OncoDNA®
THE CANCER THERANOSTIC COMPANY

International User Group Meeting

22nd and 23rd of April 2026

Lifting the Lid on Reporting

Simon Lefèvre
Production Manager

OncoDNA
THE CANCER THERANOSTIC COMPANY

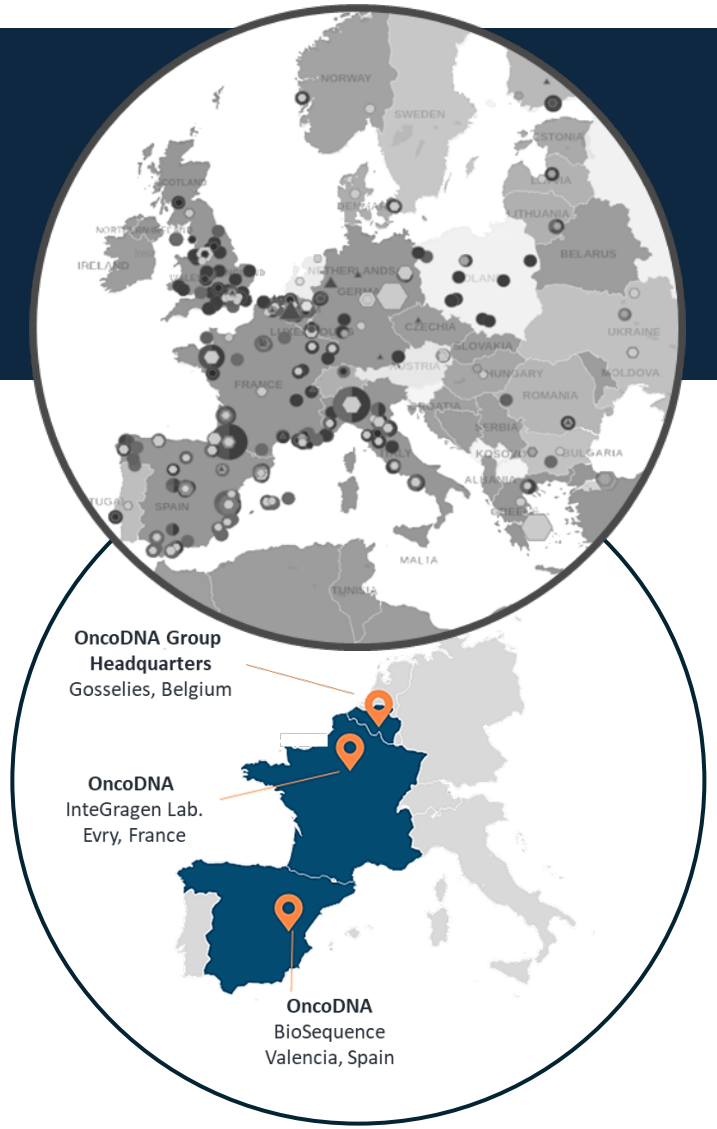
Who are we?

OncoDNA AT A GLANCE

OncoDNA was founded in 2012 and has grown exponentially since its creation, closing milestones partnerships with leading oncology organizations and expanding its footprint worldwide.

~100
Collaborators in **9** Countries

35 distributors
active on all continents



425 Hospitals
Research Centers

2,240
Oncologists

>100,000
Samples

OncoKDO, advanced oncogenomic database

Since 2013

Proprietary input

Clinical data from **25,000** patients

External sources

- > 15 public databases
- Clinical literature

Manual, daily data curation by our scientists

Accurate Data
Dynamic
Constantly growing

OncoDEEP, initiated for patients by oncology experts

More 10 years of knowledge that matters

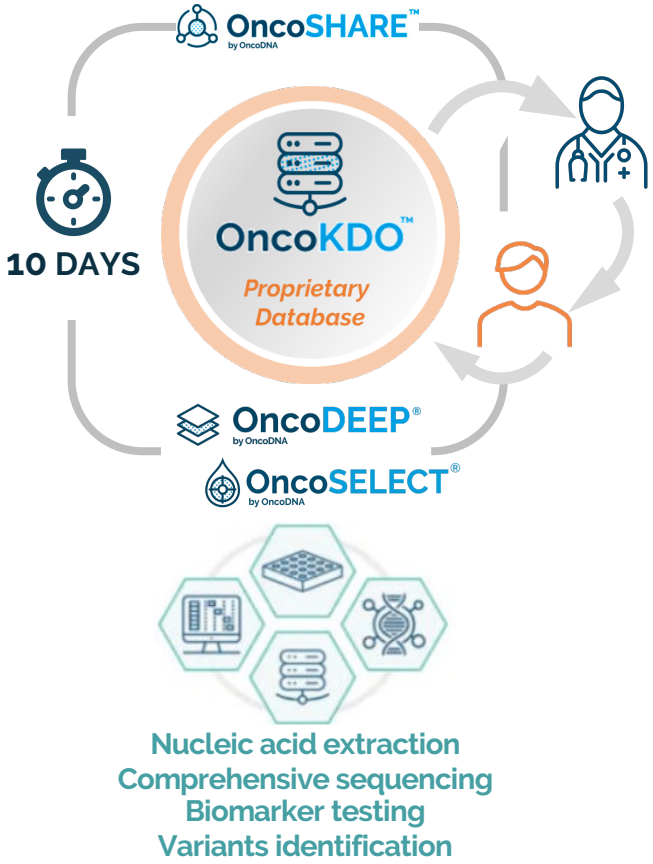
2012

OncoKDO™
Proprietary Database

2013

Centralized at OncoDNA

Clinical interpretation
Online Reporting



Nucleic acid extraction
Comprehensive sequencing
Biomarker testing
Variants identification

