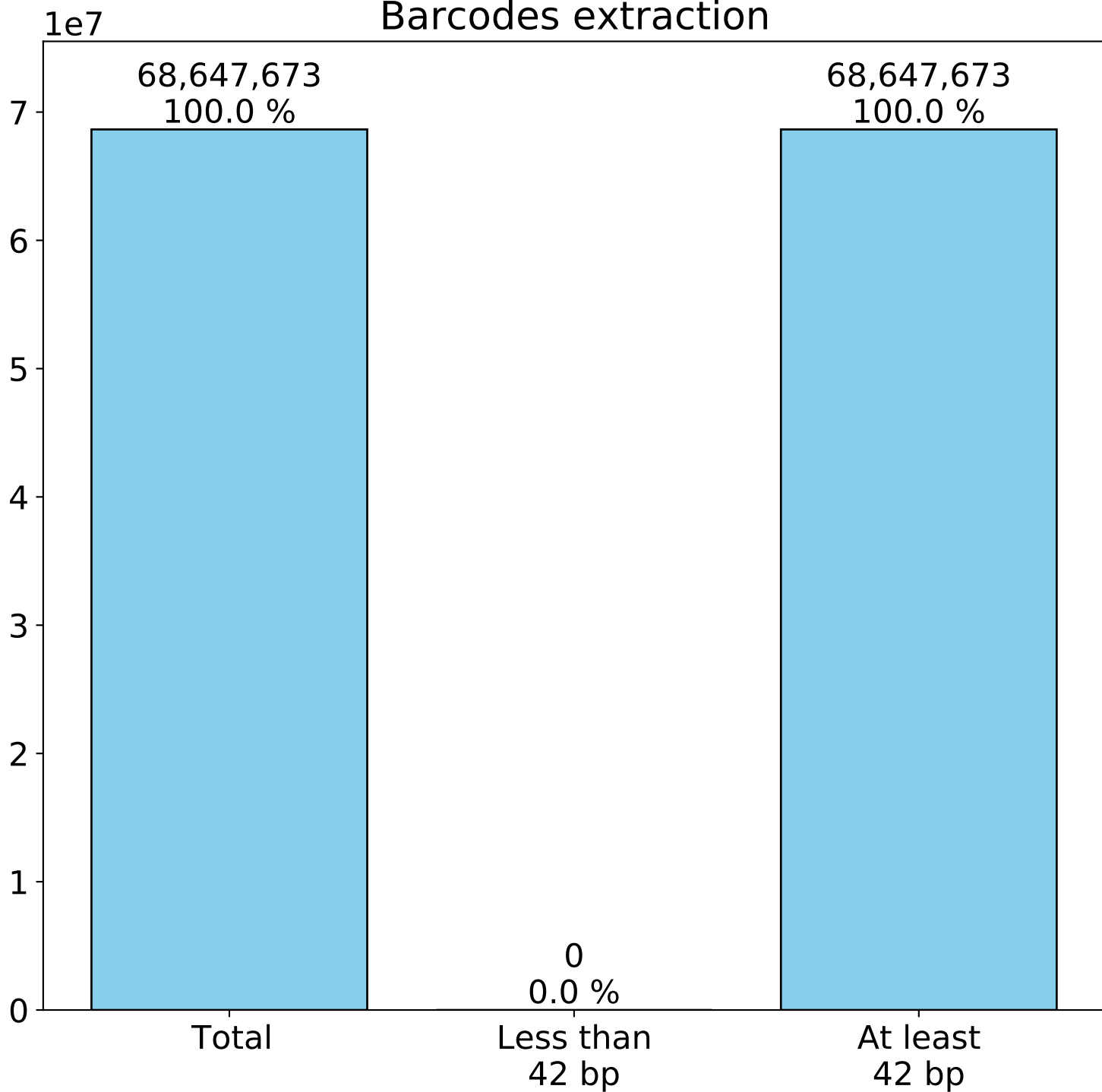
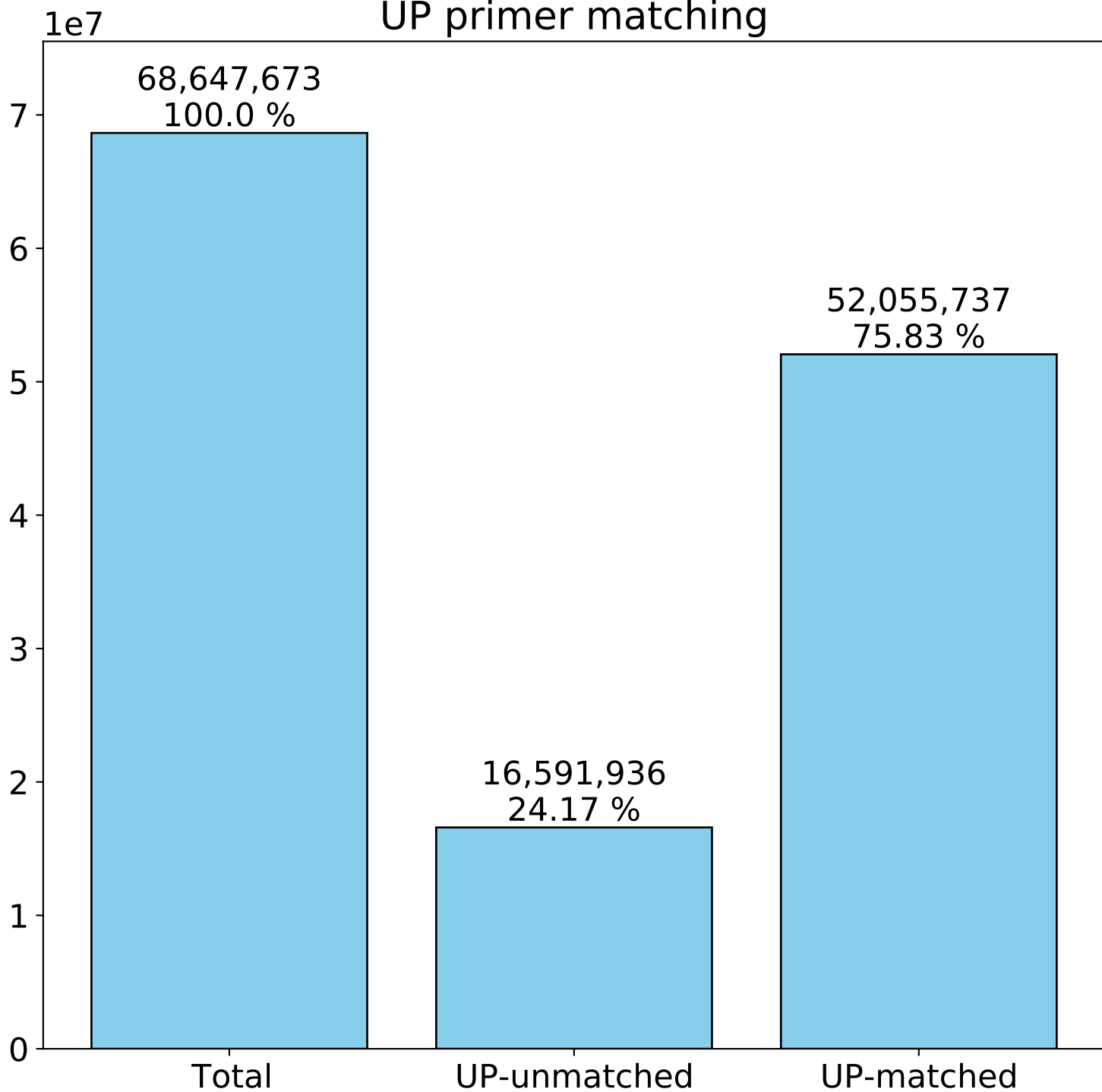


