|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| 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) |  | 0 |  | 0 |  |  |

Table S2. **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 |  | 5 |  | 56.46 |  |
| Error |  | 799 |  |  |  |
| Total |  | 804 |  |  |  |

Table S3. **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 | \* |
| 1 | 5 | 0.210 |
| 1 | 6 | 0.0692 |
| 2 | 3 | 0.126 |
| 2 | 4 | 0.376 |
| 2 | 5 | \* |
| 2 | 6 | 0.0037\* |
| 3 | 4 | 0.0024\* |
| 3 | 5 | 0.118 |
| 3 | 6 | 0.0447\* |
| 4 | 5 | \* |
| 4 | 6 | \* |
| 5 | 6 | 0.683 |

Table S4. **Post-hoc tests of Mutation Abundance in Sectors**. We used the Tukey’s HSD test 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.