



Genómica

Pontificia Universidad Católica de Chile

Juliana Vianna



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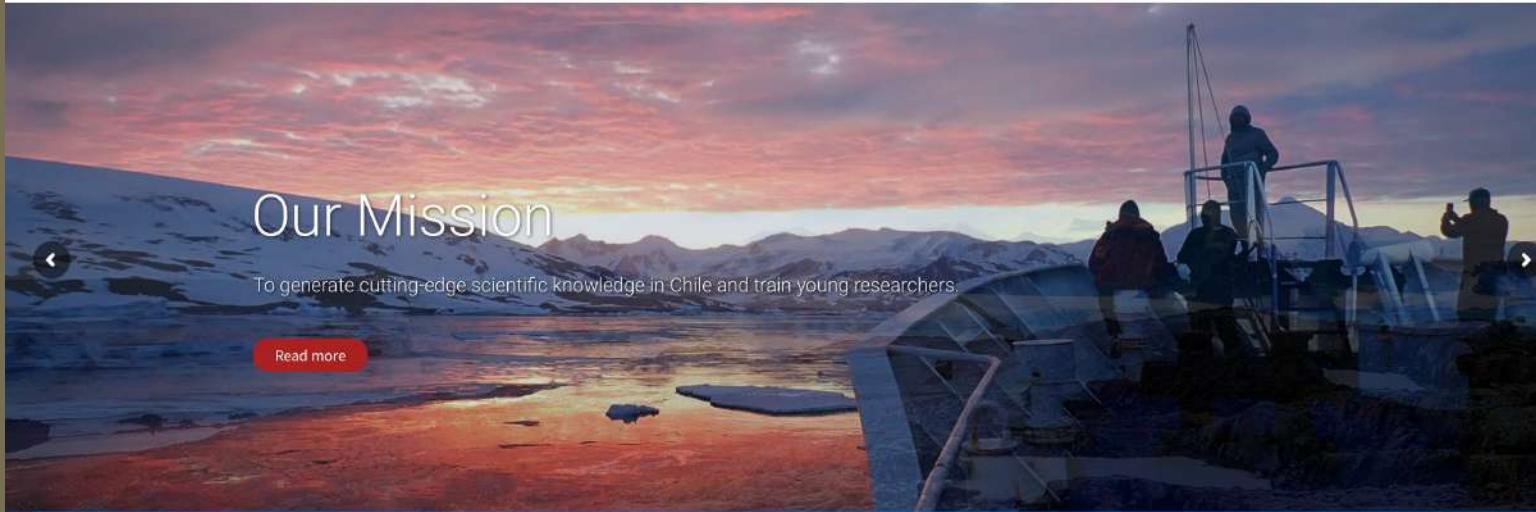
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Our Mission

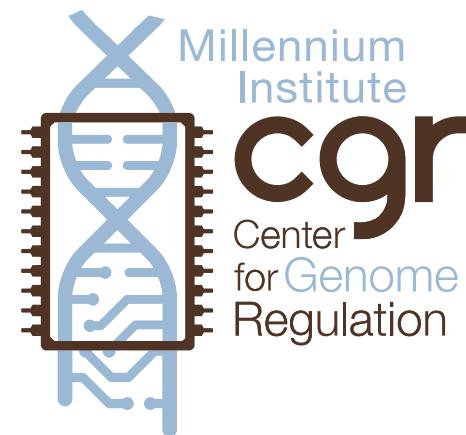
To generate cutting-edge scientific knowledge in Chile and train young researchers.

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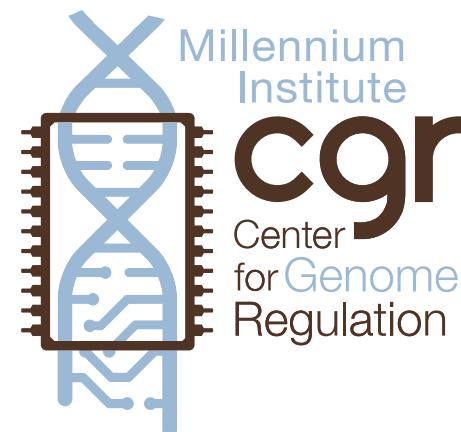
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Our Mission

To generate cutting-edge scientific knowledge in Chile

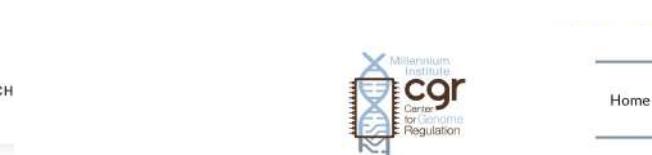
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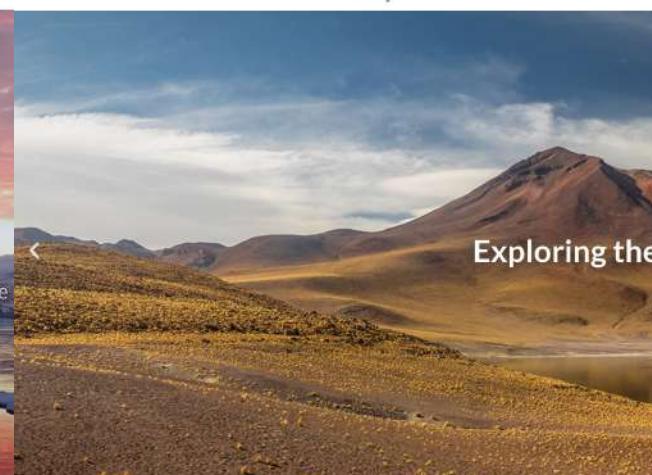
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Home

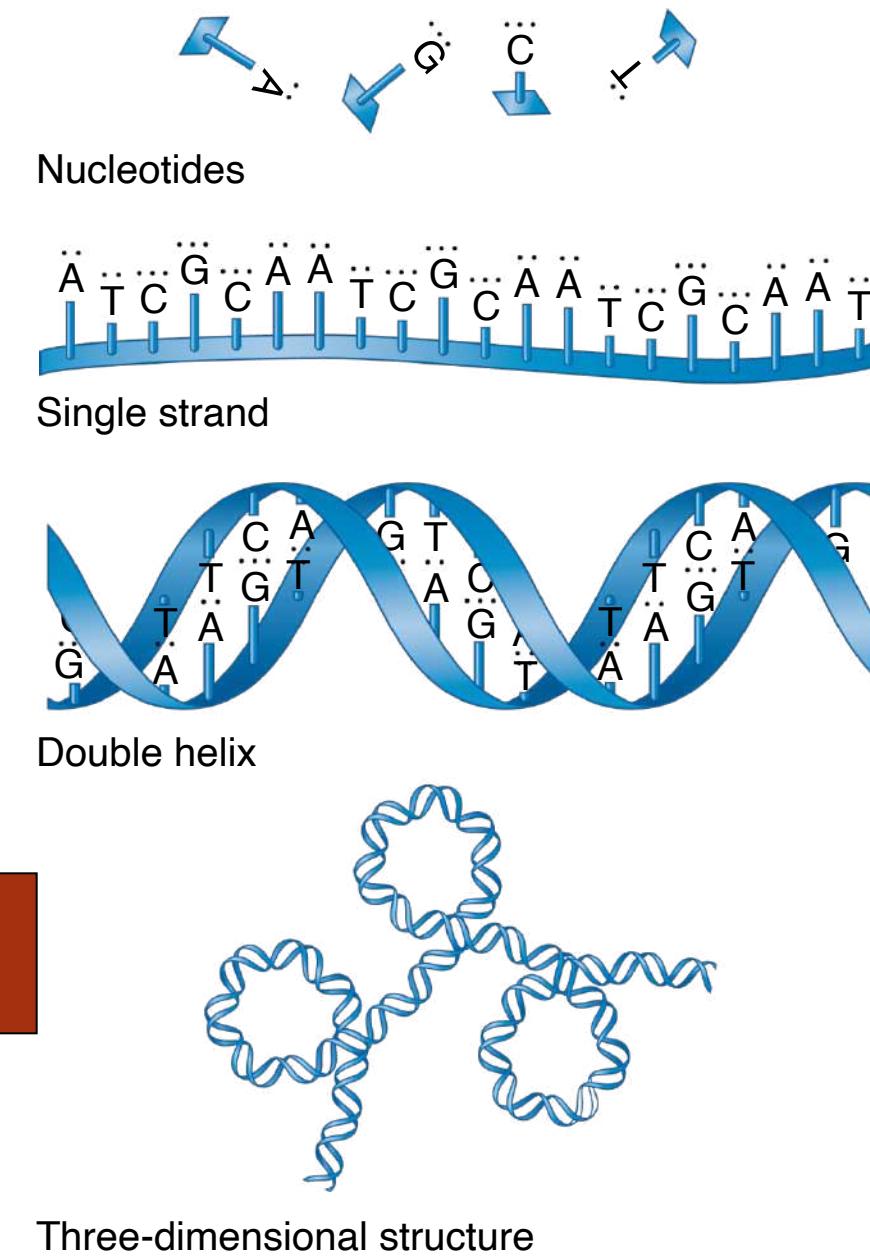
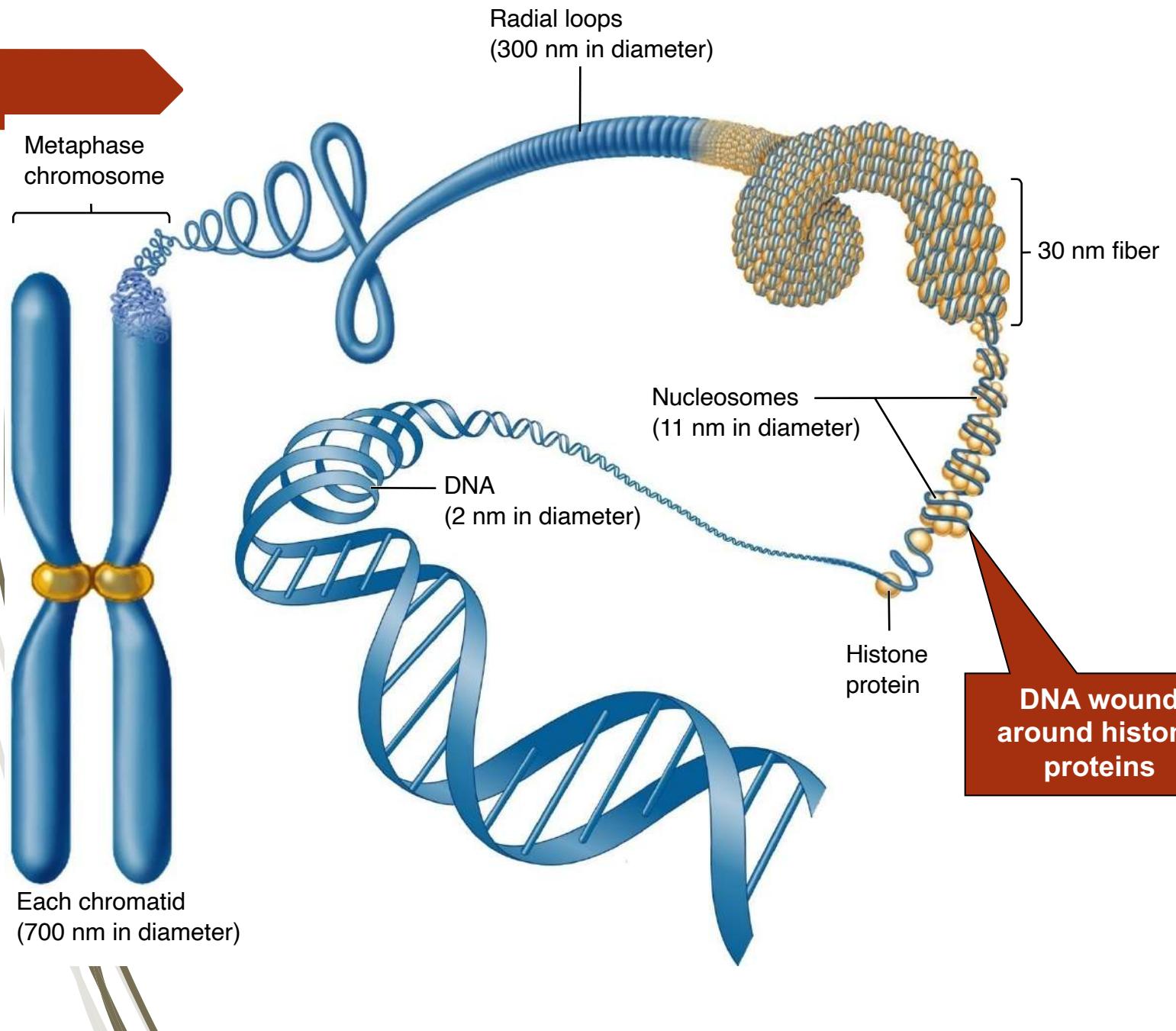




Genomas

- ▶ Genoma es el conjunto del DNA completo de un organismo.

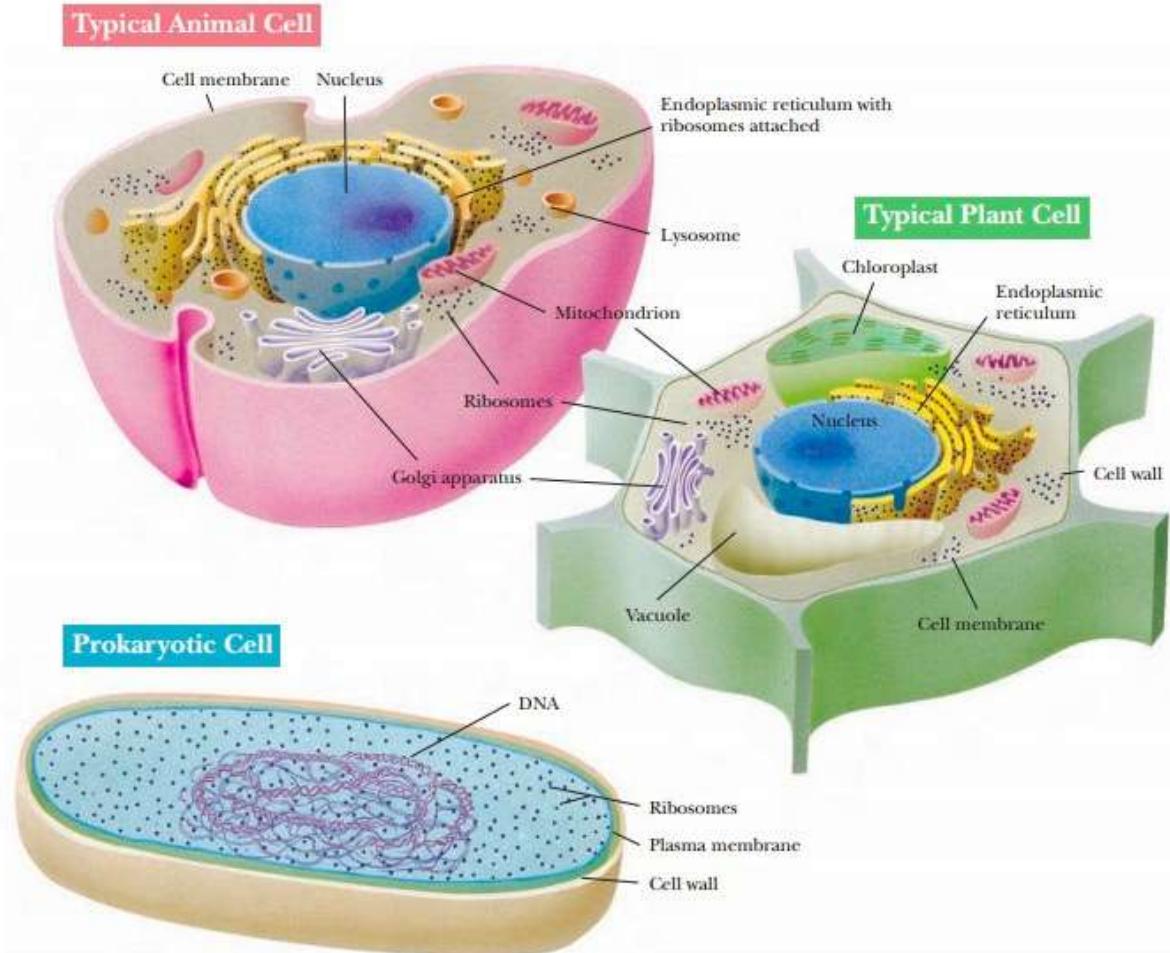




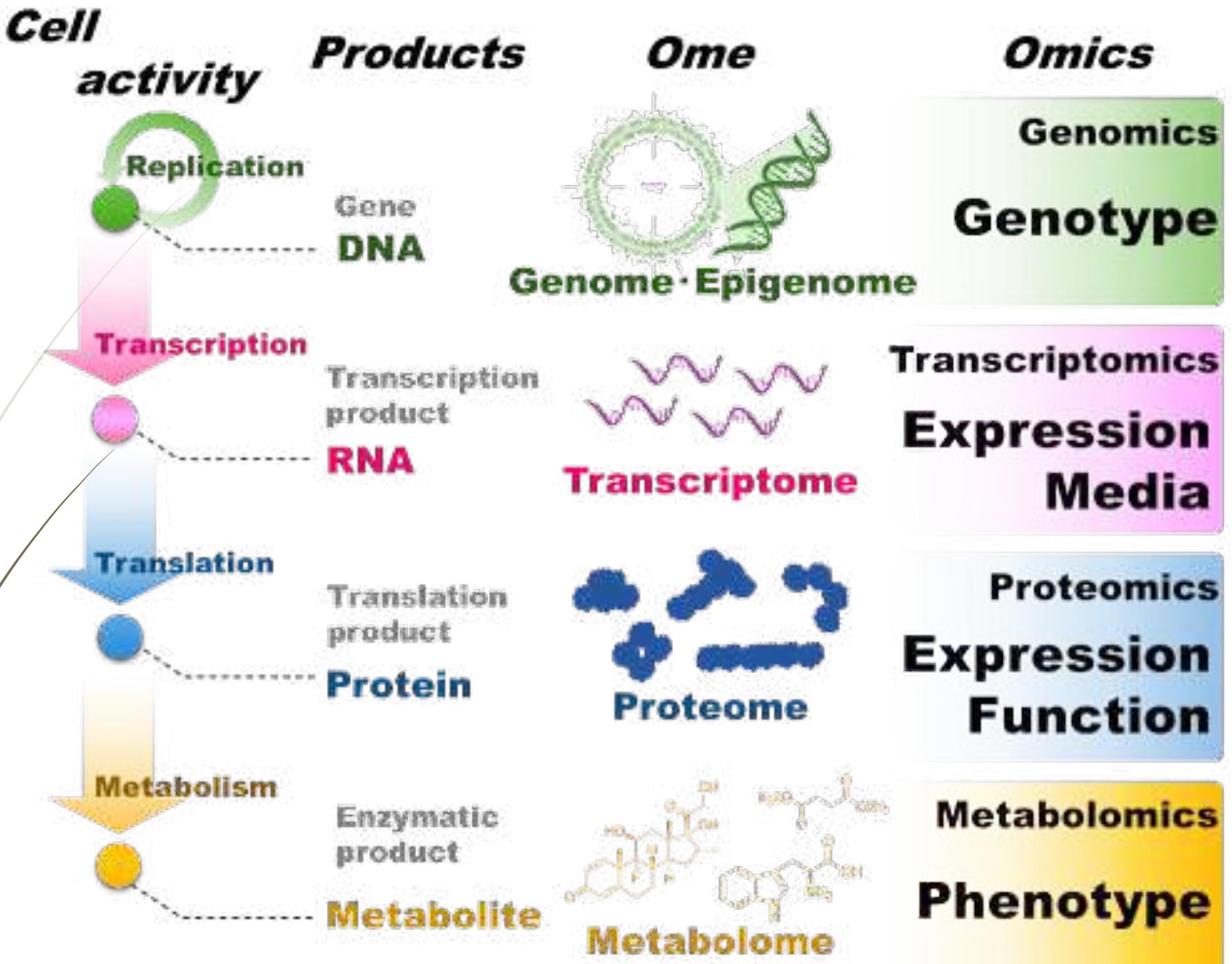
Three-dimensional structure

Tipos de genomas

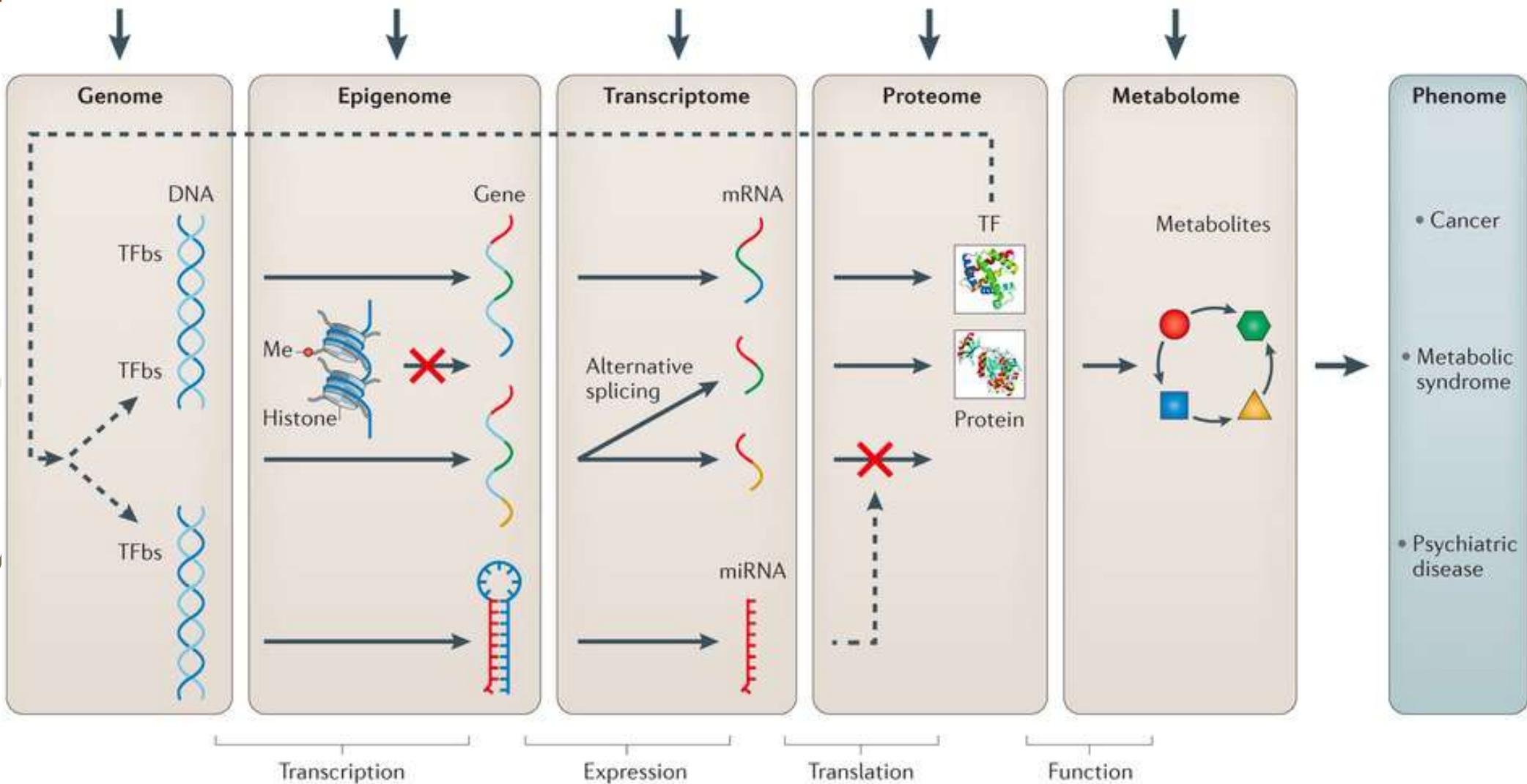
- Genoma procariota
- Genoma Eucariota:
 - Genoma nuclear
 - Genoma mitocondrial
 - Genoma cloroplasto



■ FIGURE 1.11 A comparison of a typical animal cell, a typical plant cell, and a prokaryotic cell.

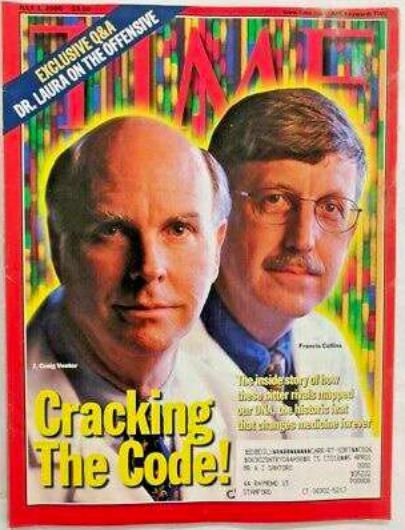


- SNP
 - CNV
 - LOH
 - Genomic rearrangement
 - Rare variant
- DNA methylation
 - Histone modification
 - Chromatin accessibility
 - TF binding
 - miRNA
- Gene expression
 - Alternative splicing
 - Long non-coding RNA
 - Small RNA
- Protein expression
 - Post-translational modification
 - Cytokine array
- Metabolite profiling in serum, plasma, urine, CSF, etc.



Genómica

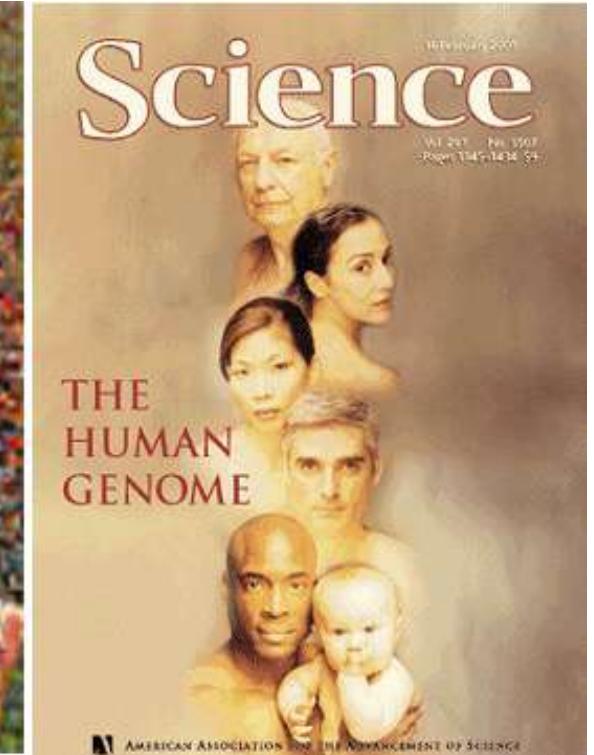
- Desde mediados de los 70s, los biólogos moleculares han sido capaces de obtener secuencias cada vez mas largas de DNA, hasta que en los 90s se logran descifrar secuencias completas de organismos.
- El más importante de estos proyectos ha sido el Proyecto Genoma Humano.



