Centro di Competenza sul Calcolo Scientifico

Piattaforma Genomica di UniTo

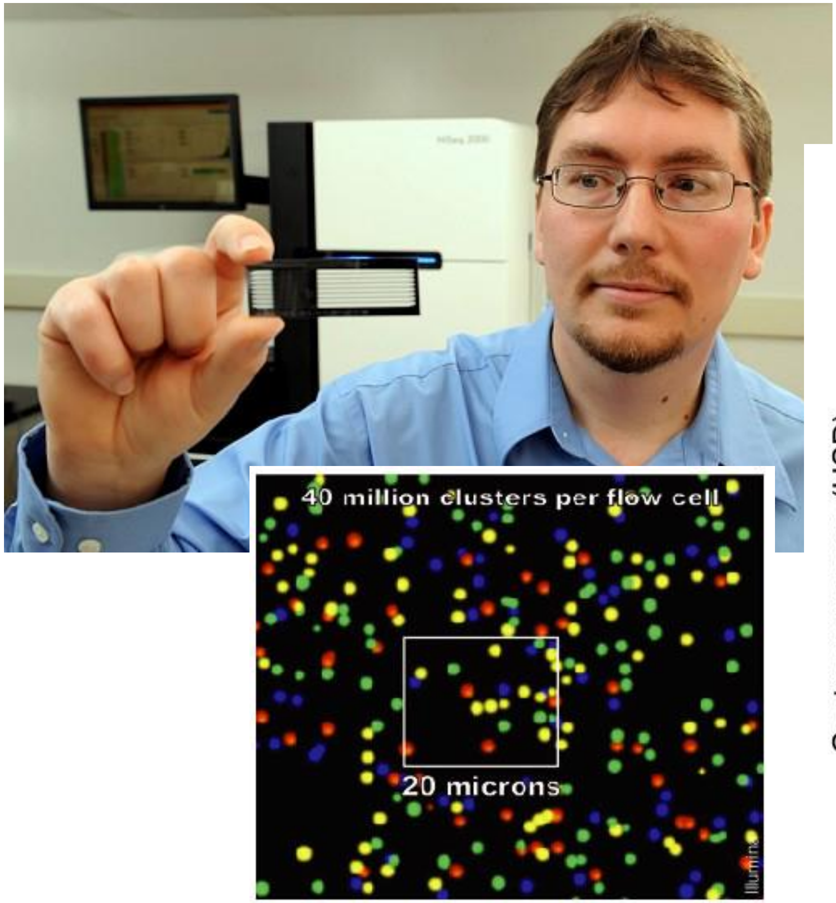
Salvatore Oliviero

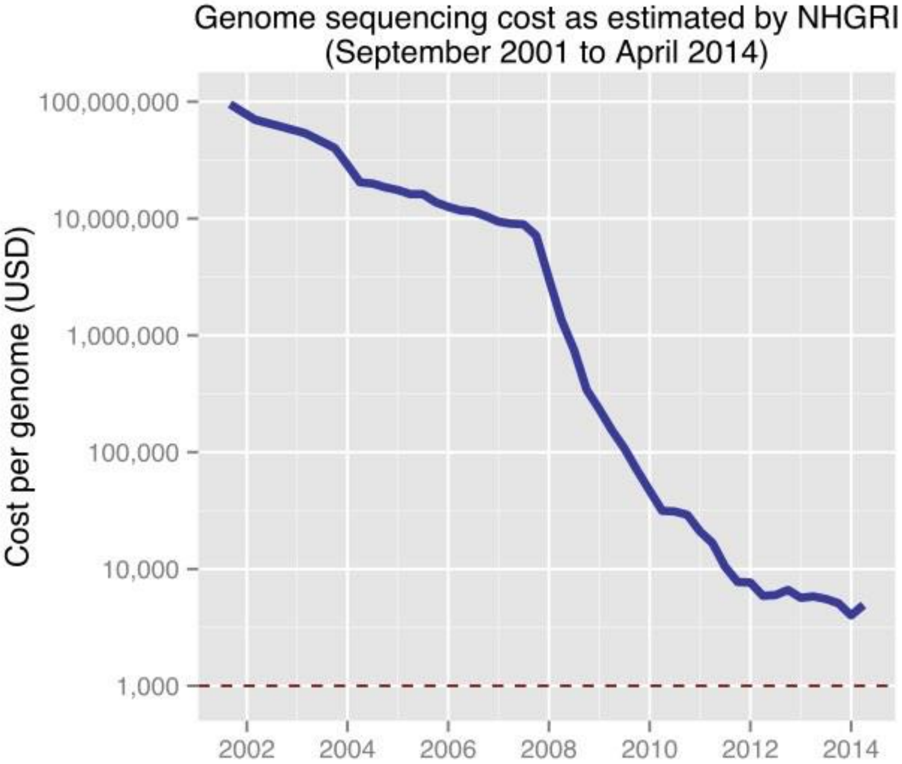
Dipartimento Scienze della Vita e Biologia dei Sistemi

