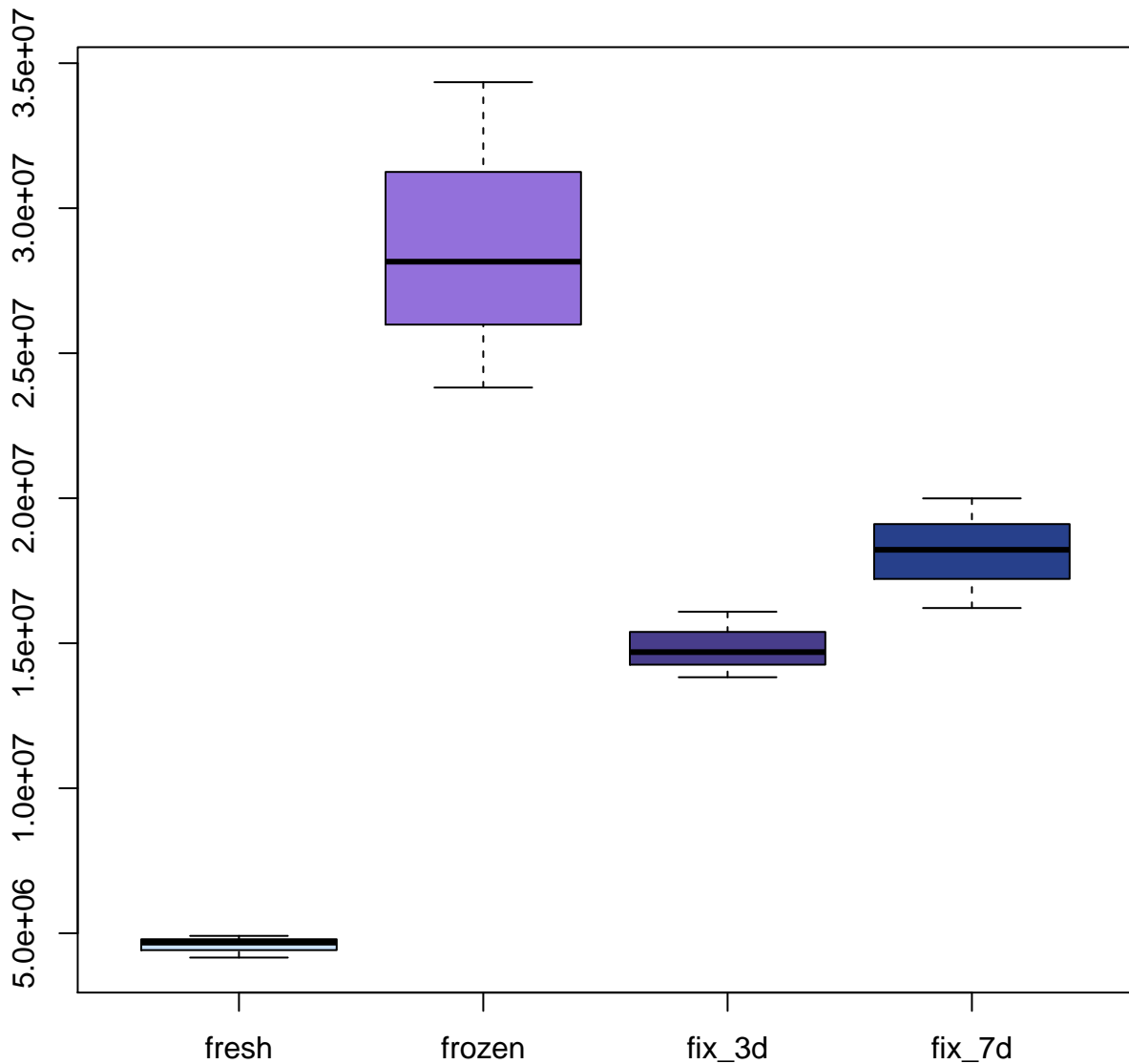
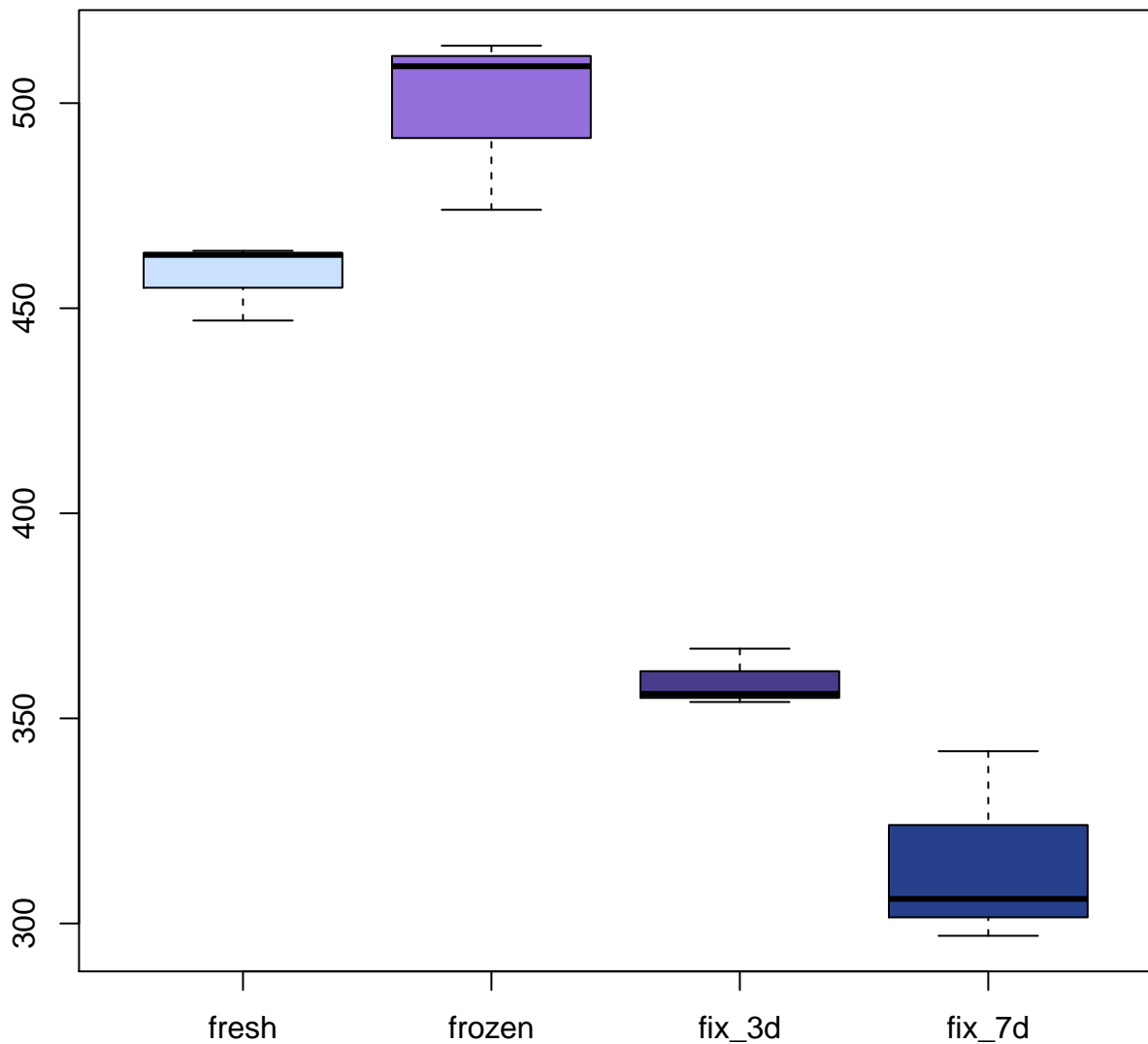