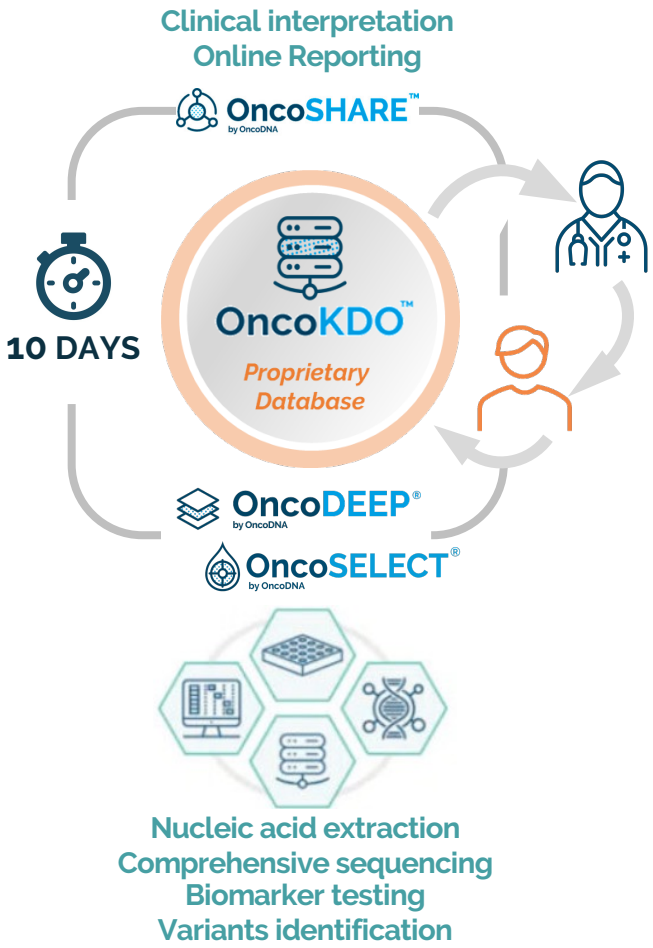
OncoDEEP, initiated for patients by oncology experts

More 10 years of knowledge that matters

2012

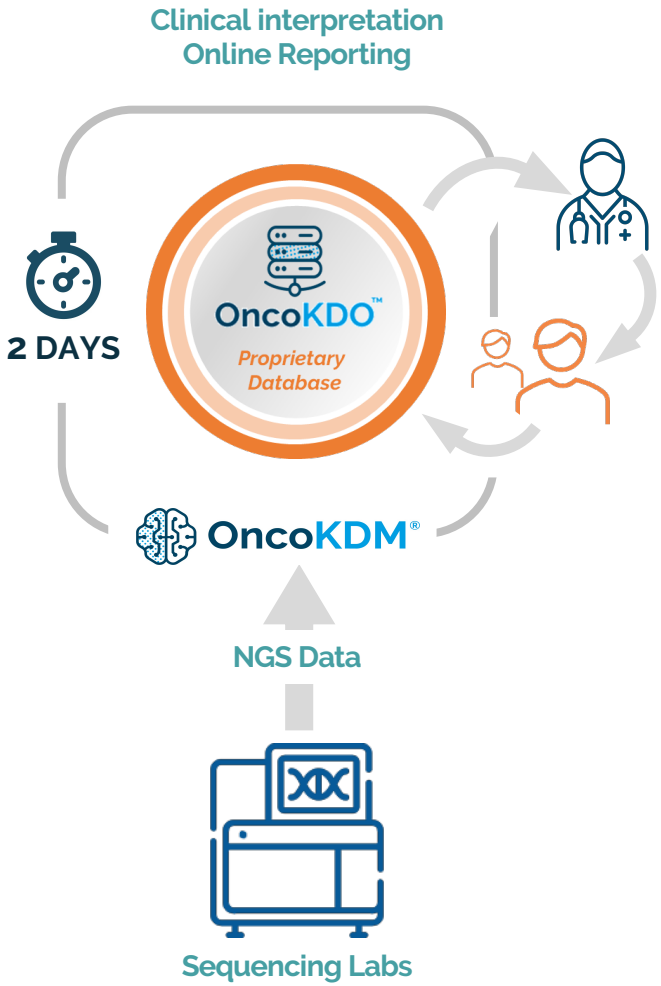
2013

Centralized at OncoDNA



2017

Decentralized Data Analysis



OncoDEEP, initiated for patients by oncology experts

More 10 years of knowledge that matters

2012

OncoKDO™
Proprietary Database

2013

Centralized at OncoDNA

Clinical interpretation
Online Reporting

OncoSHARE™ by OncoDNA

10 DAYS

OncoKDO™
Proprietary Database

OncoDEEP® by OncoDNA

OncoSELECT® by OncoDNA

Nucleic acid extraction
Comprehensive sequencing
Biomarker testing
Variants identification

