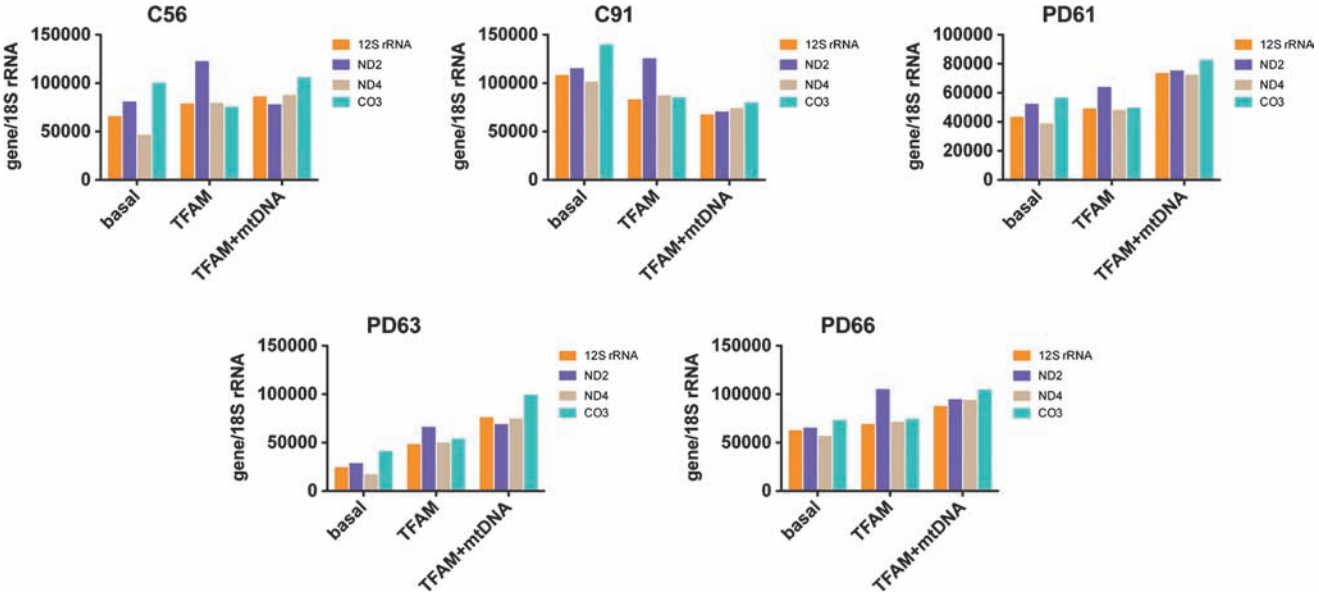
Supplementary Table 1. Demographics of CTL and PD Subjects Used to Create Cybrid Cell Lines

