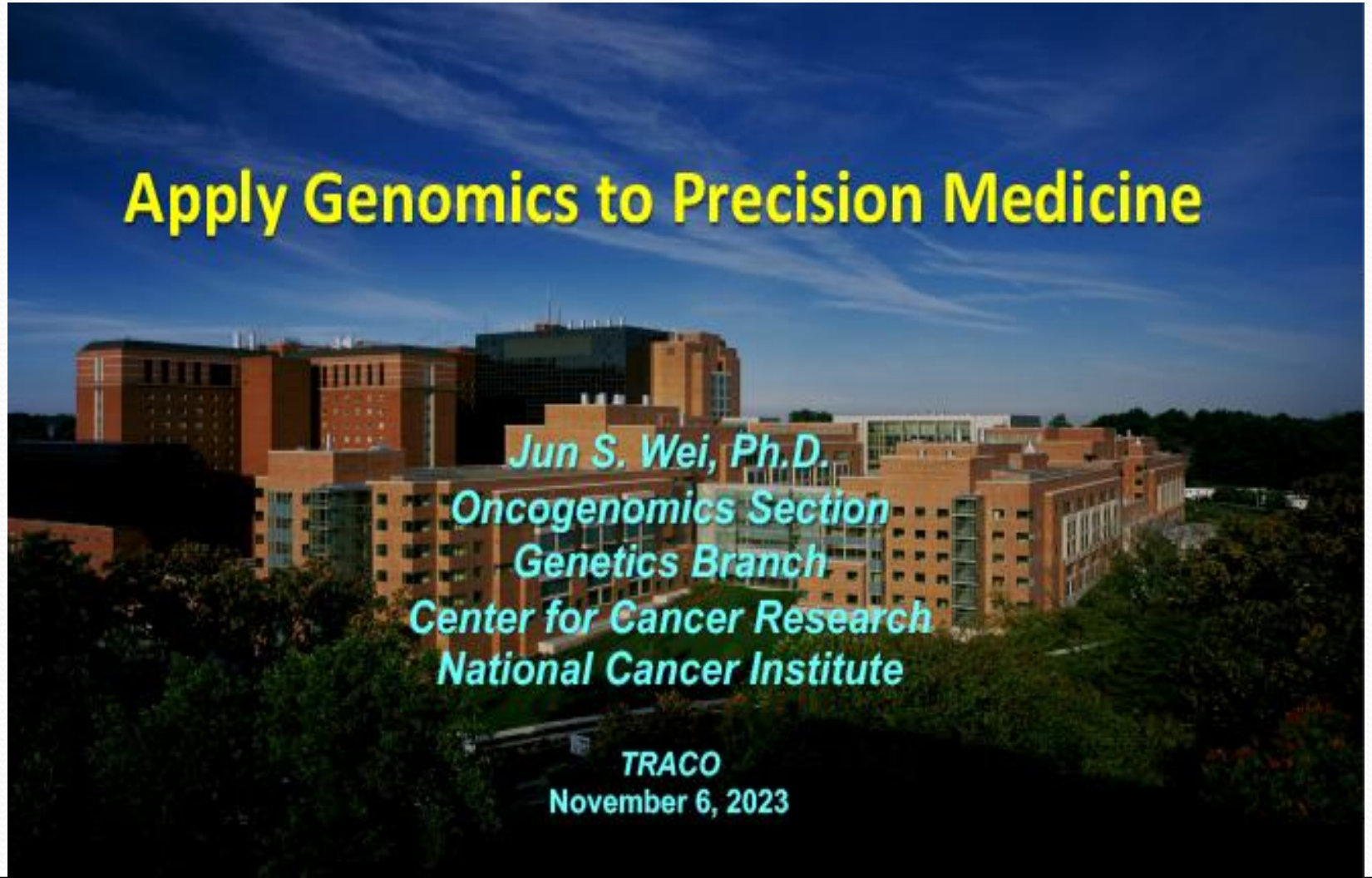
Apply genomics to precision medicine



Outline

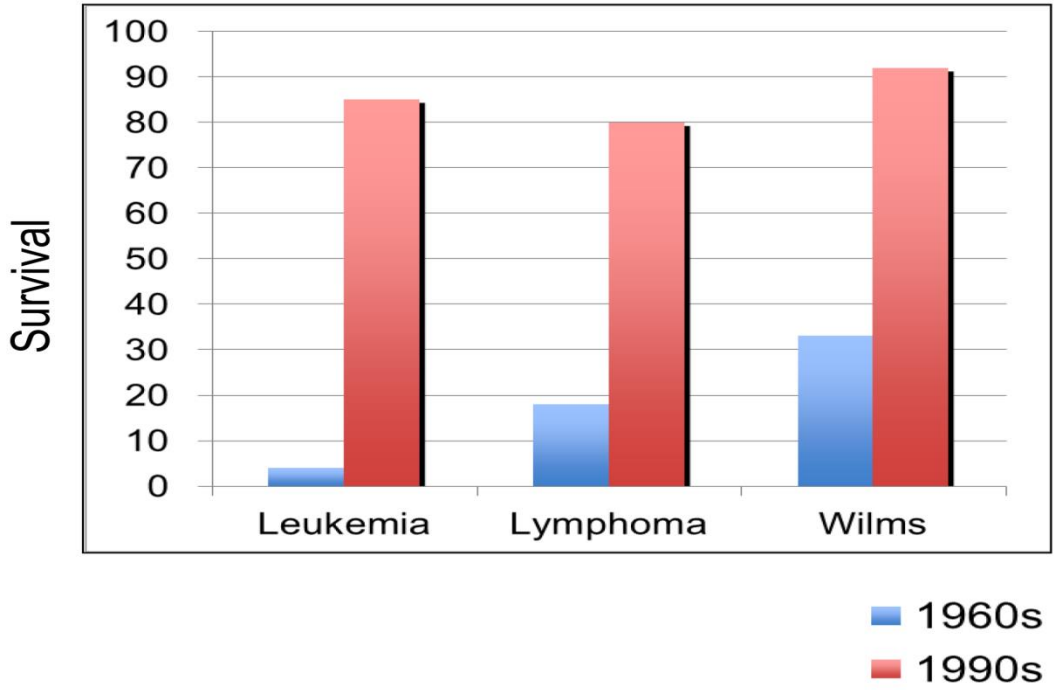
Outline

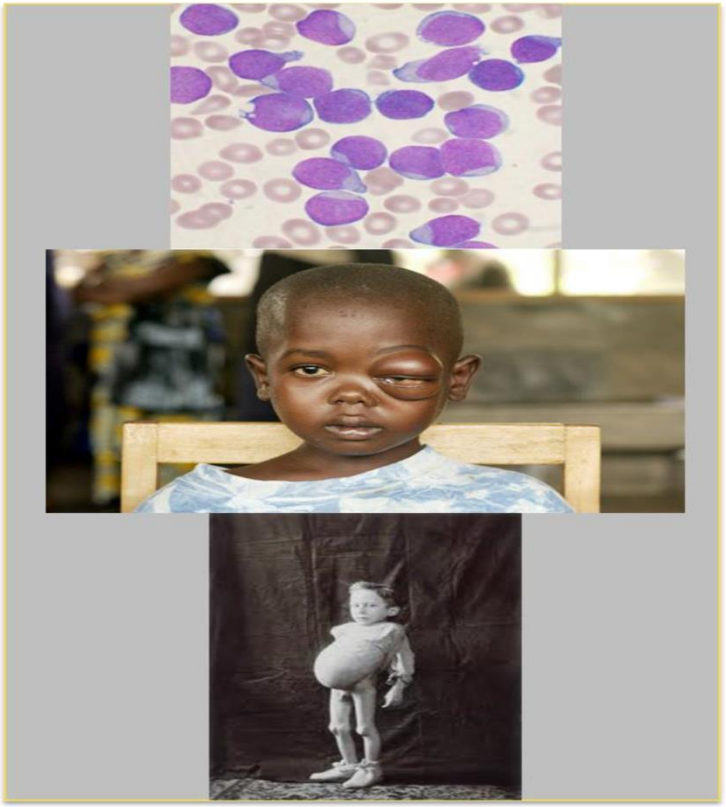
- Success and Challenges of Treating Pediatric Cancers
- Genomics
- Tool to study genomics: Next-generation Sequencing
- Precision medicine – an application of genomics

Childhood cancer

National Cancer Institute

Childhood cancer: The beginning of a modern medical success story



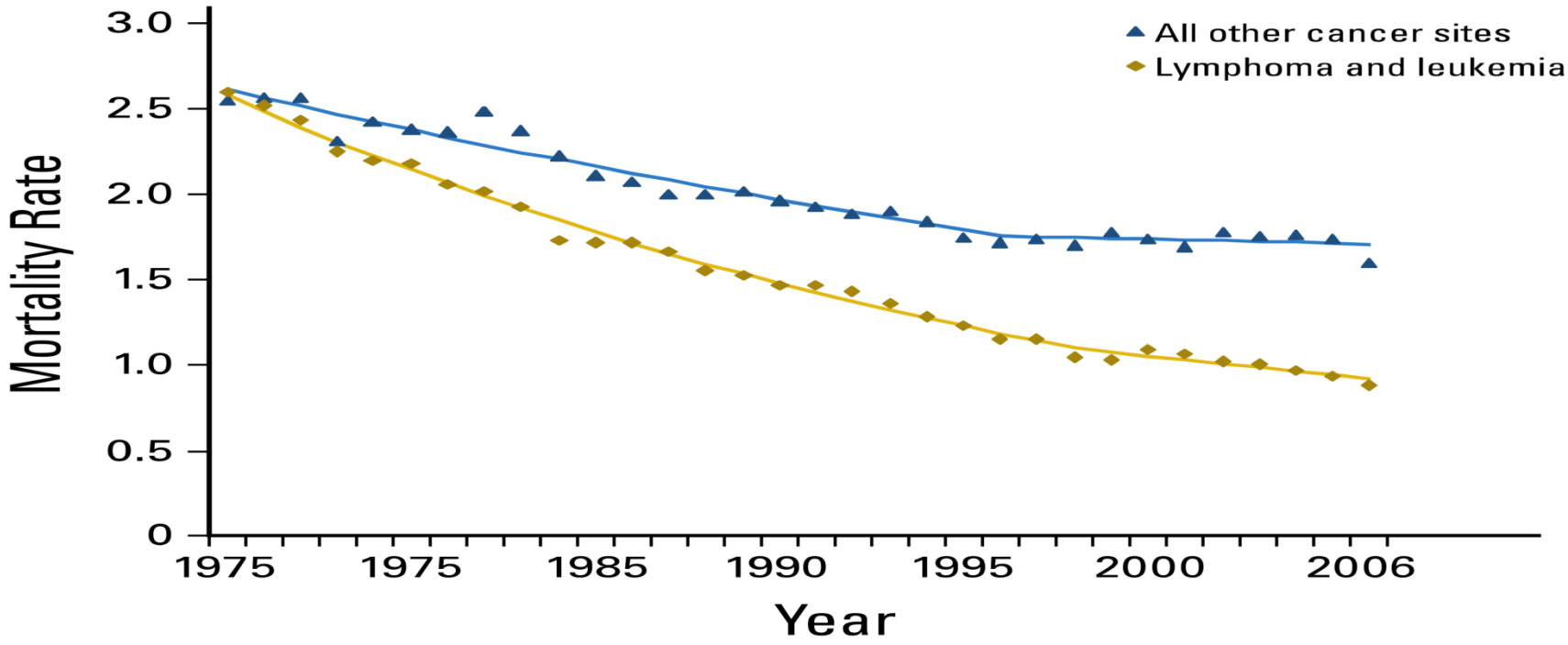


Courtesy: John Maris

Mortality rates

National Cancer Institute

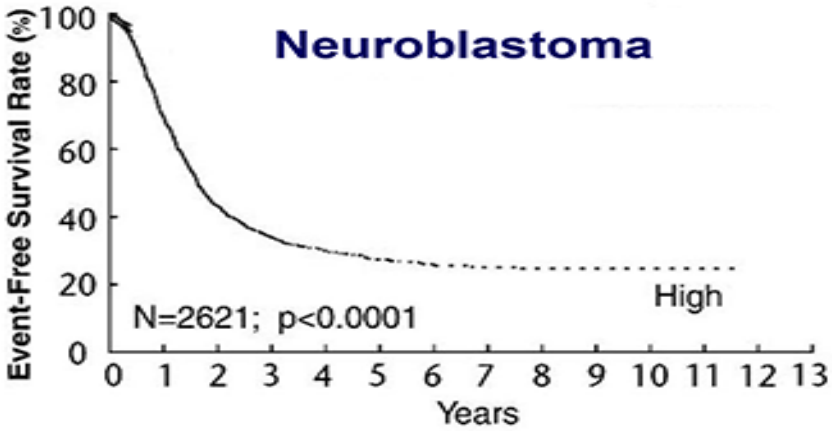
However in the past 16 years no improvement in mortality rates despite increased intensity of treatment

