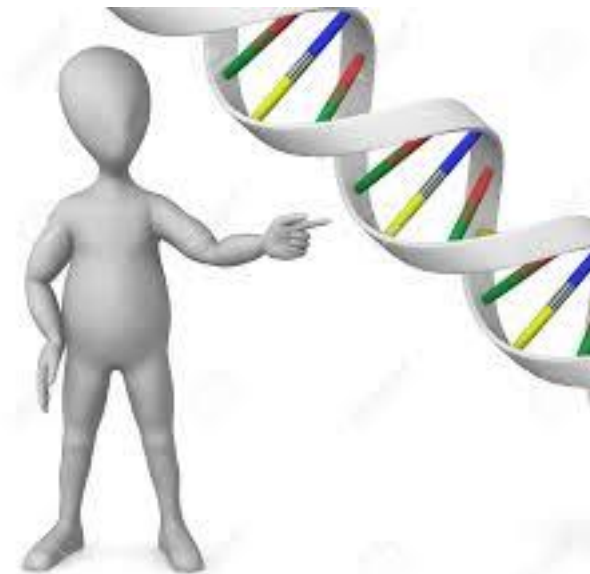


The economic advantage of in-house 1 day NGS



- *Dr. Javier Hernández Losa*
 - *30th August 2021*

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Agenda

- 1) Genexus Incorporation
- 2) Experience with OPA analysis in NSCLC
- 3) Experience in other Solid Tumors

Why perform NGS analysis?

✓ Molecular Profiling in solid tumors

Soft Tissue Tumors

Paediatric Tumors



✓ Biomarker analysis

NSCLC

CRC

Other Tumor Type



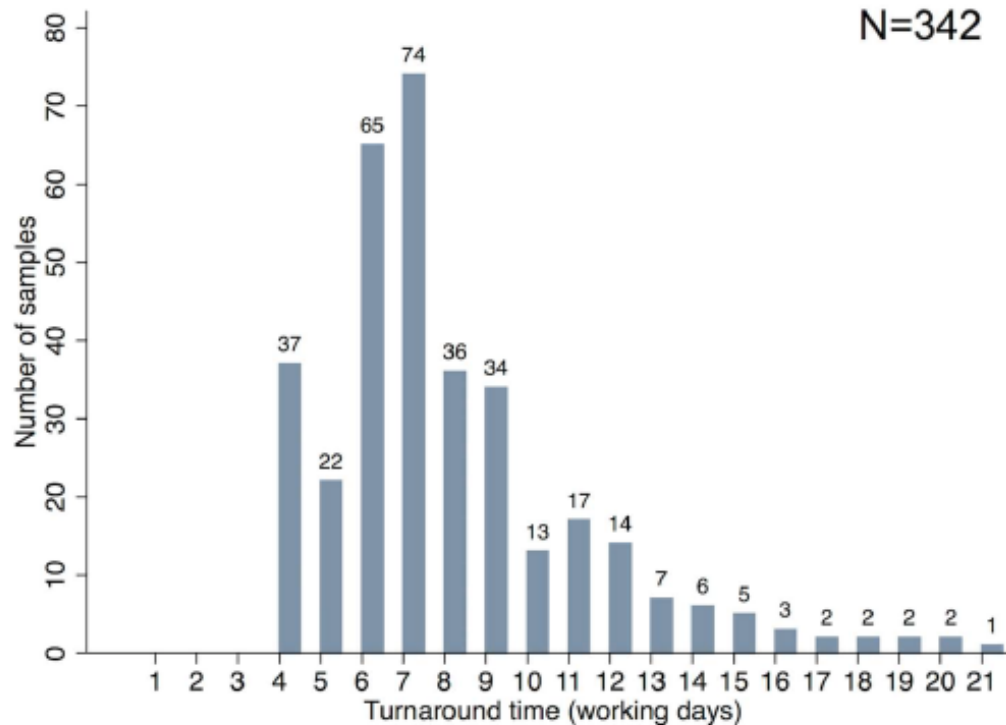
✓ Translational Research

RESEARCH ARTICLE

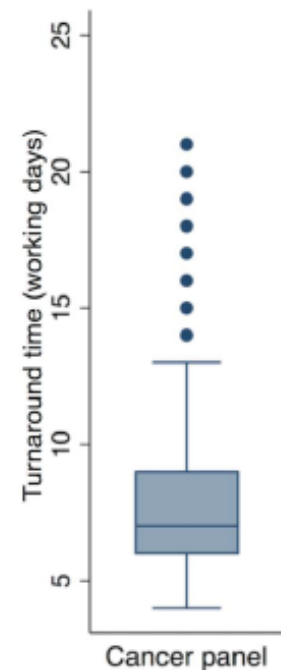
Clinical applicability and cost of a 46-gene panel for genomic analysis of solid tumours: Retrospective validation and prospective audit in the UK National Health Service



A



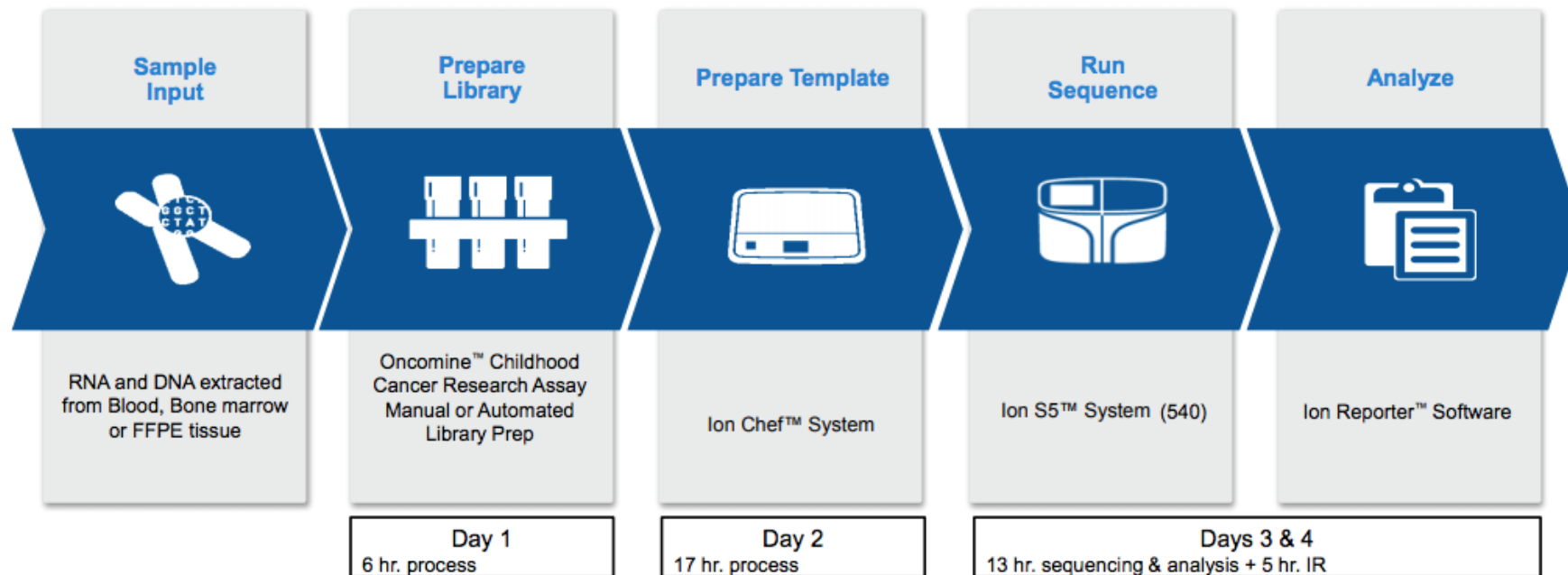
B





OCCRA Workflow

- RNA and DNA from same sample
 - Seven DNA samples plus one negative control –PLUS–
 - Seven RNA samples plus one negative control per chip



*Sample Selection and tumor area evaluation (1-2 days).
Sample collection for cost-effective batch sizes.(1-5 days)*



TAT 7-10 days

RESEARCH ARTICLE

Clinical applicability and cost of a 46-gene panel for genomic analysis of solid tumours: Retrospective validation and prospective audit in the UK National Health Service



Table 4. Total cost per sample and type of malignancy by resource category.

Cost Item	Type of Test					Combination of Single Gene Tests for Different Malignancies		
	Ion AmpliSeq Panel	cobas <i>BRAF</i>	cobas <i>EGFR</i>	cobas <i>KRAS</i>	<i>KIT</i> (Sanger Sequencing)	NSCLC (<i>BRAF</i> , <i>EGFR</i> , <i>KRAS</i>)	Melanoma (<i>BRAF</i> , <i>NRAS</i> , <i>KIT</i>)	Colorectal Carcinoma (<i>KRAS</i> , <i>NRAS</i>)
Equipment	£18 (5%)	£0 (0%)	£0 (0%)	£0 (0%)	£0 (0%)	£1 (0%)	£1 (0%)	£0 (0%)
Consumables	£185 (55%)	£34 (48%)	£62 (59%)	£93 (66%)	£83 (60%)	£177 (64%)	£159 (57%)	£134 (65%)
Staff	£48 (14%)	£23 (33%)	£23 (22%)	£23 (16%)	£30 (21%)	£48 (17%)	£65 (23%)	£35 (17%)
Miscellaneous ^a	£31 (9%)	£2 (2%)	£2 (2%)	£2 (1%)	£2 (2%)	£5 (2%)	£5 (2%)	£3 (2%)
Overheads	£56 (17%)	£12 (17%)	£17 (17%)	£23 (17%)	£28 (17%)	£46 (17%)	£50 (18%)	£35 (17%)
Total test cost	£339 (100%)	£71 (100%)	£104 (100%)	£141 (100%)	£138 (100%)	£276 (100%)	£280 (100%)	£208 (100%)
Total test cost in US dollars	\$449	\$94	\$138	\$187	\$183	\$366	\$371	\$276

