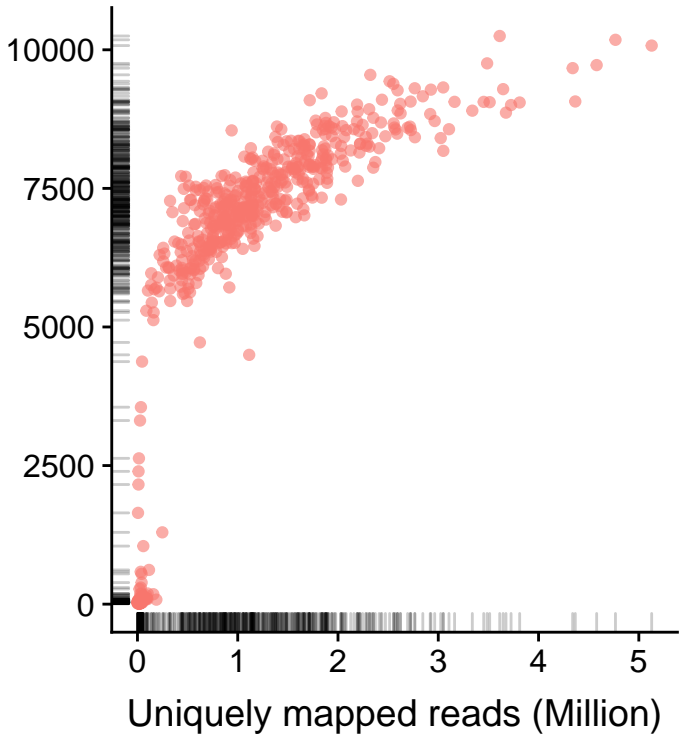


Number of detected genes

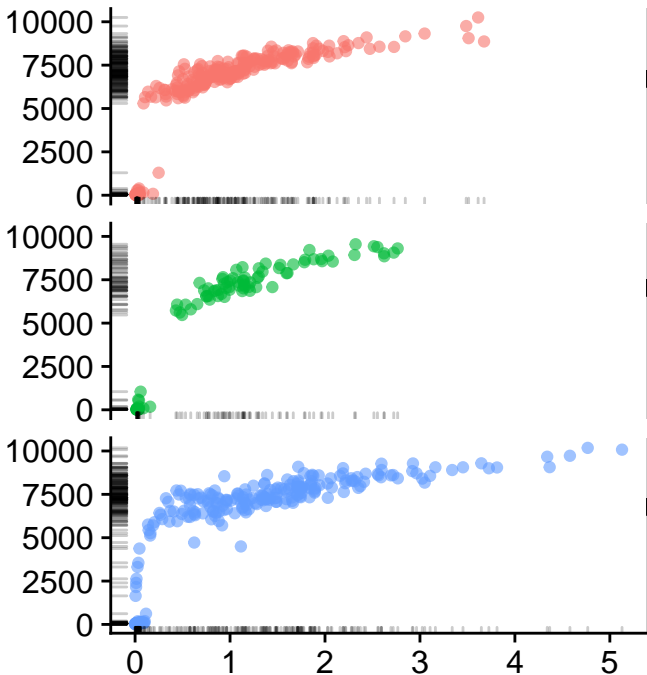


