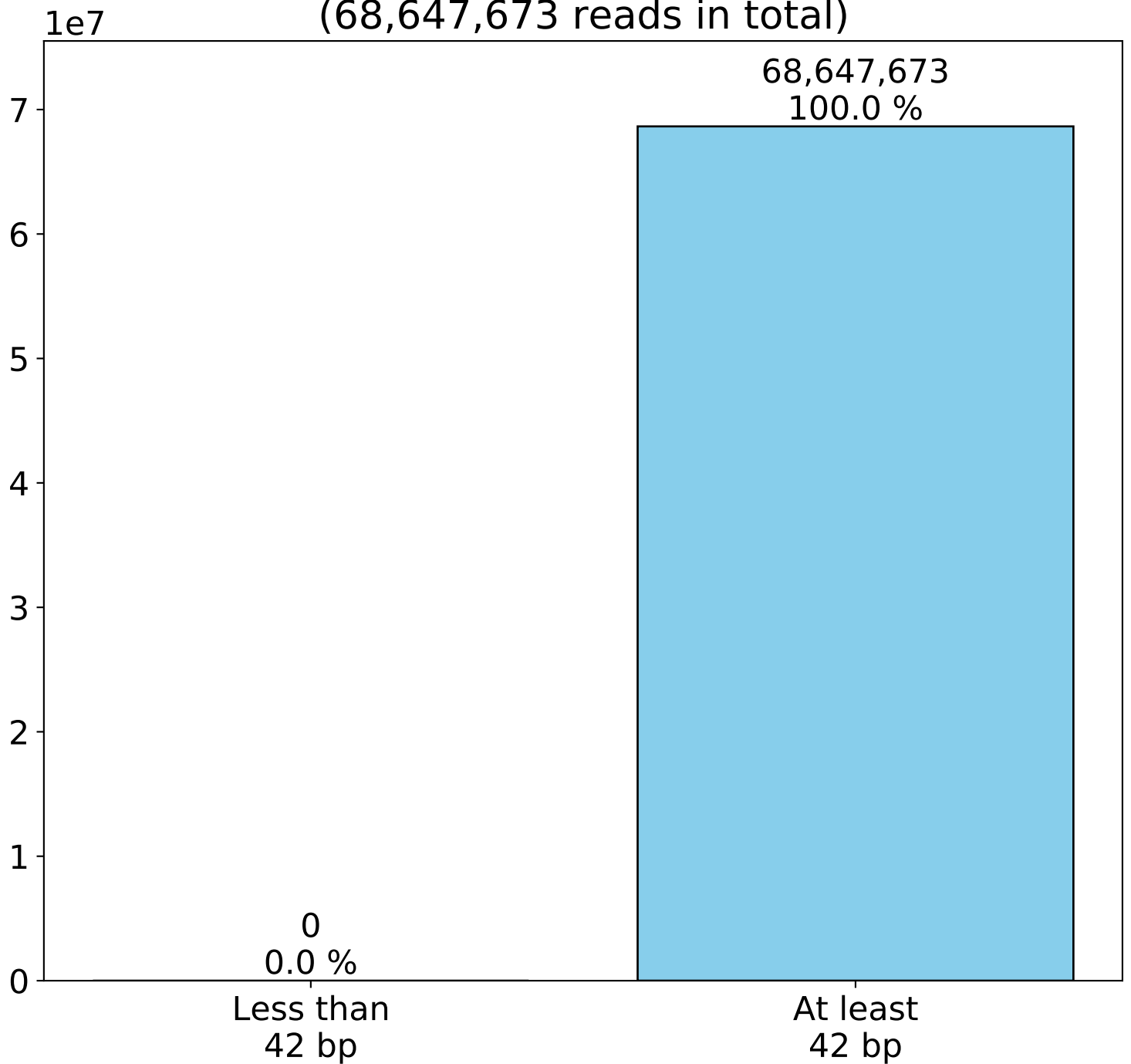
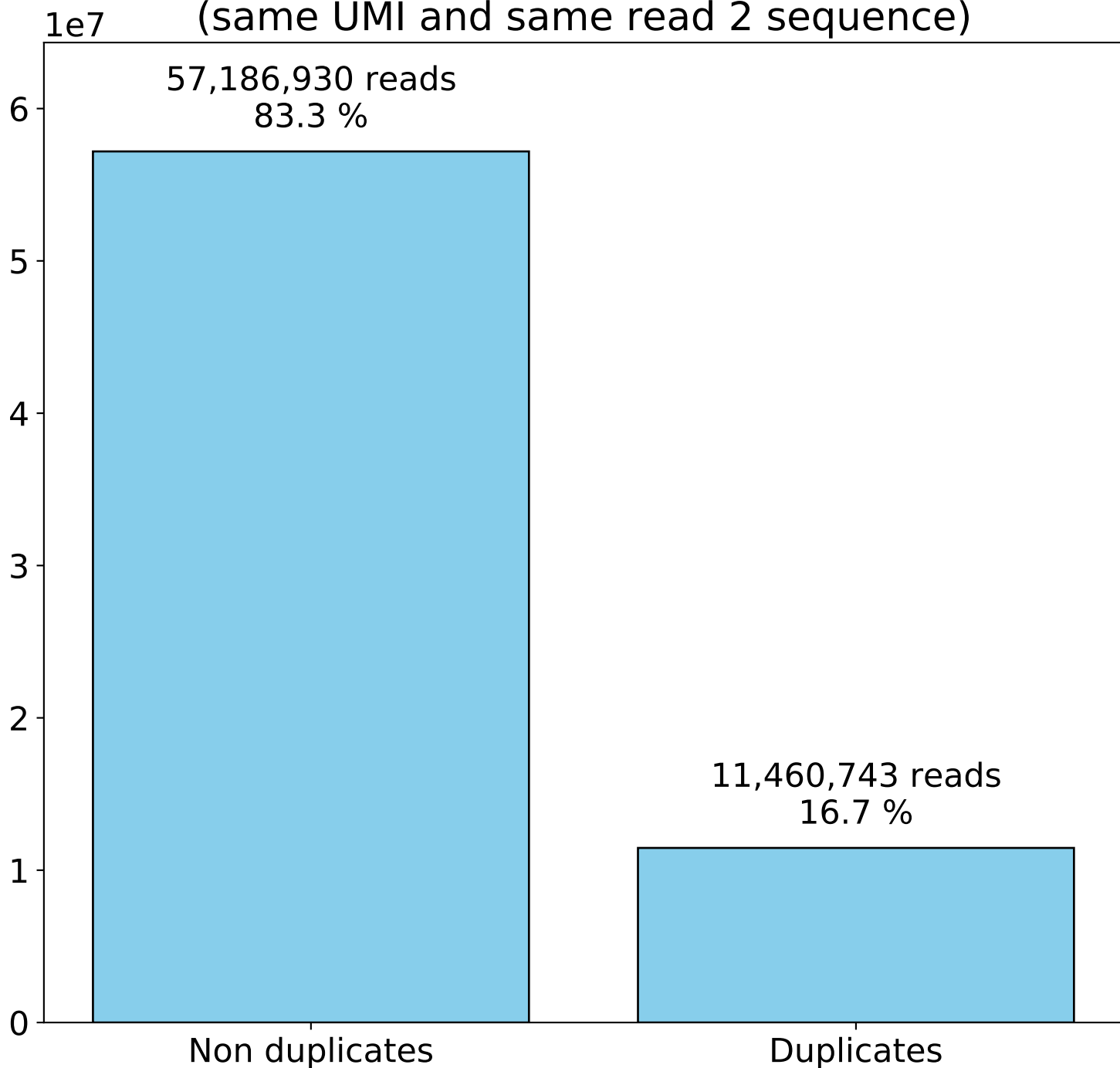


