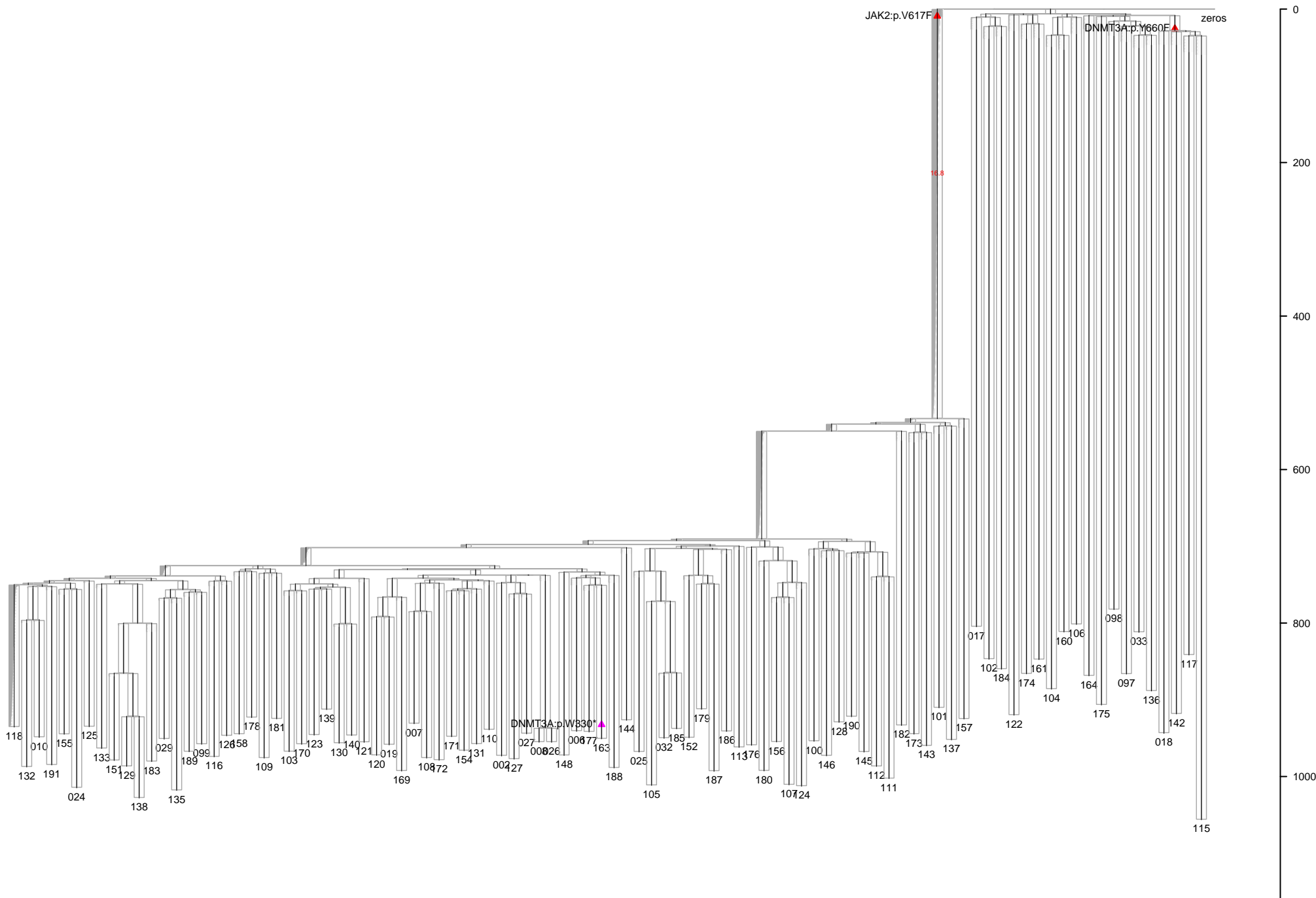
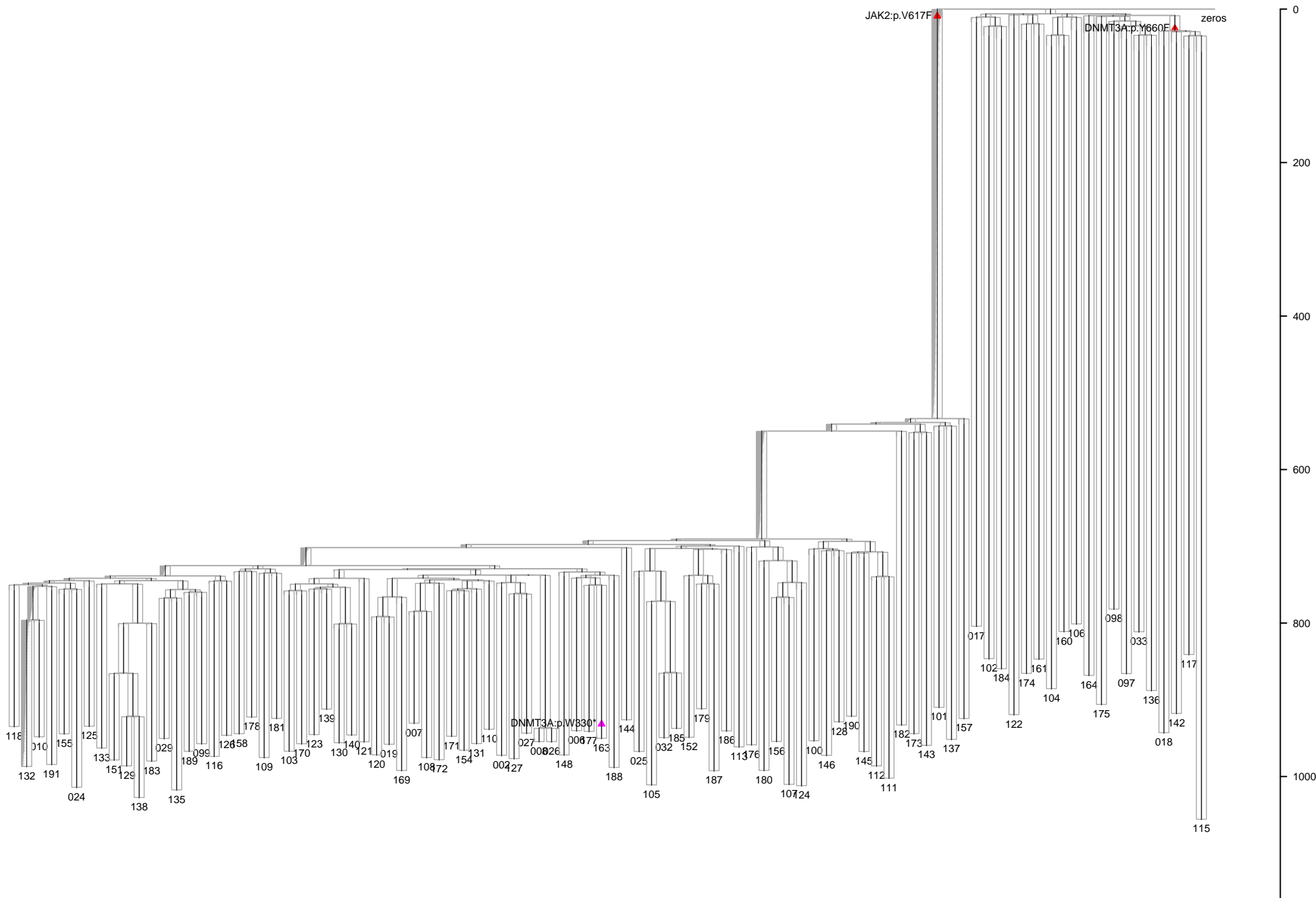
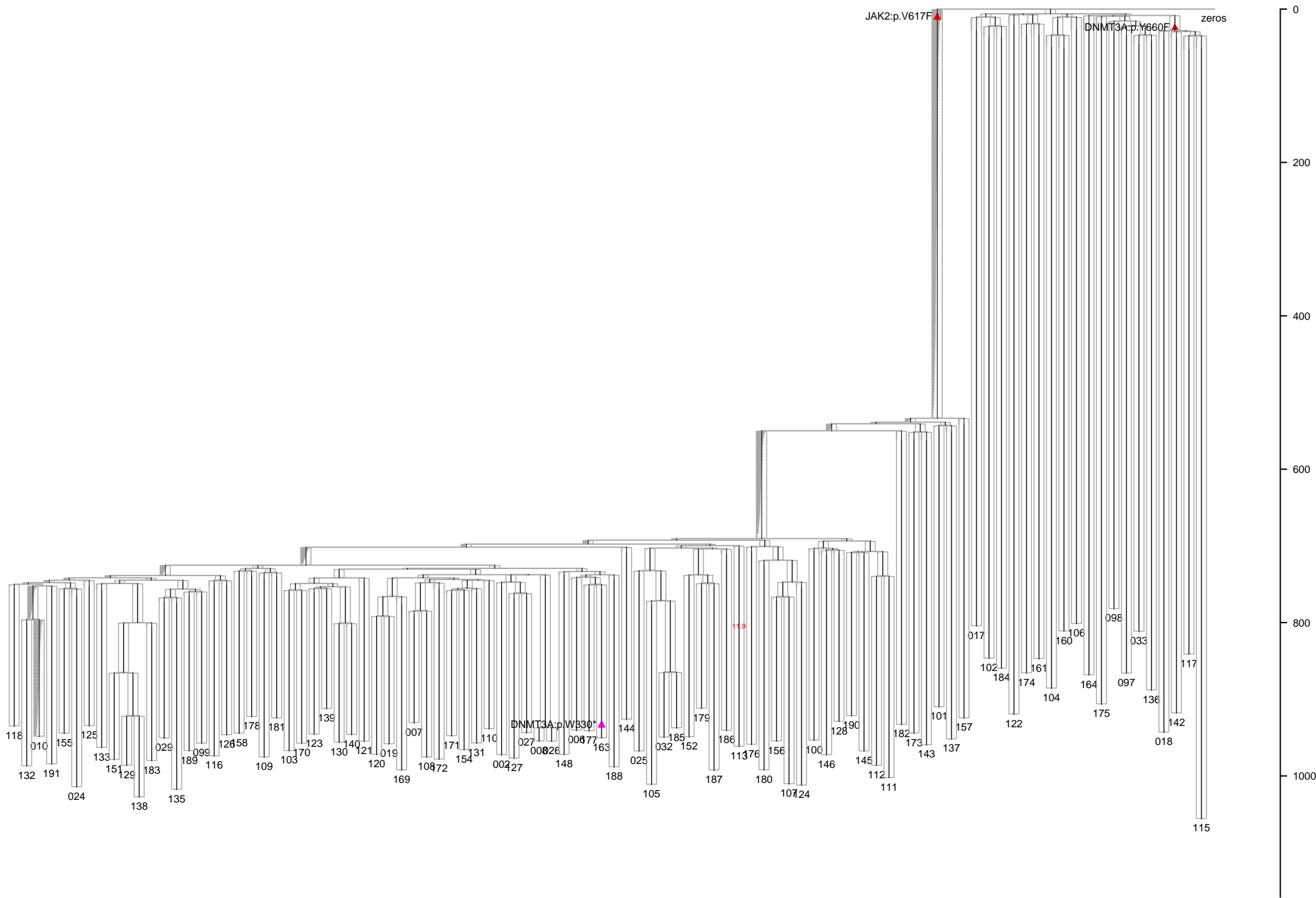


## Tree By Colony Quality Assessment

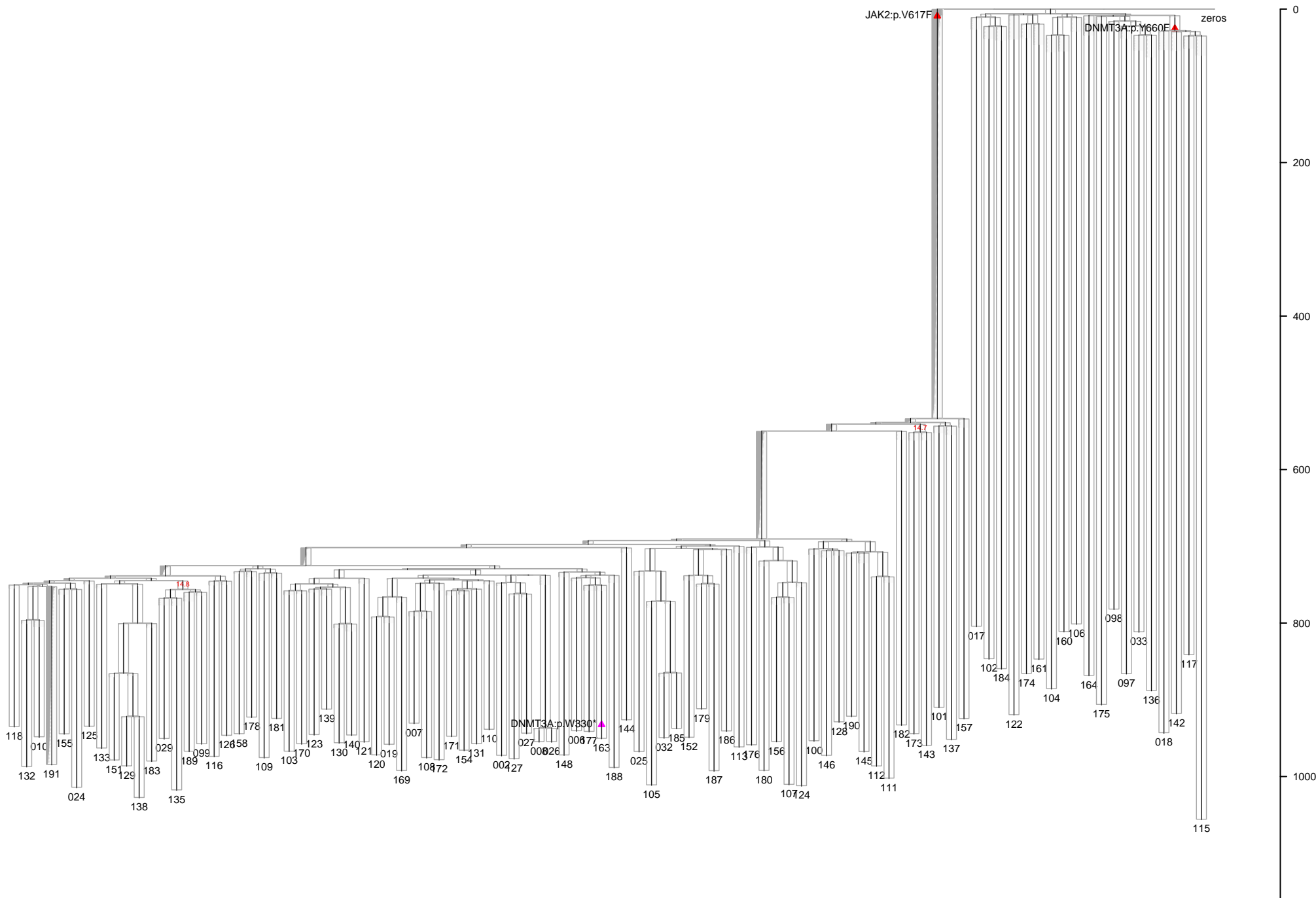
This file reports the VAF distribution of the variants assigned to each branch on a per colony basis. This allows one to 'walk through' the trees on a per colony basis to visualise both the branch placement and VAF of all the variants present in that single colony with respect to the rest of the tree. This is particularly helpful to ensure that variants belonging to a single colony are not found in non-ancestral branches whilst also allowing one to assess if other branches in the tree suffer from a lack of sensitivity for picking up specific variants. The report includes all colonies - including those that are dropped from the final tree and also some additional samples of interest. For colonies that are in the final tree it is expected that the VAFs will be clonal on branches that are ancestral to the colony of interest and zero for those that are not ancestral. Branches are highlighted if they show significant deviation from this expectation ( $VAF < 0.35$  and  $VAF > 0.05$ ; Binomial test on aggregate mutant read count and aggregate depth; blue  $p < 0.05$  and red  $p < 0.05/\text{number of branches}$ ). Branches where the depth is significantly lower than the depth of variants across the whole tree are annotated with the branch depth shown in red.



