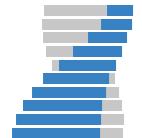


NGI Sweden

Next Generation Sequencing at the
National Genomics Infrastructure

SciLifeLab

 **NGI** stockholm

Phil Ewels

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



Research Programs

Technology Platforms

National Genomics Infrastructure

Proteomics

Metabolomics

Single-Cell Biology

Cellular & Molecular Imaging

Molecular Structure

Chemical Biology

Genome Engineering

Diagnostic Development

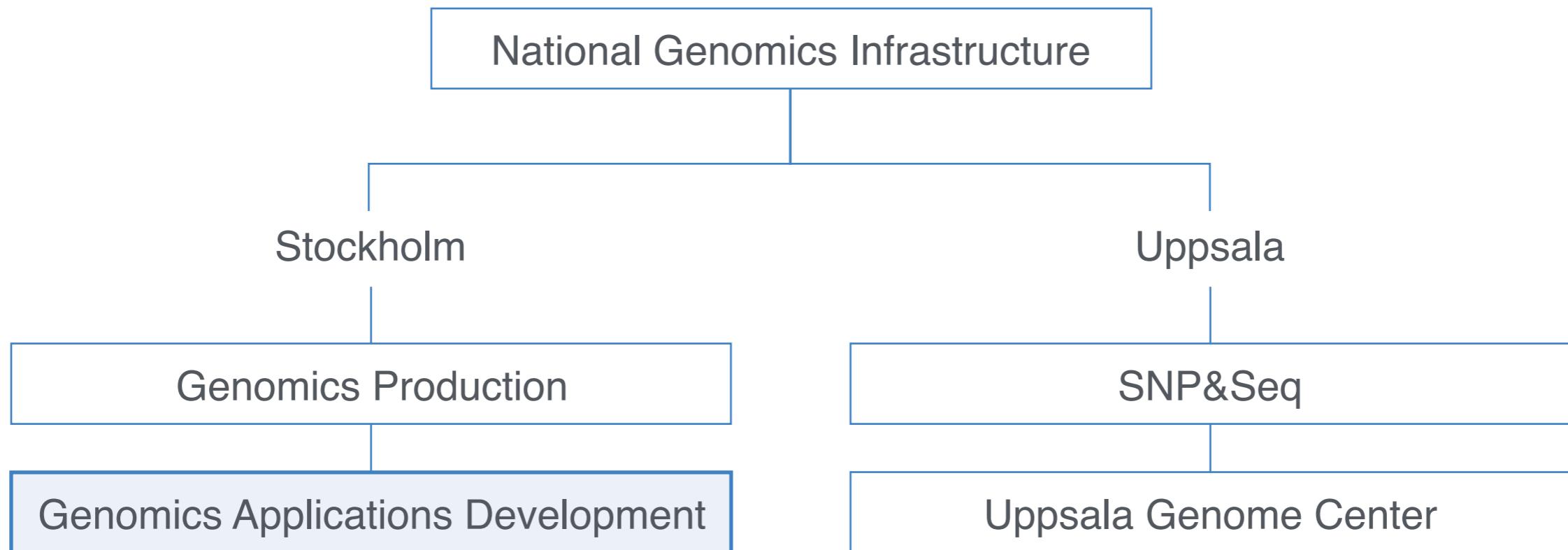
Drug Discovery & Development

National Bioinformatics Infrastructure

Data Office



SciLifeLab NGI

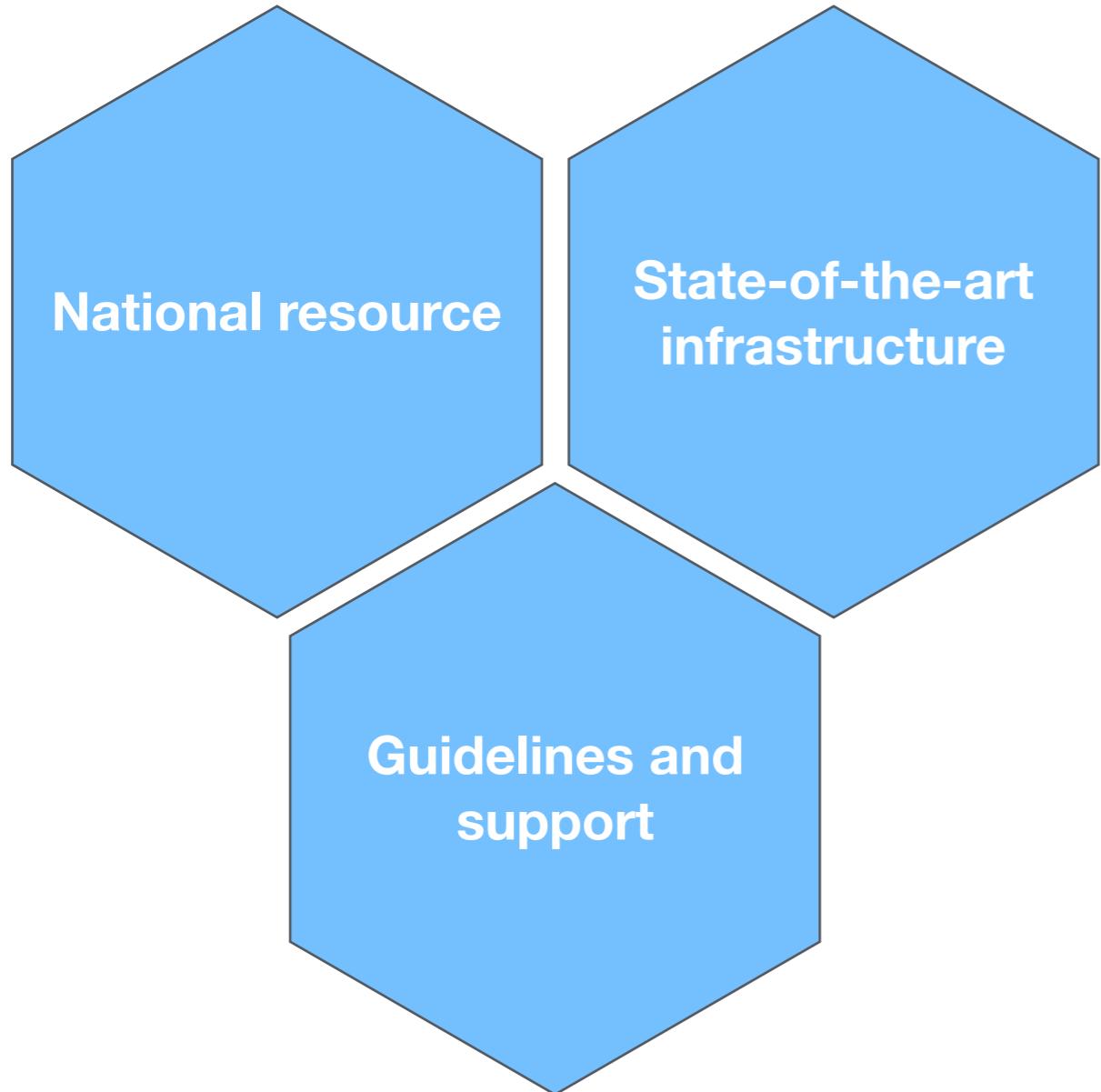


SciLifeLab NGI



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



