e table 1

Standard nerve conductions studies at the age of 59

Nerve	Stimulation	Values		
Motor		*DML (ms)*	*CMAP (mV)*	*MCV (m/s)*
Peroneal	Ankle	3.3 [5.0]	**1.8** [2.1]	
	Fibula (head)		**1.6** [2.1]	44.2 [41]
Tibial	Ankle	4.3 [5.1]	5.8 [2.9]	
	Popliteal fossa		3.6 [2.9]	46.0 [40]
Median	Wrist	**4.2** [4.5]	2.9 [2.9]	
	Elbow		**2.2** [2.9]	**41.0** [49]
Ulnar	Wrist	3.8 [3.5]	**2.1** [2.5]	
	Elbow		**1.8** [2.5]	48.0 [48]
Sensory			*SNAP (µV)*	*SCV (m/s)*
Sural	Ankle		9.0 [3.5]	47.0 [38]

Pathological values are marked bold. Reference values are given in square brackets. DML, distal motor latency (ms); CMAP, compound muscle action potential (mV); MCV, motor conduction velocity (m/s); SNAP, sensory nerve action potential (µV); SCV, sensory conduction velocity (m/s).

E table 2

mtDNA deletion species detected by single-molecule PCR in the patient's skeletal muscle

Start[a]	End[b]	Size	Flanking sequences[c]	Direct repeat	m.5789 allele	Number of detected molecules
5787	16034	10248	**GTTTGAAGCTGCCT**[CTCCGAATTTGCAA CTGTTCTTTCATGG]**GGAAGCAGATTTGG**	–	–	14
5791	16071	10281	**GAAGCTGCCTCTCC**[GAATTTGCAATTCA AAGTATTGACTCAC]**CCATCAACAACCGC**	C	C	6
5791	16073	10283	**GAAGCTGCCTCTCC**[GAATTTGCAATTCA GTATTGACTCACCC]**ATCAACAACCGCTA**	CC	C	1
5788	16073	10286	**TTTGAAGCTGCCTC**[TCCGAATTTGCAAT GTATTGACTCACCC]**ATCAACAACCGCTA**	C	–	1
5707	16069	10363	**TAACAGCTAAGCAC**[CCTAATCAACTGGC CCAAGTATTGACTC]**ACCCATCAACAACC**	C	–	1

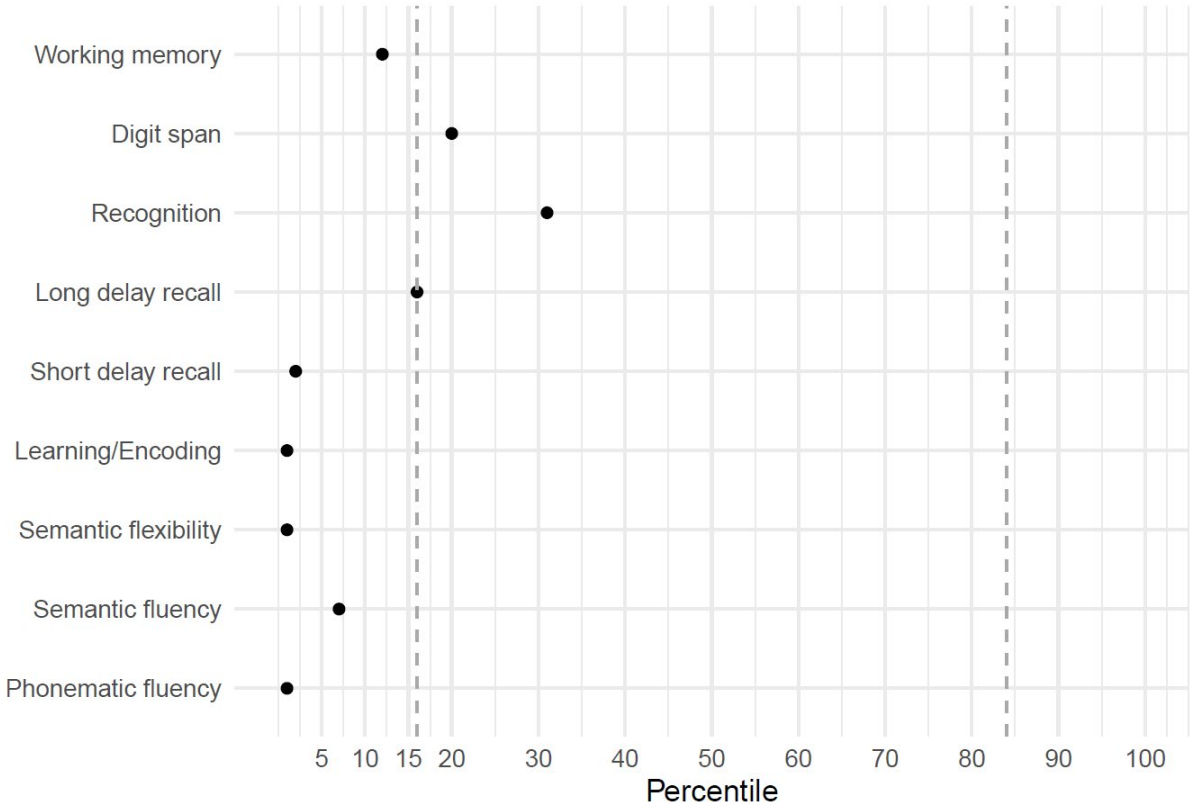
[a]Start indicates the position of the first deleted nucleotide

