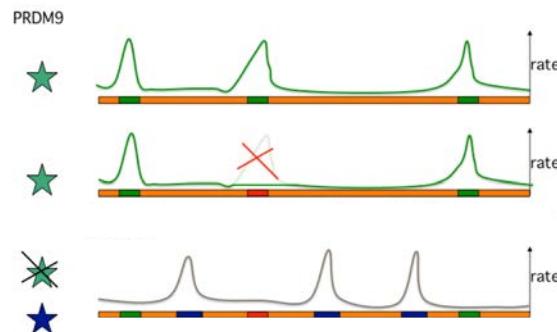


Conséquences de la variation du taux de recombinaison chez les vertébrés

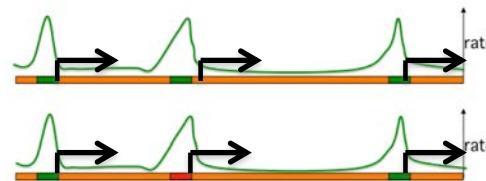
Molly Przeworski

Cours #5

Directed by PRDM9



When targeting functional elements



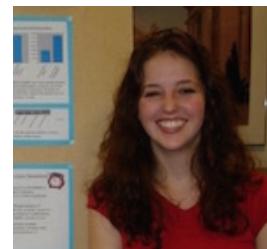
Apes, mice, others...?

Birds, yeasts,...?

How general is this?



Zachary Baker
(PhD Student, Columbia)



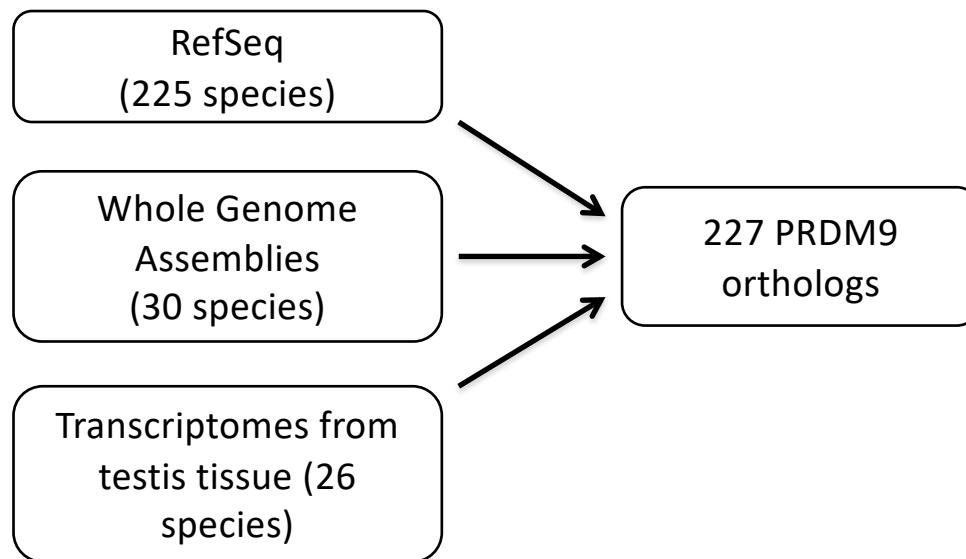
Molly Schumer
(soon, faculty at Stanford)



Yuki Haba
(MA student, now
Princeton grad)

Baker, Schumer et al. 2017 eLife

How general is this?



PRDM9 in (225) vertebrates

Key - All species have complete loss

- Some species have complete loss

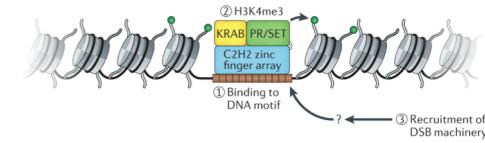
 - All species have lost a particular domain

 - Some species have lost domains in at least one paralog

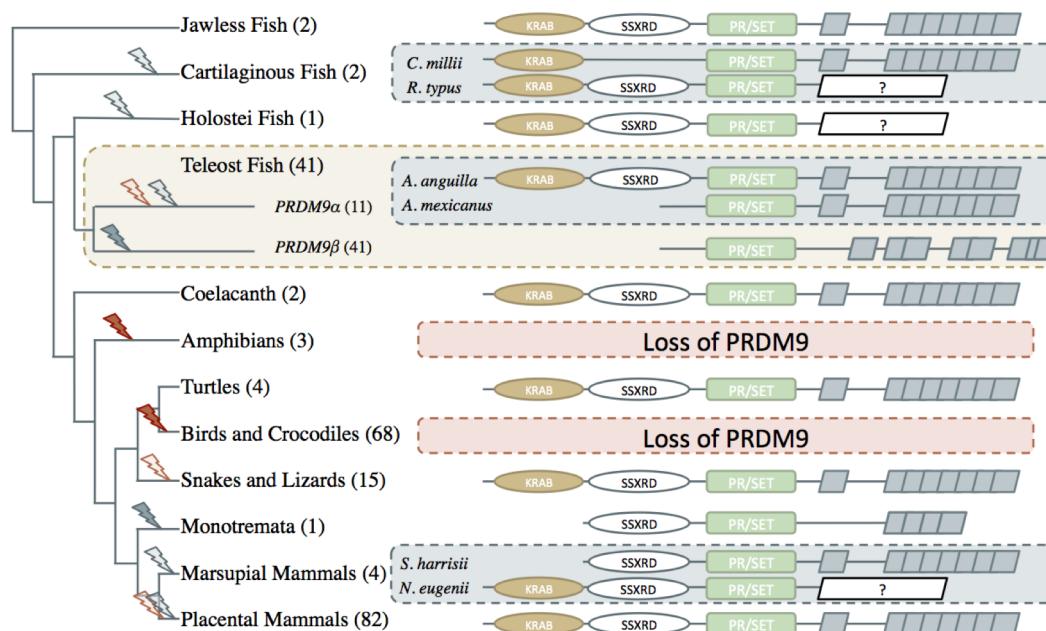
- Representative orthologs

- Representative paralogs

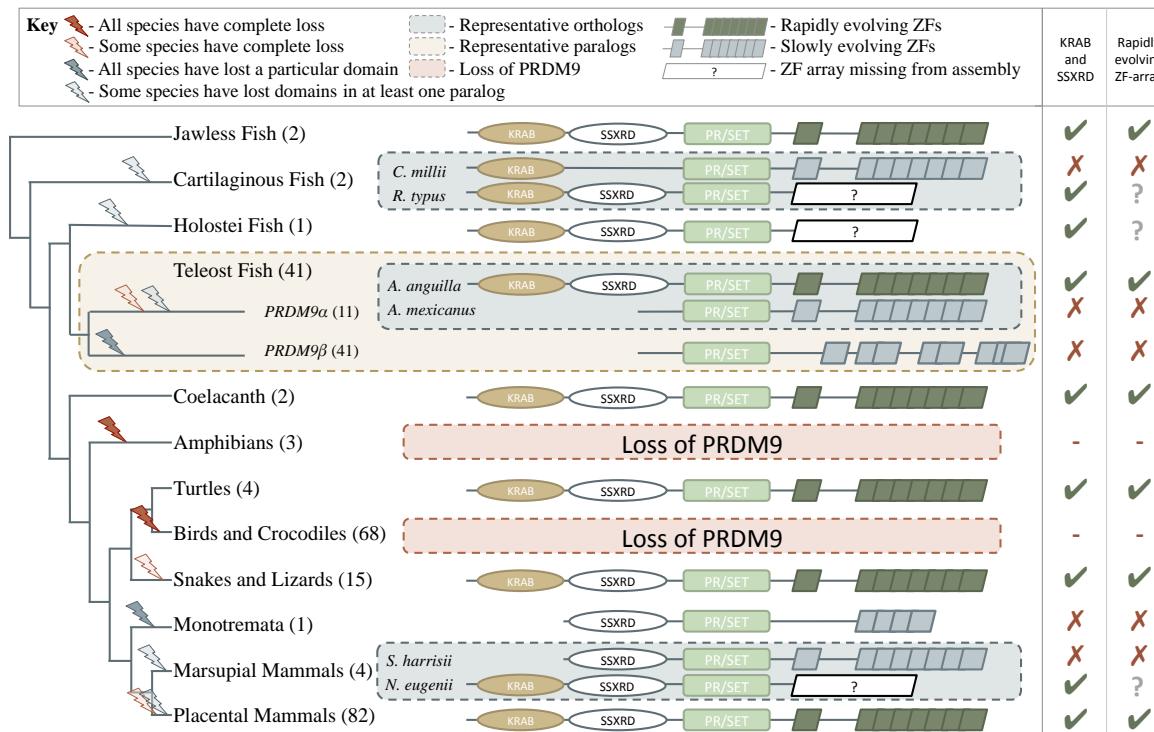
Loss of PRDM9



Partial orthologs
are constrained
(i.e., $dN/dS < 1$ in
the SET domain)

