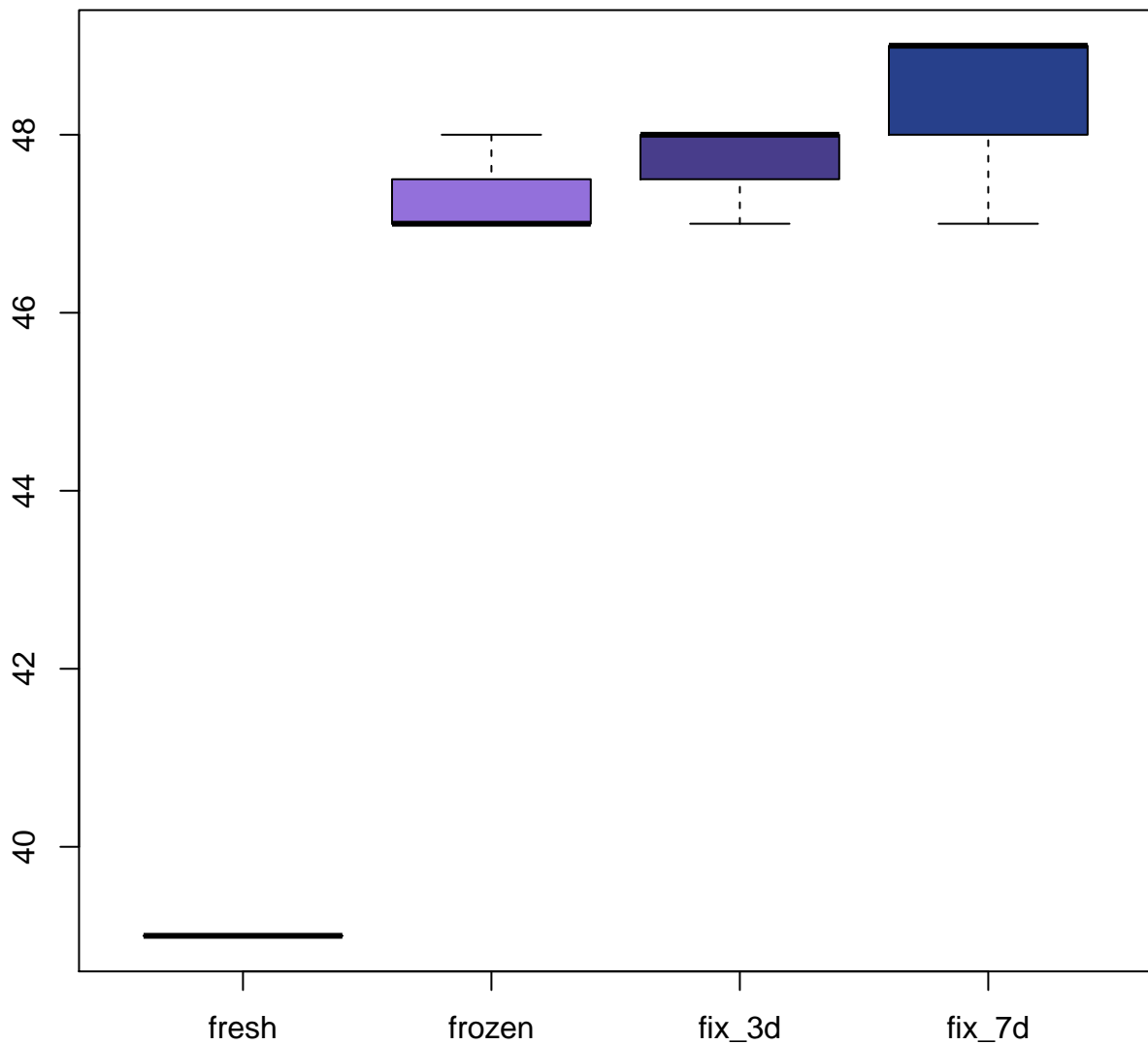
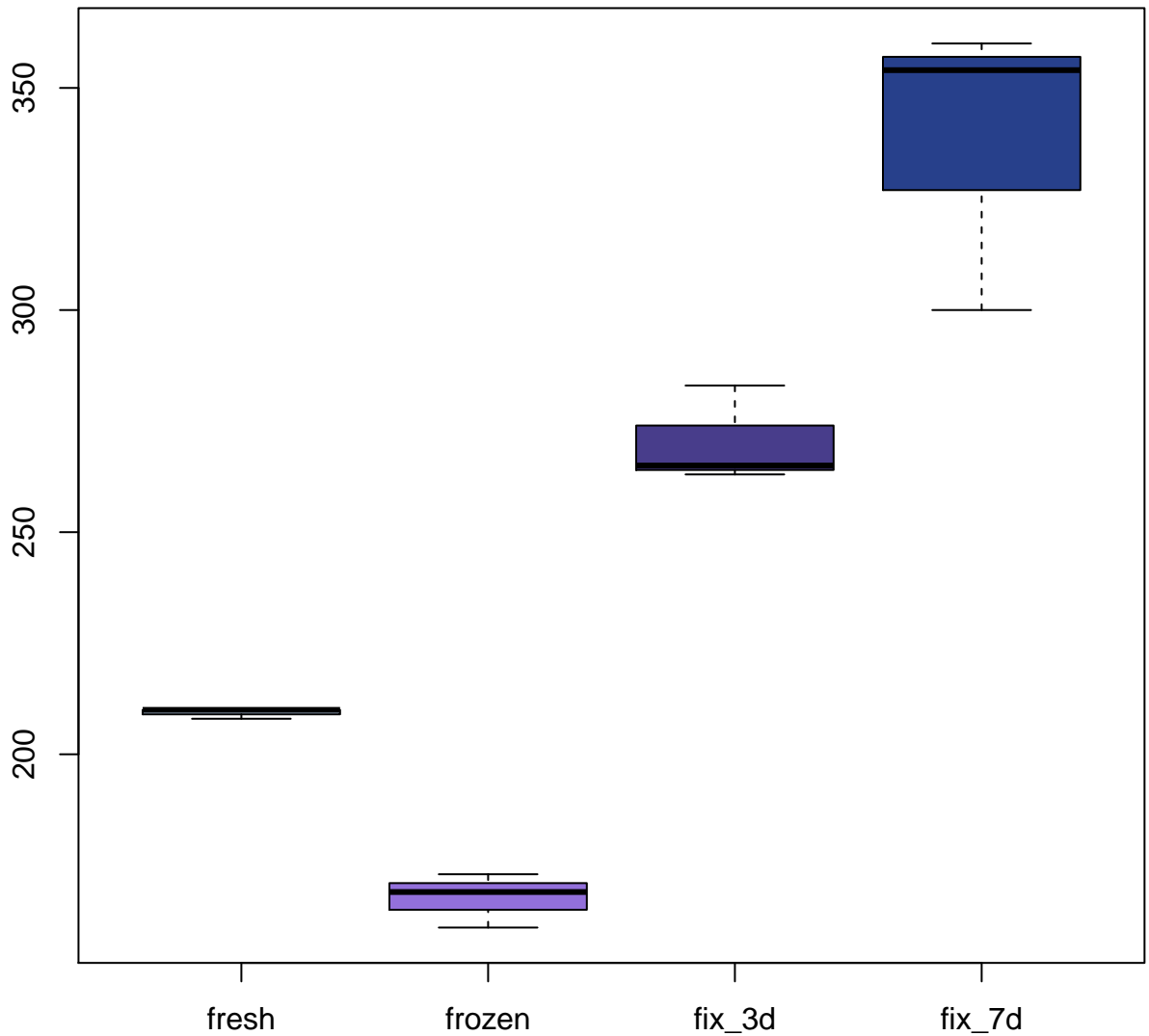


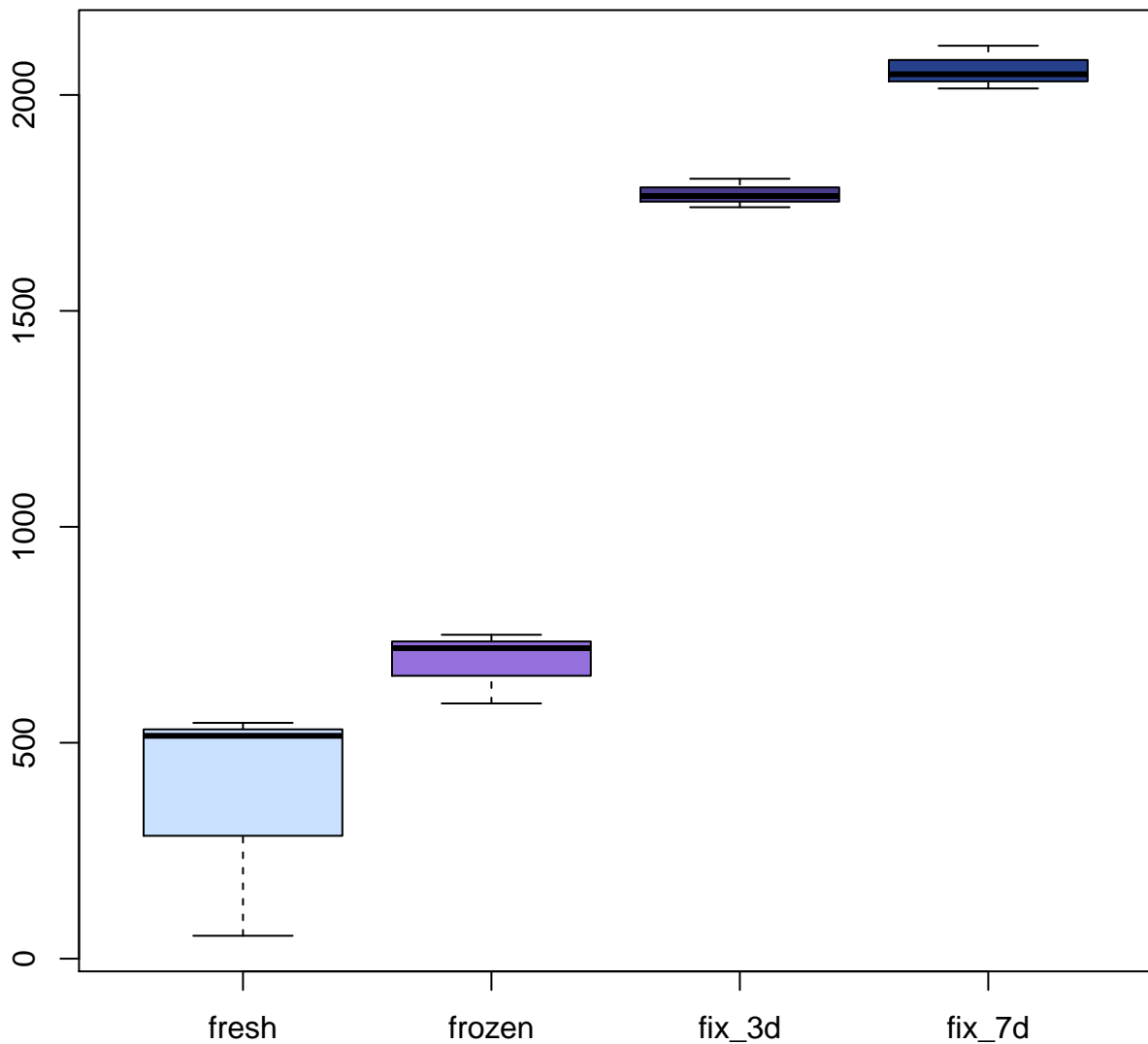
