

Understanding Diseases of Mitochondrial DNA Maintenance

May 10, 2024

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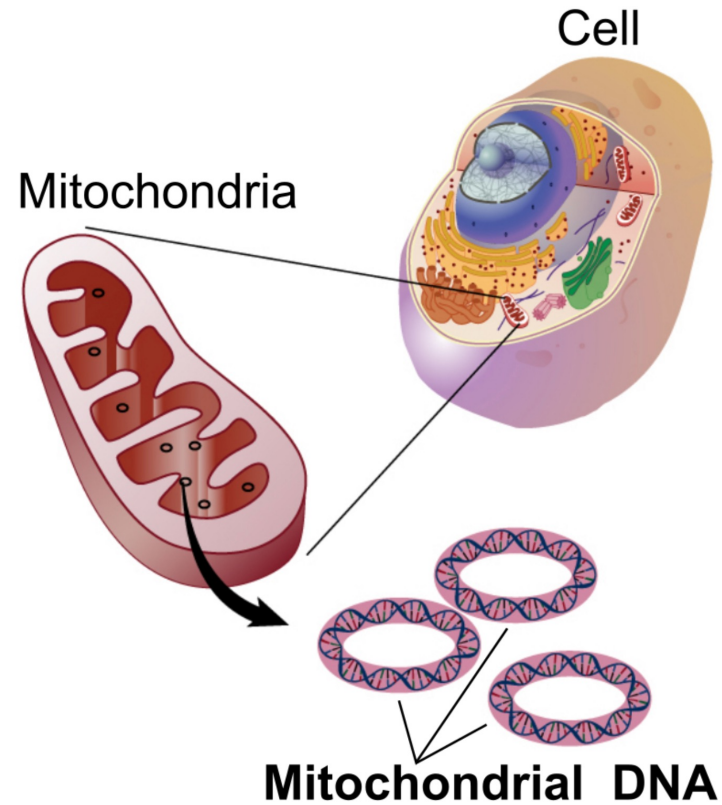
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Outline of Talk

- **Function of mitochondrial DNA (mtDNA)**
- **How mtDNA is copied (POLG, POLG2, TWNK, SSBP1)**
- **How mutations arise in mitochondrial DNA, the natural evolution of mtDNA**
- **Genetic diseases (POLG related diseases) that affect mtDNA replication**
- **MtDNA mutagenesis in POLG related diseases**
- **New therapies on the horizon**

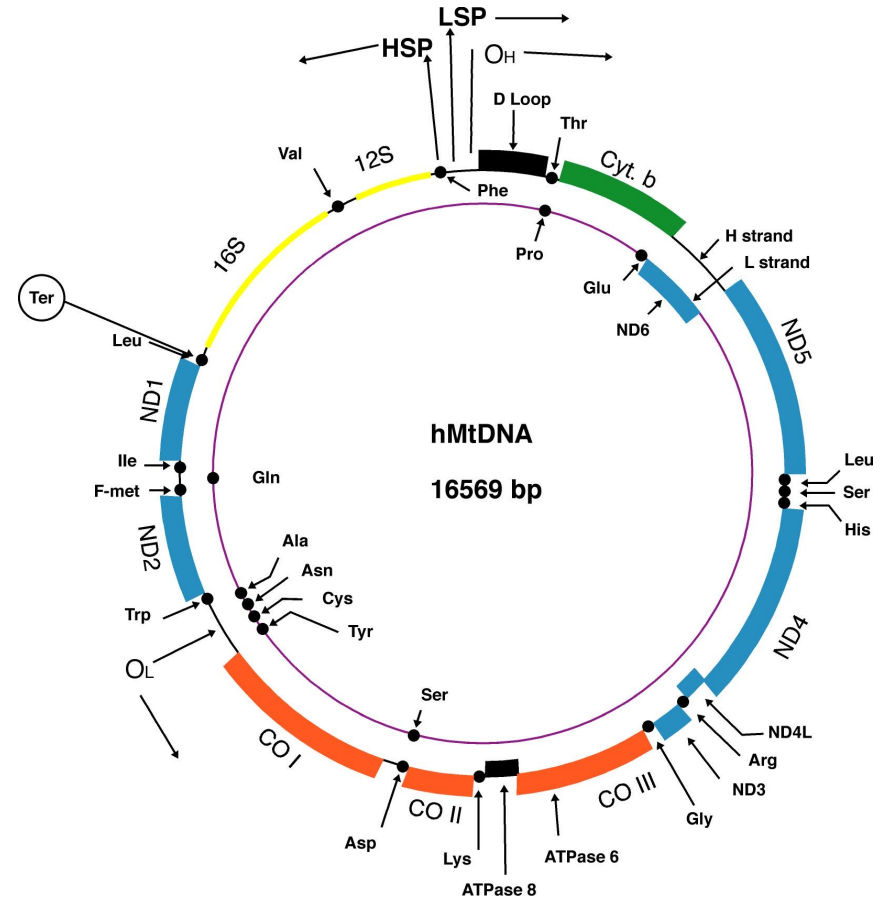
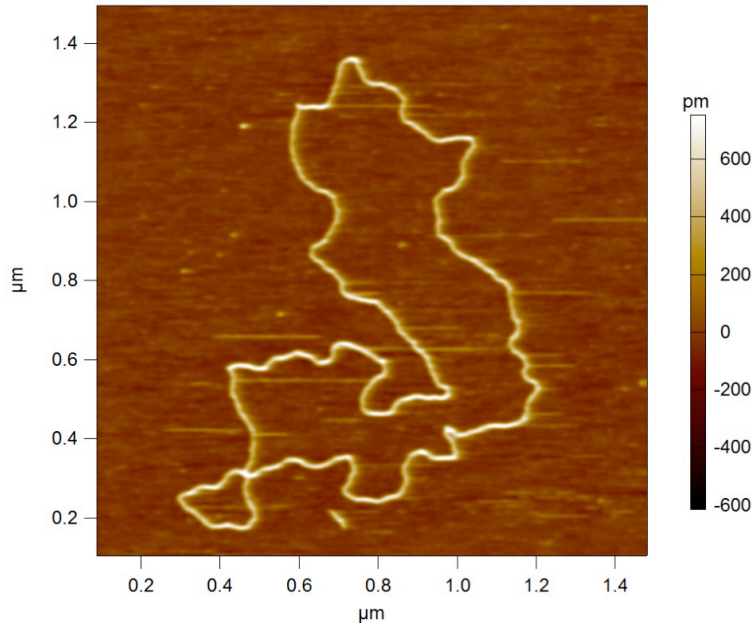
Mitochondria have their own DNA



Human mitochondrial DNA

The mitochondrial genome is a closed, circular DNA.

Maternally inherited



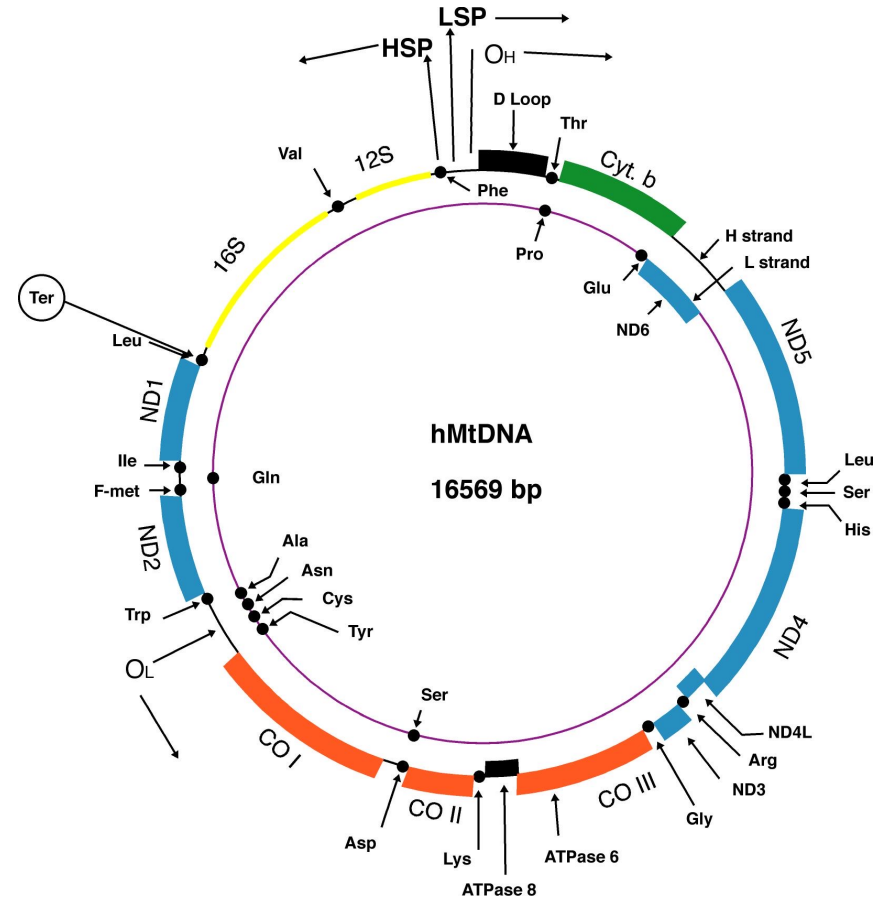
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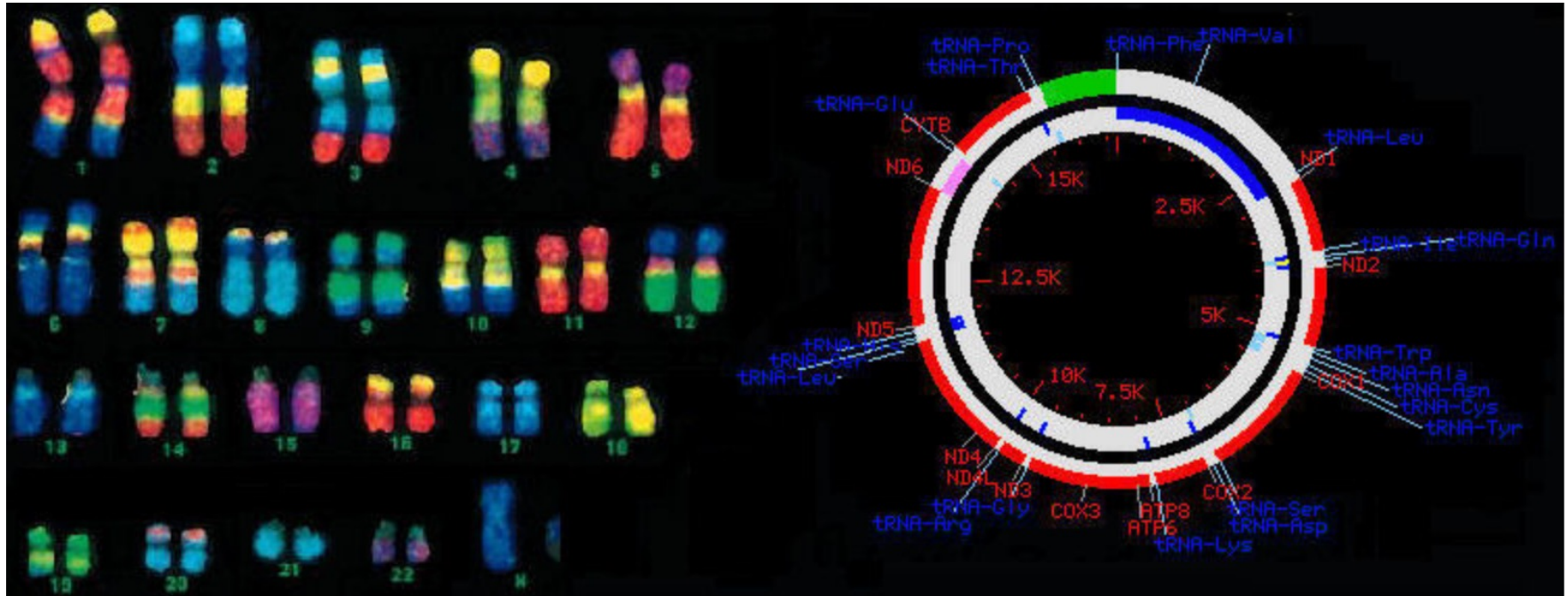
Thousands of copies per cell

