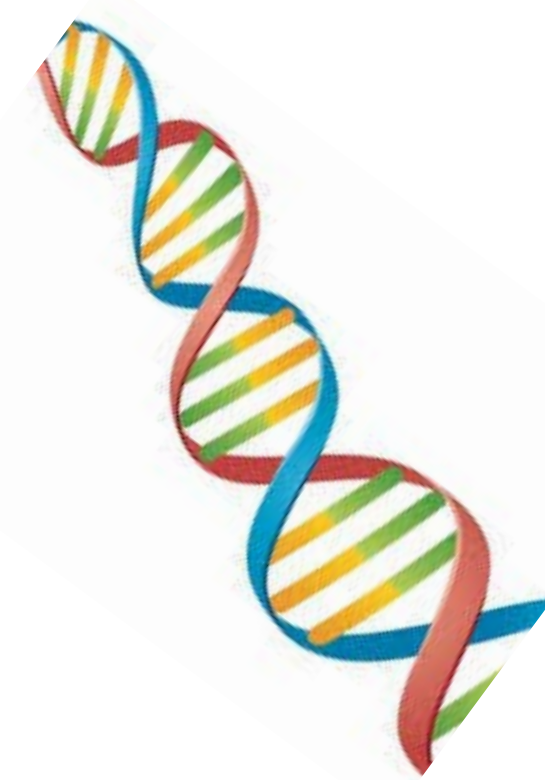


Harvard FAS Bauer Sequencing Facility

Christian Daly, Patrick Dennett, Nicole El-Ali, Emma White, Claire Hartmann - Division of Science, FAS, Harvard University

Our Core in a Nutshell

- Full-service and self-run options
- Expert consultation and training
- Customized sequencing
- Sample and library preparation support



Illumina Library Preparation

- DNA, mRNA or ribo-depleted RNA input
- Covaris shearing or enzymatic fragmentation
- Low input options
- High or low throughput
- Costs as low as \$16/sample
- Rush options available



Single Cell Sequencing

10x Genomics

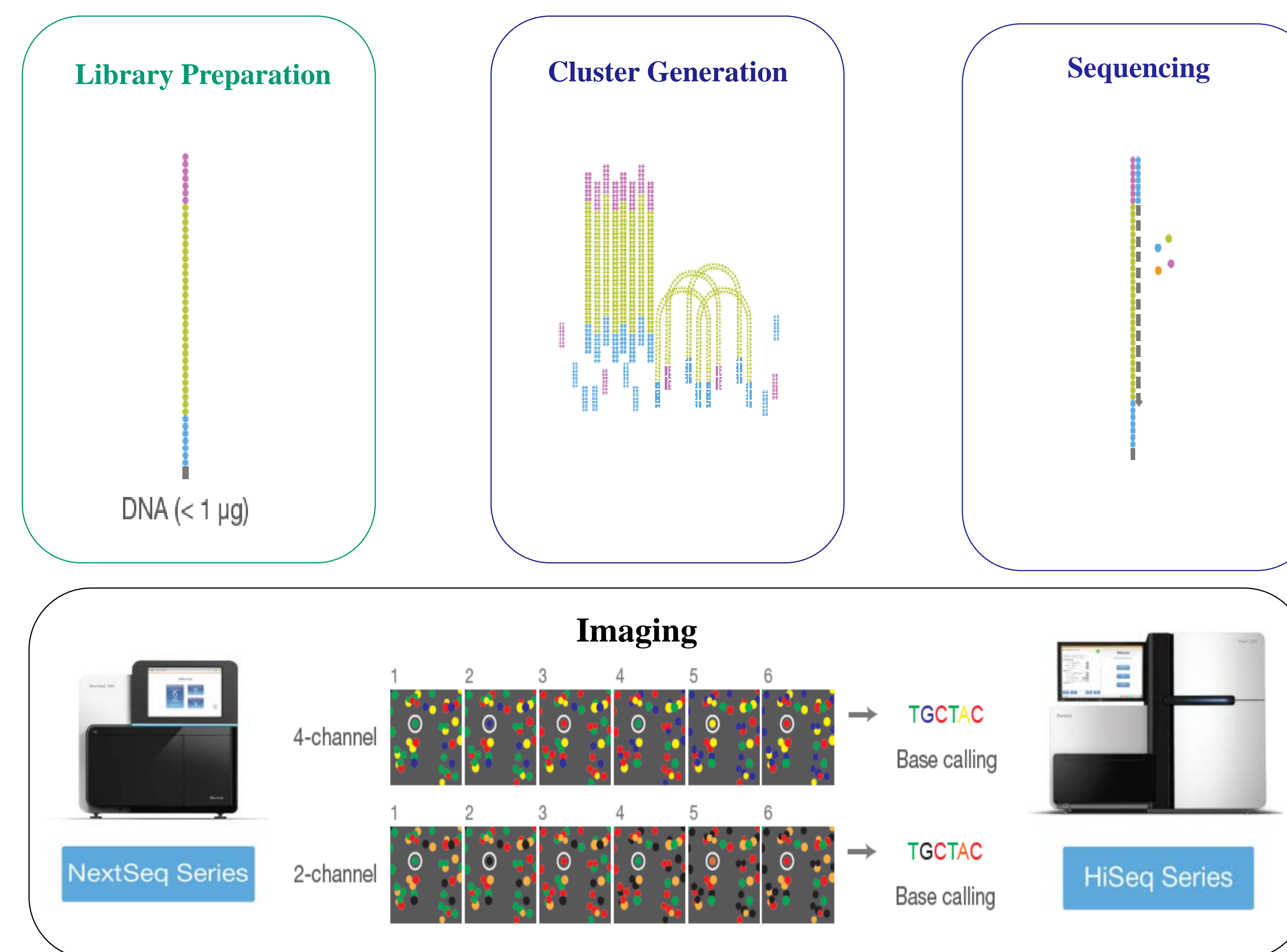
- Full-service or self-run (after training)
- 3' gene expression
- 5' gene expression + VDJ
- Coming soon: ATACseq, CNV



SmartSeq v4

- Index sorting available in our flow core
- Low cost miniature reaction volumes

Illumina Sequencing



High Capacity

- Four NextSeqs and two HiSeqs on site
- High output NovaSeq runs available

Fast Turn-Around

- Options for ~1 week turn-around available

Customizable Sequencing

- Variable read lengths
- Custom primers and unique parameters are our specialty
- Yields from 100M – 400M reads per run
- Consult with us to choose the best option for your needs

QC options

- Full-service for easy sequencing with confidence
- Self-run for lower costs with expert training and support

Sample and Library QC

- Bioanalyzer & TapeStation sizing
- Size Selection by Pippin Prep or SPRI
- Qubit, Nanodrop and QPCR Quantification



Nanopore Sequencing

- Training and support
- Full-service MinIon options (Harvard researchers only)



Other Technologies

Liquid Handling

Large and small volumes
Automated DNA Extraction



PCR

QPCR in 96 or 384
QX200 digital PCR
Biomark High Throughput QPCR



Plate Readers

Fluorescence, FP, Luminescence, Absorbance

Contact Information

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