context

Based on this paper (http://www.plantphysiol.org/content/183/2/637/tab-figures-data#fig-data-additional-files) we want to see in what category our Azolla MYC-likes fall, perhaps reproduce some trees and check if the shared domains coïncide with what is described in the paper.

this notebook

In the previous notebook, I confirmed I can align and differentiate the two subfamilies of sequences based on the J&R paper. Here I'm correcting some minor mistakes, and I'm adding some extra sequences of interest.

0 Acquire data

As in step 1

- **CHBRA15G00250 Cbrduo1 -> "g8575"**
- **LC221833 CauDUO1**
- **LC221832 CleDUO1**
- **GFZG01001741.1**
- **Mapoly0017s0071**
- **XM_024688710.1**
- **XM_024668389.1**
- **Sacu_v1.1_s1503.g028048**
- **Sacu_v1.1_s0147.g023157**
- **MA_130648g0010**
- **AmTr_v1.0_scaffold00111.43**

And for Subfamily VII

- DN3051_co_g1_i1
- **HAOX-0009745**
- **Mapoly1089s0002**
- **MN199011**
- **Sacu_v1.1_s0002.g001222**
- **Sacu_v1.1_s0041.g012546**
- **Sacu_v1.1_s0272.g027033**
- **MA_96853g0010**
- **MA_10208000g0010**
- **MA_20462g0010**
- **AmTr_v1.0_scaffold00038.91**
- **AmTr_v1.0_scaffold00037.85**

Changed in step 2

Added: Azolla MYB like sequences and Arabidopsis GAMYB: MYB33. Azolla sequences were retrieved from fernbase.org; the arabidopsis sequence from uniprot.

Second I'm replacing `XM_024688710` with `XM_024688730.1 1`. This was a typo in the last itteration of this workflow. Also I'm removing `GFZG01001741.1_rf_1_GFZG01001741.1_TSA` for this sequences behaves oddly in the tree and doesn quite fit in the alignment. I think it is something different that doesn't belong here.It was an algeal sequence so I might be too cautious here...

Now to proceed, let's

1. ~~Acquire data~~
2. linearise and combine
3. allign
4. identify domains
5. add Azolla sequences and repeat.
6. for the fun of it, make a phylogenetic tree

   I'm using code from my phylogenetics workflow here https://github.com/lauralwd/lauras_phylogeny_wf/blob/master/tree_building_workflow.ipynb (https://github.com/lauralwd/lauras_phylogeny_wf/blob/master/tree_building_workflow.ipynb)

Clean-up. Since I'm not having version2 or v3 appendices, I'm cleaning up old files to prevent confusion. These may still be retrieved from git history.

In [9]:
```
rm data/alignments_raw data/alignments_trimmed data/*_linear.fasta -rf analyses
```

1 linearise and combine

In [6]:
```
tree
```

```
.
├── data
│   ├── Azfi-v1-MYB-sequences.fasta
│   ├── MYB33_ARATH.fasta
│   ├── VII_sequences.fasta
│   └── VI_sequences.fasta
├── docs
│   └── step1_differentiate_subfamilies_VI_and_VII.html
├── envs
│   ├── conda-env-jalview.yaml
│   └── conda-env-phylogenetics.yaml
├── figures
│   └── VI-vs-VII_alignment_v1.png
├── step1_differentiate_subfamilies_VI_and_VII.ipynb
└── step2.ipynb

4 directories, 10 files
```

In [10]:
```
for i in data/*fasta
do  inseq=$(echo $i | cut -d '/' -f 2 | cut -d '.' -f 1)
    cat data/$inseq.fasta \
     | awk '/^>/ {printf("%s%s\n",(N>0?"\n":""),$0);N++;next;} {printf("%s",$0);} END {printf("\n");}' \
     > data/"$inseq"_linear.fasta
done
```

