S4 Table. Relative distribution of mutations within the macrodomains of *E. coli*.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Ori MD | NSRight | Ter MD | Right MD | Left MD | NSLeft | Pearson’s Chi-square† (df = 5) |
| *Aerobic proportion of mutations* |
| BPSs | 0.26 | 0.18 | 0.19 | 0.07 | 0.15 | 0.16 | χ2 = 2.67, *p* = 0.751 |
| SVs | 0.15 | 0.15 | 0.48 | 0.06 | 0.15 | 0.00 | χ2 = 29.47, *p* < 0.001 |
| Indels | 0.23 | 0.00 | 0.23 | 0.23 | 0.08 | 0.23 | χ2 = 10.31, *p* = 0.067†† |
| *Anaerobic proportion of mutations* |
| BPSs | 0.22 | 0.21 | 0.14 | 0.14 | 0.08 | 0.22 | χ2 = 5.31, *p* = 0.379 |
| SVs | 0.15 | 0.15 | 0.48 | 0.06 | 0.15 | 0.00 | χ2 = 23.68, *p* < 0.001 |
| Indels | 0.16 | 0.21 | 0.16 | 0.05 | 0.16 | 0.26 | χ2 = 0.63, *p* = 0.987†† |
| *Expected proportion of mutations for even distribution across the genome* |
| BPSs | 0.24 | 0.19 | 0.16 | 0.10 | 0.12 | 0.19 |  |
| GCRs | 0.18 | 0.17 | 0.41 | 0.07 | 0.09 | 0.07 |  |
| Indels | 0.19 | 0.13 | 0.19 | 0.13 | 0.13 | 0.25 |  |

†Null hypothesis is that mutations are distributed evenly across the genome.

††The criteria for the statistical test was not met as expected cell count was < 5.