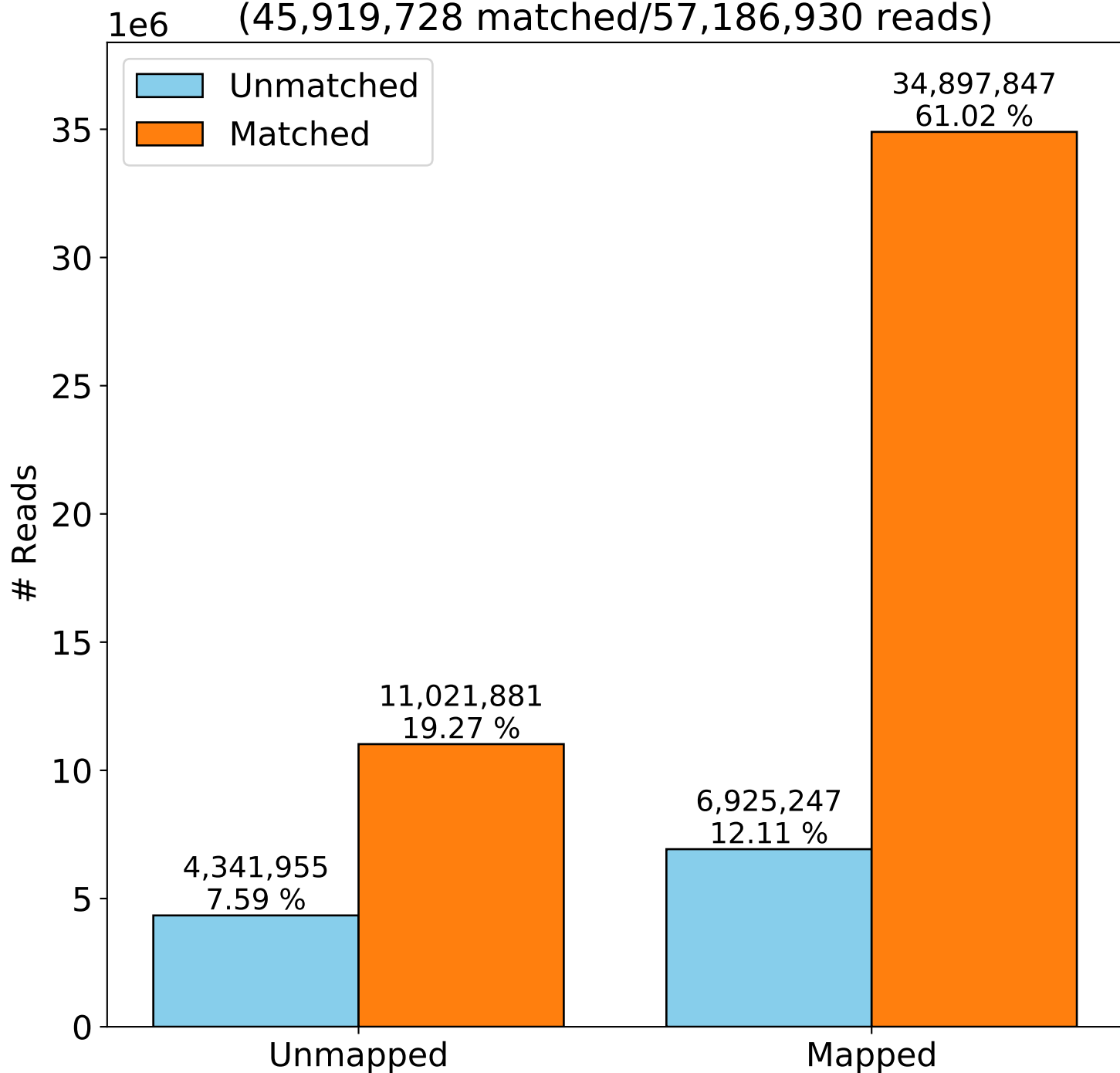
Barcode extraction (68,647,673 reads in total)



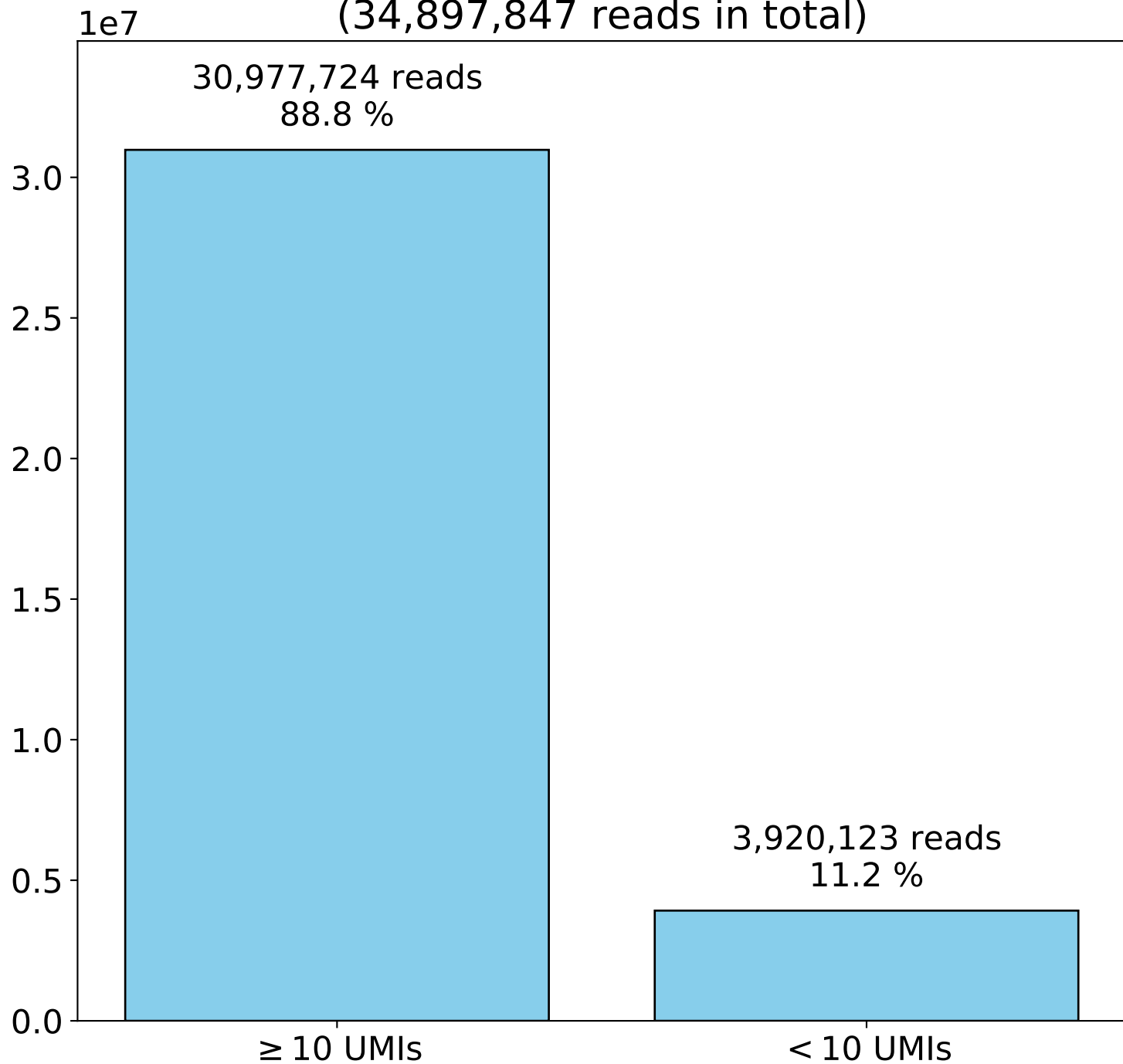
PCR duplicates (68,647,673 reads in total)
(same UMI and same read 2 sequence)



