Comprehensive Genomics Shared Resource

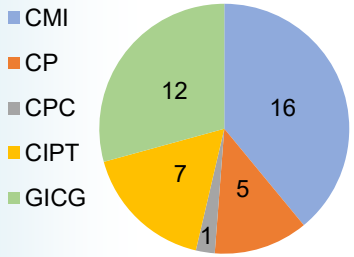
RUTGERS Cancer Institute of New Jersey
RUTGERS HEALTH

NCI Comprehensive Cancer Center
A Cancer Center Designated by the National Cancer Institute

Aims

- Co-managed by CINJ and the New Jersey Medical School we provide cutting-edge sequencing platforms to decode genomic, epigenetic, and transcriptomic information in support of clinical and basic research
- Continue to provide techniques relevant to genomics, including sample preparation, single cell sequencing, and FISH, and increase the inclusion of clinical testing panels
- Continue to evaluate new sequence technologies supported by service development surveys that will assess member needs
- Provide advanced training, workshops, seminars, and educational programs for members, trainees, and, more broadly, the Rutgers community

Research Program Support (2018–2022)



41 Members

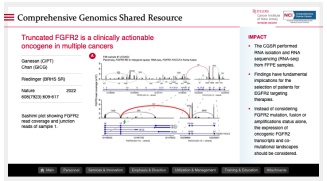
Publications

Total	30
IF >10	9

Peer-Reviewed Grants

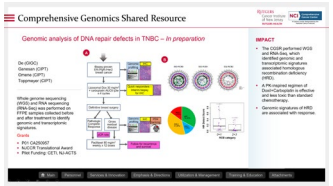
All	13 (1T)
NCI	3 (1T)

CIPT, GICG



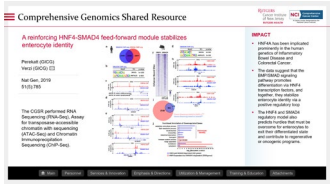
Nature, 2022

CIPT, GICG



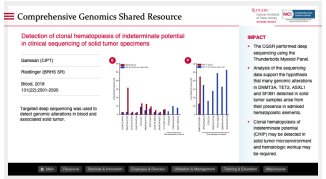
Ongoing project

GICG



Nat Genetics, 2019

CIPT



Blood, 2018

Leading Personnel & Roles

Patricia Soteropoulos, PhD
Director

Emmanuel Zachariah, PhD
Senior Molecular Biologist

Veera D'Mello, PhD
Research Technician Specialist

Curtis Krier
Manager

As Needed

Mainul Hoque, PhD
Research Genomics Supervisor

Deanna Streck
Clinical Genomics Supervisor

Alexander Lemenze, PhD
Sequencing Quality Control and Assurance

Services & Innovation

New

- Fixed RNA Single Cell Sequencing
  - 10x Genomics, Honeycomb, Parse
- Additional Educational Opportunities
  - Lectures for CINJ Trainees
  - Resident/Fellow Clinical Genomics and Cytogenetics Rotations

Continuing

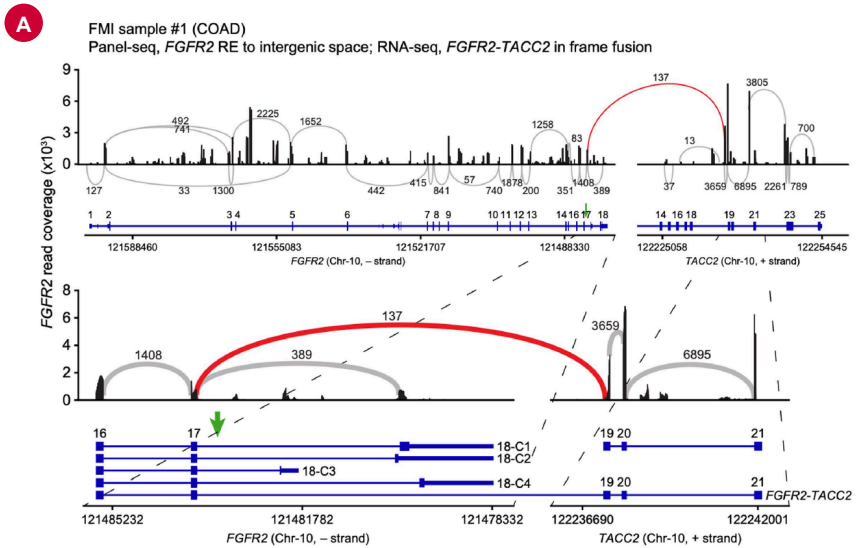
- RNA Sequencing
- DNA Sequencing
- Single Cell Sequencing
- Long Read Sequencing
- Microarray Analysis
- Quantitative PCR Analysis
- Sanger Sequencing
- Fragment Analysis
- Nucleic Acid Isolation and Q/C
- Lectures, Lab Training, Research Rotations, and Fellowships

