



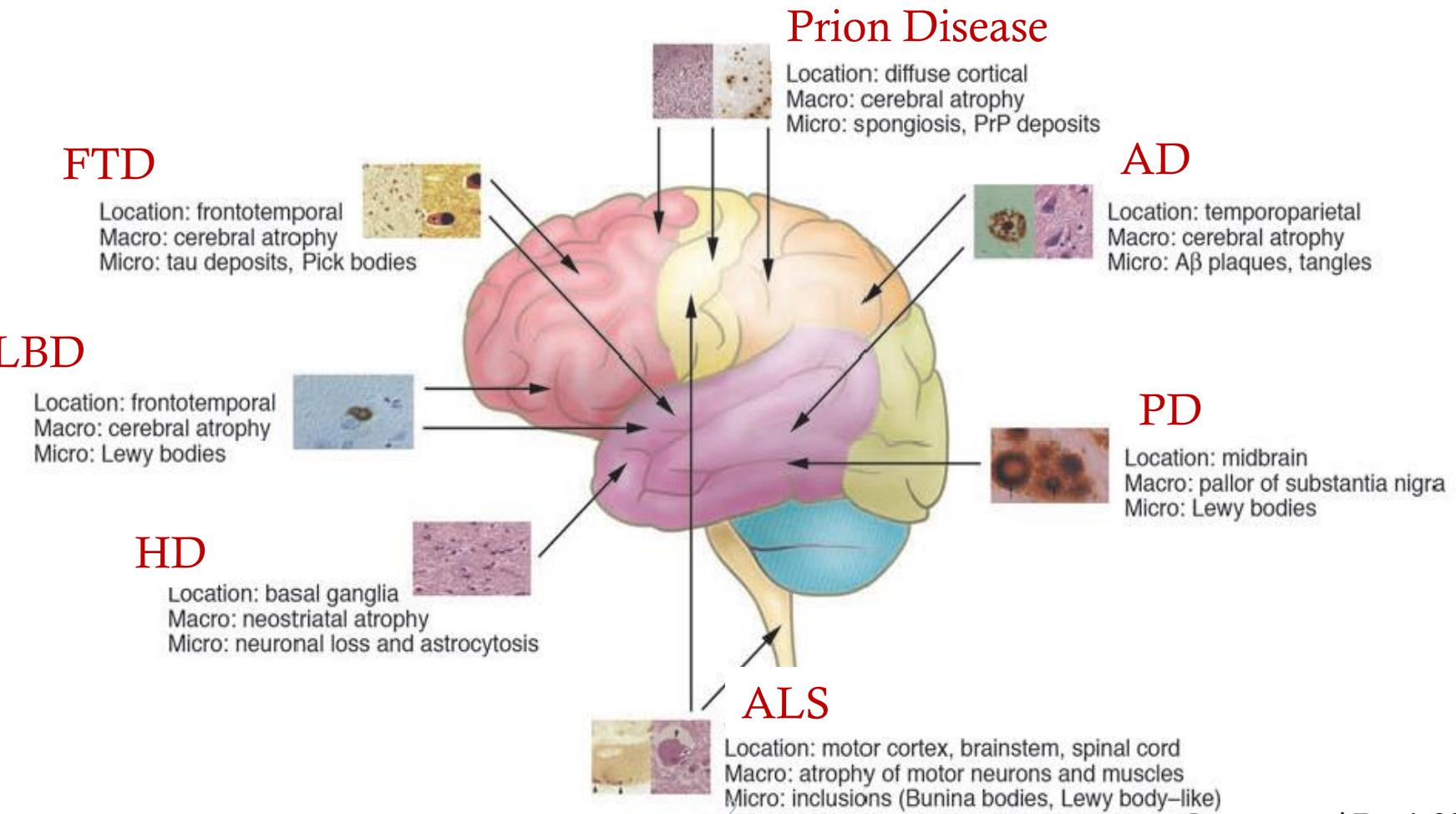
Suna and İnan Kıraç Foundation  
Neurodegeneration Research Laboratory

# Identification of Pathogenic Mutations in Neurodegenerative Disorders: Bioinformatic Analysis of Next Generation Sequencing Data



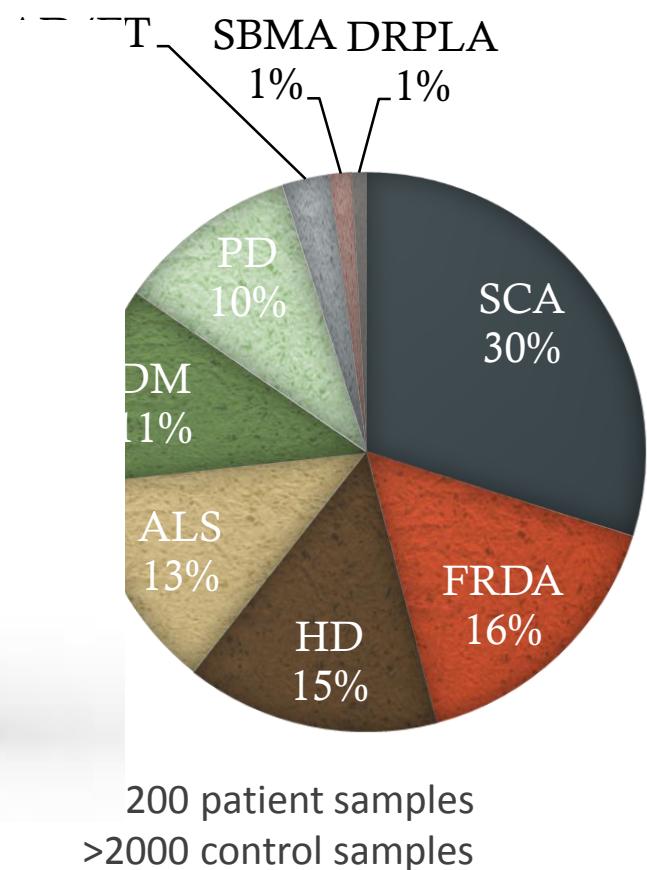
MSc Thesis Defence  
Ece Kartal  
March 17, 2015

# Selective neuron degeneration in different areas of the brain



# Patient cohort in Ndal

- Amyotrophic Lateral Sclerosis (ALS)
- Parkinson's Disease
- Alzheimer's Disease
- Frontotemporal Dementia
- Ataxias
- Triplet repeat disorders
  - Huntington's Disease
  - Spinocerebellar Atrophy
  - Friedreich's Atrophy
  - Spinal-bulbar muscular atrophy
  - Dentatorubral pallidoluysian atrophy
  - Myotonic Dystrophy



# Evolution of innovation



# Next generation sequencing for molecular diagnosis of neurological disorders using ataxias as a model

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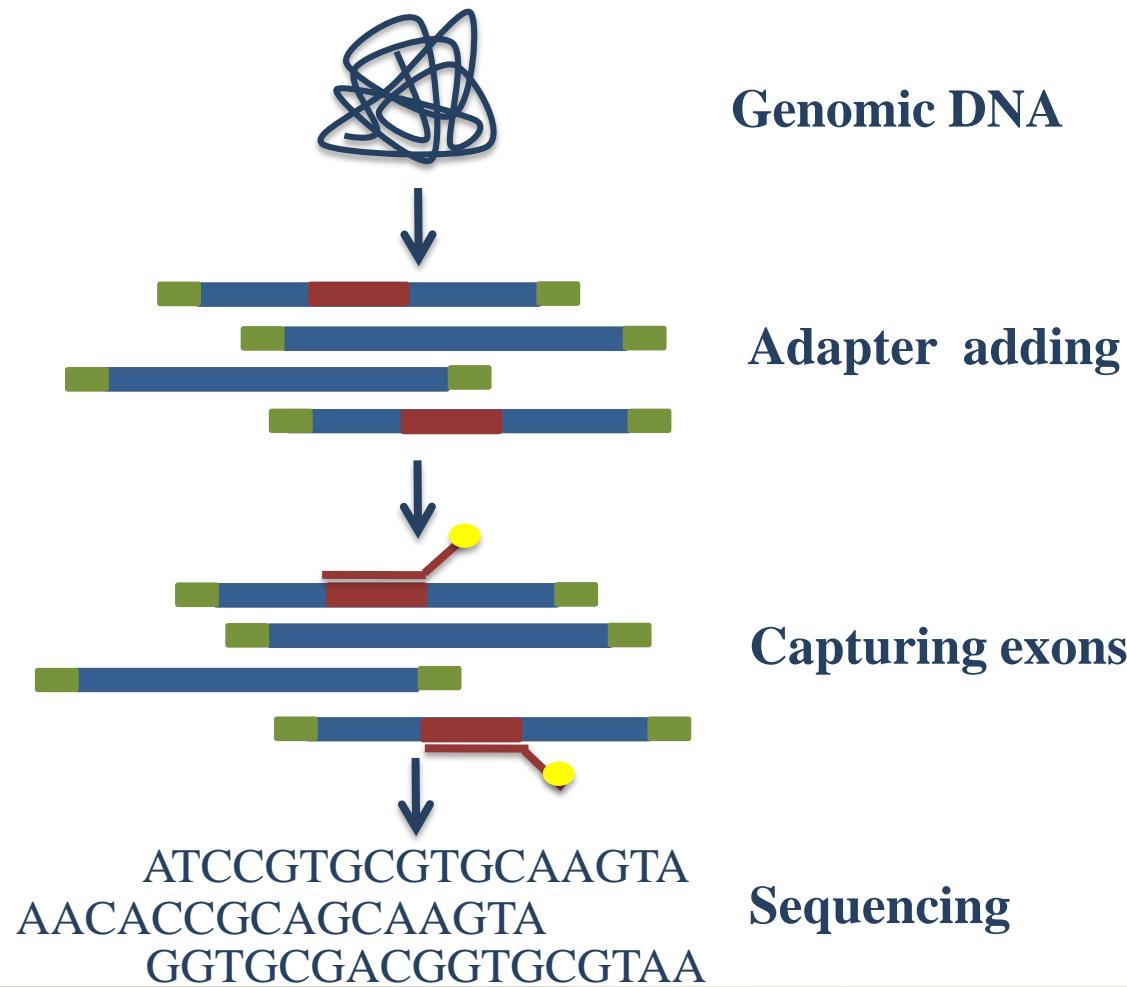
9 Department of Paediatrics, Oxford University Hospitals NHS Trust, Oxford, OX3 7DU, UK

# Exome sequencing

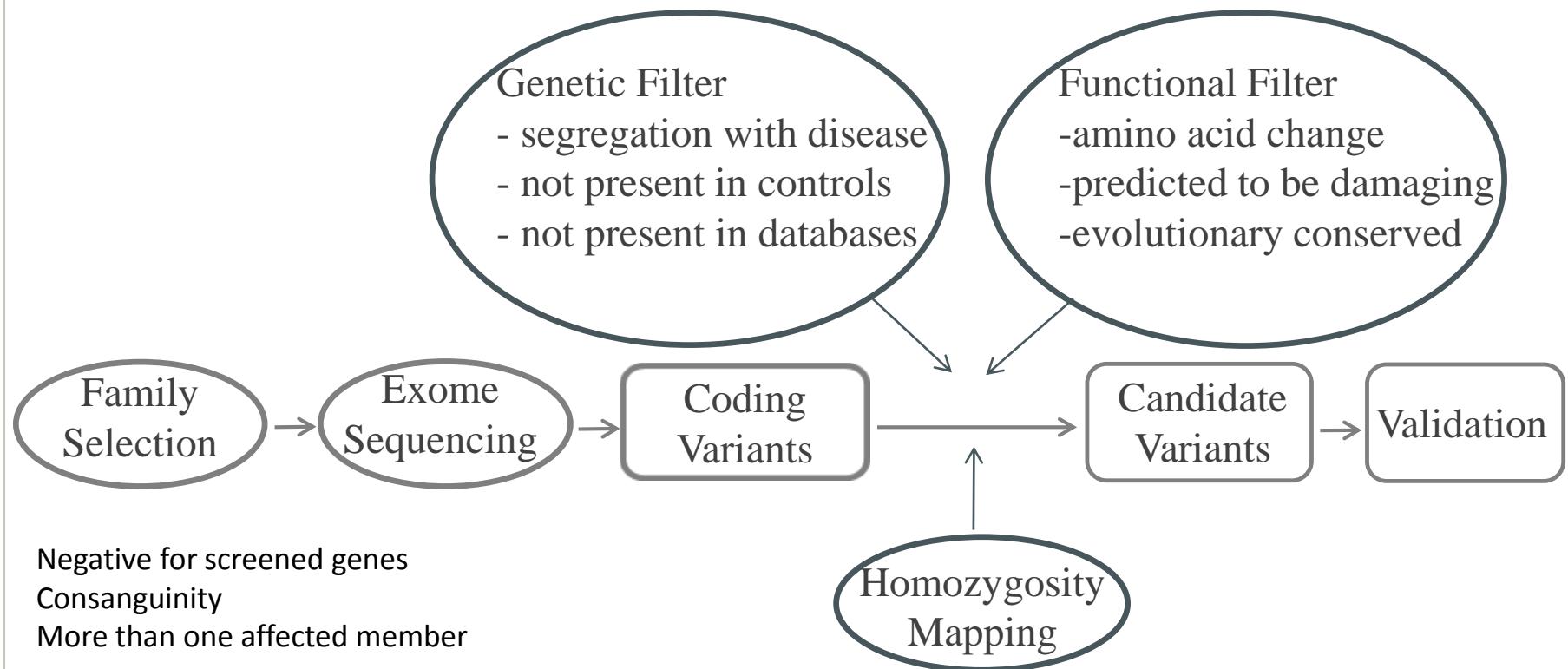
- 1% of genome, total length 30MB
- 85% of pathogenic variants
- Cost-effective
- Less data analysis



