



Characterising antibody immunity and ageing in a short-lived teleost

William John Bradshaw

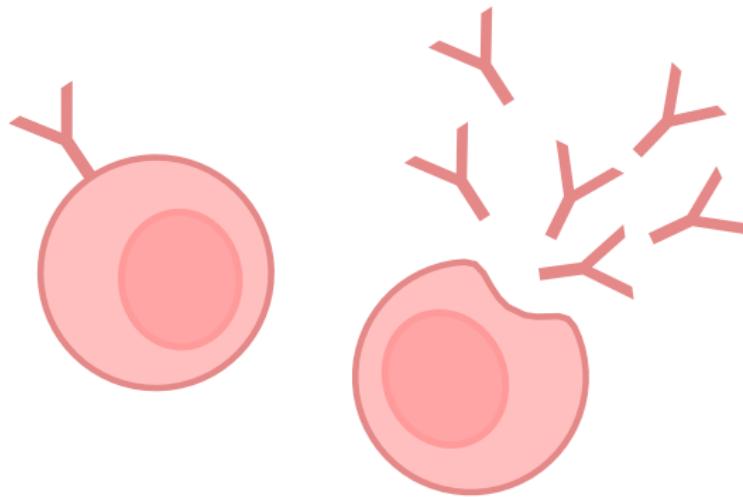
6th June 2019



University of Cologne



Antibodies



B-cells

Ageing has major effects on B-cell immunity

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- Reduced naïve B-cell output
- Fewer unique antibody sequences
- Decreased responsiveness to vaccination
- Impaired antibody quality
- ...

There's a lot we don't know about B-cell immune ageing

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- Very little known outside humans and mice

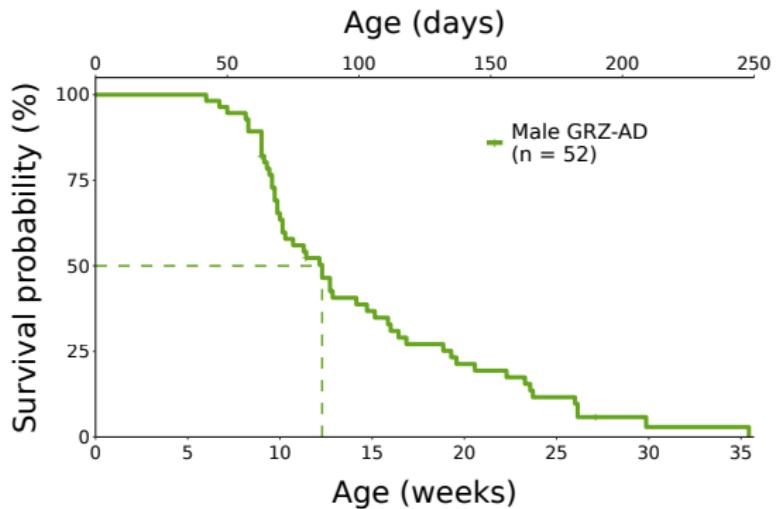
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- Very little known outside humans and mice
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- Very little known outside humans and mice
- Almost all data comes from peripheral blood
- No spatial resolution (different organs)

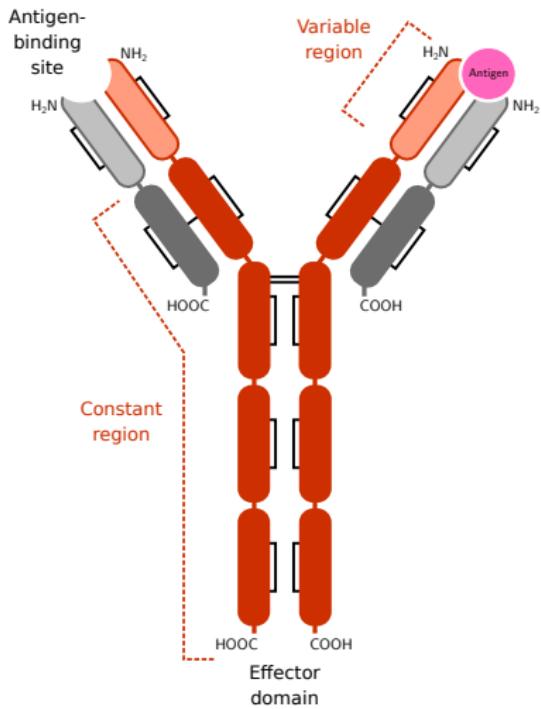
The turquoise killifish as a model for antibody ageing



Yumi Kim

How does B-cell immunity change with age in killifish?

How does the antibody heavy-chain repertoire change with age in killifish?

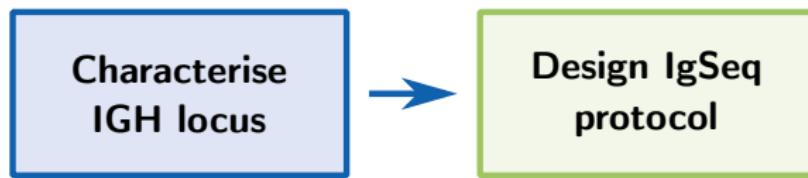


How does the **antibody heavy-chain repertoire** change with age in killifish?

**Characterise
IGH locus**



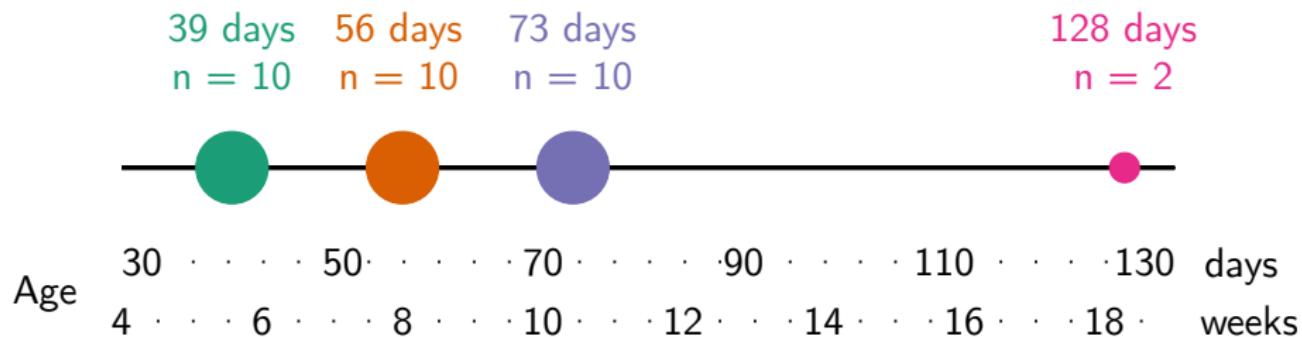
How does the **antibody heavy-chain repertoire** change with age in killifish?



How does the **antibody heavy-chain repertoire** change with age in killifish?