## Minimum fragment length



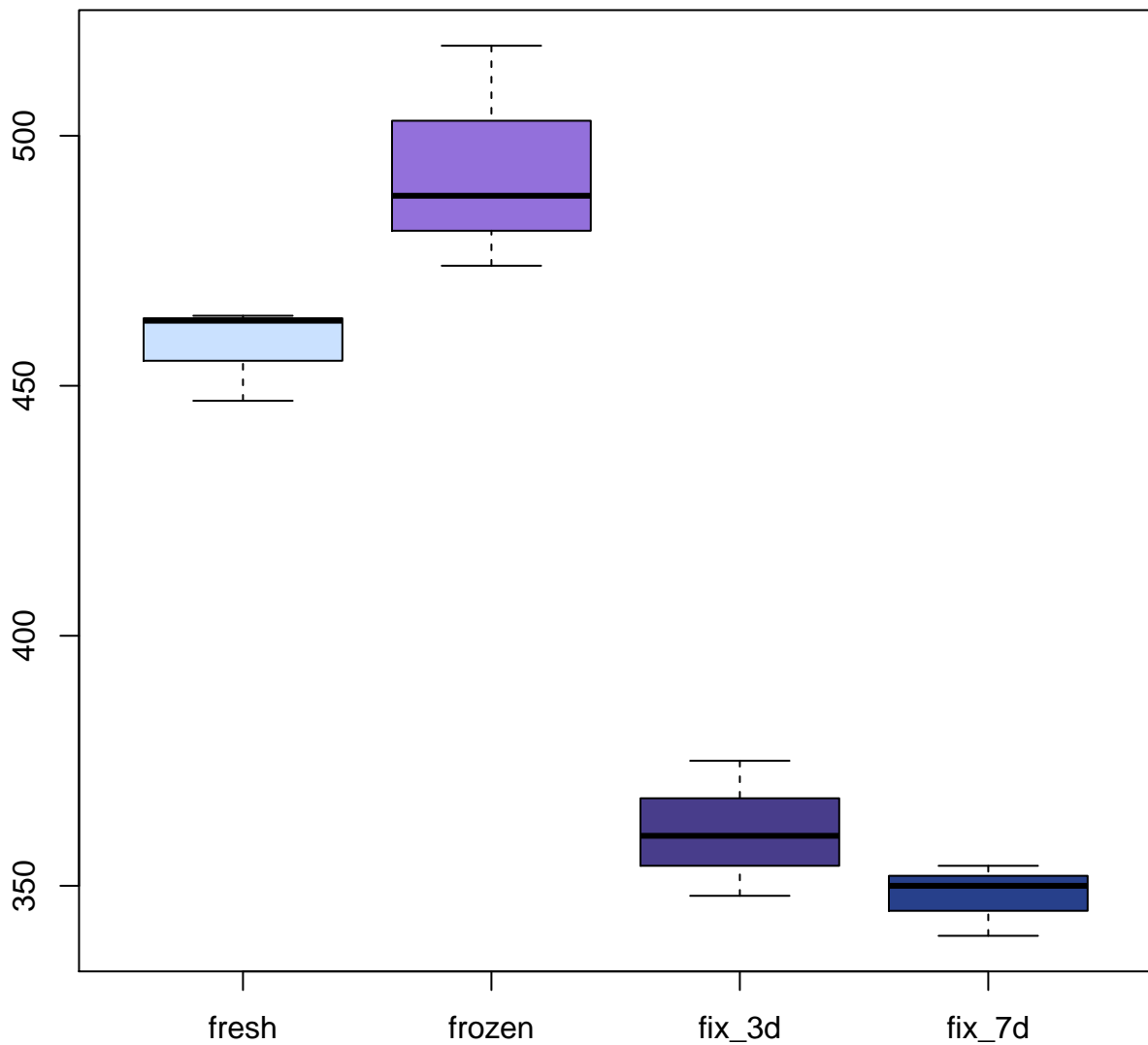
**Median fragment length**



