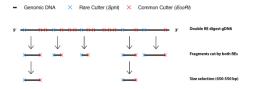
Supplementary Fig. S1. Overview of ddRADseq protocol. (A) Genomic DNA for each individual is double restriction digested and size selected, (B) individual-specific adapters are ligated, (C) samples are pooled and sequenced in multiplex, (D) resulting reads are demultiplexed by individual, (E) *de novo* assembly of loci is performed, and presence/absence and coverage are calculated across loci, (F) loci from individuals are compared, and (G) haplotypes are called for variable loci.

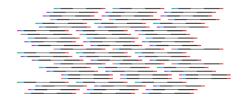
(A) Double digestion and size selection



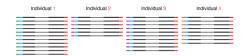
(B) Uniquely barcode fragments by individual



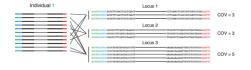
(C) Sequence multiple individuals in parallel



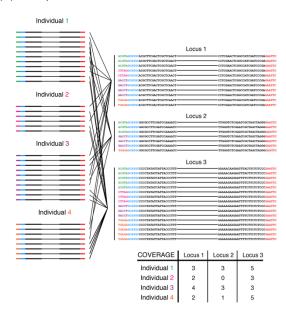
(D) Demultiplex reads by individual



(E) Assemble loci and estimate coverage



(F) Compare all loci across all individuals



(G) Call SNPs and resolve haplotypes for variable loci

