

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 smaller peak around 20,000 mutations. The other categories (C>A, C>G, T>A, and T>G) show much lower frequencies, generally below 10,000 mutations.

A bar chart illustrating the distribution of 1000 random mutations across six categories: C>A, C>G, C>T, T>A, T>C, and T>G. The x-axis represents the mutation categories, and the y-axis represents the frequency of mutations. The C>T category shows the highest frequency, peaking at 1000 mutations. The T>C category shows the lowest frequency, peaking at approximately 100 mutations. The C>A, C>G, T>A, and T>G categories show intermediate frequencies, peaking at approximately 200, 100, 100, and 100 mutations respectively.

Mutation Category	Frequency (Approximate)
C>A	200
C>G	100
C>T	1000
T>A	100
T>C	100
T>G	100

A bar chart illustrating the distribution of nucleotide substitutions across a sequence. The y-axis represents the frequency, ranging from -5 to 10. The x-axis is divided into six color-coded regions corresponding to different substitution types: C>A (blue), C>G (black), C>T (red), T>A (grey), T>C (green), and T>G (pink). The chart shows a high frequency of C>T substitutions in the middle region and T>C substitutions in the right region.