Supplementary Table 2. Proportions of genome coverage (by any unique tag) for nucleotide-space short tag alignments. Columns shown are length of tag matched; numbers in parentheses represent the number of mismatches allowed.

Species	**25(1)**	**30(1)**	**35(1)**	**50(2)**	**60(3)**	**75(4)**	**90(5)**
H. sapiens[a]	74.8%	78.3%	81.0%	83.0%	83.3%	84.6%	85.4%
M. musculus[b]	77.8%	80.6%	82.6%	83.9%	84.1%	85.0%	85.7%
C. elegans[c]	90.0%	91.2%	92.1%	92.6%	92.7%	93.3%	93.7%
D. melanogaster[d]	69.6%	70.3	70.9%	71.2%	71.2%	71.7%	72.2%

[a] Build hg19

[b] Build mm9

[c] Build ce6

[d] Build dm3