iBio - SOLID TUMOR PANEL

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SOLID TUMOR PANEL

- One test to detect genetic alterations of 52 oncogenes commonly involved in cancer.
- Detection of most common, actionable genetic alterations of lung cancer, colon cancer, pancreatic cancer, stomach cancer, melanoma, etc.
- Detection of *NTRK1, NTRK2* and *NTRK3* fusions.

Most relevant investigated genes*

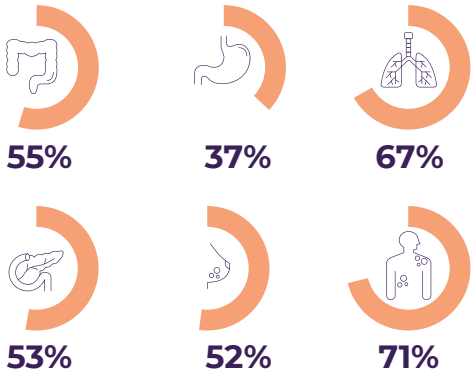
LUNG	COLON	MELANOMA	PANCREAS	BREAST	STOMACH
ALK	AKT1	BRAF	ALK	AKT1	ATM
BRAF	ALK	KIT	BRAF	ERBB2	ERBB2
EGFR	ATM	MAP2K1	ERBB2	ERBB3	ERBB3
ERBB2	BRAF	NRAS	FGFR2	ESR1	FGFR2
ERBB3	ERBB2	NTRK1	IDH1	NTRK1	NTRK1
FGFR1	KRAS	NTRK2	KRAS	NTRK2	NTRK2
KRAS	MET	NTRK3	MET	NTRK3	NTRK3
MAP2K1	NRAS		NTRK1	PIK3CA	PIK3CA
MET	NTRK1		NTRK2		RET
NTRK1	NTRK2		NTRK3		ROS1
NTRK2	NTRK3		PIK3CA		
NTRK3	PIK3CA		RET		
PIK3CA	RET		ROS1		
RET					
ROS1					

*Based on ESCAT tiers and OncoKB data

PRECISION ONCOLOGY

- Molecular diagnosis of clinically actionable mutations is the basis of precision oncology.
- Multigene tests identify such genetic alterations in over half of patients.
- Broad molecular assays are cost-efficient and indispensable for ongoing clinical studies.

Expected prevalence of mutations*



*Prevalence of potentially actionable mutations of genes tested in the panel based on cBioPortal data

- Multigene molecular tests are advisable in cases of **lung cancer, advanced cancer with poor prognosis, rare malignancies** and **cancer of unknown primary.**

METHOD

- Formalin fixed paraffin embedded (FFPE) tissue block, or other tumor-cell containing sample.
- Recommended tumor cell ratio: ≥20%
- Bioinformatic identification of single nucleotide variants (**SNV**), short insertions and deletions as well as copy number variations (**CNV**) and **fusion transcripts.**
- Variant classification and annotation (e.g., ClinVar, COSMIC, HGMD, Varsome, etc.)

LIST OF INVESTIGATED GENES

SNV, short insertions/deletions (hotspots) and copy number changes: AKT1, ALK, AR, BRAF, CCND1, CDK4, CDK6, CTNNB1, DDR2, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FGFR1, FGFR2, FGFR3, FGFR4, GNA11, GNAQ, HRAS, IDH1, IDH2, JAK1, JAK2, JAK3, KIT, KRAS, MAP2K1, MAP2K2, MET, MTOR, MYC, MYCN, NRAS, PDGFRA, PIK3CA, RAF1, RET, ROS1, SMO

Most common fusion transcripts: AB1L, ALK, AKT3, AXL, BRAF, EGFR, ERBB2, ERG, ETV1, ETV4, ETV5, FGFR1, FGFR2, FGFR3, MET, NTRK1, NTRK2, NTRK3, PDGFRA, PPARG, RAF1, RET, ROS1

COVERAGE: >95% (>500×)

AVERAGE SEQUENCING DEPTH: >1000×

TURNAROUND TIME: 2-3 WEEKS

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iBio SCIENCE

UNIVERSITY OF PÉCS
SZENTÁGOTHAI RESEARCH CENTRE

WORKFLOW

Our mission is advancing scientific research in the fields of **BIOTECHNOLOGY** and **MEDICINE** as well as applying the latest innovative technologies in diagnostics. **IBIOSCIENCE LTD.** in collaboration with **UNIVERSITY OF PÉCS SZENTÁGOTHAI RESEARCH CENTER** provides state-of-the-art next generation sequencing services and expertise for the Hungarian scientific community.

01 **CONTACT**
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02 **SAMPLE DISPATCH**
FFPE block or slides,
cell blocks or smears,
or isolated DNA/RNA

03 **SAMPLE PROCESSING**
microscopical control
of tumor cell ratio,
DNA and RNA isolation

04 **GENETIC ANALYSIS**
bioinformatic analysis,
variant identification
and annotation

05 **REPORT**
categorization of variants
based on guidelines
(pathogenic, likely
pathogenic, VUS etc.)

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