

# NGI Sweden

Next Generation Sequencing at the  
National Genomics Infrastructure

SciLifeLab



**NGI** stockholm

Phil Ewels

[phil.ewels@scilifelab.se](mailto:phil.ewels@scilifelab.se)

Introduction to Bioinformatics Using NGS Data

Umeå, 2018-11-14

# — Overview

National Genomics Infrastructure

Sequencing Technologies

Sequencing Applications

Bioinformatics at the NGI

# The National Genomics Infrastructure



# SciLifeLab NGI

SciLifeLab

Research Programs

Technology Platforms

National Genomics Infrastructure

Proteomics

Metabolomics

Single-Cell Biology

Cellular & Molecular Imaging

Molecular Structure

Chemical Biology

Genome Engineering

Diagnostic Development

Drug Discovery & Development

National Bioinformatics Infrastructure

Data Office

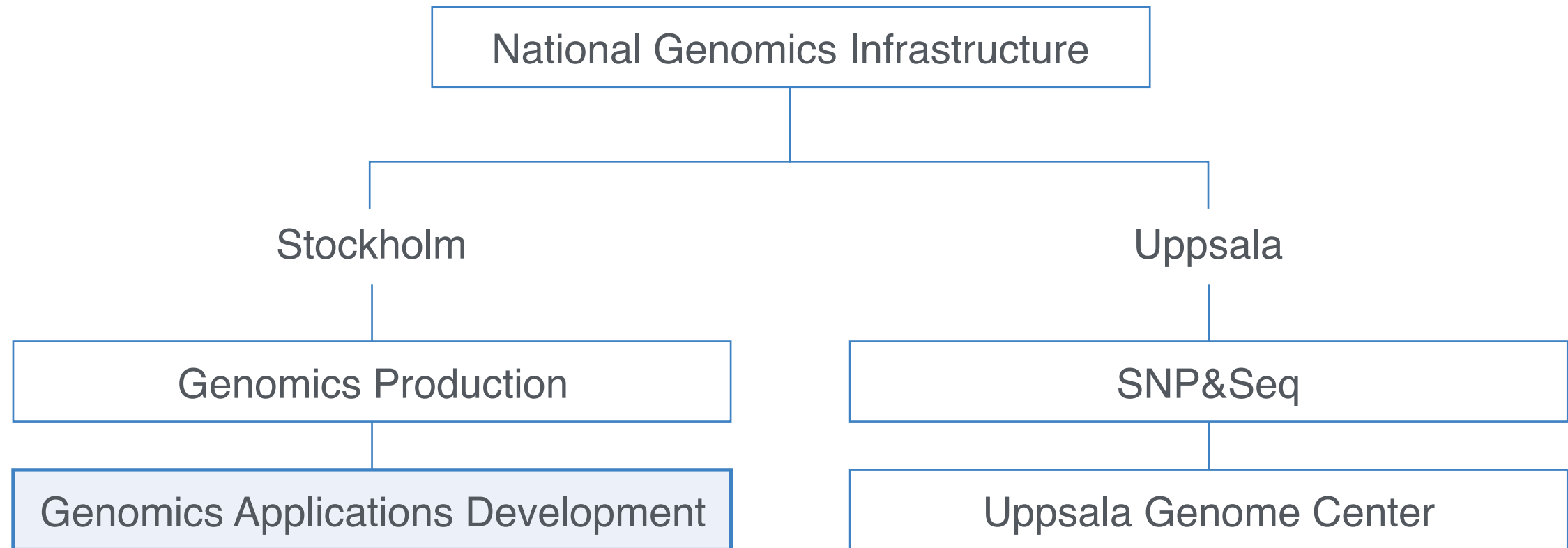
SciLifeLab



NGI stockholm



# SciLifeLab NGI



# — SciLifeLab NGI

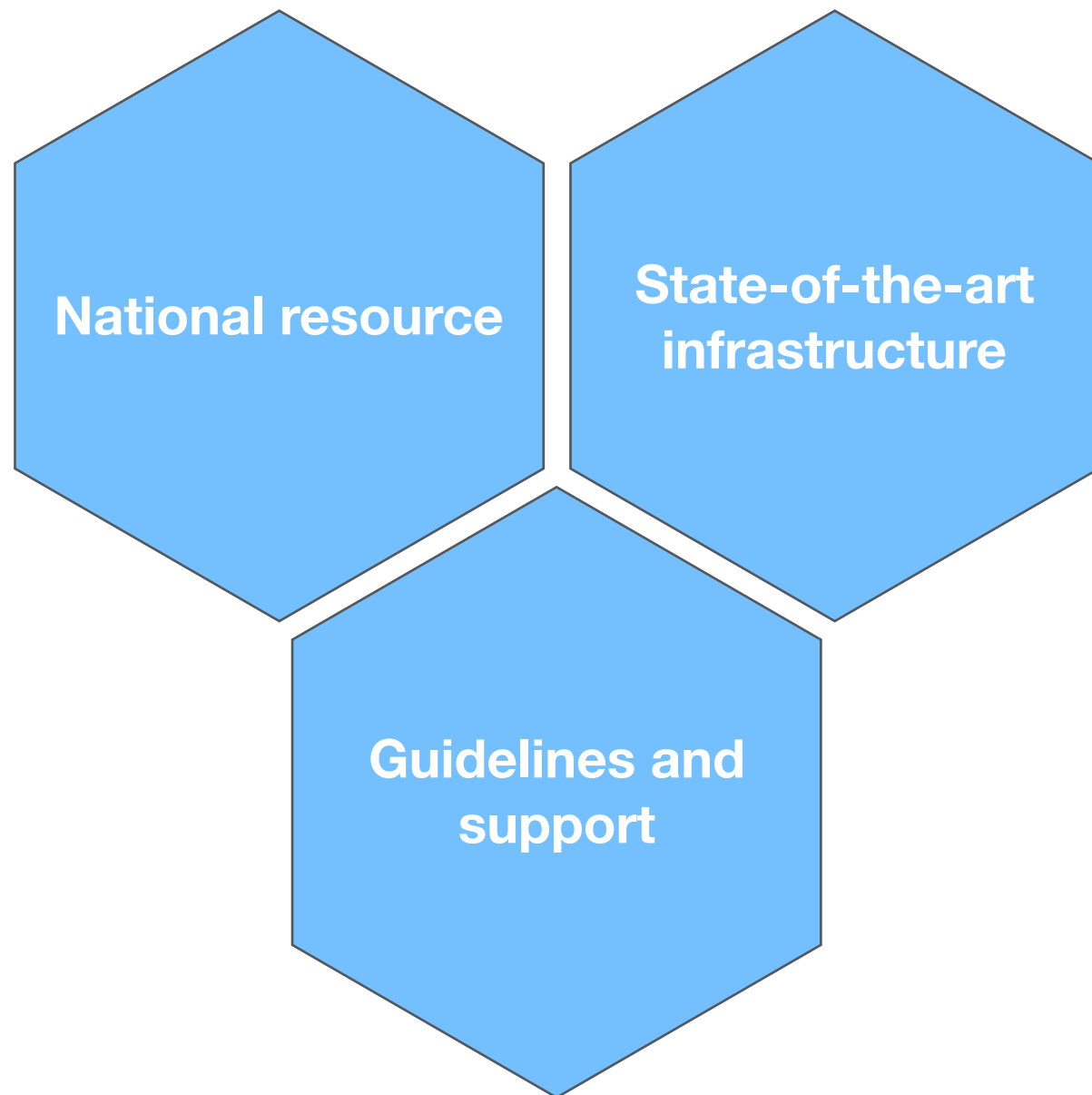


Our mission is to offer a **state-of-the-art infrastructure** for massively parallel DNA sequencing and SNP genotyping, available to researchers all over Sweden

SciLifeLab

 NGI stockholm

# SciLifeLab NGI



We provide  
**guidelines and support**  
for sample collection, study  
design, protocol selection and  
bioinformatics analysis

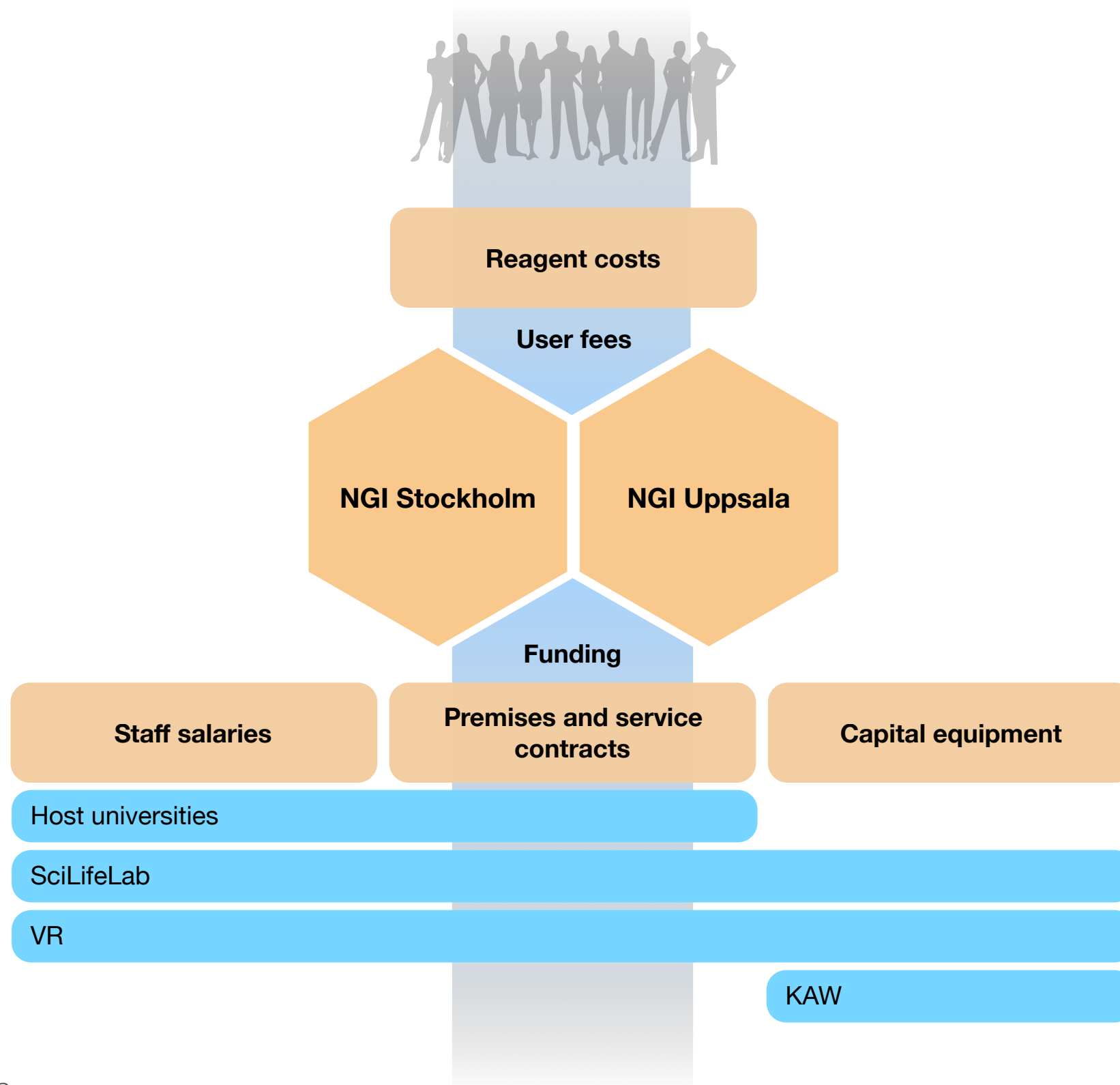
# — NGI Organisation



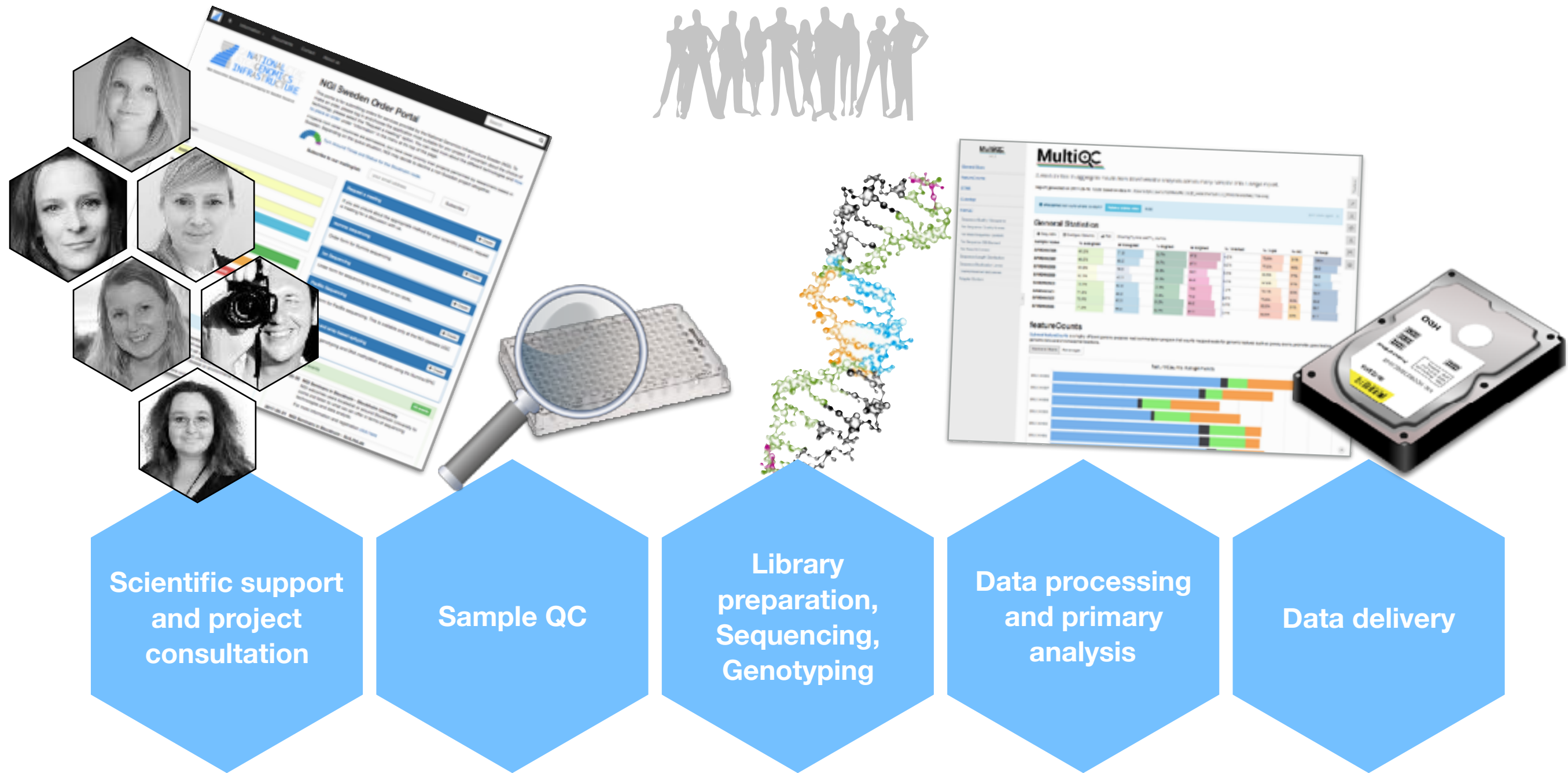
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# NGI Organisation