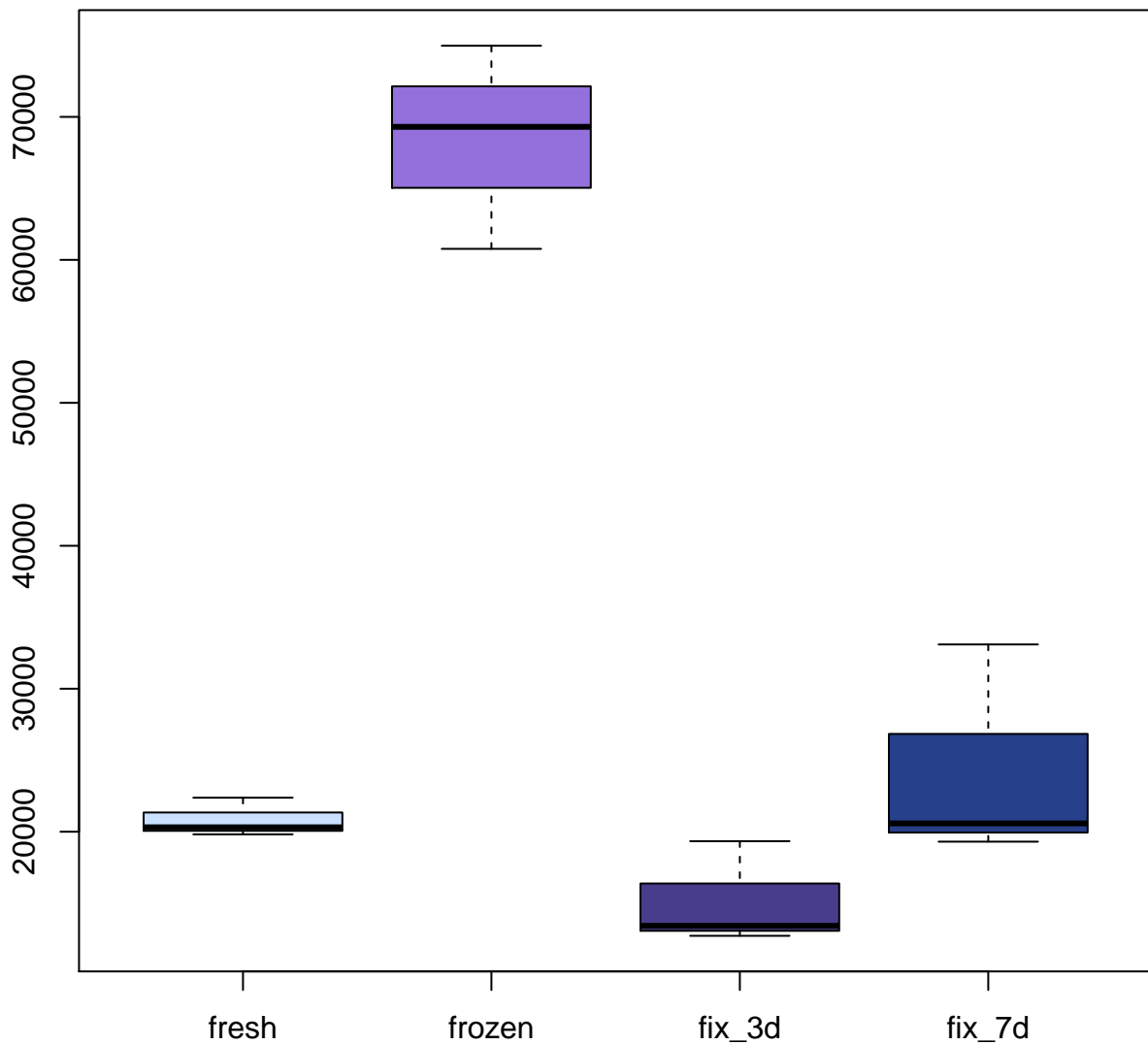
**Number of mapped reads after filtering**



