SUPPLEMENTARY INFORMATION

A ChIP-Seq Data Analysis Pipeline Based on Bioconductor Packages

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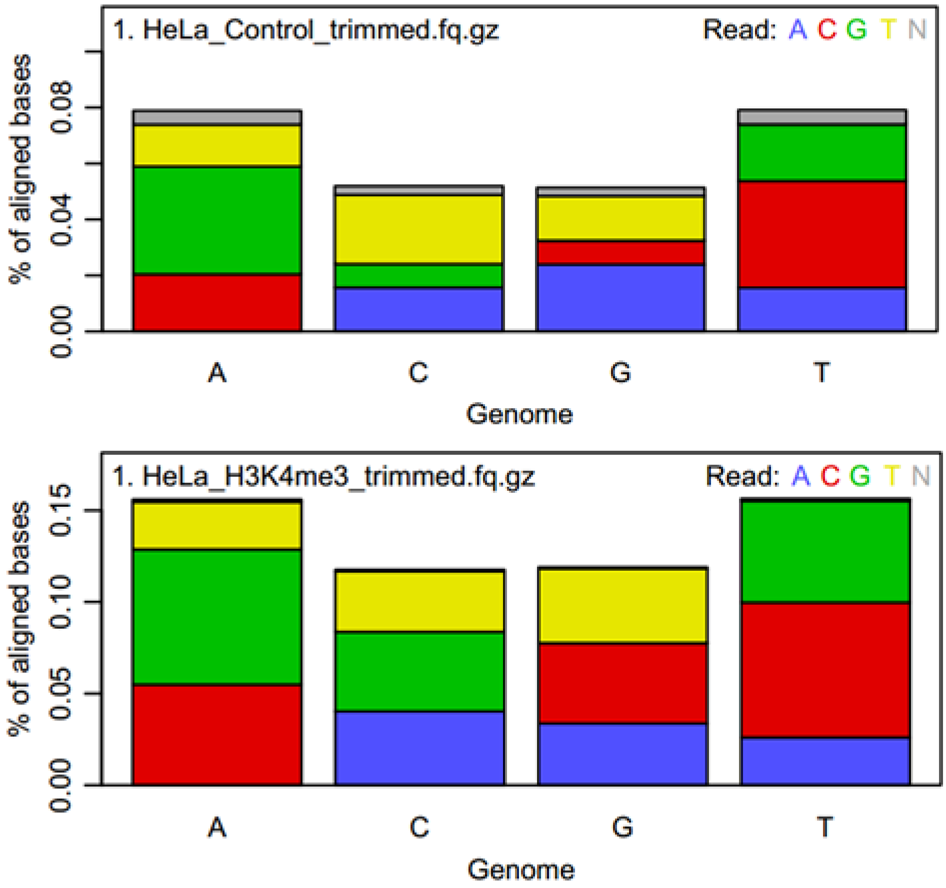
http://www.genominfo.org/src/sm/gni-15-11-s001.pdf



Supplementary Fig. 6. Mismatch type. It shows the frequency of read bases that caused mismatches in the alignments to the reference genome, separately for each genome base.