NGS vs Single Gene Approach



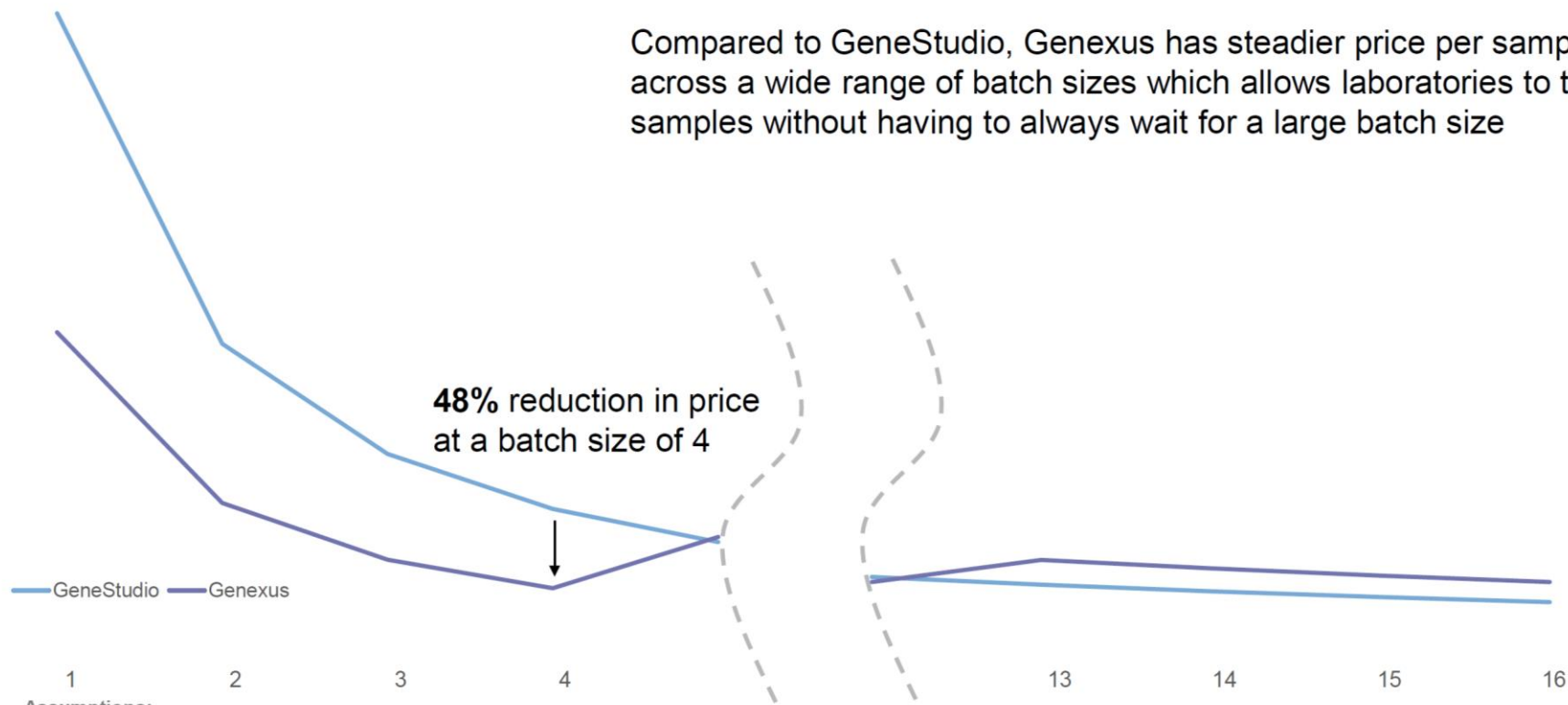
Diferencial			NSCLC							
	NGS	TOTAL (€)	EGFR MUT	ALK TRANS	ROS1 TRANS	RET TRANS	NTRK1 TRANS	MET MUT	BRAF mut	PD-L1
1505	820	2325	375	465	295	295	295	350	250	215
			CRC							
			KRAS MUT	NRAS MUT	BRAF MUT					
130		950	350	350	250					
			GIST							
			KIT MUT	PDGFRA MUT						
-170		650	300	350						

* The prices were obtained globally in Spain by different suppliers and are expressed in euros



Genexus Is Cost Effective at Low Batch Sizes

Compared to GeneStudio, Genexus has steadier price per sample across a wide range of batch sizes which allows laboratories to test samples without having to always wait for a large batch size



Assumptions:

- For Genexus, per sample pricing calculated using list prices for Oncomine Precision Assay with associated Genexus consumables (running FFPE samples)
- For GeneStudio, per sample pricing calculated using list prices for Oncomine Focus Assay with associated GeneStudio S5 consumables (Ion Chef automated library preparation)

Batch sizes are important



		8	7	6	5	4	3
Description	Number reactions	PRICE	PRICE	PRICE	PRICE	PRICE	PRICE
ArcherFusionPlexSarcomaPanel(8rx)	8	2724,2	340,53	340,53	340,53	340,53	340,53
ArcherMBCAdaptersA17-A24forIllumina							
MiseqReagentKitV2(300cycles)	8	1190,4	148,80	170,06	198,40	238,08	396,80
AB0003MBC1V2300	8	3914,6					
AgencourtFormaPure	50	440,0	8,80	8,80	8,80	8,80	8,80
AgencourtAMPureXPBeads25mL	25	285,4	11,42	11,42	11,42	11,42	11,42
iTaqUniversalSYBRGreenSupermix	160	134,0	0,84	0,84	0,84	0,84	0,84
KAPAUniversalLibraryQuantificationKit	56	615,9	11,09	11,09	11,09	11,09	11,09
QUBITESSAYTUBES*SETOF500*	500	237,12	0,47	0,47	0,47	0,47	0,47
QUBITERNAHSESSAYKIT,500	500	66,5	0,13	0,13	0,13	0,13	0,13
			522,1	543,3	571,7	611,4	770,1

Why Genexus?

Library preparation to variant interpretation

Report*

Ion Torrent™ Genexus™
Integrated Sequencer (Available November 2019)

Ion Torrent™ GX5™ Chip:
12–15M reads/lane



14 hours for a single-lane run
(approx. 24 hours for full chip)
Up to 32 Samples per run



For Research Use Only. Not for use in diagnostic procedures.

- ✓ Workflow optimization batches (n=4 samples/line)
- ✓ Full automation
- ✓ Reduction in TAT (14 hours)
- ✓ Possibility to combine FFPE and Liquid Biopsy analysis

ONCOMINE PRECISION ASSAY (OPA)

DNA

Genes con cobertura Hotspot:

AKT1	ESR1	MAP2K2
AKT2	FGFR1	MET
AKT3	FGFR2	MTOR
ALK	FGFR3	NRAS
AR	FGFR4	NTRK1
ARAF	FLT3	NTRK2
BRAF	GNA11	NTRK3
CDK4	GNAQ	PDGFRA
CDKN2A	GNAS	PIK3CA
CHEK2	HRAS	PTEN
CTNNB1	IDH1	RAF1
EGFR	IDH2	RET
ERBB2	KIT	ROS1
ERBB3	KRAS	SMO
ERBB4	MAP2K1	TP53

45 genes

CNV (ganancia y pérdida de copias):

ALK
AR
CD274
CDKN2A
EGFR
ERBB2
ERBB3
FGFR1
FGFR2
FGFR3
KRAS
MET
PIK3CA
PTEN

14 genes

RNA

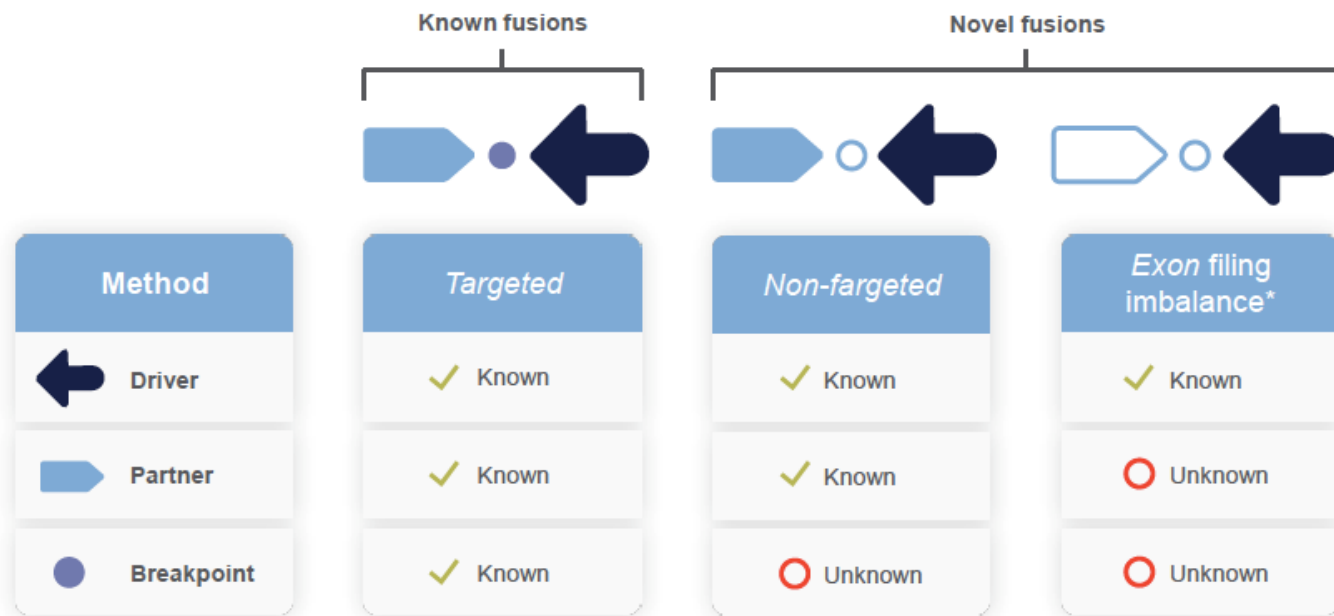
Fusiones Génicas:

