

GENETICS 101 & WHOLE GENOME SEQUENCING

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DREAM IT.
HOPE IT.

National Ataxia Foundation

Annual Ataxia Conference

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Hosted by the Southeast Region

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PRESENTER DISCLOSURES

- Vikram Shakkottai
- No relationships to disclose

WHAT IS A GENE

- A gene is the basic physical and functional unit of heredity.
- Genes, which are made up of DNA, act as instructions to make molecules called proteins.
- Every person has two copies or alleles of each gene, one inherited from each parent.

INHERITANCE

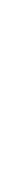
Father



Mother



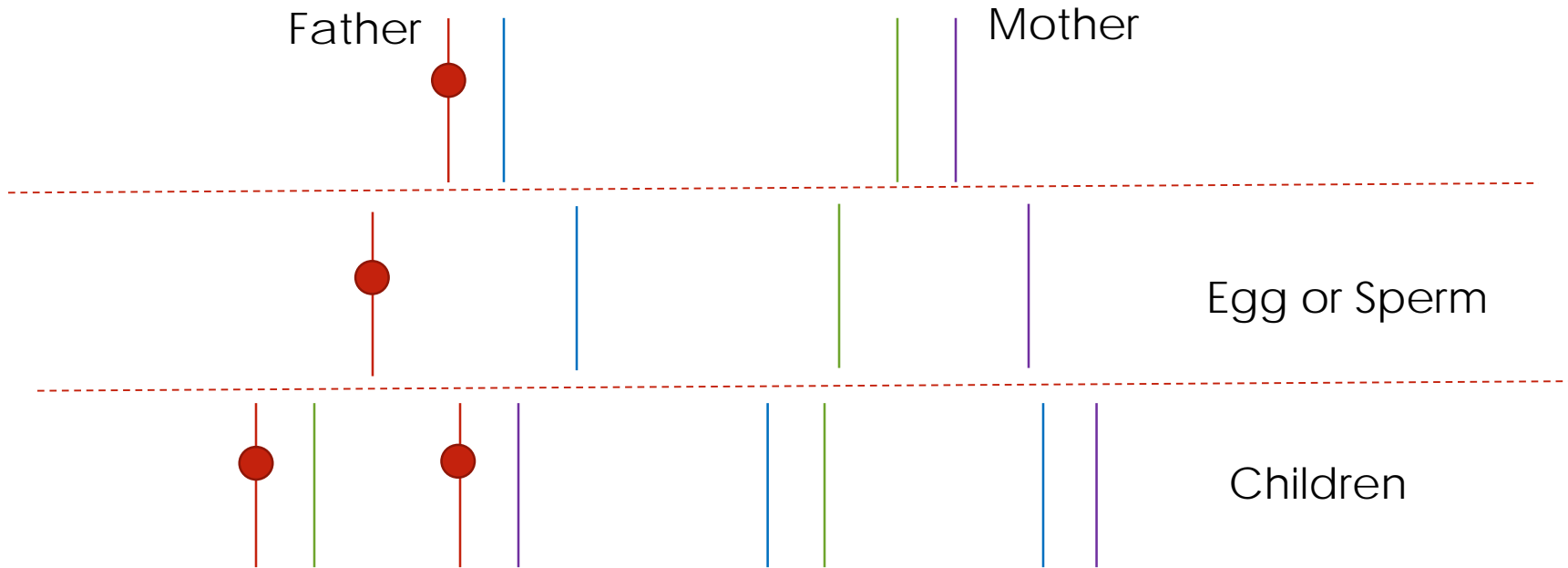
Egg or Sperm



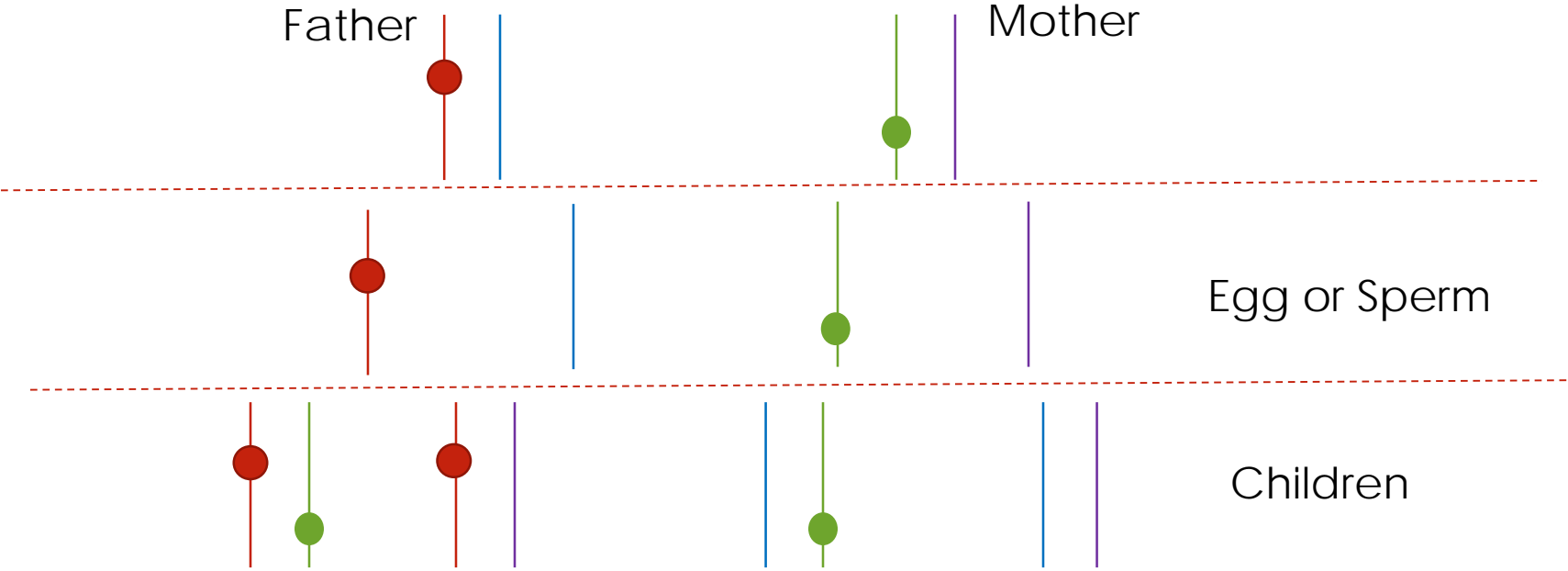
Children



DOMINANT DISEASE

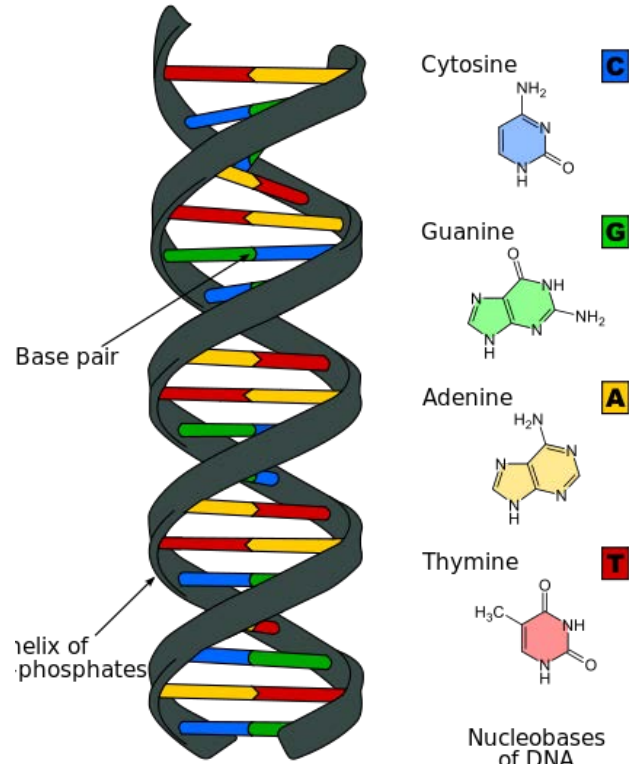


RECESSIVE DISEASE



WHAT IS A GENE MADE OF?

- DNA
- Letters-A,T,G,C
- 3 letters made a code for an amino acid



DNA
Deoxyribonucleic acid

Wikimedia commons

THE TRIPLET CODE

- A,T(U),G,C
- Examples: AAA-Lysine
- CAG-Glutamine

		Second letter					
		U	C	A	G		
First letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } UCC } Ser UCA } UCG }	UAU } Tyr UAC } UAA } Stop UAG } Stop	UGU } Cys UGC } UGA } Stop UGG } Trp	U C A G	
	C	CUU } CUC } Leu CUA } CUG }	CCU } CCC } Pro CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } CGC } Arg CGA } CGG }	U C A G	
	A	AUU } AUC } Ile AUA } AUG } Met	ACU } ACC } Thr ACA } ACG }	AAU } Asn AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G	
	G	GUU } GUC } Val GUA } GUG }	GCU } GCC } Ala GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } GGC } Gly GGA } GGG }	U C A G	
						Third letter	



