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| **S3 Table.** **Best model selection.** Estimating the best model of molecular substitution inferred using Log Bayes Factors (LBF) from Bayesian posterior distributions in Mr Bayes. Rate variation for tested models - gamma distributed rate variation across sites (gamma); gamma distributed with proportion of invariable sites (invgamma); rate variation with proportion of invariable sites (propinv); equal rate variation across sites (equal). | | | | |
| **Model** | **Harmonic Mean** | **LBF** | **Model**  **probability** |
| GTR + invgamma | -3081.46 | 0 | 0.980719 |
| GTR + propinv | -3083.54 | -4.154 | 0.015399 |
| GTR + gamma | -3099.49 | -36.062 | 2.14E-16 |
| GTR + equal | -3201.17 | -239.428 | 1.02E-104 |
| F81 + invgamma | -3451.05 | -739.180 | 0.00E+00 |
| F81 + propinv | -3409.53 | -656.136 | 1.08E-285 |
| F81 + gamma | -3447.53 | -732.140 | 0.00E+00 |
| F81 + equal | -3513.69 | -864.460 | 0.00E+00 |
| HKY + invgamma | -3126.01 | -89.100 | 1.98E-39 |
| HKY + propinv | -3084.23 | -5.532 | 0.003882 |
| HKY + gamma | -3093.67 | -24.426 | 2.42E-11 |
| HKY + equal | -3207.02 | -251.114 | 8.59E-110 |
| mixed + invgamma | -3099.09 | -35.256 | 4.79E-16 |
| mixed + propinv | -3088.50 | -14.084 | 7.50E-07 |
| mixed + gamma | -3091.90 | -20.884 | 8.35E-10 |
| mixed + equal | -3207.86 | -252.802 | 1.59E-110 |