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Supplemental Information

The relevance of mitochondrial DNA variants fluctuation during reprogramming and neuronal differentiation of human iPSCs

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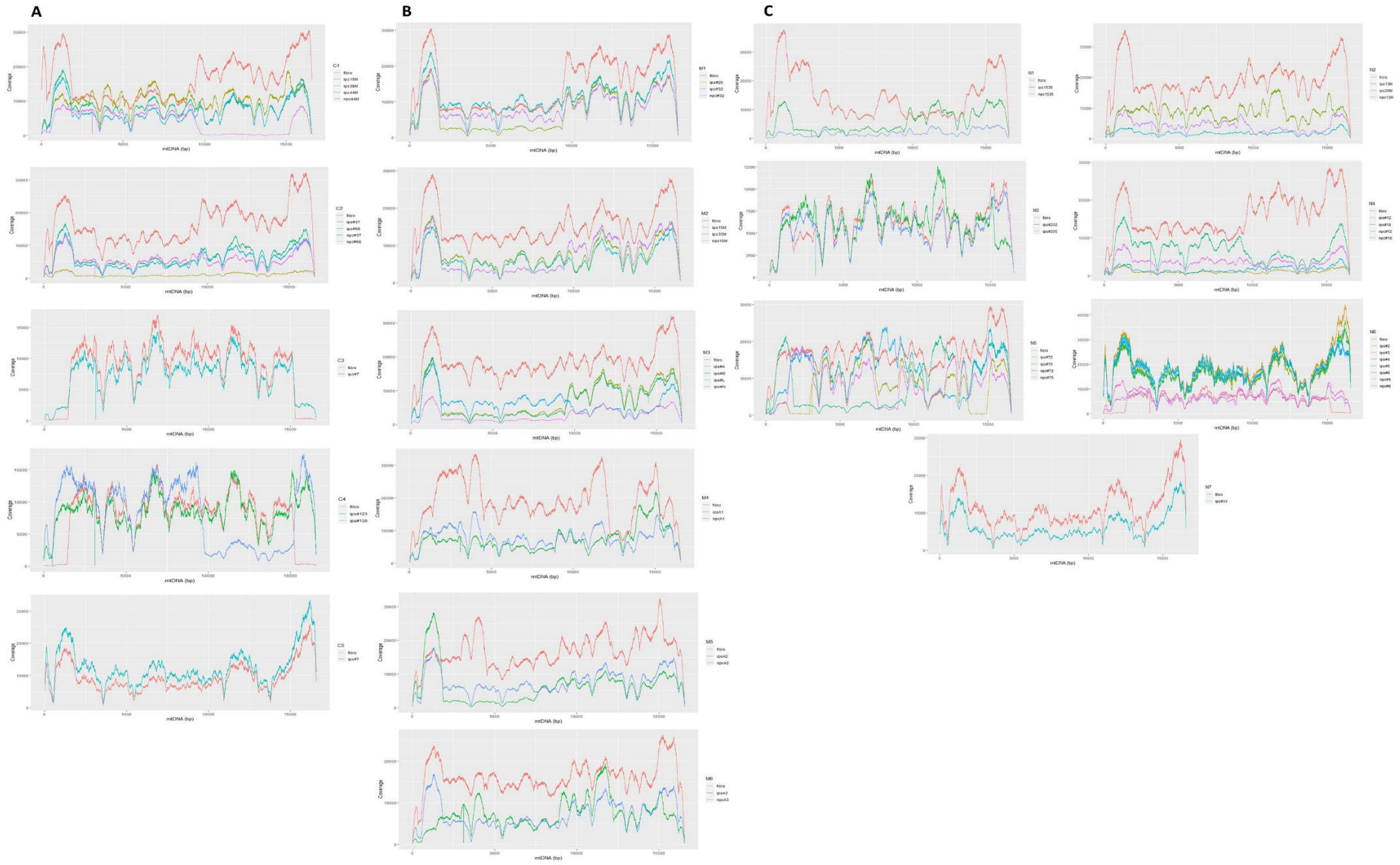

Figure S1. mtDNA NGS coverage in CONTROL (A), MITO (B) and NUCLEAR (C) group.

