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

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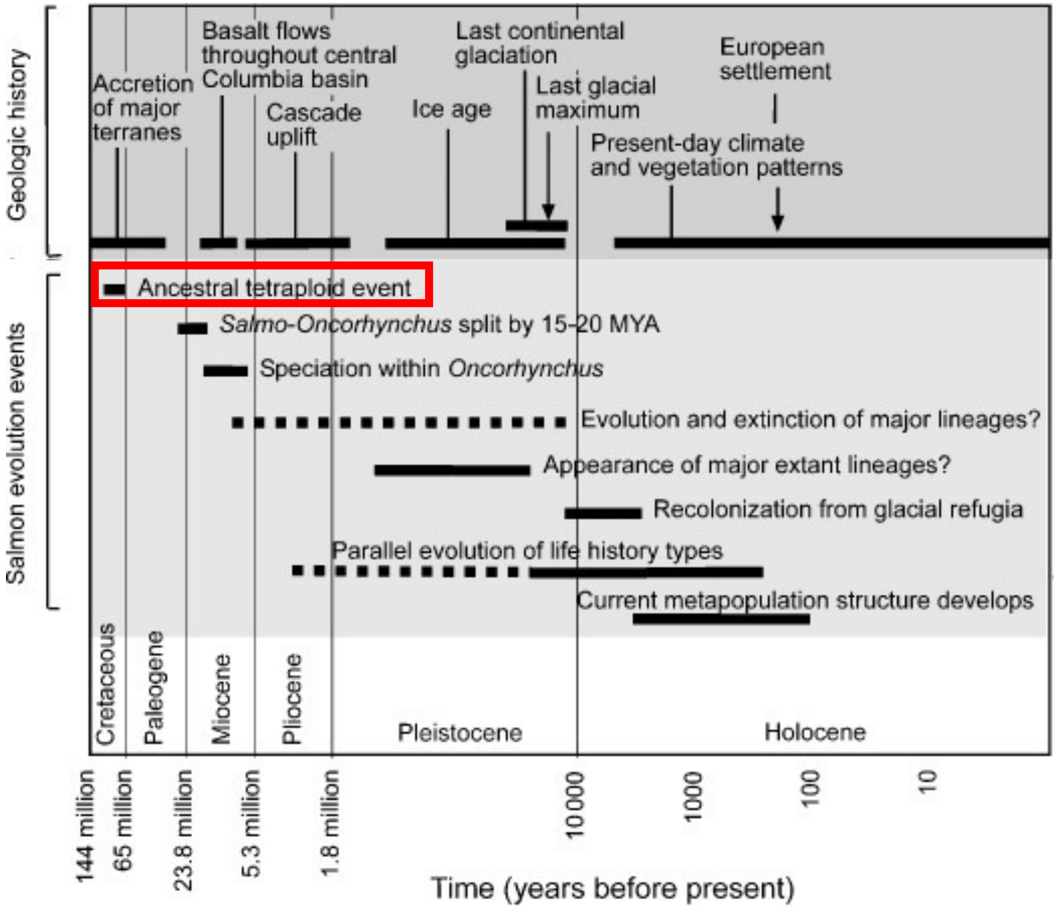
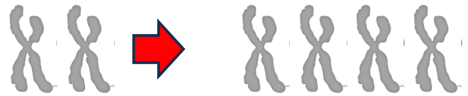
Todd Seamons, Paul Hohenlohe, Carl Ostberg, Krista Nichols

Salmonid genomes are *complicated* because of their ancient genome duplications



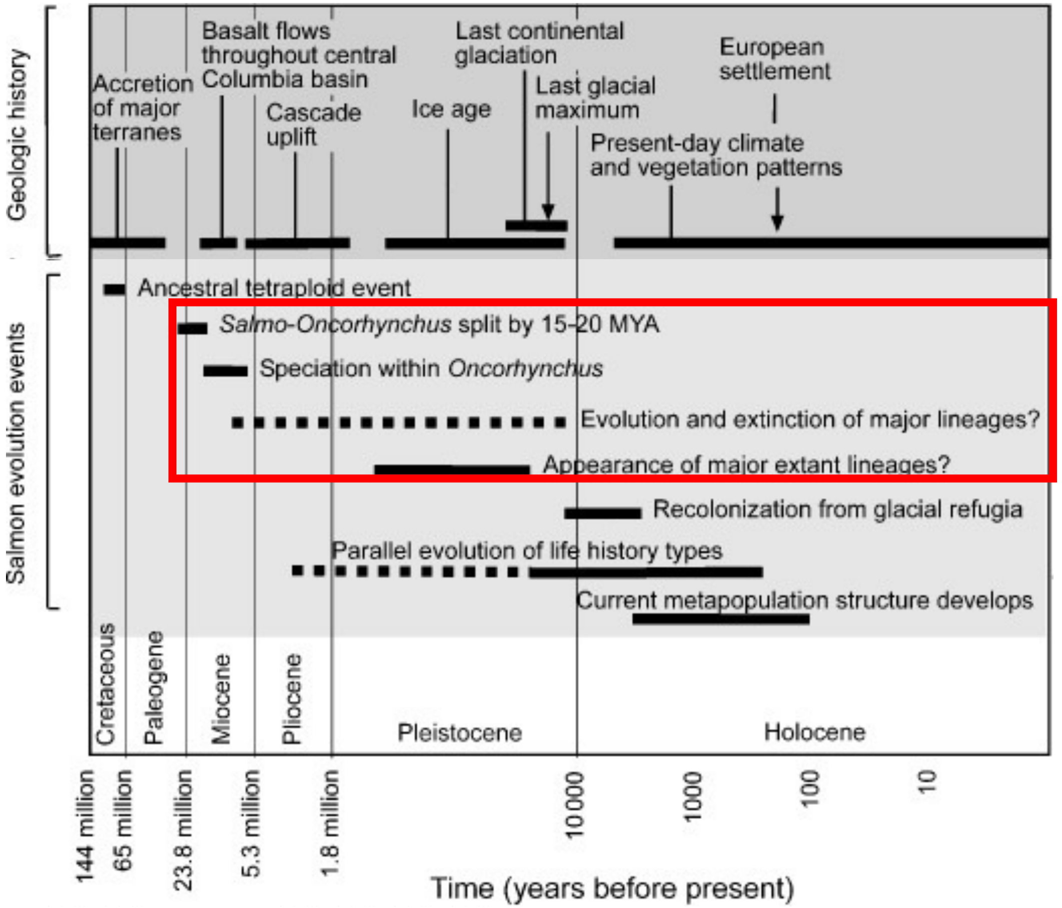


Diploid
(2 **sets of chromosomes**)

Tetraploid
(4 **sets of chromosomes**)

Waples et al. (2008) *Evol Appli.*

Speciation began *after* duplication with many genetic regions evolving independently



Diploid
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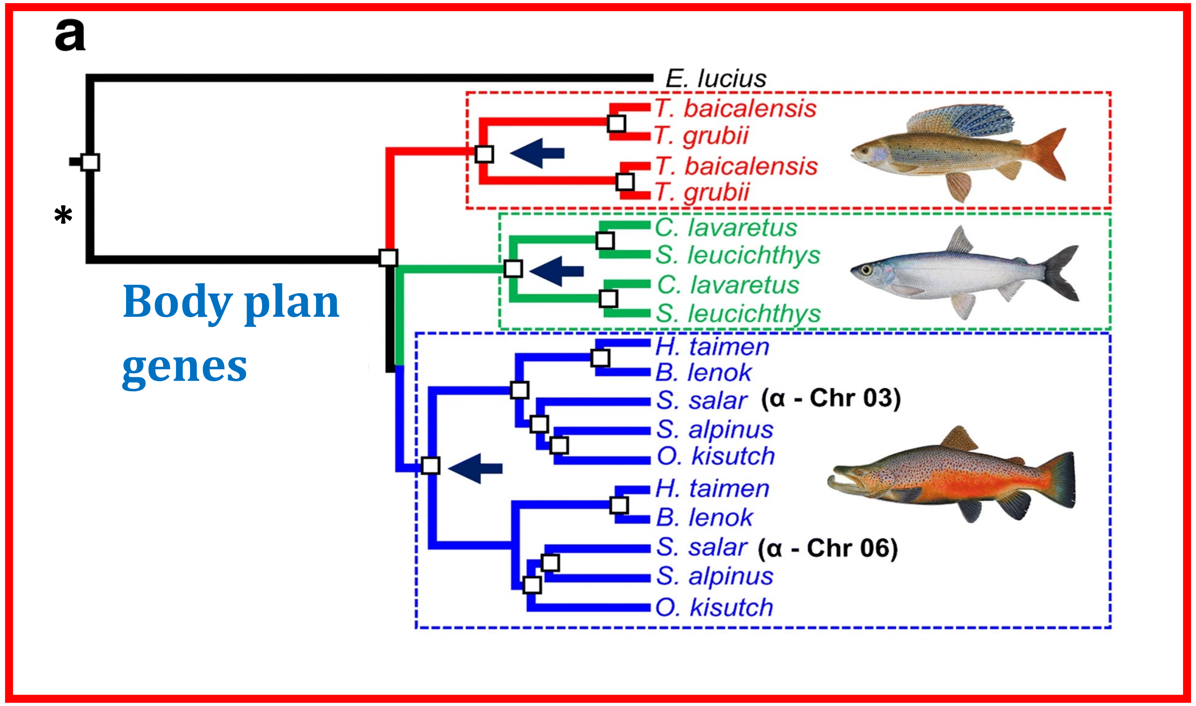
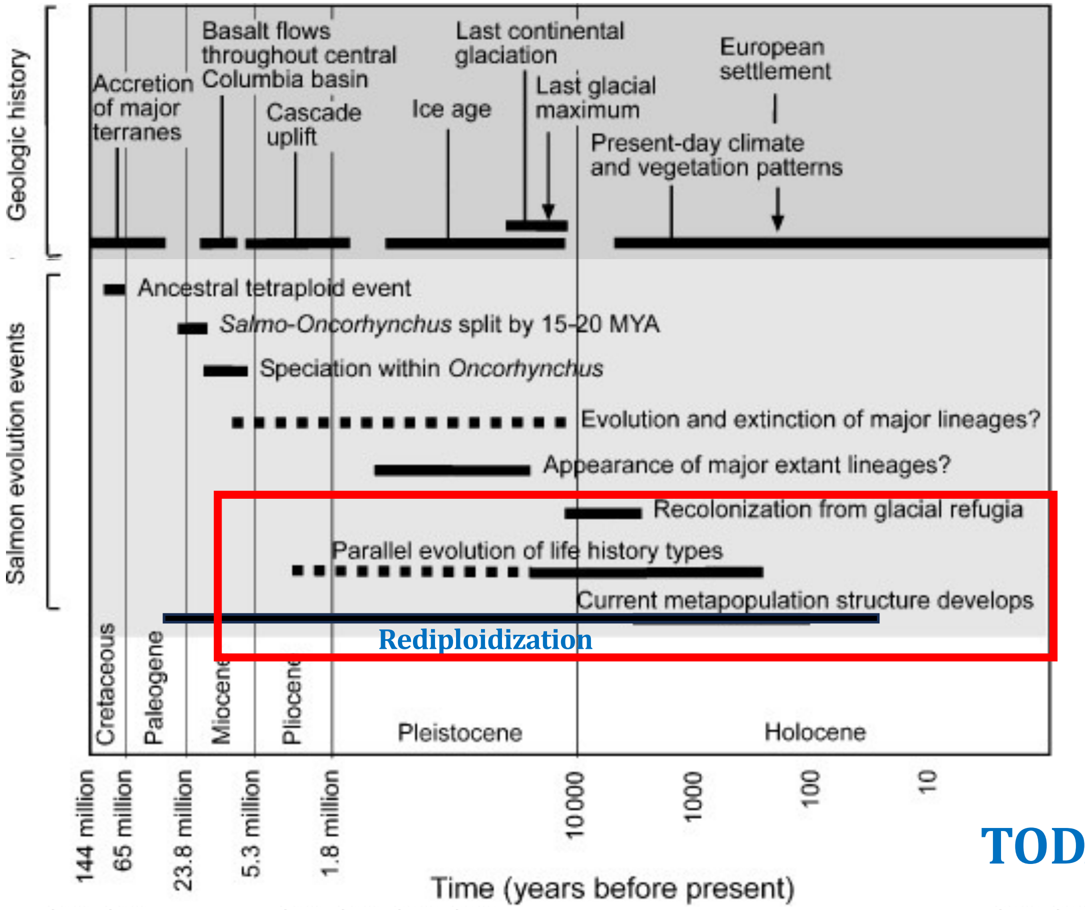


