*	25	*MUTYH*	33	*PTCH1*	41	*TSC1*
2	*APC*	10	*DICER1*	18	*KIT*	26	*NF1*	34	*PTEN*	42	*TSC2*
3	*ATM*	11	*DPYD*	19	*MAX*	27	*NF2*	35	*RET*	43	*VHL*
4	*BRCA1*	12	*EGFR*	20	*MEN1*	28	*PALB2*	36	*RNF43*		
5	*BRCA2*	13	*EPCAM*	21	*MET*	29	*PDGFRA*	37	*SMAD4*		
6	*BRIP1*	14	*ERCC3*	22	*MLH1*	30	*PMS2*	38	*SMARCA4*		
7	*CDH1*	15	*ERCC4*	23	*MSH2*	31	*POLD1*	39	*STK11*		
8	*CDKN2A*	16	*FH*	24	*MSH6*	32	*POLE*	40	*TP53*		

GENE SOLUTIONS K-TRACK | TEST INFORMATION

LIQUID BIOPSY PROFILING

125-GENE PANEL FOR THORACIC CANCERS

● Full exon ● Amplification ● Fusion

1	*ACVR2A*	22	*CAMTA1*	43	*EP300*	64	*KIT*	85	*NSD1*	106	*RB1*
2	*AFF3*	23	*CASP8*	44	*EPHA3*	65	*KMT2A*	86	*NTRK1* ●	107	*RBM10*
3	*AKT1*	24	*CDC73*	45	*EPHA5*	66	*KMT2C*	87	*NTRK2* ●	108	*RET* ●●
4	*ALK* ●●	25	*CDH1*	46	*EPHA7*	67	*KMT2D*	88	*NTRK3* ●	109	*RNF213*
5	*AMER1*	26	*CDK12*	47	*ERBB2* ●●	68	*KRAS* ●	89	*PALB2*	110	*RNF43*
6	*APC* ●	27	*CDKN2A*	48	*ERBB3*	69	*LRP1B*	90	*PBRM1*	111	*ROS1*
7	*AR*	28	*CDKN2B*	49	*ERBB4*	70	*MAP2K1* ●	91	*PDE4DIP*	112	*SETD2*
8	*ARAF*	29	*CHD4*	50	*ESR1*	71	*MAP2K4*	92	*PDGFRA*	113	*SF3B1*
9	*ARID1A*	30	*CHEK2*	51	*FAT1*	72	*MAX*	93	*PIK3C2G*	114	*SMAD4*
10	*ARID1B*	31	*CIC*	52	*FAT4*	73	*MEN1*	94	*PIK3CA* ●	115	*SMARCA4* ●
11	*ARID2*	32	*CREBBP*	53	*FBXW7*	74	*MET* ●●	95	*PIK3R1*	116	*STK11* ●
12	*ASXL2*	33	*CSDE1*	54	*FGFR2*	75	*MGA*	96	*PMS2*	117	*TERT promoter*
13	*ATM*	34	*CTCF*	55	*FGFR3*	76	*MSH2*	97	*POLD1*	118	*TP53* ●
14	*ATR*	35	*CTNNB1*	56	*FHIT*	77	*MTOR*	98	*POLE*	119	*TRRAP*
15	*AXIN1*	36	*DDR2*	57	*FOXA1*	78	*NCOR1*	99	*PREX2*	120	*TSC1*
16	*B2M*	37	*DICER1*	58	*GATA3*	79	*NF1*	100	*PRKD1*	121	*TSC2*
17	*BARD1*	38	*DNMT1*	59	*GRIN2A*	80	*NFE2L2*	101	*PTEN*	122	*TSHR*
18	*BCOR*	39	*DNMT3B*	60	*HRAS*	81	*NOTCH1*	102	*PTPRB*	123	*ZFHX3*
19	*BRAF* ●	40	*EGFR* ●	61	*IDH1*	82	*NOTCH2*	103	*PTPRD*	124	*ZMYM3*
20	*BRCA1*	41	*EIF1AX*	62	*INPP4B*	83	*NRAS* ●	104	*PTPRS*	125	*ZNF521*
21	*BRCA2*	42	*ELF3*	63	*KEAP1* ●	84	*NRG1*	105	*PTPRT*		

