



UPPSALA
UNIVERSITET

Experimental design in genomics

Olga Vinnere Pettersson, Uppsala University

Scientific Lead of Planetary Biology Capability, SciLifeLab

ERGA Vice-chair

Český Krumlov

2025-01-10

Origins (green)



Jūrmala



University of Latvia

BSc Botany

MSc Plant pathogenic fungi - taxonomy

Transmutation (genomics)



Swedish University of Agricultural Sciences /
Uppsala University



PhD in fungal taxonomy

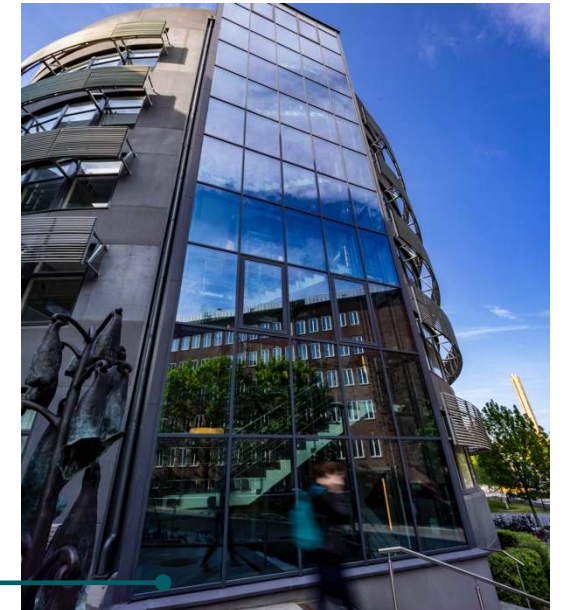
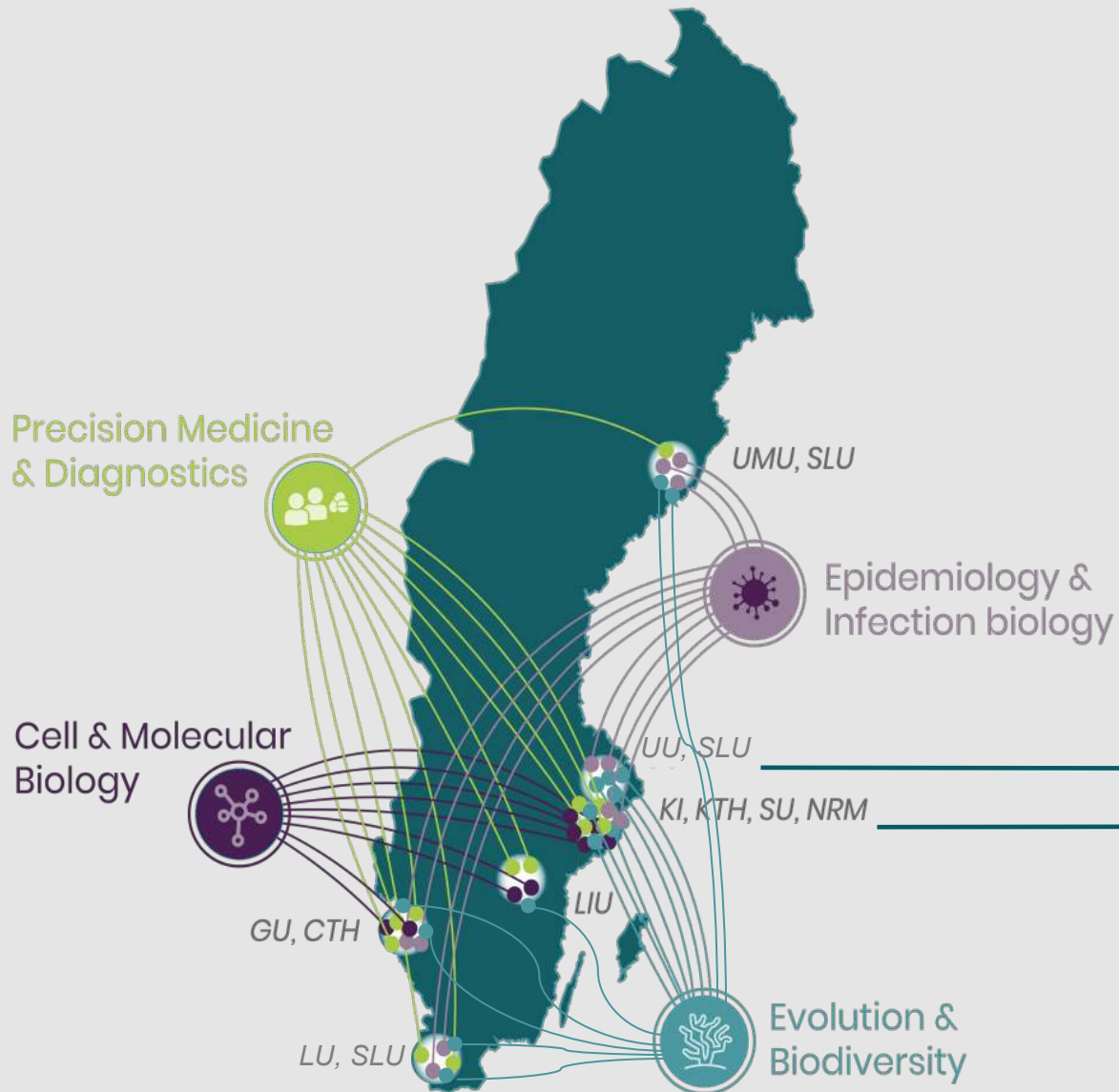
PostDoc in genome architecture of *Bartonella*

PostDoc in genomics of extremophilic fungi

SciLifeLab Genomics



Sweden's national center for molecular biosciences



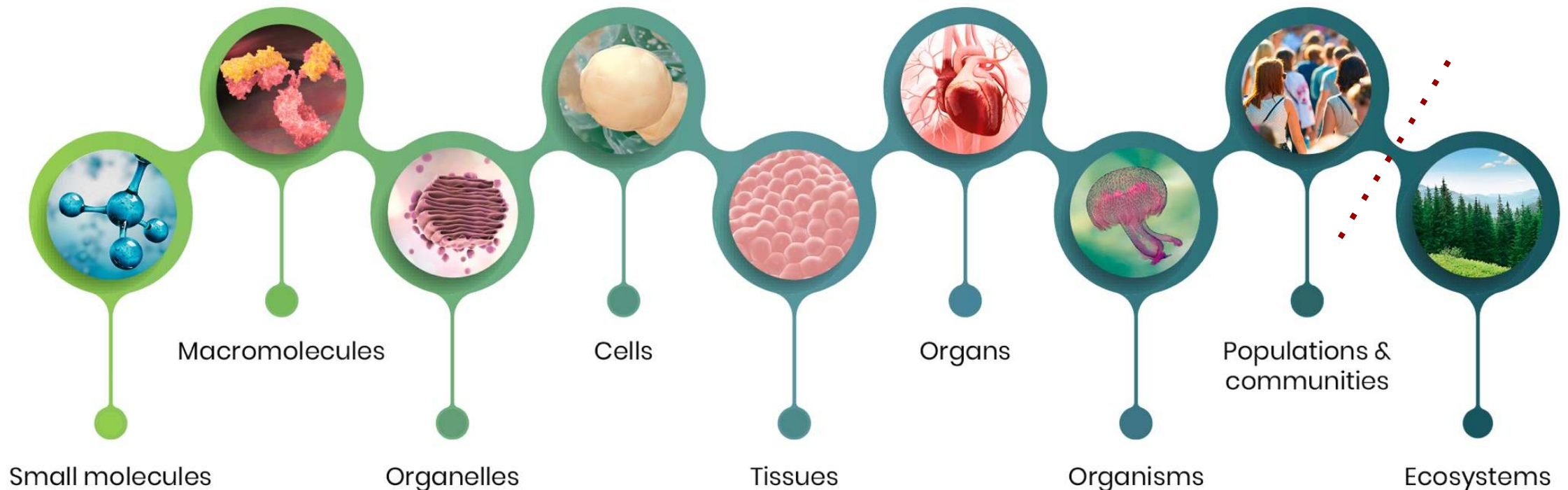
Connecting strong research environments

Enabling research across the full spectrum of life science



SciLifeLab infrastructure technologies:

- Can be used to study the molecular aspects of life **ranging from the atomic scale up to entire ecosystems**
- Are applicable across a **large spectrum of disciplines and research fields** in life science
- Are **available to all academic researchers in Sweden** on equal terms
- Are available to **healthcare and industry** all over the country, as well as international users



Who am I to tell you things...

- Since 2012 – project manager at SciLifeLab Genomics
- 2013 – long-read sequencing (and why it does not work as it should on many non-models)
- 2018 – VGP SamplePrep committee
- 2019 – EBP Sample Collection and Processing SubCommittee
- 2020 – present at conception of ERGA, since 2023 vice-chair
- 2022 – Biodiversity Genomics Europe
(building de-centralized European sequencing infrastructure, knowledge transfer)

More than a decade of project management experience, 20 years in genomics of non-models, 12 years in long-read sequencing

Also, I know what you are going through...



Now, to the lecture!



Outline

- Some perspective
- What to think about BEFORE planning a sequencing project (aka Project Design)
- Sequencing applications and experiment design specifics:
 - Whole-genome sequencing
 - Targeted sequencing
 - Transcriptome sequencing
 - Shotgun metagenomics
 - Reference genome sequencing + optimal project workflow example
- Sampling and sample quality requirements
- What every facility wish you knew before sending your samples
- Some perspective

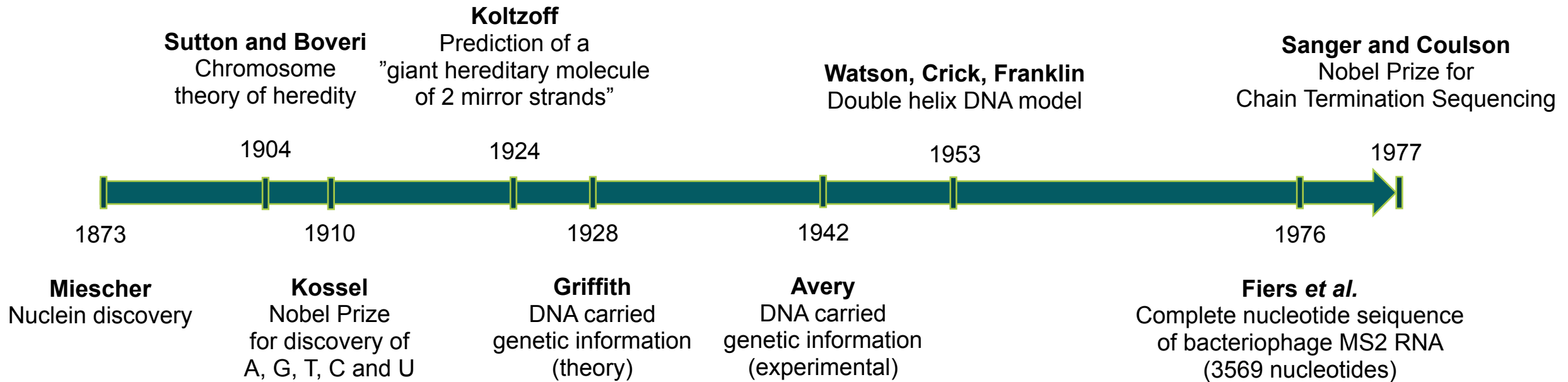


To give you a perspective

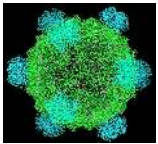


Der Rückstand nach Extraction mit Salzsäure zeigt unter dem Mikroskop noch Hülle und Inhalt und gibt die Millon'sche Reaction. In Kochsalzlösung quillt er nicht mehr, dagegen etwas in destillirtem Wasser.

From Miescher to Sanger



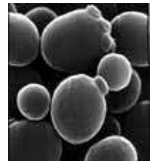
At the very beginning of genome sequencing era...



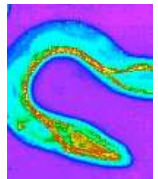
- First DNA genome: virus ϕ X 174 - 5 368 bp (1977)



- First organism: *Haemophilus influenzae* - 1.5 Mb (1995)



- First eukaryote: *Saccharomyces cerevisiae* - 12.4 Mb (1996)



- First multicellular organism: *Cenorhabditis elegans* - 100 MB (1998)



- First plant: *Arabidopsis thaliana* - 157 Mb (2000)

The Yeast Genome project



Life with 6000 Genes

A. GOFFEAU, B. G. BARRELL, H. BUSSEY, R. W. DAVIS, B. DUJON, H. FELDMANN, F. GALIBERT, J. D. HOEISEL, C. JACQ, [...] AND S. G. OLIVER

[& Affiliations](#)

SCIENCE • 25 Oct 1996 • Vol 274, Issue 5287 • pp. 546-567 • DOI: 10.1126/science.274.5287.546



*“The genome of the yeast *Saccharomyces cerevisiae* has been completely sequenced through **an international effort involving some 600 scientists in Europe, North America, and Japan**. It is the largest genome to be completely sequenced so far (a record that we hope will soon be bettered) and is the first complete genome sequence of a eukaryote.”*

*“New graduate students are already wondering how we all managed in the “dark ages” before the sequence was completed. We must now tackle a much larger challenge, that of elucidating the function of all of the novel genes revealed by that sequence. **As with the sequencing project itself, functional analysis will require a worldwide effort.** In Europe, a new research network called EUROFAN [for European Functional Analysis Network] has been established to undertake the systematic analysis of the function of novel yeast genes. Parallel activities are underway in Germany, Canada, and Japan. In the United States, the National Institutes of Health has recently sent out a request for applications for “Large-Scale Functional Analysis of the Yeast Genome.” “*



GENETICS
Subscription to Authors Editorial Board Scientific Manuscript

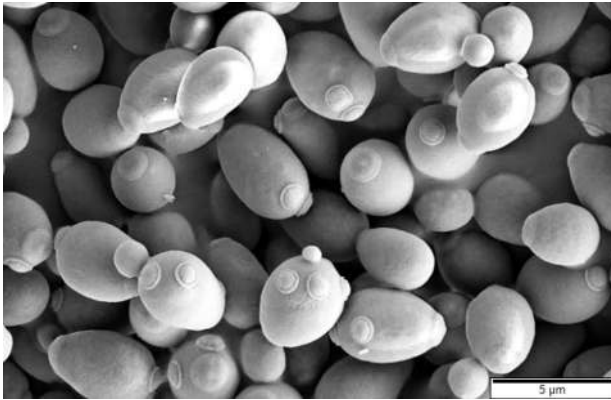
Genetics, 2013 Jun; 194(2): 291-299.
doi: [10.1534/genetics.113.151258](https://doi.org/10.1534/genetics.113.151258)

The Modest Beginnings of One Genome Project

[David B. Kaback¹](#)

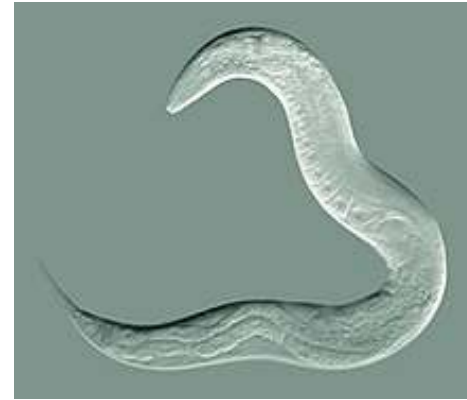
PMCID: PMC3664842
PMID: 23733847

First genomic references



1/3 of genes related to human by homology

Basic cell functions



Human disease gene discovery

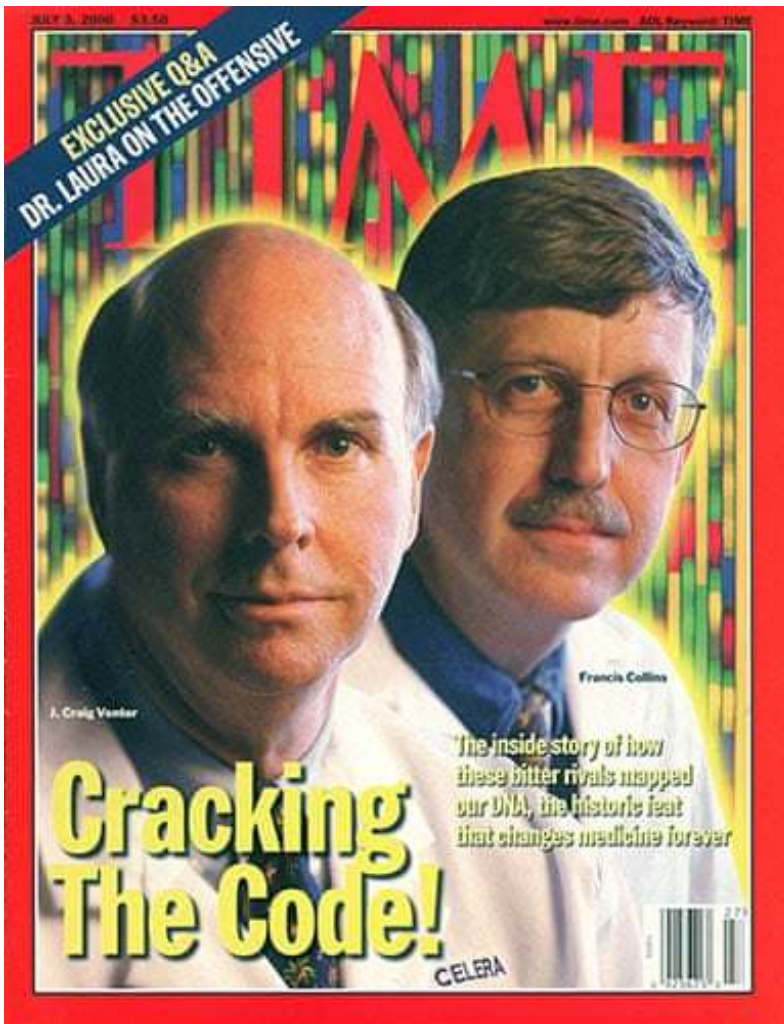


Phenotypical traits



Plant genome structure and function

But it was not enough...



