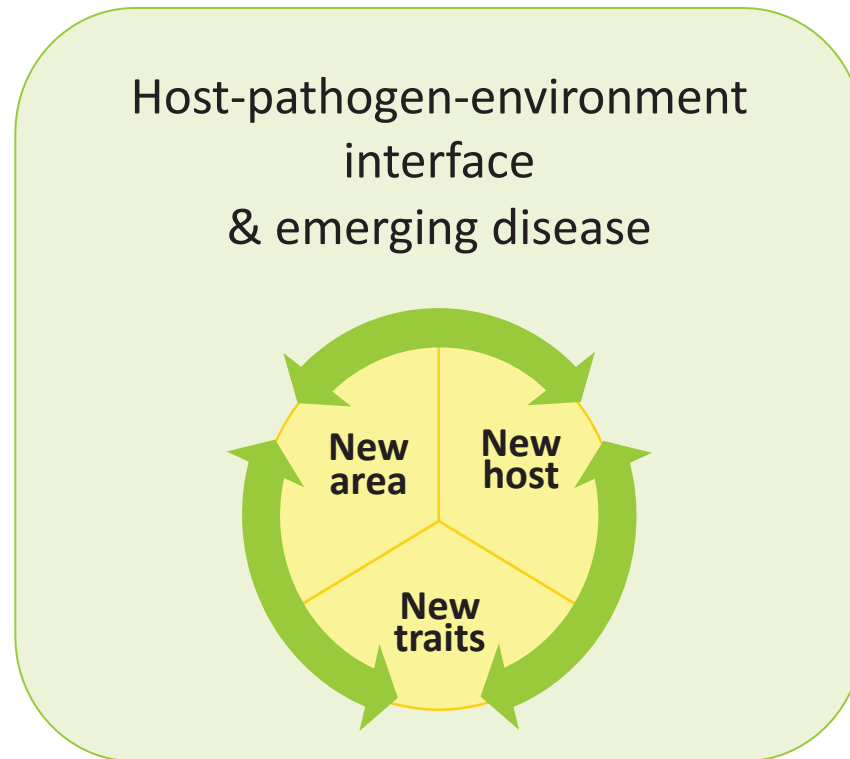


Aude Gilabert
Post-doctorante

**Pathogen emergence:
Evolution of parasitism
and
host adaptation**

PATHOGEN EMERGENCE





QUESTION: Evolution of signalling pathways



QUESTION: Evolution of signalling pathways

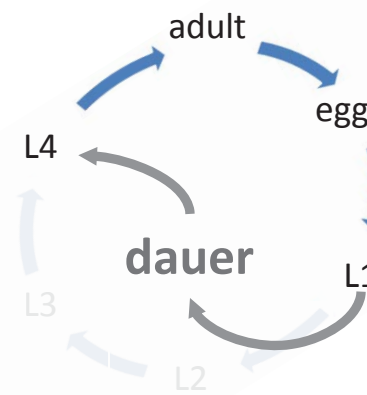
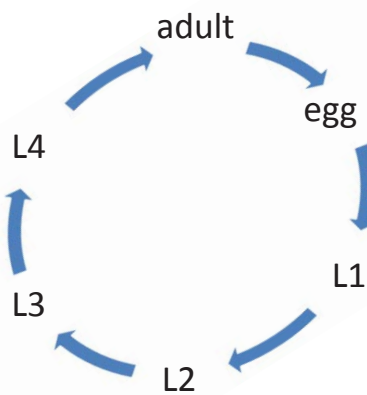
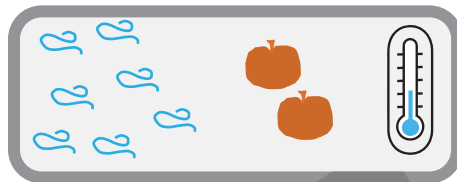
↳ The dauer signalling pathways



QUESTION: Evolution of signalling pathways

↳ The dauer signalling pathways

C. elegans life cycle





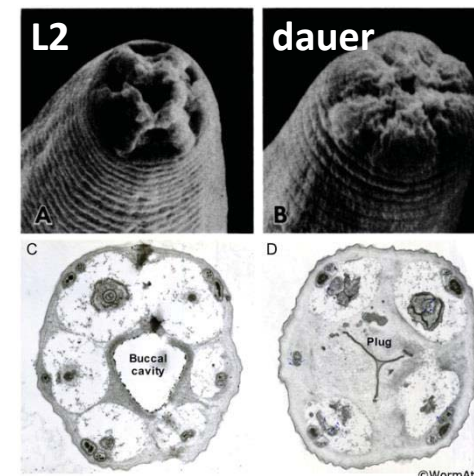
QUESTION: Evolution of signalling pathways

↳ The dauer signalling pathways

C. elegans life cycle

Daure larva:

- Arrested developmental stage
- Non-feeding
- Morphological characteristics
- ↓ metabolism
- Resistant to environmental stresses

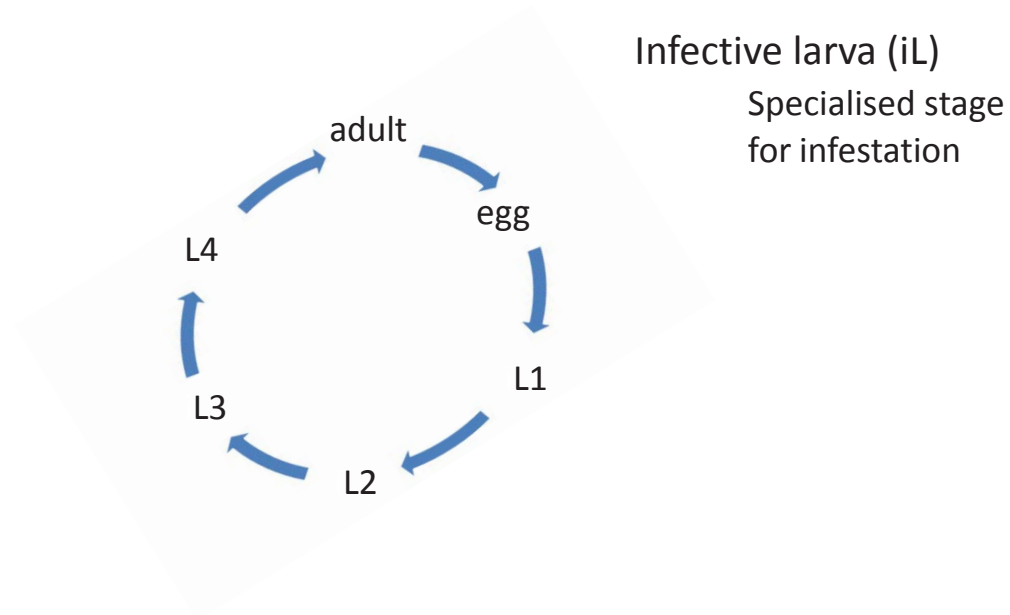




QUESTION: Evolution of signalling pathways

↳ The dauer signalling pathways

Parasitic nematodes' life cycle

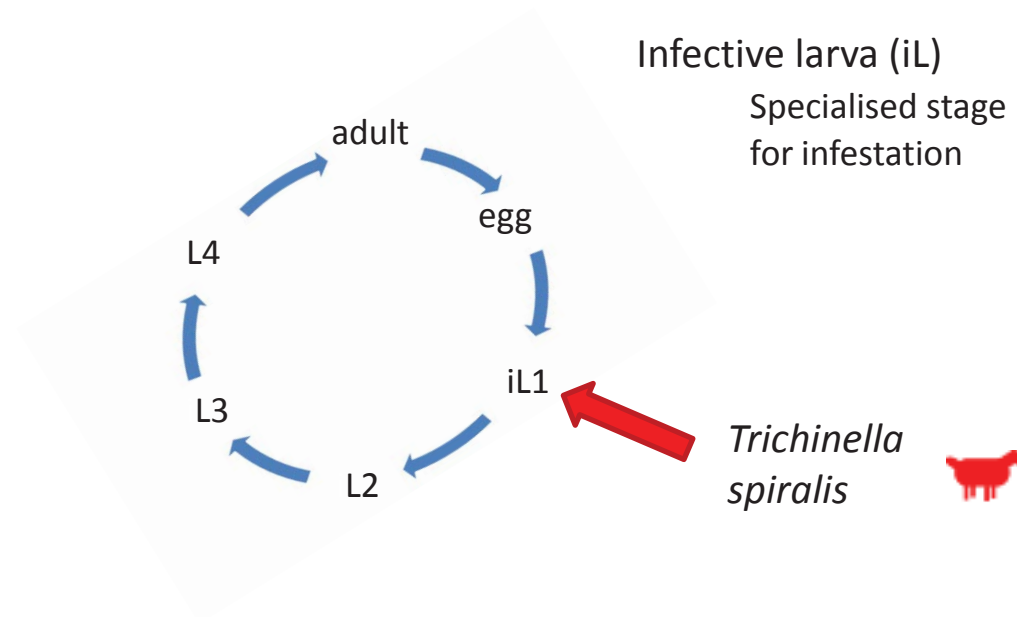




QUESTION: Evolution of signalling pathways

↳ The dauer signalling pathways

Parasitic nematodes' life cycle

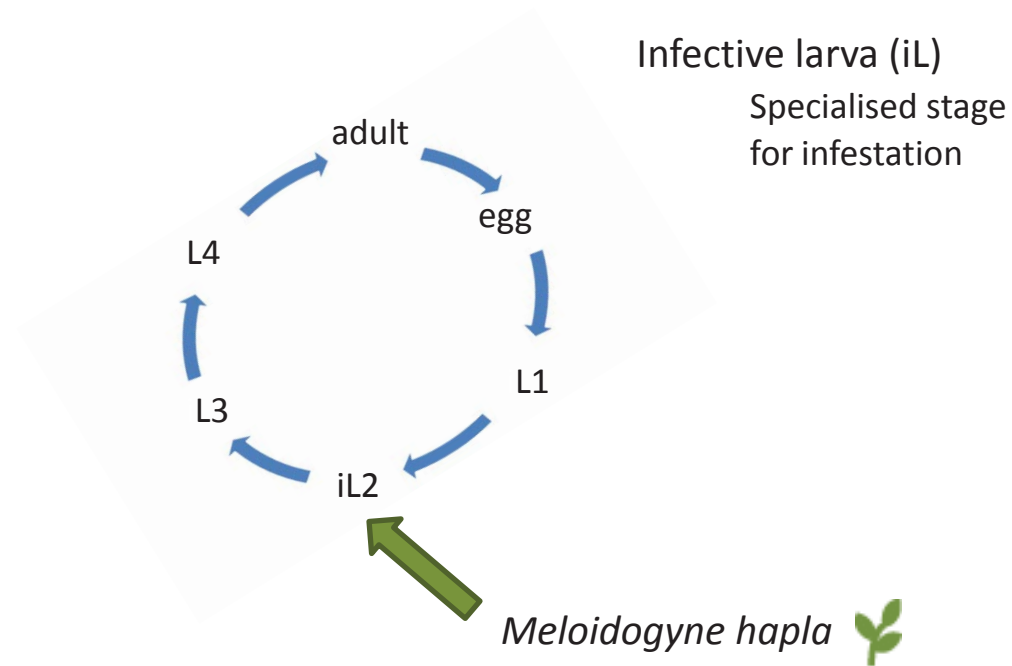




QUESTION: Evolution of signalling pathways

↳ The dauer signalling pathways

Parasitic nematodes' life cycle

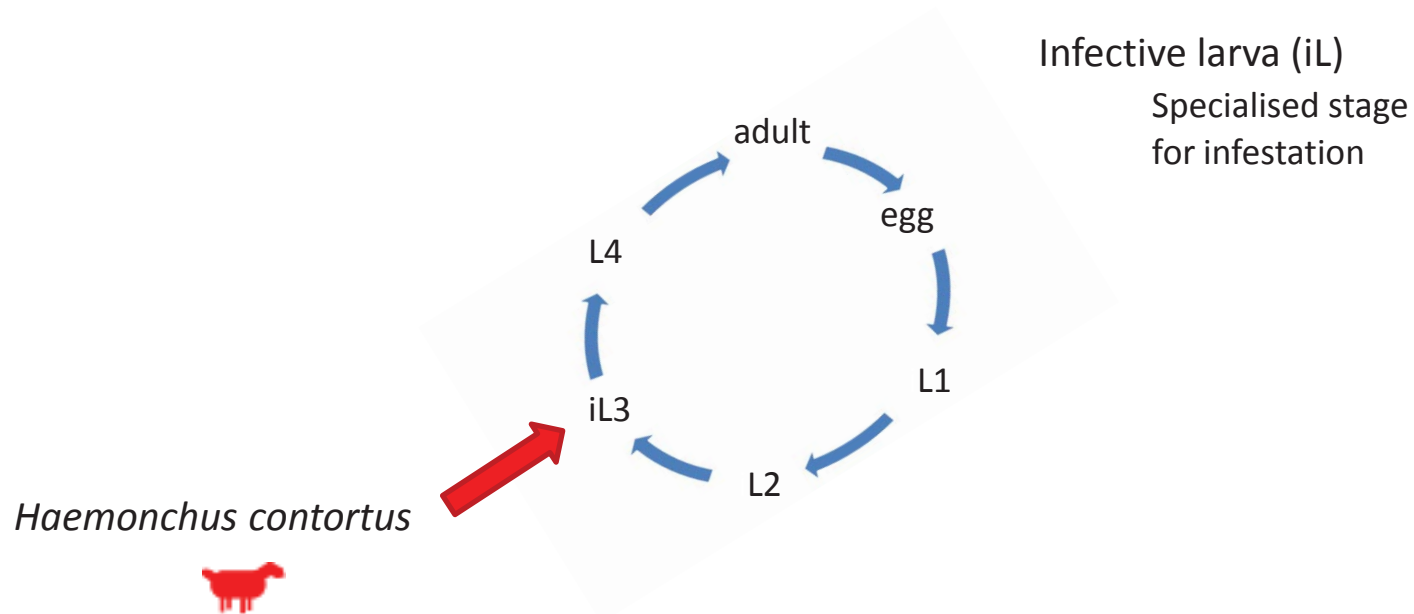




QUESTION: Evolution of signalling pathways

↳ The dauer signalling pathways

Parasitic nematodes' life cycle





QUESTION: Evolution of signalling pathways

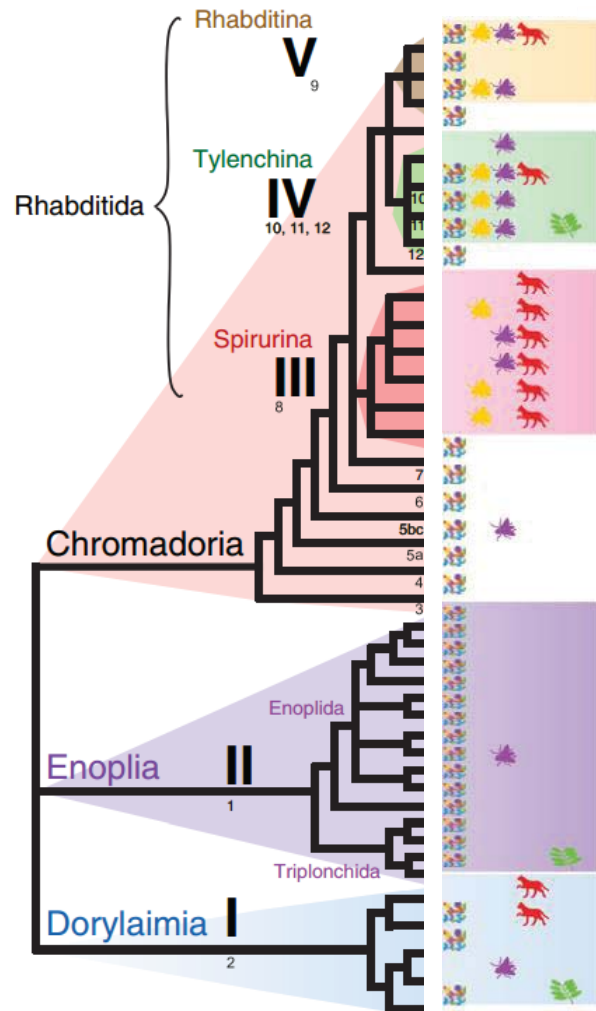
↳ The dauer signalling pathways

Parasitic nematodes' life cycle

Infective larva:

- Arrested developmental stage
 - Non-feeding
 - Morphological characteristics
 - ↓ metabolism

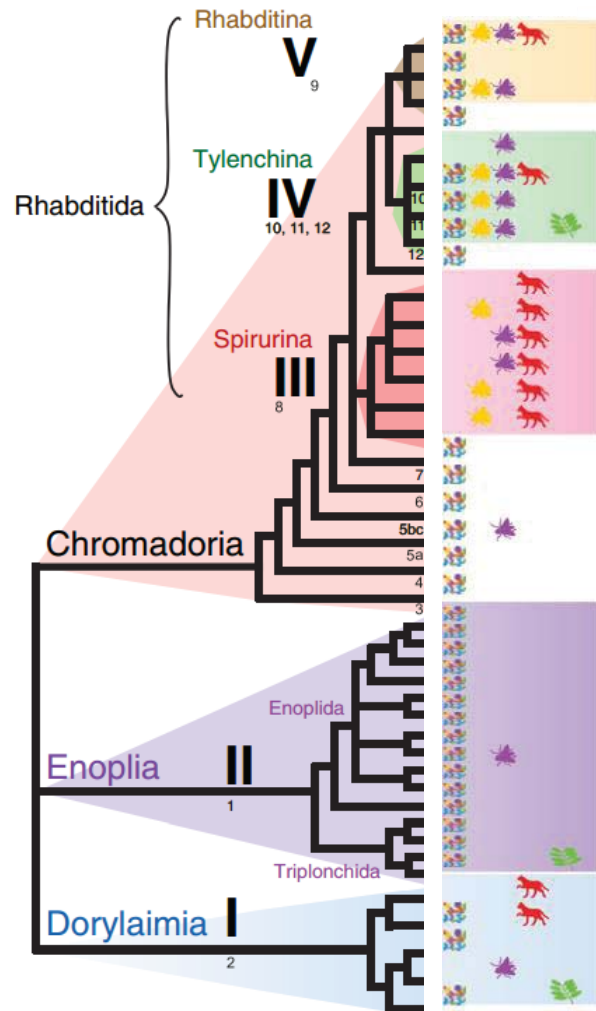
 - Resistant to environmental stresses
-



⊙ Dauer hypothesis

Pre-adaptation to parasitism

⇒ Multiple independent transitions



⇒ Multiple independent transitions

⊙ Dauer hypothesis

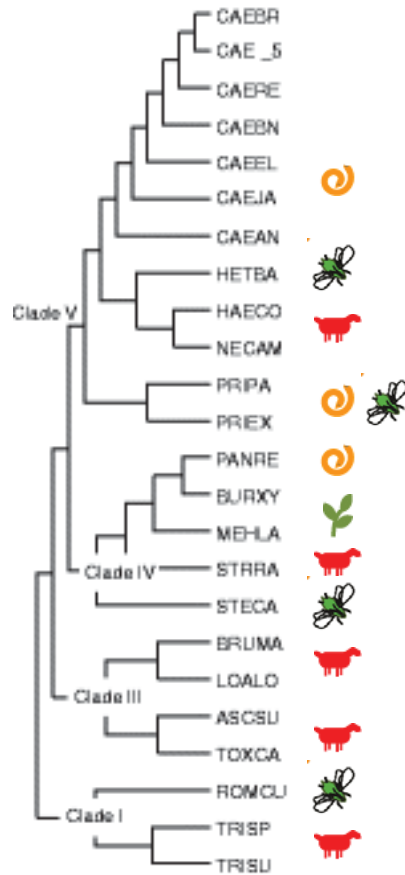
Pre-adaptation to parasitism

⊙ *Existence of common genetic pathways that would likely control the dauer transition across the phylum?*

⇒ Gene candidate approach

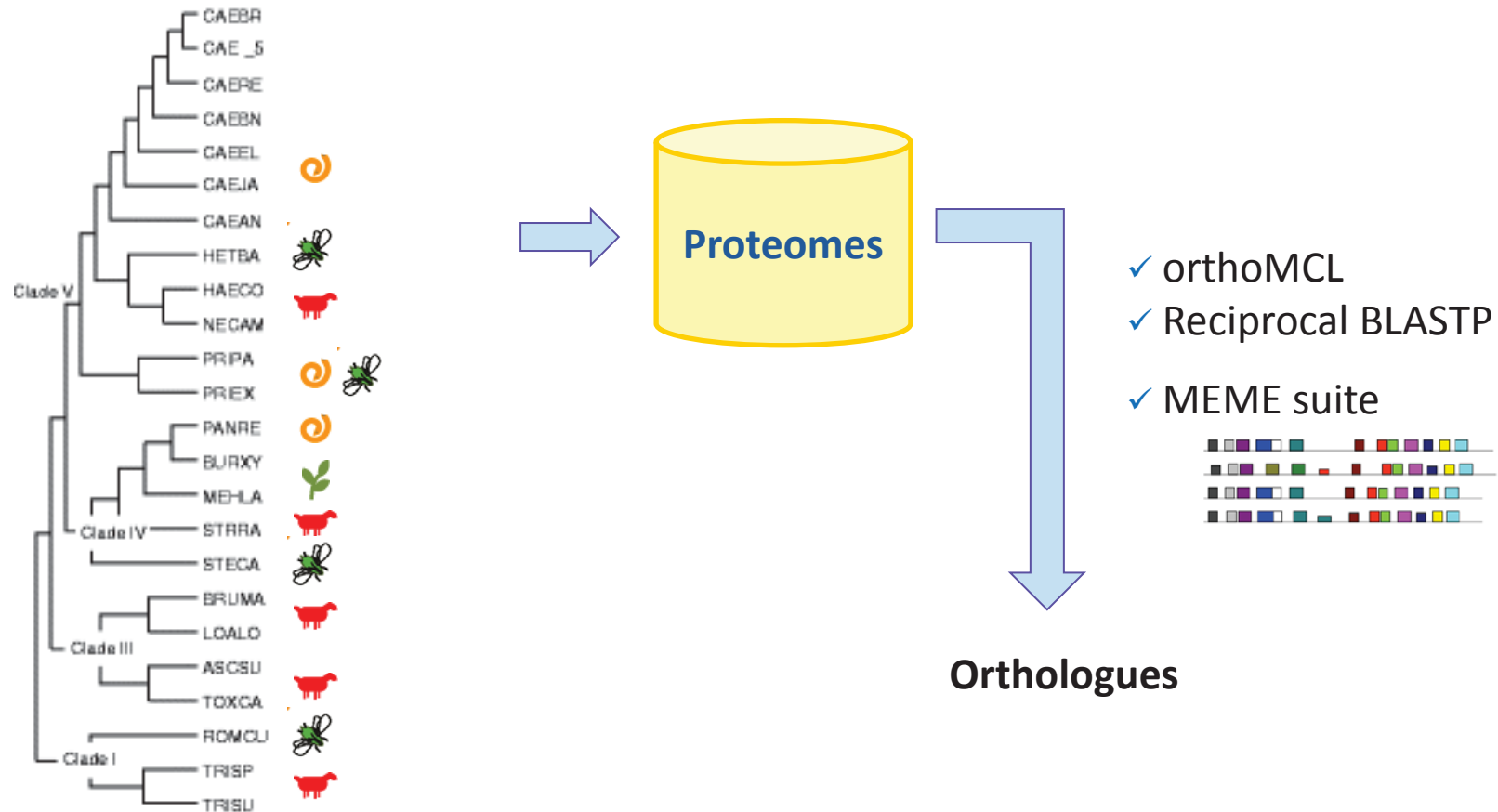


- Bioinformatic search of orthologues
 - 47 genes involved in the dauer transition
 - 24 species



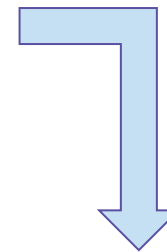
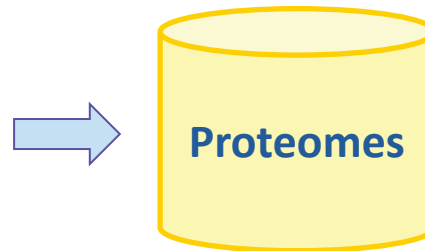
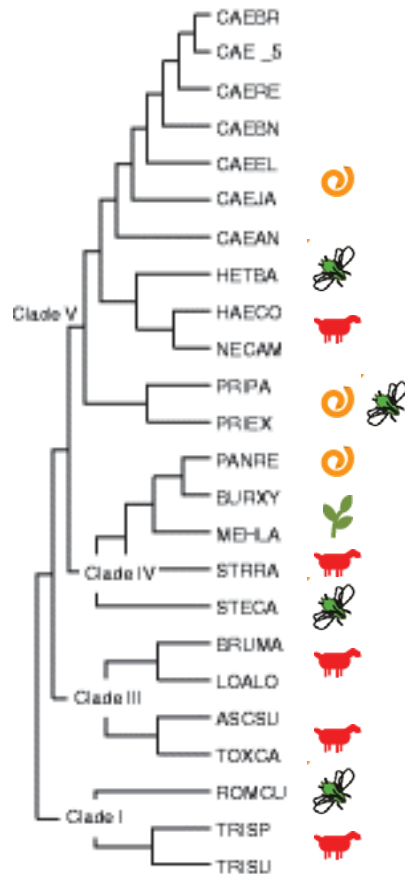


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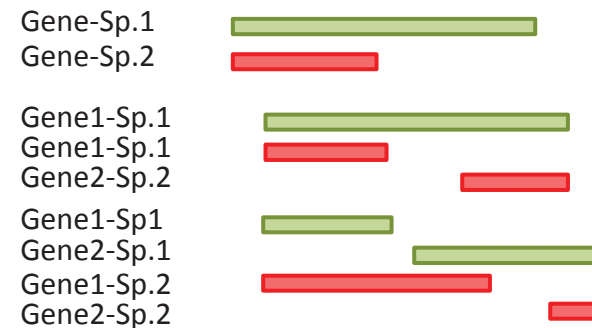
- Bioinformatic search of orthologues
 - 47 genes involved in the dauer transition
 - 24 species



- ✓ orthoMCL
- ✓ Reciprocal BLASTP
- ✓ MEME suite

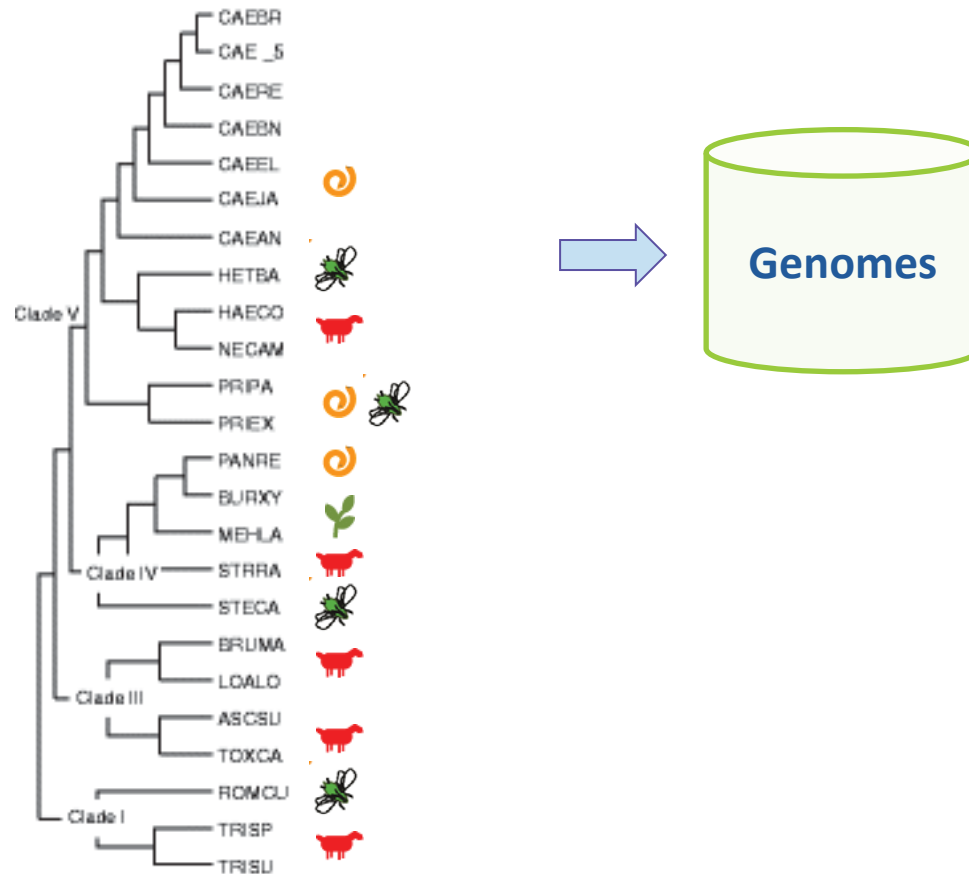
~~Orthologues~~

Gene models



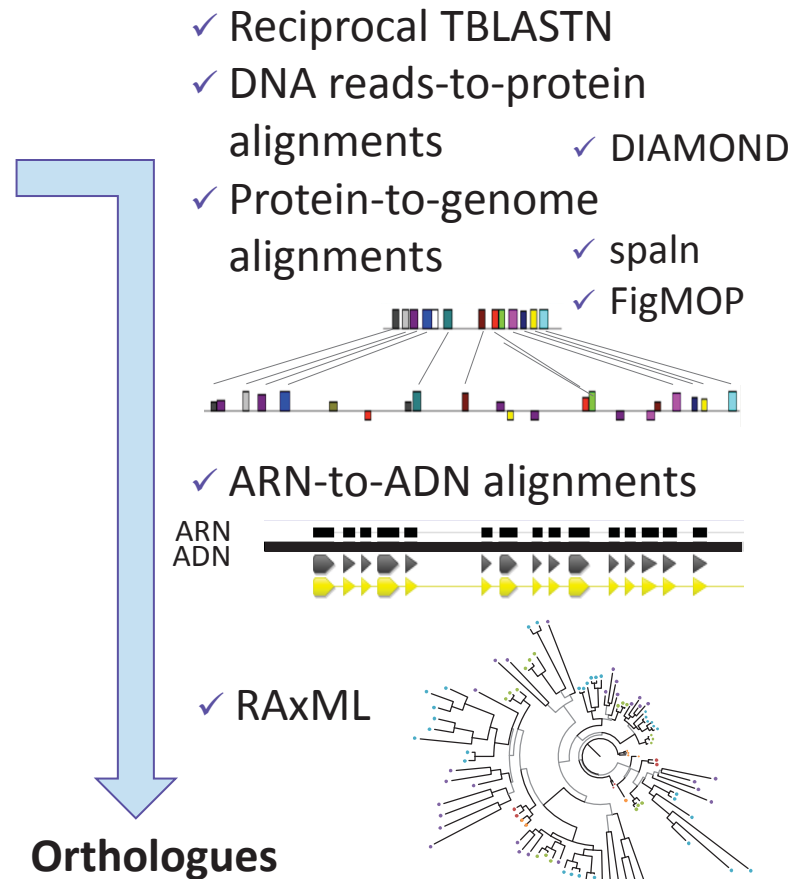
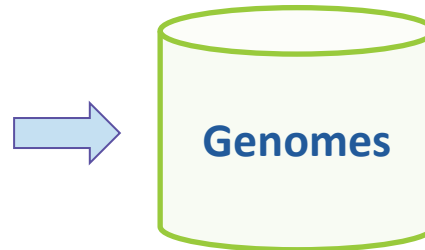
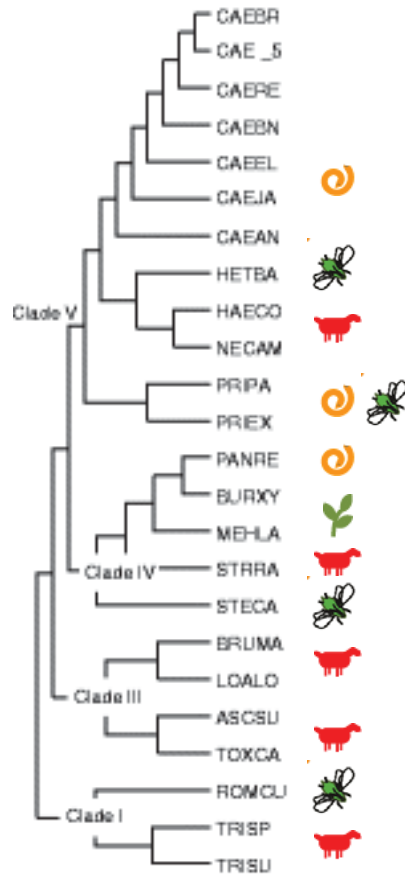