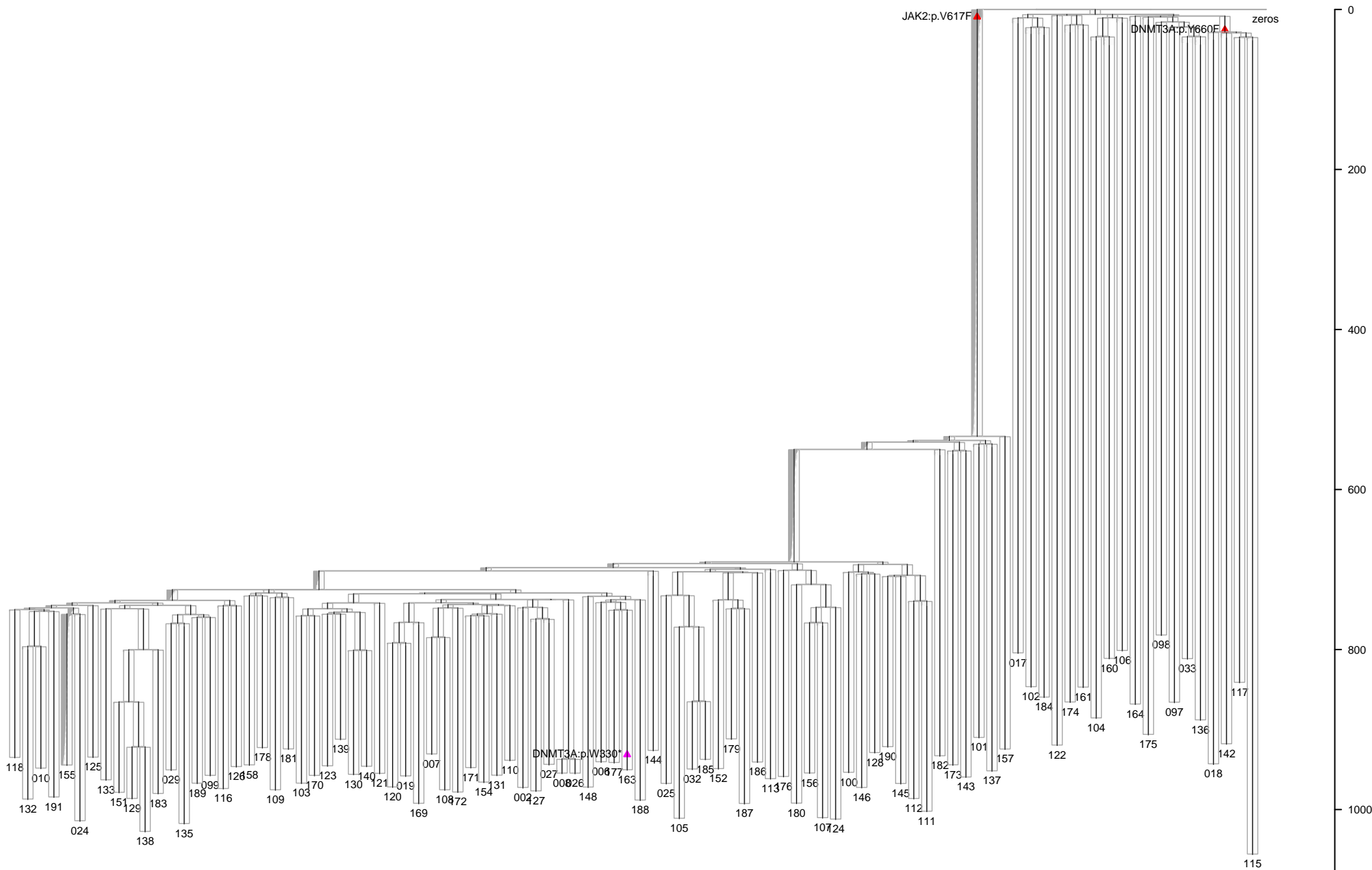


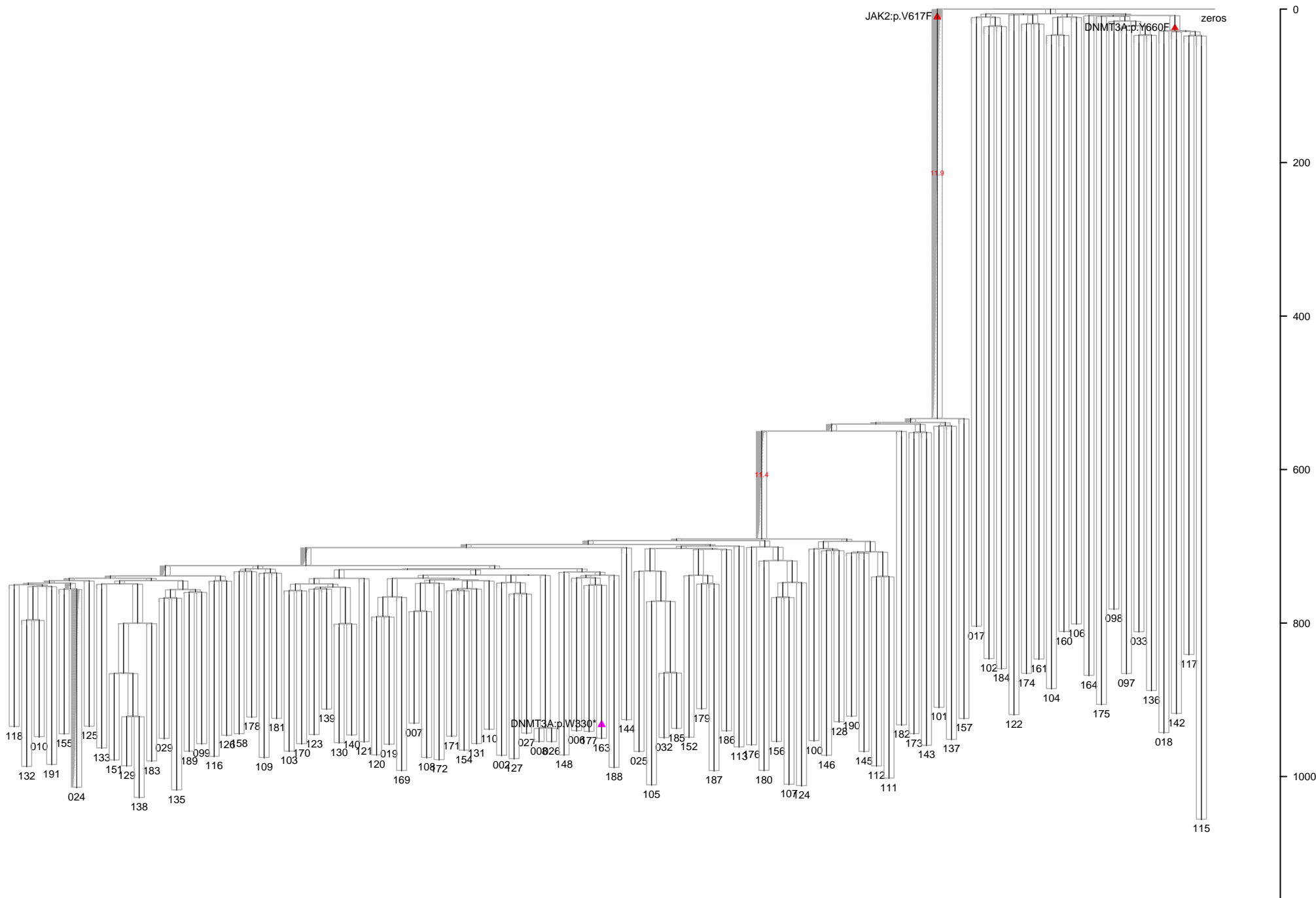


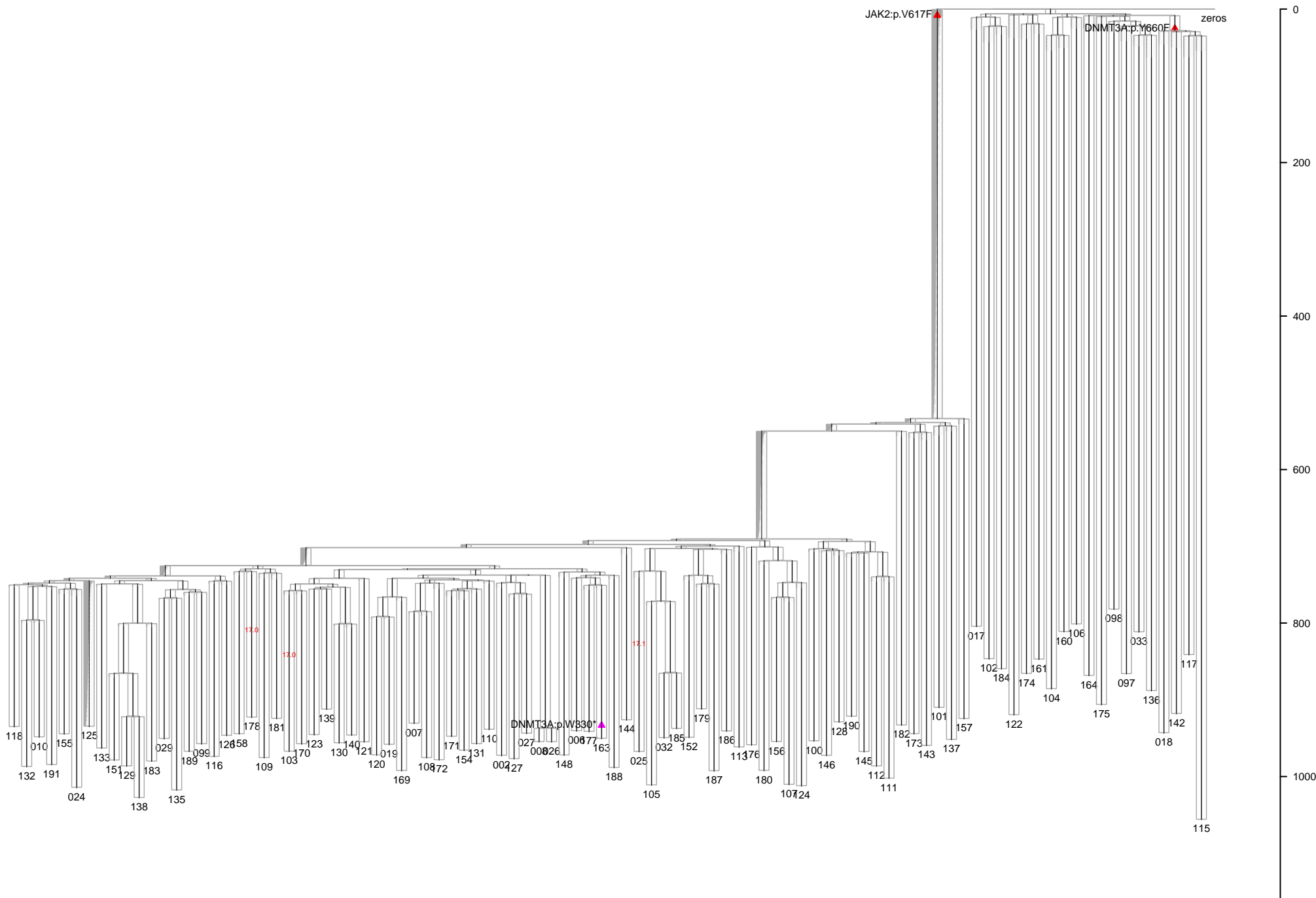
PD5847: Annotated with VAF from 191  
Mean Depth=18.27



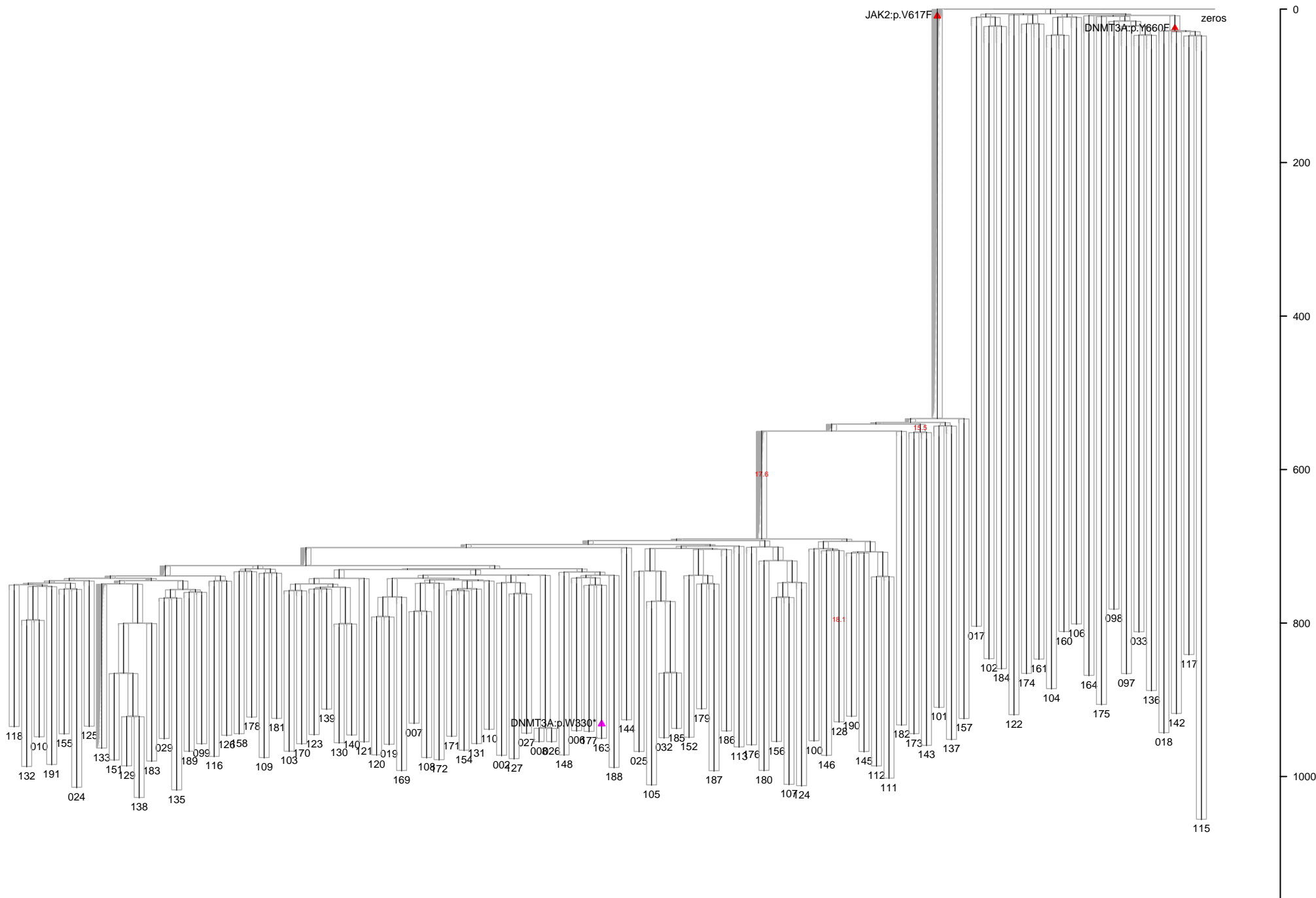
PD5847: Annotated with VAF from 155  
Mean Depth=15.92



