

De novo assembly and annotation of wild crucian carp genome

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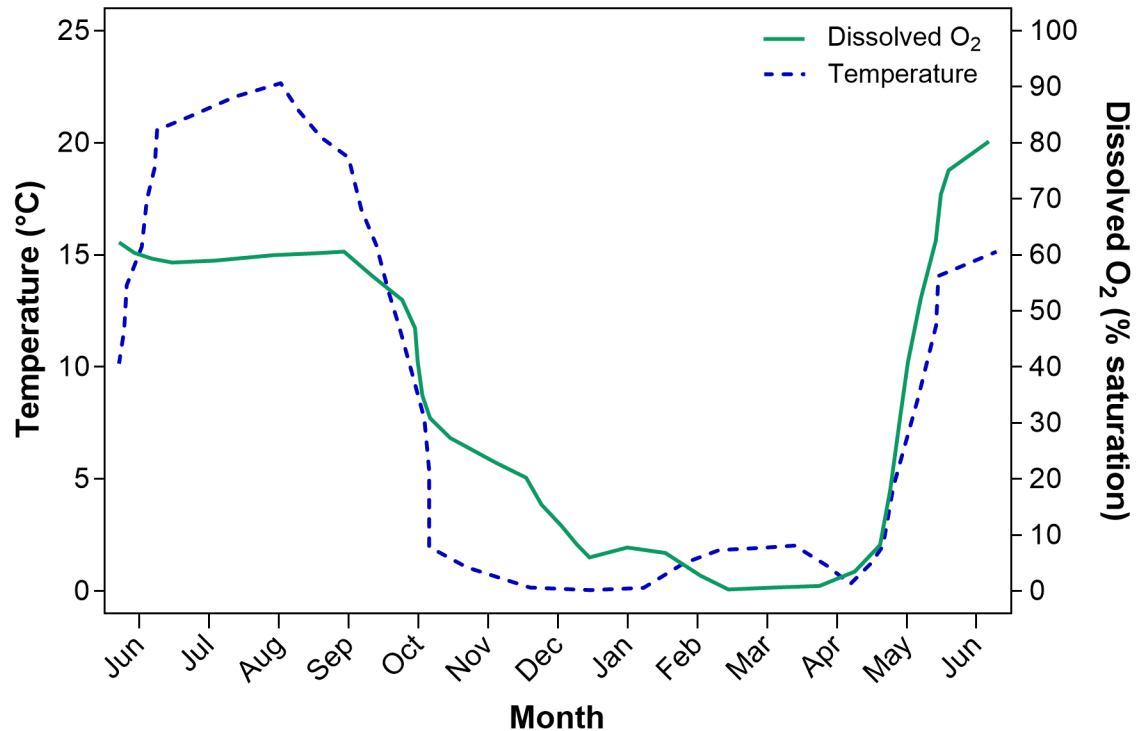


Carassius carassius



UNIVERSITY
OF OSLO

The crucian carp lives in changing environments that reach low O₂



Reproduced from Vornanen and Paajanen (2004), *Am J Physiol*



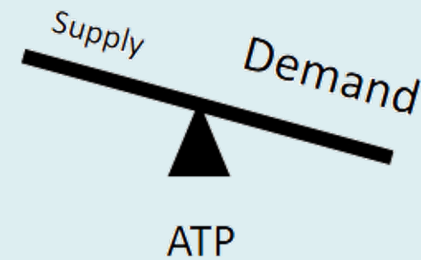
Photos by Jonathan Stecyk

Anaerobic glycolysis: 95% reduction in ATP supply (36 ATP → 2 ATP)