In [11]:
```
#cat data/*_sequences_linear.fasta > data/combi_sequences_linear.fasta
cat data/VII_sequences_linear.fasta | sed 's/>/>VII_/' > data/combi_sequences_linear.fasta
cat data/MYB33_ARATH_linear.fasta data/Azfi-v1-MYB-sequences_linear.fasta >> data/combi_sequences_linear.fasta
cat data/VI_sequences_linear.fasta | sed 's/>/>VI_/' >> data/combi_sequences_linear.fasta
head data/combi_sequences_linear.fasta
```

```
>VII_HAOX-0009745
GLKKGPWTAEEDVILSEYVMKHGEGNWNLIQKNTGLPRCGKSCRLRWANHLRPNLKKGAFSREEEALVIKLHAEIGNKWARMALQLPGRTDNEIKNFWNTRIKRRIRAGLPLHST
DLVLCPIATTTPFREKLTEYMEESRDTKPIDRDSDDCDGHTNSAHVKESSQT
>VII_Mp3g05910.1
MELGSAPDFSEDVGALKKGPWTSAEDAILVAYVTKHGEGNWNSVQKHSGLYRCGKSCRLRWANHLRPNLKKGAFTPEEERMIIELHAKLGNKWARMAAQLPGRTDNEIKNYWNTR
IKRRMRAGLPVYPPEMQNPAANSQYLFEHGEMSMSSGGESECDPGSSPSTGDFQNLSVSGMHGGCRMKSCSSLTGMSDLPLSSVVTQTLSAGQSISSPGRRMKRMHRDTQCSSMS
GASGGGGLFPQLSDESSKTMPYFKARRSCGTRNSMRLAQIAGFPYDPDPEGLHFEGMPNHGYLNLPPFSCSRPNSSLKLELPSSQSAESADSAGTPGSAMTSPYTAFSLPQNHHL
LSSEADSFGSNNSNNSSFLQALLQEAQNLDPGRDQIRSAELSDQLLVLTSANPPMDVSALMSPRKSRWGEDSDPTTPLEGRTYSMFSEDTSPNCTSNWDETSTLQSPLTTVSSNL
QAAHVGGLKIENSAQHDMPCGNYGDEENLISSLLDFARPDATPVVEWYNPPDVYTLGGQPCHSLPEAIEAAFHHQDVVAELEHLGAAGHPVANHVWELGSCPWNNMPGVCQLGDL
PTDCRPLTSIADQMNDPCAIC
>VII_ENA|MN199011|MN199011.1 Selaginella moellendorffii
MGDPMQGGVAAAAALELCEEGRGRGGGGGAVKGLKKGPWTPSEDAILVAYVHKHGEGNWNNVQKNCGLSRCGKSCRLRWANHLRPNLKKGAFTPEEERTIIELHAKLGNKWARMA
SQLPGRTDNEIKNYWNTRIKRRMRAGLPVYPPDLQDLCSNLARGGHHRKEAQDDHYLGHHHNQVVVSSSTSSKSSNSNNSSRKSGGILIAAAKNSHDHPSSIATSSYYNDDGARG
DDHHDDFAAAYHHHRLLEQINQQHQQQSQPESTSESYGSNSGGSGGGNFLRDVLFHQDHQAQRDHDHHSPDEQPLVYGKSSAANEEGIYQLRLFEVWDEDQVEQTTTATTFRGGL
VYPDEDFYALLELESQMPGPPPELIPVPVNLLSYSSGLNHPANLALMFQGEMIPALNSPSTTQLNCYPCLYNRDELPDLYQQQQQQLMWD
>VII_Sacu_v1.1_s0002.g001222 Myb transcription factor [0.077]
MENRKVWDYEGRSTPKKSGKEKHDEGGRVQRKEHGLAAAEVMKKGPWTAEEDALLLAYVSKHGEGNWNSVQKNAGVMRCGKSCRLRWTNQLRPGLKKGSLTPQEERLVIEQHALL
GNRWARIAAMLPGRTDNEIKNFWNTRMKRNLRAGKPLYPADVKLVVKPAEPTVSNYDAAADWRRQQEEERGCGSAAATDREAARHDRMIHHPVETAGHALNSVQSRSRSTNFSFL
DMQPPGDLSFGMQFHSYYHSSKRPSYNAQIPAAIDSPSYFYSDHYDESSMFAHLFPNILEVQRGPEEHGLVPNGTFACAAACDNKDIMGANFNDCCSSSSSITSTRYPFYRSAYN
GSPESCLACHDAELPSVQMAESADSSSGLSSSASPFVFCNAVPLSEADSFGATNKESPIHKRNGNLVDVLHMIKQEVDASAAGGGDNIIVEDLDLELLVDTSCNASPTSSSNYKS
SVLSANNPLTLLGLTSVNDGDDFGTLLISEEDSELNLHTSRDTRDFAYQFPAAAGTELSHLKLKQQQADTIKSEGPSVSQYVDEELLTLLMLEKPDQGLPTVEFCNENANPVRPT
VNGESQEMIMSGQGELEAMLRYVYTQDSDAAEQVMIGSVTVGWGDGSFTWDKSLEIMDEFPSVVTDYVSPAGCSKISP
>VII_Sacu_v1.1_s0041.g012546 Myb transcription factor [0.077]
MERRLSSISHSAYLRRADDSVHTFQDMKEQEHLDHLYFQEFSEDQATPLKKGPWTAEEDALLLAYVSRHGDGNWNTVQKYSGVFRNGKSCRLRWTNHLRPNLKKGAFSPEEERII
IEQHAAIGNRWSRIAAMLPGRTDNEIKNFWNTRKKRRSRAGLPLYPASILLRPVAATGNATSTVASPPESIITSLQSQQQPQKENIASVNDHLQSVVDRTTNFLLNSSTDLFNAA
LCAAEAQGNAGKTLINAKRARDADDRTHCQRYSAYQTTPPIHEQAGQQSPIPVDSRSLHHQVVLPAPPDIMTTQNGYGDSLSFSNGGNESYRNEVNSCLPVSRELPSVQSTESAD
SSSGLSTSFTVTYQMLSLSEVDSFNRSAKCETLGSNDGNLLDVVLQQRDPEFHHLRLKTDGITEQQQQQEAQTLKTYCNCPSPRSLSQFDSDPLSFLGGRSLTLLSDDLNVAMES
EGVSSDGLLAAGEEVHGEHKQKEVTSSSLCIEQEEDELLTLLAFGRLDSMSFAGLYEEQGGSSSDAASMDPDEEFMNSGGGLEAMFANVHNDTATLDSSNTSWEQQQQLDSCLLW
NNMPGAVEGRVLLMKHSLRT
```

In [12]:
```
tree
```

```
.
├── data
│   ├── Azfi-v1-MYB-sequences.fasta
│   ├── Azfi-v1-MYB-sequences_linear.fasta
│   ├── combi_sequences_linear.fasta
│   ├── MYB33_ARATH.fasta
│   ├── MYB33_ARATH_linear.fasta
│   ├── VII_sequences.fasta
│   ├── VII_sequences_linear.fasta
│   ├── VI_sequences.fasta
│   └── VI_sequences_linear.fasta
├── docs
│   └── step1_differentiate_subfamilies_VI_and_VII.html
├── envs
│   ├── conda-env-jalview.yaml
│   └── conda-env-phylogenetics.yaml
├── figures
│   └── VI-vs-VII_alignment_v1.png
├── step1_differentiate_subfamilies_VI_and_VII.ipynb
└── step2.ipynb

4 directories, 15 files
```

2 align

In [13]:
```
conda activate phylogenetics
if    [ ! -d ./data/alignments_raw/ ]
then  mkdir  ./data/alignments_raw
fi
for   i in data/*sequences_linear.fasta
do    inseq=$(echo $i | cut -d '/' -f 2 | cut -d '.' -f 1)
      if    [ ! -f "./data/alignments_raw/$inseq"_aligned-mafft-linsi.fasta ]
      then  linsi --thread $(nproc) data/$inseq.fasta > ./data/alignments_raw/"$inseq"_aligned-mafft-linsi.fasta \
                                                      2> ./data/alignments_raw/"$inseq"_aligned-mafft-linsi.log
      fi
done
conda deactivate
```

```
(phylogenetics) (phylogenetics) (phylogenetics)
```

