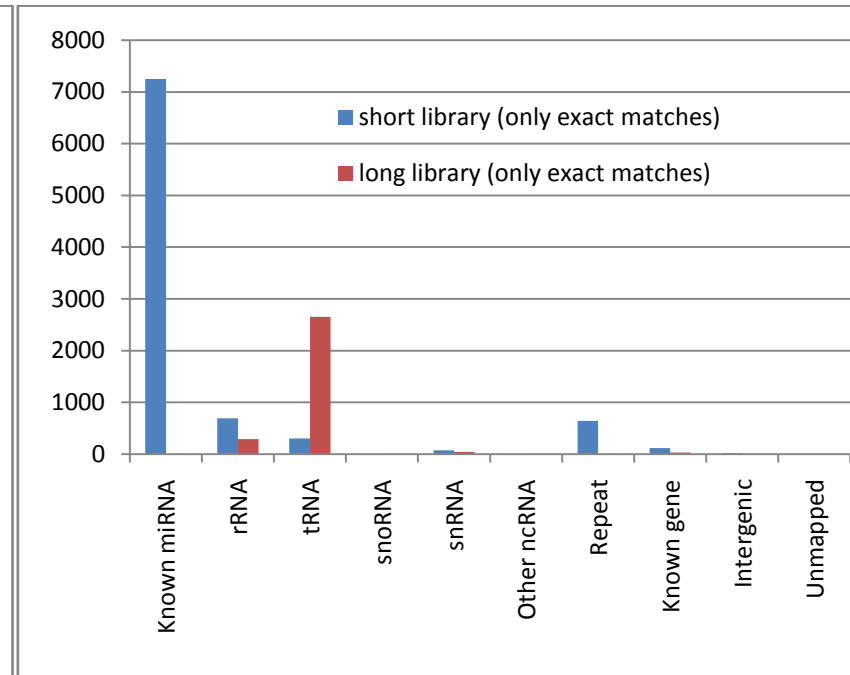


(A) Counts of the all reads



(B) counts of the reads which are perfectly aligned with the genome