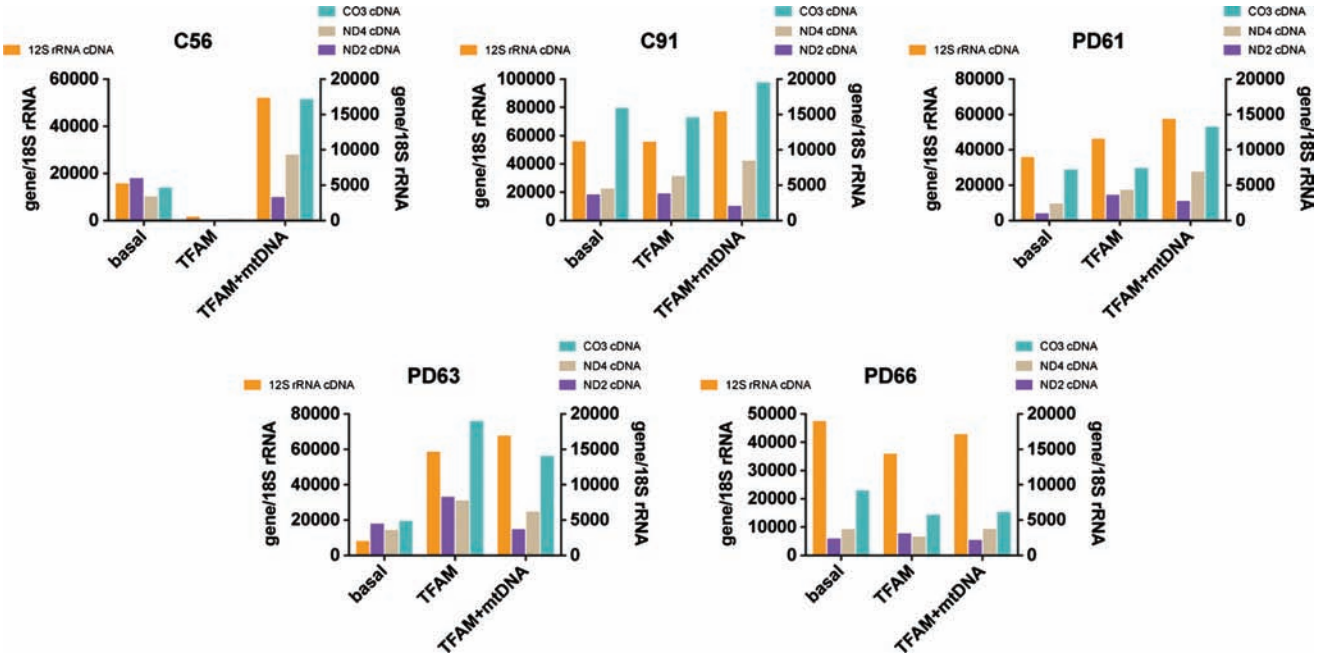
Cybrid ID	*Age at Cybrid Creation*	*Sex of Patient*	*Diagnosis*	*Ethnicity*	*H&Y*	*PD Duration in Yrs*
56	72	M	CTL	W	NA	
91	61	F	CTL	W	NA	
59	51	M	PD	W	4	11
61	65	M	PD	AA	2	15
63	73	F	PD	W	2	14
66	75	M	PD	W	2	7

Supplementary Table 2. Primer/Probe Sequences for mtDNA genes

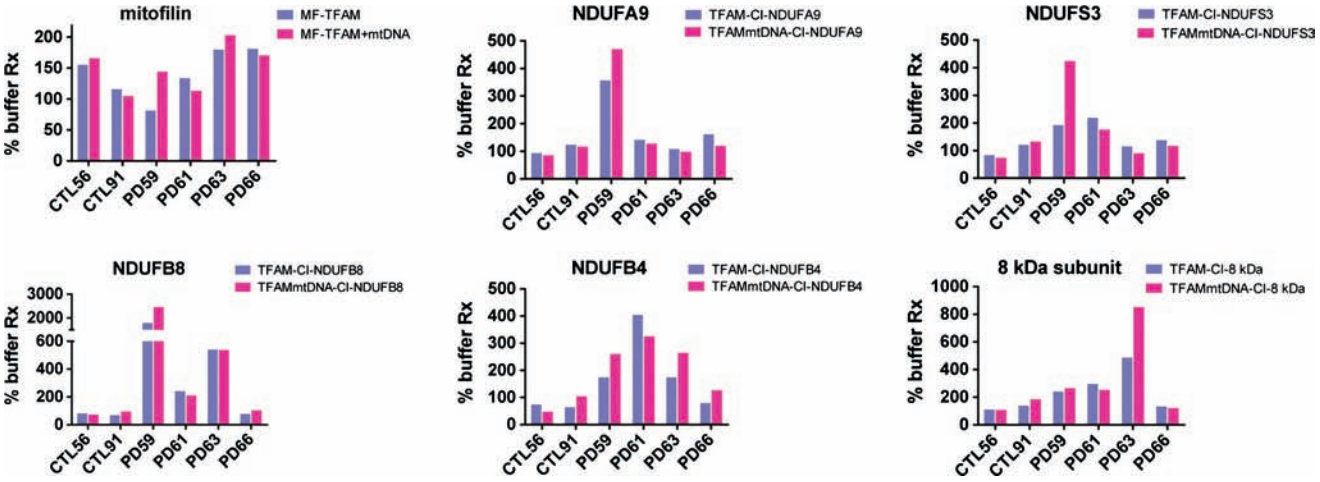
ND2 probe	CACGCAAGCAACCGCATCCATAAT	5′-FAM; 3′-BHQ1
ND2 sense	AAGCTGCCATCAAGTATTTCC	
ND2 antisense	GTAGTATTGGTTATGGTTCATTGTC	
COX3 probe	CGAAGCCGCCGCCTGATACTG	5′-TET; 3′-BHQ1
COX3 sense	TTTCACTTTACATCCAAACATCAC	
COX3 antisense	CAATAGATGGAGACATACAGAAATAG	
ND4 probe	AGCCAGAACGCCTGAACGCAG	5′-TAMRA; 3′-BHQ2
ND4 sense	TGGCTATCATCACCCGATG	
ND4 antisense	TGAGTAGTAGAATGTTTAGTGAGC	
12SRNA probe	CGCCAGAACACTACGAGCCACAG	5′-Cy5; 3′-BHQ3
12SRNA sense	CCTCAACAGTTAAATCAACAAAAC	
12SRNA antisense	CTGAGCAAGAGGTGGTGAG	