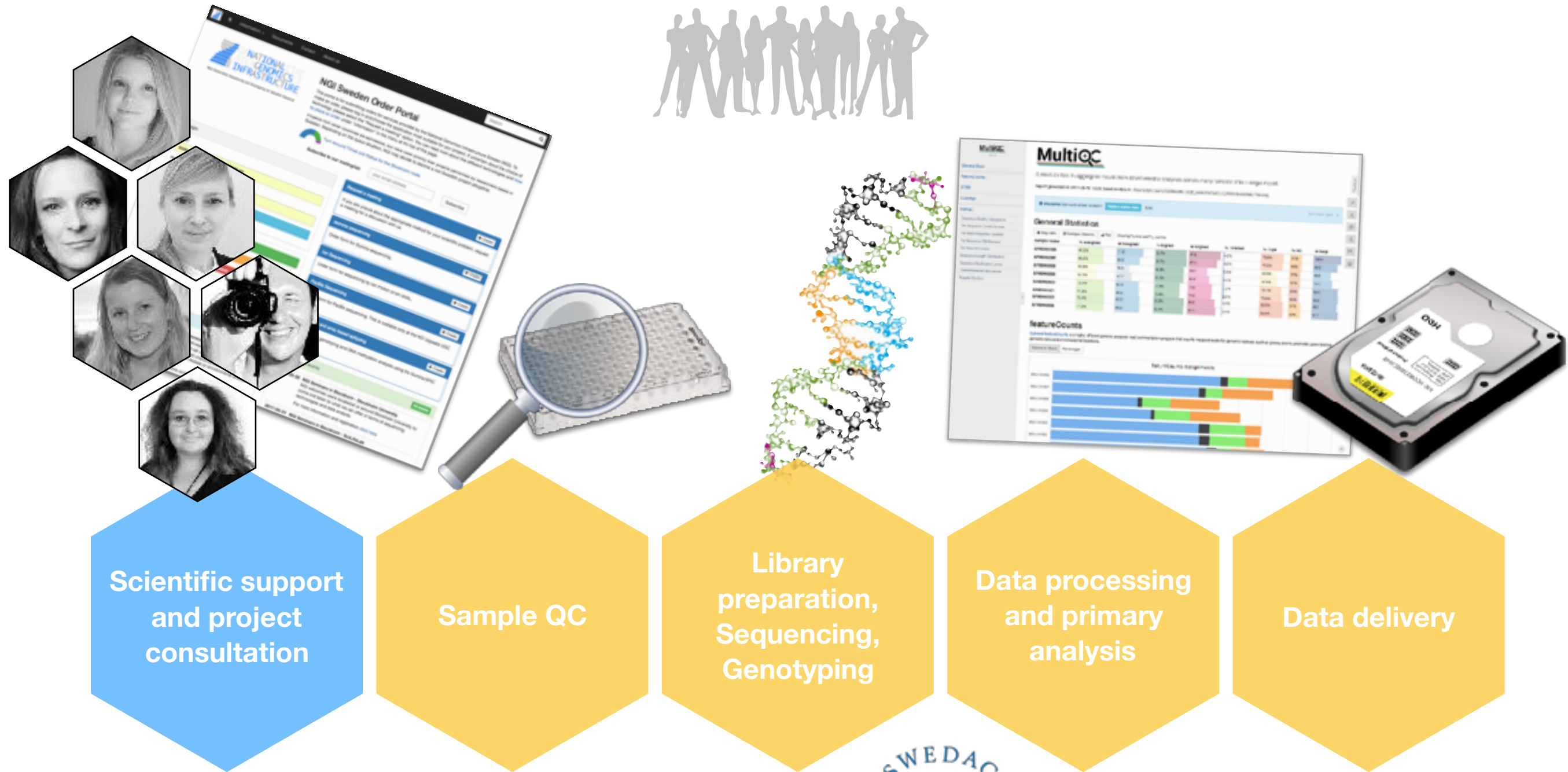


# Project timeline





# Project timeline

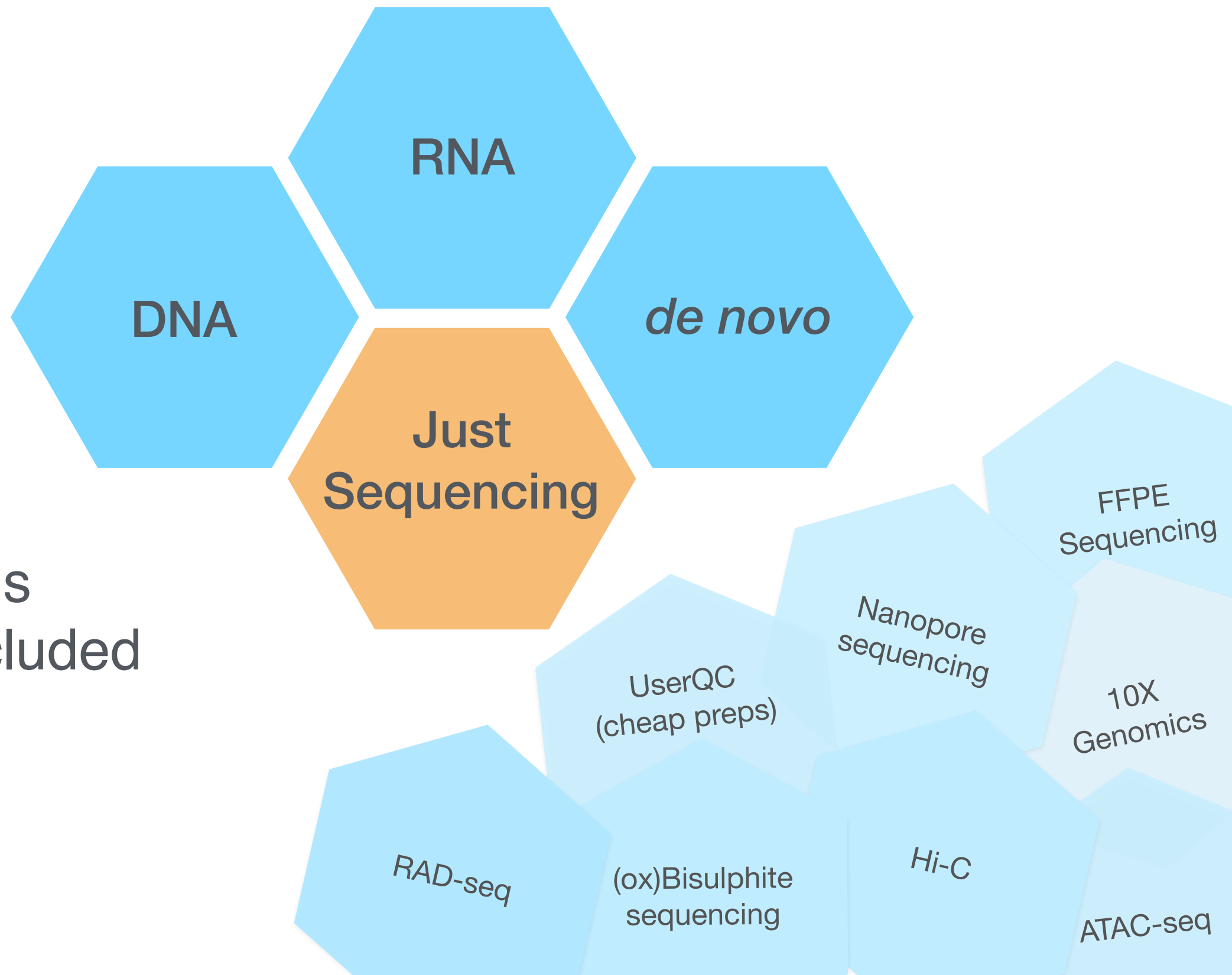


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ACKREDITERING.SWEDAC  
Ackred. nr 1850  
Provning  
ISO/IEC 17025

# Methods offered at NGI



Data analysis pipelines included

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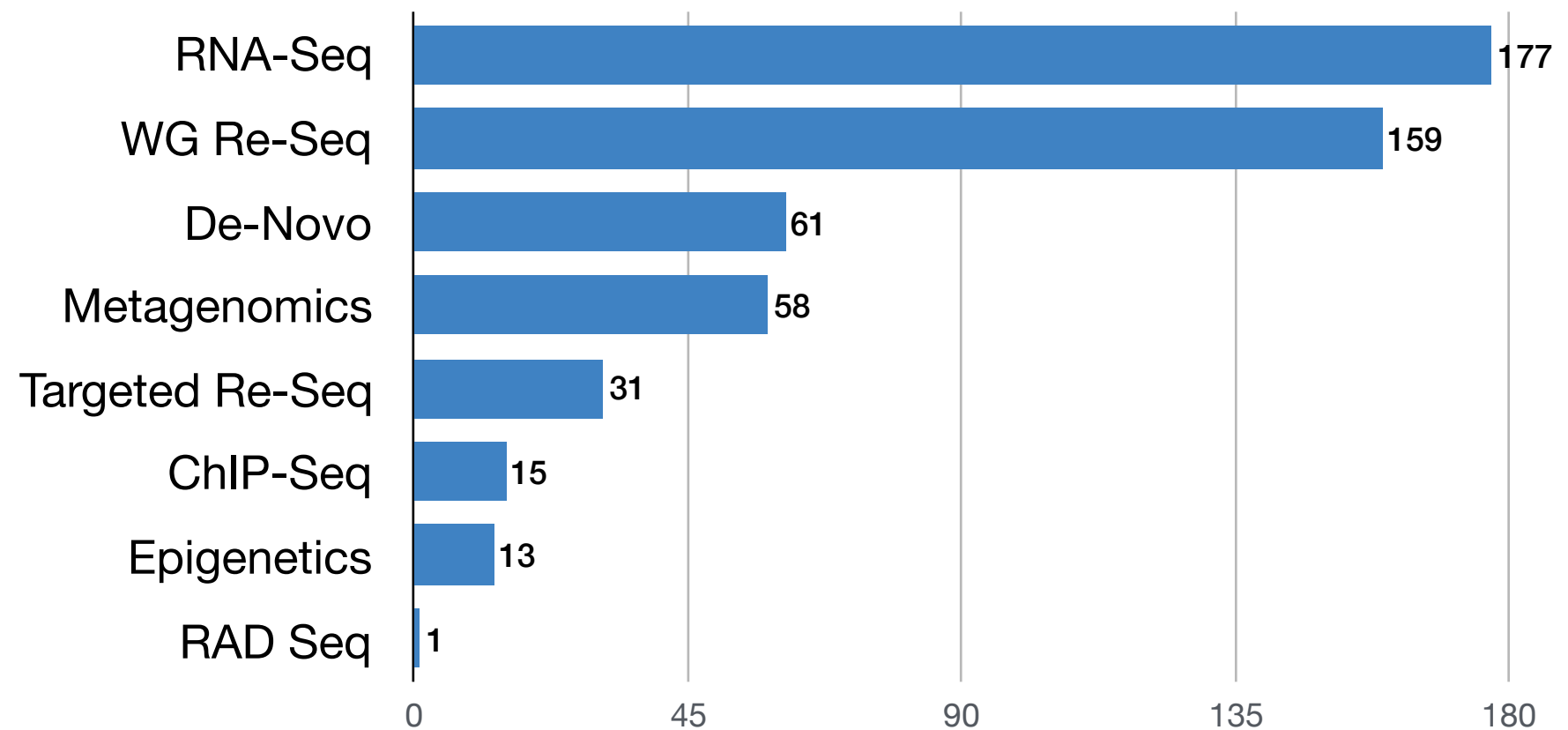
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# NGI Stockholm

- RNA-seq is the most common project type

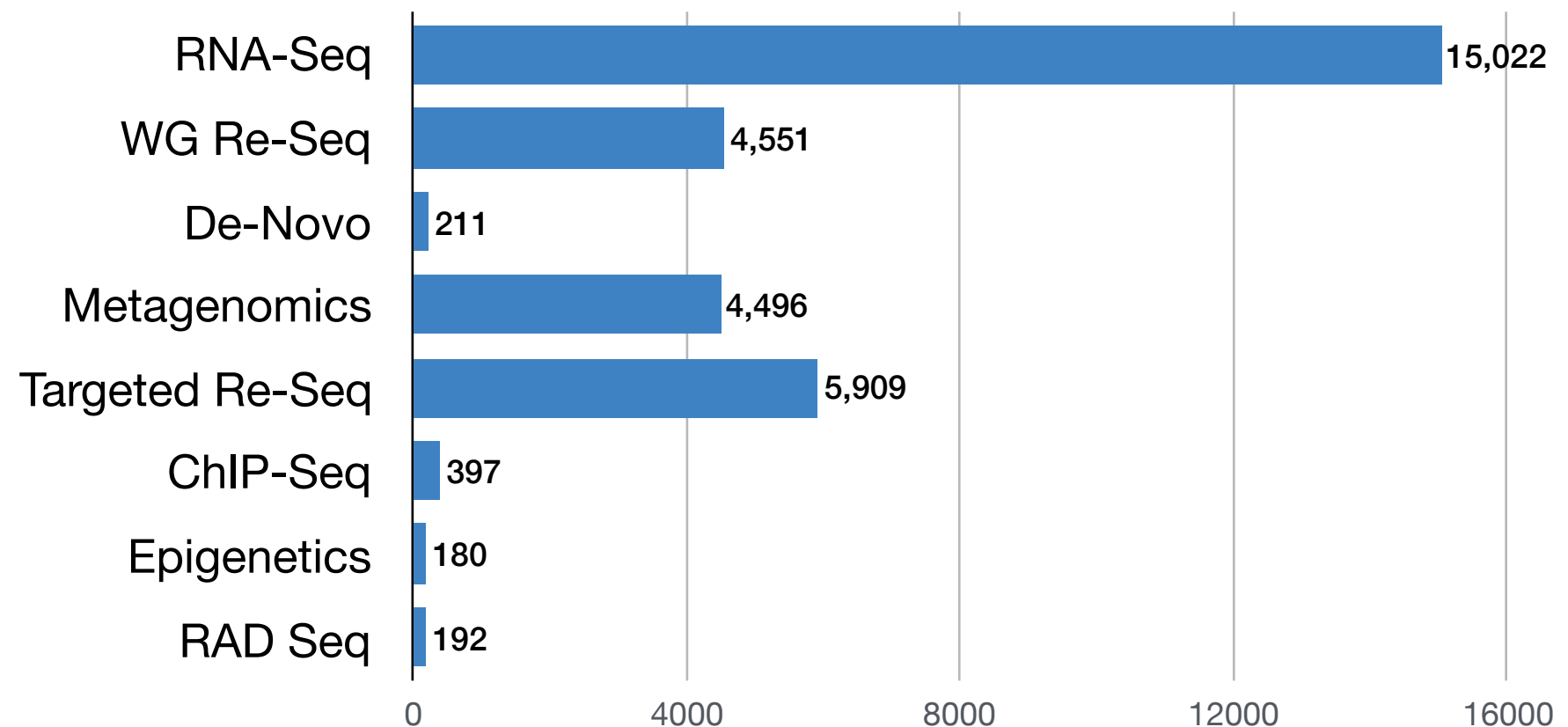
NGI Stockholm Projects in 2017



# NGI Stockholm

- RNA-seq is the most common project type
- In total, NGI Sweden processed 1068 NGS projects with almost 50 000 samples in 2017

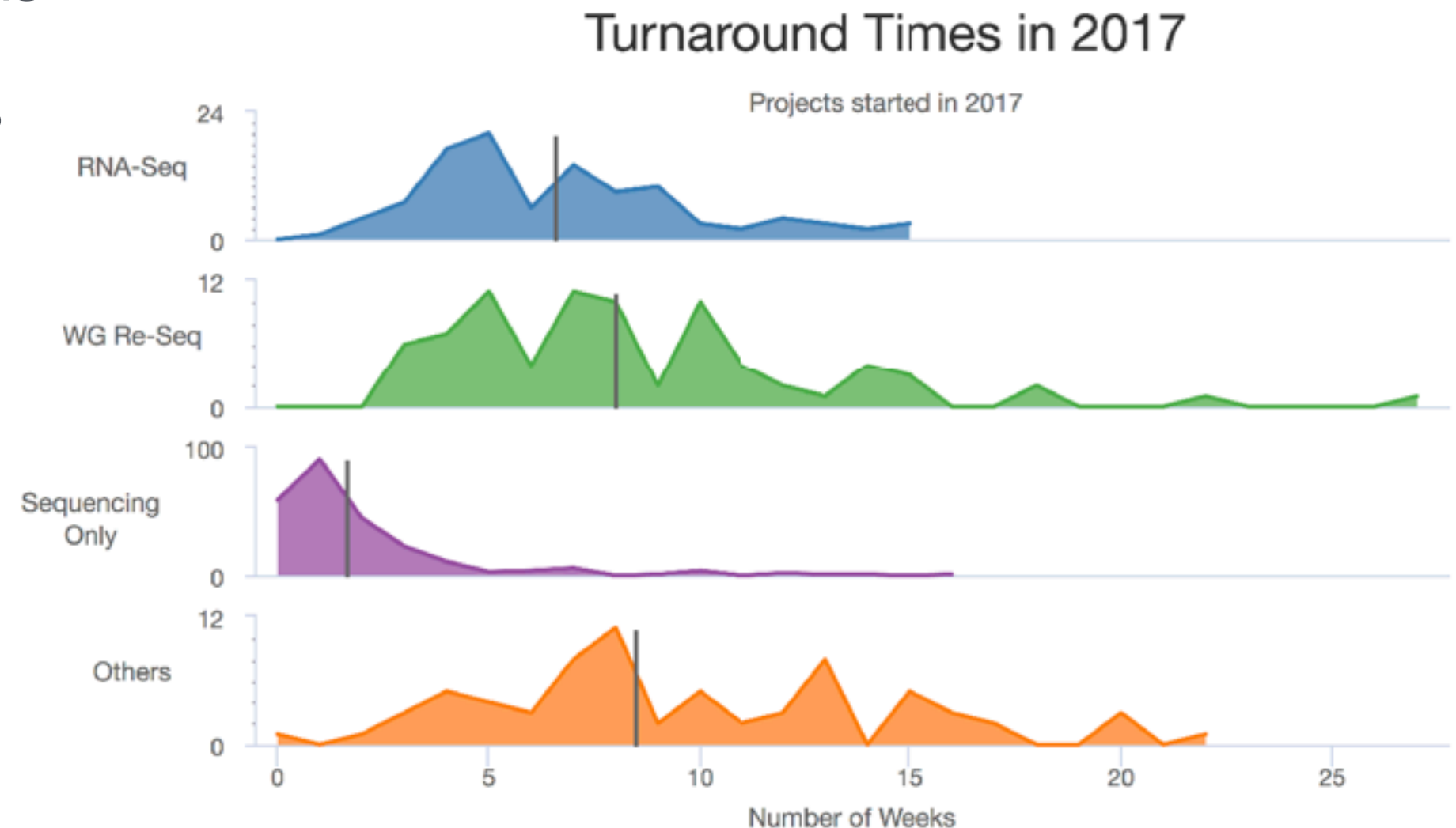
NGI Stockholm Samples in 2017



# NGI Stockholm

- Median turn around times from QC passed to data delivered for 2017
  - Sequencing only: 11.5 days
  - RNA: 6.5 weeks
  - WGS: 8 weeks

[https://ngisweden.scilifelab.se/file/stockholm\\_dashboard](https://ngisweden.scilifelab.se/file/stockholm_dashboard)



