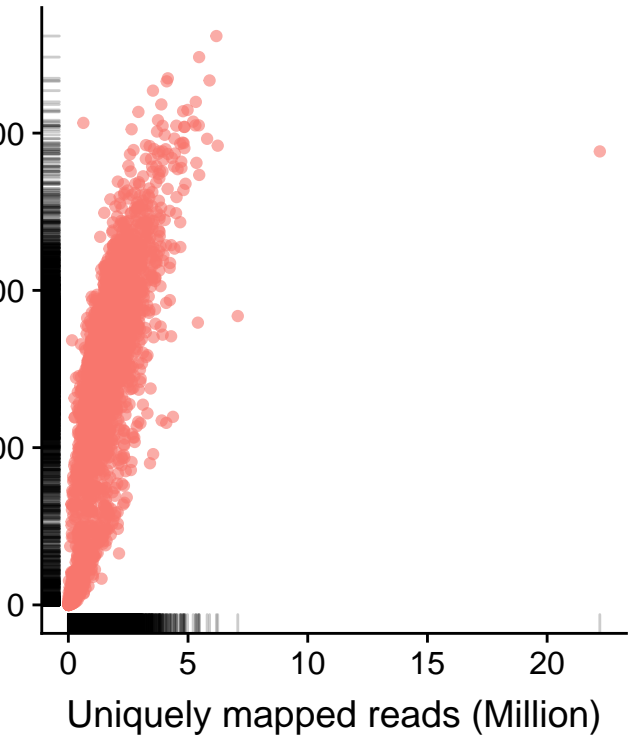


Number of detected genes

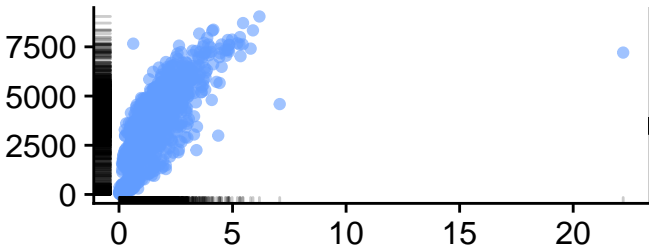
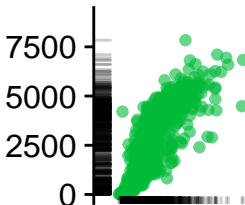
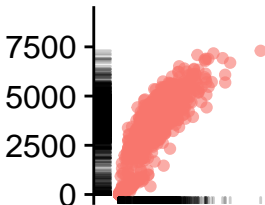


