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European User Group Meeting
OncoDEEP® Kit

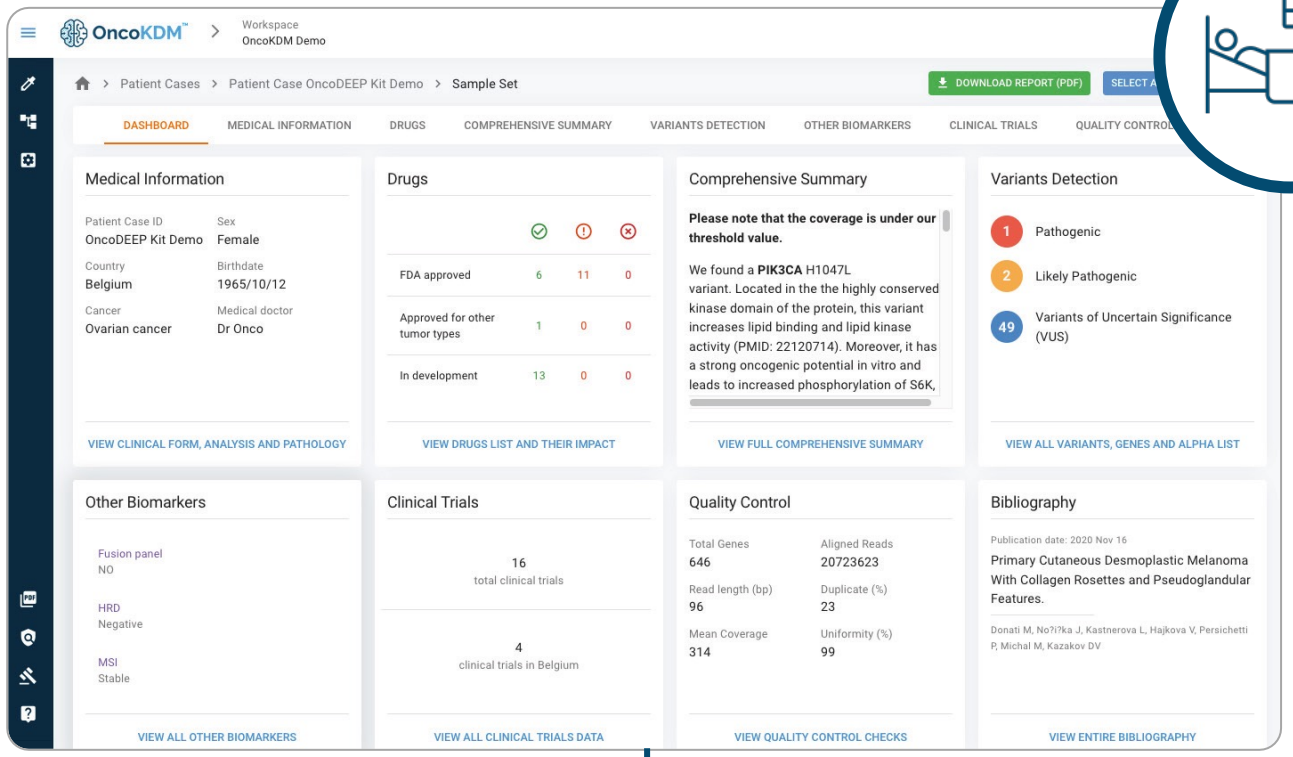
21st - 22nd October 2024

OncoDEEP® by OncoDNA KIT

- Flexible and Innovative –
Delivering on the bigger picture

Koenraad Eycken

Being at the top of a process requires mastering every single step



Wetlab

Automation

Sequencing

Analysis

Clinical interpretation

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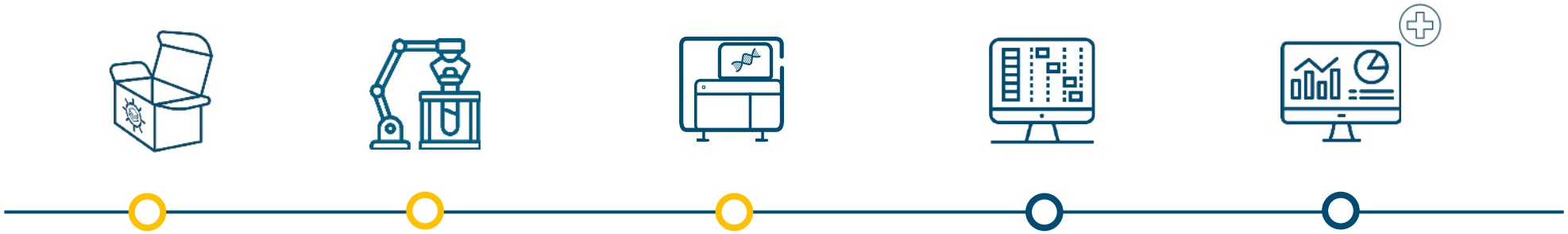
We've designed a robust, adaptive workflow to fit most lab setups



TWIST BIOSCIENCE

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DNA extraction impact

 # 3938 ***Comprehensive Genomic Profiling of solid tumor patients with the OncoDEEP assay for broad analysis in clinical diagnostics***

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Introduction

With the fast-growing number of recommended and required genomic biomarkers small gene panels have become vastly insufficient for most tumor types. Comprehensive Genomic Profiling (CGP) is amenable to screen for subtle nucleotide variants (SNVs and indels) in several hundred of cancer-related genes. Moreover, CGP can provide information on copy number variations (CNVs), gene fusions and tumor-agnostic genomic biomarkers including microsatellite instability (MSI), tumor mutation burden (TMB) and homologous recombination deficiency (HRD) for optimal clinical patient management with diagnostic, prognostic and therapeutic value in a wide variety of solid tumors. Only few CGP panels have been diagnostically validated in the clinic. Here, we report on an extensive multicentric (7 labs) comparative analysis of the novel CGP assay OncoDEEP from OncoDNA, with the diagnostically validated TSO500 assay from Illumina.

Table 1. Comparison of the number of genes for variant calling and the ability of biomarker detection for the TSO500 and OncoDEEP assays

Detection at DNA level	TSO500	OncoDEEP # genes	*in common*
SNVs and indels	523	638	*516*
Amplifications	59	638	*59*
Deletions	0	xx	*0*
pan-tumor markers			
MSI	Yes	Yes	*Yes*
TMB	Yes	Yes	*Yes*
LOH	No	Yes	*No*
HRD	No*	Yes	*No**
Detection at RNA level	**TSO500**	**OncoDEEP # genes**	**in common**
Fusions	55	11	*11*
Splice variants	3	9	*3*

**separate HRD panel has to be added to the assay*

Materials and Methods

Both assays were performed as described in the user guides of both assays. In total, 234 diagnostic DNA and RNA samples with known TSO500 data were analyzed with the OncoDEEP assay. In addition, 12 and 8 reference DNA and RNA samples resp., were analysed for exon skipping and gene fusion detection by most laboratories. The diagnostic samples included many different tumor types, representative of the real life situation in the NGS diagnostic centers. Pooled libraries of both assays were sequenced on a NextSeq500/550 or NovaSeq instrument (Illumina). The major differences between both assays are listed in Table 2.