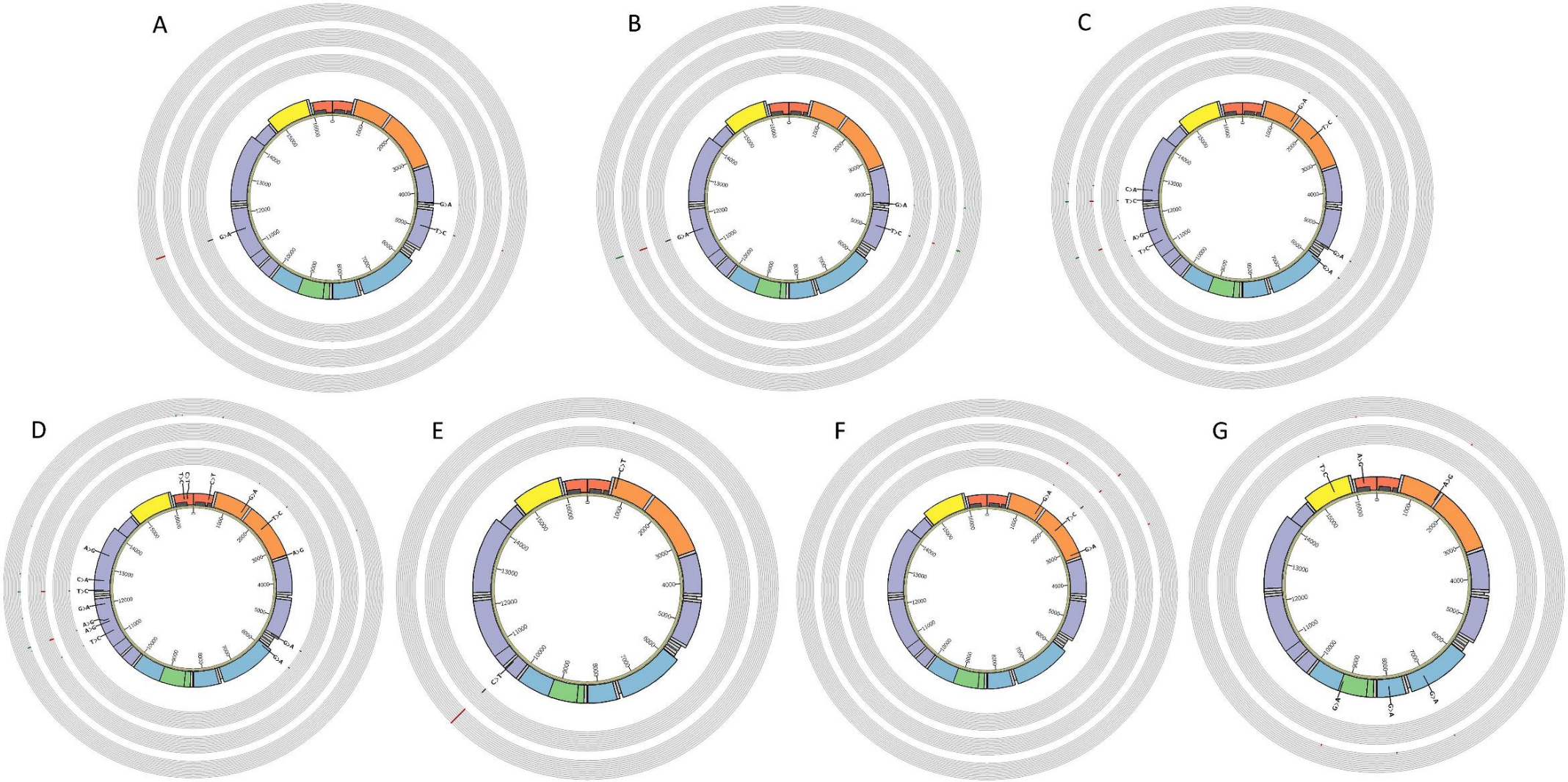

Figure S2. Circos plot of the structure of the human mitochondrial genome showing CONTROL heteroplasmic variants. Colored boxes represent: MT-DLOOP (red), transfer RNAs (light gray), ribosomal RNAs (orange), Complex I genes (purple), Complex III gene (yellow), Complex IV genes (blue) and Complex V genes (green). Shorter boxes are antisense transcripts, while others are sense transcripts. Dark gray bars represent hypervariable regions. The innermost circle with black lines showed fibroblasts heteroplasmic variants, the outer circles with red lines showed iPSCs heteroplasmic variants and the outermost circle with green lines showed NPCs heteroplasmic variants; the length of the lines are proportionate to variants heteroplasmic loads. A. C1 fibroblasts, 19M and 38M iPSC clones. B. C1 fibroblasts, 44M iPSC and NPC clones. C. C2 fibroblasts, #37 iPSC and NPC clones. D. C2 fibroblasts, #68 iPSC and NPC clones. E. C3 fibroblasts and #7 iPSC clone. F. C4 fibroblasts, #123 and #130 iPSC clones. G. C5 fibroblasts and #105 iPSC clone.

