Introduction to NGS Technologies

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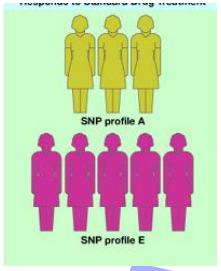
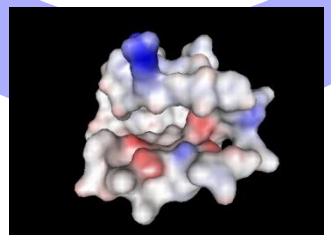
Genetic Research

Genes in the DNA...



...produces the final phenotype

...plus the environment...



...whose structure accounts for function...

>protein kinase

acctgttgatggcgacagggactgt
atgctgatctatgctgatgcatgcat
gctgactactgatgtgggggctattg
acttgatgtctatc....

From genotype to phenotype.

Genetic Research

Genes in the DNA...

...code for proteins...

>protein kinase

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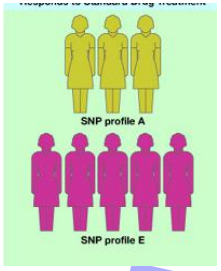

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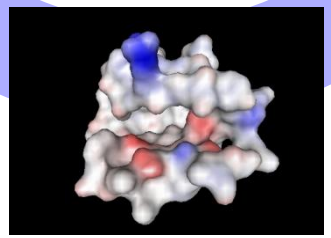

...plus the environment...

Data is information

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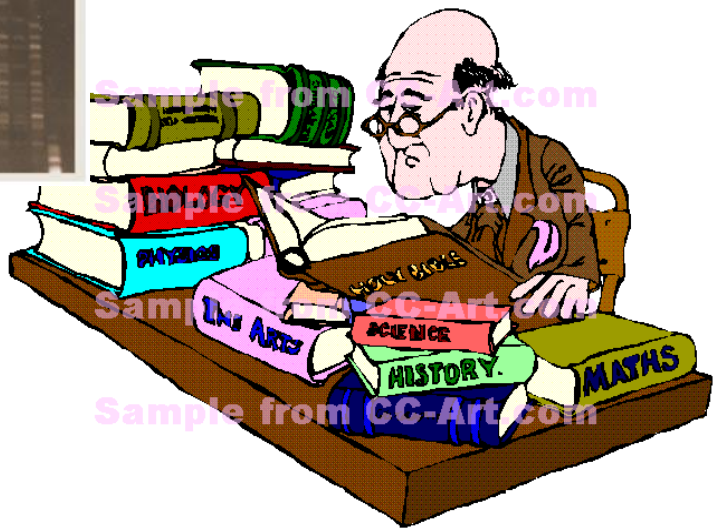
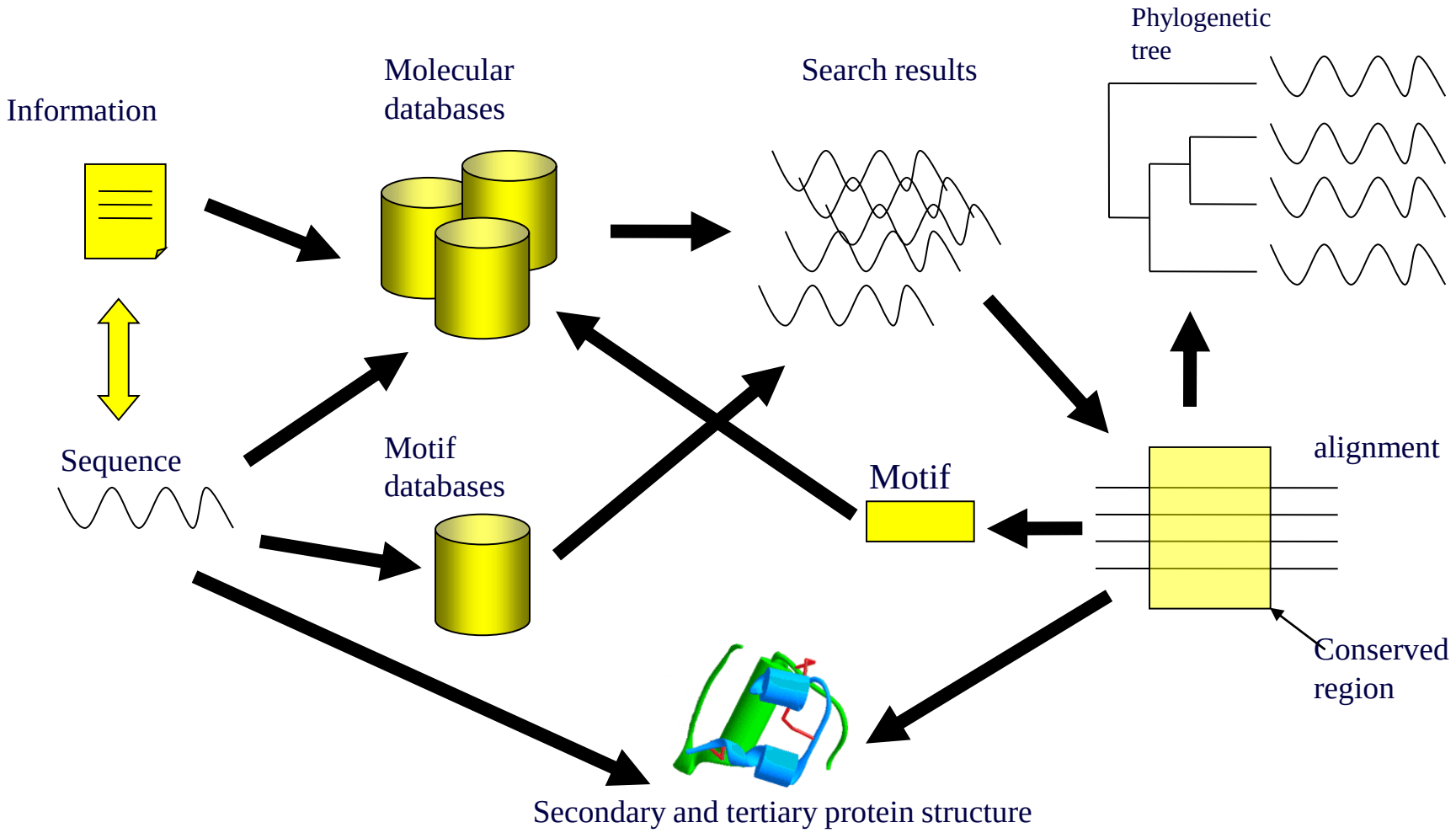
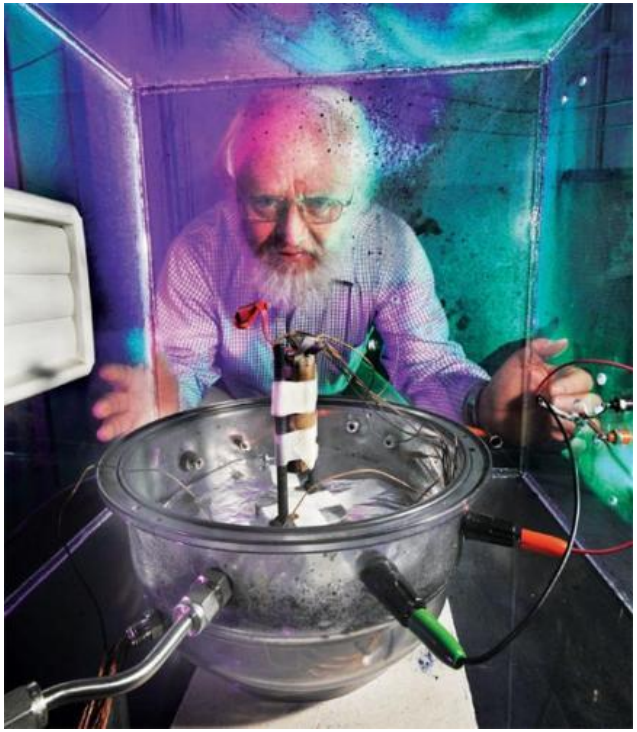


Bioinformatics tools for pre-genomic sequence data analysis





The aim:

Extracting as much information as possible for one single data

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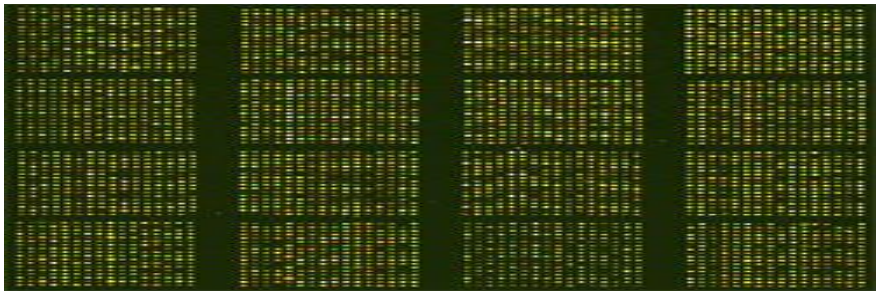
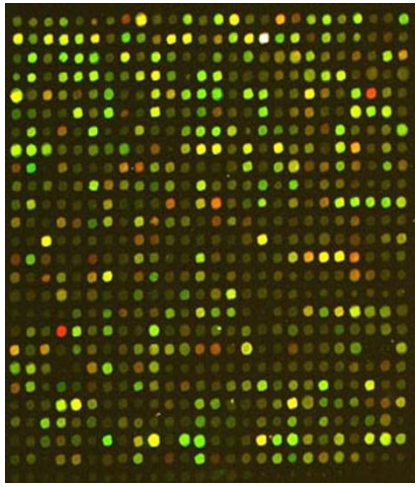
High Throughput Technologies

- 1988 arrayed DNAs were used
- 1991 oligonucleotides are synthesized on a glass slide through photolithography (Affymax Research Institute)
- 1995 DNA Microarrays
- 1997 Genome wide Yeast Microarray





Nature Milestones DNA Technologies

Next Generation Sequencing

600 **Gbp** per run

Genes in the DNA...

>protein kunase

acctgttgatggcgacagggactgtatgct
gatctatgctgatgcatgcatgctgactact
gatgtgggggctattgacttgatgtctatc...
.

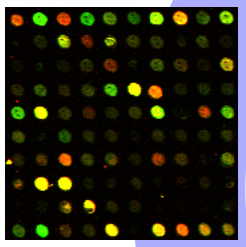
...which can be different because of the variability.

10 million SNPs

...whose final effect configures the phenotype...

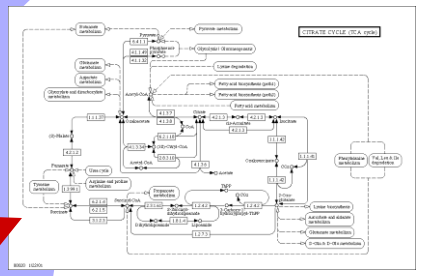
...when expressed in the proper moment and place...

A typical tissue is expressing among **5,000 and 10,000 genes**



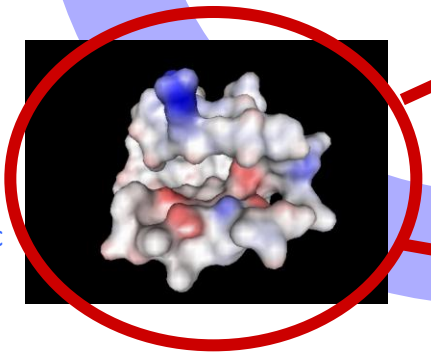
From genotype to phenotype.

(in the functional post-genomics scenario)



...conforming complex interaction networks...

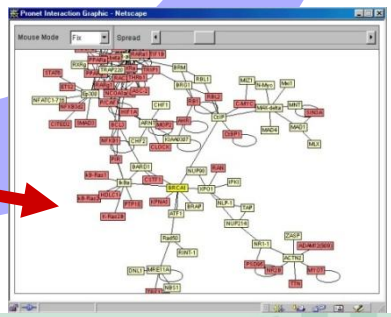
...code for proteins...



That undergo post-translational modifications, somatic recombination...

100K-500K proteins

...whose structures account for function...



Each protein has an average of **8** interactions

...in cooperation with other proteins...

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Next Generation Sequencing
SOLID **12Gbp** per round

Genes in the DNA...

>protein kunase

acctgttgatggcgacagggactgtatgct
gatctatgctgatgcatgcatgctgactact
gatgtgggggctattgacttgatgtctatc...
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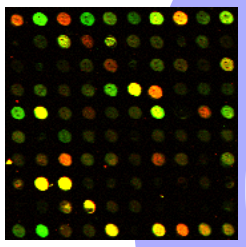
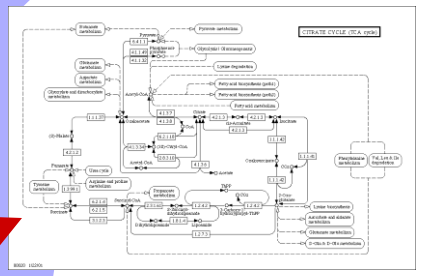


Data ≠ Information



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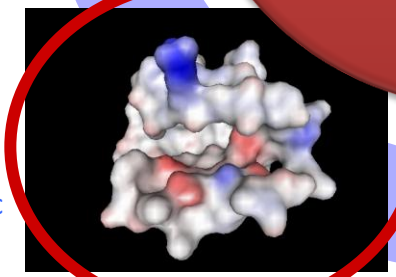

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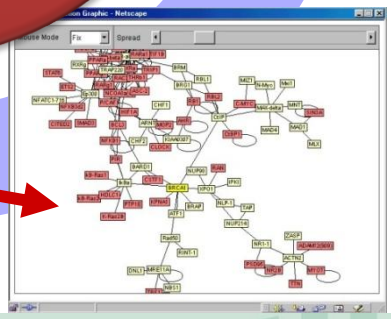

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History of DNA Sequencing

1870	Miescher: Discovers DNA
1940	Avery: Proposes DNA as 'Genetic Material'
1953	Watson & Crick: Double Helix Structure of DNA
1965	Holley: Sequences Yeast $tRNA^{Ala}$
1970	Wu: Sequences λ Cohesive End DNA
1977	Sanger: Dideoxy Chain Termination Gilbert: Chemical Degradation
1980	Messing: M13 Cloning
1986	Hood et al.: Partial Automation
1990	Capillary electrophoresis published Cycle Sequencing
2002	Improved Sequencing Enzymes Improved Fluorescent Detection Schemes
2008	Next Generation Sequencing Improved enzymes & image processing

Adapted from Eric Green, NIH; Adapted from Messing & Llaca, *PNAS* (1998)

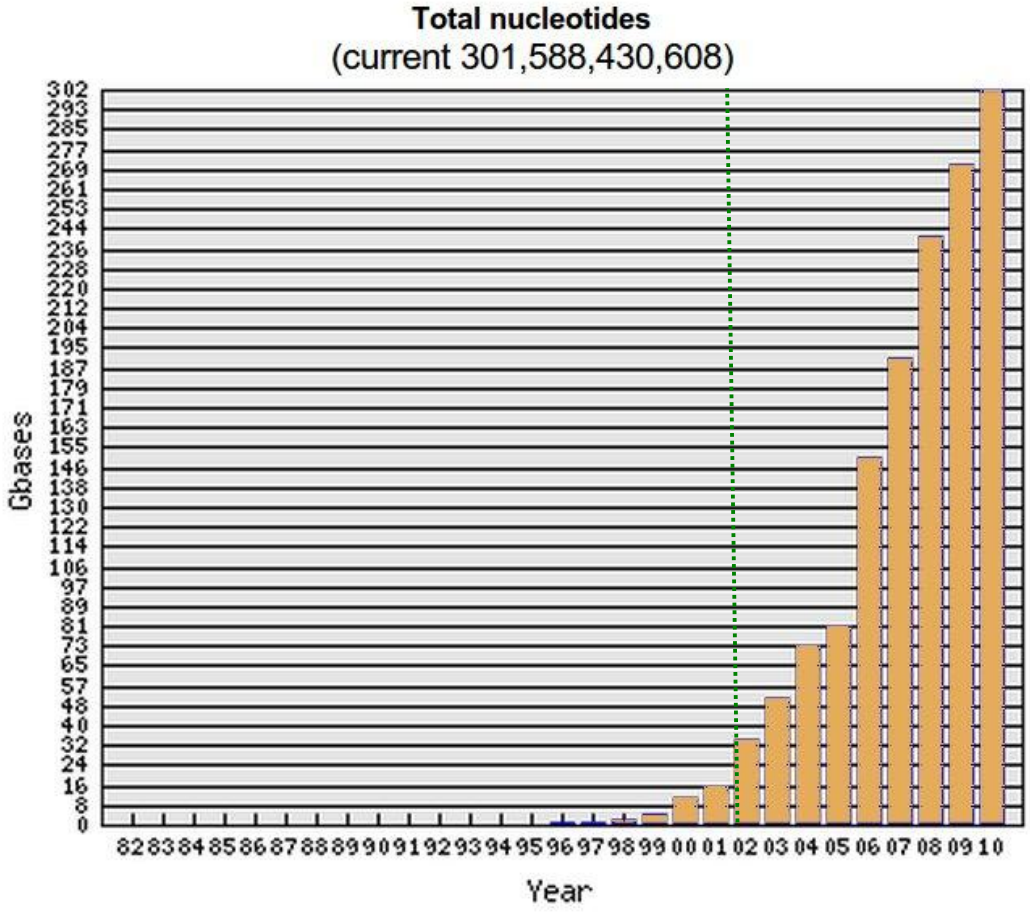
Date	Cost per Mb	Cost per Genome
Sep-01	$5,292.39	$95,263,072
Mar-02	$3,898.64	$70,175,437
Sep-02	$3,413.80	$61,448,422
Mar-03	$2,986.20	$53,751,684
Oct-03	$2,230.98	$40,157,554
Jan-04	$1,598.91	$28,780,376
Apr-04	$1,135.70	$20,442,576
Jul-04	$1,107.46	$19,934,346
Oct-04	$1,028.85	$18,519,312
Jan-05	$974.16	$17,534,970
Apr-05	$897.76	$16,159,699
Jul-05	$898.90	$16,180,224
Oct-05	$766.73	$13,801,124
Jan-06	$699.20	$12,585,659
Apr-06	$651.81	$11,732,535
Jul-06	$636.41	$11,455,315
Oct-06	$581.92	$10,474,556
Jan-07	$522.71	$9,408,739
Apr-07	$502.61	$9,047,003

Date	Cost per Mb	Cost per Genome
Jul-07	$495.96	$8,927,342
Oct-07	$397.09	$7,147,571
Jan-08	$102.13	$3,063,820
Apr-08	$15.03	$1,352,982
Jul-08	$8.36	$752,080
Oct-08	$3.81	$342,502
Jan-09	$2.59	$232,735
Apr-09	$1.72	$154,714
Jul-09	$1.20	$108,065
Oct-09	$0.78	$70,333
Jan-10	$0.52	$46,774
Apr-10	$0.35	$31,512
Jul-10	$0.35	$31,125
Oct-10	$0.32	$29,092
Jan-11	$0.23	$20,963
Apr-11	$0.19	$16,712
Jul-11	$0.12	$10,497
Oct-11	$0.09	$7,743
Jan-12	$0.09	$7,666

National Human Genome Research Institute

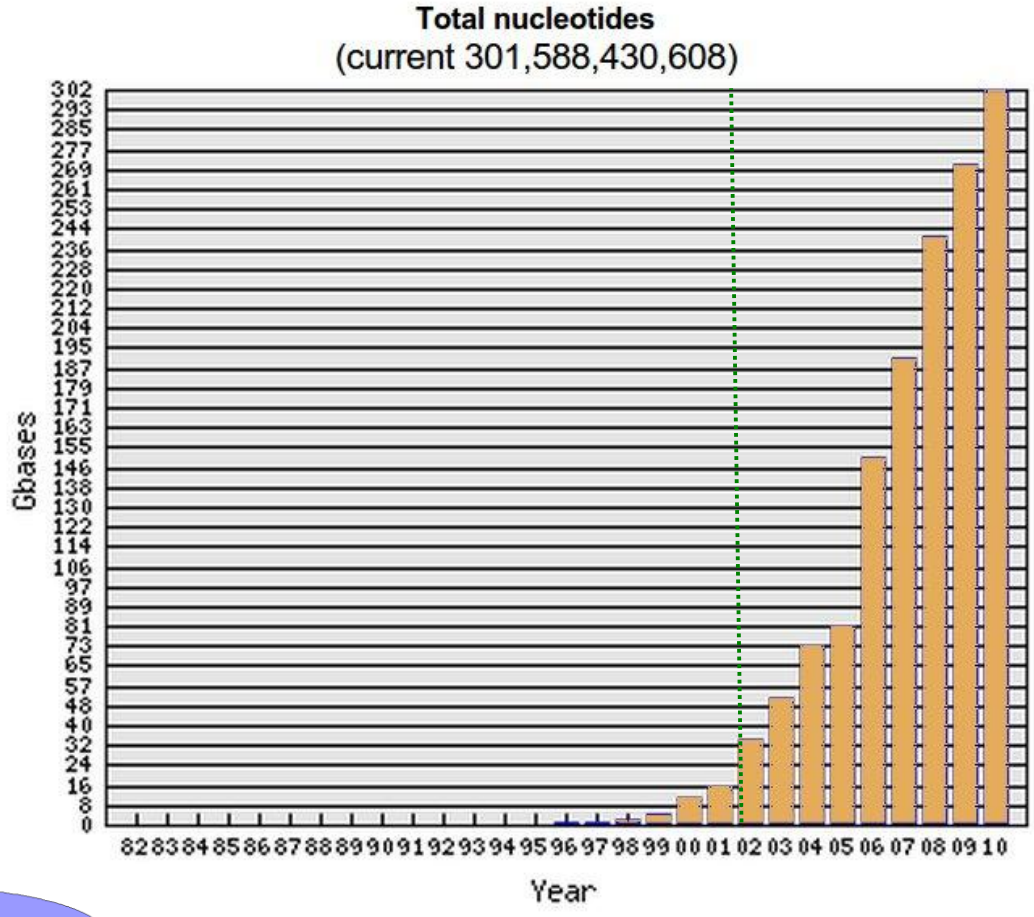
genome.gov/sequencingcosts

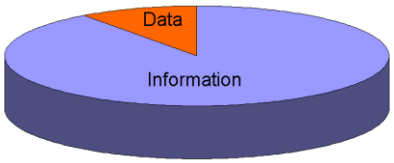
Pre & Post-genomic databases



EMBL database growth (March 2011)

Pre & Post-genomic databases





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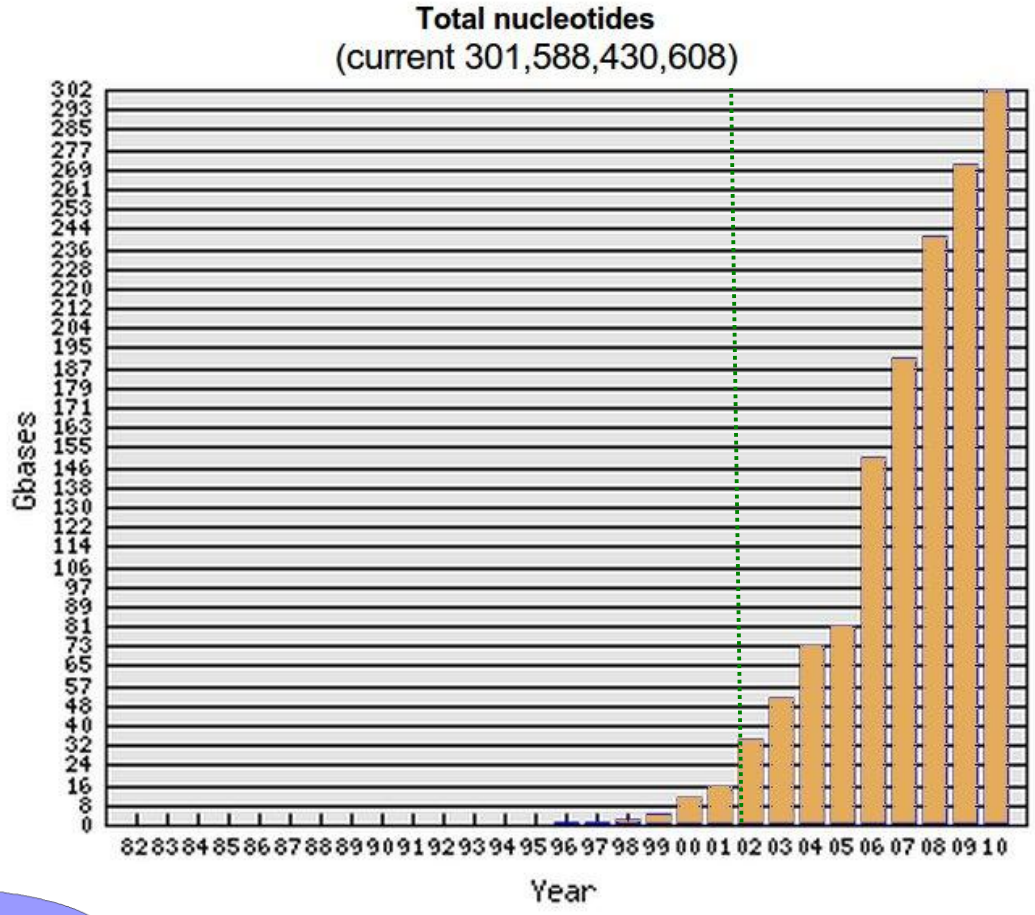

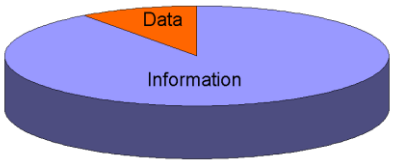

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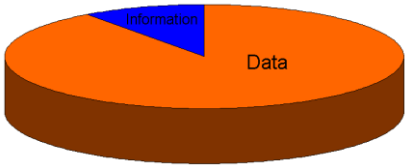

