A/T mononucleotide distributions downstream of the start sites of aligned reads in the forward and reverse strands

Estimate the average nucleosome core fragment length $L$ by minimizing the discrepancy between the A/T nucleotide distributions

Discrepancy is calculated on the central black-colored region that excludes the flanking regions of 30nt that may have Mnase sequence bias (high A/T rate followed by C/G rate).