OncoDNA®
THE CANCER THERANOSTIC COMPANY

International User Group Meeting

22nd and 23rd of April 2026

The experience of implementing OncoDEEP and OncoSELECT enabled by an MGI sequencer

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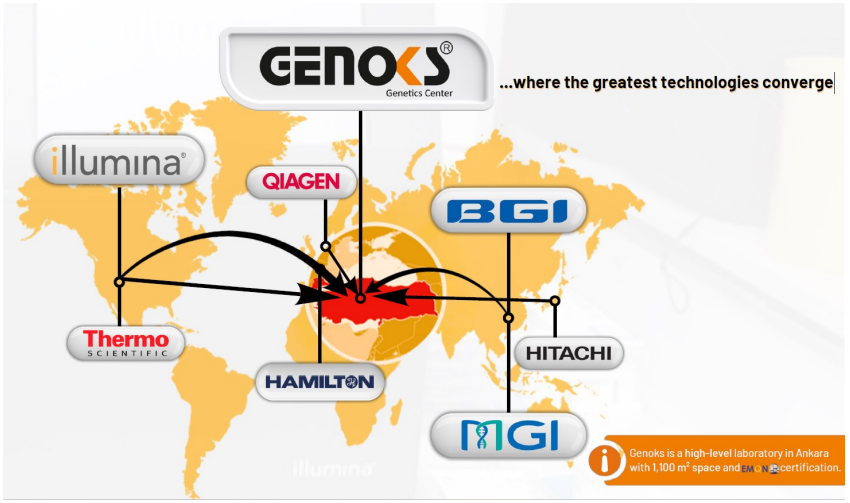
www.genoks.com.tr

T.C. SAĞLIK BAKANLIĞI Ruhsat No: GHDM-SM/06.15/01 · POWERED BY illumina · BGI · MGI · OncoDNA THE CANCER THERANOSTIC COMPANY · EMQN · CE IVD · ISO 27001 · ISO 14001 · ISO 9001

Who we are;



What we do;

- GenoXhere-PLUS
- GenoXhere-PRIME
- GenoXhere-BRCA
- GenoXhere-breast/ovarian
- GenoXhere-colon
- GenoXhere-prostate

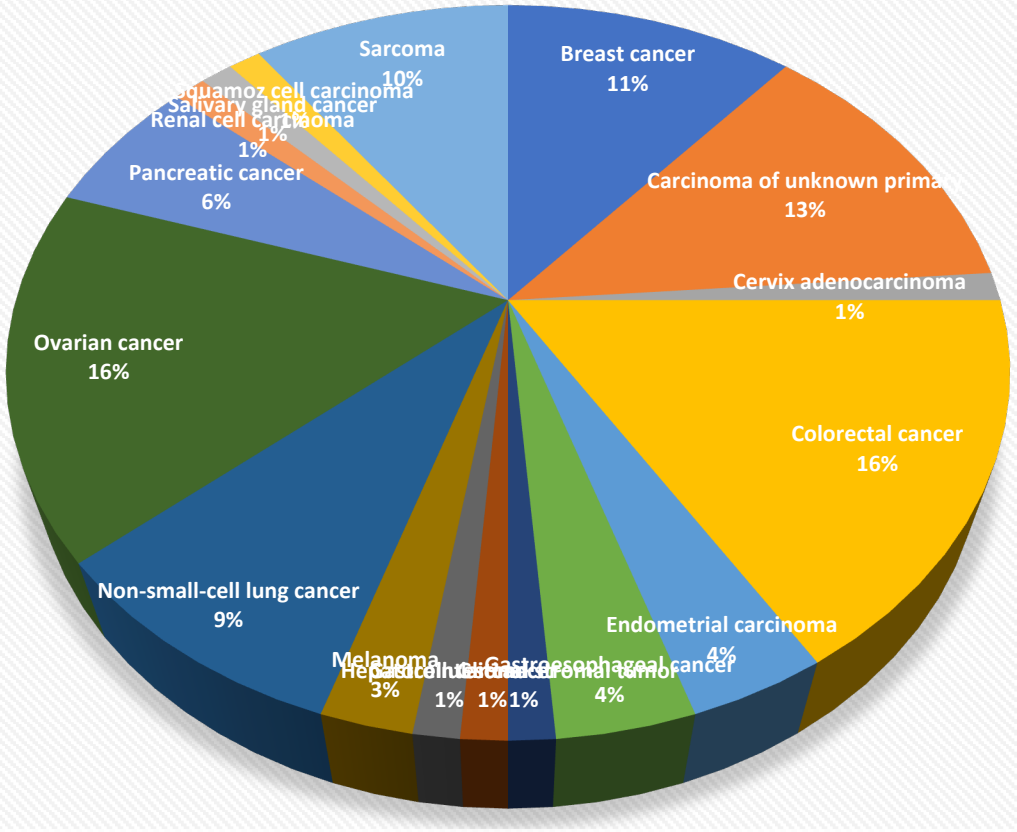
Hereditary Cancers

- GenoXolid-PLUS (OncoDeep)