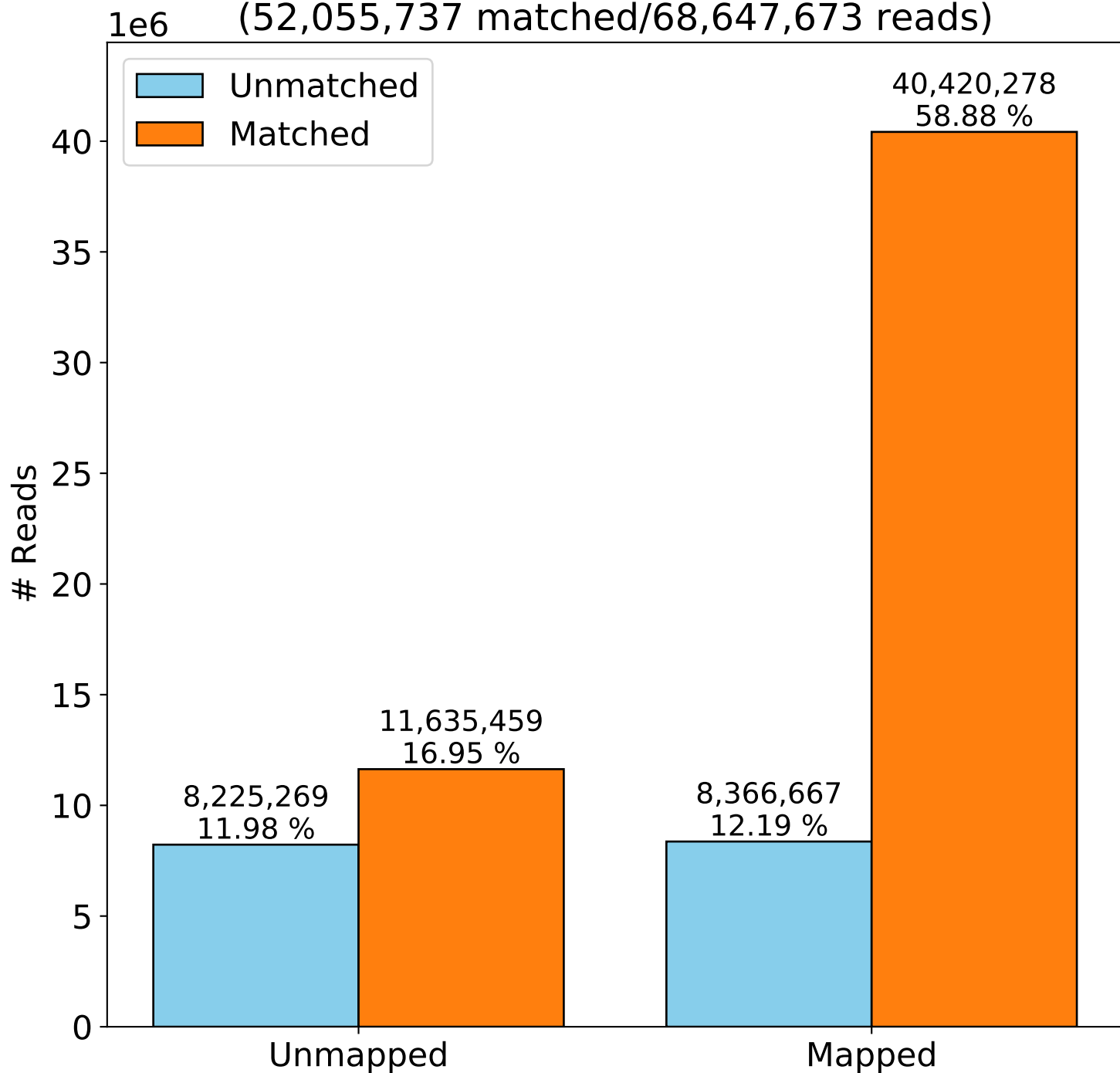
Barcodes extraction



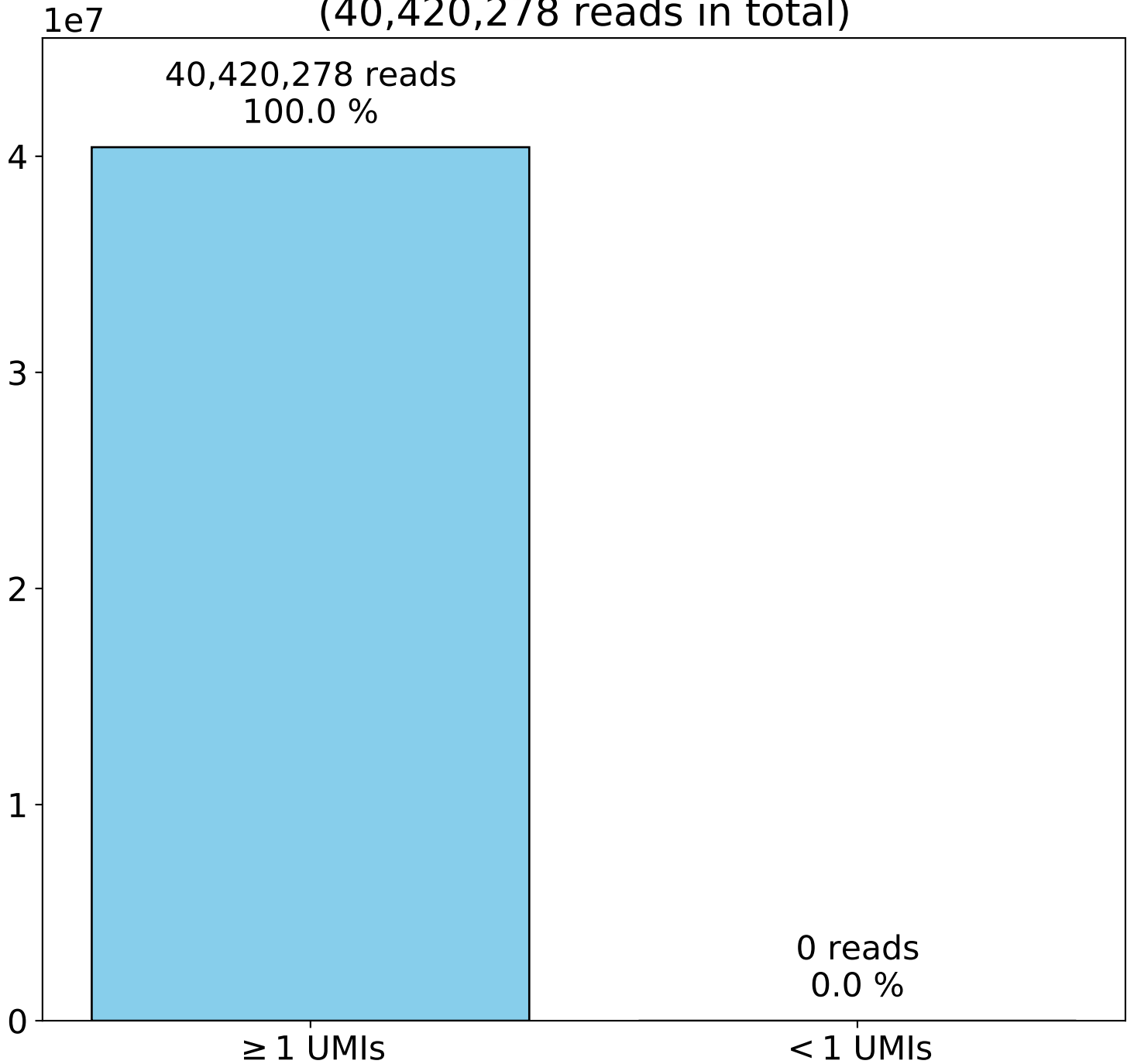
UP primer matching



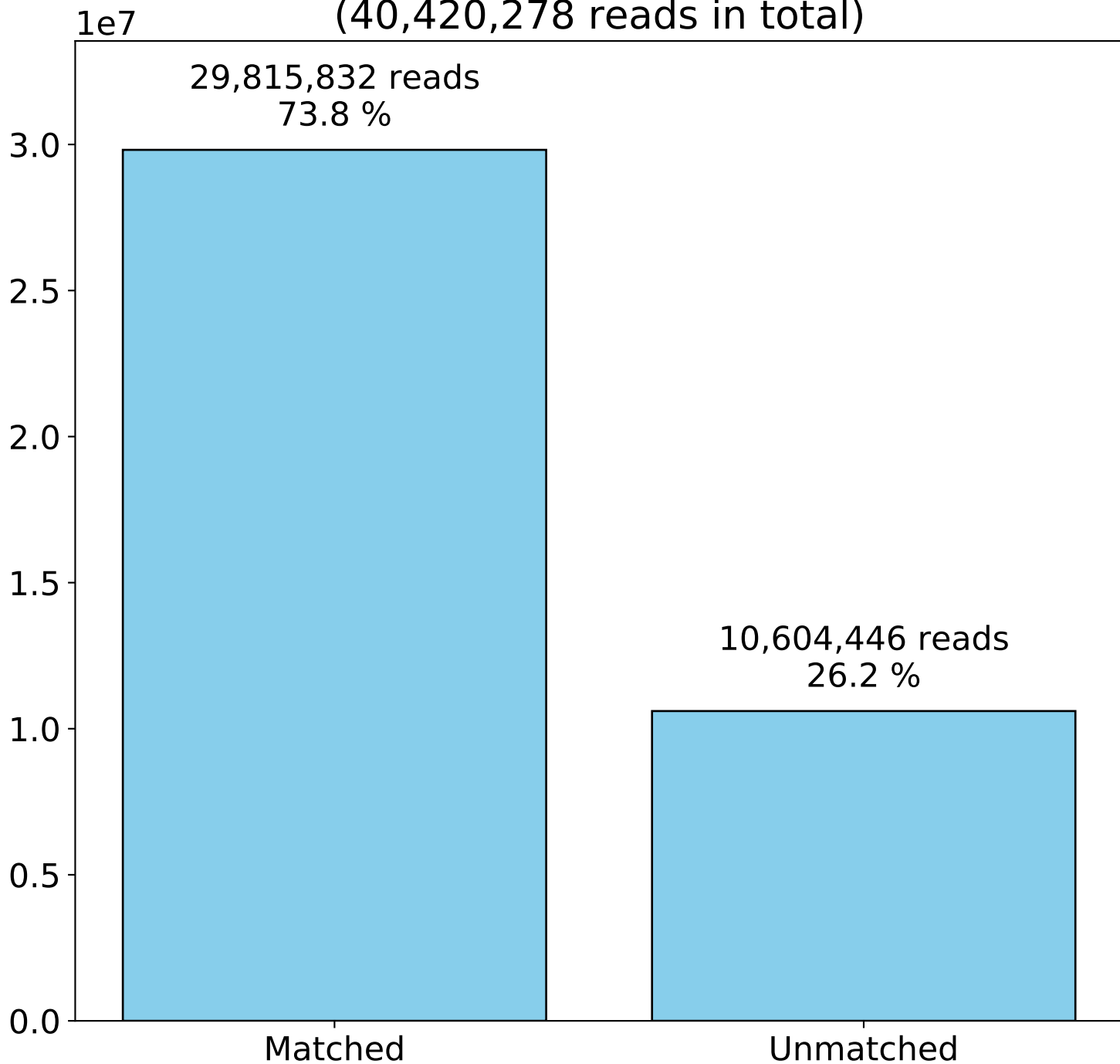