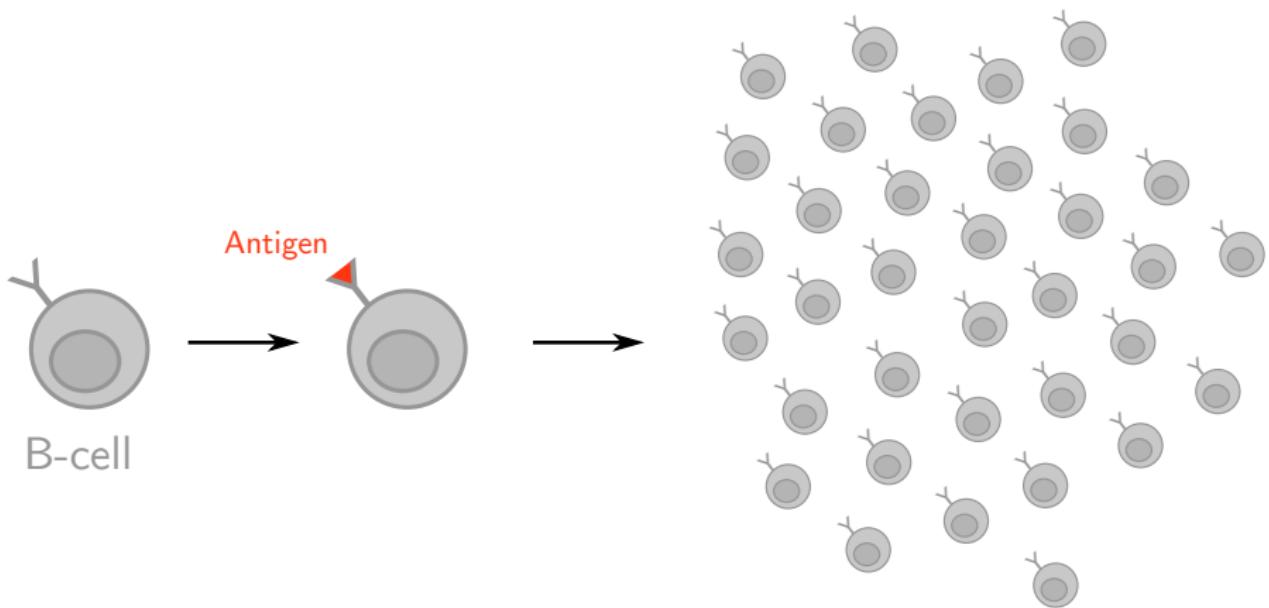


Sample design – killifish ageing study

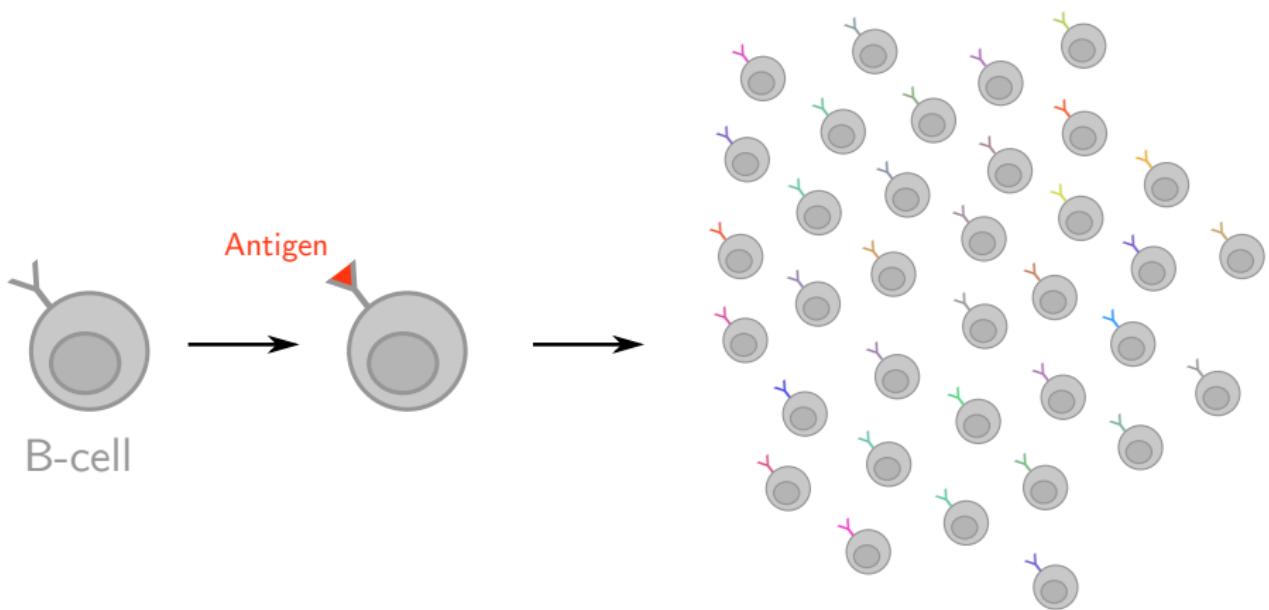


Clonal antibody diversity

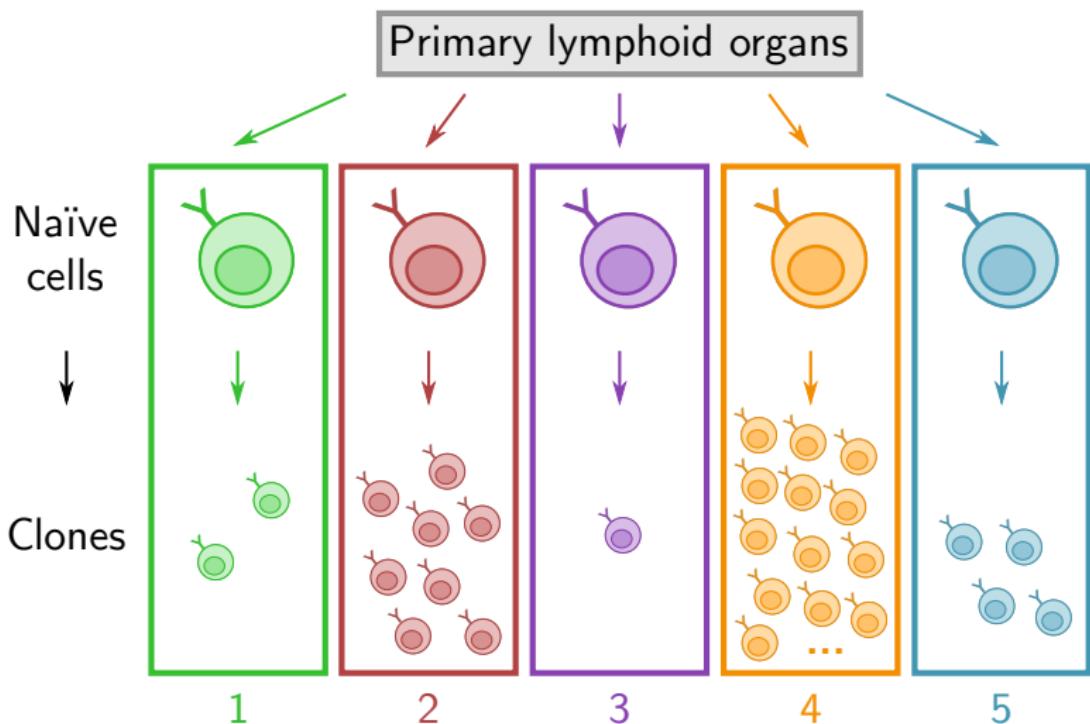
Clonal antibody diversity



Clonal antibody diversity

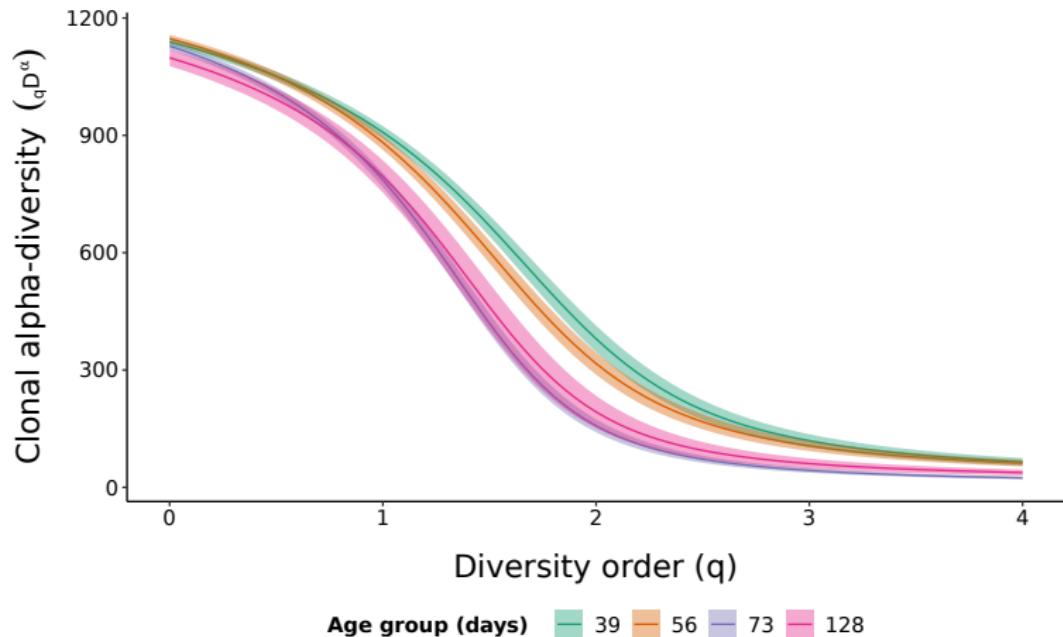


Clonal antibody diversity

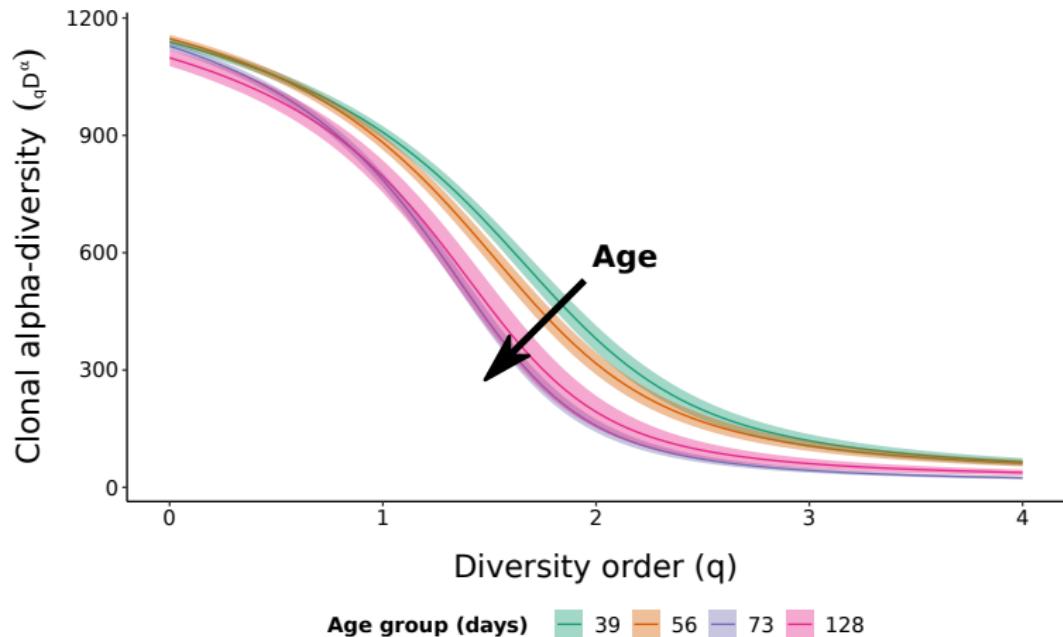


Clonal alpha diversity in the killifish antibody repertoire

Clonal alpha diversity in the killifish antibody repertoire declines with age



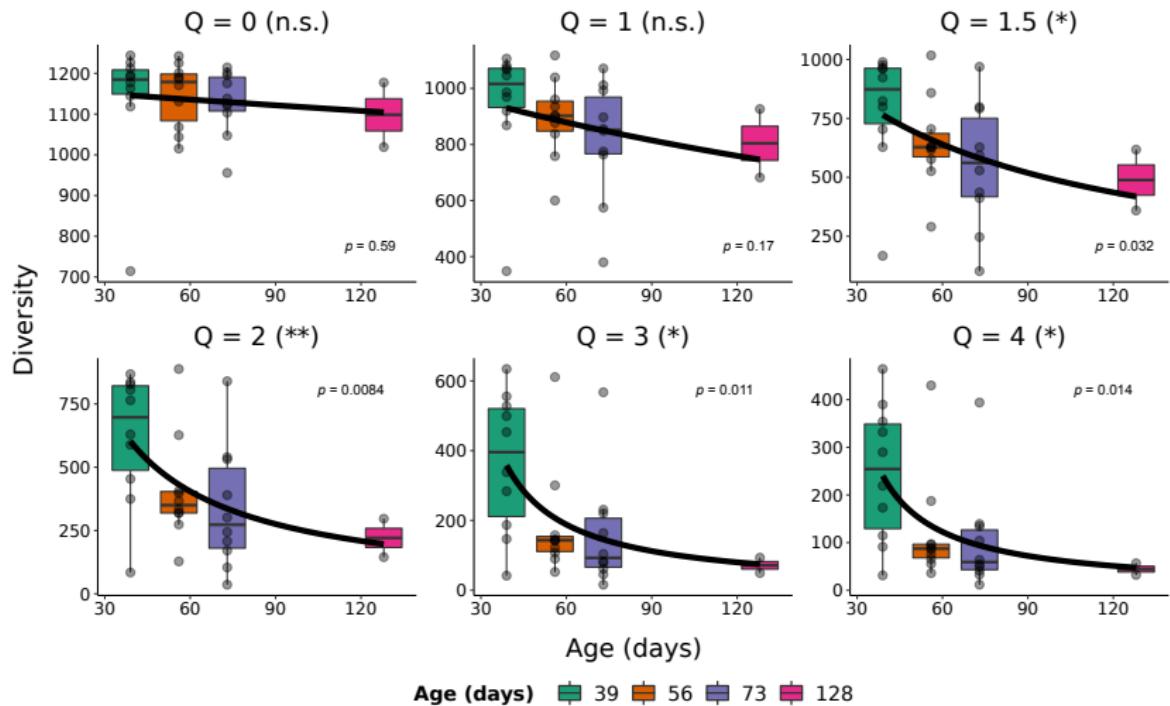
Clonal alpha diversity in the killifish antibody repertoire declines with age



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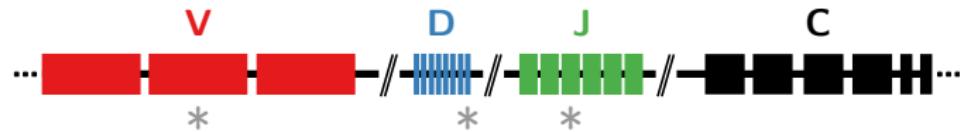
Clonal alpha diversity in the killifish antibody repertoire declines with age at high diversity orders



VJ alpha diversity in the killifish antibody repertoire



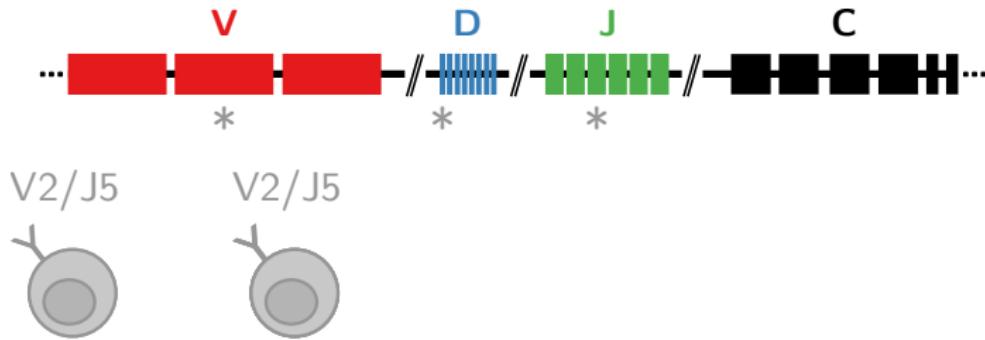
VJ alpha diversity in the killifish antibody repertoire



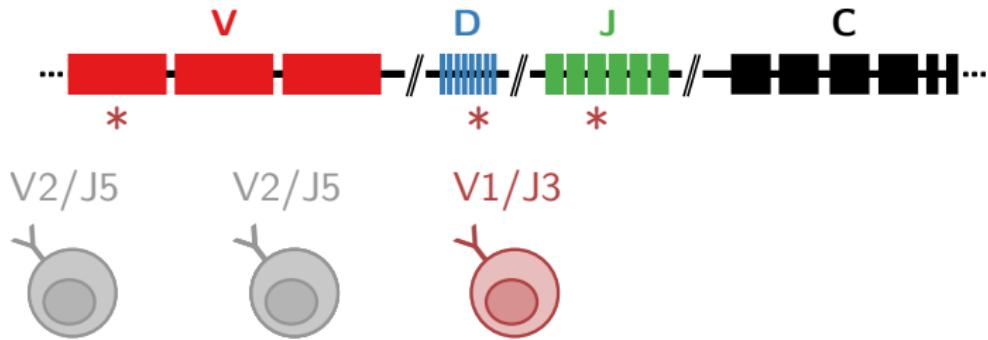
V2/J5



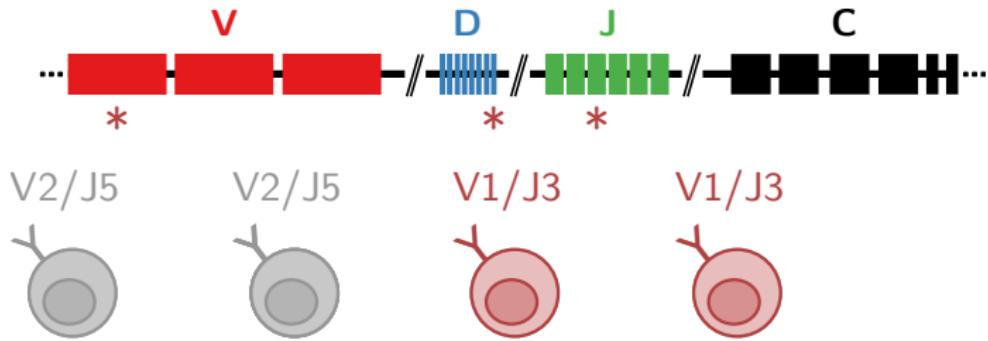
VJ alpha diversity in the killifish antibody repertoire



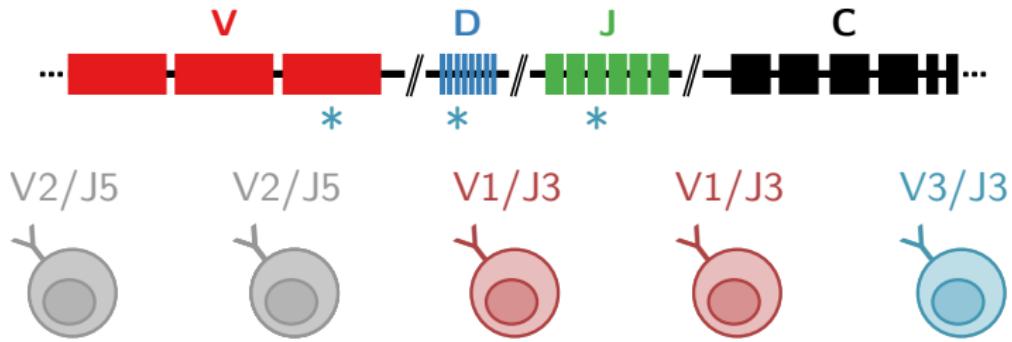
VJ alpha diversity in the killifish antibody repertoire



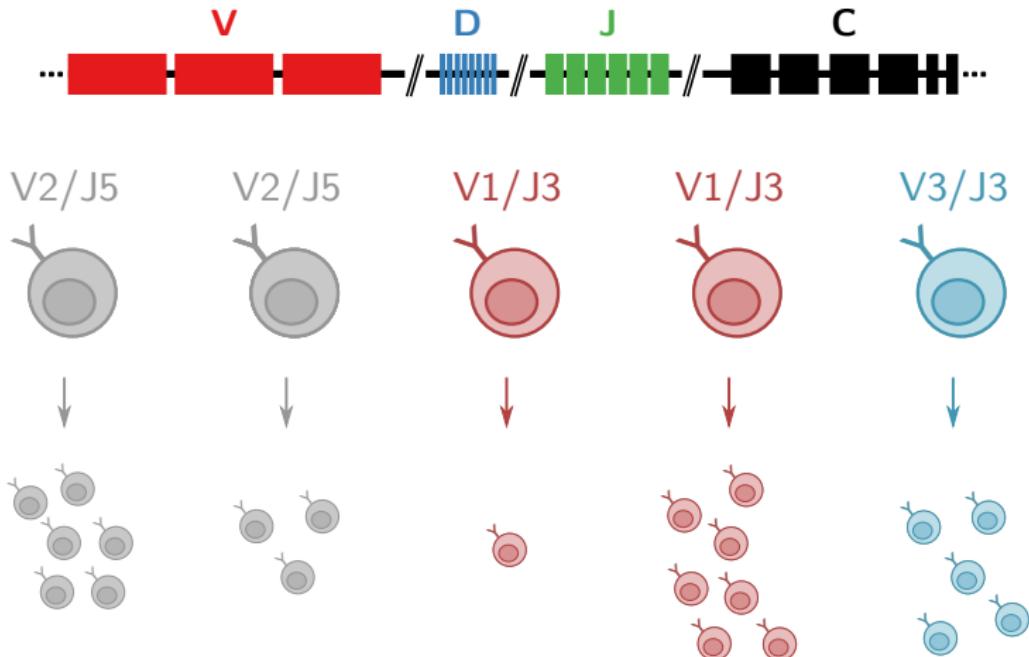
VJ alpha diversity in the killifish antibody repertoire



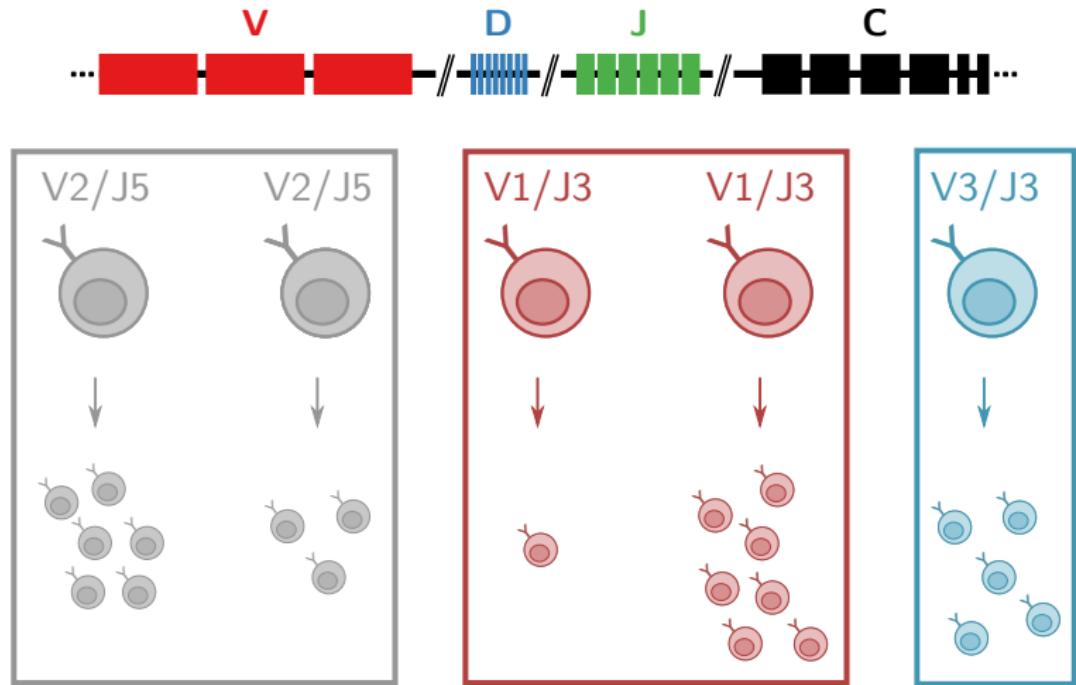
VJ alpha diversity in the killifish antibody repertoire



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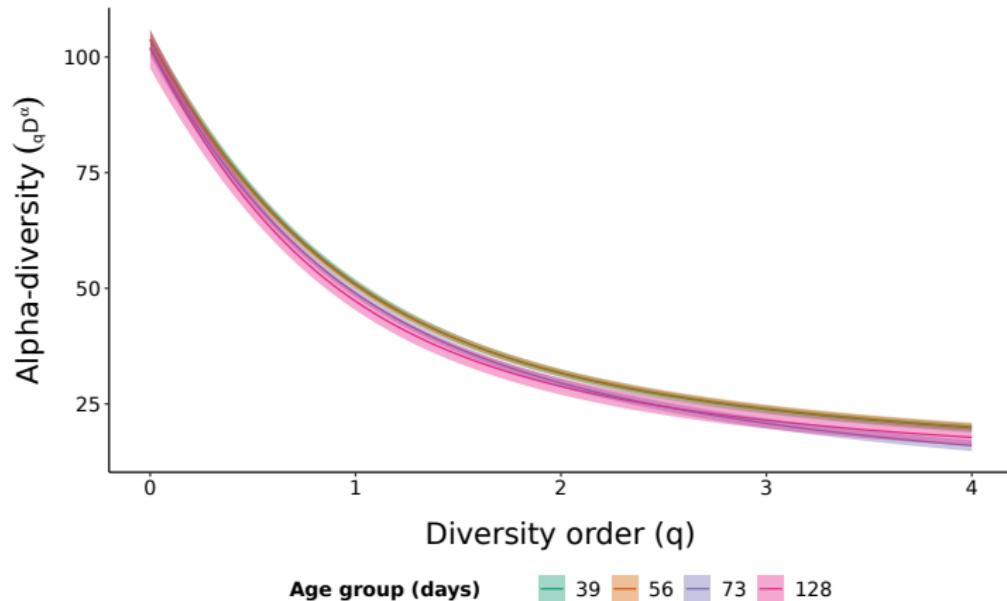


VJ alpha diversity in the killifish antibody repertoire

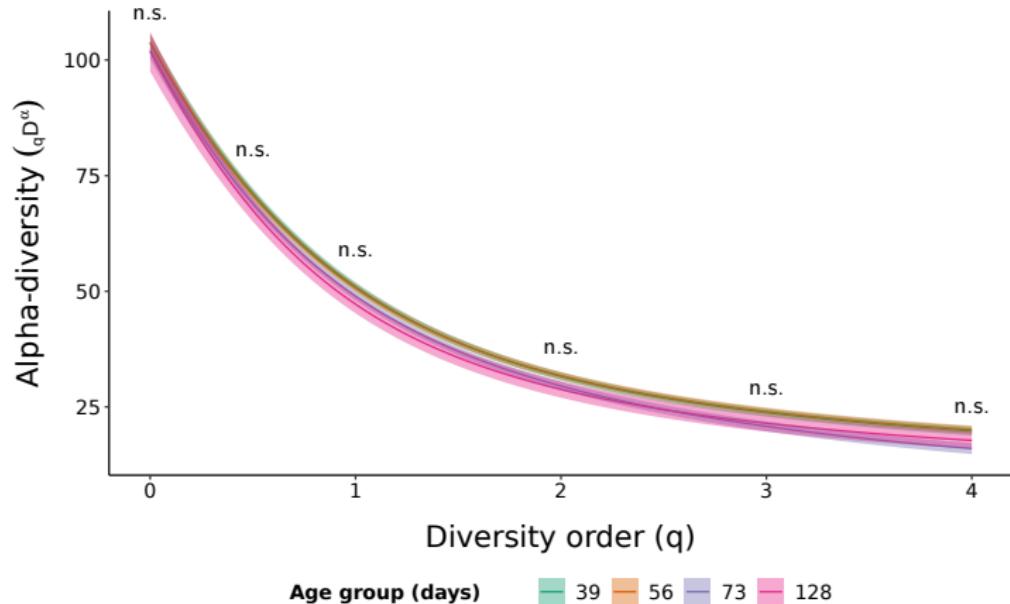


VJ alpha diversity in the killifish antibody repertoire

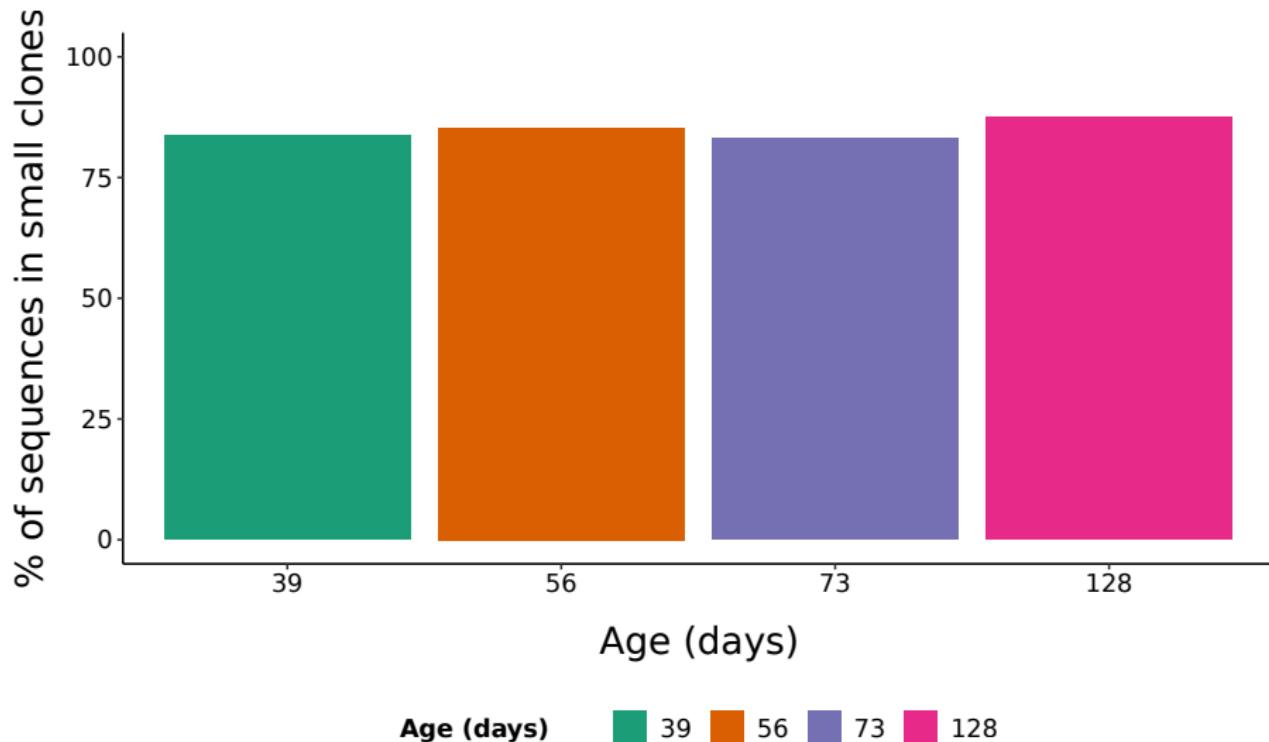
VJ alpha diversity in the killifish antibody repertoire **does not decline** with age



