Supplementary material

Supplementary Figure 1

1.14 is homoplasmic for 5958T>C substitution.

Primers were designed to produce a 139 bp amplicon encompassing residues 5930-6060 with a primer-determined *Rsa* I restriction site and would produce a second site if the 5958T>C mutation was present. Following a last cycle hot PCR reaction, the product was cleaved with *Rsa* I endonuclease at 37˚C overnight. At least 98% of the product was sensitive to *Rsa* I in clone 1.14, whilst the product from donor colon homogenate was only cut at the internal primer site.

Supplemenatry Figure 2

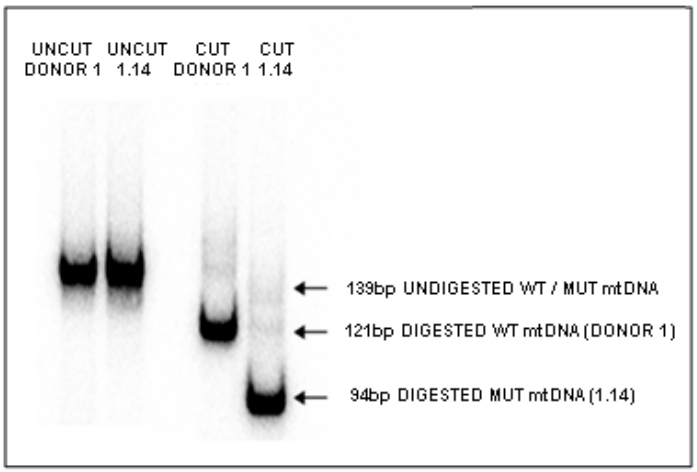
In-gel activities of mitochondrial complexes from *trans*mitochondrial clones and control lines.

One hundred micrograms of mitochondrial protein from each of the indicated cell lines was solubilised and subjected to one dimensional BN-PAGE. Following electrophoresis, gels were incubated overnight in 2 mM Tris HCl pH7.4, 0.1 mg/ml NADH, 2.5 mg/ml nitroblue tetrazolium (for complex I activity) or 50 mM KPi pH 7.4, 1 mg/ml reduced cytochrome *c*, 20 μg/ml catalase and 0.5 mg/ml diaminobenzidine (complex IV). Complex I activity produces a blue precipitate (left panel) and complex IV activity generates a brown precipitate. Mitochondria from 143B ρ^0 and 1.12 produce no visible precipitate from either enzyme, consistent with low or absent intramitochondrial translation. Conversely, although 1.14 showed comparable complex I activity to the parental control, only a very faint brown precipitate was noted, indicating a specific defect in complex IV.

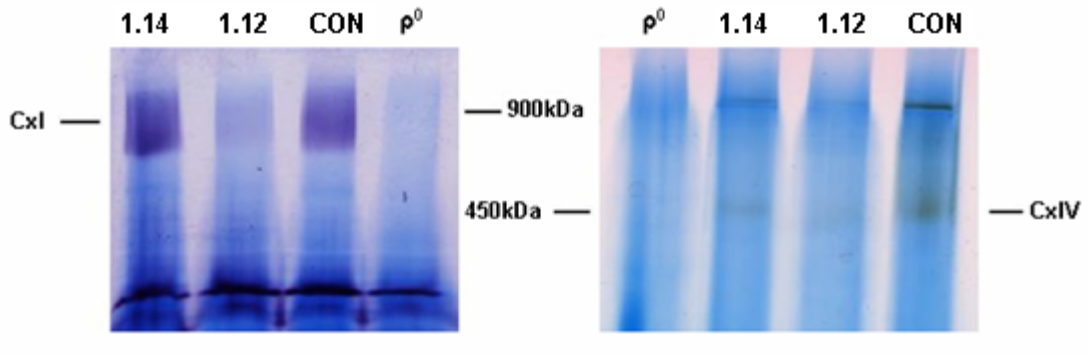
Supplementary Table 1 and 2

Complete sequences of mtDNA present in donor homogenates and all *trans*mitochondrial cybrids.

The mitochondrial genome of DNA isolated from colonic tissue and cybrids was amplified and sequenced as detailed in Materials and Methods. All base substitutions differing from the revised Cambridge Reference Sequence are listed. Substitutions that also differ from the donor tissue homogenate are highlighted for each cybrid. Donor 1 is a member of haplogroup T2, donor 2 is haplogroup H2.



