**Supplementary Table S2.** Log probabilities and number of reticulations detected for testing for introgression and reticulations using PhyloNet for different chromosomal tree sets. The max number of reticulations represents the parameter using in code, while the number detected indicates how many were observed in the resulting reticulating phylogeny.

|  |  |  |  |
| --- | --- | --- | --- |
| **Chromosome** | **Total Log Probability** | **Max Number of Reticulations Allowed** | **Number of Reticulations Detected** |
| ma1 | -2.06E+07 | 5 | 5 |
| ma2 | -1.48E+07 | 5 | 5 |
| ma3 | -1.21E+07 | 5 | 5 |
| ma4 | -4.01E+06 | 5 | 5 |
| ma5 | -4.53E+06 | 5 | 5 |
| ma6 | -2.55E+06 | 5 | 4 |
| ma7 | -2.15E+06 | 3 | 3 |
| Z | -7.85E+05 | 5 | 5 |
| mi1 | -1.53E+06 | 5 | 4 |
| mi2 | -5.98E+05 | 5 | 5 |
| mi3 | -1.05E+06 | 4 | 4 |
| mi4 | -9.20E+05 | 5 | 5 |
| mi5 | -4.23E+05 | 5 | 5 |
| mi6 | -9.86E+05 | 5 | 5 |
| mi7 | -8.64E+05 | 4 | 3 |
| mi8 | -1.29E+06 | 4 | 4 |
| mi9 | -9.94E+04 | 5 | 5 |
| mi10 | -2.16E+05 | 5 | 5 |
| All-chromosomes | -6.99E+07 | 5 | 6 |