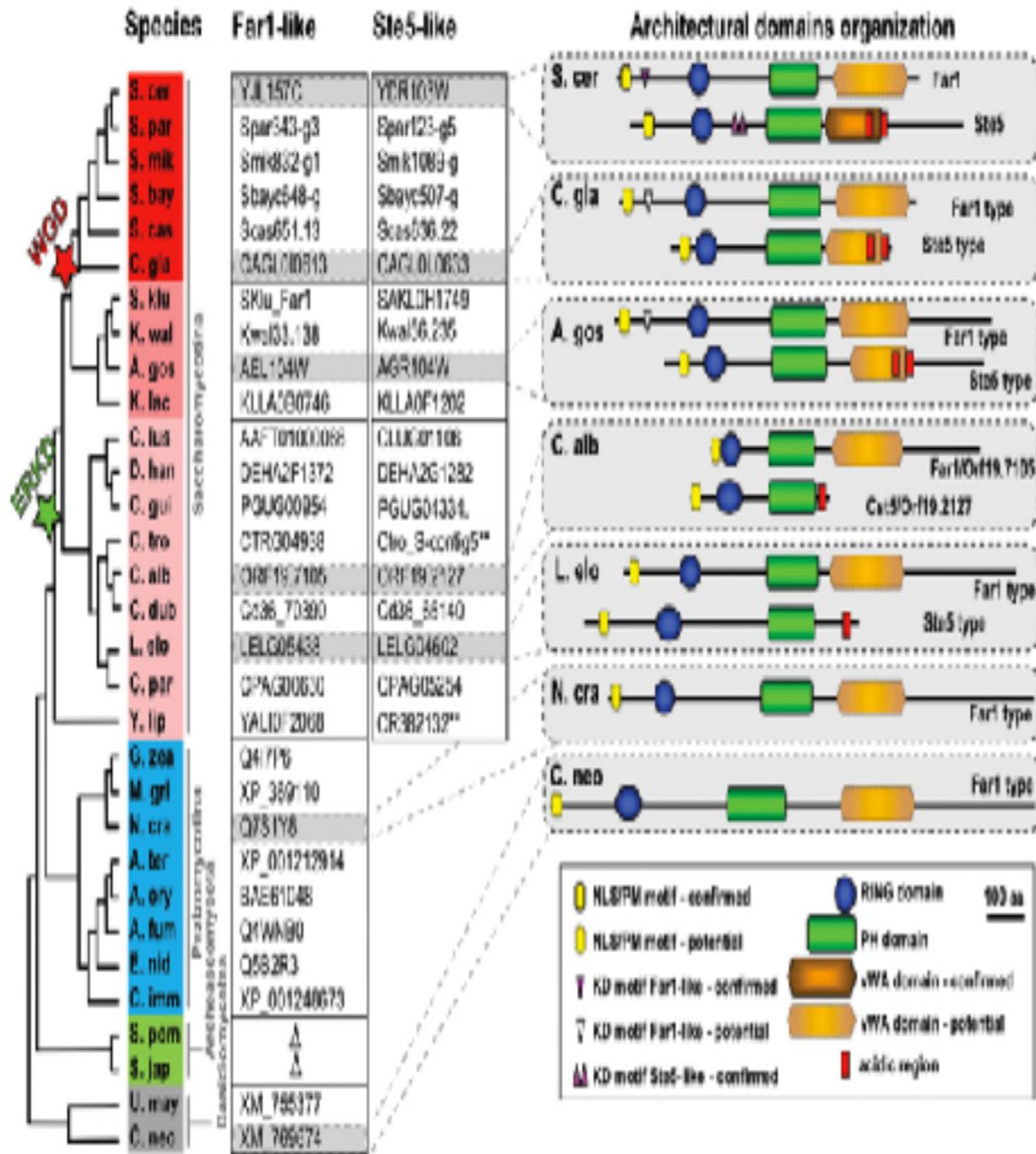


# Evolution of Yeast Scaffolding Proteins: Far1 and Ste5

Jilong Yu

# Background(A past research):

Côte et al. 2011. Evolutionary reshaping of fungal mating pathway scaffold proteins.