MtDNA copy number is very dynamic



Nuclear vs. Mitochondrial DNA

Mitochondrial DNA only accounts for ~0.3% of DNA in a cell



nucDNA genome

~3,000,000 Kbp

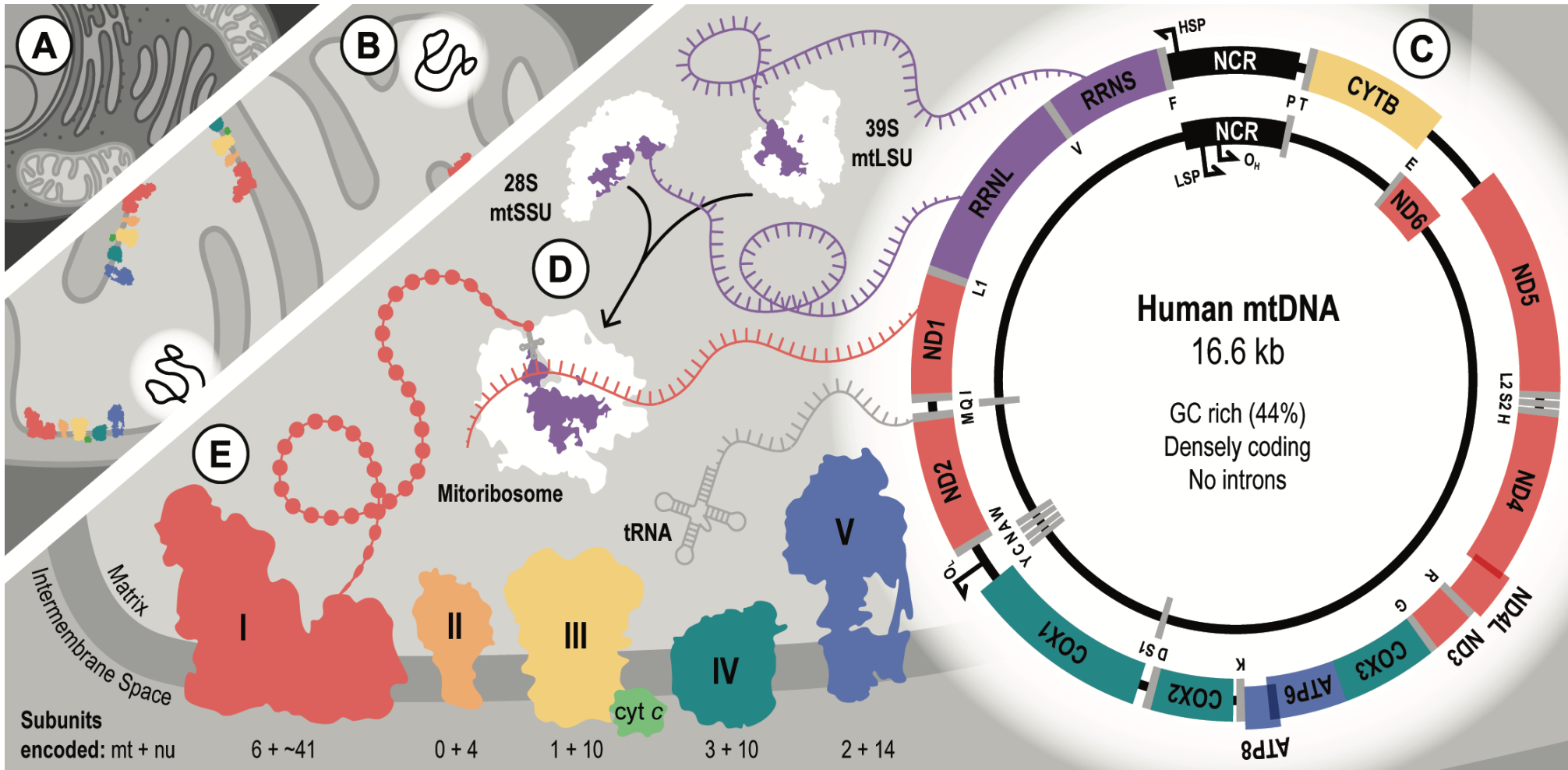
>50,000 genes

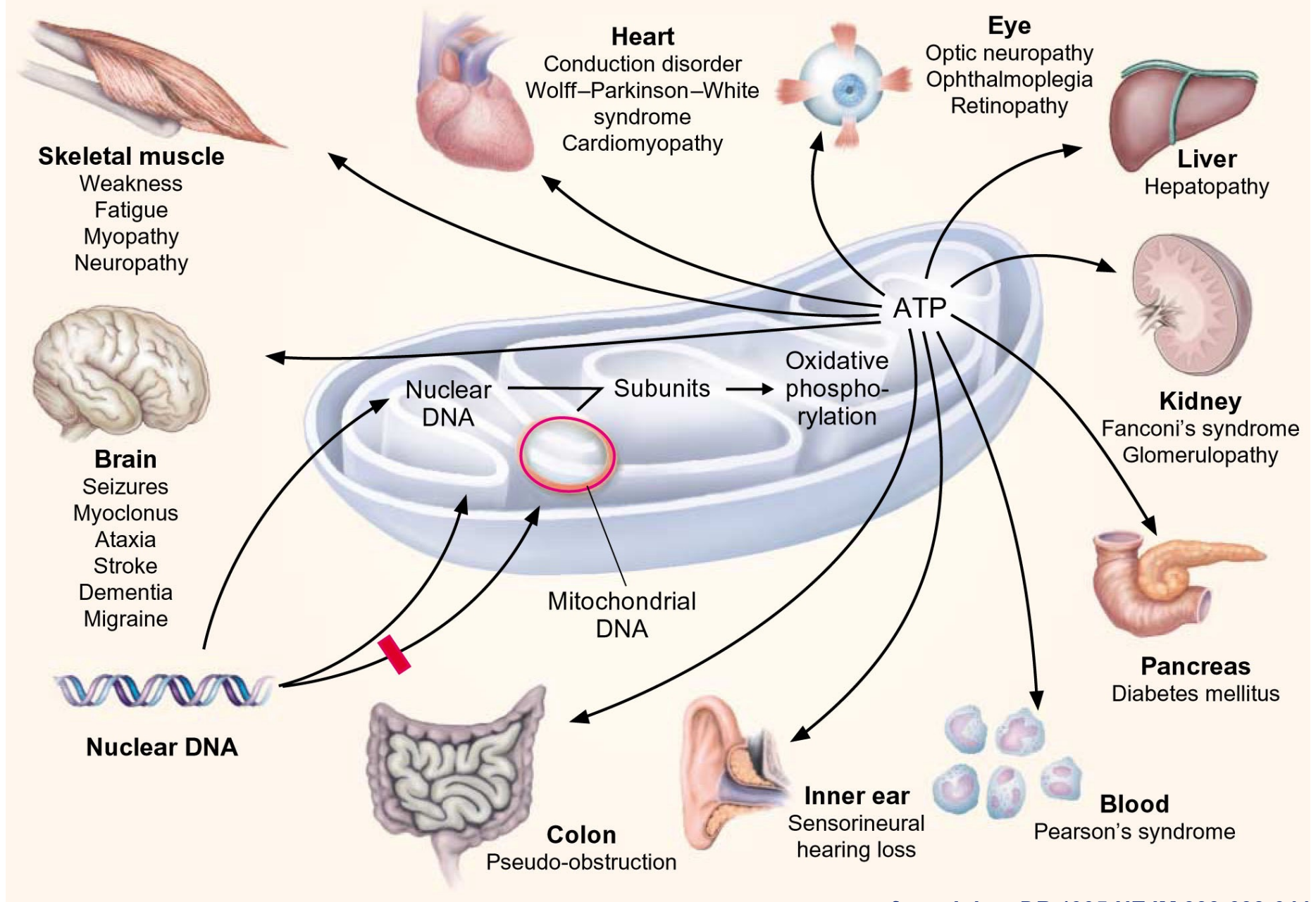
mtDNA genome

≈17 Kbp

38 genes

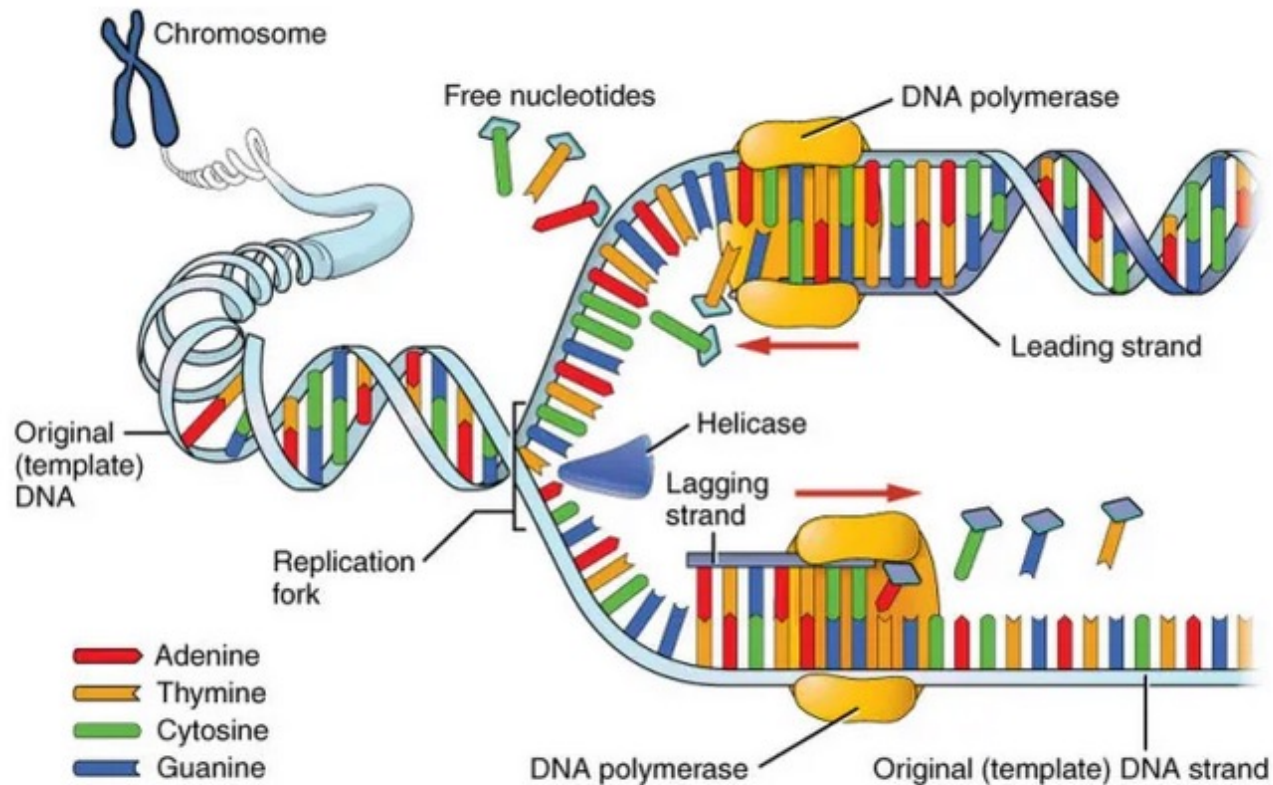
Human mitochondrial DNA





How is DNA copied

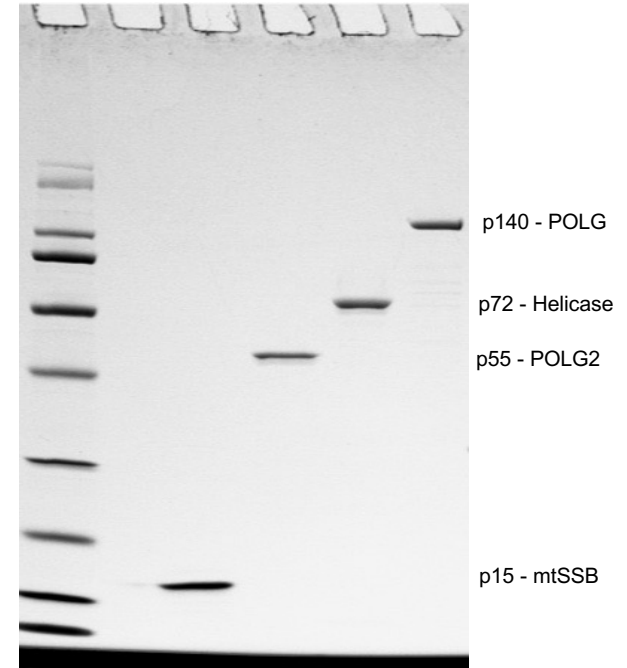
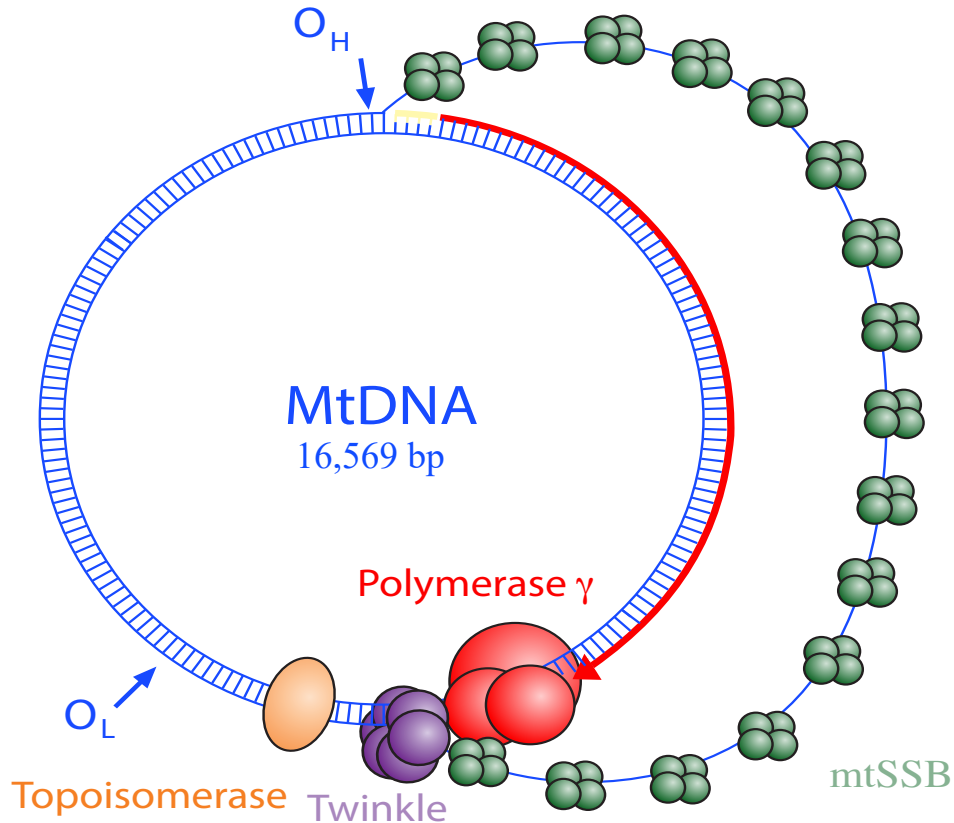
DNA is copied or replicated by enzymes called “DNA Polymerases”



17 Human DNA Polymerases

<u>Polymerase</u>	<u>Family</u>	<u>Chromosome</u>	<u>Mol. Wt. (kDa)</u>	<u>Function/Comments</u>
α (alpha)	B	Xq21.3-q22.1	165	Initiates replication
β (beta)	X	8p12-p11	39	BER, other functions
γ (gamma)	A	15q25	140	Mitochondrial replication & repair
δ (delta)	B	19q13.3-.4	125	Replication, BER, NER, MMR
ϵ (epsilon)	B	12q24.3	255	Replication, checkpoint control
ζ (zeta)	B	6q22	344	γ REV3 homolog, lesion bypass
η (eta)	Y	6p21.1	78	Lesion bypass, <i>XPV</i> , skin cancer susceptibility
θ (theta)	A	3q13.31	300	crosslink repair, <i>Dm308</i> , lesion bypass
ι (iota)	Y	18q21.1	80	Lesion bypass? BER?
κ (kappa)	Y	5q13.1	99	Lesion bypass, mutator when overexpressed
λ (lambda)	X	10q23	64	pol β homolog, meiosis? NHEJ
μ (mu)	X	7p13	55	TdT homolog, NHEJ
ν (nu)	A	4p16.3	100	lesion bypass, crosslink repair?
σ (sigma)	X	5p15	60	TRF4
Rev1	Y	2q11.1-2	125	lesion bypass
