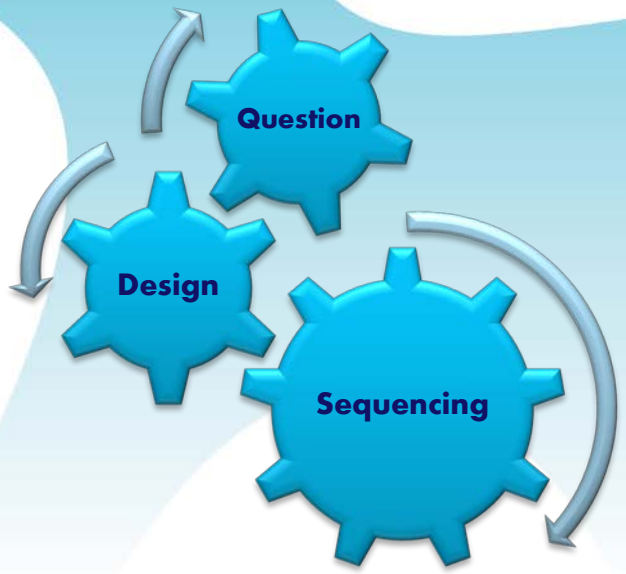
Leymus Genomics
Products and Services for Genomic Analysis

Genome Scan

Company profile
&
Introduction to NGS



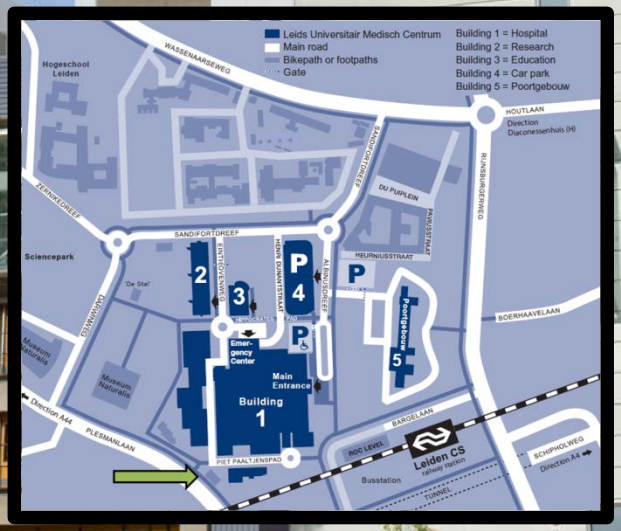
Dr. Mark de Jong
Lab Manager
2017-10-16

genomescan.nl

Leids Universitair Medisch Centrum

Erasmus MC
University Medical Center Rotterdam

Zafung



Company profile

- **Innovation**
  - Technology driven
  - Latest available technologies, instruments and software
  - Main focus on sequencing and array technology

- **Quality**
  - ISO/IEC17025 accreditation

- **Knowledge**
  - Extensive technical expertise and experience

Genome Scan

3Gb TEST

FAST-SEQ

OPTIBIOCAT

SYSVASC

decode
a ctmm project

BONE-NET

EPISTOP

EARLYNUTRITION
Long-term effects of early nutrition on later health

EUCID.net
European network of Congenital Imprinting Disorders

GenoMEL

IDEAL ageing

HEALS

TranCYST

ngsprotocol
a ctmm project

iMode-CKD

Loss of photoreceptorness and gain of genomic alterations in retinoblastoma reveal tumor progression

Irsan E. Kooi[a,†], Berber M. Mol[a,†], Annette C. Moll[b], Paul van der Valk[c], Marcus C. de Jong[d], Pim de Graaf[d], Saskia E. van Mil[a], Antoinette Y.N. Schouten-van Meeteren[e], Hanne Meijers-Heijboer[a], Gerjan L. Kaspers[f], Hein te Riele[g], Jacqueline Cloos[f,h], Josephine C. Dorsman[a,*]

RESEARCH ARTICLE

Copy number alterations and allelic relation to recurrence of rectal cancer

Inès J Goossens-Beumer[1], Jan Oosting[2], Wim L Corver[2], Marjolein JFW Jansen[3], Bart Janssen[3], Wilbert van Workum[3], Elaine CM Zeestraten[1], Cornelis JH van de Velde[1], Hans Morreau[2], Peter JK Kuppen[1] and Tom van Wezel[2*]

Toxicology in Vitro

journal homepage: www.elsevier.com/locate/tiv

Exploration of new functional endpoints in neuro-2a ce detection of the marine biotoxins saxitoxin, palytoxin a

Jonathan Nicolas[a,b,*], Toine F.H. Bovee[b], Lenny Kamelia[a], Ivonne M.C

Reduced seed germination in *Ara* SWI/SNF2 ATPase genes

Hendrika A. C. F. Leeggangers[a,†,‡], Adam Folta[a,‡], Aleksandra Muras[a], Jan-Peter Nap[b,c] and Ludmila Mlynarova[a,*]

[a]Laboratory of Molecular Biology, Plant Sciences Group, Wageningen University and Research Centre, Wageningen, The Netherlands
[b]Applied Bioinformatics, Biosicence, Plant Research International, Plant Sciences Group, Wageningen University and Research Centre, Wagenir The Netherlands
[c]Expertise Centre ALFE, Institute for Life Science & Technology, Hanze University of Applied Sciences, Groningen, The Netherlands

Identification of a Classical Mutant in the Industrial Host *Aspergillus niger* by Systems Genetics: LaeA Is Required for Citric Acid Production and Regulates the Formation of Some Secondary Metabolites

Jing Niu,[a] Mark Arentshorst,[a] P. Deepa S. Nair,[a] Zyu Dai,[a] Scott E. Baker,[b] Jens C. Frisvad,[c] Kristian F. Nielsen,[c] Peter J. Punt,[a,**] and Arthur F.J. Ram[a,*]

[a]Molecular Microbiology and Biotechnology, Institute of Biology Leiden, Leiden University, 2333 BE, Leiden, The Netherlands, [b]Chemical and Biological Process Development Group, and [c]Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory, Richland, Washington [c] University of Denmark, 2800 Kgs Lyngby, Denmark, and [**]Dute

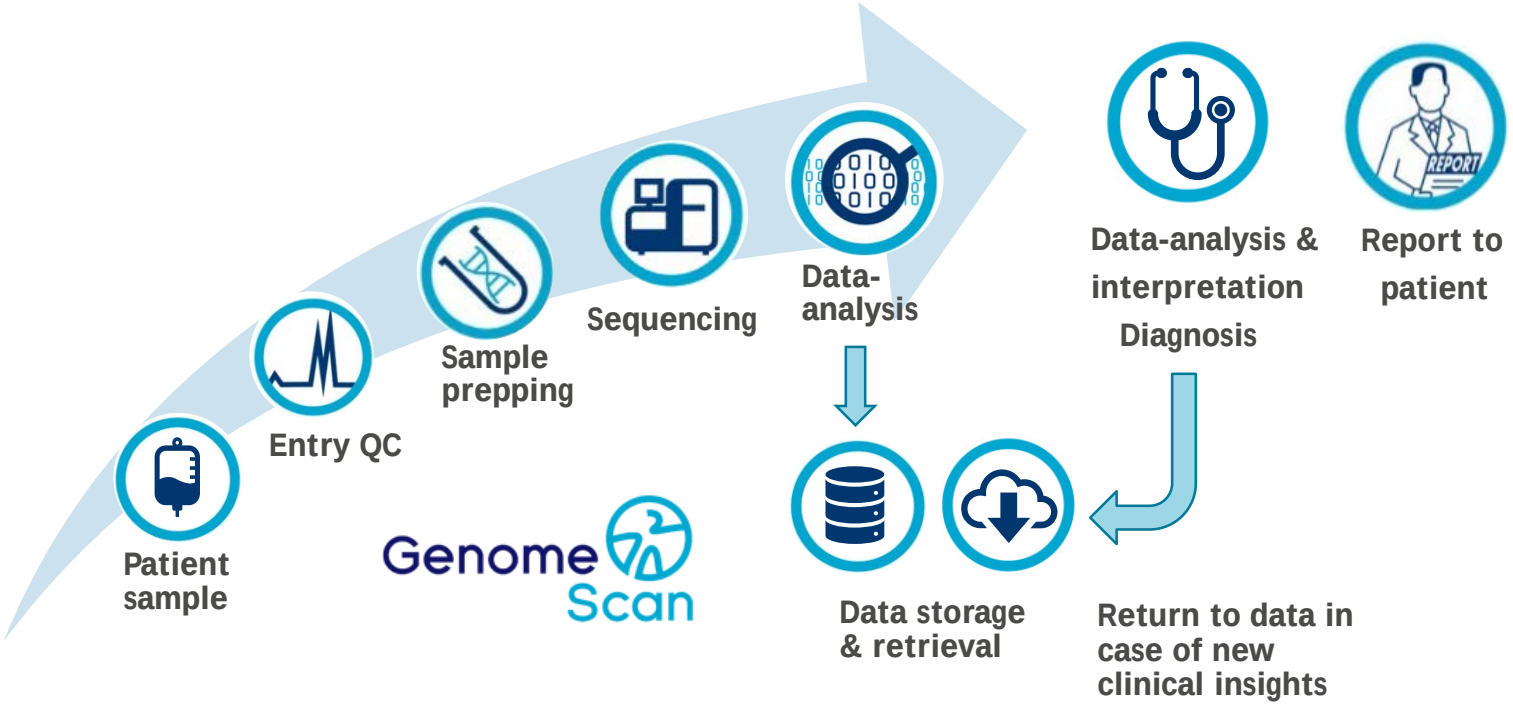
The Double-Reduction Landscape in Tetraploid Potato as Revealed by a High-Density Linkage Map

Peter M. Bourke, Roeland E. Voorrips, Richard G. F. Visser, and Chris Maliepaard[1]
Wageningen UR Plant Breeding, Wageningen University and Research Centre, Wageningen 6708 PB, The Netherlands
ORCID IDs: 0000-0002-0665-6508 (P.M.B.); 0000-0003-4388-9244 (R.E.V.)

What we provide

- Expertise in designing a clinical-grade workflow:
  high accuracy, specificity, reliability
- All instrumentation & (LUMC compatible) infrastructure
  required for optimal test development
- Guidance in the wealth of genetic applications and instruments available:
  from pilot design to fully validated service
- Bio-informatics pipelines for comprehensive data-analysis
- Speed: fastest TAT in the field
- All according to ISO17025 / ISO15189 / G(C)LP quality standards

Route towards state-of-the-art diagnostics



Provide instrumentation, expertise & infrastructure to the clinic in order to fast-track the route towards personalized treatment

Our service portfolio

DNA Sequencing

(Targeted) gene panels

Whole Genome Sequencing (WGS)
Whole Exome Sequencing (WES)
Focused Inherited Disease Scan
Custom targeted sequencing
Cancer panels
ChloroplastScan
MicrobiomeScan
MitochondrialScan
VirusScan

Transcriptomics

All RNA species

Total RNA
Messenger RNA
Long non-coding RNA, Small RNA / Micro RNA
CompoundScan

Epigenetics

Methylation and hydroxymethylation

850k methylationEPIC
Hydroxymethylation
Reduced Representation Bisulfite Sequencing (RRBS)
Whole Methylome Bisulfite sequencing (WMBS)

Bio informatics

Data analysis

Custom data analysis
Validated pipelines for all standard applications

www.genomescan.nl
info@genomescan.nl

Phases of genetic test development

Phase 1

Phase 2

Kickoff meeting

- Research question?
- Possible solutions

Design

- Reach consensus on:
  - experimental setup
  - data-analysis report format

Proof of Principle study

- Pilot experiment
- Performance of total workflow

Data-analysis

- Assess data quality and quantity

Pilot study evaluation

- Optional: adaptations to procedure to fit required results

Phases of genetic test development

Phase 3

Phase 4

Sample Isolation

- Sample shipment
- DNA purification
- Sample QC

Sample Preparation

- Sample processing according to SOPs

Sequencing

- Paired-end Sequencing on HiSeq 4000 or NextSeq 500

Data-Analysis

- Read Alignment on reference
- Detection of mutations

Reporting and evaluation

- Reporting
- Project evaluation

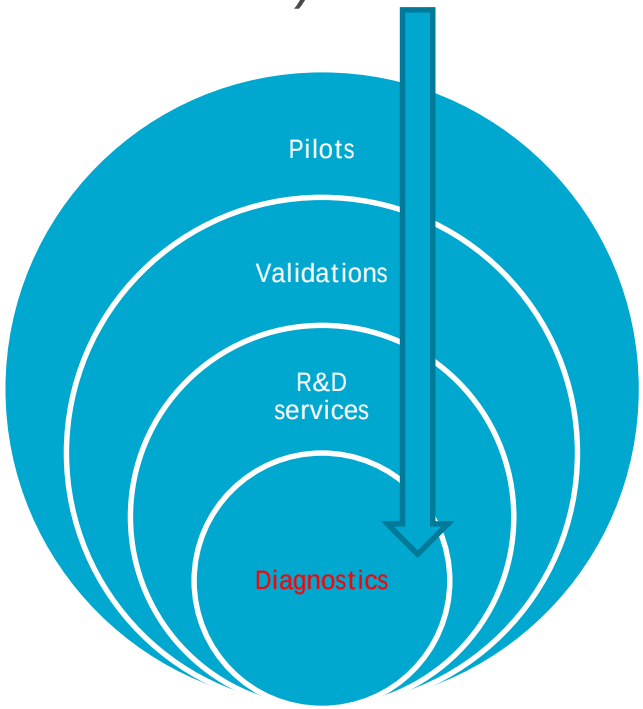
Quality Assurance

ISO17025 accreditation since April 2011 (L518 - RvA)

- All services are fully tested and validated
- Experiments performed according to Standard Operating Procedures (SOPs)
- Samples handled by continuously trained technicians
- Guaranteed deliverables for scope services
- Traceability of process
- Detailed reporting
- Transparent process
- Extensive customer support

Consultancy in experimental design

- All services rely on transparancy (NDA if needed)
- If requested: guidance from sample isolation to data analysis
- **Good experimental design crucial for optimal results**
- Clear expectations



The foundation of GenomeScan

Genome Scan

LUMC Leids Universitair Medisch Centrum

2002 — 2008 — 2011 — 2015 — 2017

ServiceXS
Your question ⇌ Our focus

TESTING
RvA L 518

Erasmus MC
Universitair Medisch Centrum Rotterdam

GCLP COMPLIANT

Illumina GAIIX Genome A
www.ebay.com/itm/Illumina-GAIIX-Genome-Analyzer-IIx-/331124096056
Apps | Bookmarks | LIMS 2.0 | LIMS 1.0 | access.lumc.nl | mail.lumc.nl | Farmatec - Vergunnin | PerfectView | 360Dx | GenomeWeb | Magzine.nu - MagZio | Bliyoo - Lees onbepe | Assembly of a humar | New Chemistry and S
Hi! Sign in or register | Daily Deals | Gift Cards | Help & Contact
iPhone 8: Available Now
Sell | My eBay
ebay Shop by category
Search for anything
All Categories
Search
Advanced
Back to home page | Listed in category: Business & Industrial > Healthcare, Lab & Life Science > Lab Equipment > Analytical Instruments

People who viewed this item also viewed

Genuine Illumina Genome Analyzer IIx & PEM IIx...
$9,229.99
~~$12,999.99~~
+ $2,250.00

Illumina Amplification Manifold for Cluster Ge...
$19.69
+ $13.50

Illumina Cluster Station for Genome Analyzer R...
$2,342.99
~~$3,299.99~~
+ $985.00

Illumina Paired End Module 181 Multiplex S...
$249.99
+ $92.84

Illumina PEM IIx Gene Sequencer Accesory -...
$144.00
+ $38.52

Illumina GAIIX Genome Analyzer IIx

Item condition: **Used**

Price: **US $19,900.00**

Buy It Now
Add to cart

Best Offer:
Make Offer

1 watching
Add to watch list
Add to collection

Longtime member | Best offer available

Shipping: May not ship to Netherlands - Read item description or contact seller for shipping options. | See details
Item location: Lake Zurich, Illinois, United States
Ships to: United States

Delivery: Varies

Payments: PayPal | See details

Returns: Seller does not offer returns.

