Appendix S1

Tissue extraction and SNP filtering details:

Tissues samples were extracted using a modified QiagenTM DNeasy blood and tissue protocol. DNA quality and quantity were assayed using agarose gel electrophoresis and Qubit® Fluorometer. Library preparation and sequencing was performed on an Ion Torrent Proton Platform (IBIS, Laval University, Quebec, CA) following the protocol developed in [1] (using enzymes *Pst*I and *Msp*I) as described in [2].

Raw sequence quality was assessed using FastQC [3] v. 0.11.4. Adapters were trimmed using cutadapt [4]; SNP filtering and discovery was conducted using *de novo* assembly in *Stacks* v. 1.44 [5]. *process\_radtags* was used to demultiplex and filter reads based on quality; reads were trimmed to 80 base pairs to remove bases with low-quality scores on the 3’ end. Key parameters included: *ustacks* minimum stack depth (-m) of 5, maximum distance between stacks (-M) of 5, maximum distance to align secondary reads (-N) of 7, *cstacks* maximum mismatches between tags (-n) of 5, *rxstacks* log likelihood > -30, *populations -*r *=* 0.8, *-*p = 11/14. GBS was performed on 14 populations, but only results for the 12 transplanted populations are presented herein.

 Downstream filtering was conducted in the *radiator* package [6] in R v. 3.3.3 [7]. Brook trout are residual tetraploids [8] making SNP identification complicated by the occurrence of paralogues [9]. To remove potential paralogues, loci with more than 4 SNPs were removed; only the first SNP was used per locus, and loci with Ho > 0.6 in 2 or more of the sampled populations were excluded. SNPs with a minor allele frequency (<0.01) were similarly excluded to remove potential sequencing errors and rare alleles. Individuals missing more than 40% of genotypes across all filtered loci were also removed.

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