Solid Tumor

- GenoXliquid (OncoSelect)
- GeneXheme

Liquid Biopsy & Hematological Malignancies


Breast cancer
11%
Carcinoma of unknown prima
13%
Cervix adenocarcinoma
1%
Colorectal cancer
16%
Endometrial carcinoma
4%
Gastroesophageal cancer
4%
Gastrointestinal stromal tumor
1%
Glioma
1%
Hepatocellular cancer
1%
Melanoma
3%
Non-small-cell lung cancer
9%
Ovarian cancer
16%
Pancreatic cancer
6%
Renal cell carcinoma
1%
Salivary gland cancer
1%
Squamoz cell carcinoma
1%
Sarcoma
10%
Breast cancer
Carcinoma of unknown primary
Cervix adenocarcinoma
Colorectal cancer
Endometrial carcinoma
Gastroesophageal cancer
Gastrointestinal stromal tumor
Glioma
Hepatocellular cancer
Melanoma
Non-small-cell lung cancer
Ovarian cancer
Pancreatic cancer
Renal cell carcinoma
Salivary gland cancer
Squamoz cell carcinoma
Sarcoma

Why Oncodeep?

RT-PCR Kits → **NGS Panel Kits (DNA)** → **NGS Panel Kits (DNA+RNA Fusion)** → **CGP Kits (DNA+RNA Fusion+HRD+MSI+TMB)**

Oncodeep

- ✓ ALL IN ONE (DNA+RNA Fusion+HRD+MSI+TMB)
- ✓ CE-IVD
- ✓ Power of marketing
- ✓ Ease of wet-lab
- ✓ Bioinformatics interface and reporting user-friendly
- ✓ Robust solution

- ✓ **Preventing unnecessary labor**
- ✓ **Saving time**
- ✓ **Fasting results** → **Early Access Targeted Therapy**

Why we use MGI platfotms;

DNBSEQ-T7

DNBSEQ-G400

MGI

- ✓ **Low library conc. ⟶ Sequencing**
- ✓ **Mix Run**
- ✓ **Different Index/Adapter**
- ✓ **Cost Effective**

Validation of Oncodeep

DNBSEQ-G400

- **First Run**

Same wet-lab

DNBSEQ-T7

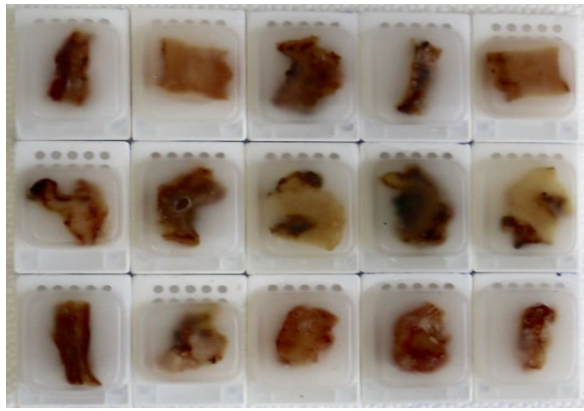
- **Routine**

- ✓ **Data comparison**
- ✓ **Concordance**
- ✓ **Evaluated by Genoks Team & OncoDNA FAS Technical Team**

Validation Challenges

- **FFPE**
- ✓ **Fixation Process**
- ✓ **Tumour Rate**
- ✓ **Tumour Necrose Rate**

