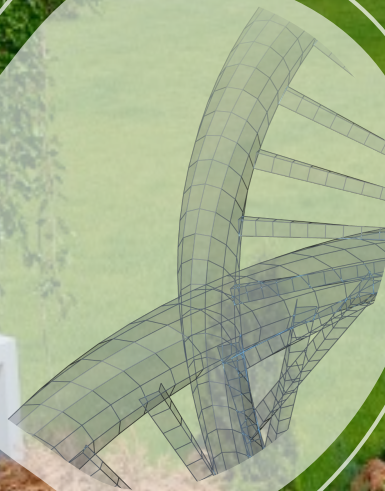
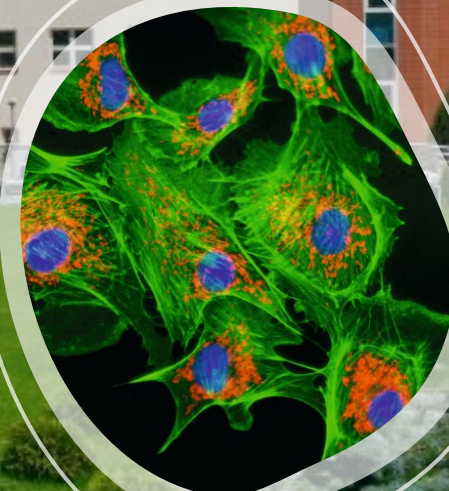
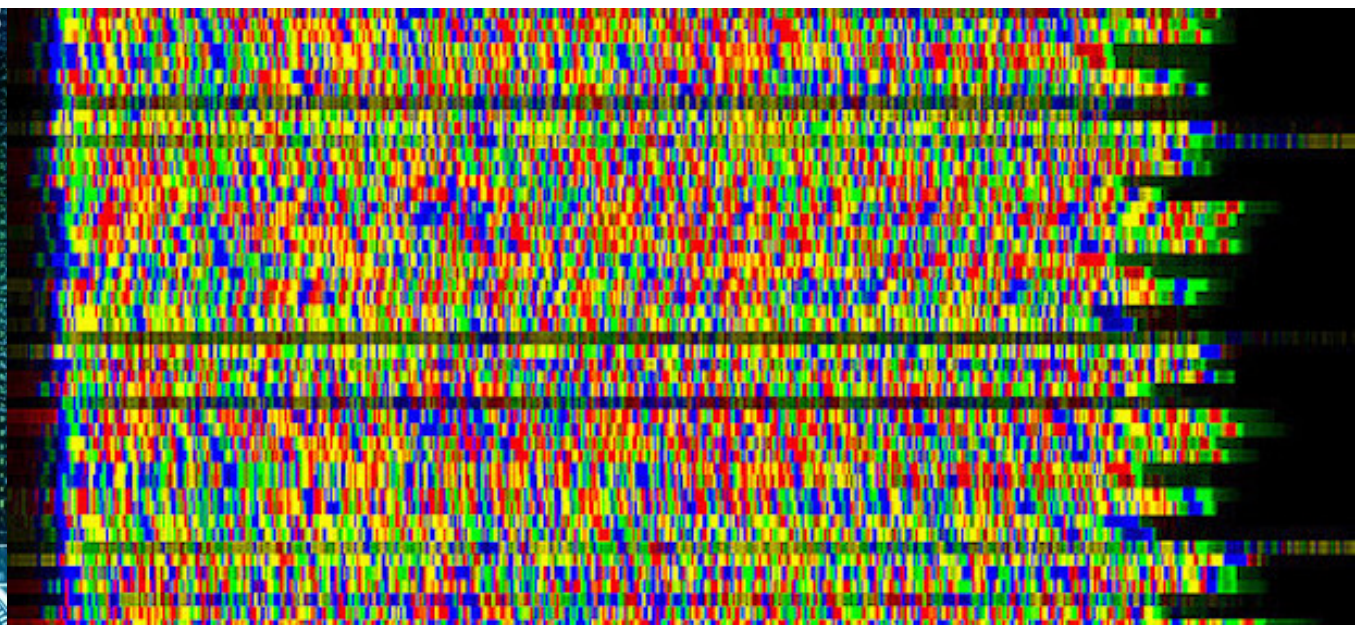
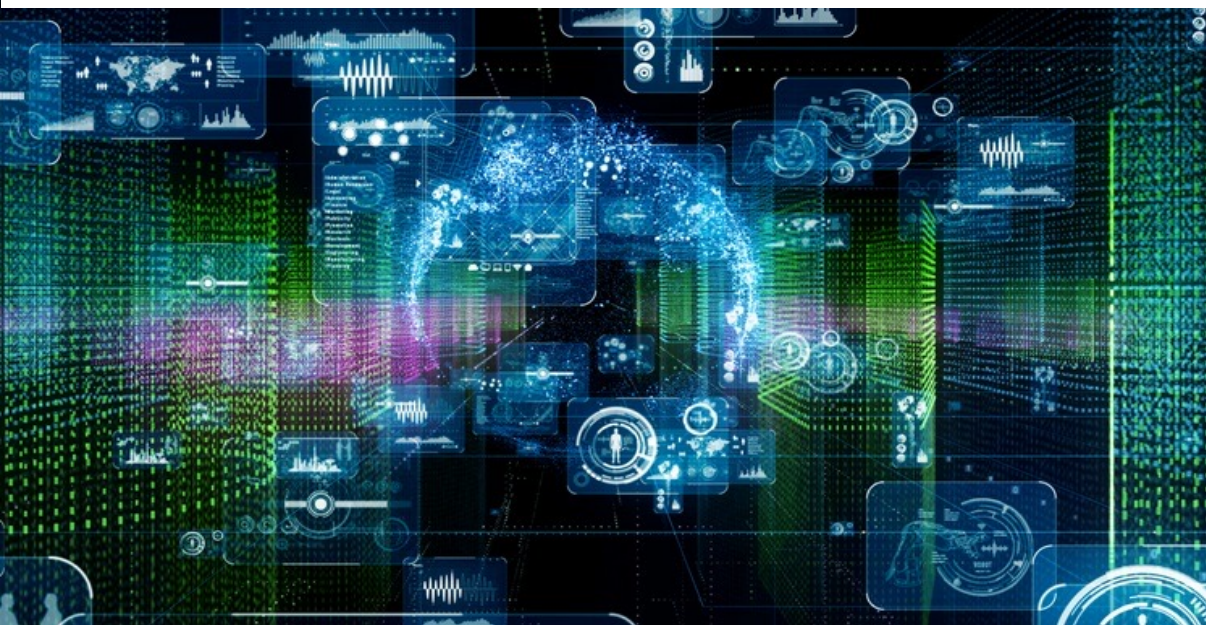