Table 2. Comparison of TSO500 and OncoDEEP assay features

	TSO500 (Illumina)	OncoDEEP (OncoDNA)
Pre-analytics		
Recommended input	DNA: 80 ng RNA: 40 ng	DNA: 100 ng RNA: 200 ng (dried)
Library prep		
DNA Fragmentation method Normalisation	Shearing With beads	Enzymatic Quantification and dilution
Hybridization capture		
Pooling before hyb # Hybridization steps	No 2	Yes (8 samples) 1
Sequencing on a NextSeq550		
Read length #Samples per run Flowcell NextSeq550Dx	101 bp 8 (DNA + RNA) High Output Kit v2.5 (300 Cycles)	74 bp 24 (DNA + RNA) High Output Kit v2.5 (150 Cycles)
Data analysis		
Secundary analysis Tertiary analysis	TSO500 local app not available	OncoKDM (OncoDNA) OncoKDM (OncoDNA)
Hands-on-time and cost		
Hands-on-time Cost/sample	5 h $$$	4 h $$

Results

General comments OncoDEEP:

- The mean **coverage** of the samples is **more uniform** than for TSO500 (Figure 1) thereby allowing to pool 2- to 3-times more samples.
- The **QC metrics** are more prone to the DNA extraction procedure.

Variant detection with OncoDEEP:

High concordance between both assays for **SNP** and **indel** detection (Figure 2). Missed variants (15%) were due to:

- *Insufficient coverage due to low QC sample metric (8%)*
- *VAF did not reach the threshold of 5% (3%)*
- *Too stringent filter settings e.g. >20 variant reads required (2%)*
- *Classified as VUS instead of (Likely) Pathogenic (1%)*
- *Different usage of NM_ transcript number (1%)*

Amplifications, if >6-fold change, were all concordant; **LOH** can not be assessed since it is not validated for TSO500.

Gene **fusions** (82) or **exon skipping** (16) events were concordant in 78 cases (80%). In the undetected cases it was due to:

- *Very low number of supporting reads in TSO500 (4 cases)*
- *Absence of driver gene in OncoDEEP panel (14 cases)*
- *Unknown reason (2 cases)*

Pan-cancer **biomarkers**:

- In general good agreement between both assays
- Compared to TSO500, the values for MSI calling tend to be somewhat higher (Figure 3) while somewhat lower for TMB
  - HRD could only be compared for few samples but were concordant

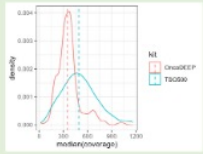

Figure 1. *Distribution of the median coverage obtained with TSO500 (blue) and OncoDEEP (red) (SD 217 vs 145) showing the higher uniformity of the OncoDEEP capture.*

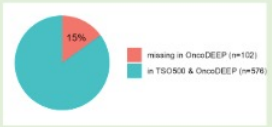

Figure 2. *Of the 678 TSO500 (Likely) Pathogenic SNV and indel variants 85% were also detected with the OncoDEEP assay (green). However, 102 (red) were absent due to a variety of reasons (see text).*

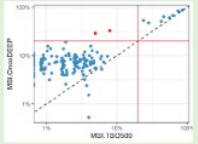

Figure 3. *MSI positive ratio plot (log-scale) for FFPE samples analyzed with TSO500 and OncoDEEP. Using a threshold of 20%, only 2 discordant calls (red) were present.*

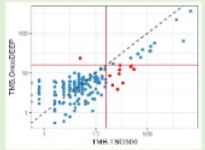

Figure 4. *Comparison of TMB values obtained with TSO500 and OncoDEEP (log-scale). With a threshold of 16 mut/Mb 11 discordant calls (red) were found.*

Conclusions

- The OncoDEEP assay can efficiently detect somatic variants and CNV's in a broad range of solid tumor samples.
- Pan-cancer biomarker analysis (MSI, TMB, HRD) is mostly in line with TSO500 but threshold settingis recommended.
- Gene fusion detection at the RNA level is only possible for 9 most common driver genes in solid tumors.
- The targeting capture provides a uniform selection of the targeted regions in a single hybridisation step.
- The assay includes variant classification and interpretation (OncoKDM) generating patient reports with local clinical trial selection.
- Successful validation (precision, sensitivity, specificity, accuracy, limit-of-detection) of the OncoDEEP assay was performed on 82 diagnostic and 8 reference samples for its implementation in clinical diagnostics.

- Multicenter OncoDEEP – TSO500 comparison
- Data sets needed to be discarded due to bad extraction techniques

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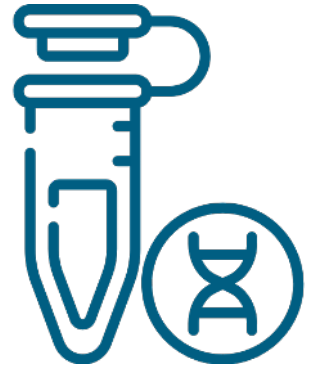
DNA extraction

DNA extration can have a big impact on the final result.



Promega

AS1450		Aligned Reads	Reads Length (bp)	Duplicate (%)	On Target reads (%)	Uniformity (%)	GC Content (%)	Mean Coverage	Target Not Covered (%)	Target Low covered (%)	Mode Insert Size (bp)	Mean Insert Size (bp)
	KDM43635	24584834	99	25	40,2	83	51,6	297	0,02	4,40	138	198
	KDM43637	17095704	97	27	46,5	97	48,8	254	0,02	1,90	114	159
	KDM43638	18847627	94	21	47,0	98	50,5	279	0,02	1,20	101	131
	KDM43639	31309418	96	22	46,4	70	52,8	450	0,01	5,00	115	150
	KDM43640	19740875	97	21	48,7	98	48,9	308	0,02	0,80	113	156
	KDM43641	34433258	96	21	45,2	67	53,2	475	0,02	3,20	113	154
	KDM43642	25718423	98	21	45,4	97	49,8	365	0,02	0,40	142	183

AS1720	RD-23-112-Or	Aligned Reads	Reads Length (bp)	Duplicate (%)	On Target reads (%)	Uniformity (%)	GC Content (%)	Mean Coverage	Target Not Covered (%)	Target Low covered (%)	Mode Insert Size (bp)	Mean Insert Size (bp)
	KDM43889	26370315	98	18	37,6	99	49,1	320	0,02	0,50	115	171
	KDM43888	22360048	97	16	39,6	99	49,3	291	0,03	0,70	114	143
	KDM43887	26911421	97	18	38,3	99	49,2	338	0,02	0,50	114	151
	KDM43886	31139055	98	17	38,4	99	49,5	388	0,03	0,30	120	163
	KDM43885	25986585	98	17	38,7	99	48,8	328	0,02	0,50	122	162
	KDM43884	21314142	97	17	38,1	99	48,9	266	0,03	1,10	110	146
	KDM43883	25971479	98	18	38,0	99	49,1	320	0,02	0,50	122	164