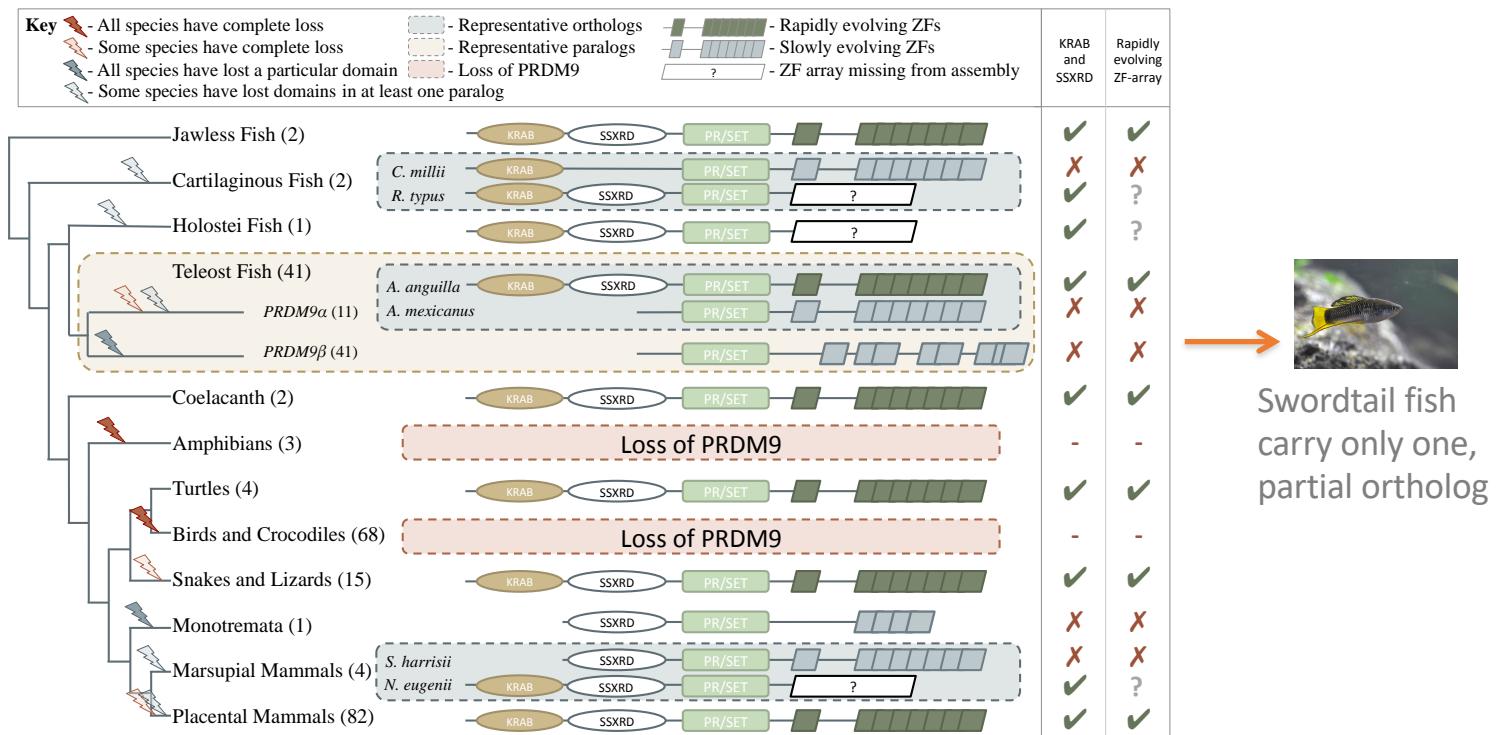


The ZF evolves rapidly if & only if the gene is intact

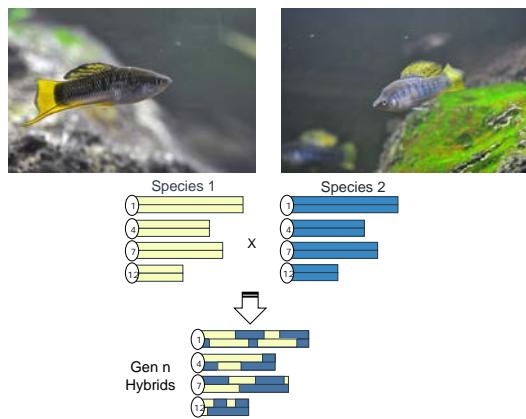
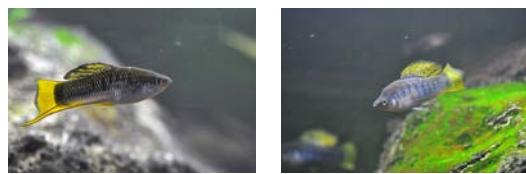


$p < 10^{-6}$, controlling for the phylogeny

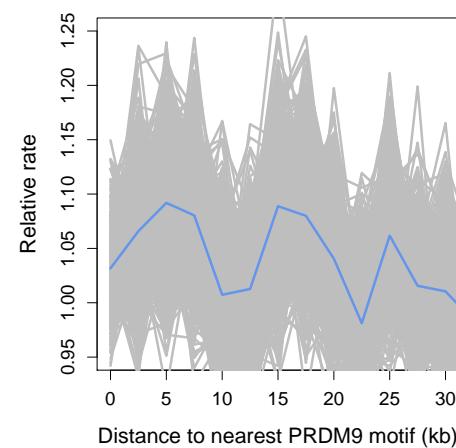
Role in recombination of partial ortholog?



An admixture-based genetic map

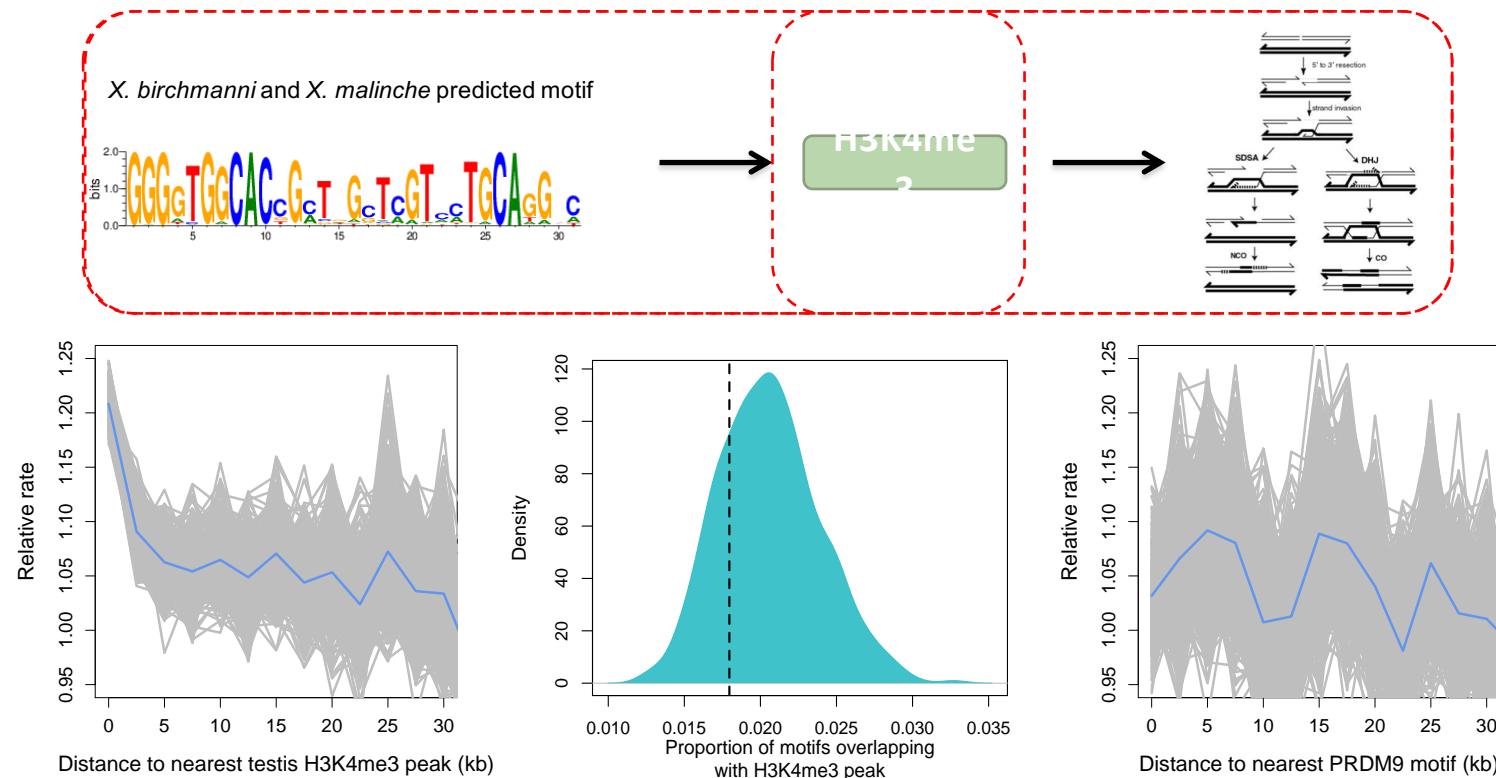


Sequenced 286 hybrids
at ~1X coverage



Role in recombination of partial ortholog?