Truncated FGFR2 is a Clinically Actionable Oncogene In Multiple Cancers

Ganesan (CIPT) ✉
Chan (GICG)

Riedlinger (BRHS SR co-author)

Nature, 2022
608(7923):609-617



Sashimi plot showing FGFR2 read coverage and junction reads

IMPACT

- The CGSR performed RNA isolation and RNA sequencing (RNA-seq) from FFPE samples
- Findings have fundamental implications for the selection of patients for FGFR2 targeting therapies
- Instead of considering FGFR2 mutation, fusion or amplifications status alone, the expression of oncogenic FGFR2 transcripts and co-mutational landscapes should be considered

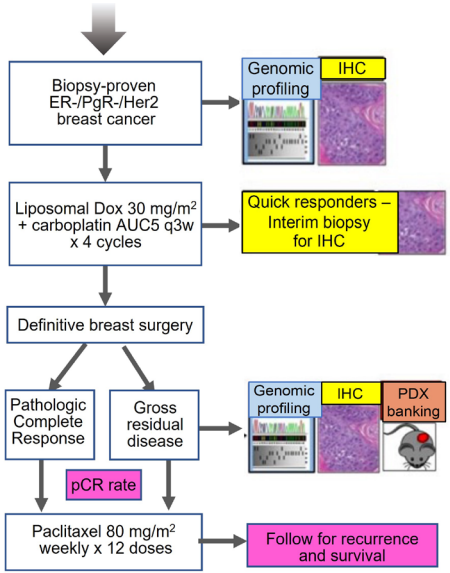
Genomic Analysis of DNA Repair Defects in TNBC – *In preparation*

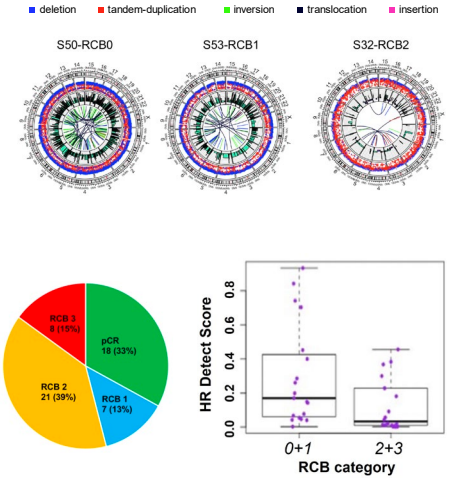
De (GIGC)
Ganesan (CIPT)
Omene (CIPT)
Toppmeyer (CIPT)

Whole genome sequencing (WGS) and RNA sequencing (RNA-Seq) was performed on FFPE samples collected before and after treatment to identify genomic and transcriptomic signatures

Grants

- P01 CA250957
- NJCCR Translational Award
- Pilot Funding: CETI, NJ-ACTS





IMPACT

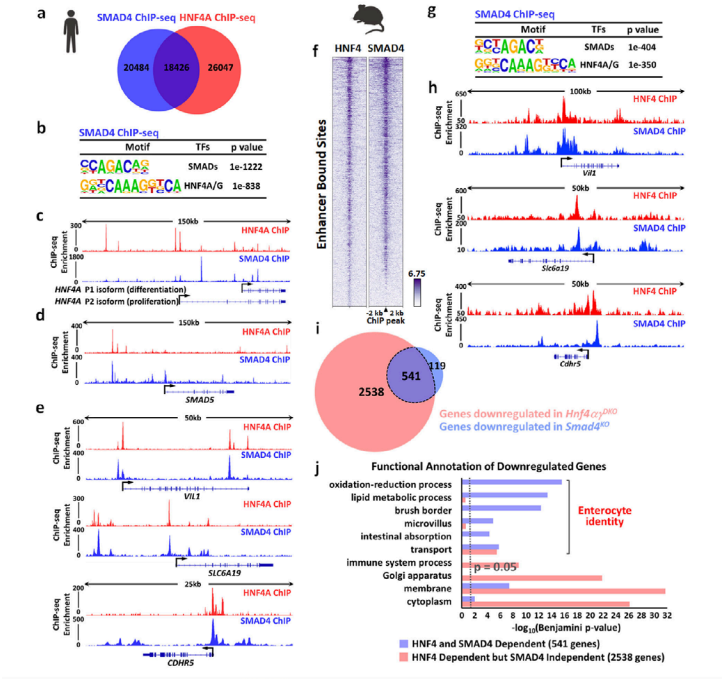
- The CGSR performed WGS and RNA-Seq, which identified genomic and transcriptomic signatures associated homologous recombination deficiency (HRD) in 50 TNBCs
- A PK-inspired regimen of Doxil+Carboplatin is effective and less toxic than standard chemotherapy
- Genomic signatures of HRD are associated with response

