

**Supplementary Data. Shared changes in WM35 and WM35 PKB cells with respect to consensus revised Cambridge mitochondrial sequence**

position	MITO <sup>1</sup>	WM35	WM35 PKB	amino acid change	transition(ti)/ transversion(tv)	sequence region	amino acid position <sup>2</sup>	protein region <sup>3</sup>	degree of conservation <sup>4</sup>
5280	A	T	T	Thr→Ser	tv	ND2 (4470-5511)	271	—	low
5319	A	C	C	Thr→Pro	tv	ND2	284	TM	low
6385	C	no seq data	G	Ala→Gly	tv	COI (5904-7445)	161	TM	high
7832, 7834	A,C	G,G	G,G	Ile→Val	ti & tv	COII (7586-8269)	83	TM	intermediate
7888	C	G	G	NC	tv	COII	101	—	—
7893	A	G	G	Gln→Arg	ti	COII	103	—	complete
7898	T	G	G	Tyr→Asp	tv	COII	105	—	high
7916	A	G	G	Thr→Ala	ti	COII	111	—	intermediate
12290	A	G	G	NC	ti	tRNA <sup>leu</sup> (12266-12336) ND5 (12337- 14148)	3	—	—
12343	A	G	G	Met→Val	ti	ND5	6	LC	low
12354	T	G	G	NC	tv	ND5	9	—	—
12361	A	G	G	Thr→Ala	ti	ND5	12	LC	low
12371	T	G	G	Leu→Arg	tv	ND5	24	LC	low
12407	T	G	G	Val→Gly	tv	ND5	—	—	very low
12437- 12438	A,T	T,G	T,G	His→Leu	tv	ND5	34	—	low
12444	A	G	G	Val→Gly	ti	ND5	36	TM	very low
12446	A	G	G	Lys→STOP	ti	ND5	37	TM	low
12448	T	G	G	Ser→Ala	tv	ND5	38	TM	low
12465	C	A	A	NC	tv	ND5	43	—	—
12468	T	A	A	Phe→Leu	tv	ND5	44	TM	high
12471	T	C	C	NC	ti	ND5	45	—	—
12474	C	G	G	Ile→Met	tv	ND5	46	TM	intermediate
12475	A	C	C	Ser→Arg	tv	ND5	47	TM	complete
12488	C	G	G	Thr→STOP	tv	ND5	51	TM	intermediate
12492	A	G	G	NC	ti	ND5	52	—	—

12507	A	G	G	NC	ti	ND5	57	—	—
12508	G	A	A	Asp→Asn	ti	ND5	58	TM	low
12513	A	G	G	NC	ti	ND5	59	—	—
12577-									
12578	A,A	G,C	G,C	Lys→Ala	ti & tv	ND5	81	—	intermediate
12594	C	G	G	NC	tv	ND5	86	—	—
12612	A	G	G	NC	ti	ND5	92	—	—
12616	T	G	G	Leu→Val	tv	ND5	94	TM	high

1. MITO refers to the Revised Cambridge Mitochondrial Sequence in which rare polymorphisms have been excluded.
2. Amino acid position denotes position within the gene product.
3. Protein region denotes whether mutation occurs in a transmembrane domain (TM) or low complexity (LC) region of the gene product.
4. Indicates degree of cross-species conservation.