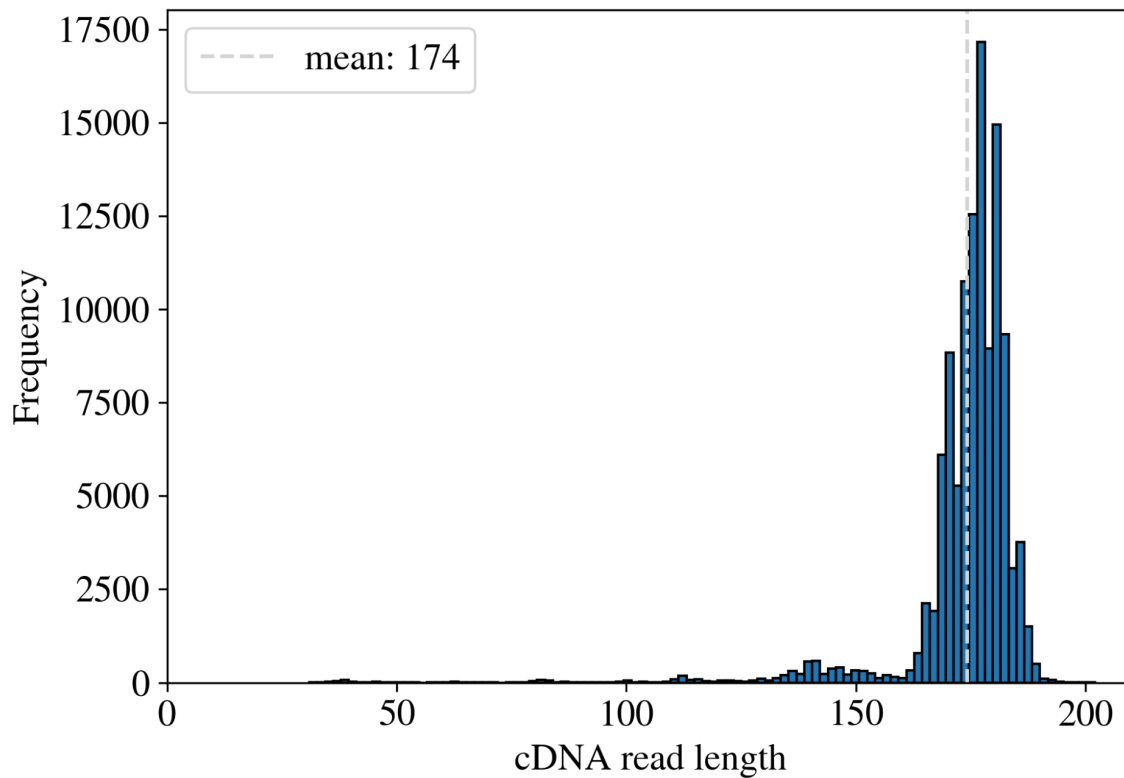


# Supplementary Material: Pseudoalignment facilitates assignment of error-prone Ultima Genomics reads

A. Sina Boeshaghi<sup>1</sup> and Lior Pachter<sup>2,3,\*</sup>

<sup>1</sup>Department of Mechanical Engineering, California Institute of Technology, Pasadena, CA  
<sup>2</sup>Division of Biology and Biological Engineering, California Institute of Technology, Pasadena, CA  
<sup>3</sup>Department of Computing and Mathematical Sciences, Pasadena, CA  
\*Address correspondence to: lpachter@caltech.edu

