

Single cell sequencing

Boris Tichý (CEITEC-MU), Andreas Sommer (VBCF)

24. 09. 2018



Genomics

Genomics Tools:

Microarrays

PCR

Sanger

FISH

...

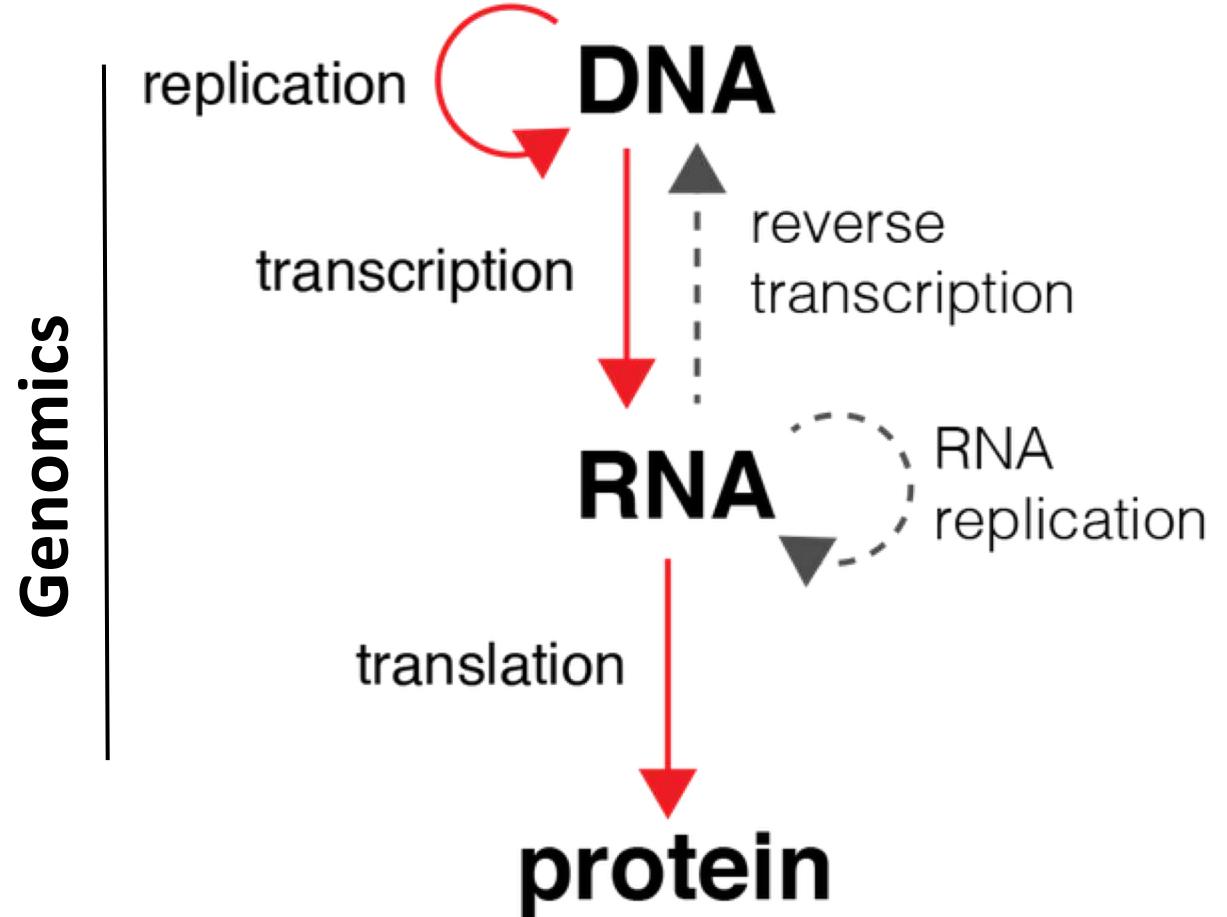
NGS

(Next Generation Sequencing)

