

**Precision medicine in NTUH**  
**Rapid diagnosis for genetic conditions by**  
**next-generation sequencing**

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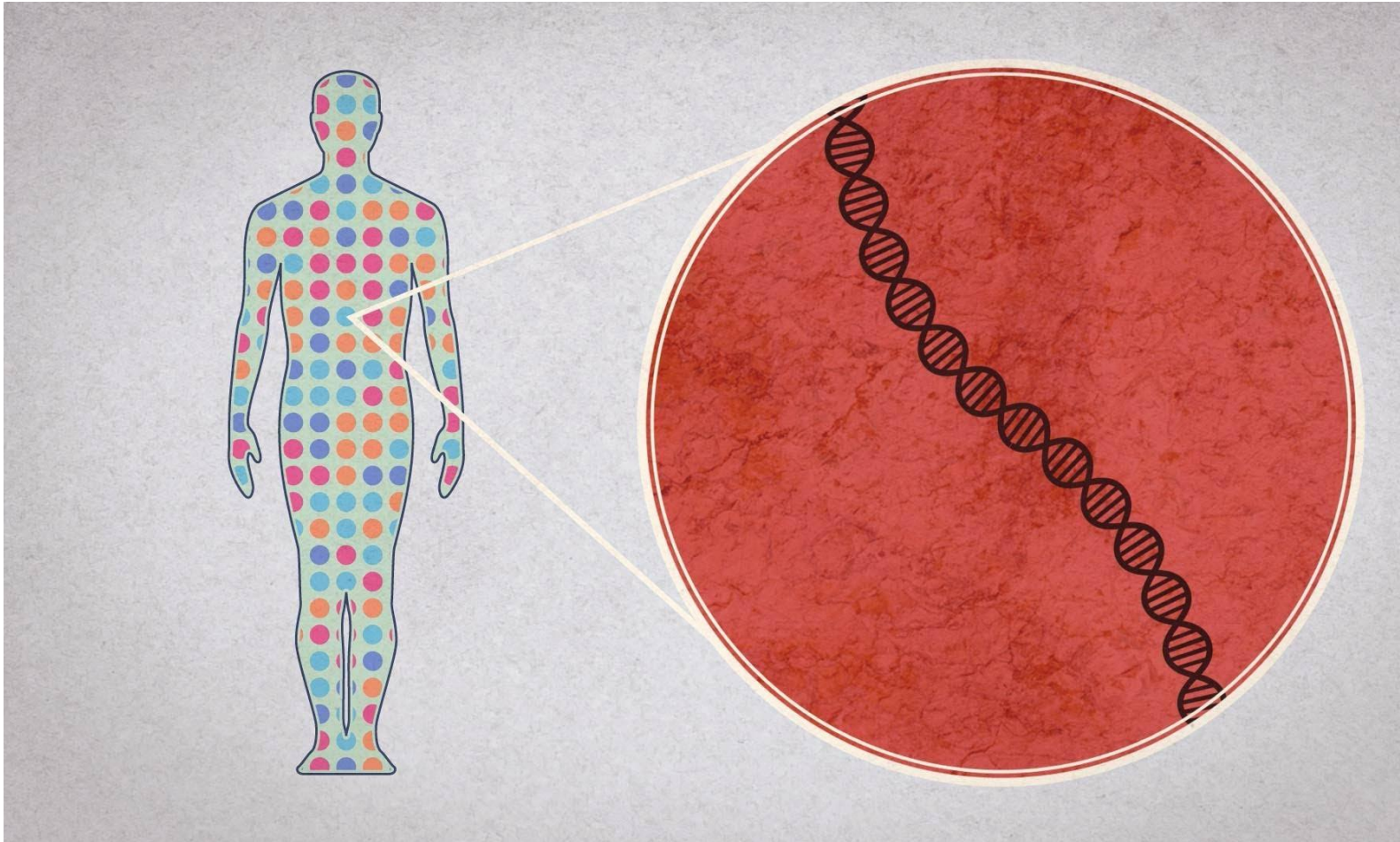
Quality

# Quality Control (QC)

Quality in medicine can't be  
achieved without a correct  
diagnosis

The Burden of Genetic Disease on Inpatient  
Care in Children's Hospitals is high

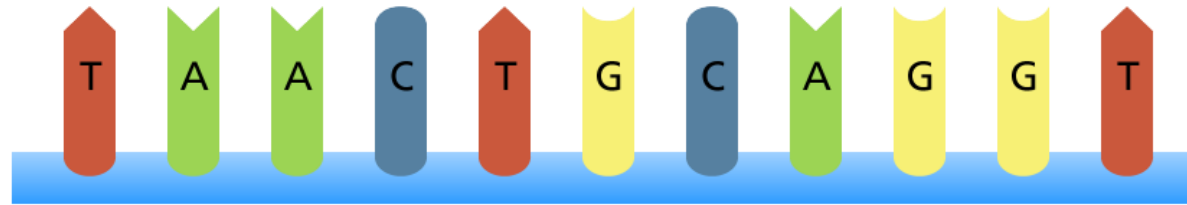
# The human genome contains over 3 billion base pair of DNA



