Supplementary Table 3. Proportions of genome coverage (by any unique tag) for color-space short tag alignments. Columns shown are length of tag matched; numbers in parentheses represent the number of mismatches allowed. Valid-adjacent errors are counted as 2 mismatches for all tag lengths except 25, where valid-adjacent errors are counted as a single mismatch.

Species	25(1)	35(3)	50(5)	60(6)
H. sapiens[a]	74.6%	79.8%	81.6%	83.8%
M. musculus[b]	77.8%	81.8%	83.0%	84.8%
C. elegans[c]	90.0%	91.9%	92.3%	93.4%
D. melanogaster[d]	69.7%	70.7%	70.8%	71.8%

[a]Build hg19

[b]Build mm9

[c]Build ce6

[d]Build dm3