Single cell sequencing



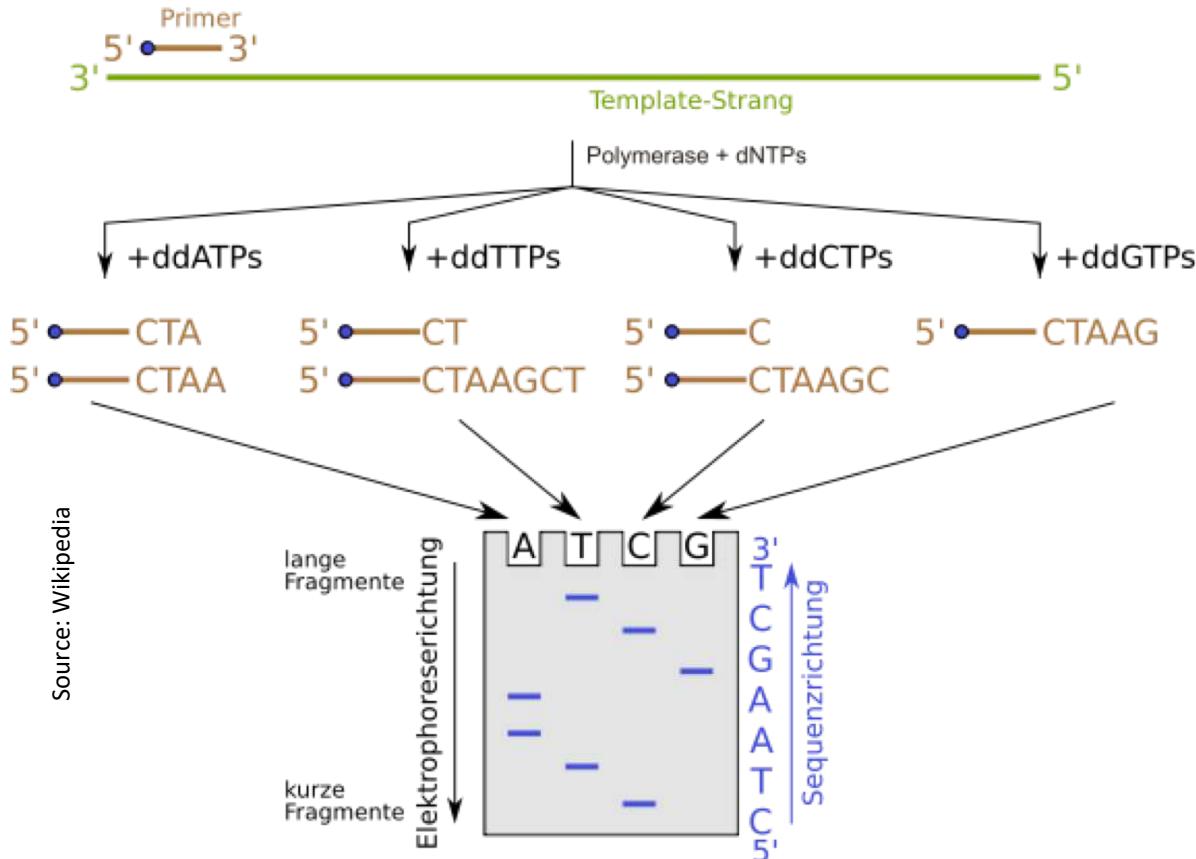
Interreg
EUROPEAN UNION
Austria-Czech Republic
European Regional Development Fund



Sanger



Interreg
Austria-Czech Republic
European Regional Development Fund



Single cell sequencing



Frederick Sanger



- ✧ First full human genome
- ✧ Large Sequencing centers from 6 countries,
- ✧ Hundreds of dedicated scientists
- ✧ Approx. 10 years
- ✧ > 3 billion USD



2005



Interreg
Austria-Czech Republic
European Regional Development Fund



2010

Massive Parallelization of sequencing reactions!

"A new generation of non-Sanger-based sequencing technologies has delivered on its promise of sequencing DNA at unprecedented speed, thereby enabling impressive scientific achievements and novel biological applications."

nature methods: method of the Year 2007

2014



2011



Pricing

Jul 24, 2018

Staphylococcus Genome Set Reveals Bug's Host-Switching History

When rese

Aug 13, 2018

aureus isol

Deep Whole-Genome Sequencing Diagnoses Early Infantile

domestic e

Epileptic

Encephalopathy

Aug 17, 2018

Researchers International Consortium Sequences, Annotates Bread Wheat Reference Genome

The consortium Research | 17 September 2018

Genomic history of the Sardinian population

Cost per which has been researchers.

\$1k

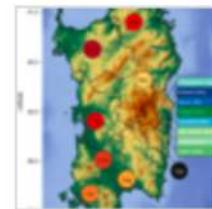
\$100

2001 2003 2005 2007 2009 2011 2013 2015 2017

Analyses of 3,514 whole-genome-sequenced individuals from Sardinia indicate that within-island substructure and sex-biased processes have impacted the genetic history of Sardinia, providing new insight into the demography of ancestral Sardinians.