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

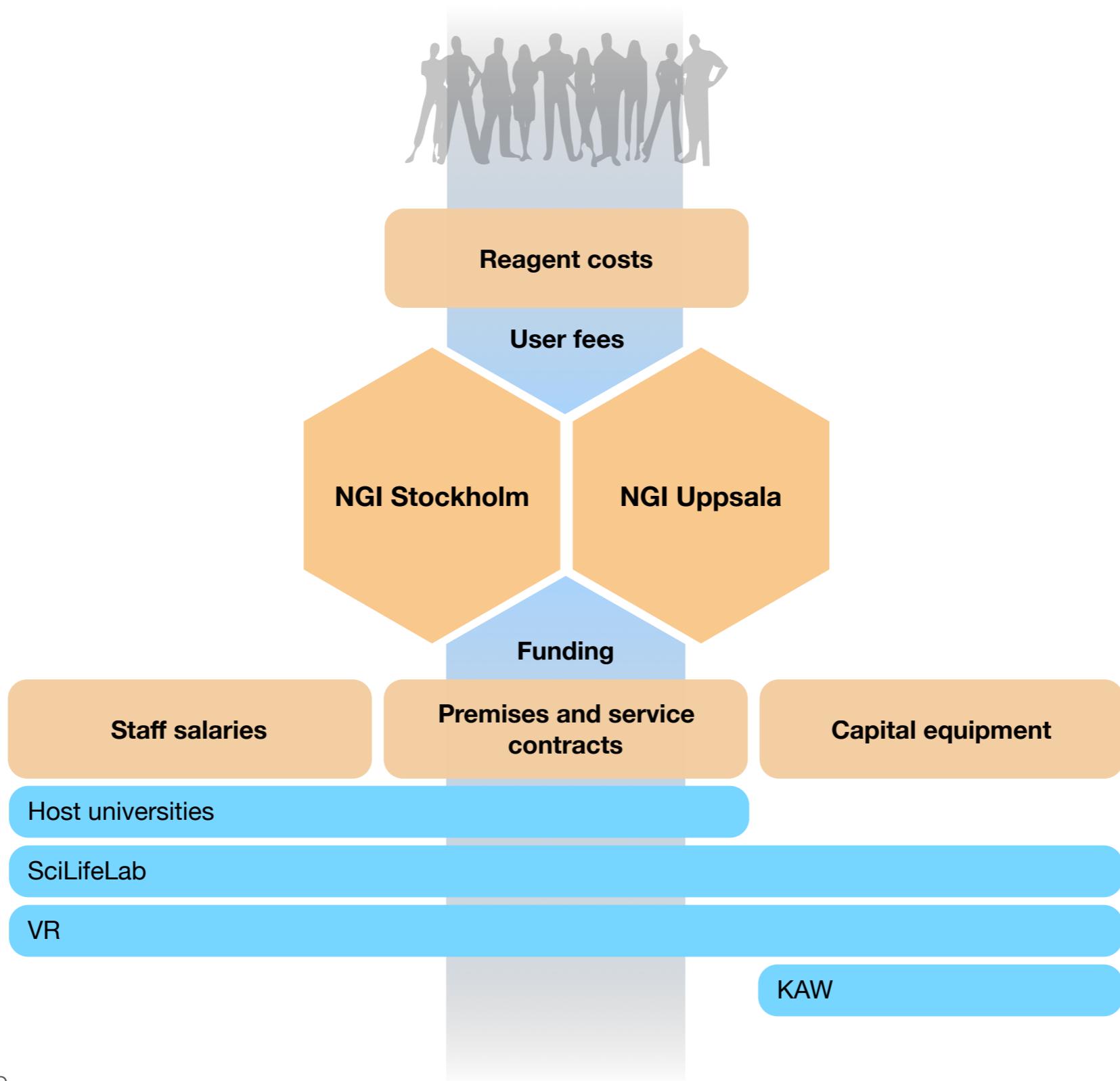
- NGI Organisation



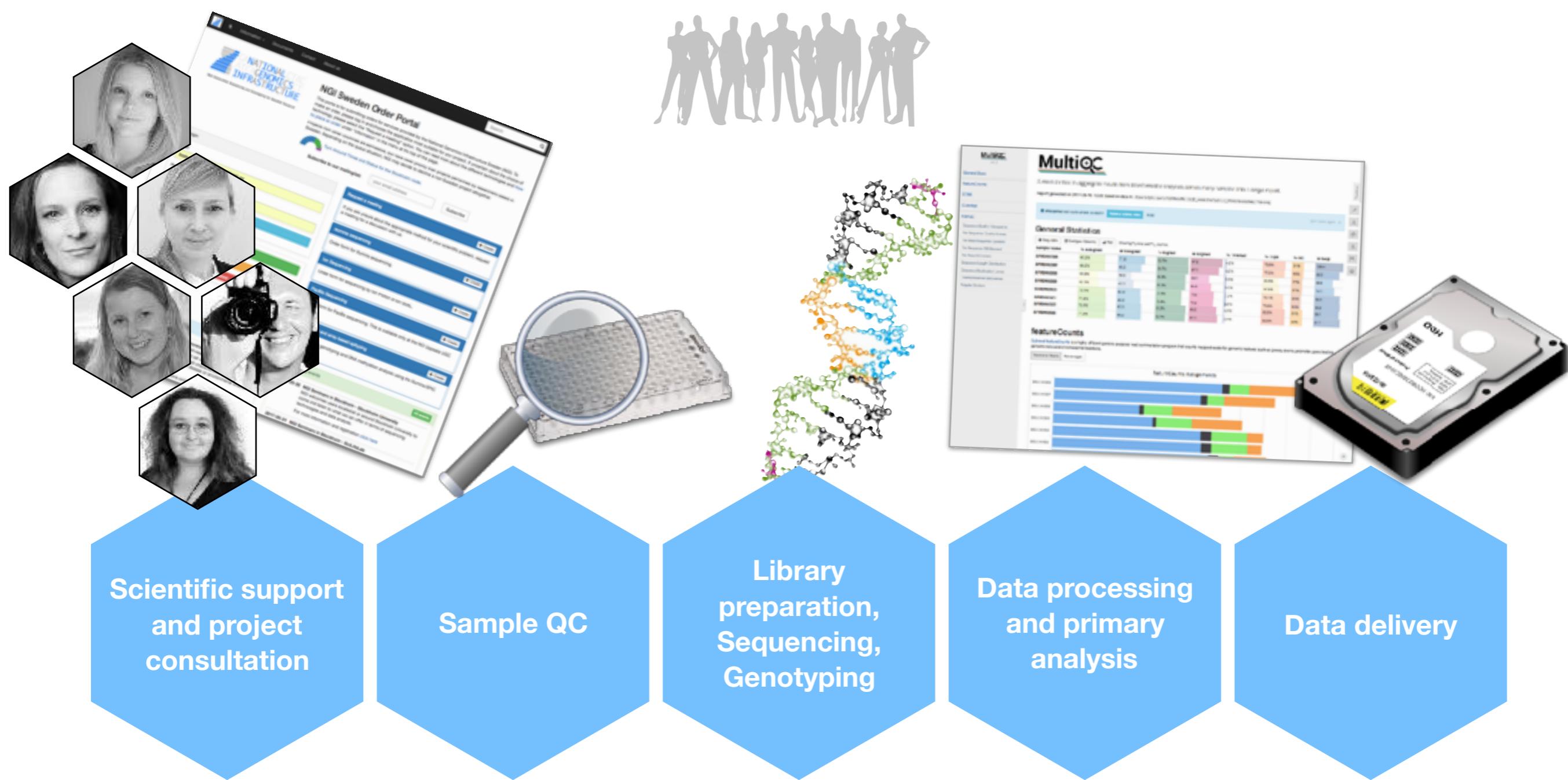
SciLifeLab

 NGI stockholm

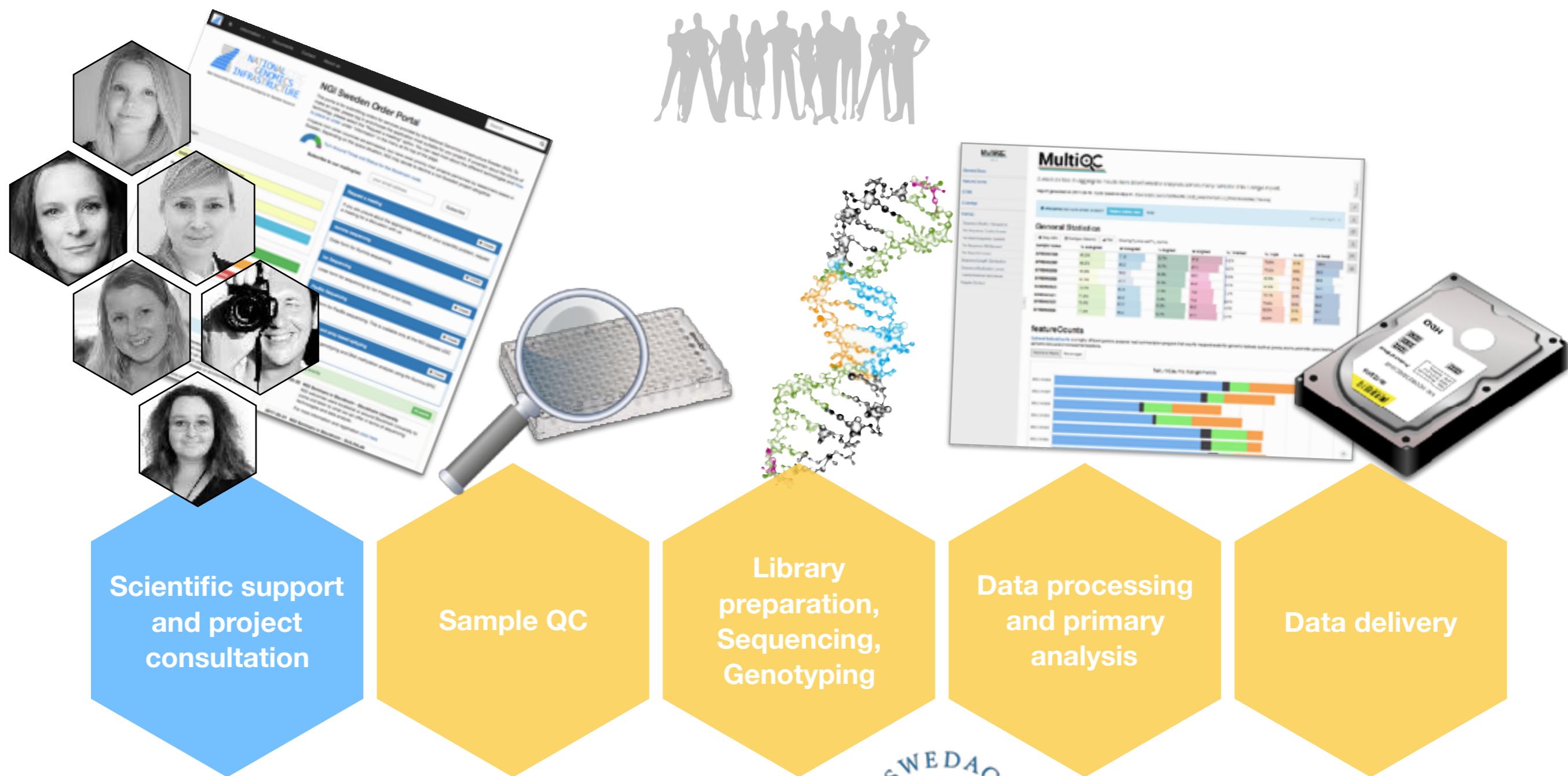
NGI Organisation



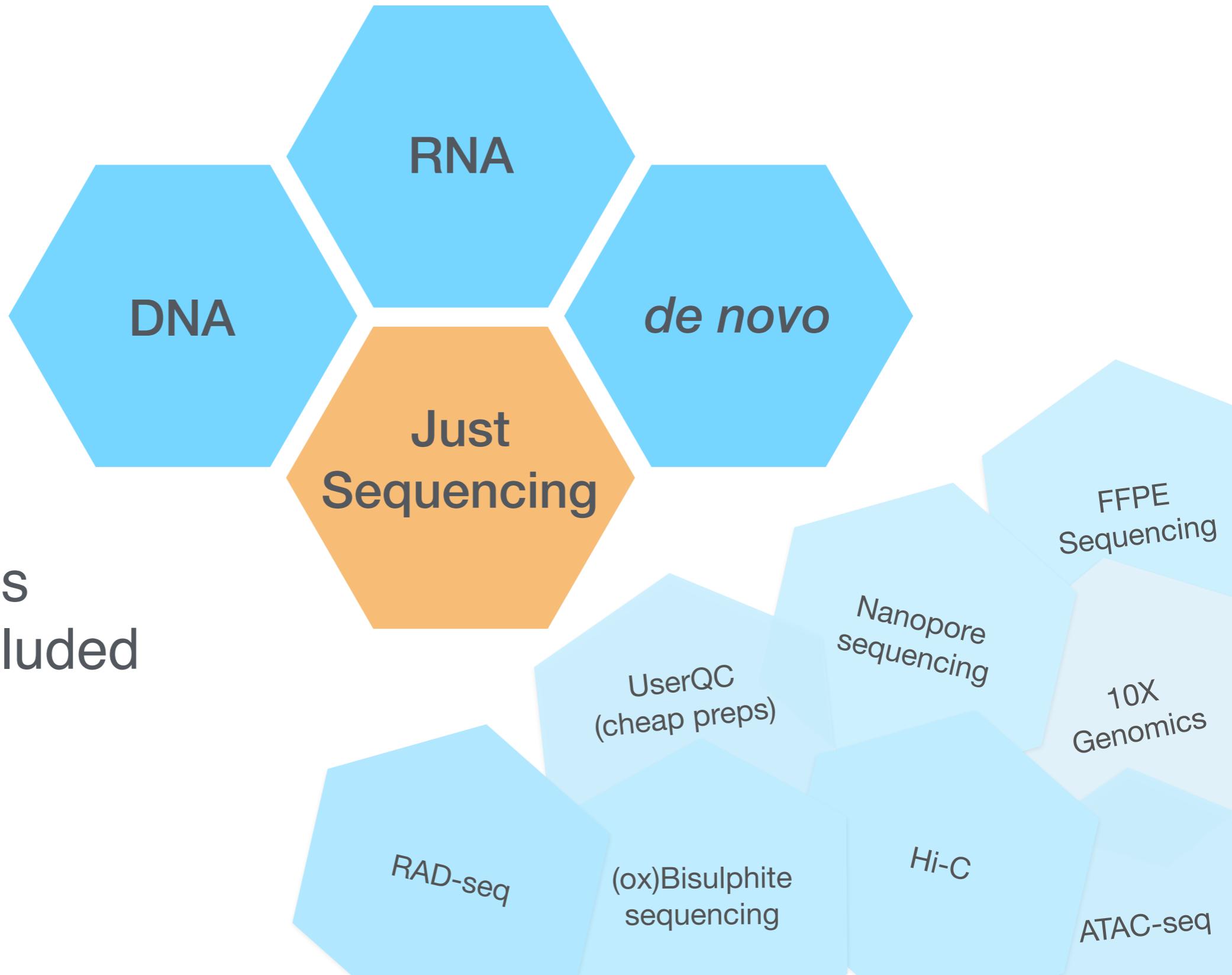
Project timeline



Project timeline



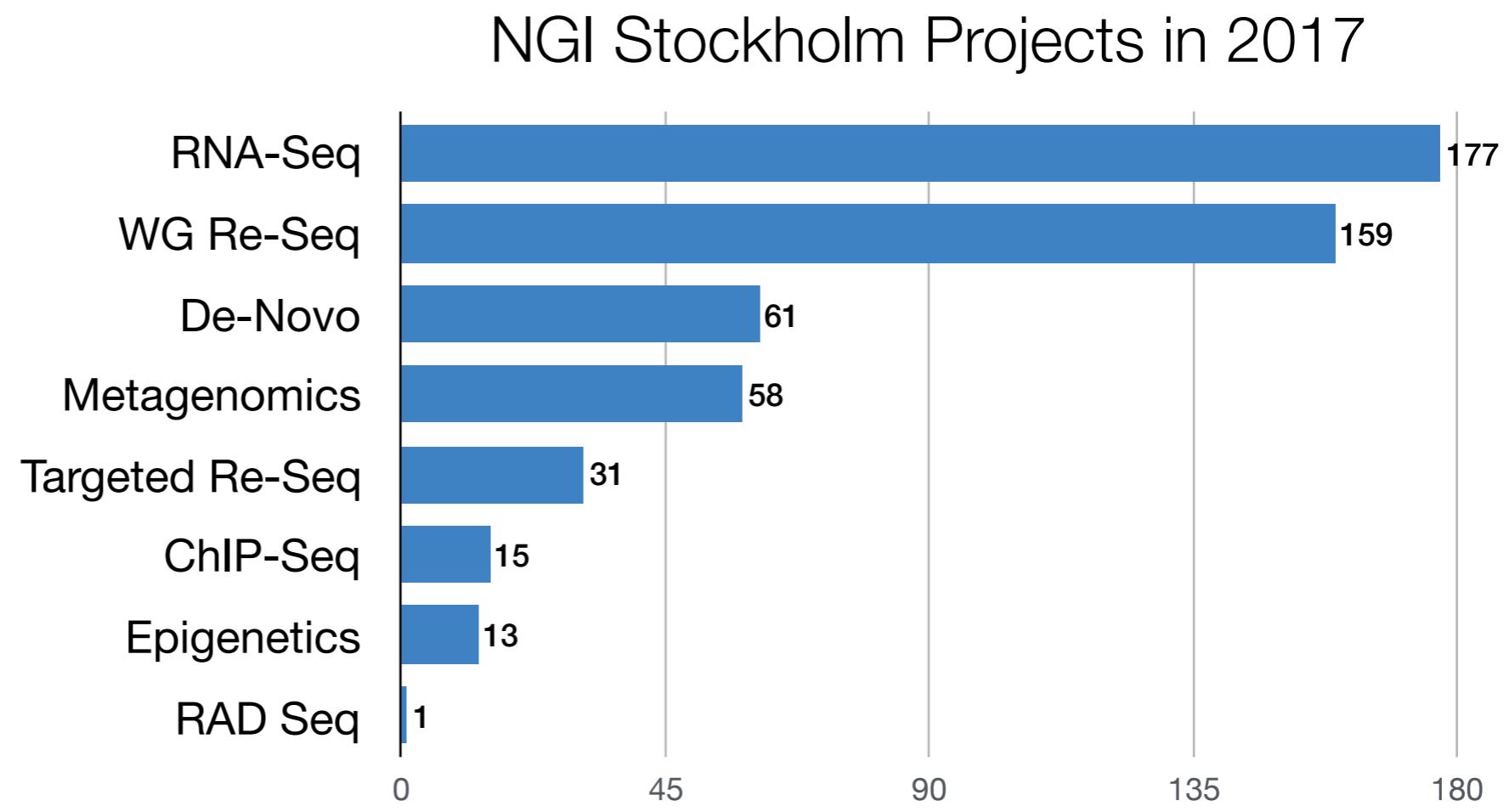
Methods offered at NGI



Data analysis
pipelines included

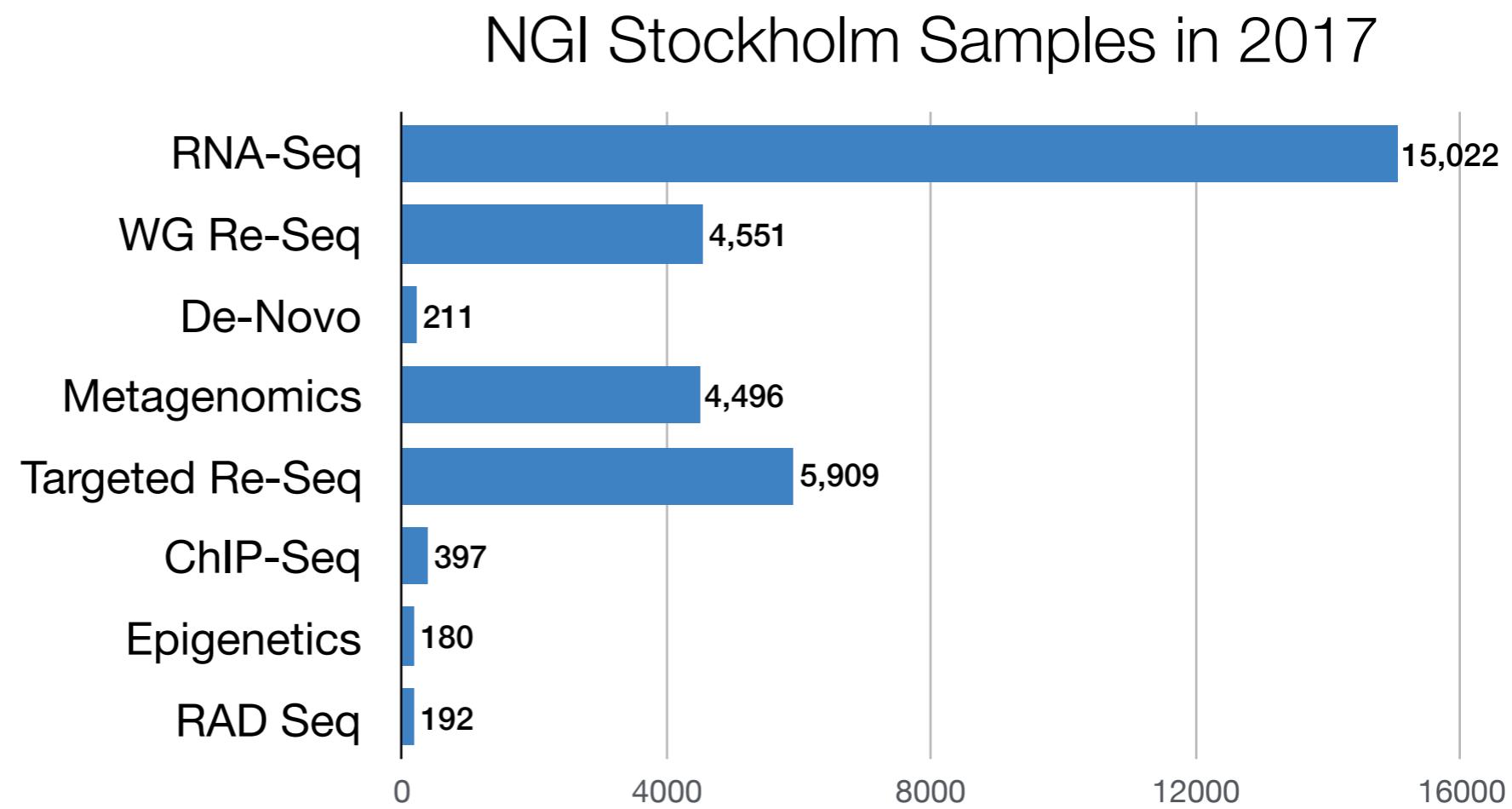
- NGI Stockholm

- RNA-seq is the most common project type



NGI Stockholm

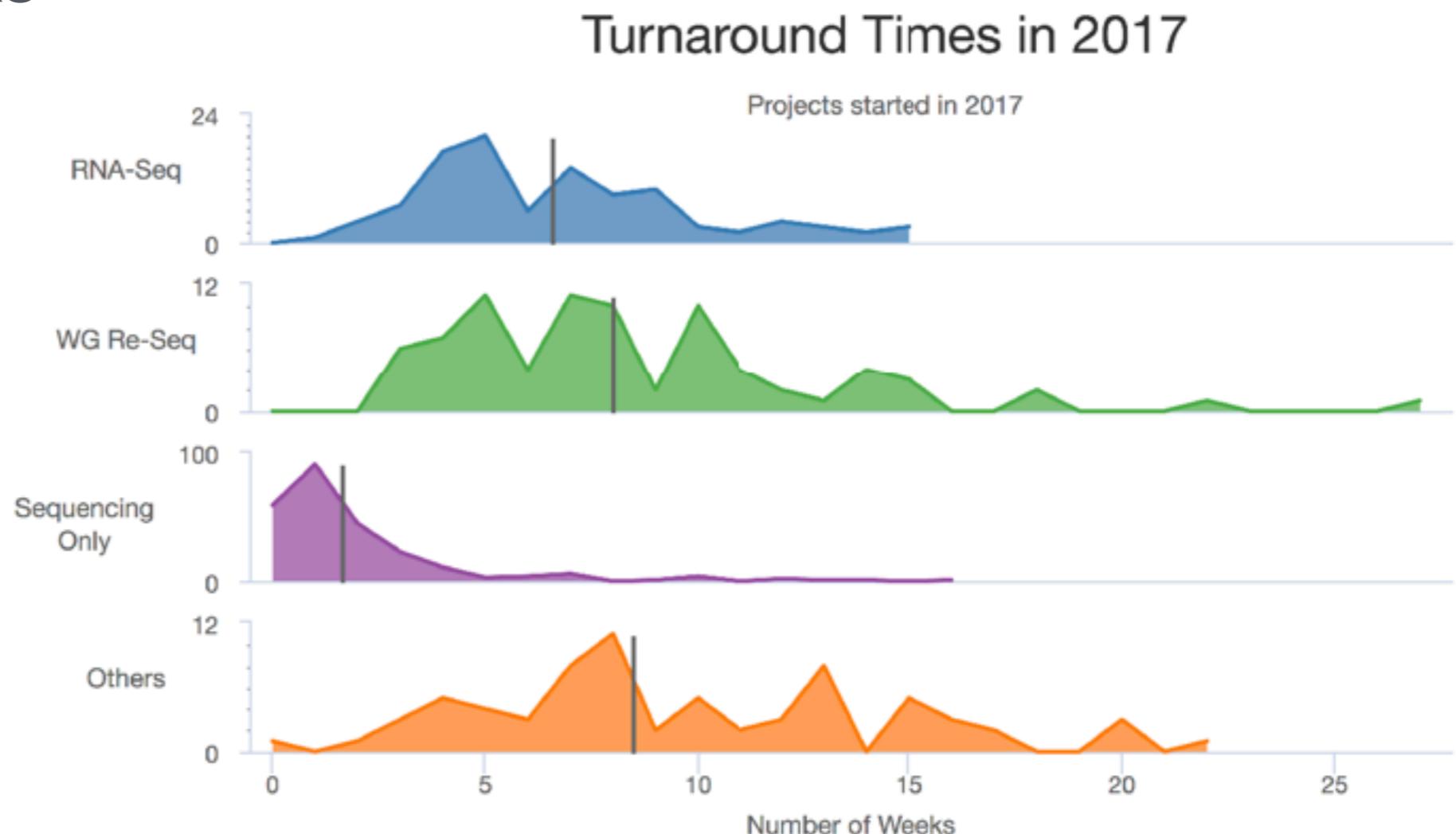
- RNA-seq is the most common project type
- In total, NGI Sweden processed 1068 NGS projects with almost 50 000 samples in 2017