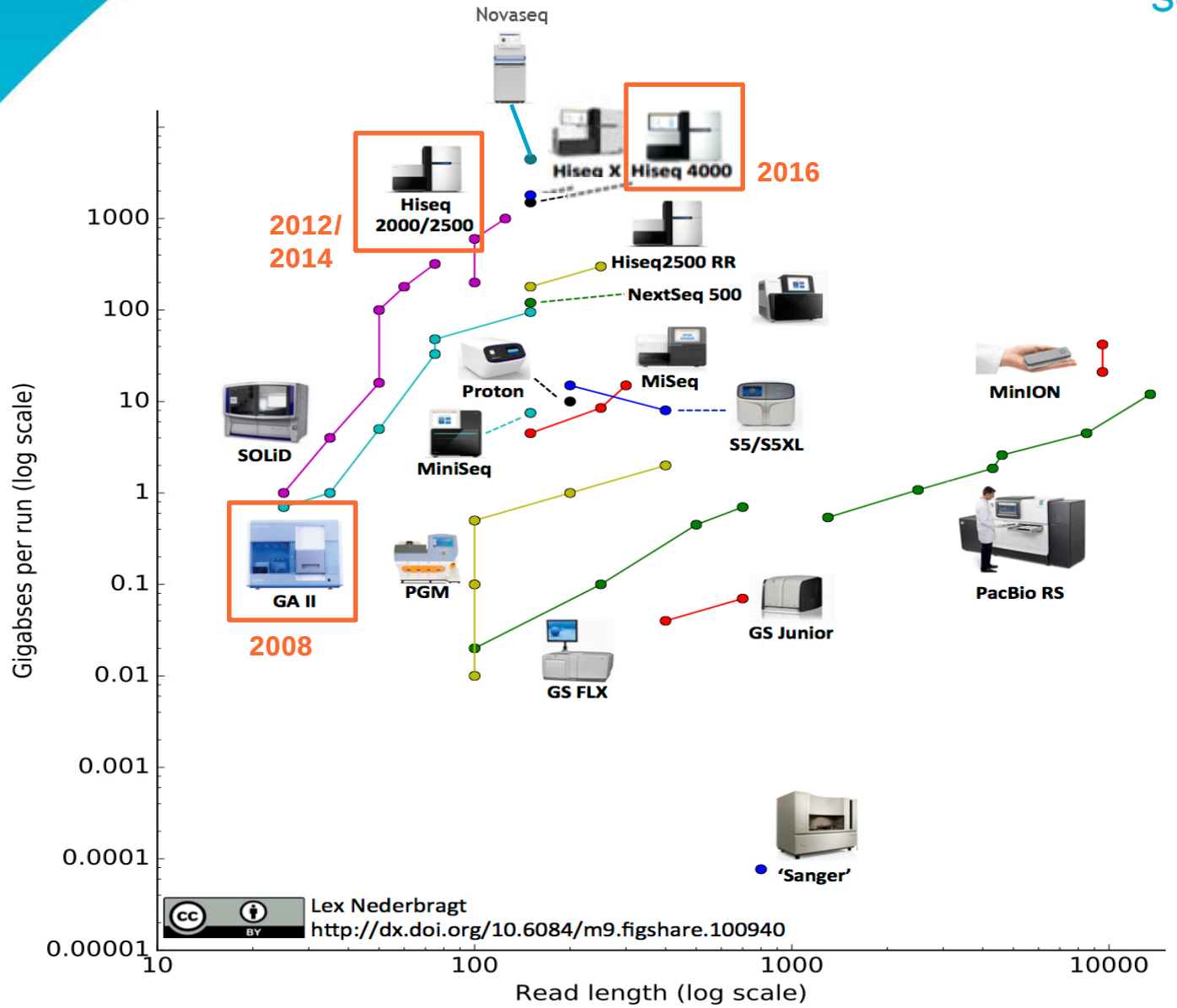
Guarantee: ebay MONEY BACK GUARANTEE | See details
Get the item you ordered or get your money back.
Covers your purchase price and original shipping.

Add to watch list

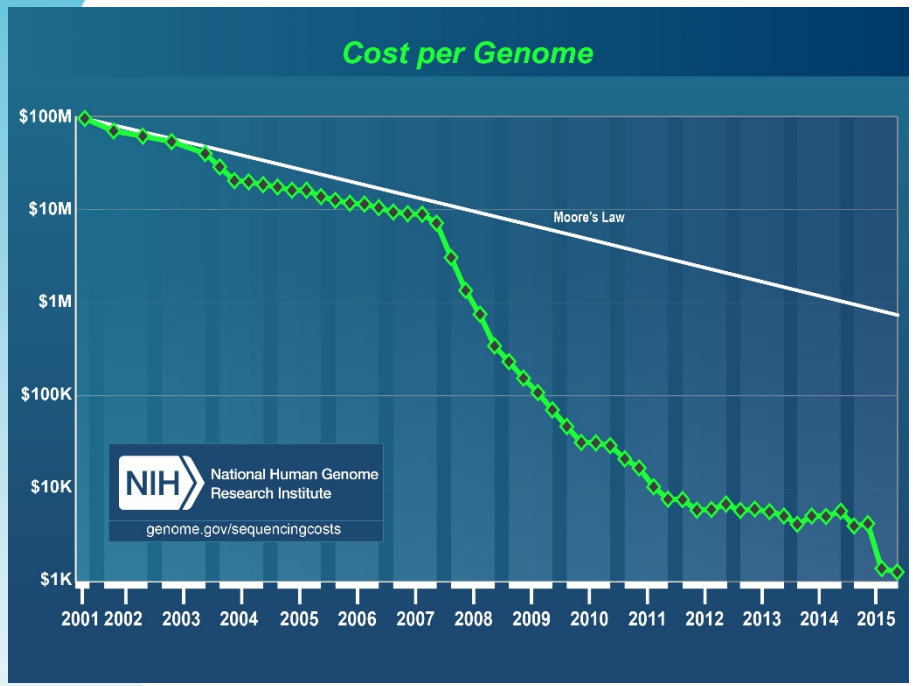
Seller information
madscientist960 (68 ★)
100% Positive feedback

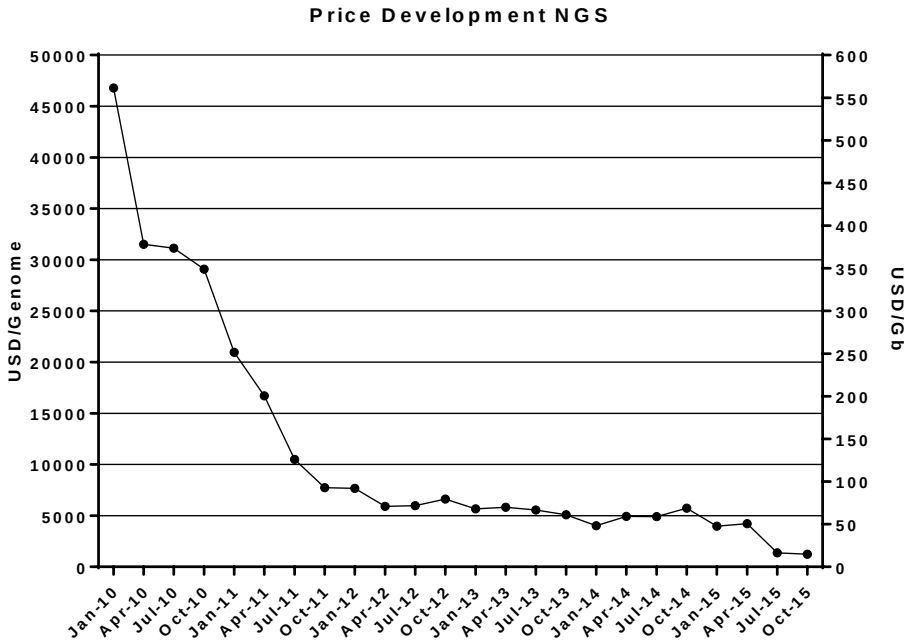
Save this Seller
See other items

Outlook 2016
Sell now
9:18 PM
9/28/2017


Novaseq
Hiseq X
Hiseq 4000
2016
Hiseq 2000/2500
2012/ 2014
Hiseq2500 RR
NextSeq 500
MiSeq
Proton
MinION
SOLiD
MiniSeq
S5/S5XL
GA II
2008
PGM
PacBio RS
GS Junior
GS FLX
'Sanger'
Lex Nederbragt
http://dx.doi.org/10.6084/m9.figshare.100940
Gigabses per run (log scale)
Read length (log scale)
0.00001
0.0001
0.001
0.01
0.1
1
10
100
1000
10
100
1000
10000

Sequencing costs





Wetterstrand KA. DNA Sequencing Costs: Data from the NHGRI Genome Sequencing Program (GSP) Available at: www.genome.gov/sequencingcostsdata. Accessed [2017-09-29].

Balanced sequencer portfolio to accommodate all research needs

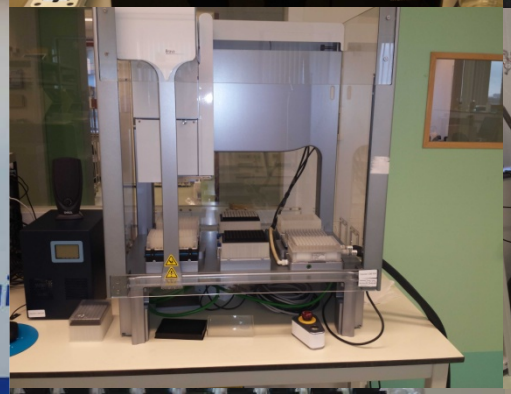
	HiSeq 4000	NextSeq 500	PacBio Sequel / RSII
Read length (max)	150 bp	150 bp	20 - 60 kb
Total run time	1 - 3.5 day	Up to 1 day	1 - 2 days
Output / run	~2000 Gb	~120 Gb	~5 Gb
Exomes per run	Up to 192	~12	~1
Major applications	**Production scale sequencer for all applications**	**Targeted panel sequencing Fast diagnostics**	**Long read seq *de novo* seq Pseudogenes**

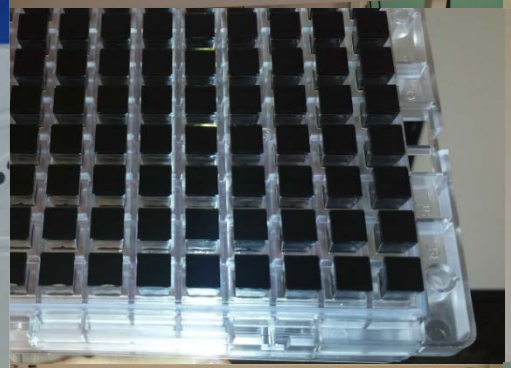
Lab Tour

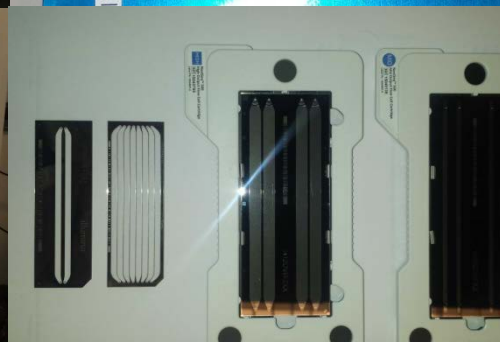
Dance
Technologies
RainDrop
Source

NextSeq 500
Welcome to NextSeq
illumina

HiSeq 2500
Illumina



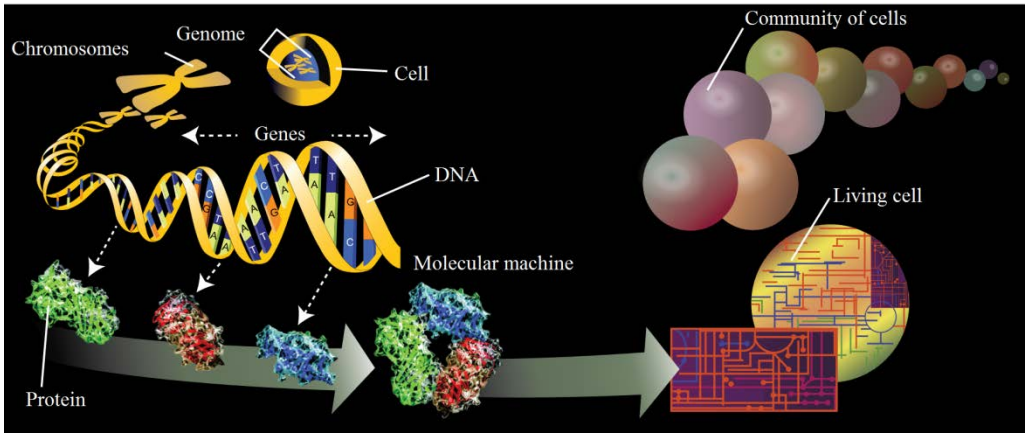




Portfolio GenomeScan

Advanced technology for ‘omics’ experimentation

- Next Generation Sequencing
- (Hydroxy)methylation
- Gene Expression
- Genotyping
- Bioinformatics



“Omics aims at the collective characterization and quantification of pools of biological molecules that translate into the structure, function, and dynamics of an organism or organisms.”

