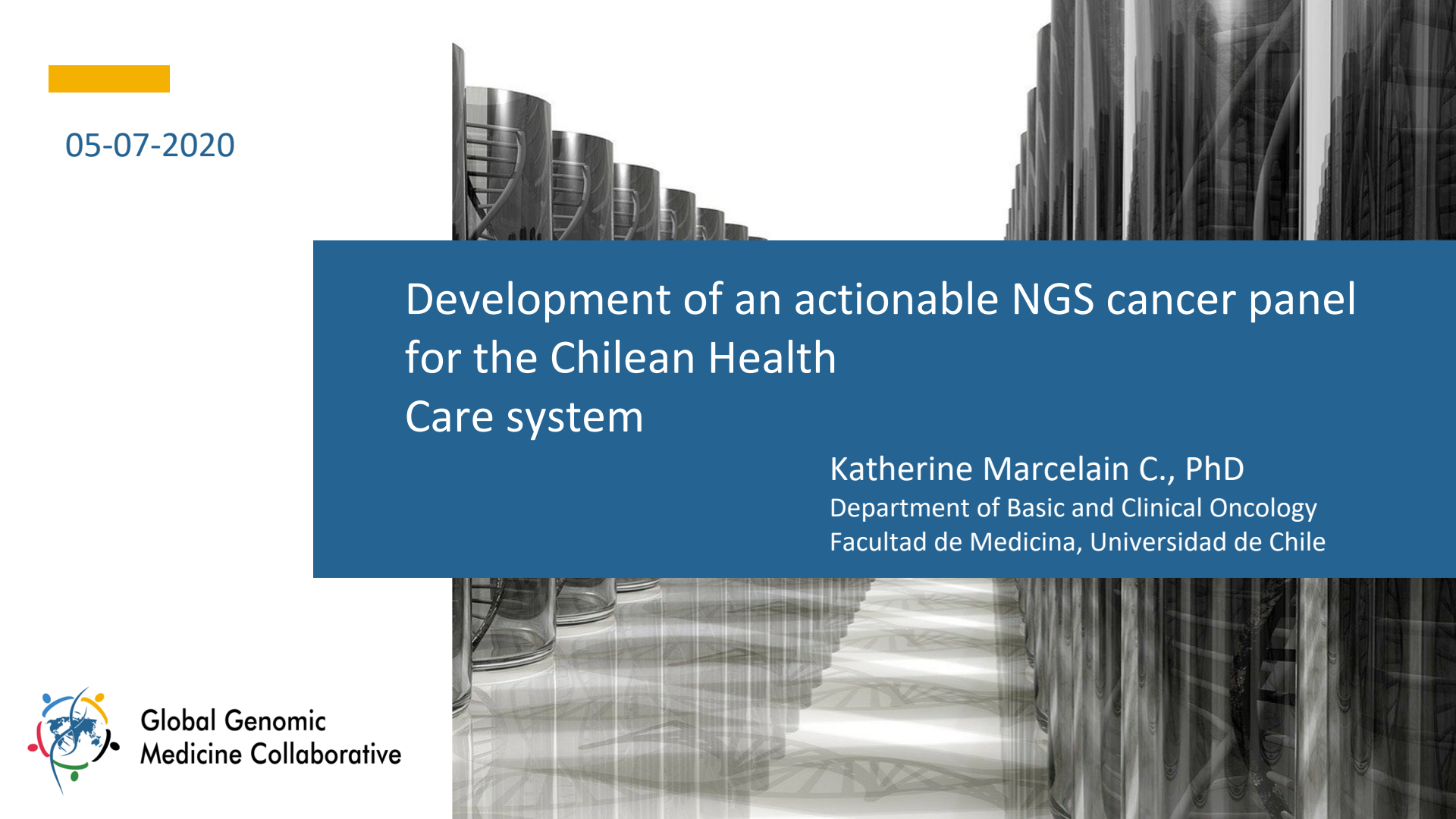




05-07-2020



Development of an actionable NGS cancer panel for the Chilean Health Care system