2017

Decentralized Data Analysis

Clinical interpretation
Online Reporting

OncoSHARE™ by OncoDNA

2 DAYS

OncoKDO™
Proprietary Database

OncoKDM®

NGS Data

Sequencing Labs

2022

Accessible to hospitals worldwide

Clinical interpretation
Online Reporting

2 DAYS

OncoKDM®

OncoKDO™
Proprietary Database

4 DAYS

NGS Data

Molecular Pathology Labs

OncoDEEP® by OncoDNA KIT

OncoSELECT® KIT

OncoXPLORE™ KIT

OncoDNA
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How does it works?

OncoDNA kit workflow

Tertiary Analysis

Field application Team

BioIT Team

Production Team

Scientific Team

Library preparation

Target enrichment

Sequencing

Files Transfer

FASTQ

QC check / Alignement

Variant Calling / Classification

Data **cross-referencing** with OncoKDO

Report validation

Clinical interpretation

OncoDEEP® DNA & RNA Kit

OncoSELECT® Kit

Illumina

MGI

Element Biosciences

HRD

MSI

TMB

CNV

LOH

OncoKDO

OncoKDM®

OncoDNA
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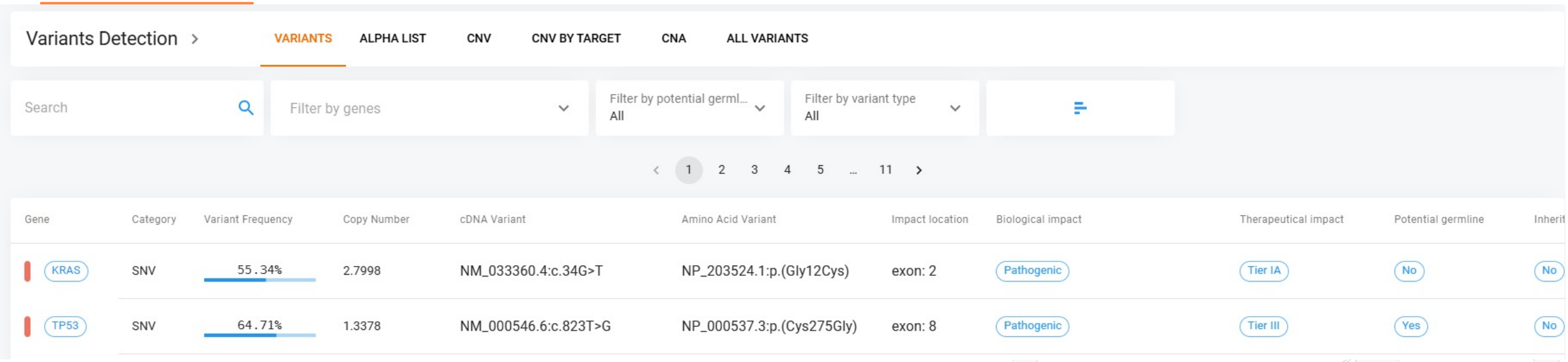
OncoKDM

Variant section



- Variants passing the filters: **>5% VAF** (except alphalist, **non-synonymous** (except pathogenic), **non-intronic, >80x** and **counted 20x.**
- Possibility to **search by genes** or **filter by several genes**
- Filter by **pathogenicity** or **potential germline**
- Information on **Biological Impact** and **Therapeutical Impact** available

Variant position

RB1	chr13:48379606	SNV	26.12%	1.7632	NM_000321.3:c.1345G>T	p.(G449*)	exon: 14	Likely Pathogenic	Tier III
STK11	-	LOH	-	1	NM_000455.5	-	-	Likely Pathogenic	Tier III
TP53	-	LOH	-	1	NM_000546.6	-	-	Likely Pathogenic	Tier III
TP53	chr17:7674954	SNV	74.09%	0.8725	NM_000546.6:c.577C>T	p.(H193Y)	exon: 6	Likely Pathogenic	Tier III

- **Position of the variant** available in « variant » section
- **Easy** copy/paste and **doublecheck** location at raw data

All Variant section

Variants Detection > VARIANTS ALPHA LIST CNV CNV BY TARGET CNA ALL VARIANTS

Genes: ABL1,ALK,ARID,... Min frequency Max frequency

< 1 2 3 4 5 ... 48 >

Gene	Category	Variant Frequency (Tumor)	Depth (Tumor)	cDNA Variant	Amino Acid Variant	Add to report
NADK	DEL	4.34%	691	NM_023018.5:c.1334_1336del	NP_075394.3:p.E445del	
NADK	INS	36.47%	691	NM_023018.5:c.1334_1336d...	NP_075394.3:p.E445dup	
NADK	SNV	49.6%	865	NM_023018.5:c.1212G>A	NP_075394.3:p.P404P	
NADK	SNV	47.88%	1180	NM_023018.5:c.786C>A	NP_075394.3:p.N262K	

