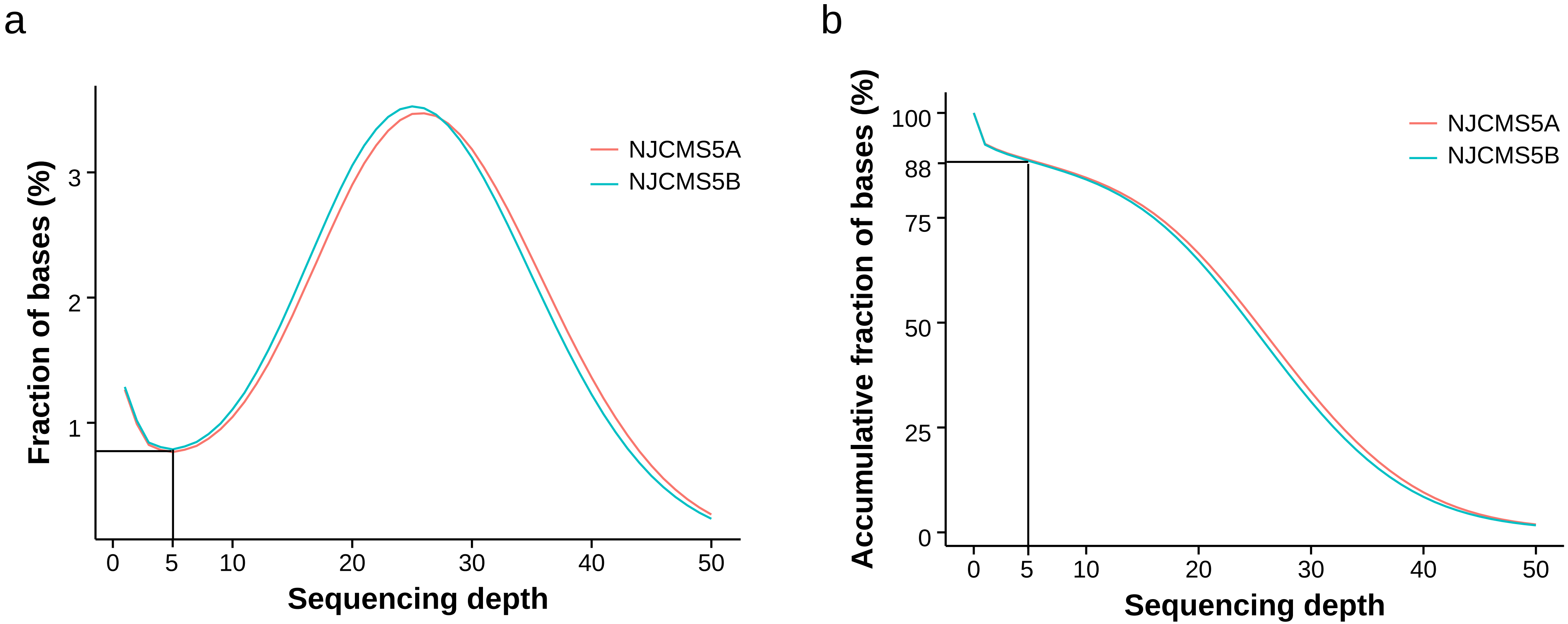

Figure S1 Data analysis of soybean genome-wide methylation sequencing. (a) Coverage of each signle-base site on the genome both NJCMS5A and NJCMS5B; The x-axis represents the coverage of sequencing depth; the y-axis represents the percentage of each signle-base site in the whole genome (Yi); **(b)** Accumulative coverage of genome sequencing both NJCMS5A and NJCMS5B；The y-axis represents the accumulative percentage of each signal-base site in the whole genome (Yj) Yj>=Yi.