# Sequencing steps of whole exome



# Exome sequencing workflow

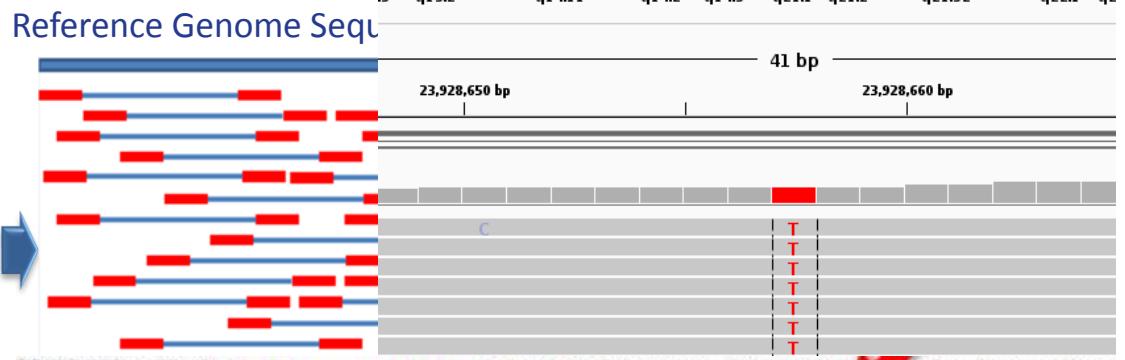


# Bioinformatic analysis steps



Sequencing signal to nucleotides  
-Result:.short reads in \*fastq files

Alignments of reads to human reference genome  
- Result:  
SAM/BAM

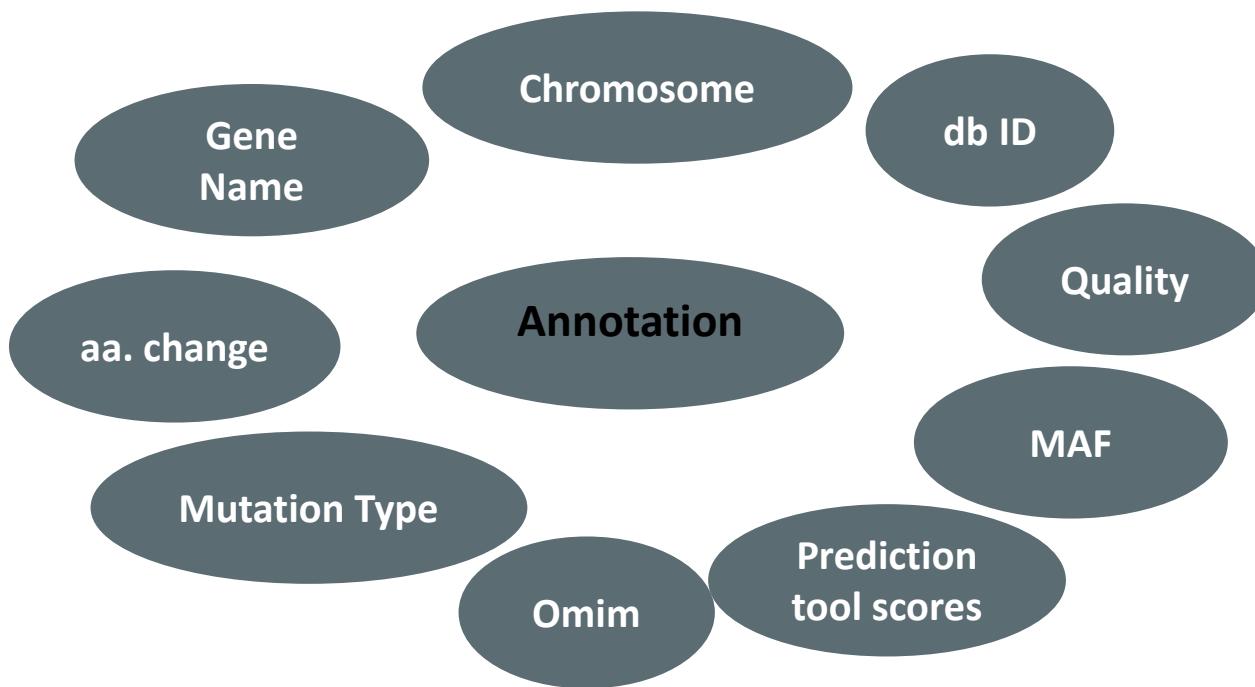


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##FILTER=<ID=N Reference allele sistent Genotype Submission or At Least One .  
#CHROM POS Reference allele QUAL FILTER INFO . . . . RSPOS=1  
1 11794553 rs12121577 C G . . . . RSPOS=1  
SAO=0;VP=050110000000050510000100;GENEINFO=AGTRAP:57085;WGT=0;VC=SNV;TPA;SLO;VLD;  
3548 (22/22)  
1 11794676 rs17875979 G A,C,T . . . . RSPOS=1  
0;SAO=0;VP=050100000000050512000104;GENEINFO=AGTRAP:57085;WGT=0;VC=SNV;SLO;VLD;  
0967741935 (12/12) | 0(0/) | 0(0/)  
1 11797186 rs12095517 T C . . . . RSPOS=1  
;SAO=0;VP=050100000000070512000100;GENEINFO=AGTRAP:57085;WGT=0;VC=SNV;SLO;VLD;G  
83870968 (184/118)  
1 11799228 rs6540992 T A . . . . RSPOS=1  
;SAO=0;VP=050100000000050512000101;GENEINFO=AGTRAP:57085;WGT=0;VC=SNV;SLO;VLD;G  
77419355 (84/66)  
1 11800048 rs11121815 T A,C,G . . . . RSPOS=1  
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2/92) | 0(0/)
```

Alternate alleles



# Annotation Step



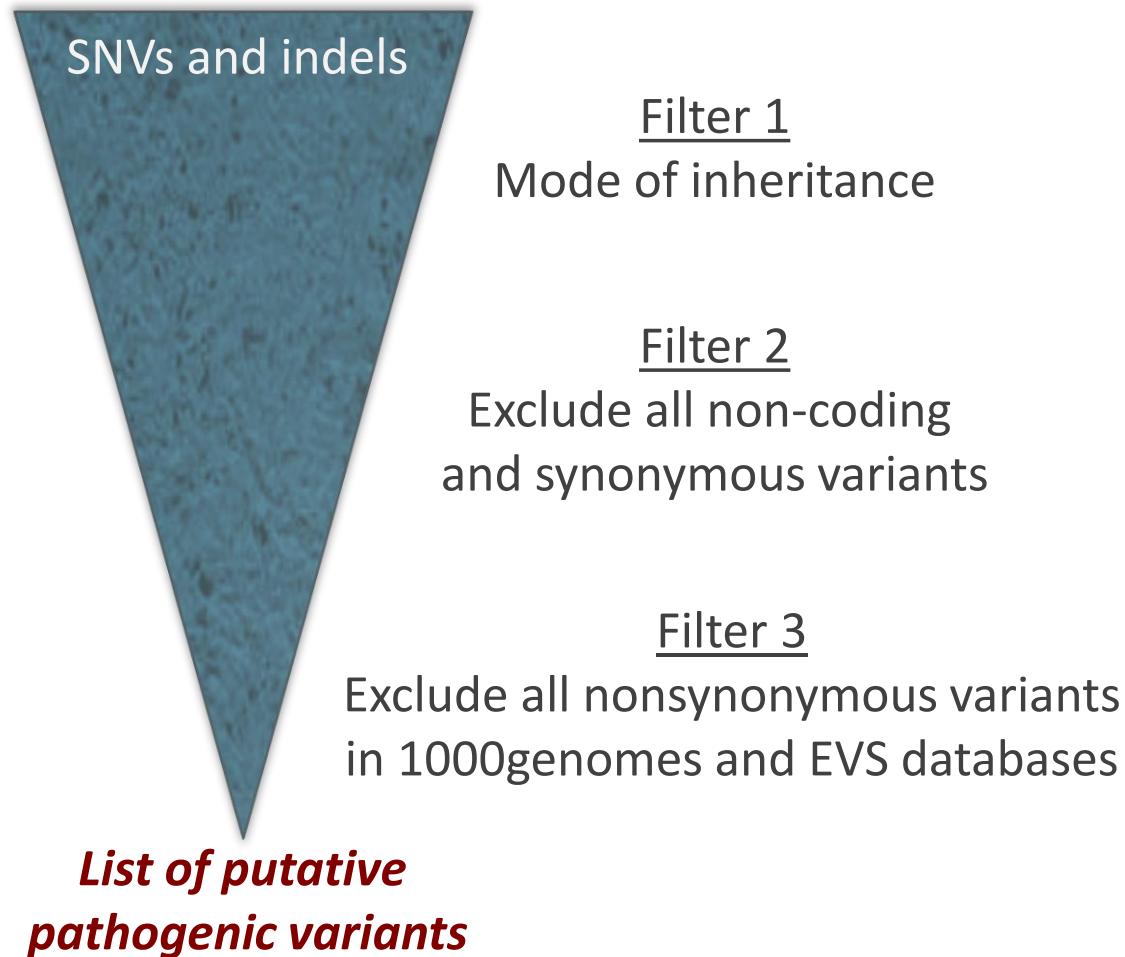
# Annotated .vcf file

<b>Chr</b>	chr1	<b>AA_Change</b>	exon1:c.G166C:p.A56P
<b>LeftFlank</b>	54355553	<b>Conserved_LOD</b>	483
<b>RightFlank</b>	54355555	<b>Segmental_Duplication</b>	0
<b>Gene_name</b>	YIPF1	<b>ESP6500_MAF</b>	0
<b>muttype</b>	SNP	<b>1000_Genome_MAF</b>	0
<b>dbID</b>	rs36013100	<b>PhyloP_score</b>	0.062946
<b>ref_allele</b>	A	<b>SIFT_score</b>	0.69
<b>var_allele</b>	C	<b>PolyPhen2_score</b>	0.026
<b>QUAL</b>	5593.41	<b>Gerp++</b>	-6.89
<b>FILTER</b>	PASS	<b>MutationTaster</b>	9.00E-06
<b>Type</b>	exonic_nonsynonymous	<b>OMIM</b>	Hypomagnesemia