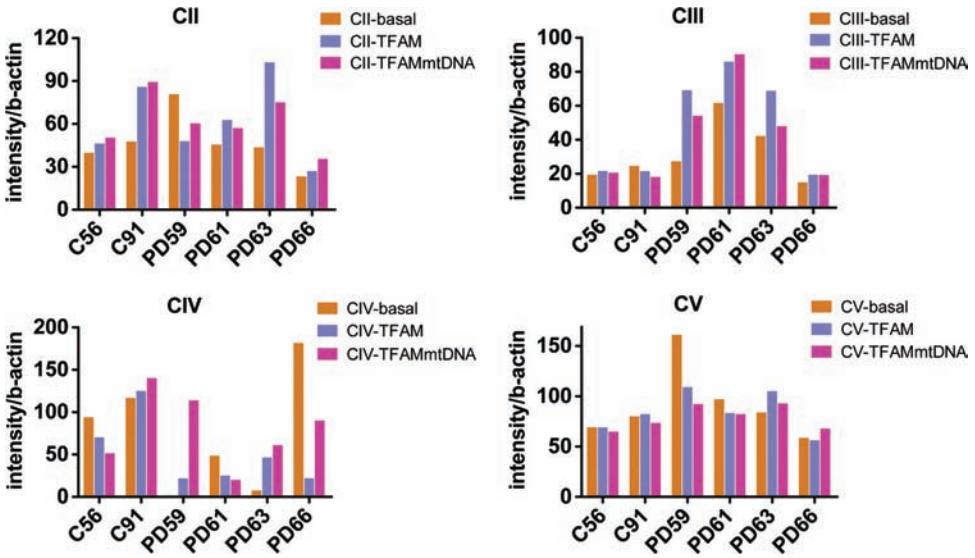
SUPPLEMENTARY FIG. 1. Shown are mtDNA gene copy numbers normalized to 18S rRNA gene levels under basal conditions and after treatment with MTD–TFAM alone or MTD–TFAM complexed with human mtDNA. Total genomic DNA was analyzed by qPCR. Shown are data from two control (CTL) and three PD cybrid lines; similar data for PD59 are presented in Fig. 2 (*top*).



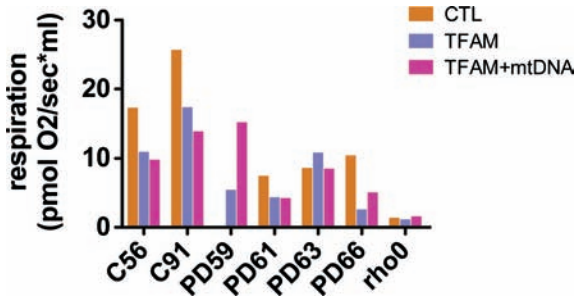
SUPPLEMENTARY FIG. 2. Shown are mtDNA gene expression data from cDNA generated from total RNA samples. Data are normalized to levels of 18S rRNA. Shown are data from two CTL and three PD cybrid lines; similar data for PD59 are presented in Fig. 2 (*bottom*).



