Functional Genomics Core Facility (FGCF)

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IRB BARCELONA
INSTITUTE FOR RESEARCH IN BIOMEDICINE

Single Cell Services at IRB Barcelona: From Groundwork to Partnership

Kick-Off meeting - SCENTINEL PROJECT
Heraklion - 21st June 2024

Freddy Monteiro. Functional Genomics Core Facility, IRB Barcelona

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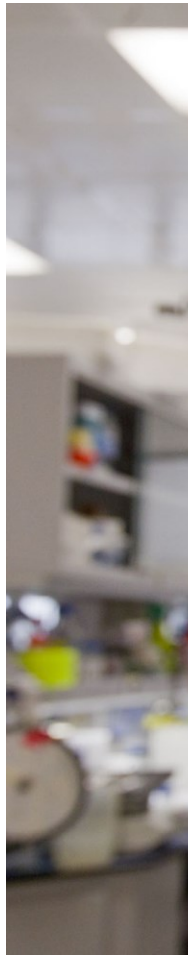
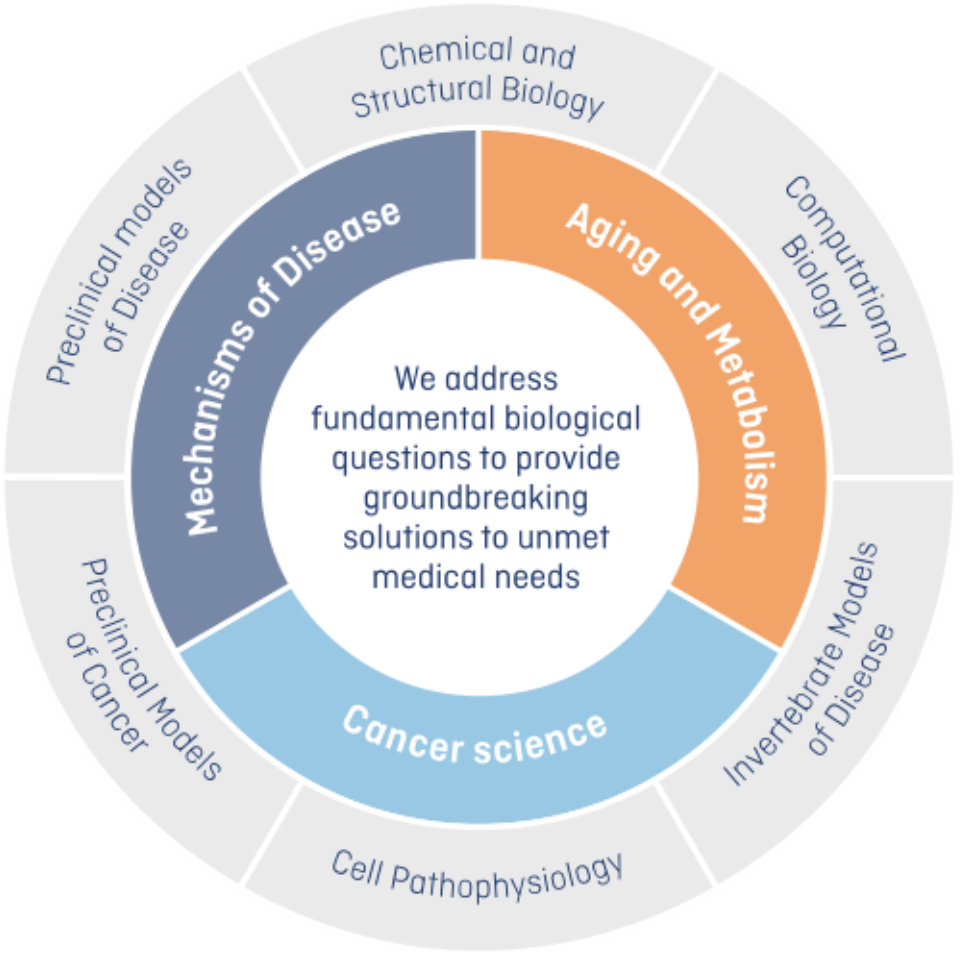
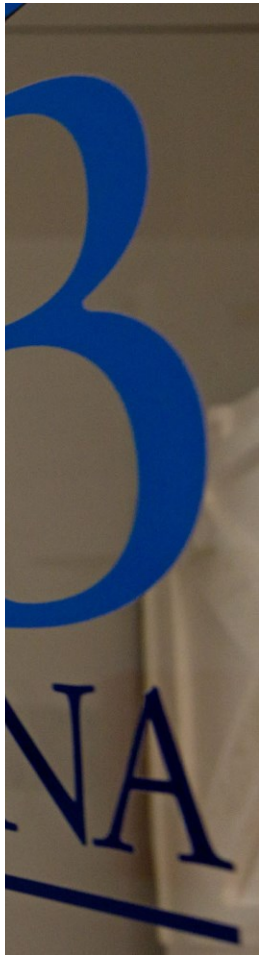
Institut de Recerca Biomèdica (IRB Barcelona)