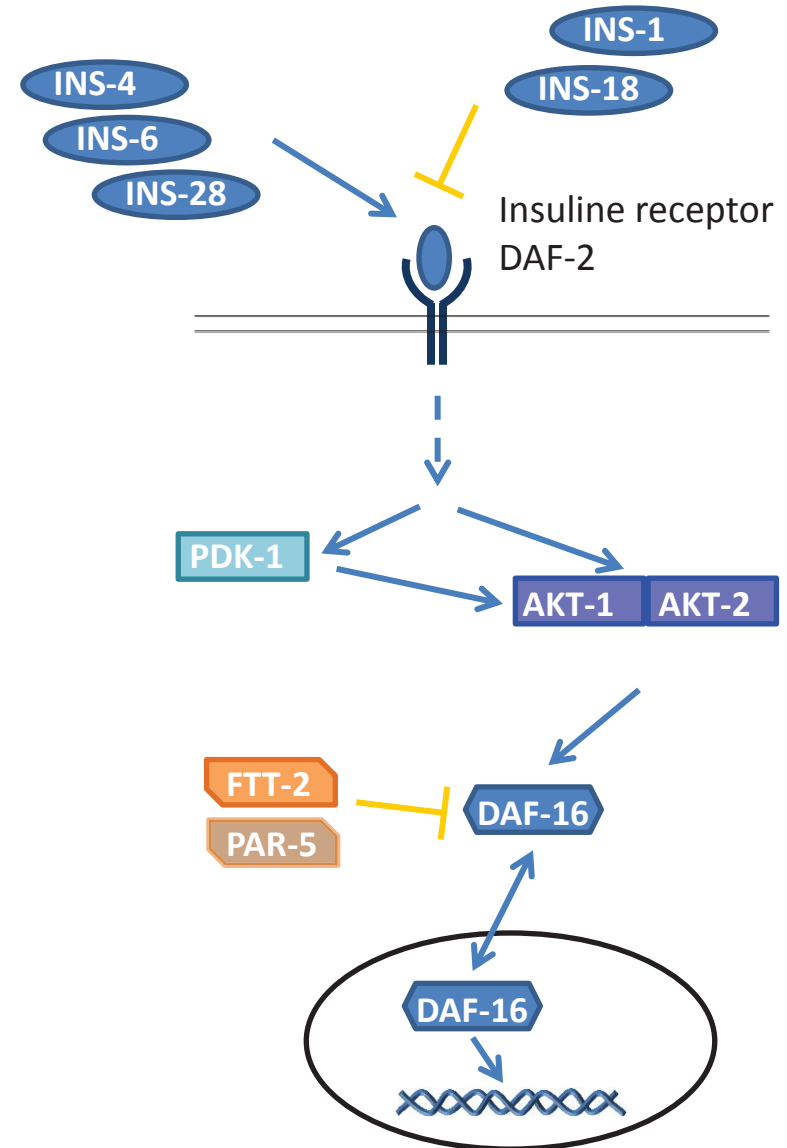
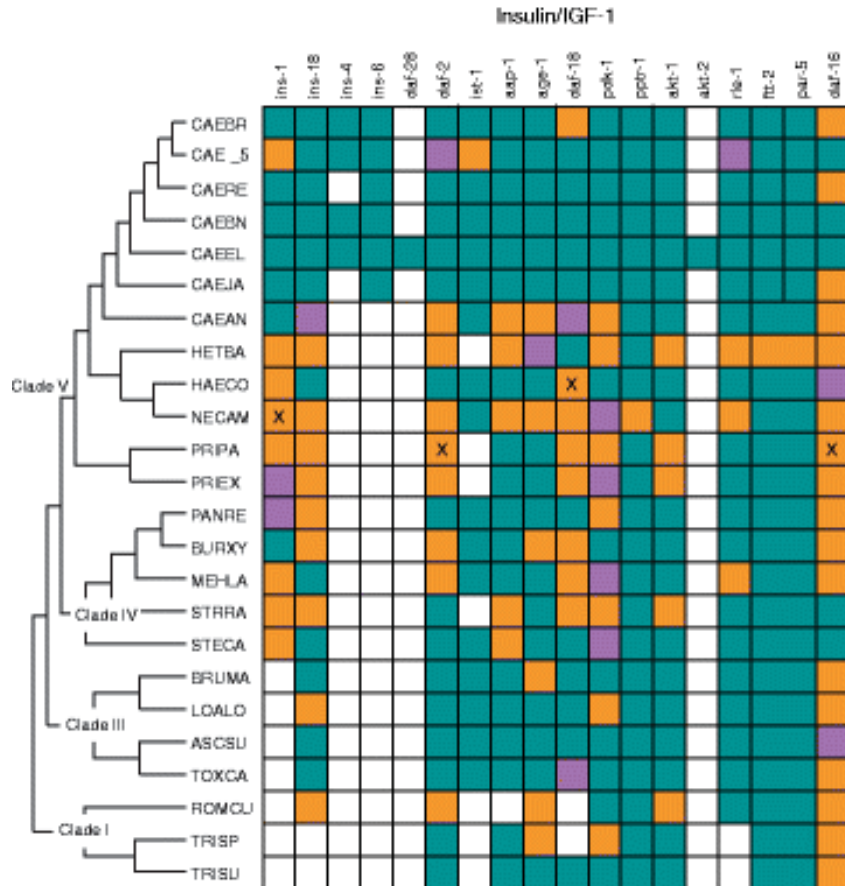
- Bioinformatic search of orthologues
 - 47 genes involved in the dauer transition
 - 24 species





- Bioinformatic search of orthologues
 - 47 genes involved in the dauer transition
 - 24 species





Not found

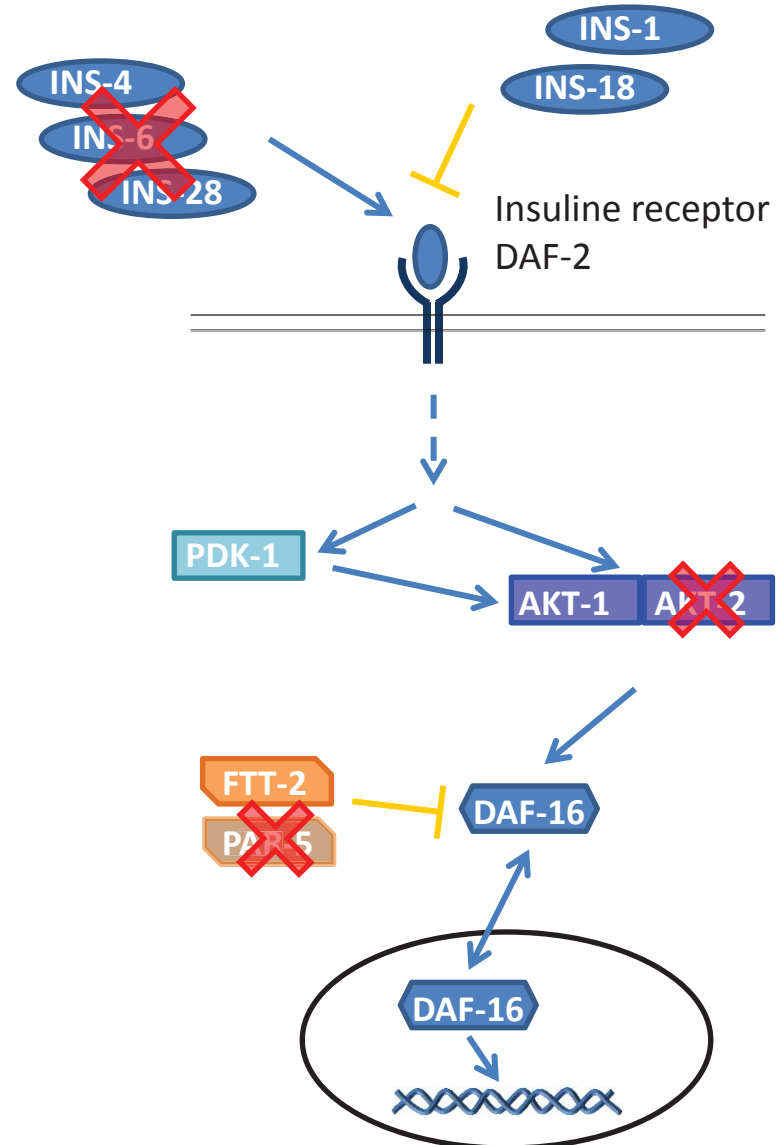
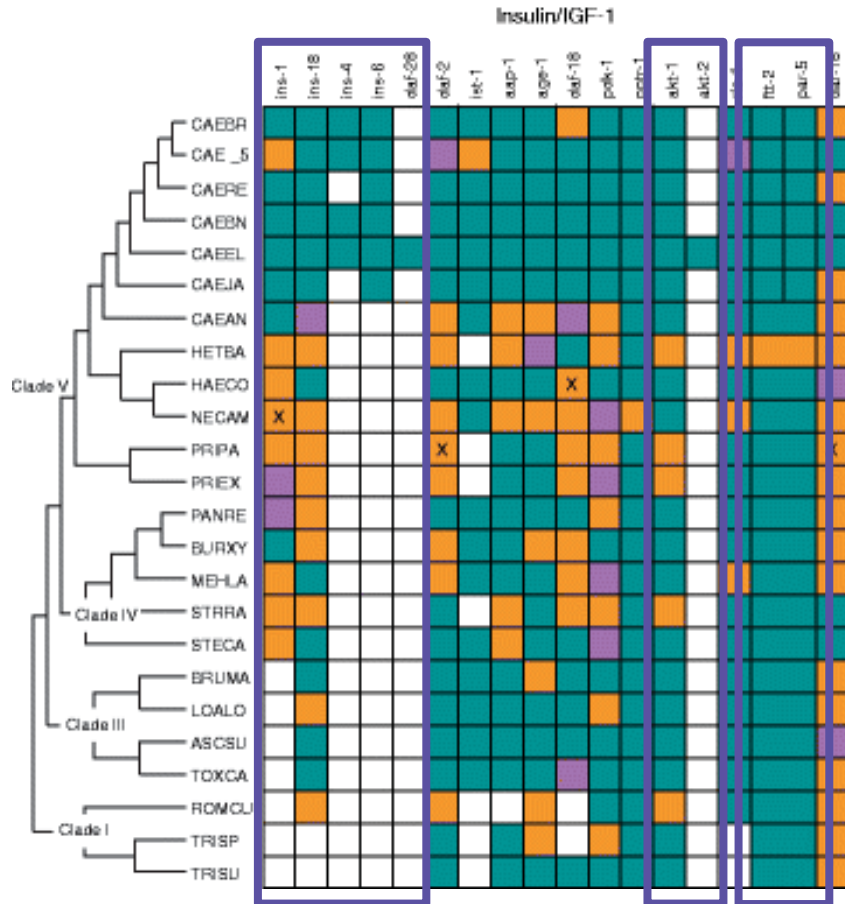
Reciprocal BLAST

Other search strategies
Minor changes

Major changes



Non-Caenorhabditis



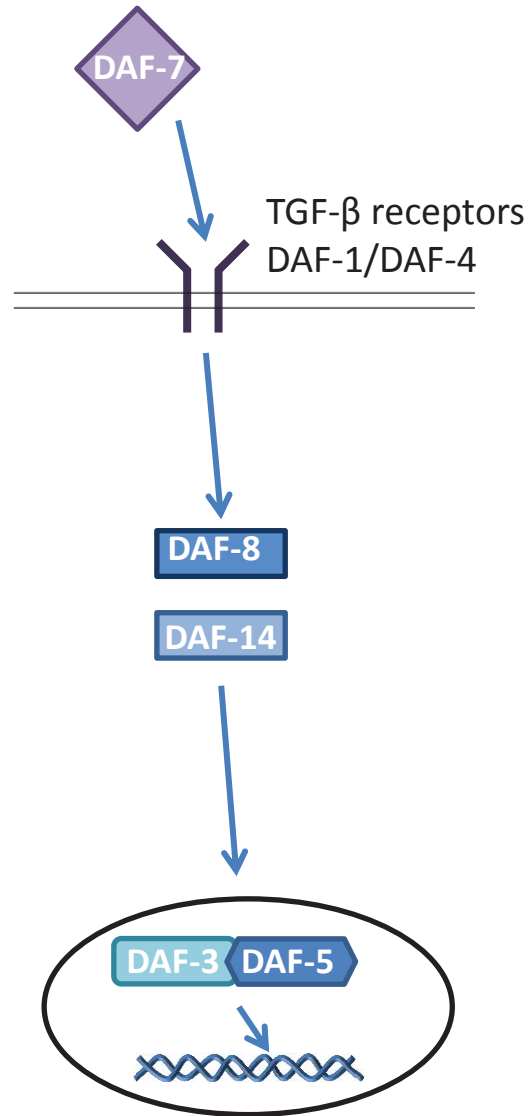
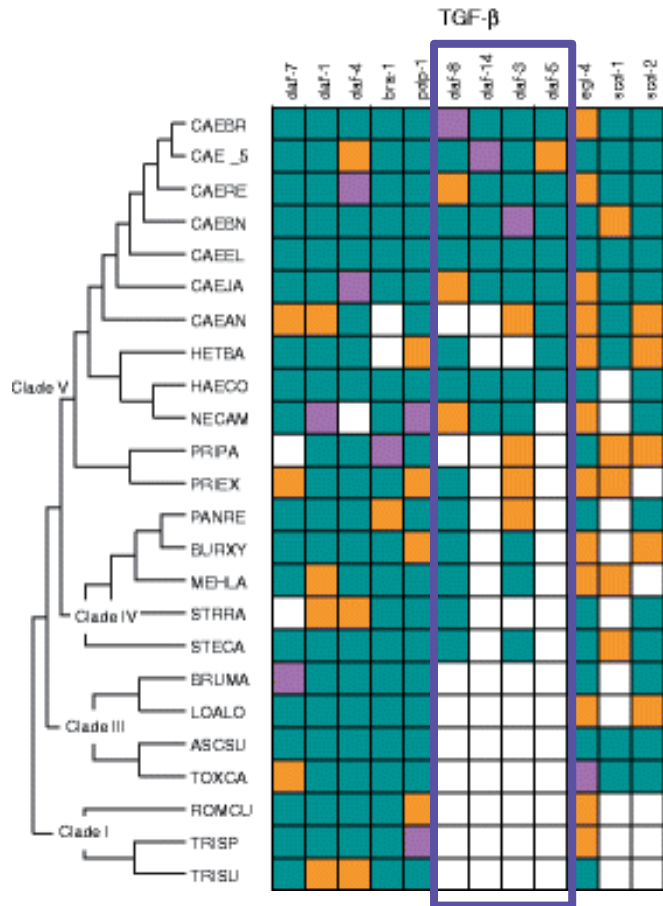
Other search strategies