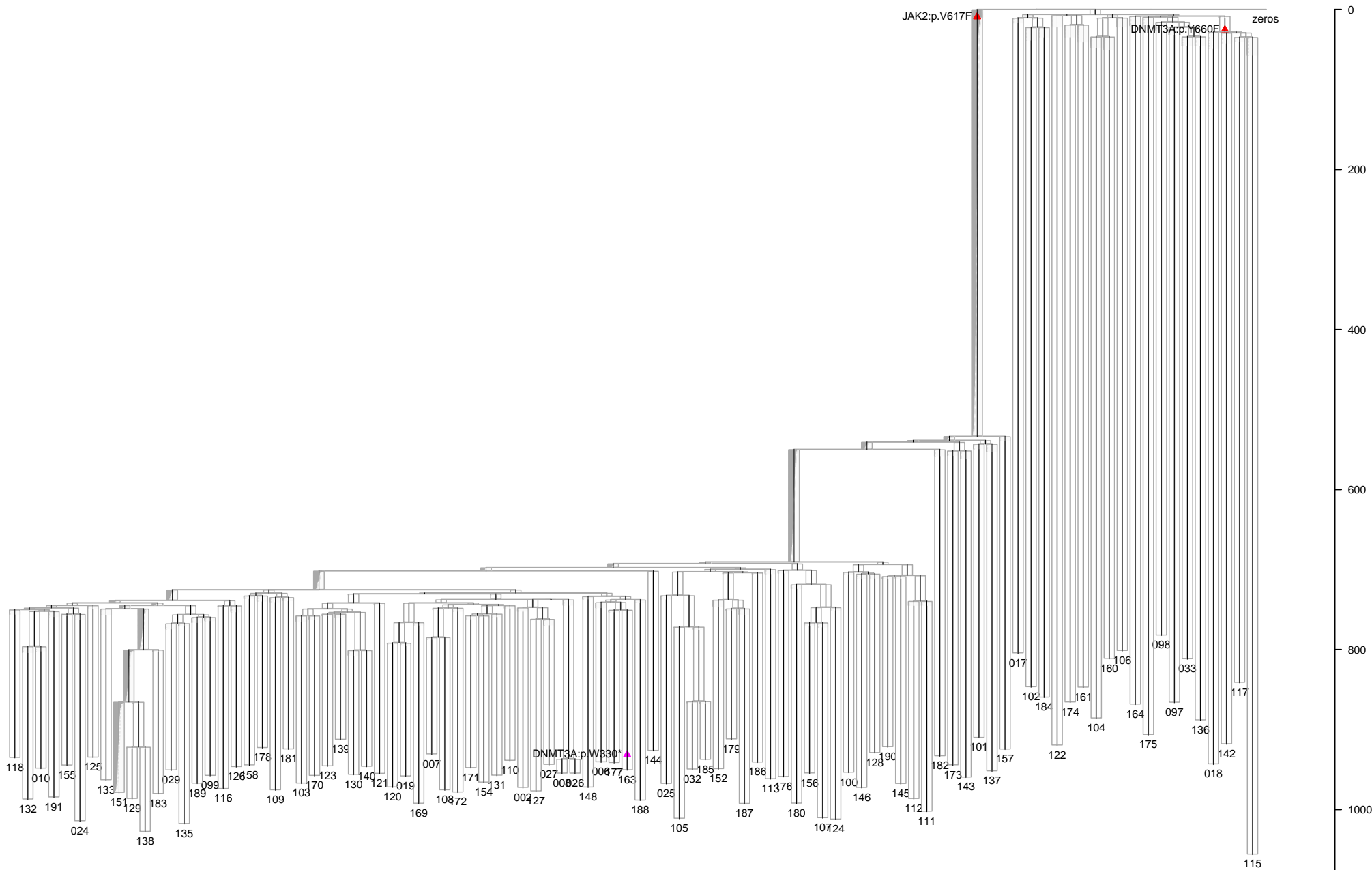


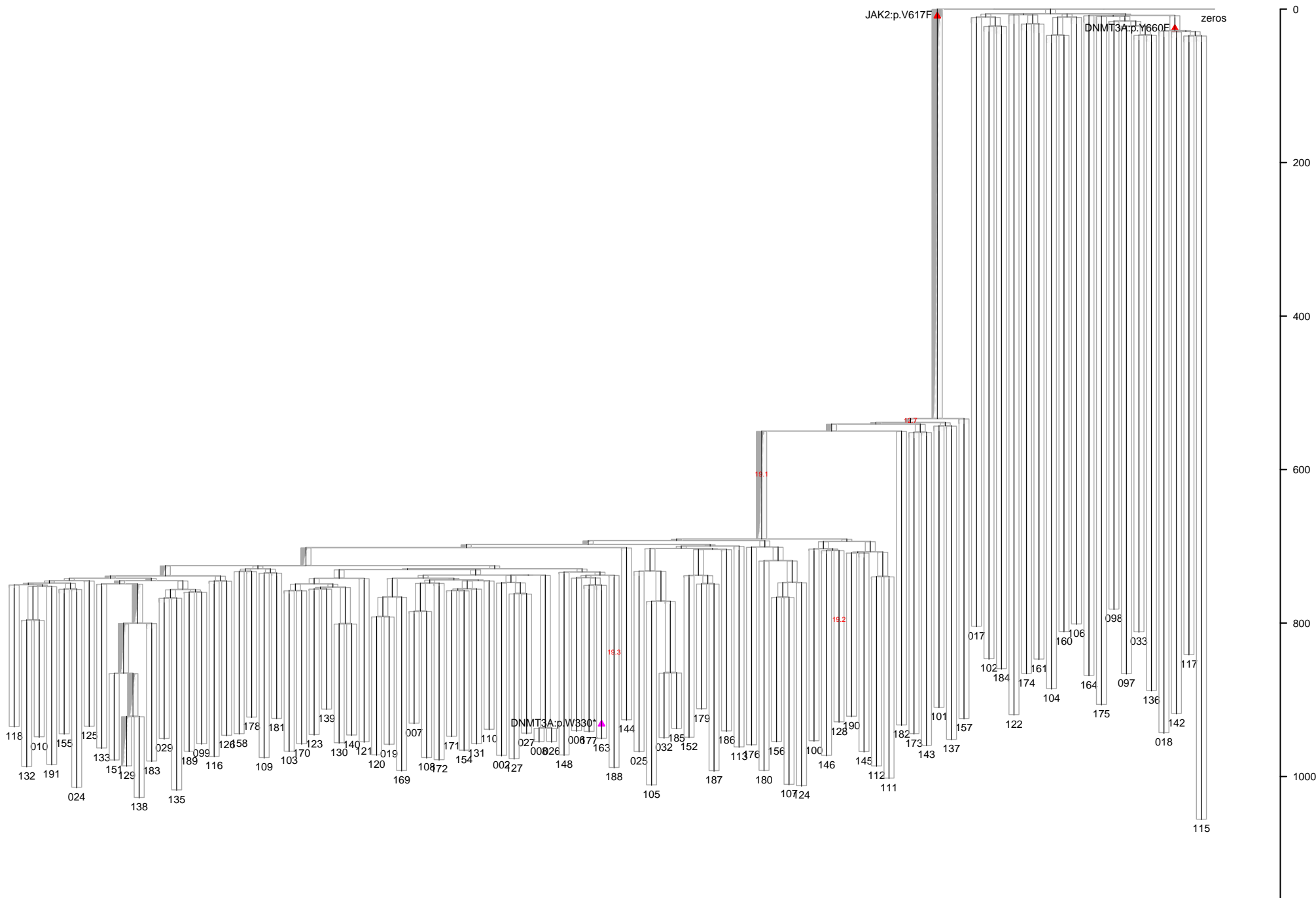


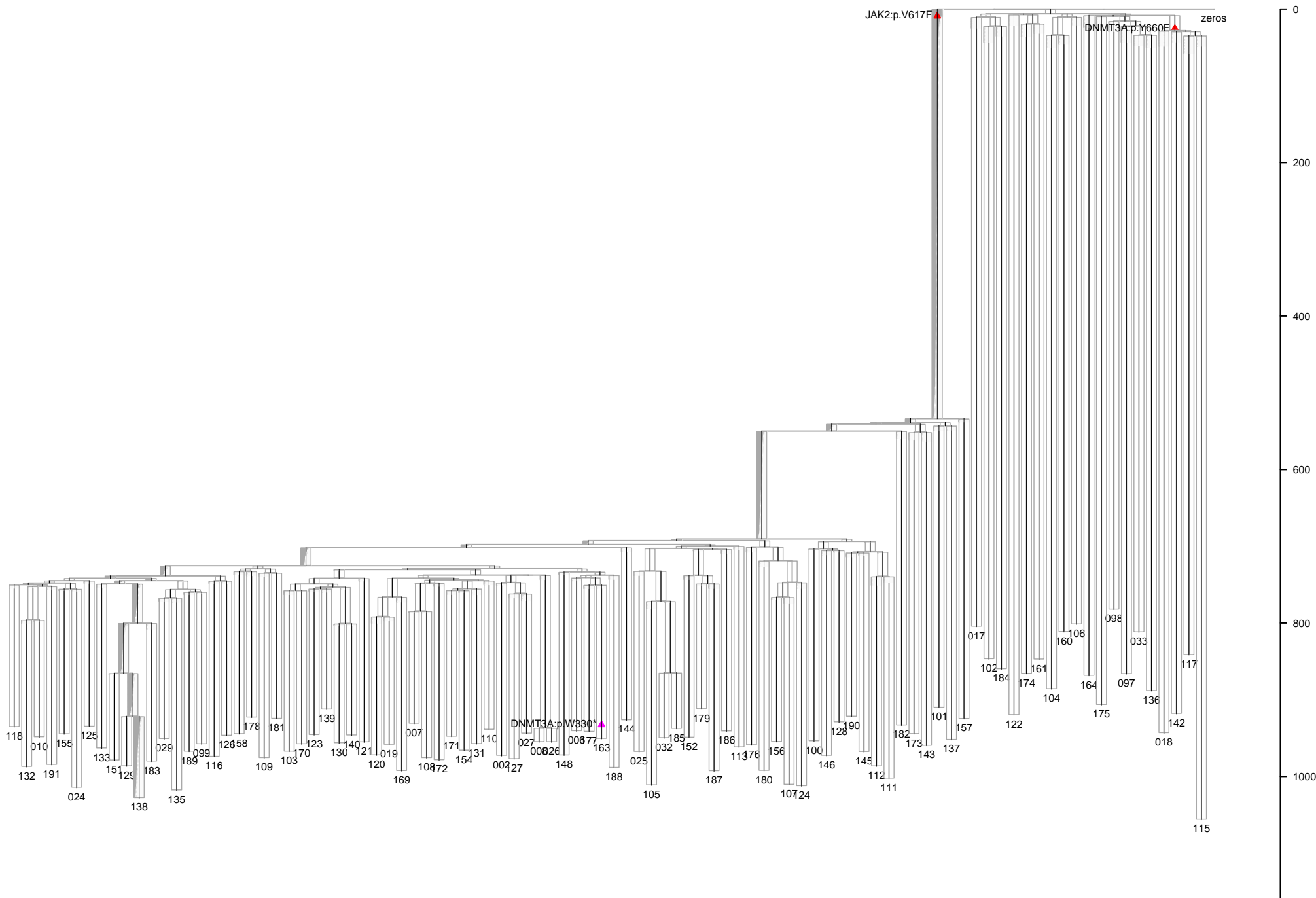


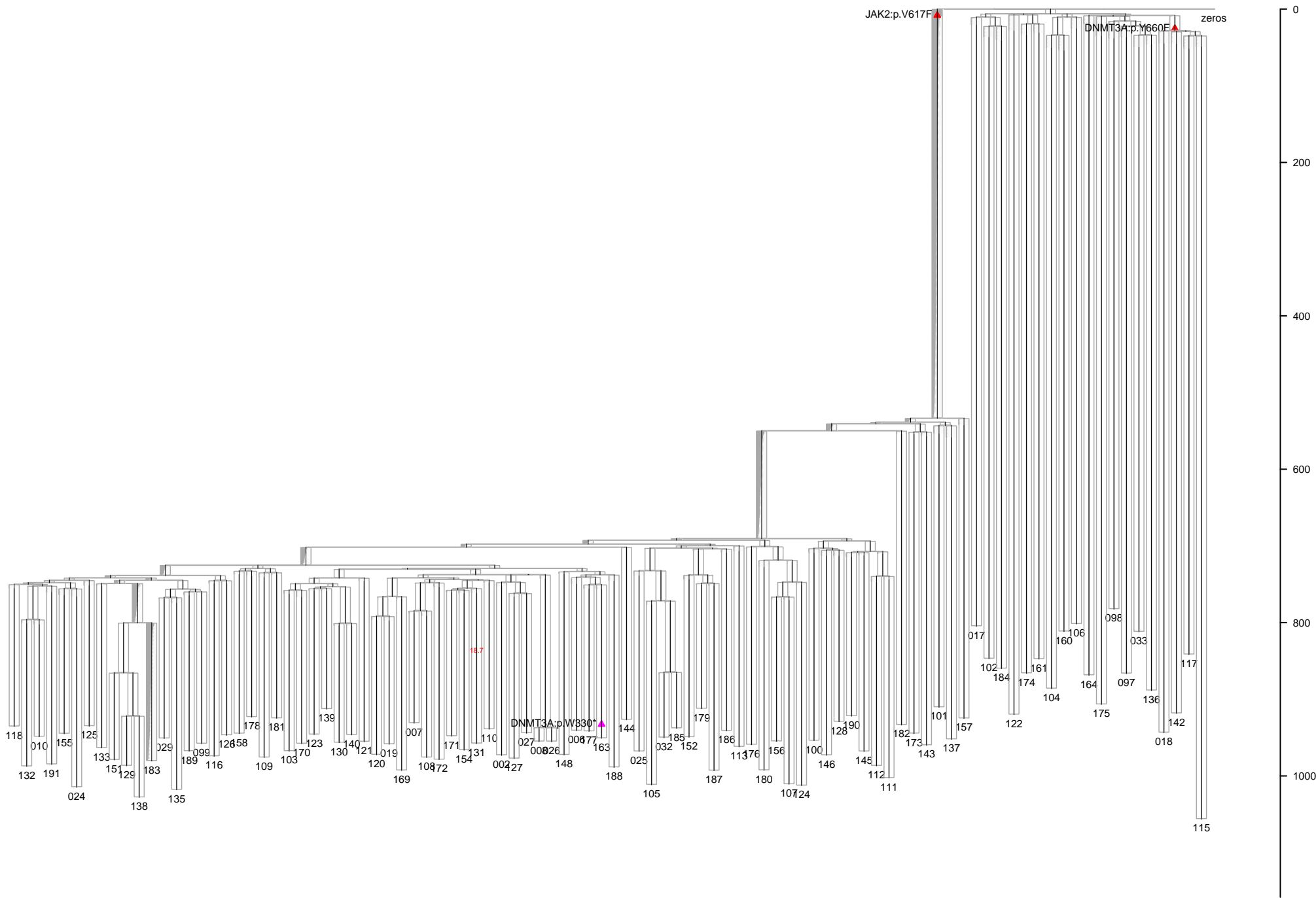


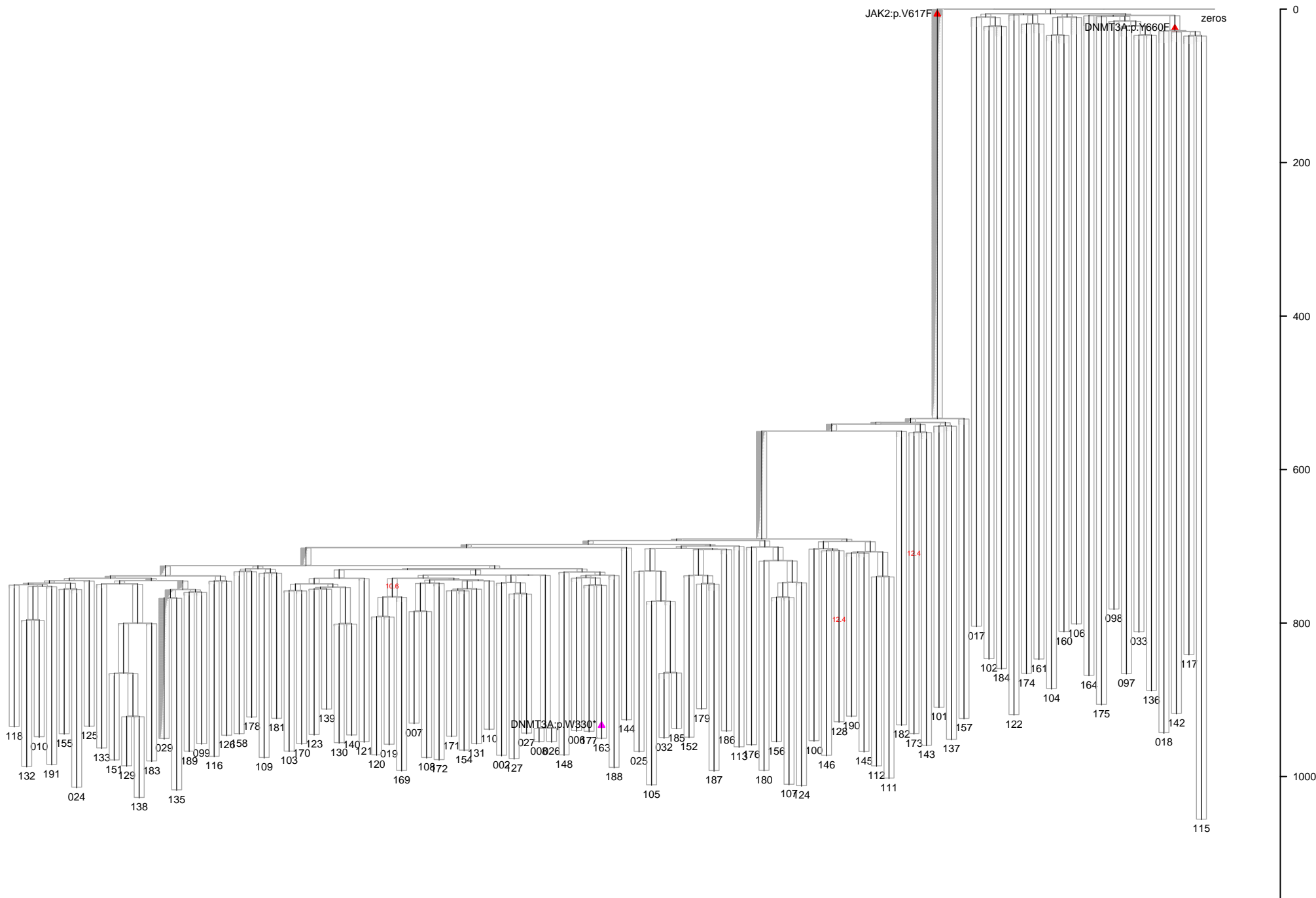
PD5847: Annotated with VAF from 151  
Mean Depth=17.51