NGI Stockholm

- 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

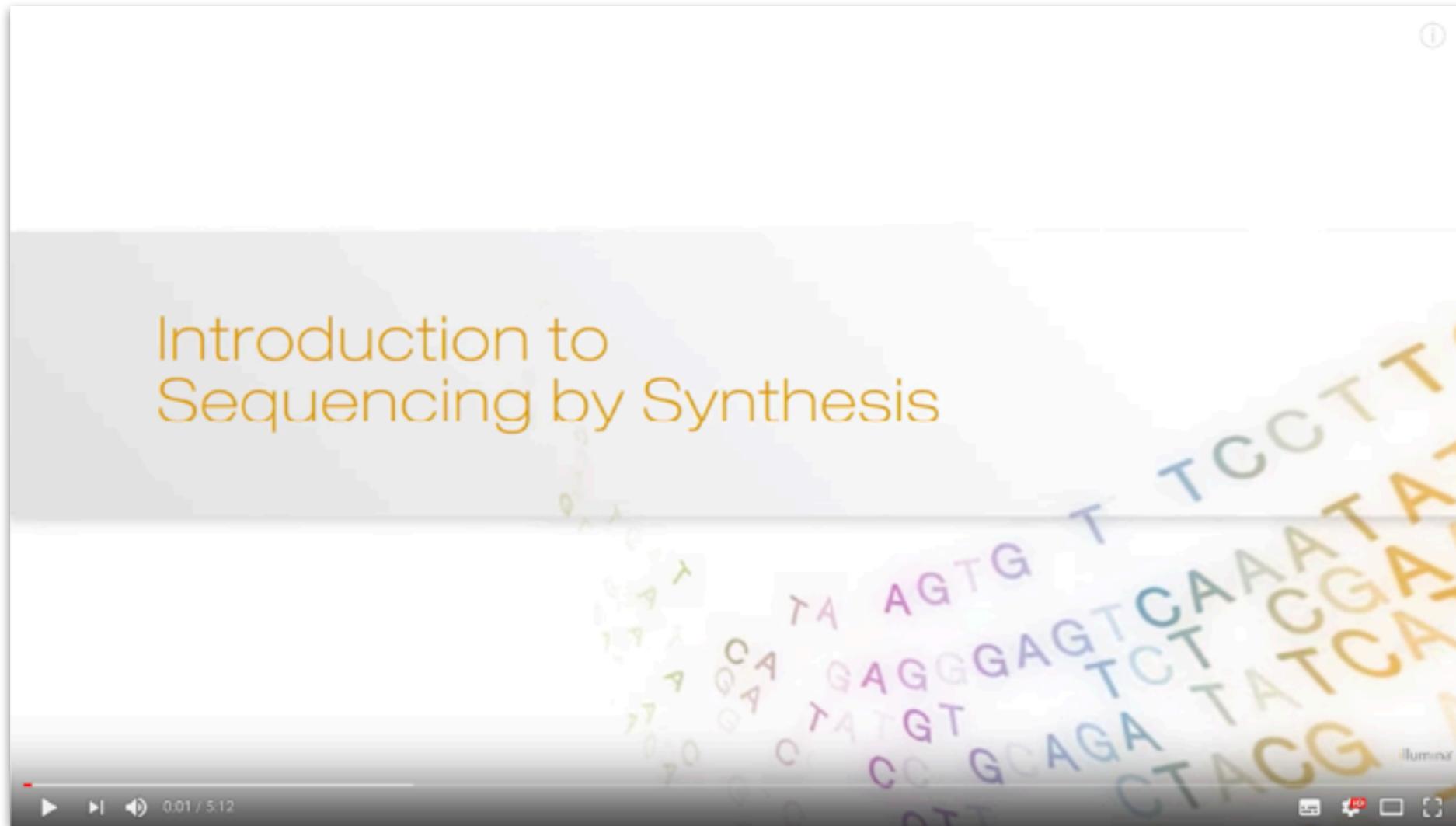
Ion Torrent

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>

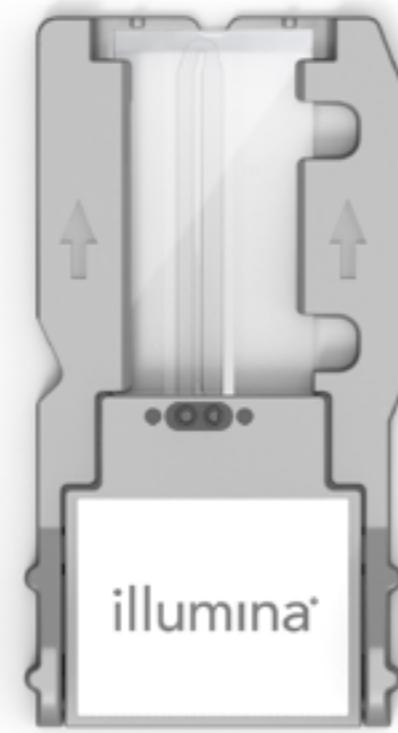
SciLifeLab

NGI stockholm

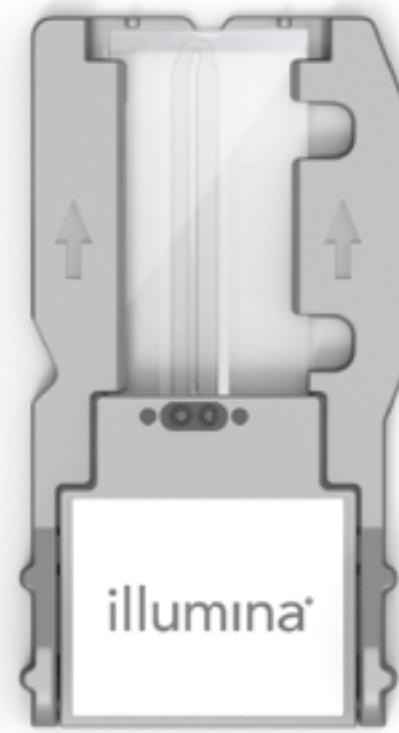
Illumina iSeq 100



Illumina MiniSeq 100



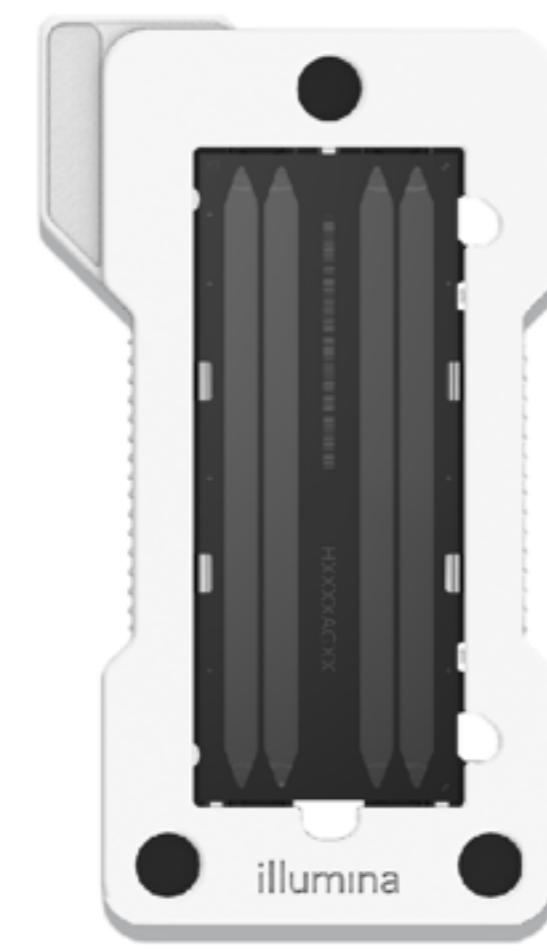
Illumina MiSeq



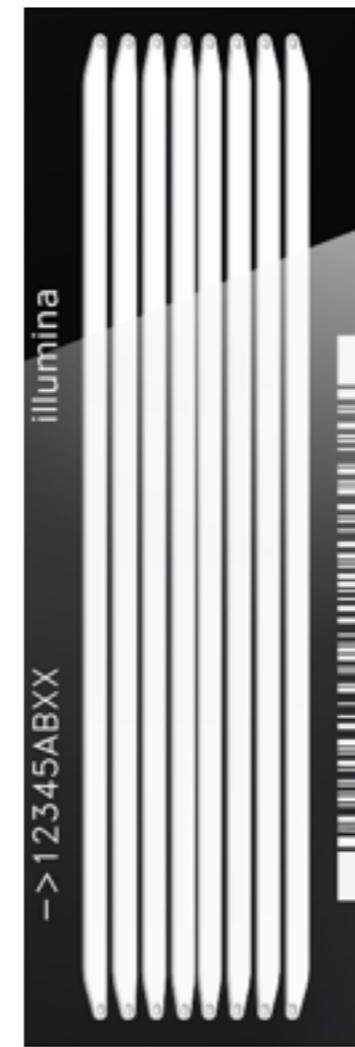
SciLifeLab

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Illumina NextSeq



Illumina HiSeq 2500



Illumina HiSeq 3000



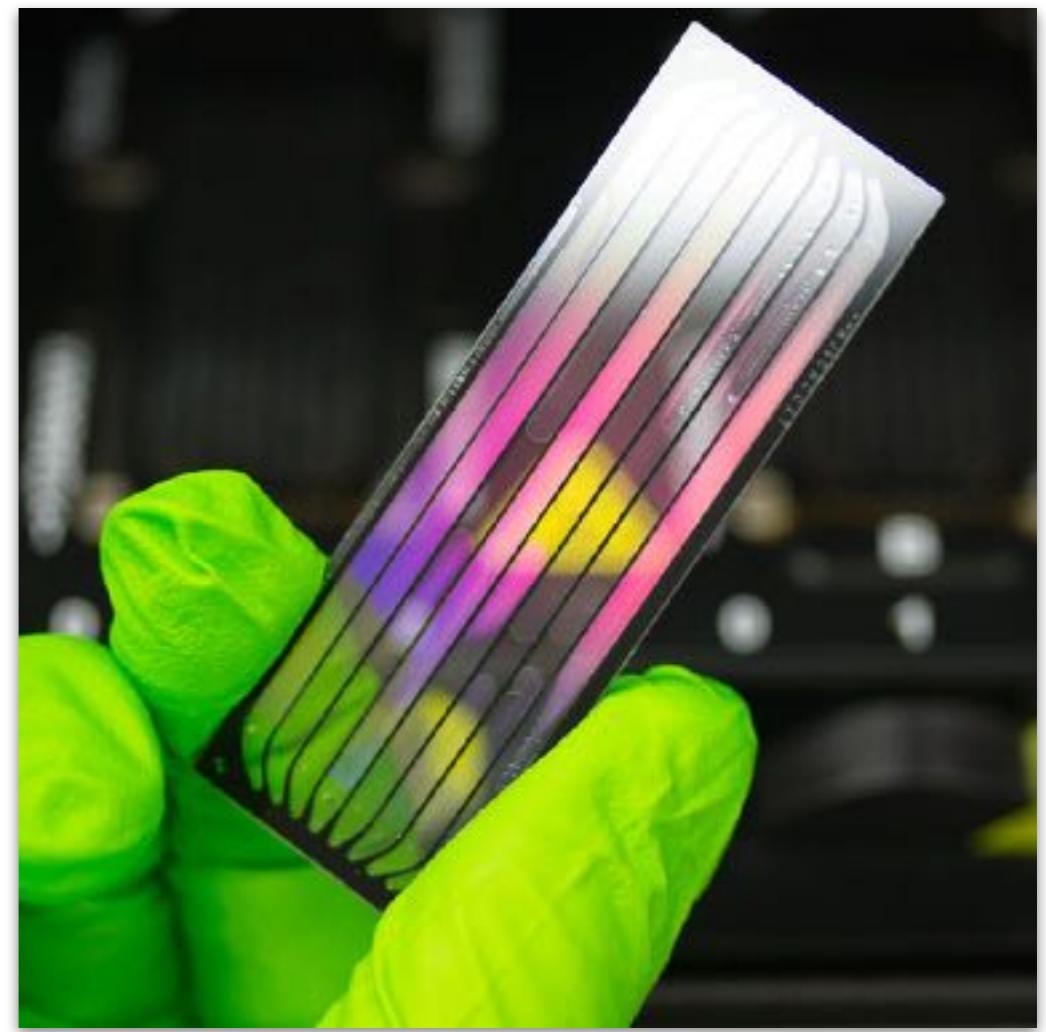
SciLifeLab

NGI stockholm

Illumina HiSeq 4000



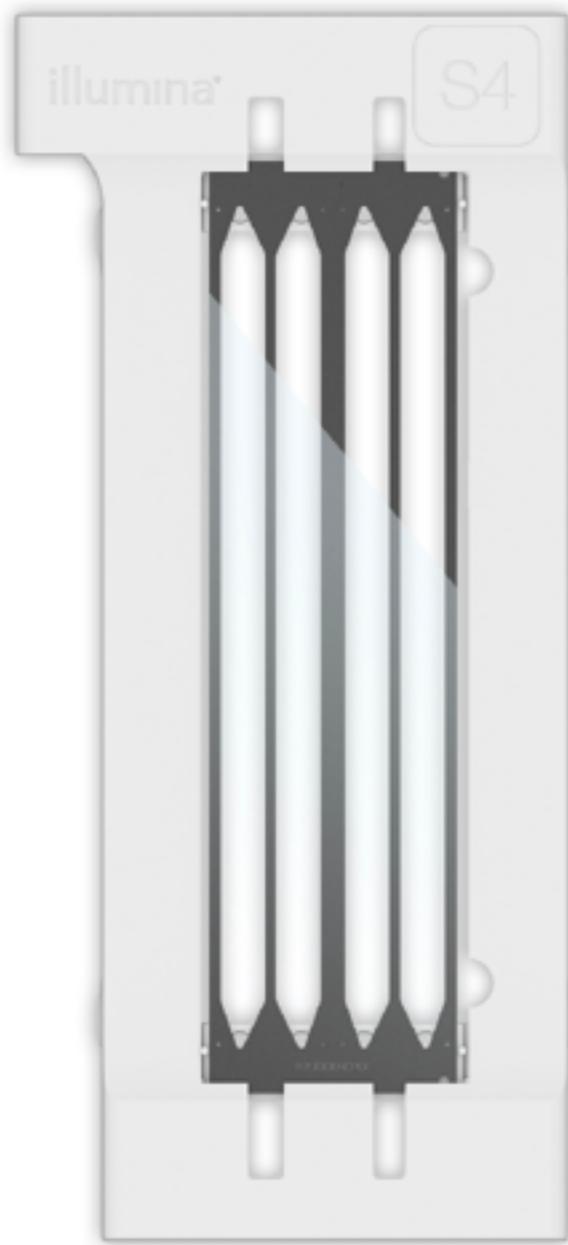
Illumina HiSeq X



SciLifeLab

NGI stockholm

Illumina NovaSeq 6000



SciLifeLab

NGI stockholm

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