MUTATION

- A defect in a gene
- Can be inherited or arise *de novo*

MUTATION

- AUGCAGAUG
- AUG CAG AUG
- Methionine-Glutamine-Methionine
- AUG **A** CAGAUG
- AUG AAG AUG
- Methionine-**Lysine**-Methionine

		Second letter							
		U	C	A	G				
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U C A G
	UUC		UCC		UAC		UGC		
	UUA	Leu	UCA		UAA	Stop	UGA	Stop	
	UUG		UCG		UAG	Stop	UGG	Trp	
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U C A G
	CUC		CCC		CAC		CGC		
	CUA	Leu	CCA		CAA	Gln	CGA	Arg	
	CUG		CCG		CAG		CGG		
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U C A G
	AUC		ACC		AAC		AGC		
	AUA	Met	ACA		AAA	Lys	AGA	Arg	
	AUG		ACG		AAG		AGG		
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U C A G
	GUC		GCC		GAC		GGC		
	GUA	Val	GCA		GAA	Glu	GGA	Gly	
	GUG		GCG		GAG		GGG		

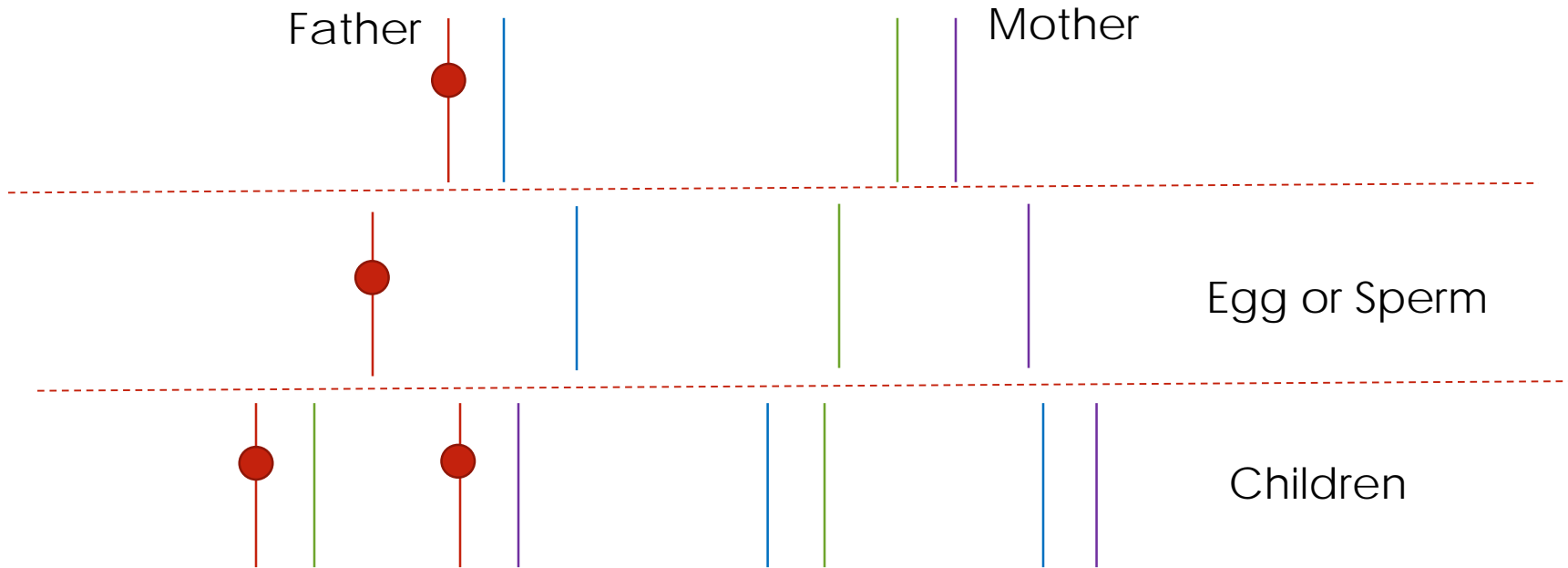
REPEAT DISORDERS

- Stretch of repeating sequence
- For example CAG CAG CAG CAG 4 repeats
- Mutation here-CAG CAG CAG CAG CAG CAG 6 repeats

SCA

- Dominantly inherited ataxia
- Numbering is based on order of discovery
- For example, SCA1 was the first to be identified