UP primer matching
(52,055,737 matched/68,647,673 reads)



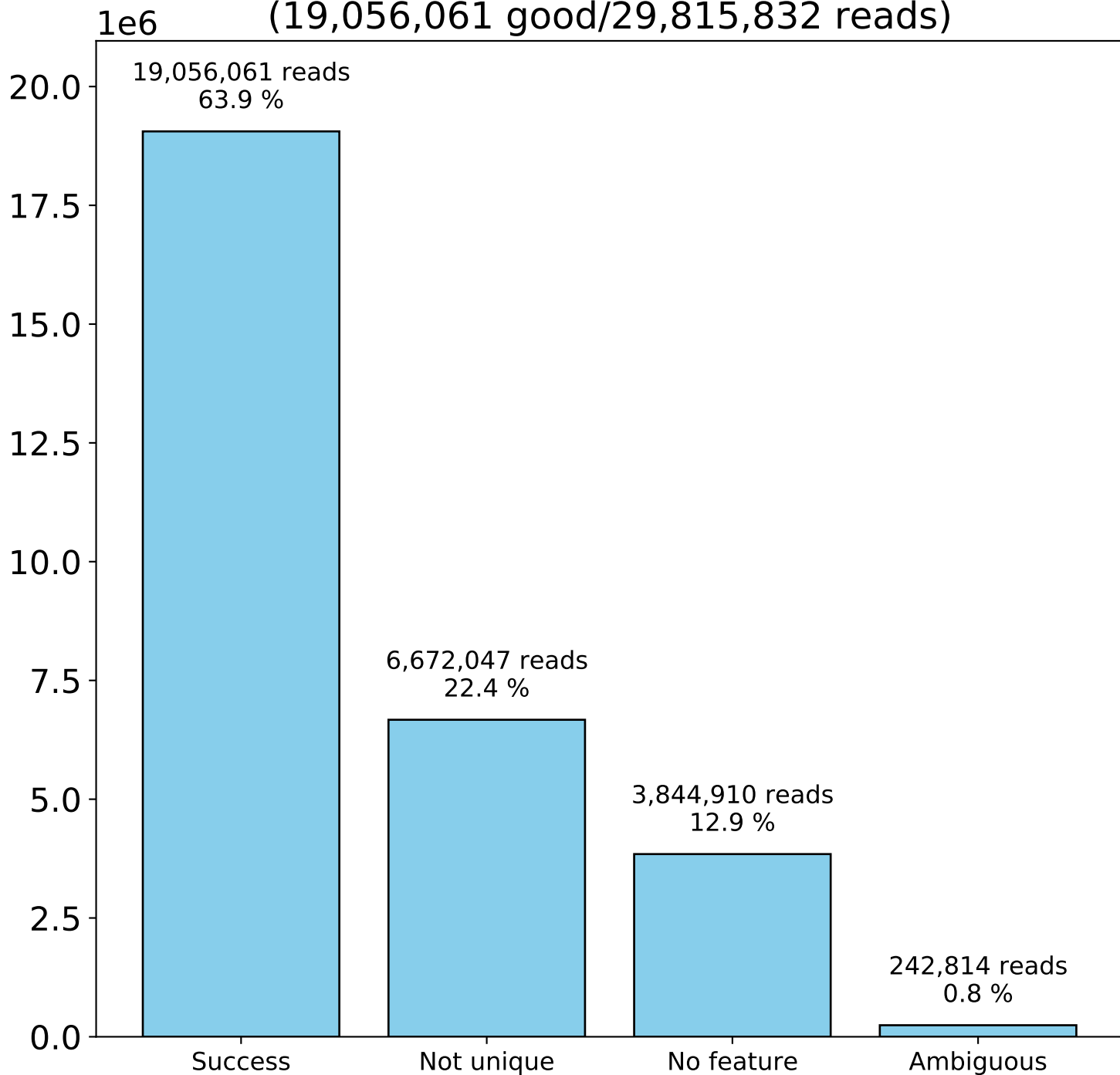
Reads with barcode that pass the UMIs threshold (40,420,278 reads in total)