Body plan genes

***Salmonidae* speciation and diversification began ~40–50 Myr later**

Robertson et al. (2017) *Gen. Biol.*
Waples et al. (2008) *Evol Appli.*

Salmonid genomes are *still* diploidizing



TODAY

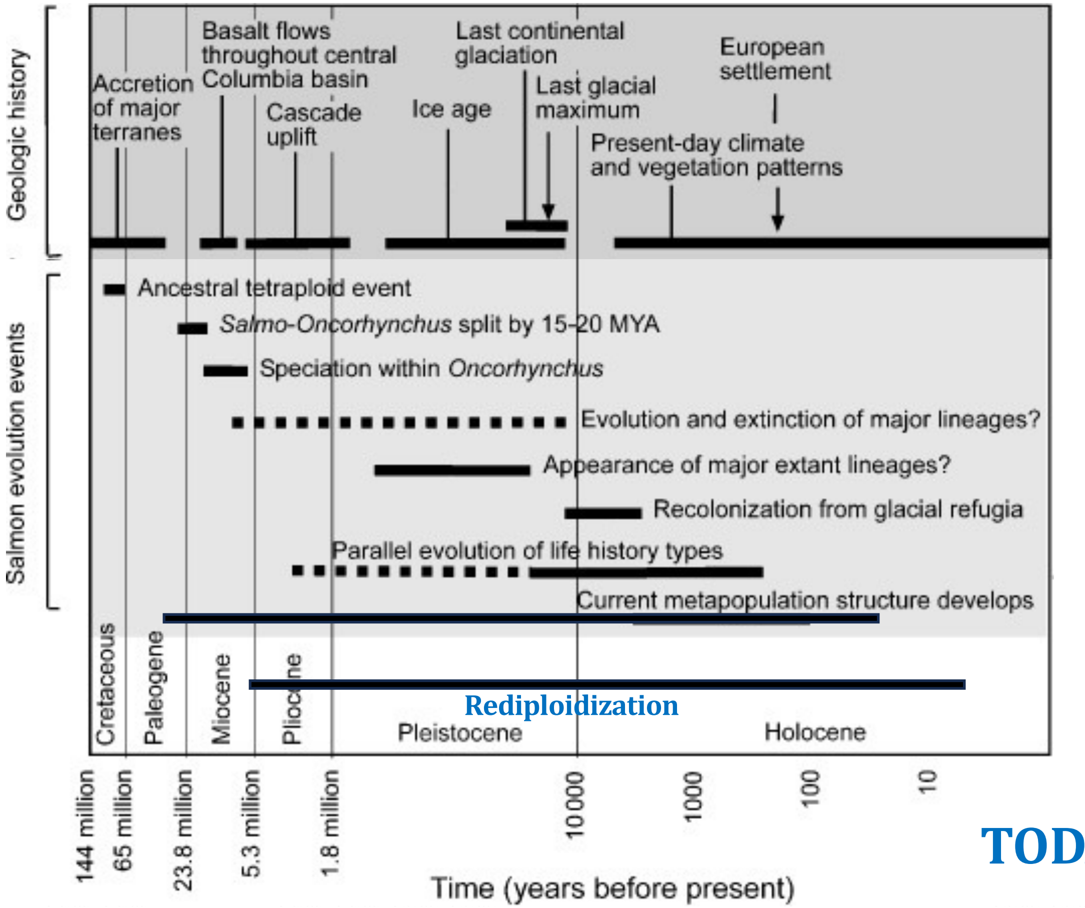
Diploid
(2 sets of chromosomes)

Tetraploid
(4 sets of chromosomes)

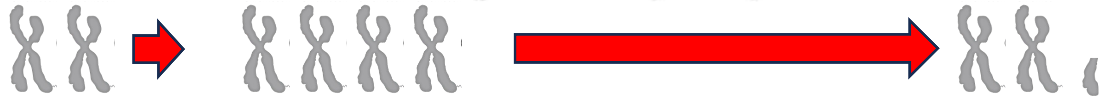
Diploid(ish)
(2 sets of chromosomes,
4 sets of some genes)

Waples et al. (2008) *Evol Appli.*
Robertson et al. (2017) *Gen. Biol.*
Loudenslager and Thoorgaard (1979) *Can J Zool.*

Salmonid genomes vary significantly in number of chromosomes (karyotype)



TODAY

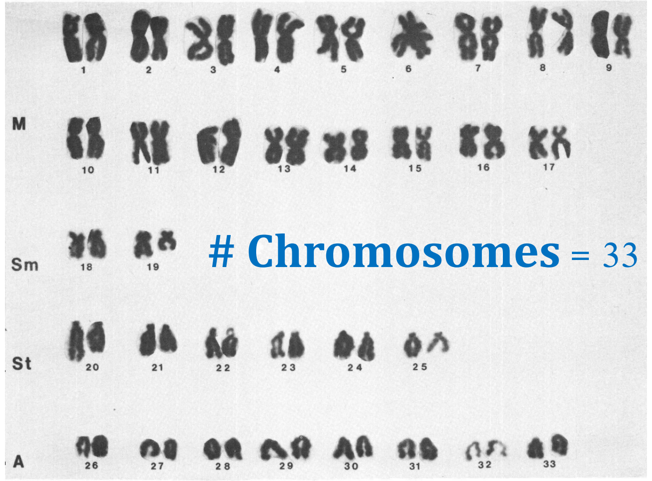


Diploid
(2 sets of chromosomes)

Tetraploid
(4 sets of chromosomes)

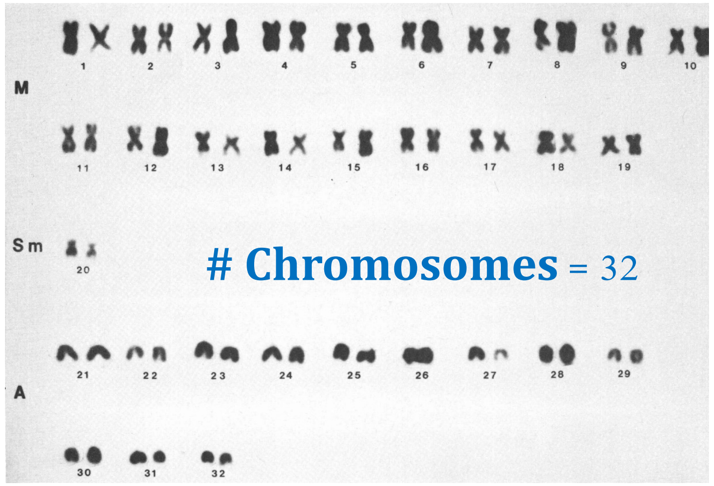
Diploid(**ish**)
(2 **sets of chromosomes,**
4 **sets of some genes**)

Yellowstone Cutthroat



 # Chromosomes = 33

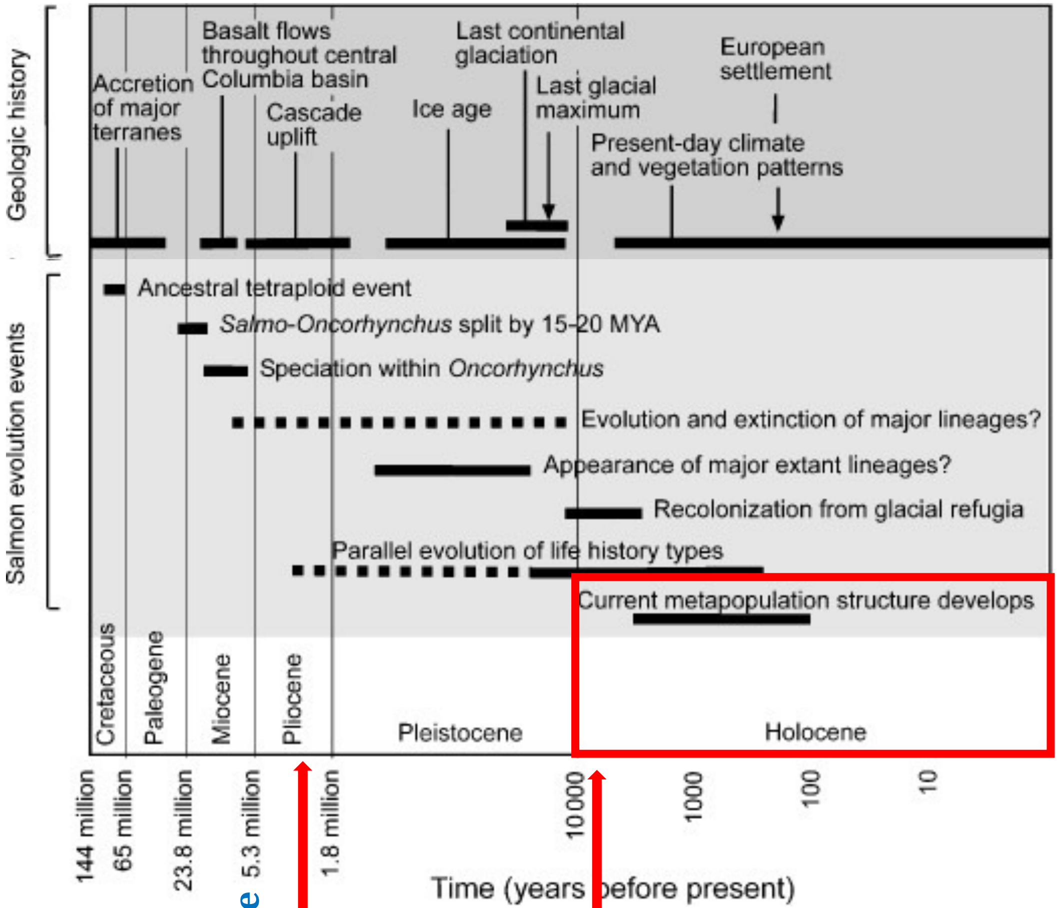
Westslope Cutthroat



 # Chromosomes = 32

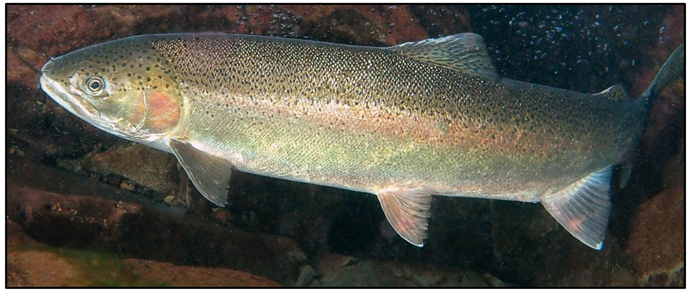
Waples et al. (2008) *Evol Appli.*
Robertson et al. (2017) *Gen. Biol.*
Loudenslager and Thoorgaard (1979) *Can J Zool.*

Coastal Cutthroat Trout and Steelhead/Rainbow Trout sympatric after last glacial maximum



Species Divergence timing

Species have been sympatric ~10 KY

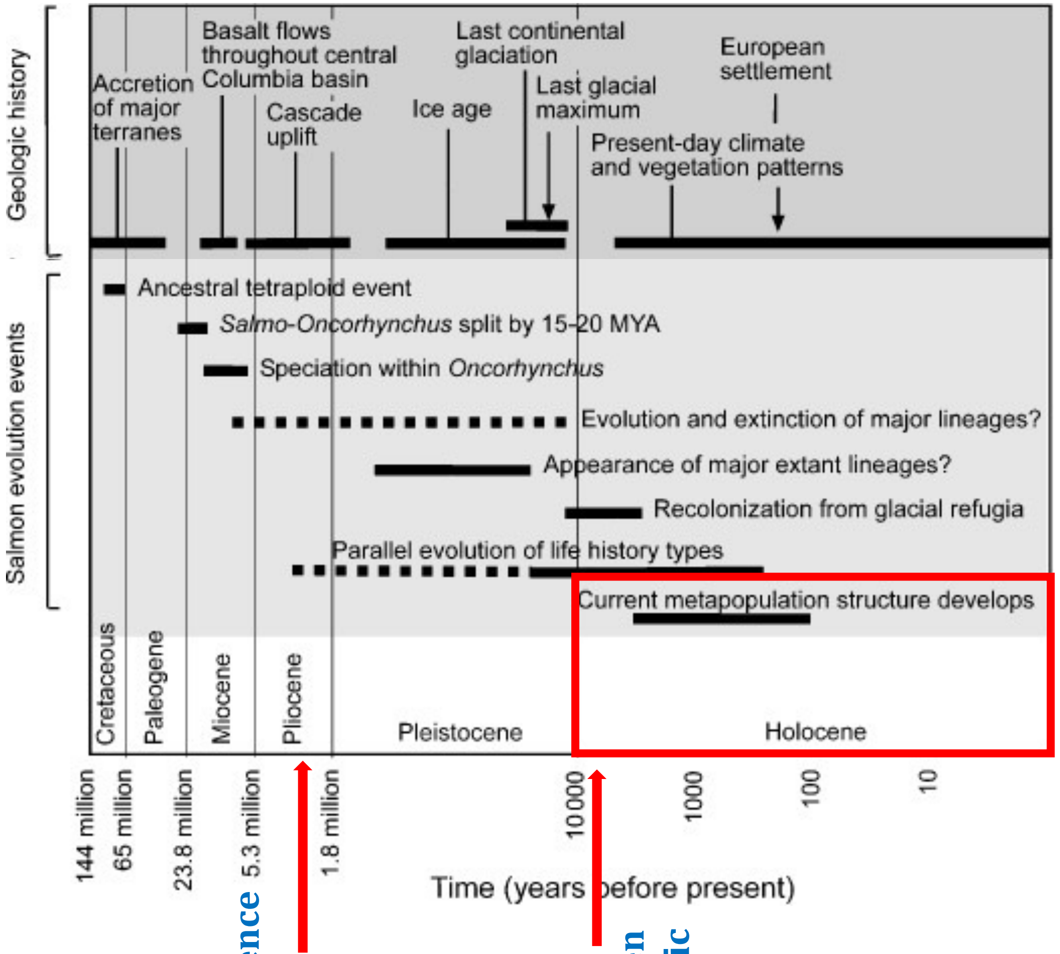


Steelhead / Rainbow Trout

Coastal Cutthroat Trout

PC: John McMillan, Jack Brill
Behnke, (2002) *Nat. Trout West. N. Am.*
Waples et al. (2008) *Evol Appli.*

Long-term introgression makes identifying species and hybrids challenging!