Proyecto Genoma Humano - 2003

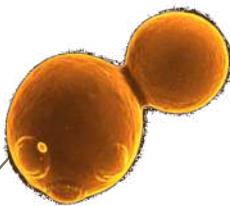


Craig Venter y Francis Collins
Celera genomics y NIH

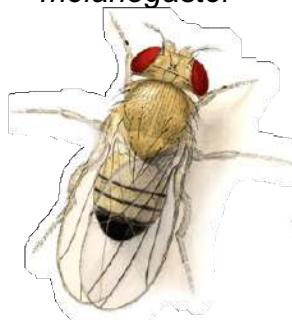


Tamaños de Genomas

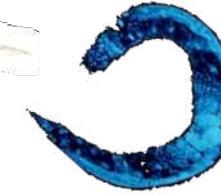
Levadura
Saccharomyces cerevisiae



Drosophila
Drosophila melanogaster



C.elegans



Arabidopsis
thaliana



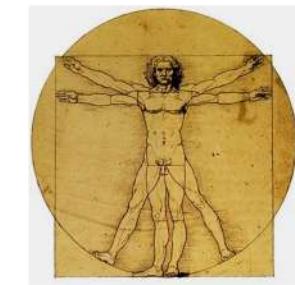
Vid
Vitis vinifera



Ratón
Rattus norvergicus
Mus musculus



Humano
Homo sapiens



12 Mbp

137 Mbp

97 Mbp

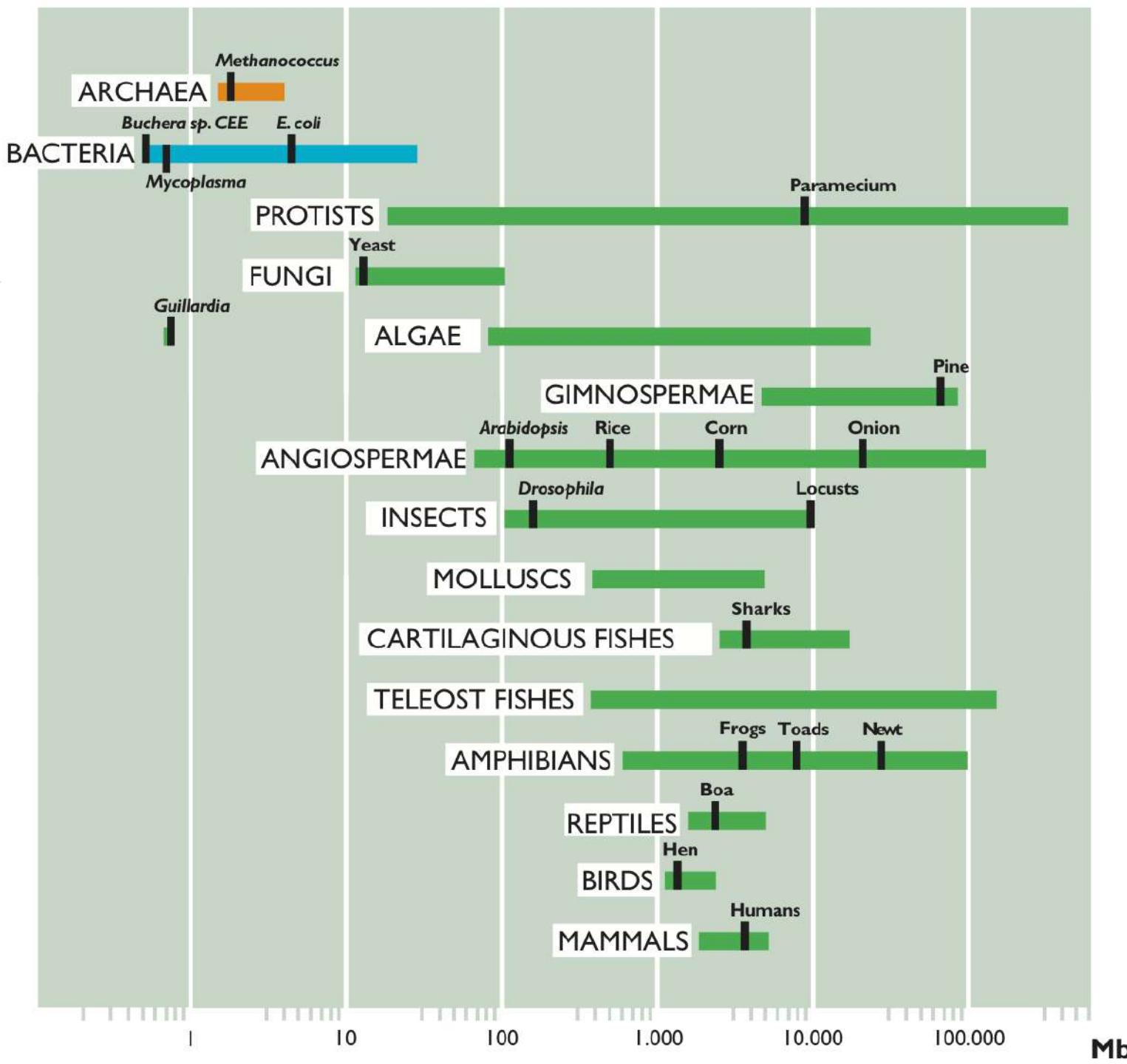
142 Mbp

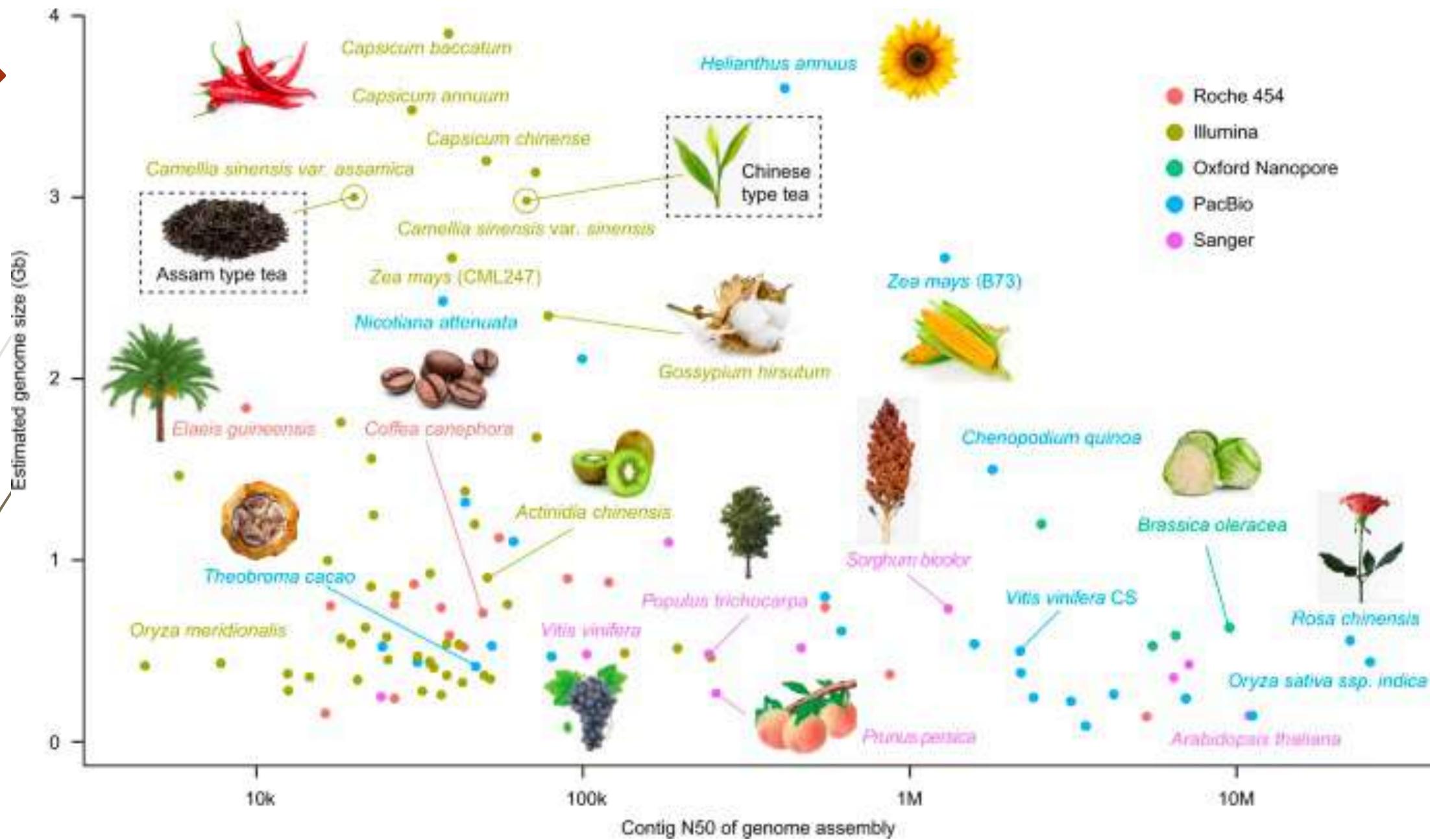
170 Mbp

2.750 Mbp

3.200 Mbp

Pares de bases (bp), kpb (o kb)= mil pb, Mpb (o MB)= un millon de pb, Gpb (o Gb) = mil millones de pb



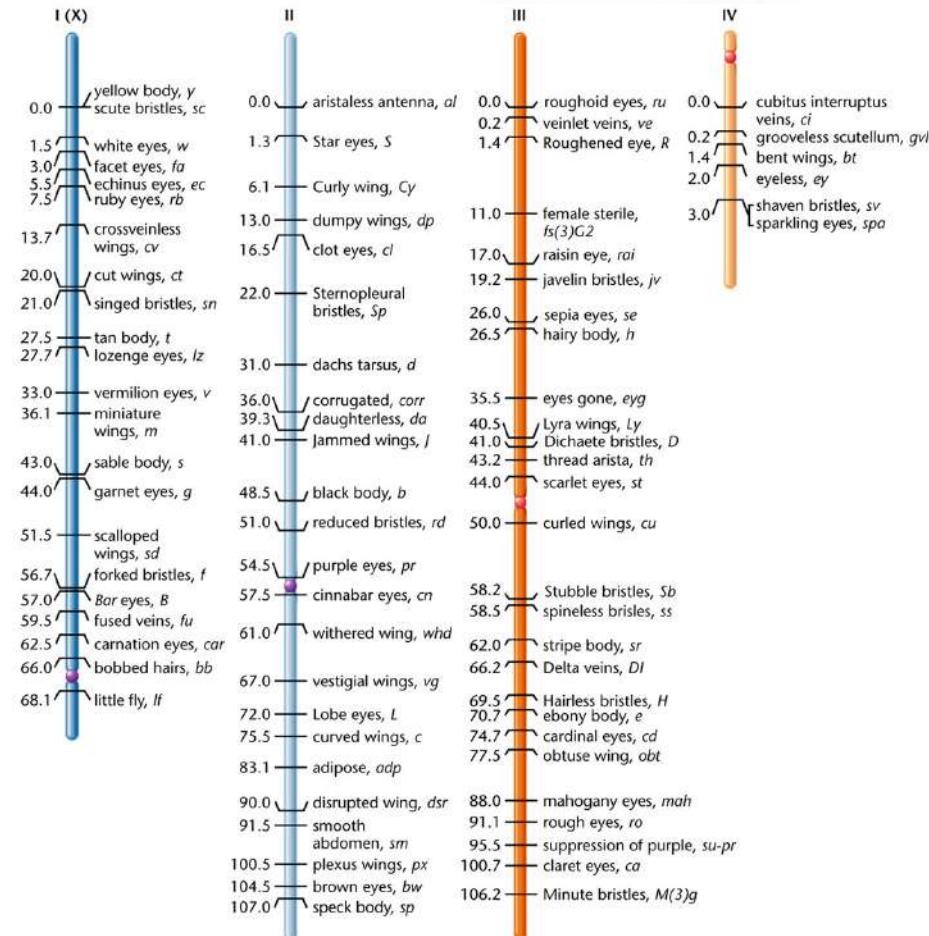


Genómica

► La genómica incluye diversos campos:

1-Genómica estructural: incluye la construcción de los datos de la secuencia del genoma, el descubrimiento de los genes y su localización, y la construcción de mapas génicos.

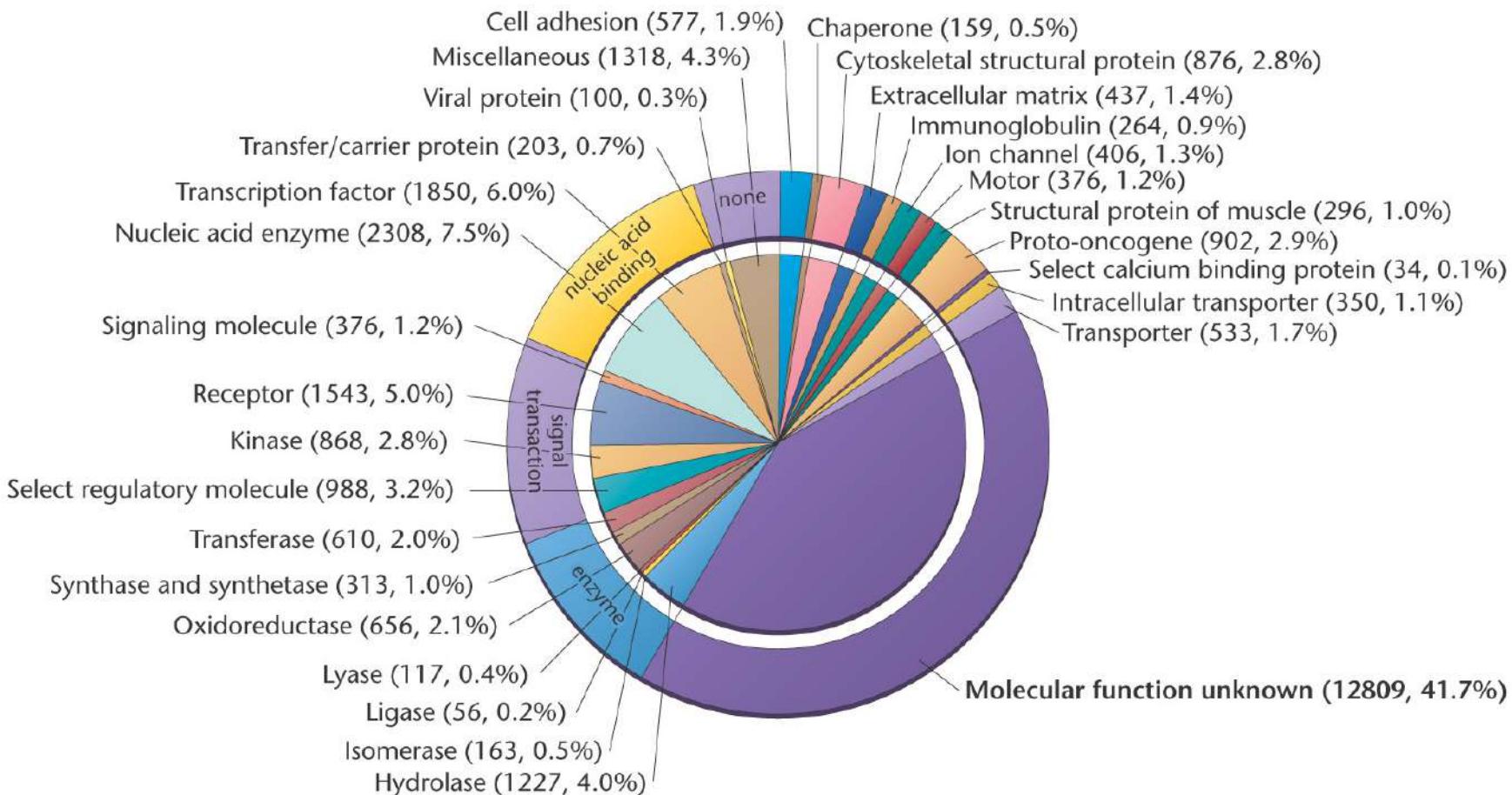
Mapa genético de los cuatro cromosomas de *Drosophila melanogaster*



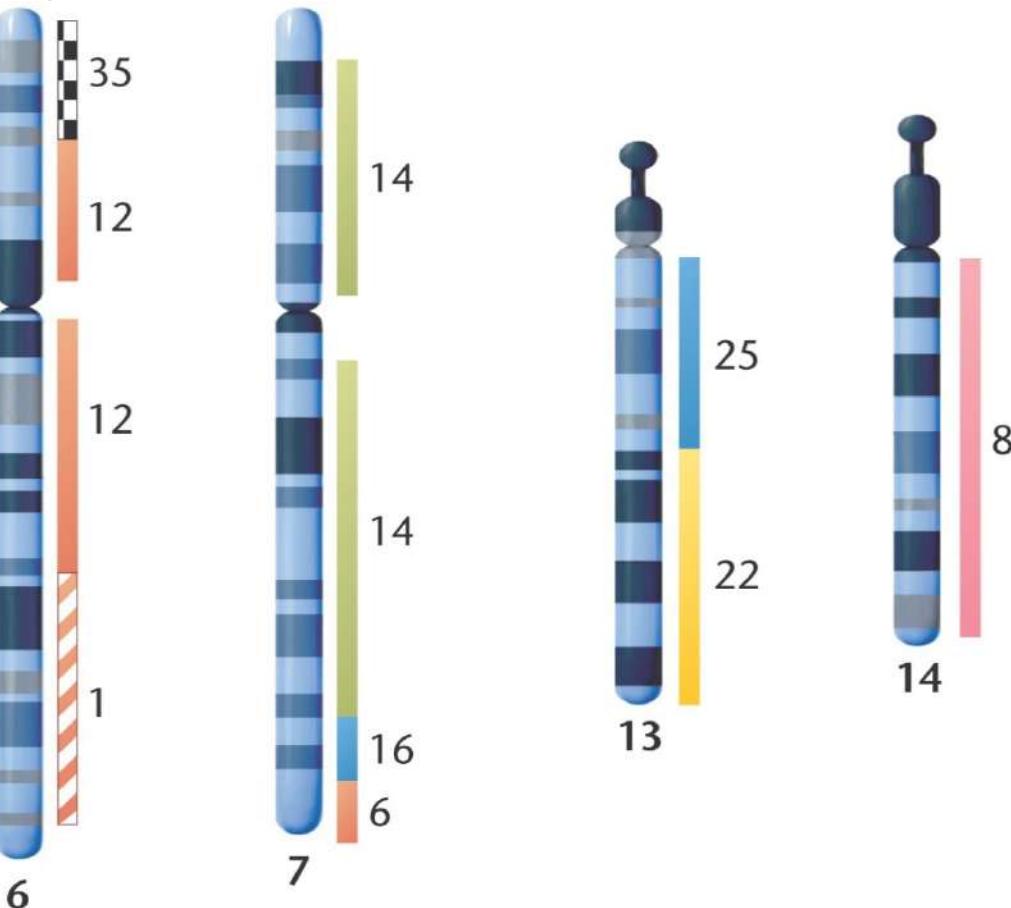
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2-Genómica funcional: La genómica funcional estudia la función biológica de los genes, su regulación y sus productos.

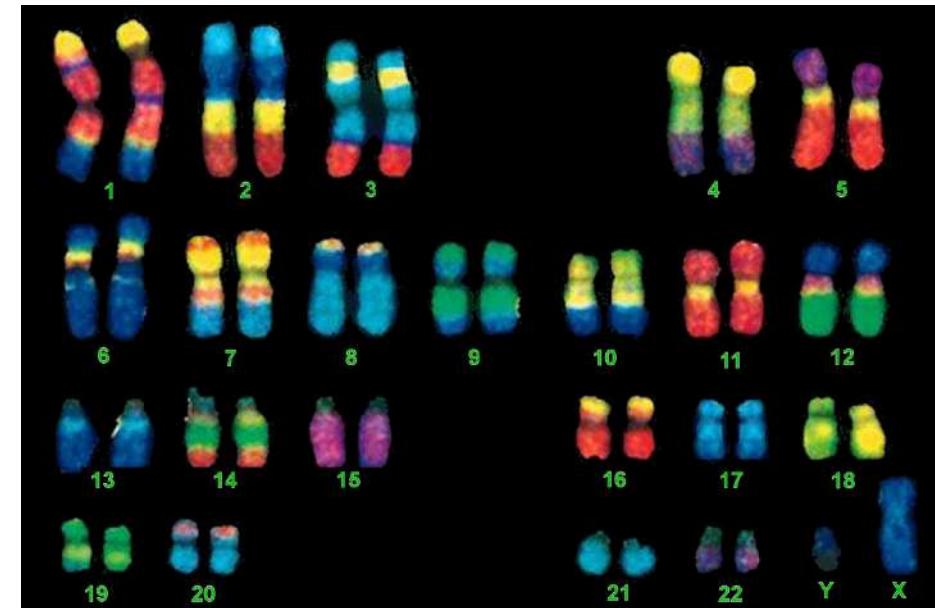
Genoma Humano



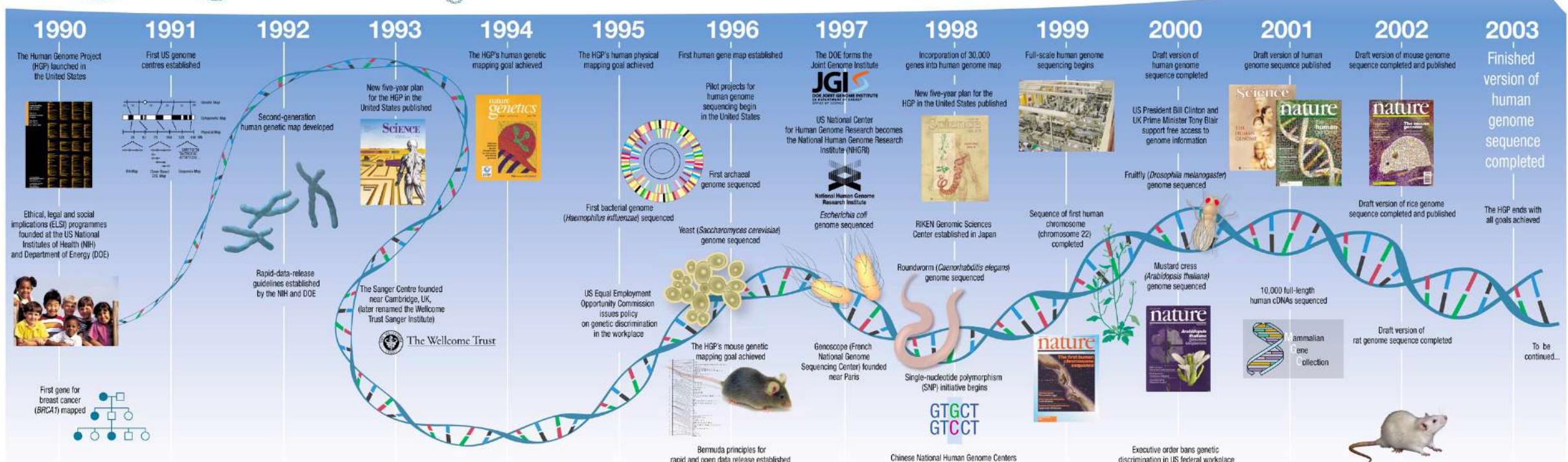
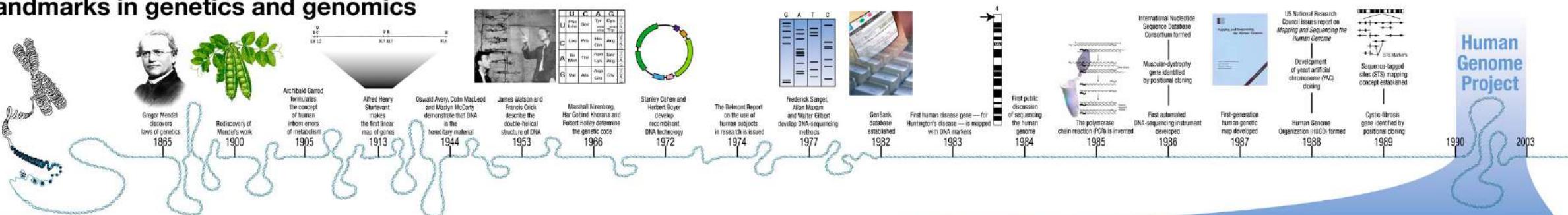
3-Genómica comparativa: compara la secuencia de genes y proteínas de diferentes genomas para elucidar las relaciones funcionales y evolutivas.



Ej: FISH- El cromosoma 6 humano tiene secuencias que se encuentran en tres cromosomas de perro (1,2 y 35).



Landmarks in genetics and genomics

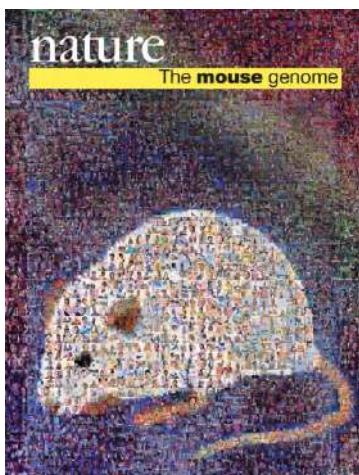


DESIGN BY DARBY LEE
PIXS COURTESY J. BLAMER, CITY UNIV., NEW YORK; WATSON & CRICK COURTESY A. BARRINGTON BROWN/SPL/AGENCE COUVET COURTESY AAAS

2000:



2002:



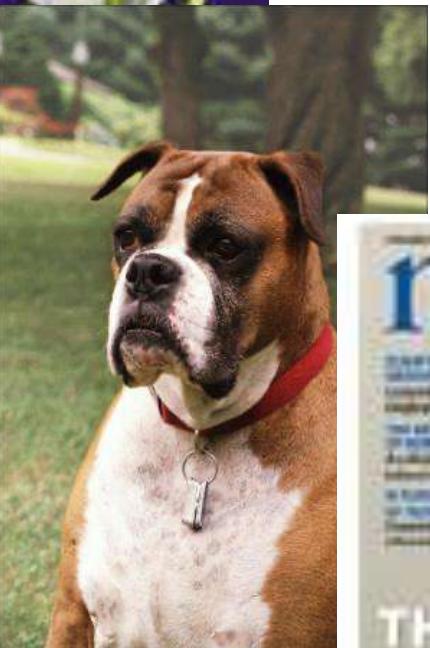
2003:



2004:

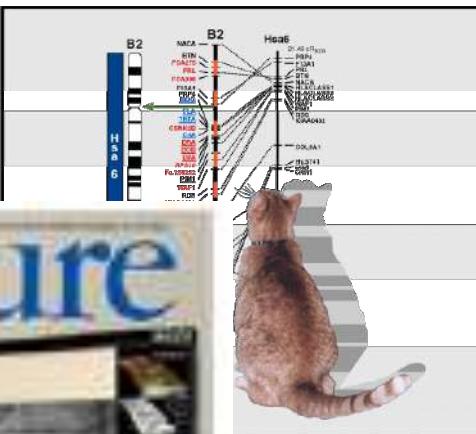


2005:



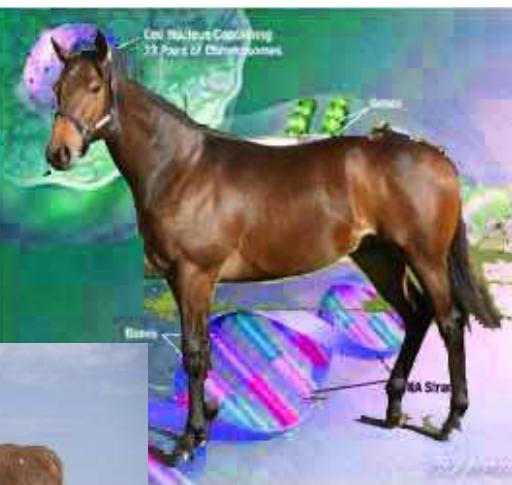
2,4 billones de bases de los 39 cromosomas

2007:



2007:

Genoma: *Equus caballus*
Aprox. 300.000 BAC
2,7 billones de bases



2009: *Bos taurus*. (2.54 Gb)

Next Generation Sequencing

- Mejoramiento en enzimas, química y análisis de imágenes a la mitad de la ultima decada aumentando la capacidad de secuenciación.
- Esta nueva tecnología llamada “next-generation sequencing”, es un potencial para acelerar las investigaciones biológicas y biomédicas
- Tornando disponible genomas y transcriptomas.
- Rápido, bajo costo y métodos fáciles en laboratorio de biología molecular.
- Primeros métodos con **short reads** y mas recientemente **long reads**

Tecnologia NGS



Cost-effective
Fast
Ultra throughput
Cloning-free
Short reads



Tecnología de NGS



GS FLX 454
(ROCHE)



HiSeq 2000
(ILLUMINA)



5500xl SOLiD
(ABI)



GS Junior

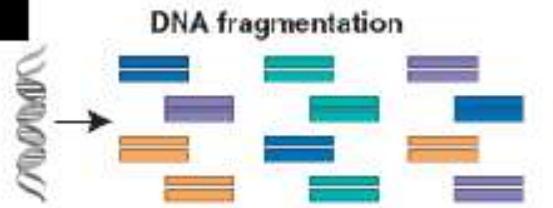


MiSeq
(ILLUMINA)

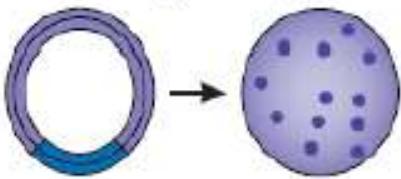


Ion TORRENT

Sanger seq.

