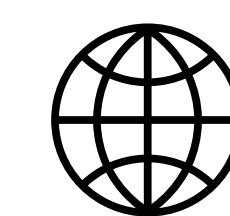


Gene trees challenge



@JLSteenwyk



<https://jlsteenwyk.com/>

SC-OGs are types of phylogenomic markers

Molecular evo. often relies on SC-OGs

Many molecular evolution studies *strictly*
rely on single-copy orthologs (SC-OGs)

Phylogenomics typically relies on SC-OGs

Many molecular evolution studies *strictly* rely on single-copy orthologs (SC-OGs)

- Phylogenomics,
- genome-wide surveys of (+) selection
- gene coevolution analysis
- others



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Many molecular evolution studies *strictly* rely on single-copy orthologs (SC-OGs)

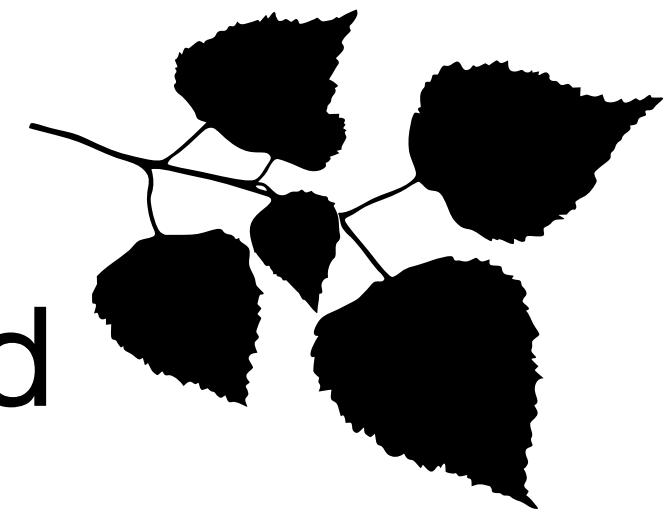
- Phylogenomics,
- genome-wide surveys of (+) selection
- gene coevolution analysis
- others

but SC-OGs are hard to find...

The quest for SC-OGs

A dataset of 35 plants

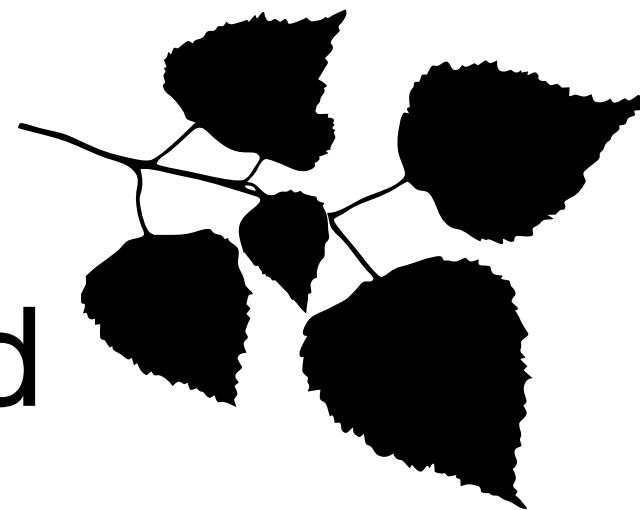
- only one single-copy orthogroup was identified



The quest for SC-OGs

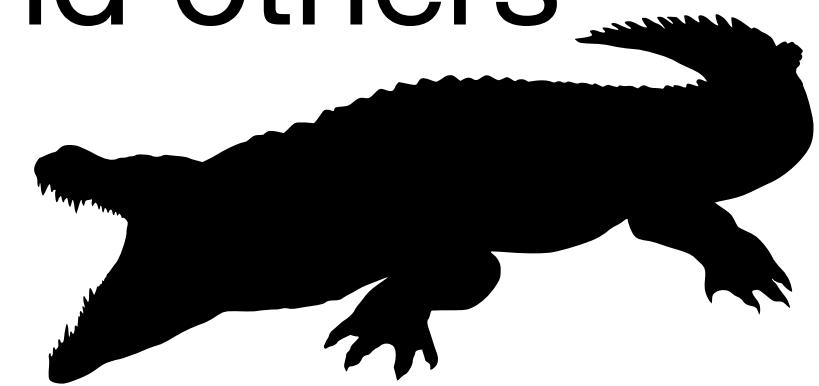
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A dataset of 30 turtles, tortoise, birds, crocodile, alligators, and others

- only 27 single-copy orthogroups identified

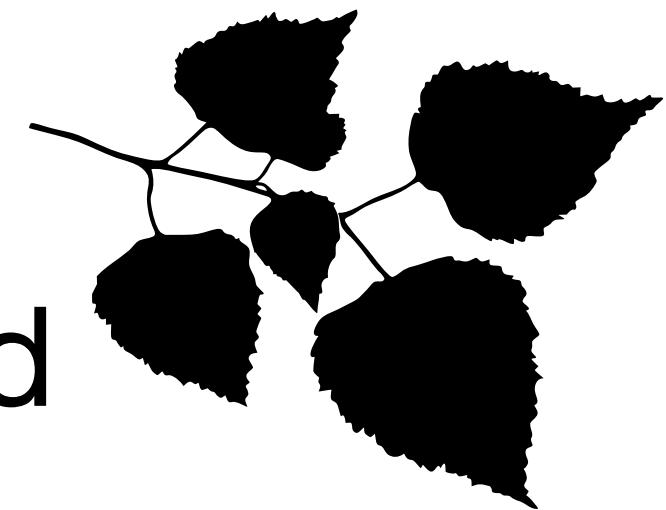


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The quest for SC-OGs

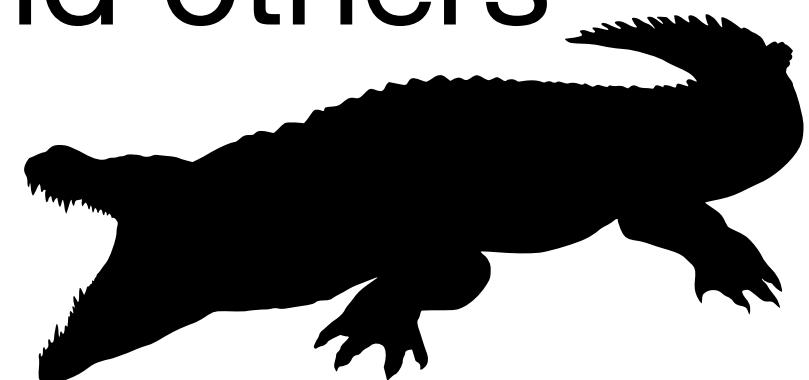
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A dataset of 76 arthropods (Thomas et al. (2020), *Genome Biology*)

- Zero single-copy orthogroups with 100% occupancy



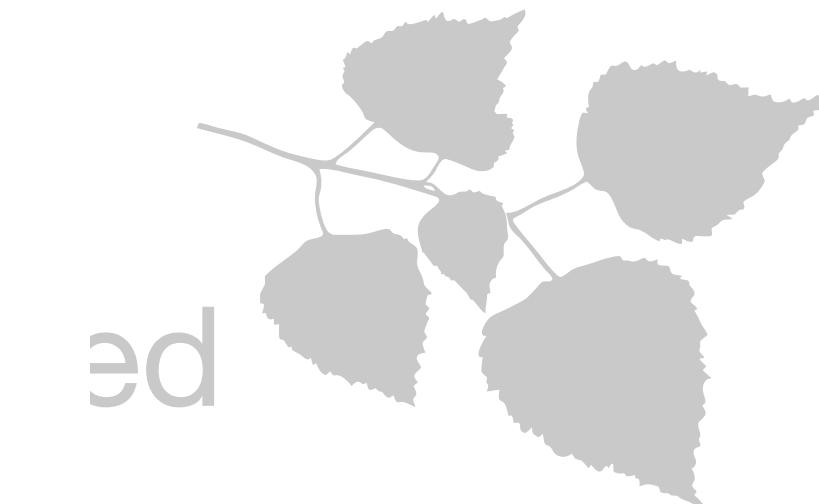
@JLSteenwyk

Too few phylogenomic markers :(

A dataset of 35 plants
• only one single-copy

A dataset of 30 turtles,
• only 27 single-copy o

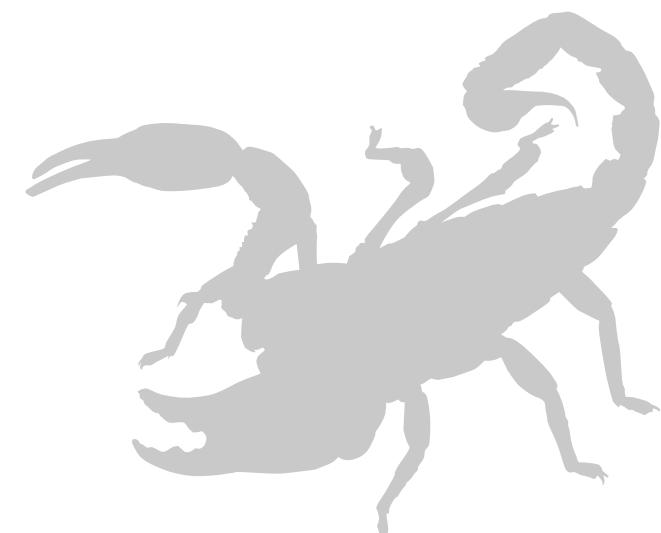
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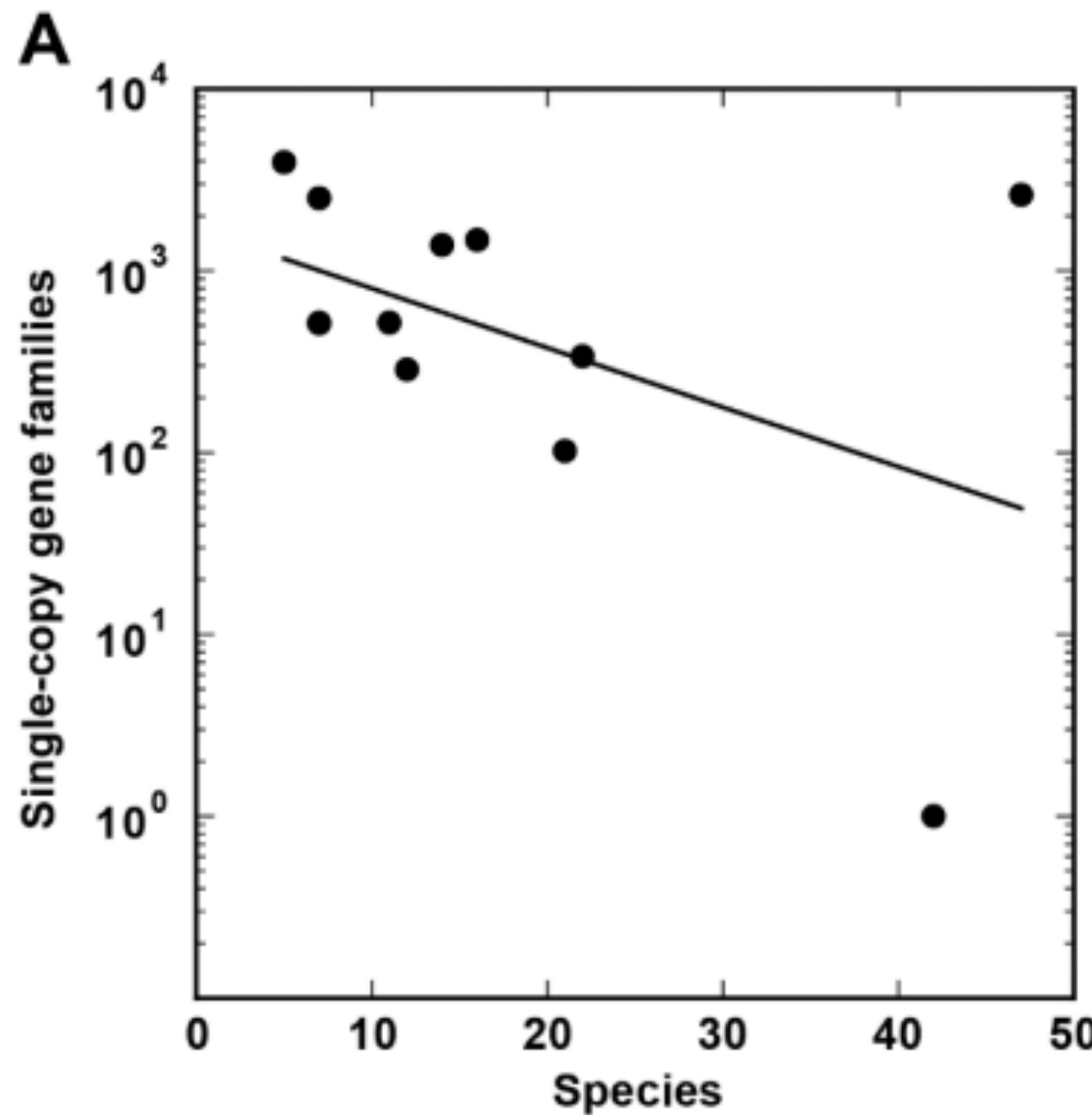
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:0), *Genome Biology*)