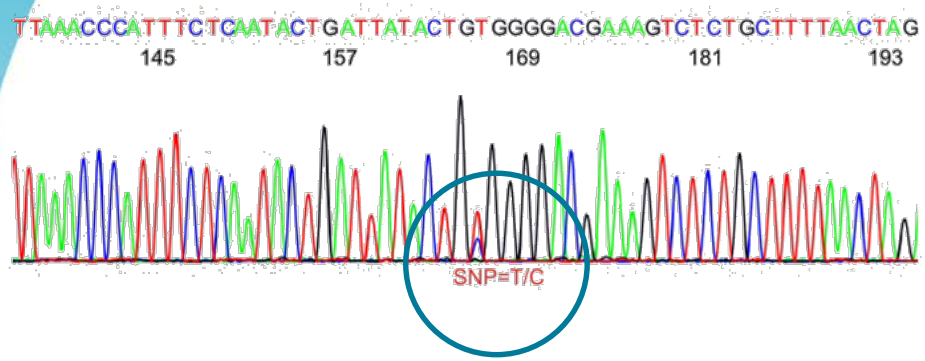
Next Generation Sequening

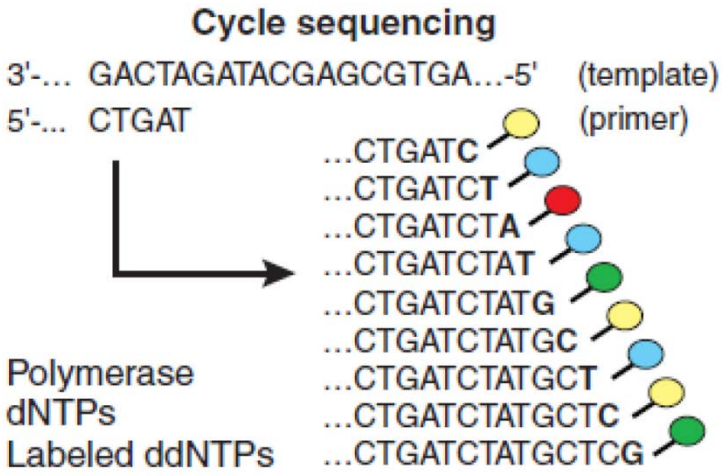
Common theme

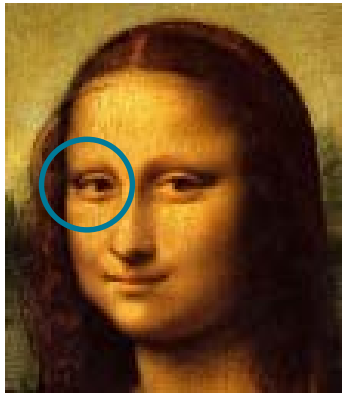
- Construction of a library
- Amplification
- Nucleotide readout (>100 million reads in parallel)
- Vast amount of digital data

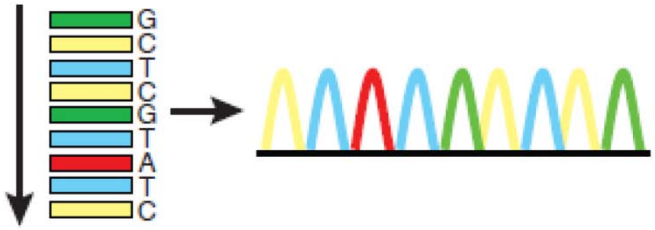
Sanger sequencing

Traditional









genomescan.nl

Advantages and limitations of NGS

- Much cheaper and higher throughput compared to Sanger
- Association of DNA/RNA features with phenotype
- Can be performed without design
- Transcriptome analysis
- Targeted (re)sequencing

- Limitations
  - Expensive equipment and “cost per sample”
  - Short(er) reads, bias, PCR-errors
  - Data-analysis can be (extremely) time-consuming
    - Systems Biology
    - Data quality; statistics

Microarrays vs sequencing

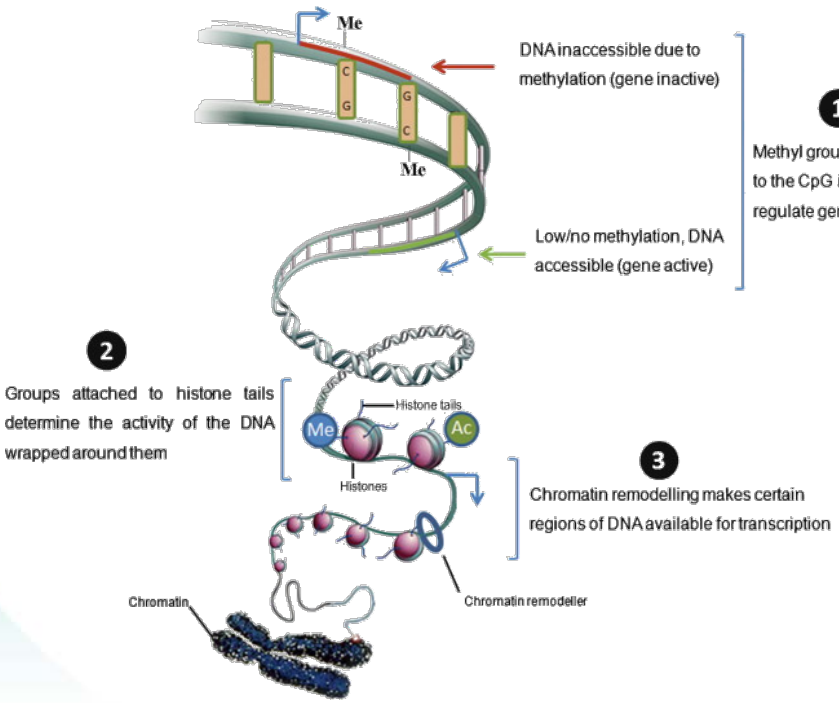
- Still cost-effective for several applications
- Fixed design; focus on data you need
- Established bioinformatics
- Ease of interpretation
- Hybridization on arrays => sequencing on arrays

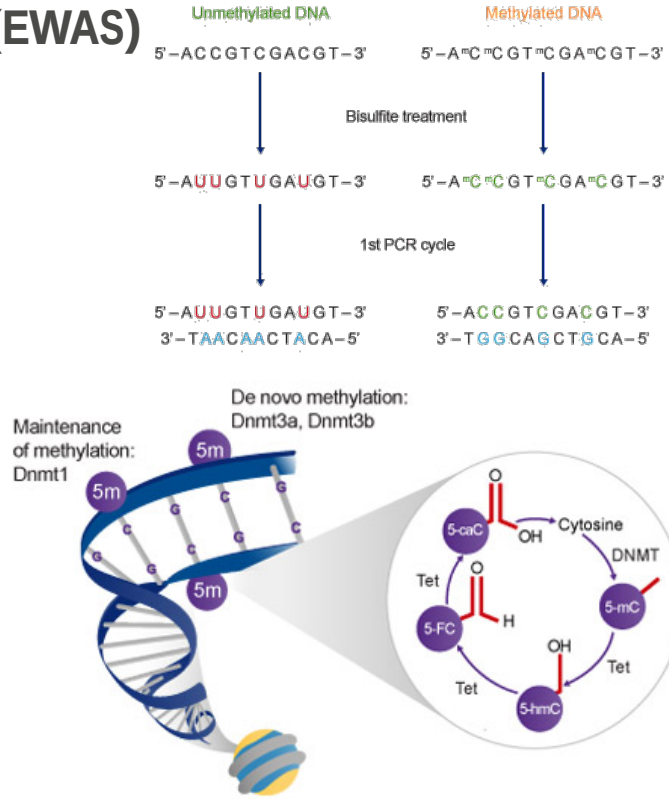
Array service

Epigenome-wide association studies (EWAS)