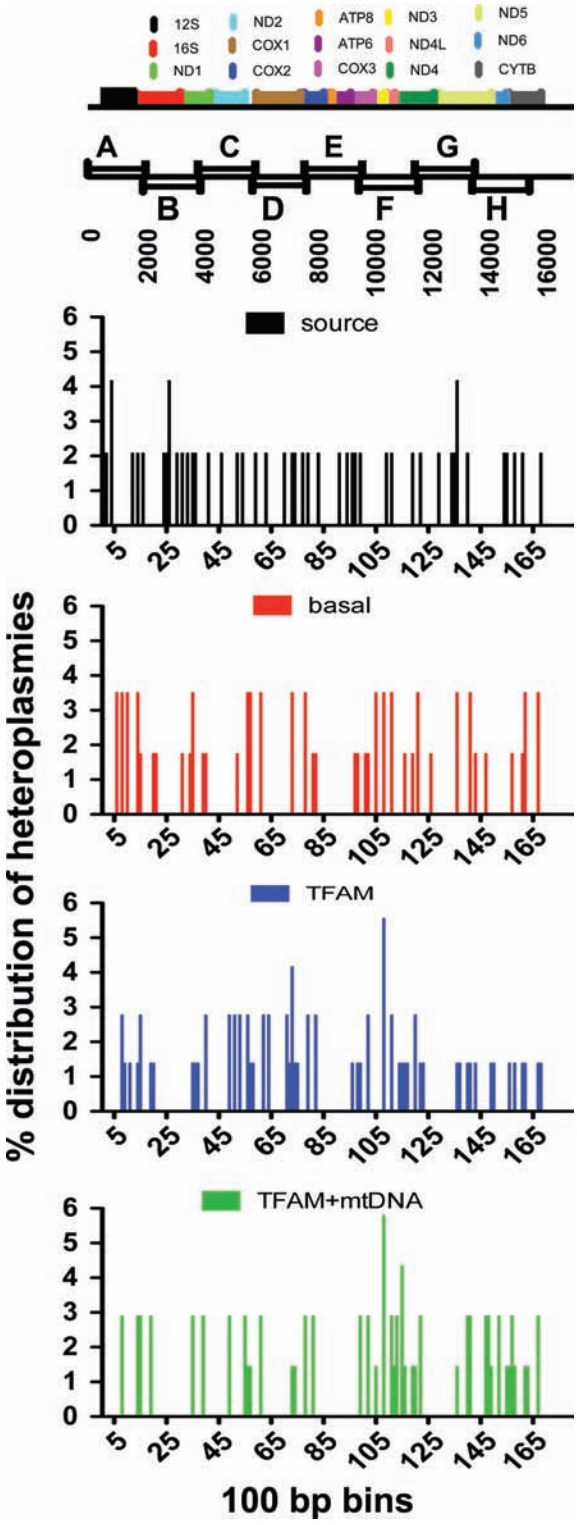
SUPPLEMENTARY FIG. 3. Effects of single treatments with MTD–TFAM or MTD–TFAM complexed with mtDNA on protein levels of mitofilin and five complex I subunits in PD and CTL cybrids. Cells were assayed 9–11 weeks after treatment. Protein levels were normalized to β-actin in each sample and are expressed as a percentage of levels in untreated cells.



SUPPLEMENTARY FIG. 4. Effects of single treatments with MTD–TFAM or MTD–TFAM complexed with mtDNA on protein levels of subunits of ETC complexes II–V. Cells were assayed 9–11 weeks after treatment. Protein levels were normalized to β-actin in each sample.



SUPPLEMENTARY FIG. 5. Effects of single treatments with MTD–TFAM or MTD–TFAM complexed with mtDNA on basal respiration rates in intact cybrid cells metabolizing glucose. Cells were assayed 9–11 weeks after treatment. Respiration rates are expressed per 10^6 live cells.



SUPPLEMENTARY FIG. 6. *Top*: Diagram of primers A–H used to generate ~2-kb amplicons of heavy circle mtDNA (Bannwarth *et al.*, 2005, 2006) and their approximate locations on the mitochondrial genome compared with 13 ETC genes and 2 rRNA genes. *Bottom*: Four graphs of heteroplasmy distributions observed in the mtDNA generated from Roche genomic DNA ("source"), and PD59 under basal conditions and after treatment with MTD–TFAM alone or complexed with mtDNA. For each amplicon analyzed with Surveyor, the Experion gel distribution of bands was determined in bins 100 bp in size. The total number of heteroplasmies found was as follows: source mtDNA (48), PD59 basal mtDNA (57), PD59 treated with MTD–TFAM (72), and PD59 treated with MTD–TFAM + mtDNA (69).