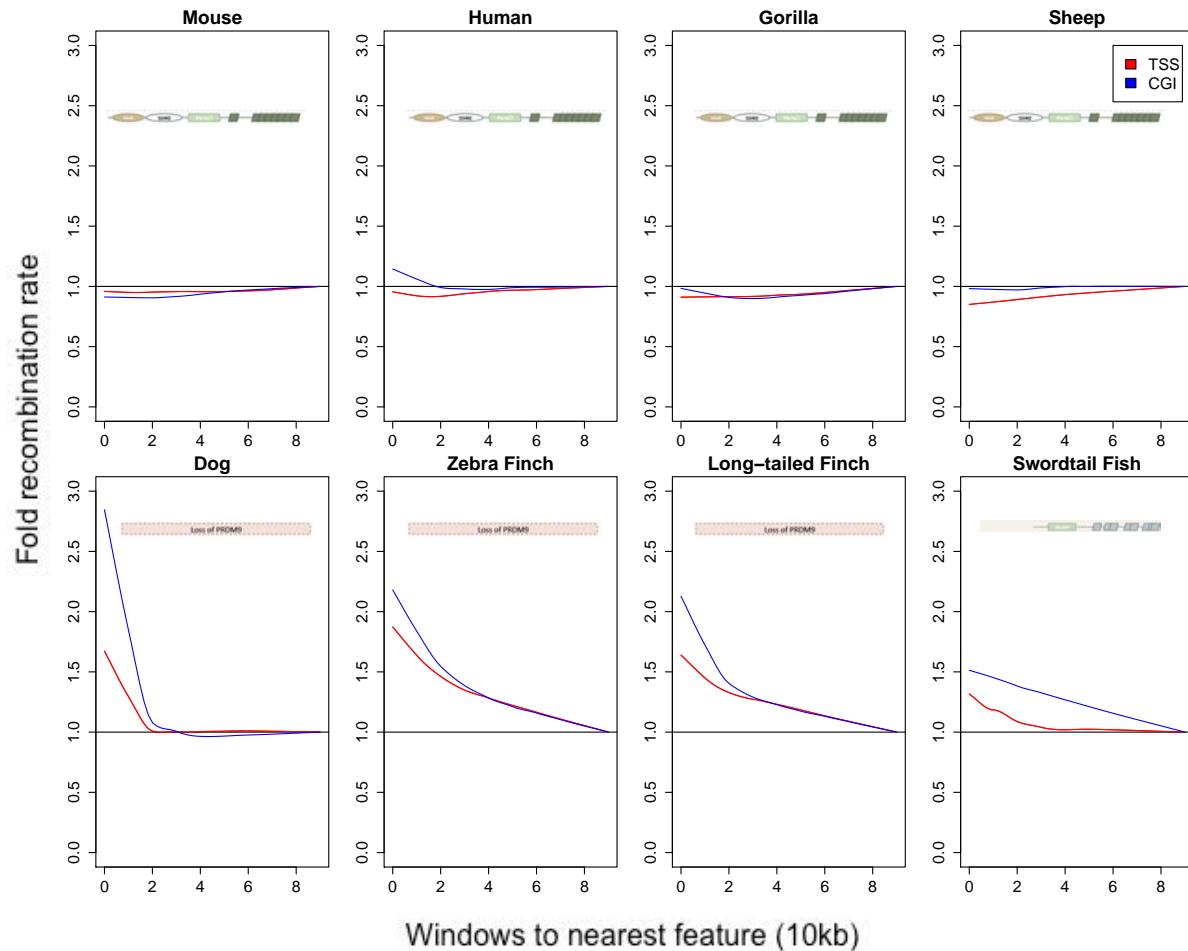




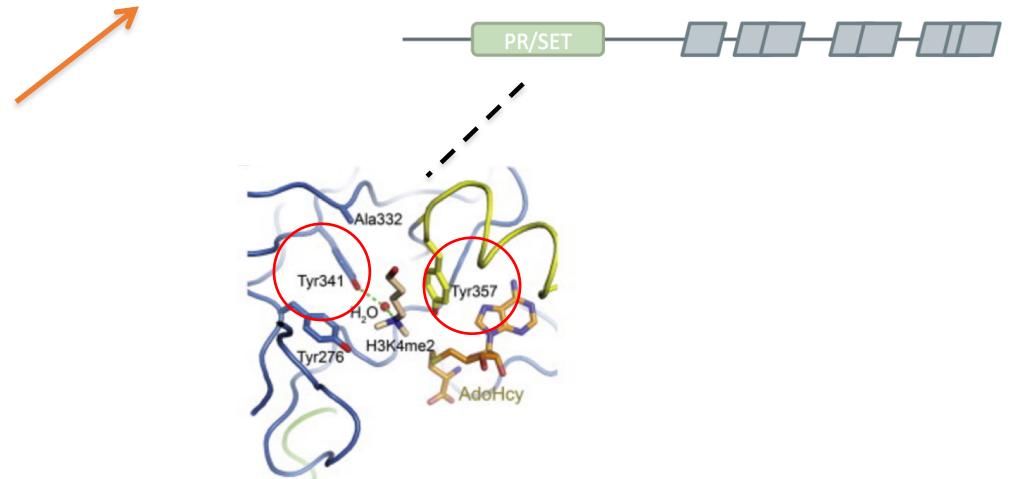
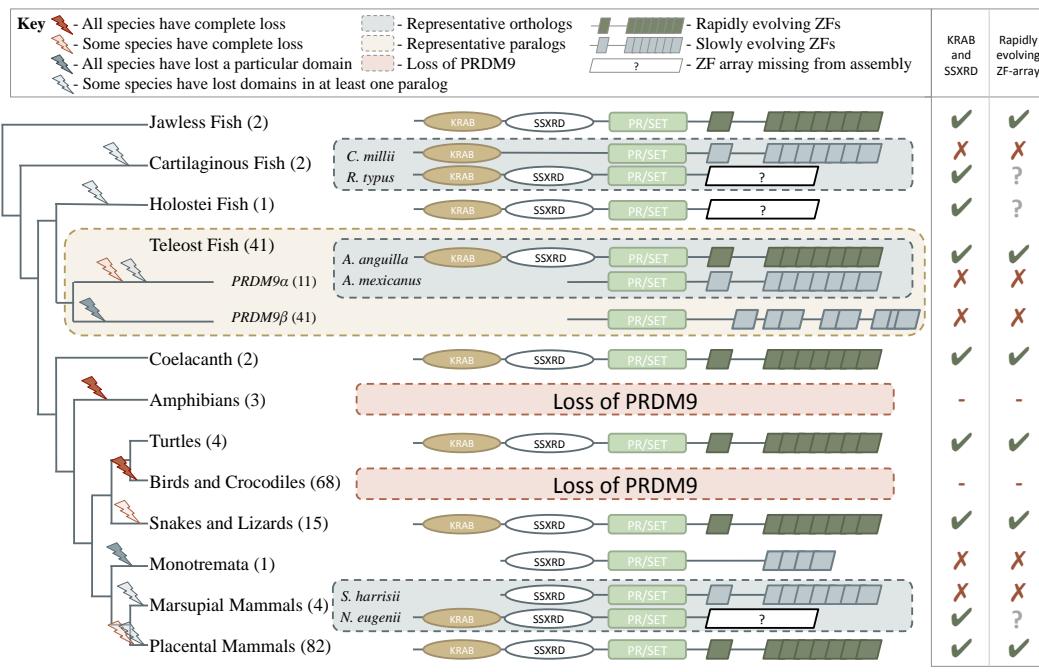
H3K4me3 is associated with the recombination rate

PRDM9 binding motif not associated with H3K4me3

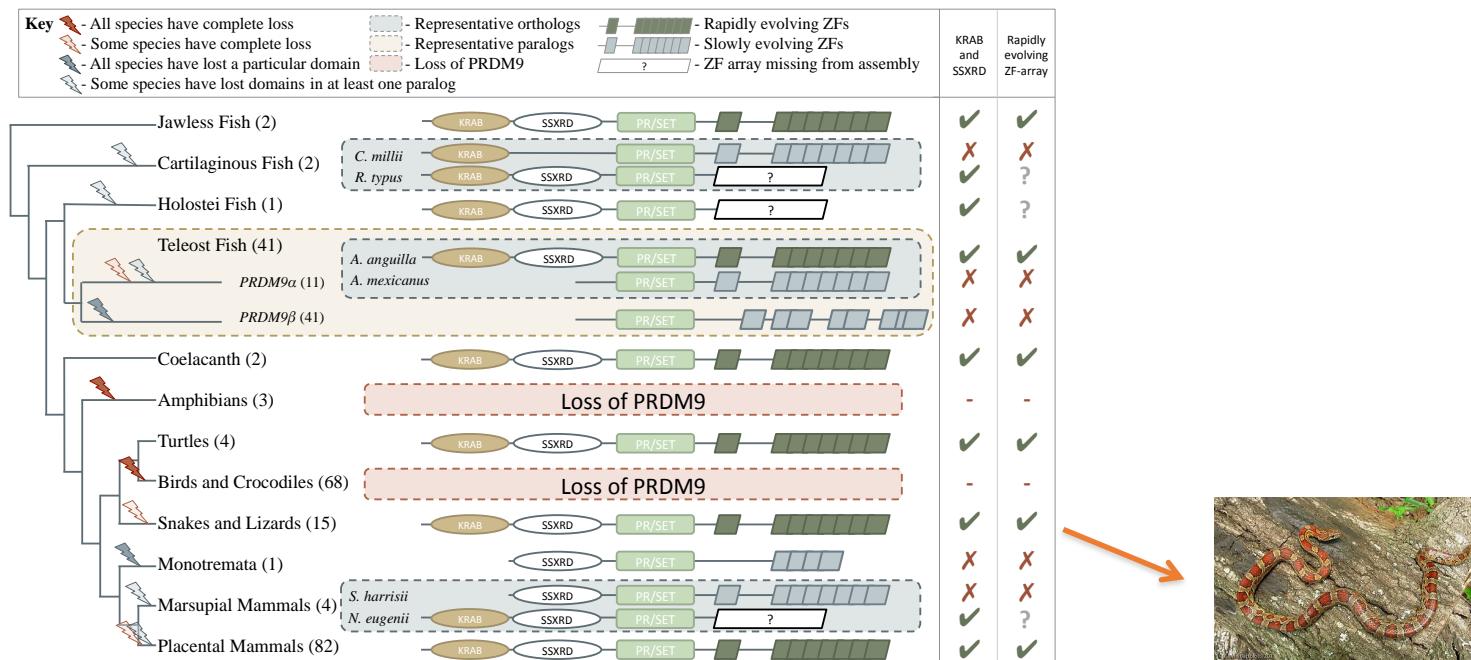
PRDM9 binding motif not associated with increased recombination



