SUPPLEMENTARY INFORMATION

A ChIP-Seq Data Analysis Pipeline Based on Bioconductor Packages

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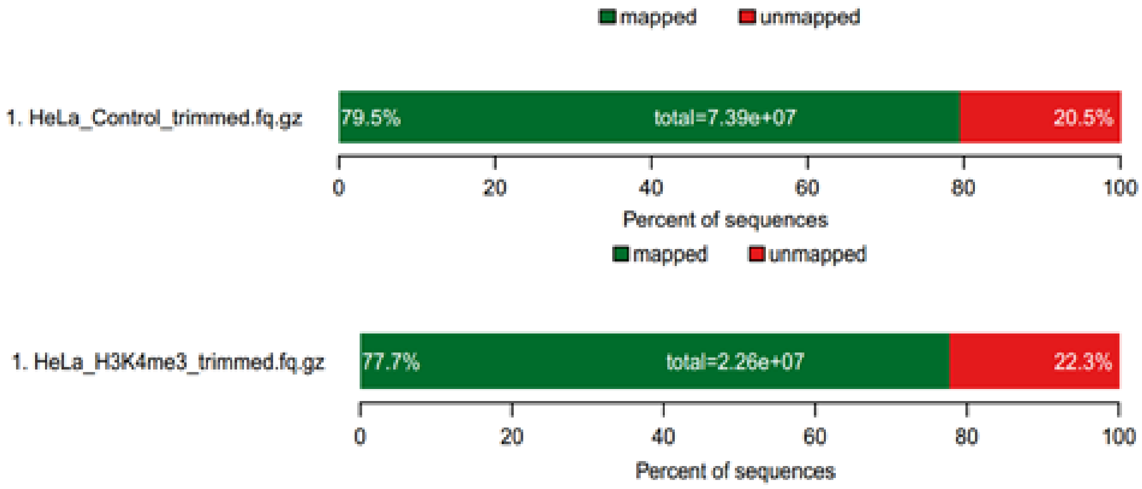
http://www.genominfo.org/src/sm/gni-15-11-s001.pdf



Supplementary Fig. 3. Mapping statistics. It shows the fraction of reads that were the portion of mappable and unmappable to the reference genome. The percentages of mapped reads were 79.5% and 77.7%, respectively.