

Supplemental Figure 3

MDA-MB-157

mRNA	Position	Complex	Heteroplasmy
Missense	A8701G	ATP8 (C-V)	45/49 (91.8%)
	A8860G	ATP8 (C-V)	
	C8932T	ATP8 (C-V)	39/41 (95.1%)
	A10398G	ND3 (C-I)	39/43 (90.7%)
	C14766T	CYTB (C-III)	
	A14769G	CYTB (C-III)	51/53 (96.2%)
	A15326G	CYTB (C-III)	
	Initiator Codon	A8527G	ATP6 (C-V)
Frameshift	GA6691G	COX1 (C-IV)	40/78 (51.3%)
	A9531AC	COX3 (C-IV)	13/24 (54.2%)
Stop gained	T15514A	CYTB (C-III)	18/40 (45.0%)
Modifiers			
D-loop	G16129A		57/62 (8.1%)
	T16209C		
	C16223T		
	C16292T		
	C16295T		54/56 (96.4%)
	T16311C		50/53 (94.3%)
	T16519C		
tRNA	G4412A		14/20 (70.0%)
	C5601T		
	CT15939C		64/70 (91.4%)
rRNA	A750G		
	A1438G		
	T1822C		
	A2706G		36/38 (94.7%)
Synonymous			
	T3396C	ND1 (C-I)	48/53 (90.6%)
	T4218C	ND1 (C-I)	
	A4769G	ND2 (C-I)	
	C7028T	COX1 (C-IV)	29/31 (93.5%)
	C7819A	COX2 (C-IV)	
	C8410T	ATP6 (C-V)	41/48 (85.4%)
	T9540C	COX3 (C-IV)	24/26 (92.3%)
	T9950C	COX3 (C-IV)	
	C10070T	ND3 (C-I)	18/20 (90.0%)
	T10873C	ND4 (C-I)	24/28 (85.7%)
	G11440A	ND4 (C-I)	
	G11719A	ND4 (C-I)	62/64 (96.9%)
	C12705T	ND5 (C-I)	
	T13602C	ND5 (C-I)	13/47 (27.7%)
	G15301A	CYTB (C-III)	
	T15514C	CYTB (C-III)	21/40 (52.5%)