Anoxia

$pO_2 = 0$

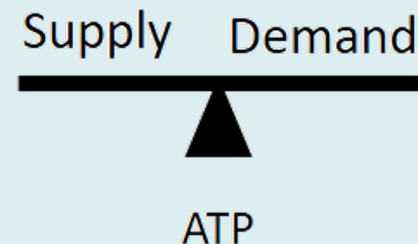
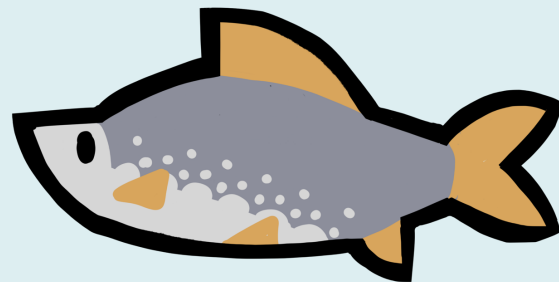
Anoxia sensitive species



Anoxic catastrophe

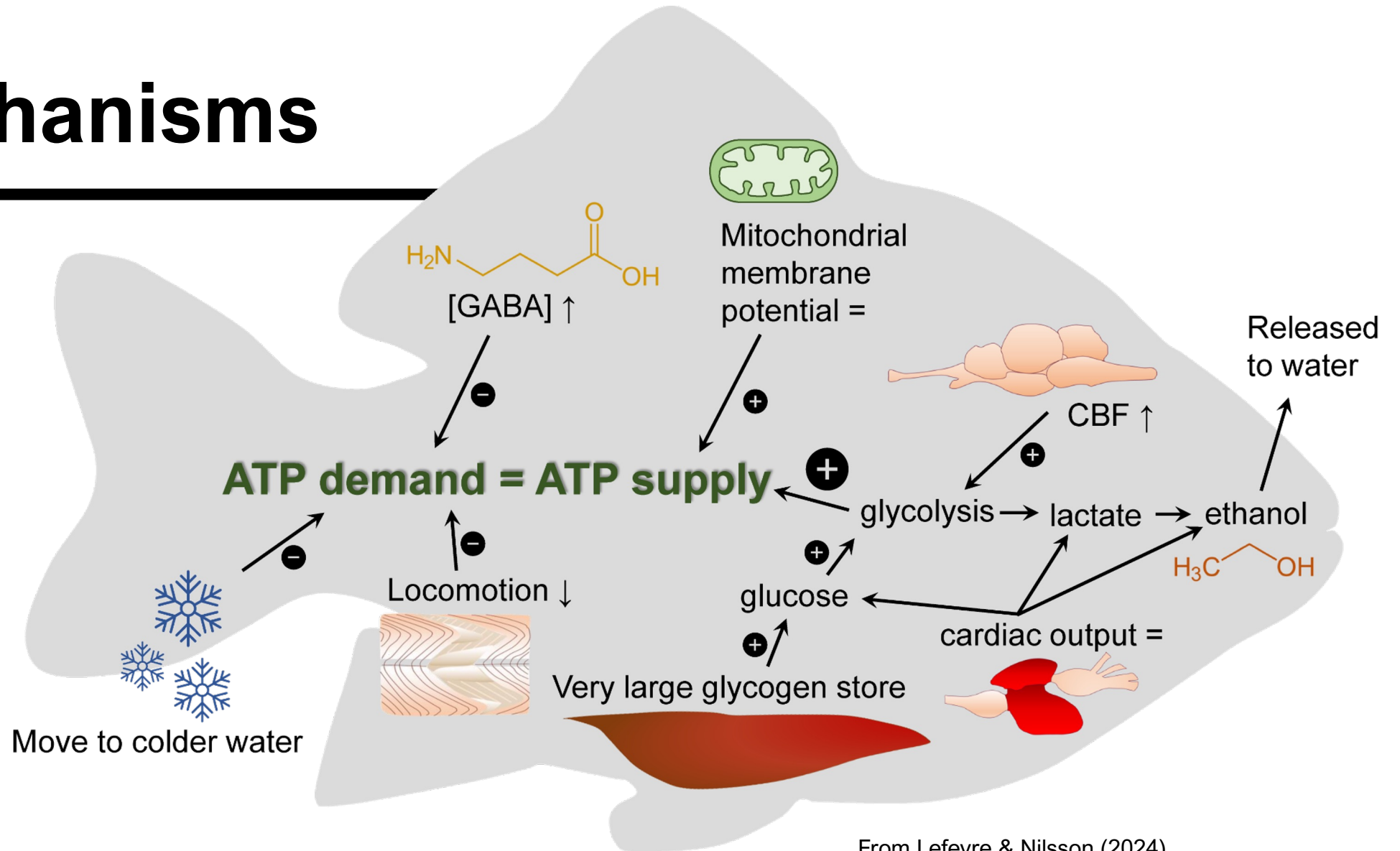
Not enough ATP for physiological functions.
Uncontrolled cell death
Ischemia: «cell betrayal»