GENOME SEQUENCING WORKSHOP

MARCH 3 & 4, 1986

SANTA FE, NEW MEXICO

SPONSOR

DOE

OFFICE OF HEALTH AND
ENVIRONMENTAL RESEARCH

HOST

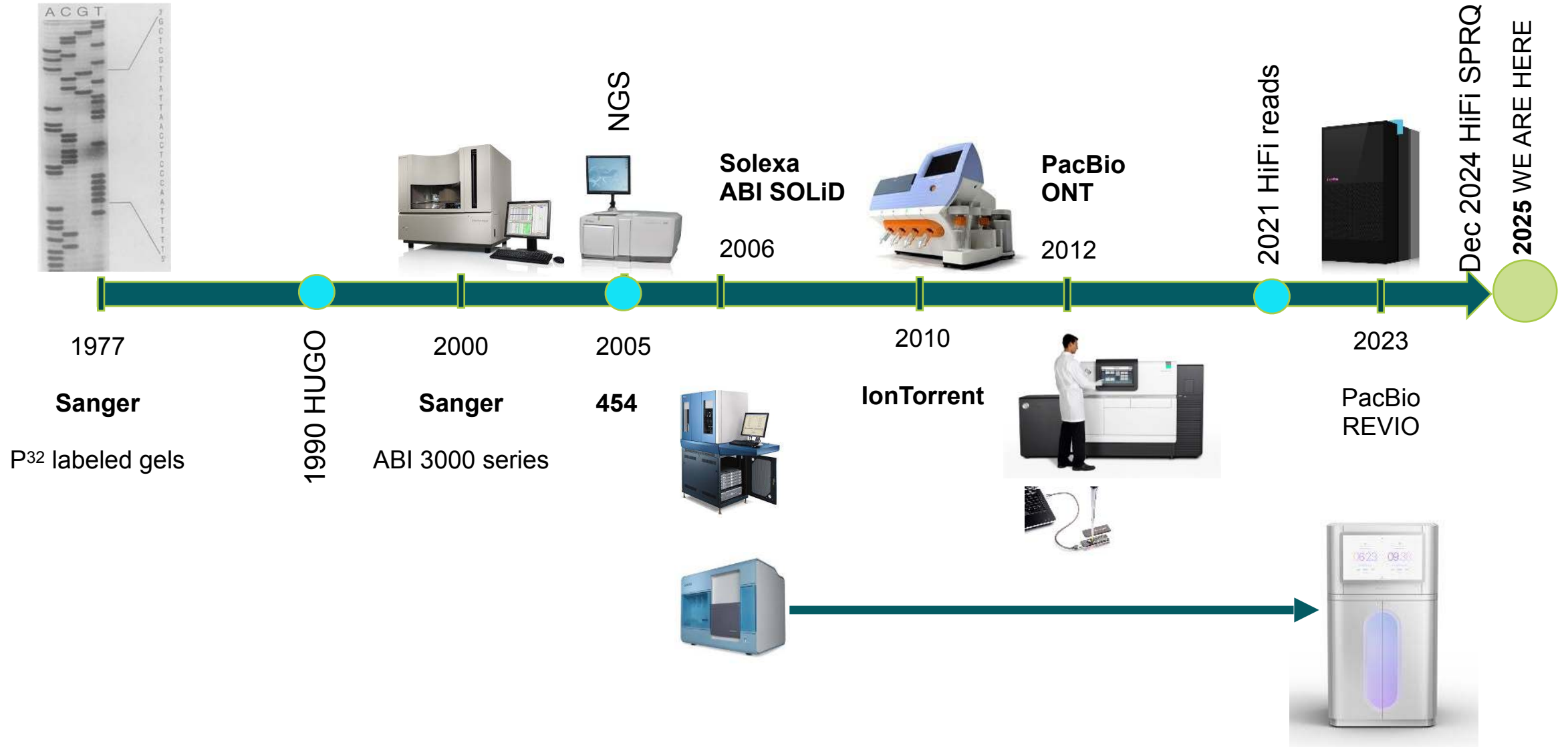
LIFE SCIENCES DIVISION
LOS ALAMOS NATIONAL LABORATORY



It is thus important that we identify here what real benefits and liabilities might emerge from the contemplated sequencing activity, which would aim at capturing the entire human genome in a period of 10 or 12 years. Do we have the technologies necessary to do this, and do we have the computational power and algorithms needed to integrate and analyze this data? Will this information provide both clinical and basic benefits of such magnitude to warrant an accelerated effort?



An outcome of HUGO – Genomic Revolution



Just a comparison

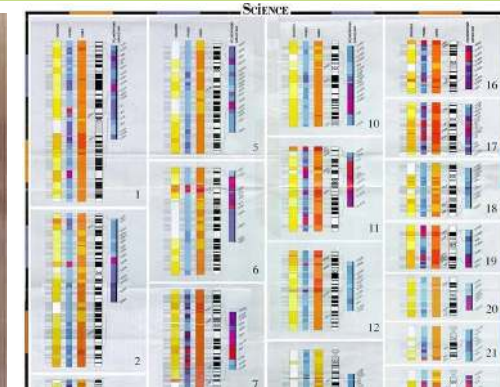


1990 - 2003

HUGO

Sanger traditional

\$2.7 bln



2007

Craig Venter's genome

Sanger ABI 3730

\$300 mln



2008

Jim Watson's genome

454 FLX

\$1 mln



TODAY
any human

\$500-800

\$800-3k

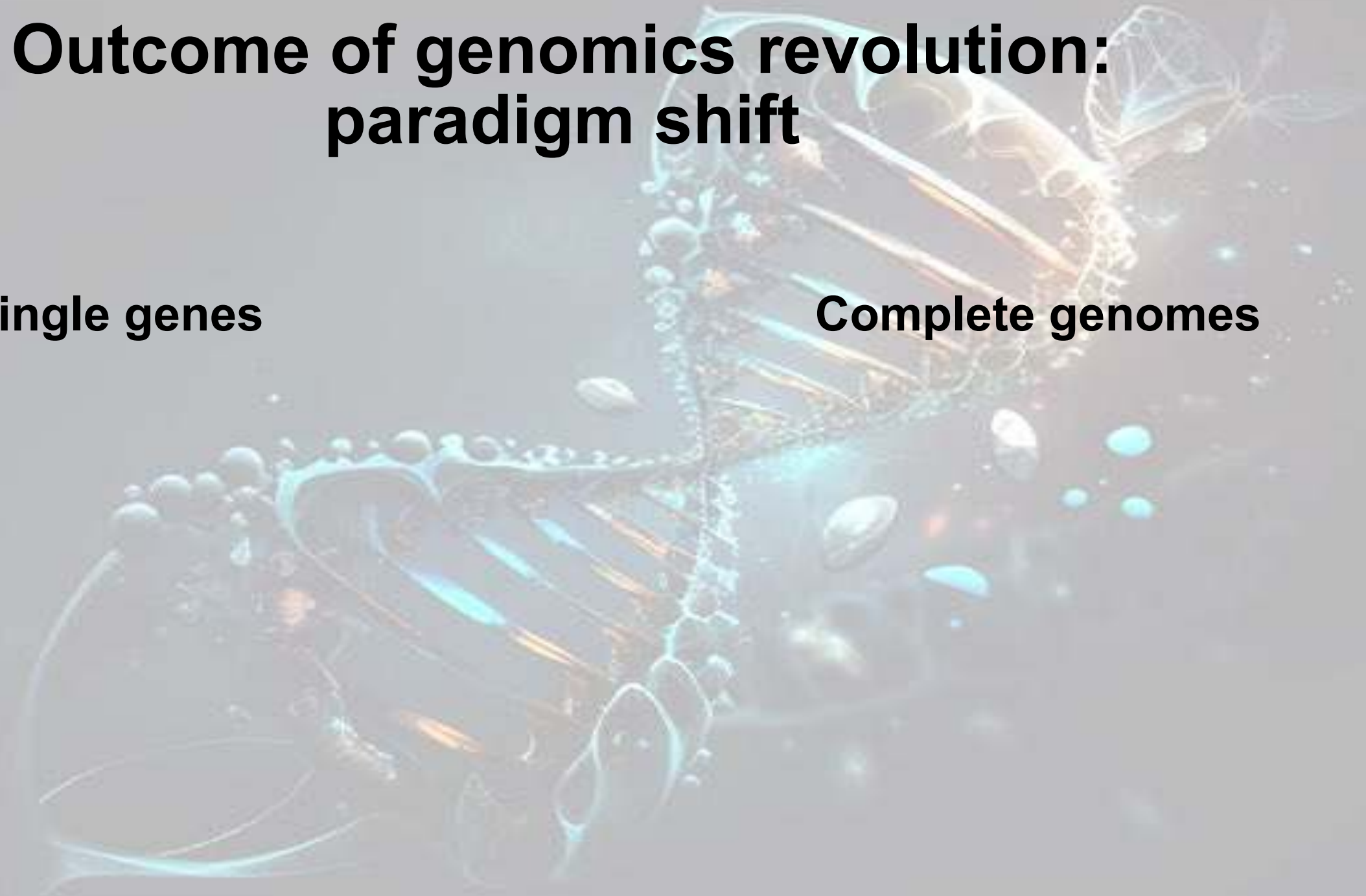
with Illumina

with long reads

Outcome of genomics revolution: paradigm shift

Single genes

Complete genomes



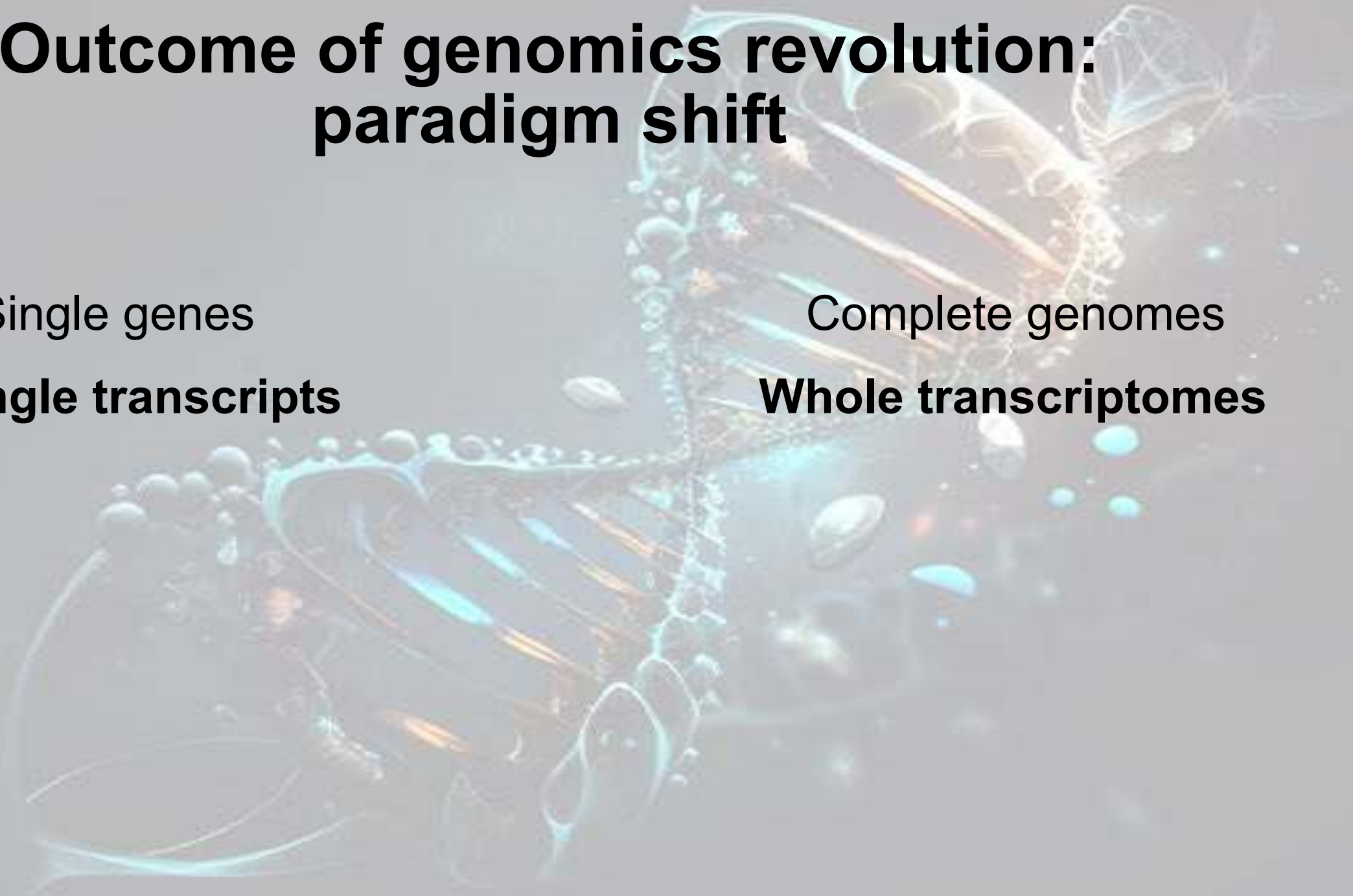
Outcome of genomics revolution: paradigm shift

Single genes

Single transcripts

Complete genomes

Whole transcriptomes



Outcome of genomics revolution: paradigm shift

Single genes

Single transcripts

Single organisms

Complete genomes

Whole transcriptomes

Metagenomes

Outcome of genomics revolution: paradigm shift

Single genes

Single transcripts

Single organisms

Model organism

Complete genomes

Whole transcriptomes

Metagenomes

Any species

Outcome of genomics revolution: paradigm shift

Single genes

Single transcripts

Single organisms

Model organism

Complete genomes

Whole transcriptomes

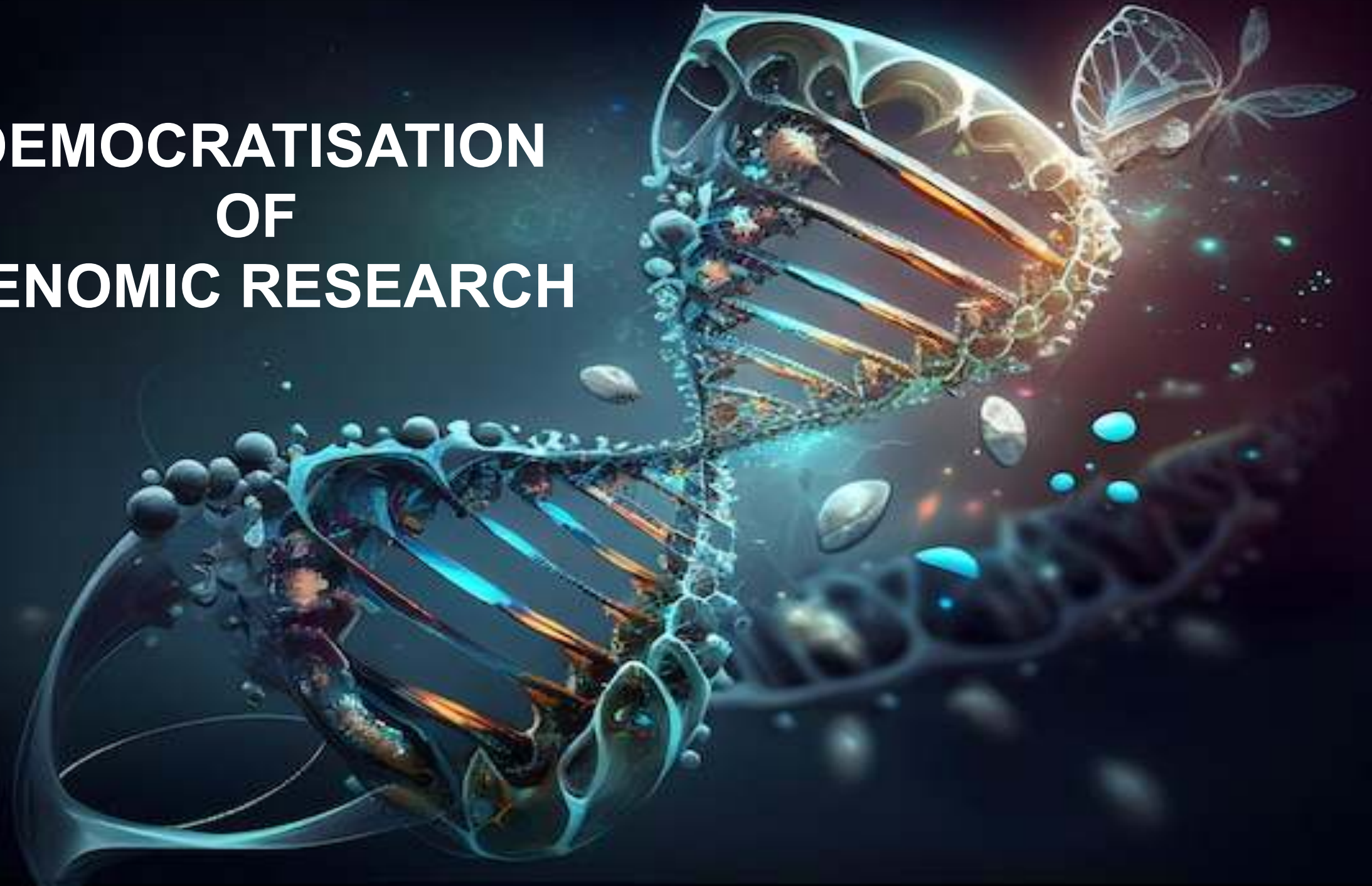
Metagenomes

Any species

Available to highly specialized labs

Available to anyone

DEMOCRATISATION OF GENOMIC RESEARCH



Drawback of genomic revolution: how to stay up to date?



- Immense speed of technological progress
- Inspiration from papers? HA!
 - Design + gathering material + conducting experiments (1 month - years)
 - Sequencing (1-6 months)
 - Analysis (...)
 - Writing paper (month - year)
 - Paper submission (weeks)
 - Reviewer #3 (weeks - months)
 - Design -> published paper 1-3 years

Drawback of genomic revolution: how to stay up to date?



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SOLUTION: talk to a sequencing center near you





Planning the sequencing project



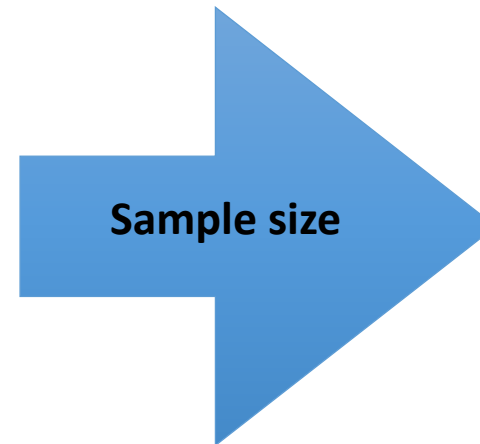
WHAT IS MY QUESTION?

- Qualitative or quantitative?
 - Avoid: “let’s sequence and see what happens”
 - Frequent scenario: “here is what I have, do your best/worst”

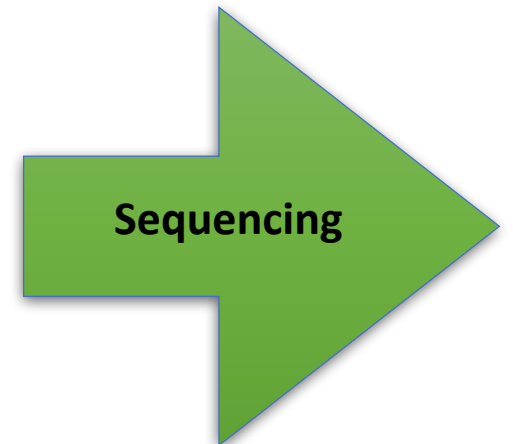
Hypothesis*



Sample size



Sequencing



**or creating a resource (e.g. variant database, reference, etc)*



Available
resources

- €€€
- Store and compute
- Who will analyse the data?
- Who will biologically interpret the data?
- Sample availability (number, quality and amount of material)

Sample size

- Statistical sensitivity: #of samples, #of replicates, #of reads (sequencing depth)

Sequencing

- Choice of application and technology

Early planning **before** writing a grant proposal is highly recommended. Get advise!



Let's dive into it

NGS Technologies and Applications



NGS technologies

Short read NGS

Long-read NGS



Whole genome re-sequencing
RNA-seq
Targeted sequencing
Amplicons up to 600 bp

De novo genome sequencing
RNA-seq
Whole-transcript sequencing
Targeted sequencing
Structural variant resolving
Allele phasing
Amplicons up to 13 kb



Whole genome sequencing (WGS)

Re-sequencing or de novo?