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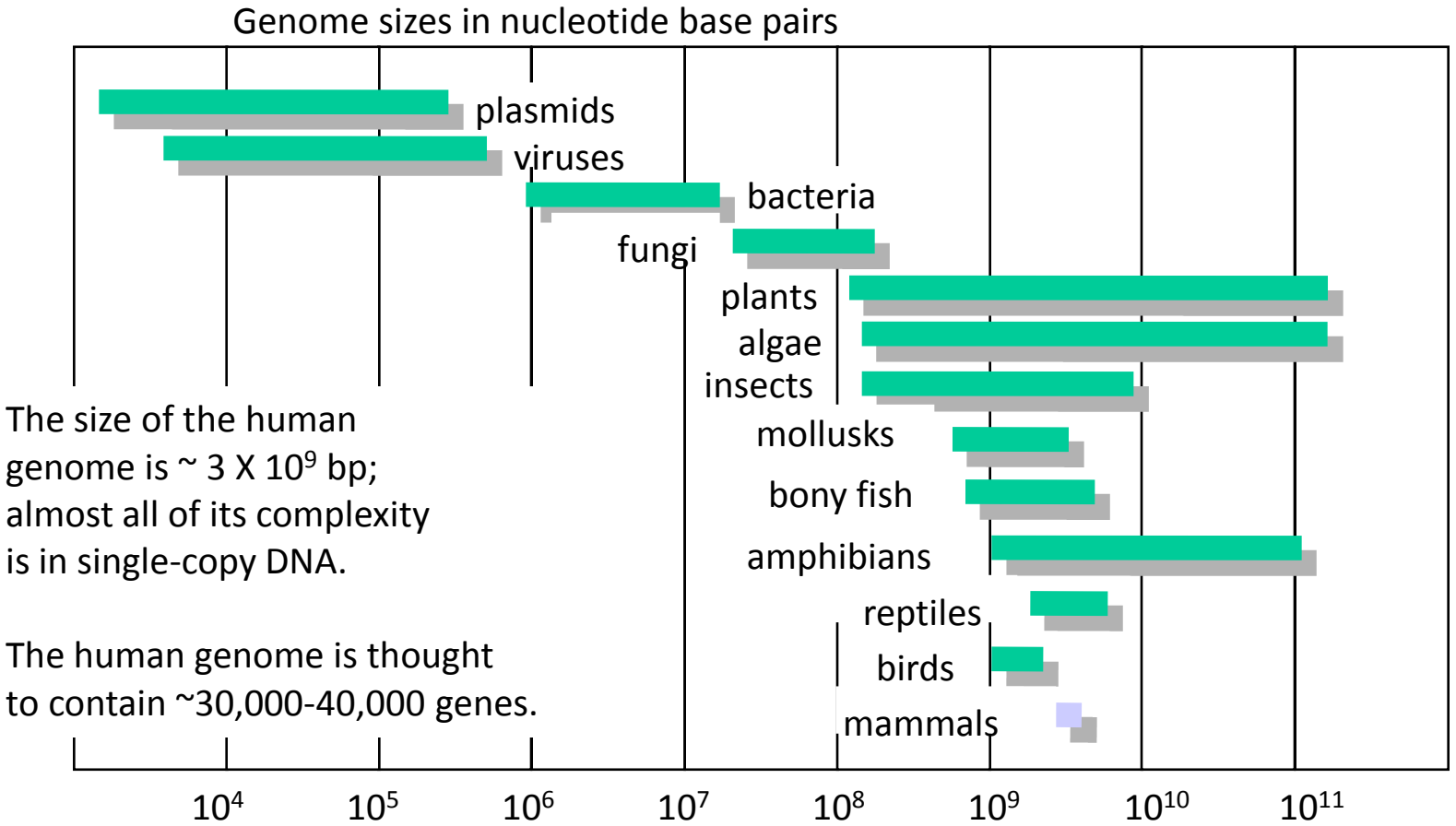
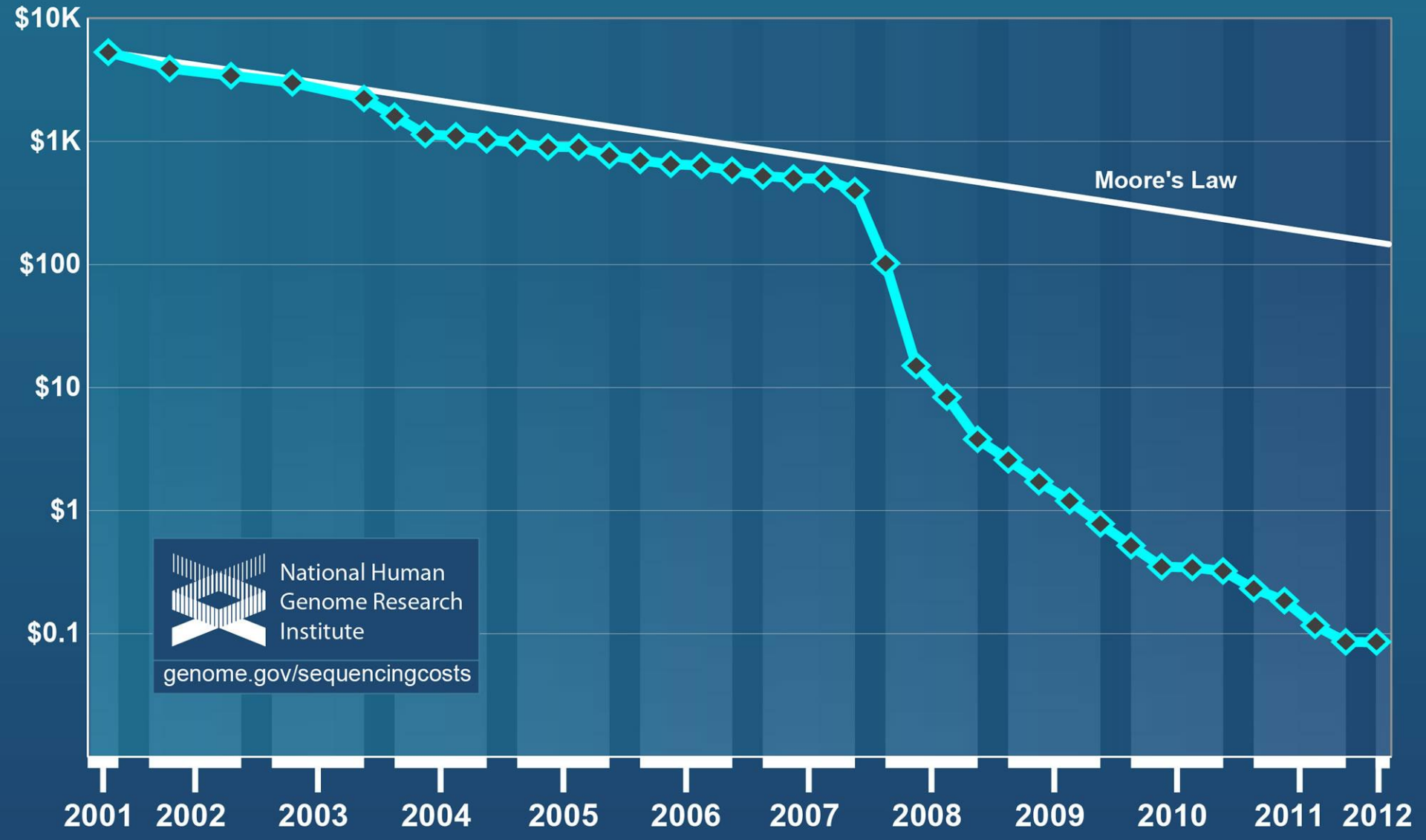


http://www3.kumc.edu/jcalvet/PowerPoint/bioc801b.ppt

Computing capabilities (*CPU power doubles in ~18-24 moths, hard drive capacity doubles in ~12 moths, network bandwidth doubles in ~20 moths*) should increase : **7-10x** in 5 years. Follows **Moors's law**

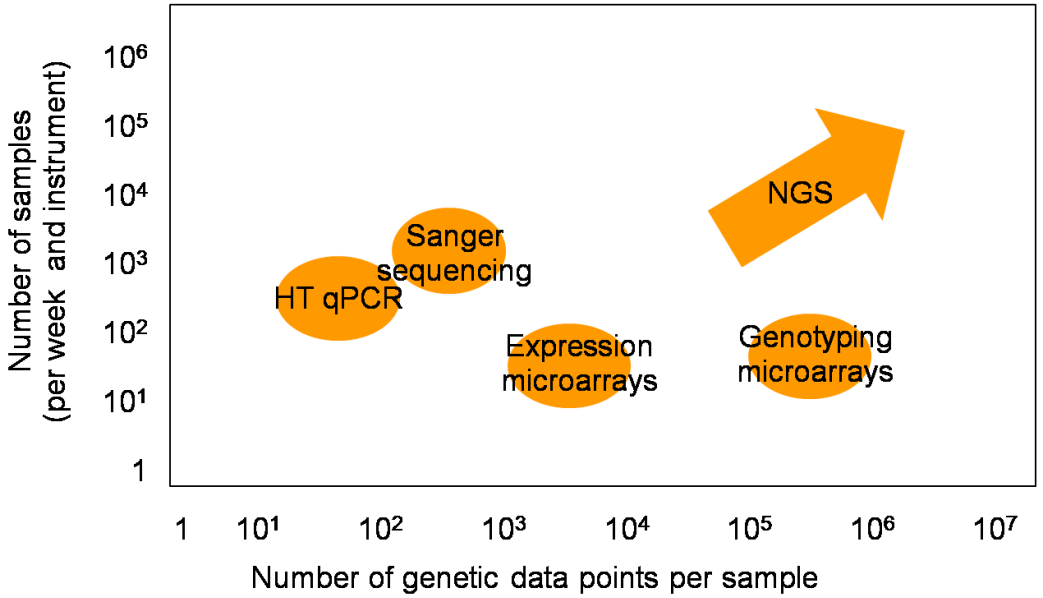
Data projection in 3-5 years: **100x** increase in sequencing volume. Still new technologies with higher throughput to come very soon !!!

Cost per Raw Megabase of DNA Sequence



Relative throughput of the different HT technologies

NGS emerges with a potential of data production that will, eventually wipe out conventional HT technologies in the years coming



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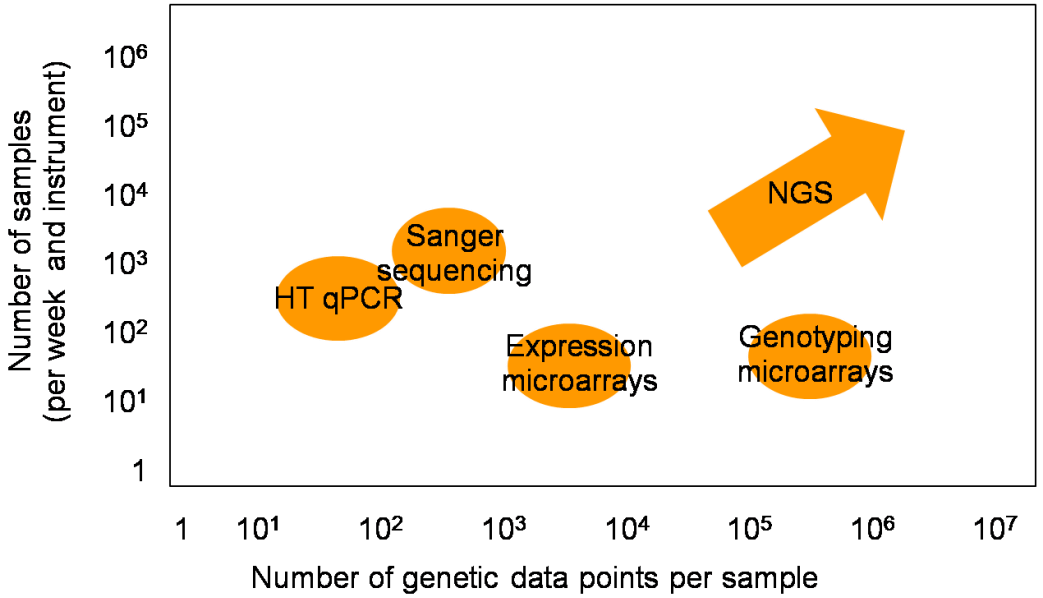

Too many sequences to be handled in a standard computer

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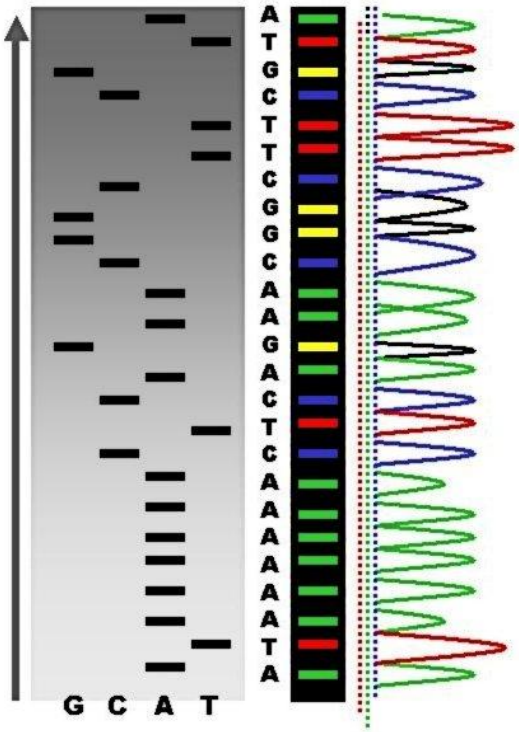
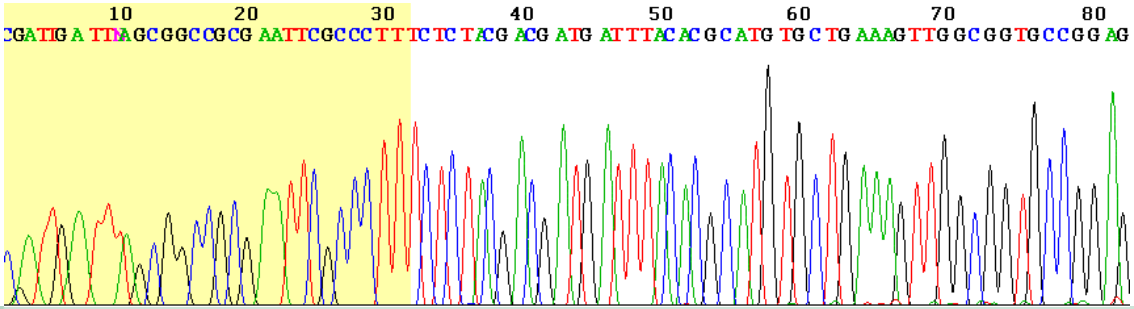
Basics of the “old” technology

- Clone the DNA.
- Generate a ladder of labeled (colored) molecules that are different by 1 nucleotide.
- Separate mixture on some matrix.
- Detect fluoroscope by laser.
- Interpret peaks as string of DNA.
- Strings are 500 to 1,000 letters long
- 1 machine generates 57,000 nucleotides/run
- Assemble all strings into a genome.





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Basics of the “new” Technology

→ Get DNA.

→ Attach it to something.

→ Extend and amplify signal with some color scheme.

→ Detect fluorochrome by microscopy.

→ Interpret series of spots as short strings of DNA.

→ Strings are 30-250 letters long

→ Multiple images are interpreted as 0.4 to 1.2 GB/run/day (1,200,000,000 letters/day).

→ Map or align strings to one or many genome.

	Sanger (1st-gen) Sequencing	Next-Gen Sequencing, and 3rd generation
Whole Genome	Human (early drafts), model organisms, bacteria, viruses and mitochondria (chloroplast), low coverage	New human (!), individual genome, exomes, 2,500 normal (1K genome project), 25,000 cancer (TCGA and ICGC initiatives), CNV, matched control pairs, time course, rare-samples
RNA	cDNA clones, ESTs, Full Length Insert cDNAs, other RNAs	RNA-Seq: Digitization of transcriptome, alternative splicing events, miRNA, allele specific transcripts
Communities	Environmental sampling, 16S RNA populations, ocean sampling,	Human microbiome, deep environmental sequencing, Bar-Seq
Other		Epigenome, rearrangements, ChIP-Seq

NGS technologies

Roche 454 SEQUENCING

Cost-effective
Fast
Ultra throughput
Cloning-free
Short reads

illumina®

life™

PACIFIC BIOSCIENCES™

ion torrent
by life technologies

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Differences between the various platforms:

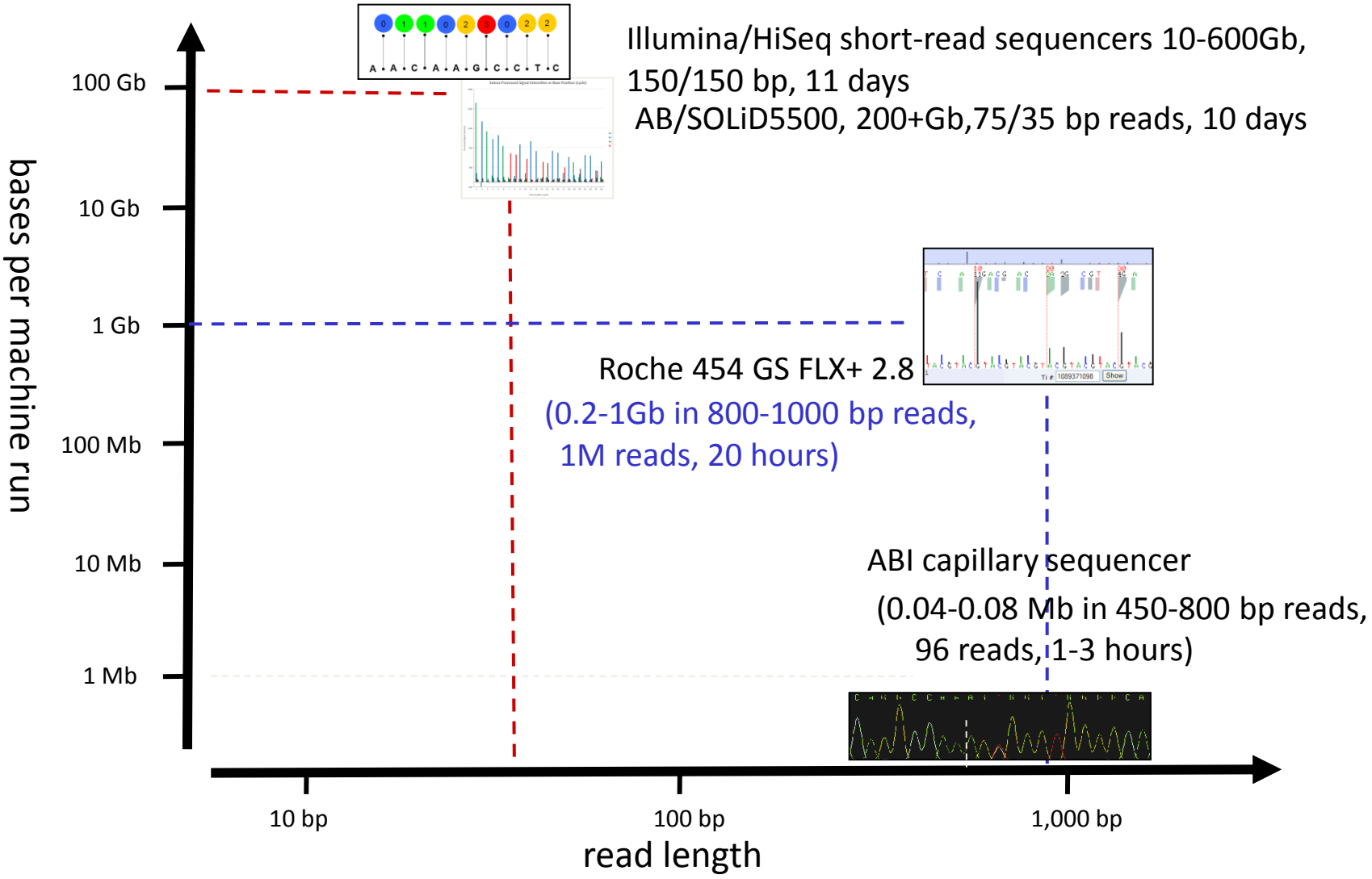
- Nanotechnology used.
- Resolution of the image analysis.
- Chemistry and enzymology.
- Signal to noise detection in the software
- Software/images/file size/pipeline
- Cost

Similarities- LOTS of DATA
General ways of dealing at the sequences

- Assemble them and look at what you have
- You map them (align against a known genome) and then look at what you have.
- Or a mixture of both!
- Sometimes you select the DNA you are sequencing
- or you try to sequence everything
- Depends on biological question, sequencing machine you have, and how much time and money you have.
- NGS is relatively cheap but think what you want to answer, because the analysis won't do magic

Next-gen sequencers

From John McPherson, OICR



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Next Generation Sequencers

3 main platforms:

- **Solexa/illumina**
- **Roche 454**
- **ABI SOLiD**

- Follow an approach similar to Sanger sequencing, but do away with separation of fragments by size and “read” the sequence as the reaction occurs
- Several different “next generation” sequencing platforms developed and commercialized, more on the way.
- Simultaneously sequence entire libraries of DNA sequence fragments

454 (Roche)

- First next generation method to be commercially available

- Uses a “sequencing by synthesis” approach:
  - DNA is broken into pieces of 500-1,400 bp, ligated to adaptors, and amplified on tiny beads by PCR (emulsion PCR)
  - Beads (with DNA attached) are placed into tiny wells (one bead per well) on a PicoTiter Plate that has millions of wells. Each well is connected to an optical fibre.
  - DNA is sequenced by adding polymerase and DNA bases containing pyrophosphate. The different bases (A,C,G,T) are added sequentially in a flow chamber
  - When a base complementary to the template is added, the pyrophosphate is released and a burst of light is produced
  - The light is detected and used to call the base

- Initially 100-150 bp, but they have been improved to 600-1000 bp

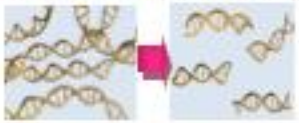
- >1 million, filter-passed reads per run (20 hours)

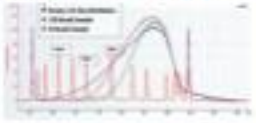
- 1 billion bases per day

Roche 454 pyrosequencing

Principel

Preparation of the DNA includes : DNA fragmentation (nebulization), DNA size selection, Fragment end polishing, Adaptor ligation, Library immobilization, fill in reaction and ssDNA library isolation. At the end of these steps, the DNA fragments are ready for the emulsion PCR (emPCR).

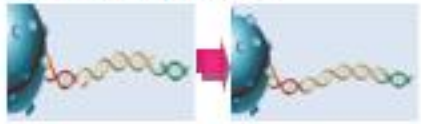

fragmentation

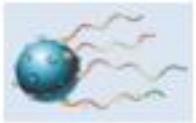

size selection


Polishing

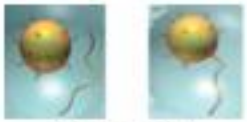

Adaptor ligation


Immobilization


Fill in reaction


ssDNA library isolation

emPCR include the immobilisation of the DNA fragments on capture beads (1 molecule / bead), emulsification (1bead / aqueous microreactor), amplification and indirect enrichment resulting in an immobilized and amplified library.


Immobilisation on capture beads


emulsification


amplification

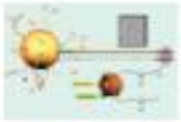

Indirect enrichment : melt, enrichment with biotinilated primer, streptavidin magnetic beads, enrich and melt

Sequencing includes a prewash, the loading DNA library beads, enzyme beads (PPiase) and packing beads on the picotiter plate (PTP). Run over night. At the end of these steps you get your data.


DNA library loading


PPiase + enzyme + packing beads loading


assembly of the PTP


sequencing

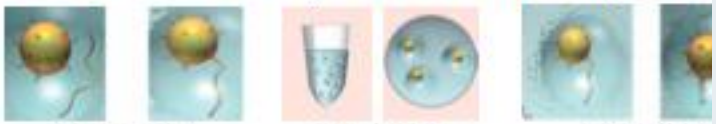
Roche 454 pyrosequencing

Principel

Preparation of the DNA includes : DNA fragmentation (nebulization), DNA size selection, Fragment end polishing, Adaptor ligation, Library immobilization, fill in reaction and ssDNA library isolation. At the end of these steps, the DNA fragments are ready for the emulsion PCR (emPCR).

fragmentation | size selection | Polishing | Adaptor | Immobilization | Fill in reaction | ssDNA library

emPCR include the immobilisation of the DNA fragments on ca
indirect enrichment resulting in an immobilized and amplified lib



Immobilisation on capture beads | emulsification | amplification

Sequencing includes a prewash, the loading DNA library bead
end of these steps you get your data.

DNA library loading | PPiase + enzyme + packing beads loading | assembly of the P

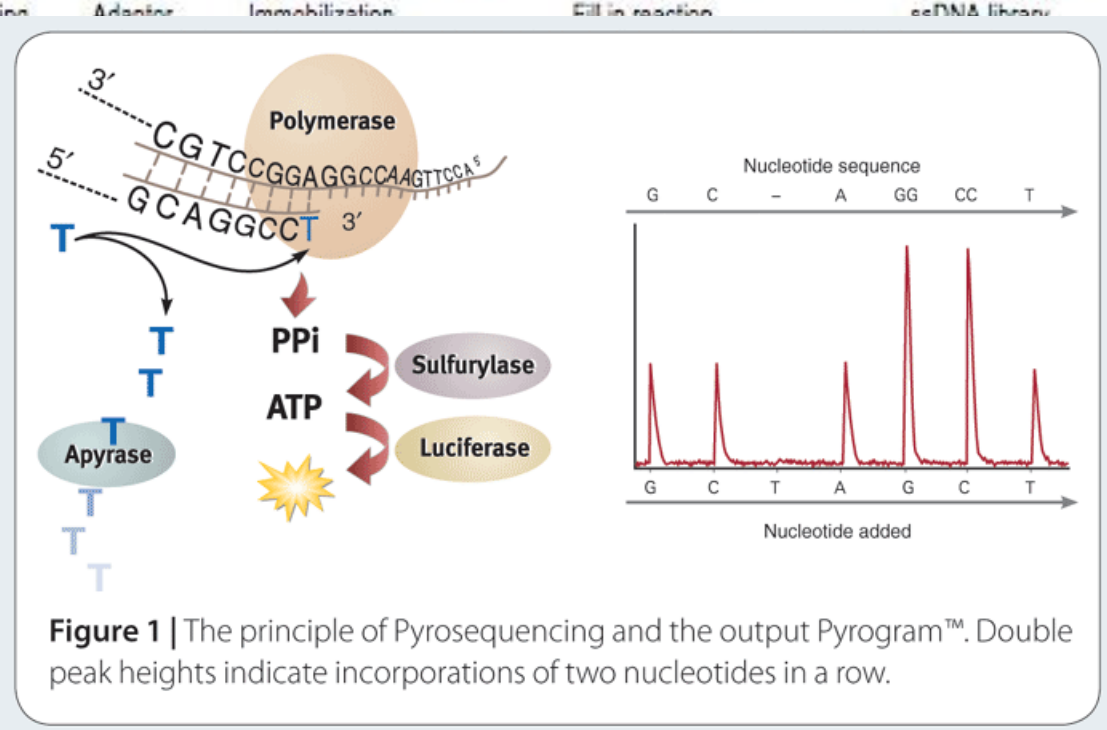
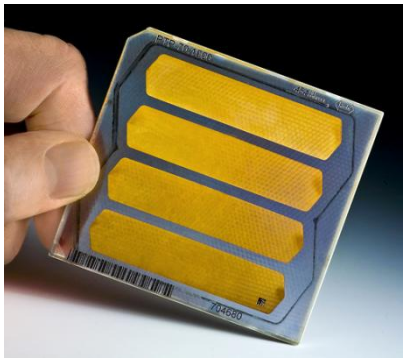


Figure 1 | The principle of Pyrosequencing and the output Pyrogram™. Double peak heights indicate incorporations of two nucleotides in a row.

Roche / 454 : GS FLX

- Good for
  - “de novo“ sequencing (longer reads).
  - Resequencing (expensive)
  - New bacterial genomes.
  - Amplicons
- Pyrosequencing. Bias with long polinucleotide streches

Roche 454



Throughput	400-600 million high-quality, filter-passed bases per run* 1 billion bases per day
Run Time	10 hours
Read Length	Average length = 400 bases
Accuracy	Q20 read length of 400 bases (99% at 400 bases and higher for prior bases)
Reads per run	>1 million high-quality reads
Data	Trace data accepted by NCBI since 2005
Computing Requirements	Cluster recommended (Roche GS FLX Titanium Cluster available)
Robustness	No complex optics or lasers; reagents have long shelf life

GS Junior, benchtop

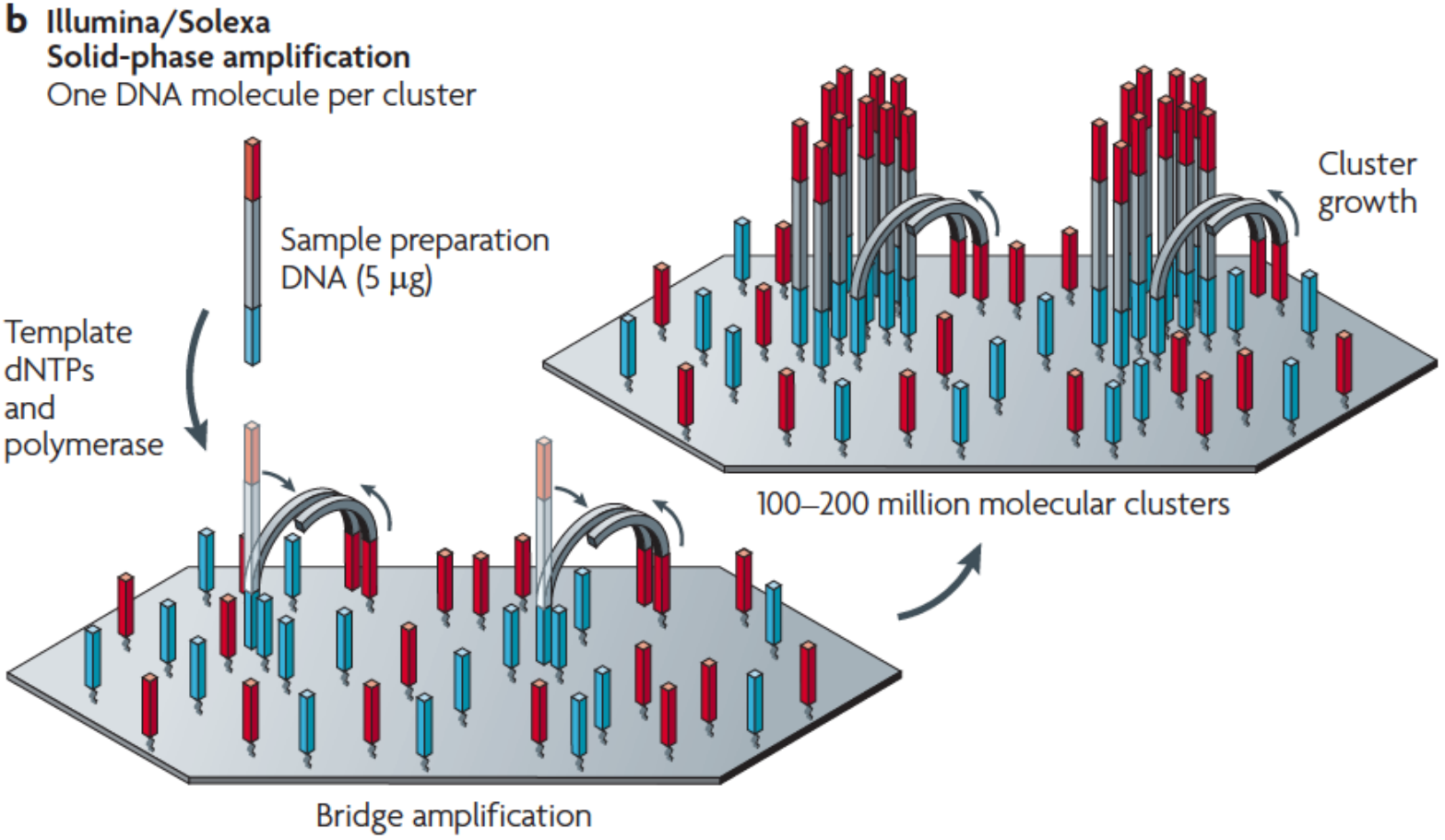
System Performance	
Throughput	35 million high-quality, filtered bases per run*
Run Time	10 hours sequencing 2 hours data processing
Avg. Read Length	400 bases*
Accuracy	Q20 read length of 400 bases (99% accuracy at 400 bases)
Reads per Run	100,000 shotgun, 70,000 amplicon
Sample Input	gDNA, amplicons, cDNA, or BACs depending on the application
Physical Dimensions	40 cm wide x 60 cm deep x 40 cm high (the size of a laser printer) Weight = 55 lbs.
Computing	Linux-based OS on HP desktop computer included. All software is point-and-click.