Species Divergence timing

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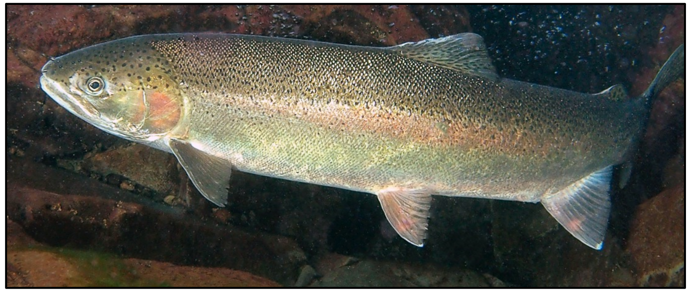


Steelhead / Rainbow Trout

↓

Hybrid

↑

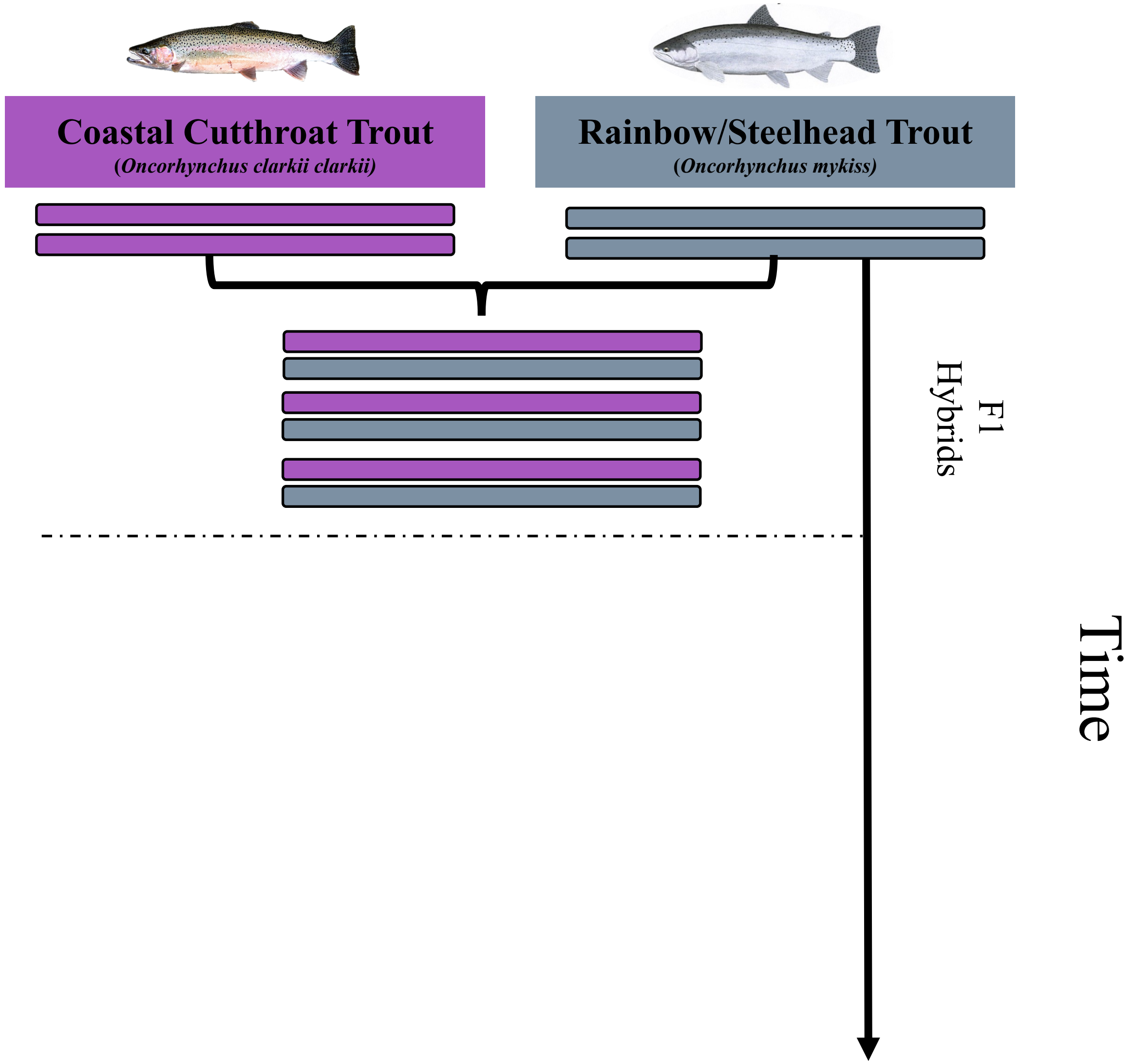
Coastal Cutthroat Trout

PC: John McMillan, Jack Brill
Behnke, (2002) *Nat. Trout West. N. Am.*
Waples et al. (2008) *Evol Appli.*

First generation hybrids get one copy of genetic information from each parent

Challenge 1:

Recombination shuffles genetic ancestry between species that hybridize



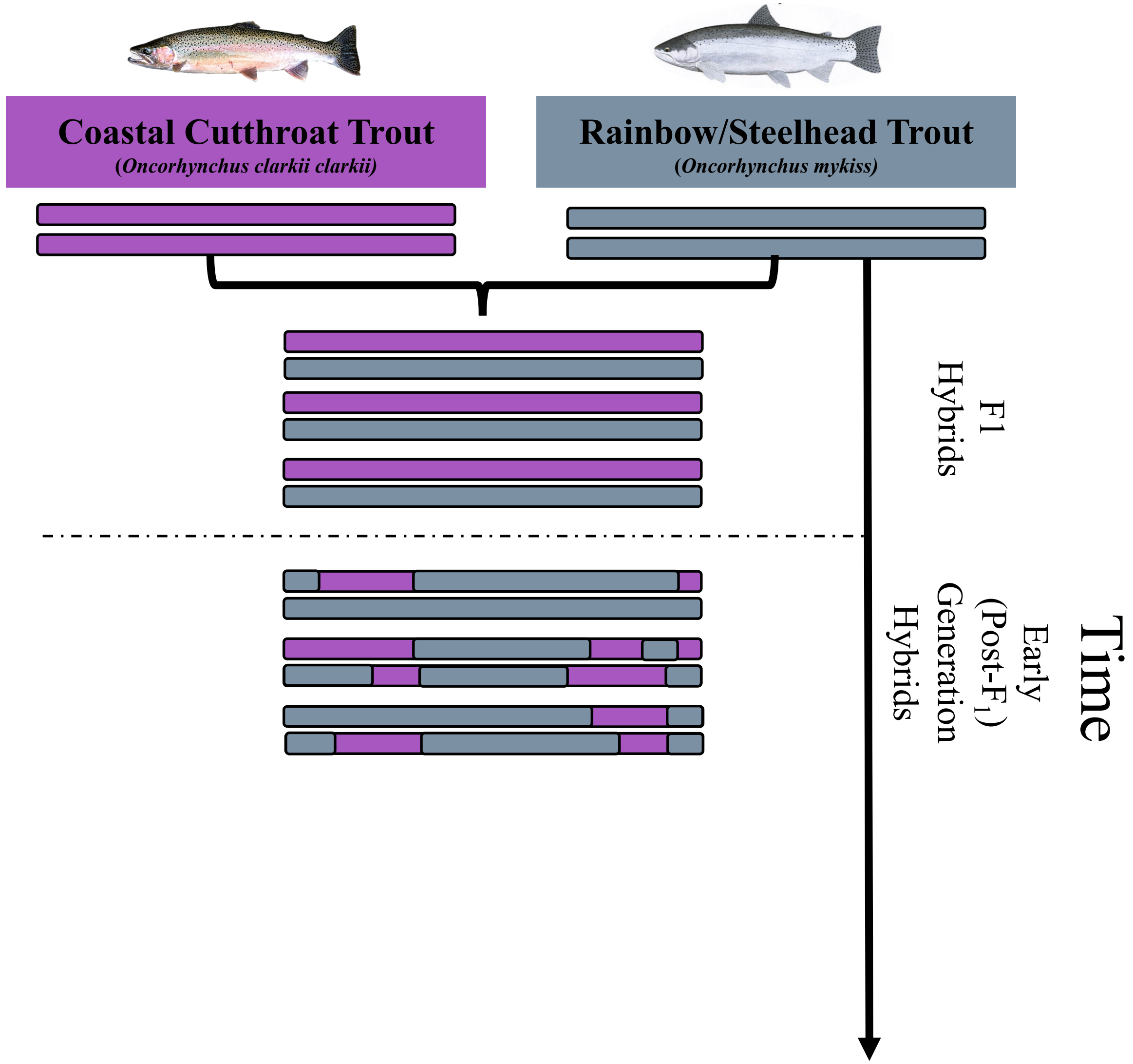
Coastal Cutthroat Trout

(Oncorhynchus clarkii clarkii)

Rainbow/Steelhead Trout

(Oncorhynchus mykiss)

Over time, recombination will begin to break down large blocks of genetic ancestry



Coastal Cutthroat Trout
(Oncorhynchus clarkii clarkii)

Rainbow/Steelhead Trout
(Oncorhynchus mykiss)