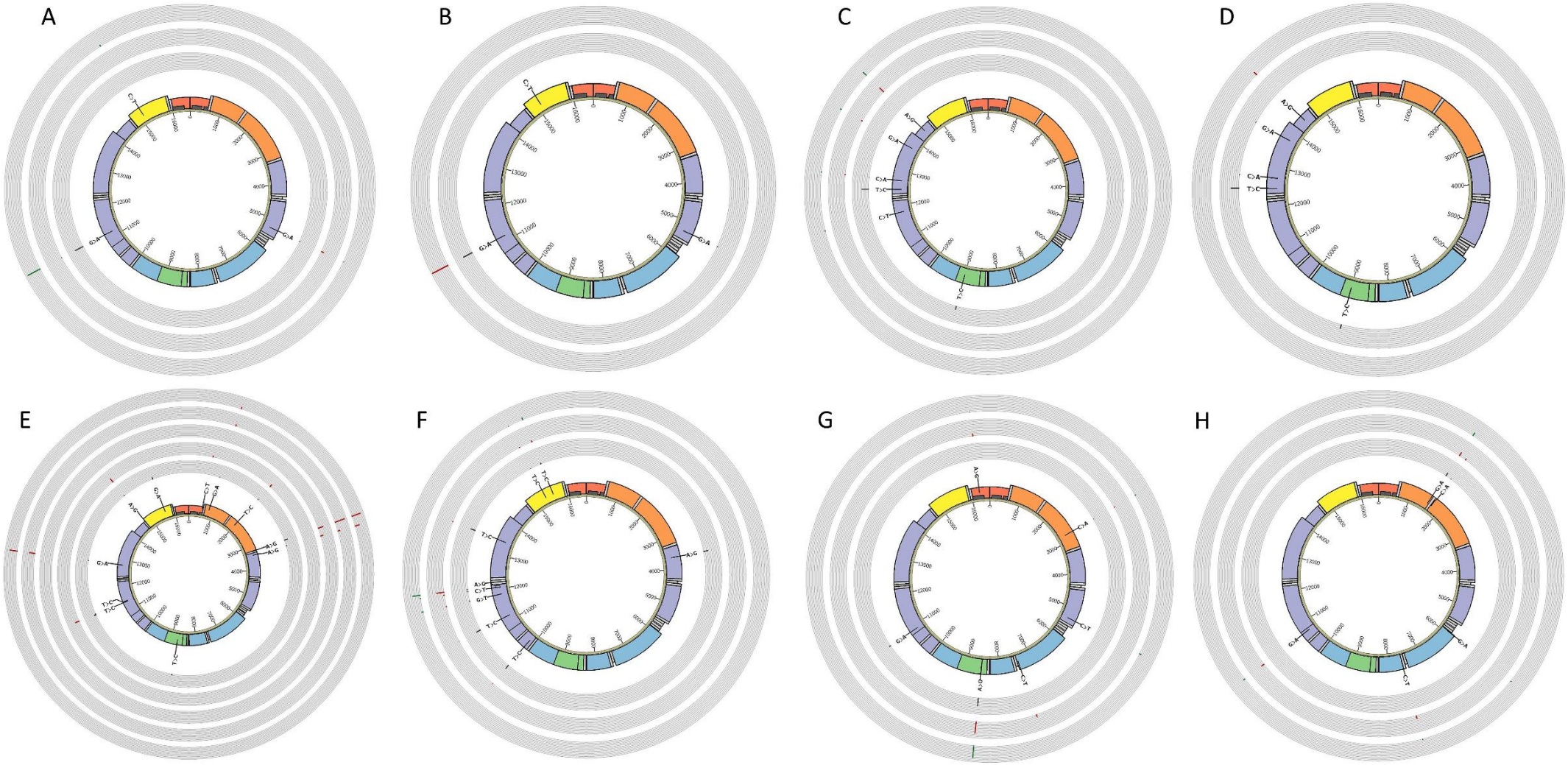

Figure S3. Circos plot of the structure of the human mitochondrial genome showing MITO heteroplasmic variants. A. M1 fibroblasts, #20 iPSC and NPC clones. B. M1 fibroblasts and #32 iPSC clone. C. M2 fibroblasts, 15M iPSC and NPC clones. D. M2 fibroblasts and 33M iPSC clone. E. M3 fibroblasts, #A, #B, #L and #N iPSC clone. F. M4 fibroblasts, A1 iPSCs and NPC clones. G. M5 fibroblasts, A2 iPSC and NPC clones. H. M6 fibroblasts, A3 iPSC and NPC clones.

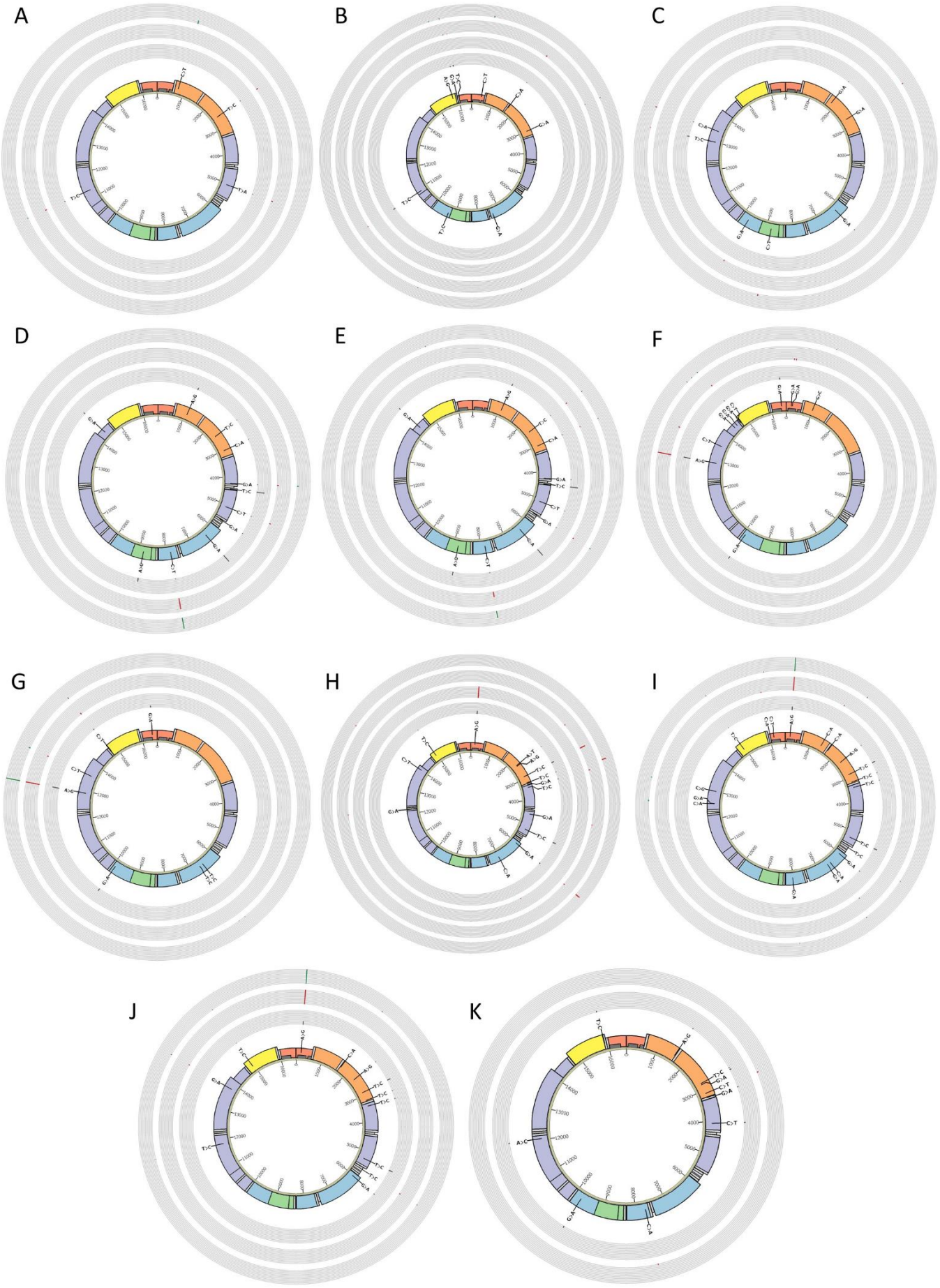

Figure S4. Circos plot of the structure of the human mitochondrial genome showing NUCLEAR heteroplasmic variants. A. N1 fibroblasts, 1535 iPSC and NPC clones. B. N2 fibroblasts, 13M iPSC and NPC clones. C. N3 fibroblasts, #202 and #205 iPSC clones. D. N4 fibroblasts, #12 iPSC and NPC clones. E. N4 fibroblasts, #18 iPSC and NPC clones. F. N5 fibroblasts, #72 iPSC and NPC clones. G. N5 fibroblasts, #75 iPSC and NPC clones. H. N6 fibroblasts, #2, #3 and #6 iPSC clones. I. N6 fibroblasts, #4 iPSC and NPC clones. J. N6 fibroblasts, #8 iPSC and NPC clones. K. N7 fibroblasts and #34 iPSC clone

