Ref_{BAC}	Ref_{EX}	Aligner	SZr	number of reads aligned to			P_{mis}	P_{uq}
				Ref_{BAC*}	Ref_{BAC}	Ref_{EX}		
CT302	CE_ch1	Eland	27	2,031,172	2,029,756	2,308	0.114%	99.930%
CT302	CE_ch1	RMAP	27	2,019,184	2,017,834	2,280	0.113%	99.933%
CT302	CE_ch1	Slider	27	1,962,980	1,962,405	1,067	0.054%	99.971%
CT302	CE_ch1	Eland	32	1,868,157	1,867,855	1,110	0.059%	99.984%
CT302	CE_ch1	RMAP	32	1,877,140	1,876,839	1,100	0.059%	99.984%
CT302	CE_ch1	Slider	32	1,709,421	1,709,287	467	0.027%	99.992%
CT302	CE_ch1	RMAP	36	1,626,071	1,625,979	266	0.016%	99.994%
CT302	CE_ch1	Slider	36	1,339,159	1,339,136	59	0.004%	99.998%
CT302	H_ch1	Eland	27	2,031,172	1,683,423	32,012	1.902%	82.879%
CT302	H_ch1	RMAP	27	2,019,184	1,674,277	32,530	1.943%	82.918%
CT302	H_ch1	Slider	27	1,962,980	1,632,788	14,062	0.861%	83.179%
CT302	H_ch1	Eland	32	1,868,157	1,596,347	32,748	2.051%	85.450%
CT302	H_ch1	RMAP	32	1,877,140	1,603,530	33,263	2.074%	85.424%
CT302	H_ch1	Slider	32	1,709,421	1,471,127	12,466	0.847%	86.060%
CT302	H_ch1	RMAP	36	1,626,071	1,420,896	33,198	2.336%	87.382%
CT302	H_ch1	Slider	36	1,339,159	1,186,272	10,789	0.909%	88.583%
CT302	H_G	Eland	27	2,031,172	1,556,836	43,454	2.791%	76.647%
CT302	H_G	RMAP	27	2,019,184	1,548,580	43,797	2.828%	76.693%
CT302	H_G	Slider	27	1,962,980	1,512,994	17,680	1.169%	77.076%
CT302	H_G	Eland	32	1,868,157	1,484,658	44,566	3.002%	79.472%
CT302	H_G	RMAP	32	1,877,140	1,491,424	44,768	3.002%	79.452%
CT302	H_G	Slider	32	1,709,421	1,370,847	16,060	1.172%	80.194%
CT302	H_G	RMAP	36	1,626,071	1,328,199	46,754	3.520%	81.681%
CT302	H_G	Slider	36	1,339,159	1,113,174	14,495	1.302%	83.125%
T02	CE_ch1	Eland	27	335,212	334,996	602	0.180%	99.936%
T02	CE_ch1	RMAP	27	334,567	334,355	578	0.173%	99.937%
T02	CE_ch1	Slider	27	329,821	329,712	115	0.035%	99.967%
T02	H_ch1	Eland	27	335,212	280,540	8,828	3.147%	83.690%
T02	H_ch1	RMAP	27	334,567	280,014	8,935	3.191%	83.694%
T02	H_ch1	Slider	27	329,821	277,160	5,399	1.948%	84.033%

Expanded Table 3: Results of aligning sequences from CT302 and T02 BACs to its reference Ref_{BAC*}, and to their reference Ref_{BAC} coupled with three extra sequences (Ref_{EX}): (CE_ch1: C.elegans chromosome I), (H_ch1: human chromosome 1) and (H_G: human genome not including chromosome 6). We see that when Ref_{EX} is added to the reference that the reads are aligned to, some reads that originally aligned to the BAC, now align to Human chromosome 1 or C.elegans chromosome 1. However, with Slider, this generally occurs less than with RMAP or Eland.