**RESEARCH CENTER
FOR FUNCTIONAL
GENOMICS,
BIOMEDICINE AND
TRANSLATIONAL
MEDICINE**





THE FUTURE IN HEALTH THROUGH INNOVATION





GEN  **omics**

2014

THE VALUES OF THE UMPH IULIU HATIEGANU GENOMICS CENTER

Creating an environment for a better quality of life through our values

Originate improvement in genomic medicine and bring them into the clinic

Commitment to offer high-quality genomic services for all the patients in need

Dedication to work for the improvement of genomic profiling to improve the standard of care

VISION

- Discoveries and innovation in genomic medicine to improve people's health in our region
- Extend the frontiers of science, continuously reinventing methods for disease understanding and exploring every source of innovation

MISSION

- Genomics – innovative environment, through integrated research services, from the initial design to the final product
- Development of new products in the field of genomic medicine to discover new diagnostic strategies and innovative therapies
- Support for researchers, doctors, PhD students, undergraduate and master's students discovering and investigating the foundation of genomics and its applicability in human medicine



**GENOMICS
PREDICTION, DIAGNOSIS AND PRECISION AND
PERSONALIZED THERAPIES FOR DIFFERENT
PATHOLOGIES
CANCER, CARDIOVASCULAR DISEASES,
DIABETES, INFECTIOUS DISEASES,
NEURODEGENERATIVE DISEASES**



GEN  **mics**

- 1. Processing of biological samples**
- 2. Extraction and qualitative and quantitative quantification of nucleic acids (blood, serum, plasma, urine, tumor tissue, CSF, cells)**
- 3. Discovery of new therapeutic compounds/testing therapeutic compounds *in vitro* models**
- 4. Fluorescence and confocal microscopy/laser capture microdissection /cell painting**
- 5. Flow cytometry**
- 6. Microarray - gene expression: complete coding, non-coding transcriptome analysis**
- 7. Next-generation sequencing - whole genome, exome sequencing, RNAseq, miRNAseq, lncRNAseq, commercial panels, custom panels**
- 8. Quantitative analysis by real-time amplification**
- 9. Bioinformatics**
- 10. Gene therapy - CRISPR**
- 11. Pathological anatomy / immunohistochemistry / digital pathology / convolutional neural networks**
- 12. Determination of water compounds / Screening mycotoxins in cereals/ Environmental metal species**



PEER REVIEW PUBLICATIONS

PUBLICATION 2014



PUBLICATION 2015



PUBLICATION 2016



PUBLICATION 2017



PUBLICATION 2018



PUBLICATION 2019



PUBLICATION 2020



PUBLICATION 2021

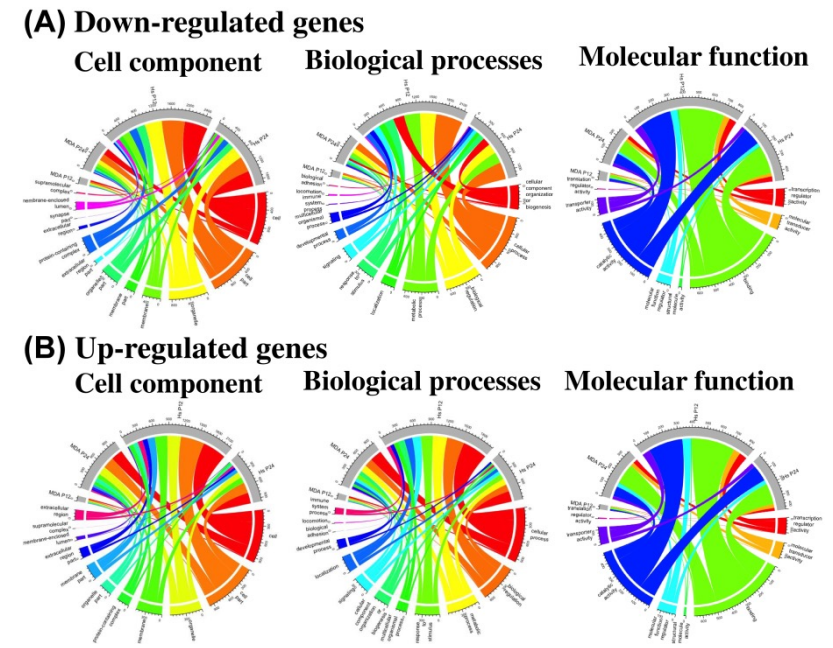
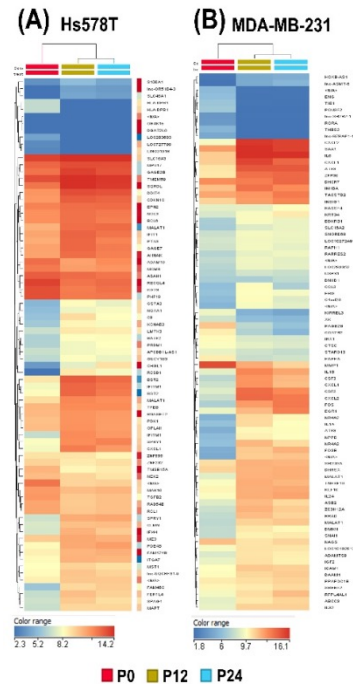
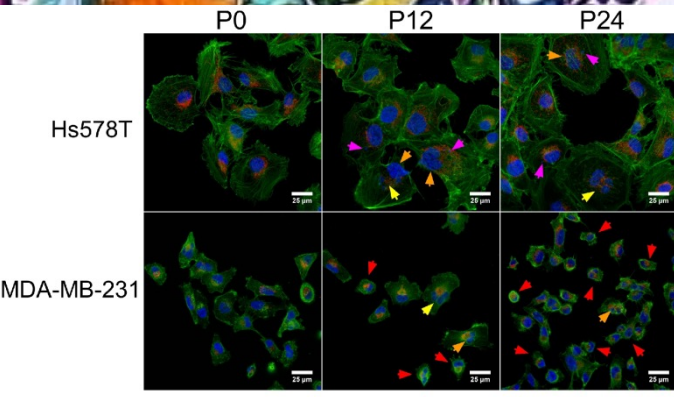
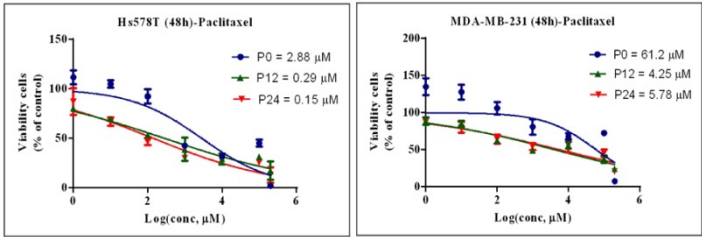