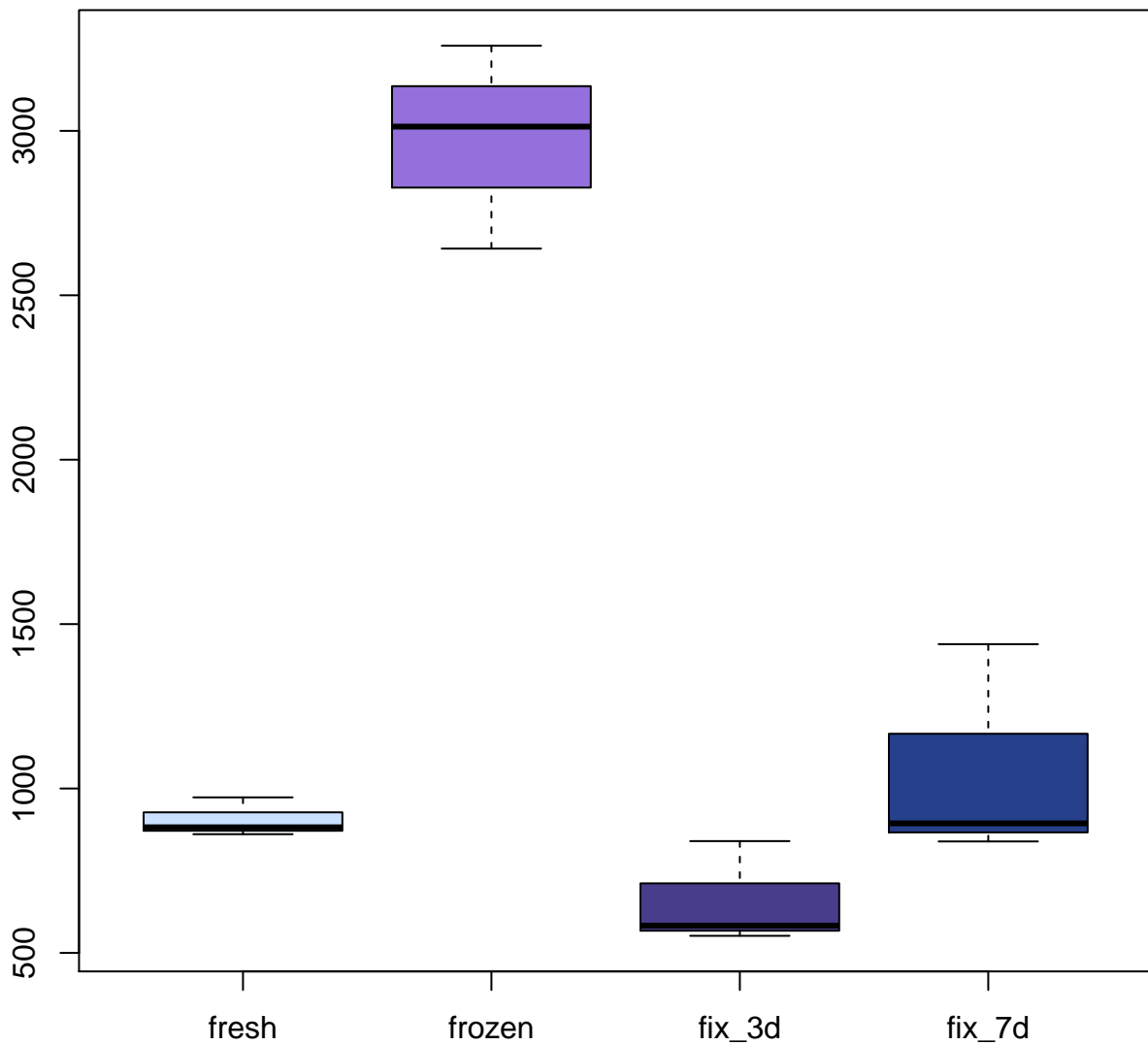
**Average fragment width**