# Sequencing Technologies



# — Sequencing Types

Illumina

PacBio

Oxford Nanopore

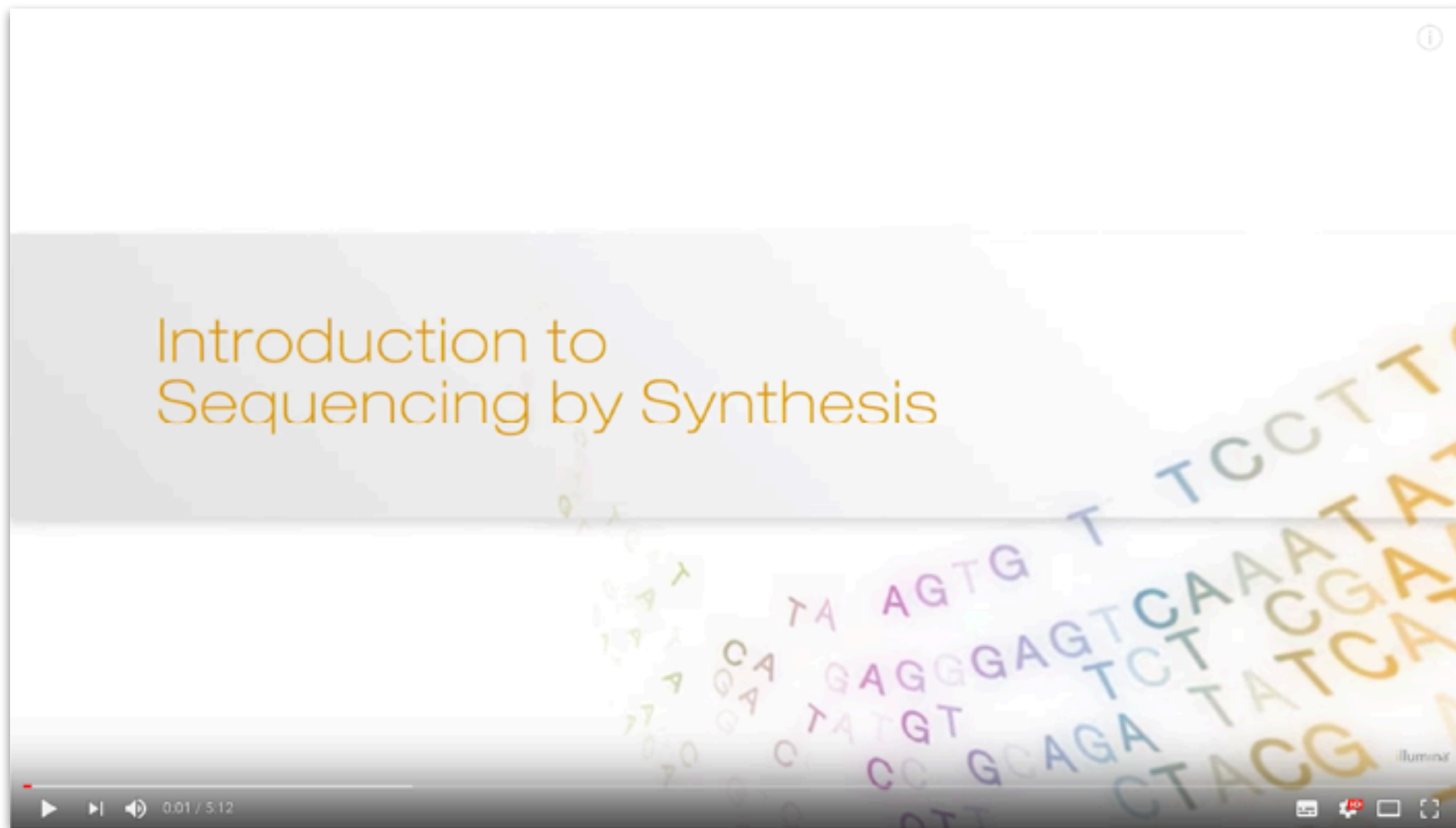
Ion Torrent

illumina®

# — Illumina Sequencing

- Largest provider of sequencing technology
- NGS machines use "Sequencing-by-synthesis"
  - Developed at the University of Cambridge in 1990s
  - Spun into a company called Solexa in 1998
  - Solexa acquired by illumina in 2007
- Responsible for vast majority of DNA sequencing experiments worldwide

# – Illumina Sequencing



<https://youtu.be/fCd6B5HRaZ8>

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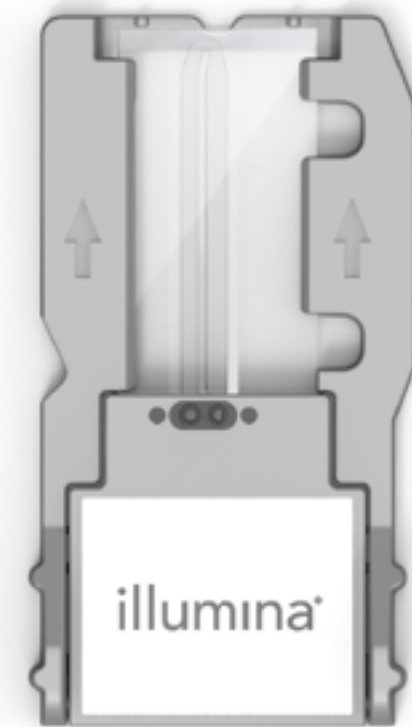
 NGI stockholm



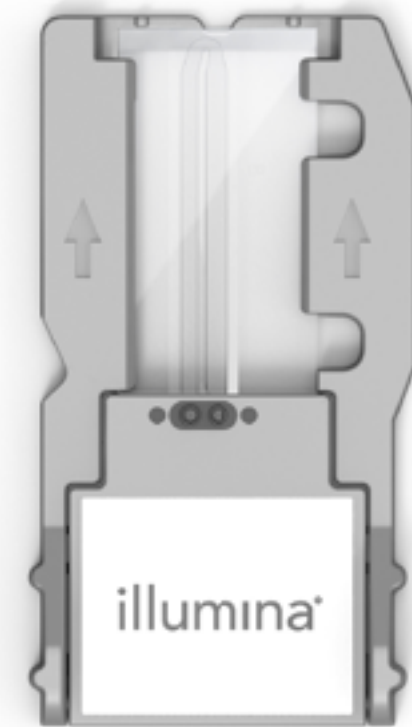
# — Illumina iSeq 100



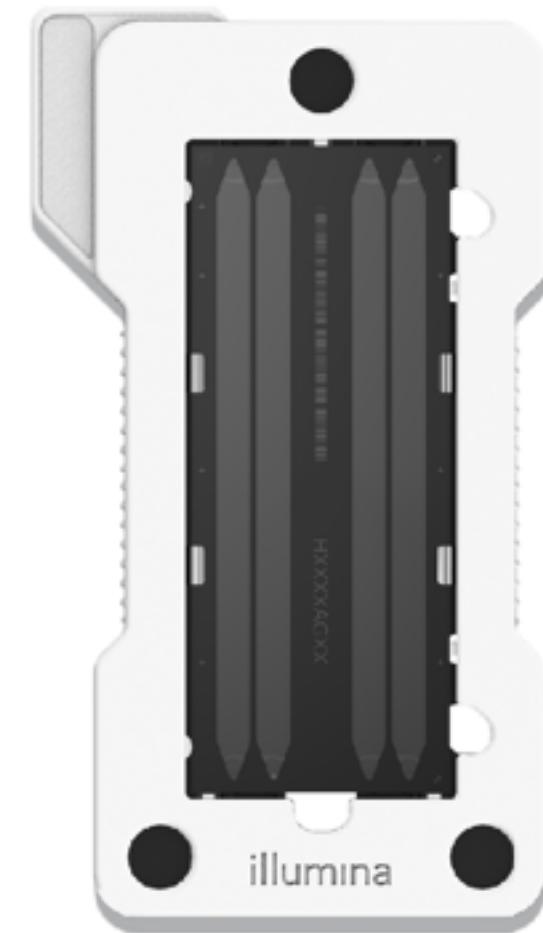
# — Illumina MiniSeq 100



# — Illumina MiSeq



# — Illumina NextSeq



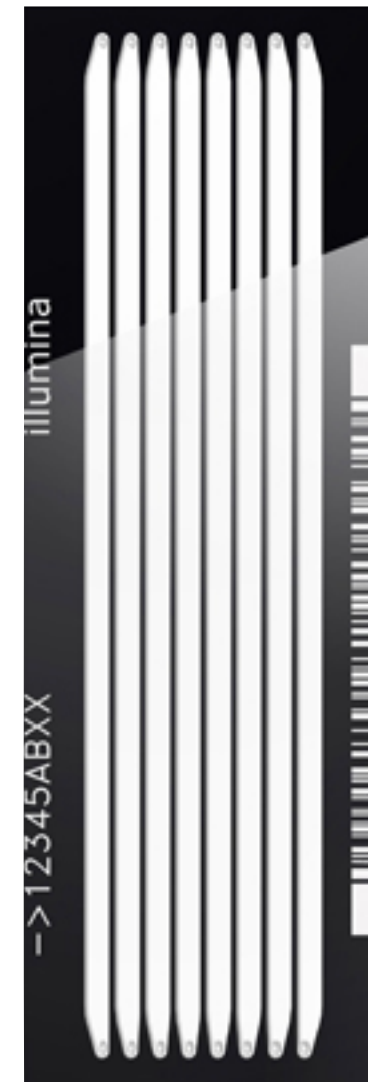
# — Illumina HiSeq 2500



# — Illumina HiSeq 3000

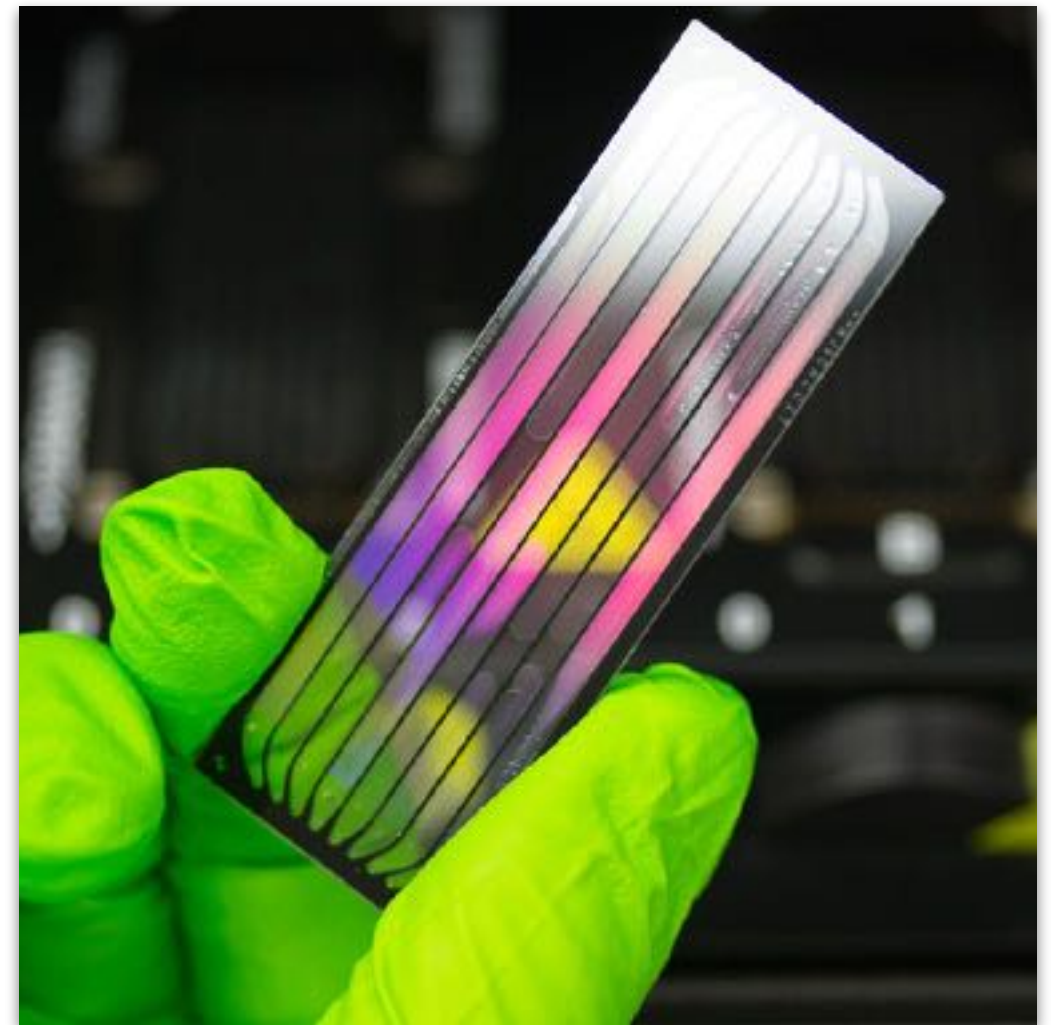


# — Illumina HiSeq 4000



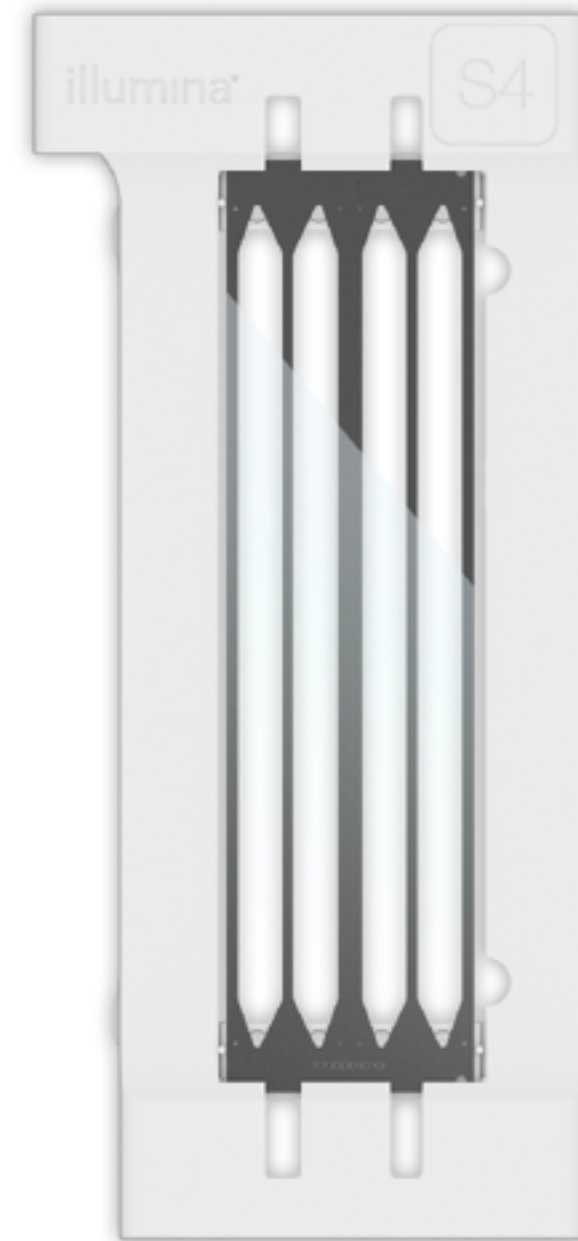


# — Illumina HiSeq X





# — Illumina NovaSeq 6000

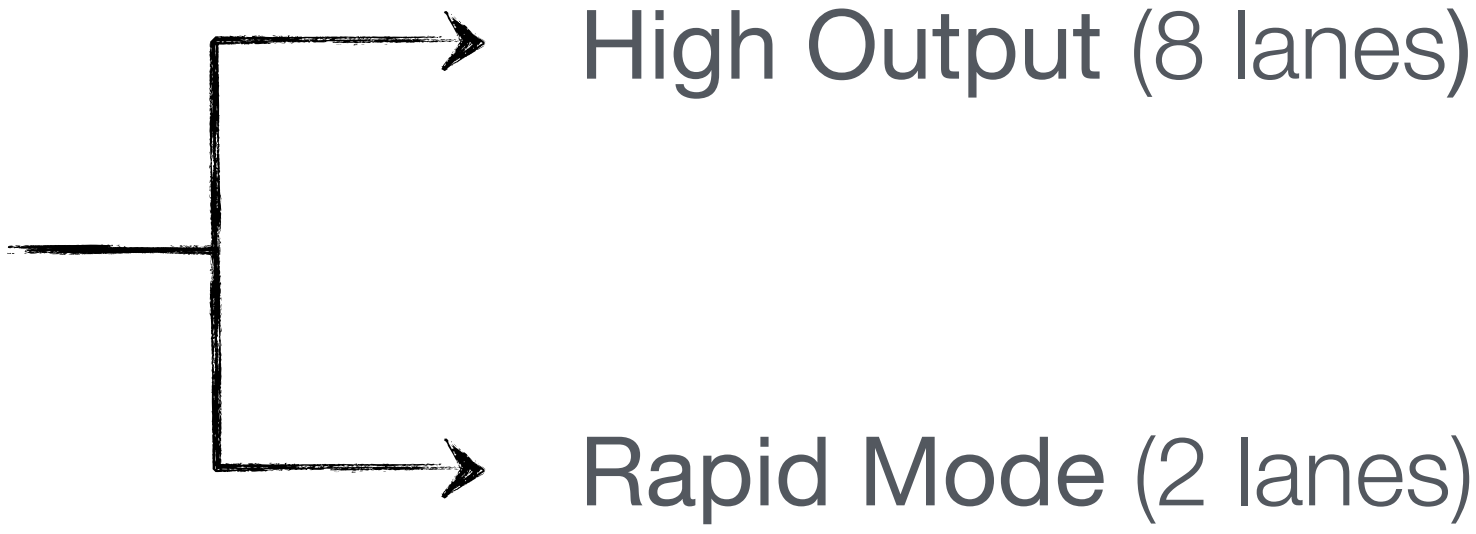


# — Illumina at NGI

iSeq 100	Coming soon to NGI Uppsala Small cheap runs
MiSeq	Small runs, long reads (2x300bp)
HiSeq 2500	Primary machine for most of NGI's history
HiSeq X	Cheap, high throughput Only allowed to run WGS with > 15X coverage
NovaSeq 6000	Newest machine, both Stockholm & Uppsala Will eventually replace HiSeq 2500

# — Illumina at NGI

iSeq 100
MiSeq
HiSeq 2500
HiSeq X
NovaSeq 6000



# — Illumina at NGI

iSeq 100
MiSeq
HiSeq 2500
HiSeq X
NovaSeq 6000

Coming soon!