DNA (hydroxy)methylation service

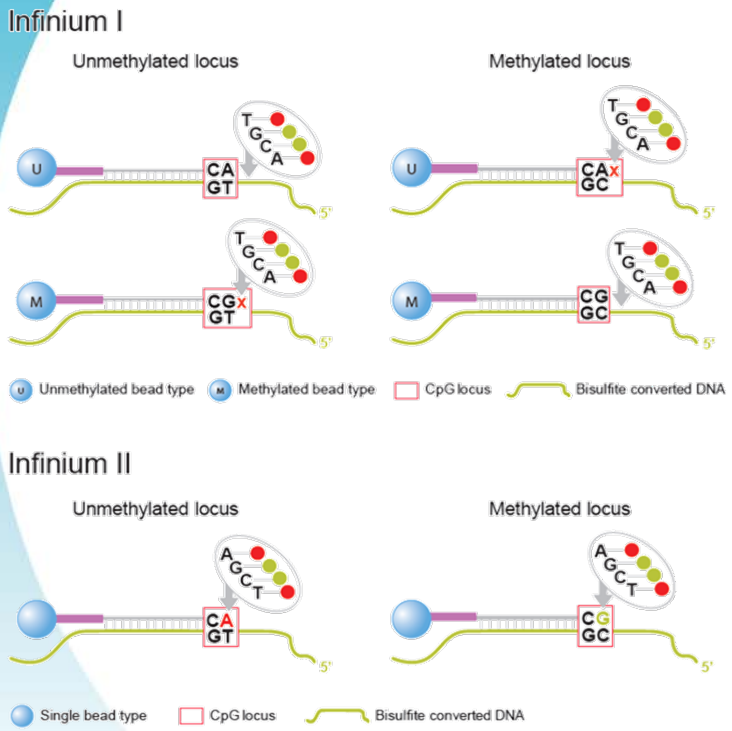
Illumina Infinium 850k

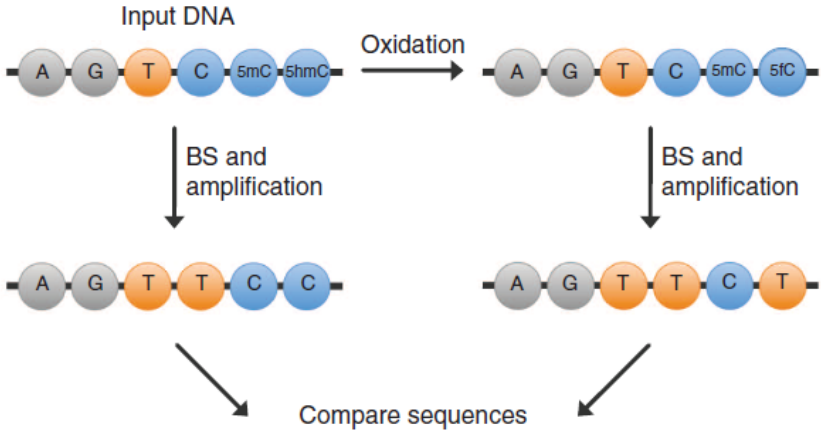




genomescan.nl

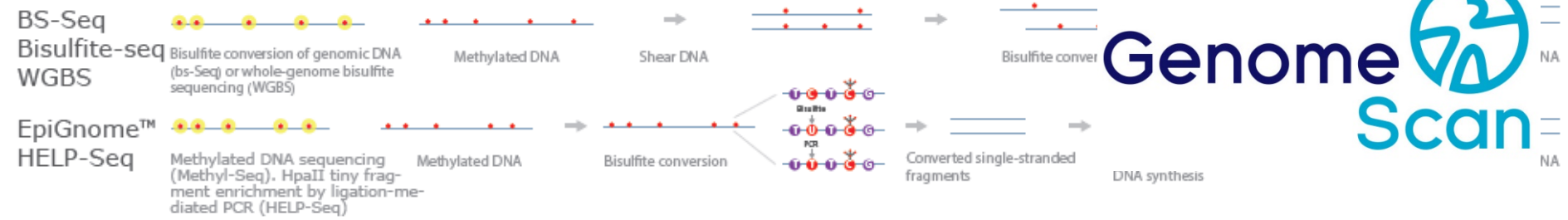
Illumina methylation BeadChip



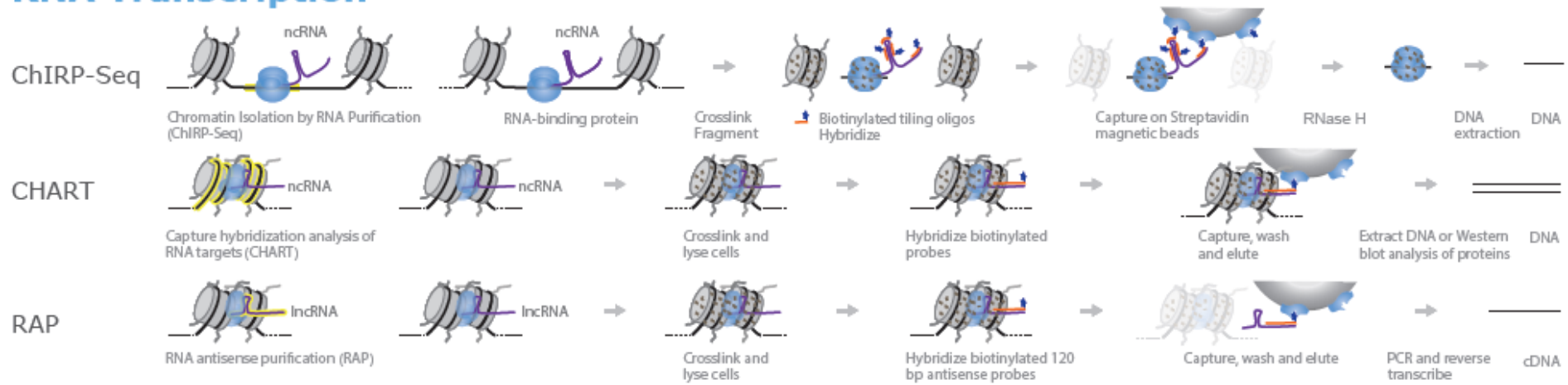


Base	Sequence	BS Sequence	oxBS Sequence
C	C	T	T
5mC	C	C	C
5hmC	C	C	T

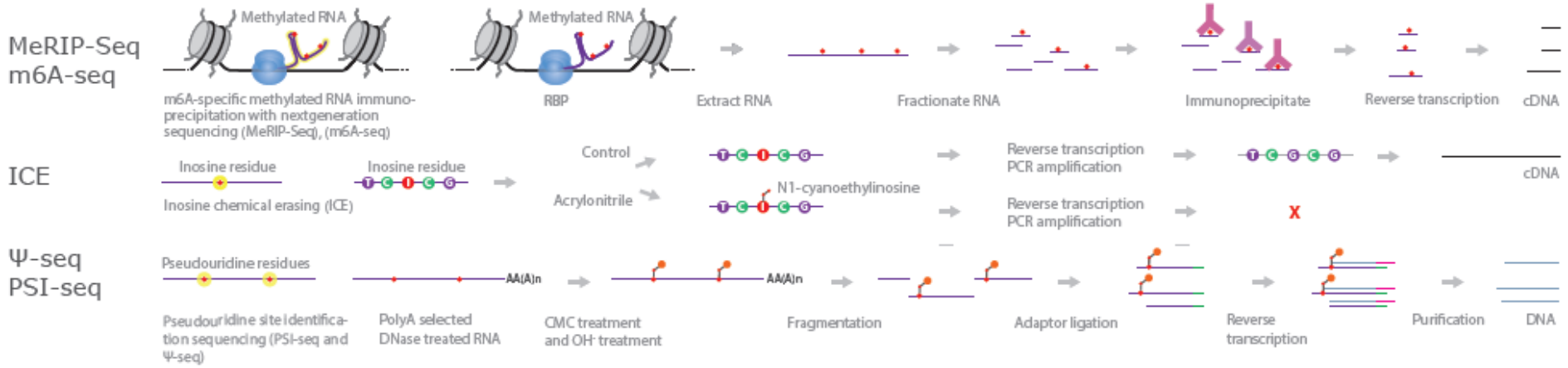
Methylation



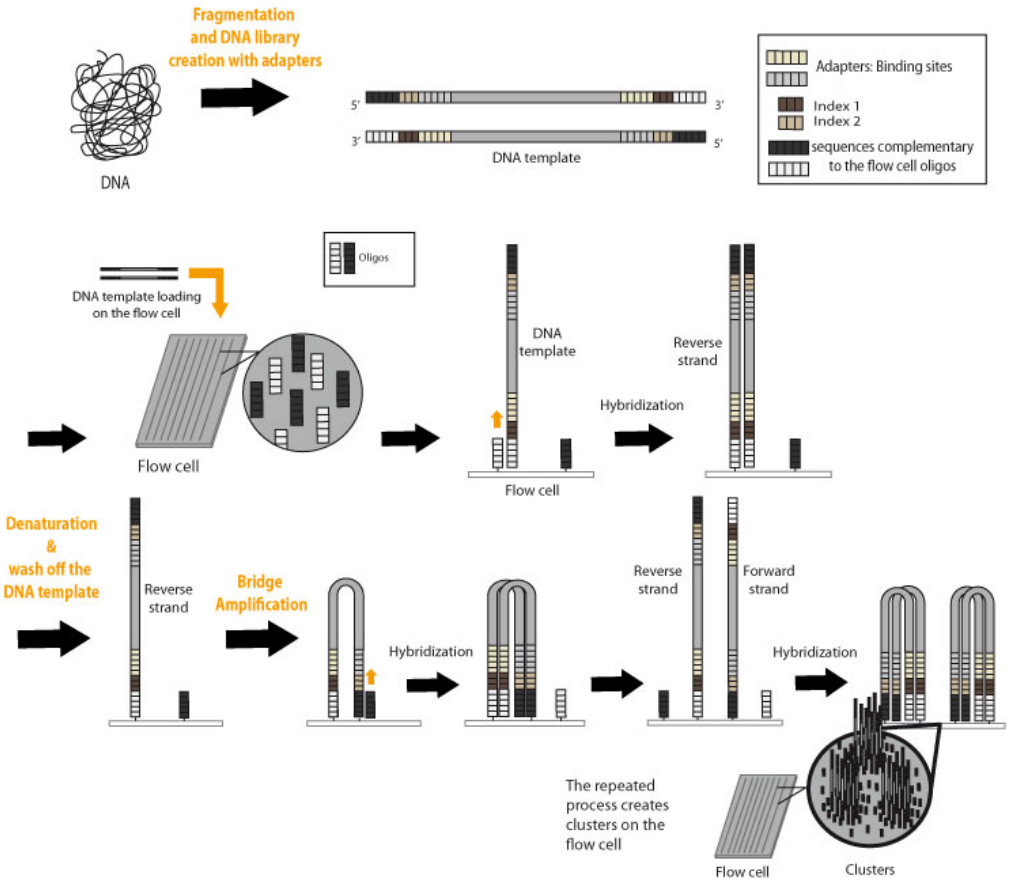
RNA Transcription

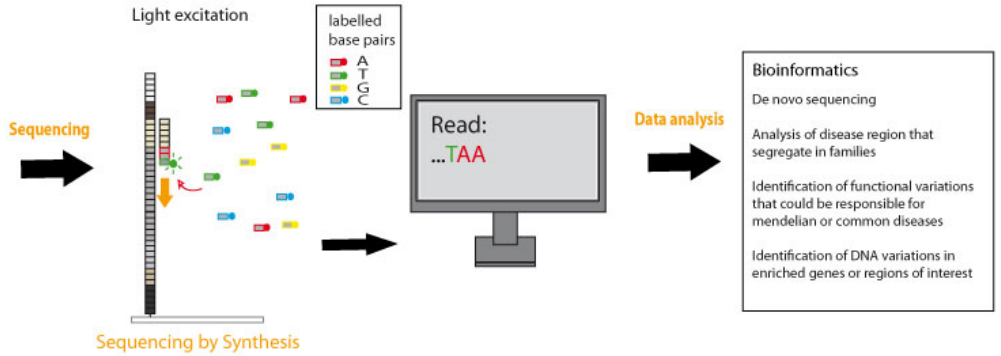


RNA Modifications



Next generation sequencing





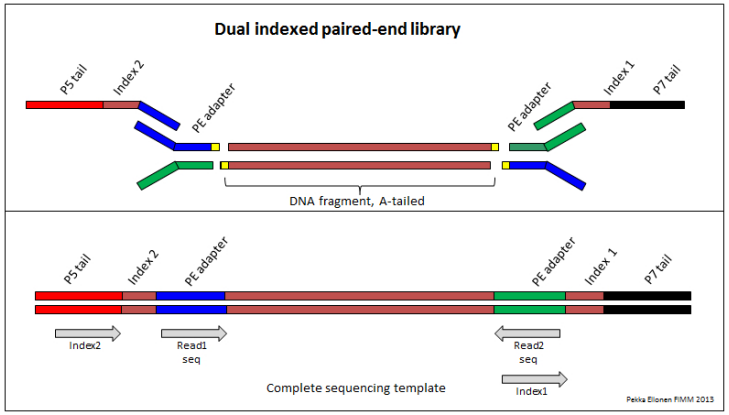
Bioinformatics

De novo sequencing

Analysis of disease region that segregate in families

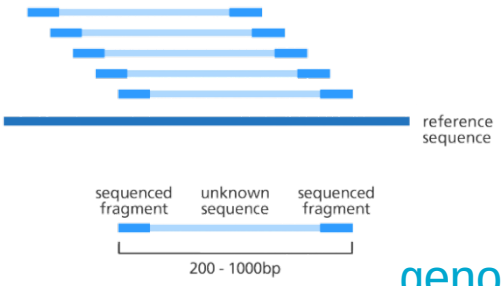
Identification of functional variations that could be responsible for mendelian or common diseases

Identification of DNA variations in enriched genes or regions of interest



Single-end reads

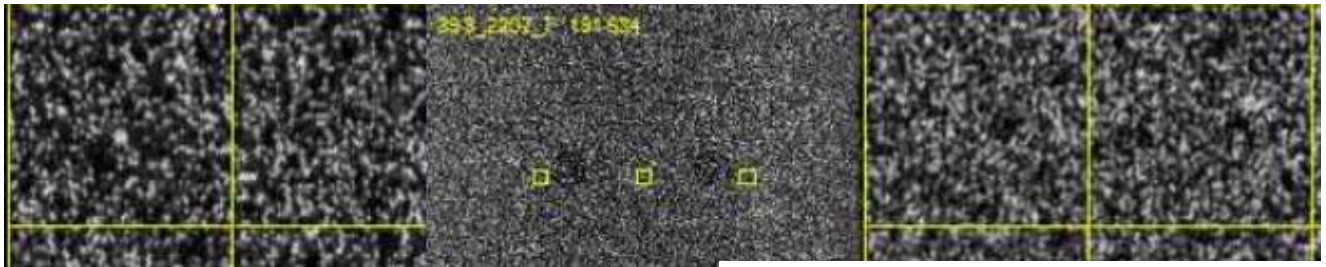
Paired-end reads

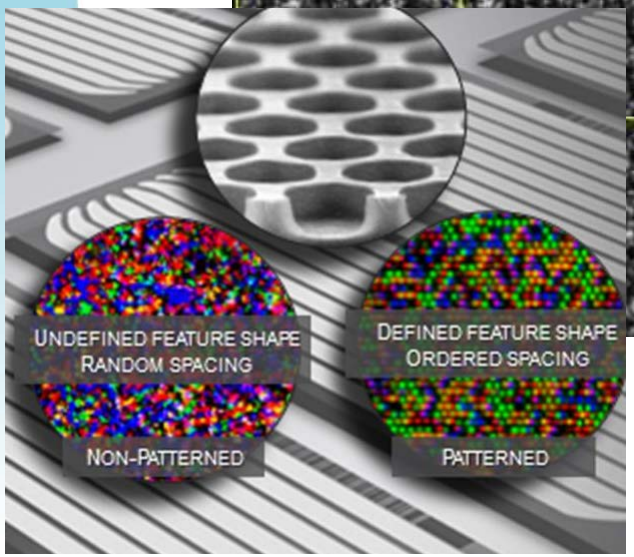


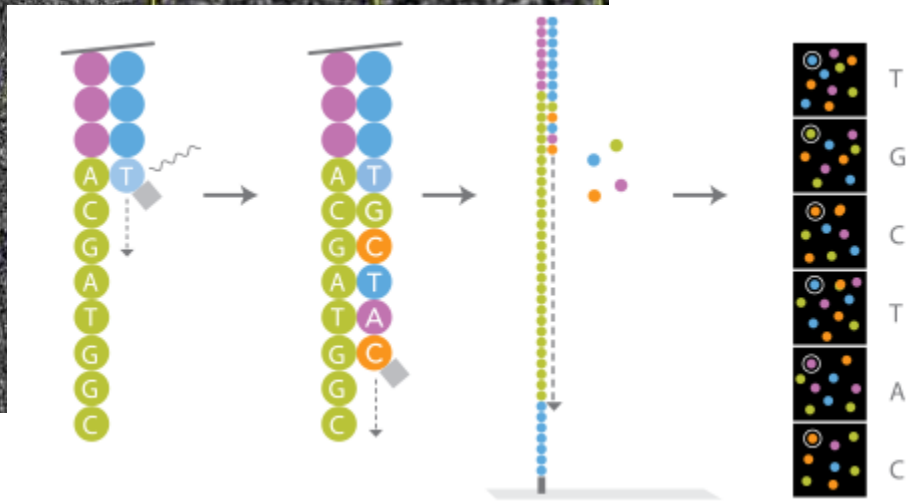
genomescan.nl

HiSeq clusters

Sequencing-by-synthesis (SBS)







NGS Services

Genome Analysis

de novo sequencing
Resequencing
ChIP sequencing
Metagenome sequencing

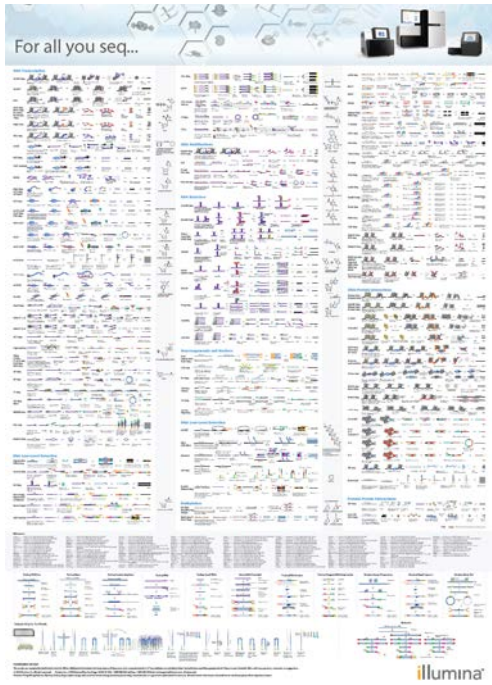
Targeted Analysis

Exome sequencing
Custom targeted sequencing
Sequencing of amplicons and genomic fragments

Transcriptome Analysis

mRNA sequencing: poly-A selection
RNA sequencing: rRNA depletion
Strand specific RNA seq
miRNA & small RNA sequencing

‘Ready-to-Run’



