

A scatter plot showing the relative frequency of nucleotide mutations in SARS-CoV-2 across the genome. The x-axis represents the Nucleotide Position (0 to 2500), and the y-axis represents the Relative Frequency (0.0 to 1.0). The plot is divided into four horizontal bands by dashed lines at y=0.25, 0.5, and 0.75. Mutations are represented by colored circles: red for A, G, and C, and teal for T. The size of the circle indicates the relative frequency of the mutation. Several mutations are labeled with their position and amino acid change: M58Q, S126F, E198K, I297V, D685G, K771N, and K771S. The plot shows a high density of mutations in the 0-500 position range, particularly in the 0.25-0.5 relative frequency band. The 0.75-1.0 band shows a high density of mutations in the 1500-2500 position range, particularly in the 0.75-1.0 relative frequency band.

- nonsyn

- nonsyn

● syn

- NA

n

● 5

● 10

● 15

● 20