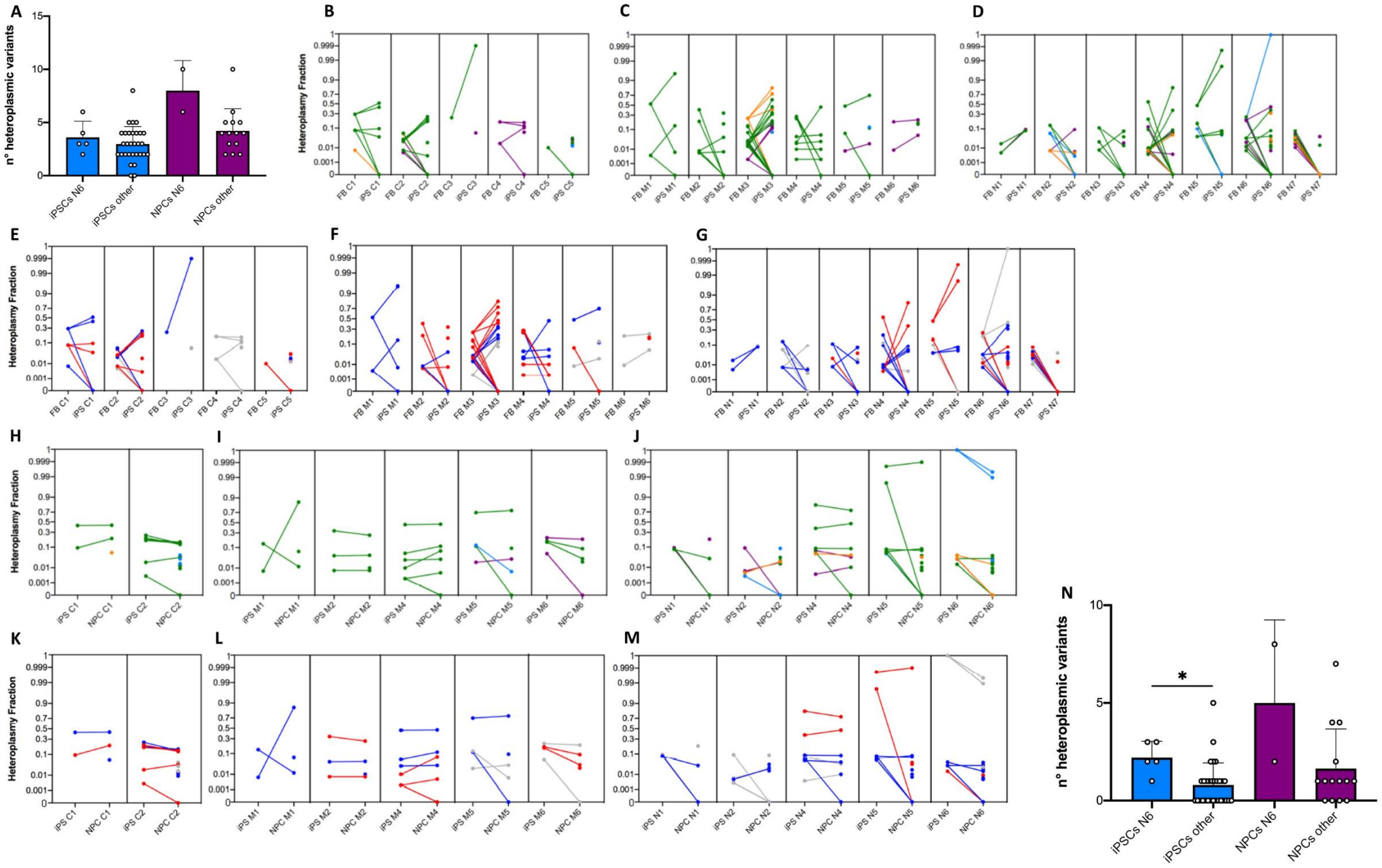
A
n° heteroplasmic variants
iPSCs N6
iPSCs other
NPCs N6
NPCs other
B
C
D
Heteroplasmy Fraction
E
F
G
H
I
J
K
L
M
N
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Figure S5. Analysis and characterization of heteroplasmic variants. A. iPSC and NPC clones obtained from the N6 patient carrying the *POLG* p.P648R mutation did not display a significantly higher number of heteroplasmic variants compared to the iPSCs (p=0.417) and the NPCs (p=0.06) derived from controls and from the MITO or NUCLEAR groups. B-D. Variants HF fluctuations during the reprogramming step from fibroblasts to iPSCs in CONTROL (B), MITO (C) and NUCLEAR (D) groups. Dots appearing in iPSC means unique variants. Non transmitted variants are highlighted with a straight line going to zero in iPSC. blue= MT-DLOOP violet=rRNA orange=tRNA green=coding genes. E-G. Variants HF fluctuations during the reprogramming step from fibroblasts to iPSCs in CONTROL (E), MITO (F) and NUCLEAR (G) groups. Dots appearing in iPSC means unique variants. Non transmitted variants are highlighted with a straight line going to zero in iPSC. blue=benign red=damaging gray=no prediction. H-J. Variants HF fluctuations during differentiation step from iPSCs to NPCs in CONTROL (H) MITO (I) and NUCLEAR (J) groups. Dots appearing in NPC means unique variants. Non transmitted variants are highlighted with a straight line going to zero in NPC. blue= MT-DLOOP violet=rRNA orange=tRNA green=coding genes. K-M. Variants HF fluctuations during differentiation step from iPSCs to NPCs in CONTROL (K), MITO (L) and NUCLEAR (M) groups. Dots appearing in NPC means unique variants. Non transmitted variants are highlighted with a straight line going to zero in NPC. blue=benign; red=damaging; gray=no prediction. N. iPSC clones obtained from the N6 patient carrying the *POLG* p.P648R mutation accumulated a significantly higher number of unique variants compared to all other iPSCs (p=0.003), differently from the NPC clones (p=0.09).