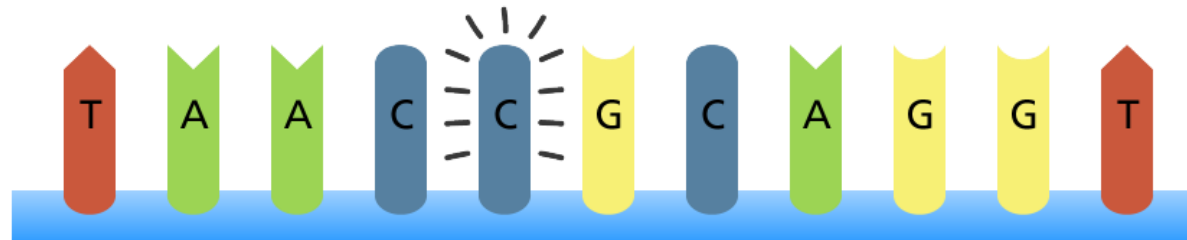
23 pairs of chromosome  
Total length: over 3 billion base pairs  
~20,000 protein coding genes

# If DNA sequences change, you may get sick

Original sequence



Point mutation



# Mutation in DNA sequence causes human diseases



Sam Berns, 17y  
Progeria



Queen Victoria  
Hemophilia

# OMIM Gene Map Statistics

## OMIM Morbid Map Scorecard (Updated February 8th, 2019)

Total number of phenotypes* for which the molecular basis is known	6,357
Total number of genes with phenotype-causing mutation	4,040

## Distribution of Phenotypes across Genes (Updated February 8th, 2019)

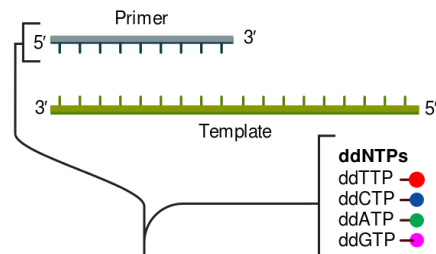
Number of genes with 1 phenotype	2,779
Number of genes with 2 phenotypes	762
Number of genes with 3 phenotypes	265
Number of genes with 4+ phenotypes	234

How to find a mutation?

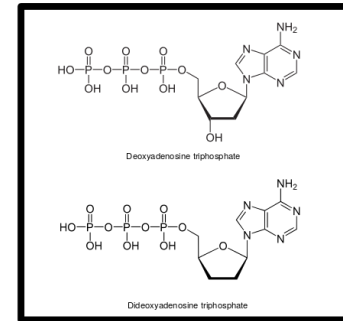
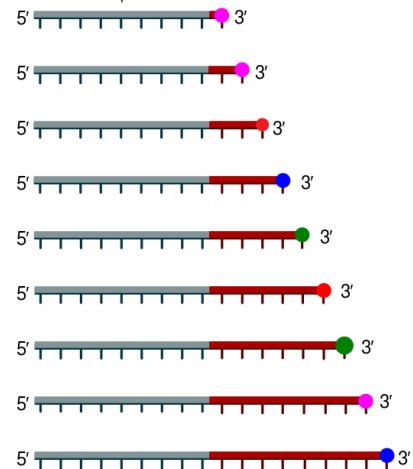
# Capillary sequencing (Sanger sequencing)

## ① Reaction mixture

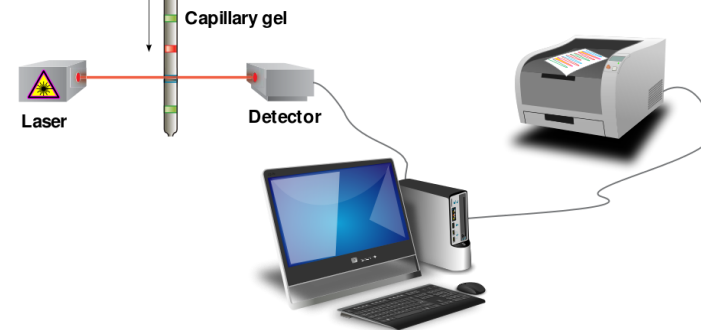
- Primer and DNA template
- DNA polymerase
- ddNTPs with flouorchromes
- dNTPs (dATP, dCTP, dGTP, and dTTP)



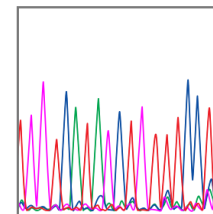
## ② Primer elongation and chain termination



