

R&D and New Test Development

Maher Albitar, MD

Senior Vice President, Chief Medical Officer and
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Dr. Albitar has served as Chief Medical Officer and Director of Research and Development since January 2012. Prior to that Dr. Albitar served as the Medical Director of Hematopathology and Oncology and Chief of R&D at Nichols Institute, Quest Diagnostics. Prior to joining Quest diagnostics, Dr. Albitar was a tenured full professor at MD Anderson Cancer Center and the University of Texas. At MD Anderson, he held the positions of Director of the Molecular Laboratory and Chief of Leukemia in the Division of Pathology and Laboratory Medicine. Dr. Albitar received training in Anatomic and Clinical Pathology at Brown University in Providence, RI and in Hematopathology at the University of Pennsylvania. Dr. Albitar also did post-doctoral training in Genetics at the Genetic Department and Howard Hughes Medical Institute at the University of Pennsylvania. Dr. Albitar received his medical degree in 1979 from Damascus Medical School in Damascus, Syria. Throughout his career, Dr. Albitar has focused on hematologic disease, cancer and molecular biology. He published almost 300 different articles, book chapters and reviews and has multiple patents and patent applications.

Key Drivers of our Leadership in Oncology Testing

- Expanding Molecular Testing: integrating molecular in Anatomic pathology, Flow cytometry, FISH and cytogenetics
- Unique molecular capabilities: Proprietary high sensitivity NGS, RNA Sequencing and Quantitative Profiling
- Leadership in Liquid biopsy (Hematologic neoplasms and prostate cancer)
- Comprehensive multimodality cancer Genomic profiling and Immunologic profiling
- Integrating deep learning

Patient DOB / Sex M
Specimen Type: Paraffin Tissue
Body Site: Abdominal Wall Mass
Specimen ID:
MRN
Reason for Referral:

M.D.
Accession / CaseNo:
Collection Date: 02/27/2017
Received Date: 03/02/2017 04:02:00 AM EST
Report Date: 03/03/2017 10:47:33 AM EST



Diagnosis:

ABDOMINAL WALL TUMOR (SGS17-2251-B8):

- FIBROSARCOMA, FAVORING "INFANTILE" VARIANT (MOLECULAR STUDIES PENDING)

Clinical Data:

Abdominal wall mass in 15 yo male.



Reason for Referral:

Result Summary:

POSITIVE: A FUSION TRANSCRIPT INVOLVING t(4;19)(q35;q13.1)/CIC-DUX4 GENES IS DETECTED.

CIC-DUX4 fusion transcript has been reported in round-cell sarcoma and is believed to be reported to be associated with significantly more aggressive disease (Histopathology. 2016 Oct;69(4):624-34).

There is no evidence of fusion transcript involving any of the other tested genes.

Sutter Medical Center, Sacramento

Patient DOB / Sex M
Specimen Type: Paraffin Tissue
Body Site: Abdominal Wall Mass
Specimen ID:
MRN:
Reason for Referral:

M.D.
Accession / CaseNo:
Collection Date: 02/27/2017
Received Date: 03/02/2017 04:02:00 AM EST
Report Date: 03/23/2017 10:13:01 AM EST



Diagnosis:

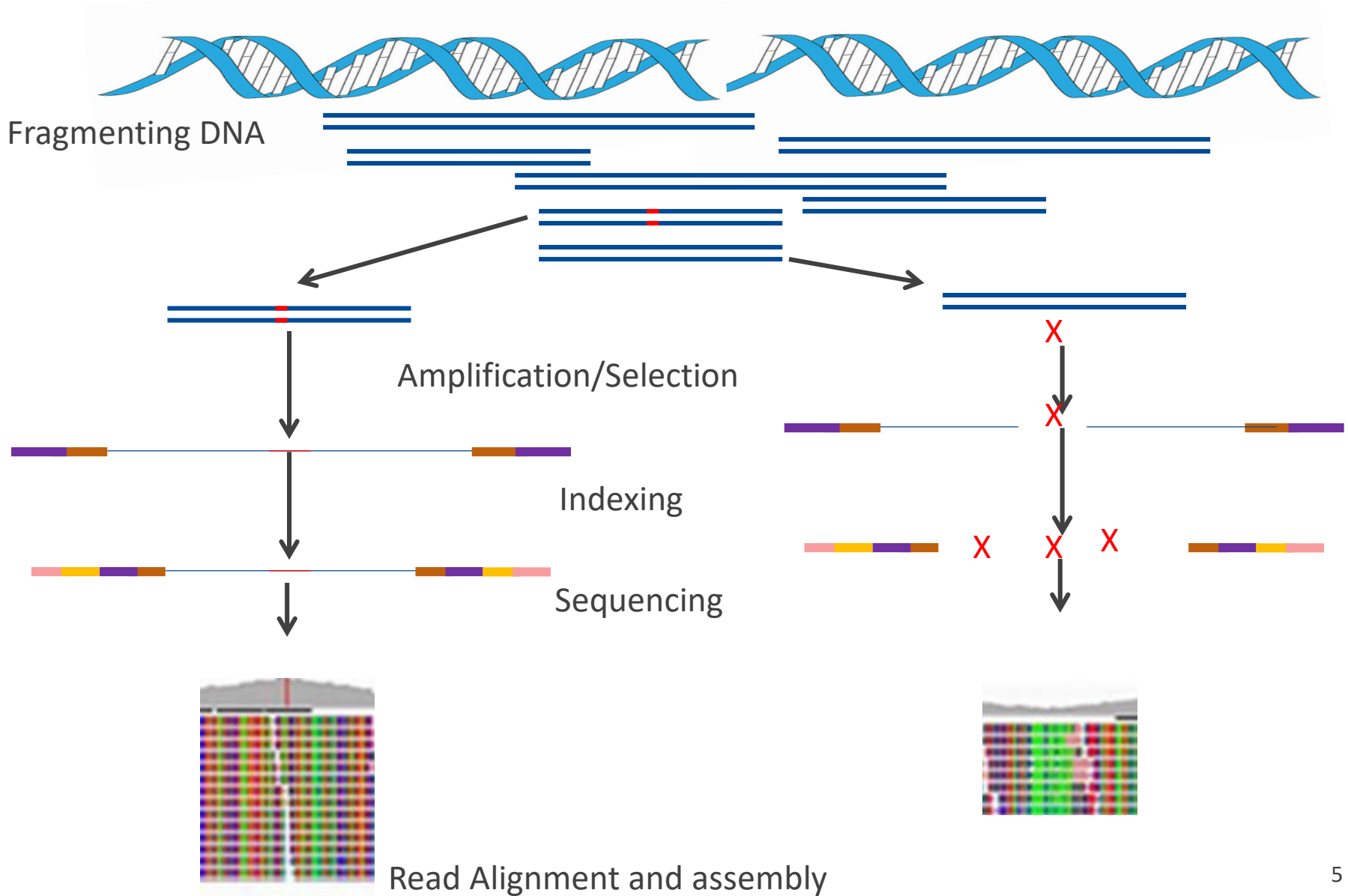
ABDOMINAL WALL TUMOR (SGS17-2251-B8):

- CIC-DUX POSITIVE ROUND CELL SARCOMA (SEE ADDENDUM DIAGNOSIS)

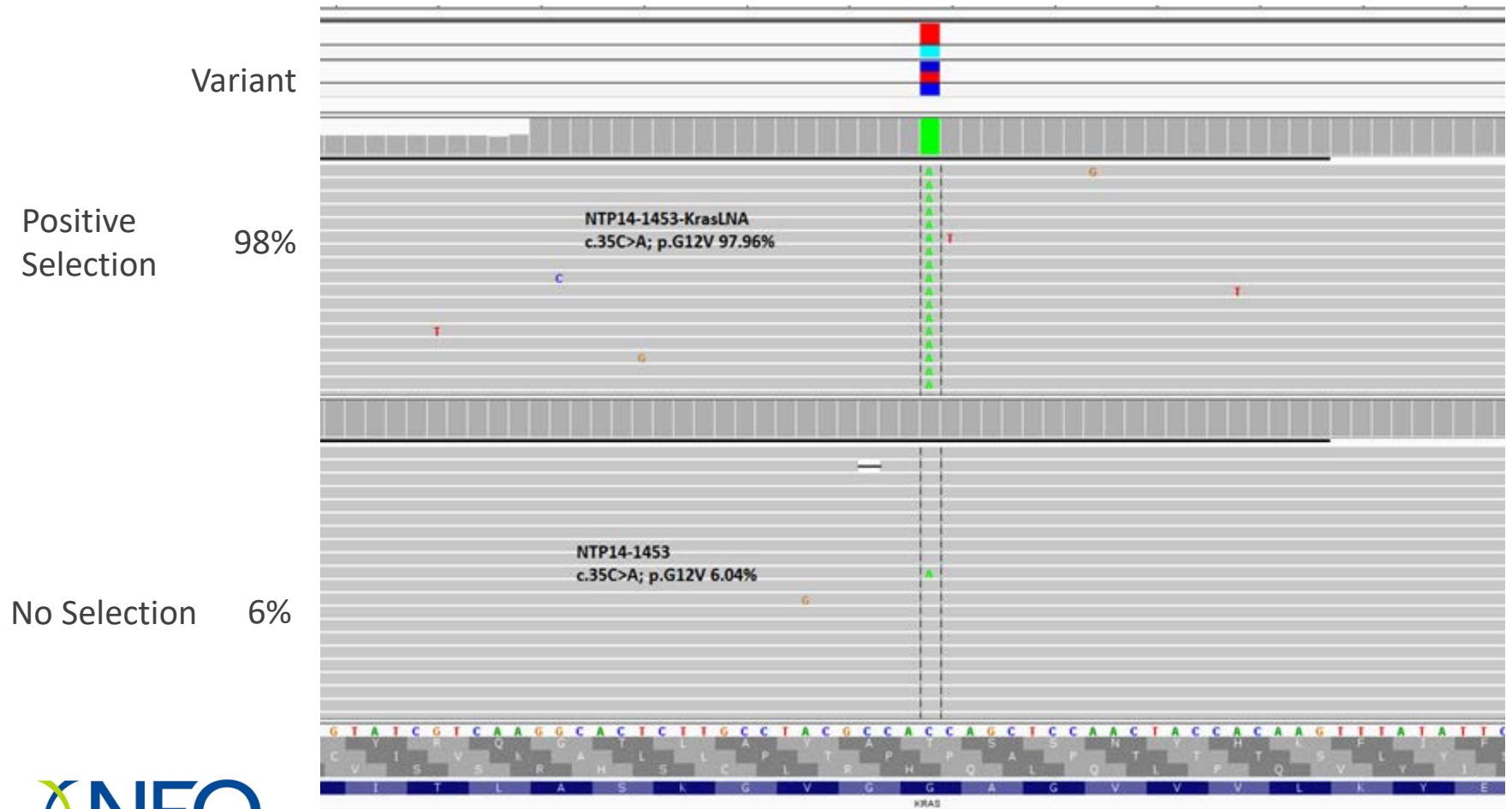
Clinical Data:

Abdominal wall mass in 15 yo male.