- Re-sequencing (WGS):
 - Pre-requisite: a reference genome to map to.Population studies (genotyping, variant discovery, allele frequency, etc)
SNPs only? Short reads.
SVs? Long reads.
SNPs and SVs? PacBio **HiFi** (January 2025).
- *De novo* (Reference genome sequencing):
 - Creating a genomic reference from scratch
 - Long reads (sometimes coupled with short-read skims)



WGS sequencing depth

Population sequencing: individual libraries or pools of many individuals

Type of Experiment	Coverage Required
Haploid SNPs/divergence	$\geq 10 \times$
Diploid SNPs/divergence	$\geq 30 \times$
Aneuploid/somatic mutations	$\geq 50 \times$
Population sequencing	$\geq 200 \times$

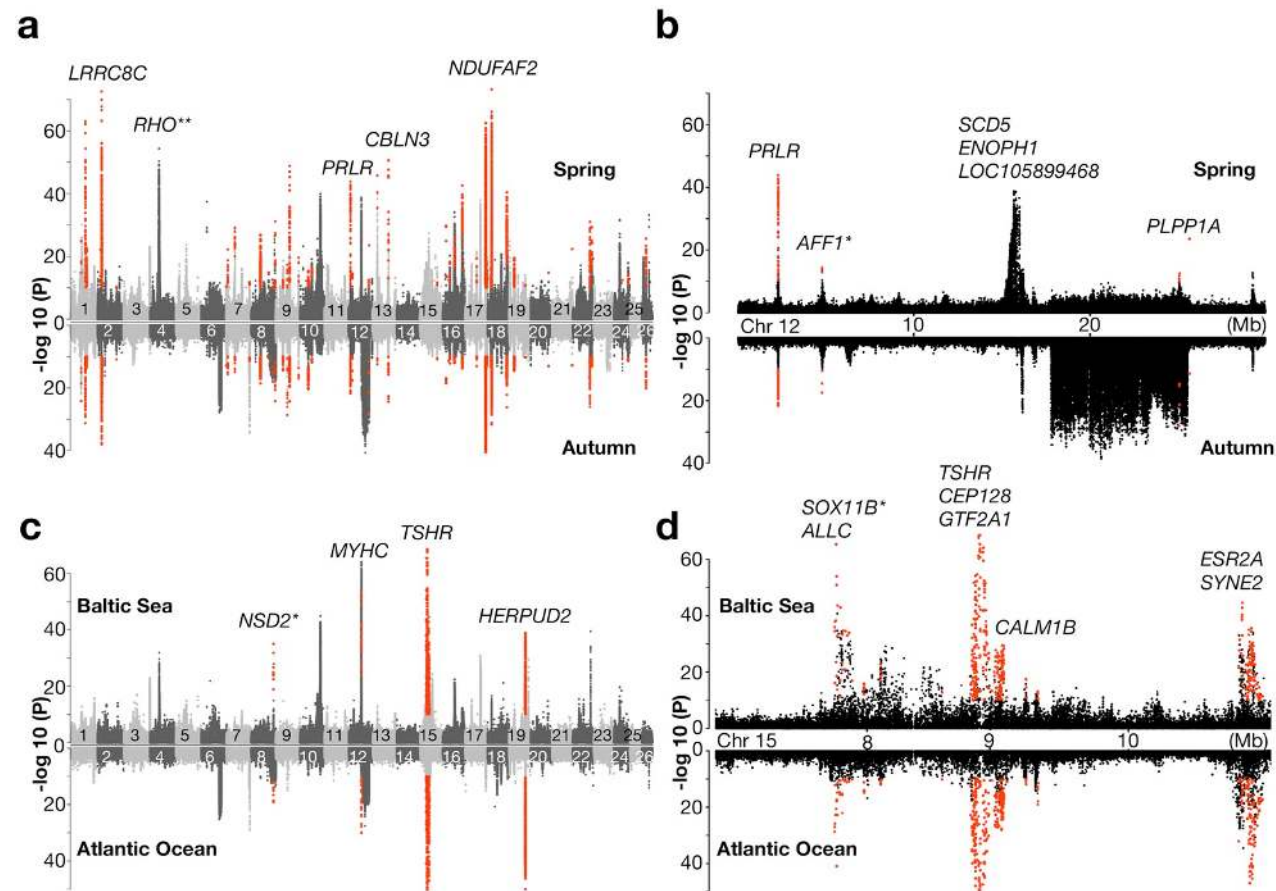
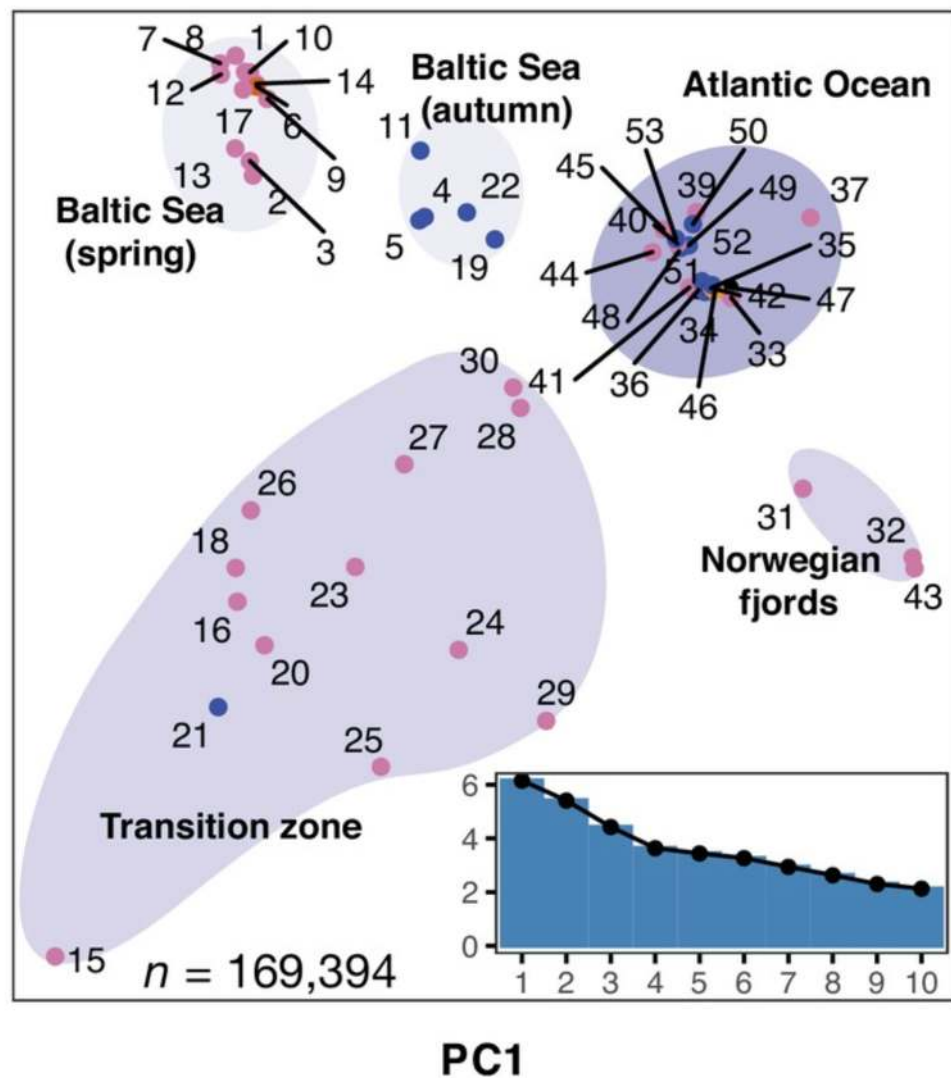
Borrowed from Mike Zody

Individual libraries give better resolution, but are more expensive

Pool sequencing: will pick up main trends (e.g. loci under selection)

Caution not to over sequence: sequencing errors vs true biology

WGS, examples



Evolutionary Biology, Genetics and Genomics

Ecological adaptation in Atlantic herring is associated with large shifts in allele frequencies at hundreds of loci

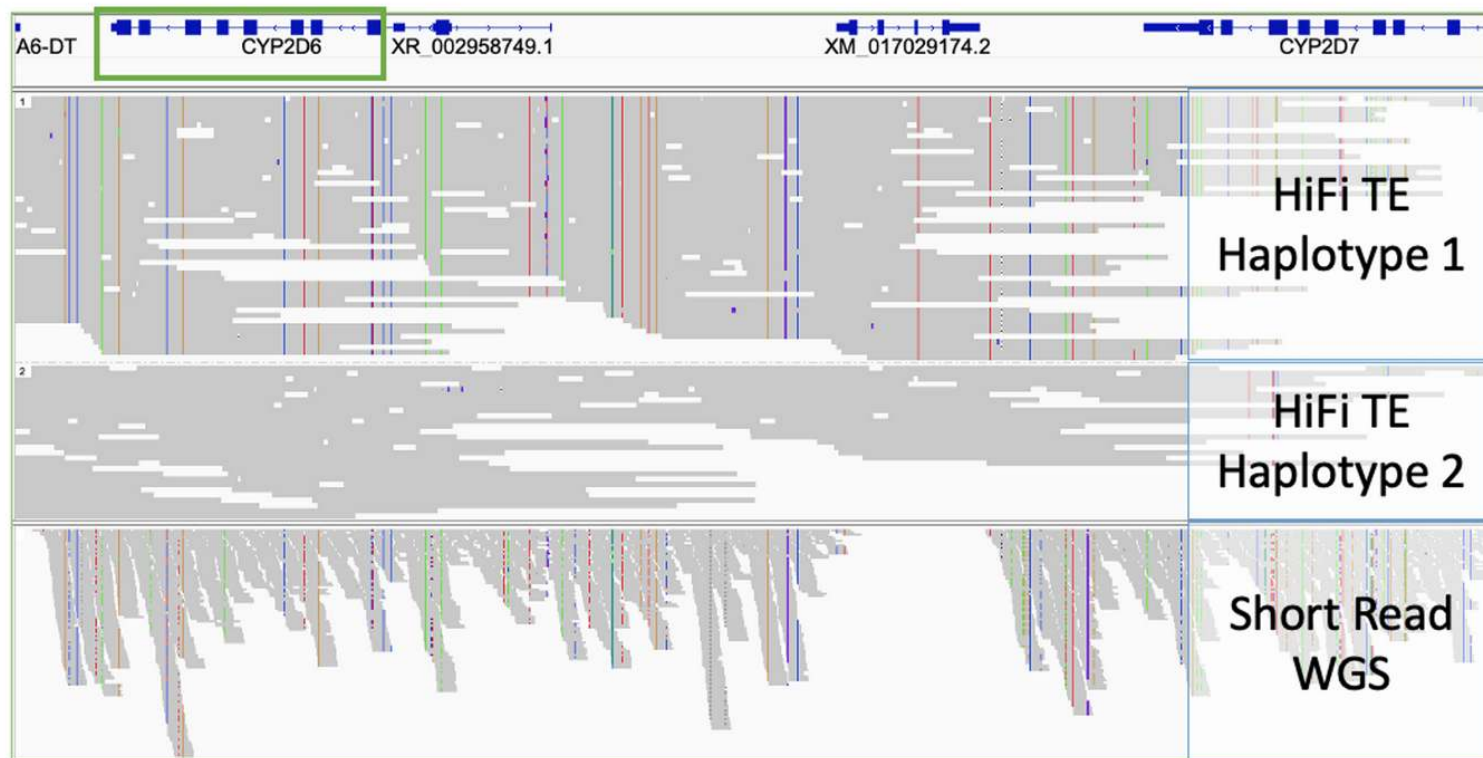
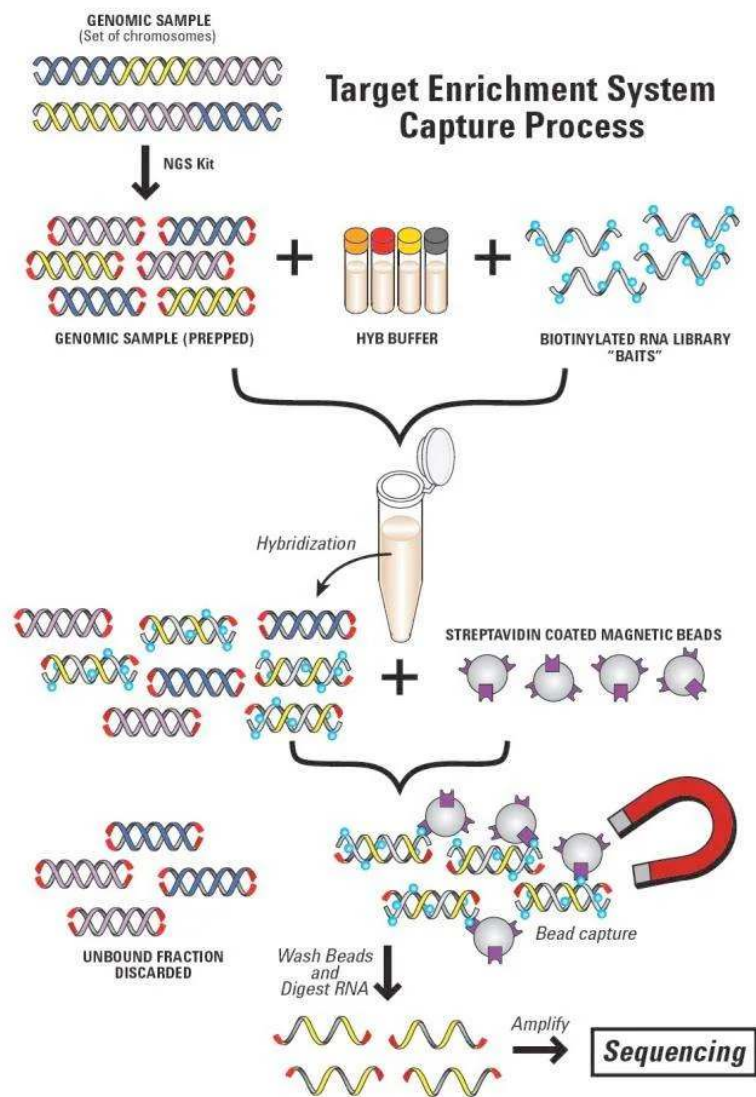
Targeted sequencing

Zooming into portions of a genome - a cost effective screening alternative

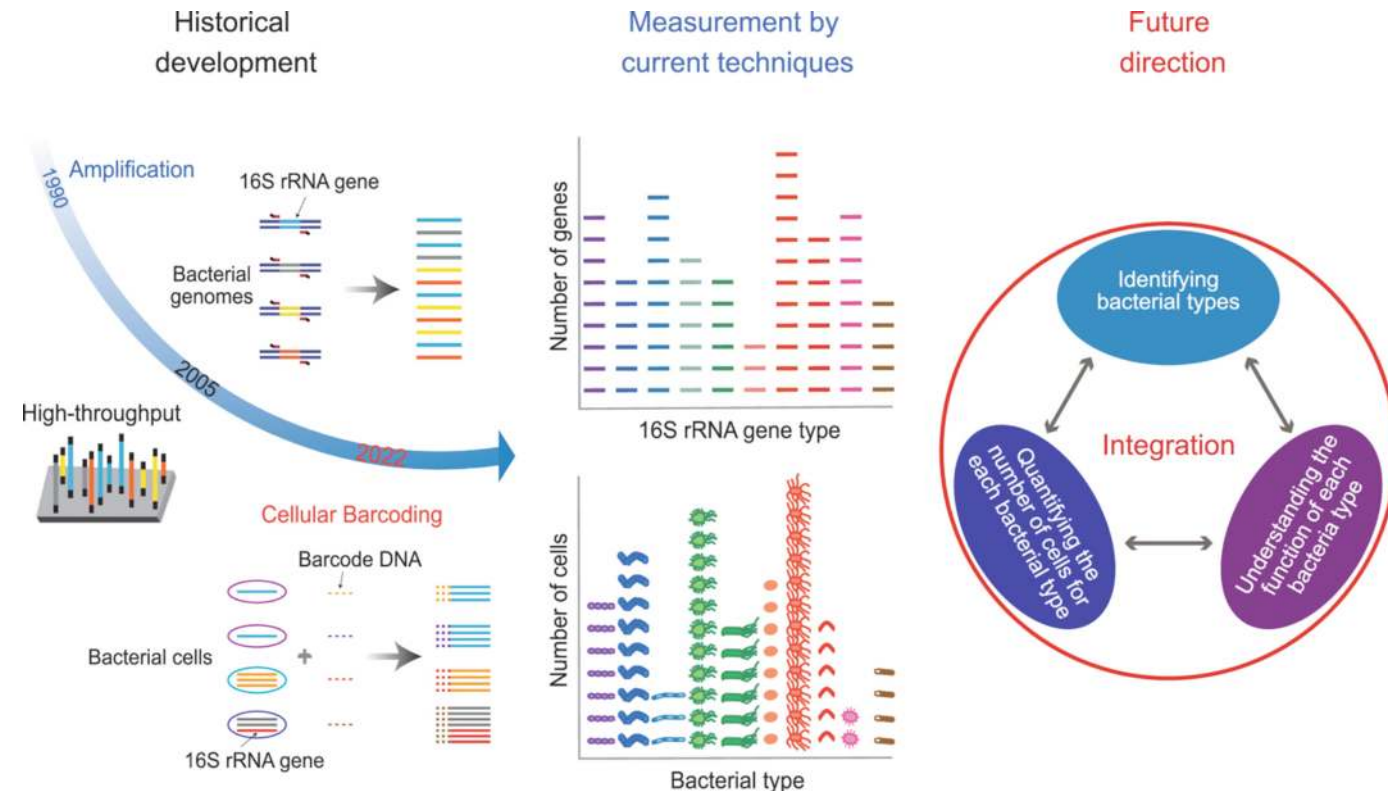
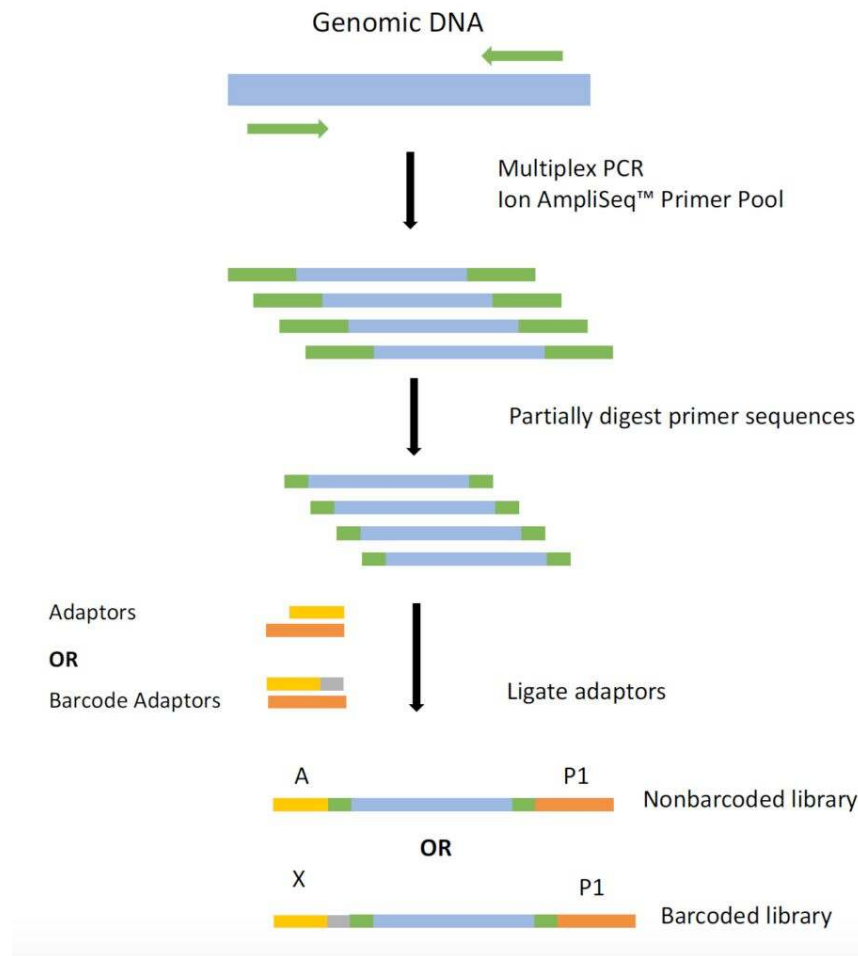