# USUAL SUSPECTS: Rare variants

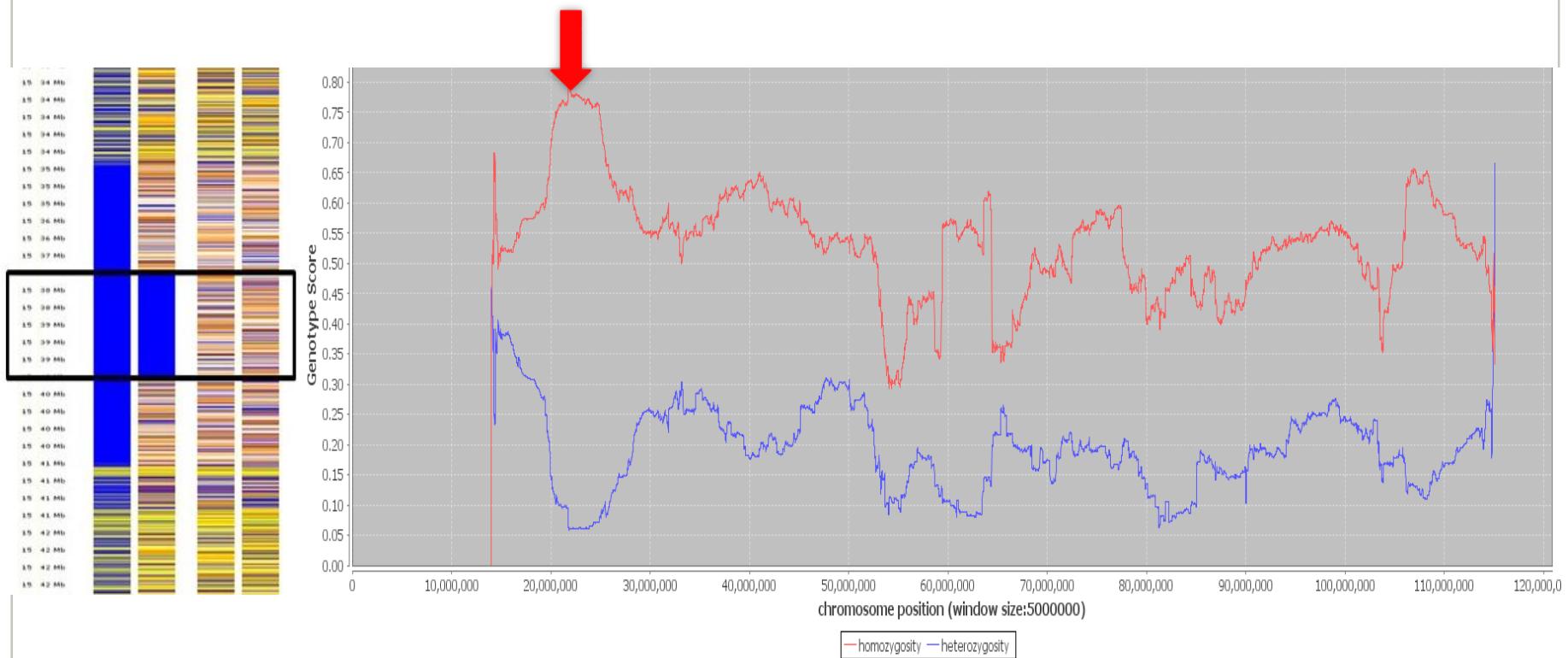


# Elimination of variants



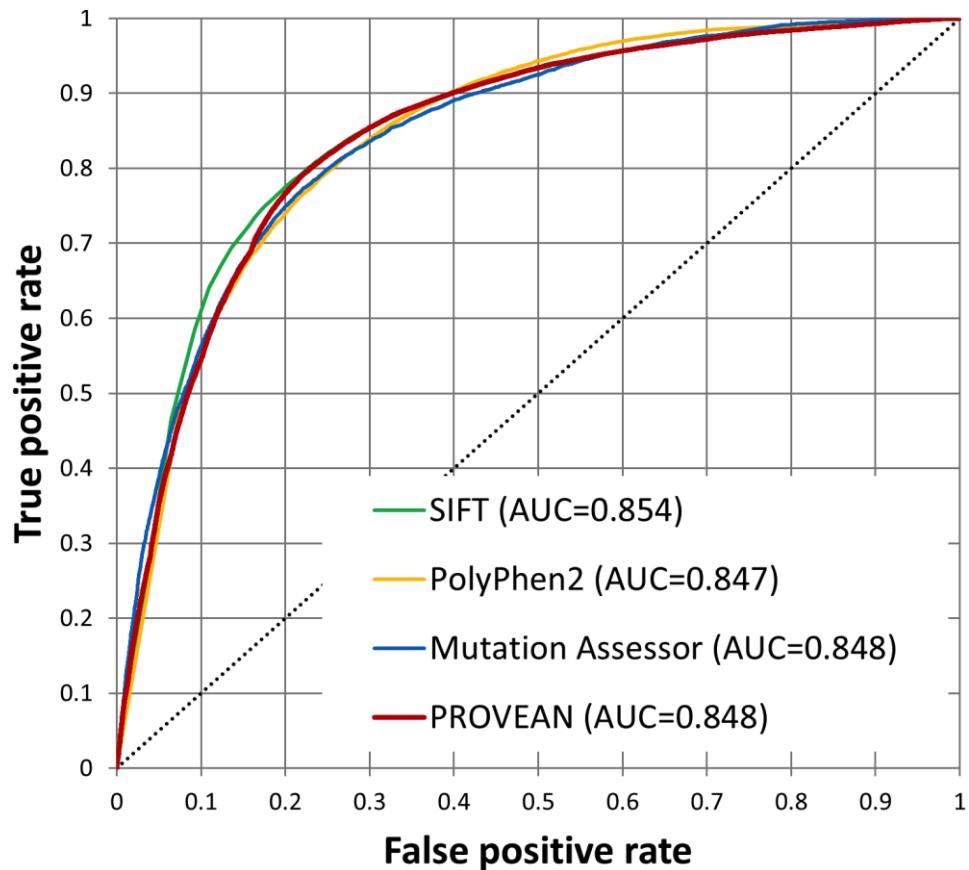
# Homozygosity mapping

- Homozygous Stretch Identifier (HomSI) (Tübitak)



# Prediction Tools

- SIFT
- Polyphen2
- Mutation Taster
- Provean
- SNP & Go
- Pylop



# Purpose

- Identification the genes/variants responsible for different neurodegenerative diseases, which could not be solved by conventional PCR-based techniques.
- This study includes 13 families:
  - Amyotrophic Lateral Sclerosis and related syndromes
  - Recessive ataxias

# Study cohort

<b>Family</b>	<b>Clinical Diagnosis</b>
1	ALS
2	ALS
3	ALS
4	ALS
5	ALD-PD
6	SCA & FRDA
7	SCA & FRDA
8	SCA & FRDA
9	SCA & FRDA
10	FRDA
11	SCA
12	SCA & FRDA
13	SCA

# STUDY COHORT

ALS

Ataxias

- Most common adult-onset motor neuron disease
- Selective death of
  - ✓ upper motor neurons in the motor cortex
  - ✓ lower motor neurons in the brainstem and spinal cord
- Symptoms:
  - spasticity
  - muscle weakness
  - muscle atrophy
  - twitching
  - breathing and talking difficulties
- Coordination of muscle movements
- dysfunction of the cerebellum
- Types
  - Friedrich's ataxia
  - Spinocerebellar ataxias
  - Ataxia oculomotor apraxia
  - Ataxia-telangiectasia
  - Episodic ataxia

# Family 1

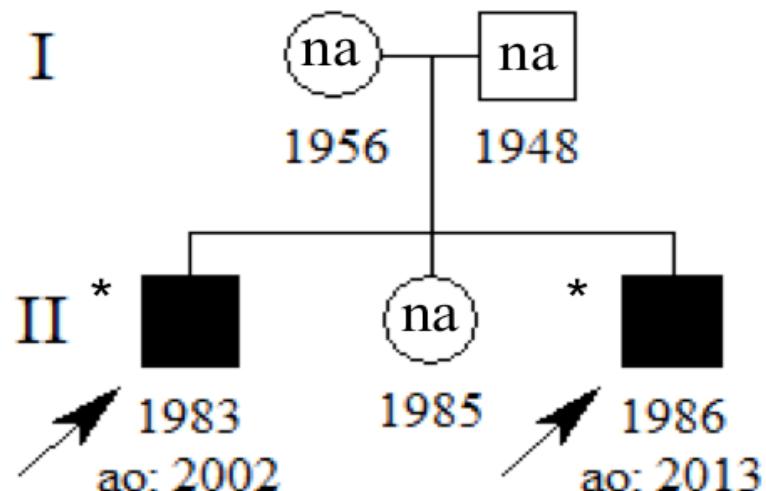
Symptoms: limb onset disease

- weakness in right hand fingers  
atrophy of hand muscles  
atrophy in the right arm
- fasciculations

Clinical diagnosis: ALS

Genetics: dominant

- C9Orf72, SOD1, UBQLN2, TDP-43 and FUS (-)

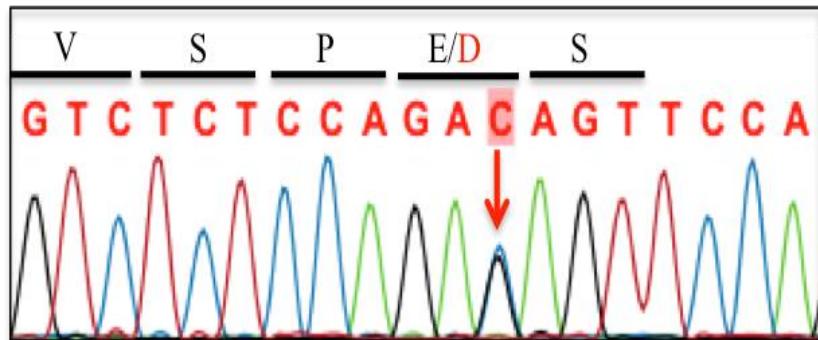


na: not available

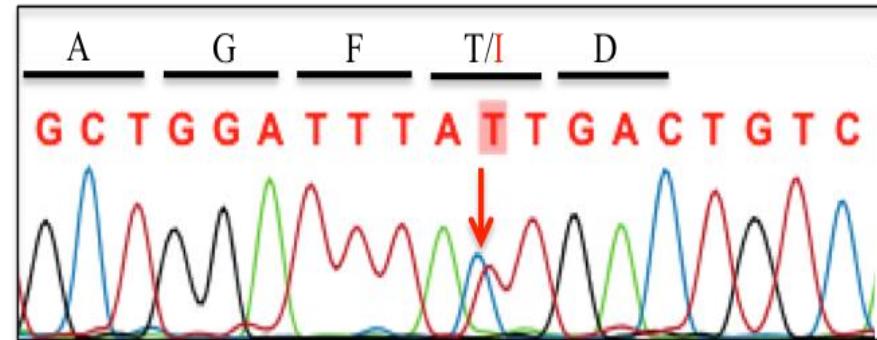
# Exome results/validation: Family 1

Candidate variations in ALS-Family 1.

Chr	Position	Gene name	dbSNP ID	Ref/A <sub>l</sub> t	Mutation