Improving Sensitivity of NGS



Developing High Sensitivity NGS



Patent Pending on High Sensitivity NGS



US 20160340725A1

(19) **United States**

(12) **Patent Application Publication**
Albitar

(10) **Pub. No.: US 2016/0340725 A1**

(43) **Pub. Date: Nov. 24, 2016**

(54) **METHOD TO INCREASE SENSITIVITY OF
NEXT GENERATION SEQUENCING**

(52) **U.S. CL.**

CPC *C12Q 1/6858* (2013.01); *C12Q 1/6869*
(2013.01); *C12Q 1/6886* (2013.01); *C12Q*
2600/156 (2013.01)

(71) Applicant: **NEOGENOMICS LABORATORIES,
INC.**, Fort Myers, FL (US)

(72) Inventor: **Maher Albitar**, Valley Center, CA (US)

(57) **ABSTRACT**

(21) Appl. No.: **15/134,302**

(22) Filed: **Apr. 20, 2016**

Related U.S. Application Data

(60) Provisional application No. 62/150,198, filed on Apr.
20, 2015.

Publication Classification

(51) **Int. Cl.**
C12Q 1/68 (2006.01)

A method for detecting a low-occurrence mutation in isolated DNA adds a blocking probe to reagents during amplification of the isolated DNA. The blocking probe is an oligonucleotide complementary to wild-type DNA corresponding to the sample. The blocking probe spans a site of a suspected mutation within a region of interest in the isolated DNA. After amplification, fragments of the amplified DNA is sequenced using next generating sequencing and an output is generated to display the sequenced fragments. In some embodiments, the blocking probe is locked nucleic acid (LNA).

NeoLAB™ Liquid Biopsy Heme Profiles

4 multiplex profiles and 10 single-gene analyses

- AML Profile (28 genes via NGS)
- BTK Inhibitor Acquired Resistance Profile (2 genes)
- MDS/CMML Profile (31 genes via NGS)
- Myeloid Disorders Profile (54 genes via NGS)
- Single gene NeoLABs
 - FLT3 Mutation Analysis
 - NPM1 Mutation Analysis
 - PML-RARA Translocation, t(15;17)
 - IDH1 Mutation Analysis
 - KIT (c-KIT) Mutation Analysis
 - RUNX1-RUNX1T1 (AML1-ETO) Translocation, t(8;21)
 - KRAS Mutation Analysis
 - NRAS Mutation Analysis
 - inv(16), CBFB-MYH11 Translocation
 - IDH2 Mutation Analysis

NeoLAB™ Solid Tumor Liquid Biopsy Profiles

NeoLAB Solid Tumor Monitor

- Plasma based test that uses cfDNA (48 genes via NGS)
- Useful for monitoring response to therapy, monitoring heterogeneity, and predicting early relapse.

NeoLAB EGFR T790M

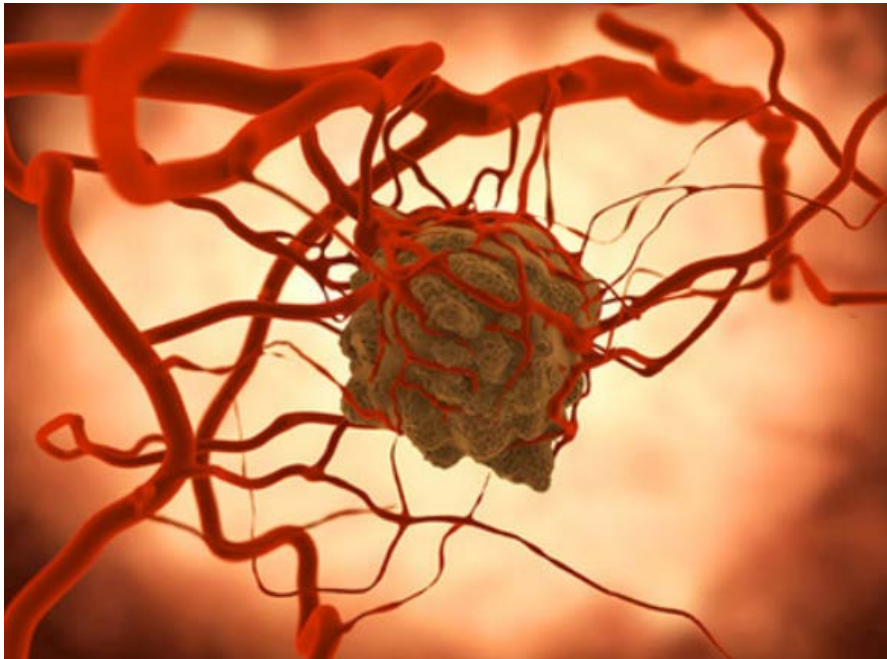
- Plasma based test that uses cfDNA for detecting resistance to EGFR kinase inhibitors

NeoLAB Prostate

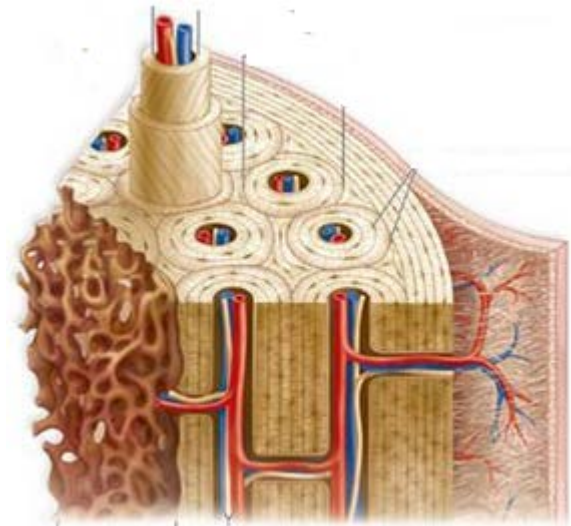
- Plasma and Urine based test
- qRT PCR examines expression levels in 12 genes
- Uses two different algorithms

Emerging Leader in Liquid Biopsies

Solid Tumors



Hematologic
Neoplasms

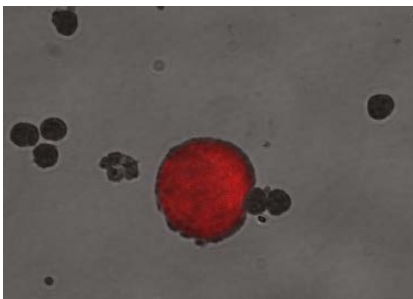


Emerging Leader in Liquid Biopsies

NeoLAB™ Liquid Biopsies

Circulating Tumor Cells
(CTC)

Solid Tumors



Cell-free DNA/RNA (and protein)

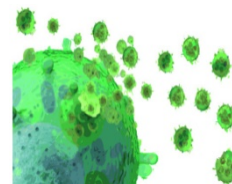
Solid Tumors

Hematologic
Neoplasms

Apoptosis
Paraptosis
Autophagy
Necrosis



Exosome
Microvessels



NEO Discovery NGS Panel: 315 Genes + 9 FISH + PD-L1 +TMB

ABL1	C11orf30 (EMSY)	DDR2	FGFR4	IL7R	MET	PIK3CA	SDHD	TSHR
ABL2	CARD11	DICER1	FH	INHBA	MITF	PIK3CB	SETD2	U2AF1
ACVR1B	CBFB	DNMT3A	FLCN	INPP4B	MLH1	PIK3CG	SF3B1	VEGFA
AKT1	CBL	DOT1L	FLT1	IRF2	MPL	PIK3R1	SLIT2	VHL
AKT2	CCND1	EGFR	FLT1	IRF4	MRE11A	PIK3R2	SMAD2	WISP3
AKT3	CCND2	EP300	FLT4	IRS2	MSH2	PLCG2	SMAD3	WT1
ALK	CCND3	EPHA3	FOXL2	JAK1	MSH6	PMS2	SMAD4	XPO1
AMER1 (FAM123B)	CCNE1	EPHA5	FOXP1	JAK2	MTOR	POLD1	SMARCA4	ZBTB2
APC	CD274	EPHA7	FRS2	JAK3	MUTYH	POLE	SMARCB1	ZNF217
AR	CD79A	EPHB1	FUBP1	JUN	MYC	PPP2R1A	SMO	ZNF703
ARAF	CD79B	ERBB2	GABRA6	KAT6A (MYST3)	MYCL (MYCL1)	PRDM1	SNCAIP	
ARFRP1	CDC73	ERBB3	GATA1	KDM5A	MYCN	PREX2	SOCS1	
ARID1A	CDH1	ERBB4	GATA2	KDM5C	MYD88	PRKAR1A	SOX10	
ARID1B	CDK12	ERG	GATA3	KDM6A	NF1	PRKCI	SOX2	
ARID2	CDK4	ERRFI1	GATA4	KDR	NF2	PRKDC	SOX9	
ASXL1	CDK6	ESR1	GATA6	KEAP1	NFE2L2	PRSS8	SPEN	
ATM	CDK8	EZH2	GID4 (C17orf39)	KEL	NFKBIA	PTCH1	SPOP	
ATR	CDKN1A	FAM46C	GLI1	KIT	NKX2-1	PTEN	SPTA1	
ATRX	CDKN1B	FANCA	GNA11	KLHL6	NOTCH1	PTPN11	SRC	
AURKA	CDKN2A	FANCC	GNA13	KMT2A (MLL)	NOTCH2	QKI	STAG2	
AURKB	CDKN2B	FANCD2	GNAQ	KMT2C (MLL3)	NOTCH3	RAC1	STAT3	
AXIN1	CDKN2C	FANCE	GNAS	KMT2D (MLL2)	NPM1	RAD50	STAT4	
AXL	CEBPA	FANCF	GPR124	KRAS	NRAS	RAD51	STK11	
BAP1	CHD2	FANCG	GRIN2A	LMO1	NSD1	RAF1	SUFU	
BARD1	CHD4	FANCL	GRM3	LRP1B	NTRK1	RANBP2	SYK	
BCL2	CHEK1	FAS	GSK3B	LYN	NTRK2	RARA	TAF1	
BCL2L1	CHEK2	FAT1	H3F3A	LZTR1	NTRK3	RB1	TBX3	
BCL2L2	CIC	FBXW7	HGF	MAGI2	NUP93	RBM10	TERC	
BCOR	CREBBP	FGF10	HNF1A	MAP2K1	PAK3	RET	TERT (promoter only)	
BCORL1	CRKL	FGF14	HRAS	MAP2K2	PALB2	RICTOR	TET2	
BLM	CRLF2	FGF19	HSD3B1	MAP2K4	PARK2	RNF43	TGFBR2	
BRAF	CSF1R	FGF23	HSP90AA1	MAP3K1	PAX5	ROS1	TNFAIP3	
BRCA1	CTCF	FGF3	IDH1	MCL1	PBRM1	RPTOR	TNFRSF14	
BRCA2	CTNNA1	FGF4	IDH2	MDM2	PDCD1LG2	RUNX1	TOP1	
BRD4	CTNNB1	FGF6	IGF1R	MDM4	PDGFRA	RUNX1T1	TOP2A	
BRIP1	CUL3	FGFR1	IGF2	MED12	PDGFRB	SDHA	TP53	
BTG1	CYLD	FGFR2	IKBKE	MEF2B	PDK1	SDHB	TSC1	
BTK	DAXX	FGFR3	IKZF1	MEN1	PIK3C2B	SDHC	TSC2	

