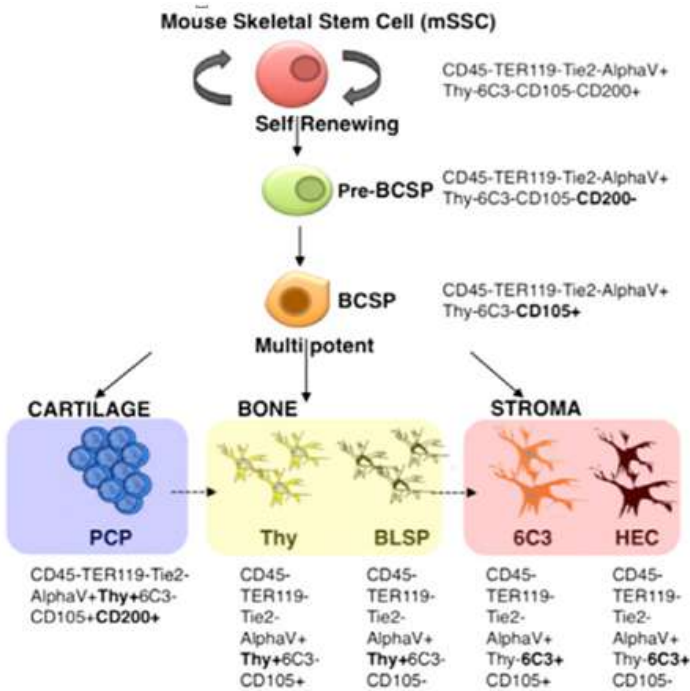# Transcriptome analysis of small synovial stromal populations in a murine model of rheumatoid arthritis

Nina Lukač, MD
Department of Anatomy
Laboratory for Molecular Immunology
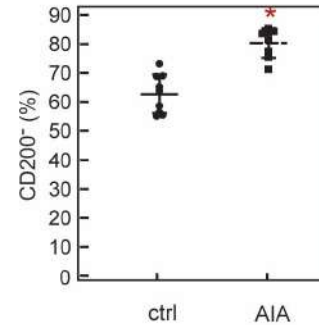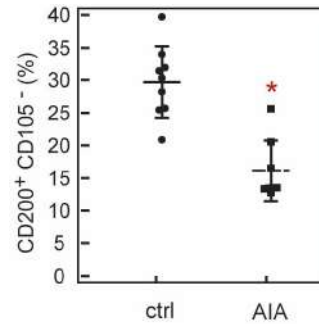Croatian Institute for Brain Research

HrZZ
Hrvatska zaklada za znanost

University of Zagreb
School of Medicine

Altered synovial stromal populations rheumatoid arthritis

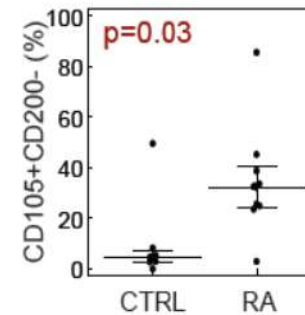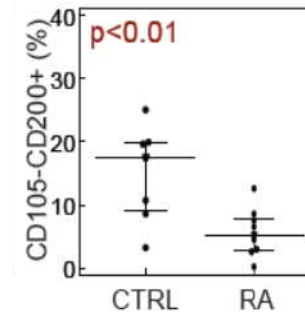*Chan et al. 2015, Cell*