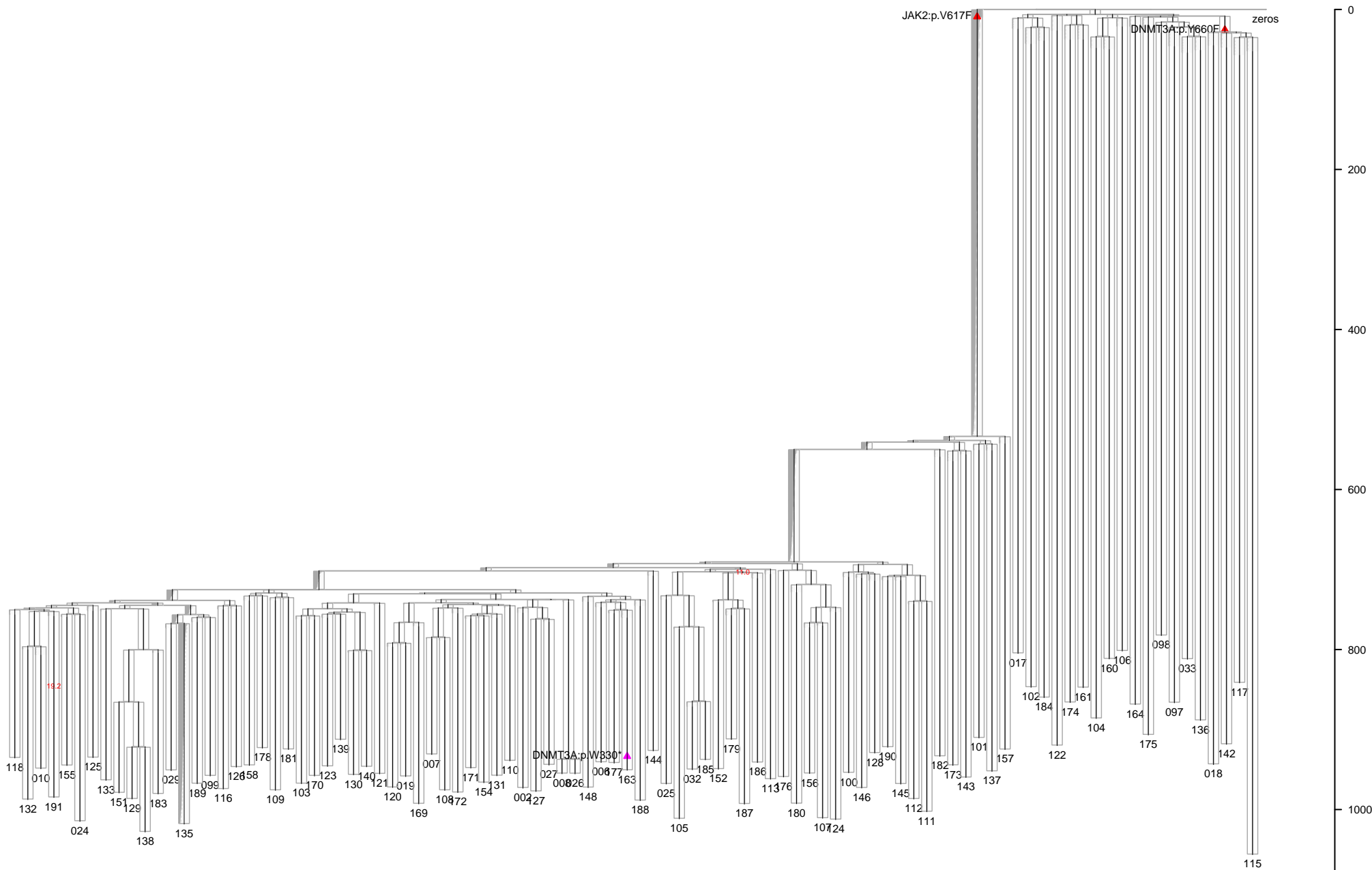


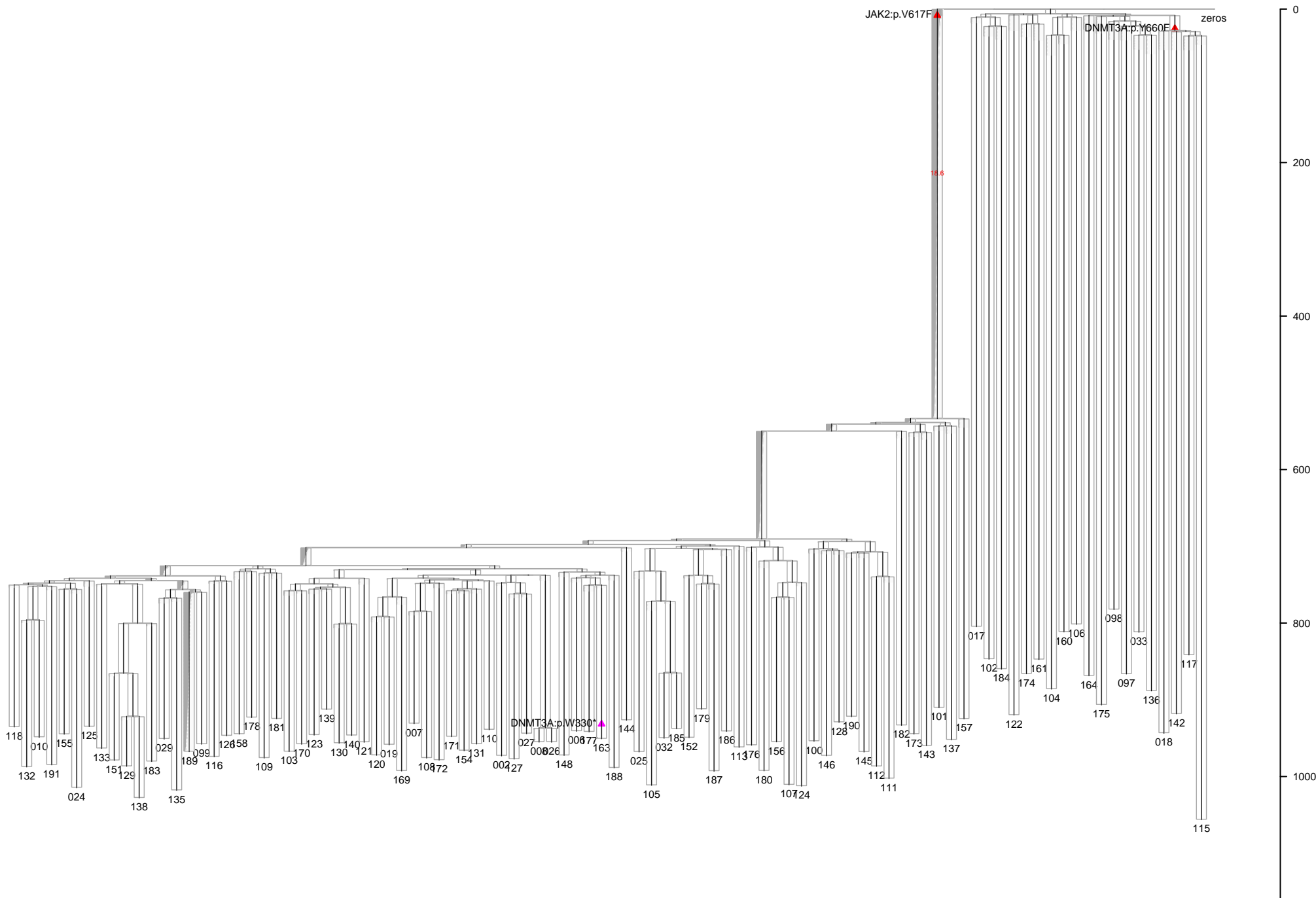




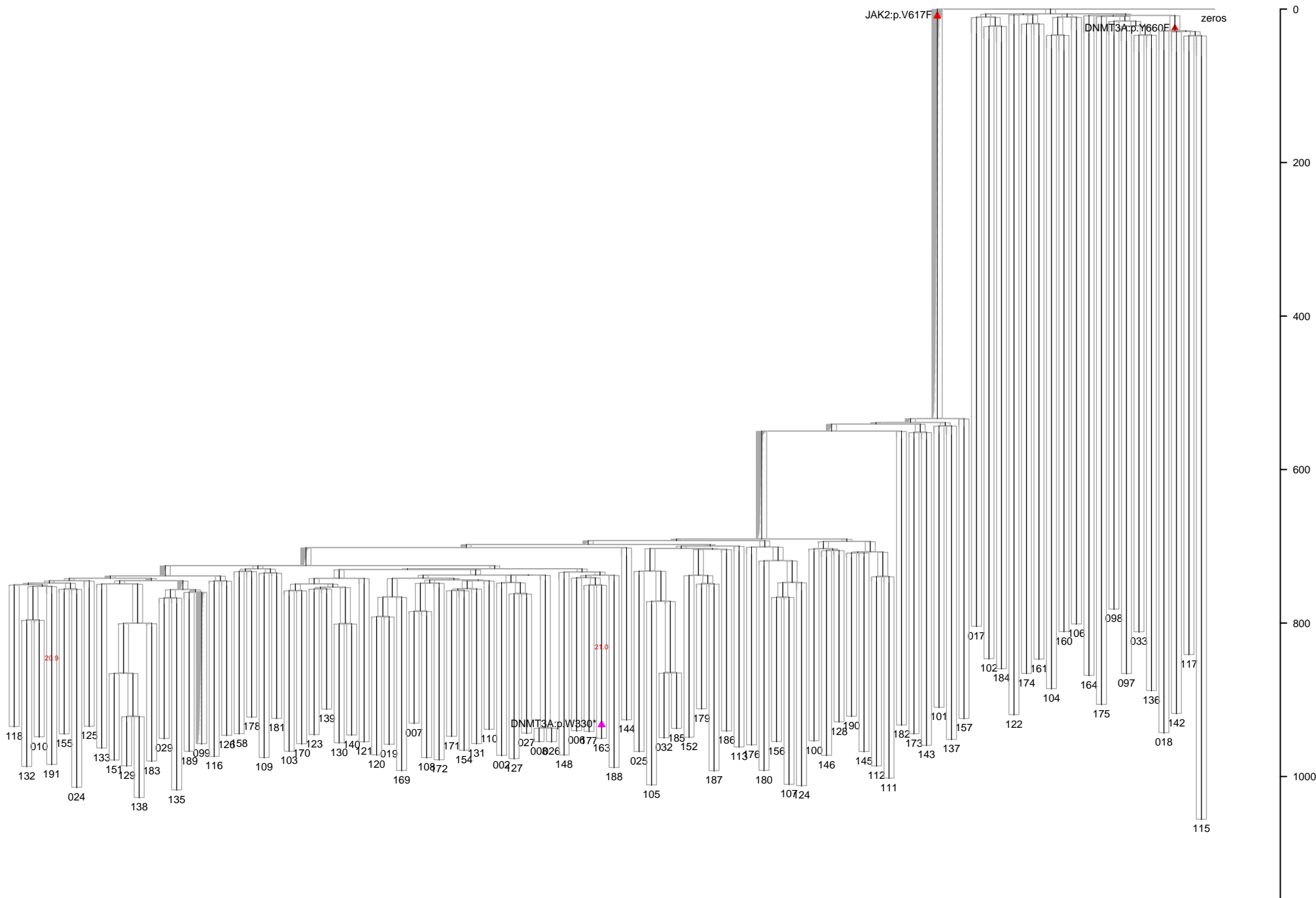


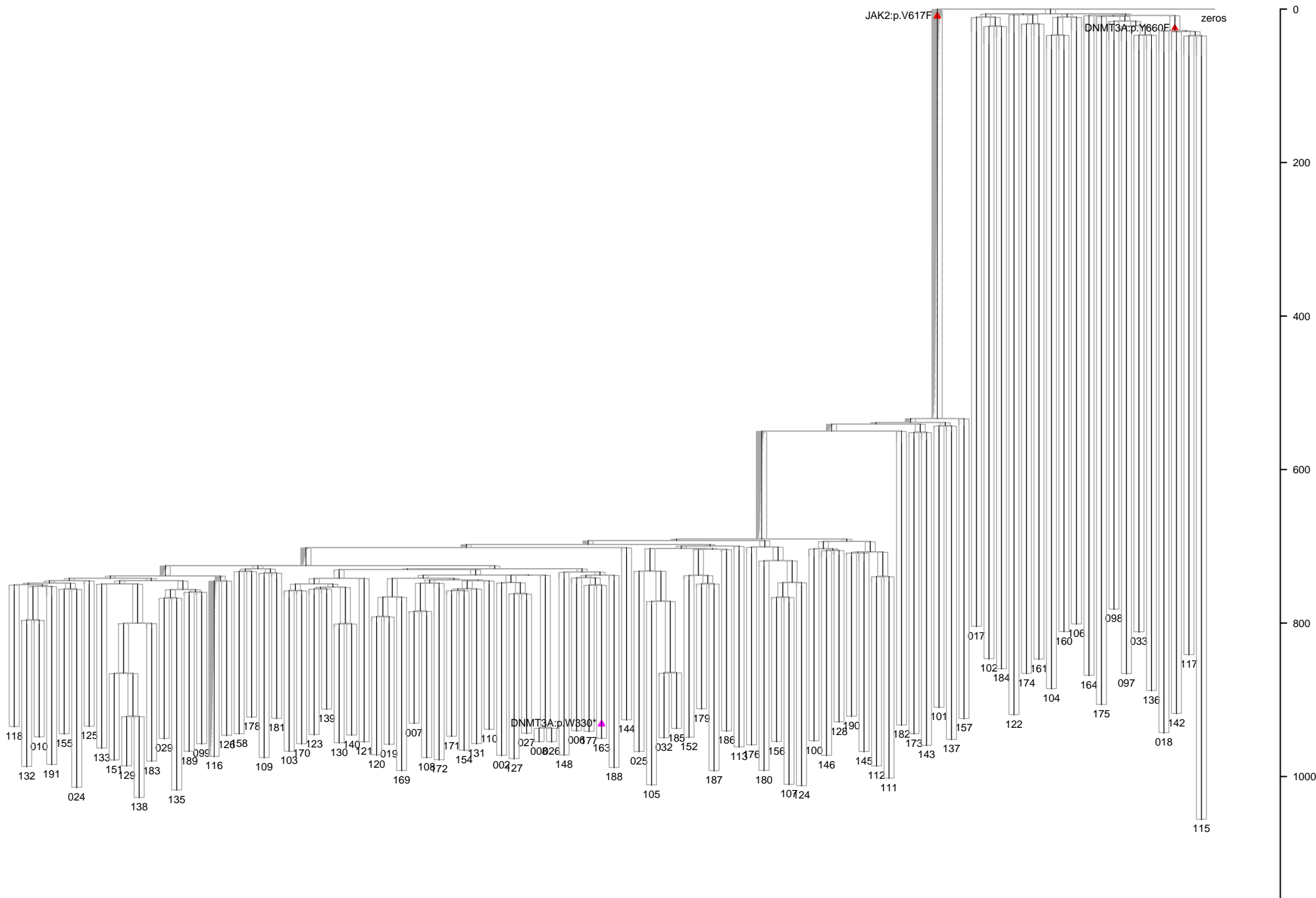
PD5847: Annotated with VAF from 135  
Mean Depth=20.20