Number of detected genes

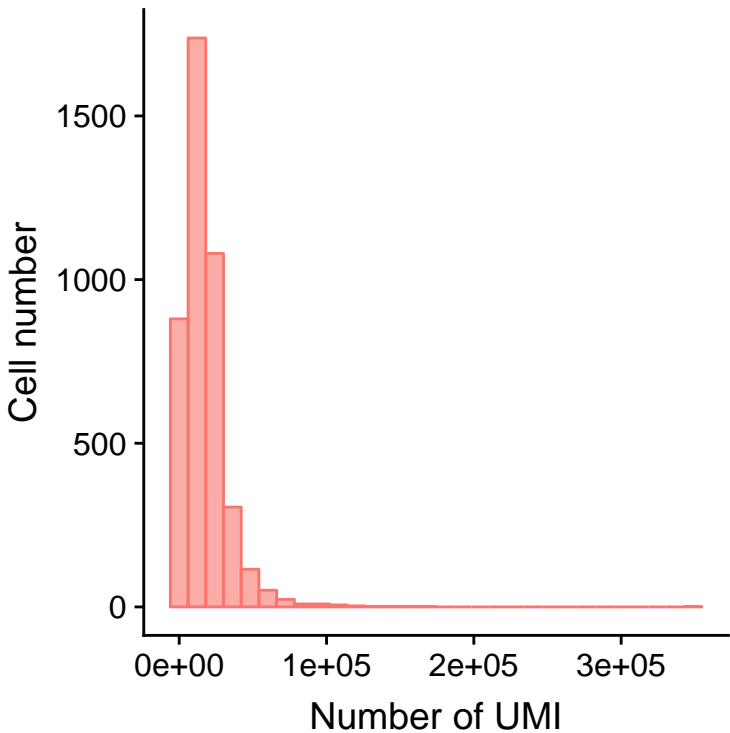
WD\_C

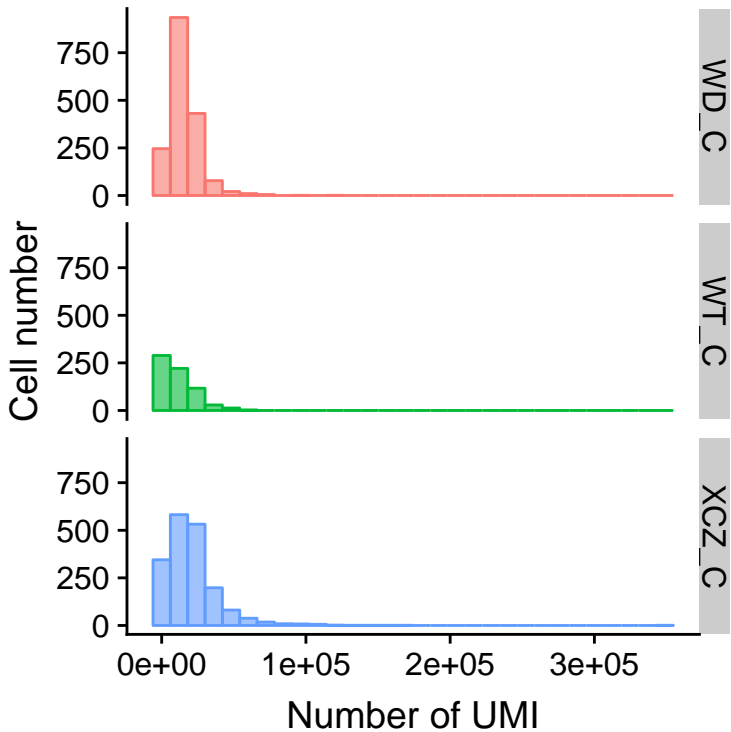
WT\_C