[b]End indicates the position of the last deleted nucleotide

[c]Upper rows, sequences at 5' breakpoints; lower rows, sequences at 3' breakpoints. Bold font indicates retained nucleotides, regular font deleted nucleotides. Square brackets represent breakpoints. Nucleotides different from the human mtDNA reference sequence (m.5785T>C and m.5789T>C) are underlined.

e figure 1

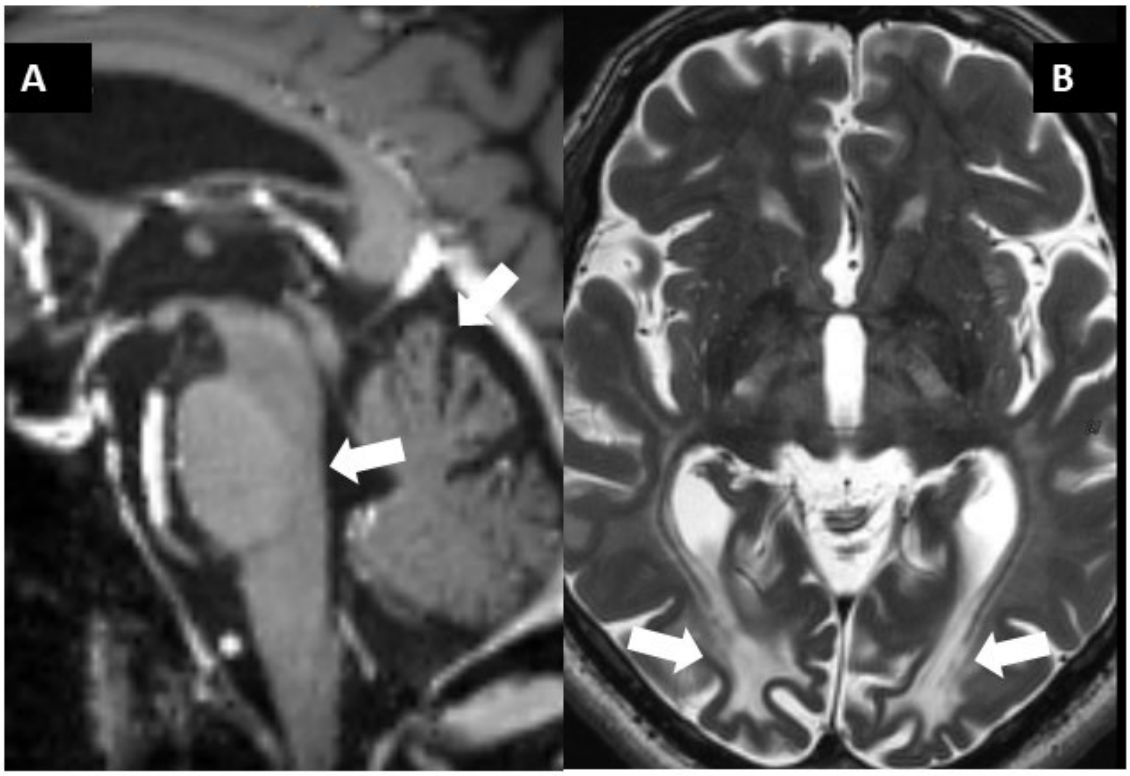
The patient's neuropsychological profile.