TdT	X	10q23-24	57	Terminal transferase
PrimPol	AEP	4q35.1	65	Restart during replication stress, Mitochondrial TLS

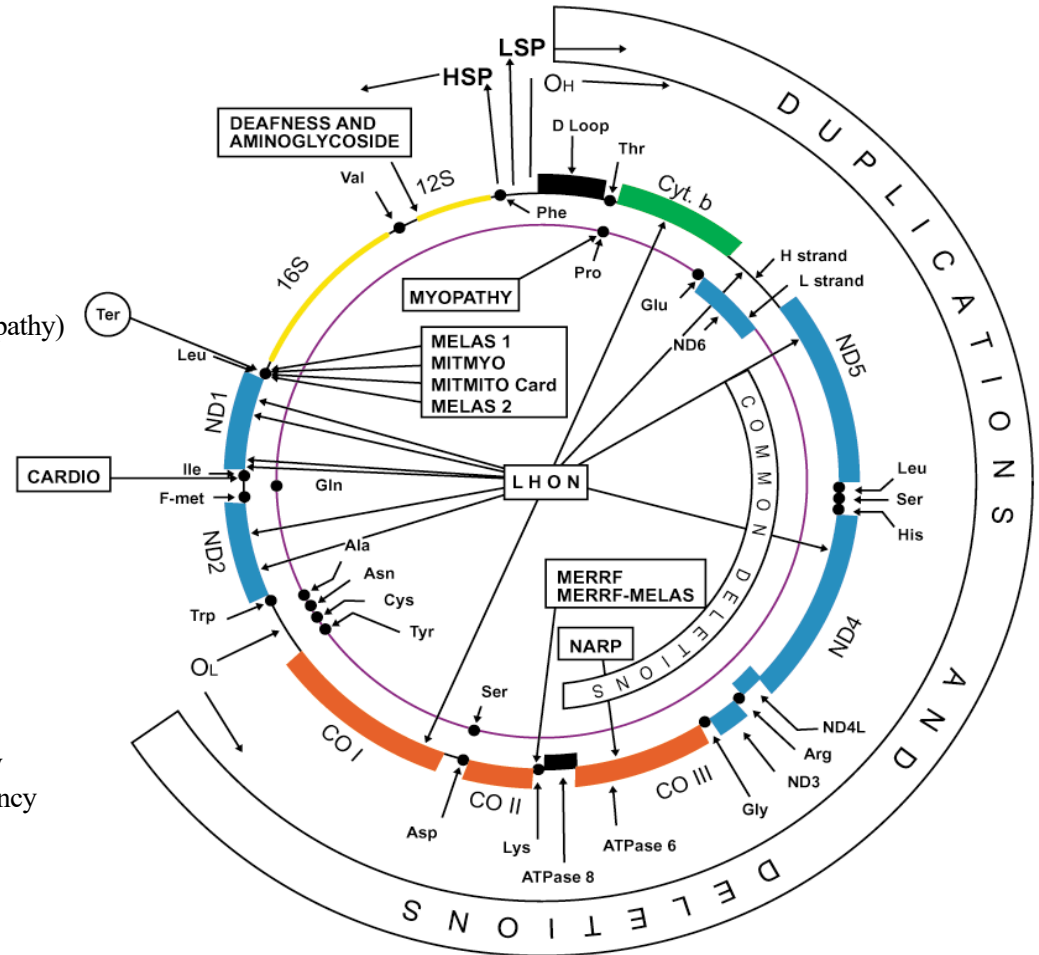
Proteins involved in mitochondrial DNA replication



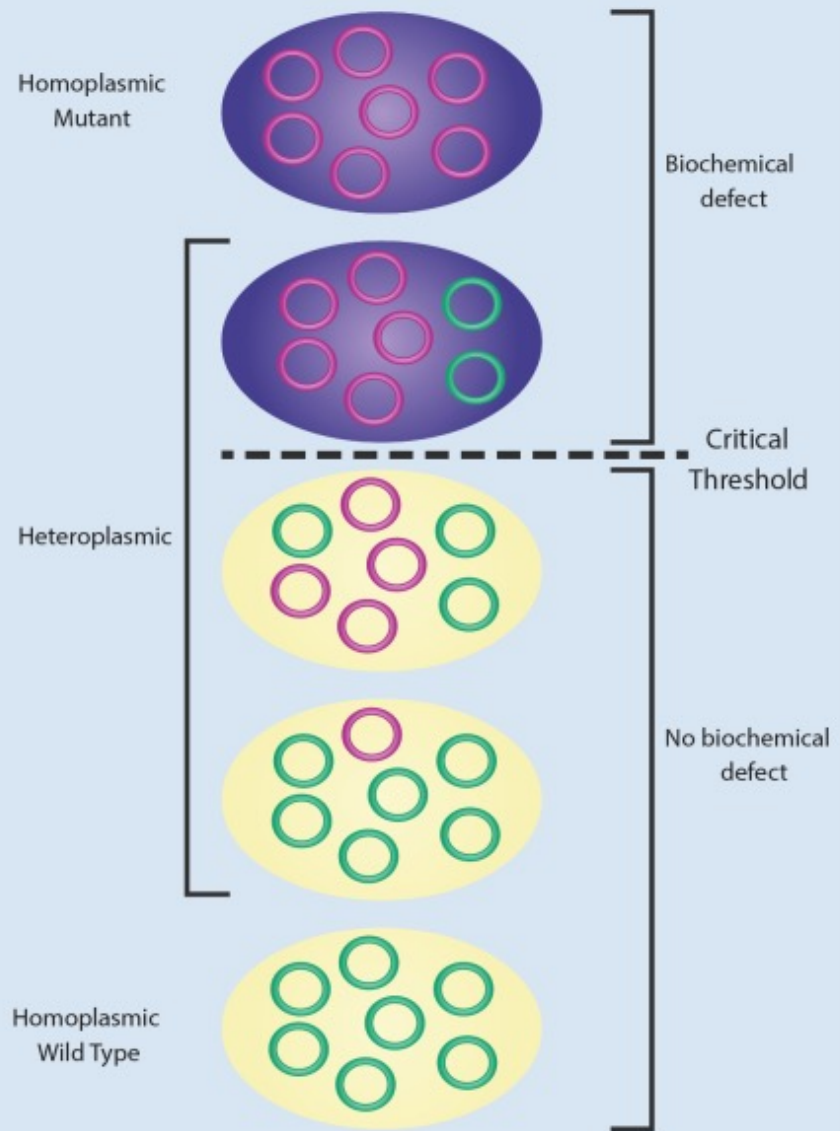
- POLG: p140, catalytic subunit of Pol γ , polymerase and exonuclease**
- POLG2: p55, accessory subunit of Pol γ , functions as processivity factor**
- TWNK: replicative DNA helicase**
- SSBP1: single-stranded DNA binding protein**

Mitochondrial DNA mutations cause or are associated with various diseases

- * Alpers Disease
- * Barth syndrome
- * Beta-oxidation Defects
- * Carnitine-Acyl-Carnitine Deficiency
- * Carnitine Deficiency
- * Co-Enzyme Q10 Deficiency
- * Complex I Deficiency
- * Complex II Deficiency
- * Complex III Deficiency
- * Complex IV Deficiency
- * Complex V Deficiency
- * COX Deficiency
- * CPEO
- * CPT I Deficiency
- * CPT II Deficiency
- * Glutaric Aciduria Type II
- * KSS
- * Lactic Acidosis
- * LCAD
- * LCHAD
- * Leigh Disease or Syndrome
- * LHON
- * LIC (Lethal Infantile Cardiomyopathy)
- * Luft Disease
- * MAD
- * MCAD
- * MELAS
- * MERRF
- * Mitochondrial Cytopathy
- * Mitochondrial DNA Depletion
- * Mitochondrial Encephalopathy
- * Mitochondrial Myopathy
- * MNGIE
- * NARP
- * Pearson Syndrome
- * Pyruvate Carboxylase Deficiency
- * Pyruvate Dehydrogenase Deficiency
- * Respiratory Chain
- * SCAD
- * SCHAD
- * VLCAD

