

### Tree QC plots following removal of low quality colonies

Page 1) Upper panel: Plot of tree with unadjusted SNV branch length. Lower panel: Plot of tree with adjusted SNV branch length correcting somatic mutation detection for germline sensitivity. Bottom track bar plot shows the sequencing depth of each sample.

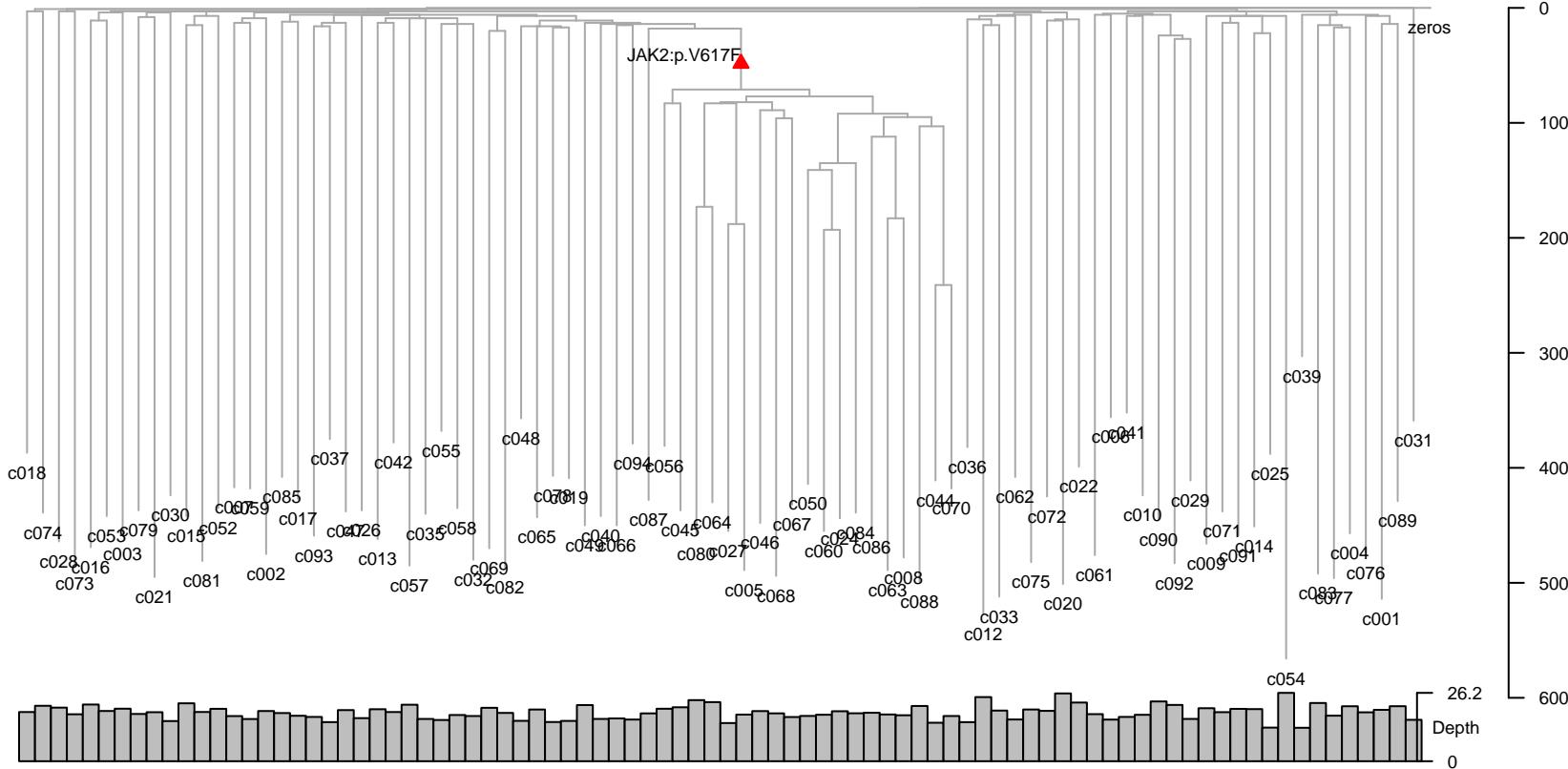
Page 2) Tree plot with chromosomal proportion of mapped variants shown. Highlights branches where the composition differs significantly ( $p<0.01$ ) from the average (Chi-Square test) to confirm that all copy number changes have been identified and accounted for and are not inadvertently affecting branch lengths.

Page 3) Box plots of VAF distribution for shared branches aggregated by the number of shared colonies. The number of colonies is specified as the top number on the x-axis axis labels. The number of loci\*shared colonies is specified in brackets (so divide by number above to get number of loci). This plot is to ensure that the VAF of variants in shared (to various degrees) versus private branches is equal with no bias across different types of branches across a tree. In particular, highly shared branches and private branches do not vary in the VAF of the variants included. Lower panel: as above but showing the VAF distribution by the number of colonies in the clade.

Page 4) Top panel: Trees annotated with pooled VAF distributions. Each branch plots the per mapped locus pooled VAF sorted by VAF. Branches highlighted in blue have VAF nominally significantly less than 0.45 ( $p<0.05$ ). Branches highlighted in red have VAF significantly less than 0.45 on a Bonferroni corrected basis ( $<0.05/\text{num.branches}$ ). Where appropriate the numerical VAF is reported on the branch. The tree includes residual germline variants that are assigned to a small germline root branch. Residual germline variants here will often exhibit low VAF and are removed from subsequent analysis. Lower panel: Trees annotated with bootstrap support. mpboot bootstrap support is obtained for each bipartition of the tree.

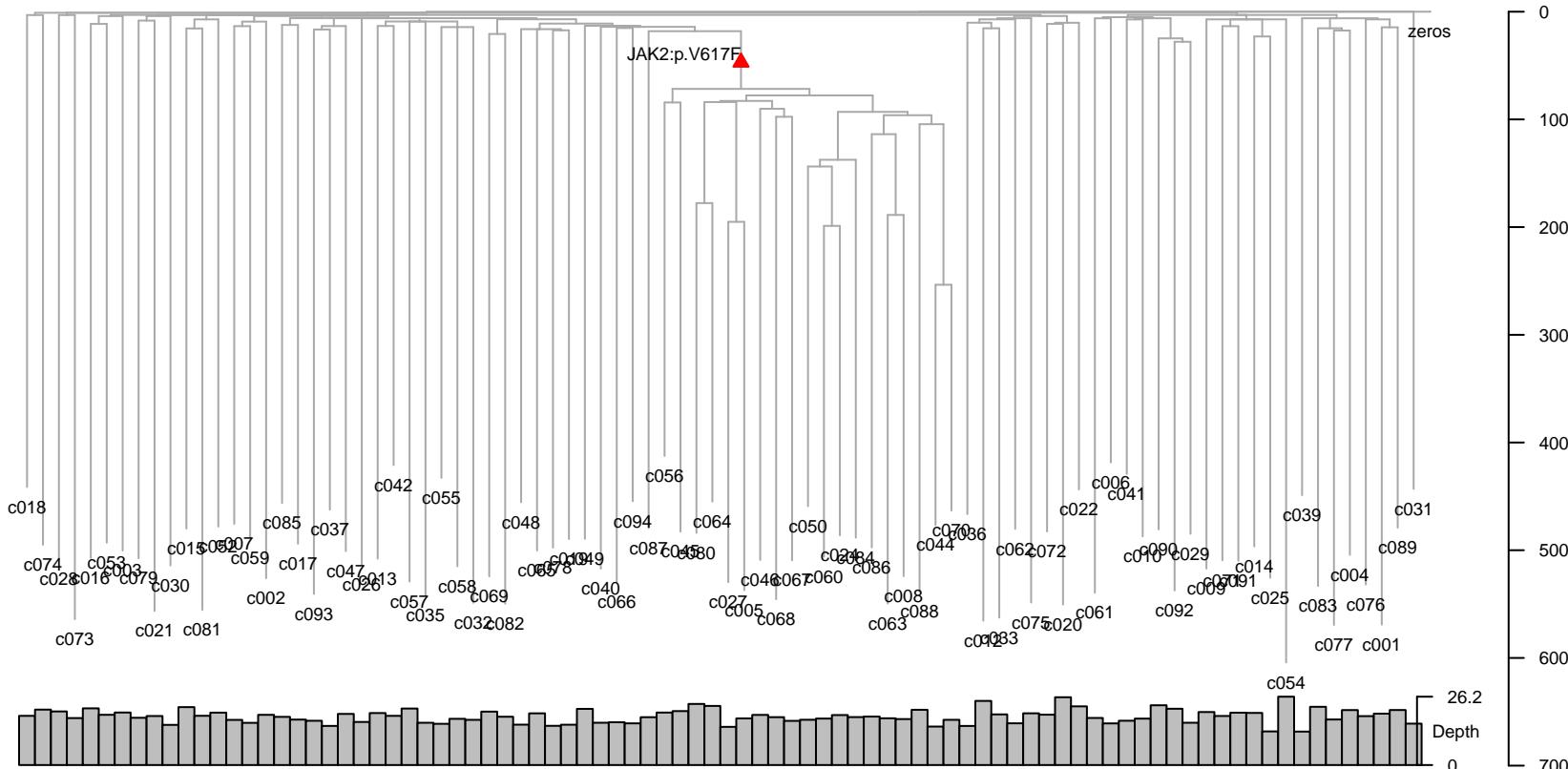
PD7271: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)

▲ missense

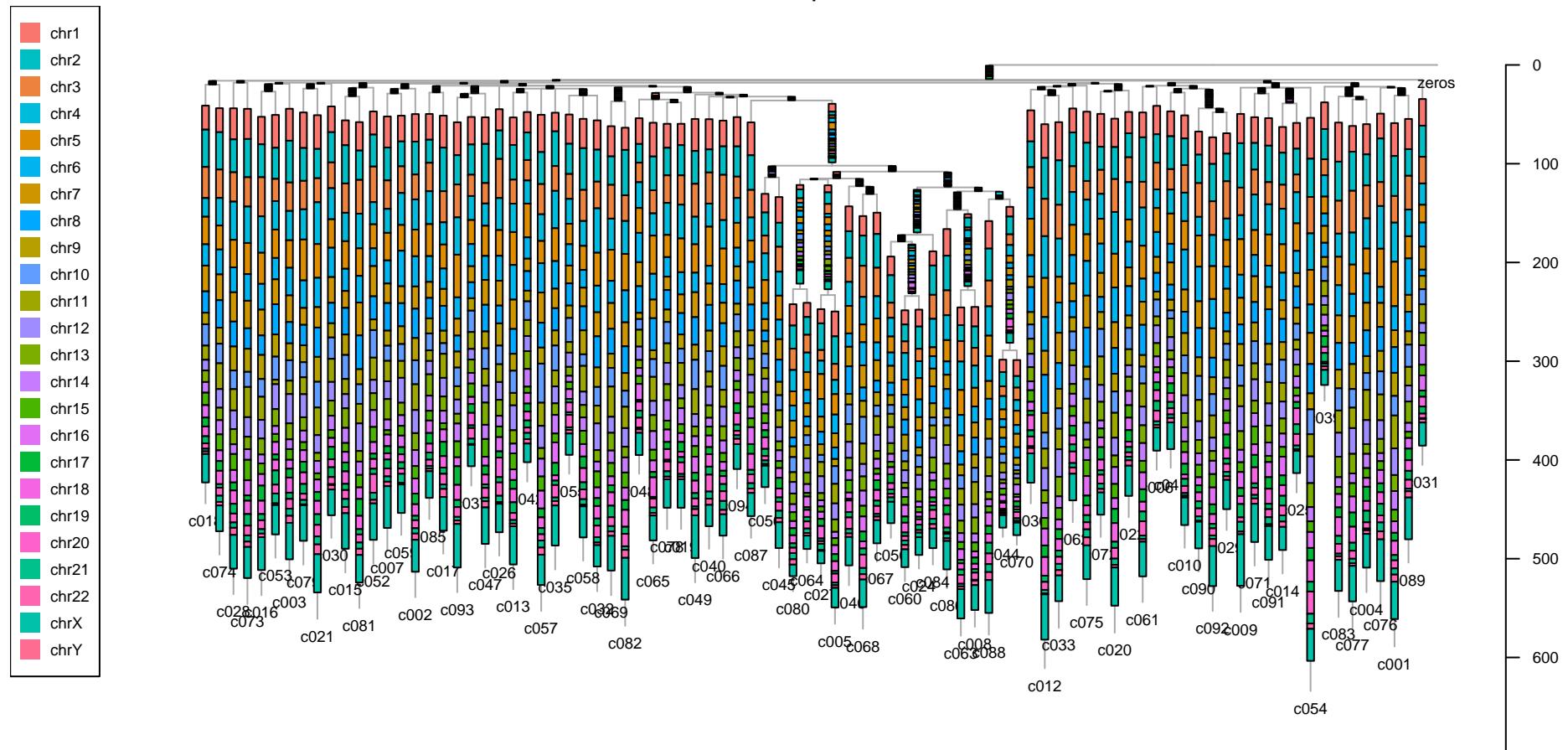


PD7271: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity

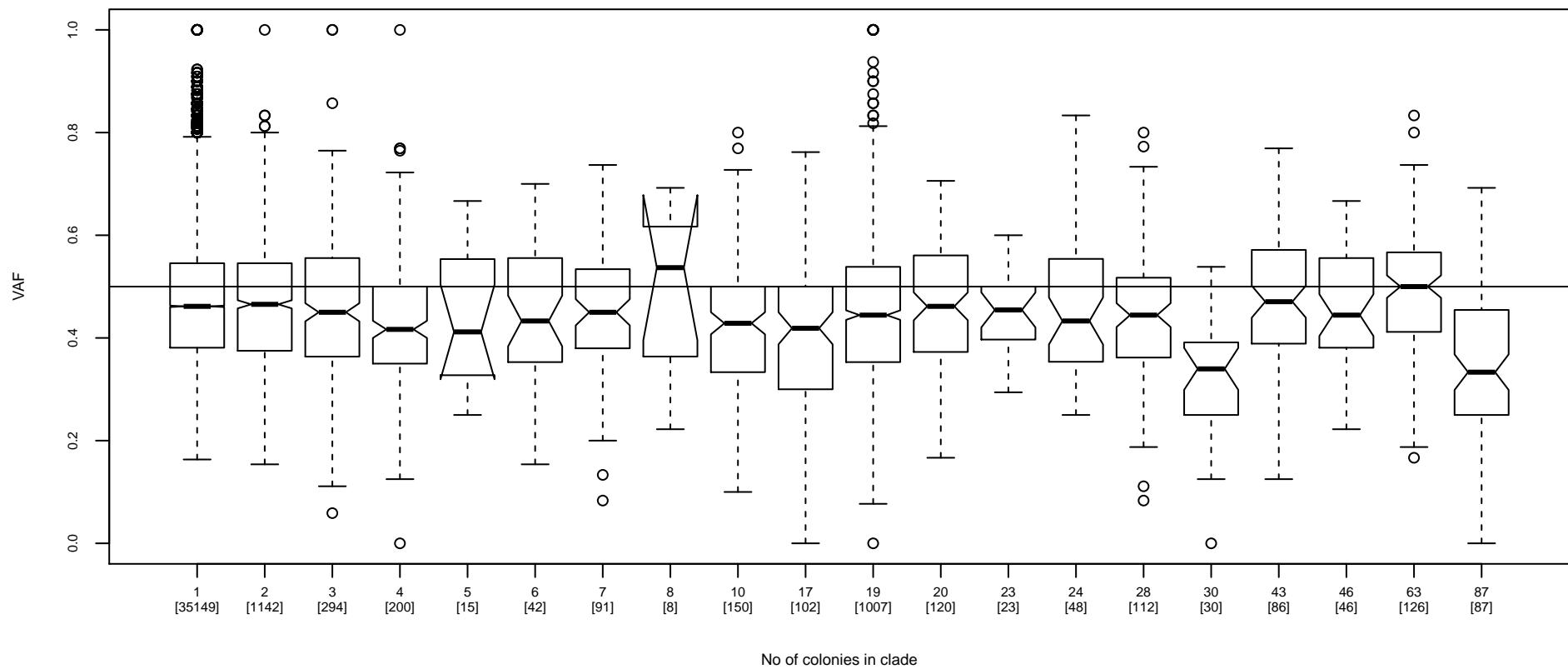
▲ missense



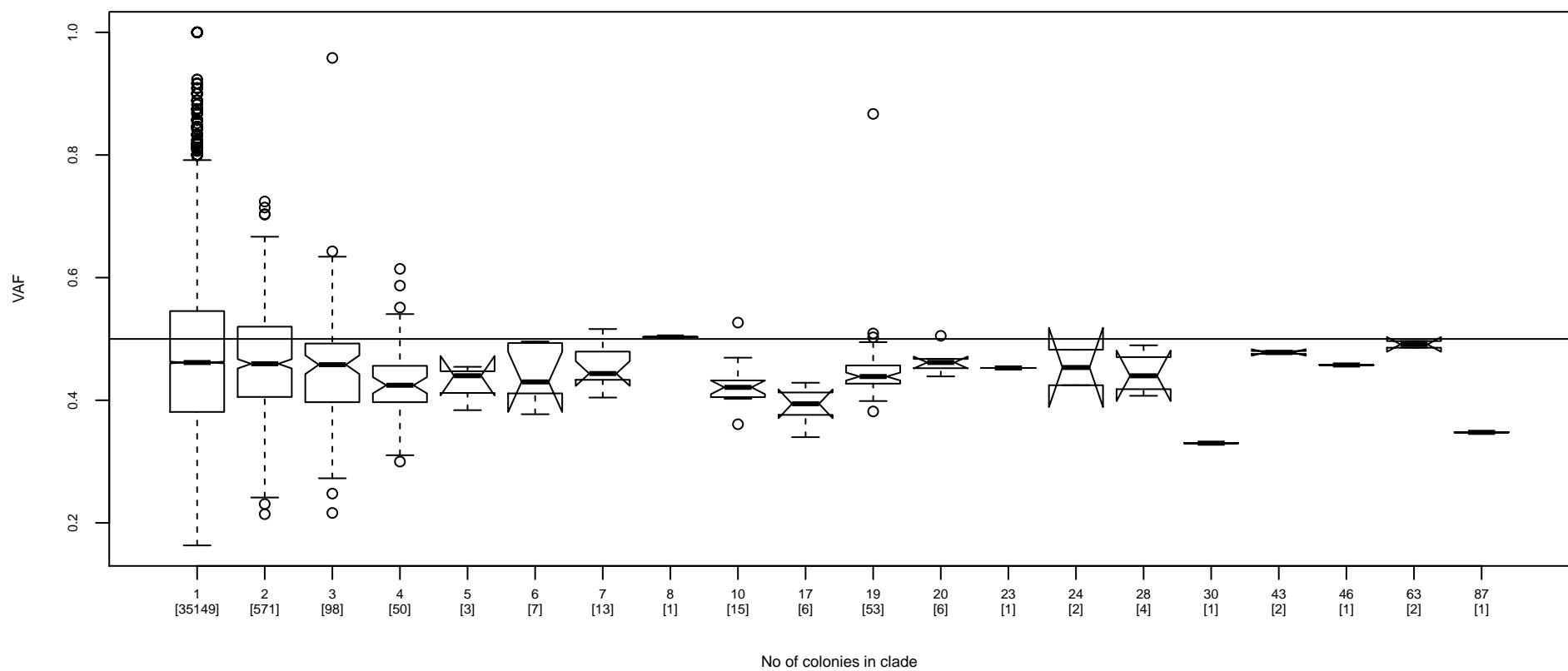
**PD7271: Chromosome composition check**



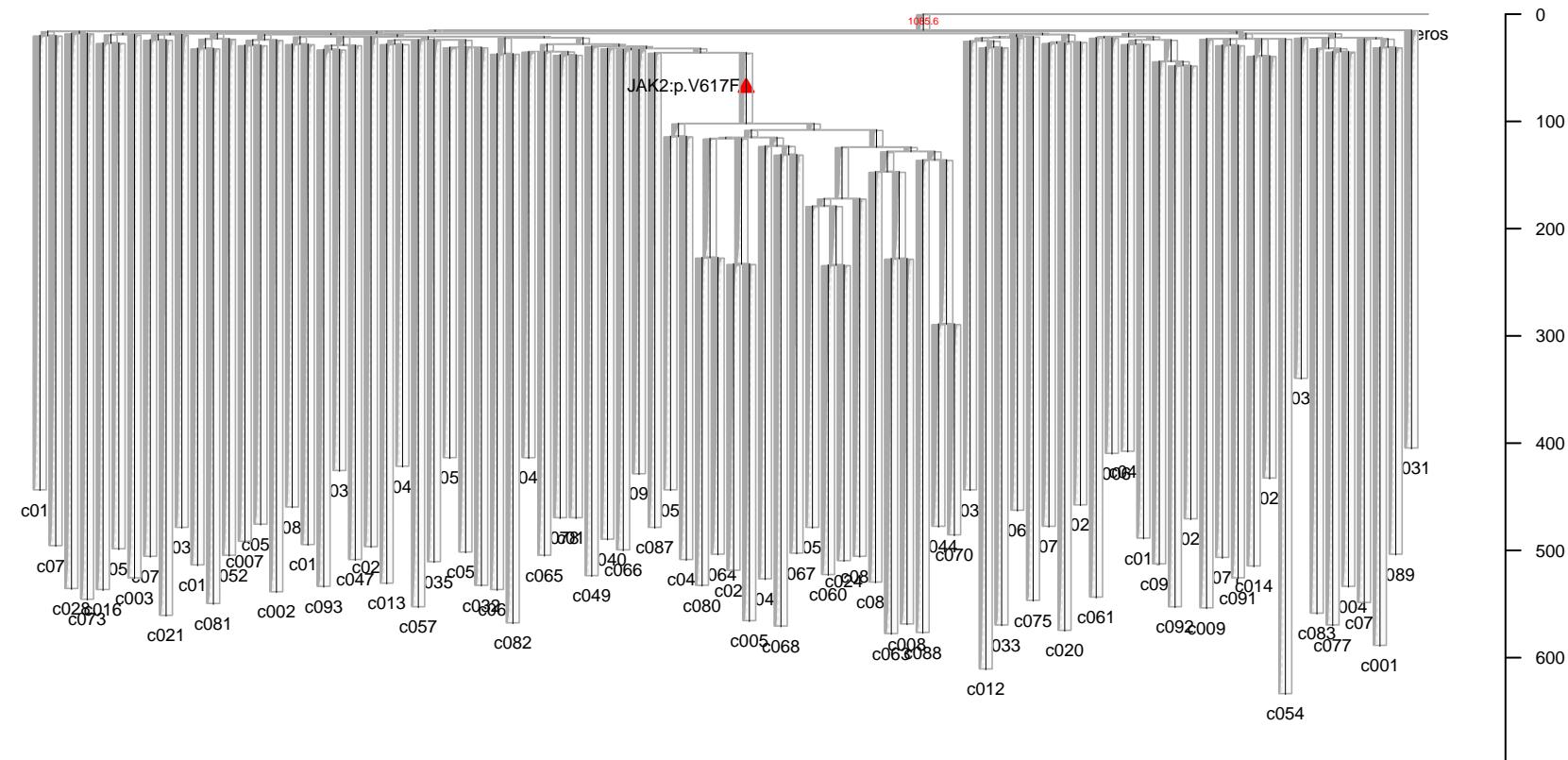
PD7271:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



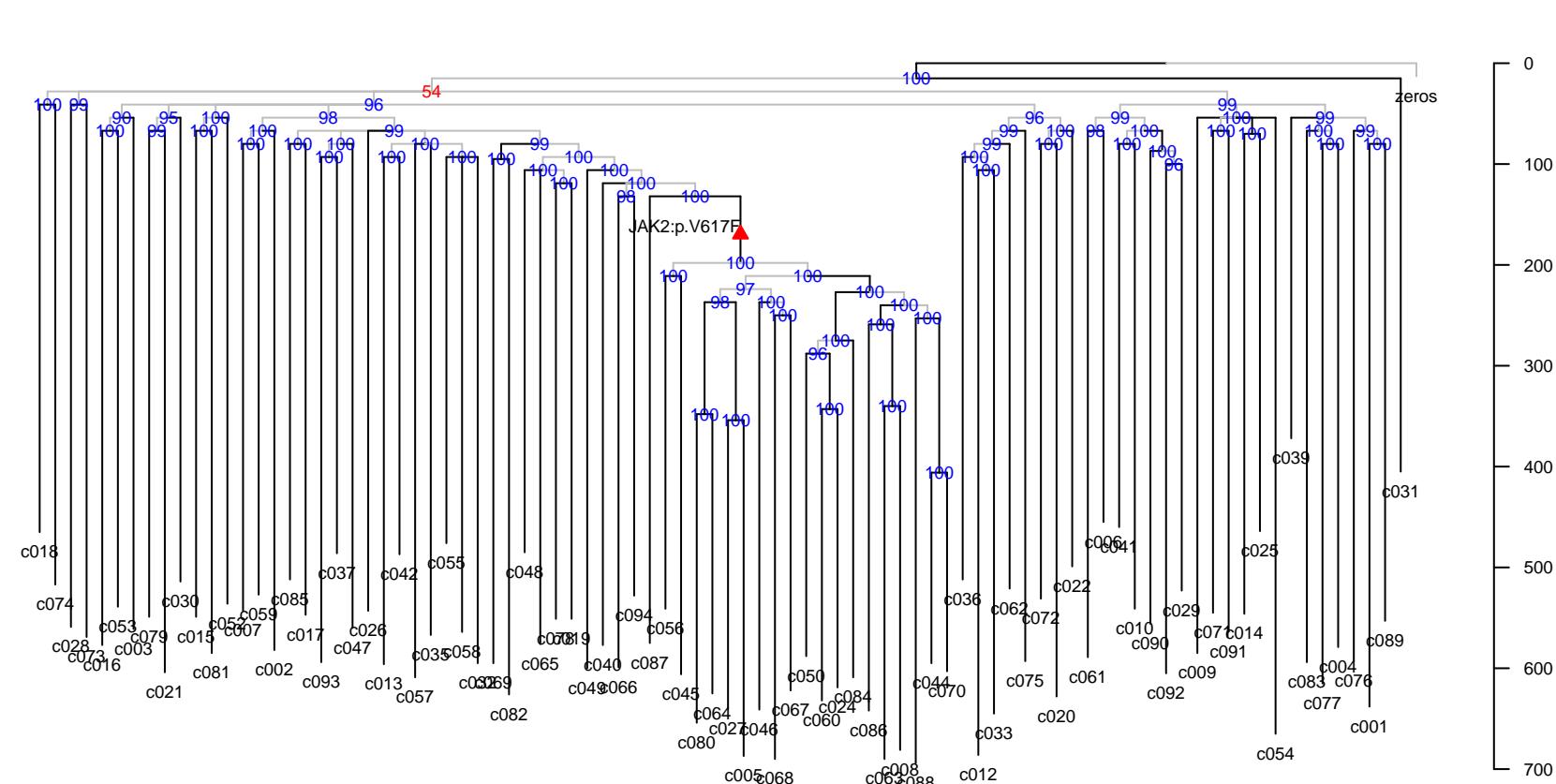
PD7271:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



### PD7271 [Pooled VAF]

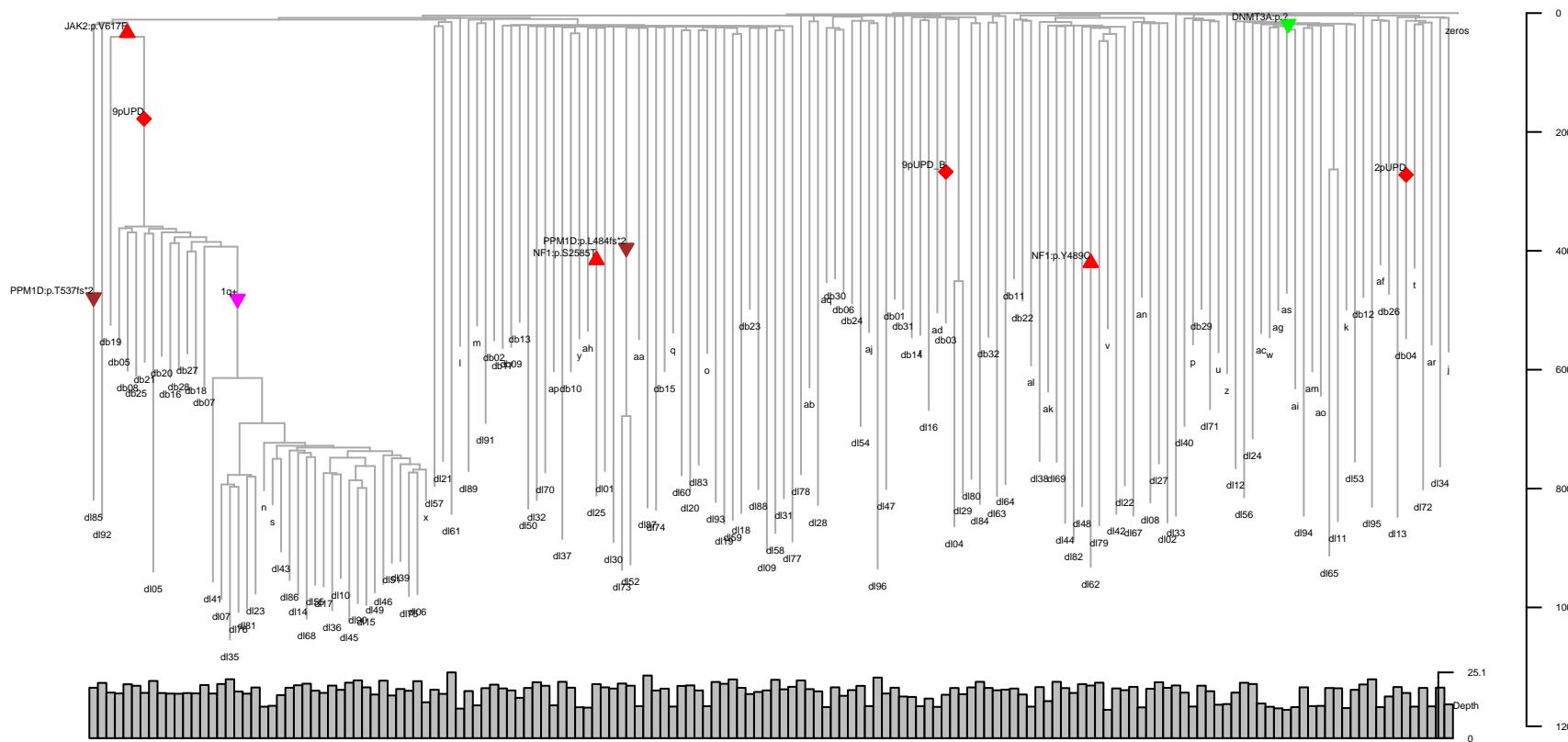
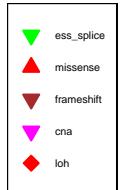


PD7271: With MPBoot Bootstrap Support (Grey branches extended to 13 Mutations)

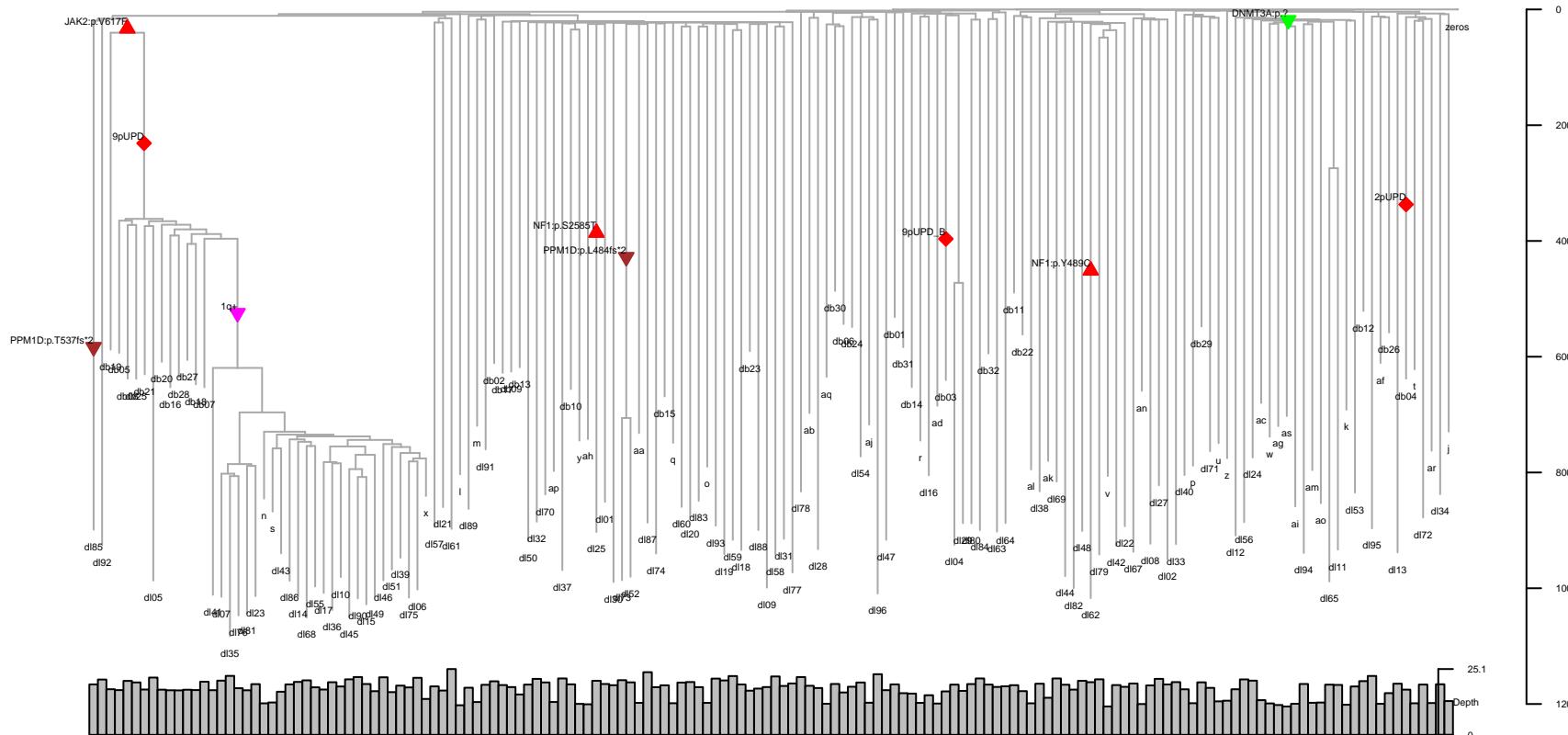
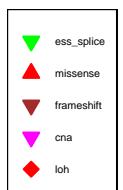


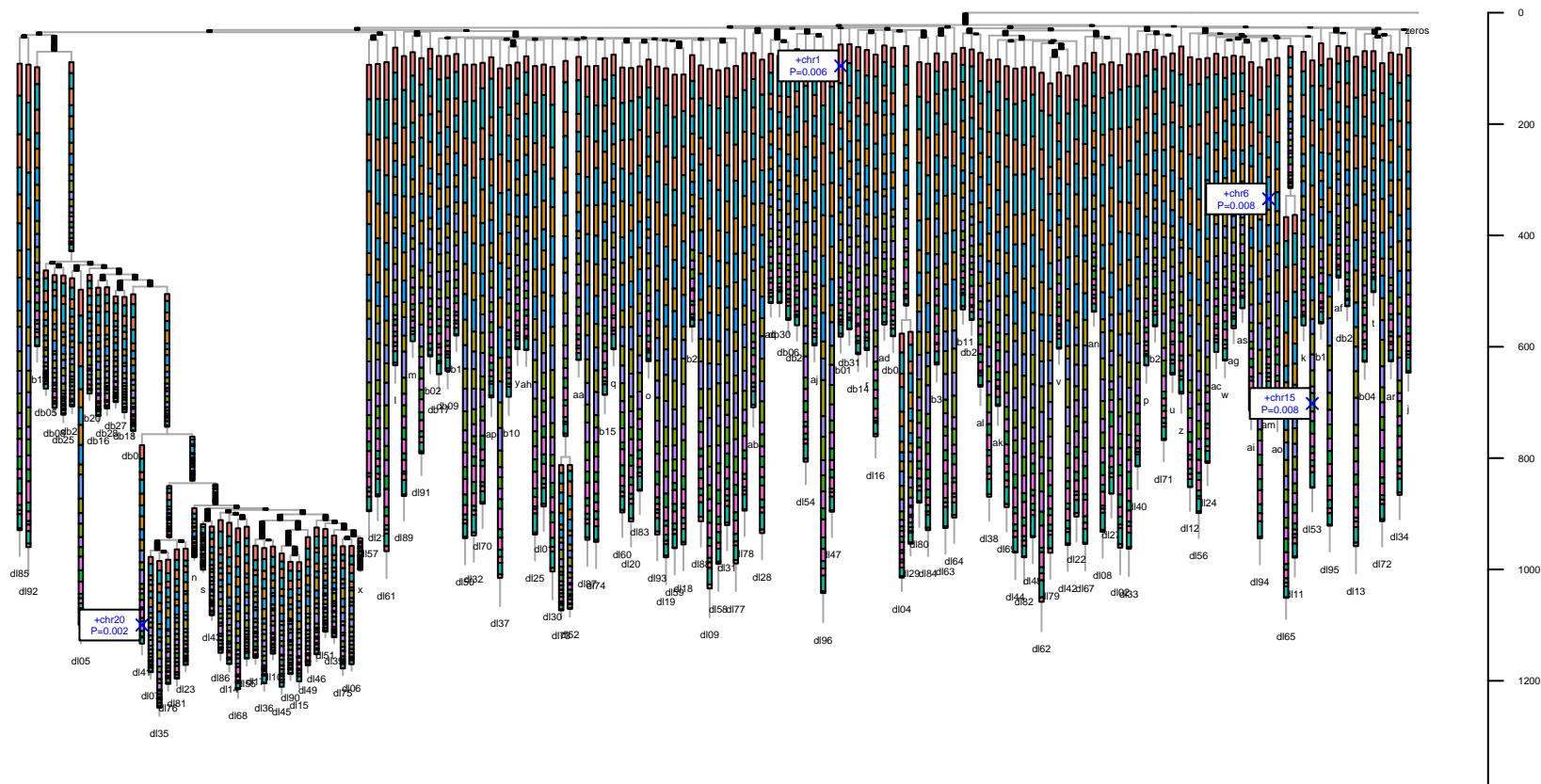
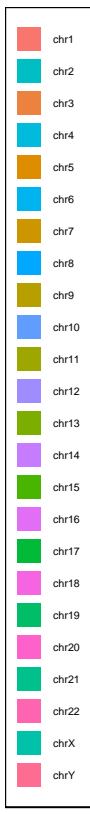
▲ missense

