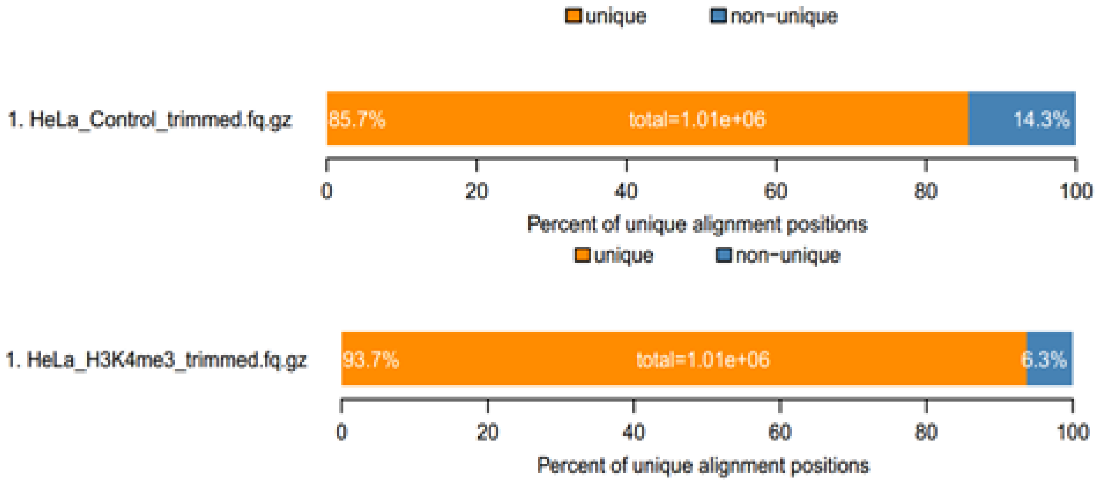
SUPPLEMENTARY INFORMATION

A ChIP-Seq Data Analysis Pipeline Based on Bioconductor Packages

Seung-Jin Park[1,2], Jong-Hwan Kim[1,2], Byung-Ha Yoon[1,2], Seon-Young Kim[1,2]*

[1]Personalized Genomic Medicine Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon 34141, Korea,
[2]Department of Functional Genomics, University of Science and Technology (UST), Daejeon 34113, Korea

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



Supplementary Fig. 4. Library complexity. It shows the fractions of unique and non-unique read alignment positions. This measure is not independent of the total number of reads in a library. The percentages of unique mapped reads are 85.7% and 93.7%, respectively.