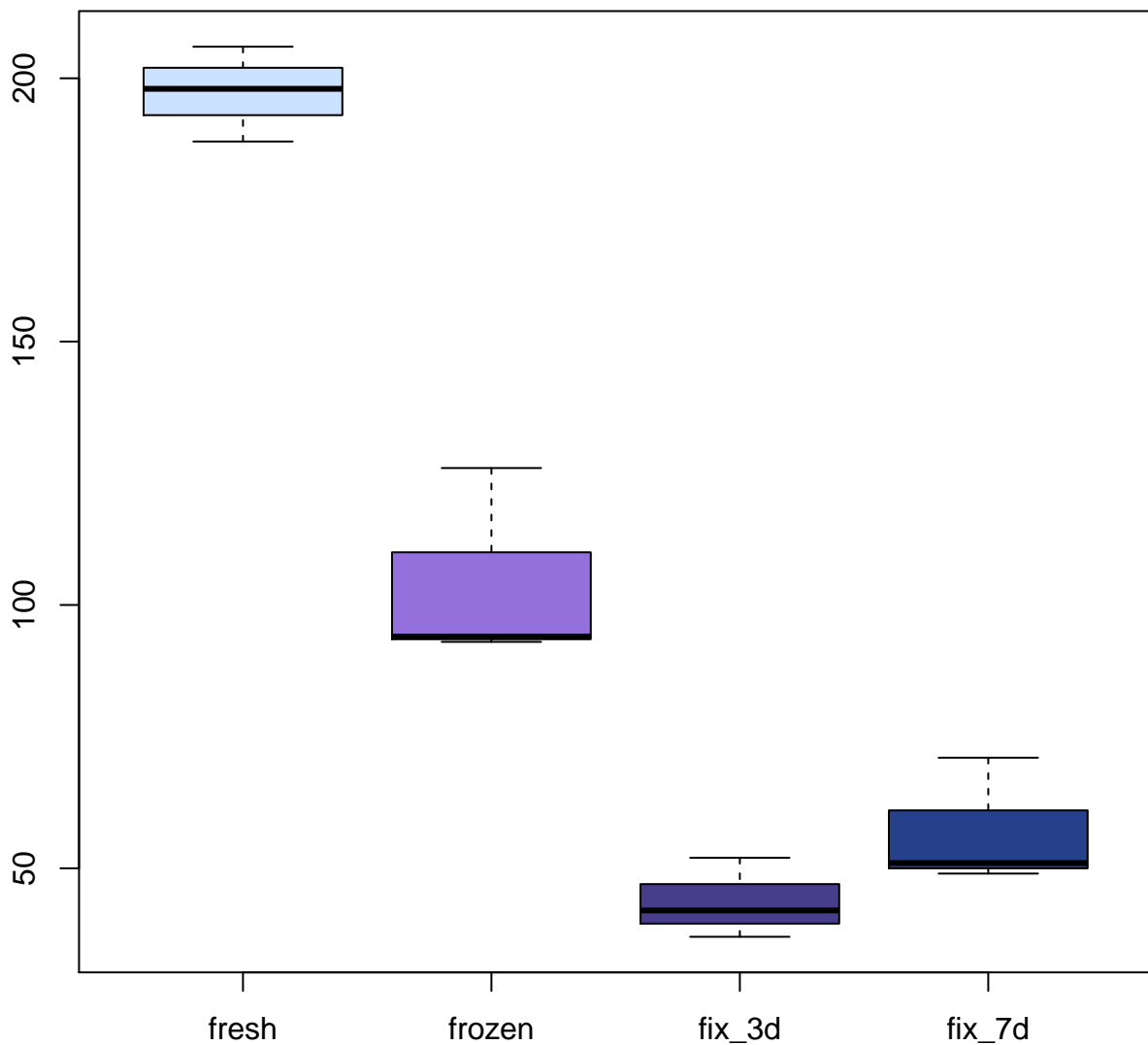
**Number of called peaks**



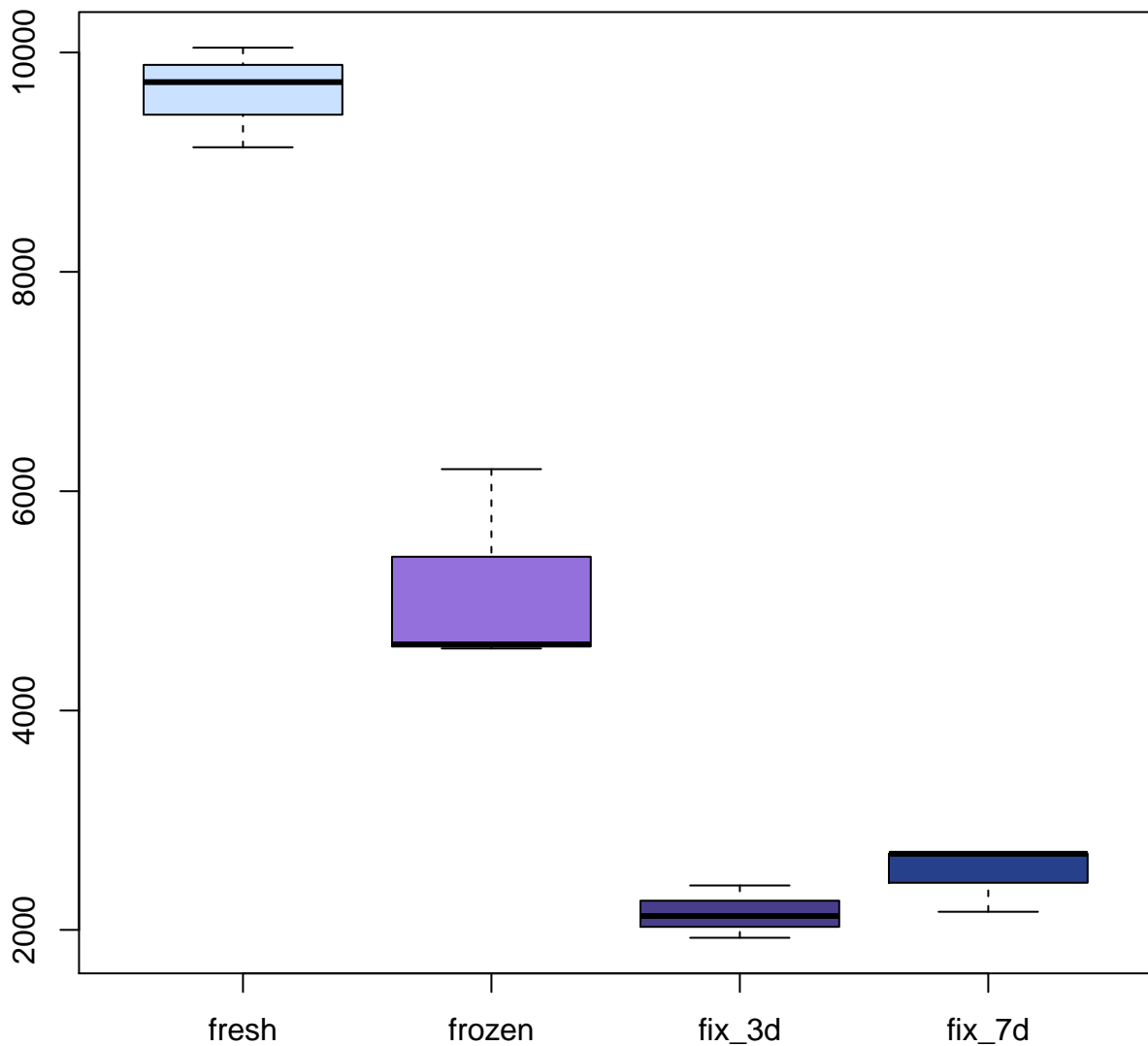
