Supplementary Table 4. Proportions of unique start sites and genome coverage (by any unique tag) for nucleotide-space short tag alignments in hg19. Columns shown are length of tag matched; numbers in parentheses represent the number of mismatches allowed. This table indicates how the presence of more sequencing error (or higher true variant rates) leads to a decrease in the uniquely mappable genome.

	50(0)	**50(1)**	**50(2)**	**50(3)**
Unique start sites	84.9%	80.5%	76.9%	73.9%
Coverage by unique tags	88.6%	85.8%	83.0%	80.5%