F1 Hybrids

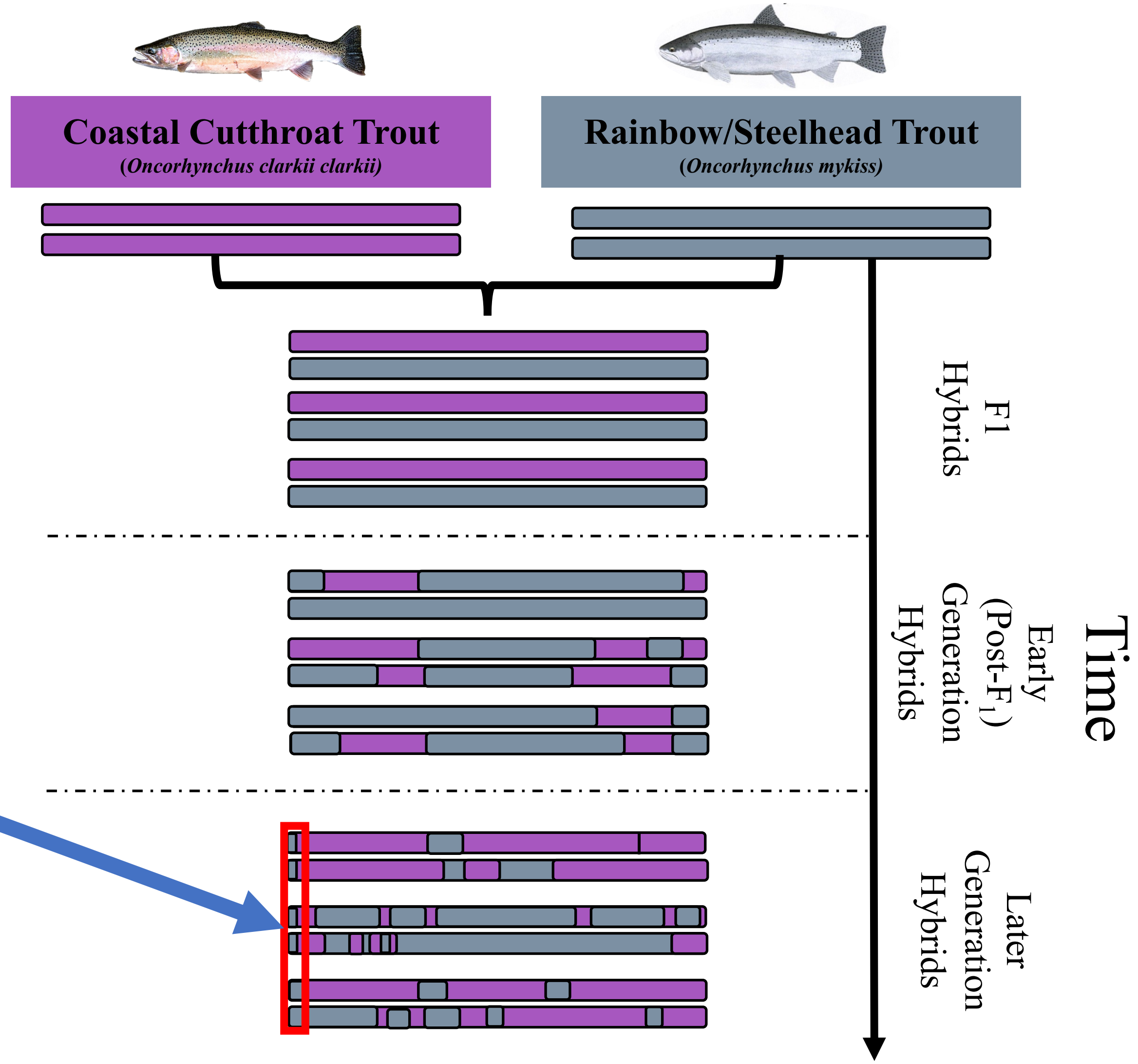
Early (Post-F_1) Generation Hybrids

Time

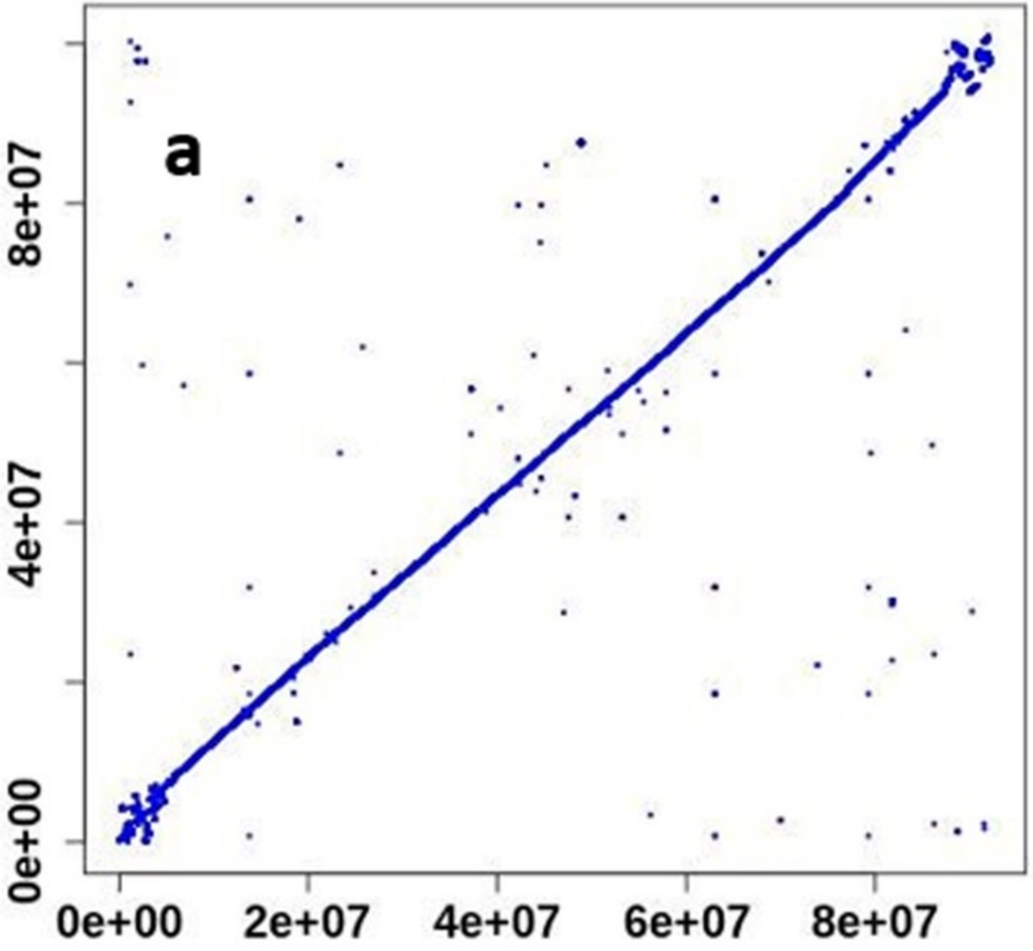
Many generations later, the non-self genetic variation is hard to identify

Challenge 2:

Populations that introgressed a long time ago can have very small, hard to identify, non-self blocks of genetic ancestry



Understanding how genetic markers are organized can give us insights into reproductive isolation



RBT Chromosome 5

(Arlee lineage)

RBT Chromosome 5

(Swanson lineage)

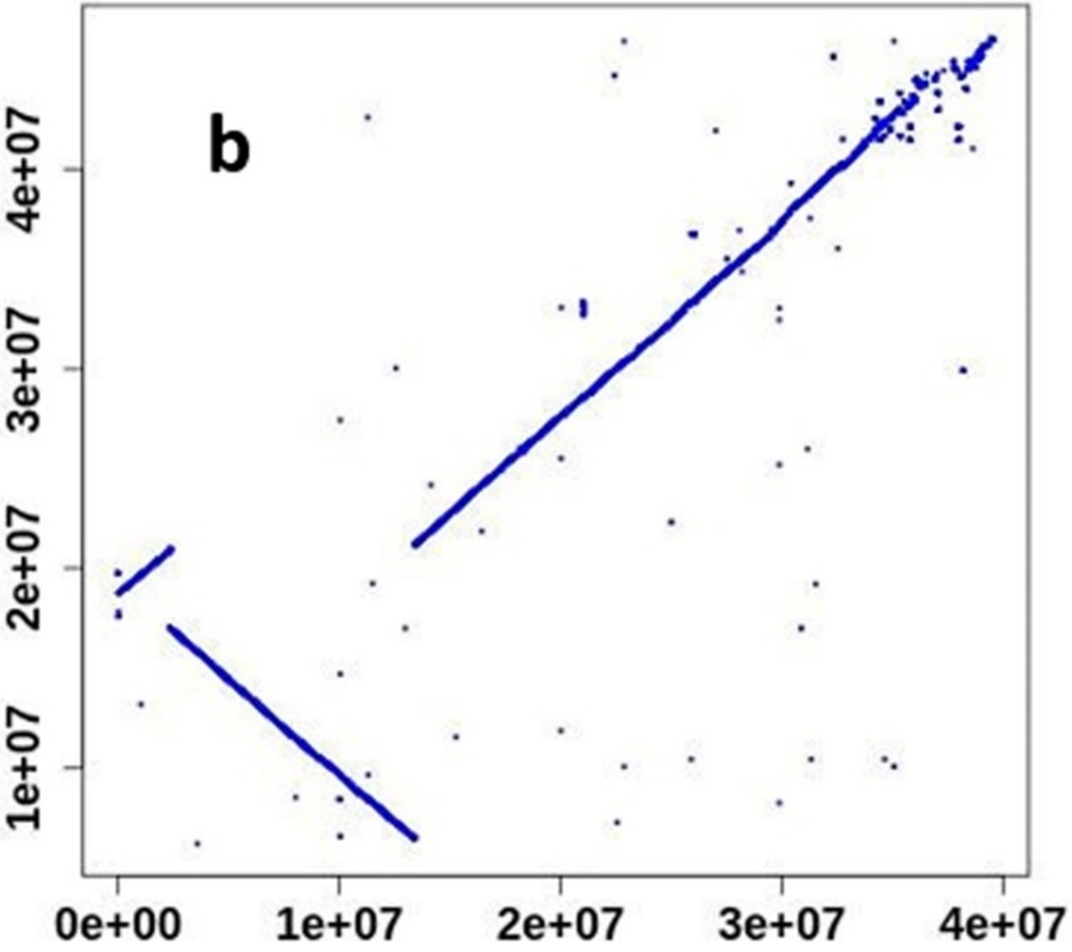
Genetic markers in different rainbow trout lineages align to similar chromosomal positions!

Each point = single position in the genome

Gao et al. 2021

Pearse et al. 2019

Chromosome 20 aligns to a different chromosome and in a different orientation of Atlantic Salmon



RBT Chromosome 20

(Arlee lineage)

Atlantic Salmon Chromosome 28

Challenge 3:

Species specific structural variation is often missed when using other species' reference genomes

Gao et al. 2021

Pearse et al. 2019

The challenges with identifying species and hybrid diagnostic markers in salmonids

1. Recombination shuffles genetic ancestry between species that hybridize

Species diagnostic markers

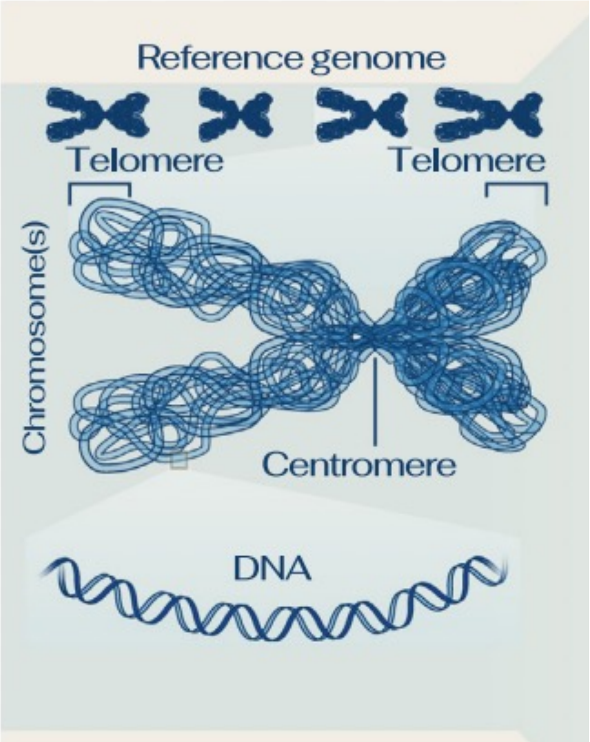
2. Populations that introgressed a long time ago can have very small, hard to identify, non-self blocks of genetic ancestry

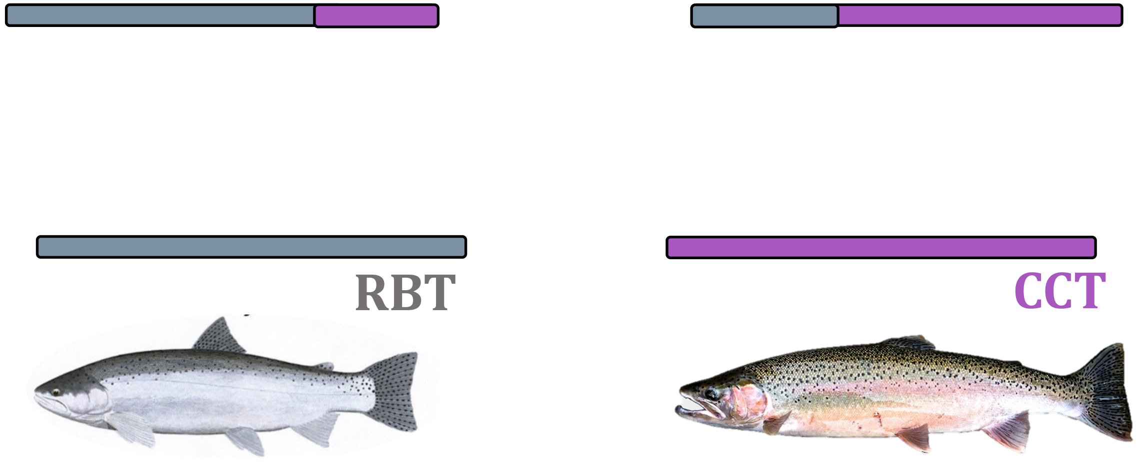
Shared variation

3. Diagnostic chromosomal and structural variation is often lost during filtering when using a different species' genome

Hybrid diagnostic markers

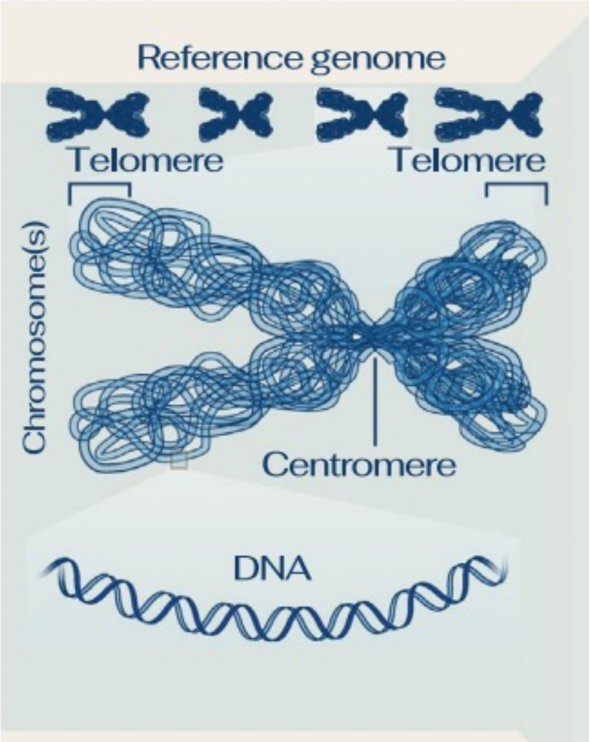
Reference genomes are maps for the structure and organization of a species’ genetic information