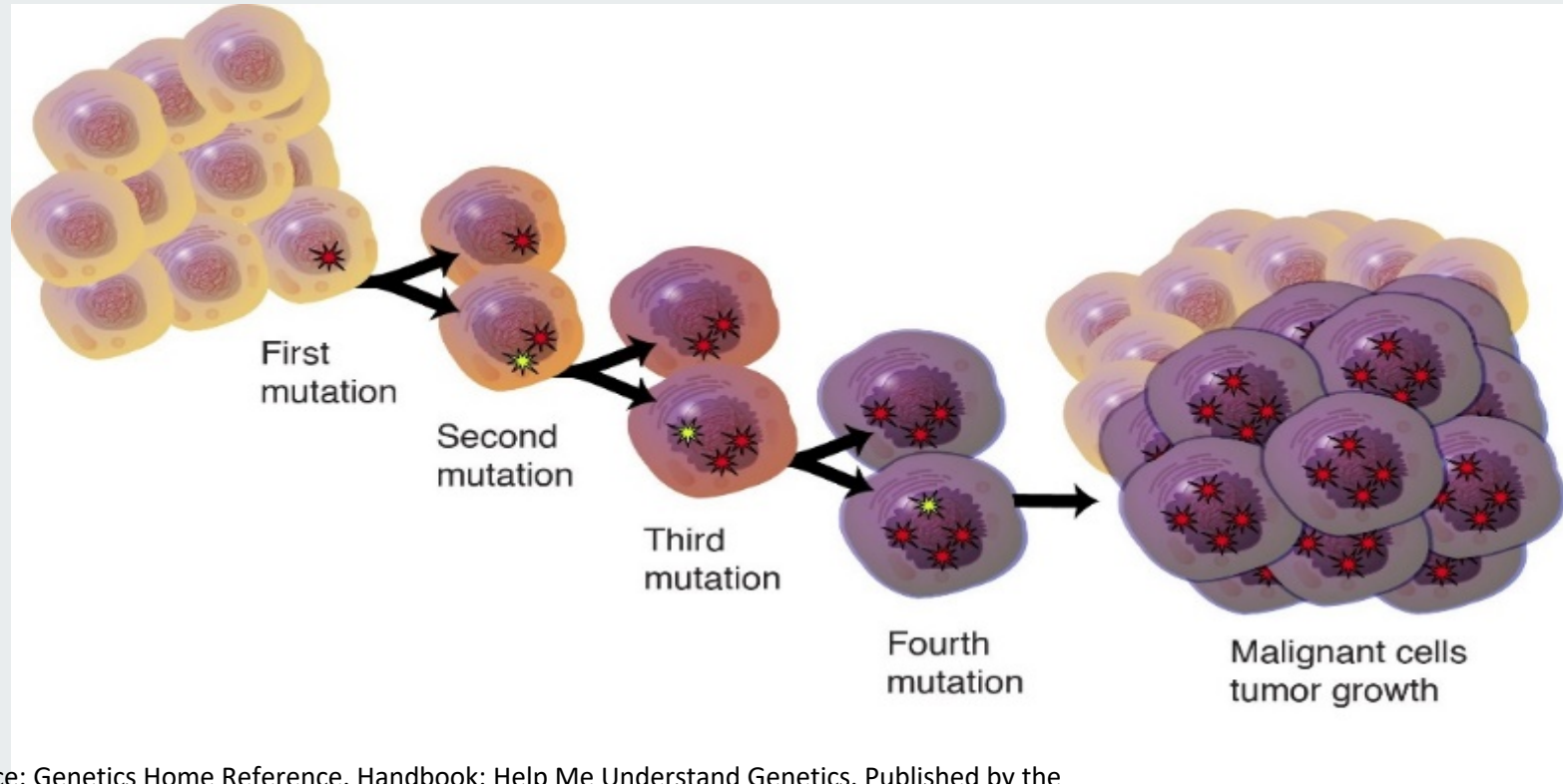
Katherine Marcelain C., PhD
Department of Basic and Clinical Oncology
Facultad de Medicina, Universidad de Chile