Number of detected genes

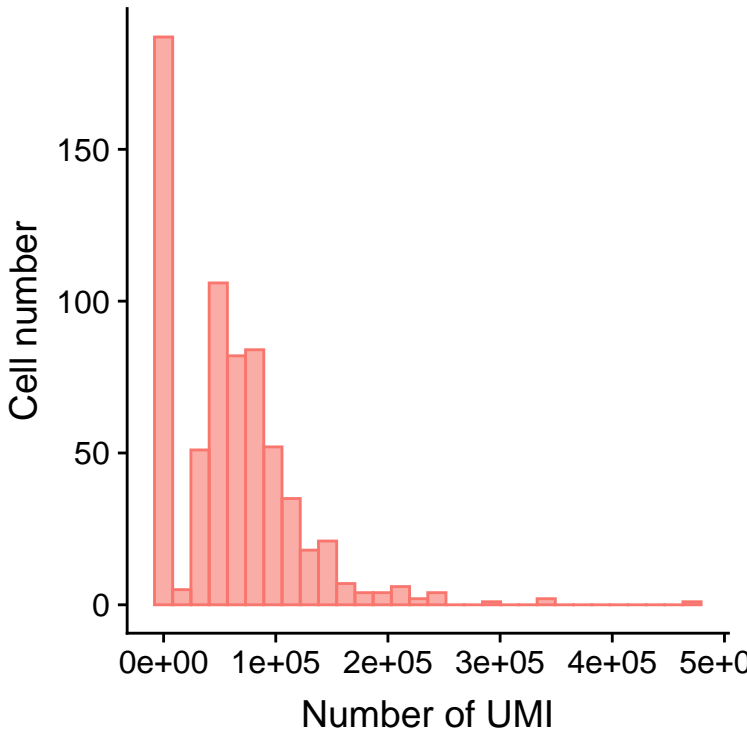
XC_FOXL1

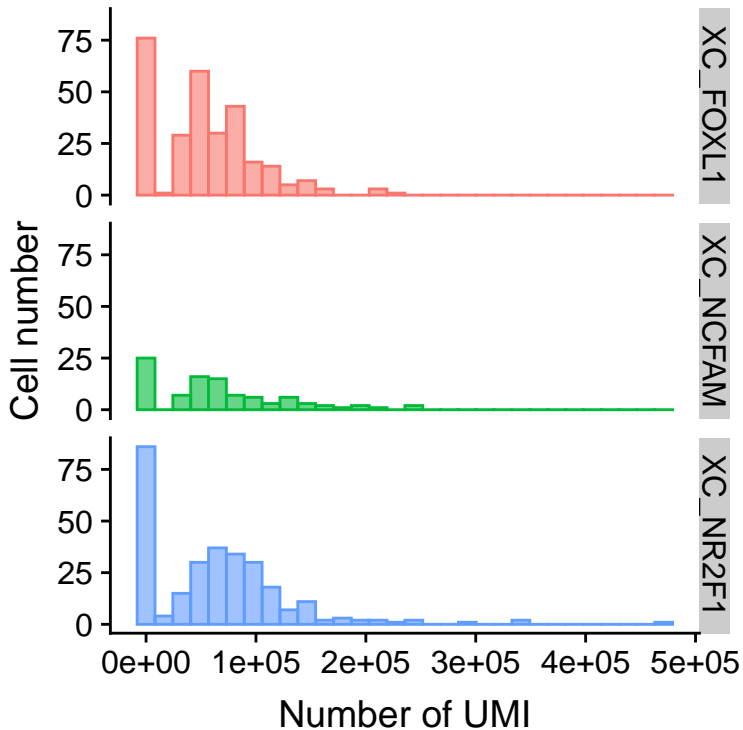
XC_NCFAM