## Number of peaks per chromosome



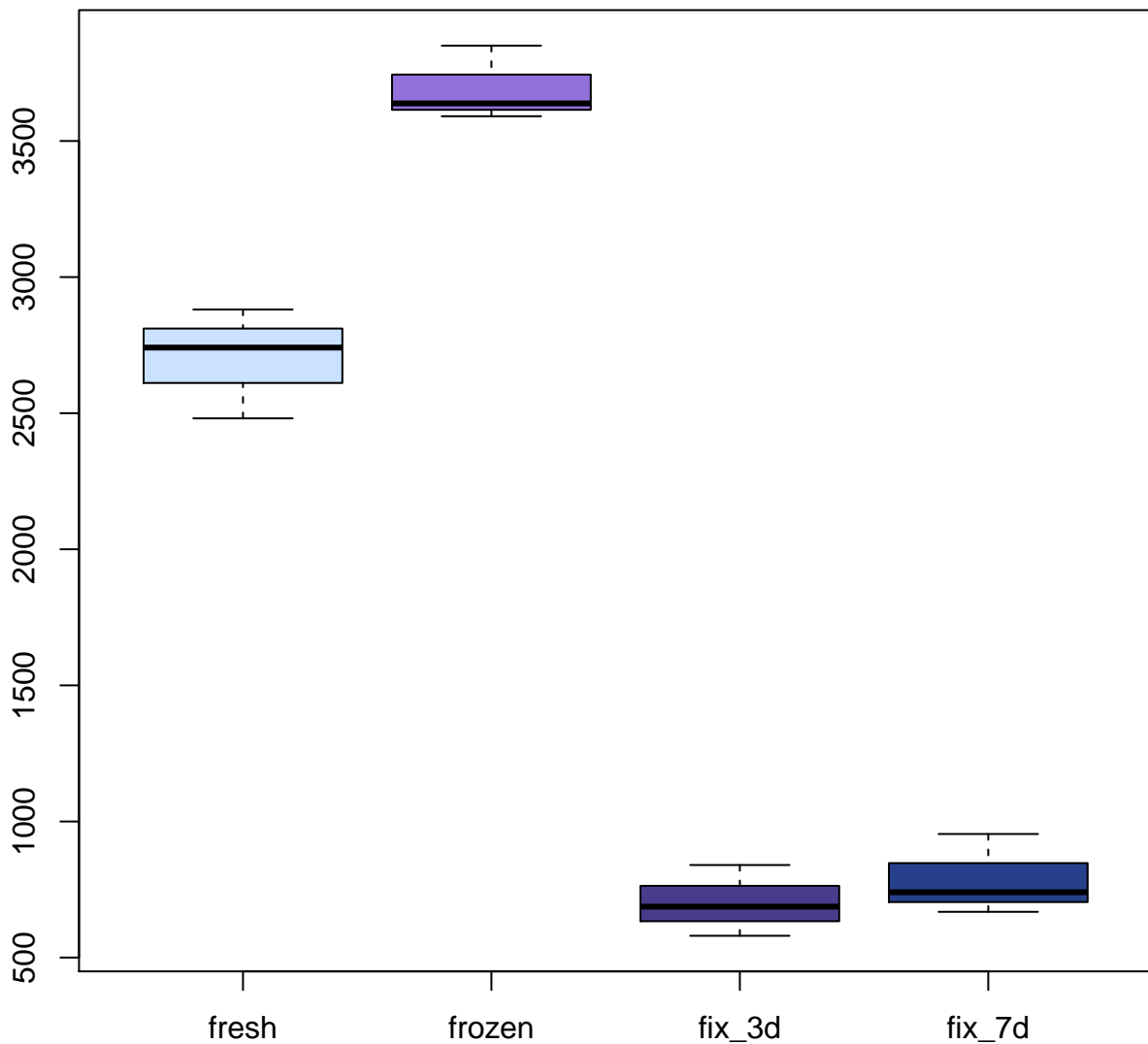