- **Lack of predefined validation of framework**



https://www.precisionformedicine.com/biospecimens/tissues/ffpe-tissue

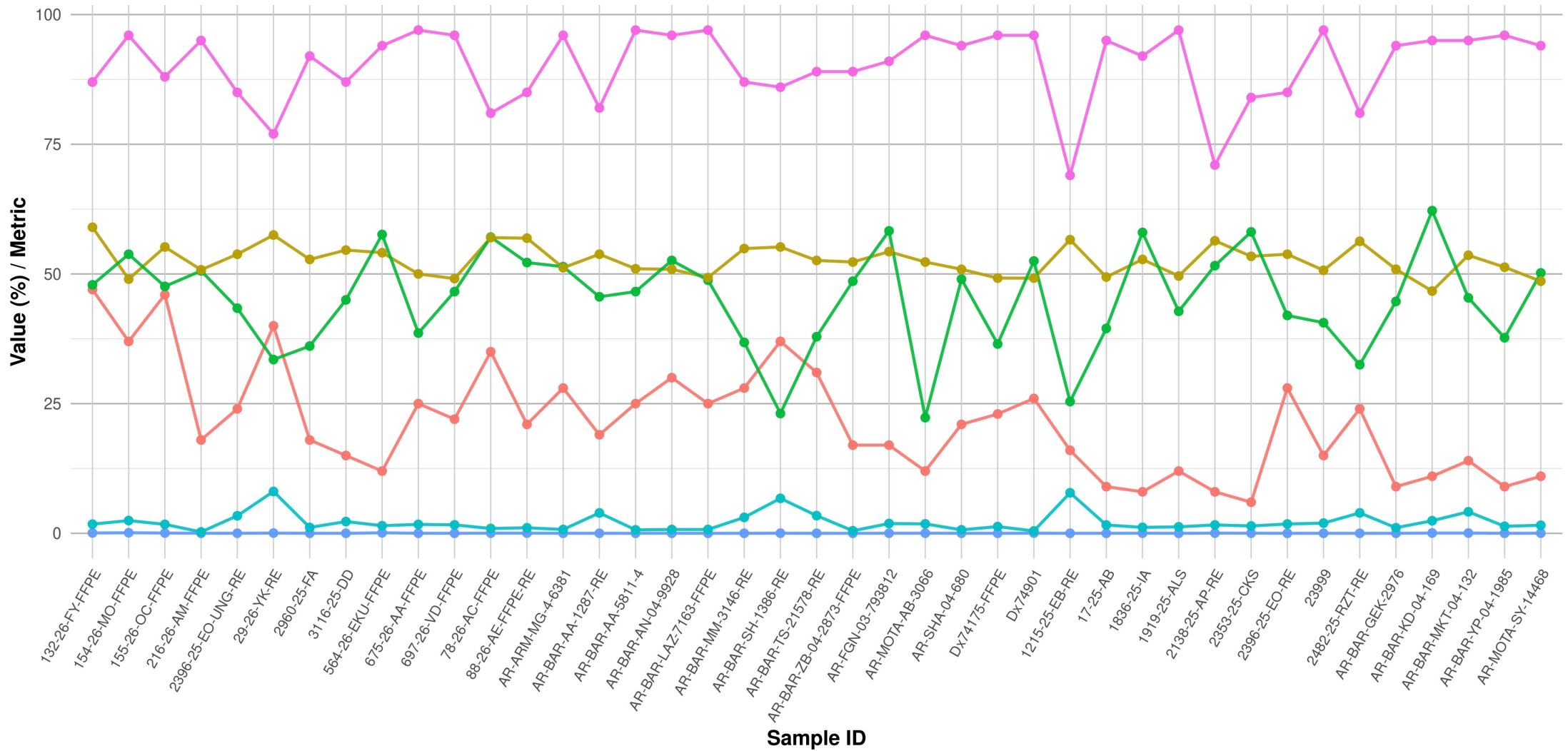
https://www.ibiospecimen.com/ffpe-specimens/

- **Platform spesific bias assesment (GC bias/Duplication Rate) -** Coverage normalization and bioinformatic GC-correction strategies

