

Supplemental Table S6. Hamster genome alignments in the RH pools

Pool	Reads				Cross-species reads (%) ^e
	Total ^a	Hamster alignments ^b	Corrected hamster ^c	Both species ^d	
1	42 000 172	37 695 387	37 595 178	100 209	0.27
2	35 358 581	30 838 307	30 754 890	83 417	0.27
3	52 166 656	45 779 128	45 668 817	110 311	0.24
4	32 756 205	28 166 022	28 092 611	73 411	0.26
5	42 876 176	38 382 035	38 167 486	214 549	0.56
6	41 449 894	37 403 393	37 193 349	210 044	0.56
Mean	41 101 281	36 377 379	36 245 388	131 990	0.36
s.e.m.	2 763 700	2 538 432	2 528 698	25 935	0.06

^a Identical to same column in Supplemental Table S5.

^b Aligned to hamster genome.

^c Hamster reads minus those that also align to human genome.

^d Aligned to both human and hamster. Identical to same column in Supplemental Table S5, apart from minor alignment differences.

^e (Aligned to both species/hamster alignments) · 100.