Anoxia tolerant crucian carp



Maintains enough ATP for physiological function

Mechanisms

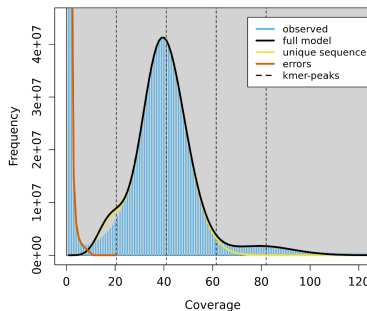


From Lefevre & Nilsson (2024)
Encyclopedia of Fish Physiology 2nd edition

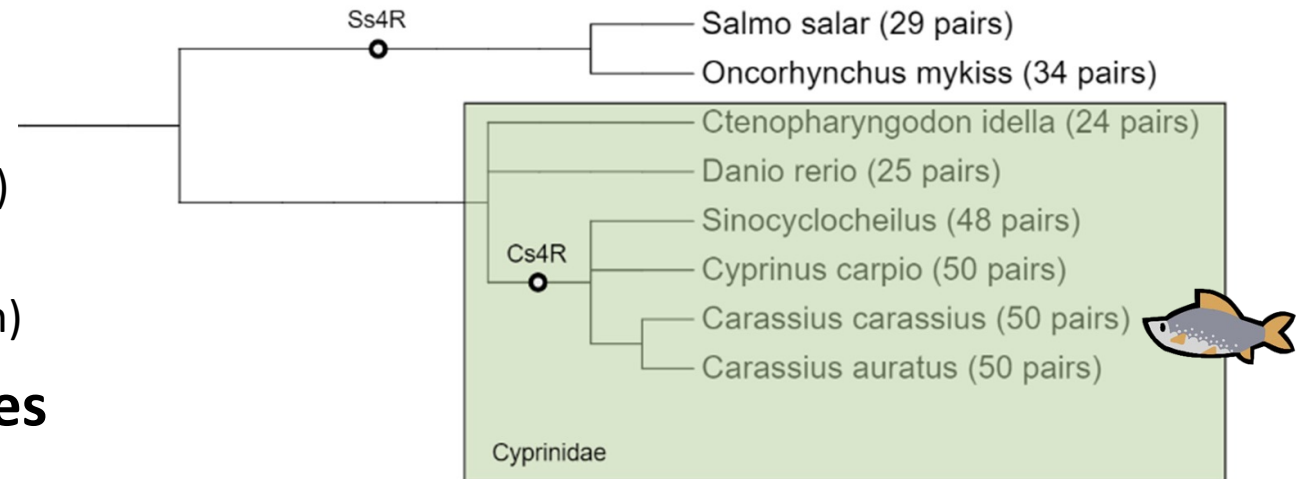
Originated as an allotetraploid, and now a diploid

Common carp-specific genome duplication (CcaGD) ~12 Mya

- 1st genome duplication (all fishes)
- 2nd genome duplication (cyprinid fishes)
- 3rd genome duplication (crucian carp, common carp and goldfish)
- **Abundance of duplicated genes**



