CFG - Practical session 2

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L'opció per desar està desactivada

Alignment questions

Which is/are the most likely mutational process/es explaining the pattern observed between the positions 1,417 and 1,438 (numbers according to the top bar of JalView).

- (●) Insertion and deletion
- ( ) Duplication and loss
- ( ) Point mutation
- ( ) Inversion

Esborra la selecció

Calculate and report the % of sites in the alignment that are gaps

26.1%

By looking at the results of the protein domain analyses, which molecular function would you assign to this set of sequences?

- ( ) Protein binding
- ( ) Catalytic activity
- (●) Extracellular matrix
- ( ) Electron transport

Esborra la selecció

Look at the 'Domain' and 'Repeat' rows at Interpro results. List all the differences that you find, if any, between the three queried sequences.

Annotate the **ungaped** positions that you want to talk about. *Max.: 500 characters*

VWF is only present in 2 (position 31 to 88), Fib_collagen_C is present in all (positions 1196 to 1447), like the collagen repeat (various positions). There is a collagen triple helix repeat for all species except Bos Mutus (extends from position 99 to 388).

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Trimming questions

By looking at the initial part of the alignment (alignment positions 70 to 163), you will see that there is a conserved region shared between some sequences.

Based on the InterProScan results, can you identify which matches (domain, repeat...) corresponds to this region?

Hint: To check the position of the aligned amino acid in the unaligned protein sequence look at the information displayed at the bottom left of the JalView software.

- [ ] Non cytoplasmatic domain
- [ ] None of them
- [x] Collagen triple helix repeat

How many sites have been trimmed in relation to the original alignment?

674

What could be the benefit from having trimmed a fraction of the alignment? Are there any potential drawbacks associated with this process?

- [ ] By trimming the alignment, there will be less informative sites, and this will always increase the computational time needed by the phylogenetic inference software to compute a phylogeny
- [x] By trimming the alignment, we may have removed informative signal
- [x] In general, we can expect alignment trimming to reduce computational time of the phylogenetic inference
- [ ] Trimming the alignment will always improve the accuracy of the phylogenetic inference

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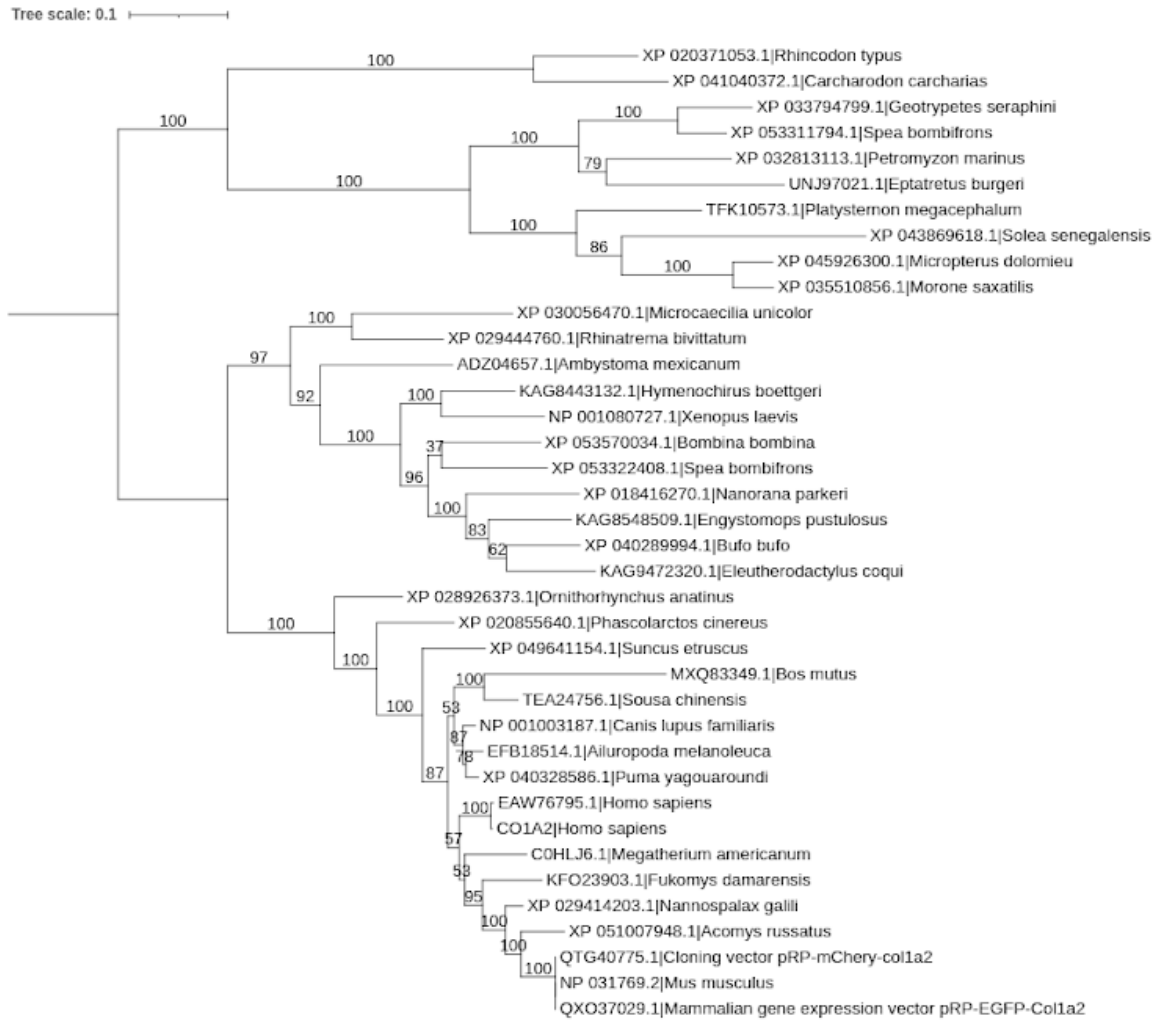
Tree inference