In [14]:
```
tree data
```

```
data
├── alignments_raw
│   ├── Azfi-v1-MYB-sequences_linear_aligned-mafft-linsi.fasta
│   ├── Azfi-v1-MYB-sequences_linear_aligned-mafft-linsi.log
│   ├── combi_sequences_linear_aligned-mafft-linsi.fasta
│   ├── combi_sequences_linear_aligned-mafft-linsi.log
│   ├── VII_sequences_linear_aligned-mafft-linsi.fasta
│   ├── VII_sequences_linear_aligned-mafft-linsi.log
│   ├── VI_sequences_linear_aligned-mafft-linsi.fasta
│   └── VI_sequences_linear_aligned-mafft-linsi.log
├── Azfi-v1-MYB-sequences.fasta
├── Azfi-v1-MYB-sequences_linear.fasta
├── combi_sequences_linear.fasta
├── MYB33_ARATH.fasta
├── MYB33_ARATH_linear.fasta
├── VII_sequences.fasta
├── VII_sequences_linear.fasta
├── VI_sequences.fasta
└── VI_sequences_linear.fasta

1 directory, 17 files
```

In [26]:
```
conda activate jalview
for   i in data/alignments_raw/*aligned*.fasta
do    prefix=$(echo $i | sed 's/\.fasta//')
      jalview -nodisplay \
              -open $prefix.fasta \
              -colour CLUSTAL \
              -png  $prefix.png > /dev/null 2> /dev/null
done
conda deactivate
```

```
(jalview) (jalview)
```

intermediate conclusions

Already from the alignments, I can see that one Azolla sequence shouldn't be in here so I ~~will remove~~ have removed that and reordered the alignment to place the Azolla sequences in the middle of the two subdomains.

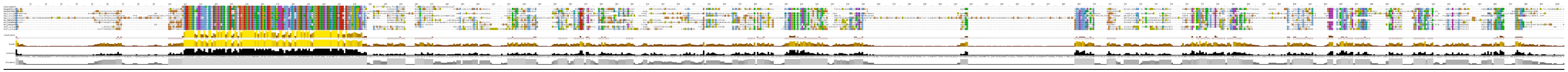
3 Identify domains

reproducing Jiang & Rao

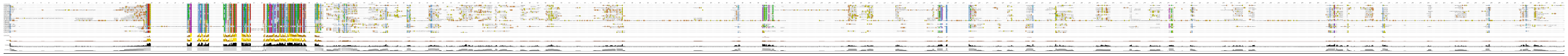
linsi alignments

Now let's look at the linsi alignments. If I open them in jalview, I get something like this for VI.