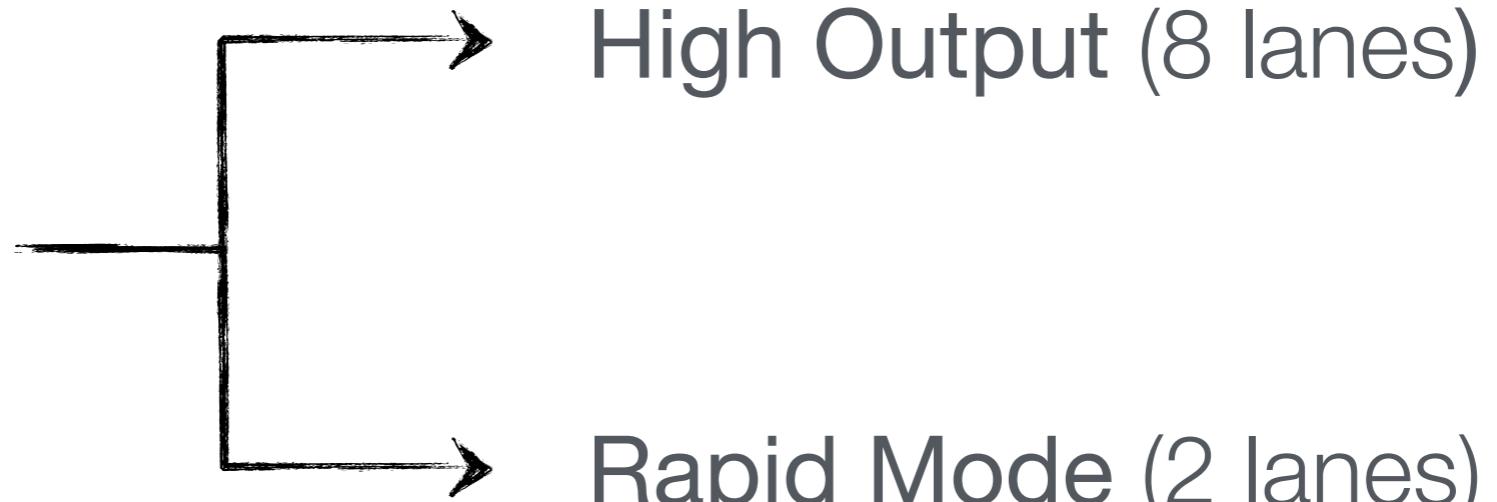
HiSeq X

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



Illumina at NGI

iSeq 100

MiSeq

HiSeq 2500

HiSeq X

NovaSeq 6000

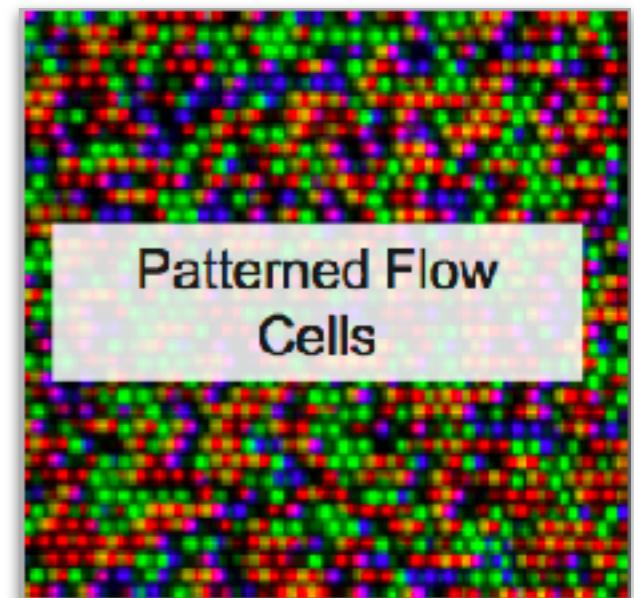
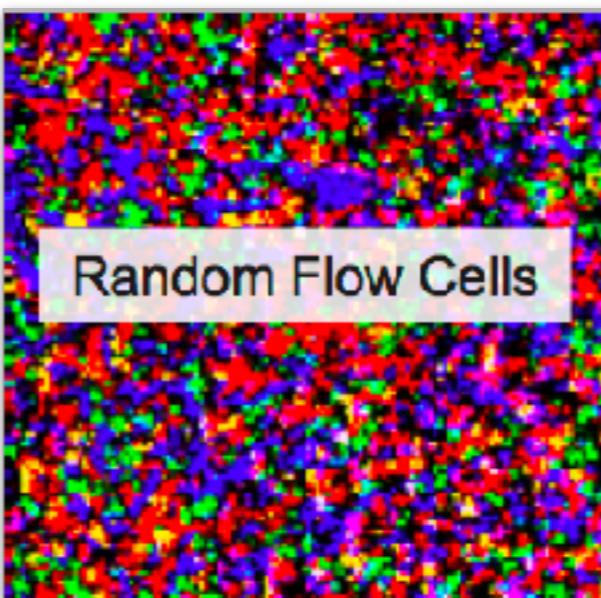
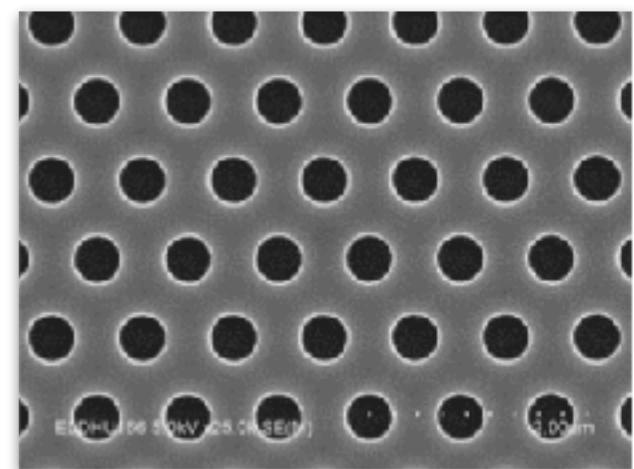
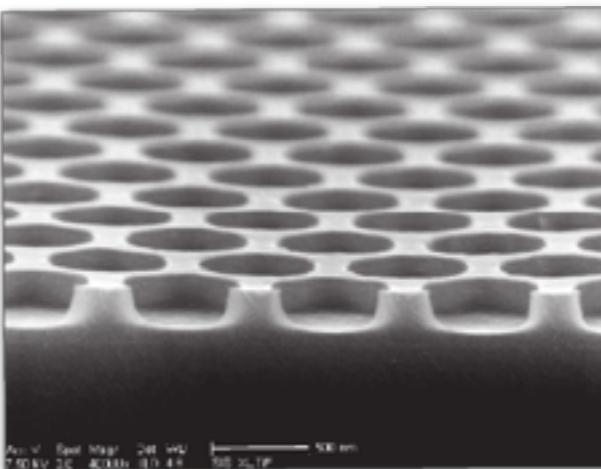


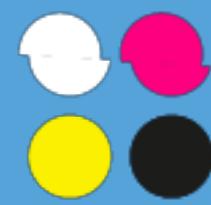
How to choose

- 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

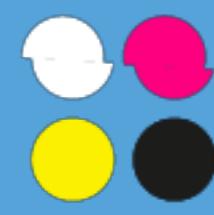




QCFAIL.com

Articles about common next-generation
sequencing problems

Phil Ewels
Simon Andrews



QCFAIL.com

Illumina Patterned Flow Cells Generate Duplicated Sequences

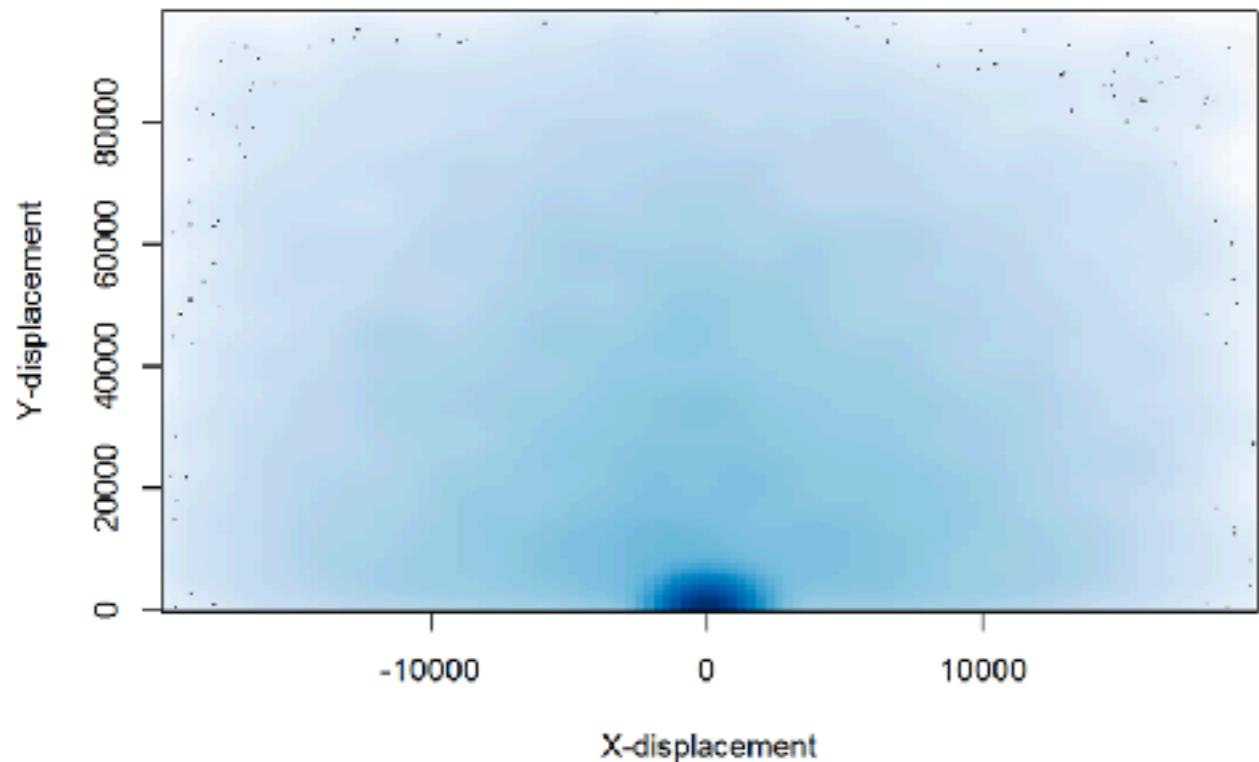
Steven Wingett



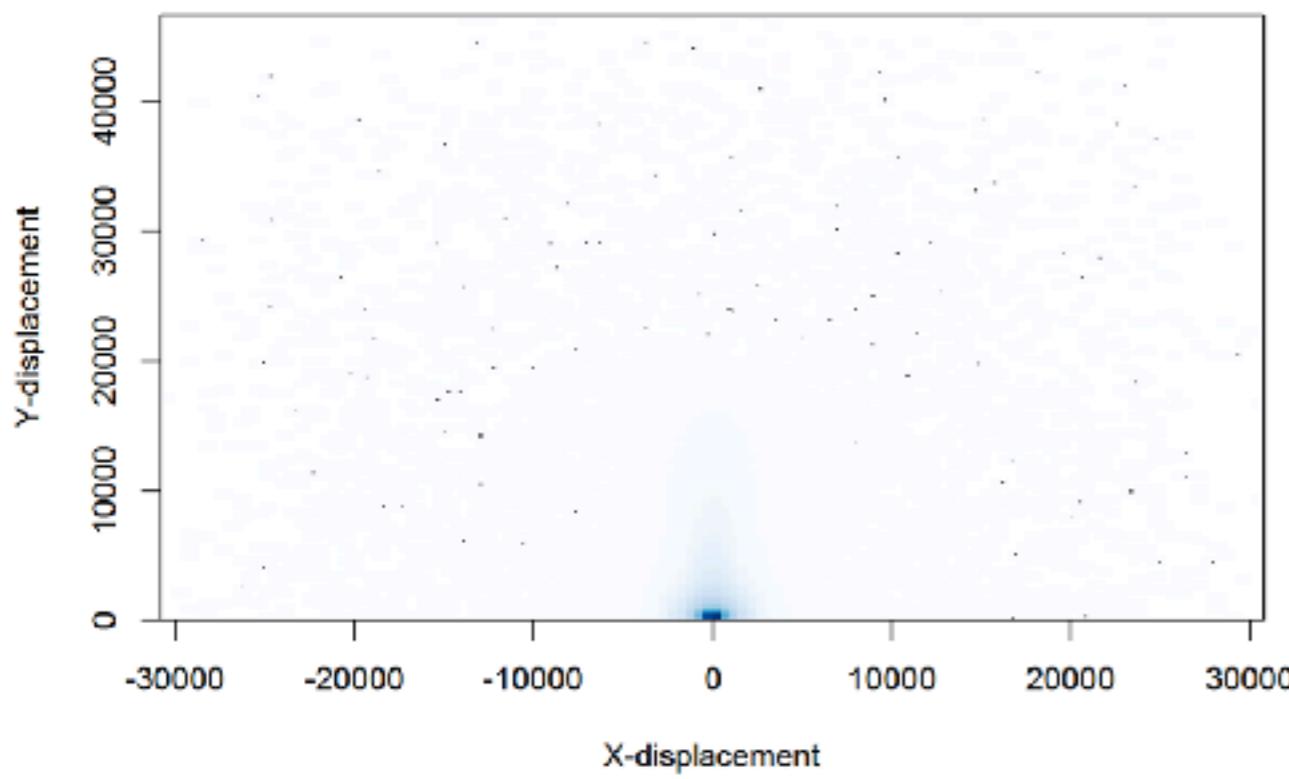
<https://sequencing.qcfail.com/articles/illumina-patterned-flow-cells-generate-duplicated-sequences/>

