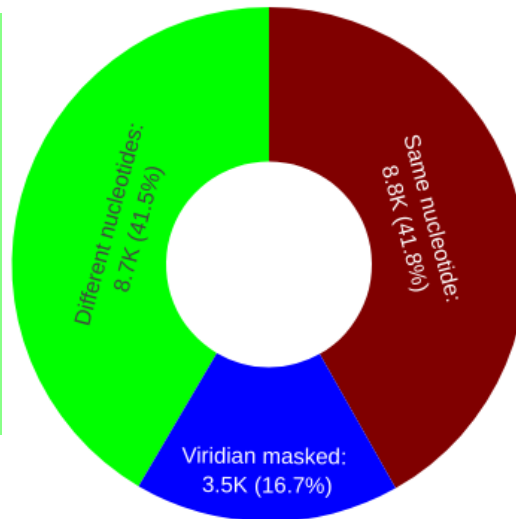
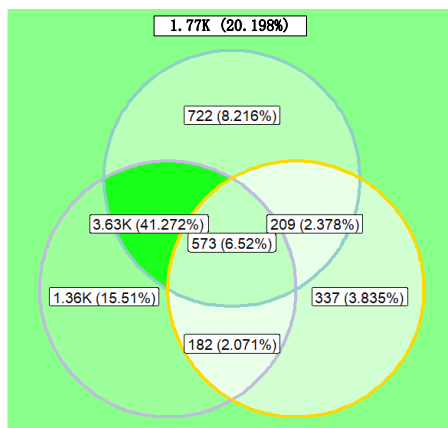
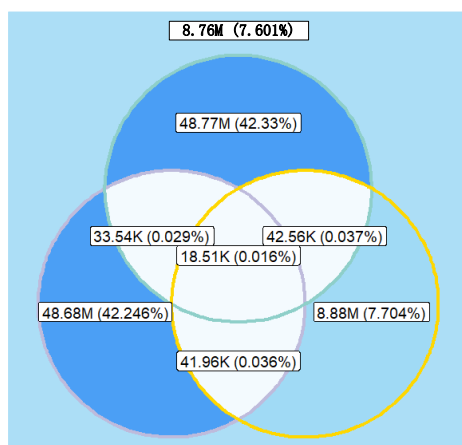
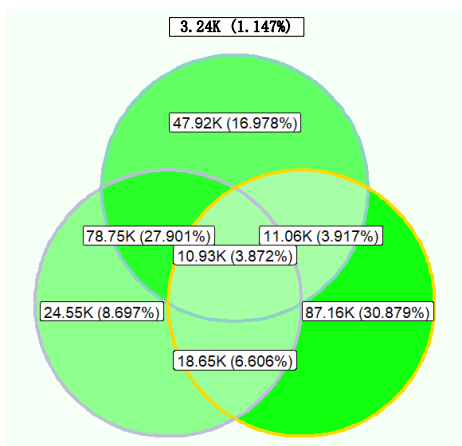
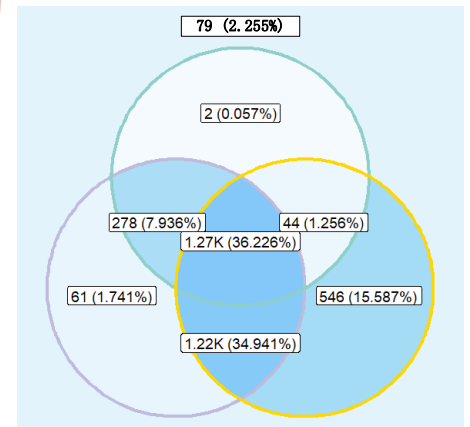
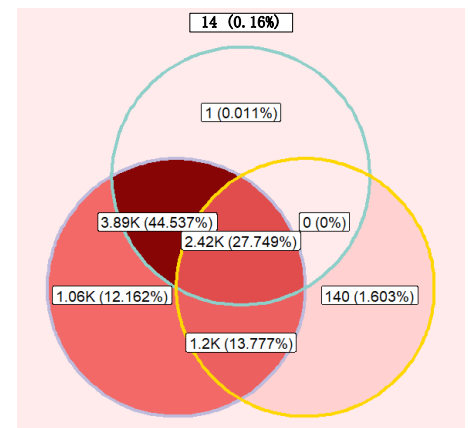


# Sequence errors inferred by MAPLE

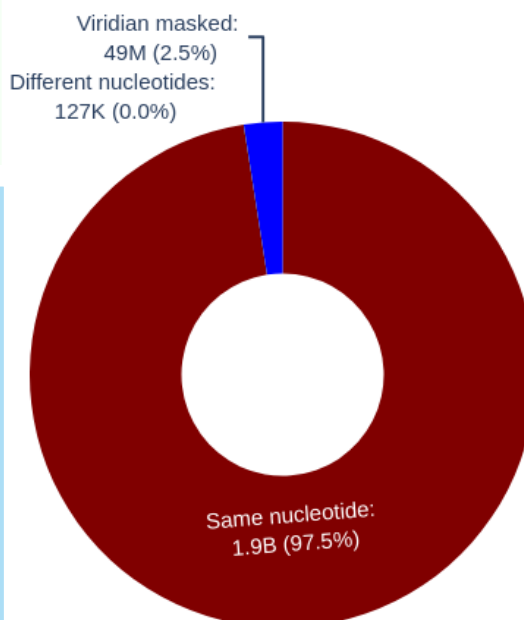


— Coverage  
— Allele Frequency

— Phred-scaled strand  
bias at this position



## All Positions



— Same nucleotide  
— Viridian masked  
— Different nucleotides