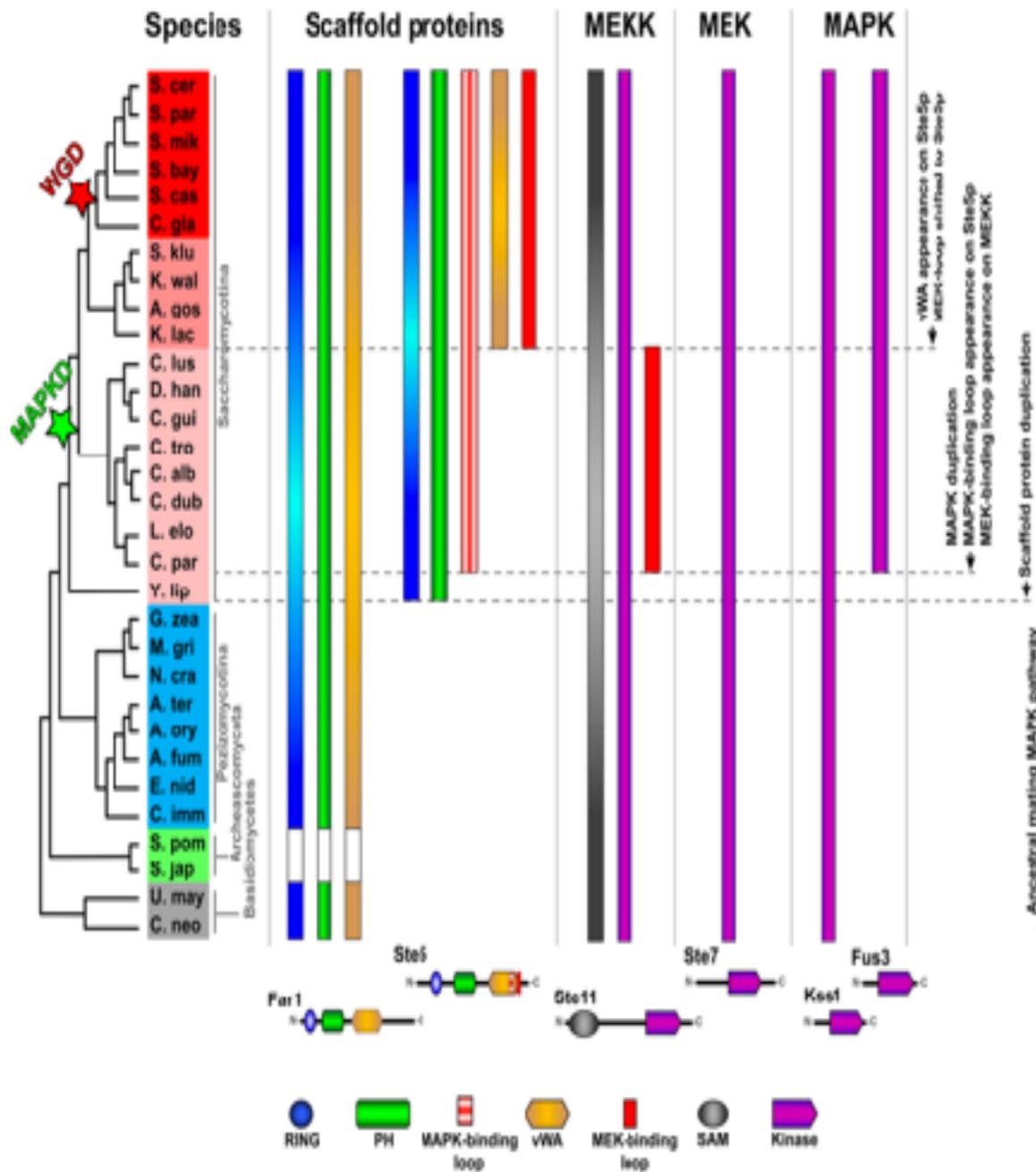
- Far1 and Ste5 are scaffolding proteins in mating pathway of *Saccharomyces cerevisiae* the Baker Yeast. Structurally similar proteins are found within the fungal kingdoms.