WHY US?

From concept - design - data analysis - interpretation of results - final product (patents, scientific articles, grants)

DO YOU HAVE AN IDEA?
BUT DON'T KNOW HOW TO DEVELOP IT?





**1600 gene expression analysis
transcriptome / miRNome**

**Biological samples
Cell lines
Animal models
Exosomes**

**Animal models
Cell lines**

**1048 gene expression samples (coding
genes and lncRNA)**

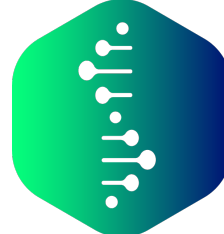
**552 gene expression samples
(noncoding genes and miRNome)**

**Tumor tissue
Normal tissue**

- Bladder cancer
- Oral cancer
- Prostate cancer
- Glioblastoma
- Hematologic diseases
- Endometriosis
- Melanoma
- Breast cancer
- Lung cancer

**Plasma samples from patients
and normal subjects**

- Colorectal cancer
- Bladder cancer
- Thyroid cancer



(A)

Mutation	Mutation											
	c.421 58 A>G ERBB4	c.352 40 A>G PIK3CA	c.3849-24 C>A KDR	c.798 54 G>A KDR	c.*37delT CSF1A	c.*35instA CSF1A	c.35 G>A HRAS	c.817 A>G HNF1A	c.1310-3 T>C FLT3	c.469 G>T TP53	c.215 C>G TP53	c.4732_4734 delGTG NOTCH1
Hs578T p0												
Hs578T p12												
Hs578T p24												

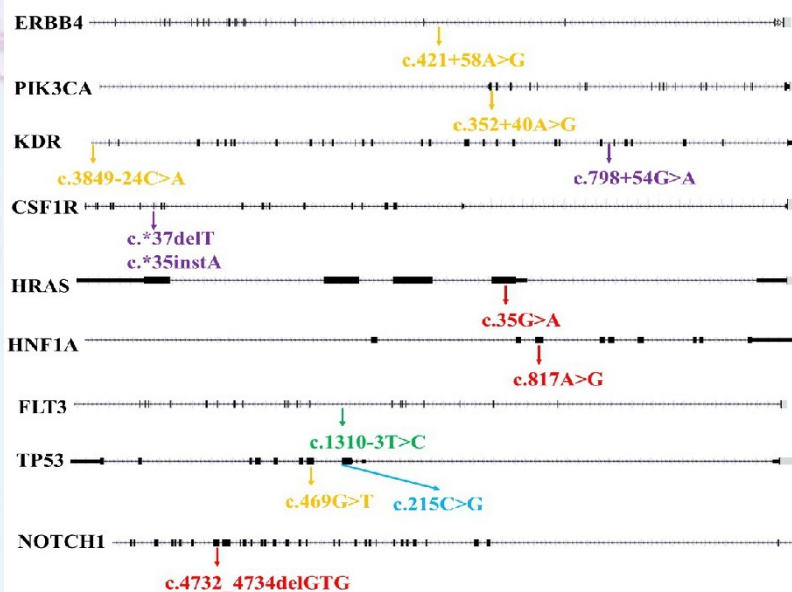
(B)

Sample	Mutation									
	G>T BRAF	G>A KRAS	G>A TP53	A>G PIK3CA	G>A KDR	c.*37delT CSF1A	c.*35instA CSF1A	C>G TP53	C>T SMAD4	
MDA-MB-231 p0										
MDA-MB-231 p12										
MDA-MB-231 p24										

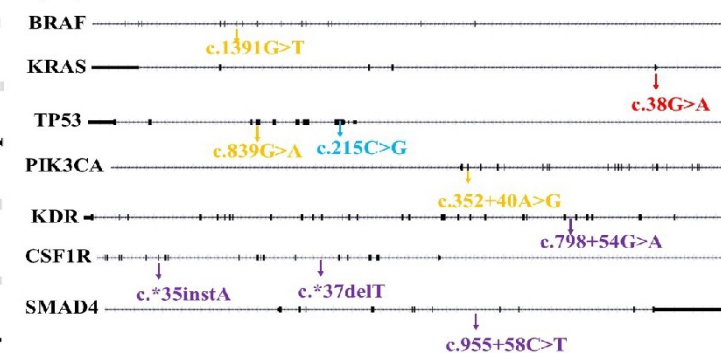
(C)

	drug response
	benign
	likely pathogenic
	pathogenic
	variant of unknown significance

(D)



(E)