PD5182: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)

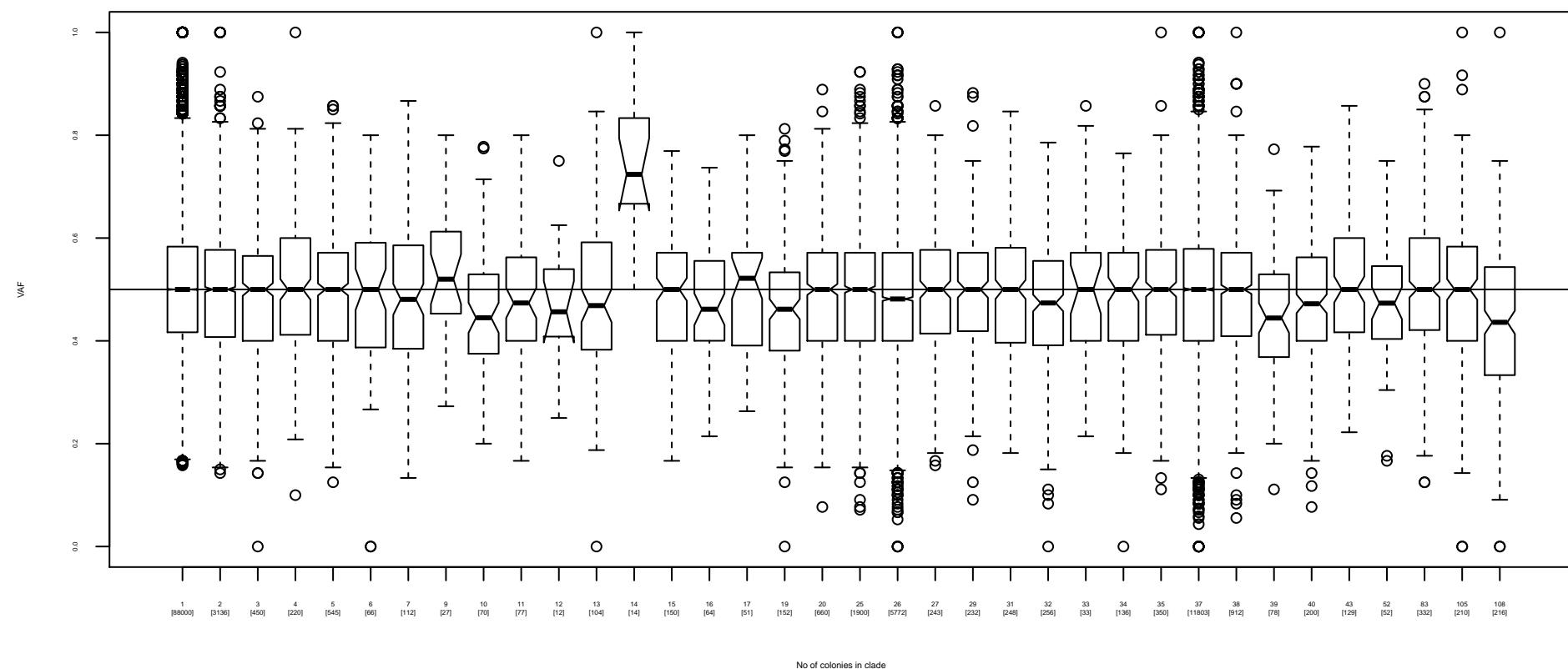


PD5182: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity

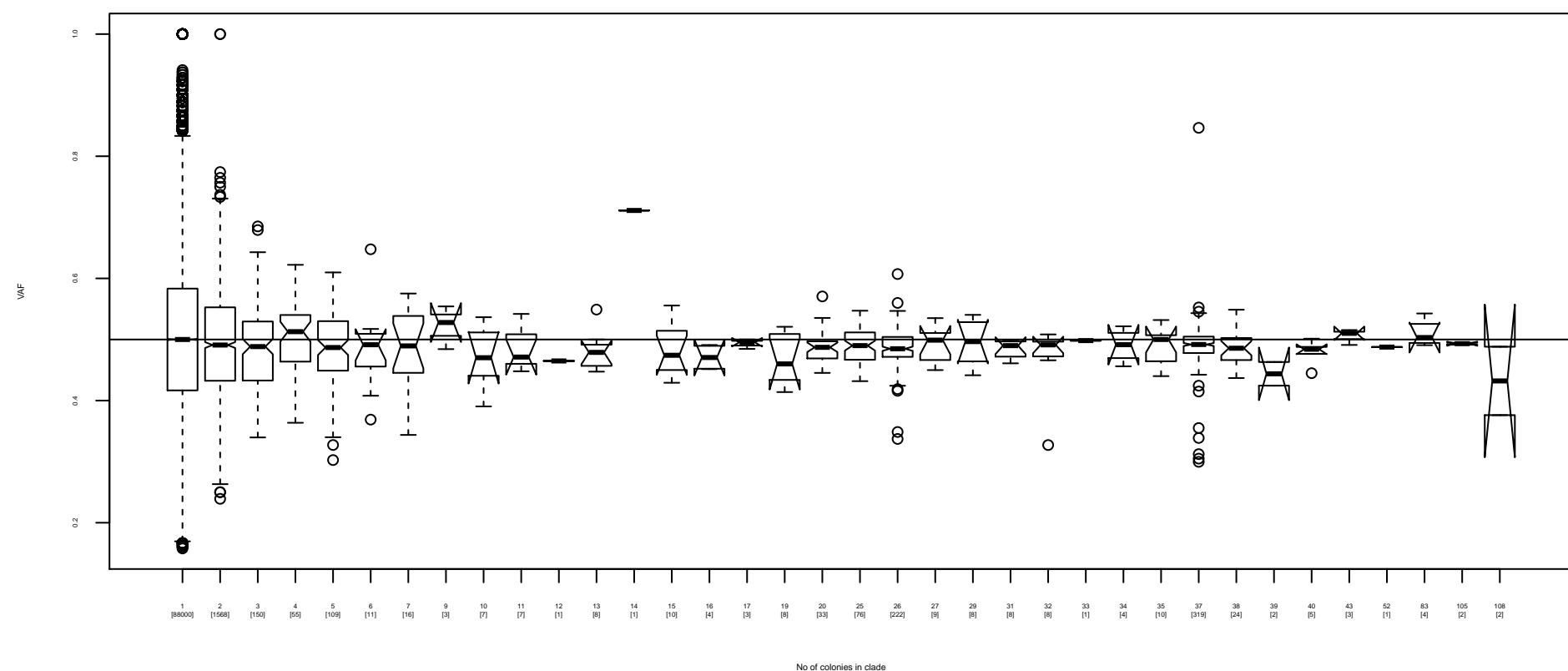




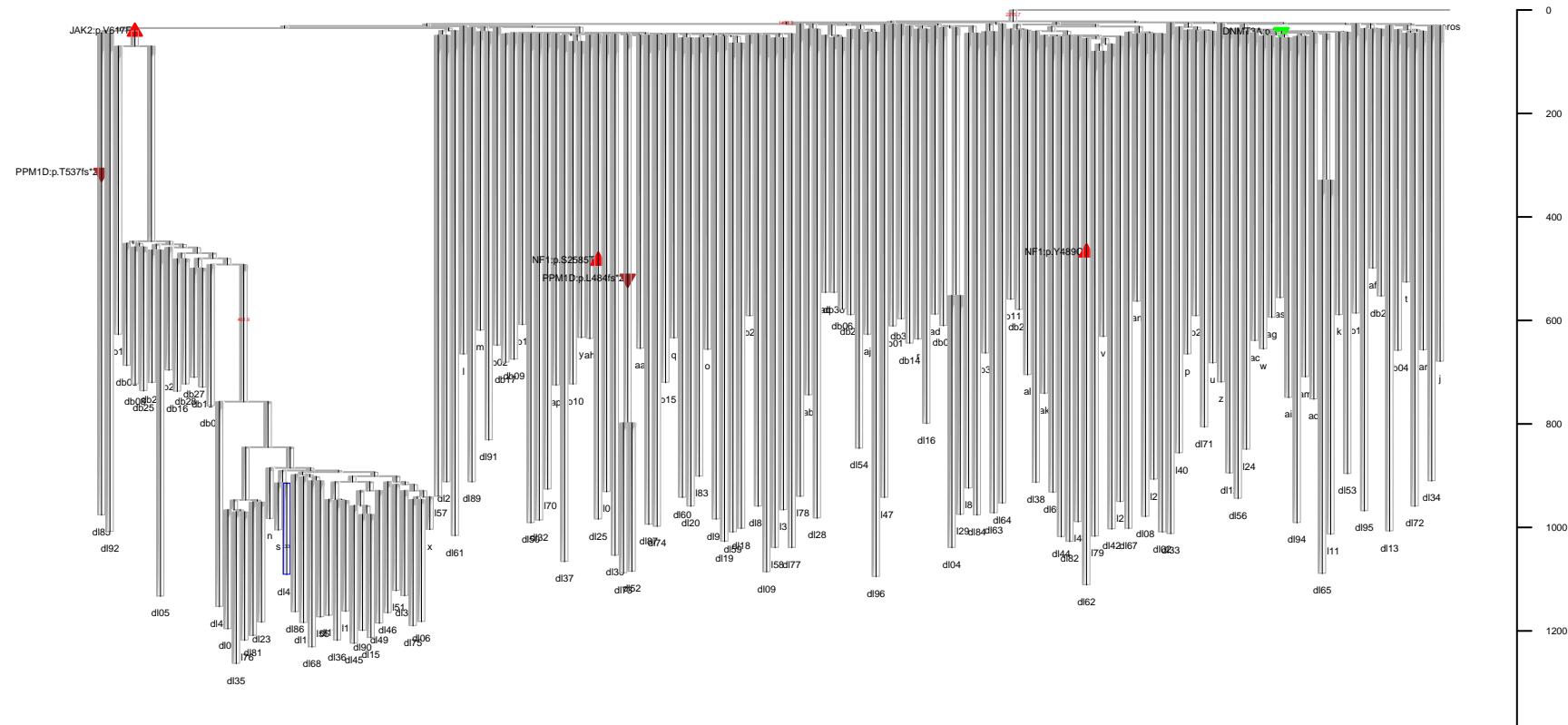
PD5182:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



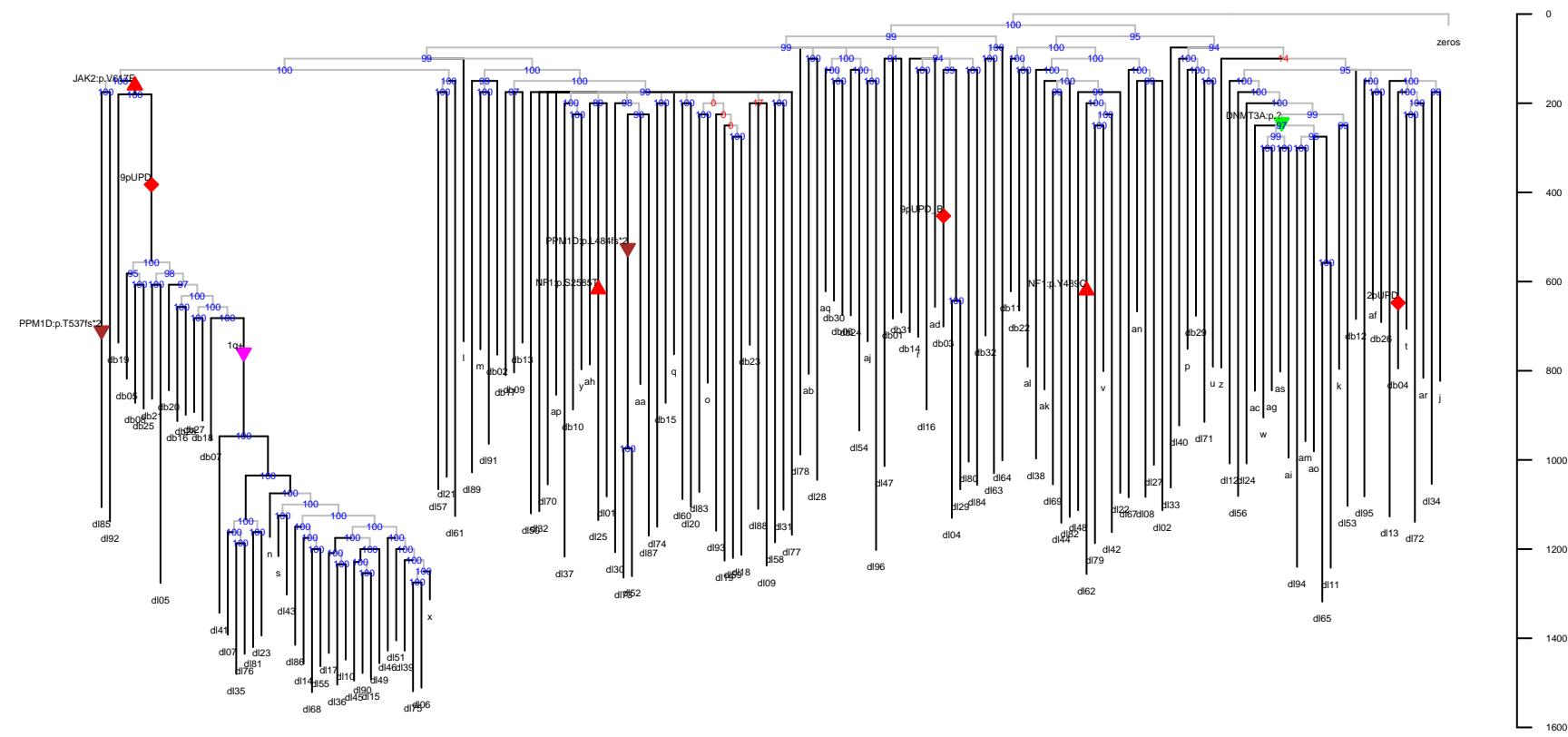
PD5182:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



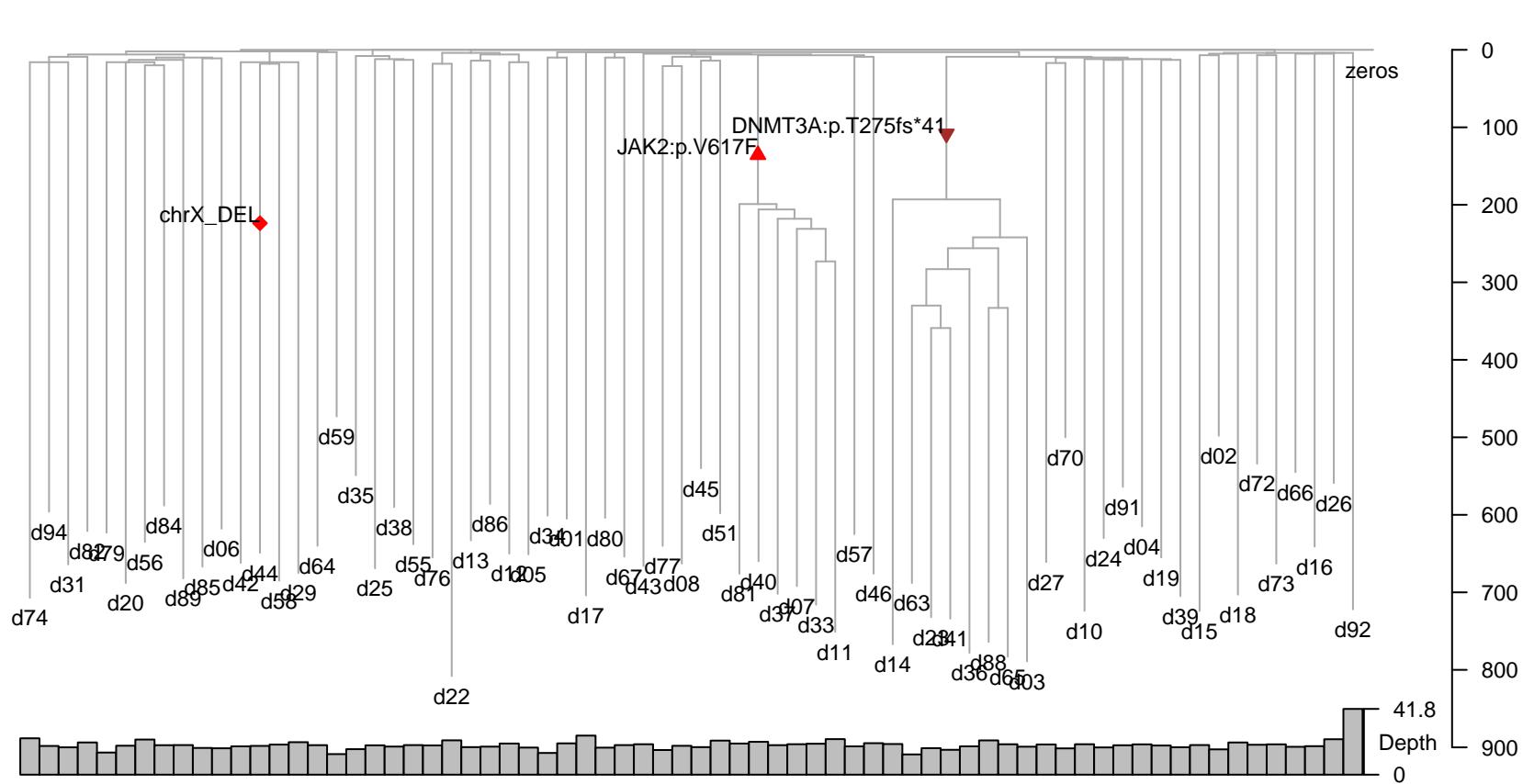
PD5182 [Pooled VAF]



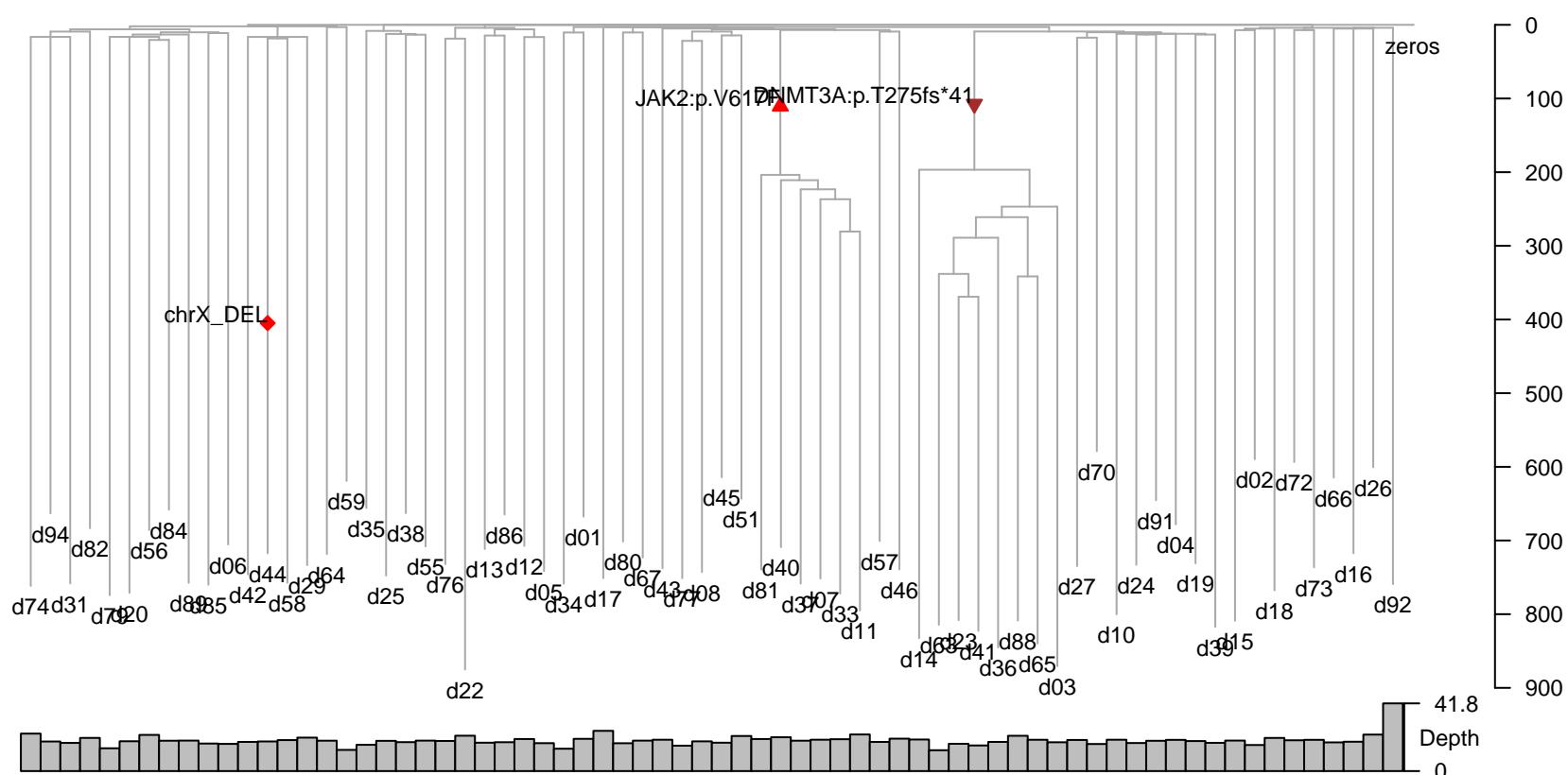
PD5182: With MPBoot Bootstrap Support (Grey branches extended to 25 Mutations)



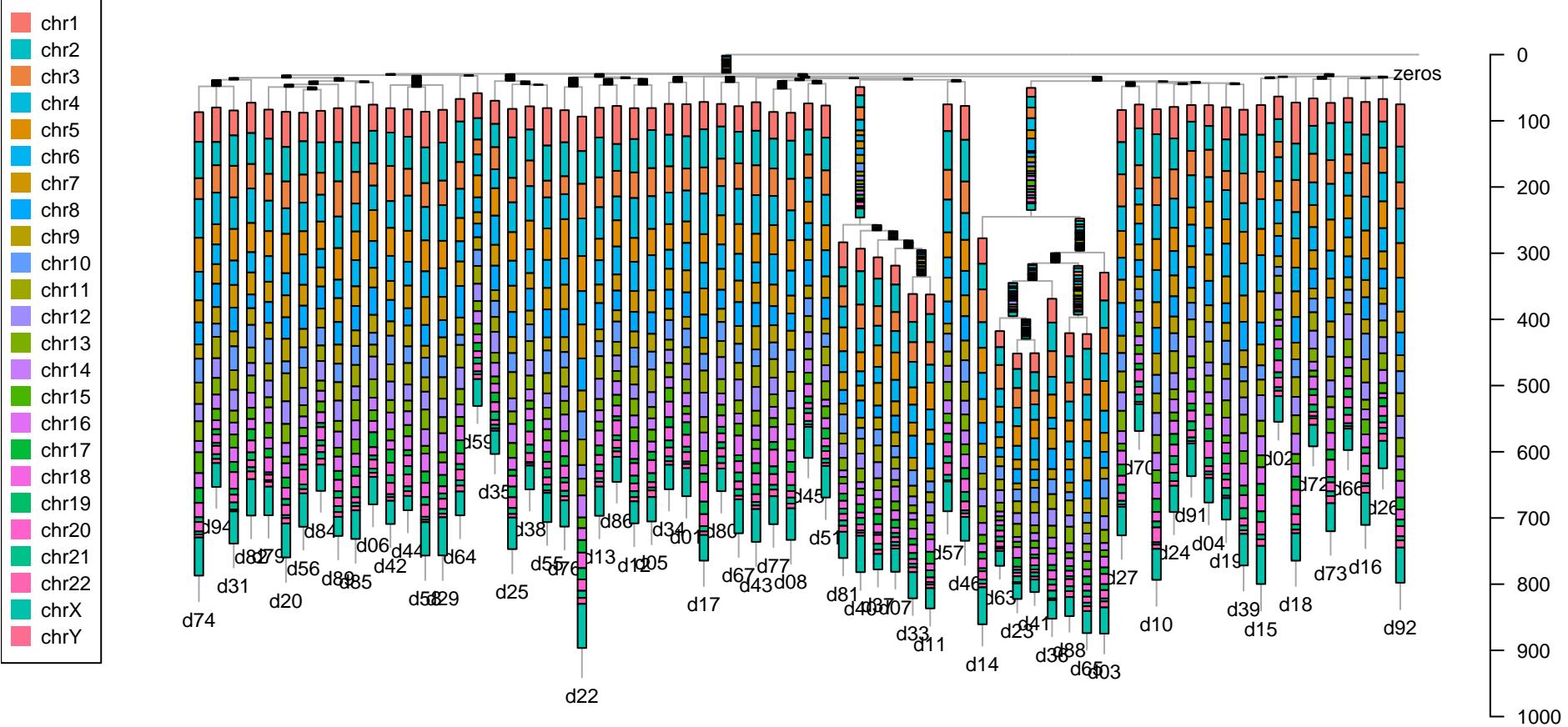
### PD5163: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)



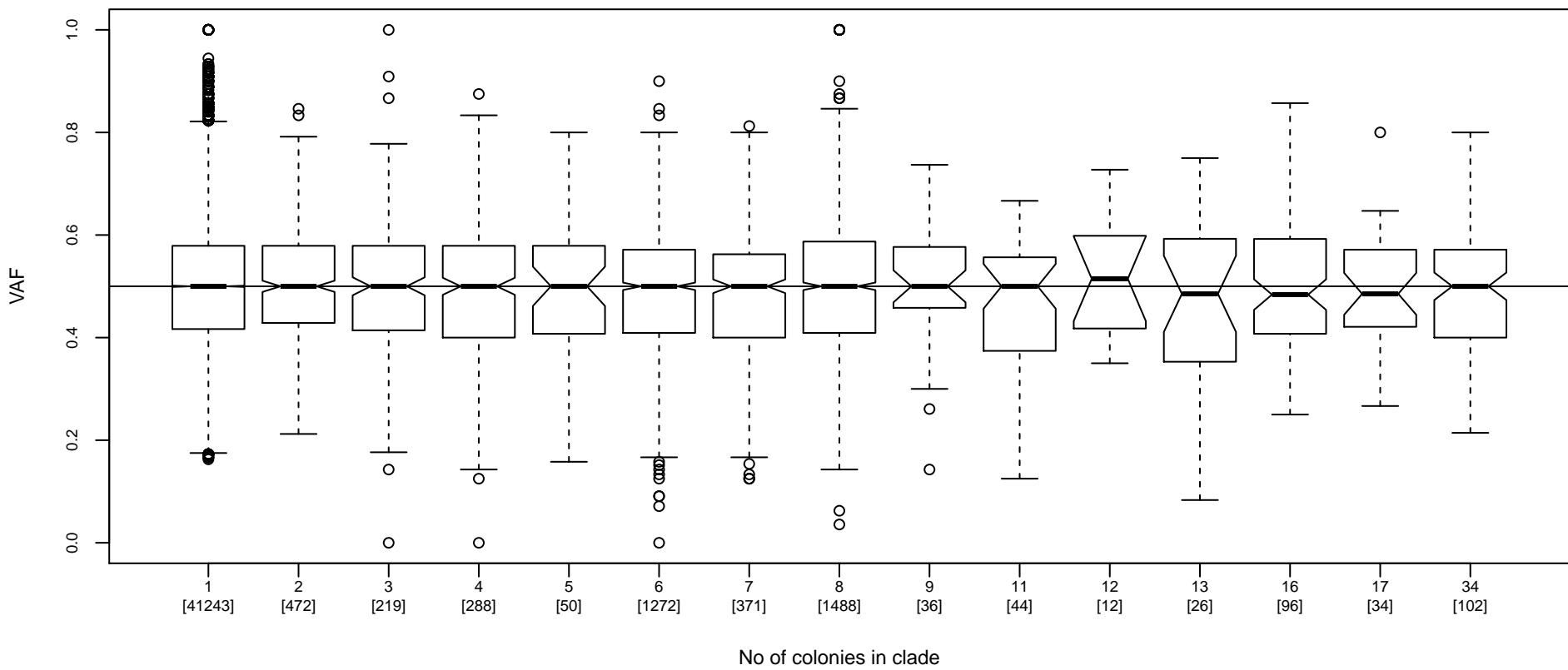
### PD5163: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



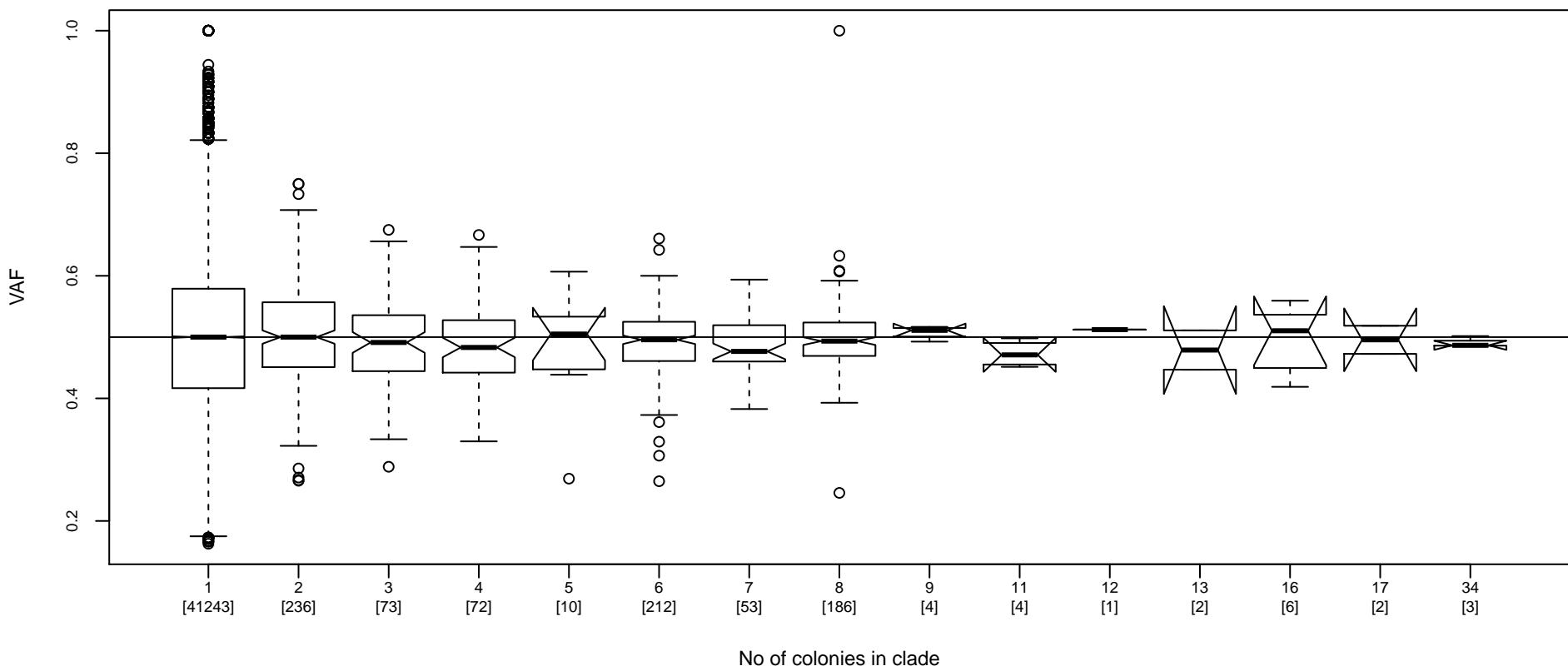
# PD5163: Chromosome composition check



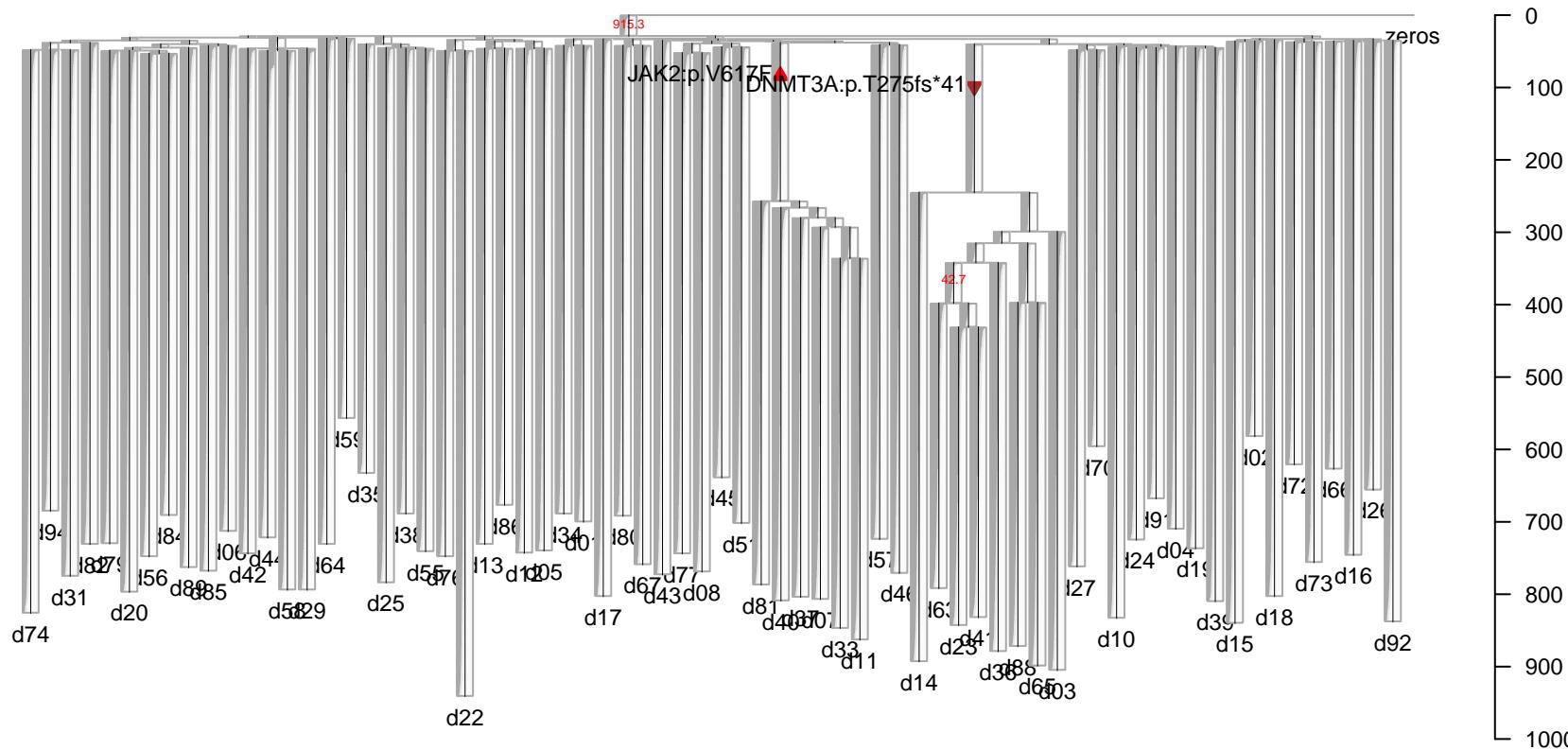
PD5163:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