General workflow

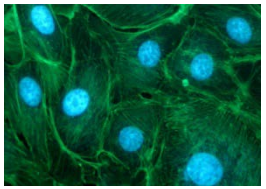
From sample to data

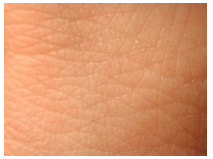
Sample selection

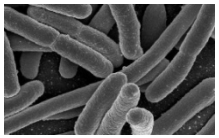
Library preparation

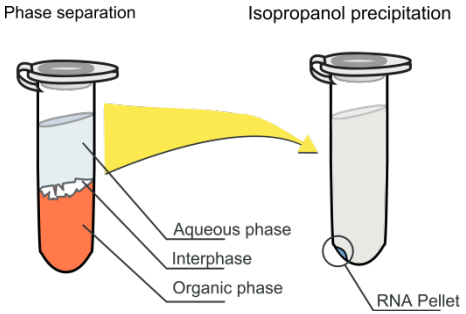
Sequencing

Bioinformatics







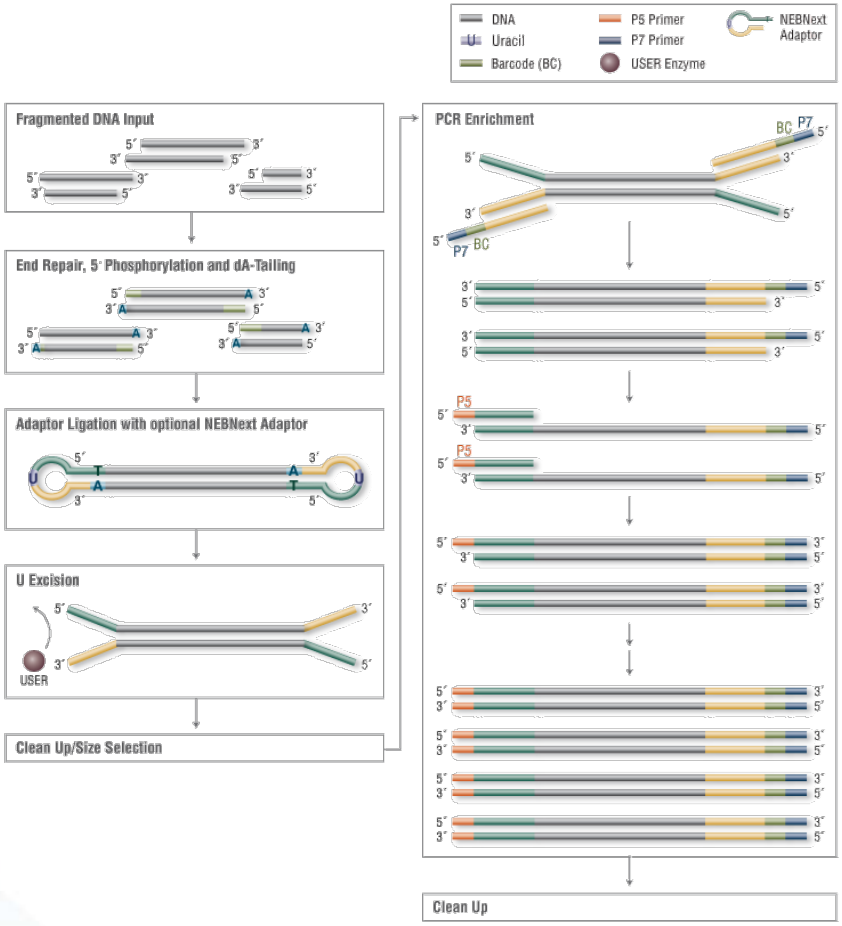


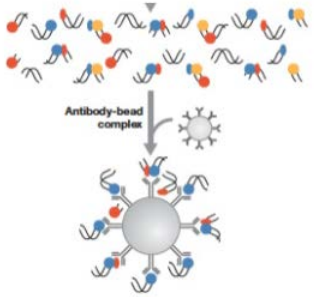
genomescan.nl

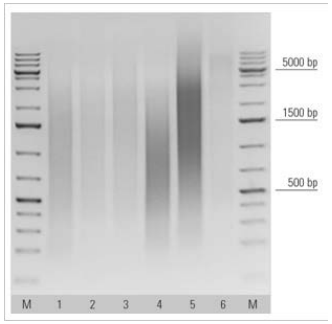
Genome Scan

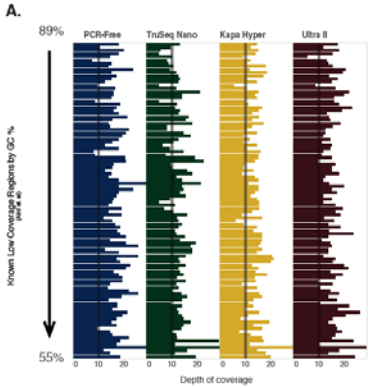
DNASeq

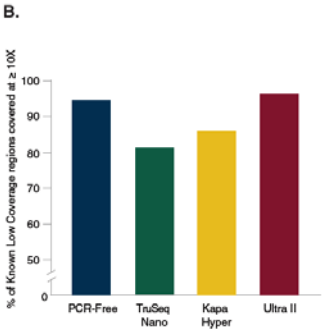
NebNext Ultra II







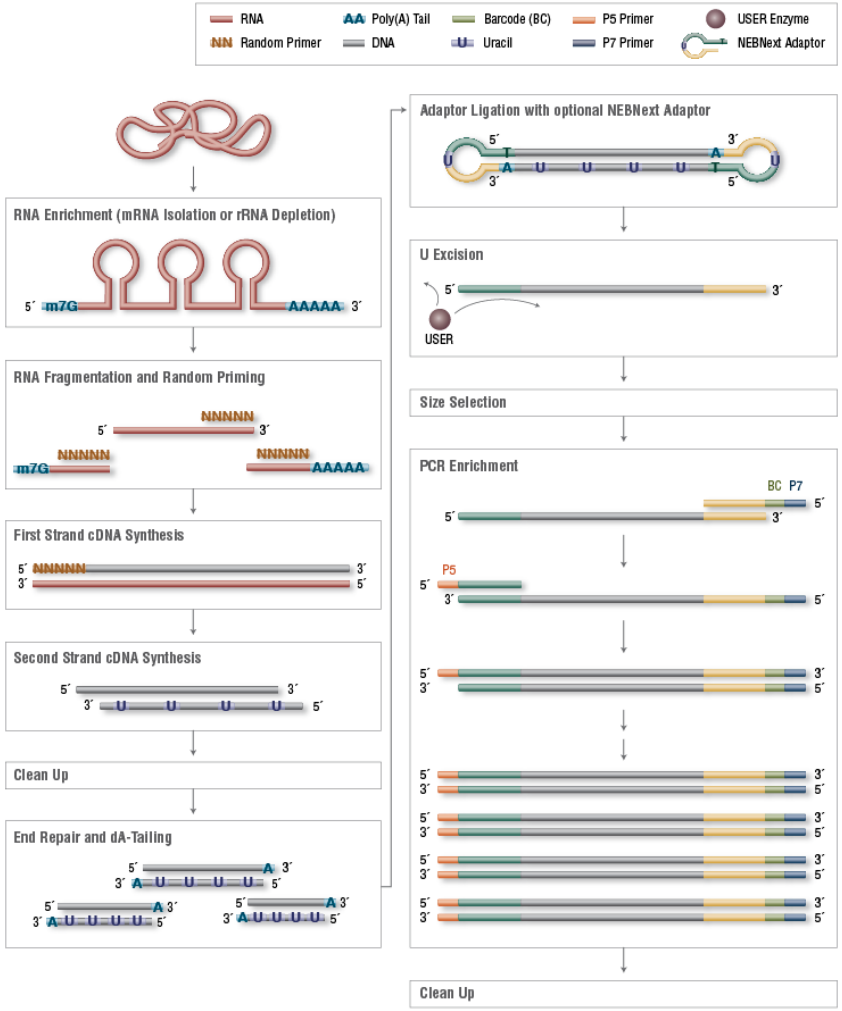


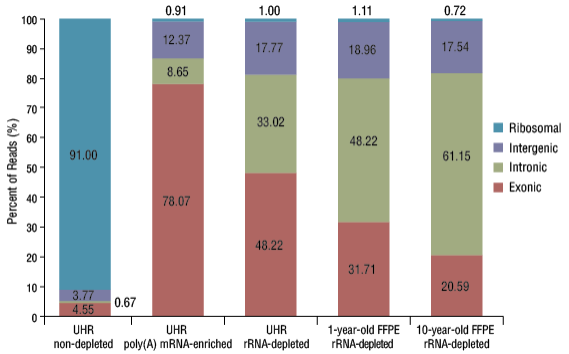


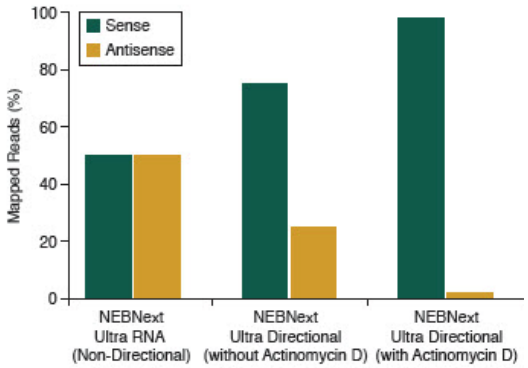
Genome Scan

Stranded RNAseq

NebNext Ultra RNA





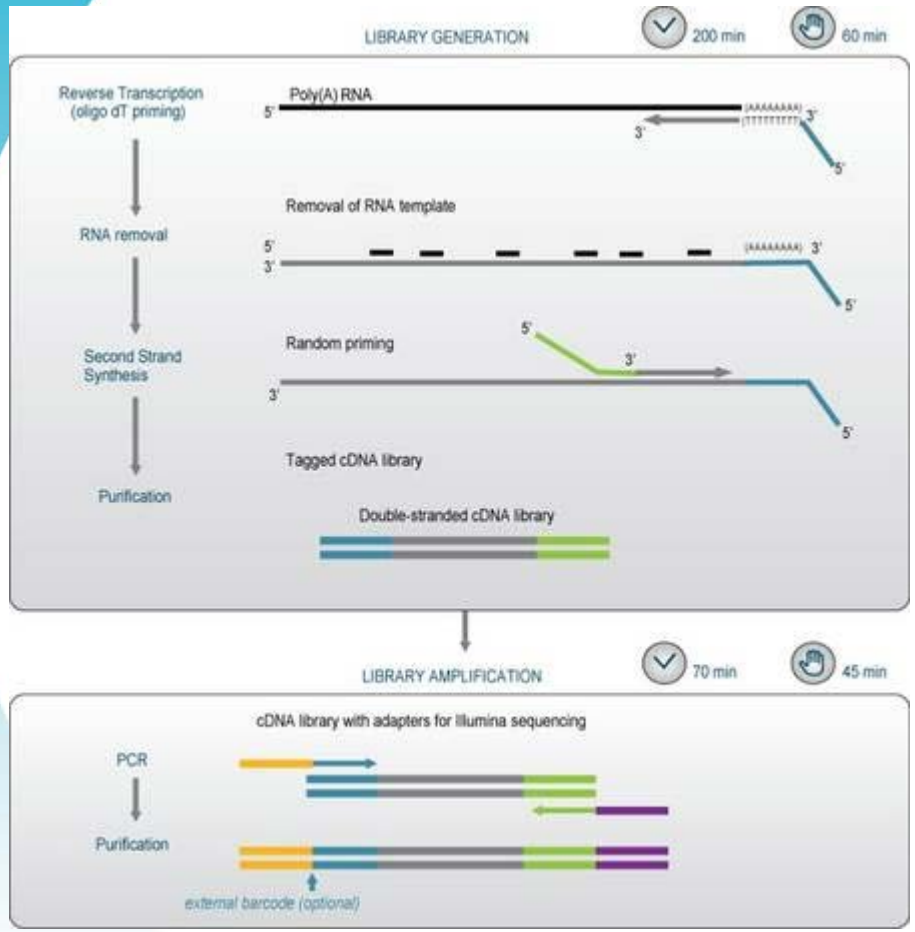


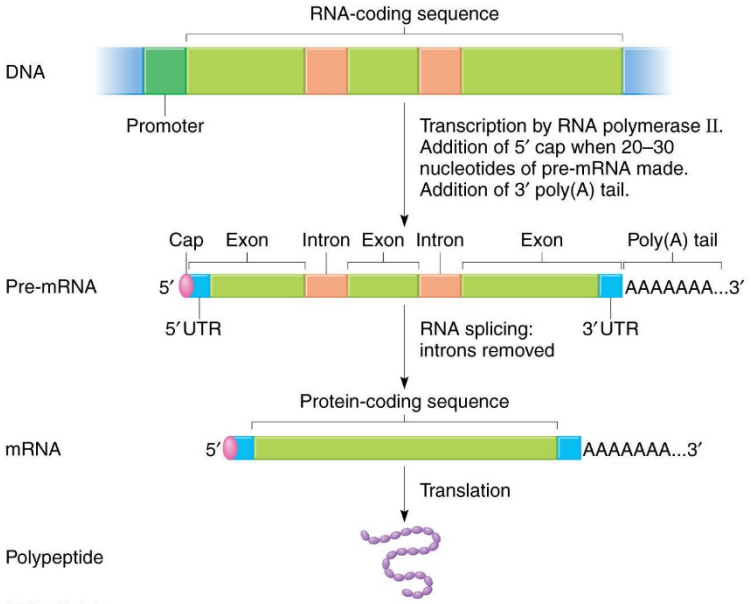
genomescan.nl

Genome Scan

Lexogen

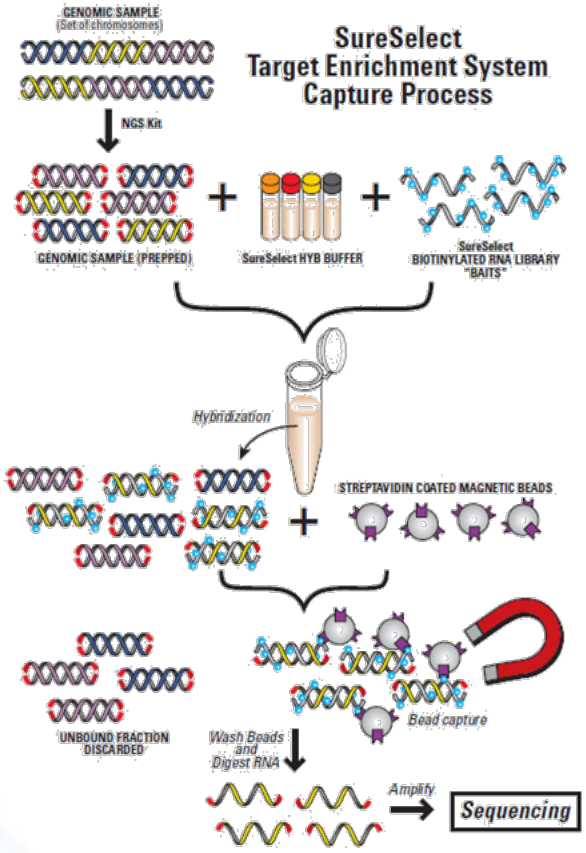
Counting 3'-ends

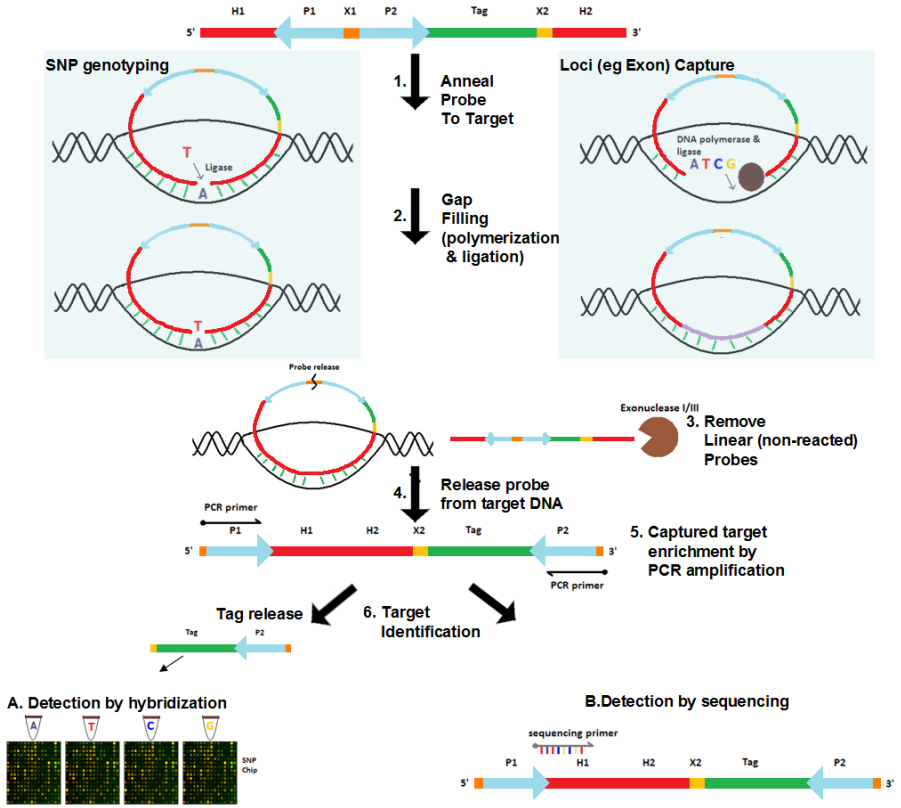




Genome Scan

Targeted (re)sequencing





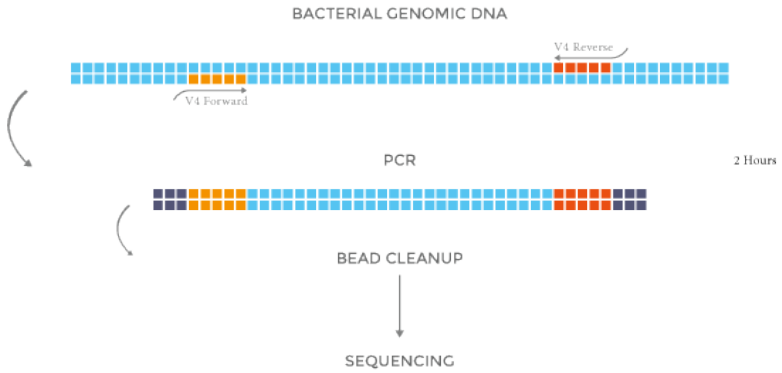
genomescan.nl

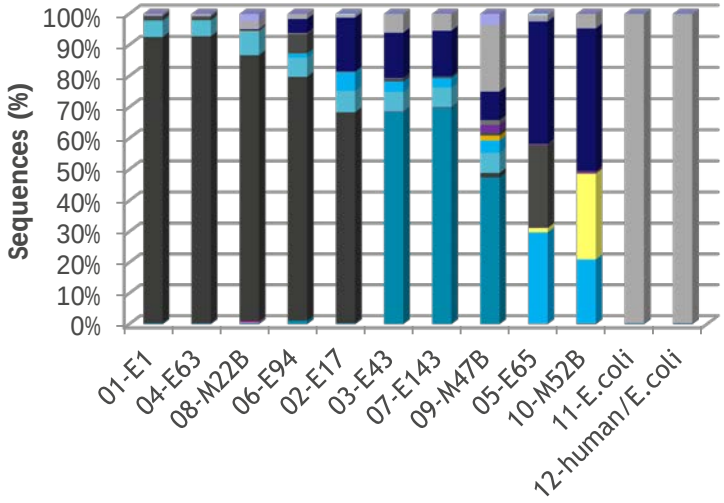
Genome Scan

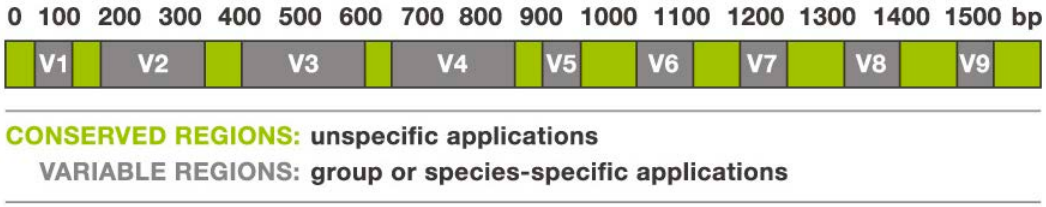
Microbiome

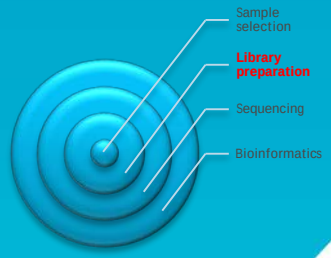
NEXTflex DNA Sequencing Kit

- Sequencing V4 region of 16S