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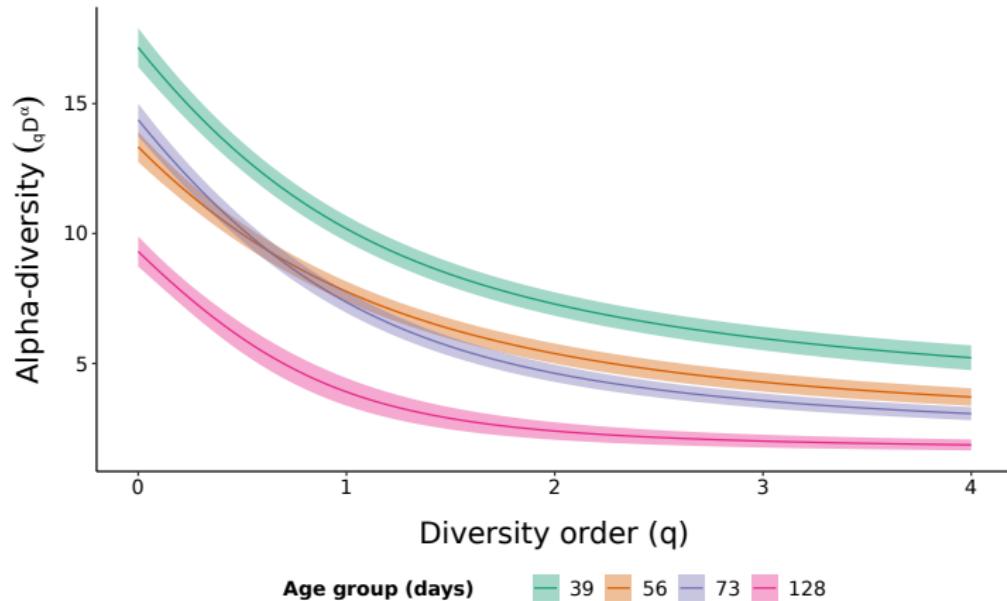


Most sequences in killifish repertoires are from small clones

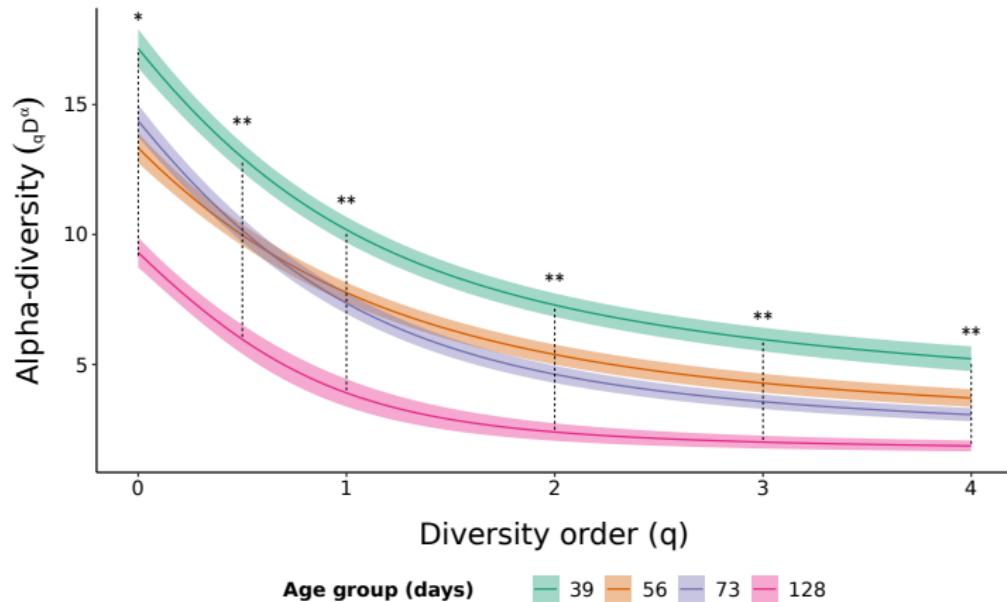


VJ alpha diversity of large clones

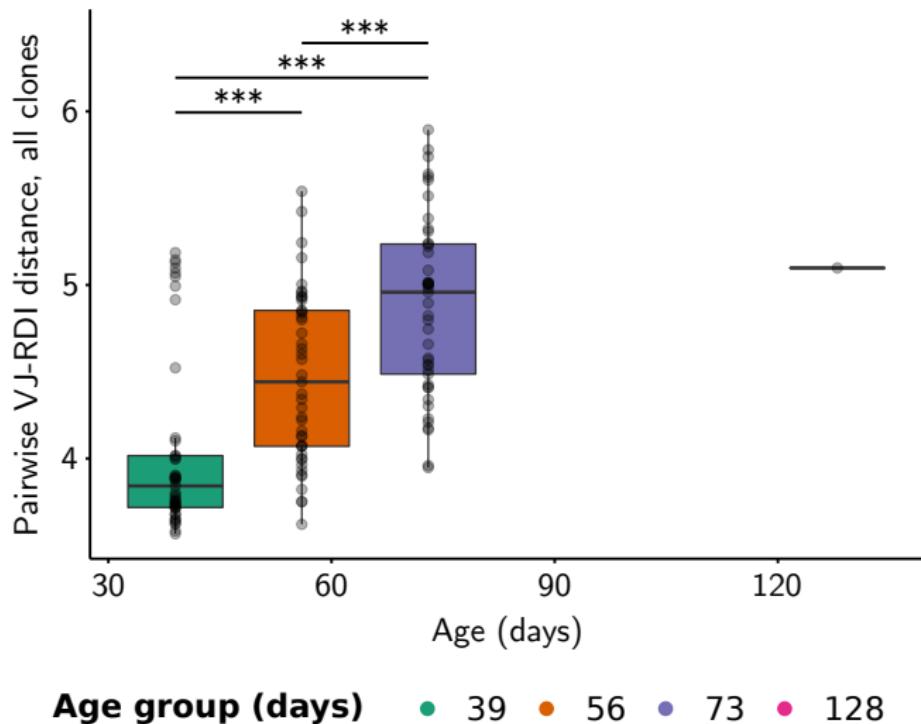
VJ alpha diversity of large clones does decline with age



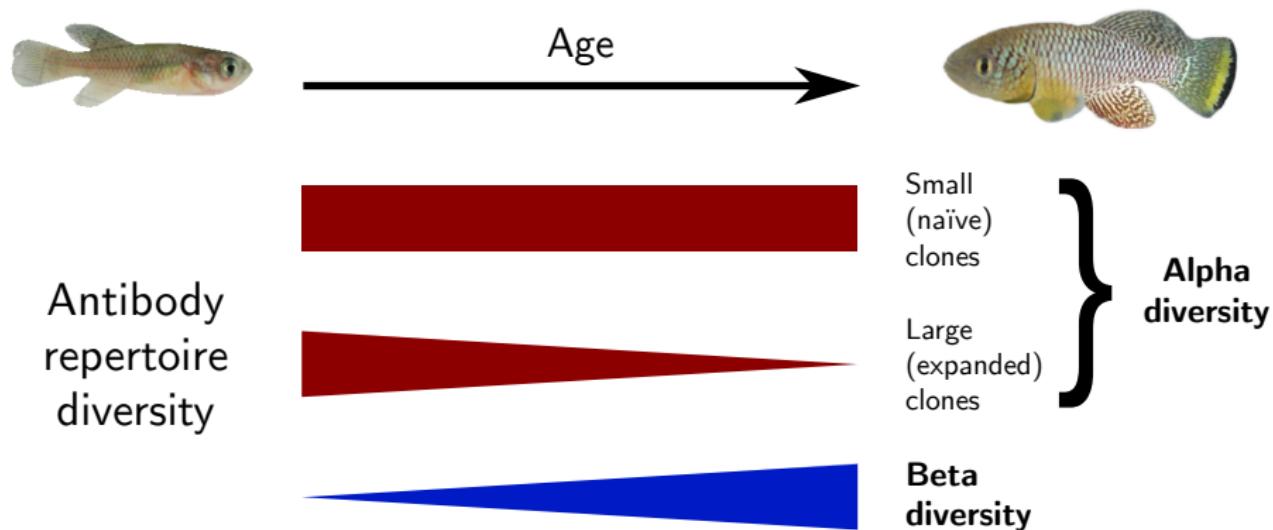
VJ alpha diversity of large clones does decline with age



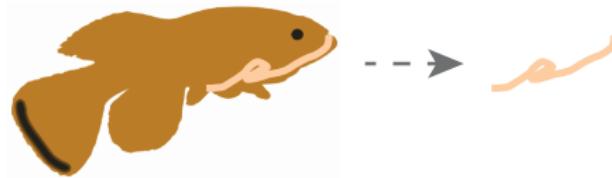
Killifish VJ repertoires become **more dissimilar** with age



Summary I

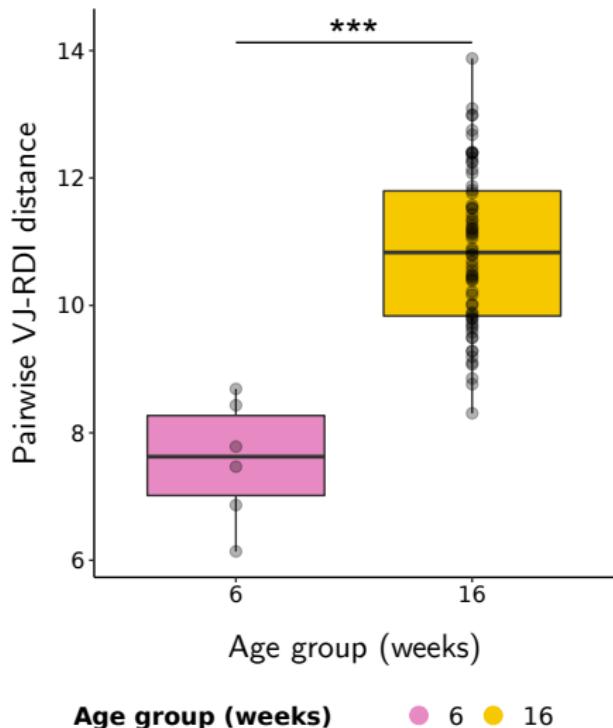


Sample design – gut repertoire study

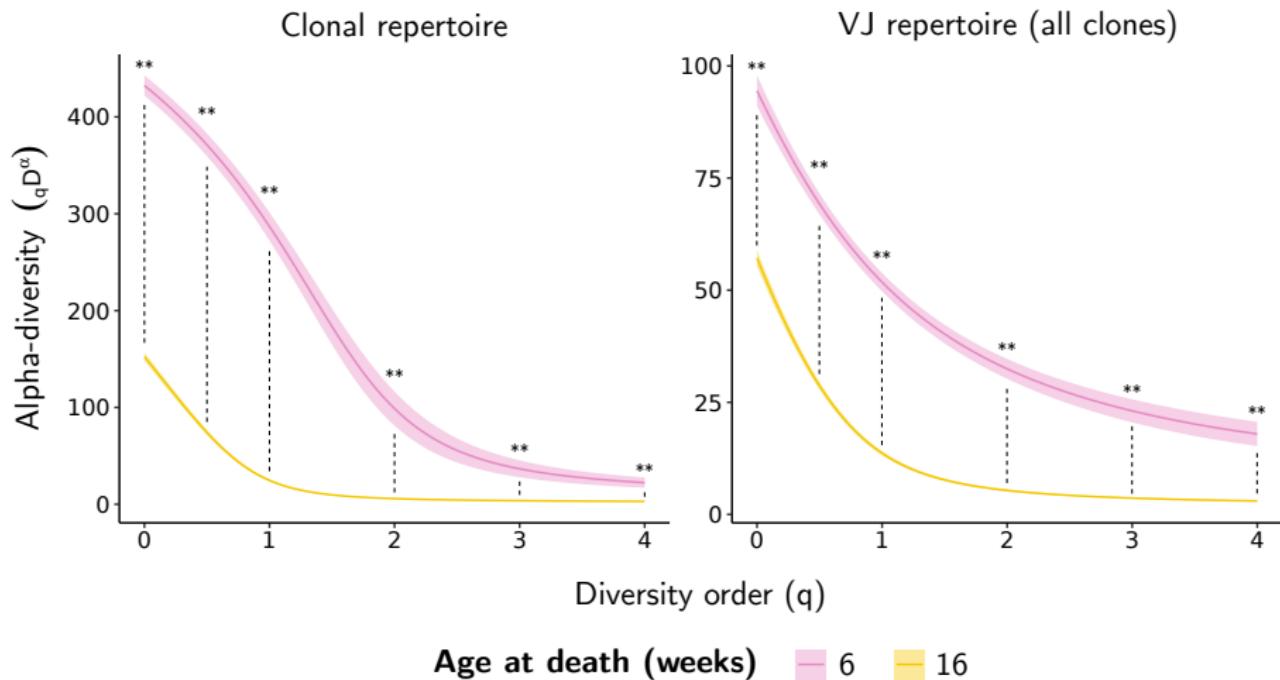


Samples collected for Smith et al., eLife 2017

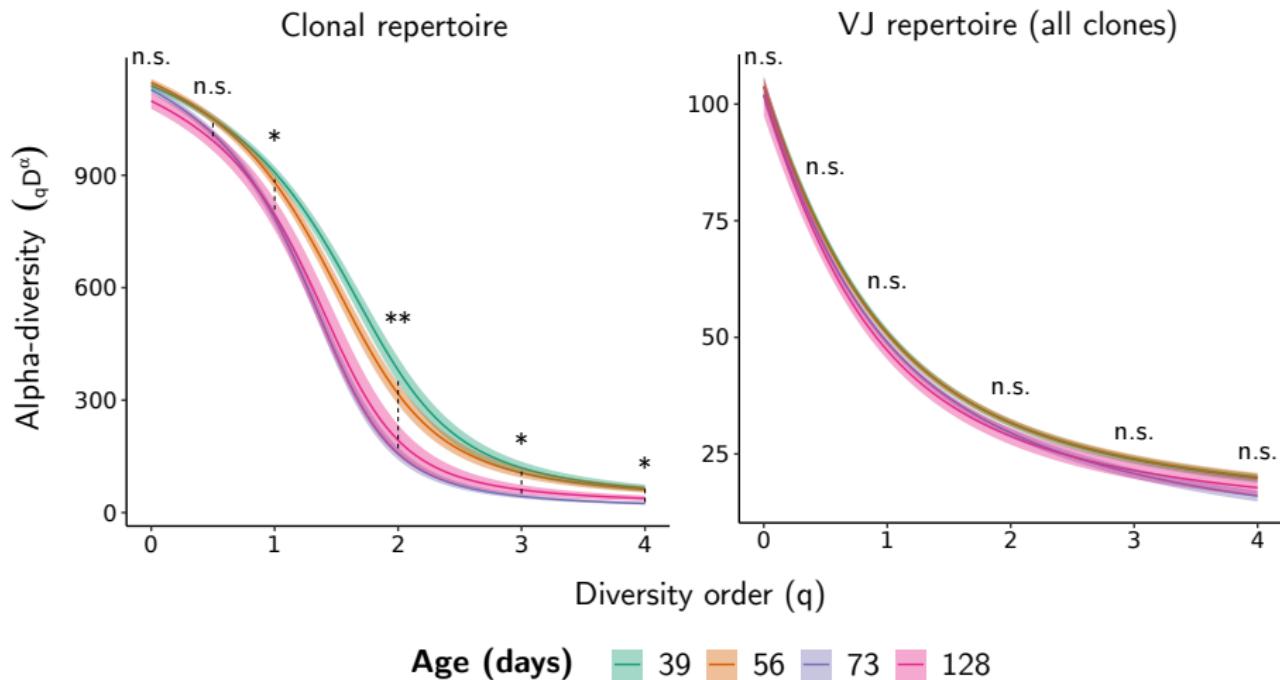
Killifish gut repertoires become much more dissimilar with age



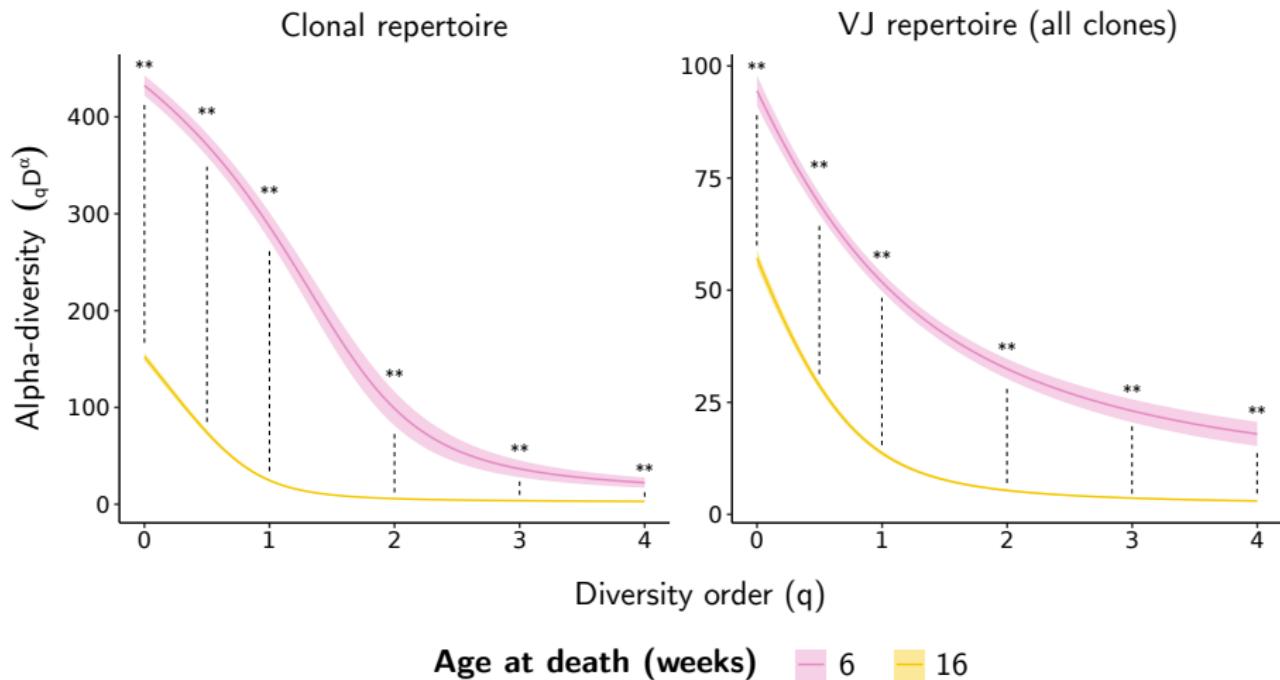
Gut repertoire alpha diversity declines dramatically with age in turquoise killifish



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Why the difference?