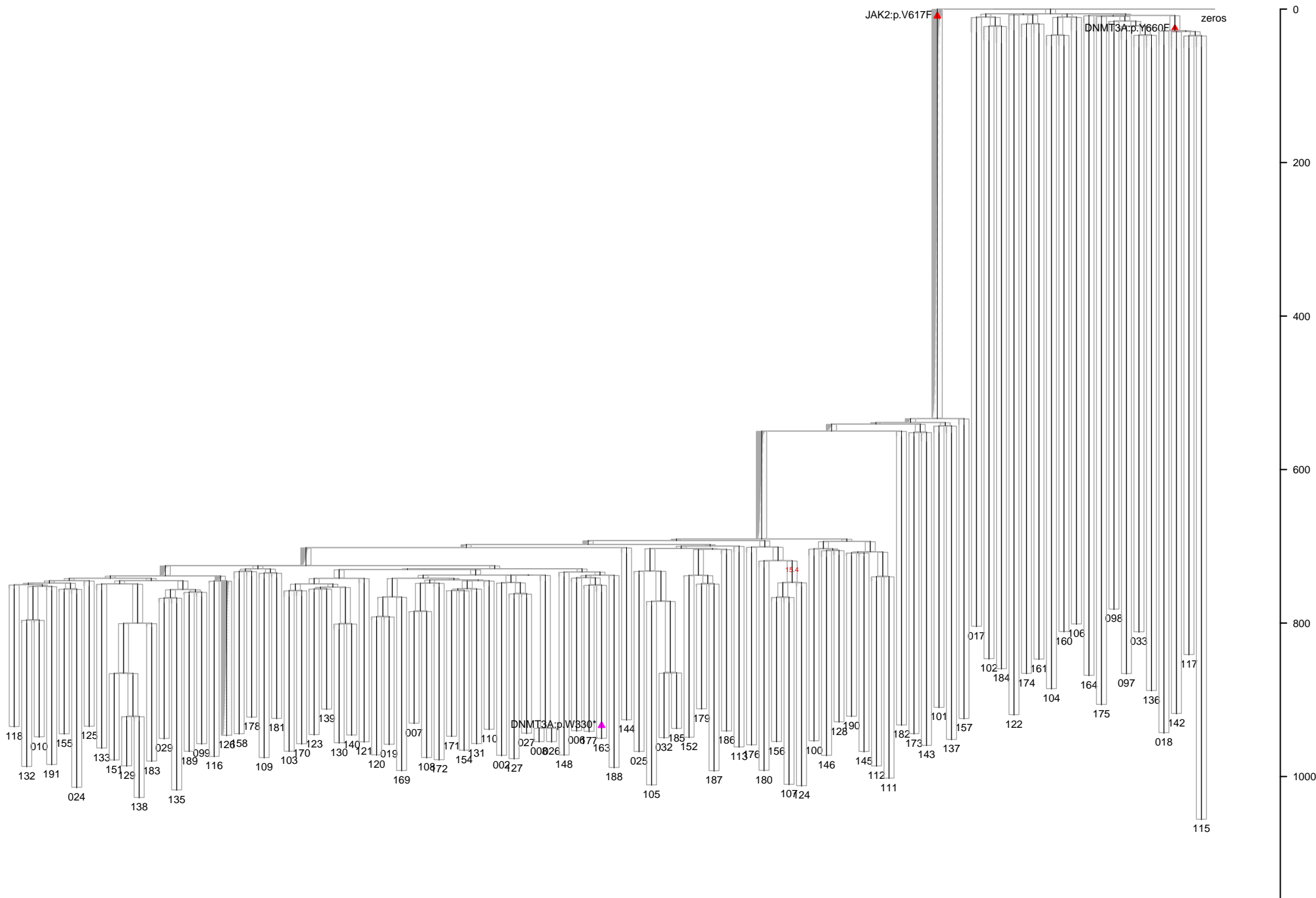


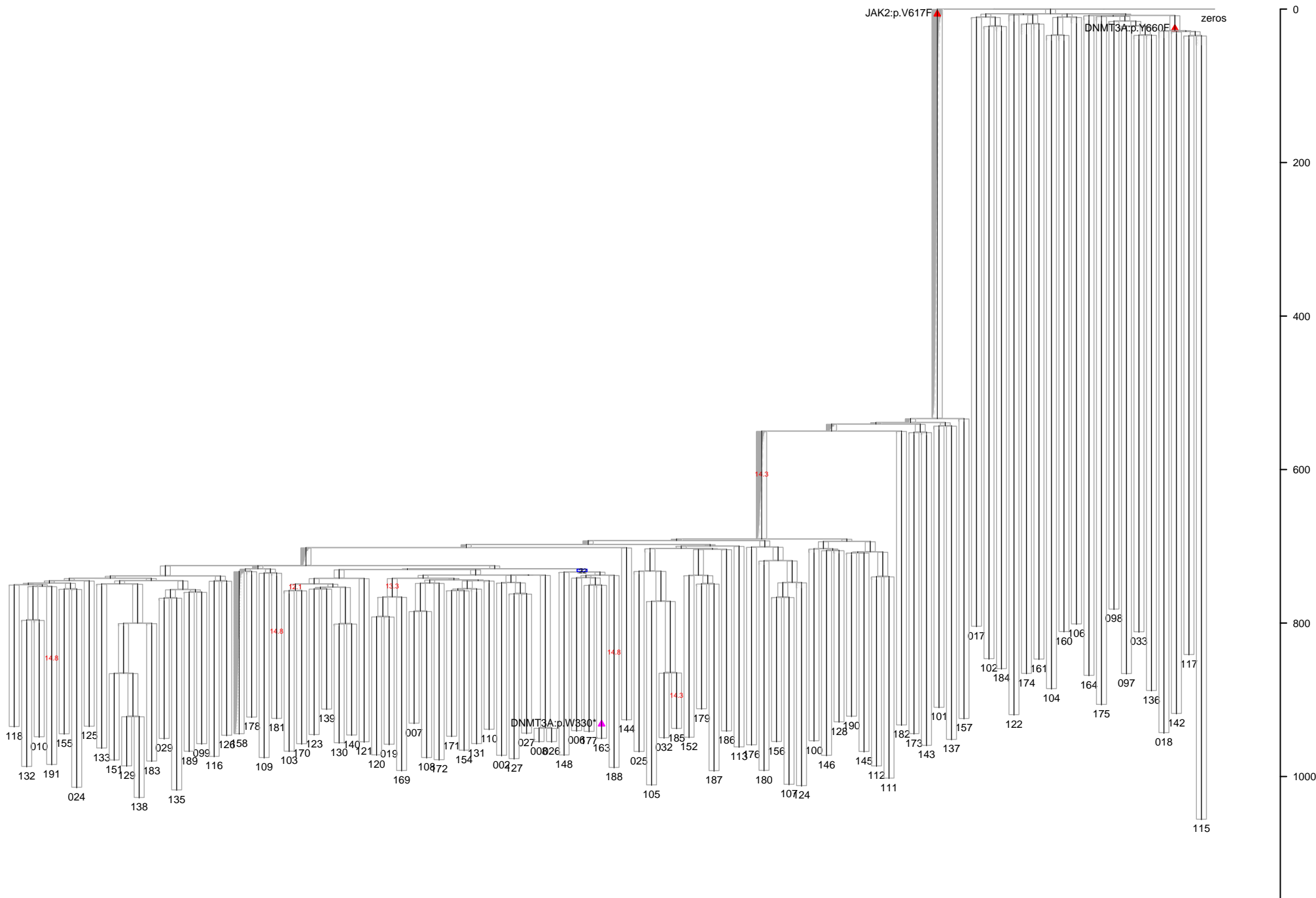


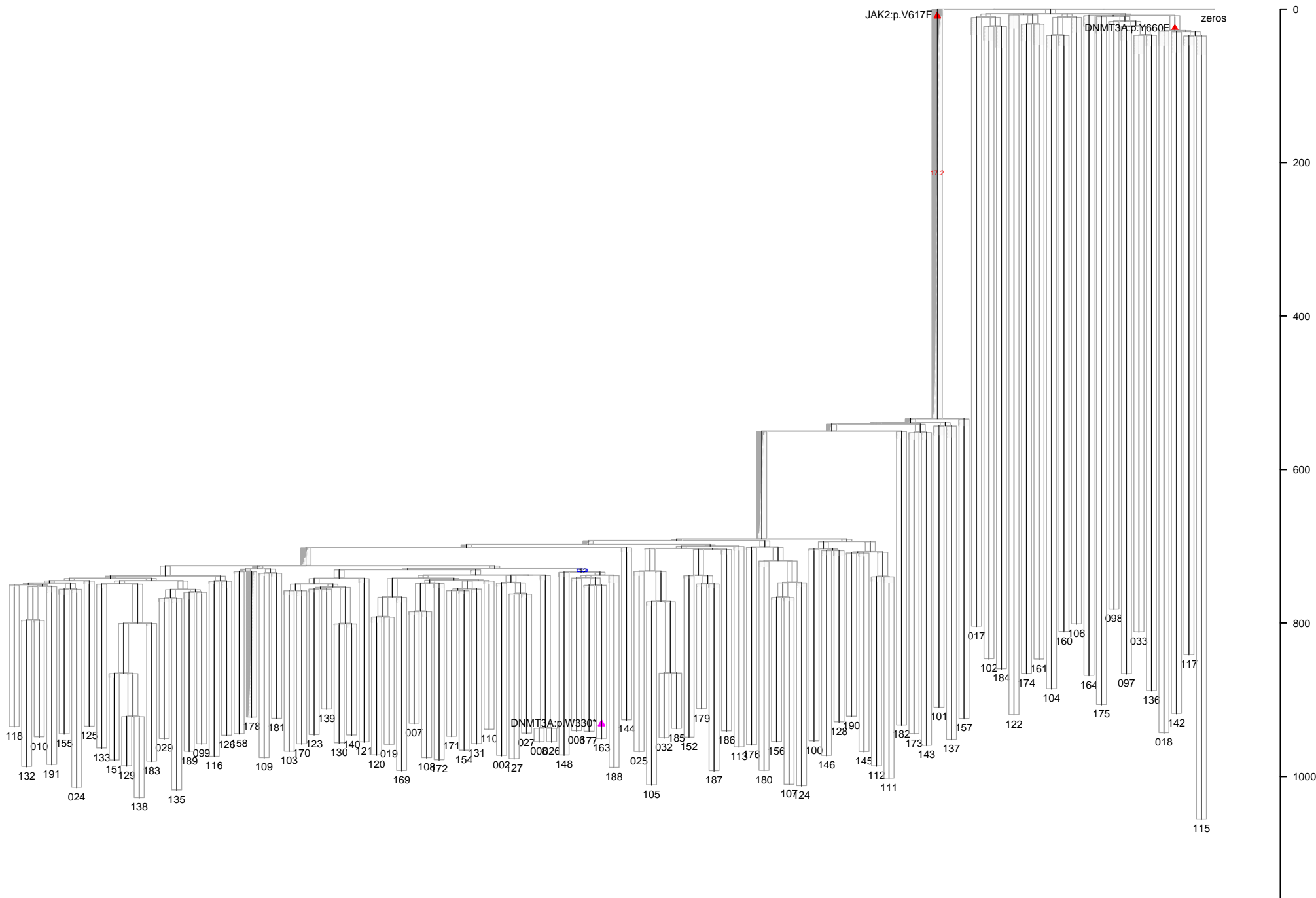


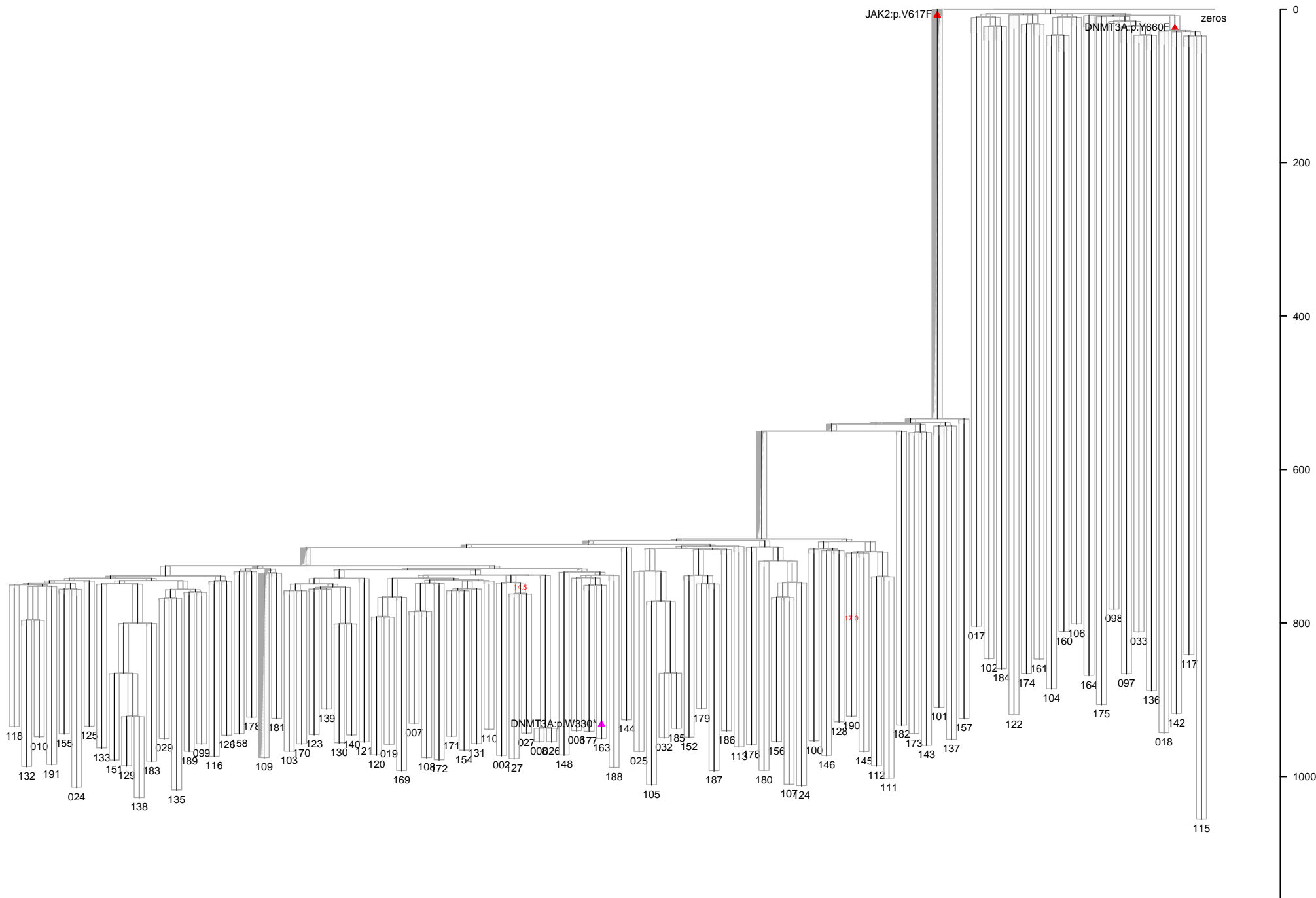


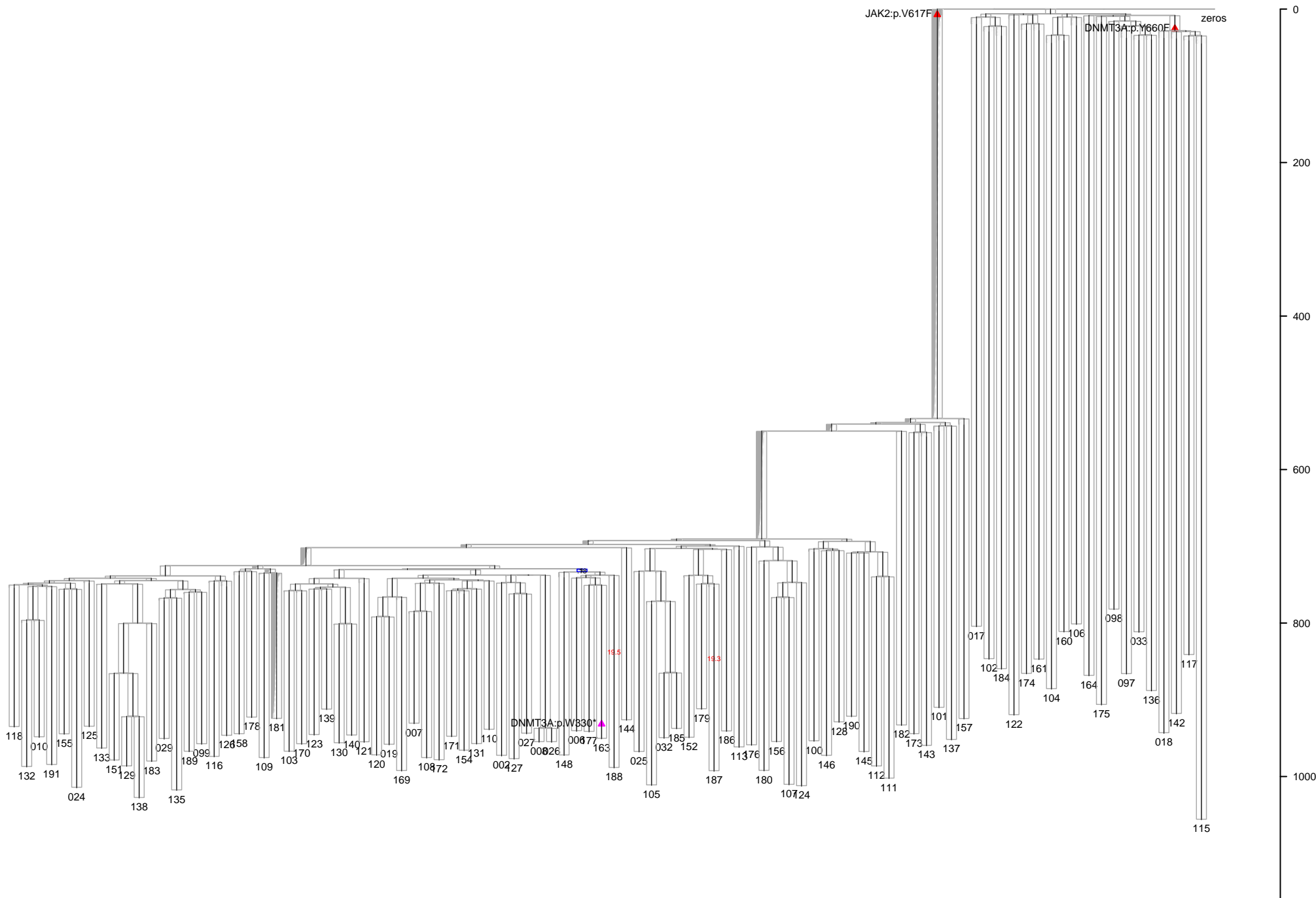




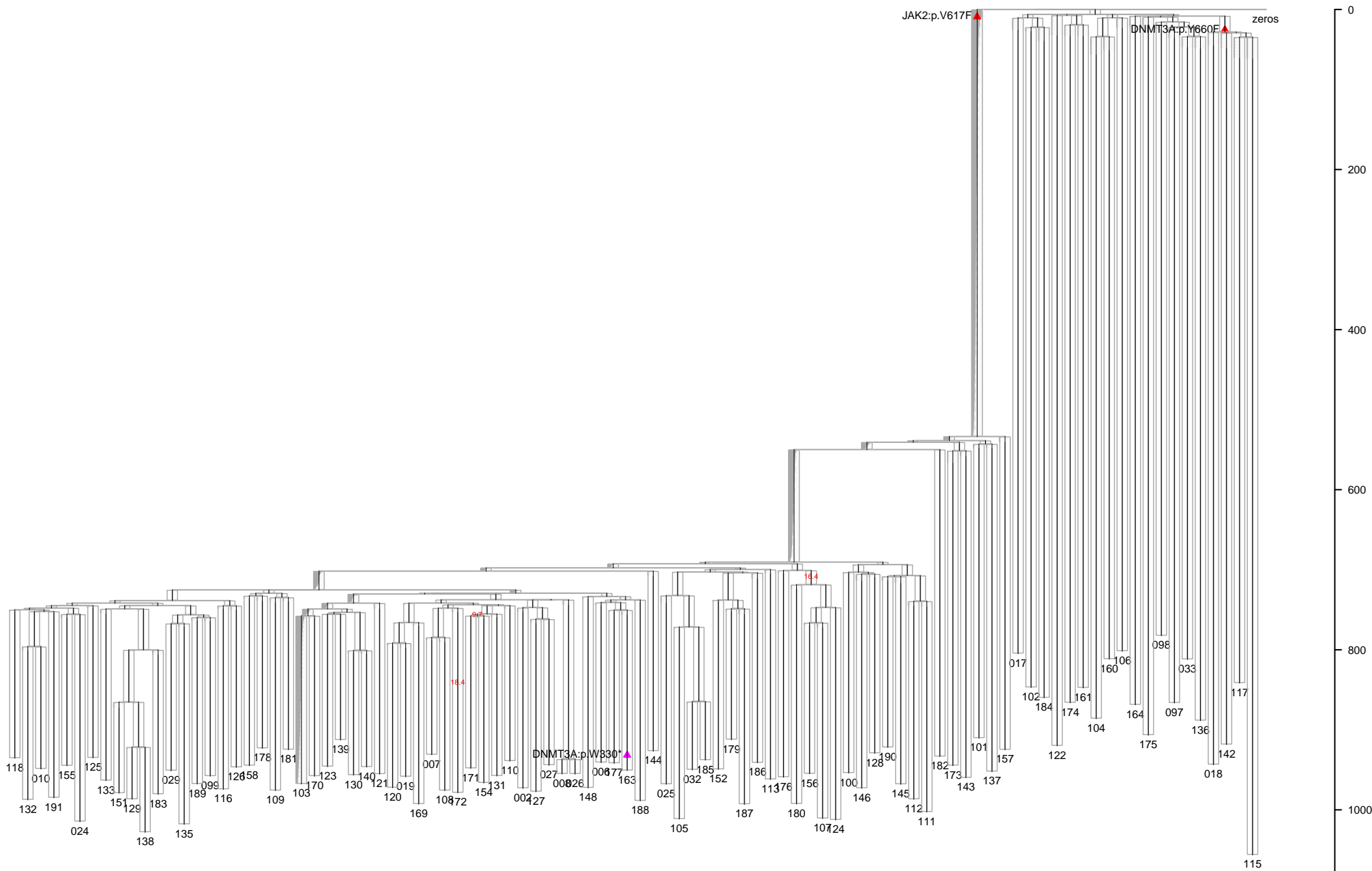




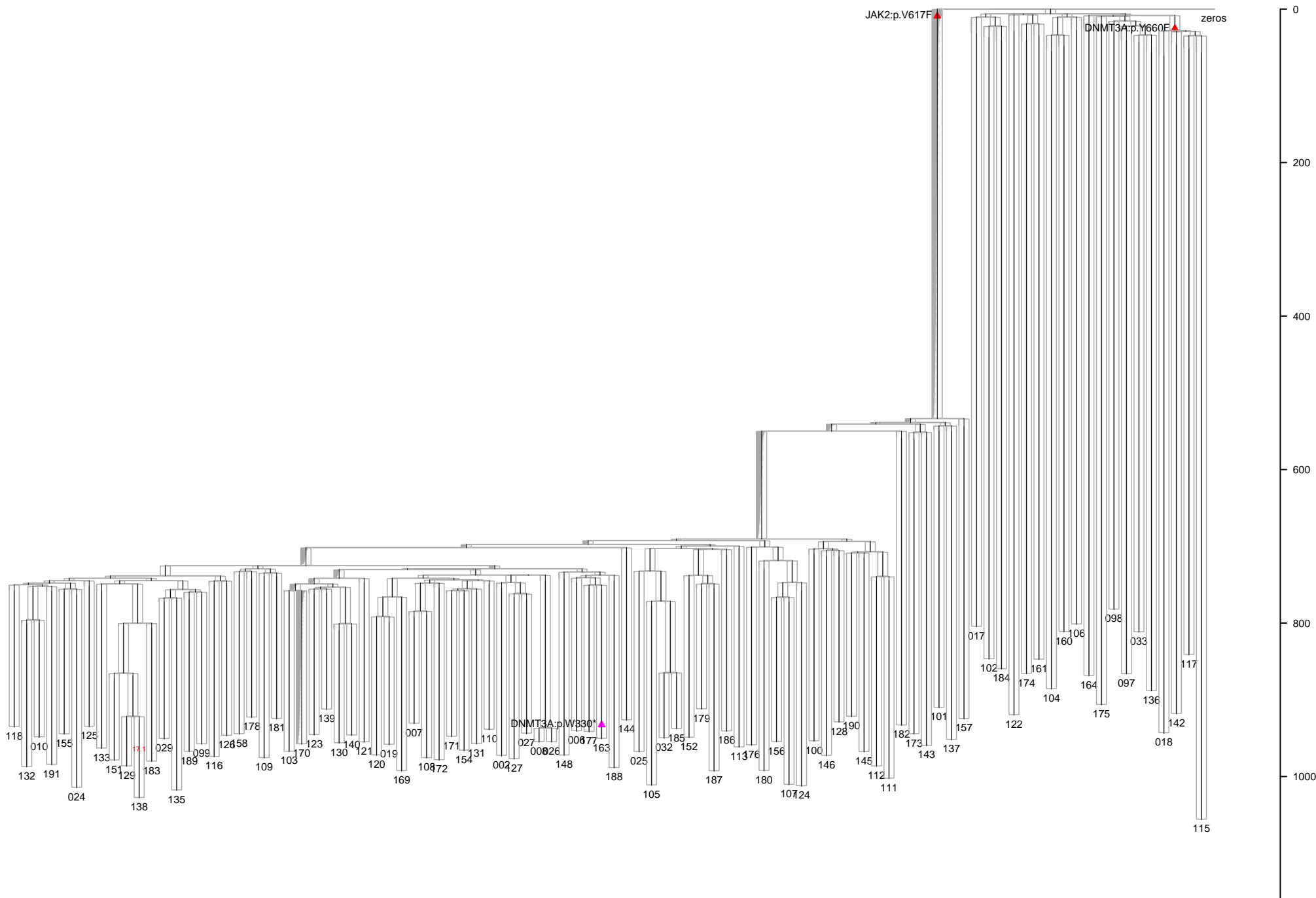


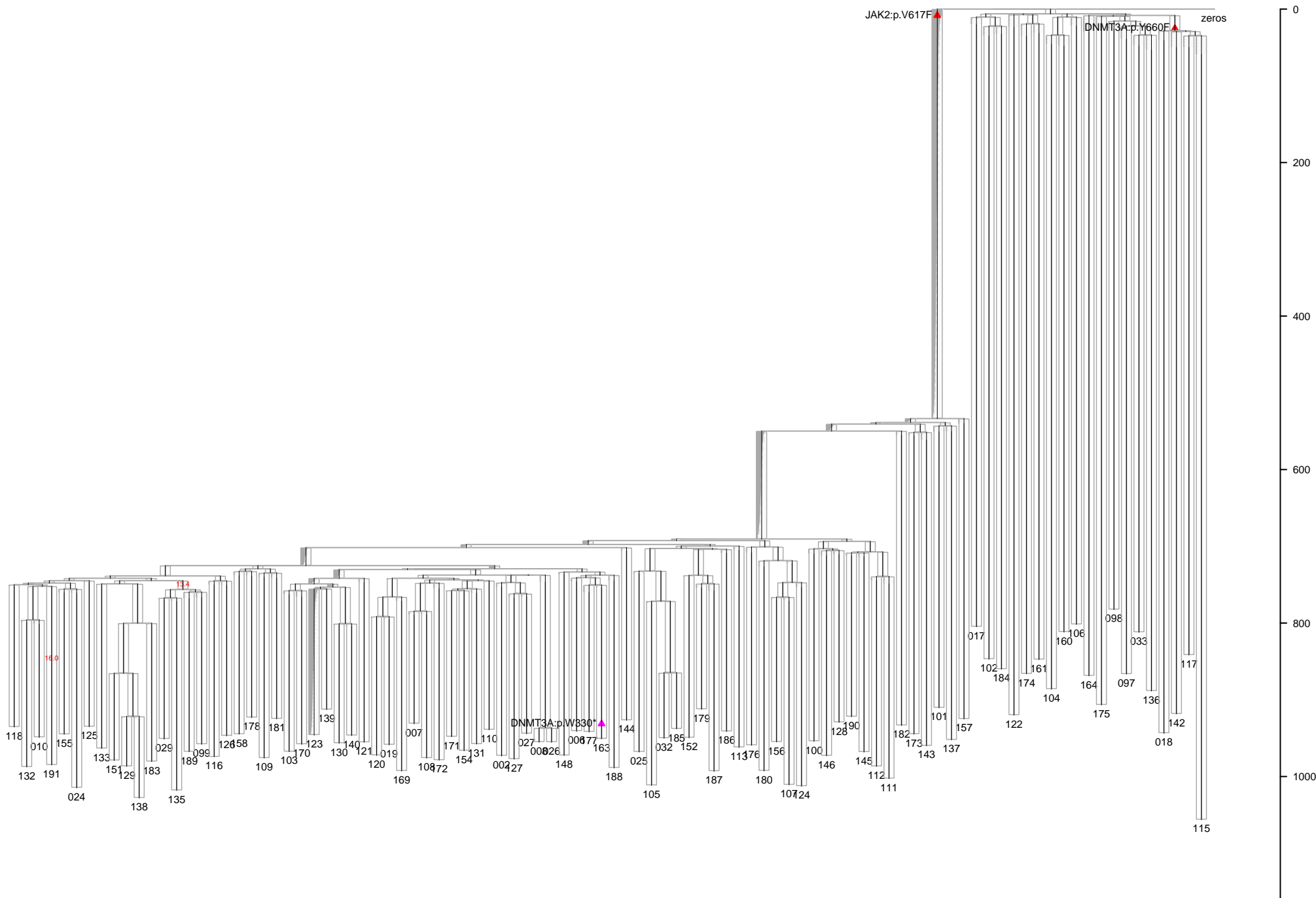


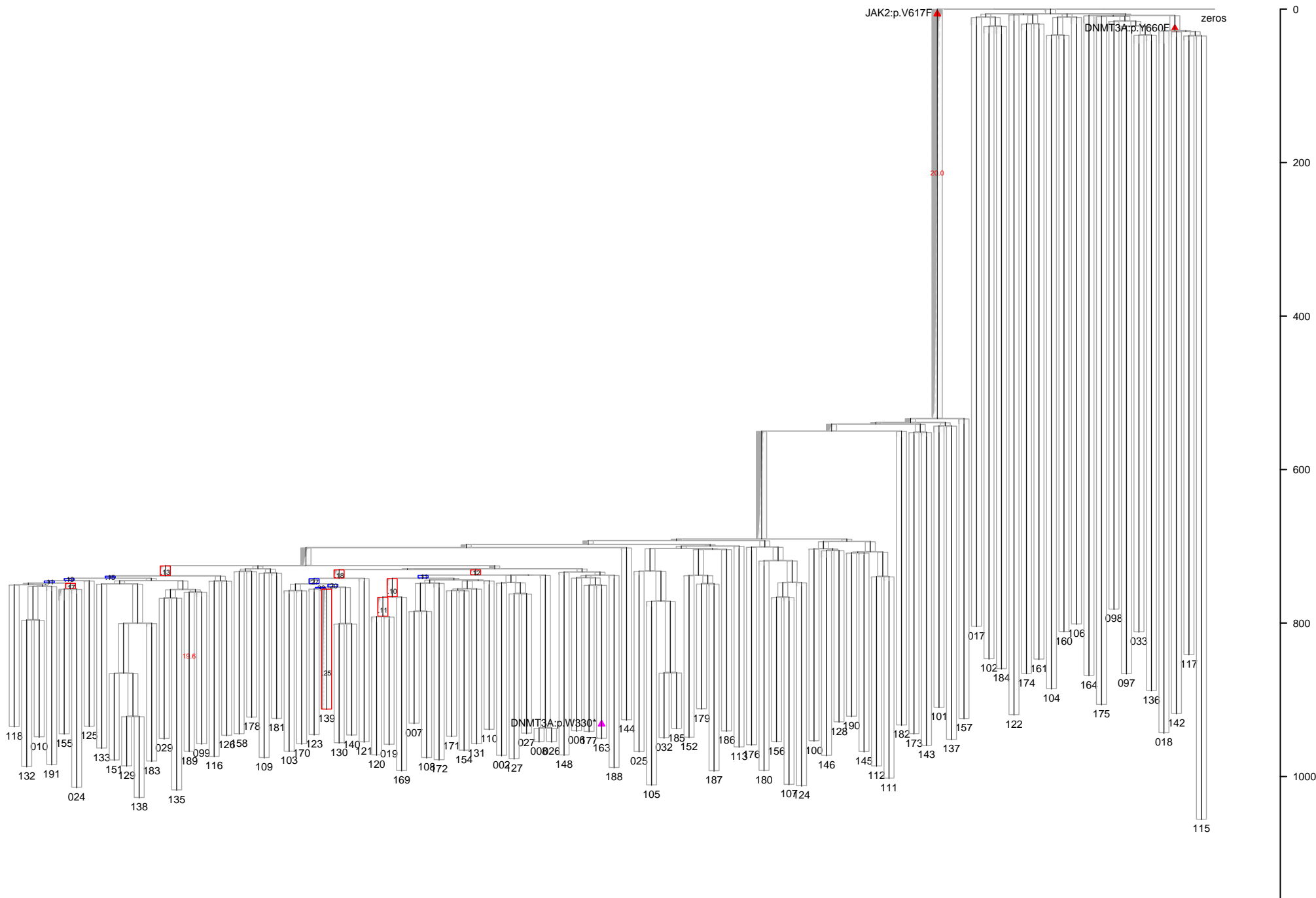
PD5847: Annotated with VAF from 103  
Mean Depth=19.38