- **Capture with probes**
 - Panels or custom (Agilent, ThermoFisher, Twist, etc)
 - Specificity varies
 - Material requirements (good quality and quantity)
 - Cost
- **PCR**
 - Own primers or custom panels (e.g. Ion AmpliSeq)
 - High sensitivity and specificity
 - Prior knowledge of sequence is needed
 - Bias and product length limitations
- **CRISPR-Cas9**
 - Prior knowledge of sequence is needed
 - Requires a lot of DNA
 - Off-target effects reported

Targeted sequencing: capture with probes



Targeted sequencing: PCR (amplicon seq)



REVIEW ARTICLE | [Open Access](#) | [CC](#) [BY](#)

Long journey of 16S rRNA-amplicon sequencing toward cell-based functional bacterial microbiota characterization

Jianshi Jin [✉](#), Xiongduo Liu, Katsuyuki Shiroguchi [✉](#)

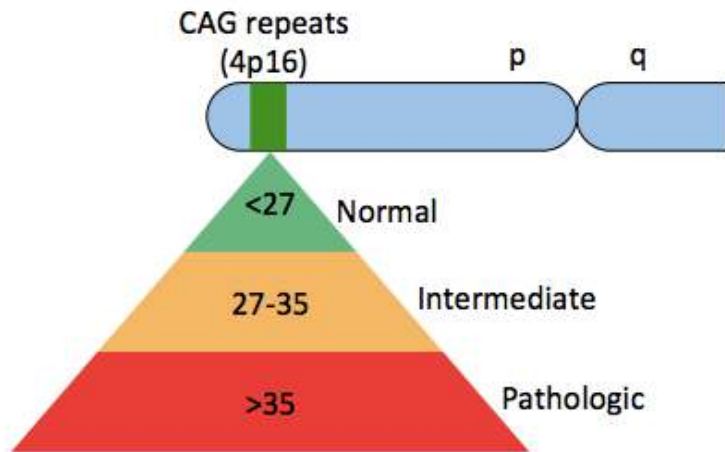
First published: 11 July 2024 | <https://doi.org/10.1002/imo2.9> | Citations: 2

Disease panels with multiple targets (e.g. Ion AmpliSeq)

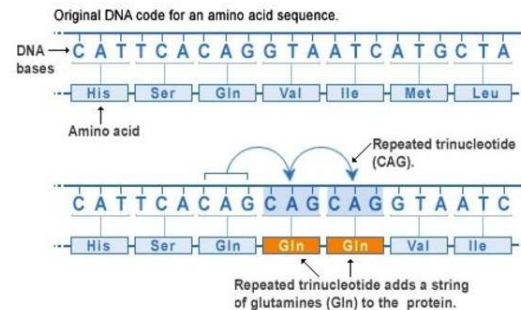
Targeted sequencing: CRISPR-Cas9



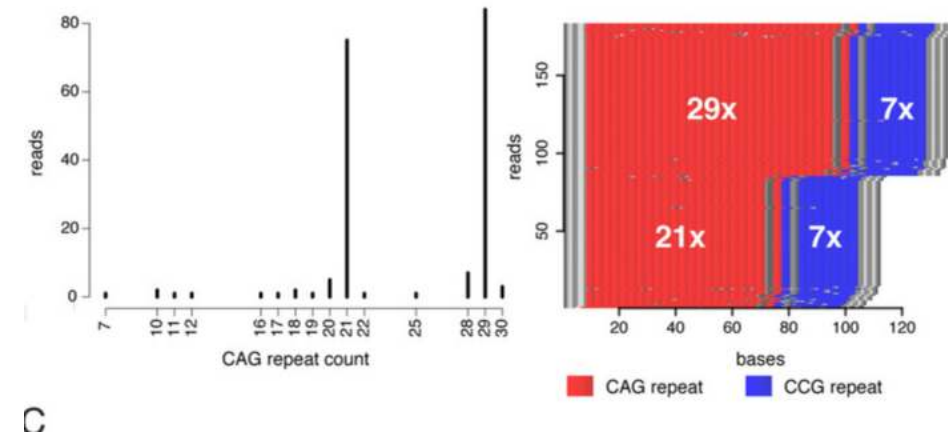
Huntington's Disease



Repeat expansion mutation



U.S. National Library of Medicine



Huntington's disease:

- Inherited disorder resulting in brain cell death
- Decline of motor and cognitive functions
- Common onset: 30-50 years of age
- No cure
- Causative genetic variant: CAG-repeat expansion in *HTT* gene

Problem: polymerase slippage – low complexity regions
PCR-based methods do not work

Detailed analysis of *HTT* repeat elements in human blood using targeted amplification-free long-read sequencing

Ida Höjjer, Yu-Chih Tsai, Tyson A. Clark, Paul Kotturi, Niklas Dahl, Eva-Lena Stattin, Marie-Louise Bondeson, Lars Feuk, Ulf Gyllenstein, Adam Ameur ✉

Targeted sequencing: technology & depth?



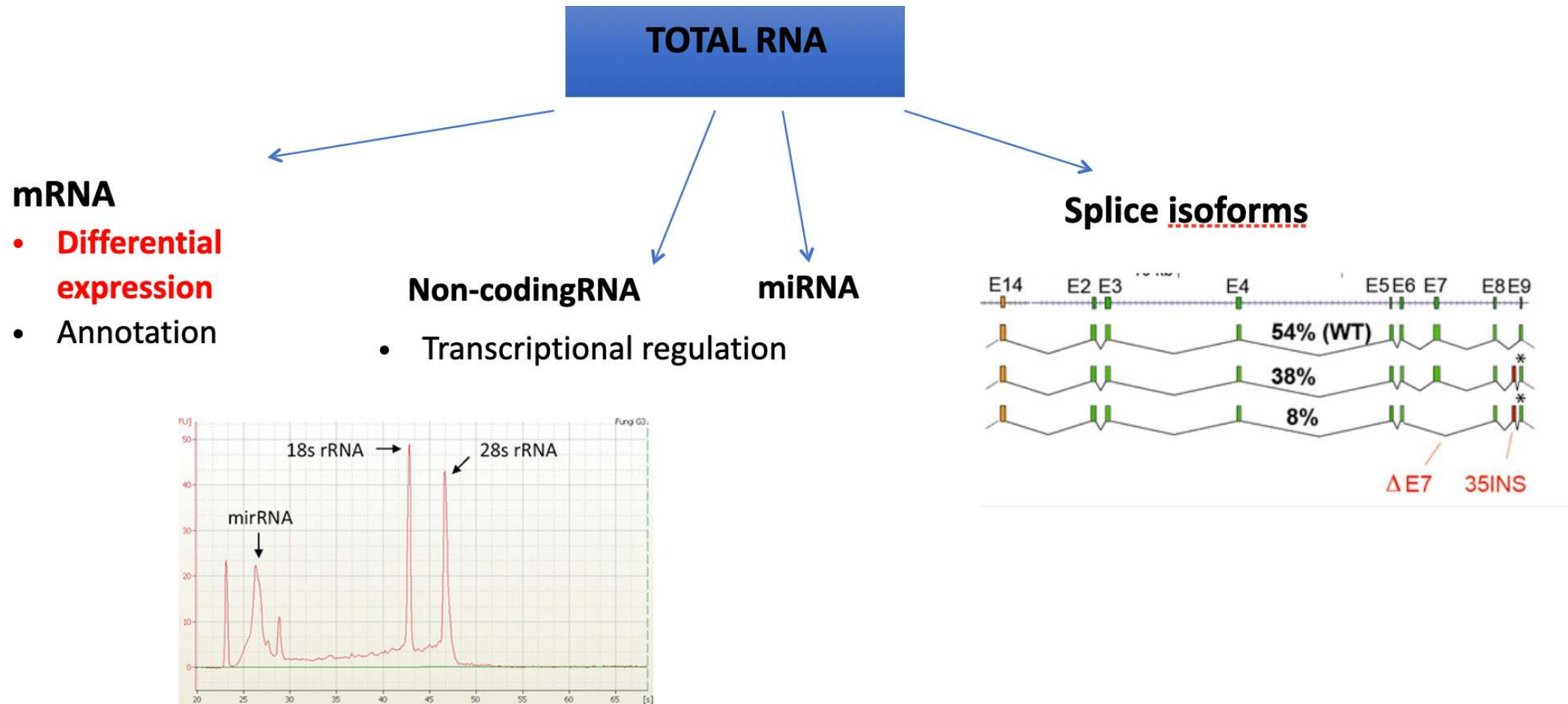
Talk to different vendors: technology-specific solutions

Run a pilot! (e.g. known truth vs real-life)

Hierarchical data reduction to determine sequencing depth

Ask for advise from your sequencing provider

Transcriptome Sequencing (RNA-seq)

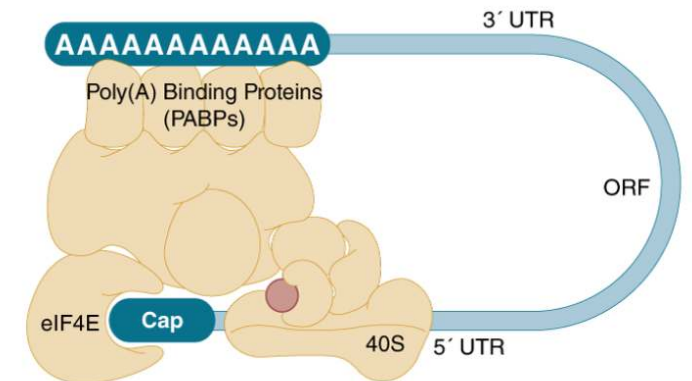
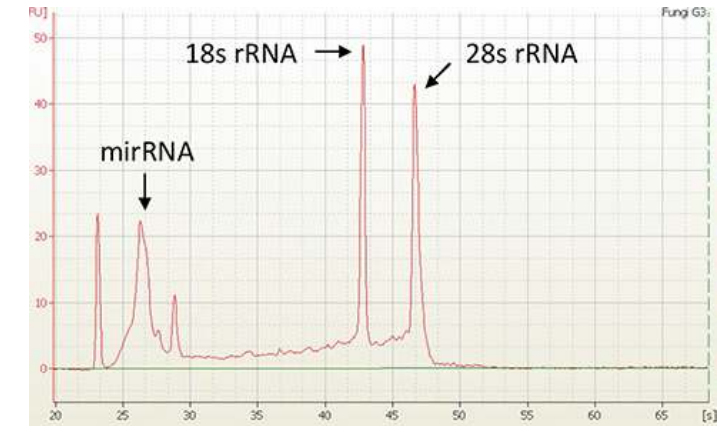


Transcriptome Sequencing (RNA-seq)



One must get rid of rRNA. To PolyA or not to PolyA?

Method	Pros	Cons
rRNA depletion	• Captures on-going transcription • Picks up non-coding RNAs	• Does not get rid of all rRNA • Messy Dif.Ex. profile
polyA selection	• Gives a clean Dif.Ex. Profile • Loses all non-polyA RNAs	• Does not pick many non-coding RNAs



Number of reads

Differential expression with a **good*** reference: 5+M PE reads (up to 100M for rare transcripts)

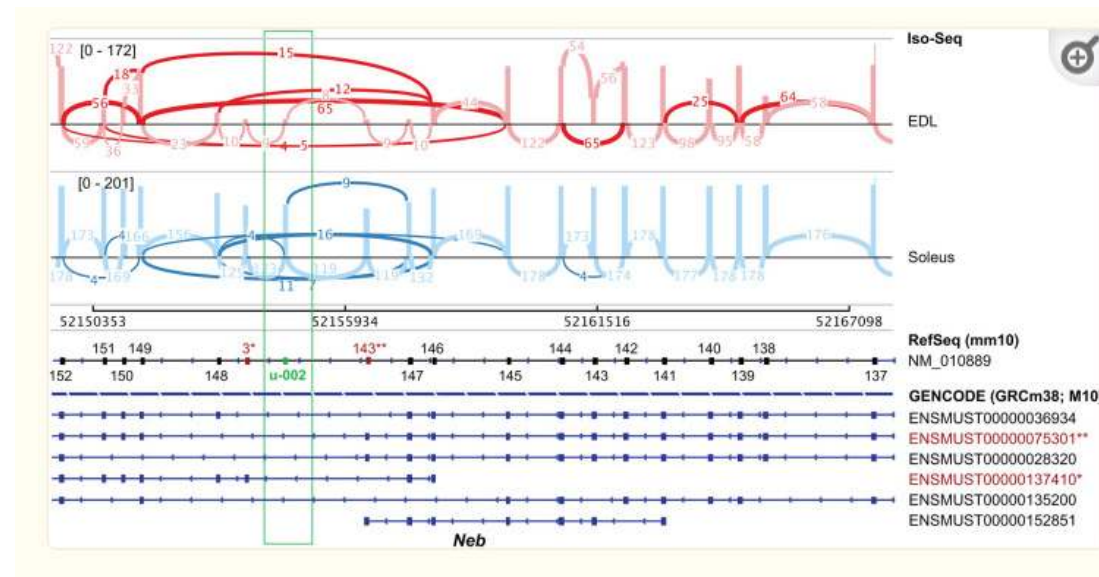
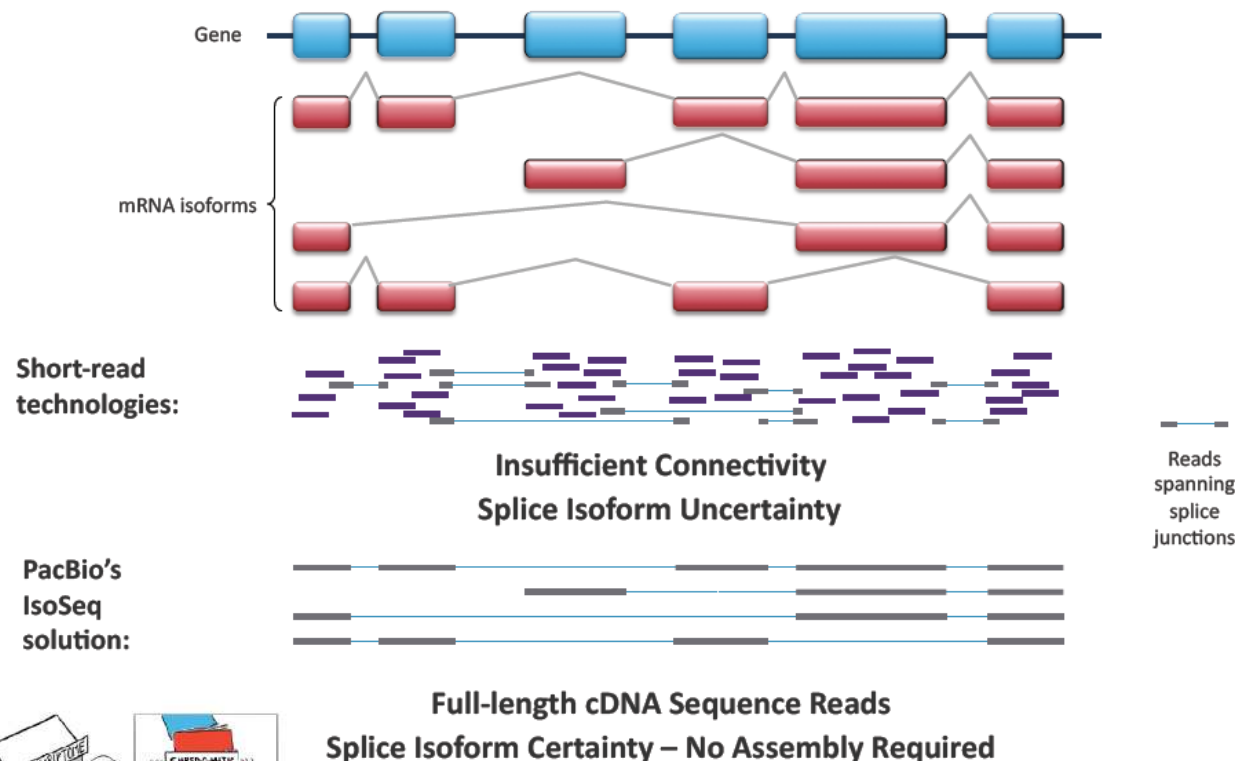
Annotation: a minimum of 50M PE reads of mixed tissue (rather 100M per tissue)

*well-annotated

RNA-seq with log reads



DETERMINATION OF TRANSCRIPT ISOFORMS



[Genome Res.](#) 2020 Jun; 30(6): 885–897.

NEB:

one of the biggest protein coding genes in vertebrates
(22kb mRNA, 183 exons)