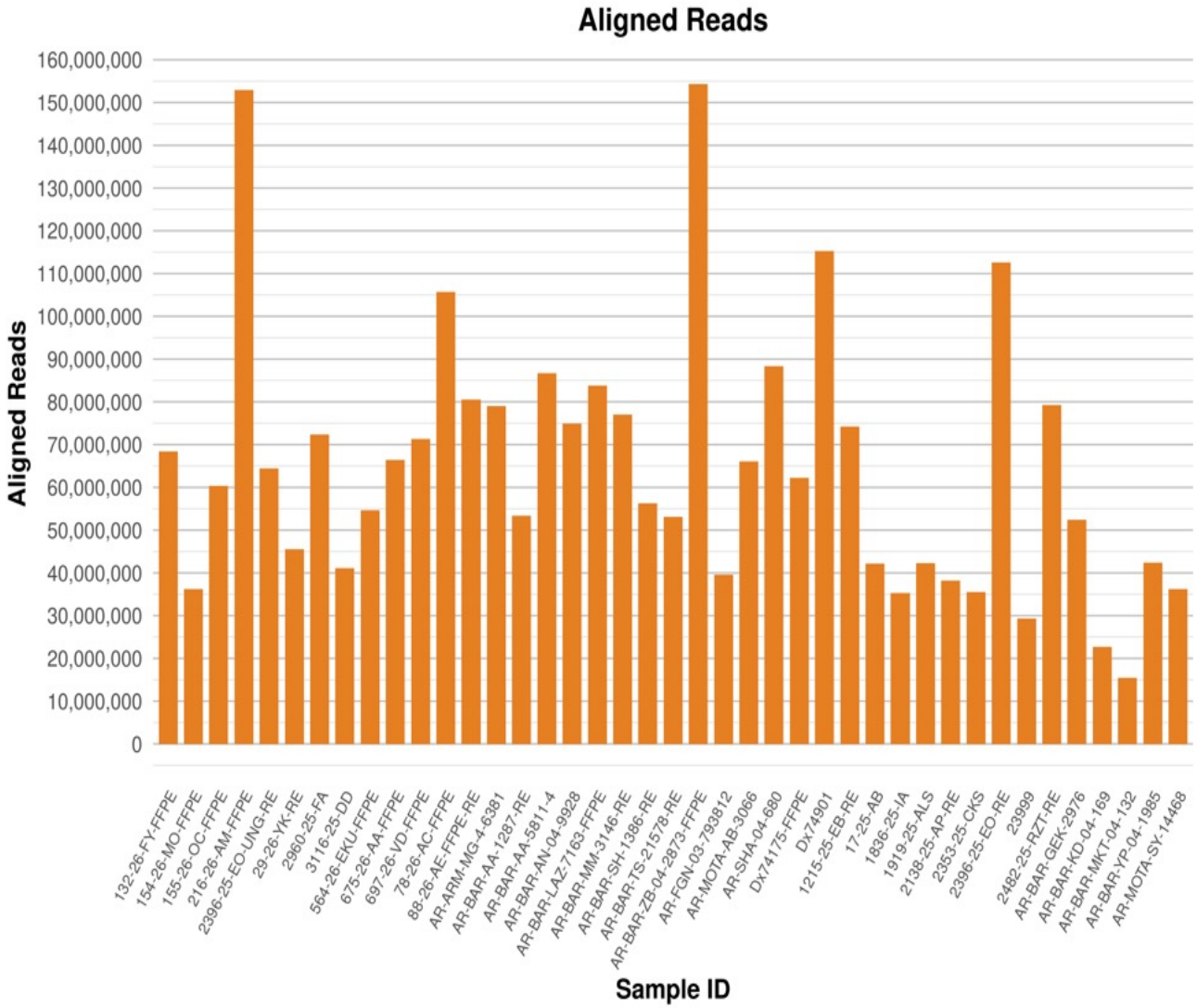
DNBSEQ-G400

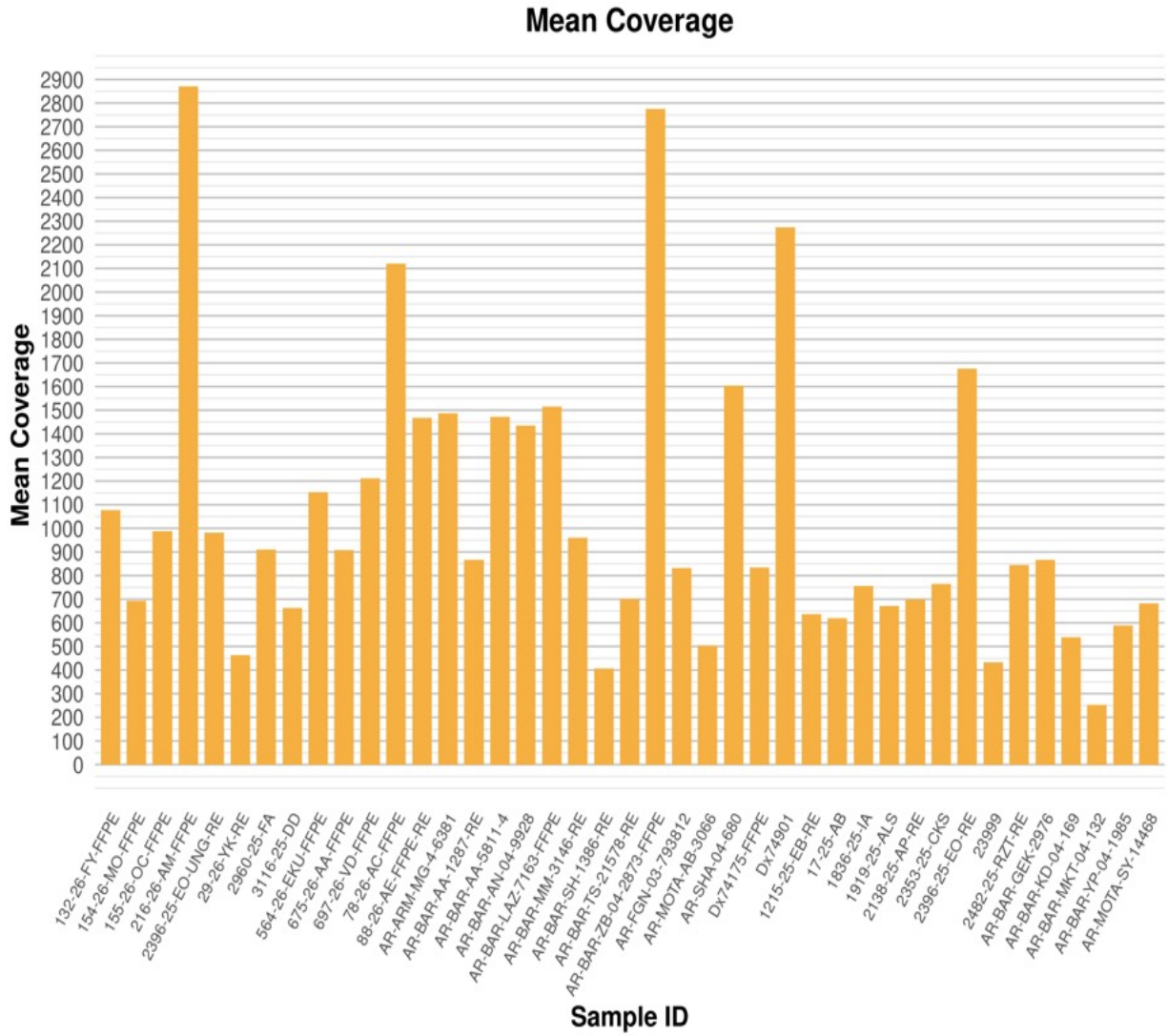
DNBSEQ-T7

QC Metrics Across Samples



DNBSEQ-T7


Aligned Reads
Aligned Reads
160,000,000
150,000,000
140,000,000
130,000,000
120,000,000
110,000,000
100,000,000
90,000,000
80,000,000
70,000,000
60,000,000
50,000,000
40,000,000
30,000,000
20,000,000
10,000,000
0
132-26-FY-FFPE
154-26-MO-FFPE
155-26-OC-FFPE
216-26-AM-FFPE
2396-25-EO-UNG-RE
29-26-YK-RE
2960-25-FA
3116-25-DD
564-26-EKU-FFPE
675-26-AA-FFPE
697-26-VD-FFPE
78-26-AC-FFPE
88-26-AE-FFPE-RE
AR-ARM-MG-4-6381
AR-BAR-AA-1287-RE
AR-BAR-AA-5811-4
AR-BAR-AN-04-3928
AR-BAR-LAZ-7163-FFPE
AR-BAR-MM-3146-RE
AR-BAR-SH-1386-RE
AR-BAR-TS-21578-RE
AR-BAR-ZB-04-2873-FFPE
AR-FGN-03-793812
AR-MOTA-AB-3066
AR-SHA-04-680
Dx74175-FFPE
Dx74901
1215-25-EB-RE
17-25-AB
1836-25-IA
1919-25-ALS
2138-25-AP-RE
2353-25-CKS
2396-25-EO-RE
23999
2482-25-RZT-RE
AR-BAR-GEK-2976
AR-BAR-KD-04-169
AR-BAR-MKT-04-132
AR-BAR-YP-04-1985
AR-MOTA-SY-14468
Sample ID


Mean Coverage