□ Not found

■ Reciprocal BLAST

■ Minor changes

■ Major changes



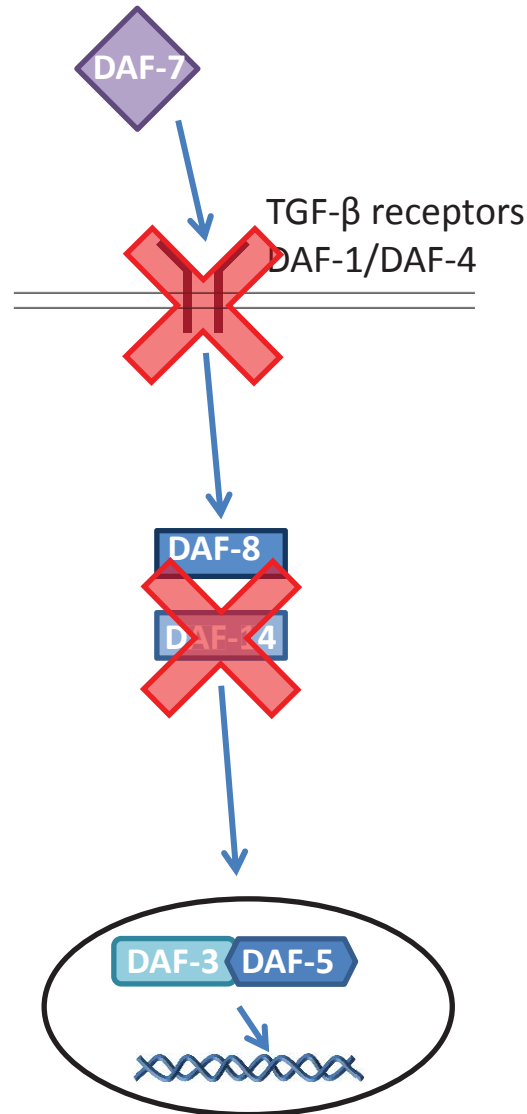
Other search strategies

Not found

Reciprocal BLAST

Minor changes

Major changes



Phenotypes:

Dauer development
Egg-laying

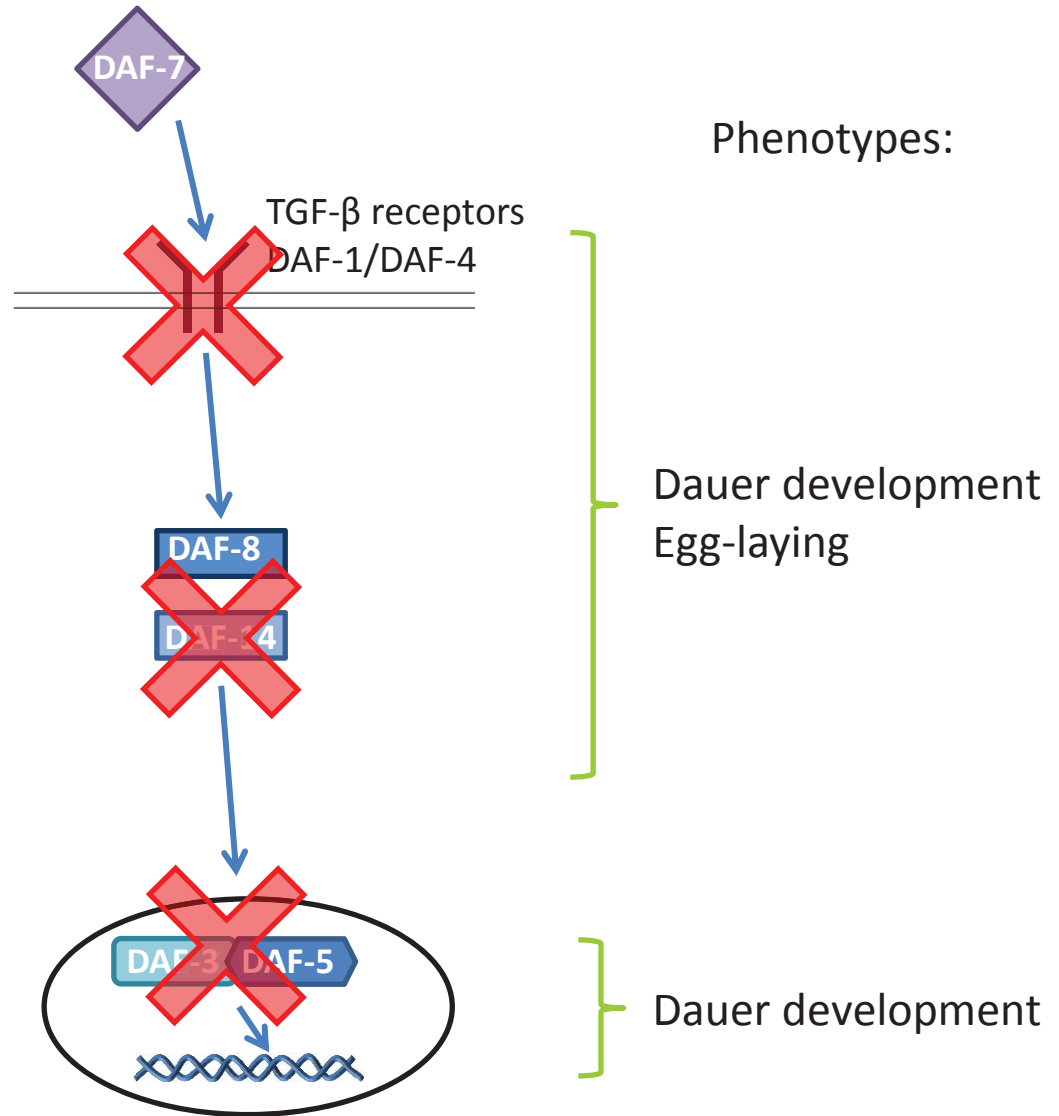
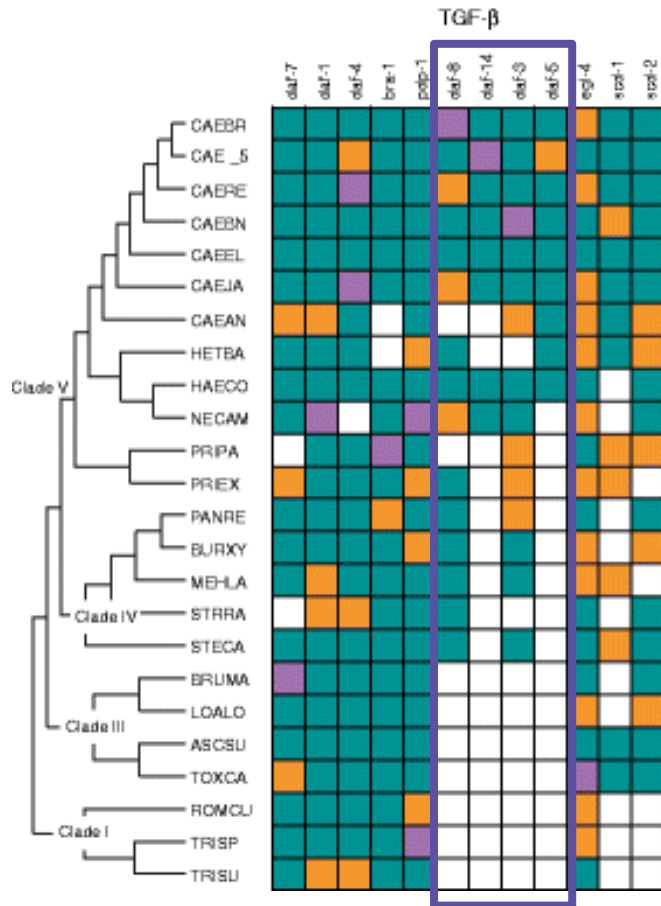
Other search strategies

