**Table I.** Curation and alignment size of genetic markers in each dataset.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | Download sequences | Number of removed sequences | | | | | Final dataset | Aligment size (bp) |
| Duplicates | No Hylidae species (e.g Phyllomedusidae) and other genetic regions | Imprecise taxonomic labels | Less than 400 bp | Singletons |
| 12s | 5484 | 2718 | 323 | 194 | 453 | 106 | 1690 | 969 |
| 16s | 10986 | 5452 | 1651 | 818 | 240 | 113 | 2712 | 658 |
| COI | 5558 | 1891 | 1284 | 501 | 98 | 47 | 1737 | 658 |
| Cytb | 6484 | 2726 | 312 | 28 | 981 | 12 | 2425 | 651 |