&

HuGeF

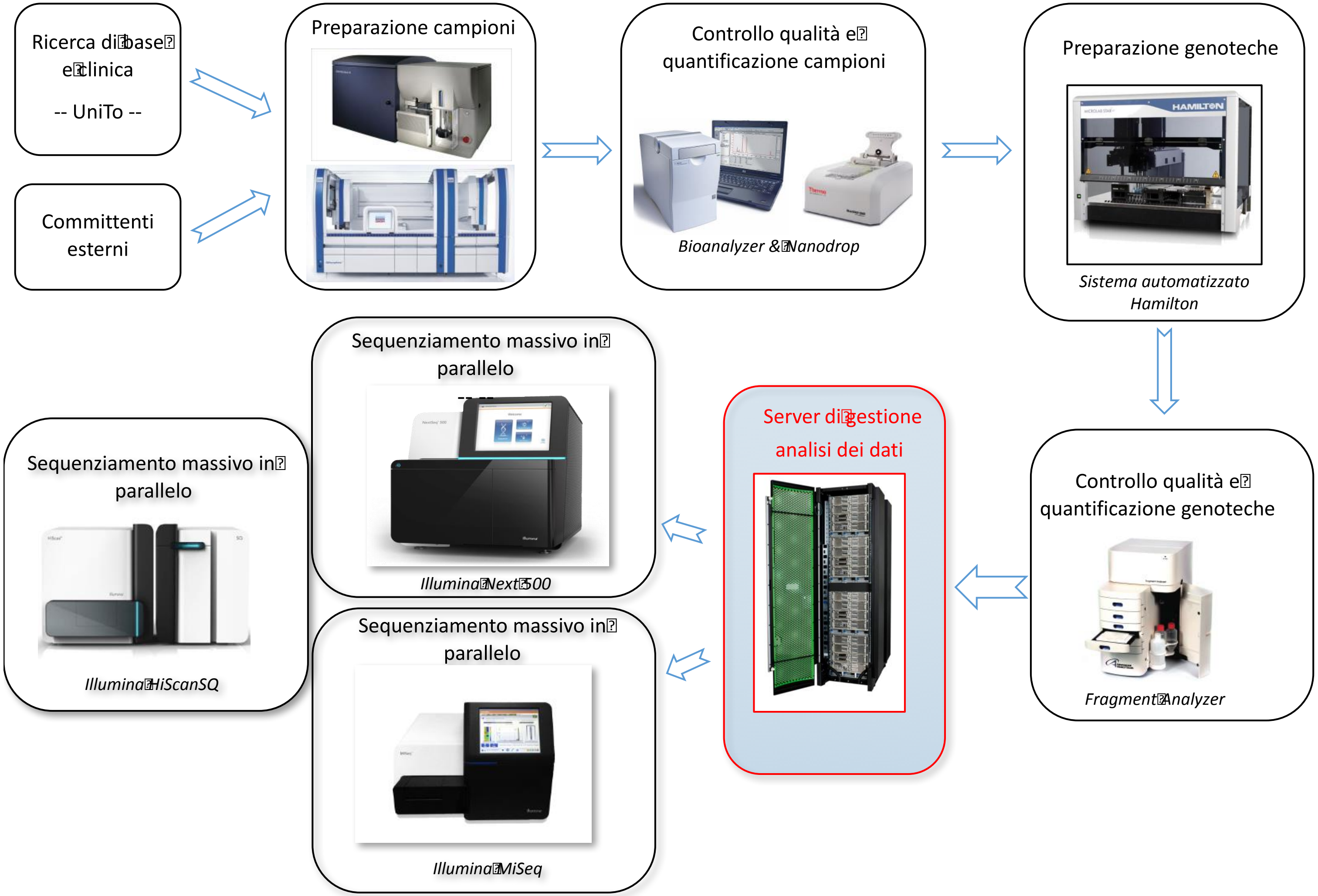
Today state of the art of DNA sequencing