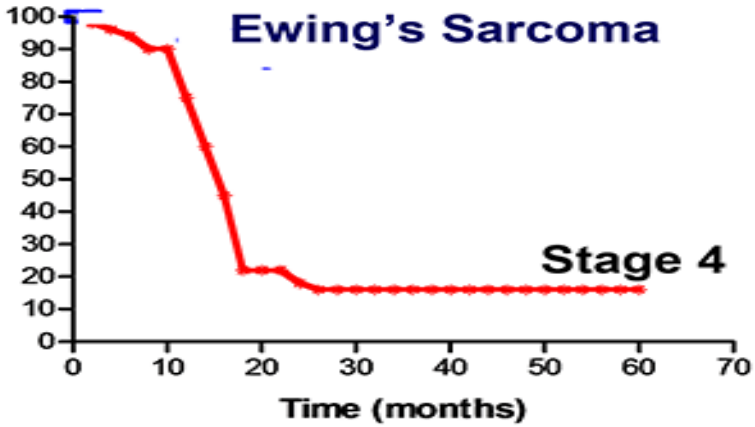


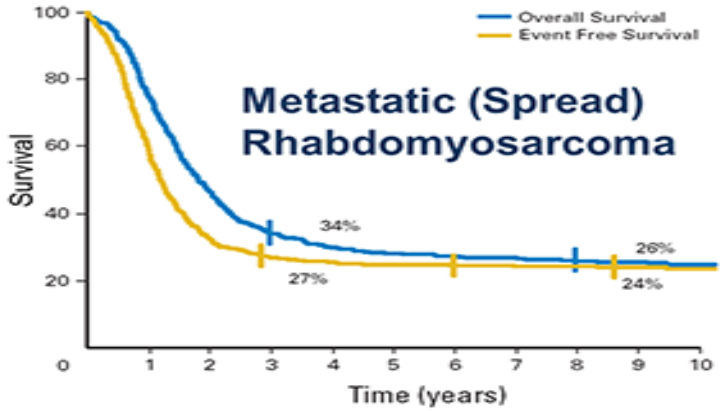
Courtesy: Malcolm Smith

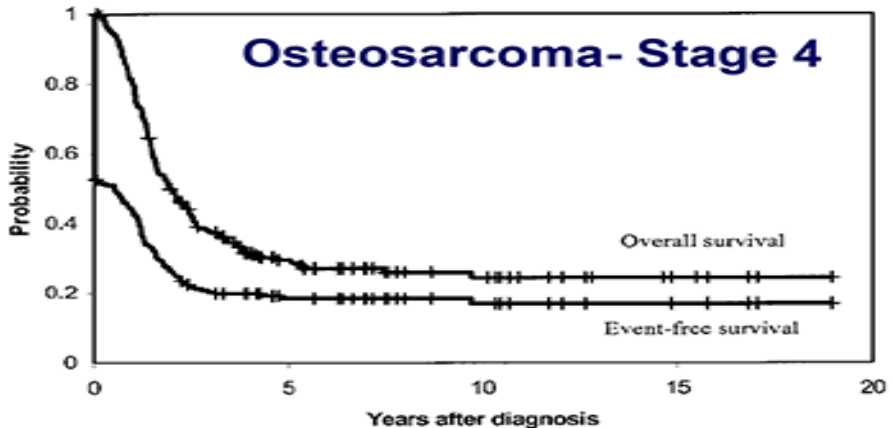
Pediatric cancers

Metastatic, Recurrent, & Refractory Disease Remains Incurable









Gene expression

The dramatic consequences of gene expression in biology

Anise swallowtail, *Papilio zelicaon*

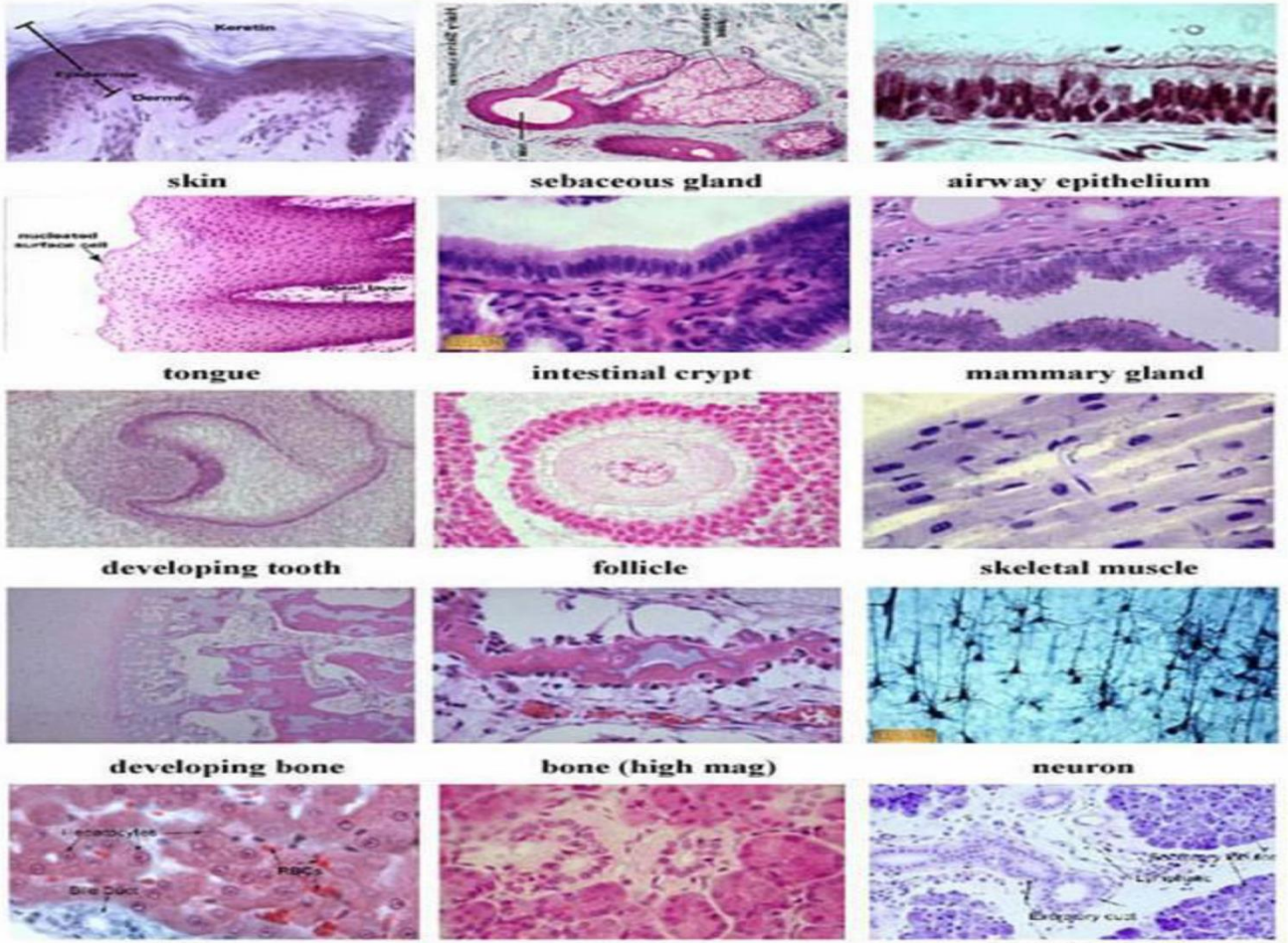
Same genome →
Different expression pattern
Different proteome
Different tissues
Different physiology

Gene expression

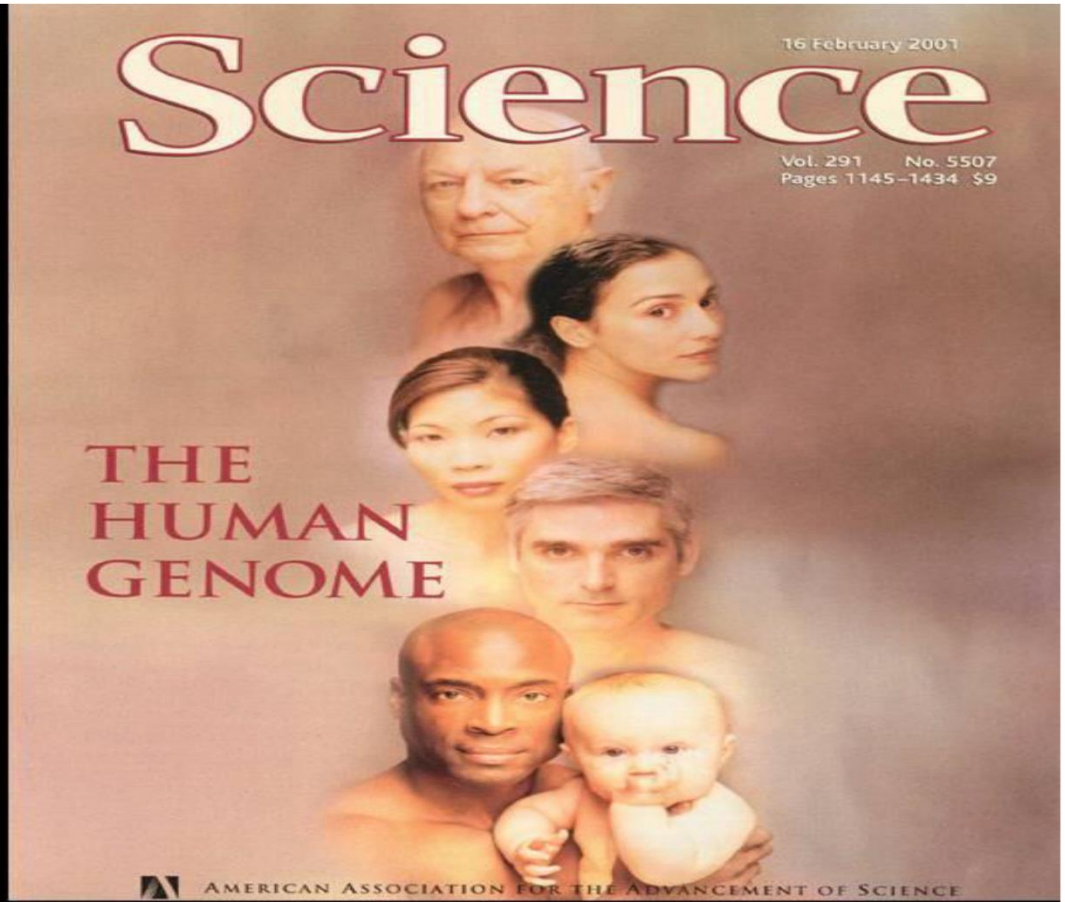
...but the complexity and diversi

Same genome or DNA →

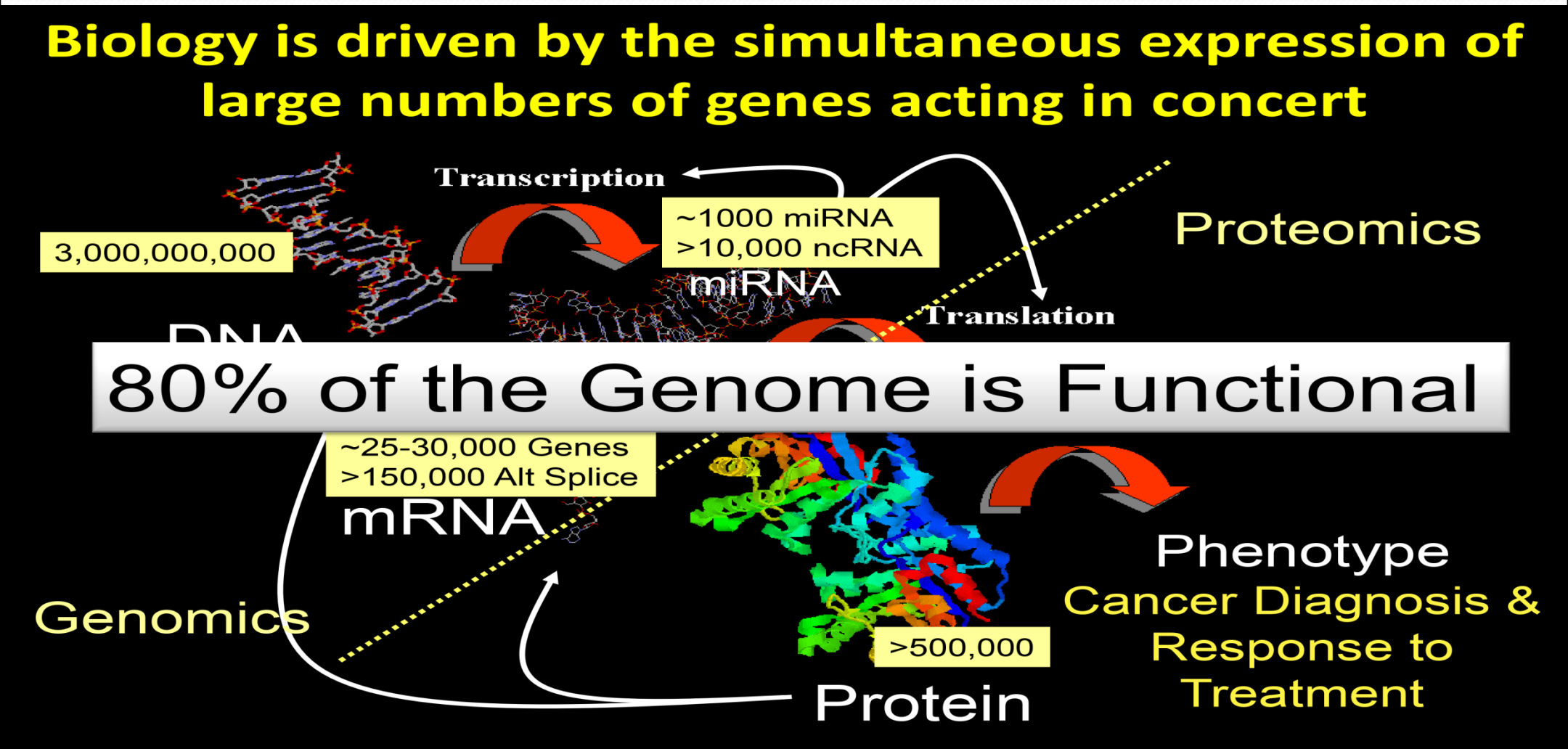
- Different expression pattern
- Different proteome
- Different tissues
- Different physiology



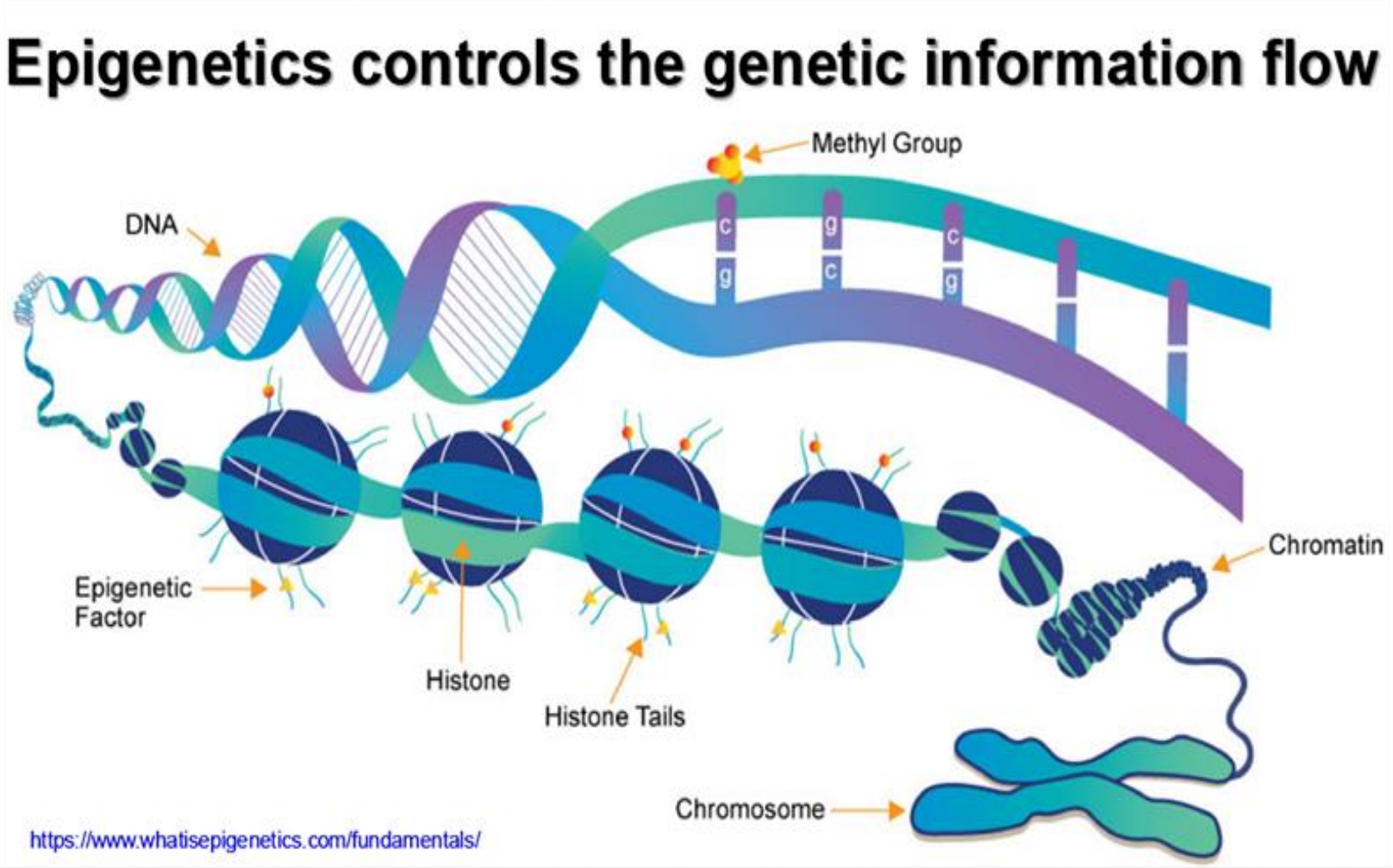
Human genome



Gene expression



Epigenetics



Challenge

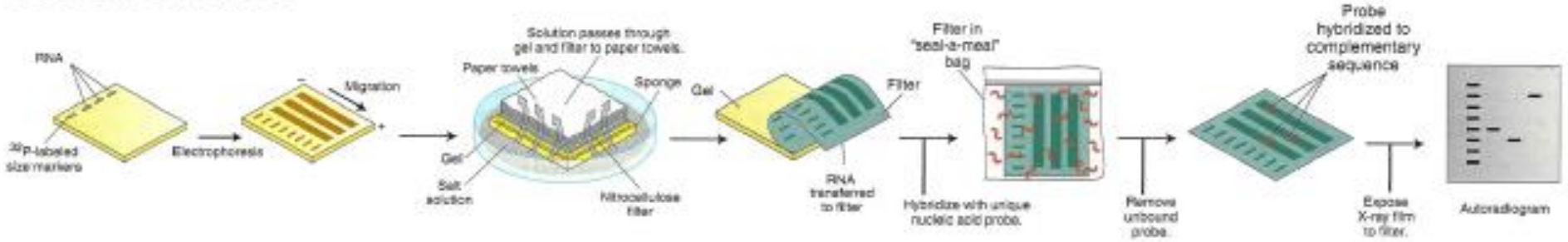
Challenge: how to measure/detect genes and their products in a massively parallel way?

