Fragment length distribution using DNAfrags

BAM file

samtools
Extracts fragment length
from a BAM file
DNAfrags::get_fragments_length()

Output:
- ***_fragment_length.txt** file

ggplot2
Plot fragment length
distribution
DNAfrags::plot_fragments_length()

Output:
- ***_distribution.txt** file
- ***_distribution.pdf** file

Fragment length distribution for sample SRR11742859

Fragment length distribution for sample SRR11742864