Charleston W. K. Chiang, Joseph H. Marcus [...] John Novembre

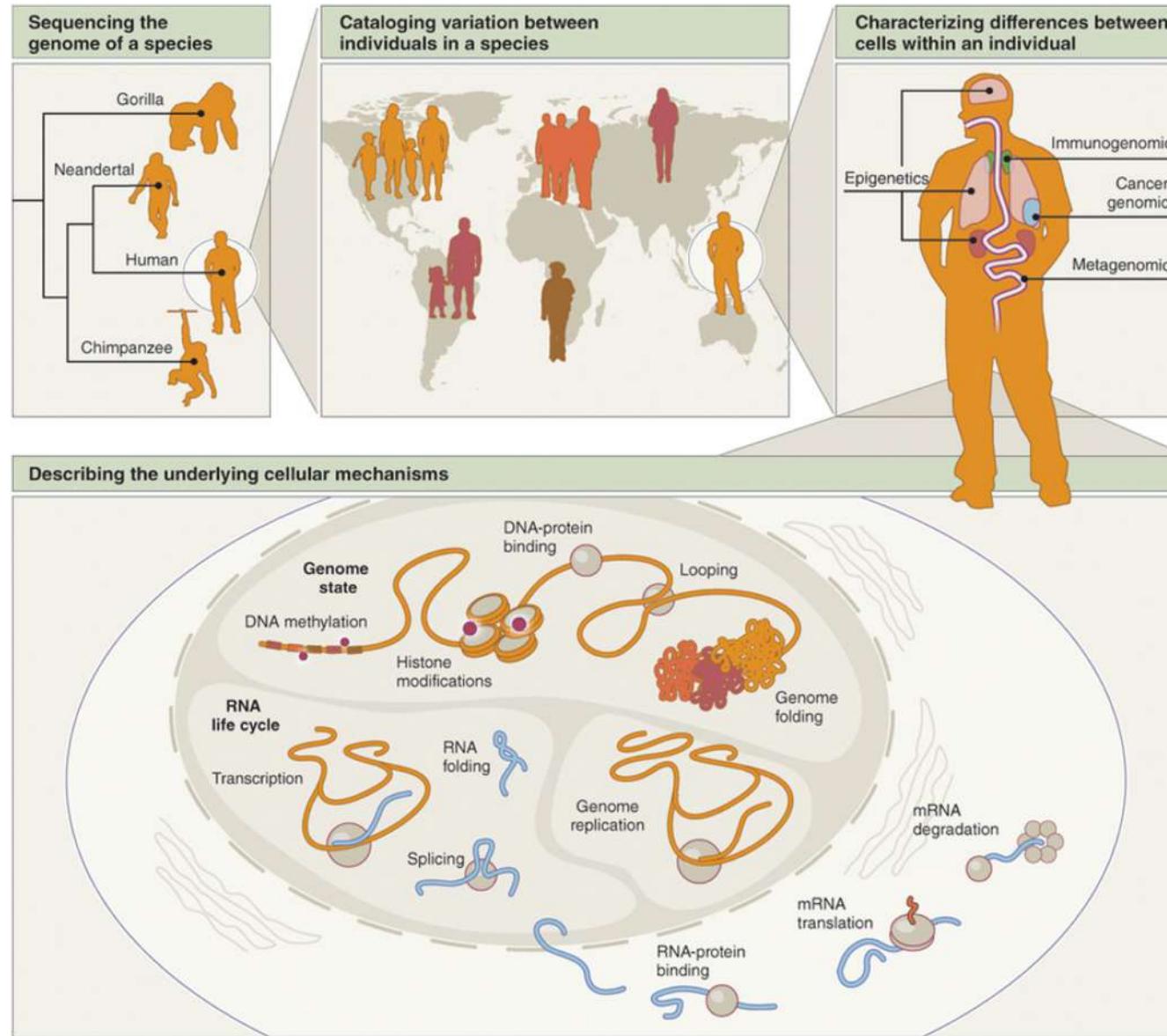
Nature Genetics, 1–9



Protocols, Flexibility



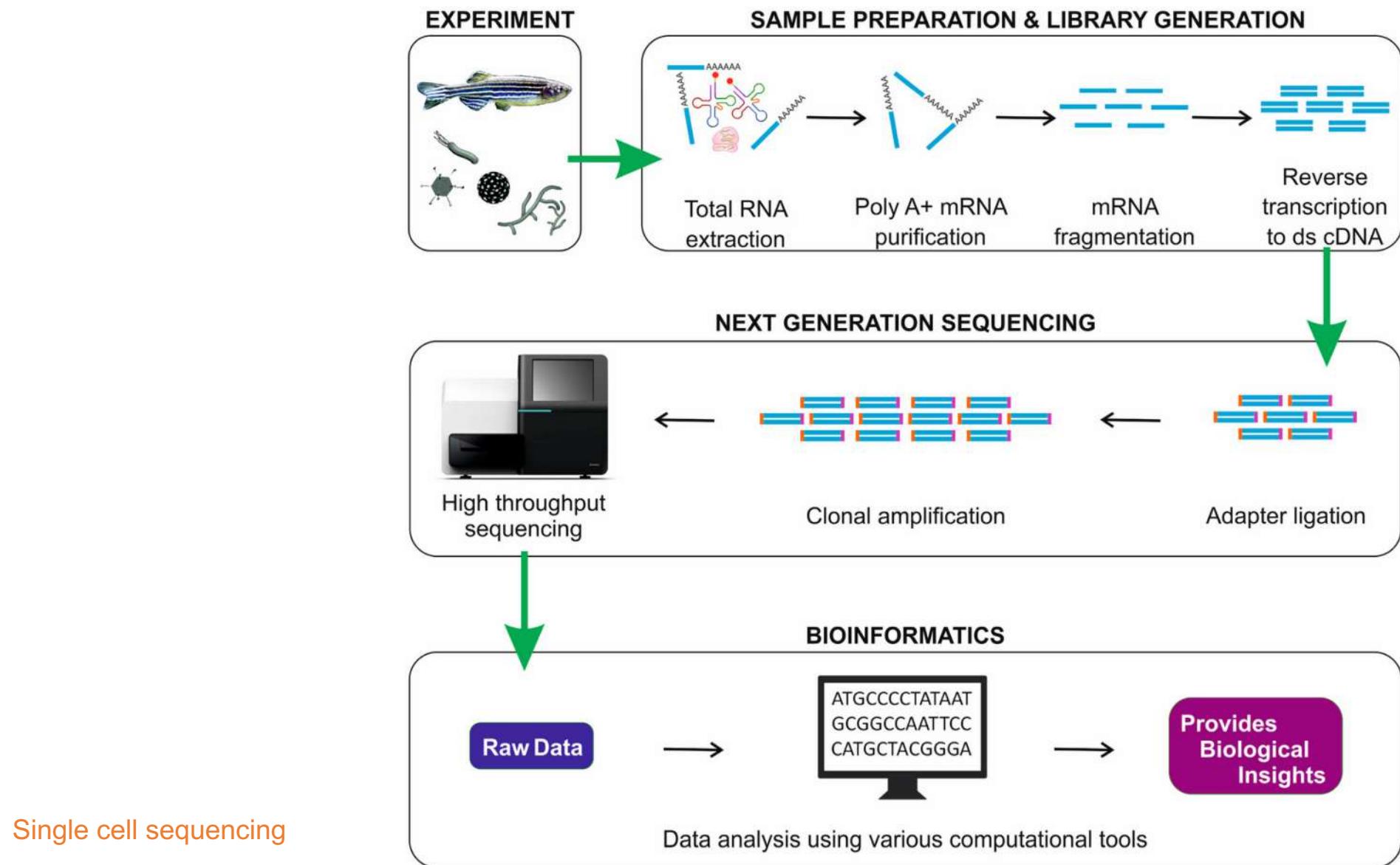
Interreg
Austria-Czech Republic