chr5	179260099	SQSTM1	rs55793208	G/C	c.G822C:p.E274D
chr15	50878630	TRPM7	rs8042919	G/A	c.C4445T:p.T1482I

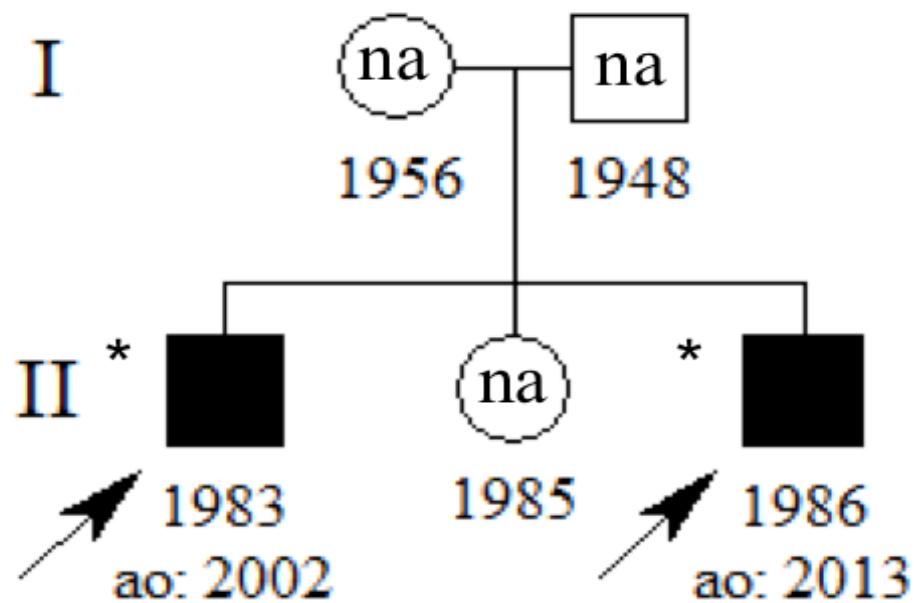


SQSTM1 gene



TRPM7 gene

# Overall results-Family 1: ALS



na: not available

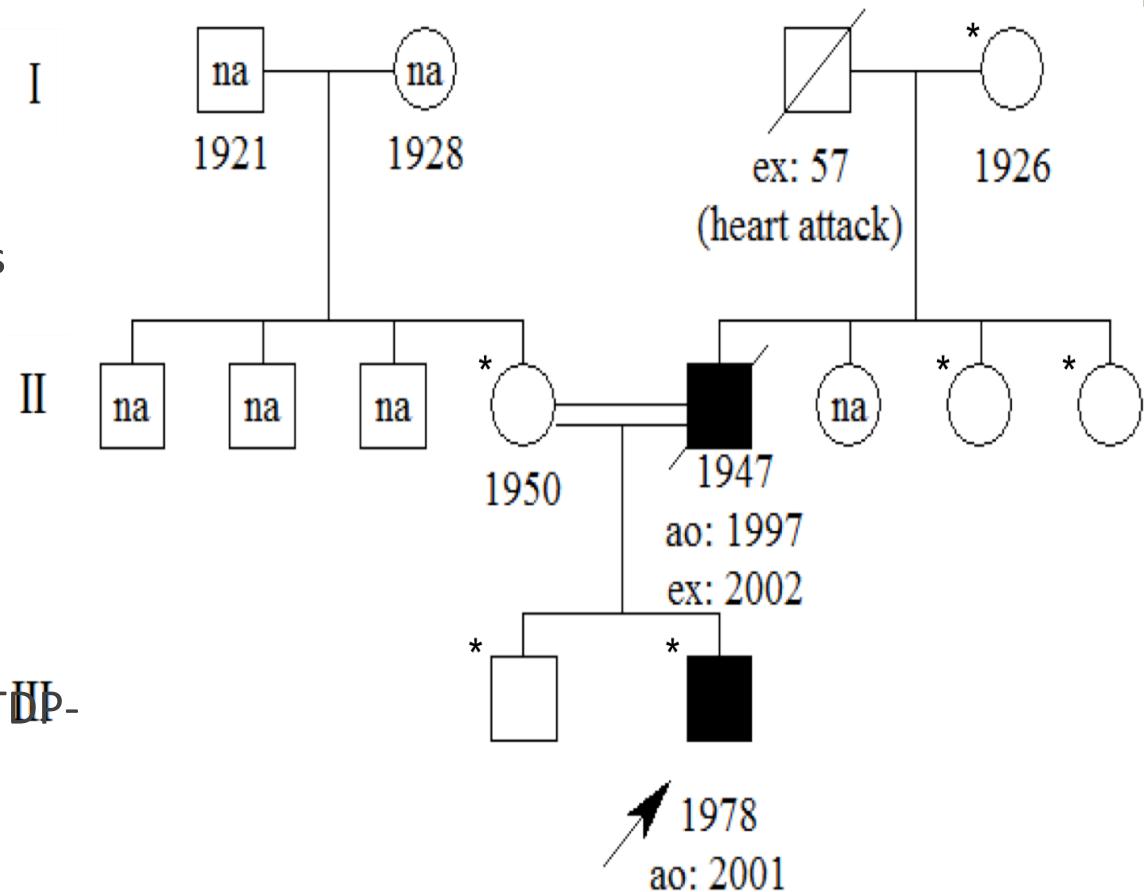
# Family 2

- Symptoms:
  - cognitive impairment
  - bilateral leg weakness
  - upper extremity weakness
  - AO: 23

Clinical diagnosis: ALS

Genetics: recessive

- C9Orf72, SOD1, UBQLN2, TDP-43, FUS and FRDA (-)



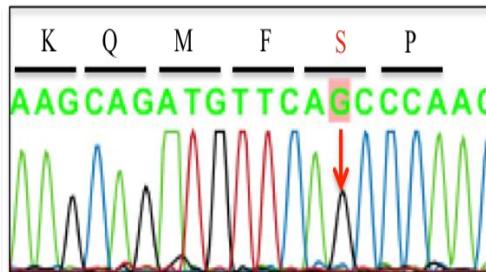
na: not available

# Exome results/validation: Family 2

Candidate variations in ALS-Family 2.

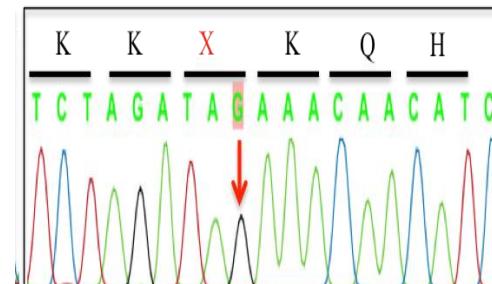
Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr15	44855496	SPG11	-	A/C	c.T6816G:p.Y2272X
chr15	44865000	SPG11	rs140824939	T/C	c.A5885G:p.N1962S
chr5	73205717	ARHGEF28	rs17634865	C/T	c.C3703T:p.P1235S

SPG11 p.N1982S mutation



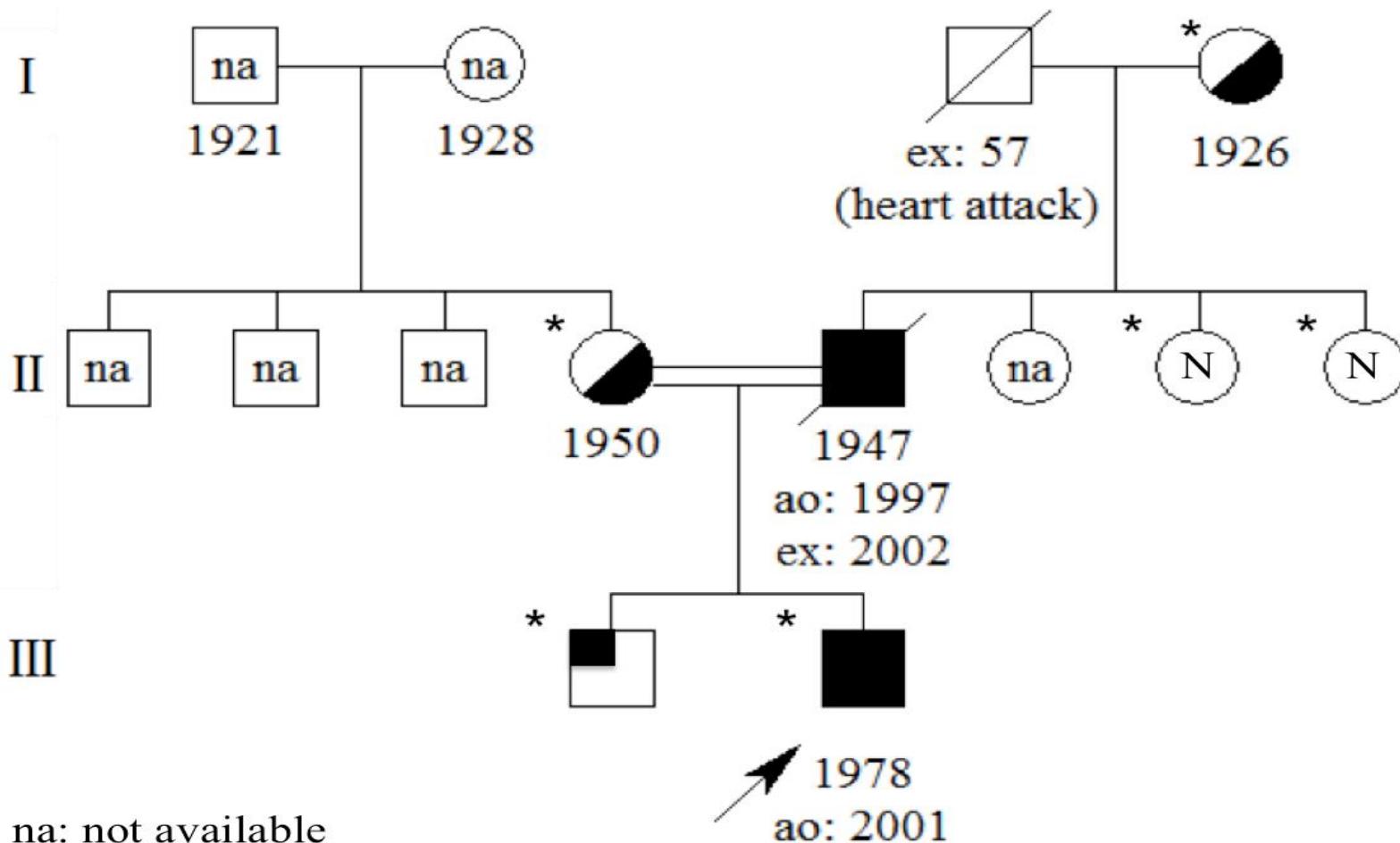
index case

SPG11 p.Y2272X mutation



index case

# Overall results-Family 2: ALS



# Family 3

Symptoms:

- involvement of anterior horn

I

II

III

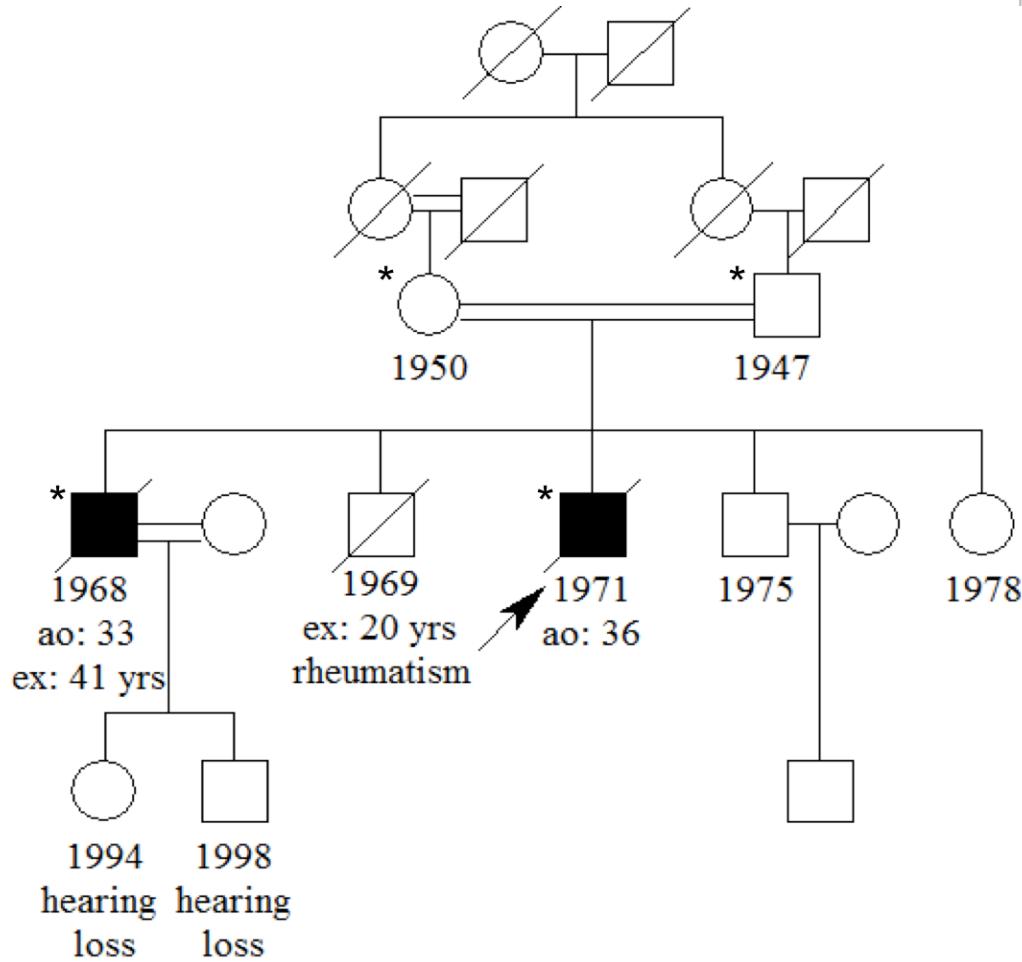
Clinical diagnosis: ALS

Genetics: recessive

- C9Orf72, SOD1, UBQLN2, TDP-43, FUS, FRDA (-)

IV

V

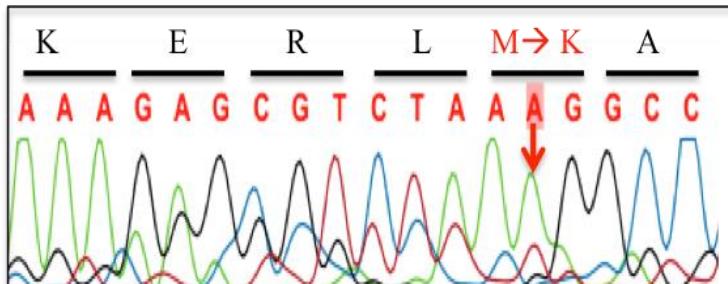


# Exome results/validation: Family 3

Candidate variations in ALS-Family 3.

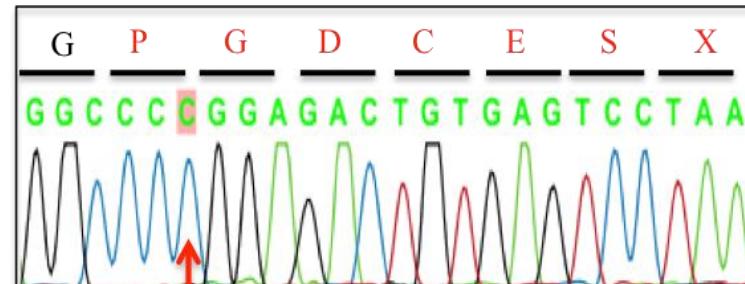
Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr10	13152400	OPTN	rs11258194	T/A	c.T293A:p.M98K
chr10	13164477	OPTN	-	G/GC	c.873dupC:p.G291fsX6

OPTN p.M98K mutation



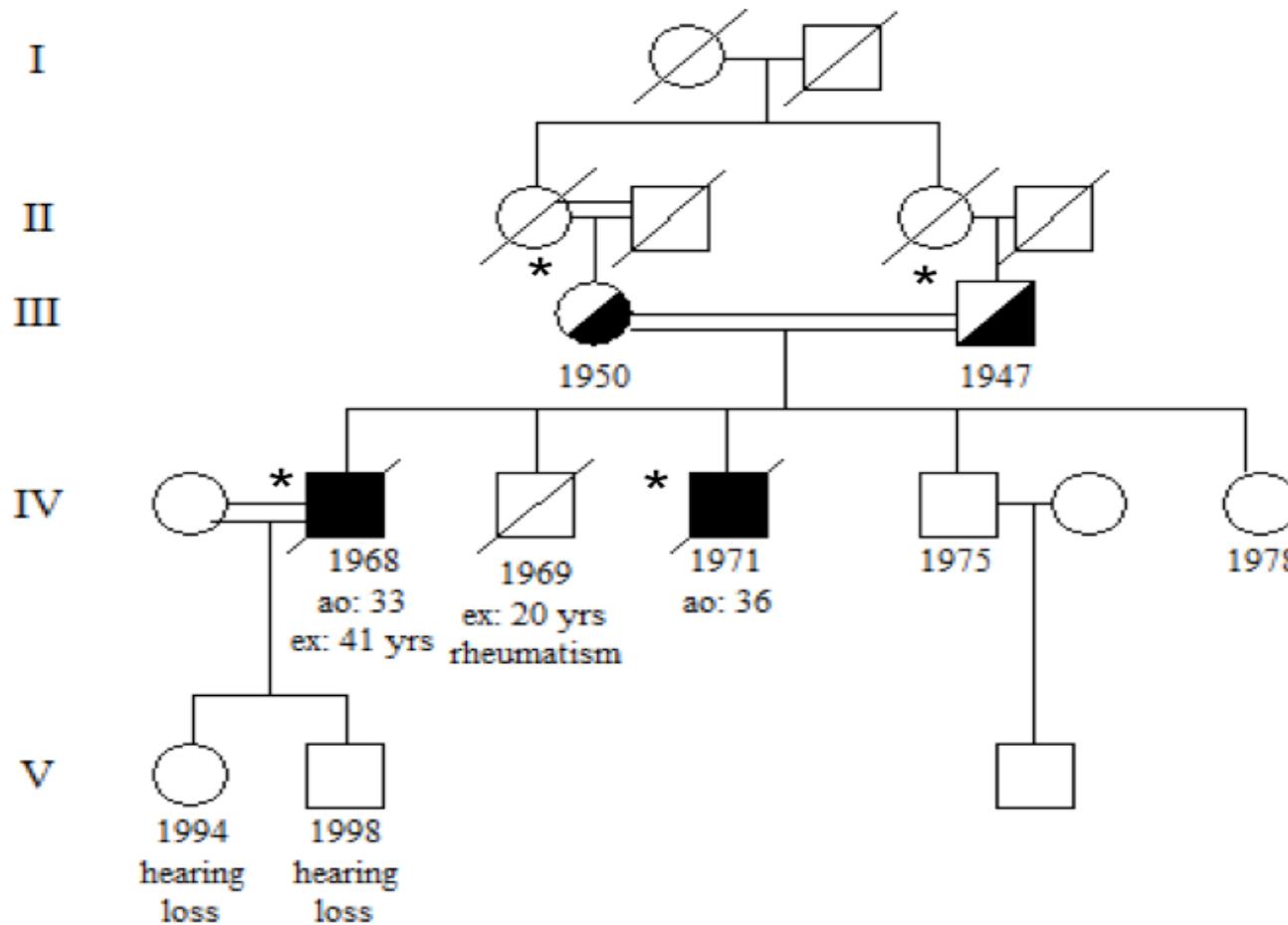
index case

OPTN p.G291fsX6 mutation

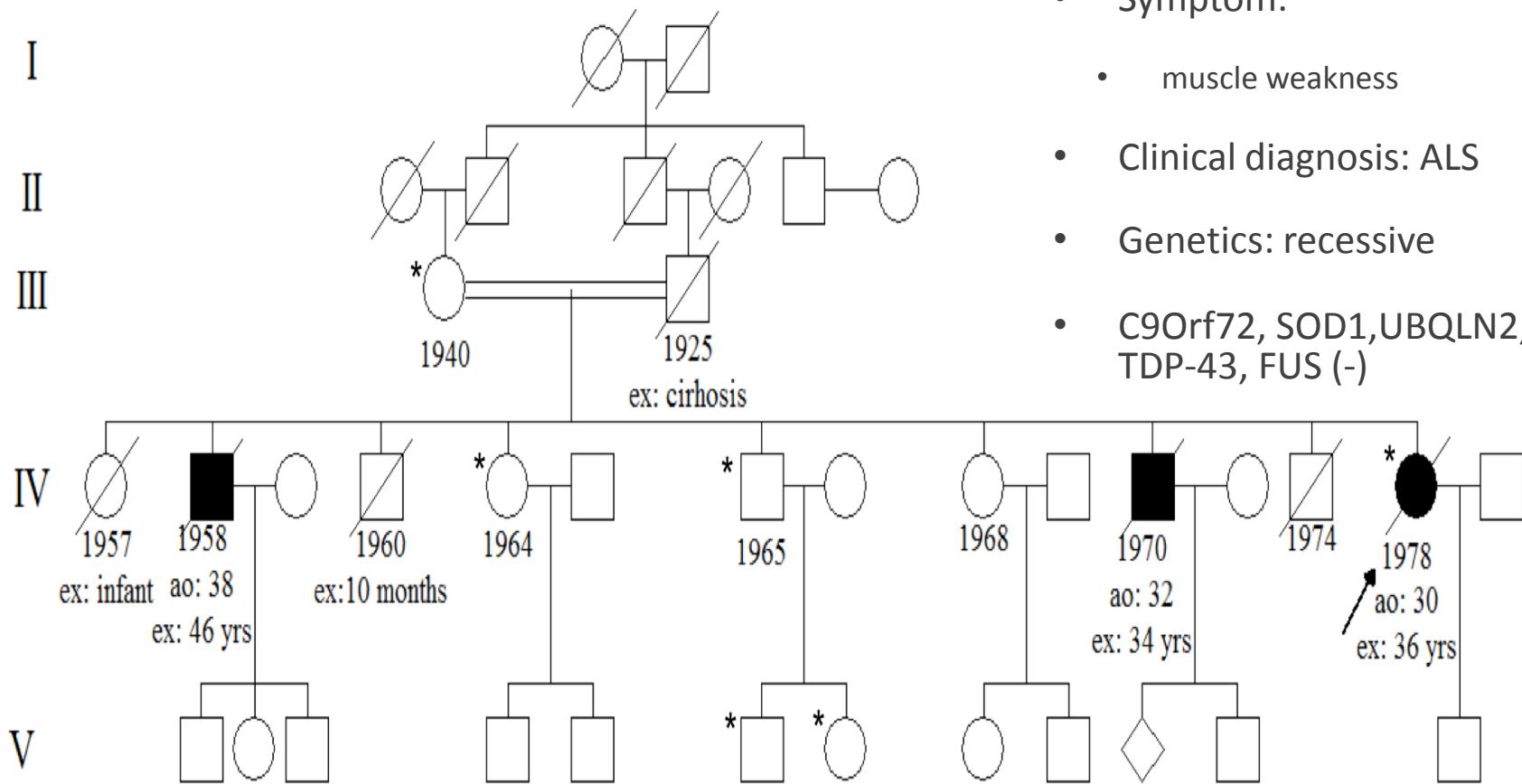


26 index case

# Overall results-Family 3: ALS



# Family 4

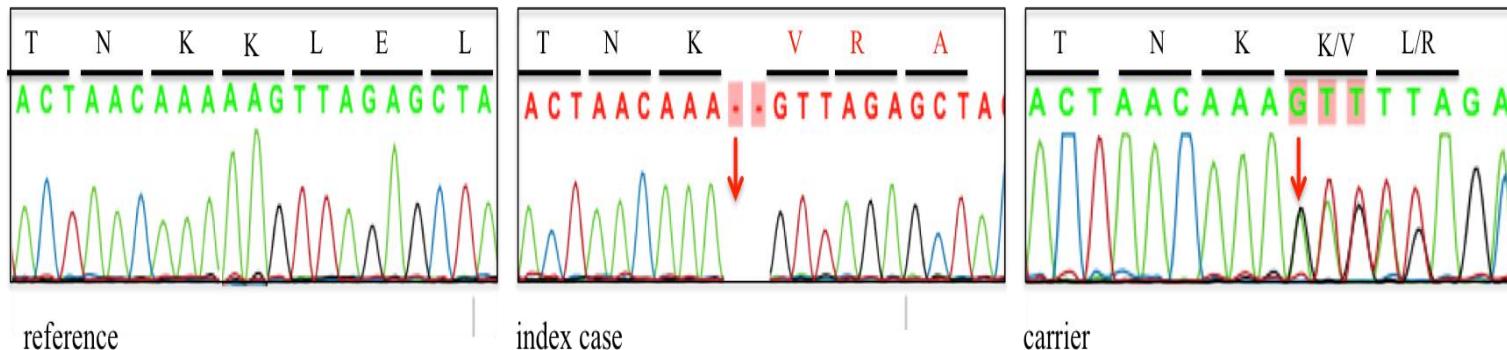


# Exome results/validation: Family 4

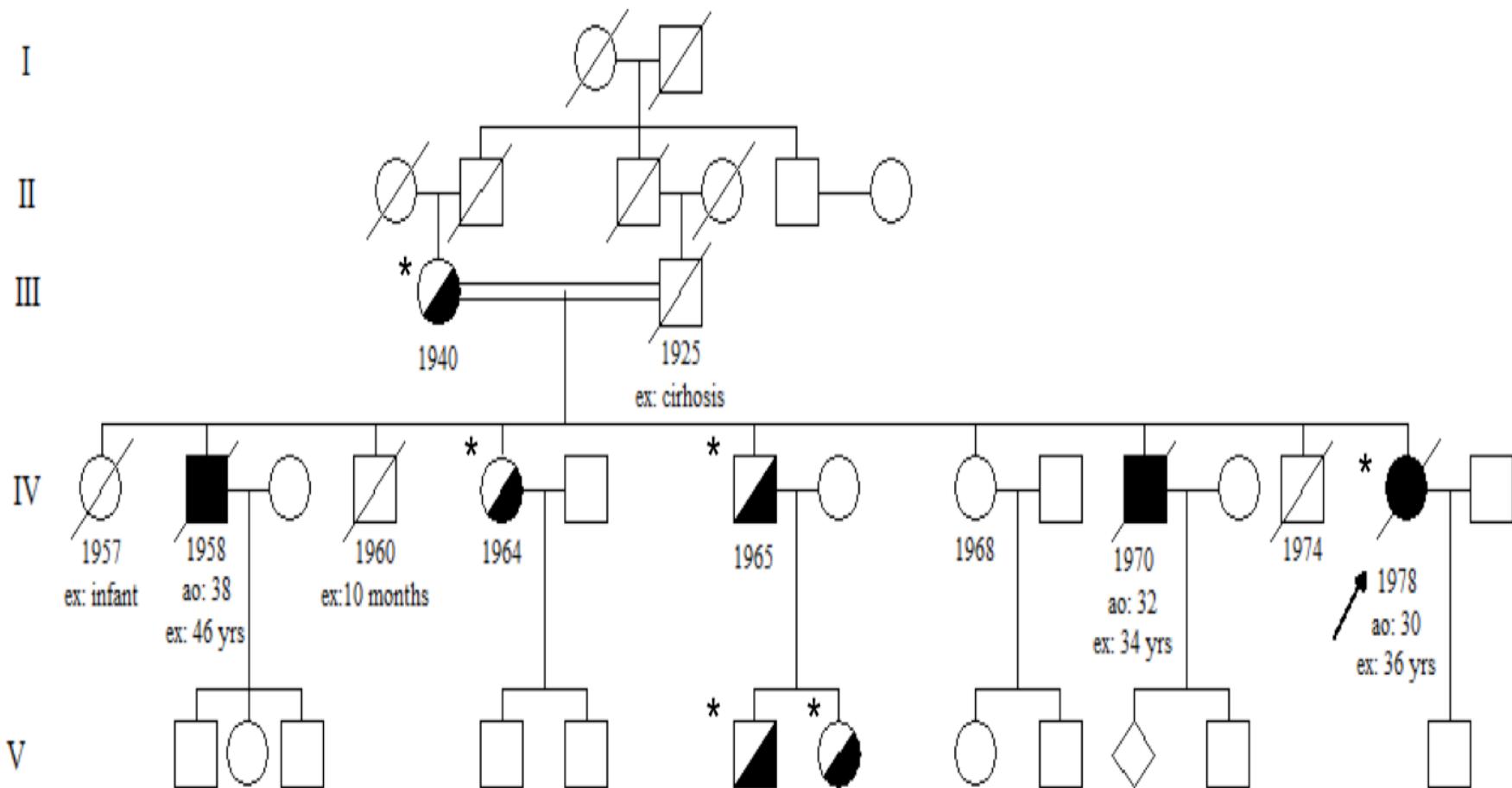