FISH Testing

Translocations: ALK,
RET, ROS, MYC,
PDGFRA, BRAF

Copy Number

Variation (CNV): PTEN,
MET, HER2

IHC
PD-L1

TMB

Extensive Menu of NeoTYPE Cancer Specific Profiles

- 18 NeoTYPE Cancer Specific Solid Tumor Genomic/Immunologic Profiles

Brain (22 MolDx, 5 FISH, PD-L1)

Breast (22 MolDx, 3 FISH, PD-L1)

Cervical (22 MolDx, 2 FISH, PD-L1)

Colorectal (24 MolDx, 2 FISH, PD-L1)

Endometrial (21 MolDx, 2 FISH, PD-L1)

Esophageal (22 MolDx, 3 FISH, PD-L1)

Gastric (22 MolDx, 3 FISH, PD-L1)

GIST Profile (11 MolDx, PD-L1)

Head & Neck (24 MolDx, 2 FISH, PD-L1,
1 ISH)

Liver/Biliary (24 MolDx, 2 FISH, PD-L1)

Liposarcoma (5 MolDx, 1 FISH)

Lung (21 MolDx, 6 FISH, PD-L1)

Melanoma (17 MolDx, 1 FISH, PD-L1)

Other Solid Tumor (24 MolDx, 2 FISH, PD-L1)

Ovarian (22 MolDx, 2 FISH, PD-L1)

Pancreas (22 MolDx, 3 FISH, PD-L1)

Soft Tissue (19 MolDx, 2 FISH, PD-L1)

Thyroid Profile (16 MolDx, 2 FISH, PD-L1)

Extensive Menu of NeoTYPE Cancer Specific Profiles

- 8 NeoTYPE Hematologic Neoplasm Profiles

AITL Peripheral T-Cell Lymph (5 MoIDx)

AML Favorable Risk (2 MoIDx)

AML Prognostic (27 MoIDx)

CLL Prognostic (5 MoIDx, 5 FISH)

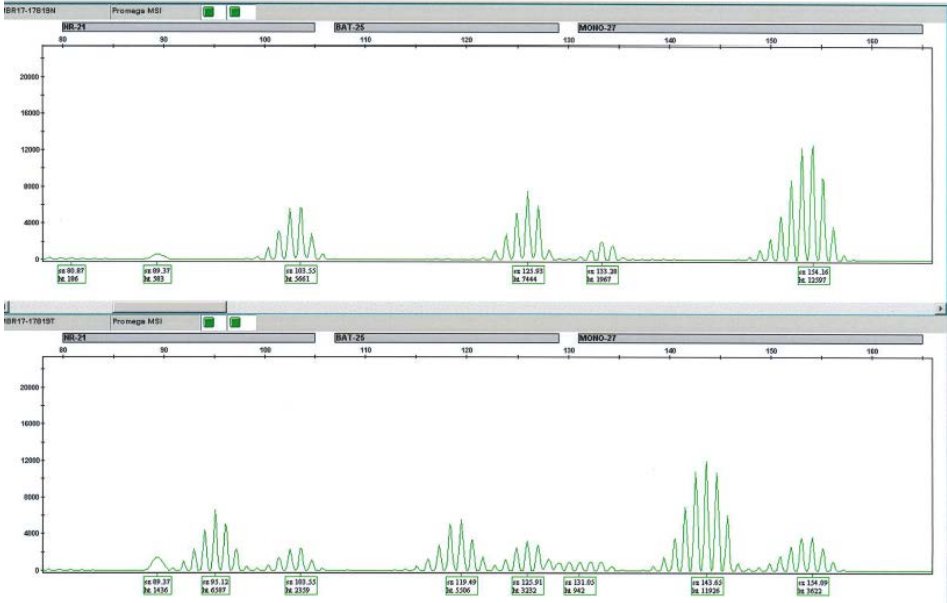
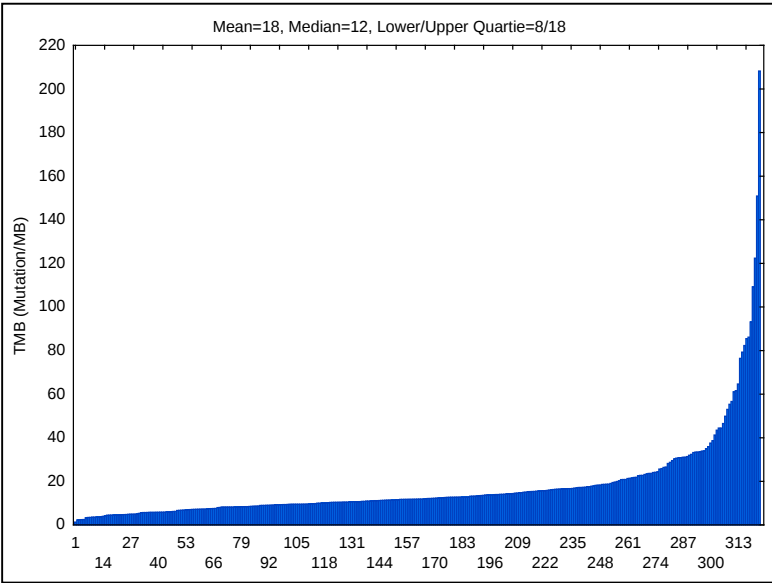
JMML (16 MoIDx)

Lymphoma (8 MoIDx)

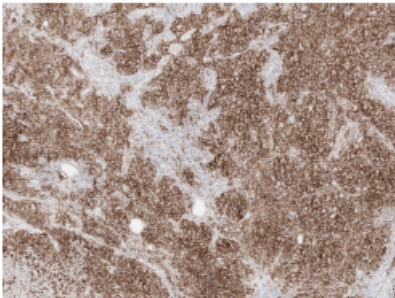
MDS/CMML (32 MoIDx)

MPN (25 MoIDx)

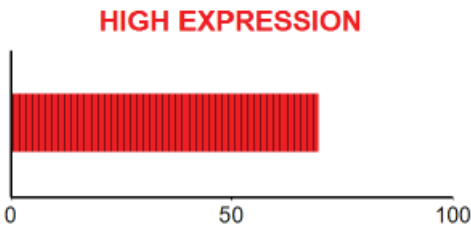
Immunoprofiling: PD-L1, Microsatellite instability and Tumor Mutation Burden (TMB)



Specimen ID: **MLS17-08752-E14**

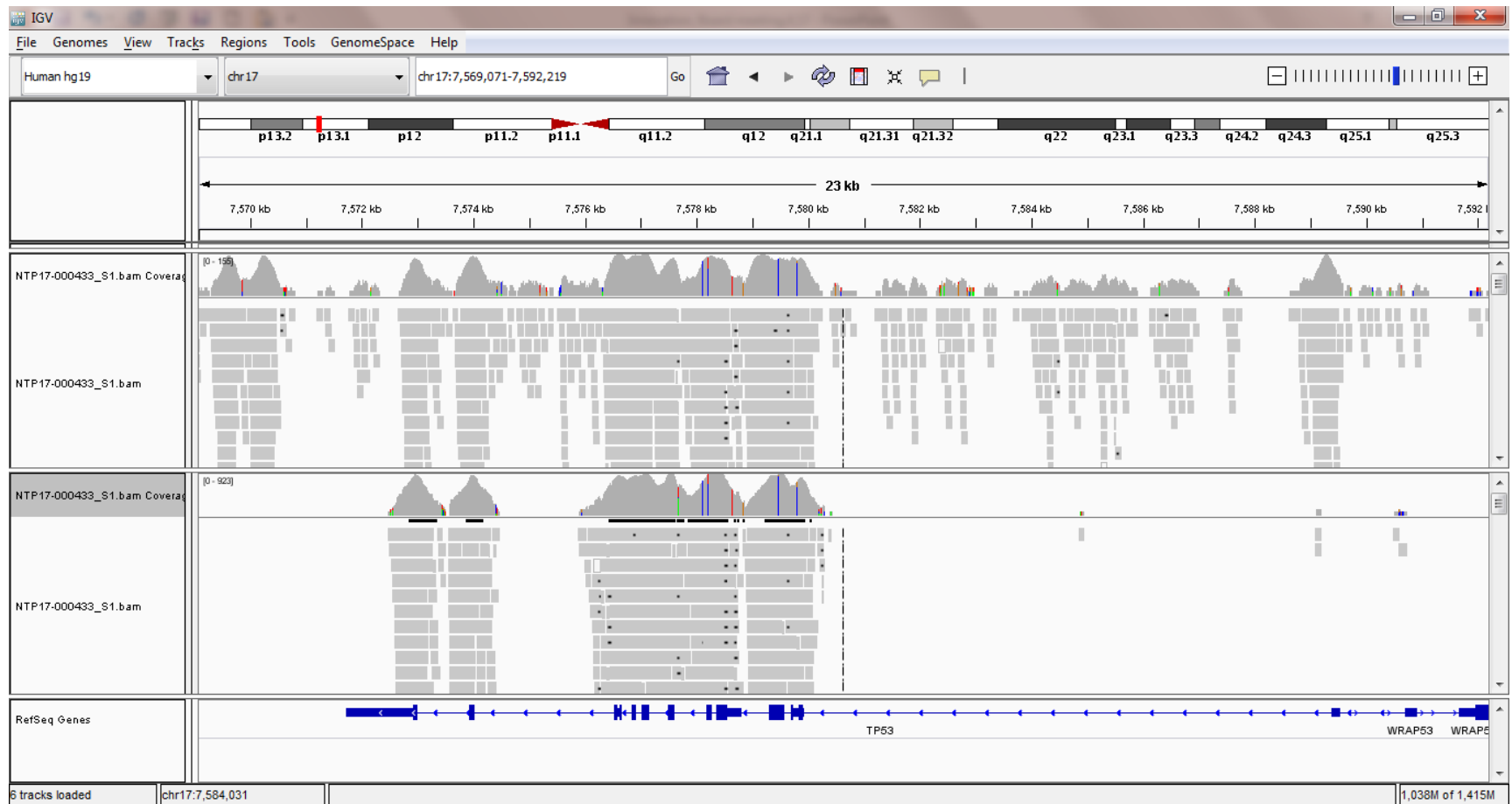


PD-L1 22C3 FDA (KEYTRUDA®): HIGH EXPRESSION
Tumor Proportion Score: 70%
Intensity: Strong