Patterned duplicates

Relative positioning of duplicates

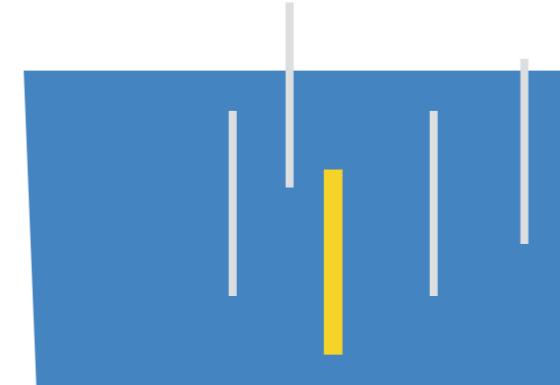


HiSeq 2500

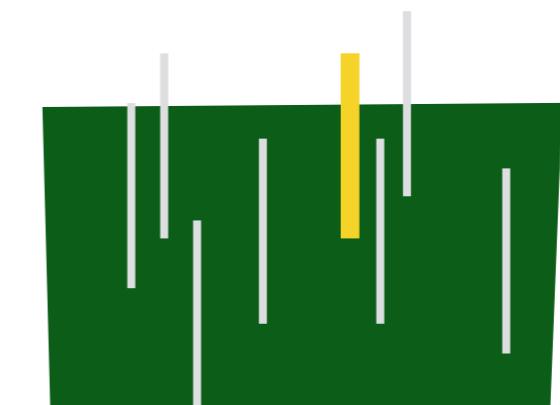


HiSeq 4000

Duplicates on
different tiles

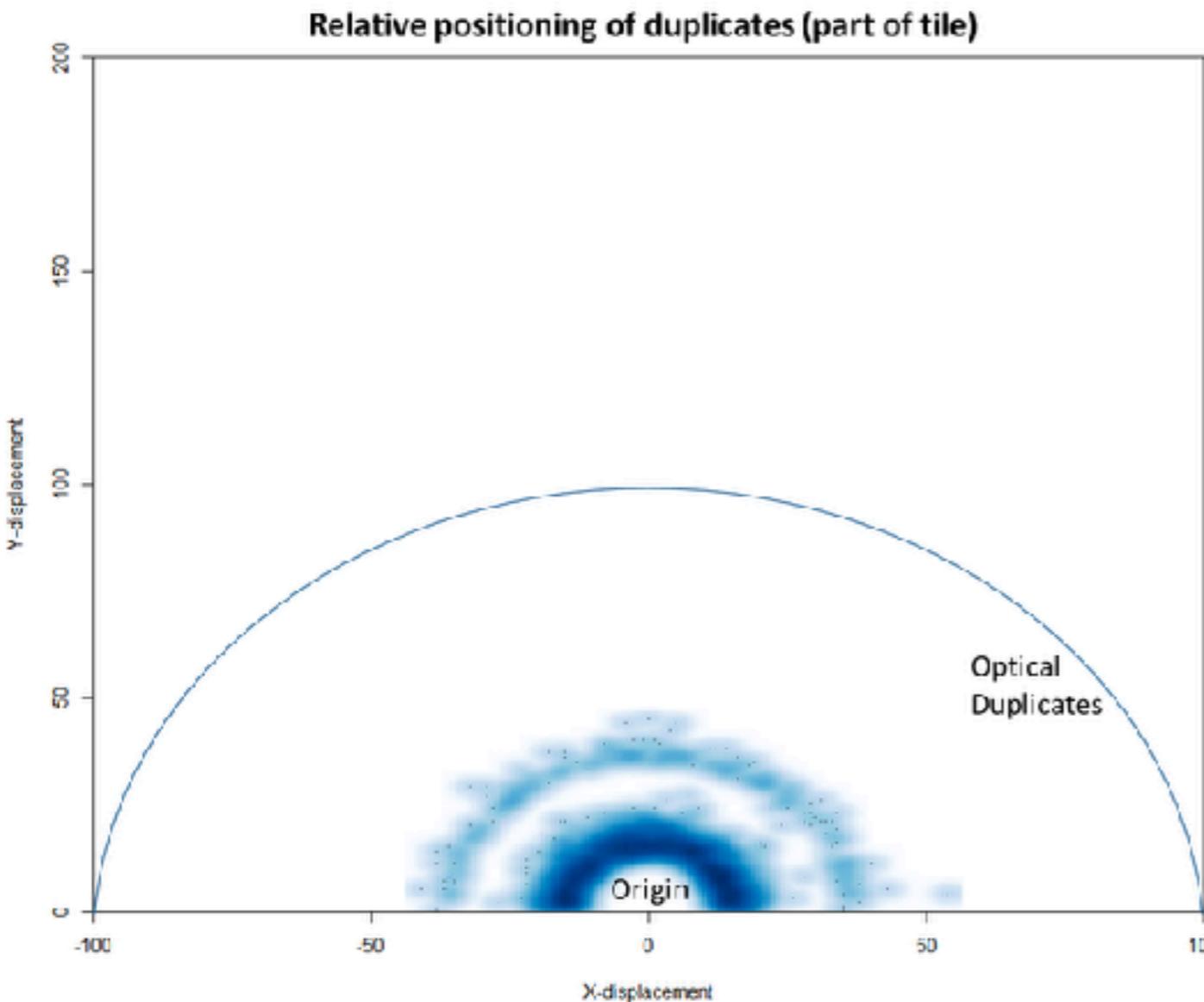


Tile A



Tile B

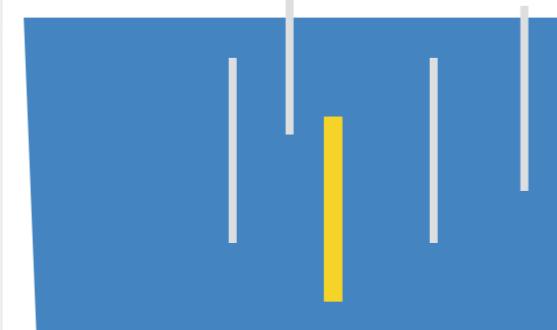
Patterned duplicates



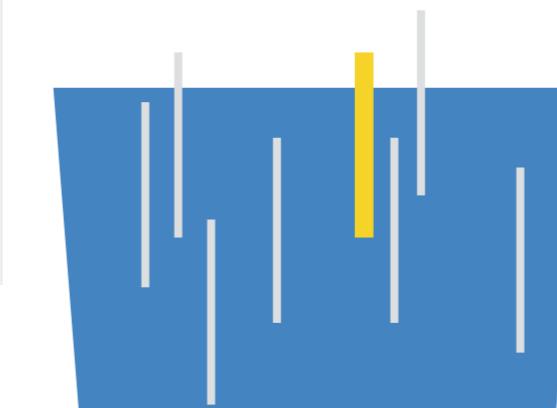
Unpatterned
flow cell

Duplicates on
the same tile

HiSeq 2500

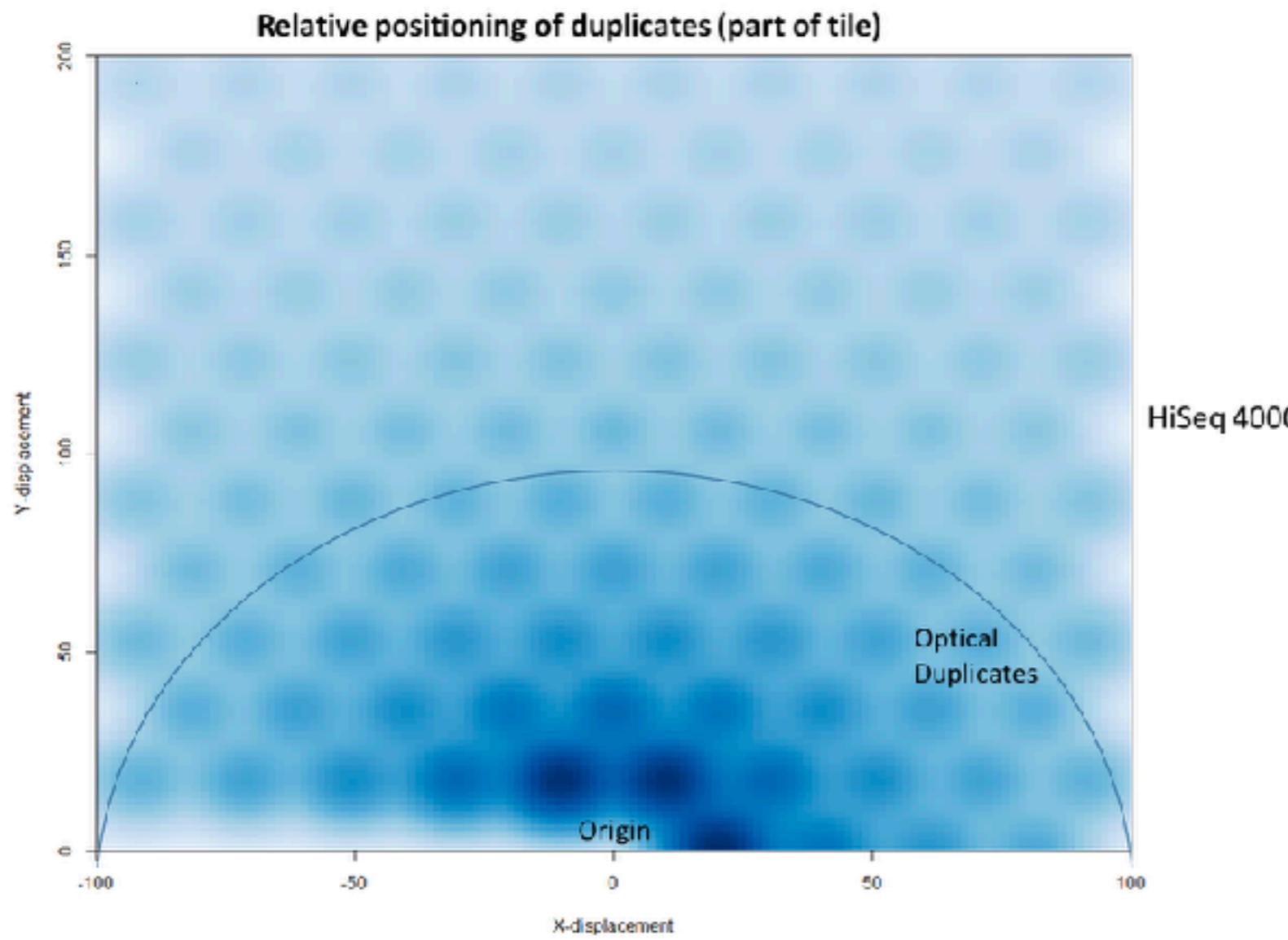


Tile A



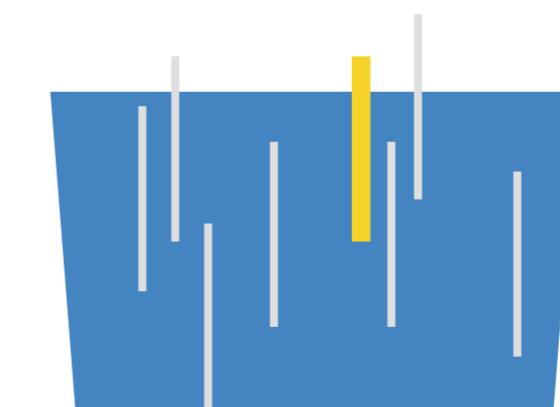
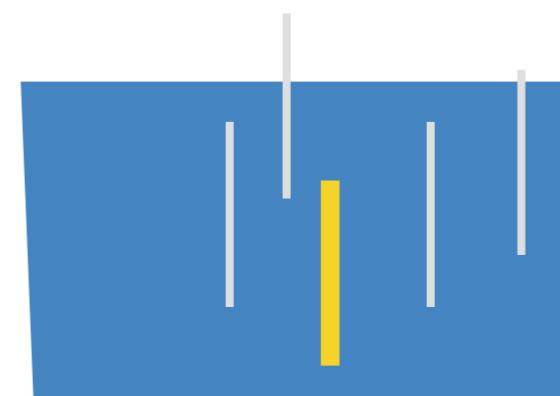
Tile A

Patterned duplicates

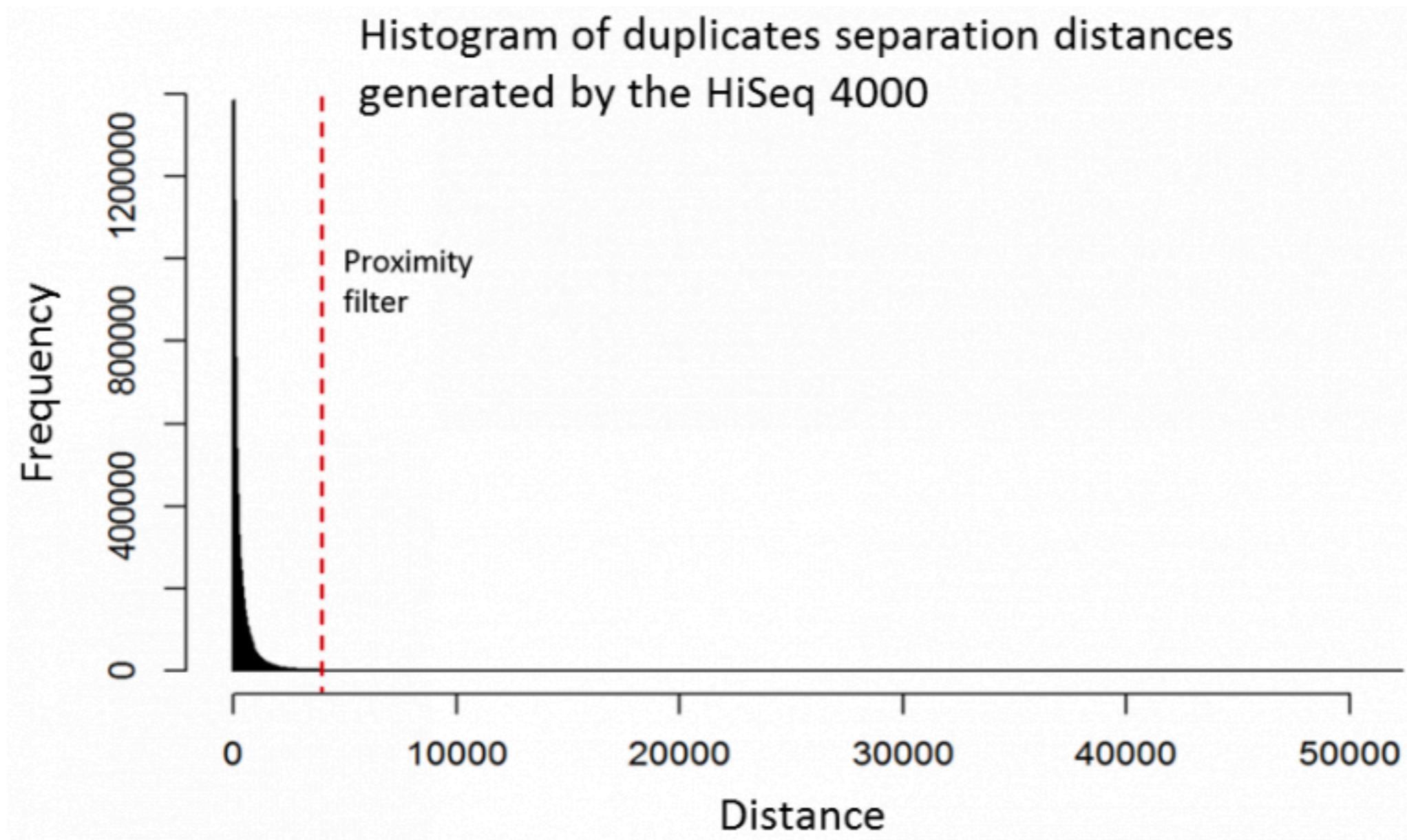


Patterned
flow cell

Duplicates on
the same tile

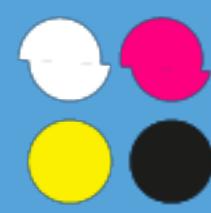


Patterned duplicates



— 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 work directly with .bcl files
 - https://github.com/EdinburghGenomics/well_duplicates



QCFAIL.com

Illumina 2 colour chemistry can
overall high confidence G bases

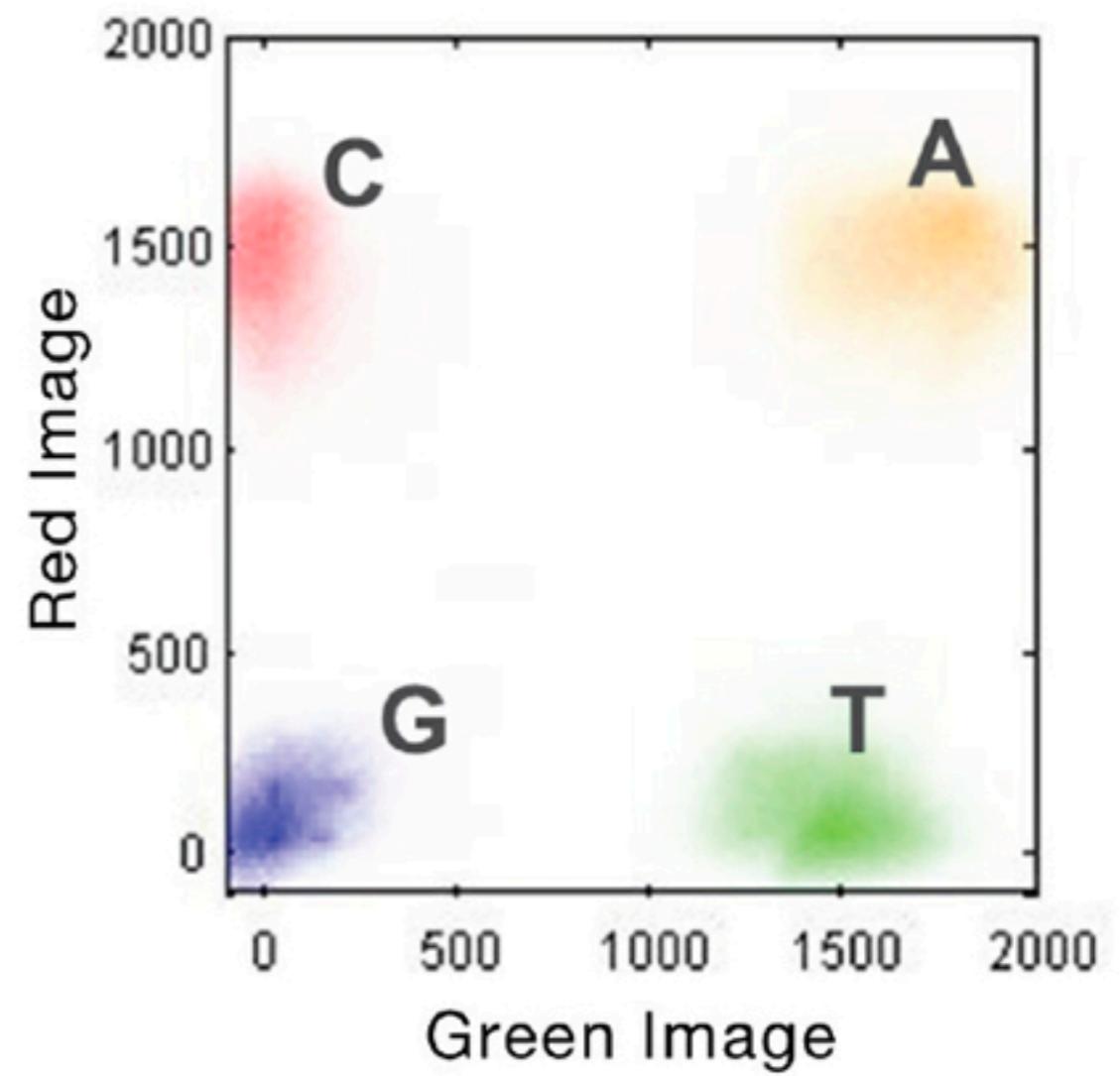
Simon Andrews



<https://sequencing.qcfail.com/articles/illumina-2-colour-chemistry-can-overall-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

GGGGGGGG_CGAGATCT



CGGAGCCT_CTATTAAG
1CDX1-423



ACTCGCTA_TCGACTAG
1CDX1-376



TAAGGCAGA_CGTCTAAAT
2CSE-2



ACTGAGCG_CTTAAAG
1CDX1-383



CGATCAGT_CTATTAAG
1CDX1-413



TGCAGCTA_CTATTAAG
1CDX1-483



Percentage of reads

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+TTTGCCT	1 475 160	1.4%
CGCTCATT+CGTTTACT	1 408 140	1.33%



Colour chemistry

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

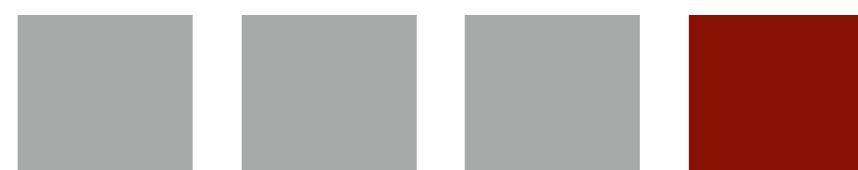
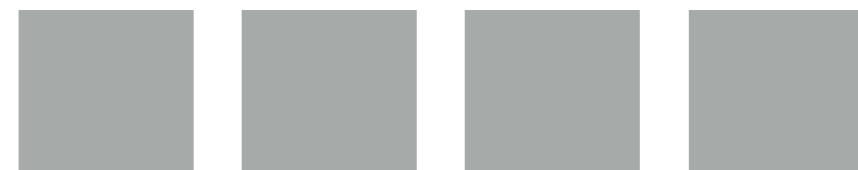
Sample 1 GGTT

