

## SUPPLEMENTARY MATERIAL

### Mitochondrial DNA Alterations and Oxidative Stress in Acute Leukemia

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### Supplementary Material 1

Primers	Sequences	Regions	Size (bp)	cycle	PCR Conditions
L1	5' ccc taa cac cag cct aac ca 3'	370-774	420	32	1 95°C for 5min denaturation step  30 95°C for 1min denaturation step 55°C for 1min annealing step 72°C for 1min elongation step  1 72°C for 10min elongation step
R1	5' att gct gcg tgc ttg atg 3'				
L2	5' tcc acc att agc acc caa ag 3'	15977-16297	360		
R2	5' ggg tgg gta gg ttt gtt ggt 3'				
L3	5' caa acc tac cca ccc tta aca 3'	16283-16549	299		
R3	5' ggg aac gtg tgg gct att ta 3'				
L4	5' aag cct aaa tag ccc aca cg 3'	16525-382	479		
R4	5' tgg tta ggc tgg tgt tag gg 3'				
D41	5' cgc ata aaa ctt aaa act tta cag 3'	3126-3277	151	38	1 37°C for 10min UDG activity  95°C for 5min denaturation step  37 95°C for 10s denaturation step 60°C for 10s annealing step 72°C for 15s elongation step
R56	5' ctt tgc gta gtt gta tat agc c 3'				
18SF	5' egg cta cca cat cca agg aa 3'	1546-1650	104		
18SR	5' gct gga att acc gcg g 3'				
β-actin F	5' gcc cta taa aac cca gcg 3'	exon 6	227		
β-actin R	5' cca cga tgg agg gga aga 3'				
TFAM F	5' gaa gaa ttg ccc agc gt 3'	exon 2	185		
TFAM R	5' cat agc ttt cct tttt aaa tgt ttg t 3'	exon 3			

## Supplementary Material 2

**A**

**Table 2.** Homoplasmic and heteroplasmic variations found in patients and healthy controls compared to rCRS

Homoplasmic variation:

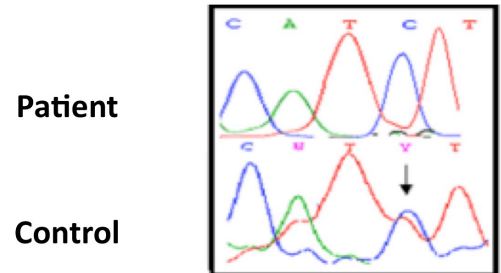
m.57T>TC, m.58T>C, m.66delG, m.73A>G, m.93A>G, m.143G>A, m.146T>C, m.150C>T, m.152T>C, m.182C>T, m.185G>T, m.189A>G, m.195T>C, m.199T>C, m.200A>G, m.204T>C, m.207G>A, m.215A>G, m.247G>A, m.248G>A, m.263A>G, m.295C>T, m.303\_309insC(2), m.308delC, m.309\_315insC, m.311insC, m.311\_315insC(2), m.318T>C, m.320C>T, m.534C>T, m.350A>C, m.357A>G, m.456C>T, m.462C>T, m.471T>C, m.489T>C, m.497C>A, m.513G>A, m.514delC, m.515delA, m.524\_525insAC, m.523delA, m.524delC, m.573insC(5), m.709G>A, m.710T>C, m.750A>G, m.16041A>G, m.16051A>G, m.16069C>T, m.16093T>C, m.16104C>A, m.16126T>C, m.16129G>A, m.16145G>A, m.16163A>G, m.16172T>C, m.16176C>T, m.16183A>CC, m.16186C>T, m.16187C>T, m.16188C>T, m.16189T>C, m.16192C>T, m.16193insC, m.16193C>T, m.16209T>C, m.16217T>C, m.16218C>T, m.16221C>T, m.16222C>T, m.16223C>T, m.16224T>C, m.16234C>T, m.16244C>T, m.16248C>T, m.16256C>T, m.16261C>T, m.16264C>T, m.16270C>T, m.16168T>C, m.16304T>C, m.16309A>G, m.16311T>C, m.16357T>C, m.16358C>T, m.16368T>C, m.16399A>G, m.16359T>C, m.16368T>C, m.16390G>A, m.16399A>G, m.16519T>C, m.16526G>A.

Heteroplasmic variation:

m.185G>A, m.259A>T, m.310T>C, m.311C>T, m.311insC, m.336A>C, m.343C>T, m.366G>A, m.452C>A, m.511C>T and m.16228C>T.

**B**

m. C343T hetero



## Supplementary Material 3