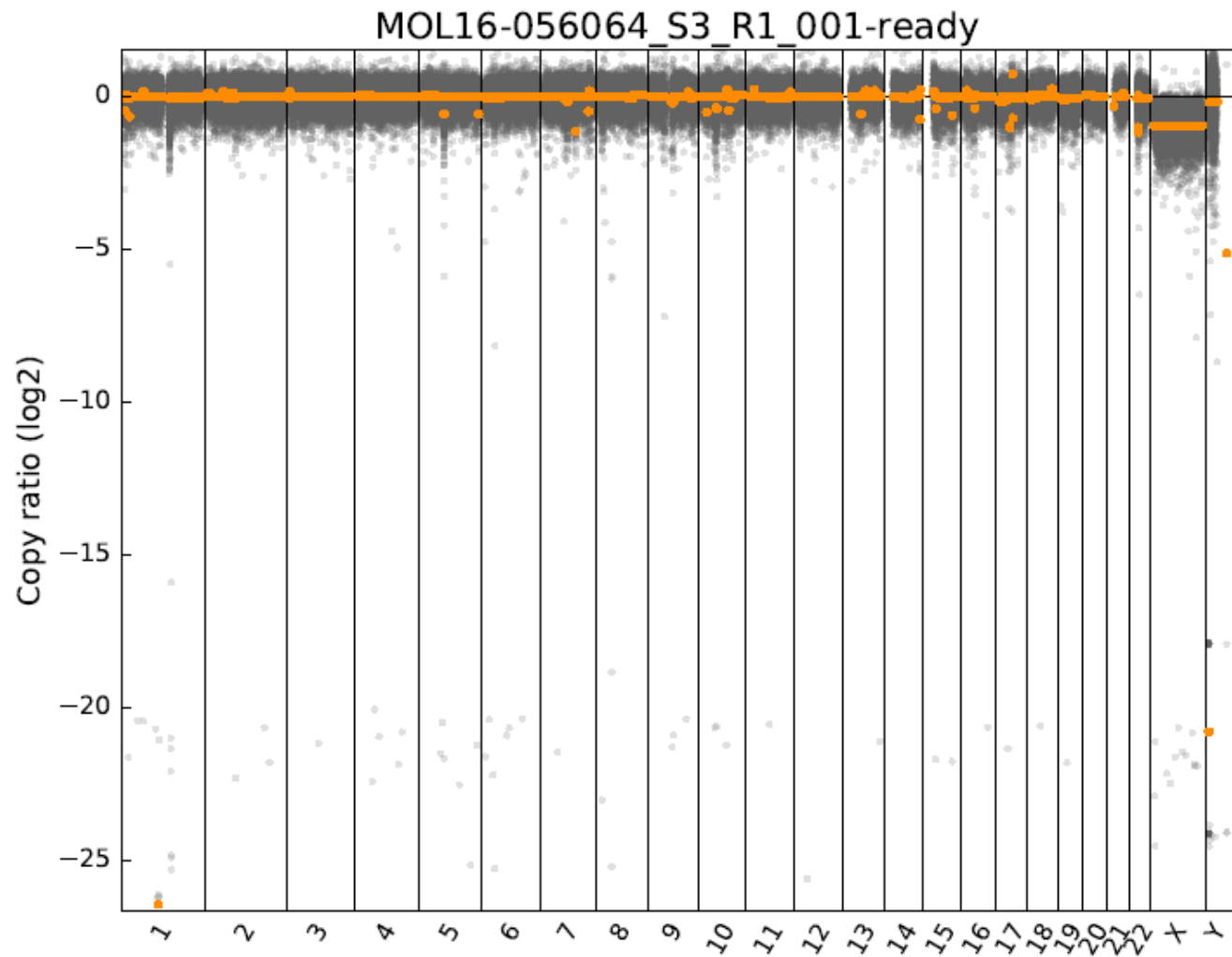


Reference Ranges	
High Expression	>=50% TPS
Expressed	1-49% TPS
No Expression	<1% TPS

Integrating Molecular Testing with Cytogenetic and FISH Analysis



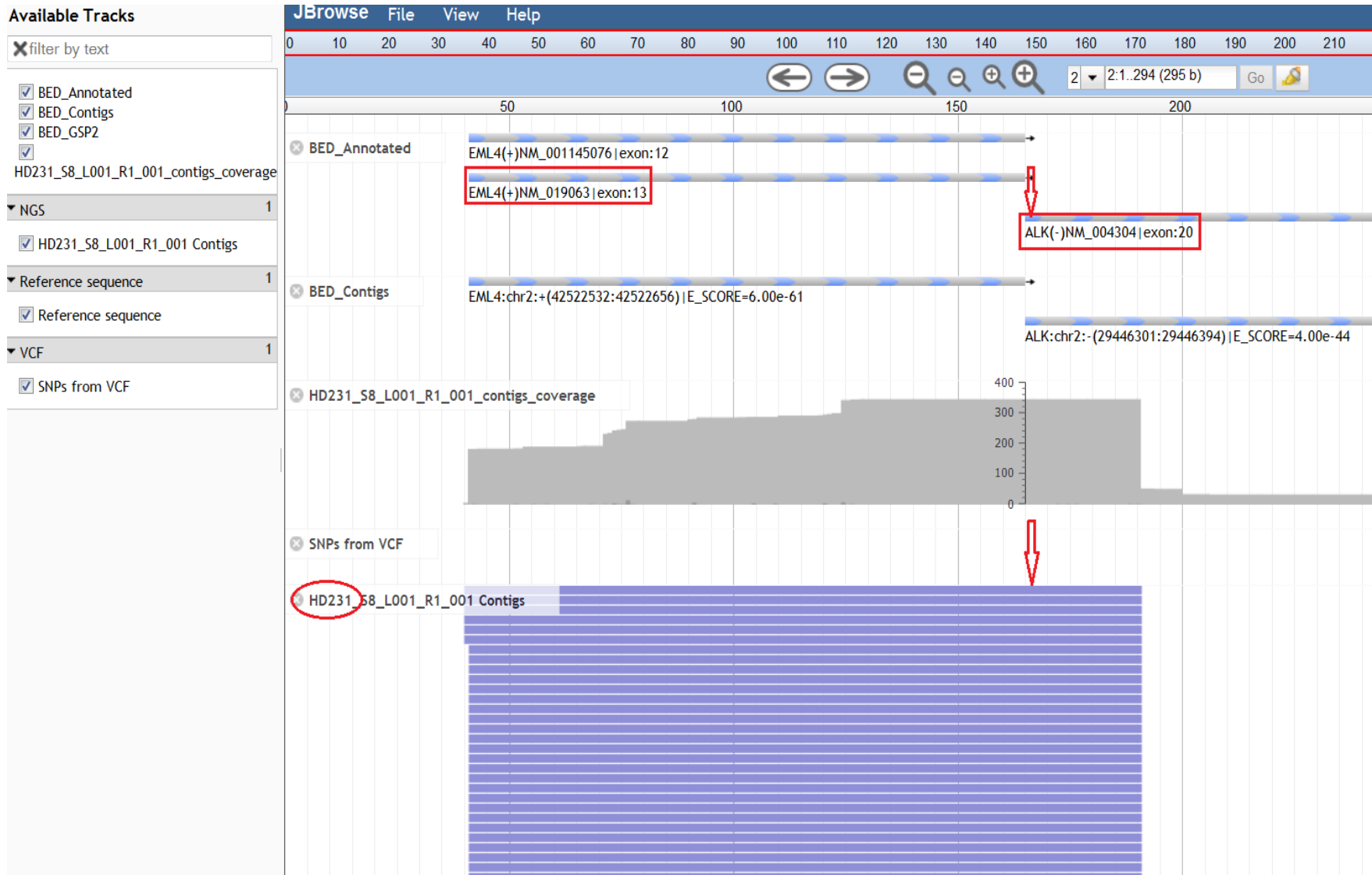
Genome-Wide Copy Number Variation Detection by NGS



Genomic Changes not Detected by FISH or Cytogenetics: Copy Number Neutral Mosaic 11q LOH in CLL