***Typical results**. Average read length and number of reads depend on specific sample and genomic characteristics*

Solexa (Illumina)

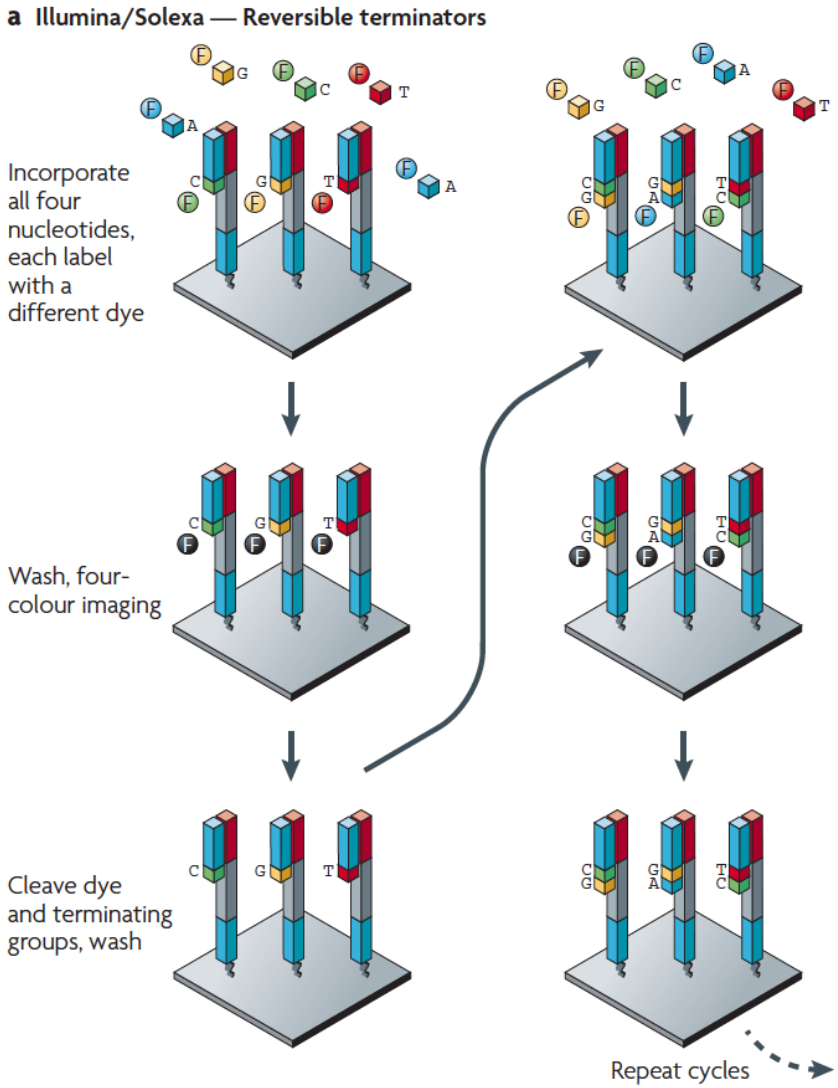
- Over 90% of all sequencing data is produced on Illumina systems.
- Uses a “sequencing by synthesis” approach:
  - DNA is broken into small fragments and ligated to an adaptor.
  - The fragments are attached to the surface of a flow cell and amplified.
  - DNA is sequenced by adding polymerase and labeled reversible terminator nucleotides (each base with a different color).
  - The incorporated base is determined by fluorescence.
  - The fluorescent label is removed from the terminator and the 3’ OH is unblocked, allowing a new base to be incorporated
- Started with 35 bp, increased now to up to 150 bp
- One run can give up to 10-600 Gb, 300-6000 million paired-end reads
- 75-85% of bases at or above Q30

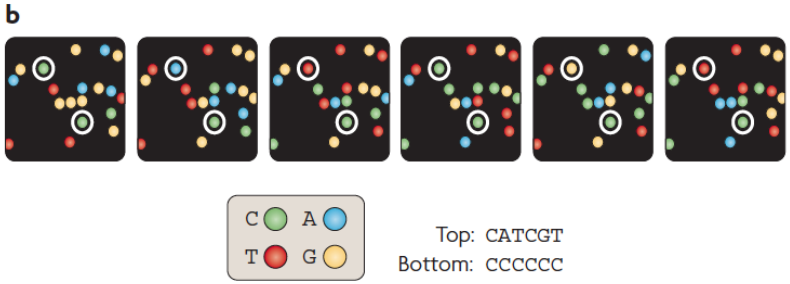
Solexa / illumina



From Michael Metzker, http://view.ncbi.nlm.nih.gov/pubmed/19997069

Solexa / illumina

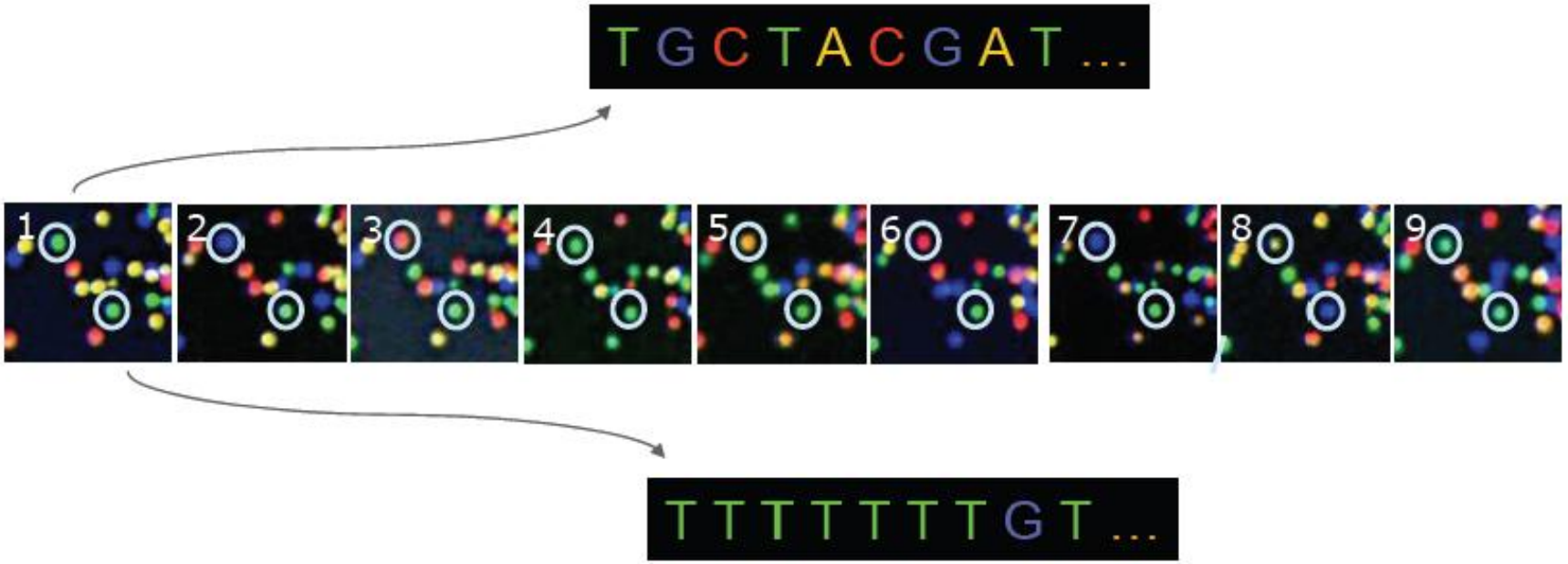




From Michael Metzker, http://view.ncbi.nlm.nih.gov/pubmed/19997069

Solexa / illumina

Base calling from raw data



From Debbie Nickerson, Department of Genome Sciences, University of Washington, http://tinyurl.com/6zbzh4

The identity of each base of a cluster is read off from sequential images

Illumina-HiSeq 2500

600 Gb/run in 11 days
2x100 bp fragments
6 billion reads per run

Illumina-MiSeq

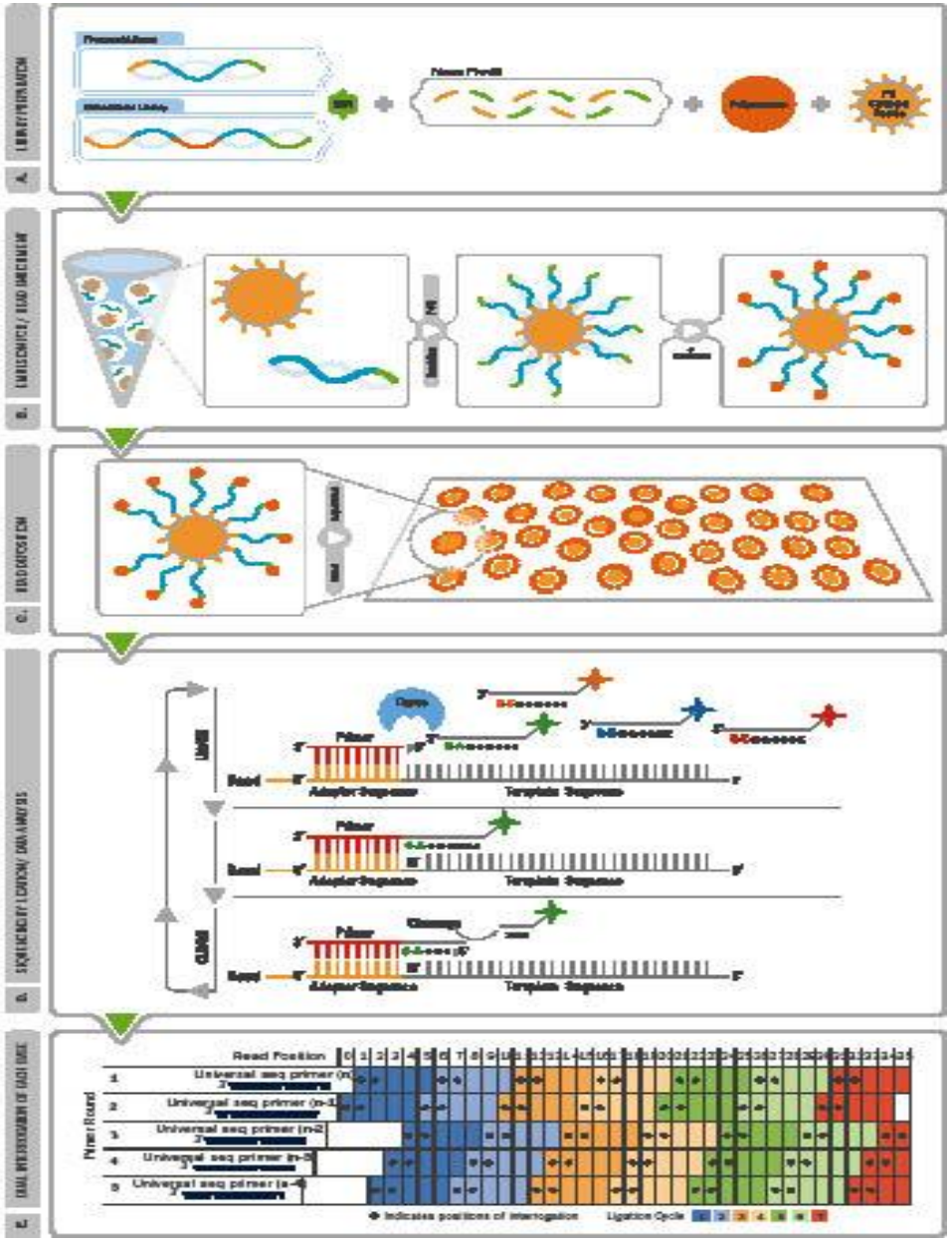
175-245 Mb 4h 1x 36bp

1.5-2.0 Gb 27h 2x150 bp

SOLiD (ABI / Life Technologies)

- **Colorspace**
- "**sequencing by ligation**" method
- Does not use polymerase, instead uses DNA ligase for sequencing:
  - DNA is broken into small fragments and ligated to an adaptor.
  - The fragments are attached to beads and amplified by emulsion PCR. Beads are attached to the surface of a glass slide.
  - DNA is sequenced by adding 8-mer fluorescently labelled oligonucleotides
  - If an oligo is complementary to the template, it will be ligated and 2 of the bases can be called.
  - The attached oligo is then cut to remove the label and the next set of labelled oligos are added
  - The process is repeated from different starting points (using different universal primers) so that each base is called twice
- 200 Gb, 1.8 billion reads per run, 35bp-75bp, 10 days

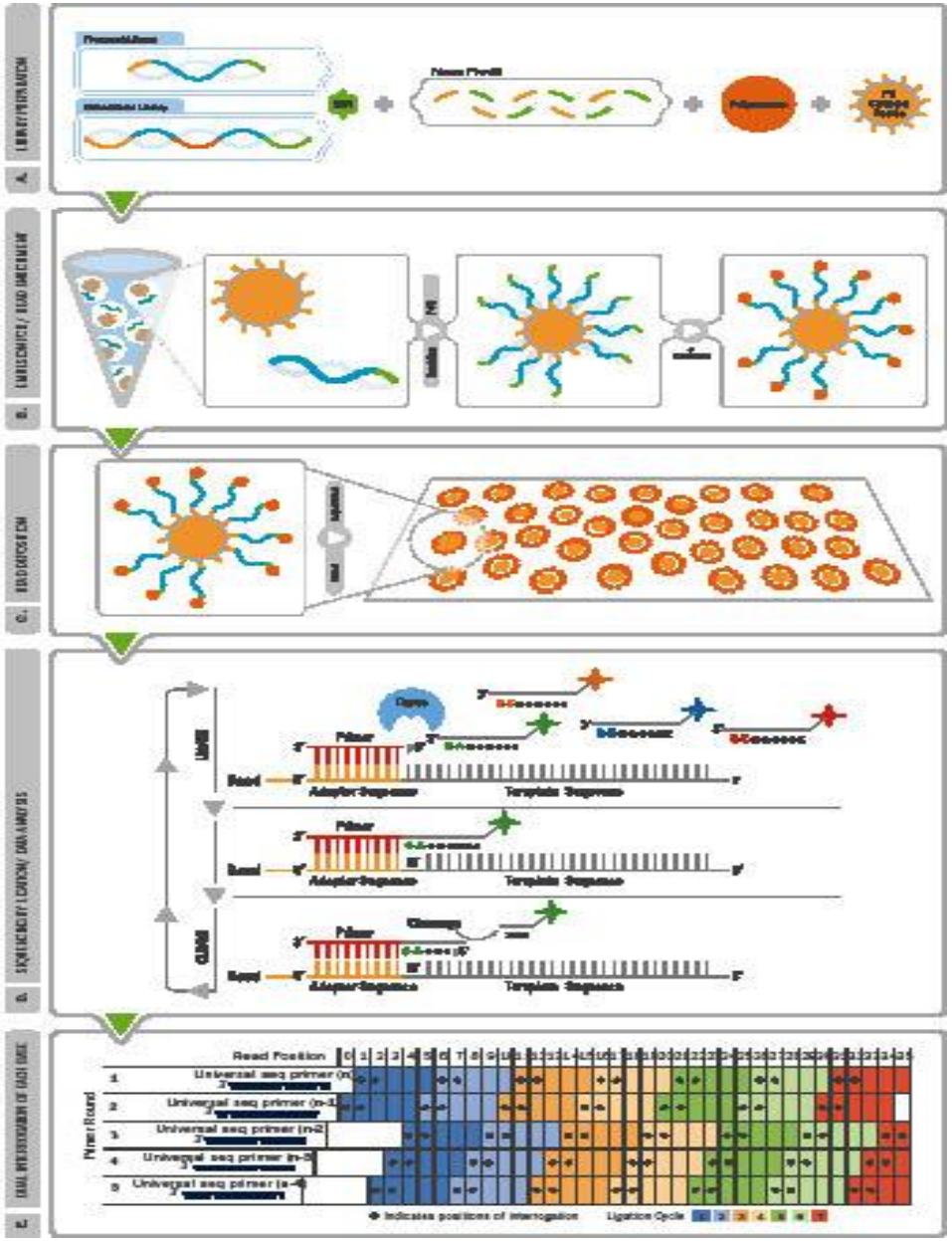
SOLiD



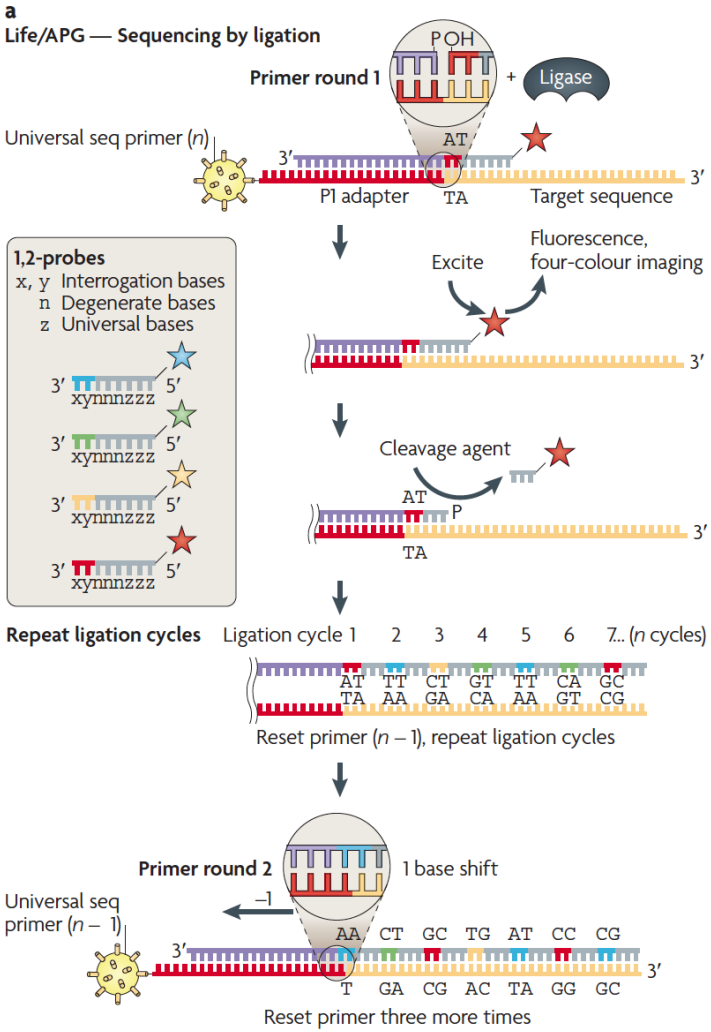
SOLiD

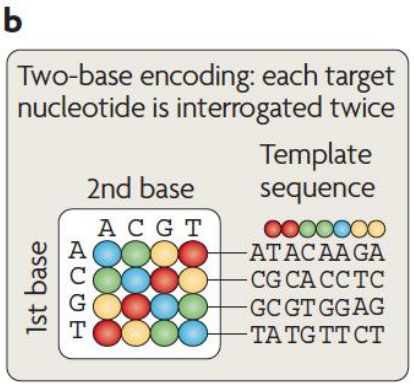
* Sequencing output in "**color space**"

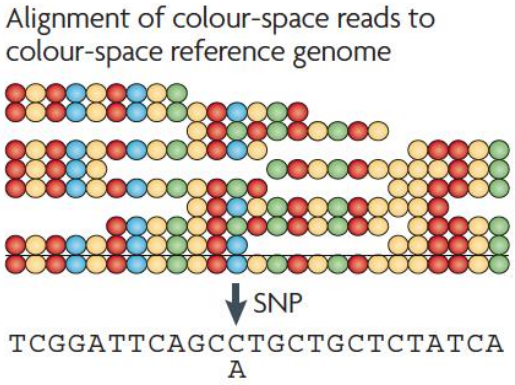
* Needs reference genome to translate to base space.



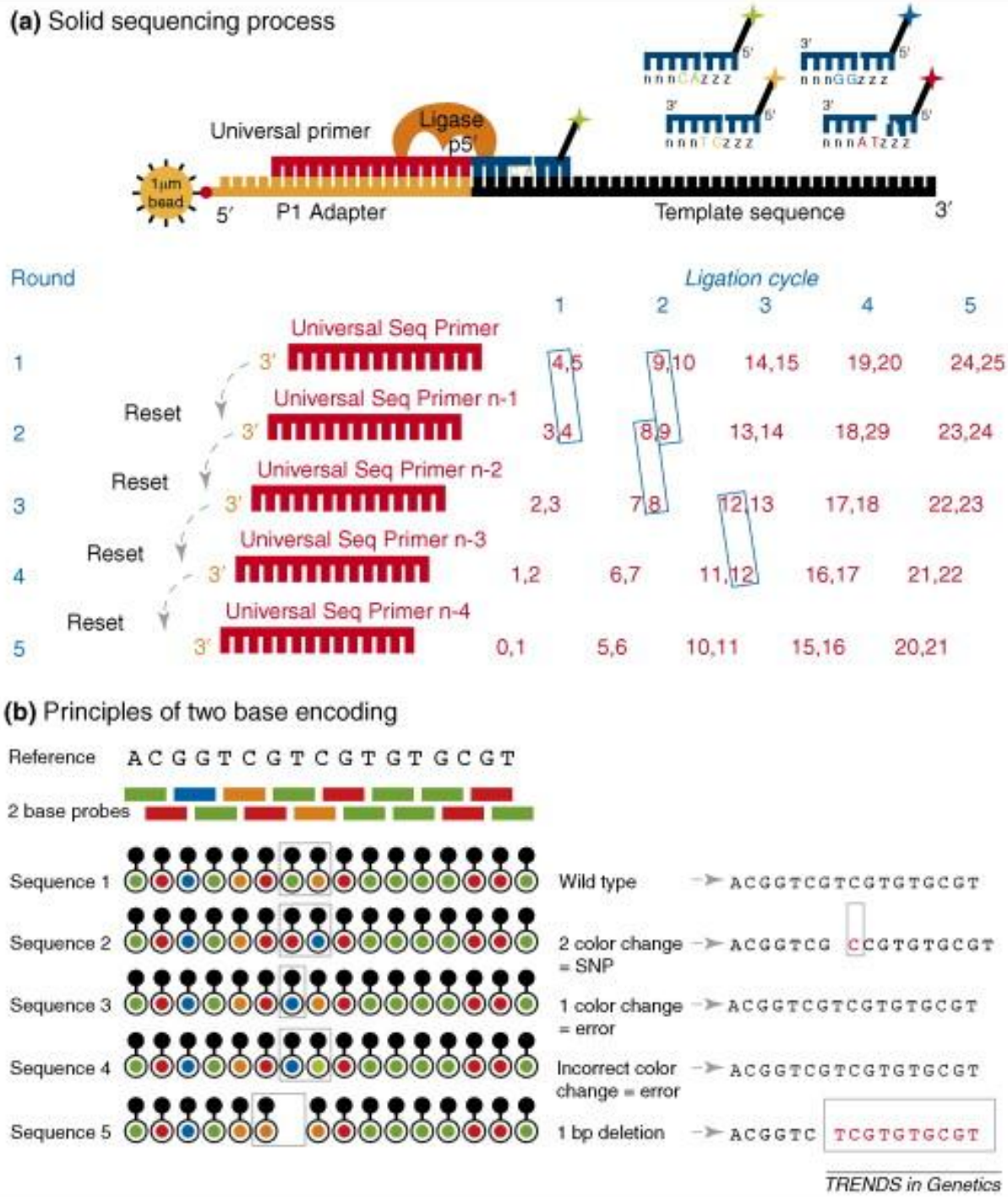
SOLiD







From Michael Metzker, http://view.ncbi.nlm.nih.gov/pubmed/19997069



TRENDS in Genetics

SOLiD color space

Use the following steps to encode a DNA sequence ATCAAGCCTC*:

1. start at the 5' end,
2. replace the di-base AT at this position with its corresponding code 3 from the table,
3. advance by one base, which exposes the TC di-base, and
4. continue, as shown below.

Base Sequence:	A	T	C	A	A	G	C	C	T	C
Color String:		3	2	1	0	2	3	0	2	2

SOLiD_Dibase_Sequencing_and_Color_Space_Analysis.pdf

Union of Biochemistry) codes. So let B = {A, C, G, T}. The color code should satisfy the following requirements:

For all bases *b*, *d*, *e* in B:

1. The available colors are 0, 1, 2, and 3:
   color (*bd*) ∈ {0, 1, 2, 3}.

2 Two different di-bases that have the same first base get *different* colors: color (bd) ≠ color (*be*) if d ≠ e.
   For example, color (AC) ≠ color (AG).

3. A di-base and its reverse get the *same* color:
   color (*bd*) = color (*db*).
   For example, color (AC) = color (CA).

4. Monodibases get the *same* color:
   color (*bb*) = color (*dd*).

		Second Base			
		A	C	G	T
First Base	A	0	1	2	3
	C	1	0	3	2
	G	2	3	0	1
	T	3	2	1	0

Panel E

SOLiD_Dibase_Sequencing_and_Color_Space_Analysis.pdf

5. Two different di-bases that nevertheless have the same second base get *different* colors:
   color (*bd*) ≠ color (*cd*), if $b \neq c$.

For example, color (AC) ≠ color (TC). Property 6 also follows from requirements 1-4, but it is most easily verified against the completed code (Figure 3, Panel E).

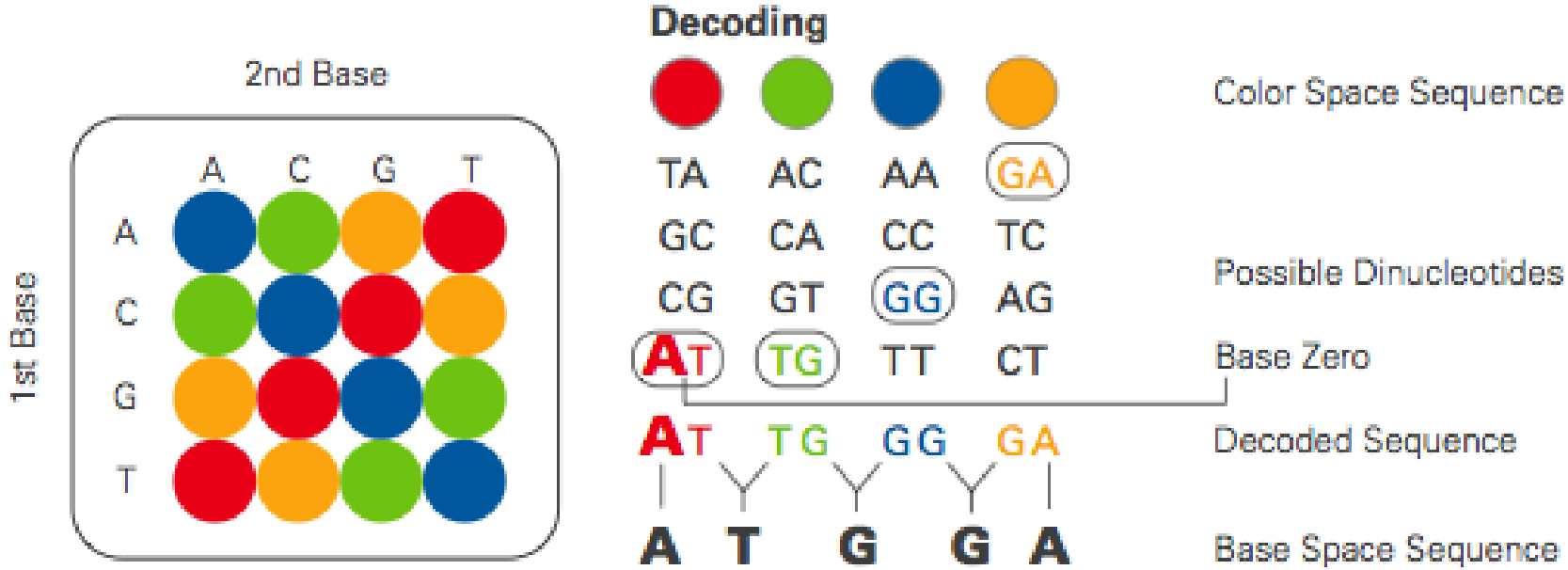
6. A di-base and its complement get the *same* color:
   color ($b^c d^c$) = color ($d^c b^c$).
   For example, color (AC) = color (TG).