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Why the difference?

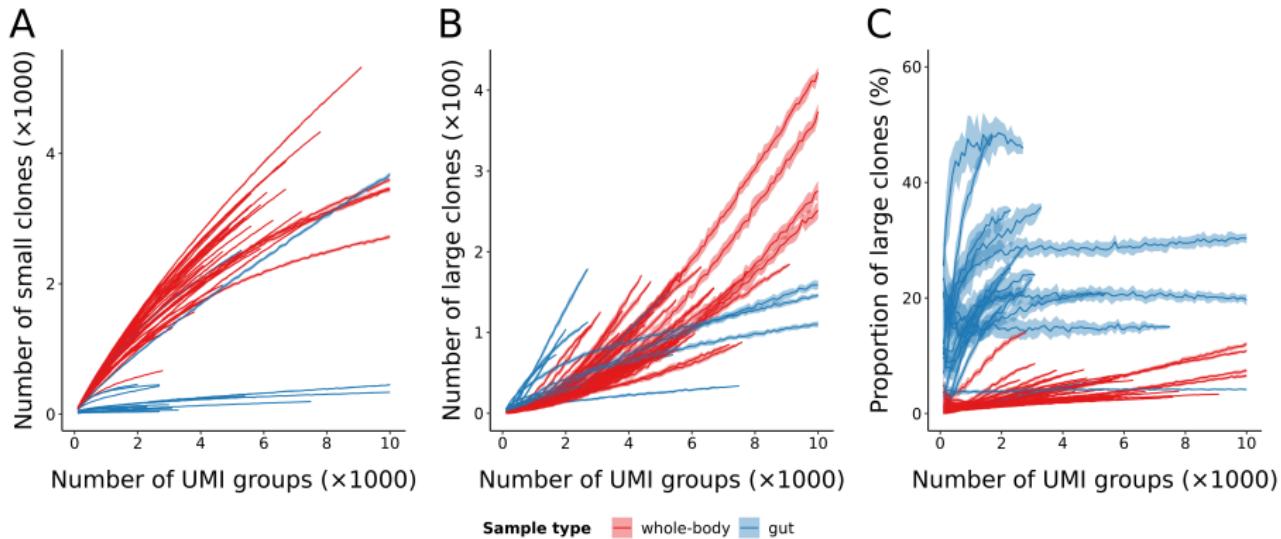
1. Difference in **environment**?

- Intense antigen exposure from gut microbiota
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2. Difference in **clonal composition**?

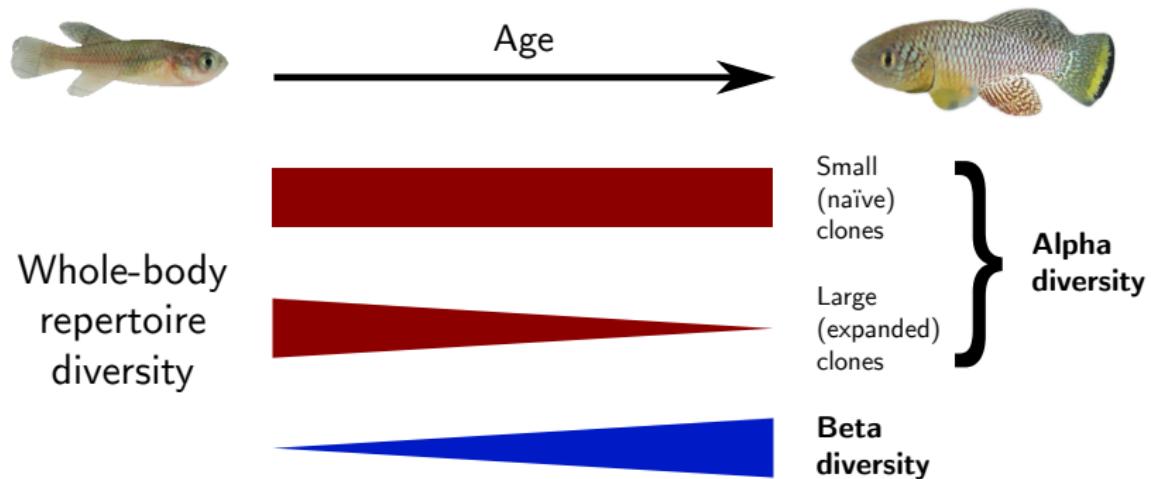
- Whole body includes primary lymphoid organs, intestine does not
- → More small naïve clones in whole-body samples than gut samples
- Larger clones more age-sensitive → stronger age effect in gut samples

Killifish gut repertoires contain fewer **small** clones than whole-body repertoires

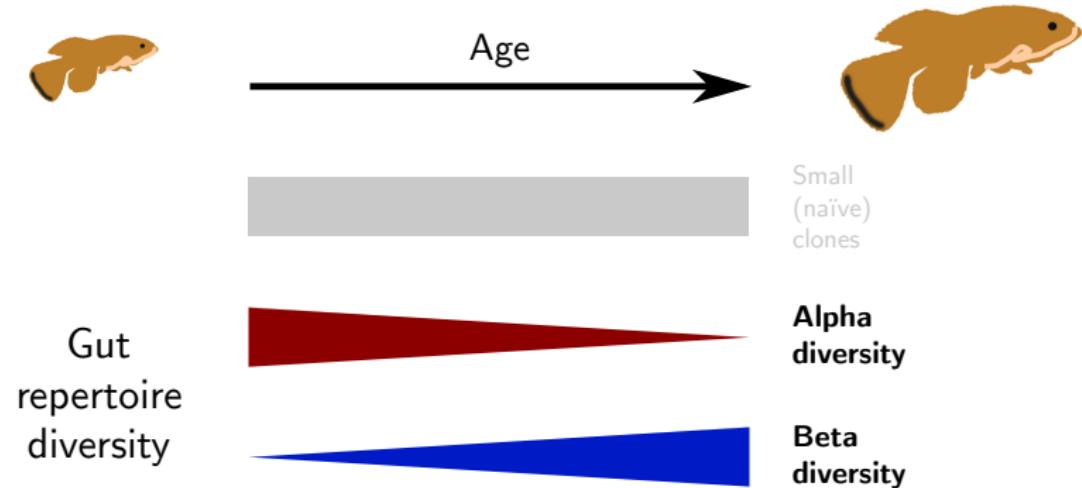


Summary II

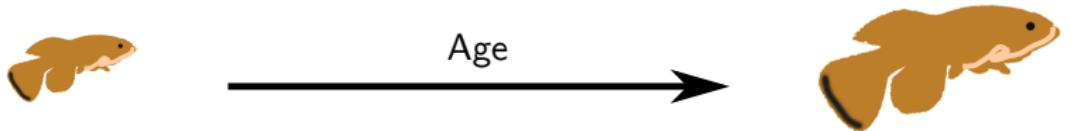
Summary II



Summary II



Summary II



Gut
repertoire
diversity

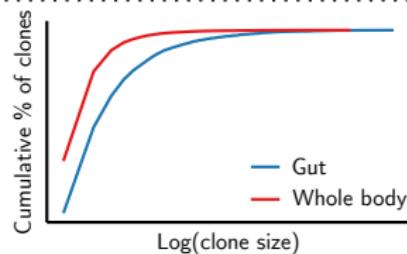


Small
(naïve)
clones

Alpha
diversity



Beta
diversity



Acknowledgements

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Bérénice Benayoun
John Beausang

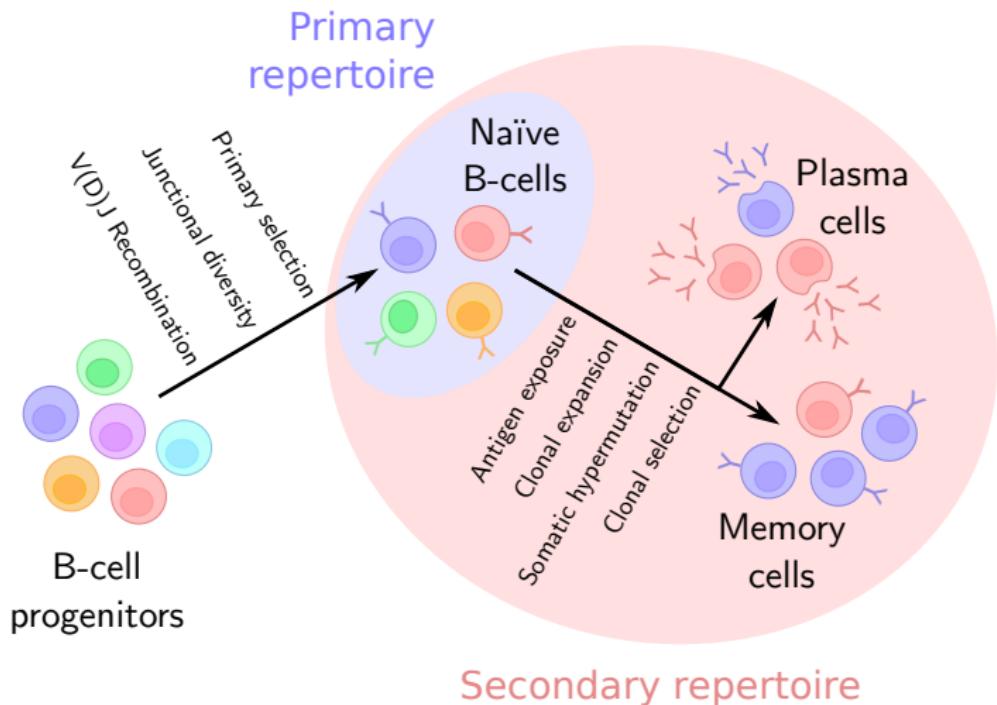


Kathrin Reichwald
Jason Vander Heiden
Quentin Marcou

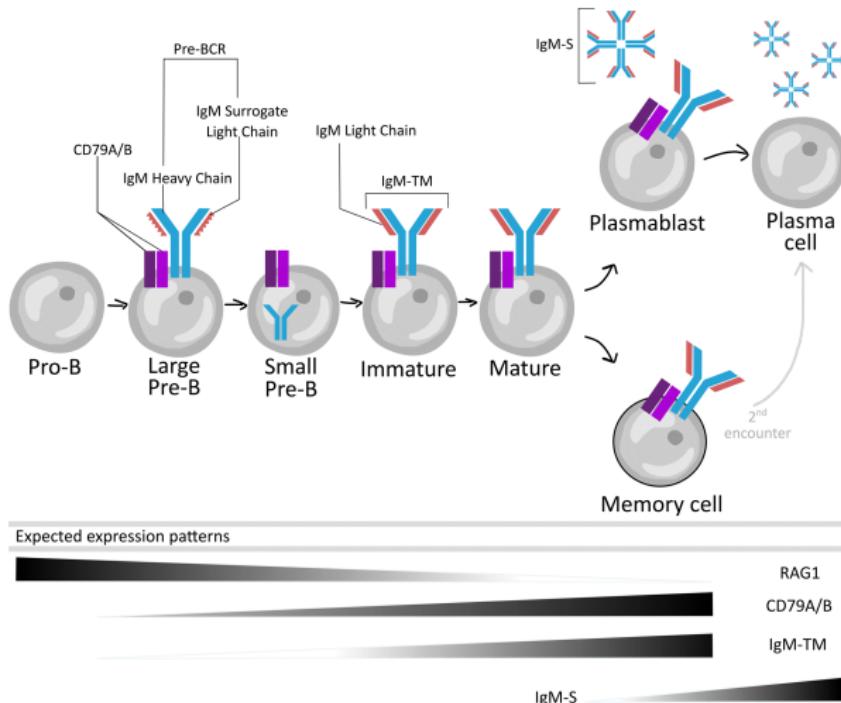
Manolis Pasparakis
Andreas Beyer
Michael Lässig

Thank you!

Primary and secondary antibody diversity

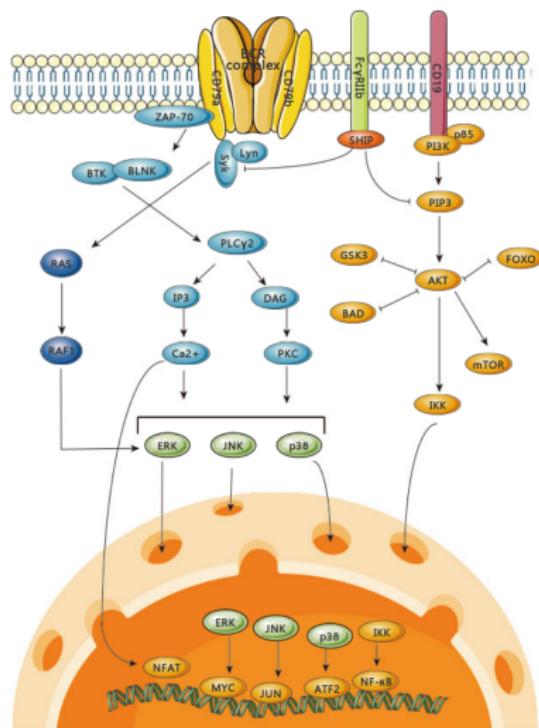


B-cell development

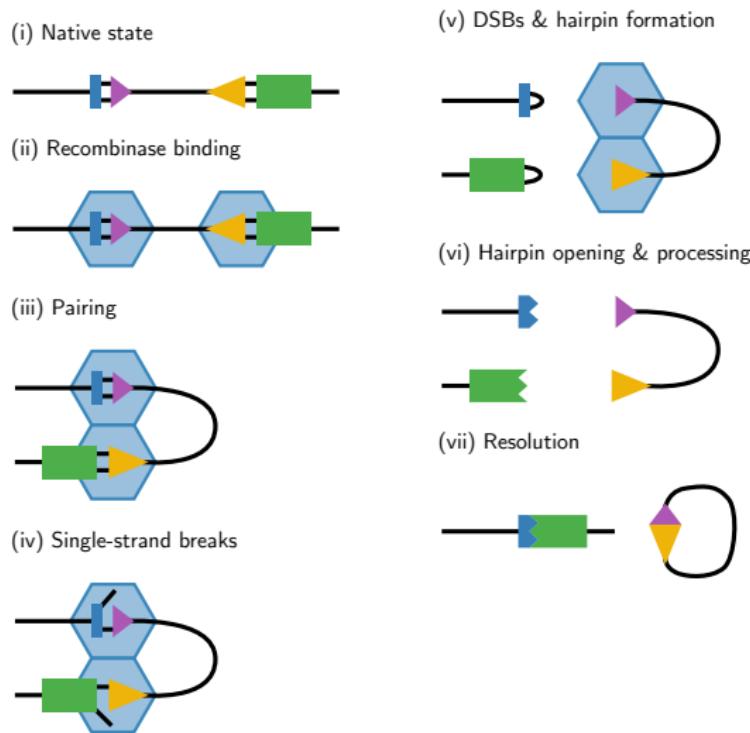


Davina Patel

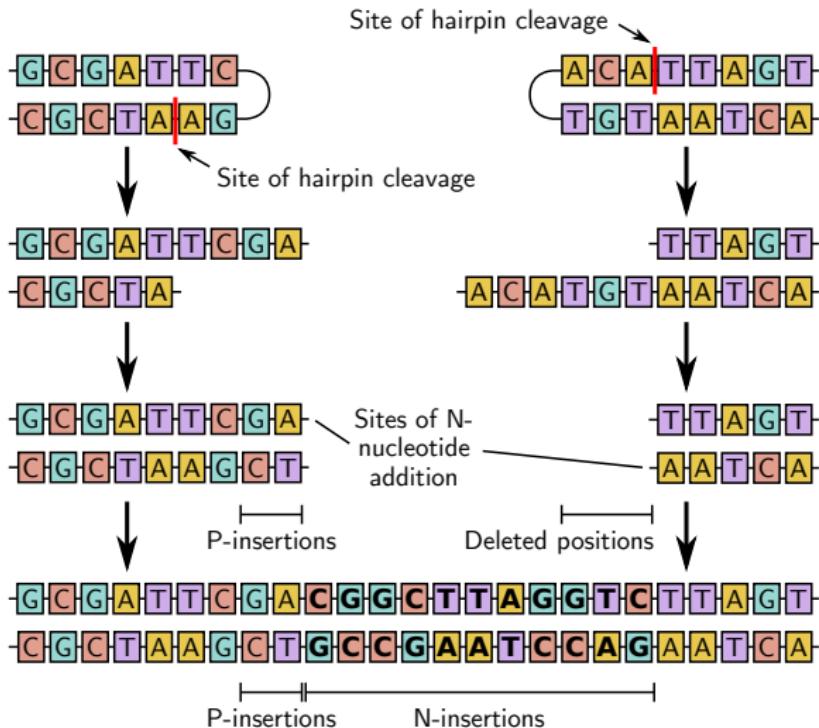
BCR signalling pathway



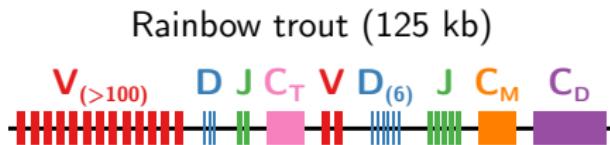
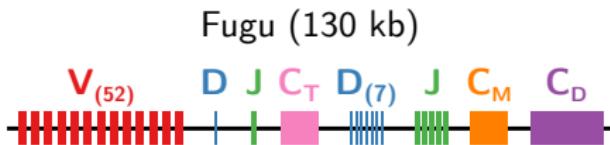
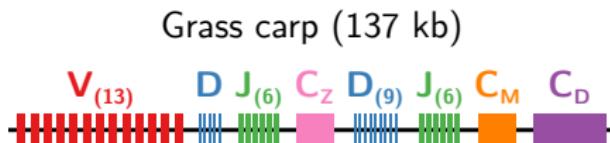
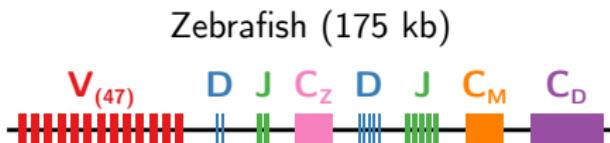
Mechanism of VDJ recombination