Candidate variation in ALS-Family 4.

Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr10	13167492	OPTN	-	CAA/A	p.359_359del

OPTN p.359\_359del mutation

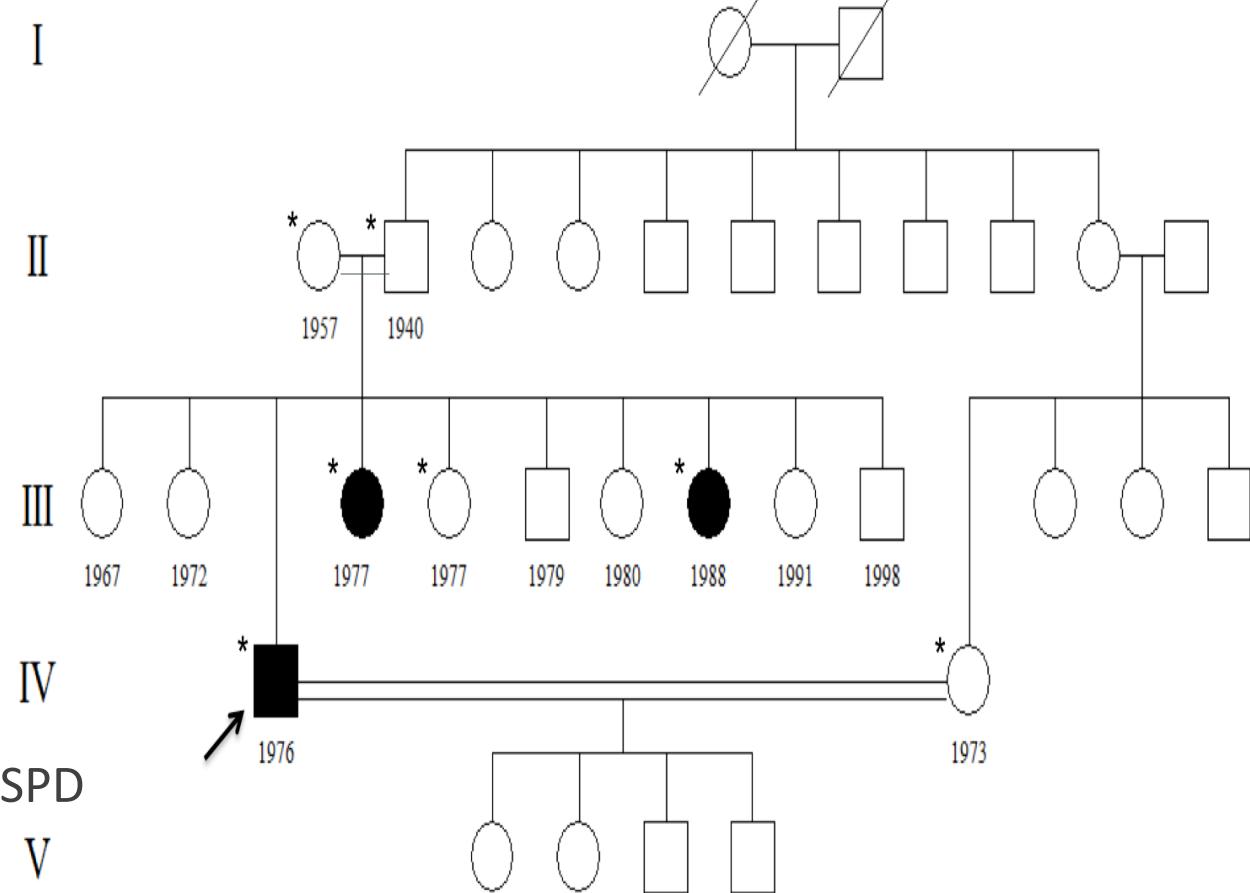


# Overall results-Family 4: ALS

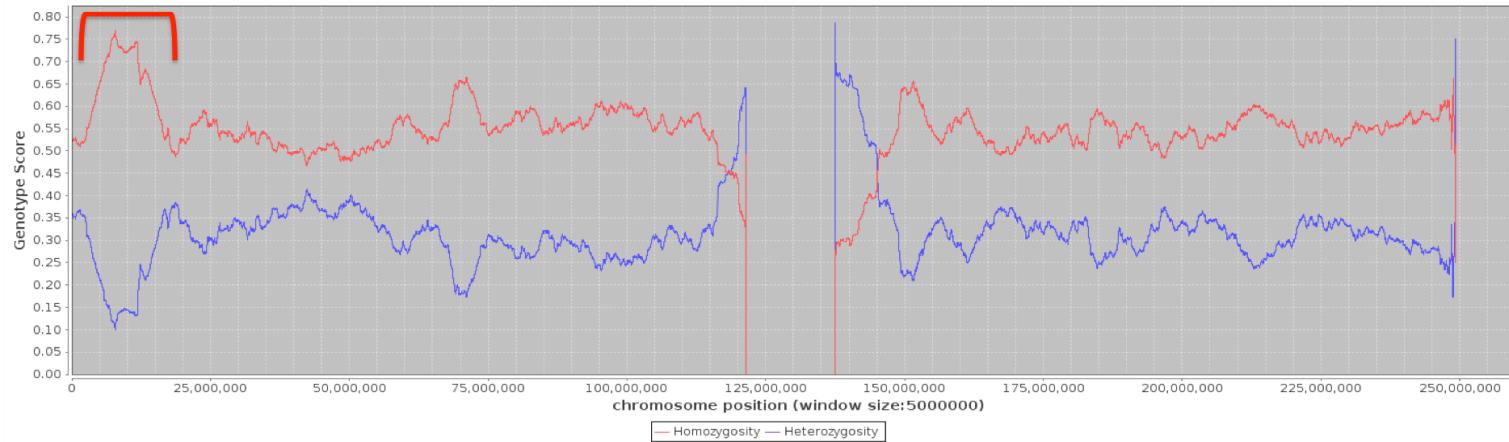


# Family 5: ALS with parkinsonism

- Symptoms:
  - bradykinesia
  - rigidity
  - tremor
  - speech problems
  - blepharospasm
  - psychosis
  - hallucination
  - AO: 24 years
- Clinical diagnosis: ALSPD
- Genetics: recessive

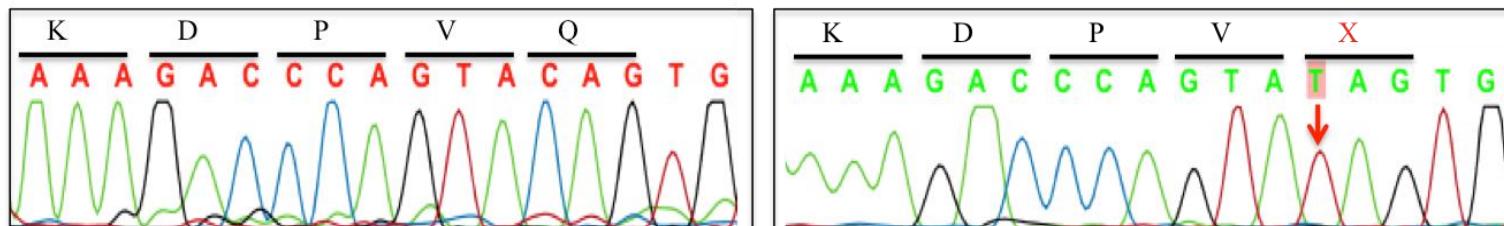


# Exome results/validation: Family 5



Candidate variation in DJ1 Family.

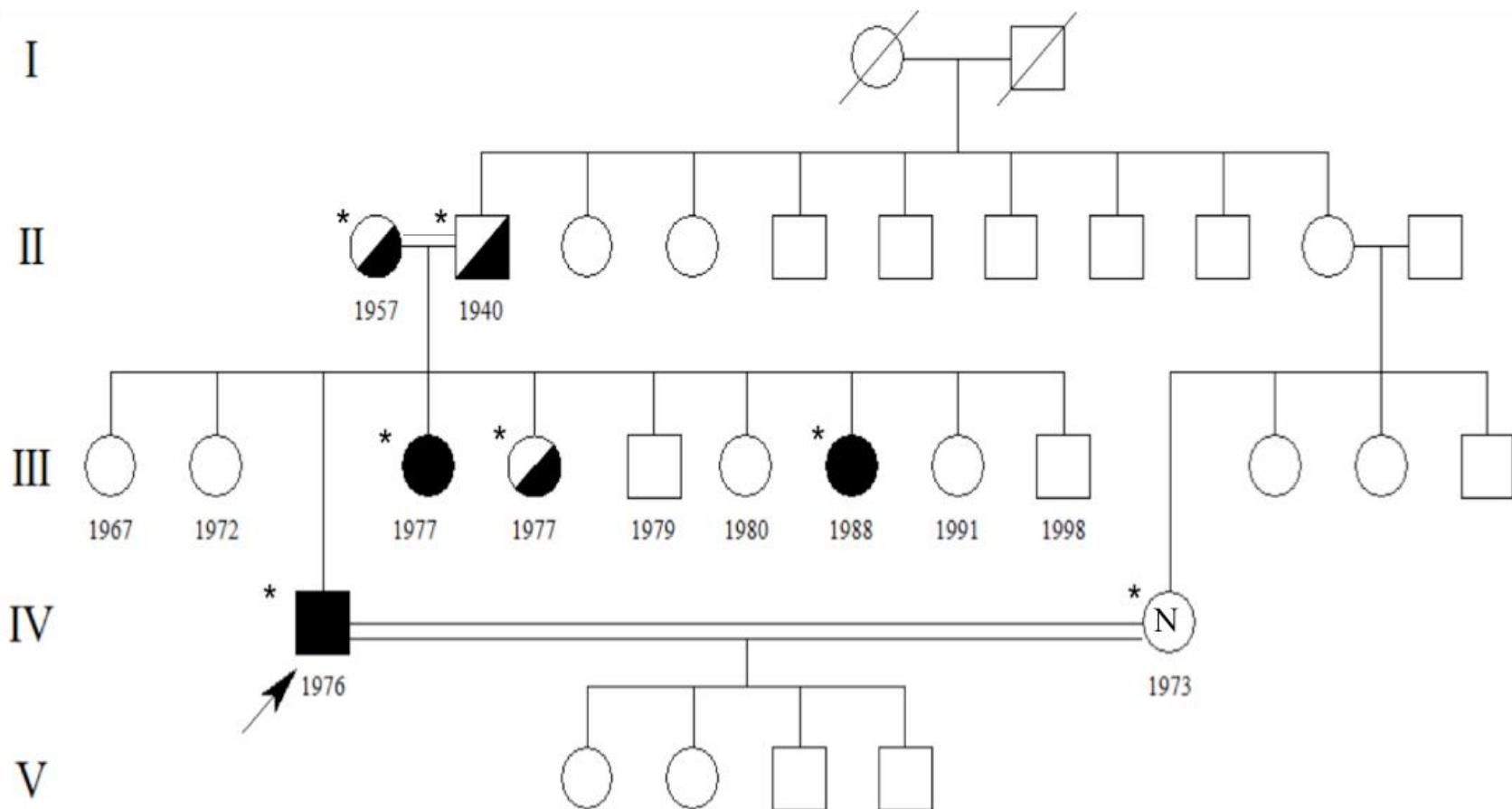
Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr1	8025425	DJ1	-	C/T	c.C133T:p.Q45X



reference

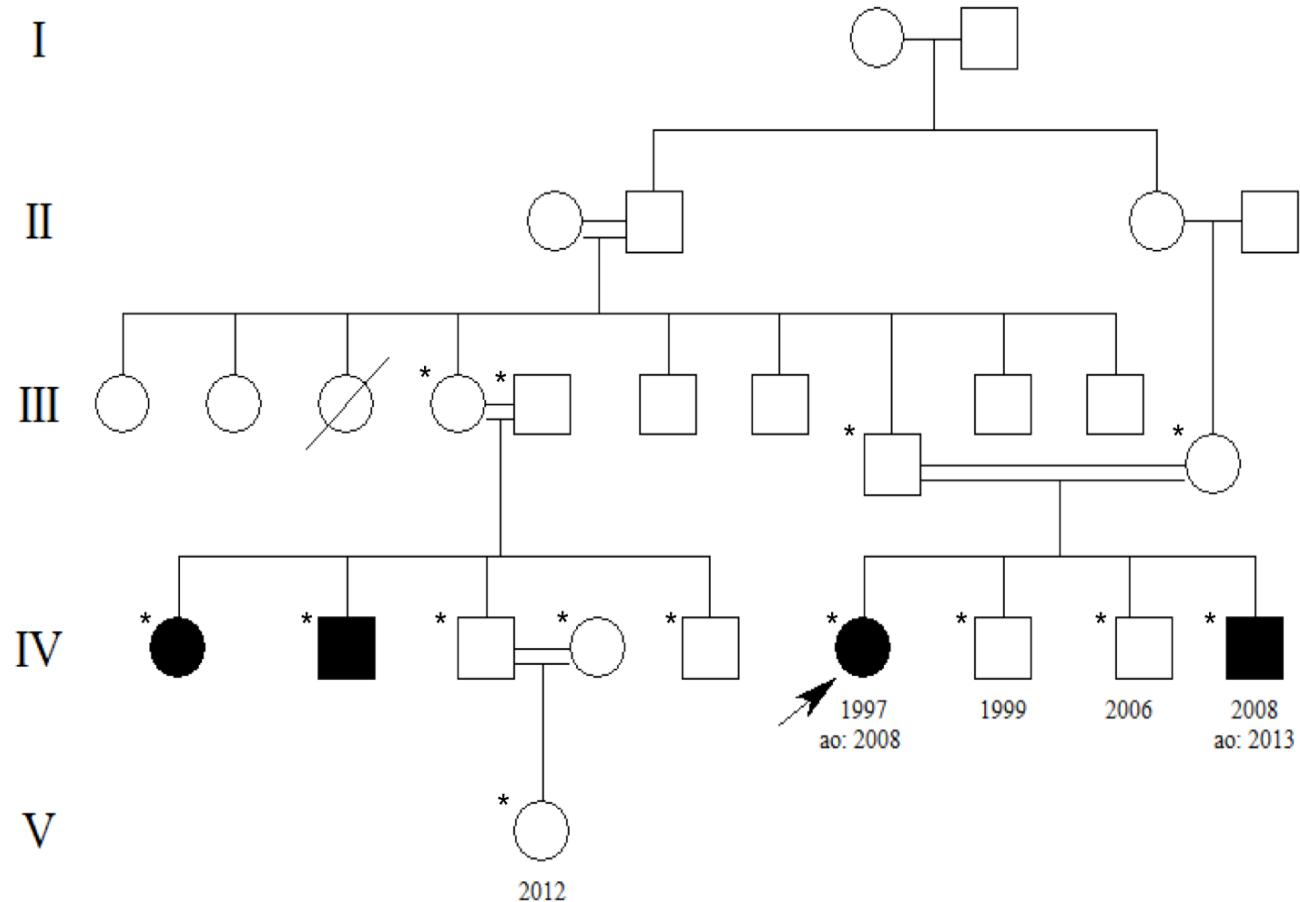
32 index

# Overall results-Family 5: ALD-PD



# Family 6

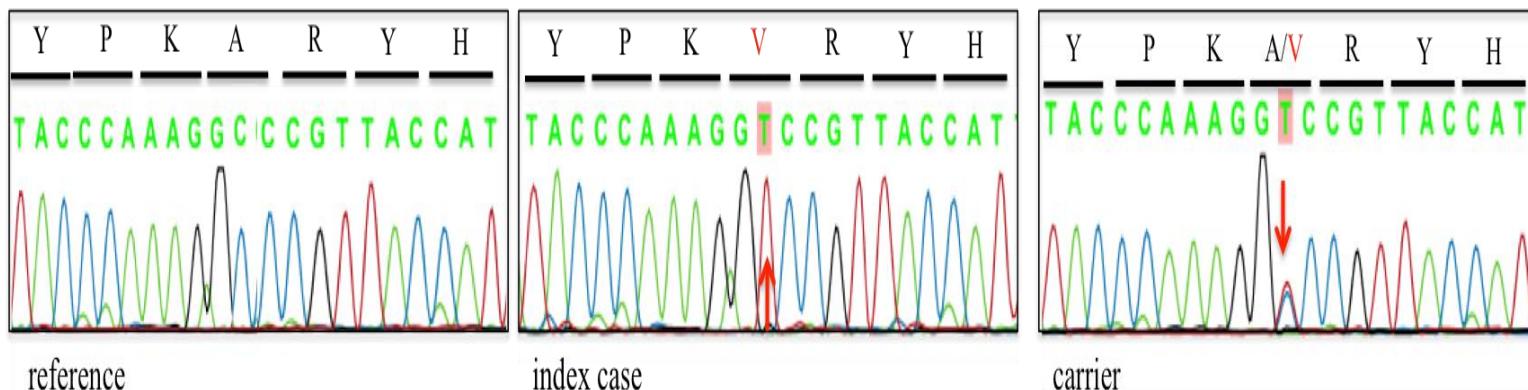
- Symptoms:
  - balance disorder
  - walking difficulties
  - cerebellar atrophy
  - polyneuropathy
- Clinical diagnosis:  
SCA and FRDA
- Genetics SCA1,3  
and FRDA(-)



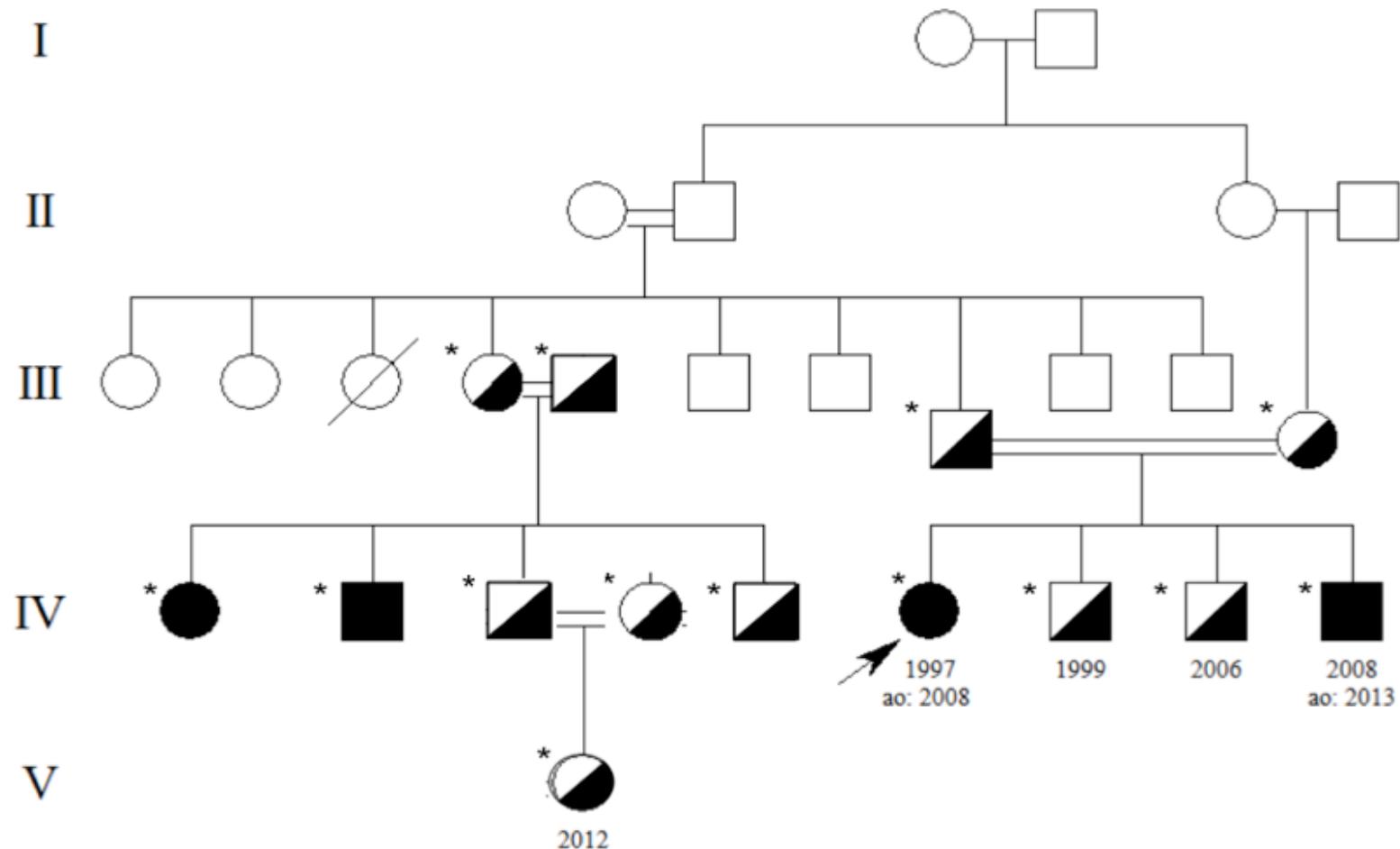
# Exome results/validation: Family 6

Candidate variation in AOA1-Family 1.

Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr9	32984806	APTX	-	G/A	c.C473T:p.A158V



# Overall results-Family 6: Ataxia with Oculomotor Apraxia type 1



# Family 7

- V.1: AO, 14 years

mental retardation

walking difficulties

- V.2: AO, 13 years

walking difficulties

no mental retardation

Clinical diagnosis:

SCA and FRDA

Genetics: recessive

SCA 1,2,3,6,7,17 and

FRDA (-)

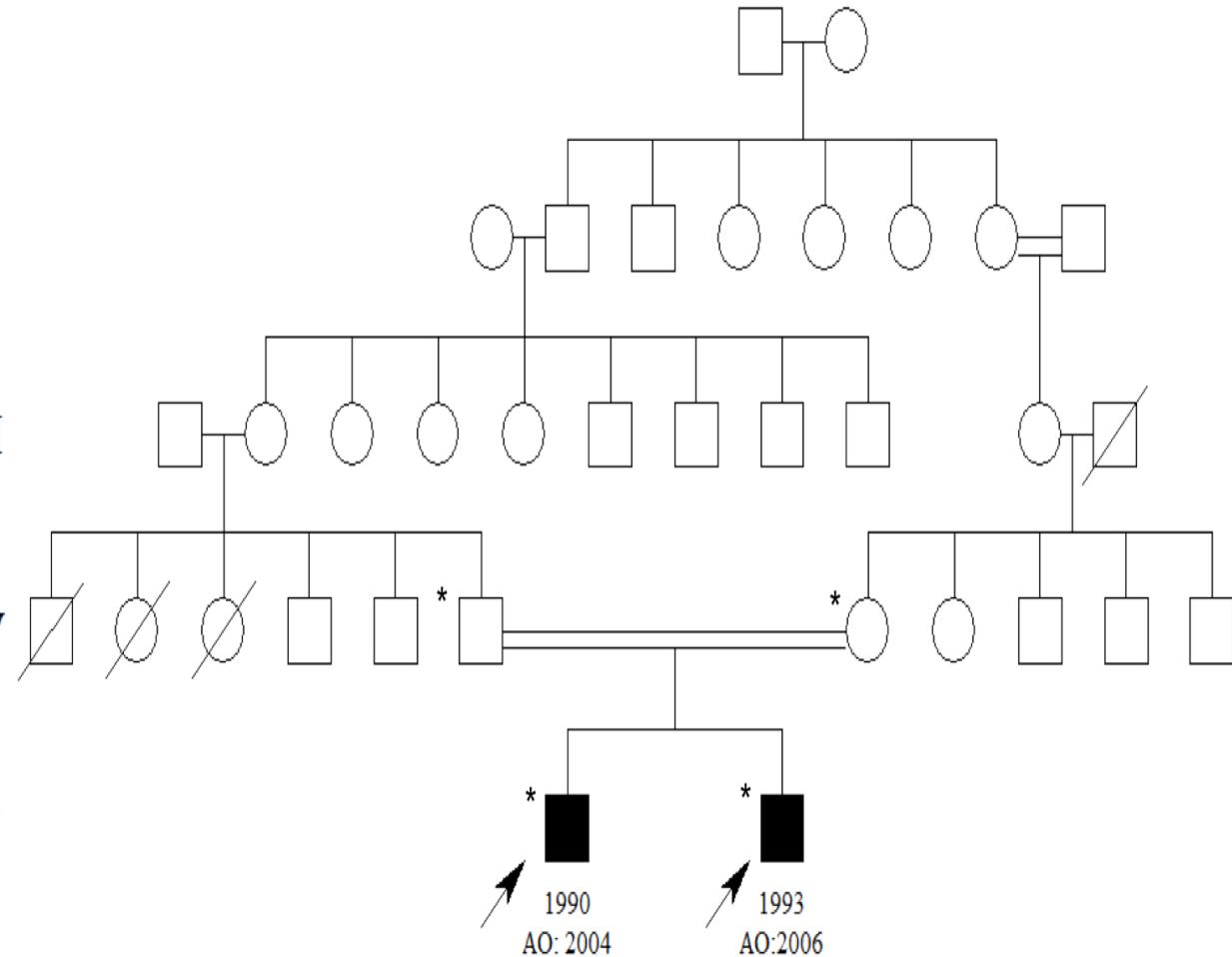
I

II

III

IV

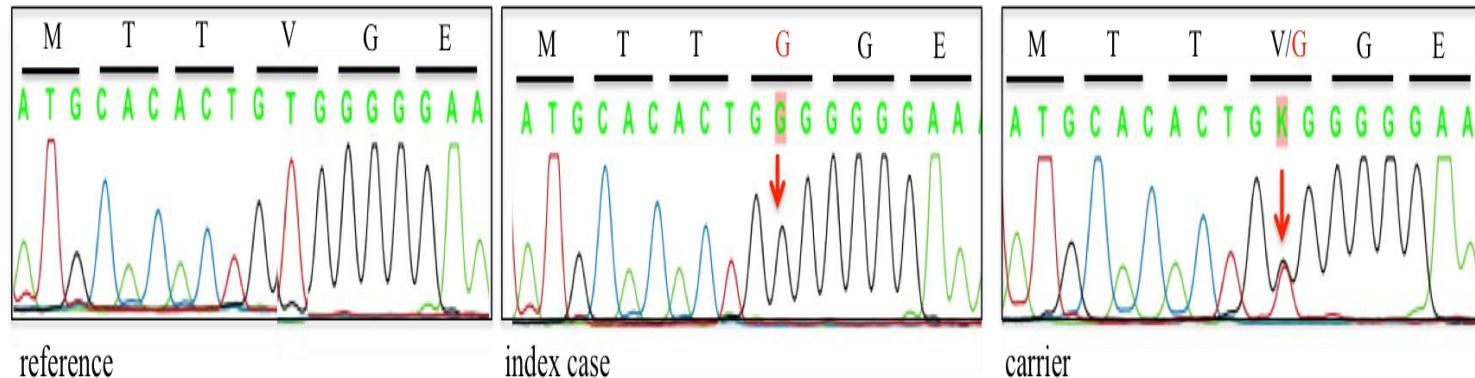
V



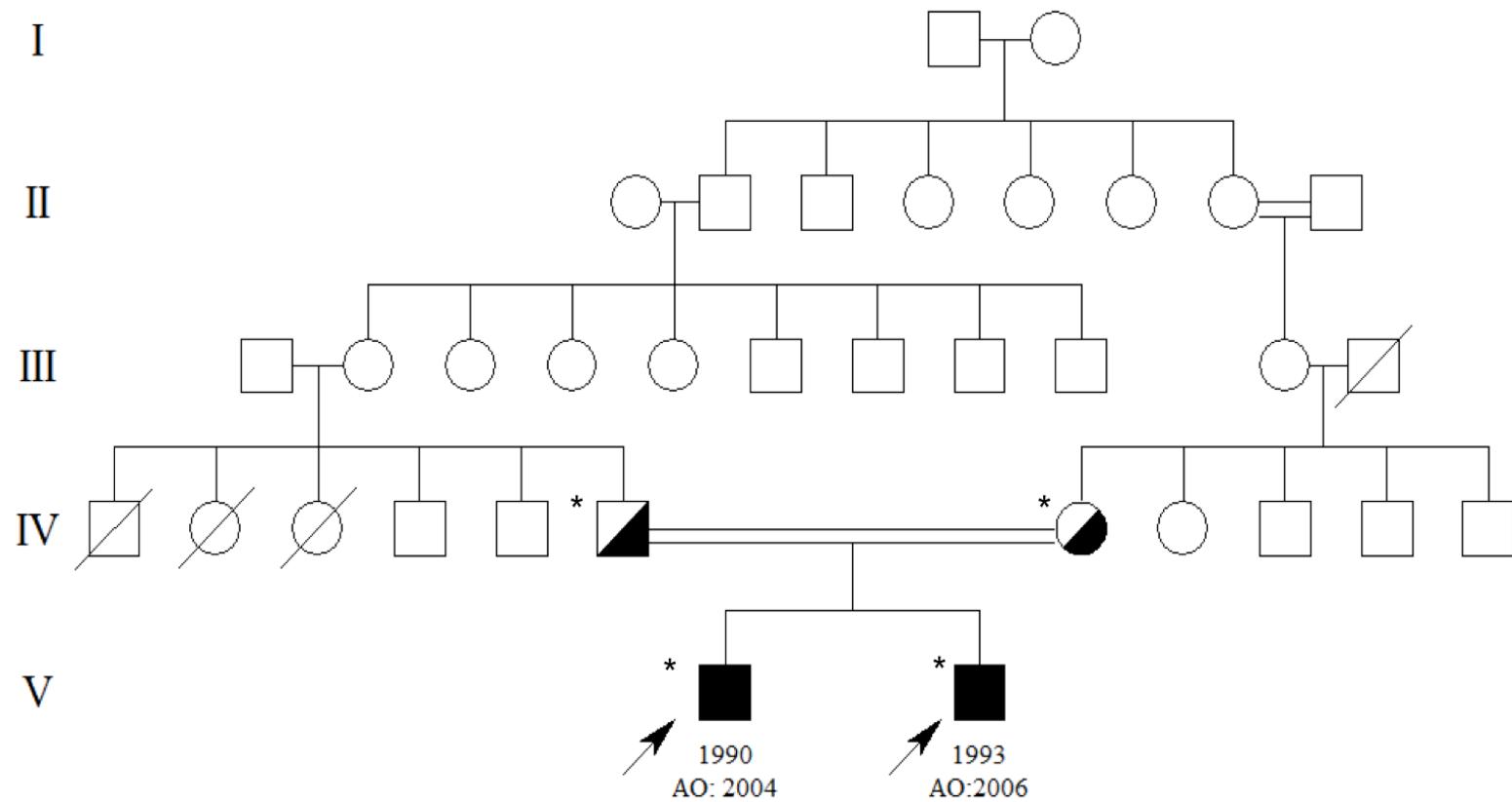
# Exome results/validation: Family 7

Candidate variation in AOA1-Family 2.

Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr9	32984710	APTX	-	A/C	c.T569G:p.V190G