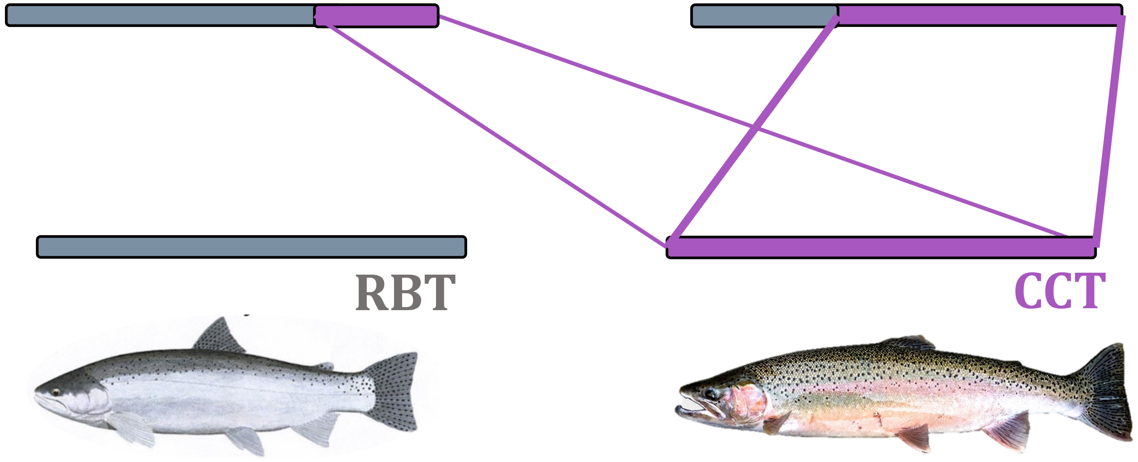




Formenti et al. 2022

Reference genomes are maps for the structure and organization of a species' genetic information





Formenti et al. 2022

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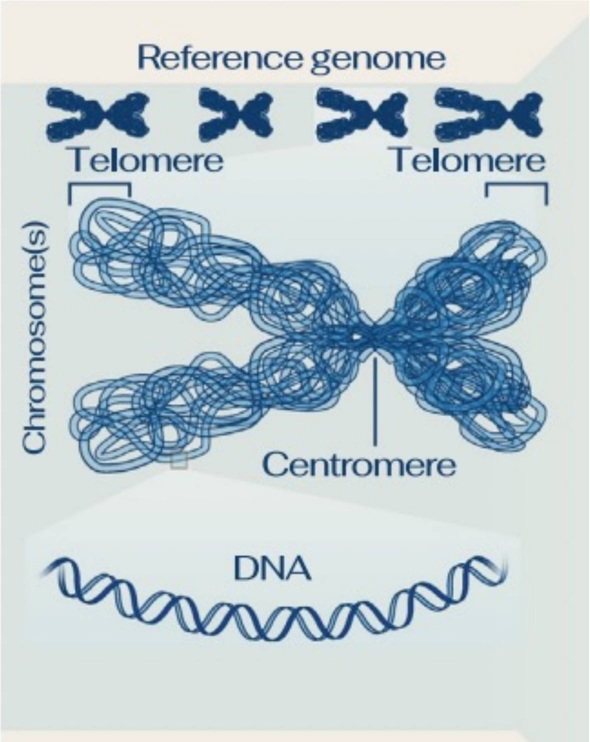
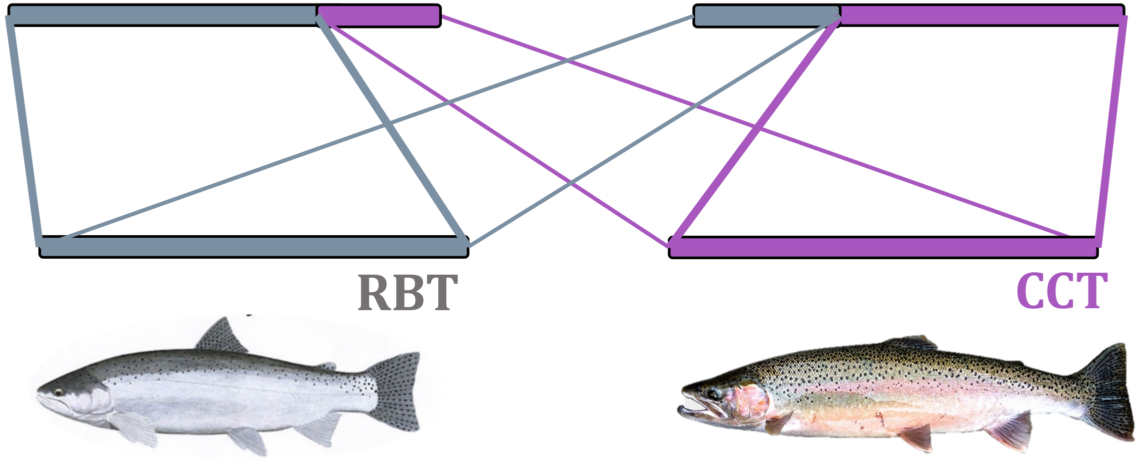


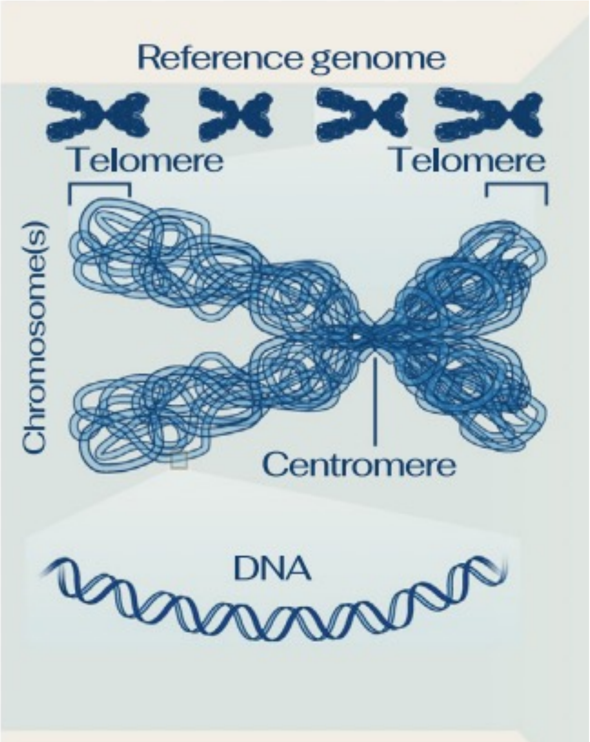


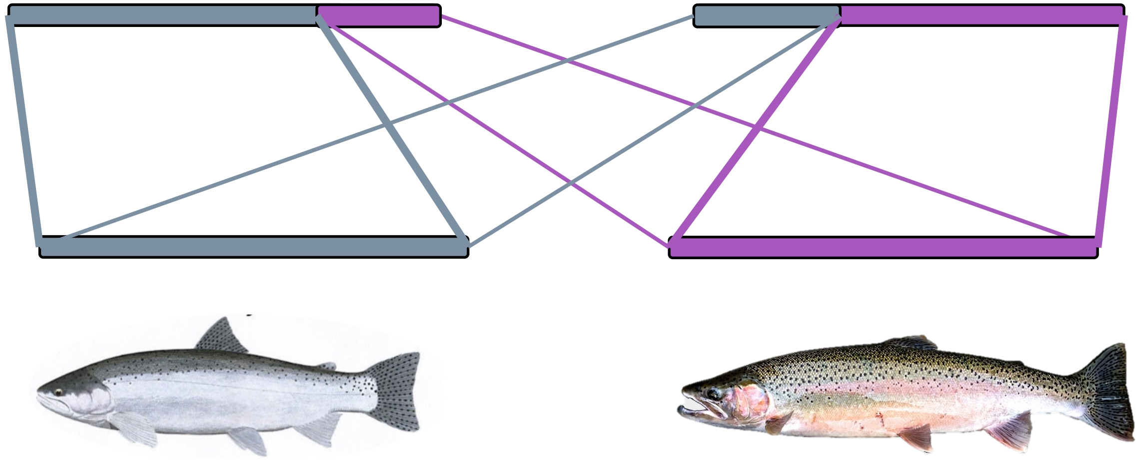
Chromosomal Features:

Gene duplications
Centromeres
Telomeres
Inversions
Fusions
Fissions

Formenti et al. 2022

Reference genomes can provide important resources for species' monitoring and management





Conservation + Management Implications

Identifying hybrids

Determining hybrid class

Inbreeding and deleterious genetic variation

Identification of genetic population or stock

Local adaptation

Genetic diversity

Chromosomal Features:

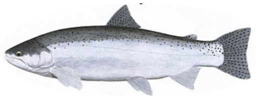
Gene duplications
Centromeres
Telomeres
Inversions
Fusions
Fissions

Formenti et al. 2022

Coastal Cutthroat Trout have different numbers of chromosomes from Rainbow Trout

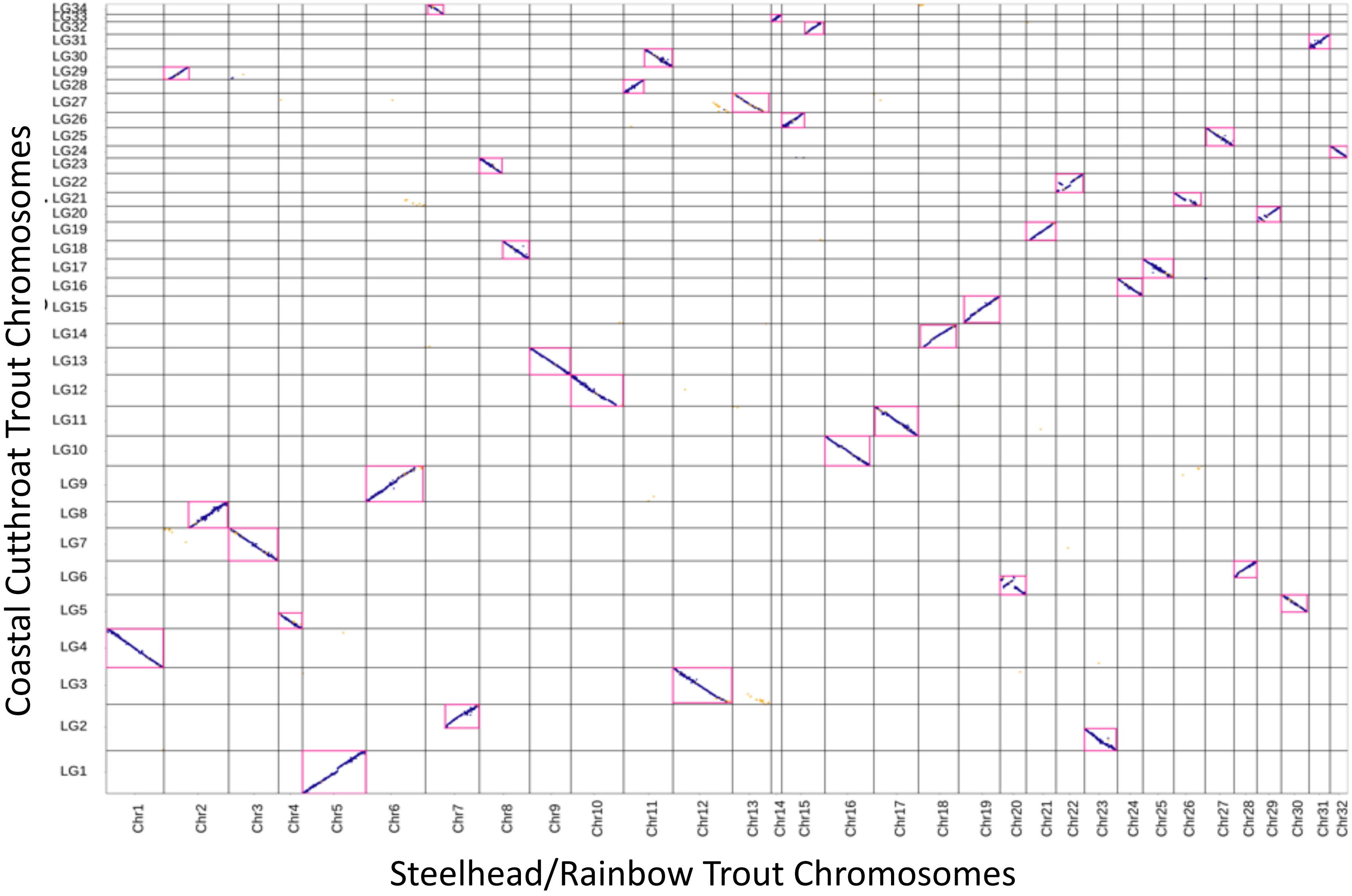
Coastal Cutthroat Trout (CCT)

n = 34 chromosomes



Steelhead/Rainbow Trout (RBT)

n = 32 chromosomes

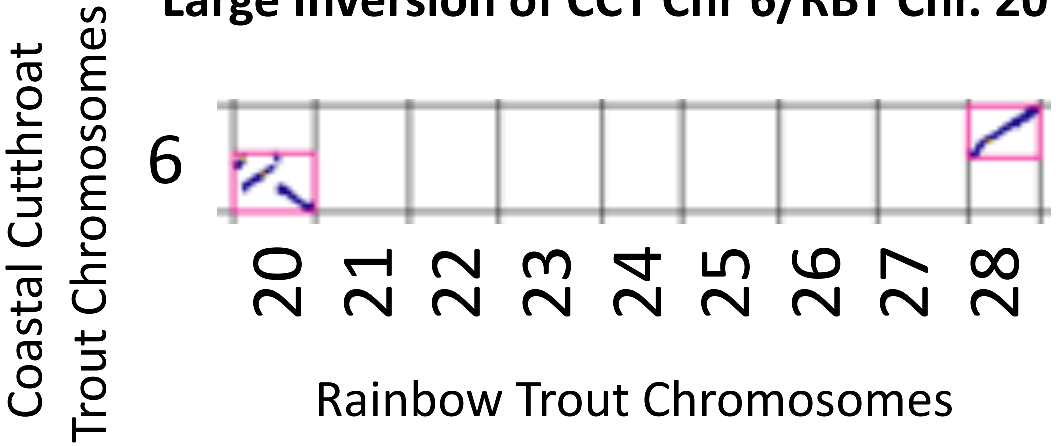


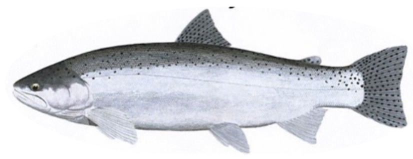
Coastal Cutthroat Trout also exhibit numerous chromosomal rearrangements