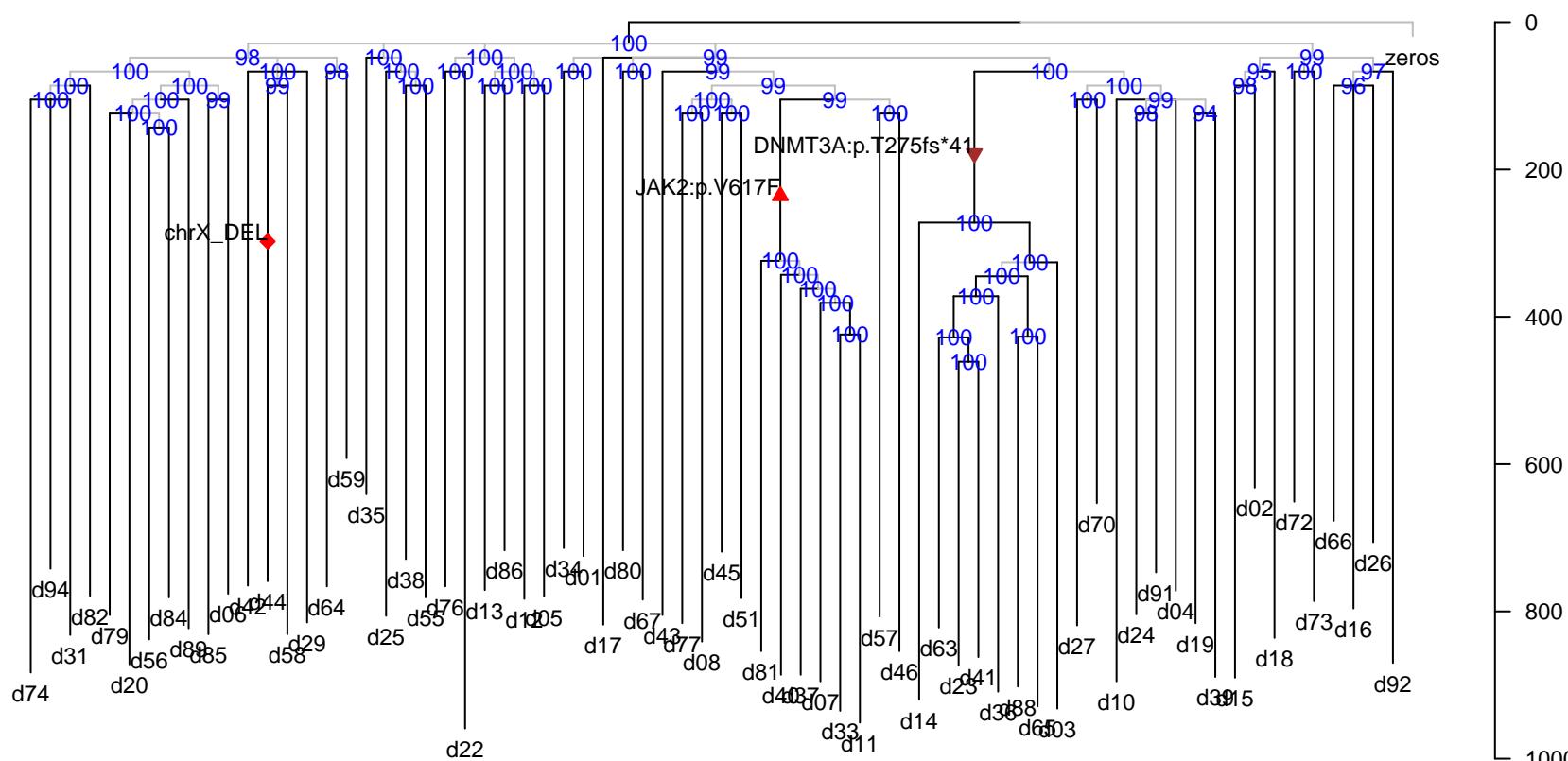
PD5163:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



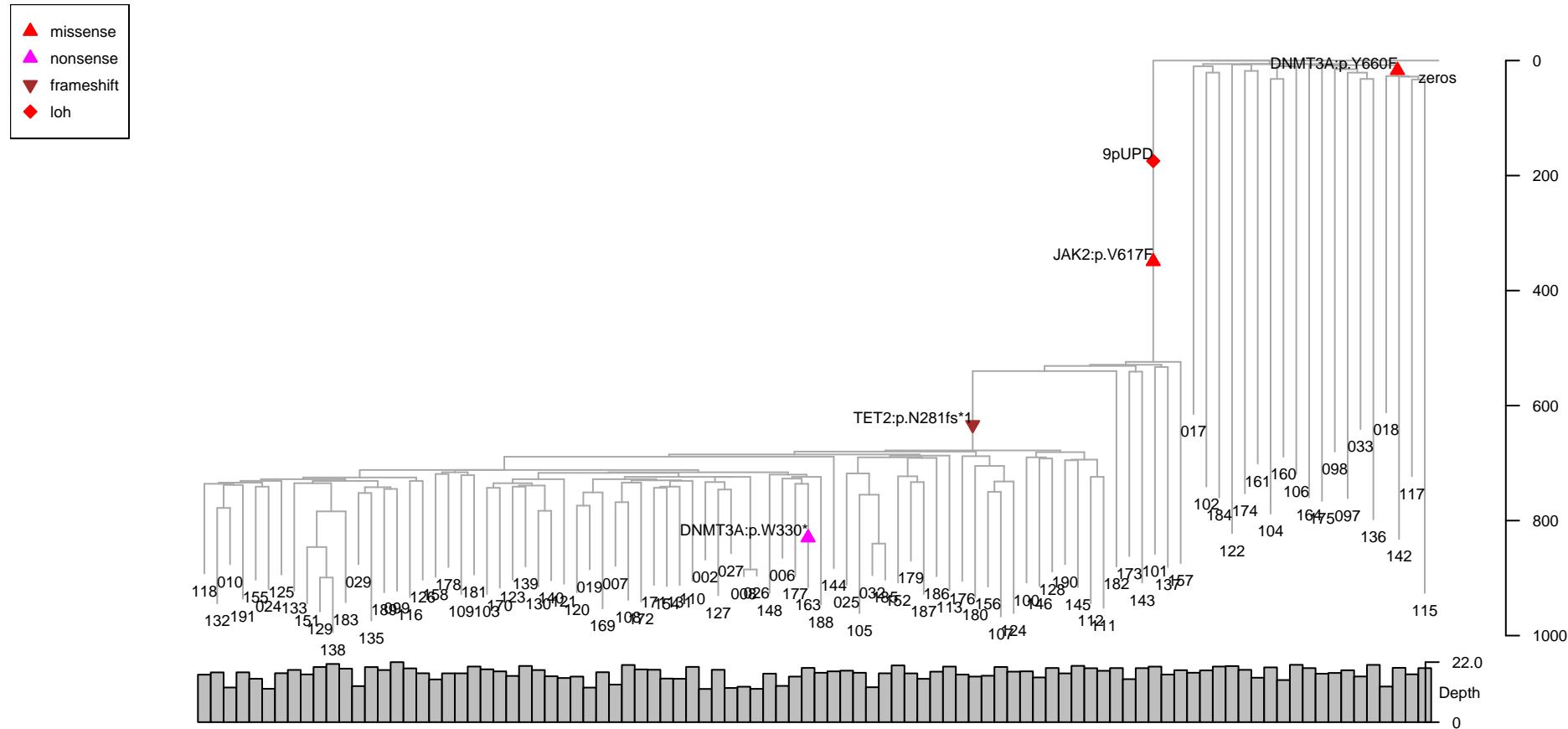
PD5163 [Pooled VAF]



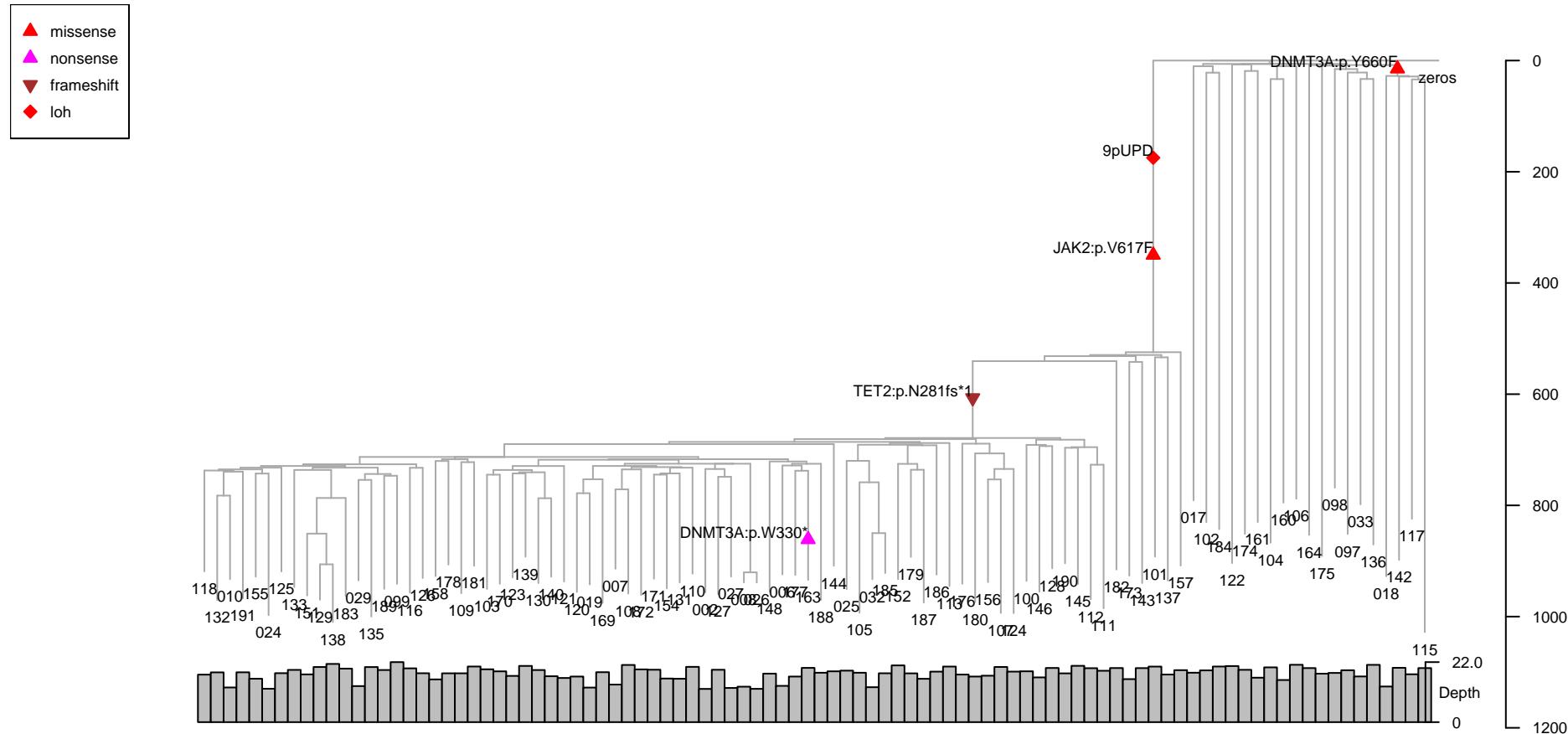
## PD5163: With MPBoot Bootstrap Support (Grey branches extended to 19 Mutations)



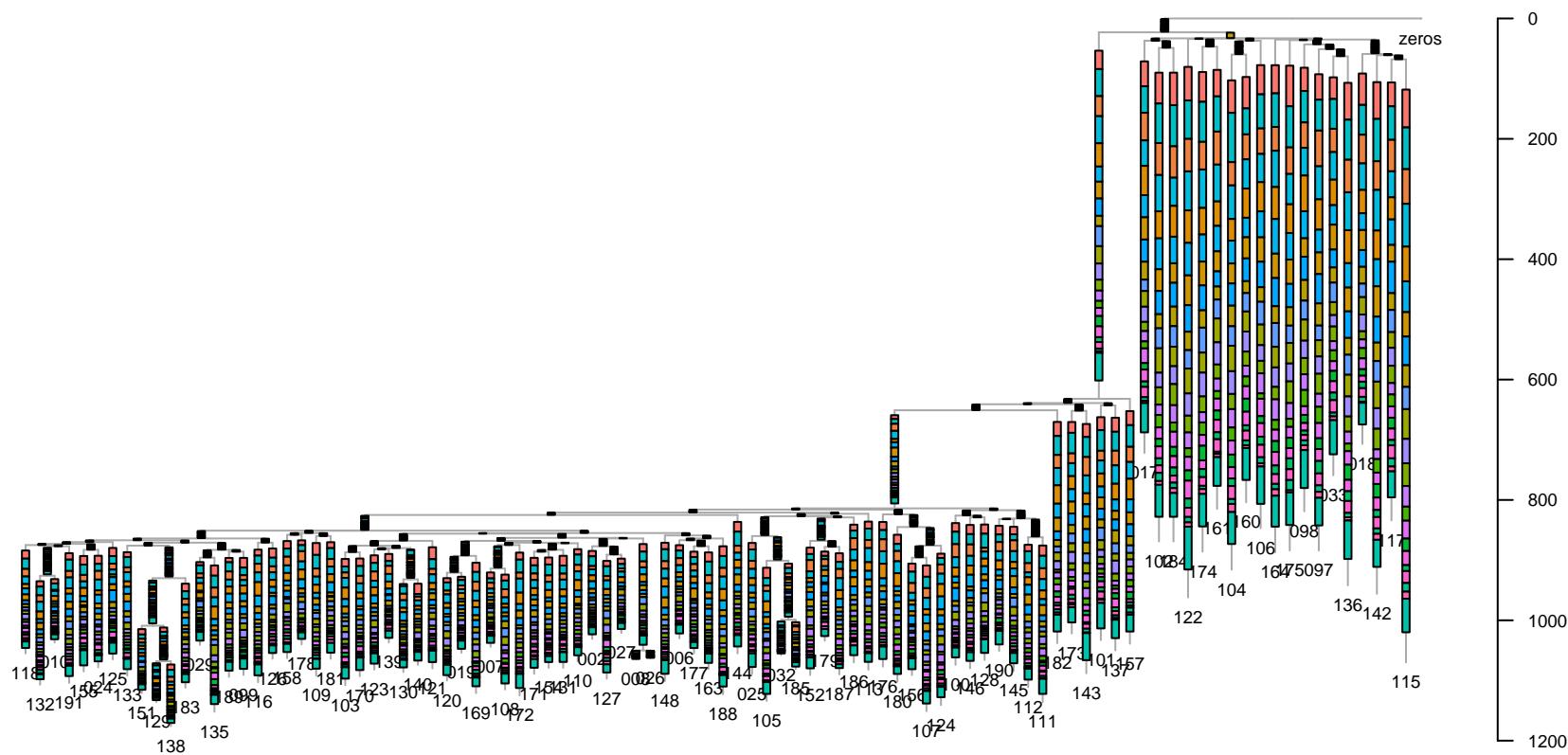
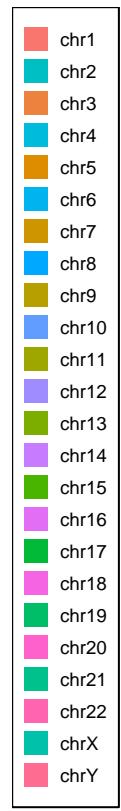
PD5847: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)



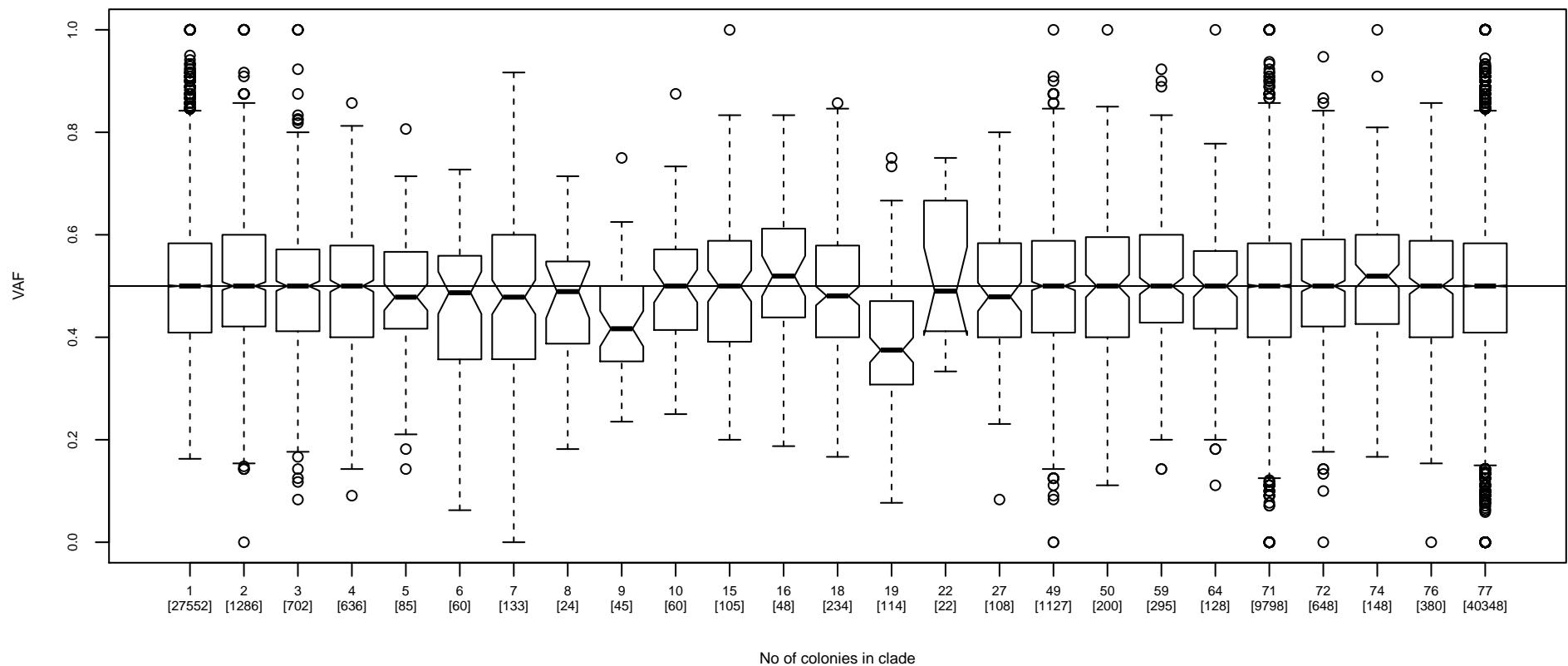
PD5847: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



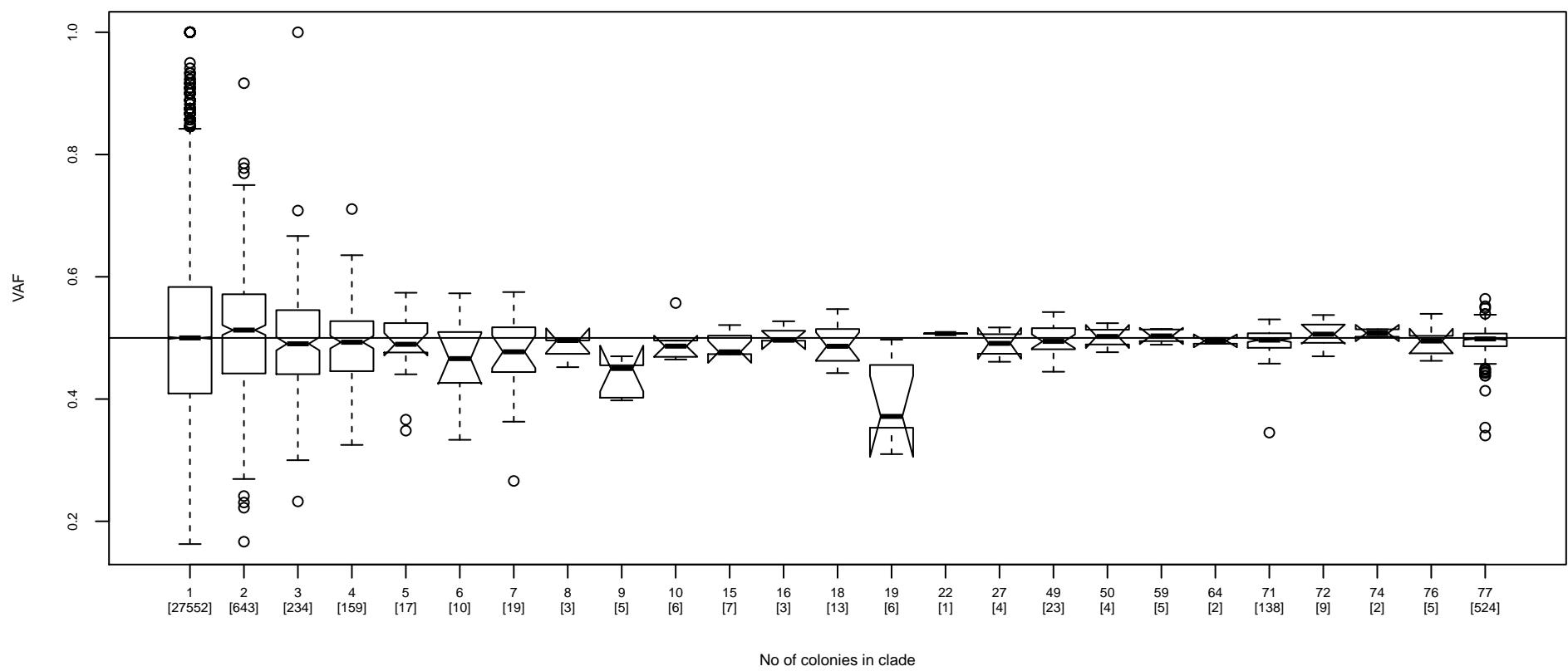
## PD5847: Chromosome composition check

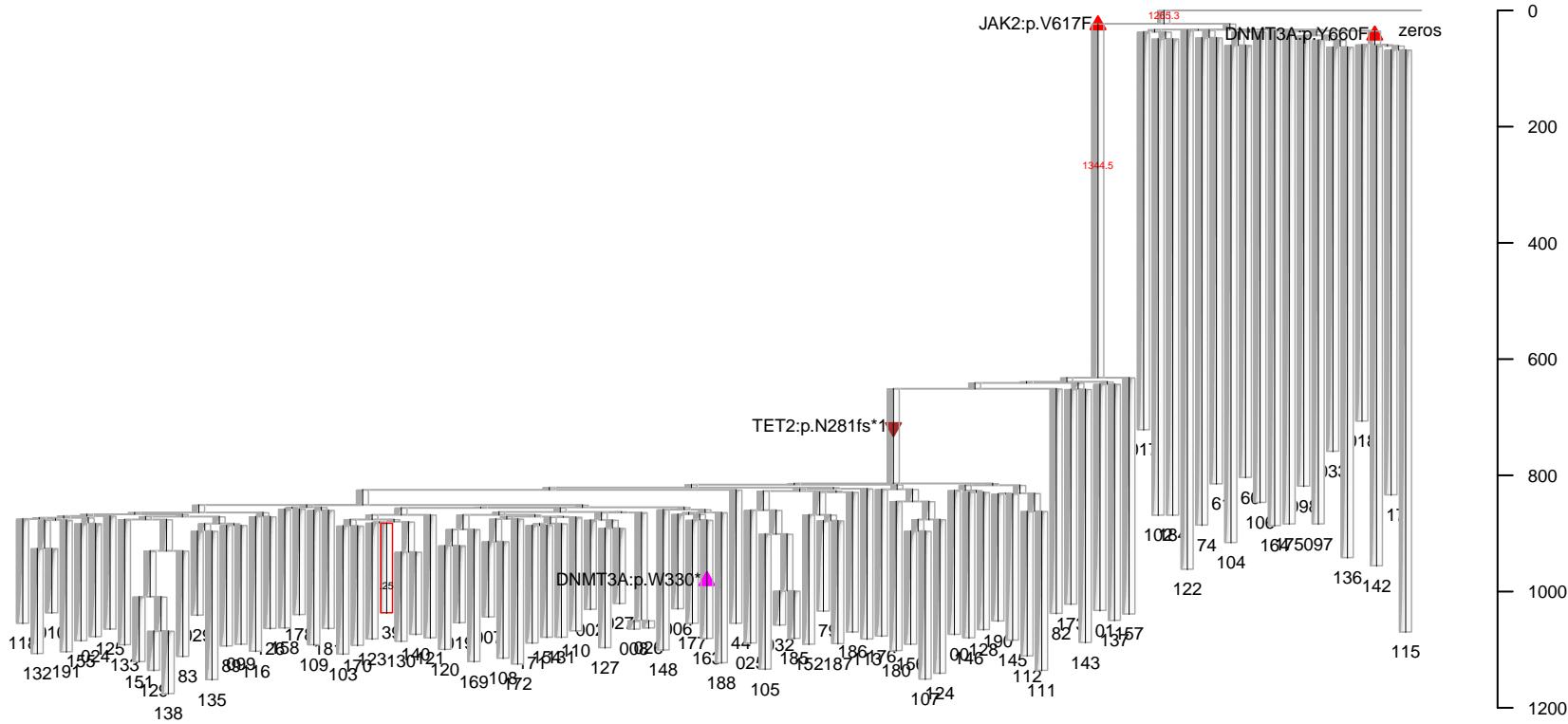


PD5847:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



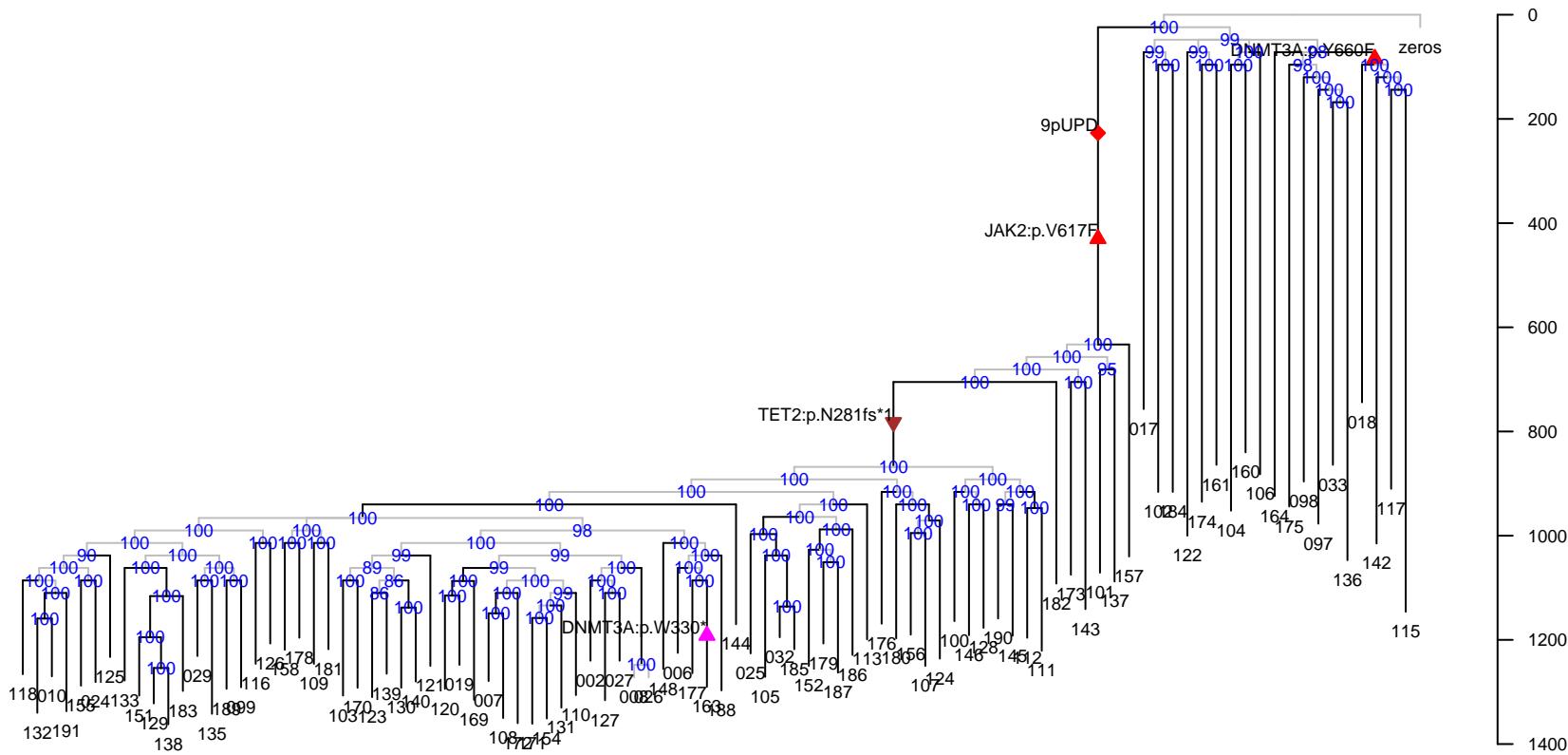
PD5847:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



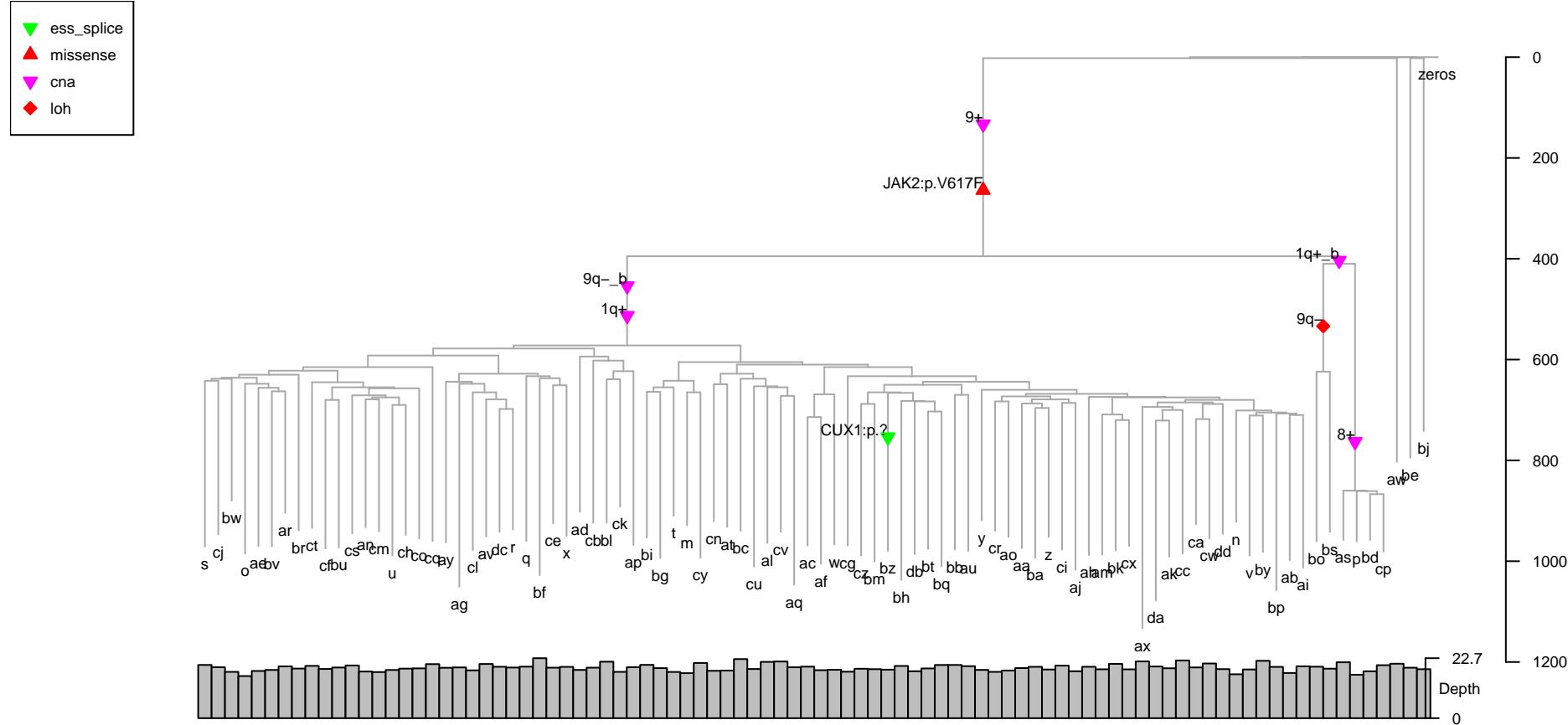


**PD5847: With MPBoot Bootstrap Support (Grey branches extended to 24 Mutations)**

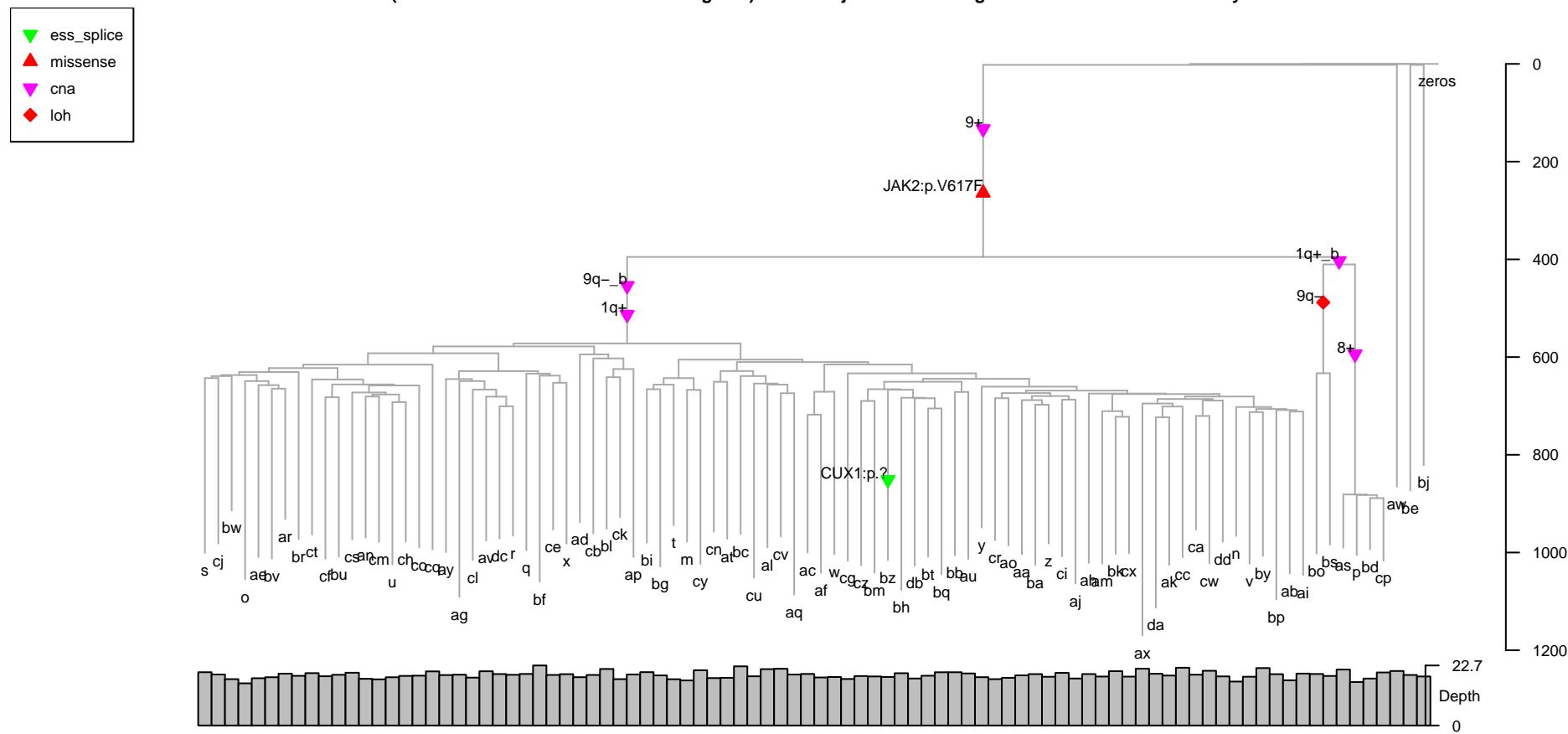
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  - ▲ nonsense
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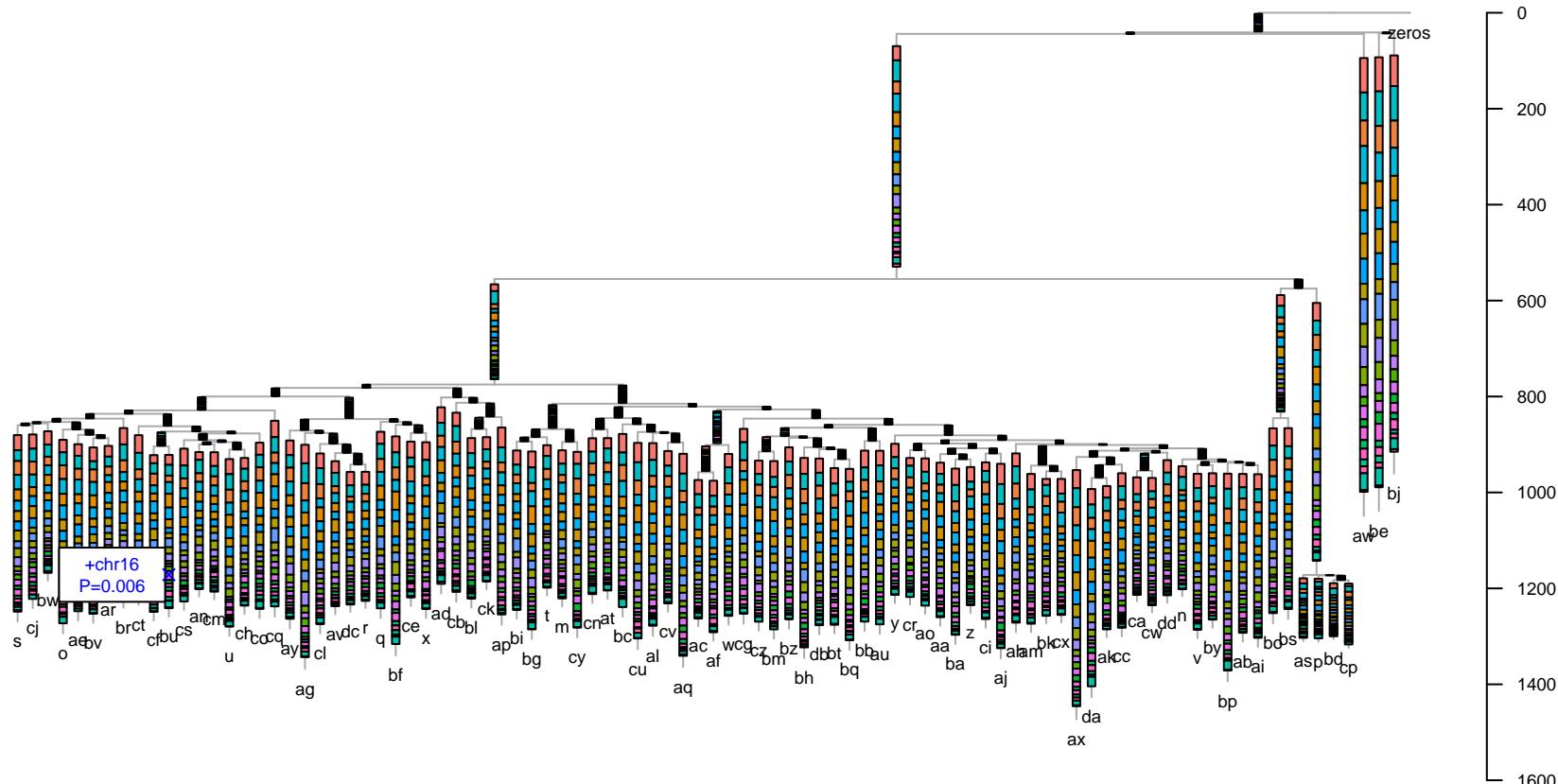
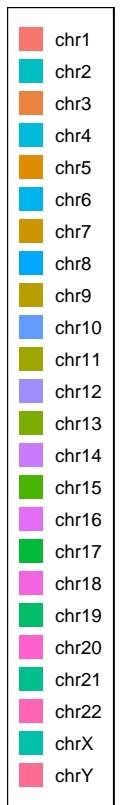
PD5179: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)