DOMINANT DISEASE



SCA

- Polyglutamine or CAG expansions
- SCA1, 2, 3, 6, 7, 17

		Seond letter								
		U	C	A	G					
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U	
	UUC		UCC		UAC		UGC		C	
	UUA	Leu	UCA	UAA	Stop	UGA	Stop	UGG	Trp	A
	UUG		UCG							UAG
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U	
	CUC		CCC		CAC		CGC		C	
	CUA	CAG	CCA	CAG	CAG	CAG	CAG	CAG	A	
	CUG		CCG						CAG	CAG
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U	
	AUC		ACC		AAC		AGC		C	
	AUA	Met	ACA	AAG	AAA	Lys	AGA	Arg	A	
	AUG		ACG				AAG		AGG	G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U	
	GUC		GCC		GAC		GGC		C	
	GUA	GUG	GCA	GAG	GAA	Glu	GGA	GGG	A	
	GUG		GCG				GAG		GGG	G



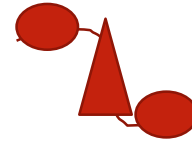
REPEATS

- Toxicity if repeats are too long

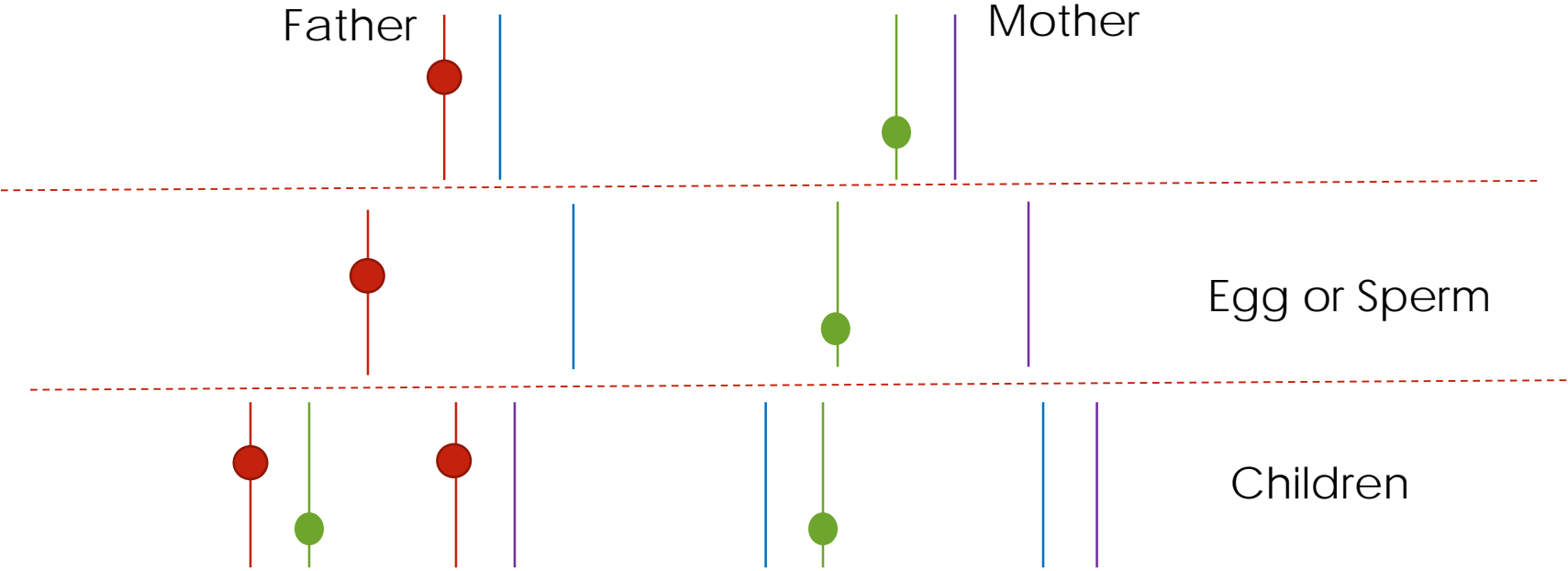
DOMINANT DISEASE

- Point mutations
 - AUGCAGAUG
 - AUG CAG AUG
 - Methionine-Glutamine-Methionine

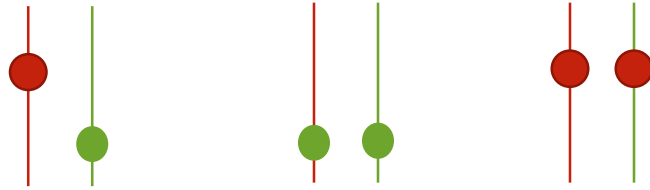
- AUGACAGAUG
- AUG AAG AUG
- Methionine-Lysine-Methionine



RECESSIVE DISEASE



RECESSIVE DISEASE



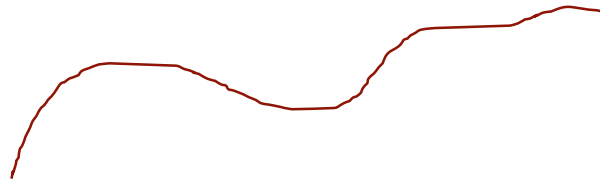
2 mutations-one on each copy of the gene