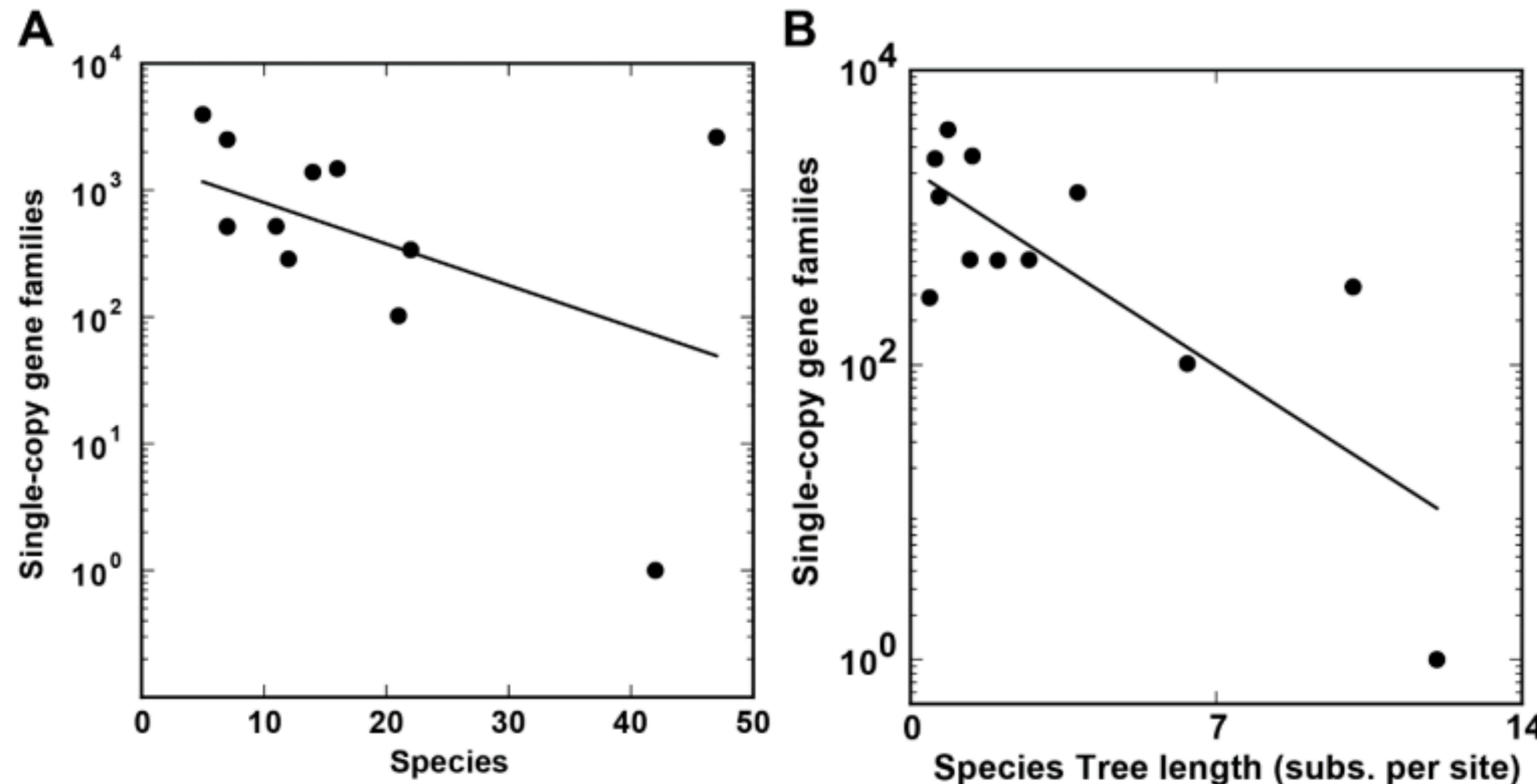


Factors that impact SC-OG identification



The number of single-copy orthologs decreases as the number of species and evolutionary distance among species increases

Factors that impact SC-OG identification

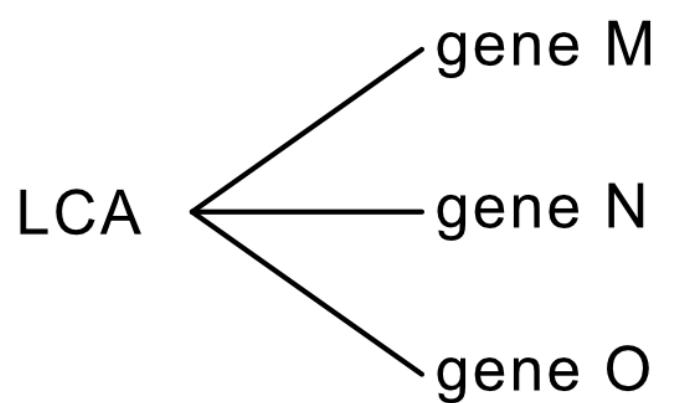


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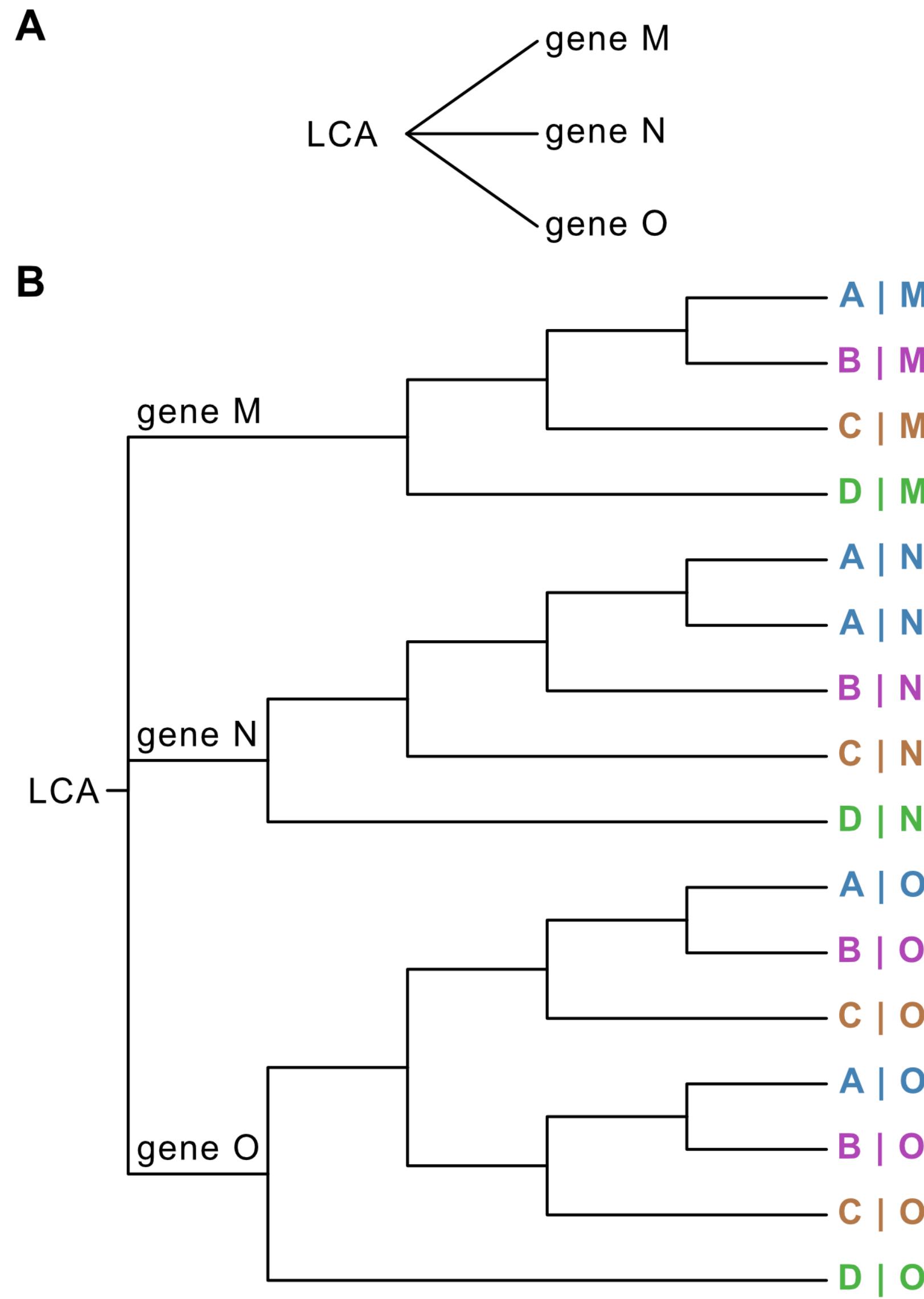
Can other types of orthologs be used for molecular evolution studies?

