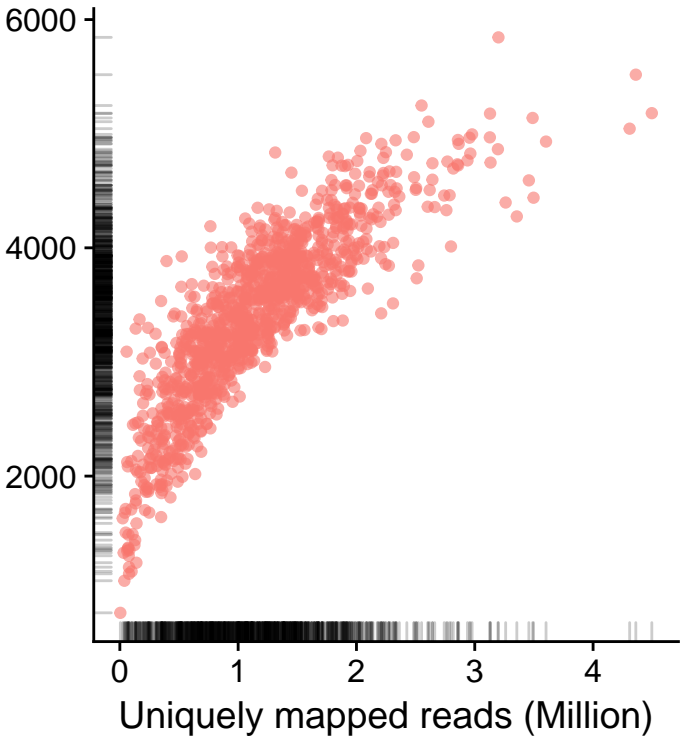
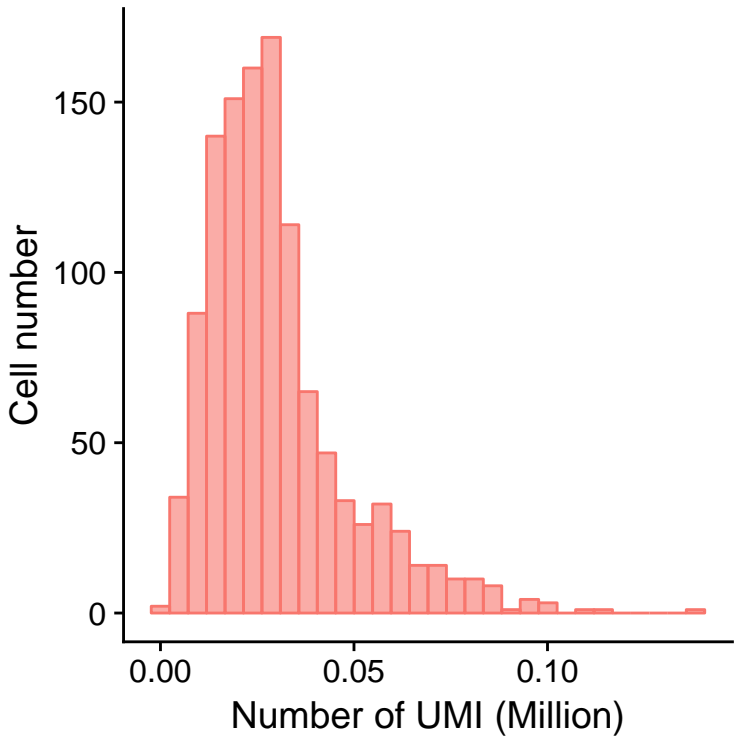
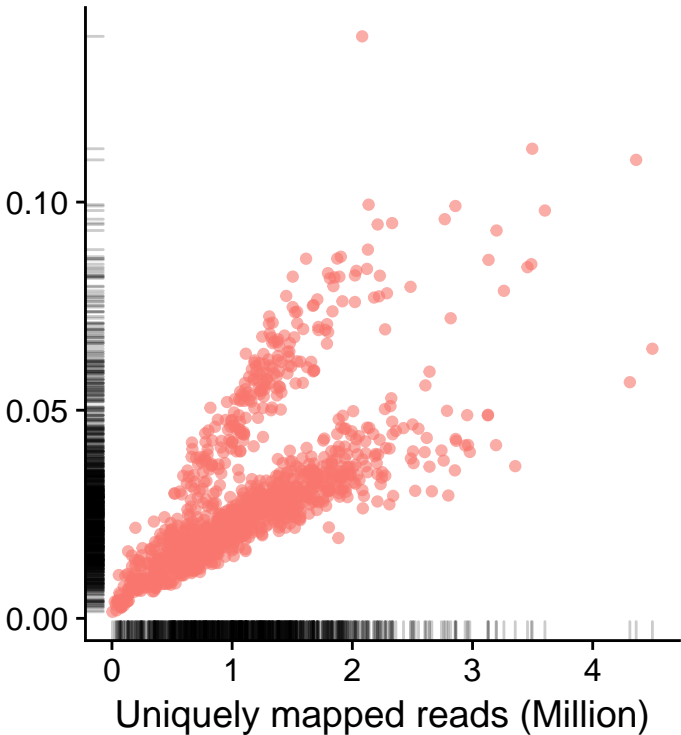