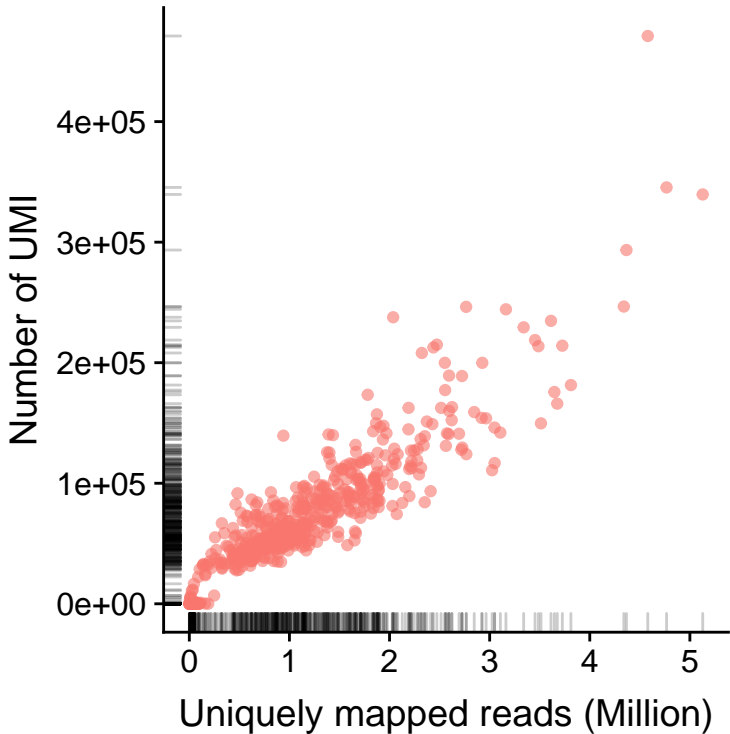
XC_NR2F1

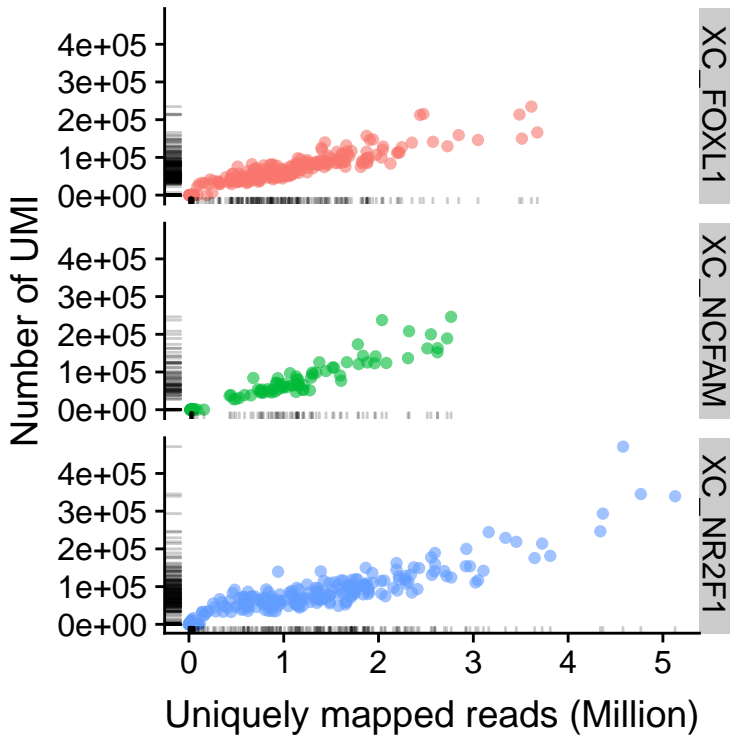


Uniquely mapped reads (Million)