Parc Científic de Barcelona. C/ Baldiri Reixac 10. 08028 Barcelona







523 Professionals

451 Scientific Staff

57% Women **43%** Men

3 Research Programmes

- Aging and Metabolism
- Mechanism of Disease
- Cancer Science

28 Research groups

9 Core facilities

6 Active spin-offs

https://www.irbbarcelona.org/annualreport2022/

Location

Parc Científic de Barcelona. C/ Baldiri Reixac 10. 08028 Barcelona

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Functional Genomics Core Facility (FGCF)

Team

Nacho Pons, Ph.D.
Senior Research officer

David Fernandez
Technical officer

Quim Perdices
Technical officer

Mariem Dris
Technical officer

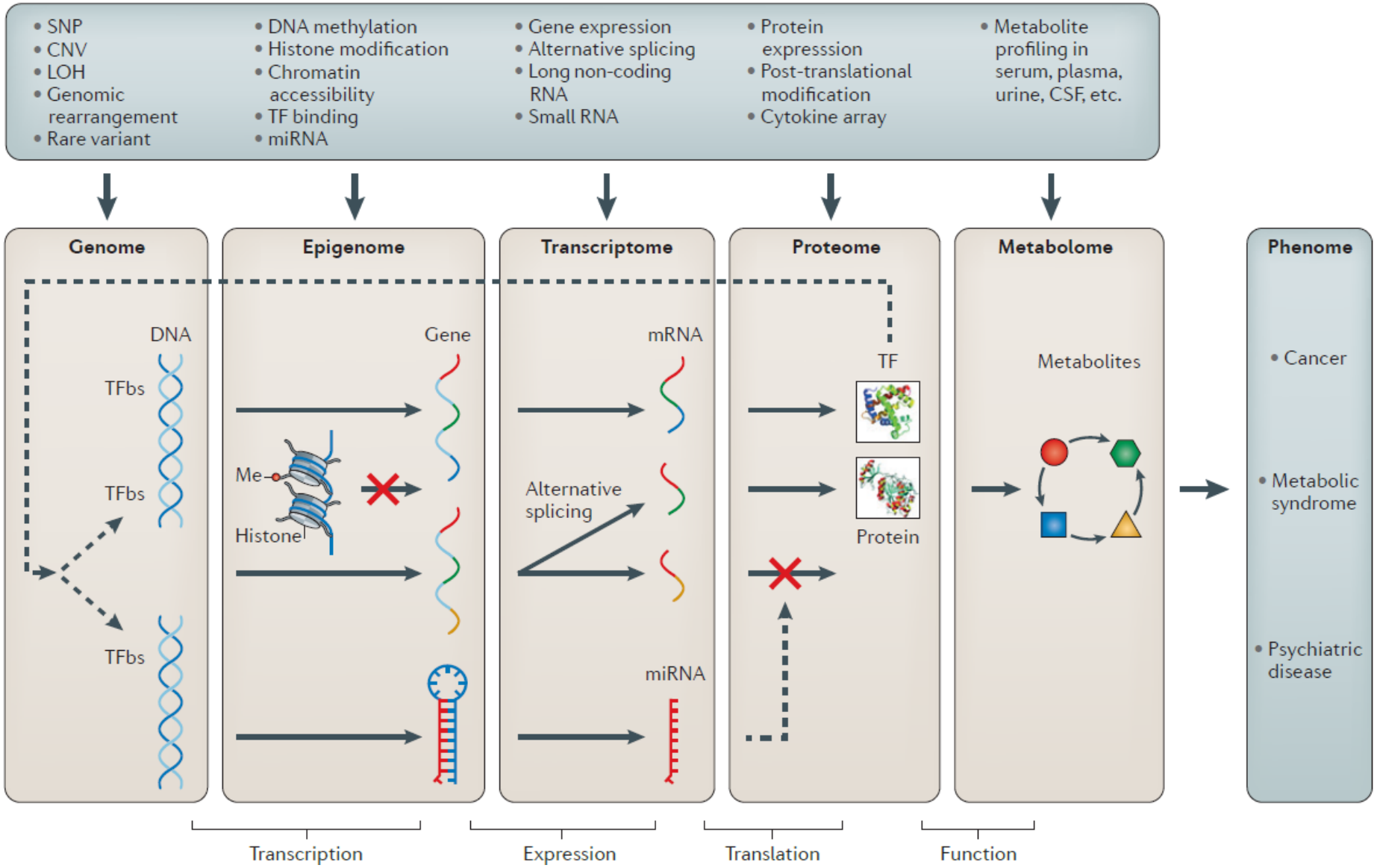
Cecilia Garcia
Research Assistant
(Comp. Genomics Lab)

