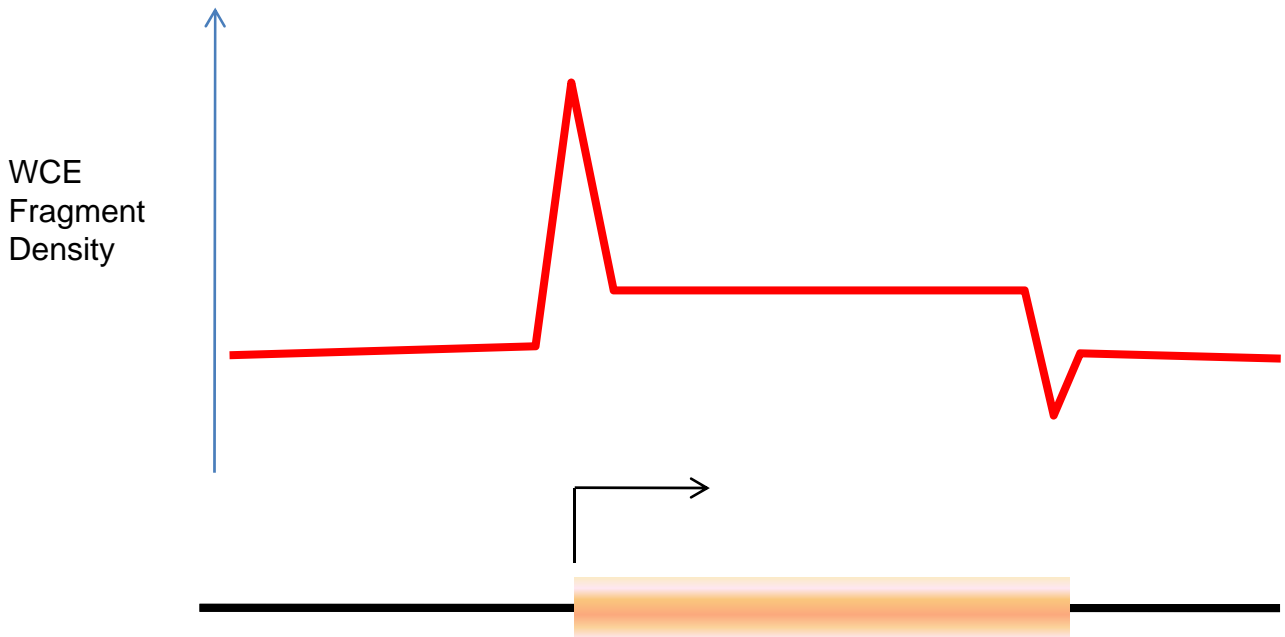


### Supplementary Figure S3



**Supplementary Figure S3.** A schematic model of WCEseq fragments distribution across a typical gene, based on observations in Figures 4 and 5. Gene region is expected to be more fragment-rich than the immediate upstream and downstream regions, with the TSS marked with a substantial increase of fragment count and the TES punctuated with lower fragment count.