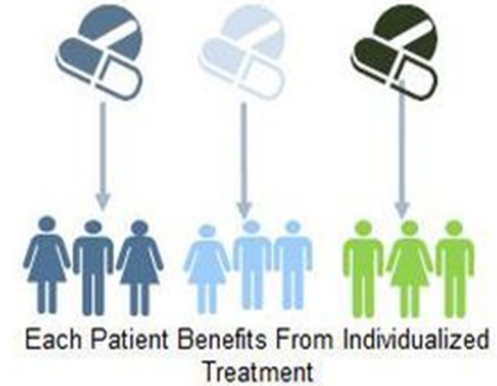
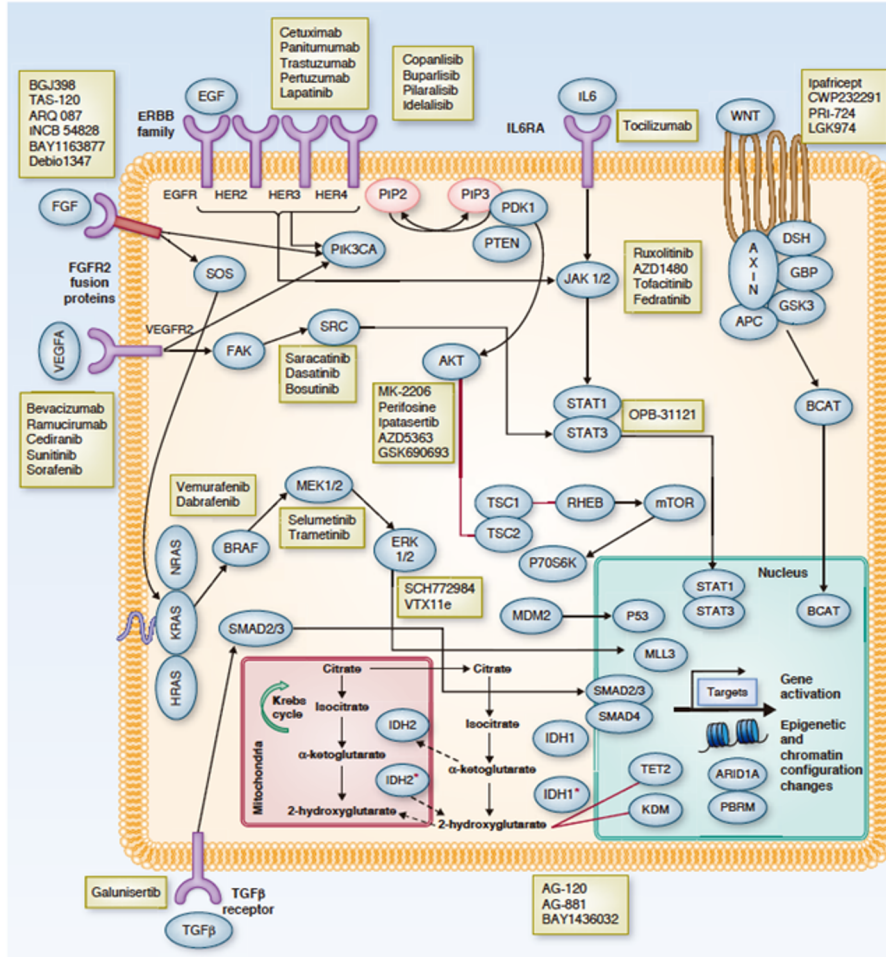
Global Genomic
Medicine Collaborative



Genomic Medicine in Oncology treatment



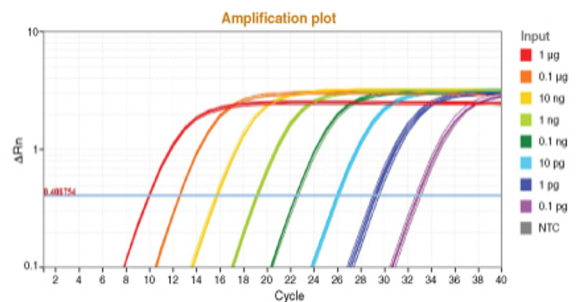
Reference: Genetics Home Reference. Handbook: Help Me Understand Genetics. Published by the Lister Hill National Center for Biomedical Communications, US National Library of Medicine, National Institutes of Health, Department of Health & Human Services. June 4, 2012.