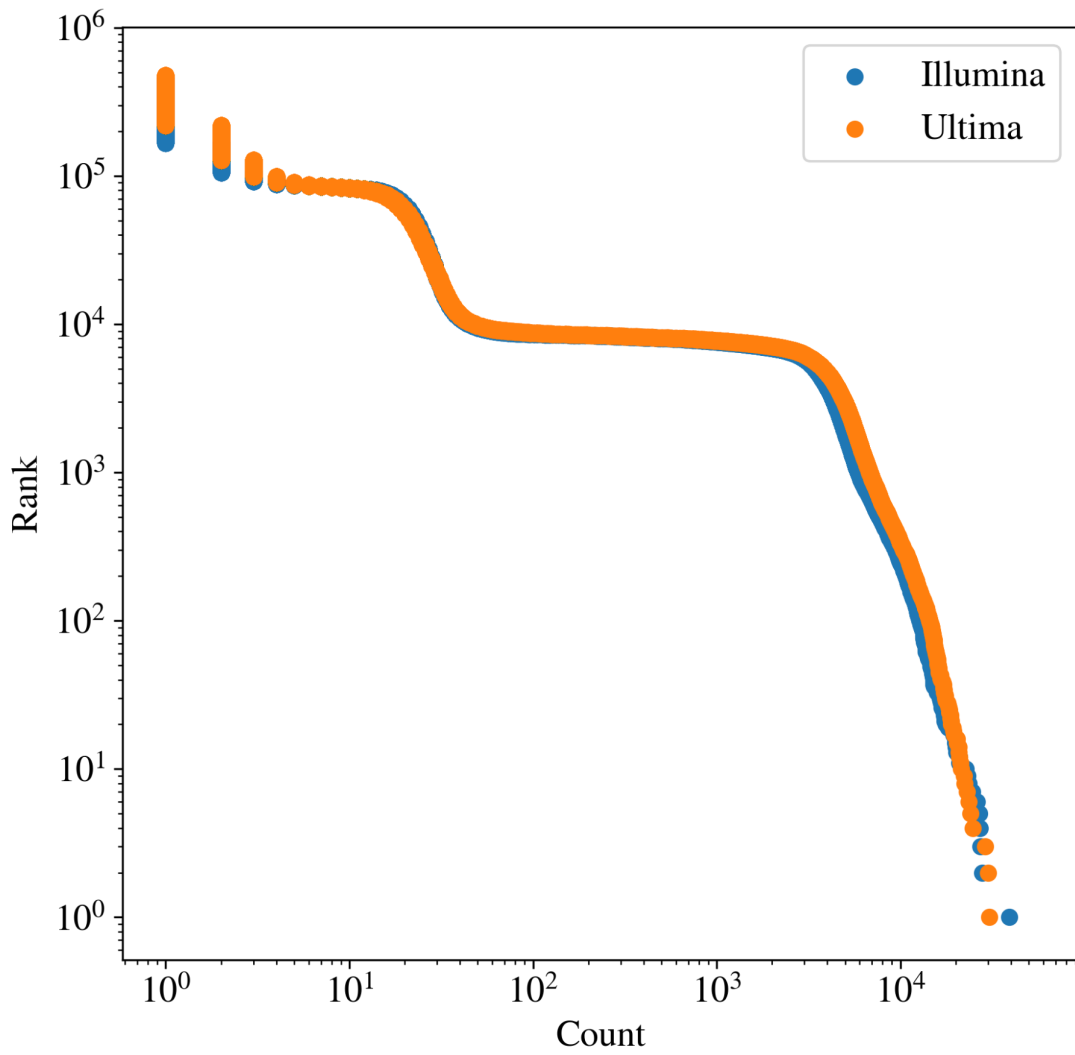


**Supplementary Figure 1:** Distribution of Ultima Genomics cDNA read lengths.

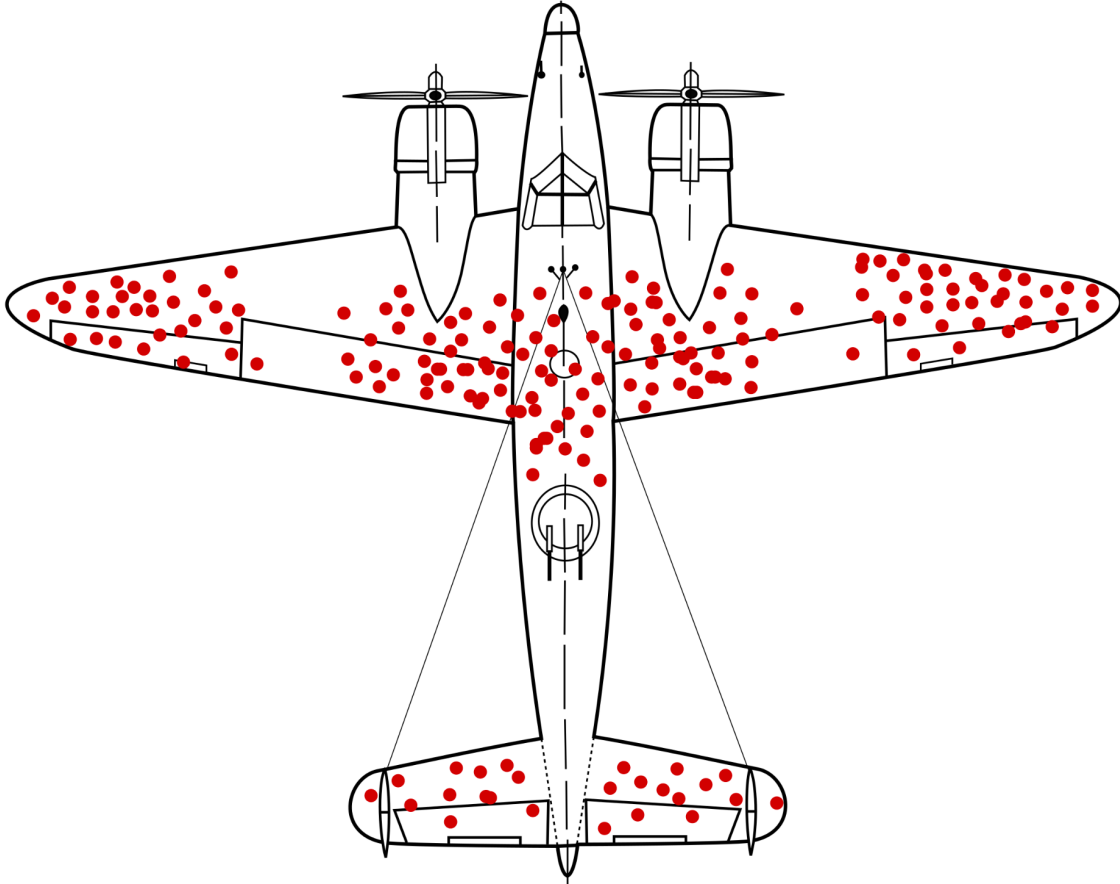


```
$ kb count -x 10xv3_Ultima -o out -i index.idx -g t2g.txt read1.fastq.gz
```

**Supplementary Figure 2:** Pre-processing Ultima Genomics single-cell RNA-seq with kallisto-bustools.



**Supplementary Figure 3:** Knee plots for the Ultima Genomics (55bp CDNA reads) - Illumina (55bp cDNA reads) comparison.



**Supplementary Figure 4:** An illustration of survivorship bias in the work of Abraham Wald on “A Method of Estimating Plane Vulnerability Based on Damage of Survivors” during WWII (1940). Source of image: [Wikipedia](#) (license [CC BY-SA 4.0](#)).