# Overall results-Family 7: Ataxia with Oculomotor Apraxia type 1



# Family 8

- Symptoms:

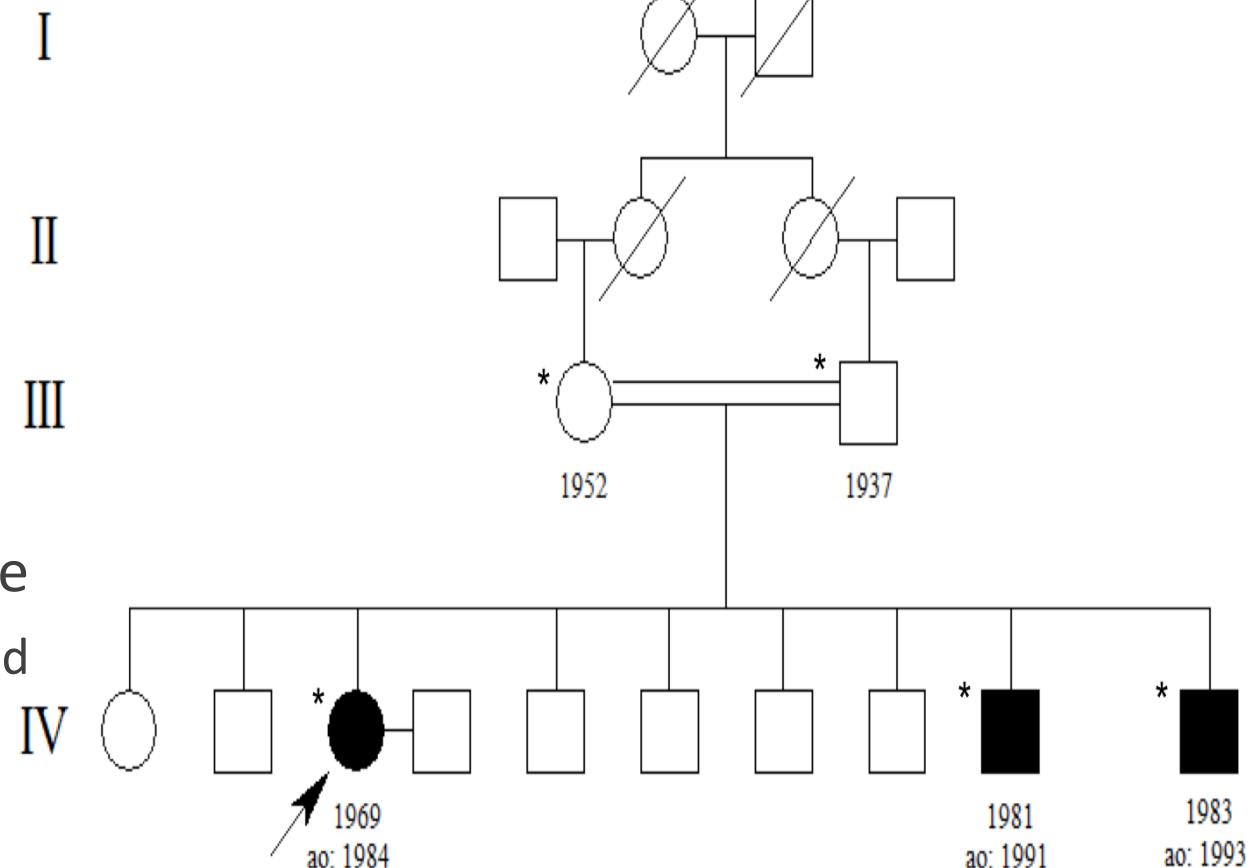
- speech problems I
- walking difficulties II
- cerebellar ataxia III

- Clinical diagnosis:

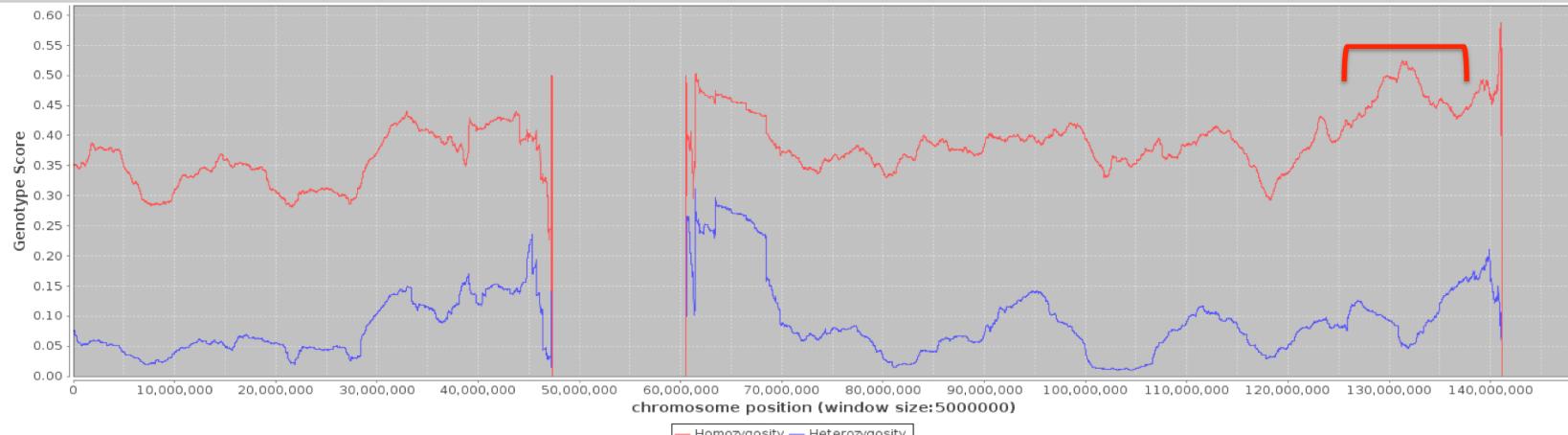
- SCA and FRDA

- Genetics: recessive

- SCA 1,2,3,6,7,17 and  
FRDA (-)

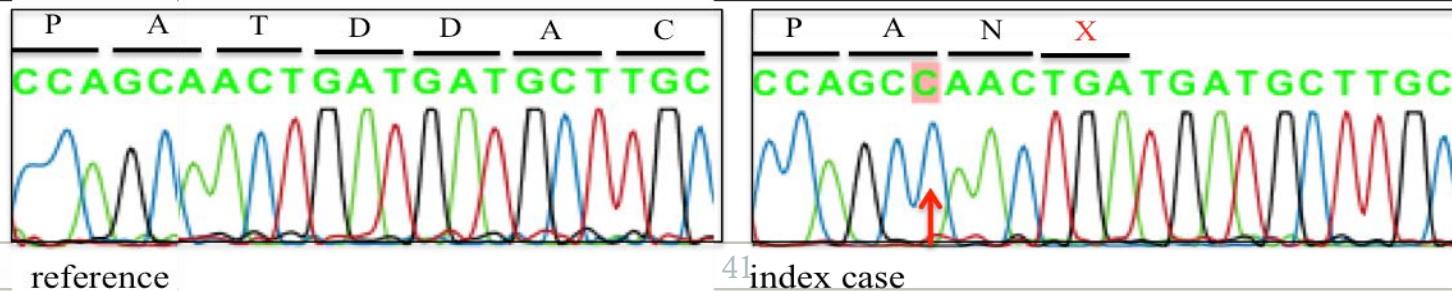


# Exome results/validation: Family 8

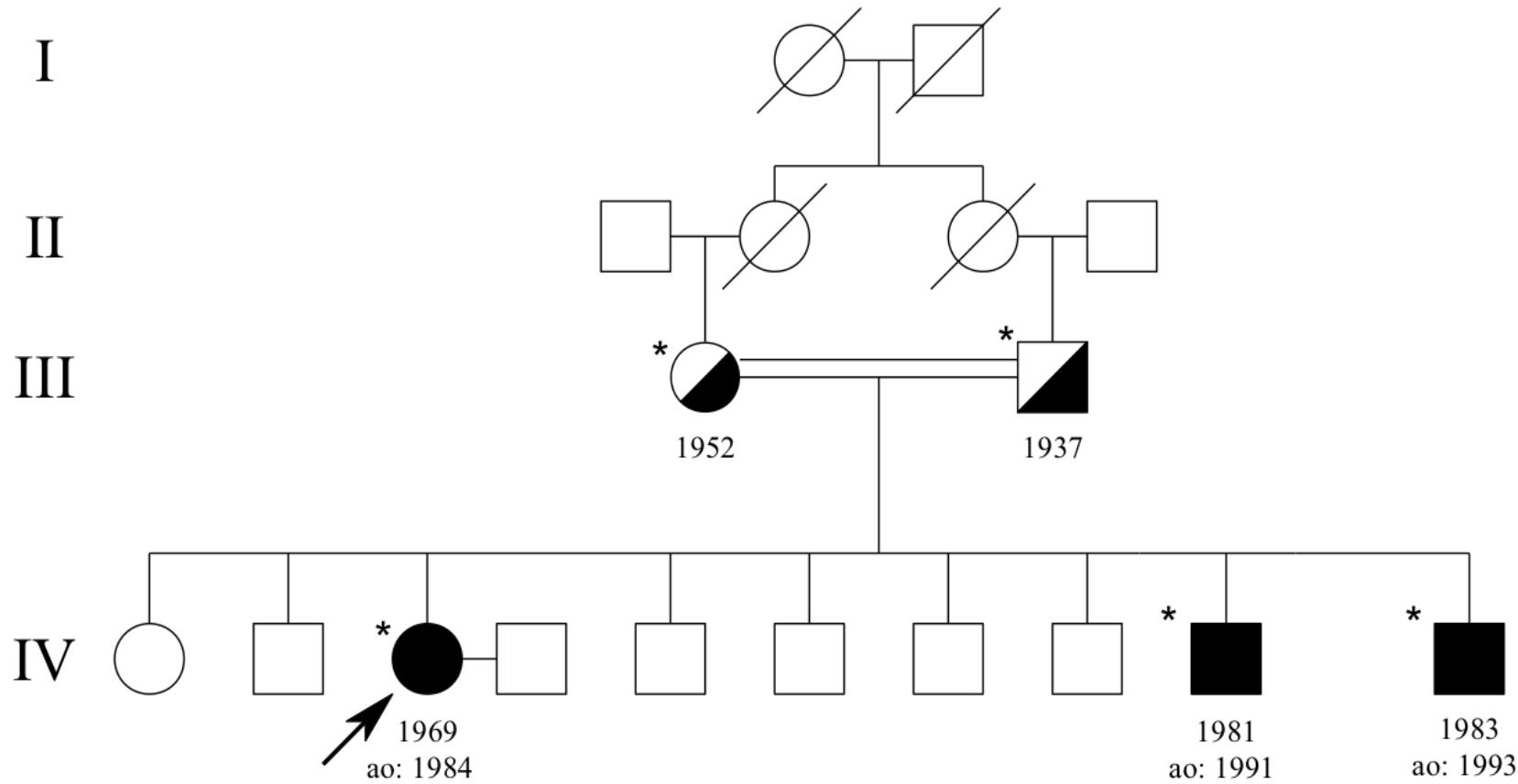


Candidate variant list

Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr9	135202689	SETX	-	T/TG	c.4296_4297insC:p.A1432fs

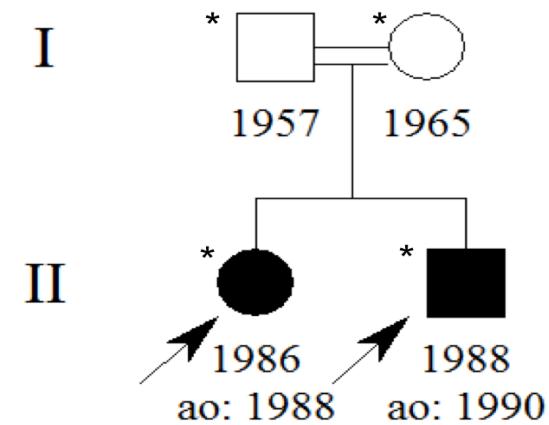


# Overall results-Family 8: Ataxia with Oculomotor Apraxia type 2



# Family 9

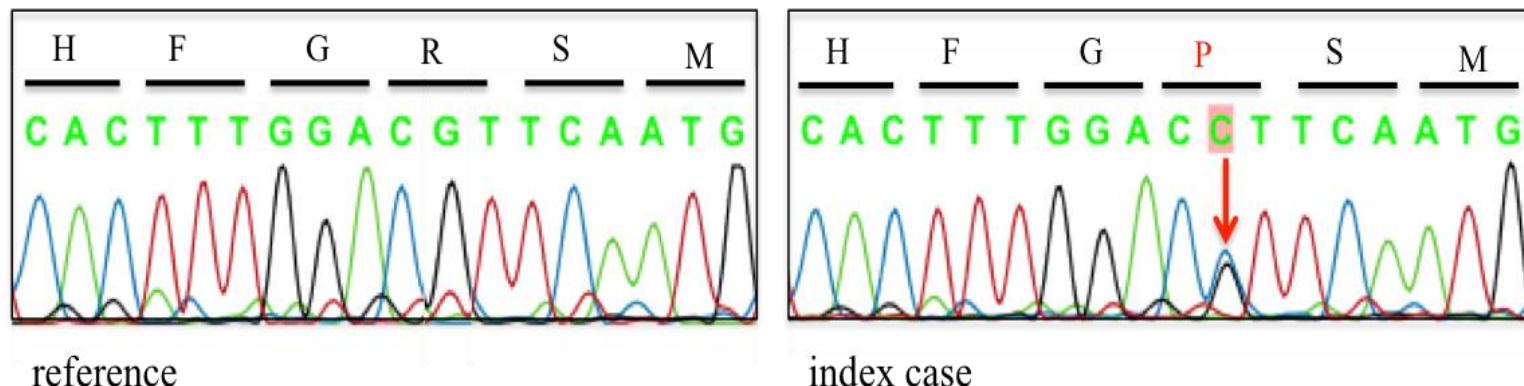
- Symptoms:
  - walking difficulties at the age of two
  - dysarthria
  - spinocerebellar atrophy
- Clinical diagnosis: SCA and FRDA
- Genetics: recessive
  - SCA 1,2,3,6,7,17 and FRDA (-)



# Exome results/ validation: Family 9

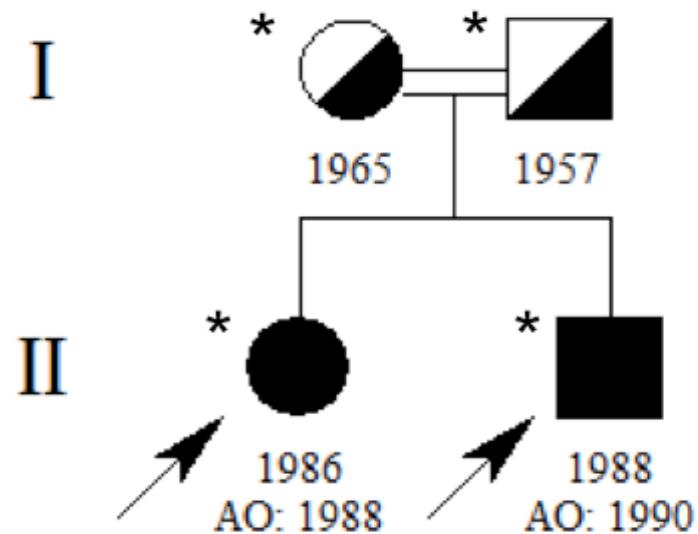
Candidate variation in the ALTD1-Family.

Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr11	94211981	MRE11A	-	C/G	c.G464C:p.R155P



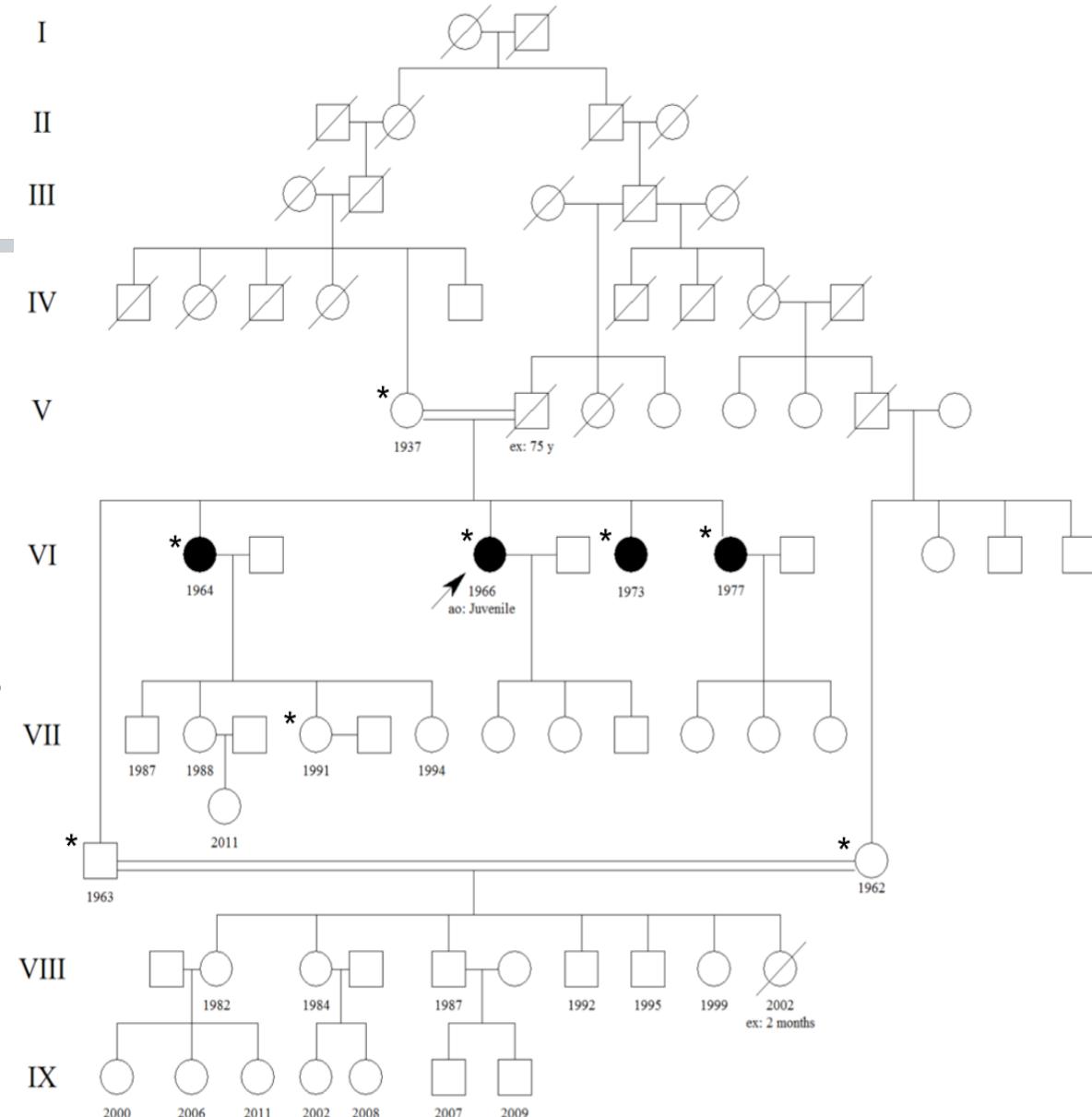
# Overall results: Family 9

## Ataxia-telangiectasia-like Disorder-1

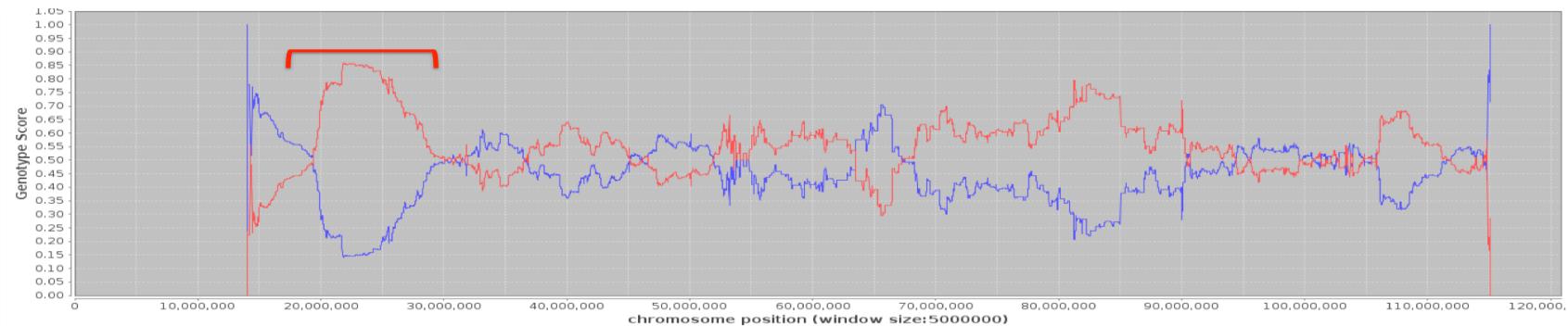


# Family 10

- Symptoms:
  - tenar
  - hypotenar
  - Interosseal
  - tibialis anterior
  - intrinsic foot
  - muscle atrophy
  - symmetrical weakness
  - dysarthria
  - spondylosis
- Clinical diagnosis: FRDA
- Genetics: recessive FRDA (-)



# Exome results/validation: Family 10

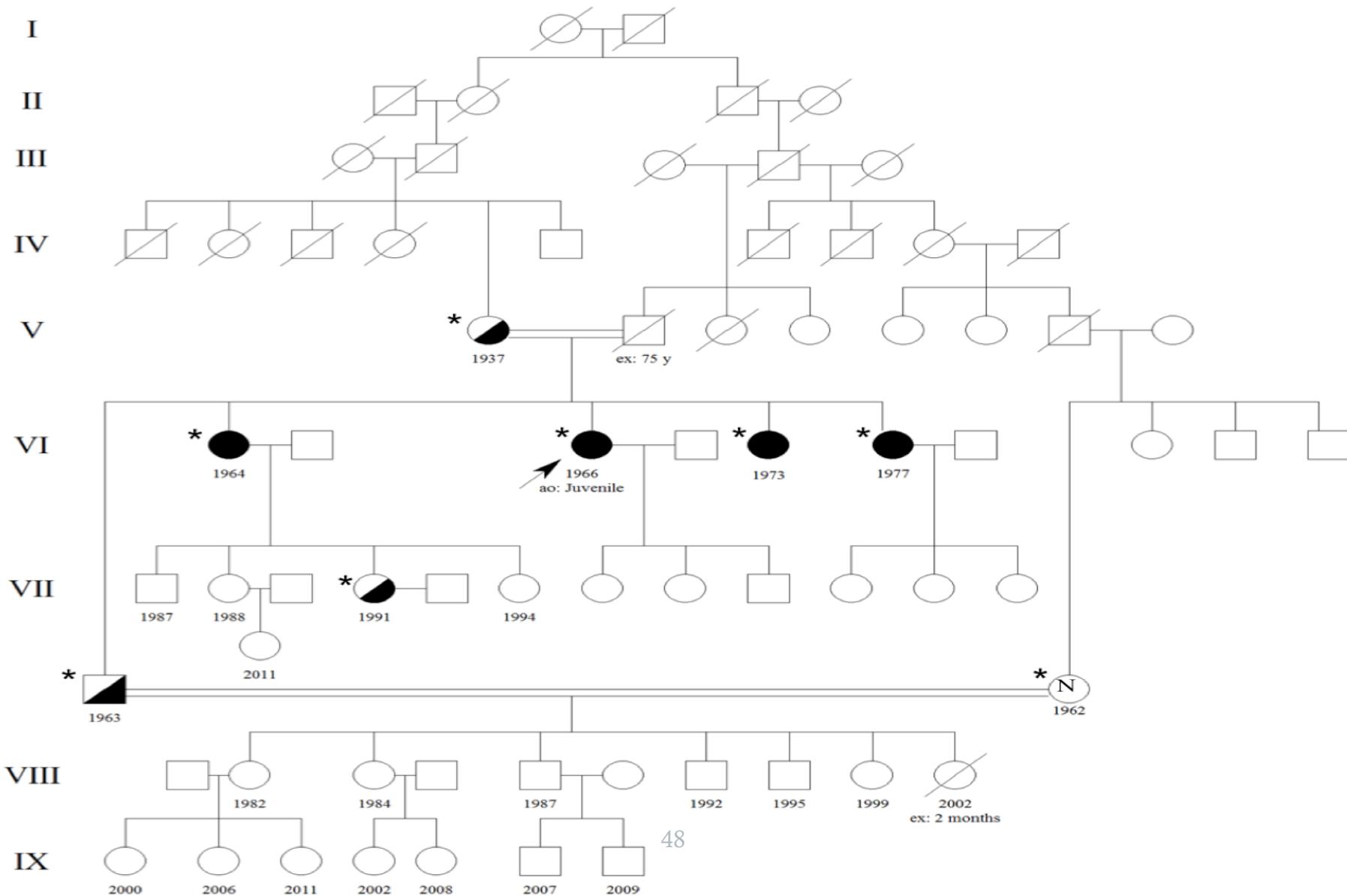


Candidate variant list in ARSACS-Family 1.

Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr13	23909699	SACS	-	C/G	c.G8315C:p.G2772A
chr13	23928656	SACS	-	C/T	c.2093+1G>A