**Number of peaks normalized by total mapped reads**



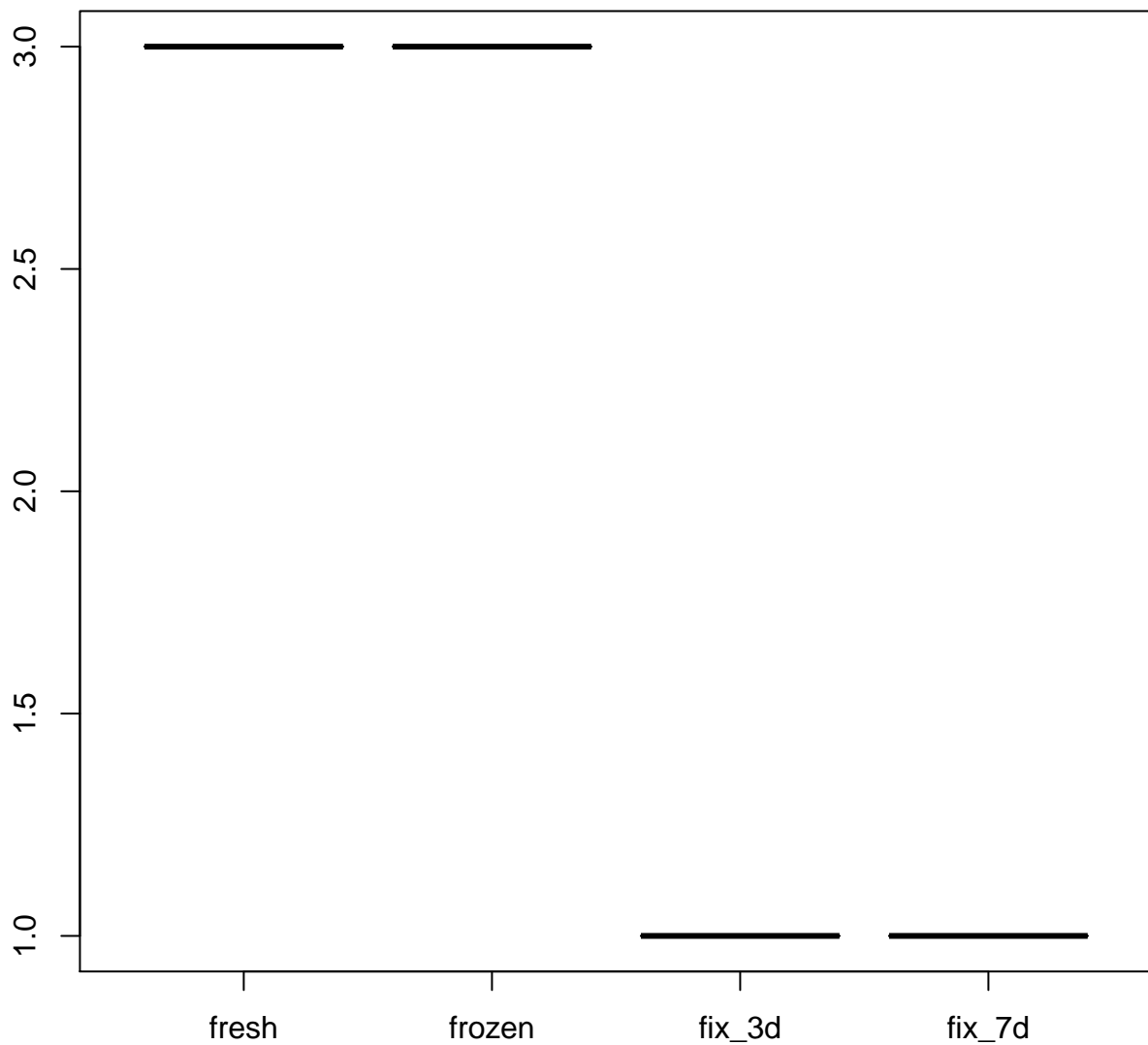
**Number of peaks normalized by reads mapped per chr**



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



## Signal to noise ratio





**Average peak width**