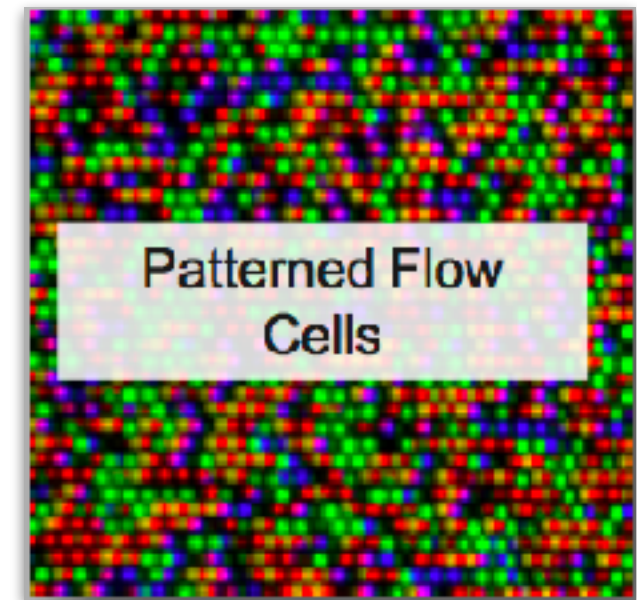
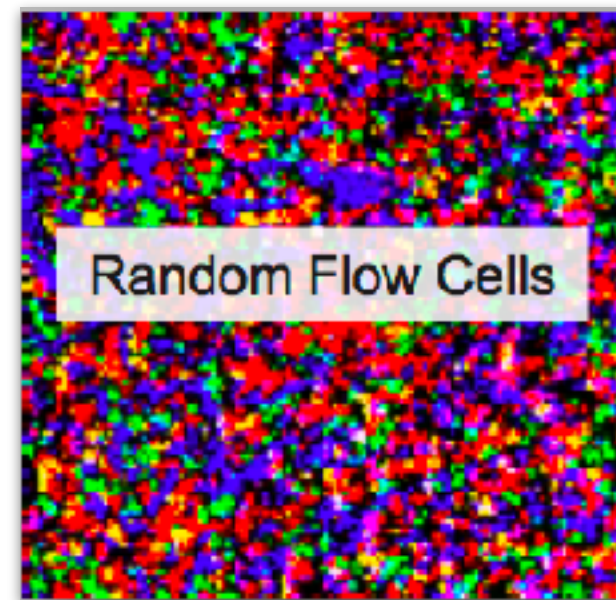
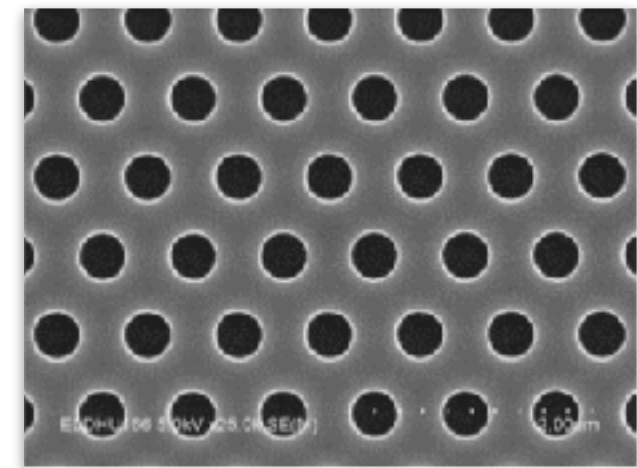
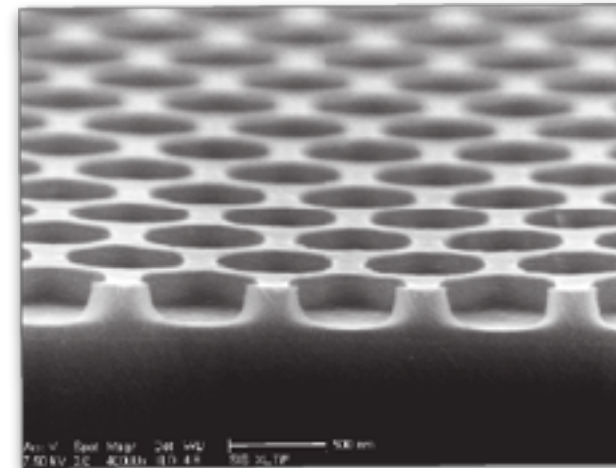


# — How to choose

- Number of reads required
  - How many samples, how deeply sequenced?
- Type of reads required
  - Single End / Paired End, length?
- Urgency and cost
  - Sharing flow cells with other users
  - Best price for the project

# Patterned flow cells

- New type of flow cell
  - HiSeq 4000, HiSeq X, NovaSeq
- Single sequence per well
  - Higher density, more data
- Different side effects
  - Index hopping
  - Duplicate reads





Articles about common next-generation  
sequencing problems

Phil Ewels  
Simon Andrews



# Illumina Patterned Flow Cells Generate Duplicated Sequences

Steven Wingett

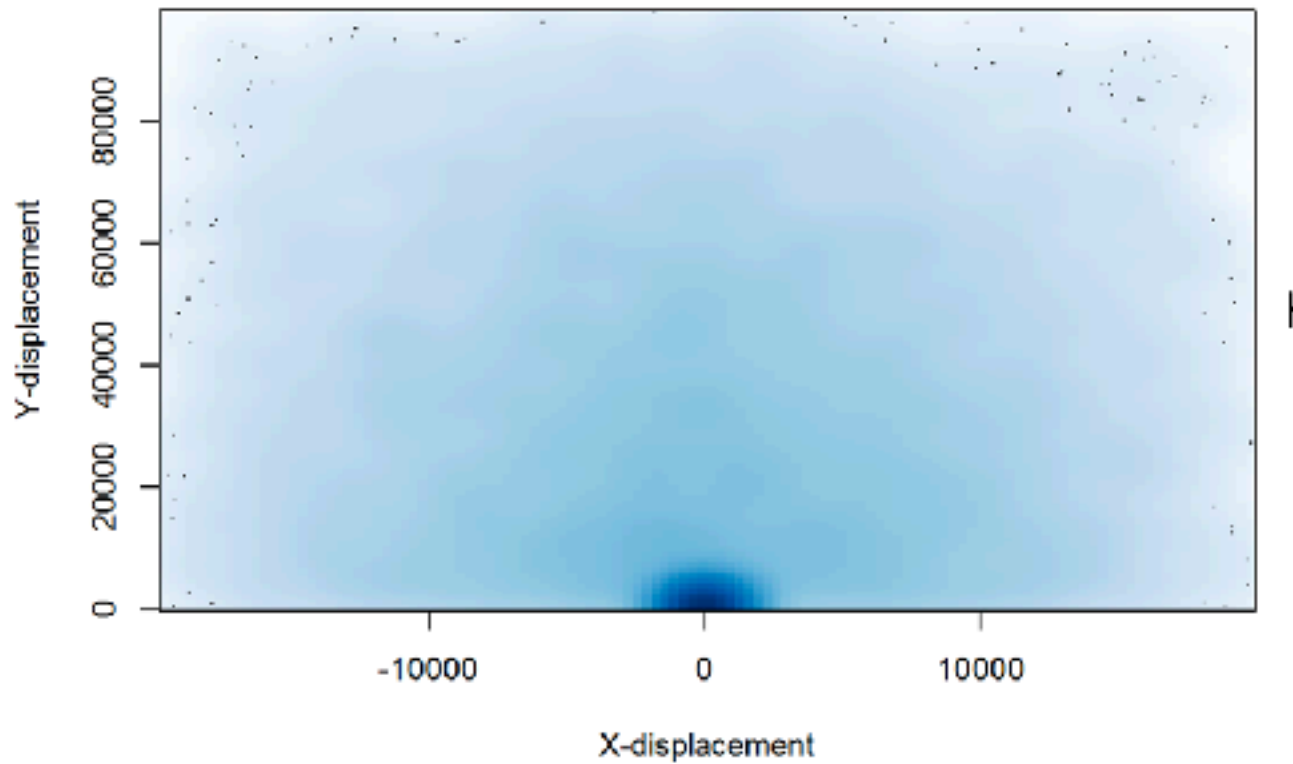


<https://sequencing.qcfail.com/articles/illumina-patterned-flow-cells-generate-duplicated-sequences/>

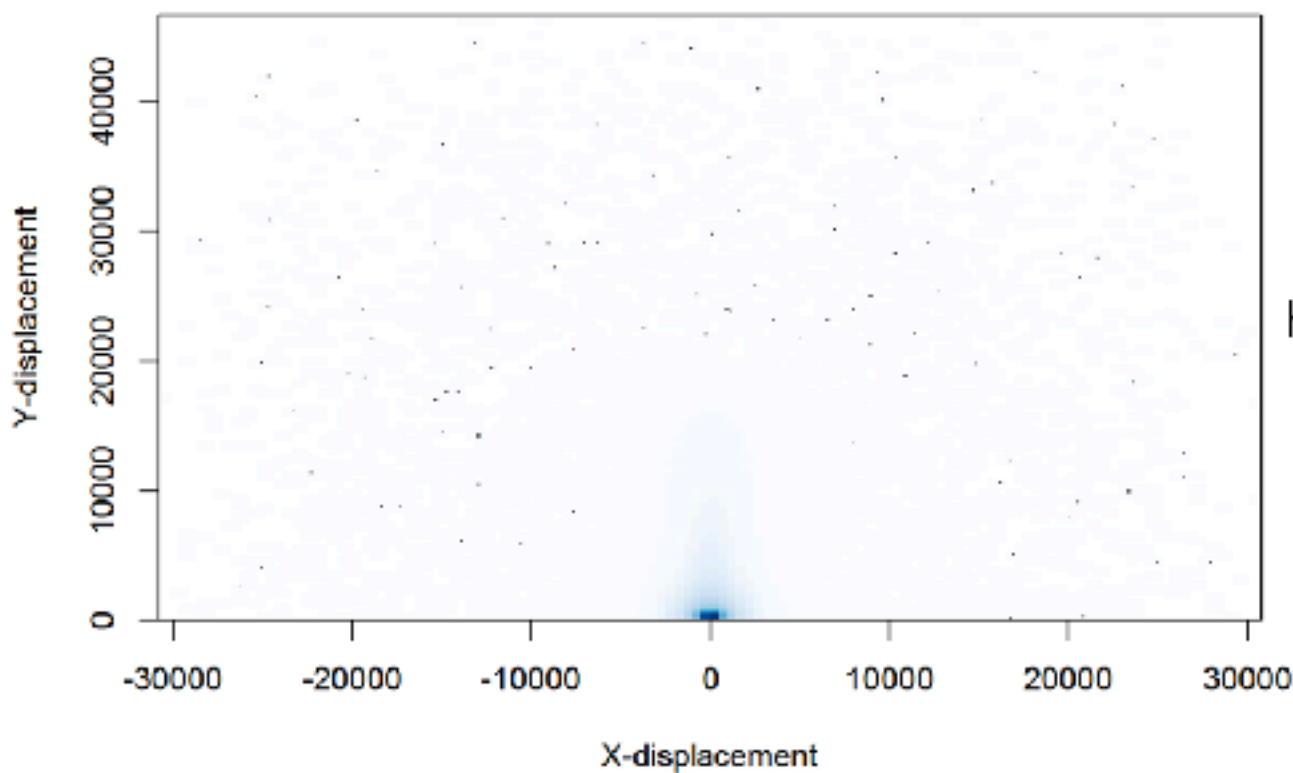


# Patterned duplicates

Relative positioning of duplicates

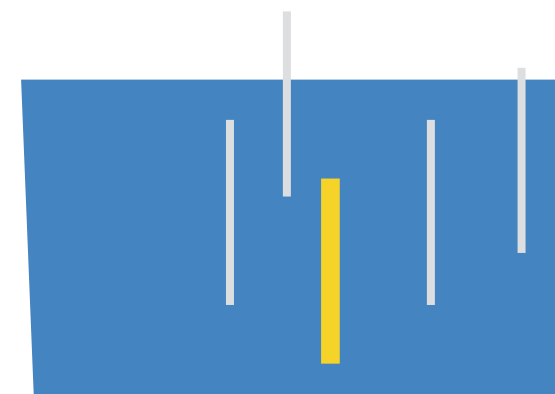


HiSeq 2500

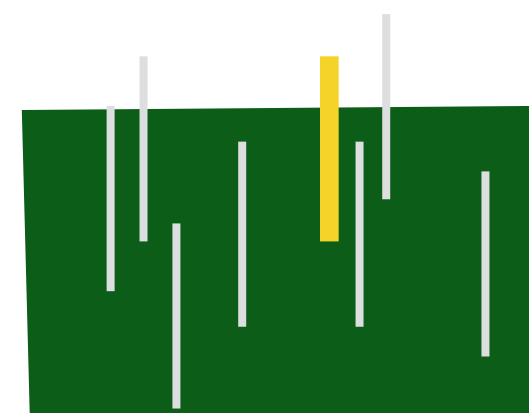


HiSeq 4000

Duplicates on different tiles



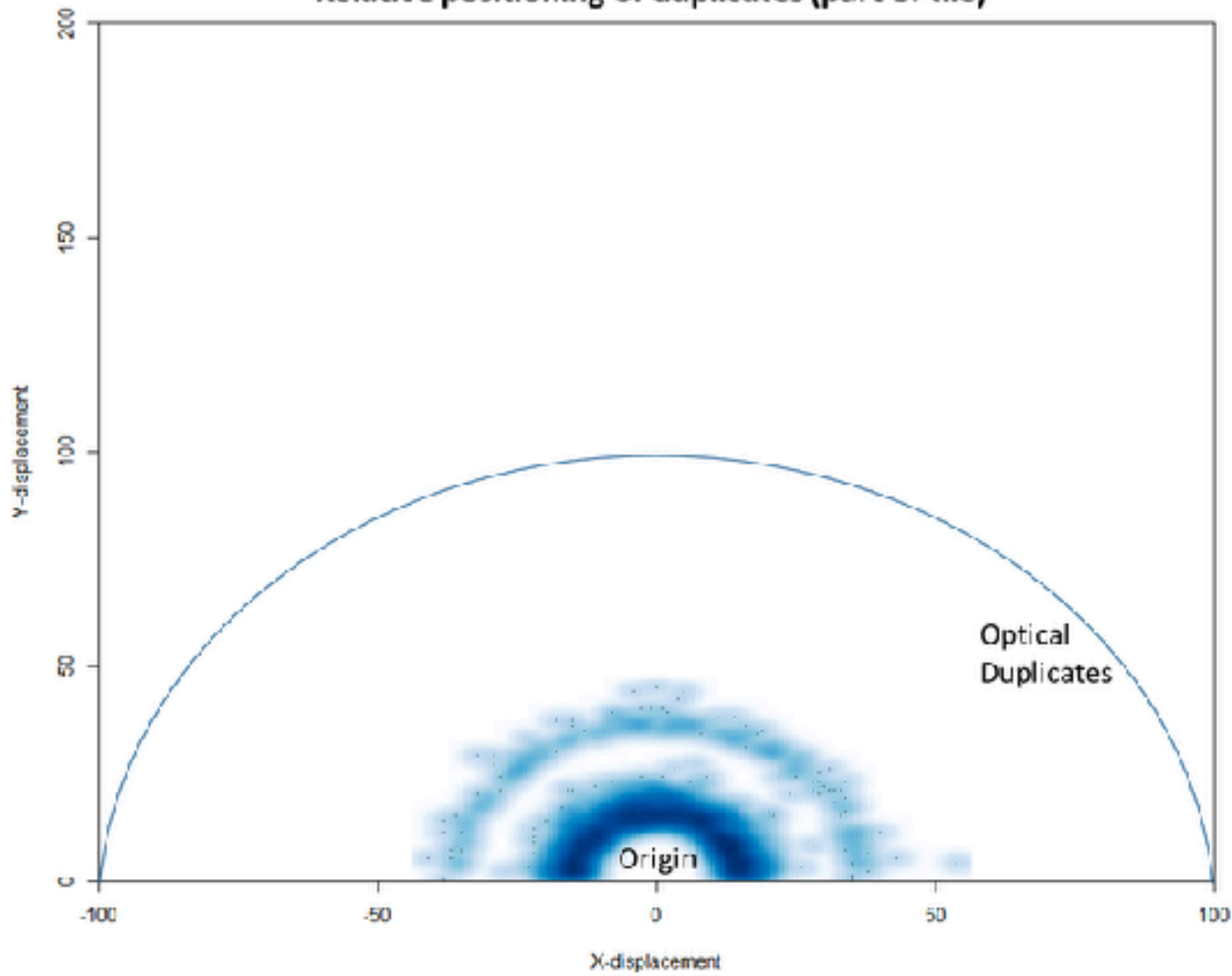
Tile A



Tile B

# Patterned duplicates

Relative positioning of duplicates (part of tile)