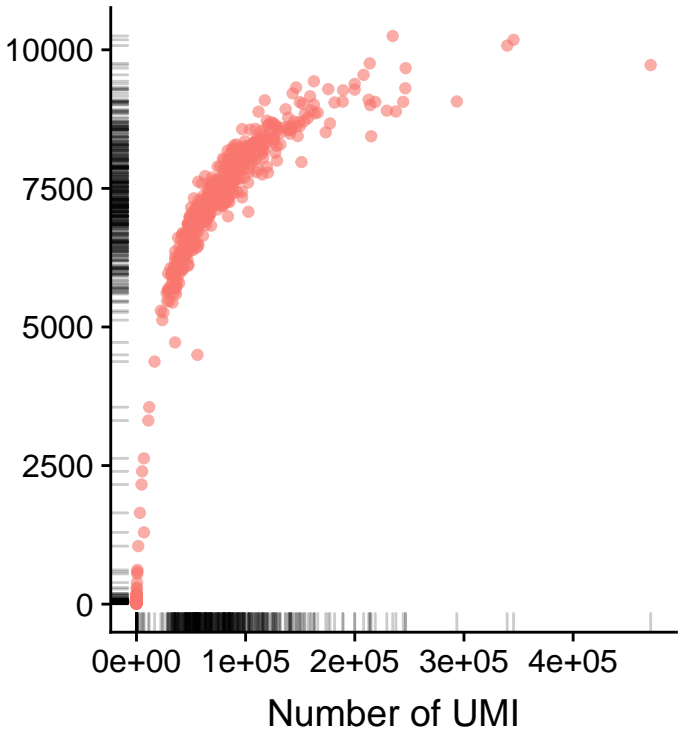








Number of detected genes

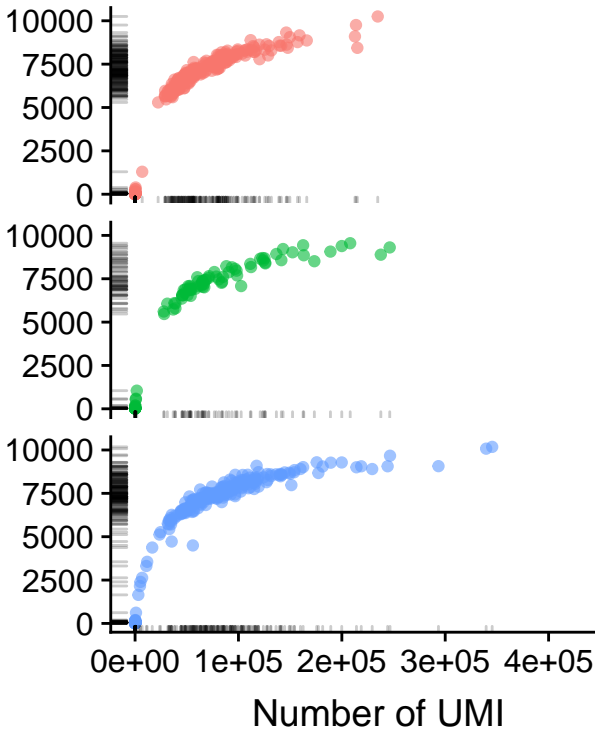


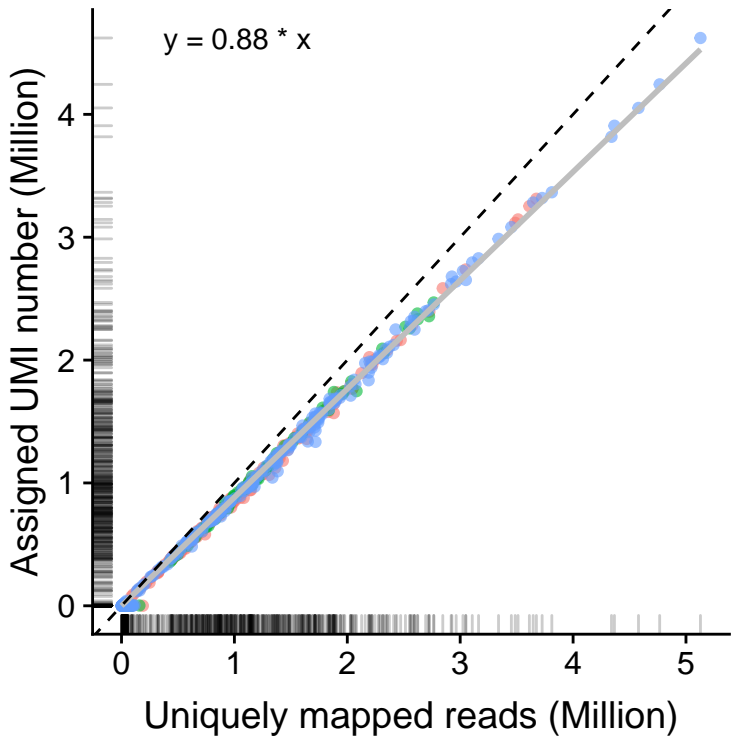
Number of detected genes

