

Suppl. 4: Table of Identified Somatic Mitochondrial Mutations

Case	Position	Reference	Variation	Coverage	Allele Frequency	Region / Gene	AA_Ref	AA_Var
1	1923	C	T	854	8.4	16S rRNA	-	-
1	2733	G	A	1069	6.5	16S rRNA	-	-
1	3842	G	A	651	6.8	ND1	W	Stop
1	4127	G	A	693	5.5	ND1	R	Q
1	9645	G	A	6531	19.1	COX3	A	T
1	10457	T	C	536	3.9	tRNA-Arg	-	-
1	14960	G	A	1984	15.9	CYTB	D	N
2	3922	G	A	947	4.2	ND1	E	K
2	5591	G	A	585	57.6	tRNA-Ala	-	-
2	7486	G	A	966	5.9	tRNA-Ser	-	-
2	15876	T	C	1083	46.6	CYTB	L	P
3	2701	G	A	851	26.8	16S rRNA	-	-
3	3002	G	A	584	3.9	16S rRNA	-	-
3	10851	G	A	113	39.8	ND4	S	N
4	7658	G	A	1167	5.1	COX2	D	N
5	3553	C	A	146	13	ND1	L	I
5	8649	A	C	959	3.9	ATP6	R	R
5	11969	G	A	1103	5.3	ND4	A	T
5	12871	G	A	2695	3.4	ND5	D	N
6	11004	G	A	1111	39.3	ND4	R	H
6	13837	G	A	831	16	ND5	A	T
7	-	-	-	-	-	-	-	-
8	813	A	G	928	3.6	12S rRNA	-	-
8	825	T	A	925	3.5	12S rRNA	-	-
9	8649	A	C	556	2.9	ATP6	R	R
9	10839	C	T	161	7.5	ND4	T	I
9	11711	G	A	2485	62.3	ND4	A	T
10	4956	A	G	1712	7.6	ND2	M	V
10	5164	G	A	371	84.1	ND2	R	H
10	9565	G	A	593	8.4	COX3	G	D
10	10522	G	A	2552	9.2	ND4L	G	D
11	1289	G	A	565	3.4	12S rRNA	-	-
11	1773	AT	-	1245	6.9	16S rRNA	-	-
11	8873	G	A	417	56.6	ATP6	G	D
11	9316	T	C	639	9.4	COX3	F	S
11	15431	G	A	416	5.8	CYTB	A	T
11	16284	A	G	240	16.2	DLOOP	-	-
11	16390	G	A	571	48.3	DLOOP	-	-
12	3000	A	G	448	25.2	16S rRNA	-	-
12	5224	G	A	541	7	ND2	G	E
12	5902	T	C	1670	9.3	non-coding	-	-
12	6825	G	A	766	15.3	COX1	A	T
12	12349	A	G	265	16.2	ND5	T	A
12	12892	T	C	1772	10.6	ND5	L	L
13	1552	G	A	612	9.3	12S rRNA	-	-
13	2701	G	A	778	3.3	16S rRNA	-	-
13	8649	A	C	487	4.3	ATP6	R	R
13	11690	G	A	1136	8.5	ND4	G	S
14	5930	T	C	984	3.5	COX1	S	S
14	10522	G	A	378	10.3	ND4L	G	E
14	13352	T	C	162	56.2	ND5	L	P
14	14612	G	A	126	84.1	ND6	S	K
14	16390	G	A	377	80.4	DLOOP	-	-
15	11390	G	A	182	3.3	ND4	G	R
15	16389	G	A	437	7.8	DLOOP	-	-
16	1334	G	A	550	3.1	12S rRNA	-	-
16	3433	T	C	568	13.2	ND1	Y	H
16	8852	G	A	408	27.9	ATP6	W	Stop
16	9774	G	A	1165	5.7	COX3	D	N
16	11072	T	C	347	6.1	ND4	S	P
16	13268	G	A	424	13.9	ND5	G	E
16	16488	C	T	444	10.8	DLOOP	-	-

Case	Position	Reference	Variation	Coverage	Allele Frequency	Region / Gene	AA_Ref	AA_Var
17	-	-	-	-	-	-	-	-
18	182	C	T	254	8.7	DLOOP	-	-
18	15718	T	C	1360	3.4	CYTB	L	L
18	16278	C	T	222	63.5	DLOOP	-	-
19	12235	T	C	448	12.7	tRNA-Ser	-	-
19	12635	T	C	207	8.7	ND5	I	T
19	12925	G	A	512	10.4	ND5	D	N
19	13393	G	A	220	22.3	ND5	E	K
19	14207	G	A	230	8.7	ND6	T	N
20	292	T	C	417	6	DLOOP	-	-
20	1623	G	A	556	3.1	tRNA-Val	-	-
20	3688	G	A	613	3.6	ND1	A	T
20	6129	G	A	364	19	COX1	G	R
20	8854	G	A	456	3.1	ATP6	A	T
20	8969	G	A	274	23	ATP6	S	N
20	12974	T	C	490	7.8	ND5	L	P
21	1080	A	C	437	54.7	12S rRNA	-	-
21	7380	G	A	127	15	COX1	E	K
22	7	A	G	691	59.6	DLOOP	-	-
22	2211	T	C	638	20.2	16S rRNA	-	-
22	16261	C	T	217	20.7	DLOOP	-	-
23	66	G	A	1011	20.2	DLOOP	-	-
23	824	T	C	977	23.2	12S rRNA	-	-
23	3082	G	A	819	9.8	16S rRNA	-	-
23	3967	G	C	905	8.1	ND1	A	P
23	4298	G	A	1367	3.3	tRNA-Ile	-	-
23	5215	T	C	465	45.7	ND2	L	P
23	6285	G	A	1661	6.3	COX1	V	I
23	14864	T	C	662	28.4	CYTB	C	R
23	16390	G	A	956	6.6	DLOOP	-	-
24	1024	G	A	976	25.1	12S rRNA	-	-
24	2149	G	A	714	54.6	16S rRNA	-	-
24	2647	G	A	2257	20.9	16S rRNA	-	-
24	4714	G	A	924	17.6	ND2	G	E
24	7805	G	A	604	7.1	COX2	V	I
24	7901	T	C	1453	3.4	COX2	W	R
24	16180	A	G	274	14.2	DLOOP	-	-
25	4752	T	C	127	11	ND2	S	P
25	6322	G	A	1190	19.5	COX1	G	E
25	8950	G	A	181	6.1	ATP6	V	I
26	1308	T	C	1388	10.9	12S rRNA	-	-
26	1611	G	A	1448	3.3	tRNA-Val	-	-
26	10230	G	A	456	3.3	ND3	V	M
26	11438	G	A	587	11.1	ND4	G	R
26	11747	G	A	1294	71.8	ND4	A	T