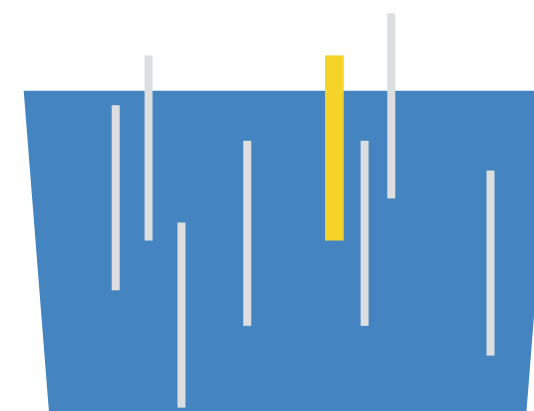
Unpatterned  
flow cell

Duplicates on  
the same tile

HiSeq 2500



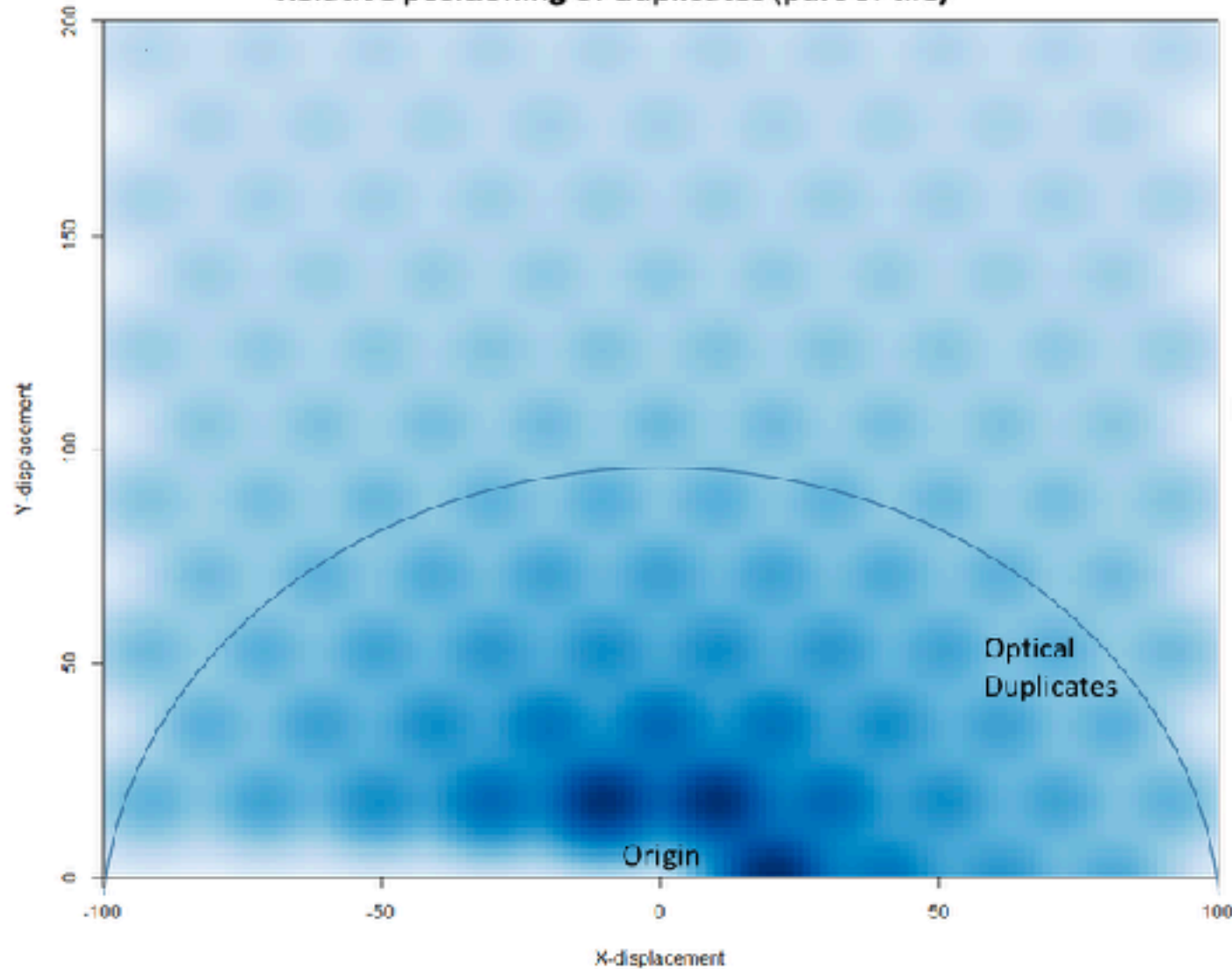
Tile A



Tile A

# Patterned duplicates

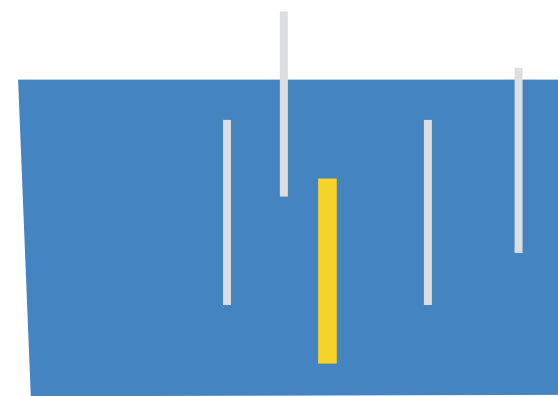
Relative positioning of duplicates (part of tile)



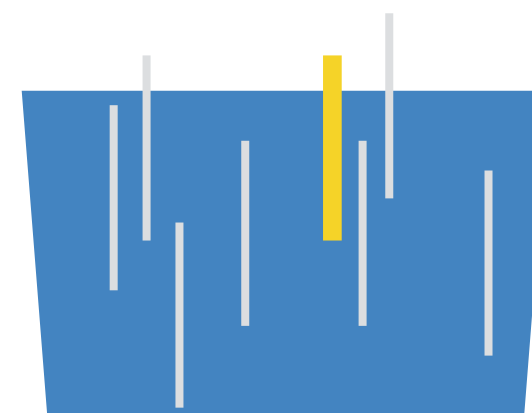
Patterned  
flow cell

Duplicates on  
the same tile

HiSeq 4000

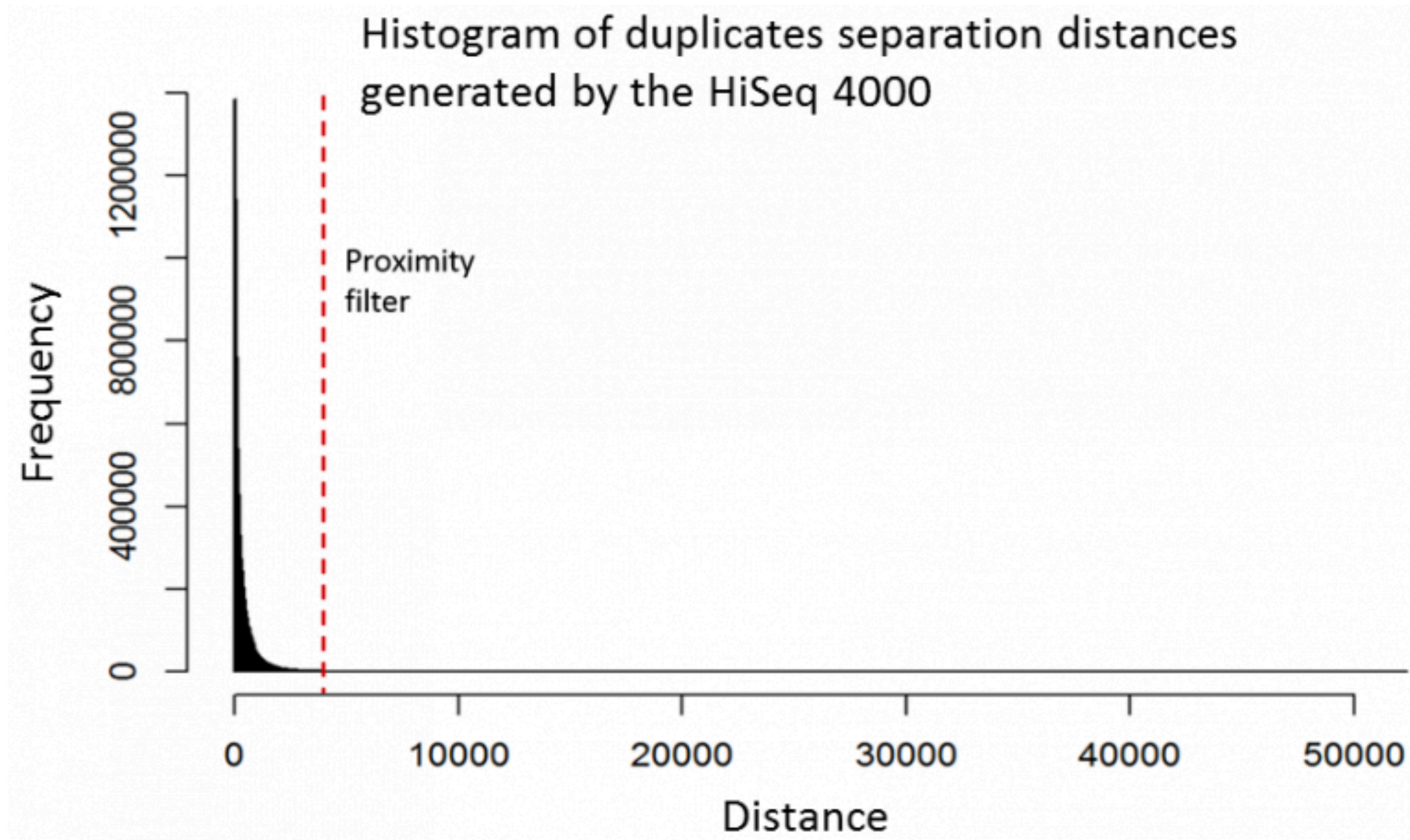


Tile A



Tile A

# Patterned duplicates



# – Patterned duplicates

- Regular duplicate removal works fine
  - Sequence alignment positions should be identical
- Can use Picard MarkDuplicate optical duplicate settings
  - May need to increase the default pixel threshold
- Specialised tools such as [EdinburghGenomics/well\\_duplicates](https://github.com/EdinburghGenomics/well_duplicates) work directly with .bcl files
  - [https://github.com/EdinburghGenomics/well\\_duplicates](https://github.com/EdinburghGenomics/well_duplicates)



Illumina 2 colour chemistry can  
overcall high confidence G bases

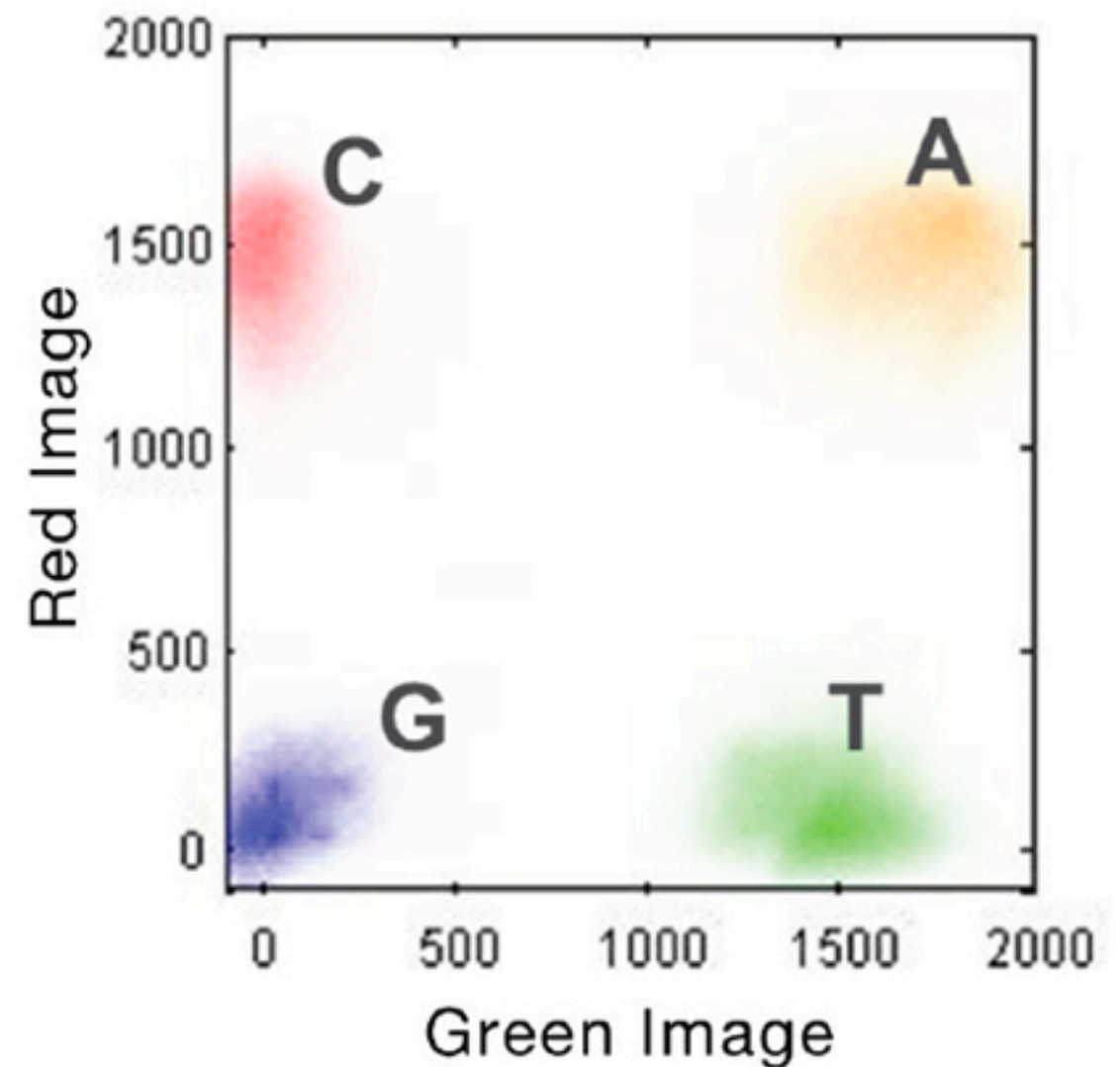
Simon Andrews



<https://sequencing.qcfail.com/articles/illumina-2-colour-chemistry-can-overcall-high-confidence-g-bases/>

# Colour chemistry

- Older SBS used four different fluorophores
  - One for each nucleotide
- New machines use two
  - Faster and cheaper
  - NextSeq, NovaSeq, iSeq



# Colour chemistry

## 4-colour chemistry

Base	G Filter	A Filter	T Filter	C Filter
G	✓	✗	✗	✗
A	✗	✓	✗	✗
T	✗	✗	✓	✗
C	✗	✗	✗	✓
N	✗	✗	✗	✗

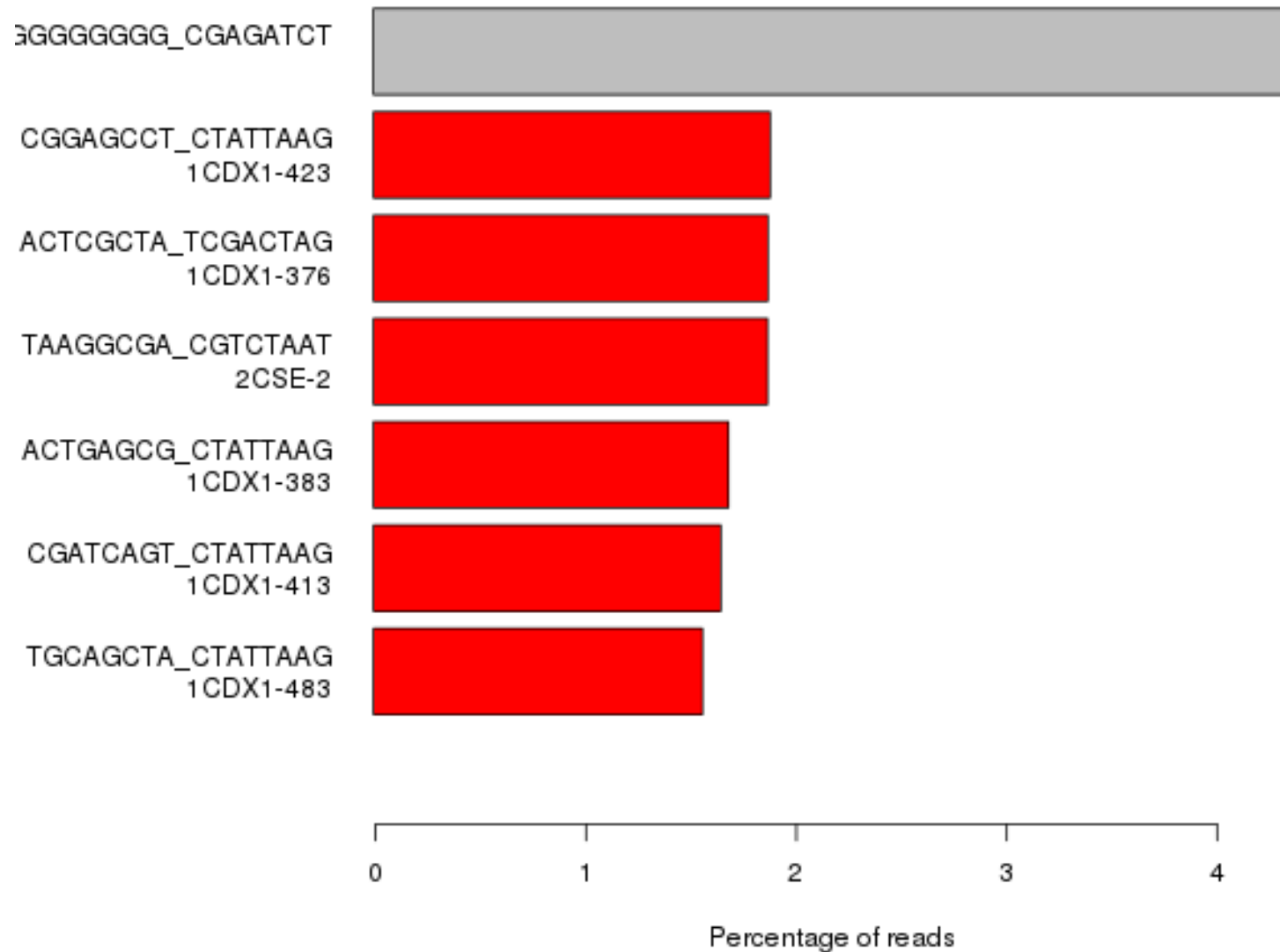


# — Colour chemistry

## 2-colour chemistry

Base	Green Filter	Red Filter
G	✗	✗
A	✓	✓
T	✓	✗
C	✗	✓
N	✗	✗

# Colour chemistry



Index	Count	Total %
AGCGATAG+ATTGTTGC	3 408 780	3.22%
GGGGGGGG+GGGGGGGG	3 051 380	2.89%
TCCGCGAA+ATTGTTGC	2 844 020	2.69%
GAGATTCC+ATTGTTGC	2 602 140	2.46%
TAATGCGC+ATTGTTGC	2 578 560	2.44%
TCTCGCGC+ATTGTTGC	2 405 340	2.28%
ATTACTCG+ATTGTTGC	2 281 500	2.16%
CGCTCATT+ATTGTTGC	2 279 700	2.16%
ATTCAGAA+ATTGTTGC	2 252 180	2.13%
CTGAAGCT+ATTGTTGC	2 249 940	2.13%
TCCGGAGA+CGTTTACT	2 236 880	2.12%
GGGGGGGG+TGTTTCCC	2 160 120	2.04%
CGGCTATG+ATTGTTGC	2 132 900	2.02%
GAATTCGT+ATTGTTGC	2 080 700	1.97%
TCCGGAGA+ATTGTTGC	2 070 820	1.96%
ATTACTCG+CGTTTACT	2 017 160	1.91%
TGCGATTG+TTTGTGGC	1 730 080	1.64%
ATTCAGAA+CGTTTACT	1 640 140	1.55%
GGGGGGGG+TTTTGCCT	1 475 160	1.4%
CGCTCATT+CGTTTACT	1 408 140	1.33%