Mean Coverage
2900
2800
2700
2600
2500
2400
2300
2200
2100
2000
1900
1800
1700
1600
1500
1400
1300
1200
1100
1000
900
800
700
600
500
400
300
200
100
0
132-26-FY-FFPE
154-26-MO-FFPE
155-26-OC-FFPE
216-26-AM-FFPE
2396-25-EO-UNG-RE
29-26-YK-RE
2960-25-FA
3116-25-DD
564-26-EKU-FFPE
675-26-AA-FFPE
697-26-VD-FFPE
78-26-AC-FFPE
88-26-AE-FFPE-RE
AR-ARM-MG-4-6381
AR-BAR-AA-1287-RE
AR-BAR-AA-5811-4
AR-BAR-AN-04-3928
AR-BAR-LAZ-7163-FFPE
AR-BAR-MM-3146-RE
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23999
2482-25-RZT-RE
AR-BAR-GEK-2976
AR-BAR-KD-04-169
AR-BAR-MKT-04-132
AR-BAR-YP-04-1985
AR-MOTA-SY-14468
Sample ID

User Friendly OncoKDM Interface

Other Biomarkers

HRD
Positive_BRCA+_GS+

Tumor Mutational Burden
High

MSI
Stable

VIEW ALL OTHER BIOMARKERS

Other Biomarkers

MSI
Stable

HRD
Positive_BRCAwt_GS+

Tumor Mutational Burden
Low

VIEW ALL OTHER BIOMARKERS

Quality Control

Total Genes 629	Aligned Reads 54599509
Read length 140.38	Duplicate (%) 12
Mean Coverage 1153	Uniformity (%) 94

