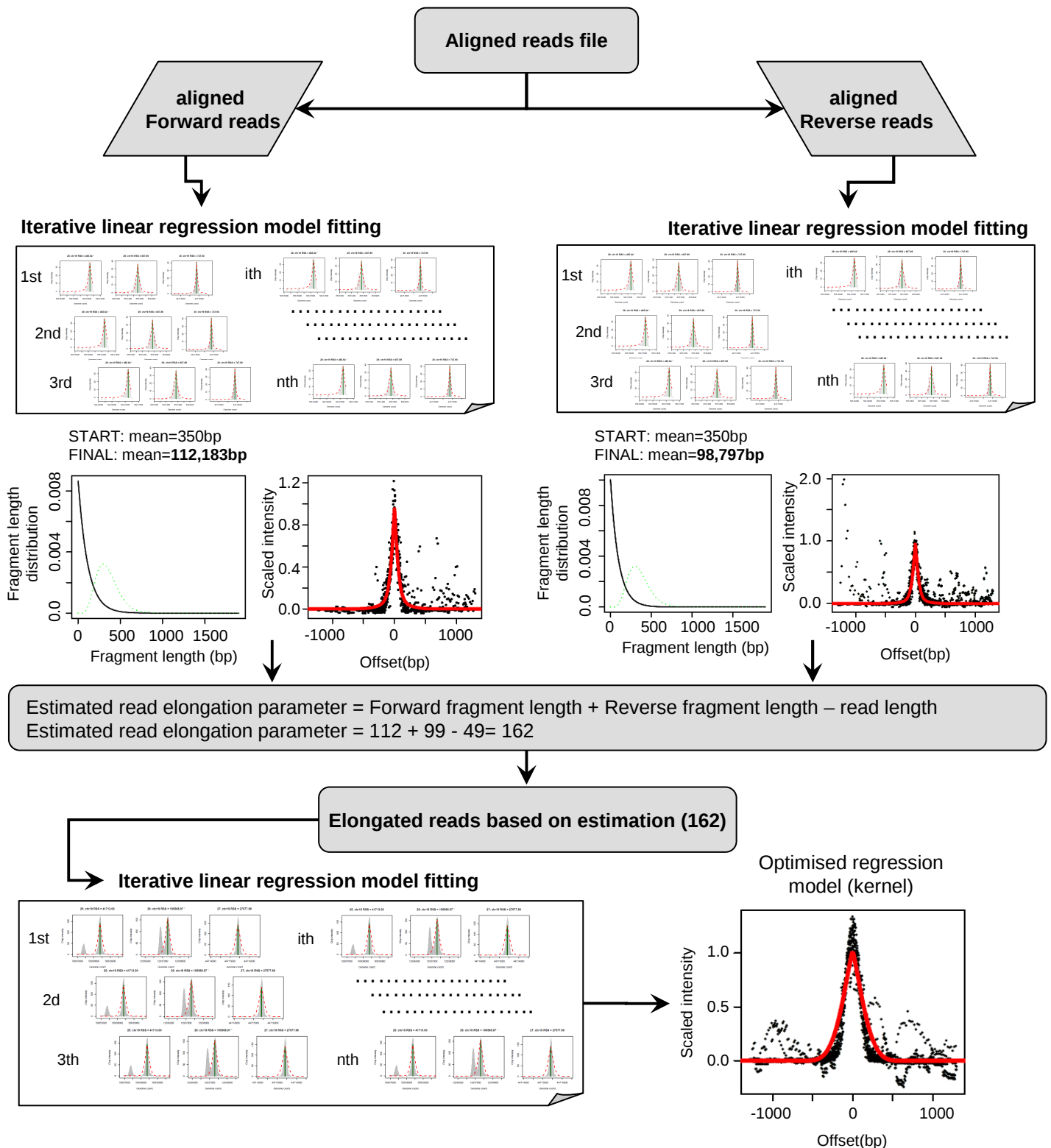




Additional file 2. Schematic representation illustrating the approach implemented in MeDiChISeq for estimating the read elongation parameter. In cases where the user is not able to propose a read elongation parameter from DNA fragmentation information, MeDiChISeq uses iterative linear regression model fitting in a strand-specific mode. From this preliminary step, the fragment length per strand is inferred, then the estimated read elongation parameter is estimated by adding the forward and reverse fragment length and subtracting the read length. In the illustrated example (CTCF dataset), this analysis estimated a read elongation parameter of 162bp.