- All the variants **without any filters**
- **VAF 1-5%,** deep **intronic** and **synonymous**
- Can be **switched to** variant section by clicking on

Alphalist

KRAS	Exon 3	Q61H/K/L/R /X	-	1191	-	-	WT	-
KRAS	Exon 3	A59T /X	-	1123	-	-	WT	-
KRAS	Exon 2	G13any-ms	-	887	-	-	WT	-
KRAS	Exon 2	G12any-ms	53.33%	870	NM_033360.4:c.34G>T	NP_203524.1:p.(G12C)	Mutated	-
NRAS	Exon 4	A146T /X	-	801	-	-	WT	-

- **Hotspot positions** directly linked to targeted therapies
- **Different filter on VAF:** 2% for indels, 3% for SNV
- Can go down to **1% depending on the coverage:** counted at least 10x (5-10x present in all variant)

Quality check control – Sequencing performance analysis

DASHBOARD | MEDICAL INFORMATION | DRUGS | COMPREHENSIVE SUMMARY | VARIANTS DETECTION | OTHER BIOMARKERS | CLINICAL TRIALS | QUALITY CONTROL

Quality Control > GENES | LOW COVERAGE | QC

Cellularity
0.7

Purity	0.66
Ploidy	3.66
Aligned Reads	34770061
Read length	99.64
Duplicate (%)	11
Mean Coverage	550
Uniformity (%)	92
Target Not Covered (%)	0.03
Mean Insert Size (bp)	174

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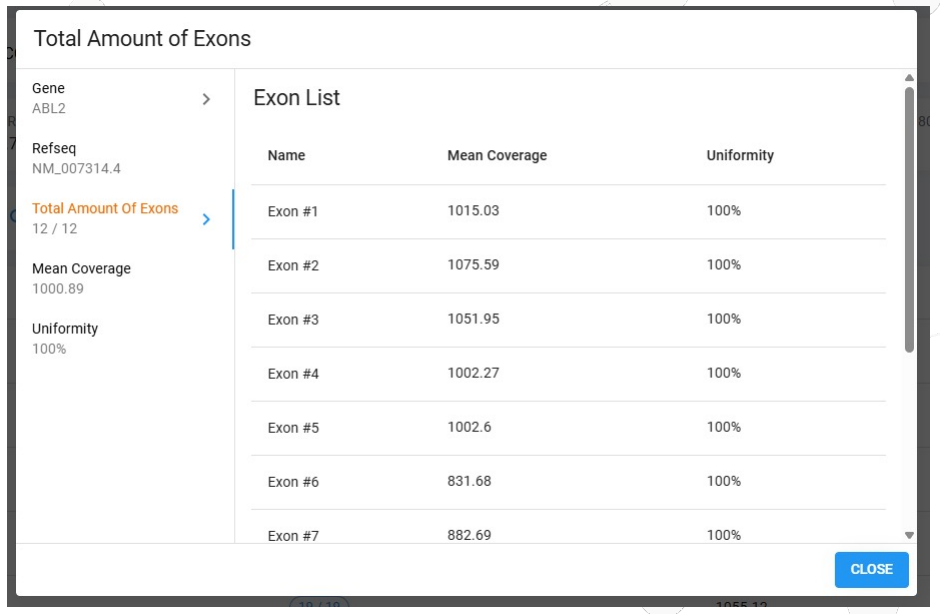
QC metrics

Gene	Refseq	Total Amount Of Exons	Mean Coverage	Uniformity
ABL1	NM_007313.3	11 / 11	924.86	100%
ABL2	NM_007314.4	12 / 12	1000.89	100%
ACVR1	NM_001105.5	9 / 11	937.82	100%
ACVR1B	NM_020328.4	10 / 10	1009.48	100%