A Reinforcing HNF4-SMAD4 Feed-Forward Module Stabilizes Enterocyte Identity

Perekatt (GICG)
Verzi (GICG) ✉

Nat Gen, 2019
51(5):785

The CGSR performed RNA Sequencing (RNA-Seq), Assay for transposase-accessible chromatin with sequencing (ATAC-Seq) and Chromatin Immunoprecipitation Sequencing (ChIP-Seq)



IMPACT

- HNF4A has been implicated prominently in the human genetics of Inflammatory Bowel Disease and Colorectal Cancer
- The data suggest that the BMP/SMAD signaling pathway promotes differentiation via HNF4 transcription factors, and together, they stabilize enterocyte identity via a positive regulatory loop
- The HNF4 and SMAD4 regulatory model also predicts hurdles that must be overcome for enterocytes to exit their differentiated state and contribute to regenerative or oncogenic programs

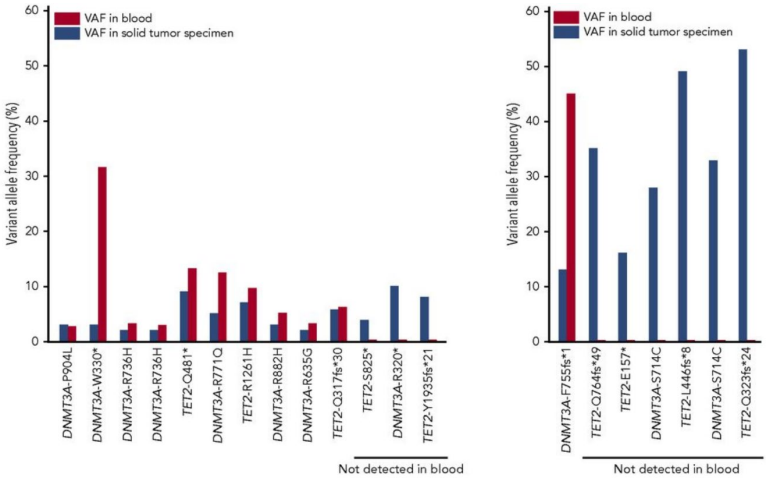
Detection of Clonal Hematopoiesis of Indeterminate Potential in Clinical Sequencing of Solid Tumor Specimens

Ganesan (CIPT)

Riedlinger (BRHS SR co-author)

Blood, 2018
131(22):2501-2505

Targeted deep sequencing was used to detect genomic alterations in blood and associated solid tumor



IMPACT

- The CGSR performed deep sequencing using the Thunderbolts Myeloid Panel
- Analysis of the sequencing data support the hypothesis that many genomic alterations in DNMT3A, TET2, ASXL1 and SF3B1 detected in solid tumor samples arise from their presence in admixed hematopoietic elements
- Clonal hematopoiesis of indeterminate potential (CHIP) may be detected in solid tumor microenvironment and hematologic workup may be required

Emphasis and Future Directions

- Work with SRM and members in New Brunswick to evaluate and perform a needs assessment for Spatial Transcriptomics Platforms
- Seek Funding to Upgrade Illumina Equipment
- Investigate New Genomics Technologies
- Survey Faculty Regarding New Services and Technologies
- Add Additional Lab Rotation and Fellowship Opportunities
- Outreach for Clinical Research and Diagnostic Services
- Expand training and education for RWJMS and NJMS residents and fellows

Training and Education

New

- Presentations to CINJ Trainees
- Presentations to CINJ Research Programs
- Resident/Fellow Training in Clinical Genomics and Cytogenetics