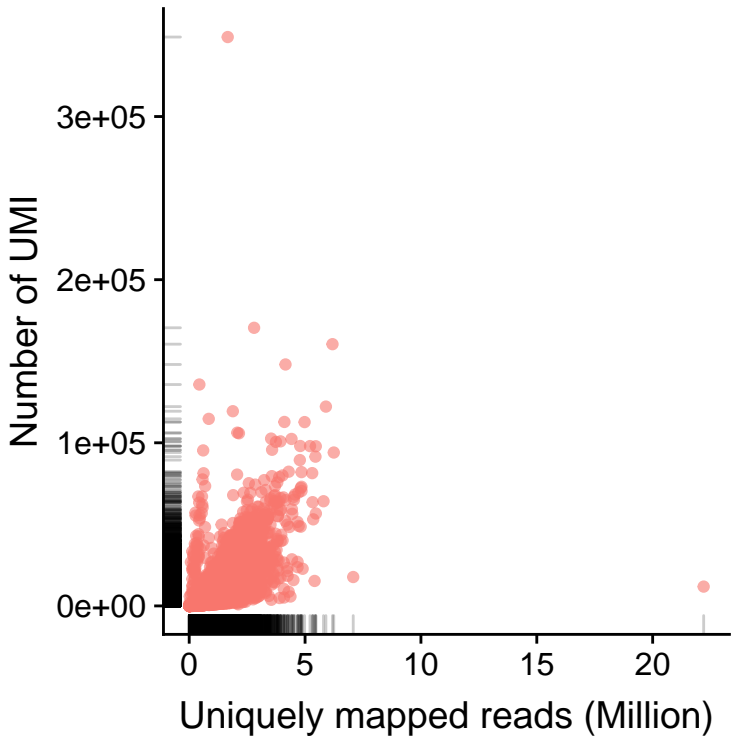
XCZ\_C

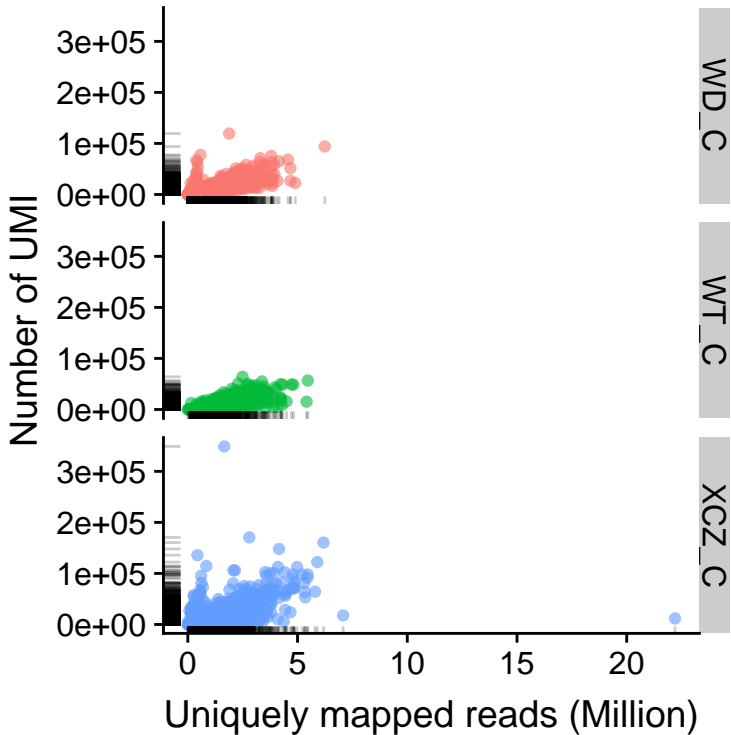


Uniquely mapped reads (Million)



