**S10 Table.** Summary of positive selection in rodent and carnivore lactoferrin using PAML. Analyses were performed using two independent codon models (F3X4, F61). Selection was inferred by comparing likelihood scores between models that allow for selection (M2, M8) relative models which exclude selection (M1, M7) in this gene. Tree length and dN/dS values are shown for the M8 calculations.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Codon freq.** | ***M1-M2*** | ***M7-M8*** | **Tree length** | **dN/dS (%)** |
| **2δ** | **p-value** | **2δ** | **p-value** |
| **Rodents (10 species)** | F3X4 | 9.0 | 0.011 | 31.0 | <0.0001 | 4.1 | 1.9 (5.1) |
| F61 | 0 | 1.0 | 24.3 | <0.0001 | 3.9 | 2.1 (4.1) |
| **Carnivores (8 species)** | F3X4 | 6.6 | 0.037 | 9.7 | 0.0079 | 1.1 | 4.3 (1.7) |
| F61 | 4.5 | 0.10 | 5.7 | 0.059 | 1.1 | 4.5 (1.2) |