



UNIVERSITÀ
DI TRENTO

Dipartimento di
Biologia Cellulare, Computazionale e Integrata - CIBIO

24 JUNE

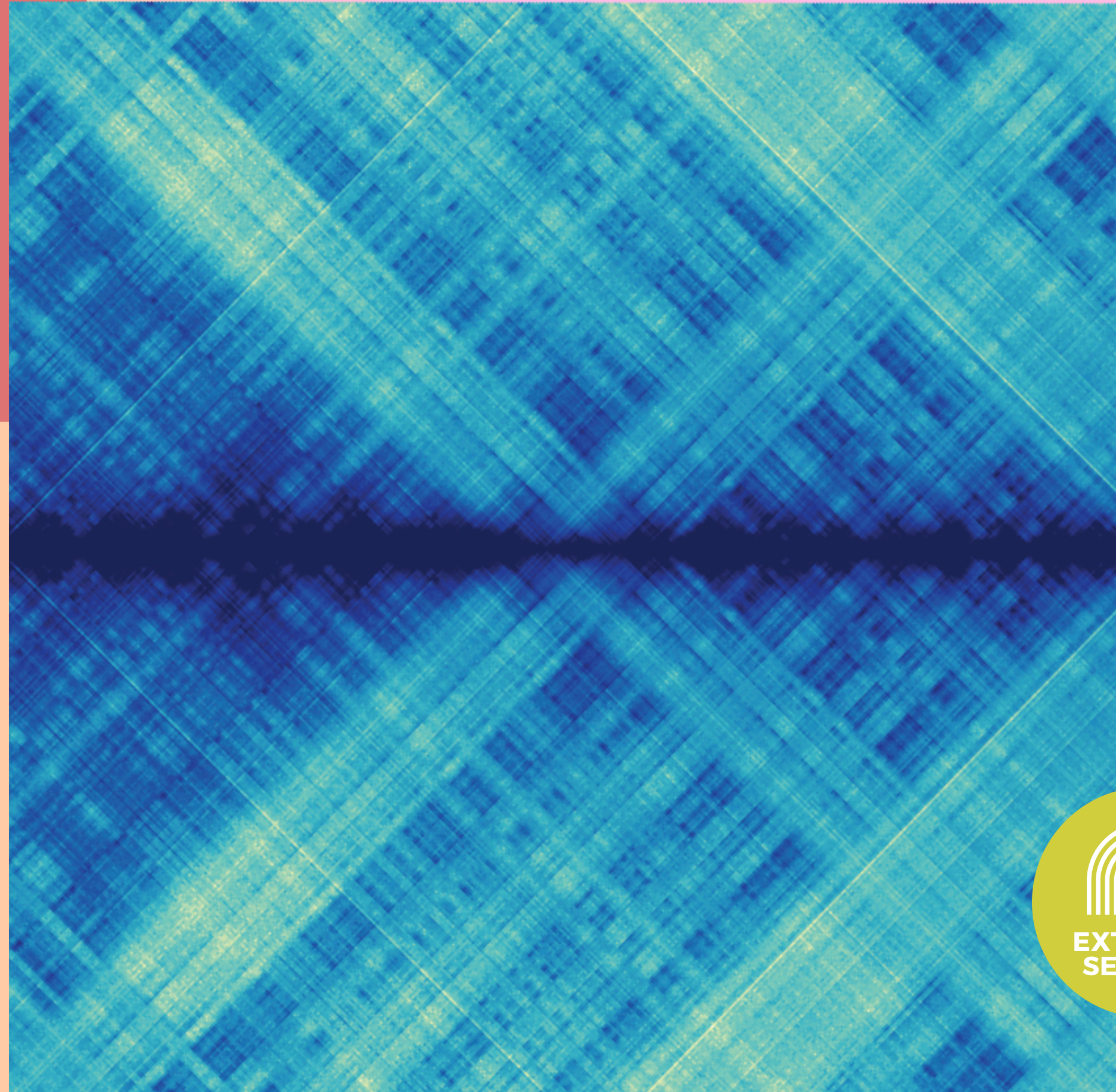
11.30 A.M.

ROOM A102 - POVO1

FRANCESCO FERRARI

IFOM, MILANO

IGM-CNR, PAVIA



● ● **MAPPING CHROMATIN**
● ● **COMPARTMENTS REMODELING**
● ● **IN CANCER BY THEIR**
BIOCHEMICAL PROPERTIES

We developed 4f-SAMMY-seq, an epigenomic method that exploits biochemical properties to map 3D chromatin compartmentalization within a single experiment using small, fresh tissue samples. Applying this to primary prostate cancer biopsies alongside transcriptome analysis revealed two patient subgroups based on structural alterations: Low (LDD) and High (HDD) Degree of Decompartmentalization. The HDD subtype exhibited extensive remodeling and tumor-suppressive transcriptional repression. From this, we derived a robust prognostic signature validated across more than 900 patients, offering a novel tool for diagnostic biopsies.