Factors that impact SC-OG identification

A

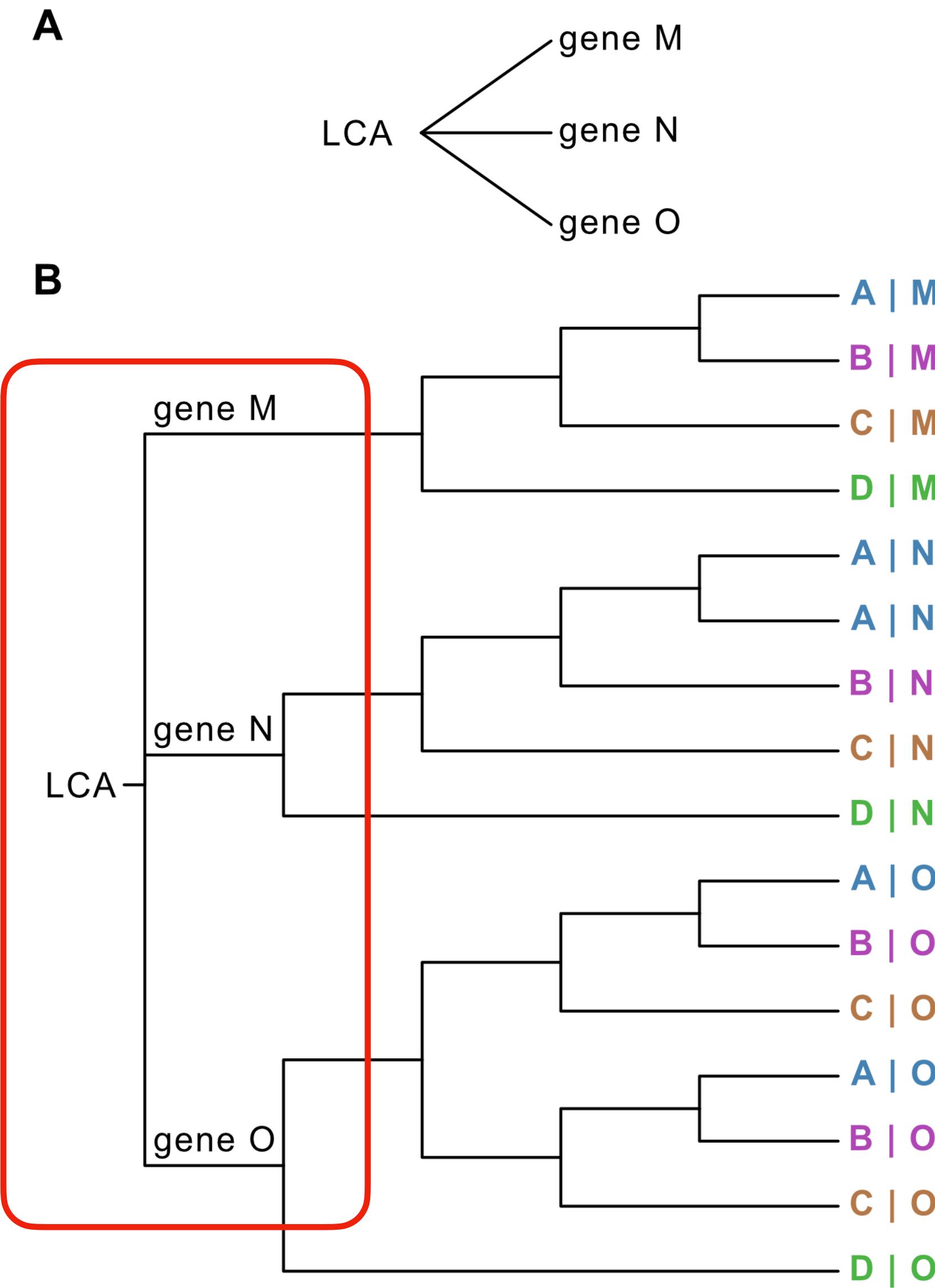


Factors that impact SC-OG identification



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Factors that impact SC-OG identification

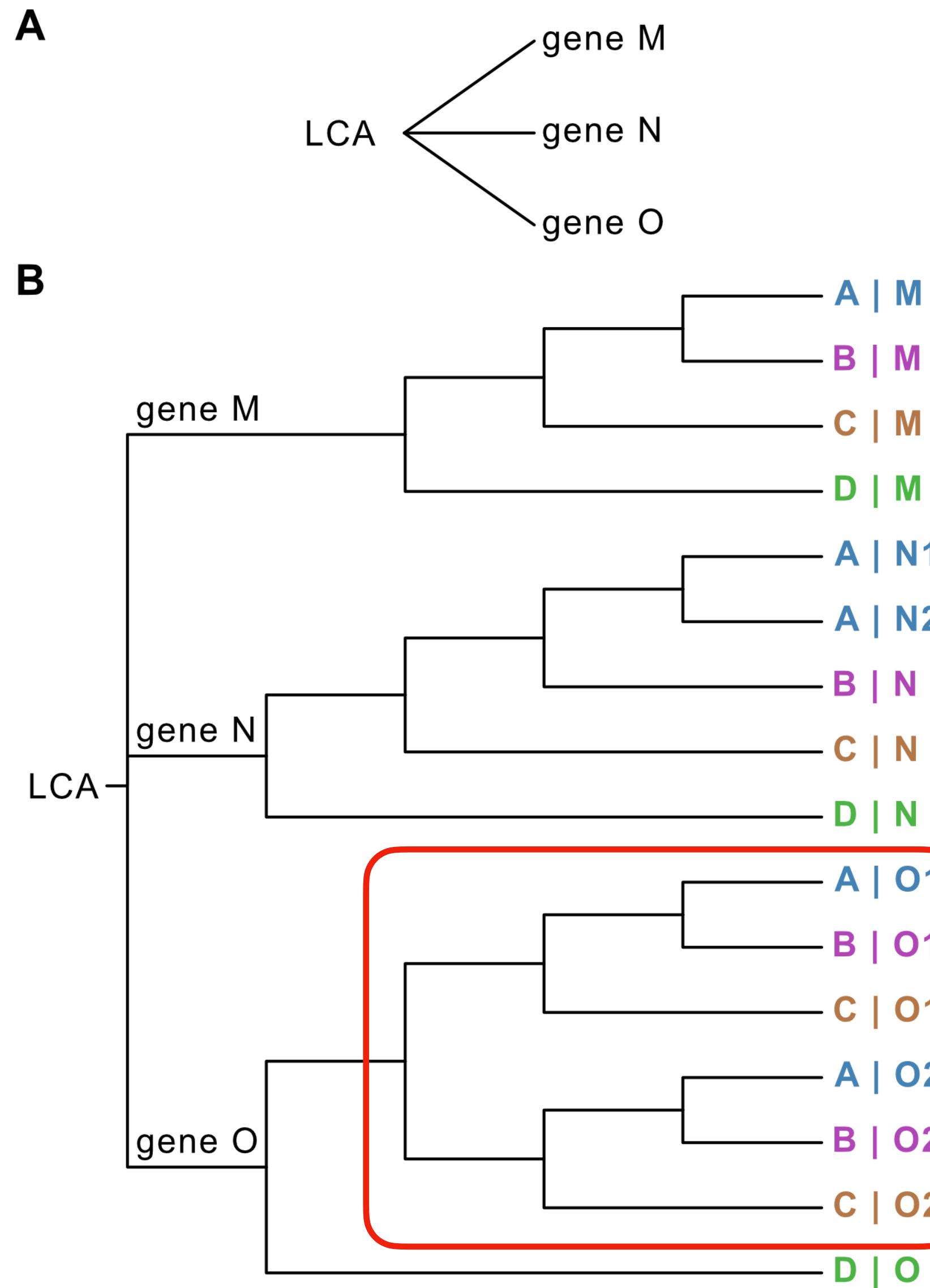


- Gene M, N, and O are outparalogs—paralogous genes wherein duplication occurred prior to a speciation event



@JLSteenwyk

Factors that impact SC-OG identification

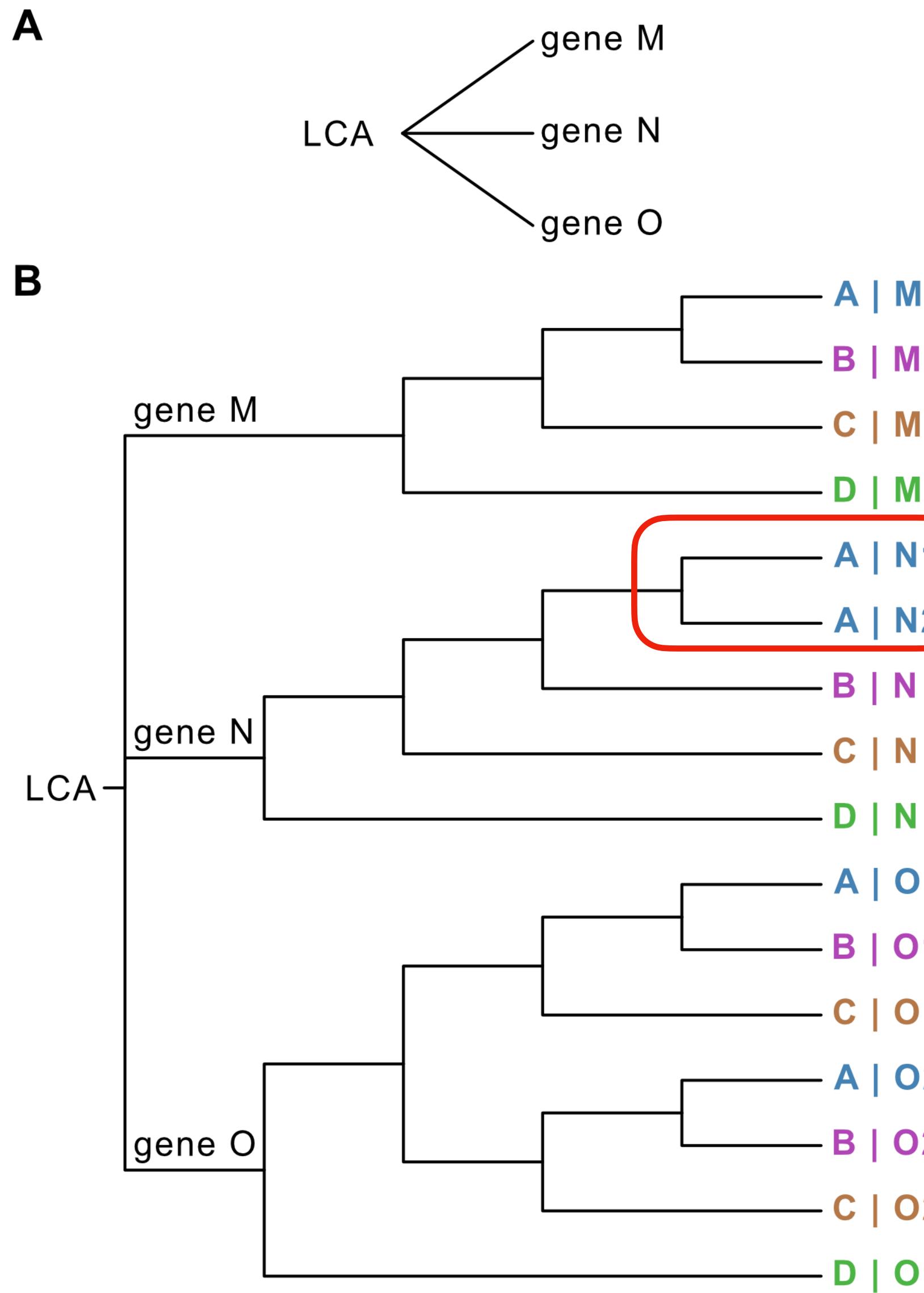


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Factors that impact SC-OG identification