The partial ortholog of PRDM9 does not direct recombination

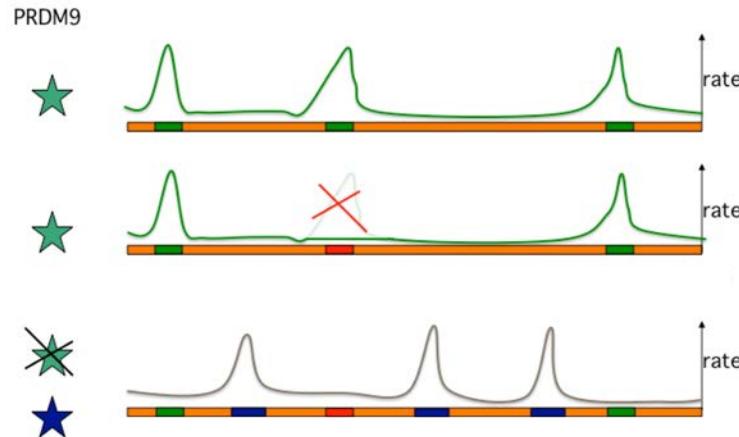


Does the complete ortholog of PRDM9 direct recombination outside of mammals?



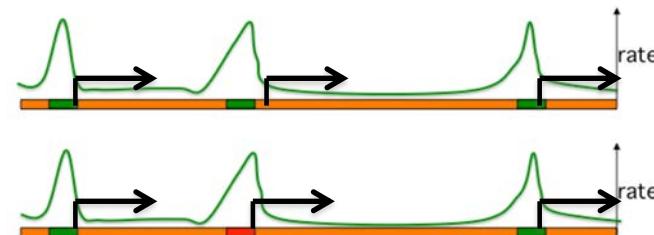
Two mechanisms for directing recombination in vertebrates

Directed by the complete PRDM9

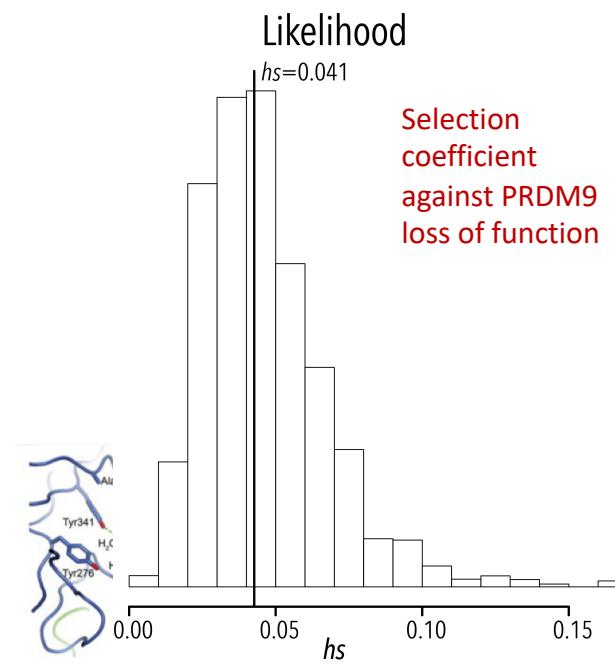
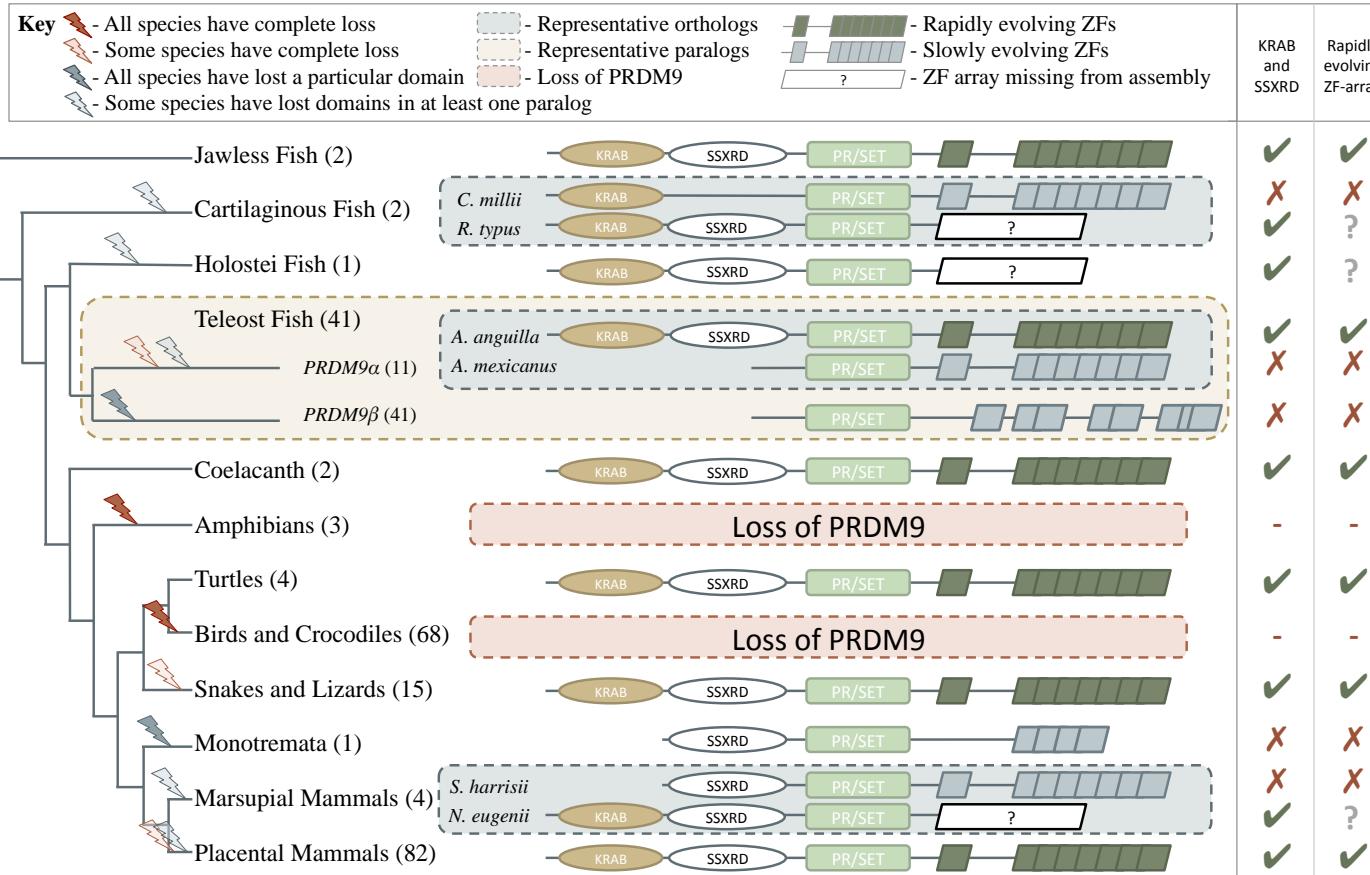


primates, rodents, snakes (?)
Also turtles, some fish?

Without a complete PRDM9

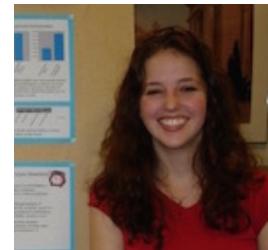


birds, some fish
amphibians, monotremes?