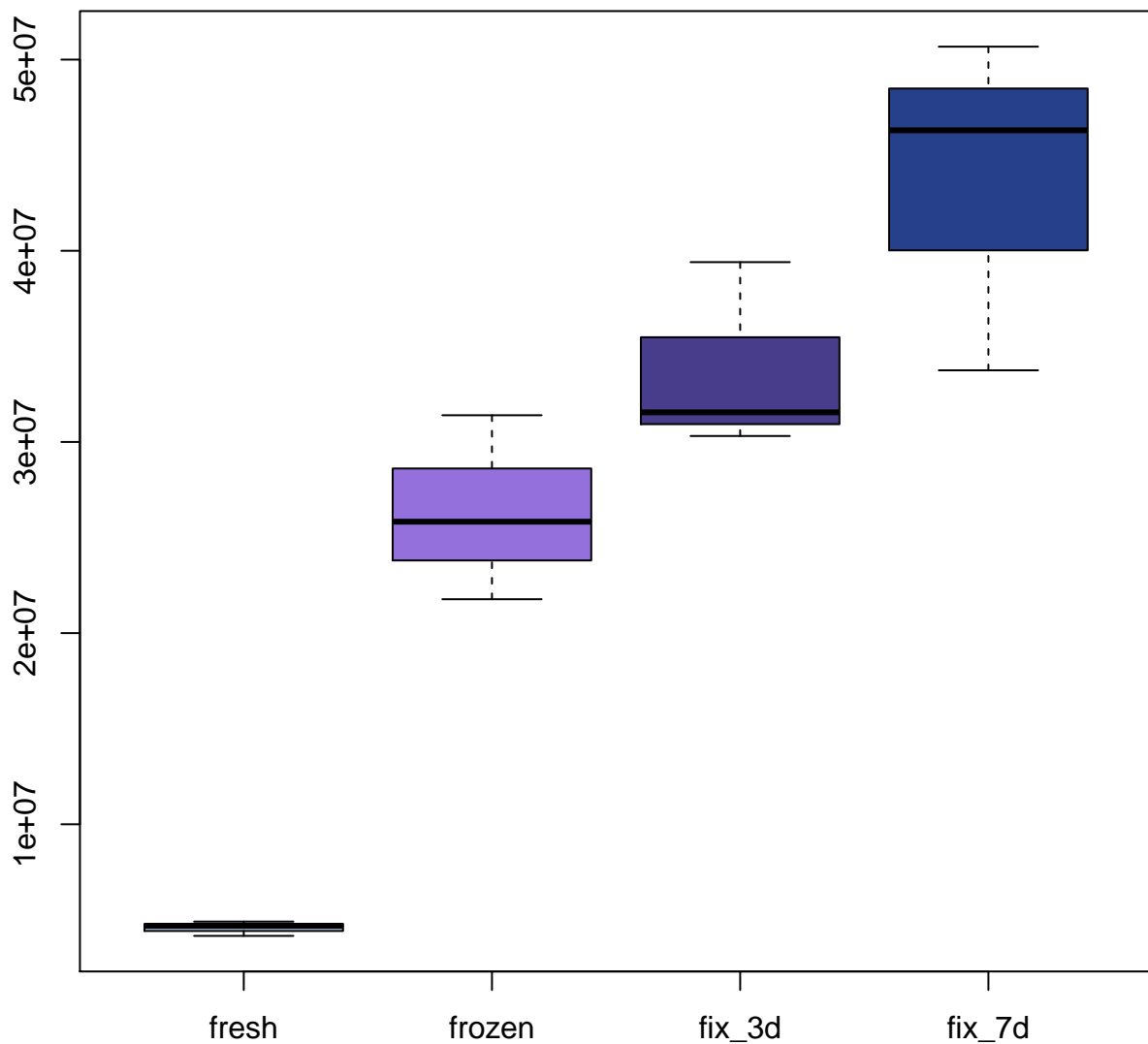
**Maximum fragment length**



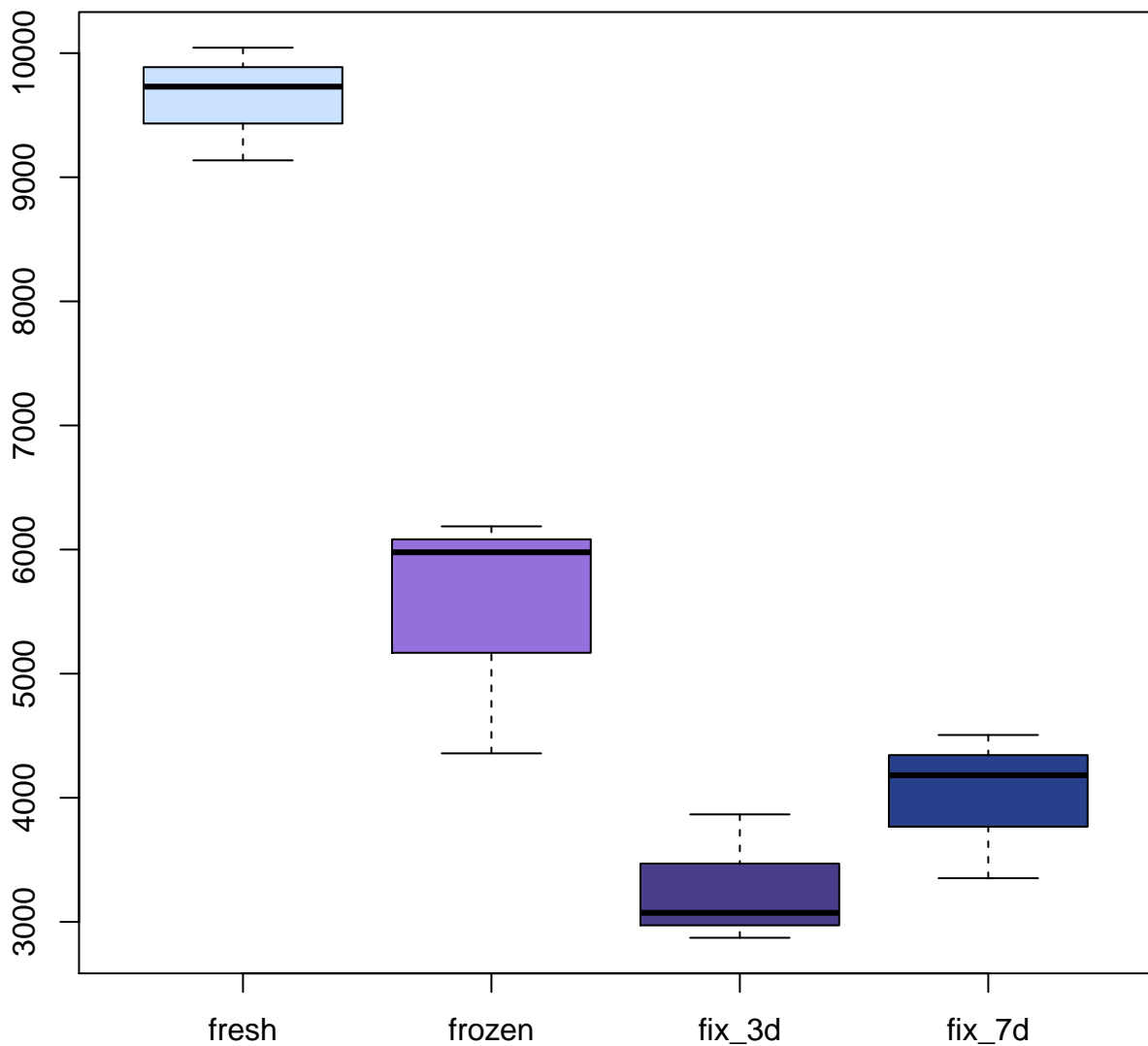