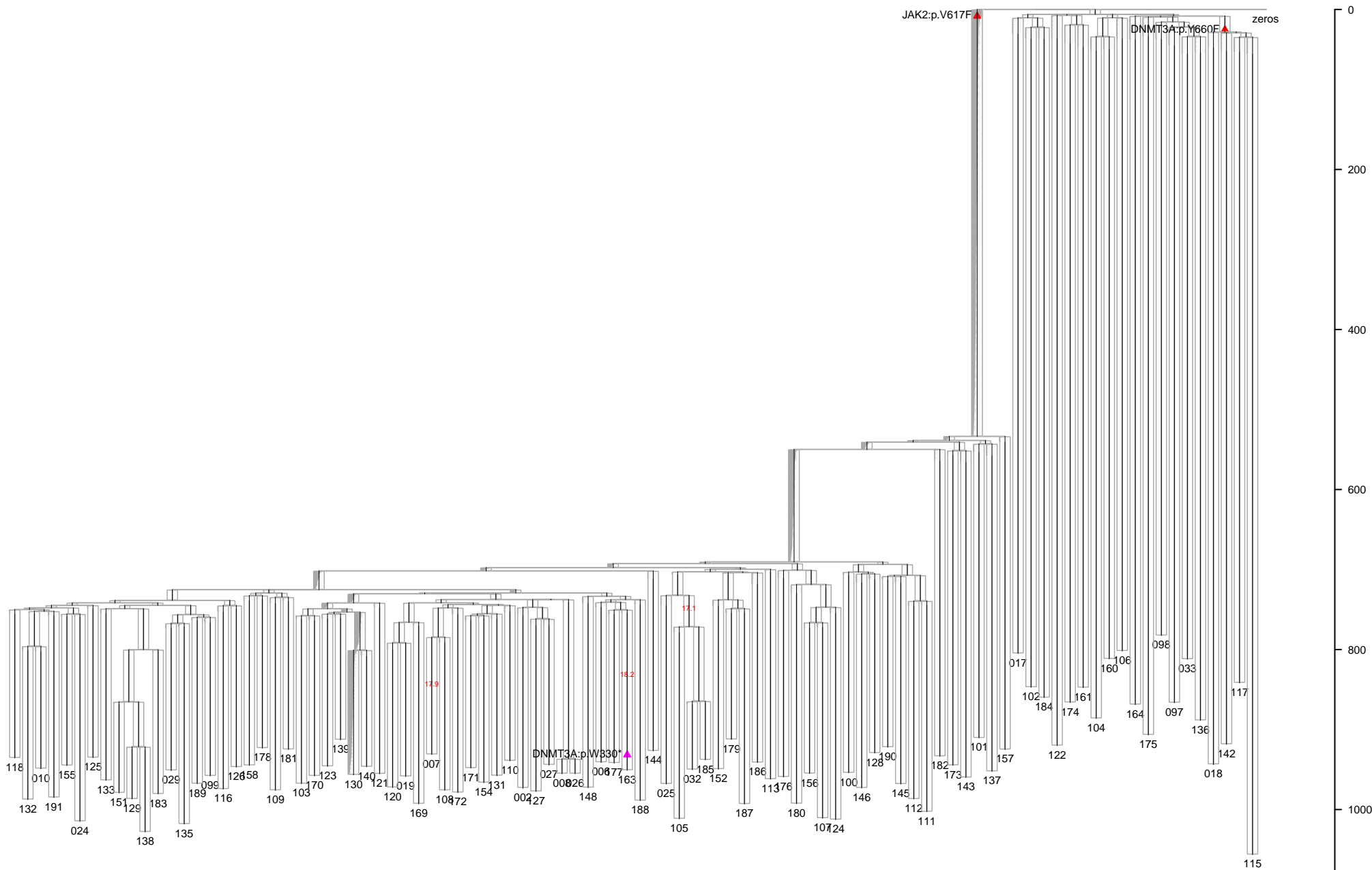


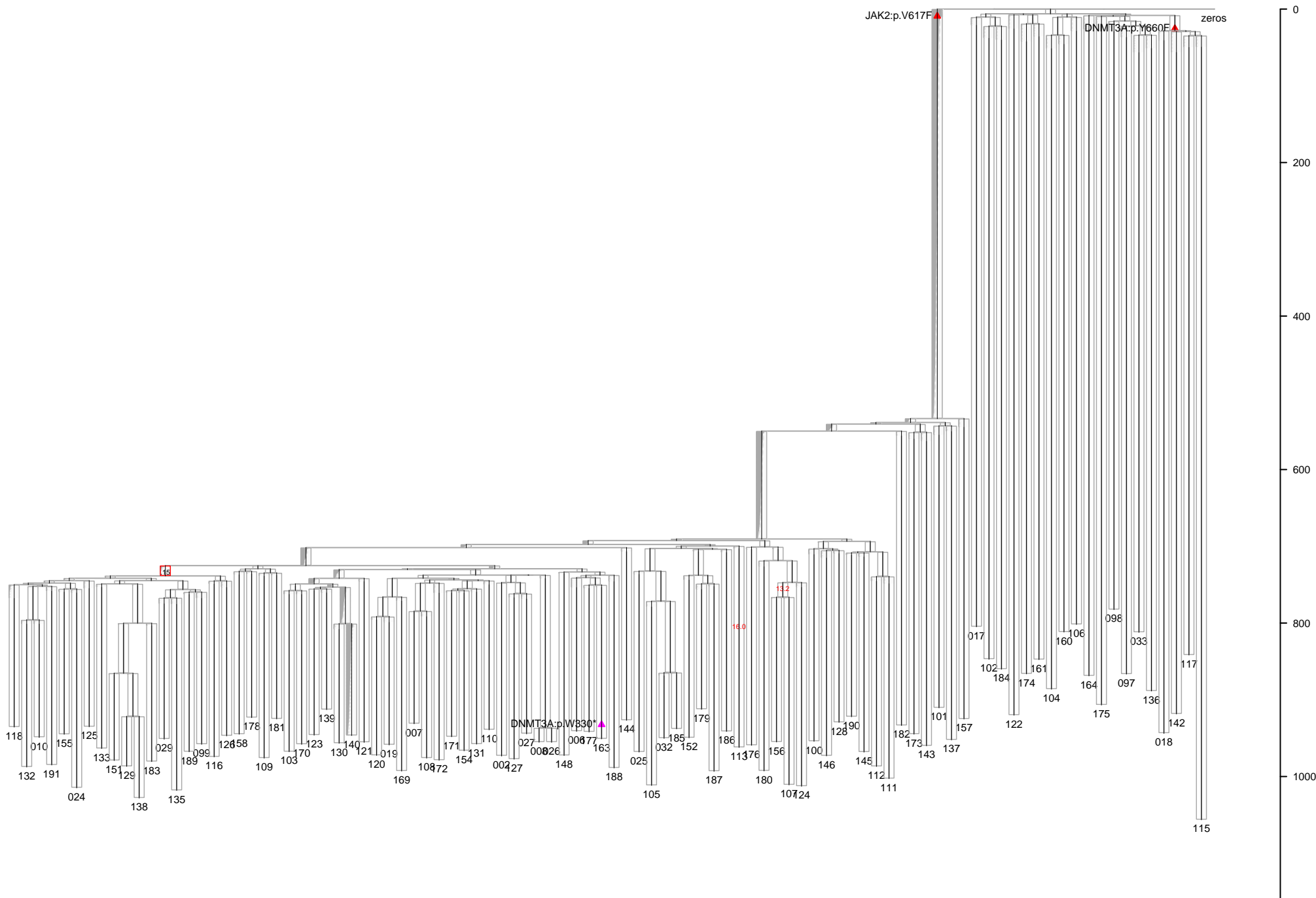




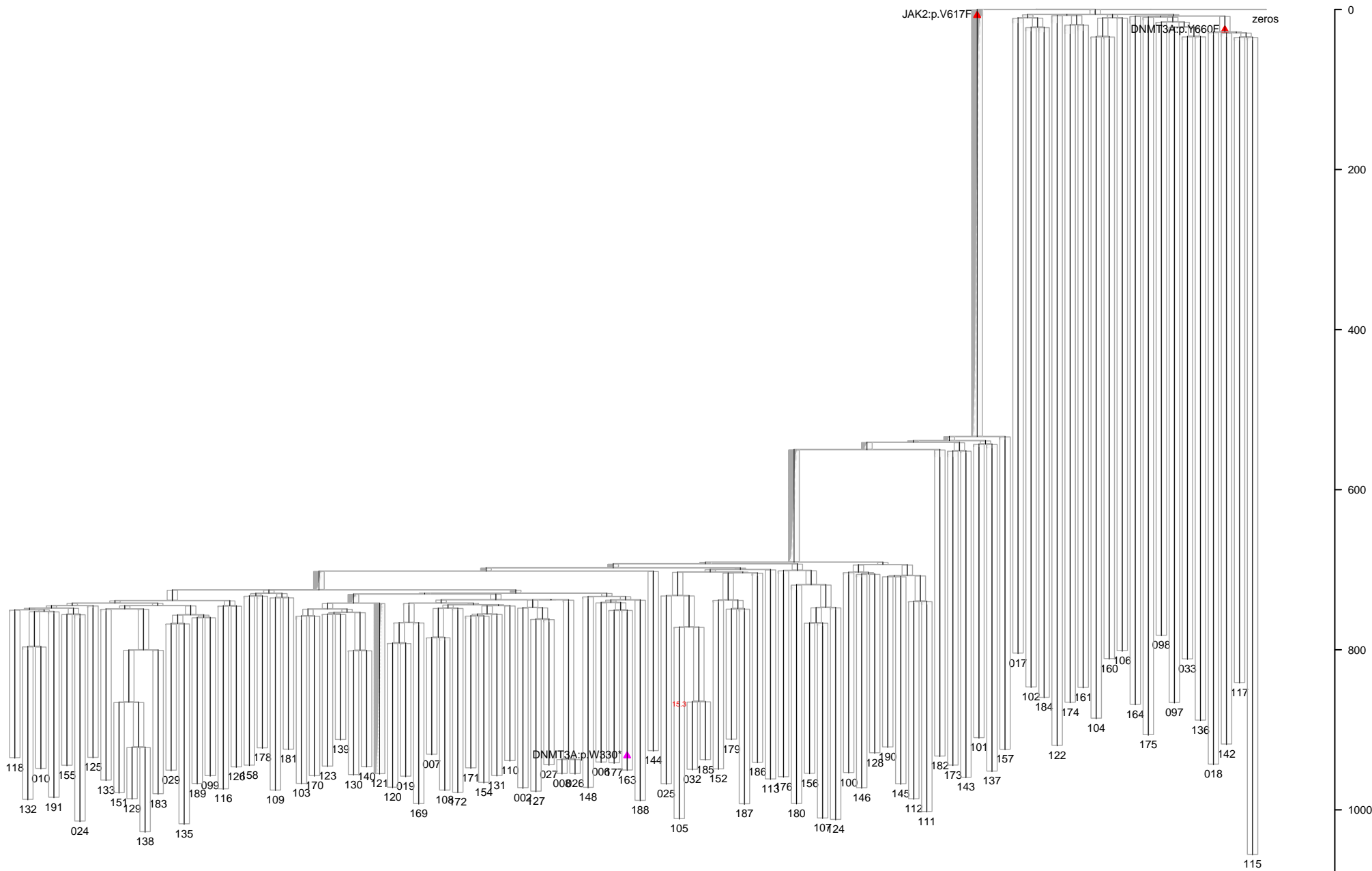


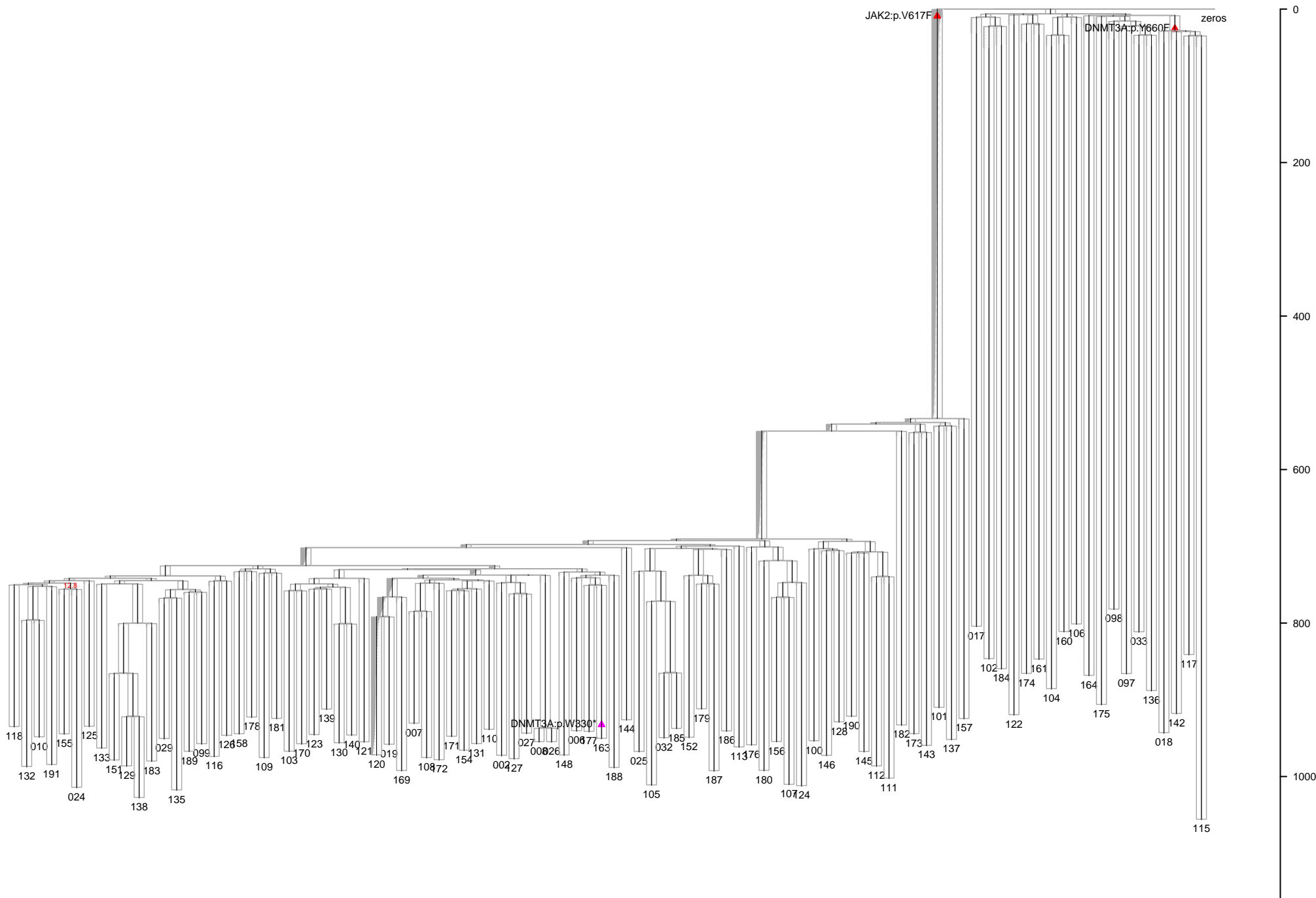
**PD5847: Annotated with VAF from 130**  
**Mean Depth=19.11**