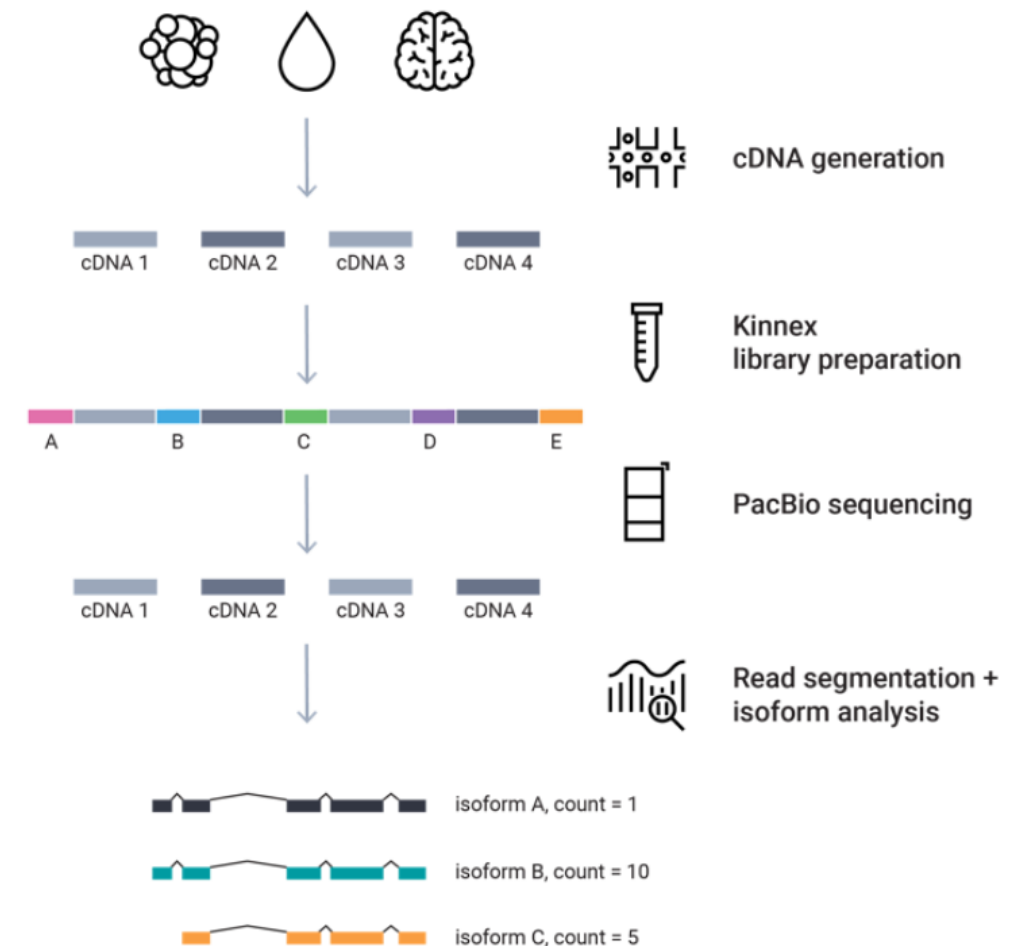
Codes for nebulin, muscle protein



Differential expression with long reads



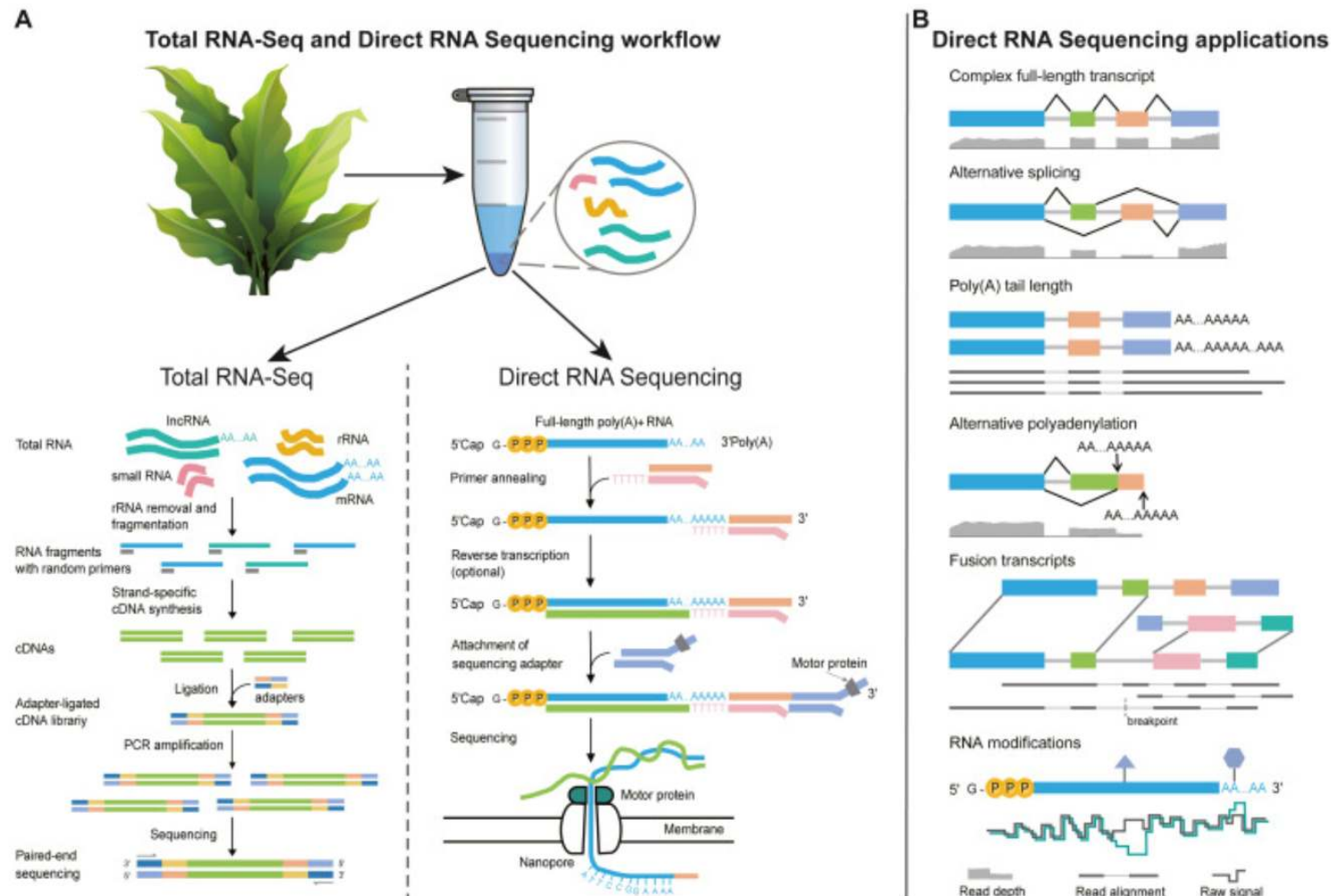
- Best of both worlds: expression values AND isoform information
- Prior to Q2 2024 - ONT only (polyA or CAP-selected)
- Now: both ONT and PacBio Kinnex



RNA-seq: direct RNA sequencing on ONT



Do not get too excited

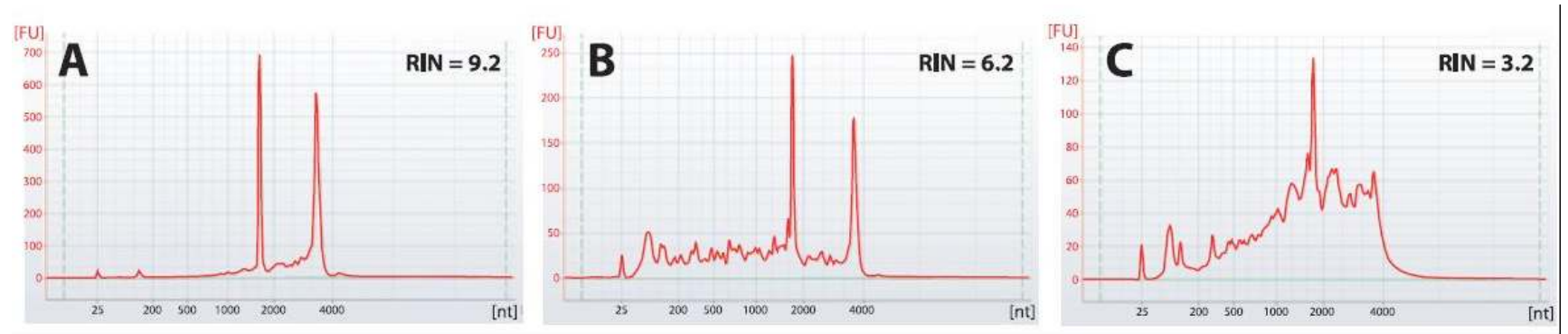


One cannot use
direct RNA-sequencing
for differential gene expression
experiments!
(January 2025)

RNA-seq considerations



- mRNA only: use any kit (for annotation and long-reads we recommend TRIZOL)
- mRNA **and** miRNA: only specialized kits
- Always use DNase!
- RIN value above 8

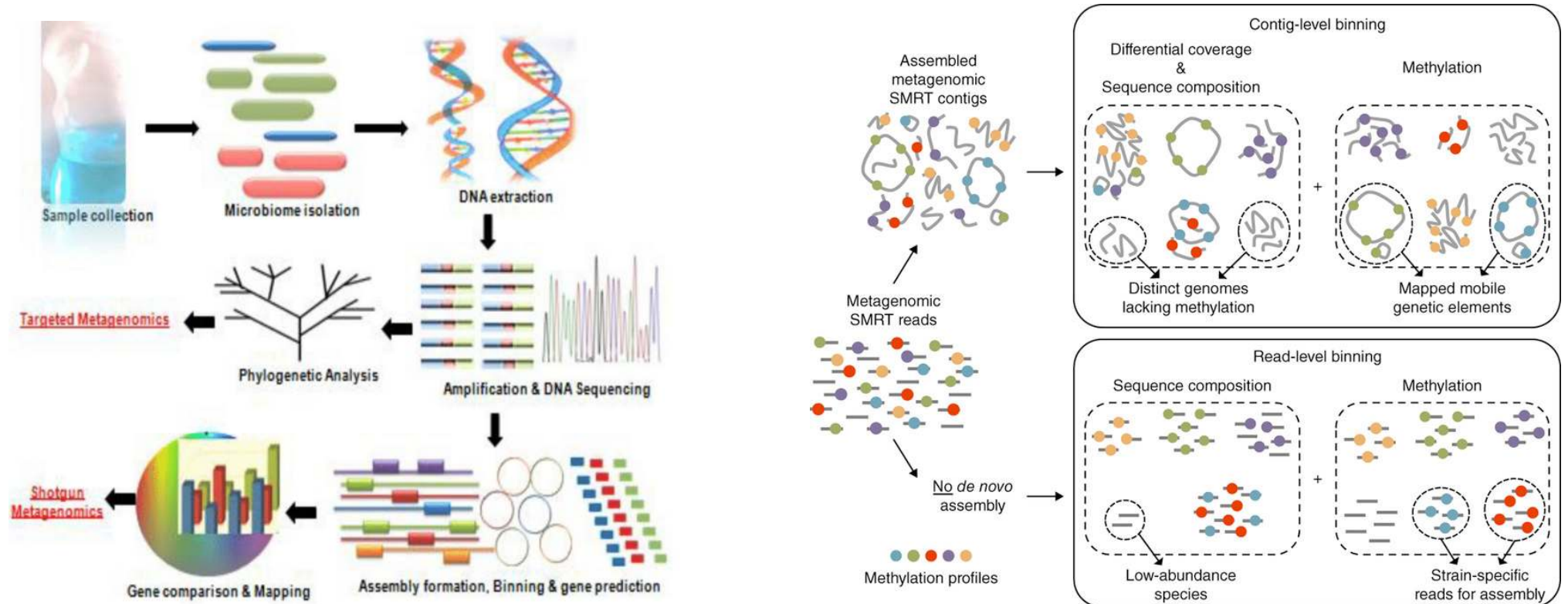


- CONTROL vs experimental conditions
- Biological replicates: a minimum of 4 is strongly recommended

Shotgun metagenomics



- Strongly recommend a pilot + hierarchical data reduction to determine the sequencing depth
- Can be done with both short and long reads
- If with long reads - consider utilizing epigenetic signature for plasmid assignment / OTU binning





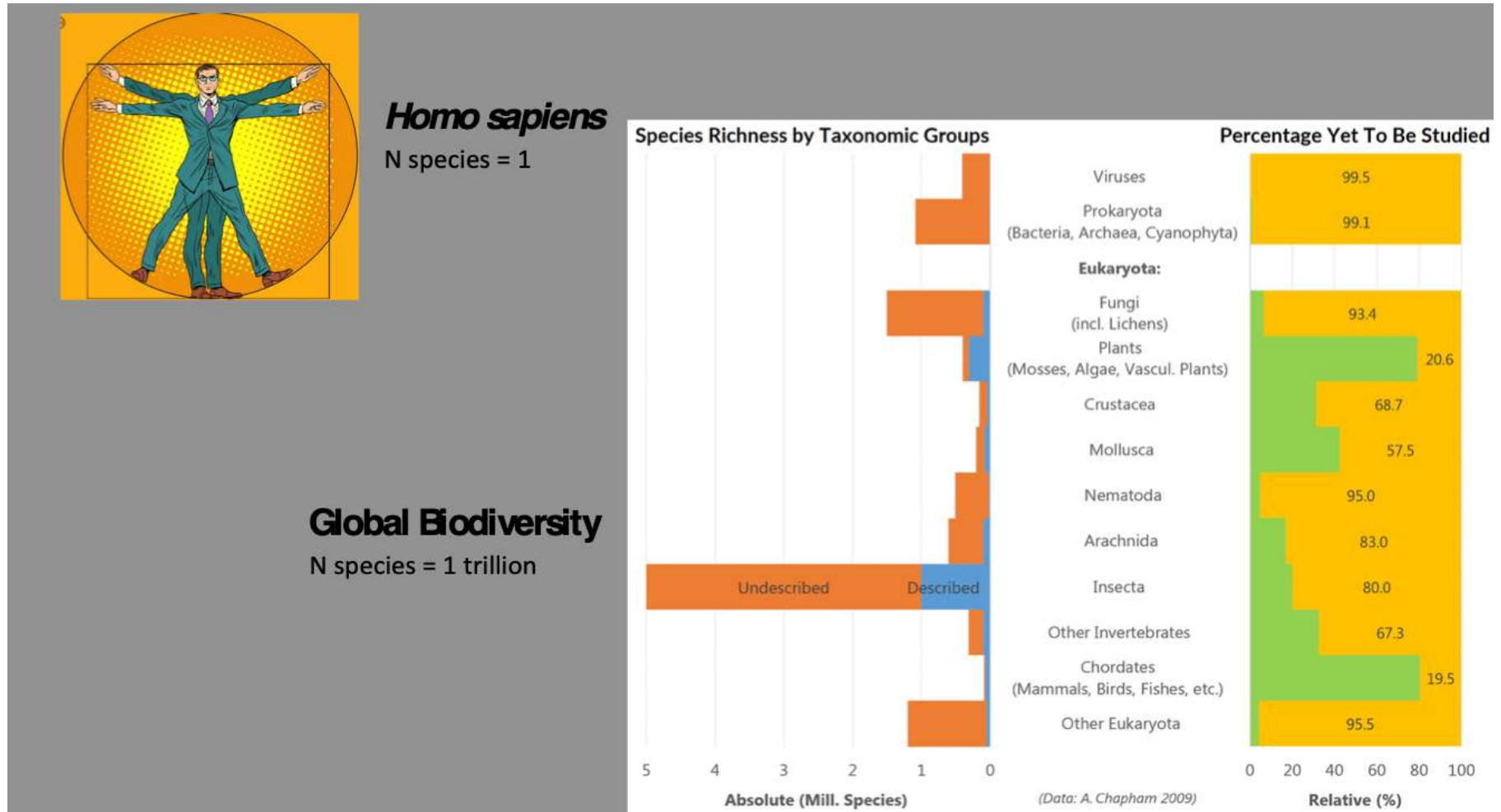
Diving into deep: reference genome sequencing of non-models

Coffee break?

De novo (reference genome) sequencing



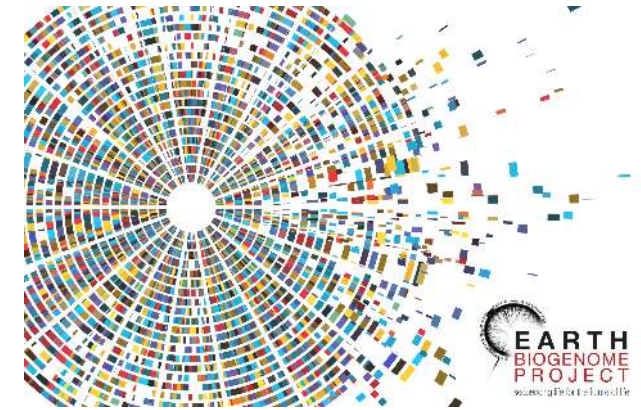
- Sequencing a genome without a prior reference



Reference genome sequencing (RefGen)



- Only closely related taxa can be used for alignment
- Always done with long reads
- Enable any kind of downstream genetic analysis



- Generating a chromosome-scale reference genome is a life-time investment. But it is costly.



- Sit tight, it is going to be a long one

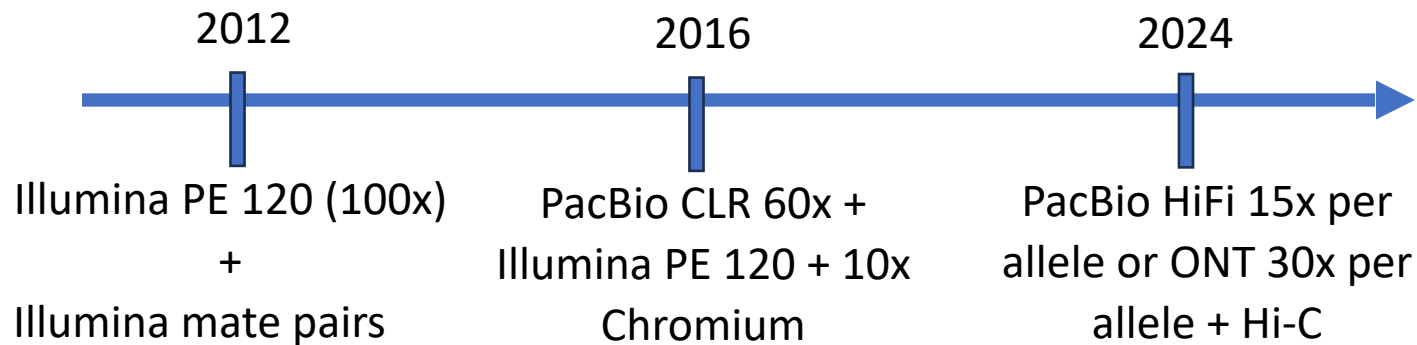


RefGen Sequencing recipes

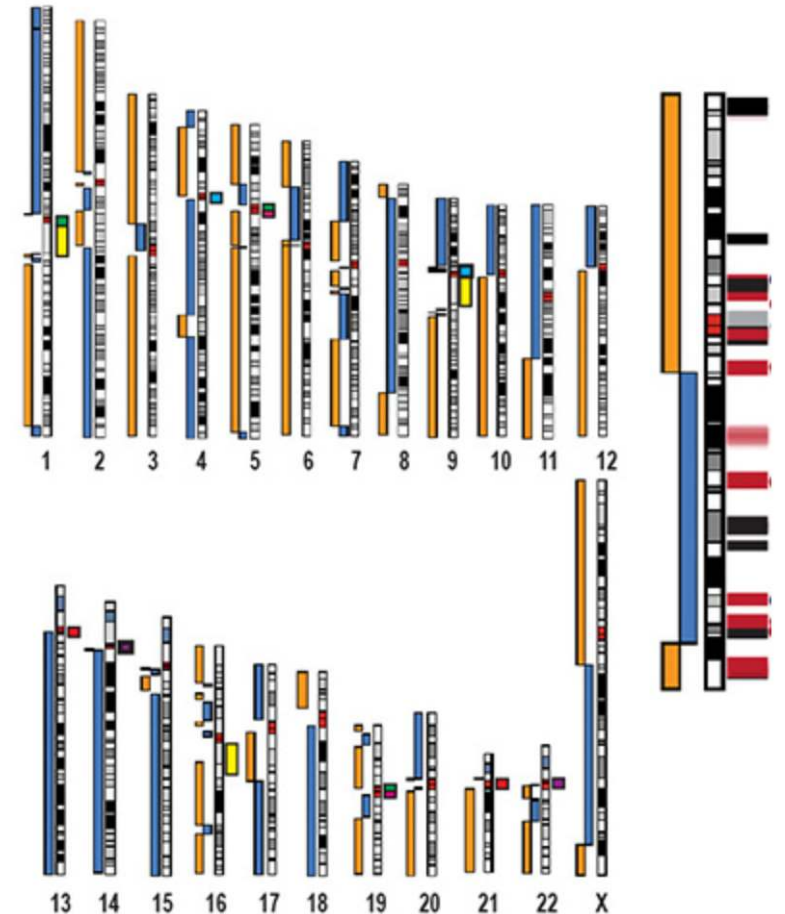


Optimal technology combination for RefGen is a moving target

Technology is constantly developing
So do the methods of analysis



Where to check? ERGA or EBP SOPs

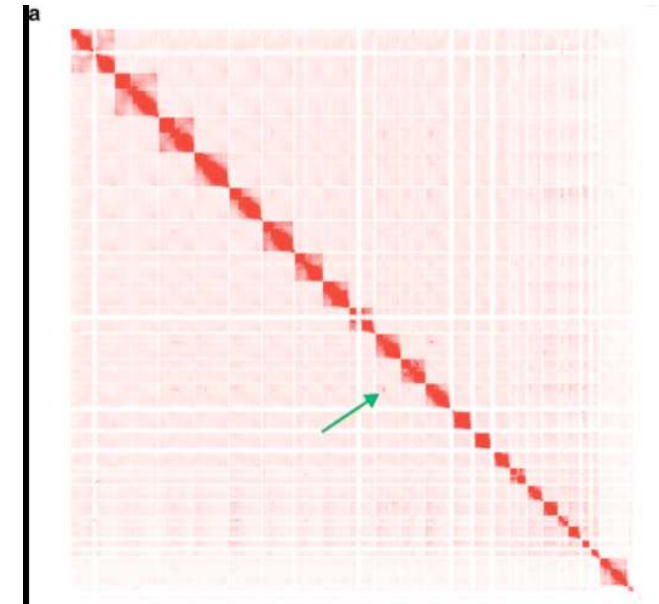
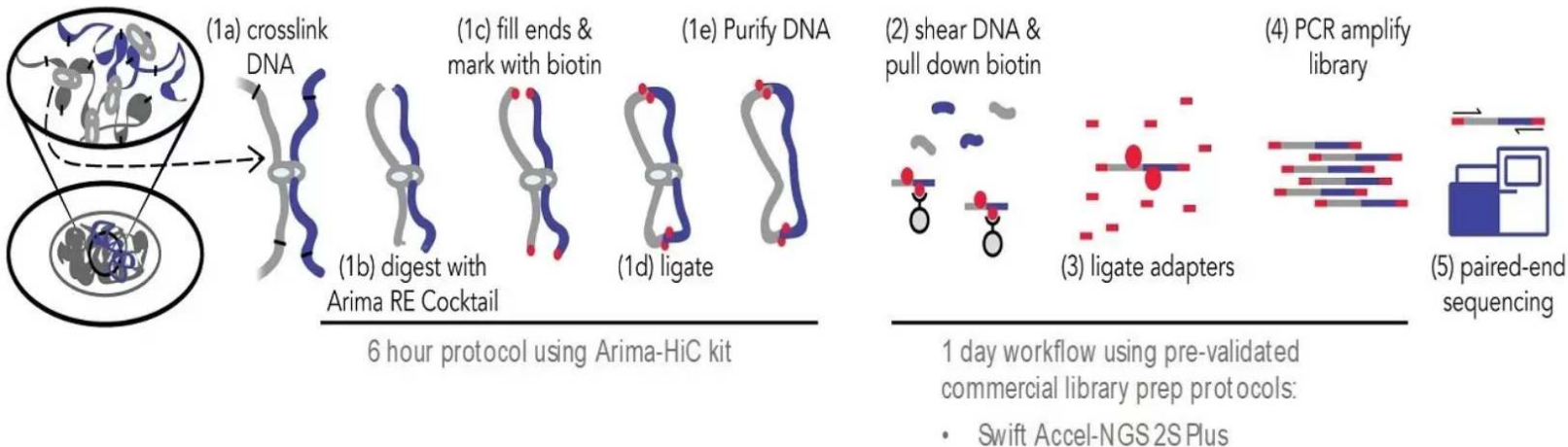