Zachary Fuller

Implications for patterns of between species introgression



Molly Schumer
(soon faculty, Stanford)

Schumer et al. 2018 Science

Many species have hybridized or are hybridizing



Staubach et al 2012



Rosenthal et al 2003



Green et al 2010



Arnold et al 1993



Brelsford et al 2011

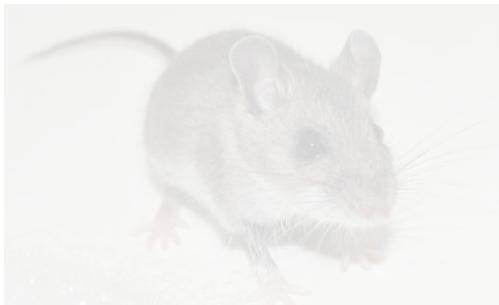


Dasmahapatra et al. 2012



Carney et al 2000

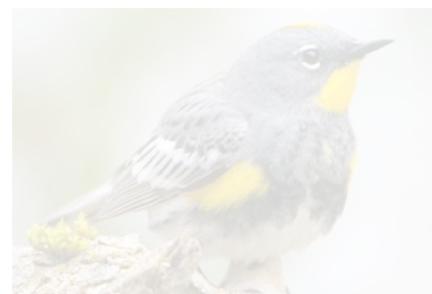
Many species have hybridized or are hybridizing



Staubach et al 2012



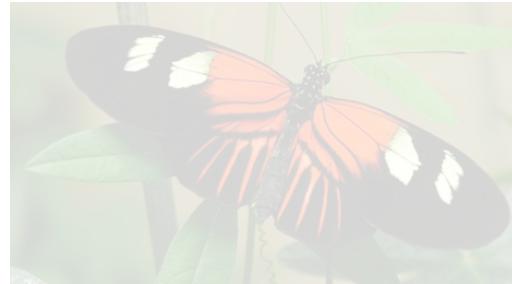
Rosenthal et al 2003



Brelsford et al 2011



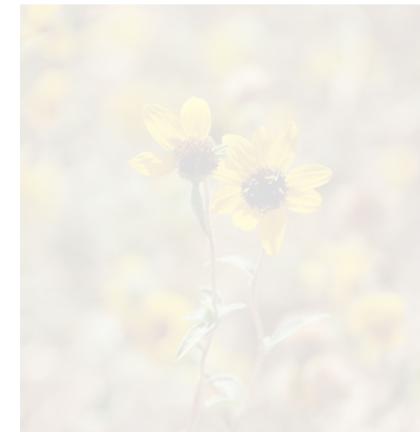
Arnold et al 1993



Dasmahapatra et al. 2012

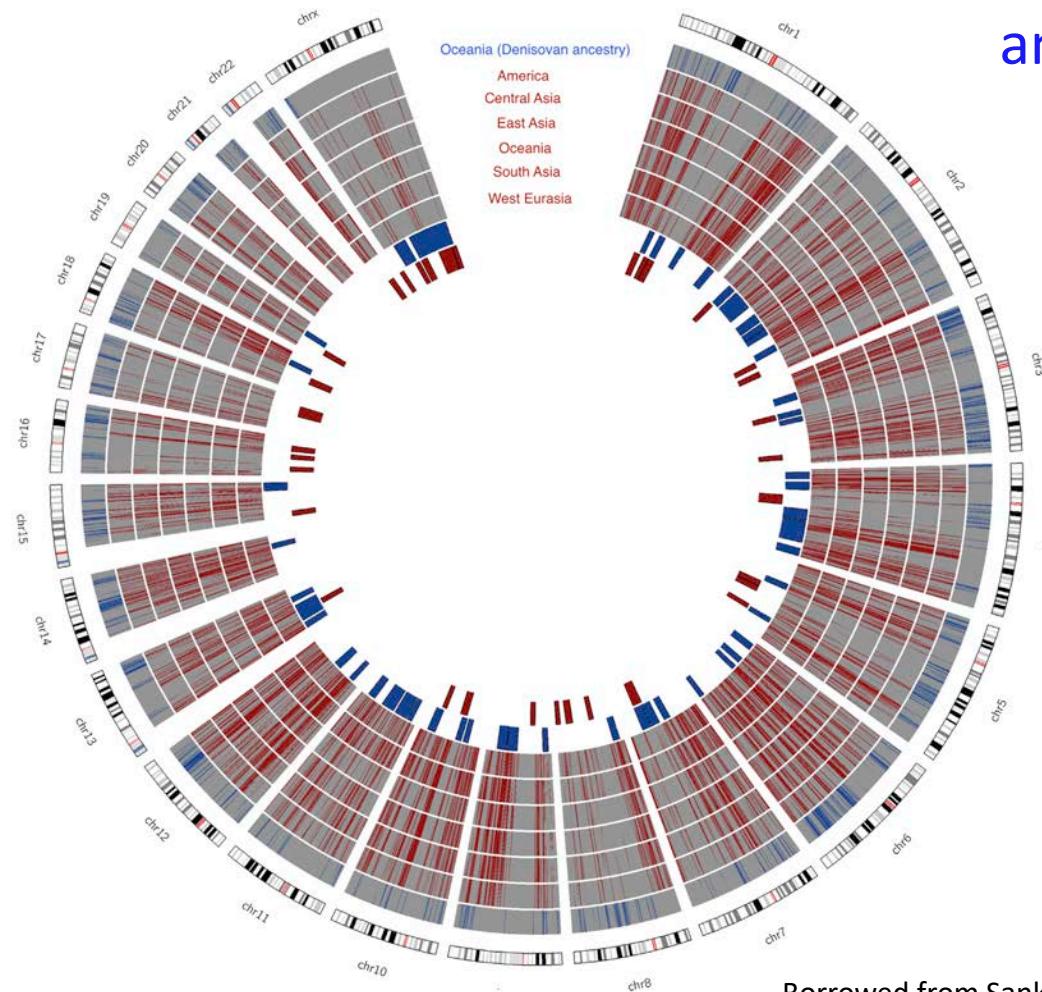


Green et al 2010

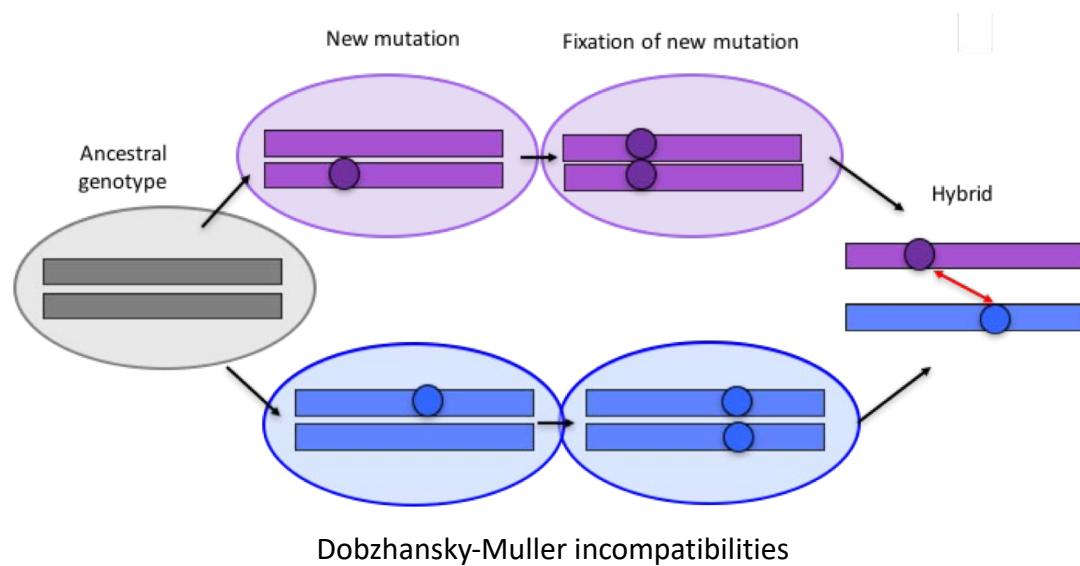


Carney et al 2000

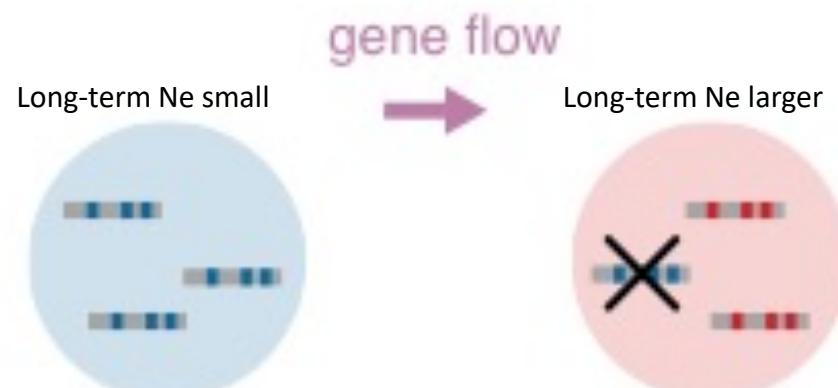
Europeans have
~2% Neanderthal
ancestry



Borrowed from Sankararaman et al. 2016



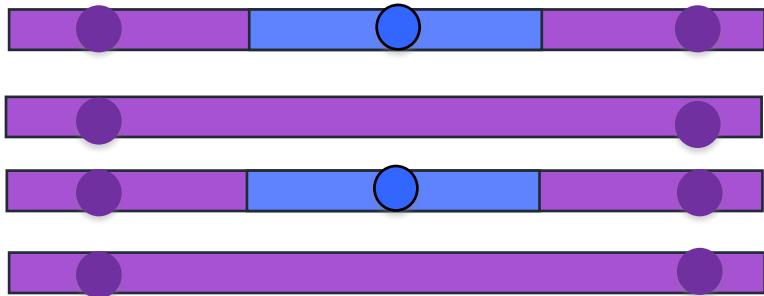
PRDM9 is an example of a DMI in some mice crosses



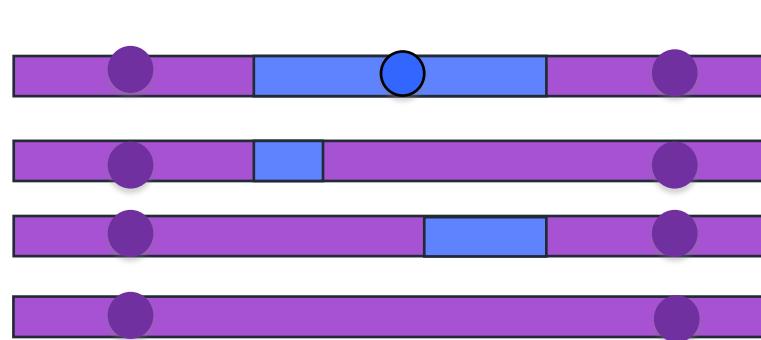
Harris & Nielsen 2016; Juric et al. 2016
Figure from Simon Aeschbacher

