Supplemental Table S12. Mitochondrial DNA in the RH pools

Pool	Total[b]	Hamster[c]	Human *TK1*[d]	Hamster mito	Human mito	Revert freq	Hamster (align)[e]	Human (align)[f]	Human (*TK1*)[g]
		Reads[a]						Mito copy number	
1	42 000 172	37 595 178	997	103 116	16	0.24	800	0.12	0.74
2	35 358 581	30 754 890	2636	109 494	474	0.2	1040	4.42	8.67
3	52 166 656	45 668 817	3302	96 305	492	0.27	615	3.09	6.57
4	32 756 205	28 092 611	3125	61 749	45	0.29	641	0.46	0.61
5	42 876 176	38 167 486	2234	89 994	0	0.28	688	0.00	0.00
6	41 449 894	37 193 349	2573	96 898	2	0.37	760	0.02	0.03
Mean	41 101 281	36 245 388	2478	92 926	172	0.28	757	1.35	2.77
s.e.m.	2 763 700	2 528 698	336	6797	99	0.02	63	0.78	1.56

[a] All reads, except "Total", purged of cross-species alignments.

[b] Identical to same column in Supplemental Tables S5, S6.

[c] Identical to "Corrected hamster" column in Supplemental Table S6.

[d] Identical to same column in Supplemental Table S7.

[e] Hamster mitochondrial copy number: $2 \cdot$ (hamster mitochondrial reads/{hamster reads − hamster mitochondrial reads}) $\cdot$ ({hamster genome length = 2 368 906 908 bp}/{hamster mitochondrial genome length = 16 283 bp}).

[f] Human mitochondrial copy number deduced from hamster genome alignments: $2 \cdot$ (human mitochondrial reads/{hamster reads − hamster mitochondrial reads}) $\cdot$ ({hamster genome length = 2 368 906 908 bp}/{human mitochondrial genome length = 16 569 bp}).

[g] Human mitochondrial copy number deduced from *TK1* alignments: $1 \times$ (human mitochondrial reads/*TK1* reads) $\cdot$ ({*TK1* window length = 1×10^6 bp}/{human mitochondrial genome length = 16 569 bp}) $\cdot$ (1 − reversion frequency).