ALK	RET
AR	ROS1
BRAF	RSPO2
EGFR	RSPO3
ESR1	
FGFR1	
FGFR2	
FGFR3	
MET	
NRG1	
NTRK1	
NTRK2	
NTRK3	
NUTM1	

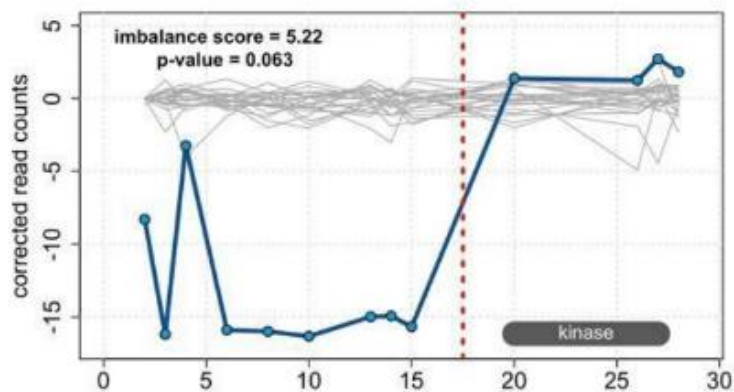
18 variants

FusionSync Detection Technology

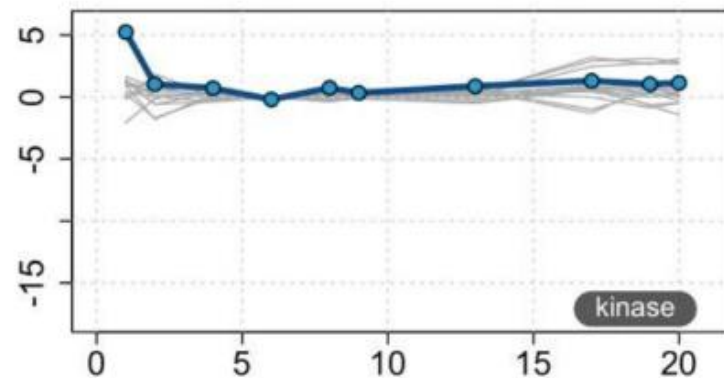
FusionSync Detection Technology is a synchronous approach that combines three methods for sensitive, specific, and broad detection of known and novel fusions



ALK FUSION



NO FUSION



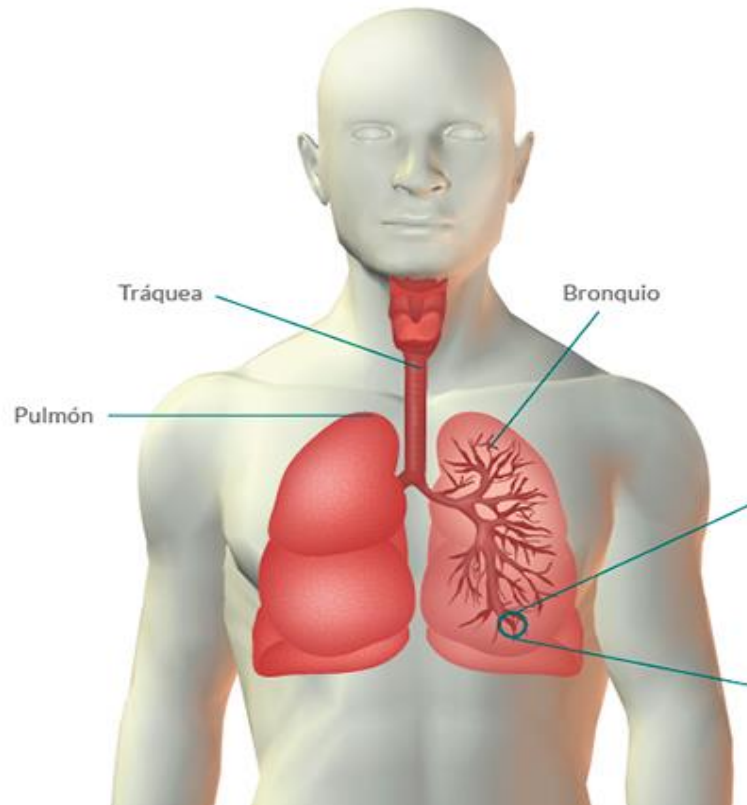
Oncomine Precision Assay Throughput on Genexus



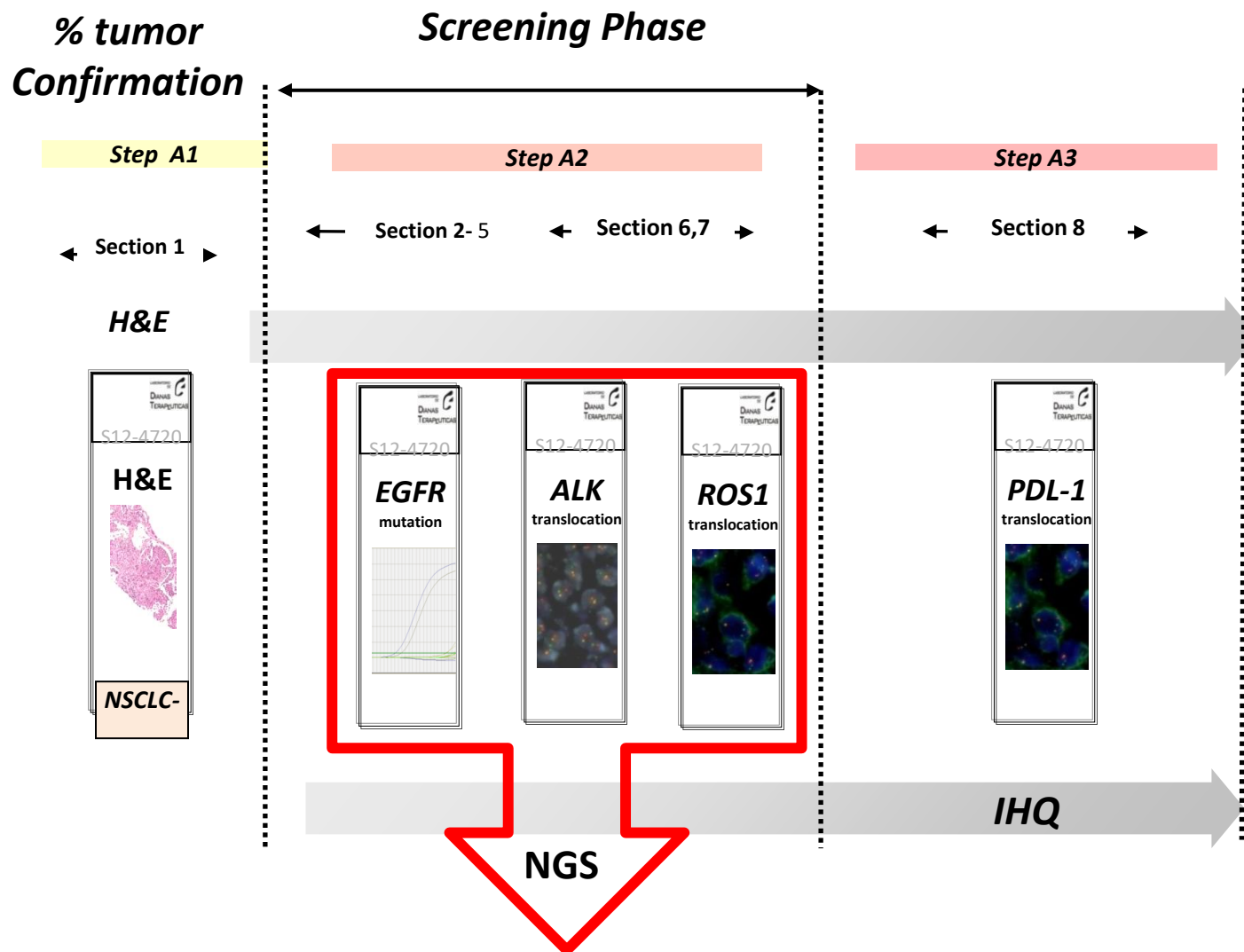
Assay		1 Lane	2 Lanes	3 Lanes	4 Lanes
Max Number of Samples	Oncomine Precision Assay (for DNA & RNA workflow)	4	8	12	16
	Oncomine Precision Assay (for cTNA workflow)	1	2	3	4

Workflow	# of samples
Simultaneous DNA- and RNA-based variant analysis	up to 16 FFPE tissue samples (one DNA reaction and one RNA reaction per sample)
DNA-only or RNA-only variant analysis	up to 32 FFPE tissue samples

