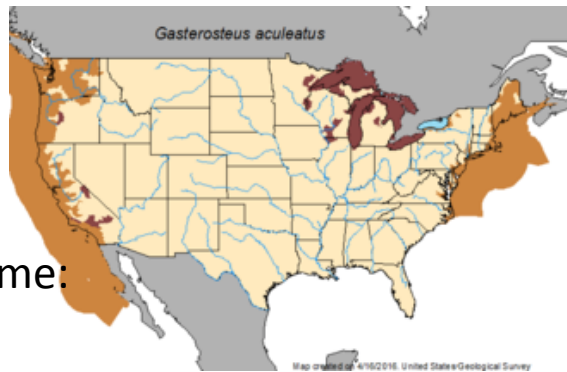


The three-spined stickleback

- Anadromous: lives at sea, breeds in rivers (exceptions)
- Wide geographical range (north of 30°)



Reference genome:
BearPaw lake,
Alaska

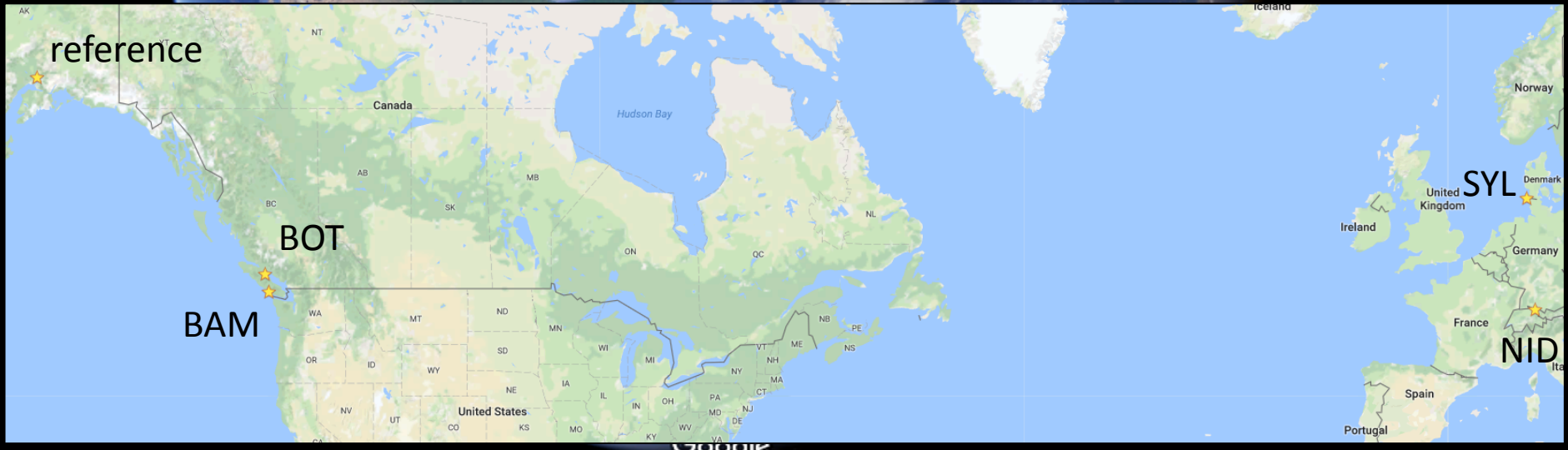
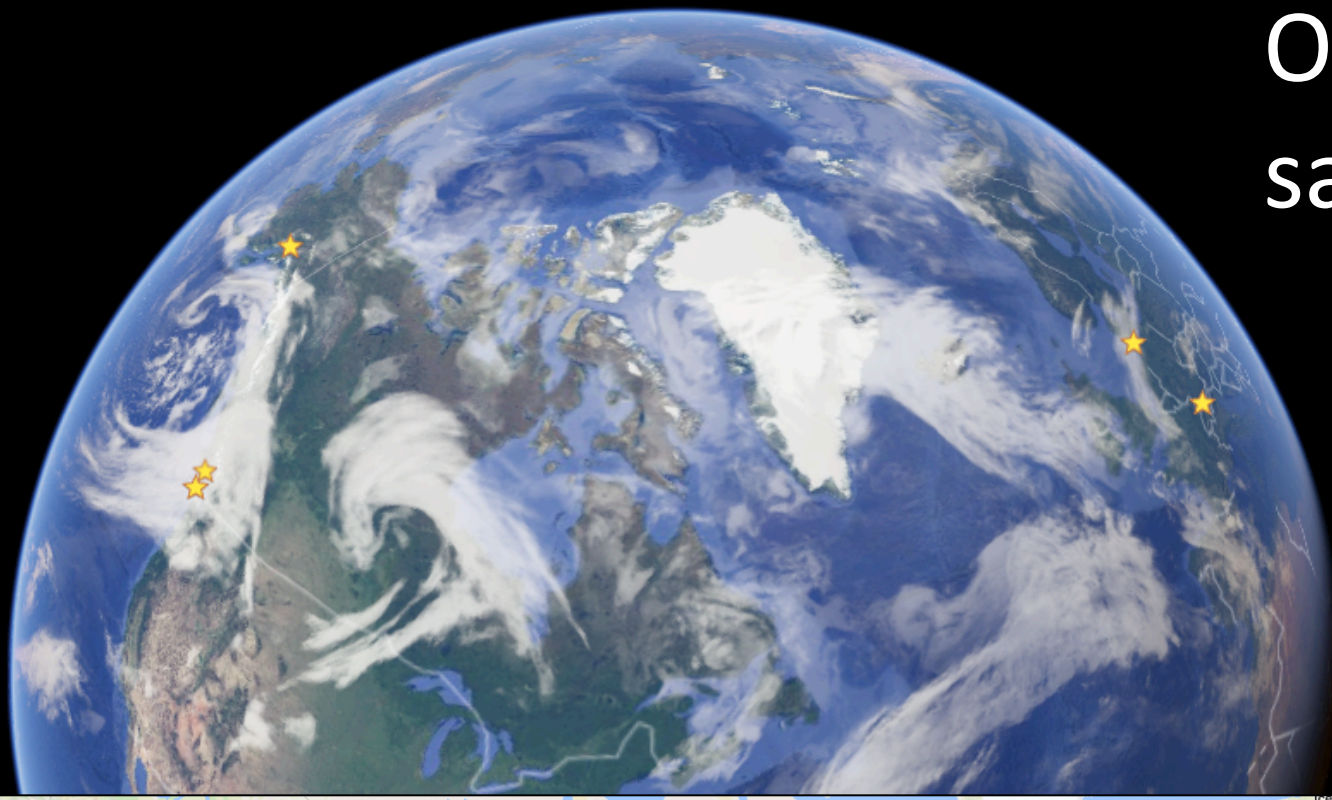