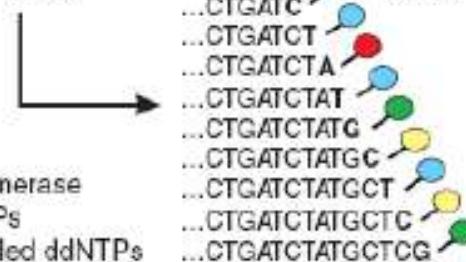


In vivo cloning and amplification



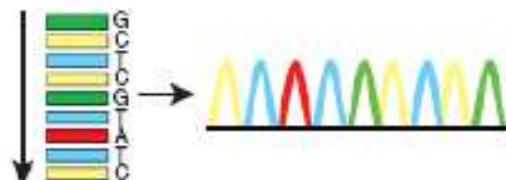
Cycle sequencing

3'... GACTAGATACGAGCGTGA...5' (template)
5'... CTGAT (primer)

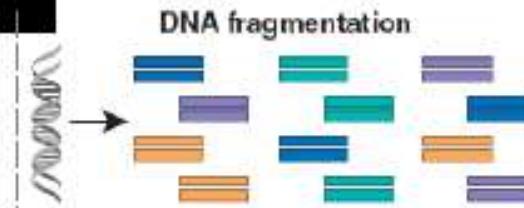


Polymerase
dNTPs
Labeled ddNTPs

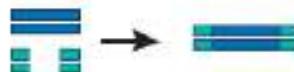
Electrophoresis (1 read/capillary)



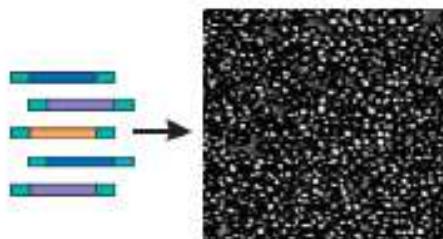
Next Generation Sequencing



In vitro adaptor ligation



Generation of polony array



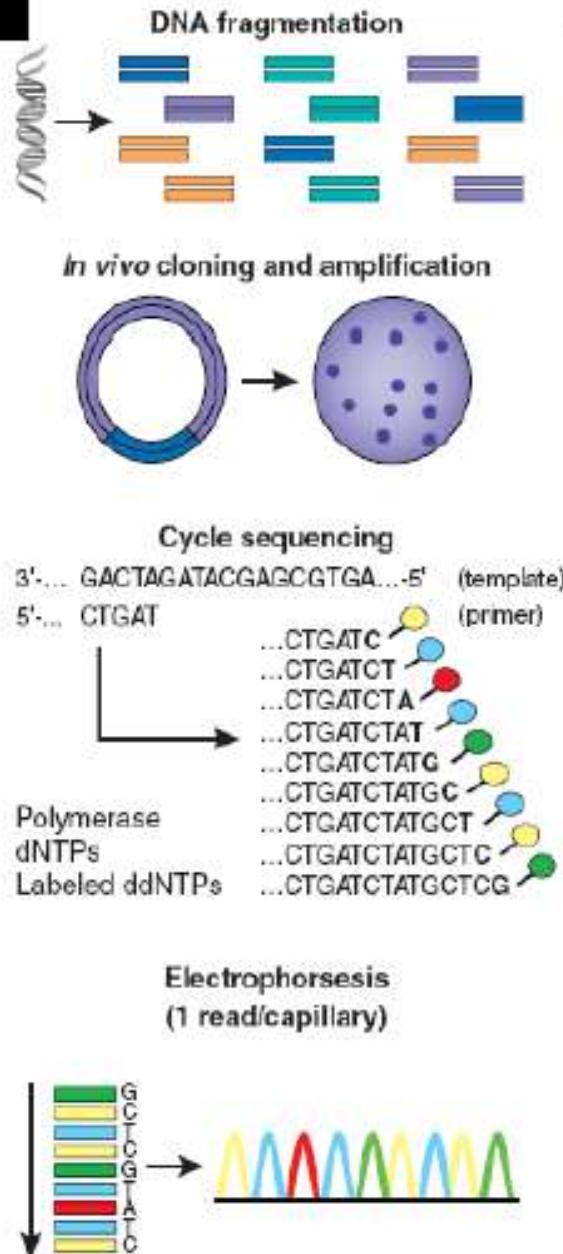
Cyclic array sequencing (>10⁶ reads/array)



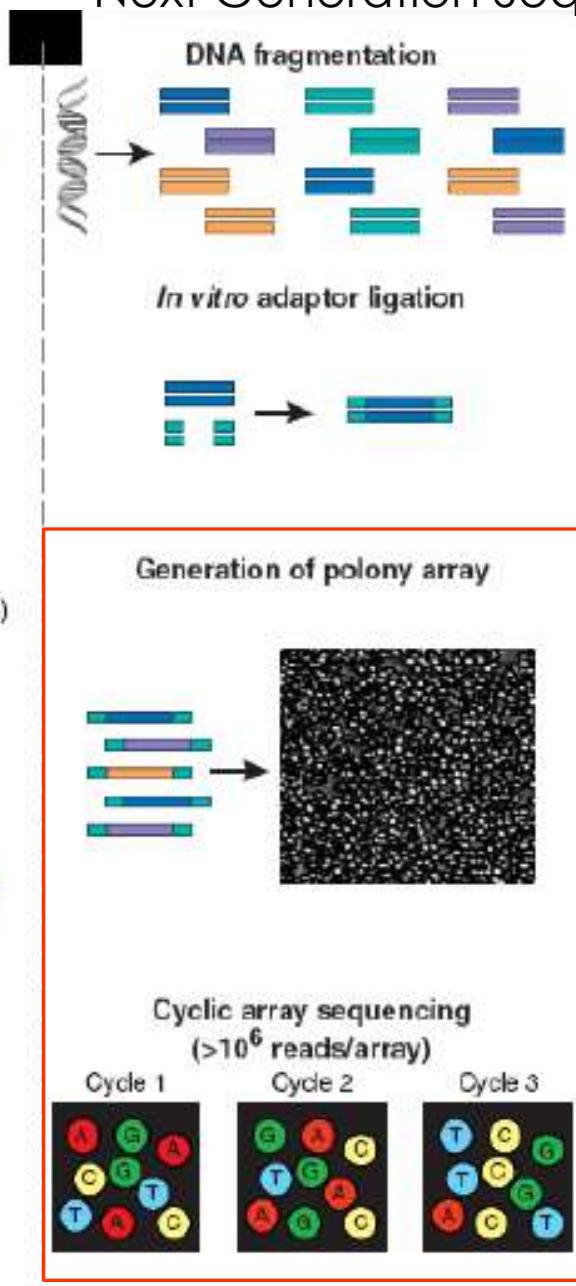
Ventajas:

- Construcción de librerías de secuenciación
- Amplificación clonal
- No utiliza clonar *in vivo*, transformación y cultivo...

Sanger seq.



Next Generation Sequencing

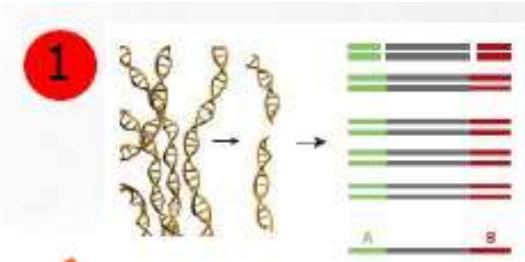


Ventajas:

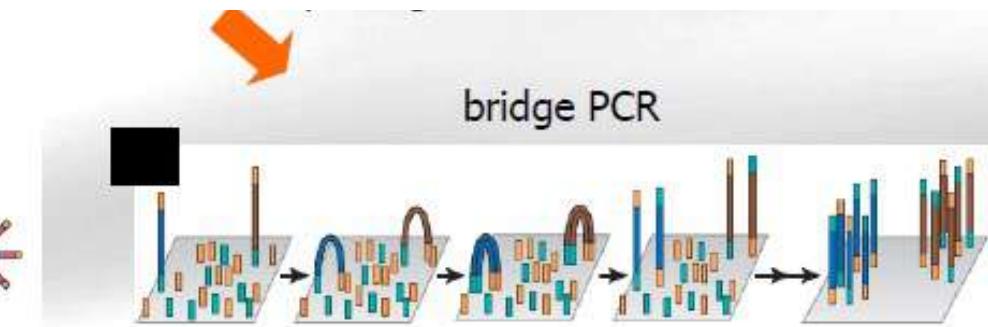
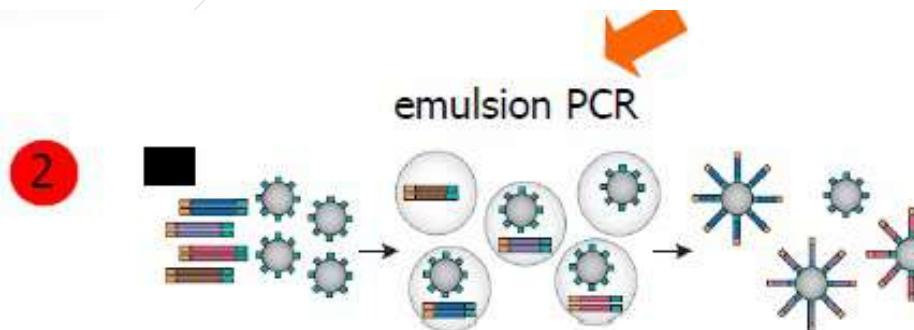
- Secuenciar en método basado en array
- Mayor grado de paralelismo que secuenciar con capilar

Métodos sec. Genomas - short reads

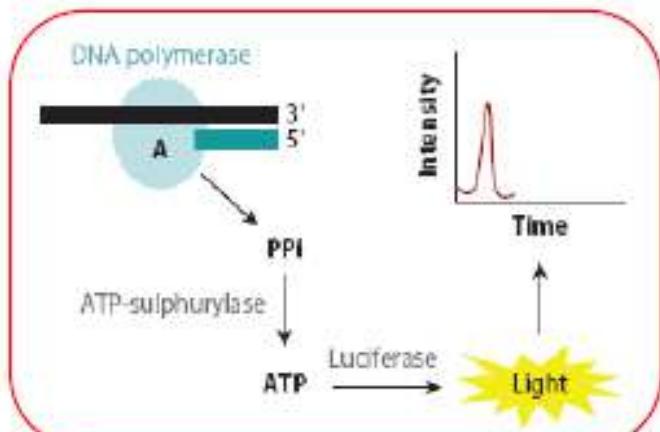
- 1 Library preparation
- 2 Clonal amplification
- 3 Cyclic array sequencing



Fragmentación del DNA y
ligación de los adaptadores in
vitro

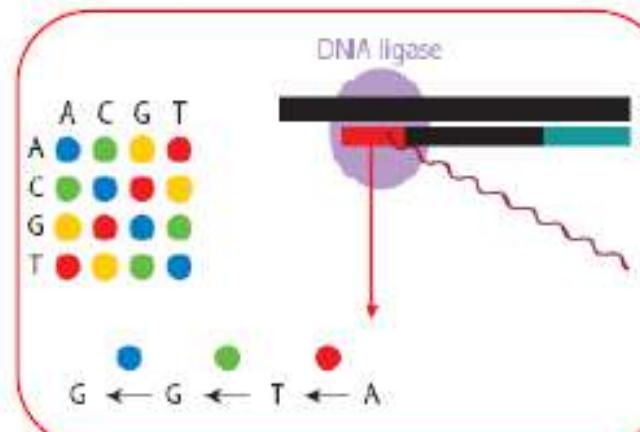


- 3 Pyrosequencing



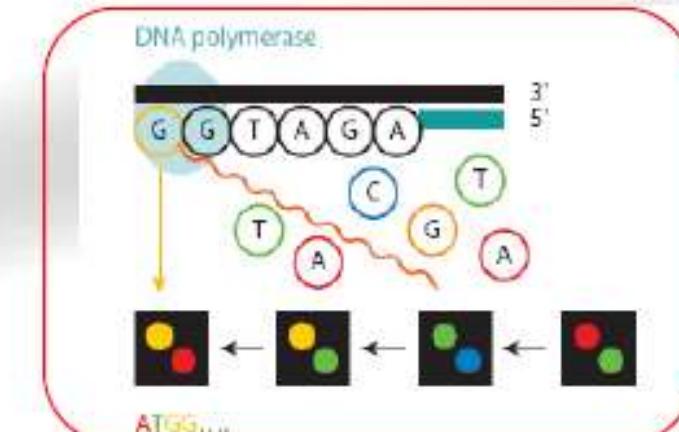
454 sequencing

- Sequencing-by-ligation



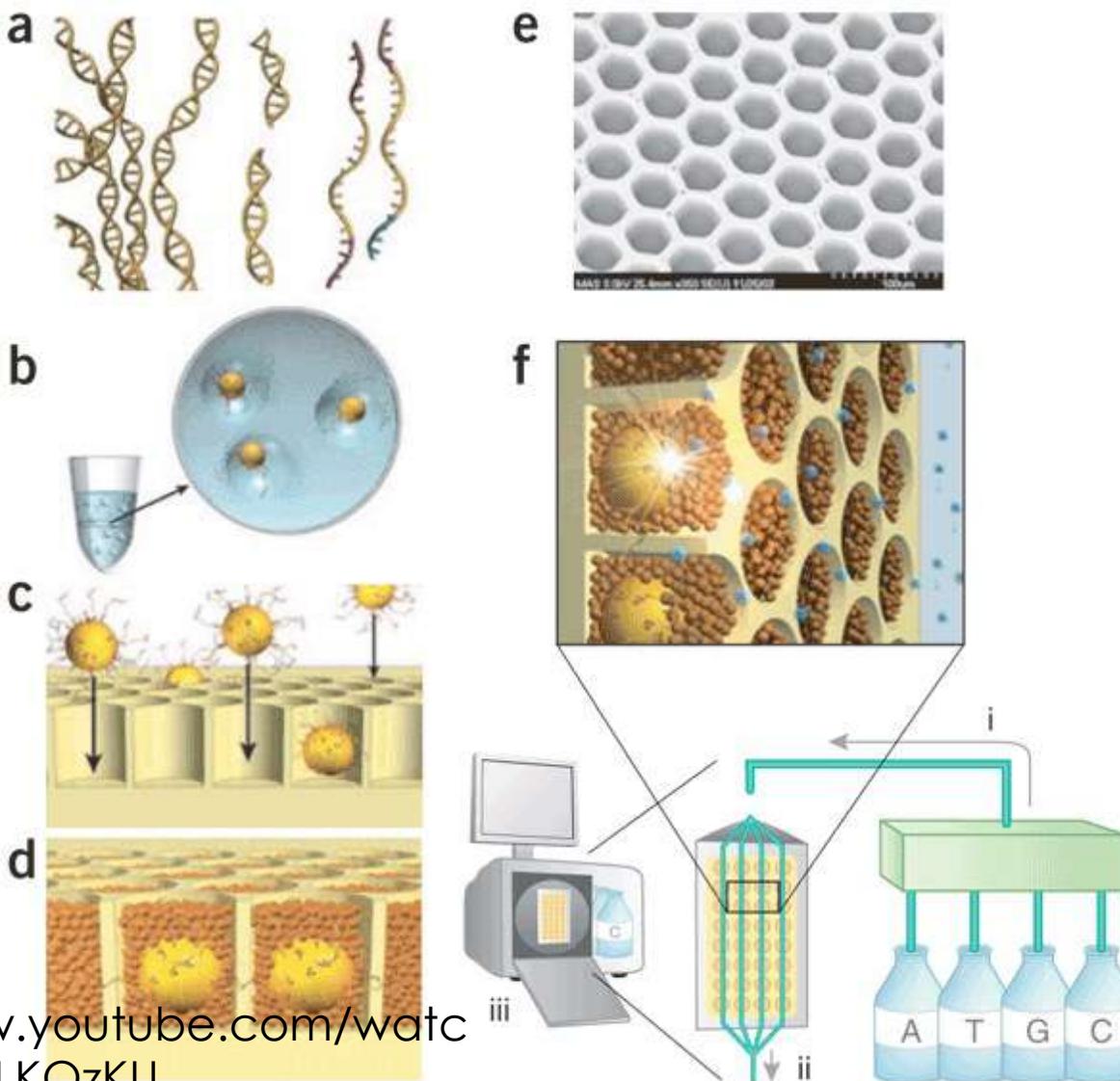
SOLID platform

- Sequencing-by-synthesis



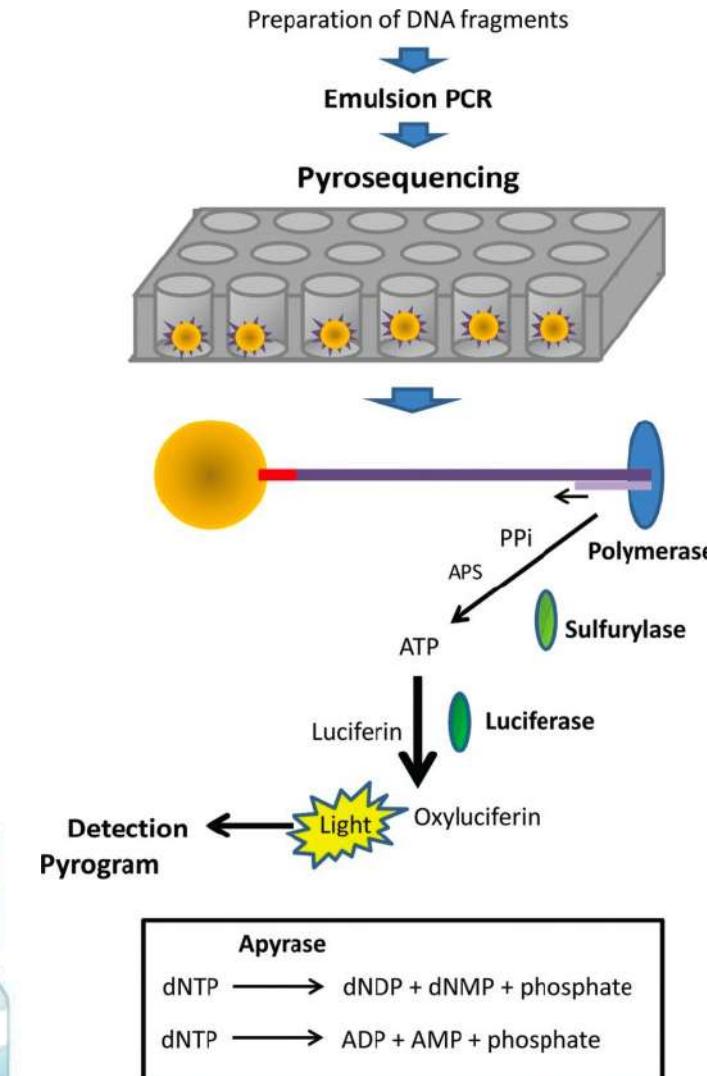
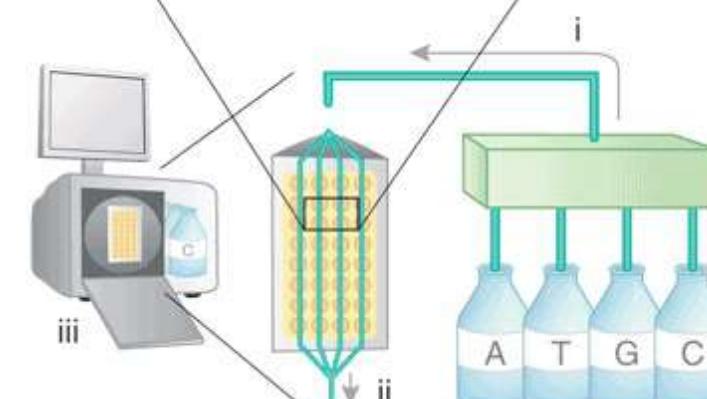
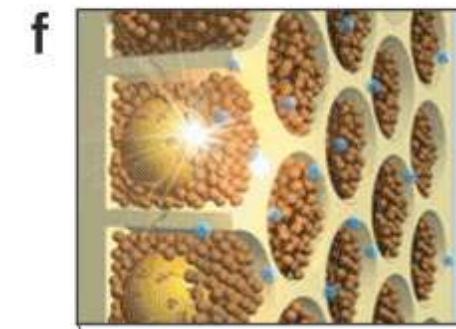
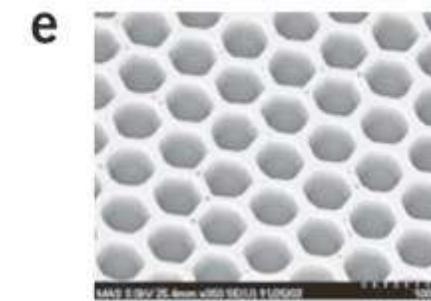
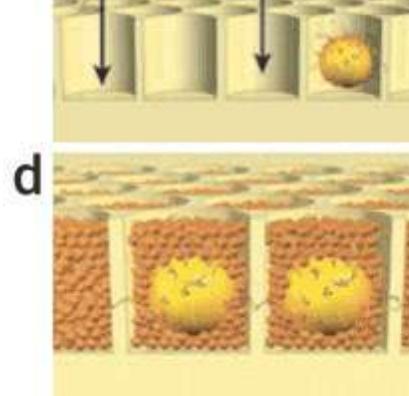
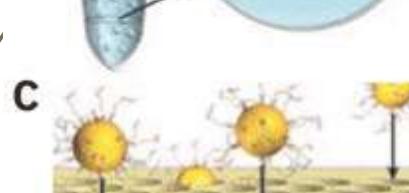
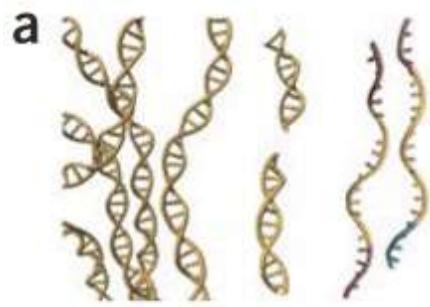
Solexa technology / Illumina

454 Sequencing - Roche



- (a) Genomic DNA is isolated, fragmented, ligated to adapters and separated into single strands.
- (b) Fragments are bound to beads (one fragment per bead). PCR-reaction-mixture-in-oil emulsion and PCR amplification occurs within each droplet, resulting in beads each carrying ten million copies of a unique DNA template.
- (c) Deposited into wells of a fiber-optic slide.
- (d) Pyrophosphate sequencing reaction are deposited into each well.
- (e) Scanning electron micrograph of a portion of a fiber-optic slide
- (f) The 454 sequencing instrument

454 Sequencing - Roche



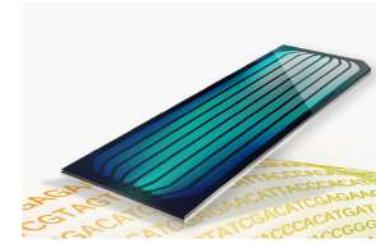
Illumina sequencing

The screenshot shows the Illumina website at illumina.com/science/technology/next-generation-sequencing/sequencing-technology.html. The page features a large banner with the text "Explore Illumina sequencing technology" and "Massively parallel sequencing with optimized SBS chemistry". The navigation bar includes links for Products, Learn, Company, Support, Recommended Links, and various sub-sections under "NEXT-GENERATION SEQUENCING".

Science and Education / Technology / Next-Generation Sequencing:
Sequencing by Synthesis (SBS) Technology

Introduction to SBS Technology

Illumina sequencing technology, sequencing by synthesis (SBS), is a widely adopted next-generation sequencing (NGS) technology worldwide, responsible for generating more than 90% of the world's sequencing data.¹ Illumina sequencing instruments and reagents support massively parallel sequencing using a proprietary method that detects single bases as they are incorporated into growing DNA strands.



Feedback



SBS Chemistry

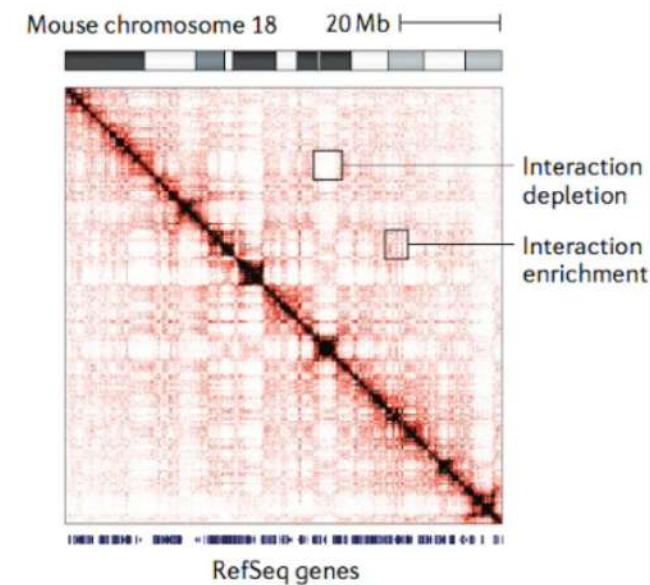
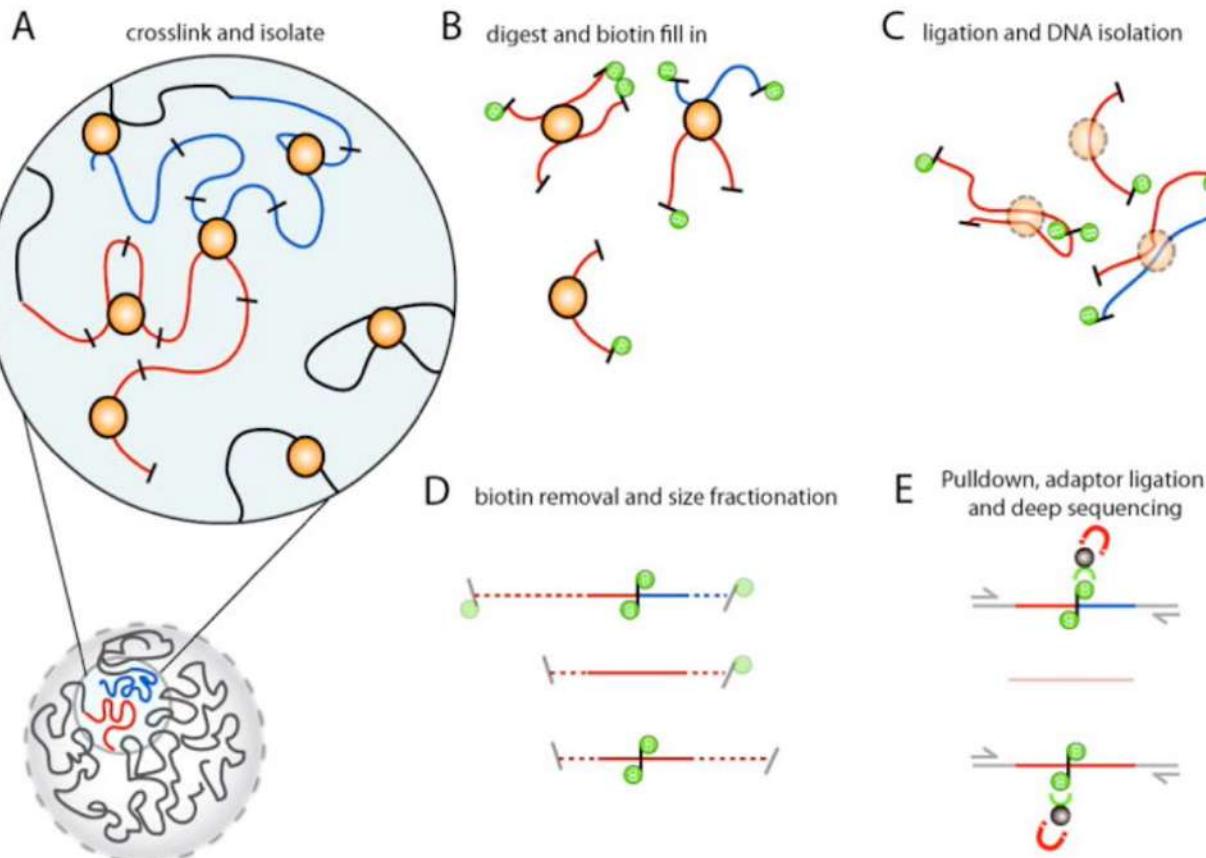
A fluorescently labeled reversible terminator is imaged as each dNTP is added, and then

► https://www.youtube.com/watch?v=fCd6B5HRaZ8&feature=emb_logo

Genomas: short read pero diferente

Hi-C

- Note: Biotin labels fragment ends without interfering with folding of bound proteins, DNA



► <https://www.youtube.com/watch?v=-MxEw3IXUWU>

Genomas: Long reads sequencing

Nanopore



Nanopore DNA sequencing devices

A range of nanopore sequencing devices are available, providing high-yields and scalable sample throughput to suit all requirements — from portable analysis using Flongle and MinION, through to flexible, high-throughput benchtop sequencing on GridION and PromethION. MinION Starter Packs are available from just \$1,000 providing low-cost access to the benefits of long-read, real-time DNA sequencing.