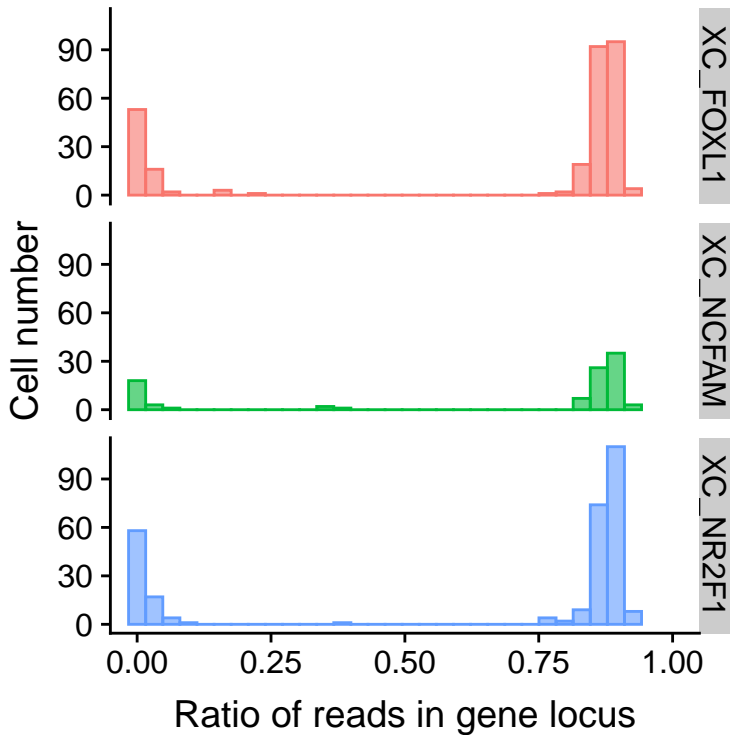
XC_FOXL1

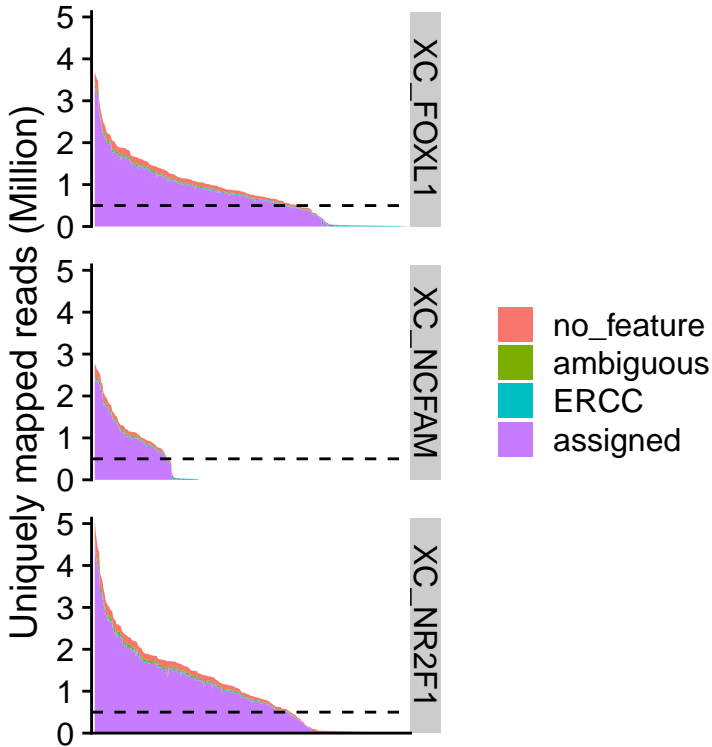
XC_NCFAM

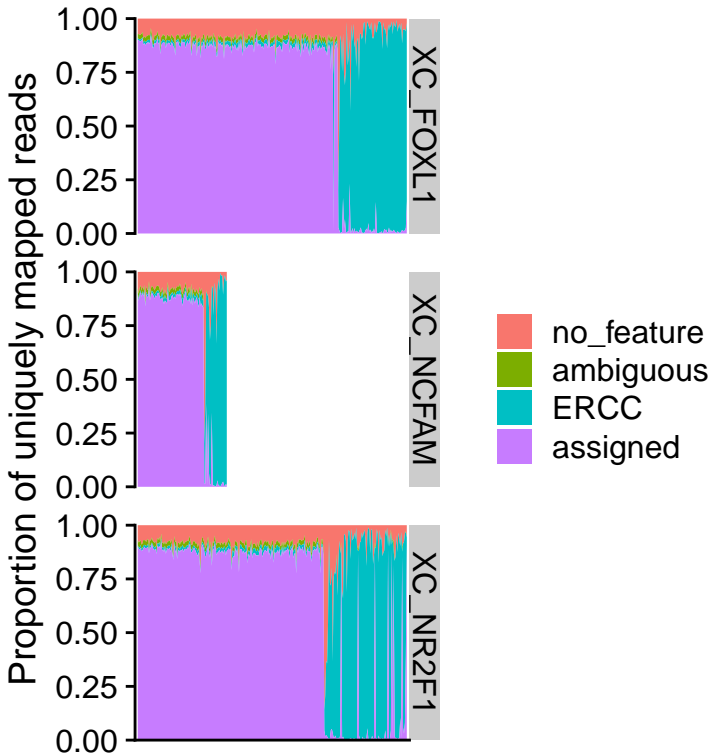
XC_NR2F1

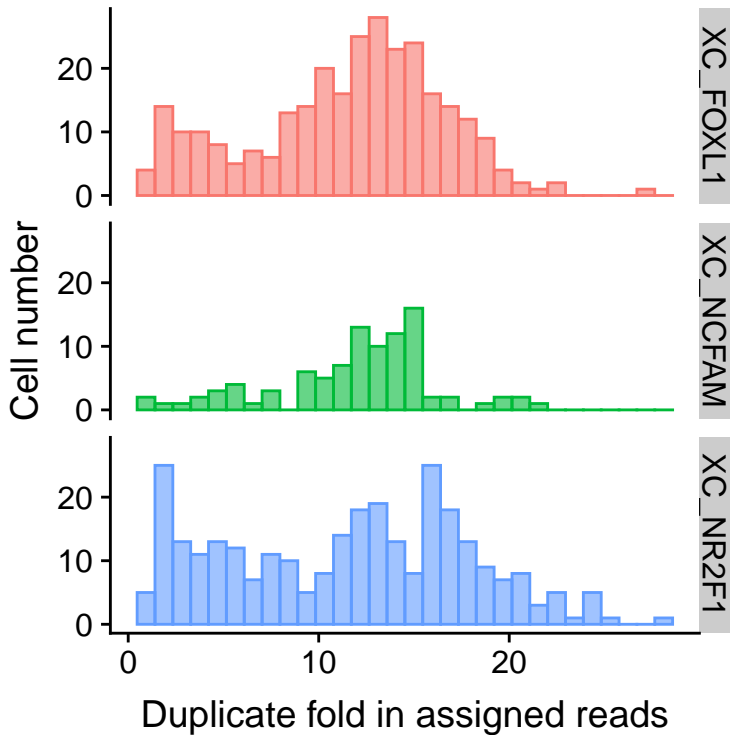