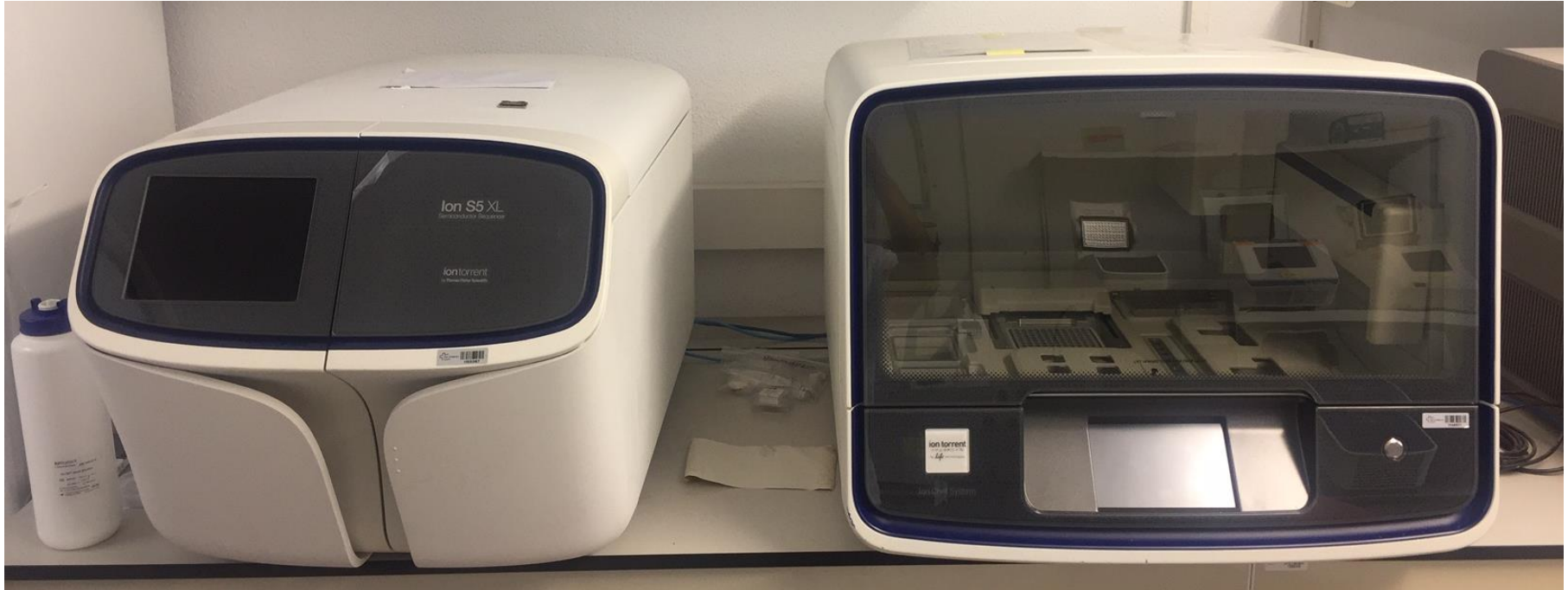
Experience in NSCLC



Workflow Modifications



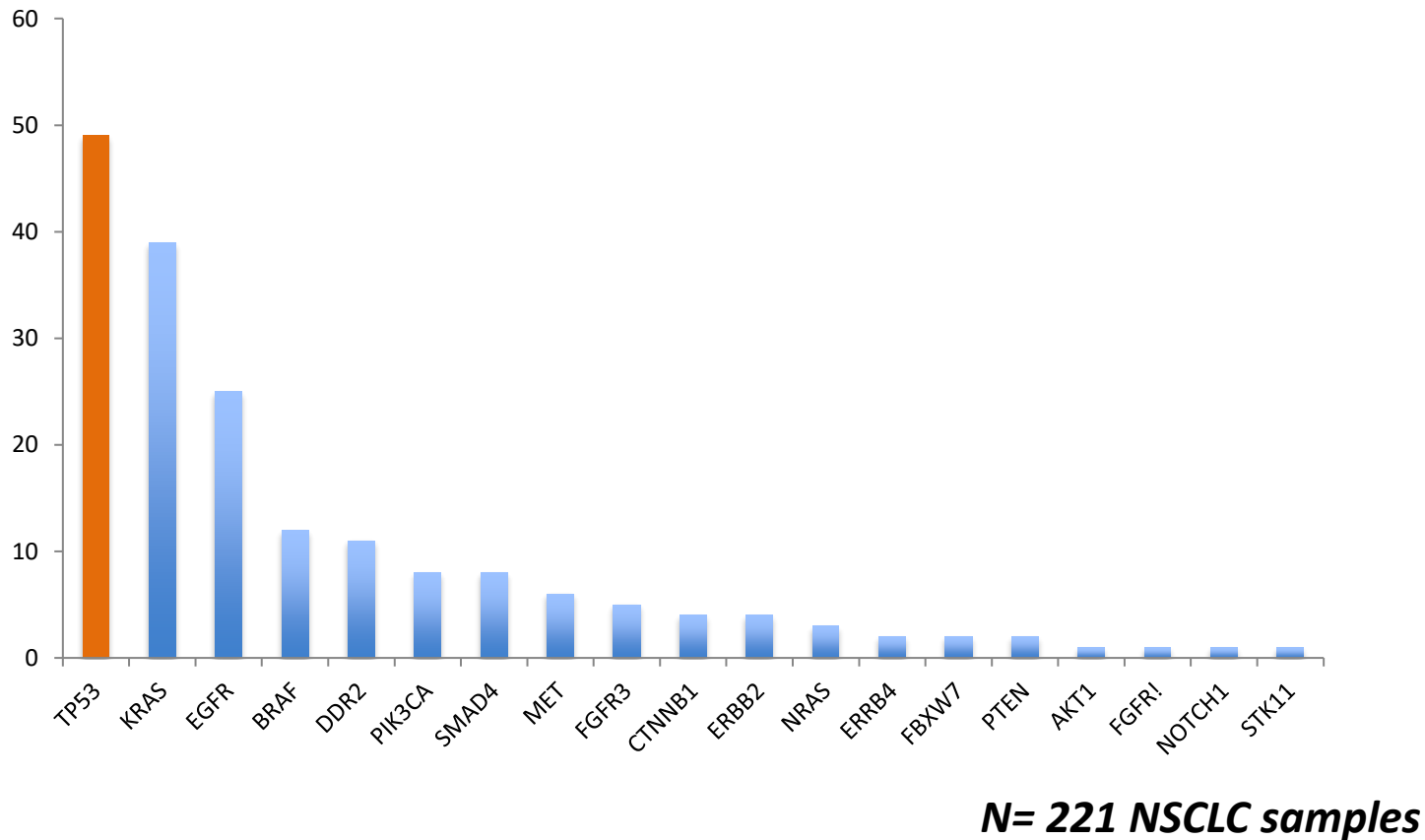
Initially IonS5xl + IonChef



- Biomarker testing in NSCLC
- Molecular Profiling in Pediatric Tumors
- Molecular Profiling in Myeloproliferative diseases



Experience in NSCLC



Genexus acquisition 2020



Jaime Vicioso. EngineerThermo Fisher Scientific

Different handicaps

Hospital Accessibility

Genexus installation

Software installation

Genexus setup

Training → *Webex*



Live Lens[®]



Rescue[®]

Comparative Study in NSCLC samples

Shared Genes		Unique Genes		
AKT1?	FGFR3?	AKT2?	FLT3?	NTRK1?
ALK?	KRAS?	AKT3?	GNA11?	NTRK2?
BRAF?	MAP2K1?	AR?	GNAQ?	NTRK3?
CTNNB1?	MET?	ARAF?	GNAS?	PDGFRA?
EGFR?	NRAS?	CDK4?	HRAS?	RAF1?
ERBB2?	PIK3CA?	CDKN2A?	IDH1?	RET?
ERBB4?	PTEN?	CHEK2?	IDH2?	??
FGFR1?	TP53?	ERBB3?	KIT?	??
FGFR2?	??	ESR1?	MAP2K2?	??
??	??	FGFR4?	MTOR?	??

?

*NSCLC Samples analyzed by reference test
n = 15 samples*

Comparative Study in NSCLC samples

ID Mostra	GEN	Canvi AA	Canvi nt	Freq Al·lèlica	Profunditat
1	KRAS	p.Gly12Asp	c.35G>A	13,2	2.577
	RET	p.Cys620Arg	c.1858T>C	3,3	849
2	BRAF	p.Gly469Ala	c.1406G>C	32,4	5.023
3	CD274 Gain-of-Function Copy Number 12,05				
4	KIT	p.Val530Ile	c.1588G>A	32	571
	TP53	p.Gly245Val	c.734G>T	37,3	643
	AR LOSS 0,82				
5	EGFR	p.Leu858Arg	c.2573T>G	20,2	4.664
6	KRAS	p.Gly12Cys	c.34G>T	11,7	2.577
7	EGFR	p.E746_A750del	c.2236_2250delGAATTAAGAGAAGCA	30	5.032
8	KRAS	p.Gln61His	c.183A>C	13,7	4.159
9	KRAS	p.Gly12Val	c.35G>T	44,8	6.961
10	EGFR	p.Leu858Arg	c.2573T>G	24,1	1.563
11	Sense Alteracions				
12	CTNNB1	p.Asp32Asn	c.94G>A	39,4	1.205
	KIT	p.Val530Ile	c.1588G>A	6,7	1.179
	TP53	p.Asp281Gly	c.842A>G	46,3	721
13	Sense Alteracions				
14	P53	p.Val157Phe	c.469G>T	22,8	5.001
	KRAS AMPLIFICATION CNV Ratio 3,52				
15	ERBB3	p.Asp297Tyr	c.889G>T	20,6	1.867
	PIK3CA	p.Glu545Asp	c.1635G>C	7,7	3.522