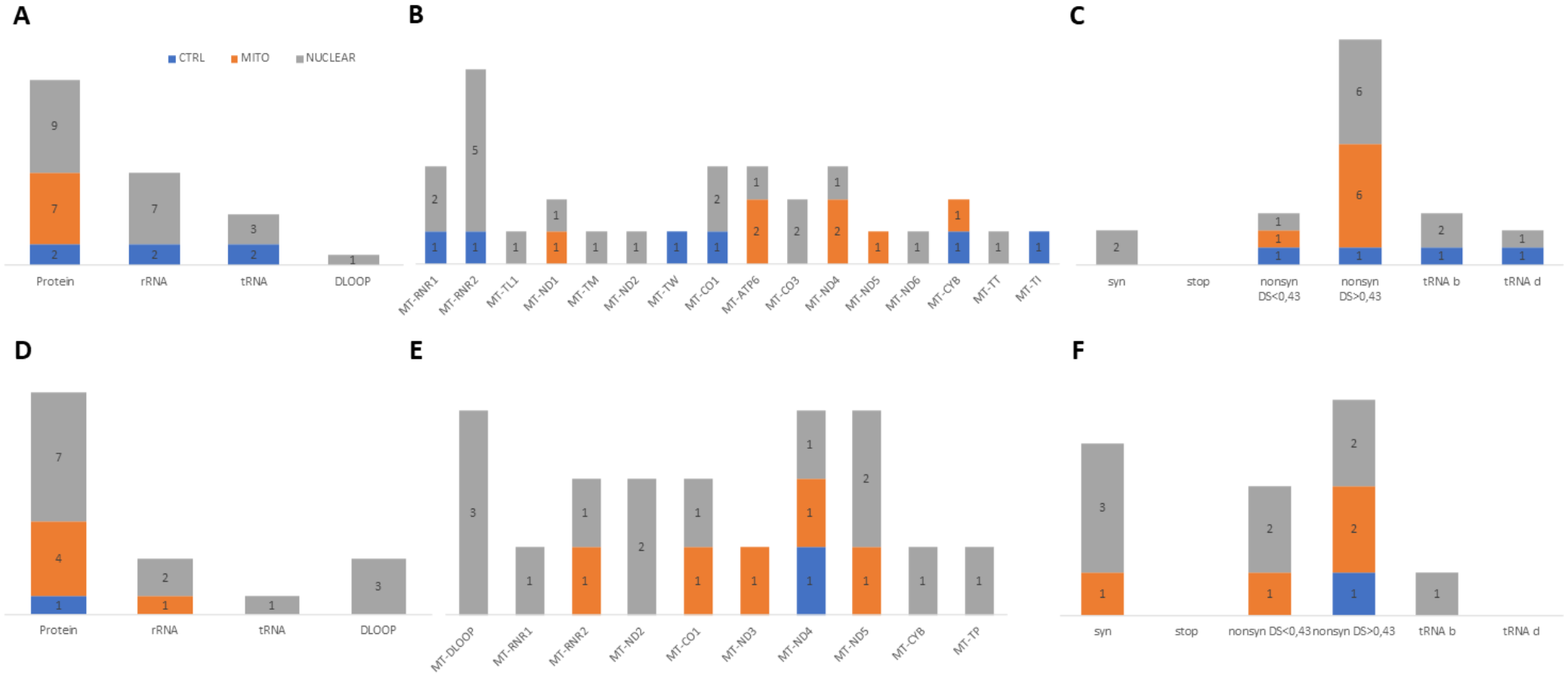

Figure S6. mtDNA localization and prediction of variants non-transmitted in reprogramming and differentiating steps in the three groups. A. Thirty-two heteroplasmic variants were non-transmitted to the iPSCs clones during the reprogramming step. B. Mitochondrial genes localization of non-transmitted variants in iPSCs. C. Predictions of non-transmitted variants in iPSCs. D. Sixteen heteroplasmic variants were non-transmitted to the NPCs clones in the differentiating step. E. Mitochondrial genes localization of non-transmitted variants in NPCs. F. Predictions of non-transmitted variants in NPCs. syn=synonymous; nonsyn=nonsynonymous; b=benign; d=damaging

Fibroblasts	Mean Coverage	% of bases above 5000X	iPSC clones	Mean Coverage	% of bases above 5000X	NPC clones mean coverage	% of bases above 5000X
C1	16,215 X	100	19M	10.433 X	94.4		
			38M	8,331 X	84.5		
			44M	7,055 X	72.7	4,057 X	51
C2	16,559 X	100	#37	1,087 X	0	5,531 X	47.1
			#68	6,653 X	56.1	5,534 X	60
C3	7,641 X	80.5	#7	7,274 X	76.5		
C4	7,874 X	78.7	#123	8,437 X	90		
			#130	8,220 X	61.5		
C5	7,740 X	89.5	#105	9,135 X	96.3		
M1	14,751 X	100	#20	7,282 X	49.2	7,231 X	82
			#32	8,798 X	94.2		
M2	15,206 X	100	15M	6,785 X	75.4	6,230 X	50
			33M	6,095 X	65.5		
M3	18,298 X	100	#A	6,171 X	49.2		
			#B	5,923 X	48.4		
			#L	5,904 X	63.2		
			#N	2,726 X	16		
M4	18,917 X	100	A1	7,189 X	72.8	7,417 X	85.3
M5	7,537 X	68.5	A2	6,271 X	56.3	7,002 X	82
M6	16,034 X	100	A3	7,138 X	74.2	6,618 X	70.8
N1	14,648 X	100	1535	5,970 X	45.6	1,913 X	0
N2	19,002 X	100	13M	8,458 X	90.4	4,074 X	27.6
			20M	1,857 X	0		
N3	6,453 X	68.3	#202	6,238 X	75.3		
			#205	5,711 X	67.4		
N4	15,839 X	100	#12	1,136 X	0	1,655 X	0
			#18	6,857 X	67.2	3,776 X	13.7
N5	17,048 X	100	#72	7,793 X	66.6	12,425 X	85.2
			#75	8,388 X	49.8	7,232 X	75.7
N6	5,698 X	89.9	#2	15,998 X	98.3		

			#3	14,770 X	97.9		
			#4	11,107 X	94.2	6,114 X	77
			#6	11,723 X	95.7		
			#8	13,095 X	97.3	7,229 X	86.3
N7	10,640 X	96.3	#34	5,606 X	49.5		

Table S1. mtDNA NGS coverage.