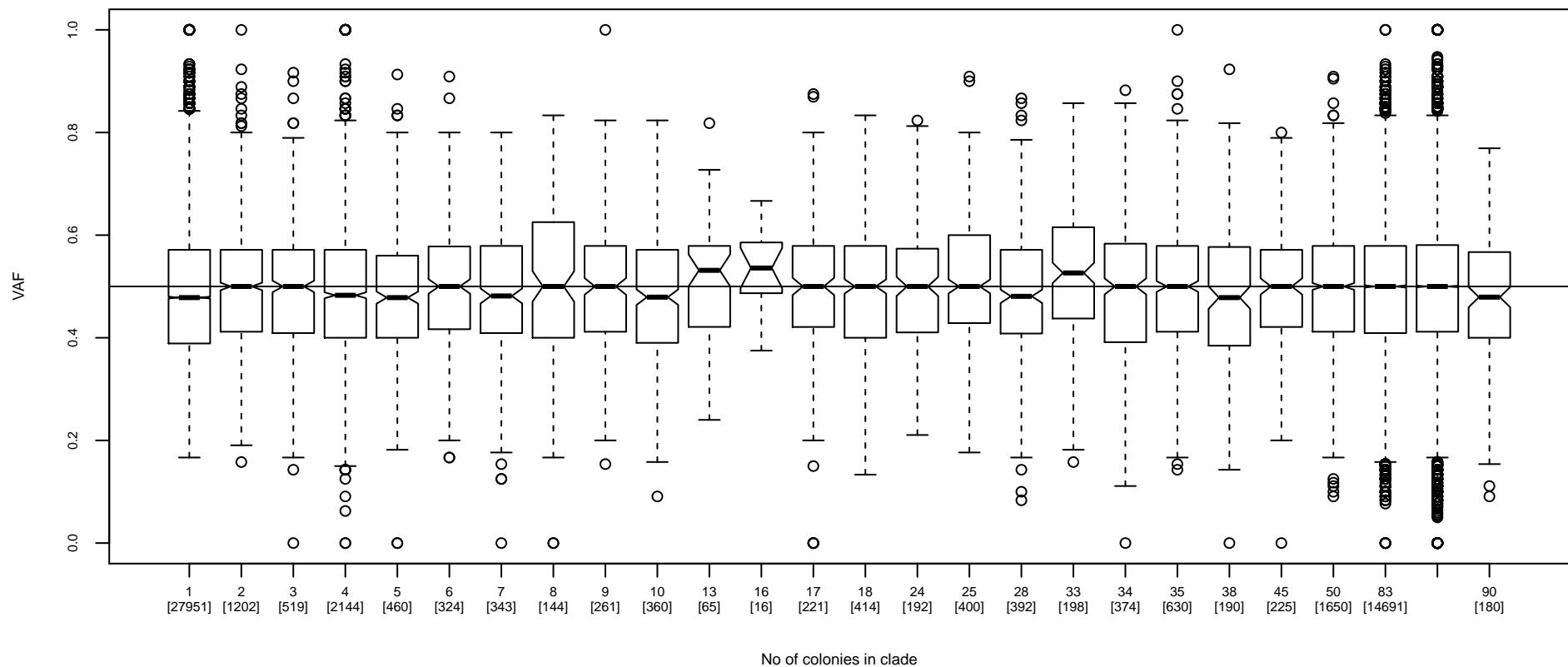
PD5179: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



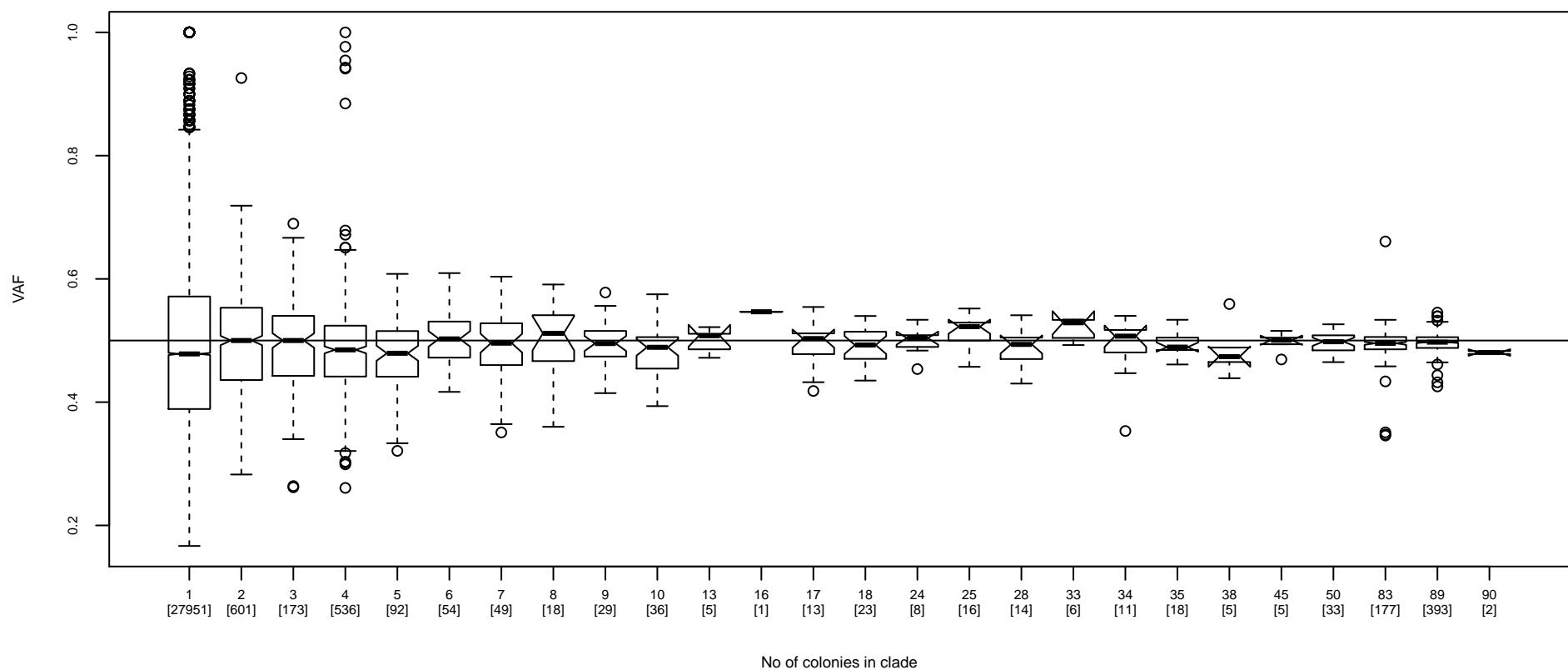
## PD5179: Chromosome composition check



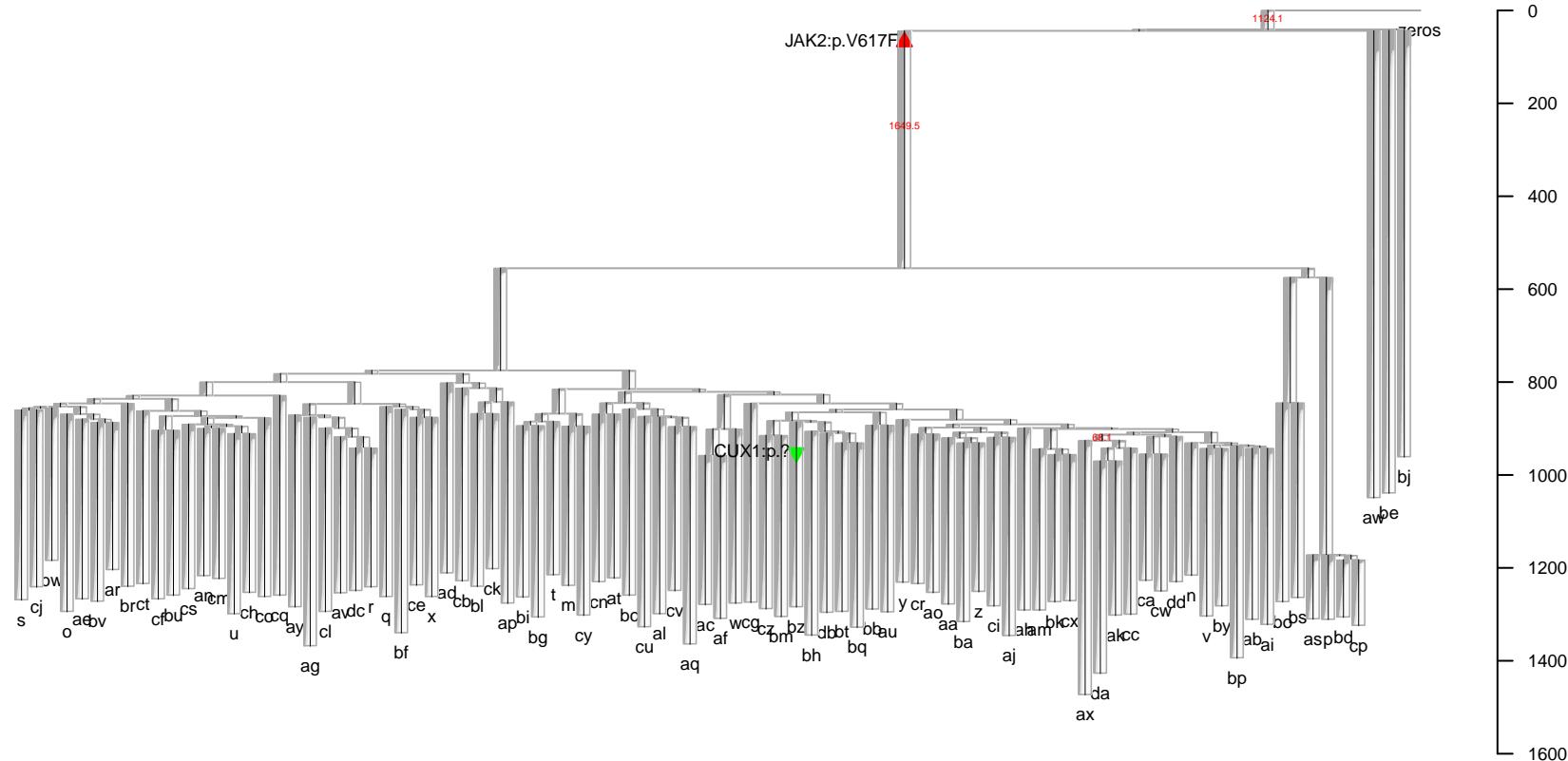
PD5179:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



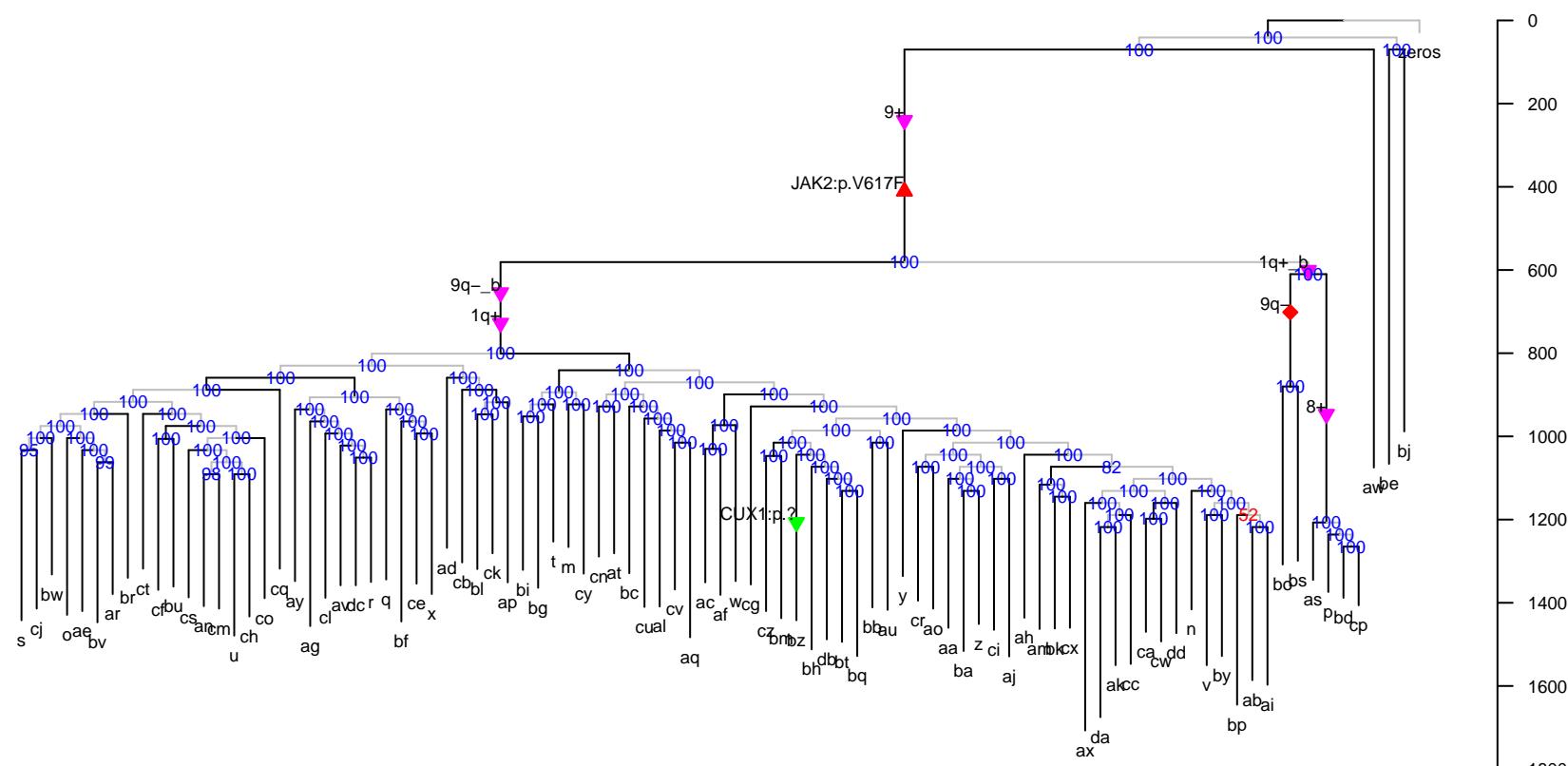
PD5179:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



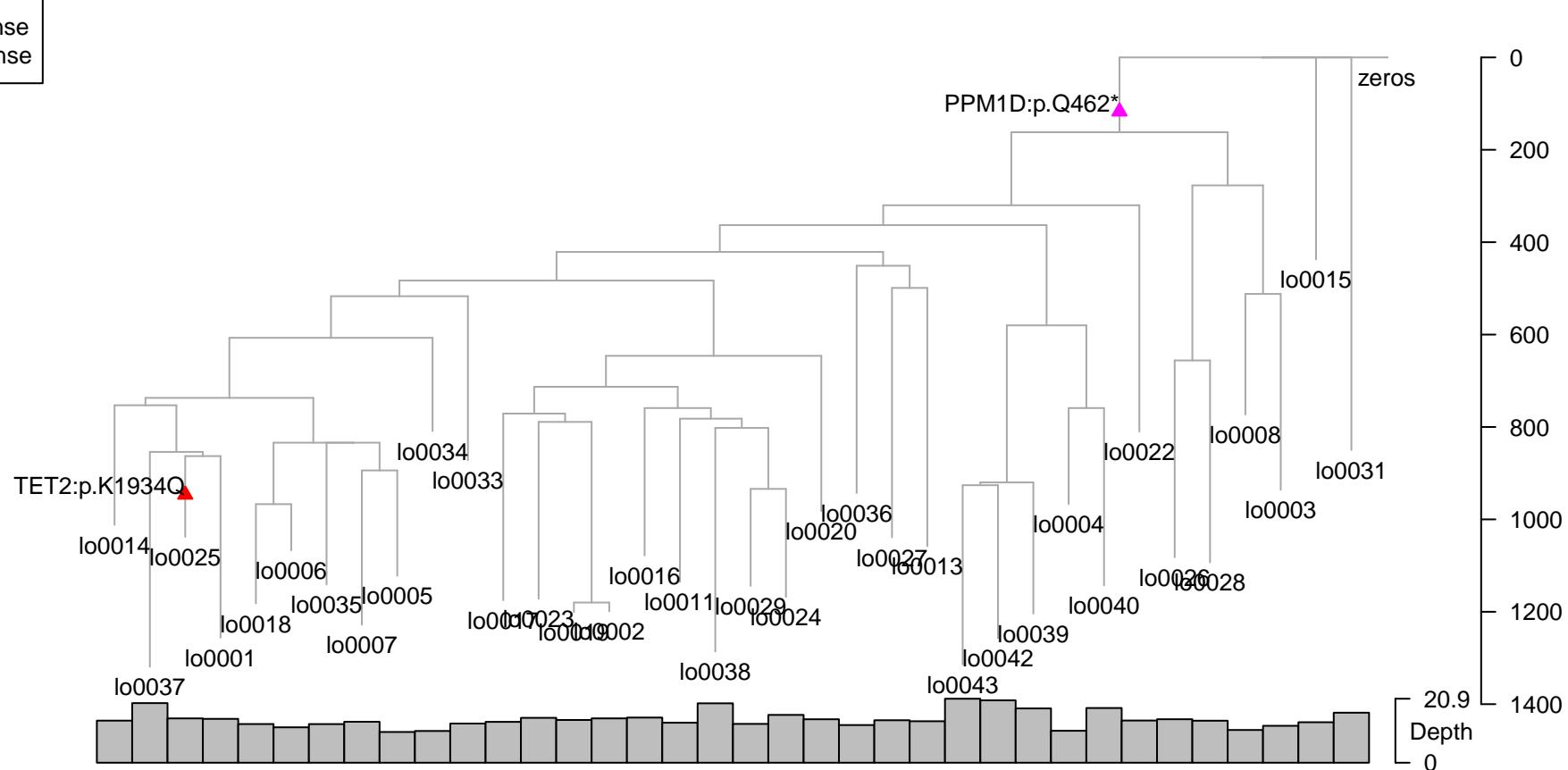
### PD5179 [Pooled VAF]



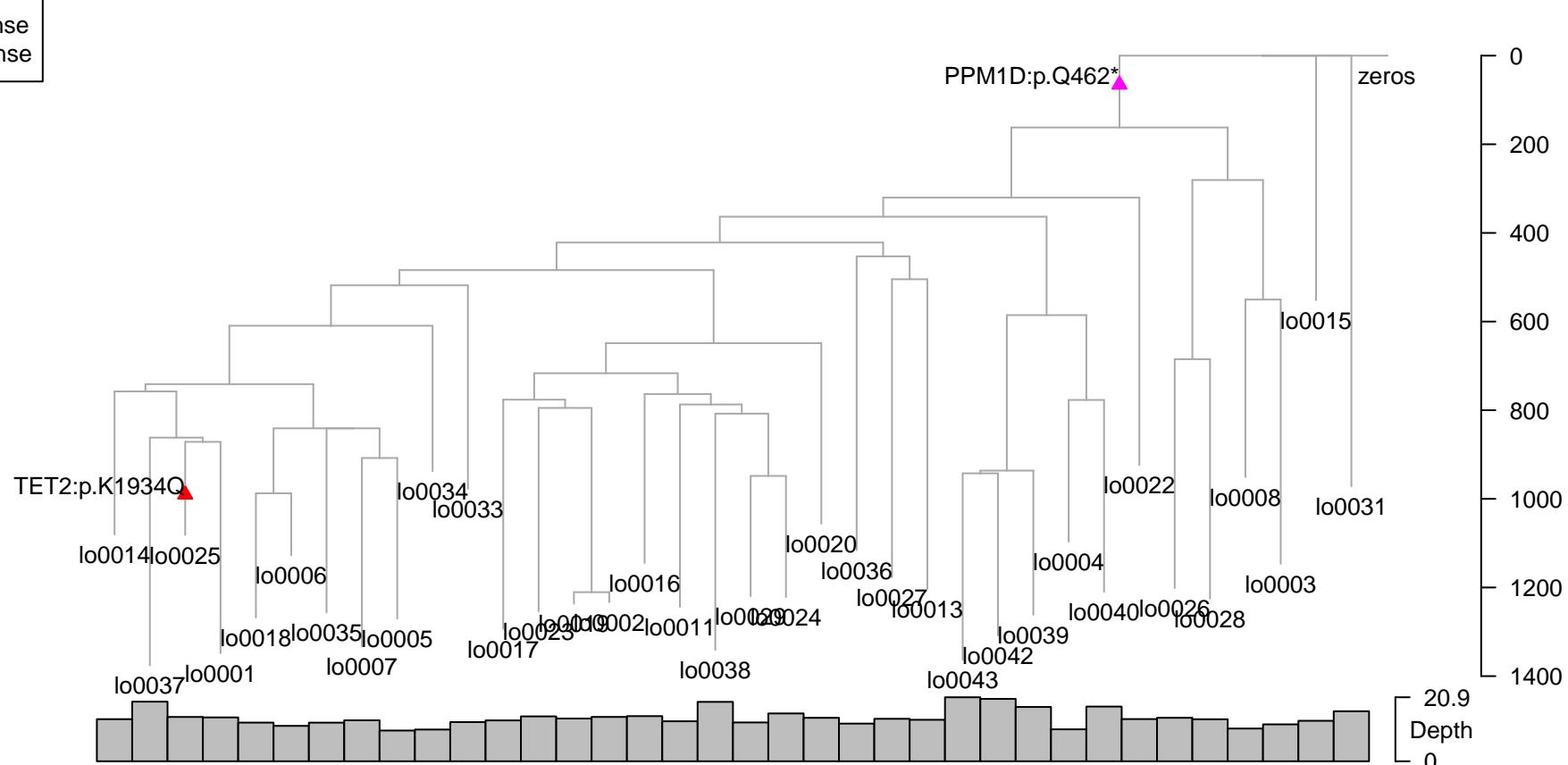
### PD5179: With MPBoot Bootstrap Support (Grey branches extended to 29 Mutations)



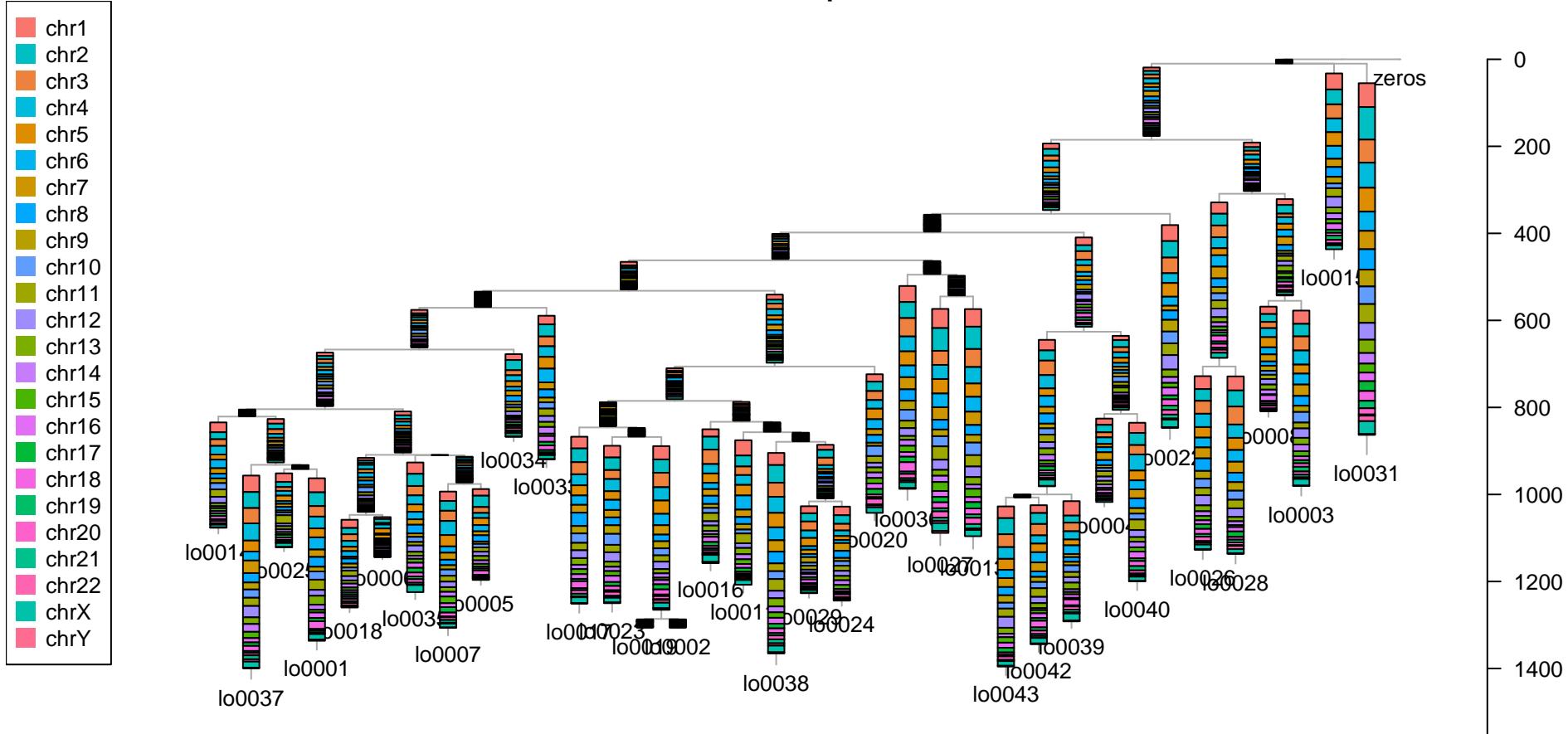
### PD6634: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)



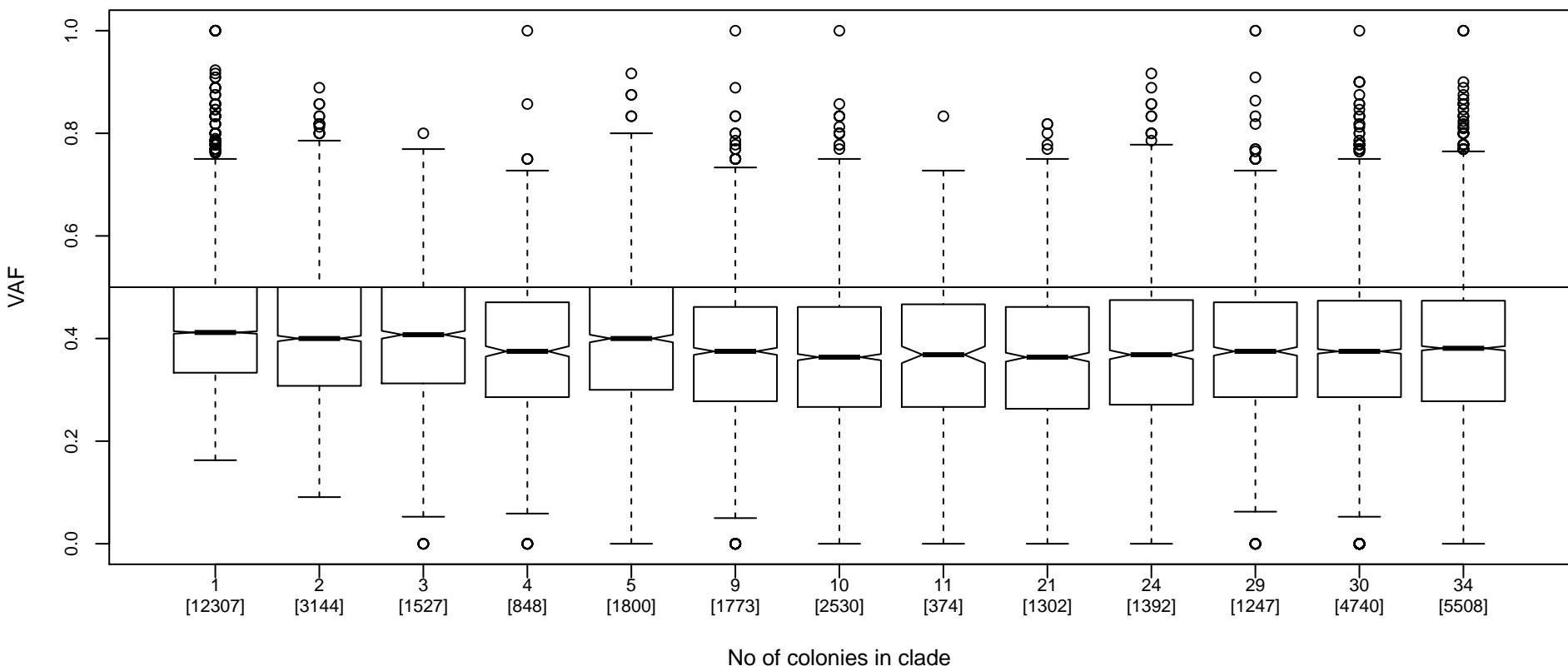
### PD6634: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



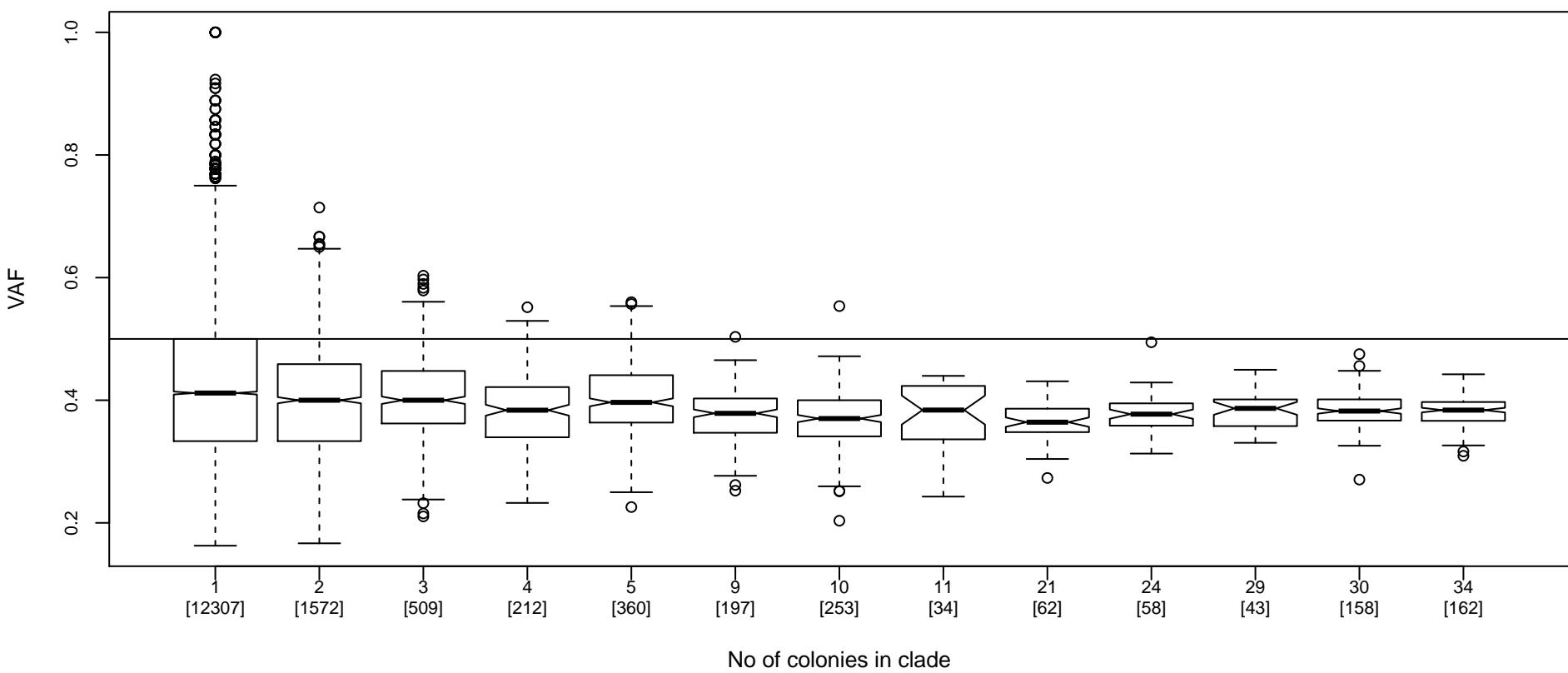
# PD6634: Chromosome composition check



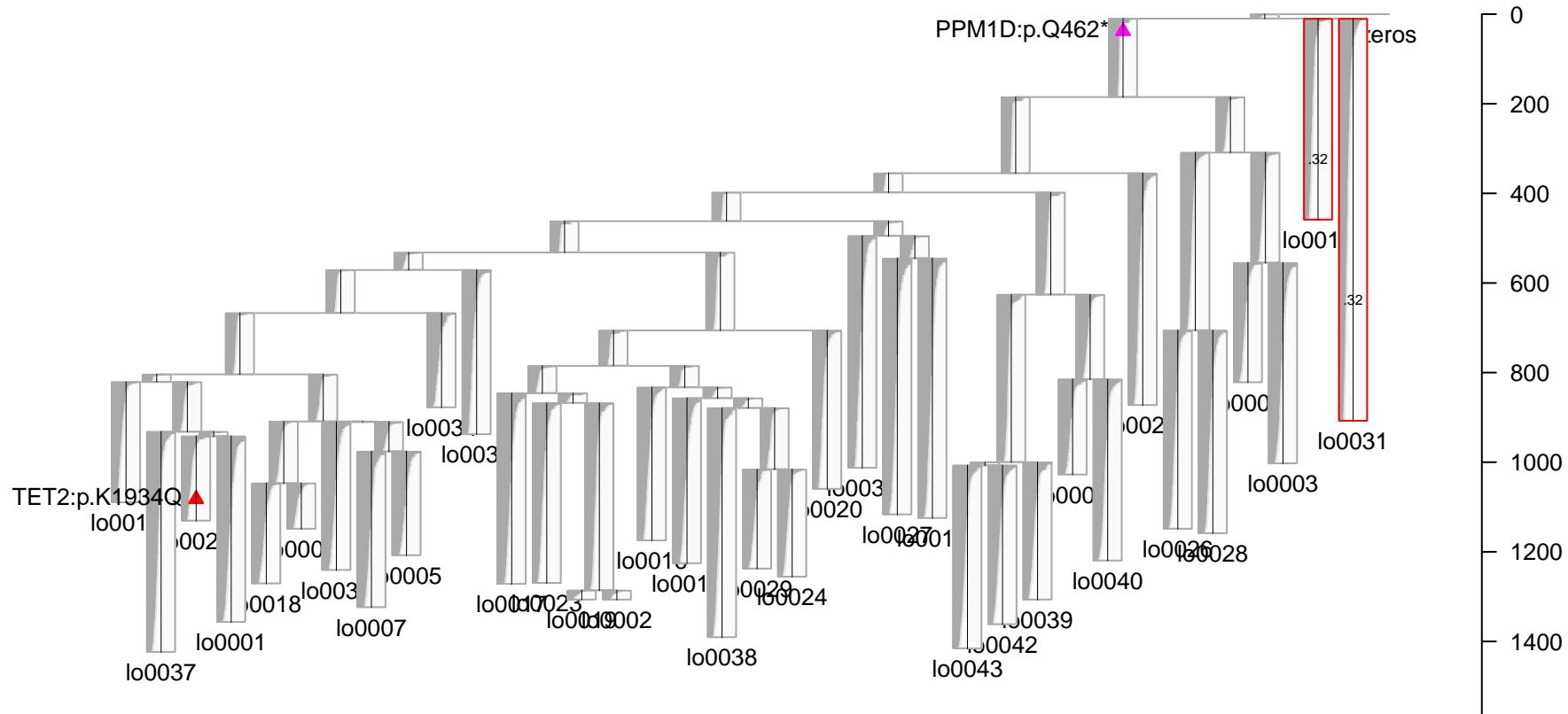
### PD6634:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