Comparative Study in NSCLC samples

ID Mostra	GEN	Canvi AA	Canvi nt	Freq Al·lèlica	Profunditat
1	KRAS	p.Gly12Asp	c.35G>A	6,32	1.771
2	BRAF	p.Gly469Ala	c.1406G>C	28,96	2.738
3	SMAD4	p.His132Tyr	c.394C>T	34,77	3.103
	TP53	p.Glu349Ter	c.1045G>T	16,65	2.721
4	ERBB4	p.Gln346His	c.1038G>T	22,12	3.996
	TP53	p.Gly245Val	c.734G>T	34,7	3.971
5	EGFR	p.Leu858Arg	c.2573T>G	18,2	3.988
6	KRAS	p.Gly12Cys	c.34G>T	11,96	3.963
	TP53	p.Gln104Ter	c.310C>T	12,68	1.554
7	EGFR	p.Glu746_Ala750del	c.2236_2250delGAATTAAGAGAAGCA	22,85	3.921
8	KRAS	p.Gln61His	c.183A>C	12,91	3.998
9	KRAS	p.Gly12Val	c.35G>T	41,6	3.966
	TP53	p.Arg110Pro	c.329G>C	30,4	1.589
	DDR2	p.Met441Ile	c.1323G>A	21,08	4.000
10	EGFR	p.Leu858Arg	c.2573T>G	25,35	3.988
11	Sense Alteracions				
12	CTNNB1	p.Asp32Asn	c.94G>A	52,89	2.320
	TP53	p.Arg110His	c.329G>A	74,98	2.370
	TP53	p.Asp281Gly	c.842A>G	54,29	2.387
13	TP53	p.Val217fs	c.649delG	30,21	3.969
14	TP53	p.Val157Phe	c.469G>T	35,8	3.109
	DDR2	p.Met441Ile	c.1323G>A	26,46	3.998
15	SMAD4	p.Gln256Leu	c.767A>T	5,15	1.185
	PIK3CA	p.Glu545Asp	c.1635G>C	4,9	3.960

Oncomine precision assay is labeled For Research Use Only. Not for use in diagnostic procedures.

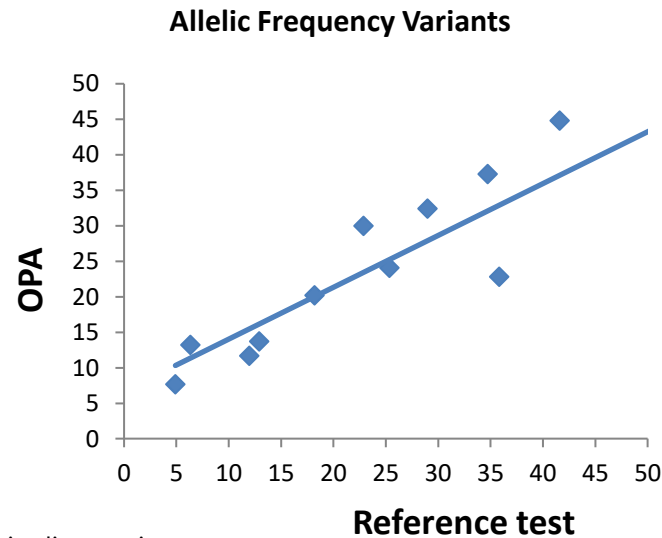
Results by reference test

Comparative Study in NSCLC samples

Sample ID	GEN	Aminoacid	Nucleotide	Reference test		OPA	
				FA	Reads	FA	Reads
1	KRAS	p.Gly12Asp	c.35G>A	6,32	1771	13,2	2577
2	BRAF	p.Gly469Ala	c.1406G>C	28,96	2738	32,4	5023
4	TP53	p.Gly245Val	c.734G>T	34,7	3971	37,3	643
5	EGFR	p.Leu858Arg	c.2573T>G	18,2	3988	20,2	4664
6	KRAS	p.Gly12Cys	c.34G>T	11,96	3963	11,7	2577
7	EGFR	p.Glu746_Ala750del	c.2236_2250delGAATTAAGAGAAGCA	22,85	3921	30	5032
8	KRAS	p.Gln61His	c.183A>C	12,91	3998	13,7	4159
9	KRAS	p.Gly12Val	c.35G>T	41,6	3966	44,8	6961
10	EGFR	p.Leu858Arg	c.2573T>G	25,35	3988	24,1	1563
12	TP53	p.Asp281Gly	c.842A>G	54,29	2387	46,3	721
12	CTNNB1	p.Asp32Asn	c.94G>A	52,89	2320	39,4	1205
14	TP53	p.Val157Phe	c.469G>T	35,8	3109	22,8	5001
15	PIK3CA	p.Glu545Asp	c.1635G>C	4,9	3960	7,7	3522

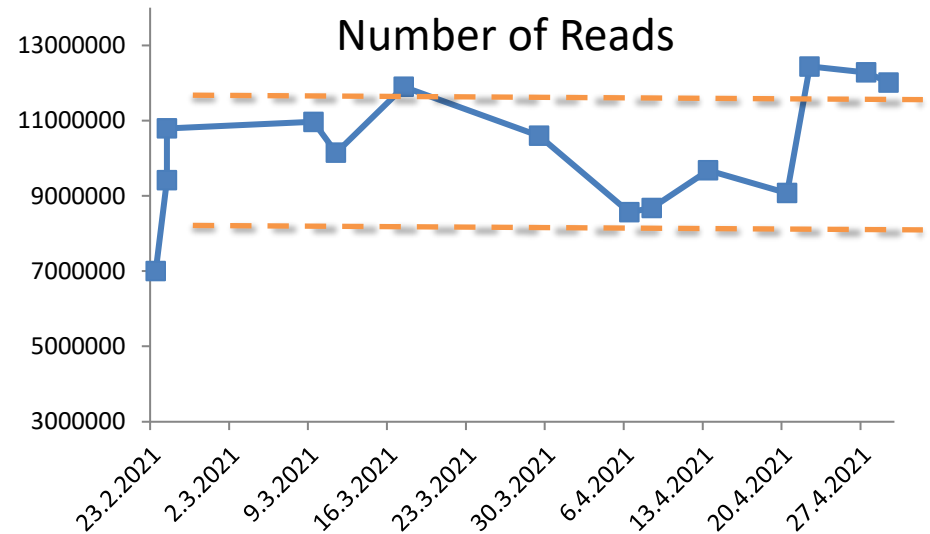
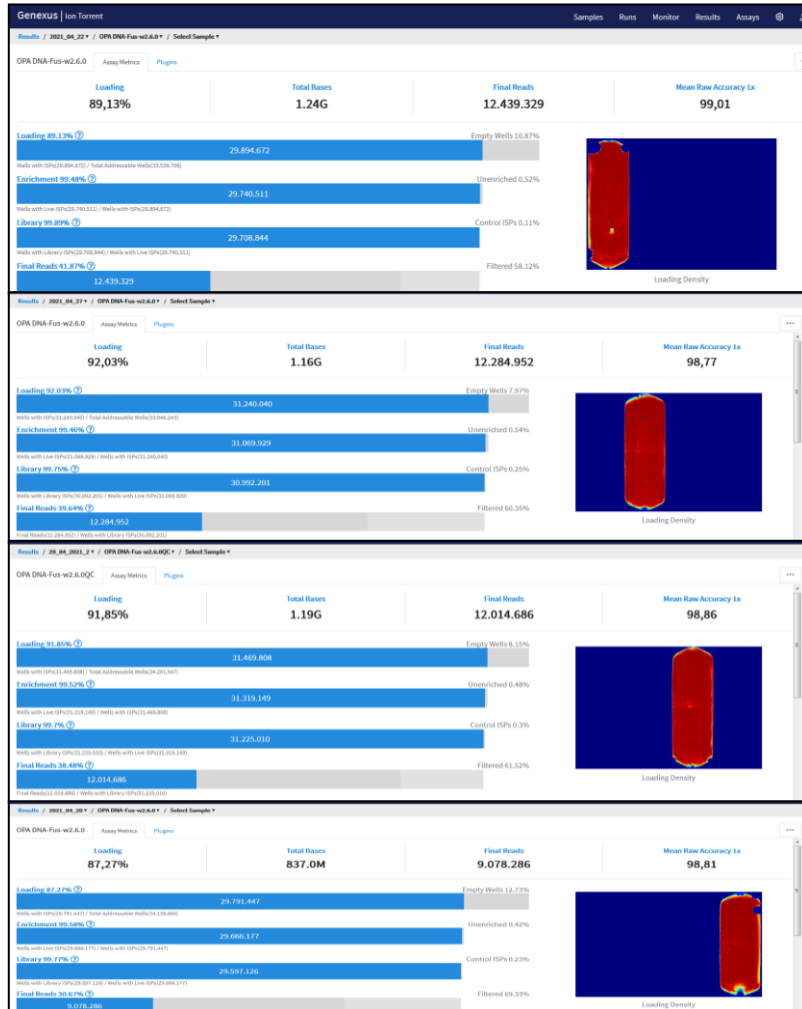
7

NSCLC retrospective cases
n = 15 samples



Oncomine precision assay is labeled For Research Use Only. Not for use in diagnostic procedures.