Sample 2 GTTC

Green



Red



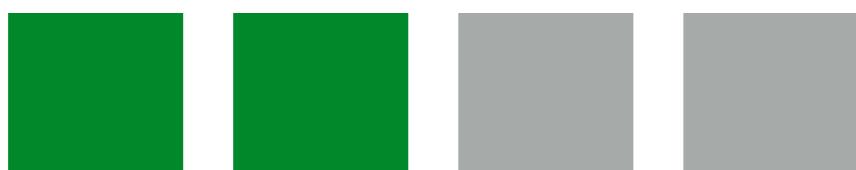
Colour chemistry

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

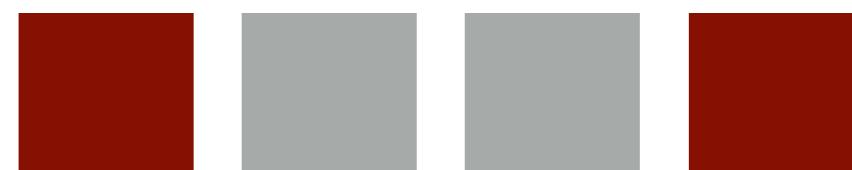
Sample 1 GCAT

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-100000041074.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>

PacBio RS II



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PacBio Sequel



SciLifeLab

NGI stockholm

PacBio Sequencing

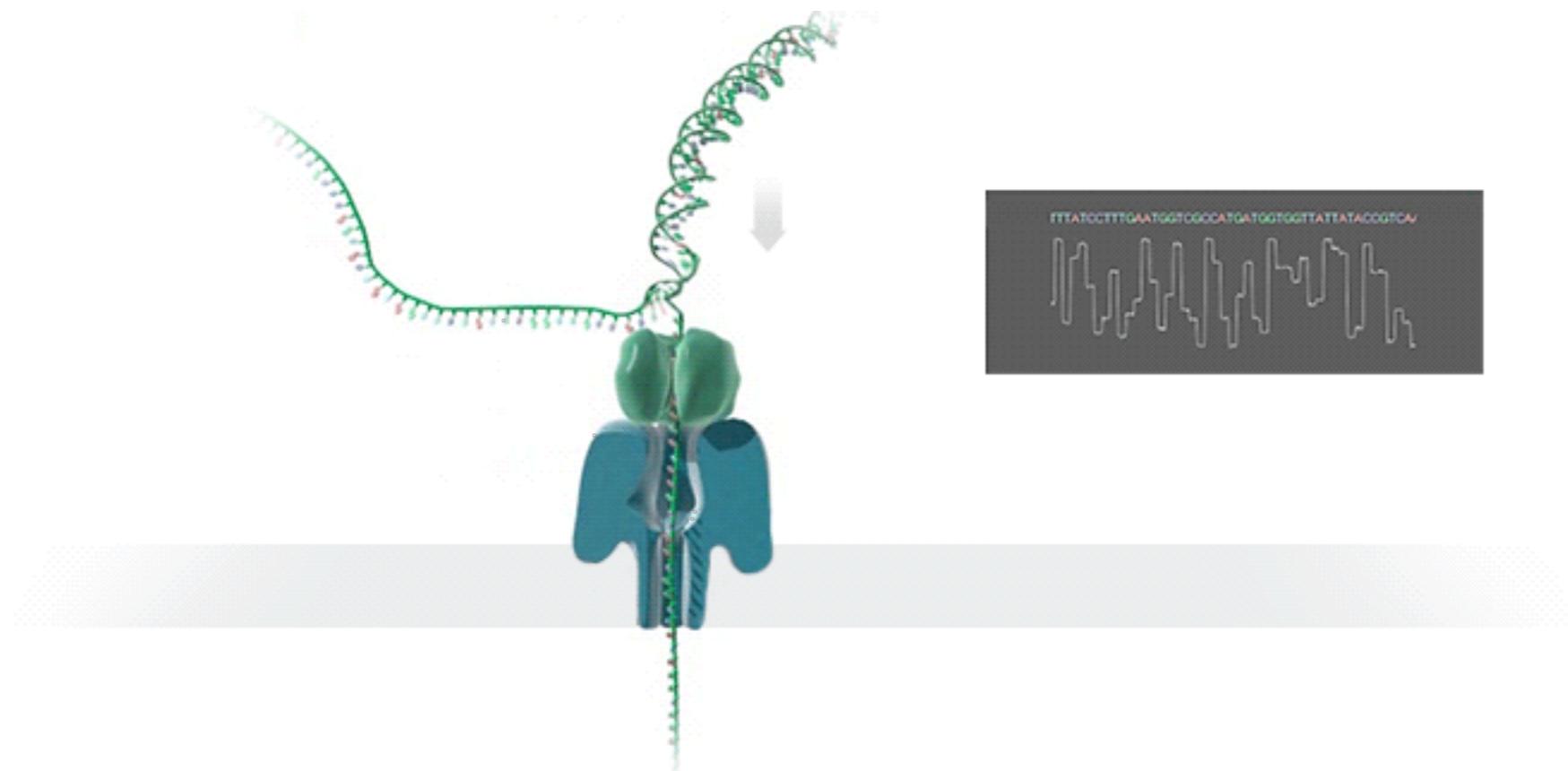
- Long reads are excellent for *de-novo* genome assembly, haplotype phasing and isoform detection
- Output is expensive compared to illumina, but getting better
 - Small genomes are no problem. Larger genomes are now becoming more feasible.
- New amplification-free enrichment using CRISPR-Cas9



- Oxford Nanopore

- 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



SciLifeLab

NGI stockholm

MinION



SciLifeLab

NGI stockholm

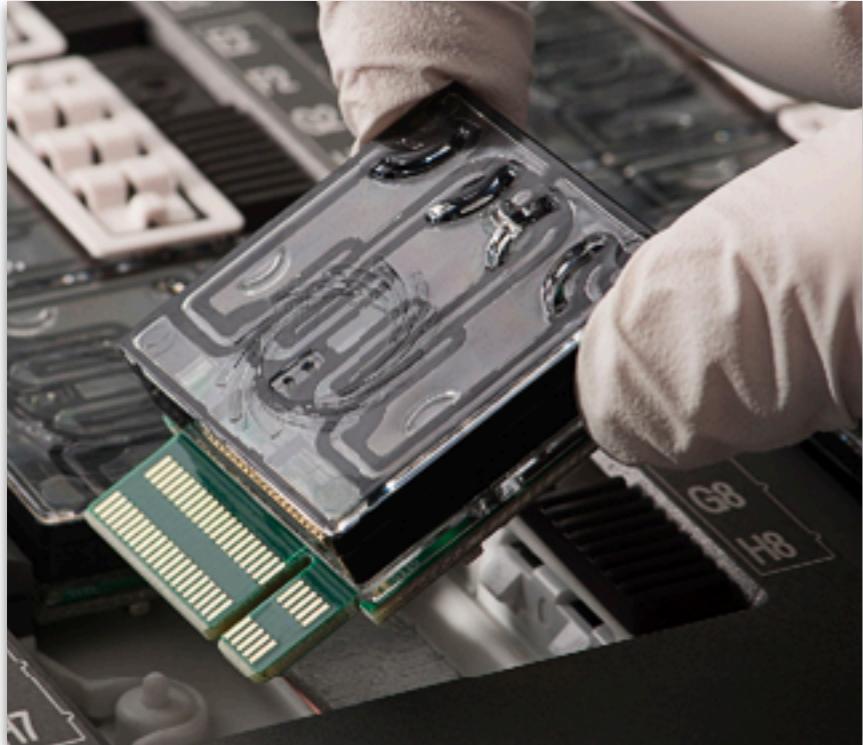
GridION



SciLifeLab

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PromethION



SciLifeLab

NGI stockholm

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

iontorrent

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

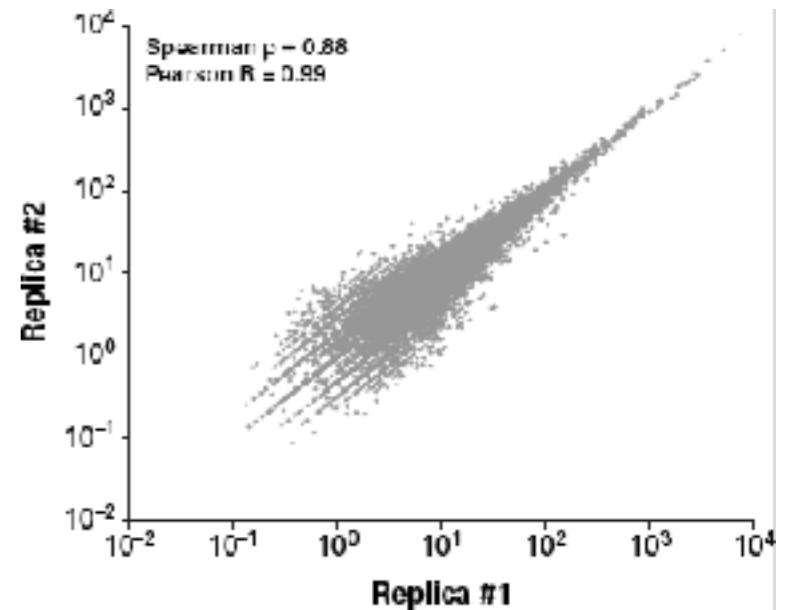


Library Preparation

- 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
- Define your limitations
 - Low-input material
 - Low quality material (eg. FFPE)
- Choose your question
 - Differential gene expression
 - Differential isoform detection & quantification
 - Fusion gene detection

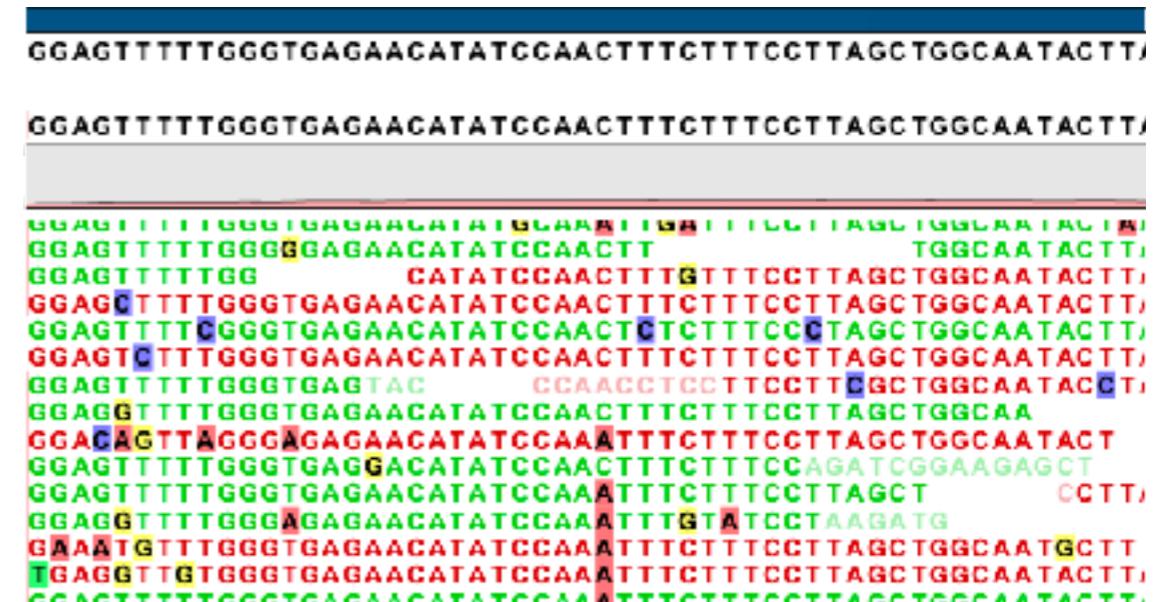


RNA Sequencing

- 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

- Choose your question
 - SNP, SNV, indel calling
 - Structural variant detection
 - *De-novo* genome assembly
- Define your requirements
 - Low-input material
 - Low quality material (eg. FFPE)
- Choose your priorities
 - Sequencing accuracy
 - Sequencing depth
 - Ultra-long reads



- DNA Sequencing

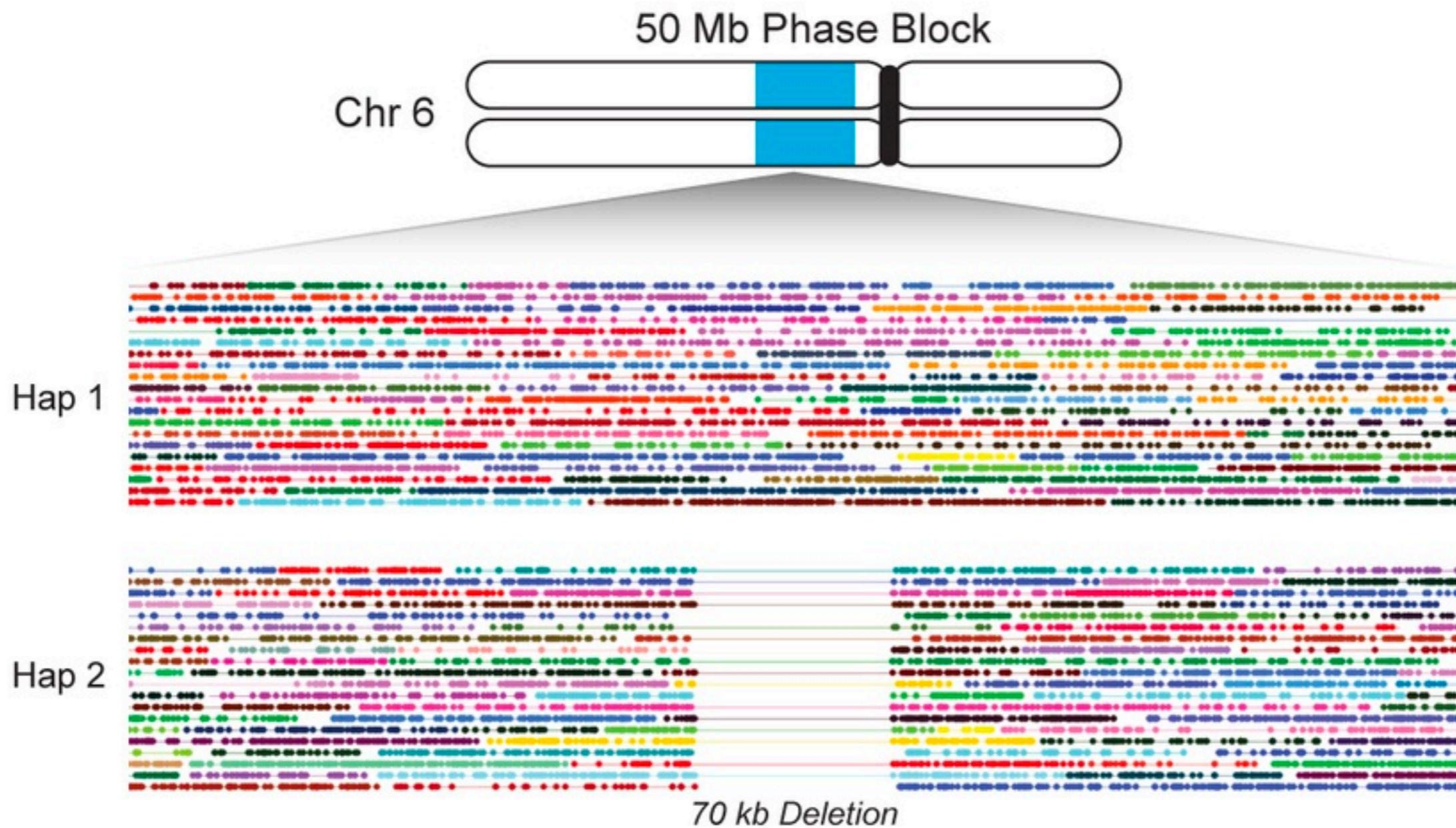
- Illumina sequencing DNA library prep kits
 - Illumina TruSeq DNA PCR Free *Best quality*
 - Rubicon ThruPLEX *Low input*
 - Illumina Nextera XT *Cheap (plate format)*
 - Illumina Nextera Flex *Fast and simple*
 - 10X Genomics *Linked reads*
- Oxford Nanopore, PacBio, IonTorrent