Flongle



MinION



MinION Mk1C



GridION



PromethION

<https://www.youtube.com/watch?v=RcP85JHLmnI>

Genomas: Long reads sequencing

PACBIO

The screenshot shows the PacBio website's "SEQUENCING SYSTEMS" section. It features three main products: the Revio long-read system, the Onso short-read system, and the Sequel long-read systems. Each product has a corresponding image and a brief description.

REVIO SYSTEM
Long-read sequencing

Highly accurate HiFi sequencing for complete views of genomes, epigenomes, and transcriptomes

Throughput to run up to 1,300 human HiFi genomes per year

Smart consumables for simple handling and less plastic waste

Powerful compute with Google Health DeepConsensus onboard

[Learn more](#)

ONSO SYSTEM
Short-read sequencing

Greater level of sensitivity to detect rare variants

Reduced requirement for sequencing coverage depth versus SBS sequencers

Contiguous reads through homopolymer and difficult to sequence regions

Low duplication rate, no index hopping

Rapid conversion of existing P5/P7 libraries for sequencing on the Onso system

SEQUEL IIe SYSTEM
Long-read sequencing

Long, accurate HiFi reads with DNA methylation direct from the instrument in every run

Supports a wide range of applications – targeted sequencing, RNA sequencing, and whole-genome sequencing

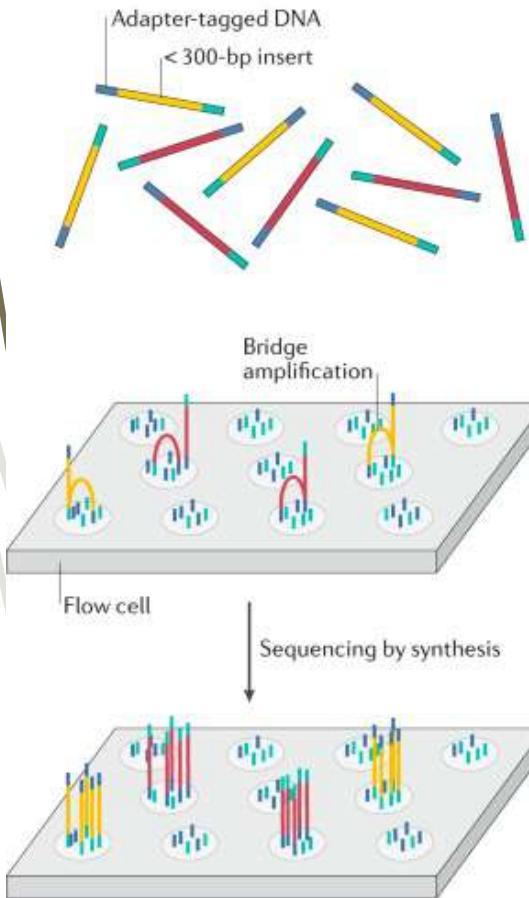
Throughput match for microbial genome sequencing, AAV vector sequencing, Iso-Seq, and more

Featured in hundreds of peer-reviewed publications

Genomas: short read x Long read sequencing

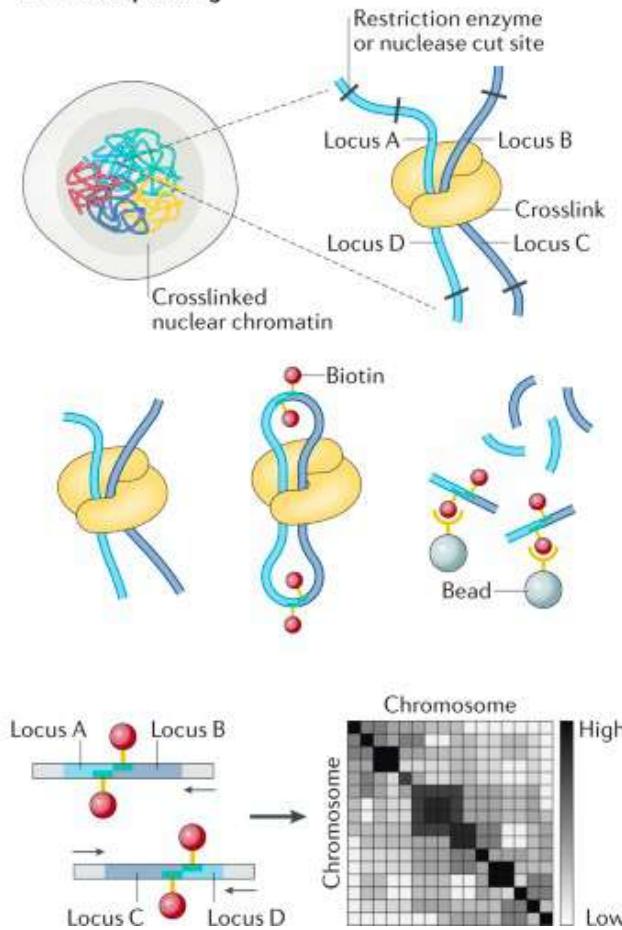
Short reads Illumina

a Illumina short-read sequencing



Hi-C

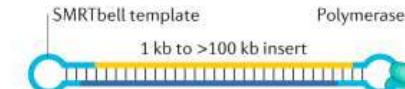
b Hi-C sequencing



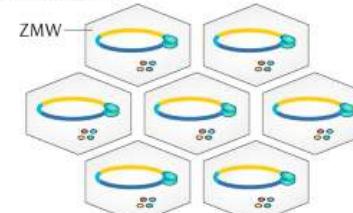
PacBio

a PacBio SMRT sequencing

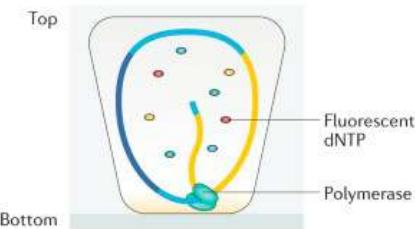
Template topology



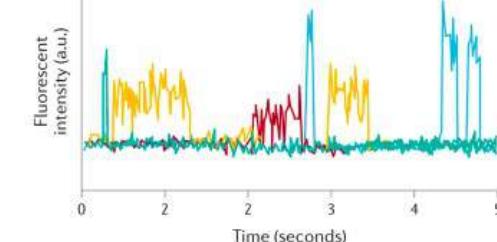
Flow cell (top view)



Single ZMW (cross section)



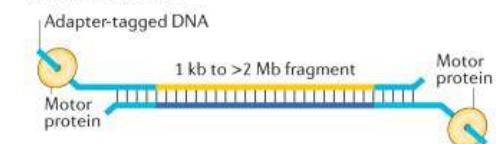
Readout



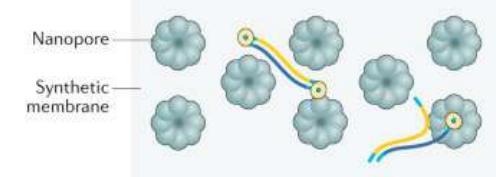
Nanopore

b ONT sequencing

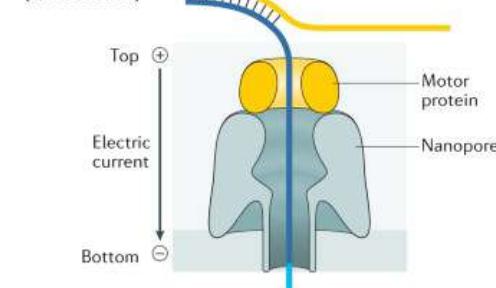
Template topology



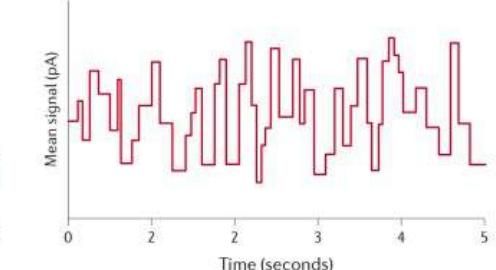
Flow cell (top view)



Single nanopore (cross section)



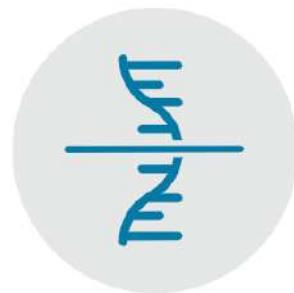
Readout



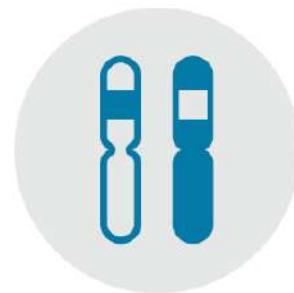
Genoma de referencia: *de novo*



SNP & INDEL



Methylation



Structural Variation



Phasing

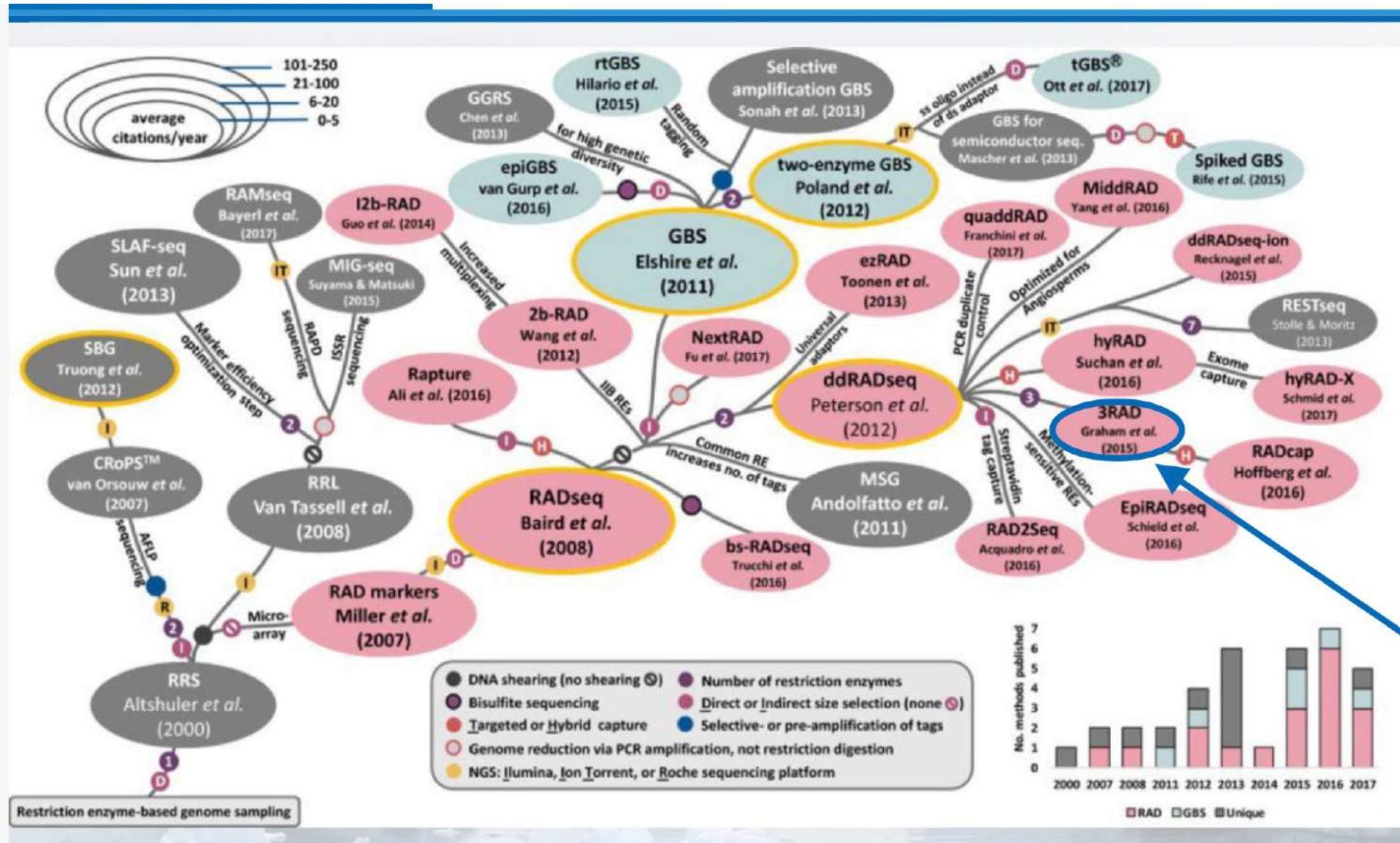


Assembly

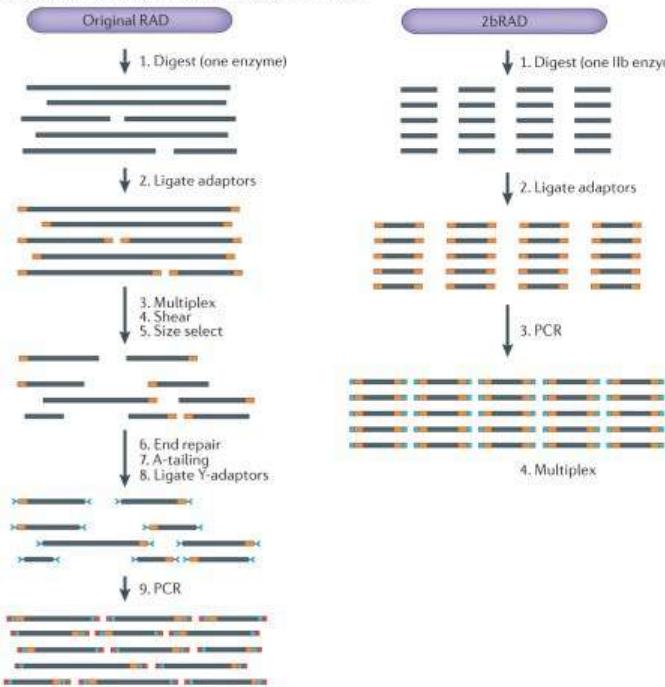
Resequencing

- Identificación SNP
- Estudio poblacional
- Genómica comparativa

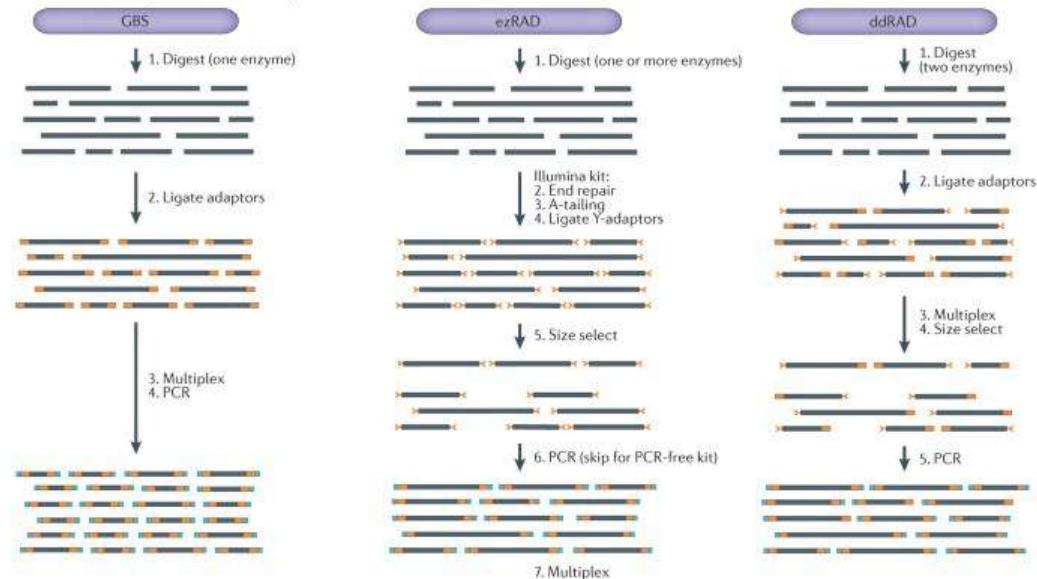
Técnicas de representación Reducida del genoma

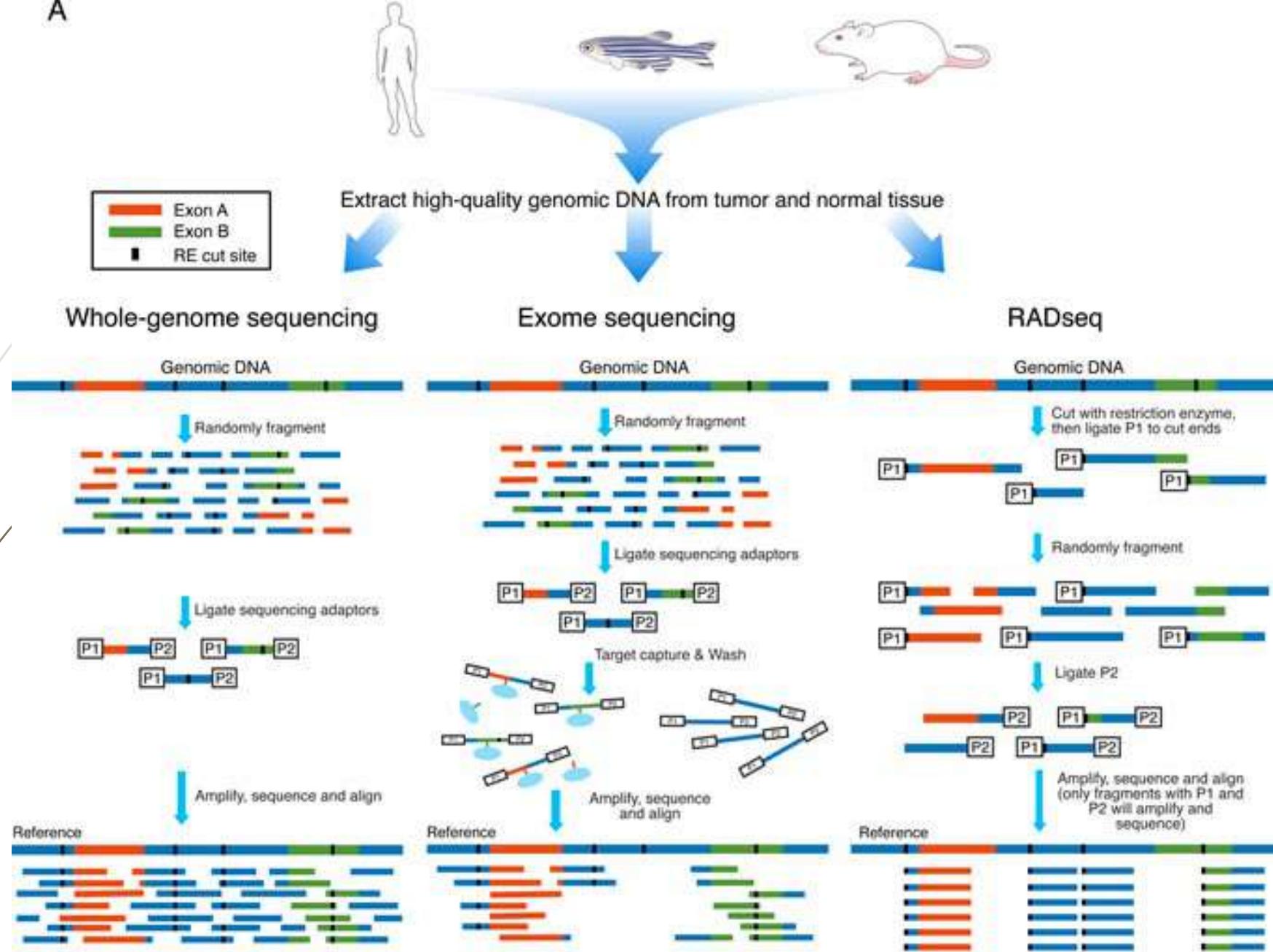


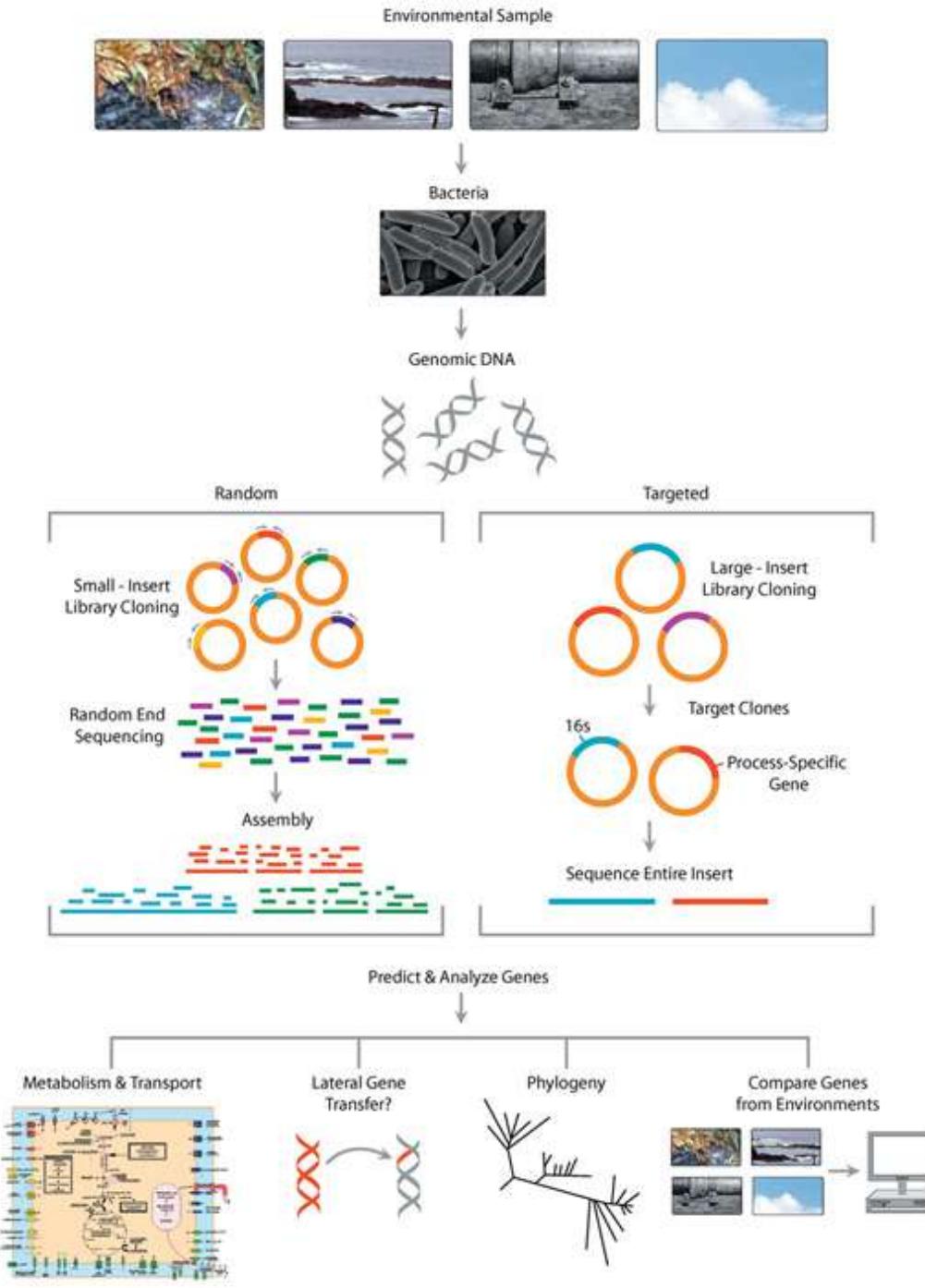
Sequence next to single restriction enzyme cut sites



Sequence flanked by two restriction enzyme cut sites



A



Metagenómica

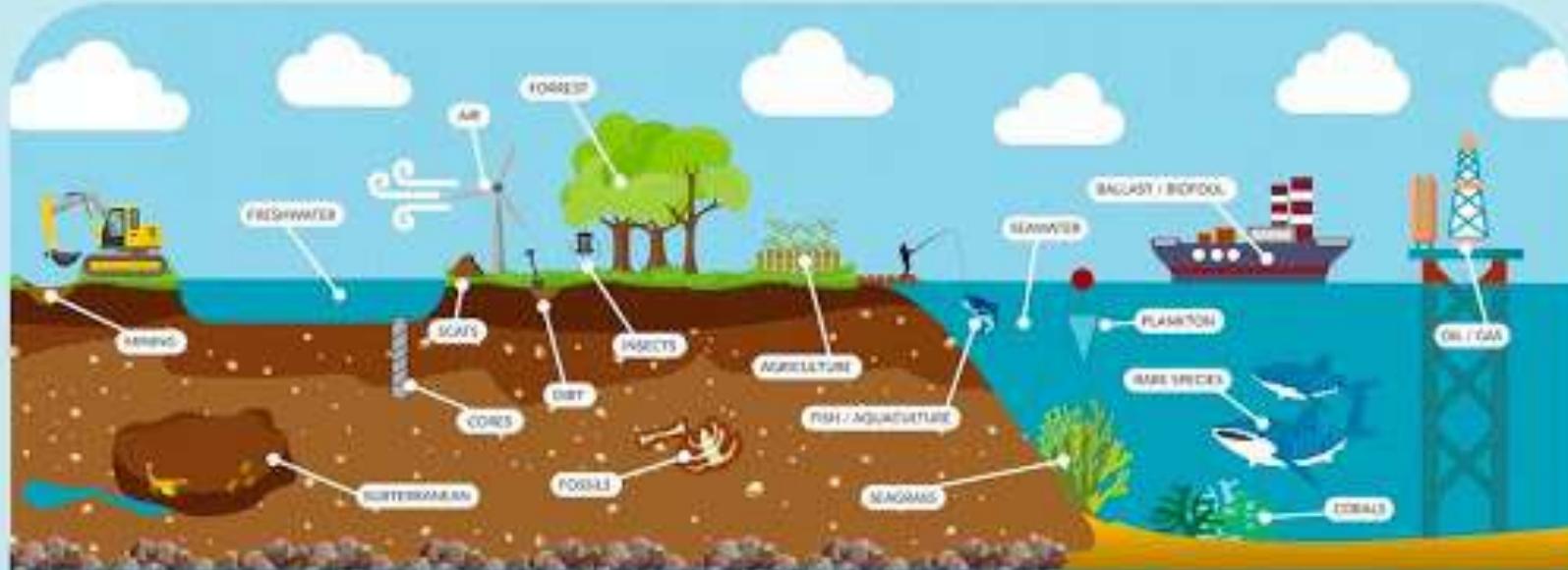
Metagenómica estudia colección de material genético (genomas) de una mezcla de comunidades o organismos.

