Table S3. ddRAD assembly statistics for phylogenetic analyses.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| *Minimum samples per locus* | *Loci* | *Variable sites* | *Parsimony informative sites* | *Alignment length (bp)* | *% missing sites in alignment* |
| 4 | 170,742 | 865,883 | 376,685 | 13,771,990 | 86% |
| 20 | 34,953 | 253,130 | 192,551 | 2,810,232 | 63% |
| 40 | 9,584 | 77,410 | 44,691 | 765,090 | 47% |