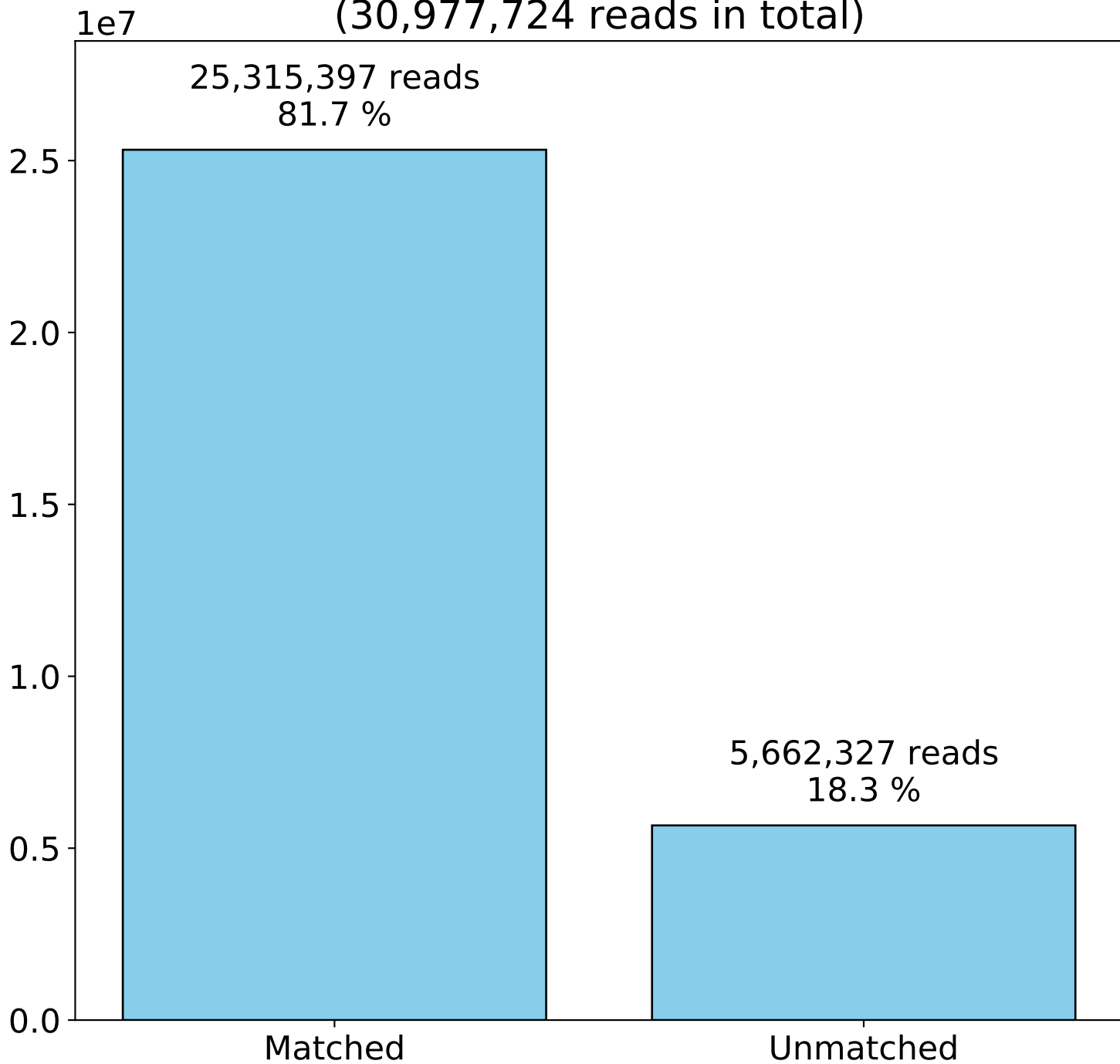
UP primer matching
(45,919,728 matched/57,186,930 reads)



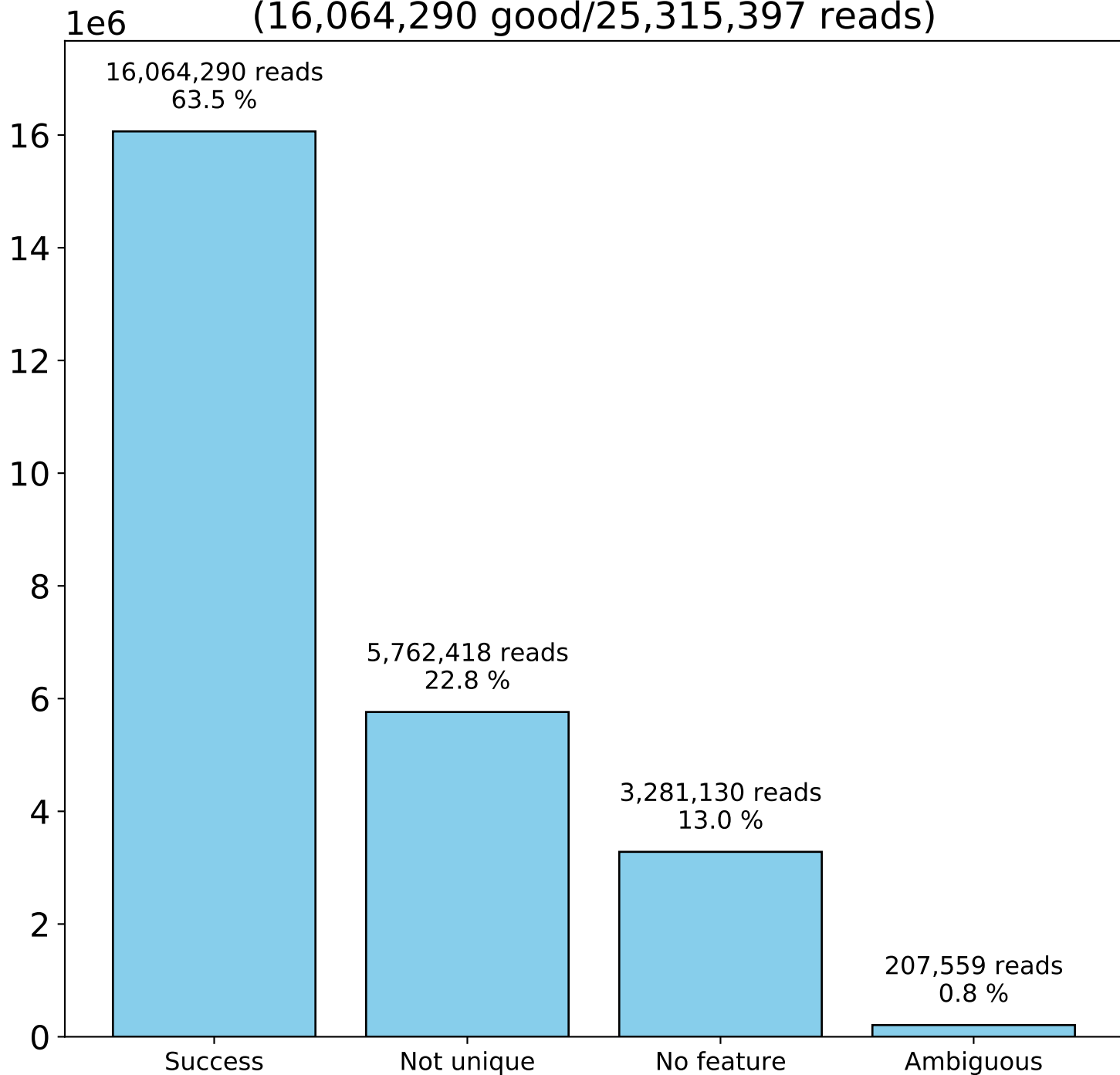
Reads with barcode that pass the UMIs threshold
(34,897,847 reads in total)