Freddy Monteiro, Ph.D.
FGCF Manager

genomics@irbbarcelona.org

https://www.irbbarcelona.org/en/research/functional-genomics

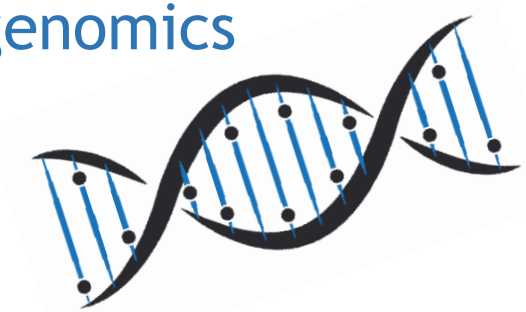
The scope of our work



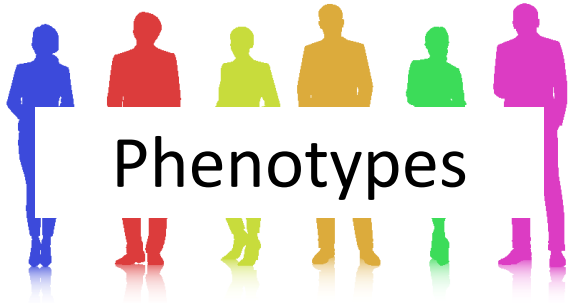
Ritchie et al. Nat. Rev. Genet. 2015 https://www.nature.com/articles/nrg3868

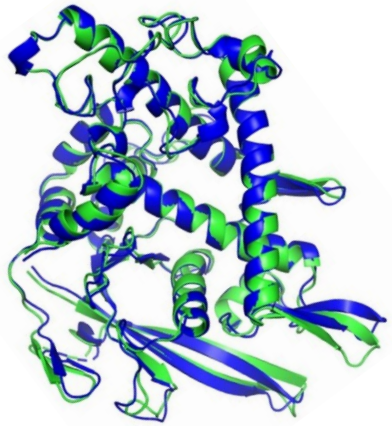
Functional Genomics scope (I)

Genomics and Epigenomics

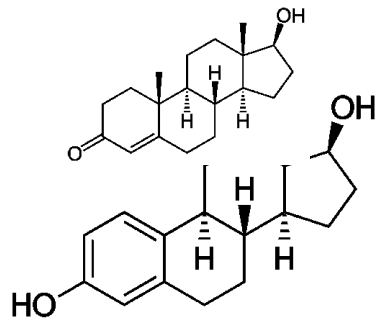


Transcriptomics





Proteomics



Metabolomics

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Workflows

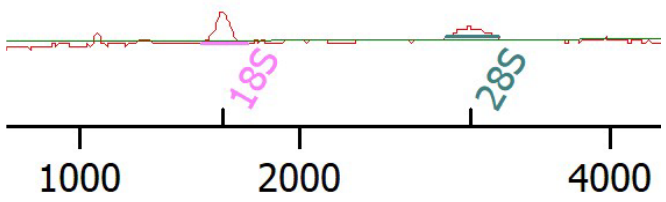
- Common discussion focused on experimental design, troubleshooting, pilot studies, review of results, data interpretations and publication.
- Sample and Library Quality Control
- Nucleic Acids Extraction and Purification
- qPCR
- Affymetrix Microarrays
- Pico profiling
- Single-cell transcriptomics and epigenomics
- NGS libraries for WGS, RNA-seq, ChIP-seq, HI-C sequencing
- *in house* Illumina NextSeq550 Sequencing and externalized sequencing
- *E. coli* ORF and shRNA clone collections (OpenBiosystems 2008 and Mission 2009)

Workflows

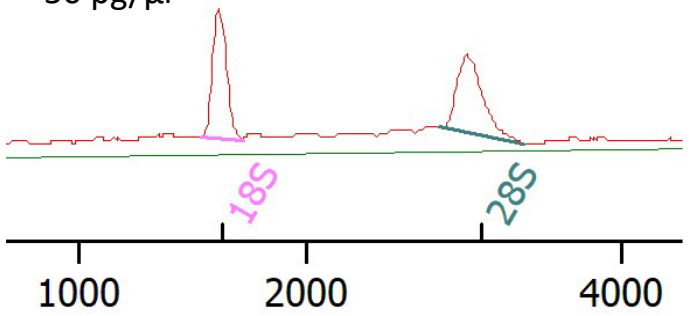
Nucleic Acids Extraction and Purification

- Technical support and troubleshooting of your extractions.
- RNA extraction from single embryos (2.5 onwards), or dozens of flow cytometry-sorted cells.
- DNA, total RNA, poly-A RNA, and small RNA purifications.
- 2021:

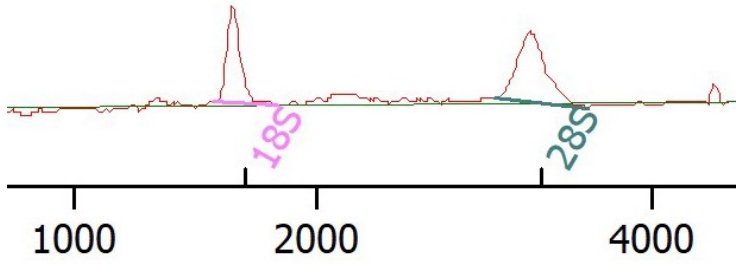
1 mouse embryo (E2.5)
~10 pg/µl



5 mouse embryos (E2.5)
~50 pg/µl



1 human embryo (E3.5)
~68 pg/µl



Workflows

Pico profiling

- Methodology developed at IRB Barcelona.