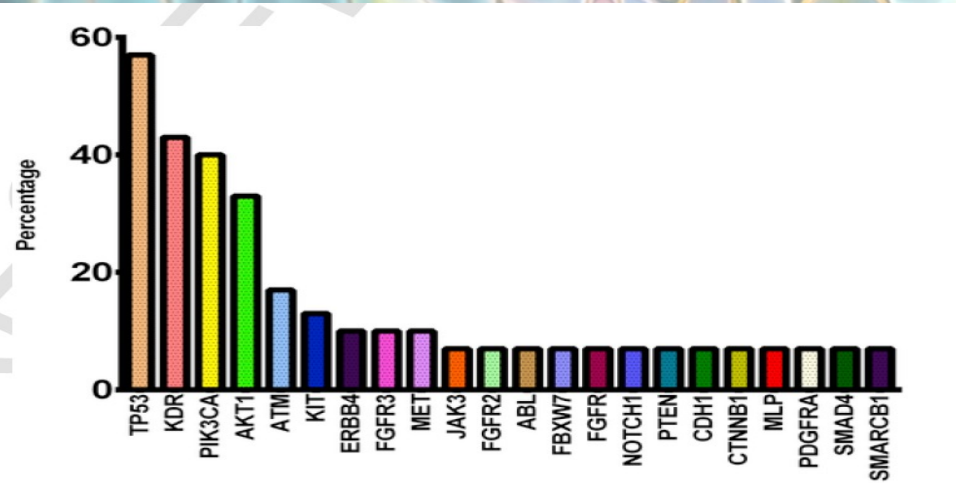
Evaluation of mutation patterns in TNBC cell lines, Hs578T/Pax and MDA-MB-231/Pax, post-therapy with paclitaxel using Ion Torrent PGM Machine and Ion AmpliSeq Cancer Hotspot Panel Pool



Next generation sequencing

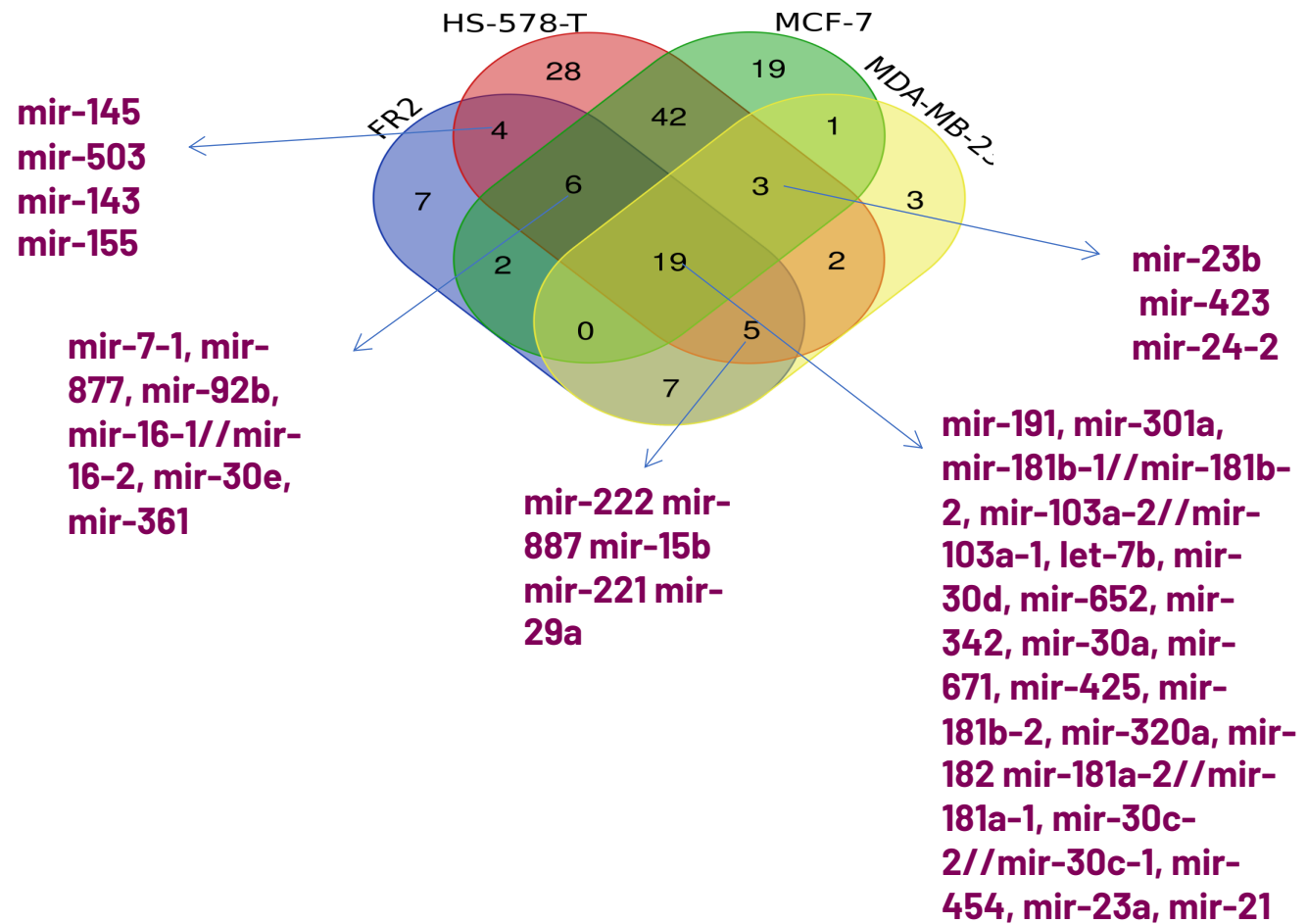
600 Cancer panel analysis
Patients
Cell lines
Animal models