- Coverage and uniformity per gene or per exons
- Can be searched by genes

QC metrics

Quality Control > GENES LOW COVERAGE QC

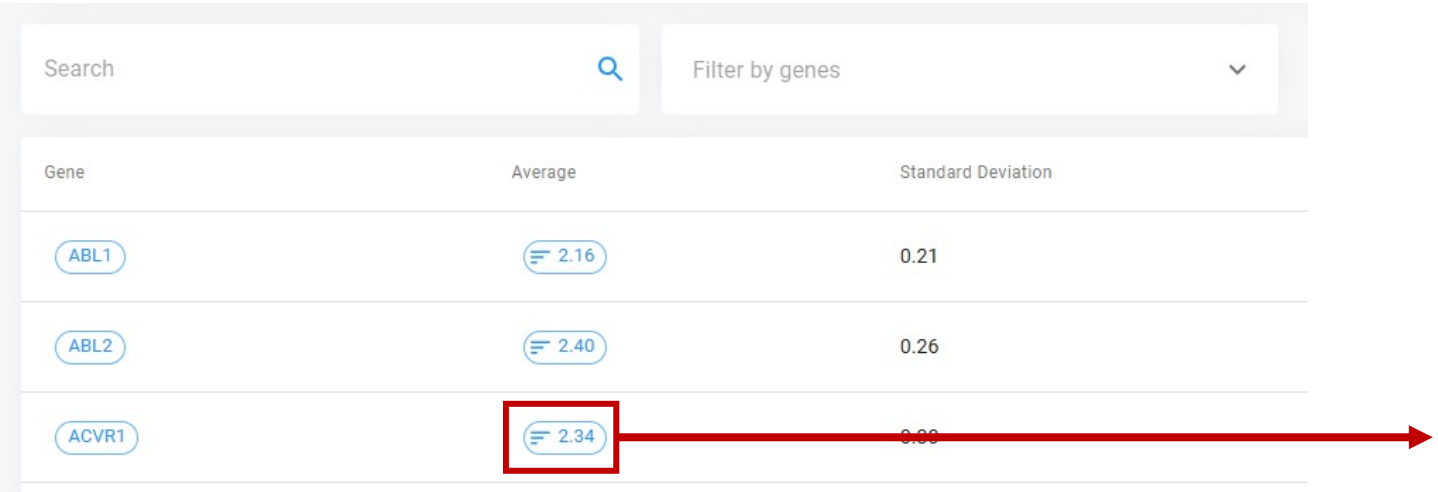
Search

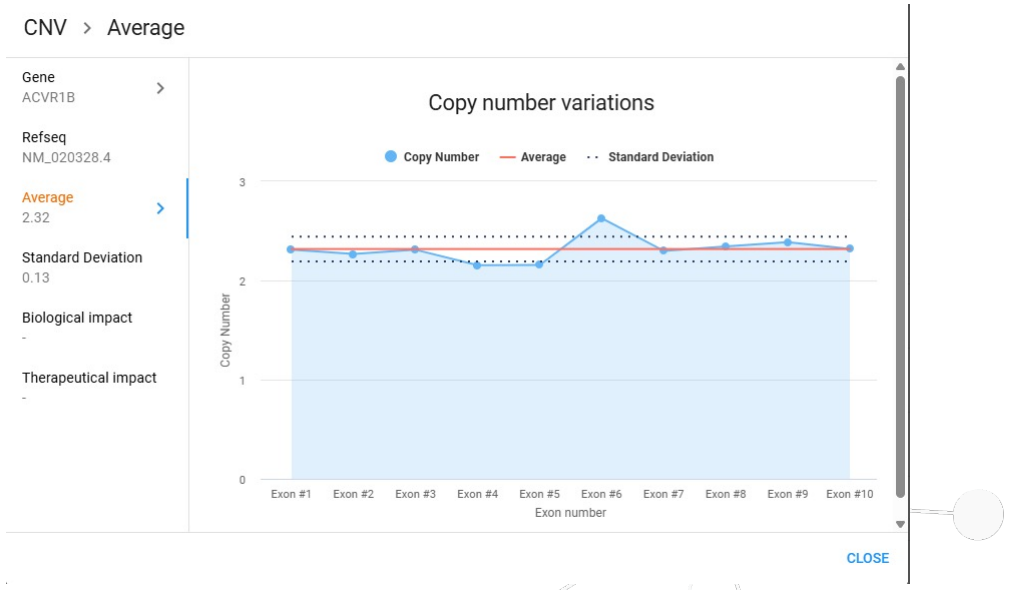
Filter by genes

Region	CDNA Start	CDNA End	Size	Minimum	Maximum	Average	Gene	Refseq	Exon	Target
chr3:63912640-63912672	42	74	33	69	89	78	ATXN7	NM_001377406.1	2	TGT00002789
chr6:156778569-156778575	889	895	7	77	80	79	ARID1B	NM_001374820.1	2	TGT00005287
chr6:156778583-156778587	903	907	5	77	80	79	ARID1B	NM_001374820.1	2	TGT00005287
chr7:78019436-78019644	4039	4247	209	21	80	45	MAGI2	NM_012301.4	22	TGT00005679

- All **region covered <80x** visible in low coverage
- Can be searched by genes
- **Classical QC metrics** of the sample in QC