Number of detected genes

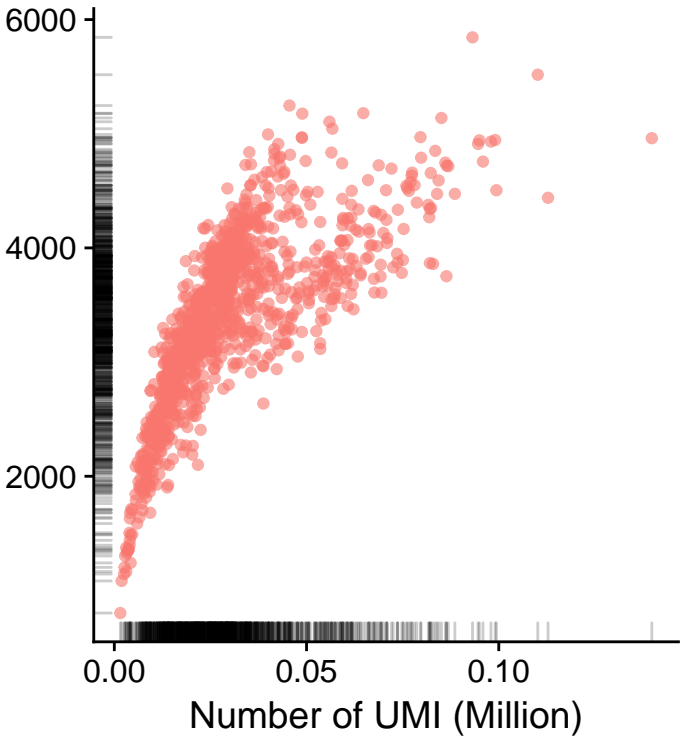




Number of UMI (Million)



Number of detected genes



Assigned UMI number (Million)

