

End positions from single end sequencing of sonicated input chromatin

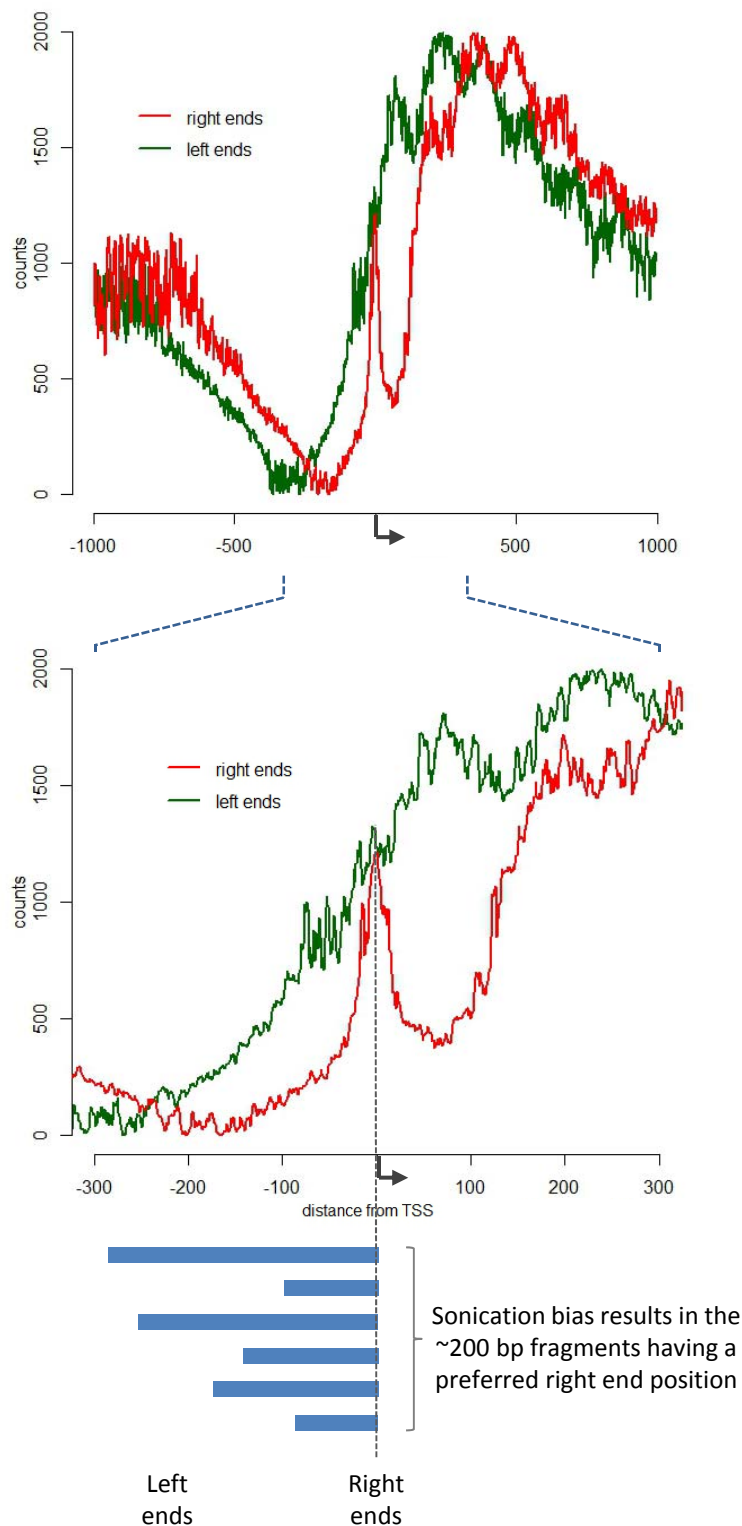


Figure 1 – figure supplement 1 – Sonication bias at promoter regions. The left ends (5' position on forward strand reads) and right ends (3' position on reverse strand reads) of fragments from single-end sequencing data of sonicated input chromatin was aligned to the TSS (reads corresponding to genes on the reverse strand were flipped). The non-uniform distribution indicates a bias with the distinct peak at the TSS arising from non-random chromatin fragmentation, with a high probability of having a right end just downstream of the TSS. The input dataset from modENCODE ID#3953 (GSE47229) was used. Due to the sonication bias, it is clear that the sonicated fragments do not represent the minimally protected DNA footprint, and as such the length of the recovered DNA fragments provides no information.