Metagenómica usualmente refiere al estudio de comunidad microbiana



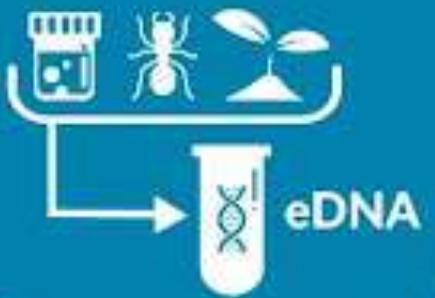
Environmental DNA (eDNA)

Applications and Workflow

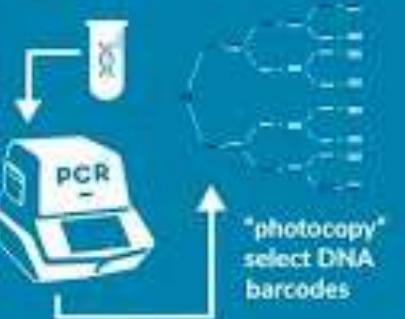


1. Choose an Application

2. Collect Samples and Extract DNA



3. Amplify Target DNA 'Barcodes'



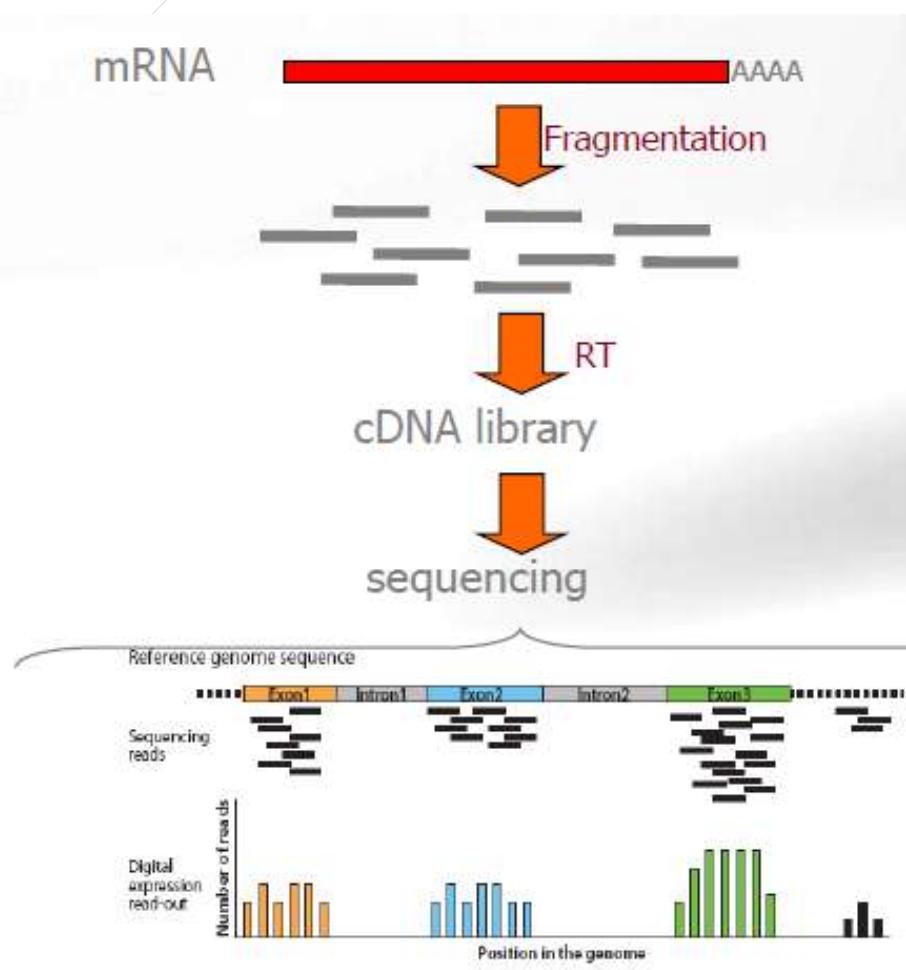
4. Sequence and Interpret DNA Barcodes

- Species assemblage
- Baseline biodiversity surveys
- Impact assessment
- Invasive / feral species detection
- Endangered species detection
- Disease and pathogen detection
- Food webs



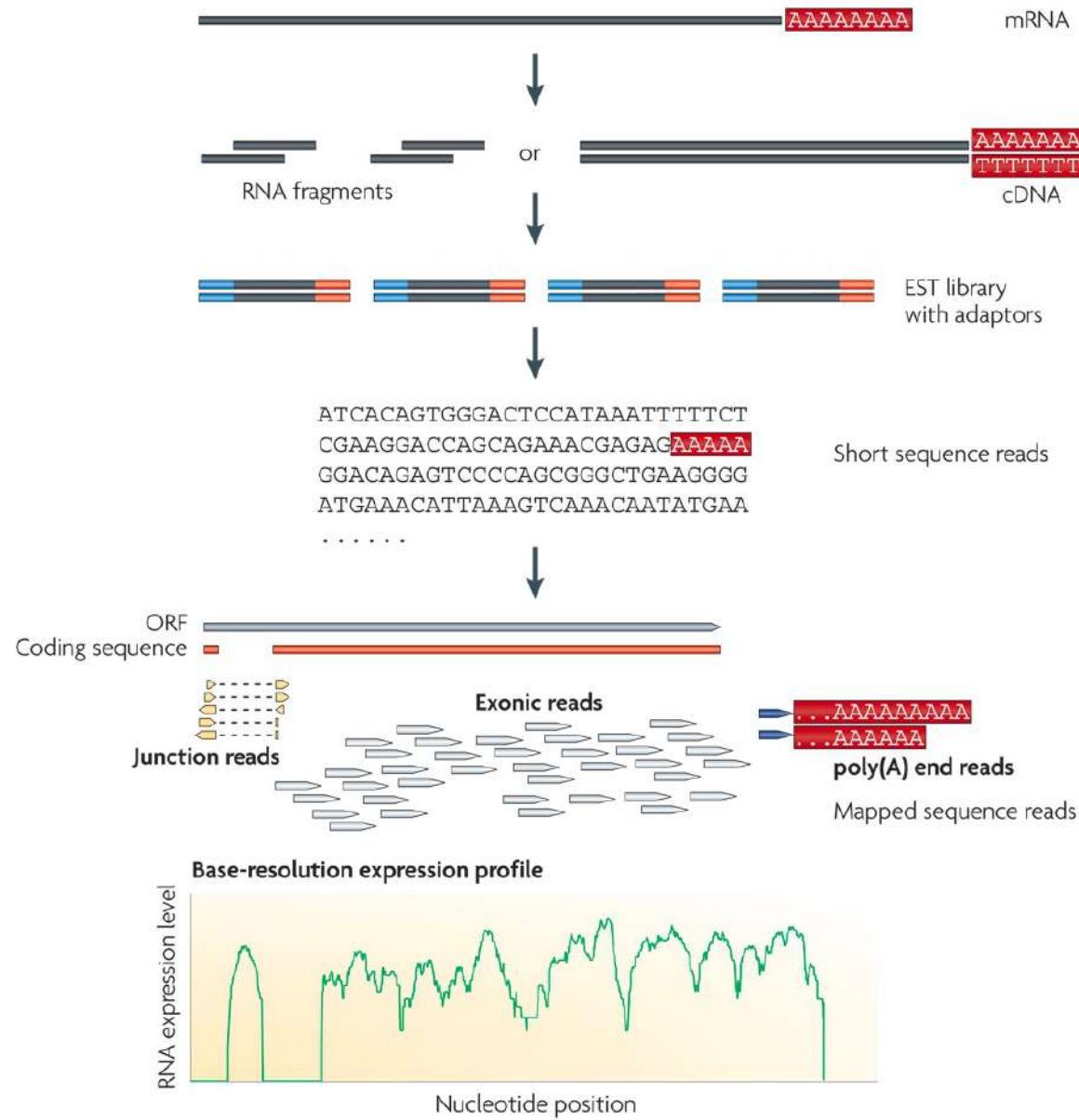
Genómica funcional

Transcriptoma por NGS: RNAseq



- Detectar expresión diferencial y describir un RNAm nuevos
- Identificar eventos de splicing alternativos
- Detectar expresión de SNPs o mutaciones
- Identificar alelos específicos en patrones de expresión.

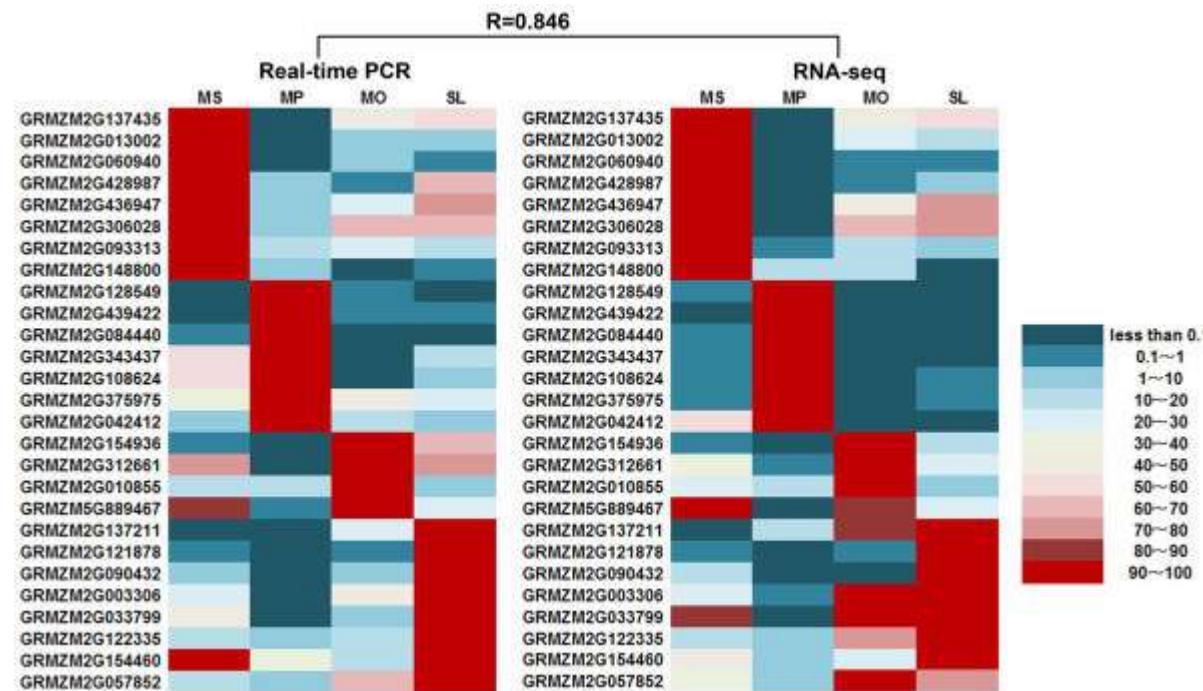
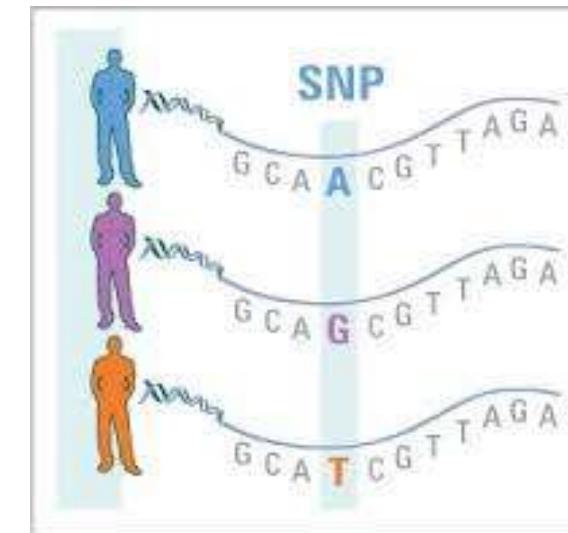
RNA seq



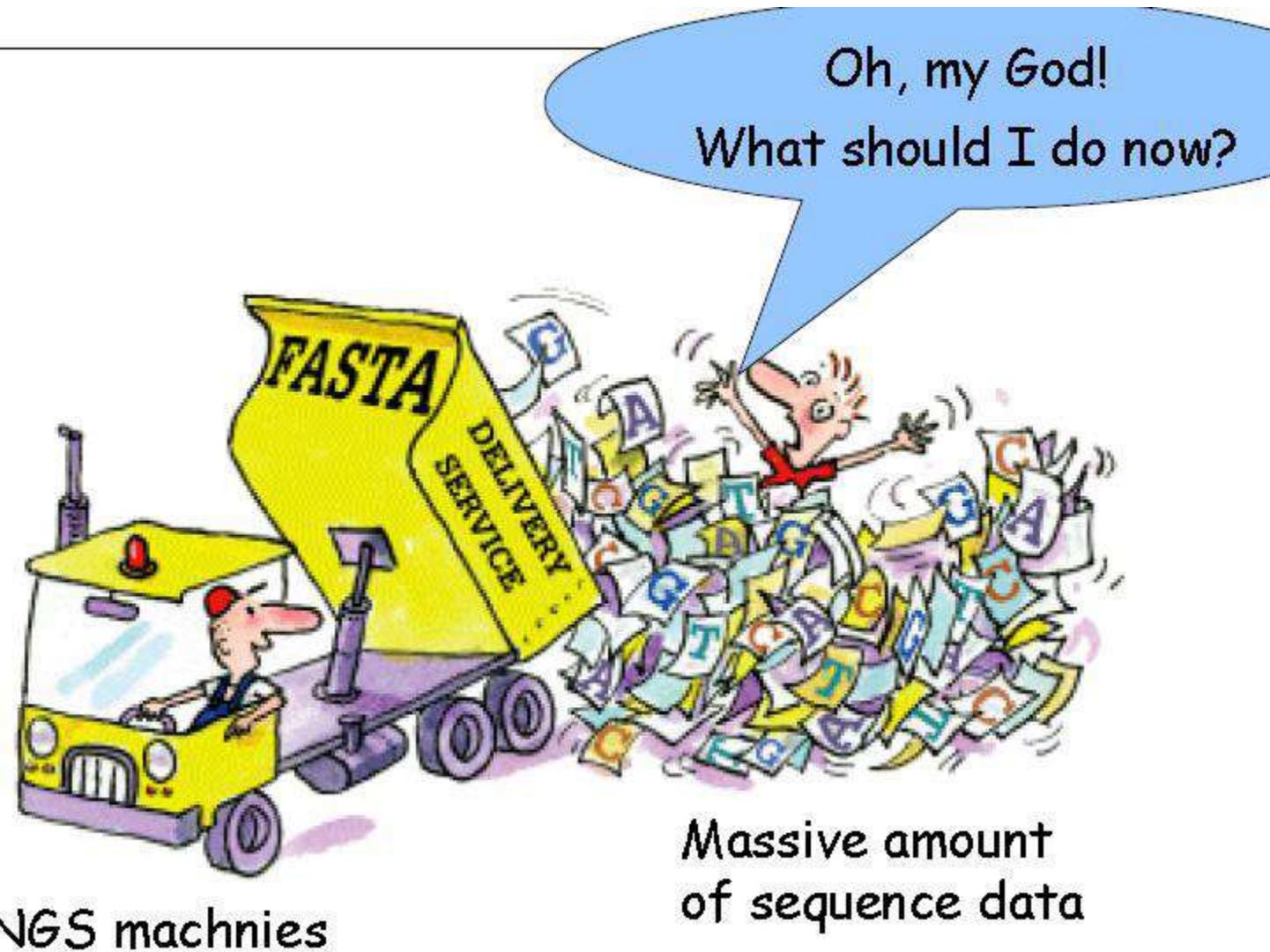
RNA seq

Dos aspectos pueden ser estudiados

- Variaciones en genes expresados
- Expresión diferencial entre individuos



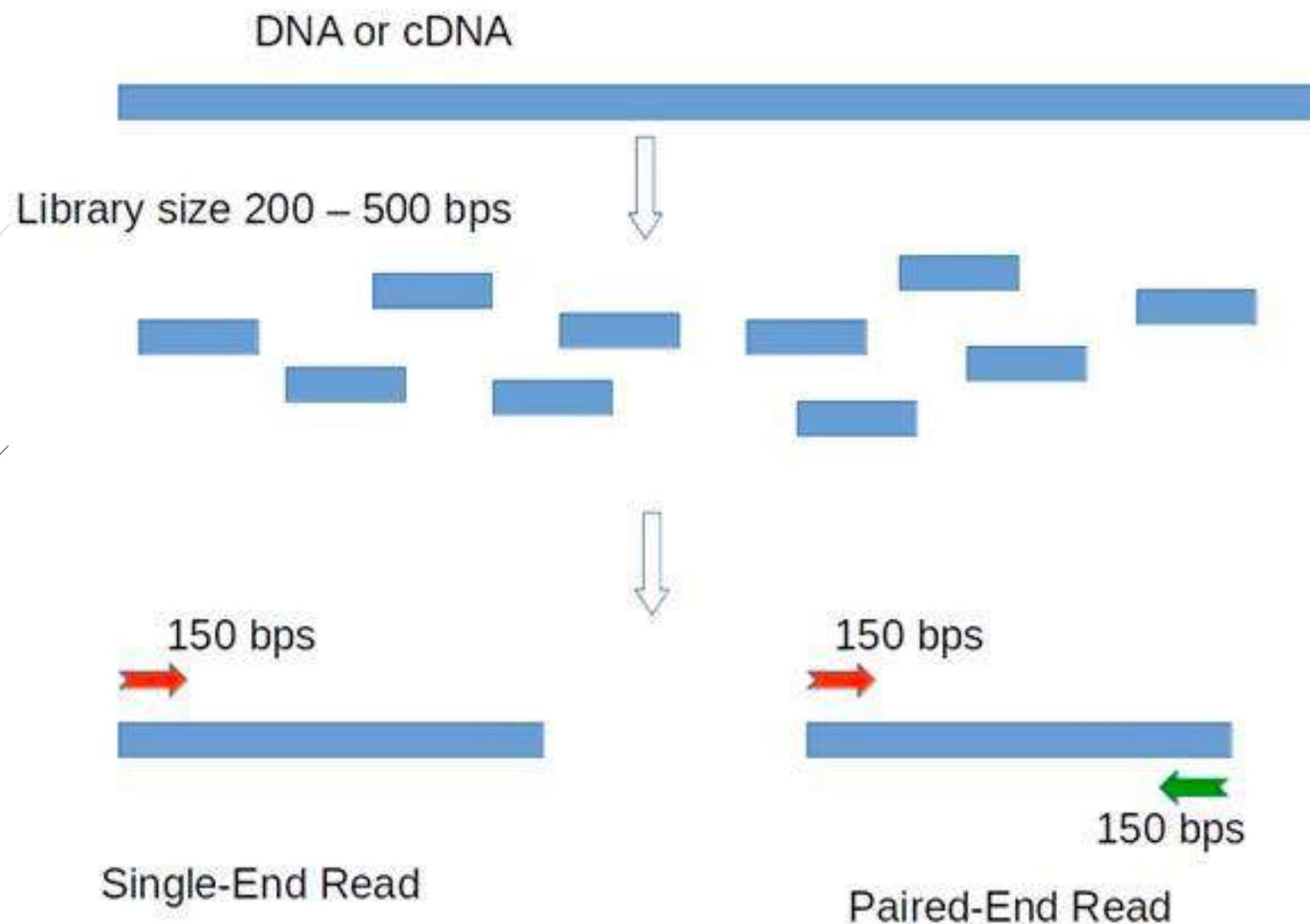
Secuenciamos el genoma... y ahora?



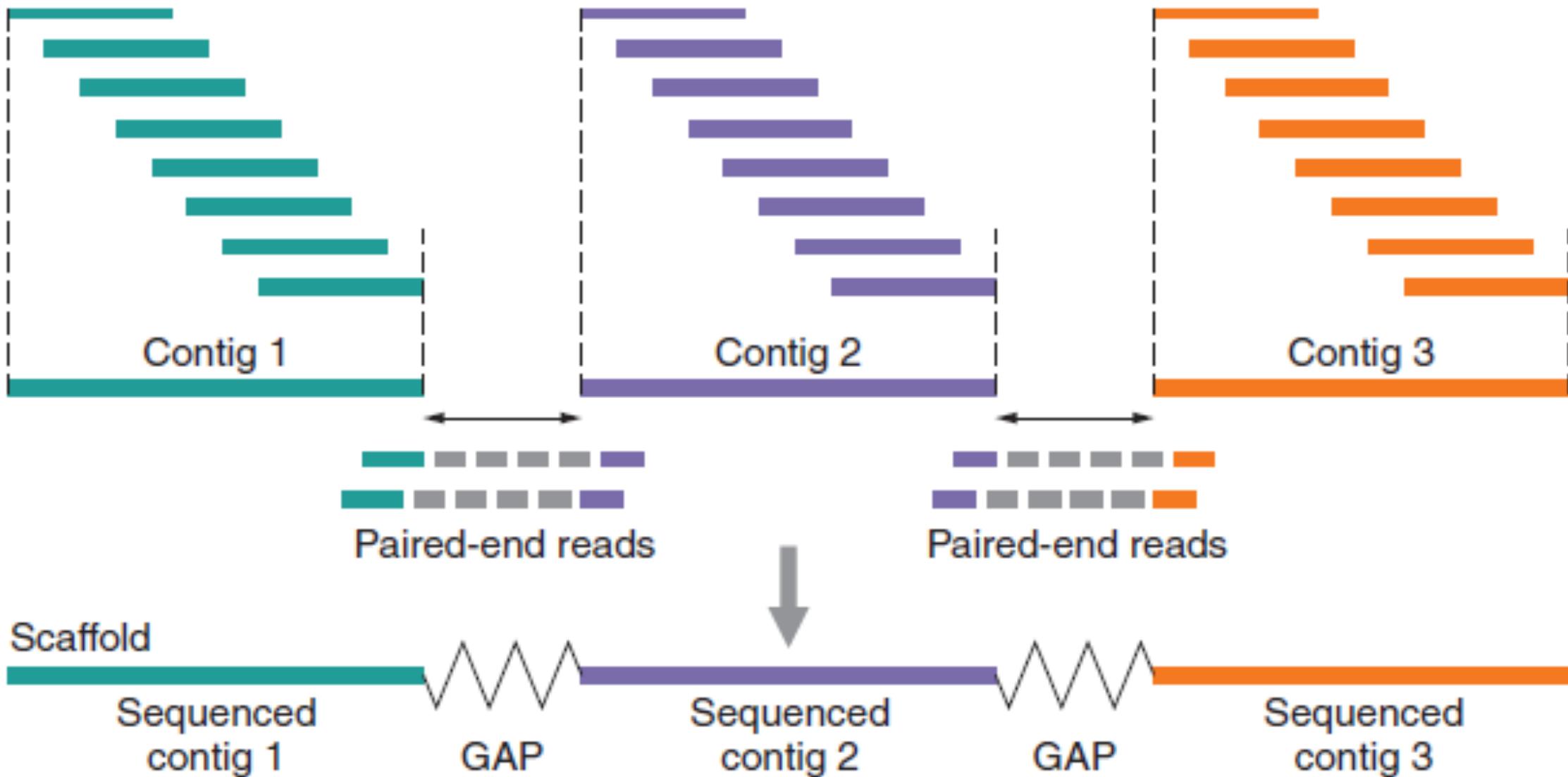


Bioinformatica

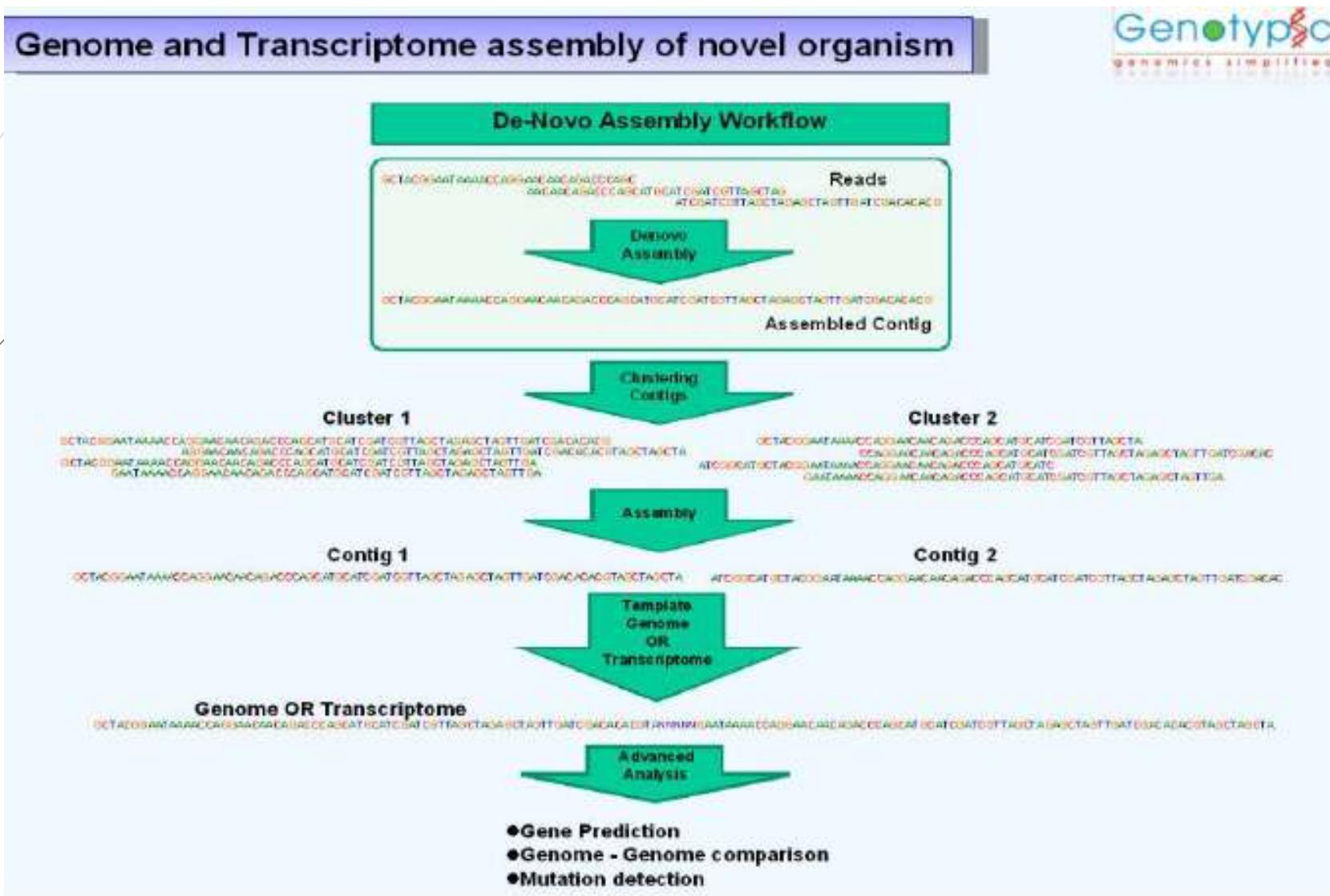
- ▶ Análisis de un grande volumen de datos genómicos, proteomico y metabolomico requiriendo algoritmos sofisticados y computadores muy capaces
- ▶ Área en rápido desarrollo con pocos profesionales capacitados para desarrollar programas y analizar datos



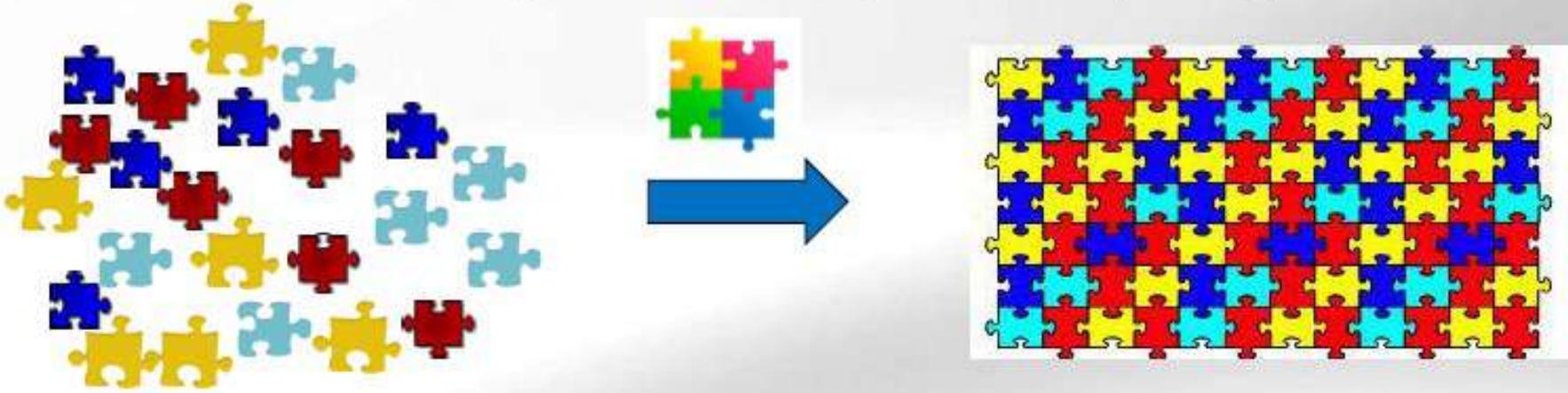
Strategy for whole-genome shotgun sequencing assembly



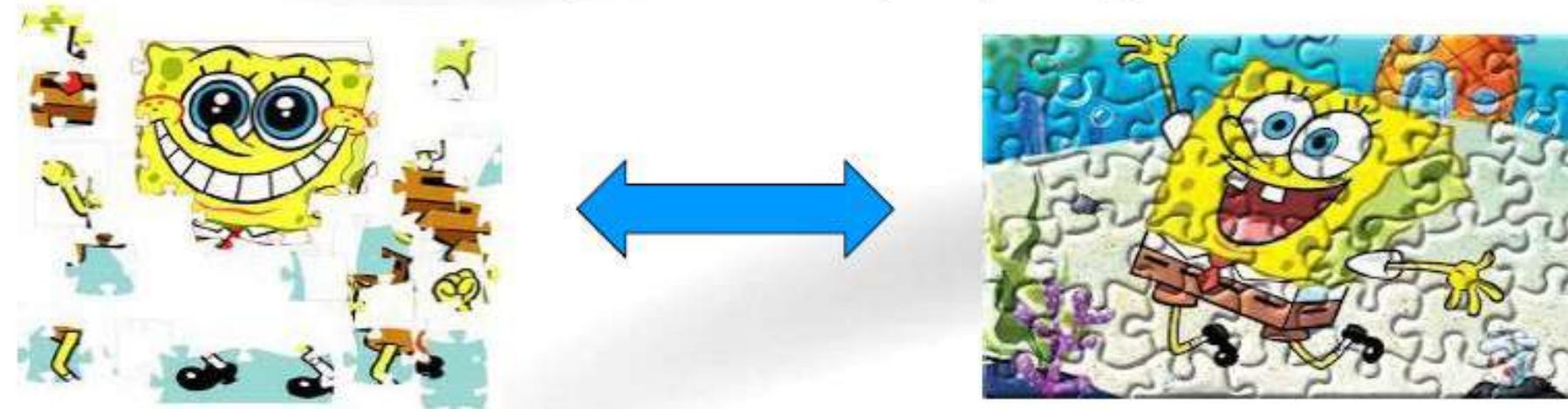
De novo sequencing (no hay genoma de referencia....)