		Second Base			
		A	C	G	T
First Base	A	0	1	2	3
	C	1	0	3	2
	G	2	3	0	1
	T	3	2	1	0

Panel E

SOLiD_Dibase_Sequencing_and_Color_Space_Analysis.pdf

SOLiD color space



SOLiD_Dibase_Sequencing_and_Color_Space_Analysis.pdf

Its format is

```
>TAG_ID
Color_space
```

e.g.

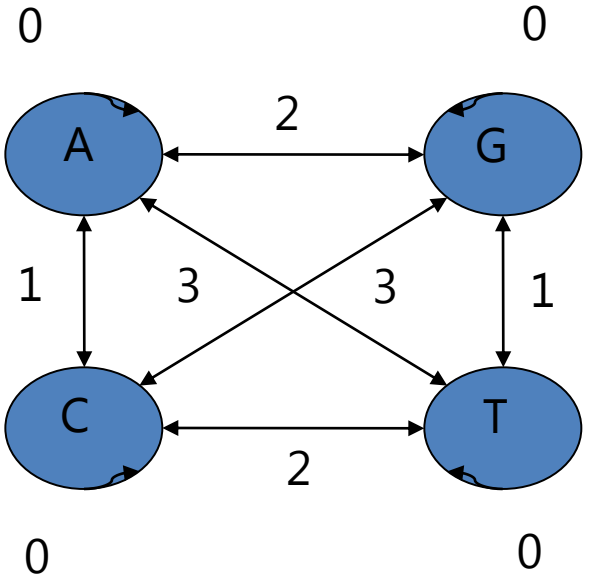
```
>1_88_1830_R3
G3211312320130023232O
>1_89_1562_R3
G2313313123333310132O
```

AB SOLiD: Dibase Sequencing

AB SOLiD reads look like this:

T012233102 T012033102

	A	C	G	T
A	0	1	2	3
C	1	0	3	2
G	2	3	0	1
T	3	2	1	0



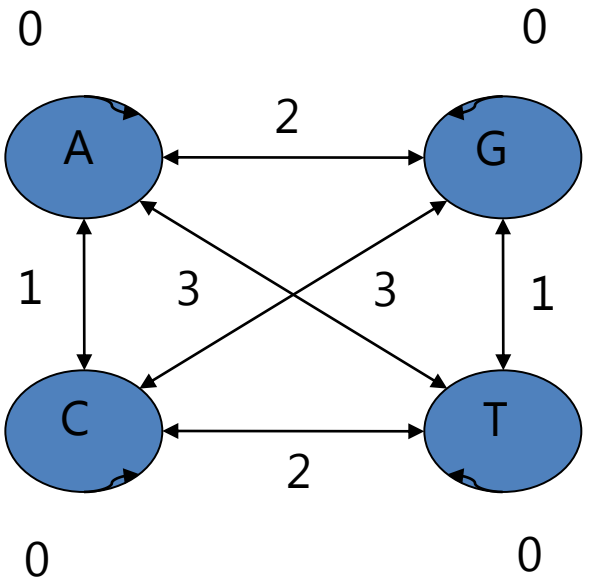
Mike Brudno, U of Toronto http://bioinformatics.ca/files/CBW - presentations/HTSeq_2009_Module 2/HTSeq_2009_Module 2.ppt

AB SOLiD: Dibase Sequencing

AB SOLiD reads look like this:

```
T012233102    T012033102
 TGAGCGTTC     TGAATAGGA
```

	A	C	G	T
A	0	1	2	3
C	1	0	3	2
G	2	3	0	1
T	3	2	1	0



Mike Brudno, U of Toronto http://bioinformatics.ca/files/CBW - presentations/HTSeq_2009_Module 2/HTSeq_2009_Module 2.ppt

AB SOLiD: Dibase Sequencing

AB SOLiD reads look like this:

Mike Brudno, U of Toronto http://bioinformatics.ca/files/CBW - presentations/HTSeq_2009_Module 2/HTSeq_2009_Module 2.ppt

AB SOLiD: Variations

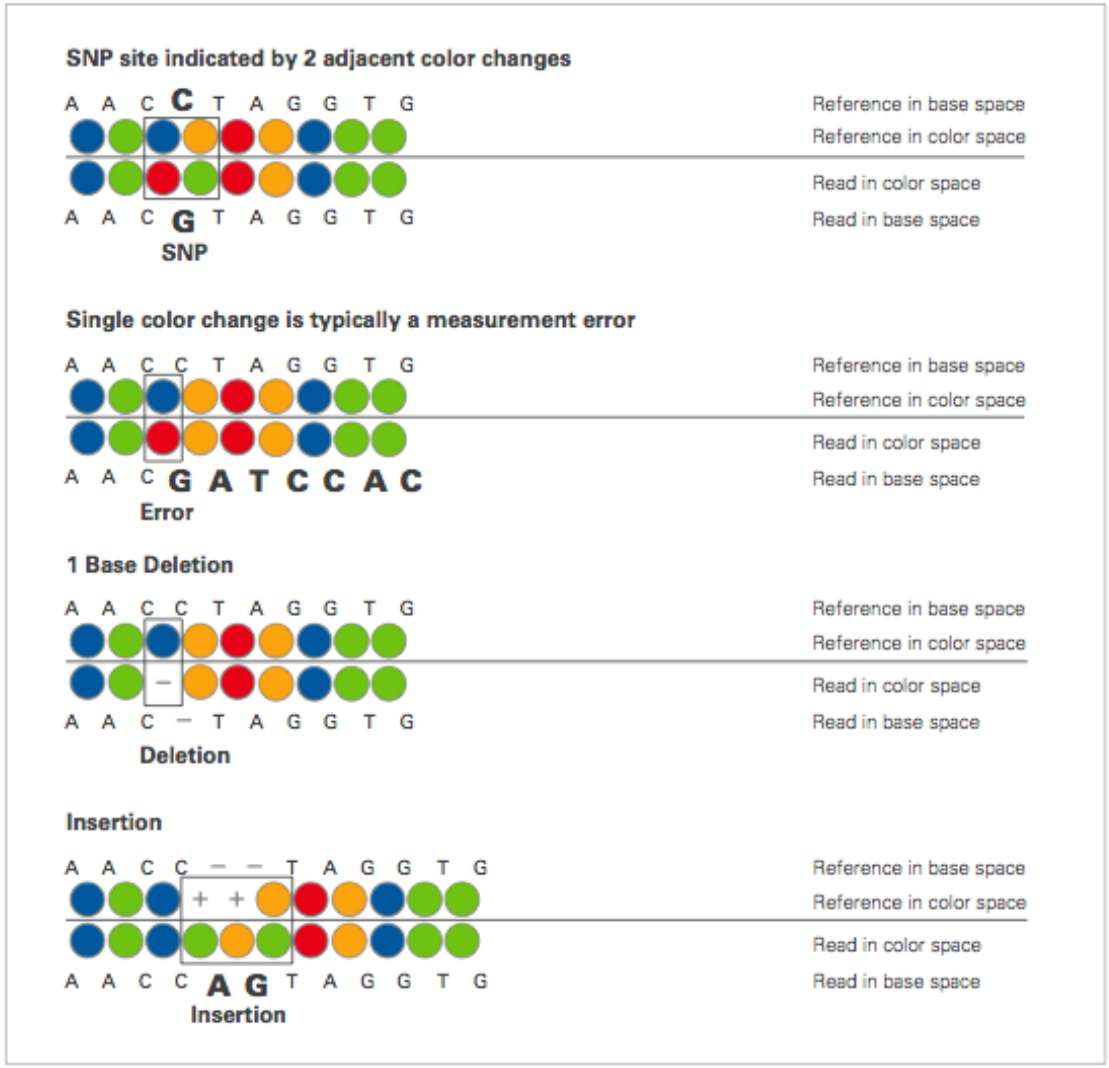


Figure 5. Examples of polymorphisms in color space.

SOLiD_Dibase_Sequencing_and_Color_Space_Analysis.pdf

5500XL SOLiD

200 Gb/run (microbeads)
300 Gb/run (nanobeads)

35-75 bp fragments

1.8 - 4.8 billion reads/run

2x6 lanes/run
96 bar-codes

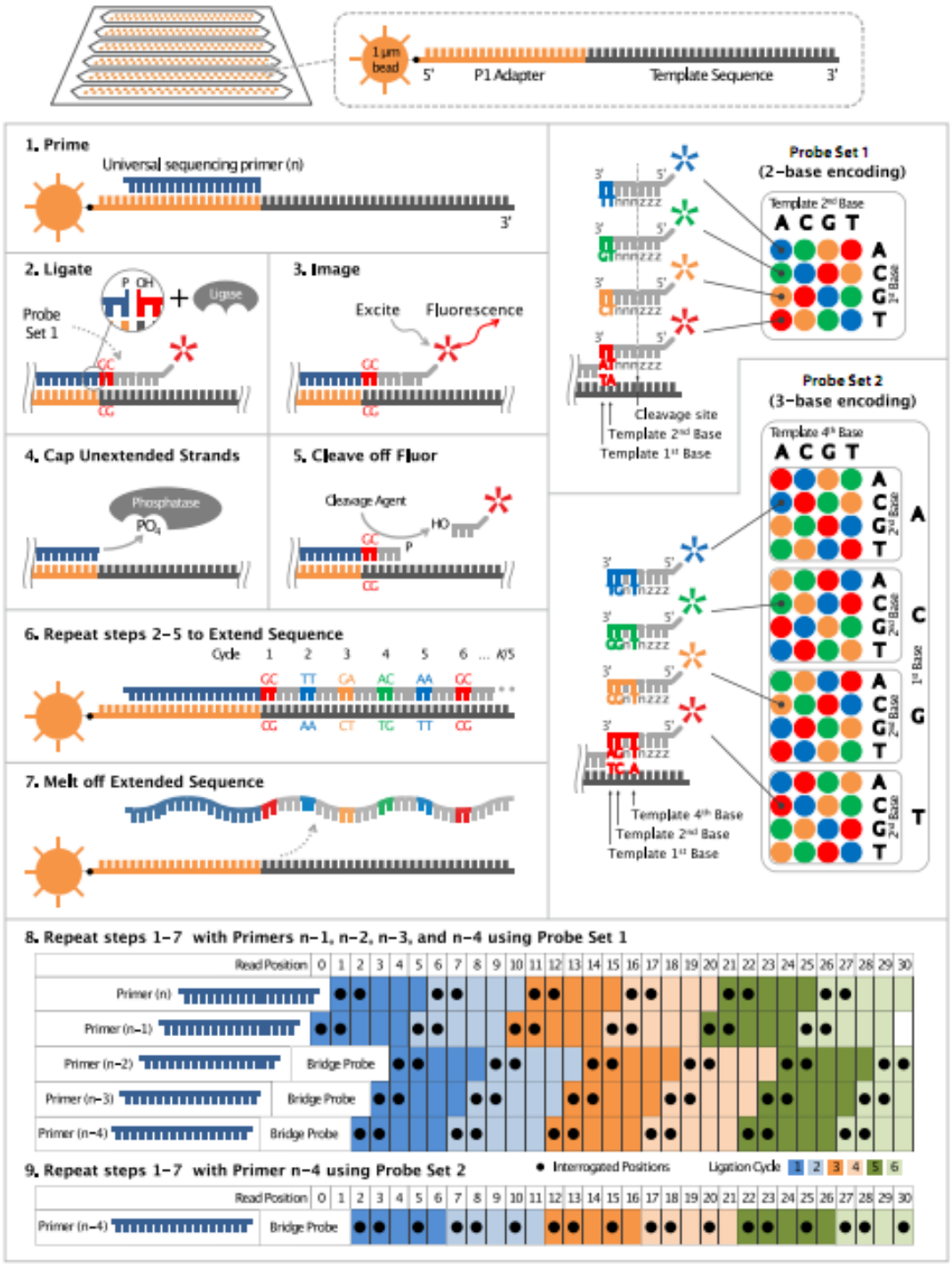
ECC: 99.99% accuracy

SOLiD 5500

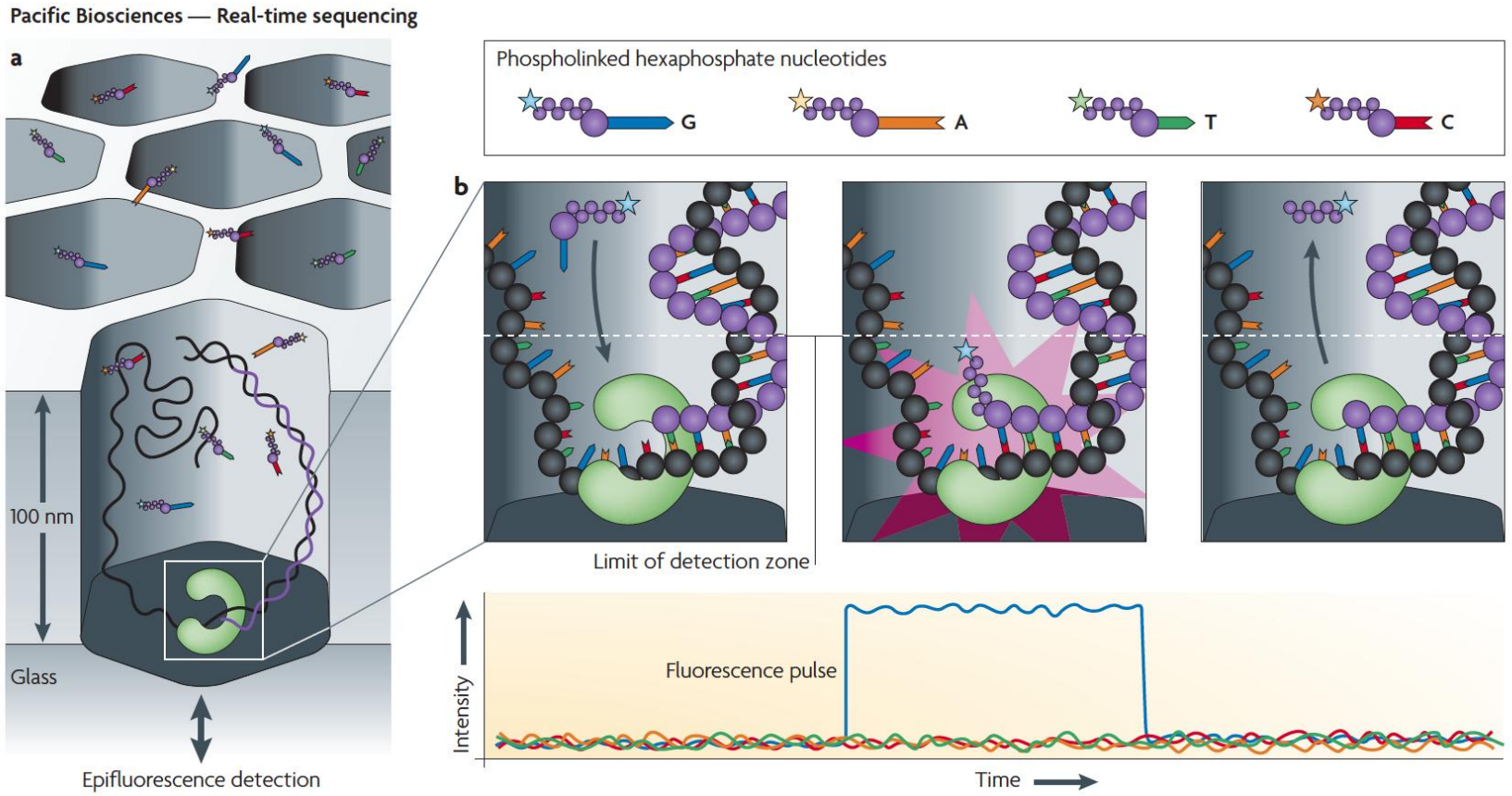
*Sixth 3-based encoded primer

*Sequencing output in base space

* No reference needed



PacBio

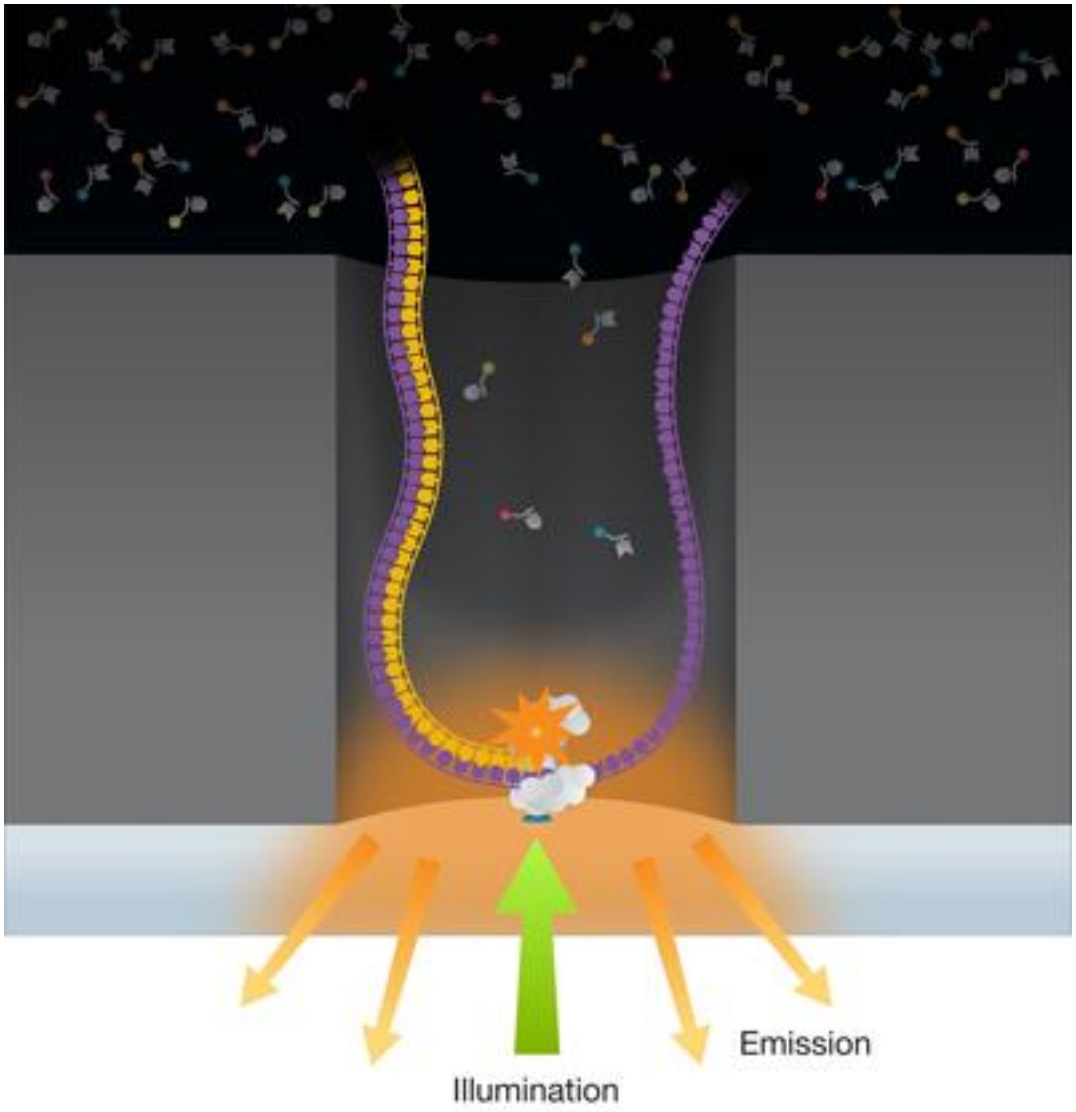


From Michael Metzker, http://view.ncbi.nlm.nih.gov/pubmed/19997069

Pacific Bioscience

SMRT: Singel Molecule Real time DNA synthesis
Up to 12000 nt
50 bases/second

ZMW: Zero Mode Waveguide



Ion Torrent

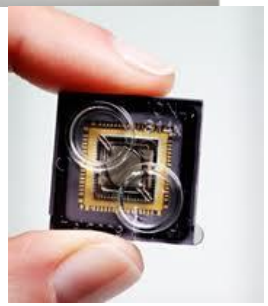
$ 50.000

$ 500 /sample

1 hour/run

> 200 nt lengths

Reads H+ released by DNA polymerase



Ion Proton

"Cost, speed, and accuracy are key elements in the use of DNA sequencing. The technological advances in the new Ion Proton™ instrument promise to be game-changing for both research and clinical applications."

DR. RICHARD LIFTON
YALE SCHOOL OF MEDICINE, USA

Human-exome sequencing

Using the next generation of semiconductor technology, the Ion Proton™ I Chip will deliver whole-exome sequencing in just a few hours.

ION PROTON™ SEQUENCER

HUMAN GENOMES
HUMAN EXOMES
WHOLE TRANSCRIPTOMES

Human-genome sequencing

The Ion Proton™ II Chip will enable fast, affordable, whole-genome sequencing on your benchtop.

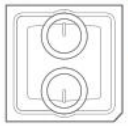
2-hour run times

Rapid 100-base sequencing runs on the Ion Proton™ I Chip.

THE ONLY BENCHTOP GENOME CENTER

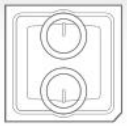
The Ion Proton™ Sequencer* is based on the next generation of semiconductor sequencing technology that made the Ion PGM™ Sequencer the fastest selling sequencer in the world. New high-throughput chips will enable the Ion Proton™ Sequencer to sequence a human genome with similar run times, and single-day workflow, as the Ion PGM™ Sequencer.

Data analysis, which has long been a bottleneck for whole-genome sequencing, can also be completed in the same day on a single stand-alone server. In the time it takes for other systems to batch sequence 6 genomes, the Ion Proton™ Sequencer can sequence and analyze 10 genomes for a small fraction of the cost.



Proton I*

The Ion Proton™ I Chip
165 million wells
2 human exomes



Proton II*

The Ion Proton™ II Chip
660 million wells
1 human genome

*The content provided herein may relate to products that have not been officially released and is subject to change without notice.

OXFORD NANOPORE

The MinION is a memory key–sized disposable unit that can be plugged into a laptop for under $1,000, according to the company.

Oxford Nanopore

JUNTA DE ANDALUCIA
CONSEJERÍA DE SALUD

CASEGH
Centro Andaluz de Secuenciación Genómica Humana

UNIÓN EUROPEA
FONDO EUROPEO DE DESARROLLO REGIONAL
"Una manera de hacer Europa"

GOBIERNO DE ESPAÑA
MINISTERIO DE CIENCIA E INNOVACIÓN

Comparison

Roche 454

- Long fragments
- Errors: poly nts
- Low throughput
- Expensive

- De novo sequencing
- Amplicon sequencing
- RNASeq

Illumina

- Short fragments
- Errors: Hexamer bias
- High throughput
- Cheap

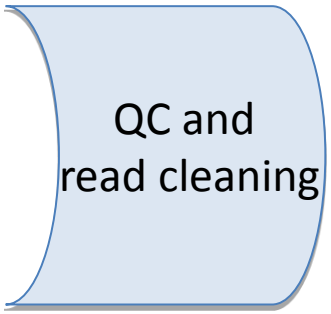
- Resequencing
- ChipSeq
- RNASeq
- MethylSeq

SOLiD

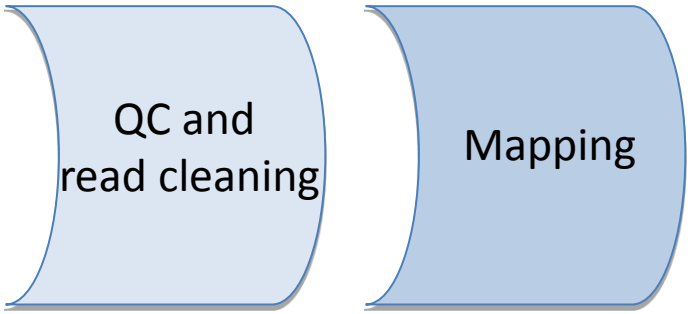
- Short fragments
- Color-space
- High throughput
- Cheap