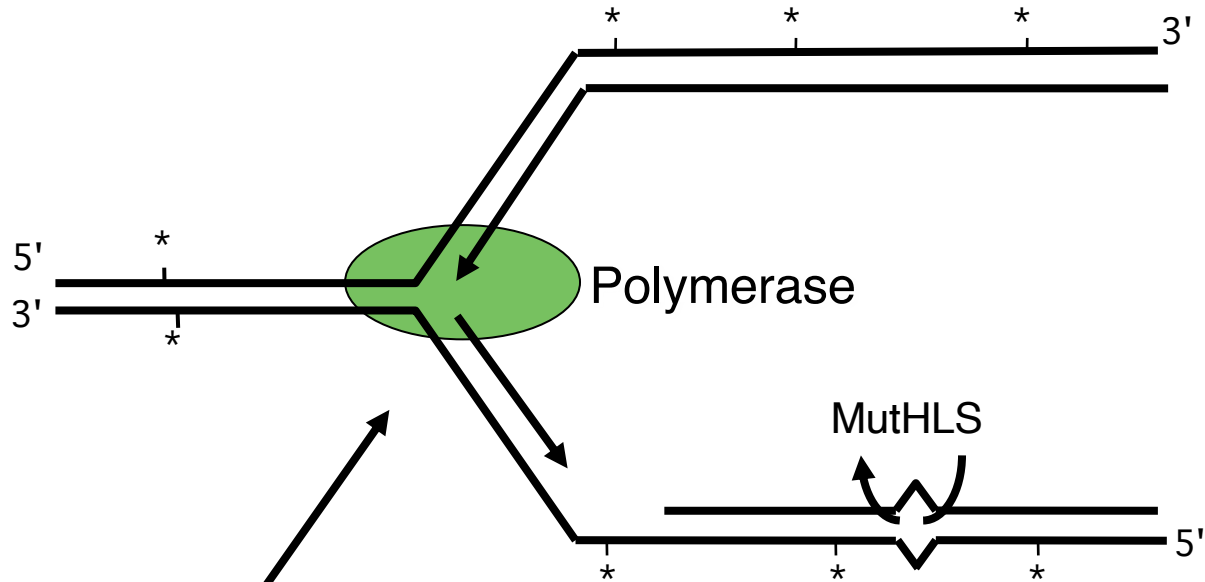


○ = Mutant mitochondrial DNA
○ = Wild Type mitochondrial DNA



MtDNA mutates or evolves faster than nuclear DNA,
with estimates suggesting that MtDNA mutates/evolves
~20-100-fold faster than nuclear DNA

Fidelity of nuclear DNA Replication: 10^{-10}



1. Insertion fidelity (DNA polymerase): 10^{-5}
2. Proofreading (*Exonuclease*): 10^{-2}
3. DNA mismatch repair: 10^{-3}

1. Typing
2. Delete (backspace)
3. Spell check

Fidelity of Human DNA Polymerase γ

- DNA polymerase γ has high DNA synthetic fidelity at single base pairs. (<1 error per 1,000,000 nucleotides synthesized)
- Pol γ proofreading contributes ~100-fold to base substitution and frameshift fidelity.

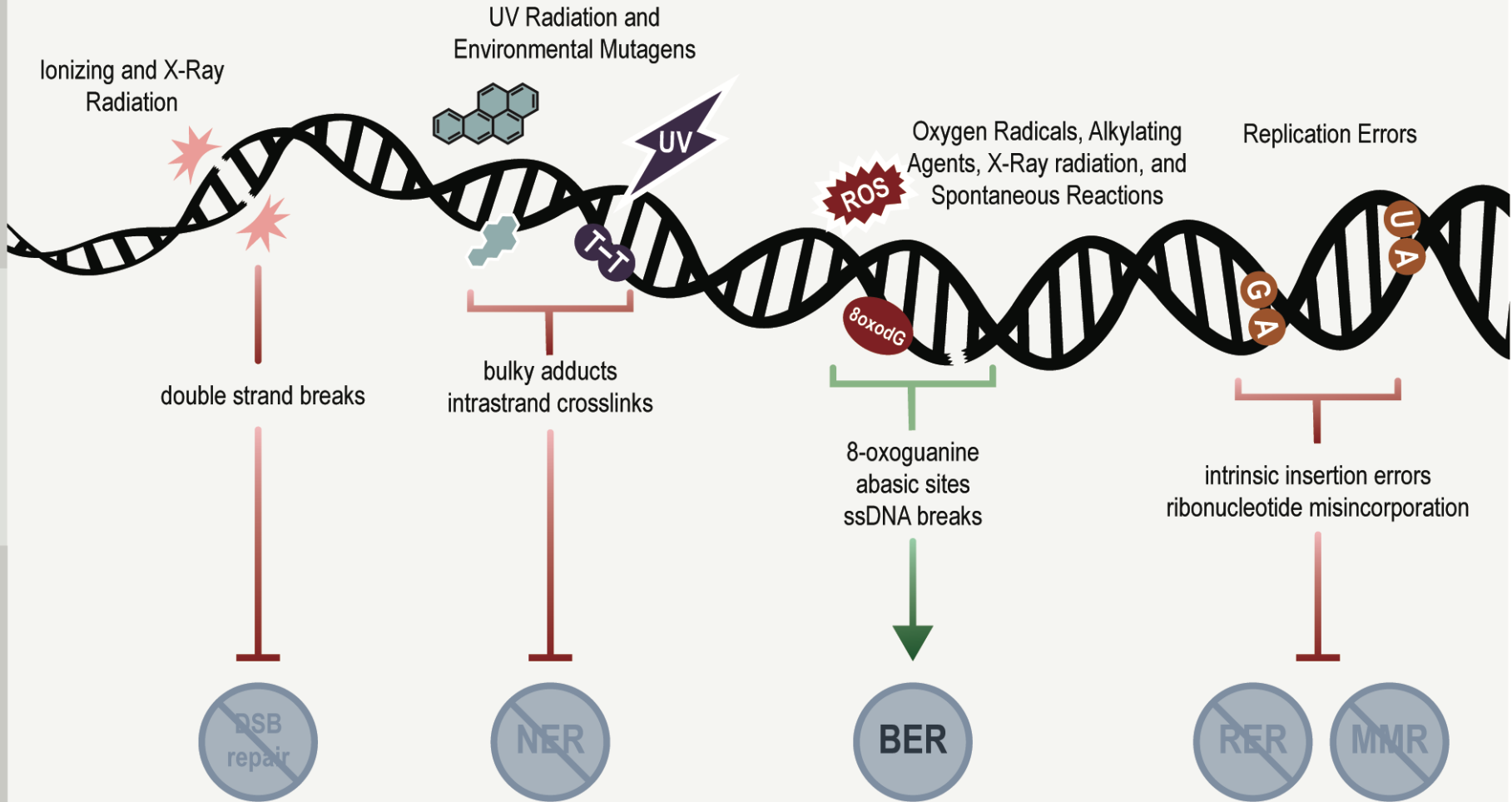
Nuclear and Mitochondrial DNA Repair

Repair system	Nuclear	Mitochondrial
Nucleotide Excision Repair	XPA, XPC, RPA, TFIIH, XPF9, XPG Pol ϵ , PCNA, RFC, DNA ligase I/III	None
Mis Match Repair	hMSH2, hMSH3, hMSH5, hMSH6, hMLH1, PMS2	No clear MMR activity
Base Excision Repair	Base glycosylase, UDG, TDG APE, PARP <u>Short patch repair</u> - pol β <u>Long patch repair</u> - pol δ/ϵ or pol β FEN1, DNA2, PCNA, RFC DNA ligase I/III	UDG, OGG, hMYH APE1 <u>Short patch repair</u> – pol γ <u>Long patch repair</u> – pol γ , FEN1, DNA2, DNA ligase III
Ribonucleotide Excision Repair	Rnase H2	None

Source of DNA Damage

Damage Type

Repair Pathway

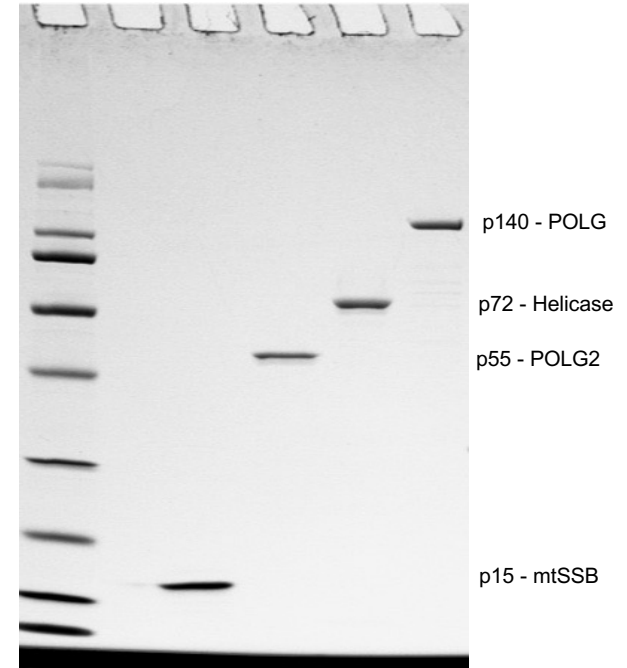
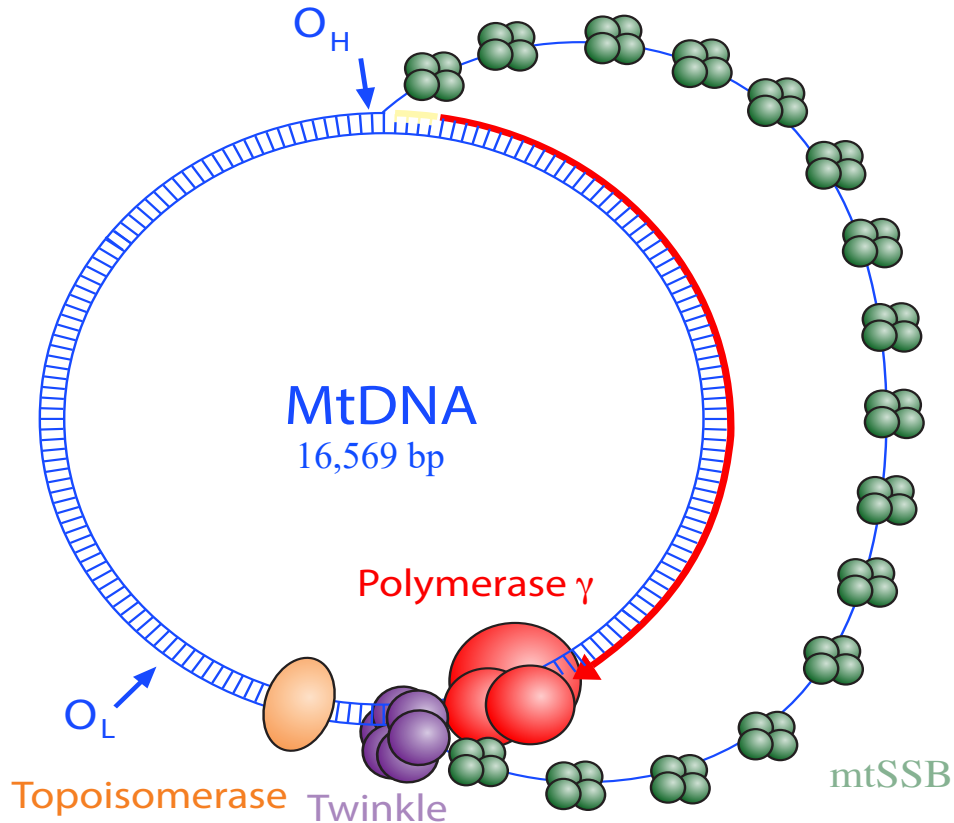


MtDNA mutates or evolves faster than nuclear DNA, with estimates suggesting that MtDNA mutates/evolves ~20-100-fold faster than nuclear DNA

The highly mutation rate is mostly due to the lack of mitochondrial mismatch repair.