last ice-age
trapped sticklebacks
in rivers/lakes leading to

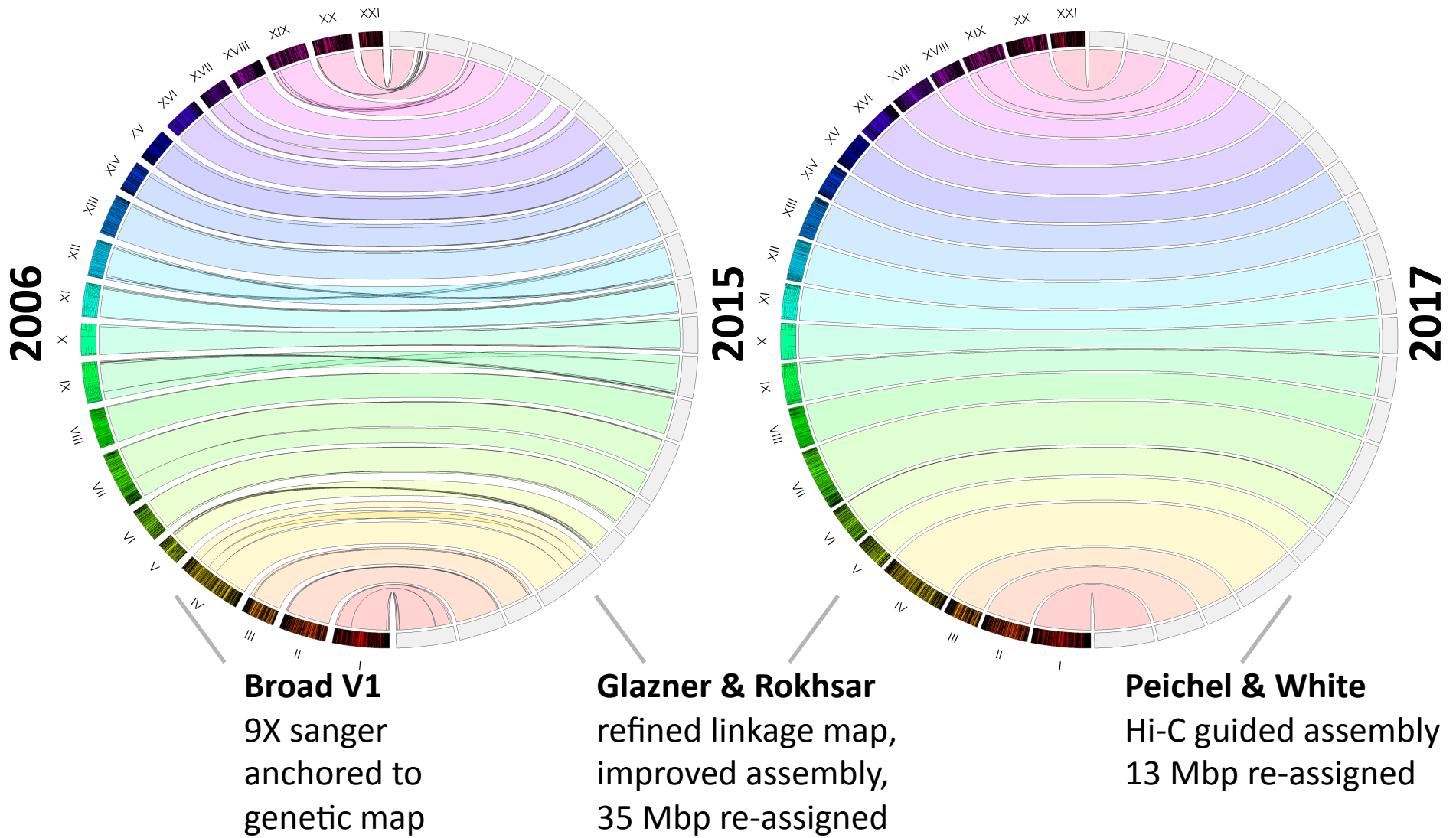
-quick adaptation
-morphological change
-behavioral diversity

- Morphological differences (armour plates)
- Elaborate breeding, behavior; adaptable
- Model for evolution / population genetics, behavioral ecology
- Four supernova genome drafts, 4 genotypes
 - Atlantic / Pacific : fresh / saltwater