## ③ Capillary gel electrophoresis separation of DNA fragments

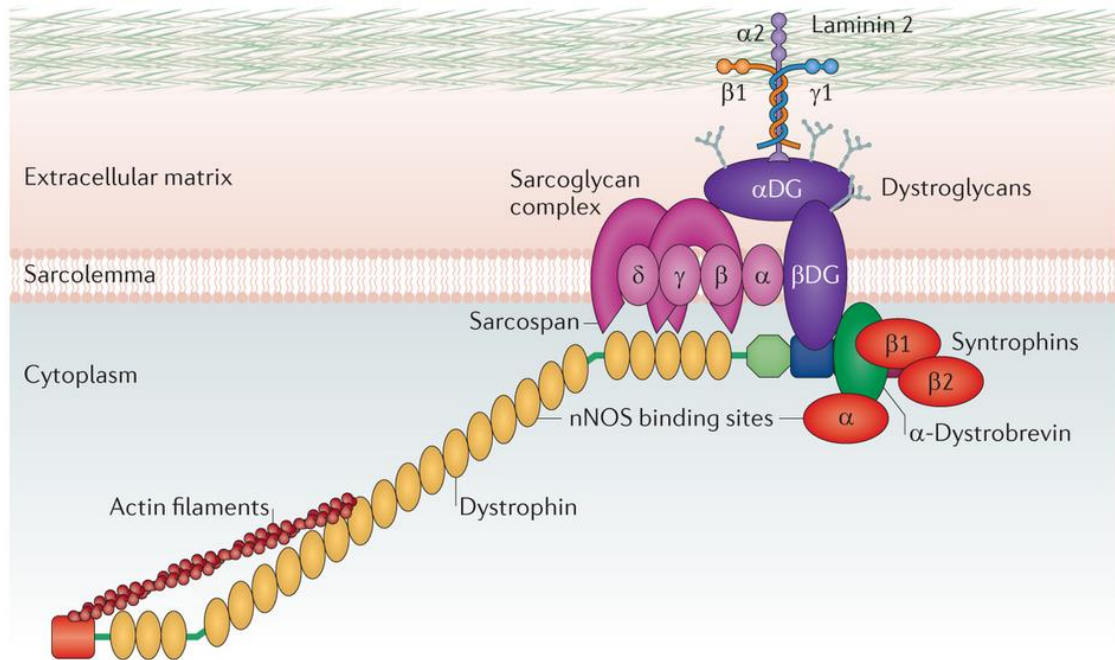


## ④ Laser detection of flouorchromes and computational sequence analysis

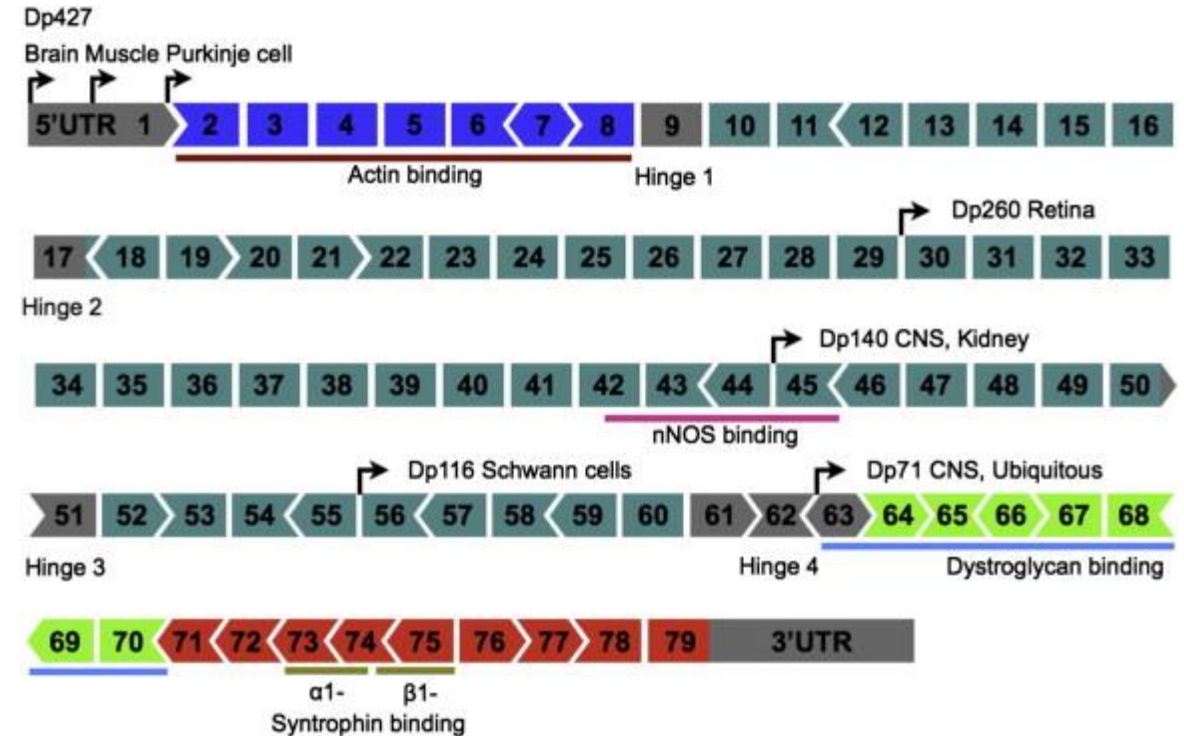


Chromatograph

# Dystrophin gene

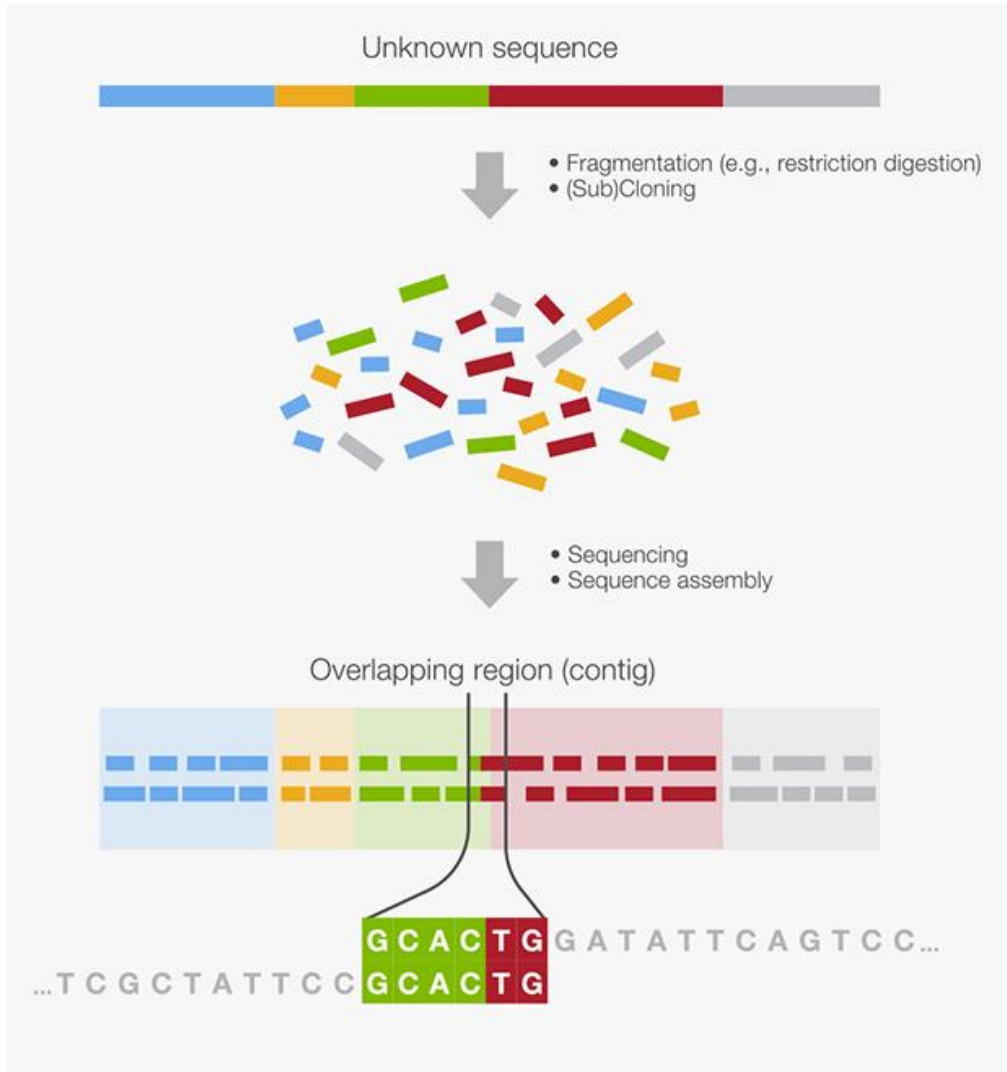


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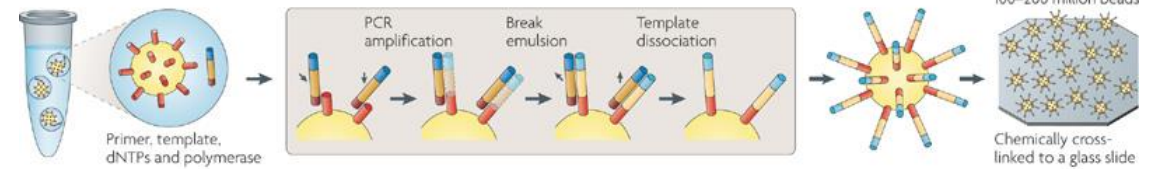
This big gene is quite refractory to Sanger sequencing

# Next generation sequencing



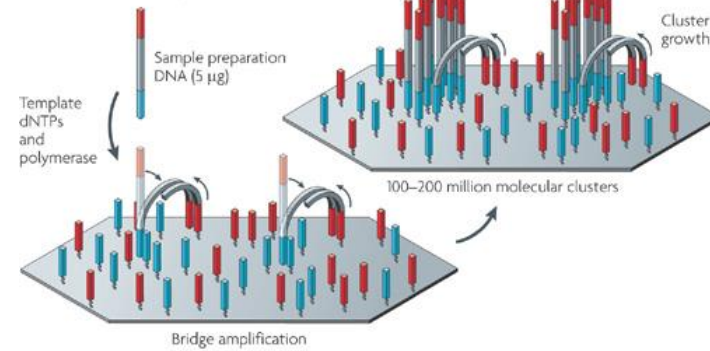