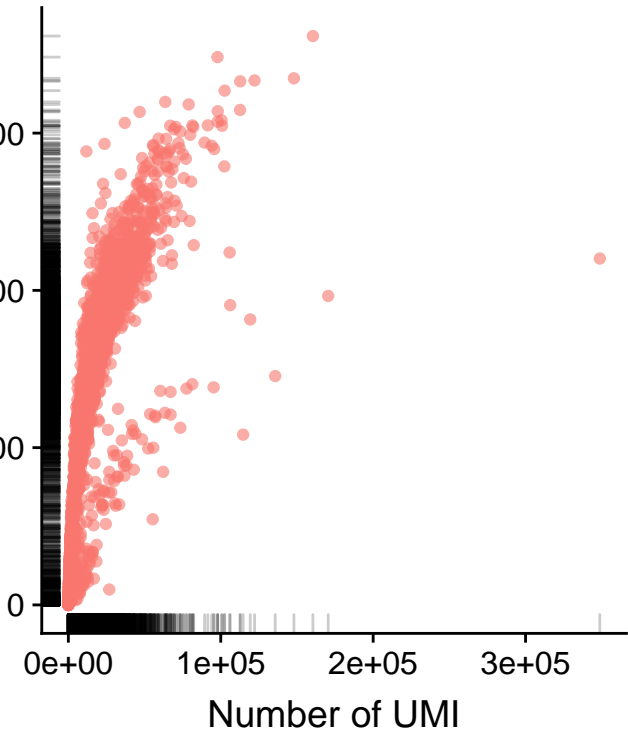








Number of detected genes

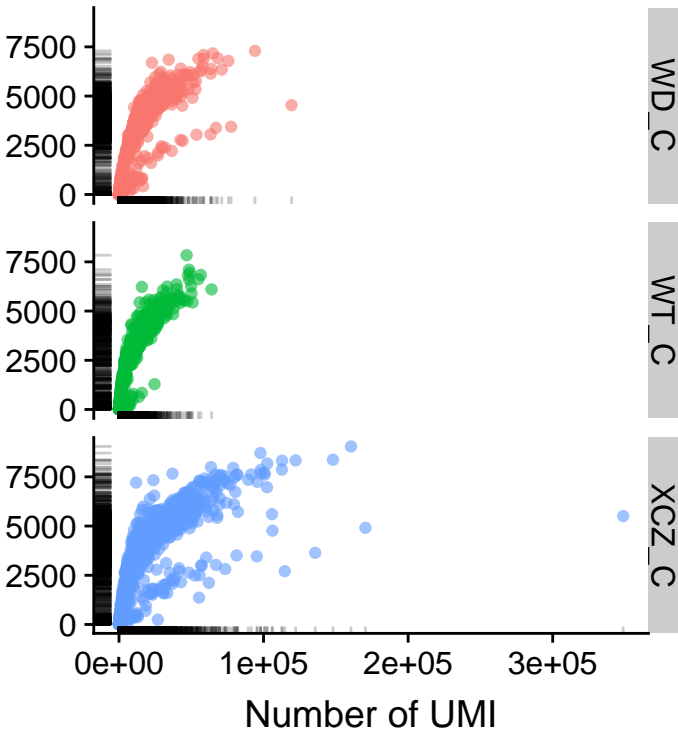


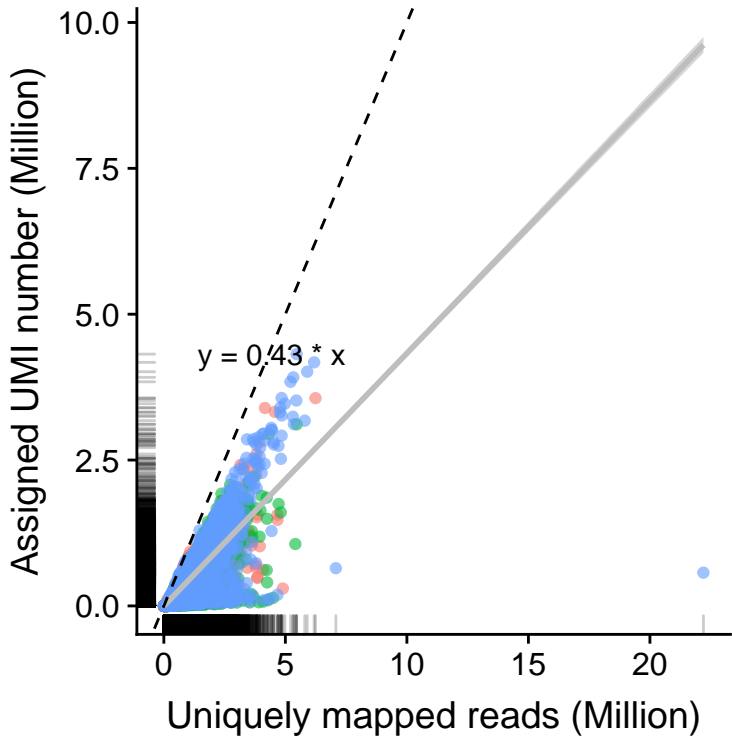
Number of detected genes

