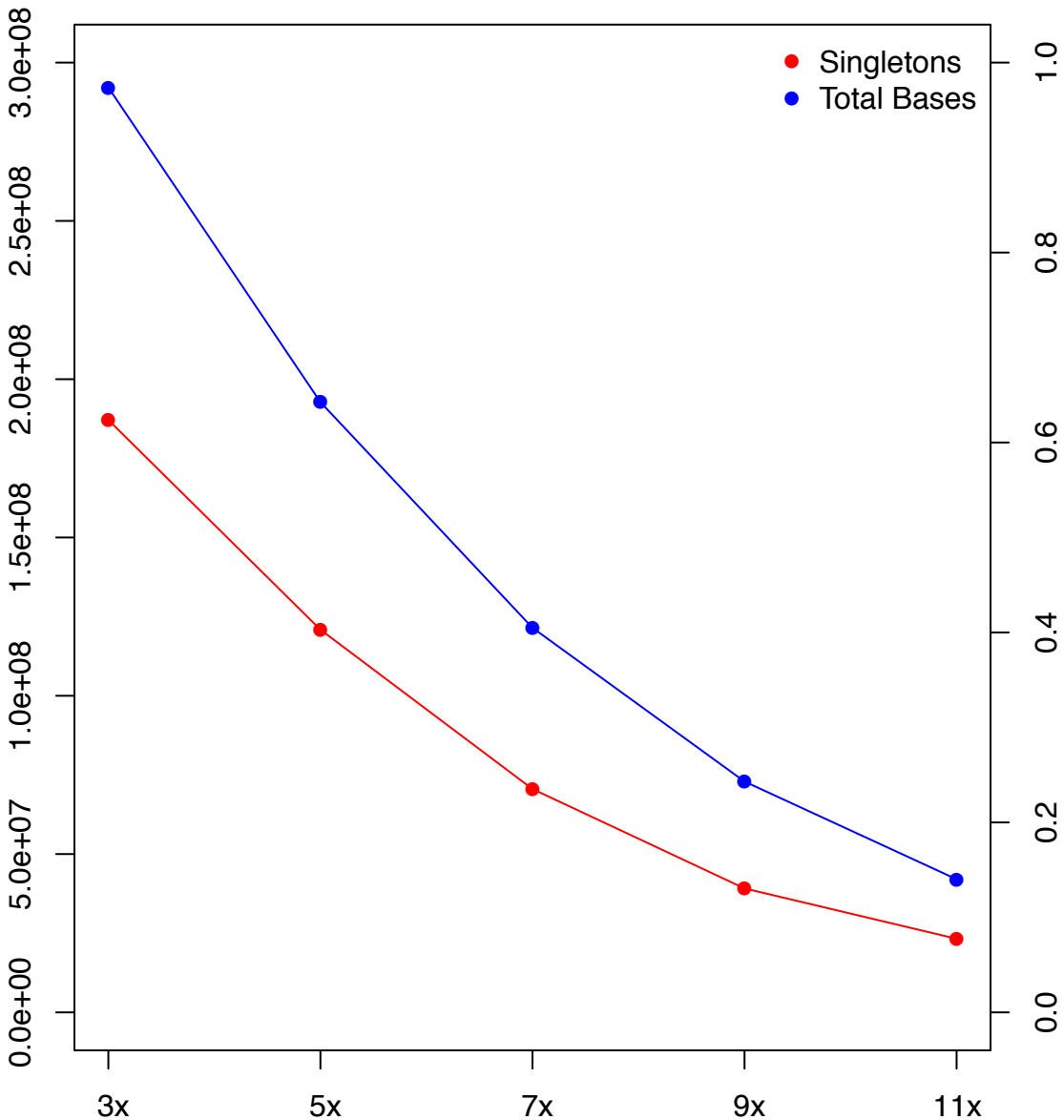


Total Bases in Alignments



Minimum Read Depth

• Singletons
• Total Bases

Number of Singletons/Locus