Murine model of RA

Human RA

mSSC
CD45-CD31-TER119-
CD51+**CD200+ CD105-**
(AIA, NI ctrl)
BCSP
CD45-CD31-TER199-
CD51+**CD200- CD105+**
(AIA)
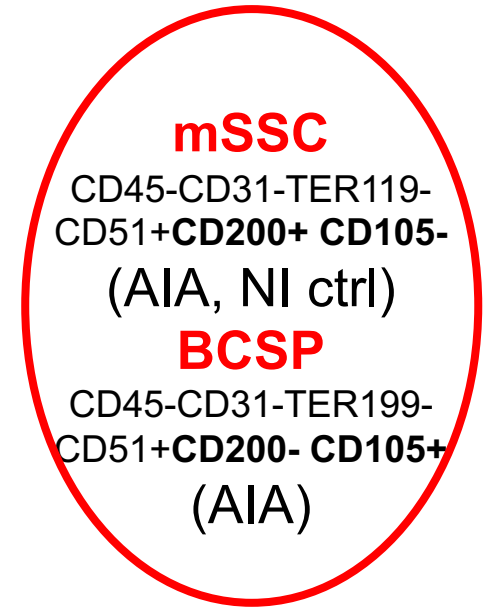
**Transcriptome analysis
(RNA sequencing)**
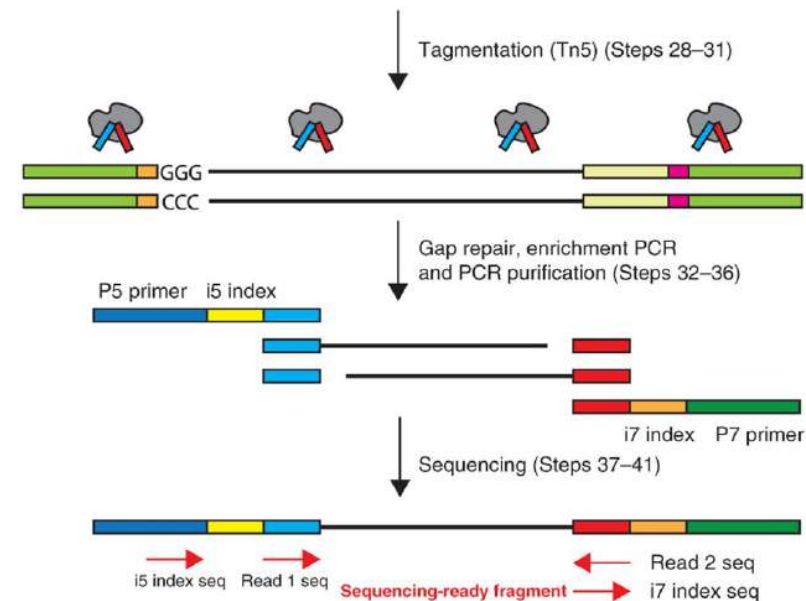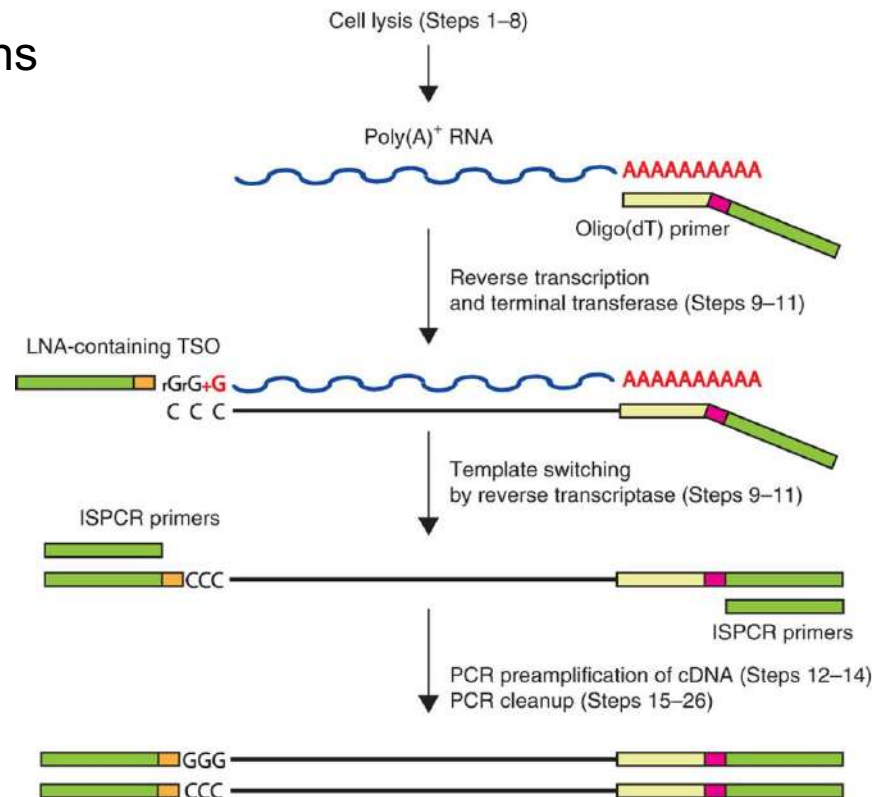
Picelli et al. 2014, Nat Protoc.

