Supplemental Table S7. Human DNA retention in the RH pools

	Reads[a]				Retention		
Pool	Human reads[b]	Hamster reads[b]	Human *TK1*[c]	Revert freq	align (%)[d]	*TK1* (%)[e]	mean (%)
1	76	15 130	997	0.24	1.00	5.82	3.41
2	194	12 372	2636	0.20	3.14	5.88	4.51
3	246	18 255	3302	0.27	2.70	5.45	4.07
4	259	11 237	3125	0.29	4.61	5.85	5.23
5	155	15 082	2234	0.28	2.06	4.96	3.51
6	154	14 877	2573	0.37	2.07	3.79	2.93
Mean	181	14 492	2478	0.28	2.60	5.29	3.94
s.e.m.	28	1003	336	0.02	0.50	0.33	0.34

[a] All reads purged of cross-species alignments.
[b] Medians of non-overlapping 1 Mb windows.
[c] Maximum 1 Mb window encompassing *TK1*.
[d] $2 \cdot$ (Human reads/hamster reads) $\cdot$ 100.
[e] (Human reads$/TK1$) $\cdot$ $(1 -$ reversion frequency$) \cdot 100$.