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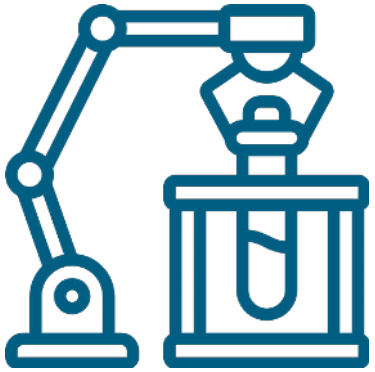
Automation



Customized support

- Protocol review with the company
- Proposals of workflow fitting our assay requirements but getting around the tricky steps to automate
- Active role in the script development and testing phases

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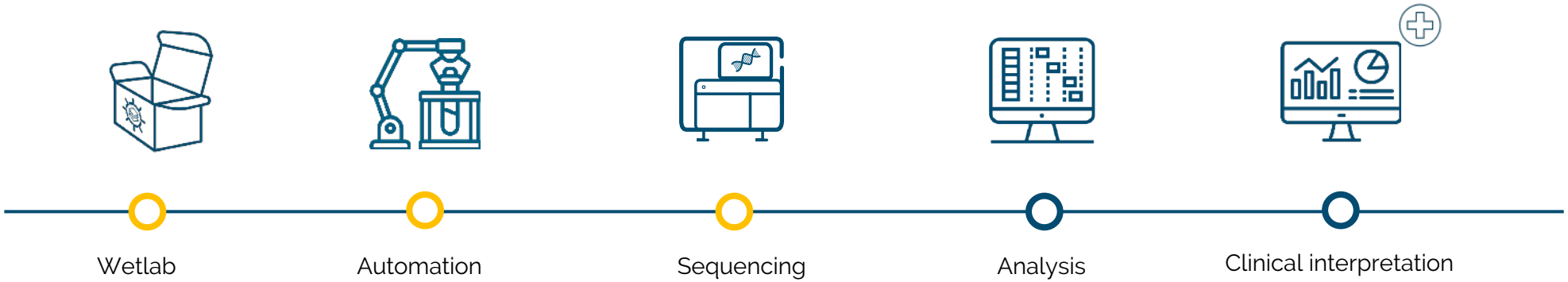
Sequencers



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What has been done

➡ Clinical samples, carrying known variants/fusion/genomic signatures previously detected with OncoDEEP® kit combined with Illumina sequencing, were selected (**Table 1**). Reference standards were also used: 6 from Horizon for variants & fusions and 3 from Seracare for tumor mutational burden (TMB). DNA inputs of 6ng, 50ng & 100ng were used and some samples were replicated. In total, 90 samples (54 clinical & 36 reference samples) were sequenced to evaluate the performance of MGI System.

Table 1: Samples used to compare OncoDEEP® panel based on Illumina or MGI sequencer

Samples	Aim	n
Clinical samples	Variant/fusion calling and MSI	34
Ovarian clinical samples*	HRD	20
HD678, HD789, HD798, HD799, HD803, HD832, GM24149	Variant/fusion calling	29
Seracare samples	TMB	7

*FFPE ovarian clinical samples coming from the Hospital 12 Octubre (Madrid, Spain)

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Sequencing

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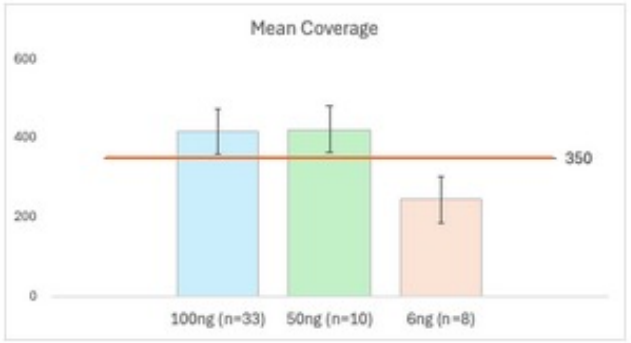
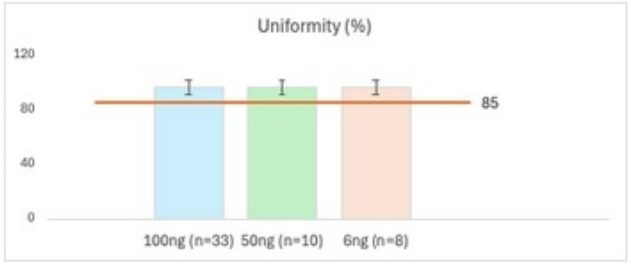
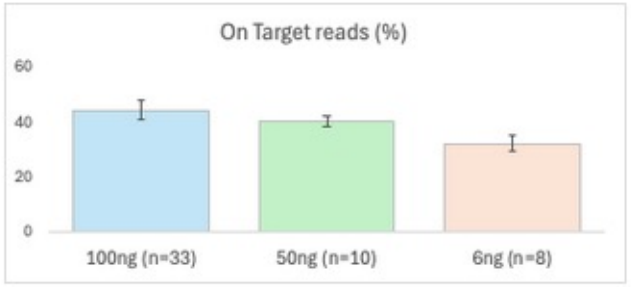
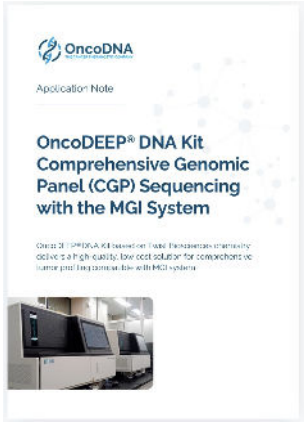
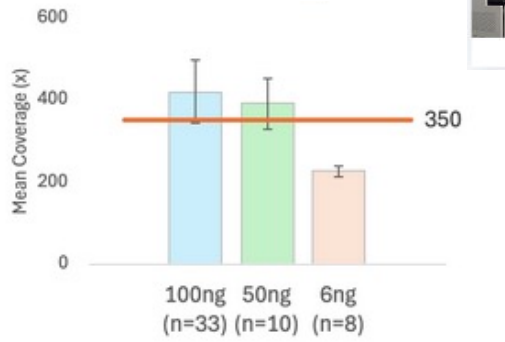