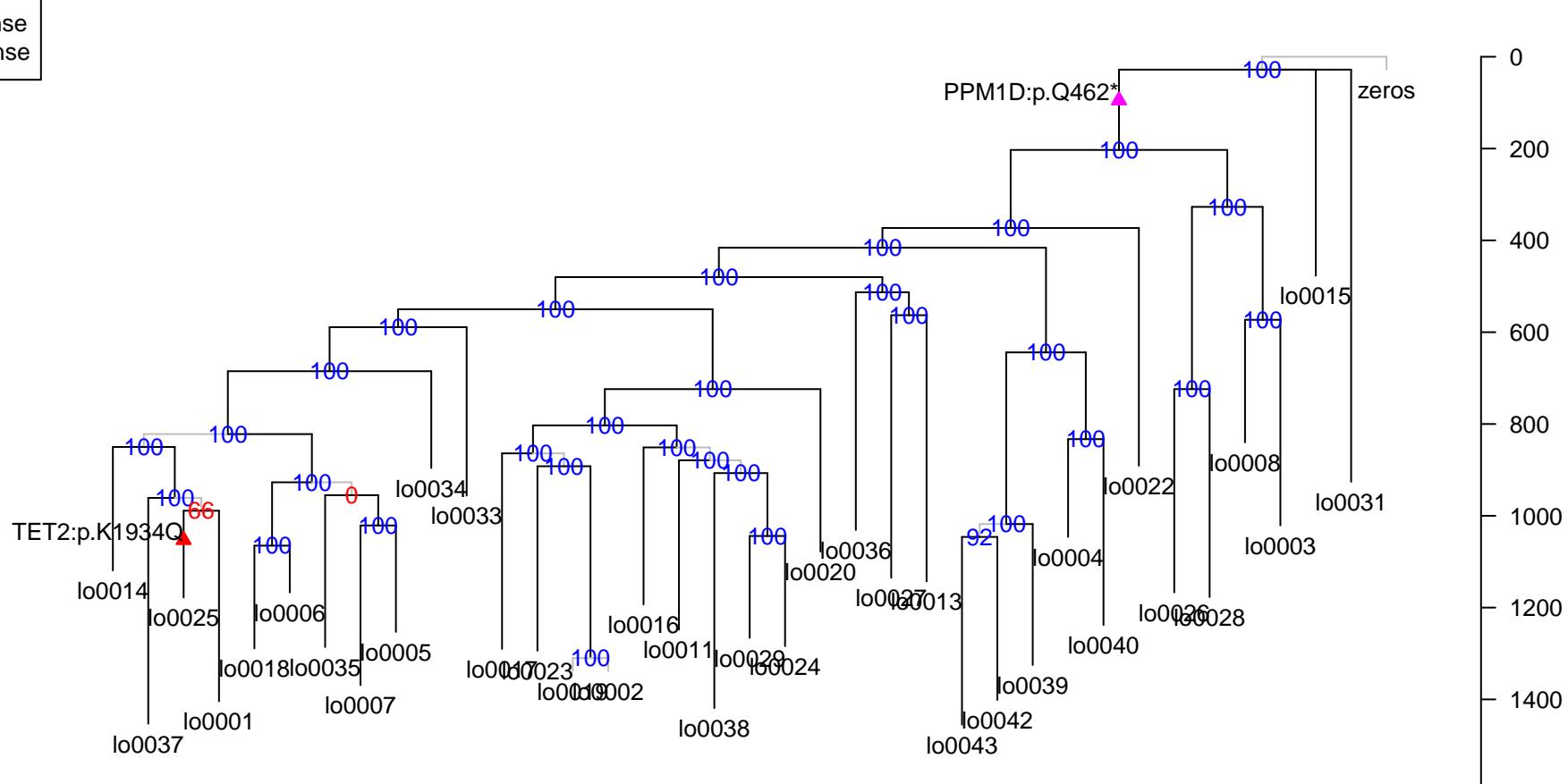
### PD6634:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



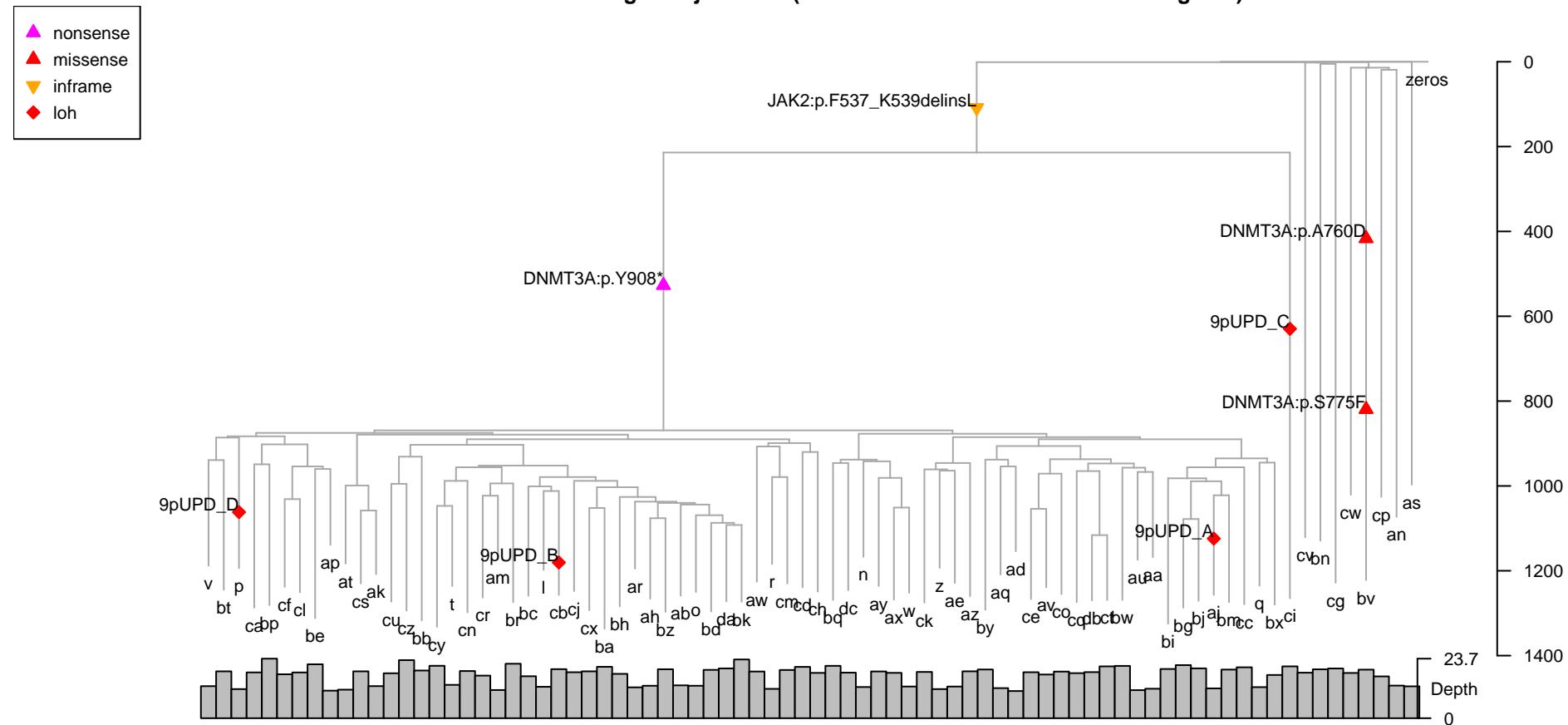
# PD6634 [Pooled VAF]



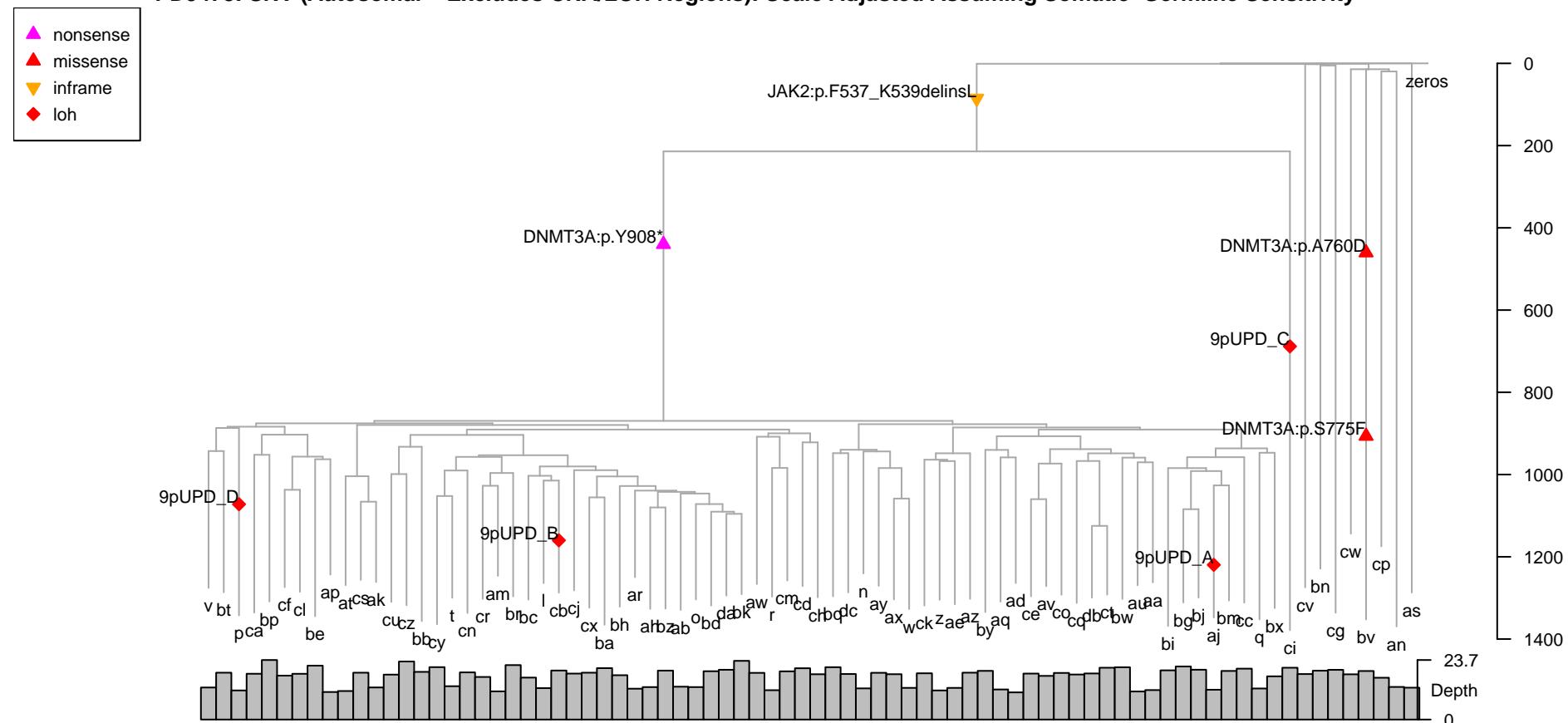
## PD6634: With MPBoot Bootstrap Support (Grey branches extended to 28 Mutations)



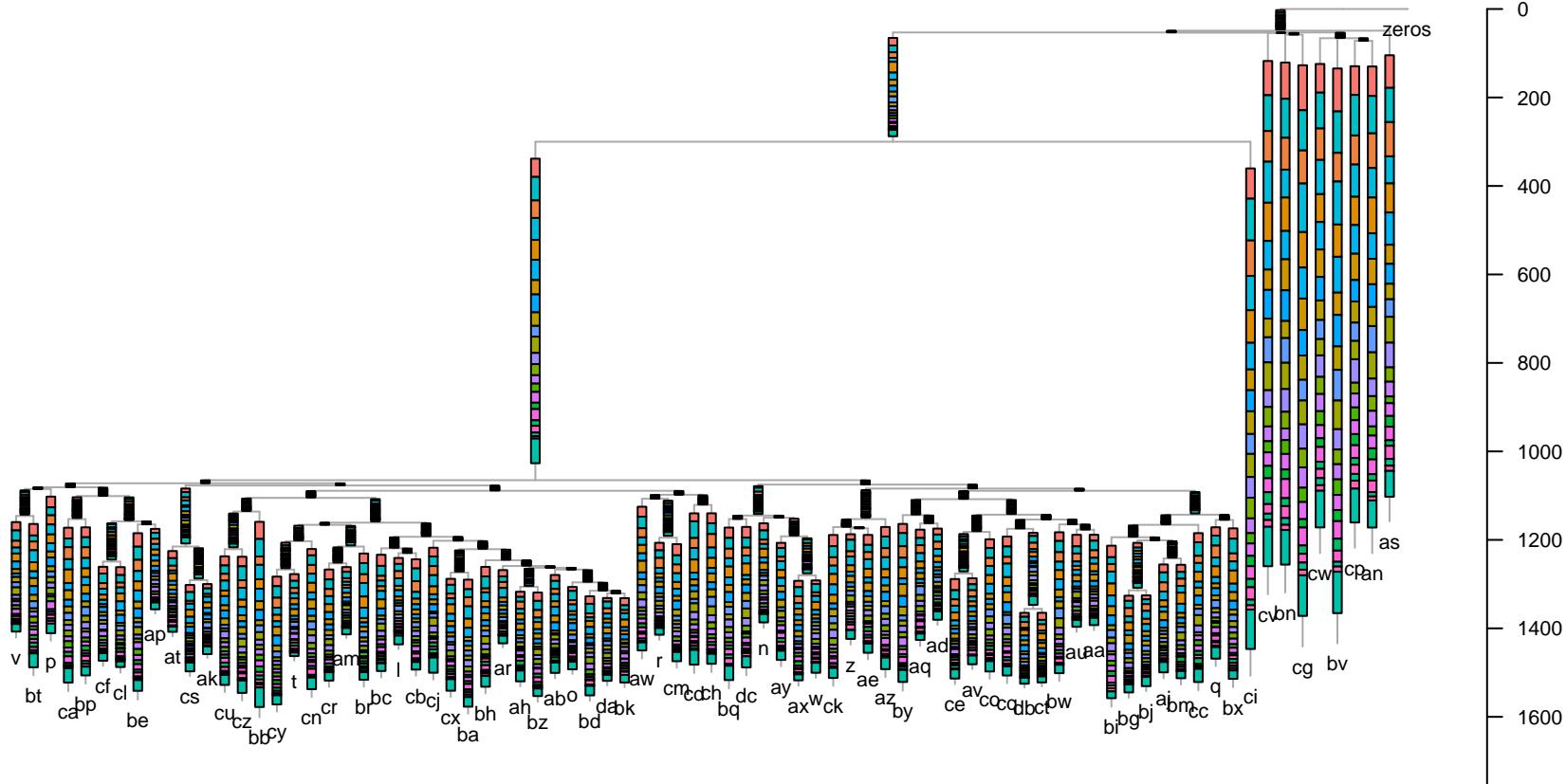
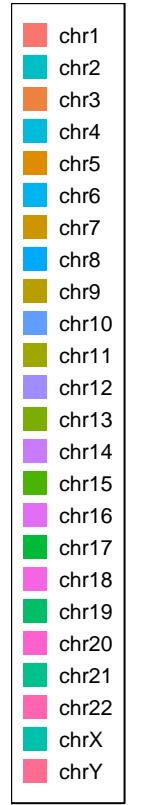
### PD9478: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)



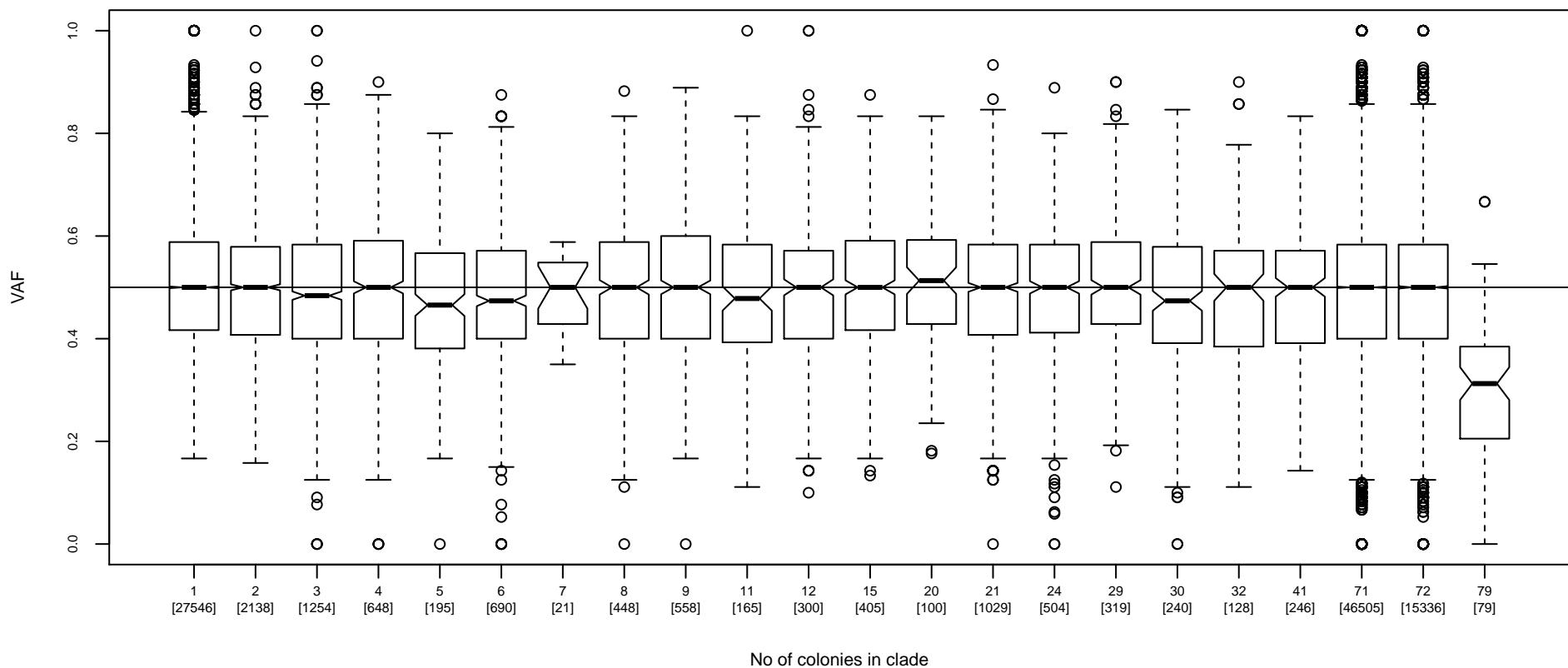
### PD9478: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



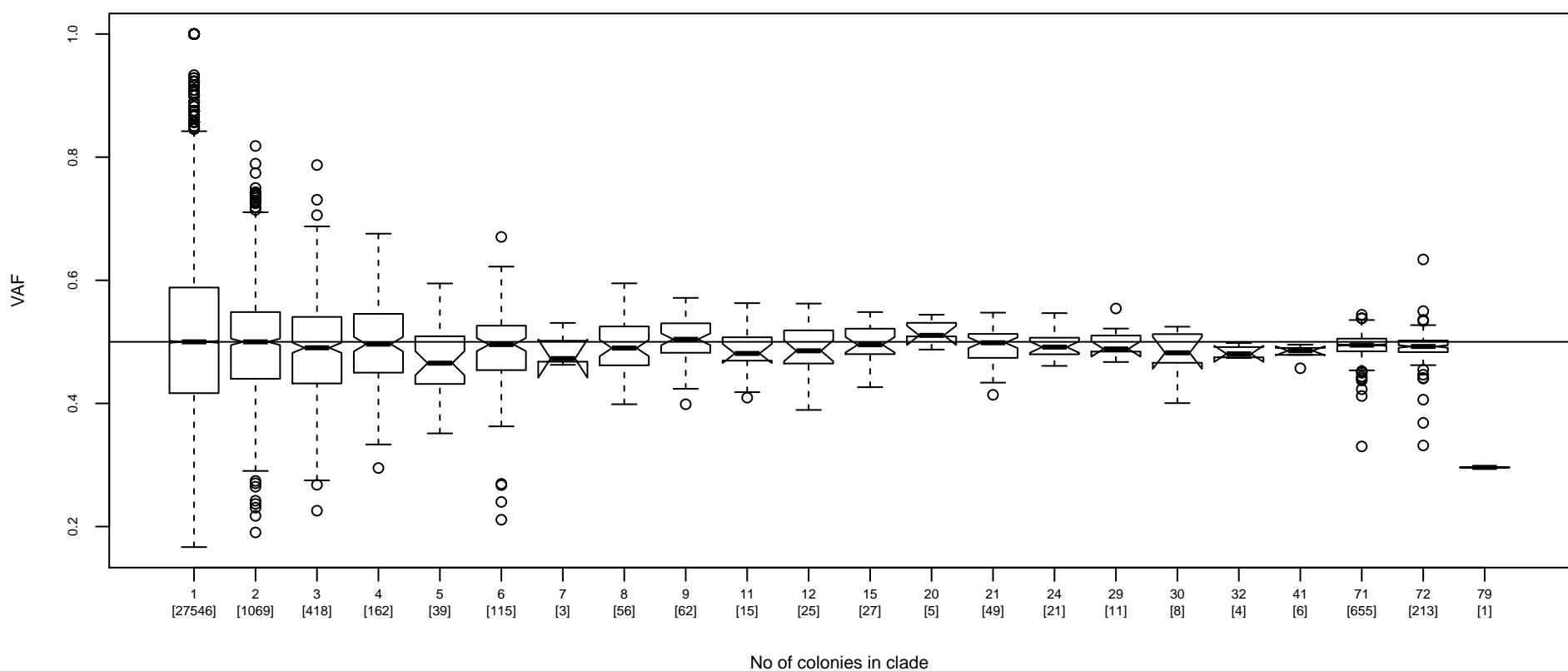
# PD9478: Chromosome composition check



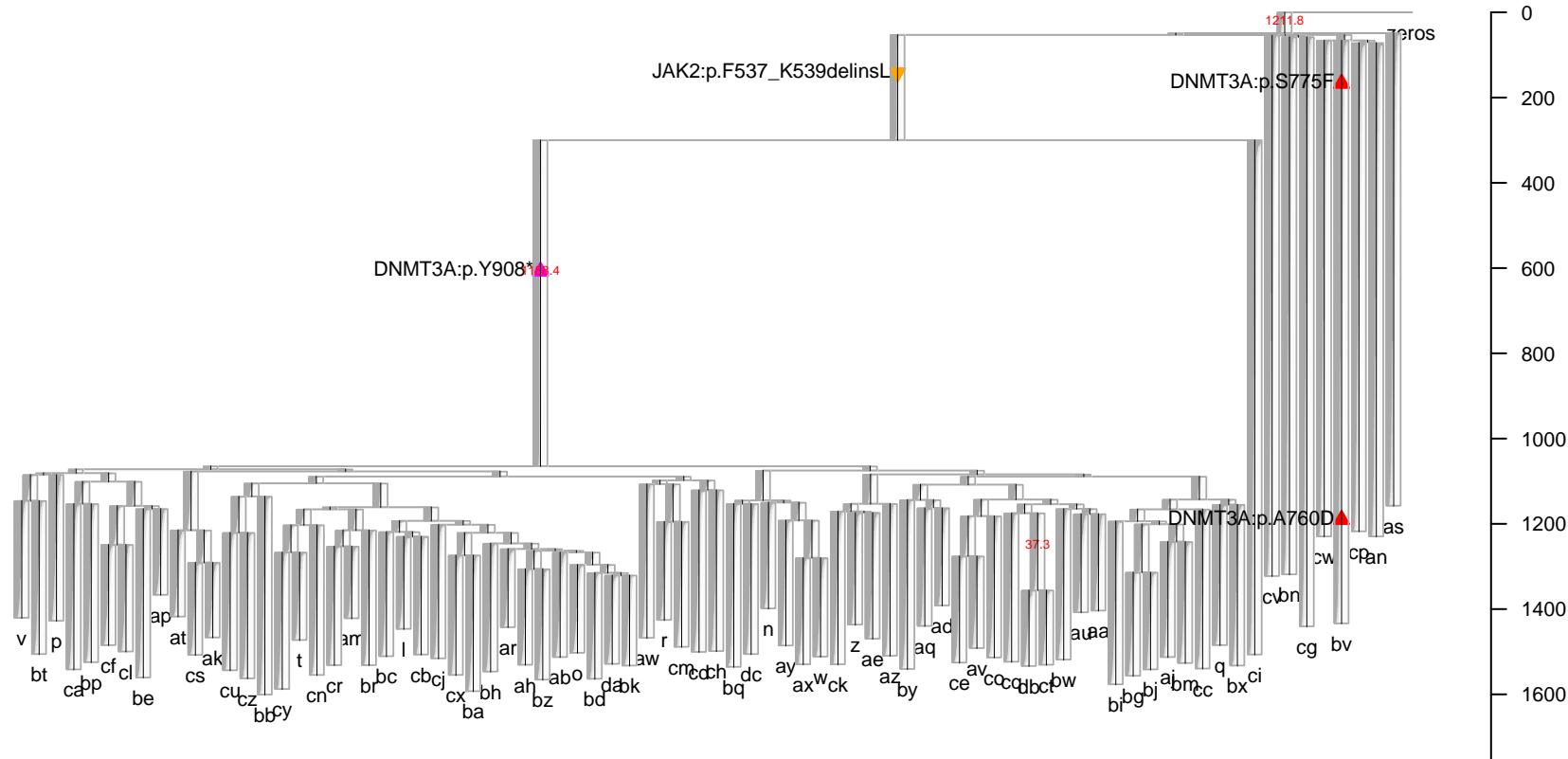
### PD9478:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



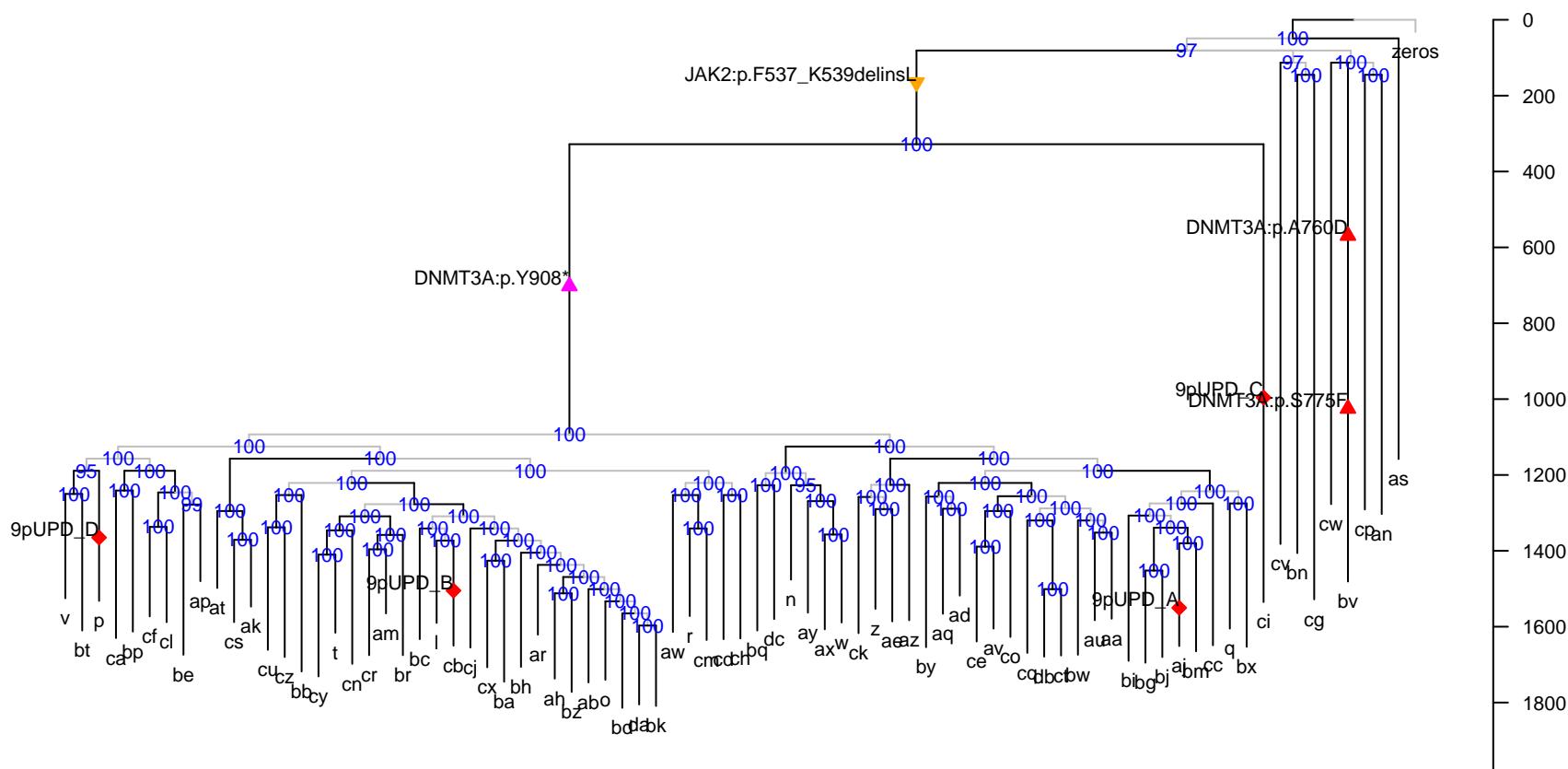
### PD9478:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



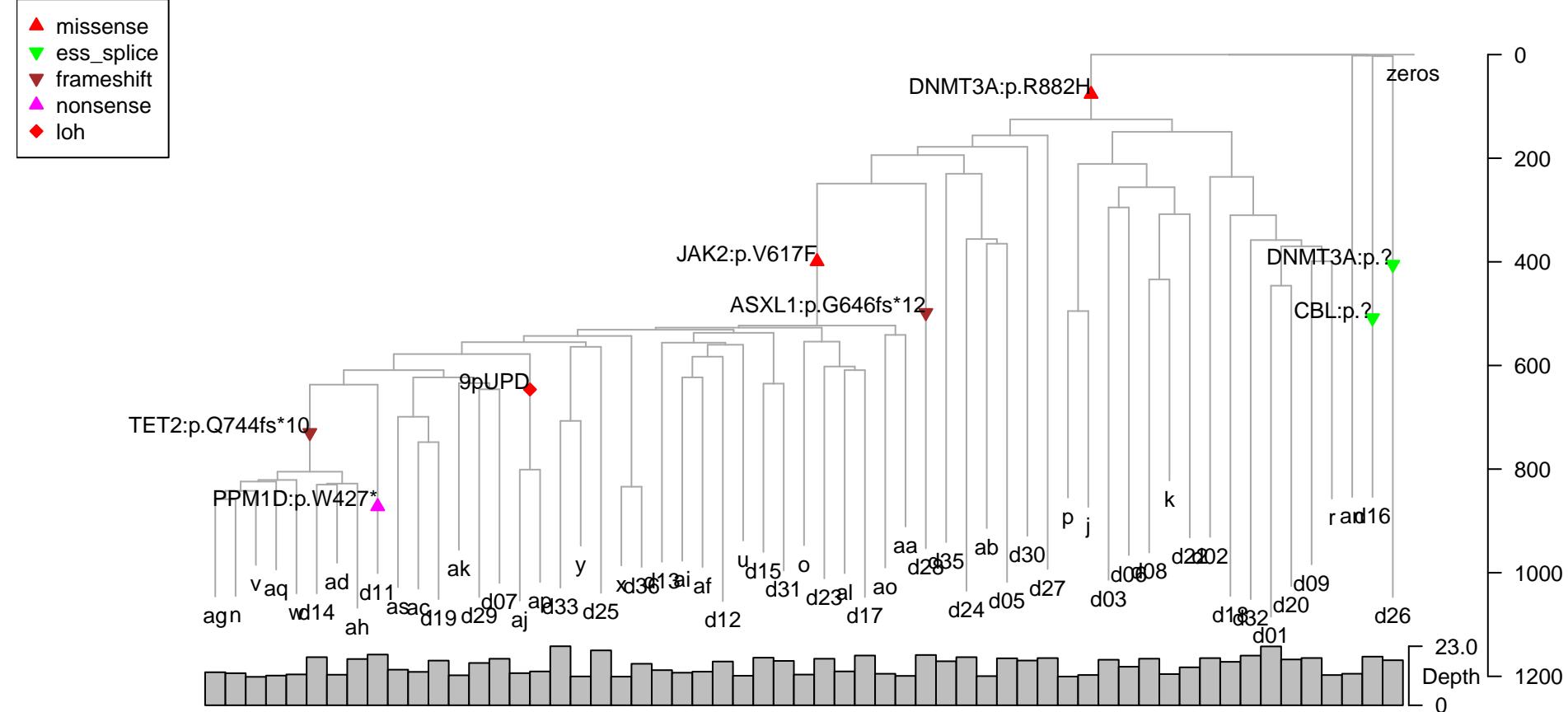
### PD9478 [Pooled VAF]



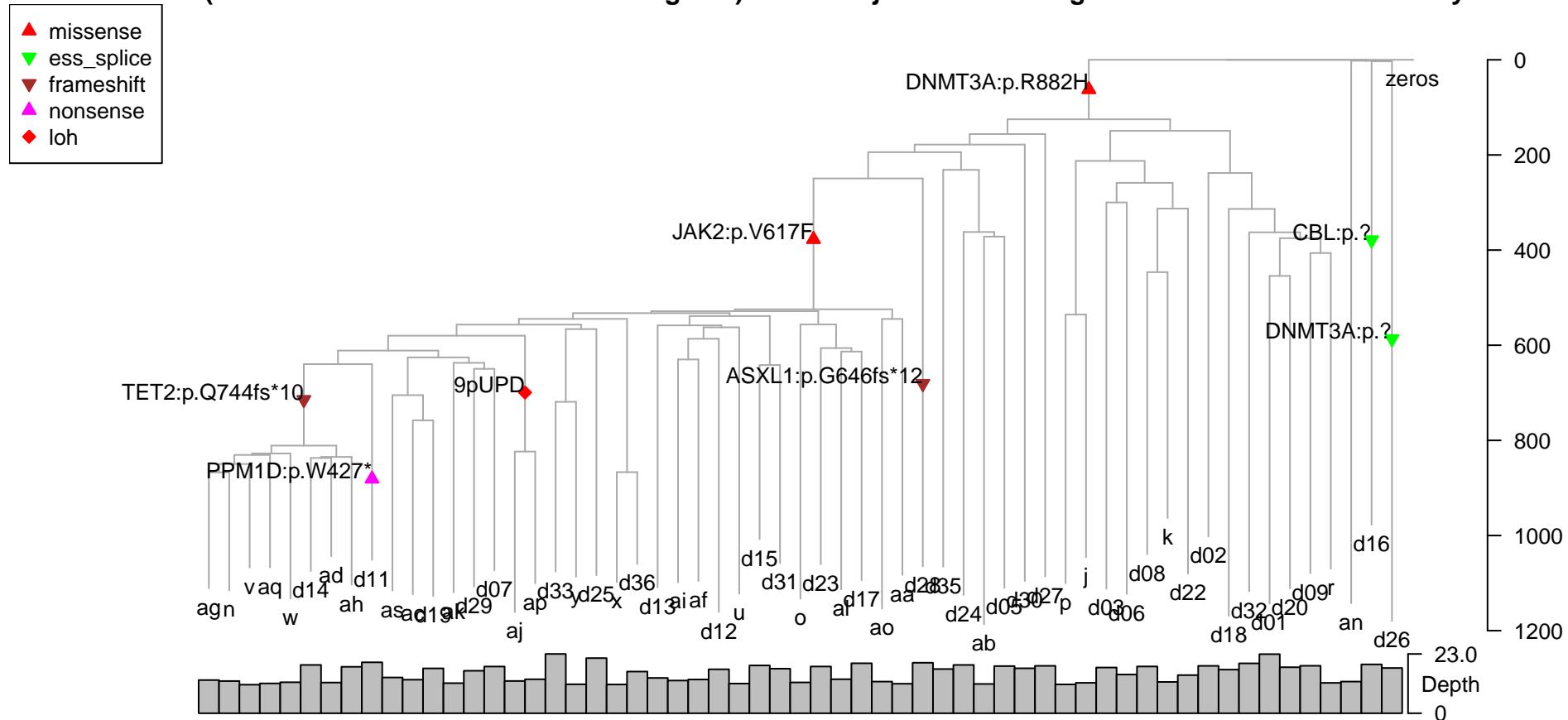
### PD9478: With MPBoot Bootstrap Support (Grey branches extended to 32 Mutations)