Mechanisms of junctional diversity

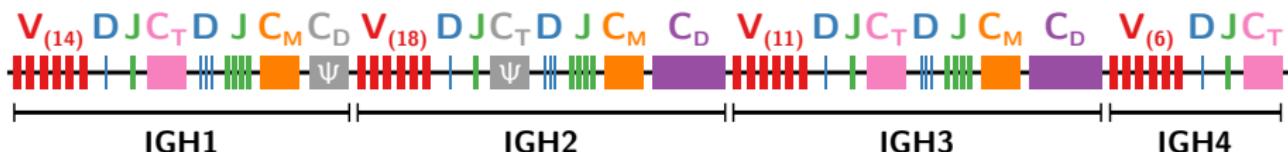


Other teleost loci: simple

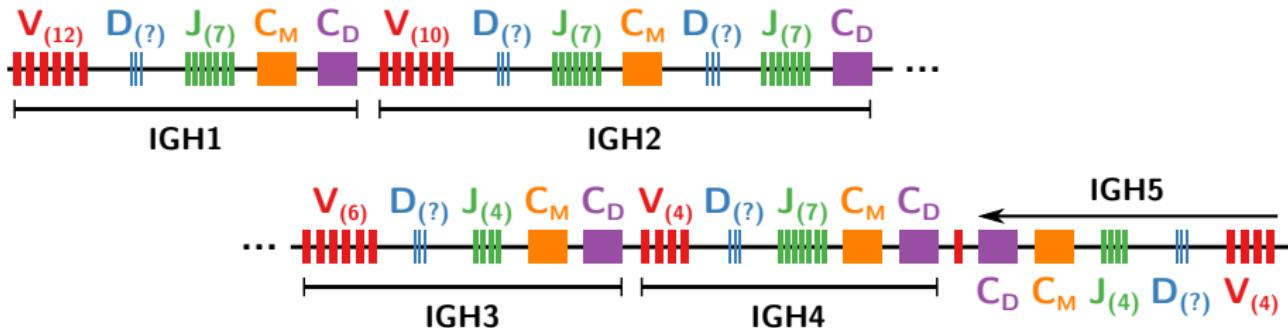


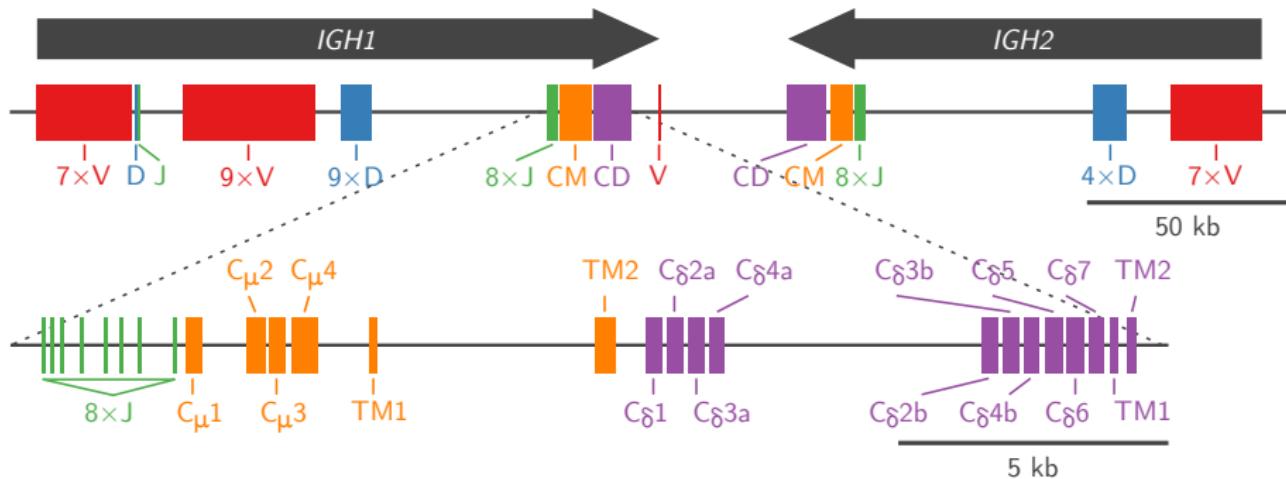
Other teleost loci: complex

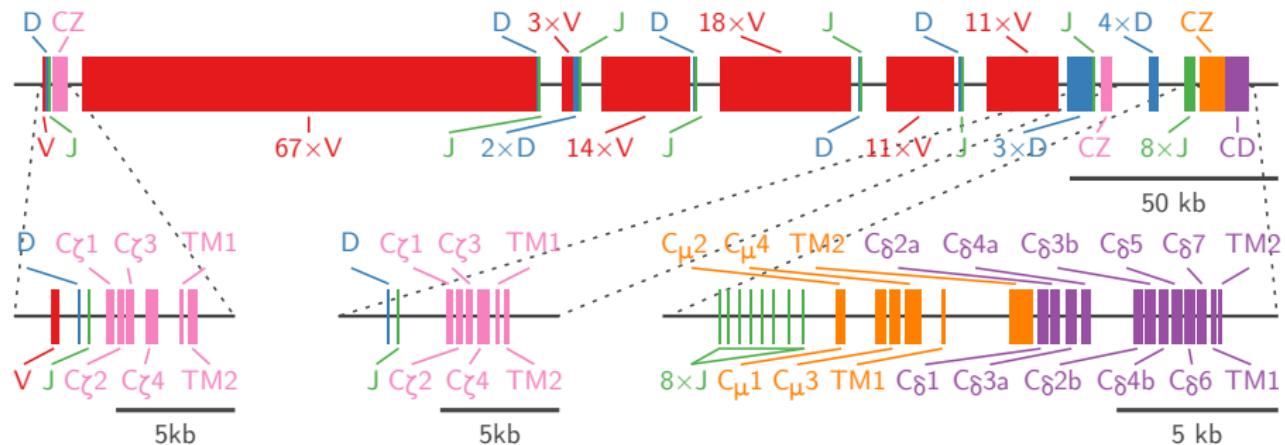
Three-spined stickleback (200 kb)

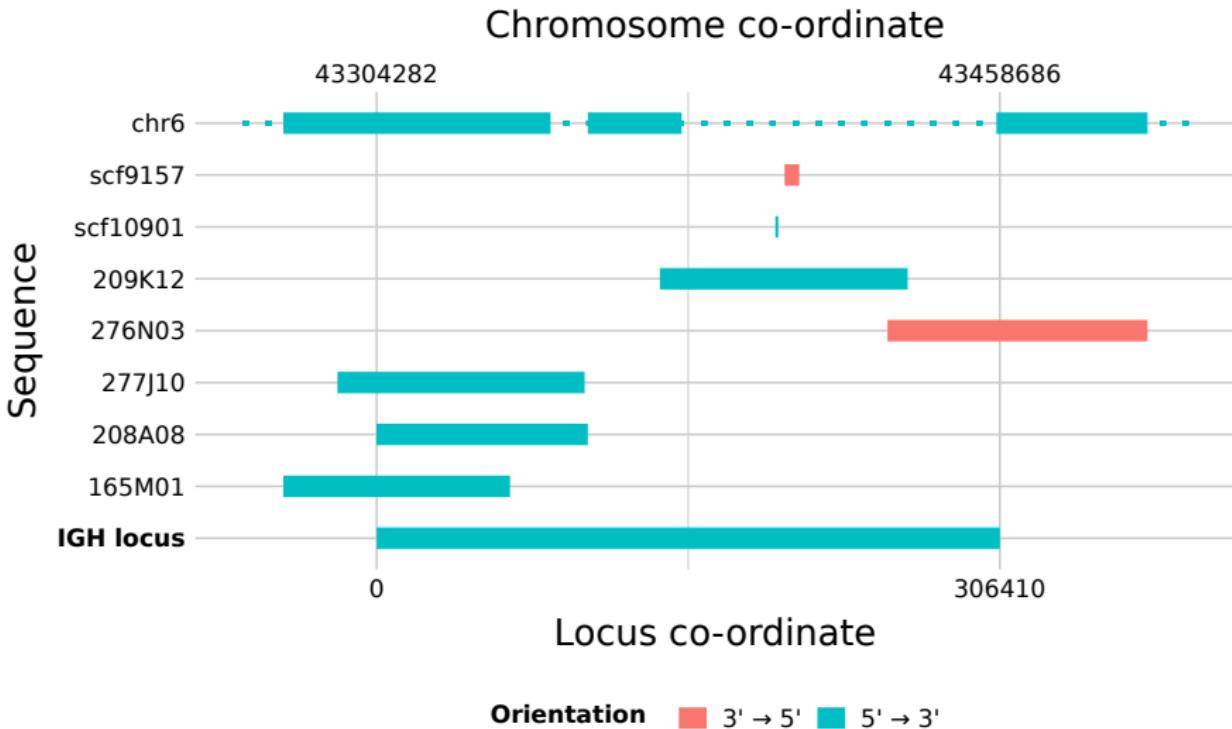


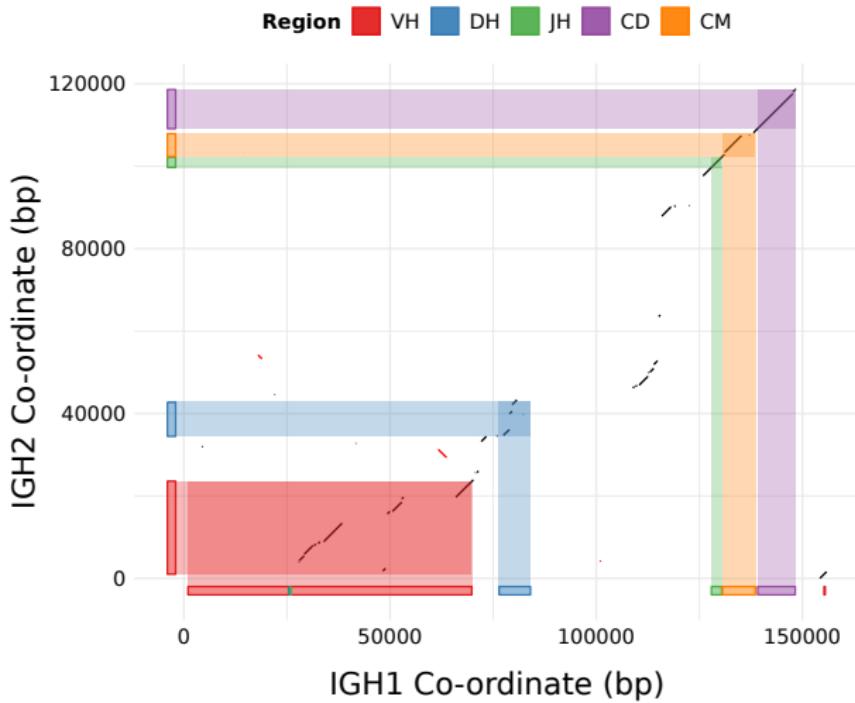
Medaka (450 kb)



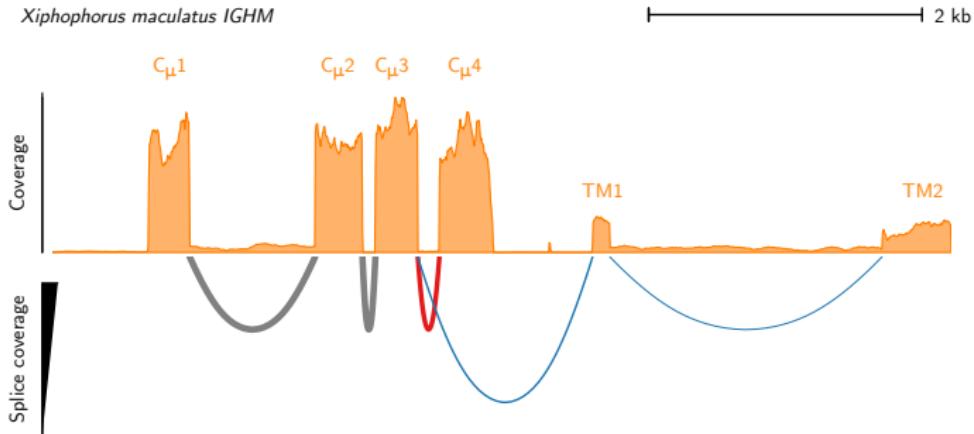
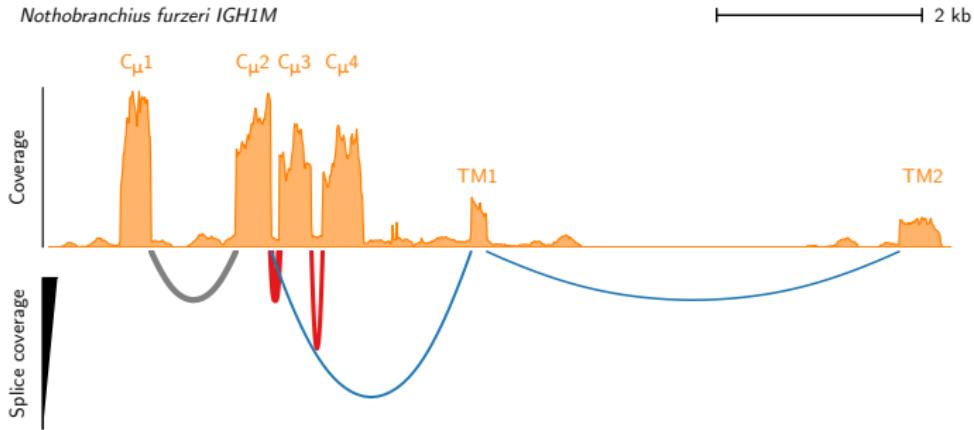
Nothobranchius furzeri IGH

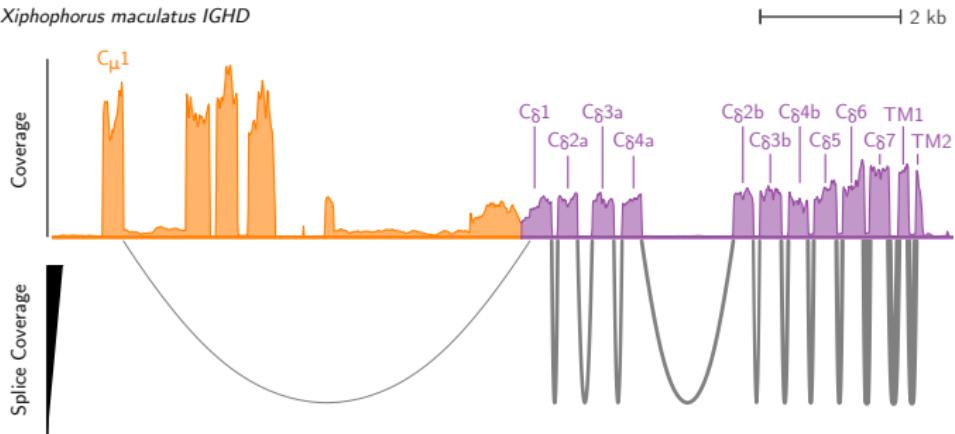
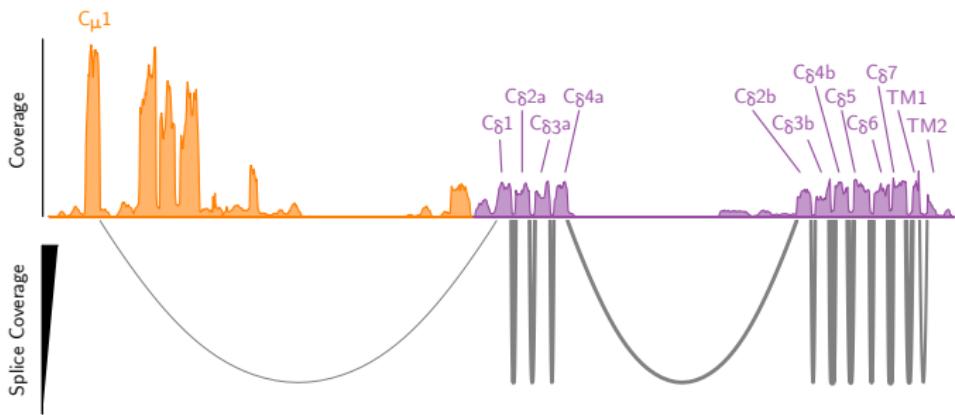
Xiphophorus maculatus IGH