POSITION	REF	ALT	LOCUS	AA CHANGE	tRNA	MitoTIP	DISEASE SCORE	POLYPHEN2	WHO
183	A	G	MT-DLOOP						N6
811	G	A	MT-RNR1						M3
1489	G	A	MT-RNR1						C4
1562	G	A	MT-RNR1						M6
1693	C	A	MT-RNR2						N2
1693	C	A	MT-RNR2						M6
1975	T	C	MT-RNR2						M3
2256	T	C	MT-RNR2						C4
2404	T	C	MT-RNR2						N4
2522	T	C	MT-RNR2						N1
2766	C	A	MT-RNR2						M5
2895	T	C	MT-RNR2						N6
3009	C	A	MT-RNR2						N4
3243	A	G	MT-TL1		14;0;DL;A;Y	pathogenic			M3
3399	A	G	MT-ND1	Syn					M3
3404	T	C	MT-ND1	L33P			0.84	0.991	N6
4244	G	A	MT-ND1	S313N			0.11	0.0	N4
4933	T	C	MT-ND2	L155P			0.857	0.99	C1
5068	T	A	MT-ND2	M200K			0.417	0.184	N1
5107	C	T	MT-ND2	T213I			0.244	0.101	N4
5293	G	A	MT-ND2	S275N			0.189	0	M1
5610	G	A	MT-TA		50;II;TS;C;N	possibly benign			N4
6018	G	A	MT-CO1	A39T			0.14	0.015	N6
7824	C	T	MT-CO2	S80F			0.835	0.913	N4
8537	A	G	MT-ATP8	I58V			0.341	0.326	M5
10158	T	C	MT-ND3	S34P			0.397	0.202	M4
10377	C	T	MT-ND3	Syn					C3
10861	T	C	MT-ND4	Syn					N2
11150	G	A	MT-ND4	A131T			0.161	0.035	M1
11154	T	C	MT-ND4	I132T			0.72	0.99	C2
11157	T	C	MT-ND4	I133T			0.794	0.99	M4
11299	T	C	MT-ND4	Syn					N1
11361	T	C	MT-ND4	M201T			0.709	0.949	M3

11511	A	G	MT-ND4	N251S			0.153	0	C2
11546	G	A	MT-ND4	V263M			0.137	0	C1
11835	G	T	MT-ND4	W359L			0.73	0.995	M4
12049	C	T	MT-ND4	Syn					M4
12100	A	G	MT-ND4	Syn					M4
12371	T	C	MT-ND5	L12P			O.502	na	C2
12721	C	A	MT-ND5	L129M			0.62	0.965	M2
12778	G	A	MT-ND5	Stop-gain					M3
12926	A	G	MT-ND5	D197G			0.485	0.65	N5
13020	A	C	MT-ND5	Syn					N3
13424	T	C	MT-ND5	L363P			0.857	0.995	M4
13425	C	A	MT-ND5	Syn					N3
13759	G	A	MT-ND5	A475P			0.08	0	M2
14750	A	G	MT-CYB	T2A			0.051	0	M3
14761	C	T	MT-CYB	Syn					N5
15293	T	C	MT-CYB	F183L			0.74	0.999	M4
15541	T	C	MT-CYB	Syn					M4
15959	G	A	MT-TP		70;II;AS;C;N	possibly benign			N2
16044	T	C	MT-DLOOP						N2

Table S2. Variants transmitted from fibroblasts to iPSCs clones.

POSITION	REF	ALT	LOCUS	AA CHANGE	tRNA	MitoTIP	DISEASE SCORE	POLYPHEN2	WHO
183	A	G	MT-DLOOP						N6
1562	G	A	MT-RNR1						M6
2404	T	C	MT-RNR2						N4
2766	C	A	MT-RNR2						M5
3009	C	A	MT-RNR2						N4
3010	G	A	MT-RNR2						N2
4244	G	A	MT-ND1	S313N			0.11	0	N4
4933	T	C	MT-ND2	L155P			0.857	0.99	C1
5293	G	A	MT-ND2	S275N			0.189	0	M1
5610	G	A	MT-TA		50;II;TS;C;N	possibly benign			N4
5654	T	C	MT-TA		2;II;AS;A;N	possibly benign			N6
7592	C	T	MT-CO2	H3Y			0.718	0.991	M6
7824	C	T	MT-CO2	S80F			0.835	0.913	N4
8537	A	G	MT-ATP8	I58V			0.341	0.326	M5
10695	G	A	MT-ND4L	A76T			0.74	0.931	M6
11150	G	A	MT-ND4	A131T			0.161	0.035	M1
11299	T	C	MT-ND4	Syn					N1
11511	A	G	MT-ND4	N251S			0.153	0	C2
11546	G	A	MT-ND4	V263M			0.137	0	C1
11835	G	T	MT-ND4	W359L			0.73	0.995	M4
12049	C	T	MT-ND4	Syn					M4
12100	A	G	MT-ND4	Syn					M4
12371	T	C	MT-ND5	L12P			0.502	No Info	C2
12649	C	A	MT-ND5	L105M			0.67	1	C2
12721	C	A	MT-ND5	L129M			0.62	0.965	M2
12926	A	G	MT-ND5	D197G			0.485	0.65	N5
13575	C	T	MT-ND5	Syn					N5
13759	G	A	MT-ND5	A475T			0.08	0	M2

13813	G	A	MT-ND5	V493I			0.14	0.002	N6
14424	A	G	MT-ND6	S84P			0.832	1	M2
14761	C	T	MT-CYB	Syn					N5
15293	T	C	MT-CYB	F183L			0.74	0.999	M4
15541	T	C	MT-CYB	Syn					M4
15959	G	A	MT-TP		70;II;AS;C;N	possibly benign			N2
16254	A	G	MT-DLOOP						M5

Table S3. Variants transmitted from iPSCs to NPCs clones.