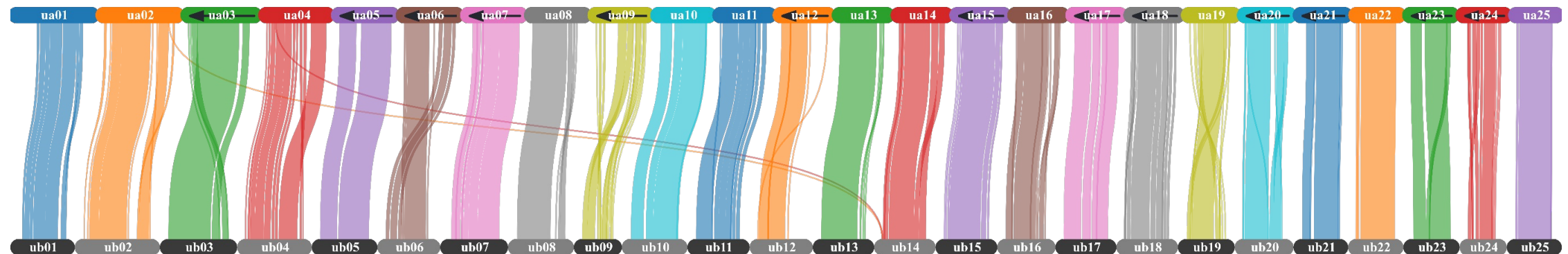
Kmer spectra looks like a diploid!