1. Amplicon QC & quantification

QC
(Bioanalyzer)

Ideal: peak spanning 400 - 10,000 bp
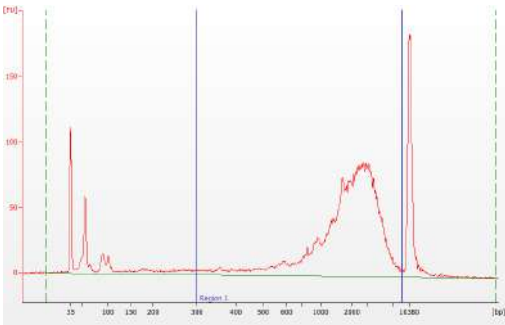
SMART-Seq® v4 Ultra® Low Input RNA Kit for Sequencing User Manual
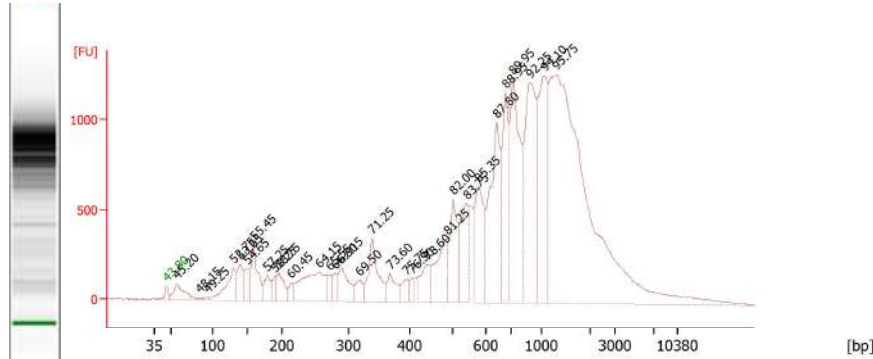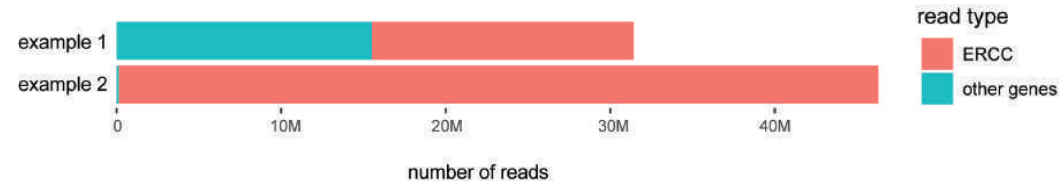
ERCC Spike-In overrepresentation
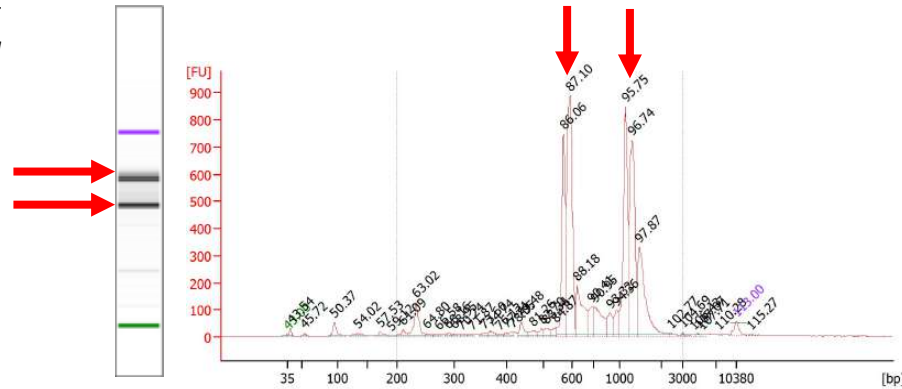
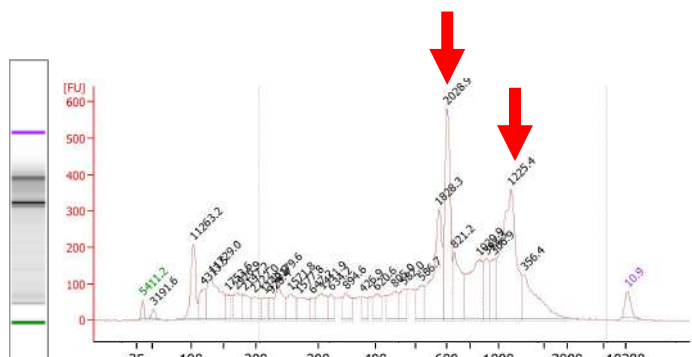## Concentration
(Qubit)
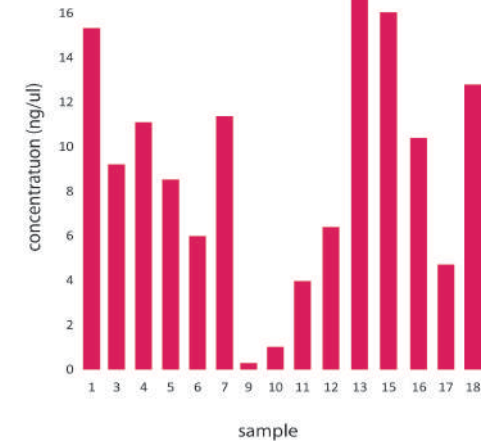
Housekeeping genes
(qPCR)
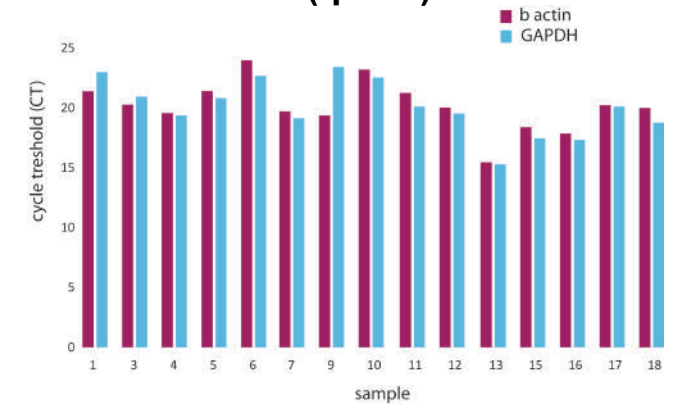
ERCC Spike-In overrepresentation