**Average fragment length**



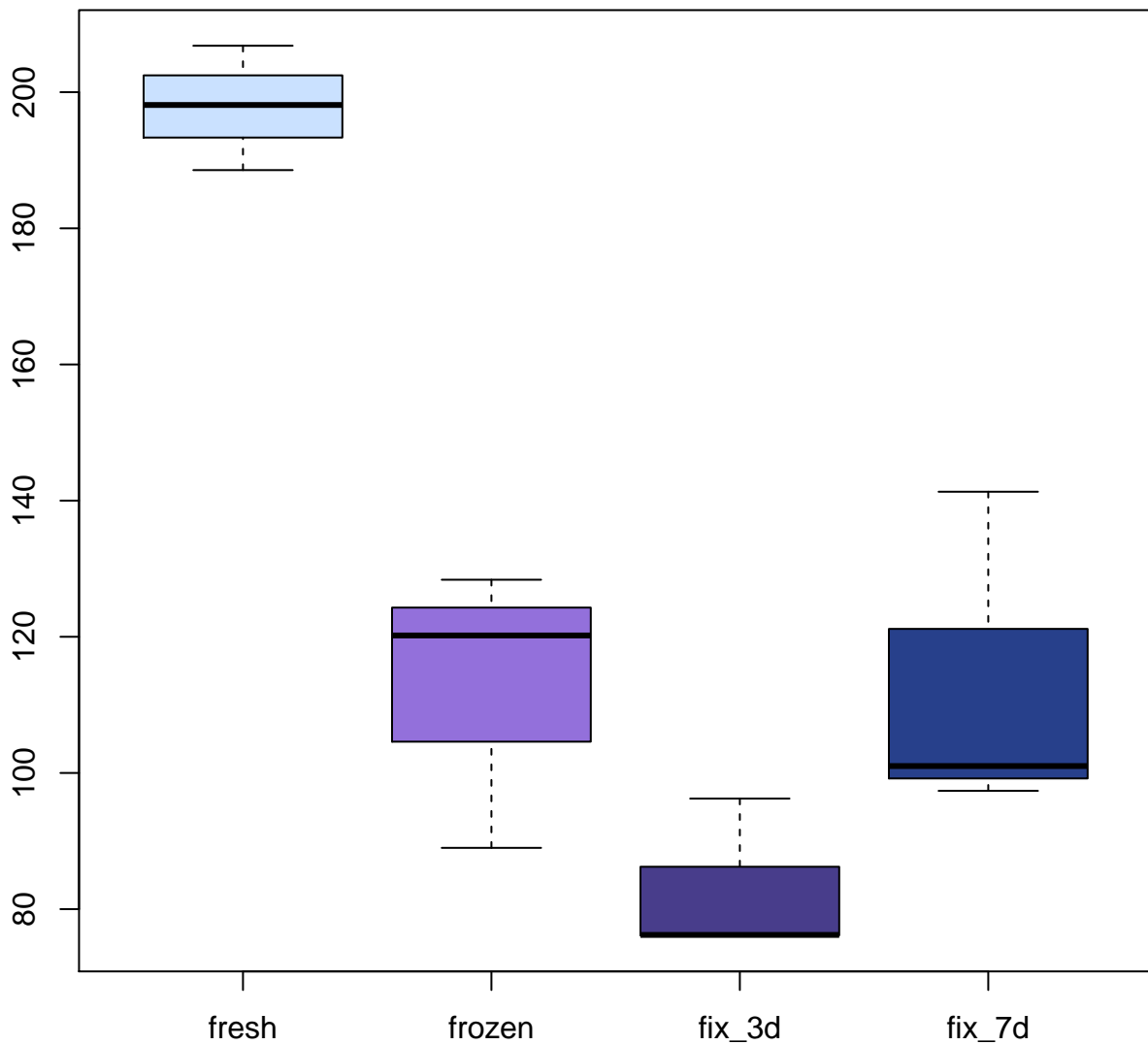
**Number of mapped reads after filtering**