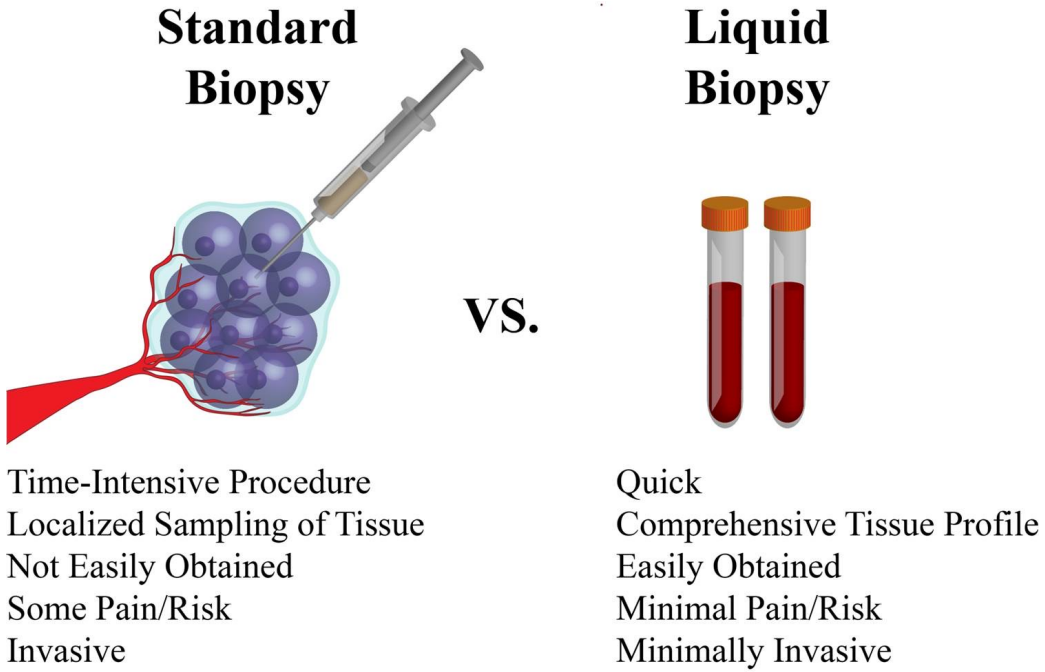
VIEW QUALITY CONTROL CHECKS

Gene	Position	Category	Variant Frequency	Copy Number	cDNA Variant	Amino Acid Variant	Impact location	Biological impact	Therapeutical impact	Potential germline	Inherited incidental findings	Depth	Visib
AKT1	chr14:104780214	SNV	25.43%	4.867	NM_005163.2:c.49G>A	p.(E17K)	exon: 2	Pathogenic	Tier IA	No	Yes	527	
PIK3CA	chr3:179218294	SNV	10.95%	1.1487	NM_006218.4:c.1624G>A	p.(E542K)	exon: 10	Pathogenic	Tier IA	No	Yes	274	
TP53	chr17:7674241	SNV	27.67%	2.3956	NM_000546.6:c.722C>T	p.(S241F)	exon: 7	Pathogenic	Tier IID	Yes	Yes	524	

Name	Results	Score	Type	Conclusion	Usual Markers	Visibility
EML4::ALK v3	YES	-	SEQ	We have identified a **EML4::ALK v3** gene fusion. Several variants of EML4::ALK gene fusions have been identified, depending on the breakpoint within EML4, and therefore the length of the corresponding fused protein. The EML4::ALK v3 gene fusion involves breakpoints in the exon 6 of EML4 and exon 20 of ALK, leading to the expression of a small protein, harboring the full tyrosine kinase domain of ALK (exon 20-29) linked to the NTD domain of EML4 (exon 1-6), but lacking the TAPE domain of EML4. EML4::ALK v3 fusion has been linked to shorter PFS, increased frequency of metastasis and shorter response to TK inhibitors due to a higher frequency of ALK resistance variants (PMID: 37149843; PMID: 28872581). In addition, EML4::ALK v3 has been associated with increased IC50 for all ALK TK inhibitors compared to the EML4:ALK v1, especially for crizotinib (205.3nm vs 23.3nm) and ceritinib (75.1nm vs 12.47nm). Alectinib, brigatinib, ensartinib and lorlatinib showed also higher IC50, but comparable to the one of crizotinib in a EML4:ALK v1 context (PMID: 34175504). NSCLC patients with EML4::ALK v3 rearrangement have been reported to be sensitive to crizotinib (PMID: 20979469; PMID: 32974126), lorlatinib (https://ascopubs.org/doi/10.1200/JCO.2022.40.16_suppl.9070; PMID: 37187318; PMID: 37541389; PMID: 37223611) and ceritinib treatments (PMID: 34890832). A case of NSCLC has been reported to respond to subsequent treatment with alectinib and crizotinib (https://doi.org/10.1200/JCO.2021.39.15_suppl.e21014). Interestingly, a study with chinese NSCLC treated with crizotinib has reported that patients harboring EML4::ALK v3 displayed significantly lower PFS and OS than those with other variants. Furthermore, patients with a single EML4::ALK rearrangement event displayed favorable PFS compared to those harboring multiple ALK rearrangements (PMID: 30895431). **Remark**: Co-occurrence of EML4::ALK v3 and TP53 alteration has been associated with shorter PFS when treated with ALK inhibitors; such as alectinib, brigatinib, ceritinib, crizotinib, or lorlatinib (https://ascopubs.org/doi/10.1200/JCO.2023.41.16_suppl.9029; https://doi.org/10.1200/JCO.2021.39.15_suppl.e21014; PMID: 38433979; PMID: 35579989; PMID: 37541389; PMID: 35870258)	-	✓✓ Published

Validation of OncoSELECT

- **Liquid Biopsy**
  - **Metastasis info**
  - **Insufficient input DNA**
  - **MRD, Resistant mutations**



https://www.gene-quantification.de/liquid-biopsy.html

Why OncoSELECT ?