**a Roche/454, Life/APG, Polonator**  
**Emulsion PCR**

One DNA molecule per bead. Clonal amplification to thousands of copies occurs in microreactors in an emulsion

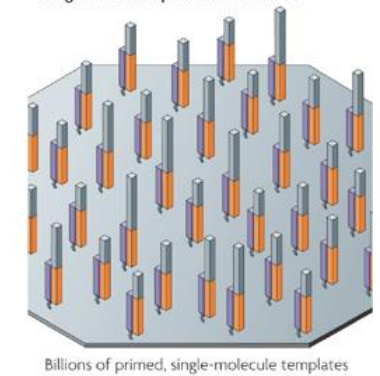


**b Illumina/Solexa**  
**Solid-phase amplification**

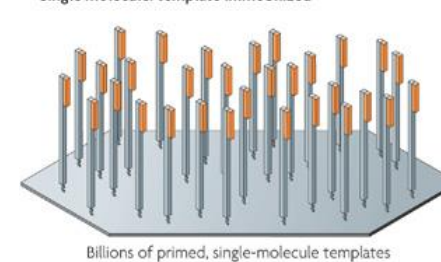
One DNA molecule per cluster



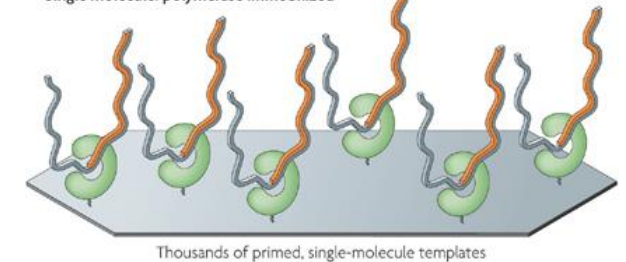
**c Helicos BioSciences: one-pass sequencing**  
**Single molecule: primer immobilized**