Not found

Reciprocal BLAST

Minor changes

Major changes



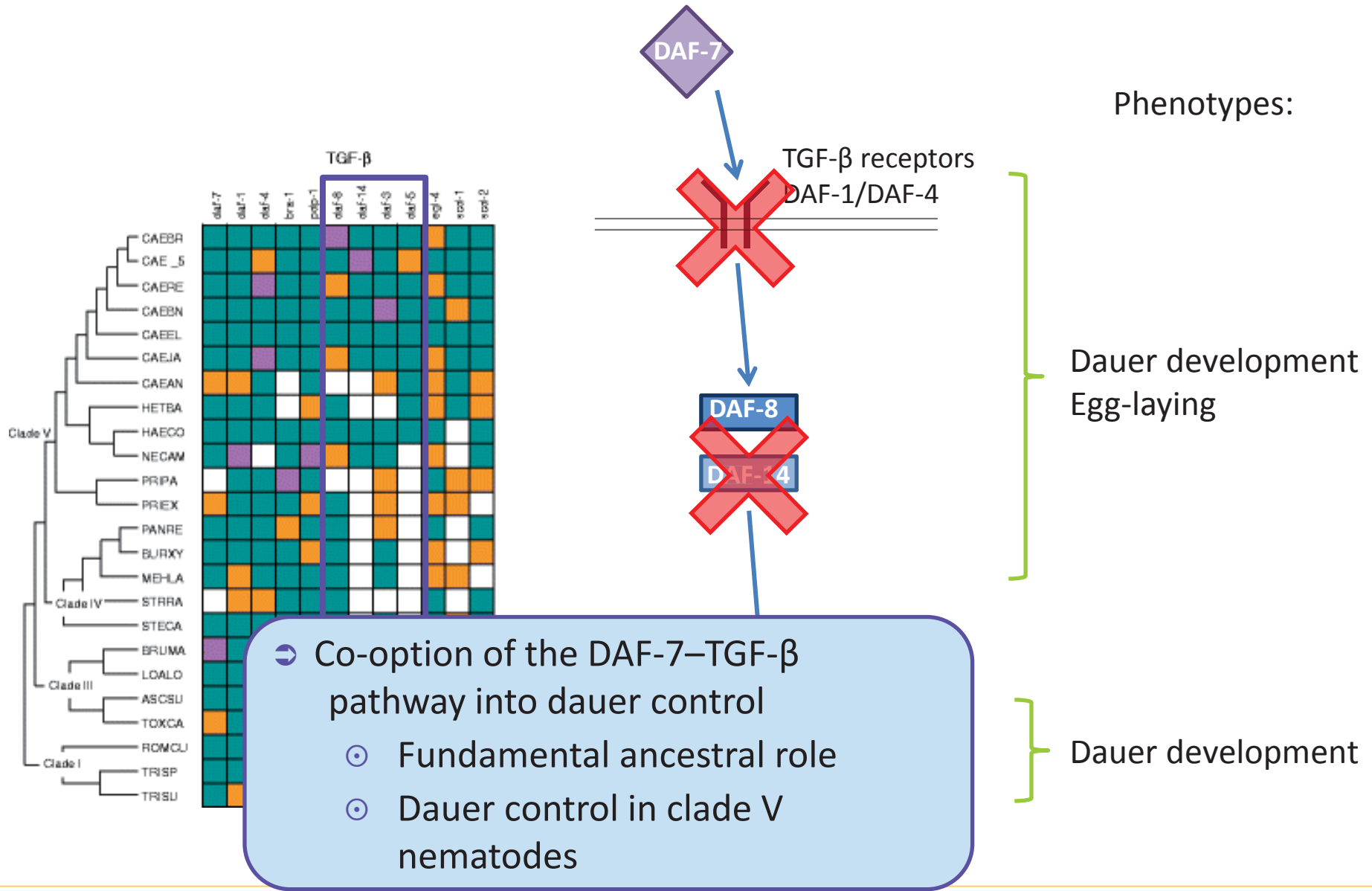
Not found

Reciprocal BLAST

Minor changes

Major changes

Other search strategies



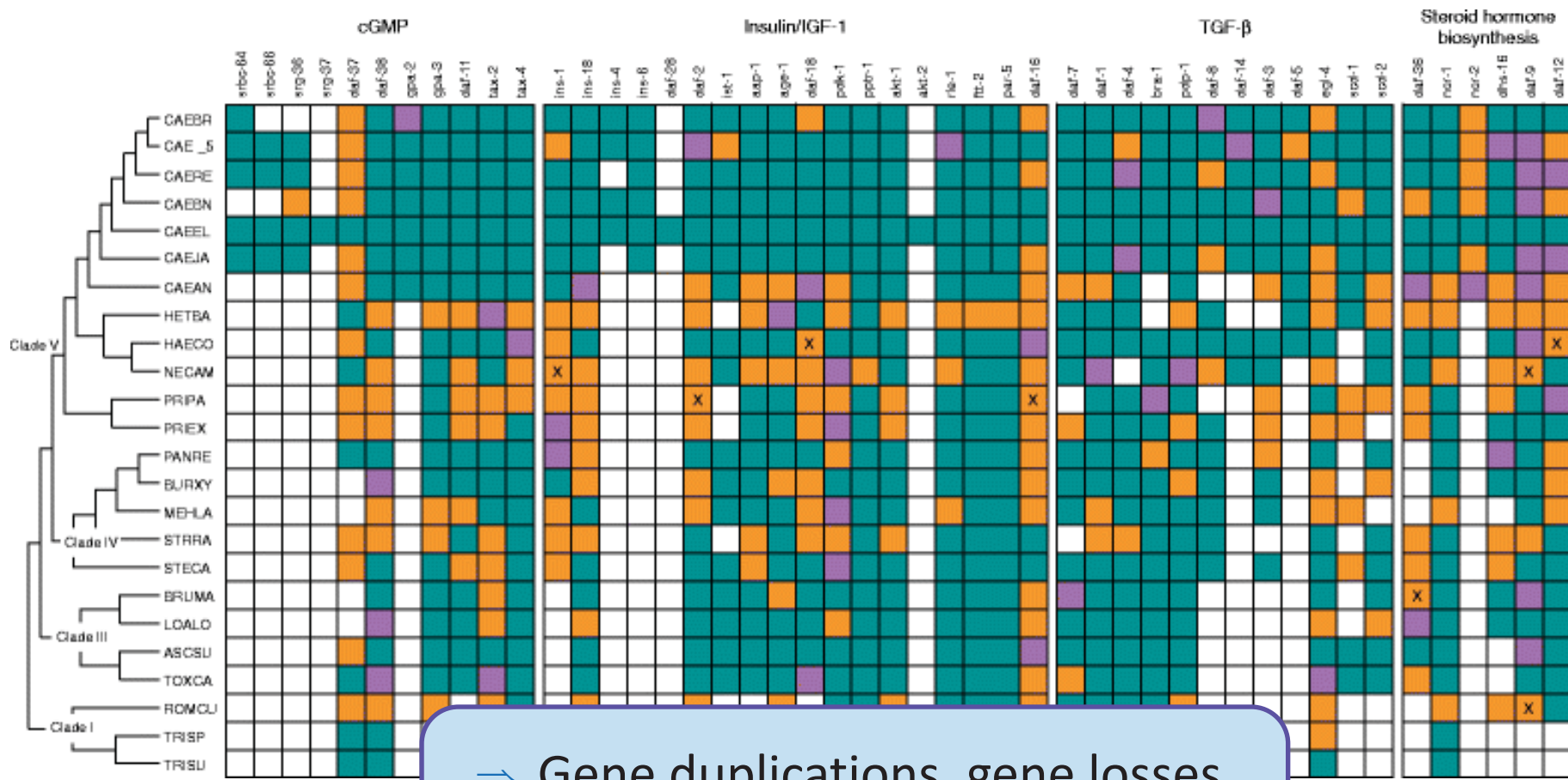
Not found

Reciprocal BLAST

Minor changes

Major changes

Other search strategies



⇒ Gene duplications, gene losses & pathway co-option

Other search strategies

Not found
 Reciprocal BLAST
 Minor changes
 Major changes

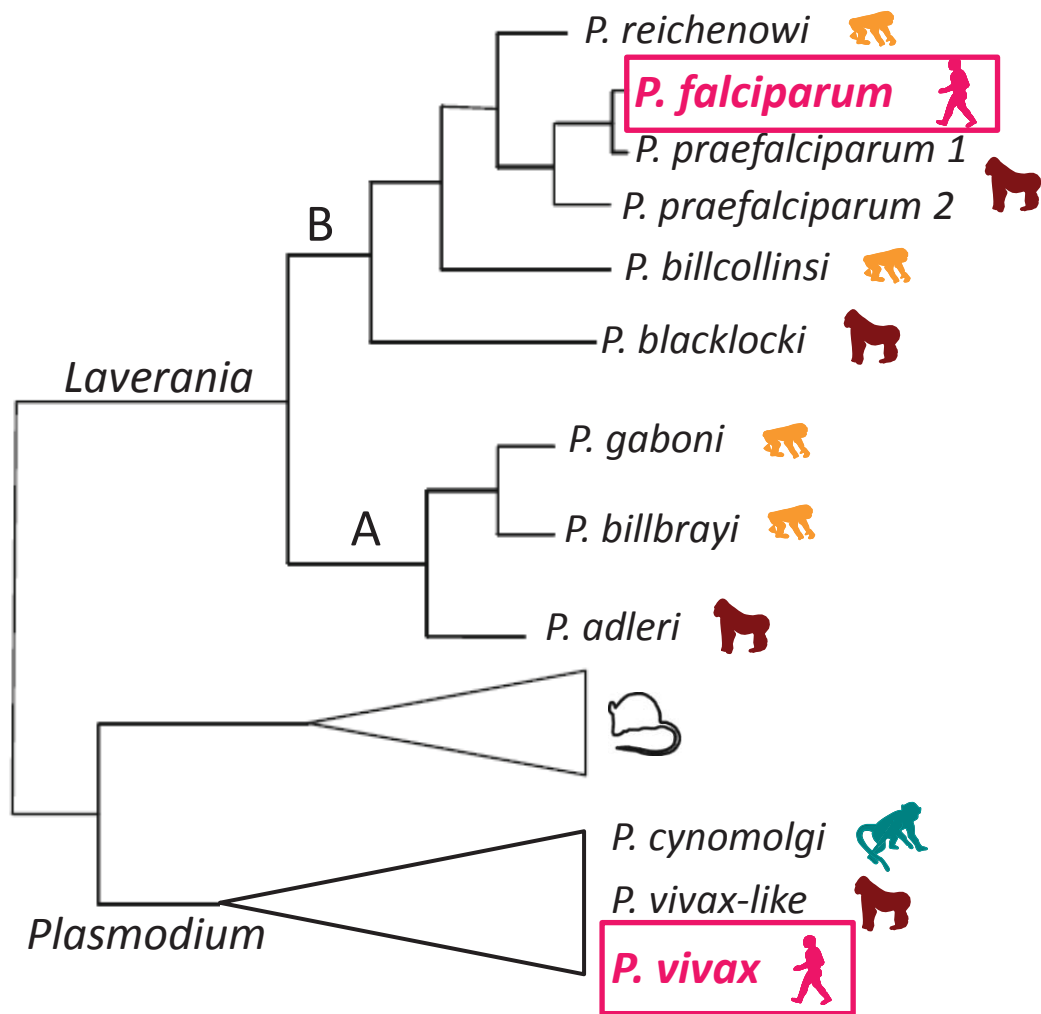
HOST ADAPTATION IN *PLASMODIUM* SPECIES

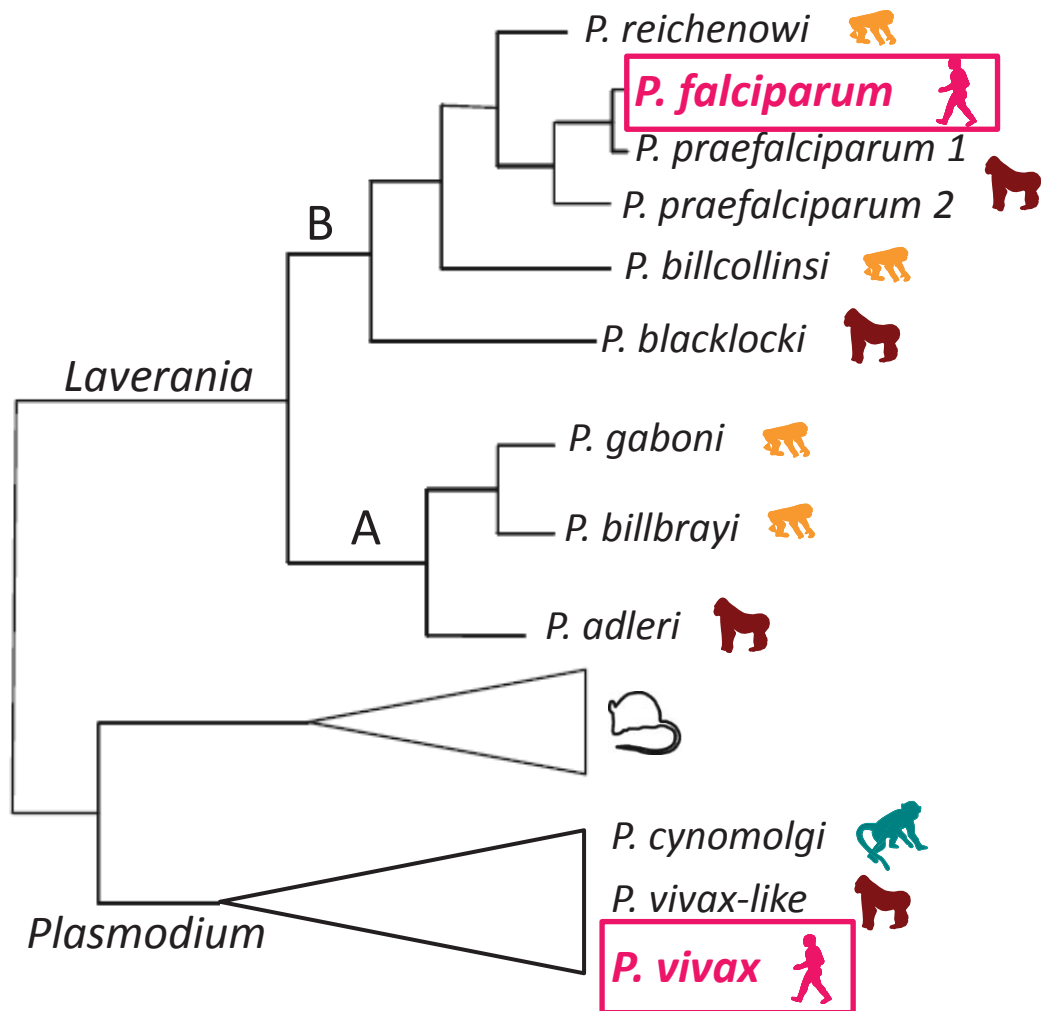




QUESTION: Human pathogens emergence

↳ *Plasmodium falciparum* & *Plasmodium vivax*,
malaria causing pathogens





⇒ Origins

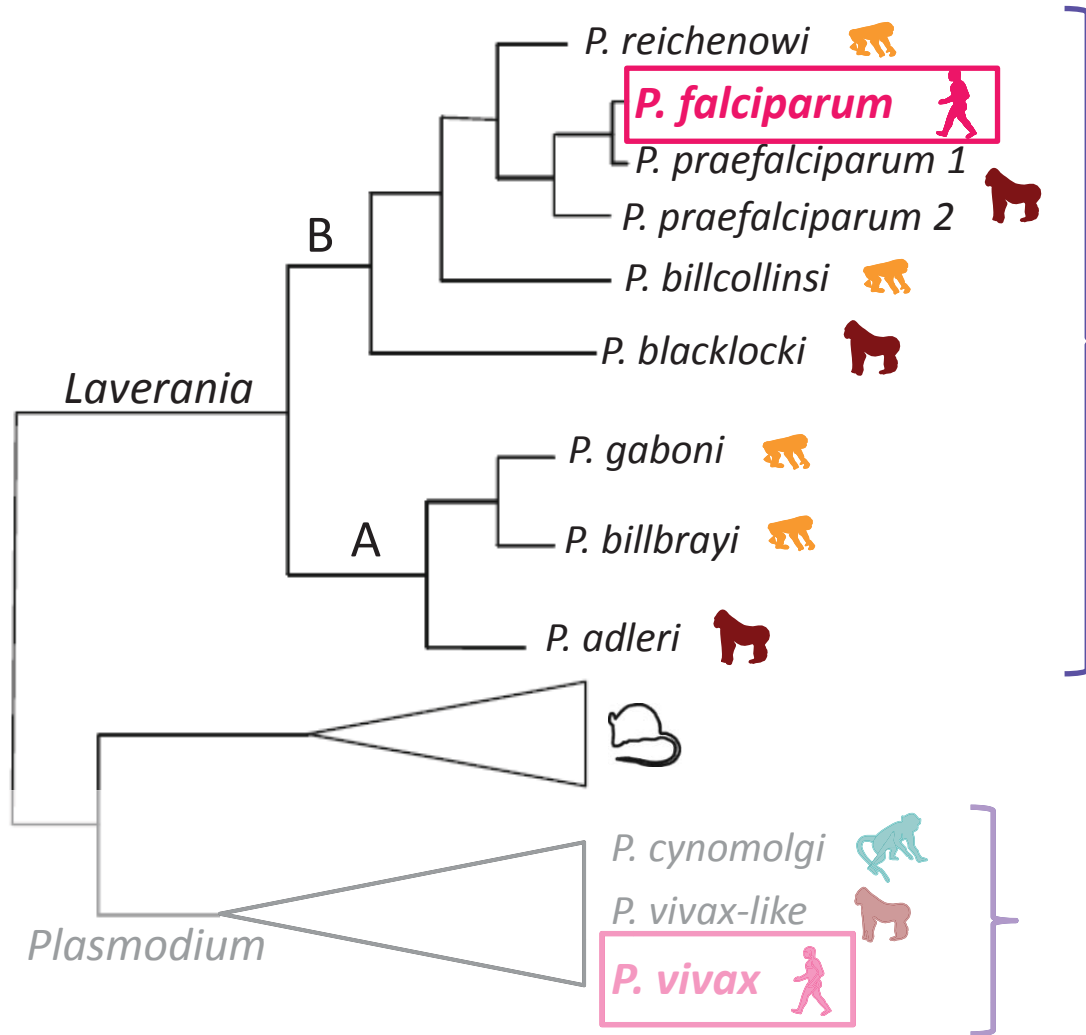
⇒ Host adaptation

⇒ Comparative genomics





○ Comparative genomics & bioinformatics



- i. Gene transfer, convergent evolution
- ii. Selection
- iii. Multi-genic families

Diversity & genetic differentiation (SNPs)



◉ *Laverania* genomics

Technical challenges:

- Low parasitemia
- Co-infections
- Host contamination
- AT rich



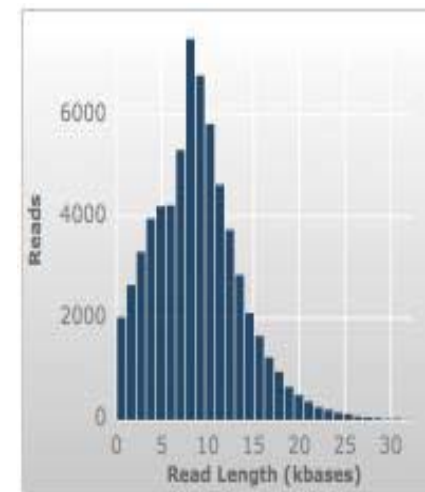
◉ *Laverania* genomics

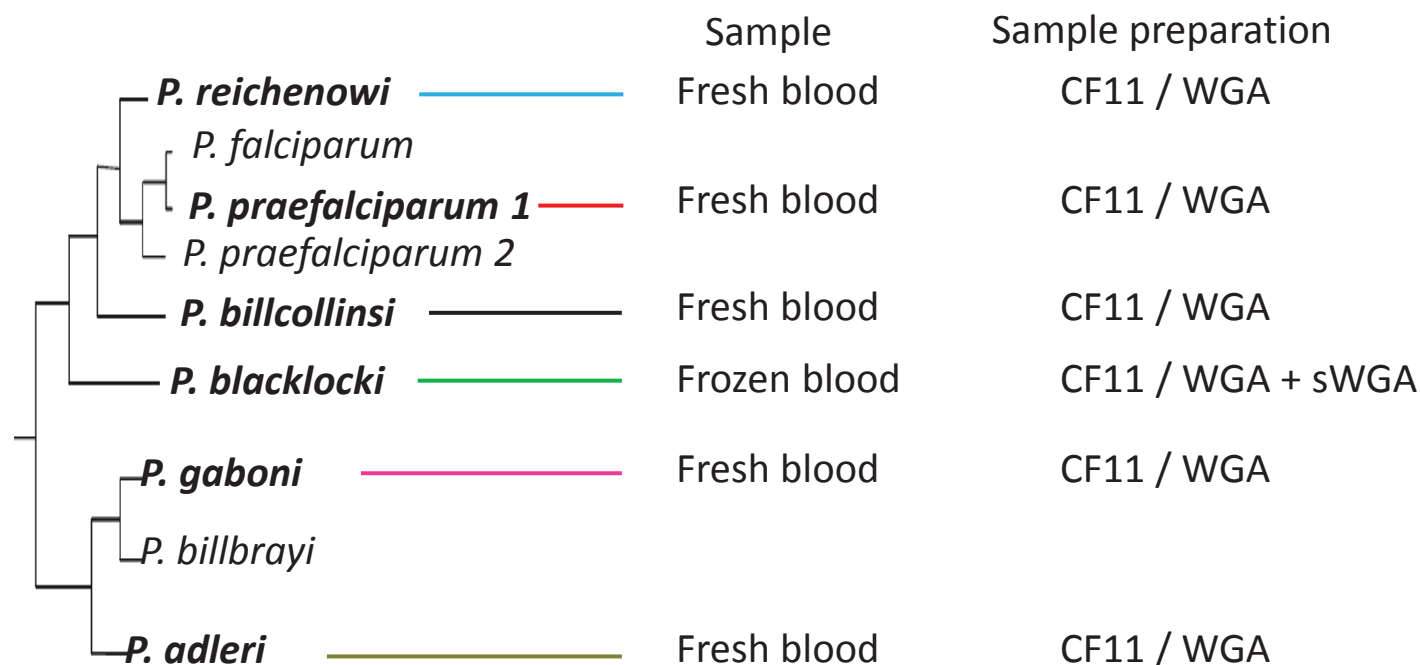
Technical challenges:

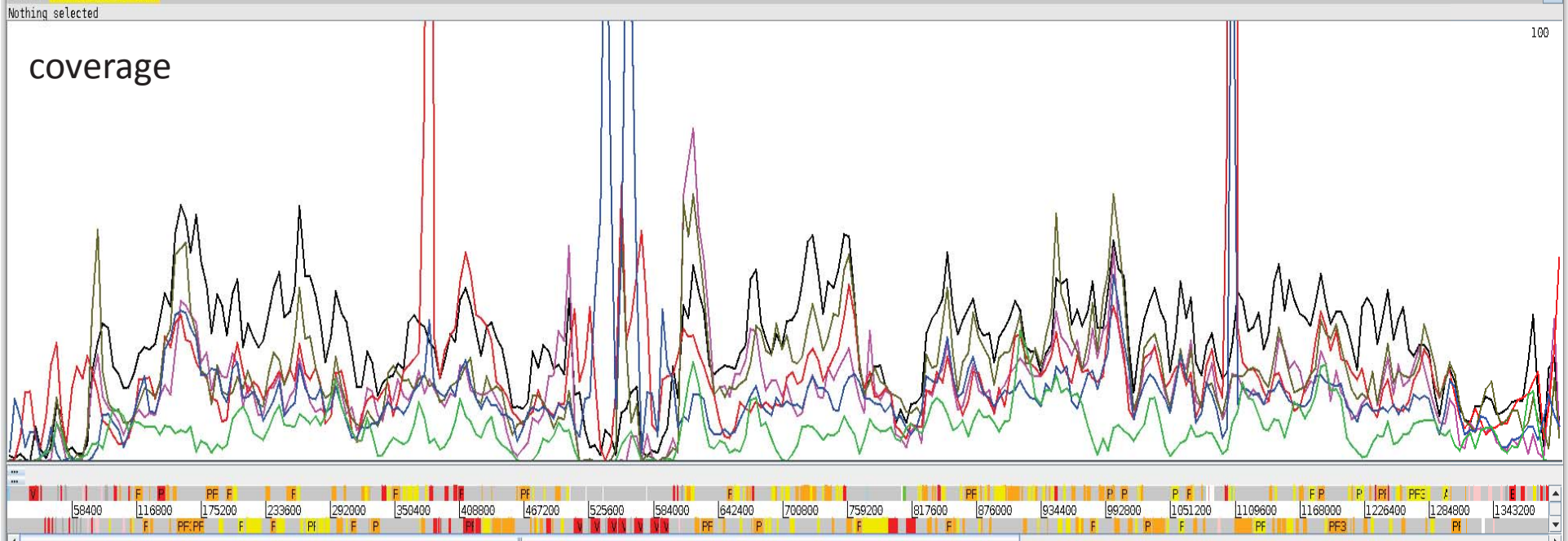
- Low parasitemia
- Co-infections
- Host contamination
- AT rich

⇒ CF11 cellulose columns,
whole genome amplification (WGA)
& PacBio

long reads
(mean = 10kb)







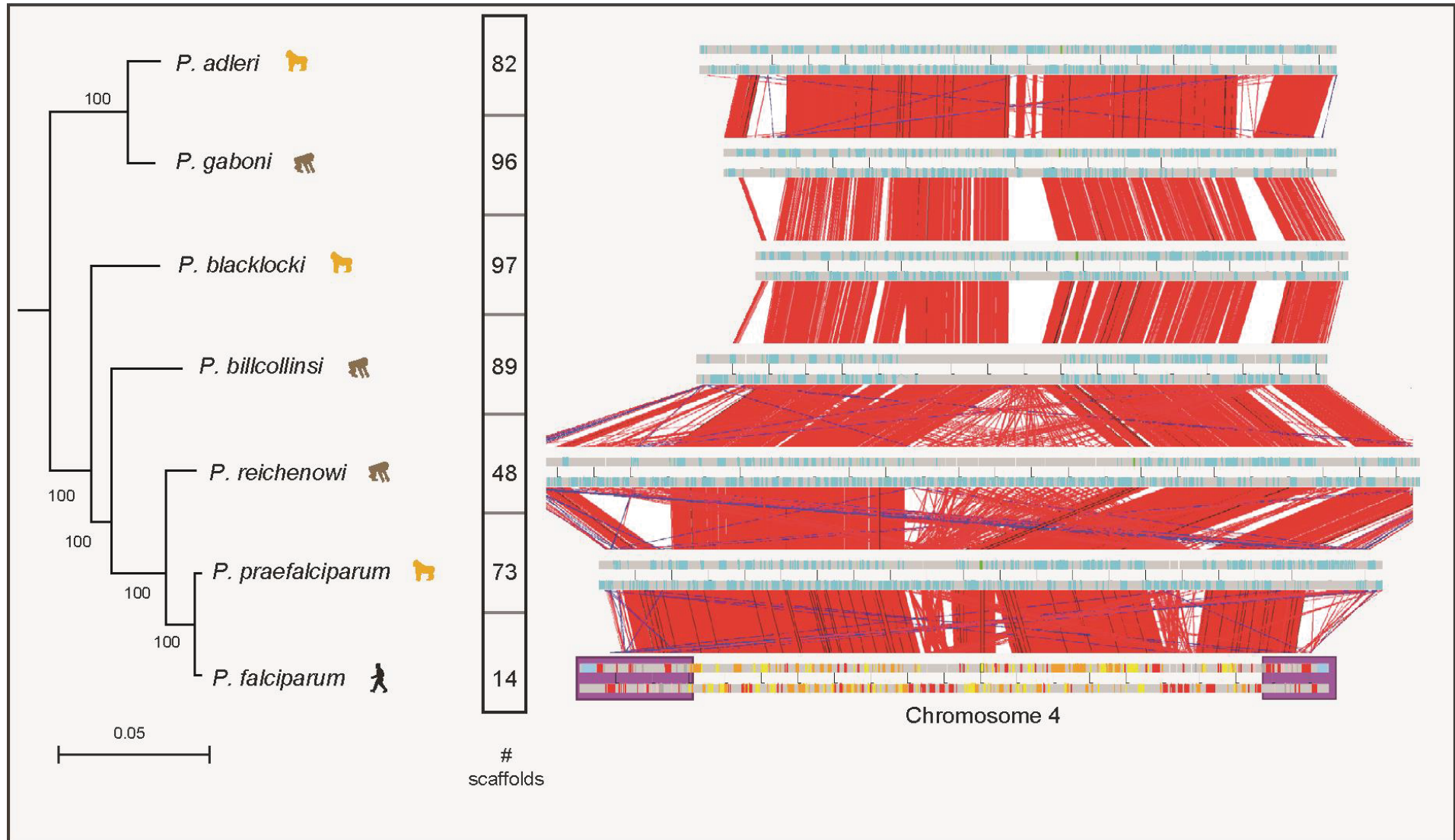
	Sample	Sample preparation	# genes
<i>P. reichenowi</i>	Fresh blood	CF11 / WGA	5941
			<i>P. falciparum</i>
<i>P. praefalciparum</i> 1	Fresh blood	CF11 / WGA	6476
			<i>P. praefalciparum</i> 2
<i>P. billcollinsi</i>	Fresh blood	CF11 / WGA	5637
<i>P. blacklocki</i>	Frozen blood	CF11 / WGA + sWGA	5346
<i>P. gaboni</i>	Fresh blood	CF11 / WGA	5421
			<i>P. billbrayi</i>
<i>P. adleri</i>	Fresh blood	CF11 / WGA	5515

**4269
one-to-one
orthologues**



Species tree

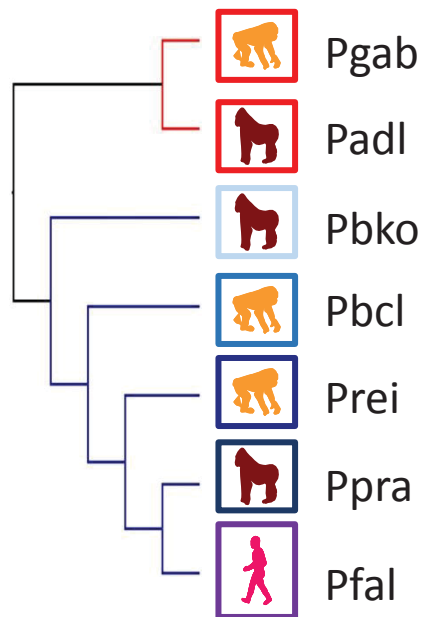
Reference genome assemblies





○ Gene transfer & convergent evolution

Species tree
topology

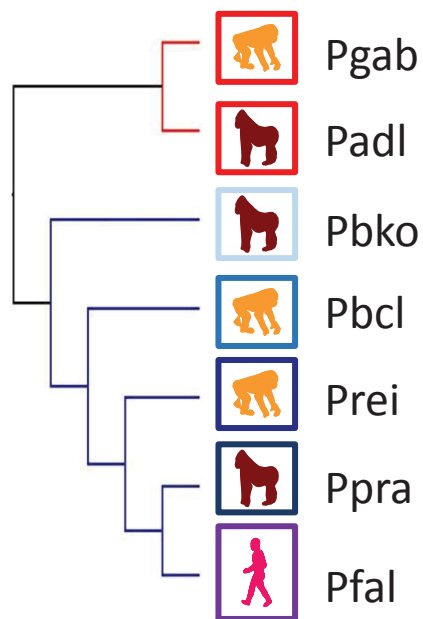


4269 CDS



○ Gene transfer & convergent evolution

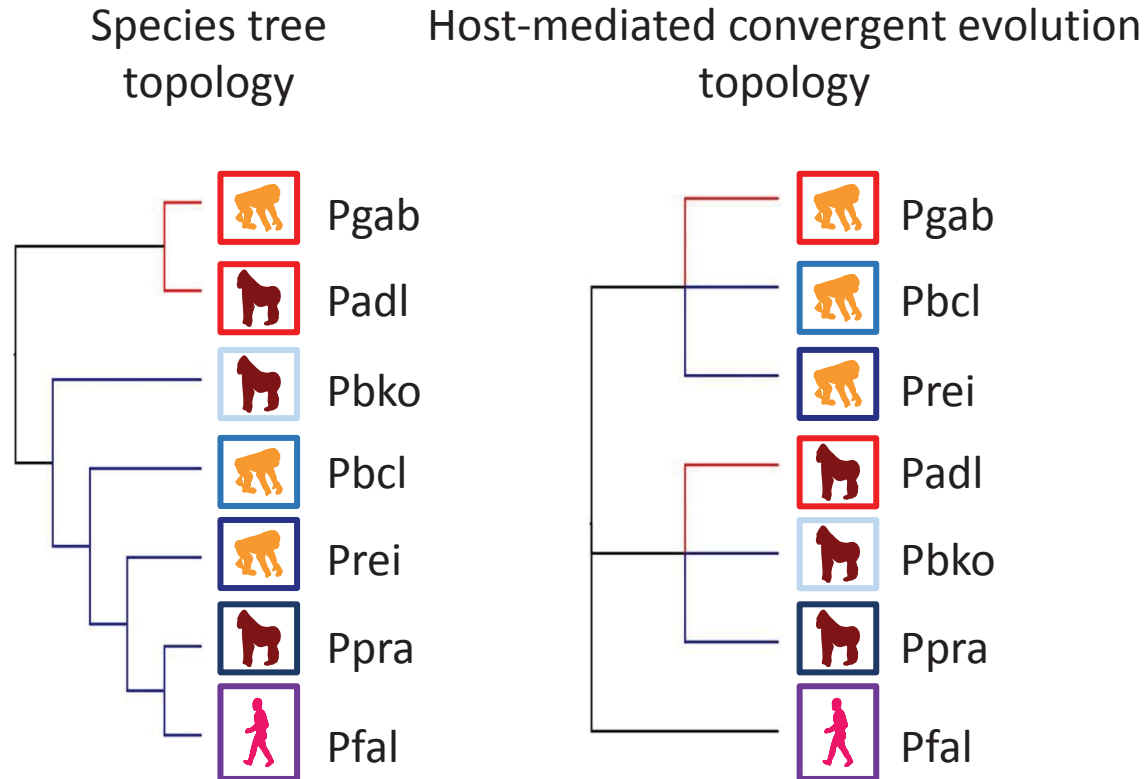
Species tree
topology



4269 CDS \Rightarrow 4251 CDS



○ Gene transfer & convergent evolution

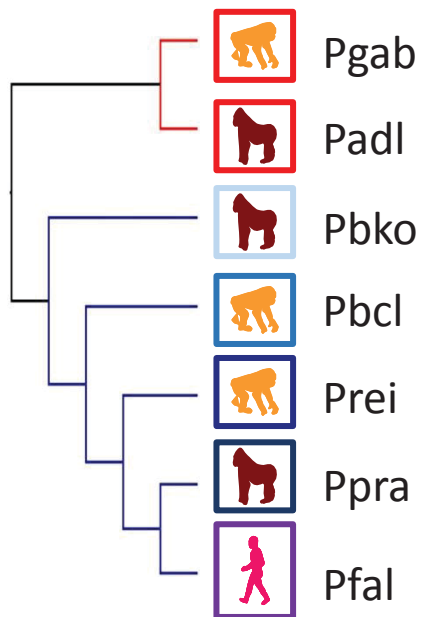


4269 CDS \Rightarrow 4251 CDS

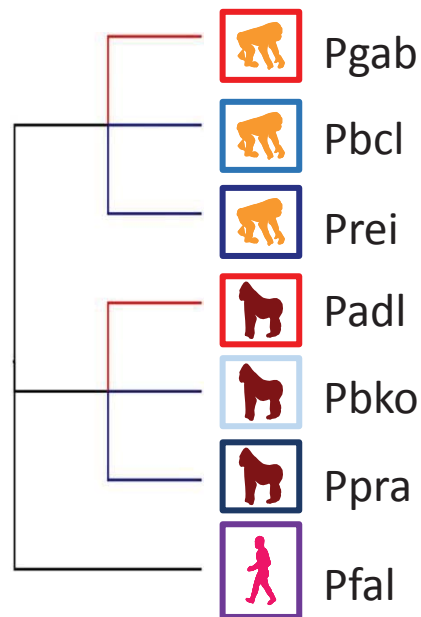


○ Gene transfer & convergent evolution

Species tree
topology



Host-mediated convergent evolution
topology



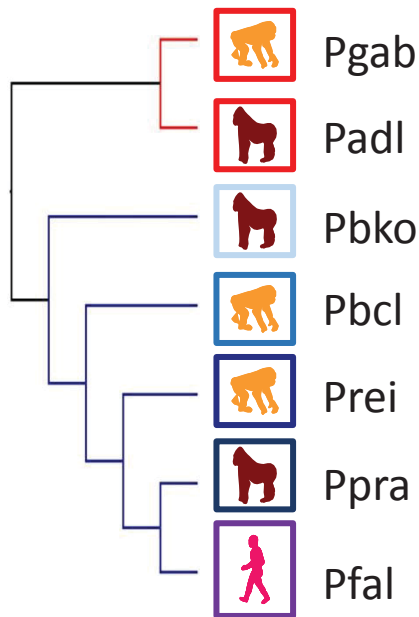
4269 CDS \Rightarrow 4251 CDS

\Rightarrow 0 CDS

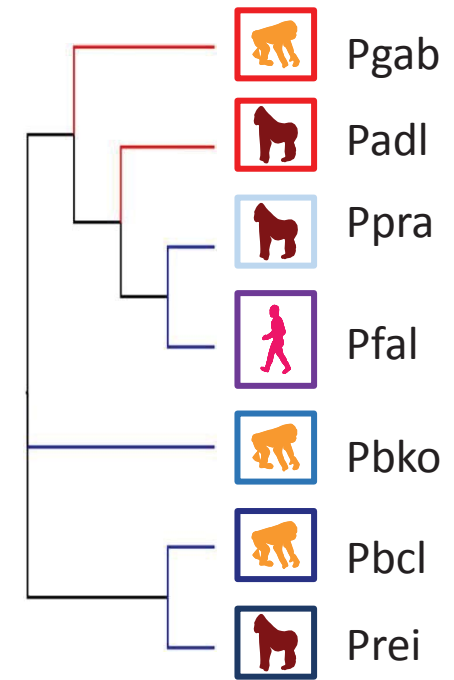
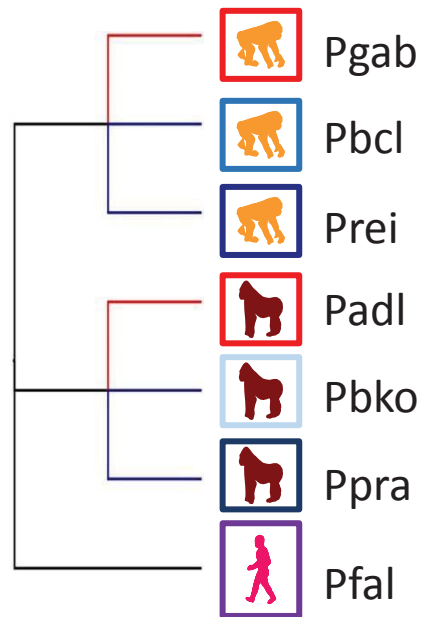