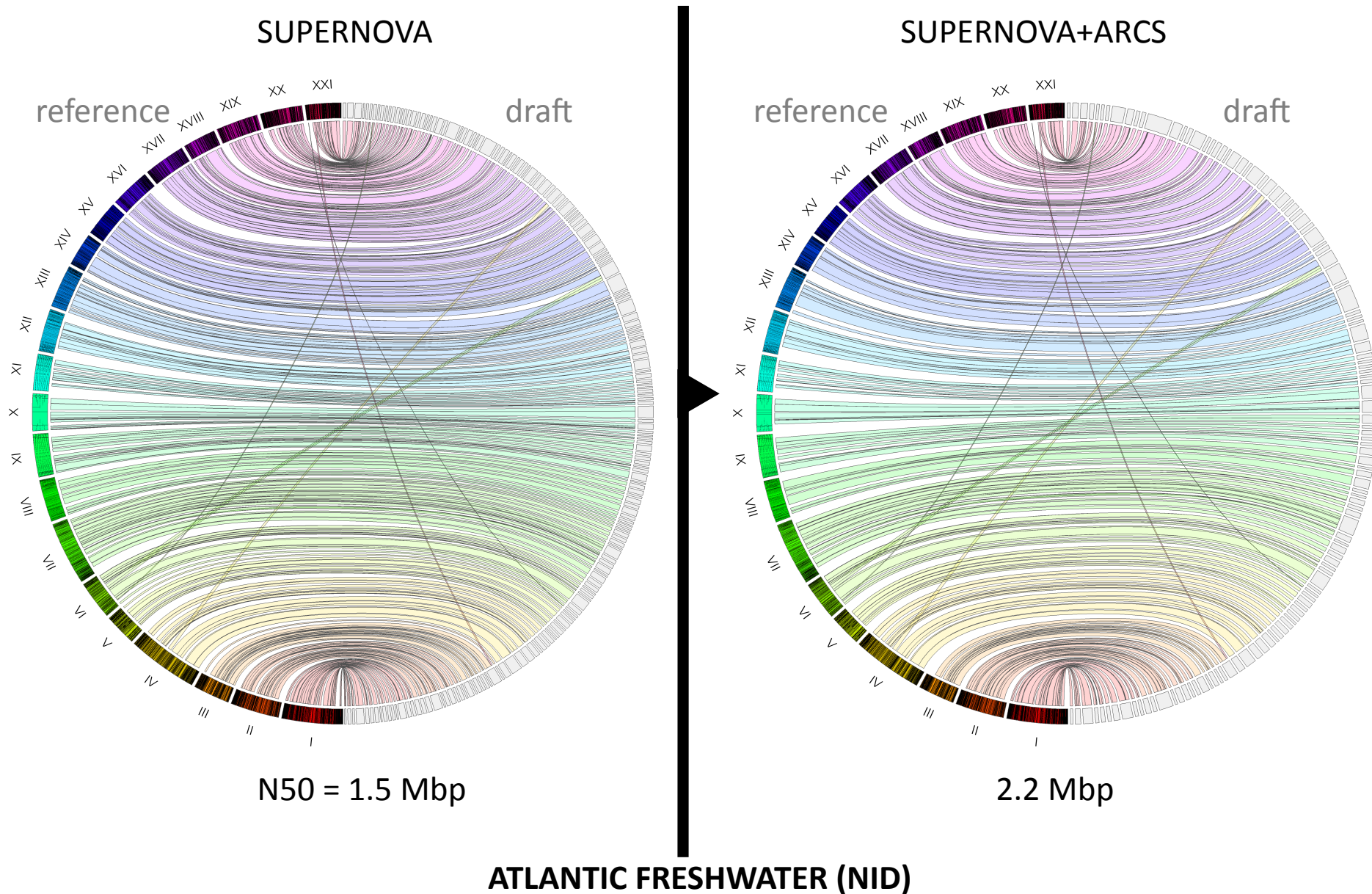
Origins of samples



Gasterosteus aculeatus genome reference improvements



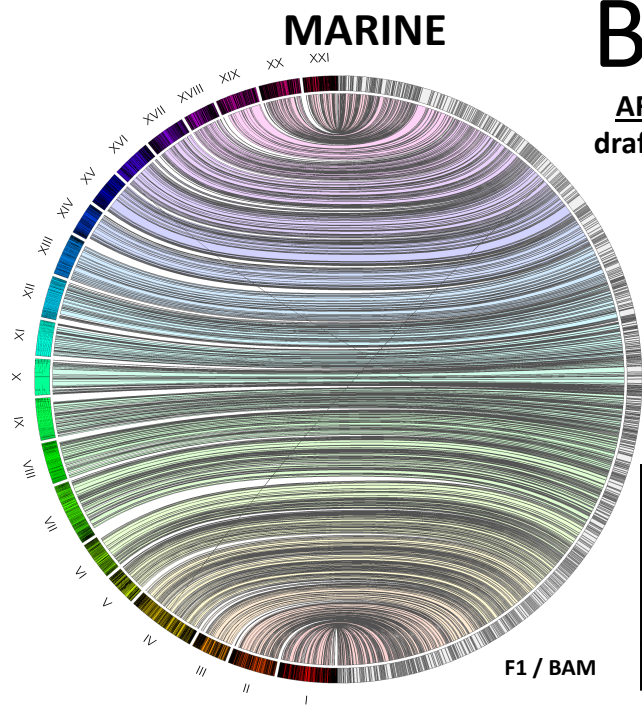
ARCS scaffolding



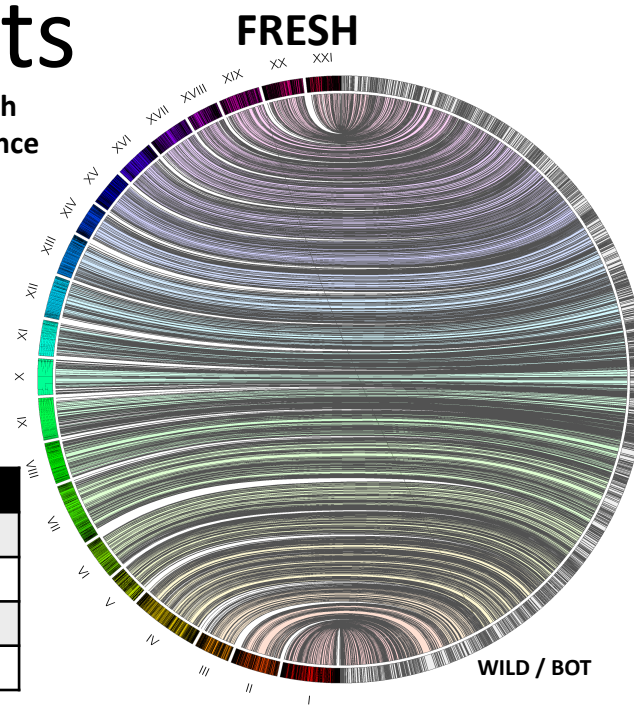
Breakpoints

AFTER ARCS SCAFFOLDING, each draft was aligned to the reference