Synteny is the conservation of blocks of sequence between chromosomes

Synteny plotting detects the genome duplication of the crucian carp

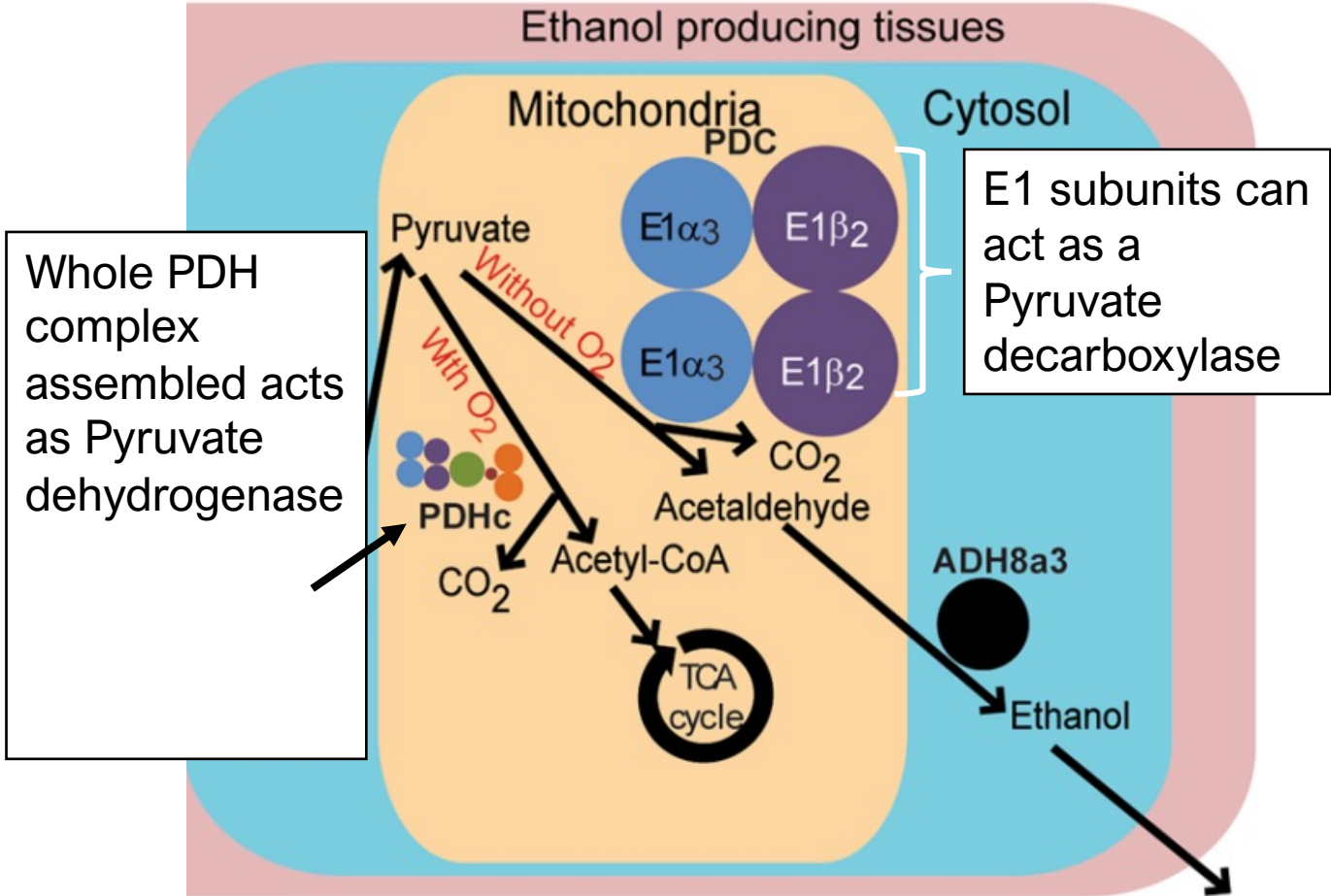
Subgenome A: 25 chromosomes



Subgenome B: 25 chromosomes

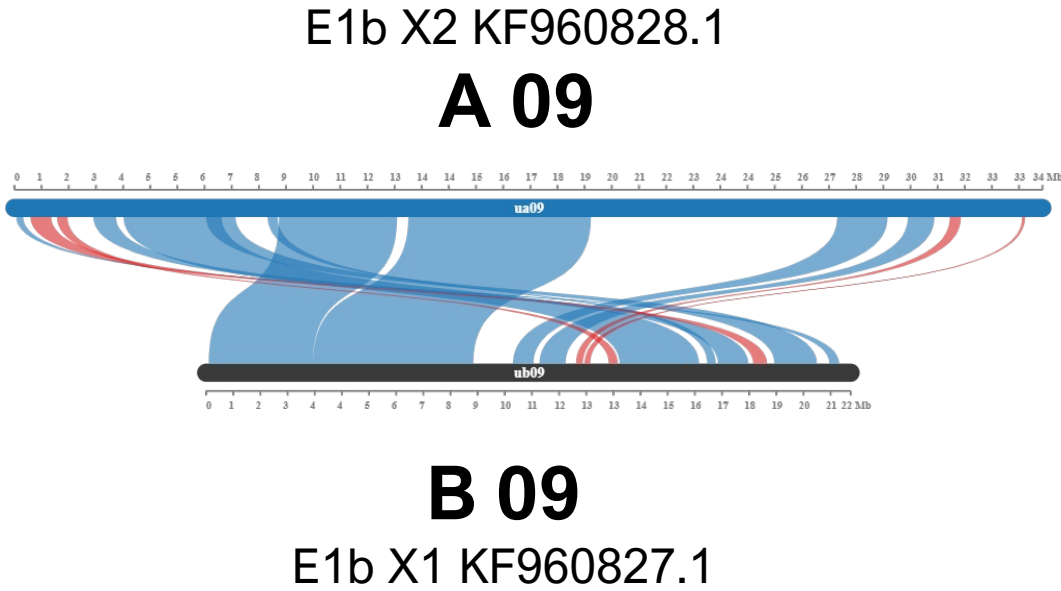
Sequences from our genome assembly at chromosome level