- Resequencing
- ChipSeq
- RNASeq
- MethylSeq

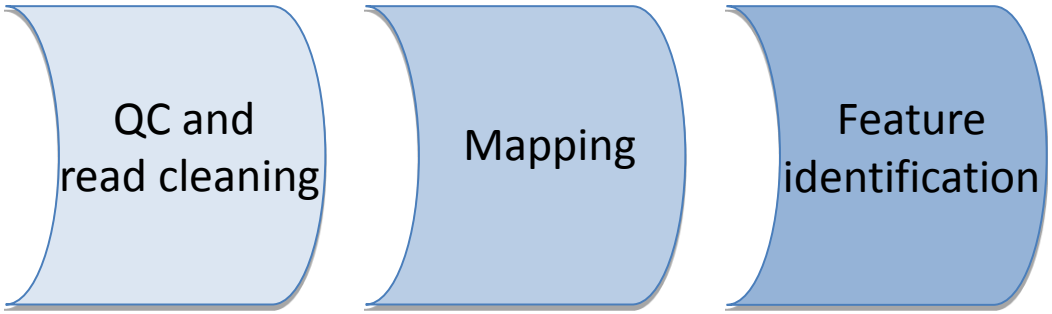
Basic steps NGS data processing



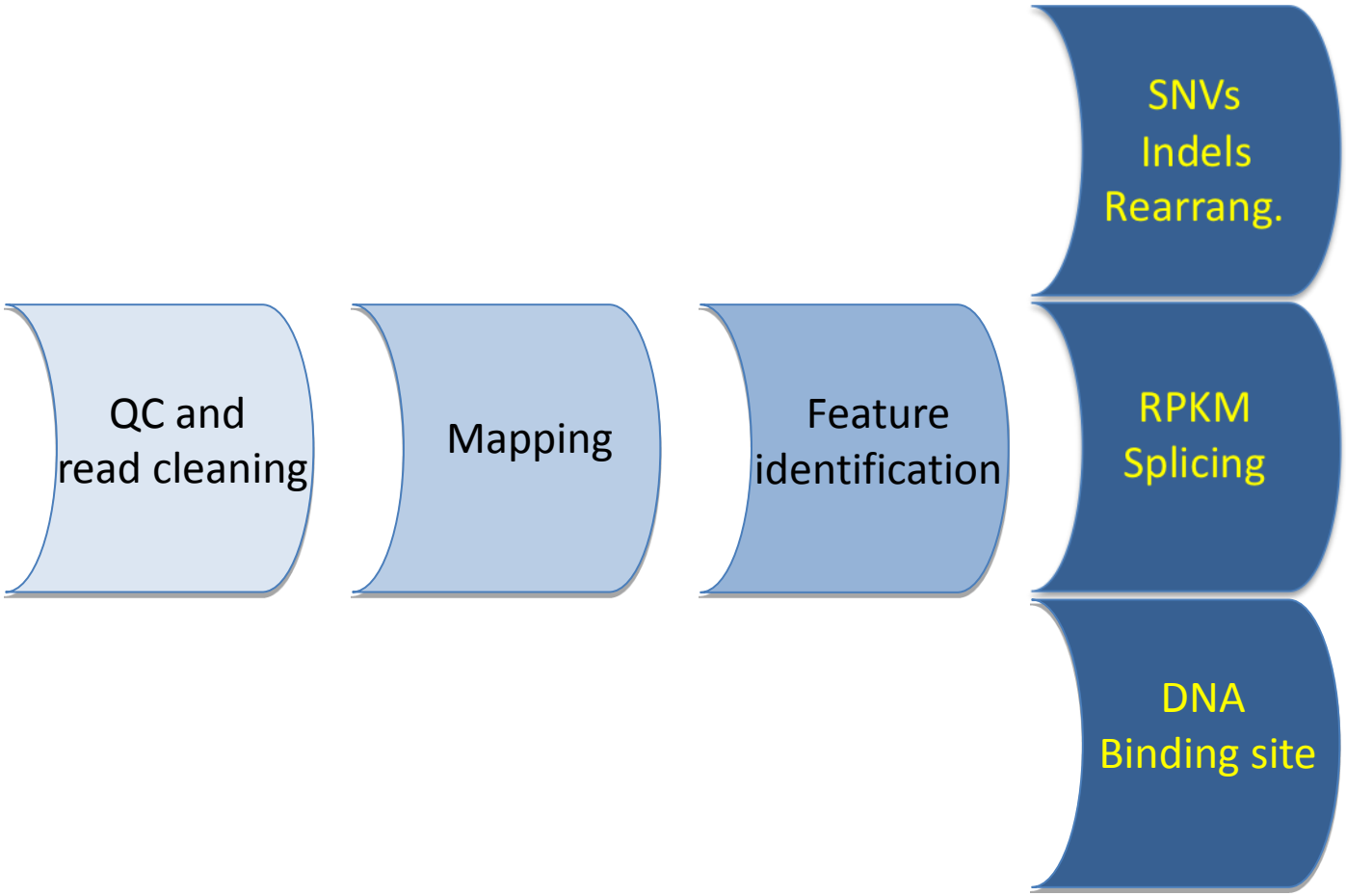
Basic steps NGS data processing



Basic steps NGS data processing



Basic steps NGS data processing



File formats

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jcarbonell@bender:/scratch2/jcarbonell$ samtools view ivia15_06_pair1.remdup_bwa_bwa_ref01_upper_mapped.bam | head -n 10
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0       XM:i:0  XO:i:0  XG:i:0  MD:Z:38
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2       XM:i:1  XO:i:0  XG:i:0  MD:Z:12G25
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2       XM:i:0  XO:i:0  XG:i:0  MD:Z:38
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1       XO:i:0  XG:i:0  MD:Z:8A29
```

fastq: sequence data and qualities

SAM/BAM: mapping data and qualities

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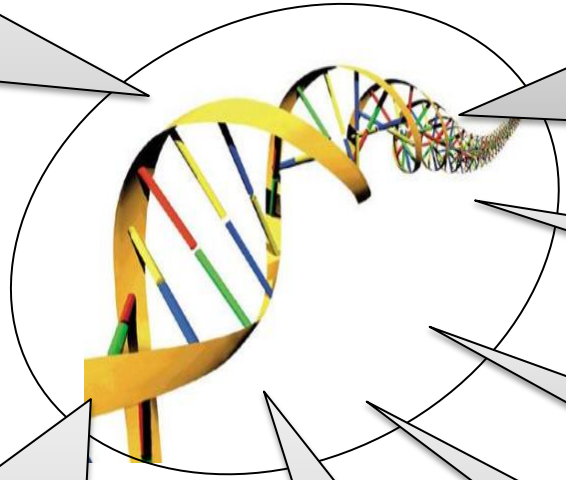
"Una manera de hacer Europa"
GOBIERNO DE ESPAÑA
MINISTERIO DE CIENCIA E INNOVACIÓN

Most common applications of NGS

RNA-seq /Transcriptomics
- Quantitative
- Descriptive
  - Alternative splicing
- miRNA profiling



Resequencing
- Mutation calling
- Profiling
- Genome annotation

***De novo* sequencing**

Exome sequencing
Targeted sequencing

Copy number variation

Metagenomics
Metatranscriptomics

ChIP-seq /Epigenomics
- Protein-DNA interactions
- Active transcription factor binding sites
- Histone methilation

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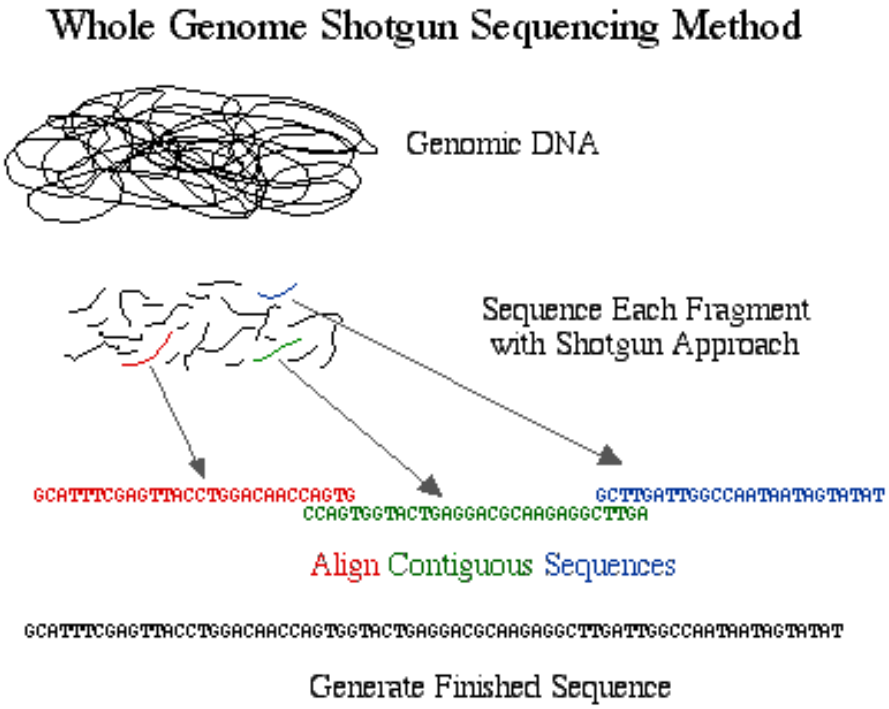
DNA sequencing - 1

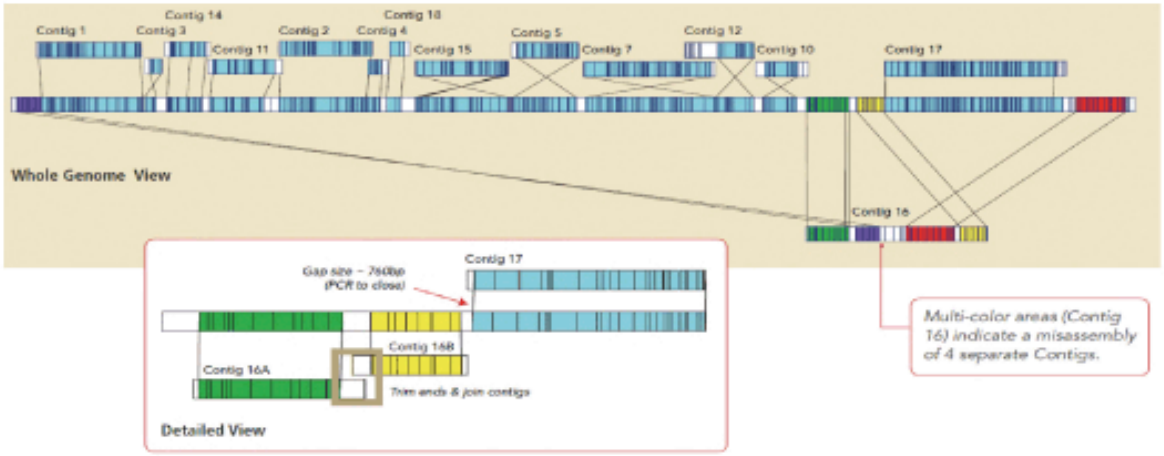
- **Whole GENOME Resequencing**
  - Need reference genome
  - Variation discovery



DNA sequencing - 2

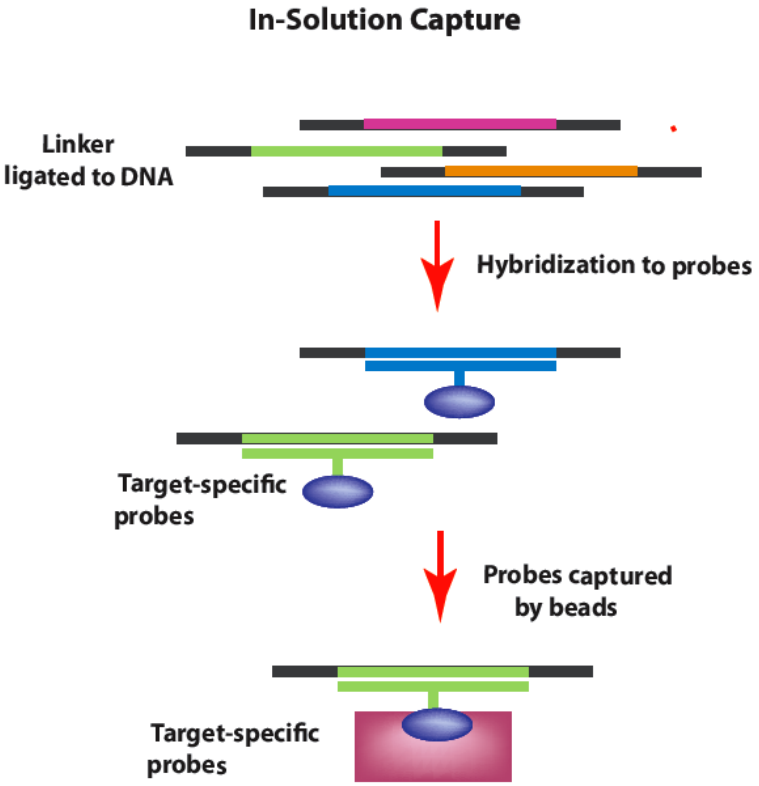
- **Whole GENOME "de novo" sequencing**
  - Uncharacterized genomes with no reference genome available
  - known genomes where significant structural variation is expected.
  - Long reads or mate-pair libraries. Sequencing mostly done by Roche 454
  - Assembly of reads is needed: Computational intensive

- E.g. Genome bacteria sequencing



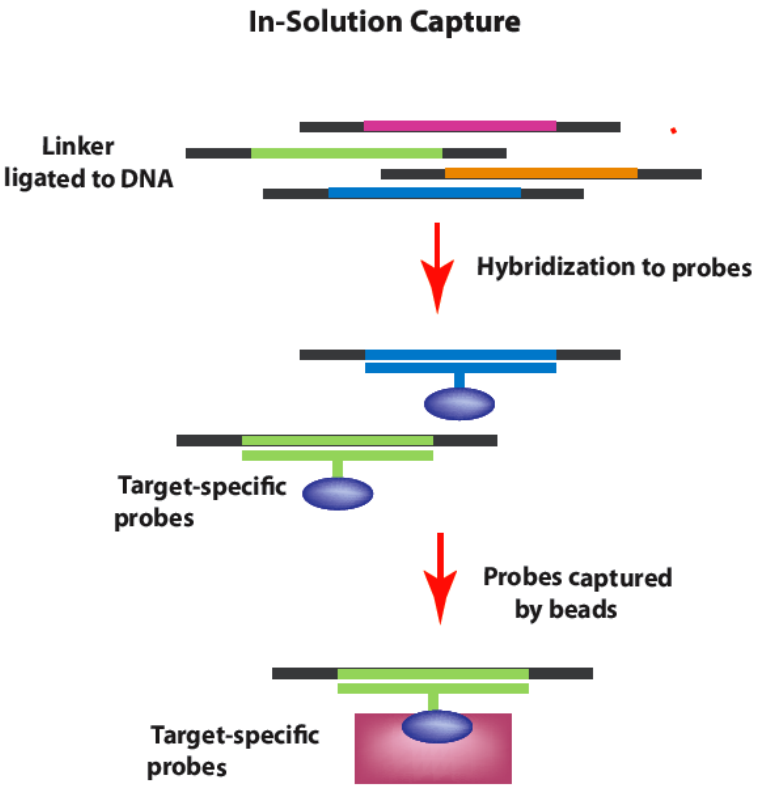
DNA sequencing - 3

- **Whole EXOME Resequencing**
  - Need reference genome
    - Available for Human and Mouse
  - Variation discovery on ORFs
    - 2% of human genome (lower cost)
    - 85% disesease mutation are in the exome
  - Need probes complementary to exons
    - Nimblegen
    - Agilent
- E.g. Human exome



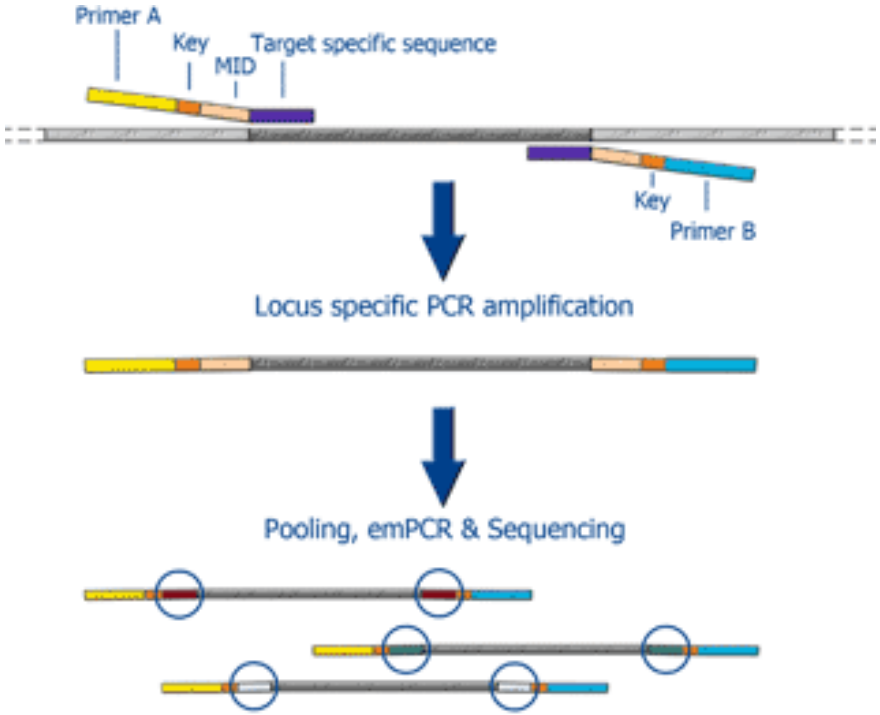
DNA sequencing - 4

- **Targeted Resequencing**
  - Capture of specific regions in the genome
- **Custom genes panel sequencing**
  - Allows to cover high number of genes related to a disease
  - *E.g. Disease gene panel*
- Low cost and quicker than capillary sequencing
- Multiplexing is possible
- Need custom probes complementary to the genomic regions
  - Nimblegen
  - Agilent



DNA sequencing - 5

- **Amplicon sequencing**
  - Sequencing of regions amplified by PCR.
  - Shorter regions to cover than targeted capture
  - No need of custom probes
  - Primer design is needed
  - High fidelity polymerase
  - Multiplexing is needed



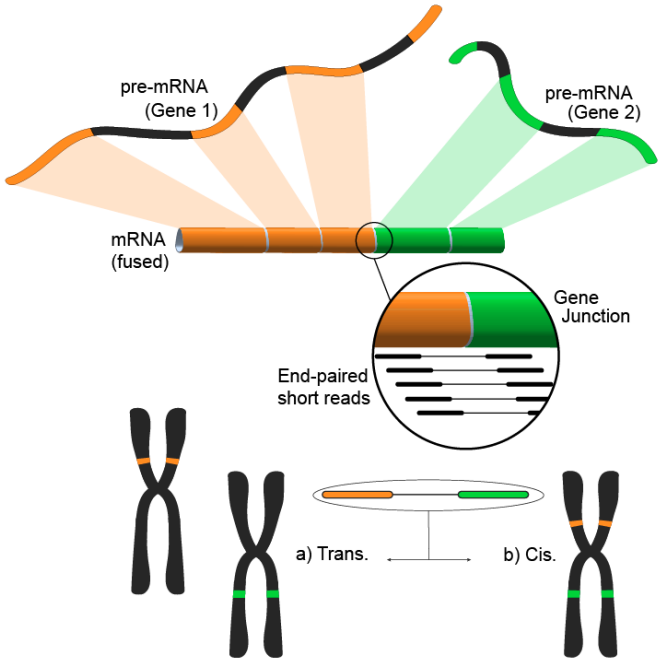
- *E.g. P53 exon amplicon sequencing*

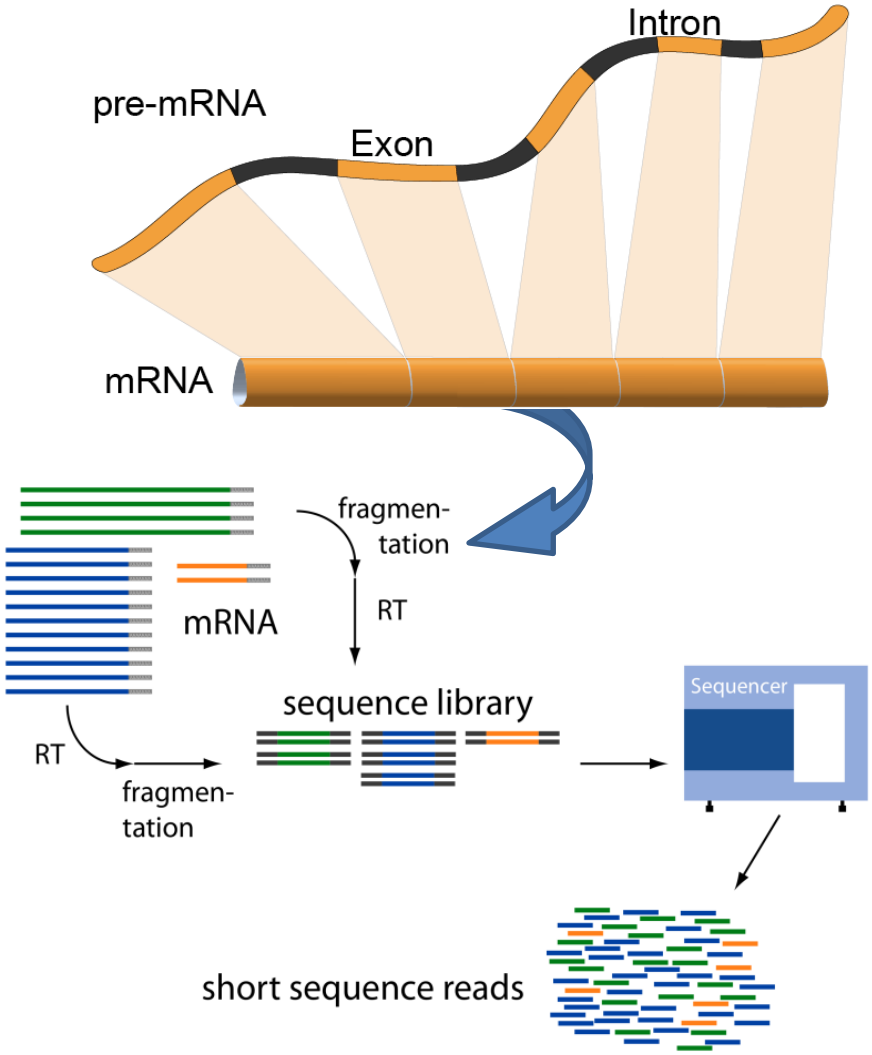
Transcriptomics - 1

- **RNA-Seq**
  - Sequencing of mRNA
  - rRNA depleted samples
  - Very high dynamic range
  - No prior knwoledge of expressed genes
  - Gives information about (richer than microarrays)
    - Differential expression of **known or unknown** transcripts during a treatment or condition
    - **Isoforms** and
    - New **alternative splicing** events
    - **Non-coding** RNAs
    - Post-transcriptional mutations or **editing**,
    - **Gene fusions**.

Transcriptomics - 1

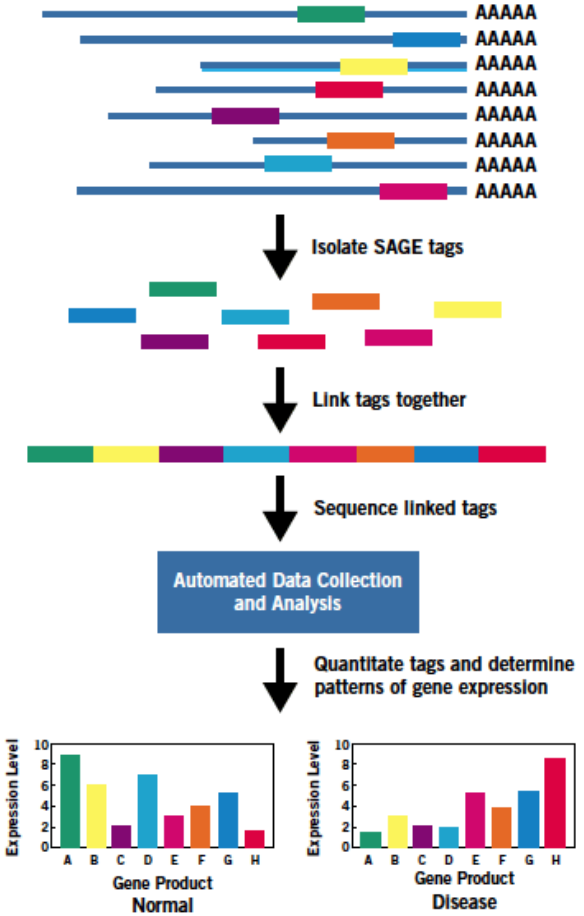
- **RNA-Seq**
  - Sequencing of **mRNA**
  - **Detecting gene fusions**





Transcriptomics - 2

- **SAGE**. Serial Analysis of Gene Expression
  - Quantification of gene expression levels on a genome-wide scale.
  - Determines mRNA expression by **sequencing unique sequence tags** isolated from the 3' ends of mRNAs
  - Advantages over microarrays:
    - Detects known and novel mRNAs.
    - Is highly reproducible with a dynamic range of > 105.
  - SAGE strategy is the better if looking at changes in **expression levels of known transcripts** during a treatment or condition.



Applications of RNAseq

Qualitative:
* Alternative splicing
* Antisense expression
* Extragenic expression
* Alternative 5’ and 3’ usage
* Detection of fusion transcripts