RECESSIVE ATAXIA

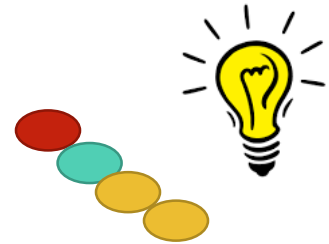
- Friedreich ataxia
- Also a repeat disorder-but non coding

NON-CODING REPEATS



RNA (the code)

Translational
machinery



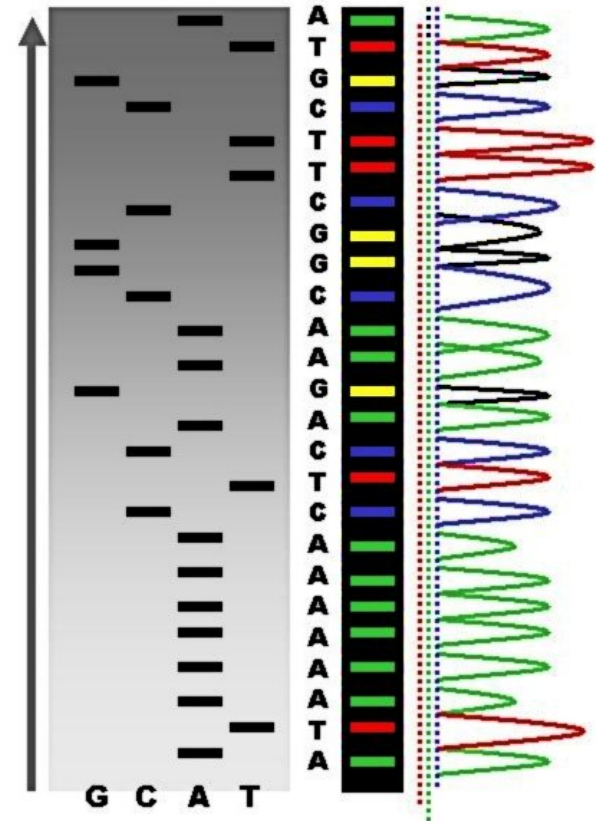
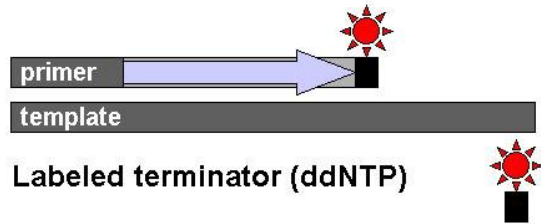
Protein