CNV





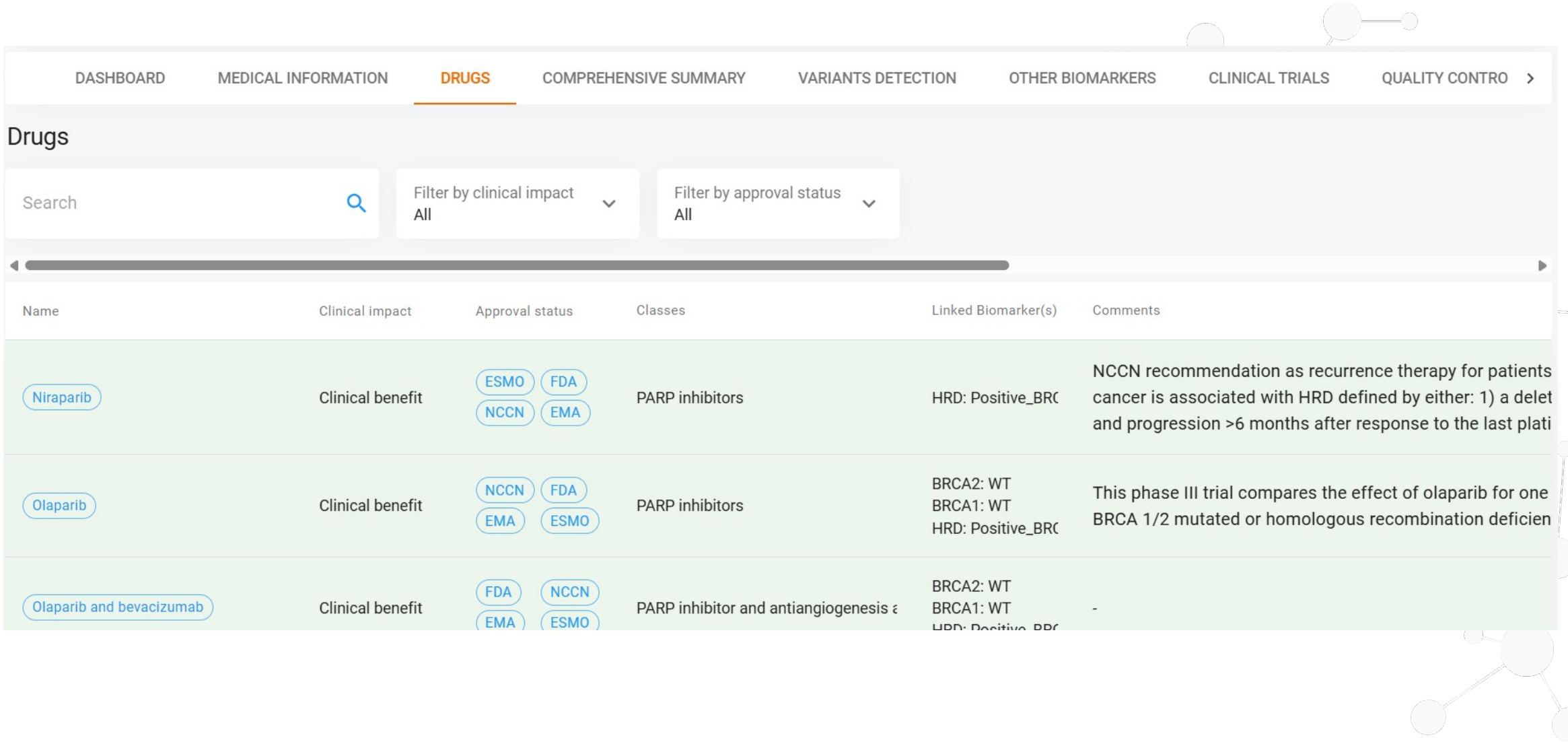
- Can **search by gene or filter on several genes**
- Click on the CNV average value to open the **CNV distribution by exon**
- **If above 6 copies (min 3 probes and 75%)**: amplification and reported in variant section
- **If below 0,6 copies (min of 3 probes and 75%):** CNV-LOSS and reported in variant section

Other Biomarkers

Name	Results	Score	Type	Conclusion	Usual Markers	Visibility
HRD	Negative	16.8	HRD	We **did not demonstrate** the presence of a deleterious (or suspected deleterious) BRCA1/2 variant. This category includes variants for which published data demonstrate a loss of function of the corresponding proteins as well as the large rearrangements. We observed a **negative genomic scar** for this patient. Therefore, the test results demonstrate a **homologous recombination proficiency** for this patient. This status is based on the absence of BRCA1/2 variant (including large rearrangement) and a genomic instability status of negative. Treatment based on PARP inhibitors could be associated with potantial lack of clinical benefit.	-	Published
MSI	Stable	3.32%	MSI	We did not observe a high level of microsatellite instability (MSI). MSI-High has been linked to increased sensitivity to immune checkpoint inhibitor drugs (PD-1/PD-L1 inhibitors) (PMID: 28877075). Therefore, PD-1/PD-L1 inhibitors would be associated with a lack of clinical benefit for this patient. Nonetheless, this information may need to be combined with other biomarkers like the ones present in the personalized immunogram. **Rmk:** dMMR negatively affects the response of CRCs to chemotherapeutics such as pyrimidine analogues, oxaliplatin, cisplatin, temozolomide and procarbazine. Moreover, fluorouracil-based adjuvant chemotherapy seems to improve patient outcome, in particular those with colon cancer with microsatellite-stable or MSI-Low tumours but not those with tumours exhibiting MSI-H (PMID: 12867608; PMID: 20627535; PMID: 20498393; PMID: 25474278). Nonetheless, the approved treatments for CRC involve several chemotherapy combinations, and the ESMO 2018 guidelines advice not to base the choice of the chemotherapy combination on the MSI status. Therefore, MSI-H should not be considered as a marker related to lack of clinical benefit for the approved chemotherapies in colorectal cancer.	**BAT-25**: Stable **BAT-26**: Stable **D2S123**: Unstable **NR-21**: Stable **NR-27**: Stable	Published
RET Fusion DNA	NO	-	Seq	We didn't observe any translocation variant in RET. Therefore treatment targeting RET gene fusions would be associated with a potential lack of clinical benefit for this patient.	-	Published
Tumor Mutational Burden	Low	4.44 Mut/Mb	TMB	We did not observe a high tumor mutational burden (TMB). In patients with high TMB, checkpoint inhibitors (PD-1/PD-L1 blockade) have been associated with clinical benefits across diverse tumors (PMID: 28835386). Therefore, treatments based on PD-1/PD-L1 inhibitors would be associated with a lack of clinical benefit for this patient. Nonetheless, this information may need to be combined with other biomarkers like the ones present in the personalized immunogram.	-	Published

