

Gene	Sequence variation	N° of occur	Phylogenetic conservation	Haplogroup	Presence in mtDB database	Polyphen 2	SIFT
<i>MTTF</i>	m.579T>C	1	-	V	No	-	-
	m.592C>T	1	-	J1	No	-	-
	m.636A>G	1	-	H	No	-	-
	m.645A>G	1	-	H	No	-	-
<i>MTRNR1</i>	m.1151C>A	1	Low	K	No	-	-
	m.1386T>C	1	Low	H	No	-	-
<i>MTTV</i>	m.1645A>G	1	-	H	No	-	-
<i>MTRNR2</i>	m.1917A>G	1	High	T	No	-	-
	m.1938A>T	2	Low	H, J1	No	-	-
	m.2050A>T	1	High	J1	No	-	-
	m.2108G>A	1	High	L1	No	-	-
	m.2137C>T	1	High	L1	No	-	-
	m.2418_2419delAC	1	-	H	No	-	-
	m.2639C>A	1	Low	L2	No	-	-
	m.2865C>T	1	Low	V	No	-	-
m.3170C>T	1	Low	U	No	-	-	
<i>MTTL1</i>	m.3258T>C	1	-	U	No	-	-
<i>MTND1</i>	m.3460G>A (p.Ala52Thr)	1	Medium	J1	2	Damaging	Not tolerated
	m.3488T>C (p.Leu61Pro)	1	Low	H	No	Damaging	Not tolerated
	m.3764C>T (p.Thr153Met)	1	Low	U	1	Damaging	Tolerated
<i>MTT1</i>	m.4317A>G	1	-	T	No	-	-
	m.4317delA	1	-	ND	No	-	-
<i>MTTM</i>	m.4449G>A	1	-	J1	No	-	-
<i>MTND2</i>	m.4746T>C (p.Tyr93His)	1	Low	T	No	Damaging	Tolerated
	m.4935A>G (p.Thr156Ala)	1	Low	T	No	Benign	Tolerated
<i>MTTW</i>	m.5560G>A	1	-	U	No	-	-
<i>MTTN</i>	m.5667G>A	1	-	H	No	-	-
	m.5728T>C	1	-	H	No	-	-
<i>MTTC</i>	m.5800A>G	1	-	T	No	-	-
<i>MTTY</i>	m.5865T>C	1	-	H	No	-	-
<i>MTCO1</i>	m.6736T>C (p.Met278Thr)	1	Medium	T	No	Benign	Not tolerated
<i>MTTS1</i>	m.7472_7473InsC	1	-	H	No	-	-
<i>MTCO2</i>	m.7745A>G (p.Asn54Asp)	1	Low	T	No	Benign	Tolerated
	m.7887G>C (p.Gly101Ala)	1	High	T	No	Damaging	Not tolerated
<i>MTTK</i>	m.8362T>G	1	-	T	No	-	-
<i>MTATP8</i>	m.8394C>T (p.Pro10Leu)	1	Low	L2	No	Damaging	Tolerated
<i>MTATP6</i>	m.8563A>C (p.Thr13Pro)	1	Low	H	No	Damaging	Not tolerated
	m.8609_8610InsC (p.Leu29Serfs*36)	1	-	ND	No	-	-
	m.8866A>G (p.Ile114Val)	1	Low	T	No	Benign	Tolerated
	m.8902G>A (p.Ala126Thr)	1	Medium	ND	No	Benign	Not tolerated
	m.9145G>T (p.Ala207Ser)	1	High	H	No	Damaging	Not tolerated
	m.9185T>C (p.Leu220Pro)	2	High	H, M1	No	Damaging	Not tolerated
<i>MTCO3</i>	m.9909T>C (p.Phe235Leu)	1	High	W	No	Damaging	Not tolerated
<i>MTTG</i>	m.10010T>C	1	-	M1	No	-	-
<i>MTND3</i>	m.10111T>C (p.Met18Thr)	1	Low	T	No	Damaging	Tolerated
	m.10191T>C (p.Ser45Pro)	2	Low	U, M1	No	Damaging	Not tolerated
<i>MTND4</i>	m.10826A>G (p.Ile23Val)	1	Low	T	No	Damaging	Tolerated
	m.10856A>G (p.Ile33Val)	1	Low	H	No	Damaging	Tolerated
	m.10866T>C (p.Ile36Thr)	1	Low	H	No	Benign	Tolerated
	m.11778G>A (p.Arg340His)	1	High	K	2	Damaging	Not tolerated
	m.11936C>G (p.Leu393Val)	1	Low	T	No	Benign	Not tolerated
	m.12134T>A (p.Ser459Thr)	1	Low	H	No	Benign	Tolerated
<i>MTHH</i>	m.12168G>A	1	-	H	No	-	-
	m.12197_12198InsC	1	-	W	No	-	-
<i>MTTS2</i>	m.12236G>A	1	-	ND	21	-	-

<i>MTTL2</i>	m.12276G>A	1	-	H	No	-	-
	m.12316G>A	1	-	H	No	-	-
	m.12324C>T	1	-	W	No	-	-
<i>MTND5</i>	m.12414delT (p.Asn27Thrfs*10)	1	-	H	No	-	-
	m.12706T>C (p.Phe124Leu)	2	High	K, ND	No	Damaging	Not tolerated
	m.13108T>C (p.Phe258Leu)	1	Medium	K	No	Damaging	Not tolerated
	m.13336T>C (p.Phe334Leu)	1	Medium	ND	No	Damaging	Not tolerated
	m.13339T>C (p.Phe335Leu)	1	High	J1	No	Damaging	Not tolerated
	m.13513G>A (p.Asp393Asn)	4	High	H, H, T, ND	No	Damaging	Not tolerated
	m.13514A>G (p.Asp393Gly)	2	High	K, ND	No	Damaging	Not tolerated
	m.13604G>C (p.Ser423Thr)	2	High	I, ND	No	Damaging	Not tolerated
	m.13804G>A (p.Ala490Thr)	1	Medium	H	No	Damaging	Not tolerated
	m.13931T>C (p.Ile532Thr)	1	Medium	V	No	Benign	Tolerated
	m.13945A>G (p.Ile537Val)	1	Low	L3	No	Benign	Tolerated
	m.14065A>G (p.Thr577Ala)	1	Low	H	No	Benign	Tolerated
<i>MTND6</i>	m.14328C>T (p.Val116Met)	1	Low	K	No	Benign	Tolerated
	m.14487T>C (p.Met63Val)	3	Medium	H, H, T	No	Damaging	Not tolerated
	m.14535_14536InsC (p.Phe46fs*61)	1	-	T	No	-	-
<i>MTTE</i>	m.14710G>A	1	-	H	No	-	-
	m.14724G>A	1	-	T	No	-	-
<i>MTCYB</i>	m.14924T>C (p.Ser60Pro)	1	Low	T	No	Damaging	Not tolerated
	m.15295C>A (p.Phe183Leu)	1	High	U	No	Damaging	Not tolerated
	m.15537C>G (p.Thr264Ser)	1	High	J1	No	Benign	Not tolerated
	m.15542C>T (p.Pro266Ser)	1	Medium	H	No	Damaging	Not tolerated
	m.15699G>C (p.Arg318Pro)	1	Medium	H	No	Damaging	Not tolerated
<i>MTTT</i>	m.15926C>T	1	-	U	No	-	-
<i>MTTP</i>	m.15992A>T	1	-	J1	No	-	-

Sup. table 4 : Mitochondrial DNA variants identified by Surveyor analysis