Case A: There is no reference genome available (“*de novo*” sequencing)



Case B: There exists a reference genome available (resequencing)



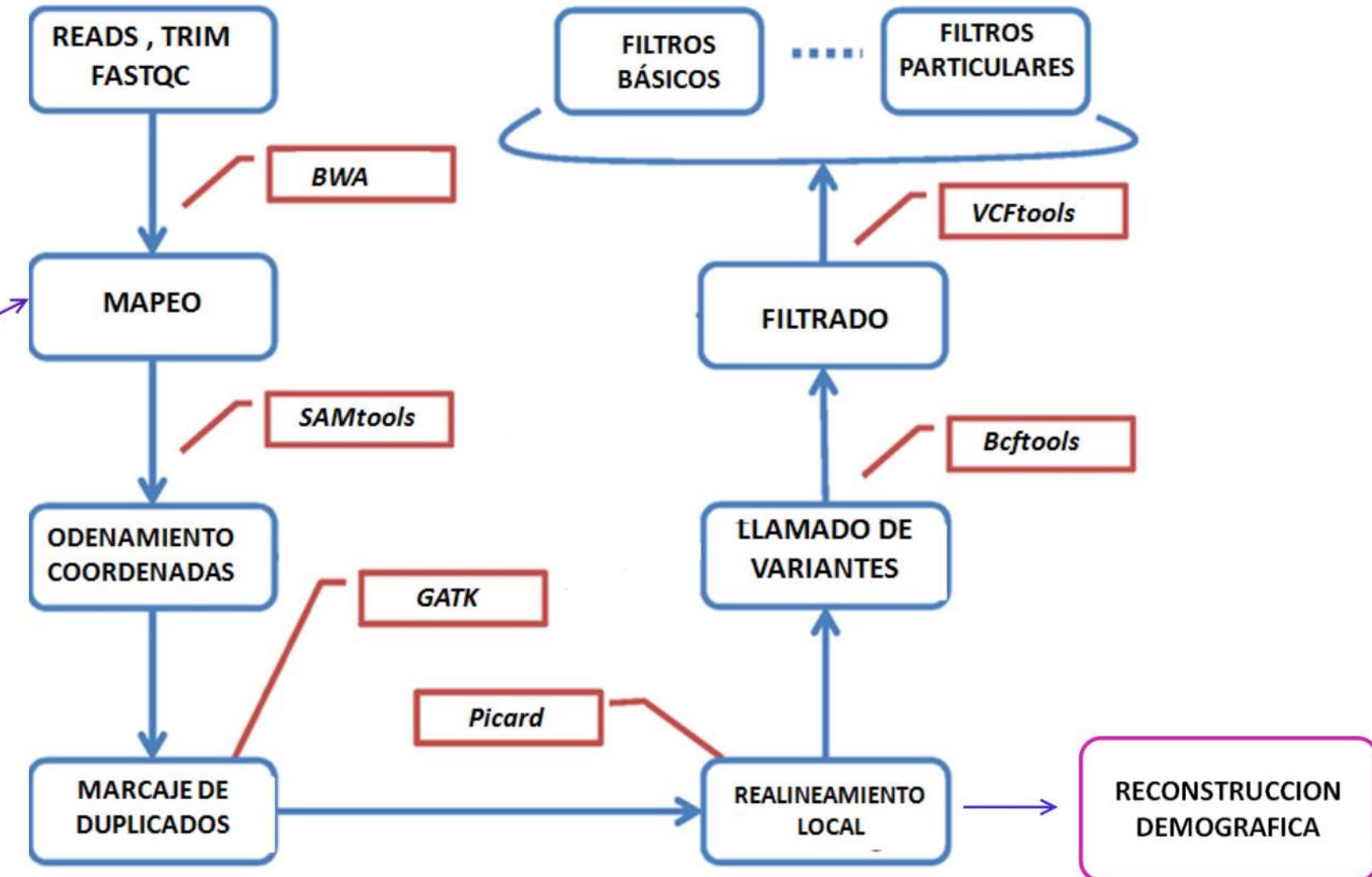
Pipeline Bioinformático

Genoma de referencia



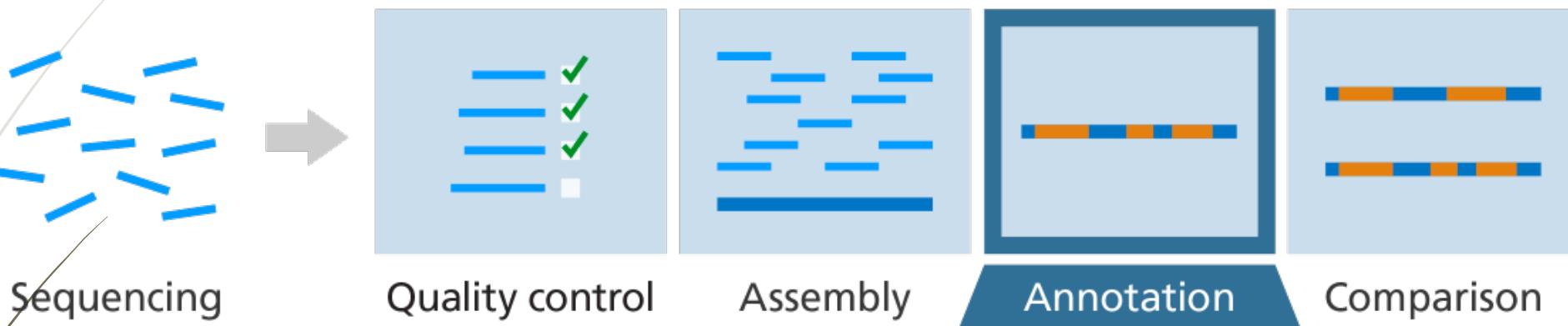
Pequeño pinguino azul

Eudyptula minor



ANOTAR EL GENOMA

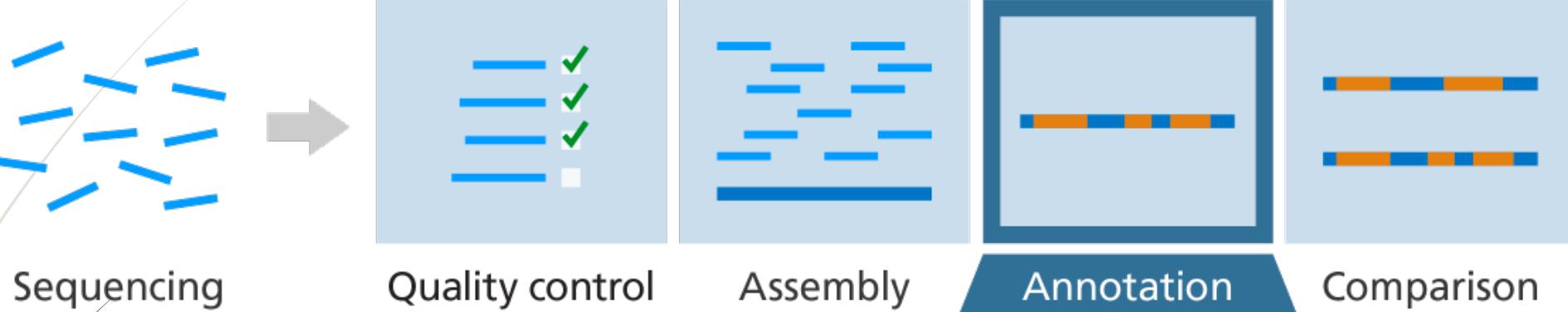
- Predecir la posición de los genes y la región en el cromosoma



Open Reading Frame (ORF)
Fragmento de DNA sin stop codón

Secuencia codificante (CDS)
Una ORF que puede codificar proteína

Métodos para anotar



► **Transcriptoma**

► **Homología de secuencias**

Buscando proteicas en base de datos por similitud

► **Composición de secuencias**

Predicción (codones inicio, stop..) e funciones de secuencias.
Utilizando métodos Machine learning para reconocer patrones

Enriquecimiento

Example of a Swiss-Prot Record

UniProtKB - Q9H479 (FN3K_HUMAN)

Display

Entry

Publications

Feature viewer

Feature table

None

Function

Names & Taxonomy

Subcell. location

Pathol./Biotech

PTM / Processing

Expression

Interaction

Structure

Family & Domains

Sequence

Cross-references

Function

Protein | Fructosamine-3-kinase

Gene | FN3K

Organism | Homo sapiens (Human)

Status | Reviewed - Annotation score: ●●●●○ - Experimental evidence at protein levelⁱ

May initiate a process leading to the deglycation of fructoselysine and of glycated proteins. May play a role in the phosphorylation of 1-deoxy-1-morpholinofructose (DMF), fructoselysine, fructoseglycine, fructose and glycated lysozyme.

GO - Molecular functionⁱ

- fructosamine-3-kinase activity Source: UniProtKB
- kinase activity Source: Reactome

Complete GO annotation...

GO - Biological processⁱ

- epithelial cell differentiation Source: UniProtKB
- fructosamine metabolic process Source: GO_Central
- fructoselysine metabolic process Source: UniProtKB
- post-translational protein modification Source: Reactome

Complete GO annotation...

Gene Ontology (GO):
Structured vocabulary for defining molecular functions, biological processes, and cellular components.

GO

- Componente celular
Parte de la celular
- Función molecular
Ej. Ligand binding
- Proceso Biológico
Que hace

Enriquecimiento

Blast

An official website of the United States government [Here's how you know](#)

NIH National Library of Medicine
National Center for Biotechnology Information

BLAST®

Home Recent Results Saved Strategies Help

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)

NEWS

BLAST+ 2.13.0 is here!
Starting with this release, we are including the blastn_vdb and tblastn_vdb executables in the BLAST+ distribution.

Thu, 17 Mar 2022 12:00:00 EST [More BLAST news...](#)

Web BLAST

Nucleotide BLAST
nucleotide ► nucleotide

blastx
translated nucleotide ► protein

tblastn
protein ► translated nucleotide

Protein BLAST
protein ► protein

BLAST Genomes

Enter organism common name, scientific name, or tax id **Search**

Human Mouse Rat Microbes

EN

Standalone and API BLAST

Genomas secuenciados

The screenshot shows the homepage of the Genomes OnLine Database (GOLD). The page has a blue header with the GOLD logo and the text "Welcome to the Genomes OnLine Database". Below the header, there are three main sections: "Metagenomes", "Isolate Genomes", and "Genome Distribution". The "Metagenomes" section shows statistics for classification, studies (376), and samples (2639). The "Isolate Genomes" section shows statistics for complete projects (4910), incomplete projects (17870), and targeted projects (1585). The "Genome Distribution" section has links for Project Type, Sequencing Status, and Phylogenetic. At the bottom, there are three large buttons: "1. Register" (with a GOLD logo), "2. Annotate" (with a bioinformatics icon), and "3. Publish" (with a SIGS logo). The footer includes links for "Inicio", "Materials", "Introduction to", "Our Timeline", "Home - google...", and "ESRI". It also features logos for the U.S. Department of Energy Office of Science and the JGI (Joint Genome Institute).

www.genomesonline.org/cgi-bin/GOLD/Index.cgi

GOLD Genomes Online Database

Last update: 2019-03-10
Total # of genomes: 21923
Download GOLD

HOME Genome Map Genome Earth Search News Statistics Team Reference Contact

[f](#) [W](#) [Blogger](#)

Welcome to the Genomes OnLine Database

GOLD: Genomes Online Database, is a World Wide Web resource for comprehensive access to information regarding genome and metagenome sequencing projects, and their associated metadata, around the world.

Metagenomes

Classification

- Studies: 376
- Samples: 2639

Isolate Genomes

Complete Projects: 4910

Incomplete Projects: 17870

Targeted Projects: 1585

Genome Distribution

- Project Type
- Sequencing Status
- Phylogenetic

1. Register

Register your project information and Metadata in Genomes Online Database

2. Annotate

Annotate your microbial genome or metagenome with IMG/ER or MG/ER

3. Publish

Publish your genome or metagenome in open access standards-supportive journal

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Disclaimer | Credits

U.S. DEPARTMENT OF ENERGY Office of Science

www.ncbi.nlm.nih.gov/genomes/browse/submit-genome/

Inicio Materials Introduction to Our Timeline Home - google... ESRI 4:130 PM

Genomas secuenciados

The screenshot shows the NCBI homepage. At the top, there is a blue header bar with the NCBI logo, a "Resources" dropdown, a "How To" dropdown, and a "My NCBI" link. Below the header is the main search interface, featuring the NCBI logo, a search bar set to "All Databases", a search button, and a clear button. On the left side, there is a sidebar titled "Resources" with a list of links including "NCBI Home", "All Resources (A-Z)", "Data & Software", "DNA & RNA", "Domains & Structures", "Genes & Expression", "Genetics & Medicine", "Genomes & Maps", "Homology", "Literature", "Proteins", "Sequence Analysis", "Small Molecules", "Taxonomy", "Training & Tutorials", and "Variation". The main content area has a heading "Welcome to NCBI" and a sub-section "Genome" with the text "1000 prokaryotic genomes are now completed and available in the Genome database." There is also a small image of bacterial cells.

Resources

[NCBI Home](#)

[All Resources \(A-Z\)](#)

[Data & Software](#)

[DNA & RNA](#)

[Domains & Structures](#)

[Genes & Expression](#)

[Genetics & Medicine](#)

[Genomes & Maps](#)

[Homology](#)

[Literature](#)

[Proteins](#)

[Sequence Analysis](#)

[Small Molecules](#)

[Taxonomy](#)

[Training & Tutorials](#)

[Variation](#)

Welcome to NCBI

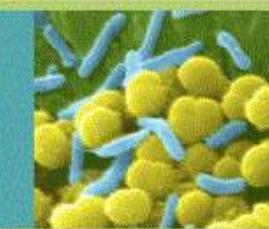
The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

[More about the NCBI](#) | [Mission](#) | [Organization](#) | [Research](#) | [RSS](#)

Genome

1000 prokaryotic genomes are now completed and available in the Genome database.

1 2 3 4



How To...

- [Determine conserved synteny between the genomes of two organisms](#)
- [Find a homolog for a gene in another organism](#)
- [Obtain the full text of an article](#)
- [Design PCR primers and check them for specificity](#)

Popular Resources

- [BLAST](#)
- [Bookshelf](#)
- [Gene](#)
- [Genome](#)
- [Nucleotide](#)
- [OMIM](#)
- [Protein](#)
- [PubChem](#)
- [PubMed](#)
- [PubMed Central](#)
- [SNP](#)

NCBI News

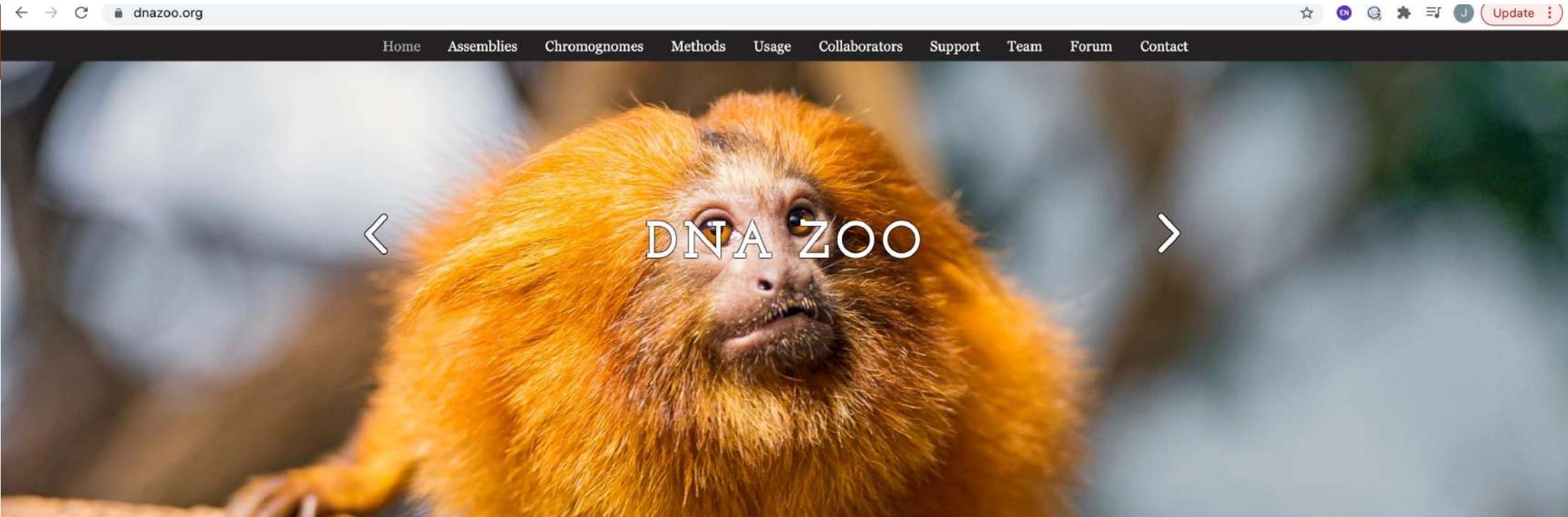
[Education resource information in the May NCBI News](#)

07 Jun 2010

[May NCBI News is available.](#)

[OMIM's new look, Epigenomics in April NCBI News](#)

Iniciativas genómicas



D. Lim, P. Kaur, B. Halaska, G. Rulli

2 hours ago • 2 min

Fin-al fantasy

Next to the blue whale, the fin whale is the second-largest mammal in the world. Unlike blue whales, fin whales have pointed heads and...

Utiliza Hi-C

Iniciativas genómicas

earthbiogenome.org

EN J Update



ABOUT EBP GOVERNANCE COMMITTEES REPORTS MEDIA CONTACT

CREATING A NEW FOUNDATION FOR BIOLOGY

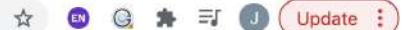
Sequencing Life for the Future of Life

What is the Earth Biogenome Project?

Powerful advances in genome sequencing technology, informatics, automation, and artificial intelligence, have propelled humankind to the threshold of a new beginning in understanding, utilizing, and conserving biodiversity. For the first time in history, it is possible to efficiently sequence the genomes of all known species, and to use genomics to help discover the remaining 80 to 90 percent of species that are currently hidden from science.

Iniciativas genómicas

naturalhistory.si.edu/research/global-genome-initiative



Smithsonian

VISIT EXHIBITS RESEARCH EDUCATION EVENTS ABOUT JOIN US DONATE



NATIONAL
MUSEUM of
**NATURAL
HISTORY**

Glob (GGI)

The Global Genome Initiative (GGI) is a collaborative science-based endeavor to collect the Earth's genomic biodiversity, preserve it in the world's biorepositories and make it available to researchers everywhere. The Global Genome Initiative aims to capture half of the world's genomic diversity by 2022.

The Global Genome Initiative led the development of and hosts the secretariat of the [Global Genome Biodiversity Network](#)—a consortium of the world's major biorepositories and genomic research collections. As of June 2021, it has nearly 100 collaborating [member institutions](#). The Global Genome Biodiversity Network will serve to accelerate and optimize research everywhere. Its goal is to achieve one federated database of the world's genomic resources—tissues and DNA—accessible to all stakeholders.

Our Vision

Preserving and understanding the genomic diversity of life on Earth

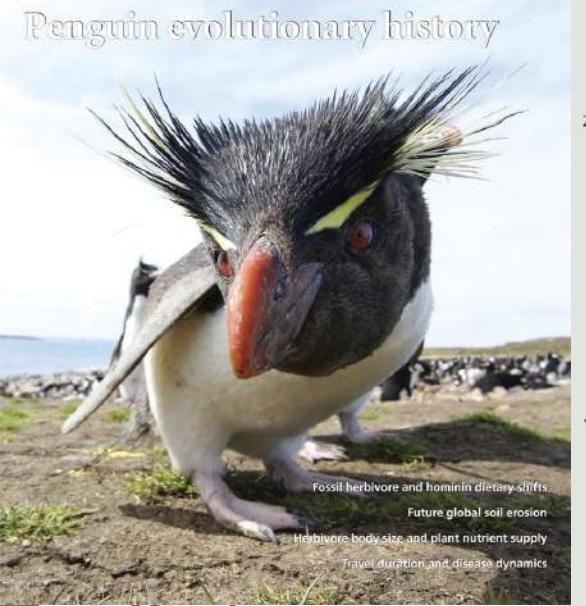
[MORE ABOUT GGI](#)

IMG_7217.JPG, IMG_7205.JPG, IMG_7200.JPG, IMG_7179.JPG, IMG_7110.JPG, Doussangetal.20...pdf

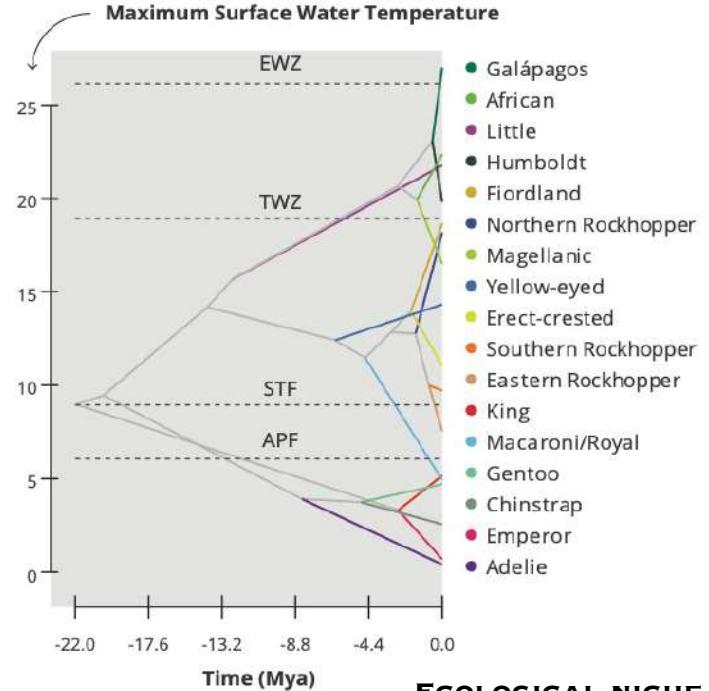
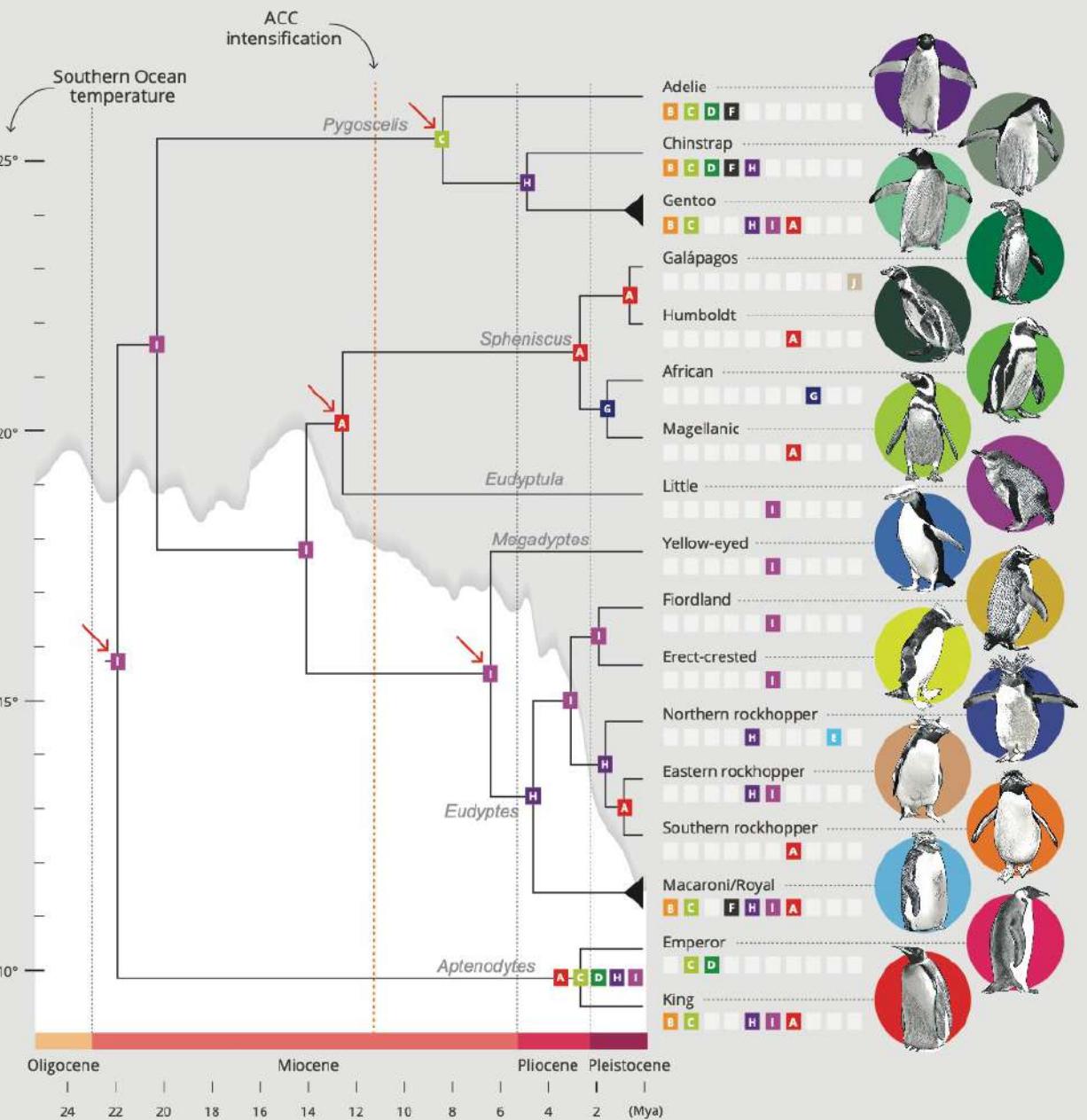
Home / Our Research / Global Genome Initiative

EVOLUTIONARY HISTORY

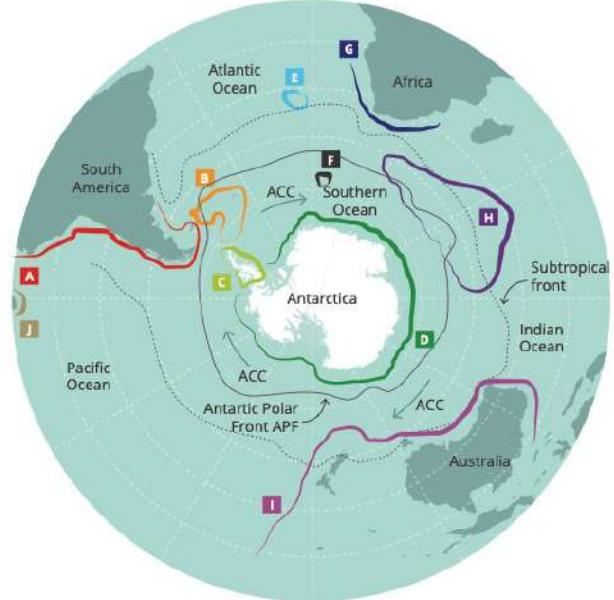
September 8, 2020 | vol. 117 | no. 36 | pp. 21625–22664
PNAS
Proceedings of the National Academy of Sciences of the United States of America
www.pnas.org