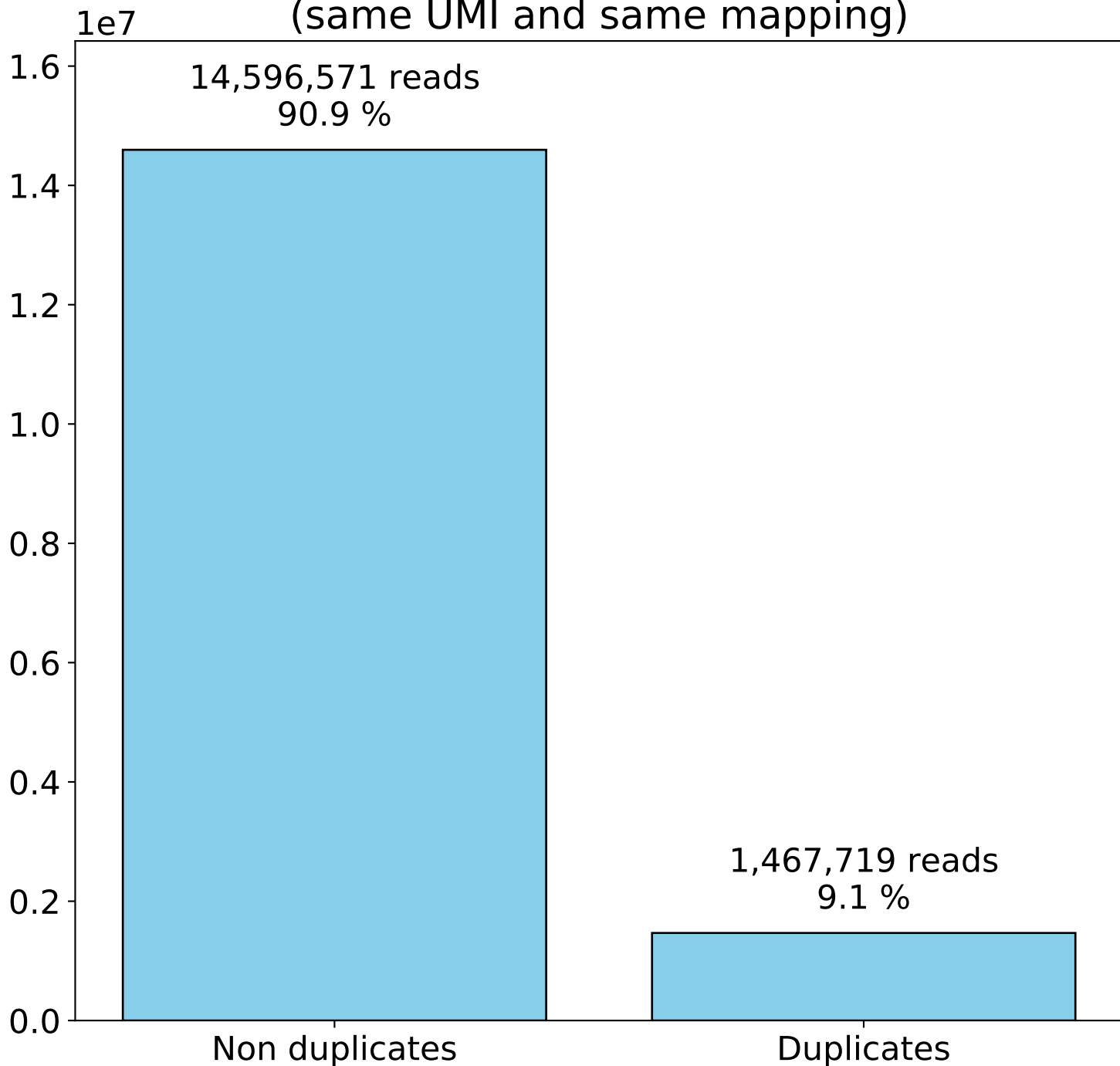
Barcode matching (30,977,724 reads in total)



Gene annotation of the reads (16,064,290 good/25,315,397 reads)

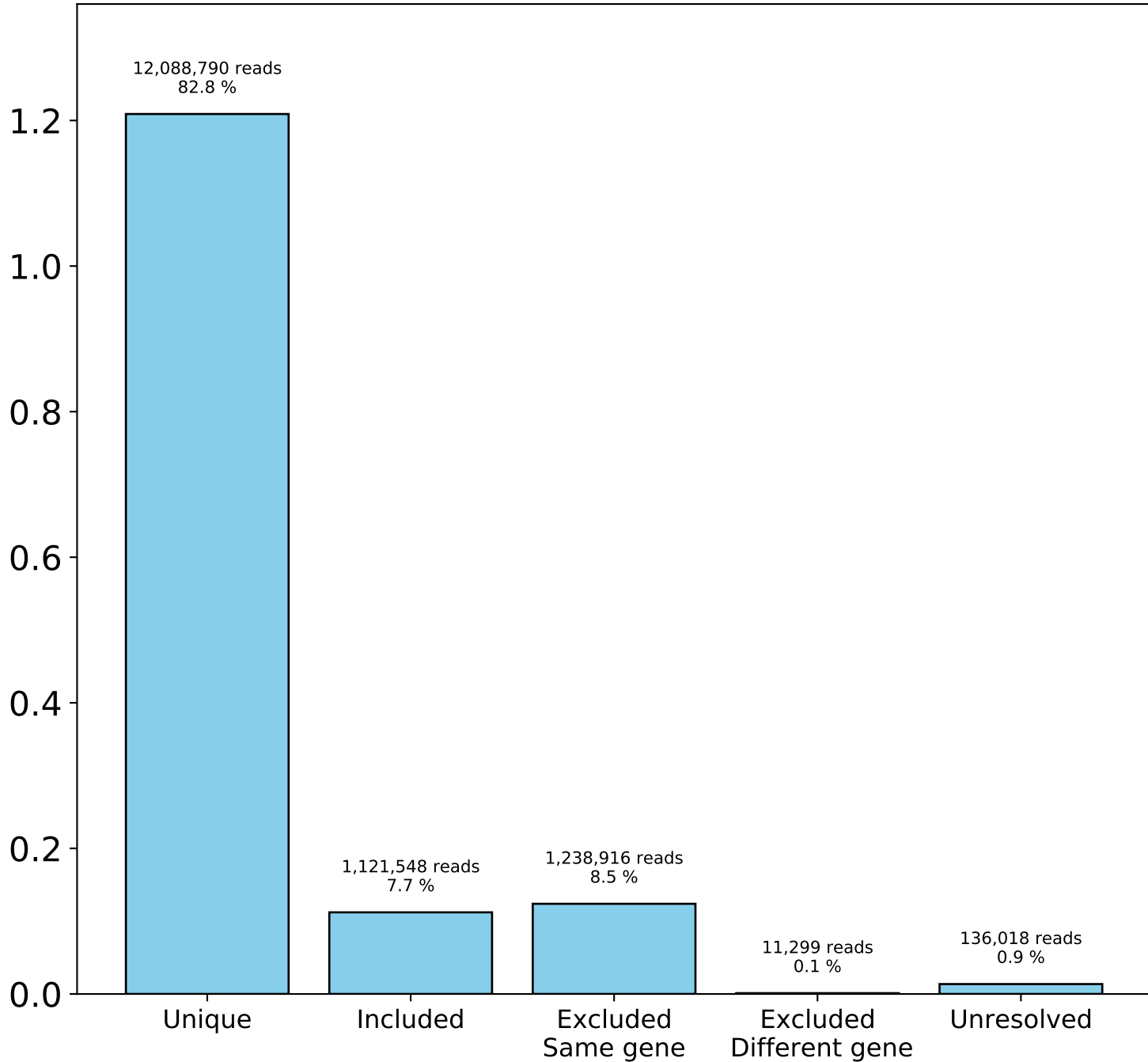


Position duplicates (16,064,290 reads in total)
(same UMI and same mapping)