Rearrangements in CCT

CCT Chr. 6 = fusion RBT Chr. 20 + RBT Chr. 28

Large Inversion of CCT Chr 6/RBT Chr. 20



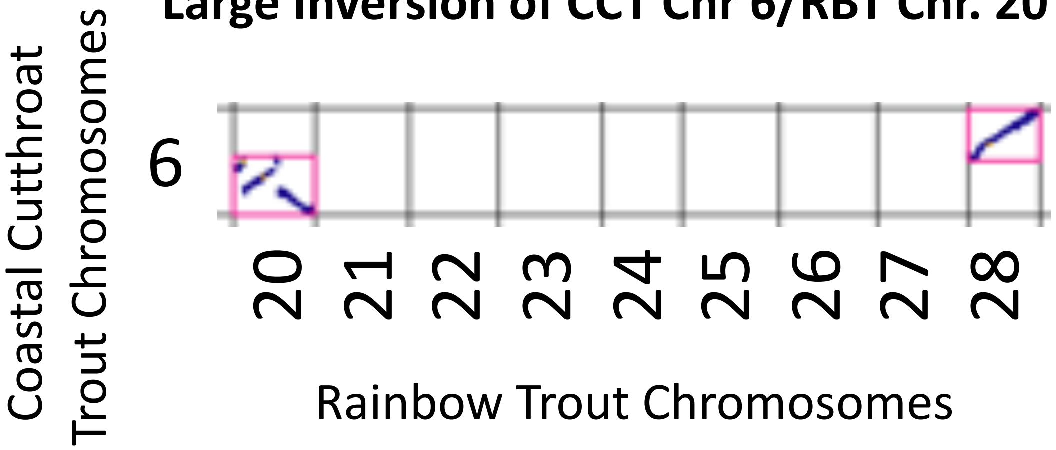


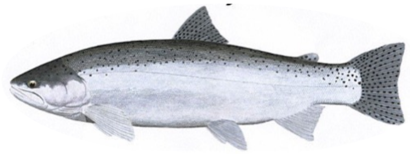
Can we use structural variation as species and hybrid diagnostic markers?

Rearrangements in CCT

CCT Chr. 6 = fusion RBT Chr. 20 + RBT Chr. 28

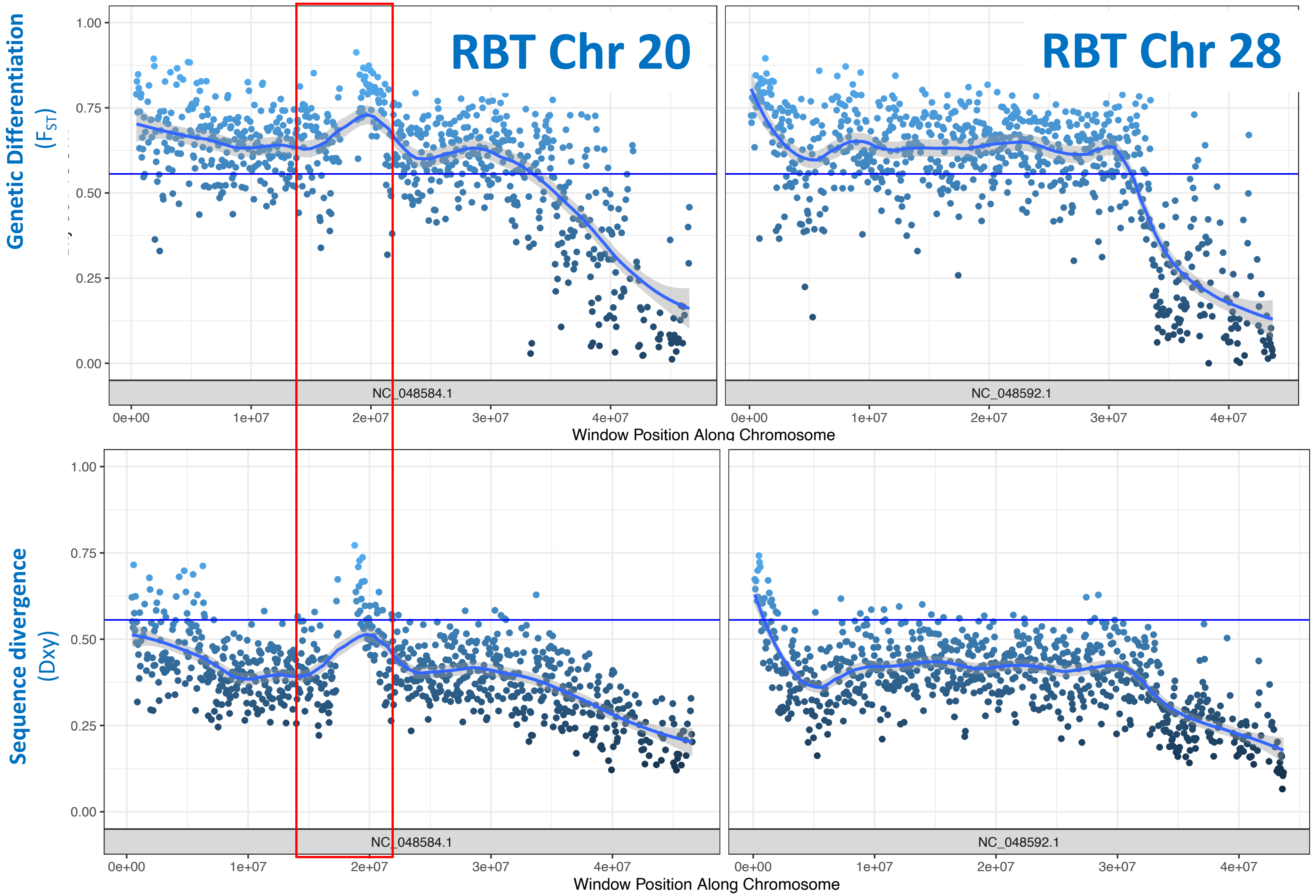
Large Inversion of CCT Chr 6/RBT Chr. 20



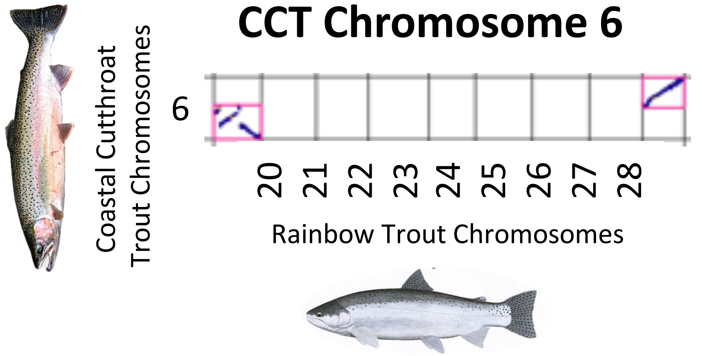


Structural variation can result in reduced recombination!

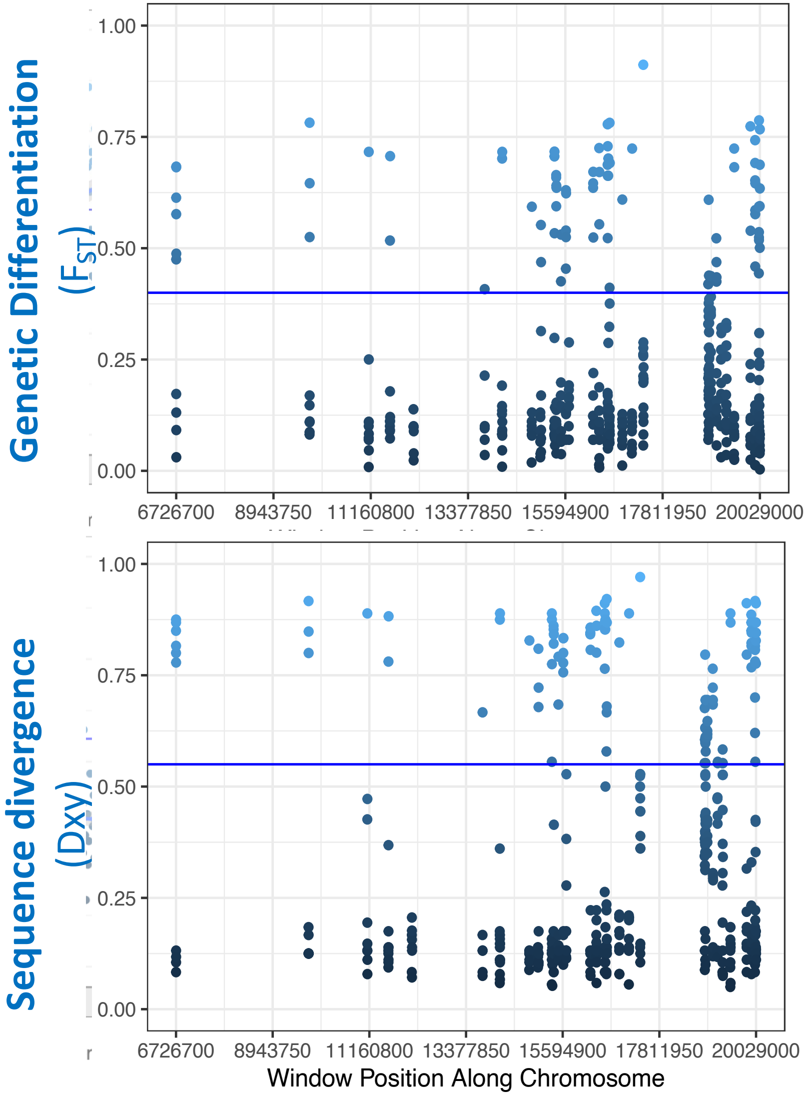
We can leverage the reference genome to look at divergence in the rearranged chromosome



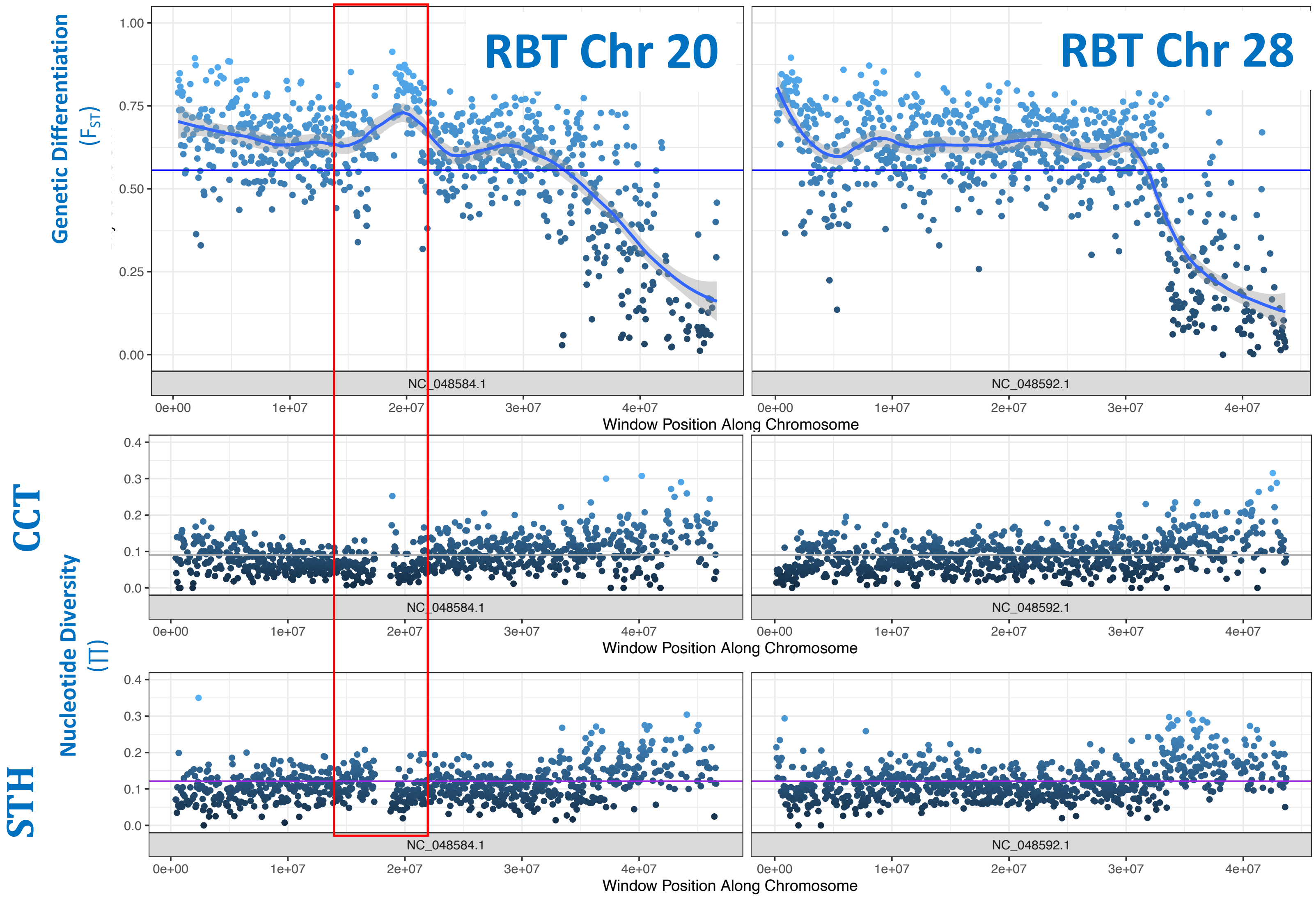
High genetic differentiation between CCT and STH near the Chr. 20 inversion