$$y = 0.63 * x$$

2

1

0

0

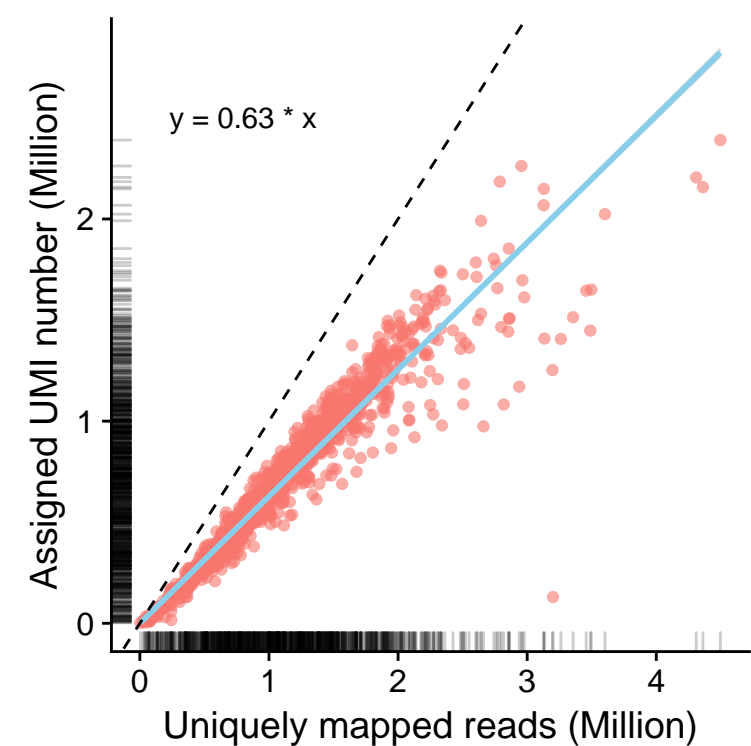
1

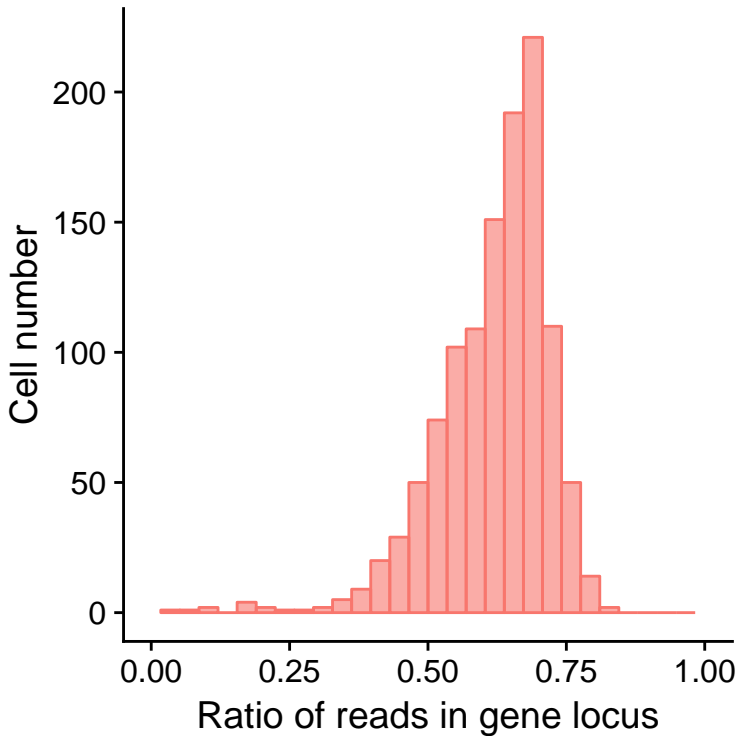
2

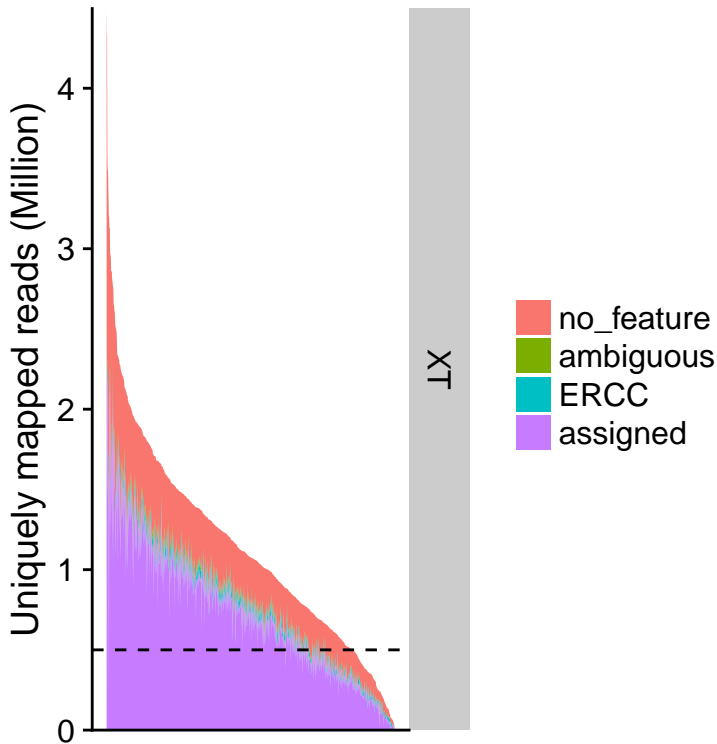
