Supplemental Table S4. Mitochondrial alignments and misalignments

Source	Reads			Cross-species alignments (%)[b]	Copy number[c]
	Aligned[a]	Human mito	Hamster mito		
HEK293	40 128 368	153 367	289	0.19	2145
A23	33 234 329	138	95 975	0.14	843

[a] Identical to corresponding values in Supplemental Table S3.

[b] Percentage cross-species reads after alignment to other species: (Hamster mitochondrial reads/human mitochondrial reads) · 100 for HEK293; (human mitochondrial reads/hamster mitochondrial reads) × 100 for A23.

[c] $3 \cdot$ (Human mitochondrial reads/{aligned human reads − human mitochondrial reads}) · ({human genome = 3 088 269 832 bp}/{human mitochondrial genome = 16 569 bp}) for HEK293 which is pseudotriploid (Lin et al. 2014); $2 \cdot$ (hamster mitochondrial reads/{aligned hamster reads − hamster mitochondrial reads}) · ({hamster genome = 2 368 906 908 bp}/{hamster mitochondrial genome = 16 283 bp}) for A23.