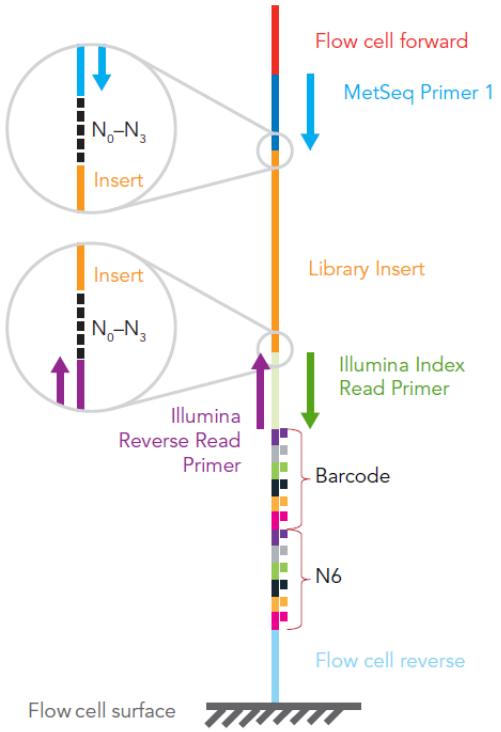


Genome Scan

Methylome

850k arrays, Capture, RRBS, WGBS

- Illumina 850k EPIC
  - Also suitable for hydroxymethylation
- SeqCap Epi CpGiant, RRBS & WGBS



5′ (Ad)YGG(BCOT)TCG(Ad) 3′

and

3′ (Ad)GCT(BCOB)GGY(Ad) 5′

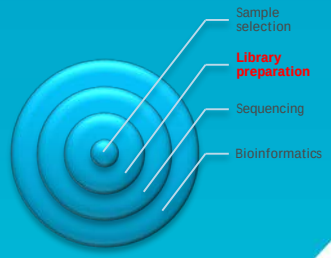
BCOT = Bisulfite Converted Original Top genomic strand

BCOB = Bisulfite Converted Original Bottom genomic strand

Y = C or T, depending on methylation status

Blue = DNA sequence derived from library construction

0 diversity bases added	5′	YGG(BCO)	BCO = Bisulfite-Converted Original genomic strand
1 diversity base added	5′	DYGG(BCO)	Y = C or T, depending on methylation status
2 diversity bases added	5′	DDYGG(BCO)	D = A, G, or T
3 diversity bases added	5′	RDDYGG(BCO)	R = A or G



Genome Scan

Methylome CpGs

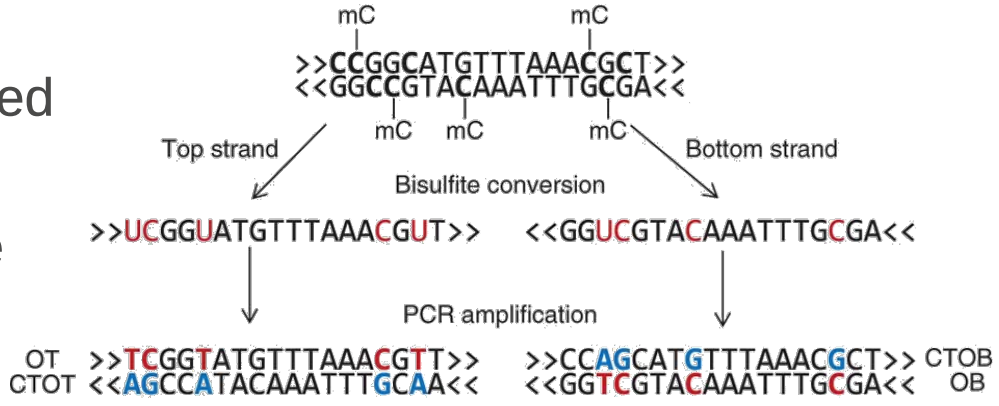
Technology	CpGs *10^6	Data
850k	~0.9	'Array'
Capture	~5.5	6-8 Gb
RRBS	~6.8	7.5 Gb
WGBS	~28	3-100 Gb

Genome Scan

Methylome analysis

(BioIT) challenges

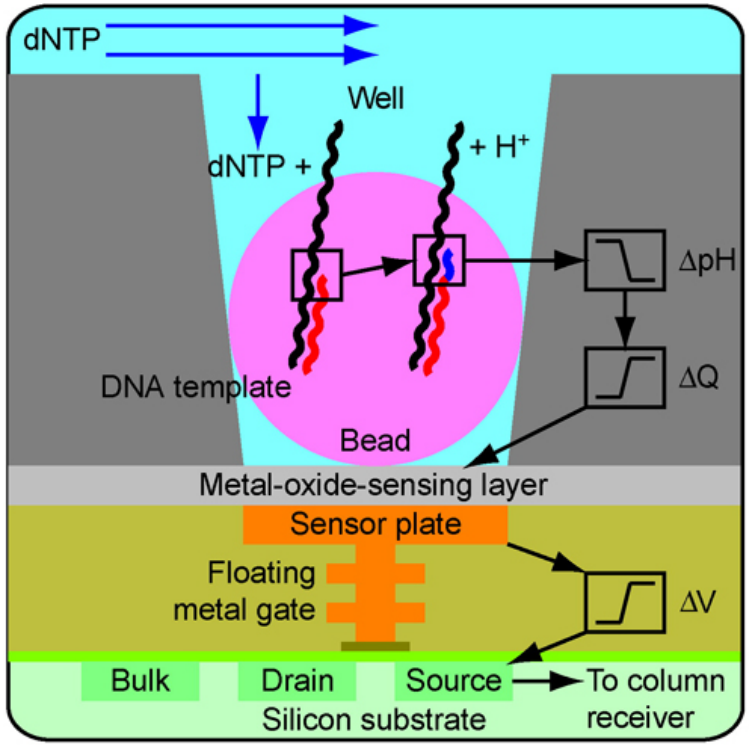
- No ‘exact’ mapping
- Complexity from 4 to 3 (or 5) bases
- T can align to G; G doesn’t align to T
- 4 possible strands
- Occurrence of C/T SNPs
- Cluster complexity reduced
- Sticky *MspI*-sites
- Completeness of bisulfite treatment
- SBR vs DMR