PLOS ONE

OPEN ACCESS PEER-REVIEWED

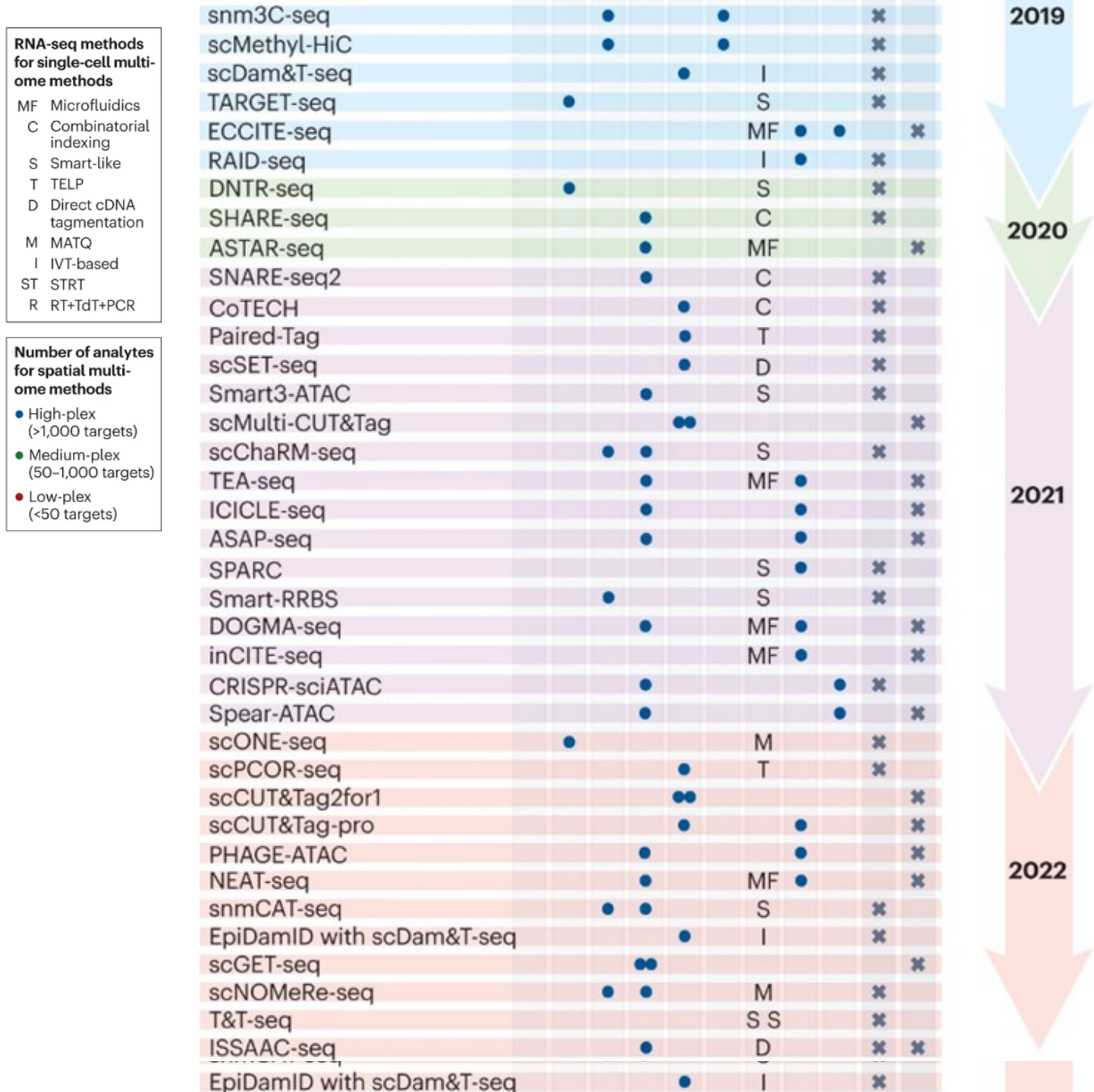
RESEARCH ARTICLE

Accurate Expression Profiling of Very Small Cell Populations

Eva Gonzalez-Roca, Xabier Garcia-Albéniz, Silvia Rodriguez-Mulero, Roger R. Gomis, Karl Kornacker, Herbert Auer

Published: December 28, 2010 • https://doi.org/10.1371/journal.pone.0014418

- Consists of RNA isolation from very small cell populations (10 cells), cDNA synthesis and amplification, labeling of cDNA using biotin and hybridization to Affymetrix expression arrays.
- Current demand from IRB and external groups focus on cDNA synthesis and amplification for gene expression analysis by qPCR.
- 2021: Single mouse embryos (E2.5) yield ~3 µg cDNA at approx. ~70 ng/µl (Ct 15-17 cycles).