VII

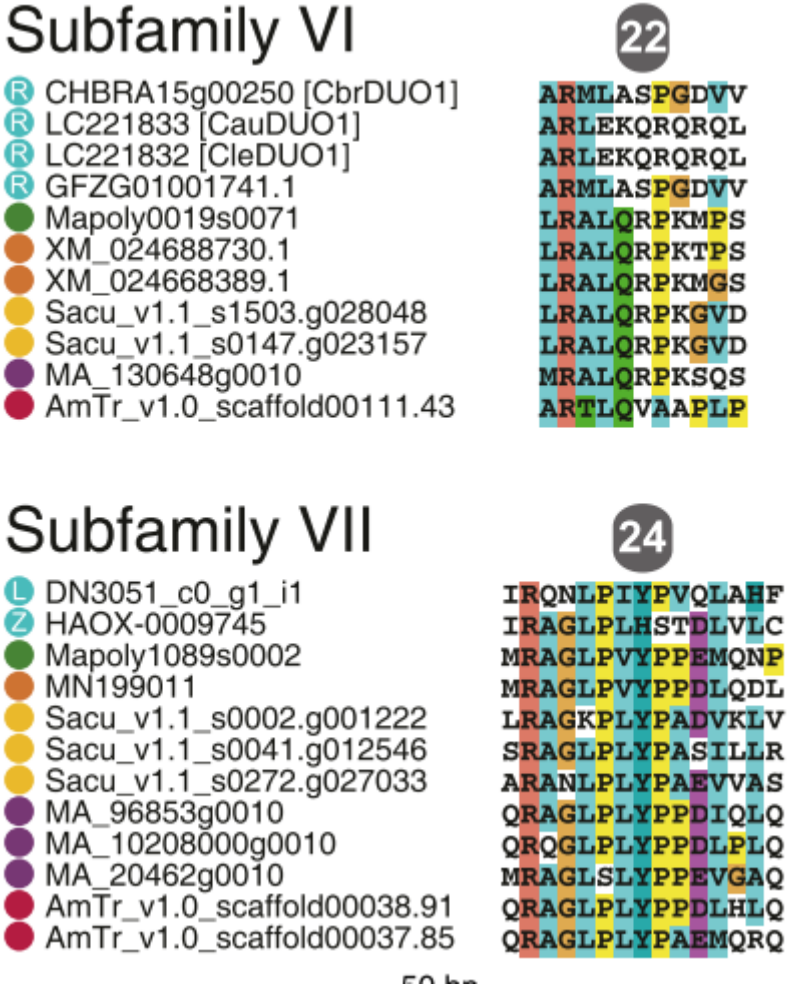


and both combined



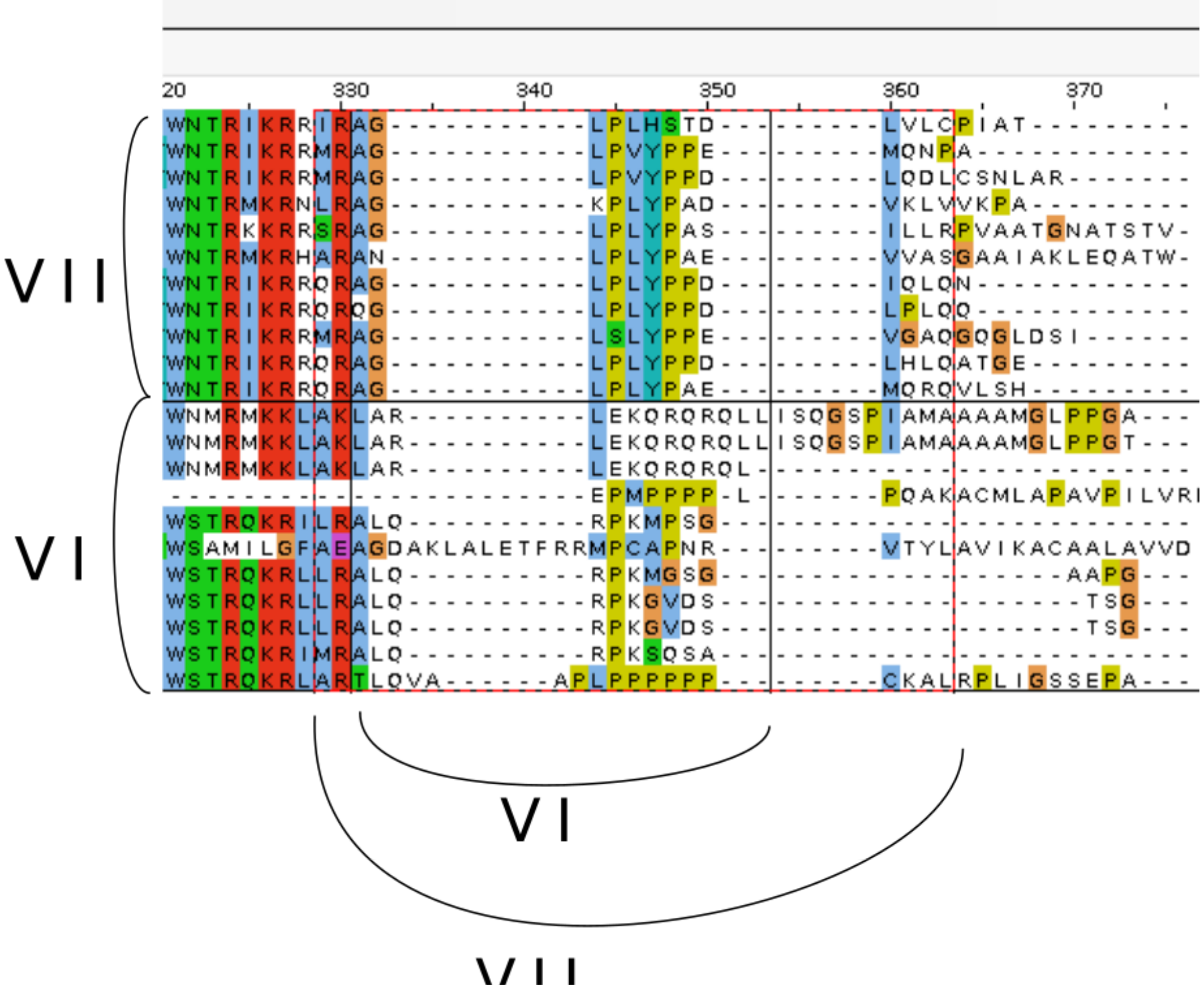
There are clearly conserved domains, and especially in VI, there is a super long tail of extra sequence in one of the rows.

And I'm looking for these...