- Basidiomycetes(gray) and Pezizomycotina (blue) has only Far1 like proteins, while Saccharomycotina(red and pink) has both Far1 like and Ste5 like proteins.

- Based on structural differences of these scaffolding proteins and protein protein interaction study, the author propose an interpretation of evolutionary history of the proteins.

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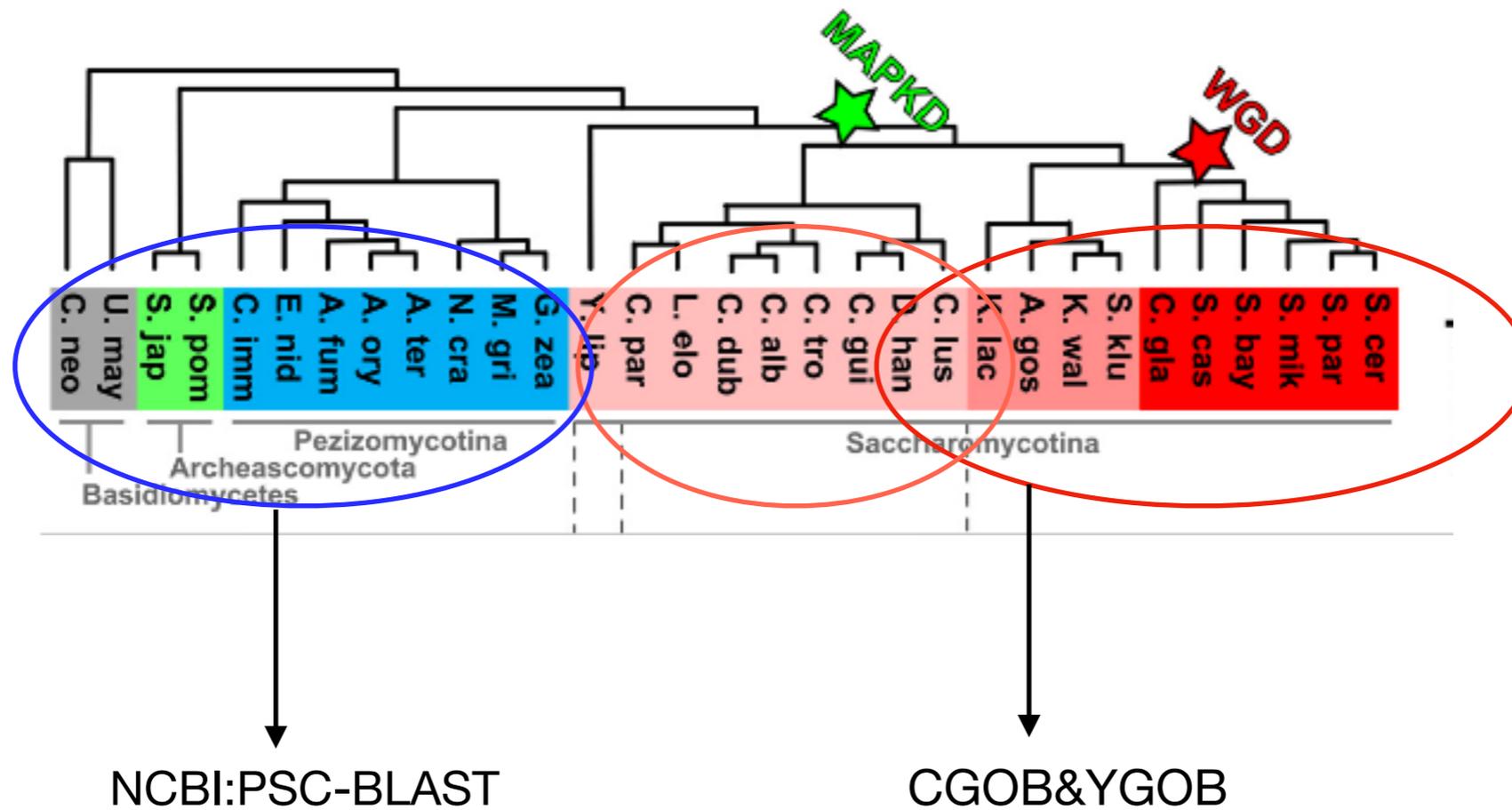