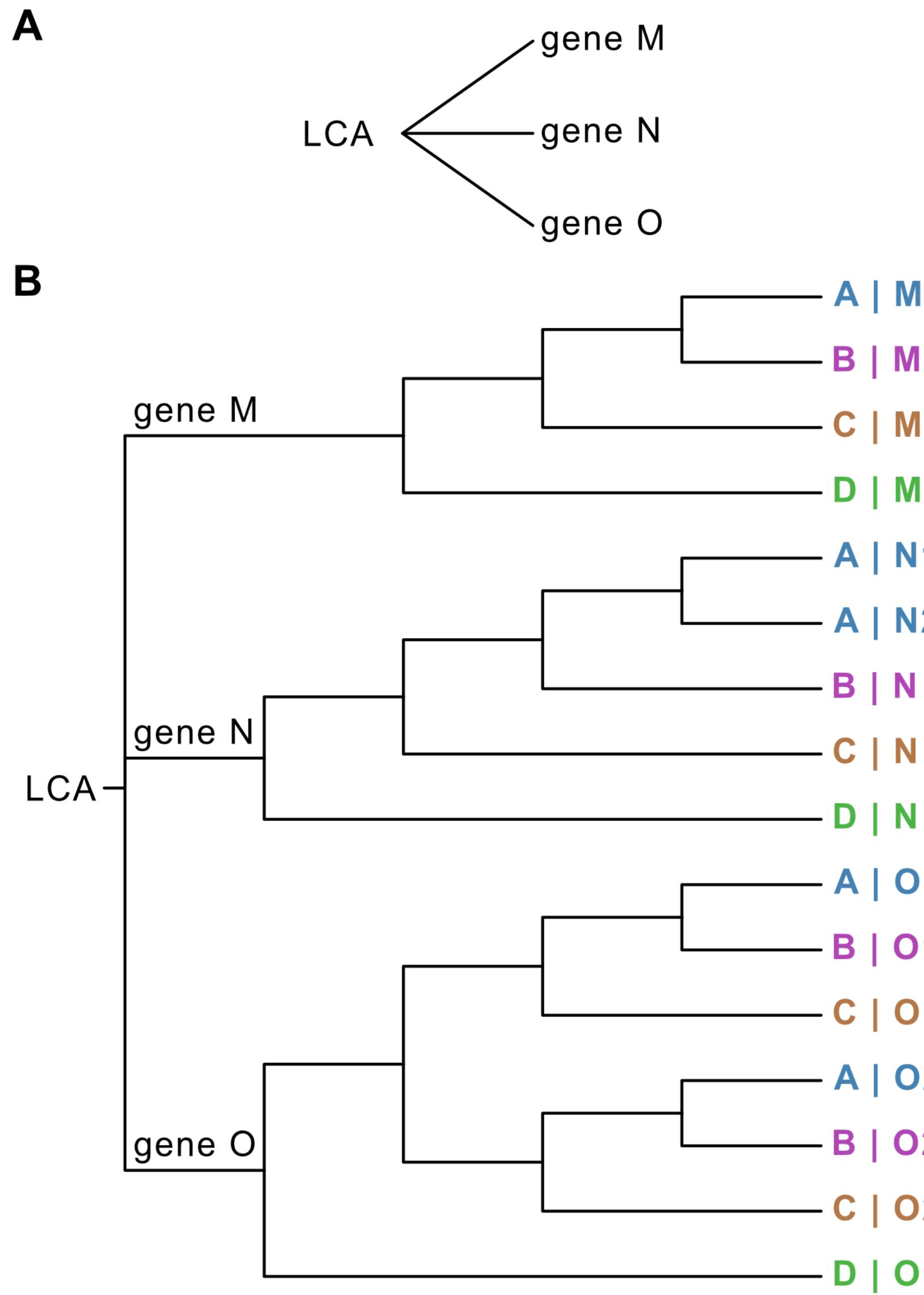


- Gene M, N, and O are outparalogs—paralogous genes wherein duplication occurred prior to a speciation event
- A, B, and C O1 and O2 are inparalogs—paralogous genes wherein duplication occurred after a speciation event
- A | N1 and A | N2 are within species inparalogs



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Factors that impact SC-OG identification



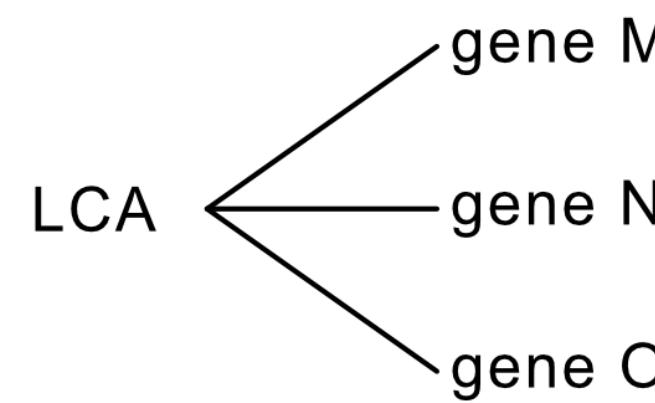
Note, splitting this tree will result in multiple subgroups of single-copy orthologs