chr15	89399451	ACAN	-	C/T	c.C3635T:p.T1212I
chr16	89399454	ACAN	-	C/T	c.C3638T:p.A1213V

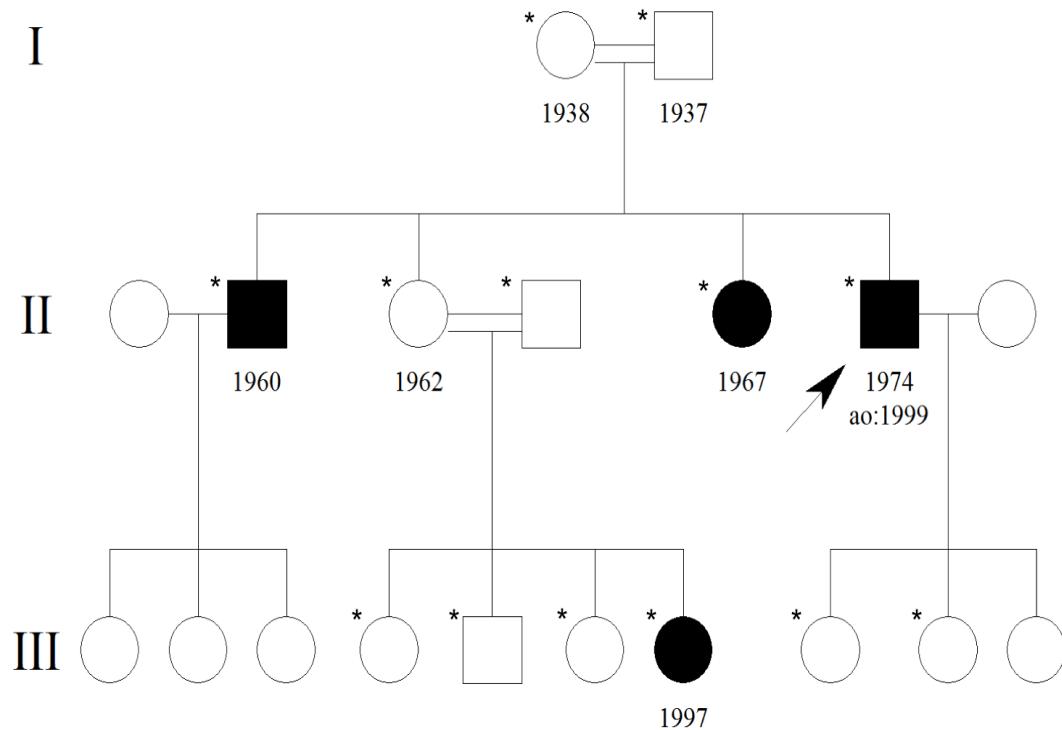
# Overall results-Family 10

## Autosomal recessive spastic ataxia of Charlevoix-Saguenay



# Family 11

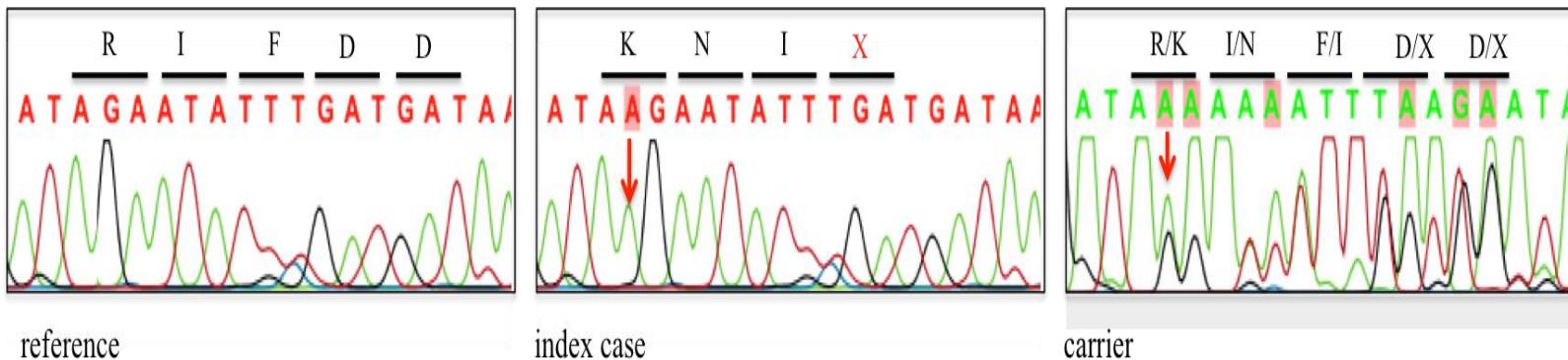
- Symptoms: -
- Clinical diagnosis: SCA
- Genetics: recessive
  - SCA 1,2,3,6,7,17 (-)



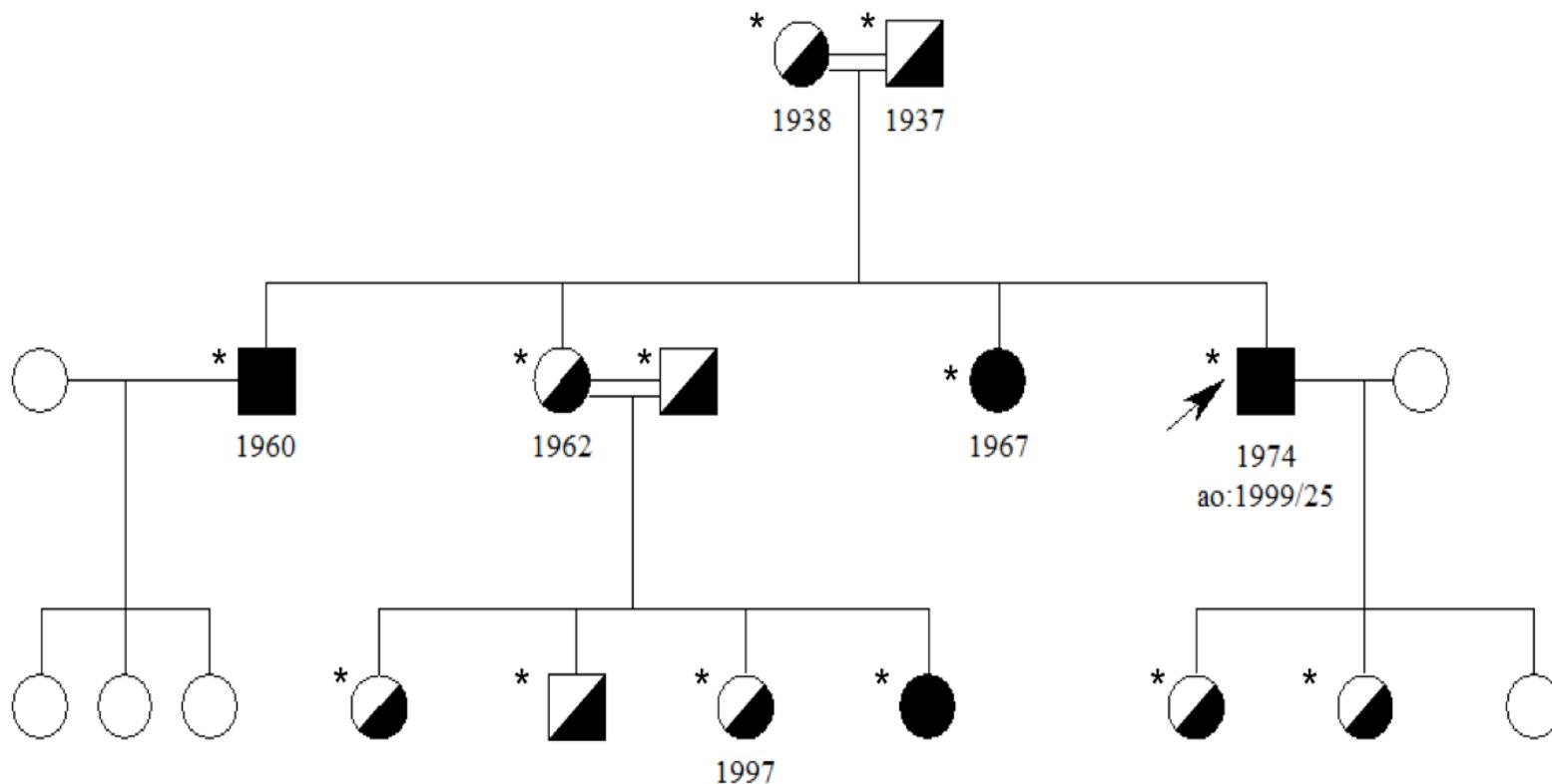
# Exome results/validation: Family 11

Variation list in ARSACS-Family 2.

Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr13	23910294	SACS	-	C/CT	c.7279dupA:p.R2574fs

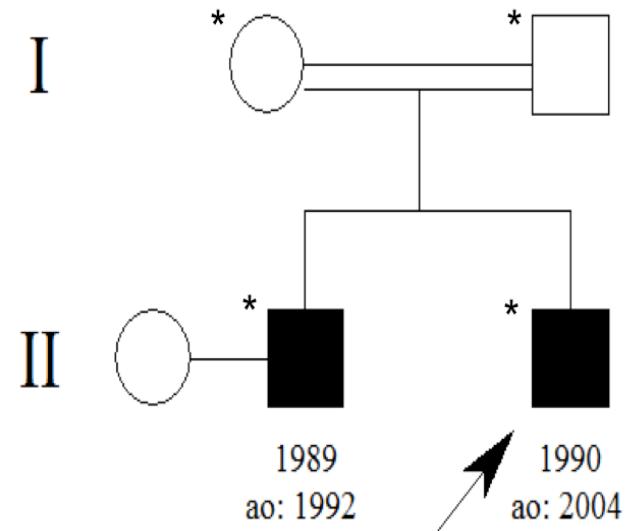


# Overall results-Family 11: Autosomal recessive spastic ataxia of Charlevoix-Saguenay



# Family 12

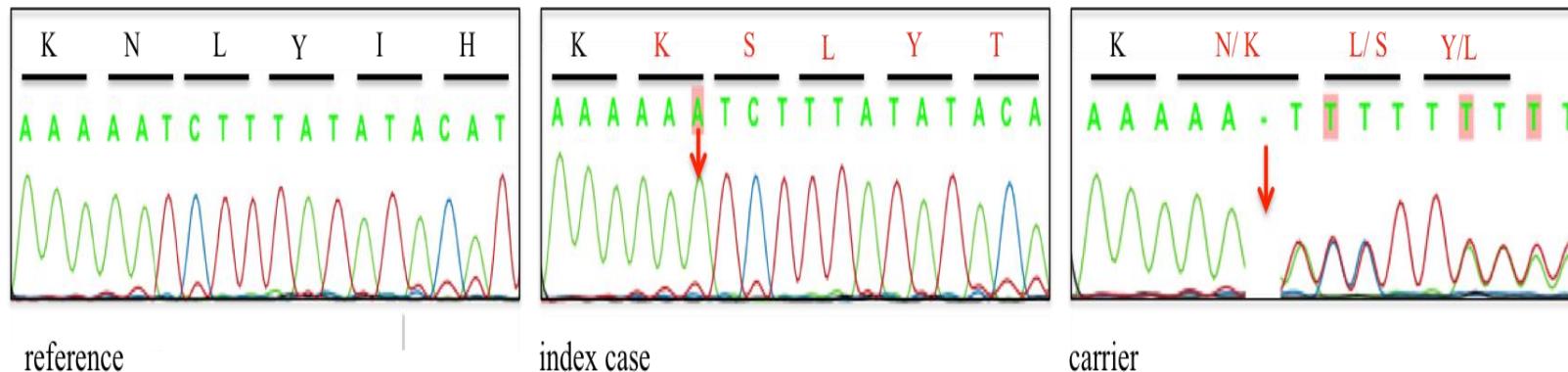
- Symptoms:
  - cerebellar dysfunction
  - nystagmus
  - speech problems
- Clinical diagnosis: SCA and FRDA
- Genetics: recessive
  - SCA 1,2,3,6,7,17 (-)
  - II.2 GAA expansion in FXN



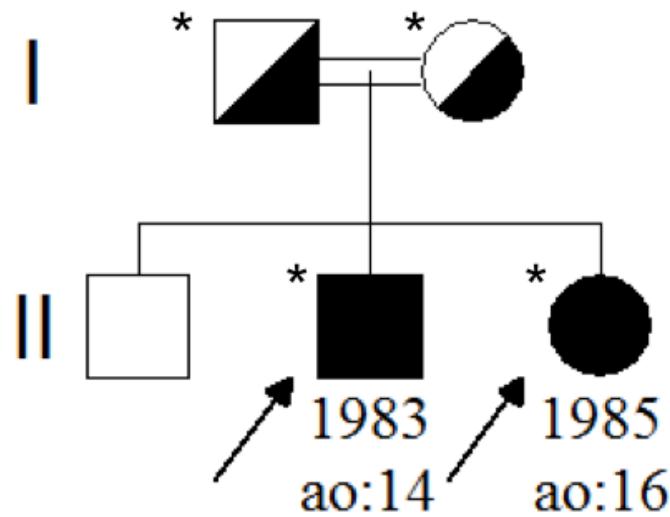
# Exome results/validation: Family12

Candidate variation in ARSACS-Family 3.

Chr	Position	Gene name	dbSNP ID	Ref/A <sub>l</sub> t	Mutation
chr13	23915660	SACS	-	A/AT	c.2355_2356insA:p.N785fsX12

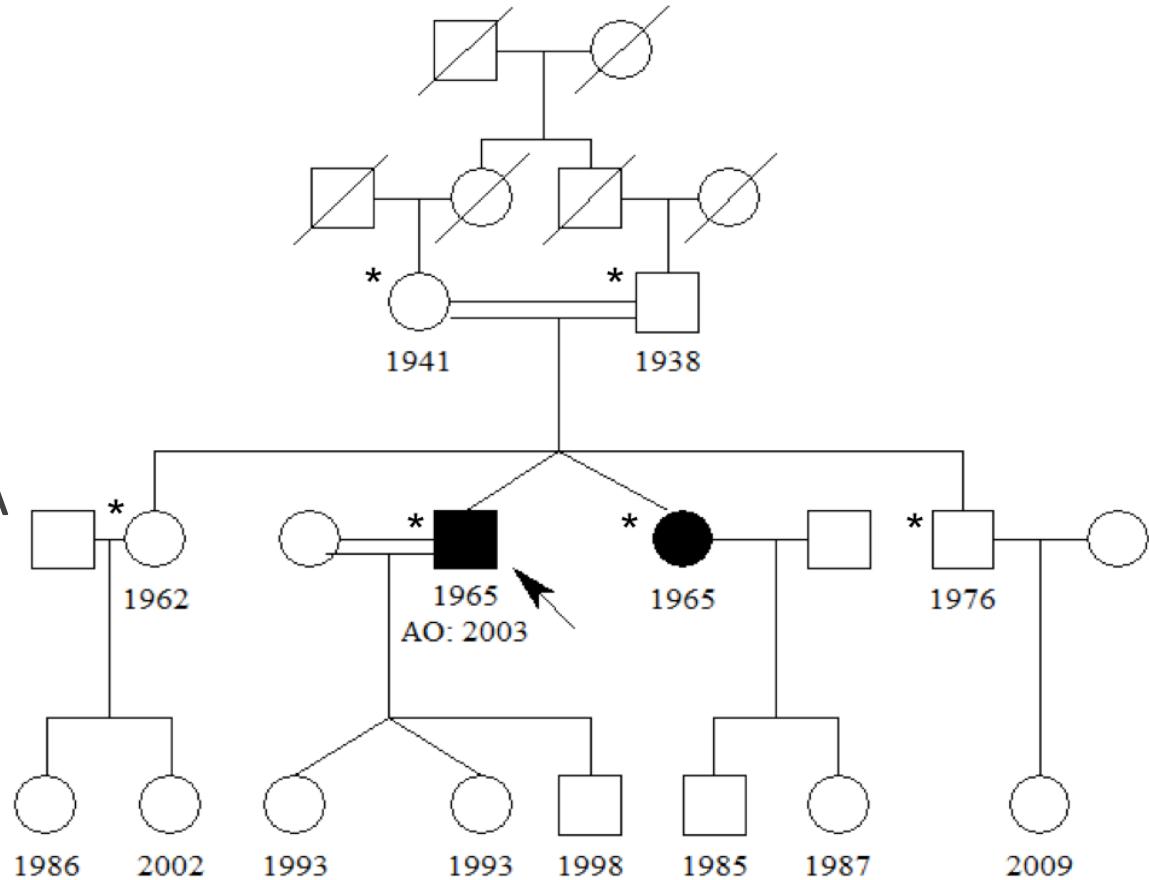


# Overall results-Family 12: Autosomal recessive spastic ataxia of Charlevoix-Saguenay



# Family 13

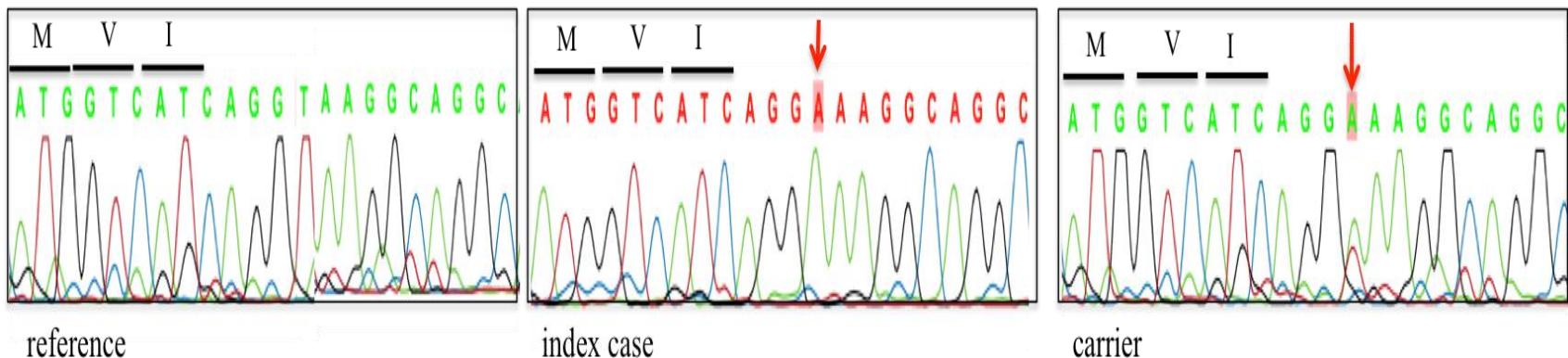
- Symptoms:
  - slowly progressive cerebellar ataxia
  - dementia
  - speech, balance and walking problems
- Clinical Diagnosis: SCA
- Genetics: recessive



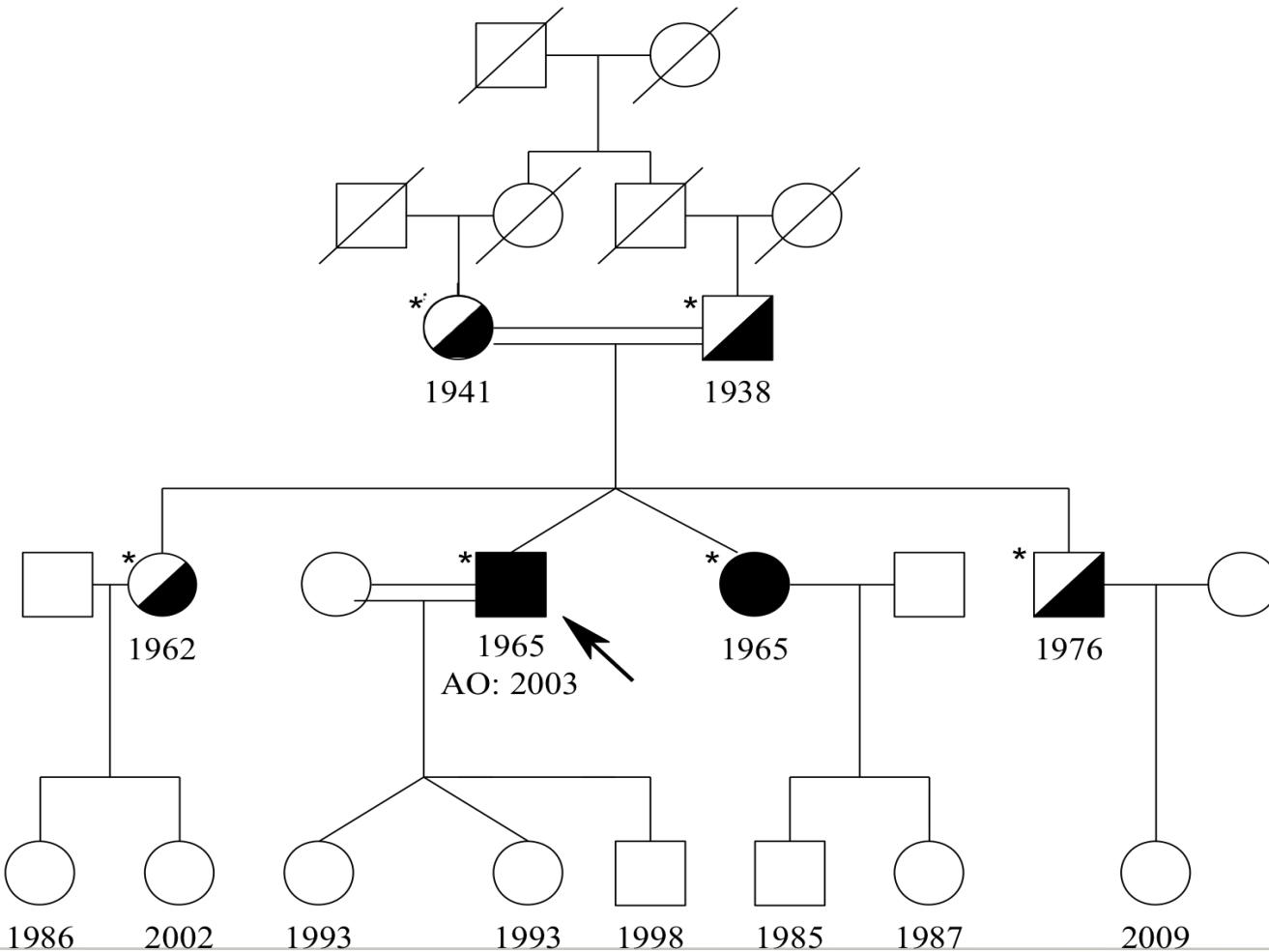
# Exome results/validation: Family 13

Variant list in the family.

Chr	Position	Gene name	dbSNP ID	Ref/Alt	Mutation
chr 1	17314815	ATP13A2	-	A/T	c.2747+2T>A



# Overall results-Family 13: Kufor-Rakeb Syndrome



# Overall results

<b>Family</b>	<b>Diagnosis</b>	<b>Results</b>	<b>Final diagnosis</b>