Supplementary Figure 1:



Supplementary Figure 2:

BASE SUBSTITUTION	DONOR 1	1.12	1.14	CHARACTERISATION (GENE PRODUCT, AA CHANGE)
750 A>G	+	+	+	Polymorphism
1411 G>A	-	+	-	12S rRNA
1438 A>G	+	+	+	Polymorphism
1888 G>A	+	+	+	Polymorphism
1758 T>C	-	+	-	16S rRNA
2706 A>G	+	+	+	Polymorphism
3039 T>C	-	+	-	16S rRNA
3107Cdel	+	+	+	Polymorphism
4216 T>C	+	+	+	Polymorphism
4769 A>G	+	+	+	Polymorphism
4917 A>G	+	+	+	Polymorphism
5277 T>C	+	+	+	Polymorphism
5426 T>C	+	+	+	Polymorphism
5958 T>C	-	-	+	COX1 (Y19H)
6489 C>A	+	+	+	Polymorphism
7028 C>T	+	+	+	Polymorphism
8270 C>T	+	+	+	Polymorphism
9bp deletion 8269→8279 (CACCCCCTC)	+	+	+	Polymorphism
8697 G>A	+	+	+	Polymorphism
8860 A>G	+	+	+	Polymorphism
10463 T>C	+	+	+	Polymorphism
11251 A>G	+	+	+	Polymorphism
11719 G>A	+	+	+	Polymorphism
11812 A>G	+	+	+	Polymorphism
13368 G>A	+	+	+	Polymorphism
14233 A>G	+	+	+	Polymorphism
14766 C>T	+	+	+	Polymorphism
14905 G>A	+	+	+	Polymorphism
15028 C>A	+	+	+	Polymorphism
15043 G>A	+	+	+	Polymorphism
15326 A>G	+	+	+	Polymorphism
15452 C>A	+	+	+	Polymorphism
15607 A>G	+	+	+	Polymorphism
15928 G>A	+	+	+	Polymorphism
16126 T>C	+	+	+	Polymorphism
16294 C>T	+	+	+	Polymorphism
16296 C>T	+	+	+	Polymorphism
16298 T>C	+	+	+	Polymorphism
16519 T>C	+	+	+	Polymorphism
73 A>G	+	+	+	Polymorphism
195 T>C	+	+	+	Polymorphism
263 A>G	+	+	+	Polymorphism
310Cins	+	+	+	Polymorphism
312Cins	+	+	+	Polymorphism
709 G>A	+	+	+	Polymorphism

BASE SUBSTITUTION	DONOR 2	2.3	2.7	2.10	2.12	2.17	2.19	CHARACTERISATION (GENE PRODUCT, AA CHANGE)
750 A>G	+	+	+	+	+	+	+	Polymorphism
1438 A>G	+	+	+	+	+	+	+	Polymorphism
1888 G>A	+	+	+	+	+	+	+	Polymorphism
2141 T>C	+	+	+	+	+	+	+	Polymorphism
2706 A>G	+	+	+	+	+	+	+	Polymorphism
2943 G>A	-	-	+	-	-	-	-	**16S rRNA**
3107Cdel	+	+	+	+	+	+	+	Polymorphism
4216 T>C	+	+	+	+	+	+	+	Polymorphism
4647 T>C	-	-	-	-	-	-	+	**ND2 gene** (F60L)
4769 A>G	+	+	+	+	+	+	+	Polymorphism
4917 A>G	+	+	+	+	+	+	+	Polymorphism
5458 T>C *	-	-	-	-	-	+	-	**ND2 gene** (I330T)
7028 C>T	+	+	+	+	+	+	+	Polymorphism
7802 C>T	+	+	+	+	+	+	+	Polymorphism
8697 G>A	+	+	+	+	+	+	+	Polymorphism
8860 A>G	+	+	+	+	+	+	+	Polymorphism
9117 T>C	+	+	+	+	+	+	+	Polymorphism
10463 T>C	+	+	+	+	+	+	+	Polymorphism
11055 T>A *	-	+	-	-	-	-	-	**ND4 gene** (L99Q)
11251 A>G	+	+	+	+	+	+	+	Polymorphism
11719 G>A	+	+	+	+	+	+	+	Polymorphism
11812 A>G	+	+	+	+	+	+	+	Polymorphism
13368 G>A	+	+	+	+	+	+	+	Polymorphism
13965 T>C	+	+	+	+	+	+	+	Polymorphism
13966 A>G	+	+	+	+	+	+	+	Polymorphism
14233 A>G	+	+	+	+	+	+	+	Polymorphism
14361 A>G *	-	-	-	-	+	-	-	**ND6 gene** (W105R)
14687 A>G	+	+	+	+	+	+	+	Polymorphism
14766 C>T	+	+	+	+	+	+	+	Polymorphism
14905 G>A	+	+	+	+	+	+	+	Polymorphism
15326 A>G	+	+	+	+	+	+	+	Polymorphism
15452 C>A	+	+	+	+	+	+	+	Polymorphism
15607 A>G	+	+	+	+	+	+	+	Polymorphism
15928 G>A	+	+	+	+	+	+	+	Polymorphism
16126 T>C	+	+	+	+	+	+	+	Polymorphism
16294 C>T	+	+	+	+	+	+	+	Polymorphism
16296 C>T	+	+	+	+	+	+	+	Polymorphism
16324 T>C	+	+	+	+	+	+	+	Polymorphism
16519 T>C	+	+	+	+	+	+	+	Polymorphism
73 A>G	+	+	+	+	+	+	+	Polymorphism
263 A>G	+	+	+	+	+	+	+	Polymorphism
315Cins	+	+	+	+	+	-	+	Polymorphism
709 G>A	+	+	+	+	+	+	+	Polymorphism

Supplementary table 2: