

TCGA and Beyond: Whole-Genome Data Powering the Next Era of Cancer Intelligence

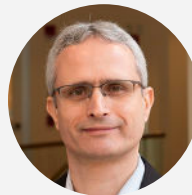
Monday, April 20th at 12:30 PM - Theater A

Learn about a transformational cancer genome initiative by Broad Institute and Inocras analyzing over 8,500 TCGA tumor-normal samples using whole-genome bioinformatics pipelines from Broad and Inocras. Professors Getz and Rheinbay will present novel findings showing how whole-genome analytics expand the variant landscape, improve driver gene discovery, and enable new

actionable insights. Professor Ju will introduce an AI-powered whole genome analytics platform built to power cancer whole genome analysis and insights at scale. Join us to learn how cancer whole genome analysis unlocks new insights and explore our next initiative to advance precision oncology.



Jehee Suh, MBA
CEO Inocras



Gad Getz, PhD
Harvard Medical School, Massachusetts General Hospital Cancer Center, Broad Institute



Esther Rheinbay, PhD
Harvard Medical School, Massachusetts General Hospital Cancer Center, Broad Institute



Youngseok Ju, MD, PhD
Co-Founder at Inocras, Korea Advanced Institute of Science and Technology

Cancer Genome Collaboration Posters

Uncovering therapeutically targetable mutations from The Cancer Genome Atlas (TCGA) whole-genome datasets

Presenter: Ryul Kim / Inocras

April 19th, 2026 2:00 p.m.- 5:00 p.m. | Poster #492

Origins of Structural Variant Junctional Insertions Across >8,000 TCGA Whole Genomes

Presenter: Youyun Zheng / Beroukhim Lab / Broad Institute

April 20th, 2026 2:00 p.m.- 5:00 p.m. | Poster #3247

Discovery of Coding and Non-coding Driver Mutations Across >8,000 TCGA Whole Genomes

Presenter: Ron Solan / Getz Lab / Broad Institute

April 20th, 2026 9:00 a.m.-12:00 p.m. | Poster #2001

Systematic Discovery of Structural Variant Drivers Across >8,000 TCGA Whole Genomes

Presenter: Antonia Kowalewski / Getz Lab / Broad Institute

April 20th, 2026 9:00 a.m.-12:00 p.m. | Poster #1989

Pan-cancer PCR-free whole-genome sequencing refines the somatic driver landscape beyond exome sequencing alone

Presenter: Gengchao Wang / Rheinbay Lab / Broad Institute

April 20th, 2026 9:00 a.m.-12:00 p.m. | Poster #1990

Copy number analysis of regulatory regions reveal recurrent promoter/enhancer somatic copy number alterations across >8000 TCGA samples

Presenter: Haruna Tomono / Meyerson Lab / Broad Institute

April 20th, 2026 9:00 a.m.-12:00 p.m. | Poster #1978

The pan-cancer landscape of chromosome Y alterations

Presenter: Luis Antonio Corchete Sanchez / Rheinbay Lab / Broad Institute

April 20th, 2026 9:00 a.m.-12:00 p.m. | Poster #1986

The landscape of X chromosome copy number alterations in cancer

Presenter: Matthew Joseph Leventhal / Zhang Lab / Broad Institute

April 20th, 2026 9:00 a.m.-12:00 p.m. | Poster #2002

Germline predisposition in The Cancer Genome Atlas (TCGA) whole-genome sequencing datasets

Presenter : Ryul Kim / Inocras

April 20th, 2026 9:00 a.m.-12:00 p.m. | Poster #1991

Pan-cancer LINE-1 retrotransposition landscapes in TCGA whole-genome sequences

Presenter: Beomki Lee / Kaist

April 20th, 2026 9AM-12 PM | Poster #1980

Whole-genome sequencing of >8,000 TCGA samples reveals diverse and atypical spectra of homologous recombination deficiency in primary human cancers

Presenter: Joonoh Lim / Inocras

April 20th, 2026 9:00 a.m.-12:00 p.m. | Poster #1977

Genomic signatures of chromosomal instability from a pan-cancer landscape of haplotype-specific copy-number alterations

Presenter: Chunyang Bao / Inocras

April 21st, 2026 2:00 p.m.-5:00 p.m. | Poster #5934

Structural Variant Signature Discovery Across >8,000 TCGA Whole Genomes Using QuantHDP

Presenter: Gregory Raskind / Beroukhim Lab / Broad Institute

April 22nd 9:00 a.m.-12:00 p.m. | Poster #7274

Fast and Cost-effective Cloud-based Pipelines to Analyze Cancer Sequencing Data

Presenter: Sam Wiseman / Getz Lab / Broad Institute

April 22nd 9:00 a.m.-12:00 p.m. | Poster #6881

Comprehensive mutation profiling from The Cancer Genome Atlas (TCGA) whole-genome sequencing datasets

Presenter: Chunyang Bao / Inocras

April 22nd, 2026 9:00 a.m.-12:00 p.m. | Poster #7270

AI-Driven stratification of cancer patients using The Cancer Genome Atlas (TCGA) whole-genome sequencing data

Presenter: Jonghoon Lee / Inocras

April 22nd, 2026 9 AM-12 PM | Poster #7268