- **High-throughput technologies**
- **Computational power**

Gene expression

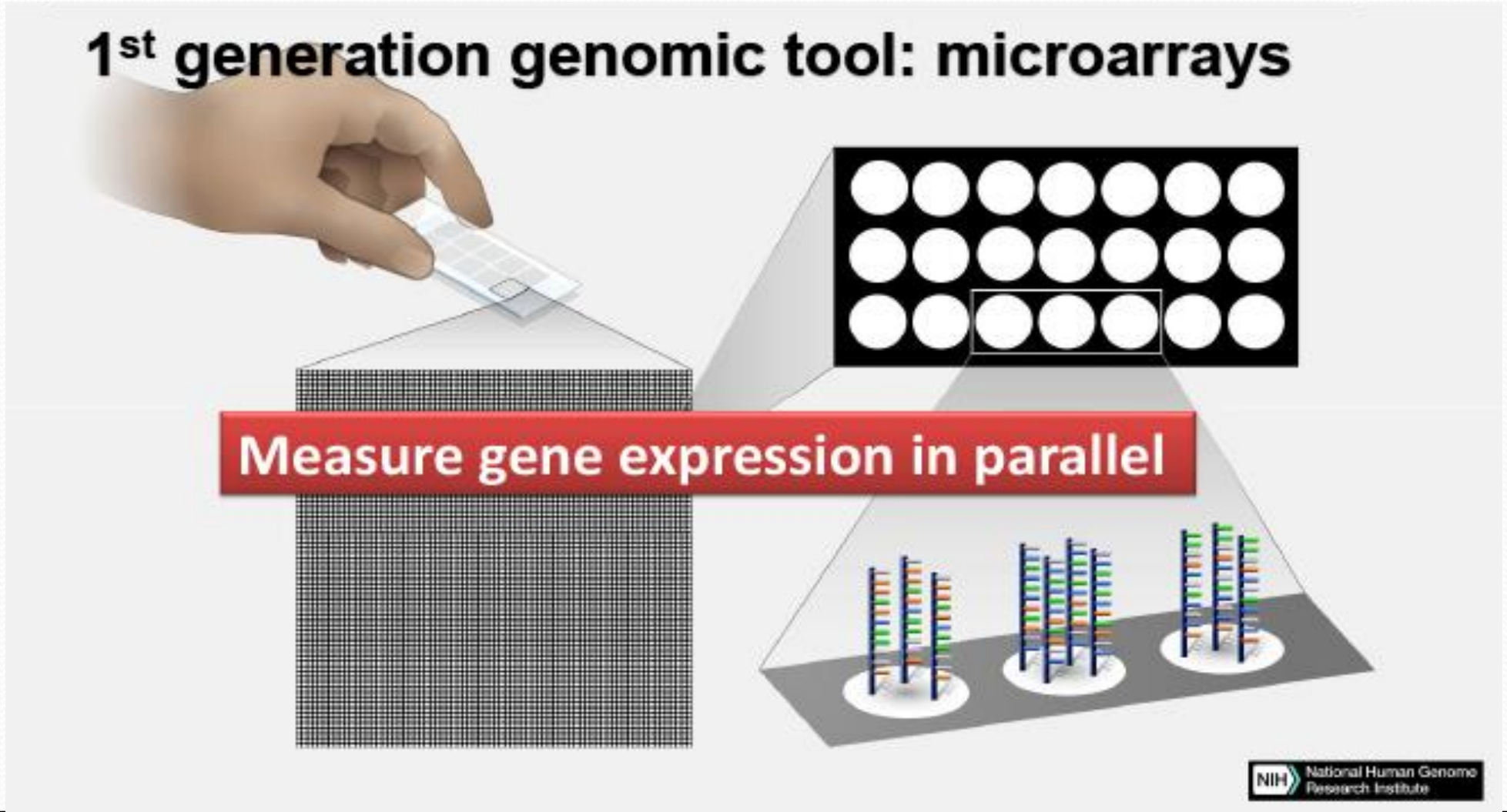
How to measure the expression of genes

Northern blot

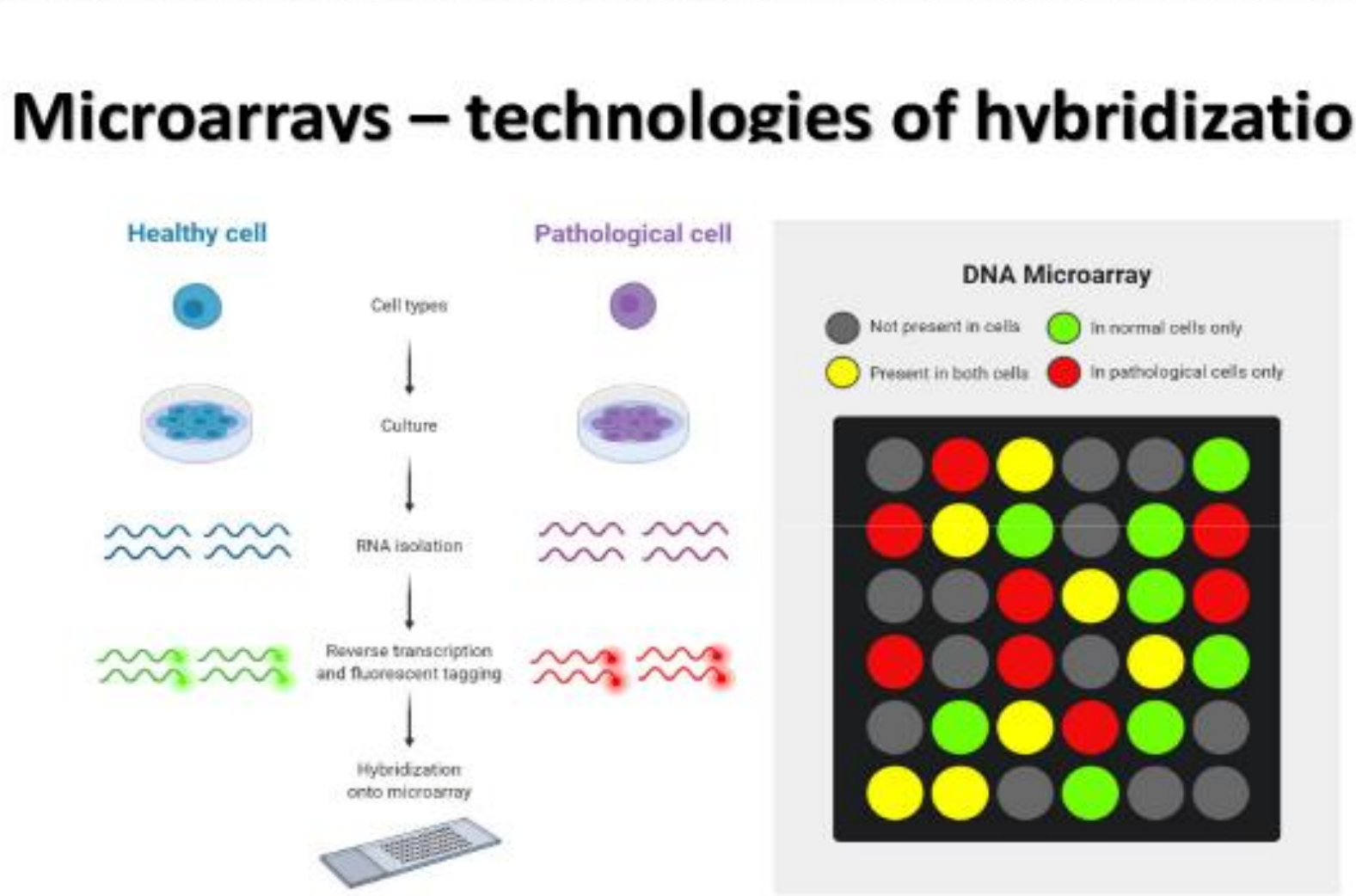


laborious and low throughput

Microarrays

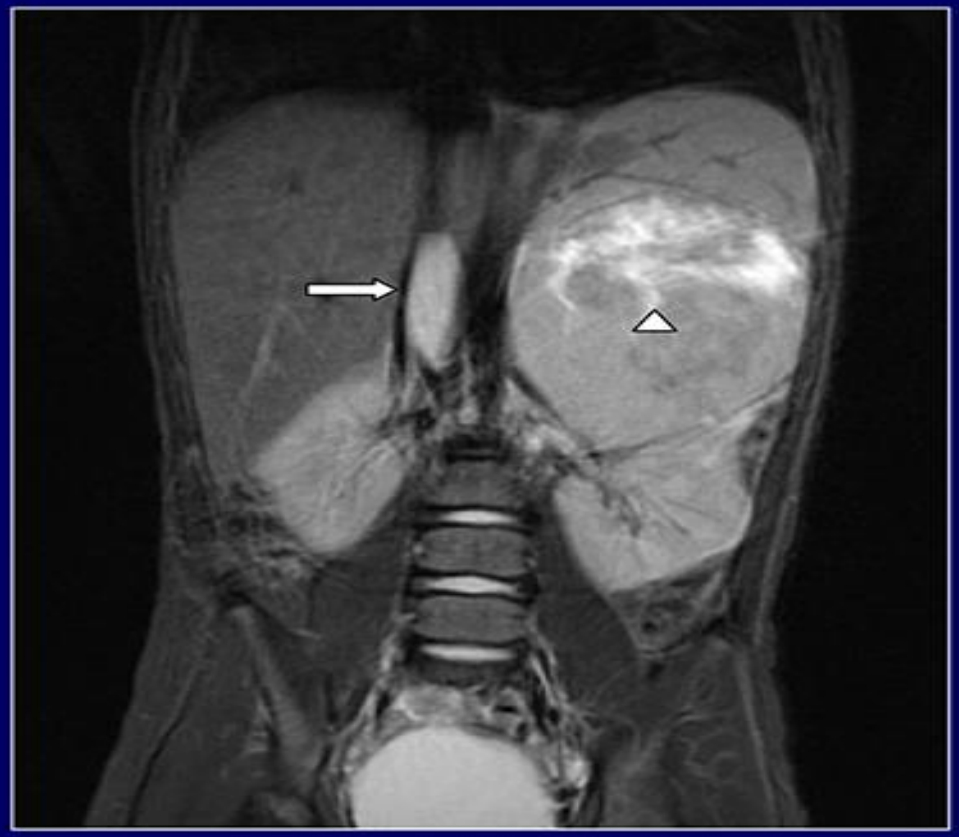


Microarrays

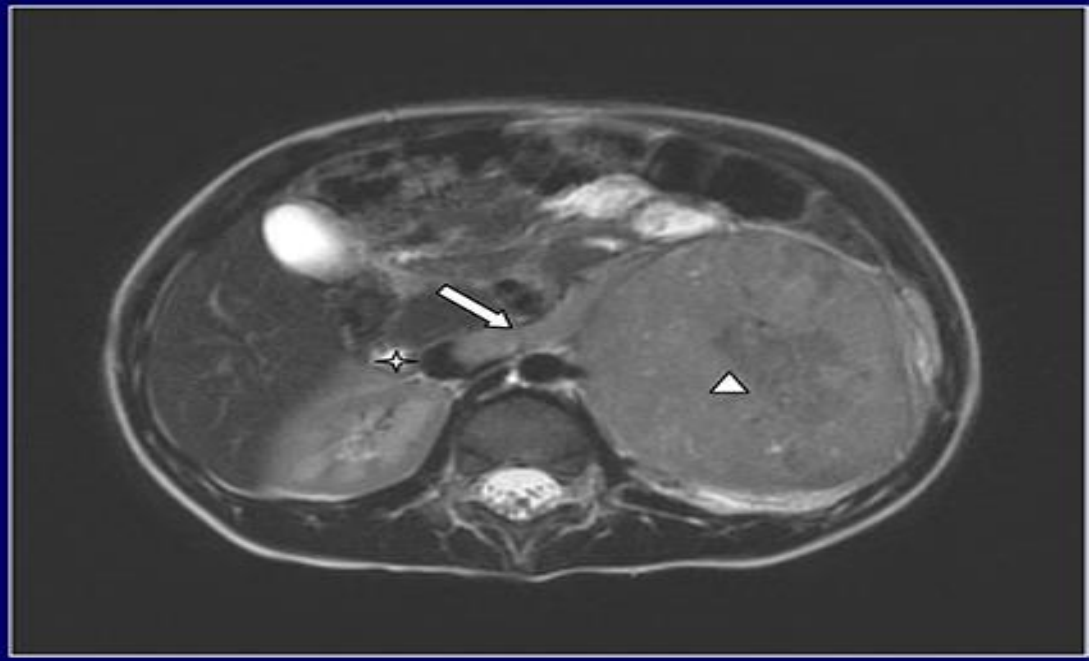


Wilms tumor

MRI: 9 x 8 x 9 cm mass in upper pole left kidney, tumor in Left renal vein and inferior vena cava