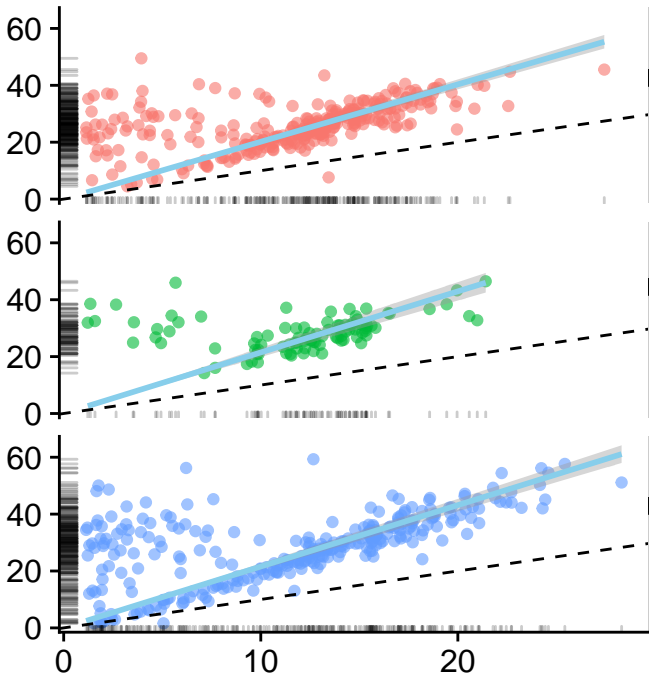
Duplicate fold in ERCC reads

XC_FOXL1

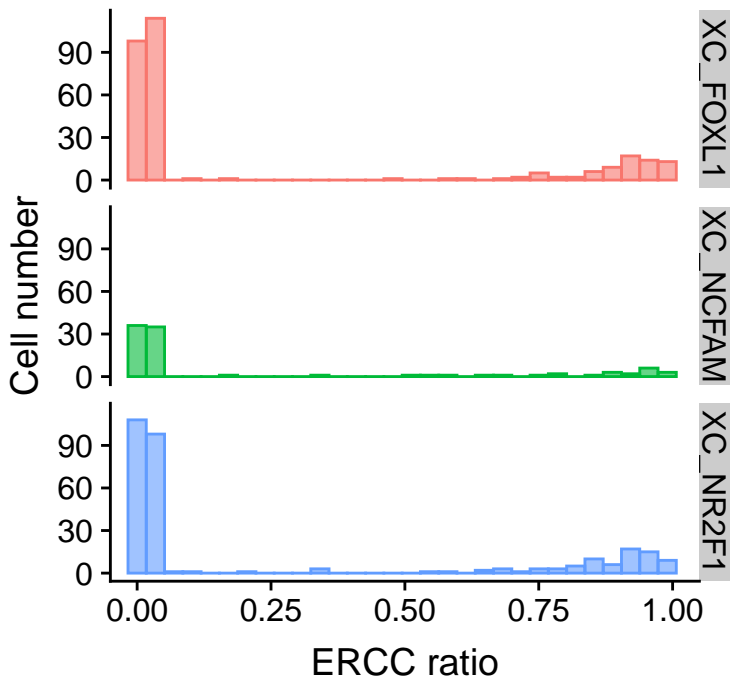
XC_NCFAM

XC_NR2F1

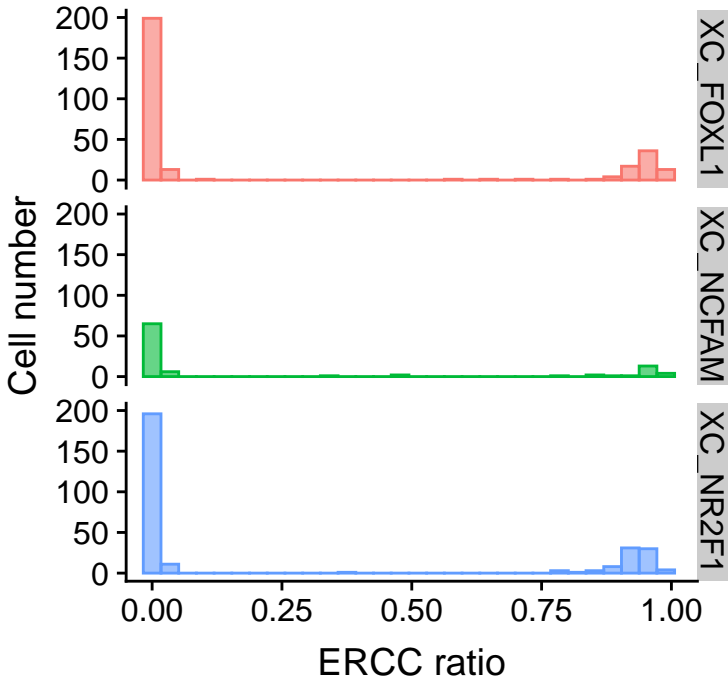