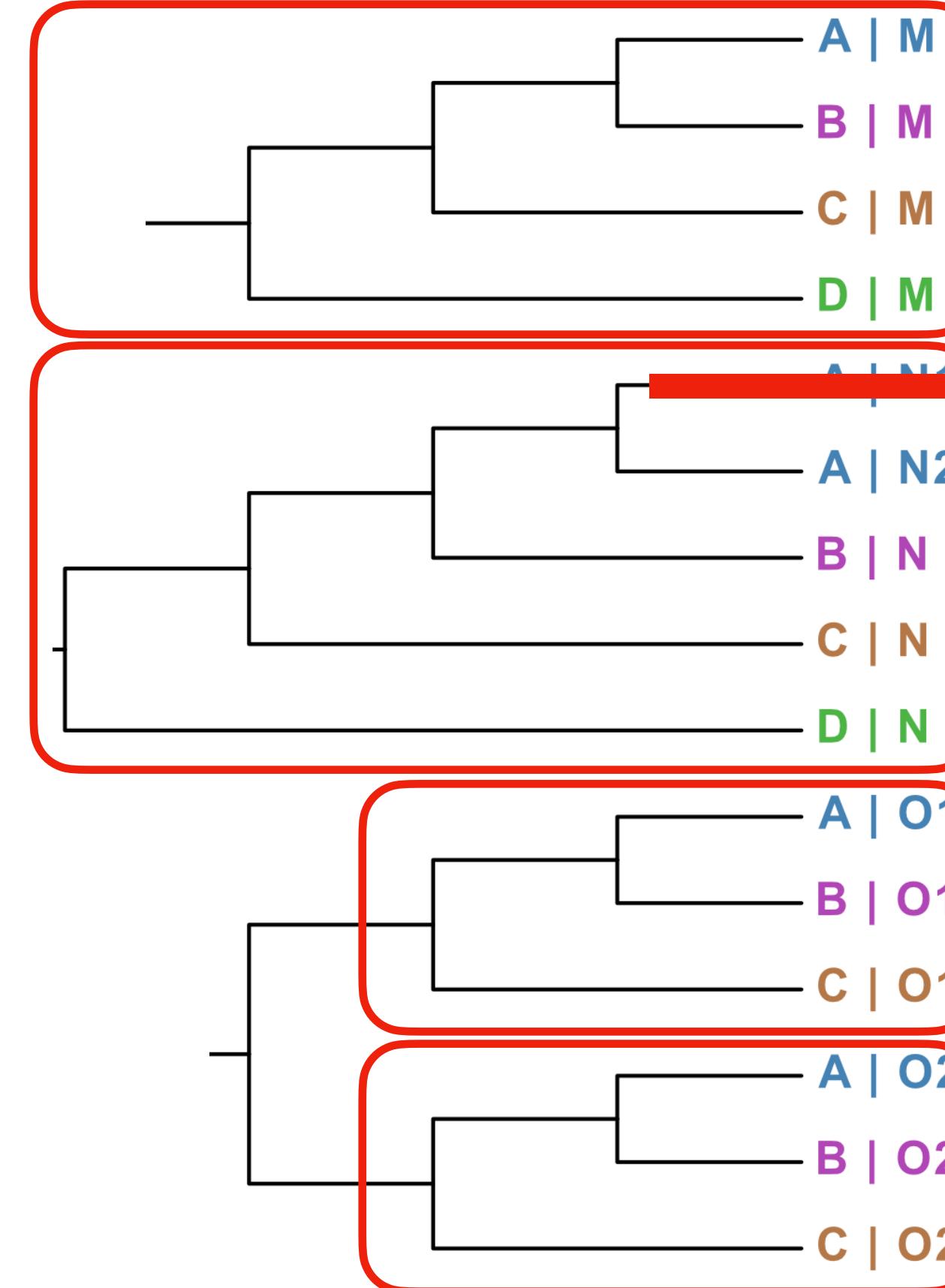
@JLSteenwyk

Factors that impact SC-OG identification

A



B

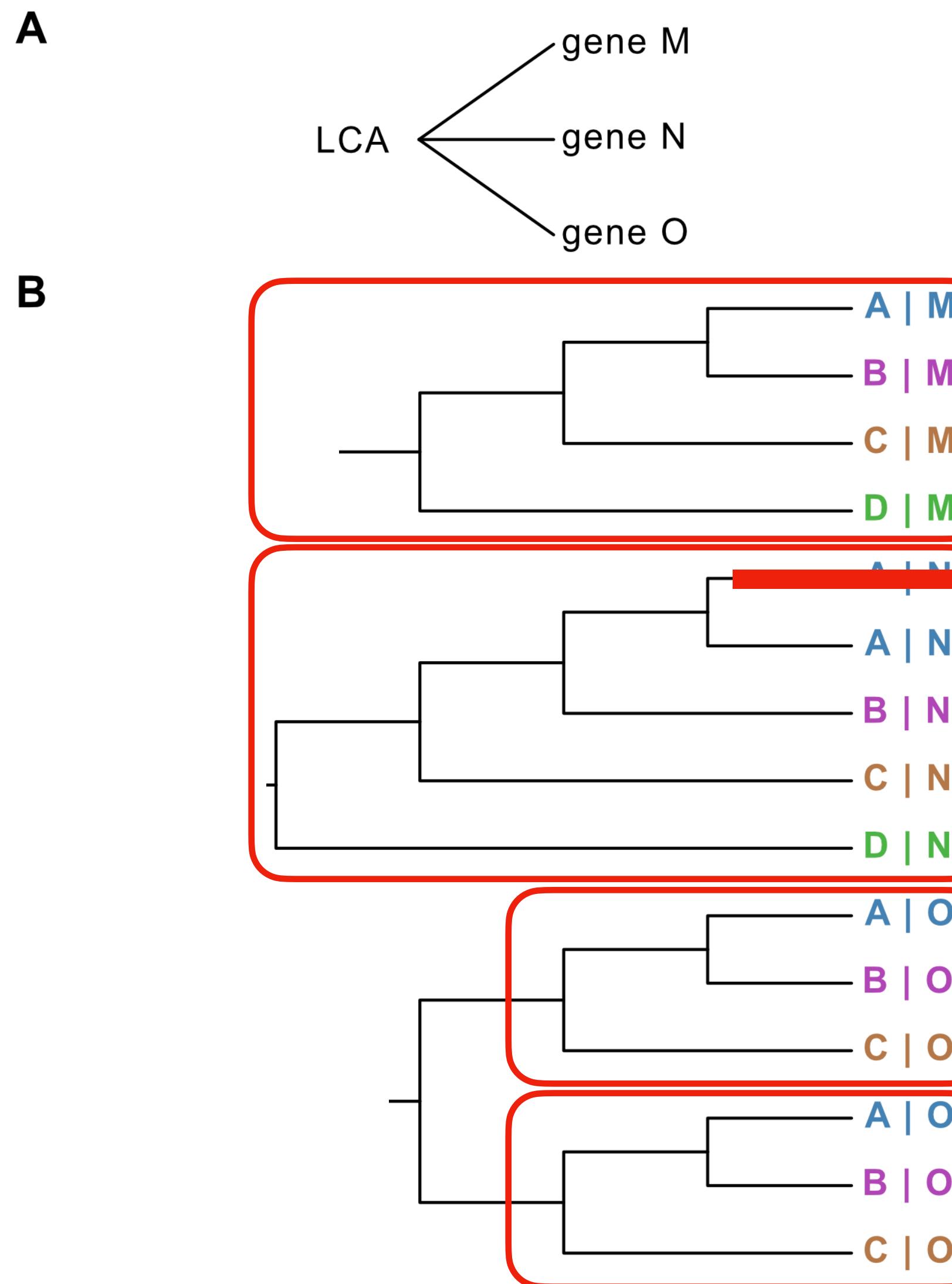


subgroups of single-copy in- and outparalogs from multi-copy orthologous groups of genes



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Factors that impact SC-OG identification



subgroups of single-copy in- and outparalogs from multi-copy orthologous groups of genes

We term these SNAP-OGs because they are orthologs that have undergone a splitting and pruning procedure



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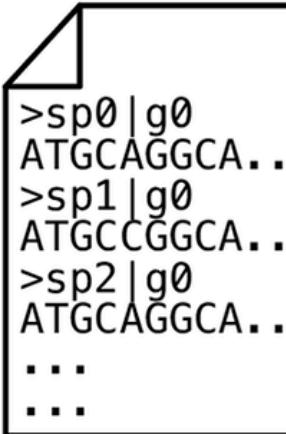
Ortho^{SNAP}

