### Table 3: The most frequently recovered topologies across all 10kb windows. RS = *Rhyncomys soricoides*, GD = *Grammomys dolichurus*, RD = *Rhabdomys dilectus*, MM = *Mus musculus*, HA = *Hylomyscus alleni*, MN = *Mastomys natalensis*, PD = *Praomys delectorum*.

|  |  |  |  |
| --- | --- | --- | --- |
| Rank | Topology | # of windows | Proportion of windows |
| 1 | (RS,((GD,RD),(MM,((HA,MN),PD)))); | 23864 | 0.146 |
| 2 | (RS,((GD,RD),(MM,((HA,PD),MN)))); | 23836 | 0.146 |
| 3\* | (RS,((GD,RD),(MM,(HA,(MN,PD))))); | 21509 | 0.131 |
| 4 | (RS,(MM,((GD,RD),((HA,MN),PD)))); | 14417 | 0.088 |
| 5 | (RS,(MM,((GD,RD),((HA,PD),MN)))); | 14321 | 0.0874 |
| 6 | (RS,(MM,((GD,RD),(HA,(MN,PD))))); | 14044 | 0.0858 |
| 7 | (RS,(((HA,PD),MN),(MM,(GD,RD)))); | 11723 | 0.0716 |
| 8 | (RS,(((HA,MN),PD),(MM,(GD,RD)))); | 11308 | 0.0691 |

\*The topology recovered from concatenation of genes or UCEs

### Table 4: Summaries of phylogenies per chromosome.

|  |  |
| --- | --- |
| Chromosome | # of unique topologies recovered |
| 1 | 184 |
| 2 | 123 |
| 3 | 114 |
| 4 | 144 |
| 5 | 134 |
| 6 | 172 |
| 7 | 218 |
| 8 | 133 |
| 9 | 116 |
| 10 | 110 |
| 11 | 93 |
| 12 | 179 |
| 13 | 186 |
| 14 | 173 |
| 15 | 96 |
| 16 | 94 |
| 17 | 188 |
| 18 | 75 |
| 19 | 82 |
| X | 207 |