Many Targeted therapies, many biomarkers. Some of these biomarkers are specific gene mutations (SNV, Indels, Fusions, Amplifications)



Current Methods for detection of somatic mutations in solid tumours in the clinical practice



RT-qPCR

Few mutations in one or a couple of genes
Example: Cobas (Roche)

\$\$
U\$ 500

Categorized by somatic alteration type

52
GENES

Categorized by published relevance

Hotspot genes

AKT1, ALK, AR, BRAF, CDK4, CTNND1, DDR2, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FGFR2, FGFR3, GNA11, GNAQ, HRAS, IDH1, IDH2, JAK1, JAK2, JAK3, KIT, KRAS, MAP2K1, MAP2K2, MET, MTOR, NRAS, PDGFRA, PIK3CA, RAF1, RET, ROS1, SMO

Copy number variants

ALK, AR, BRAF, CCND1, CDK4, CDK6, EGFR, ERBB2, FGFR1, FGFR2, FGFR3, FGFR4, KIT, KRAS, MET, MYC, MYCN, PDGFRA, PIK3CA

Fusion drivers

ABL1, AKT3, ALK, AXL, BRAF, EGFR, ERBB2, ERG, ETV1, ETV4, ETV5, FGFR1, FGFR2, FGFR3, MET, NTRK1, NTRK2, NTRK3, PDGFRA, PPARG, RAF1, RET, ROS1

Labels

ALK, BRAF, EGFR, ERBB2, KRAS, NRAS, ROS1

Guidelines

ALK, AR, BRAF, EGFR, ERBB2, KIT, KRAS, MET, NRAS, NTRK1, NTRK2, NTRK3, PDGFRA, RET, ROS1

Drug targets in clinical trials

ABL1, AKT1, AKT3, ALK, AR, AXL, BRAF, CCND1, CDK4, CDK6, DDR2, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FGFR1, FGFR2, FGFR3, FGFR4, GNA11, GNAQ, HRAS, IDH1, IDH2, KIT, KRAS, MAP2K1, MAP2K2, MET, MTOR, MYC, MYCN, NRAS, NTRK1, NTRK2, NTRK3, PDGFRA, PIK3CA, RAF1, RET, ROS1, SMO

NGS

Medium size panels
Ex. Oncomine Focus Assay (Thermo)

\$\$\$
U\$2,000



NGS

Large panels
Foundation One CDx

\$\$\$\$\$
U\$2,200 – 4,230



Design and validation of a 25 genes NGS panel for treatment indication in Solid Tumours

Currently **only 18 genes** are FDA or NCCN-recommended biomarkers for solid tumours (Level A).
(Level B: Standard of care; Level C: Clinical evidence)

Custom Panel adapted to local requirements (Chile and Latinoamerican countries): mostly FDA or NCCN-recommended biomarkers + in late trials. For solid tumours

