**Supplementary Table 5: Intra-species polymorphism in *rpoB* and *rpoC* genes and inter-species substitution frequency in *rpoB* and *rpoC* comparison between *Ec, Kp,* and *Se* as well as between *Sa* and *Sp*.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Comparison | Bacteria group | Bacteria | *rpoB* | *rpoC* |
| Intra-species\*  (polymorphism) | g-proteobacteria | *Ec* | 50 | 39 |
| *Kp* | 15 | 12 |
| *Se* | 111 | 55 |
| Firmicutes | *Sa* | 25 | 33 |
| *Sp* | 177 | 137 |
| Inter-species\*\*  (substitution) | g-proteobacteria | *Ec* and *Kp* | 257 | 273 |
| *Ec* and *Se* | 243 | 243 |
| *Se* and *Kp* | 242 | 291 |
| Firmicutes | *Sa* and *Sp* | 1222 | 1251 |

\* We have studied polymorphism and substitution in RNA polymerase genes *rpoB* and *rpoC* of each bacterium. Base substitutions are found out by doing inter species comparison of the reference gene sequence of *rpoB* and *rpoC*. Maximum number of polymorphisms in any strain is presented in the table.

\*\* Inter-species base substitution in *rpoB* and *rpoC* genes is found out by comparing reference sequence of two species belonging to a bacterial group. Intra-species polymorphisms in all the five bacteria are always found to be smaller than the inter-species base substitution values.