**The major driver of mtDNA mutations is
spontaneous errors of mtDNA replication from
POLG**

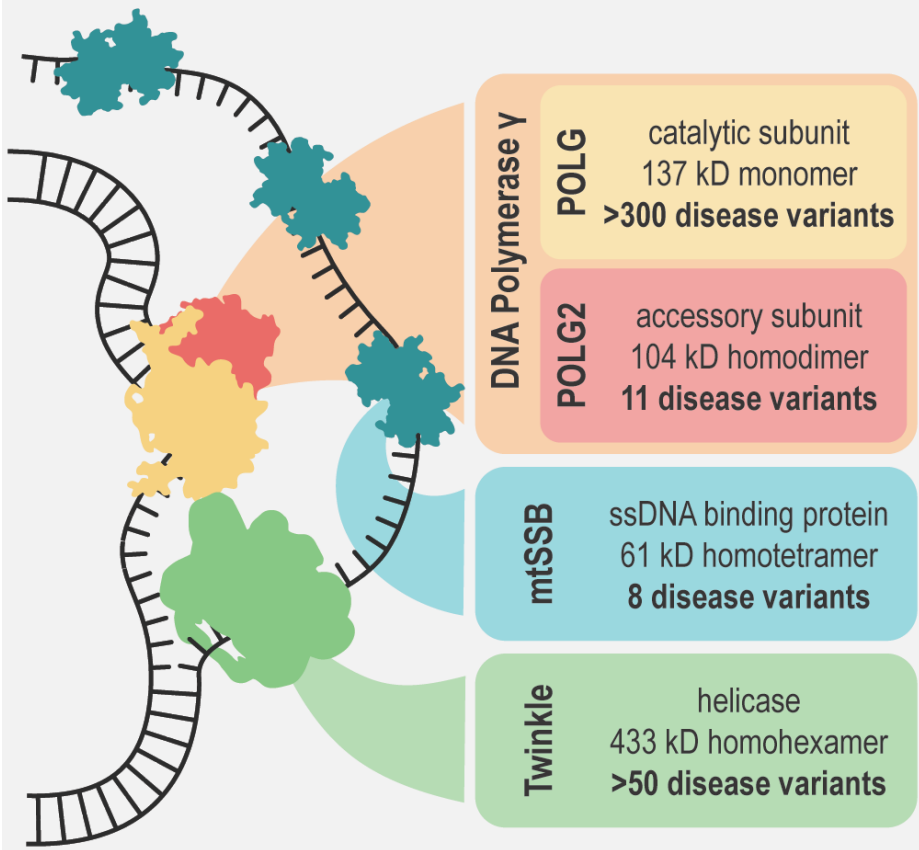
Proteins involved in mitochondrial DNA replication



- POLG: p140, catalytic subunit of Pol γ , polymerase and exonuclease**
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- SSBP1: single-stranded DNA binding protein**

A

Minimal mtDNA Replisome Components

**B**

Disease Outcomes Associated with Mutations

Alpers-Huttenlocher Syndrome, Chronic Progressive External Ophthalmoplegia, Kearns-Sayre Syndrome, Myoclonic Epilepsy Myopathy Sensory Ataxia, Ataxia Neuropathy Spectrum, Leigh Syndrome, Childhood Myocerebrohepatopathy Spectrum, Hepatocerebral Mitochondrial DNA Depletion Syndrome

Chronic Progressive External Ophthalmoplegia, Ataxia Neuropathy Spectrum, Leigh Syndrome, Hepatocerebral Mitochondrial DNA Depletion Syndrome

Optic Atrophy, Kearns-Sayre Syndrome, Pearson Syndrome, Leigh Syndrome

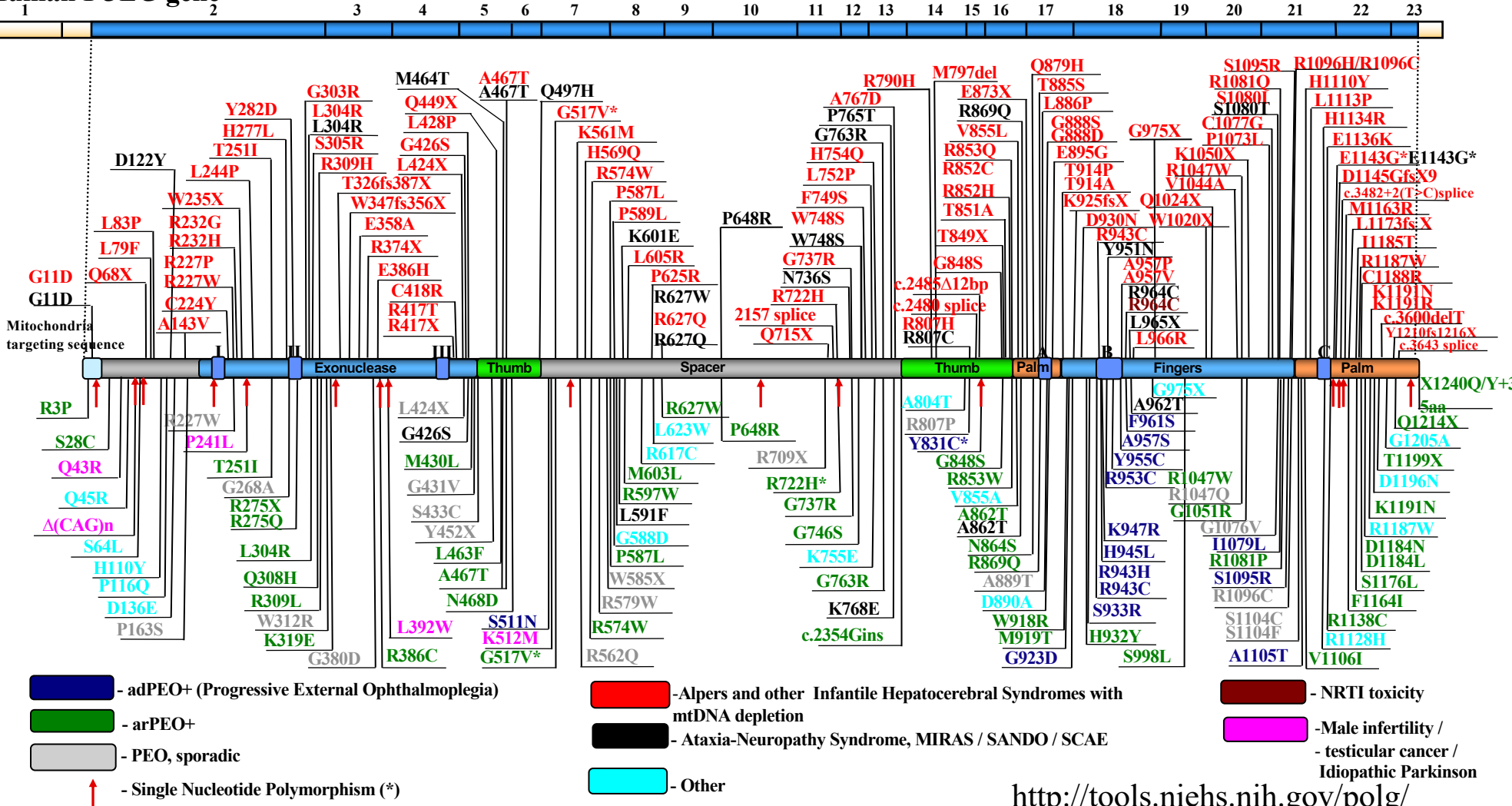
Chronic Progressive External Ophthalmoplegia, Ataxia Neuropathy Spectrum, Hepatocerebral Mitochondrial DNA Depletion Syndrome, Infantile-Onset Spinocerebellar Ataxia, Perrault Syndrome

Nuclear loci that affect the stability of mitochondrial DNA

Gene	Disorder	Locus	Function
<u>mtDNA replication and repair</u>			
<i>POLG</i>	PEO, Alpers, ataxia	15q25	Pol γ catalytic subunit
<i>POLG2</i>	PEO	17q23-24	Pol γ accessory subunit
<i>TWINK</i>	PEO, mtDNA depletion, IOSCA	10q24	Mitochondrial DNA helicase
<i>MGME1</i>	PEO, mtDNA depletion	20p11.23	Single-strand DNA nuclease
<i>DNA2</i>	mtDNA deletions, PEO	10q21.3-22.1	Mito/nuclear helicase-nuclease
<i>RNASEH1</i>	encephalomyopathy, mtDNA deletions	2p25	RNA/DNA hybrid endoribonuclease
<i>TFAM</i>	mtDNA depletion	10q21.1	Organizes mtDNA transactions
<i>SSBP1</i>	Optic atrophy, mtDNA dep/del	7q34	Single strand DNA binding protein
<u>nucleotide pool metabolism</u>			
<i>ANT1</i>	PEO	4q34-35	Adenine nucleotide translocator
<i>TP</i>	MNGIE, mtDNA deletions/depletion	22q13.32	Thymidine phosphorylase
<i>DGUOK</i>	mtDNA depletion	2p13	Deoxyguanosine kinase
<i>TK2</i>	PEO, mtDNA depletion	16q22-23.1	Mitochondrial thymidine kinase
<i>MPV17</i>	mtDNA deletions, depletion	2p23.3	Mito inner membrane protein
<i>SUCLA2</i>	mtDNA depletion	13q14.2	ATP-dep Succinate-CoA ligase
<i>SUCLG1</i>	mtDNA depletion	2p11.2	GTP-dep Succinate-CoA ligase
<i>RRM2B</i>	PEO, mtDNA depletion	8q23.1	p53-Ribonucleotide reductase, small subunit
<i>ABAT</i>	mtDNA deletions, depletion	16p13.2	4-Aminobutyrate aminotransferase
<u>mitochondrial homeostasis / dynamics</u>			
<i>OPA1</i>	Dominant optic atrophy, mtDNA deletions, ataxia	3q28-29	Dynamin related GTPase
<i>MFN2</i>	DOA, mtDNA deletions	1p36.22	Mitofusin 2
<i>FBXL4</i>	mtDNA depletion, encephalopathy	6q16.1-16.3	Mitochondrial LLR F-Box protein
<i>AFG3L2</i>	Spinocerebellar ataxia, mtDNA deletions	18p11.21	Mitochondrial IM metalloprotease
<i>SPG7</i>	ataxia, spastic paraplegia	16:89.49-89.56	Mito IM metalloprotease component
<i>GFER</i>	mtDNA deletions, myopathy	16:1.98-1.99	Protein import to IMS

Mutations in DNA polymerase γ , *POLG*

Human *POLG* gene



***POLG* Disease Burden**

- *POLG* mutations are the most common cause of inherited mitochondrial disorders (Saneto and Naviaux, 2010).
- Approximately 2% of the population carries a pathogenic genetic variant of *POLG* (Saneto and Naviaux, 2010).
- The combined prevalence of recessive and dominant disease caused by *POLG* mutations is ~1:10,000.

Major clinical syndromes associated with *POLG* mutations

Age of Onset	Syndrome	mtDNA defect
Neonatal/Infancy	Myocerebrohepatopathy spectrum (MCHS)	Depletion
Infancy/Childhood	Alpers-Huttenlocher syndrome (AHS)	Depletion
Adolescent/young adult	Ataxia neuropathy spectrum (ANS)	Deletions
	Myoclonus, epilepsy, myopathy, sensory ataxia (MEMSA)	Deletions
	Progressive external ophthalmoplegia (PEO) with or without sensory ataxic neuropathy and dysarthria (SANDO)	Deletions

T251I + P587L in the Literature

Allele 1	Allele 2	Sex	Age of Onset (yr)	Clinical Phenotype	Reference
T251I+P587L	T251I+P587L	F	41	PEO	Stewart JD, et al. (2009)
T251I+P587L	T251I+P587L	M	63	PEO & myopathy	Horvath R, et al. (2006).
T251I+P587L	G848S	M	0.5	Alpers	Wong LJ, et al. (2008)
T251I+P587L	G848S	F	51	PEO	Blok MJ, et al. (2009)
T251I+P587L	G848S	M	73	SANDO	Weiss MD, et al.(2010)
T251I+P587L	L304R	F	45	PEO, ataxia & myopathy	Horvath et al. (2006)
T251I+P587L	L304R	M	60	PEO & neuropathy	Horvath, et al. (2006)

Table 1. Summaries of the case histories of the four patients.