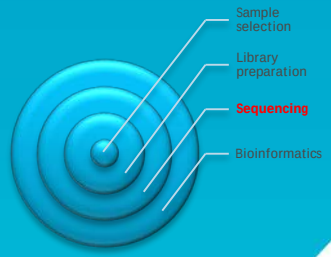


Genome Scan

‘Post-light’ sequencing

Ion Proton



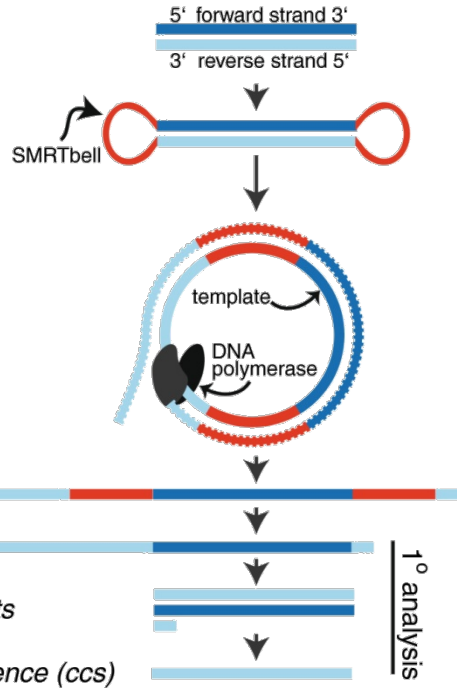


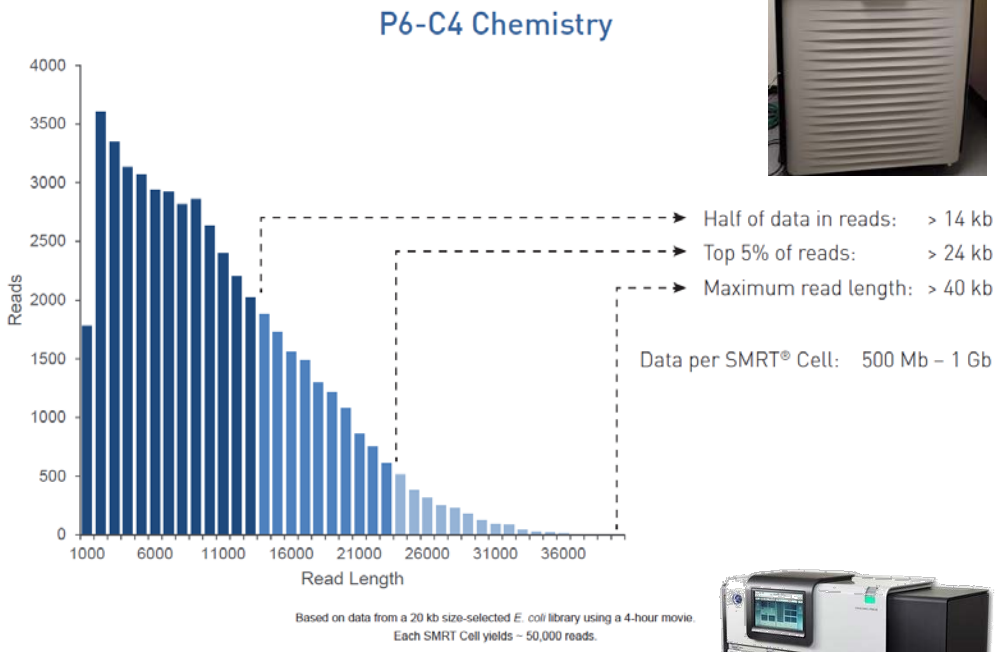
Genome Scan

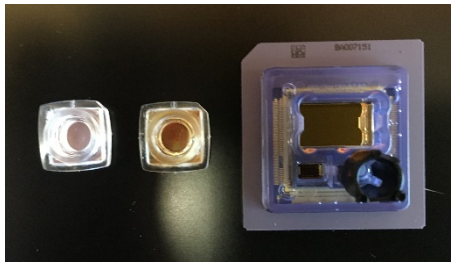
Ultra-long reads

PacBio *RSII* / Sequel

1. generate amplicon
2. ligate adaptors
3. sequence
4. data analysis

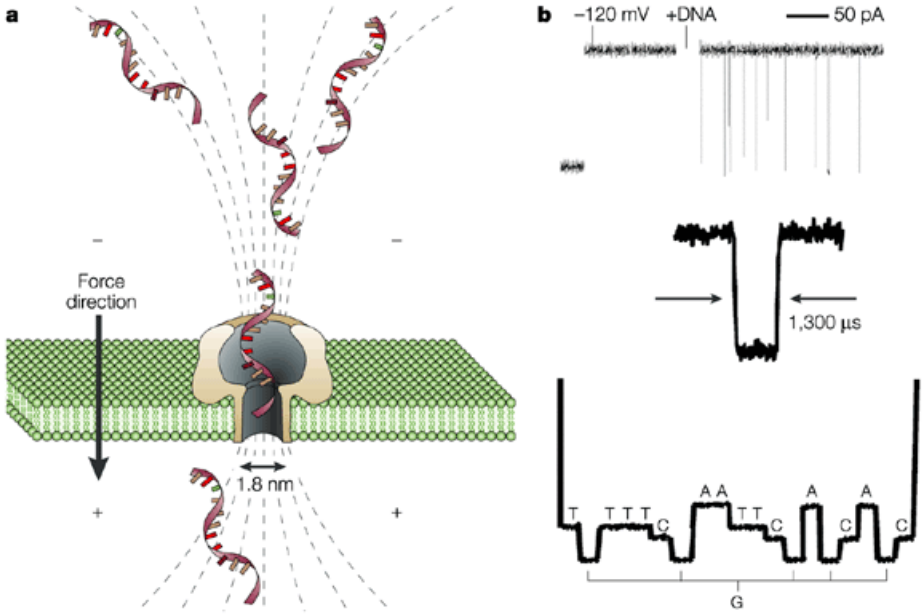






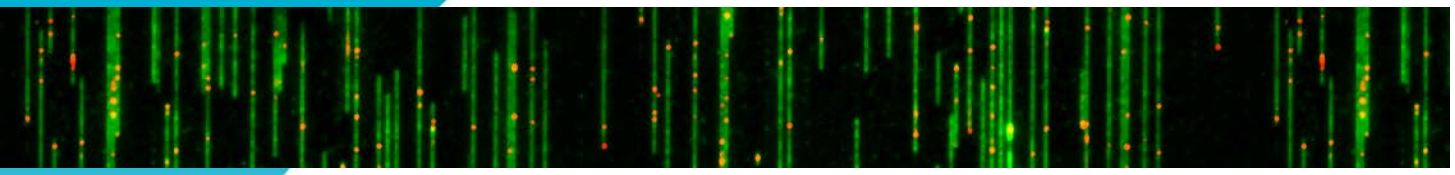
genomescan.nl

Oxford Nanopore

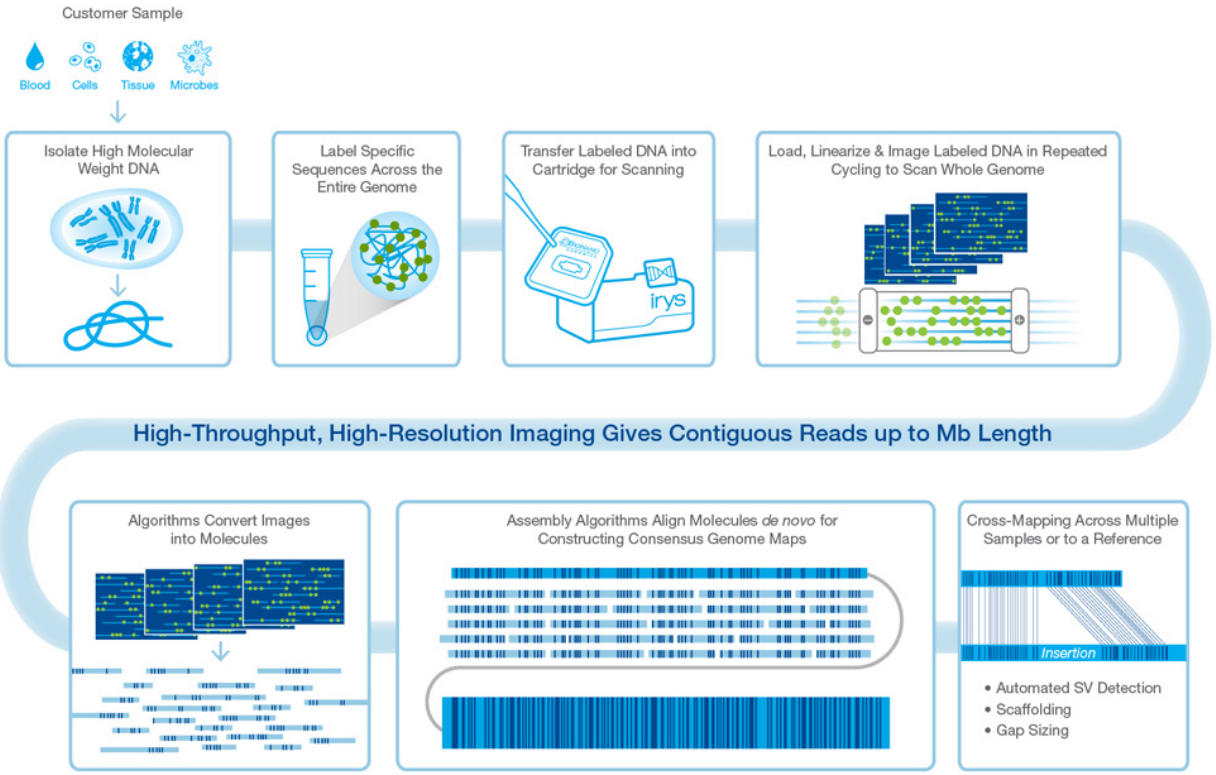


genomescan.nl

Genome Scan



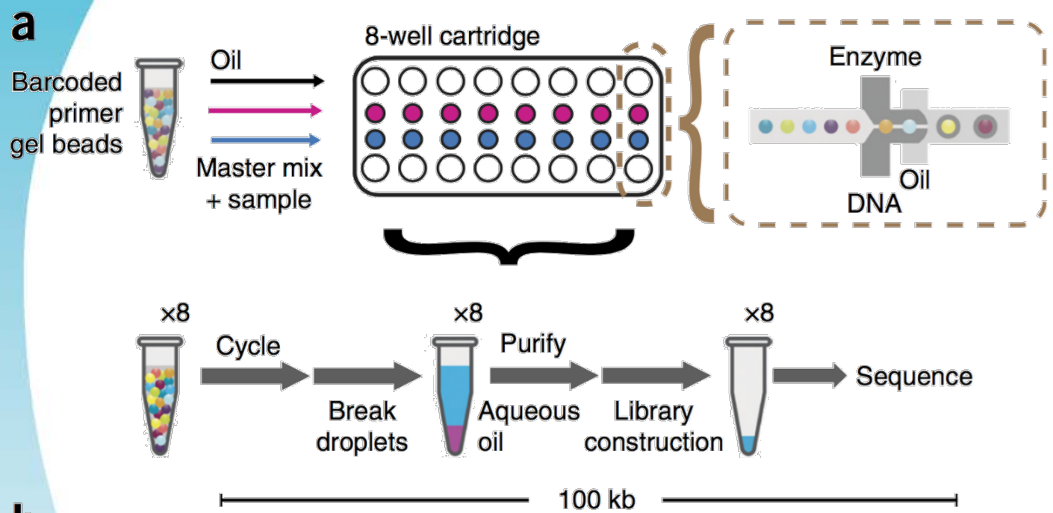
BioNanoGenomics

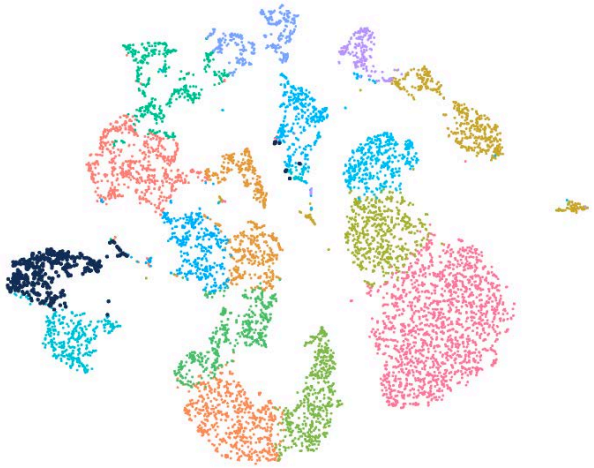


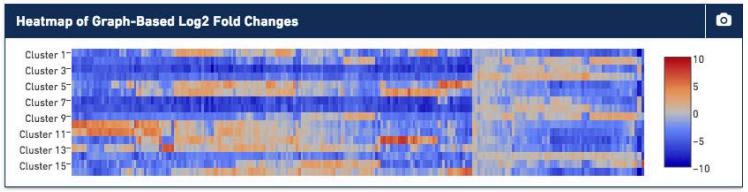
genomescan.nl

Genome scan

10X Genomics



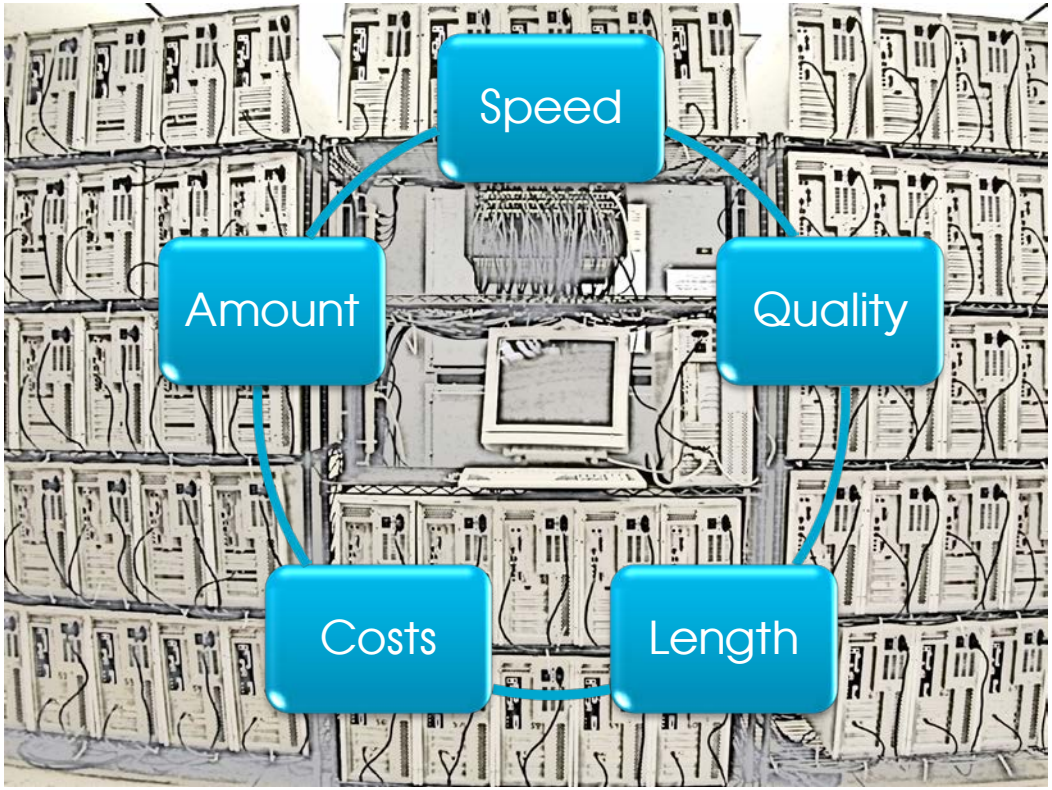




genomescan.nl

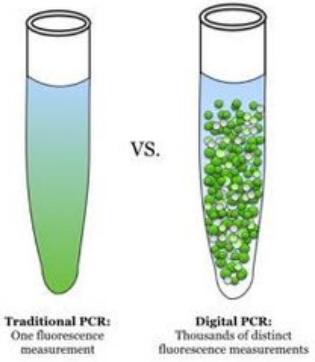
Genome Scan

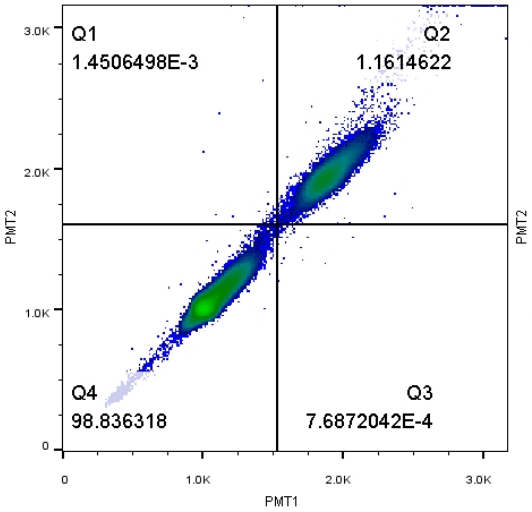
Sequencing trade-off

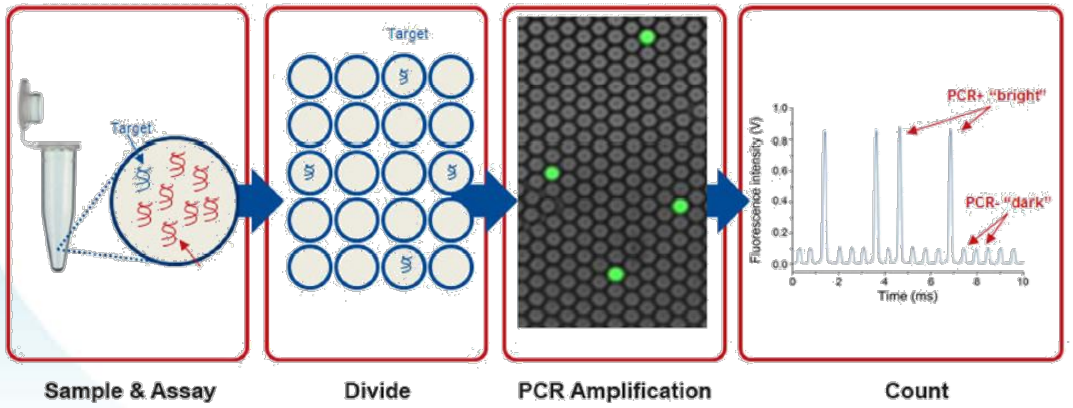


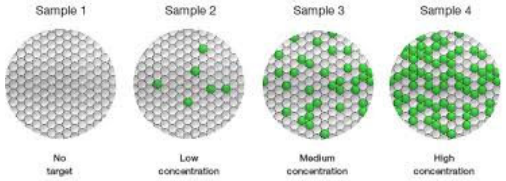
Digital droplet PCR

Bio-Rad



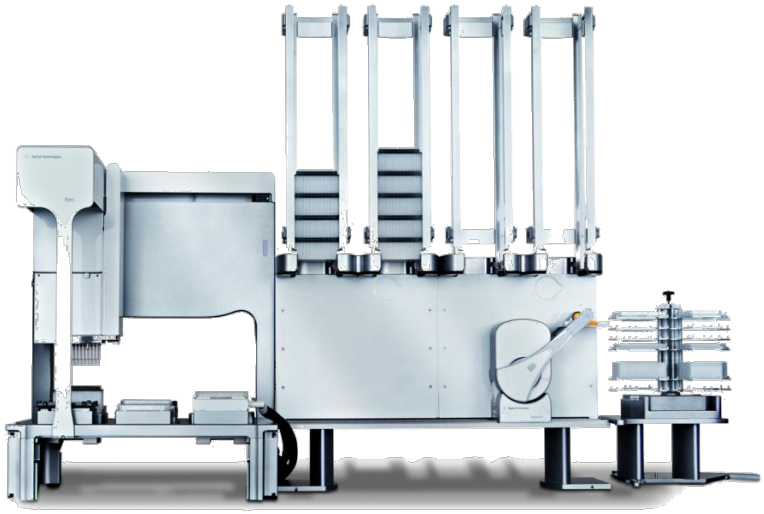


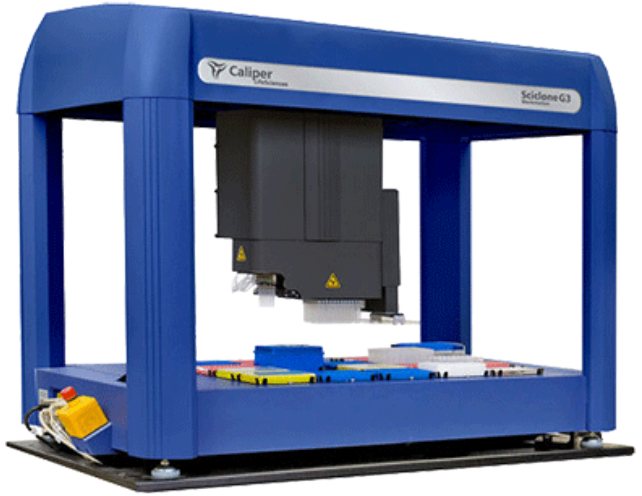


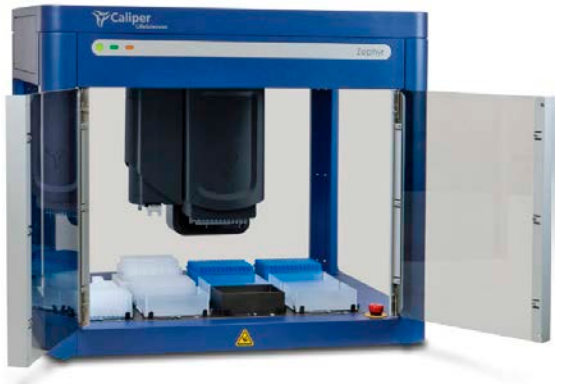


Genome Scan

Robotics & advanced HT-QC



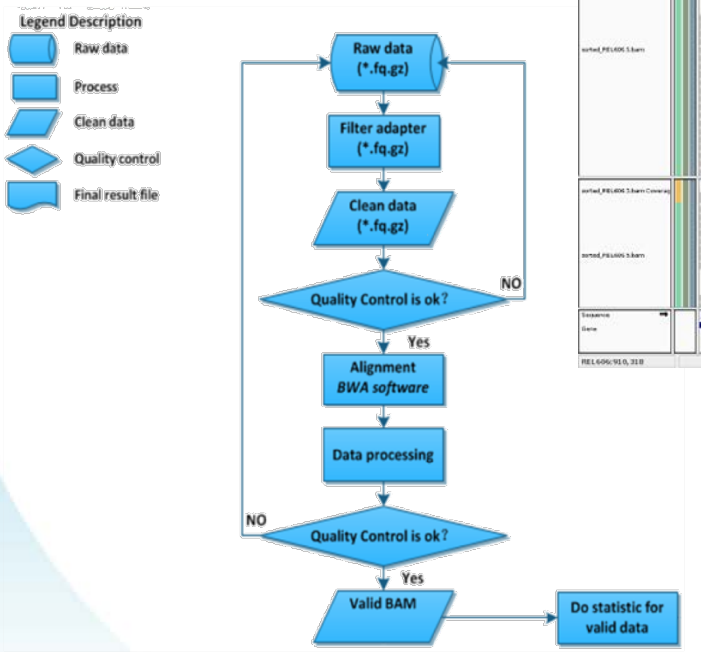


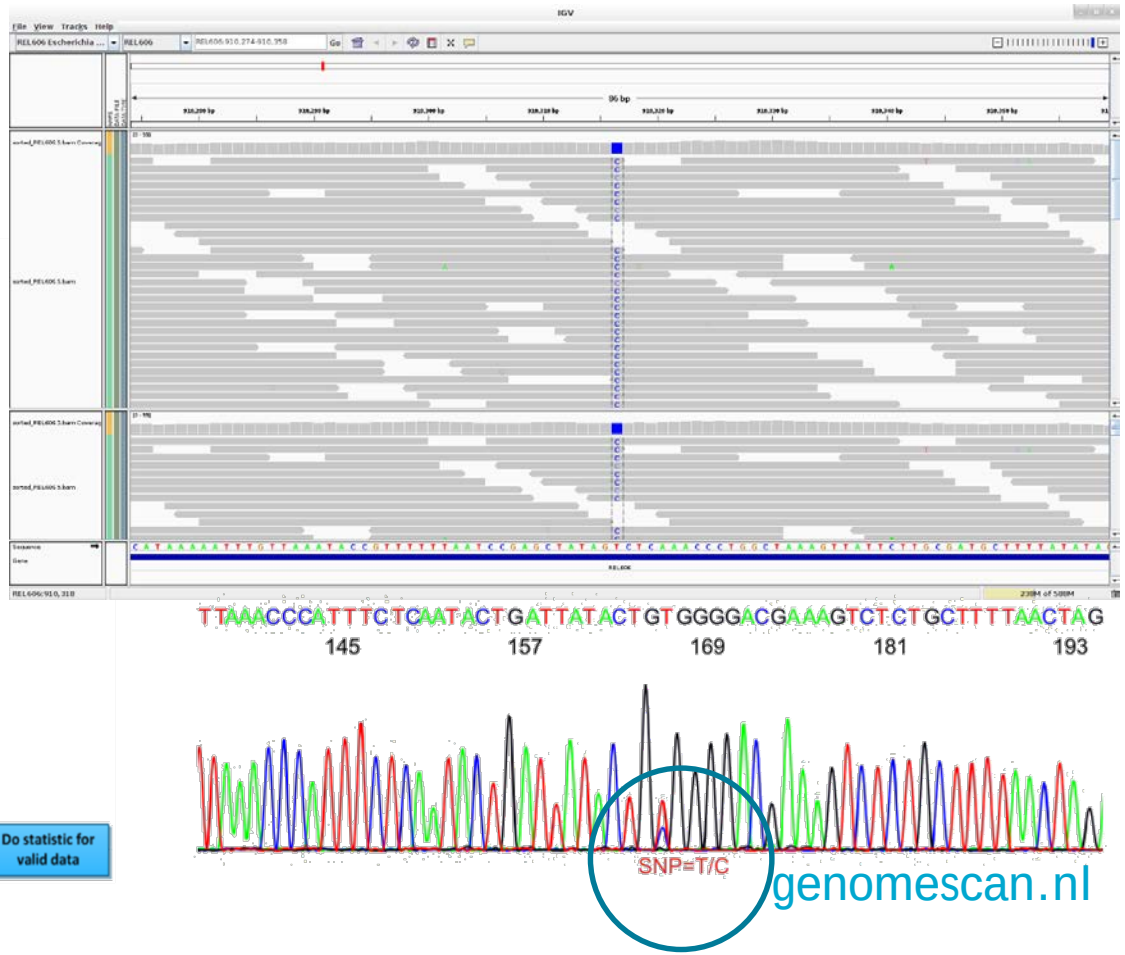


genomescan.nl

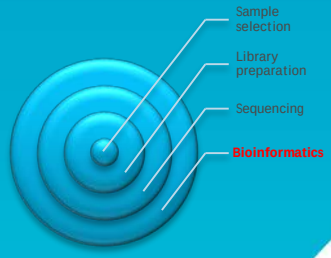
Genome Scan

Bioinformatics