Duplicate fold in assigned reads



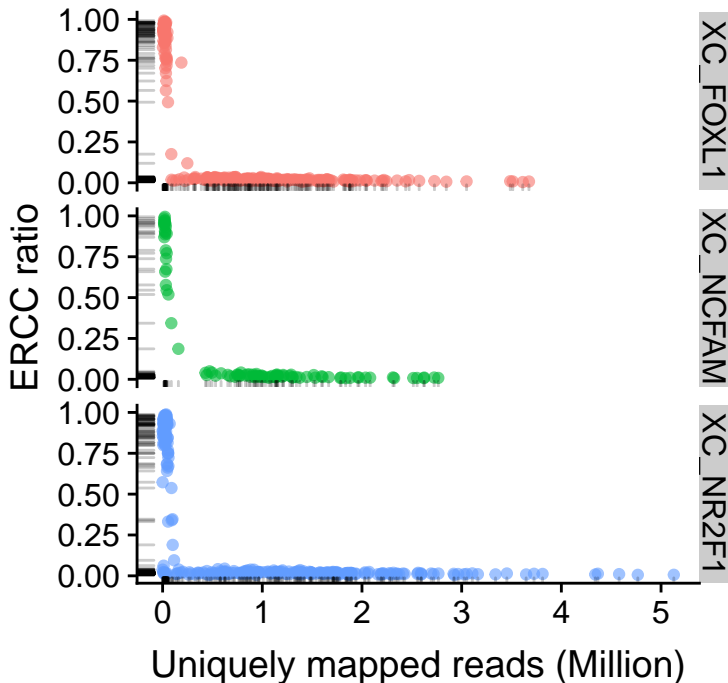
Before removing duplicates



After removing duplicates



Before removing duplicates



After removing duplicates