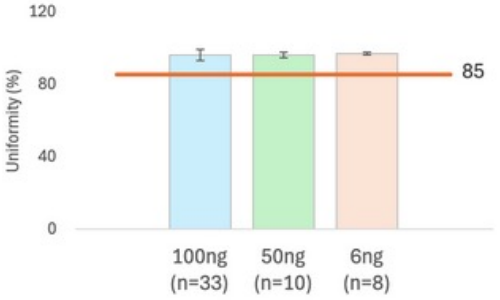


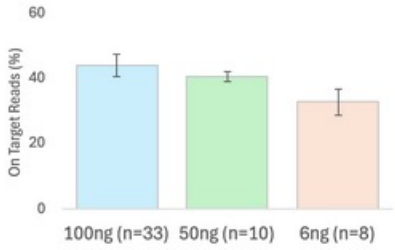


MGI









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MGI

Gene	Variant (VAF%)ø	HD798 (mild)				HD799 (moderate)				HD803 (severe)				HD832					
		Illumina		MGI		Illumina		MGI		Illumina		MGI		Illumina			MGI		
		50ng *	6ng	50ng *	6ng	50ng *	6ng	50ng *	6ng	50ng *	6ng	50ng *	6ng	100ng	50ng **	6ng	100ng	50ng **	6ng
BRAF	V600E (10.5/10.7)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
KIT	D816V (10)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
EGFR	E746_A750 del (2/1.9)	✓	✓	✓	✓	✓	✘▲	✓	✓	✓	✘▲	✓	✘▲	✓	✓	✓	✓■	✓◌◌	✓■
	L858R (3/2.8)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
	T790M (1/0.9)	✓	✓■	✓◌◌	✓■	✓	✘▲	✓	✘▲	✓	✘▲	✓	✓	✓■	✓◌◌	✓	✓	✓◌	✓■
	G719S (24.5)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
KRAS	G13D (15)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
	G12D (6/6.3)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
NRAS	Q61K (12.5)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
PIK3CA	H1047R (17.5)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
	HD803	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

ø VAF in green is specific for Reference HD832

* Duplicated

** Quadruplicate

▲Detected but discarded due to failing QC cut-off

■ Detected but not reported due to VAF <1%

◌ 1 duplicate detected but not reported due to VAF <1%

◌◌ 2 duplicates detected but not reported due to VAF <1%

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Gene	Variant (VAF%)ø	HD798 (mild)				HD799 (moderate)				HD803 (severe)				HD832					
		Illumina		EB		Illumina		EB		Illumina		EB		Illumina			EB		
		50ng *	6ng	50ng *	6ng	50ng *	6ng	50ng *	6ng	50ng *	6ng	50ng *	6ng	100ng	50ng **	6ng	100ng	50ng **	6ng
BRAF	V600E (10.5/10.7)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
KIT	D816V (10)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
EGFR	E746_A750 del (2/1.9)	✓	✓	✓	✘▲	✓	✘▲	✓△	✘▲	✓	✘▲	✓	✓	✓	✓	✓	✓■	✓△△	✘▲
	L858R (3/2.8)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
	T790M (1/0.9)	✓	✓■	✓△	✘▲	✓	✘▲	✓	✘▲	✓	✘▲	✓◎	✓	✓■	✓◎◎	✓	✓	✓	✓	✓
	G719S (24.5)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
KRAS	G13D (15)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
	G12D (6/6.3)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
NRAS	Q61K (12.5)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
PIK3CA	H1047R (17.5)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
	E545K (9/8.8)	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

ø VAF in green is specific for Reference HD832

* Duplicated

** Quadruplicate

▲Detected but discarded due to failing QC cut-off

△ 1 duplicate detected but discarded due to failing QC cut-off

△△ 2 duplicates detected but discarded due to failing QC cut-off

■ Detected but not reported due to VAF <1%

◎ 1 duplicate detected but not reported due to VAF <1%

◎◎ 2 duplicates detected but not reported due to VAF <1%

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Provider	Sequencer	FC type	Lanes	Total Reads/FC	Read Lengths	Data Output	Run Time	Nb OncoDEEP DNA+RNA samples ‡
Illumina	Next Seq 500 / 550	Mid Output	4	260M	PE75	16-19 Gb	~15 hrs	8
				260M	PE150	32-39 Gb	~26 hrs	8
		High Output	4	800M	PE75	50-60 Gb	~18 hrs	16
				800M	PE150	100-120 Gb	~29 hrs	24
	NextSeq 2000	P1	1	200 M	PE150	30 Gb	~19 hrs	8
		P2	1	800M	PE100	80 Gb	~21 hrs	24
					PE150	120 Gb	~29 hrs	24-32
		P3	1	2400M	PE100	240 Gb	~33 hrs	72-96
					PE150	360 Gb	~48 hrs	96
	Novaseq 6000	SP	2	1300-1600M	PE100	134-167 Gb	~19 hrs	48
		SP	2		PE150	200-250 Gb	~25 hrs	48-56
		S1	2	2600-3200M	PE100	266-333 Gb	~19 hrs	112
		S1	2		PE150	400-500 Gb	~25 hrs	112-120
		S2	2	6600-8200M	PE100	667-833 Gb	~25 hrs	232*
		S2	2		PE150	1000-1250 Gb	~36 hrs	240*
	Novaseq X	1.5B	2	3200M	PE100	330 Gb	~18 hrs	112
		1.5B	2		PE150	500 Gb	~21 hrs	112-120
MGI	DNBSEQ-G400	FCS	2	1100M	PE100	110 Gb	~22/26 hrs	16-24
					PE150	165 Gb	~31/37 hrs	24*
		FCL	4	3000M~3600M	PE100	300-360 Gb	~35/38 hrs	96
					PE150	450-540 Gb	~50/56 hrs	96-104*
	DNBSEQ-T7	DNBSEQ-T7RS HT V3.0	1	11600M	PE100	1160 Gb~4640 Gb	16hrs ~18hrs	368*
					PE150	1750 Gb~7000 Gb	22hrs ~24hrs	368-376*
		DNBSEQ-T7RS HT V2.0	1	10000M	PE100	1000 Gb~4000 Gb	20hrs ~22hrs	320*
					PE150	1500 Gb~6000 Gb	24hrs ~30hrs	320-328*
	DNBSEQ-G50	FCL	1	1000M	PE100	~100 Gb	~26 hrs	24*
					PE150	~150 Gb	~40 hrs	24-32*
	DNBSEQ-G99	FC	1	160M	PE150	24-48 Gb	12 hrs	4-5*
Element	AVITI	Low Output	2	500M	PE150	75 Gb	27 hrs	8*
		Medium Output	2	1000M	PE75	75 Gb	20 hrs	24
					PE150	150 Gb	31 hrs	32*
		High Output	2	2000M	PE75	150 Gb	24 hrs	48
					PE150	300 Gb	38 hrs	56-64*
PacBio	Onso			800-1000M	PE100	80-100 Gb	32 hrs	24**
					PE150	120-150 Gb	48 hrs	24-32**