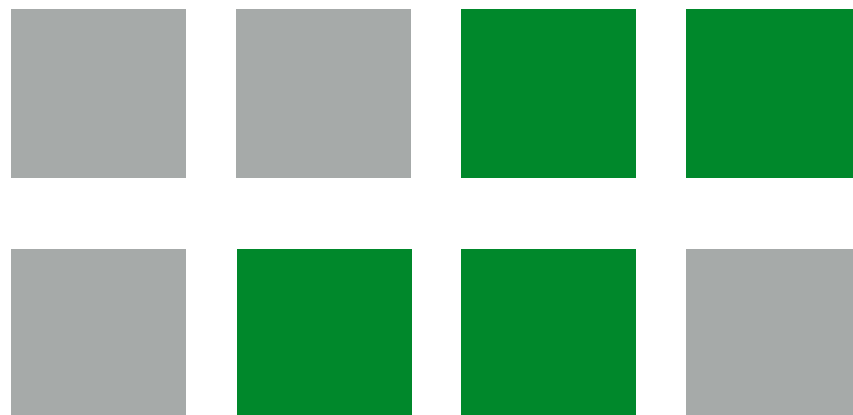
# Colour chemistry

Base	Green Filter	Red Filter
G	✗	✗
A	✓	✓
T	✓	✗
C	✗	✓
N	✗	✗

Sample 1 GGTT

Sample 2 GTTC

Green



Red



# Colour chemistry

Base	Green Filter	Red Filter
G	✗	✗
A	✓	✓
T	✓	✗
C	✗	✓
N	✗	✗

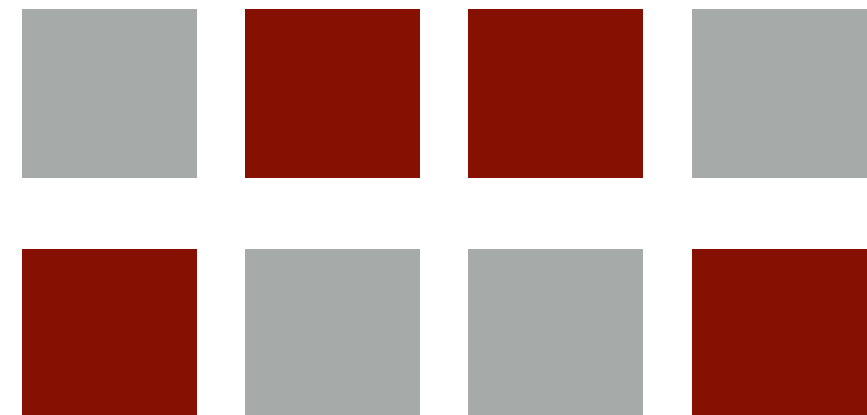
Sample 1 GCAT

Sample 2 ATGC

Green



Red



# — Colour chemistry

- Poor quality reads may show up as G instead of N
  - For example, missing bases from short insert sizes
- Trimming tools such as cutadapt now updated to handle this
- Careful colour balancing of indexes can avoid problems with deduplication
  - This isn't new - it's just more sensitive than before
- Check the illumina recommendations:
  - <http://emea.support.illumina.com/downloads/index-adapters-pooling-guide-1000000041074.html?langsel=/se/>

# Balanced pooling

- New NovaSeqs make the S4 the best option
- Proper sample concentration normalisation more important than ever
  - Big (expensive) flow cells = high stakes!
- Our plans: always improving library quantitation and normalisation
  - Constant benchmarking of quant tools
  - More accurate automation

illumina®



PACIFIC  
BIOSCIENCES®

# — PacBio

- Pacific Biosciences - specialists in long reads
  - Also uses fluorescent nucleotides
  - Polymerases immobilised at the bottom of tiny wells give off pulses as the nucleotides are incorporated
- Each well is independent, doesn't use sequencing rounds like illumina
- Can work with much longer DNA fragments
  - 250 bp – 60 kb (max ~160 kb)



# — PacBio



<https://youtu.be/NHCJ8PtYCFc>

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# - PacBio RS II



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# - PacBio Sequel



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# — PacBio Sequencing

- Long reads are excellent for *de-novo* genome assembly, haplotype phasing and isoform detection
- Output is expensive compared to illumina, but getting better
- Small genomes are no problem. Larger genomes are now becoming more feasible.
- New amplification-free enrichment using CRISPR-Cas9



Oxford

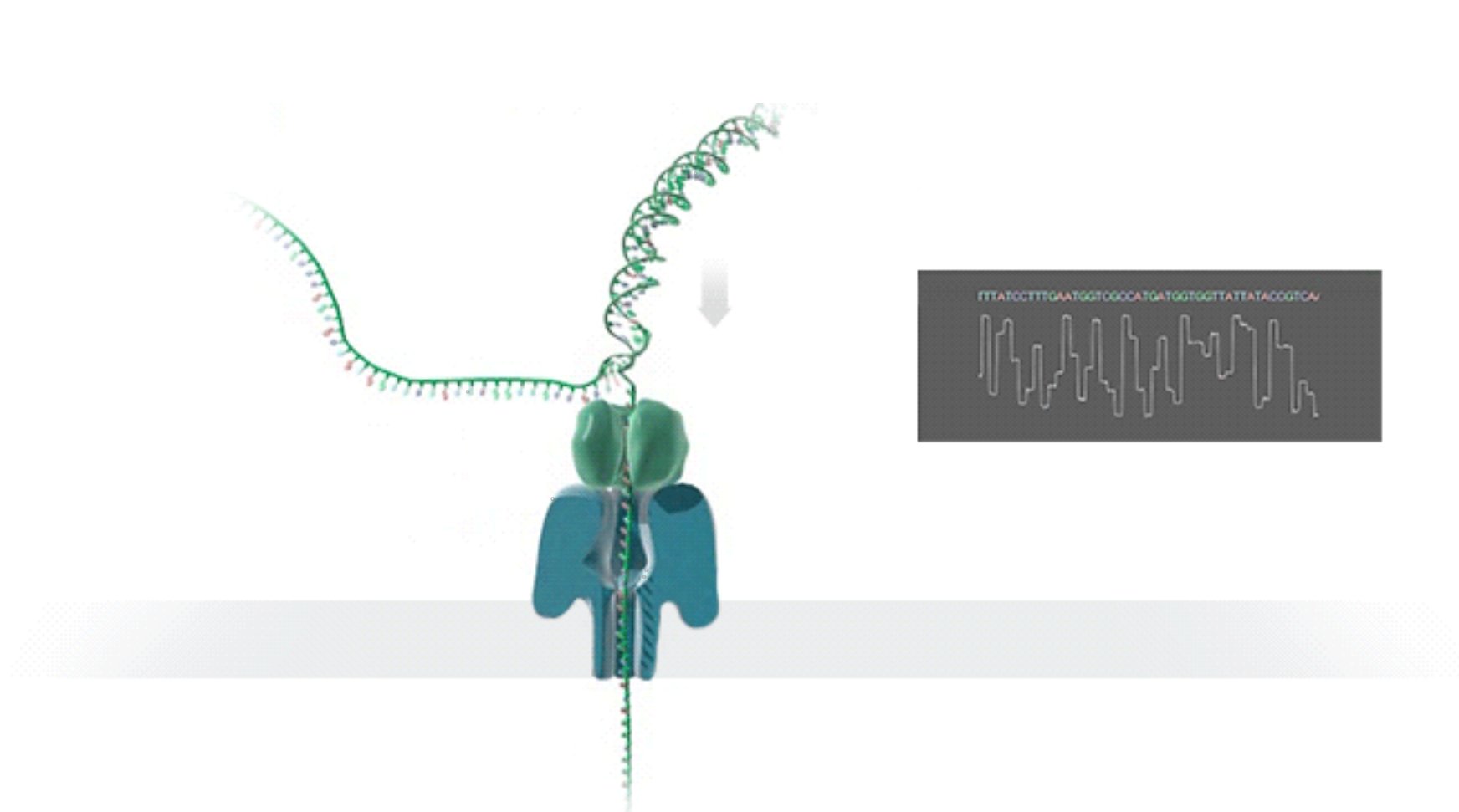
**NANOPORE**

Technologies

# — Oxford Nanopore

- Newest contender in the sequencing world
  - Lots of hype and taken several years to become a reality
- Still developing very fast
  - Quality, yield and cost changing almost monthly
- High error rates (but better than they used to be)
  - Now 2-13% depending on sequencing type

# — Oxford Nanopore



# MinION



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# MinION



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# GridION

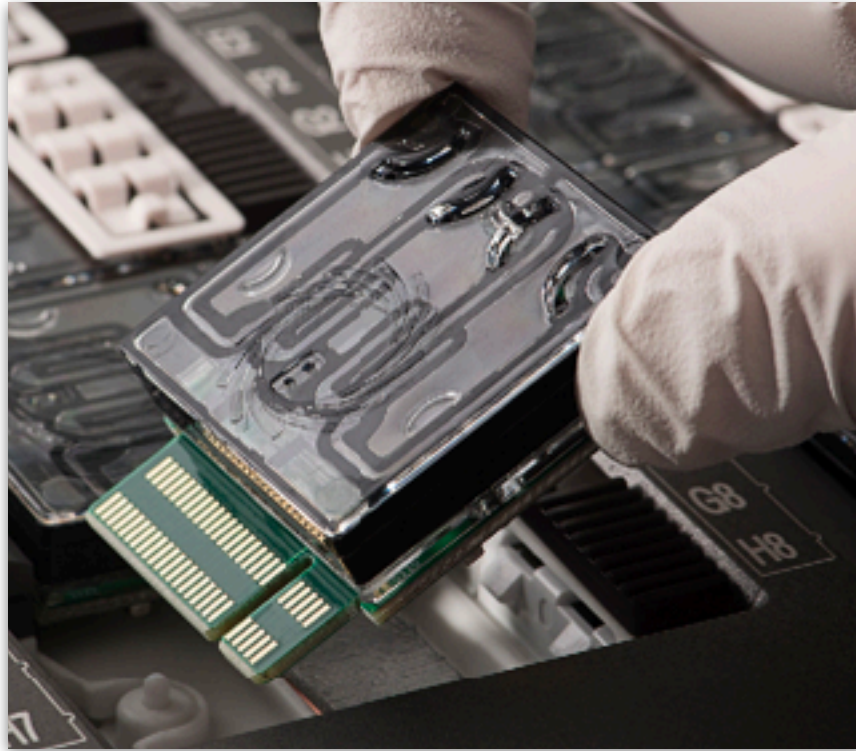


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# PromethION



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# - SmidgION



(not yet released)

# — Oxford Nanopore

- The best technology available for ultra long reads
- Twitter users report getting reads over 1 Mbp long
- "Whale spotting" - finding the longest reads on the end of the distribution curve
- Need to balance yield with read length
- Price dropping rapidly, but still expensive compared to illumina
- NGI has 2x MinIONs and a PromethION

ion torrent

by **Thermo Fisher Scientific**

# — Ion Torrent

- Main application
  - Microbial and metagenomic sequencing
  - Targeted re-sequencing (gene panels)
  - Clinical sequencing
- Short, single-end reads
- Fast run times



# — Ion Torrent PGM



- Yield
  - 0.1 - 1 Gbp
- Run time
  - 3 hrs
- Read length
  - 200 - 400 bp



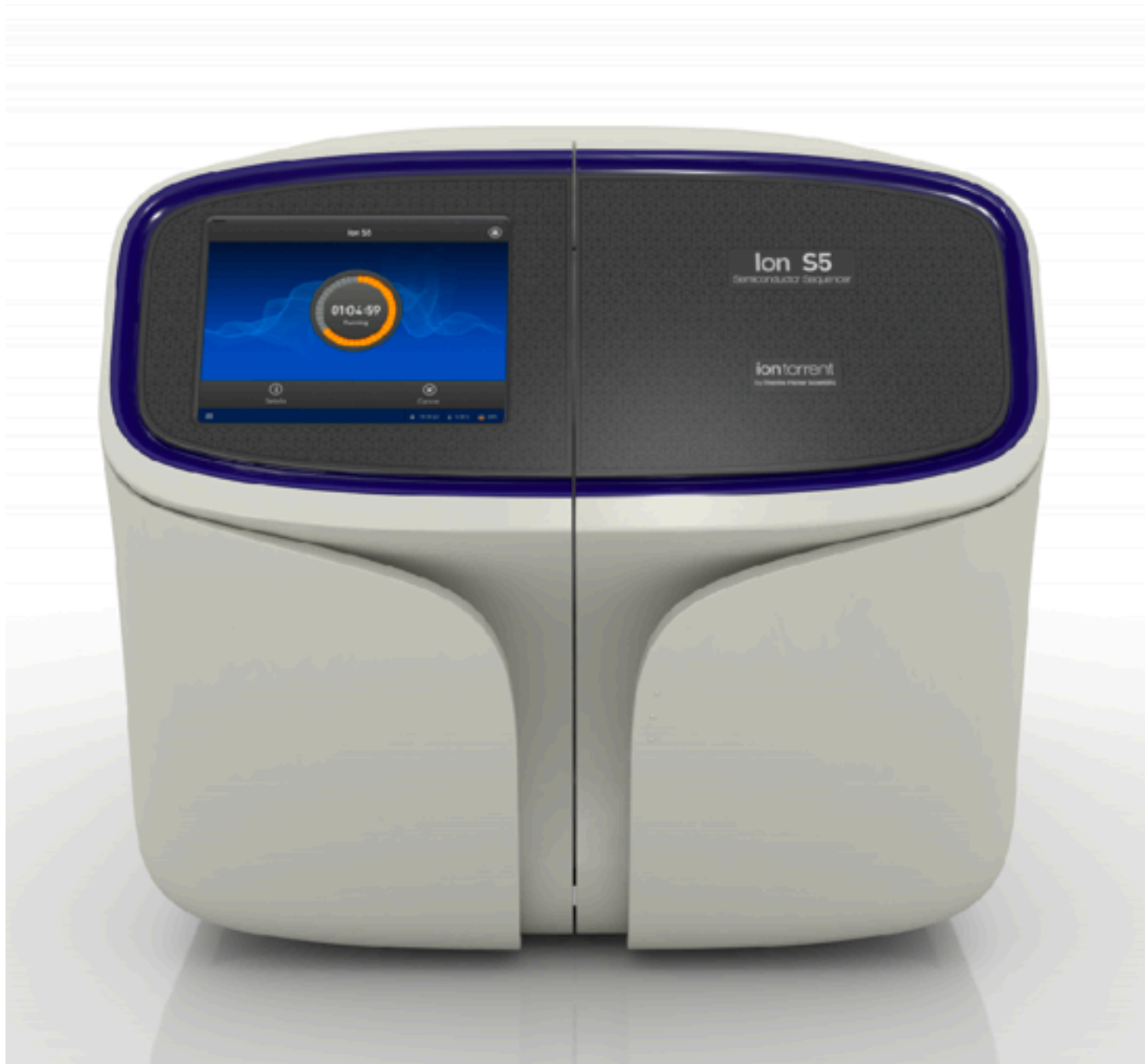
# — Ion Torrent Proton



- Yield
  - 10 Gbp
- Run time
  - 4 hrs
- Read length
  - 200 bp



# – Ion Torrent S5 XL



- Yield
  - 1-13 Gbp
- Run time
  - 3 hrs
- Read length
  - 200 - 600 bp

# – Sequencing Type

- No need to remember all of this
  - Many considerations, changing all the time
- We are experts - come and speak to us!

