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.

1. Mascher M, Wu S, St. Amand P, Stein N, Poland J. 2013 Application of genotyping-by-sequencing on semiconductor sequencing platforms: a comparison of genetic and reference-based marker ordering in barley. *PLoS One* **8**, 1–11. (doi:10.1371/journal.pone.0076925)

2. Perreault-Payette A, Muir AM, Goetz F, Perrier C, Normandeau E, Sirois P, Bernatchez L. 2017 Investigating the extent of parallelism in morphological and genomic divergence among lake trout ecotypes in Lake Superior. *Mol. Ecol.* **26**, 1477–1497. (doi:10.1111/mec.14018)

3. Andrews S. 2010 FastQC: A quality control tool for high throughput sequence data. *Online*. See https://www.bioinformatics.babraham.ac.uk/projects/fastqc/.

4. Martin M. 2011 Cutadapt removes adapter sequences from high-thoughput sequencing reads. *EMBnet.journal* **17**, 10–12. (doi:http://dx.doi.org/10.14806/ej.17.1.200)

5. Catchen J, Hohenlohe PA, Bassham S, Amores A, Cresko WA. 2013 Stacks: an analysis tool set for population genomics. *Mol. Ecol.* **22**, 3124–3140. (doi:10.1111/mec.12354)

6. Gosselin T. 2017 radiator: RADseq Data Exploration, Manipulation and Visualization using R. (doi:10.5281/zenodo.154432)

7. R Development Core Team. 2017 R: a language and environment for statistical computing. *R Found. Stat. Comput. Vienna Austria* **0**, {ISBN} 3-900051-07-0. (doi:10.1038/sj.hdy.6800737)

8. Crete-Lafreniere A, Weir LK, Bernatchez L. 2012 Framing the Salmonidae family phylogenetic portrait: a more complete picture from increased taxon sampling. *PLoS One* **7**. (doi:10.1371/journal.pone.0046662)

9. Paris JR, Stevens JR, Catchen JM. 2017 Lost in parameter space: a road map for STACKS. *Methods Ecol. Evol.* **8**, 1360–1373. (doi:10.1111/2041-210X.12775)