….

Quantitative:
* Differential expression
* Dynamic range of gene expression
….

Applications of RNAseq

Qualitative:
* Alternative splicing
* Antisense expression
* Extragenic expression
* Alternative 5’ and 3’ usage
* Detection of fusion transcripts
....

Tophat/Cufflinks
Scripture
Alexa

Quantitative:
* Differential expression
* Dynamic range of gene expression
....

edgeR
DESeq
baySeq
NOISeq

Advantages of RNAseq?

RNAseq

* Non targeted transcript detection
* No need of reference genome
* Strand specificity
* Find novels splicing sites
* Larger dynamic range
* Detects expression and SNVs
* Detects rare transcripts

....

microarrays

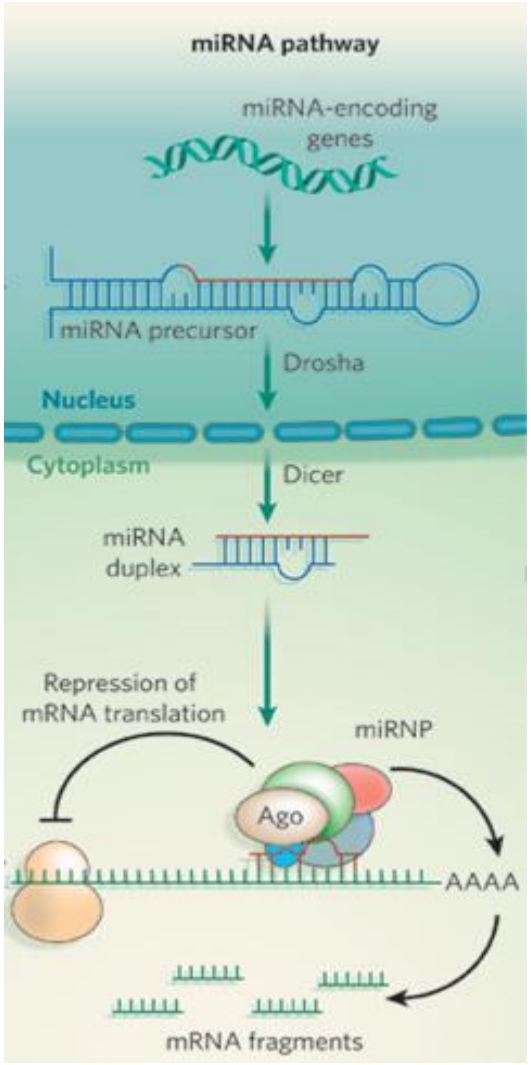
* Restricted to probes on array
* Needs genome knowledge
* Normally, not strand specific
* Exon arrays difficult to use
* Smaller dynamic range
* Does not provide sequence info
* Rare transcripts difficult

....

and…. are there any disadvantages?????

Transcriptomics - 3

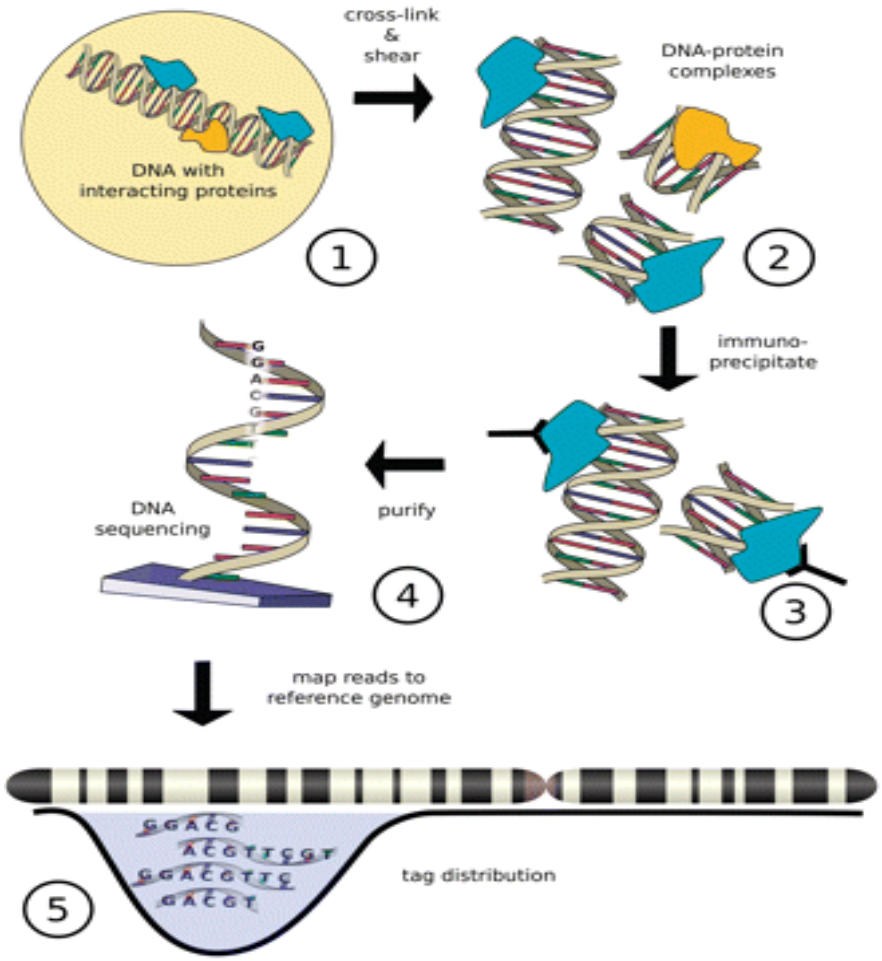
- **miRNA/small nonCoding RNA sequencing**
  - RNA Size selection step
    - 18-40 bp
  - Profiling of known miRNAs
  - miRNA discovery



TFBS detection

ChIP-Seq

- Identification of genomic region for gDNA binding proteins:
  - Transcription Factor binding site detection



Egigenomics - I

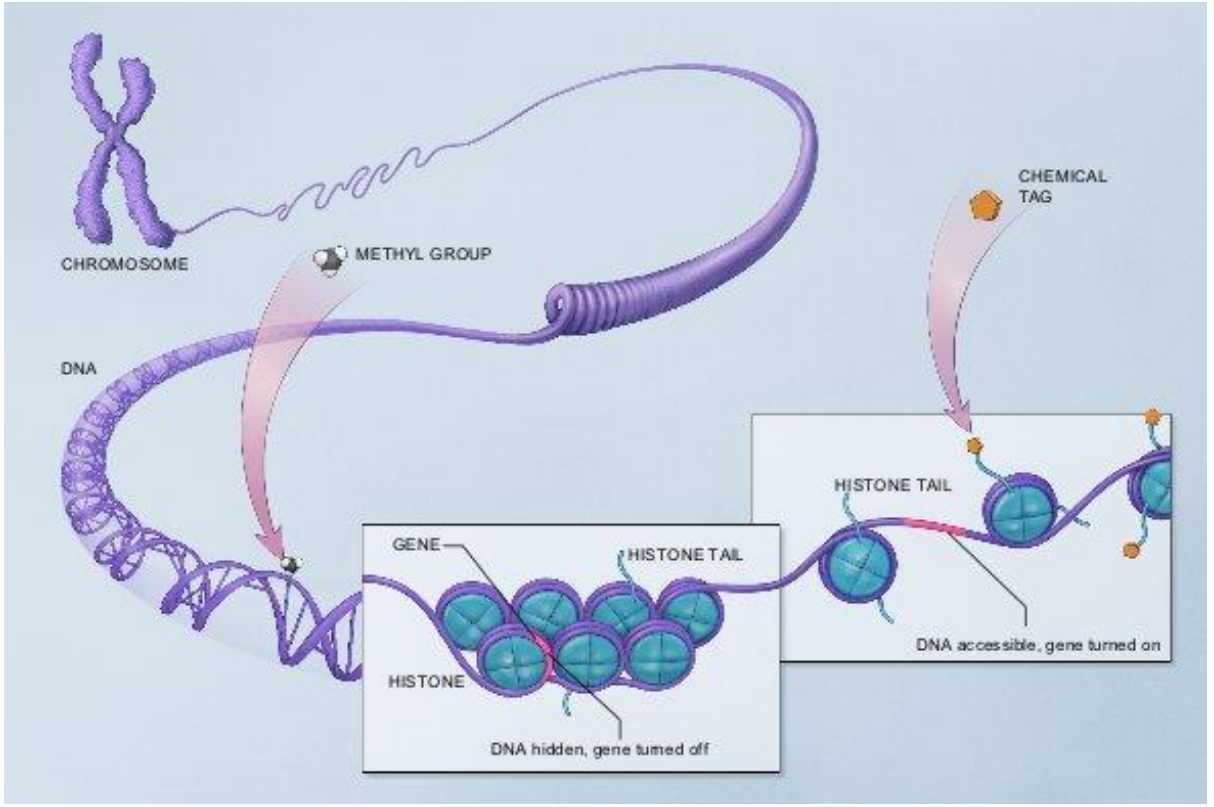
Epigenomics refers to functionally relevant modifications to the genome that do not involve a change in the nucleotide sequence

- *Play a role in turning genes off or on*

Epigenomic Marks.

a) Methyl groups attach to the backbone of a DNA molecule.

b) A variety of chemical tags attach to the tails of histones. This action affects how tightly DNA is wound around the histones.



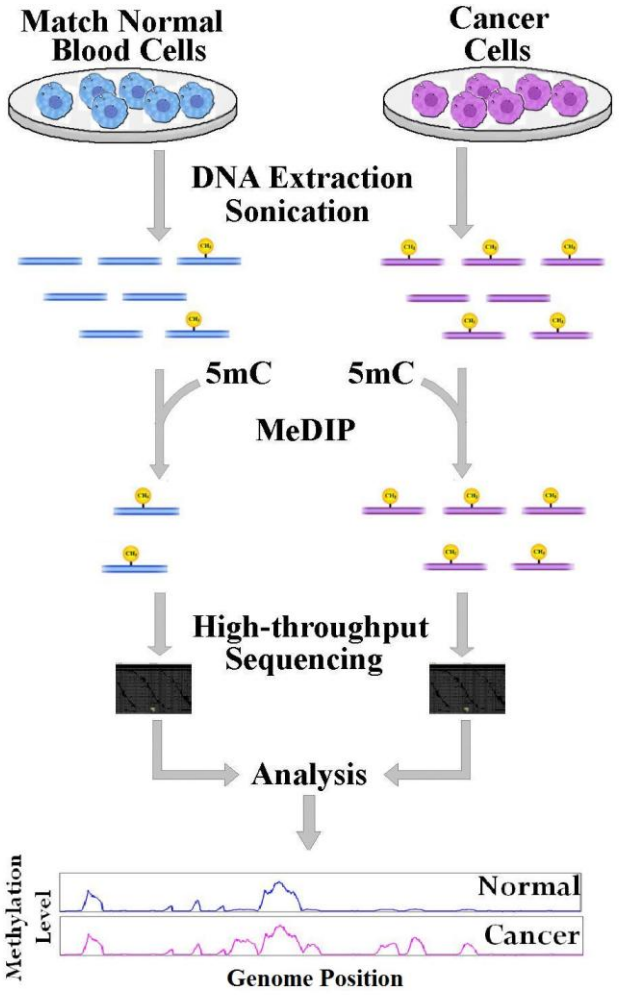
ChIP-Seq: Histone methylation detection

Egigenomics - 2

- **Methyl-Seq**
  - CpG island methylation
  - Bisulfite sequencing-based method

> E.g. Cancer studies.

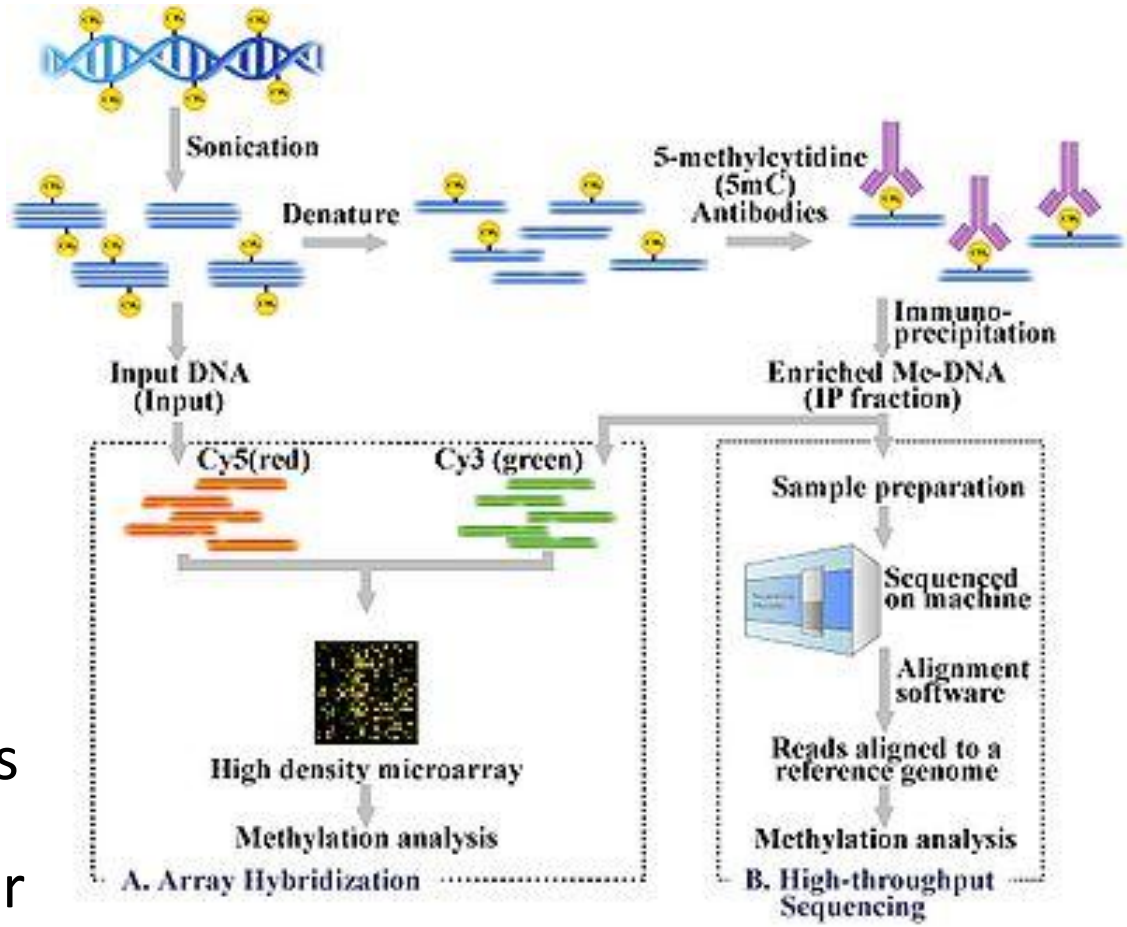
- Different degree of chromatin methylation affects expression of genes



Egigenomics - 2

MeDIP-Seq, methylated-DNA immunoprecipitation

- Similar to ChIP-Seq
- Immunoprecipitating methylated DNA with an antibody raised against 5′-methylcytosine.
- The unmethylated DNA is washed away, leaving the material highly enriched for methylated DNA

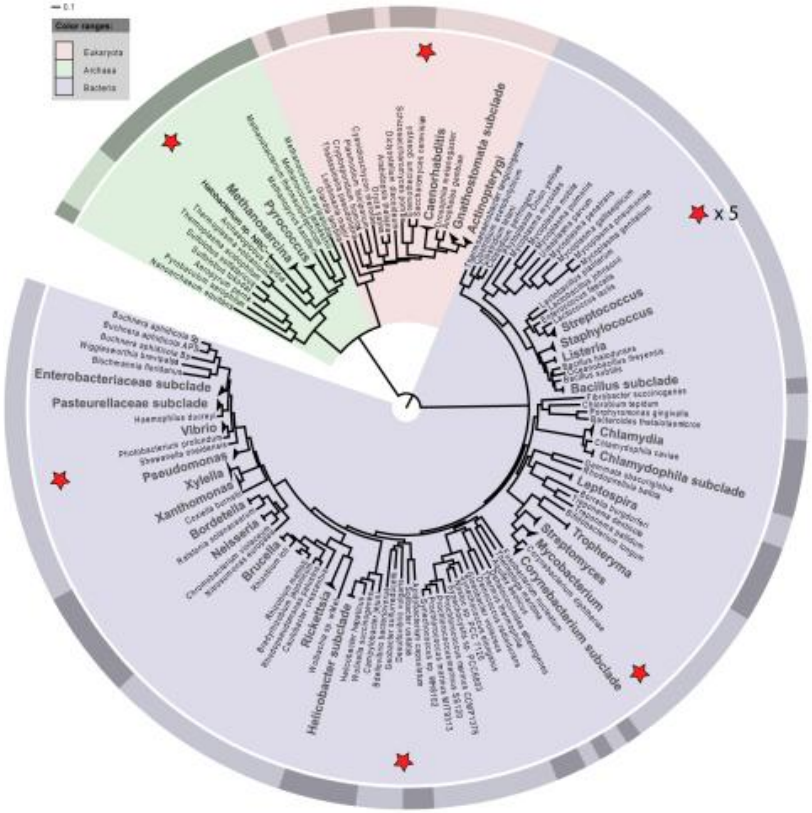


Metagenomics

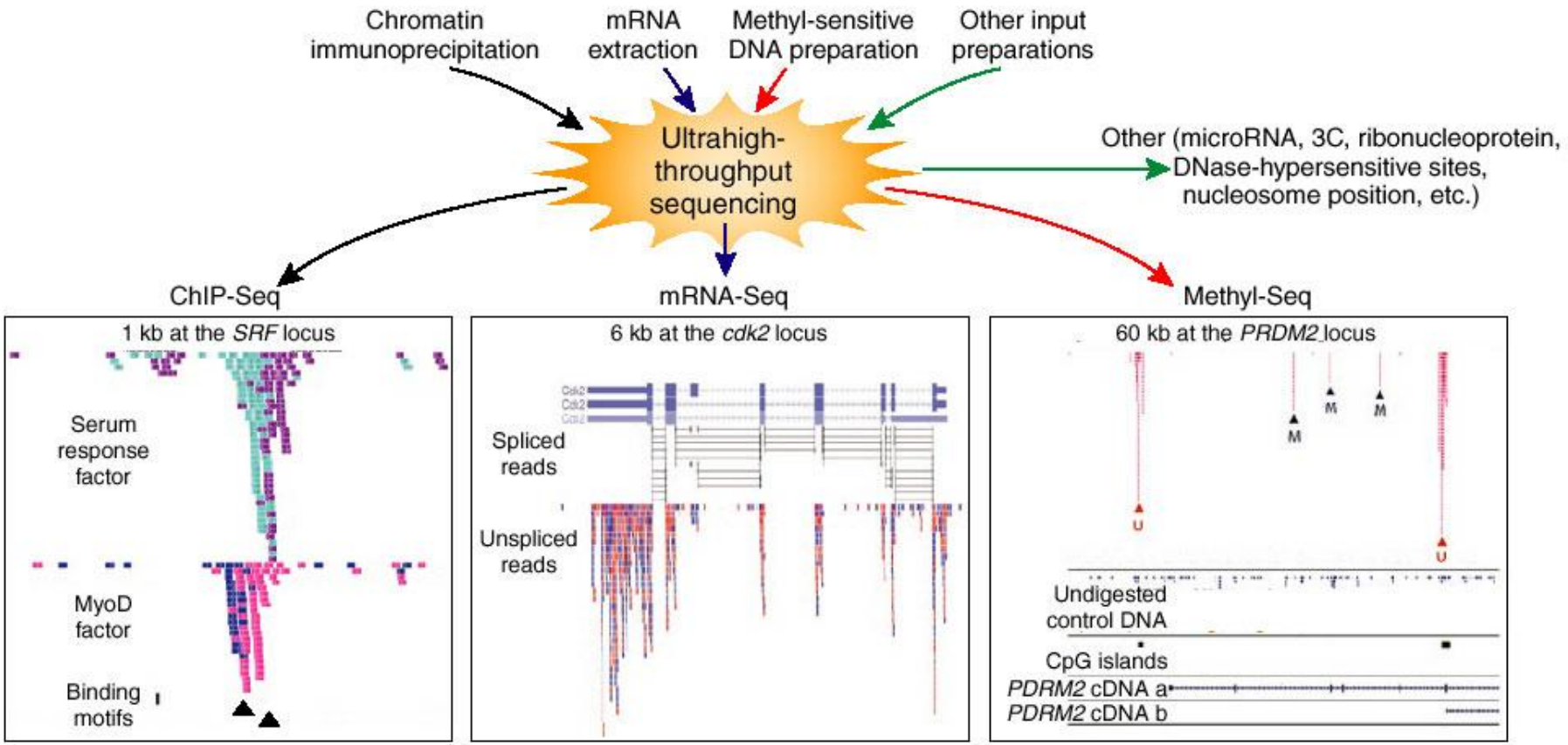
The application of modern genomics techniques to the **study of communities of microbial organisms** directly in their natural environments, bypassing the need for isolation and lab cultivation of individual species

- A sample may contain many different microorganisms,

- **16s Sequencing**
- **Shotgun genome sequencing**
- **Transcriptome sequencing**



Census NGS methods



Successful NGStories

NATURE | ARTICLE OPEN

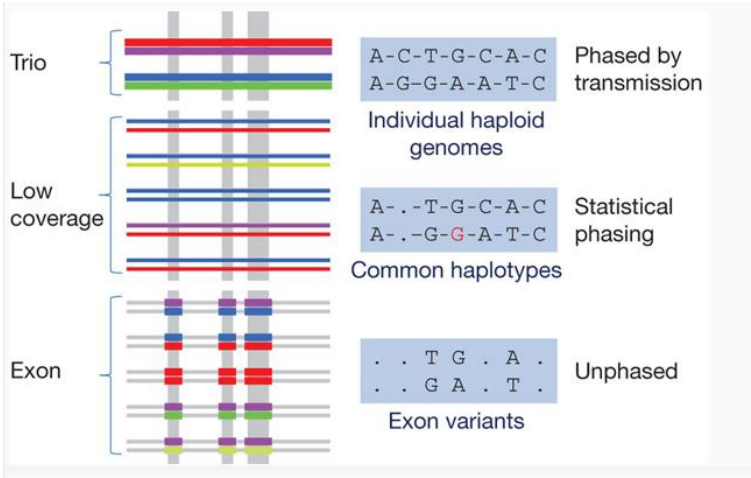
previous article next article

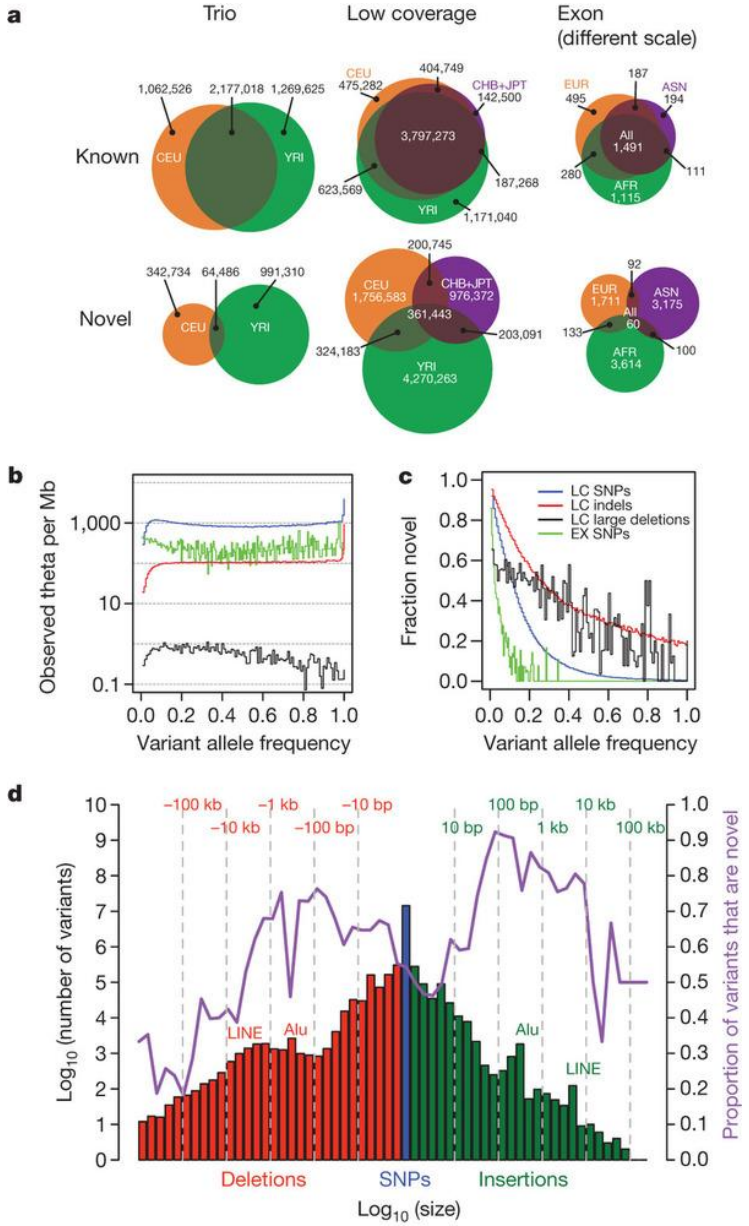
A map of human genome variation from population-scale sequencing

The 1000 Genomes Project Consortium

Affiliations | Contributions | Corresponding author

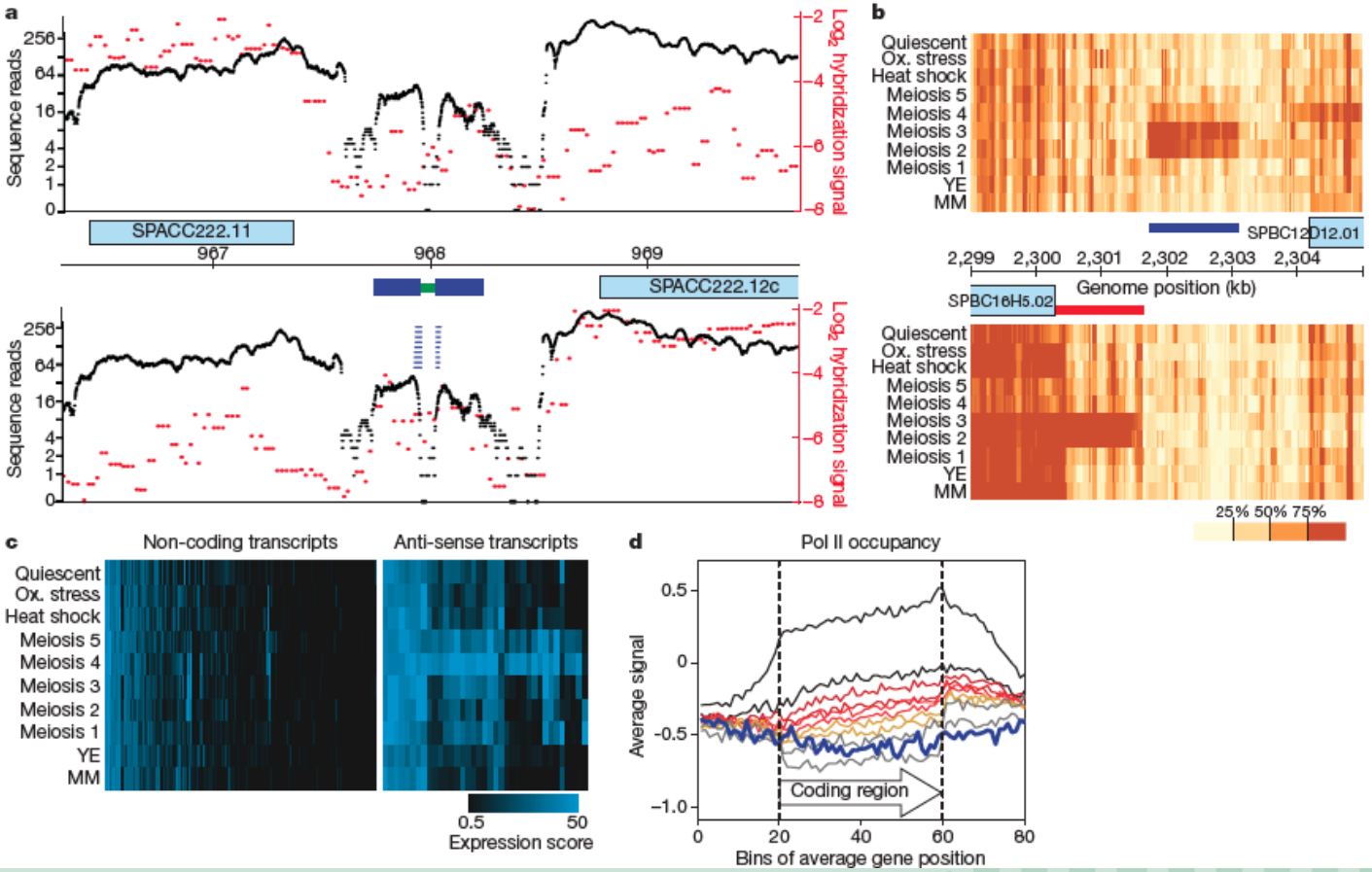
Nature **467**, 1061–1073 (28 October 2010) | doi:10.1038/nature09534
Received 20 July 2010 | Accepted 30 September 2010 | Published online 27 October 2010





Dynamic repertoire of a eukaryotic transcriptome surveyed at single-nucleotide resolution

Brian T. Wilhelm[1]*†, Samuel Marguerat[1]*†, Stephen Watt[1]†, Falk Schubert[1]†, Valerie Wood[1], Ian Goodhead[1]†, Christopher J. Penkett[1]†, Jane Rogers[1] & Jürg Bähler[1]†



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Published in final edited form as:
Nat Genet. 2010 January ; 42(1): 30–35. doi:10.1038/ng.499.

Exome sequencing identifies the cause of a Mendelian disorder

Sarah B. Ng[1,*], **Kati J. Buckingham**[2,*], **Choli Lee**[1], **Abigail W. Bigham**[2], **Holly K. Tabor**[2], **Karin M. Dent**[3], **Chad D. Huff**[4], **Paul T. Shannon**[5], **Ethylin Wang Jabs**[6,7], **Deborah A. Nickerson**[1], **Jay Shendure**[1,†], and **Michael J. Bamshad**[1,2,8,†]

[1]Department of Genome Sciences, University of Washington, Seattle, Washington, USA [2]Department of Pediatrics, University of Washington, Seattle, Washington, USA [3]Department of Pediatrics, University of Utah, Salt Lake City, Utah, USA [4]Department of Human Genetics, University of Utah, Salt Lake City, Utah, USA [5]Institute of Systems Biology, Seattle WA, USA [6]Department of Genetics and Genomic Sciences, Mount Sinai School of Medicine, New York, New York, USA [7]Department of Pediatrics, Johns Hopkins University, Baltimore, Maryland [8]Seattle Children's Hospital, Seattle, Washington, USA