‡ Sample number includes DNA samples only or DNA samples plus the same number of RNA samples (eg; 8 would mean 8 DNA samples or 8 DNA samples plus 8 RNA samples)

*Please contact the support team to discuss on the feaseable number of samples

** Under evaluation

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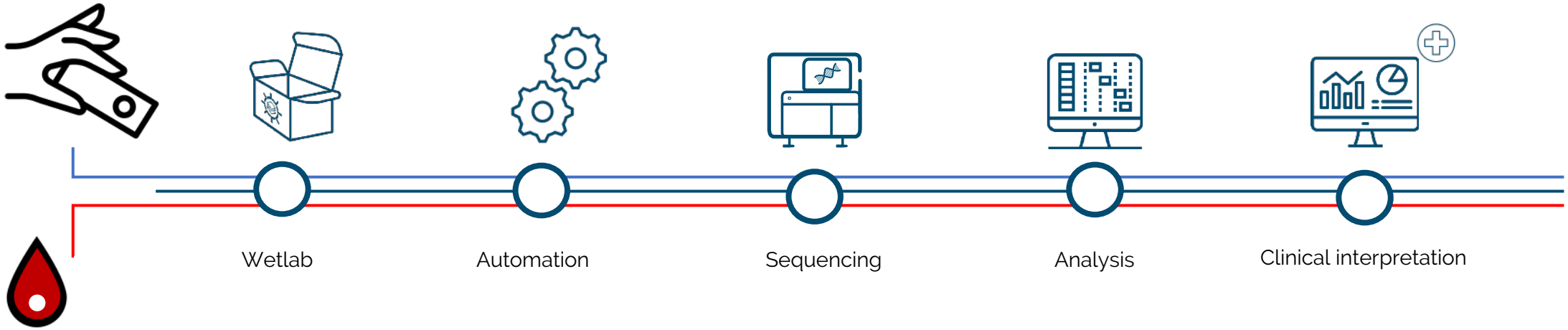
Versatile



Solid Biopsy

OncoDEEP® by OncoDNA KIT

Solid Tumor WES

RNA Panels

LargeRNA

FocusRNA

Liquid Biopsy

OncoSELECT® by OncoDNA KIT

OncoDEEP

Monitoring

TWIST MRD 500

+ New developments

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Most comprehensive genomic profiling panel

Designed by oncology experts, the OncoDEEP® panel contains **the most relevant and complete cancer gene panel**. Over time this panel was optimized to include all clinically-relevant oncology targets. The DNA and RNA panels comprise **638 and 22 genes** reporting **genomic alterations** (SNV, insertion, deletion, CNV, fusions, unusual splicing, ...) and **complex genomic signature** (HRD, MSI and TMB).

Article — HRD assessment for clinical management using the OncoDEEP® Kit

DNA (638 GENES)

Genes alterations

- SNV (Including TERT PROMOTER)
- CNV
- DELETION
- INSERTION
- LOH

Complex signatures

- HRD
- MSI
- TMB

Translocation (intronic)

- ALK
- ROS1
- RET
- MET-EX14

RNA (22 DRIVER GENES)

Gene fusions

- ALK
- ROS1
- RET
- FGFR1
- FGFR2
- FGFR3
- NTRK1
- NTRK2
- NTRK3
- BRAF
- NRG1
- EWSR1
- TMPRSS2

Unusual Splicing

- BRCA1
- BRCA2
- PTEN
- AR
- EGFR
- ERBB2
- MET
- PALB2
- RB1

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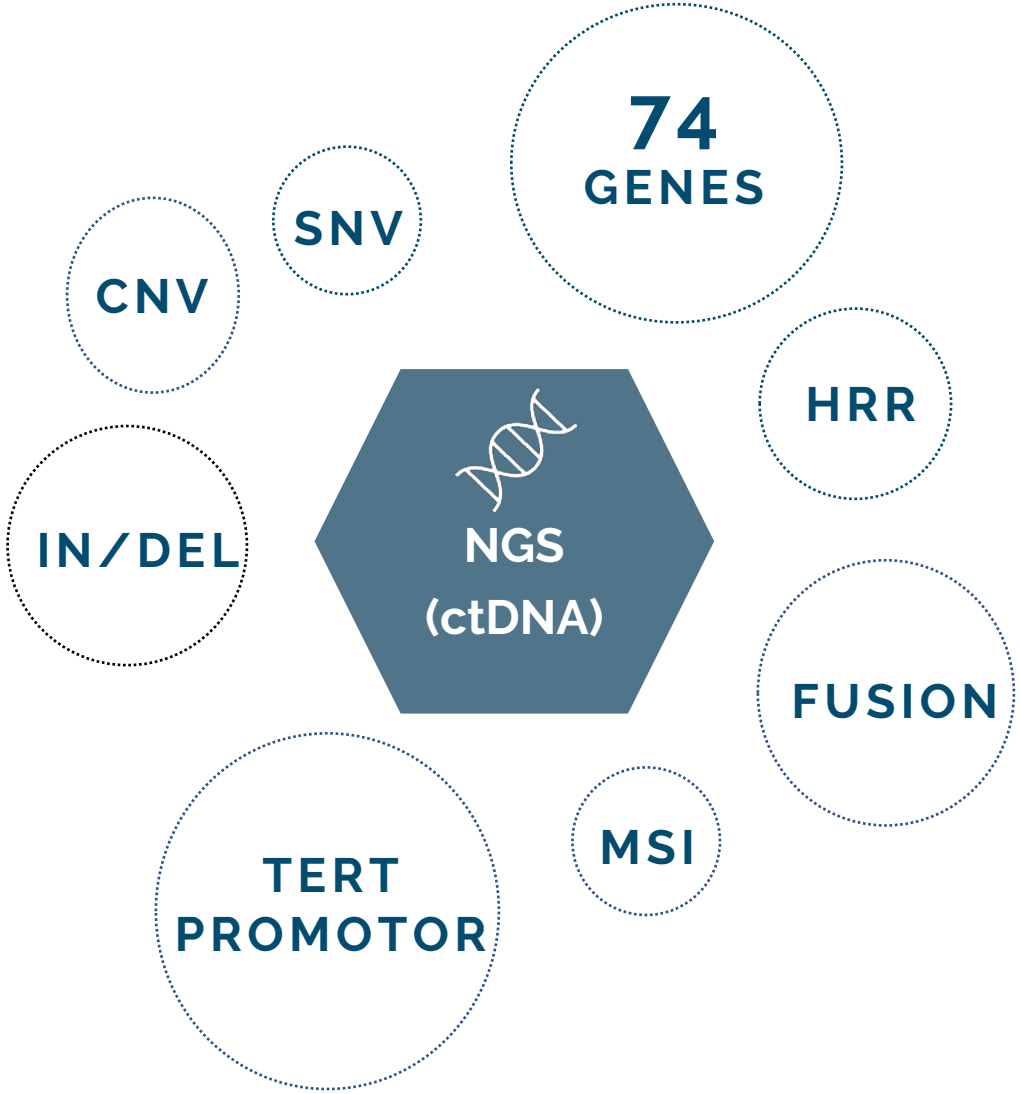
Targeted Liquid Biopsy to Support Your Clinical Decisions

Designed by oncology experts, the **OncoSELECT** panel contains the most relevant cancer gene panel associated with metastatic solid cancer, including **all clinically-relevant oncology targets**.