identify single-copy orthologous genes
nested within larger gene families

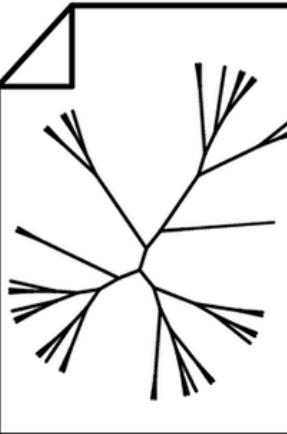
OrthoSNAP methods

A

Gene family sequences
with multiple homologs
in one or more species

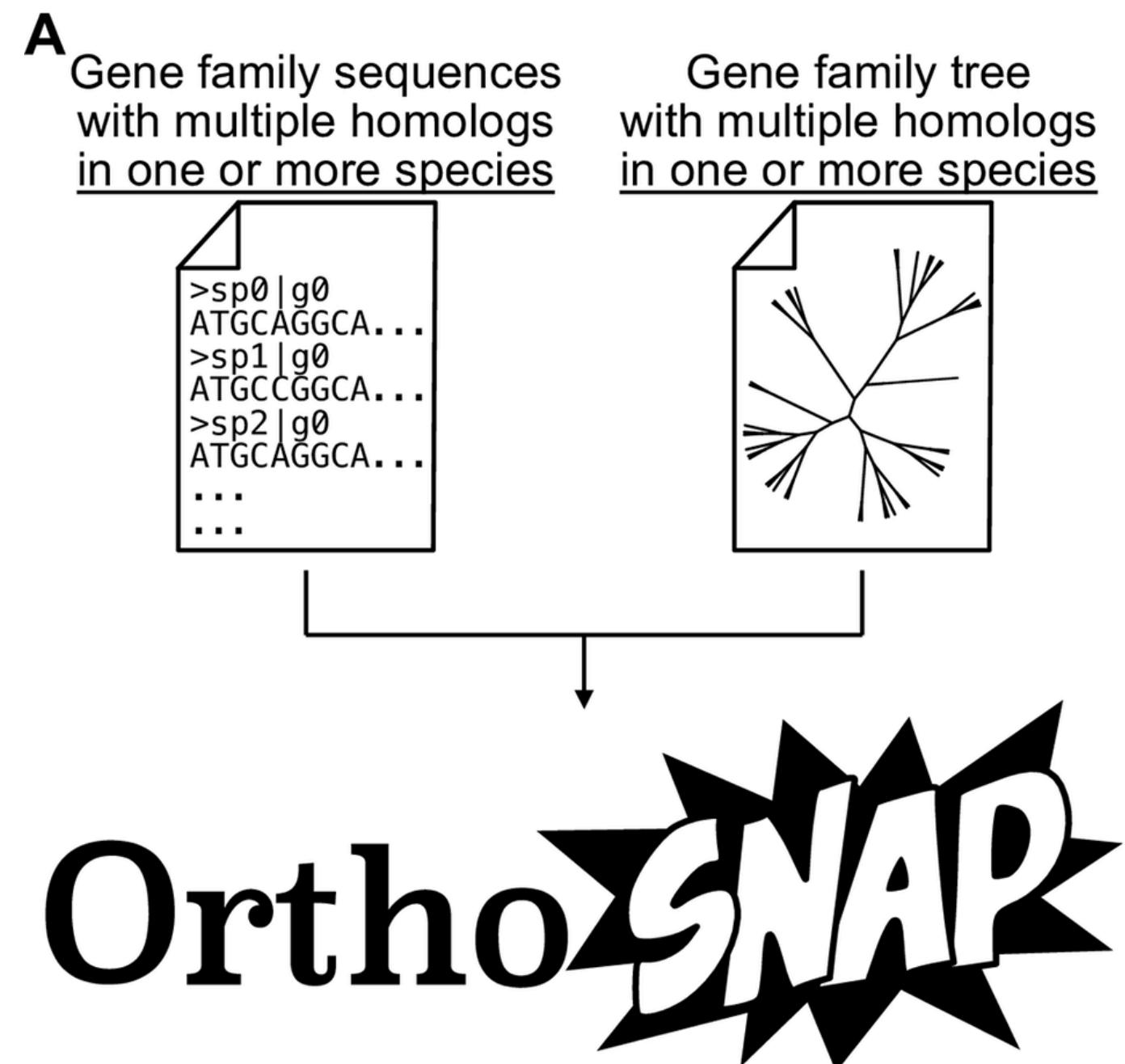


Gene family tree
with multiple homologs
in one or more species

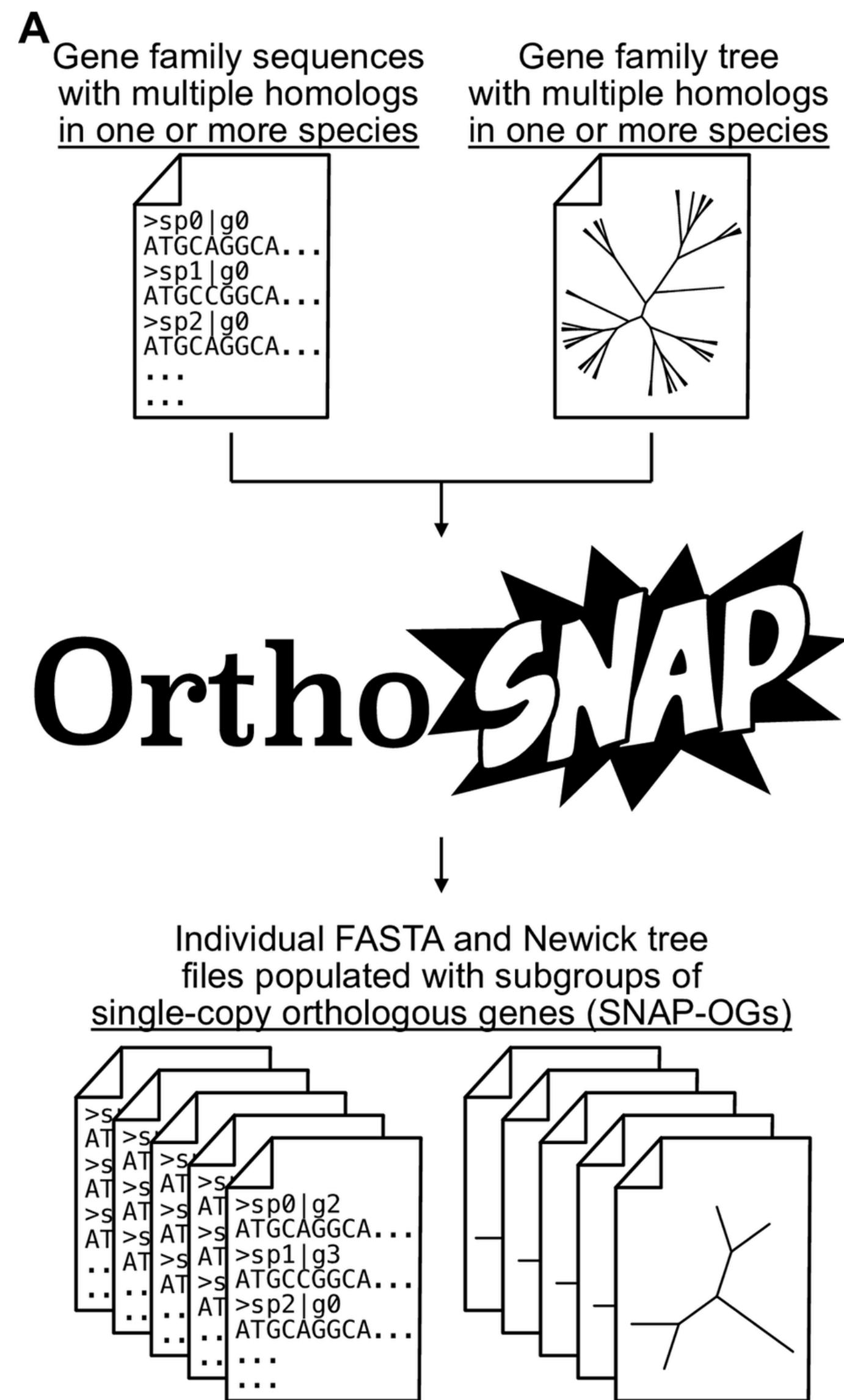


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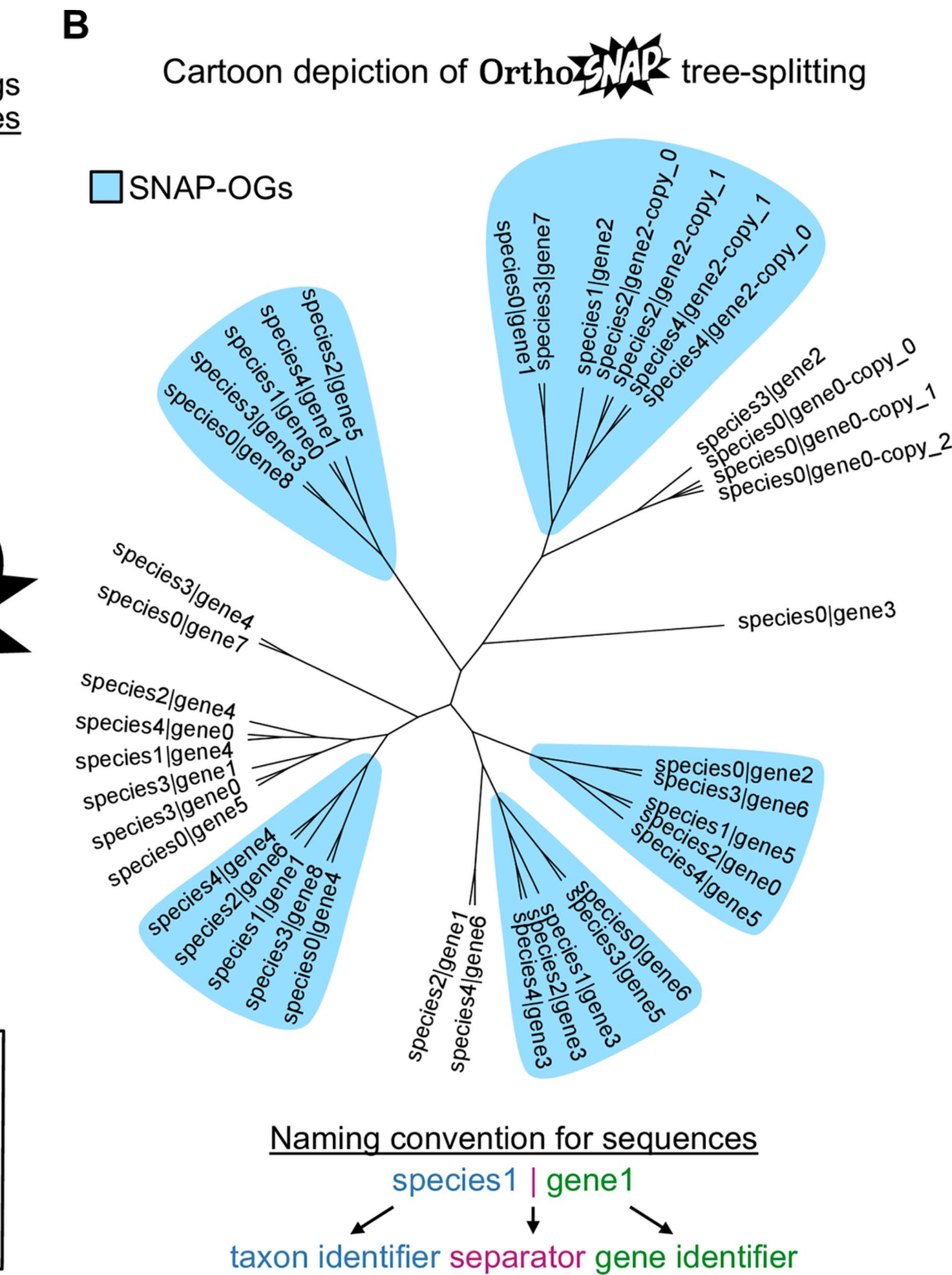
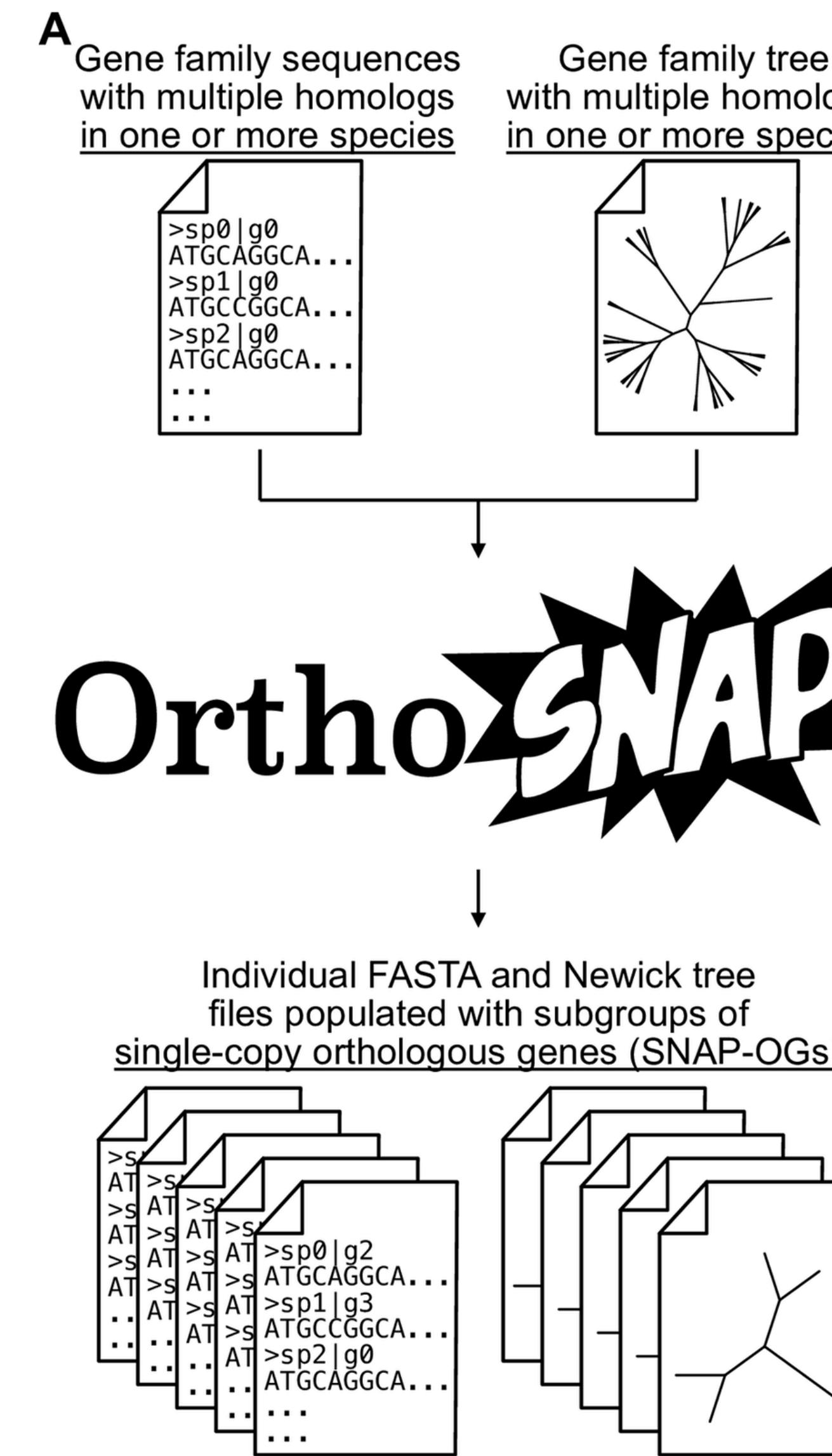
OrthoSNAP methods



OrthoSNAP methods



OrthoSNAP methods



SNAP-OGs can substantially increase datasets

	SC-OGs	SNAP-OGs	Fold difference
Budding yeast (No WGD)	1,668	1,392	0.83

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SNAP-OGs can substantially increase datasets