Gene transfer & convergent evolution

Species tree topology



Host-mediated convergent evolution topology



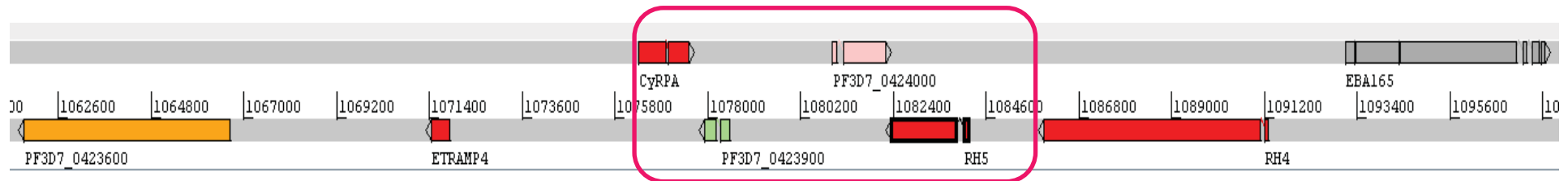
4269 CDS ⇒ 4251 CDS

⇒ 0 CDS

⇒ 4 CDS



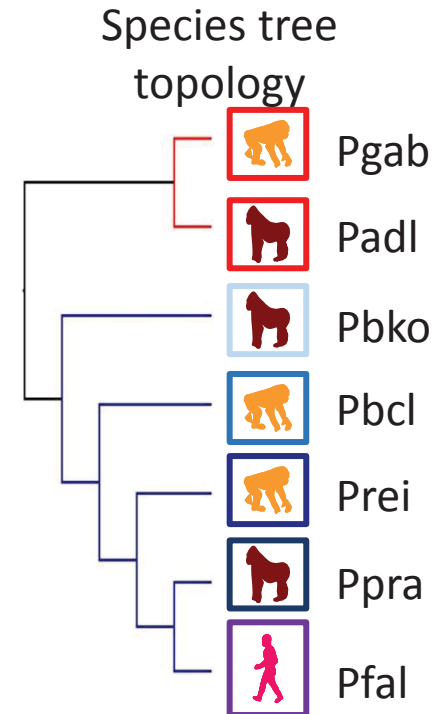
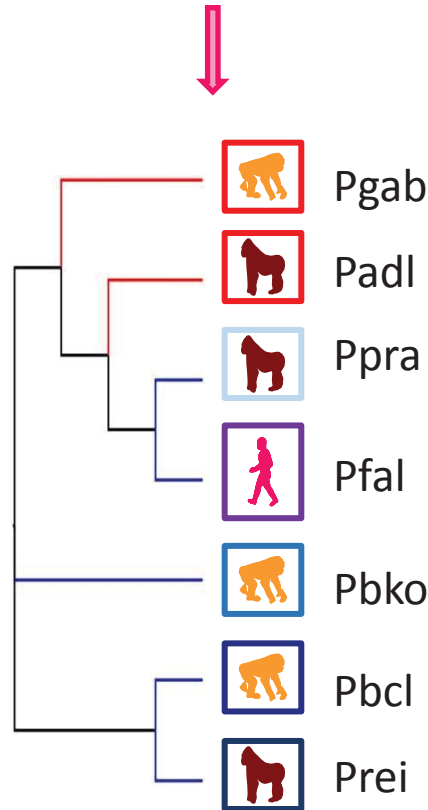
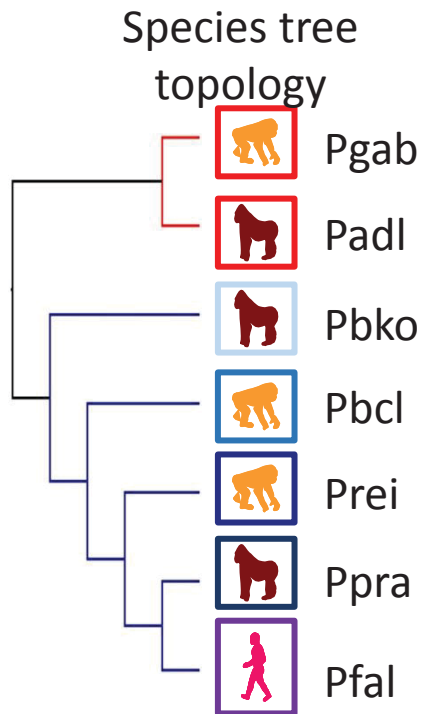
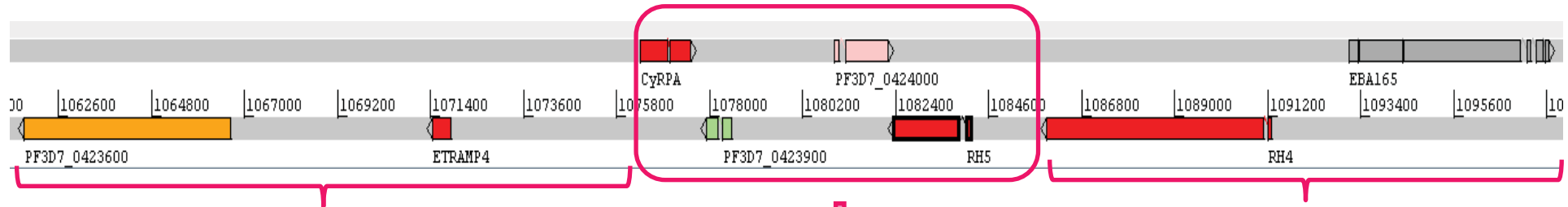
Gene transfer & convergent evolution

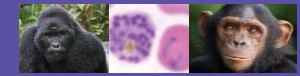




Gene transfer & convergent evolution

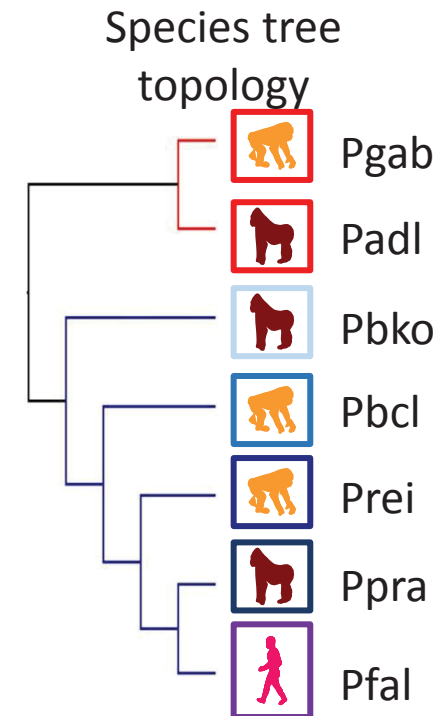
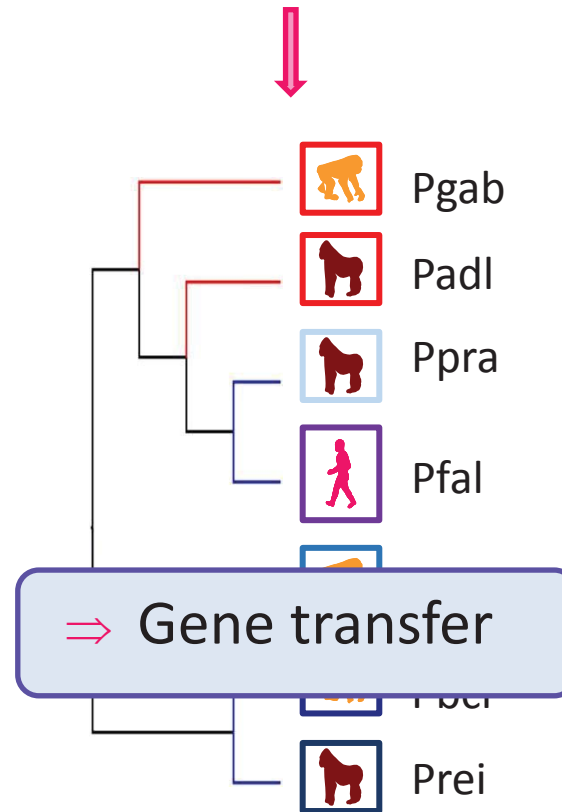
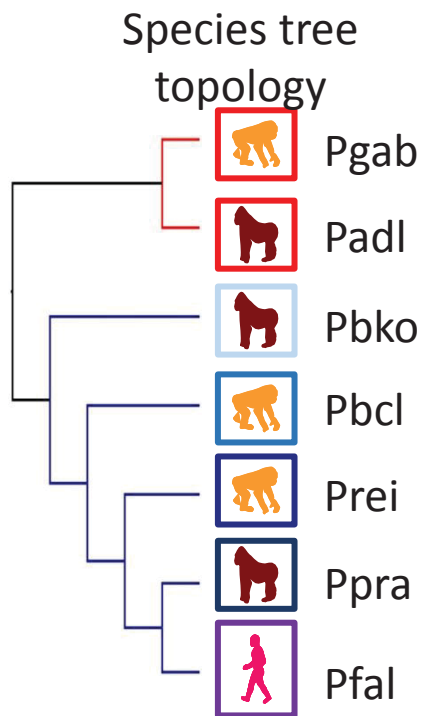
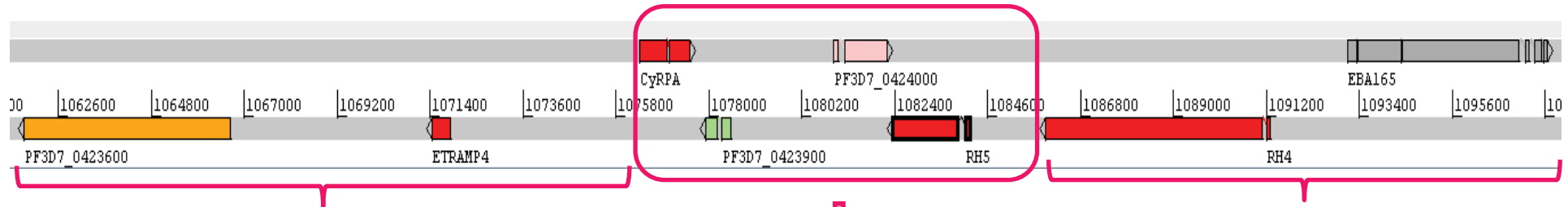
CDS & intergenic regions