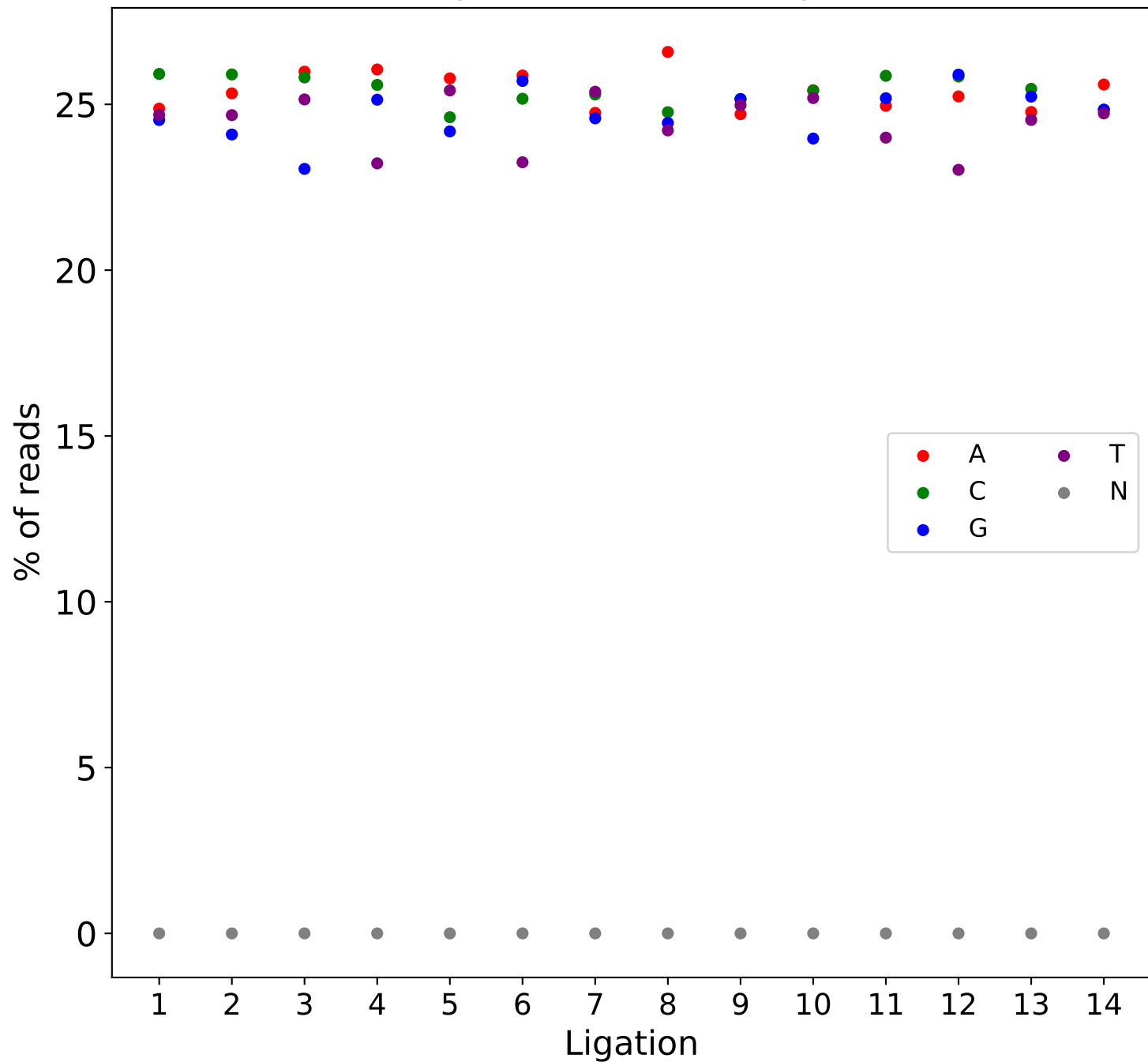


Selecting multi-mapped UMIs (majority vote)

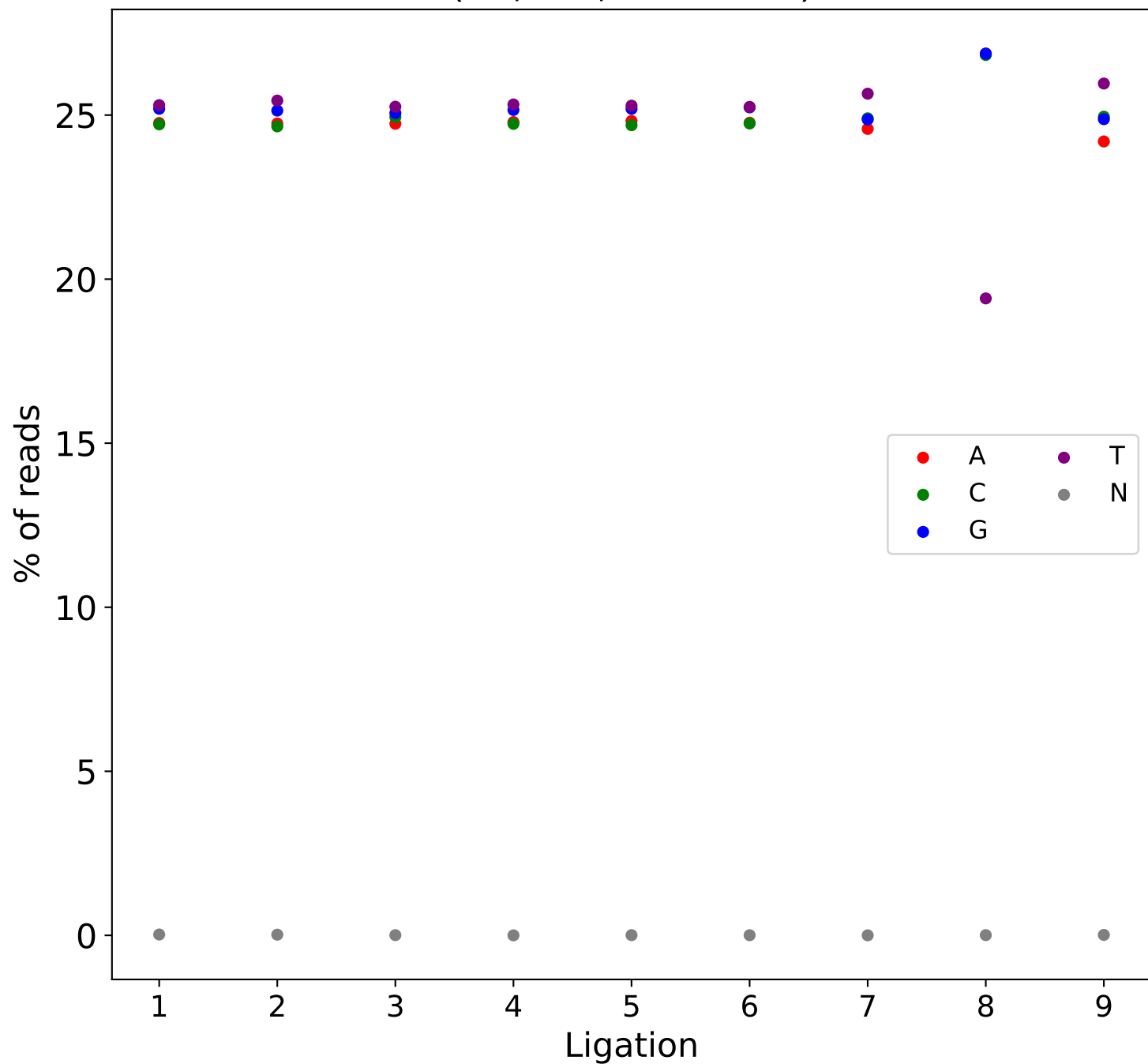
1e7 (13,210,338 unambiguous/14,596,571 reads)



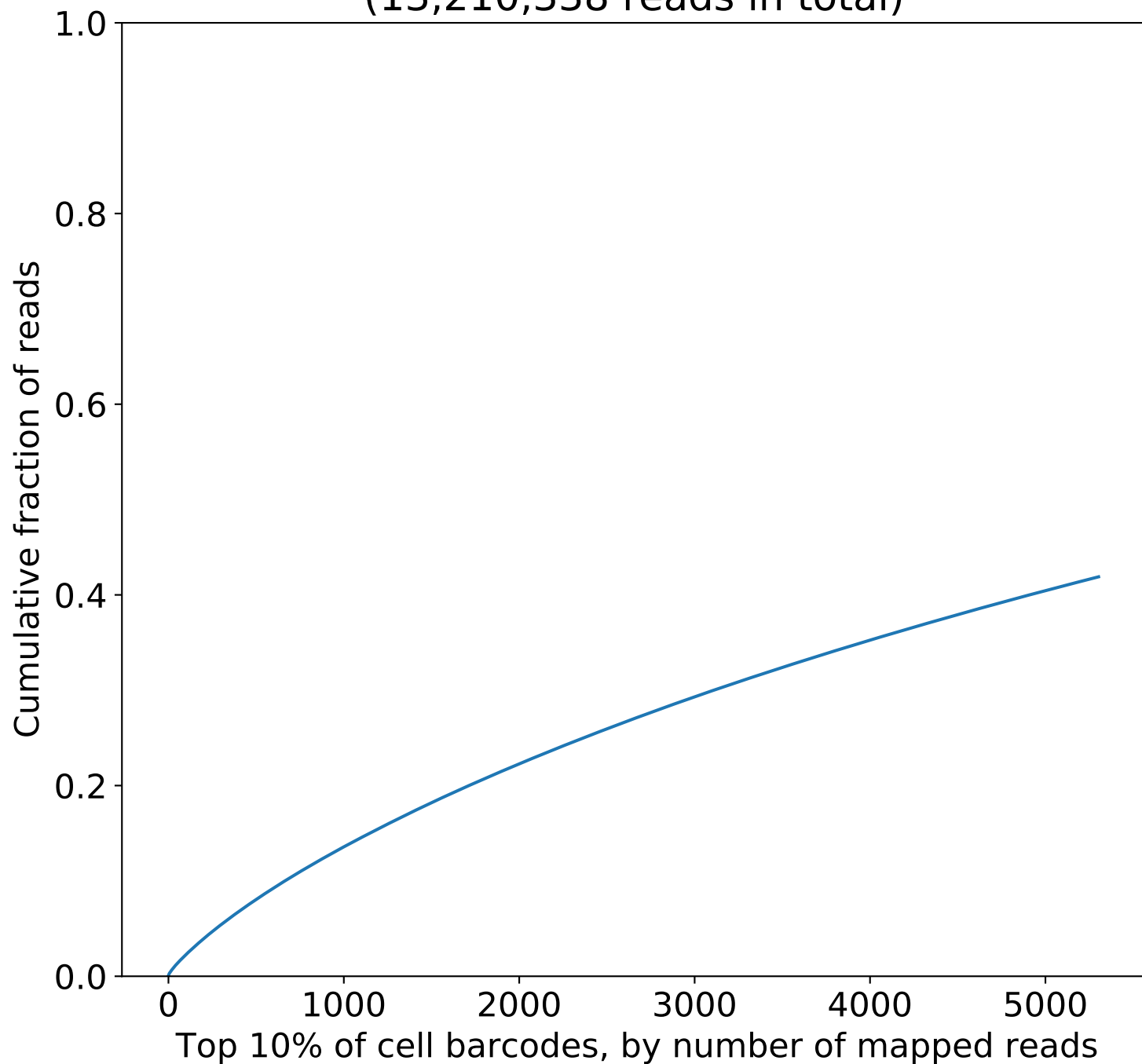
Barcode for bead-matched reads (13,210,338 reads)