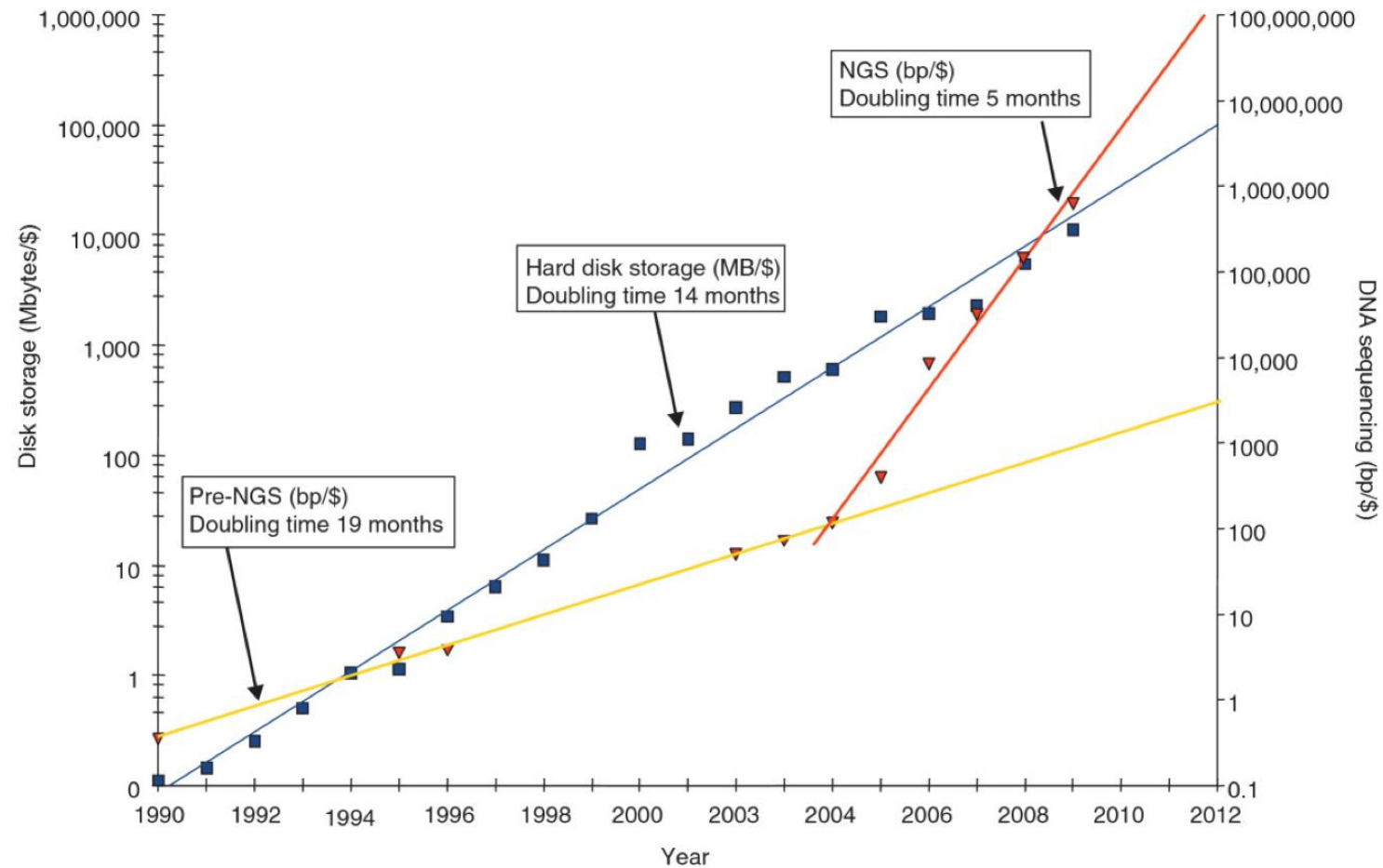
**d Helicos BioSciences: two-pass sequencing**  
**Single molecule: template immobilized**