- ✓ **Similar protocol Oncodeep/ User friendly**
- ✓ **Low input**
- ✓ **Robust solution**
- ✓ **Targeted therapy related genes**
- ✓ **Low VAF + MSI + HRR**

1st Run on T7

DNBSEQ–T7

Quality Control	GENES	LOW COVERAGE	QC
Read count at input			167535666
Coverage pre-consensus			33013.93
On Target pct pre-consensus			72.82
Uniformity pre-consensus			79.05
Low coverage pct pre-consensus			25.82
Coverage post-consensus			2280.86
Low coverage pct post-consensus			8.64
Uniformity post-consensus			98.38
Singleton Pct for consensus			16.43
Mean insert size			154.19

Quality Control	GENES	LOW COVERAGE	QC
Read count at input			60723668
Coverage pre-consensus			11229.09
On Target pct pre-consensus			73.58
Uniformity pre-consensus			82.19
Low coverage pct pre-consensus			63.51
Coverage post-consensus			246.5
Low coverage pct post-consensus			100
Uniformity post-consensus			99.14
Singleton Pct for consensus			13.18
Mean insert size			156.1

Quality Control	GENES	LOW COVERAGE	QC
Read count at input			244355618
Coverage pre-consensus			44936.88
On Target pct pre-consensus			73.99
Uniformity pre-consensus			84.48
Low coverage pct pre-consensus			18.05
Coverage post-consensus			3383.49
Low coverage pct post-consensus			7.47
Uniformity post-consensus			97.62
Singleton Pct for consensus			14.62
Mean insert size			148.25

Gene	Position	Category	Variant Frequency (Tumor)	Depth (Tumor)	Origin	cDNA Variant	Amino Acid Variant	Add to report
KRAS	chr12:25225617	SNV	0.1%	965	-	NM_033360.4:c.447A>C	NP_203524.1:p.R149S	
KRAS	chr12:25225637	SNV	0.26%	1172	-	NM_033360.4:c.427G>A	NP_203524.1:p.E143K	
KRAS	chr12:25227255	SNV	0.07%	1495	-	NM_033360.4:c.269T>A	NP_203524.1:p.F90Y	
KRAS	chr12:25227341	SNV	0.17%	2333	-	NM_033360.4:c.183A>C	NP_203524.1:p.Q61H	

Low VAF!!!!

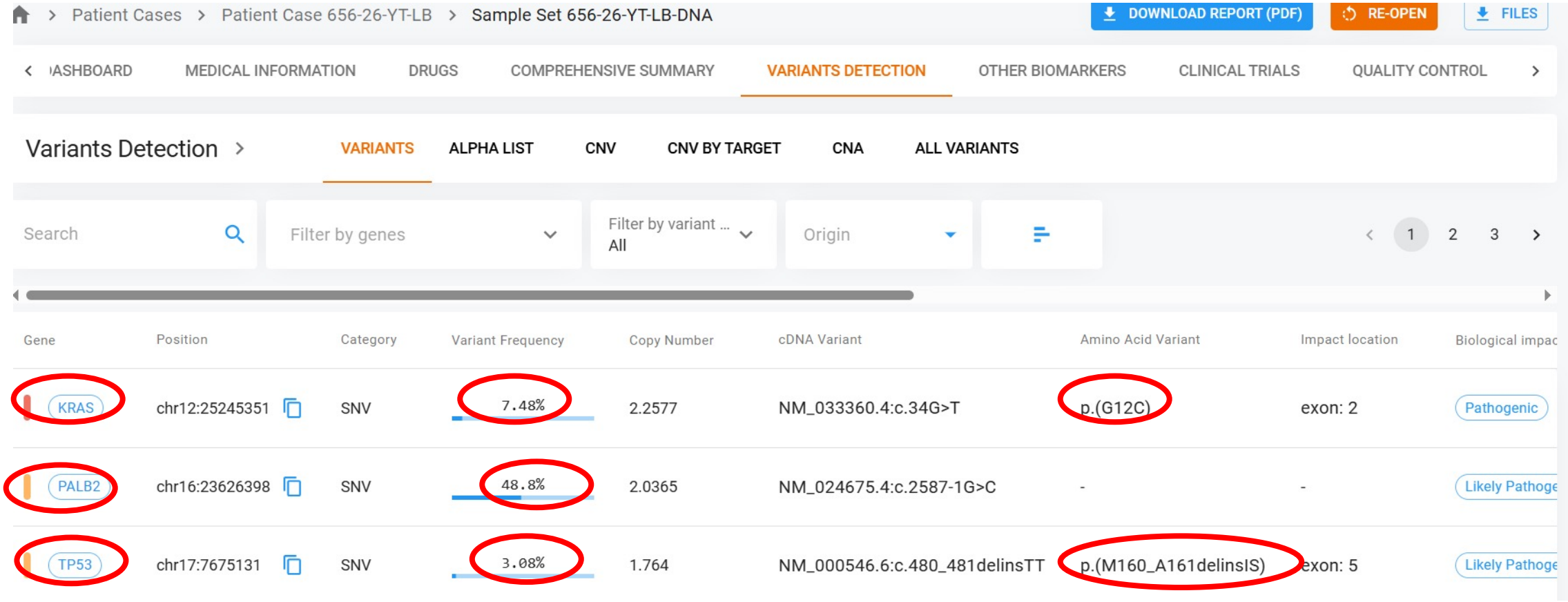
KRAS	chr12:25227374	SNV	0.1%	1910	-	NM_033360.4:c.150C>T	NP_203524.1:p.T50T	
KRAS	chr12:25227415	SNV	0.25%	1177	-	NM_033360.4:c.112-3C>T	-	
KRAS	chr12:25245276	SNV	0.14%	1453	-	NM_033360.4:c.109G>A	NP_203524.1:p.E37K	
KRAS	chr12:25245276	SNV	0.07%	1453	-	NM_033360.4:c.109G>T	NP_203524.1:p.E37*	
KRAS	chr12:25245350	SNV	0.11%	1879	-	NM_033360.4:c.35G>C	NP_203524.1:p.G12A	