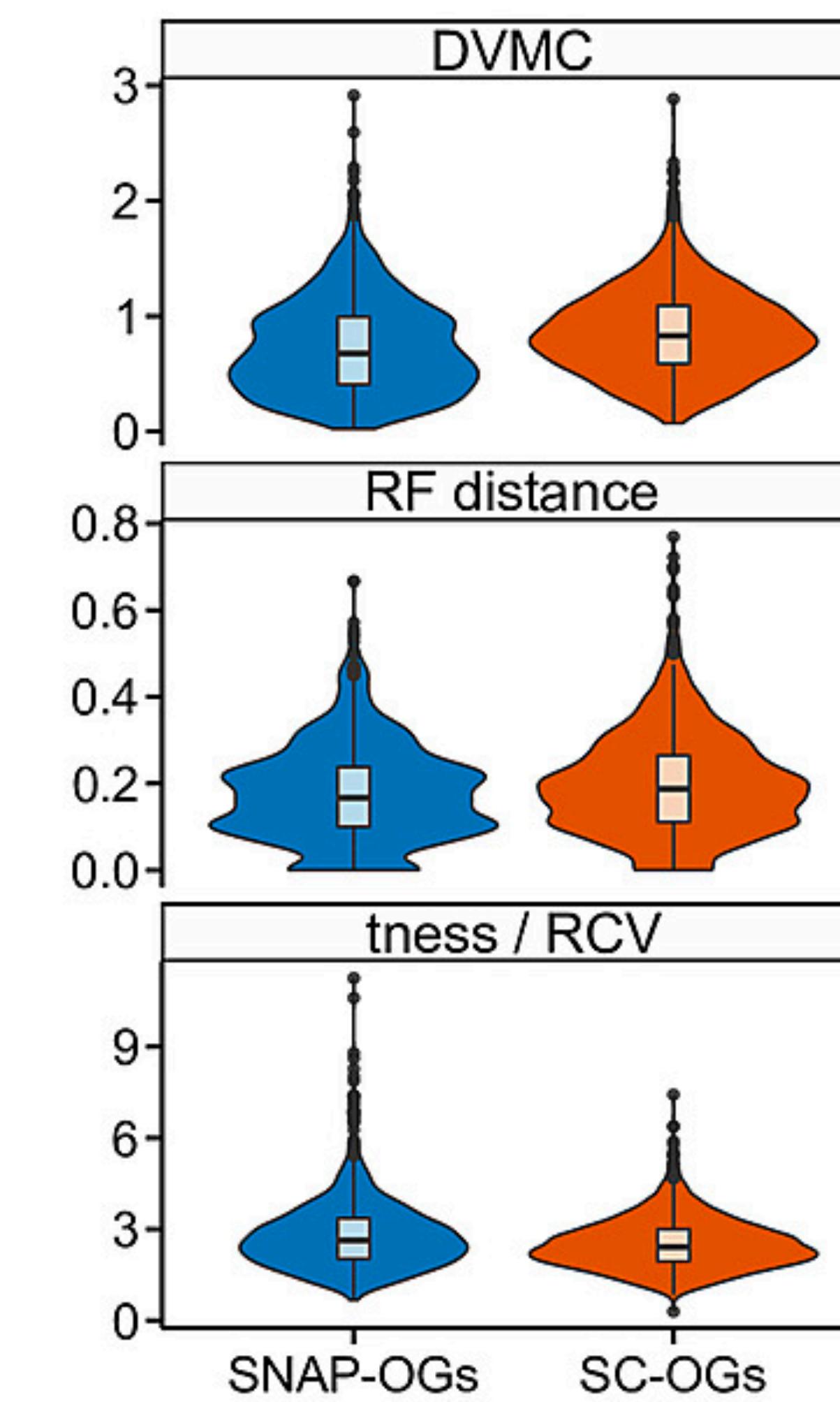
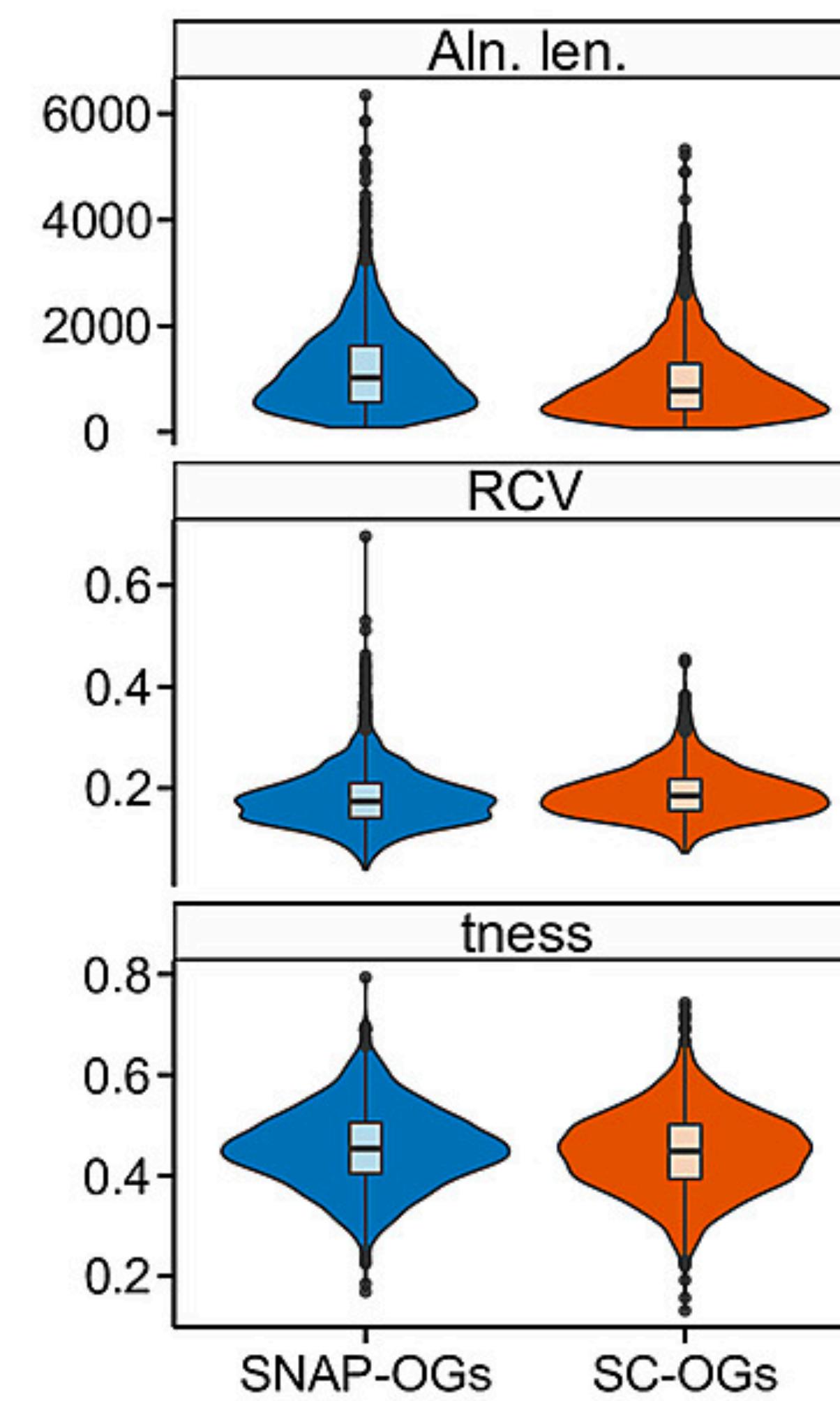
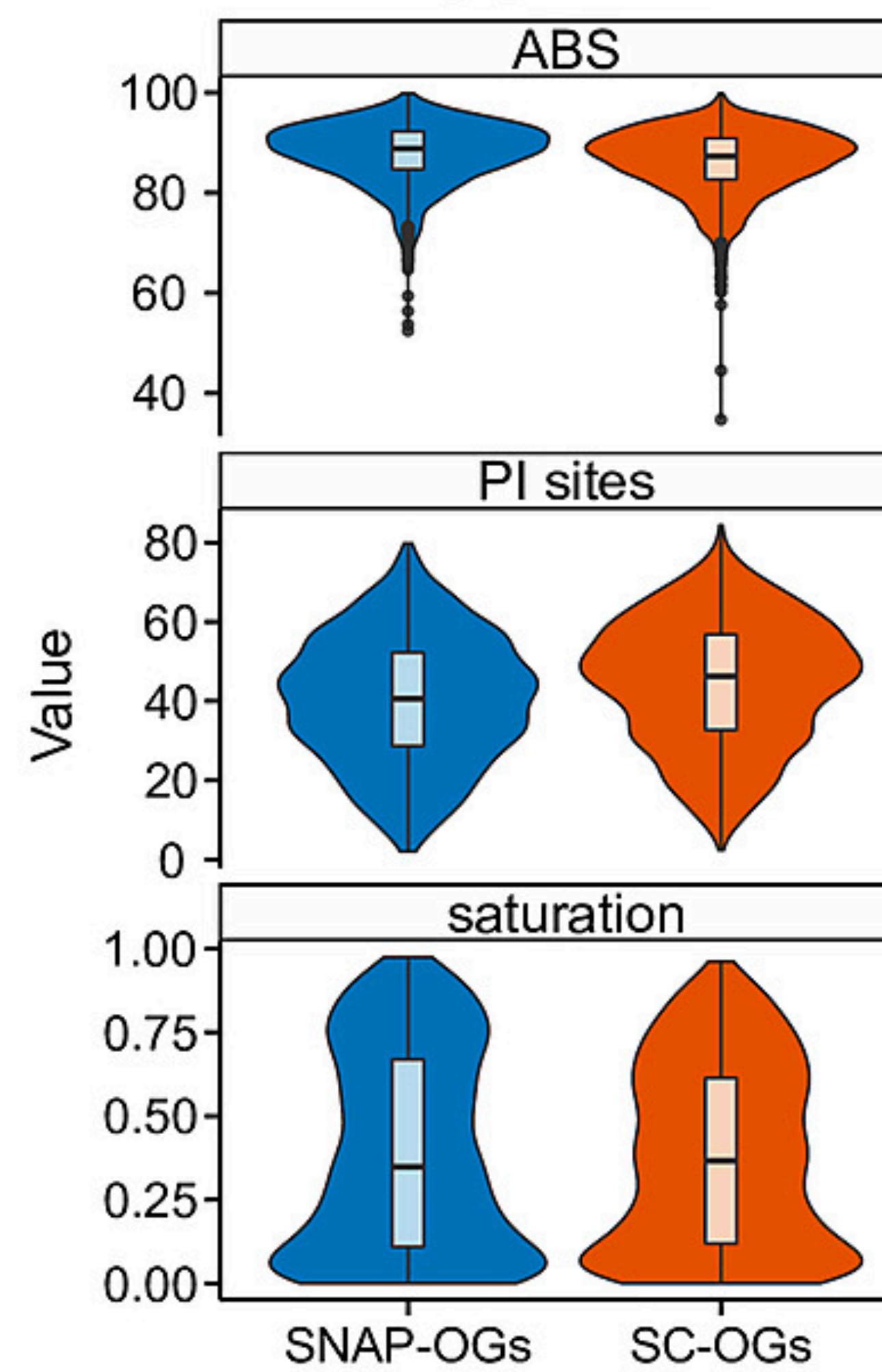
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Plants (Complex dup. And	15	653	43.53
Choanoflagellate (Transcriptomes)	390	2,087	5.35

But are SNAP-OGs bad markers?