- 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

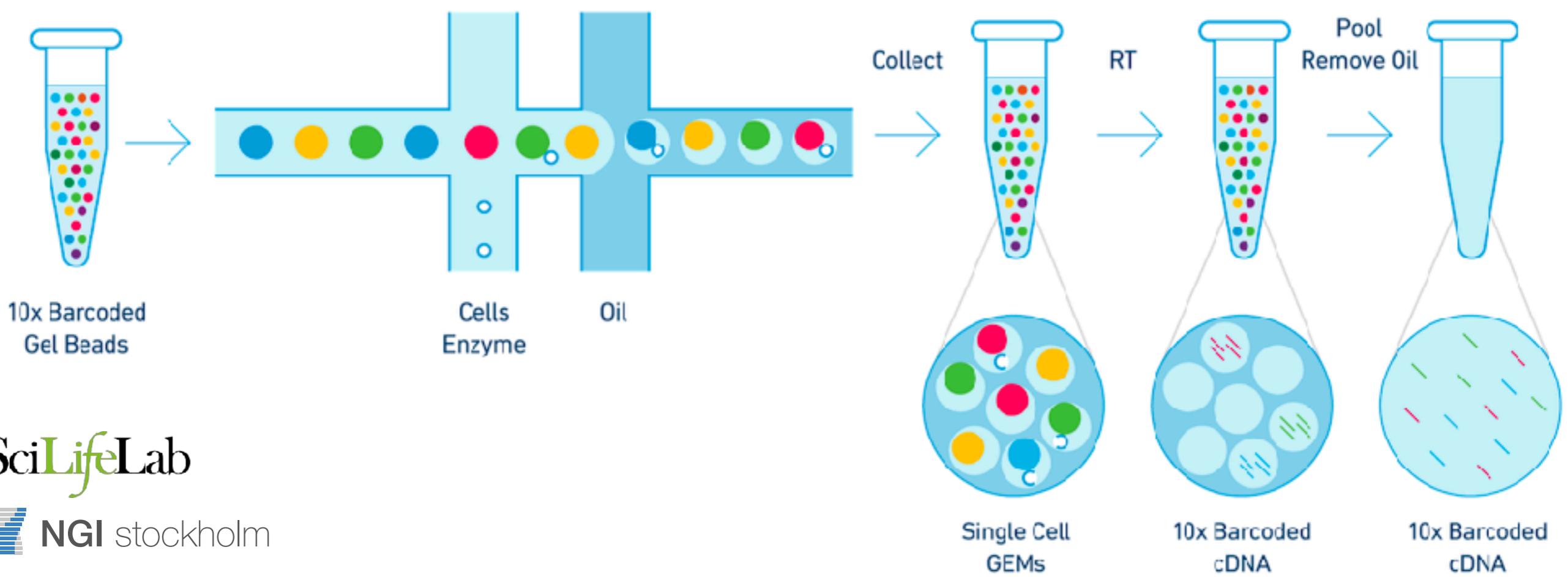


10X Genomics



10X Genomics

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

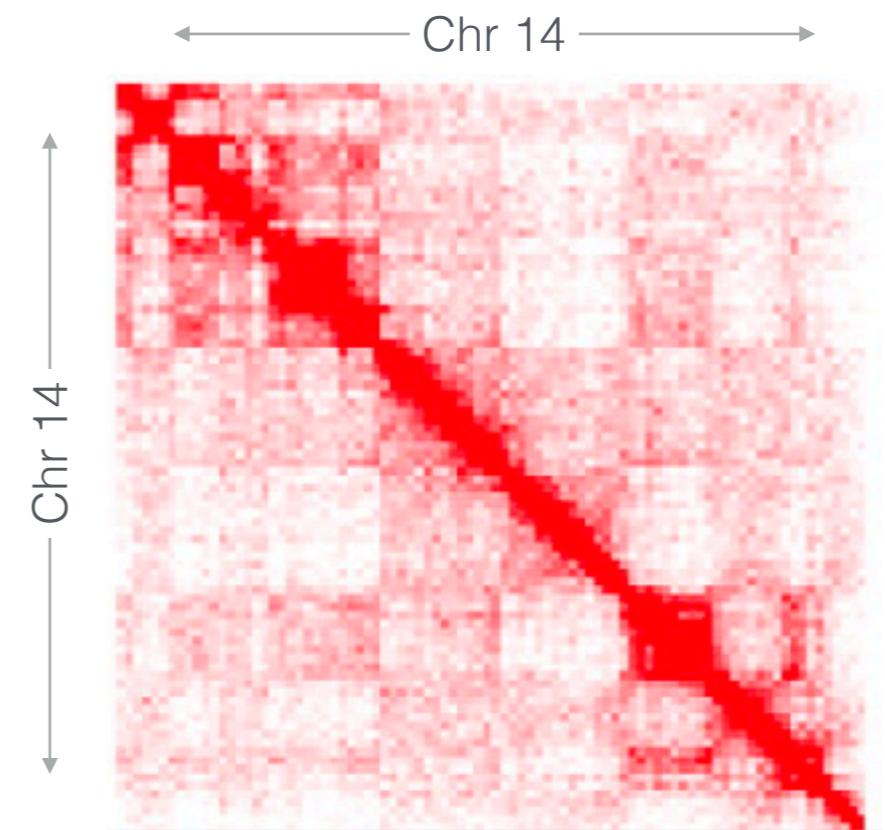


SciLifeLab

NGI stockholm

Hi-C

- Now testing Hi-C in NGI Stockholm
 - Proximity ligation assay to detect physical colocation 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

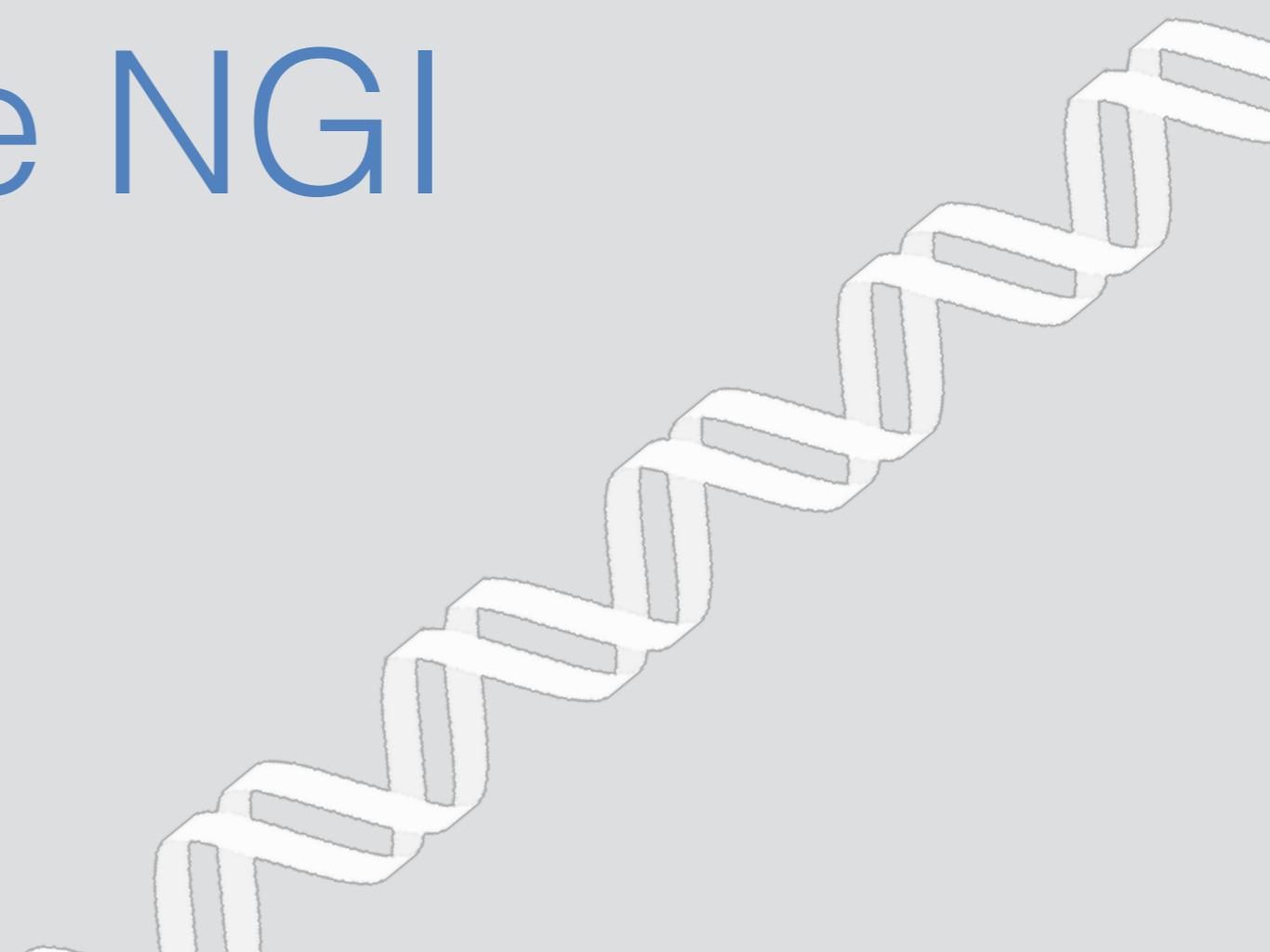
RAD Sequencing

- 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

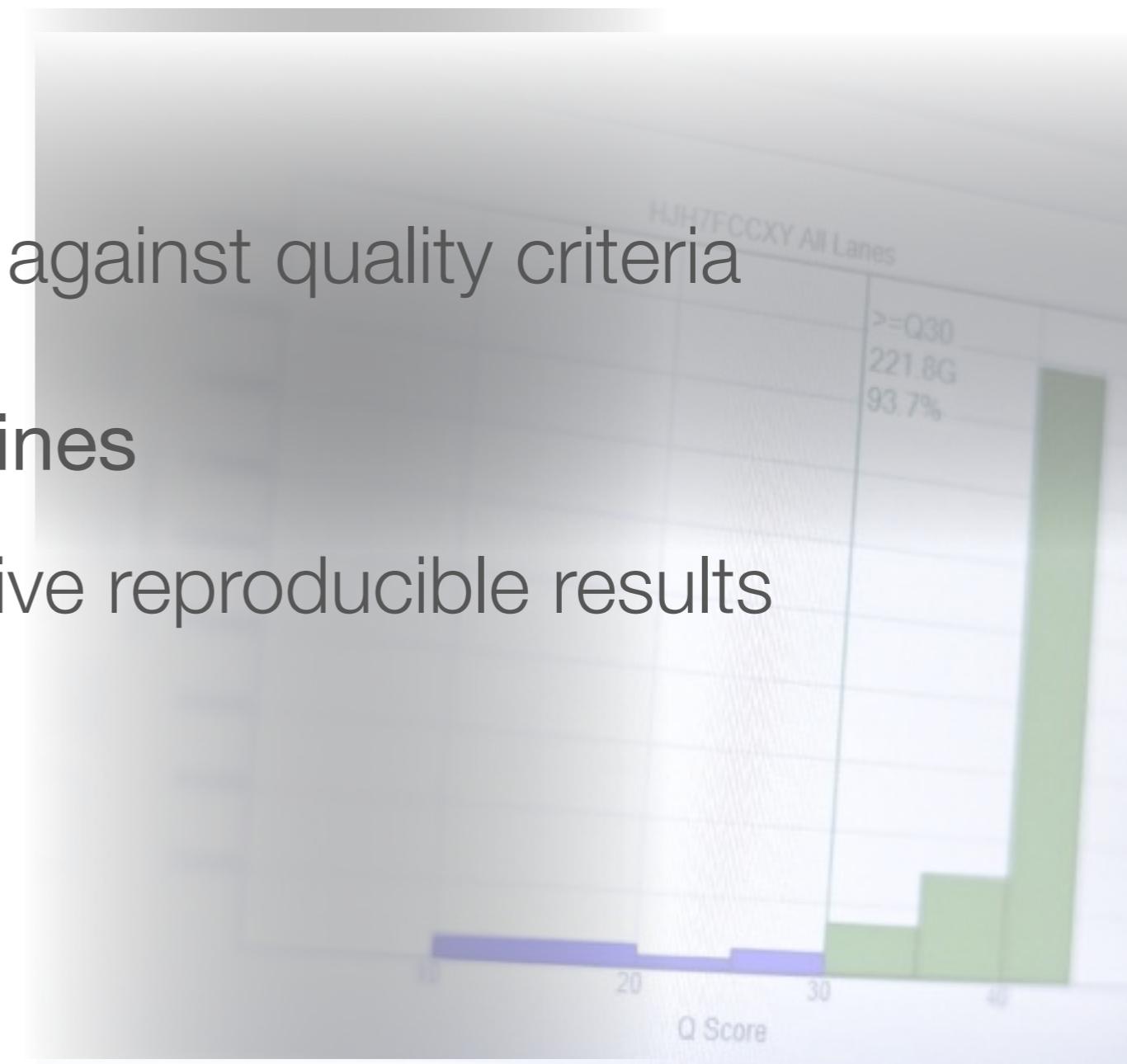
- 16S / 18S / Custom amplicons
- High sample throughput
 - Plates of 96 samples processed using liquid handling automation
 - Large numbers of index combinations allow large pools
- Cheap and convenient for metagenomics and metabarcoding sequencing projects
 - Contact us to talk about a pilot project