2nd Run on T7

DNBSEQ-T7

Sample_ID	Sample	Mean Coverage Before Consensus	On Target Reads (%) Before Consensus	Target Low Covered (%) Before Consensus	Mean Coverage After Consensus	Target Low Covered (%) After Consensus	Singleton (%) After Consensus	Mean Insert Size (bp) After Consensus	Mode Insert Size (bp) After Consensus	Median Insert Size (bp) After Consensus	GC Content (%) After Consensus	Mean Read per Cons (%) After Consensus	Initial Read Quantity Before Consensus	Uniformity (%) Before Consensus	Uniformity (%) After Consensus	Project	Flowcell
TWIST-CF-DNA-5-DNA	KDM73588	51318	77	5	1839	7	7	161	147	157	44	41	293045742	98	99	GENOKSANKA1	Run23_140426
TWIST-CF-DNA-05-DNA	KDM73587	56471	77	5	1502	12	8	159	147	157	45	55	321402960	98	100	GENOKSANKA1	Run23_140426
RC-LB-DNA	KDM73586	51051	76	5	2371	5	6	169	165	167	43	31	309289224	98	99	GENOKSANKA1	Run23_140426
656-26-YT-LB-DNA	KDM73585	49138	78	5	2502	5	6	171	165	168	42	28	300304110	98	99	GENOKSANKA1	Run23_140426

2nd Run on T7


Patient Cases > Patient Case 656-26-YT-LB > Sample Set 656-26-YT-LB-DNA
DOWNLOAD REPORT (PDF)
RE-OPEN
FILES
ASHBOARD
MEDICAL INFORMATION
DRUGS
COMPREHENSIVE SUMMARY
VARIANTS DETECTION
OTHER BIOMARKERS
CLINICAL TRIALS
QUALITY CONTROL
Variants Detection
VARIANTS
ALPHA LIST
CNV
CNV BY TARGET
CNA
ALL VARIANTS
Search
Filter by genes
Filter by variant ...
All
Origin
1
2
3
Gene
Position
Category
Variant Frequency
Copy Number
cDNA Variant
Amino Acid Variant
Impact location
Biological impac
KRAS
chr12:25245351
SNV
7.48%
2.2577
NM_033360.4:c.34G>T
p.(G12C)
exon: 2
Pathogenic
PALB2
chr16:23626398
SNV
48.8%
2.0365
NM_024675.4:c.2587-1G>C
-
-
Likely Pathoge
TP53
chr17:7675131
SNV
3.08%
1.764
NM_000546.6:c.480_481delinsTT
p.(M160_A161delinsIS)
exon: 5
Likely Pathoge

Take Away Notes for Validation;

DNBSEQ-T7

- ✓ The platform-independent wet-lab workflow of the **OncoDEEP and OncoSELECT kits**, with identical protocols, facilitated streamlined validation.
- ✓ The open manipulation capability on T7 sequencing allowed rapid validation and optimization, facilitated by our wet-lab expertise.
- ✓ Mixed-run capability allows simultaneous processing of different materials, regardless of index / adaptors used.
- ✓ A flexible, open, and robust workflow enabling rapid validation, consistent throughput, and scalable sequencing performance on **MGI T7** instrument.

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