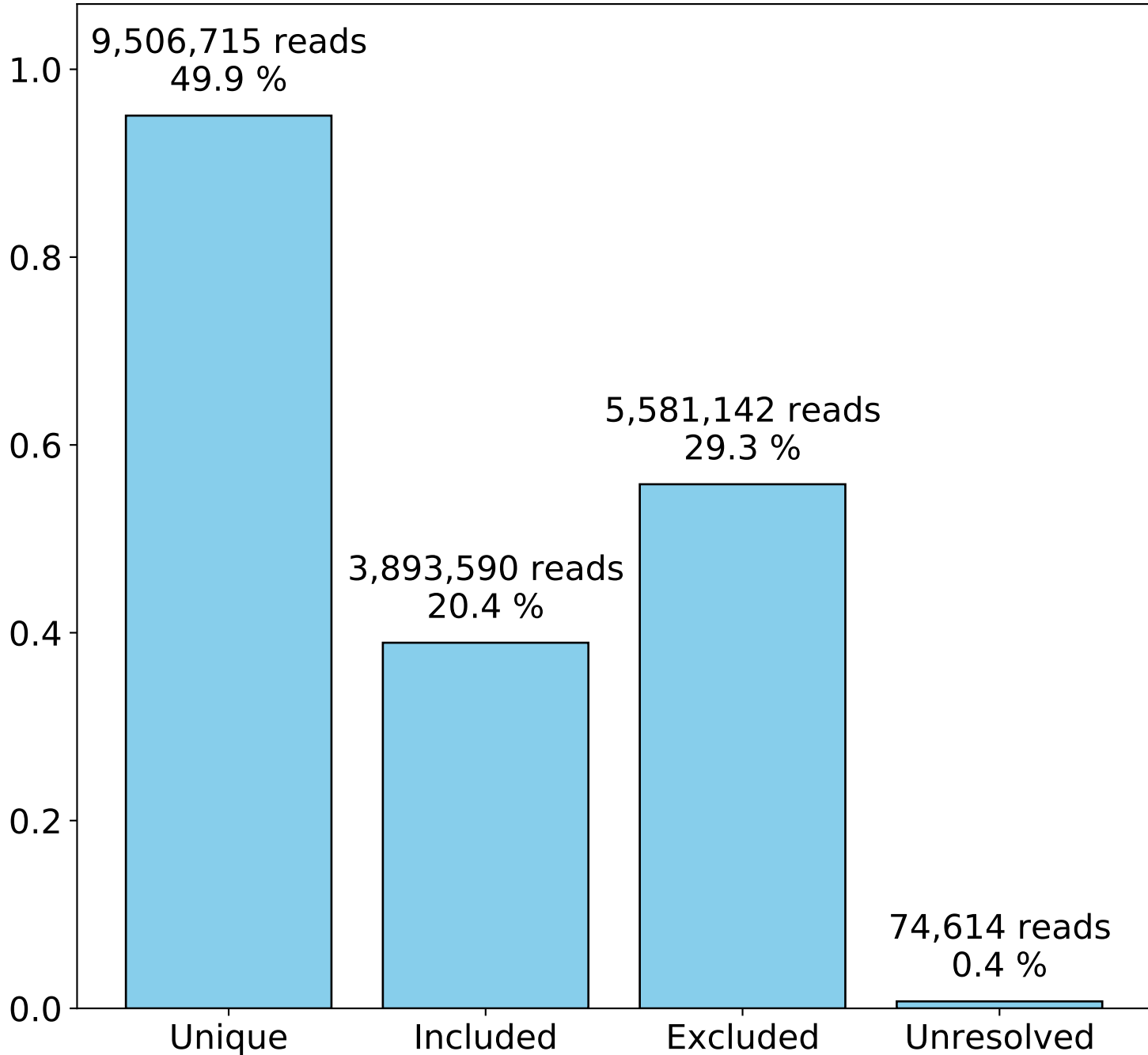
Barcode matching (40,420,278 reads in total)



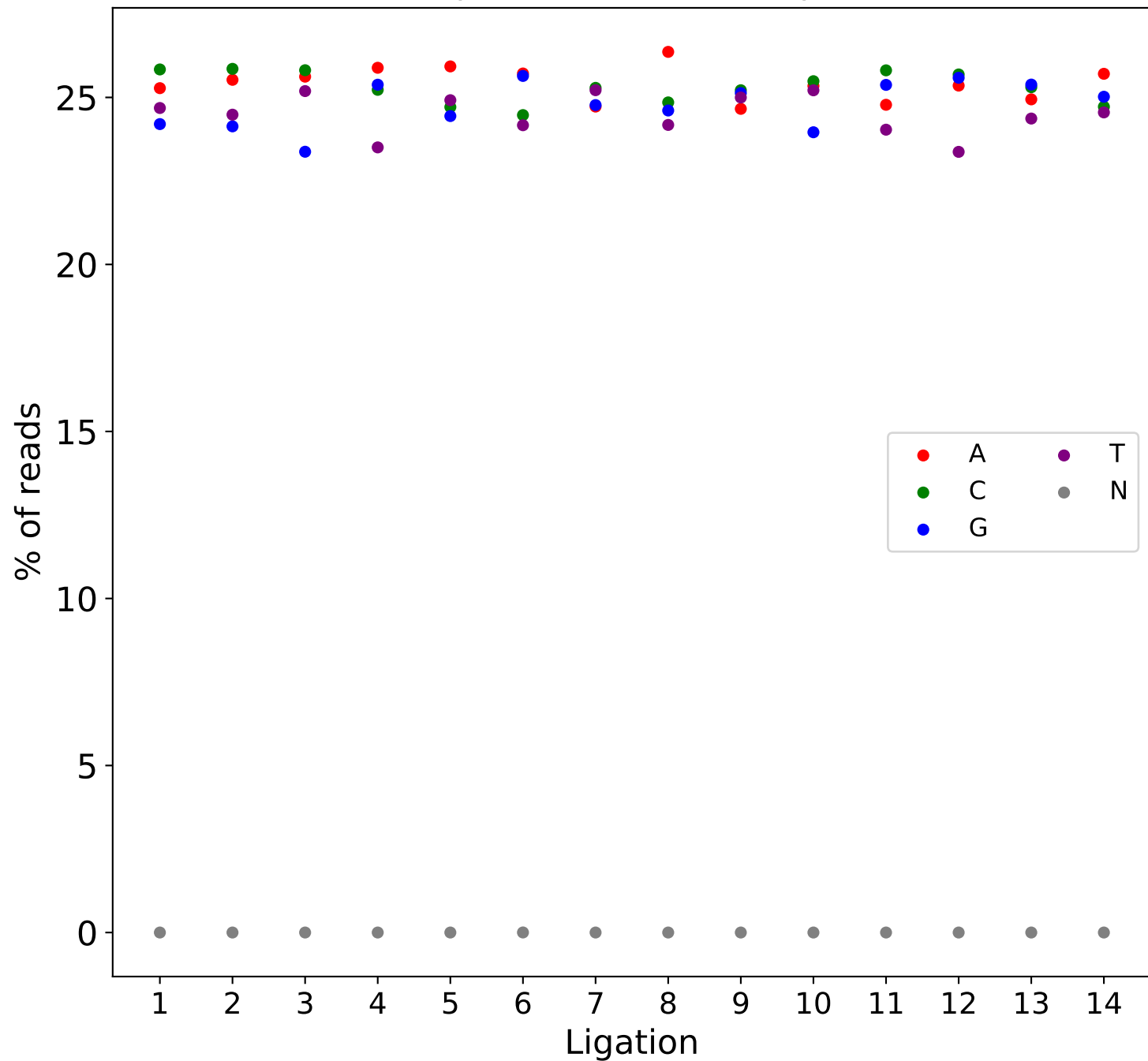
Gene annotation of the reads (19,056,061 good/29,815,832 reads)