RefGen recipe, details



- 15x PacBio HiFi per allele / ONT 30x per allele + low-coverage Illumina
- HiC 50M reads per Gb of genome (Arima HiC or DoveTail OmniC)
- RNA-seq for annotation
 - 50M reads per tissue mix (EBP standard)
 - Rather 100M reads per tissue, use as many tissues as possible

HiC library principle: DNA arrangement in chromosomes Invaluable for chromosome reconstruction



FAQ: What data should I add to improve my existing fragmented assembly?



A: Do not waste your time and just do it from scratch.

Time of a bioinformatician is more expensive than sequencing.

Long-read technologies nowadays is not what they used to be 5 years ago.

Do not “polish” your HiFi reads with Illumina - you will just introduce errors.



Important to keep in mind
while planning
reference genome sequencing

RefGen: sampling methodology is IMPORTANT

Taxon-specific sampling and preservation

(GIGA)ⁿ
SCIENCE

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GigaScience



Volume 11
2022

Article Contents

Abstract

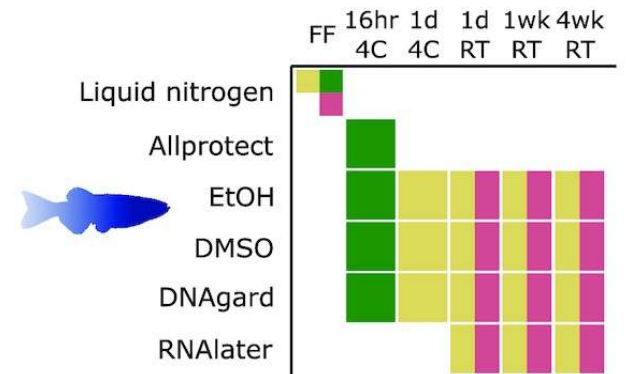
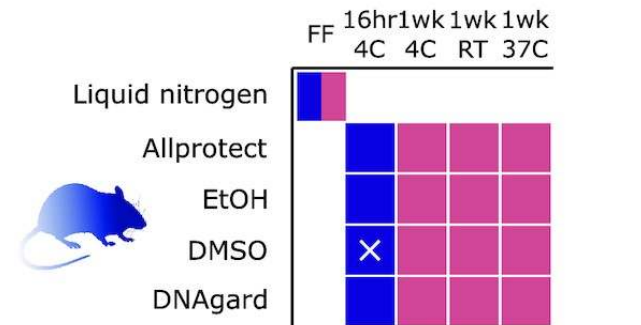
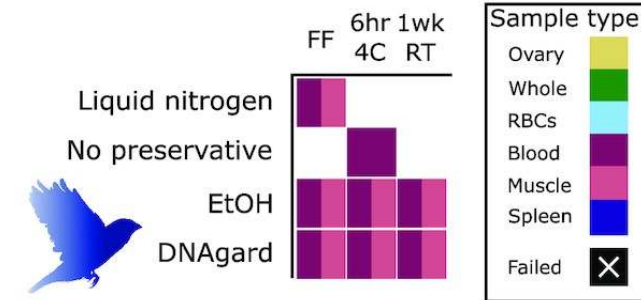
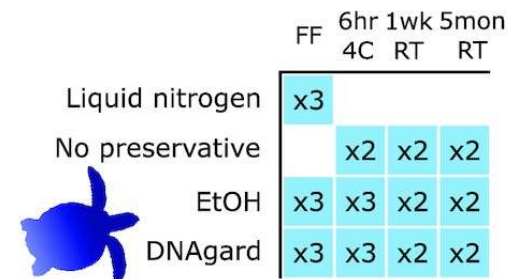
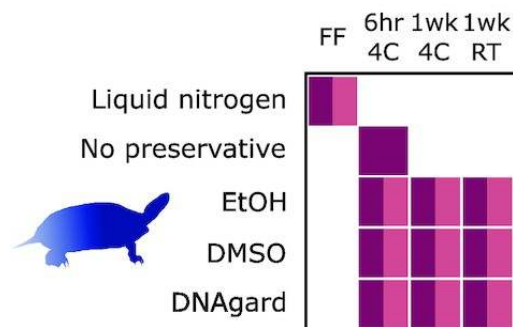
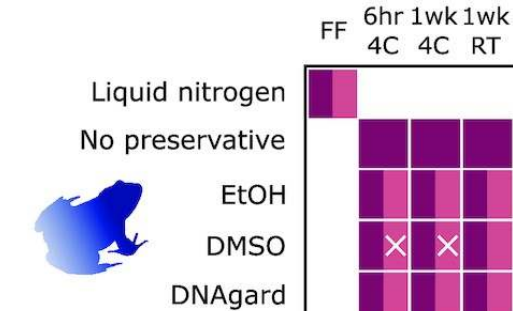
JOURNAL ARTICLE

Benchmarking ultra-high molecular weight DNA preservation methods for long-read and long-range sequencing

Hollis A Dahn, Jacquelyn Mountcastle, Jennifer Balacco, Sylke Winkler, Iliana Bista, Anthony D Schmitt, Olga Vinnere Pettersson, Giulio Formenti, Karen Oliver, Michelle Smith ... [Show more](#)
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GigaScience, Volume 11, 2022, giac068, <https://doi.org/10.1093/gigascience/giac068>

Published: 10 August 2022 [Article history](#)

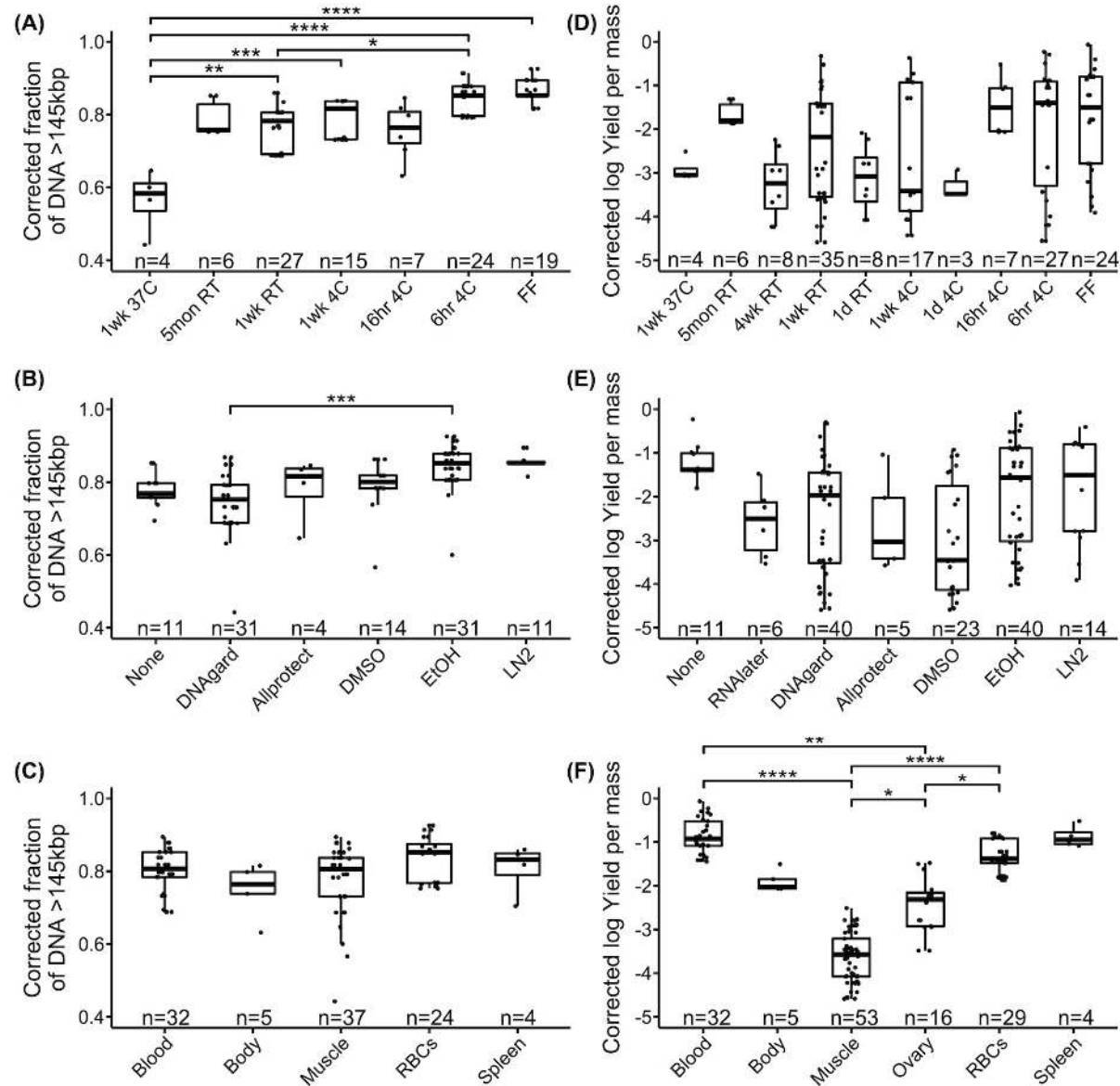


Sample type

- Ovary
- Whole
- RBCs
- Blood
- Muscle
- Spleen
- Failed

Dahn et al, 2022

RefGen: Sampling parameters matter



The most important one –
TEMPERATURE after collection



RefGen: Sample processing in the lab or field



- Optimally – keep the organism alive as long as possible
 - Do not freeze before dissection

- If large organism:
 - Dissect on ice
 - Lentil-size tissue parts are the best

Weight the sample if possible



Picture by Mara Lawnizak

- Place the parts into **pre-chilled** separate (barcoded) tubes
 - Make sure the tubes are suitable for -70°C

Please, do not send us a whole frozen mammal.....

RefGen: Correct taxonomic identification



- Make sure that the specimen is correctly identified!
- Ask for second opinion if unsure

Note: the heterogametic sex is always preferred

- Sanger-sequence DNA barcodes
 - Will help ID
 - Will be used as a tracker to safeguard against sample mix-up
- Take a picture including a **measurement instrument** (=digital voucher)
(if possible – include a colour chart)

Before going to the field, check list



- How much material is needed? How many individuals?
- What should I bring to the field if the sample must be processed there? Can we invest in a dry shipper or a portable fridge?
- Can my sample be preserved in ethanol (check with seq center and literature!)
- If the genome is supposed to be annotated – bring along RNALater or TRIZOL for the dedicated sample
- Record metadata (FAIR):
 - living stage of the organism
 - sex
 - body / organism part
 - time and temperature between sampling and preservation
 - GPS coordinates





How to check if someone is already sequencing the species you are interested in?

- Talk to the GoaT! <https://goat.genomehubs.org/>

Genomes on a Tree (GoaT)

Genomes on a Tree (GoaT): A versatile, scalable search engine for genomic and sequencing project metadata across the eukaryotic tree of life. Challis et al. 2023. Wellcome Open Res 2023, 8:2 doi:10.12688/wellcomeopenres.18658.1

GoaT has been built using [GenomeHubs](#) to help coordinate efforts across the [Earth Biogenome Project](#) (EBP) Network at all stages from planning through sequencing and assembly to publication, [read](#).

Search GoaT

Type to search GoaT taxon index (e.g. Canidae)

☐ include descendants ☐ include estimates ☐ empty columns ☐ result columns ☐ query builder

☐ Off ☐ On ☐ Off ☐ On ☐ On ☐ On

Type to search GoaT taxon index (e.g. Canidae)

tax_name(Xeromyces bisporus)

☐ include descendants ☐ include estimates ☐ empty columns ☐ result columns ☐ query builder

☐ Off ☐ On ☐ Off ☐ On ☐ On ☐ On

scientific_name	taxon_id	assembly_level	assembly_span	genome_size	chromosome_number	haploid_number
<i>Xeromyces bisporus</i>	89491	Scaffold	22M	30.7M	8	4

[TSV](#)

When using these data, please cite [Genomes on a Tree](#) and the original data

Xeromyces bisporus (species)

89491

1 species
1 assembly
0 chromosomal
1 project

[BlobToolKit](#) [ENA](#) [NCBI](#)

snail plot CCCX01

assembly_span	assembly_level	genome_size	haploid_number	chromosome_number
22M primary, n=1	Scaffold primary, n=1	30.7M median, n=4	4 mode_low, n=1	8 mode, n=2

Lineage
Eukaryota Opisthokonta Fungi Dikarya Ascomycota saccharomyceta Pezizomycotina leotiomyceta Eurotiomycetes Eurotiomycetidae Eurotiales Aspergillaceae Xeromyces

Names
Xeromyces bisporus L.R. Fraser, 1953 - authority
Xeromyces bisporus - scientific name
Xeromyces bisporus - synonym
Monascus bisporus - synonym
[gpXerBisp - toid_prefix](#)
[gpXerBisp - tol_id](#)

Analyses

Title	Files	Assemblies	Taxa	Source
btK-CCCX01	2 files	GCA_90006255.1	89491	BlobToolKit

Attributes

Attribute	Value	Summary	Source
assembly_level	Scaffold	primary	direct (1)
assembly_span	22M	primary	direct (1)
bioproject	PRJEB6149	list	direct (1)
biosample	SAMEA2500982	list	direct (1)

Not just RefGen: Legal issues - Nagoya & CITES



TAKE IT SERIOUSLY

Non-compliance: jail sentence, fine, paper retraction, etc

EU ABS regulation (Regulation (EU) Nr. 511/2014) ...

→ **What KIND OF MATERIAL** are you using? (material scope)

„genetic material of actual or potential value“

“any material of plant, animal, microbial or other (**non human**) origin containing functional units of heredity i.e. genes.”

Biological material that contains DNA/RNA (dead or alive)

excludes: human DNA ≠ **human pathogens & microbiome**, plant genetic resources under the ITPGRFA and influenza strains under the PIP framework if they are used under treaty conditions (**plant example**)



CITES - trade with endangered species ([cites.org](https://www.cites.org))



A paperwork nightmare from HELL
Get in touch with your governmental authorities
at least 4 months prior to intended shipment

Courtesy: Scarlett Sett, Kiel University, Germany

And do not forget all other “normal” import/export permits for shipment of biological material!



Sample quality requirements

Garbage in – garbage out:

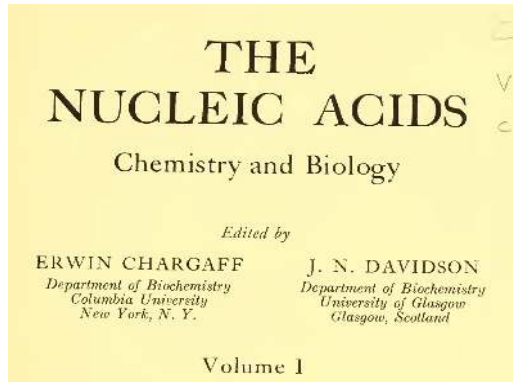


Sequencing success **always** depends on the
sample quality

NGS-quality DNA and
PCR-quality DNA
are two completely different things

Especially for long-read sequencing

Considering DNA extractions...



a. Extraction with Strong Salt Solution. Deproteinization with Chloroform

(1) *Sodium Deoxyribonucleate of Calf Thymus*.⁹⁸ Fresh frozen calf thymus glands (54.5 kg.) were minced and suspended in 0.9% sodium chloride (54 l.) and milled to produce a fine suspension. This suspension was centrifuged (6300 r.p.m.) and the solid material resuspended in 0.9% sodium chloride (45.5 l.) and milled and centrifuged as before. The tissues, which were now free of material containing pentose, were suspended in 10% sodium chloride (214 l.) with vigorous mechanical stirring at 0°. At this stage the viscosity of the solution increased considerably. After extraction at 0° for 48 hours, the insoluble material was removed by centrifuging (6300 r.p.m.) and the deoxypentose nucleoprotein precipitated from the resultant solution (pH 6.5) by the addition of an equal volume of industrial methanol. The precipitated solid was washed with 70%, then 100% industrial methanol and dried in a vacuum at room temperature. Yield, 1.69 kg. of a very slightly yellow fibrous solid.

THE PREPARATION OF DEOXYRIBONUCLEIC ACIDS BY THE *p*-AMINOSALICYLATE-PHENOL METHOD

K. S. KIRBY

*Chester Beatty Research Institute, Institute of Cancer Research,
Royal Cancer Hospital, London (Great Britain)*

(Received February 17th, 1959)

A general method for isolation of high molecular weight DNA from eukaryotes

Nikolaus Blin and Darrel W. Stafford

Department of Zoology, University of North Carolina, Chapel Hill, NC 27514, USA

Received 24 June 1976

ABSTRACT

A new method for isolation of high molecular weight DNA from eukaryotes is presented. This procedure allows preparation of DNA from a variety of tissues such as calf thymus or human placenta and from cells which were more difficult to lyse until now (e.g. *Cryptosporidium parvum*, a dinoflagellate). The DNA obtained in such a way has an average molecular weight of about 200×10^6 d and contains very few, if any, single strand breaks.

