



**Supplementary Figure 1. Schematic representation of pronuclear transfer in abnormally fertilised human embryos.** The main findings are potential development to blastocyst stage *in vitro* and very low levels of donor mtDNA carry over (<2%)

**Embryo 1**

	D3S1358	D16S539	D8S1179
Recipient sperm	15/16	11/11	10/11
Recipient follicular cells	16/16	11/11	12/13
Embryo	14/16	12/12	14/14
Donor sperm	14/16	11/12	13/14
Donor follicular cells	14/16	11/12	13/14

**Embryo 2**

	PentaD	D21S11	PentaE	CSF1PO	D8S1179
Recipient sperm	9/11	28/32.2	10/16	10/12	13/13
Recipient follicular cells	10/14	30/30	10/11	10/14	12/15
Embryo	13/13	30/32	10/13	11/12	11/15
Donor sperm	13/13	30/32	10/10	11/12	15/15
Donor follicular cells	10/13	30/30	7/13	11/12	11/15

**Embryo 3**

	D21S11	TPOX	FGA
Recipient sperm	29/31.2	9/11	23/25
Recipient follicular cells	28/28	11/11	23/25
Embryo	29/31.2	8/8	22/22
Donor sperm	29/31.2	8/8	20/22
Donor follicular cells	31.2/31.2	8/8	22/25

**Supplementary Table 1. Informative microsatellite markers from ovarian follicular cells, sperm and pronuclear transfer embryos.** The nuclear genotype of ovarian follicular cells (maternal), sperm (paternal) and embryos was determined using the PowerPlex<sup>®</sup> 16 System. Informative markers are shown. Recipient samples are those parental samples for the embryo in which the pronucleus is removed as a karyoplast. Donor samples are those parental samples of the embryo which is the pronuclear donor. In the third embryo we were also able to analyse the removed karyoplast from the recipient embryo – only the D21S11 marker amplified and this marker was 28 confirming that we had removed the female pronucleus from the embryo.

mtDNA sequence variant	Primer sequences (5' to 3')	Annealing temperature	Restriction enzyme*	Product sizes (bp)		
				Uncut	Wildtype	Mutant
m.93A>G	F TG <b>T</b> AAAACGACGGCCAGTcaccctattaacc <b>G</b> ctacg R ttgaacgtaggtgcgataataat	60°C	<i>AciI</i>	180	30 + 150	30 + 64 + 86
m.497C>T	F gtatgcactttaacagtcacc R ggggtgtctttgggittgg	61°C	<i>AciI</i>	159	27 + 44 + 88	44 + 115
m.16126T>C	F TG <b>T</b> AAAACGACGGCCAGTtacattactgccagccacca R CAGGAAACAGCTATGACCgtggctttggagttgcagtt	60°C	<i>HpyCH4V</i>	199	33 + 166	33 + 47 + 119
m.16129G>A	F attctcgttcttcatgggg R gggtttgatgtggattggg	55°C	<i>KpnI</i>	171	37 + 53 + 81	37 + 134
m.16519T>C	F TG <b>T</b> AAAACGACGGCCAGTcagtcaaatcccttctcgtc R gggaacgtgtggctatta	60°C	<i>HaeIII</i>	223	91 + 132	31 + 60 + 132

F: forward; R: reverse. Primer M13-tails are listed in capital letters. Mismatch bases are highlighted in bold. \* Digests were performed overnight with 10U restriction enzyme.

### Supplementary Table 2. Hot last cycle PCR/RFLP assay conditions.