Sector	1	2	3	4	5	6
Total Mutations	3690	1038	1036	4827	85	9
Expected Number	2233.7	2582.8	1465.9	116.9	767.84	628.24
Chi-squared Value	949.41	23551	126.07	12325	607.25	610.37
p value (df = 1)	7.80×10^{-202}	0	8.64×10^{-25}	0	6.35×10^{-128}	1.35×10^{-128}

Table 2. Chi-squared test of Mutation Enrichment in Sectors. Chi squared tests were performed on each sector to test the null hypothesis that mutations occur evenly across residues. The expected counts of mutation were generated from the proportions of the sectors in the whole sequence multiplied with the number of total mutations.

Source	SS	df	MS	Chi-sq	p value
Groups	2.66×10^6	5	5.32×10^5	56.46	6.54×10^{-11}
Error	3.52×10^7	799	4.41×10^4		
Total	3.79×10^7	804			

Table 3. Kruskal-Wallis Test of Somatic Mutation Abundance in Non-Human Sequences. We used the Kruskal-Wallis test because the data was not parametric. The single factor was sector index, and this table validated that the sectors were a factor on the distribution of mutations in non-human sequences.

Sector	Sector	p value
1	2	0.0012*
1	3	0.984
1	4	7.49×10^{-6}*
1	5	0.210
1	6	0.0692
2	3	0.126
2	4	0.376
2	5	5.53×10^{-4}*
2	6	0.0037*
3	4	0.0024*
3	5	0.118
3	6	0.0447*
4	5	1.29×10^{-5}*
4	6	5.28×10^{-4}*
5	6	0.683

Table 4. Post-hoc tests of Mutation Abundance in Sectors. Tukey's HSD test is used to compare the average counts of mutated sequences in sectors. Although the average counts from low to high is sector 4 < 2 < 3 < 1 < 5 < 6, the results do not show a clear alternative hypothesis.