Bioanalyzer

Read duplication levels
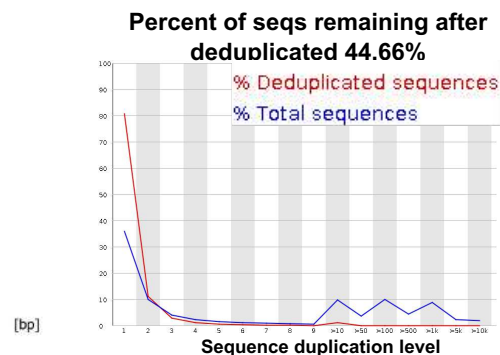
Per sequence GC content

Read distribution

Example 1

Example 2

Percent of seqs remaining after deduplicated 44.66%

Percent of seqs remaining after deduplicated 16.15%
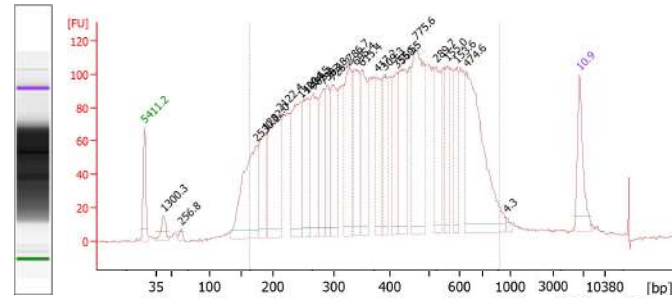
Amplicon QC