European Regional Development Fund



mRNA Sequencing



Interreg
Austria-Czech Republic
European Regional Development Fund

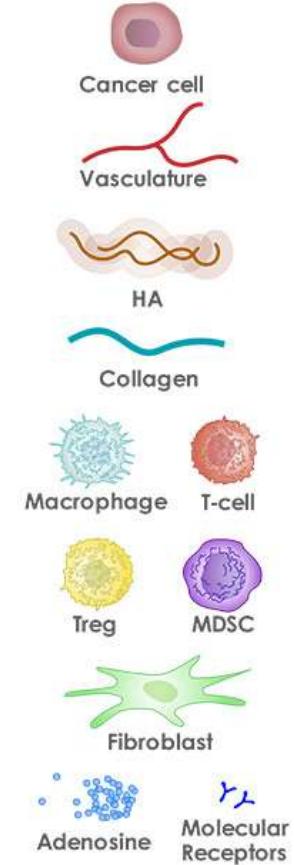
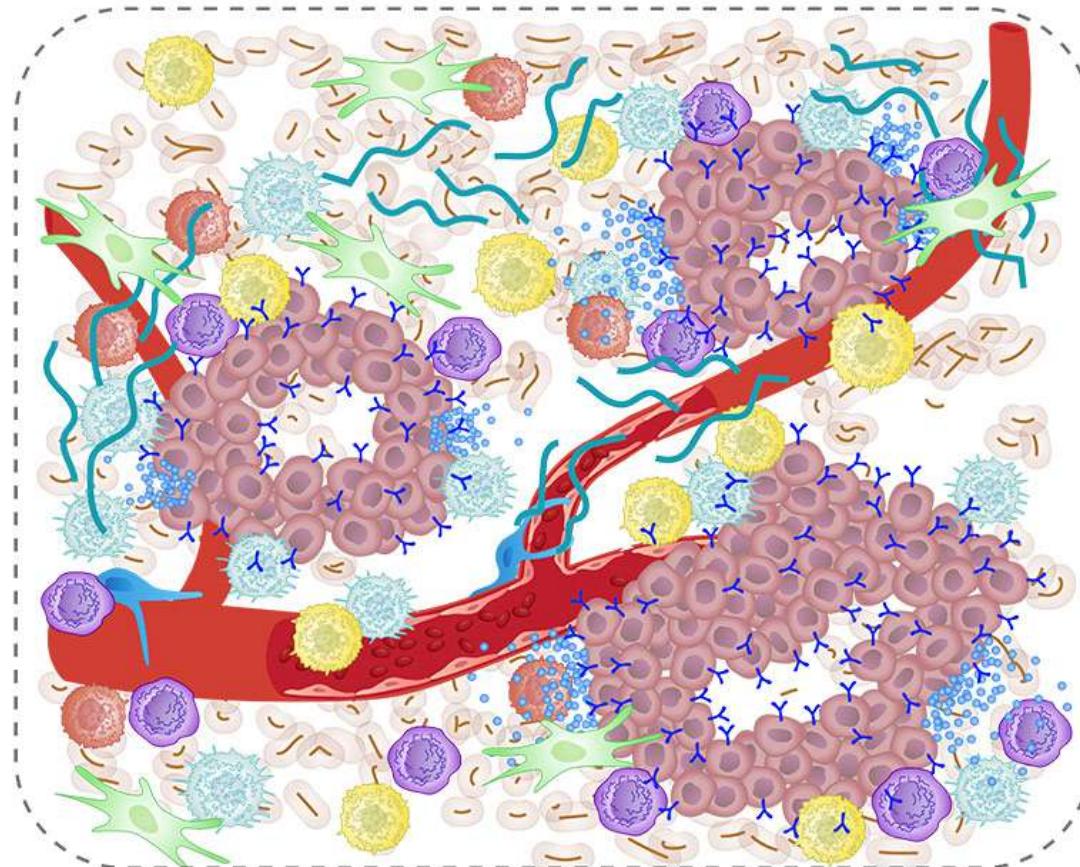


