Sample	Sequence variation	Haplogroup
Leukemia		
LAA	16362-16482-16526-239-263	H
AGM	16182C-16183C-16189-16217-16482-16519-73-263-499	B4b
MFSS	16189-16223-16245-16278-16294-16309-16390-73-143-146-152-263	L2a
JCS	16038-16209-16223-16294-16311-16519-73-146-263-374+A	L3f
DC	16223-16278-16286-16294-16309-16390-16519-73-146-152-195-263	L2a
OAM	16223-16260-16325-16362-16519-73-152-183-263-489	D1
EMB	16223-16239-16288-16325-16362-73-210-228-263-489	D1
ERR	16111-16126-16223-16259-16290-16319-16327-16362-16519-73-146-153-235-263-(523-524)delAC	A2
UPN21	16223-16325-16362-73-200-263-489	D1
UPN1	16126-16292-16294-16519-73-146-152-263-279	T2
UPN16	16069-16126-73-185-228-263-295-462-482-489	J1c
UPN22	16222-16519-263-319	H
UPN18	16086-16111-16223-16290-16319-16362-64-73-146-153-235-263-(523-524)delAC	A2
UPN20	16111-16209-16223-16290-16293C-16319-16362-16519-64-73-146-153-235-263-(523-524)delAC	A2
UPN17	16183C-16189-16223-16278-16519-73-153-189R-195-225-226-263	X2b
UPN2	16069-16126-73-185-188-228-234-260-263-295-462-489	J1c
UPN3	16093-16129-16519-152-263	H
UPN19	16519-146-263	H
Healthy control		
Donor 1	16192-16270-73-150-263	U5b
Donor 2	16223-16278-16294-16390-73-146-152-195-263-(523-524)delAC	L2a
Donor 3	16093-16129-16148-16168-16172-16187-16188G-16189-16223-16230-16278-16293-16311-16320-93-95C-185-189-236-247-263-(523-524)delAC	L0a1
Donor 4	16126-16294-16296-16519-73-263	T2
Donor 5	16270-16292-16362-73-150-263-517	U5b
Donor 6	16209-16223-16240-16324-73-263-489-(523-524)delAC	M7a1
Donor 7	16172-16219-16235-16278-16355-16519-73-146-263	U6
Donor 8	16169-16299-16519-263	H
Donor 9	16111-16189-16224-16256-16311-16519-56+C-58-73-263-497-(523-524) insAC	K1a
Donor 10	16298-16519-72-263	pre-V

Note: Sequence variation of each individual was scored according to the consensus sequence of the single cells. Positions were numbered according to the revised Cambridge Reference Sequence (CRS) [1]. Suffixes C and G indicated transversions, and

‘‘+’’ indicated insertions. Indels (insertion / deletion) were recorded at the last possible site. The length mutations of the C-tract in regions 16184-16193 and 303-309 were not included. All samples had 315+C in the second hypervariable segment of mtDNA control region. Healthy donors 1 to 5 are from Ogasawara et al. [2], donors 6 (35/M), 7 (32/M), 8 (25/M), 9 (57/M), and 10 (39/M) are newly sequenced in this study. Each mtDNA was assigned to respective haplogroup based on the classification system of world mtDNA phylogeny [3-7].