POSITION	REF	ALT	HF	LOCUS	AA CHANGE	tRNA	MitoTIP	DISEASE SCORE	POLYPHEN2	WHO	GB
185	G	A	6%	MT-DLOOP						N5 #72	3445
228	G	A	5%	MT-DLOOP						N5 #72	1901
537	C	T	8%	MT-DLOOP						M3 A	114
722	C	T	6%	MT-RNR1						C3 #7	62
1388	C	A	2.9%	MT-RNR1						N6 #4	NA
1573	A	G	2.9%	MT-RNR1						C5 #105	NA
2297	A	T	0.7%	MT-RNR2						N6 #3	NA
2643	G	A	2%	MT-RNR2						N3 #205	2
3010	G	A	0.6%	MT-RNR2						N2 13M	7223
3110	C	T	4.3%	MT-RNR2						N7 #34	10
3123	G	A	7%	MT-RNR2						C4 #130	NA
3281	G	A	32%	MT-TL1		50;0;TS;G;N	possibly benign			N6 #6	2
4596	G	A	1.4%	MT-ND2	V43I			0.12	0.006	N6 #3	NA
5654	T	C	4.4%	MT-TA		2;II;AS;A;N	possibly benign			N6 #8	5
6486	C	A	15%	MT-CO1	L195I			0.73	0.99	N6 #4	NA
7002	C	A	1.1%	MT-CO1	L367M			0.75	0.999	N6 #2	NA
7026	G	A	1.5%	MT-CO1	A375T			0.87	1.0	C5 #105	NA
7412	C	T	11%	MT-CO1	syn					M5 A2	11
7592	C	T	16%	MT-CO2	H3Y			0.718	0.991	M6 A3	1
7687	C	A	1.5%	MT-CO2	I34M			0.77	0.969	N7 #34	NA
7970	T	A	2%	MT-CO2	E129K			0.13	0.0	C5 #105	NA
8815	C	T	8%	MT-ATP6	Stop-gain					N3 #205	NA
9163	G	A	3.4%	MT-ATP6	V213I			0.81	0.975	C5 #105	58
9715	G	A	4%	MT-CO3	G170D			0.842	0.999	N3 #202	NA
10695	G	A	17%	MT-ND4L	A76T			0.74	0.931	M6 A3	2
12192	G	A	2.2%	MT-TH		59;II;TL;G;N	likely benign			N6 #3	112
12649	C	A	2%	MT-ND5	L105M			0.67	1.0	C2 #37	NA

13575	C	T	8% 7%	MT-ND5	syn					N5 #72 N5 #75	24
13813	G	A	3%	MT-ND5	V493I			0.14	0.002	N6 #8	22
14004	C	T	2.5%	MT-ND5	syn					N6 #6	7
14424	A	G	34% 16%	MT-ND6	S84P			0.832	1.0	M2 #15 M2 #33	1
16019	C	A	3%	MT-TP		5;II;AS;G;N	possibly benign			N6 #4	NA
16240	A	G	1.3%	MT-DLOOP						C5 #105	358
16254	A	G	12%	MT-DLOOP						M5 A2	229

Table S4. *Unique* variants of iPSCs clones.

POSITION	REF	ALT	HF	LOCUS	AA CHANGE	tRNA	MitoTIP	DISEASE SCORE	POLYPHEN2	WHO	GB
438	C	T	8.8%	MT-DLOOP						N2 13M	15
456	C	T	4.6%	MT-DLOOP						C2 #68	1911
765	C	T	18.9%	MT-RNR1						N1 1535	NA
991	G	C	1%	MT-RNR1						N5 #72	NA
1693	C	A	2.8% 1.9%	MT-RNR2						N6 #4 N6 #8	NA
3243	A	G	1.2%	MT-TL1		14;;DL;A;Y	confirmed pathogenic			C2 #68	9
5366	C	T	9.4%	MT-ND2	syn					M5 A2	3
5917	G	A	2.2%	MT-CO1	R5H			0.76	0.999	M6 A3	NA
6512	T	C	1%	MT-CO1	syn					N5 #75	8
6610	G	A	3.1%	MT-CO1	Stop-gain					N6 #4	NA
6641	T	C	0.7%	MT-CO1	syn					N5 #75	40
7337	G	A	2.3%	MT-CO1	syn					N2 13M	589
8007	G	A	0.9%	MT-CO2	R141Q			0.8	1.0	N6 #4	NA
9311	T	C	1.6%	MT-CO3	syn					N2 13M	47
11443	A	G	0.9%	MT-ND4	syn					C2 #68	4
11788	C	T	1%	MT-ND4	syn					M2 15M	33
11827	T	C	0.5%	MT-ND4	syn					N6 #8	80
11969	G	A	1.5%	MT-ND4	A404T			0.26	0.002	C2 #68	742
12549	C	A	2%	MT-ND5	syn					N6 #4	NA
12561	G	A	1.5%	MT-ND5	syn					N6 #4	230
13011	C	G	4.2%	MT-ND5	syn					N6 #4	NA
13395	A	G	1.3%	MT-ND5	syn					C2 #68	337
14438	G	A	4.2%	MT-ND6	P79L			0.91	1.0	N5 #72	NA
14560	G	A	1.8%	MT-ND6	syn					N5 #72	1140
14710	G	A	3.5%	MT-TE		36;II;CL;C;N	confirmed pathogenic			N5 #72	NA *Encephalomyopathy + Retinopathy

15100	C	T	7%	MT-CYB	syn					M1 #20	16
15643	C	T	1%	MT-CYB	syn					N4 #18	9
15758	A	G	3.4%	MT-CYB	I338V			0.15	0.001	N2 13M	389
16148	C	T	2.5%	MT-DLOOP						N6 #4	3350
16304	T	C	3%	MT-DLOOP						C2 #68	11367
16400	C	T	1.7%	MT-DLOOP						C2 #68	322

Table S5. *Unique* variants in NPCs clones.