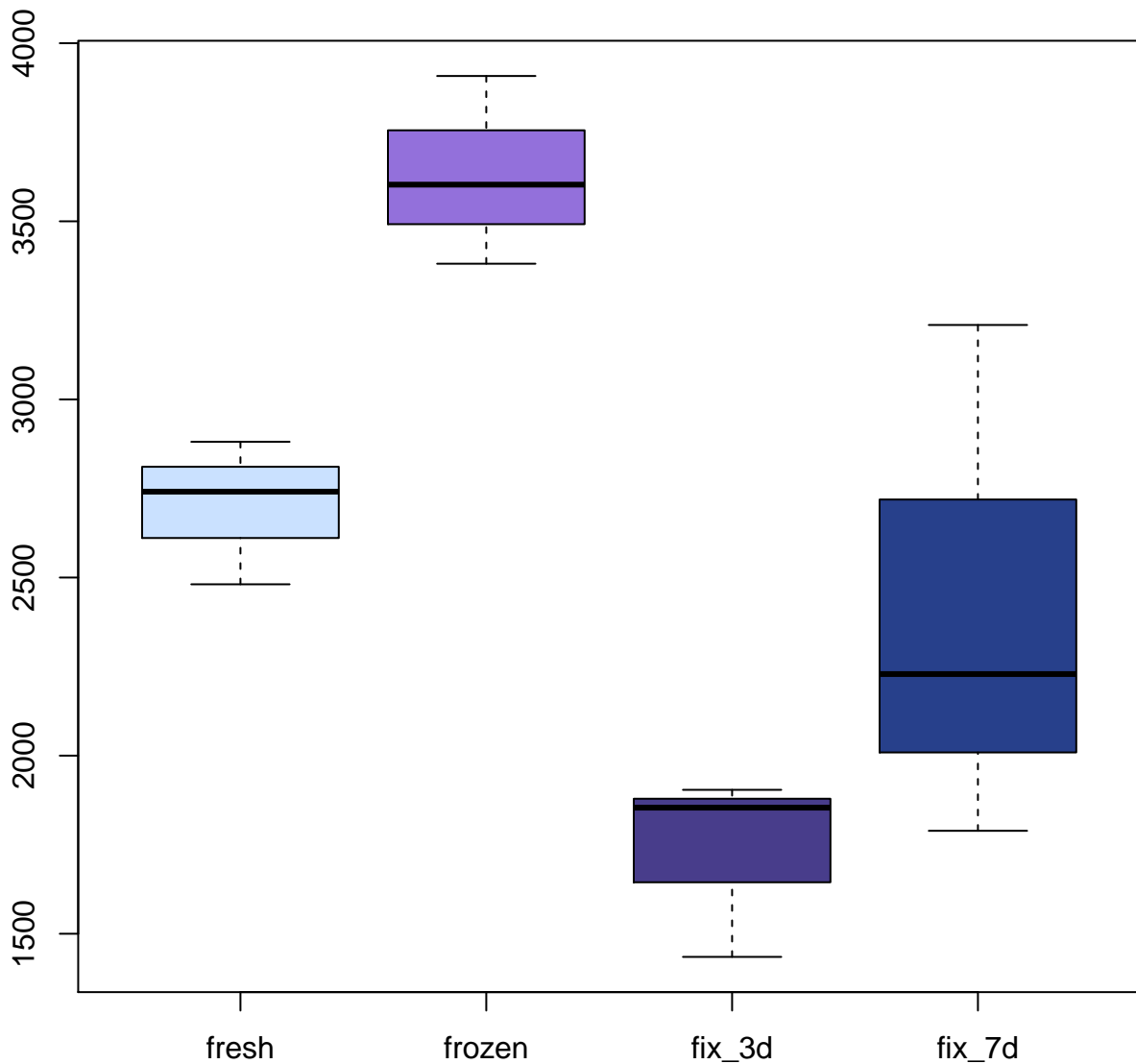
**Number of peaks normalized by reads mapped per chr**



**Number of peaks per