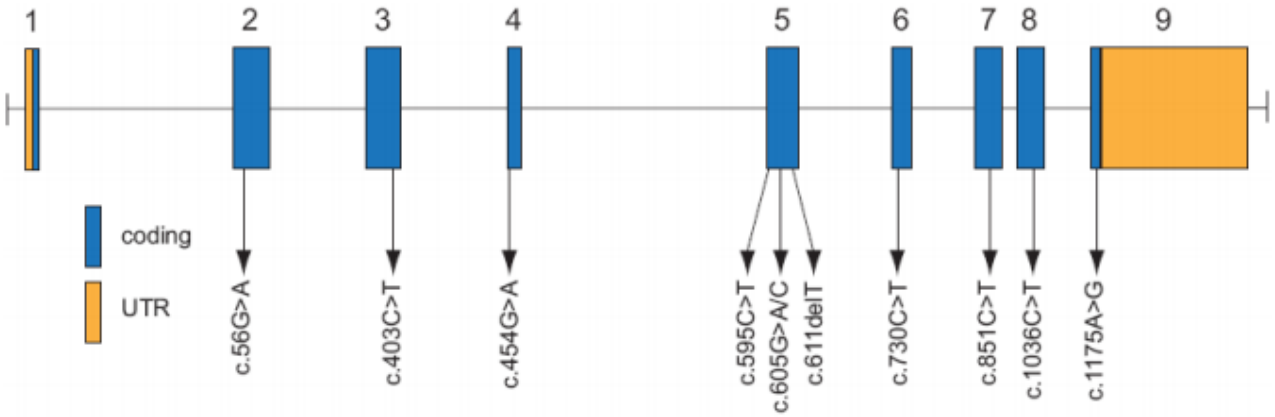


Figure 2. Genomic structure of the exons encoding the open reading frame of *DHODH*

DHODH is composed of 9 exons that encode untranslated regions (orange) and protein coding sequence (blue). Arrows indicate the locations of 11 different mutations found in 6 families with Miller syndrome.

Miller syndrome

Method

Open Access

Targeted next-generation sequencing of a cancer transcriptome enhances detection of sequence variants and novel fusion transcripts

Joshua Z Levin*, Michael F Berger†, Xian Adiconis*, Peter Rogov*, Alexandre Melnikov*, Timothy Fennell‡, Chad Nusbaum*, Levi A Garraway†§ and Andreas Gnirke*

Addresses: *Genome Sequencing and Analysis Program, Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA. †Cancer Program, Broad Institute of MIT and Harvard, 5 Cambridge Center, Cambridge, MA 02142, USA. ‡Sequencing Platform, Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA. §Department of Medical Oncology and Center for Cancer Genome Discovery, Dana-Farber Cancer Institute, Harvard Medical School, 44 Binney Street, Boston, MA 02115, USA.

Figure 3
Sequences from NUP214-XKR3 fusion transcripts detected after hybrid selection. After hybrid selection, 152 reads were aligned to the transcriptome and detected as *NUP214-XKR3* fusions. From top to bottom, we observed 137, four, eight, and three reads for these transcripts. The *NUP214* (exon 27) to *XKR3* (exon 4) has a stop codon downstream (not shown). Only *NUP214* (exon 29) to *XKR3* (exon 4) retains an open reading frame downstream of the fusion. Before hybrid selection, eight reads were aligned to the transcriptome and detected as *NUP214-XKR3* fusions; only the *NUP214* (exon 29) to *XKR3* (exon 2) transcript was detected. Sequence from *NUP214* DNA is shown as lower case, and from *XKR3*, as bold and upper case.

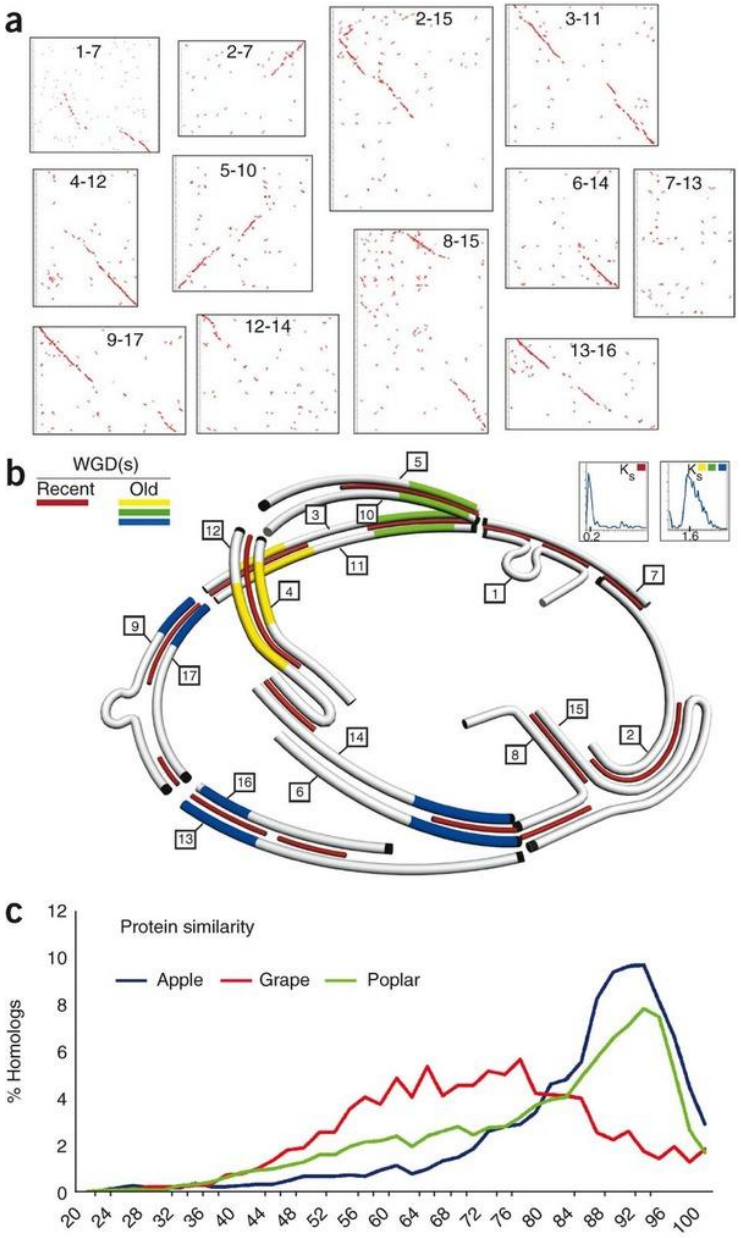
NATURE GENETICS | ARTICLE

The genome of the domesticated apple (*Malus* × *domestica* Borkh.)

Riccardo Velasco, Andrey Zharkikh, Jason Affourtit, Amit Dhingra, Alessandro Cestaro, Ananth Kalyanaraman, Paolo Fontana, Satish K Bhatnagar, Michela Troggio, Dmitry Pruss, Silvio Salvi, Massimo Pindo, Paolo Baldi, Sara Castelletti, Marina Cavaiuolo, Giuseppina Coppola, Fabrizio Costa, Valentina Cova, Antonio Dal Ri, Vadim Goremykin, Matteo Komjanc, Sara Longhi, Pierluigi Magnago, Giulia Malacarne, Mickael Malnoy + *et al.*

Affiliations | Contributions | Corresponding author

Nature Genetics **42**, 833–839 (2010) | doi:10.1038/ng.654
Received 19 November 2009 | Accepted 03 August 2010 | Published online 29 August 2010

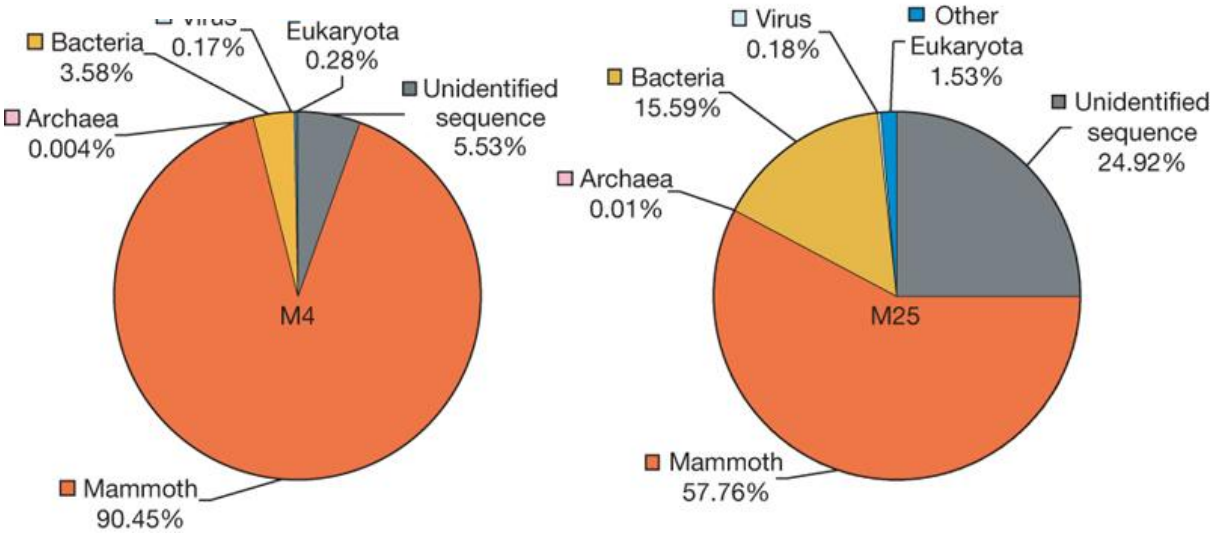


Letter

Nature **456**, 387-390 (20 November 2008) | doi:10.1038/nature07446; Received 12 May 2008; Accepted 22 September 2008

Sequencing the nuclear genome of the extinct woolly mammoth

Webb Miller[1], Daniela I. Drautz[1], Aakrosh Ratan[1], Barbara Pusey[1], Ji Qi[1], Arthur M. Lesk[1], Lynn P. Tomsho[1], Michael D. Packard[1], Fangqing Zhao[1], Andrei Sher[2,9], Alexei Tikhonov[3], Brian Raney[4], Nick Patterson[5], Kerstin Lindblad-Toh[5], Eric S. Lander[5], James R. Knight[6], Gerard P. Irzyk[6], Karin M. Fredrikson[7], Timothy T. Harkins[7], Sharon Sheridan[7], Tom Pringle[8] & Stephan C. Schuster[1]



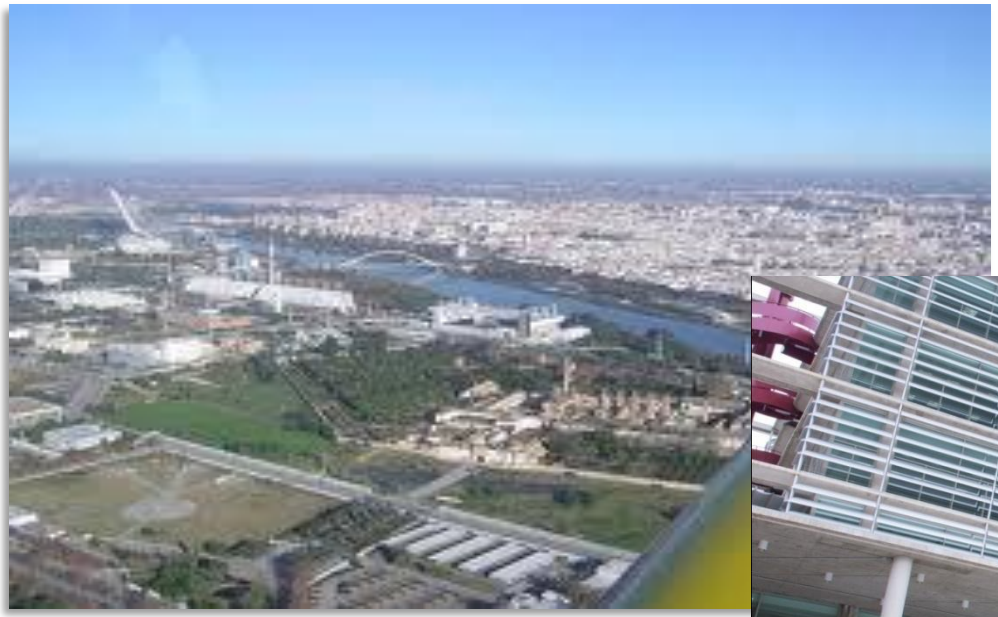
Species composition of metagenomic DNA extracted from mammoth hair

nature

No so far…. Sequencing Centers

Andalusian Human Genome Sequencing Center

CASEGH



Cartuja 93

Scientific and Technology Park

Sevilla

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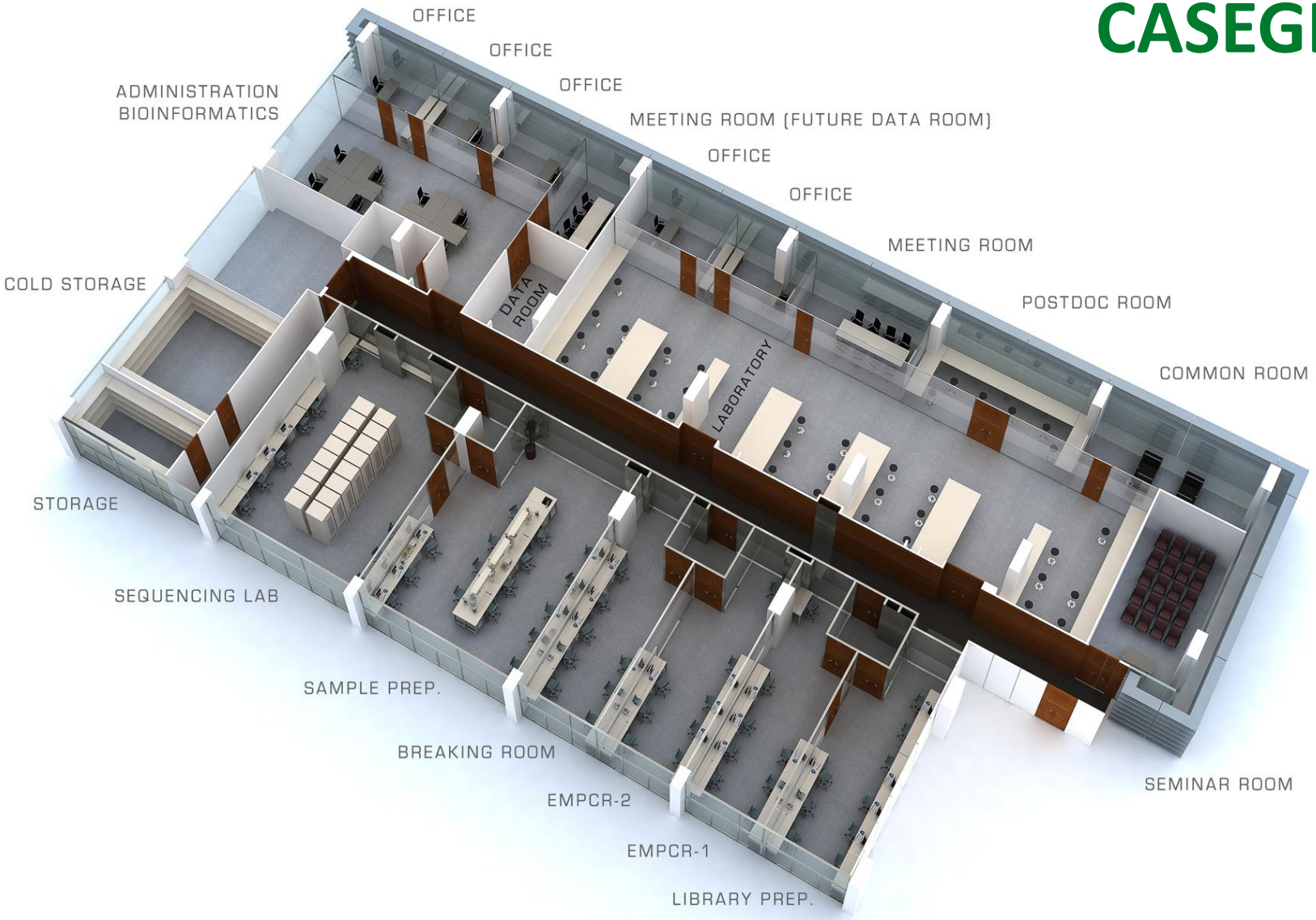
OFFICE
OFFICE
OFFICE
ADMINISTRATION
BIOINFORMATICS
MEETING ROOM (FUTURE DATA ROOM)
OFFICE
OFFICE
MEETING ROOM
COLD STORAGE
DATA ROOM
POSTDOC ROOM
LABORATORY
COMMON ROOM
STORAGE
SEQUENCING LAB
SAMPLE PREP.
BREAKING ROOM
EMPCR-2
SEMINAR ROOM
EMPCR-1
LIBRARY PREP.

SEQUENCING LAB

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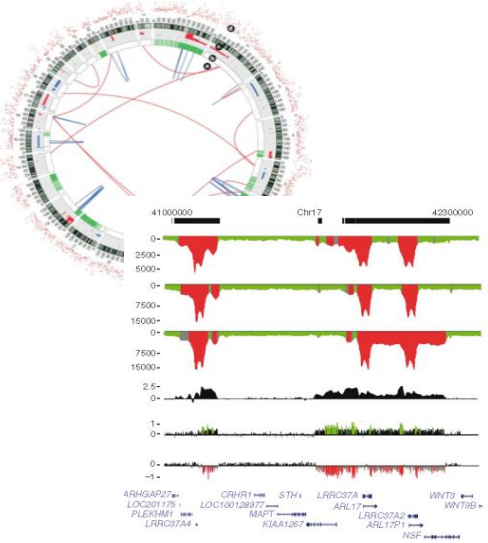
Genomics Unit

Two technologies to scan for variations

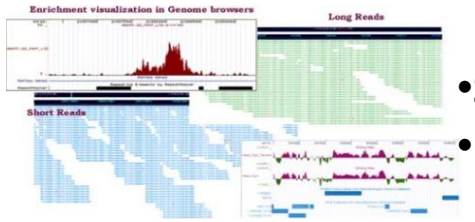
454 Roche
Longer reads
Lower coverage



Structural variation

- Amplifications
- Deletions
- CNV
- Inversions
- Translocations

SOLiD ABI
Shorter reads
Higher coverage



Variants

- SNVs
- Small indels

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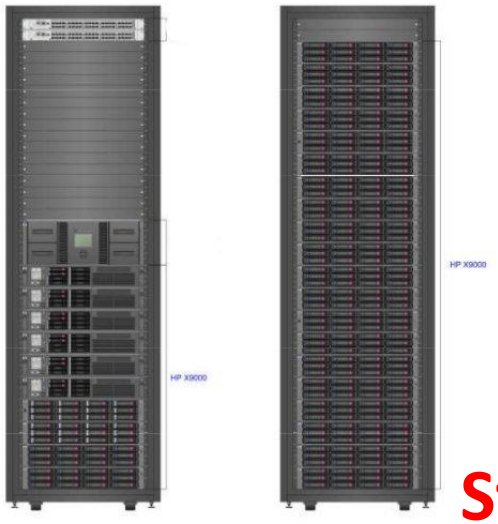
High
Performance
Computing
Cluster

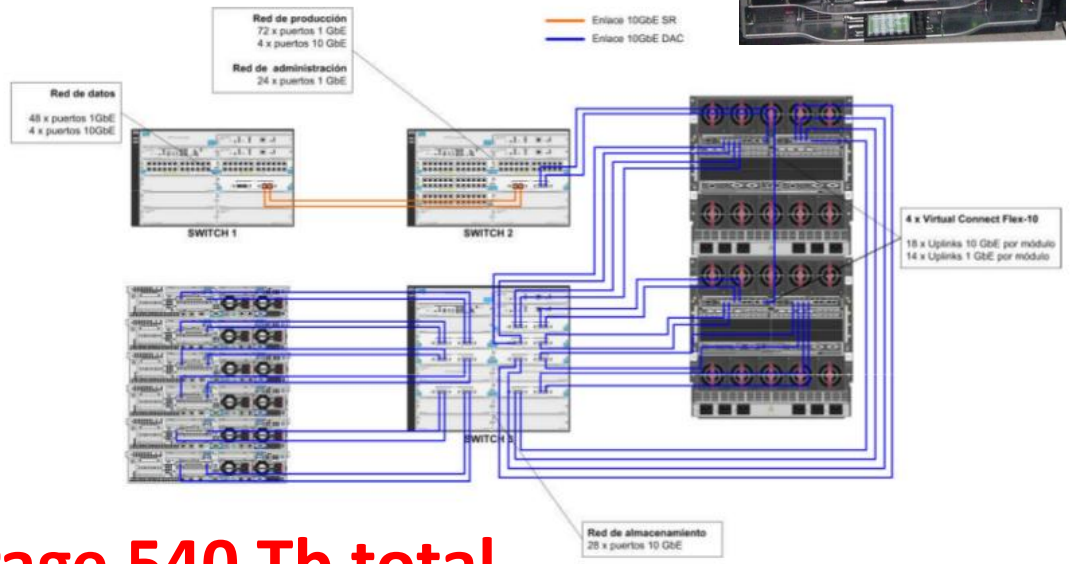
Bioinformatics Unit