Complimenting FISH Testing Using NGS: ALK Exon20/ELM4 Exon13 Fusion



Using RNA in NGS Testing: Fusion/Expression (1385 gene) Panel

BACC3	BAP1	CCND3	COX6C	EDIL3	FCRL4	GOT1	IDH1	LAMA5	MET	NOTCH1	PLCB4	RAD50	SGK1	SUV39H2	TRPS1
AB11	BARD1	CCNE1	CPNE1	EDNRB	FEN1	GPC3	IDH2	LAMP2	METTL18	NOTCH2	PLCG1	RAD51	SGGP2	SUZ12	TSC1
ABL1	BAX	CCNG1	CP51	EED	FEV	GPHN	IFNG	LASP1	METTL7B	NOTCH3	PLCG2	RAD51B	SH2D5	SVK	TSK
ABO1	BCL11A	CCND2	BA22A	EGF	FEZ1	GPR124	IFNG1	LC16A	MGAT1	NOTCH4	PLCH1	RAD51C	SH2D6	SYNR1	TSHR
ABLIM1	BCAS3	CD19	CRADD	EGF	FGF10	GPR125	IGF1	LBP1	MGEA5	NPM1	PML	RAD51D	SH3D19	TACC1	TTK
ACACA	BCAS4	CD22	CREB1	EGFR	FGF13	GPR34	IGF1R	LEF1	MGMT	NPM2	PMS1	RAD52	SH3GL2	TACC2	TTL
ACEA	BCL10	CD24	CREB1A	EGR1	FGF14	GPR134	IGF1R2	MYD88	MLL2	NRC3C1	PMS2	RAF1	SH3GL1	TACC3	TUSC3
ACER1	BCL1B3L2	CD28	CREB1B	EGFR	FGF19	GPR135	IGFBP3	PENG	MPOL1	NRC3C2	PMLUT1	RAD53	SH3GL3	TACC4	TYRO3
ACKR3	BCL11B	CD36	CREBBP	EGR3	FGF2	GRHPR	IKBKB	LGALS3	MITF	NRAA1	POLD1	RANBP17	SHC2	TAF15	TYMS
ACCSBG1	BCL2	CD44	CRKL	EGR4	FGF23	GRID1	IKBKE	LGR5	MIK167	NRA5	POLD3	RANBP2	SIK3	TAL1	U2AF1
ACSLA1	BCL2L1A	CD44	CRKL	EGF2	FGF23	GRID1	IKBKE	LGR5	MIK167	NRA5	POLD3	RANBP2	SIK3	TAL1	U2AF1
ACSL6	BCL2L1	CD70	CRTC3	ELF4	FGF4	GRIN2B	IKZF2	LHX2	MLK1	NT5C2	POM121	RARA	SIRT1	TAOK1	UBE2C
ACVRI1B	BCL2L2	CD74	CRTC3	ELF4	FGF6	GRM1	IKZF5	LHX4	MLF1	NTF3	POM121	RASAL1	SKP2	TBLIXR1	UBE2C
ACVRI1C	BCL3	CD79A	CSF1	ELK4	FGF8	GRM3	IL12RB2	LIFR	MLH1	NTF4	POSTN	RASGEF1	SLC1A2	TBX15	UFEC1
ACVRI1A	BCL3B	CD79B	CSF1B	ELK4	FGF8	GRM3	IL12RB2	LIFR	MLH1	NTF4	POSTN	RASGEF1	SLC1A2	TBX15	UFEC1
ADD3	BCL7A	CD84	CSF3	ELN	FGFR1	GSN	IL13RA2	LINC0059	MLL1	NTF1	POSTN	RASGEF1	SLC1A2	TBX15	UFEC1
ADM	BCL9	CD84A	CSF3R	ELVOL2	FGFR1OP	GSTT1	IL15	LINGO2	MLLT11	NTRK3	POU5F1	RASGRP1	SLC7A5	TCF3	USP42
AFB1	BCOR	CD148	CSF3R1G2	ELVOL2	FGFR1OP	GSTT1	IL15	LINGO2	MLLT11	NTRK3	POU5F1	RASGRP1	SLC7A5	TCF3	USP42
AFB2	BCOR1	CD148B	CSF3R1G2	ELVOL2	FGFR1OP	GSTT1	IL15	LINGO2	MLLT11	NTRK3	POU5F1	RASGRP1	SLC7A5	TCF3	USP42
AFB3	BCOR2	CD148C	CSF3R1G2	ELVOL2	FGFR1OP	GSTT1	IL15	LINGO2	MLLT11	NTRK3	POU5F1	RASGRP1	SLC7A5	TCF3	USP42
AFB4	BCR	CD25C	CTCF	EML4	FGFR3	H2AFX	IL11R1	LMO2	MLLT6	NUP214	PPARGC1B	RBM6	SMAD2	TC6	USP7
AGR3	BDNF	CD25P2	ENPP2	FGFR4	H3F3A	IL2	LMO2	MLLT6	NUP214	PPARGC1B	RBM6	SMAD2	TC6	USP7	
AGV1	BHLH122	CD148	CSF3R1G2	ELVOL2	FGFR1OP	GSTT1	IL15	LINGO2	MLLT11	NTRK3	POU5F1	RASGRP1	SLC7A5	TCF3	USP42
AHL1	BICCN1	CDH1	EP300	FHIT	HDAC1	IL13R1	LMO2	MLLT6	NUP214	PPARGC1B	RBM6	SMAD2	TC6	USP7	
AHR	BIN1	CDH11	CTNNA1	EPCL1	FHL2	HDAC2	IL3	LPAR1	NN1	NUTM2A	PPP1CB	RECQL4	SMAP1	TEAD3	VGLL3
AHR1	BIRC3	CDK1	CTNND2	EPICAM	FHIT	HDAC3	IL6	LPP	MNX1	NUTM2B	PPP1R13B	REEP3	SMARCA1	TEAD4	VHL
AK1	BIRC5	CDK2	CTNND2	EPICAM	FHIT	HDAC3	IL6	LPP	MNX1	NUTM2B	PPP1R13B	REEP3	SMARCA1	TEAD4	VHL
AK2	BLM	CDK2	CTSA	EPHA2	FLCN	HDAC5	INHBA	LRIG3	MRE11A	OLIG1	PPP2C8	RELN	SMARCA2	TENM1	WASF2
AK5	BMP4	CDK4	CUX1	EPHA3	FLI1	HDAC6	INPP4A	LRMP	MSH2	OLIG2	PPP2R1A	RERG	SMARCB1	TERF1	WDFY3
AKAP12	BMPRI1A	CDKSRAP	CXCL8	EPHA5	FLNA	HDAC7	INPP4B	LRP18	MSH3	OLR1	PPP2R1B	RETB	SMC1A	TERF2	WDR1
AKAP9	BMPRI1B	CDKSRAP	CXCL8	EPHA5	FLNA	HDAC7	INPP4B	LRP18	MSH3	OLR1	PPP2R1B	RETB	SMC1A	TERF2	WDR1
AKAP9	BRCA1	CDK7	CXCA4	EPHB1	FLT1	HEPH	INPP5D	LRPPRC	MSI2	P2RY8	PPP2R4	RHBDF2	SMO	TET1	WDR70
AKR1C3	BRCA2	CDK8	CYFIP2	EPHB6	FLT3	HERPUD1	IQCC	LRRC37B	MSN	PAFAH1B	PPP3CA	RHOA	SNAPC3	TET2	WDR90
AKT1	BRD1	CDK9	CYLD	EPO	FLT3LG	HESE1	IRF1	LRRCC59	MTCP1	PAG1	PPP3C8	RHOD	SNCG	TFAP2A	WEE1
AKT2	BRD2	CDK15	BRD1	EPH2	FLT3	HESE1	IRF1	LRRCC59	MTCP1	PAG1	PPP3C8	RHOD	SNCG	TFAP2A	WEE1
AKT3	BRD4	CDKN1A	CYP2C19	EPS15	FLYWCH1	HEY1	IRF4	LRRK2	MTU52	PAK3	PPP3R1	RICTOR	SNW1	TFE3	WHSC1L1
ALDH1A1	BRIP1	CDKN1B	DAB2IP	ERBB2	FOSB1	HGF	IRF8	LTBP1	MUC1	PAK6	PPP3R2	RLTPR	SNX29	TFEB	WIF1
ALDH3	BRIP2	CDKN1B	DAB2IP	ERBB2	FOSB1	HGF	IRF8	LTBP1	MUC1	PAK6	PPP3R2	RLTPR	SNX29	TFEB	WIF1
ALDO	BRWD3	CDKN3A	DACH2	ERBB4	FNSB	HIP1A	IRS2	LYN	MYB	PALB2	PQLS	RNF213	YOC51	TFPT	WNT10A
ALK	BTBD18	CDKN2B	DAXX	ERC1	FOSL1	HIP1	IRS4	MACROD1	MYBL1	PAPPA	PRCC	RNF43	SOCS2	TFRC	WNT10B
AMER1	BTG1	CDKN2C	DCLLX	ERCC1	FOXO1	LHPK1	ITGA5	MAD2L1	MYC	PASK	PRDM1	ROBO1	SOC53	TGFB2	WNT11
ANGPT1	BTG2	CDKN2D	DCLLX	ERCC1	FOXO1	LHPK1	ITGA5	MAD2L1	MYC	PASK	PRDM1	ROBO1	SOC53	TGFB2	WNT11
ANGPT1	BTG2	CDKN2D	DCLLX	ERCC1	FOXO1	LHPK1	ITGA5	MAD2L1	MYC	PASK	PRDM1	ROBO1	SOC53	TGFB2	WNT11
ANKRD28	BTLA	CDX1	DD2	ERCC3	FOXO3	HIST1H1C	ITGA8	MAF	MYCN	PAX3	PRDM7	ROS1	SORBS2	TGFB1	WNT2B
ANLN	BU81B	CDX2	DDIT3	ERCC4	FOXO4	HIST1H1D	ITGAV	MAFB	MYD88	PAX5	PRF1	RPA3	SORT1	TGFB2	WNT3
APH1A	C11orf30	CEBPA	DDX20	ERG	FRMPD4	HIST1H1E	ITGB3	MAGED1	MYH11	PAK7	PRG2	RPL32	SOS1	TGFB3	WNT4
APLD	C11orf35	CEBPD	DDX39B	ERL1N2	FRS2	HIST1H2A	JAG2	MALT1	MYO1F	PBX1	PRKAC	RPS21	SOX1	THBS1	WNT6
APOL2	C11orf44	CEBPE	DDX39B	ERL1N2	FRS2	HIST1H2A	JAG2	MALT1	MYO1F	PBX1	PRKAC	RPS21	SOX1	THBS1	WNT6
ARAF	C2orf44	CEP170B	DDX6	ETS2	FUS	HIST1H2B	JAK3	MAP2	NAPA	PCL0	PRKCB	RPTOR	SPEN	TLR4	WT1
ARFRP1	C3orf27	CEP57	DEK	ETV1	FUT1	HIST1H2B	JARID2	MAP2K1	NAV3	PCM1	PRKCD	RPTOR	SPEN	TLR4	WT1
ARHGAP20	CACNA1F	CHD2	DGKI	ETV5	FZD2	HIST1H3B	JUN	MAP2K3	NBN	PCSK7	PRKDC	RRM1	SPR1	TLX3	WNT10X
ARHGAP26	CACNA1G	CHD2	DGKI	ETV5	FZD2	HIST1H3B	JUN	MAP2K3	NBN	PCSK7	PRKDC	RRM1	SPR1	TLX3	WNT10X
ARHGEF12	CACNA2D3	CHD2	DGKZ	ETV6	FZD3	HIST1H4I	KALRN	MAP2K4	NBR1	PCD1	PRKG2	RRM2B	SPRY2	TMEM127	WBP1
ARHGEF7	CAD	CHD6	DICER1	EXTS1	FZD6	HLMF	KANK1	MAP2K5	NCOA1	PD1	PRMT1	RUNX1	SPRY4	TMEM32A	XAP
ARID2	CAMK2A	CHD2	DICER1	EXTS1	FZD6	HLMF	KANK1	MAP2K5	NCOA1	PD1	PRMT1	RUNX1	SPRY4	TMEM32A	XAP
ARID2	CAMK2A	CHD2	DICER1	EXTS1	FZD6	HLMF	KANK1	MAP2K5	NCOA1	PD1	PRMT1	RUNX1	SPRY4	TMEM32A	XAP
ARIH2	CAMK2A	CHD2	DICER1	EXTS1	FZD6	HLMF	KANK1	MAP2K5	NCOA1	PD1	PRMT1	RUNX1	SPRY4	TMEM32A	XAP
ARIH2	CAMK2A	CHD2	DICER1	EXTS1	FZD6	HLMF	KANK1	MAP2K5	NCOA1	PD1	PRMT1	RUNX1	SPRY4	TMEM32A	XAP
ARN1	CAMK2G	CHL1	DKK1	EXT2	GAB1	HMG1B	KAT6B	MAP3K14	NCOA3	PDGFA	PRRX1	RUNX1T1	QSMTM1	TNC	XPC
ARNT	CARD11	CHN1	DLEC1	EZH2	GANAB	HNRNP2A2	KDM2B	MAP3K7	NCOA2	PDGFA	PRRX1	RUNX1T1	QSMTM1	TNC	XPC
ASMTL	CANT1	CHN1	DLEC1	EZH2	GANAB	HNRNP2A2	KDM2B	MAP3K7	NCOA2	PDGFA	PRRX1	RUNX1T1	QSMTM1	TNC	XPC
ASPH	CAPRIN1	CHST11	DLL1	EZR	GAS1	HOOK3	KDM4C	MAPK1	NCS1N	PDGFRB	PSEN3	SARNP	SRRM3	TNFRSF10	YAP1
ASPSR1	CARM1	CHUK	DLG3	FAT1	GAS1	HOOK3	KDM4C	MAPK1	NCS1N	PDGFRB	PSEN3	SARNP	SRRM3	TNFRSF10	YAP1
ASTN2	CARD11	CHN1	DLEC1	EZH2	GANAB	HNRNP2A2	KDM2B	MAP3K7	NCOA2	PDGFA	PRRX1	RUNX1T1	QSMTM1	TNC	XPC
ASXL1	CARM1	CHUK	DLG3	FAT1	GAS1	HOOK3	KDM4C	MAPK1	NCS1N	PDGFRB	PSEN3	SARNP	SRRM3	TNFRSF10	YAP1
ATF1	CARS	CIRH1A	DMRTA2	FAM19A5	GATA2	HOXA3	KDM6A	MAPK8IP1	NDRG1	PER1	PTBP1	PTCH1	SDHA	SNRNP100	TNFRSF10
ATF3	CASP3	CKB	DNM1	FAM64A	GAT6	HOCX11	KEAP1	MATK	NEURL1	PHF1	PTEN	SDHB	SSX1	TOP2A	ZC3H7B
ATG13	CASP5	CKB	DNM1	FAM64A	GAT6	HOCX11	KEAP1	MATK	NEURL1	PHF1	PTEN	SDHB	SSX1	TOP2A	ZC3H7B
ATG5	CASP7	CKS1B	DNM2	FANCA	GBP2	HOCX13	KIAA0232	MAX	NF1	PHF23	PTGS2	SDHC	SSX2	TOP2B	ZFP64
ATIC	CASP8	CLP1	DNM3	FANCB	GDGF	HOCX13	KIAA1524	MB21D2	NF2	PHF6	PTK2	SDHD	SSX4	TP53	ZFPM2
ATM	CBAF2T3	CLTC	DNMT3A	FANCD2	GHR	HOCX9	KIAA1598	MBTD1	NFATC2	PI4KA	PTK7	SEPT2	STAT2	TP63	ZIC2
ATP1B4	CBFB	CLTCL1	DOCK1	FANCE	GID4	HRA5	KIF5B	MCL1	NFE2L2	PICALM	PTPN11	SEPT5	STAT1	TP73	ZMI21
ATP8A2	CBL	CMCKLR1	DOCK1	FANCE	GID4	HRA5	KIF5B	MCL1	NFE2L2	PICALM	PTPN11	SEPT5	STAT1	TP73	ZMI21
ATRLN1	CBLC	CNOT2	DPYD	FANCI	GLI3	HSPA1A	LKLH6	MDM2	NFKB2	PI3KCD	PTPRA	SERP2	STAT5A	TPM4	ZMYND11
ATRX	CCAR2	CNTN1	DST	FANCL	GMPS	HSPA2	KLK2	MDM4	NFKBIA	PIK3CG	PTPRK	SERPINE1	STAT5B	TPO	ZNF207
AURKA	CCNA2	CNTN1	DST	FANCL	GMPS	HSPA2	KLK2	MDM4	NFKBIA	PIK3CG	PTPRK	SERPINE1	STAT5B	TPO	ZNF207
AURKB	CCNB1	CNTN1	DST	FANCL	GMPS	HSPA2	KLK2	MDM4	NFKBIA	PIK3CG	PTPRK	SERPINE1	STAT5B	TPO	ZNF207
AUTS2	CCDC88C	COL11A1	DUSP2	FANL3	GASL3	GNA13	HTR1A	KMT2B	MECOM	NIN	PTTG1	SETBP1	STK11	TRAF3	ZNF331
AXIN1	CKK	COL1A1	DUSP2	FANL3	GASL3	GNA13	HTR1A	KMT2B	MECOM	NIN	PTTG1	SETBP1	STK11	TRAF3	ZNF331
BACH1	CCNA2	COL3A1	DUSP9	FBXW7	GOLGA5	ID1	KSR1	MEN1	NOS3	PLCB1	RAD21	SFRP4	SULF1	TRIP11	ZRSR2
BACH2	CCNB1P1	COL3A1	DUSP9	FBXW7	GOLGA5	ID1	KSR1	MEN1	NOS3	PLCB1	RAD21	SFRP4	SULF1	TRIP11	ZRSR2
BAG4	CCNB3	COL3A1	DUSP9	FBXW7	GOLGA5	ID1	KSR1	MEN1	NOS3	PLCB1	RAD21	SFRP4	SULF1	TRIP11	ZRSR2
BAIAP2L1	CCND2	CCND2	CTSL	ECT2L	GOSR1	ID4	LAMA1								