- Genomic Signature **HRD** (>37) + **TMB** (≥ 10 mut/Mb) **+ MSI** (≥ 40%)
- **Fusion and splice event:** >10x, all genes if **exonic breakpoints**, ALK/RET/ROS1 if **intronic breakpoints**

Drugs


DASHBOARD
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Filter by clinical impact
All
Filter by approval status
All
Name
Clinical impact
Approval status
Classes
Linked Biomarker(s)
Comments
Niraparib
Clinical benefit
ESMO
FDA
NCCN
EMA
PARP inhibitors
HRD: Positive_BRC
NCCN recommendation as recurrence therapy for patients
cancer is associated with HRD defined by either: 1) a delet
and progression >6 months after response to the last plati
Olaparib
Clinical benefit
NCCN
FDA
EMA
ESMO
PARP inhibitors
BRCA2: WT
BRCA1: WT
HRD: Positive_BRC
This phase III trial compares the effect of olaparib for one
BRCA 1/2 mutated or homologous recombination deficien
Olaparib and bevacizumab
Clinical benefit
FDA
NCCN
EMA
ESMO
PARP inhibitor and antiangiogenesis a
BRCA2: WT
BRCA1: WT
-

Clinical trials

DASHBOARD | MEDICAL INFORMATION | DRUGS | COMPREHENSIVE SUMMARY | VARIANTS DETECTION | OTHER BIOMARKERS | CLINICAL TRIALS | QUALITY CONTRO