C3S

GENOMIC PLATFORM



Ricerca di base e clinica

-- UniTo --

Committenti esterni

Preparazione campioni

Controllo qualità e quantificazione campioni

Bioanalyzer & Nanodrop

Preparazione genoteche

Sistema automatizzato Hamilton

Controllo qualità e quantificazione genoteche

Fragment Analyzer

Server di gestione analisi dei dati

Sequenziamento massivo in parallelo

Illumina Next 500

Sequenziamento massivo in parallelo

Illumina HiScanSQ

Sequenziamento massivo in parallelo

Illumina MiSeq

UNIVERSITÀ DEGLI STUDI DI TORINO

INFN SEZIONE DI TORINO ISTITUTO NAZIONALE DI FISICA NUCLEARE

Compagnia di San Paolo

HUGEF HUMAN GENETICS FOUNDATION · TORINO

C3S

Lab members:

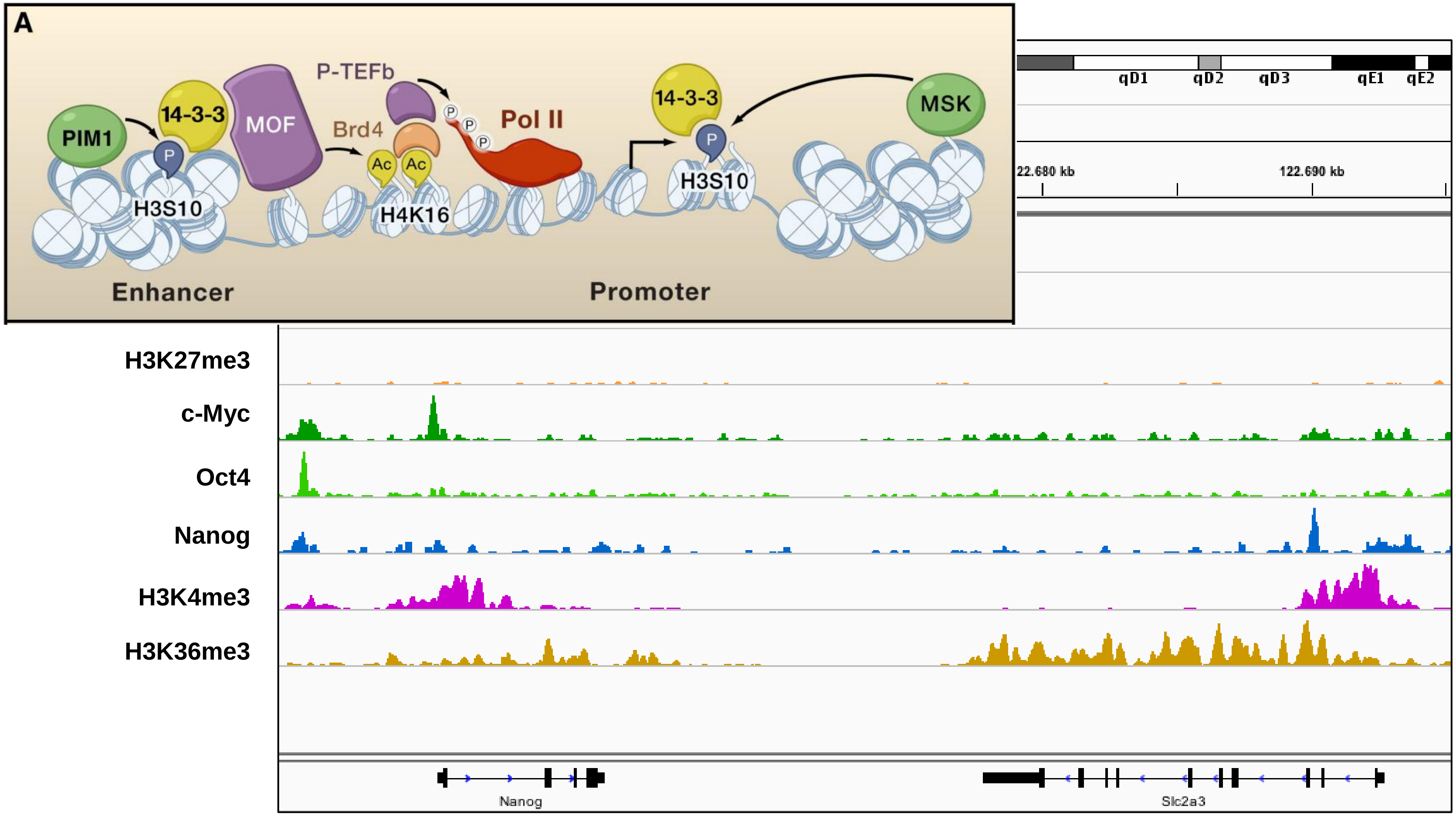
Francesca Anselmi
Giulia Basile
Alessandro Castellino
Matteo Cereda
Stefano Gallo
Danny Incarnato
Ilaria Lupoi
Mara Maldotti
Edoardo Morandi
Caterina Parlato
Valentina Proserpio
Stefania Rapelli

