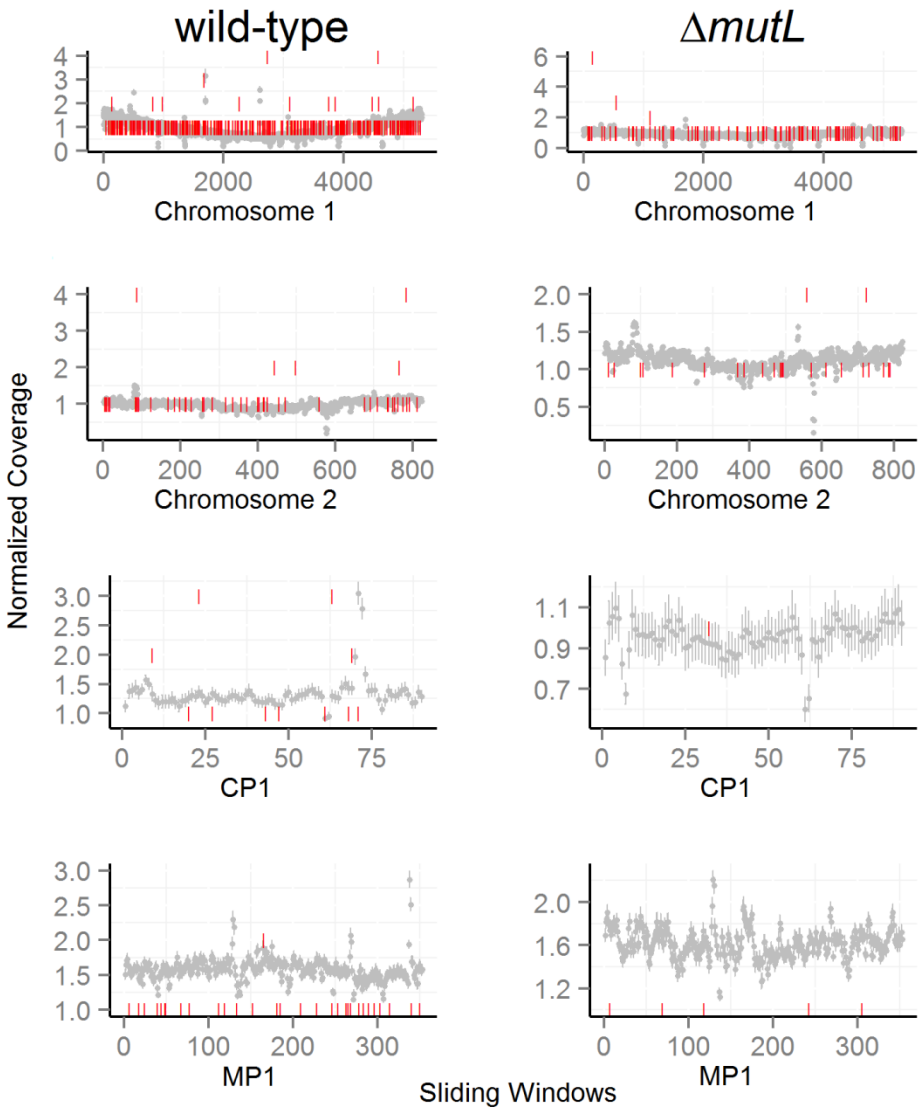

Figure S1. Sequencing depth of coverage and mutation distribution in chromosomes and plasmids. Gray dots with standard error bars show the normalized coverage; red bars show mutations and their heights denote mutation numbers; note the y-axis labels are shared by the gray dots and red bars. Each line's normalized depth of coverage at a sliding window was calculated by dividing the mean coverage of the 1-kb sliding window with the mean coverage of the whole genome. The mean and standard error of all lines' normalized coverage at the sliding window was then plotted. x-axis shows genomic position in sliding windows.