Percentiles are interpreted the following way: <5 = far-below average; 5-15: below average; 16-84 normal range; 85-94 above average; >95 far-above average. The average for each function refers to the normalized value of the corresponding neuropsychological test.

e figure 2

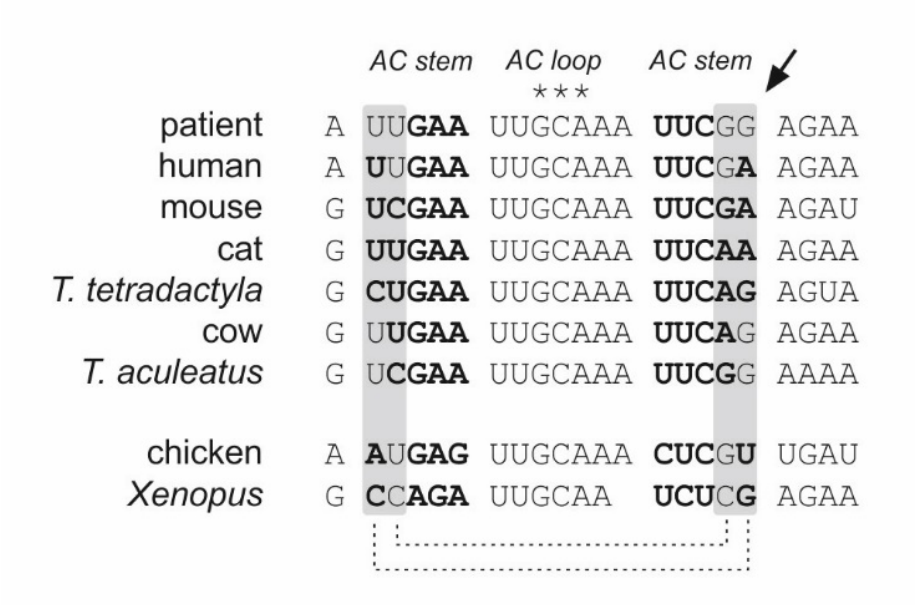
Brain MRI of the patient



Brain 1.5T MRI showing pontocerebellar atrophy on sagittal T1-weighted imaging (A) and bilateral occipital leukoencephalopathy on T2-weighted imaging (B), indicated by arrows.

e figure 3

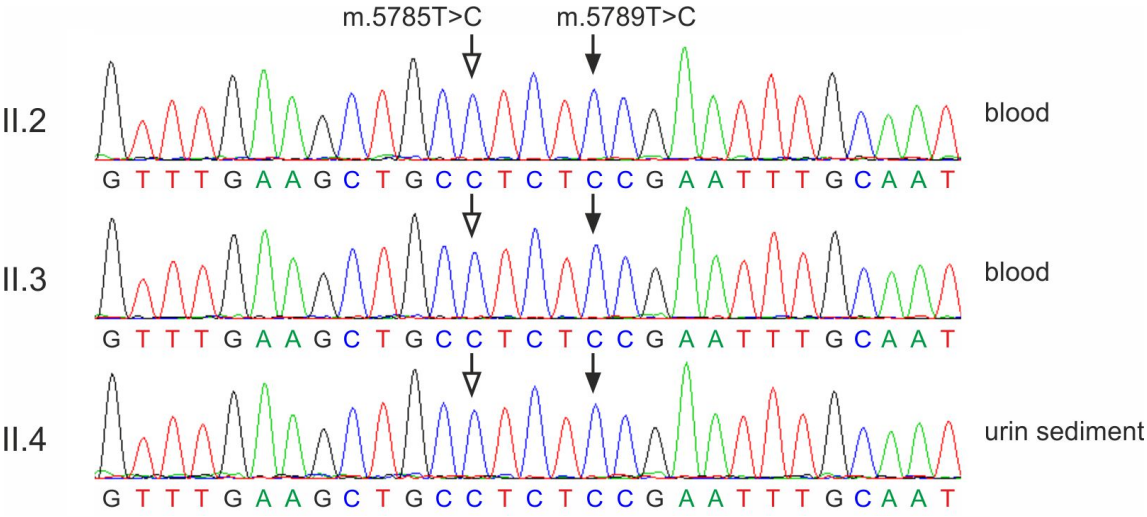
Evolutionary conservation of the mitochondrial tRNA^{Cys} anticodon stem in vertebrates



Bold letters indicate nucleotides that are parts of perfect Watson–Crick base pairings in the anticodon stem (AC stem). Note that the three base pairs adjacent to the anticodon loop (AC loop) are invariably perfect. One of the other two base pairs (grey shading and dashed lines) represents a wobble base pair (G-U) in some species. The m.5789T>C mutation (arrow) leads to two wobble base pairs in the anticodon stem of the mitochondrial tRNA^{Cys}. Stars indicate the anticodon. Sequences were retrieved from the Mamit-tRNA database[23].

e figure 4

The m.5789T>C mutation is detectable in tissue samples of the patient's siblings.



Sequencing chromatograms of single-molecule amplicons from blood and urine sediment DNA of the patient's siblings. Individuals are indicated on the left according to figure 1A. Prior to amplification, DNA was depleted for the wild-type m.5789T allele by Taq$^{\alpha}$I restriction endonuclease digestion. Filled arrow, m.5789T>C mutation; empty arrow m.5785T>C polymorphism.