Homozygous A467T patients

	Patient 1	Patient 2	Patient 3	Patient 4
Age at presentation (years)	3	6	20	24
Age at death (years)	5.5	Alive at 16	44	Alive at 31
Symptoms at presentation	Seizures	Encephalitis-type presentation	Diplopia	Seizures
Clinical phenotype	Alpers-Huttenlocher	MEMSA+	SANDO	“MELAS-like”
Blood/CSF results	GGT 170 IU/l (reference <20 IU/L), AST 490 IU/L (reference range 5 to 45 IU/l)	↑lactate 2.6mmol/L (<2) Liver function normal; ↑Plasma alanine 537 mcmmol/L (150–450); ↓Plasma arginine 28 mcmmol/L (40–120); CSF lactate 1.6mmol/L (<2); ↑CSF protein 1.32 g/L (0.15–0.6); CSF 5MTHF 29 (46–120)	↑ lactate 2.3mmol/L (< 1.65); CK 329	Normal lactate; Normal CSF exam
Neurophysiology	-	EEG: Intermittent runs of rhythmic delta activity; CS: sensory neuropathy affecting legs	NCS: Severe axonal neuropathy	NCS: Moderately severe axonal sensory motor neuropathy
Radiology	Chronic grey matter ischaemia	MRI: Bilateral occipital lesions around calcarine sulci	-	MRI: Right occipital infarct
Neuropathology	Cortical degeneration in the occipital and parietal lobes, typical of PNDC. Bilateral hippocampal sclerosis. Hepatic microsteatosis	Brain biopsy: Non-specific; Muscle histology: COX-negative fibres	Muscle histology: ↑ no. of ragged red fibres and > 10 COX-negative fibres	Muscle histology: Ragged red fibres and COX-negative fibres and marked variation in fibre size with scattered groups of atrophic fibres.
Muscle Respiratory Chain enzymes	-	Complex I 0.126 (0.104–0.268); Complex II 0.159 (0.040–0.204); Complex IV 0.026 (0.014–0.034)	Complex I 0.170 (0.104–0.268); Complex II 0.077 (0.040–0.204); Complex IV 0.024 (0.014–0.034)	-

Key: 5MTHF, 5-methyltetrahydrofolate; AST, aspartate aminotransferase; COX, cytochrome oxidase; EEG, electroencephalogram; GGT, gamma-glutamyltranspeptidase; MELAS, mitochondrial encephalomyopathy, lactic acidosis, stroke-like episodes; MEMSA, myoclonic epilepsy, myopathy, sensory ataxia; NCS, nerve conduction studies; PNDC, progressive neuronal degeneration of childhood; SANDO, Sensory Ataxia Neuropathy Dysarthria Ophthalmoplegia.

GENETIC & ENVIRONMENTAL INTERACTIONS RESULTING IN MITOCHONDRIAL DYSFUNCTION

Environmental Factors

Inhibitors

Smoking
Cyanide
Nitric Oxide
Hydrogen Sulfide
Fungal Toxins
Pesticides
Industrial Chemicals
Streptozotocin
Antibiotics
Antivirals
Anti-cancer drugs

Activators

Benzofibrate
Resveratrol
Rosiglitazone

mtDNA Variants

Ancient Adaptive Polymorphisms
Recent Deleterious Mutations

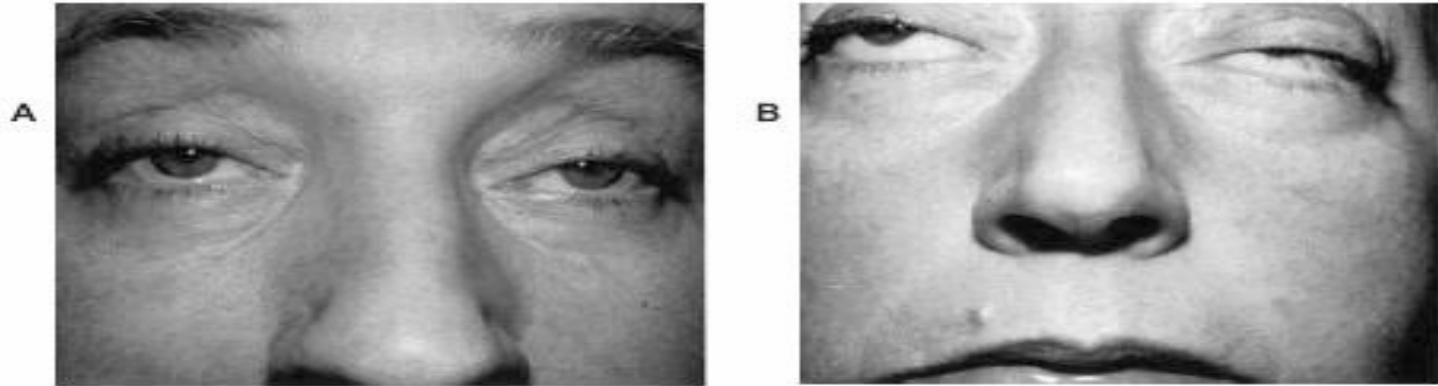
nDNA Variants

ANT1
POLG
POLG2
Twinkle
MGME1
SUV3
OPA1
MPV17
TK2
dGuoK
RRM2B
PPAR γ
PGC-1 α , β
nDNA Polymorphisms

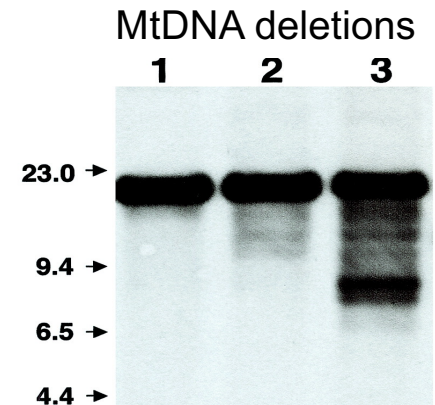
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graph TD; A[Environmental Factors] --> D[OXPHOS INHIBITION and MITOCHONDRIAL DYSFUNCTION]; B[mtDNA Variants] --> D; C[nDNA Variants] --> D;
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**OXPHOS INHIBITION
and
MITOCHONDRIAL DYSFUNCTION**

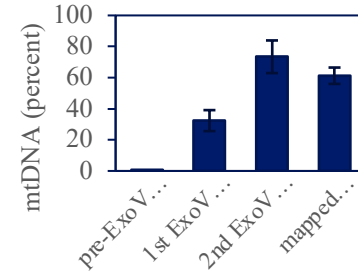
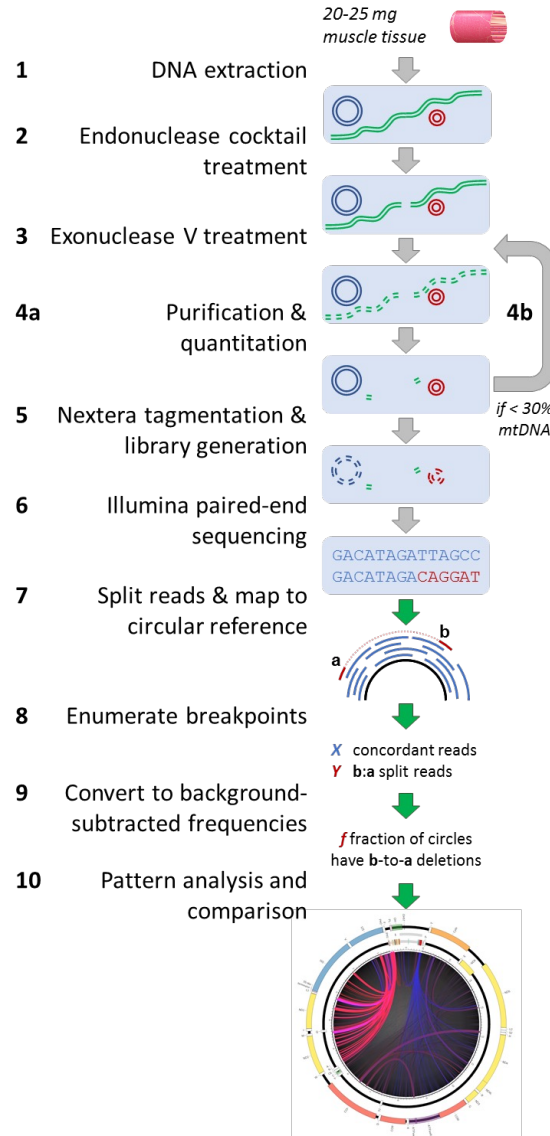
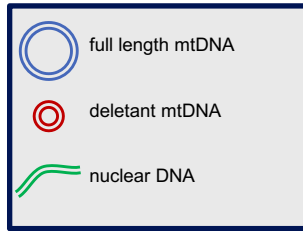
Progressive External Ophthalmoplegia



- Weakening of the external eye muscles
- Ophthalmoparesis, inability to look right and left
- Bilateral ptosis, droopy eyelids
- Multiple deletions in the mtDNA
- Many other associated symptoms



Pipeline for MtDNA Deletion Detection and Mapping: **LostArc**



LostArc TEAM

Scott Lujan
Matt Longley
Maggie Humble
Andy Lavender
Adam Burkholder
Robert Taylor, Newcastle, UK
Robert McFarland, Newcastle, UK
Grainne Gorman, Newcastle, UK
Doug Turnbull, Newcastle, UK
Tom Kunkel

Lujan et al., 2020 *Genome Biology*
 21:248

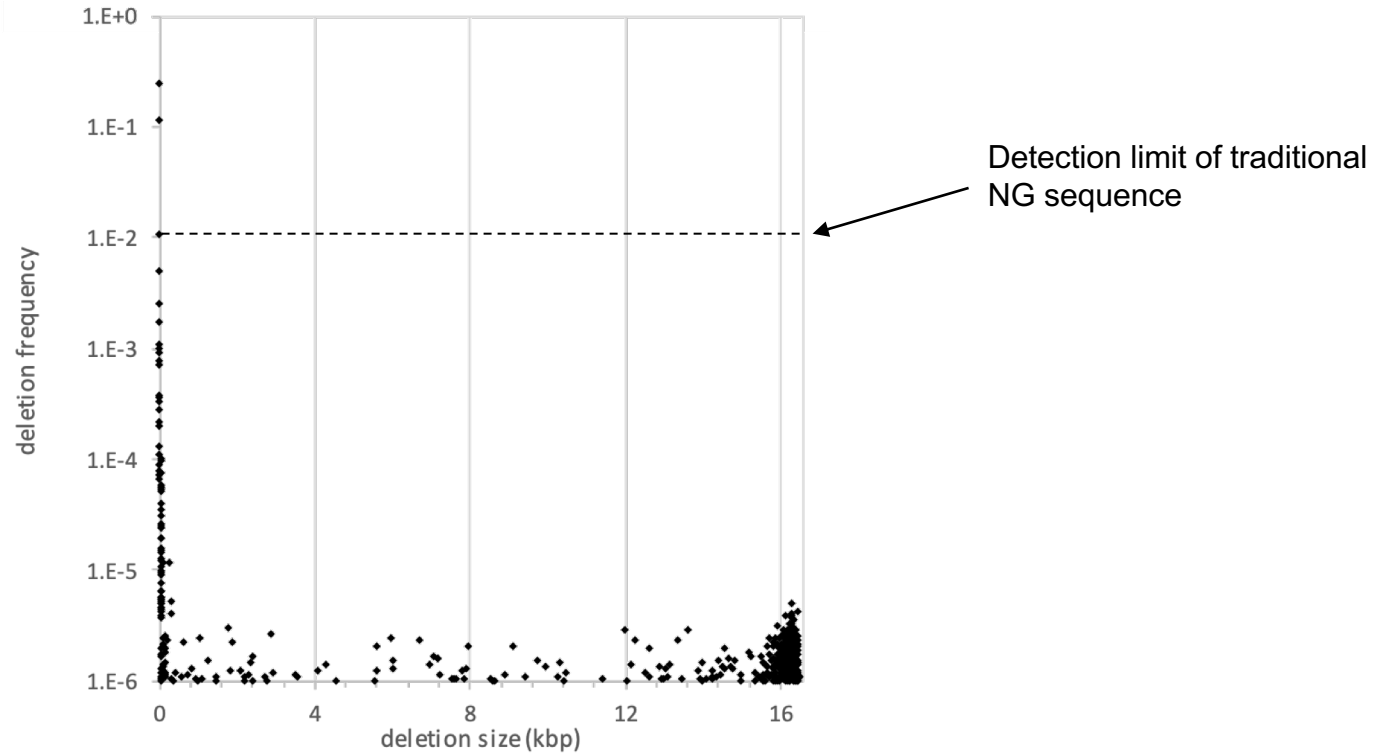
Analyzed

- 22 PEO patients with POLG mutations ranging in age from 17 – 80
- 19 Wildtype subjects, ages 19-93