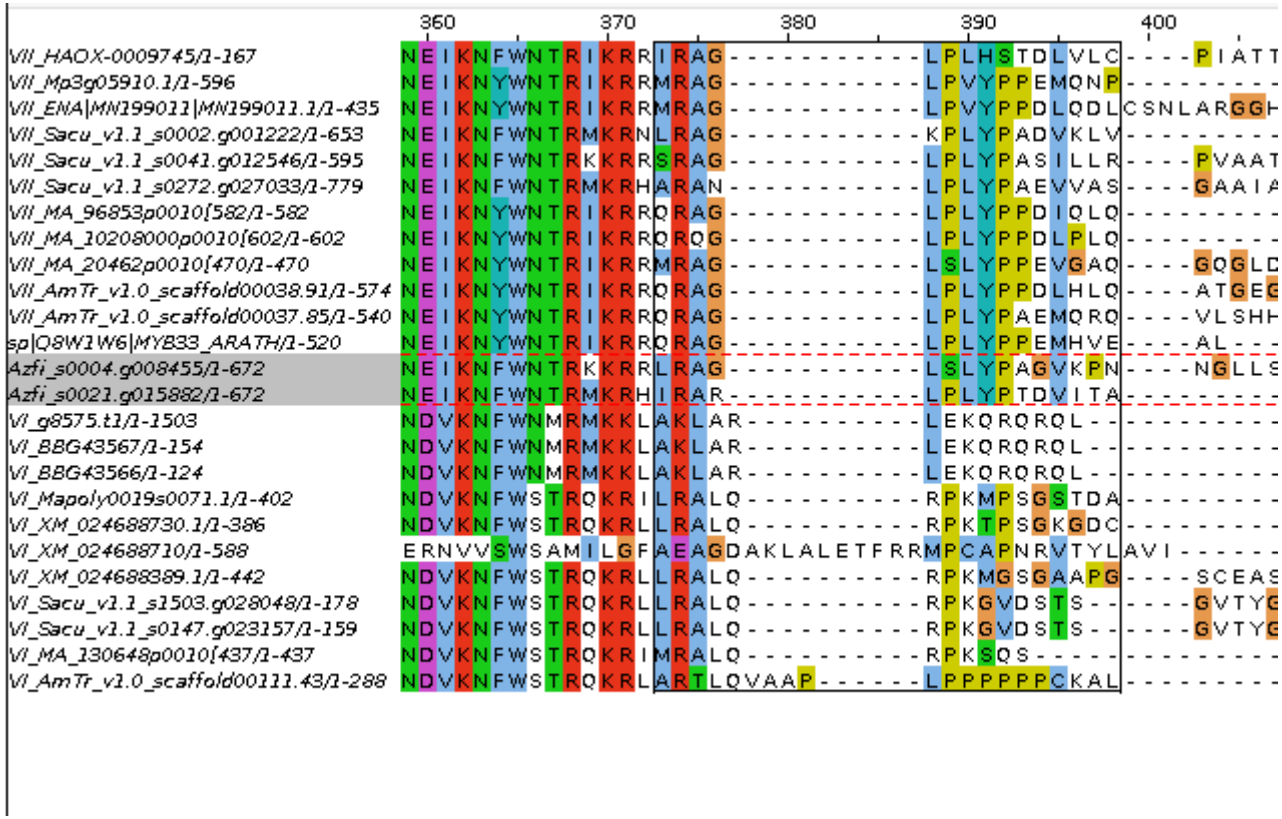


combi alignment from step1

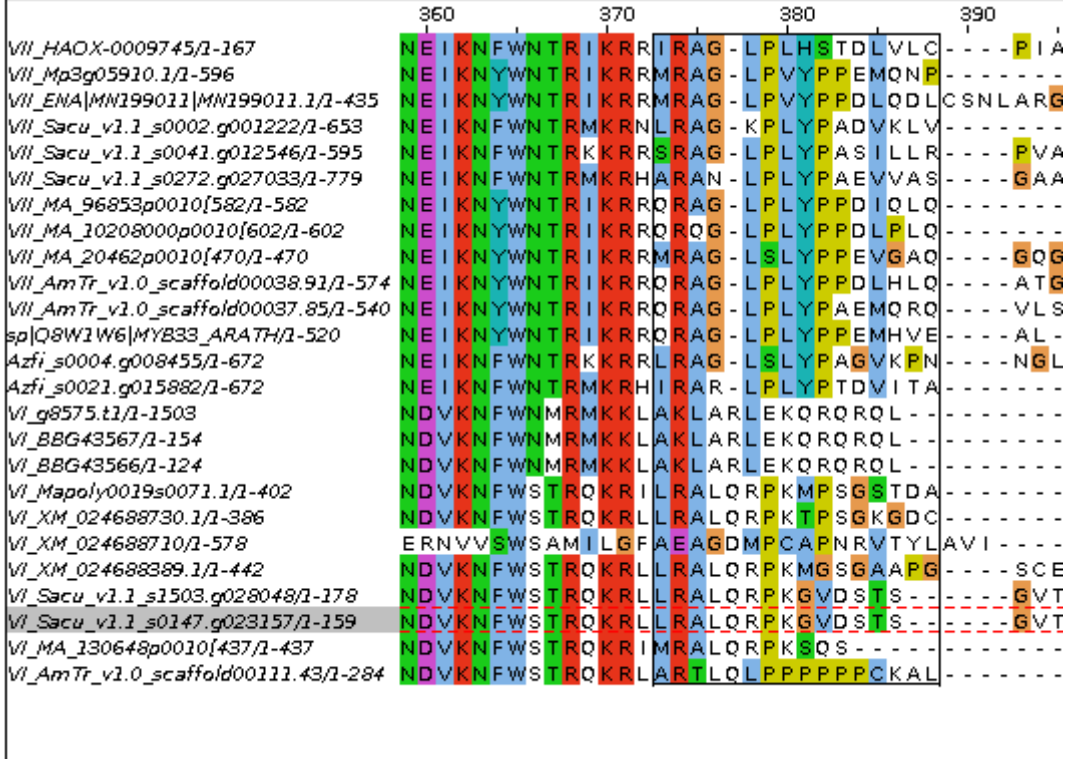
Now let's have a look at the combi alignment, to see if we can actually overlap these regions and use them to differentiate between the two subfamilies.


20
330
340
350
360
370
VII
VI
VI
VII

Now let's have a look at the analysis done above but with our two *Azolla* sequences of interest, and one Arabidopsis sequence.



When I boldly remove that gap that seems to split up this differentiating domain, it looks like so:



Just this alignment indicates that the Azolla sequence sof interest belong to the VII subfamily

The XM....710 sequence is still in, I thought I had removed it but somehow I managed to keep it in there... I won't change that now but remove the sequence from the tree instead.

4. Combi alignment with Azolla sequences

as done above

5. phylogeny

Now let's run the phylogenies again on these two new alignments

5.1 trimming

In [18]:
```
conda activate phylogenetics
if    [ ! -d data/alignments_trimmed ]
then  mkdir  data/alignments_trimmed
fi

# define appendix only once here:
trimappendix='trim-gt4'

inseq=combi_sequences_linear
for a in "data/alignments_raw/$inseq"_aligned*.fasta
do  appendix=$(echo $a | cut -d '/' -f 3- | sed "s/$inseq\_//" | sed "s/.fasta//")
    if    [ ! -f data/alignments_trimmed/"$inseq"_"$appendix"_"$trimappendix".fasta ]
    then  echo "trimming alignment $a"
          sed -i 's/ /_/g' $a
          trimal -in $a   \
                 -out data/alignments_trimmed/"$inseq"_"$appendix"_"$trimappendix".fasta \
                 -gt .4 \
                 -htmlout data/alignments_trimmed/"$inseq"_"$appendix"_"$trimappendix".html
    fi
done
conda deactivate
```

```
(phylogenetics) (phylogenetics) (phylogenetics) (phylogenetics) (phylogenetics) (phylogenetics) (phylogenetics) tri
mming alignment data/alignments_raw/combi_sequences_linear_aligned-mafft-linsi.fasta
(phylogenetics)
```

In [25]:
```
conda activate jalview
for   i in data/alignments_trimmed/*.fasta
do    prefix=$(echo $i | sed 's/\.fasta//')
      jalview -nodisplay \
              -open $prefix.fasta \
              -colour CLUSTAL \
              -png  $prefix.png > /dev/null 2> /dev/null
done
conda deactivate
```