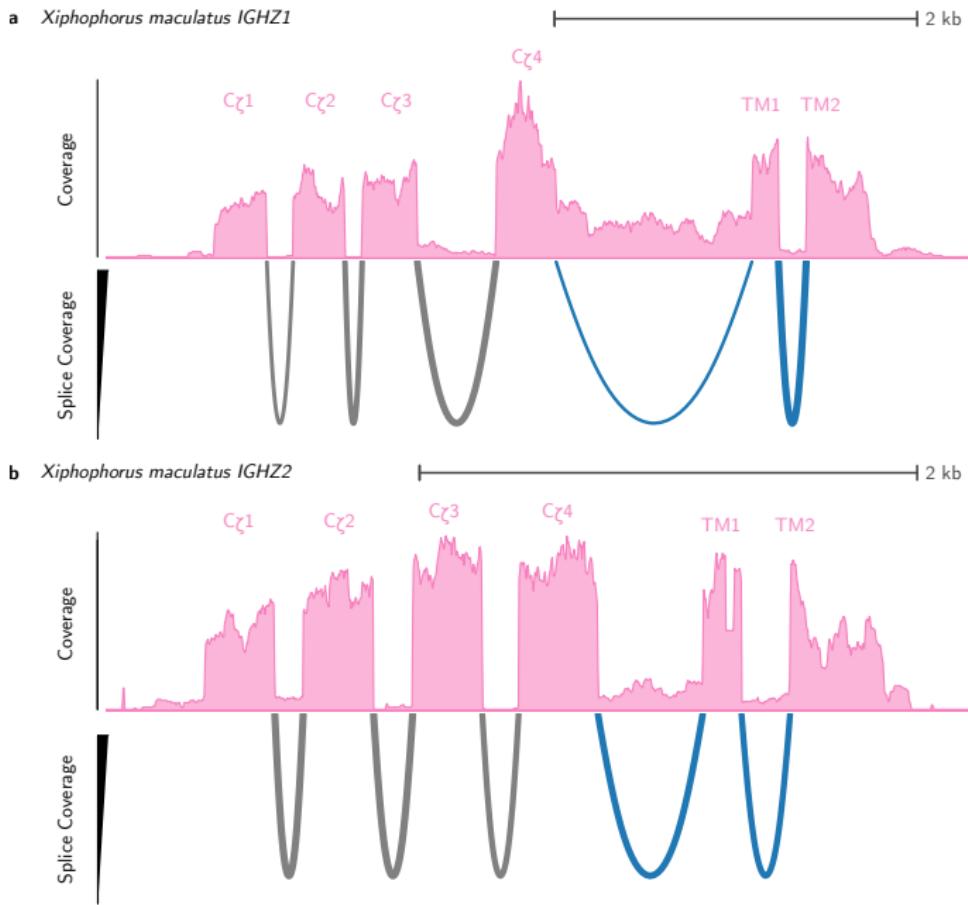




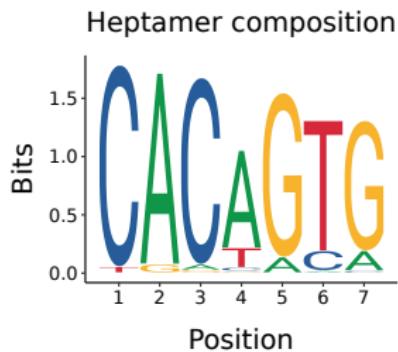
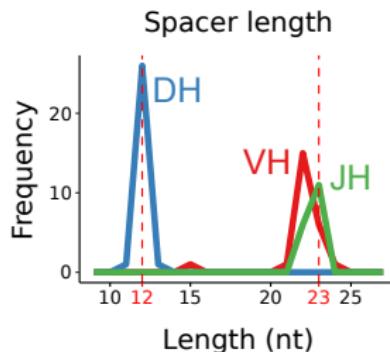
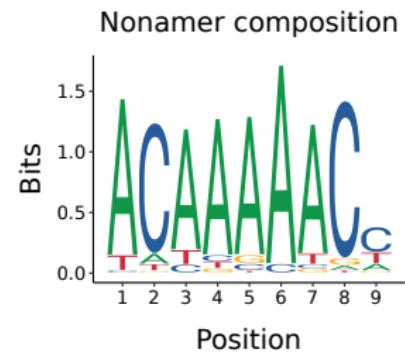
A IGHM constant region (genomic configuration)**B** Secreted IGHM**C** Transmembrane IGHM (tetrapods)**D** Transmembrane IGHM (most teleosts)**E** Transmembrane IGHM (medaka)

a Xiphophorus maculatus IGHM**b Nothobranchius furzeri IGH1M**

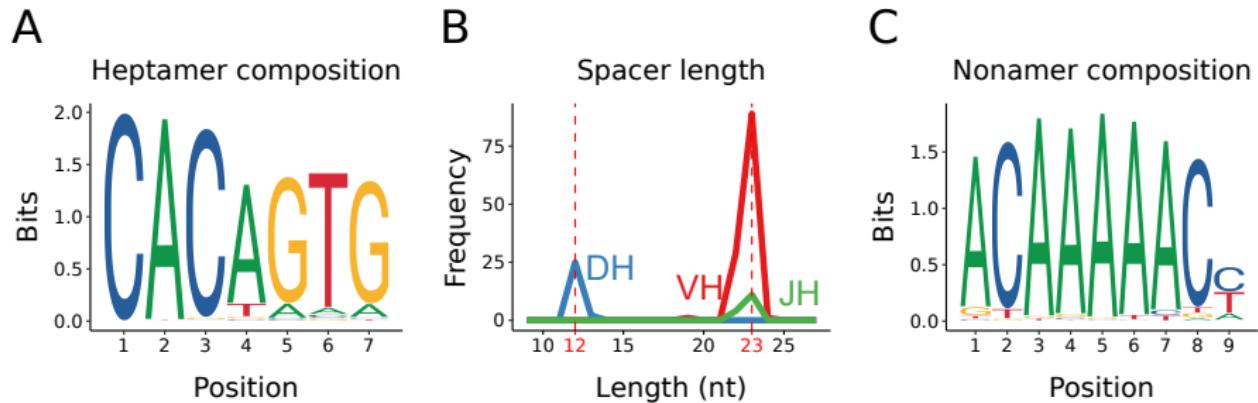
a *Xiphophorus maculatus* IGHD**b** *Nothobranchius furzeri* IGH1D

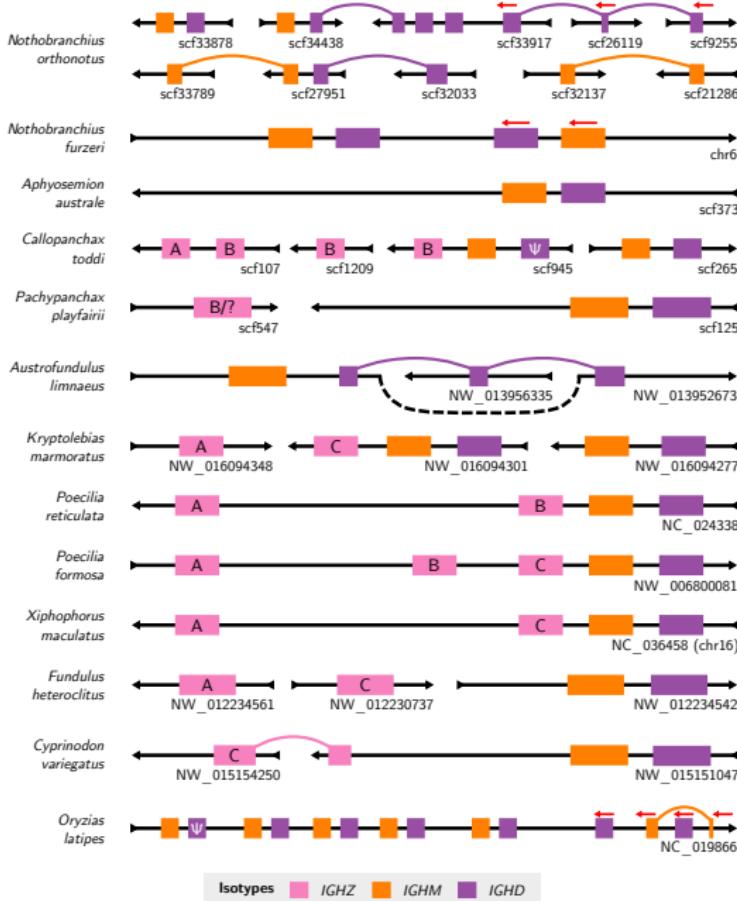


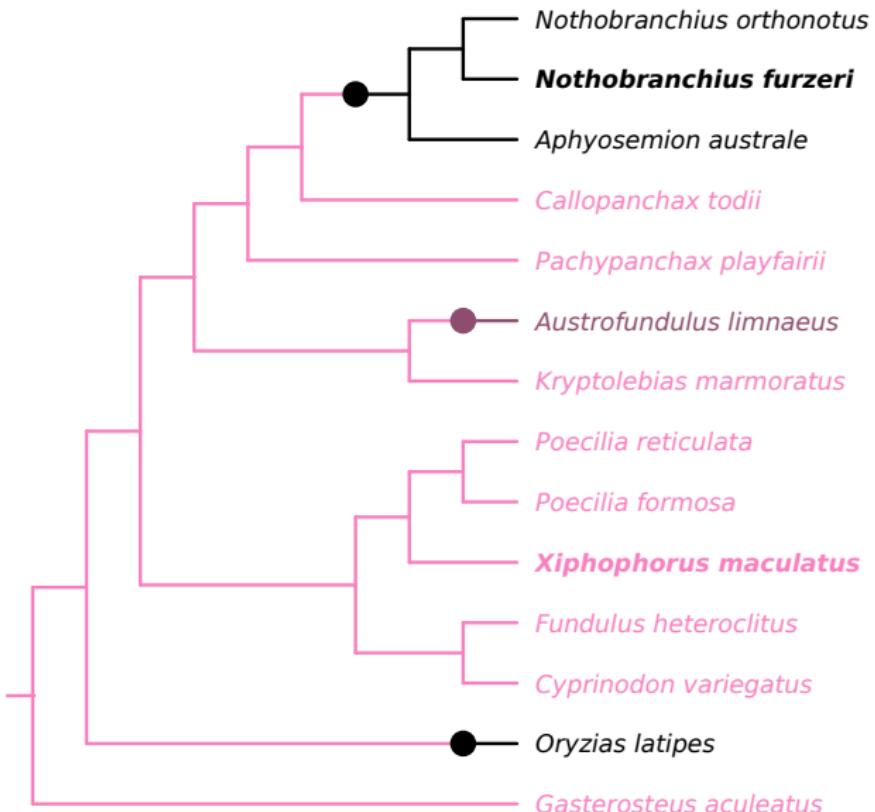
N. furzeri RSS composition

A**B****C**

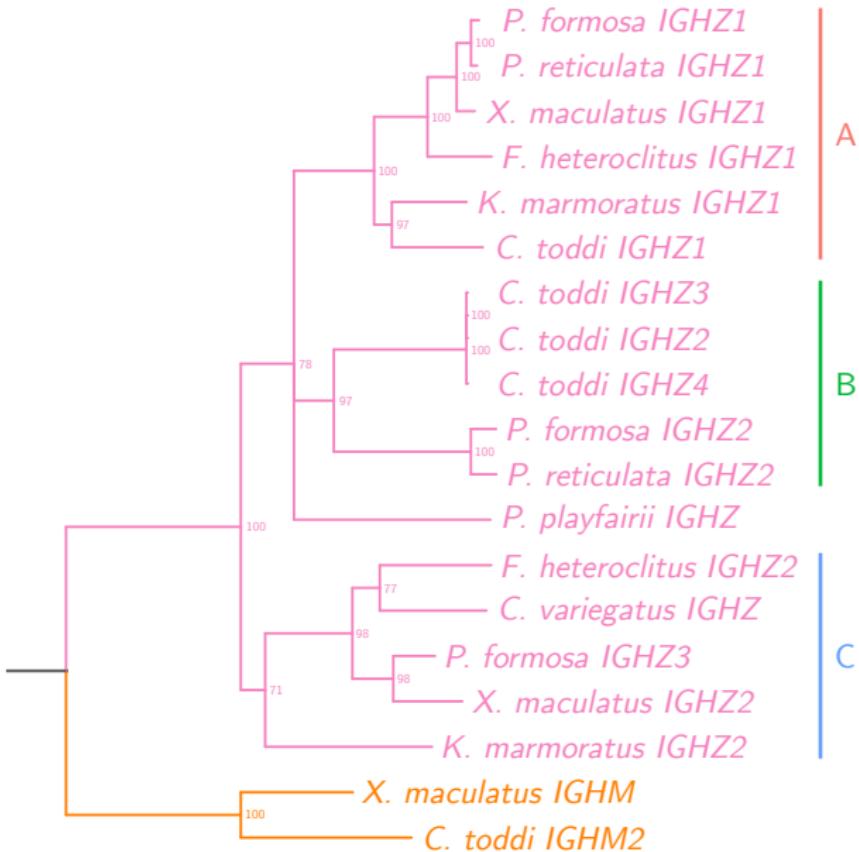
X. maculatus RSS composition



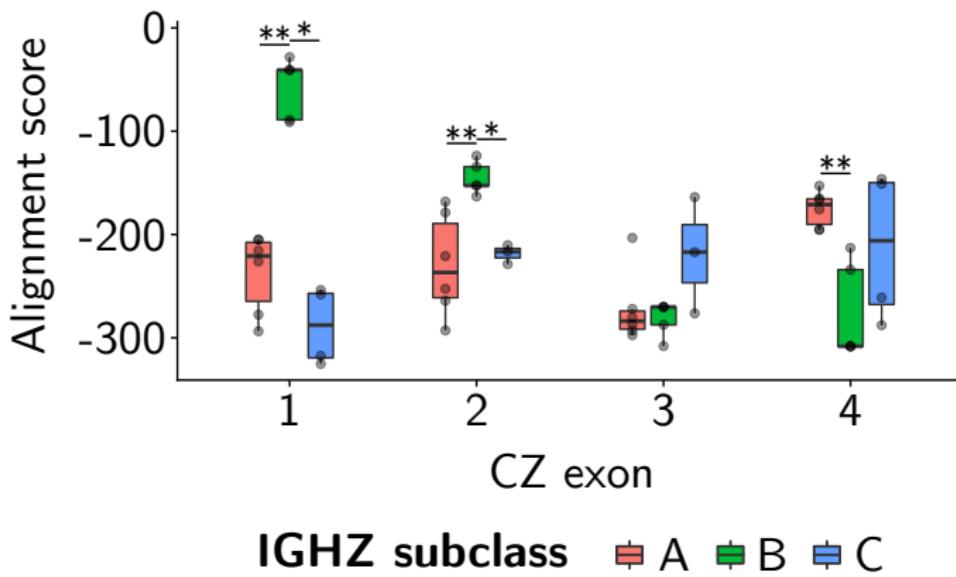


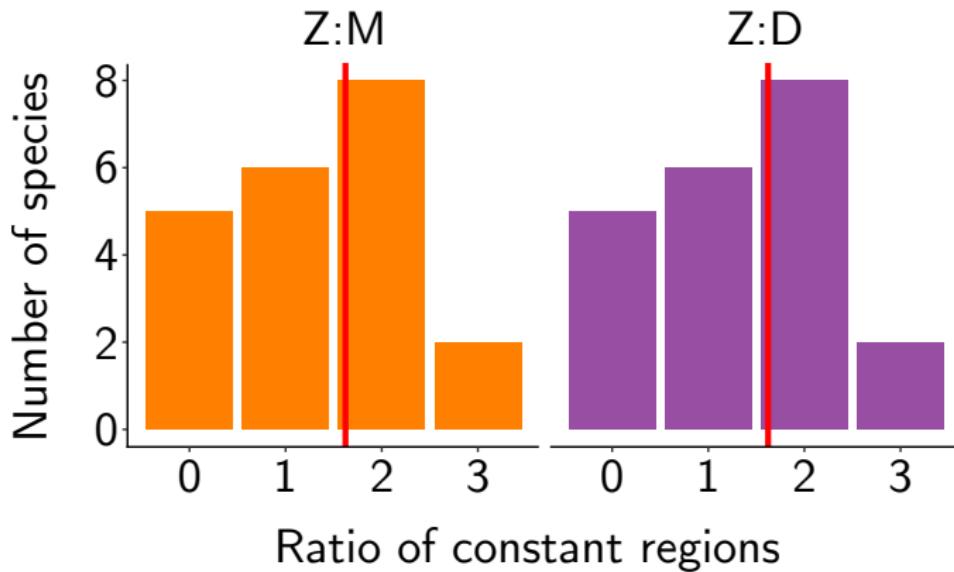


IGHZ? ■ Present ■ Suspected absent ■ Absent

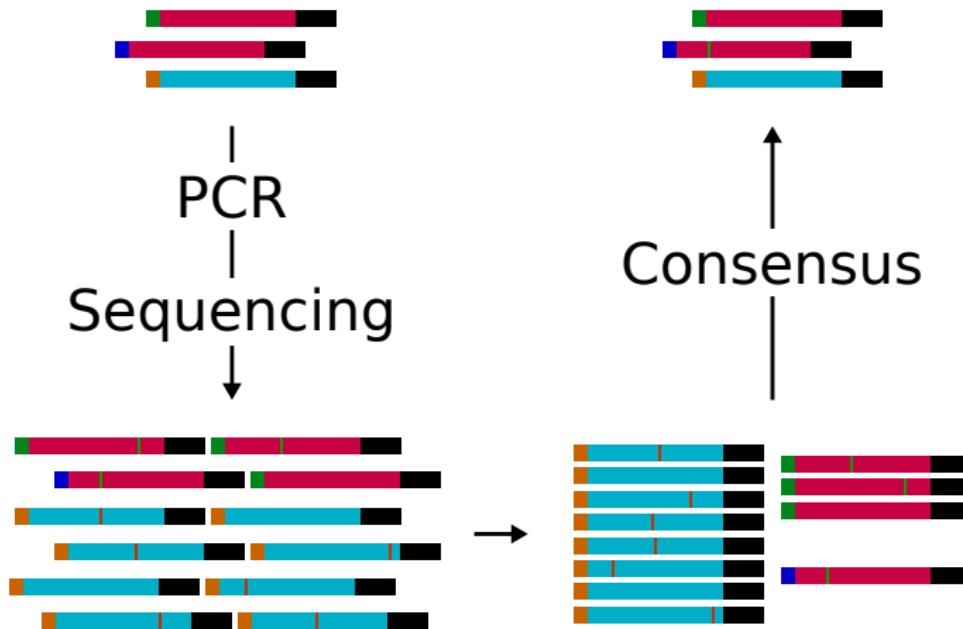


Tree	Species	# IGHZ-A	# IGHZ-B	# IGHZ-C
	<i>N. orthonotus</i>	0	0	0
	<i>N. furzeri</i>	0	0	0
	<i>A. australe</i>	0	0	0
	<i>C. toddi</i>	1	0	3
	<i>P. playfairii</i>	Unknown	1	Unknown
	<i>A. limnaeus</i>	0	0	0
	<i>K. marmoratus</i>	1	0	1
	<i>P. reticulata</i>	1	1	0
	<i>P. formosa</i>	1	1	1
	<i>X. maculatus</i>	1	0	1
	<i>F. heteroclitus</i>	1	0	1
	<i>C. variegatus</i>	0	0	1
	<i>O. latipes</i>	0	0	0