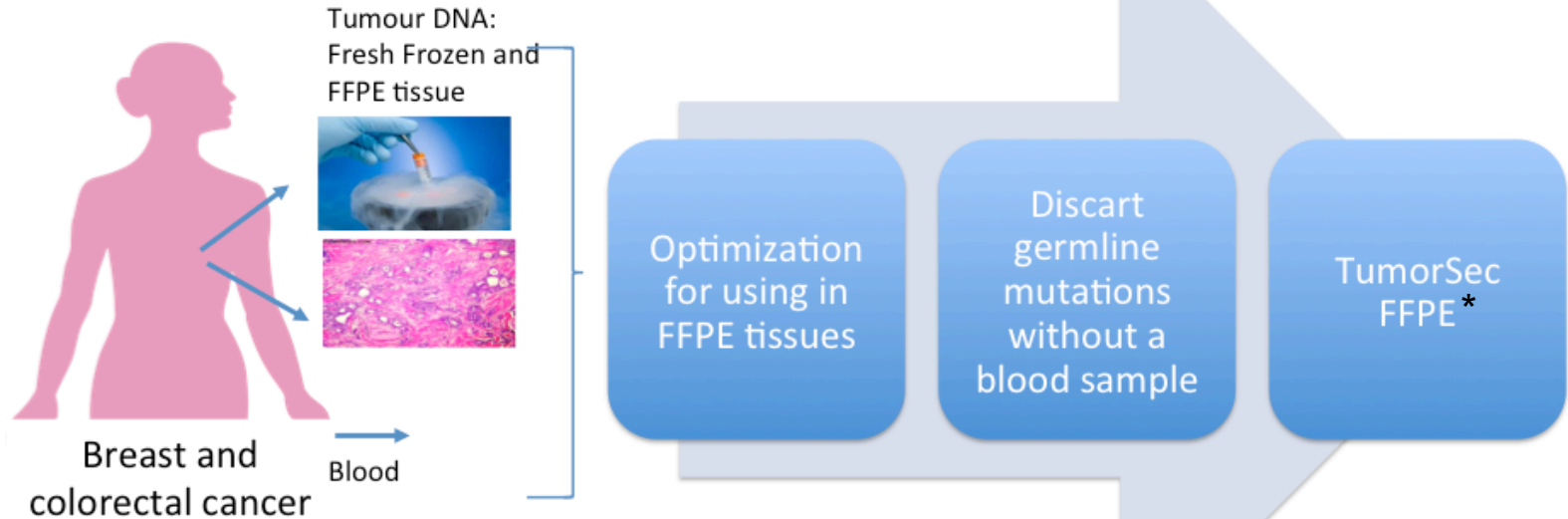


TumorSec (Hibridization Capture)

GENE	REGION	MUT TYPE	DRUGS	TUMOR TYPE	EVIDENC E
AKT1	all exons	Point	AZD-5363	BC, OV, Endom	B
ALK	Target	Point	Crizotinib, inh ALK	LUNAD	B
ARID1A	all exons	Point	inh ATM, erlotinib	BC, OV	C
BRAF	all exons	Point	Vemurafenid, dabrafenib, cetuximab, etc	MEL, NSCLC, CRC, THY	A
BRCA1	all exons	Point	Olaparib	OV, BC, CRC, MEL, SAR, PRO	A
BRCA2	all exons	Point	Olaparib	OV, BC, CRC, MEL, SAR, PRO	A
Cdk4	all exons	Amplification	Palbociclib/Abemaciclib	liposarc, MEL	B
EGFR	Target	Point/Amplif	Erlotinib, gefitinib, neratinib, osimertinib, etc	NSCLC	A
ERBB2	Target	Amplification	Trastuzumab	BC, Gastric	A
ESR1	Target	Point	Palbociclib	BC	B
IDH2	Target	Point	Enasidenib	AML	A
KIT	Target	Point	Nilotinib, imatinib, dasotinib,	MEL, GIST, AML	A
KRAS	all exons	Point	Cetuximab, erlotinib, regorafenib, etc	CRC, Panc, NSCLC	A
MET	Target	Point/Amplif	Foretinib, Rilotumumab	Papillary RCC, MEL, NSCLC	B
MTOR	all exons	Point	mTOR inhibitors	RCC	B
NRAS	all exons	Point	EGFR inhibitors	CCR	A
PDGFRA	Target	Point	Imatinib, Sunitinib	GIST	A,B
PI3KCA	all exons	Point/Amplif	Buparlisib, Serabelisib, Alpelisib, Copanlisib	BC	A
PTCH1	all exons	Point	Vismodegib	MDB, SC	B
PTEN	all exons	Point	Everolimus	Various	B
ROS1	Target	Point	Crizotinib	NSCLC	C
SMO	Target	Point	Vismodegib	Basal CC	B
TP53	all exons	Point	Prognosis	various	A
TSC1	all exons	Point	MTOR inh, Everolimus	RCC, Bladder C	A
TSC2	all exons	Point	MTOR inh	CNS, RCC	A, B