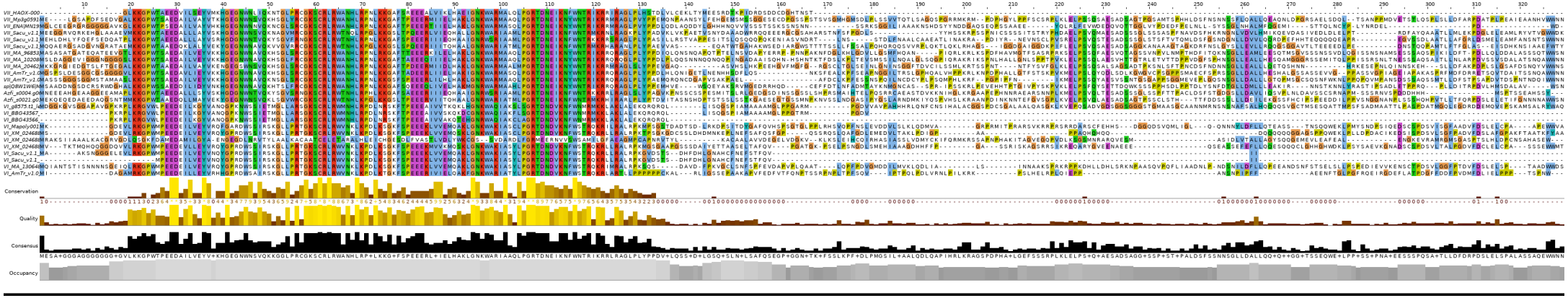
```
(jalview) (jalview)
```

In [22]:
```
tree data/alignments_trimmed
```

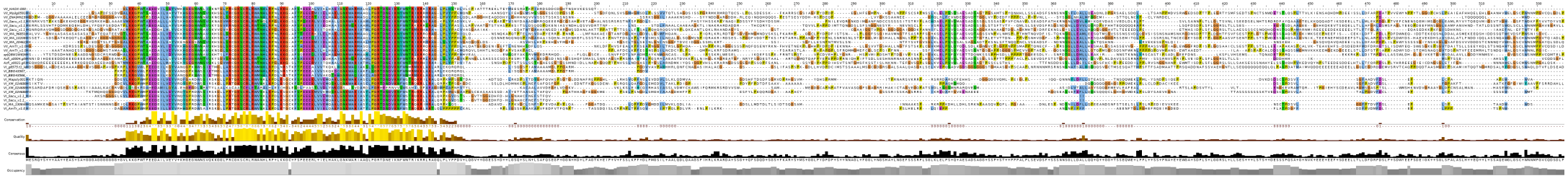
```
data/alignments_trimmed
├── combi_sequences_linear_aligned-mafft-linsi_trim-gt4.fasta
├── combi_sequences_linear_aligned-mafft-linsi_trim-gt4.html
├── combi_sequences_linear_aligned-mafft-linsi_trim-gt4.png
├── combi_sequences_linear_aligned-mafft-linsi_trim-gt6.fasta
├── combi_sequences_linear_aligned-mafft-linsi_trim-gt6.html
└── combi_sequences_linear_aligned-mafft-linsi_trim-gt6.png

0 directories, 6 files
```

For gap threshold 60%



For gap threshold 40%



All allignments contain the differentiating domain as published in J&R. 40% is too gappy for my taste, so I will take the 60% all for tree inference. However, supervisor will like 40% better so I'll run that too.

5.2 tree inference

In [27]:
```
inseq=combi_sequences_linear
echo $inseq
```

```
combi_sequences_linear
```

In [28]:
```
ls data/alignments_trimmed/"$inseq"_aligned*gt[46].fasta
```

```
data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt4.fasta
data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt6.fasta
```

In [29]:

```
conda activate phylogenetics
for a in data/alignments_trimmed/"$inseq"_aligned*gt[46].fasta
do  #iqpendix='iqtree-b100'
    iqpendix='iqtree-bb2000-alrt2000'

    echo "making a tree of file $a"
    echo "The first lines of alignment $a look like this"
    head $a

    file_appendix=$(echo $a | cut -d '/' -f 3- | sed "s/$inseq\_//" | sed "s/.fasta//")

    if   [ ! -d    analyses/"$inseq"_trees/"$file_appendix" ]
    then echo "Making a directory $file_appendix to store trees (name based on alignment filename)"
         mkdir -p  analyses/"$inseq"_trees/"$file_appendix"
    fi

    iqprefix=analyses/"$inseq"_trees/"$file_appendix"/"$inseq"_"$file_appendix"_"$iqpendix"
    if   [ ! -f "$iqprefix".tree ]
    then nice iqtree -s $a \
                     -m MFP \
                     -bb 2000 -alrt 2000 \
                     -nt AUTO \
                     -ntmax $(nproc)  \
                     -pre  "$iqprefix" \
                     2>   "$iqprefix".stderr \
                      >    "$iqprefix".stdout
    #cat "$iqprefix".log | mail -s "IQtree_run $a" laura
    fi
done
conda deactivate
```

```
(phylogenetics) making a tree of file data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt4.f
asta
The first lines of alignment data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt4.fasta look
like this
>VII_HAOX-0009745
---------------------------------GLKKGPWTAEEDVILSEYVMKHGEGN
WNLIQKNTGLPRCGKSCRLRWANHLRPNLKKG-AFSREEEALVIKLHAEIGNKWARMALQ
LPGRTDNEIKNFWNTRIKRRIRAG-LPLHSTDLVLCPIATTTREKLTEYMEESRDTKPID
RDSDDCDGHTNSHVKESSQT----------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
Making a directory aligned-mafft-linsi_trim-gt4 to store trees (name based on alignment filename)
making a tree of file data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt6.fasta
The first lines of alignment data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt6.fasta look
like this
>VII_HAOX-0009745
------------------GLKKGPWTAEEDVILSEYVMKHGEGNWNLIQKNTGLPRCGKS
CRLRWANHLRPNLKKGAFSREEEALVIKLHAEIGNKWARMALQLPGRTDNEIKNFWNTRI
KRRIRAGLPLHSTDLVLCEKLTYMEESRDTKPIDRDSDDCDGHTNST-------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------
>VII_Mp3g05910.1
ME----LGSAPDFSEDVGALKKGPWTSAEDAILVAYVTKHGEGNWNSVQKHSGLYRCGKS
CRLRWANHLRPNLKKGAFTPEEERMIIELHAKLGNKWARMAAQLPGRTDNEIKNYWNTRI
Making a directory aligned-mafft-linsi_trim-gt6 to store trees (name based on alignment filename)
(phylogenetics)
```