-  Incompatibility with 
-  Major ancestry - Human
-  Minor ancestry - Neanderthal

Low recombination rate



High recombination rate



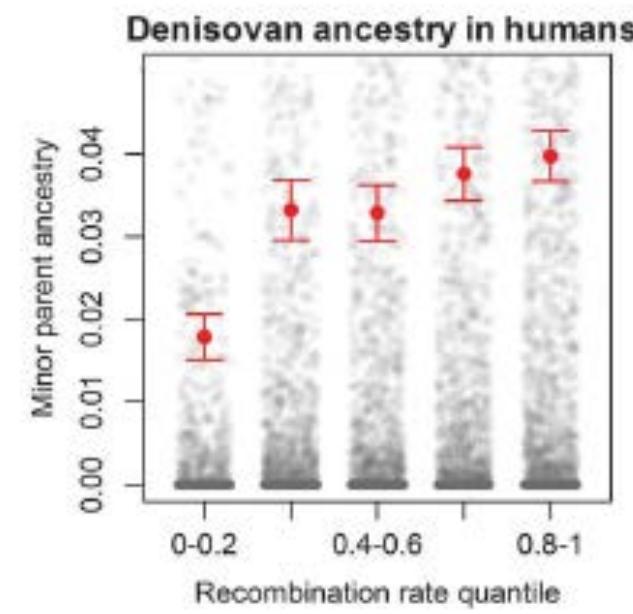
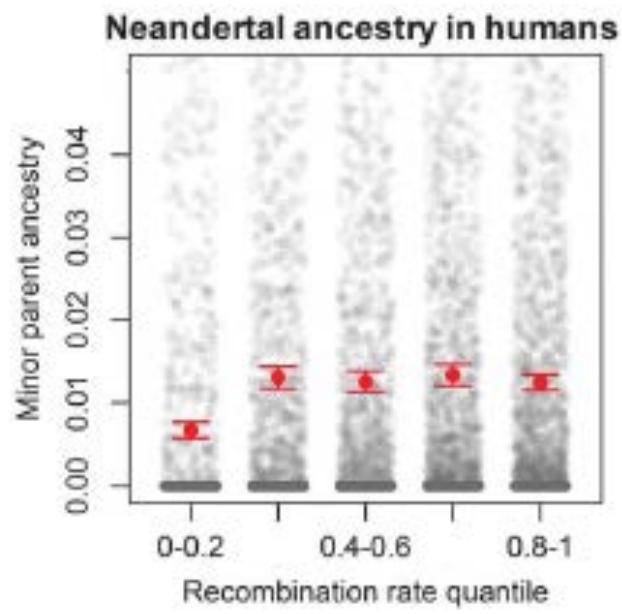
-  Incompatibility with 
-  Major ancestry - Human
-  Minor ancestry - Neanderthal

Low recombination rate



High recombination rate



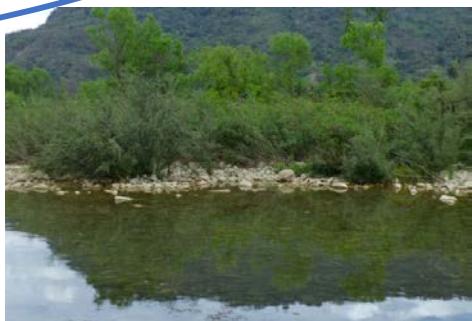


Population	Spearman's correlation between minor ancestry and rate		
	50 kb	250 kb	500 kb
Neandertal ancestry in humans (diCal-admix)	$p = 0.09$ $p = 10^{-17}$	$p = 0.17$ $p = 10^{-33}$	$p = 0.19$ $p = 10^{-42}$
Denisovan ancestry in humans	$p = 0.08$ $p = 10^{-14}$	$p = 0.14$ $p = 10^{-24}$	$p = 0.15$ $p = 10^{-29}$

Hybridization between swordtail species



X. birchmanni
(~400 meters)



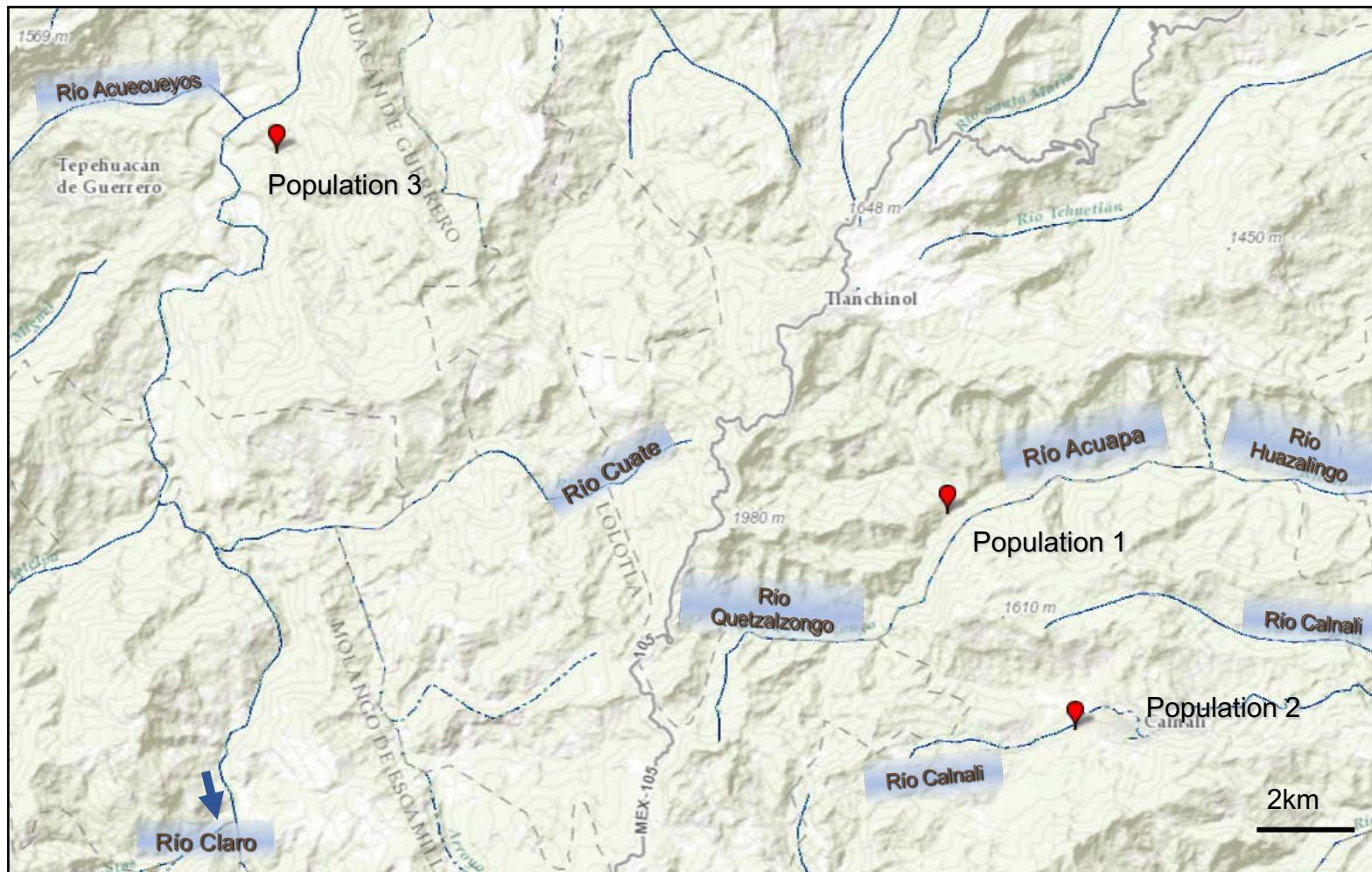
0.5% sequence divergence



X. malinche
(~1200 meters)



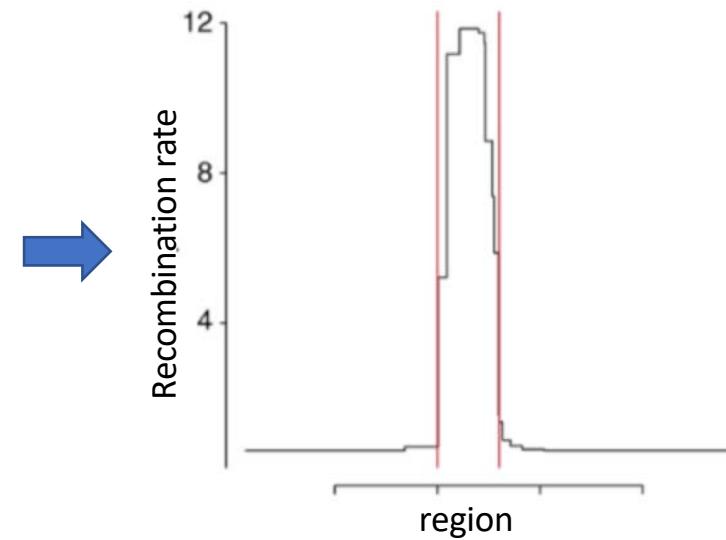
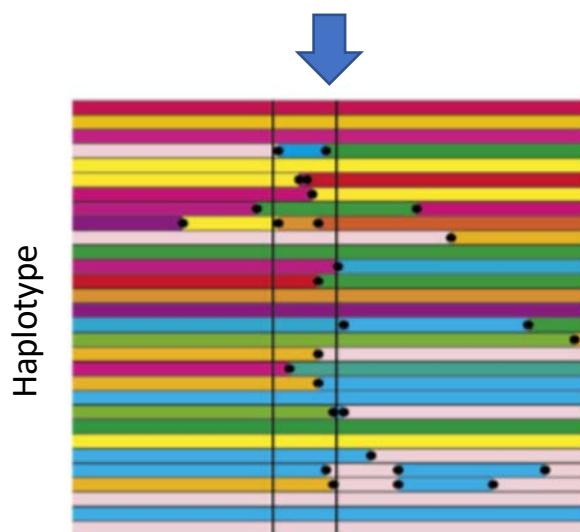
Three independent hybrid populations in Mexico