Clinical Trials

Search

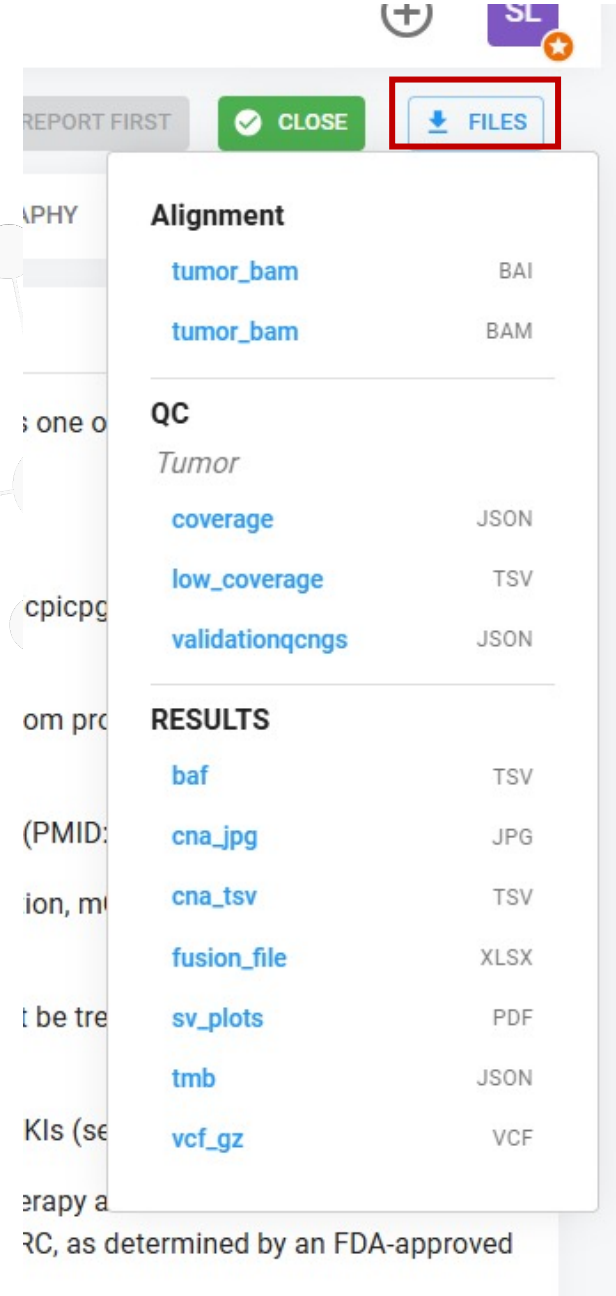
Filter by phase
All

Filter by country
All

Title	Phase	NCT ID	Countries	Visibility
A Phase I/II Study of Sacituzumab Govitecan Plus Berzosertib in Small Cell Lung Cancer, Extra-Pulmonary Small Cell Neuroendocrine Cancer and Homologous Recombination-Deficient Cancers Resistant to PARP Inhibitors	2	NCT04826341	US United States	Published
Phase 1/2 Clinical Trial of CP-506 (HAP) in Monotherapy or With Carboplatin or ICI	2	NCT04954599	NL Netherlands BE Belgium ES Spain	Published
EIS-12656 as Single Agent and in Combination in Patients With Specified Solid Tumors	2	NCT06525298	US United States	Published
Testing Olaparib for One or Two Years, With or Without Bevacizumab, to Treat Ovarian Cancer	3	NCT06580314	US United States JP Japan PR Puerto Rico	Published

Downloadable files

- **All intermediate files generated can be downloadable**
- **BAM and BAI** to check on IGV
- **QC files**
- **Raw results: Fusions and sv image, unfiltered VCF, TMB, CNA files**



Reporting Thresholds

QC

	PASSED	WARNING	FAILED
Coverage	>350	<350 and >150	<150
Uniformity	>90	<90 and >85	<85
Aligned reads	≥ 20000000	<20000000	
Read lentgh	≥50	<50	
Duplicates ratio	≤30	>30 and ≤50	>50
Missed amplicon pct	<0.1	≥0,1	≥1
Mean Insert Size	≥100	<110	
Mode Insert Size	≥100	<110	
Pct low coverage bases	≤1	>1	
GC content	47 - 50	<47 and >50	
On target pct	≥30	<30	<25

CNV

	Amplification	CNV-LOSS
Threshold	> 6 copies	<0.6copies
Note	Min 3 probes & 75% @ >6	Min 3 probes & 75% @ <0.6

LOH

	Imbalanced Gene	Homozygous Gene	DEL Gene
PLUS	BAF <33%	>8 total SNPs in gene	1 copy/DEL Region OR >66% SNPs+Total SNPs≥8

Variant

	Variant Calling	AlphaList
Threshold	≥ 5%	≥ 2% for indels ≥ 3% for SNV
Note	>80x coverage and counted 20x	>80x coverage Can go down to 1% (at least counted 10x)

Fusion & Splicing

	Counts
Threshold	>10x
Note	Not a hard threshold (Depends if actionable/pathognomonic/prognosis)

Genomic Signatures

	TMB	MSI	HRD
Threshold	≥ 10mut/Mb	≥ 40%	>37

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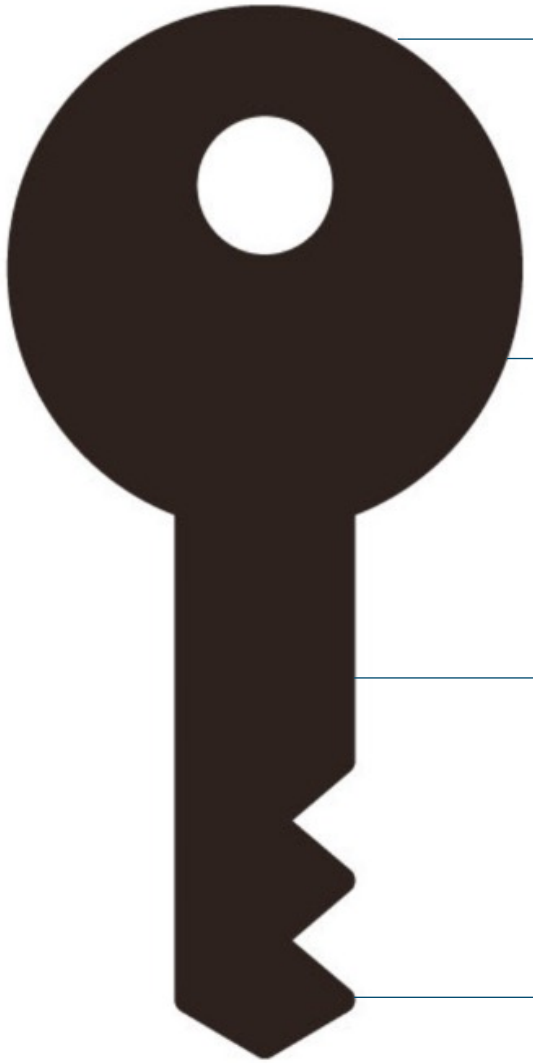
OncoKDM is in constant evolution

What do YOU need?

Key Take Away



1. OncoKDM was initially developed to deliver actionable NGS results for Oncologists

2. OncoDNA's move to a decentralized model launched a significant transformation of OncoKDM

3. OncoKDM is now further evolving to fit Kit Customers needs

4. OncoKDM is your platform so work with us to ensure it is not only fit for purpose but exceeds other software available.