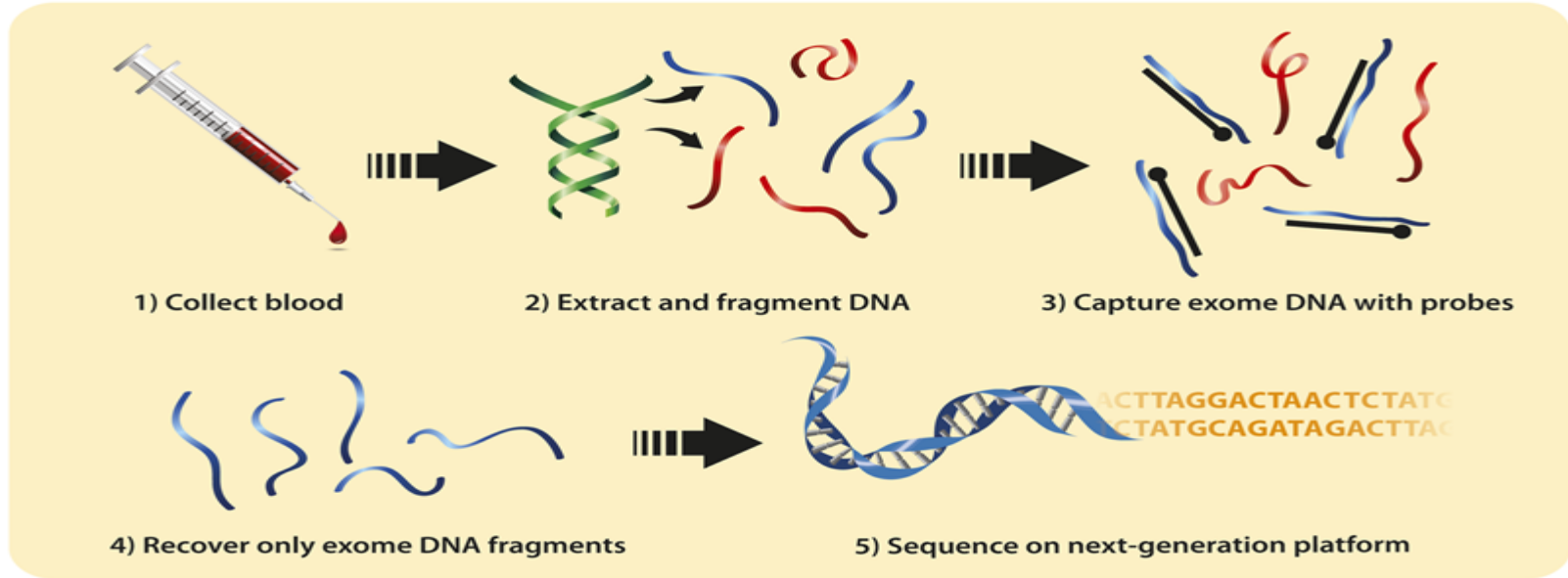
Translational
machinery

No protein

GENE SEQUENCING



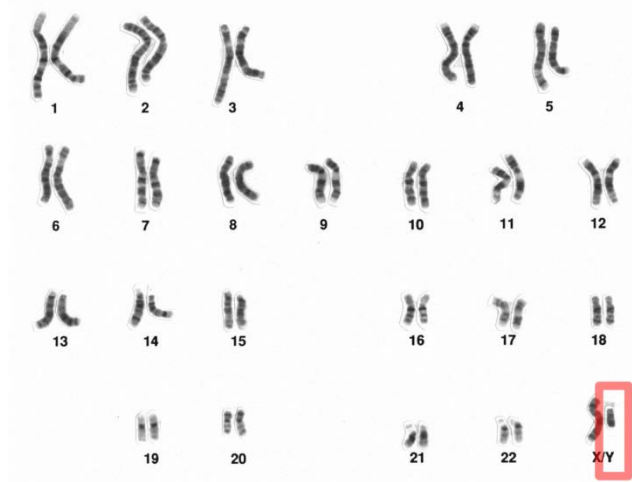
WHOLE EXOME SEQUENCING



Paria N, Copley LA, Herring JA, Kim HK, Richards BS, Sucato DJ, Wise CA, Rios JJ. (2013) **Whole-exome sequencing: discovering genetic causes of orthopaedic disorders.** *J Bone Joint Surg Am* 95(23), e1851-8

EXOME

- Simplified definition: The part of the genome that codes for protein



1% of the genome

WHY EXOME SEQUENCING?

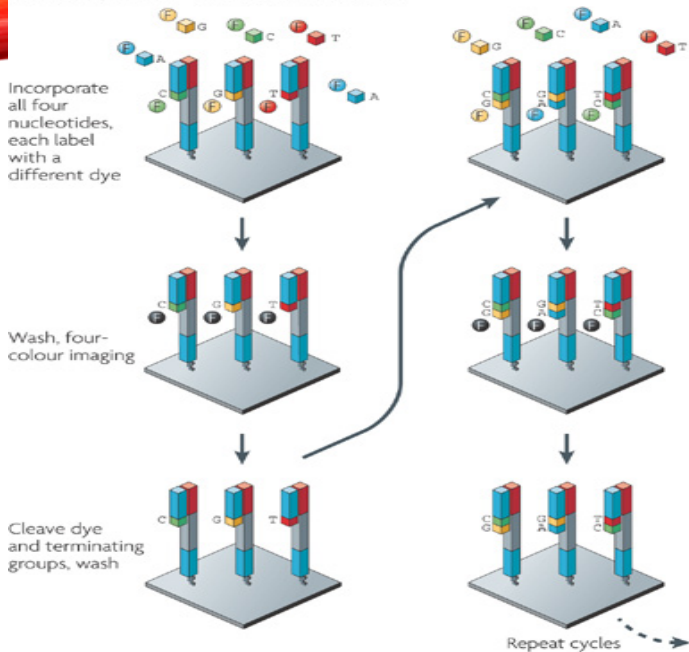
- A way to survey all the coding genes at the same time
- If you don't know where to look, look at it all
- Over 300 gene mutations can cause ataxia
- Can be cost effective