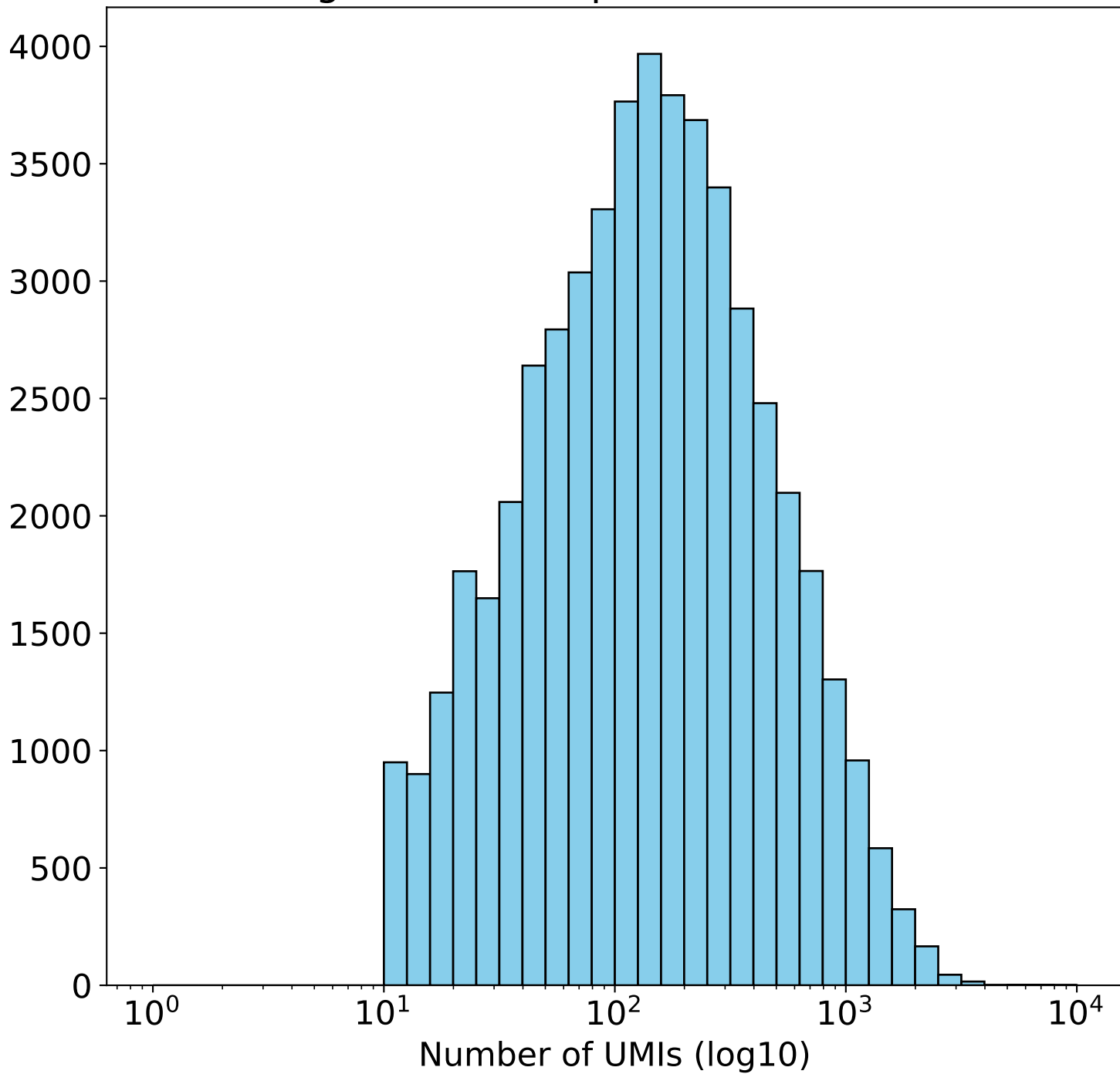
UMI for bead-matched reads (13,210,338 reads)



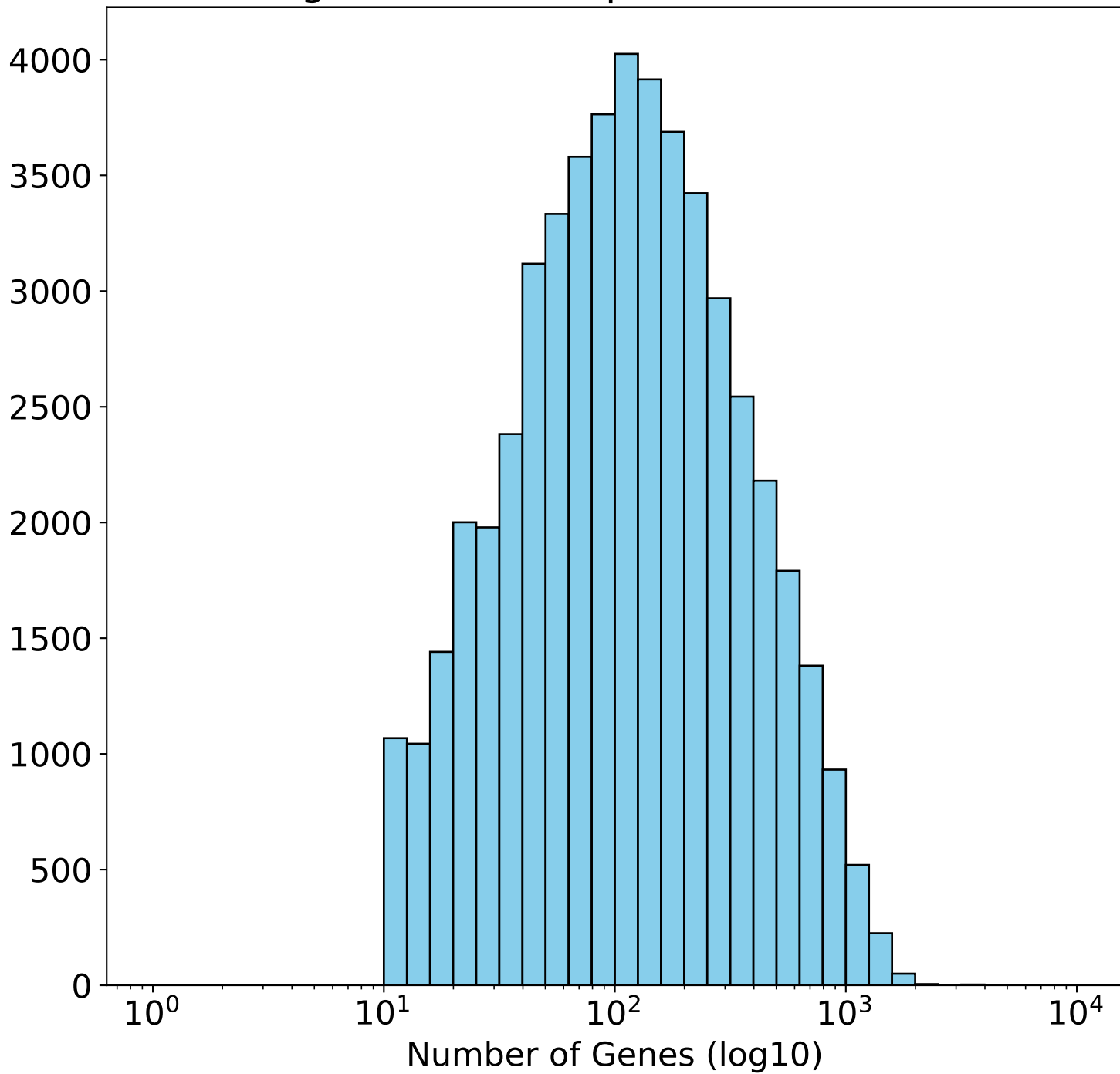
Cumulative fraction of reads per cell barcode (13,210,338 reads in total)