A fine-scale genetic map for *X. birchmanni*



>30X genomes
20 unrelated *X. birchmanni*
& five offspring of two individuals

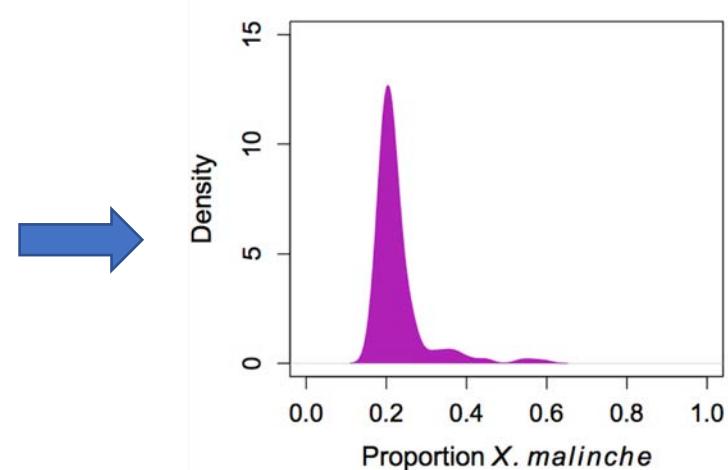
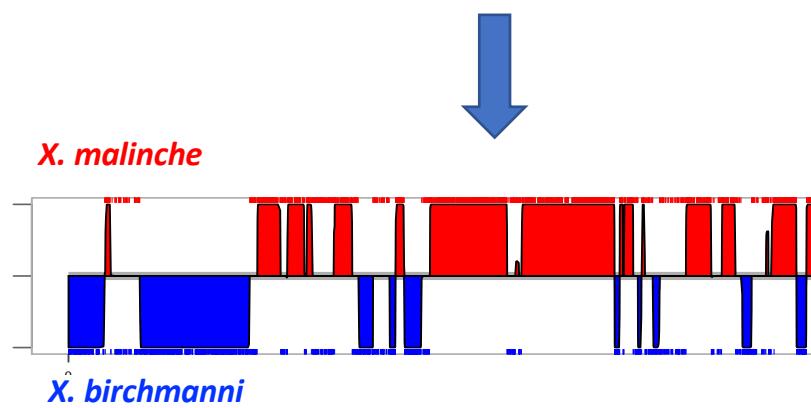


Borrowed from Hellenthal & Stephens 2006

Ancestries of the three hybrid populations

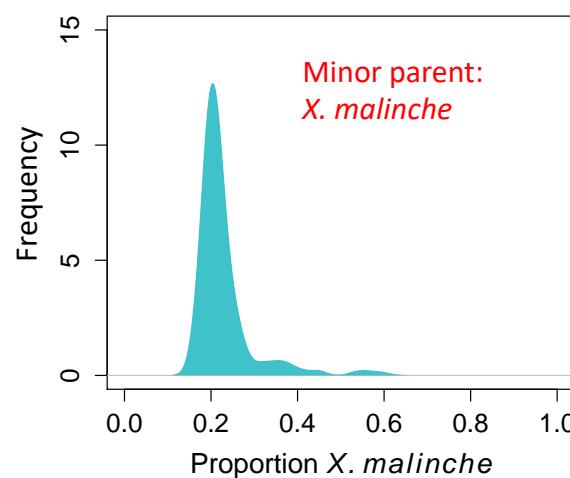


~1X genome coverage for 690 hybrids
from the three hybrid populations

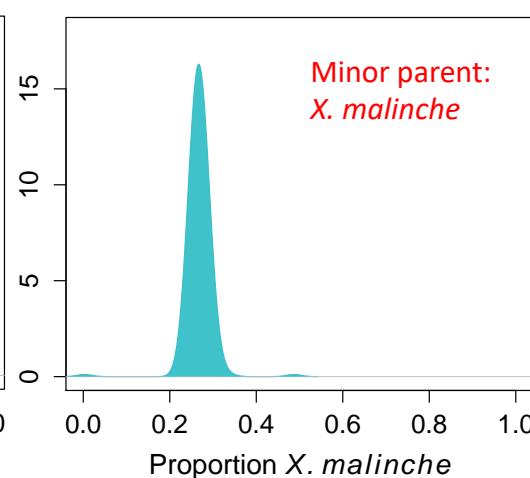




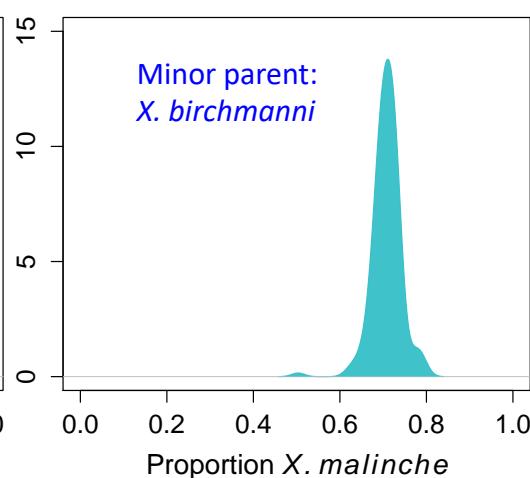
Population 1

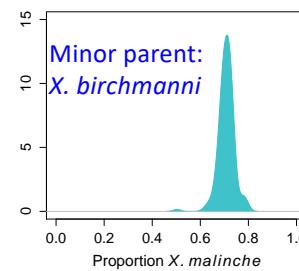
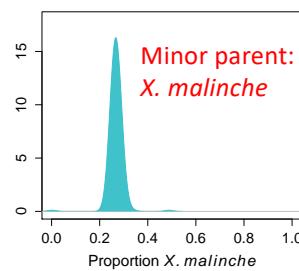
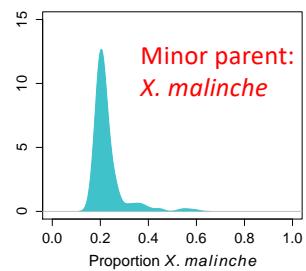


Population 2

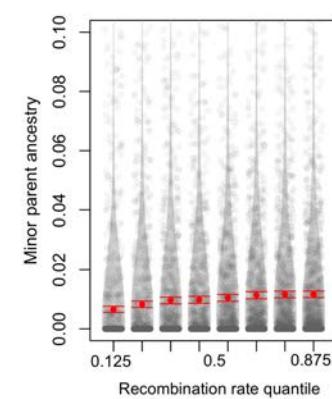
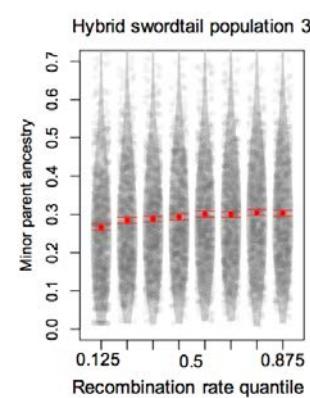
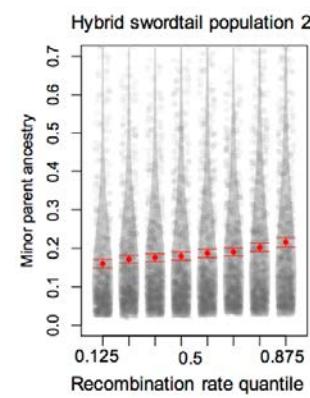
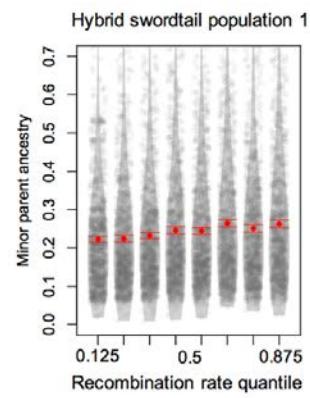


Population 3

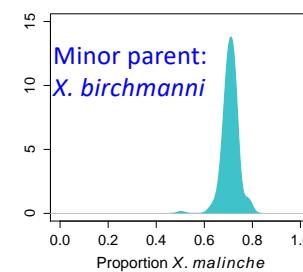
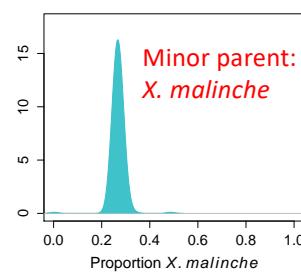
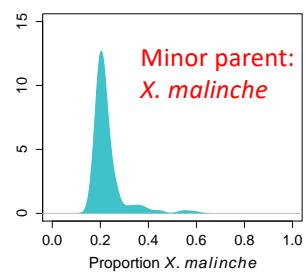




