To the editor,

Thank you for your comments and all the work handling this manuscript so far. We agree with your suggestions and those of reviewer 3 and have significantly revised the manuscript in response. Our revisions are focused on four intertwined issues in the previous draft: (1) the manuscript was too long, (2) analysis of multiple datasets was difficult to follow or justify, (3) redundant analyses cluttered the results, and (4) the discussion was too long and unfocused. We summarize how our revisions address each of these related issues below. We also briefly address minor comments.

Your comments and those of reviewer 3 are noted in blue text.

Overall Length

“The maximum length is usually reserved for papers where the topic or approach is too complex to transmit the important points in that length, but your work is not in this category.”

At 8,985 words, the previously submitted manuscript was too long for the simple message we were trying to convey. The length also exceeded the maximum article length of 8,000 words. The length of our revised manuscript has been reduced to 6,439 words including title, abstract, keywords, body of the text, figures, and tables but excluding authors affiliations, references and on-line supplementary material. We believe the revised manuscript concisely conveys our most important results and their salience to conservation of salmonid life-history diversity.

The revised length was achieved by limiting our analysis to two datasets, eliminating redundant analyses, and by shortening the discussion.

Datasets

“Normally one would a create a dataset composed of putatively neutral loci…One could then add in the potentially adaptive markers for a combined dataset or alternatively examine those loci separately for correlations with observed phenotypes.”

“Neutral (without markers in LD) vs adaptive should suffice and would additionally simplify the methods and streamline the manuscript”

“I strongly recommend a more logical construction of datasets”

Following the recommendations above, our revised manuscript focuses on just two datasets: an LD-thinned neutral dataset, and a set of 12 migration timing associated markers. In the revised manuscript, we restrict analyses of population genetic structure to the neutral dataset. We then examine diversity within the migration timing dataset, and its relationship to observed phenotypes.

Redundant Analyses

“The multitude of analyses on different versions of the dataset, not only detract from the results, but make it hard to extract the important points.”

“As mentioned above, much of the exploratory analysis can be removed - even though these figures appear primarily as supplements, there is still an inordinate amount of text dedicated to their explanation”

“Please focus on your salient results and make your manuscript both accessible and appropriate for a journal”

We removed redundant and unnecessary analyses from the revised manuscript. For example, the previously submitted manuscript conducted PCA, *a priori DAPC, de novo* DAPC, and STRUCTURE on the same dataset. While each of these analyses provide somewhat different inferences, the differences were not salient to our conclusions and did not add to the manuscript in a meaningful way. The revised draft includes one analysis of population structure suited to identifying genetic clusters (STRUCTURE) and one more suited to identifying continuous patterns of genetic variation (PCA).

Additional redundancy stemmed from application of similar methods to multiple datasets. While this approach sometimes provides interesting insights, (e.g. FST at neutral markers is correlated to FST at migration timing markers), it often only added unneeded complexity. For example, the previous draft included hypothesis testing for differences in genetic diversity among groups across multiple subsets of the data.

Removing redundant analyses also obviated the need for the supplemental methods. We moved some additional detail to the main methods, and streamlined the manuscript by removing the supplemental methods altogether.

As an indication of the number of redundant analyses removed from the revised manuscript, our revised results section contains 67% of the words as the previously submitted draft.

Discussion

“In an effort to keep up with the sprawling and meandering Methods, the Discussion is much too long and unfocussed; this is especially true of the almost 5 pages of Conservation Implications.”

“The Discussion is very, very wordy with a lot of tangential information.”

“There is also an extraordinary amount of review and speculation in the Discussion. Much of this text is a re-hashing of the Results and I would be more comfortable if the authors limited themselves to what can be directly inferred from their data and what cannot, in clear and decisive language”

We removed rehashed results, unnecessary review, and speculation from our discussion section. After streamlining datasets and analyses, it became possible to briefly remind the reader of our key results, without going into extraordinary detail about, for example, the differences between structure revealed by *de novo* DAPC and STRUCTURE. We also removed much of the literature review, particularly within the lengthy *Conservation Implications* section*.* Finally, wecompletely removed our speculative discussion about the evolutionary basis of the half-pounder life-history, and much of our speculation about the evolutionary forces responsible for maintaining diversity at the region of the genome associated with adult migration timing. The total length of the discussion section was reduced to just 42% of its previous length.

Minor Changes

In addition to the major revisions described above, we also addressed minor comments and understand that the journal does not provide copy editing services, nor a phase of the pre-publication process where that occurs. We proofed the table and figure formatting, main text, and references according the author submission guidelines. We also attempted to apply a consistent style throughout. For example, we use “early-migrating salmon but early migrators, or half-pounder returns, but half pounders,” throughout the text.