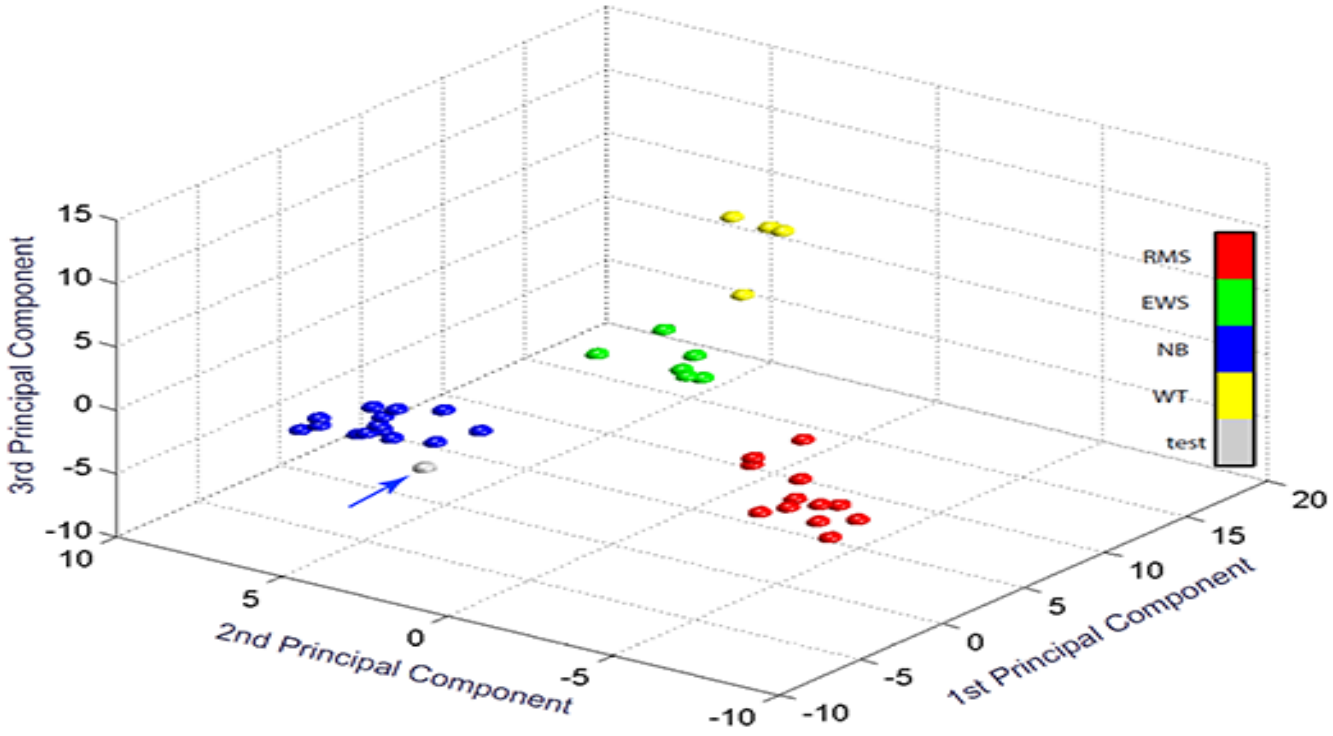


Initial diagnosis: Wilm's tumor



Cancer diagnosis

Diagnosis of cancers using gene expression profiles



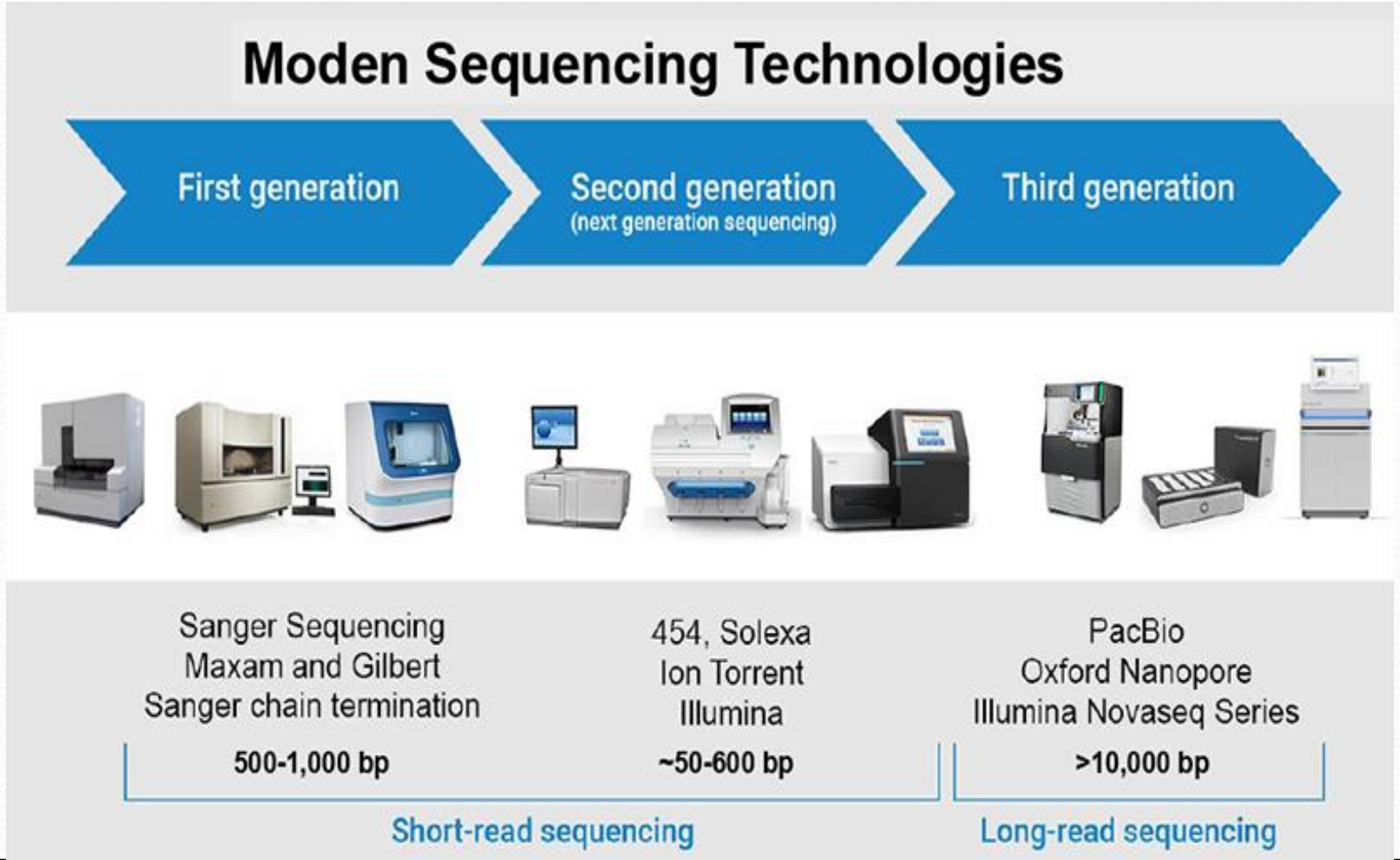
Wilm's tumor

↓

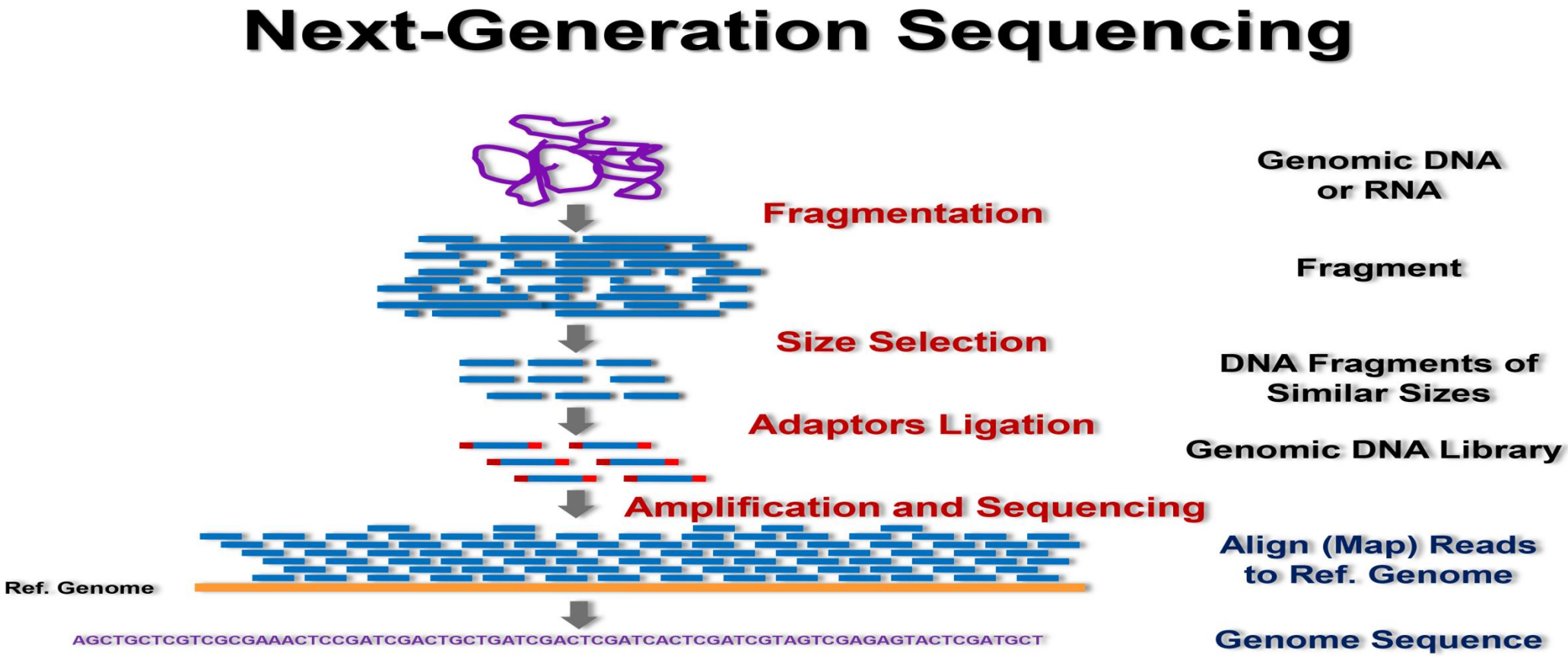
Neuroblastoma

- **Patient was switched to high risk neuroblastoma treatment included stem cell transplant**
- **Doing well 1 yr after diagnosis**

Sequencing

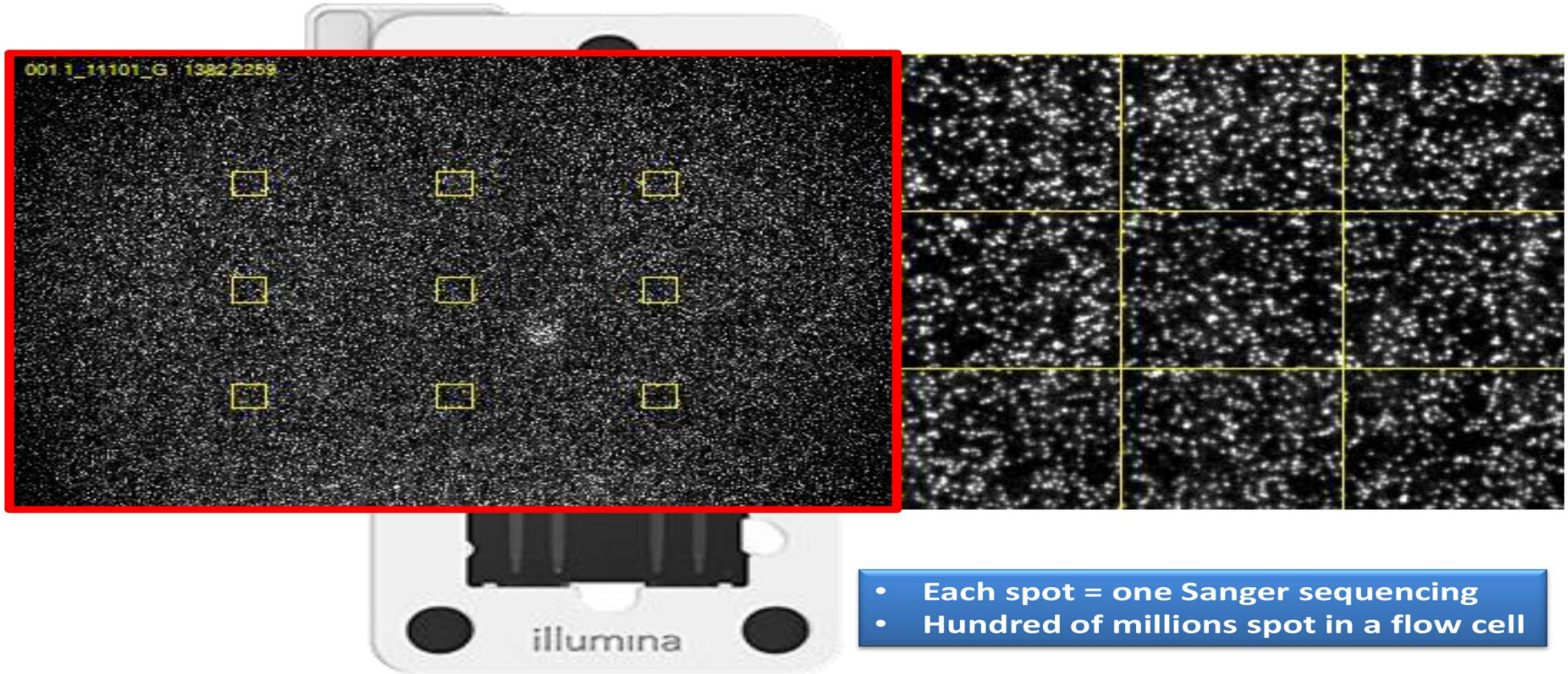

Moden Sequencing Technologies
First generation
Second generation
(next generation sequencing)
Third generation
Sanger Sequencing
Maxam and Gilbert
Sanger chain termination
500-1,000 bp
454, Solexa
Ion Torrent
Illumina
~50-600 bp
PacBio
Oxford Nanopore
Illumina Novaseq Series
>10,000 bp
Short-read sequencing
Long-read sequencing

Next-generation sequencing



Massively Parallel Sequencing

Massively Parallel Sequencing



- Each spot = one Sanger sequencing
- Hundred of millions spot in a flow cell

Desktop sequencers

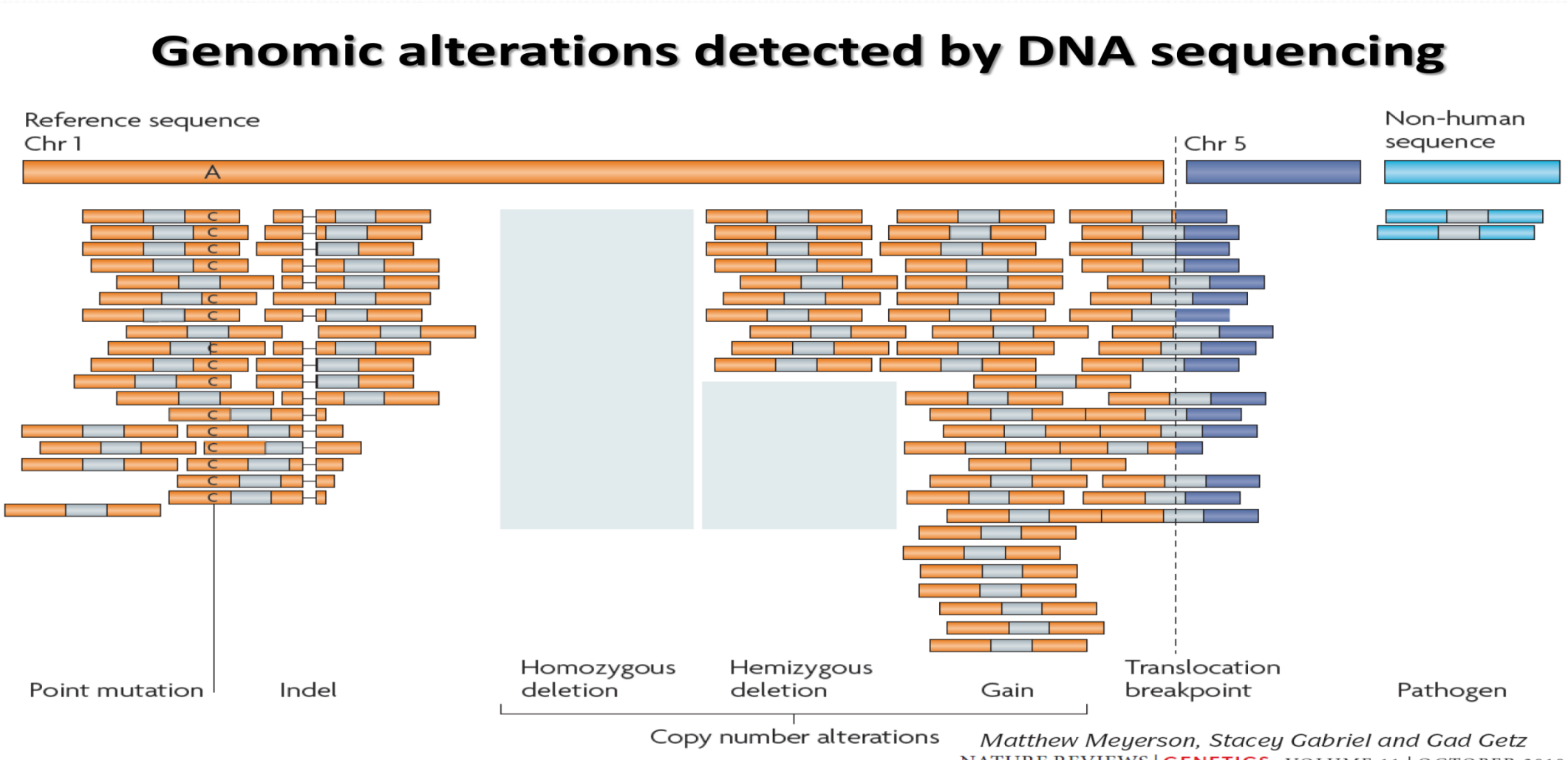
Modern desktop sequencers

Patterned
Flow Cell

Super-Resolution
Optics

- 1.2 billion reads
- 400 Gb (~133 human genomes)
- <40 hours

Genomic Alterations



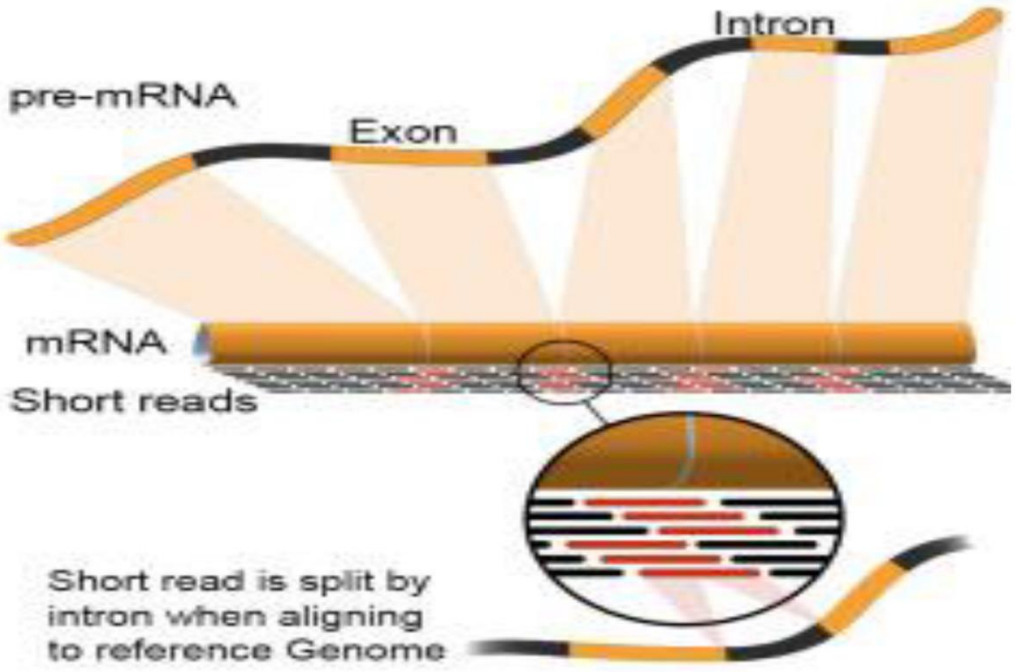
Sequencing

Next-generation sequencing: a platform for many applications to study genome and epigenome