**e Pacific Biosciences, Life/Visigen, LI-COR Biosciences**  
**Single molecule: polymerase immobilized**



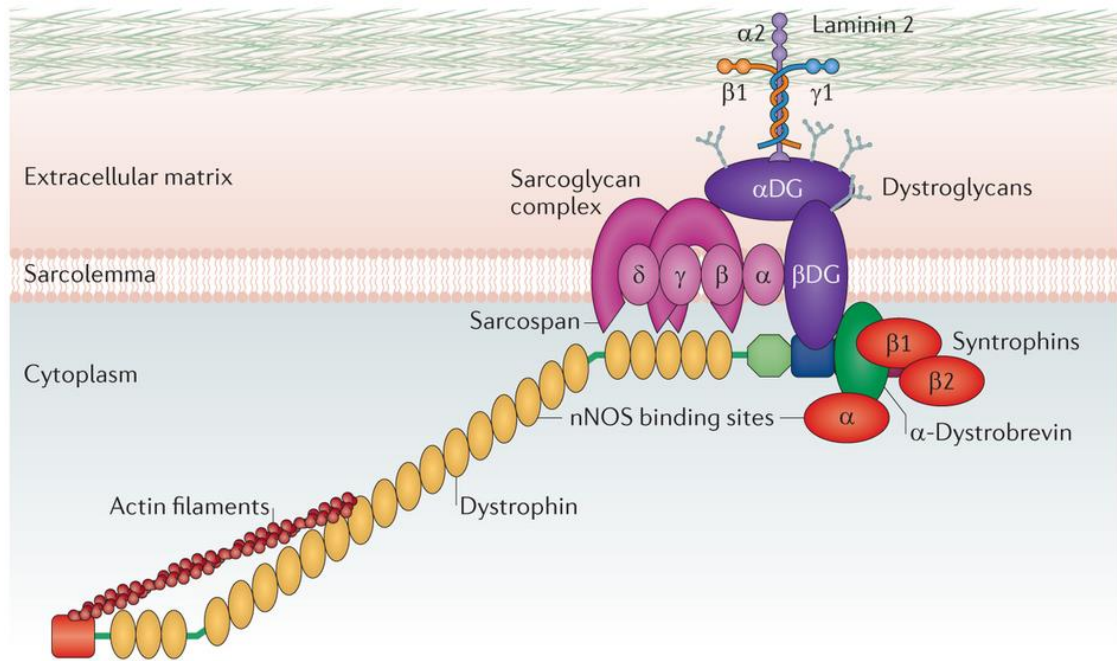
# NGS a Game-Changer



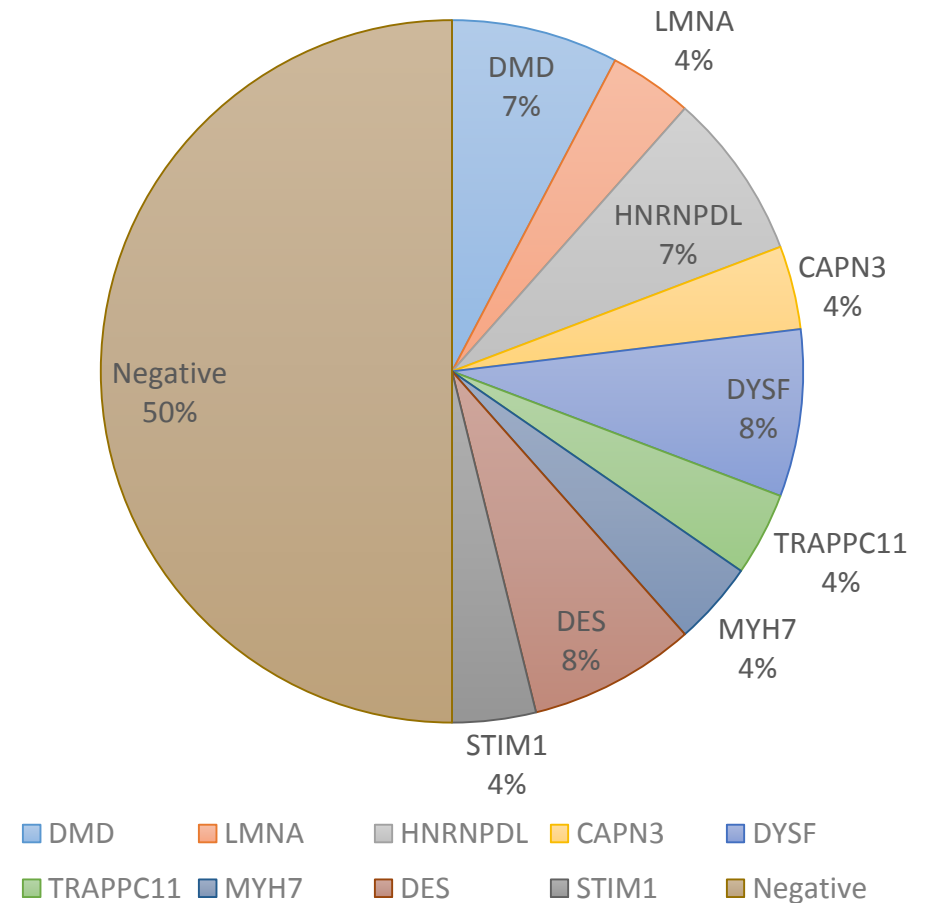
# NTUH 400-gene NGS panel

- Neuromuscular diseases
- Skeletal diseases
- Metabolic diseases

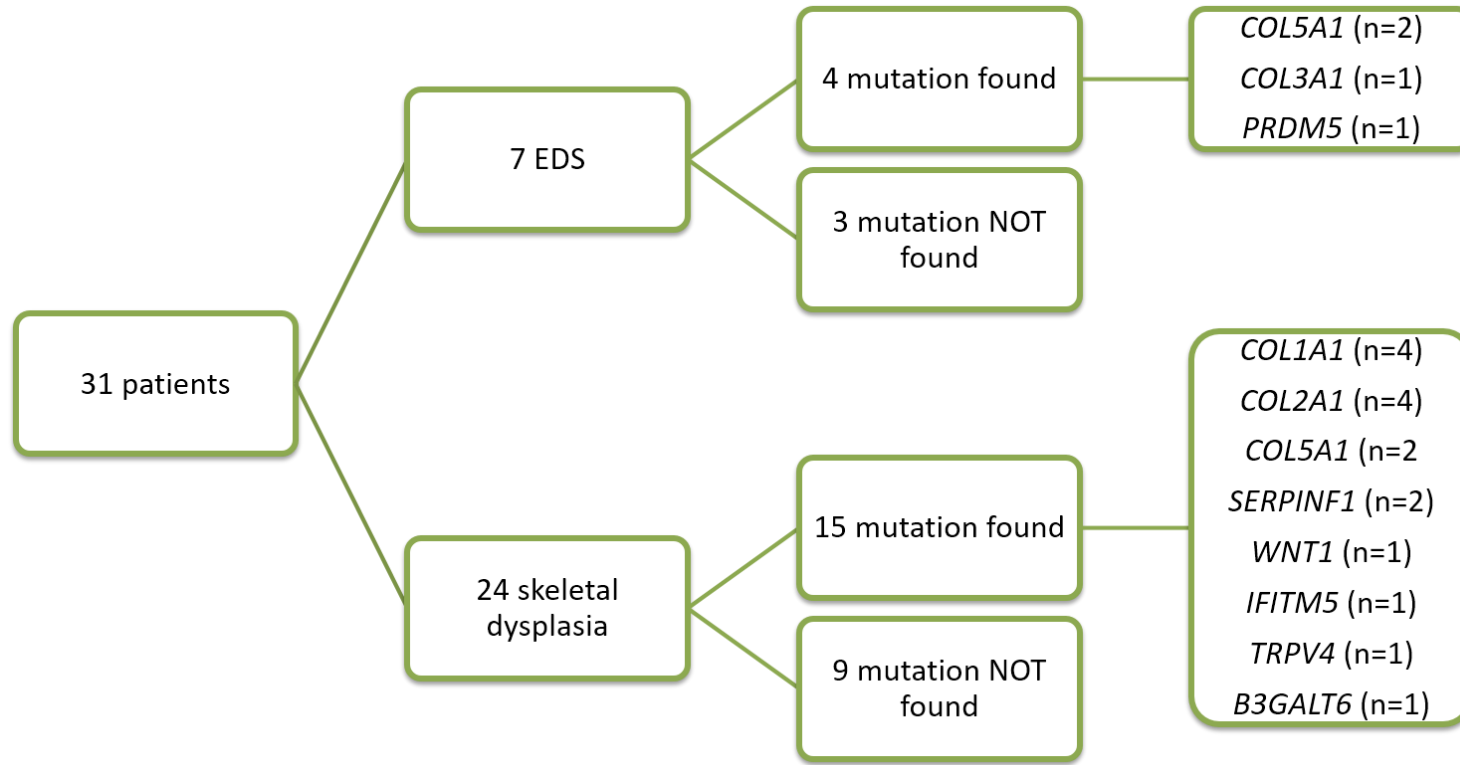
# NGS diagnosis of 26 cases of Muscular Dystrophy in NTUH 2017



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# Diagnosis of osteogenesis imperfect (OI) and Ehlers-Danlos syndrome (EDS) in NTUH



	EDS subtype	Associated genes
1	Classical (cEDS)	<i>COL5A1</i> , <i>COL5A2</i> (rarely <i>COL1A1</i> )
2	Classical-like (clEDS)	<i>TNXB</i>
3	Cardiac-valvular (cvEDS)	<i>COL1A2</i>
4	Vascular (vEDS)	<i>COL3A1</i> (rarely <i>COL1A1</i> )
5	Hypermobile (hEDS)	Unknown
6	Arthrochalasia (aEDS)	<i>COL1A1</i> , <i>COL1A2</i>
7	Dermatosparaxis (dEDS)	<i>ADAMTS2</i>
8	Kyphoscoliotic (kEDS)	<i>PLOD1</i> , <i>FKBP14</i>
9	Brittle cornea syndrome (BCS)	<i>ZNF469</i> , <i>PRDM5</i>
10	Spondylodysplastic (spEDS)	<i>B4GALT7</i> , <i>B3GALT6</i> , <i>SLC39A13</i>
11	Musculocontractural (mcEDS)	<i>CHST14</i> , <i>DSE</i>
12	Myopathic (mEDS)	<i>COL12A1</i>
13	Periodontal (pEDS)	<i>C1R</i> , <i>C1S</i>

# Whole exome sequencing (WES)

Sequencing of more than 200,000 exons  
(> 37 Mb)