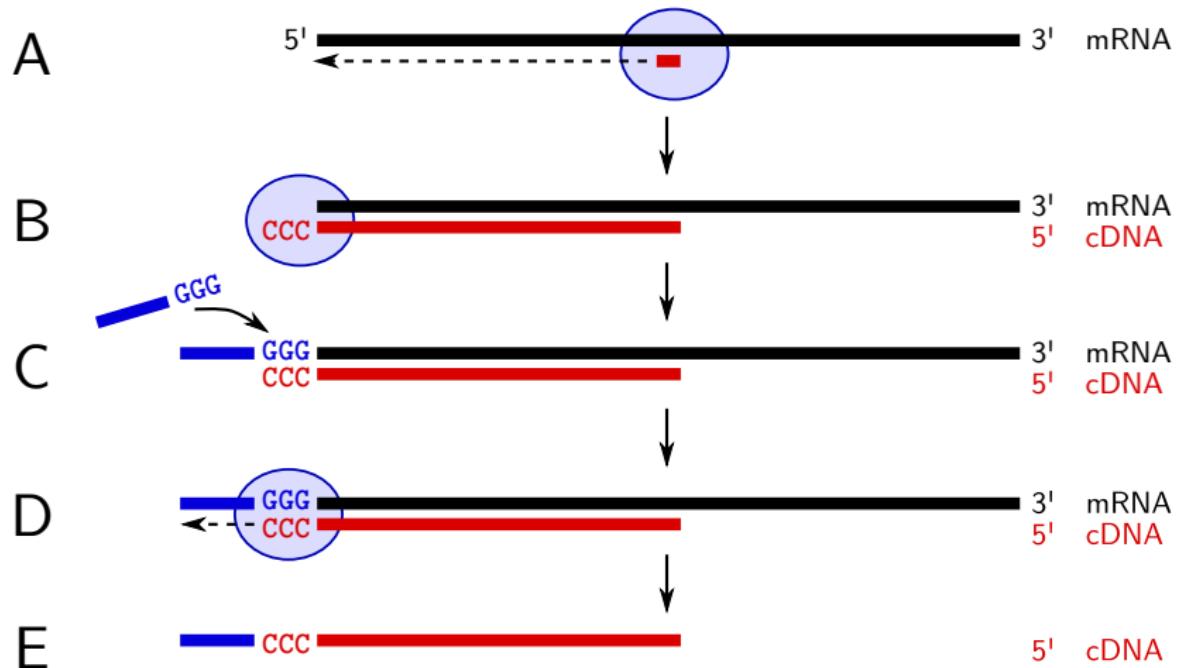




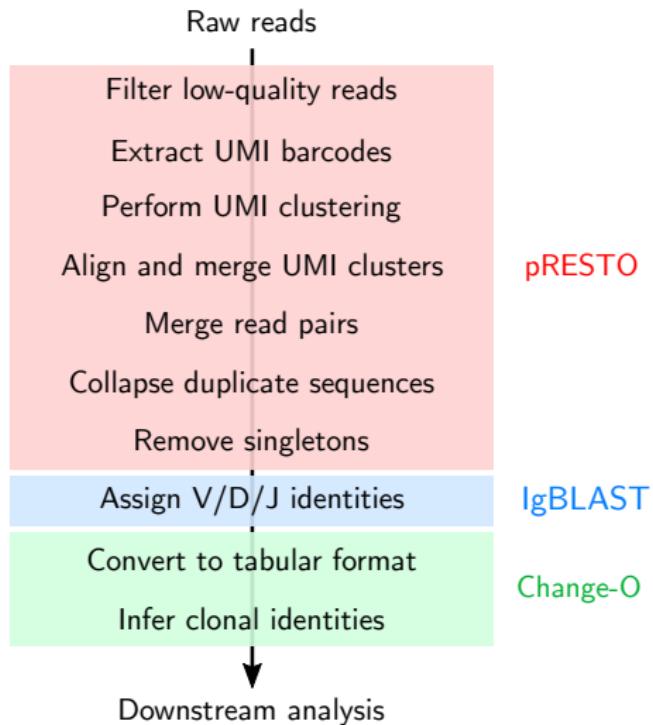
Error correction with UMIs



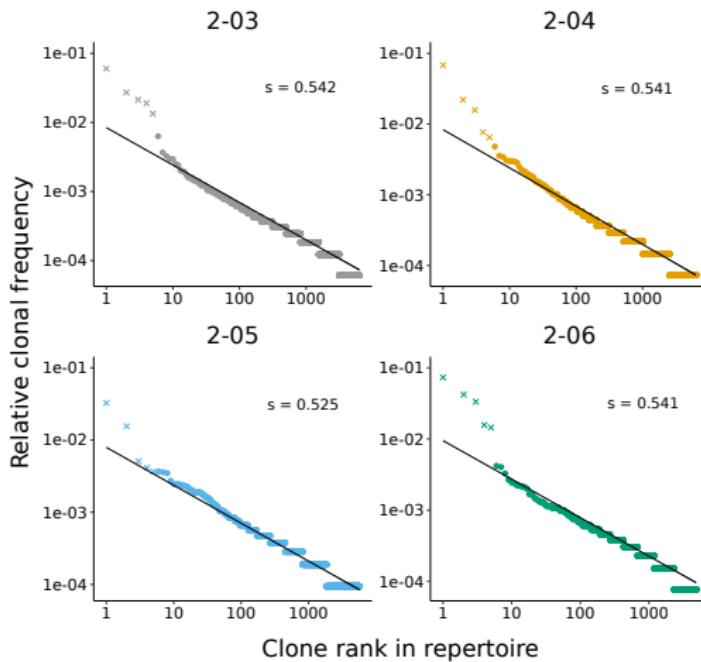
Template switching



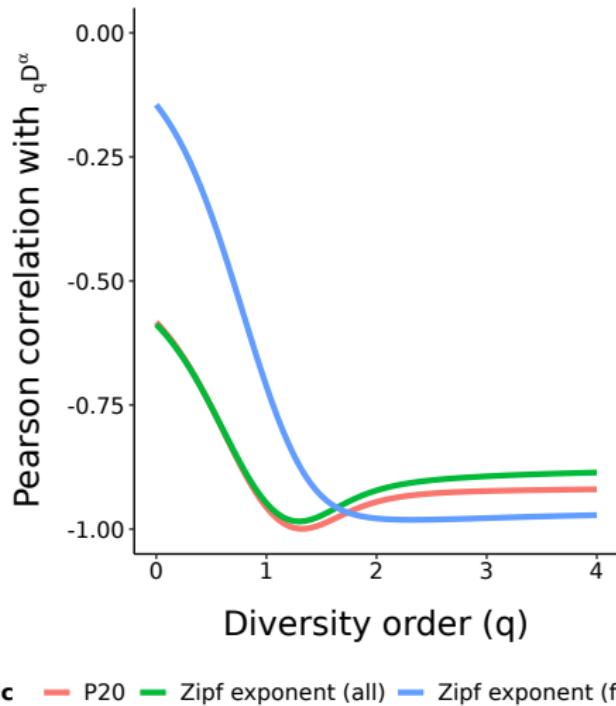
Bioinformatics pipeline



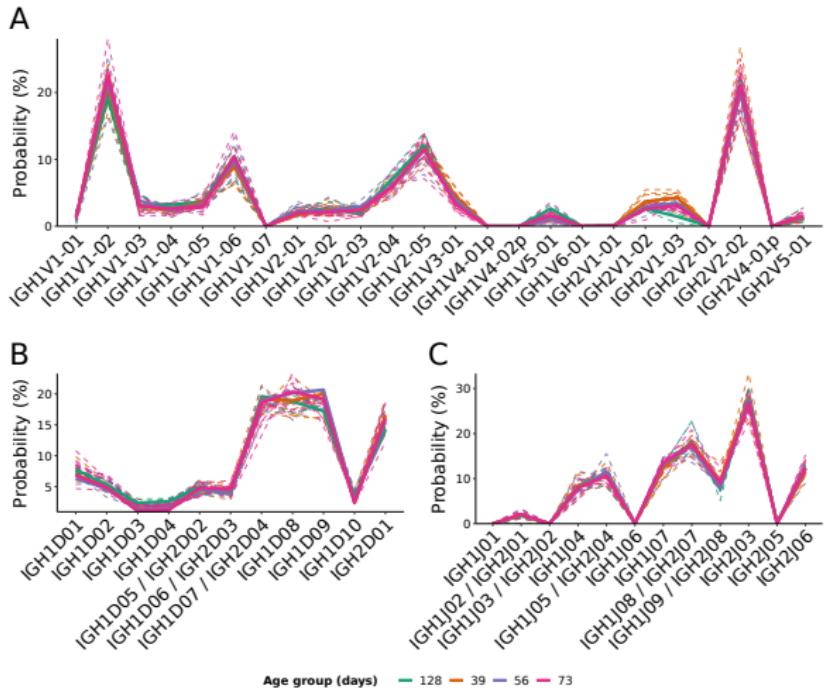
Best-fit zipf distributions of pilot clonal repertoires



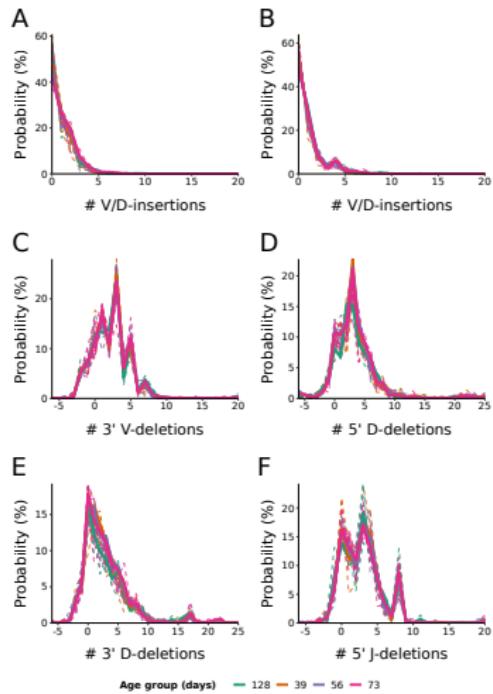
Correlation between Hill α -spectra and other diversity metrics



V/D/J usage probabilities in the killifish generative repertoire



Insertion/deletion in the killifish generative repertoire



Entropy composition of the killifish generative repertoire

N. furzeri

Recombination events (total): 31.72 bits									
Gene choice: 8.26 bits			Insertions: 12.17 bits				Deletions: 11.28 bits		
V	D	J	VD nts	VD len	DJ nts	DJ len	delV	delD	delJ

H. sapiens

recombination events : 78 bits									
gene : 11 bits			insertions : 53 bits				deletions : 14 bits		
V	D	J	VD nts	VD length	DJ nts	DJ length	delV	delD	delJ

Elhanati et al., Phil. Trans. R. Soc. B (2015)

The generative entropy of the naïve antibody repertoire does not change with age

Age (days) = 39

Recombination events (total): 30.38 bits									
Gene choice: 8.22 bits			Insertions: 10.91 bits			Deletions: 11.25 bits			
V	D	J	VD nts	VD len	DJ nts	DJ len	delV	delD	delJ

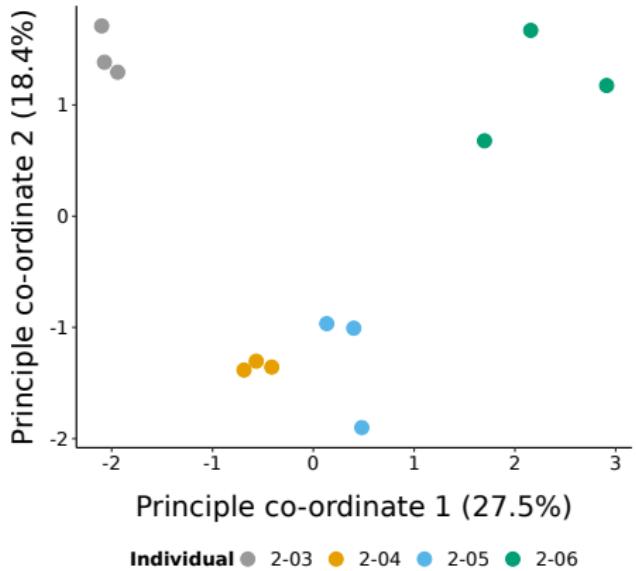
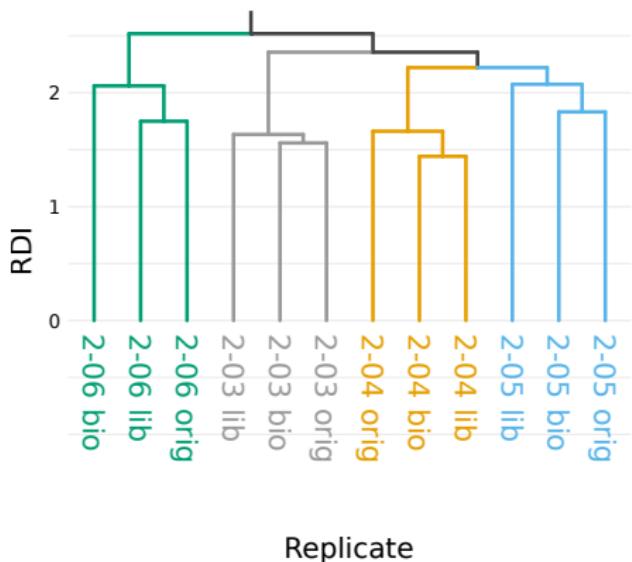
Age (days) = 56

Recombination events (total): 30.78 bits									
Gene choice: 8.21 bits			Insertions: 11.22 bits			Deletions: 11.36 bits			
V	D	J	VD nts	VD len	DJ nts	DJ len	delV	delD	delJ

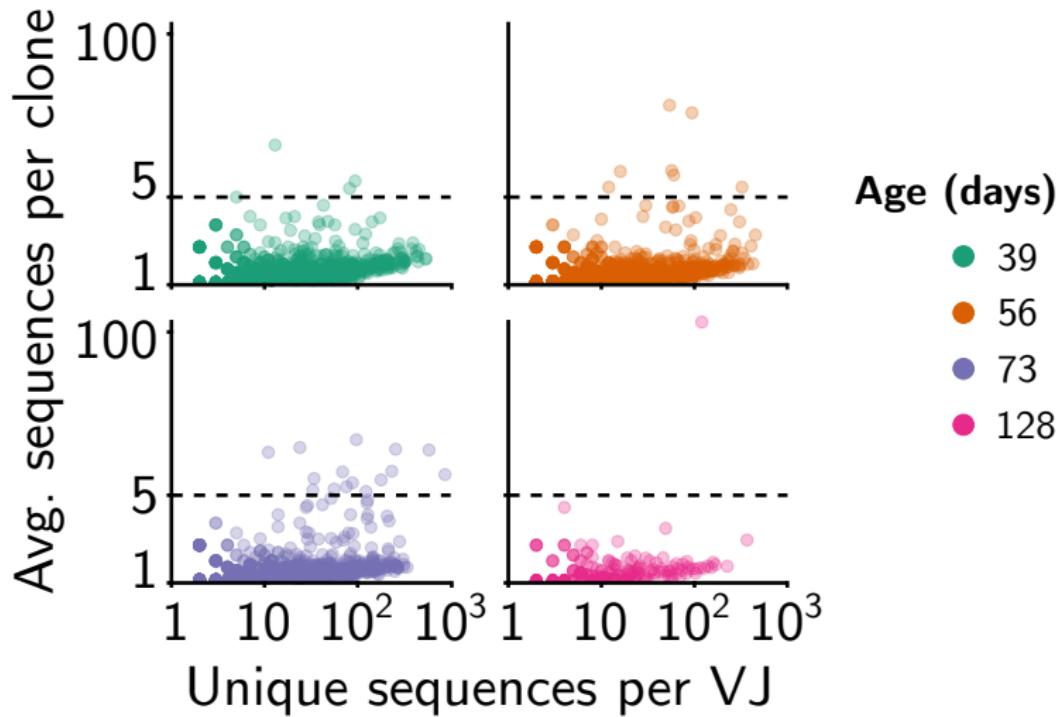
Age (days) = 73

Recombination events (total): 31.2 bits									
Gene choice: 8.17 bits			Insertions: 11.8 bits			Deletions: 11.23 bits			
V	D	J	VD nts	VD len	DJ nts	DJ len	delV	delD	delJ