Vianna et al. 2020



**ECOLOGICAL NICHE
DISPARITY THROUGH
TIME (DTT)**



EWZ: Equatorial Waters Zone (<26°C)

TWZ: Tropical Waters Zone (18°C)

STF: Subtropical Front (9°C)

APF: Antarctic Polar Front (<6°C)

INTROGRESSION

DFOIL

Pygoscelis



Adelie

Chinstrap

Ant

Falk

Ker

Cro

Gentoo

Galapagos

Humboldt

Magellanic

African

Fiordland

Erect-
crested

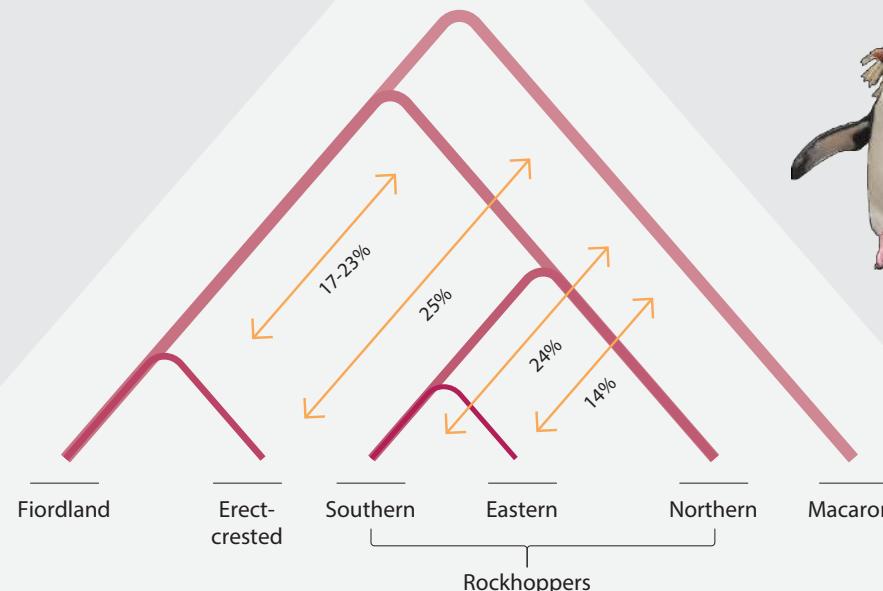
Southern

Eastern

Northern

Macaroni

Rockhoppers



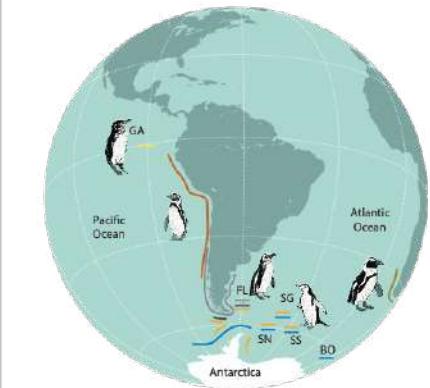
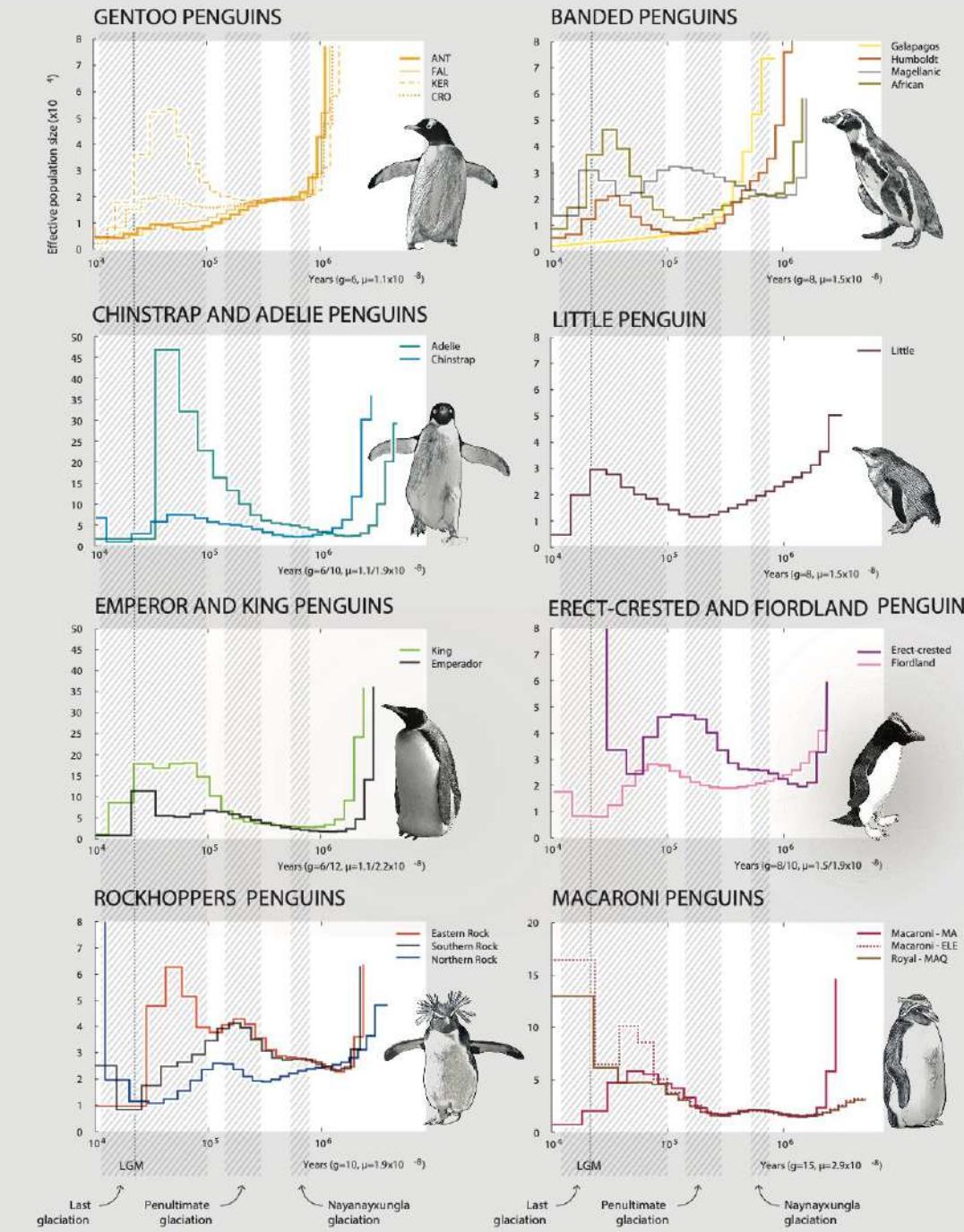
Sphenisc
US



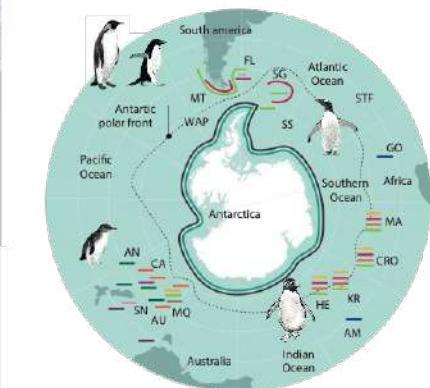
DEMOGRAPHIC HISTORY (PSMC: PAIRWISE SEQUENTIALLY MARKOVIAN COALESCENT)

MOST PENGUINS (11 OF 18 PENGUIN SPECIES) BEING AN INCREASED Ne BETWEEN 40 AND 70 KYA, FOLLOWED BY A PRECIPITOUS DECLINE DURING THE LAST GLACIAL MAXIMUM

LOWEST Ne FOR ISLAND SPECIES (GALAPAGOS, NORTHERN ROCKHOPPER, FIORDLAND)- FOUNDER EFFECT

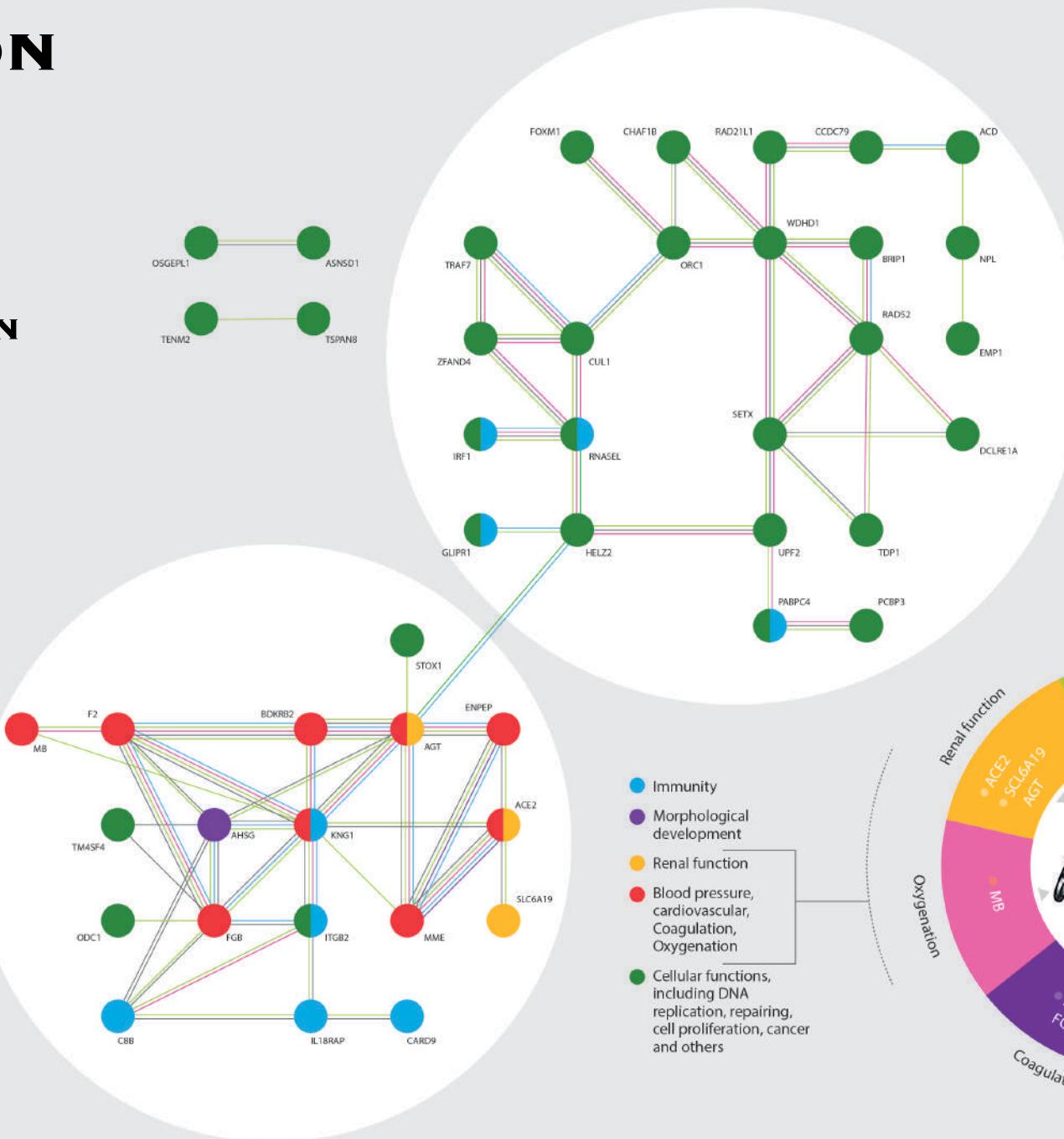


Emperor	Yellow-eyed
King	Little
Royal	Galapagos
Macaroni	Humboldt
Eastern Rockhopper	African
Southern Rockhopper	Magellanic
Northern Rockhopper	Gentoo
Fiordland	Chinstrap
Erect-crested	Adelie

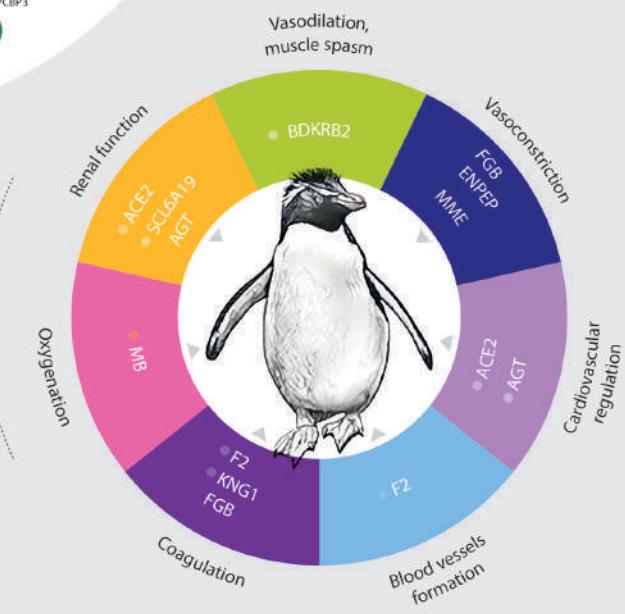


ADAPTATION

104 GENES UNDER
POSITIVE SELECTION

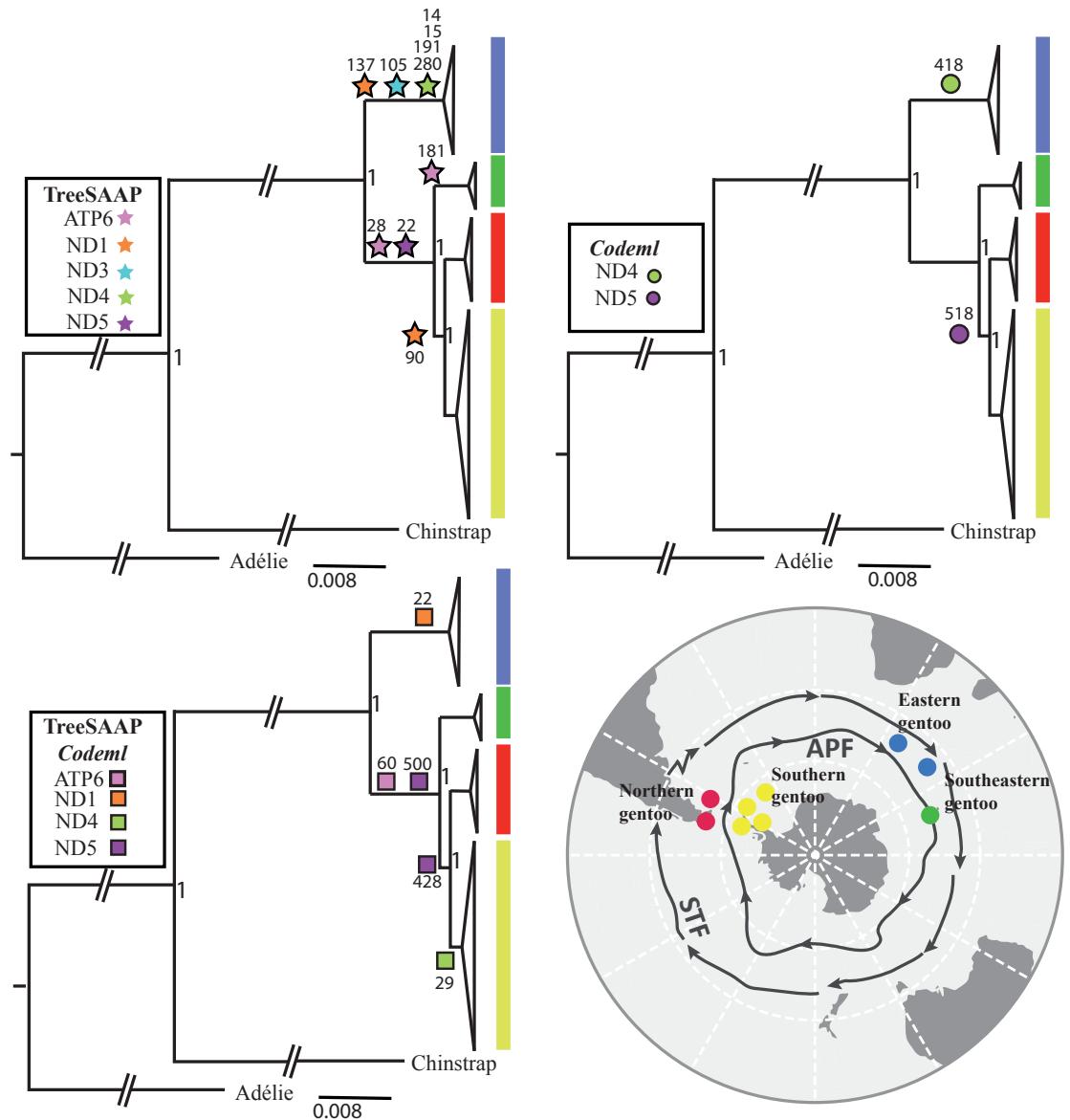
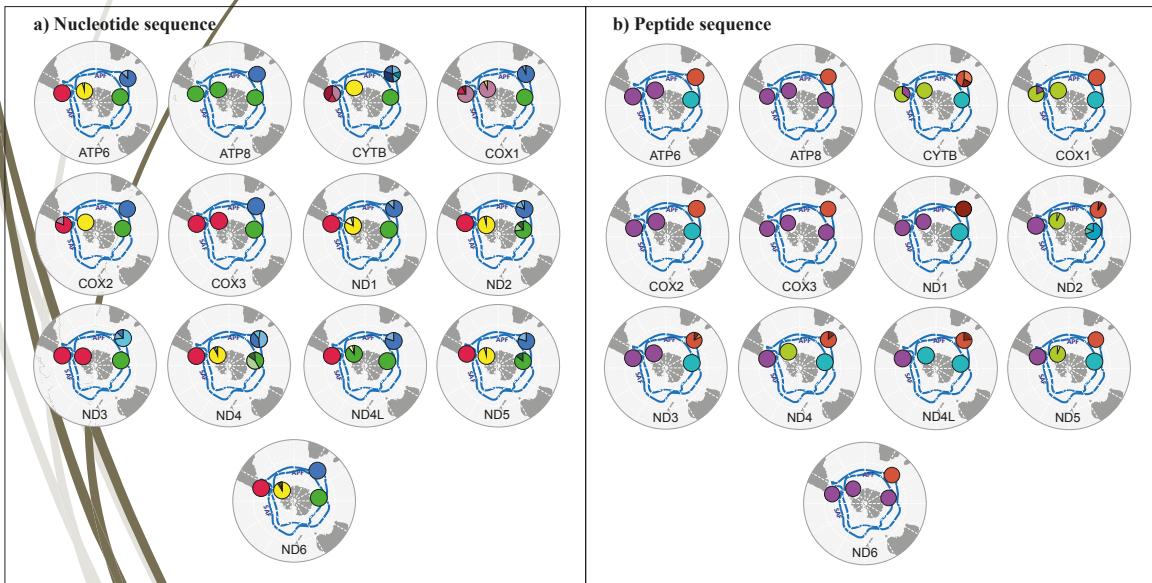


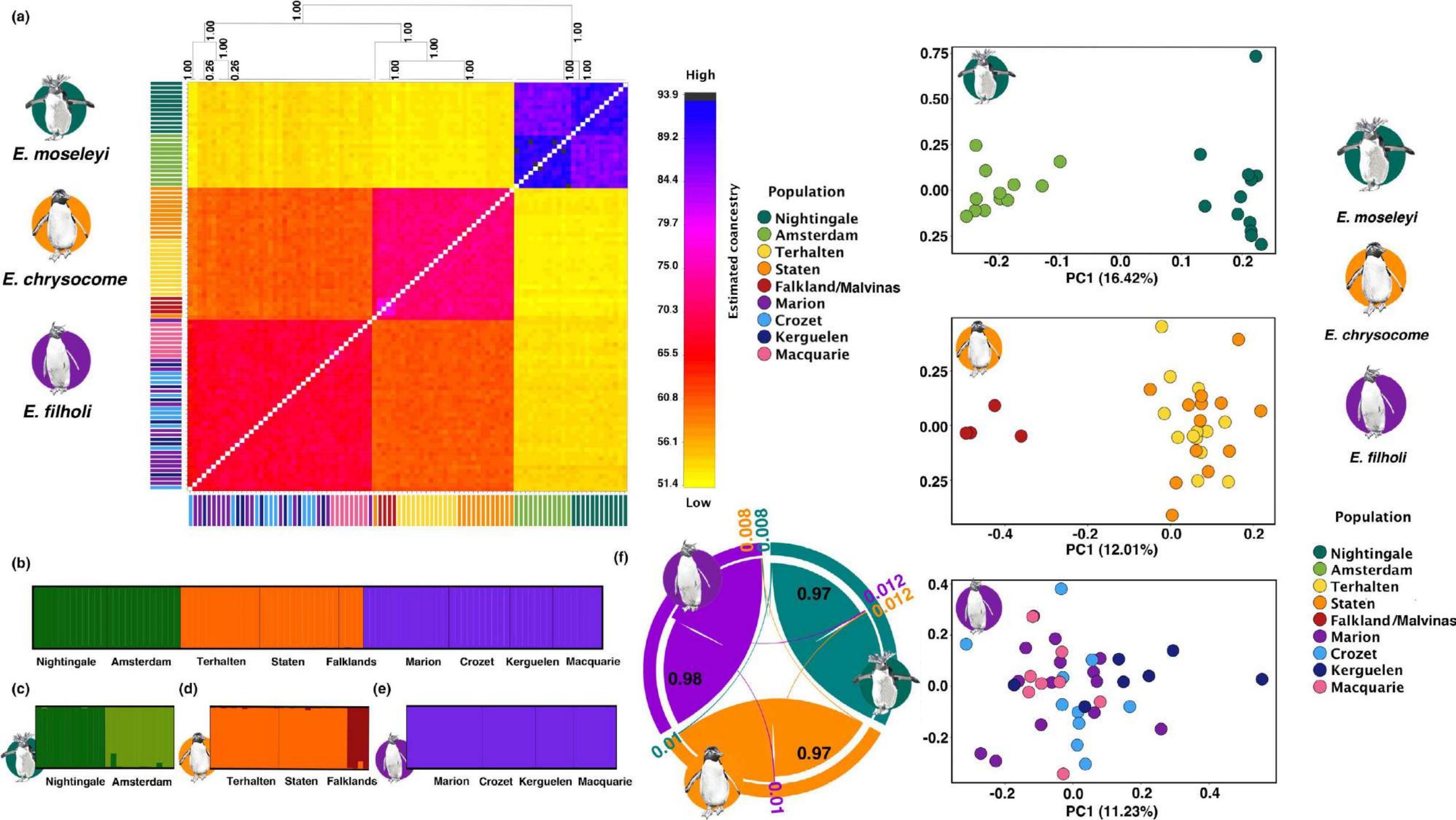
Thermoregulation
Osmoregulation
Diving

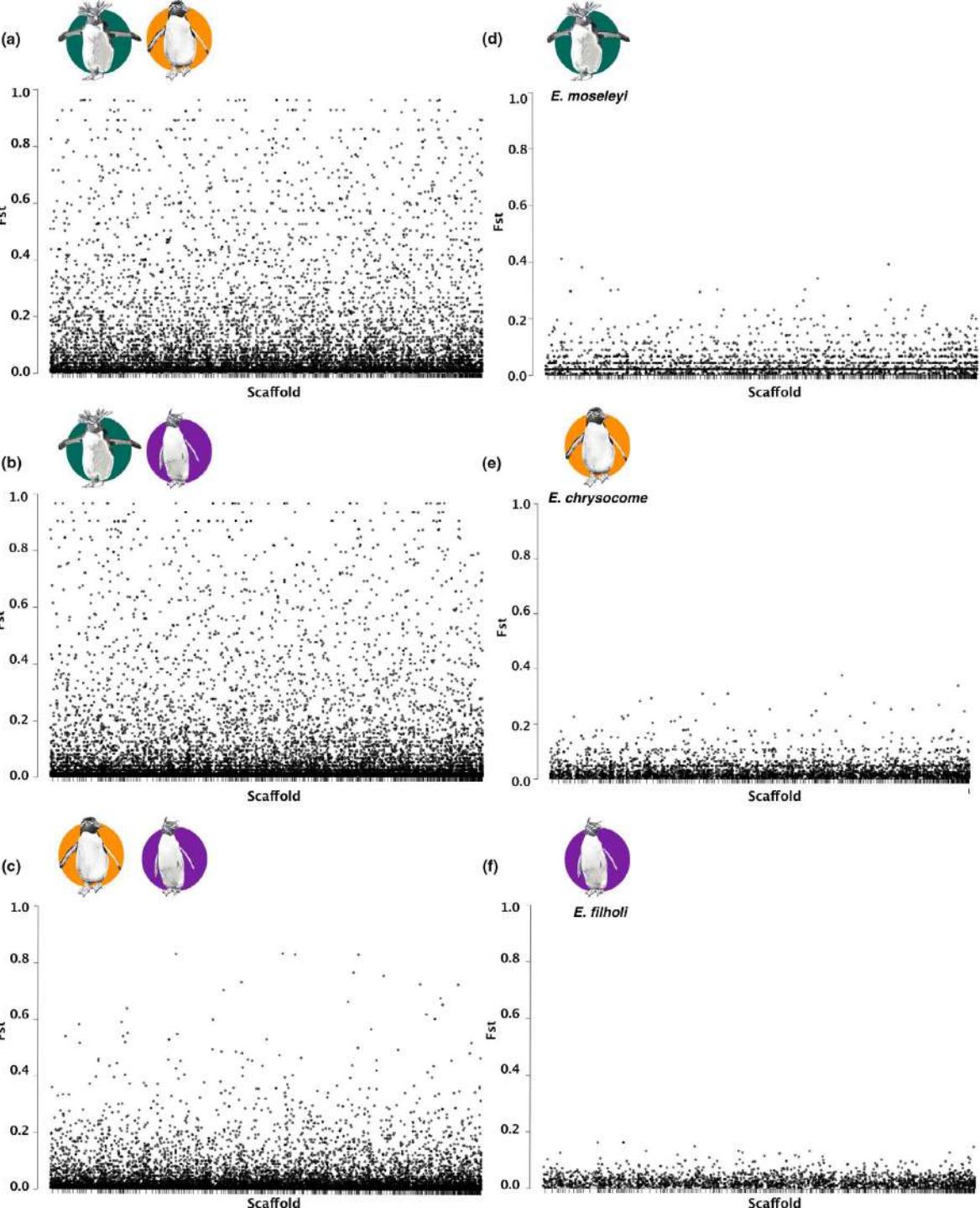
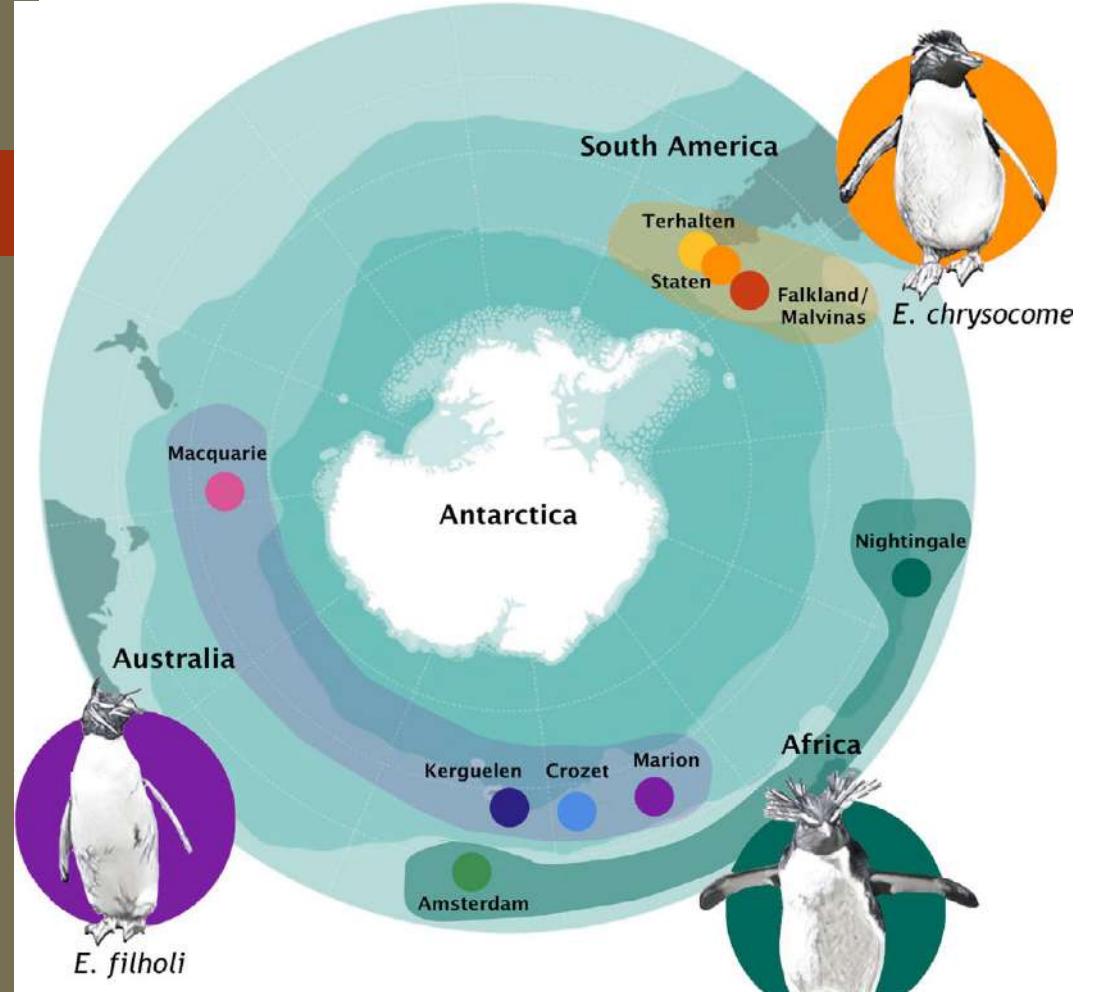




- Positive selection was mostly present in codons of the Complex I (NADH genes), supported by two different codon-based methods at the ND1 and ND4 in the most divergent lineages, the eastern gentoo penguin..