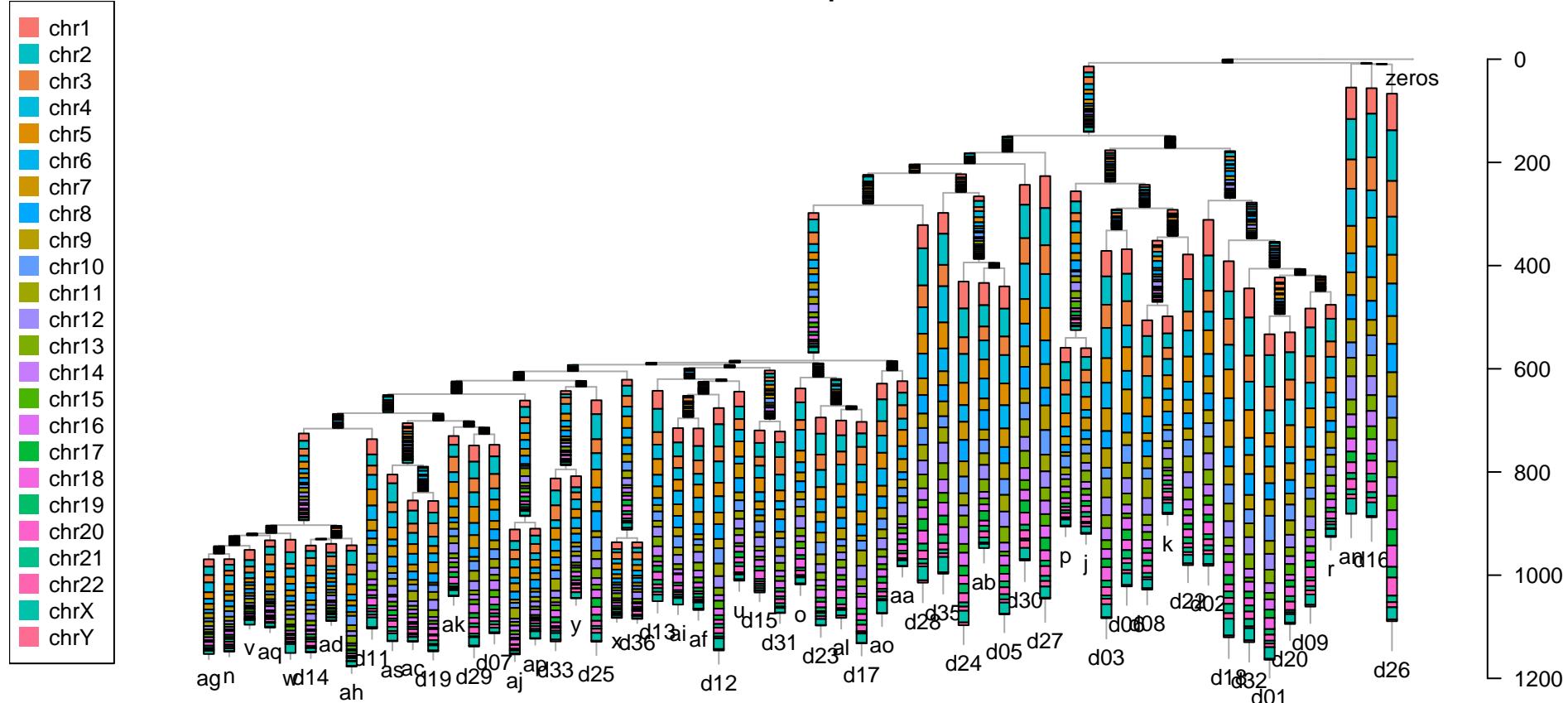
### PD6629: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)



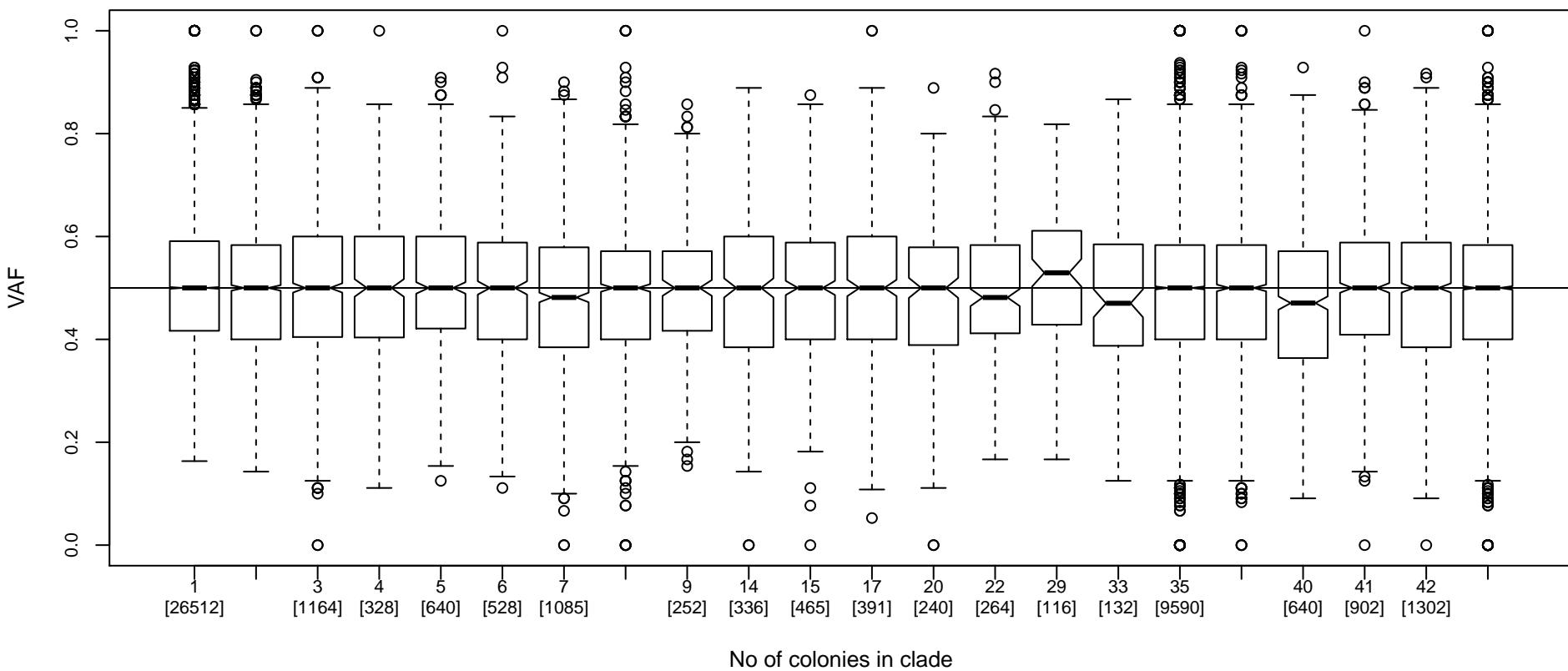
### PD6629: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



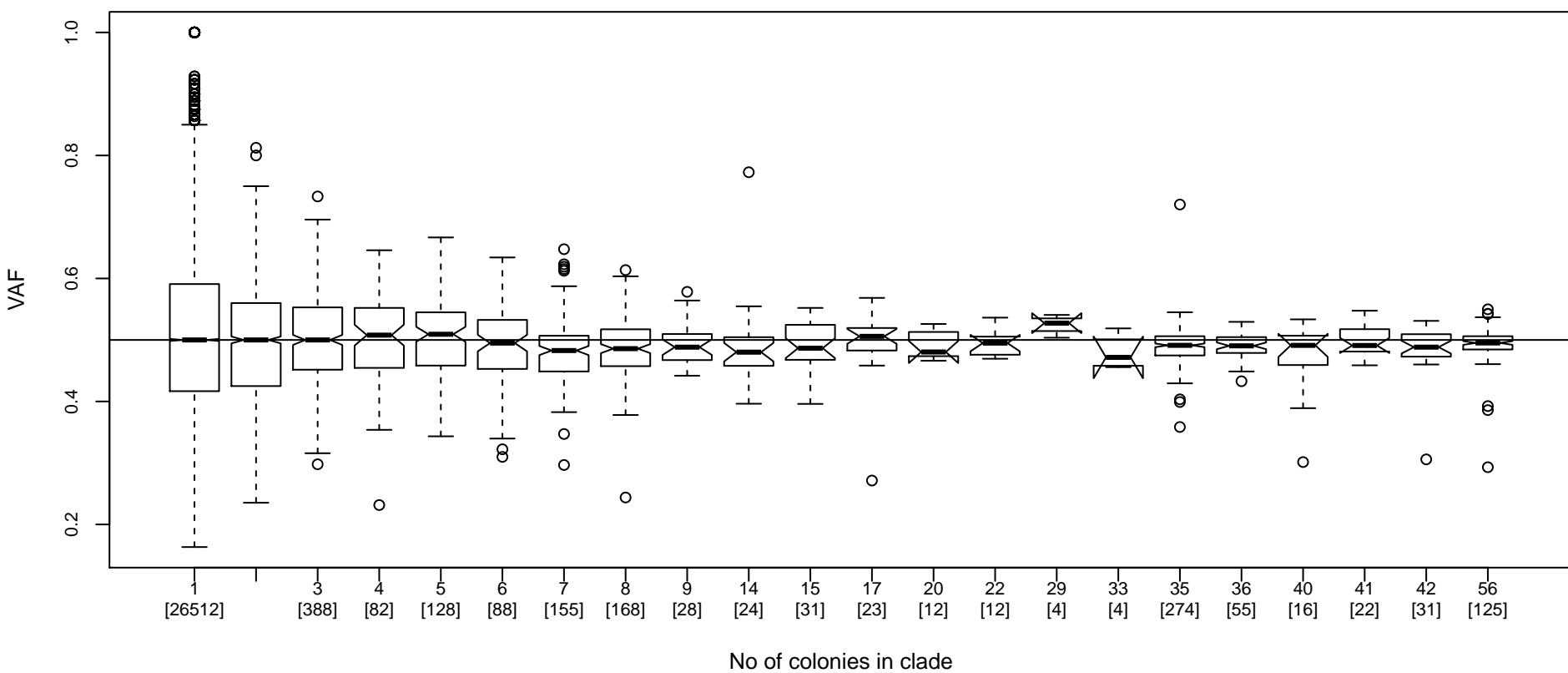
# PD6629: Chromosome composition check



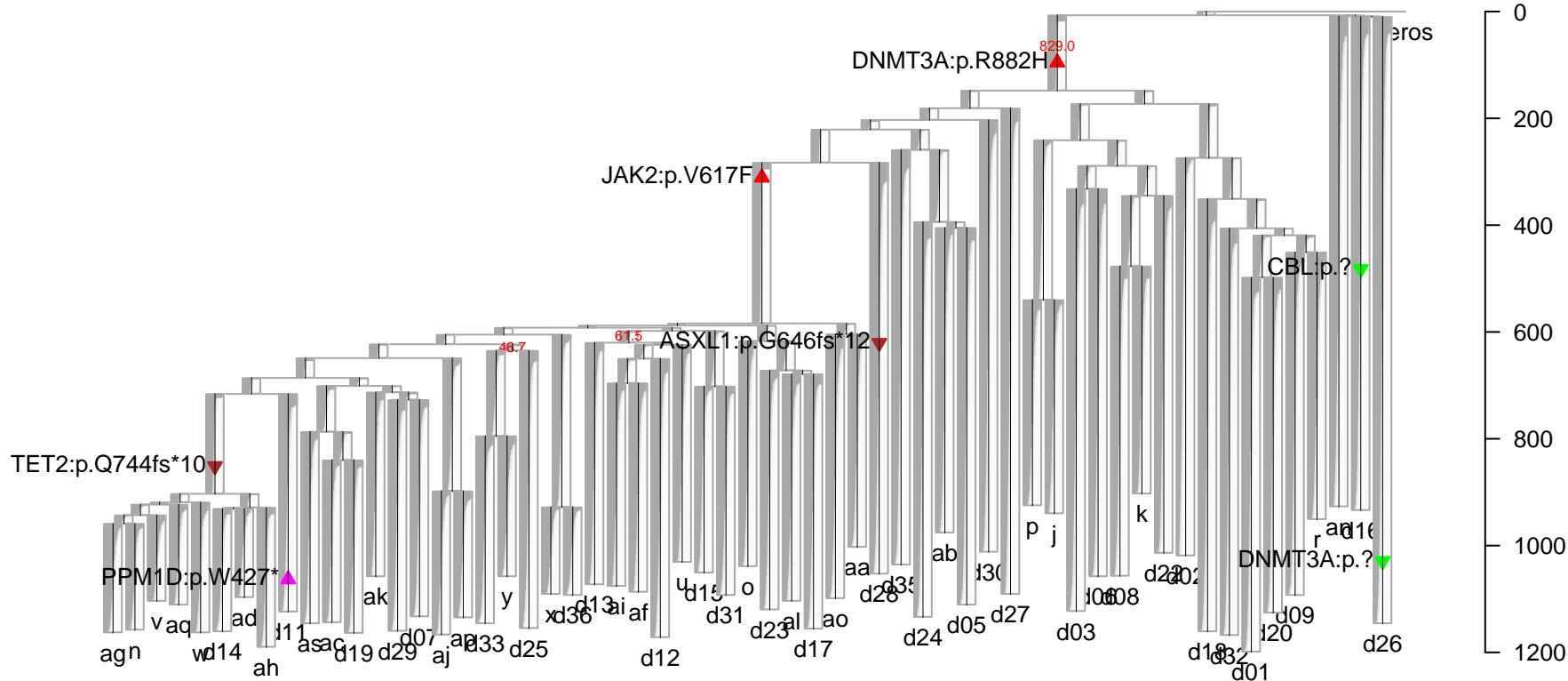
### PD6629:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



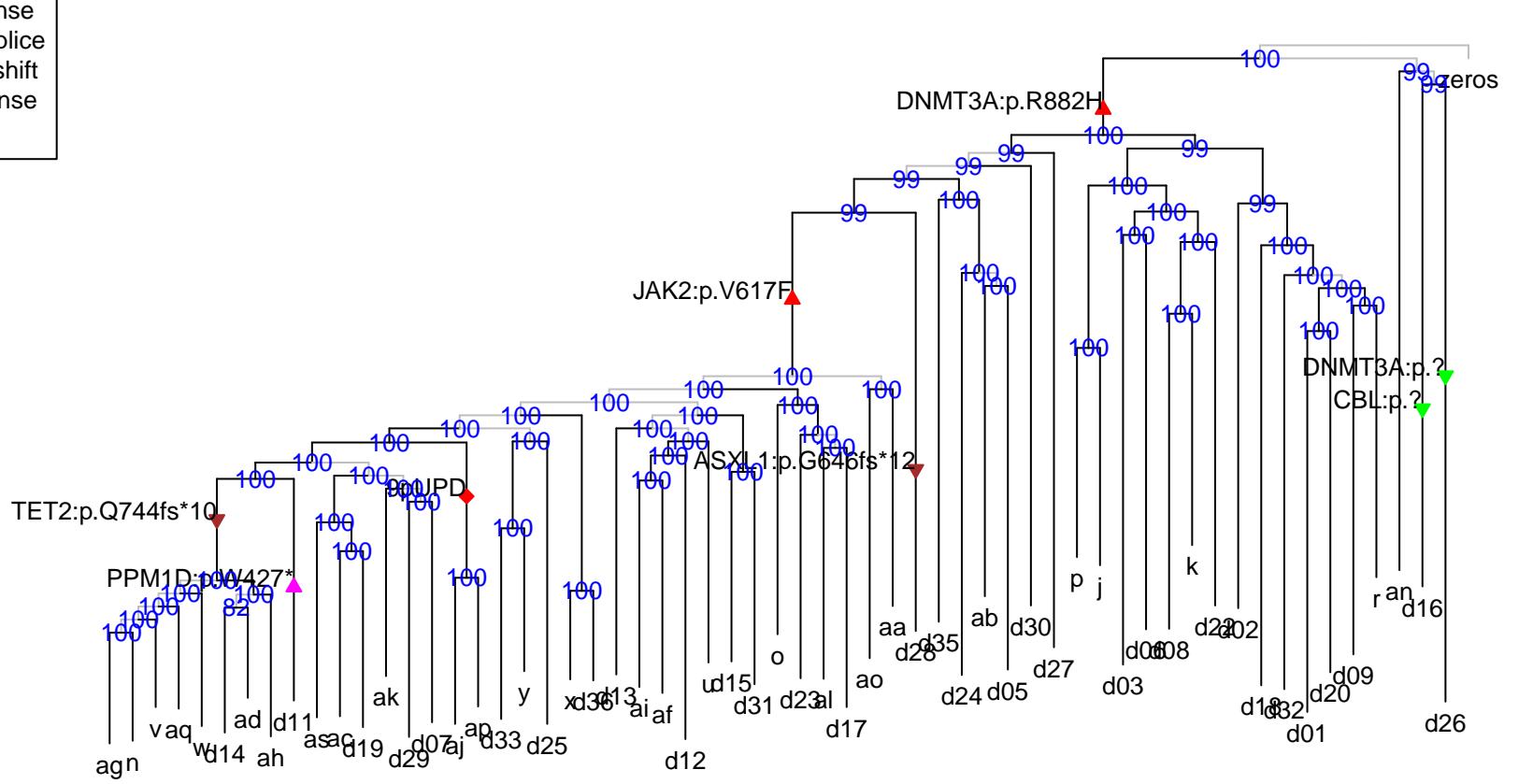
### PD6629:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



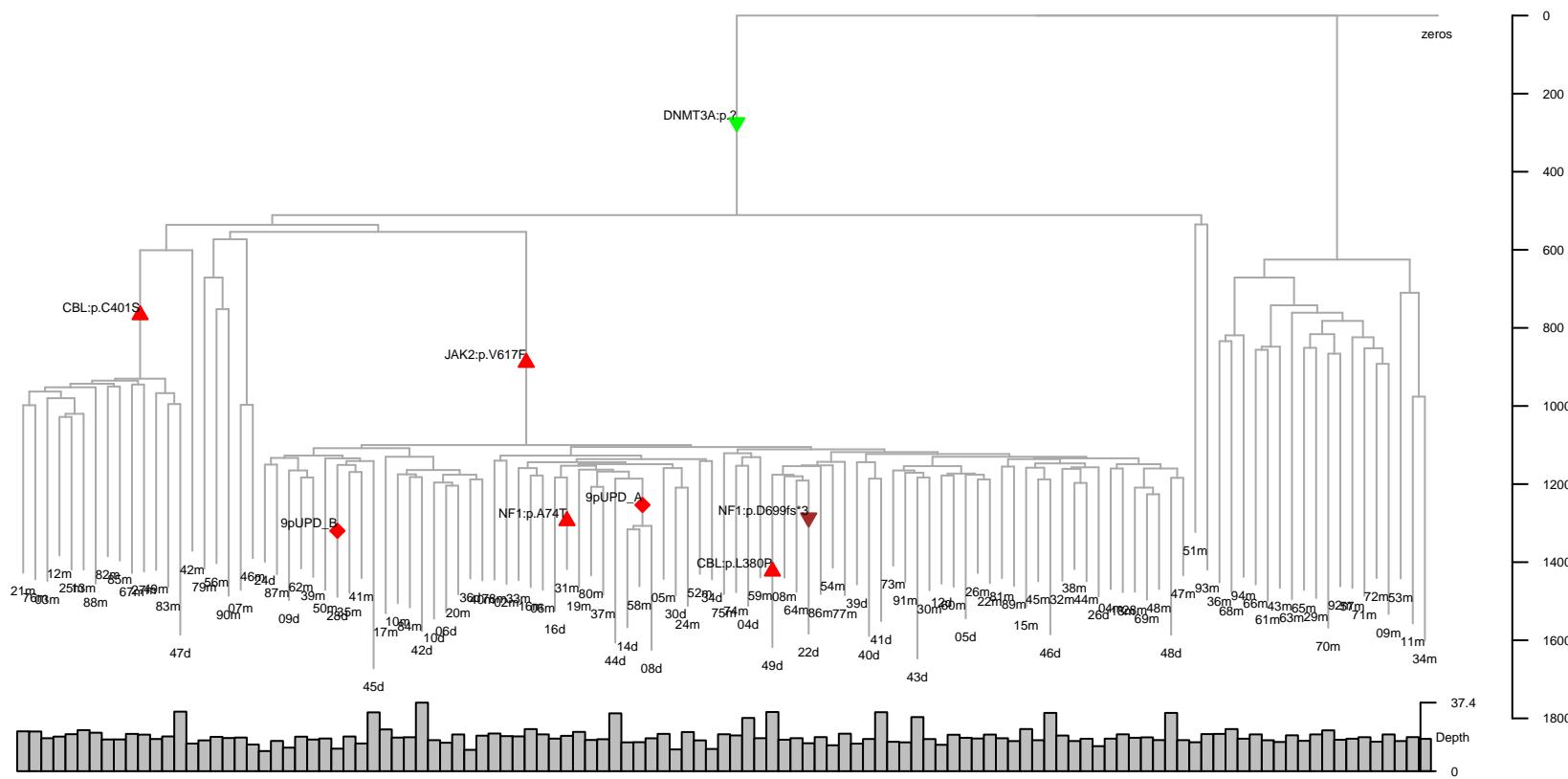
# PD6629 [Pooled VAF]



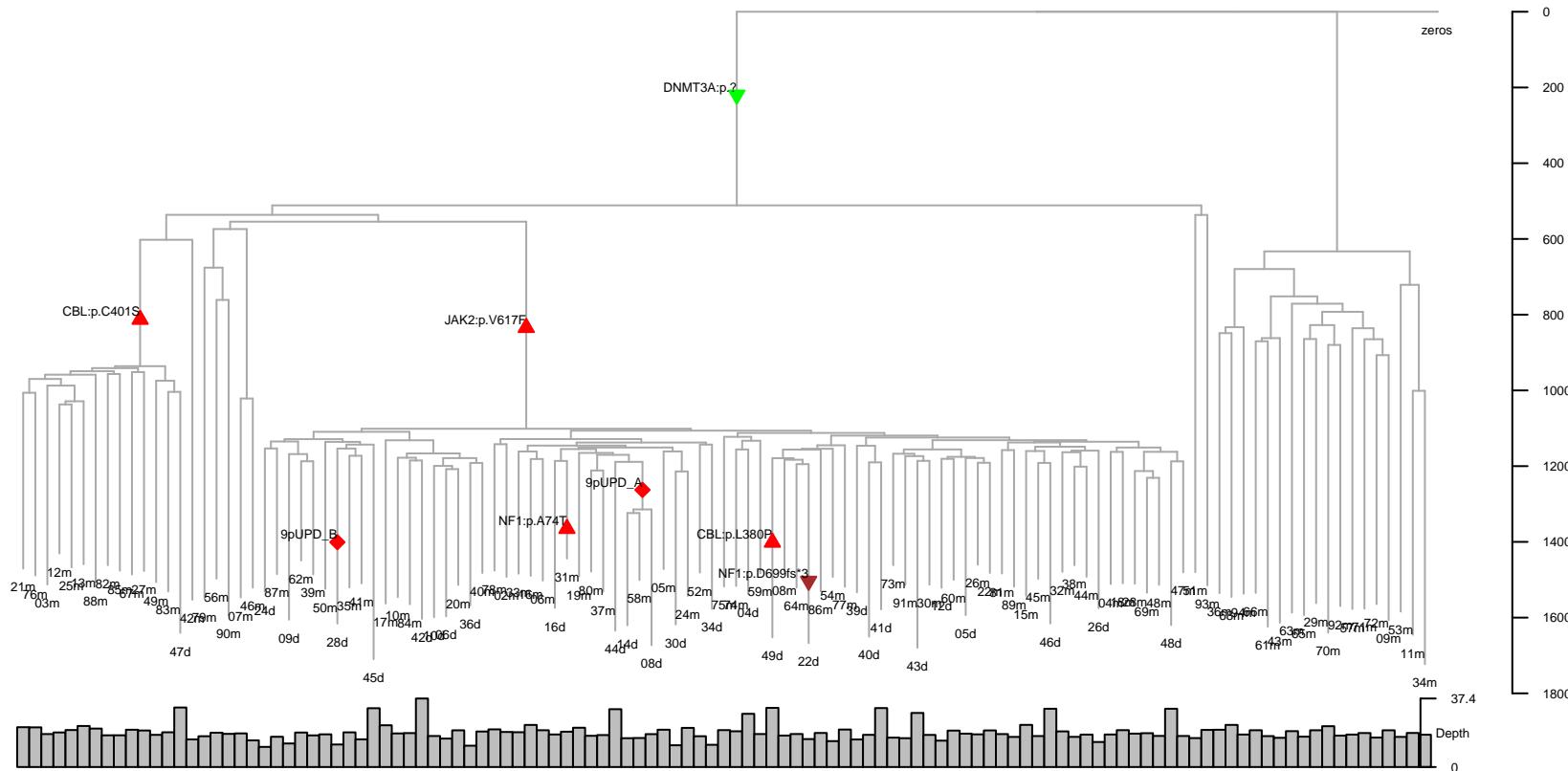
## PD6629: With MPBoot Bootstrap Support (Grey branches extended to 24 Mutations)



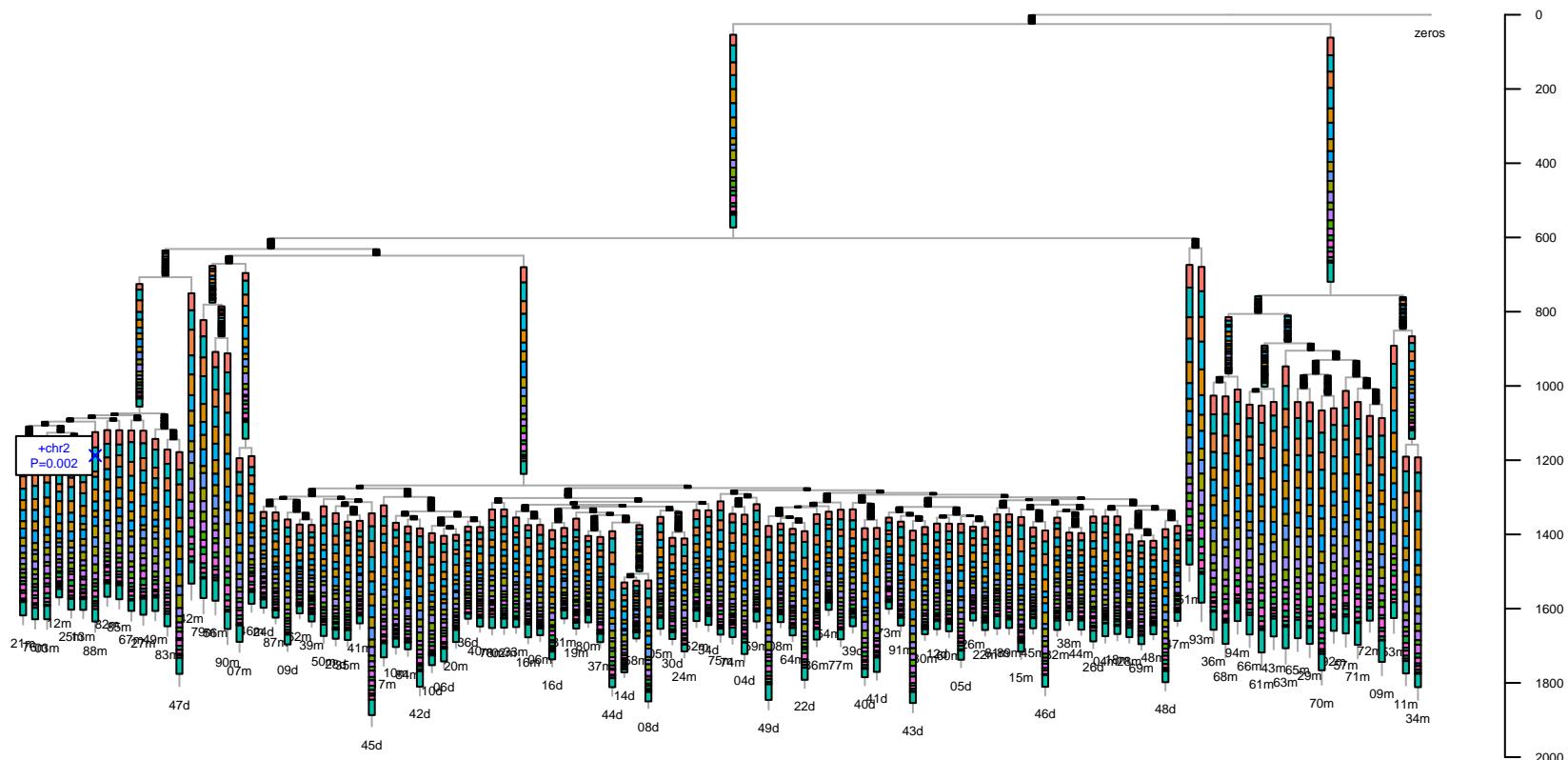
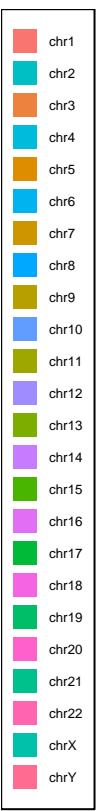
PD6646: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)



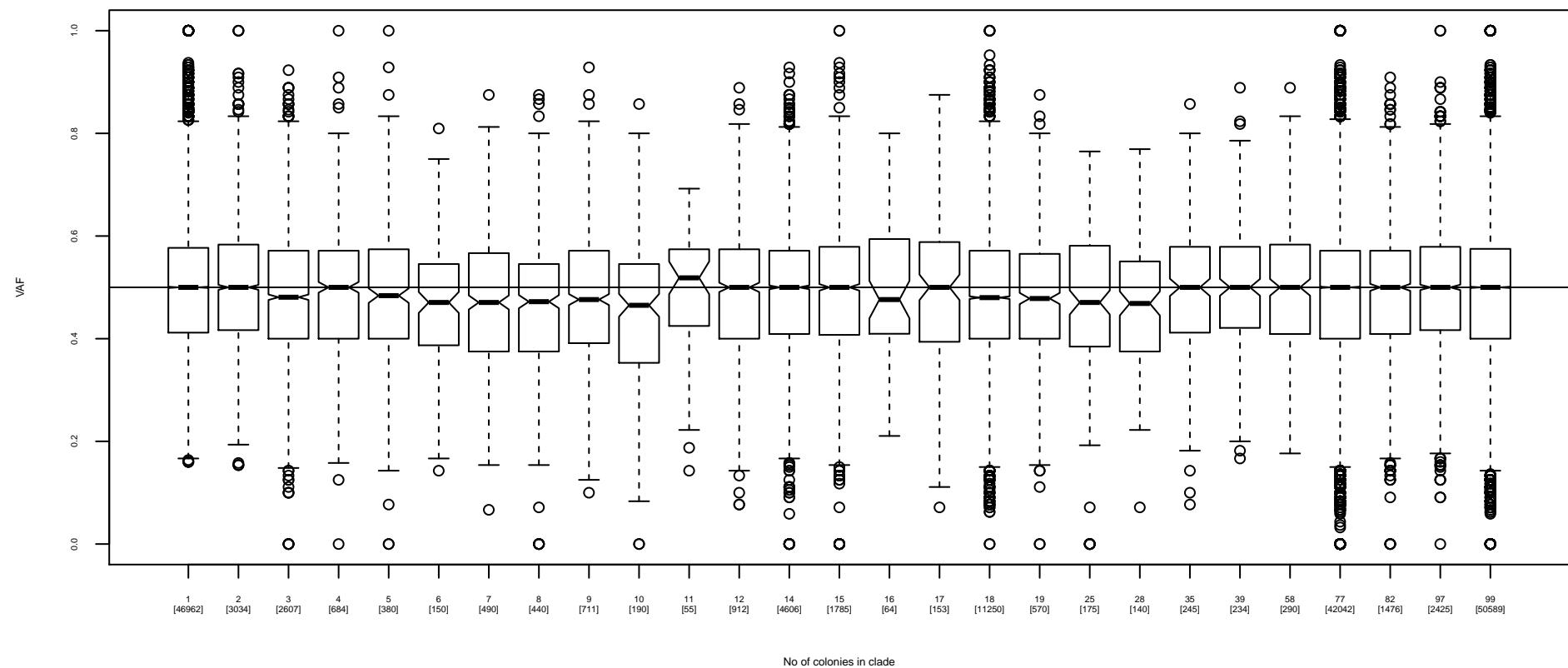
PD6646: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



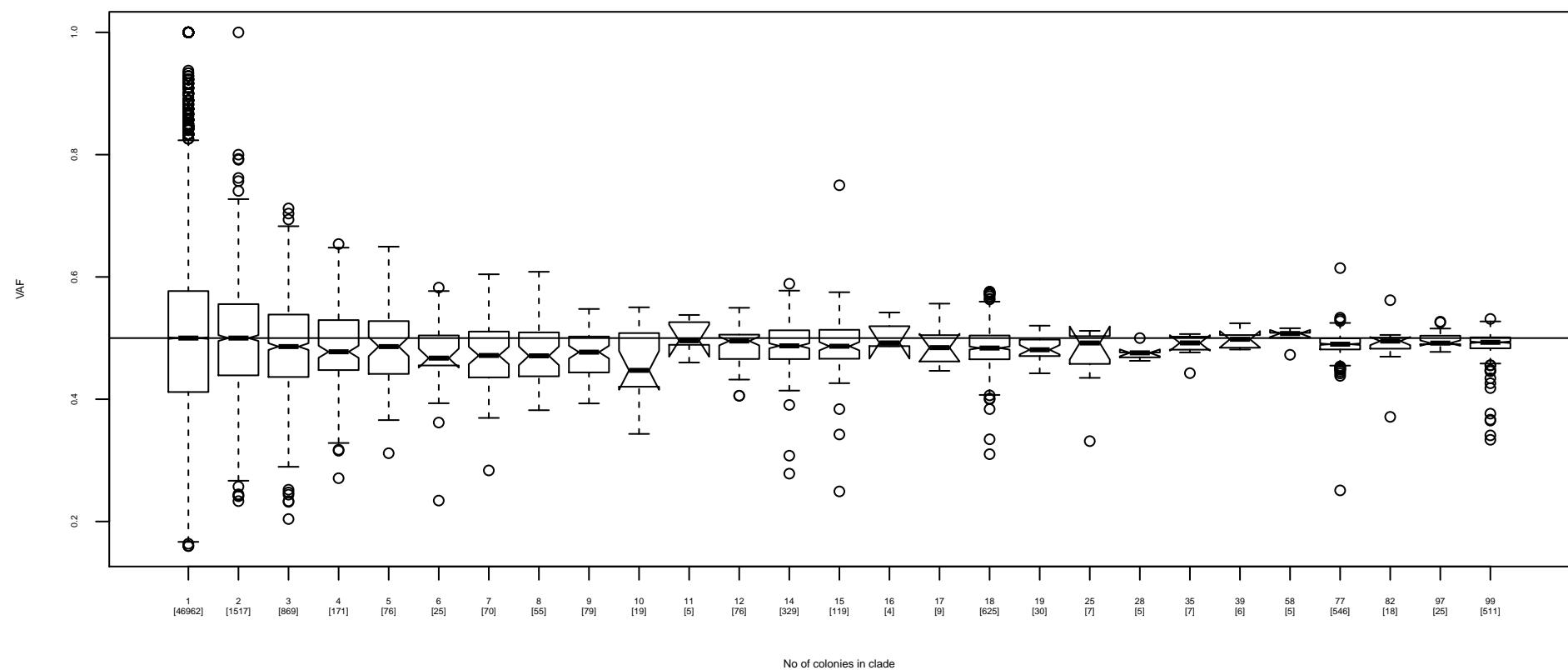
## PD6646: Chromosome composition check



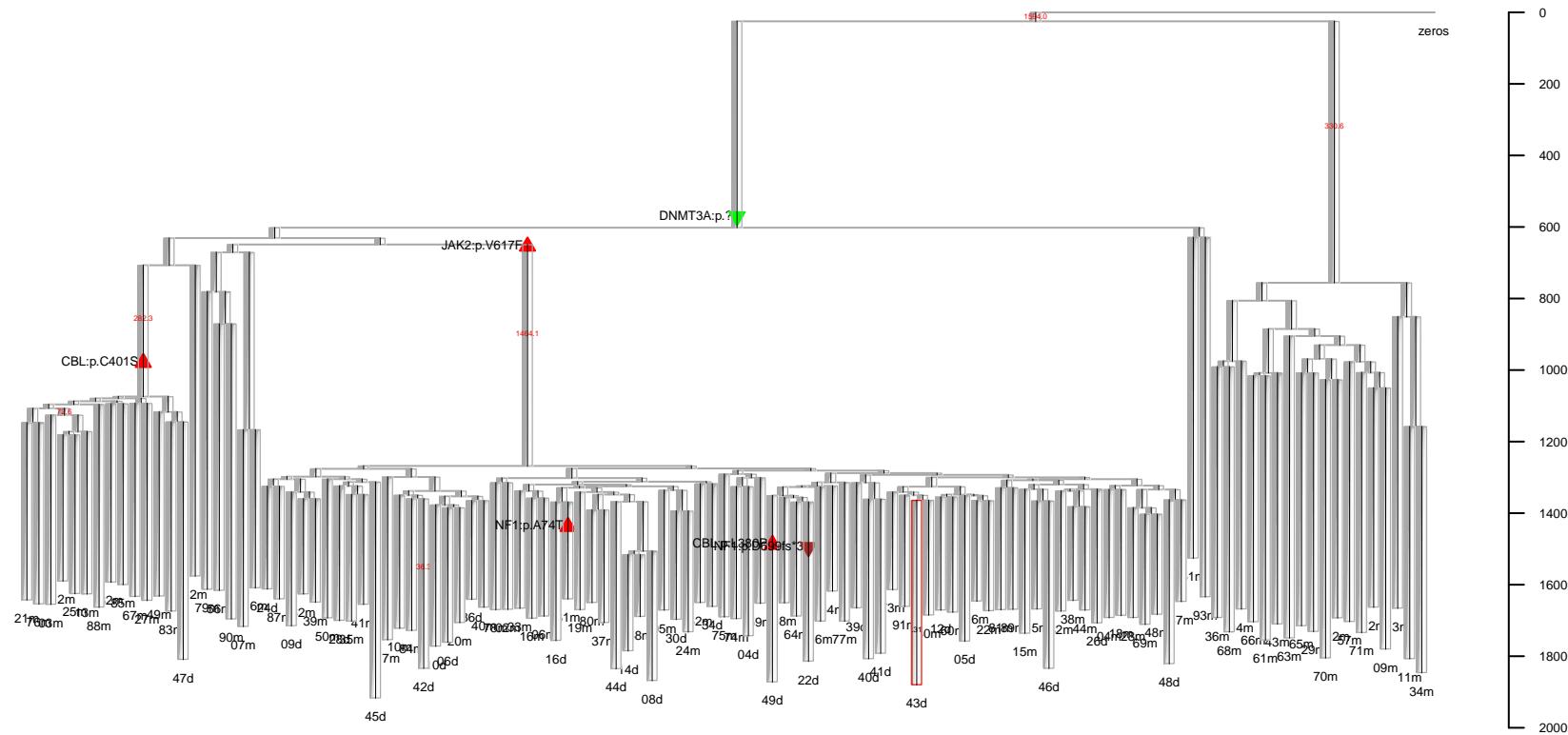
PD6646:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