- **No prior knowledge is needed for probe design as in microarrays**
- **Massive capacity at a base-pair resolution**
  - Then: *~13 years for the 1st human genome* using Sanger sequencing by *20 centers in 7 countries*
  - Now: *multiple human genomes in 2 days* using a NGS sequencer
- **A single platform for different types of genomic and epigenomic information**

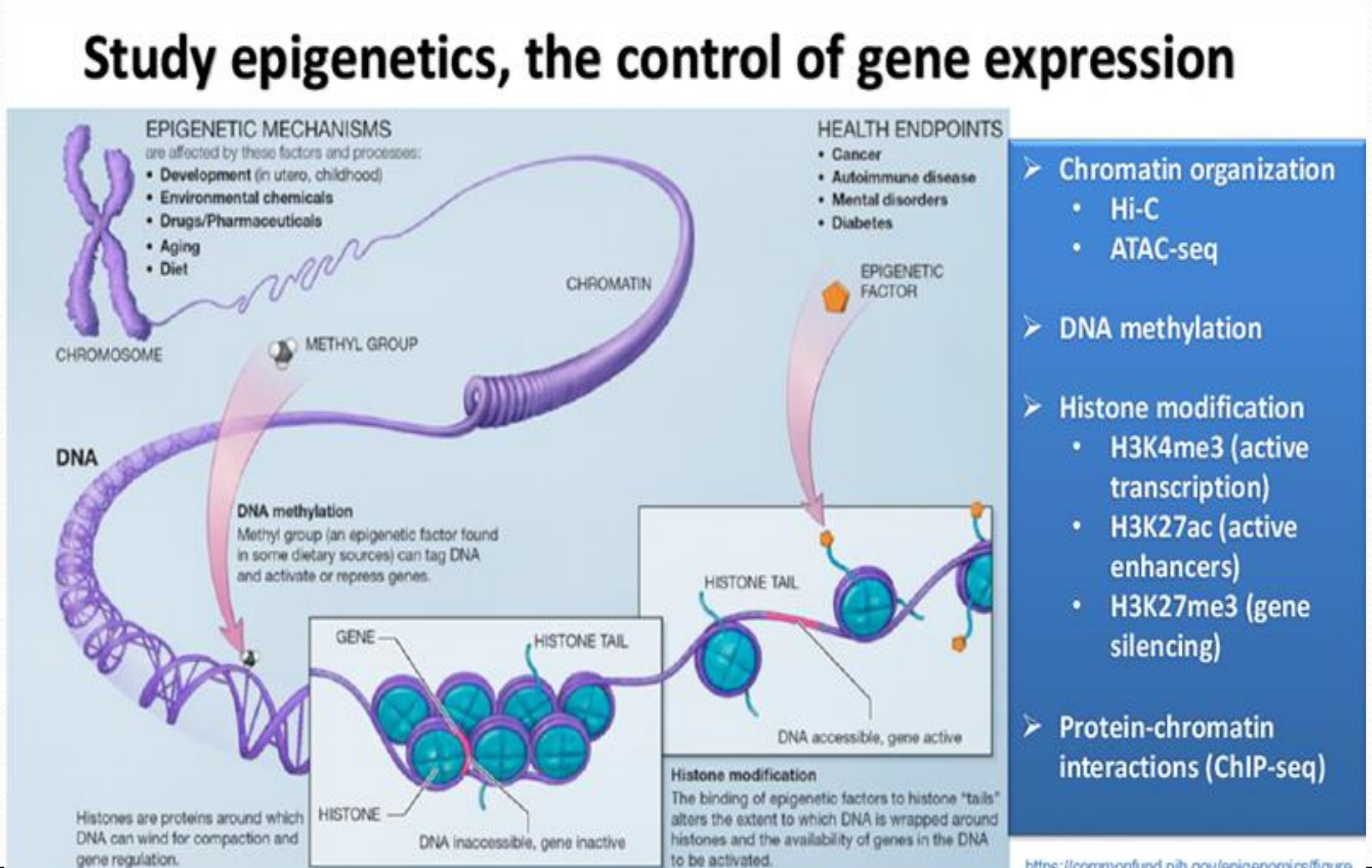
Genomic Alterations

Genomic Alterations Detected by RNA Transcriptome Sequencing



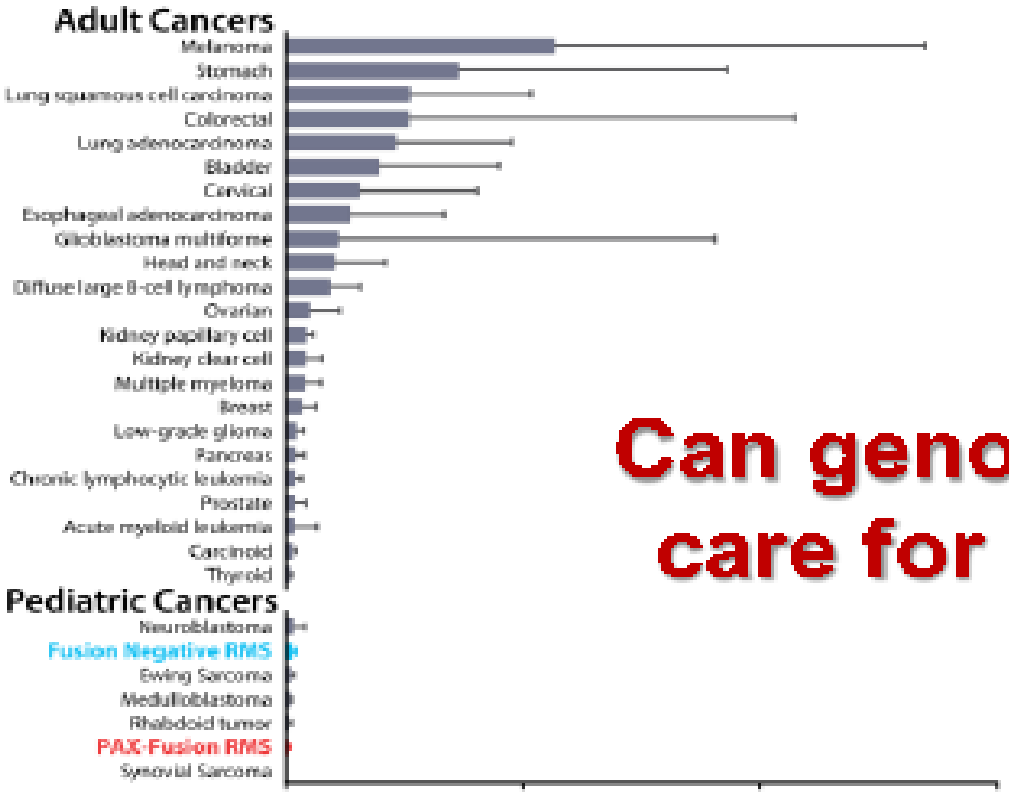
- Digital Gene Expression
- Expressed Mutations
- Alternative Splicing Events
- Expressed Fusion Transcripts
- RNA editing
- Novel Transcripts
- Non-coding RNAs

Epigenetics



Pediatric cancer mutations

Pediatric Cancers Have A Low Number of Somatic and Actionable Mutations At Initial Diagnosis



Can genomics help clinical care for cancer patients?

Clinomics for precision medicine

Personalized Medicine and Imaging

Clinical Cancer Research

MultiDimensional ClinOmics for Precision Therapy of Children and Adolescent Young Adults with Relapsed and Refractory Cancer: A Report from the Center for Cancer Research

Wendy Chang[1,2,3], Andrew S. Brohl[1,4], Rajesh Patidar[1], Sivasish Sindiri[1], Jack F. Shern[1,2], Jun S. Wei[1], Young K. Song[1], Marielle E. Yohe[1,2], Berkley Gryder[1], Shile Zhang[1], Kathleen A. Calzone[5], Nityashree Shivaprasad[1], Xinyu Wen[1], Thomas C. Badgett[1,6], Markku Miettinen[7], Kip R. Hartman[8,9], James C. League-Pascual[2,8], Toby N. Trahair[10], Brigitte C. Widemann[2], Melinda S. Merchant[2], Rosandra N. Kaplan[2], Jimmy C. Lin[1], and Javed Khan[1]

Clin Cancer Res. May 2016

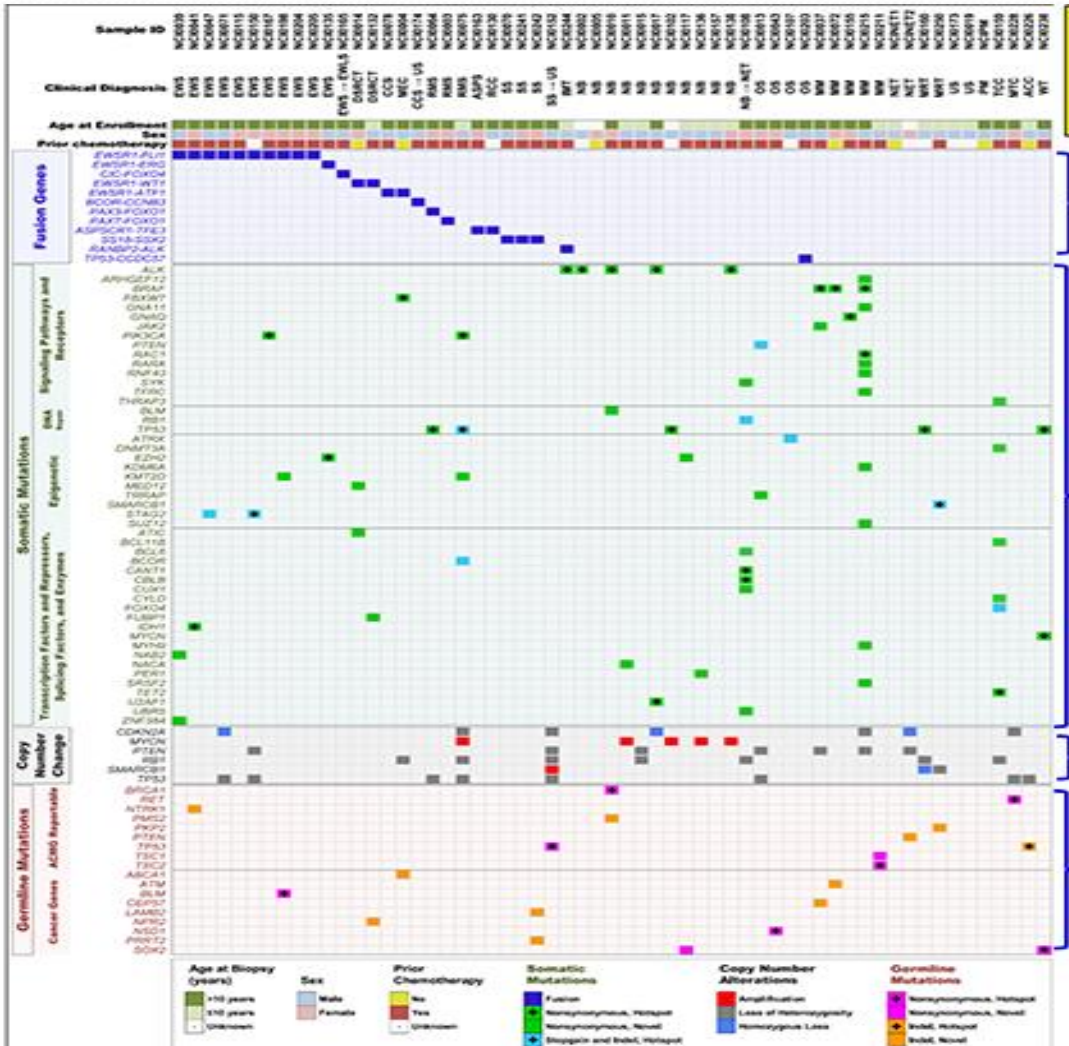
Protocol Number: 10-C-0086
Title: "Comprehensive Omics Analysis of Pediatric Solid Tumors and Establishment of a Repository for Related Biological Studies" or Omics protocol

Study design

Study Design

- Pilot study to determine the utility and feasibility of performing comprehensive genomic analyses to identify clinically actionable mutations in pediatric and young adult patients with metastatic, refractory or relapsed solid tumors
- 59 patients enrolled to the pediatric oncology branch, Center for Cancer Research (CCR), NCI (2010-2014)
- Age 7 months-25 years
- 20 diagnostic categories (non-CNS, solid tumors)
- Comprehensive multi-omics exome germline & tumor, RNAseq tumor & Illumina Omni SNP arrays of tumor

Multi-omics integrated landscapeFusion genes



Multi-Omics Integrated Landscape

RNAseq
Diagnostic, Driver, Actionable

DNAseq and RNAseq
Somatic: Driver, Actionable

DNA copy number & RNAseq
Somatic: Driver, Actionable

DNAseq
Germ line: Disease causing, Actionable

Germline mutations

~10% of Pediatric and Adolescent Young Adults with Cancers have Actionable Germline Mutations

Table 1. Germline mutations in American College of Medical Genetics (ACMG) reportable genes and tumor suppressor genes identified in 7 patients

Sample	Diagnosis	Gene	Mutation	Disease	Hotspot	Notes	Reportable by Strict ACMG Criteria
NCI0072	MM	*ATM*	p.Y380fs	Ataxia-Telangiectasia and cancer predisposition syndrome	No	Frameshift insertion of tumor suppressor gene	Yes
NCI0010	NB	*BRCA1*	Q1313X	Hereditary breast and ovarian cancer syndrome	Yes	Pathogenic, reportable	Yes
NCI0010	NB	*PMS2*	p.K356fs	Lynch syndrome and mismatch repair cancer syndrome	No	Frameshift deletion of tumor suppressor gene	Yes
NCINET2	NET	*PTEN*	p.R14fs	PTEN Hamartoma tumor syndrome	No	Frameshift deletion of tumor suppressor gene	Yes
NCI0228	MTC	*RET*	M918T	Multiple endocrine neoplasia 2B	Yes	Pathogenic, reportable	Yes
NCI0152	SS → US	*TP53*	R175H	Li-Fraumeni syndrome	Yes	Patient tumor has LOH of wild-type tp53 on other allele	No
NCI0226	ACC	*TP53*	A159K	Li-Fraumeni syndrome	Yes	Tumor has LOH of wild-type tp53 on other allele, novel, 2 base non-frameshift substitution, c.358_359delGCinsTT	No
NCI0211	MM	*TSC1*	p.S828R	Tuberous sclerosis type 1, lymphangioleiomyomatosis, focal cortical dysplasia, and everolimus sensitivity	No	Nonsynonymous SNV, autosomal dominant, patient also has a germline TSC2 mutation	No
NCI0211	MM	*TSC2*	p.T246A	Tuberous sclerosis type 2, and lymphangioleiomyomatosis	Yes	Nonsynonymous SNV, autosomal dominant, patient also has a germline TSC1 mutation	No

NOTE: Mutations were confirmed by direct visualization on an IGV viewer, and by Sanger sequencing.

Abbreviations: ACC, adrenocortical carcinoma; MM, malignant melanoma; MTC, medullary thyroid carcinoma; NET, neuroendocrine tumor; RMS, rhabdomyosarcoma; SS, synovial sarcoma; US, undifferentiated sarcoma; horizontal arrow indicates change in diagnosis.