3

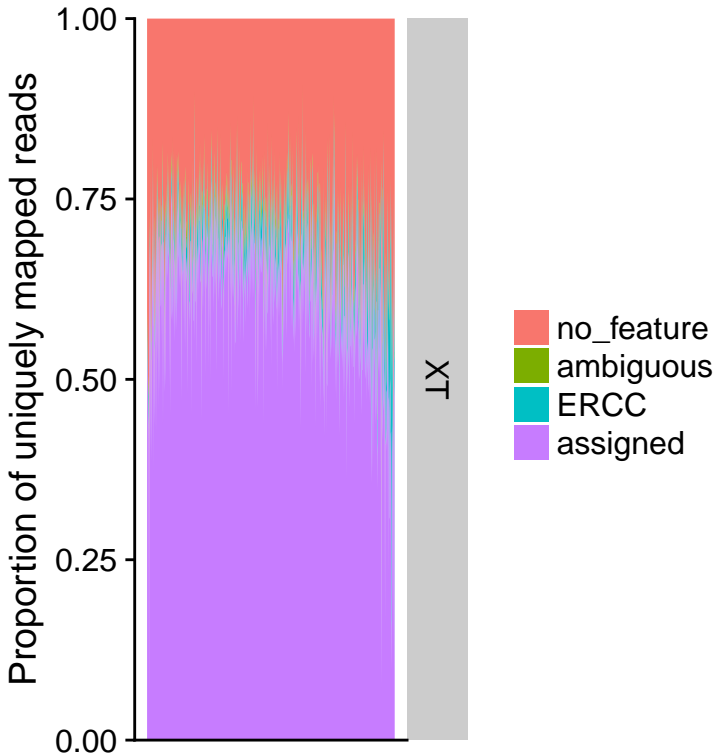
4

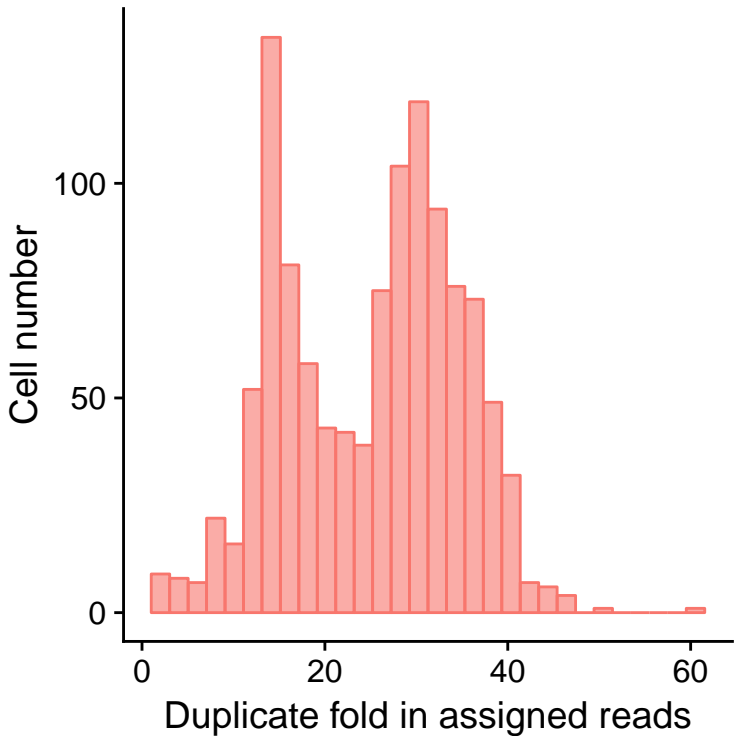
Uniquely mapped reads (Million)



