Supplemental Table Captions

**Supplemental Table 1.** Appendix of samples, taxon sets analyzed, hybrid index estimates, and raw sequencing data. SampleID corresponds to a sequencing replicate for an individual. Columns A-K is sample information, L-N lists taxon sets, O-R indicates hybrid index from three different population genomic data sets, the first containing 12 diagnostic SNPs, the second corresponding to one SNP per locus, and the third consisting of the full set of SNPs. Lemmon and Juenger (2017) indicates the hybrid index estimates based on microsatellites taken from that paper, S-AI are summary statistics from the raw sequence data.

**Supplemental Table 2.** Characteristics of target loci evaluated at the phylogenetic level.

**Supplemental Table 3.** Characteristics of target loci evaluated at the phylogeography level.

**Supplemental Table 4.** Characteristics of target loci evaluated at the population genomic level.

**Supplemental Table 5.** Locus quality metric to answer the question: what class of target loci produce the highest supported gene trees? For example, "TestStat=1/2" refers to the test statistic comparing the first and second highest ranked locus sets for this metric.

**Supplemental Table 6.** Locus quality metric to answer the question: what class of target loci produces the least discordant gene trees?

**Supplemental Table 7.** Locus quality metric to answer the question: what class of target loci produce alignments with the most variants per locus?

**Supplemental Table 8.** Locus quality metric to answer the question: what class of target loci produce the most diagnostic SNPs per sequencing effort? Note that all results are from POP taxon set.

**Supplemental Table 9.** Locus quality metric to answer the question: what class of target loci have the cleanest mapping during assembly?

**Supplemental Table 10.** Locus quality metric to answer the question: what class of target loci have the lowest copy number?

**Supplemental Table 11.** Locus quality metric to answer the question: what class of target loci produce alignments with the lowest proportion of potentially misaligned bases?

**Supplemental Table 12.** Locus quality metric to answer the question: what class of target loci produce alignments with the lowest percentage of ambiguous characters?

**Supplemental Table 13**. Locus quality metric to answer the question: what class of target loci produce alignments with the lowest percentage of missing sequences/characters in alignments?

**Supplemental Table 14**. The relative merit of models involving one-way and two-way gene flow between allopatry and sympatry in the river drainages 1 and 2 (refer to Figs. 3 and 7).

**Supplemental Table 15**. The relative merit of models involving one-way and two-way gene flow between allopatry and sympatry in the river drainages 2 and 3 (refer to Figs. 3 and 7).

**Supplemental Table 16**. The relative merit of models involving one-way and two-way gene flow between allopatry and sympatry in the river drainages 3 and 4 (refer to Figs. 3 and 7).

**Supplemental Table 17**. The relative merit of models involving one-way and two-way gene flow between allopatry and sympatry in the river drainages 4 and 5 (refer to Figs. 3 and 7).

**Supplemental Table 18**. Estimates of parameters (N=effective population size, m=migration rate) for models involving river systems 1 and 2 (4 populations).

**Supplemental Table 19**. Estimates of parameters (N=effective population size, m=migration rate) for models involving river systems 2 and 3 (4 populations).

**Supplemental Table 20**. Estimates of parameters (N=effective population size, m=migration rate) for models involving river systems 3 and 4 (4 populations).

**Supplemental Table 21**. Estimates of parameters (N=effective population size, m=migration rate) for models involving river systems 4 and 5 (4 populations).

**Supplemental Table 22.** The effect of data set type on precision of population size (Ne) and migration rate (m) estimates. Parameter estimates derived from two different data sets were compared in each pairwise randomization test. Data sets included, D=deep-scale, S=shallow-scale, A=all-loci, D1=deep-scale w/one SNP per locus, S1=shallow-scale w/one SNP per locus, A1=All loci w/one SNP per locus.

**Supplemental Table 23.** Overview of *Pseudacris* sequence characteristics for the three final empirical data sets.

**Supplemental Table 24.** *Pseudacris* summary statistics for deep-scale and shallow-scale loci used in population genomics analyses.

**Supplemental Table 25.** Population genomic loci length distributions after trimming (deep-scale and shallow-scale loci).

**Supplemental Table 26**. Population genomic results of hybrid class distribution across three replicates of each data set.