Bioinformatics

new NGS protocols

RNA-sec, Exome-seq, ChIP-seq

ChIP-seq: to map on the genome DNA binding proteins, epigenetic modifications



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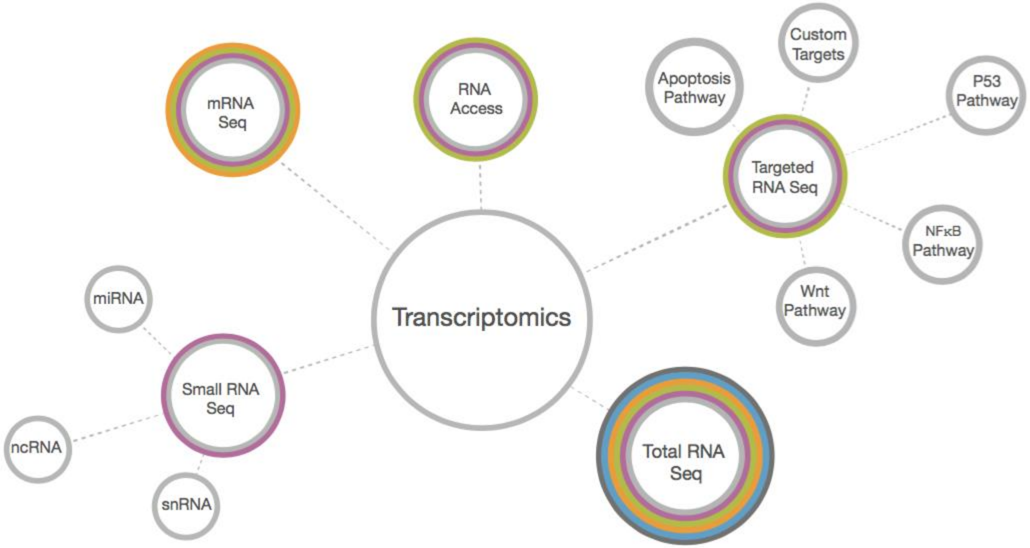
RNA-seq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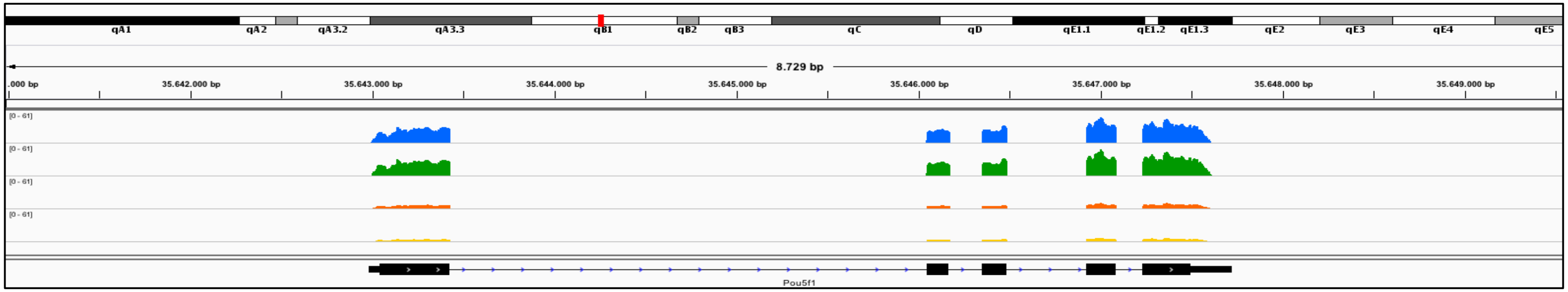
RNA Access
Apoptosis Pathway