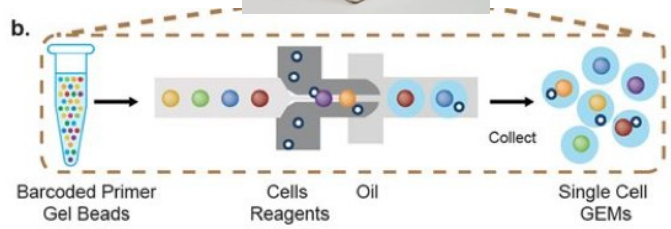


Vandereyken et al., *Nat Rev Genet* (2023).
https://www.nature.com/articles/s41576-023-00580-2

Single-cell cabapilities

Single Cell Transcriptomics, Epigenomics and Multiomics

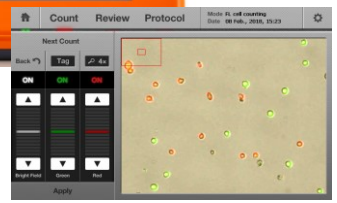
Chromium Controller 10x Genomics™



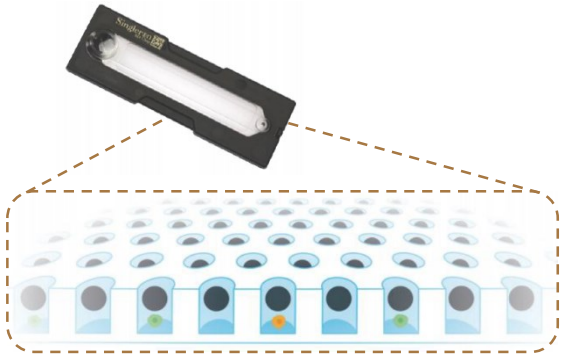
Matrix Singleron Biotechnologies™

Python Singleron Biotechnologies™

x8



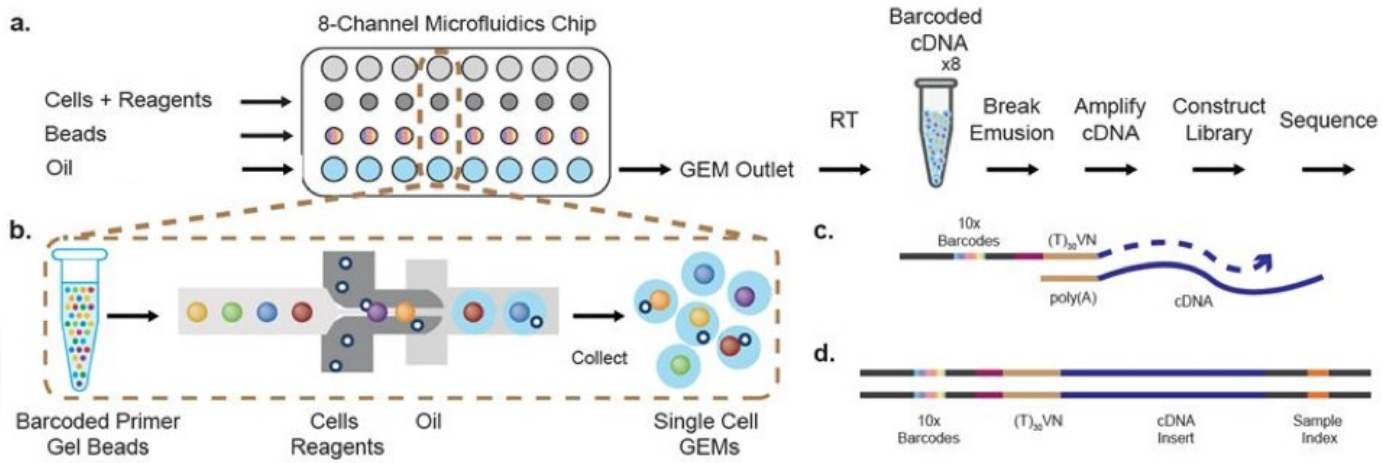
LUNA-FL Cell counter



10x Genomics

Single-cell transcriptomics and epigenomics

- Microfluidics technology from 10x Genomics for sc whole/targeted transcriptome interrogation, immune profiling, assay for transposase accessible chromatin, and Multiomics.
- Fast (18 minutes encapsulation + 9 hours library preparation)
- High-throughput (100-10.000 cells Singleplex; 500-30.000 Multiplex)

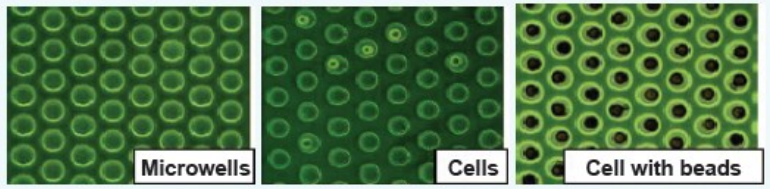


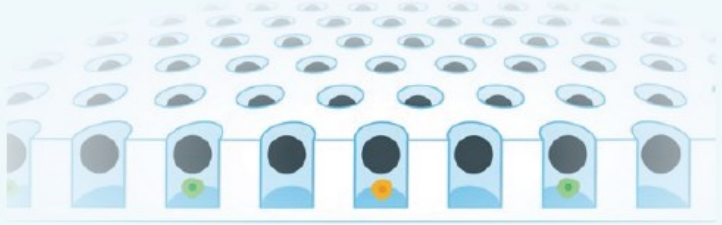
source: https://medicine.uiowa.edu/humangenetics/genomics-division/genome-sequencing/single-cell-expression-analysis-scrna-seq

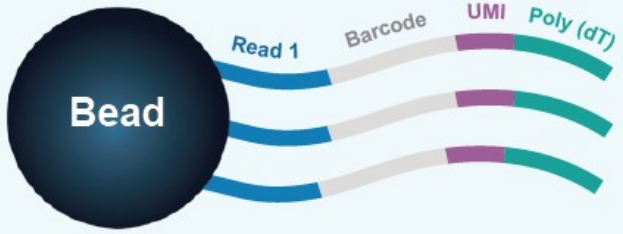
Singleron

Single-cell transcriptomics and epigenomics

- SCOPE-chip from Singleron captures single cells by partitioning them into hundreds of thousands of microwells
- Standard chip: 500-10,000 single cells; High-density chip up to 30,000 cells per sample, or up to 120,000 cells on one HD chip when multiplexing samples with Clindex.
- Large-well chips ensure analysis of cell sizes up to 100 µm
- Manual or Automated workflow.