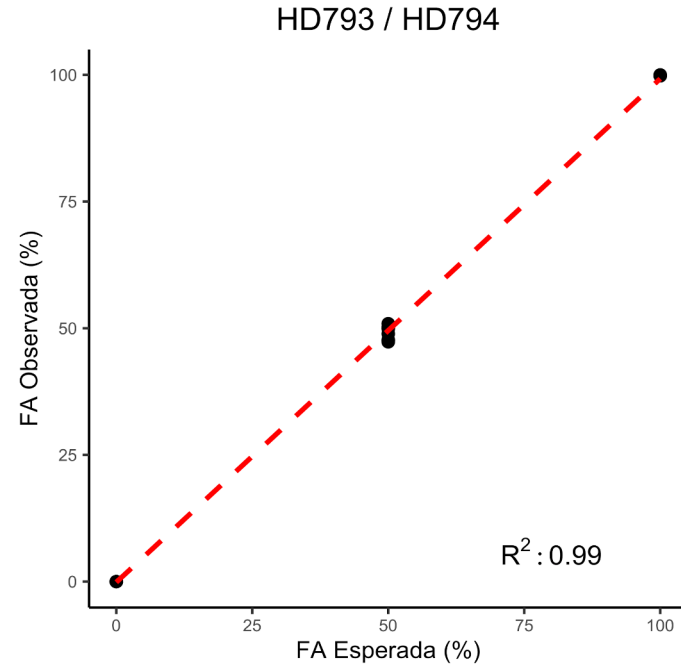
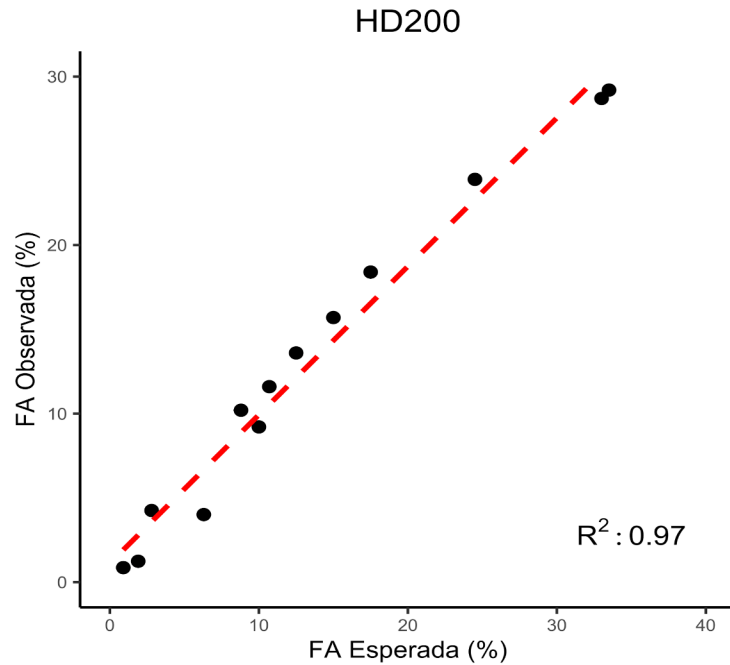
Optimization of protocol and Bioinformatic Flow works



*FFPE: Formalin-Fixed Paraffin Embedded tissues



Analytical Precision of TumorSec





Technical Validation

Repeatability (inter-run)

*same library, different run (3 samples)

Reproducibility (intra-run)

*different library, same run (3 samples)