Quality Control Metrics



New Genexus Software



Genexus | Ion Torrent

Samples Runs Monitor Results Assays  

[Samples](#) / Manage Samples

Filter Samples by... Sample Name Enter Sample Name 									+ Create Sample + Import Samples Delete Export + Prepare Library Batch	
☐	Sample Name	Collection Date	Created On 	Disease Category	Cancer Type	Sample Type	Gender	Actions		
☐	DNA_21_1374_RNA_21_1437	2021-04-13	2021-04-13 12:51	Cancer	Non-Small Cell Lung Cancer	FFPE	Male	Edit Audit Notes		
☐	DNA_21_1492-2_RNA_21_1493	2021-04-13	2021-04-13 12:51	Cancer	Unknown Primary Origin	FFPE	Female	Edit Audit Notes		
☐	DNA_21_1490-2_RNA_21_1491	2021-04-13	2021-04-13 12:48	Cancer	Non-Small Cell Lung Cancer	FFPE	Female	Edit Audit Notes		
☐	DNA_21_1539_RNA_21_1540	2021-04-13	2021-04-13 12:47	Cancer	Non-Small Cell Lung Cancer	FFPE	Male	Edit Audit Notes		
☐	DNA_21_1537_RNA_21_1538	2021-04-13	2021-04-13 12:47	Cancer	Non-Small Cell Lung Cancer	FFPE	Male	Edit Audit Notes		
☐	DNA_21_1535_RNA_21_1536	2021-04-13	2021-04-13 12:46	Cancer	Non-Small Cell Lung Cancer	FFPE	Female	Edit Audit Notes		
☐	DNA_21_1529_RNA_21_1530	2021-04-13	2021-04-13 12:45	Cancer	Non-Small Cell Lung Cancer	FFPE	Male	Edit Audit Notes		
☐	DNA_21_1542_RNA_21_1543	2021-04-13	2021-04-13 12:42	Cancer	Non-Small Cell Lung Cancer	FFPE	Male	Edit Audit Notes		

Quality Control Metrics

Results / 2021_04_27 / OPA DNA-Fus-w2.6.0 / DNA_21_1784_RMA_21_1785

DNA_21_1784_RMA_21_1785SummaryQC ✓VariantsPlugins

Run QC

Key Signal	---	57
Not Set		
Percent Loading	---	92%
Not Set		
Raw Read Accuracy	---	98,8
Not Set		

Templating Control QC - CF-1

Average Reads Per Lane	---	69.168
Not Set		
Base Call Accuracy	---	96,7%
Not Set		
Mean AQ20 Read Length (bp)	---	73
Not Set		

Sample QC - DNA

✓

MAPD	✓	0,24
[0-0.5]		
Mapped Reads	---	1.523.989
Not Set		
Mean AQ20 Read Length (bp)	---	81
Not Set		
Mean Read Length (bp)	---	93
Not Set		
Uniformity Of Base Coverage	---	96,13
Not Set		

Read Length Histogram

Sample QC - RNA

✓

Mapped Reads	---	440.090
Not Set		
Mean Read Length (bp)	---	90
Not Set		
RNA Expression Ctrls Detected	✓	7
>=5		

Read Length Histogram

Table 6 Example QC metrics for FFPE DNA+RNA isolated from tumor FFPE samples (continued)

QC metric	Value
Sample QC – DNA	
MAPD	0.18–0.24
Mapped Reads	525,000–1,000,000
Mean AQ20 Read Length (bp)	85–95
Mean Read Length (bp)	85–100
Uniformity Of Base Coverage	97–99%
Sample QC – RNA	
Mapped Reads	105,000–650,000
Mean Read Length (bp)	70–100
RNA Expression Ctrls Detected	5–7

DNA_21_1537_RNA_21_1538

Summary **QC ** Variants Plugins

...

Sample Details

Sample Name:
Collection Date:
Gender:
Sample Type:
Disease Category:
Cancer Type:
Cancer Stage:
% Cellularity:

DNA_21_1537_RNA_21_1538
13 APR 2021
Male
FFPE
Cancer
Non-Small Cell Lung Cancer
Stage IV - Metastatic
40

Key Metrics

Average Base Coverage Depth: 2466
Uniformity Of Base Coverage: 97.26%
% Base Reads On Target: 91.38%

Variant Summary

A default filter has been applied. Go to Variants Tab to remove or modify variant filter.

Filter Chain Applied: Variant Matrix Summary (5.14)

SNVs/Indels: 1 Detected

Fusions: 0 Detected

CNVs: 0 Detected

Gene	AA Change	Allele Fraction	OncoPrint Variant Class
KRAS	p.G12V	0.319	Hotspot

DNA_21_1537_RNA_21_1538

Summary **QC ** Variants Plugins

•

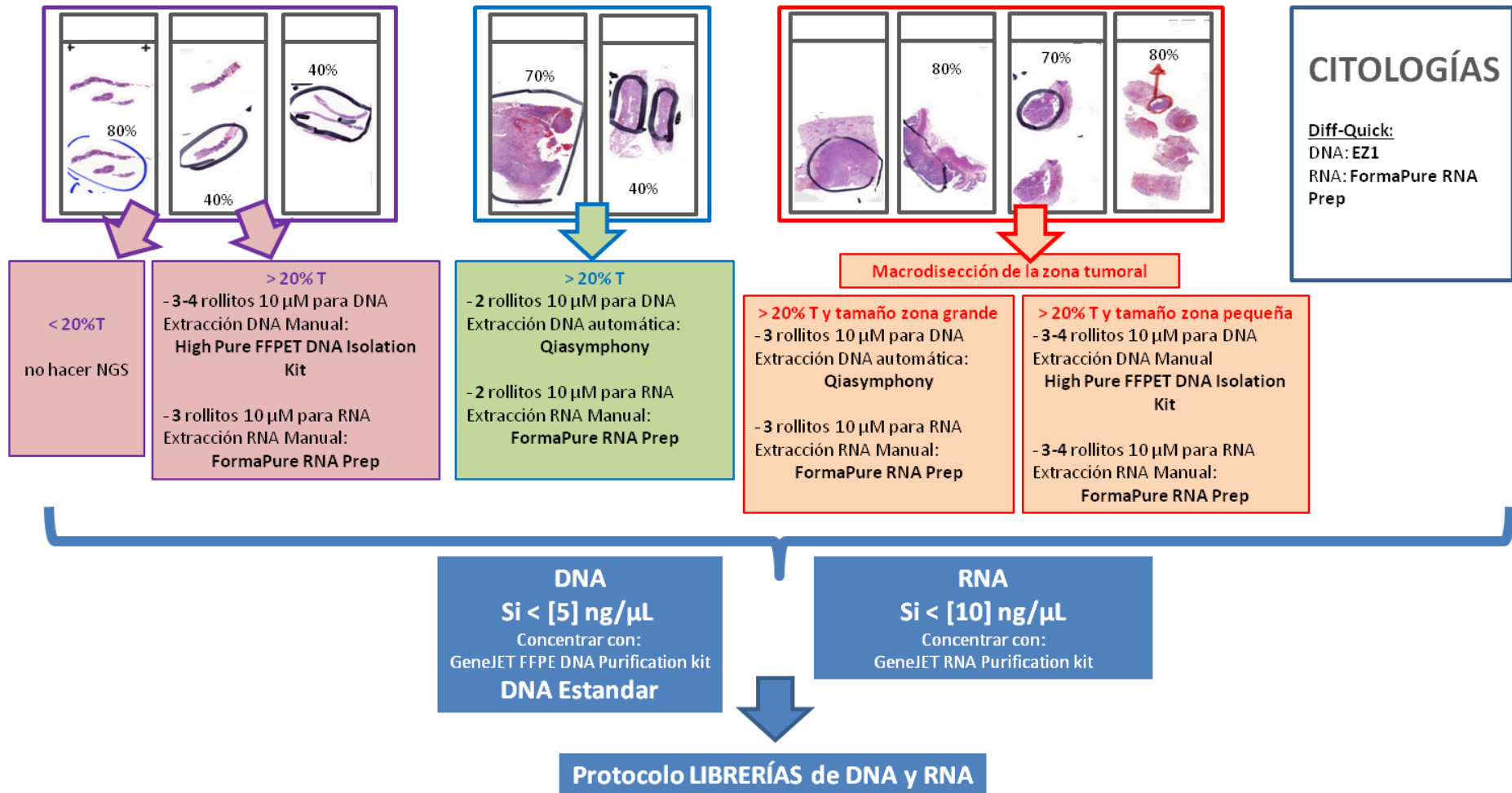
SNVs/Indels		Fusions	CNVs	Filter	Variant Matrix Summary (5.14) (1 of 1773 Variants)							Export	Columns
	OncoPrint Gene Class	Gene	AA Change	Allele Fraction	Ref	Alt	Type	Call	Effective Read Depth	Alt Allele Read Counts	Raw Read Depth		
	Gain-of-Function	KRAS	p.G12V	0.319	C	A	snp	PRESENT (HETEROZYGOUS)	3478	1108	3475		

Workflow of NGS by Genexus

<i>Monday</i>	<i>Tuesday</i>	<i>Wednesday</i>	<i>Thursday</i>	<i>Friday</i>
				
DNA +RNA extraction 	Quantification 	DNA +RNA extraction 	Molecular Tumor Board	 Analysis 
	Genexus Load 	Analysis  	Quantification 	Tissue Selection  
	Tissue Selection  		Genexus Load 	

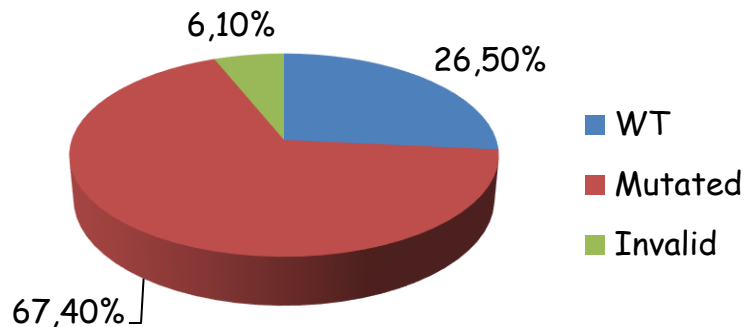
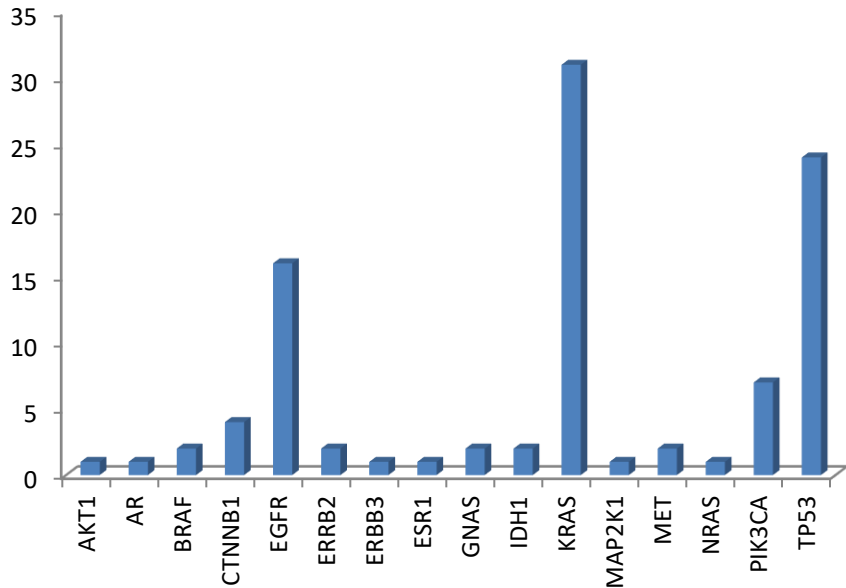
Sample Optimization (pre-analytics)