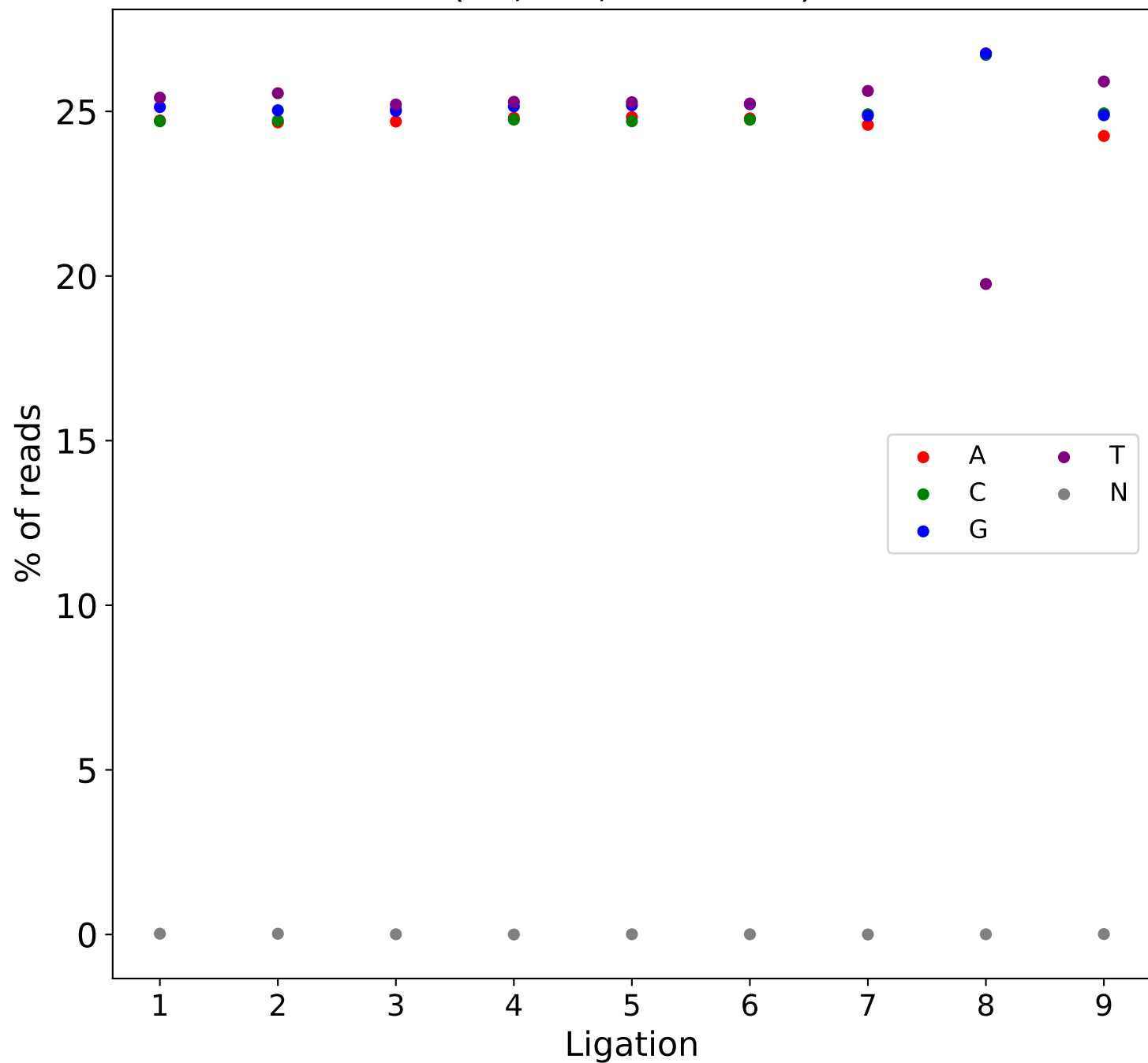
Selecting multi-mapped UMIs based on score 1e7 (13,400,305 unambiguous/19,056,061 reads)



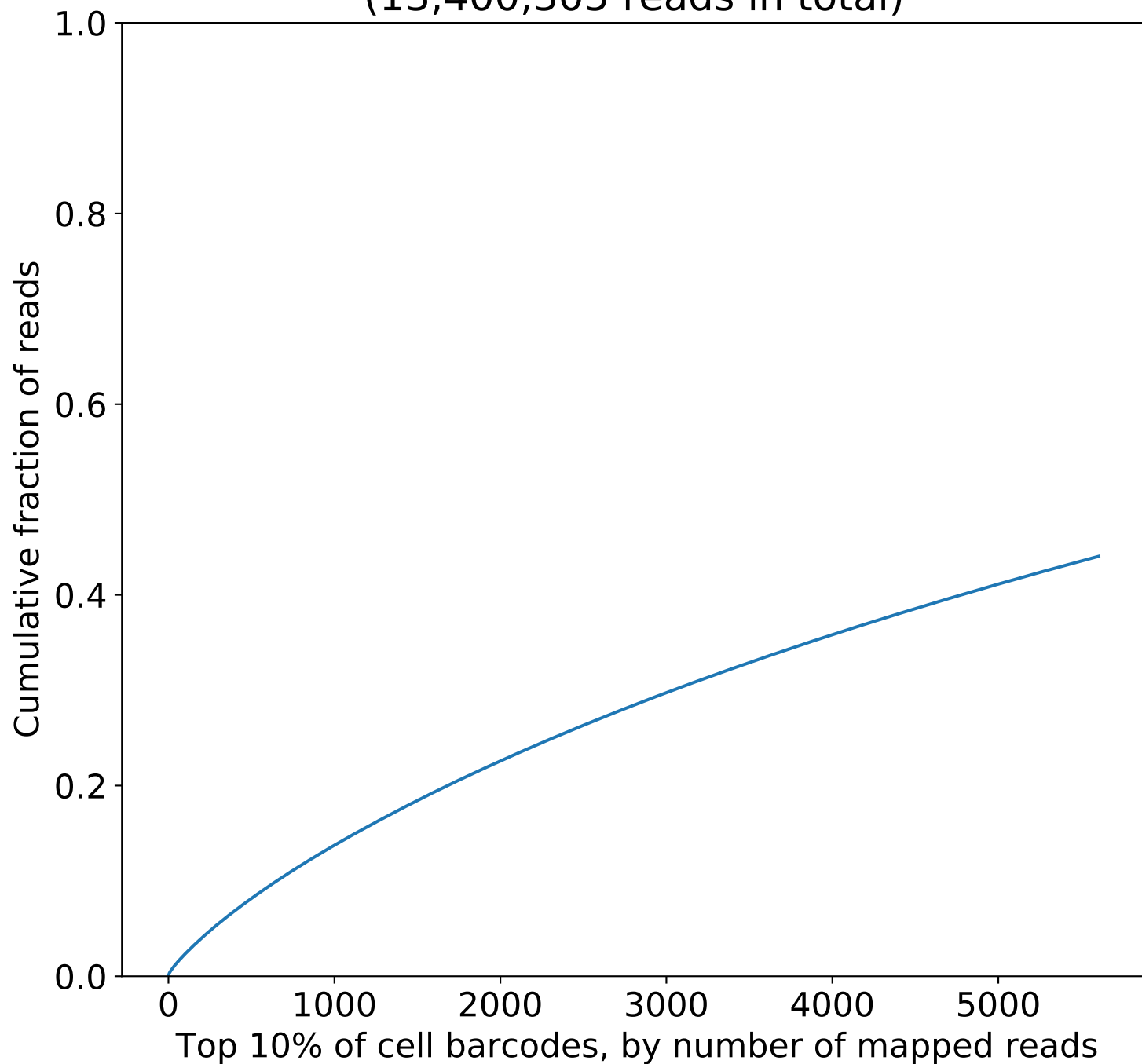
Barcode for bead-matched reads (13,400,305 reads)