Genome duplication offers neofunctionalization of duplicated genes

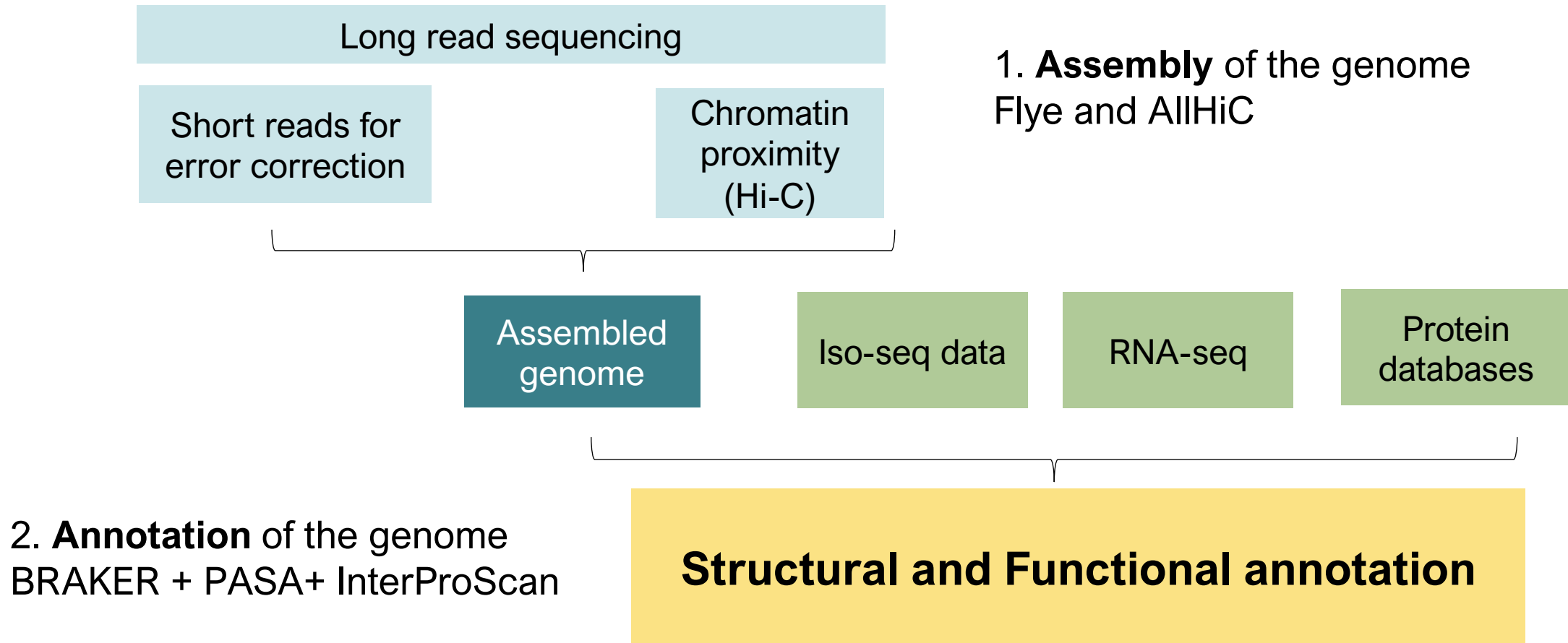


Fagernes, 2017

E1b X1 and E1b X2 have different expression levels at different oxygen states



De novo assembly of a genome and its annotation



2. **Annotation** of the genome
BRAKER + PASA+ InterProScan

Structural annotation with BRAKER

Teleosts protein database
(OrthoDB) + Isoseq predicted
proteins

Curated Genome assembly
softmasked

RNA-seq cruciancarp:
diverse tissues

- Eye
- Brain
- muscle
- liver
- scale
- skin
- Kidney
- Spleen
- Heart
- Intestine
- Gonad
- Gills