Heterogenous Material



Interreg
EUROPEAN UNION
Austria-Czech Republic
European Regional Development Fund

The Tumor Microenvironment

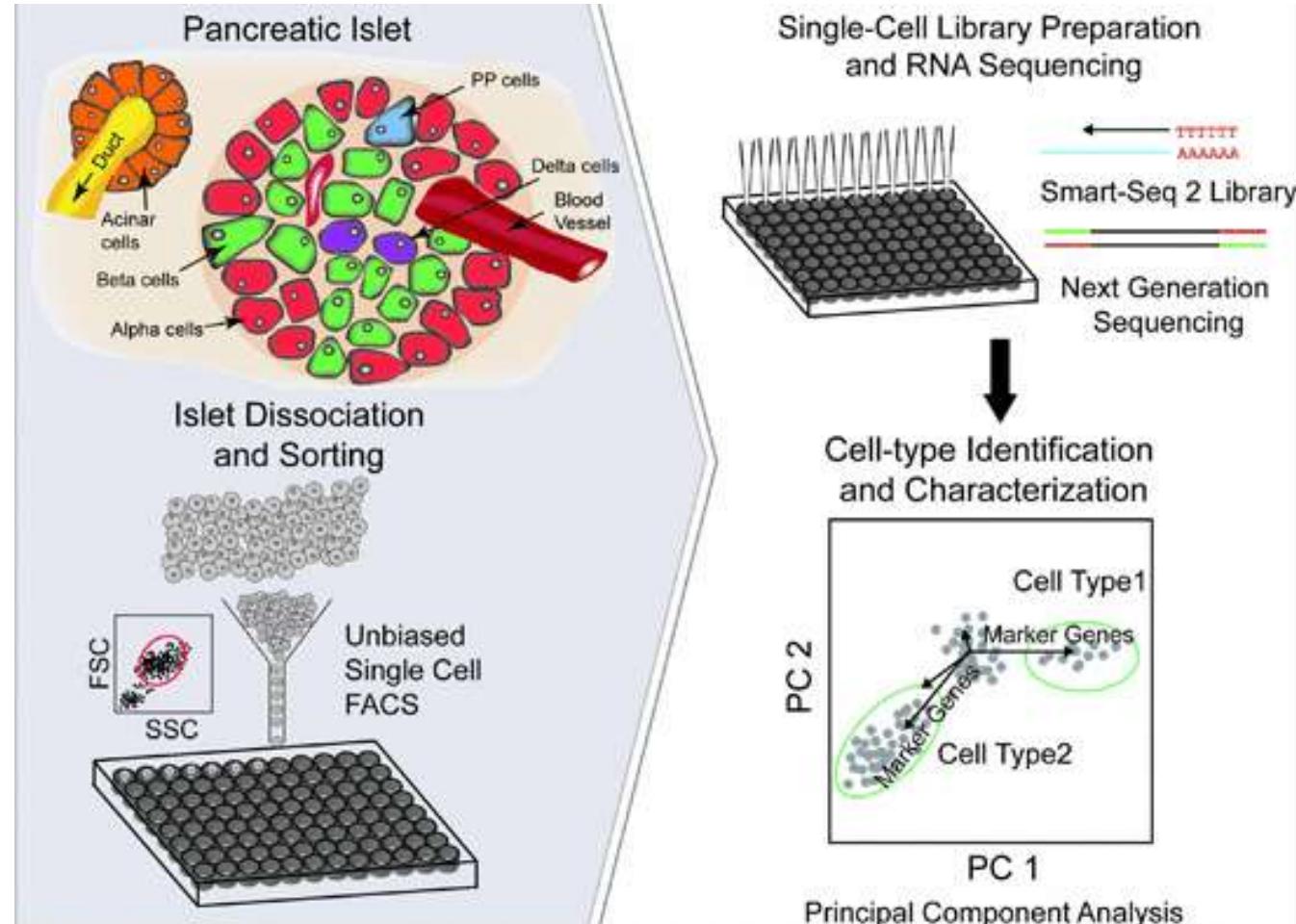


Source: <https://www.halozyme.com/science/>

Single RNA cell sequencing



Interreg
Austria-Czech Republic
European Regional Development Fund

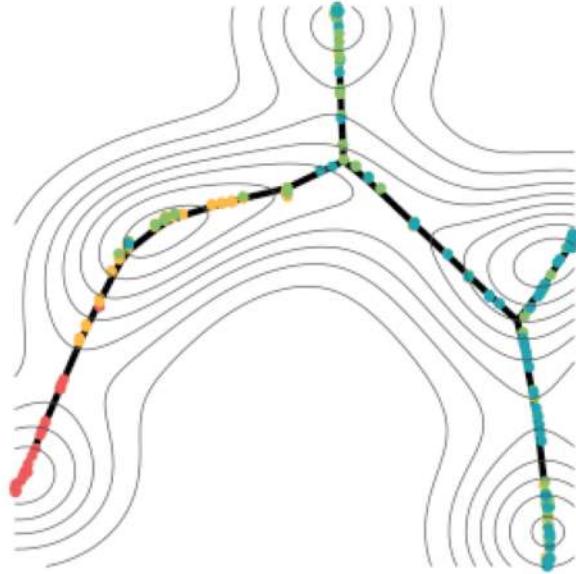


EMBO Reports (2016) 17:178–187

Data Analysis



Interreg
Austria-Czech Republic
European Regional Development Fund



Pseudotime

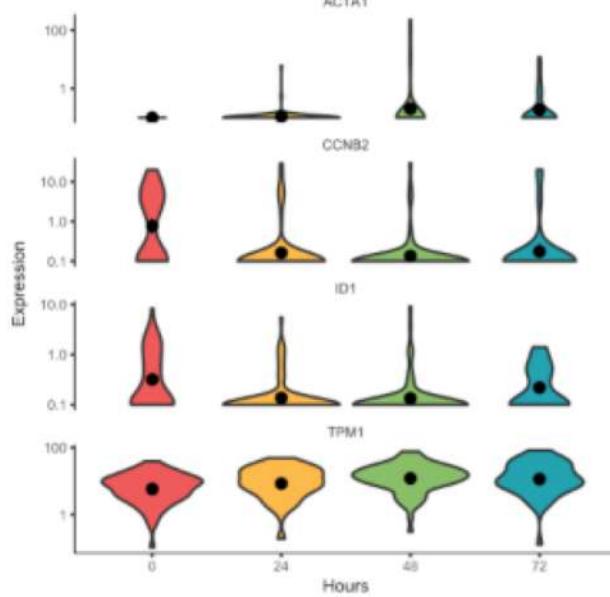
Build single-cell trajectories with the software that introduced pseudotime. Find cell fate decisions and the genes regulated as they're made.



Clustering

Group and classify your cells based on gene expression. Identify new cell types and states and the genes that distinguish them.

Single cell sequencing



Differential expression

Find genes that vary between cell types and states, over trajectories, or in response to perturbations using statistically robust, flexible differential analysis.

Source: 10X Genomics

Smart-seq 2



Interreg
EUROPEAN UNION
Austria-Czech Republic
European Regional Development Fund

Cell lysis (Steps 1-8)

Poly(A)⁺ RNA

AAAAAAA

oligo(dT) primer

Reverse transcription & terminal transferase (Steps 9-11)

LNA-containing TSO

C C C

AAAAAAA

ISPCR primers

CCC

Template switching by reverse transcriptase (Steps 9-11)

ISPCR primers

PCR pre-amplification of cDNA (Steps 12-15)
PCR cleanup (Steps 16-27)

GGG

CCC

Tagmentation (Tn5) (Steps 28-32)



GGG

CCC

Single cell sequencing

Nature Protocols volume 9, pages 171–181 (2014)