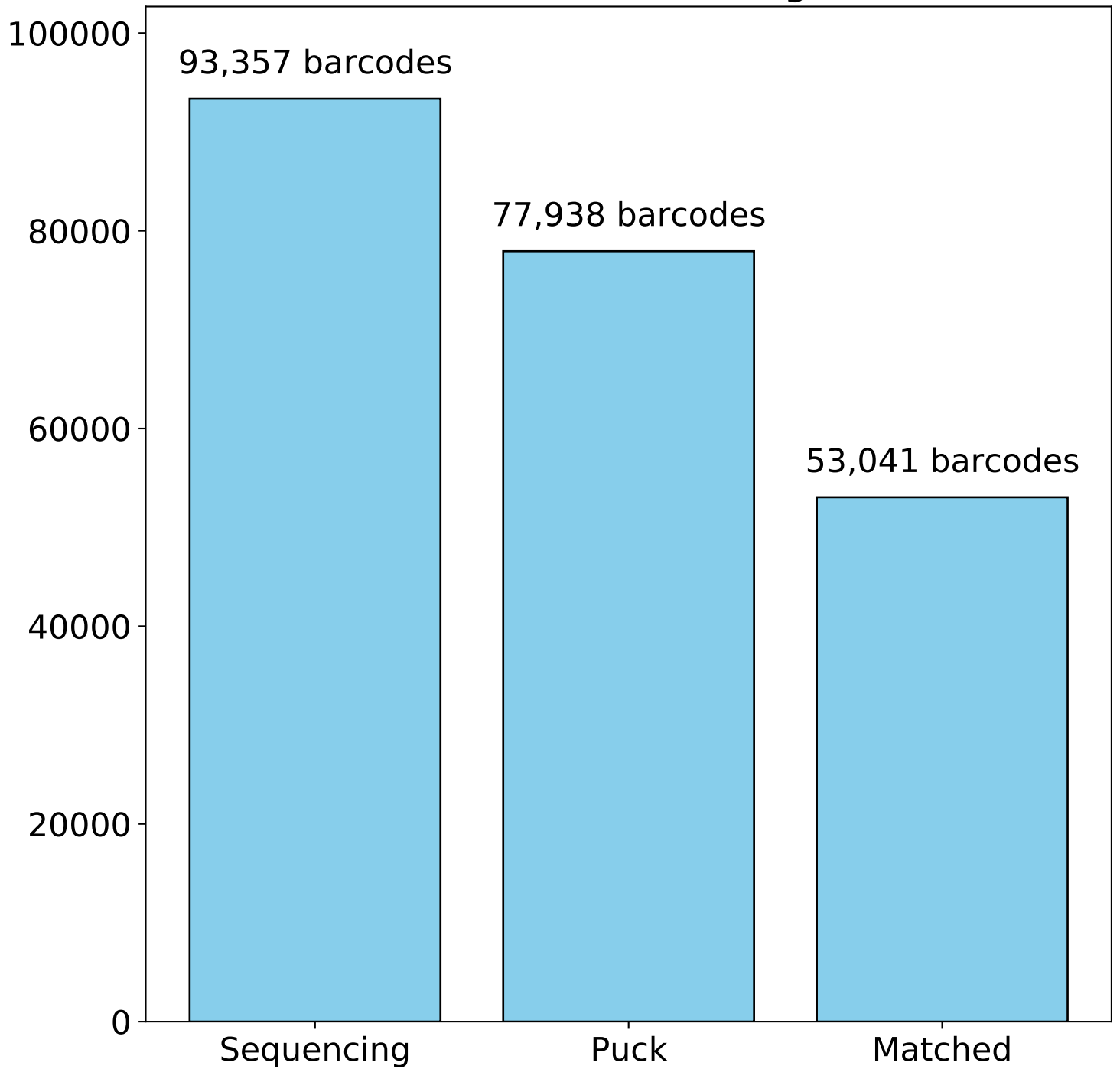
Histogram of UMIs per matched barcode



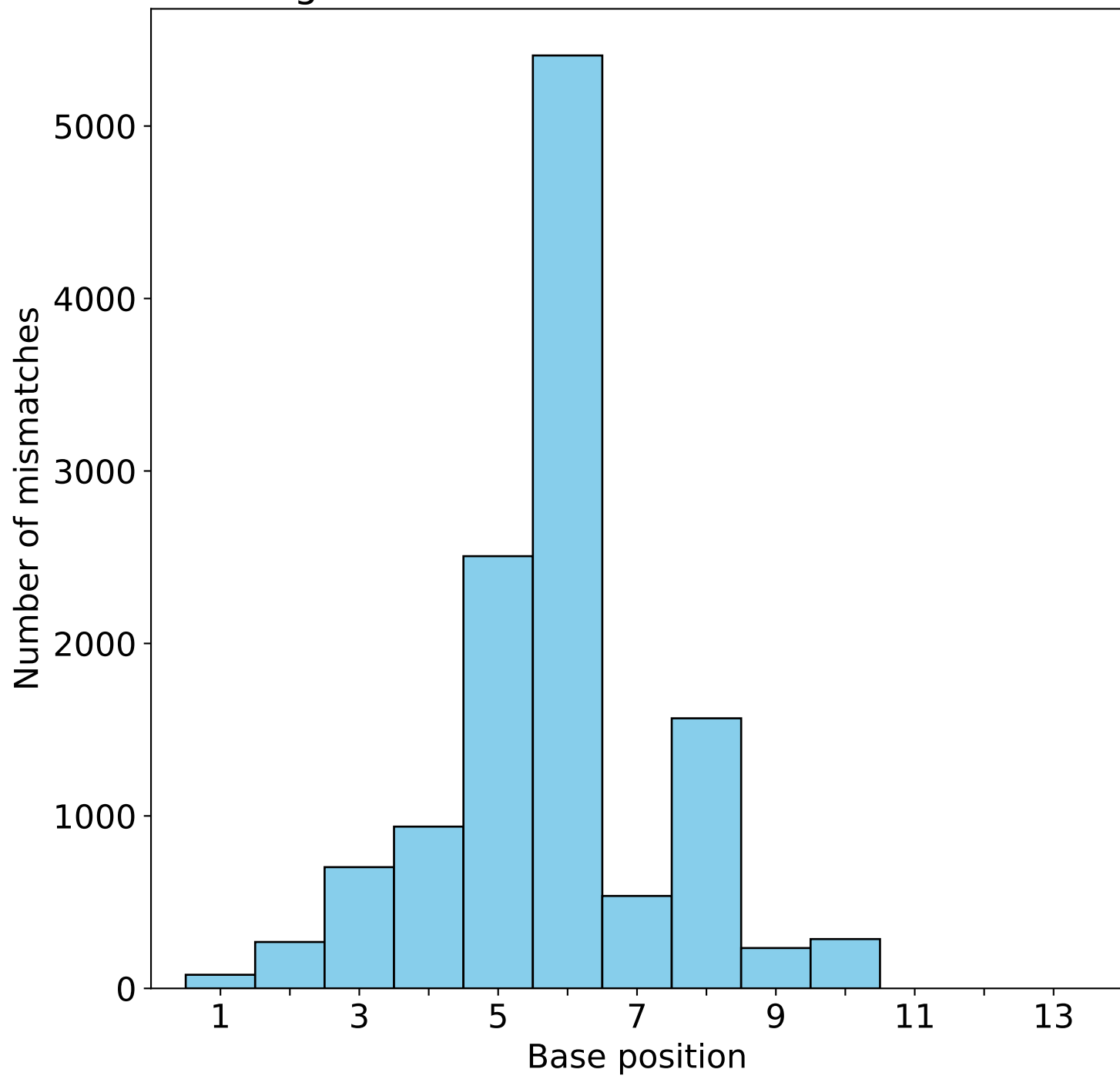
Histogram of Genes per matched barcode



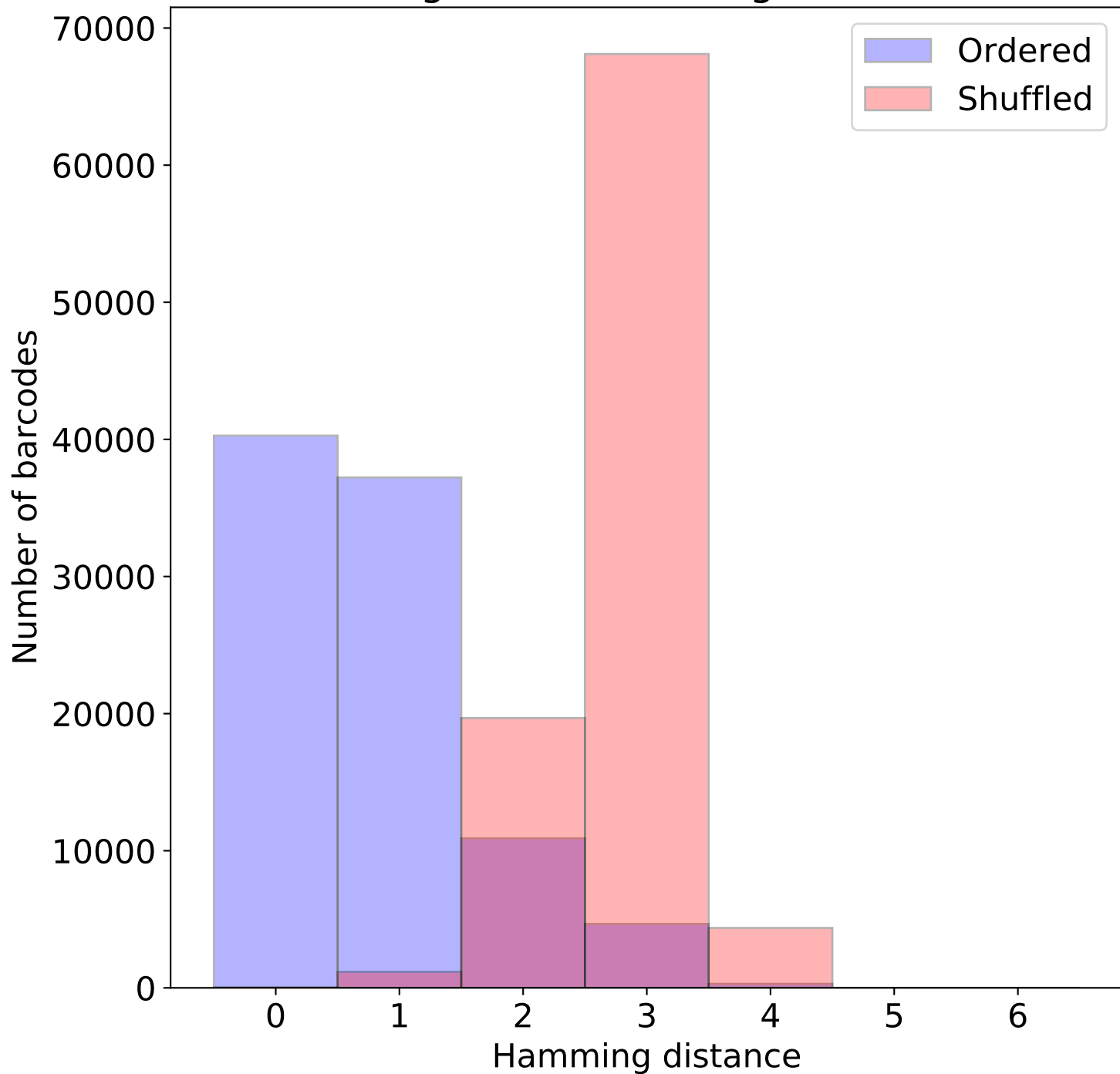