PACIFIC

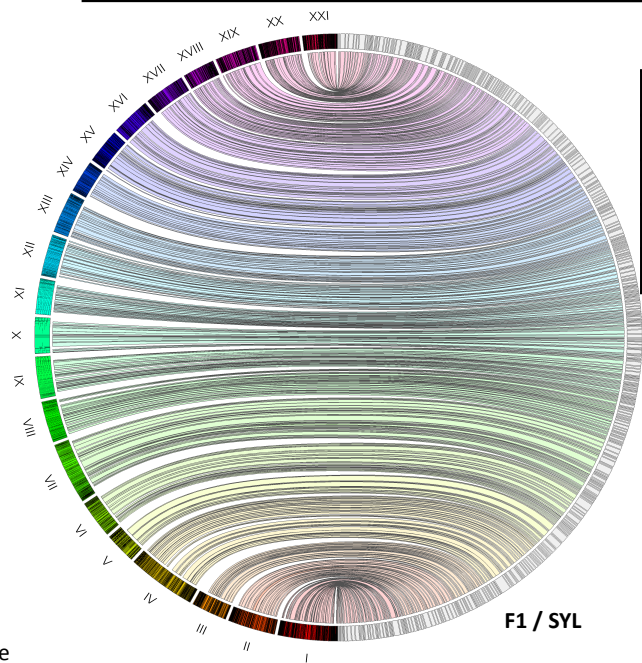


breakpoints	
all	4529
scaff	113
inter	38
intra	75



breakpoints	
all	4540
scaff	96
inter	42
intra	54

ATLANTIC

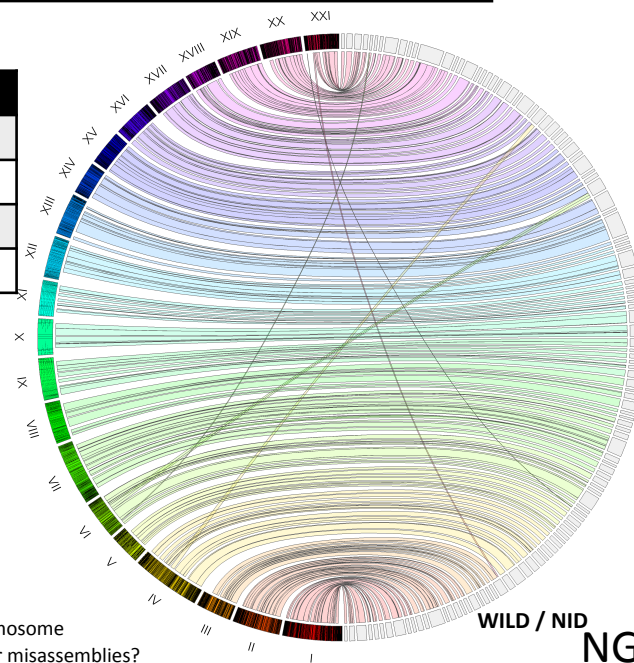


breakpoints	
all	4979
scaff	151