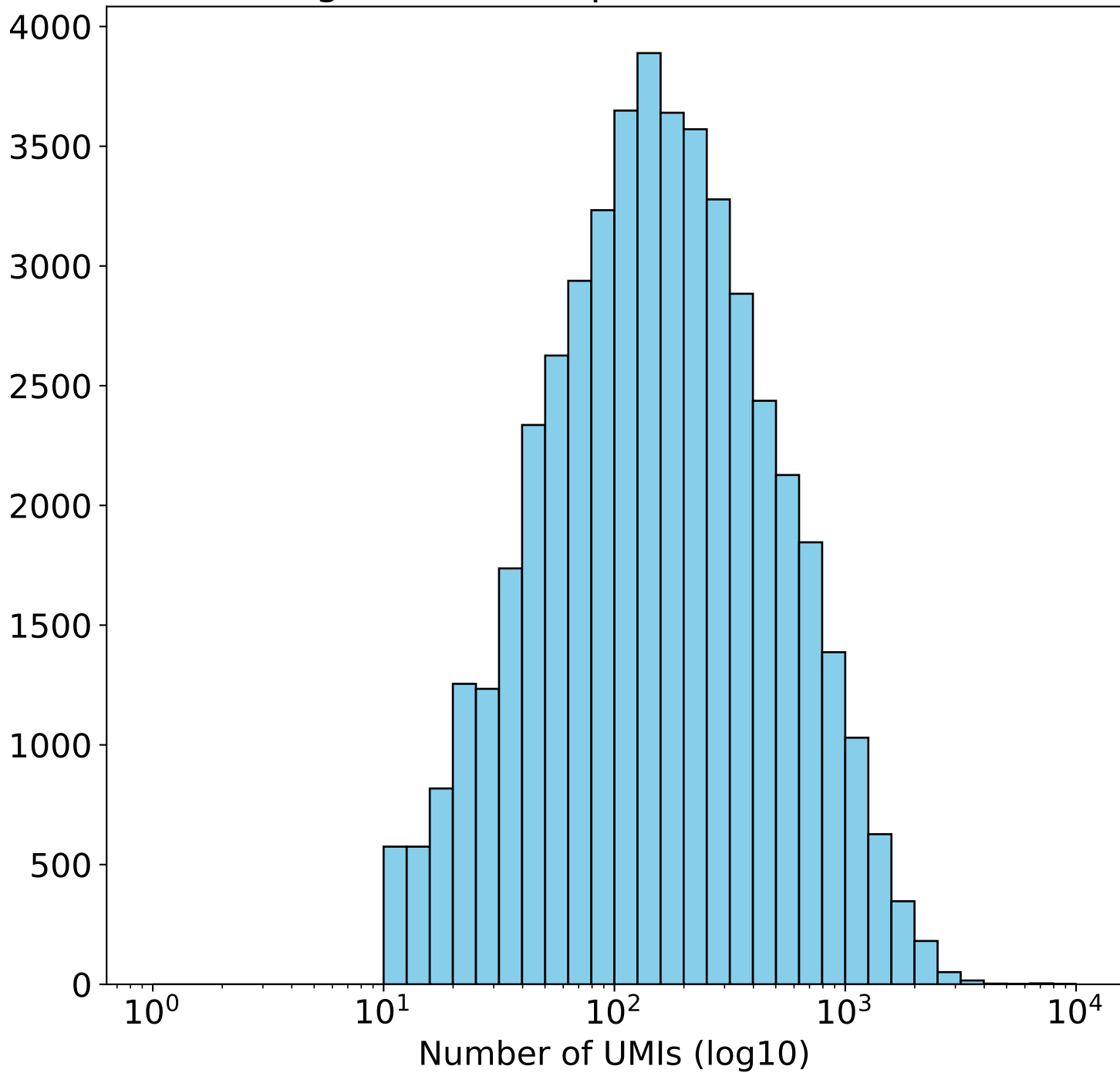
UMI for bead-matched reads (13,400,305 reads)



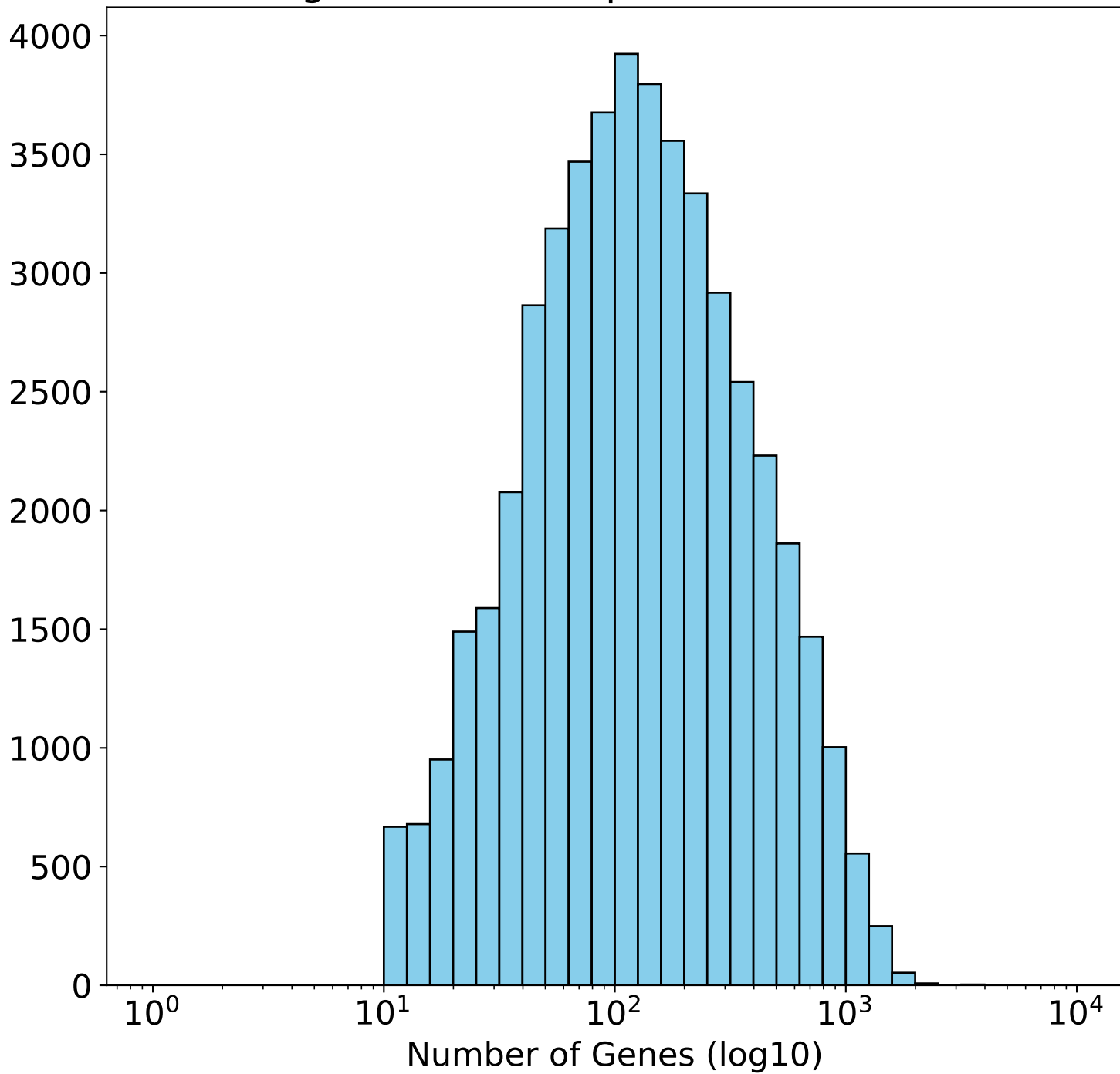
Cumulative fraction of reads per cell barcode (13,400,305 reads in total)