411
BRCA1/2



	Locus BRCA1	HGVS	Amino-acid	Mutation	Nb.	Percentage
1	chr17:41209079	c.5266dupC	p.Gln1777fs	Frameshift Insertion	11	36.67%
2	chr17:41234559	c.4218delG	p.Lys1406fs	Frameshift Deletion	1	3.33%
3	chr17:41276044	c.68_69delAG	p.Glu23fs	Frameshift Deletion	1	3.33%
4	chr17:41243941	c.3607C>T	p.Arg1203Ter	Nonsense	9	30%
5	chr17:41245861	c.1687C>T	p.Gln563Ter	Nonsense	2	6.67%
6	chr17:41258504	c.181T>G	p.Cys61Gly	Missense	4	13.34%
7	chr17:41226539	c.4485-1G>T		Splicesite	1	3.33%
8	chr17:41258472	c.212+1G>T		Splicesite	1	3.33%
				Total	30	100%

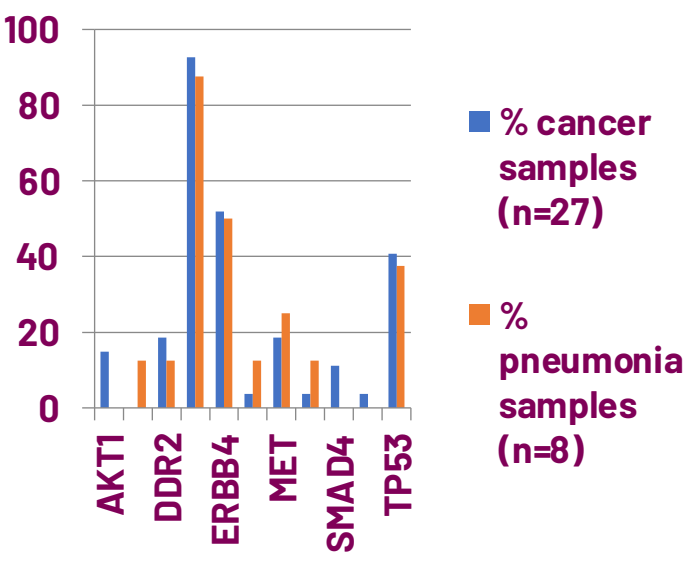
29 miRNA seq





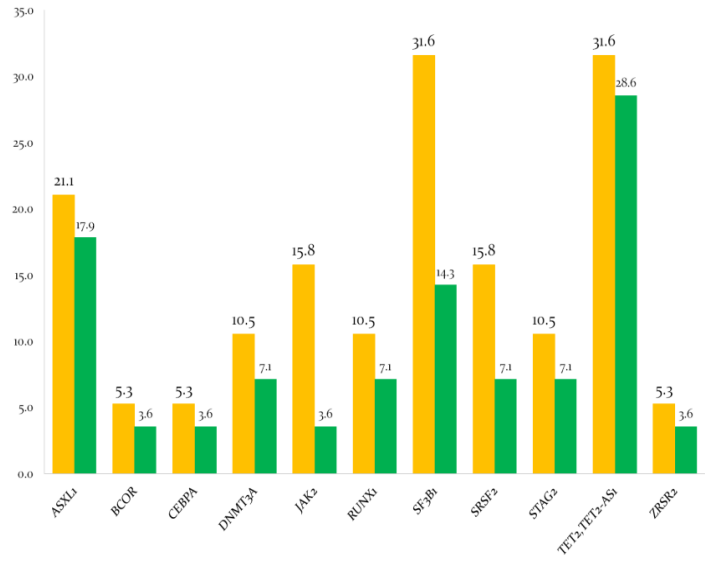
35

Lung and Colon Panel



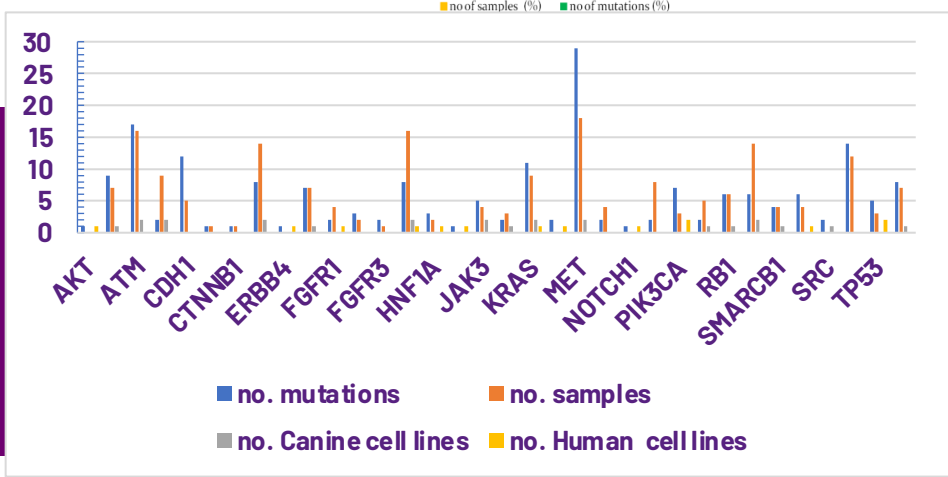
19

Oncomine Myeloid panel



19

Custom cancer panel for dog samples



HID NGS Panel

snp	GENE	chr
rs1490413		1
rs7520386		1
rs4847034		1
rs560681	LY9	1
rs10495407		1
rs891700	CHRM3-AS2	1
rs1413212		1
rs876724		2
rs1109037	LOC105373422	2
rs993934		2
rs12997453	CERKL	2
rs907100		2
rs1357617		3
rs4364205		3
rs1872575	QTRT2	3
rs1355366		3
rs6444724	ATP13A4	3
rs2046361		4
rs6811238	PALLD	4
rs1979255		4
rs717302		5
rs159606		5
rs7704770	PWWP2A	5
rs251934		5
rs338882	ADAMTS2	5
rs13218440	HIVEP1	6
rs214955	SYNE1	6