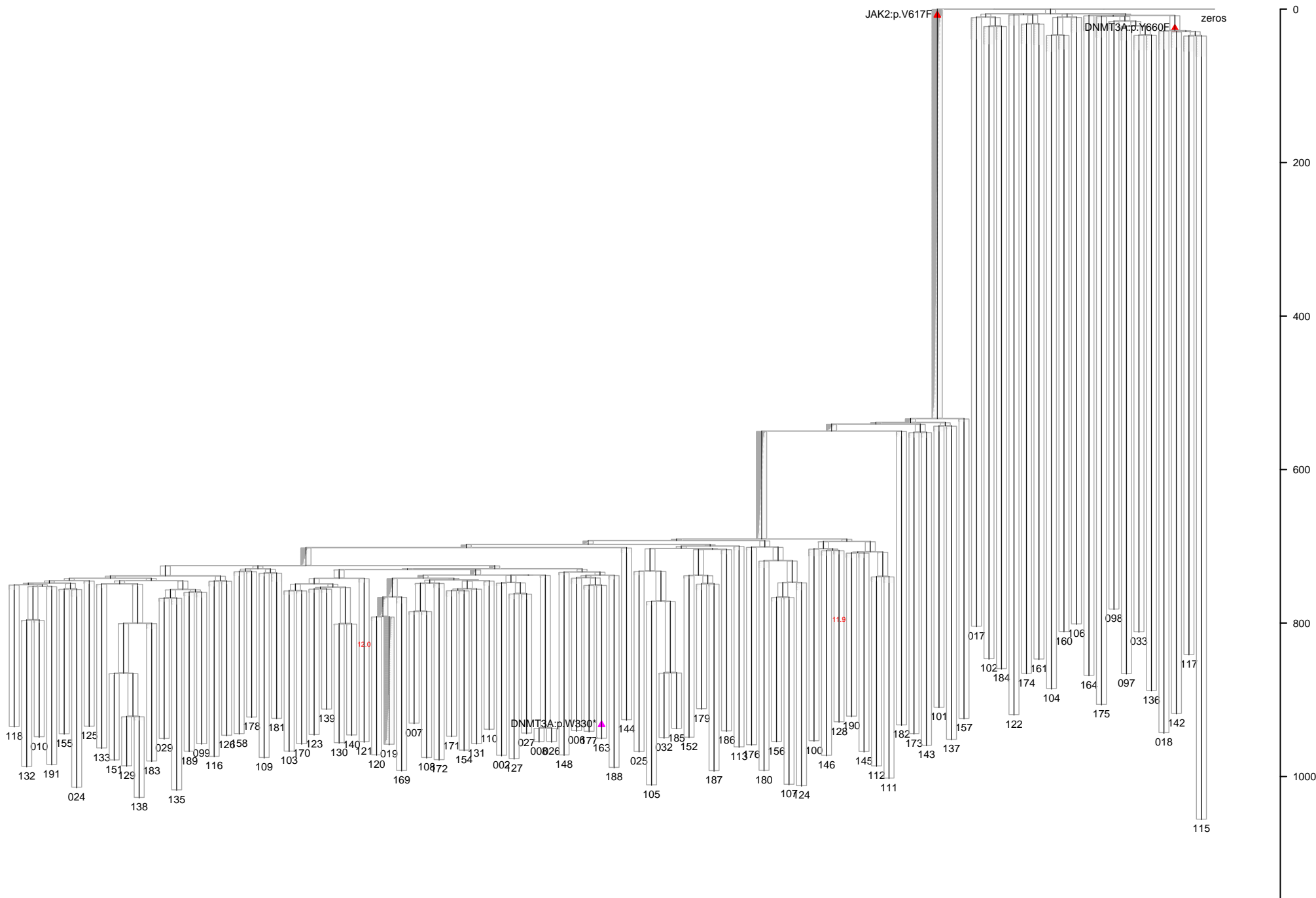




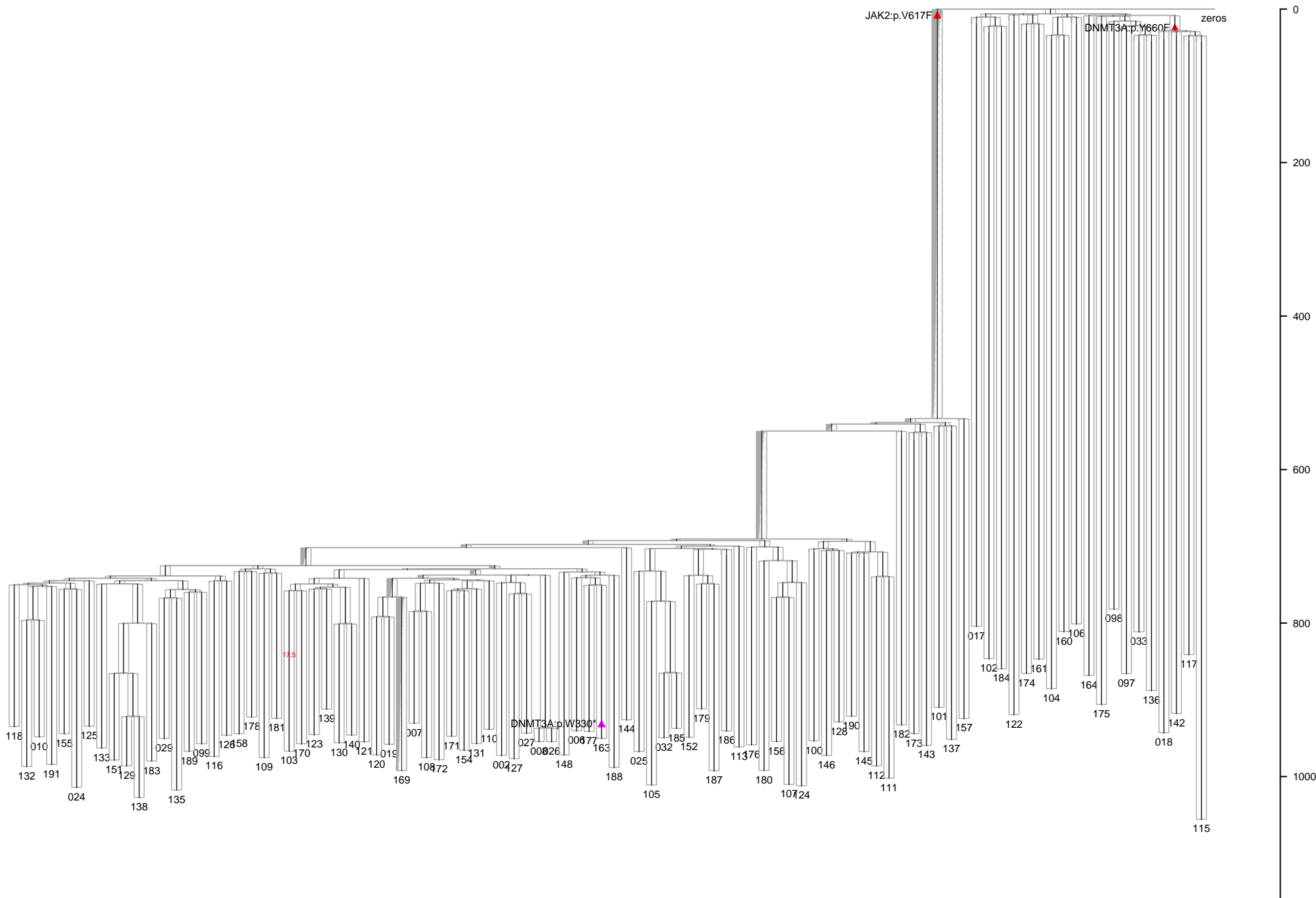
PD5847: Annotated with VAF from 121  
Mean Depth=16.19



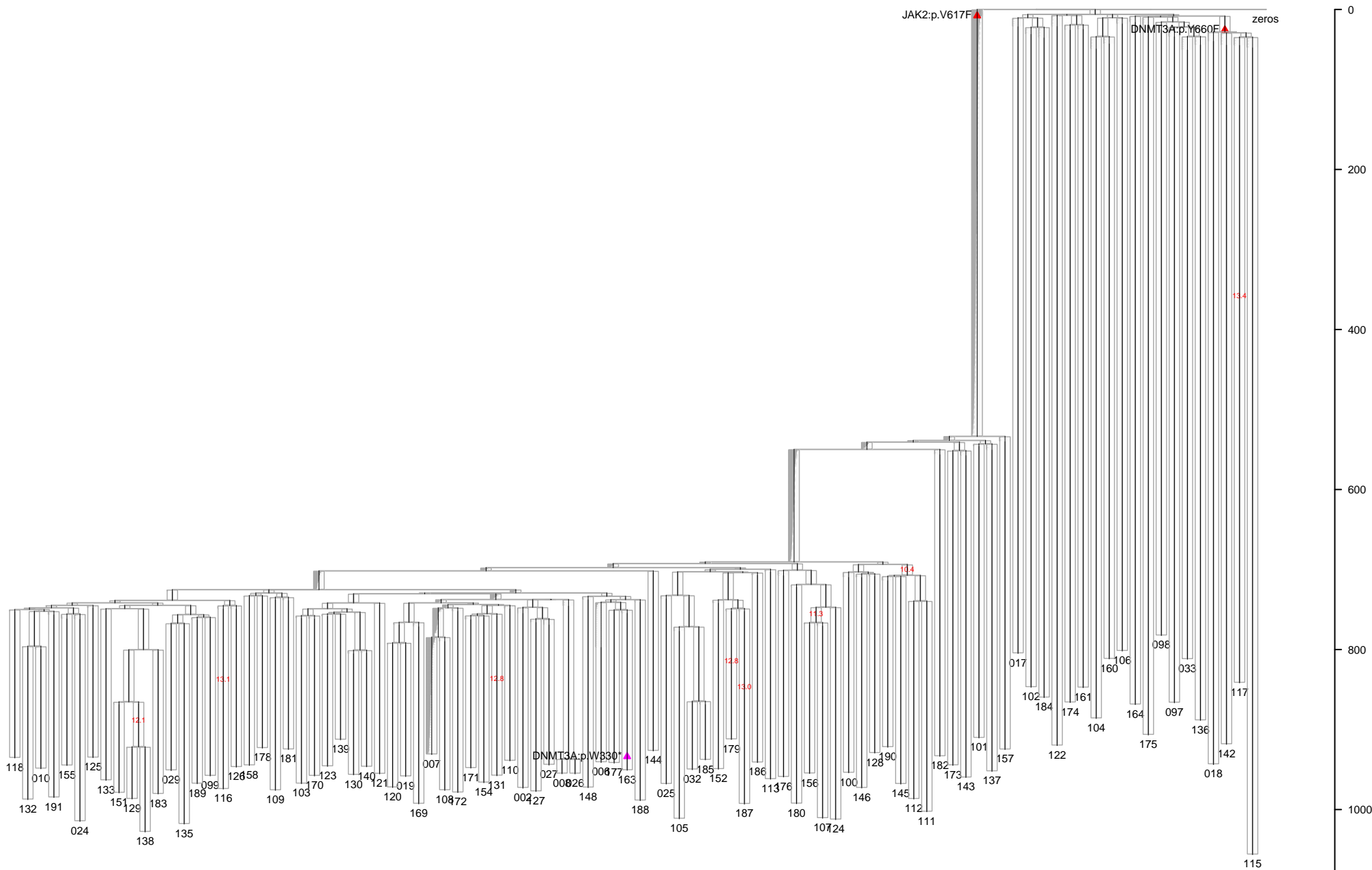


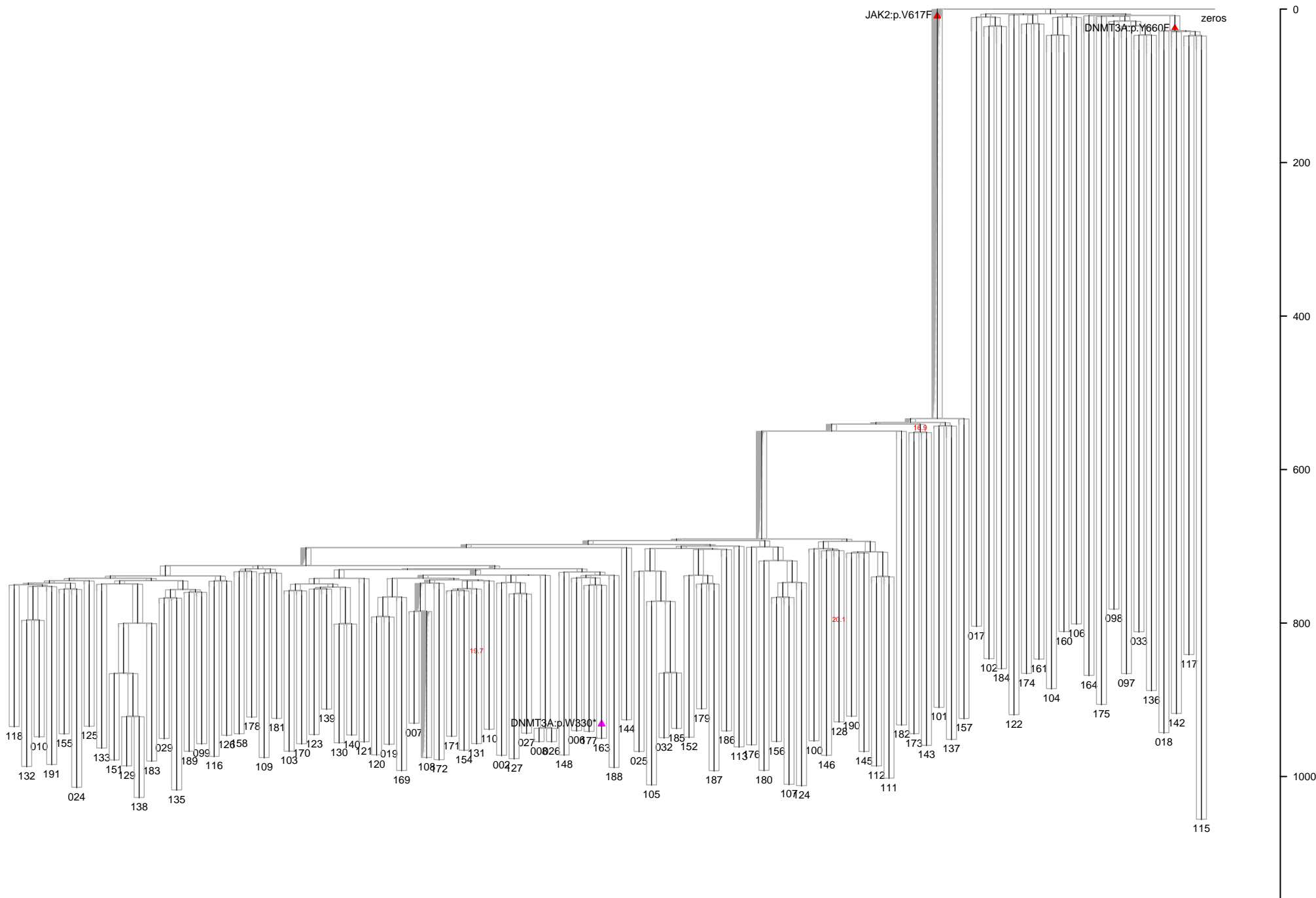


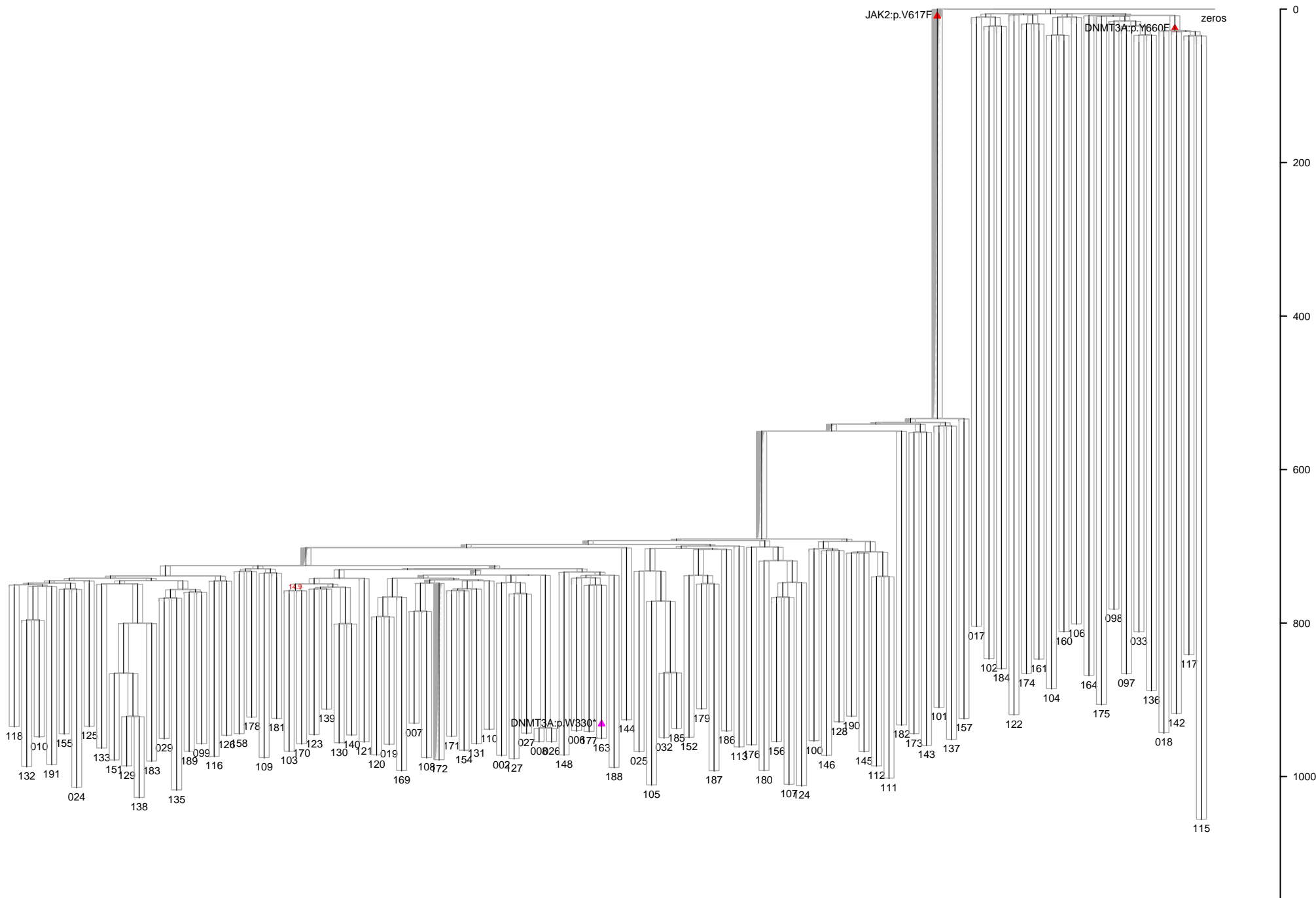




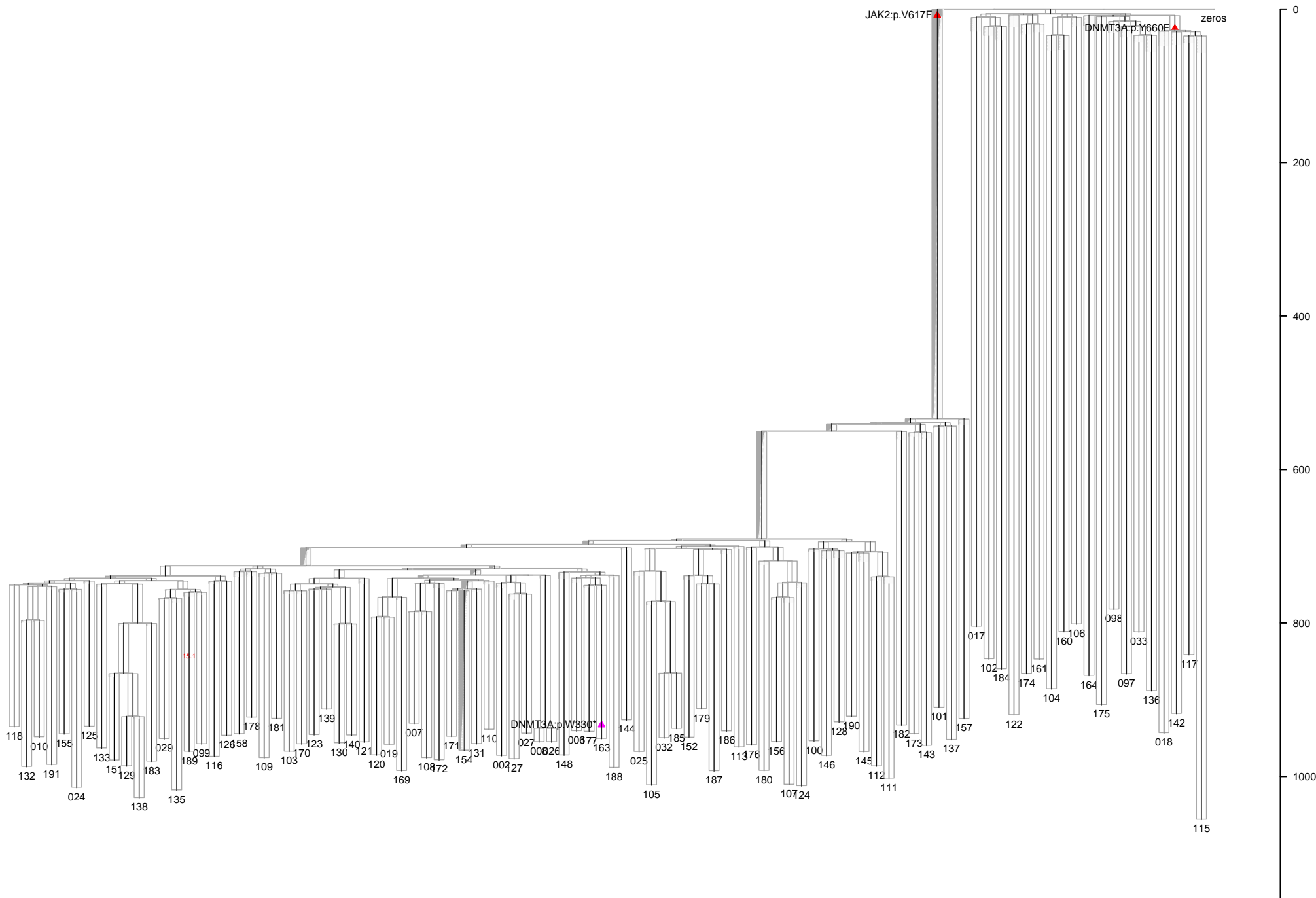
PD5847: Annotated with VAF from 007  
Mean Depth=13.77