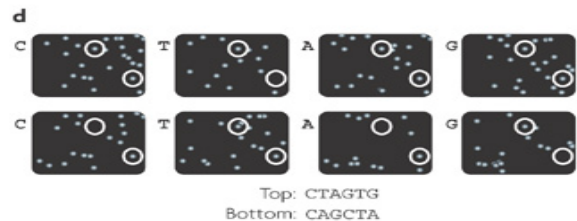
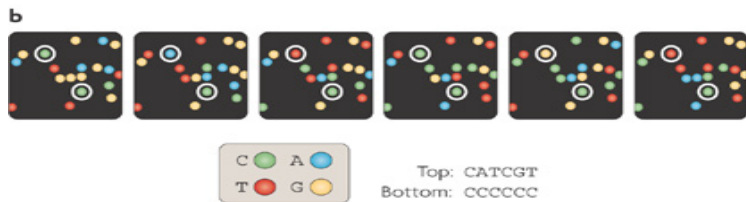
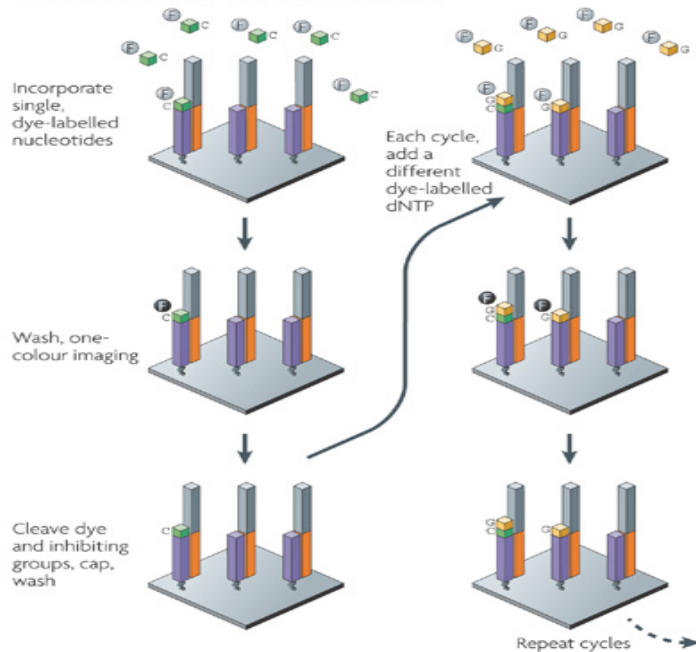
NGS PLATFORMS

- 454 Life Sciences
- Illumina
- Applied BioSystems
- Helicos Biosciences
- Danaher Motion
- Oxford Nanopore Technologies
- Pacific Biosciences.

a Illumina/Solexa — Reversible terminators



c Helicos BioSciences — Reversible terminators

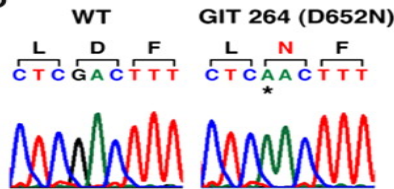


A

Reference	P L N I E V P K I S L H S L I L [*] F S A V S F L D V S S V R G L K
GIT 264-1	P L N I E V P K I S L H S L I L N F S A V S F L D V S S V R G L K
Sense	5' - CCTCTCAACATTGAGGTCCCAAAATCAGCCTCCACAGCCTCATTCTGAC [*] TTTTTCAGCAGTGTCTTTTCTTGATGTTTCTTCAGTGAGGGGCCTTAAA-3'
Antisense	3' - GGAGAGTTGTAAC [*] TCCAGGGGTTTTAGTCGGAGGTGTCGGAGTAAGAGCTGAAAAGTCGTACAGGAAAGAACTACAAAGAAGTCACTCCCCGGAATT-5'

3' - GGAGCGTTGTAAC^{*}TCCAGGGGTTTTAGTCGGAGGTGTCGGAGTAAGAGTT-5'
 3' - GTTGTAACTCCAGGGGTTTTAGTCGGAGGTGTCGGAGTAAGAGTTGAAAA-5'
 3' - AACTCCAGGGGTTTTTCGTCCGAGGGGTCGGAGTAAGAGTTGAAAAGTCGT-5'
 5' - ctccaggggttttagtcggaggtgtcggagtaagagtgtgaaaagtcgtca-3'
 3' - CCAGGGGTTTTAGTCGGAGGTGTCGGAGTAAGAGTTGAAAAGTCGTACACA-5'
 5' - ggggttttagtcggaggtgtcggagtaagagtgtgaaaagtcgtcacagga-3'
 3' - TTTTGGTGGGAGGTGTCGGAGTAAGAGTTGAAAAGTCGTACAGGAAAG-5'
 3' - TTTAGTCGGAGGTGTCGGAGTAAGAGTTGAAAAGTCGTACAGGAAAGAA-5'
 3' - GTCGAGGGCGTCGGAGTAAGAGTTGAAAAGTCGTACAGGAAAGAACTAC-5'
 5' - cggaggtgtcggagtaagagtgtgaaaagtcgtcacaggaagaactacaa-3'
 3' - GGGGGGTCGGAGTAAGAGTTGAAAAGTCGTACAGGAAAGAACTACAAA-5'
 5' - gaggtgtcggagtaagagatgaaaagtcgtcacaggaagaactacaaag-3'
 3' - GGGTCGGAGTAAGAGTTGAAAAGTCGTACAGGAAAGAACTACAAAGAAG-5'
 5' - tcggagtaagagtgtgaaaagtcgtcacaggaagaactacaaagaagtca-3'
 3' - GAGTAAGAGTAGAAAAGTCGTACAGGAAAGAACTACAAAGAAGTCACTC-5'
 5' - agagtgtgaaaagtcgtcacaggaagaactacaaagaagtcactccccgg-3'
 3' - GTTAAAAGTCGTACAGGAAAGAACTACAAAGAAGTCACTCCCCGGAAT-5'