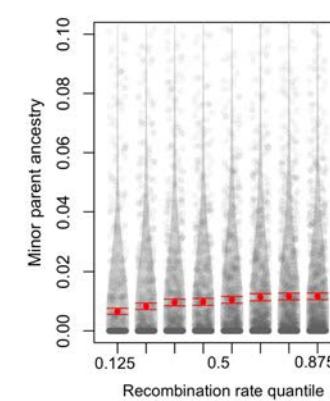
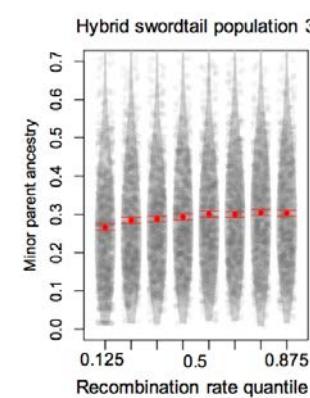
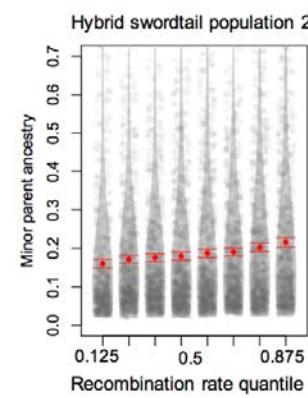
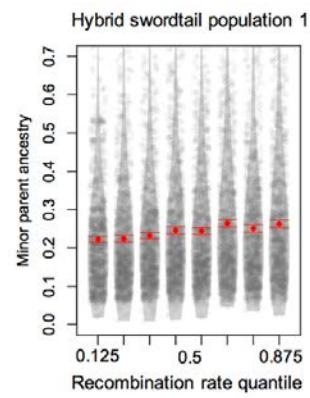
Minor parent:
Neanderthal

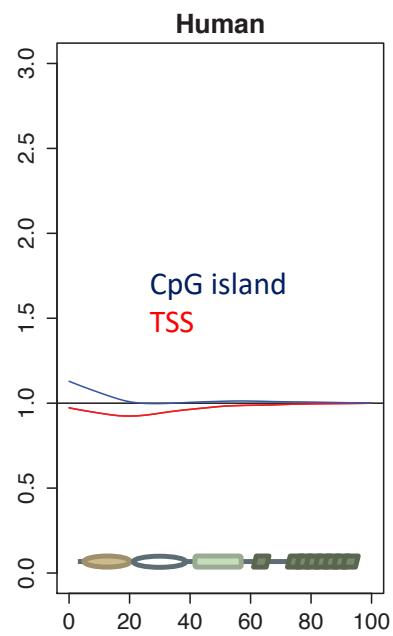
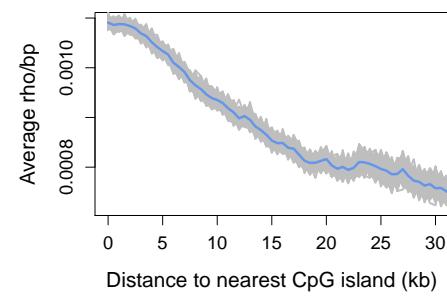
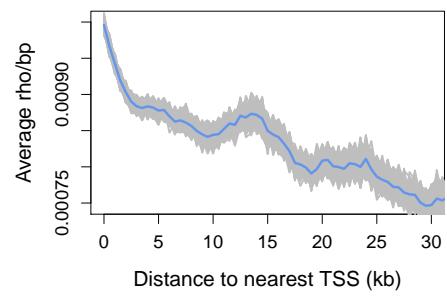


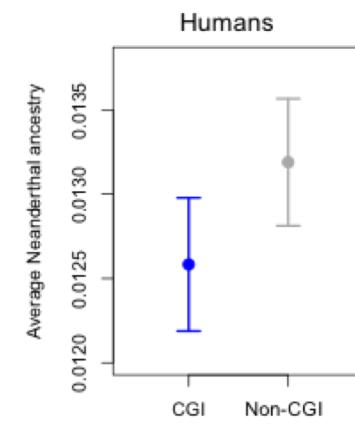
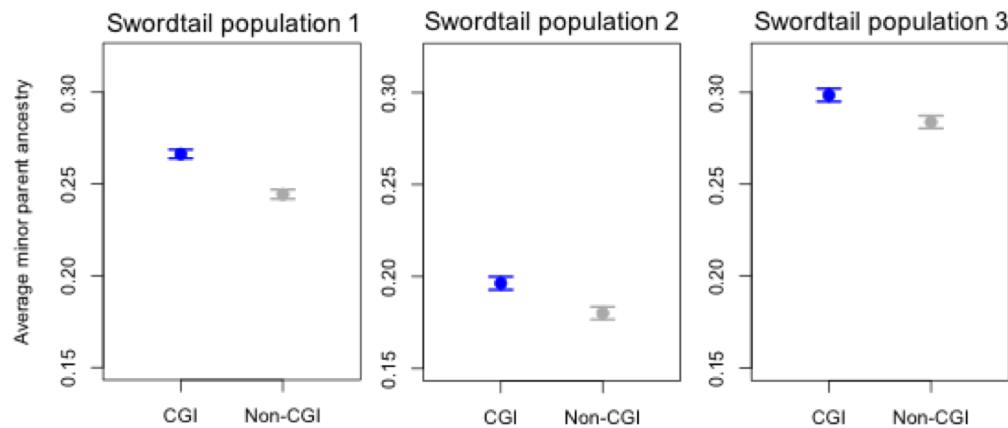
at a 50 kb scale, $\rho=0.15$, $p=10^{-7}$ in pop. 1; $\rho = 0.10$, $p=8\times 10^{-4}$ in pop. 2; $\rho = 0.10$, $p=10^{-4}$ in pop. 3; $\rho = 0.08$, $p=10^{-8}$ in humans



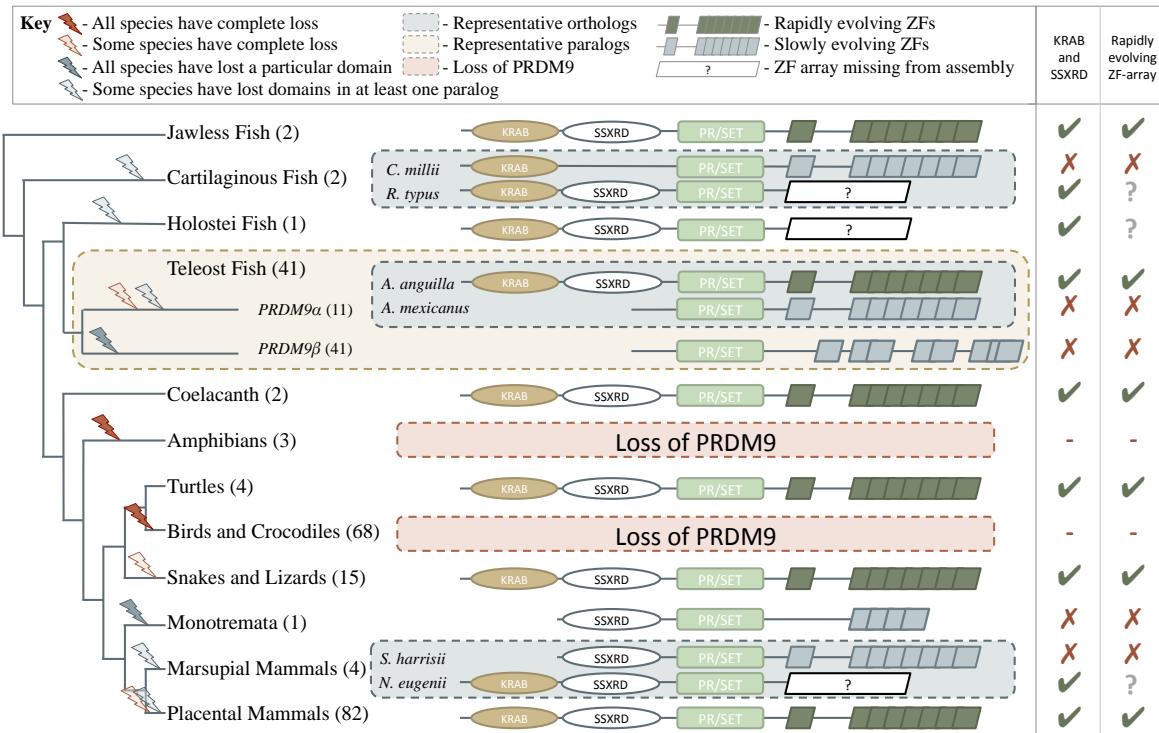
Minor parent:
Neanderthal







One-tailed $p < 0.005$ in all three populations



Summary

- ❖ Vertebrates seem to employ at least two strategies to direct recombination to the genome: through PRDM9 binding or by using promoter-like features
- ❖ The use of PRDM9 to direct recombination is associated with rapid evolution of the zinc finger and of recombination hotspots. In contrast, using promoter like features is associated with the conservation of hotspots.
- ❖ Recombination is an important predictor of where introgression occurs between hybridizing species. Therefore introgression patterns may differ between species that do and do not use PRDM9.