

Supplementary Table 1. The rescue achieved for determining the most likely origin of multi-mapping tags with (a) a high complexity sample (lower effective coverage); and (b) a low complexity sample (higher effective coverage). In both cases, the genome matched against was human (hg18), mapping 35mer and 30mer tags allowing no more than 3 color-space mismatches. No more than 10 multi-mapping positions were recorded for each tag, and the window size used for the rescue was 10. The weighting assigned to a tag's location refers to the probability that the tag derived from that location.

(a) High complexity sample with 11685074 single mapping tags and 3782953 multi-mapping tags.

Weighting Category	Number of Tags	Percentage of Tags
No weighting assigned	2092125	55.3%
0-0.1	59	0.0%
0.1-0.2	238	0.0%
0.2-0.3	2568	0.1%
0.3-0.4	20651	0.5%
0.4-0.5	104974	2.8%
0.5-0.6	78970	2.1%
0.6-0.7	114287	3.0%
0.7-0.8	127066	3.4%
0.8-0.9	115944	3.1%
0.9-1.0	1126071	29.8%
Total	3782953	100.0%

(b) Low complexity sample with 11605650 single mapping tags and 4395351 multi-mapping tags.

Weighting Category	Number of Tags	Percentage of Tags
No weighting assigned	1530298	34.8%
0-0.1	332	0.0%
0.1-0.2	266	0.0%
0.2-0.3	2799	0.1%
0.3-0.4	18105	0.4%
0.4-0.5	87936	2.0%
0.5-0.6	162980	3.7%
0.6-0.7	216004	4.9%
0.7-0.8	256090	5.8%
0.8-0.9	253389	5.8%
0.9-1.0	1867152	42.5%
Total	4395351	100.0%