inter*	70
intra	81

breakpoints	
all	5157
scaff	315
inter*	113
intra	202

*XII - II
XII - X
XIV - VI
XV - IV

shared inter-chromosome rearrangements or misassemblies?



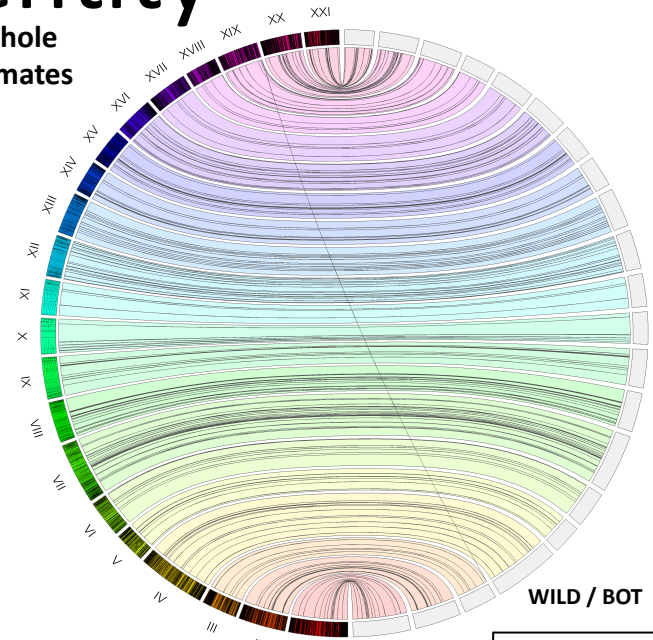
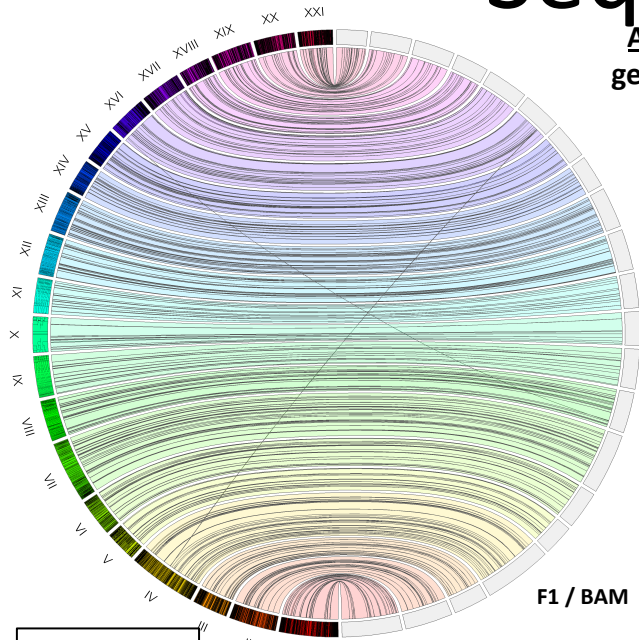
Sequence Identity