Custom Targets
P53 Pathway
Targeted RNA Seq
NFκB Pathway
Wnt Pathway
Transcriptomics
miRNA
Small RNA Seq
ncRNA
snRNA
Total RNA Seq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qA2
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qE2
qE3
qE4
qE5
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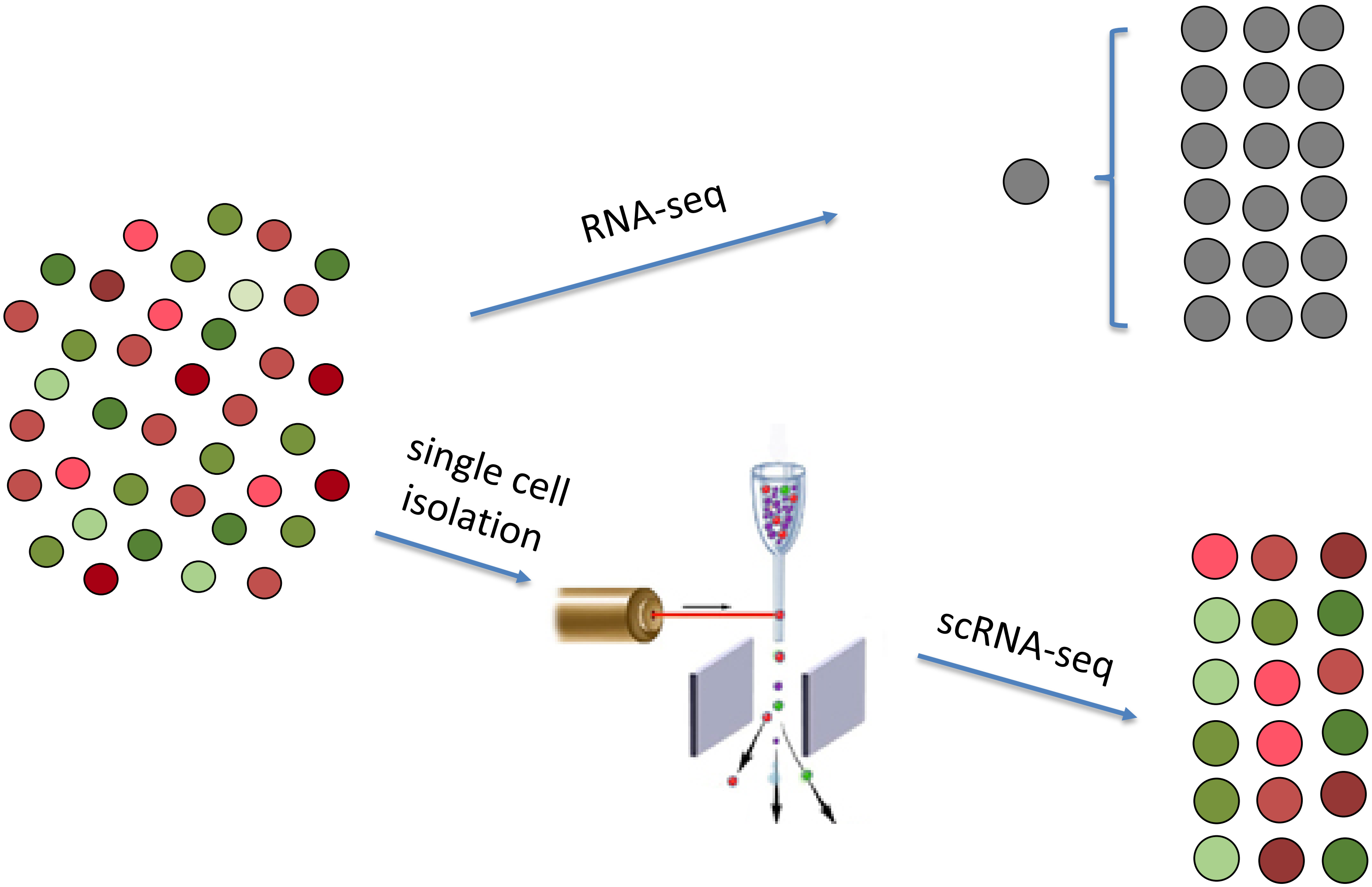
Single cell RNA-seq