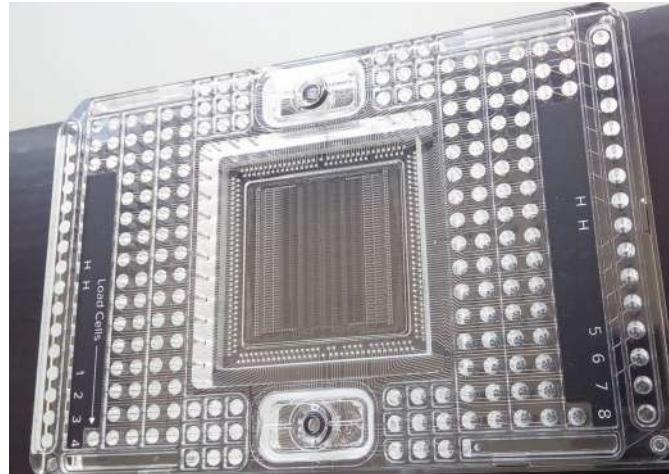
Pilot project introduction



- Project partners:
 - **VBCF – NGS Core Facility, CEITEC – Genomics Core Facility**
- Complementary equipment/expertise:
 - **Library preparation expertise, NGS sequencers, FACS, LCM, Fluidigm C1**
- Basic project idea:
 - **Set up a protocol for single cell RNA sequencing used at both sites**
- Project goal:
 - **Broadening the range of our services based on requirements of our users**
- End-users:
 - **Academic users (eg. oncology research)**

Project implementation