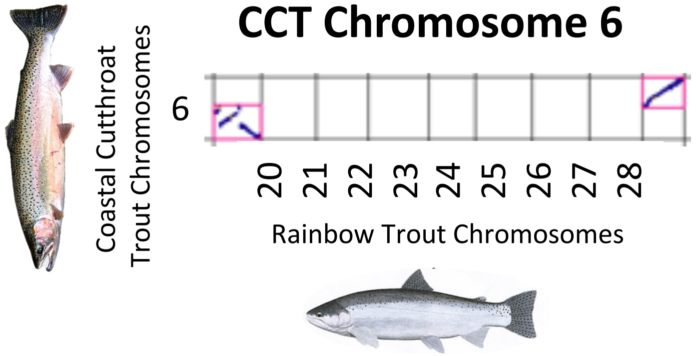
High genetic differentiation between RBT and CCT in the inversion (magnified)



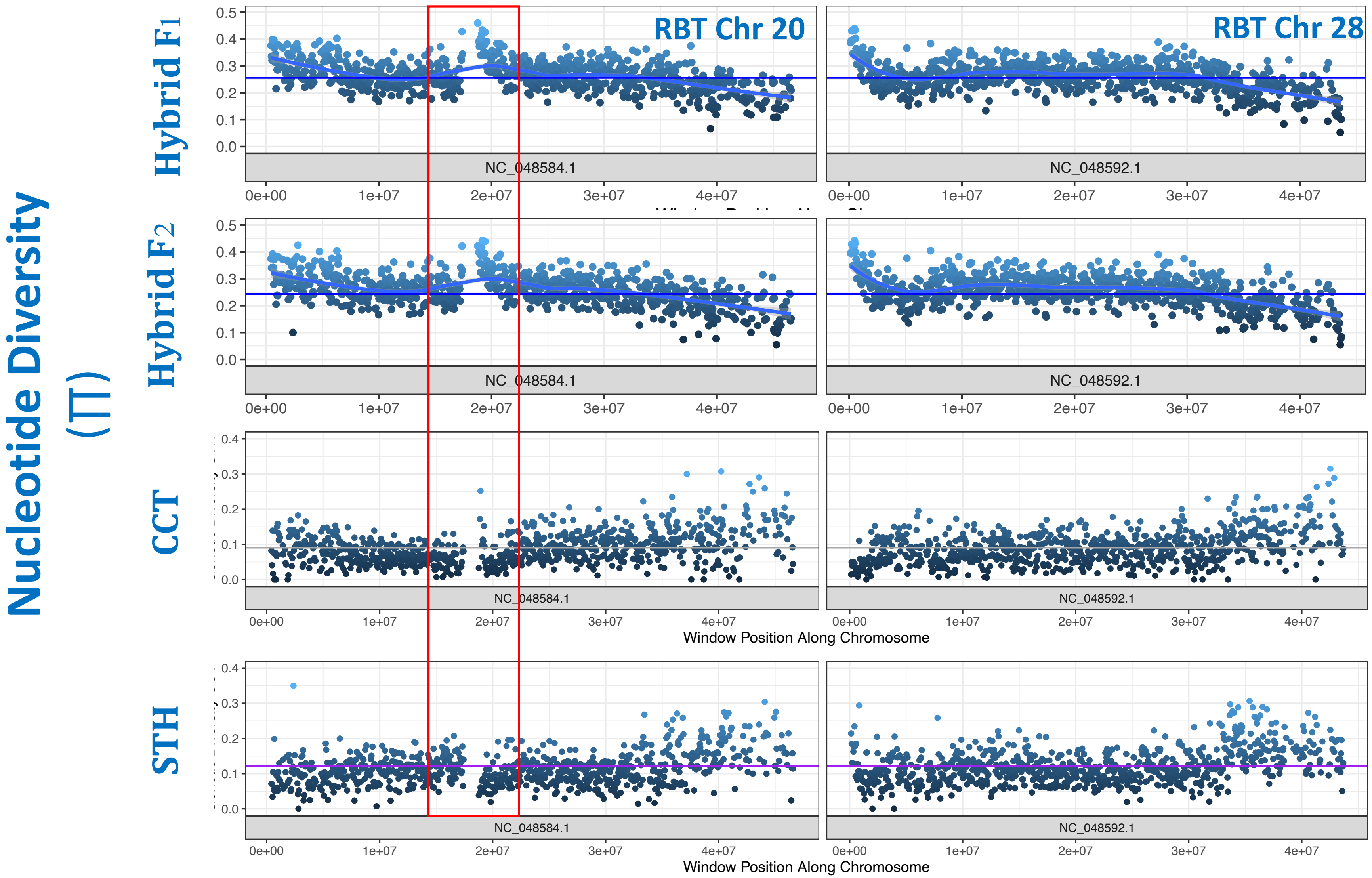
High levels of differentiation and low diversity in structural variants across species



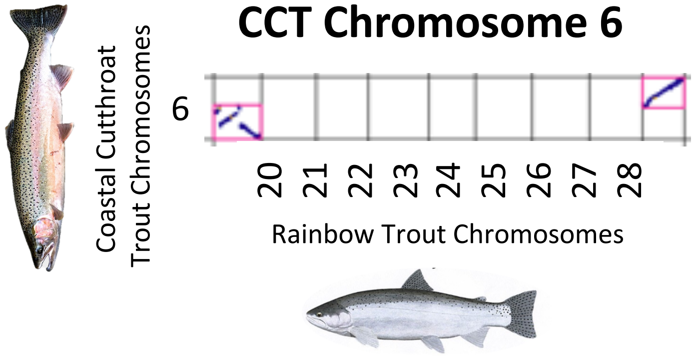
Lower diversity in this region in STH than CCT



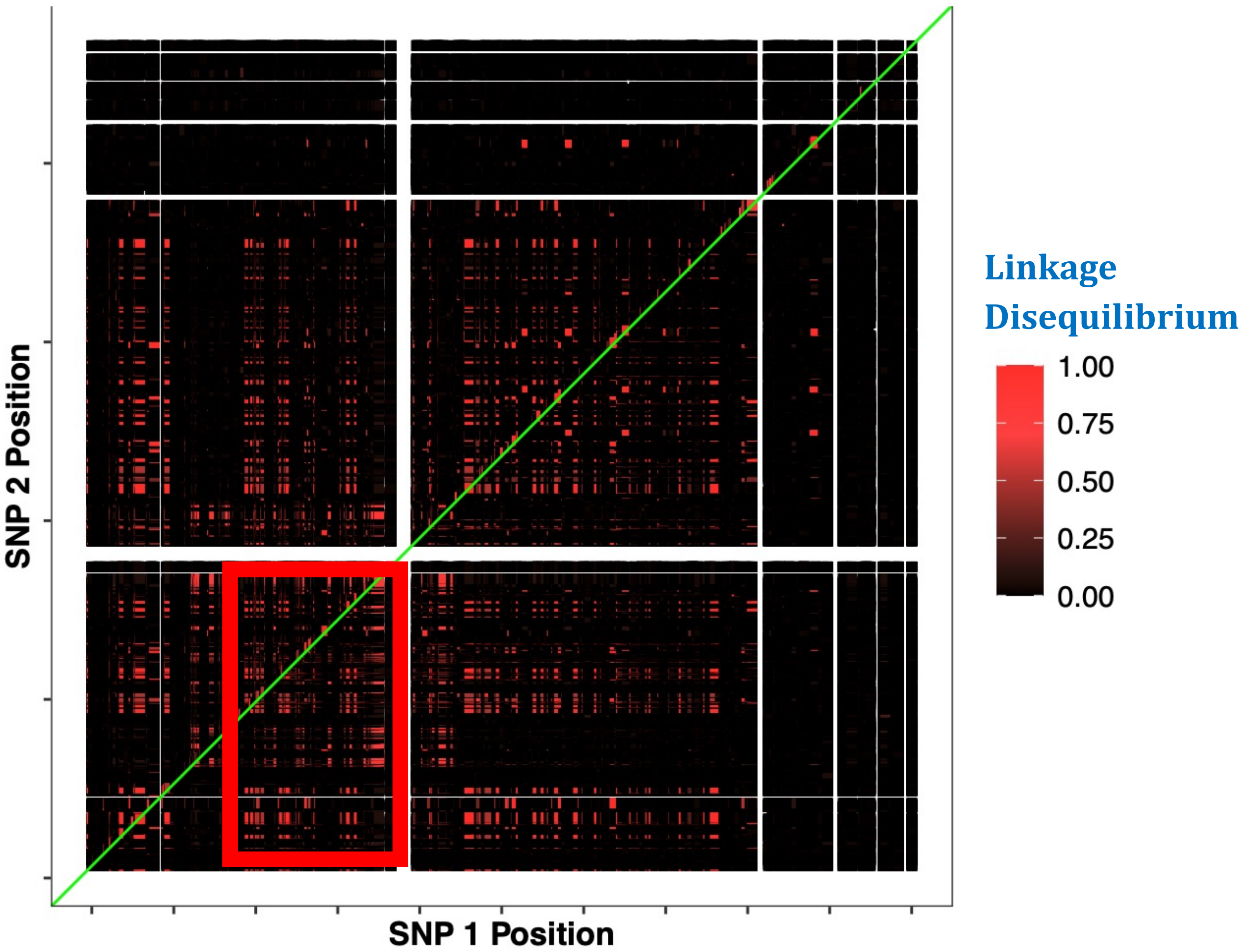
High levels of genetic diversity in this structural variants in hybrids

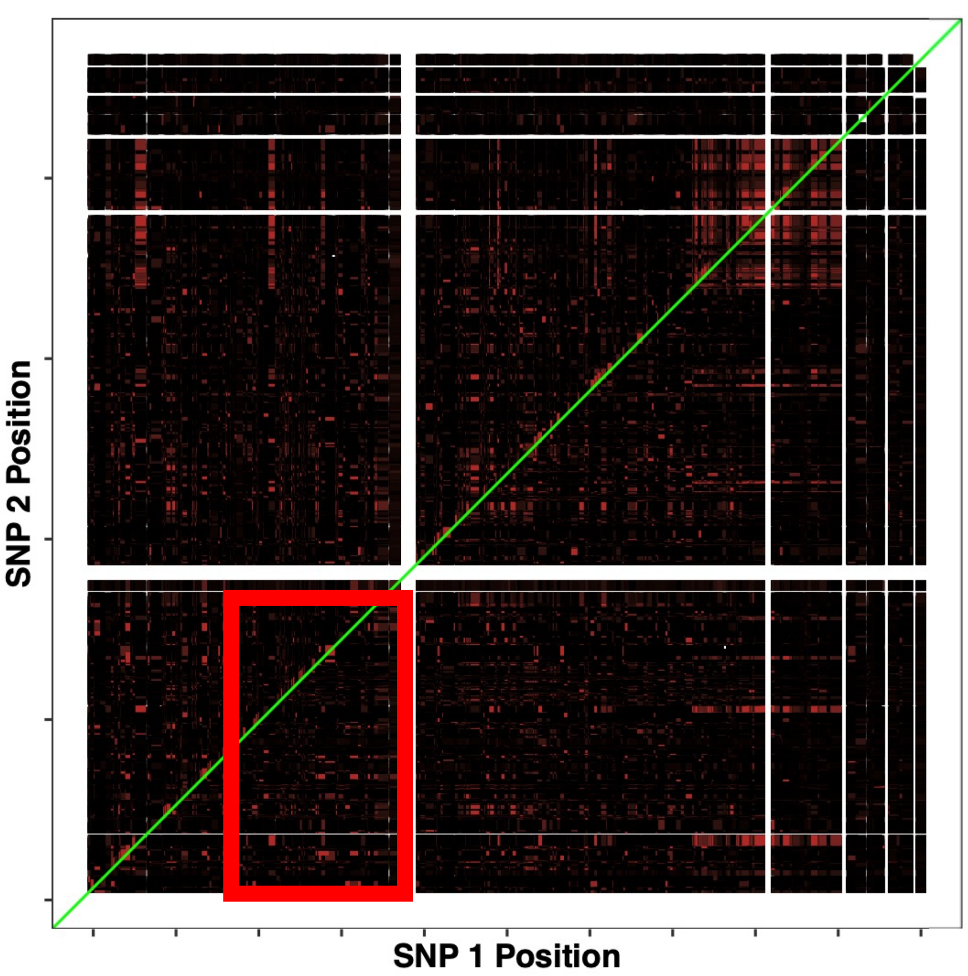


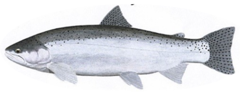
Highest genetic diversity in this region in hybrids