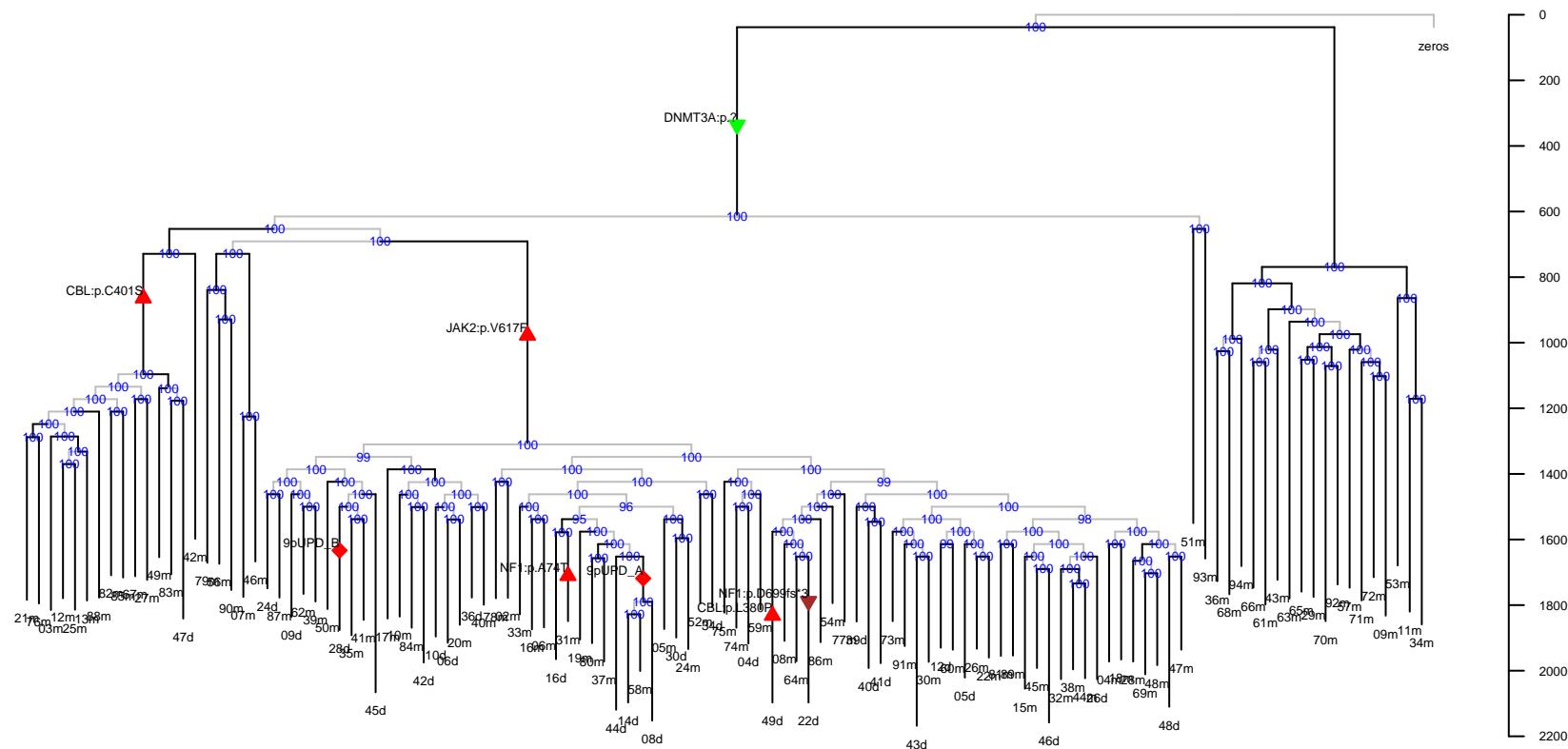
PD6646:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



PD6646 [Pooled VAF]

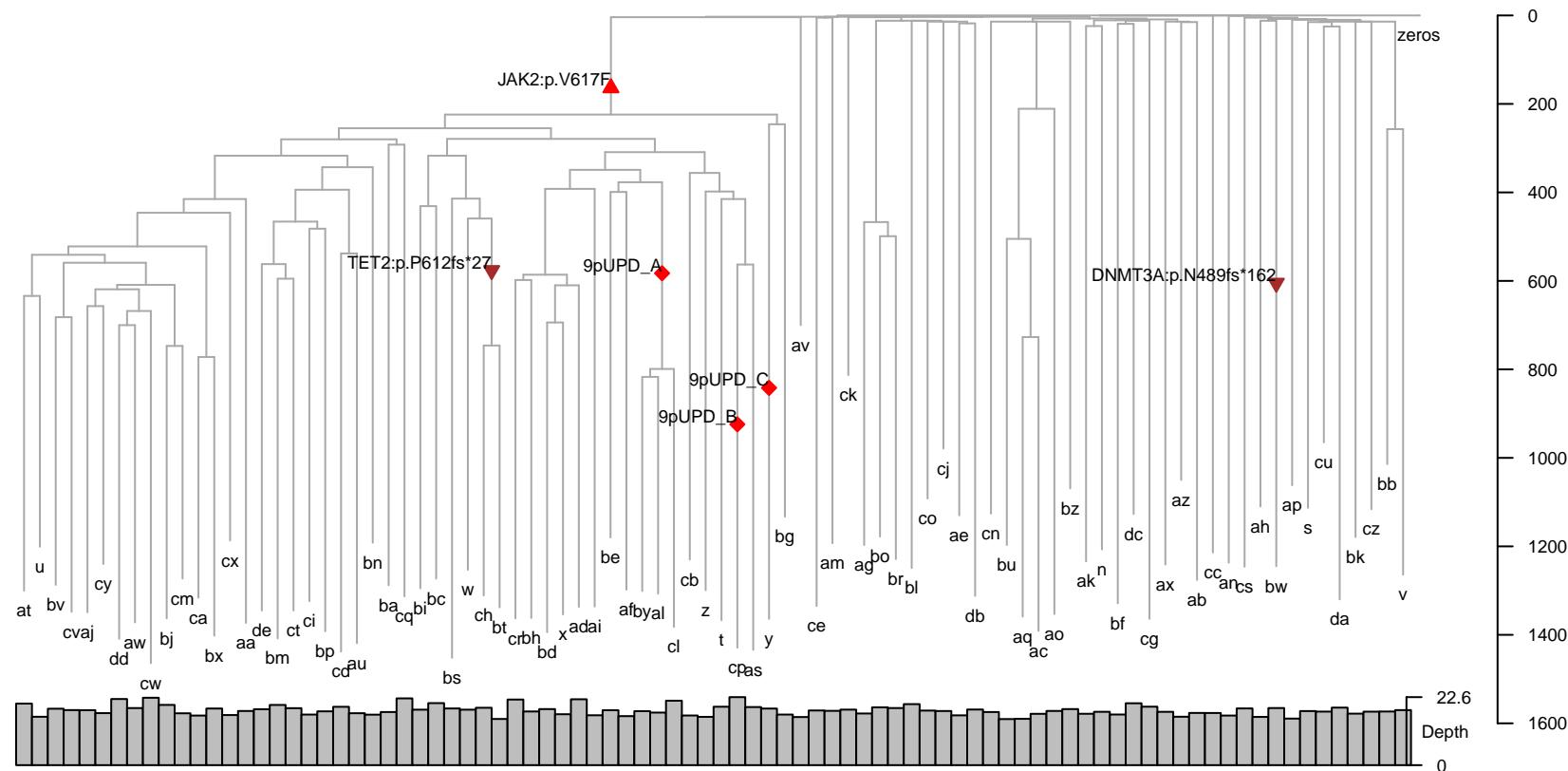


PD6646: With MPBoot Bootstrap Support (Grey branches extended to 38 Mutations)

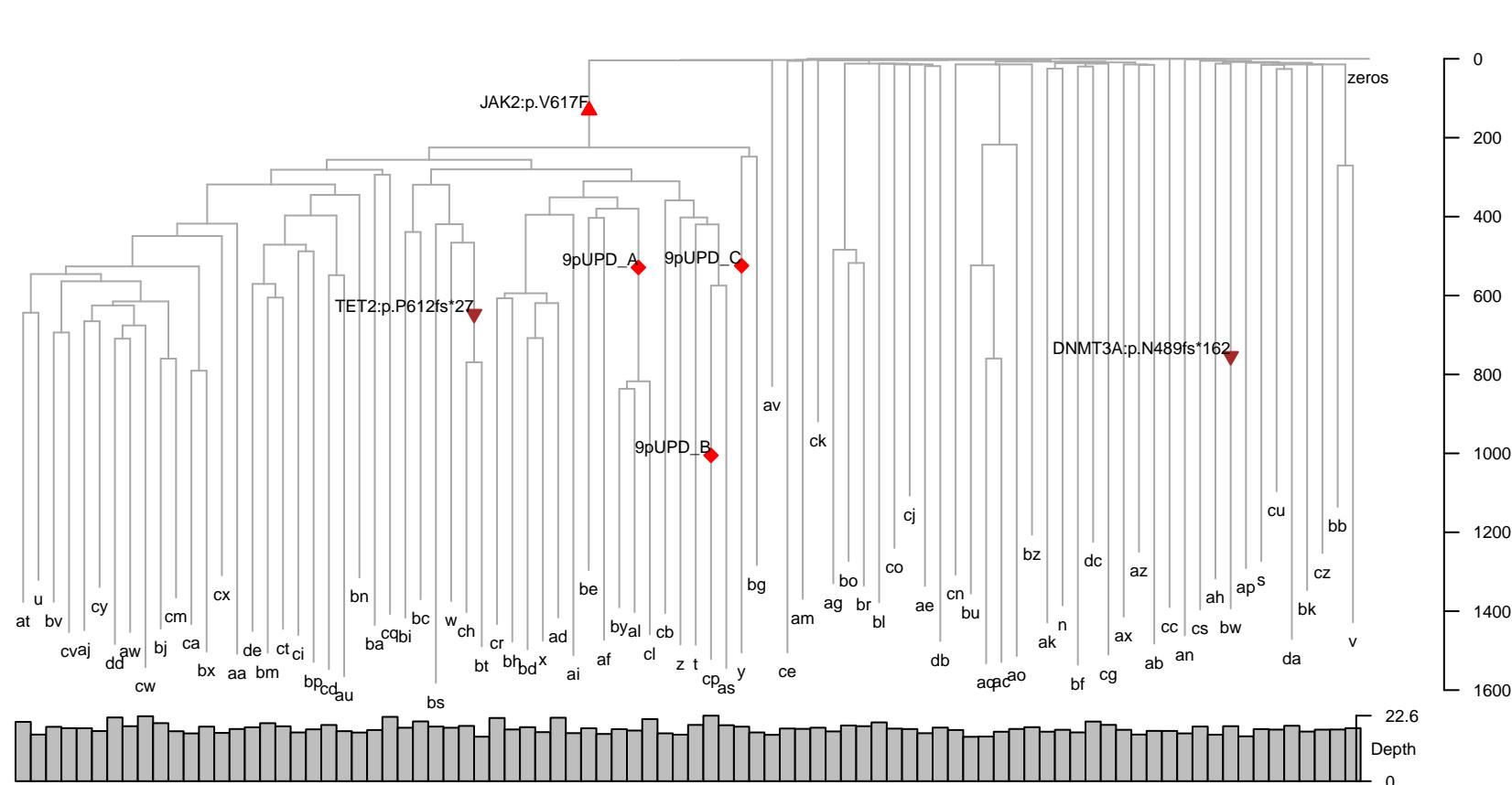


PD5117: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)

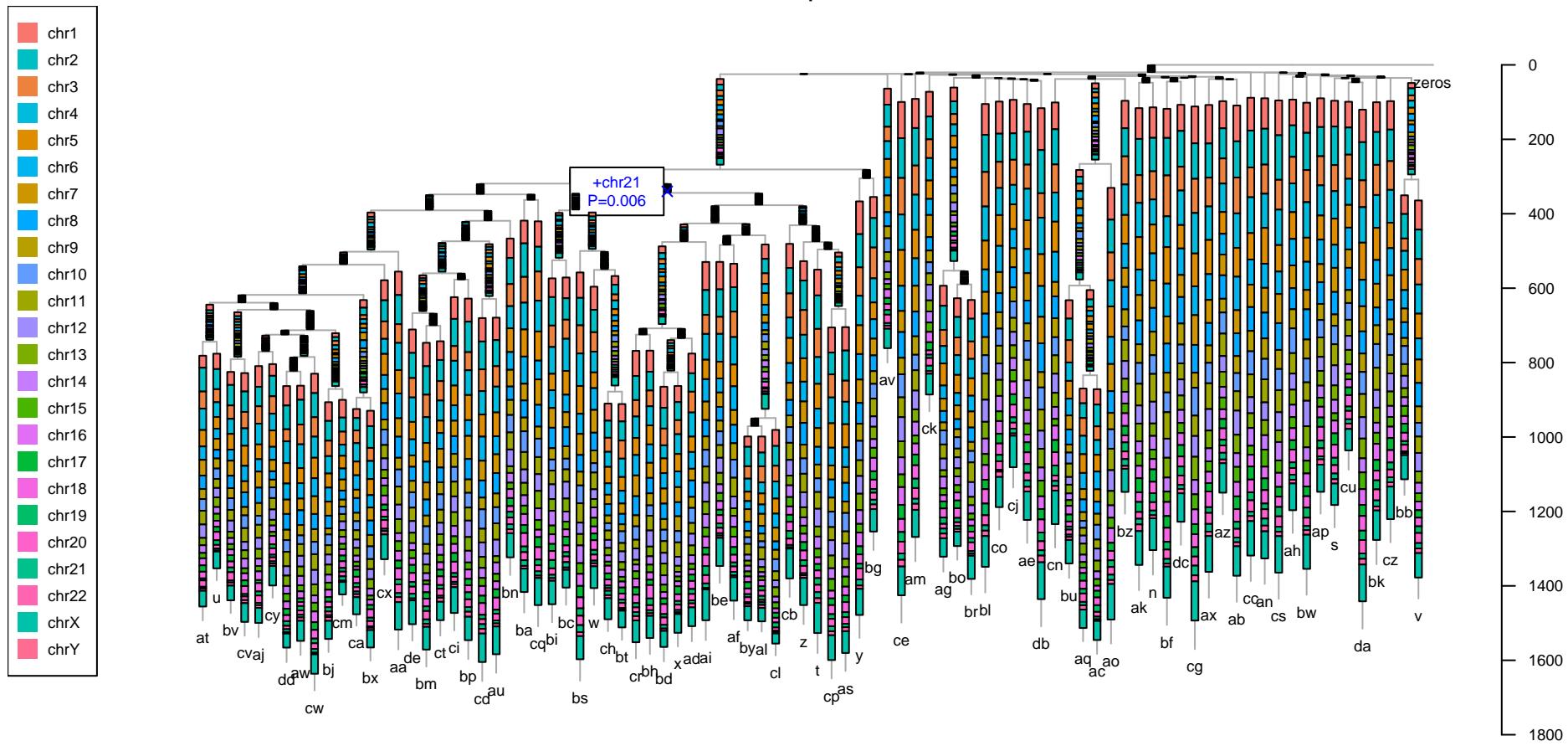
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- ◆ loh



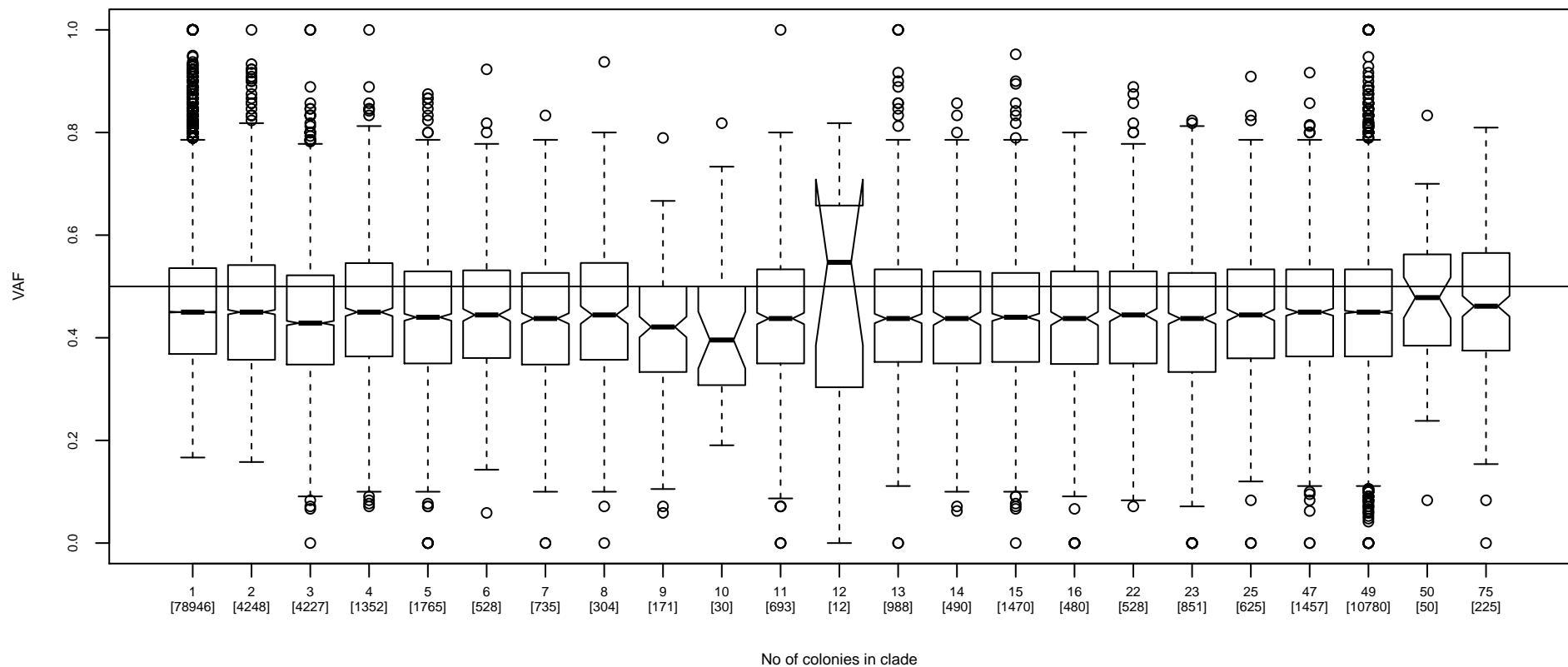
PD5117: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



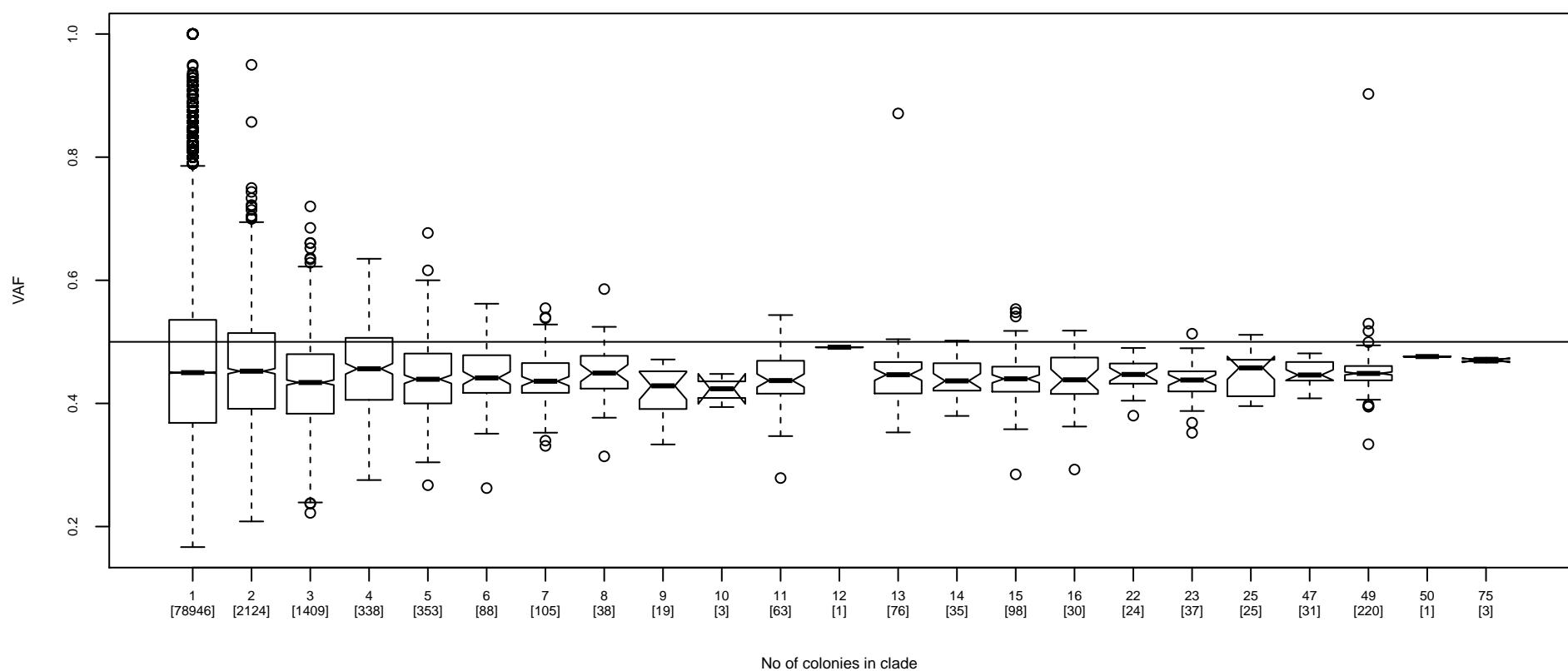
PD5117: Chromosome composition check



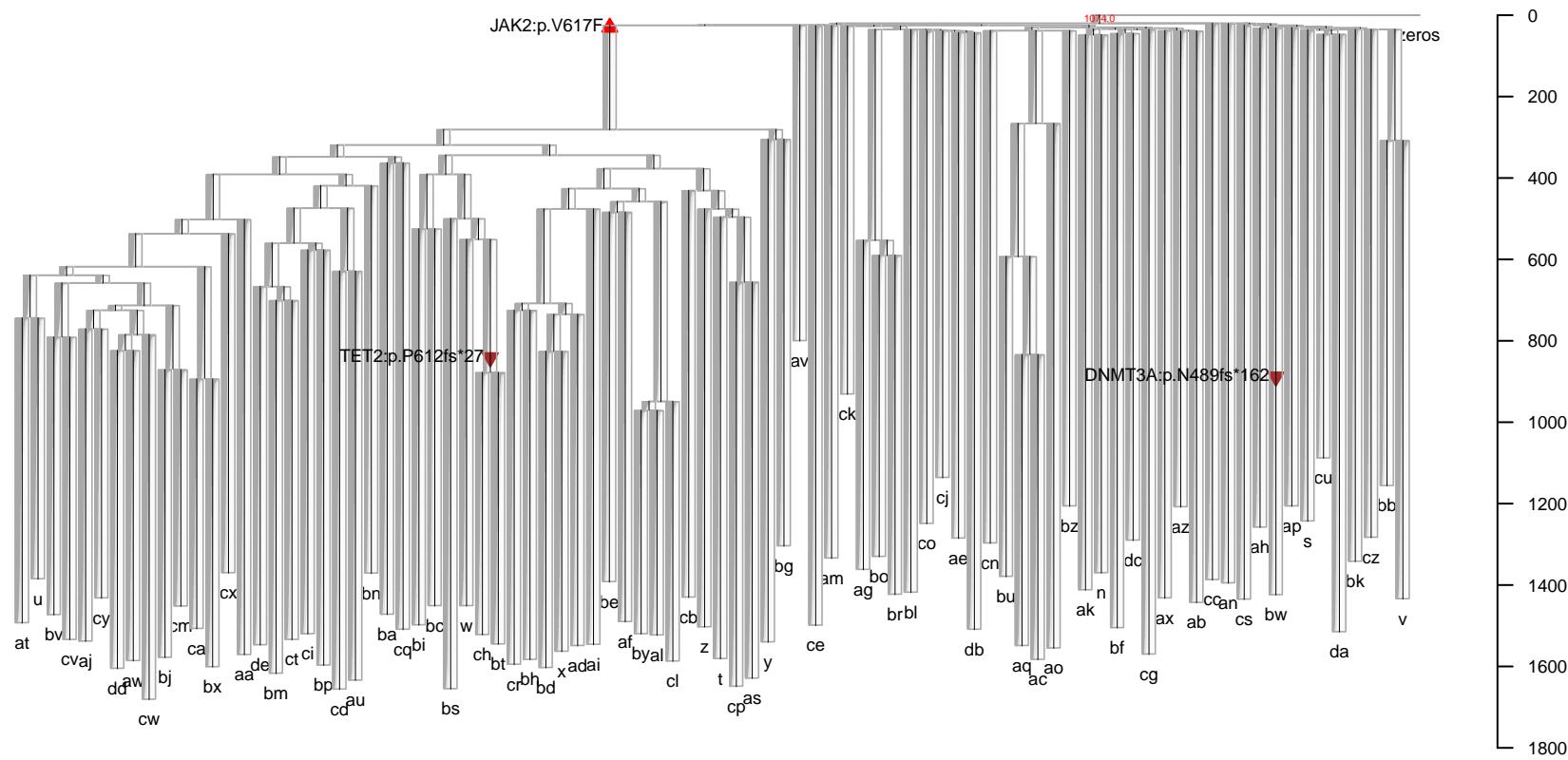
PD5117:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



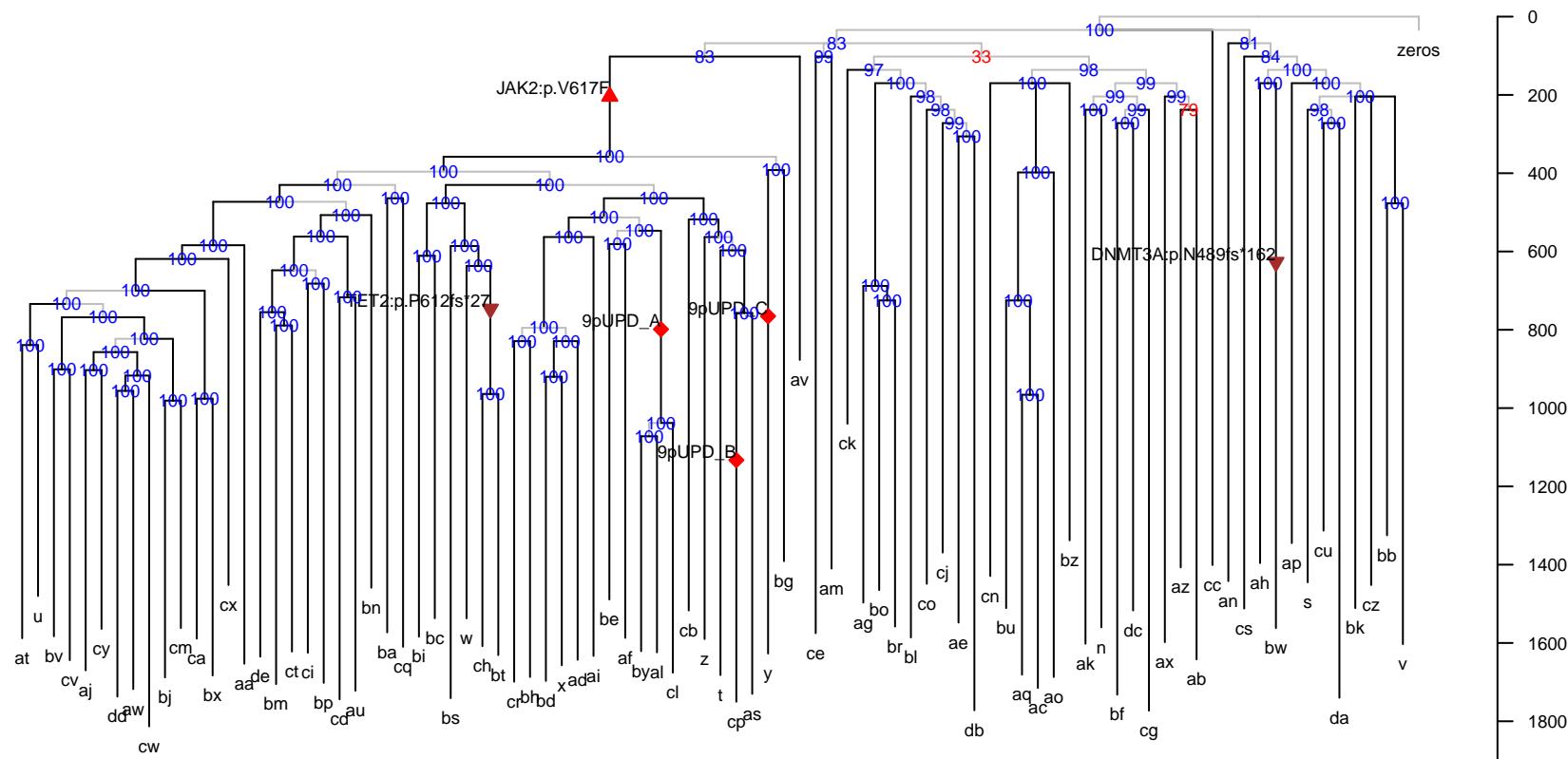
PD5117:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



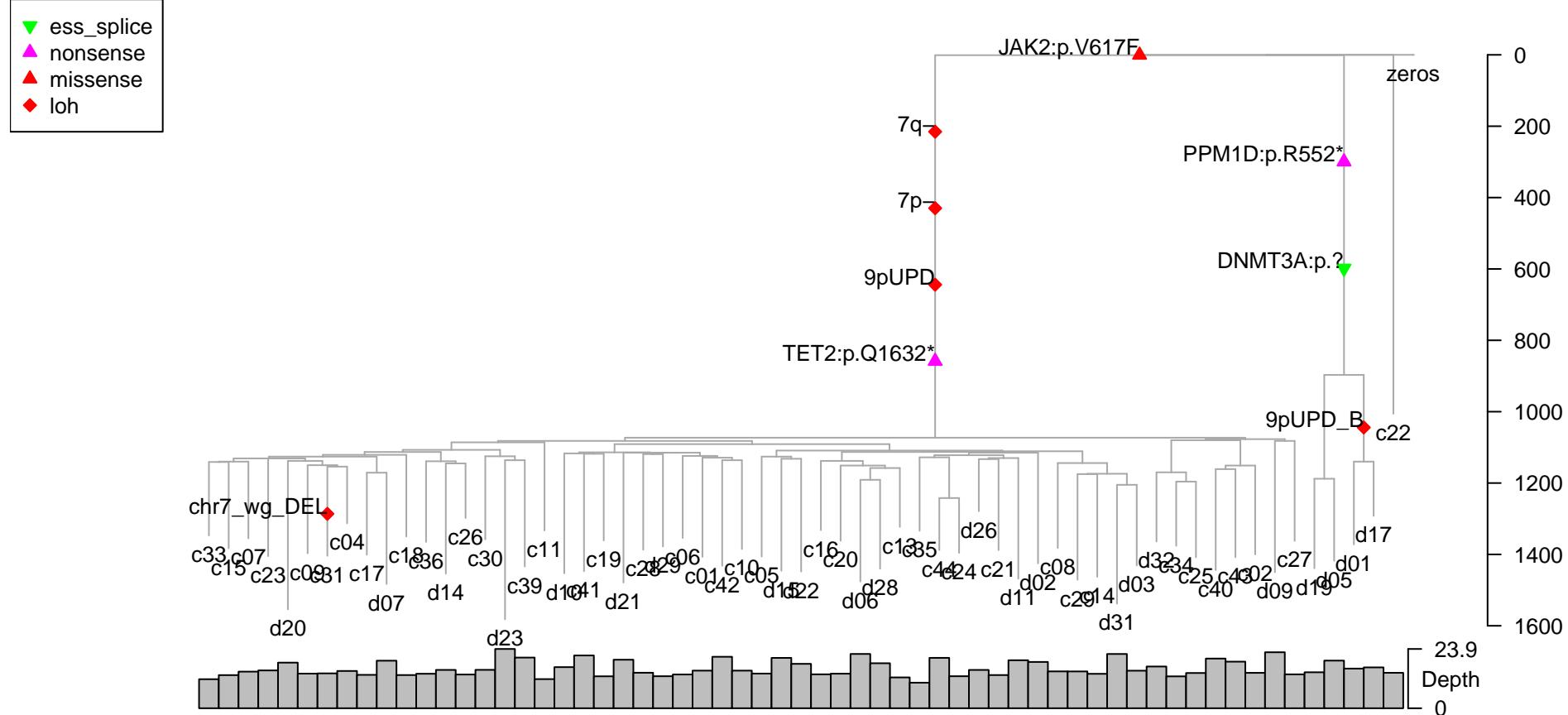
### PD5117 [Pooled VAF]



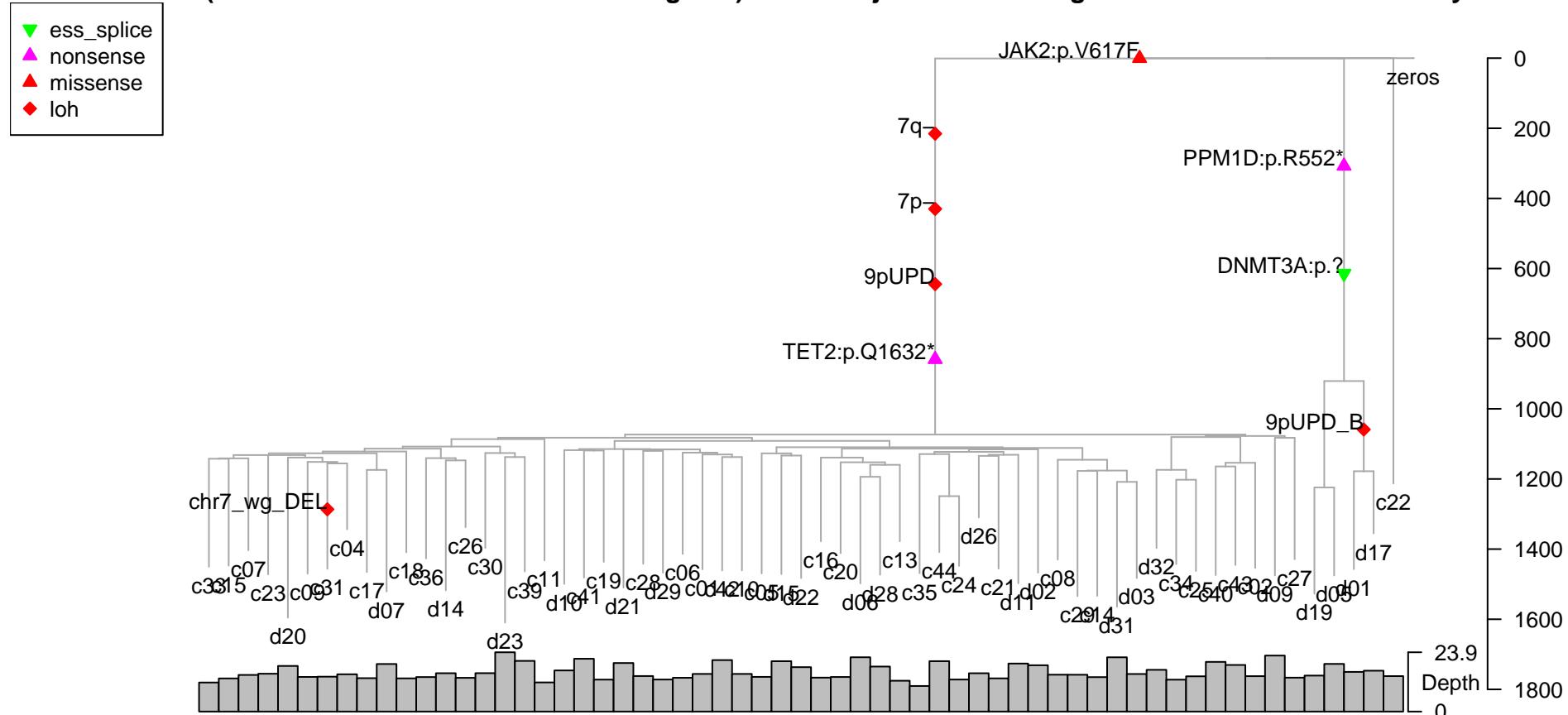
### PD5117: With MPBoot Bootstrap Support (Grey branches extended to 34 Mutations)