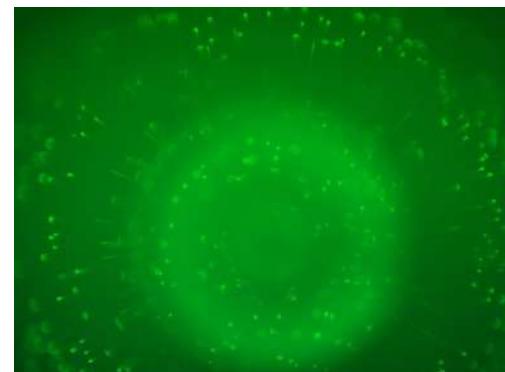
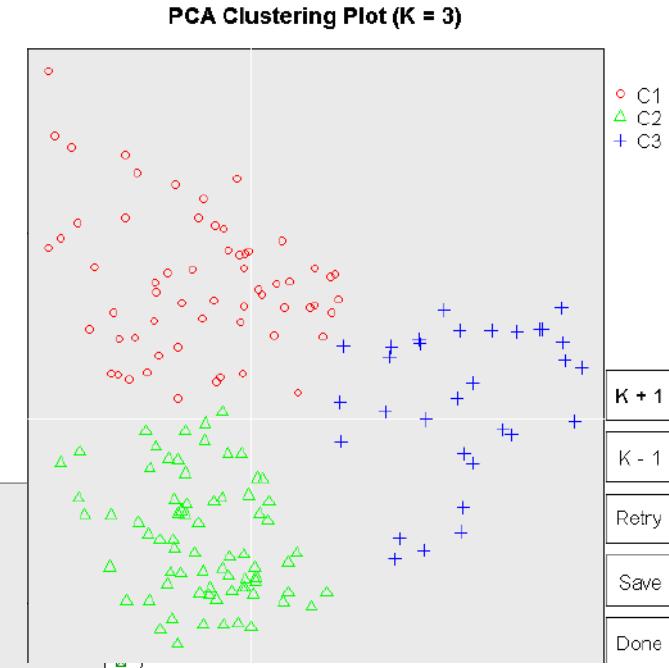
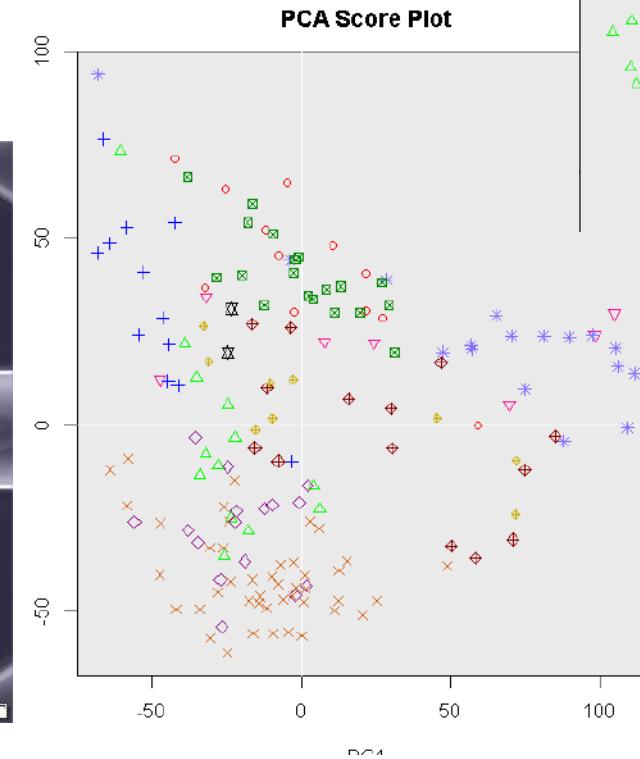
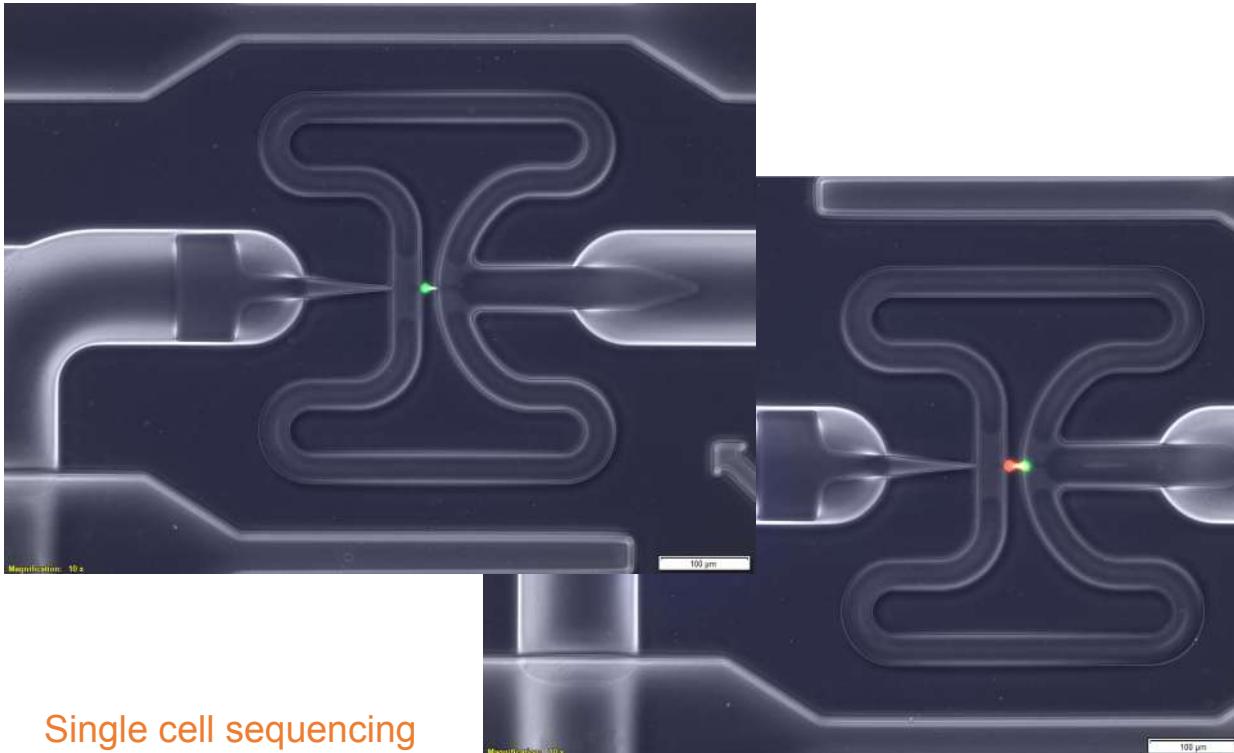
- Approach/methodology
 - **Library protocols based on SMART-Seq2 method**
 - Open solution according to *Picelli 2014*
 - Solution using Fluidigm C1 + commercial kit
- Implementation
 - **Implementation of Smart-Seq2 at VBCF** → transfer of the protocol to CEITEC
 - Staff exchange (Filip Pardy at VBCF)
 - **Implementation of Smart-Seq2 on Fluidigm C1 at CEITEC**



