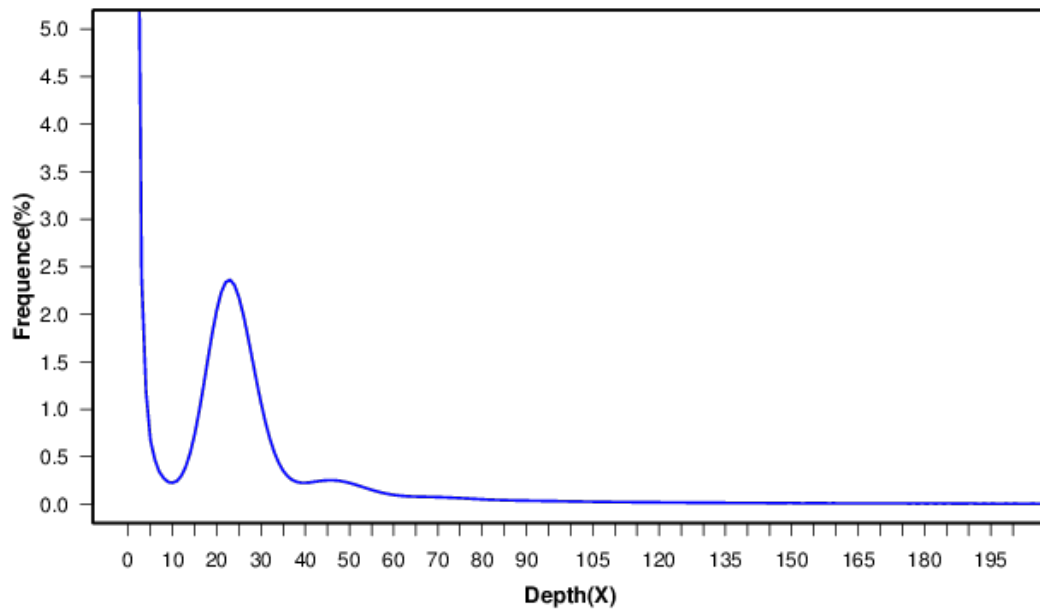**17–mer Depth Distribution Curve**

Figure S2. Genome size and heterozygosity of *A. montana* estimated using 17 *k*-mer distribution. It can be observed from the figure that the K-mer distribution curve is an abnormal Poisson distribution, showing a single peak distribution, and there is a peak near 23x. At the same time, the kmer curve has a certain tailing phenomenon, and the genome is a low repeat sequence content.