Comprehensive cancer panel 400 genes

Locus	Genotype	Ref	Genes	% Frequency	Strand	Exon	Transcript	Coding
chr1:144866643	G/A	G	PDE4DIP	22.96	-		NM_0011988 3434.3	c.5599C>T
chr1:144879090	T/C	T	PDE4DIP	38	-		NM_0011988 2734.3	c.4360A>G
chr1:144879264	G/G	A	PDE4DIP	100	-		NM_0011988 2734.3	c.4186T>C
chr1:144909956	G/A	G	PDE4DIP	63.64	-		NM_0011988 1734.3	c.2232C>T
chr1:144918957	T/A	T	PDE4DIP	42.18	-		NM_0011988 1034.3	c.1229A>T
chr1:144931087	T/C	T	PDE4DIP	36.36	-	intron 5	NM_0011988 34.3	c.637-7266A>G
chr1:144931392	G/A	G	PDE4DIP	43.94	-	intron 8	NM_0011988 34.3	c.637-7571C>T
chr1:144994658	C/A	C	PDE4DIP	22.39	-		NM_0011988 134.3	c.74G>T

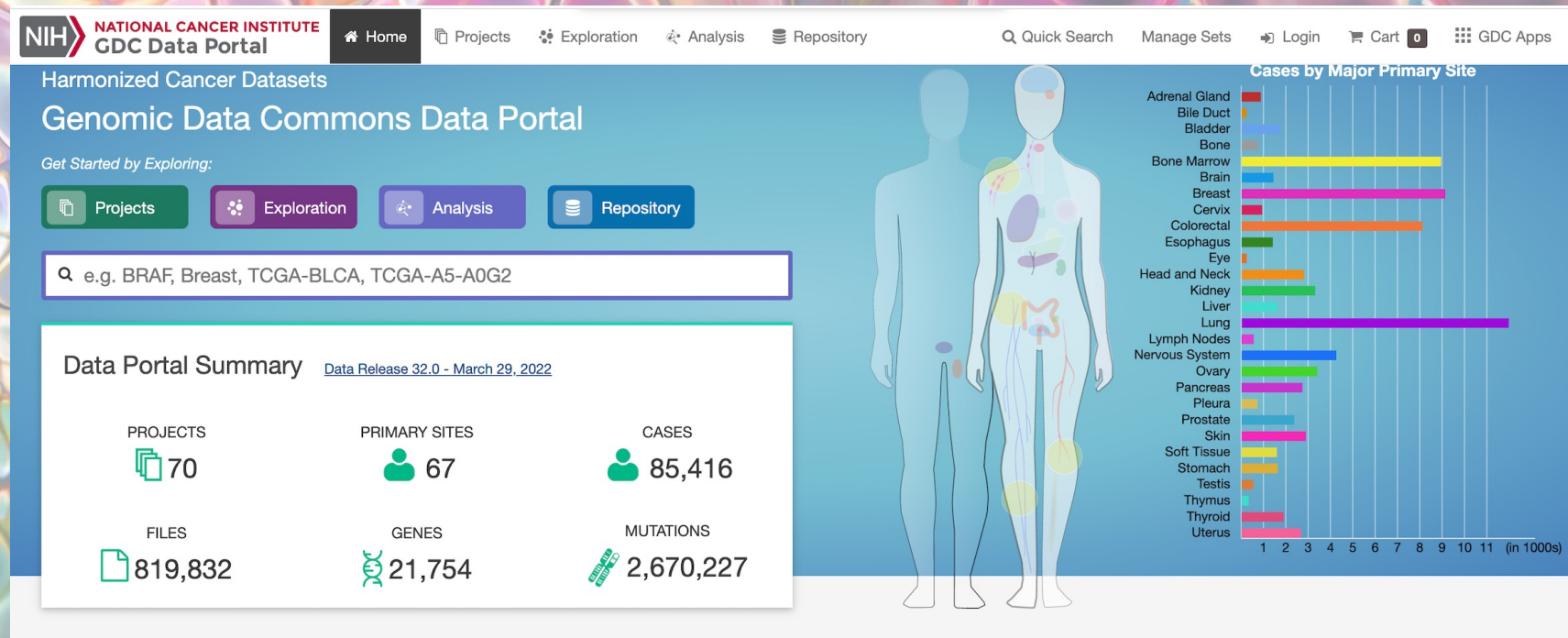
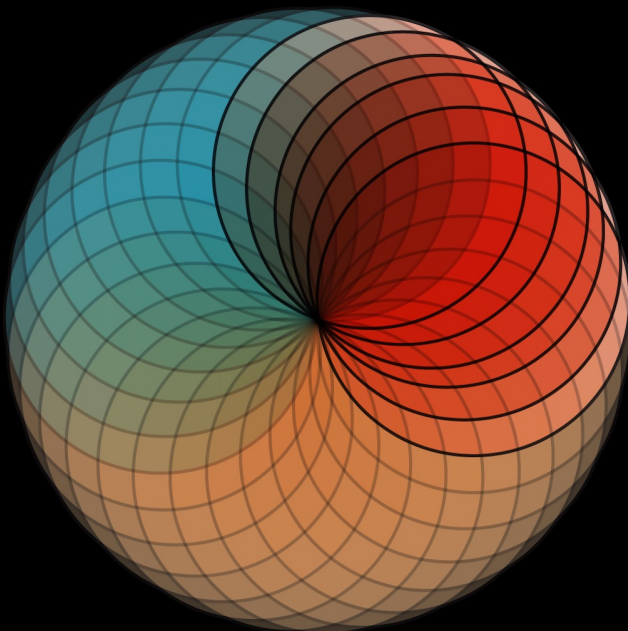
Custom NGS Panels for different diseases (COVID, Lymphoma, Hereditary Telangiectasia Type 2, etc)

Locus Hq 19	Genes	Coding
chr1:214524509	PTPN14	c.*6756T>C
chr1:214524613	PTPN14	c.*6652A>G
chr1:214524620	PTPN14	c.*6645insG
chr1:214524622	PTPN14	c.*6643T>C
chr1:214524754	PTPN14	c.*6511G>A
chr1:214525316	PTPN14	c.*5949T>G
chr1:214525603	PTPN14	c.*5662T>C
chr1:214526332	PTPN14	c.*4933T>C
chr1:214526363	PTPN14	c.*4902A>T
chr1:214526612	PTPN14	c.*4653A>C
chr1:214526964	PTPN14	c.*4301A>G
chr1:214527252	PTPN14	c.*4013C>T
chr1:214529147	PTPN14	c.*2118C>G