POSITION	REF	ALT	HF	LOCUS	AA CHANGE	tRNA	MitoTIP	DISEASE SCORE	POLYPHEN2	WHO	GB
1082	A	G	12%	MT-RNR1						N4	NA
1489	G	A	0.5%	MT-RNR1						C2	NA
1578	A	G	1.1%	MT-RNR1						N7	NA
1816	G	A	2.3%	MT-RNR2						N3	1
2256	T	C	2.6%	MT-RNR2						C2	NA
2338	A	G	1.2%	MT-RNR2						N6	NA
2778	T	C	1.8%	MT-RNR2						N7	NA
2819	G	A	6.1%	MT-RNR2						N7	NA
3193	T	C	2.2%	MT-RNR2						N6	NA
3248	G	A	2.4%	MT-TL1		18;0;DL;G;Y	possibly benign			N7	1
3628	A	G	25.3%	MT-ND1	T108A			0.135	0.001	M4	NA
4059	C	T	4.9%	MT-ND1	syn					N7	57
4445	T	C	55.4%	MT-TM		48;II;VL;U;Y	possibly benign			N4	NA
5296	T	C	25.1%	MT-ND2	L276P			0.69	0.988	N6	NA
5540	G	A	5.6%	MT-TW		30;II;CS;G;N0.65	possibly pathogenic			C2	NA *Encephalomyopathy/ DEAF
5970	G	A	6%	MT-CO1	G23S			0.26	0.04	C2	3
6261	G	A	2.3%	MT-CO1	A120T			0.664	0.988	N3	361
6382	G	A	55.2%	MT-CO1	G160E			0.869	0.992	N4	NA
8728	T	C	7.4%	MT-ATP6	W68R			0.874	0.999	M3	NA
8817	A	G	21.5%	MT-ATP6	syn					N4	54
8993	T	C	19.6%	MT-ATP6	L156P			0.902	0.999	M2	2 *NARP/Leigh Disease /MILS /other
9753	G	A	8%	MT-CO3	E183K			0.76	0.983	N7	1
9906	G	A	15.7%	MT-CO3	G234S			0.758	1.0	N5	NA
10863	G	A	6.9%	MT-ND4	S35N			0.762	0.995	M5	3
11340	T	C	12.9%	MT-ND4	L194S			0.699	0.978	M3	NA
12040	A	C	3.2%	MT-ND4	K427N			0.7	0.994	N7	11
12460	T	C	40.5%	MT-ND5	S42P			0.711	0.978	M2	NA
14384	G	A	9.1%	MT-ND6	A97V			0.073	0.0	N4	83

15441	T	C	1%	MT-CYB	L232S			0.66	0.981	C5	NA
15612	G	A	13.9%	MT-CYB	G289E			0.844	1.0	M3	NA
15898	T	C	3.8%	MT-TT		11;II;DS;U;N	possibly pathogenic			N7	1
16390	G	A	9.7%	MT-DLOOP						N5	7404

Table S6. Variants non-transmitted from fibroblasts to iPSCs.

POSITION	REF	ALT	HF	LOCUS	AA_CHANGE	tRNA	MitoTIP	DISEASE SCORE	POLYPHEN2	WHO	GB
185	G	A	5.5%	MT-DLOOP						N5 #72	3445
228	G	A	5.2%	MT-DLOOP						N5 #72	1901
1388	C	A	2.9%	MT-RNR1						N6 #4	NA
1693	C	A	5.6% 9%	MT-RNR2						M6 A3; N2 13M	NA
2522	T	C	9%	MT-RNR2						N1 1535	NA
5068	T	A	8%	MT-ND2	M200K			0.417	0.184	N1 1535	NA
5107	C	T	6%	MT-ND2	T213I			0.244	0.101	N4 #12	NA
6486	C	A	1.5%	MT-CO1	L195I			0.73	0.99	N6 #4	NA
7412	C	T	11.3%	MT-CO1	syn					M5 A2	11
10158	T	C	0.2%	MT-ND3	S34P			0.397	0.202	M4 A1	NA
10861	T	C	0.3%	MT-ND4	syn					N2 13M	42
11154	T	C	0.3%	MT-ND4	I132T			0.72	0.99	C4 #68	NA
11157	T	C	0.2%	MT-ND4	I133T			0.794	0.99	M4 A1	2
13424	T	C	0.2%	MT-ND5	L363P			0.857	0.995	M4 A1	NA
16019	C	A	3%	MT-TP		5;II;AS;G;N	possibly benign			N6 #4	NA
16044	T	C	0.3%	MT-DLOOP						N2 13M	5

Table S7. Variants non-transmitted from iPSCs to NPCs.

POSITION	REF	ALT	HF	WHO iPSC	DEPTH	FORWARD	REVERSE
2297	A	T	0.7%	N6 #3	16359	7985	8374
2643	G	A	2%	N3 #205	5774	2805	2969
3010	G	A	0.6%	N2 13M	10821	5220	5601
4596	G	A	1.4%	N6 #3	12618	6066	6552
7002	C	A	1.1%	N6 #2	17465	7040	10425
7026	G	A	1.5%	C5 #105	12452	5048	7404
7687	C	A	1.5%	N7 #34	3615	1605	2010
7970	T	A	2%	C5 #105	9320	5279	4041
12649	C	A	2%	C2 #37	1237	571	666
POSITION	**REF**	**ALT**	**HF**	**WHO NPC**	**DEPTH**	**FORWARD**	**REVERSE**
991	G	C	1%	N5 #72	5772	3086	2686
1693	C	A	1.9%	N6 #6-#8	8154	4812	3342
3243	A	G	1.2%	C2 #68	4260	1957	2303
6512	T	C	1%	N5 #75	11985	6789	5196
6641	T	C	0.7%	N5 #75	13436	7282	6154
8007	G	A	0.9%	N6 #4	6026	2920	3106
9311	T	C	1.6%	N2 13M	5891	2603	3288
11443	A	G	0.9%	C2 #68	5953	3028	2925
11788	C	T	1%	M2 15M	14260	6871	7389
11827	T	C	0.5%	N6 #8	11247	5127	6120
11969	G	A	1.5%	C2 #68	5185	2447	2738
12549	C	A	2%	N6 #4	5804	2903	2901
12561	G	A	1.5%	N6 #4	5514	2595	2919
13395	A	G	1.3%	C2 #68	4672	2233	2439
14560	G	A	1.8%	N5 #72	10719	5947	4772
15643	C	T	1%	N4 #18	6378	3380	2998
16400	C	T	1.7%	C2 #68	11278	6161	5117

Table S8. Coverage and reads strand orientation of *unique* variants with HF≤2% in iPSCs and NPCs.