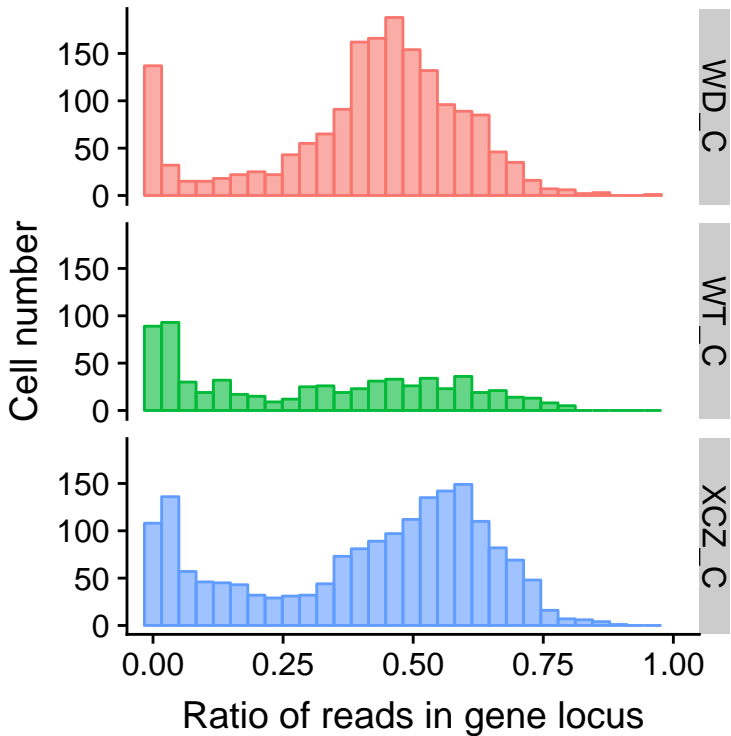
WD\_C

WT\_C

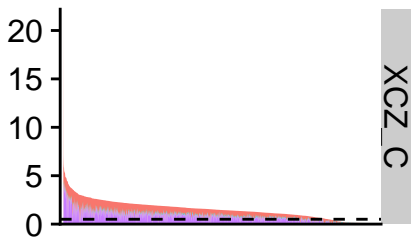
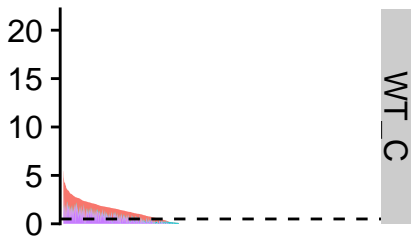
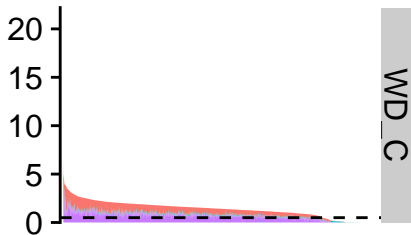
XCZ\_C