AFTER REFERENCE ORDERING whole genome %Sequence Identity estimates with ABySS-Bloom

MARINE

FRESH

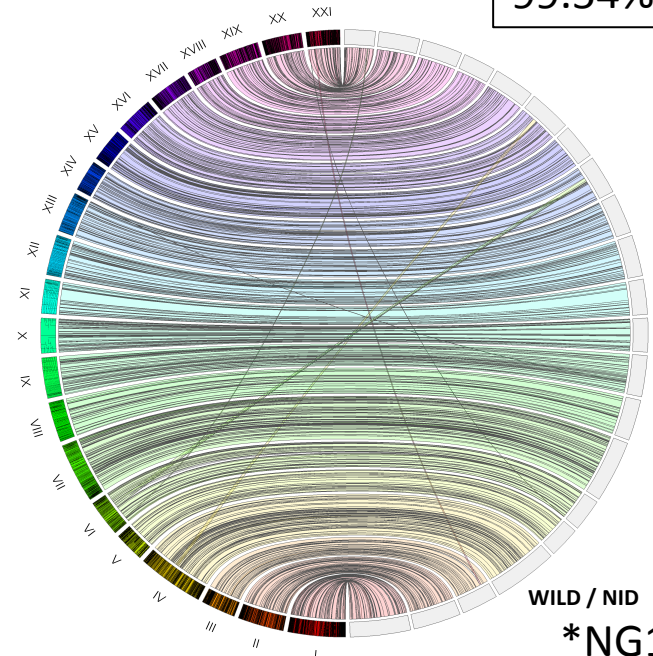
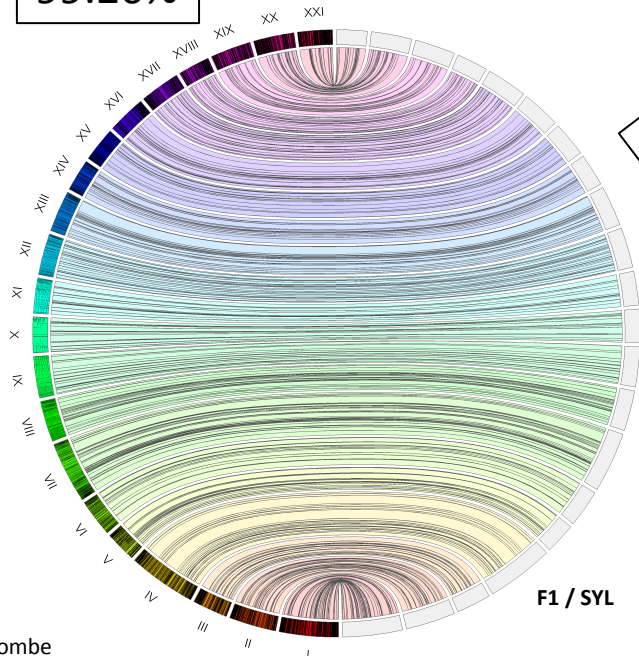
PACIFIC