support@ngisweden.se

<https://ngisweden.scilifelab.se/>

# Sequencing Applications



# Library Preparation

- All high throughput sequencing requires some kind of library preparation
  - Add adapters for sequencing chemistry
  - Adjust DNA fragment lengths
  - Incorporate biological signal into sequence
  - Add required enzymes
- Different library preps enable different applications

# RNA Sequencing

- Choose a type of RNA

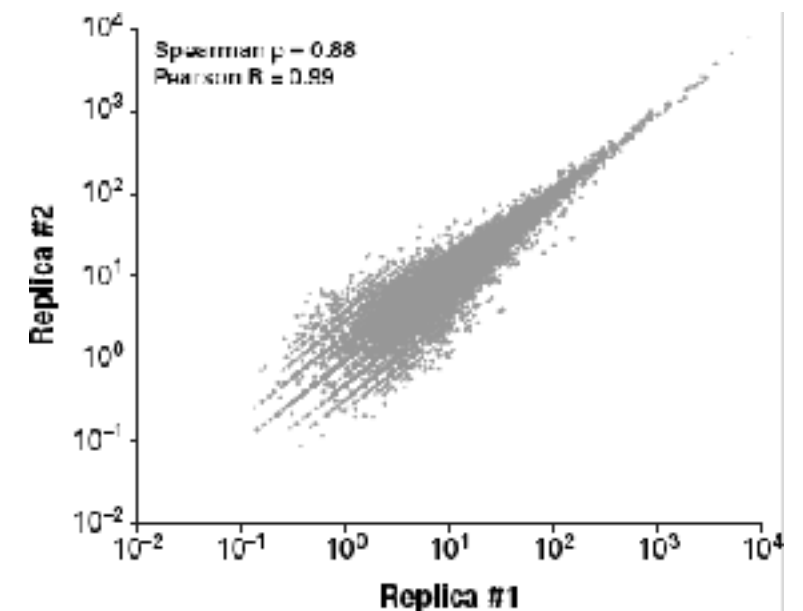
- Protein coding mRNA (poly-A)
- All RNA (rRNA depletion)
- Small RNA

- Choose your question

- Differential gene expression
- Differential isoform detection & quantification
- Fusion gene detection

- Define your limitations

- Low-input material
- Low quality material (eg. FFPE)



# RNA Sequencing

- Illumina sequencing RNA library prep kits
  - Illumina TruSeq RNA *Protein-coding poly-A*
  - Illumina RiboZero *rRNA depletion*
  - Illumina TruSeq RNA Exome *FFPE / low quality*
  - Clontech SMARTER Pico *low input*
  - Illumina TruSeq Small RNA *small RNA*
- Oxford Nanopore, PacBio, IonTorrent





# DNA Sequencing

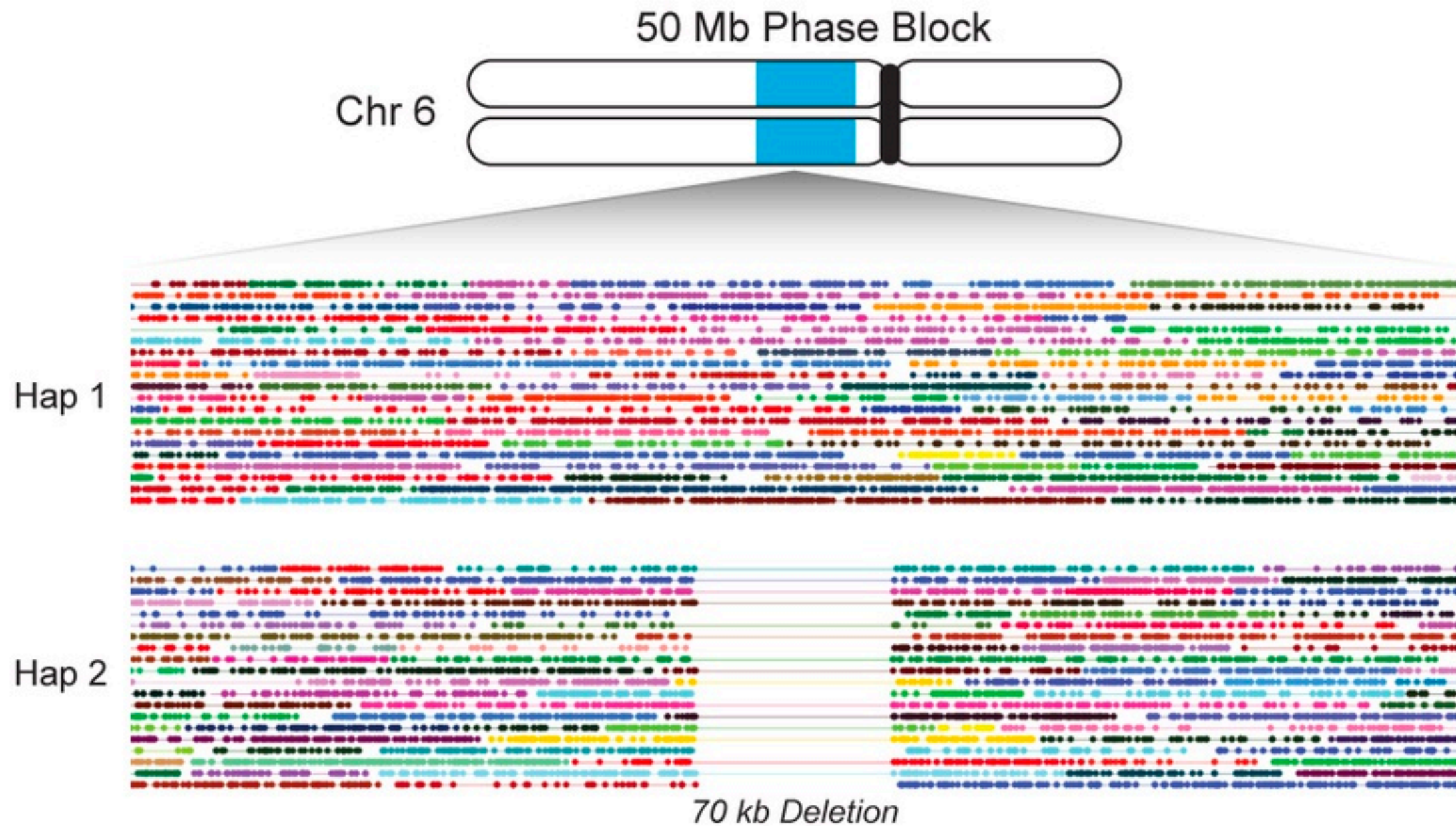
- Illumina sequencing DNA library prep kits
  - Illumina TruSeq DNA PCR Free *Best quality*
  - Rubicon ThruPLEX *Low input*
  - Illumina Nextera XT *Cheap (plate format)*
  - Illumina Nextera Flex *Fast and simple*
  - 10X Genomics *Linked reads*
- Oxford Nanopore, PacBio, IonTorrent

# 10X Genomics

- Chromium instrument uses droplet emulsion technology for nanoliter reaction volumes
- Linked-read sequencing
  - Large molecules fragmented in droplets and barcoded
  - Normal short-read illumina sequencing used
  - Long fragments (20-100+ Kbp) reassembled from barcodes
- Regular illumina sequencing libraries produced



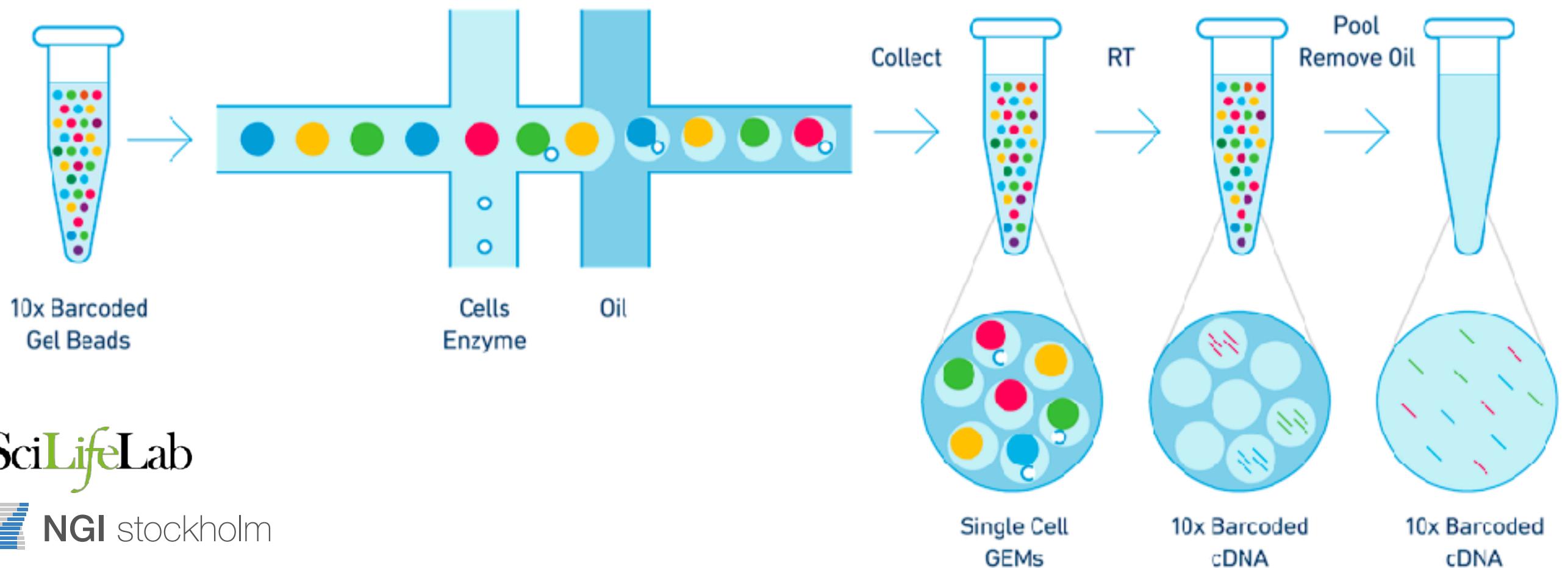
# 10X Genomics





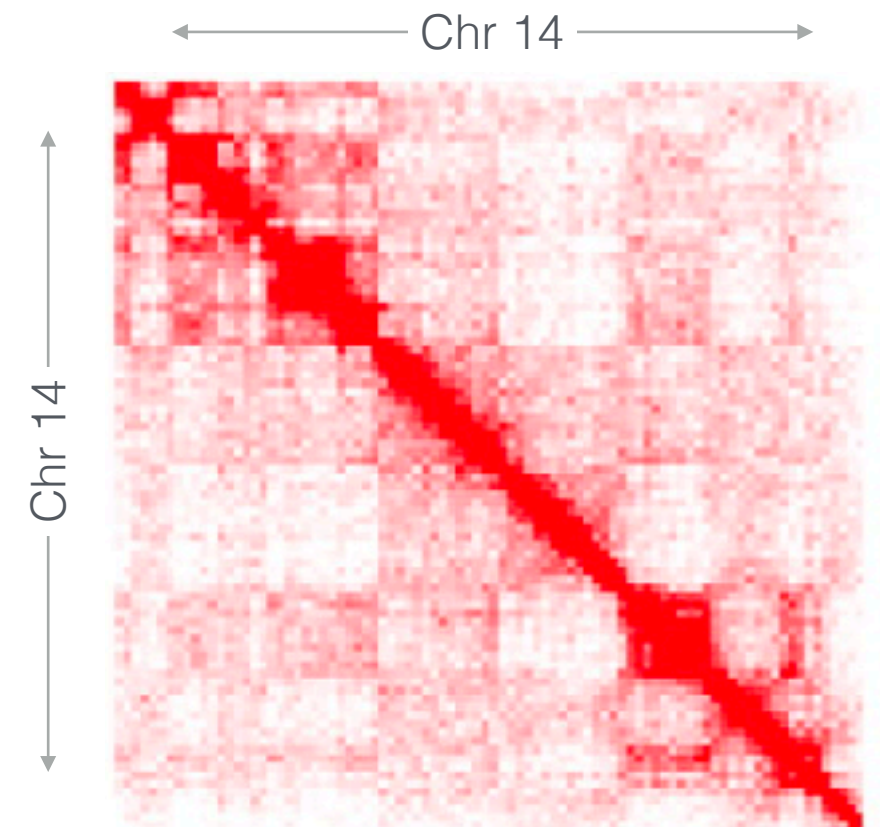
# 10X Genomics

- Single cell RNA sequencing
  - Thousands of cells captured in droplets
  - Each RNA molecule tagged with droplet barcode



# Hi-C

- Now testing Hi-C in NGI Stockholm
  - Proximity ligation assay to detect physical colocalization of DNA fragments within cell nuclei
- Multiple applications for data
  - Epigenetics
  - De-novo genome assembly
  - Structural variation detection



# – Methylation Sequencing

- **Bisulphite sequencing detects Cytosine methylation in genomic DNA**
  - Unmethylated Cs converted to Uracil by bisulfites and sequenced as T
  - Methylated Cs are protected and sequenced as C
- **Oxidative bisulphite informs about hydroxy-methylation**
  - Current under development at NGI Stockholm
- **PacBio and Oxford Nanopore able to detect some native base modifications**

# — RAD Sequencing

- Restriction-site Associated DNA sequencing, also known as GBS (Genotyping By Sequencing)
  - Genome fragmented using a restriction enzyme
  - Narrow size range purified - same regions of genome for all individuals
- Allows cheap high-depth variant calling for large numbers of samples, without a reference genome
  - Excellent for population genomics and ecology

# – Amplicon Sequencing

- 16S / 18S / Custom amplicons
- High sample throughput
  - Plates of 96 samples processed using liquid handling automation
  - Large numbers of index combinations allow large pools
- Cheap and convenient for metagenomics and metabarcode sequencing projects
  - Contact us to talk about a pilot project



# Bioinformatics at the NGI

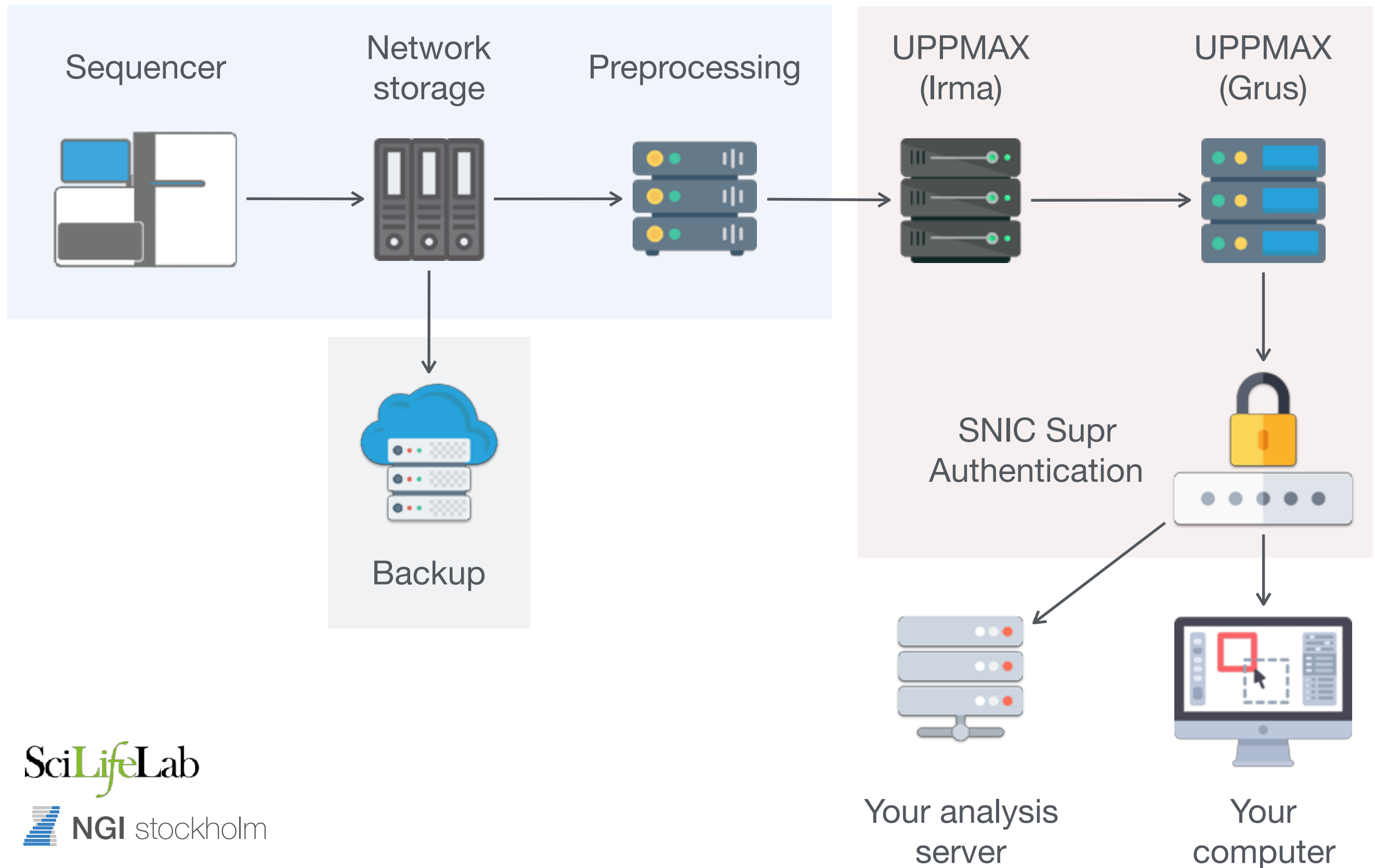


# Bioinformatics at NGI

- Raw sequencing data management
  - Demultiplexing, data transfers, backups, delivery
- Quality control
  - Every project is checked against quality criteria
- Automated analysis pipelines
  - Standardised pipelines give reproducible results
- Software development



