Document for calc_RPKM

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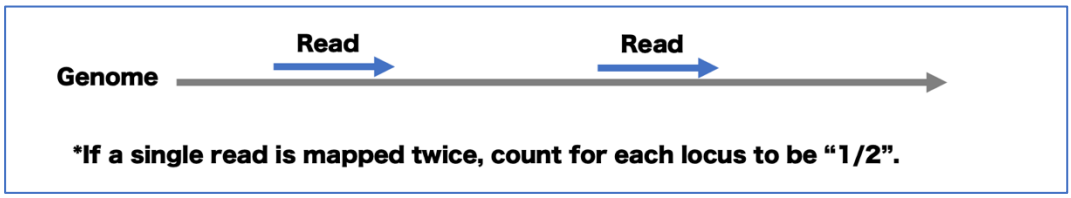
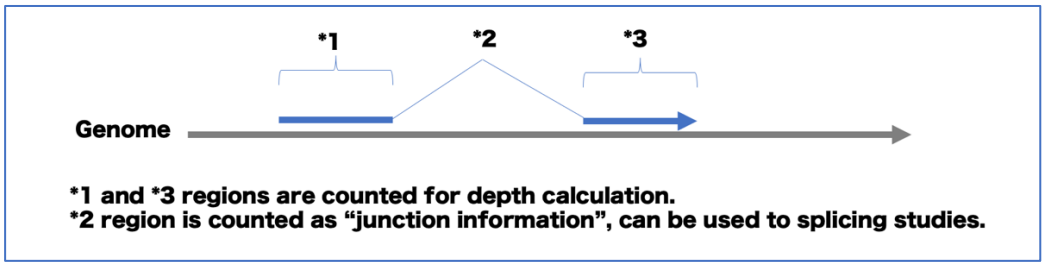
This document is under preparation.
I describe some things about how the depth of RNA-seq and RPKM is calculated.

1. Multiple mapped reads are capable. Depth for each locus is treated as 1/n when the read mapped into n loci.



2. For an RNA-seq reads mapped over Exon-Exon Junctions, only exonic regions provide depth.



3. For Single-End (SE) Reads, "strand" option is for treating the directions as is in the bam files. For Paired-End (PE) Reads, "stranded" option is for treating the RNA-seq reads as FR-firstsrtrand.