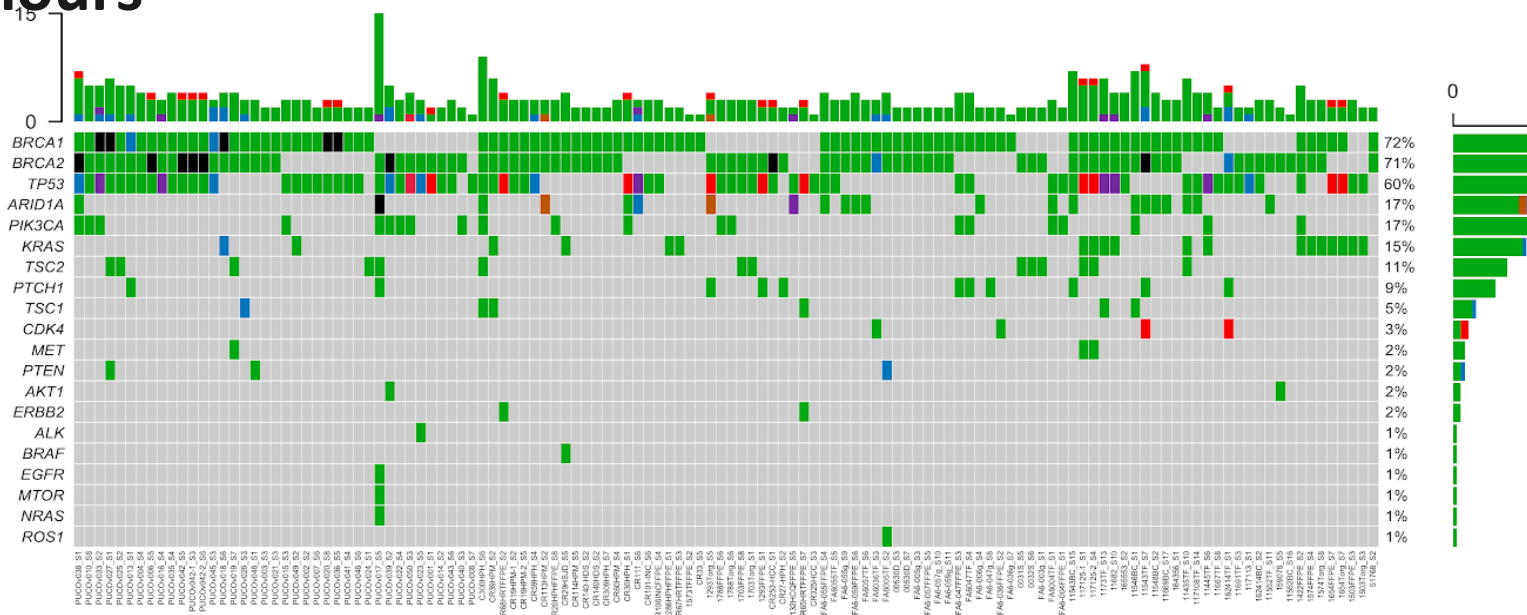
Reproducibility (inter e intra-run)

*different libraries, different runs (1 sample)

100% concordance



Identification of mutations in different types of solid tumours



- Missense_Mutation
- In_Frame_Del
- Frame_Shift_Del
- Frame_Shift_Ins

- Nonsense_Mutation
- In_Frame_Ins
- Multi_Hit

- Tejido
- CVB
 - Ovario
 - Colon

- Mama
- Páncreas
- Gastrico

- Tipo_de_muestra
- FFPE
 - BC
 - TF

Tejido
Tipo_de_muestra



Sequencing



Data Pre-Processing

Demultiplexing

QC

Trimming

Alignment

Remove Dups

QS Recalibration

Realignment near INDELS

BAM

(>80% 300x)

Annotation

ANNOVAR
ExAC

VCF

Somatic Variant Calling

Somaticseq snv and
indel calling
Votes
3/5 SNV
3/6 INDEL

VCF

REST

CGI

REST

Variant Filtering

$dp \text{ alt} \geq 12$
 $AF > 0.05$
Exac == null
protein
affecting

VCF

Reporting

Clinical Report
(Web,
SQLight)



Technical
Report
(R, Python)



Reporte TumorSec: Control de calidad de los datos generados.