Raw reads QC

Alignment QC
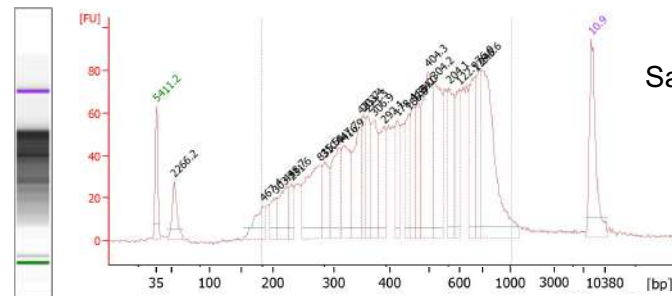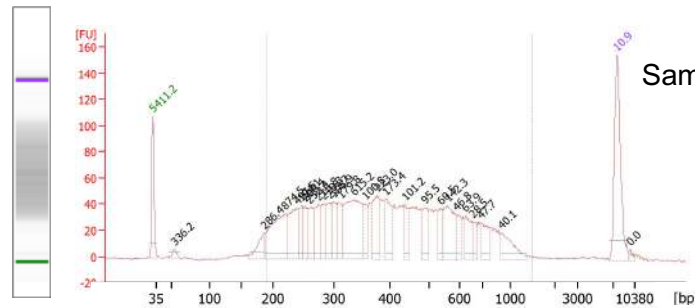
3. Library QC & quantification
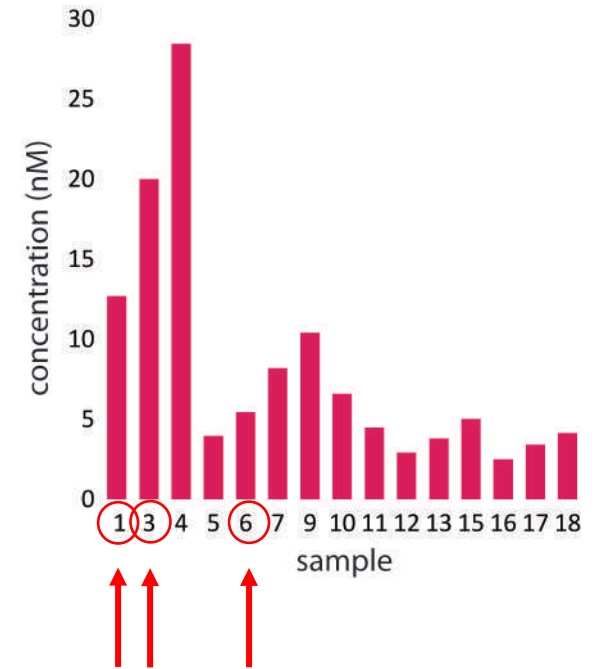
QC
(Bioanalyzer)
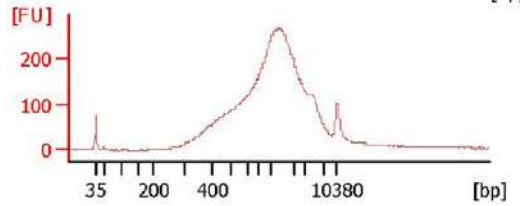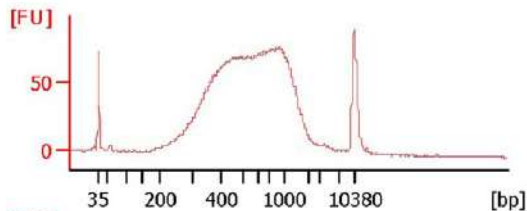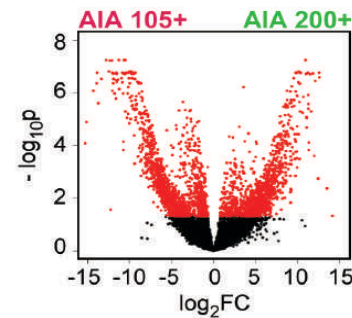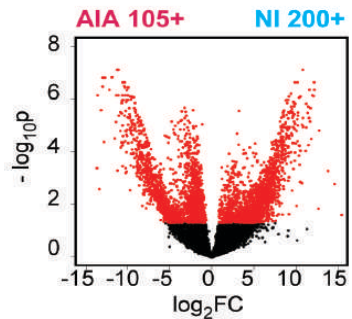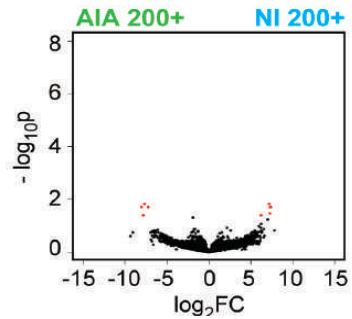
Nextera XT DNA Library Prep Kit Reference Guide
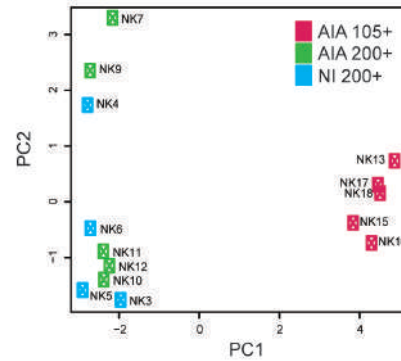
Sample 6

Sample 1

Concentration
(Bioanalyzer)

CD200+ cells have distinct transcriptional profile from CD105+ cells

Differential expression

Principal component analysis

Enriched gene sets (GSEA)

Ven diagram of DEGs