INTRODUCTION

Isolation of large quantities of nick-free, high molecular weight DNA from eukaryotic organisms has heretofore presented considerable technical difficulties. DNA prepared by conventional techniques has been a heterogeneous population of molecules ranging in molecular weight from 10×10^6 to 20×10^6 d (1, 2). The single strand molecular weight was often around

1983: P C R



Journal of Microbiological Methods

Volume 19, Issue 3, March 1994, Pages 167-172



A general method for the extraction of DNA from bacteria

Michael W Lema, Arnold Brown , Jo H Calkins

 Show more

[https://doi.org/10.1016/0167-7012\(94\)90066-3](https://doi.org/10.1016/0167-7012(94)90066-3)

Protocol | Published: November 1990

A rapid and inexpensive method for isolation of total DNA from dehydrated plant tissue

Thomas H. Tai & Steven D. Tanksley 

Plant Molecular Biology Reporter 8, 297–303(1990) | [Cite this article](#)

1176 Accesses | 183 Citations | 3 Altmetric | [Metrics](#)

A simple, rapid, inexpensive and widely applicable technique for purifying plant DNA

S Gilmore, PH Weston and JA Thomson

Australian Systematic Botany 6(2) 139 - 148

Published: 1993

Simple, Efficient, and Nondestructive DNA Extraction Protocol for Arthropods

Aloysius J. Phillips, Chris Simon

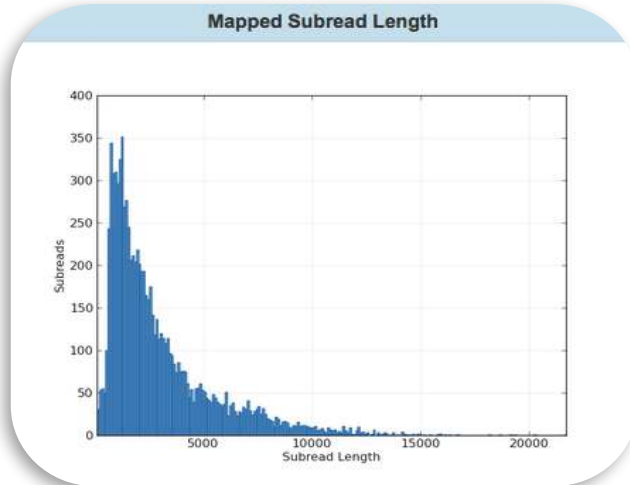
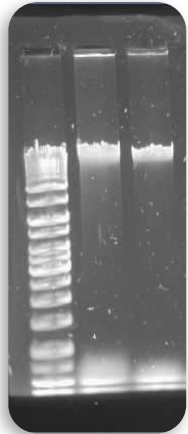
Annals of the Entomological Society of America, Volume 88, Issue 3, 1 May 1995,

Pages 281–283, <https://doi.org/10.1093/aesa/88.3.281>

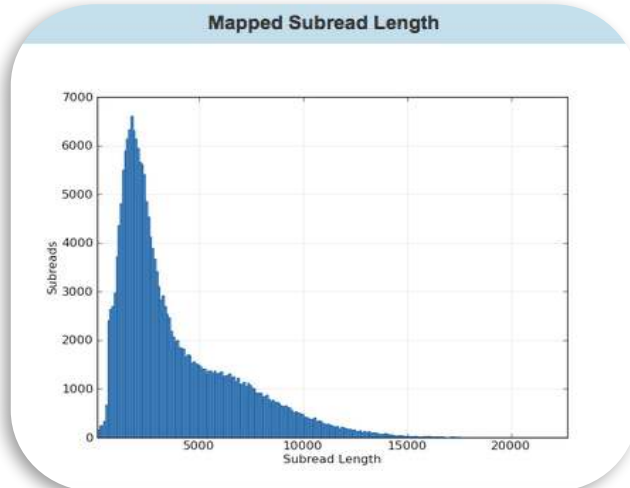
Published: 01 May 1995 [Article history](#) ▼



2013: a wake-up call



Polished Contigs	223	Max Contig Length	36,298
N50 Contig Length	2,932	Sum of Contig Lengths	480,087



Polished Contigs	9	Max Contig Length	1,508,929
N50 Contig Length	1,353,702	Sum of Contig Lengths	7,813,244



For Long Reads one needs to have *long and pure* DNA

SciLifeLab

DNA quality and inhibition of sequencing



Short-read technologies: PCR inhibition

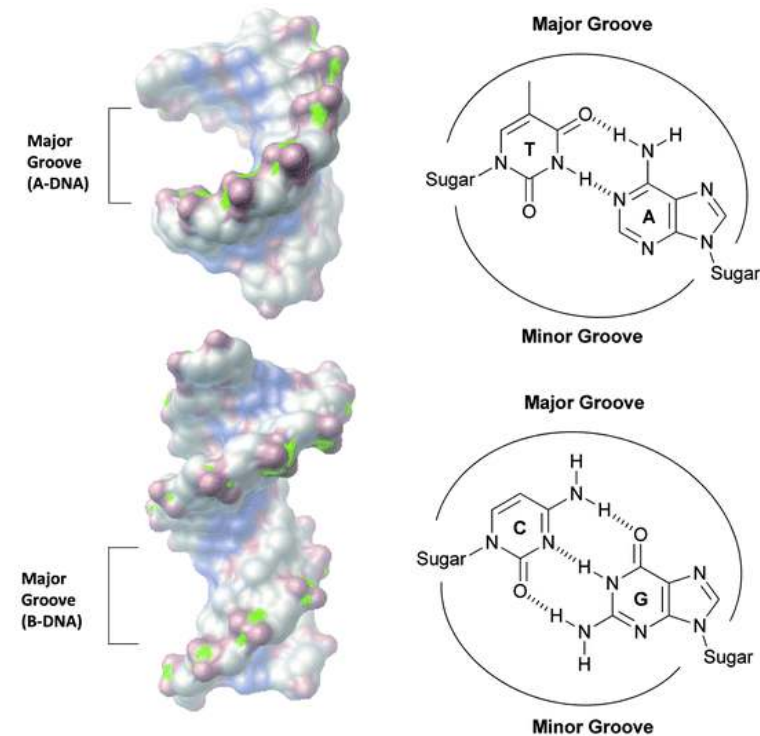
Long-read technologies are PCR-free, but one sequences native DNA “as is”.

DNA-binders:

- Proteins
- Polyphenols
- Secondary metabolites (e.g. toxins)
- Pigments
- Polysaccharides

Polymerase inhibitors:

- Salts
- Phenol
- Alcohols



[Hamilton & Arya, Nat. Prod. Rep., 2012, 29, 134-143](#)

Physical inhibiting factors – debris

What do absorption ratios tell us?



Pure DNA 260/280: 1.8 – 2.0

< 1.8:

Too little DNA compared to other components of the solution; presence of organic contaminants: proteins and phenol; glycogen - **absorb at 280 nm**.

> 2.0:

High share of RNA.

Pure DNA 260/230: 2.0 – 2.2

<2.0:

Salt contamination, humic acids, peptides, aromatic compounds, polyphenols, urea, guanidine, thiocyanates (latter three are common kit components) – **absorb at 230 nm**.

>2.2:

High share of RNA, very high share of phenol, **high turbidity**, dirty instrument, wrong blank.

*Photometrically active contaminants:
phenol, polyphenols, EDTA, thiocyanate, protein,
RNA, nucleotides (fragments below 5 bp)*

Help! My absorption values are bad!!!



Qiagen DNeasy Power Cleanup Pro

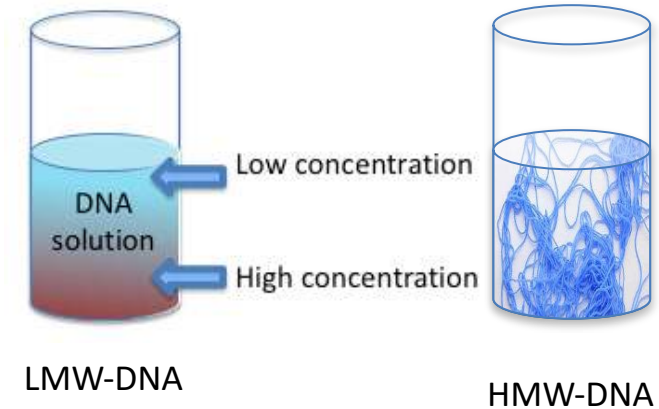


Zymogen gDNA cleanup and concentrator

Besides: AMPure beads, phenol-chloroform-CTAB, etc

Check [protocols.io](https://www.protocols.io)!

How to make a correct DNA measurement



- Thaw DNA completely
- Mix gently (**never vortex!**)
- Put the sample on a thermoblock: 37°C, 15-30 min
- Mix gently
- **Dilute 1:100** (if HMW)
- Mix gently
- Make a measurement with an appropriate blank
- **NANODROP is Bad.** Point.
- Use Qubit, or PicoGreen.
- Nanodrop value : Qubit value $\leq 50\%$

Causes of DNA degradation/damage

Mechanical damage during tissue homogenization.

Wrong pH and ionic strength of extraction buffer (-> hydrolysis).

Incomplete removal / contamination with **nucleases**.

Phenol: too old, or inappropriately buffered (**pH 7.8 – 8.0**); incomplete removal.

Wrong pH of the **DNA solvent** (acidic water).

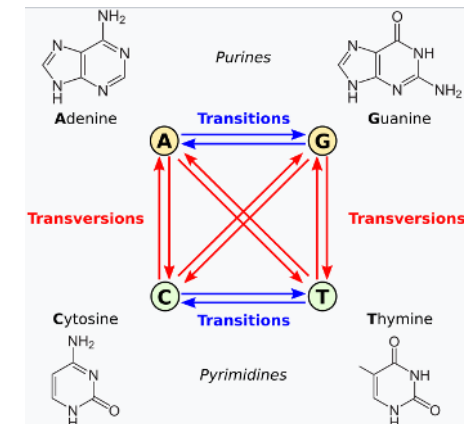
Recommended: Low TE for short-term storage, 1xTE for long-term storage.

Vigorous pipetting (wide-bore pipet tips).

Vortexing of DNA in high concentrations.

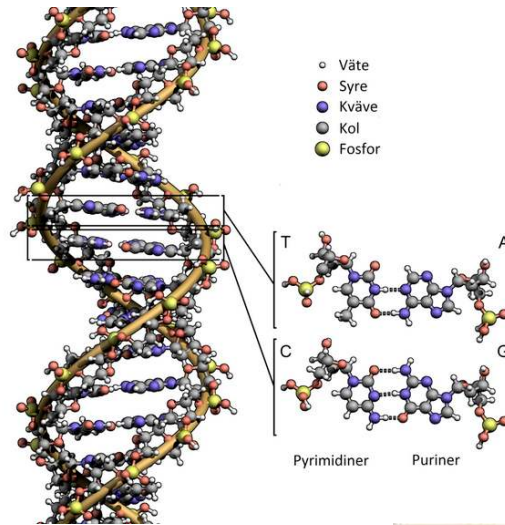
Too many **freeze-thaw** cycles (*we tested 5, still Ok*).

Sequence-dependency: depurination, deamination, T-C transitions... <https://www.biorxiv.org/content/10.1101/254276v3>



To keep in mind

There are lots of surprises, more so in non-model organisms

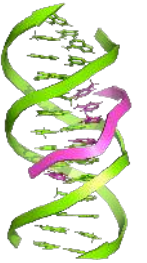
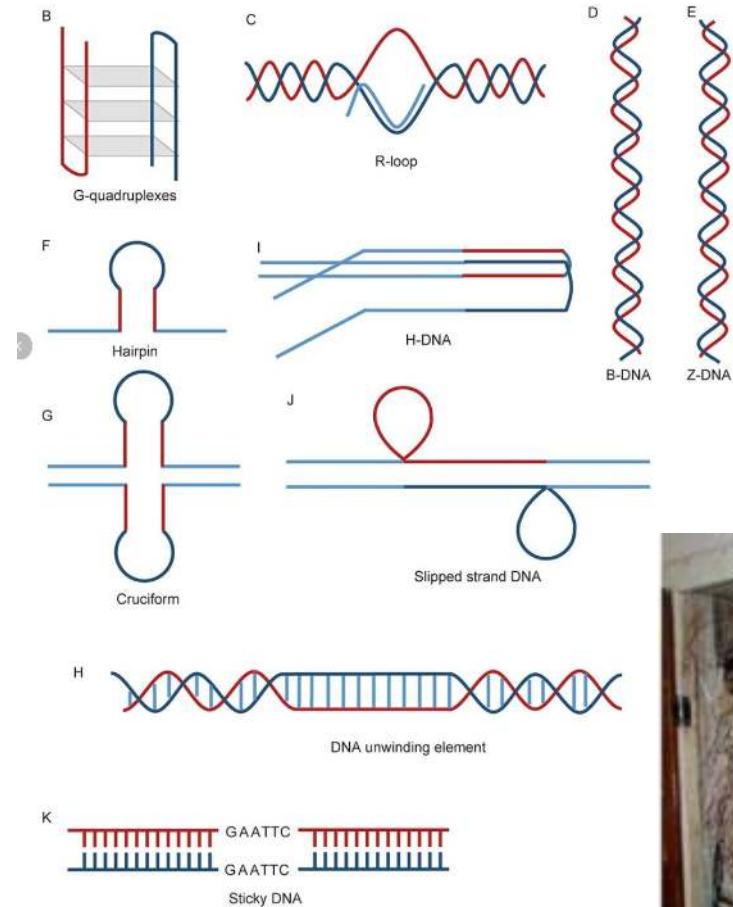


What textbook
tells you



Brutal reality

Do not forget:
DNA in solution behaves differently





What every sequencing facility wished you
knew before starting your project

Sequencing facilities and their sample requirements



Two types: commercial and non-profit (university-based)

Some can do DNA / RNA extractions, some do not

Number of samples and tissues vary (from 1 to 20)

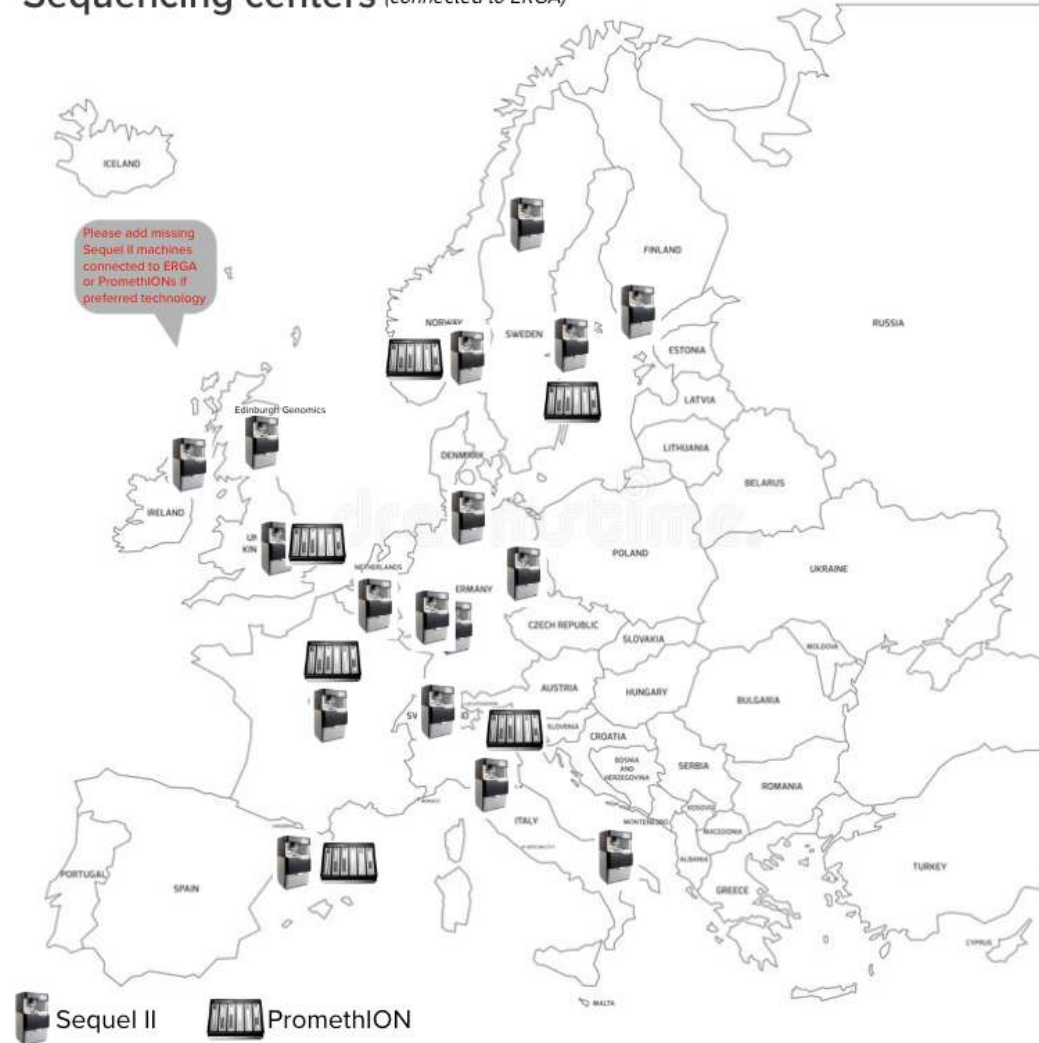
Amount of tissue / DNA vary a lot

Some accept ethanol-preserved samples, some do not

Proximity is important

No-one can answer how long time it will take

Sequencing centers (connected to ERGA)



Shipment...

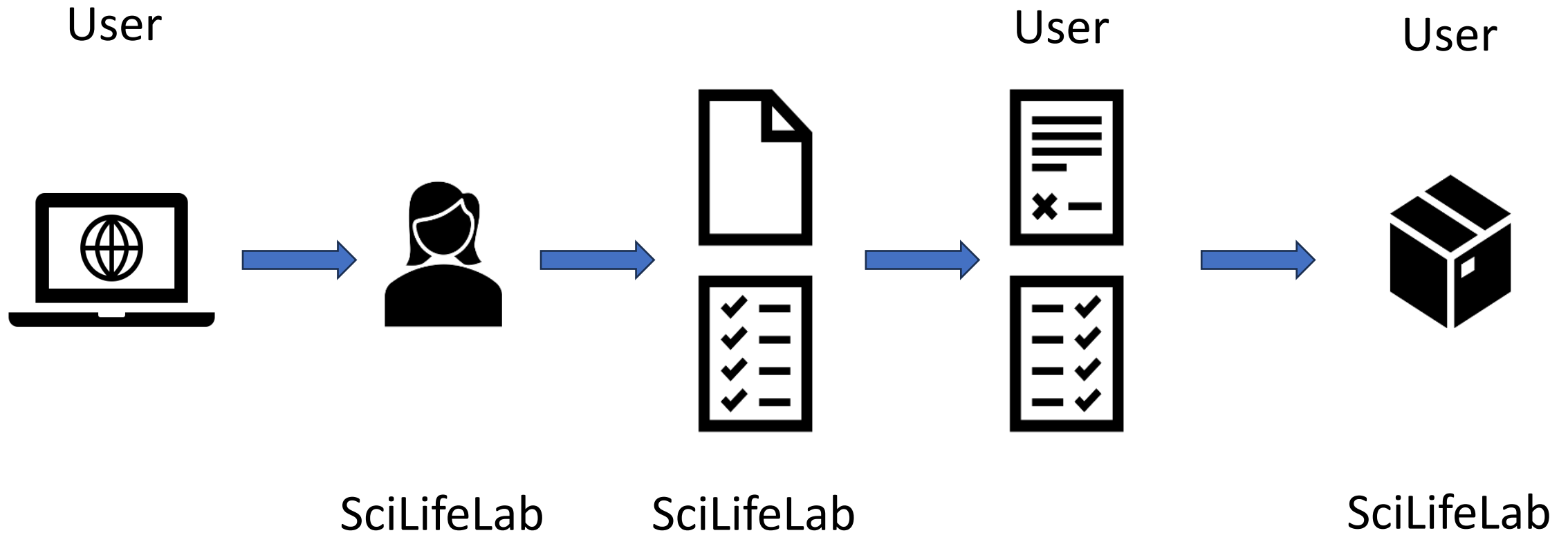


- ALWAYS solid-frozen on dry ice
- Ask for dry-ice top-up
- DHL, FedEx, UPS – all have issues, unfortunately
- BIOCAIR – used to ship human transplants. Expensive, but worth it.
- WorldCourier is very good as well. Not cheap either.

