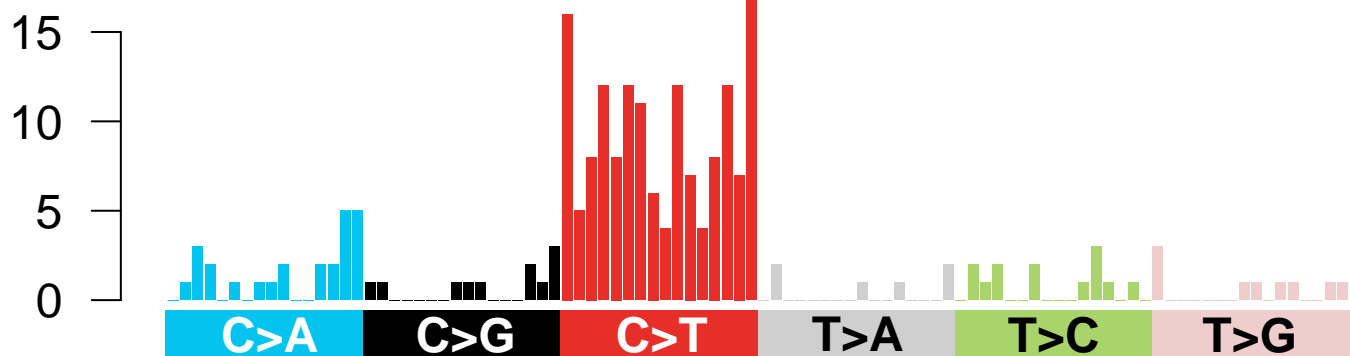
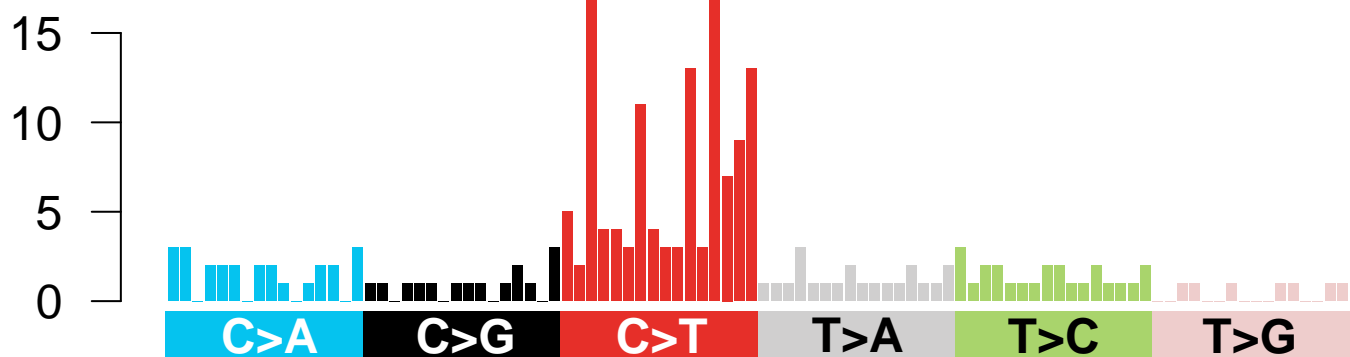


A bar chart illustrating the distribution of 100,000 random mutations across six categories. The categories are color-coded and labeled at the bottom: C>A (blue), C>G (black), C>T (red), T>A (grey), T>C (green), and T>G (pink). The y-axis represents the number of mutations, with a scale from 0 to 100,000. The C>T category shows the highest frequency, with a prominent peak reaching nearly 100,000 mutations. The T>C category shows a moderate frequency, peaking around 20,000 mutations. The other categories (C>A, C>G, T>A, and T>G) show lower frequencies, generally below 10,000 mutations.



A bar chart illustrating the distribution of 1000 random mutations across six categories. The y-axis represents the number of mutations, ranging from 0 to 1000. The x-axis categories are C>A (blue), C>G (black), C>T (red), T>A (grey), T>C (green), and T>G (pink). The C>T category shows the highest frequency, with several bars exceeding 1000 mutations.



A bar chart illustrating the distribution of nucleotide substitutions across a genomic region. The x-axis represents genomic positions, and the y-axis represents the frequency of each substitution type. The chart is divided into six color-coded categories: C>A (blue), C>G (black), C>T (red), T>A (grey), T>C (green), and T>G (pink). The C>T category shows the highest frequency, particularly in the central region, while C>A and T>G are more frequent in the flanking regions.