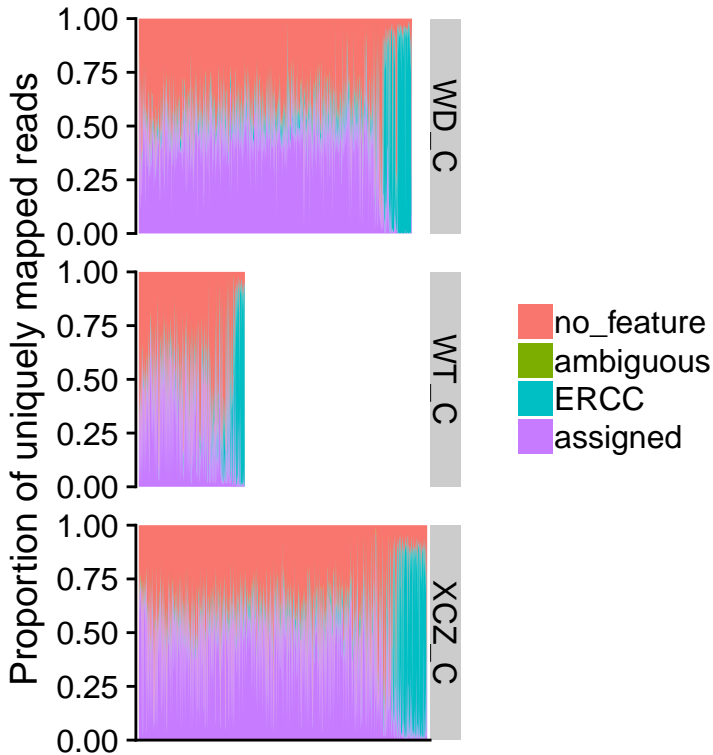


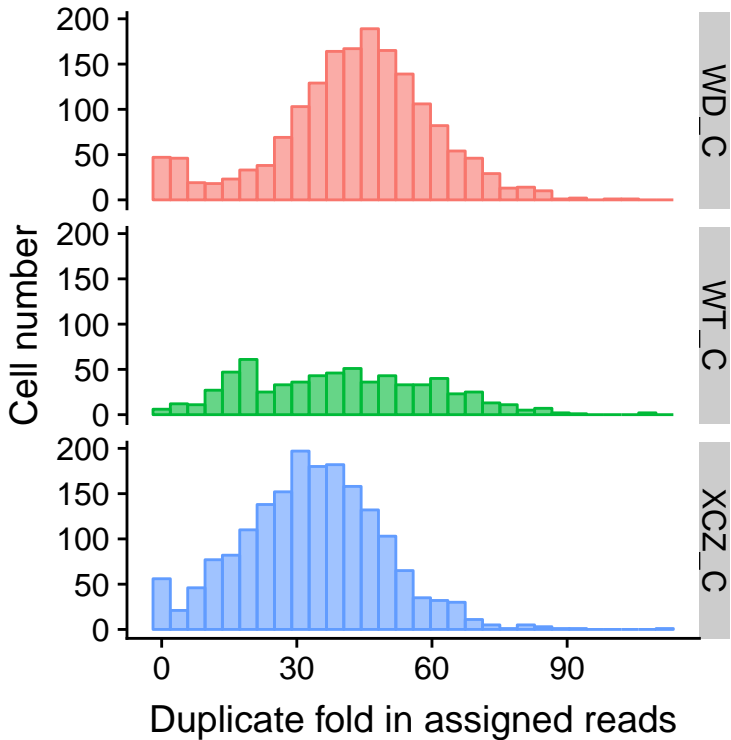


Uniquely mapped reads (Million)