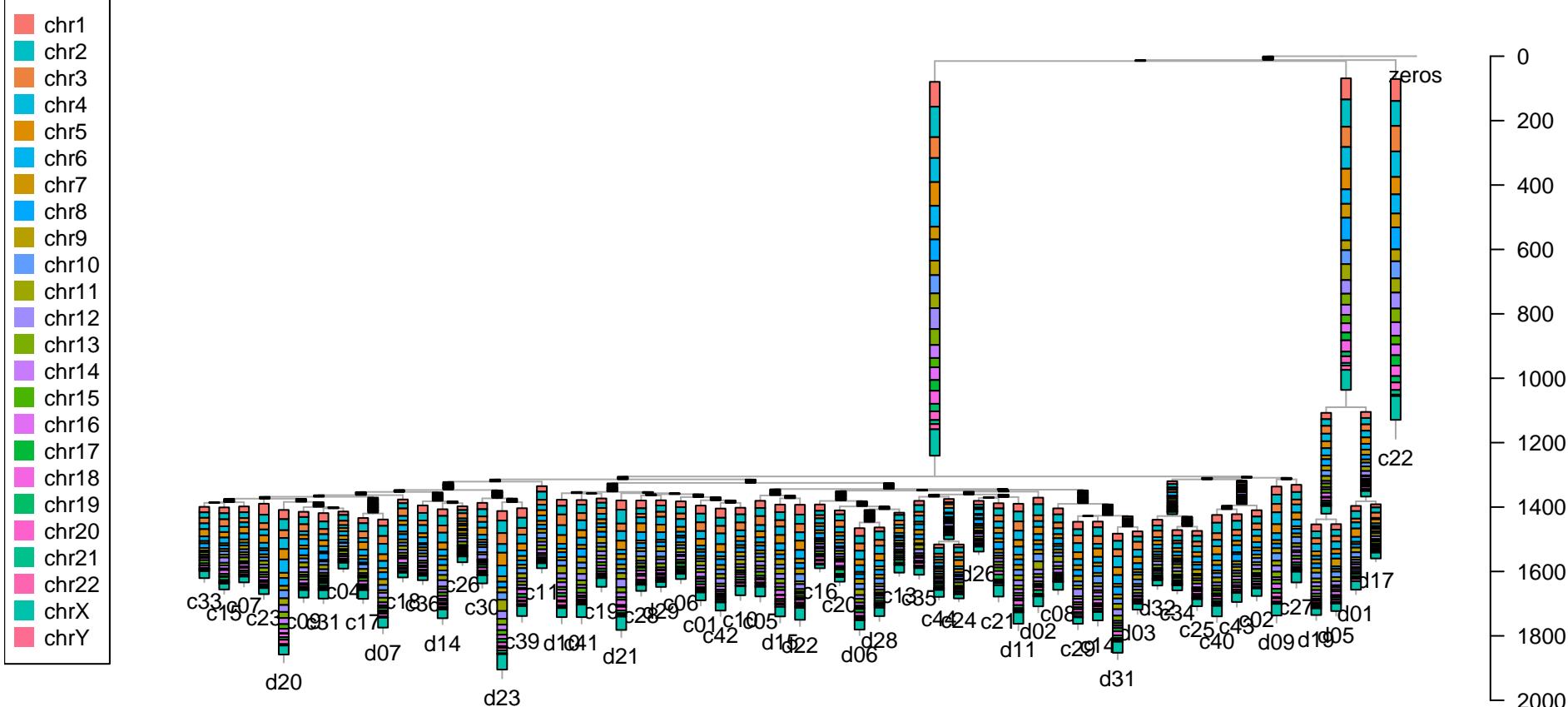
### PD4781: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)



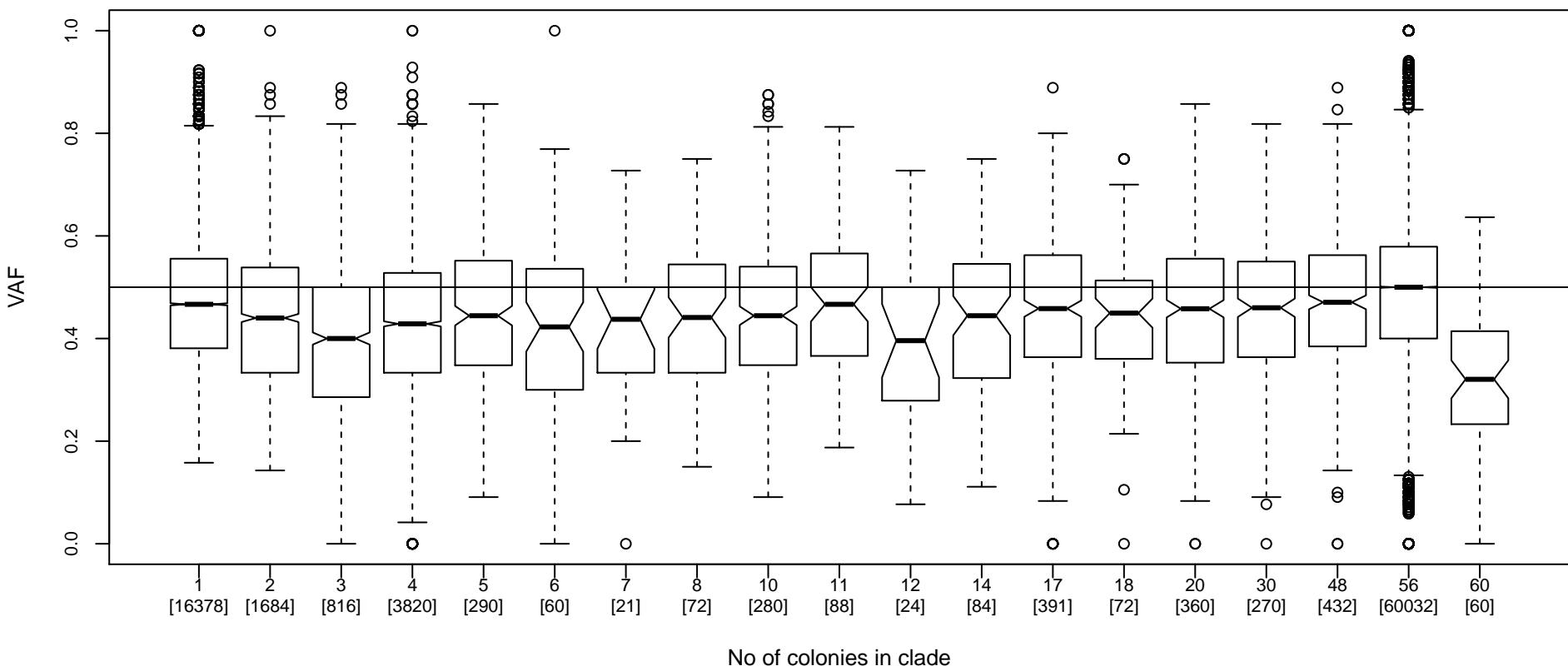
### PD4781: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity



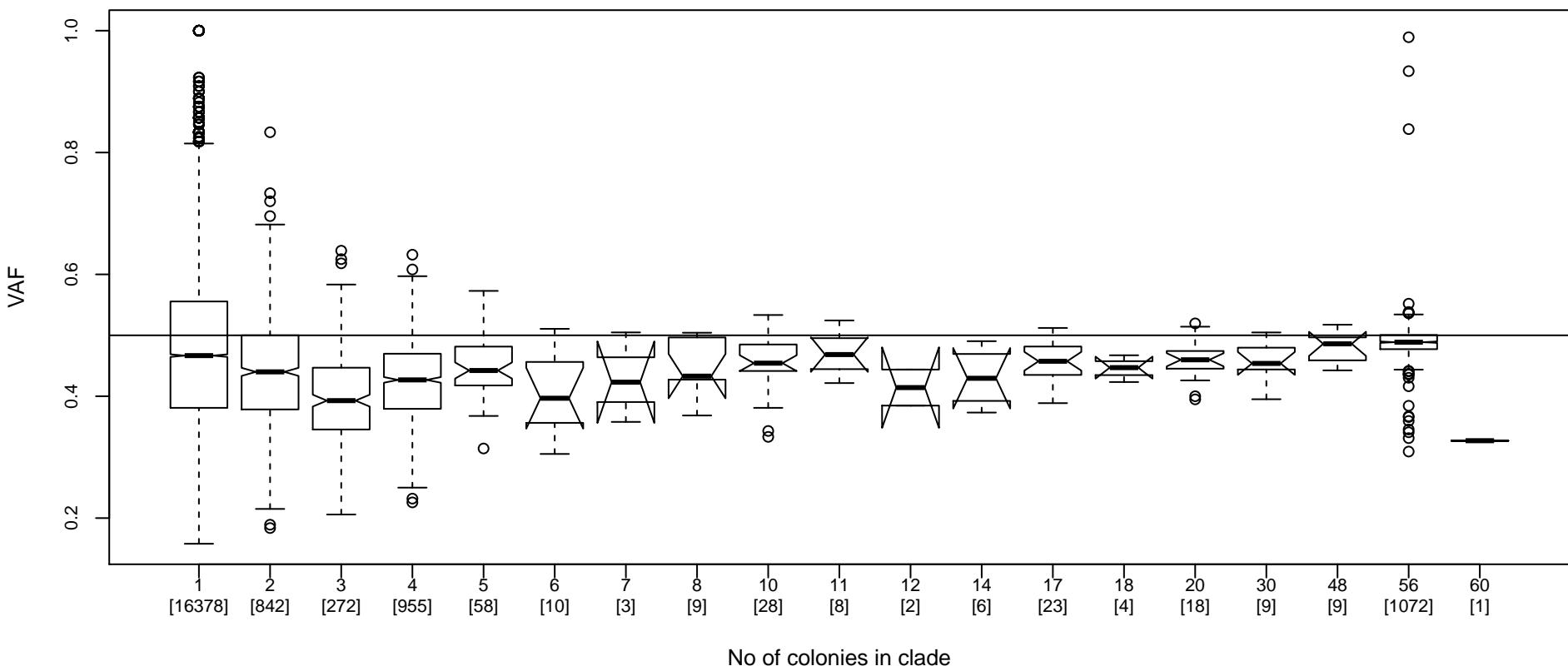
# PD4781: Chromosome composition check



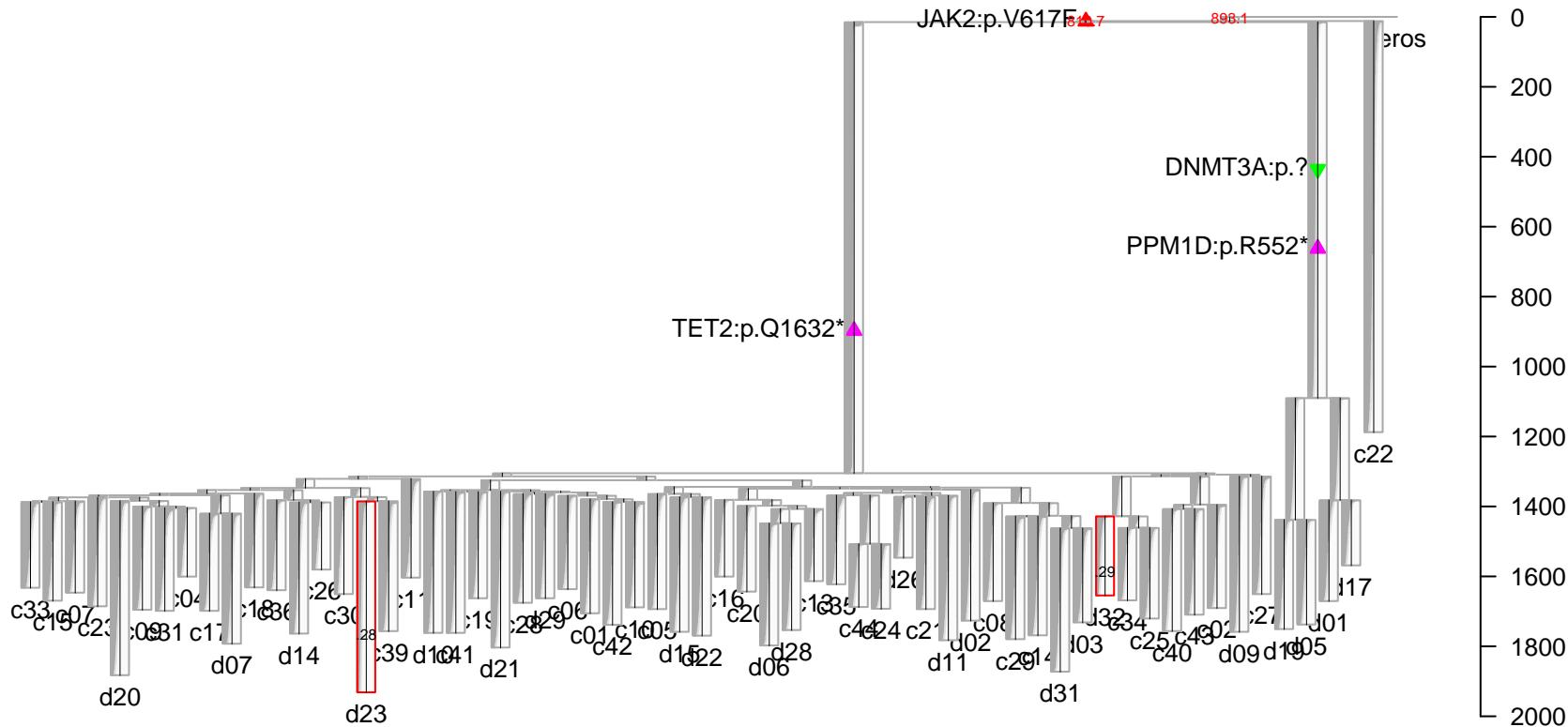
**PD4781:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)**



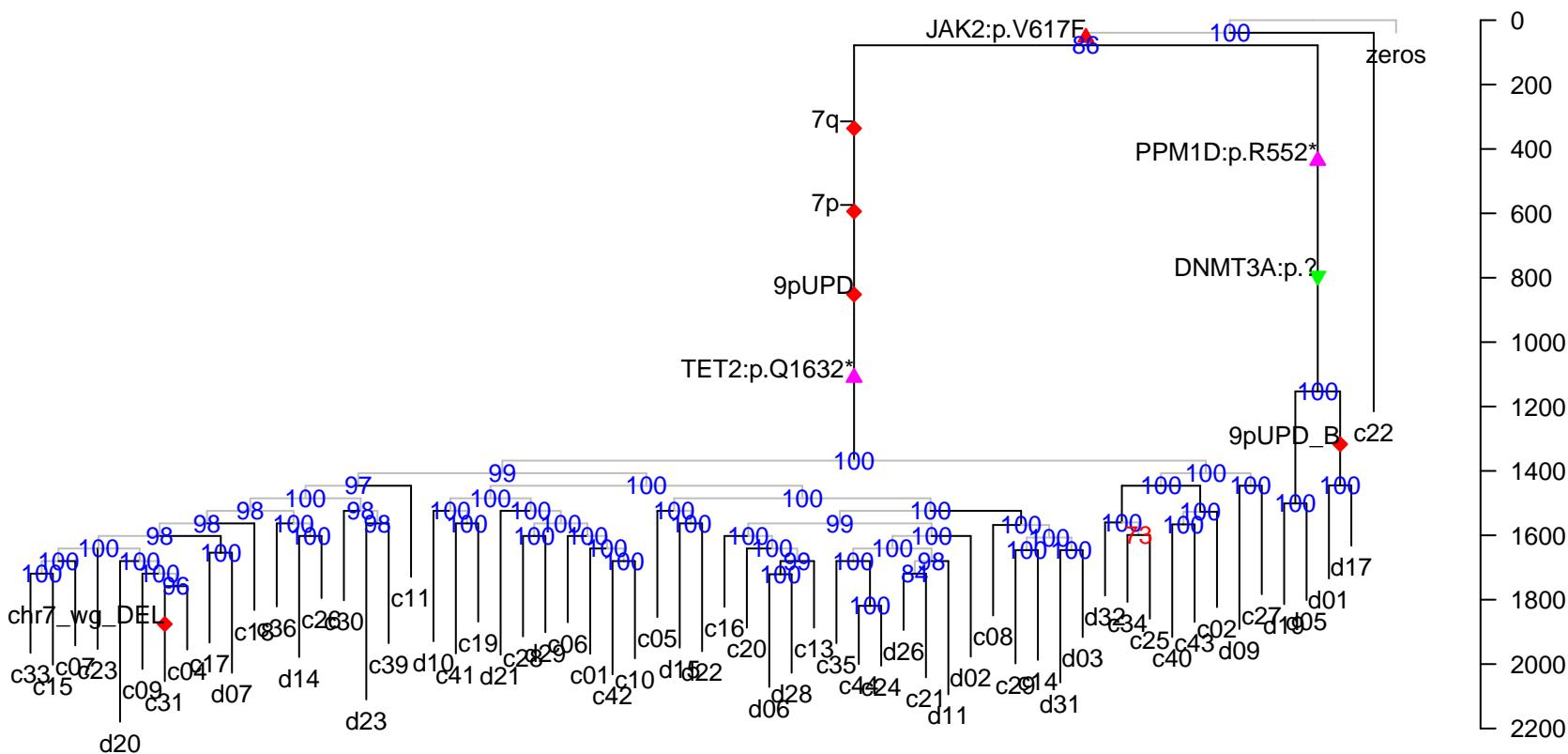
**PD4781:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))**



# PD4781 [Pooled VAF]

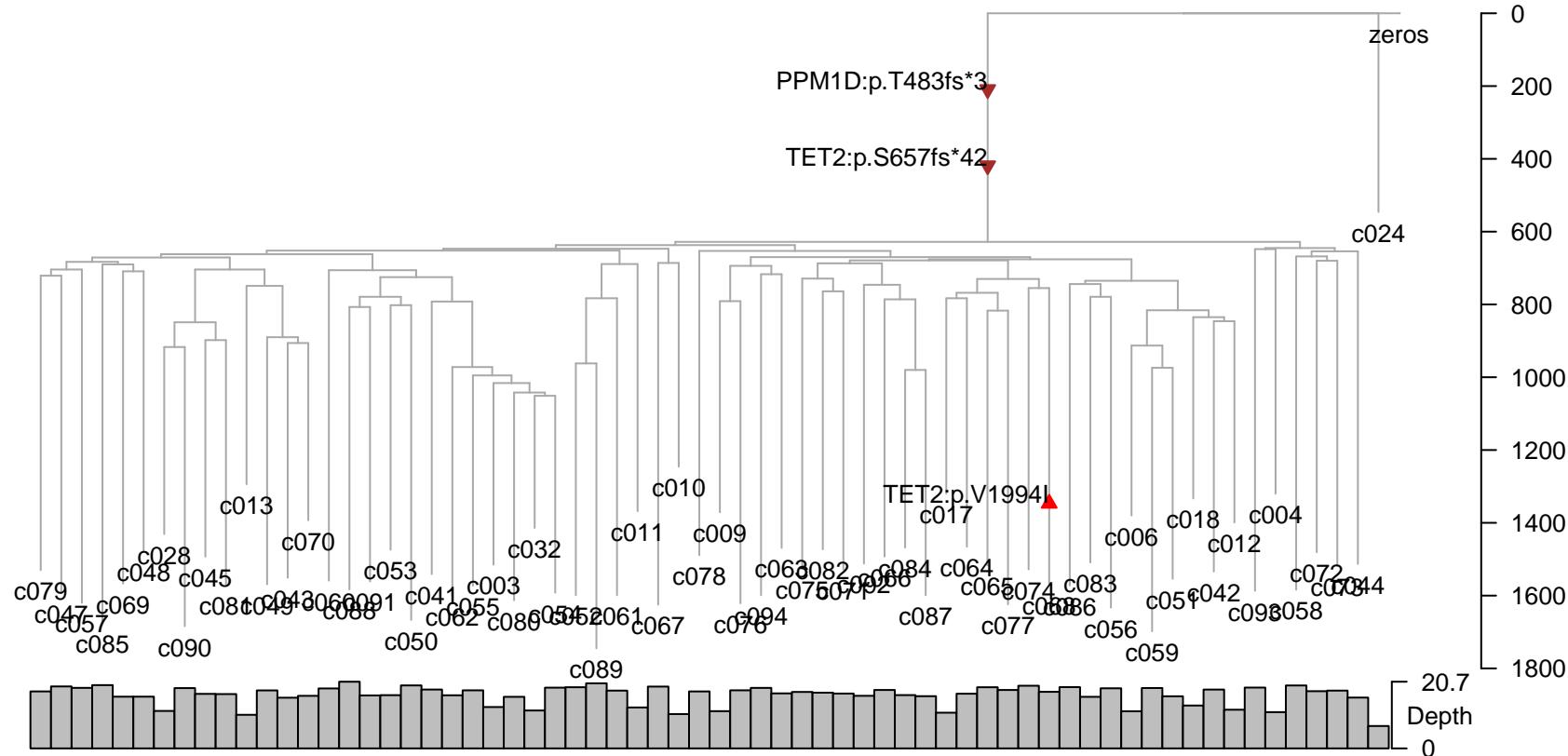


## PD4781: With MPBoot Bootstrap Support (Grey branches extended to 39 Mutations)



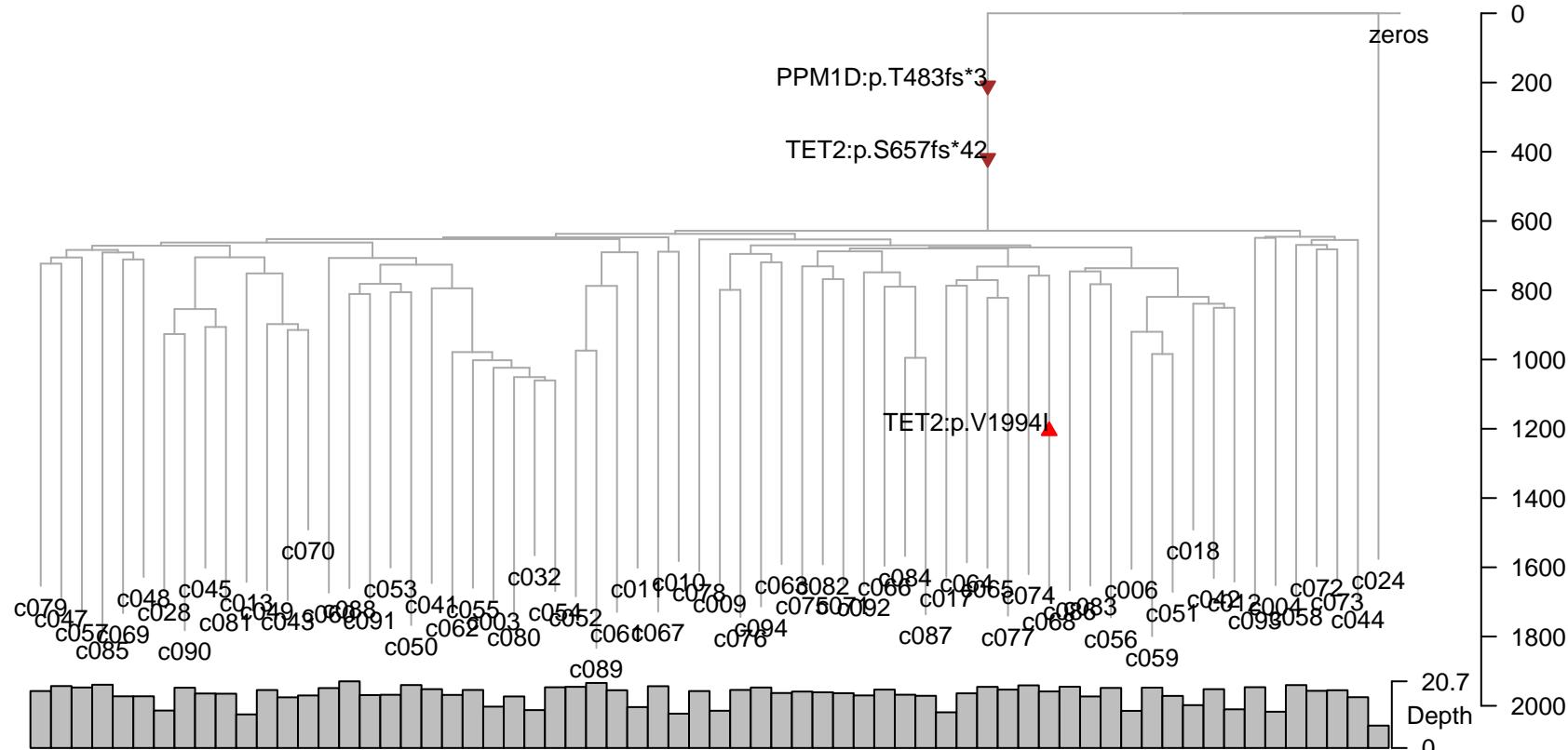
### PD5147: SNV With No Branch Length Adjustment (Autosomal – Excludes CNA/LOH Regions)

▼ frameshift  
▲ missense

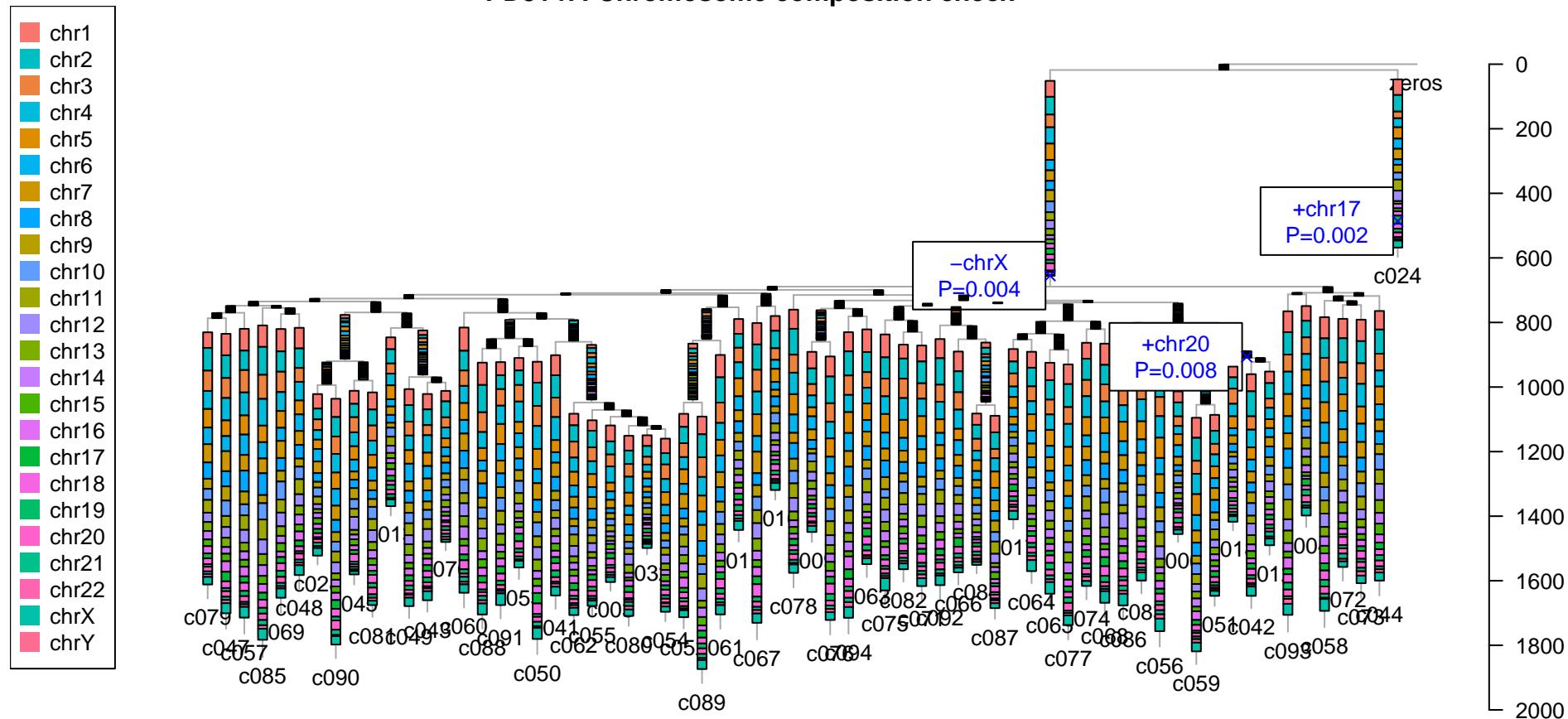


### PD5147: SNV (Autosomal – Excludes CNA/LOH Regions): Scale Adjusted Assuming Somatic=Germline Sensitivity

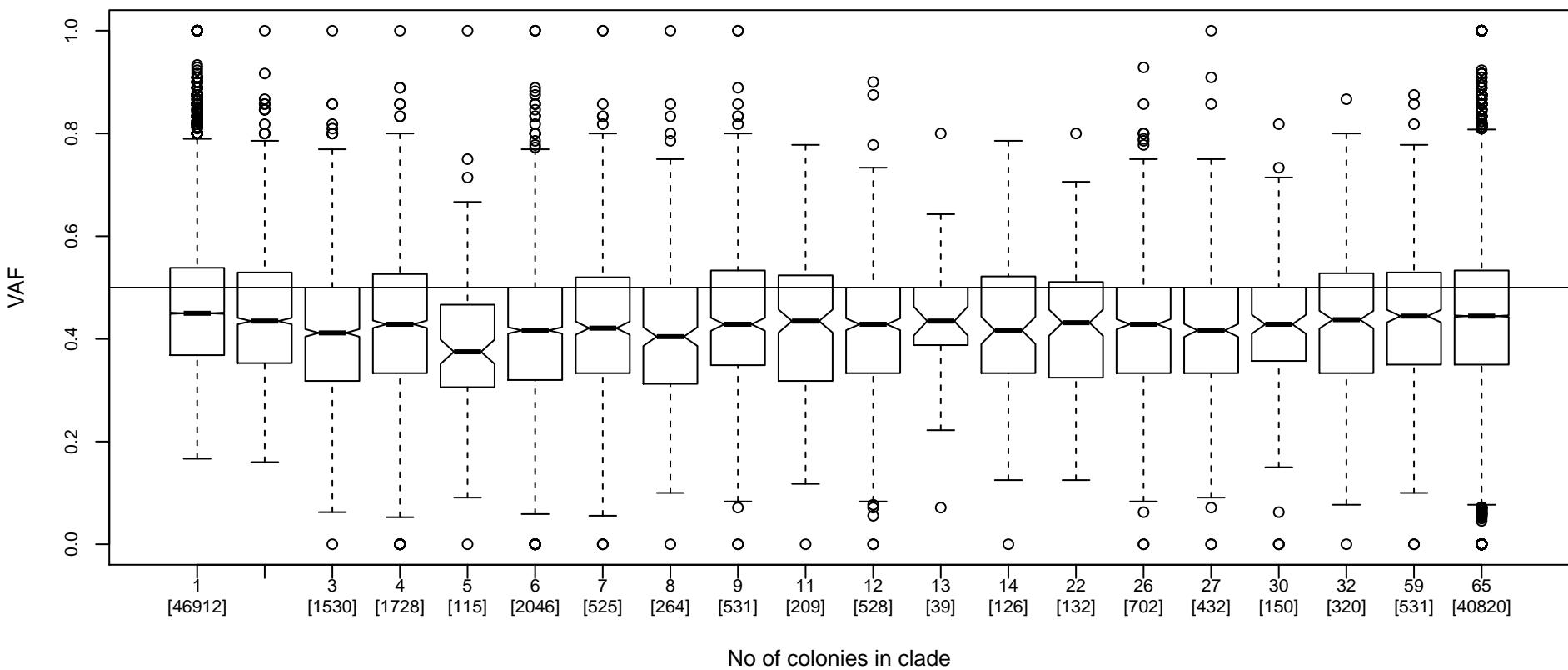
▼ frameshift  
▲ missense



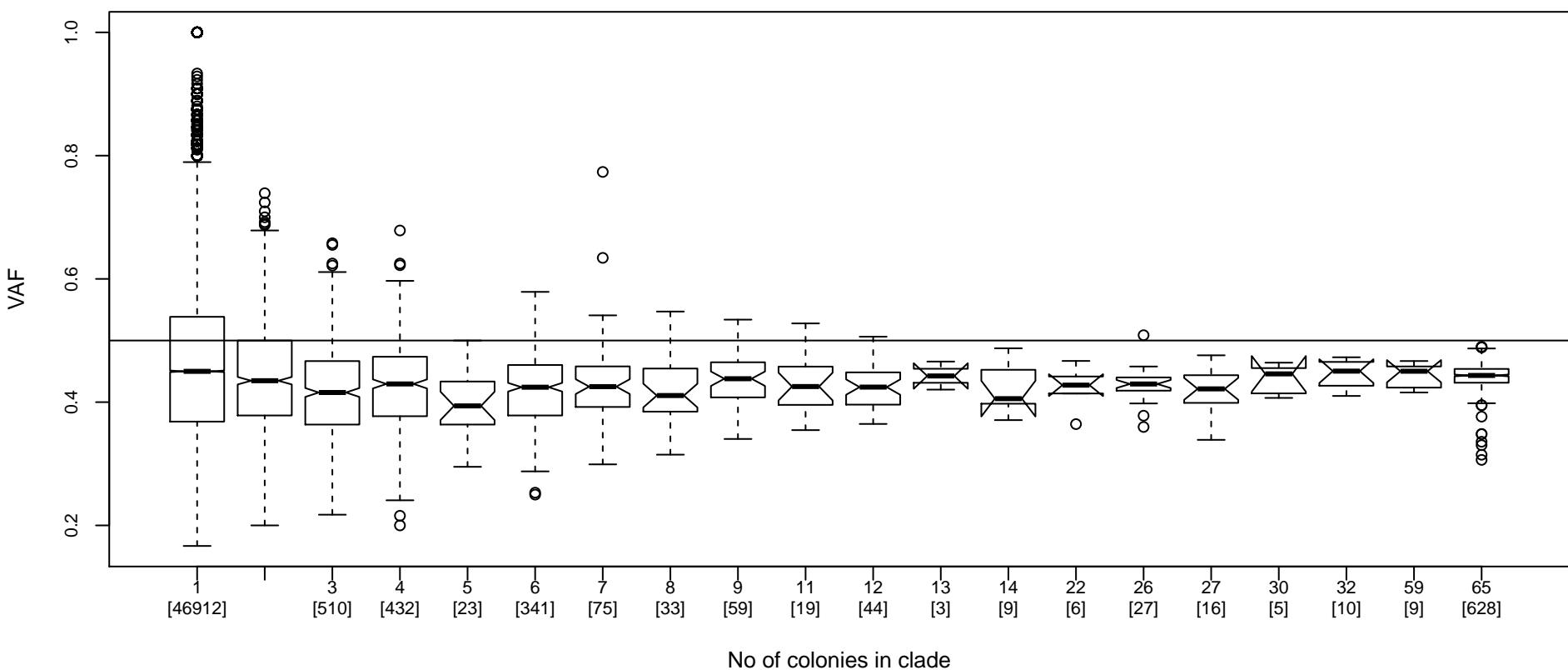
# PD5147: Chromosome composition check



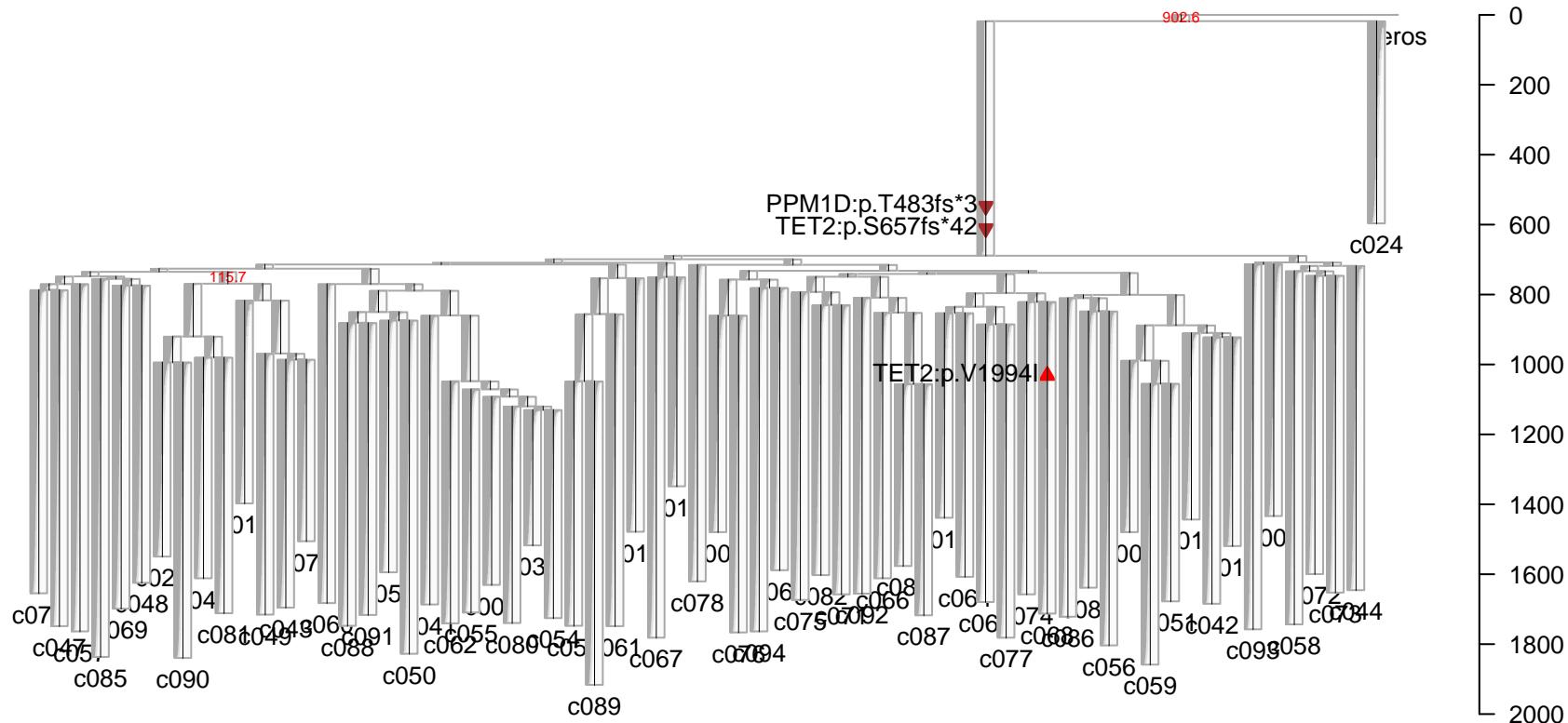
### PD5147:VAF Distribution By No. Colonies in Clade (Per Sample/Locus)



### PD5147:VAF Distribution By No. Colonies in Clade (Per Locus (Pooled over Samples))



PD5147 [Pooled VAF]



**PD5147: With MPBoot Bootstrap Support (Grey branches extended to 38 Mutations)**

- ▼ frameshift
- ▲ missense