Chang et al. Clin Cancer Res. 2016

Somatic mutations

Approximately 50% (30/59) of Pediatric and Adolescent Young Adults with Cancers Have Actionable Somatic Mutations

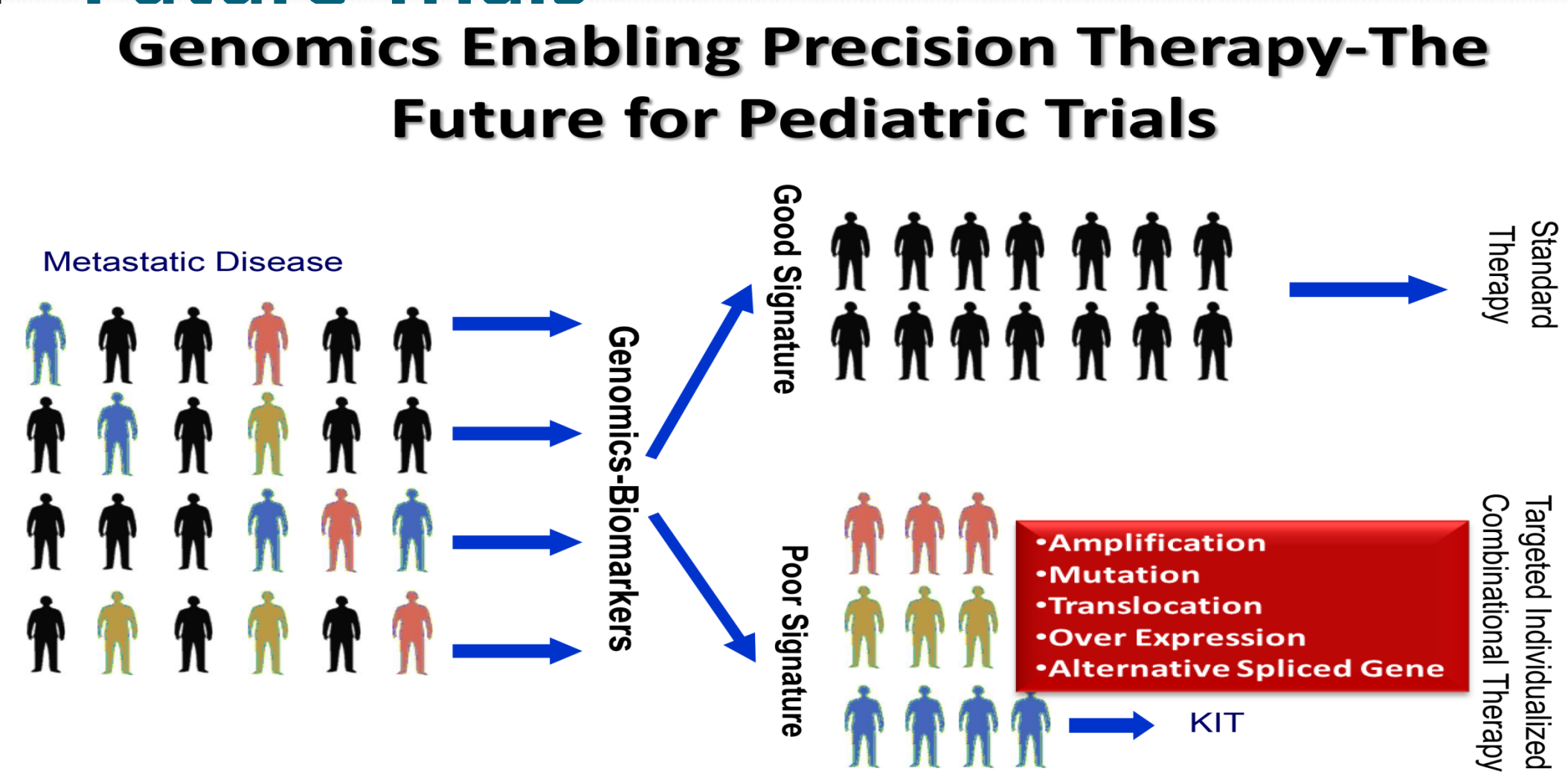
Table 2. Summary of actionable mutations in relapsed and refractory pediatric solid tumors

Sample	Diagnosis	Gene	Stage	Modality	Mutation	AA Change	Level	Drug	Clinical trial: Pediatric	FDA-Approval in adults	Exact mutation vs. hotspot	Reference preclinical data for level 3
NCI0037	MM	*BRAF*	Relapsed	WES/WTS	NS SNV	p.V600E	1	Vemurafenib, dabrafenib	Yes	Yes	Exact	—
NCI0072	MM	*BRAF*	Diagnostic	WES/WTS	NS SNV	p.V600E	1	Vemurafenib, dabrafenib	Yes	Yes	Exact	—
NCI0215	MM	*BRAF*	Relapsed	WES/WTS	NS SNV	p.V600E	1	Vemurafenib, dabrafenib	Yes	Yes	Exact	—
NCI0155	MM	*GNAQ*	Relapsed	WES/WTS	NS SNV	p.Q209L	1	Temsirolimus, trametinib, vorinostat	No	Yes	Exact	—
NCI0002	NB	*ALK*	—	WES/WTS	NS SNV	p.R1275Q	2a	Crizotinib	Yes	Yes	Exact	—
NCI0010	NB	*ALK*	Relapsed	WES/WTS	NS SNV	p.F1174V	2a	Crizotinib	Yes	Yes	Exact	—
NCI0017	NB	*ALK*	Relapsed	WES/WTS	NS SNV	p.F1174L	2a	Crizotinib	Yes	Yes	Exact	—
NCI0158	NB	*ALK*	Relapsed	WES/WTS	NS SNV	p.Y1278S	2a	Crizotinib	Yes	Yes	Exact	—
NCI0244	IMT	*ALK*	Relapsed	WTS	*RANBP2-ALK* fusion	—	2a	Crizotinib	No	Yes	Exact	—
NCI0244	IMT	*ALK*	Relapsed	WES/WTS	NS SNV	p.I1171T	2a	Ceritinib	No	Yes	Exact	—
NCI0215	MM	*GNA11*	Relapsed	WES/WTS	NS SNV	p.S236F	2a	Trametinib	No	Yes	—	—
NCI0041	EWS	*IDH1*	Relapsed	WES/WTS	NS SNV	p.R132C	2a	IDH1 Inhibitors	No	No	Exact	—
NCI0075	RMS	*PIK3CA*	Relapsed	WES/WTS	NS SNV	p.P104Q	2a	PI3K/AKT/mTOR Inhibitors	Yes	Yes	Exact	—
NCI0157	EWS	*PIK3CA*	Refractory	WES/WTS	NS SNV	p.D1037G	2a	PI3K/AKT/mTOR Inhibitors	Yes	Yes	Exact	—
NCI0013	OS	*PTEN*	Relapsed	WES/WTS	Frameshift deletion	p.K80fs	2a	PI3K/AKT/mTOR Inhibitors	Yes	No	—	—
NCINET2	NET	*PTEN*	—	WES/WTS	Germline frameshift deletion/somatic LOH	p.R14fs	2a	PI3K/AKT/mTOR Inhibitors	Yes	No	—	—
NCI0229	MTC	*RET*	Relapsed	WES/WTS	Germline SNV	p.M918T	2a	Vandetanib	Yes	Yes	Exact	—
NCI0017	NB	*CDKN2A*	Relapsed	SNP Array/WTS	Homozygous loss	—	3	CDK4/6 Inhibitor	No	No	—	36
NCI0071	EWS	*CDKN2A*	Relapsed	SNP Array/WTS	Homozygous loss	—	3	CDK4/6 Inhibitor	No	No	—	36
NCINET2	NET	*CDKN2A*	—	SNP Array/WTS	Homozygous loss	—	3	CDK4/6 Inhibitor	No	No	—	36
NCI0011	NB	*MYCN*	Relapsed	SNP Array/WTS	Amplification	—	3	Bromodomain Inhibitors	No	No	—	37
NCI0175	RMS	*MYCN*	Relapsed	SNP Array/WTS	Amplification	—	3	Bromodomain Inhibitors	No	No	—	37
NCI0102	NB	*MYCN*	—	SNP Array/WTS	Amplification	—	3	Bromodomain Inhibitors	No	No	—	37
NCI0136	NB	*MYCN*	Relapsed	SNP Array/WTS	Amplification	—	3	Bromodomain Inhibitors	No	No	—	37
NCI0138	NB	*MYCN*	Relapsed	SNP Array/WTS	Amplification	—	3	Bromodomain Inhibitors	No	No	—	37
NCI0238	WT	*MYCN*	Relapsed	WES/WTS	NS SNV	p.P44L	3	Bromodomain Inhibitors	No	No	—	37, 38
NCI0160	MRT	*SMARCB1*	—	SNP Array/WTS	Homozygous loss	—	3	EZH2 Inhibitors	No	No	—	39, 40
NCI0250	MRT	*SMARCA4*	Refractory	WES/WTS	NS SNV	p.R40X	3	EZH2 Inhibitors	No	No	—	39, 40
NCI0047	EWS	*STAG2*	Relapsed	WES/WTS	NS SNV	p.E984X	3	PARP Inhibitors	Yes	No	—	41
NCI0150	EWS	*STAG2*	—	WES/WTS	NS SNV	p.R286X	3	PARP Inhibitors	Yes	No	Hotspot	41
NCI0211	MM	*TSC1*	Relapsed	WES/WTS	NS SNV	p.S820R	3	Everolimus	No	Yes	—	42
NCI0211	MM	*TSC2*	Relapsed	WES/WTS	NS SNV	p.T246A	3	Everolimus	No	Yes	—	42

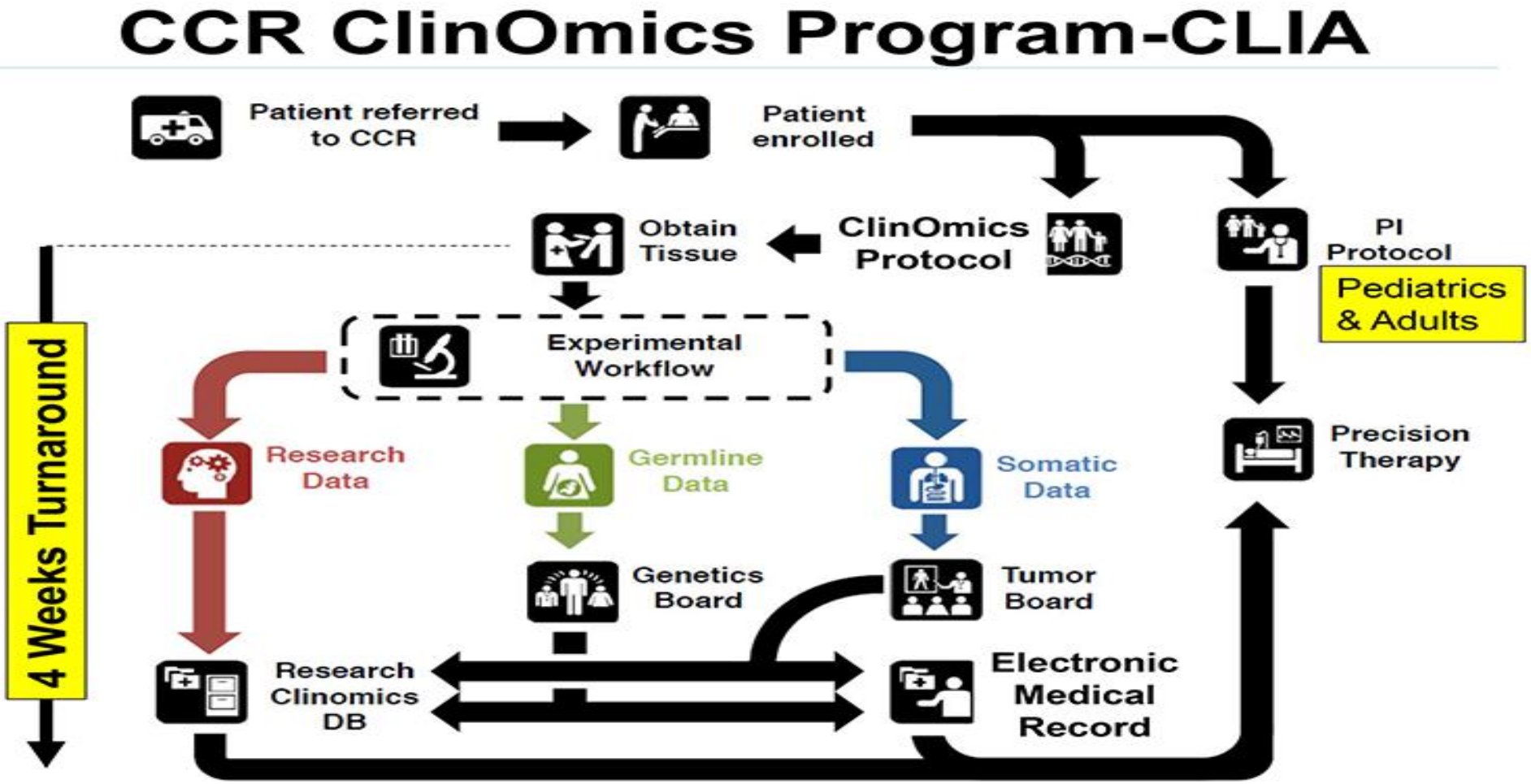
NOTE: SNVs were confirmed by direct visualization on an IGV viewer, and validation by Sanger sequencing or confirmation CLIA-certified laboratories.

Abbreviations: EWS, Ewing sarcoma; IMT, epithelioid inflammatory myofibroblastic sarcoma; MM, malignant melanoma; MRT, malignant rhabdoid tumor; MTC, medullary thyroid carcinoma; NB, neuroblastoma; NET, neuroendocrine tumor; OS, osteosarcoma; RMS, rhabdomyosarcoma; WT, Wilms tumor.