Histogram of UMIs per matched barcode

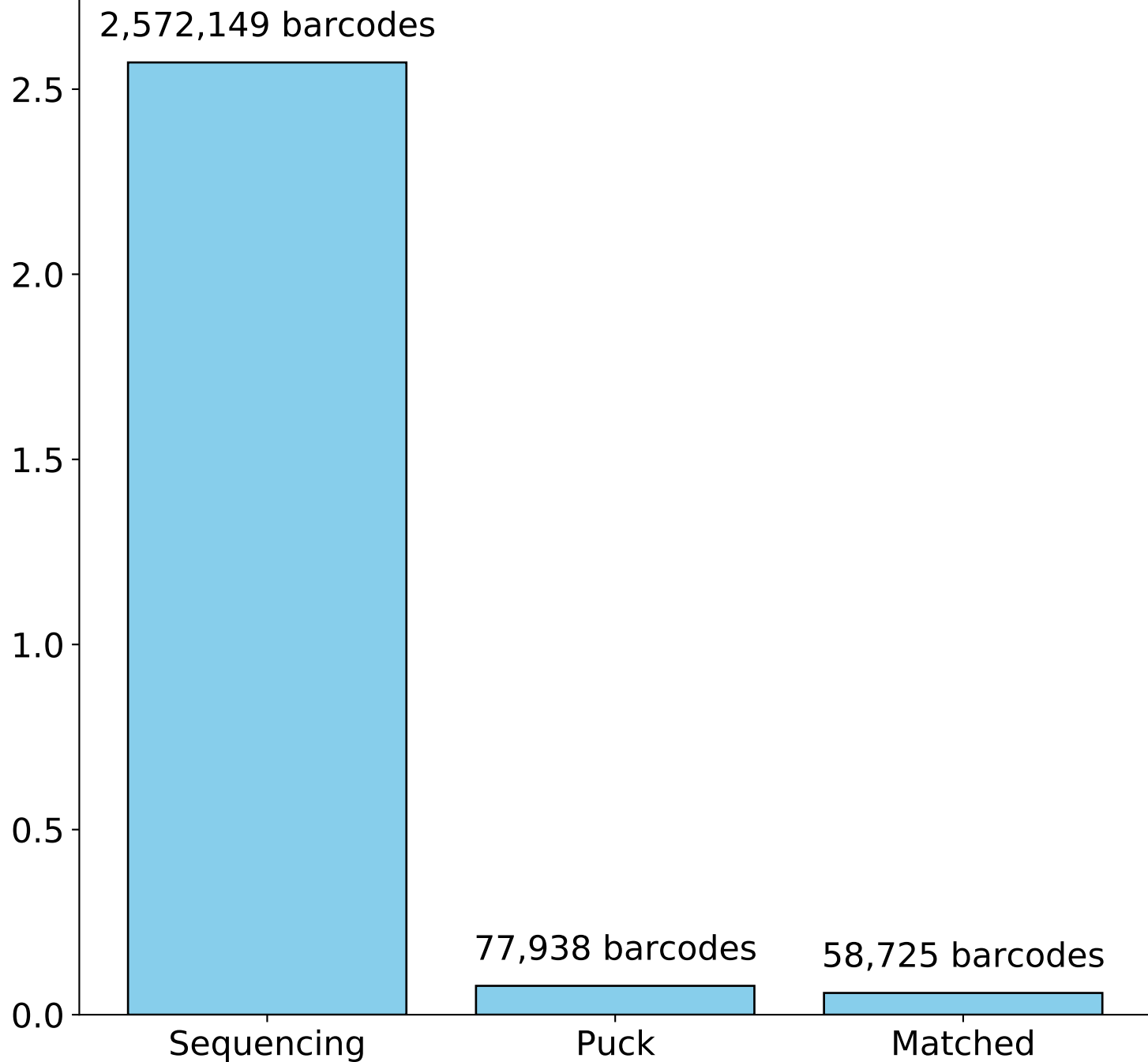


Histogram of Genes per matched barcode

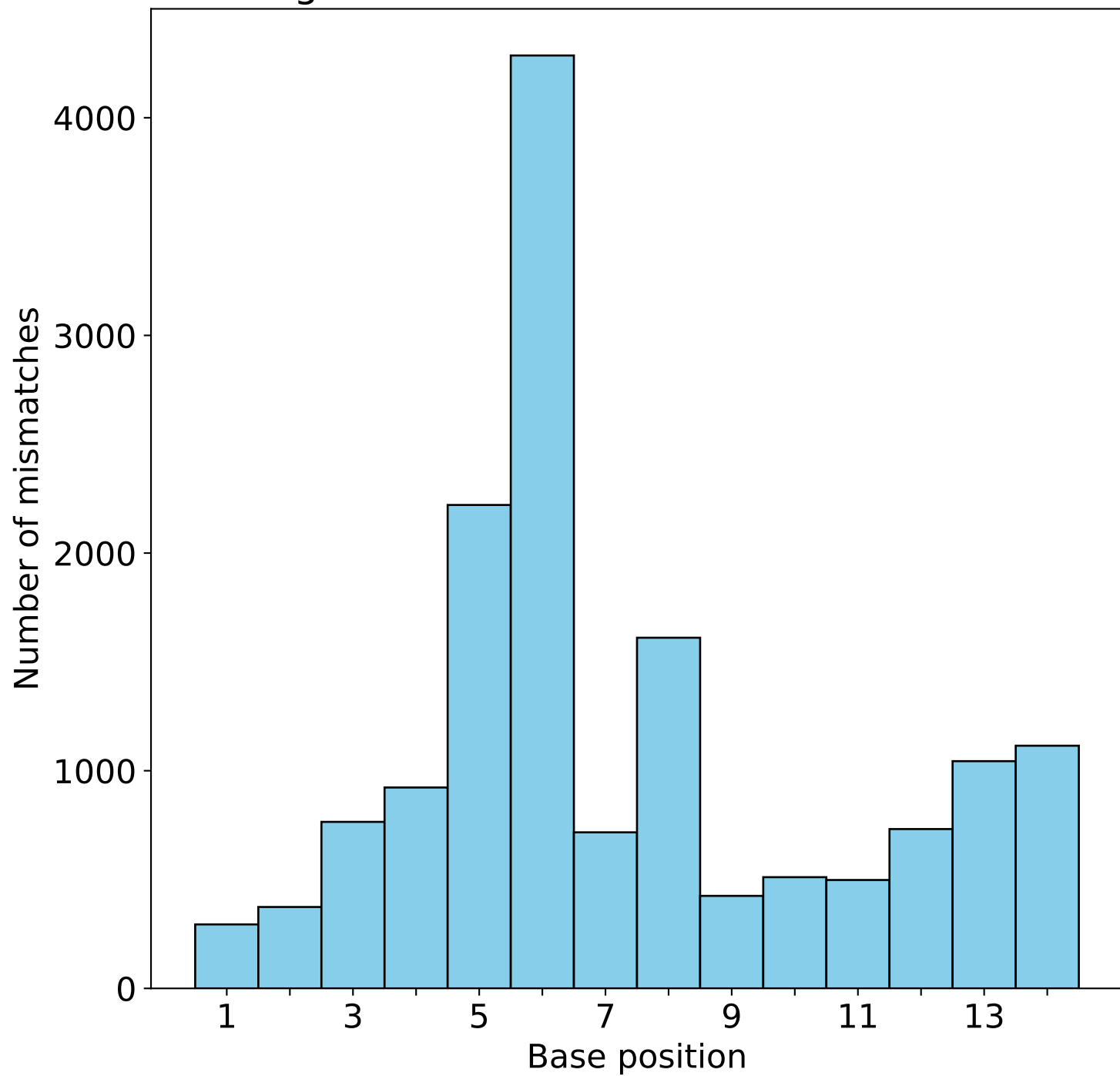


Barcode matching