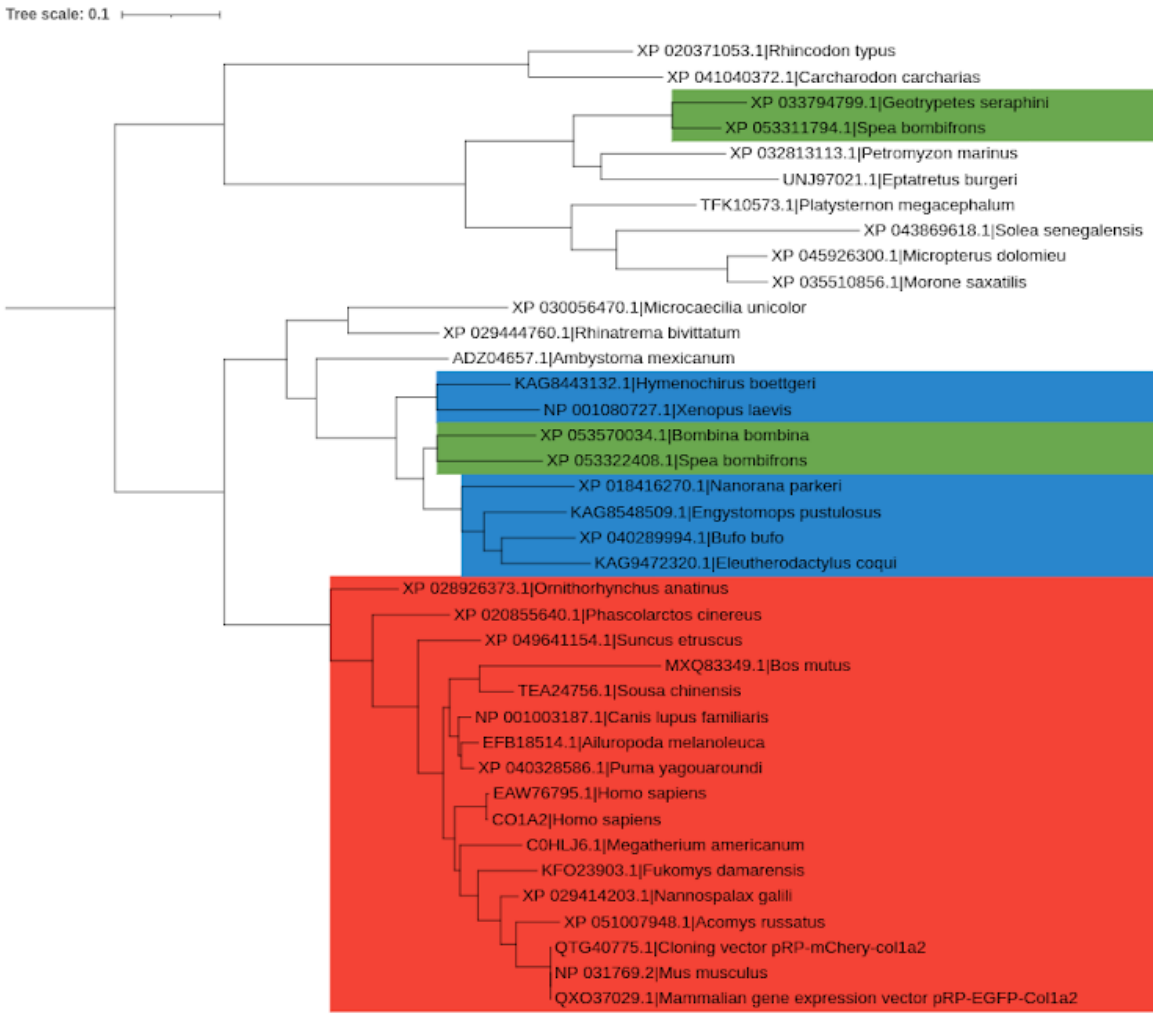
Which of the following branches would you trust the least?