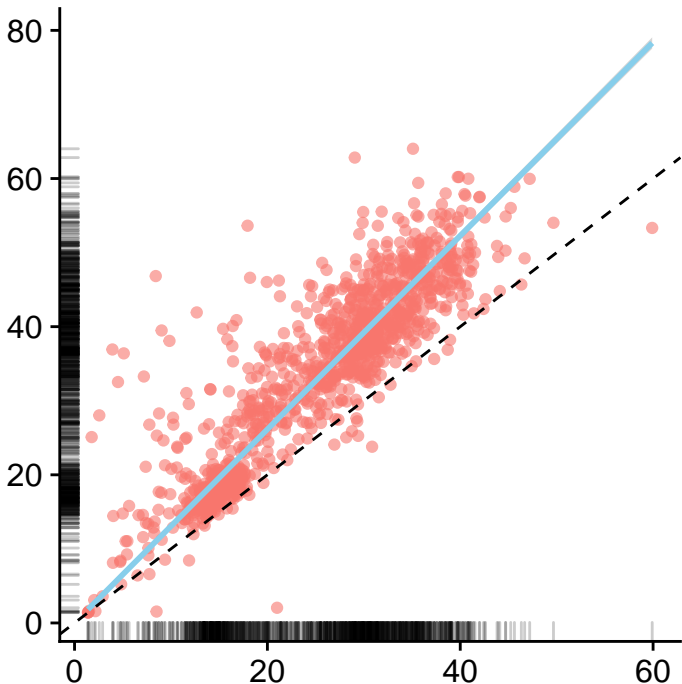






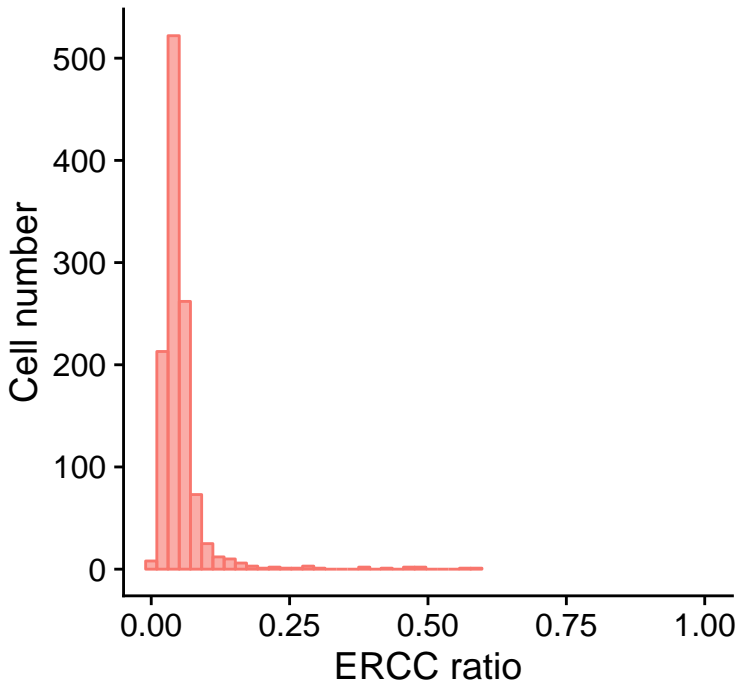


Duplicate fold in ERCC reads

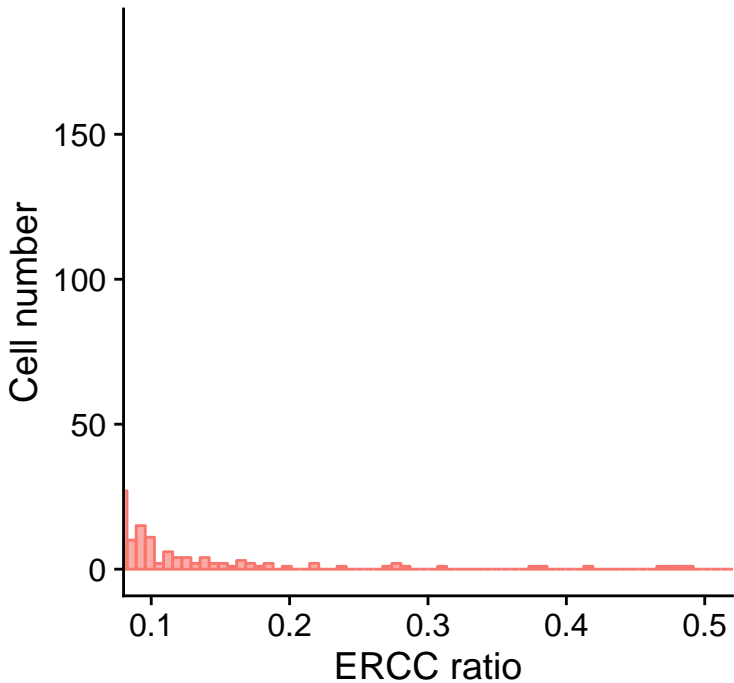


Duplicate fold in assigned reads

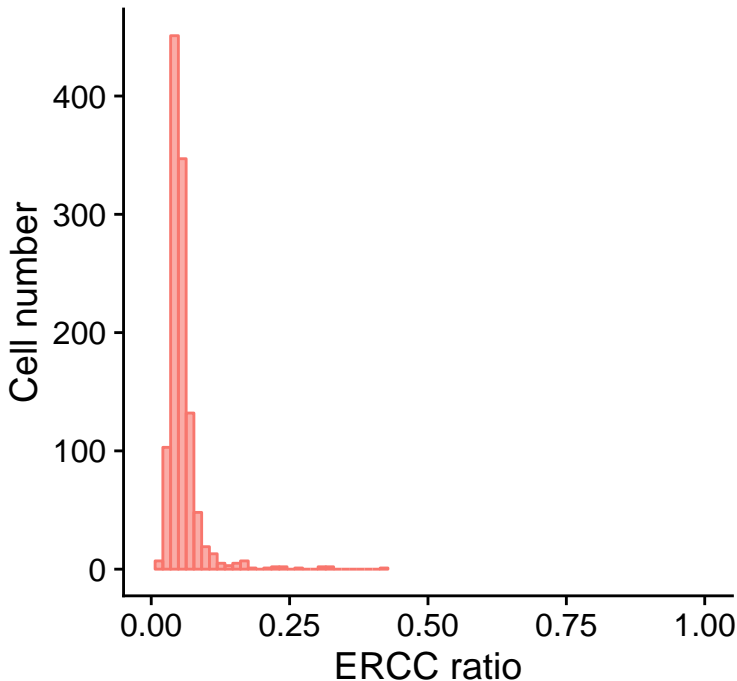