- A previous idea: Previous study with *Candida albicans* reveals that loss of function of its Far1p would cause loss of almost all of its scaffolding function. Which is not the case in *S.cer*. A hypothesis say Ste5 originates from duplication and subfunctionalization of Far1.

- New findings and idea: The author found that there are multiple changes in the structural organization of the MAPK pathway, Ste5-like scaffolding is more functional conserved than structurally conserved, therefore suggesting all Ste5-like proteins originates from the duplication in the ancestor of Saccharomycotina.

- My doubt and purpose: Its not very convincing by either structural analysis or functional analysis. Phylogenetic analysis should be provided to either support or deny it.

## Sequence Retrieval:

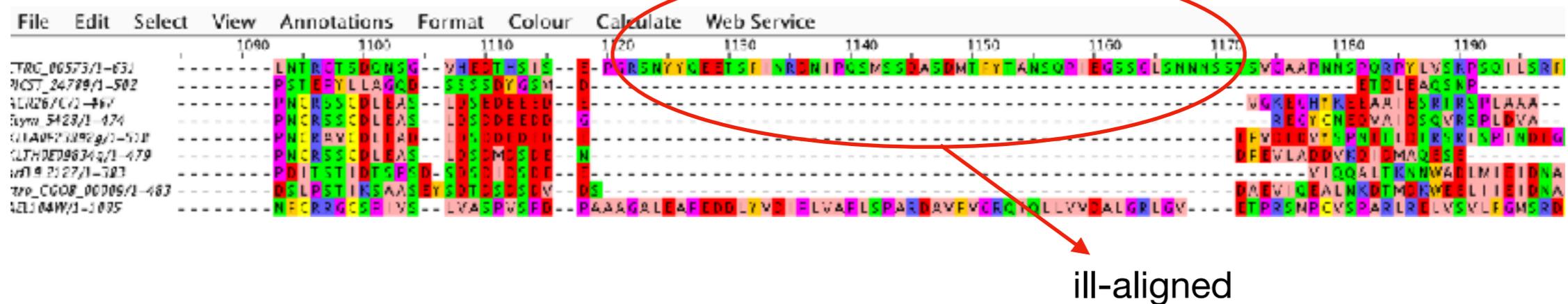


I could not find exactly the same set of sequences as in the paper. However, the purpose is to confirm if there the duplication happens in the ancestor of Saccharomycotina or after the speciation of candida.

# Sequence Preprocessing:

Problems:

1. Can't identify the species of some sequences
2. Should remove redundant sequences.
3. Some sequences can't be well aligned.
4. Balance the number of sequences in different species group.



Tip: We can also identify the inappropriate sequences by looking at overview window or alignment tree.

## Sequence Preprocessing:

Raw Sequences:

- 1.Far1-like YGOB
- 2.Far1-like CGOB
- 3.Far1-like Baz\_Pez
- 4.Ste5-like YGOB
- 5.Ste5-like CGOB
- 6.Ste5-like Baz\_Pez

