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Title: The utility of reference genomes for fisheries management: a tool for understanding hybridization in Coastal Cutthroat Trout

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Abstract:

Understanding the evolutionary consequences of hybridization is crucial for the management and persistence of the culturally and economically significant salmonid species in the west. One major challenge to species and fisheries management is the identification of hybridized taxa that have been sympatric for a long time, such as Coastal Cutthroat Trout (*Oncorhynchus clarkii*) and Steelhead/Rainbow Trout (*Oncorhynchus mykiss*). While numerous studies have documented candidate loci for hybridization between *O. mykiss* and *O. clarkii* and other cutthroat species (i.e. *O. lewisi*), their efficacy in delineating hybrids seems to vary across the range. This could be due to variances across species in karyotypes, or challenges identifying diagnostic markers without high quality reference genomes. To resolve this, we generated a high-quality, reference genome assembly and linkage map for Coastal Cutthroat Trout to identify shared and variable chromosomal structure between the two species. This will aid in identification of loci diagnostic of species and hybrids. We will evaluate the ability to delineate naturally hybridized and introgressed fish from the Skagit and Elwha Rivers as well as from lab crosses.