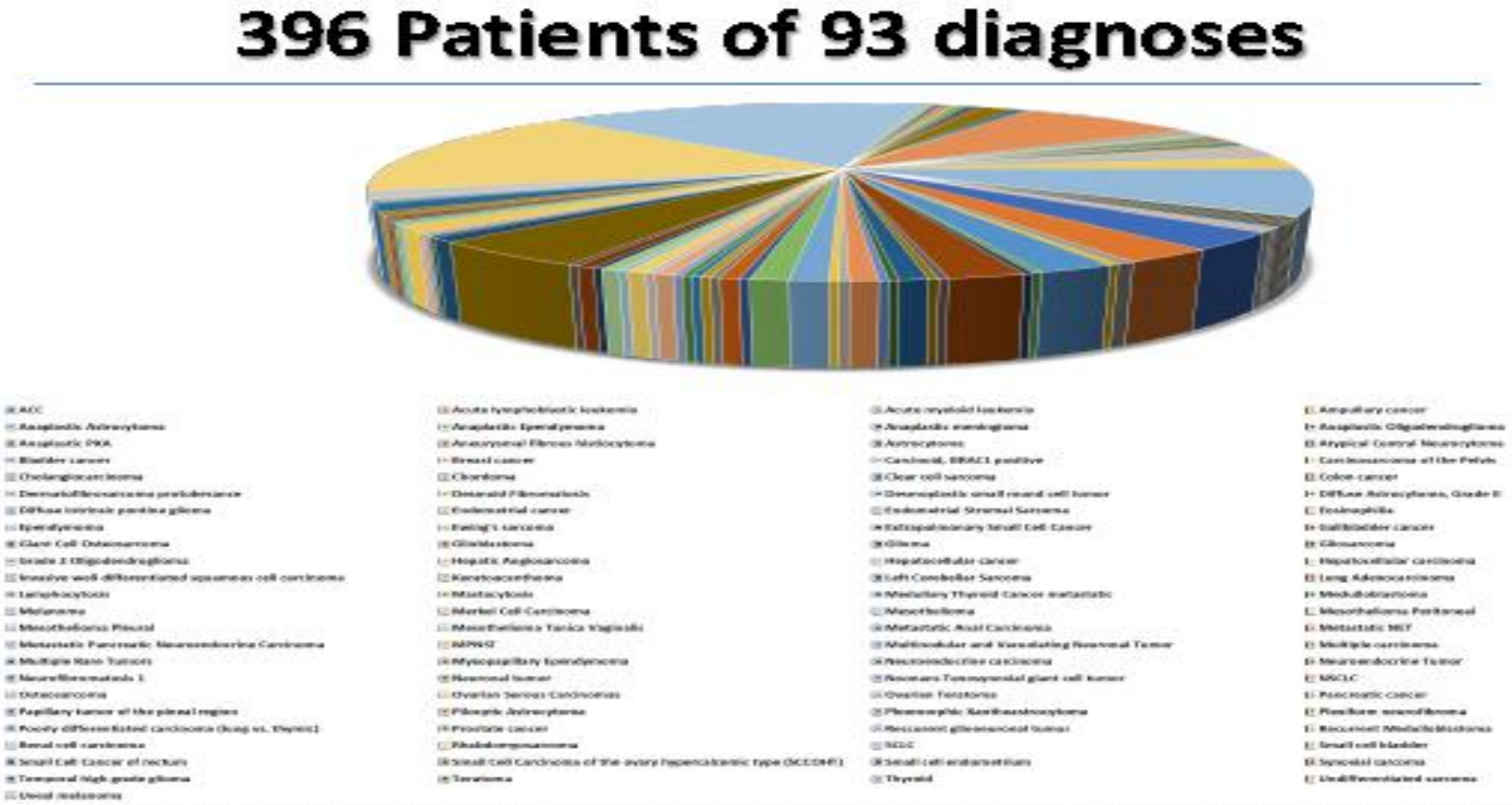
Future Trials



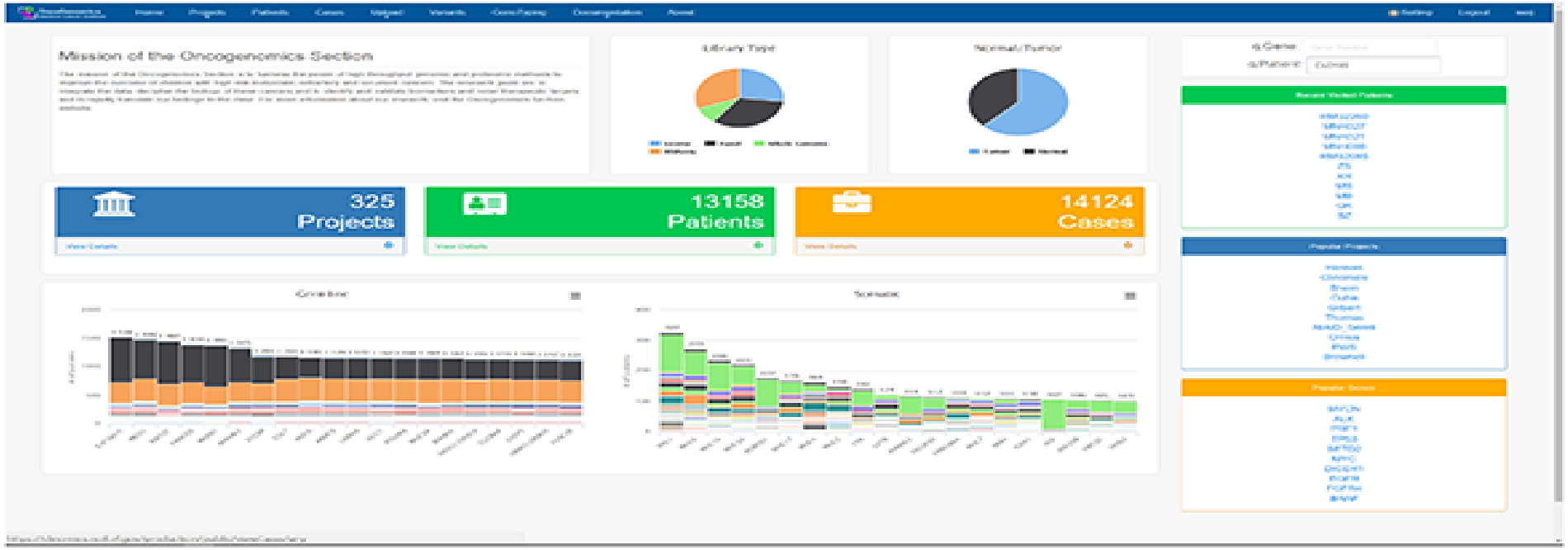
ClinOmics program



Patient diagnoses

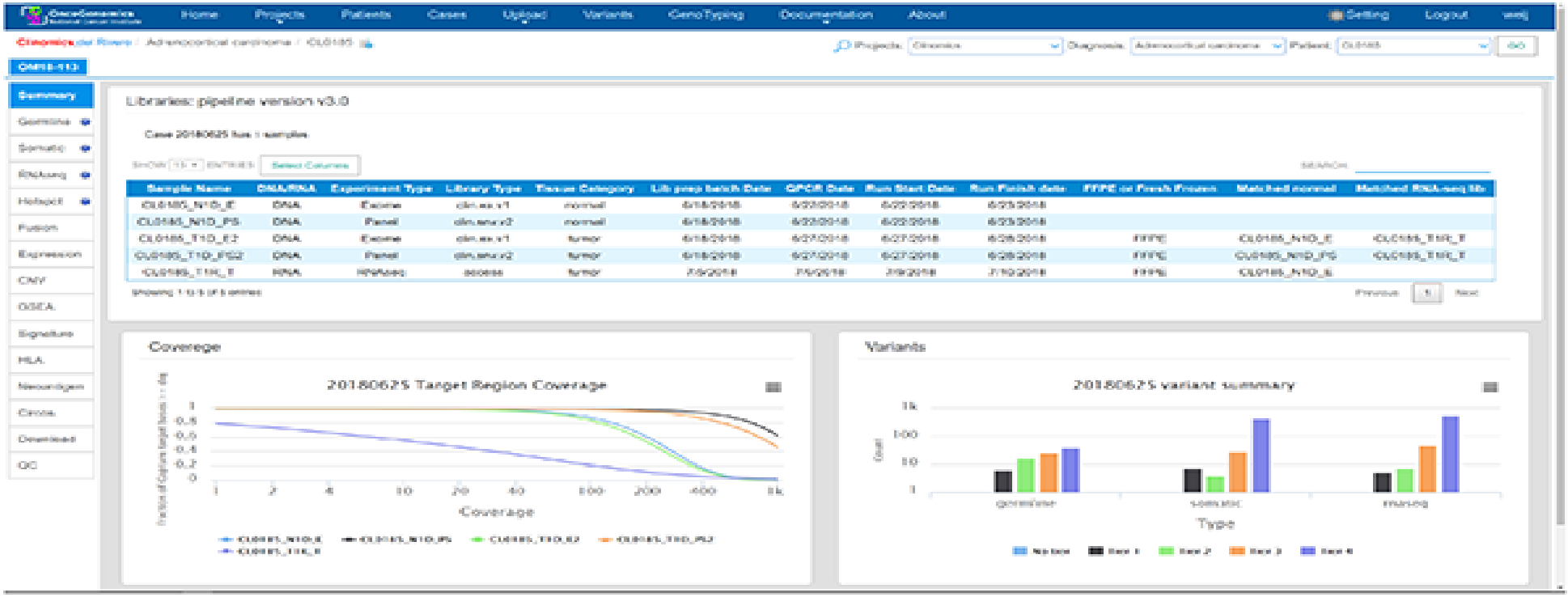


ClinOmics Data Portal



Patient Summary

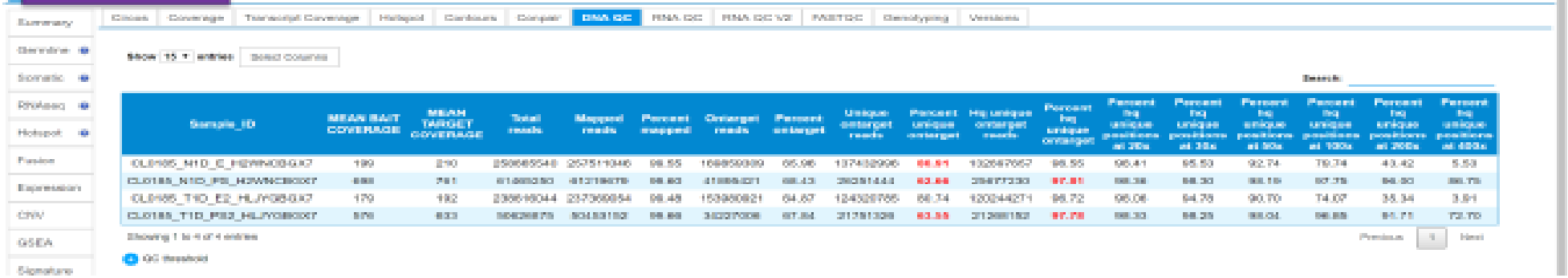
Patient Summary Page



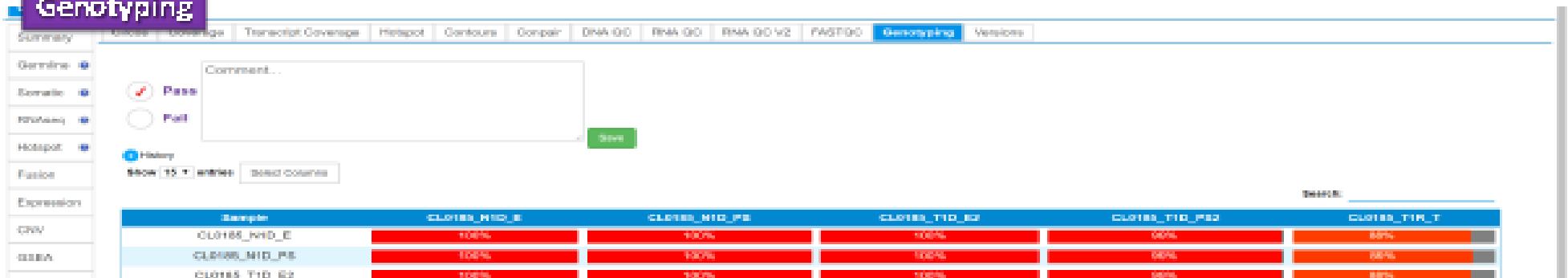
QC report

QC Report:
Sequencing Statistics & Genotyping

Run Statistics



Genotyping

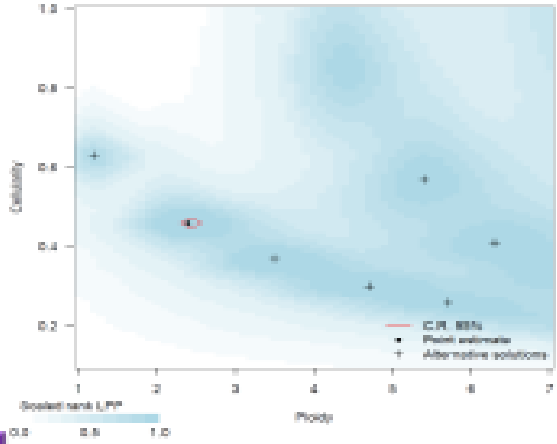


QC Report: Coverage

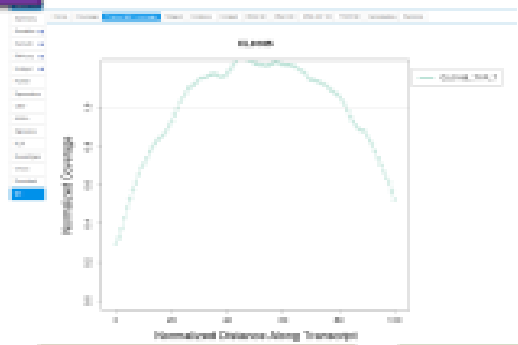
QC Report: Coverage

Circos

Tumor Content



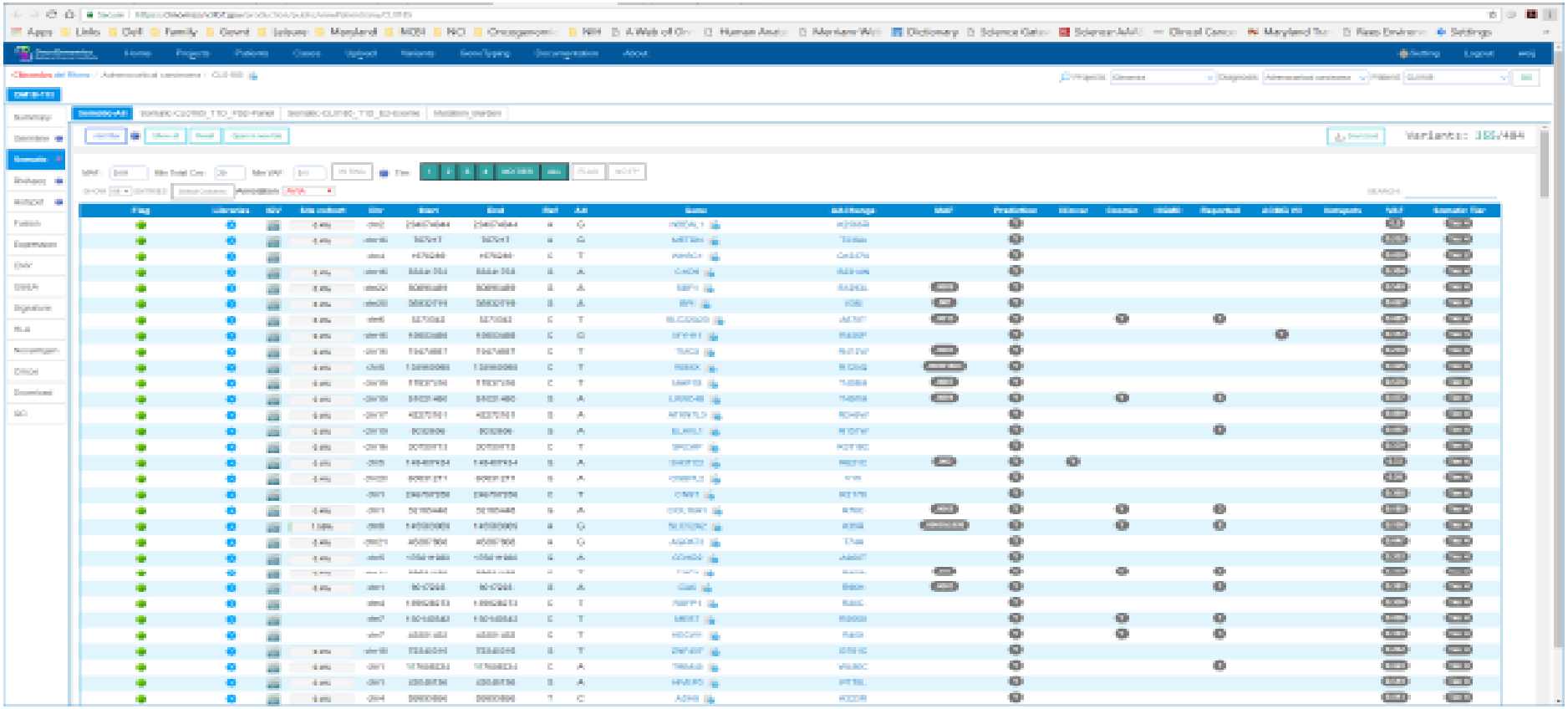
RNA Coverage



Hotspot Coverage

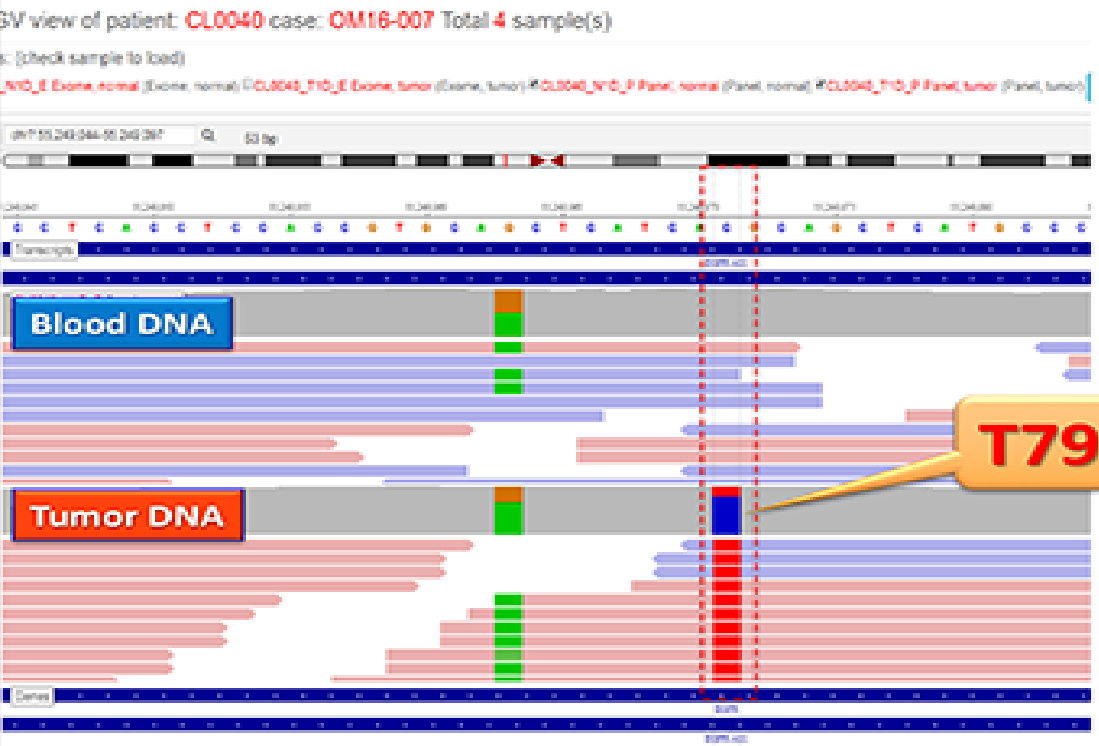
Germline and somatic mutations

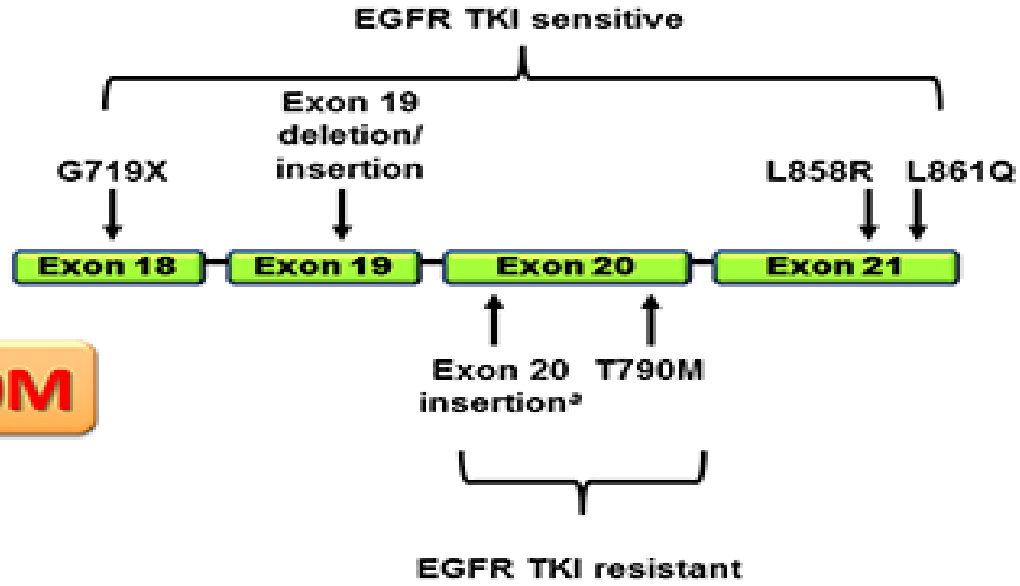
Germline and Somatic Mutations



EGFR mutations

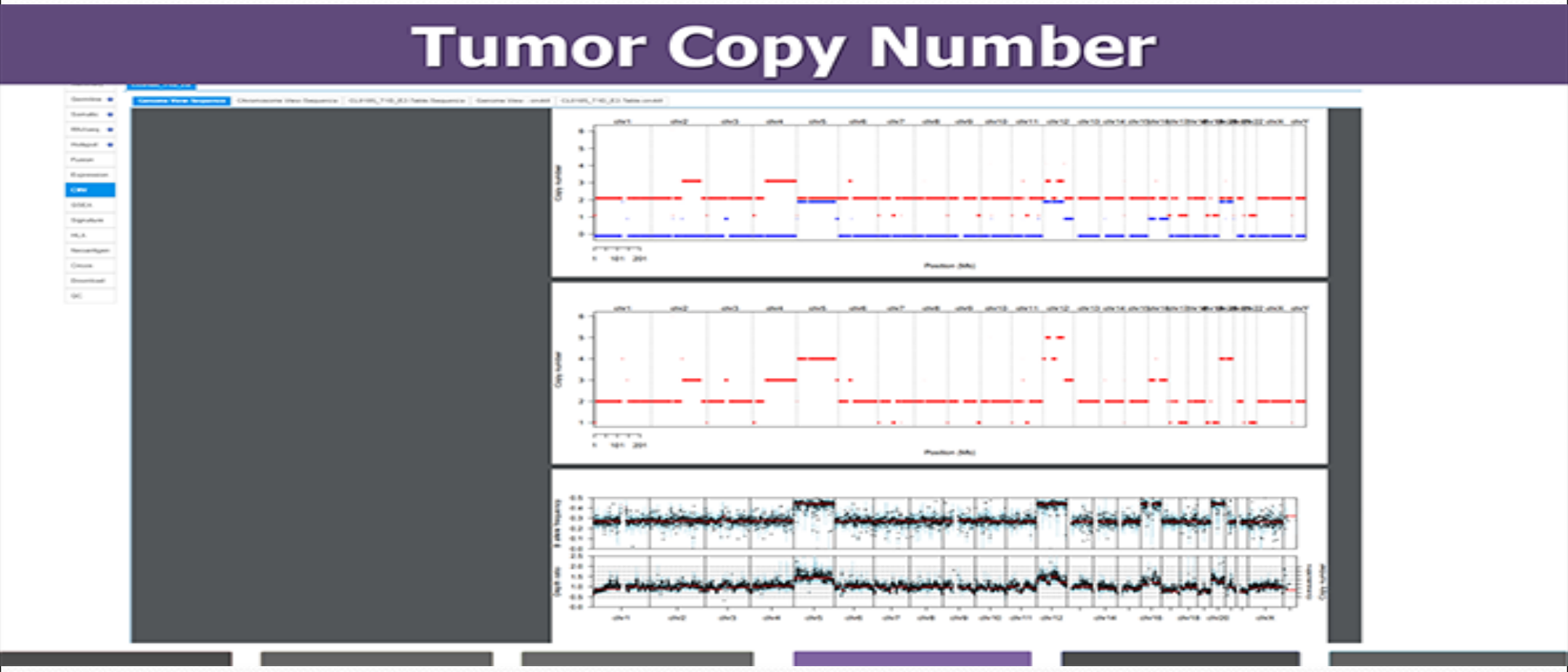
EGFR mutations in NSCLC





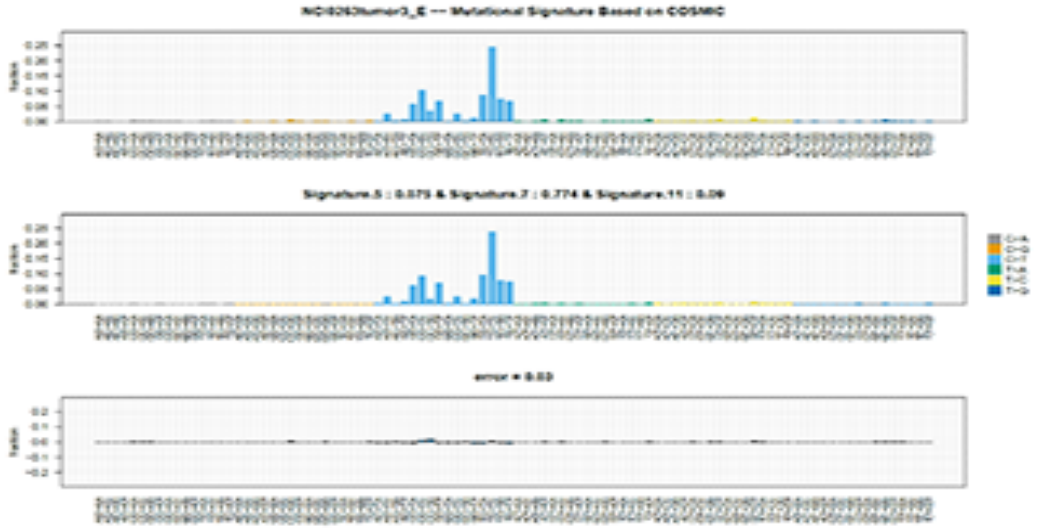
https://www.mycancergenome.org/content/disease/lung-cancer/egfr/

Tumor Copy Number



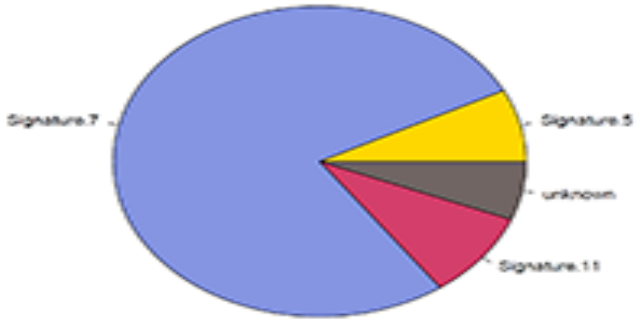