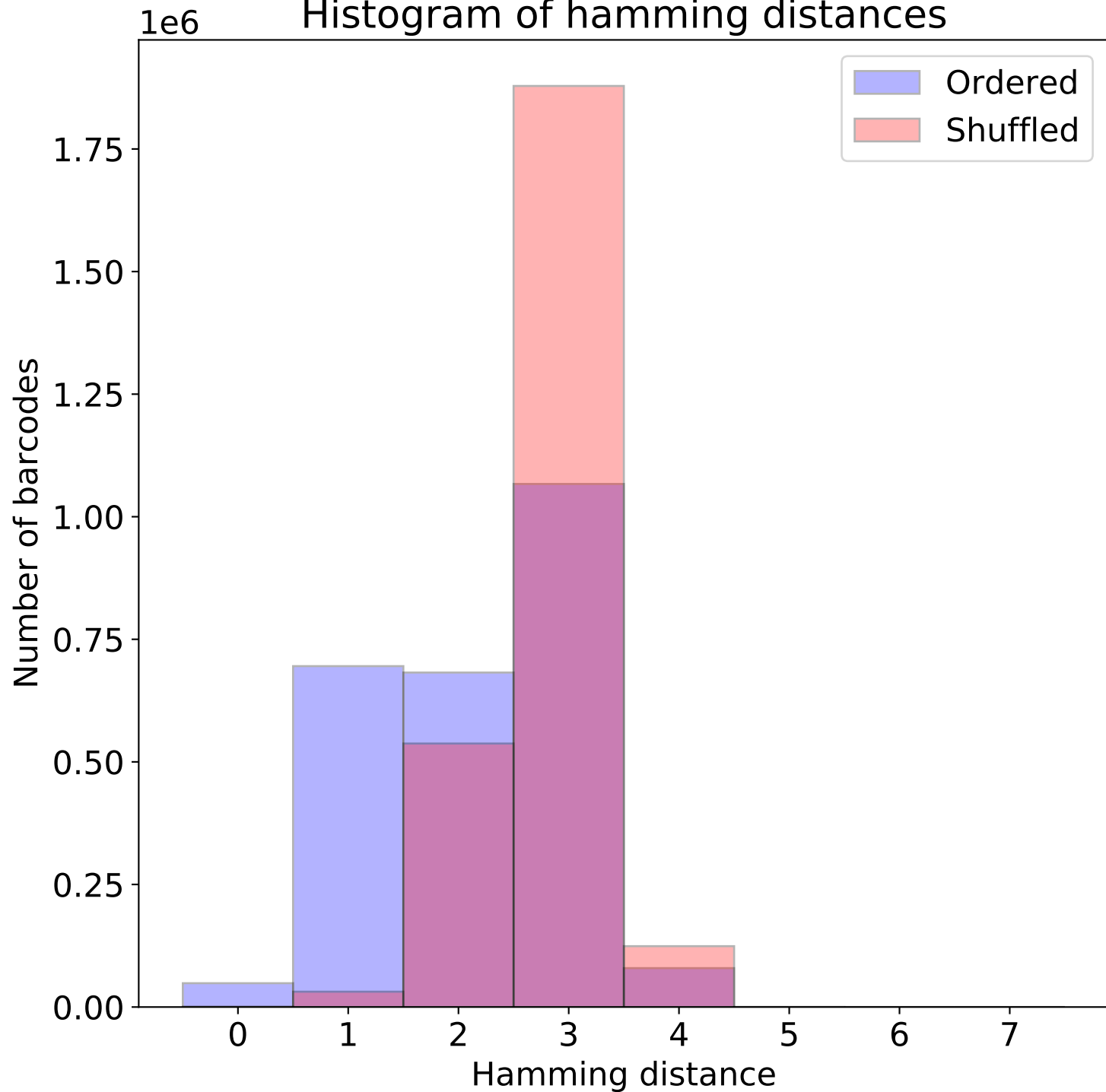
1e6



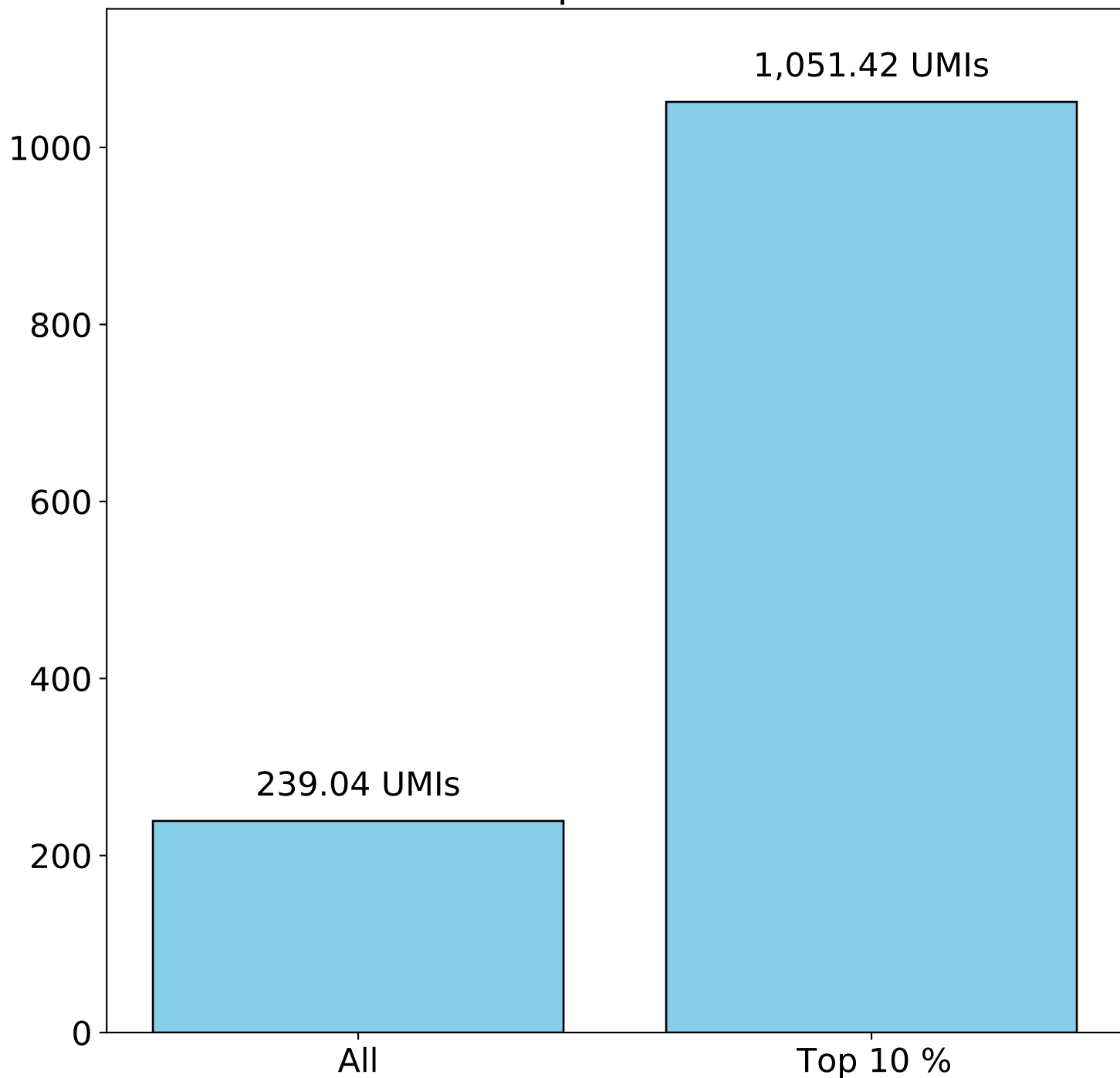
Histogram of the errors in matched barcodes



Histogram of hamming distances



Number of UMIs per matched barcodes



UMIs per bead

