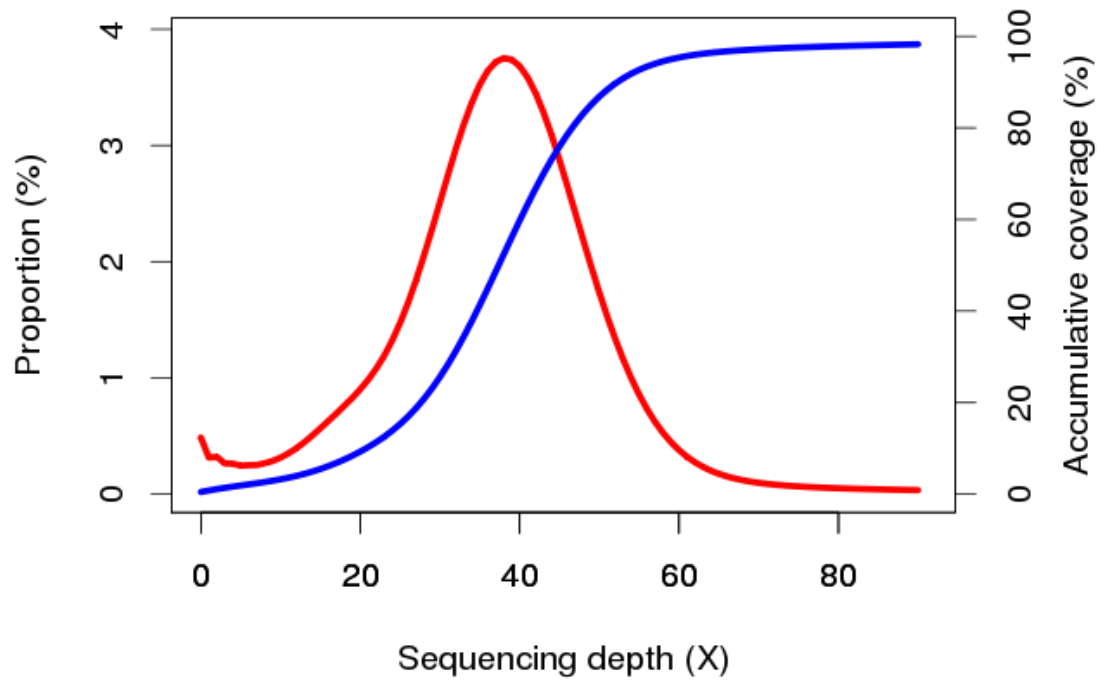




Supplementary Figure 3: Distribution of the read depth for the *de novo* assembled *S. caffer* genome. The x-axis is the number of reads aligned to a nucleotide position; the y-axis is the percentage of such genome positions. The mean sequencing depth is 38X.