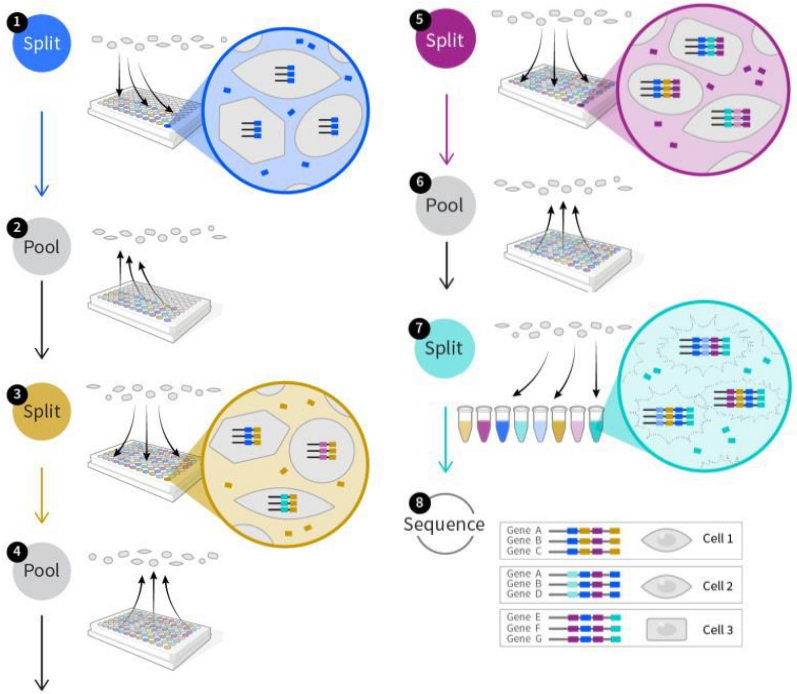




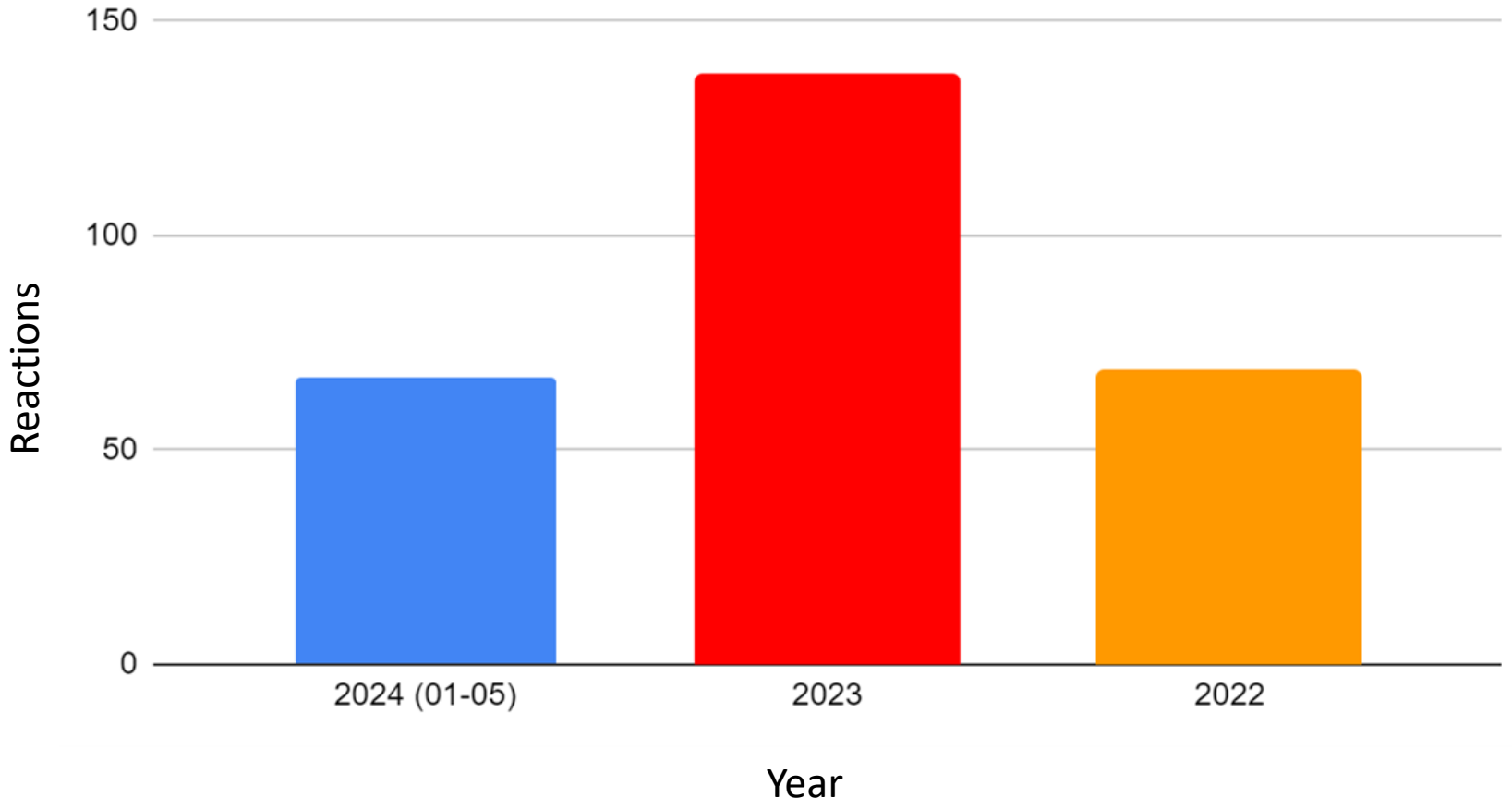


Split-pool (Parse Bio. / Scale Bio.)

- Combinatorial indexing solution for large-scale projects that aim to profile up to 100,000 cells/nuclei, across 1 to 48 samples
- Fixation solution for sample storage that enables pooling of multiple samples from different time points into a single experiment.
- Lower multiplets than microfluidics-based methodologies