no\_feature  
ambiguous  
ERCC  
assigned





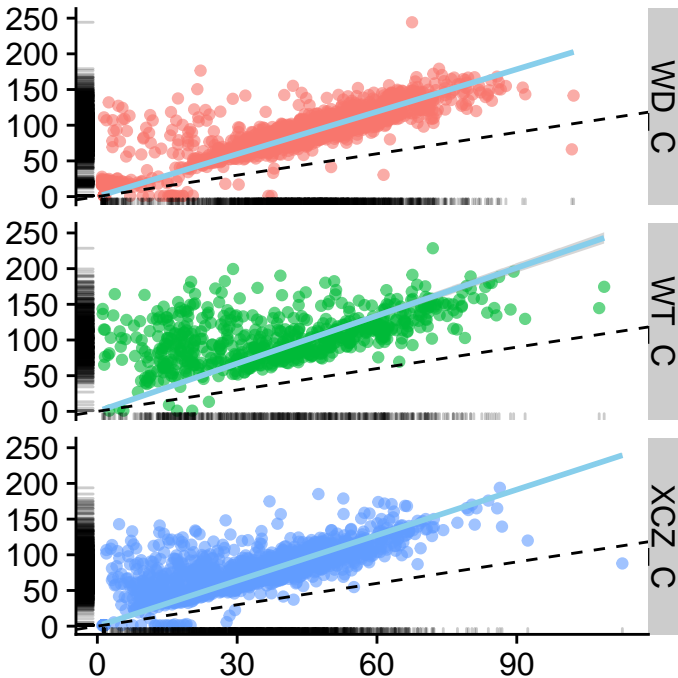
Duplicate fold in ERCC reads

WD\_C

WT\_C

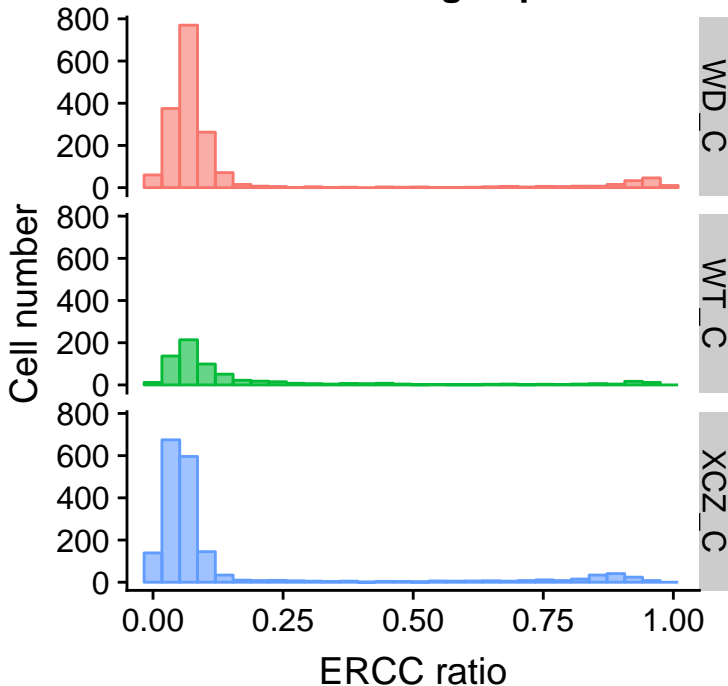
XCZ\_C

Duplicate fold in assigned reads

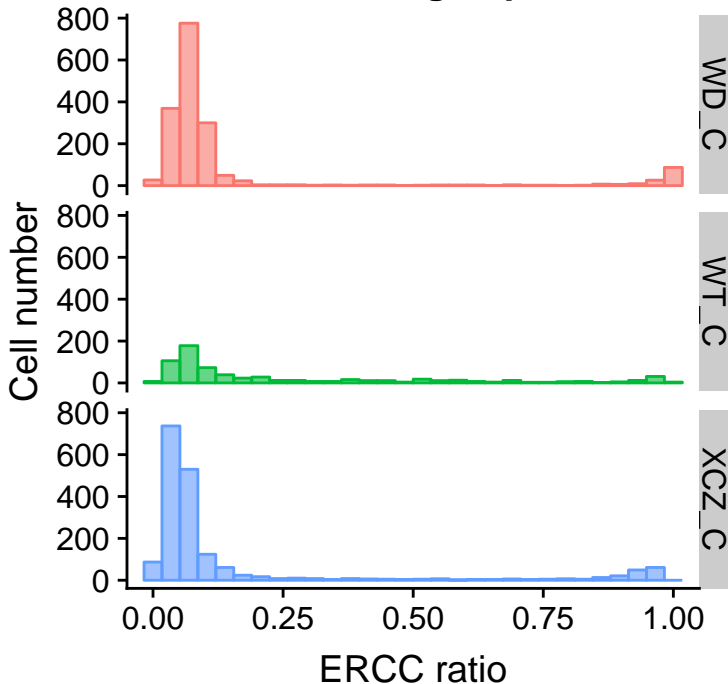




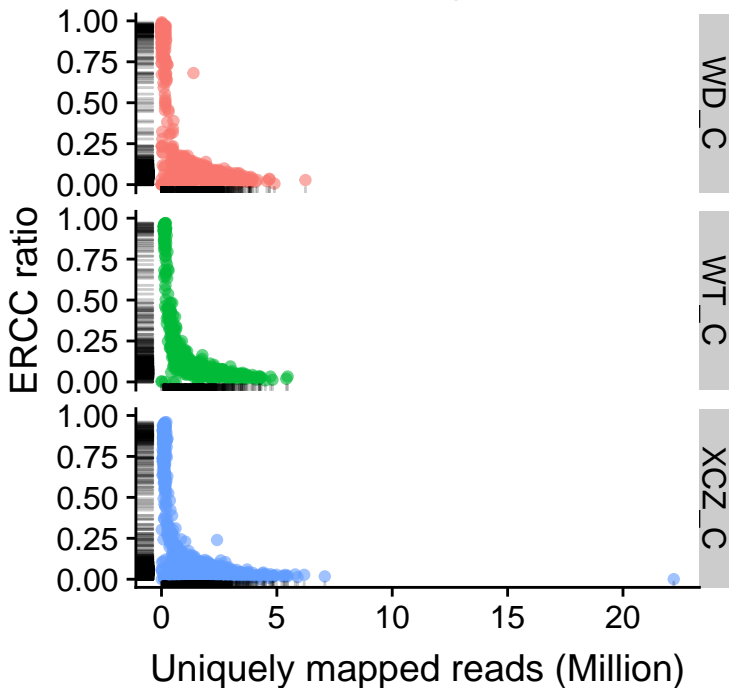
## Before removing duplicates



# After removing duplicates



## Before removing duplicates



## After removing duplicates