Bioinformatic analysis 20.000

TCGA, MIRNA, GENESPRING, GENE EXPRESSION, FEATURE EXTRACTION, STRING, Ingenuity Pathway Analysis, MIRBASE, MRNA-MIRNA NETWORK MIRTARGETLINK, VARIANT CALLER

Cell-of-Origin Patterns

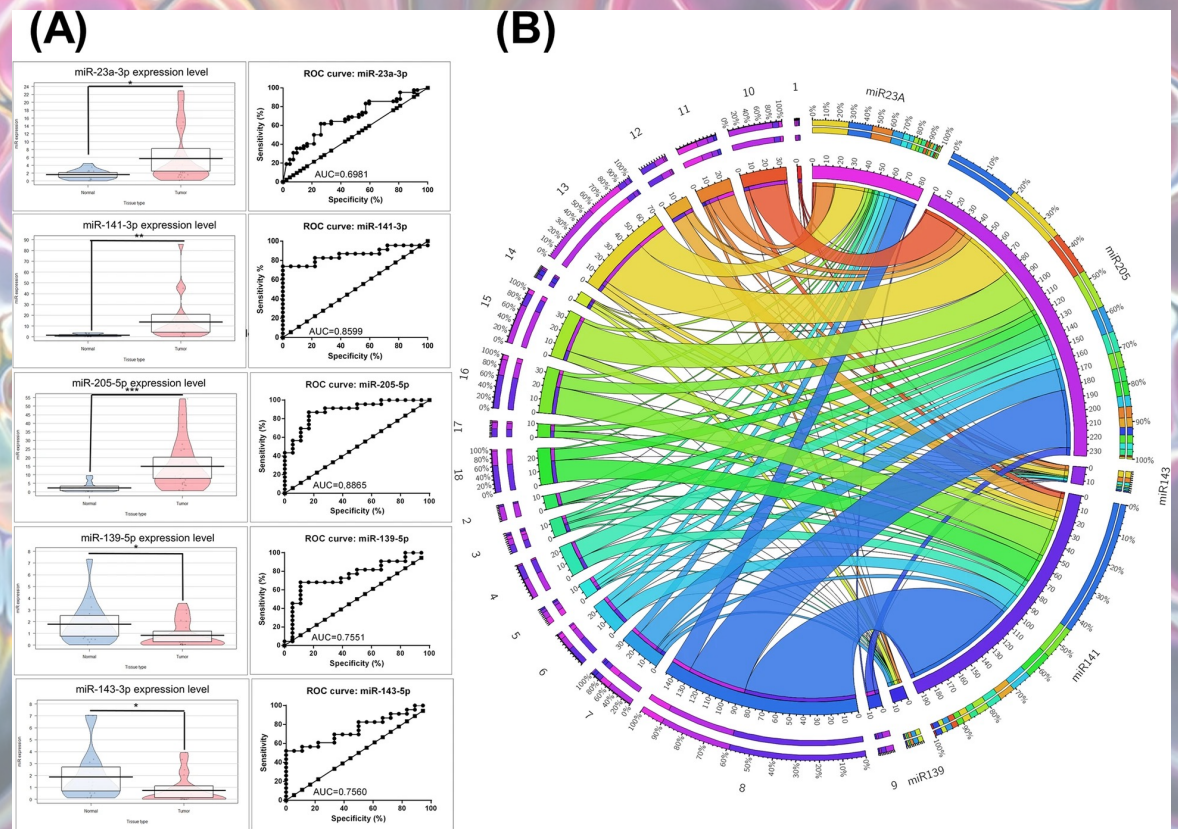
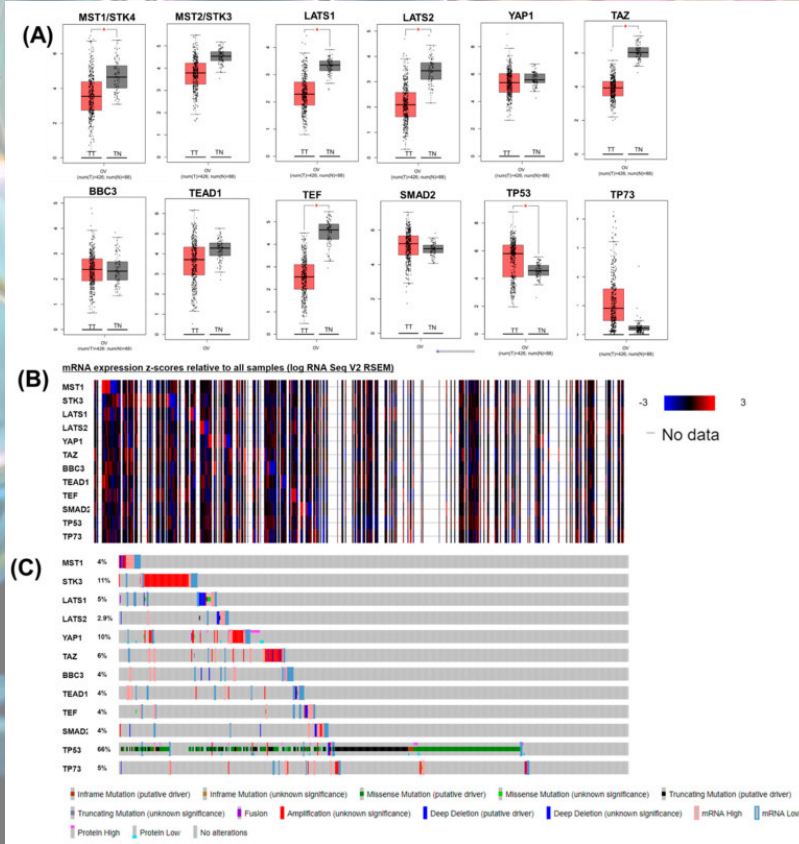