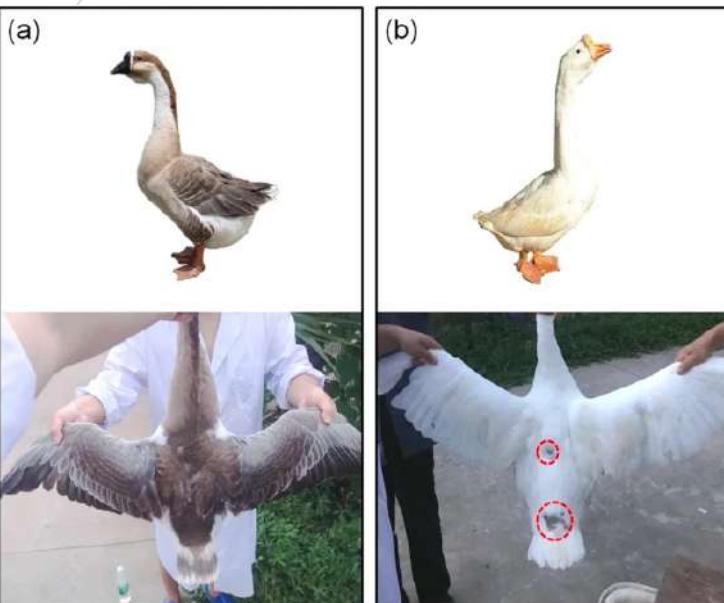


RESEARCH ARTICLE

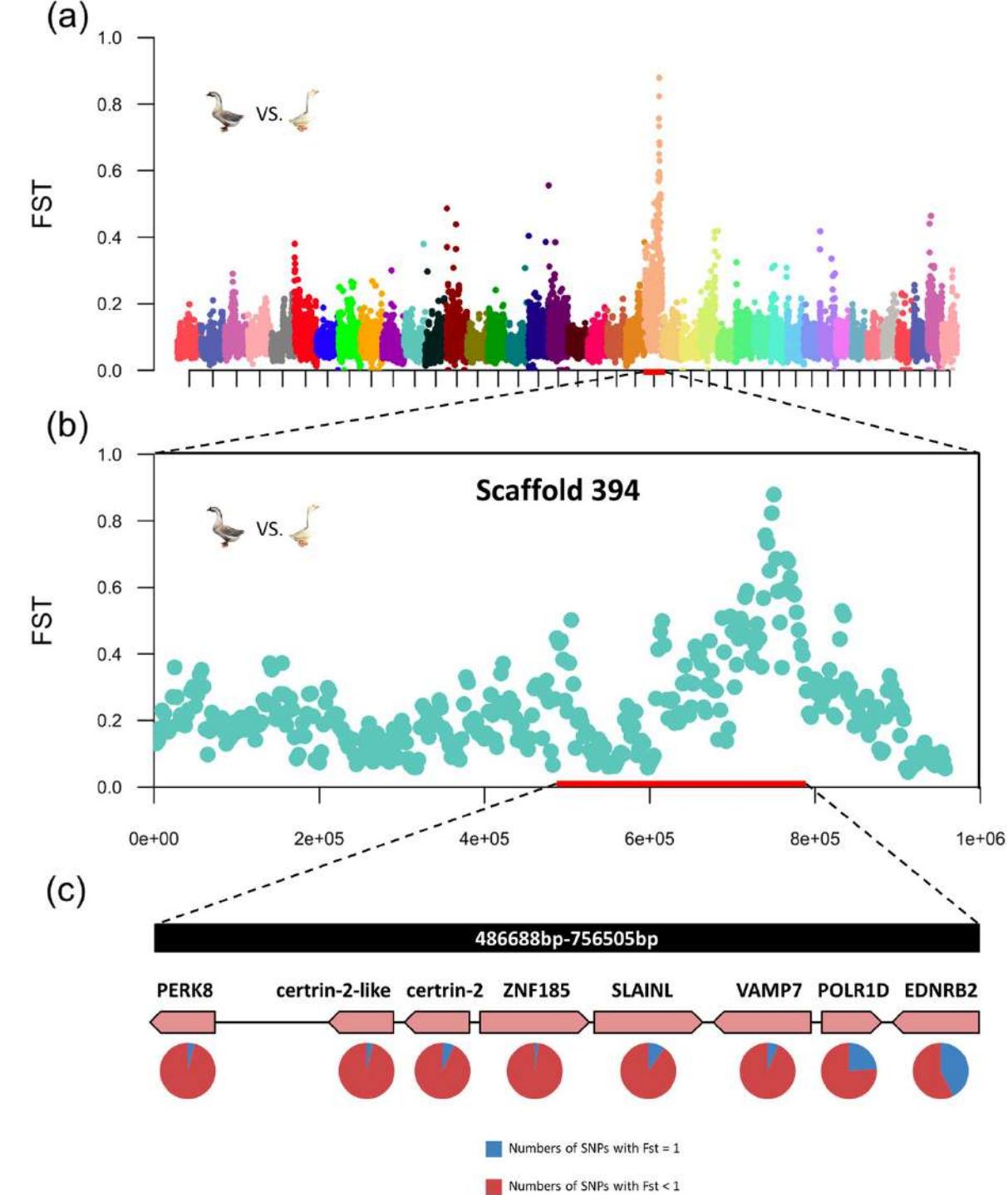
Open Access

A 14-bp insertion in endothelin receptor B-like (EDNRB2) is associated with white plumage in Chinese geese

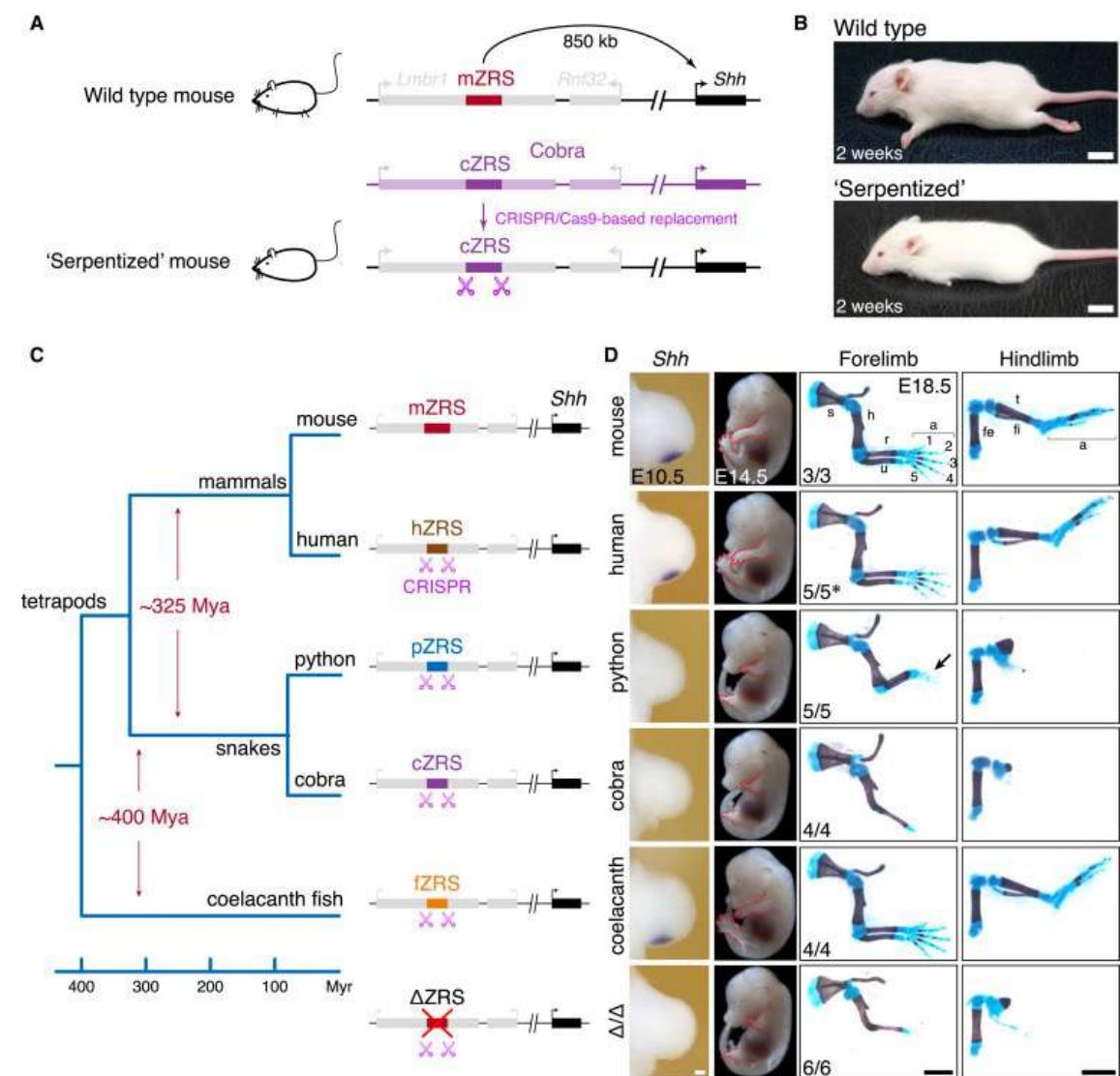
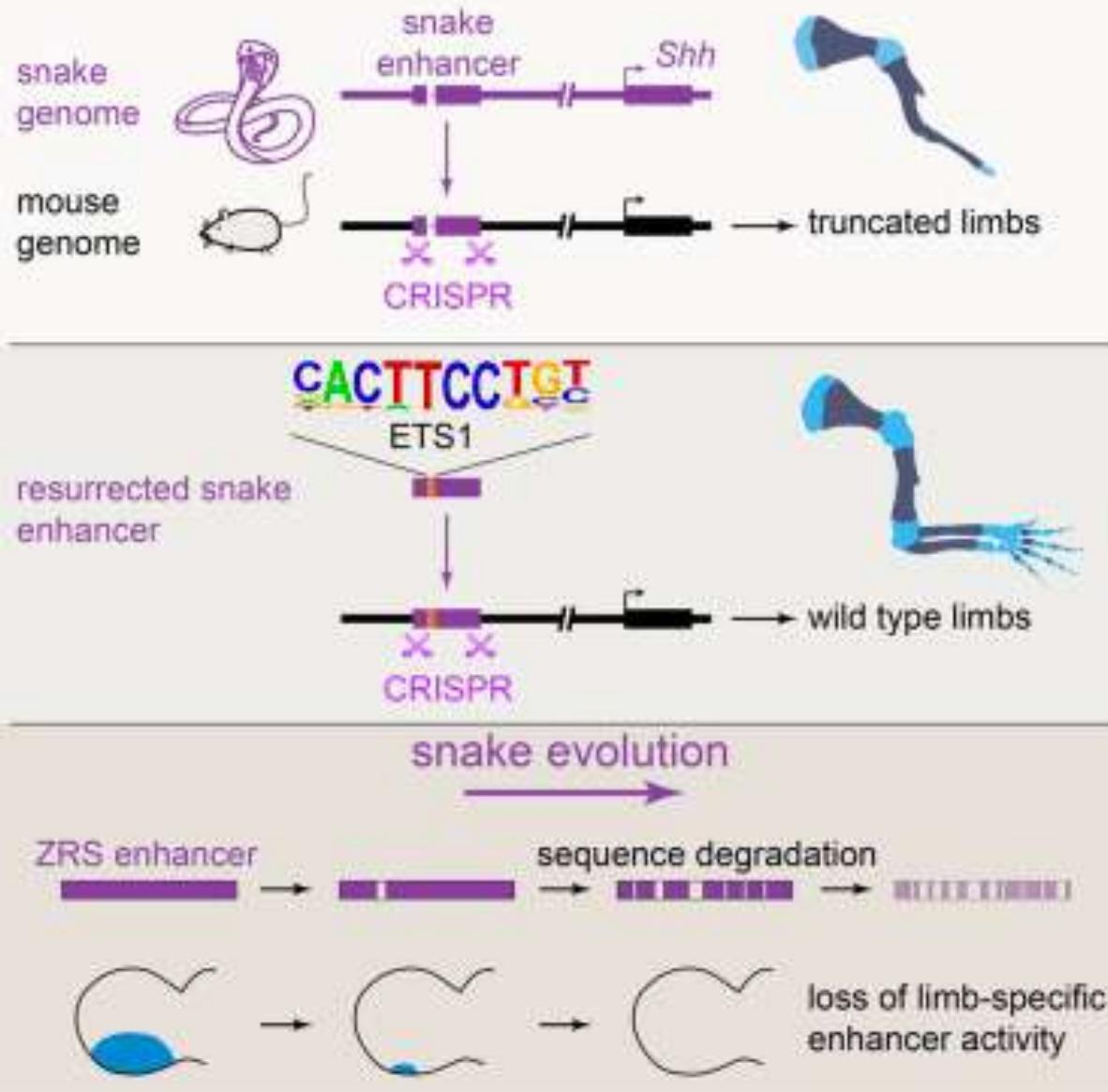
Yang Xi¹, Lei Wang¹, Hehe Liu^{1*}, Shengchao Ma¹, Yanying Li¹, Liang Li¹, Jiwen Wang¹, Han Chunchun¹, Lili Bai¹, Ahsan Mustafa² and Hua He¹



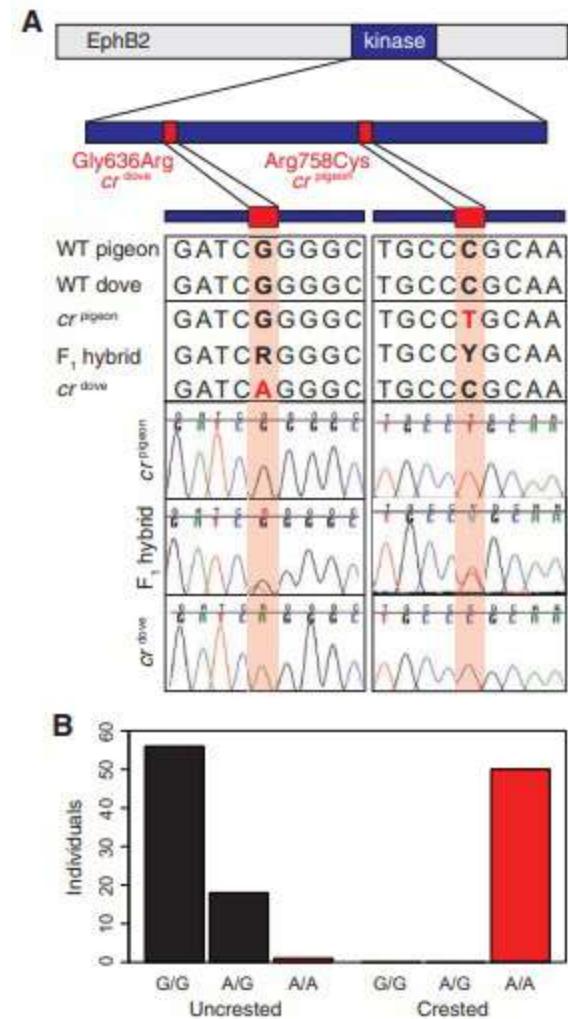
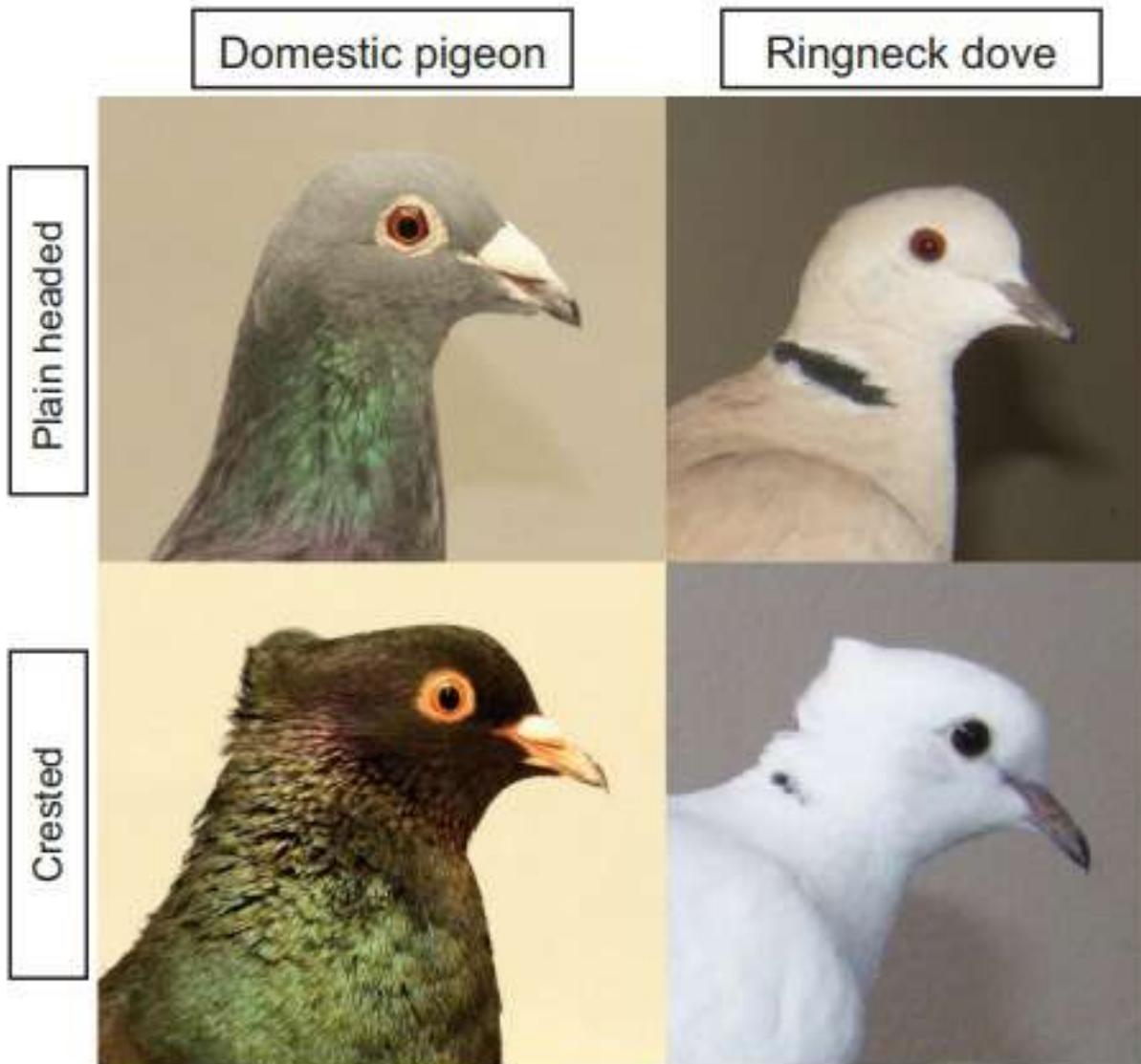
EDNRB2, a key gene that affects the migration of melanoblasts



Como se conoce la función de los genes?



Convergencia adaptativa



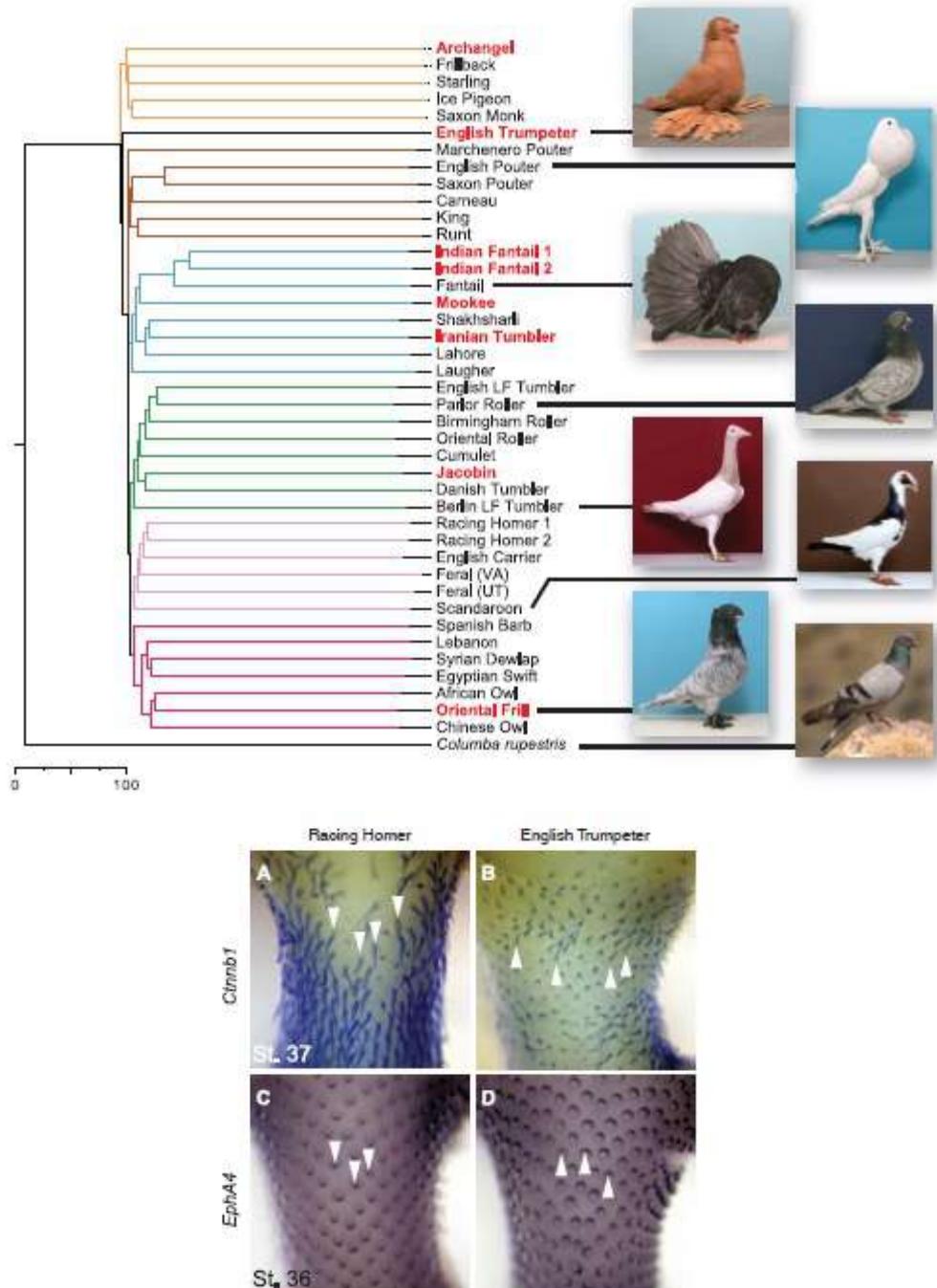
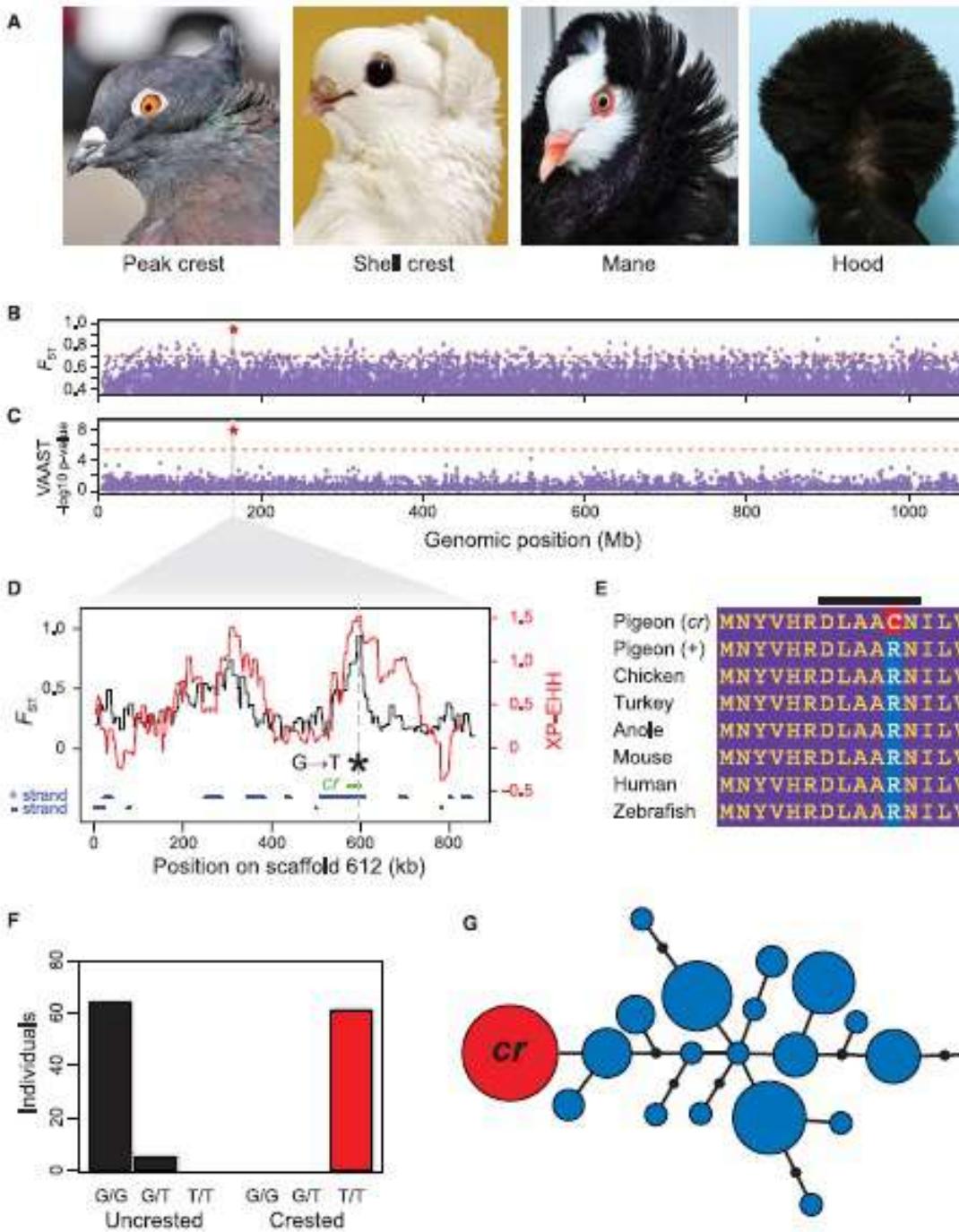
Convergent Evolution of Head Crests in Two Domesticated Columbids Is Associated with Different Missense Mutations in *EphB2*

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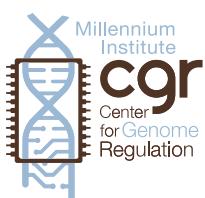
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