Bioinformatics at the NGI

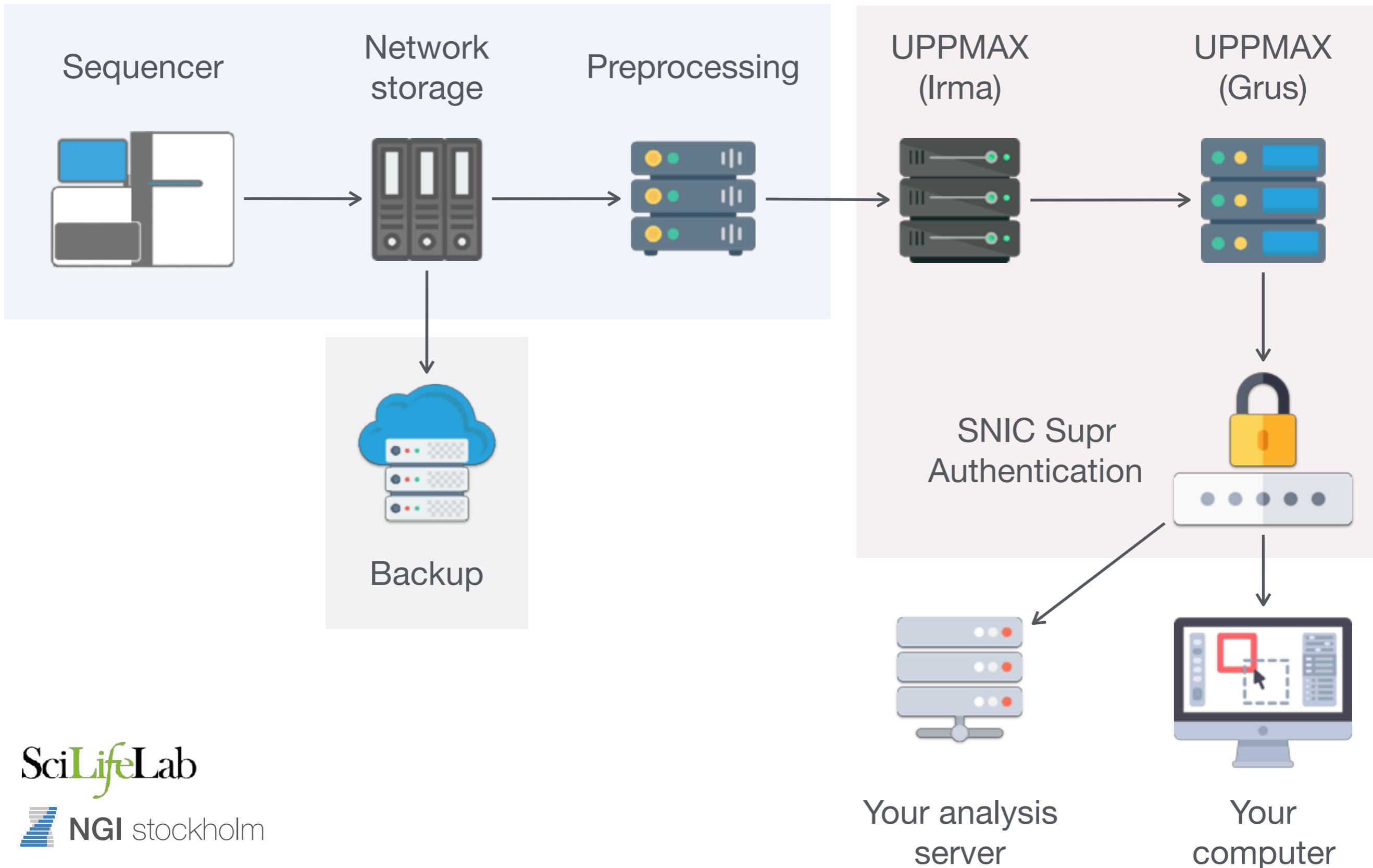


Bioinformatics at NGI

- 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



Ackred. nr 1850
Provning
ISO/IEC 17025

- Analysis Requirements

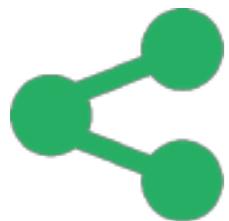


Automated



Reliable

nextflow



Easy for others to run



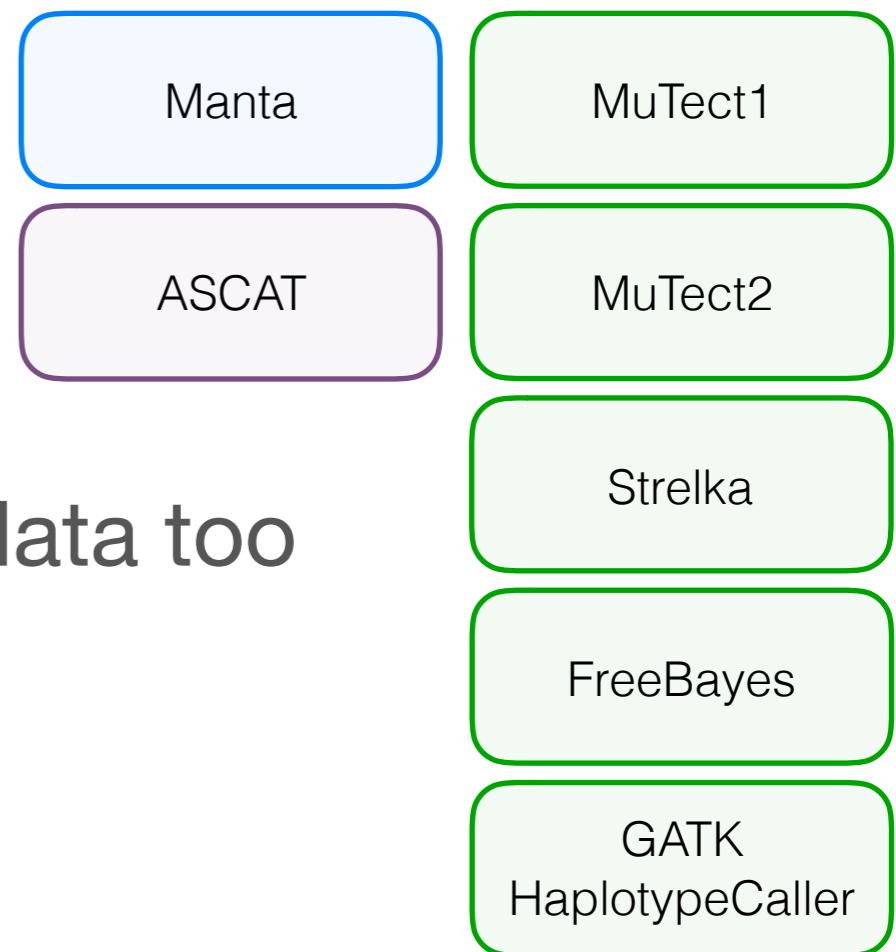
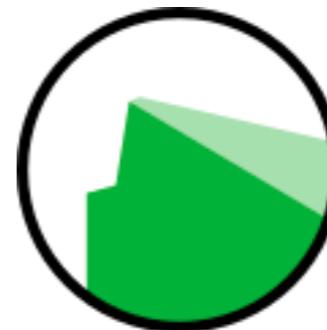
Reproducible results

Sarek



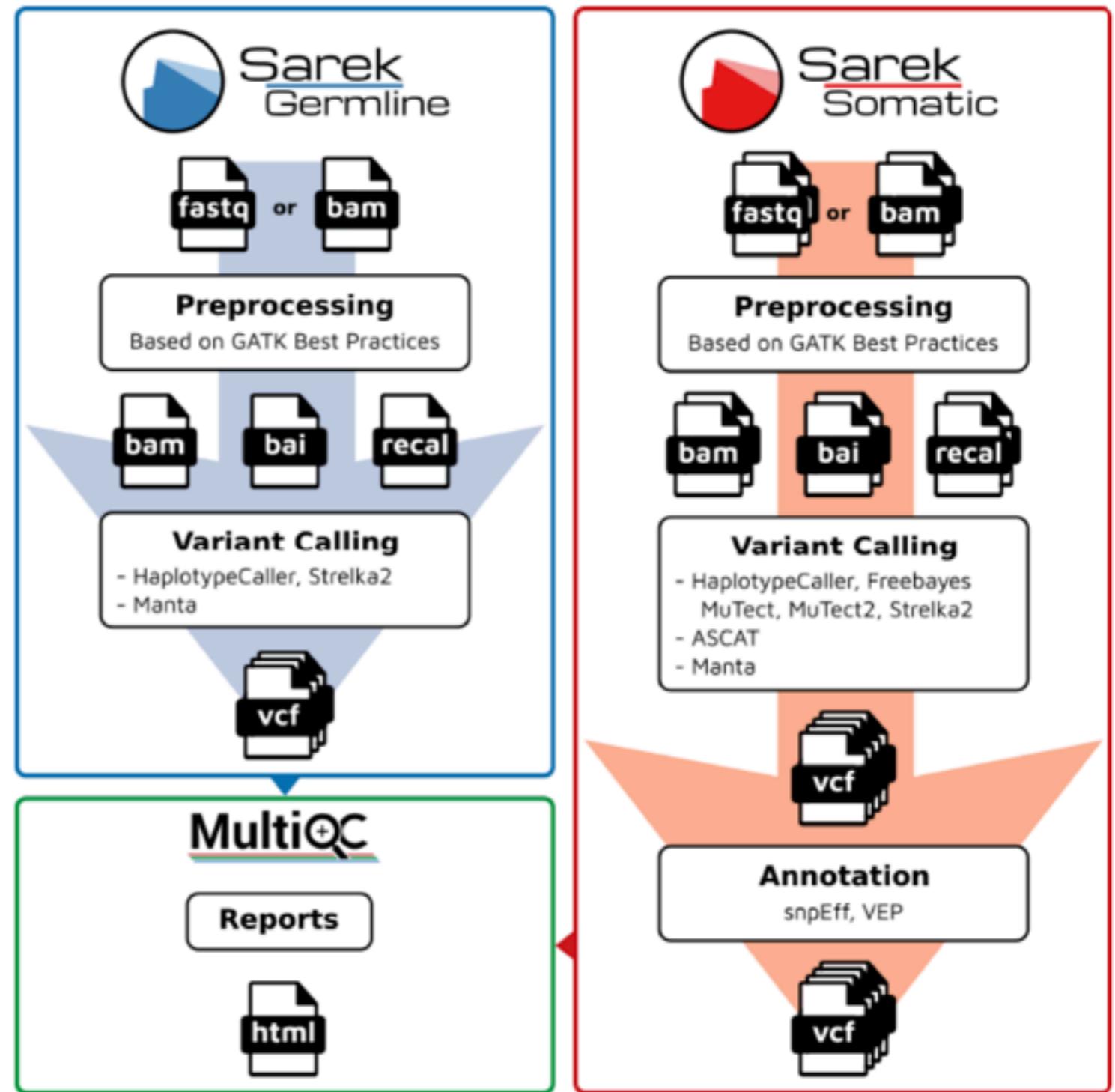
<https://github.com/SciLifeLab/Sarek>

- 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

- 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

nf-core 
<https://nf-co.re>

nf-core

The screenshot shows the nf-core website homepage. At the top, there's a navigation bar with links for Home, Pipelines, Tools, Docs, and About. Below the header, the nf-core logo is displayed with a small green icon. A sub-header states: "A community effort to collect a curated set of analysis pipelines built using Nextflow." A large green button labeled "VIEW PIPELINES" is prominent. Below this, three main sections are highlighted: "For facilities", "For users", and "For developers". Each section has a brief description and a corresponding icon. The "For facilities" section says: "Highly optimised pipelines with excellent reporting. Validated releases ensure reproducibility." The "For users" section says: "Portable, documented and easy to use workflows. Pipelines that you can trust." The "For developers" section says: "Companion templates and tools help to validate your code and simplify common tasks." Further down, a statement says: "Nextflow is an incredibly powerful and flexible workflow language. nf-core pipelines adhere to strict guidelines - if one works, they all will." Below this, there are six cards arranged in two rows of three. The first row contains: "Documentation" (with a clipboard icon), "CI Testing" (with a person wearing a hard hat icon), and "Stable Releases" (with a green checkmark icon). The second row contains: "Docker" (with a Docker logo icon), "Singularity" (with a Singularity logo icon), and "Bioconda" (with a Bioconda logo icon).



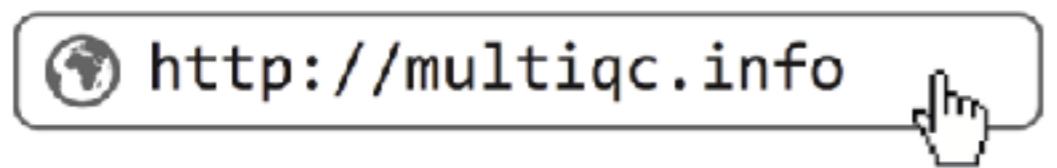
- Easy to run pipelines
- Helpful community
- Super reproducible results

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

General Stats

NGI-RNAseq

Sample Similarity

MDS Plot

STAR

Cutadapt

FastQC

Sequence Quality Histograms

Per Sequence Quality Scores

Per Base Sequence Content

Per Sequence GC Content

Per Base N Content

Sequence Length Distribution

Sequence Duplication Levels

Overrepresented sequences

Adapter Content

P1234: Test_NGI_Project

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

Contact E-mail: 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 22/22 rows and 6/6 columns.

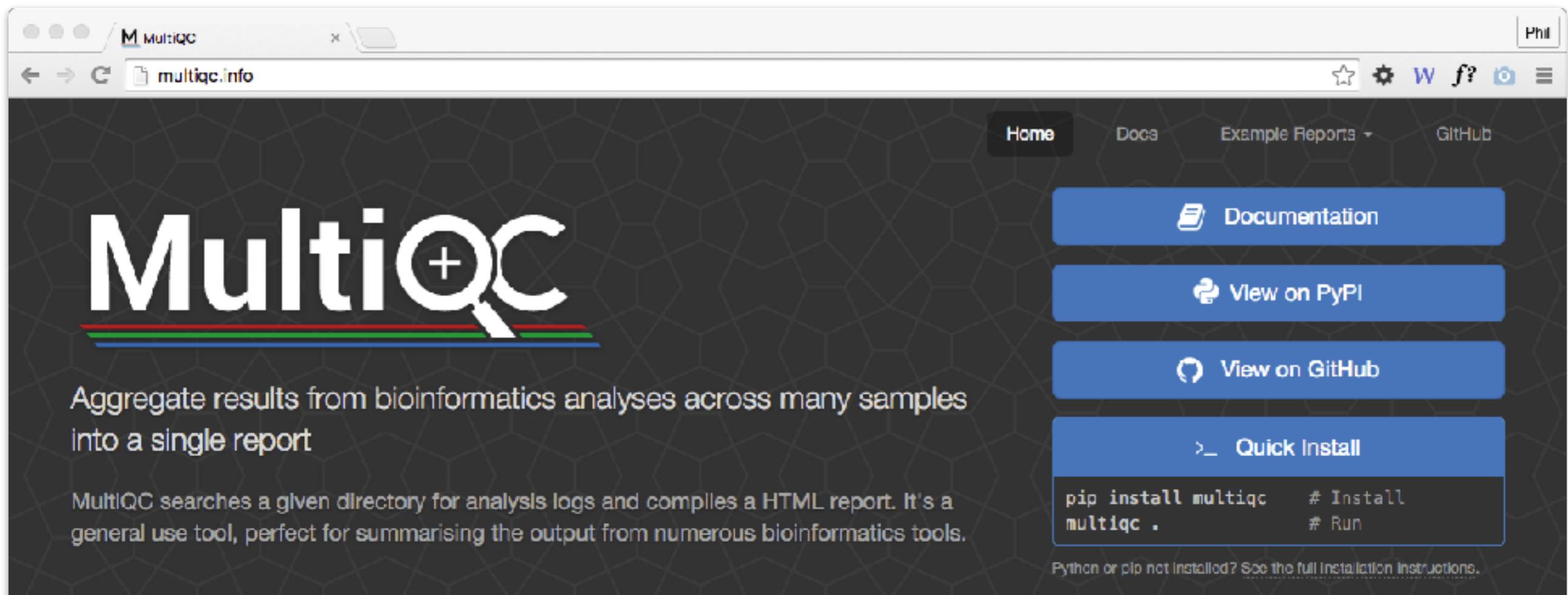
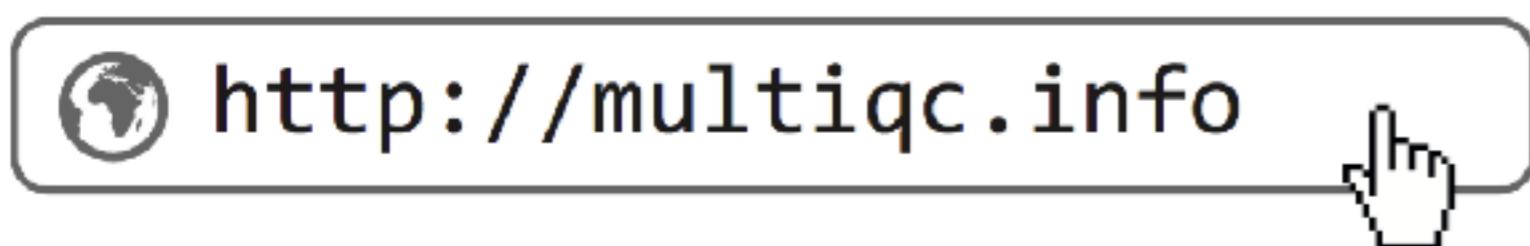
Sample Name	% Aligned	M Aligned	% Trimmed	% Dups	% GC	M Seqs
P1234_1001	68.2%	22.8	10.3%	71.3%	49%	33.7
P1234_1002	67.9%	20.9	10.7%	70.1%	50%	31.1
P1234_1003	64.7%	21.7	11.0%	72.3%	50%	33.7
P1234_1004	55.2%	17.0	13.2%	73.4%	51%	31.2
P1234_1005	53.0%	17.7	15.9%	75.8%	52%	33.8
P1234_1006	52.7%	16.1	14.1%	73.8%	52%	30.8
P1234_1007	33.0%	7.0	32.0%	60.5%	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



BIOCONDA



The screenshot shows the official MultiQC website at <http://multiqc.info>. The page has a dark background with a hexagonal grid pattern. On the left, there's a large "MultiQC" logo with a magnifying glass icon. Below it, a tagline reads: "Aggregate results from bioinformatics analyses across many samples into a single report". A paragraph explains: "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, there's a navigation bar with links for "Home", "Docs", "Example Reports", and "GitHub". Below the navigation, there are four blue call-to-action buttons: "Documentation", "View on PyPI", "View on GitHub", and "Quick Install". The "Quick Install" button contains the command: `pip install multiqc # Install
multiqc . # Run`. At the bottom, a note says: "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

<https://ngisweden.scilifelab.se>

support@ngisweden.se

The screenshot shows the NGI Sweden Order Portal homepage. At the top, there's a navigation bar with links for 'Information', 'Documents', 'Contact', and 'About us'. Below the navigation is the NGI logo and the text 'NATIONAL GENOMICS INFRASTRUCTURE' along with the subtitle 'Next-Generation Sequencing and Genotyping for Swedish Research'. To the right of the logo, there's a section titled 'NGI Sweden Order Portal' with a brief description of the portal's purpose and a note about non-Swedish projects. Below this is a 'Turn Around Times and Status for the Stockholm node' section with a rainbow-colored progress bar. Further down, there are sections for 'Subscribe to our mailing list' (with fields for email address and a 'Subscribe' button) and 'Request a meeting' (with a 'Create' button). On the right side, there are five blue boxes, each with a title and a 'Create' button: 'Illumina Sequencing', 'Ion Sequencing', 'PacBio Sequencing', 'Genotyping and array-based epityping', and 'All news'. At the bottom left, there's a note about sample submission closing from June 29 to August 6, and at the bottom right, there's a note about summer library preparation and sequencing.

SciLifeLab

NGI stockholm

Find our tools

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

<http://opensource.scilifelab.se>

The screenshot shows a GitHub repository page for the SciLifeLab open-source tools. The header features the SciLifeLab logo with the tagline "Open Source is in our DNA". Below the header, there is a list of tools, each with a small icon, a name, and a brief description.

Icon	Name	Description
	AWS-iGenomes	Reference genomes on AWS S3
	Chanjo	Coverage analysis for clinical sequencing
	CheckQC	Quick quality control of Illumina runs
	Cluster Flow	Simple pipelines for bioinformatics
CONCOCT Clustering metagenomic contigs		
cutadapt removes adapters from your reads		
	FRC	De Novo Assembly Evaluation Tool
	genmod	Inheritance in family studies
	MultiQC	Summarise results across samples
	NGI-ChIPseq	ChIP-seq analysis pipeline

Acknowledgements

Phil Ewels

✉ phil.ewels@scilifelab.se

👤 ewels

🐦 tallphil

Thanks to:

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Olga Vinnere Pettersson

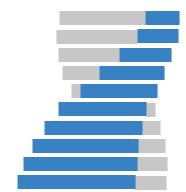
NGI Sweden



support@ngisweden.se

<http://ngisweden.scilifelab.se>

<http://opensource.scilifelab.se>



NGI Stockholm