qRT-PCR

24.000 gene expression tests, miRNA, lncRNA

Cells, exosomes, tissues, serum, plasma, blood, urine samples





GEN  **mics**

qRT-PCR

60.000 tests done for SARS-CoV-2 diagnosis

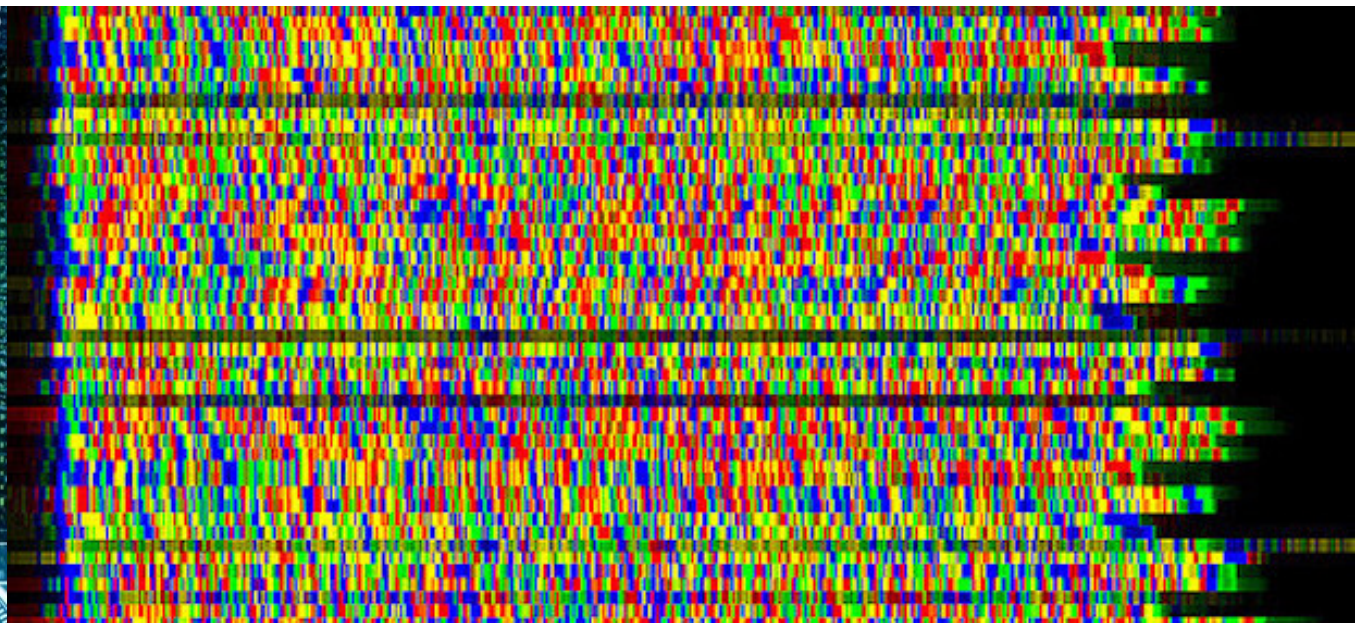
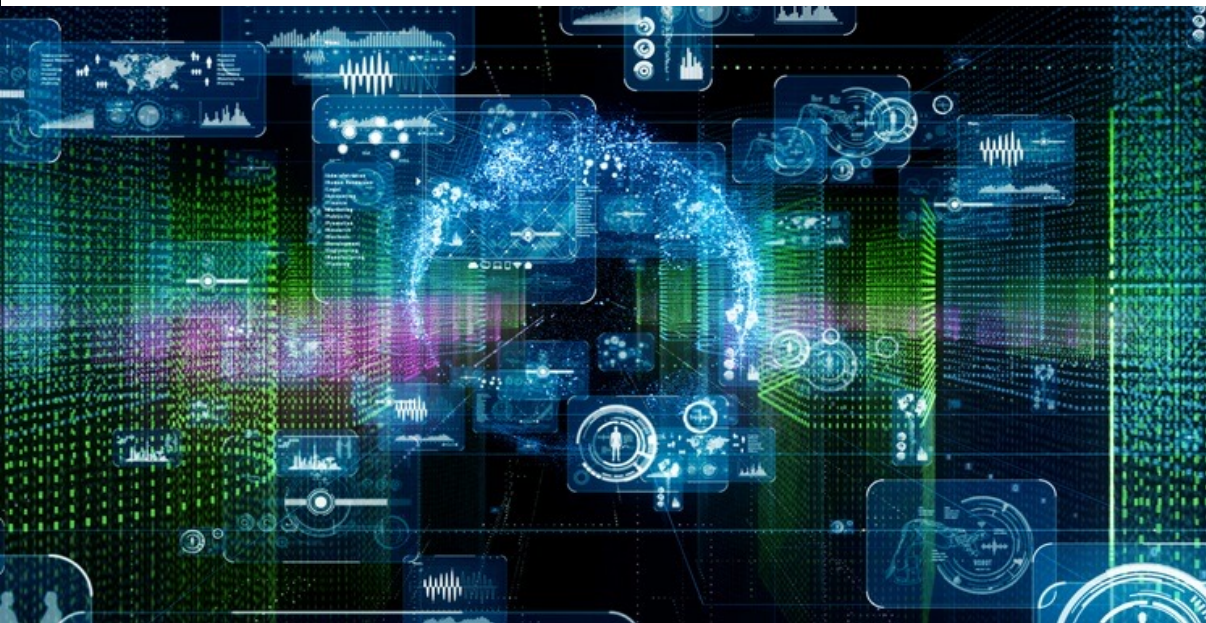


GEN  **MICS**

**GENOMICS TEAM
TOP 2% MOST CITED
AUTHORS WORLDWIDE
IN 2020, 2021**



THE FUTURE IN HEALTH THROUGH INNOVATION





GENOMICS



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