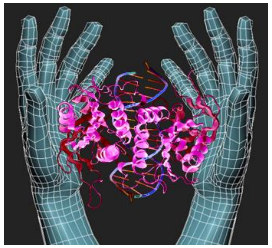


RNA-seq

single cell isolation

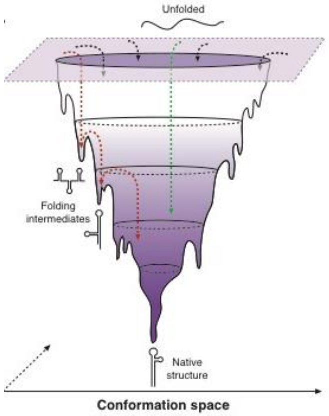
scRNA-seq

New algorithms and NGS protocols



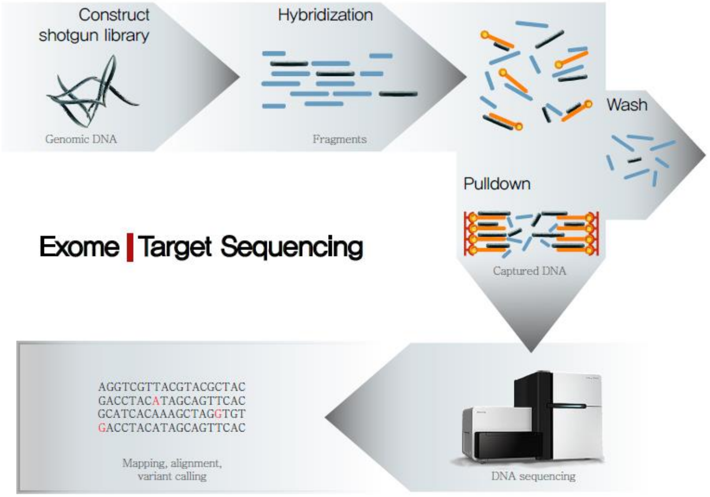
- **MREdictor tool** An highly accurate method for the identification of *bona-fide* microRNAs targets within mammalian genes.
  Incarnato et al. *Nucleic Acids Res. 2013* http://mredictor.hugef-research.org

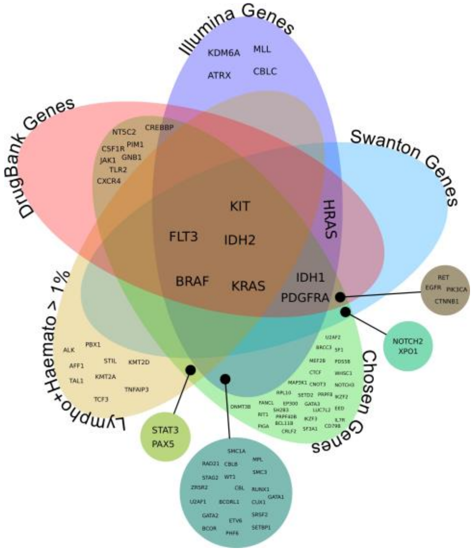
- Single-Base Resolution Analysis of 5-Formyl and 5-Carboxyl Cytosine Reveals Promoter DNA Methylation Dynamics.
  Neri, et al. *Cell Reports. 2015.* Neri et al. *Nature Protocol 2016*



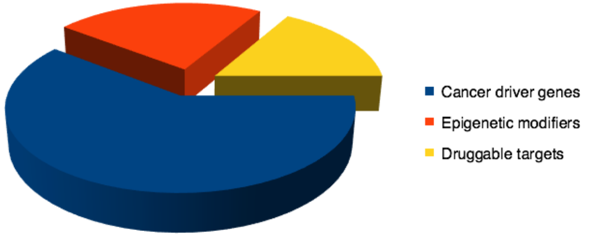
- High-throughput single-base resolution mapping of RNA 2'-O-methylated residues. Incarnato et al. *Nucleic Acids Res. 2016.*
- The RNA *epistructurome*: uncovering RNA function by studying structure and post-transcriptional modifications. Incarnato & Oliviero, *TIBS Submitted*.
- RNA structure framework: automated transcriptome-wide reconstruction of RNA secondary structures from high-throughput structure probing data.
  Incarnato et al. *Bioinformatics* 2016
- Genome-wide profiling of mouse RNA secondary structures reveals key features of the mammalian transcriptome. Incarnato et al. *Genome Biol.* 2014