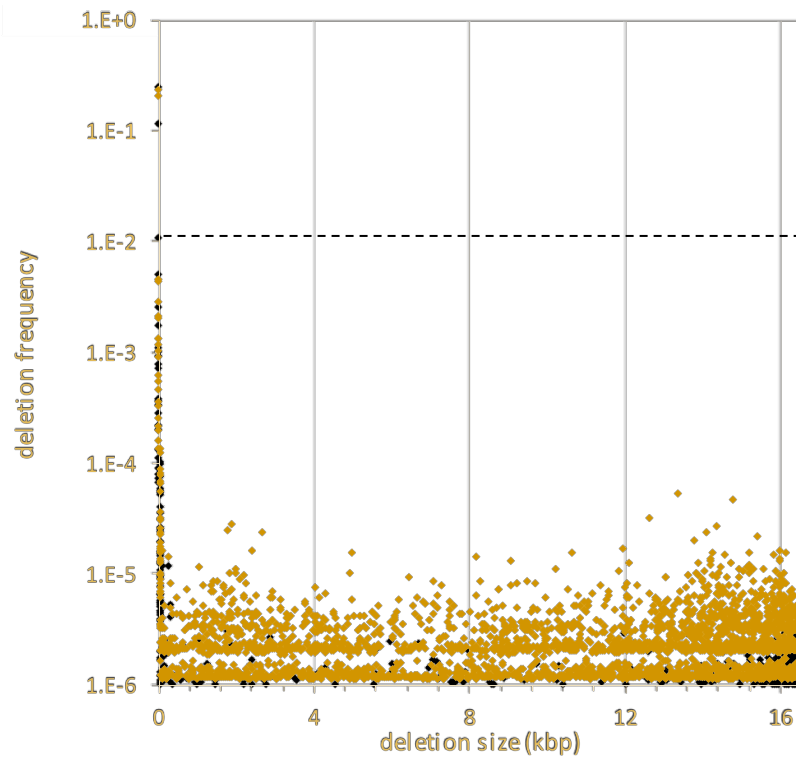
Identified:

- 35 million mtDNA deletions
- 470,000 unique deletions

HEK293 cells (weighted mean, n = 3)



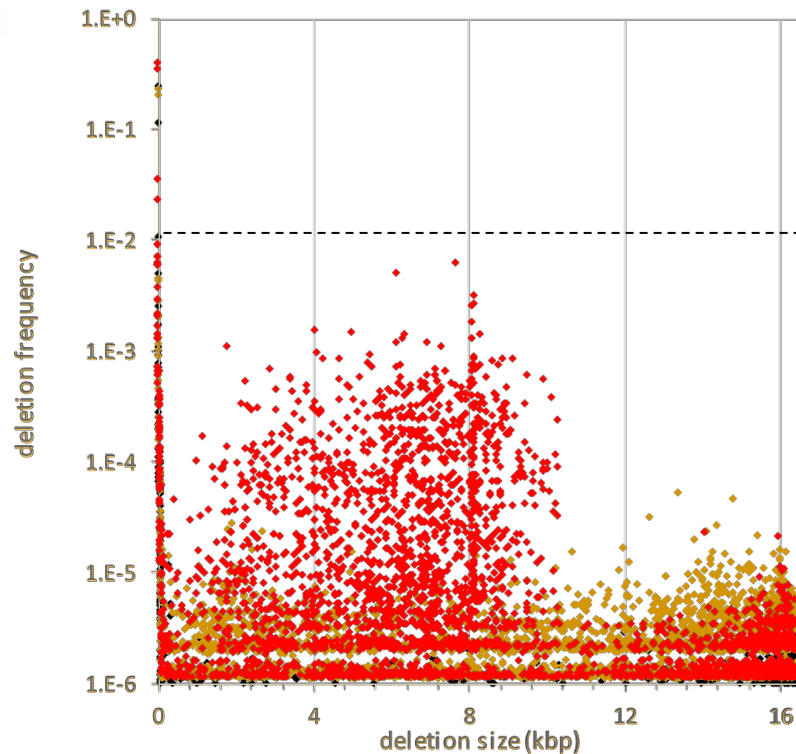
HEK293 cells (weighted mean, n = 3)
M314 (WT *POLG*, 17 years old at biopsy)



HEK293 cells (weighted mean, n = 3)

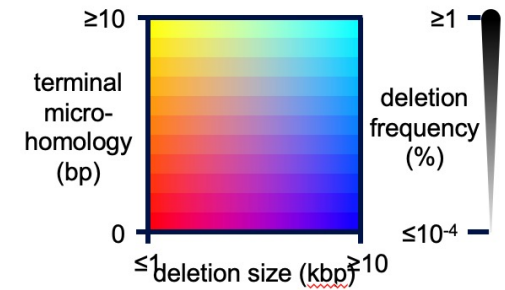
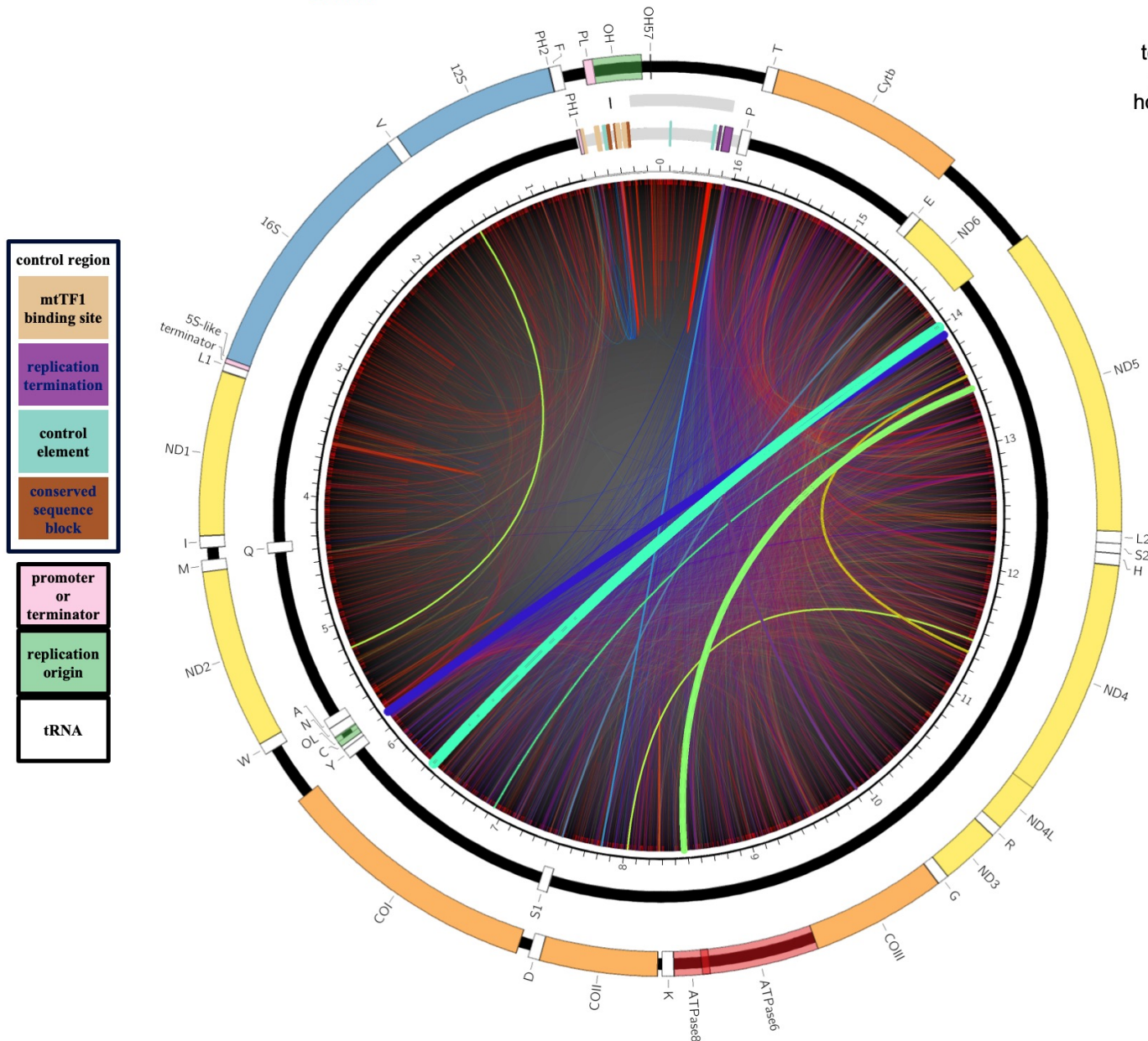
M314 (WT *POLG*, 17 years old at biopsy)

M508 (A467T/A467T *POLG*, 45 years old at biopsy)