99.26%

99.54%

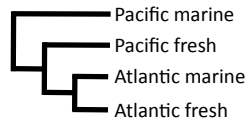
ATLANTIC



99.79%

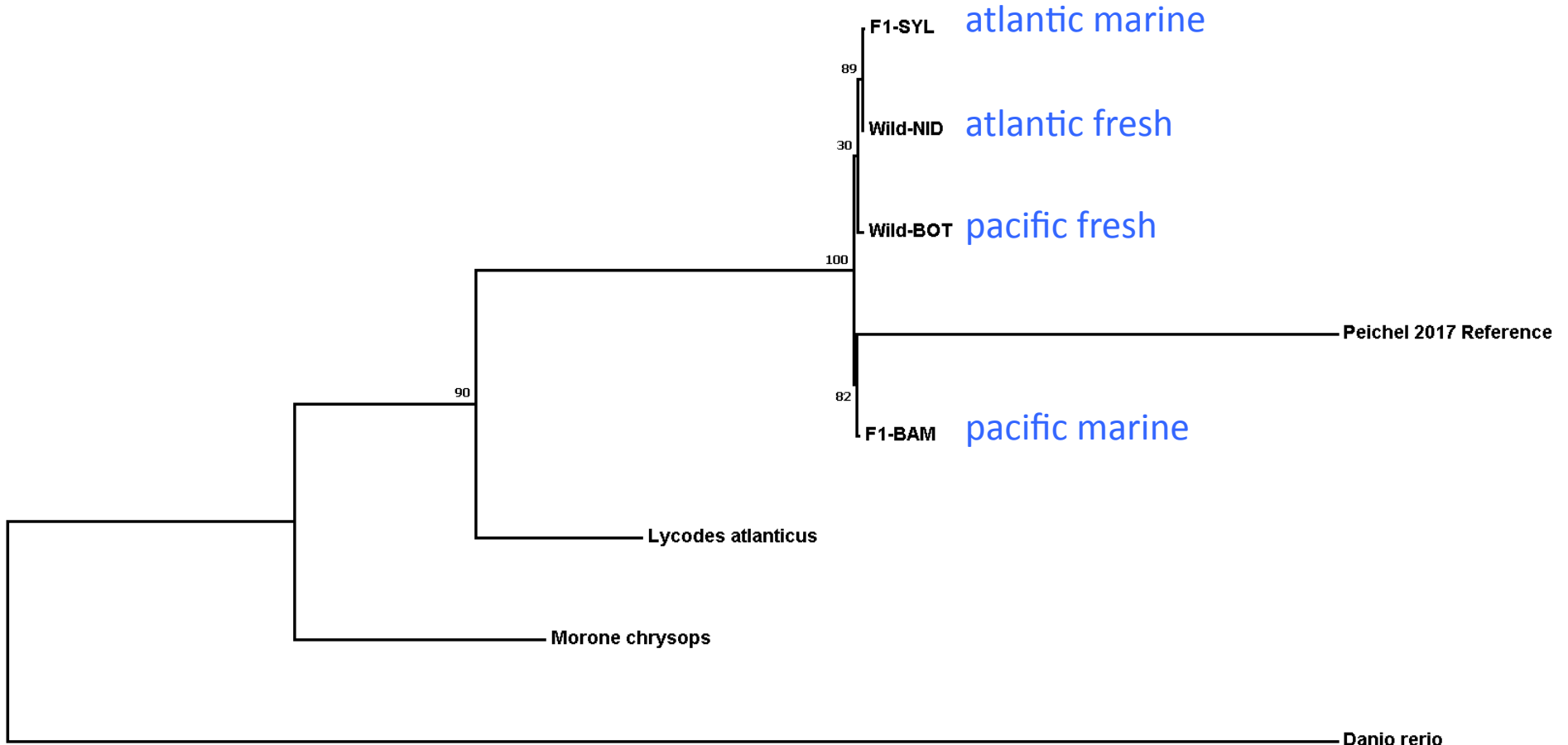
99.25%

Possible phylogeny?



Phylogenetic analysis

- Based on ten 8 single-copy nuclear gene markers (Li et al. 2007 BMC Evol Biol. 2007; 7: 44)
- ENC1, serb2, RYR3, ~~plag1~~^{not found in SYL}, tbr1, zic1, glyt, SH3PX3, ~~myh6~~^{on different chr at 100% seq. id.}, ch211-105n9.1-like : 6.3 kbp
- Corroborates: 1) breakpoint analysis 2) global estimates of sequence identity



0.02

Molecular Phylogenetic analysis by Maximum Likelihood method (bootstrap n=500)