Tumor whole exomes and targeted gene panels

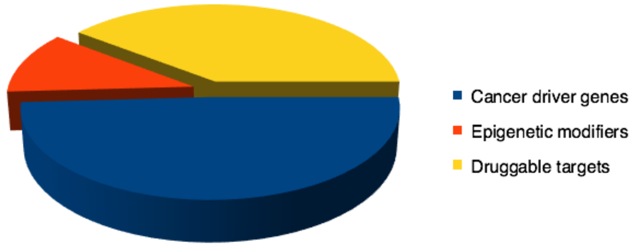




Haematopoietic Panel *
(139 genes)



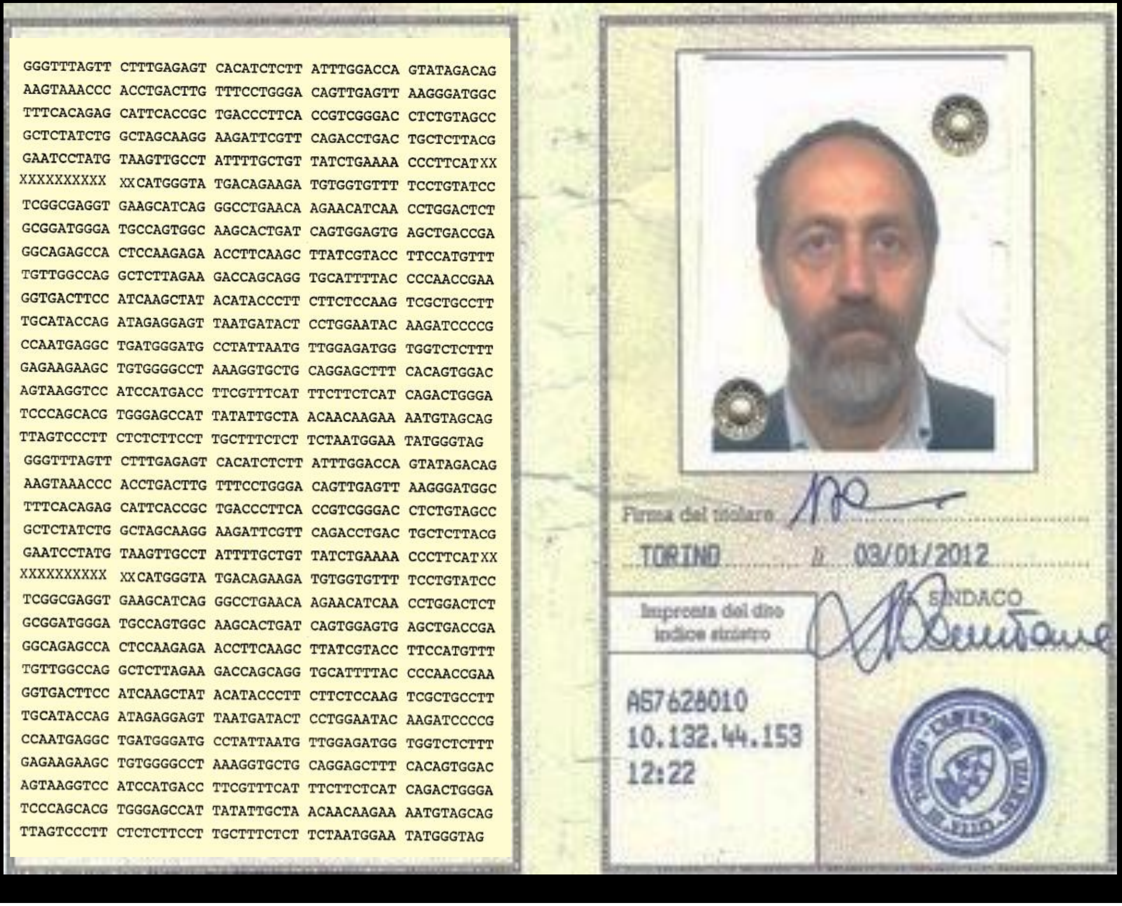
Sarcoma Panel #
(283 genes)



*In collaboration with Anatomia Patologica Molinette

In collaboration with Proff. Silvia Deaglio (HuGeF) and Franca Fagioli (Regina Margherita)

Soon …



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Firma del titolare

TORINO li 03/01/2012

SINDACO

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