**>70% of the mtDNA
genomes carried a
deletion**

45 y.o. PEO patient; A467T / T251I-P587L



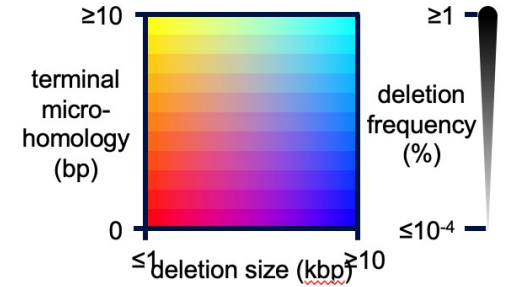
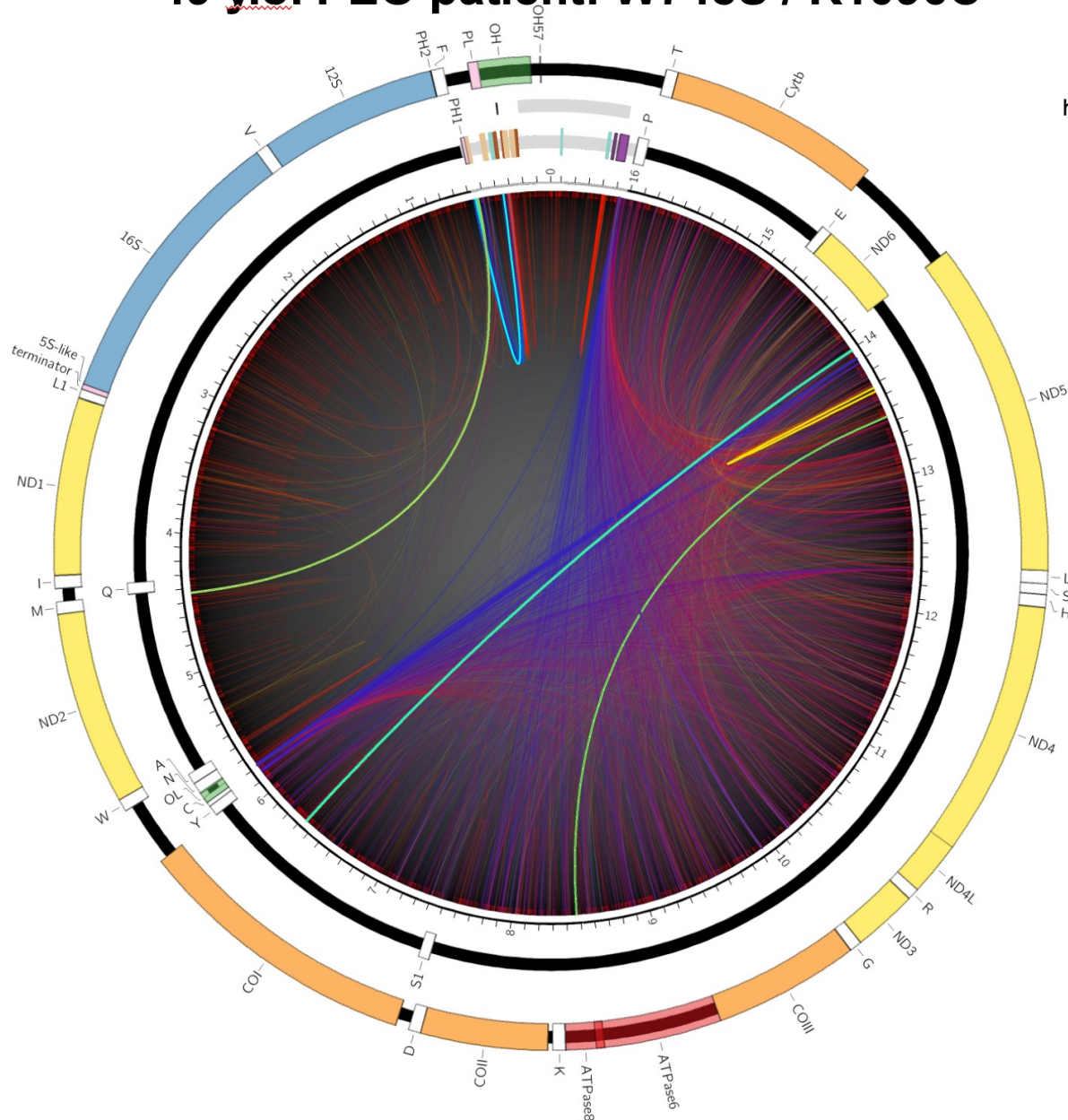
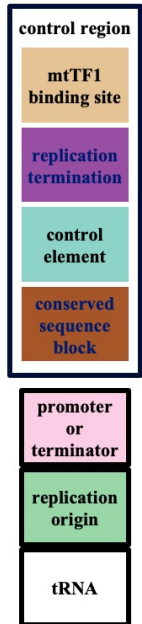
POLG A467T and T251I/P587L:

- Age of on-set at 45 yrs.
- Patient diagnosed with PEO, ptosis, and proximal weakness
- 25% COX negative muscle fibers and positive for ragged red fibers
- Long range PCR detected mtDNA deletions

Mito Deletion Mapping Results

- Over 87 million reads aligned
- 79% of the mtDNA genomes contained a deletion
- 446,000 deletions detected
- 25,933 unique deletions

49 y.o. PEO patient: W748S / R1096C



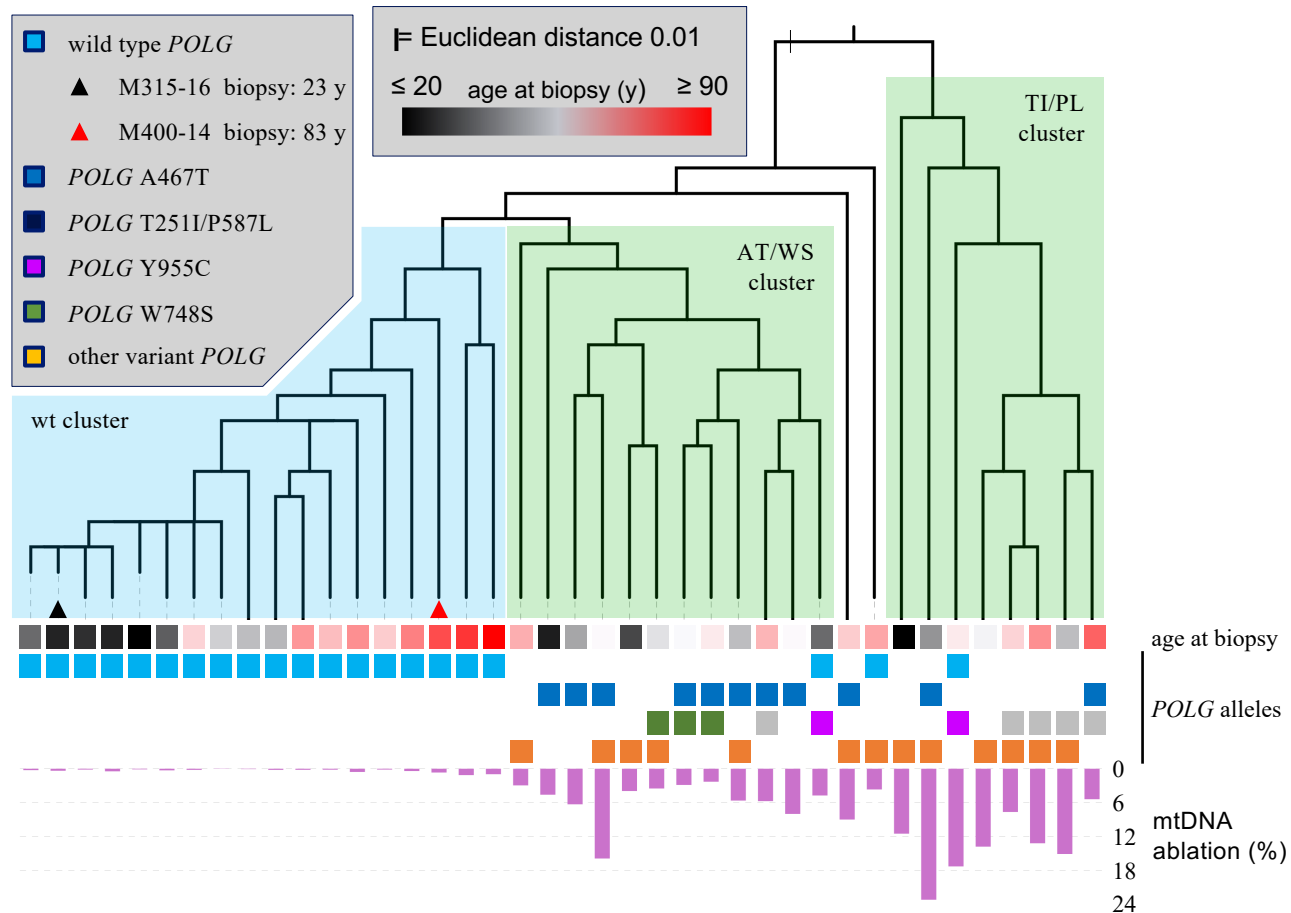
POLG W748S/R1096C:

- This patient is a 49 y.o. male with age of on-set at 25 yrs
- Diagnosed with PEO, ptosis, peripheral neuropathy, and epilepsy
- Has 16% COX negative muscle fibers and 5% ragged red fibers

Mito Deletion Mapping Results

- Over 700 million reads
- 74% of the mtDNA genomes contained a deletion
- 2.9 million deletions detected
- 24,360 unique deletions

MtDNA deletion clusters



Samples cluster by deletion pattern, WT control samples independently from *POLG* patient samples.

What does the future hold for POLG- related disorder

More accurate and faster diagnosis

- Lots of published literature available for the clinicians, families and patients
- WGS and WES genome sequencing to quickly identify POLG and related disease mutation
<http://tools.niehs.nih.gov/polg/>
- Sequencing mostly covered by health insurance

What does the future hold for POLG- related disorder

Better disease models to develop therapies

- Cell based models
- Mouse models of POLG, POLG2 and Twinkle
- Zebra Fish models of POLG and POLG2 disease
- Organoids

Human Molecular Genetics, 2005, Vol. 14, No. 13 1775–1783
doi:10.1093/hmg/ddi184
Advance Access published on May 11, 2005

Mitochondrial DNA polymerase gamma is essential for mammalian embryogenesis

Nicole Hance, Mats I. Ekstrand and Aleksandra Trifunovic*

Department of Medical Nutrition and Department of Biosciences at Novum, Karolinska Institute, Stockholm, Sweden

Received April 13, 2005; Revised and Accepted May 4, 2005

Human Molecular Genetics, 2013, Vol. 22, No. 5 1017–1025
doi:10.1093/hmg/ddt506
Advance Access published on November 29, 2012

Polg2 is essential for mammalian embryogenesis and is required for mtDNA maintenance

Margaret M. Humble¹, Matthew J. Young¹, Julie F. Foley², Arun R. Pandiri³, Greg S. Travlos⁴ and William C. Copeland^{1,*}

What does the future hold for POLG- related disorder

Better disease models to develop therapies

- Cell based models
- Mouse models of POLG, POLG2 and Twinkle
- Zebra Fish models of POLG and POLG2 disease
- Organoids

ARTICLE OPEN



Zebrafish *polg2* knock-out recapitulates human POLG-disorders; implications for drug treatment

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Hallmark Molecular and Pathological Features of POLG Disease are Recapitulated in Cerebral Organoids

Anbin Chen, Tsering Yangzom, Yu Hong, Bjørn Christian Lundberg, Gareth John Sullivan, Charalampos Tzoulis, Laurence A. Bindoff, and Kristina Xiao Liang*

What does the future hold for POLG- related disorder

Therapies in the works

- Antioxidant therapy
- Anti-seizure, anti-epileptic drugs
- Nucleotide therapy
- Metformin
- Repurposing drugs and identifying new drugs
- Gene therapy

NOVEL VITAMIN K ANALOGS SUPPRESS SEIZURES IN ZEBRAFISH AND MOUSE MODELS OF EPILEPSY

J. J. RAHN, J. E. BESTMAN, B. J. JOSEY, E. S. INKS,
K. D. STACKLEY, C. E. ROGERS, C. J. CHOU* AND
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National Institute of Neurological Disorders and Stroke (NINDS) Anticonvulsant Screening Program. Compound 2h reduced seizures particularly well in the minimal clonic seizure (6 Hz) and corneal-kindled mouse models of epilepsy, with no observable toxicity. As VK3 affects mitochondrial function, we tested the effects of our compounds on mitochondrial respiration and ATP production in a mouse hippocampal cell line. We demonstrate that these com-

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Nucleoside supplements as treatments for mitochondrial DNA depletion syndrome

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RESEARCH ARTICLE

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Deoxyribonucleoside treatment rescues EtBr-induced mtDNA depletion in iPSC-derived neural stem cells with POLG mutations

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Nicotinamide Riboside and Metformin Ameliorate Mitophagy Defect in Induced Pluripotent Stem Cell-Derived Astrocytes With *POLG* Mutations

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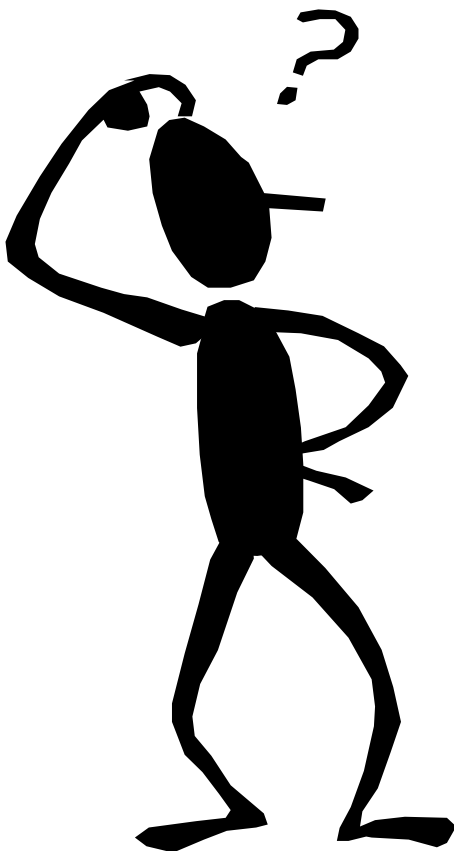
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Questions