The panel is composed of **74 genes**, reporting genomic alterations (SNV, insertion, deletion, intron aberrations such as gene translocations and unusual splicing) and TERT promoter



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Targeted Liquid Biopsy to Support Your Clinical Decisions

Optimized process to achieve **greater sensitivity and specificity**

VAF =0,25%	VAF =0,1%
98,5 > % sensitivity	87,5% > % sensitivity
99,9 > % specificity	99,9 > % specificity
99,9 > % accuracy	99,9 > % accuracy

Translocation - 24 genes

*All CDS - 28 genes

AKT1	BRCA2*	EML4	FGFR3*	IDH2	NBN*	PIK3CA	SLC34A2
ALK	BRIP1*	ERBB2	FOXL2	KEAP1*	NF1*	POLE	STK11*
AR	CD74	ERBB4	GNA11	KIF5B	NPM1	PTEN*	pTERT
ARAF	CDK12*	ESR1	GNAQ	KIT	NRAS	RAD51B*	TP53
ARID1A*	CDKN2A*	ETV6	GNAS	KRAS	NRG1	RAD51C*	
ATM*	CHEK1*	EZR	H3F3A	MAP2K1	NTRK1	RAD51D*	
ATR*	CHEK2*	FANCA*	H3F3B	MET	NTRK2	RAD54L*	
BARD1*	CTNNB1	FANCL*	H3C2	MLH1*	NTRK3	RET	
BRAF	DICER1	FGFR1*	HRAS	MRE11A*	PALB2*	ROS1	
BRCA1*	EGFR	FGFR2*	IDH1	MYOD1	PDGFRA	SDC4	

** Detection of MSI and CNV**

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Details

- Gene list: *AKT1 (3), **ALK**(20-25), **BRAF** (6-8, 11, 12, 14, 15), BRCA1*, BRCA2*, **CD74**, CDKN2A*, CTNNB1 (3), DICER1 (24,25), **EGFR** (18-21), **EML4**, ERBB2 (3, 6-8, 12, 16-21), ERBB4 (10, 12), ESR1 (5-8), **ETV6**, **EZR**, **FGFR1*, FGFR2*, FGFR3***, FOXL2 (1), GNA11 (4,5), GNAQ (4,5), GNAS (8), H3-3A (H3F3A) (2), H3-3B (H3F3B) (2), H3C2 (HIST1H3B) (1), HRAS (2-5), IDH1 (4), IDH2 (4), KEAP1*, **KIF5B**, KIT (8, 9, 11, 13, 14, 17-19), KRAS (2-4), MAP2K1 (2,3), **MET** (13-20), MYOD1 (1), **NPM1**, NRAS (2-4), **NRG1, NTRK1** (14, 15)**, NTRK2** (12, 13)**, NTRK3** (16, 17), PDGFRA (12, 14, 18), PIK3CA (2, 3, 5-8, 10, 14, 19, 21), POLE*, PTEN*, **RET** (8, 10-16)**, ROS1** (37, 38, 40)**, SDC4, SLC34A2**, STK11*, TERT (promotor), TP53**
- *AR, ARAF, ARID1A*, ATM*, ATR*, BARD1*, BRIP1*, CDK12*, CHEK1*, CHEK2*, FANCA*, FANCL*, MLH1*, MRE11A*, NBN*, NF1*, PALB2*, RAD51B*, RAD51C*, RAD51D*, RAD54L**

- MSI, genomic backbone for CNV detection (amplification, LOH, deletion…)

*Whole gene

Translocations

(X) exon targeted for SNV/Indels

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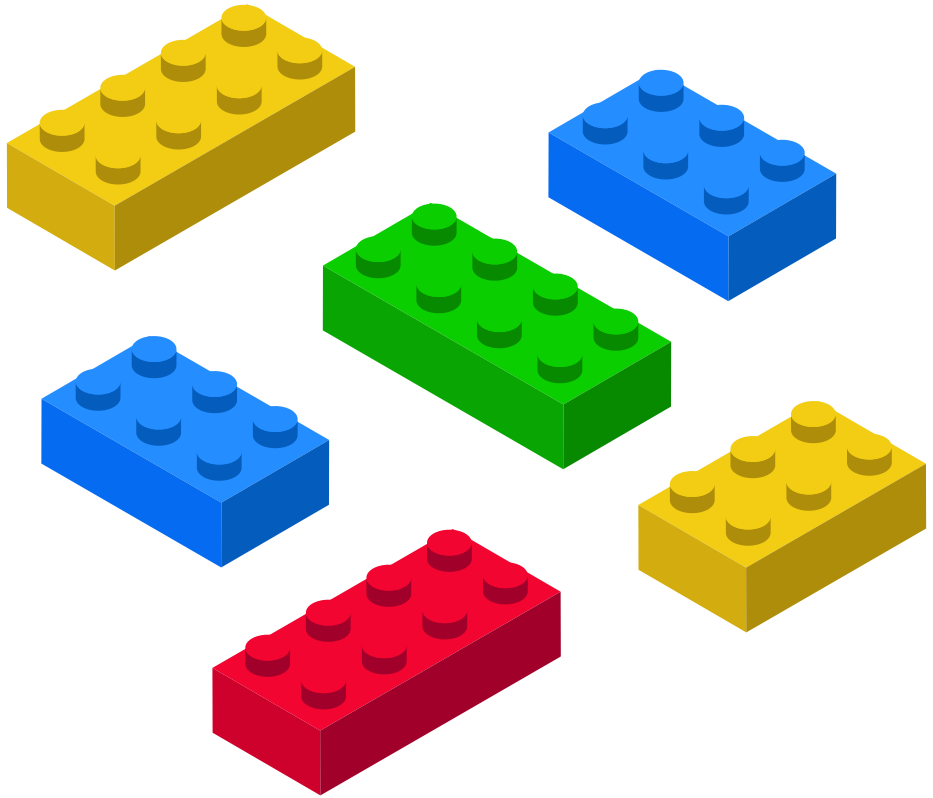
Use cases – Start combing



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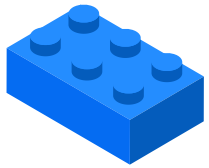
Start combining – scenario 1 – low throughput



(400 samples / year)

