

**Supplemental Table S5.** Human genome alignments in the RH pools

Pool	Reads				Cross-species reads (%) <sup>d</sup>
	Total	Human alignments <sup>a</sup>	Corrected human <sup>b</sup>	Both species <sup>c</sup>	
1	42 000 172	398 642	298 433	100 209	25.1
2	35 358 581	868 990	785 571	83 419	9.6
3	52 166 656	1 173 763	1 063 450	110 313	9.4
4	32 756 205	1 121 927	1 048 516	73 411	6.5
5	42 876 176	853 173	638 622	214 551	25.1
6	41 449 894	842 565	632 519	210 046	24.9
Mean	41 101 281	876 510	744 518	131 992	16.8
s.e.m.	2 763 700	112 354	118 120	25 936	3.7

<sup>a</sup> Aligned to human genome.

<sup>b</sup> Human reads minus those that also align to hamster genome.

<sup>c</sup> Aligned to both human and hamster.

<sup>d</sup> (Aligned to both species/human alignments) · 100.