Family 1	ALS	SQSTM1 p.E274D & TRPM7 p.T1482I	ALS
Family 2	ALS	SPG11 p.Y2272X & p.N1962S	ALS
Family 3	ALS	OPTN p.M98K & p.G291fsX	ALS
Family 4	ALS	OPTN p.359del AA	ALS
Family 5	ALD-PD	DJ1 p.Q45X	ALS-PD
Family 6	SCA & FRDA	APTX p.A158V	AOA1
Family 7	SCA & FRDA	APTX p.V190G	AOA1
Family 8	SCA & FRDA	SETX p.A1482fsX	AOA2
Family 9	SCA & FRDA	MRE11 p.R155P	A-TLD
Family 10	FRDA	SACS p.G2772A & ACAN p.T1212I-p.A1213V	ARSACS
Family 11	SCA	SACS p.R2574fsX	ARSACS
Family 12	SCA & FRDA	SACS p.N785fsX12	ARSACS
Family 13	SCA	ATP13A2 c.2747+2T>A	KRS

# Discussion & Conclusion



# Computational Challenges of Exome Sequencing

- Missing regions: repeat expansions, copy number variations (CNVs), repetitive and satellite regions
- Exon capture problem (GC-rich region)
- False-positive and false-negative rates
- Algorithms and coverage
- Educated people



# What do we need???

Better tools for:

- annotating variants
- manipulating variant data
- prioritizing variants  
(both coding & non-coding)
- prioritizing candidate genes
- pathway analysis for genetic heterogeneity
- methods for functional analysis



# Biological Challenges of Exome Sequencing

- Differential diagnosis in NDD
- Consanguinity, inter- and intra-familial heterogeneity, oligogenic inheritance pattern, incomplete penetrance, de novo mutations
- High number of variations in sporadic and dominant cases
- MAF in open-source databases
- Variant frequency of Turkish population
- Complex genetic and epigenetic factors



# A new era in molecular diagnosis

- Mechanisms leading to neurodegeneration
- Genetic counseling
- Personalized medicine
- More targeted therapies





# Acknowledgements



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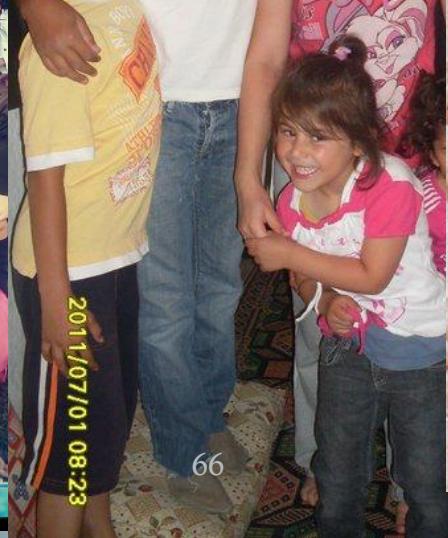
Clinicians

Pınar Kavak

Patients and families







66



# Thank you for listening

Any Questions?