Sequencing facility documentation

Paperwork is a necessary evil.

SciLifeLab example:



Optimal project workflow



1. Check the latest sequencing recipe / application
2. Get in touch with the sequencing center(s), ask for their sample requirements and necessary paperwork
3. Study papers on similar taxonomic groups – check how were the samples collected and preserved
4. Check **ALL THE PERMITS** (ethics, collection, ABS, Nagoya, CITES, import / export)
5. Collect in the field / request from biobank / assess own stock
6. **Record metadata**
7. *For RefGen:* ID the sample (use DNA barcodes for non-models)
8. *For RefGen:* Deposit a voucher / biobank accession
9. Arrange all documentation required by the sequencing facility
10. Get in touch with a courier company
11. Ship to the sequencing center



Considering costs

Sequencing project cost = collection + sample processing + nucleic acid extraction + shipment* + sequencing + data storage + data compute + data analysis + work hours

** Shipment field-lab, lab-sequencing facility, lab-vouchering collection (left-over material?)*

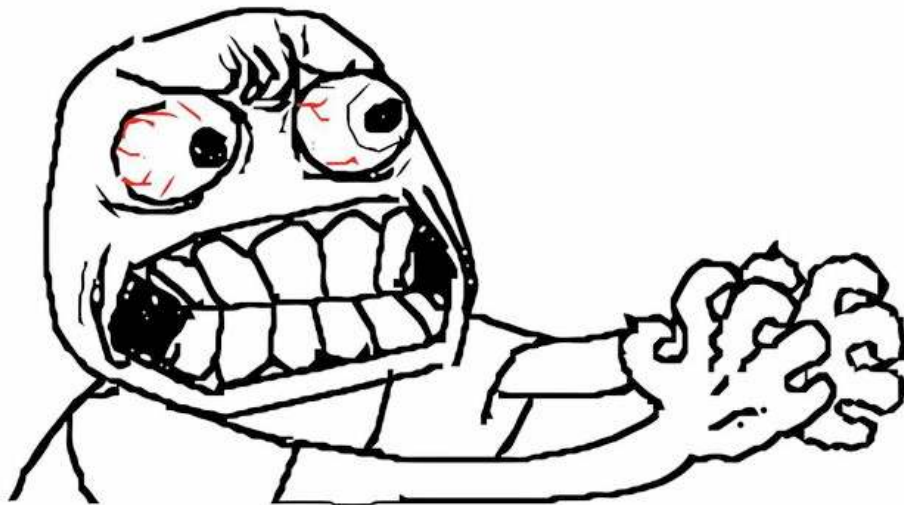
Collection + your & bioinformatician's salaries = **MOST EXPENSIVE** part of the project
Sequencing is the **CHEAPEST** part

(Never EVER believe the sequencing technology vendor prices!)

Data storage and computing resources cost (a lot of) money

Reagent Cost PacBio, Sequel		Price per kit (SEK)	Units per kit	Price / Unit	Units	Cost (SEK)	Price* / Unit	Units	Cost (SEK)	Cost (SEK)
Sample preparation										
HiFi SMRTbell Express Template Prep Kit 2.0+ Enz Clean Up	Cost per library	16279	9	1809	1	1809	2532	1	2532	2532
AMPure Clean-up	Cost per library	2898	20	145	1	145	203	1	203	203
QC and Size Selection										
Megaruptor DNA shearing 2-20 kb fragments	Per sample up to 10 µg DNA	N/A	N/A	105	2	210	155	1	155	155
SageELF	Cost per library			378	1	378	612	1	612	612
Femto PFGE	Input QC, 1-11 samples	N/A	N/A	960	4	3840	1350	4	5400	5400
Consumables tubes, tips, Ampure Beads	Cost per library	N/A	N/A	220	1	220	220	1	220	220
Sequencing Reagents										
Sequel™ SMRT® Cell 8M v3 Tray (4 cells)	Per SMRT cell	40801	4	10200	1	10200	14280	1	14280	14280
Sequel Sequencing Kit 2.0 Bundle 4rxn	Per SMRT cell	46292	20	2315	1	2315	3240	1	3240	3240
Sequel Sequencing consumables	Per run (4 SMRT cells)	N/A		850	0,25	213	927	0,25	232	232
Reagent Cost, SEK						19329			26875	26875
Additional cost, SEK										
Instrument related cost, run time (HiFi30, CLR15, IsoSeq24)	Per hour / Per SMRT cell	I		300	0	Paid	300	30	9000	9000
Work hour cost (external users only)	Per hour			400	0	Paid	400	32	0	12800
TOTAL project cost excl OH									35875	48675
University overhead	Per project 29%								0	29 %
TOTAL project cost incl OH						19329			35875	62790
*Including costs of re-run, auxilliary equipment, other reagents, etc.						1.9 k€			3.5 k€	6.3 k€

Expectations vs reality★



HUMAN CELL LINES ONLY!!!

HiFi sequencing at scale

With a high-density SMRT Cell, up to 4 SMRT Cells per run, and 24-hour run times³, the Revio system with SPRQ chemistry delivers up to 480 Gb^{2.5} of HiFi reads per day, equivalent to 2,500 human whole genomes⁴ per year.

The \$500⁶ complete, phased genome

HiFi sequencing provides small variants, structural variants, repeat expansions, methylation, and haplotype phasing from a single library and sequencing run. With a comprehensive genome, you can replace multiple assays, saving valuable time and resources while gaining deeper insights in one streamlined process.

Long-read genomes at scale, with 4x less DNA input required

SPRQ chemistry on the Revio system unlocks the ability to sequence more sample types than ever before, using just 500 ng of native DNA – without sacrificing the high throughput or exceptional quality you rely on.

On-instrument 5mC and 6mA caller for multiomic Fiber-seq chromatin assay

SPRQ chemistry, paired with Google Health DeepConsensus algorithms, delivers exceptional read accuracy plus confident 5mC and 6mA methylation detection in every run. Optimized file formats reduce data storage needs through quality value binning and smart read ordering, streamlining data handling and maximizing efficiency.



Applicable to ANY vendor



Revo: Tree of Life CCS Yield by Clade
CCS yield of sequencing completed in the last 60 days



Courtesy: James Watt, Sanger Institute (DTOL)

Finally: Recognize the sequencing facility personnel

Shift from specialized labs to sequencing facilities

Sequencing of non-model organisms, especially for RefGen generation:

- Heavily reliant on pure, HMW-DNA

- High failure rate both for PacBio and ONT

- Everything is non-model

- Every project is practically R&D

- Some projects require weeks of full-time expert lab engineer



Wrapping it all up:

- Some perspective
- What to think about BEFORE planning a sequencing project (aka Project Design)
- Sequencing applications and experiment design specifics:
 - Whole-genome sequencing
 - Targeted sequencing
 - Transcriptome sequencing
 - Single-cell sequencing
 - Shotgun metagenomics
 - Reference genome sequencing + optimal project workflow example
- Sampling and sample quality requirements
- What every facility wish you knew before sending your samples

Experimental design in genomics – take home



VERY fast development

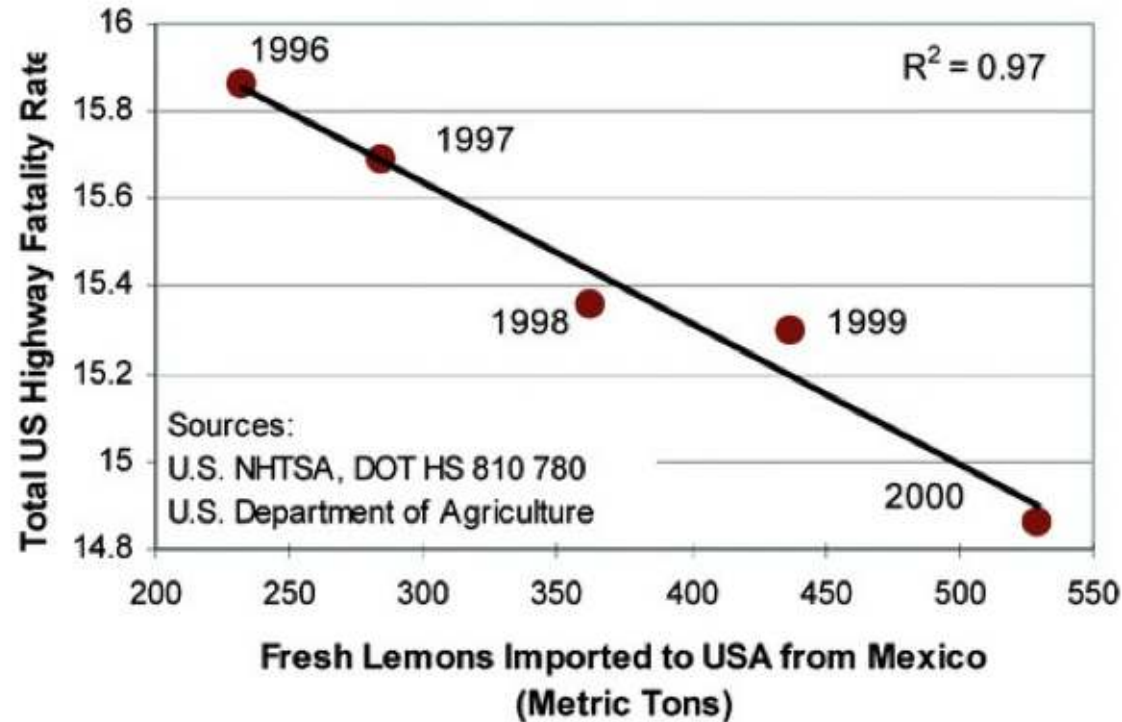
Difficult to keep oneself updated

Ask your sequencing service provider about the latest updates

Sequencing itself is the CHEAPEST part of the project

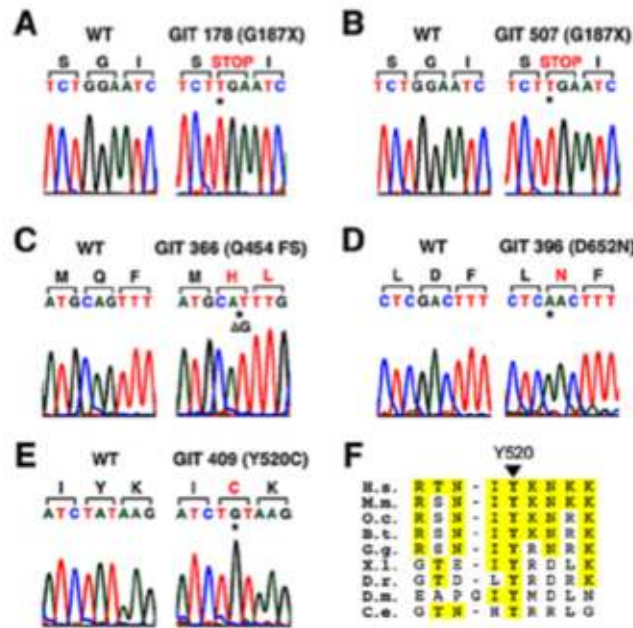
Finally, 2 minutes of philosophy

Never forget: Correlation vs Causation



Reduction in export of fresh lemons from Mexico causes significant reduction of highway traffic fatality rates in the US!

Genome is not a linear string of bases!!



Mutations in coding regions only



Transcriptional & post-transcriptional regulation

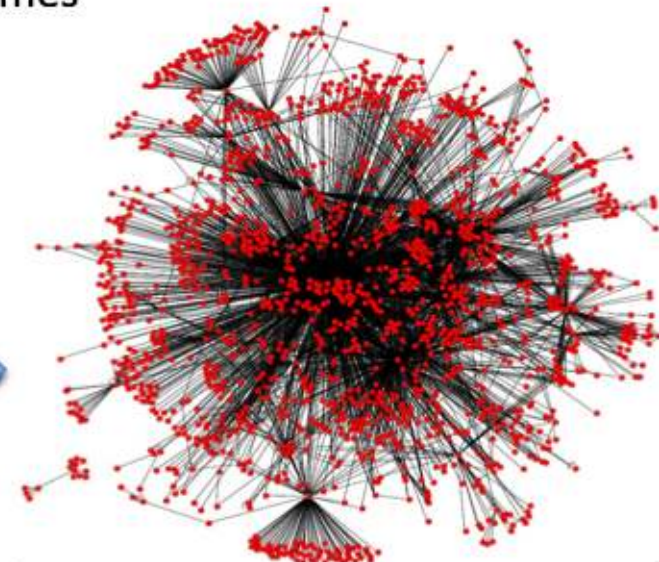


Epigenetics

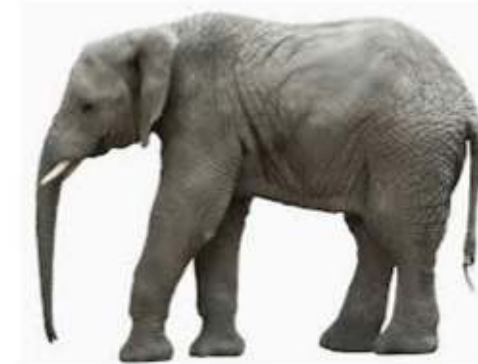
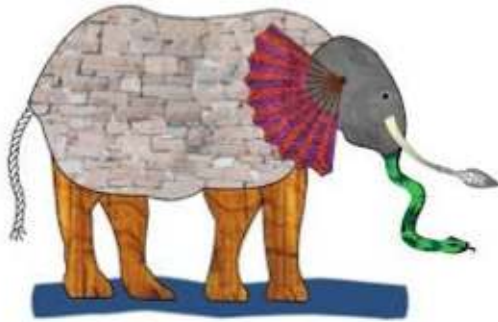


Proximity in chromosomes

```
>gi|30018278|ref|NC_004722.1| Bacillus cereus ATCC 14579, complete genome
TAGCCACTTTTTTTGATATTATAGTTGTGTTTTCACTTTGAATAAGTTTTCCACATCTTTATCTTATCC
ACAAITTTGTGTATAACATGTGGACAGTTTTAATCACATGTGGGTAAATAGTTGTCCACATTTGCTTTTTT
TGTCGAAAACCCCTTTCTCAATACAAACGACGTTTTAGGTTTTTAAATCGTTTTTCGTATAAATATACATTT
TAATTTATTAGGTTGTACATTTGTTGCACAACCTTTATTCTTTTACCAACTTAGTAAAGGAGGGACACCT
TTGGAAAATATCTCTGATTTATGGAATAGTGCCTTAAAAGAATTAGAAAAAAGGTAAGCAAGCCTAGTT
ATGAGACATGGTTAAAATCCACAACGGCTCATAACTGAAGAAAGACGTATTAACGATTACAGCTCCGAA
TGAATTTGCTCGTGACTGGCTAGAACTCTCATTACTCCGAACATAATTCAGAAACACTATACGATTTAACA
GGGGCAAAATTAGCAATTTCGCTTTTATTATTCGCCAAAGTCAAGCTGAAGAGGACATTGATCTGCCTCCAG
TTAAGCCGAATCCAGCACAAGATGATTGAGCTCATTACCACAGAGCATGTTAAATCCAAAATATACATT
CGATACATTTGTTATTGGCTCTGGTAACCGTTTTGCCCATGCAGCTTCATTAGCTGTAGCTGAGGCGCCA
GCTAAAGCGTATAATCCACTCTTTATTTACGGGGGAGTTGGACTTGGAAAGACACATTTAATGCACGCAA
TTGGTCATTATGTAATTGAACATAATCCAAATGCAAAAGTTGTATTTTATCATCAGAAAAATTTACAAA
TGAATTTATTAACCTTATTTCGTGATAATAAAGCTGTTGATTTTCGTAATAAATATCGTAACGTAGATGTT
TTATTGATAGATGATATTCAATTTCTTGCTGGAAAAGAACAGACTCAAGAAGAGTTTTTCCATACATTTA
ACGCATTACACGAAGAAAGTAACAAATTGTAATTTCTAGTGACCGACCACCAAAAGAAATTTCCAACCTTT
```



Blind men & an elephant



Letter

Genome-wide association study identifies five new schizophrenia loci

The Schizophrenia Psychiatric Genom Article

Nature Genetics **43**, 969–976 (2011)

doi:10.1038/ng.940

[Download Citation](#)

Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia

Zhiqiang Li, Jianhua Chen [...] Yongrong Shi

Nature Genetics **49**, 1576–1583 (2017)

doi:10.1038/ng.3973

[Download Citation](#)

Received: 17 April 2017

Accepted: 19 September 2017

Published online: 09 October 2017

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Schizophrenia and the dynamic genome

Patrick F. Sullivan

17 April 2017

doi:10.1038/s41587-017-0018-2

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2017

Current opinion in psychiatry

Author Manuscript

HOVS Public Access

Genome-wide association studies (GWAS) of schizophrenia: does bigger lead to better results?

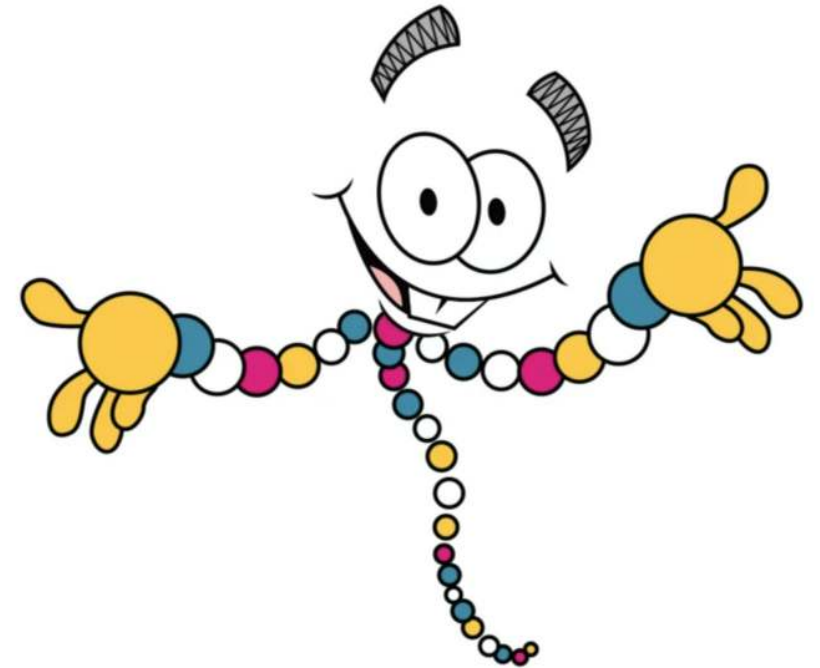
Sarah E. Bergen, PhD and Tracey L. Petryshen, PhD

Summary

Copy number variation (CNV) is a widely replicated risk factor for psychiatric disorders, including schizophrenia, although the mechanisms by which CNVs confer risk are unclear. Recent studies have provided robust evidence of CNVs associated with schizophrenia and have highlighted a potential role for schizophrenia risk-associated



Thank you!



Swedish
Research
Council



UPPSALA
UNIVERSITET



SciLifeLab



Horizon Europe
2021-2027