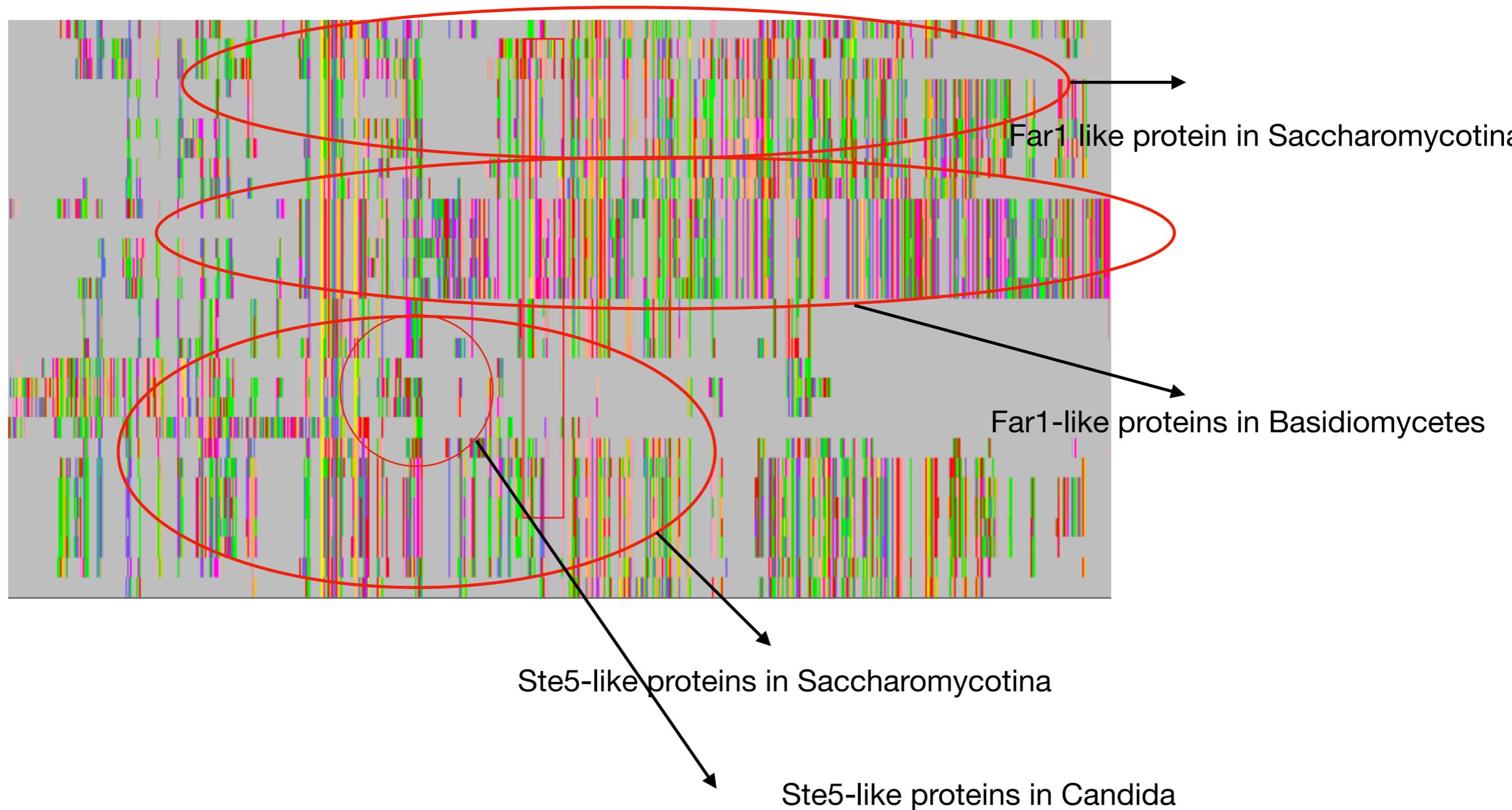
Process:

- 1.recursively align using accuracy oriented Mafft in Jalview.
- 2.delete ill-aligned sequences
- 3.remove redundancy
- 4.combine files and balance sequence number.