En el siguiente reporte se presentan diversas métricas de calidad correspondiente a la corrida 191002_TumorSec este informe fue generado el día 03/10/19 por el pipeline bioinformático de TumorSec desarrollado por el laboratorio de Genómica del Cáncer, Universidad de Chile. Estas métricas representan una guía para verificar la calidad de los resultados obtenidos por cada muestra en la secuenciación.

2.- Control de calidad de la corrida:

2.1.- Información de la corrida:

Nombre kit	MiSeq Standard Reagent Kit V2
Longitud de Lecturas	2x150 bp
Maximum Output	5.1 Gb
Cantidad de Lecturas	24-30 Millones
Calidad de Lecturas	80% > Q30.
Fecha	02-10-2019
ID_Flow Cell	CGMN9
Modo	Paired End
Equipo	MiSeq
N° Serie	M03158
Ciclos	2x150
Kit Preparación Librería	SeqCap EZ HyperCap Roche
Regiones Blanco	326,00
Largo Total Regiones Blanco (pb)	88.277,00
Calidad de Lecturas	87.24 % > Q30

Tabla 1: Información de la corrida

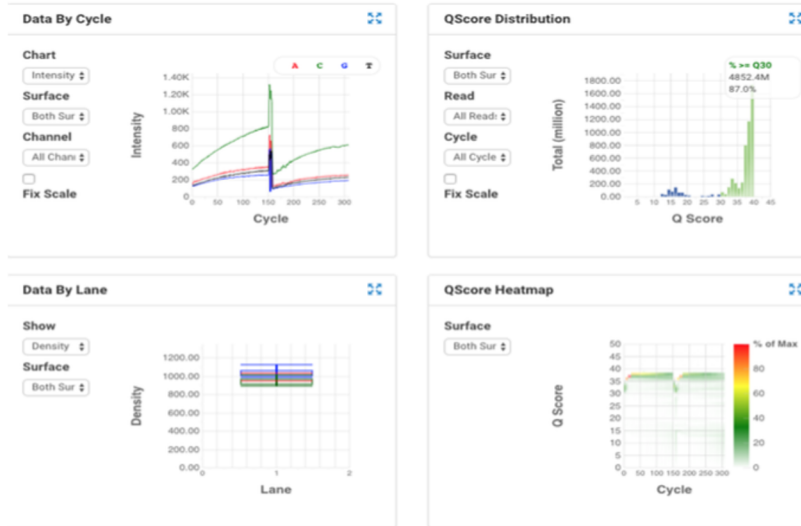


Imagen 1: Métricas de BaseSpace Illumina MiSeq.





Reporte aceptado

Reportes e

Nº de muestra
T00005S
DA001

Reportes a



REPORTE SECUENCIACIÓN TumorSec^(MR)

Katherine Marcelain	Nombre: Katherine Marcelain	ID de la muestra: 123456
Facultad de Medicina, UChile	Rut: 12903456-4	Tipo de muestra: FFPE
Independencia 1027, Independencia	Fecha de Nacimiento: 1975-01-09	Fecha de recolección: 2018-12-31
(+56) 2 29789562	Sexo: Mujer	Fecha de recepción: 2019-01-01
kmarcelain@gmail.com	Dirección: Independencia 1027, Independencia	Fecha de Secuenciación: 2019-01-02
	E-mail: kmarcelain@gmail.com	Fecha de Reporte: 2019-06-03

INFORMACION CLÍNICA

Descargar resultados Descargar vcf Descargar pdf Descargar docx Cancelar

Nº de muestra	Fecha	Estado
123456	2019-06-03 14:54:47	
T00005S	2019-05-10 19:05:41	

Acknowledgments



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- Valentina Garate (Study coordinator GBC)
- Ignacio Maureira (Ms. Genetics)
- Nicolás Miranda (Ms Genetics)
- Nicole Castillejo (Student)
- Vania Montecinos (Study Coordinator Assistant)



- Mauricio Salvo



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- Alicia Colombo (Biobank Director)
- Profesionales Biobanco.



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- Ana María Carrasco (MD)
- Johanna Wettlin
- Equipo médico



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