ALGORITMO MANEJO DE LA MUESTRA PARA NGS EN CÁNCER DE PULMÓN

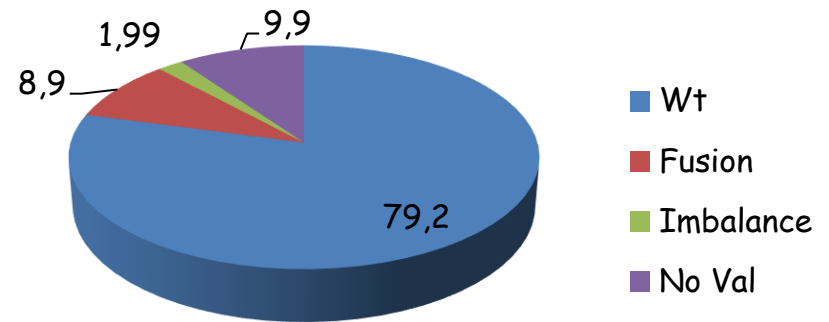


Biomarker Testing in NSCLC by OPA

- 01/03/2021 to 30/06/2021
- 4-8 samples/week



DNA analysis (n=98)



RNA analysis (n=101)

Internal Molecular Committee

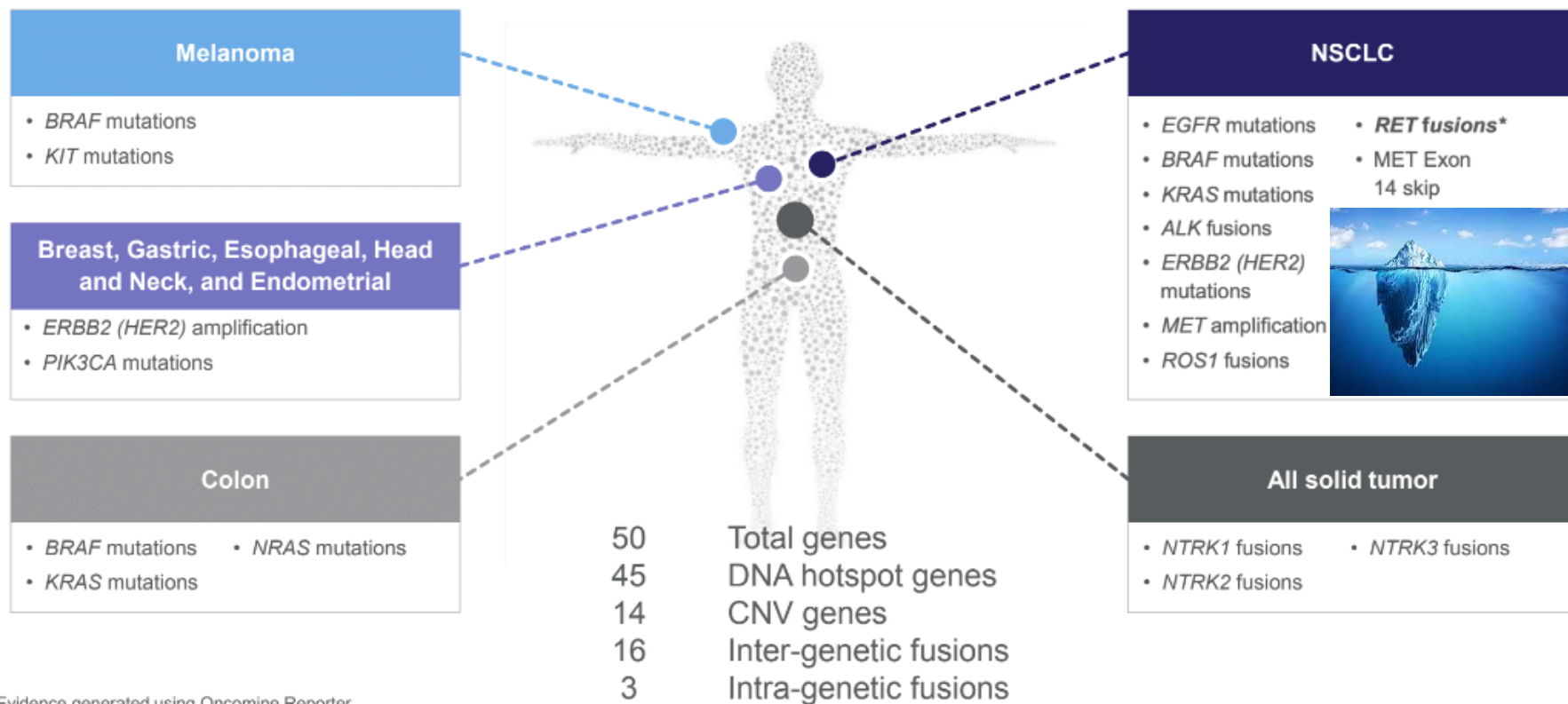
- Weekly (Thursday 8.30h) sample prioritization and results discussion internally with Pathologist.
- Bibliography update
- Pathologist + Molecular Biologist



Molecular Tumor Board

- Weekly (Thursday 8.00h) Molecular analysis results, with other sample results.
- Pathologist + Molecular Biologist + Oncologist.
- Next steps (invite external Pathologists + Medical Oncologists)

OPA Applications in Cancer



Evidence generated using Oncomine Reporter

OPA Analysis beyond NSCLC profiling

- ***Unknown Primary Tumors (UPT)***
- ***Gliomas***
- ***Soft Tissue Tumors***

Genexus Ion Torrent							Samples
Samples / Manage Samples							
Filter Samples by...	Sample Name	Enter Sample Name	Q				+ Create Sam
☐	Sample Name	Collection Date	Created On ↓	Disease Category	Cancer Type	Sample Type	
☐	DNA_21_1829_RNA_21_1830	2021-04-29	2021-04-29 10:01	Cancer	Glioblastoma	FFPE	
☐	DNA_21_1807_RNA_21_1808	2021-04-29	2021-04-29 10:00	Cancer	Non-Small Cell Lung Cancer	FFPE	
☐	DNA_21_1805_RNA_21_1806	2021-04-29	2021-04-29 09:59	Cancer	Unknown Primary Origin	FFPE	
☐	DNA_21_1624_RNA_21_1625	2021-04-29	2021-04-29 09:58	Cancer	Non-Small Cell Lung Cancer	FFPE	
☐	DNA_21_1784_RNA_21_1785	2021-04-27	2021-04-27 11:02	Cancer	Non-Small Cell Lung Cancer	FFPE	
☐	DNA_21_1780_RNA_21_1781	2021-04-27	2021-04-27 11:01	Cancer	Non-Small Cell Lung Cancer	FFPE	
☐	DNA_21_1766_RNA_21_1767	2021-04-27	2021-04-27 11:00	Cancer	Non-Small Cell Lung Cancer	FFPE	
☐	DNA_21_1759_RNA_21_1760	2021-04-27	2021-04-27 11:00	Cancer	Melanoma	FFPE	