In [30]:

```
conda activate phylogenetics
for a in data/alignments_trimmed/"$inseq"_aligned*gt[46].fasta
do  iqpendix='iqtree-b100'
    #iqpendix='iqtree-bb2000-alrt2000'

    echo "making a tree of file $a"
    echo "The first lines of alignment $a look like this"
    head $a

    file_appendix=$(echo $a | cut -d '/' -f 3- | sed "s/$inseq\_//" | sed "s/.fasta//")

    if   [ ! -d    analyses/"$inseq"_trees/"$file_appendix" ]
    then echo "Making a directory $file_appendix to store trees (name based on alignment filename)"
         mkdir -p  analyses/"$inseq"_trees/"$file_appendix"
    fi

    iqprefix=analyses/"$inseq"_trees/"$file_appendix"/"$inseq"_"$file_appendix"_"$iqpendix"
    if   [ ! -f "$iqprefix".tree ]
    then nice iqtree -s $a \
                     -m MFP \
                     -b 100 \
                     -nt AUTO \
                     -ntmax $(nproc)  \
                     -pre  "$iqprefix" \
                     2>   "$iqprefix".stderr \
                      >    "$iqprefix".stdout
    cat "$iqprefix".log | mail -s "IQtree_run $a" laura
    fi
done
conda deactivate
```

```
(phylogenetics) making a tree of file data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt4.f
asta
The first lines of alignment data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt4.fasta look
like this
>VII_HAOX-0009745
---------------------------------GLKKGPWTAEEDVILSEYVMKHGEGN
WNLIQKNTGLPRCGKSCRLRWANHLRPNLKKG-AFSREEEALVIKLHAEIGNKWARMALQ
LPGRTDNEIKNFWNTRIKRRIRAG-LPLHSTDLVLCPIATTTREKLTEYMEESRDTKPID
RDSDDCDGHTNSHVKESSQT-----------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
------------------------------------------------------------
making a tree of file data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt6.fasta
The first lines of alignment data/alignments_trimmed/combi_sequences_linear_aligned-mafft-linsi_trim-gt6.fasta look
like this
>VII_HAOX-0009745
------------------GLKKGPWTAEEDVILSEYVMKHGEGNWNLIQKNTGLPRCGKS
CRLRWANHLRPNLKKGAFSREEEALVIKLHAEIGNKWARMALQLPGRTDNEIKNFWNTRI
KRRIRAGLPLHSTDLVLCEKLTYMEESRDTKPIDRDSDDCDGHTNST-------------
------------------------------------------------------------
------------------------------------------------------------
-----------------------------
>VII_Mp3g05910.1
ME----LGSAPDFSEDVGALKKGPWTSAEDAILVAYVTKHGEGNWNSVQKHSGLYRCGKS
CRLRWANHLRPNLKKGAFTPEEERMIIELHAKLGNKWARMAAQLPGRTDNEIKNYWNTRI
(phylogenetics)
```

5.3 tree results

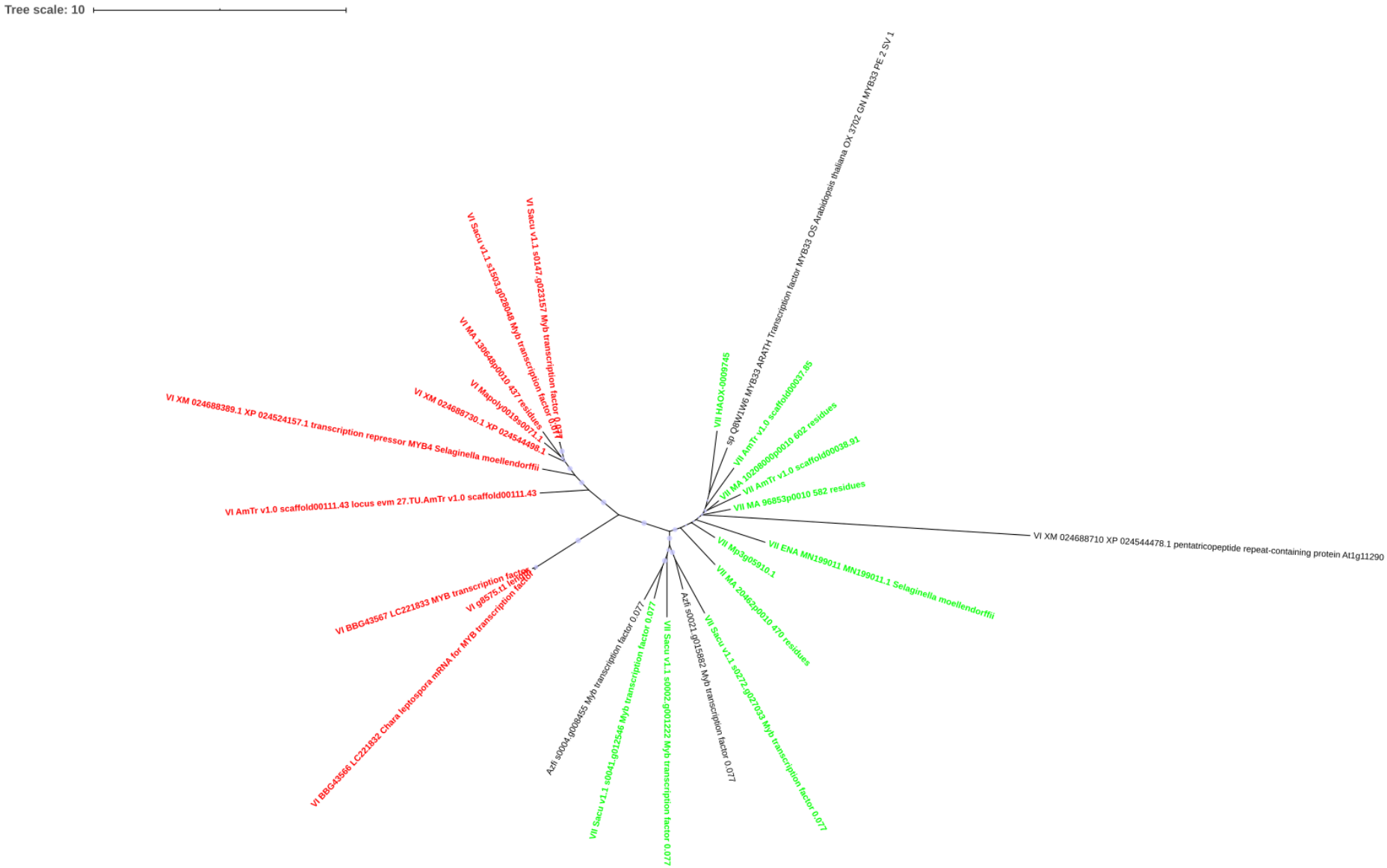
Uploading the trees to iToL, see links.

