

**Table S.5 - Insertion/deletion rates inferred from the maximum likelihood analysis assuming different rates on each branch of the phylogeny (cut-off: expect value less than  $10^{-10}$  and  $> 70\%$  match length)**

| Rate           | Reversible |         | Deleted once <sup>a</sup> |         |
|----------------|------------|---------|---------------------------|---------|
|                | MLE        | LnL     | MLE                       | LnL     |
| constant $\mu$ | 0.97       | -8257.3 | 0.93                      | -8329.8 |
| $\mu_1$        | 1.02       |         | 0.96                      |         |
| $\mu_2$        | 0.46       |         | 0.46                      |         |
| $\mu_3$        | 4.60       |         | 2.96                      |         |
| $\mu_4$        | 13.85      | -7981.3 | 20.15                     | -8014.5 |
| $\mu_5$        | 0.66       |         | 0.71                      |         |
| $\mu_6$        | 2.13       |         | 2.00                      |         |
| $\mu_7$        | 1.95       |         | 1.75                      |         |
| $\mu_8$        | 0.001      |         | 0.01                      |         |

<sup>a</sup>Genes can not be regained after deletion.