Gene transfer & convergent evolution

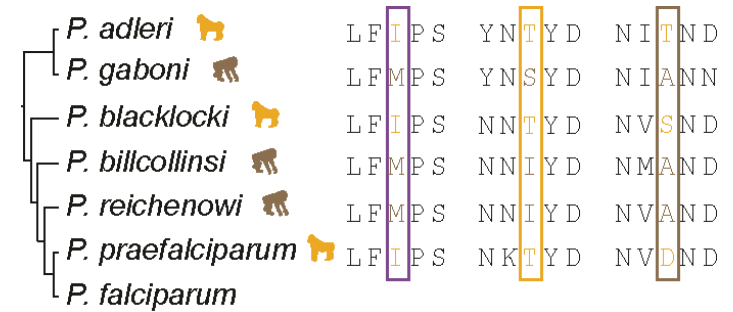
CDS & intergenic regions





○ Convergent evolution

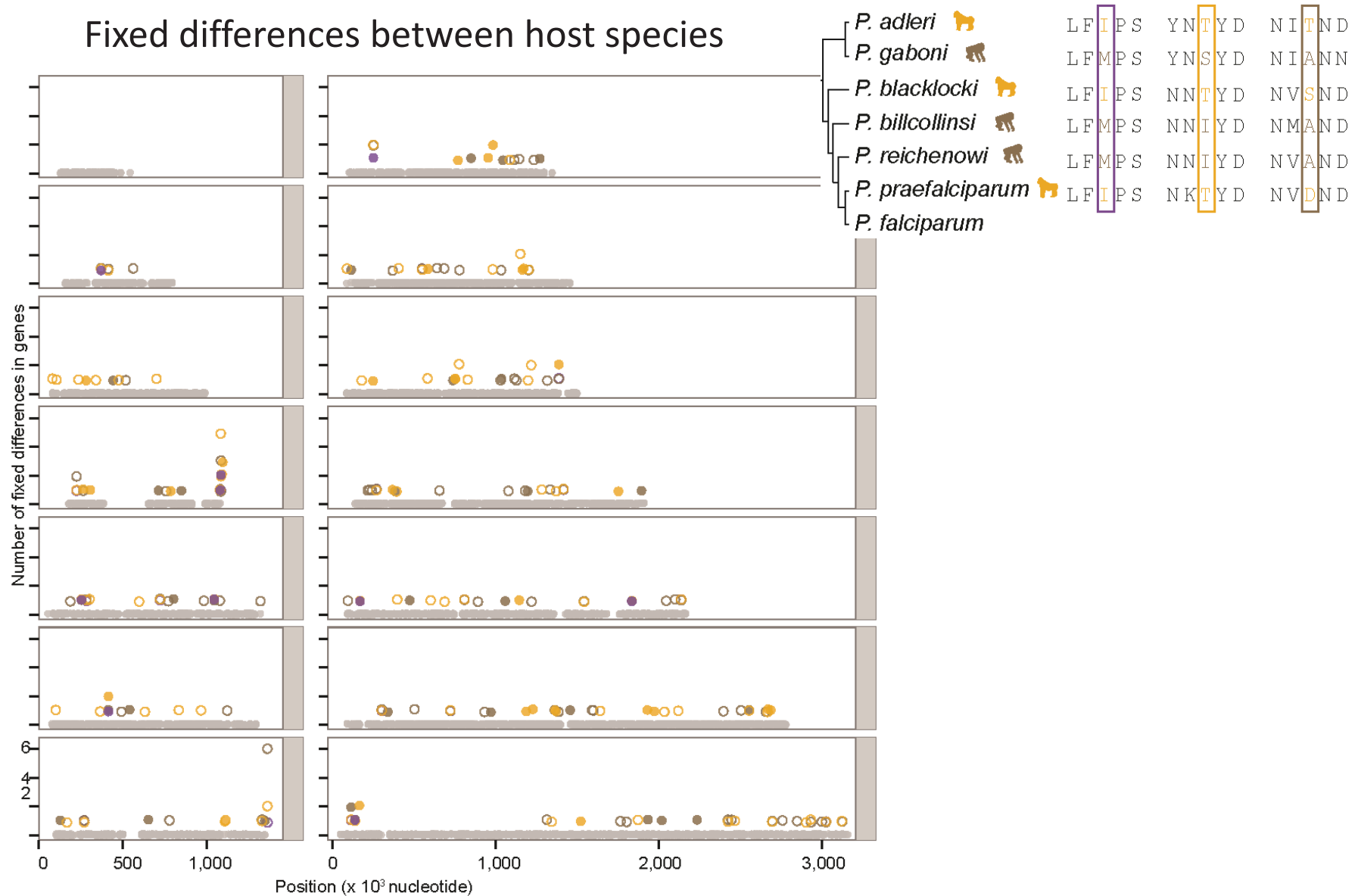
Fixed differences between host species





Convergent evolution

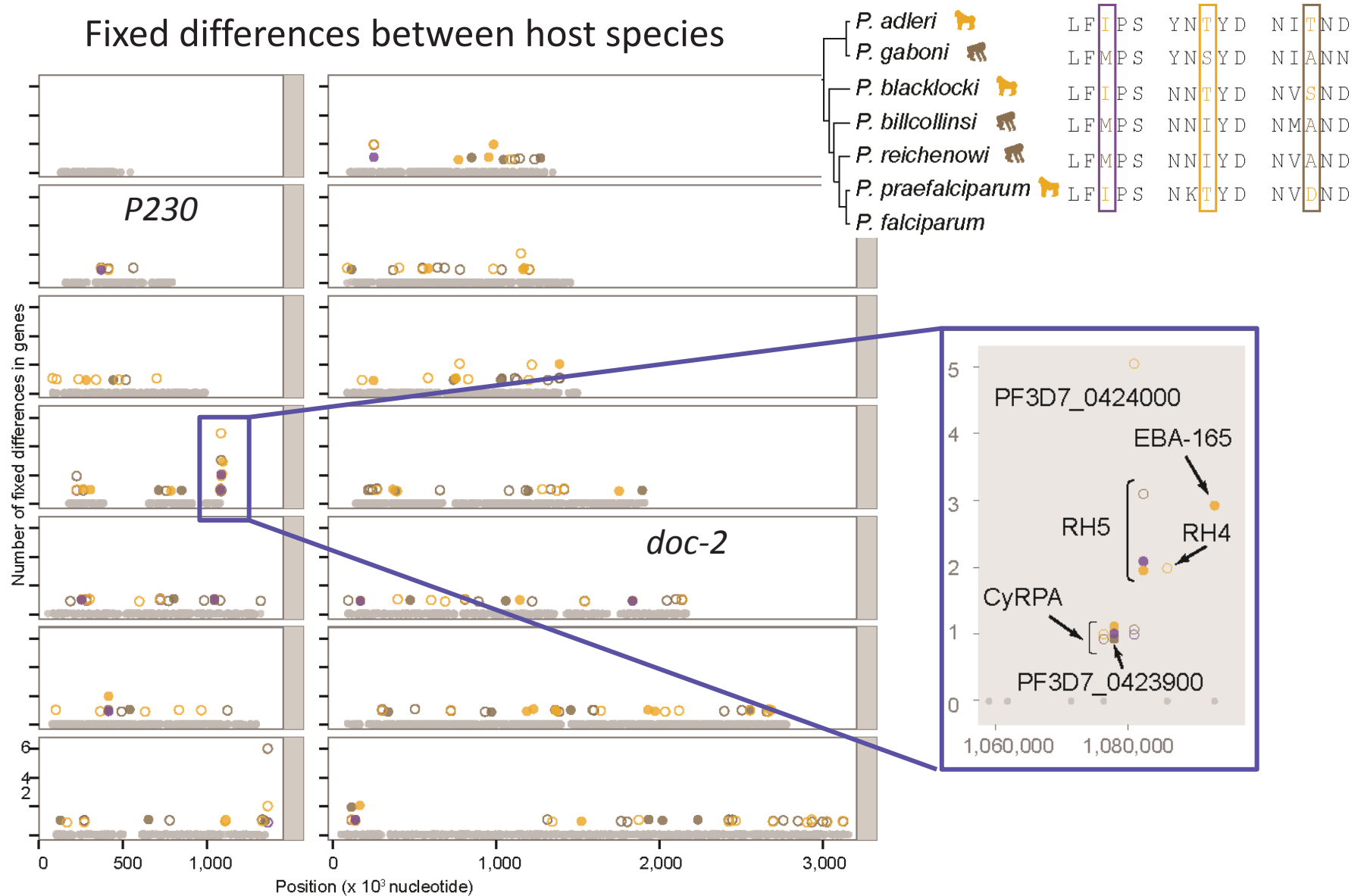
Fixed differences between host species





Convergent evolution

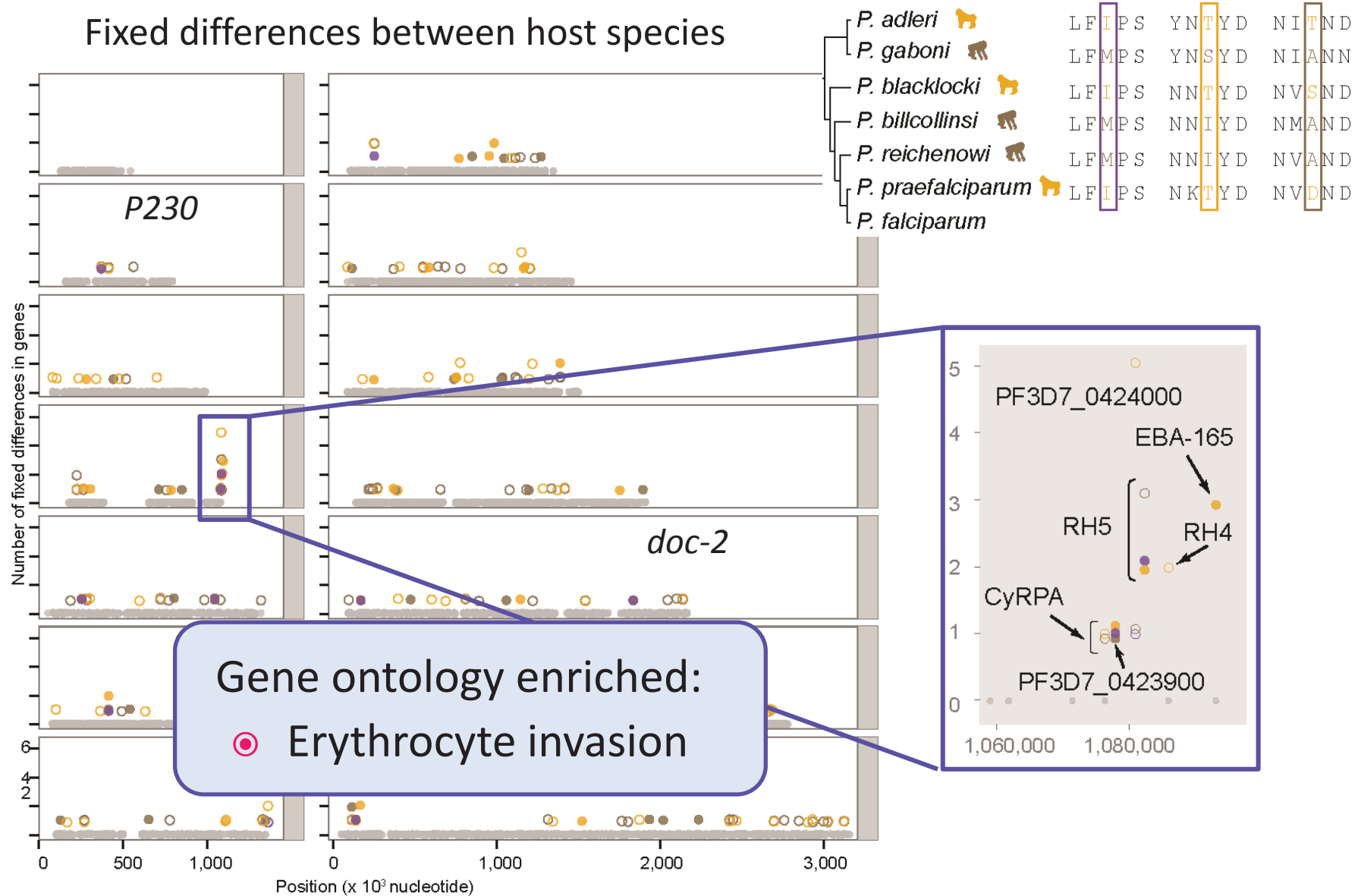
Fixed differences between host species





Convergent evolution

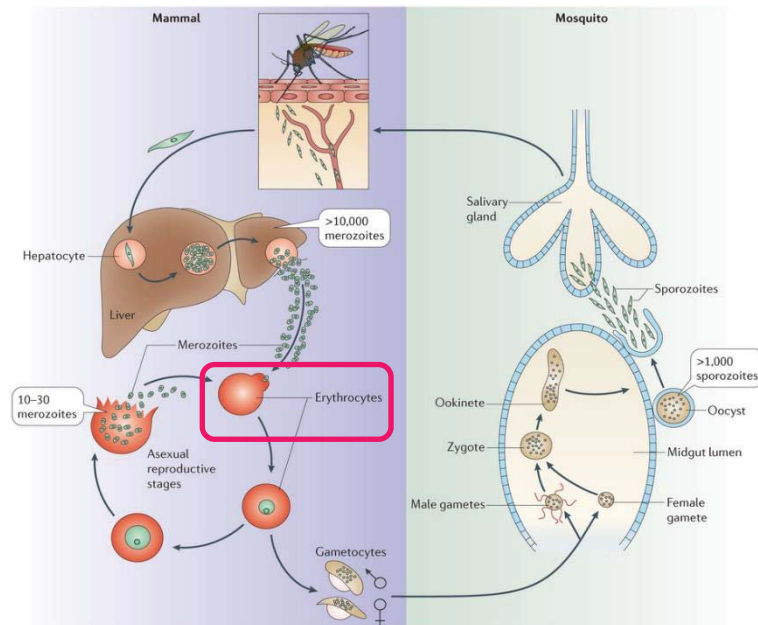
Fixed differences between host species



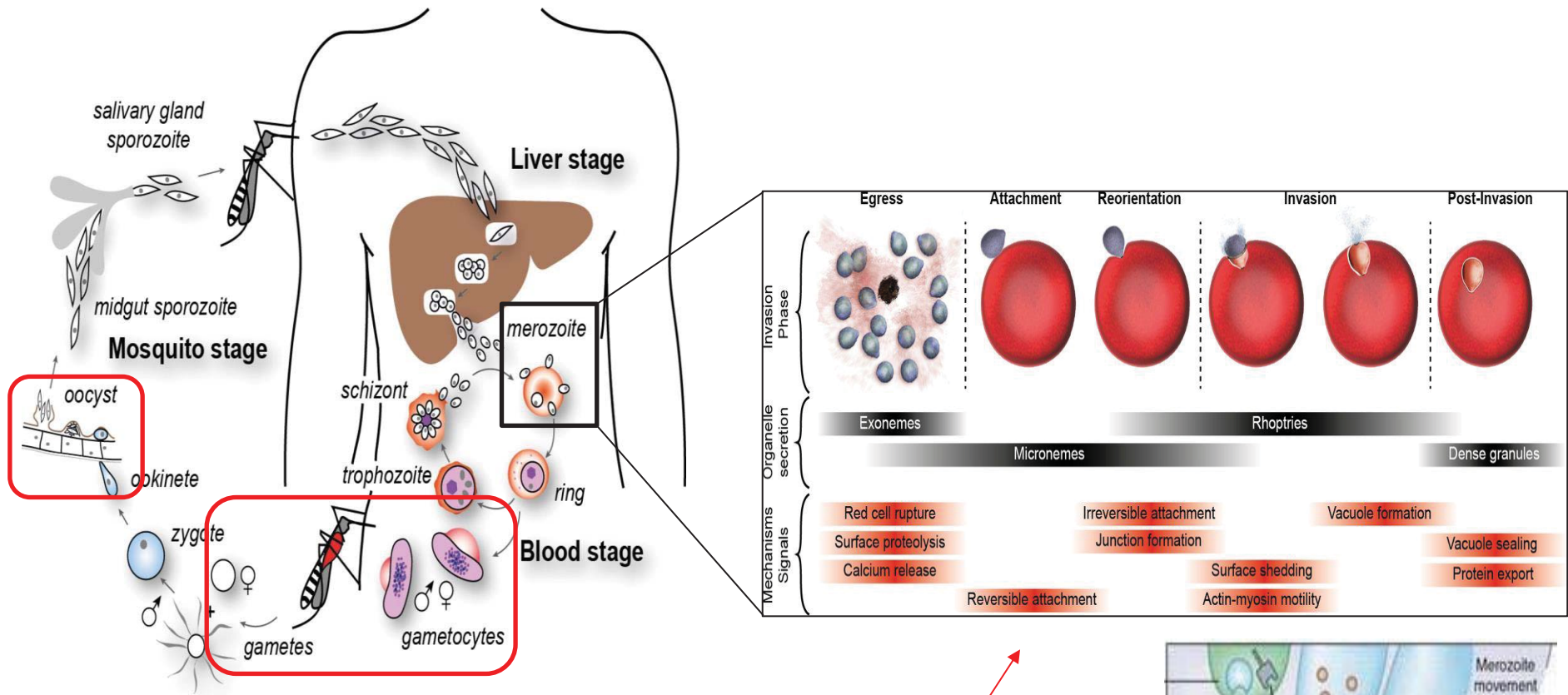


⇒ Gene transfer & convergent evolution

P. falciparum Chr. 4

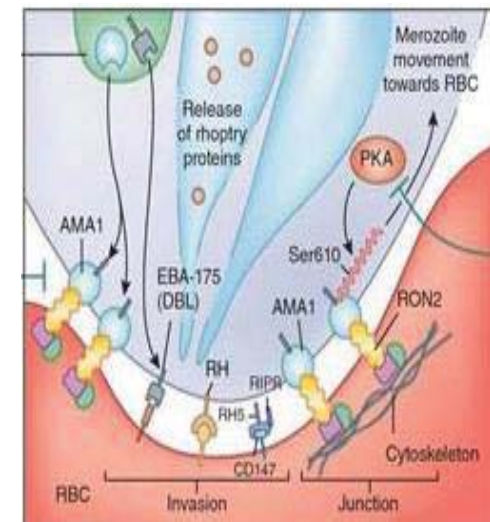


- CyRPA/Ripr/RH5 complex
 - ⇒ Interaction with the human receptor basigin
 - ⇒ Erythrocyte invasion & host tropism



6-cysteine protein P230
(pre-zygotic reproductive barrier)

DOC2
(Microneme secretion)



RH3, RH5 + CyRPA, EBA-175

Miller *et al.* (2013) Nature Medicine 19, 156–167



James Wasmuth
Dave Curran
Brian McDonald
Keyu Li
Jeff Wintersinger
Ivan Kryukov



John Gilleard



Thank you!



Céline Arnathau
Lionel Brazier
Patrick Durand
Franck Prugnonle
François Renaud
Virginie Rougeron



Matthew Berriman
Ulrike Böhme
Thomas D Otto
Samuel Oyola
Mandy Sanders



Chris Newbold