Before removing duplicates



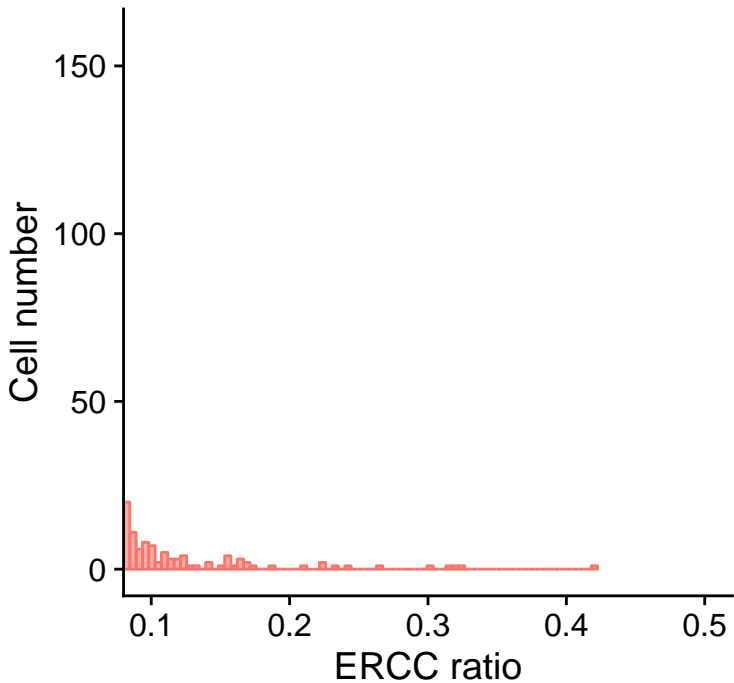
Before removing dup. (Zoom in)



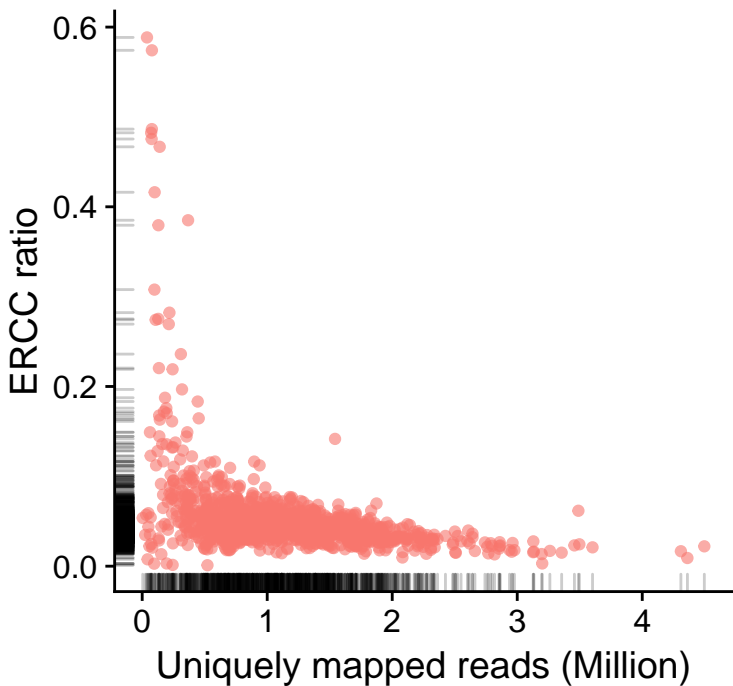
After removing duplicates



After removing dup. (Zoom in)



Before removing duplicates



After removing duplicates