All Sequences file:29 sequences

## Alignment:

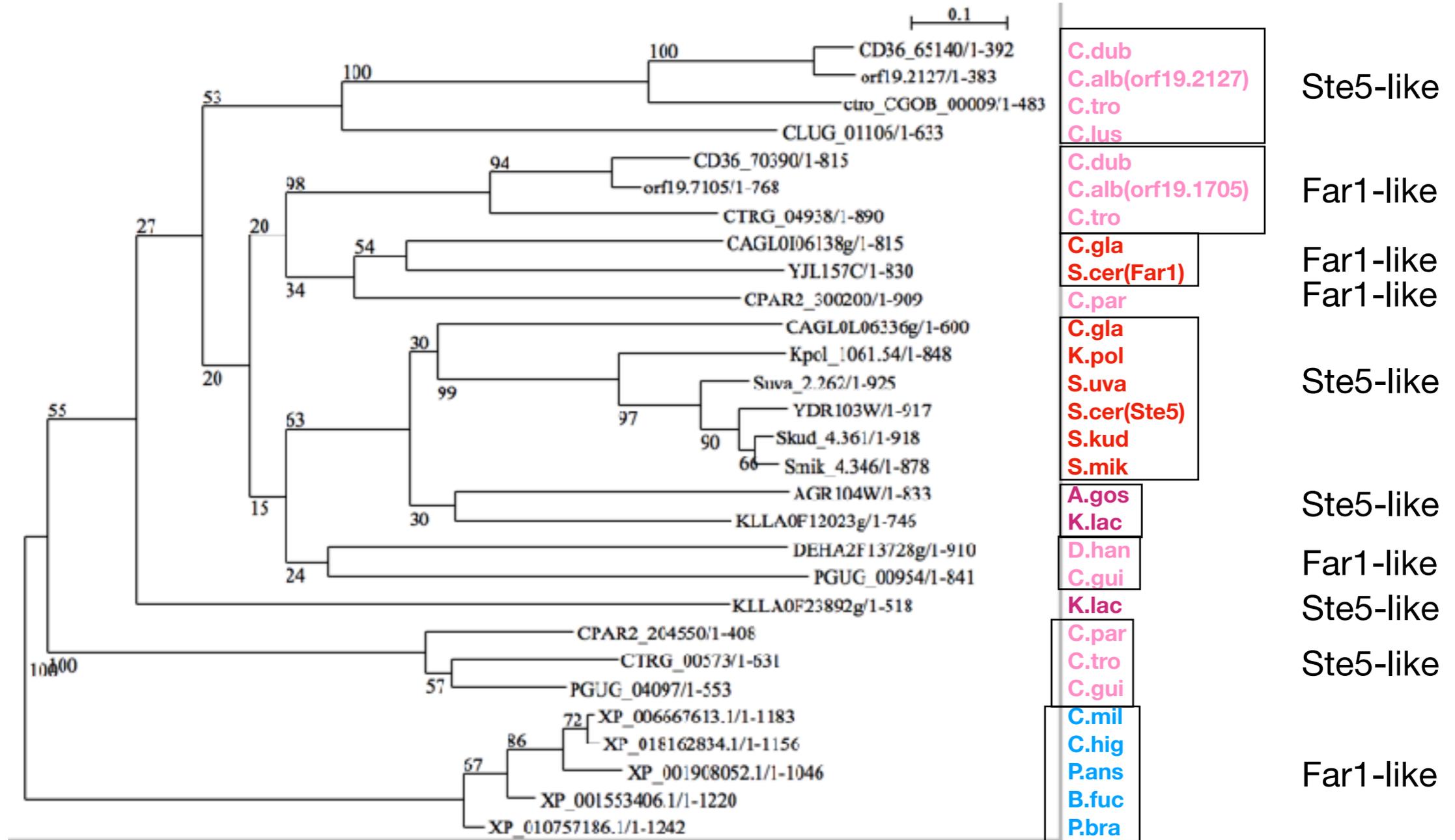
In the last step of processing, using Accuracy oriented Mafft for alignment of all 29 sequences



# Tree building:

Use Seaview – Tree – Distance Method – bootstrap 100 replicates

\* can't use too many bootstrap replicates, some sequences are too distant



# Questions