Barcode matching



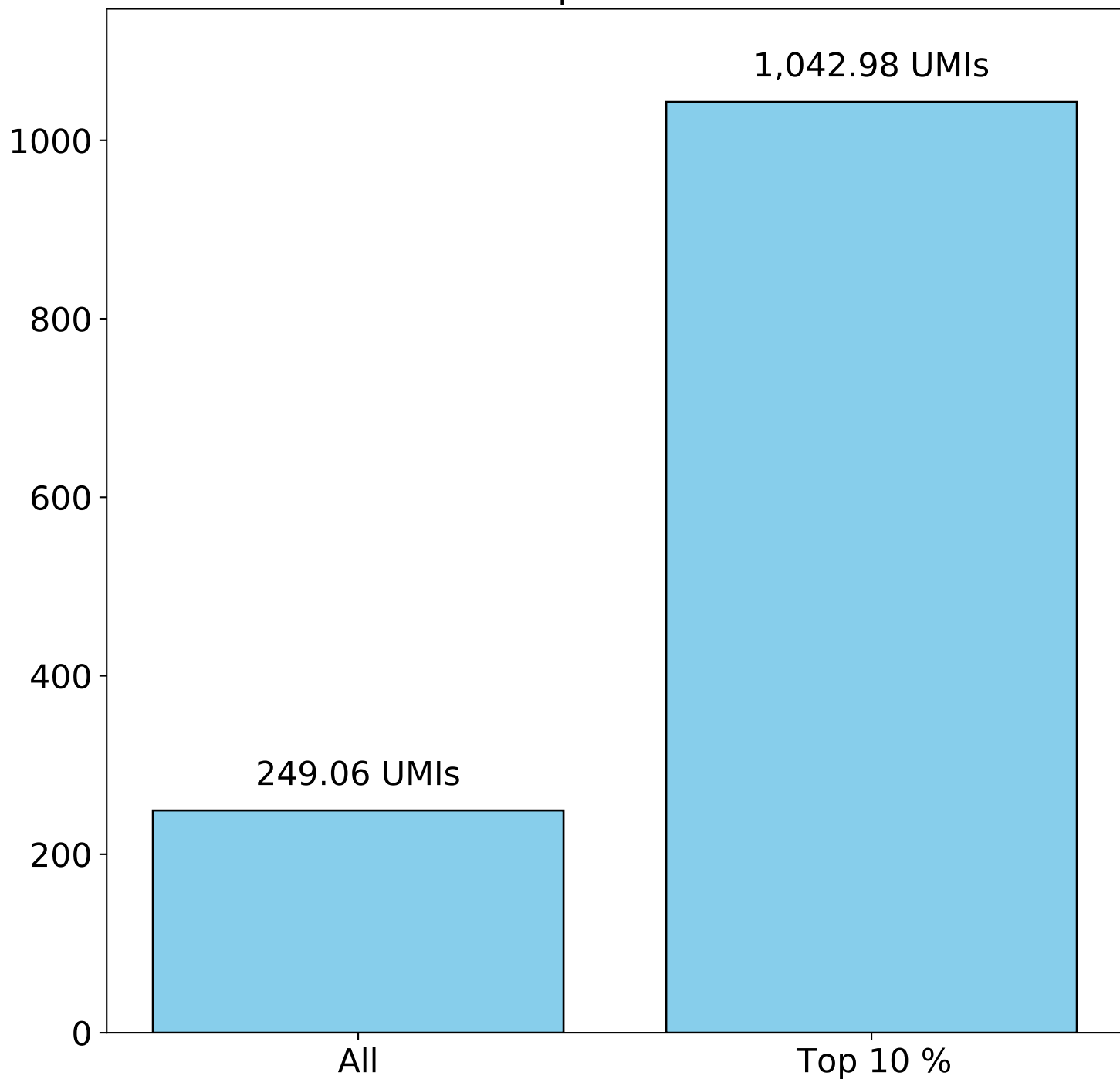
Histogram of the errors in matched barcodes



Histogram of hamming distances



Number of UMIs per matched barcodes



UMIs per bead