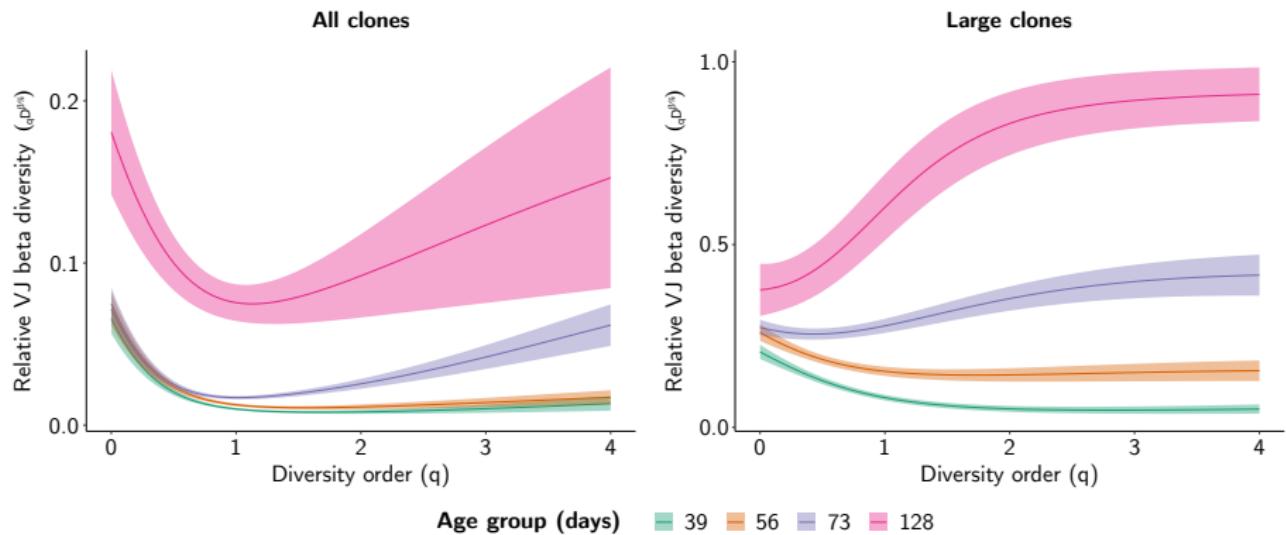
RDI measures can reliably distinguish between individual repertoires



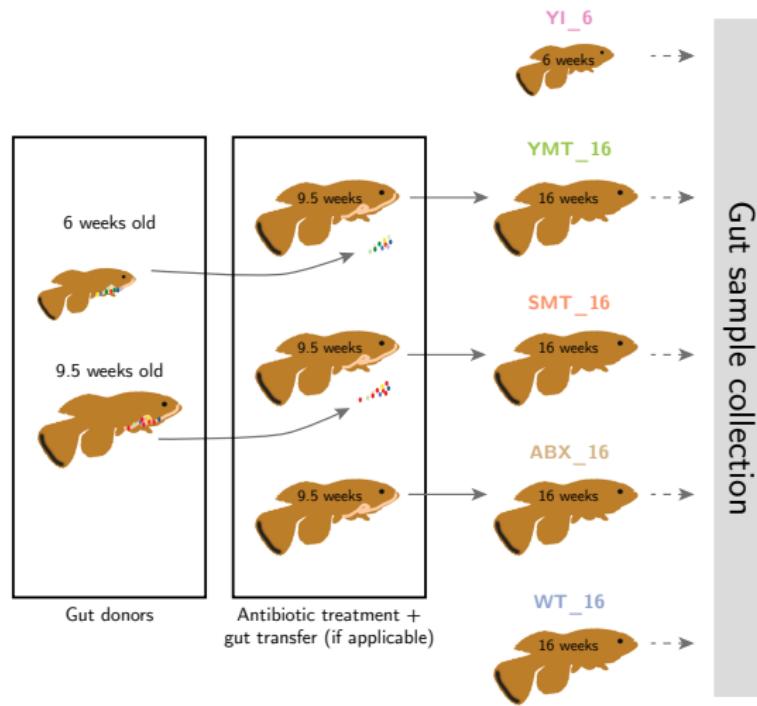
Most VJ combinations are dominated by small clones



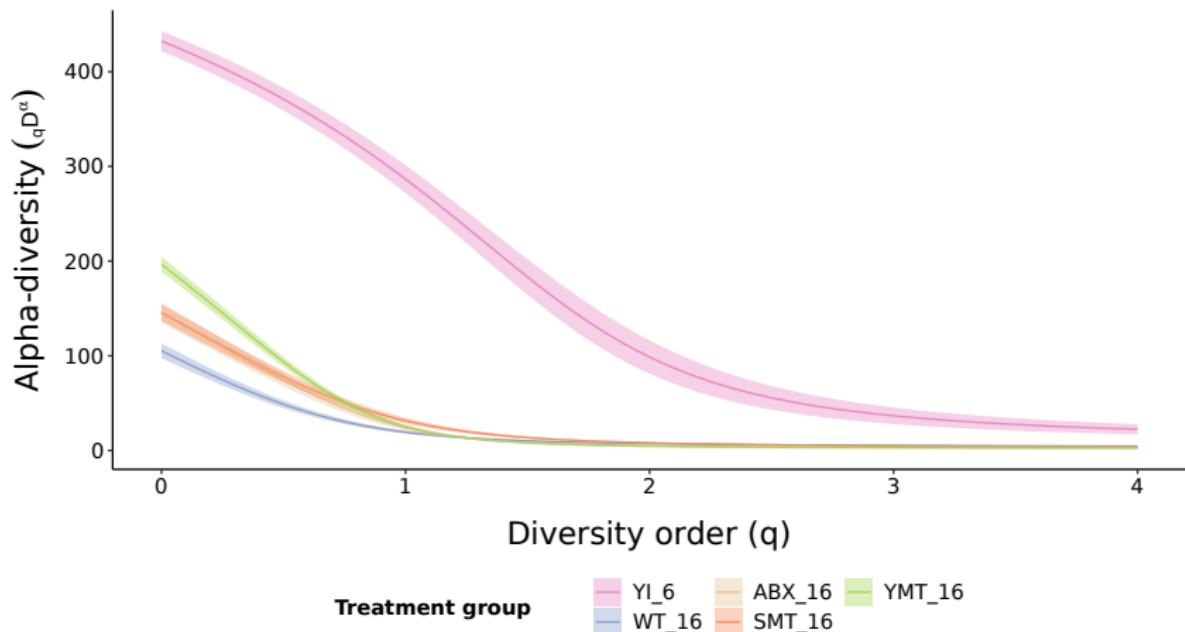
Beta-diversity spectra: ageing cohort



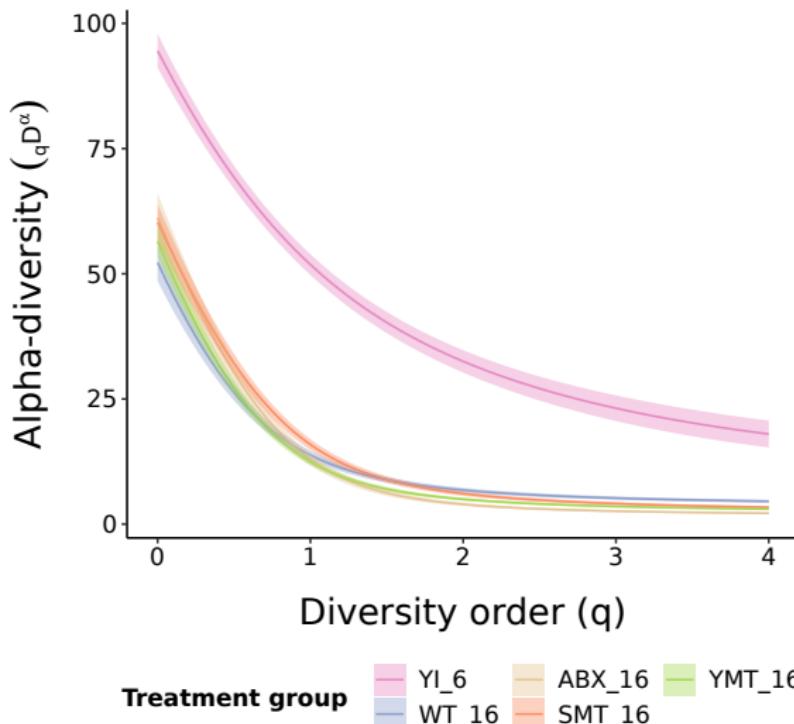
Gut microbiota transfer design



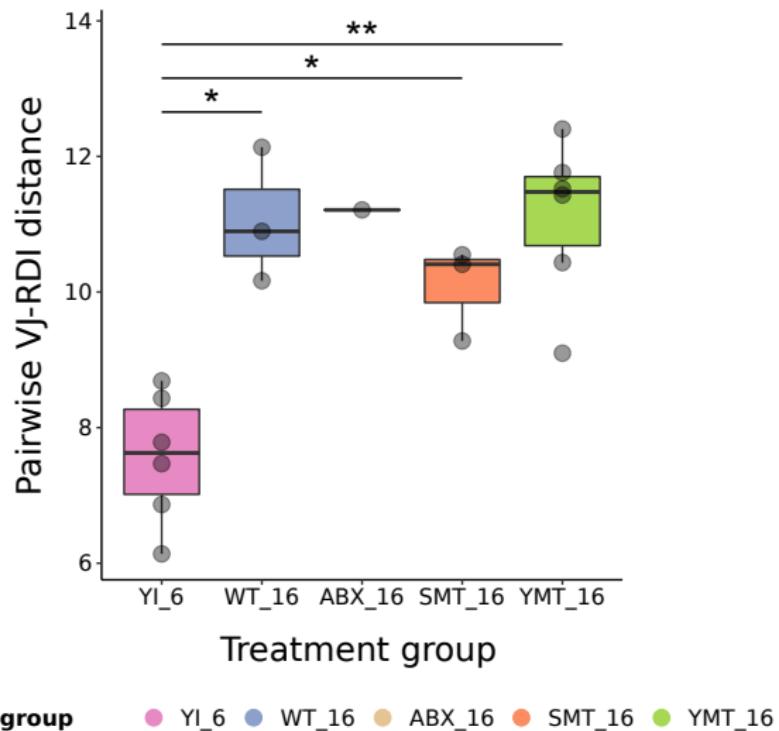
Transfer-group clonal alpha diversity



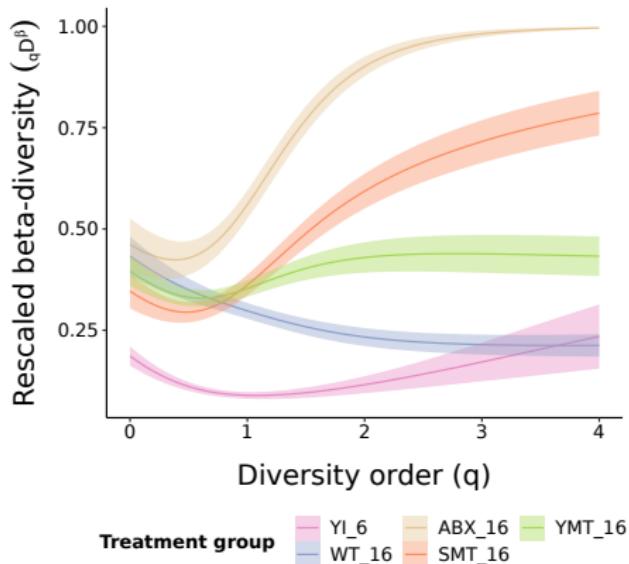
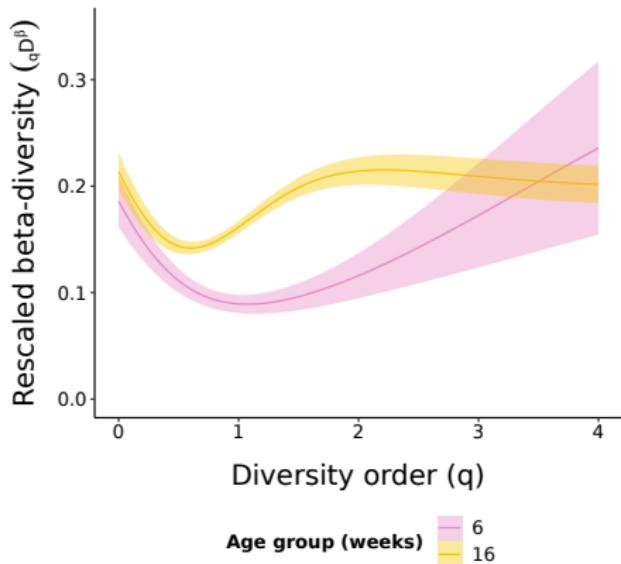
Transfer-group VJ alpha diversity



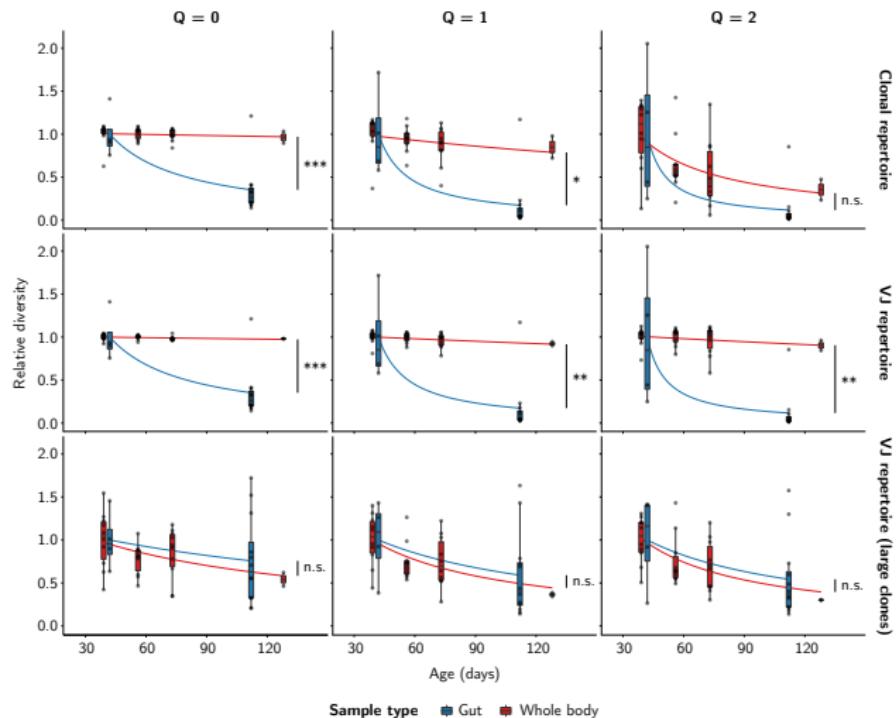
Transfer-group VJ beta diversity



Beta-diversity spectra: gut samples



Relative rate of repertoire diversity loss



Hill diversity for a unitary population X

$${}^q D(X) = \begin{cases} \left(\sum_{s \in S} p_s^q \right)^{\frac{1}{1-q}} & q \neq 1 \\ \exp \left(- \sum_{s \in S} p_s \cdot \ln p_s \right) & q = 1 \end{cases}$$

Hill diversity for a structured population C

$${}^q D_\gamma(C) = {}^q D(C)$$

$${}^q D_\alpha(C) = \begin{cases} \left(\frac{1}{M} \sum_{X \in C} [{}^q D(X)]^{1-q} \right)^{\frac{1}{1-q}} & q \neq 1 \\ \exp \left(\frac{1}{M} \sum_{X \in C} \ln {}^1 D(X) \right) & q = 1 \end{cases}$$

$${}^q D_\beta(C) = \frac{{}^q D_\gamma(C)}{{}^q D_\alpha(C)}$$

Burrows-Wheeler Transform (BWT)

(a)

\$ a c a a c g
a a c g \$ a c
a c a a c g \$
a c a a c g \$ → a c g \$ a c a → g c \$ a a a c
c a a c g \$ a
c g \$ a c a a
g \$ a c a a c

(c)

a a c	a a c	a a c
\$ a c a a c g	\$ a c a a c g	\$ a c a a c g
a a c g \$ a c	a a c g \$ a c	a a c g \$ a c
a c a a c g \$	→ a c a a c g \$	→ a a c g \$ a c
a c g \$ a c a	→ a c g \$ a c a	→ a c g \$ a c a
c a a c g \$ a	c a a c g \$ a	c a a c g \$ a
c g \$ a c a a	c g \$ a c a a	c g \$ a c a a
g \$ a c a a c	g \$ a c a a c	g \$ a c a a c

(b)

g	c g	a c g	a a c g	c a a c g	a c a a c g
\$ a c a a c g					
a a c g \$ a c					
a c a a c g \$					
a c g \$ a c a					
c a a c g \$ a					
c g \$ a c a a					
g \$ a c a a c					

Needleman-Wunsch Algorithm

Needleman-Wunsch

match = 1

mismatch = -1

gap = -1

	G	C	A	T	G	C	U	
G	0	-1	-2	-3	-4	-5	-6	-7
A	-1	0	0	1	0	-1	-2	-3
T	-2	0	0	1	0	-1	-2	-3
T	-3	-1	-1	0	2	1	0	-1
A	-4	-2	-2	-1	1	1	0	-1
A	-5	-3	-3	-1	0	0	0	-1
C	-6	-4	-2	-2	-1	-1	1	0
A	-7	-5	-3	-1	-2	-2	0	0

The diagram illustrates a dynamic programming matrix for the Needleman-Wunsch algorithm. The matrix is an 8x8 grid where rows represent the first sequence and columns represent the second sequence. The sequences are: Row 1: G, C, A, T, G, C, U; Column 1: G, C, A, T, G, C, U. The matrix contains numerical values representing scores for matches, mismatches, and gaps. Blue arrows point along the main diagonal, indicating matches between identical nucleotides. Red arrows point from the main diagonal towards the bottom-right corner, indicating long gaps in the second sequence. The values in the matrix are: Row 1: G(-1), C(-2), A(-3), T(-4), G(-5), C(-6), U(-7); Column 1: G(0), C(-1), A(-2), T(-3), G(-4), C(-5), U(-6). Subsequent rows and columns show the cumulative scores for matches, mismatches, and gaps.

Smith-Waterman Algorithm