Braker pipeline B:
Annotation with protein

Braker pipeline A:
Annotation with RNA-seq

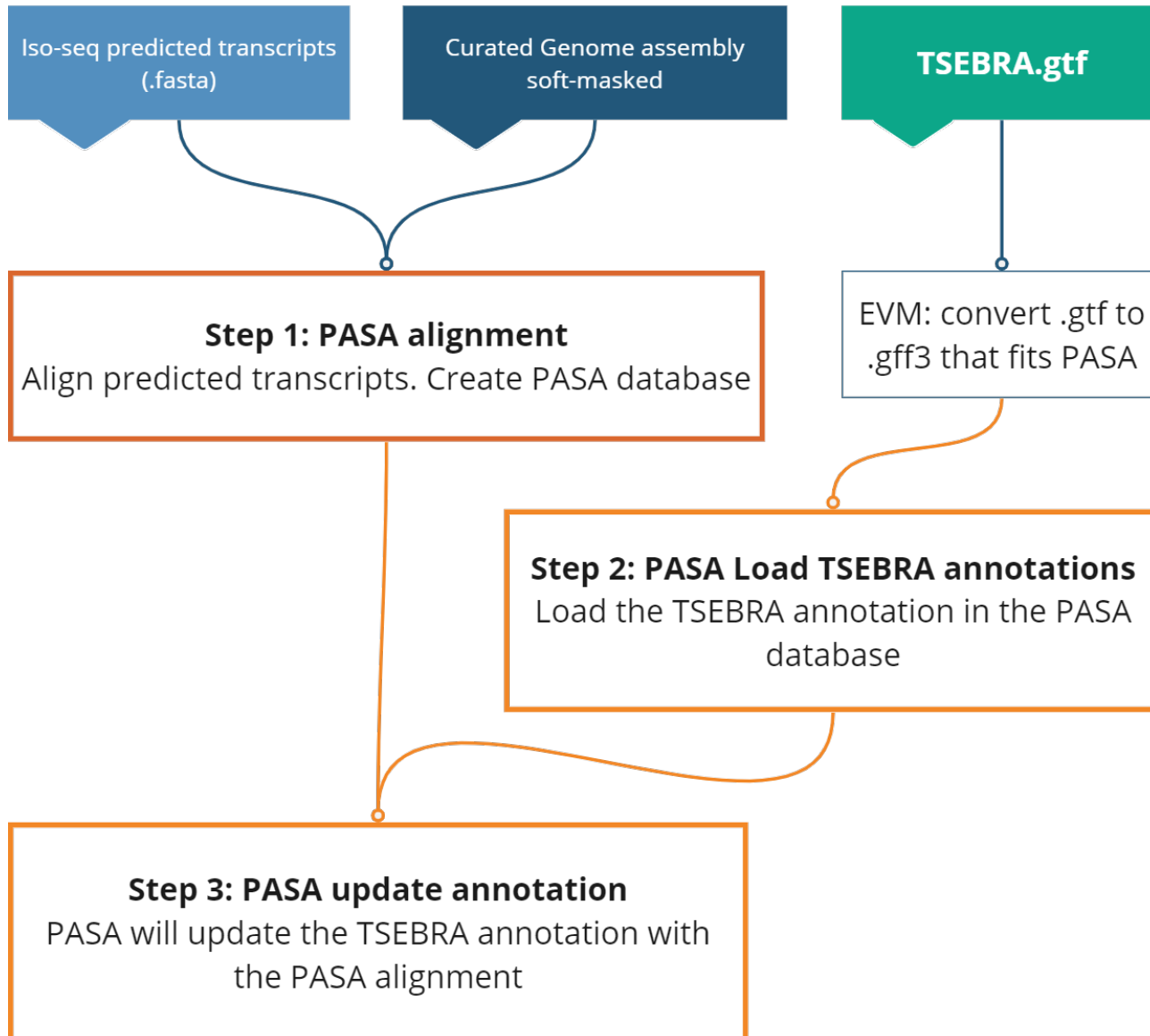
braker2.gtf

braker1.gtf

TSEBRA: Join annotation files (.gtf)
Compare transcripts
Remove low evidence transcripts