chromosome**

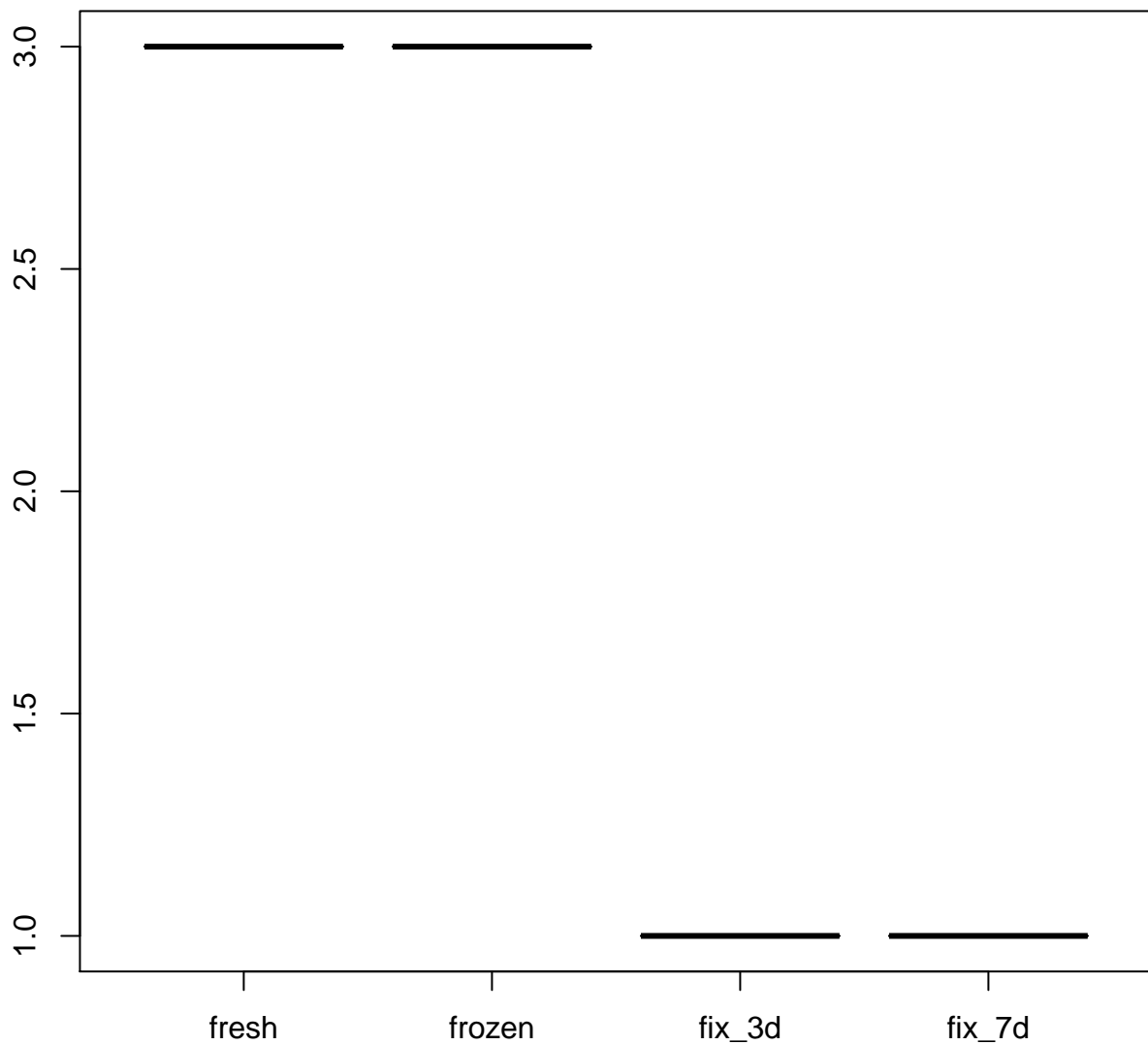


**Reads in peaks normalized by total mapped reads**