Picelli et al., Nature Protocols 2014

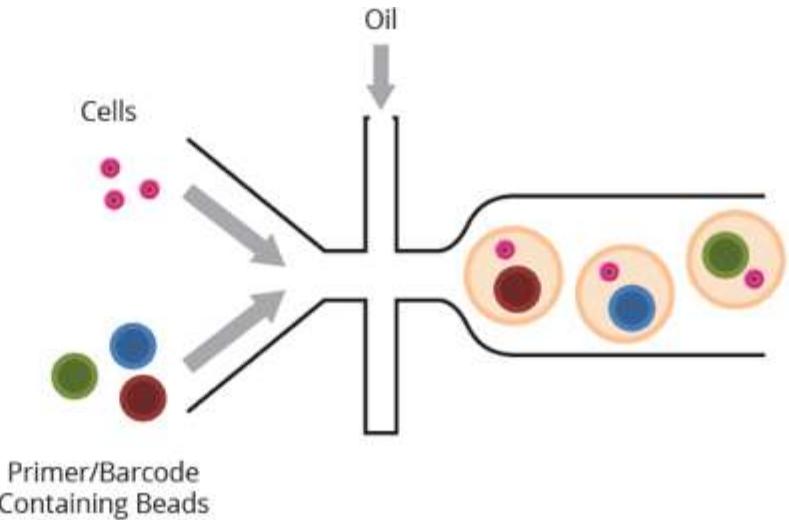
Project results

- Results:
 - **Method for single-cell RNA sequencing at both sites**
- Benefits for the users:
 - **No averaging of gene expression**
 - **Screening for cell subpopulations**



Future

- New protocols?
 - 3' single-cell RNA-Seq
 - sci-RNA-Seq (single-cell combinatorial indexing RNA sequencing)
 - 10x Genomics single-cell RNA-Seq



Single cell sequencing