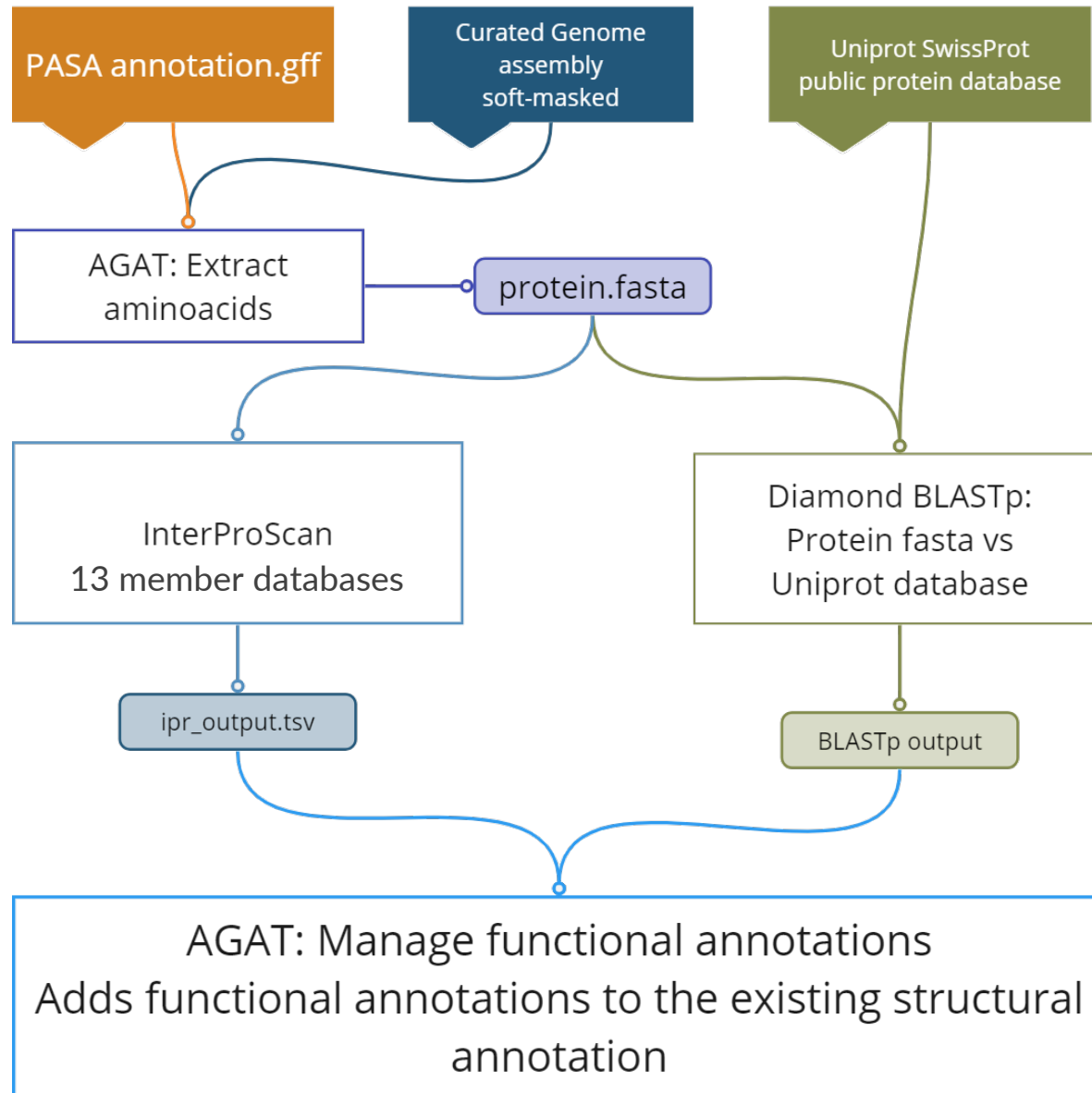


Annotation of UTRs with PASA pipeline



UTR annotation is useful to study long non-coding RNA

Functional Annotation



Future work: Comparison with goldfish

Goldfish is a very close species which has lost anoxia tolerance due to domestication

Pathway differences can indicate evolutionary processes

Go beyond In silico: Physiology experiments
Anoxia experiments with RNA-seq and plasma.



Utagawa Kuniyoshi (1798-1861) "All kind of goldfishes"

Thank you

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