Proposed Resident/Fellow Clinical Genomics and Cytogenetics Rotation

Schedule	1	2	3	4	5
	Introduction to Clinical Molecular Genomics and Cytogenetics	Clinical Molecular Genomics	Clinical Molecular Genomics	Clinical Molecular Genomics & Clinical Cytogenetics	Clinical Cytogenetics
	Tour	Microarray, MLPA, Fragment Analysis	Next Generation Sequencing: Library Generation, Quantification, Normalization, Alignment, Coverage	Specimen Types, Harvesting, Banding Techniques and FISH, Karyotyping	Interpretation of Prenatal, Pediatric, Adult, Hematolymphoid and Solid Tumor Cytogenetics
	Introductory Lectures: Laboratories, Testing Types, Methods, Equipment utilized, Laboratory Accreditation	Result Analysis, Allele Frequency, Risk Assessment, Review of Report formats	Databases and Variant Interpretation NGS Panels and Medical Exome	Review of NGS data, Oncology Tiers, Research Opportunities: Single Cell Sequencing, Transcriptomics, Whole Genome, ChIP-seq	Correlation of Karyotyping Data with Clinical History, and other Studies Including Morphology, Immunohistochemistry and Molecular Findings

Continuing

- Laboratory Training in Genomics Methods
- Research Rotations
- Laboratory Genetics and Genomics Fellowship
- Core Facilities Technology Series
- Intro to Genomics, Proteomics and Bioinformatics Grad School Course
- Lecture in Medical School and Graduate School Courses

Comprehensive Genomics Shared Resource

Rutgers Cancer Institute of New Jersey
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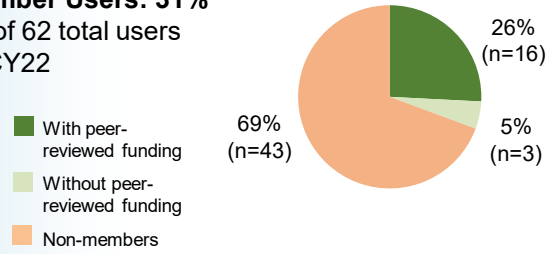
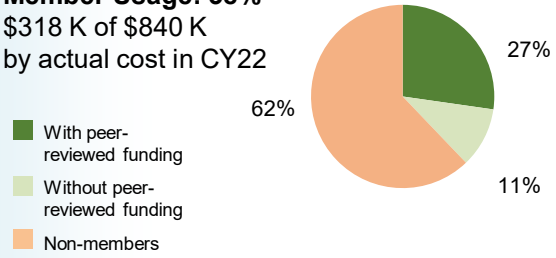
NCI Comprehensive Cancer Center
A Cancer Center Designated by the National Cancer Institute

Management & Accounting

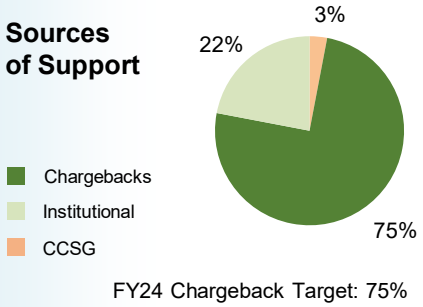
Member Users: 31%
19 of 62 total users in CY22



Member Usage: 38%
$318 K of $840 K by actual cost in CY22

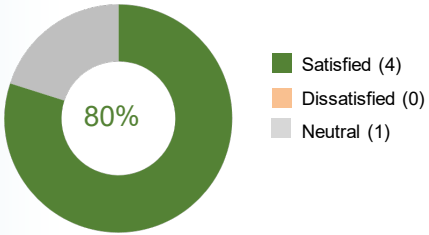


Sources of Support



FY24 Chargeback Target: 75%

Satisfaction Survey for CY22 services



Participated: 5 of 19 members (26%)

Organization & Governance

CGSR

2.1 FTE

SRACs

- Advisory Committee meets annually
- Discusses operational and scientific progress
- SRM supports organization

SRM

- SR Faculty Directors report to the ADSR
- SRM tracks and supports SRAC recommendations, productivity, service development, outreach

CINJ Director

- RLC
- Finance & Admin
- EAB

Supporting Information

Program Support

- Publications
- Grants
- 5-Year User List

Advisory Committee

- FY23 Presentation
- Action Items
- Notes

Quality Satisfaction

- Annual Survey Action Items

SR Usage

- CY22 Usage

Submitted Information

- Research Strategy
- Aims
- SRM Research Strategy