B



C

D652

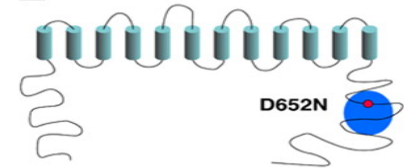
H.s.	S	L	I	L	D	F	S	A	V
M.m.	S	L	I	L	D	F	S	A	V
O.c.	S	L	I	L	D	F	S	A	V
B.t.	S	L	I	L	D	F	S	A	V
G.g.	S	I	V	L	D	F	S	A	V
X.l.	S	I	I	L	D	F	G	H	V
D.r.	S	L	I	L	D	F	C	A	V
D.m.	V	L	V	L	D	F	S	M	L
C.e.	H	I	I	I	D	C	S	T	I

D

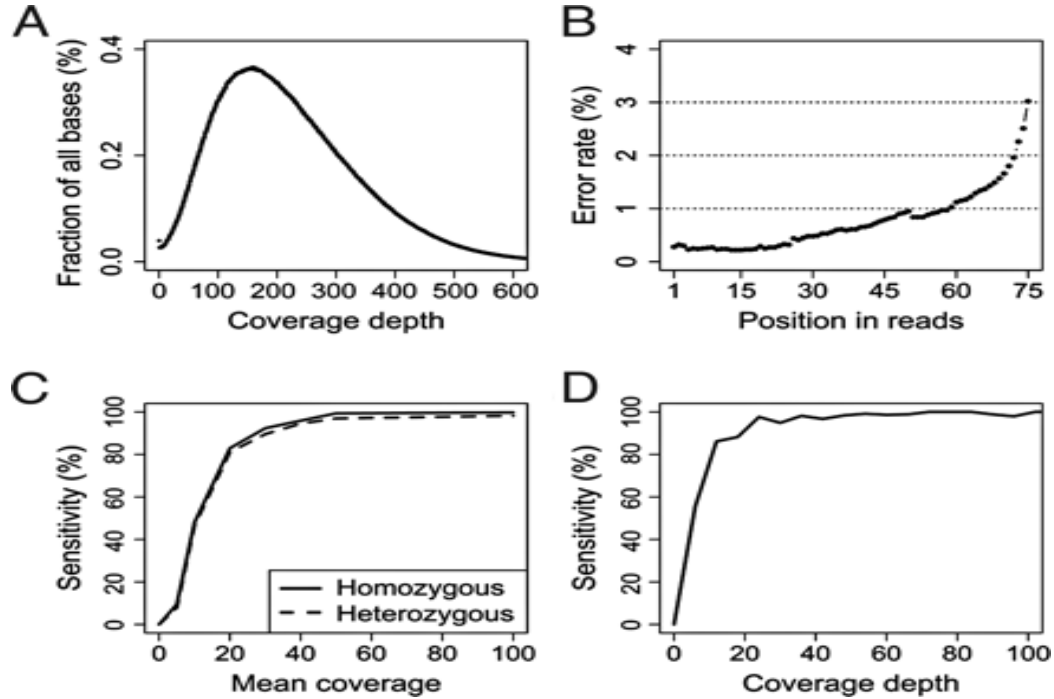
D652

SLC26A3	S	L	I	L	D	F	S	A	V
SLC26A1	T	V	V	I	D	C	A	P	L
SLC26A2	T	I	V	I	D	C	S	A	I
SLC26A4	S	L	V	L	D	C	G	A	I
SLC26A5	T	V	I	L	D	F	T	Q	V
SLC26A6	S	L	I	L	D	L	G	A	L
SLC26A7	Y	L	I	L	D	C	S	G	F
SLC26A8	T	I	I	L	D	F	S	M	V
SLC26A9	T	L	I	L	D	M	S	G	V
SLC26A11	C	L	V	L	E	C	T	H	V

E



DEPTH OF COVERAGE





QUESTIONS?