Mutation Signatures

Mutation Signatures for Tumor



COSMIC (https://cancer.sanger.ac.uk/cosmic/signatures)

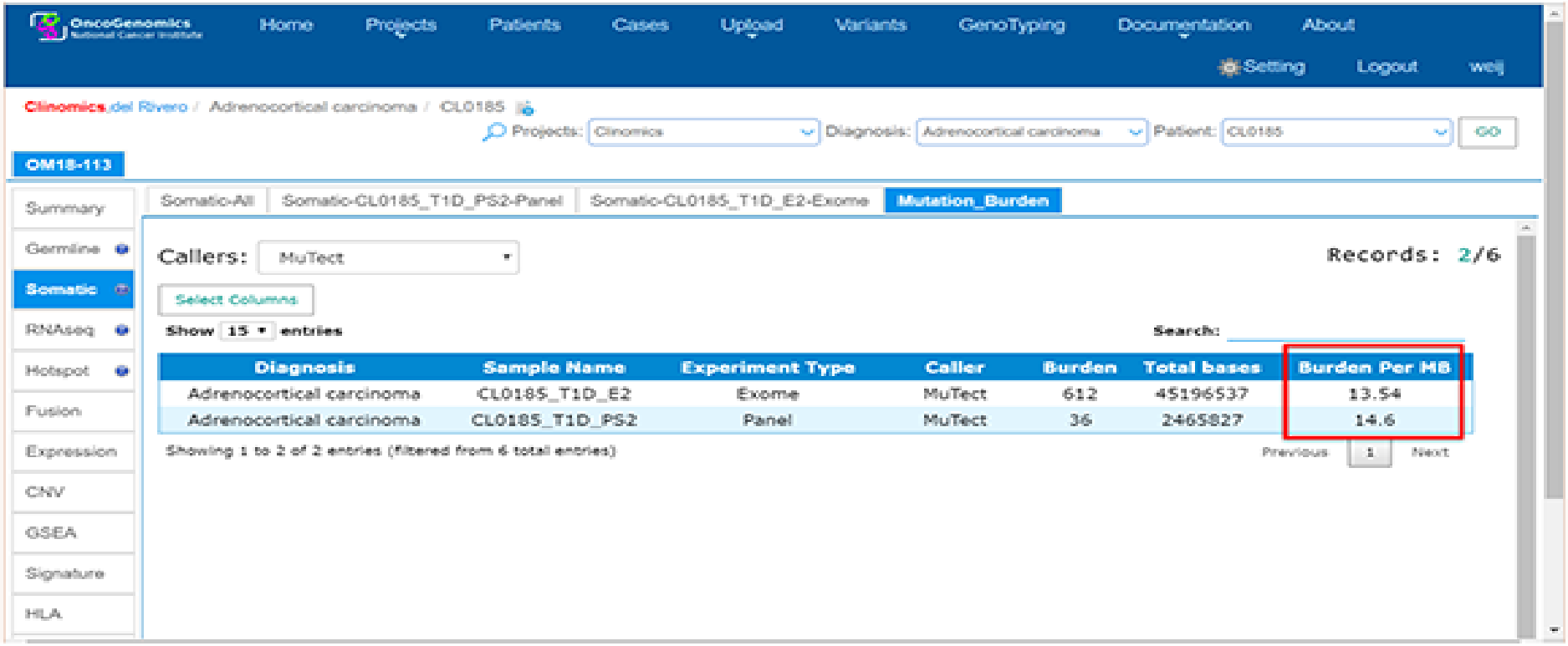
NCI0263: Melanoma



Signature 7: UV signature

Mutation Burden

Mutation Burden



Fusion Gene Detection

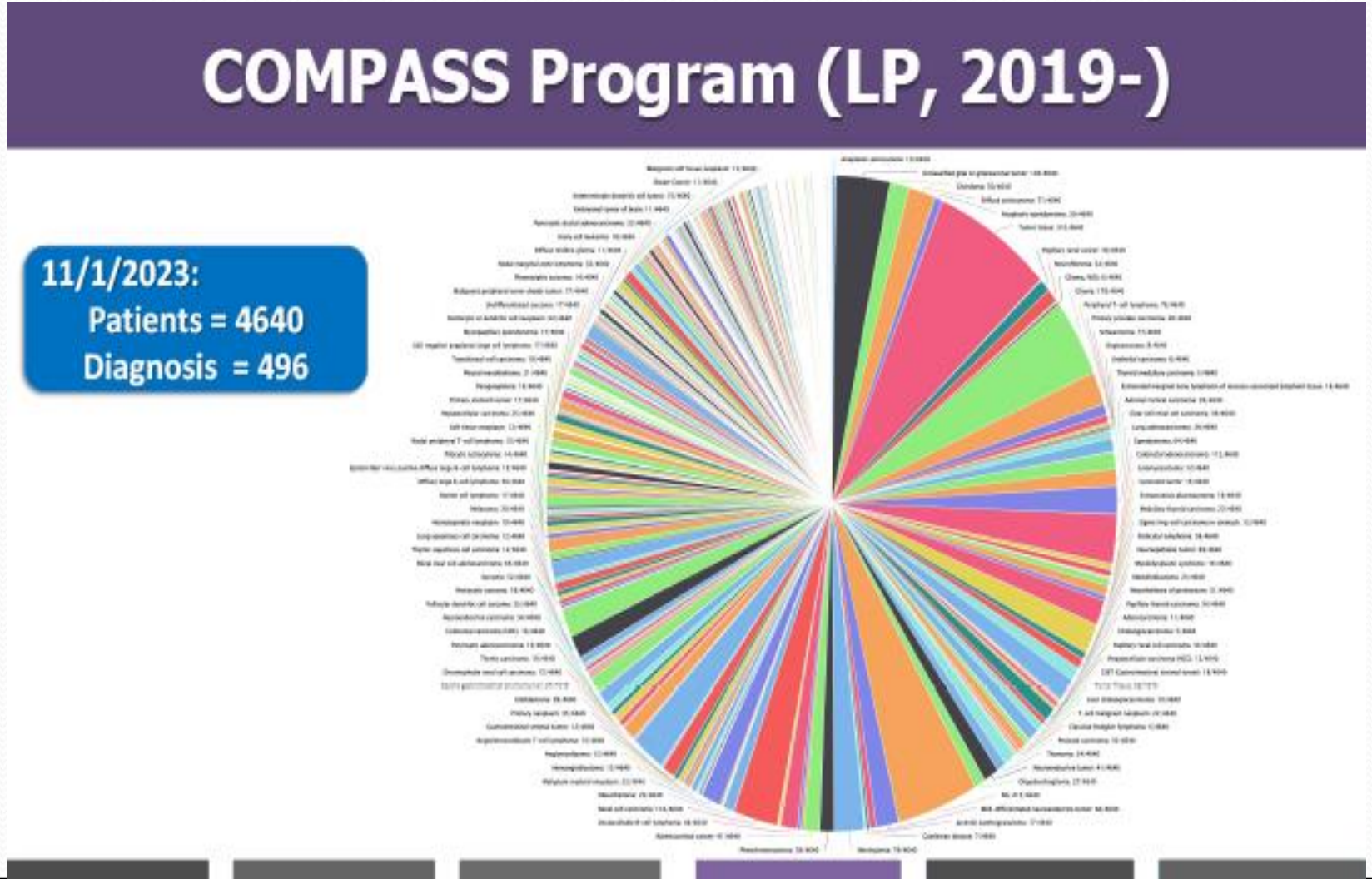
Fusion Gene Detection from RNA-seq experiments

Useful Genomic Information

Other Useful Genomic Information

- HLA typing (Tissue typing)
- Neoantigen prediction
- Gene expression
- Gene Set Enrichment Analysis (GSEA)
- Survival analysis if outcome data is available

COMPASS


COMPASS Program (LP, 2019-)
11/1/2023:
Patients = 4640
Diagnosis = 496

Conclusions

Conclusions

- Next-generation sequencing is an important genomic tool to study the genomics and epigenetics of tumors
- Genomic research has significantly advanced our understanding of human cancers
- Routine integrated omics analyses of patient tumors can pinpoint rational molecular targets to improve the outcomes of childhood cancers

Acknowledgements