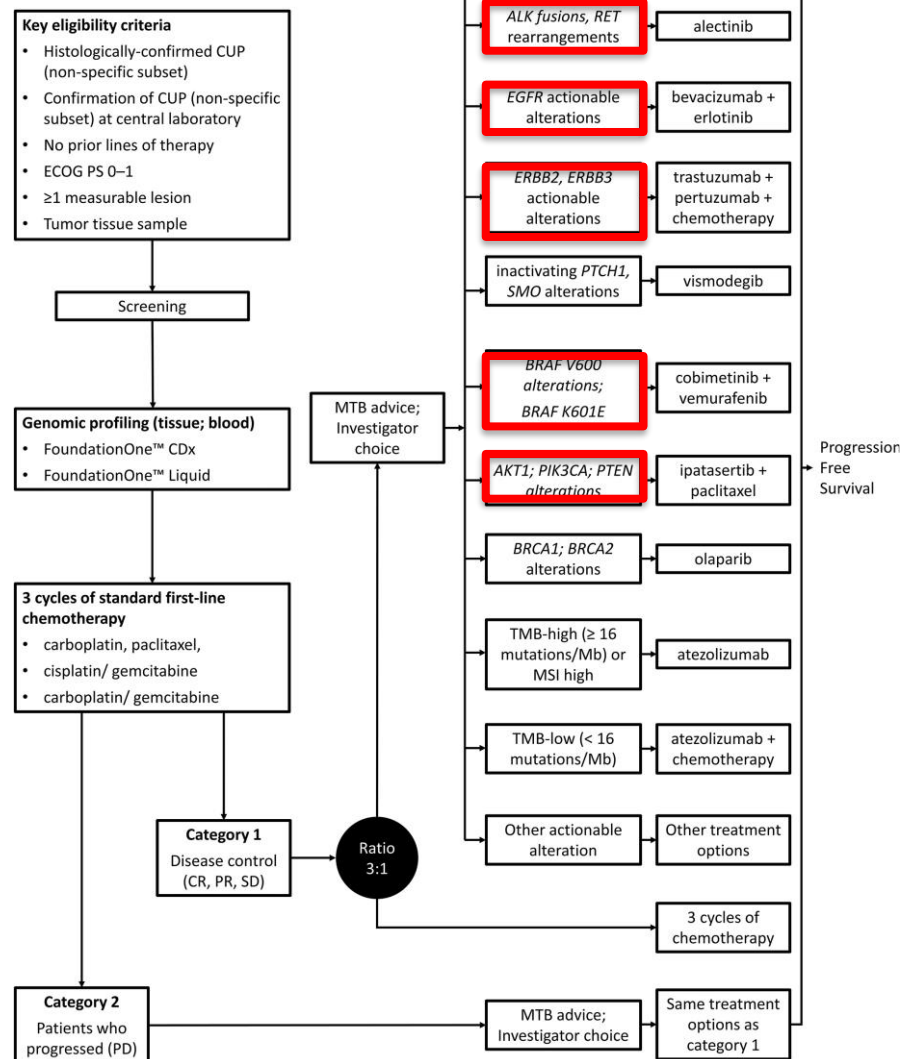
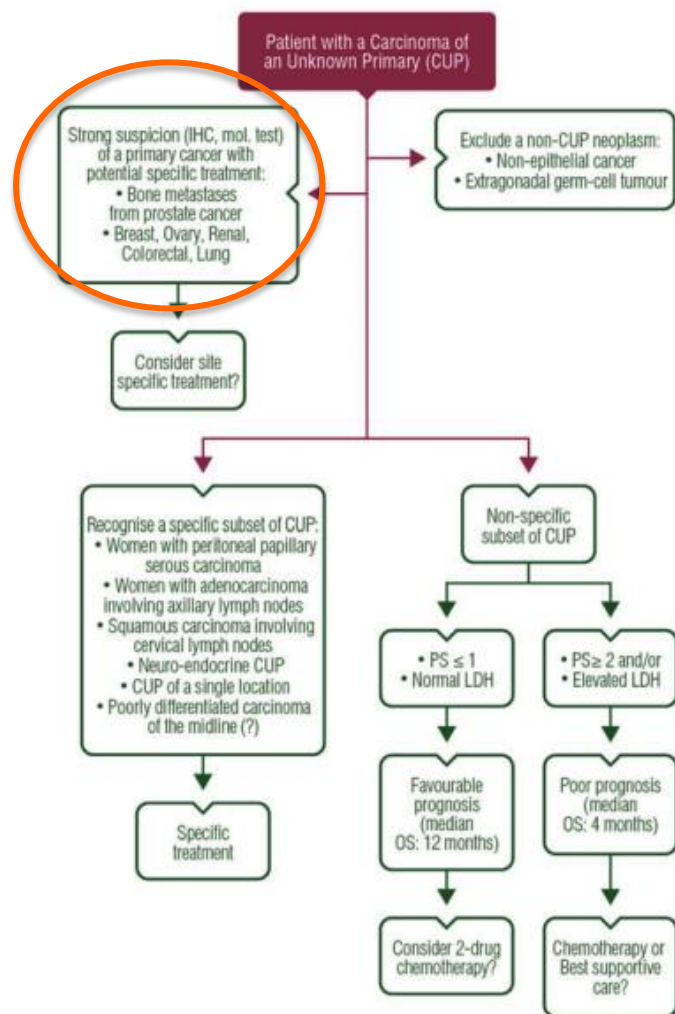
Cancers of unknown primary site: ESMO Clinical Practice Guidelines for diagnosis, treatment and follow-up[†]

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Other Solid Tumor Types

	Sample	Gene	Protein	DNA	FA	Cosmic
1	CNS	TP53	p.R273H	c.818G>A	42	COSM10660
2	CUP	MET	p.R988C	c.2962C>T	50,9	COSM1666978
3	CUP	KRAS	p.G12C	c.34G>T	69,5	COSM516
4	CNS	CDKN2A		CNV10,25		
5	Soft Tissue	TP53	p.R248Q	c.743G>A	42	COSM10662
6	CNS	KRAS	p.G12V	c.35G>T	31,9	COSM520
7	Soft Tissue	TP53	p.R213*	c.637C>T	96	COSM10654
8	CNS	EGFR	p.G598V	c.1793G>T	77,2	COSM21690
9	CNS	EGFR		CNV2,61		
10	CNS	CDKN2A		CNV10,09		
11	CNS	IDH1	p.Arg132His	c.395G>A	42,6	COSM27846
		TP53	p.Arg248Gln	c.743G>A	3,6	COSM10662
12	CNS	TP53	p.Arg273Leu	c.818G>T	63,9	COSM10779
13	CCR	ERBB2		CNV18,18		

DNA-analysis

?

	Sample	Gene	Fusion	Reads
1	CNS	BRAF	GTF2I(6)-BRAF(10)	1.637
2	CNS	NTRK2	KANK1(3)-NTRK2(12)	3.433
3	CNS	MET	PTPRZ1(1)-MET(2)	3.197
4	Melanoma	ALK	TPM3(7)-ALK(20)	107
5	Thyroid	RET	NCOA4(7)-RET(12)	255
6	CNS	MET	CAPZA2-MET	1245

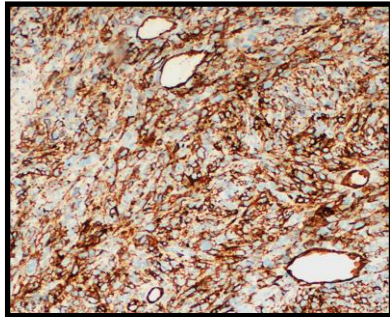
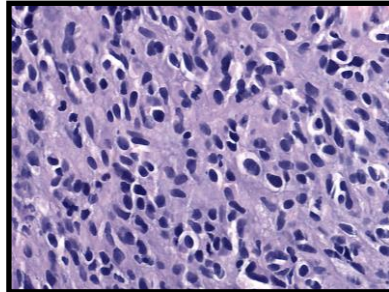
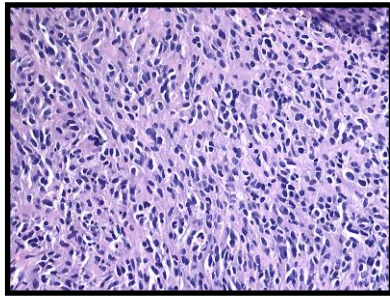
RNA-analysis

?

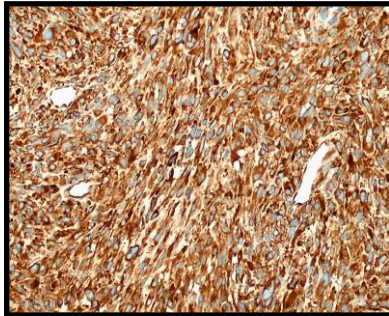
CNS: Central Nervous System Tumors.

CUP: Carcinoma of Unknown Primary Tumor.

Malignant Mesenchymal Tumour MNPST??

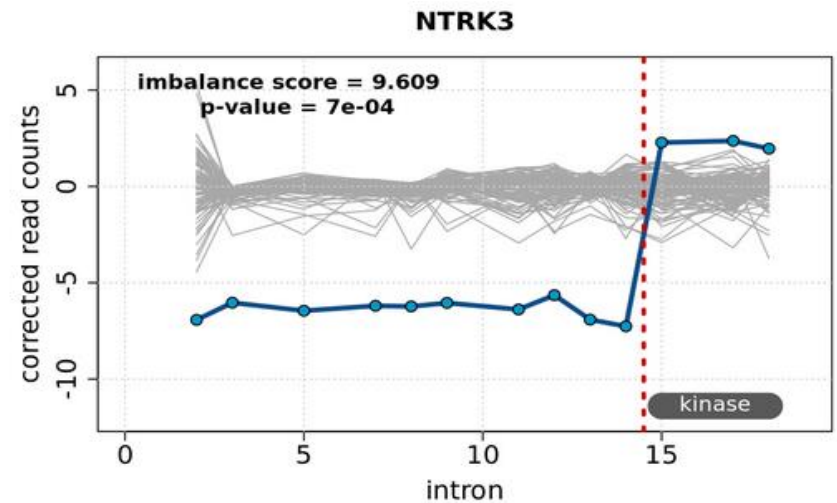
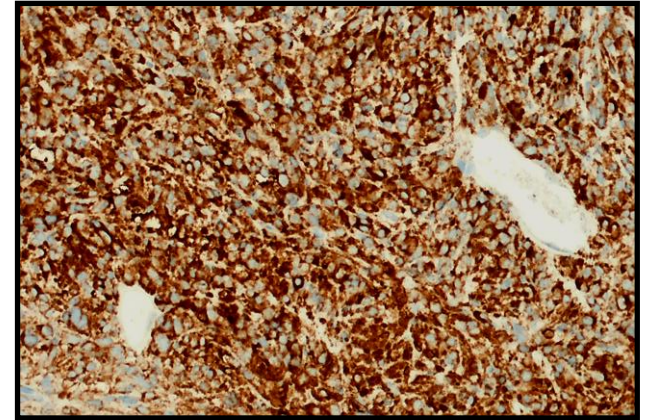


CD34



Vimentin

NTRK



Take Home Messages



- 1. Optimal OPA NGS analysis Workflow with Genexus in FFPE samples (4 samples batch)***
- 2. TAT to Complete NGS analysis from samples arrival is currently done in less than 5 working days***
- 3. All cases analyzed by NGS are discussed in the internal Comitee, and some of them in the MTB***
- 4 OPA analysis could be extended to other Solid Tumor Types***

Thank You



Multidisciplinary Team



Molecular Biology. Vall d'Hebron