# NGI Data Handling



# Grus Deliveries

- UPPMAX tool for NGI data deliveries
  - NGI creates a SNIC Supr "delivery project" for each NGI sequencing project
  - Project PI and contact person given access, according to what was put on the order form
  - Email sent with project ID and instructions
- Grus is for secure short term storage only
  - Requires two-factor authentication



# Analysis Pipelines

- Initial data analysis for major protocols
- Internal QC and standardised starting point for users
- All software open source and on GitHub
  - <http://opensource.scilifelab.se/>
  - <http://github.com/SciLifeLab/>
- Accredited facility

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Akkred. nr 1850  
Provning  
ISO/IEC 17025

# - Analysis Requirements



Automated



Reliable



Easy for others to run



Reproducible results

**nextflow**



# Sarek



**GitHub**

<https://github.com/SciLifeLab/Sarek>

- Tumour/Normal pair WGS analysis based on GATK best practices

- SNPs, SNVs and indels
- Structural variants
- Heterogeneity, ploidy and CNVs

- Works with regular WGS and Exome data too



**Sarek**

Manta

MuTect1

ASCAT

MuTect2

Strelka

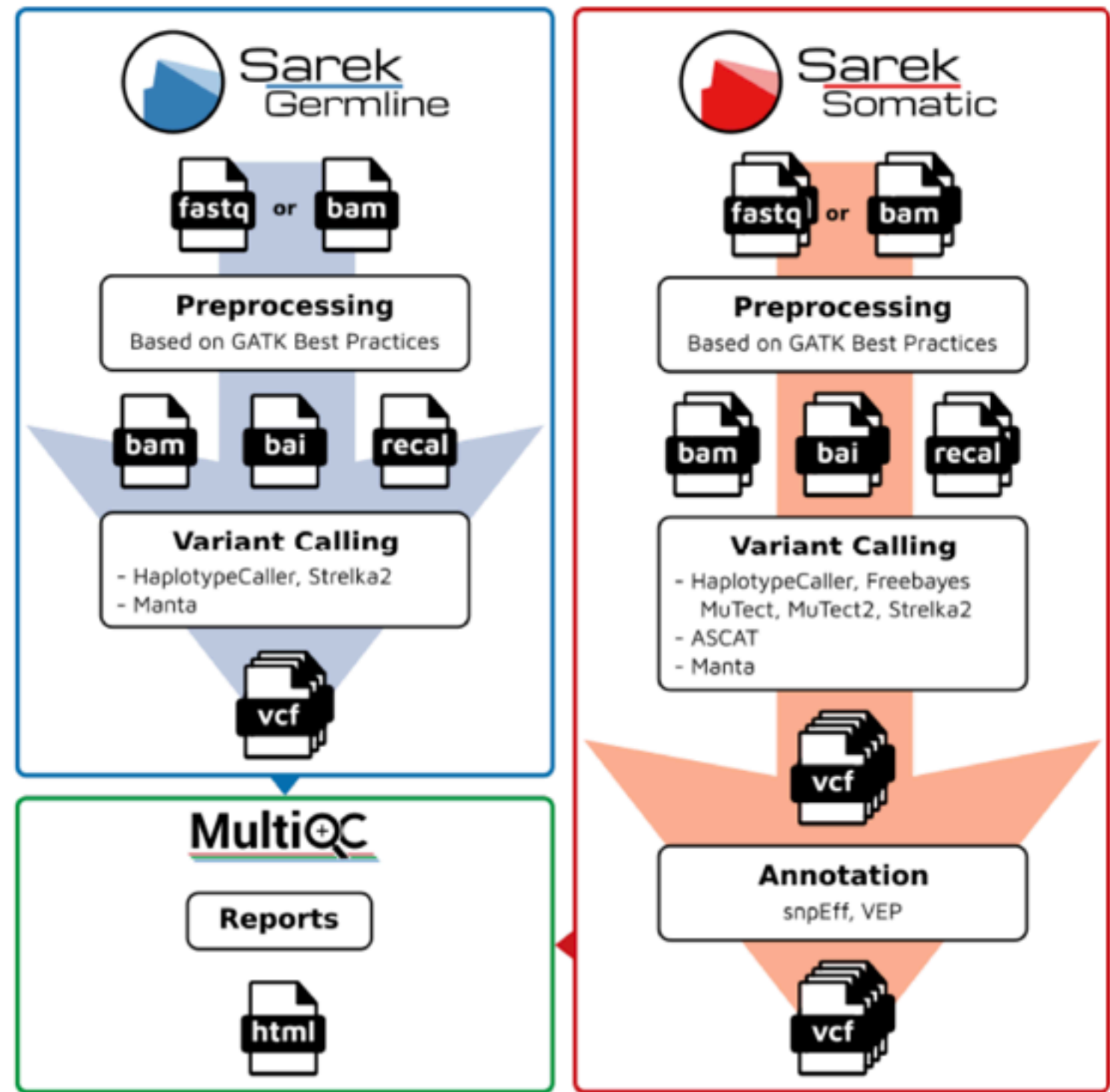
FreeBayes

GATK  
HaplotypeCaller



# Sarek

- Tool split into sub-workflows
- Preprint available on bioRxiv
  - <https://www.biorxiv.org/content/early/2018/05/09/316976>
- Will soon be main DNA pipeline at NGI





# — nf-core

- A community effort to collect a curated set of Nextflow analysis pipelines
  - GitHub organisation to collect pipelines in one place
  - No institute-specific branding
  - Strict set of guideline requirements
  - Automated testing for code style and function

SciLifeLab

 NGI stockholm

**nf-core**

<https://nf-co.re>



# nf-core



The screenshot shows the nf-core website homepage. At the top, there is a navigation bar with links for Home, Pipelines, Tools, Docs, and About. The main header features the nf-core logo and a tagline: "A community effort to collect a curated set of analysis pipelines built using Nextflow." Below this is a prominent "VIEW PIPELINES" button. A green banner highlights three key benefits: "For facilities" (Highly optimised pipelines with excellent reporting), "For users" (Portable, documented, and easy to use workflows), and "For developers" (Companion templates and tools). Below the banner, a paragraph states: "Nextflow is an incredibly powerful and flexible workflow language. nf-core pipelines adhere to strict guidelines - if one works, they all will." The bottom section consists of six feature cards: Documentation (Extensive documentation covering installation, usage and description of output files ensures that you won't be left in the dark.), CI Testing (Every time a change is made to the pipeline code, nf-core pipelines use continuous-integration testing to ensure that nothing has broken.), Stable Releases (nf-core pipelines use GitHub releases to tag stable versions of the code and software, making pipeline runs totally reproducible.), Docker (Software dependencies are always available in a bundled docker container, which Nextflow can automatically download from dockerhub.), Singularity (If you're not able to use Docker, built-in support for Singularity can solve your HPC container problems. These are built from the docker containers.), and Bioconda (Where possible, pipelines come with a bioconda environment file, allowing you to set up a new environment for the pipeline in a single command.).

nf-core



<https://nf-co.re>

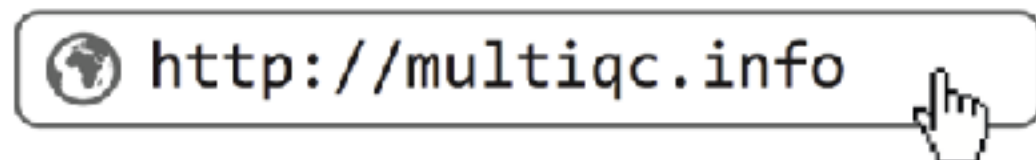
- Easy to run pipelines
- Helpful community
- Super reproducible results

# Quality Control

- Every project has some level of quality control checks
  - Sequencing quality
  - FastQC, FastQ Screen
- Analysis pipelines give application-specific QC
  - Qualimap, RSeQC
- Reporting is done using MultiQC

# MultiQC

- Reporting tool, parses logs from completed analysis
- Creates single HTML report for all samples & steps in a project
- Interactive plots for data exploration
- Current version now has 67 supported tools
- Works with anything from tens → thousands of samples
- Highly customisable



P1234: Test\_NGI\_Project

# P1234: Test\_NGI\_Project

This is an example project. All identifying data has been removed.

**Contact E-mail:** [phil.ewels@scilifelab.se](mailto:phil.ewels@scilifelab.se)  
**Application Type:** RNA-seq  
**Sequencing Platform:** HiSeq 2500 High Output V4  
**Sequencing Setup:** 2x125  
**Reference Genome:** hg19

Report generated on 2017-05-17, 18:43 based on data in:

`/Users/philewels/GitHub/MultiQC_website/public_html/examples/ngi-rna/data`

☰ NGI names

👤 User supplied names

## General Statistics

📄 Copy table

⚙️ Configure Columns

📊 Plot

Showing <sup>22</sup>/<sub>22</sub> rows and <sup>6</sup>/<sub>9</sub> columns.

Sample Name	% Aligned	M Aligned	% Trimmed	% Dups	% GC	M Seqs
P1234_1001	68.2%	22.8	10.3%	71.3%	49%	33.7
P1234_1002	67.9%	20.9	10.7%	70.1%	50%	31.1
P1234_1003	64.7%	21.7	11.0%	72.3%	50%	33.7
P1234_1004	55.2%	17.0	13.2%	73.4%	51%	31.2
P1234_1005	53.0%	17.7	15.9%	75.8%	52%	33.8
P1234_1006	52.7%	16.1	14.1%	73.8%	52%	30.8
P1234_1007	33.0%	7.0	32.0%	80.5%	52%	21.8
P1234_1008	27.5%	4.3	44.2%	79.1%	50%	16.7
P1234_1009	52.3%	10.5	20.9%	64.2%	48%	20.5





# Getting MultiQC



ewels / MultiQC

BIOCONDA



PyPI



`http://multiqc.info`

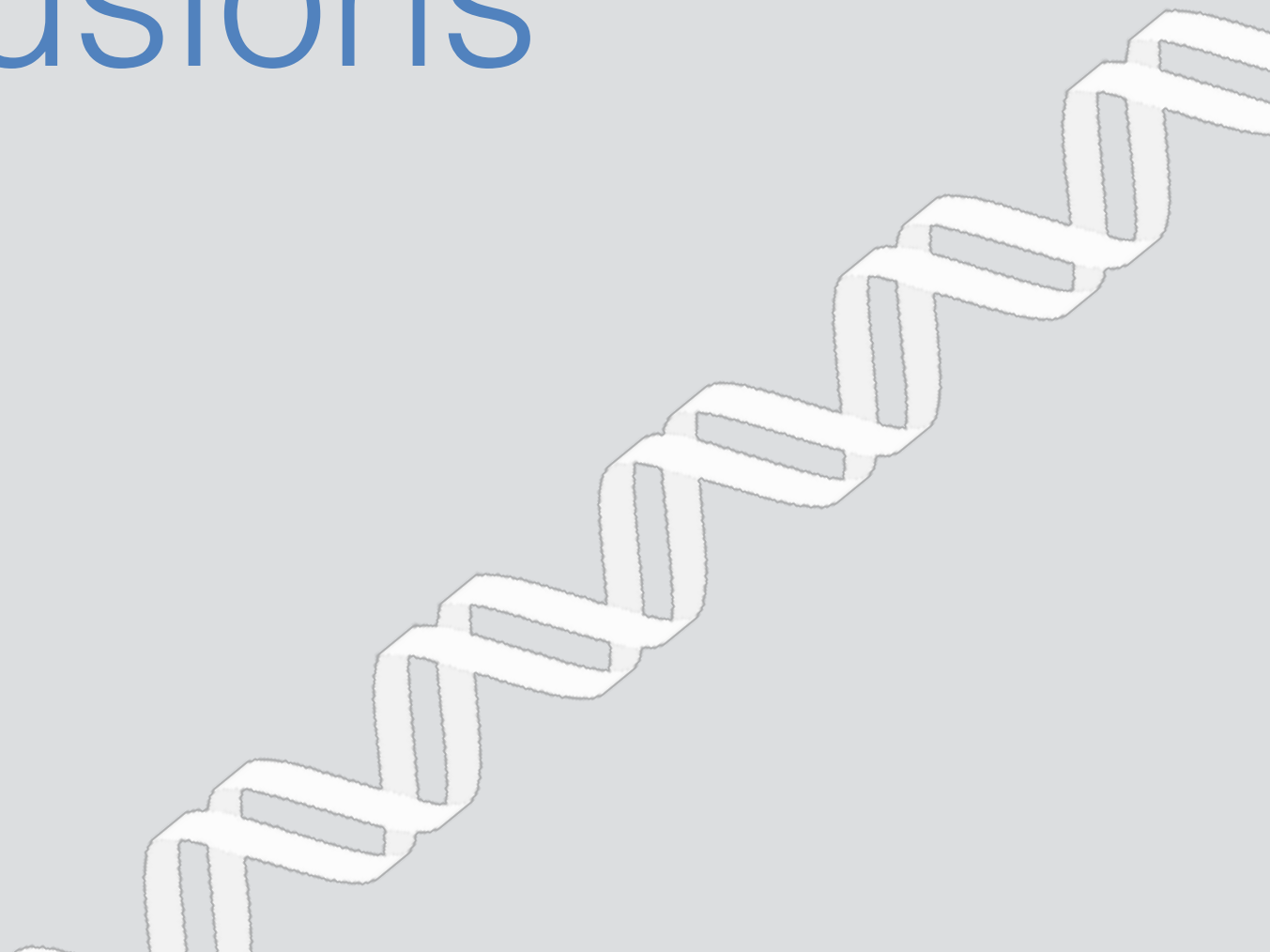


The screenshot shows a web browser window with the URL `multiqc.info`. The page features a dark background with a hexagonal pattern. The main heading is "MultiQC" in a large, white, sans-serif font, with a plus sign inside the 'Q'. Below the heading is a sub-heading: "Aggregate results from bioinformatics analyses across many samples into a single report". A paragraph of text follows: "MultiQC searches a given directory for analysis logs and compiles a HTML report. It's a general use tool, perfect for summarising the output from numerous bioinformatics tools." On the right side, there is a navigation menu with "Home", "Docs", "Example Reports", and "GitHub". Below the menu are four blue buttons: "Documentation", "View on PyPI", "View on GitHub", and "Quick Install". The "Quick Install" button contains a code block: 

```
pip install multiqc # Install
multiqc . # Run
```

 At the bottom right, there is a small link: "Python or pip not installed? See the full installation instructions."

# Conclusions





# If you have a project

- Visit our order portal
- Create projects
- Request meetings
- Send us an email

Information Documents Contact About us

**NGI Sweden Order Portal**

This portal is for submitting orders for services provided by the National Genomics Infrastructure Sweden (NGI). To make an order, please log in and choose the application most suitable for your project. If uncertain about the choice of technology, please select the "Request a meeting" option. You can read more about the different technologies and [How to place an order](#) under "Information" in the menu at the top of the page.

Projects from other countries are admissible, but have lower priority than projects performed by researchers based in Sweden. Depending on the queue situation, NGI may decide to decline a non-Swedish project altogether.

Turn Around Times and Status for the Stockholm node.

Subscribe to our mailing list:

**Login**

Email

Password

**Request a meeting**

If you are unsure about the appropriate method for your scientific problem, request a meeting for a discussion with us.

**Illumina Sequencing**

Order form for Illumina sequencing.

**Ion Sequencing**

Order form for sequencing by Ion Proton or Ion S5XL.

**PacBio Sequencing**

Order form for PacBio sequencing. This is available only at the NGI Uppsala UGC node.

**Genotyping and array-based epityping**

Order form for genotyping and DNA methylation analysis using the Illumina EPIC beadchip.

summer. Library preparation and sequencing will continue at a reduced pace.  
August 4. Only complete orders will be processed at June 18.

Sample submission will be closed from June 29 to August 6.

**Director and Co-Director positions for SciLifeLab genomics and high-throughput sequencing (2018-04-16)**  
Are you a visionary researcher within genomics with experience of operating or supervising infrastructures? Are you ready to take a major leadership roles in genomics? SciLifeLab now seeks a Director and a Co-Director to head the national Genomics Platform and high-throughput sequencing. An expressions of interest to these positions from both national and international candidates are welcomed!  
Read more at [SciLifeLab website](#).

**Vacancies: Forskningsingenjör (vikariat) at NGI Uppsala (2018-04-16)**  
Är du en utbildad biotekniker, molekylärbiolog eller linjando med hög noggrannhet, ansvarsfull och god samarbetsförmåga? Har du praktisk erfarenhet av stortskaligt laboratoriearbete, gläda i ackrediterad miljö och med datorstyrda laboratorieinstrument? NGI Uppsala söker nu en forskningsingenjör till sekvenseringsenheten av DNPA/SCQ-teknologiplattformen. Arbetet omfattar DNA-sekvensering med modern instrumentering från Illumina såsom HiSeqX, NovaSeq, HiSeq2500 och MiSeq.  
Läs mer om tjänsten och ansök på [UU hemsida](#).

**Vacancies: 2 Bioinformatikerna at NGI Uppsala (2018-04-11)**

<https://ngisweden.scilifelab.se>  
[support@ngisweden.se](mailto:support@ngisweden.se)

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# Find our tools

- View our open-source software
- All code available on GitHub

<http://opensource.scilifelab.se>



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# Acknowledgements

## Phil Ewels

 phil.ewels@scilifelab.se

 ewels

 tallphil

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Olga Vinnere Pettersson

NGI Sweden

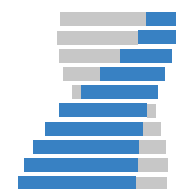
 *ngisweden*

support@ngisweden.se

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