

Figure 1 displays three panels (a, b, c) showing the distribution of nucleotide frequencies (A, C, G, T) across different genomic regions (MBFV-NC_009029.2 to MBFV-NC_032088.1) for the three species (H. pylori, H. cina, H. cina).

Panel (a) shows the distribution of nucleotide frequencies (A, C, G, T) across different genomic regions (MBFV-NC_009029.2 to MBFV-NC_032088.1) for the three species (H. pylori, H. cina, H. cina). The x-axis represents the genomic region, and the y-axis represents the frequency of each nucleotide (A, C, G, T). The distribution is highly variable across the regions, with A and G being the most frequent nucleotides in most regions.

Panel (b) shows the distribution of nucleotide frequencies (A, C, G, T) across different genomic regions (MBFV-NC_009029.2 to MBFV-NC_032088.1) for the three species (H. pylori, H. cina, H. cina). The x-axis represents the genomic region, and the y-axis represents the frequency of each nucleotide (A, C, G, T). The distribution is highly variable across the regions, with A and G being the most frequent nucleotides in most regions.

Panel (c) shows the distribution of nucleotide frequencies (A, C, G, T) across different genomic regions (MBFV-NC_009029.2 to MBFV-NC_032088.1) for the three species (H. pylori, H. cina, H. cina). The x-axis represents the genomic region, and the y-axis represents the frequency of each nucleotide (A, C, G, T). The distribution is highly variable across the regions, with A and G being the most frequent nucleotides in most regions.