RNA Quantification by NGS is very Reliable for Cancer Profiling

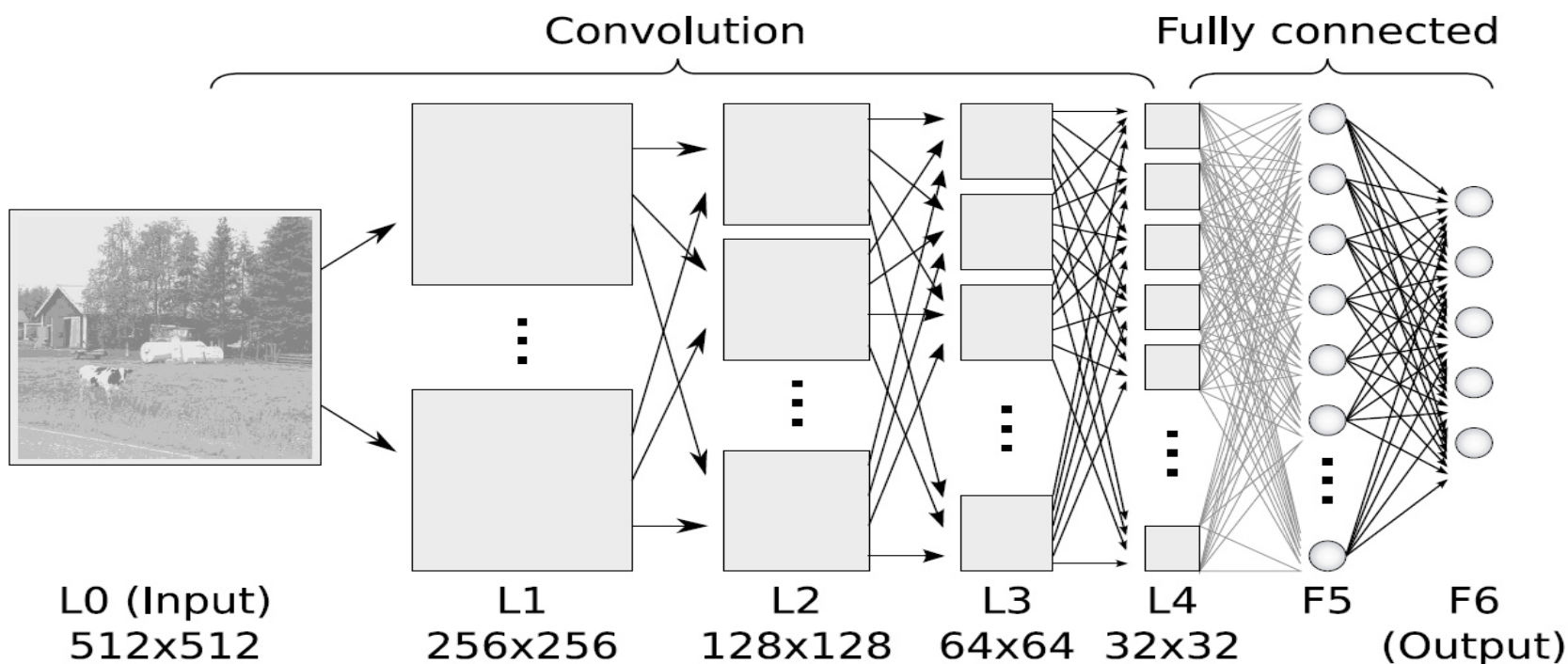


Using NGS RNA Expression for Differential Diagnosis and Immunoprofiling

Gene	Location	Sarcoma1	UHR	KTP-4	KTP-8	KTP-33	ALL	Sarcoma2
BCL10	chr1:85731459-85743771	0.32	0.83	1.25	0.96	1.39	0.90	1.25
BCL2	chr18:60790578-60986613	0.35	1.34	3.81	5.54	14.53	3.11	0.44
BCL6	chr3:187416046-187463513	3.46	1.06	9.55	13.43	18.82	0.81	0.91
CD19	chr16:28943259-28950668	0.71	1.31	293.21	347.17	326.02	616.33	0.17
CD22	chr19:35820068-35838264	1.20	1.16	254.48	269.75	364.59	72.56	0.77
PD-L1	chr9:5450502-5470567	0.66	0.76	8.61	2.72	2.84	0.32	2.95
CD28	chr2:204571197-204603636	0.20	0.96	0.92	0.33	0.20	0.01	0.08
CD36	chr7:80231503-80308593	55.63	1.09	2.17	18.38	2.41	0.68	33.44
CD44	chr11:35160416-35253949	1.12	1.04	1.52	1.10	0.15	0.32	0.54
CD58	chr1:117057155-117113715	0.66	0.83	2.09	2.36	0.73	13.98	1.79
CD70	chr19:6585849-6591163	0.04	1.17	0.57	0.30	0.46	0.01	2.68
CD74	chr5:149781199-149792499	15.85	1.42	79.83	74.79	34.99	35.51	14.01
CD79A	chr19:42381189-42385439	1.29	1.57	500.77	510.95	418.12	450.01	0.87
CD79B	chr17:62006097-62009704	4.02	1.74	1016.32	298.30	322.10	232.72	1.49
CD8A	chr2:87011727-87035519	1.76	1.44	84.78	57.25	25.55	5.40	22.40
CRLF2	chrX:1314893-1331616	0.34	1.23	0.22	0.26	0.26	211.16	0.22
KMT2D	chr12:49412757-49449107	0.81	1.04	1.80	1.32	1.34	1.89	0.62
MEF2D	chr1:156433512-156470634	1.90	1.41	2.30	2.20	1.41	3.05	1.31
MYC	chr8:128748314-128753680	0.14	0.92	0.16	0.16	0.20	0.07	0.25
PAX5	chr9:36833271-37034476	0.46	0.62	372.89	291.90	416.05	155.92	0.70
ZNF384	chr12:6775642-6798738	0.85	1.25	1.34	0.89	1.46	1.34	0.53
JAK2	chr9:4985244-5128183	1.46	0.87	2.66	2.31	1.58	1.95	1.65
FLT3	chr13:28577410-28674729	14.39	0.53	11.54	6.66	4.32	1044.77	2.51