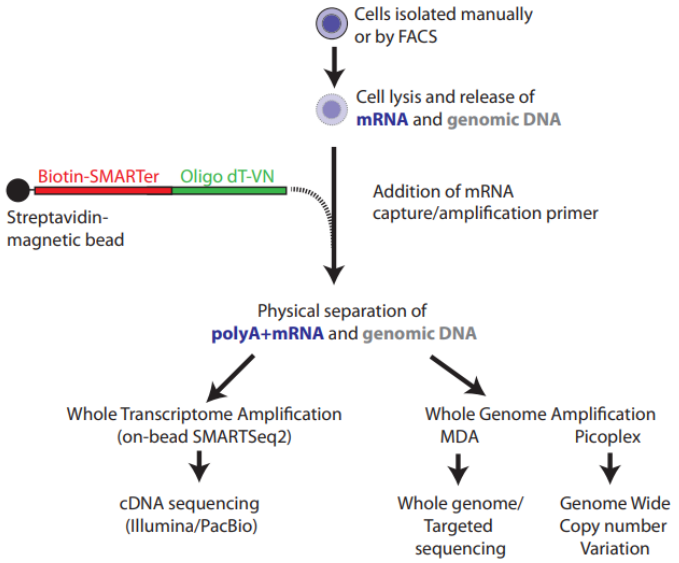
Single-cell samples/reactions in figures

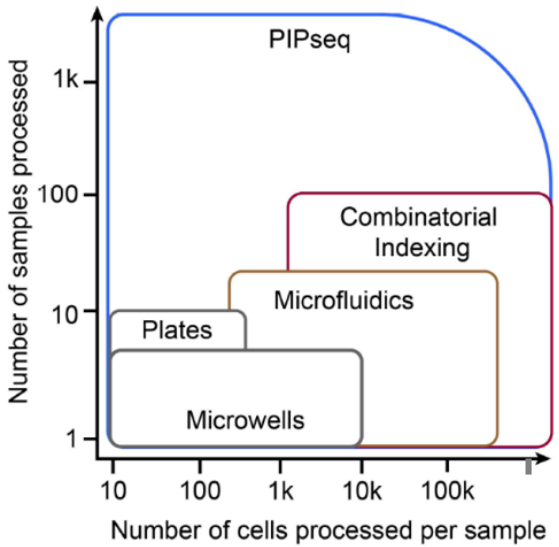


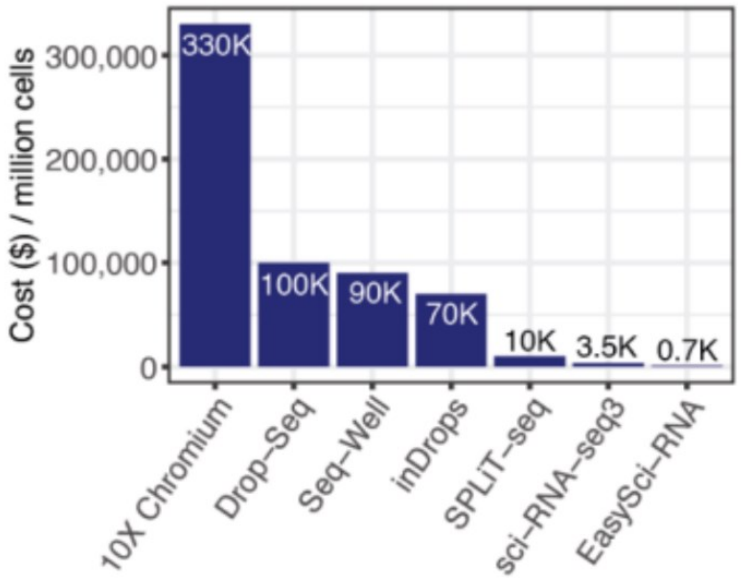
Novel Methodologies

Single-cell transcriptomics and epigenomics

- Implementation of novel non-commercial techniques and approaches.
- Simultaneous analysis of genome and transcriptome of the same single cell
- Plate-based and applicable to a limited number of cells