genomescan.nl



Genome Scan

Bioinformatics

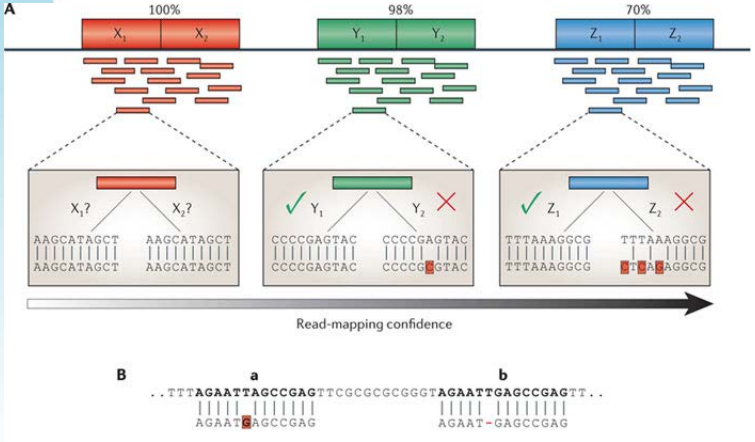
Data quality assessment

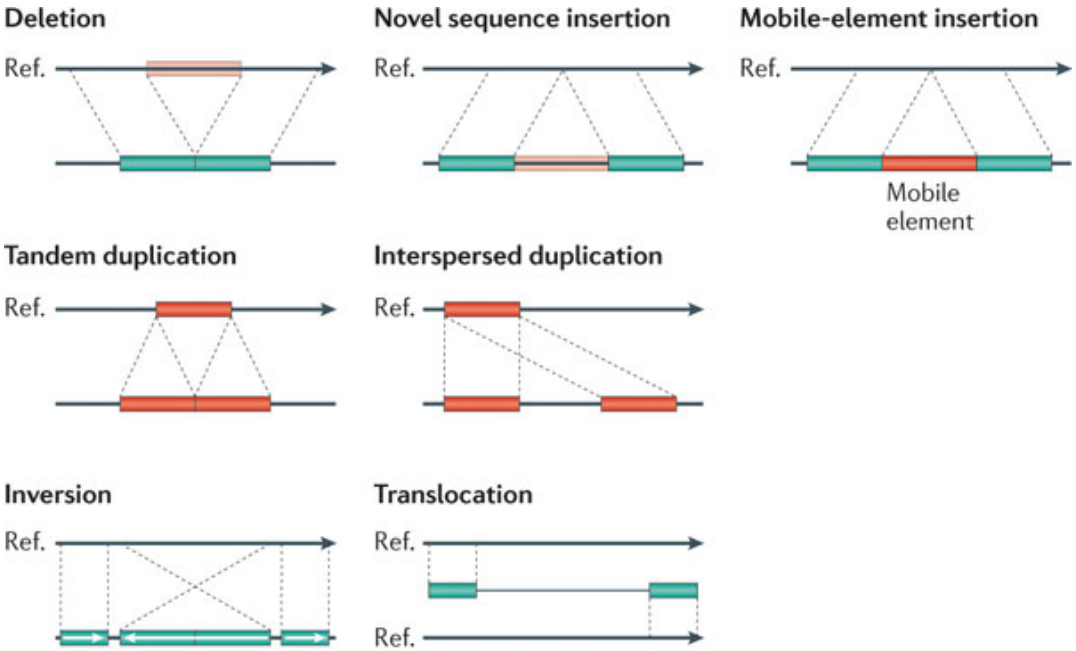
Data quality metrics & filtering

Data analysis pipelines

Whole Genome (re)sequencing
Targeted (re)sequencing
Genotyping, SNP, mutation analyses
Copy Number Variation
de novo assembly
Whole Transcriptome Sequencing (RNA-Seq)
Digital Gene Expression
ChIP Seq analysis
Functional annotation
Visualisation in a genome browser
miRNA and small RNA Analysis

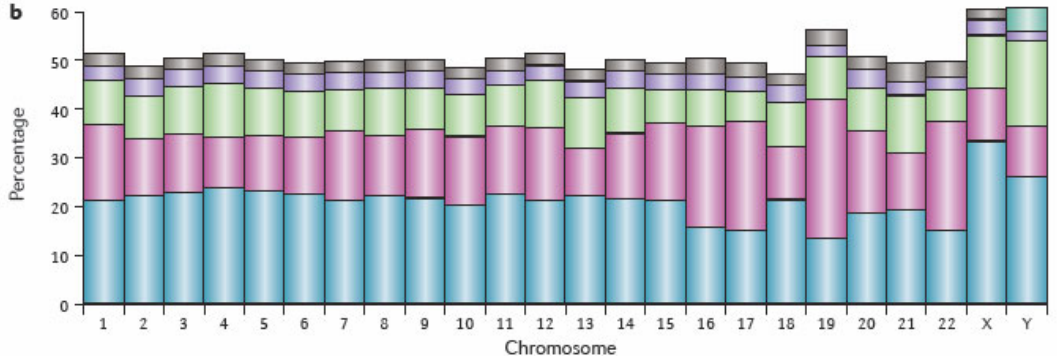
Challenges
DNA



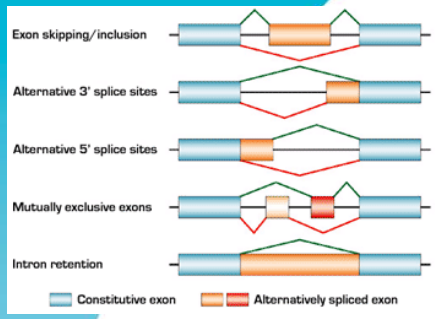


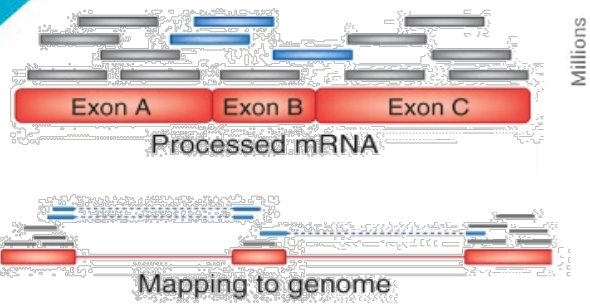
a

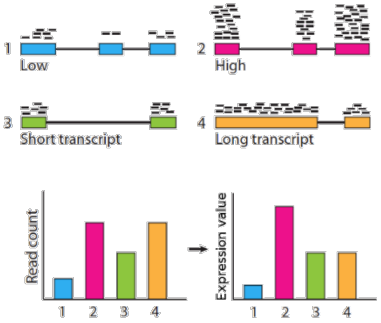
Repeat class	Repeat type	Number (hg19)	Cvg	Length (bp)
Minisatellite, microsatellite or satellite	Tandem	426,918	3%	2–100
SINE	Interspersed	1,797,575	15%	100–300
DNA transposon	Interspersed	463,776	3%	200–2,000
LTR retrotransposon	Interspersed	718,125	9%	200–5,000
LINE	Interspersed	1,506,845	21%	500–8,000
rDNA (16S, 18S, 5.8S and 28S)	Tandem	698	0.01%	2,000–43,000
Segmental duplications and other classes	Tandem or interspersed	2,270	0.20%	1,000–100,000

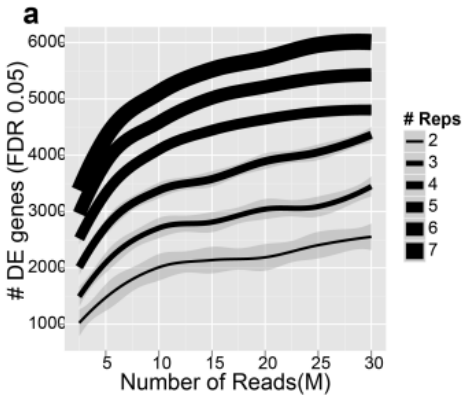


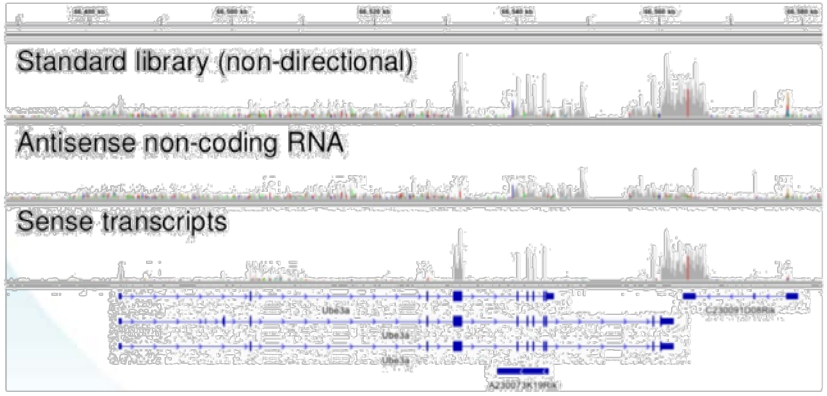
Challenges
RNA

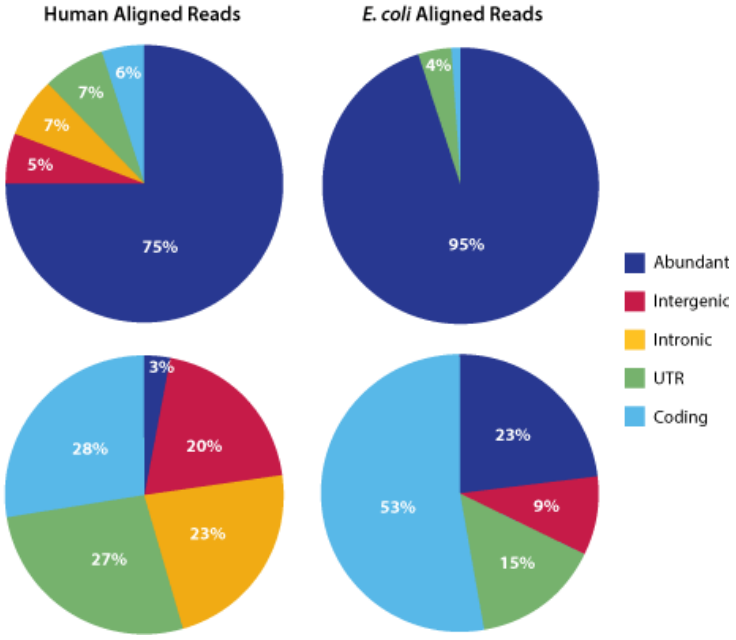












Genome Scan

Your Question

Our Focus

www.genomescan.nl
info@genomescan.nl