40% gt

Red is VI

Green is VII

gt 40% propper bootstraps:



propper bootstrap (https://itol.embl.de/tree/1312115964466181596025313) and ultrafast (https://itol.embl.de/tree/1312115964273141596034188#)

60% gt

gt 60% propper bootstraps:

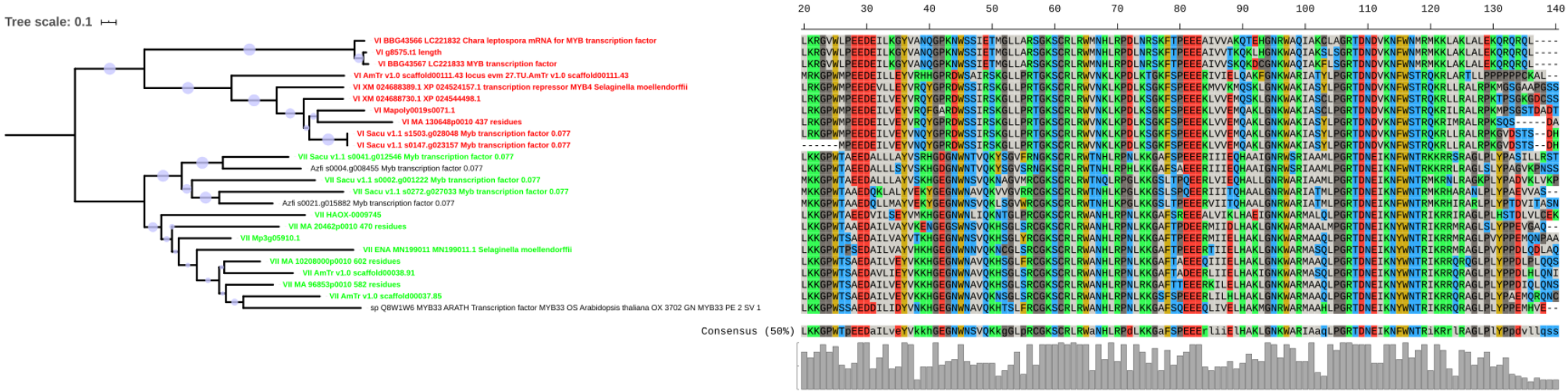
Conclusions

The selected Azolla myb sequences (candidates from RNA seq analysis fit in the VII subfamily of MYBs as identified by R&J. This is supported by (1) inspecting the alignment on the specific area that R&J annotated as characteristic for both sequences. And (2) by the phylogenetic trees. I do wonder if I should include more subfamilies in the phylogeny.

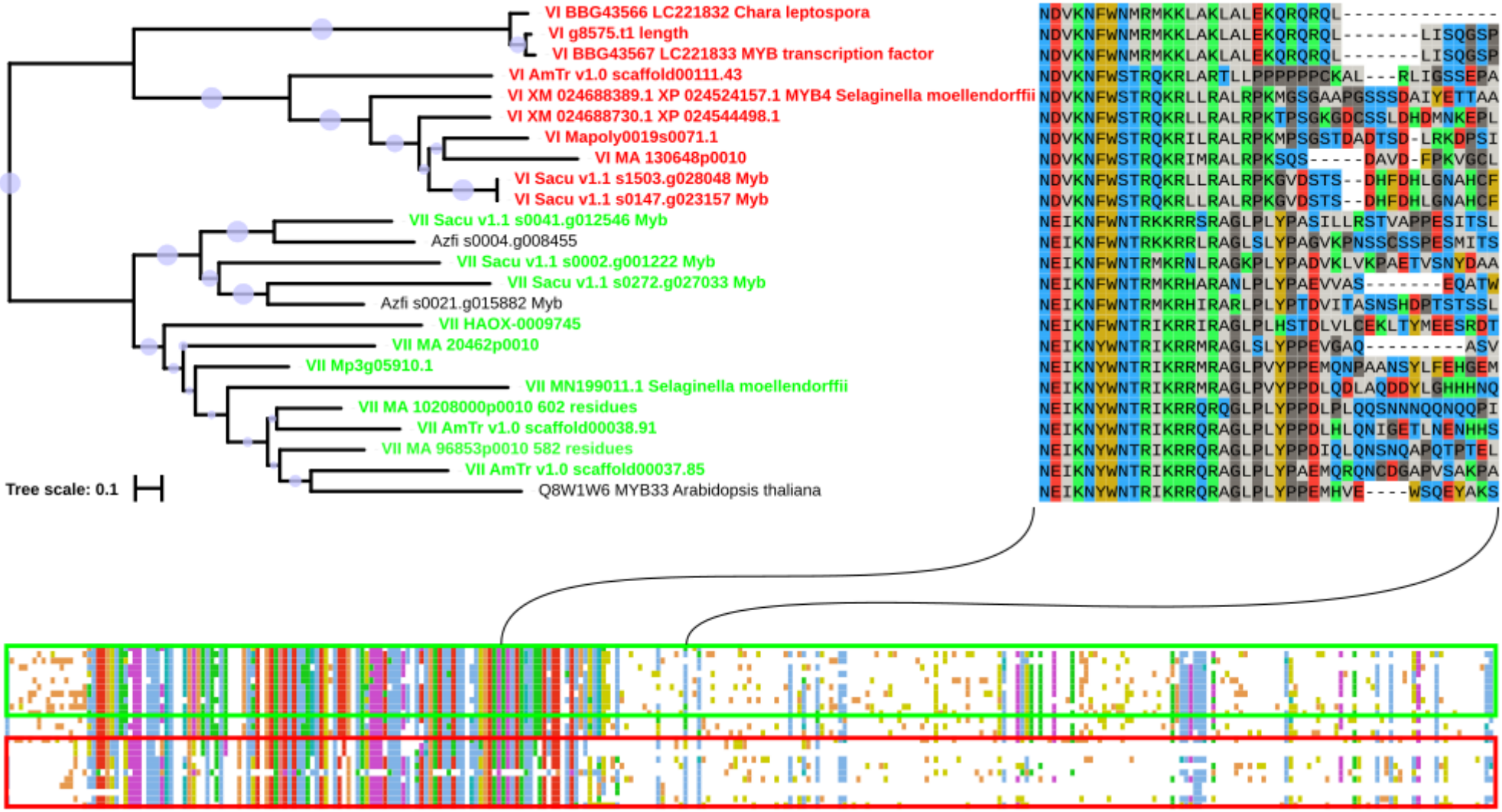
At the very least I need to remove the XM_...710 and the GFZG...1741.1 sequences still, and prepare this into a draft figure.

Another big improvement would be to clean up the sequence names with just an accession nr and add the genus and species names for better interpretation and judgement by the readers.

A figure with the tree and MSA combined could look like this:



Or a bit polished like so:



There's quite some improvements needed still, just thinking out loud here:

1. it's anoying that the two alignments don't have the same colour scheme
2. in the bottom panel, some of the blanks are actually filled with sequence, but they are blank...
3. Better annotation in top right panel of what residues differentiate VI from VII