- ○ The branch separating Rhinatrema bivittatum and Microcaecilia unicolor
- ◉ The branch separating Spea bombifrons and Bombina bombina
- ○ The branch separating the two human sequences
- ○ The branch separating Megatherium americanum and its sister group

Esborra la selecció

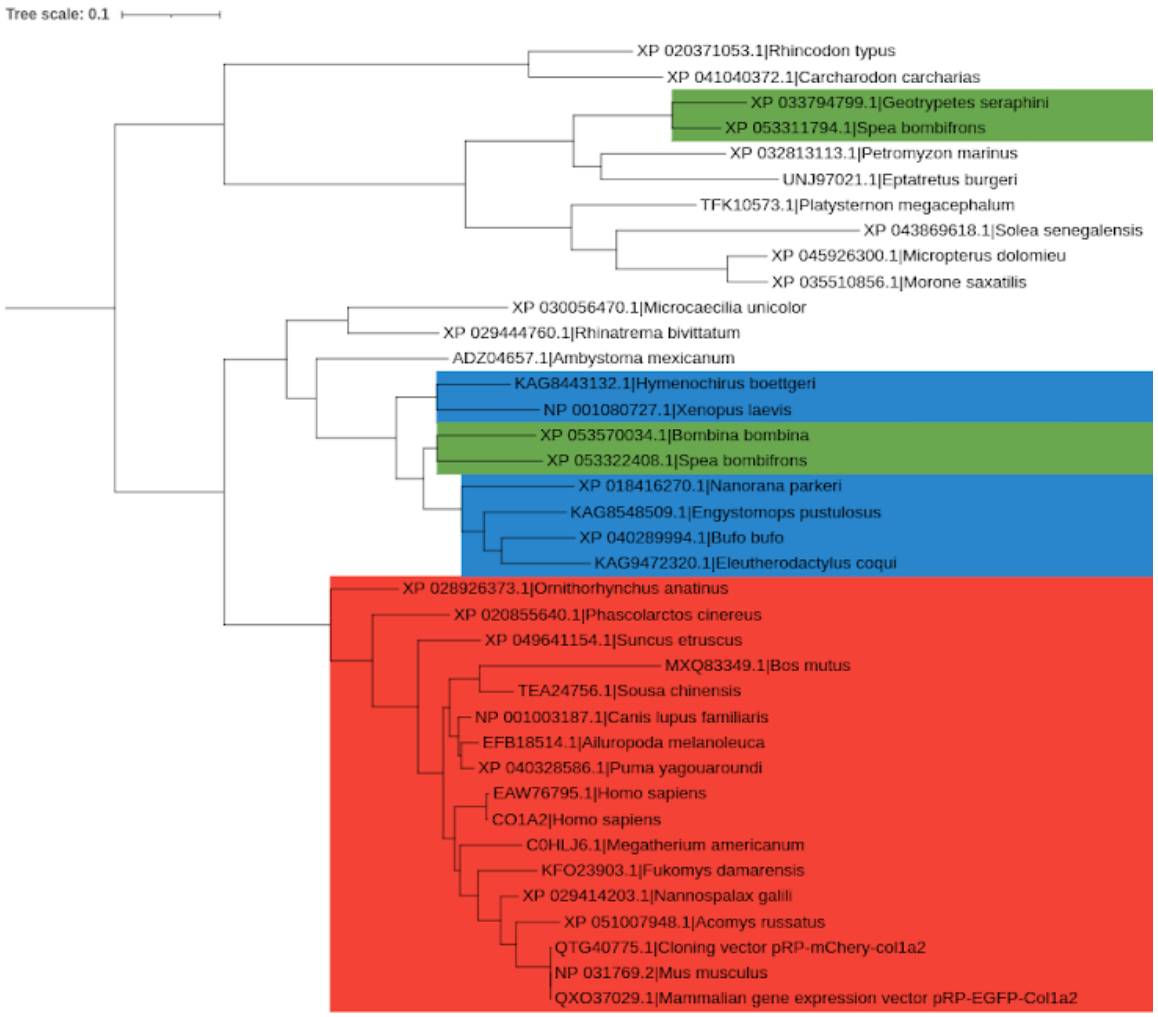
The red group is:



- ○ Paraphyletic
- ○ Polyphyletic
- ◉ Monophyletic

Esborra la selecció

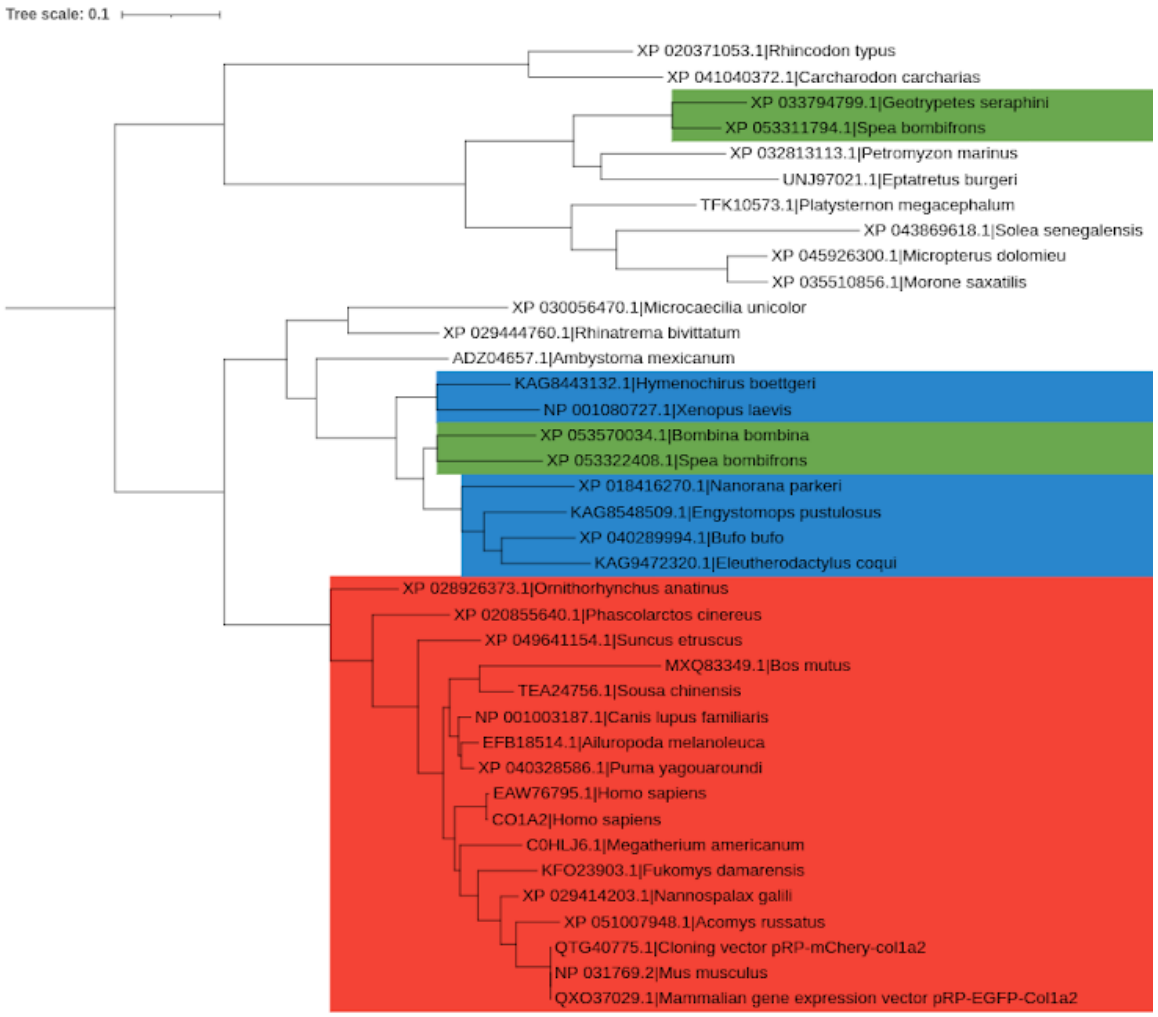
The blue group is:



- ○ Monophyletic
- ◉ Paraphyletic
- ○ Polyphyletic

Esborra la selecció

The green group is:

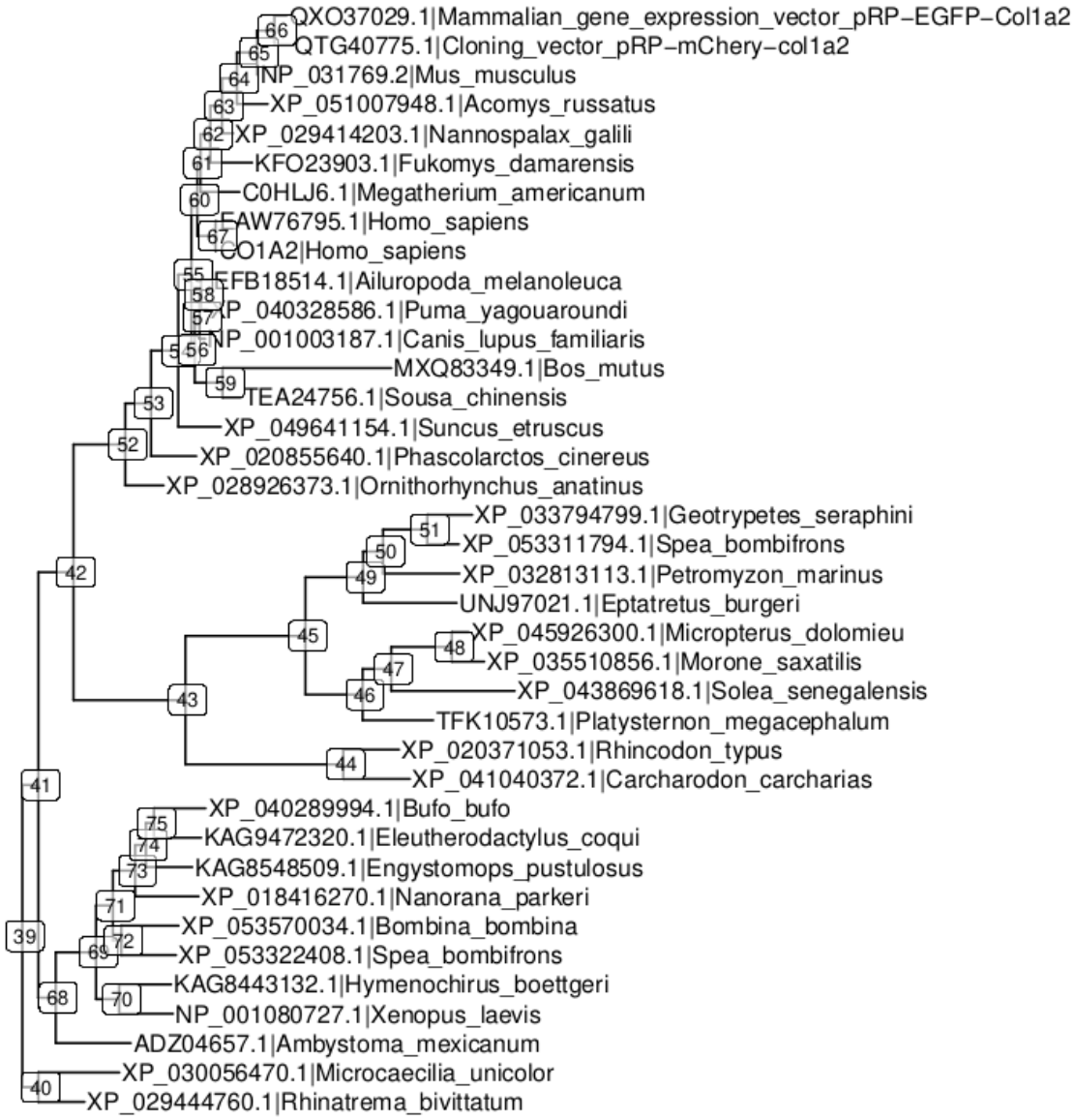


- ○ Paraphyletic
- ◉ Polyphyletic
- ○ Monophyletic

Esborra la selecció

Identify nodes that correspond to species-specific duplications

Write the number of the node/ nodes in the figure using the following format: XX, XX, XX, XX, ...



67, the only one where the specie is mantaine

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