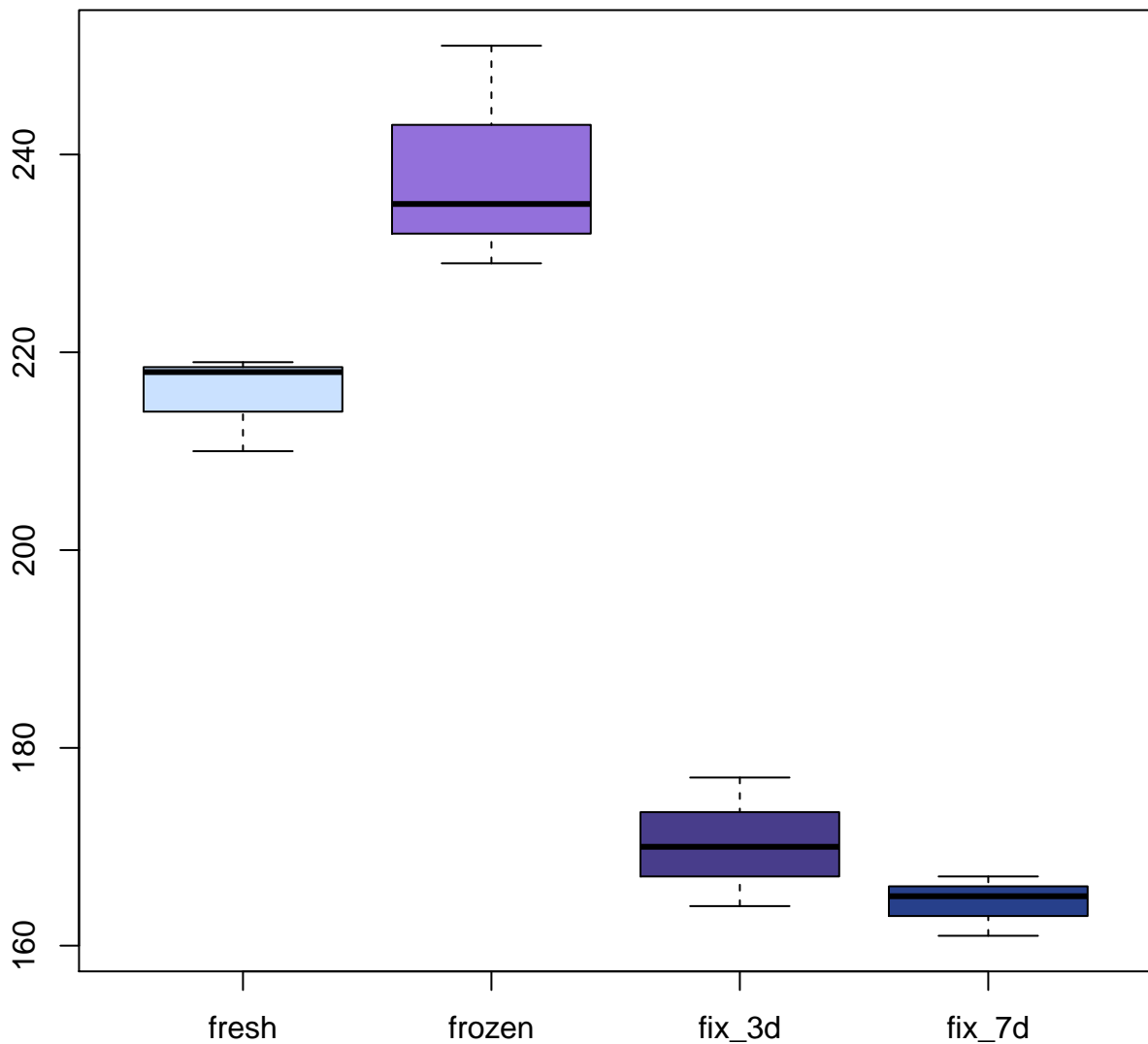




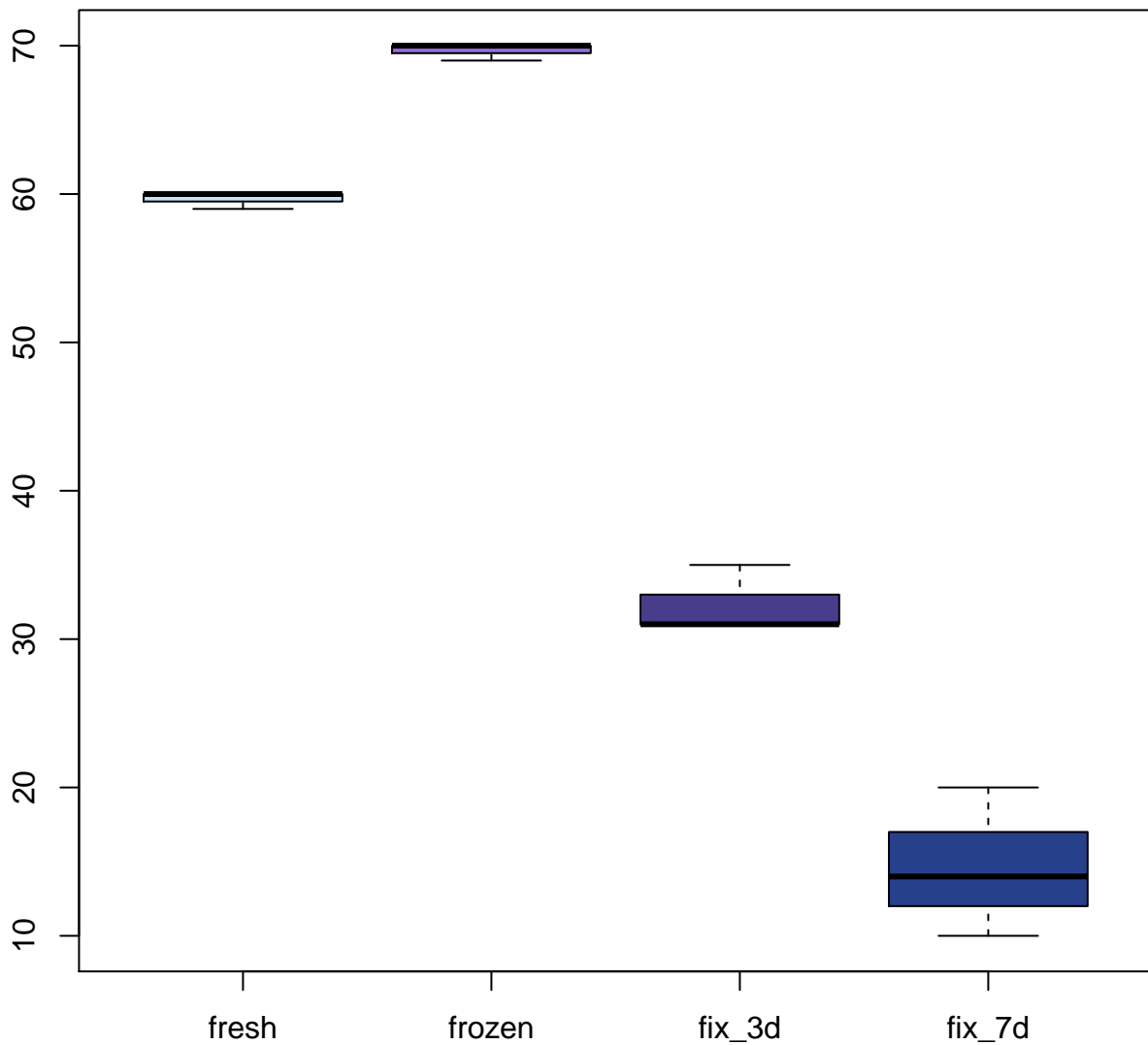
## Signal to noise ratio



**Average peak width**



## Overlap between replicates within each condition



## Overlap with DNase1 peaks for K562