High linkage disequilibrium near the inversion in natural Steelhead, not Coastal Cutthroat Trout



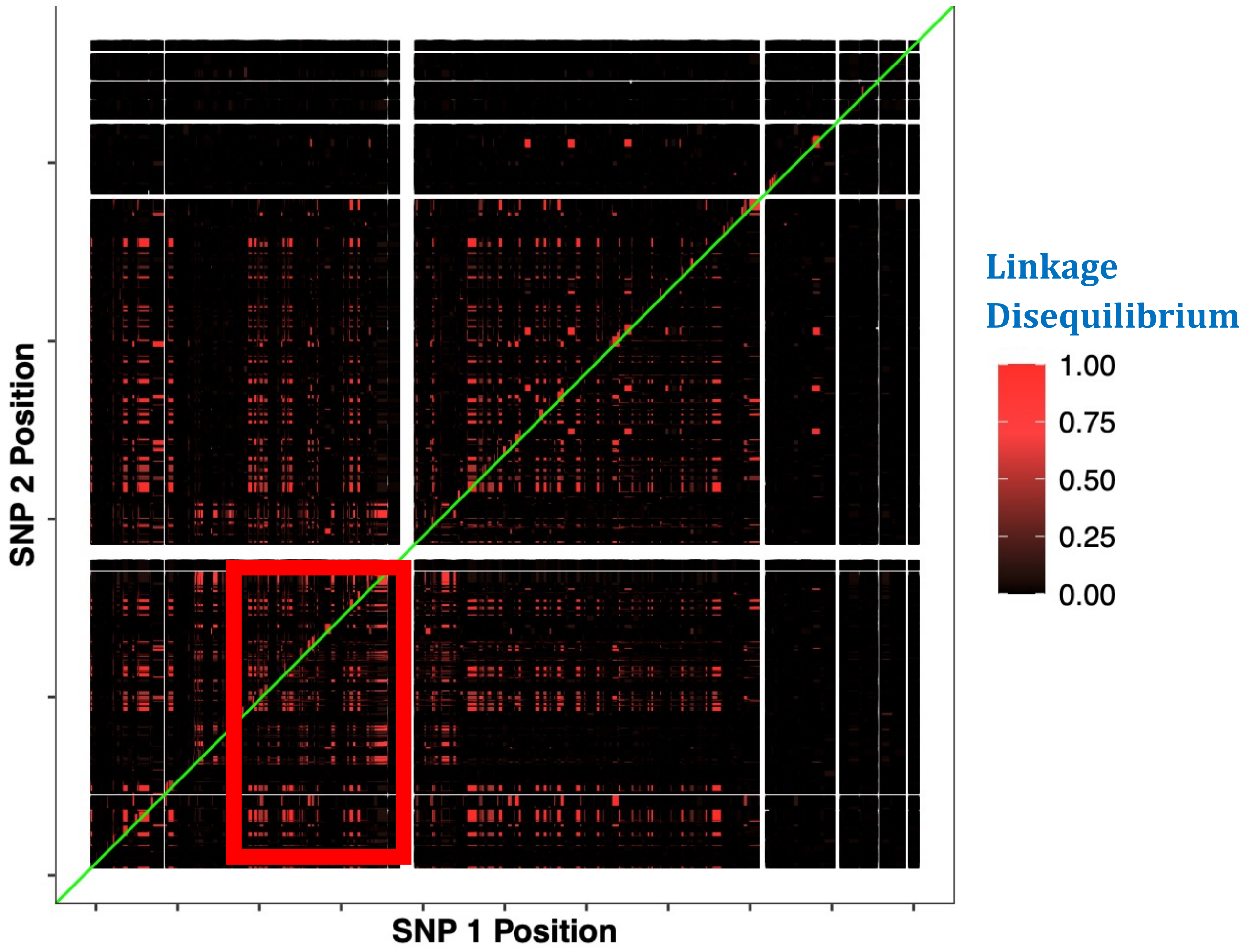


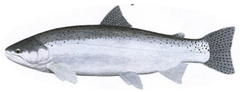


STH

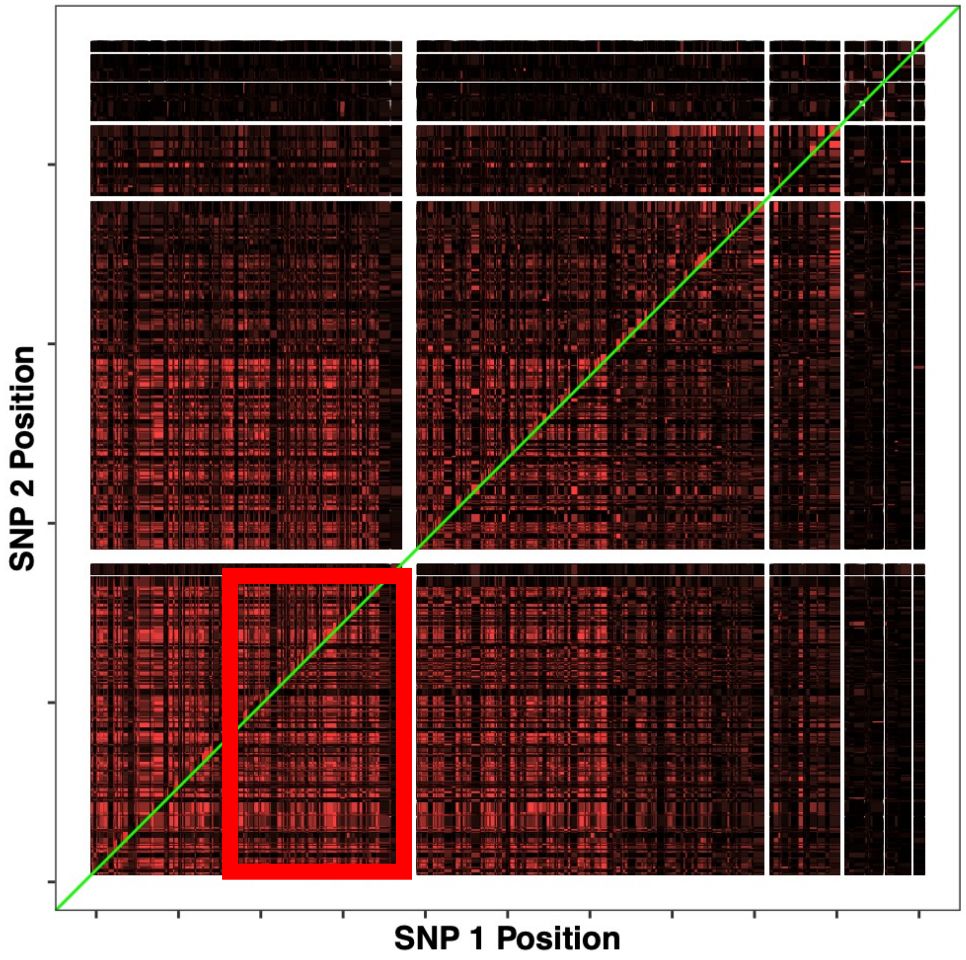
CCT

In natural populations, we see high linkage disequilibrium in hybrids broadly across chromosome 20





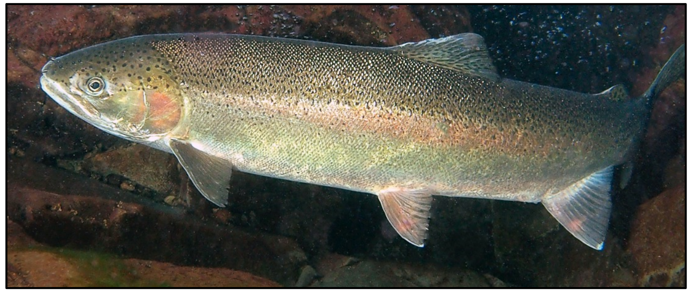
STH



Hybrids

Reference genomes improve our ability to identify Coastal Cutthroat Trout and their hybrids

- Salmonid genomes are complex because of their evolutionary history!
- Patterns of hybridization can vary, making identification of diagnostic markers challenging
- Reference genomes can guide our selection of species and hybrid markers
- Provide tools for developing species-specific markers for monitoring and management
- We can use reference genomes to identify regions of genomic incompatibility

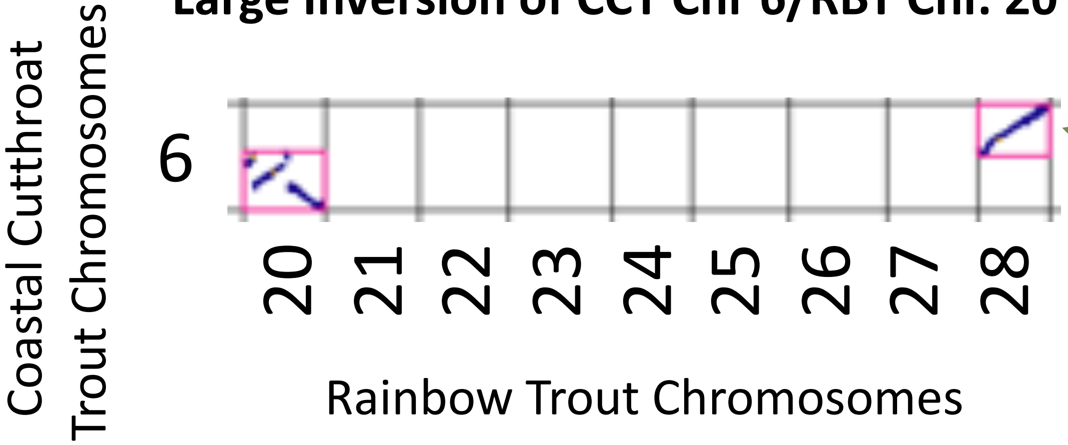


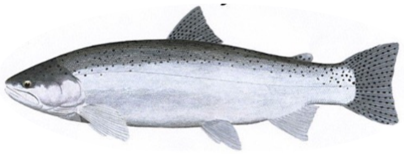
We can also use reference genomes to look for shared underlying shared life-history traits

Rearrangements in CCT

CCT Chr. 6 = fusion RBT Chr. 20 + RBT Chr. 28

Large Inversion of CCT Chr 6/RBT Chr. 20



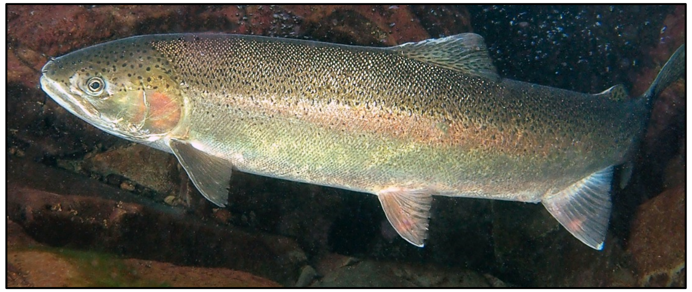


Chromosome 28 contains a gene related to ocean-migration timing in numerous Salmonids

National Genomics Center
FOR WILDLIFE AND FISH CONSERVATION

Acknowledgements, Funding and Coauthors

Rocky Mountain Research Station



Funding

USDA ARS
National Research Council NRC
NSF

Genome assembly and linkage mapping

USDA ARS
NOAA
University of Idaho
Forest Service U.S. Department of Agriculture
Washington Department of Fish and Wildlife
USGS

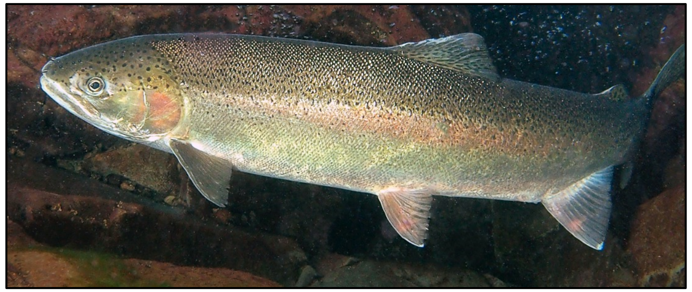
Elwha River samples + lab crosses

USGS
Washington Department of Fish and Wildlife
NOAA
Elwha Klallam Tribe
National Park Service
Trout Unlimited

National Genomics Center
FOR WILDLIFE AND FISH CONSERVATION

Thanks for listening, any questions?

Rocky Mountain Research Station



Funding

USDA ARS

NRC

NSF

Coastal CUTTHROAT COALITION

Genome assembly and linkage mapping

USDA ARS

NOAA

University of Idaho

FOREST SERVICE U.S. DEPARTMENT OF AGRICULTURE

WASHINGTON DEPARTMENT OF FISH AND WILDLIFE

USGS

Elwha River samples + lab crosses

USGS

WASHINGTON DEPARTMENT OF FISH AND WILDLIFE

NOAA

ELWHA KLALLAM TRIBE

NATIONAL PARK SERVICE

TROUT UNLIMITED