Advances in Artificial Intelligence

- Pattern recognition (70s and 80s)
- Machine Learning (90s): choose an algorithm, and wait for the computations to finish
- ***Deep Learning (Today)***: Convolutional Neural Nets (CNN)



Utilizing Deep Learning/Artificial Intelligence (AI)

- Reducing subjectivity in:
 - Diagnosis
 - Predicting response
 - Predicting prognosis
 - Predicting relapse and MRD
- Laboratory Processes and procedures

Example - Quantifying and Capturing Image Data As Numerical Values

	A	C	D	E	F	G	H	I	J	K	L	M	N	O
1	File		File	Node	GatedOn	SubGate	X-marker	Y-marker	Weight	mean(X)	mean(Y)	cov(XX)	cov(XY)	cov(YY)
47840	673710	041287 00	673710	90	Lymphocytes 2	quad 4	CD10 APC	CD23 ECD	0.011421	387.627907	117.9767442	9890.838291	-1133.10168	11648.045
47841	673710	041287 00	673710	93	Lymphocytes 2	quad 1	CD5 APCA 700	CD23 ECD	0.074369	20.30178571	320.2214286	3234.217854	-66.2096811	4172.9009
47842	673710	041287 00	673710	93	Lymphocytes 2	quad 2	CD5 APCA 700	CD23 ECD	0.016733	465.4126984	284.6428571	8479.289997	-1331.20181	1569.4518
47843	673710	041287 00	673710	93	Lymphocytes 2	quad 3	CD5 APCA 700	CD23 ECD	0.129615	31.72233607	125.8688525	3896.493599	-179.630677	7586.5996
47844	673710	041287 00	673710	93	Lymphocytes 2	quad 4	CD5 APCA 700	CD23 ECD	0.779283	521.7597137	113.5185753	5222.165848	-74.8828918	4060.1538
47845	673710	041287 00	673710	168	Lymphocytes 2	gate 1	CD20 V450	CD19 PC5.5	5.31E-04	159.75	461.5	15546.1875	629.625	2297.25
47846	673710	041287 00	673710	168	Lymphocytes 2	gate 2	CD20 V450	CD19 PC5.5	0.069323	727.6762452	567.4482759	4802.138478	2428.94398	4289.0902
47847	673710	041287 00	673710	168	Lymphocytes 2	gate 3	CD20 V450	CD19 PC5.5	0.086985	383.2412214	52.04732824	7726.311278	2095.22828	5063.1137
47848	673710	041287 00	673710	168	Lymphocytes 2	gate 4	CD20 V450	CD19 PC5.5	0.843161	19.26492361	45.40384312	2735.92824	195.819615	3276.7098
47849	673710	041288 00	673710	165	CD45 KO+CD16 FITC	gate 1	CD45 KO	CD16 FITC	1	527.8291021	345.6703944	11327.80971	2881.07371	64451.797
47850	673710	041288 00	673710	103	Mononuclear 3	quad 1	CD117 PC5.5	CD34 APC	0.012956	107.1961722	620.5645933	6721.028502	-80.8954465	2626.3510
47851	673710	041288 00	673710	103	Mononuclear 3	quad 2	CD117 PC5.5	CD34 APC	0.019092	468.4090909	633.7207792	5442.780697	684.812279	3529.1817
47852	673710	041288 00	673710	103	Mononuclear 3	quad 3	CD117 PC5.5	CD34 APC	0.933734	52.8706101	165.372303	3858.700579	1388.99672	13445.287
47853	673710	041288 00	673710	103	Mononuclear 3	quad 4	CD117 PC5.5	CD34 APC	0.034218	409.4583333	275.4746377	5826.943916	3622.15021	15810.227
47854	673710	041288 00	673710	104	Mononuclear 3	quad 1	HLA-DR PB	CD34 APC	1.86E-04	219	738.3333333	24000.66667	-23622.3333	23994.888
47855	673710	041288 00	673710	104	Mononuclear 3	quad 2	HLA-DR PB	CD34 APC	0.027833	627.467706	641.4209354	14187.25118	-393.553221	1950.9831
47856	673710	041288 00	673710	104	Mononuclear 3	quad 3	HLA-DR PB	CD34 APC	0.643628	100.6548204	205.2509872	12382.15746	4631.36575	8721.1853
47857	673710	041288 00	673710	104	Mononuclear 3	quad 4	HLA-DR PB	CD34 APC	0.328354	608.3575609	103.193317	20834.43964	-4093.8288	18730.590
47858	673710	041288 00	673710	105	Mononuclear 3	quad 1	CD33 PC7	CD34 APC	0.016799	90.60147601	628.0738007	7723.317193	-155.701216	2916.5406
47859	673710	041288 00	673710	105	Mononuclear 3	quad 2	CD33 PC7	CD34 APC	0.014381	403.0474138	635.4784483	8179.157235	-1445.91493	2944.6719
47860	673710	041288 00	673710	105	Mononuclear 3	quad 3	CD33 PC7	CD34 APC	0.8136	33.17074286	183.9835429	2481.695266	1726.29645	12063.420
47861	673710	041288 00	673710	105	Mononuclear 3	quad 4	CD33 PC7	CD34 APC	0.155219	515.6034345	94.05990415	7393.591538	-5792.00899	17599.292
47862	673710	041288 00	673710	105	Mononuclear 3	quad 1	CD33 PC7	CD34 APC	0.833183	101.1833333	638.1313848	5383.61368	-175.518388	3885.8183

Recent NeoGenomics Filed Patents

Date

10/02/14	Methods for early detection of esophageal cancer
03/13/14	Automated fish reader using learning machines
11/13/14	Compositions and methods for detecting and determining a prognosis for prostate cancer
05/12/16	Deep sequencing of peripheral blood plasma DNA as a reliable test for confirming the diagnosis of myelodysplastic syndrome
05/12/16	Determining tumor load and biallelic mutation in patients with CALR mutation using peripheral blood plasma
06/16/16	Automated flow cytometry analysis method and system
11/24/16	Method to increase sensitivity of next generation sequencing
01/05/17	Method for high sensitivity detection of MYD88 mutations
02/23/17	High-sensitivity sequencing to detect BTK inhibitor resistance

Prostate Cancer Is the Most Common Cancer in Men

Estimated New Cases

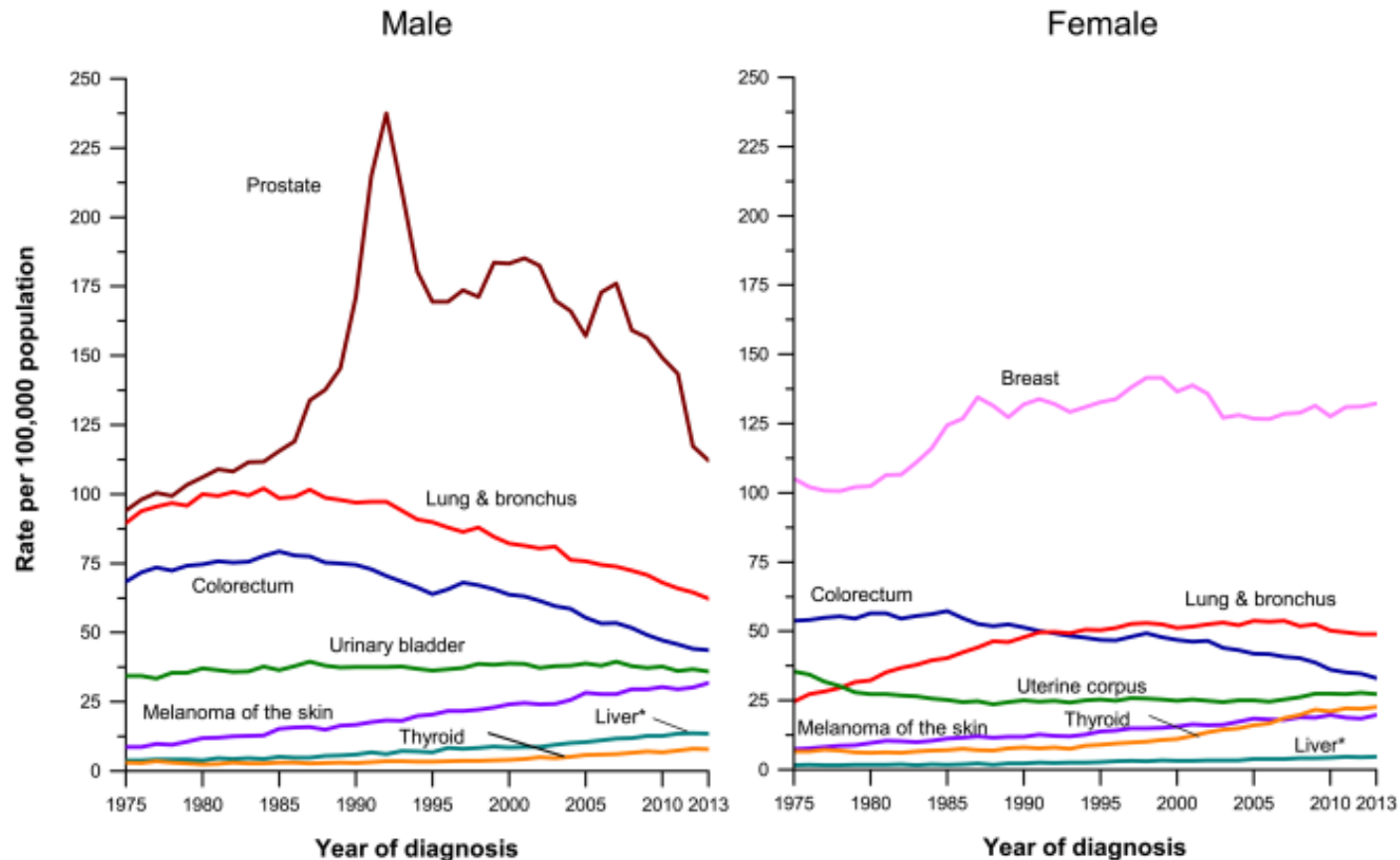
			Males	Females			
Prostate	161,360	19%			Breast	252,710	30%
Lung & bronchus	116,990	14%			Lung & bronchus	105,510	12%
Colon & rectum	71,420	9%			Colon & rectum	64,010	8%
Urinary bladder	60,490	7%			Uterine corpus	61,380	7%
Melanoma of the skin	52,170	6%			Thyroid	42,470	5%
Kidney & renal pelvis	40,610	5%			Melanoma of the skin	34,940	4%
Non-Hodgkin lymphoma	40,080	5%			Non-Hodgkin lymphoma	32,160	4%
Leukemia	36,290	4%			Leukemia	25,840	3%
Oral cavity & pharynx	35,720	4%			Pancreas	25,700	3%
Liver & intrahepatic bile duct	29,200	3%			Kidney & renal pelvis	23,380	3%
All Sites	836,150	100%			All Sites	852,630	100%