113-GENE PANEL FOR DIGESTIVE CANCERS

● Full exon ● Amplification ● Fusion

1	*ACVR2A*	20	*BRCA1* ●	39	*ERBB4*	58	*KMT2C*	77	*NTRK3* ●	96	*RNF43*
2	*ADGRG6*	21	*BRCA2* ●	40	*ESR1*	59	*KMT2D*	78	*PALB2* ●	97	*ROS1*
3	*AFF3*	22	*CAMTA1*	41	*FANCA*	60	*KRAS* ●	79	*PBRM1*	98	*RPTOR*
4	*AKT1*	23	*CASP8*	42	*FAT1*	61	*LRP1B*	80	*PDE4DIP*	99	*SETD2*
5	*ALK*	24	*CDH1*	43	*FAT4*	62	*MAP2K1*	81	*PDGFRA* ●	100	*SF3B1*
6	*AMER1*	25	*CDK12*	44	*FBXW7*	63	*MAP3K1*	82	*PIK3CA* ●	101	*SMAD4*
7	*ANKRD11*	26	*CDKN2A*	45	*FGFR2* ●	64	*MET* ●●	83	*PIK3R1*	102	*SMARCA4*
8	*APC* ●	27	*CIC*	46	*FGFR3* ●	65	*MSH6*	84	*POLD1*	103	*SOX9*
9	*AR*	28	*CREBBP*	47	*FOXP1*	66	*MTOR*	85	*POLE* ●	104	*STK11*
10	*ARAF*	29	*CTCF*	48	*GATA3*	67	*NCOR1*	86	*PREX2*	105	*TCF7L2*
11	*ARID1A*	30	*CTNNB1*	49	*GNAS*	68	*NF1*	87	*PTEN*	106	*TERT*
12	*ARID1B*	31	*DOT1L*	50	*GRIN2A*	69	*NFE2L2*	88	*PTPN13*	107	*TP53* ●
13	*ARID2*	32	*EGFR*	51	*HRAS*	70	*NOTCH1*	89	*PTPRB*	108	*TRRAP*
14	*ATM*	33	*ELF3*	52	*IDH1* ●	71	*NOTCH2*	90	*PTPRT*	109	*TSC1*
15	*ATR*	34	*EP300*	53	*IDH2* ●	72	*NRAS* ●	91	*RB1*	110	*TSC2*
16	*AXIN1*	35	*EPCAM*	54	*KDM6A*	73	*NRG1*	92	*RBM10*	111	*TSHR*
17	*B2M*	36	*EPHA5*	55	*KEAP1*	74	*NSD1*	93	*RET* ●●	112	*ZFHX3*
18	*BCOR*	37	*ERBB2* ●●	56	*KIT* ●	75	*NTRK1* ●	94	*RHOA*	113	*ZNF521*
19	*BRAF* ●	38	*ERBB3*	57	*KMT2A*	76	*NTRK2* ●	95	*RNF213*		

149-GENE PANEL FOR BREAST & GYNECOLOGICAL CANCERS

● Full exon ● Amplification ● Fusion

1	*ACVR2A*	26	*CHD7*	51	*GLI1*	76	*MED12*	101	*PIK3CA* ●	126	*SF3B1*
2	*AFF3*	27	*CIC*	52	*GLI2*	77	*MEN1*	102	*PIK3R1*	127	*SMAD4*
3	*AKT1* ●	28	*CREBBP*	53	*GNAS*	78	*MET* ●●	103	*PMS2*	128	*SMARCA4*
4	*ALK*	29	*CTCF*	54	*GRIN2A*	79	*MGA*	104	*POLD1*	129	*SMARCB1*
5	*AMER1*	30	*CTNNB1*	55	*HRAS*	80	*MLH1*	105	*POLE* ●	130	*SMYD3*
6	*APC* ●	31	*DICER1*	56	*IDH1*	81	*MRE11*	106	*PPP2R1A*	131	*SNCAIP*
7	*AR*	32	*DNMT3A*	57	*IDH2*	82	*MTOR*	107	*PRDM14*	132	*SOX9*
8	*ARID1A*	33	*DOT1L*	58	*IGF1R*	83	*NCOR1*	108	*PREX2*	133	*SPEN*
9	*ARID1B*	34	*EGFR*	59	*IKZF1*	84	*NCOR2*	109	*PRKD1*	134	*SPOP*
10	*ARID2*	35	*EP300*	60	*IRS1*	85	*NF1*	110	*PTEN* ●	135	*STAG2*
11	*ATM*	36	*ERBB2* ●●	61	*JAK1*	86	*NFE2L2*	111	*PTPN13*	136	*STAT5A*
12	*ATR*	37	*ERBB3*	62	*JAK3*	87	*NOTCH1*	112	*PTPRB*	137	*STK11*
13	*AXIN1*	38	*ERBB4*	63	*KDM5A*	88	*NOTCH2*	113	*PTPRD*	138	*STK40*
14	*BAP1*	39	*ERCC3*	64	*KDM5C*	89	*NOTCH4*	114	*PTPRT*	139	*TBX3*
15	*BCOR*	40	*ERCC4*	65	*KDM6A*	90	*NRAS*	115	*RAD54L*	140	*TCF7L2*
16	*BRAF* ●	41	*ESR1* ●	66	*KEAP1*	91	*NRG1*	116	*RARA*	141	*TEK*
17	*BRCA1* ●	42	*FAT1*	67	*KIT*	92	*NSD1*	117	*RASA1*	142	*TOP1*
18	*BRCA2* ●	43	*FAT4*	68	*KMT2A*	93	*NTRK1* ●	118	*RB1*	143	*TP53* ●
19	*BRD4*	44	*FBXW7*	69	*KMT2C*	94	*NTRK2* ●	119	*RBM10*	144	*TRRAP*
20	*CASP8*	45	*FGFR2*	70	*KMT2D*	95	*NTRK3* ●	120	*RET* ●●	145	*TSC1*
21	*CBFB*	46	*FGFR3*	71	*KRAS* ●	96	*PALB2* ●	121	*RNF213*	146	*TSC2*
22	*CDH1*	47	*FOXA1*	72	*LRP1B*	97	*PARP1*	122	*RNF43*	147	*VHL*
23	*CDK12*	48	*FOXP1*	73	*MAP2K4*	98	*PBRM1*	123	*ROS1*	148	*ZFHX3*
24	*CDKN2A*	49	*GABRG1*	74	*MAP3K1*	99	*PDE4DIP*	124	*RUNX1*	149	*ZNF521*
25	*CHD4*	50	*GATA3*	75	*MAX*	100	*PIK3C2G*	125	*SETD2*		

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