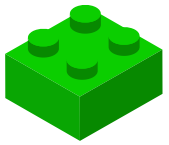
OncoDEEP® by OncoDNA KIT

+

illumina

NextSeq 500/550 mid 2x75/2x150

50 flow cells / year

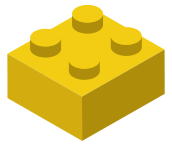


OR

Element Biosciences

EB AVITI Low output

50 flow cells / year

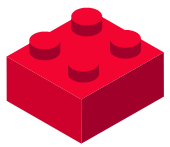


OR

MGI

DBSNQ400 MGI FCS 2x100

50 flow cells / year



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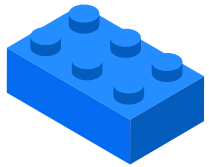
Start combining – scenario 2 – Medium throughput



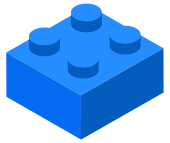
(800 samples / year)

OncoDEEP® by OncoDNA KIT

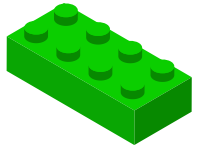
+

OncoSELECT® by OncoDNA KIT

(300 samples / year)



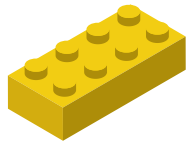
illumina



NextSeq 550/550 high 2x75/2x150 for OncoDEEP	50 flow cells / year
NextSeq 500/550 high 2x150 for OncoSelect	50 flow cells / year
NextSeq 1000/2000 P2 2x100/2x150 for OncoDEEP	50 flow cells / year
NextSeq 1000/2000 P2 2x150 for OncoSELECT	50 flow cells / year
NextSeq 2000 P3 2x150 combining OncoDEEP and OncoSELECT	50 flow cells / year

OR

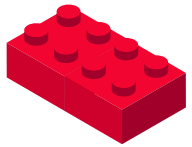
Element Biosciences



EB Aviti Medium output 2x75 for OncoDEEP	50 flow cells / year
EB Aviti Medium output 2x150 for OncoSELECT	50 flow cells / year
EB Aviti High output 2x150 combining OncoDEEP and OncoSELECT	50 flow cells / year

OR

MGI



DBSNQ400 MGI FCS 2x100 for OncoDEEP	50 flow cells / year
DBSNQ400 MGI FCS 2x150 for OncoSELECT	50 flow cells / year
DBSNQ400 MGI FCL 2x150 combining OncoDEEP and OncoSELECT	50 flow cells / year

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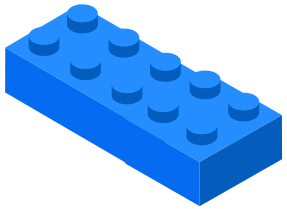
Start combining – scenario 3 – high throughput



(1200 samples / year)

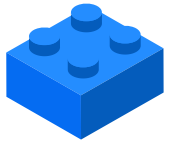
OncoDEEP® by OncoDNA KIT

DNA

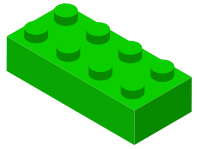
+

OncoSELECT® by OncoDNA KIT

(600 samples / year)



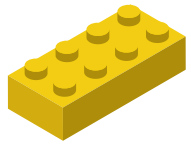
illumina



NextSeq 500/550 High 2x75/2x150 for OncoDEEP	50 flow cells / year
2x NextSeq 550 high for OncoSelect	100 flow cells / year
NextSeq 1000/2000 P2 2x100/2x150 for OncoDEEP	50 flow cells / year
2x NextSeq 1000/2000 P2 2x150 for OncoSELECT	100 flow cells / year
NextSeq 2000 P3 2x150 combining OncoDEEP and OncoSELECT	50 flow cells / year

OR

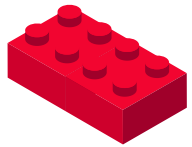
Element Biosciences



EB Aviti Medium output 2x75/2x150 for OncoDEEP	50 flow cells / year
EB Aviti High output 2x150 for OncoSELECT	50 flow cells / year
	50 flow cells / year

OR

MGI



DBSNQ400 MGI FCS 2x150 for OncoDEEP	50 flow cells / year
DBSNQ400 MGI FCL 2x150 combining OncoDEEP and OncoSELECT	50 flow cells / year
	50 flow cells / year

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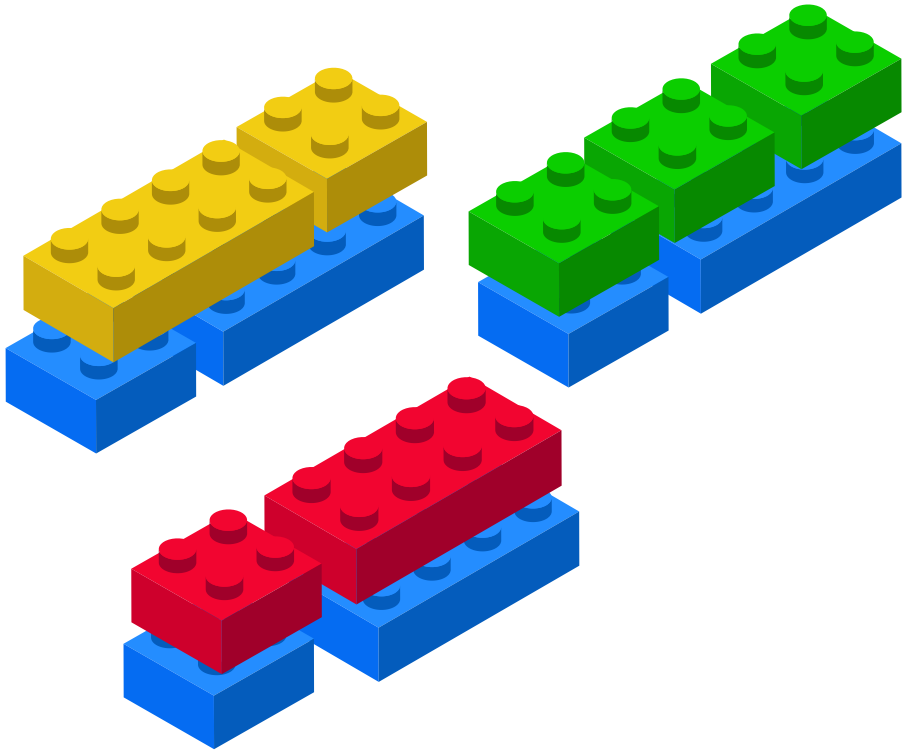
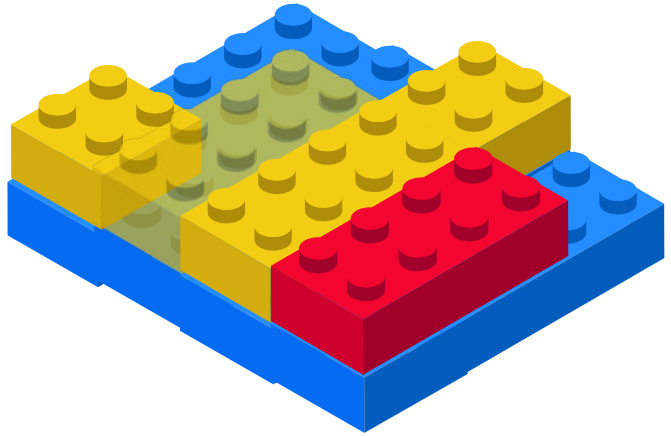
Our workflow offers multiple combinations to optimize efficiency and cost…