# More than 40,000 variants arise from WES



40,000-100,000 variants



**MViewer software and  
Variant Prioritizer**



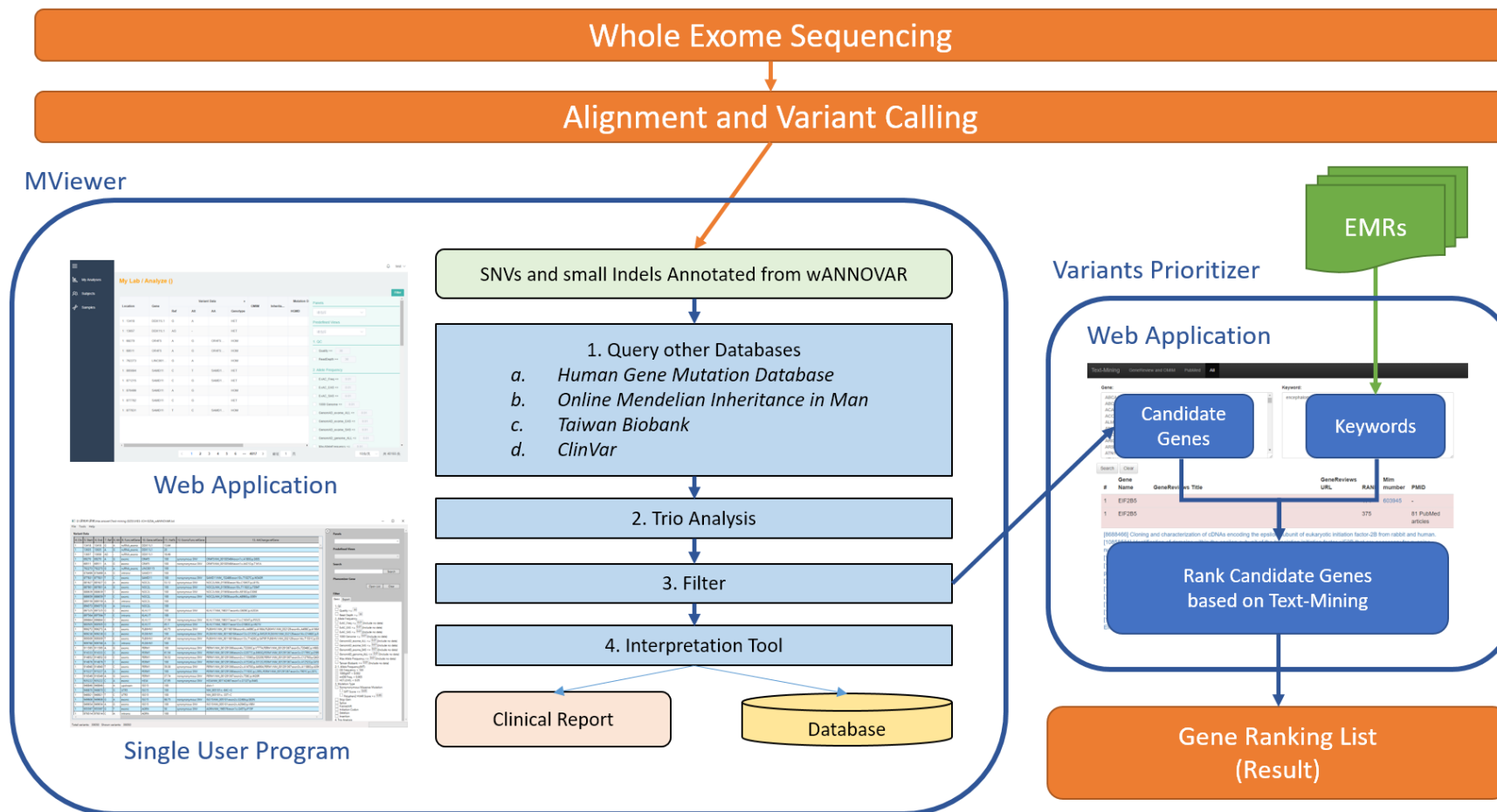
1-2 variants in 1 gene

# Previous turnaround time of WES

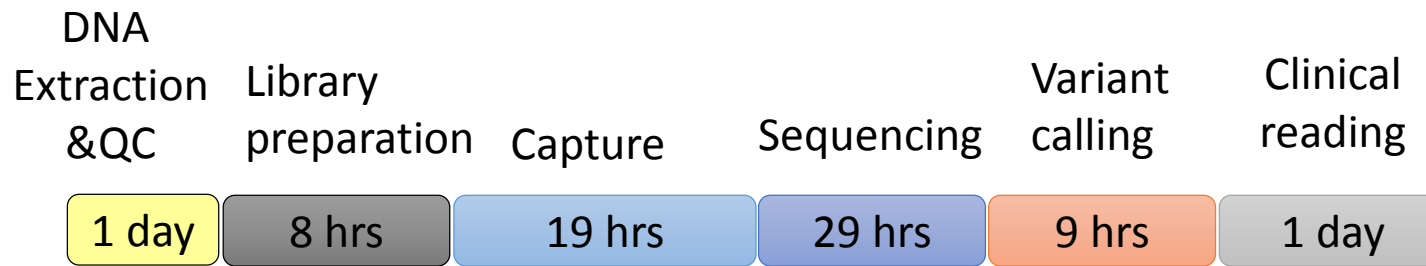
3 months



# The MViewer software: Developed by NTU/NTUH



# Rapid WES trio analysis for infants and children with acute illness (Funded by MOST)



**Turn-around time: 7 days**

# Diagnostic yield: 52.1% (37/71)

	Total (n=71)	Positive (n=37)
Mean age $\pm$ SD	15 $\pm$ 2.9	18 $\pm$ 29.8
Sex (M/F)	40/31	18/18
Turn around time (working days)		
Mean $\pm$ SD	6.0 $\pm$ 1.0	<b>5.8<math>\pm</math>0.9</b>
Median (Range)	4.3-9.9	4.3-8.4

**55.6% (20/36) of the cases are first identified in Taiwan**

# Benefits from molecular diagnosis

HPO	Positive cases	Specific treatment (%)		Total cases	Redirection of treatment (%)
Nervous system	11	6 (55%)		22	8 (36%)
Cardiovascular system	3	3 (100%)		13	2 (15%)
Metabolism/homeostasis	10	8 (80%)		16	6 (38%)
Immune system	3	3 (100%)		8	3 (38%)
Liver	3	3 (100%)		5	3 (60%)
Genitourinary system	2	2 (100%)		2	2 (100%)
Musculature	2	0 (0%)		2	2 (100%)
Multiple congenital anomaly	3	0 (0%)		3	1 (33%)

# Prizes and exhibitions



# Thanks

- Ministry of science and technology
- All the team members of NTU Medical Genetics
- Referring physicians
- Patients and families