Estimated Deaths

			Males	Females			
Lung & bronchus	84,590	27%			Lung & bronchus	71,280	25%
Colon & rectum	27,150	9%			Breast	40,610	14%
Prostate	26,730	8%			Colon & rectum	23,110	8%
Pancreas	22,300	7%			Pancreas	20,790	7%
Liver & intrahepatic bile duct	19,610	6%			Ovary	14,080	5%
Leukemia	14,300	4%			Uterine corpus	10,920	4%
Esophagus	12,720	4%			Leukemia	10,200	4%
Urinary bladder	12,240	4%			Liver & intrahepatic bile duct	9,310	3%
Non-Hodgkin lymphoma	11,450	4%			Non-Hodgkin lymphoma	8,690	3%
Brain & other nervous system	9,620	3%			Brain & other nervous system	7,080	3%
All Sites	318,420	100%			All Sites	282,500	100%

CA: A Cancer Journal for Clinicians
 Volume 67, Issue 1, pages 7-30,
 5 JAN 2017 DOI:
 10.3322/caac.21387
<http://onlinelibrary.wiley.com/doi/10.3322/caac.21387/full#caac.21387-fig-0001>

Over Diagnosis Of Prostate Cancer and the Effects US Preventive Task Force



CA: A Cancer Journal for Clinicians

Volume 67, Issue 1, pages 7-30, 5 JAN 2017 DOI: 10.3322/caac.21387

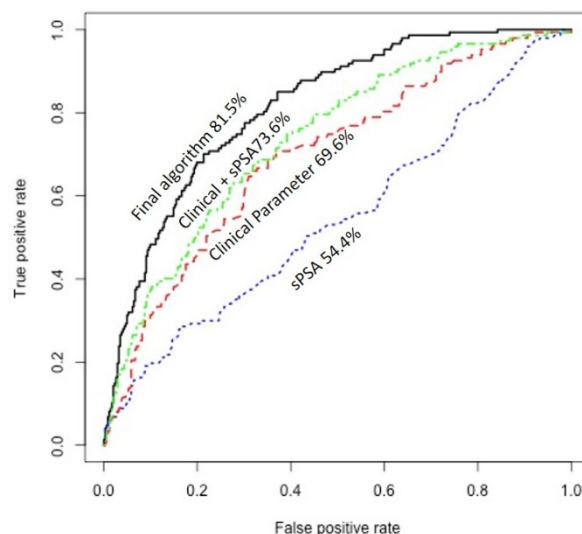
<http://onlinelibrary.wiley.com/doi/10.3322/caac.21387/full#caac21387-fig-0003>

Currently Unmet Needs in Prostate Cancer Screening and Management

- Better Screening approach
- Reducing unnecessary biopsies
- Reducing overtreatment
- Better selection of patients for active Surveillance
better monitoring

Combined Urine and Plasma Biomarkers are Highly Accurate for Predicting High Grade Prostate Cancer

Urine/Plasma Assay (**NeoLAB Liquid Biopsy**) for predicting Gleason $\geq 3+4$ using cell-free RNA (cfRNA) levels of UAP1, PDLIM5, IMPDH2, HSPD1, PCA3, PSA, TMPRSS2, ERG, AR, PTEN, and ERG
Clinical Parameters: sPSA, age, race, history of prior Bx, DRE



Multi-Center Prospective Study of **489 Patients**

	Cut-off	Sensitivity		Specificity		NPV		PPV		Total
		$\geq 3+4$	$\geq 4+3$	$\geq 3+4$	$\geq 4+3$	$\geq 3+4$	$\geq 4+3$	$\geq 3+4$	$\geq 4+3$	Missed
Actual										
Predicted positive	Low	86%	96%	57%	59%	90%	98%	46%	46%	21 (4.3%)
	Standard	91%	97%	51%	44%	93%	98%	44%	52%	13 (2.7%)
	High	97%	99%	36%	37%	97%	99%	40%	40%	4 (0.8%)

Predicting Prostatectomy Findings

Objective: Clinical validation of the Urine/Plasma test using Prostatectomy data

Age (Median, Min-Max)	61 (36-77)
Prostate size (gm) (Median, Min-Max)	34 (9.22-160)
Gleason	
3+3	90 (29.4%)
3+4	122 (39.8%)
4+3	50 (16.3%)
3+5, 4+4, 4+5, 5+4	44 (14.4%)
sPSA (ng/ml) (Median, Min-Max)	
≤4	62 (20%)
4 to 10	198 (65%)
>10	46 (15%)
Race	
Caucasian	246 (80.4%)
African American	50 (16.3%)
Hispanic	1 (0.3%)
Asian	1 (0.0.3%)
Missing	8 (2.6%)
DRE	
Normal	202 (66%)
Abnormal	64 (21%)
Unknown	40 (13%)
Family Hx	
No	188 (61.4%)
Yes	93 (30.3%)
Unknown	25 (8.2%)
Stage	

Stage	
T1	90 (29%)
T1a	50 (16%)
T1b	20 (7%)
T1c	122 (40%)
T2	1 (0.3%)
T2a	5 (2%)
T2b	14 (5%)
T2c	4 (1%)
Bx performed by	
Ultrasound	304 (99%)
MRI	2 (1%)
Prostate sizedetermined by	
TRUS-Ultrasound	293 (96%)
MRI	10 (3%)
Unknown	3 (1%)

NeoLAB Liquid Biopsy Test is More Accurate Than Biopsy in Predicting Prostatectomy Results

Urine/Plasma Test in Predicting **Biopsy** Findings

	High sensitivity			Standard sensitivity			Low sensitivity		
	Value	Lower Limit	Upper Limit	Value	Lower Limit	Upper Limit	Value	Lower Limit	Upper Limit
Sensitivity	95%	91%	98%	92%	87%	95%	88%	83%	92%
PPV	71%	65%	76%	70%	65%	76%	70%	64%	75%
NPV	29%	10%	58%	28%	13%	50%	22%	10%	40%

Discrepancy Between Biopsy and Prostatectomy

Upgraded		Downgraded	
Gleason Score	No (%)	Gleason Score	No (%)
3+3 to 3+4	49 (16%)	3+4 to 3+3	11 (4%)
3+3 to 4+3	9 (3%)	4+3 to 3+3	1 (0.3%)
3+4 to 4+3	14 (5%)	4+4 to 3+3	1(0.3%)
3+4 to 4+4	2 (1%)	4+4 to 3+4	2 (0.7%)
3+4 to 4+5	2 (1%)	4+4 to 4+3	11 (4%)
4+3 to 4+4	3 (1%)	4+5 to 4+3	8 (3%)
4+3 to 5+4	1 (0.3%)	5+4 to 4+5	1 (0.3%)
4+4 to 4+5	1 (0.3%)	5+5 to 4+5	1 (0.3%)
4+5 to 5+4	1 (0.3%)		
Total	82 (27%)	Total	36 (12%)

Urine/Plasma Test in Predicting **Prostatectomy** Findings

	High sensitivity			Standard sensitivity			Low sensitivity		
	Value	Lower Limit	Upper Limit	Value	Lower Limit	Upper Limit	Value	Lower Limit	Upper Limit
Sensitivity	97%	94%	99%	94%	90%	96%	92%	87%	95%
PPV	87%	82%	90%	87%	83%	91%	87%	83%	91%
NPV	43%	19%	70%	36%	19%	57%	31%	17%	50%

Sensitivity and Specificity of Prostate **Biopsy in Predicting Prostatectomy** Findings

	Estimated Value	95% Confidence Interval	
		Lower Limit	Upper Limit
Sensitivity	78%	72%	83%
Specificity	71%	55%	83%
PPV	94%	90%	97%
NPV	36%	26%	46%

NeoLAB Prostate Test Indications

- Prior to performing biopsy
- When Biopsy findings are questionable
- To determine if patients patient should be put on active surveillance
- To monitor patients on Active Surveillance

Independent Validation of NeoLAB Prostate Testing Performed in Odense University, Denmark

Pre-Bx samples (41 patients)

Pre/High sensitivity			
	Estimated	95 % Confidence Interval	
	Value	Lower Limit	Upper Limit
Sensitivity	100 %	63 %	100 %
Specificity	56 %	38 %	73 %
PPV	39 %	20 %	61 %
NPV	100 %	78 %	100 %

Pre/standard and low			
	Estimated	95 % Confidence Interval	
	Value	Lower Limit	Upper Limit
Sensitivity	100 %	63 %	100 %
Specificity	63 %	44 %	78 %
PPV	43 %	23 %	66 %
NPV	100 %	80 %	100 %

Post-Bx samples (41 patients)

Post/high and standard			
	Estimated	95 % Confidence Interval	
	Value	Lower Limit	Upper Limit
Sensitivity	89 %	51 %	99 %
Specificity	28 %	14 %	47 %
PPV	26 %	13 %	45 %
NPV	90 %	54 %	99 %

Post/Low			
	Estimated	95 % Confidence Interval	
	Value	Lower Limit	Upper Limit
Sensitivity	89 %	51 %	99 %
Specificity	34 %	19 %	53 %
PPV	28 %	13 %	47 %
NPV	92 %	60 %	100 %

Key Takeaways

- ✓ Rapid and continuous innovation to improve patient care
- ✓ Utilization of cutting edge science and technologies.
- ✓ Multiple proprietary technologies
- ✓ Extensive menu of multi-modality tumor profiles
- ✓ Leading provider of Liquid Biopsies



Questions and Answers

This Concludes our Investor Day Presentations. Thank you for joining us. Should you have any questions on any of these materials, please contact:

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Thank you for joining us.