Even when the backlog become critical



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Use Case – High Throughput lab

- **The ask**
  - Medim size targeted tumor panel (SNV, InDel, CNV, fusion, MSI, PgX) and small RNA panel 2000 samples
  - Large CGP tumor panel (SNV, InDel, CNV, fusion, MSI, PgX; HRD) and large RNA panel 800
  - Targeted tumor panel for heamatological samples (SNV, InDel,, fusion) 672
  - CF DNA panel 500 samples

- **The OncoDNA proposal**
  - OncoDEEP for all solid tumor panels and heamatological samples
  - OncoSelect and potentially OncoDEEP on Liquid Biopsy panel
  - Large RNA panel

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	OncoDEEP Library Preparation and Capture - up to 48 samples batch		Duration	Hands-on Time Manual	Hands-on Time Automatized
D1 8h30	STEP 1	DNA Fragmentation, End-Repair and dA-tailing dA-tailed DNA samples	1 hour	30 min.	40 min.
	STEP 2	Universal Adapter Ligation and Clean-up Ligation products	1 hour	15 min. 30 min. Clean-up	
	STEP 3	PCR Amplification with UDI Primers, Clean-up and QC Individual indexed libraries	1 hour	15 min. 30 min. Clean-up 15 min. QC	
	STEP 4	Preparation of libraries and pools for hybridization Pool of Individual indexed libraries	1 hour	15 min. + 15 min.	20 min.
D1 15h30	STEP 5	Capture probes hybridization Hybridized targets in solution	16 hour	15 min.	
D2 8h30	STEP 6	Hybridized targets binding to the streptavidin beads Captured targets on beads	1,5 hour	30 min. 30 min. Clean-up	15 min.
D2 14H	STEP 7	Post-capture PCR amplification, clean-up and QC Enriched libraries ready to be sequenced	1 hour	30 min.	

Why is this important

		Monday	Tuesday	Wednesday	Thursday	Friday
Automation	AM		Lib Prep RNA	Capture Washes & Post-Capture Amplification	Lib Prep RNA	Capture Washes & Post-Capture Amplification
	PM	Lib Prep DNA	Hybridization and Capture Launch	Lib Prep DNA	Hybridization and Capture Launch	
Manual		cDNA synthesis		Sequencing Run launch		Sequencing Run launch
				cDNA synthesis		

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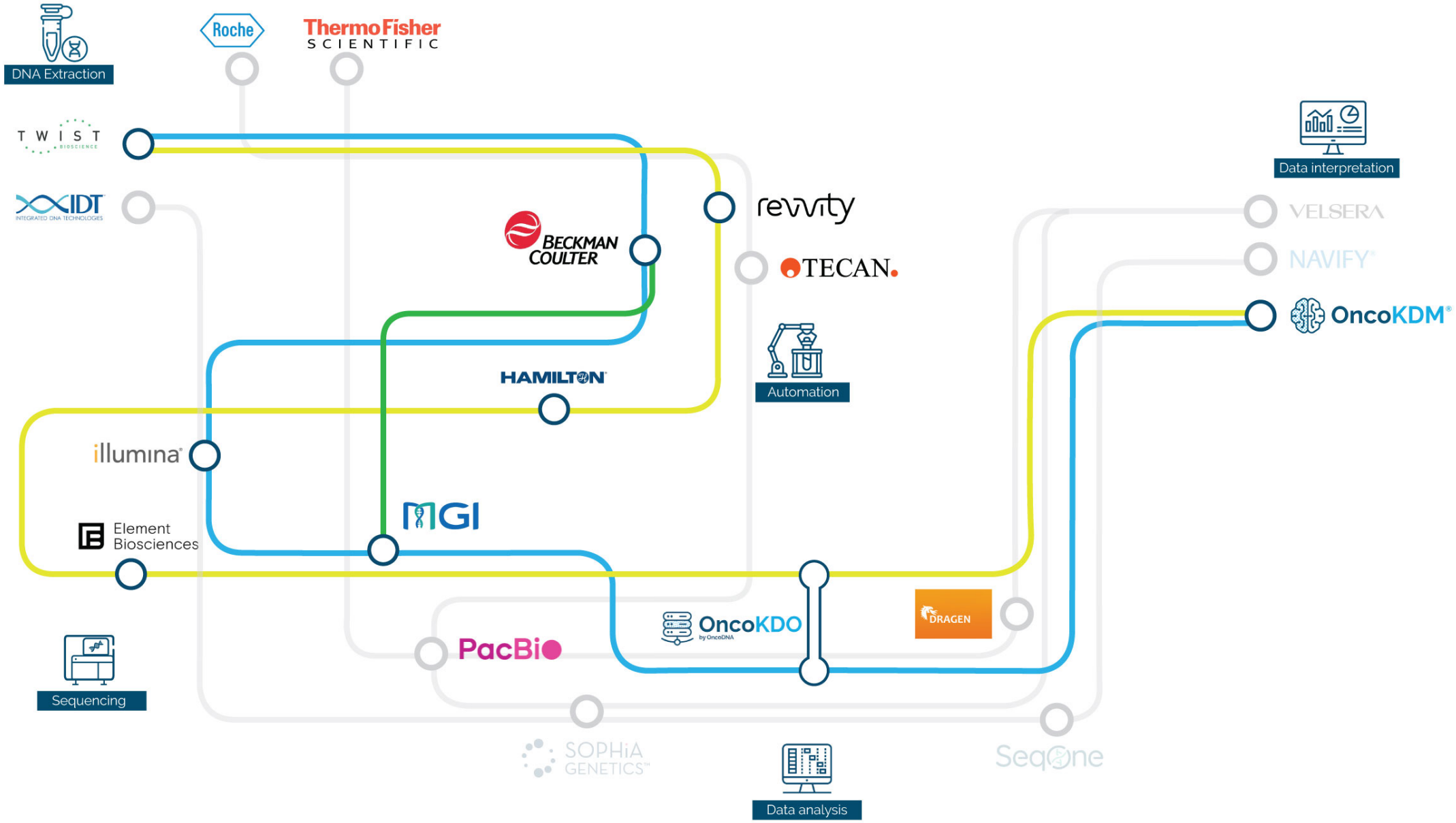
We are your partner to navigate a complex ecosystem



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Data Data Data – Live demo

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