SNAP- & SC-OGs are statistically indistinguishable

A

Budding yeasts

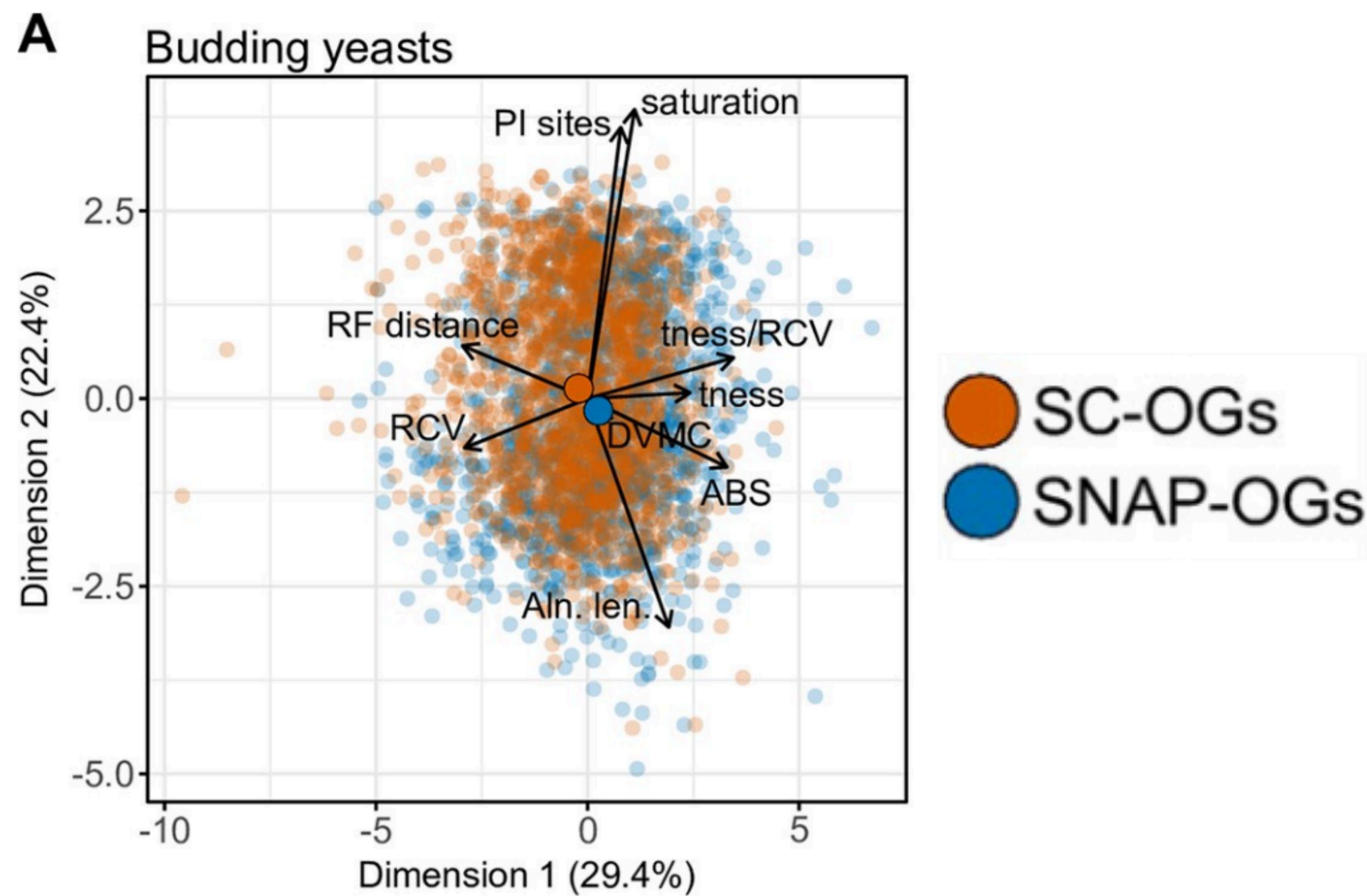


SC-OGs
SNAP-OGs

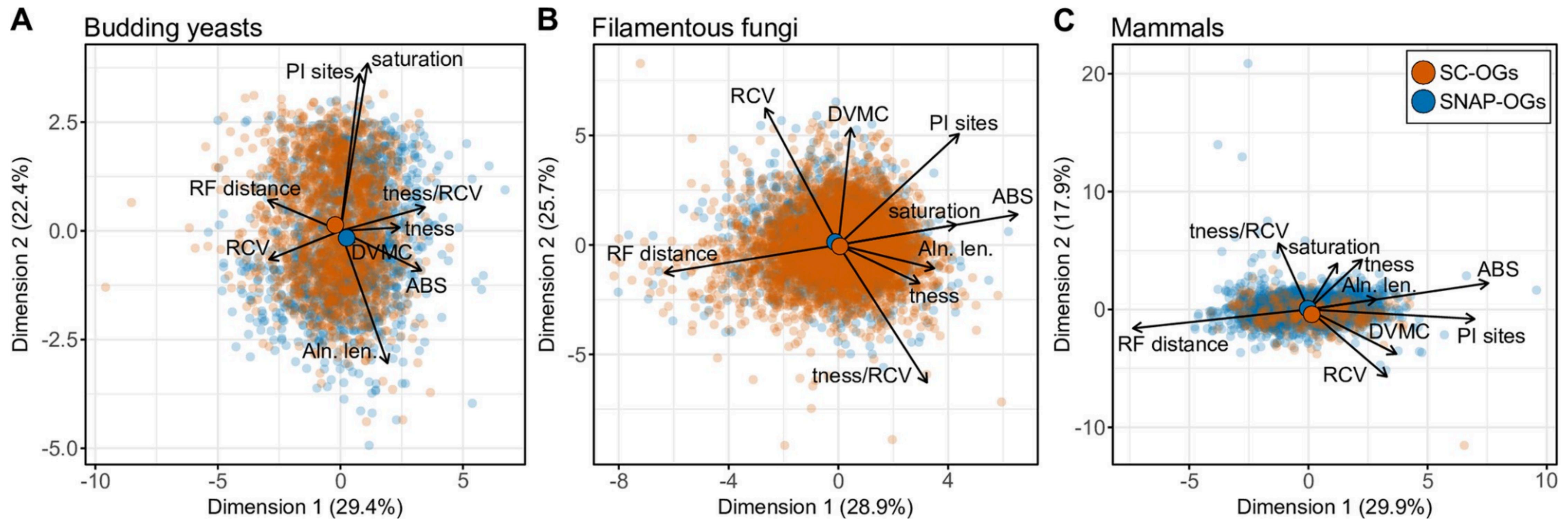


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SNAP- & SC-OGs are statistically indistinguishable



SNAP- & SC-OGs are statistically indistinguishable



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Phylogenomics typically relies on SC-OGs

- High-throughput screens of (+) selection requires SC-OGs

Phylogenomics typically relies on SC-OGs

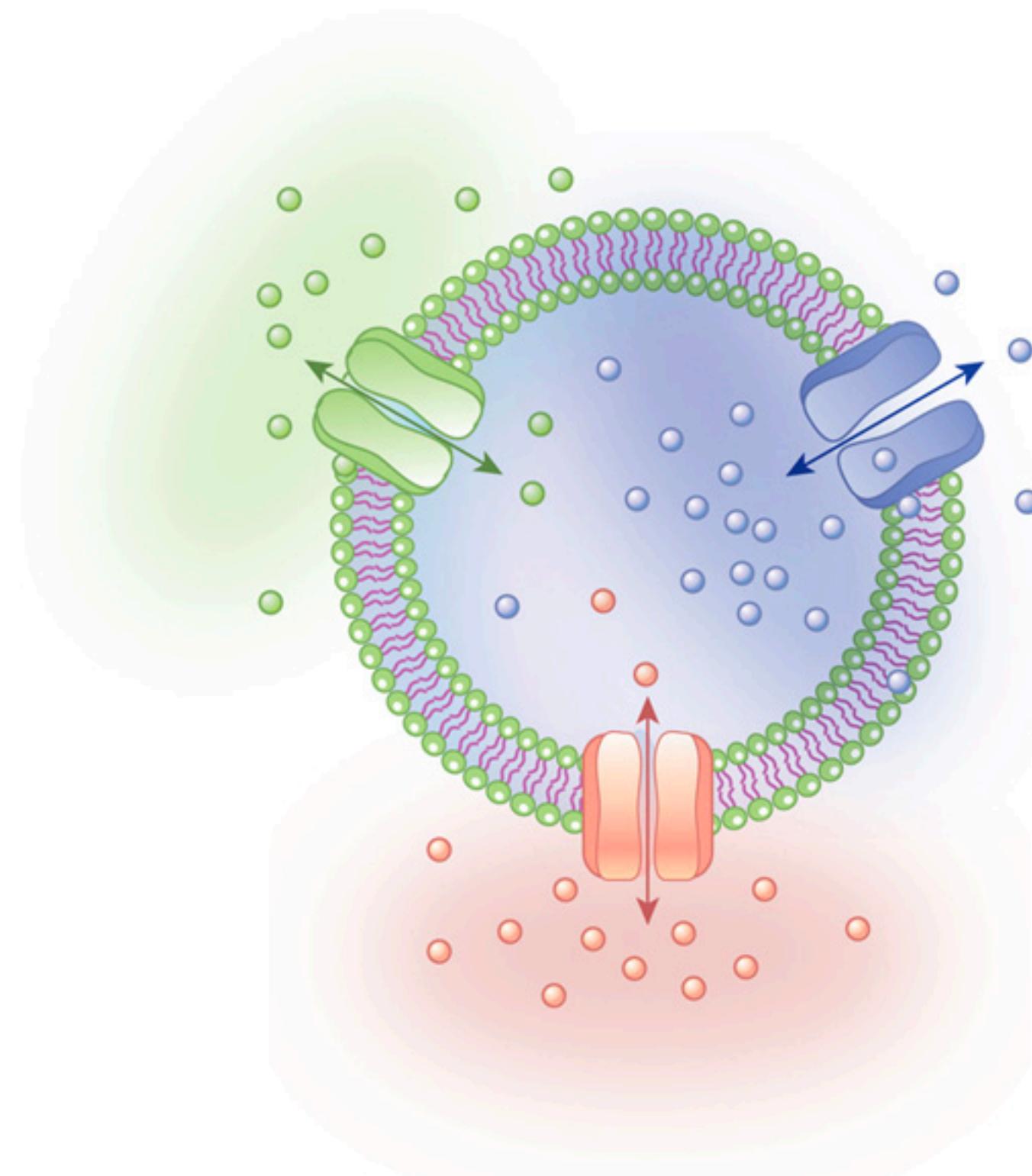
- High-throughput screens of (+) selection requires SC-OGs
- What types of genes are not typically SC-OGs?
 - Receptors
 - Heat shock proteins
 - Transporters
 - Transcription factors
 - Kinases
 - Etc...



@JLSteenwyk

Molecular evolution of *all* types of genes

- 5 SNAP-OGs were identified in OGs of transcription factors
- 5 SNAP-OGs were identified in OGs of MFS transporters
- 4 SNAP-OGs were identified in an OG of kinases



Phylogenomics typically relies on SC-OGs

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- What types of genes are not typically SC-OGs?
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 - **Heat shock proteins**
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Ortho^{SNAP}

identify single-copy orthologous genes
nested within larger gene families

Gene trees challenge