24 High Performance Computing nodes – **72-192** Gb RAM
2 Control nodes - **24** Gb RAM

- 2 x Quad core CPU
- 16 threads
- 2 x 10Gb Network interface

Execution of **400 jobs in parallel**





Storage 540 Tb total

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Services at CASEGH

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The Medical Genome Project (MGP)

Public Funding:

- Andalucia Health System.
- Central government.
- European Regional Development Fund (ERFD).

Private Funding:

- 454 Life Sciences (Roche).

The MGP Scope and Aims

- Medical Genome Project's (MGP) general goals are:
  - Identify novel genes responsible for inherited rare diseases
  - Identify susceptibility genes for common diseases
  - Use the results of genetic research to discover new drugs acting on new targets (new genes associated with human disease pathways)

The MGP Scope and Aims

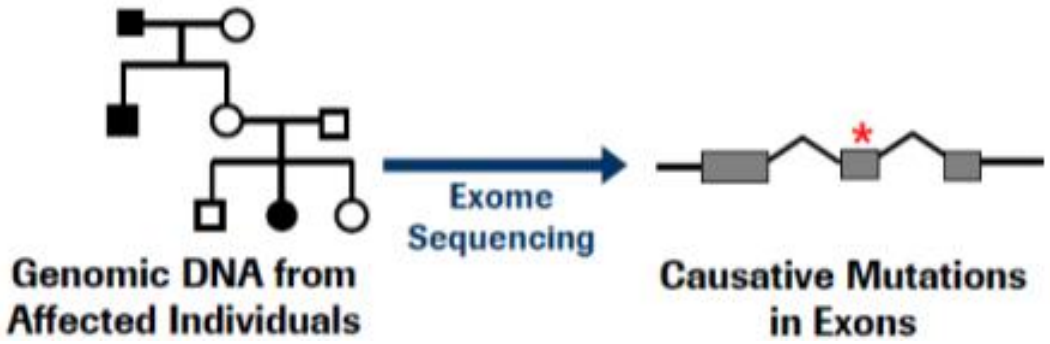
- Medical Genome Project's (MGP) specific goals are:
  - The characterization of a great number of genetic diseases by means of **exome sequencing**.
    - Diseases on study are genetic Rare Diseases
    - Monogenic diseases
  - To characterize SNPs in a healthy **control population**
    - 300 Individuals

- MGP will be used as the first steps towards the implementation of **genomic and personalized medicine** in the Andalusian HEALTHCARE SYSTEM. A system covering a population of 8.5 million.

Exome capture

- Focus on the Most Relevant Portion of the Genome

- "Exome" (all exons in the genome):
  - the most functionally relevant ~2% of the genome.
  - where the majority of known inherited disease-causing mutations reside.



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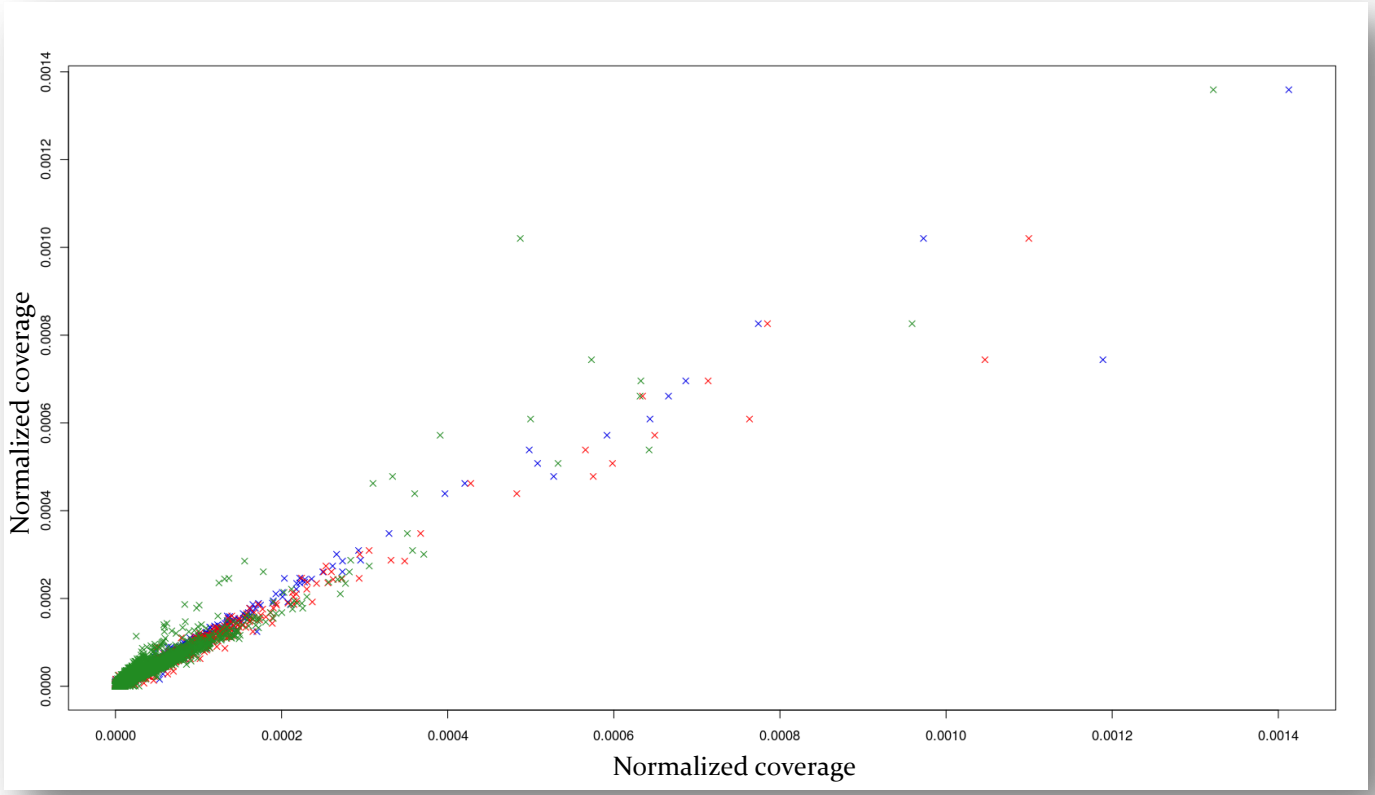
Exome capture reproducibility

Normalized coverage per exon for different samples



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Exome capture reproducibility

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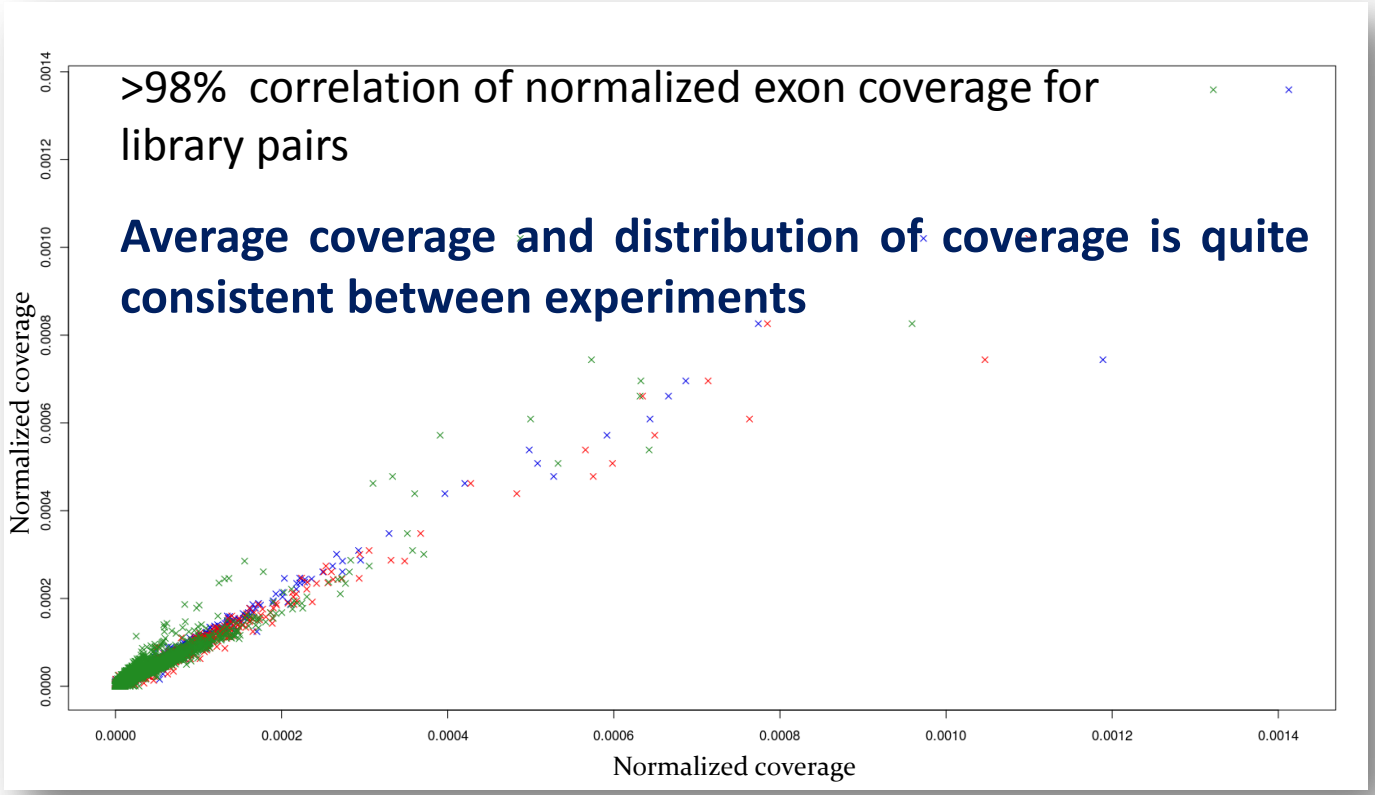

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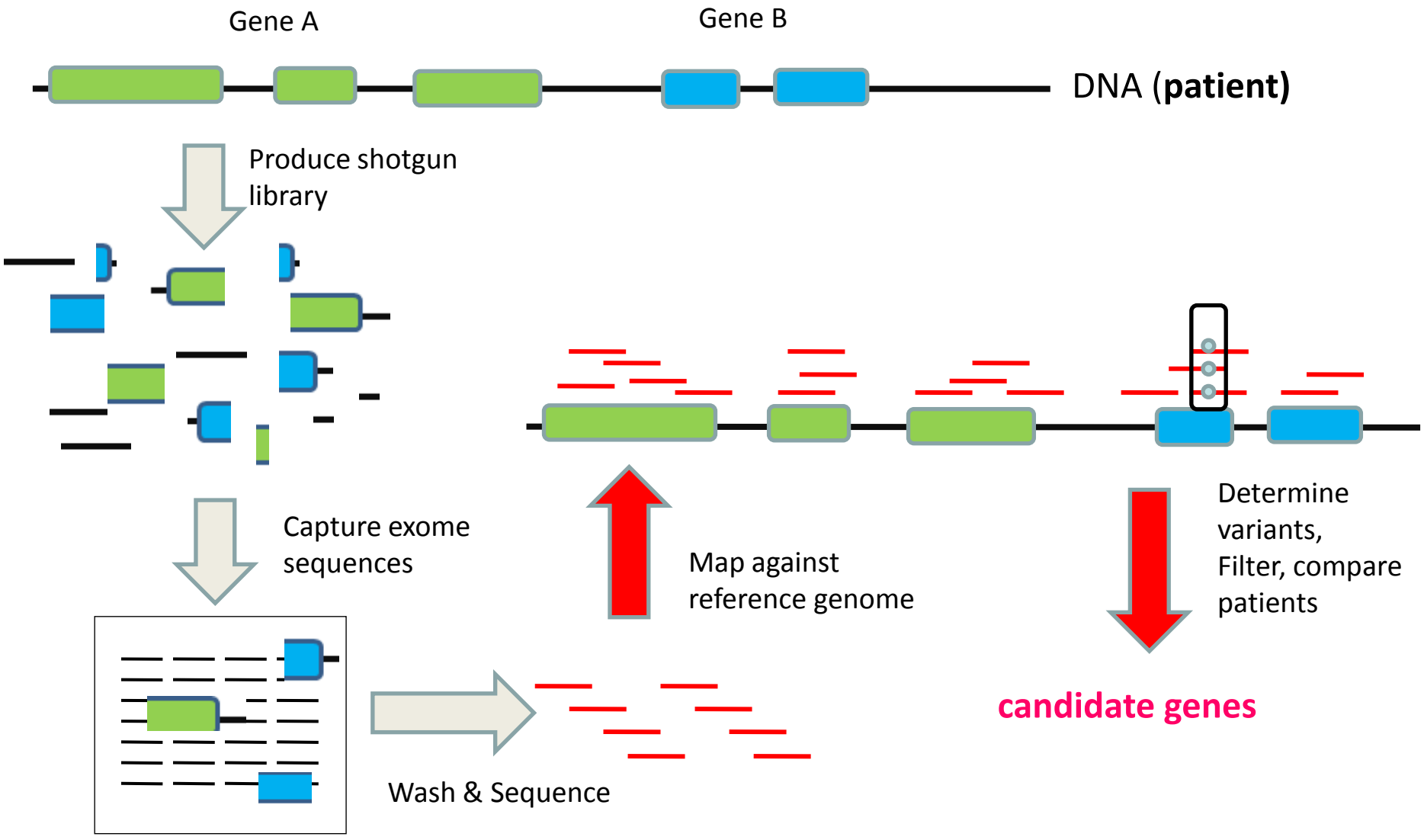
Exome sequencing work-flow for Variant detection



Bioinformatic analysis
Primary analysis pipeline (Automatic)

FastQ
Color space
200M reads

Automatic QC

Preprocess

Position / quality

Base composition

Nucleotide QC

Sequence cleaning

Mapping

BFAST

Variant Calling

SAM to BAM
Sort BAM
Clean BAM
Index BAM

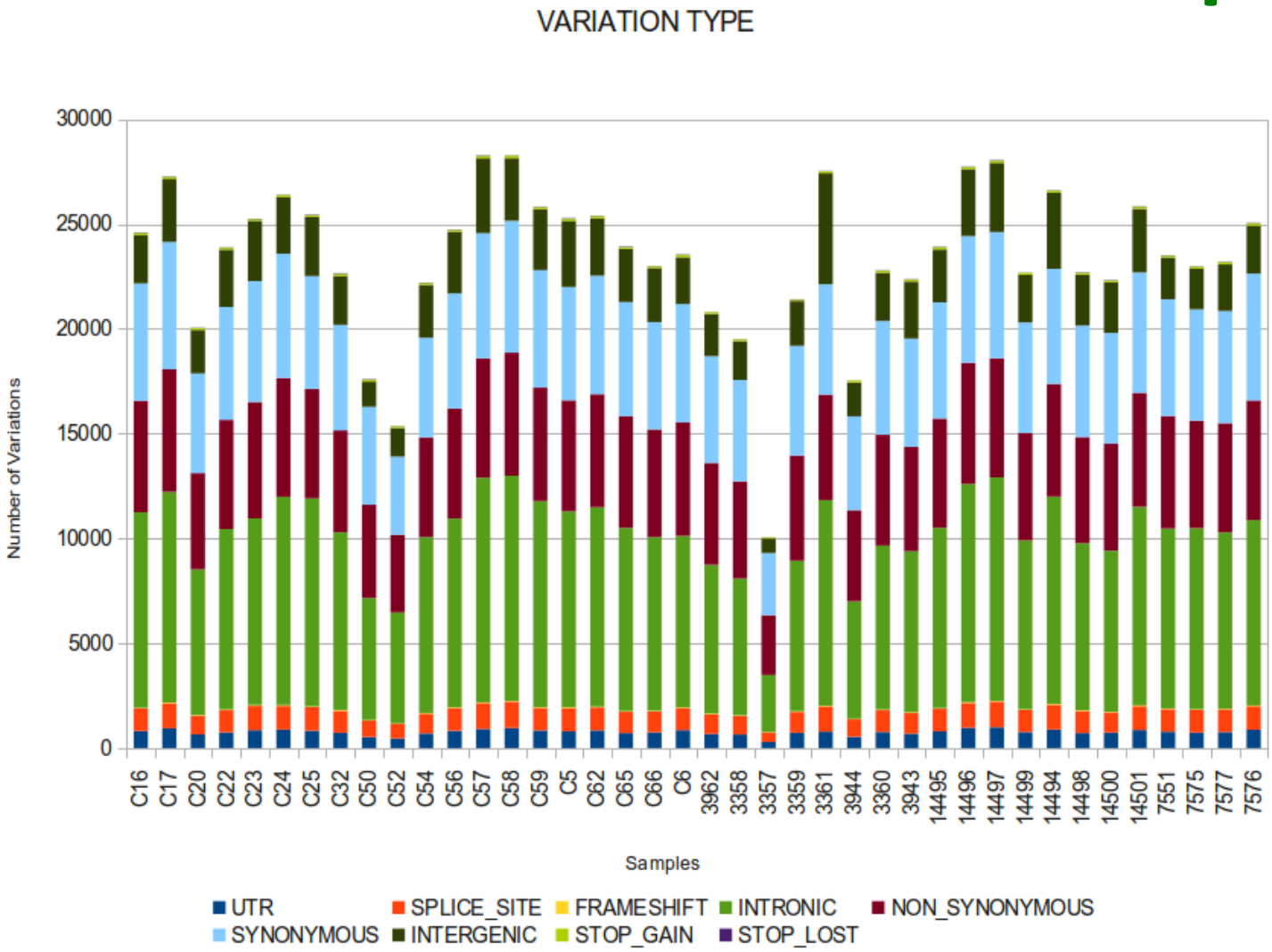
Annotation and filtering

Variation

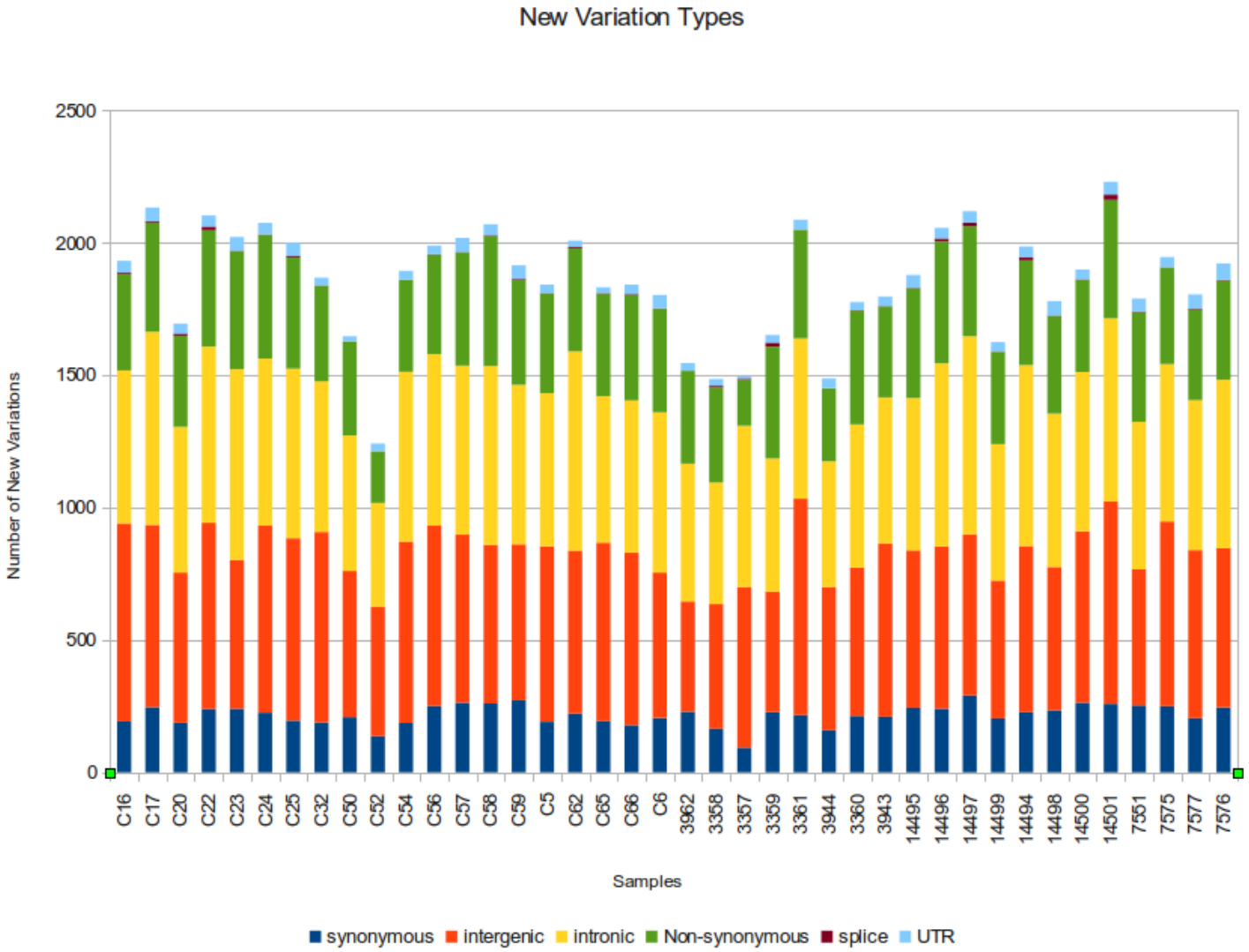
4-6 hours* **8-12 hours*** **8-12 hours*** **minutes**

** 8CPUs 200Mreads (>25-30 Exomes per week)*

SNPs distribution across samples



New Variation Types



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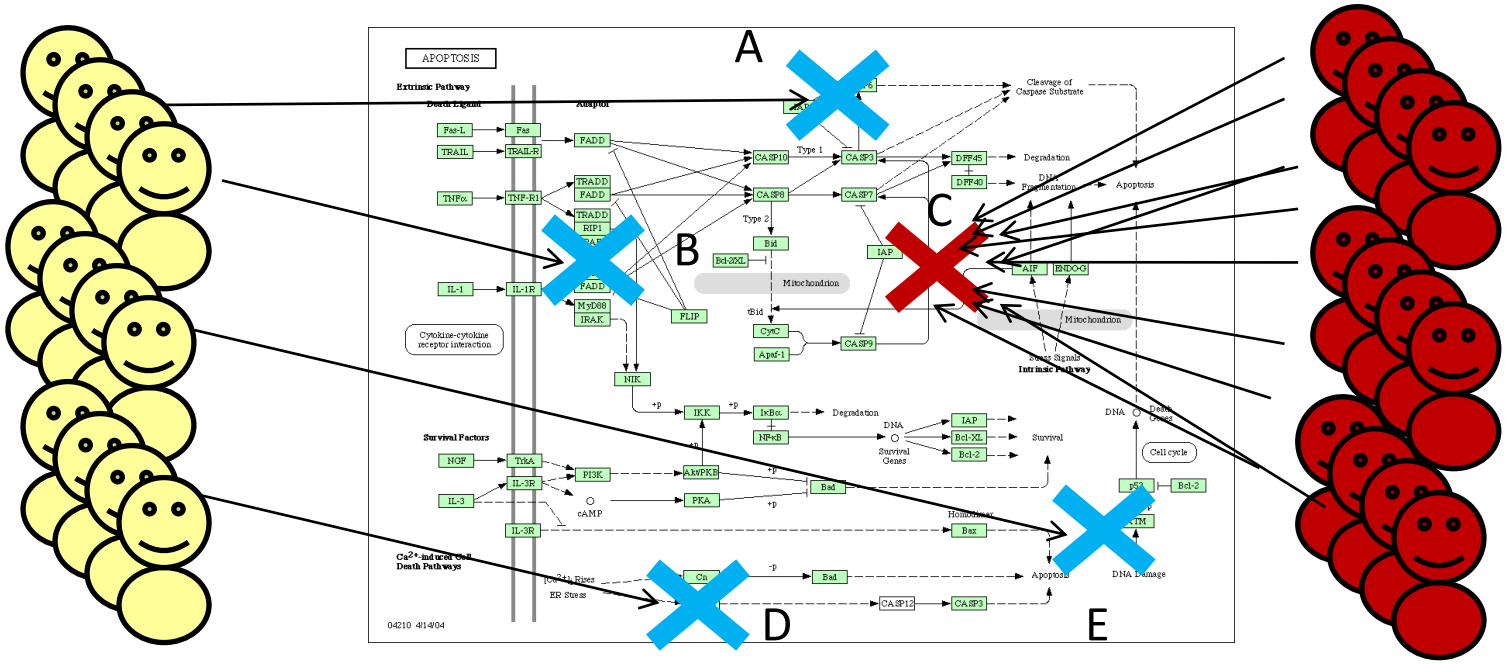
Secondary analysis:
Finding the mutations causative of diseases

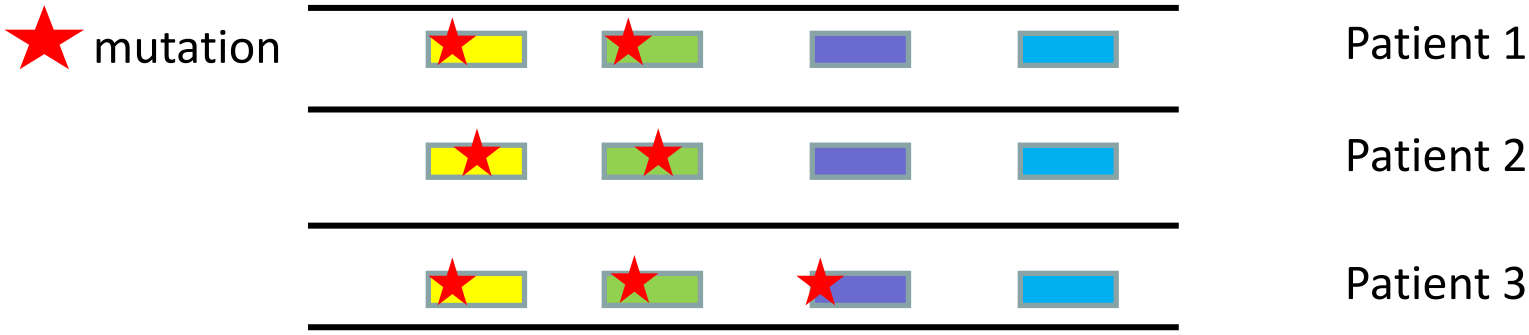
The simplest case: monogenic disease due to a single gene



Controls

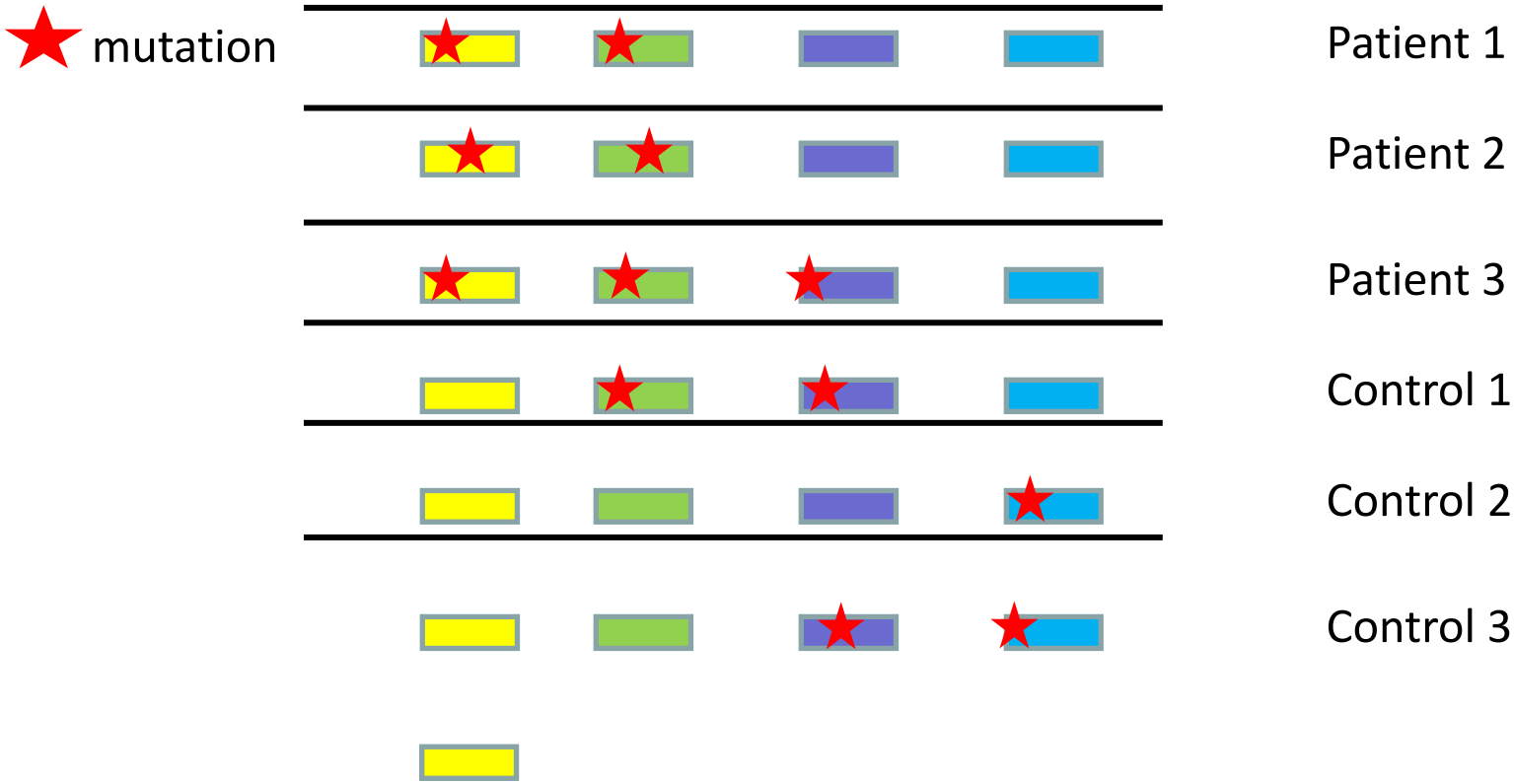
Cases

The principle: comparison of patients (or families) and reference controls



The principle: comparison of patients (or families) and reference controls

The principle: comparison of patients (or families) and reference controls



candidate gene (shares mutation for all patients but no controls)

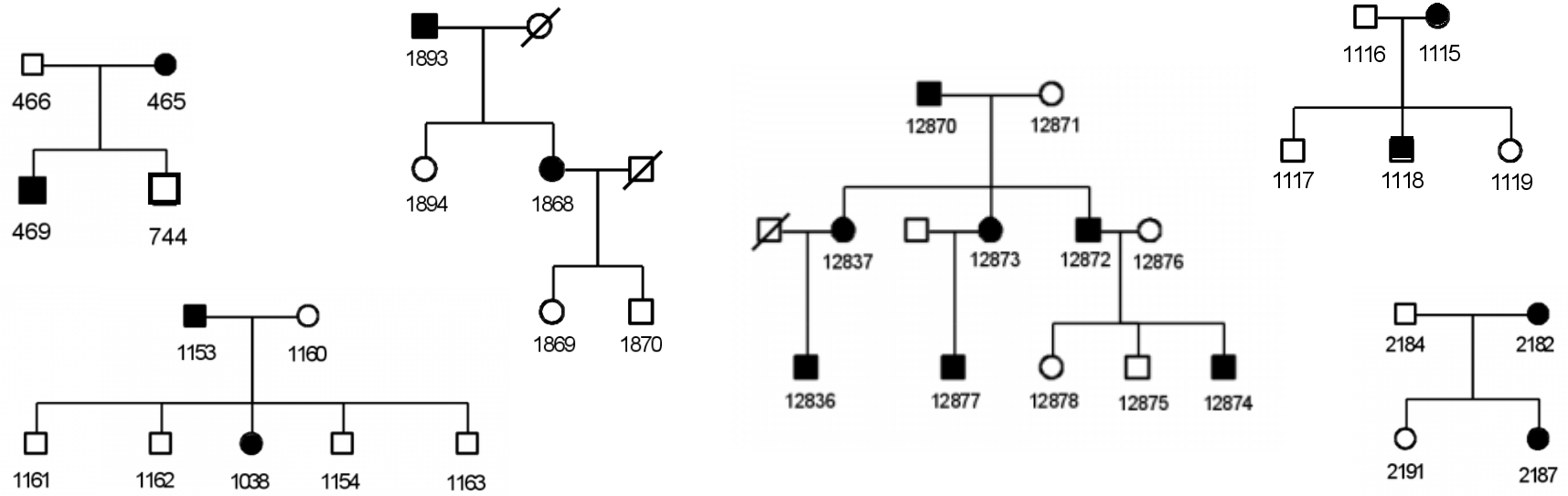
Is this approach realistic?
Can we detect such rare variants so easily?

a) Interrogating 50Mb produces too many variants

b) In many cases we are not hunting new but known variants

c) Same phenotype can be due to different mutations and different genes

Filtering with multiple family information



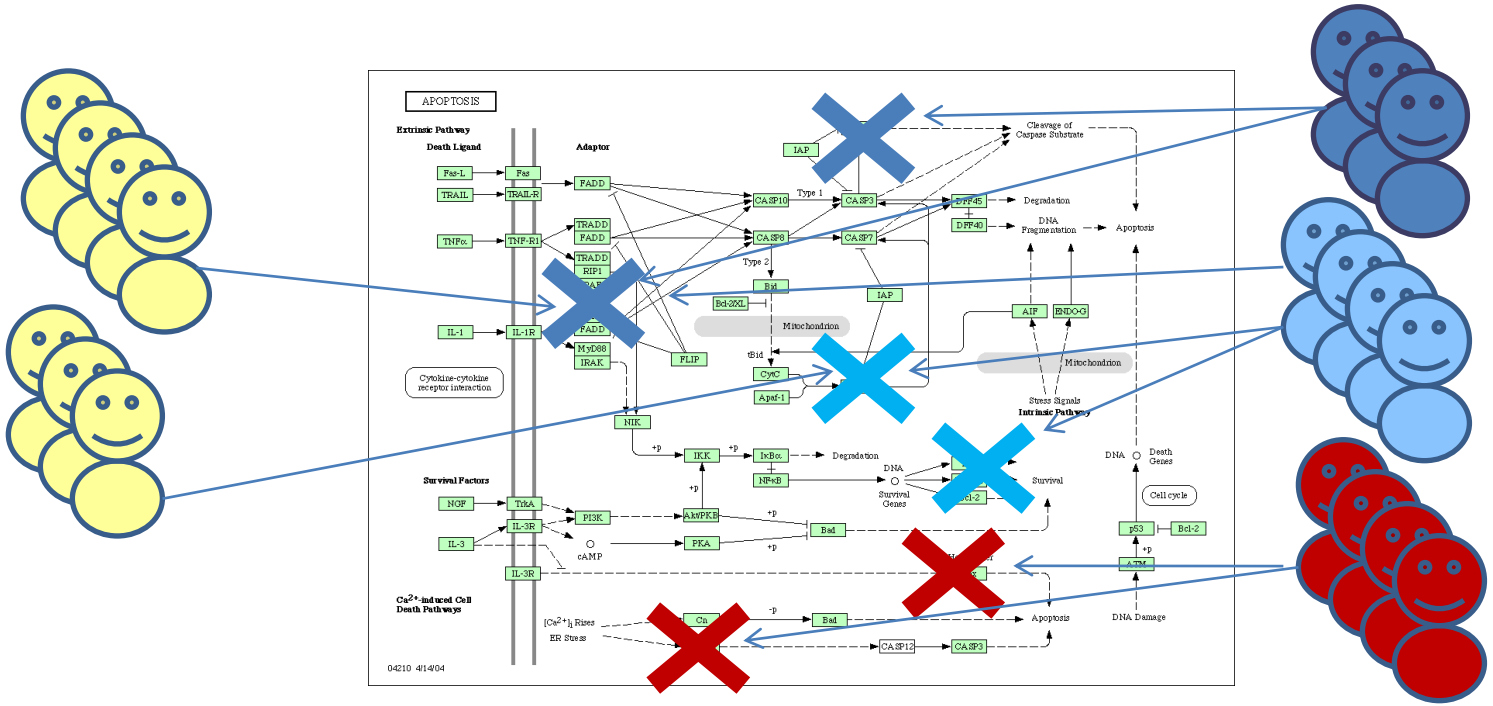
	Families					
	1	2	3	4	5	6
Variants	3403	82	4	0	0	0
Genes	2560	331	35	8	1	0

Problem: how to prioritize putative candidate genes

Clear individual gene associations are difficult to find in some diseases

Controls

Cases



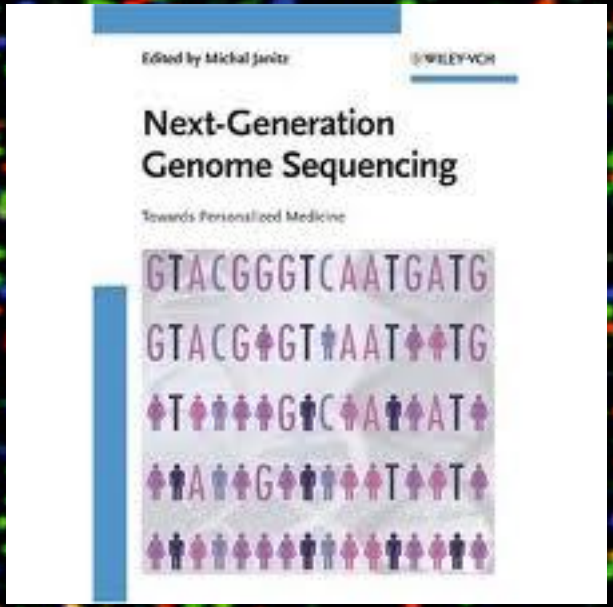
They can have different mutations (or combinations).

Many cases have to be used to obtain significant associations to many markers.

The only common element is the pathway (yet unknow) affected.

Conclusions

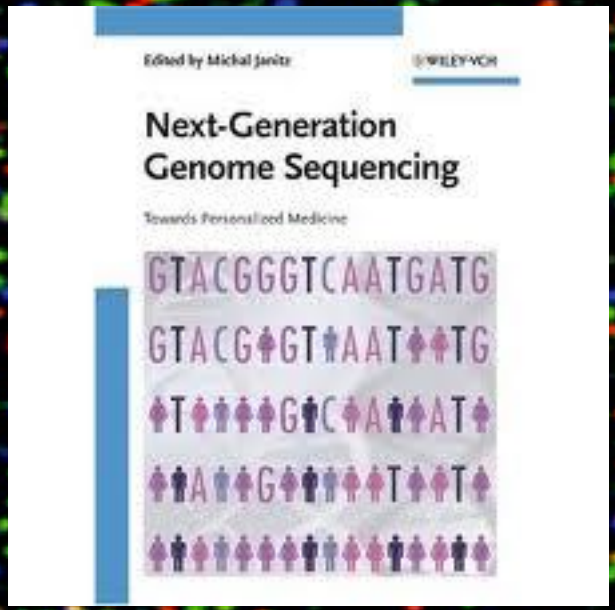
NGS is revolutionizing how we do genome research



Conclusions

NGS is revolutionizing how we do genome research

But it will also revolutionize our lives….

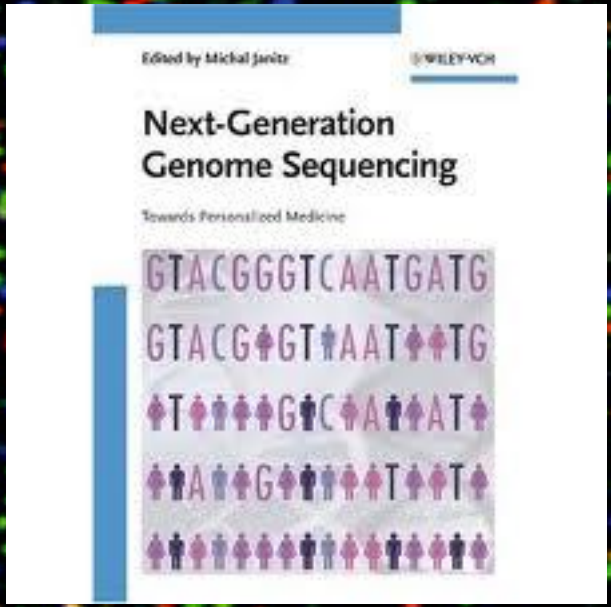


Conclusions

NGS is revolutionizing how we do genome research

But it will also revolutionize our lives….

If we manage to process and analyze ALL the DATA




THANK YOU