Clark, Nat Biotechnol (2023). https://www.nature.com/articles/s41587-023-01685-z

Sziraki et al. bioRxiv 2022 doi: 10.1101/2022.09.28.509825v1.full → Nature Genetics 2023 doi: 10.1038/s41588-023-01572-y

Support infrastructure@ the FGCF

Massively Parallel Sequencing

Illumina™

NextSeq2000
Illumina™

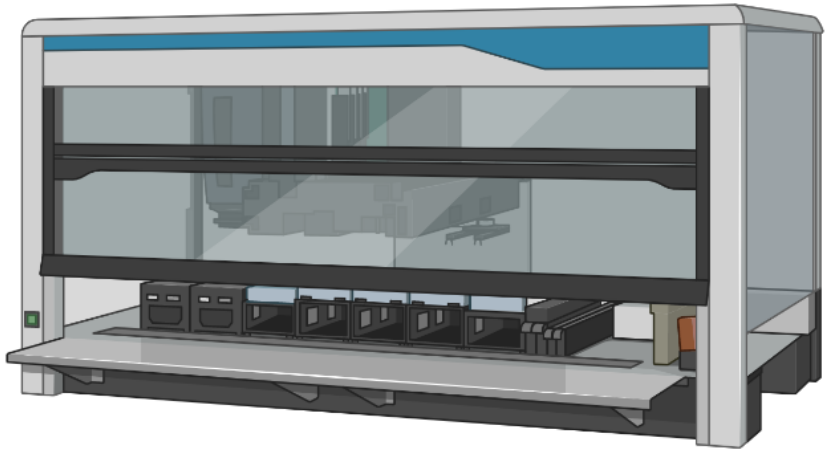
400 Million reads

1,800 Million reads (P4)

Support Infrastructure @ the FGCF

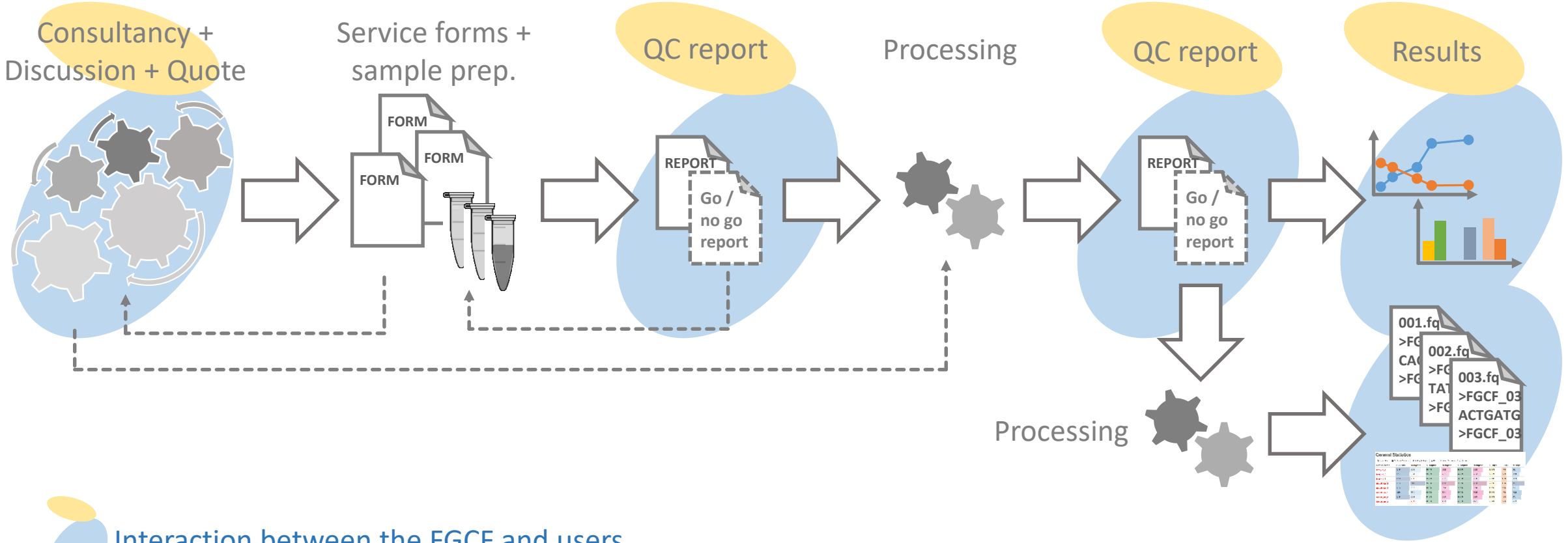
High throughput sample processing and automation

TapeStation 4200
Agilent™



MicroLab STAR
Hamilton™

FGCG services life cycle



Interaction between the FGCF and users