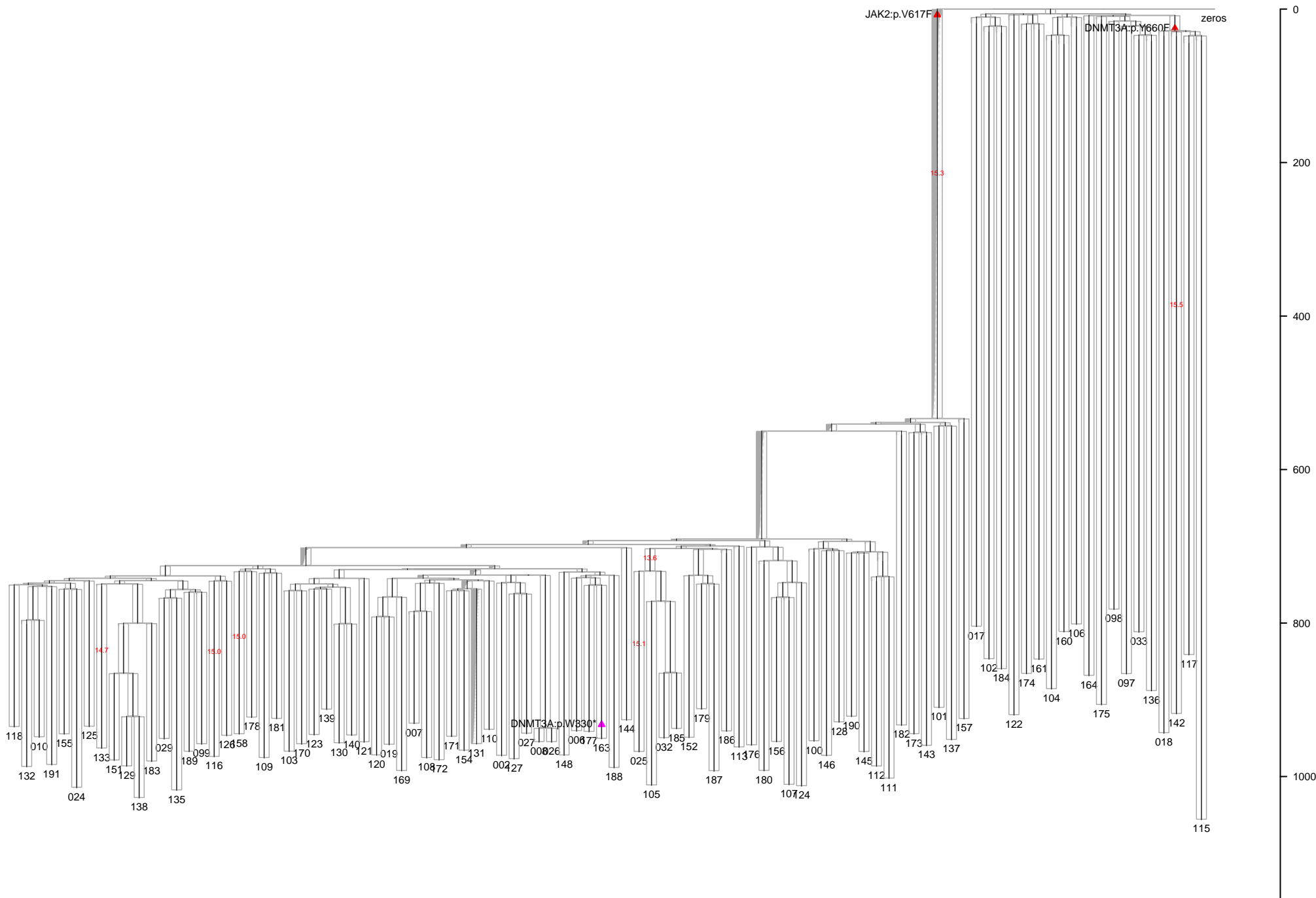


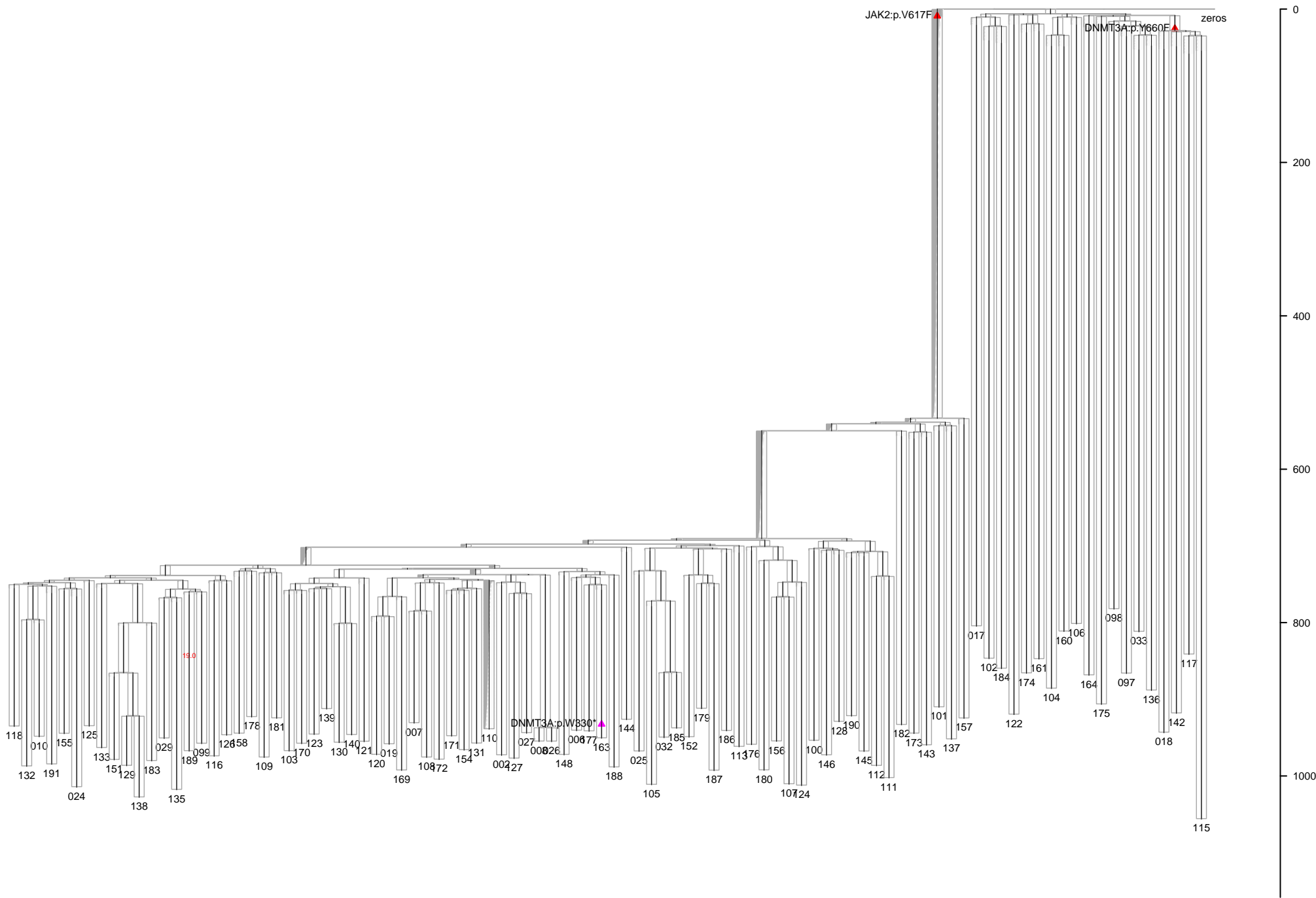




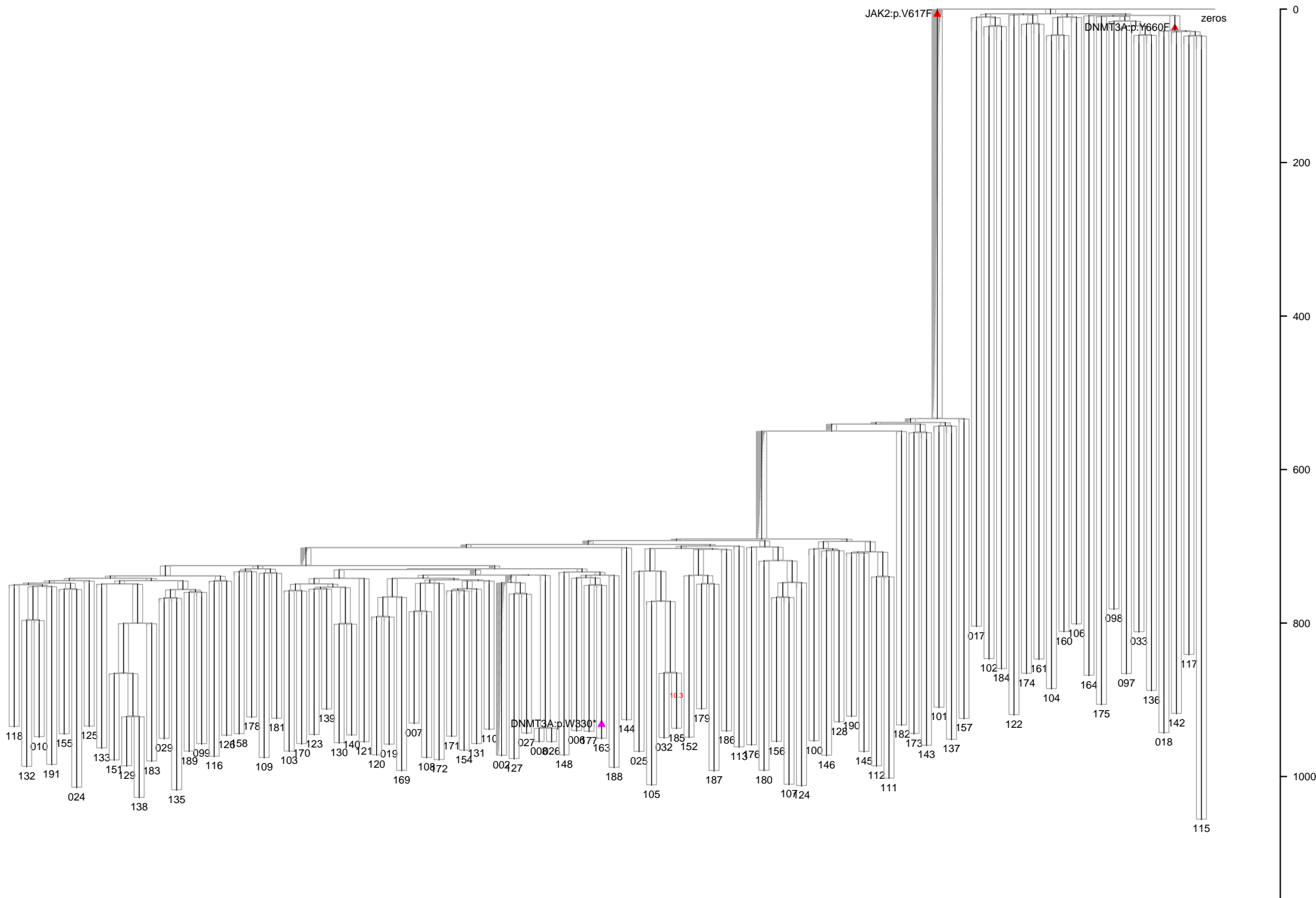
191 samples are clustered hierarchically. The dendrogram shows a primary split between a large cluster on the left and a smaller cluster on the right. The left cluster further divides into several subgroups, while the right cluster is more homogeneous. A vertical axis on the right indicates a scale from 0 to 1000. Key labels include 'JAK2:p.V617F' at the top left, 'DNMT3A:p.Y660F' at the top right, and 'zeros' at the top right. A specific sample, 00877, is highlighted with a pink triangle and labeled 'DNMT3A:p.W390\*'. Other labeled samples include 118, 010, 155, 125, 133, 151, 129, 183, 029, 099, 116, 126, 178, 181, 139, 123, 140, 121, 101, 169, 007, 171, 110, 027, 008, 026, 148, 163, 188, 144, 025, 105, 185, 152, 179, 186, 113, 176, 156, 100, 146, 145, 112, 111, 128, 190, 182, 173, 143, 137, 157, 101, 137, 102, 184, 174, 161, 104, 160, 106, 164, 175, 098, 097, 033, 136, 142, 117, 018, 115, 132, 191, 024, 138, 135, 130, 120, 108, 172, 154, 002, 027, 008, 026, 148, 163, 188, 144, 025, 105, 185, 152, 179, 186, 113, 176, 156, 100, 146, 145, 112, 111, 128, 190, 182, 173, 143, 137, 157, 101, 137, 102, 184, 174, 161, 104, 160, 106, 164, 175, 098, 097, 033, 136, 142, 117, 018, 115.

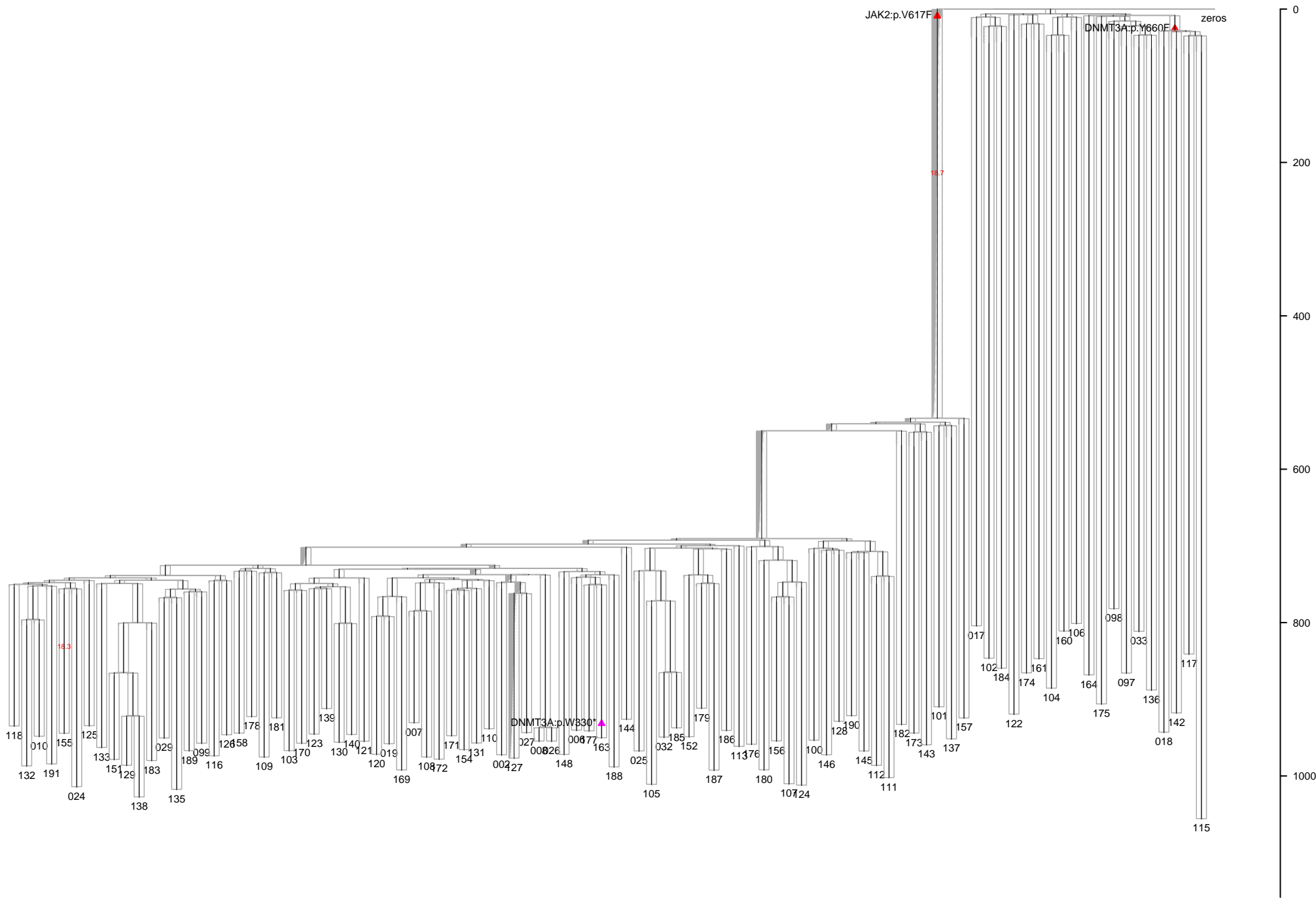




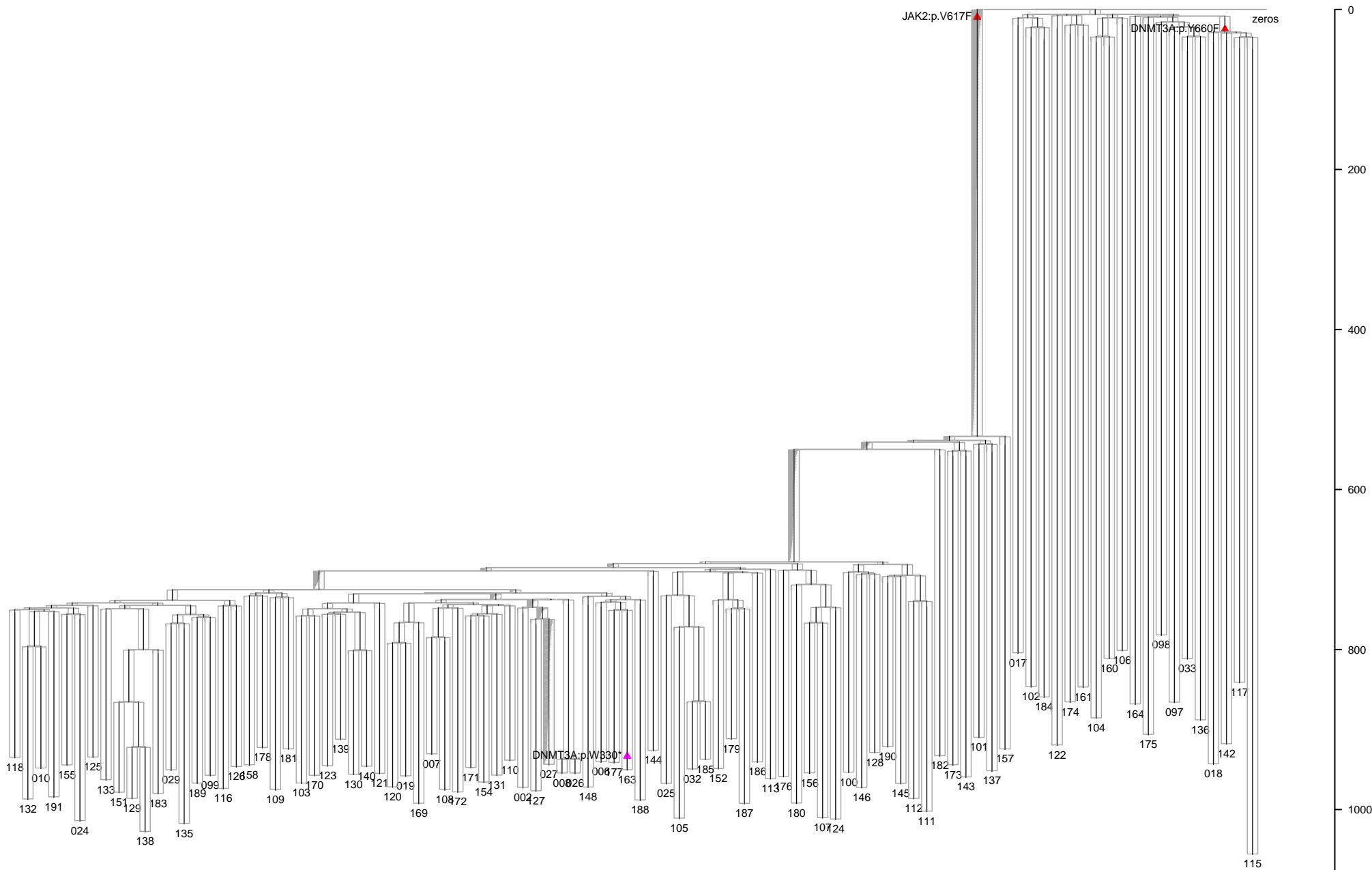




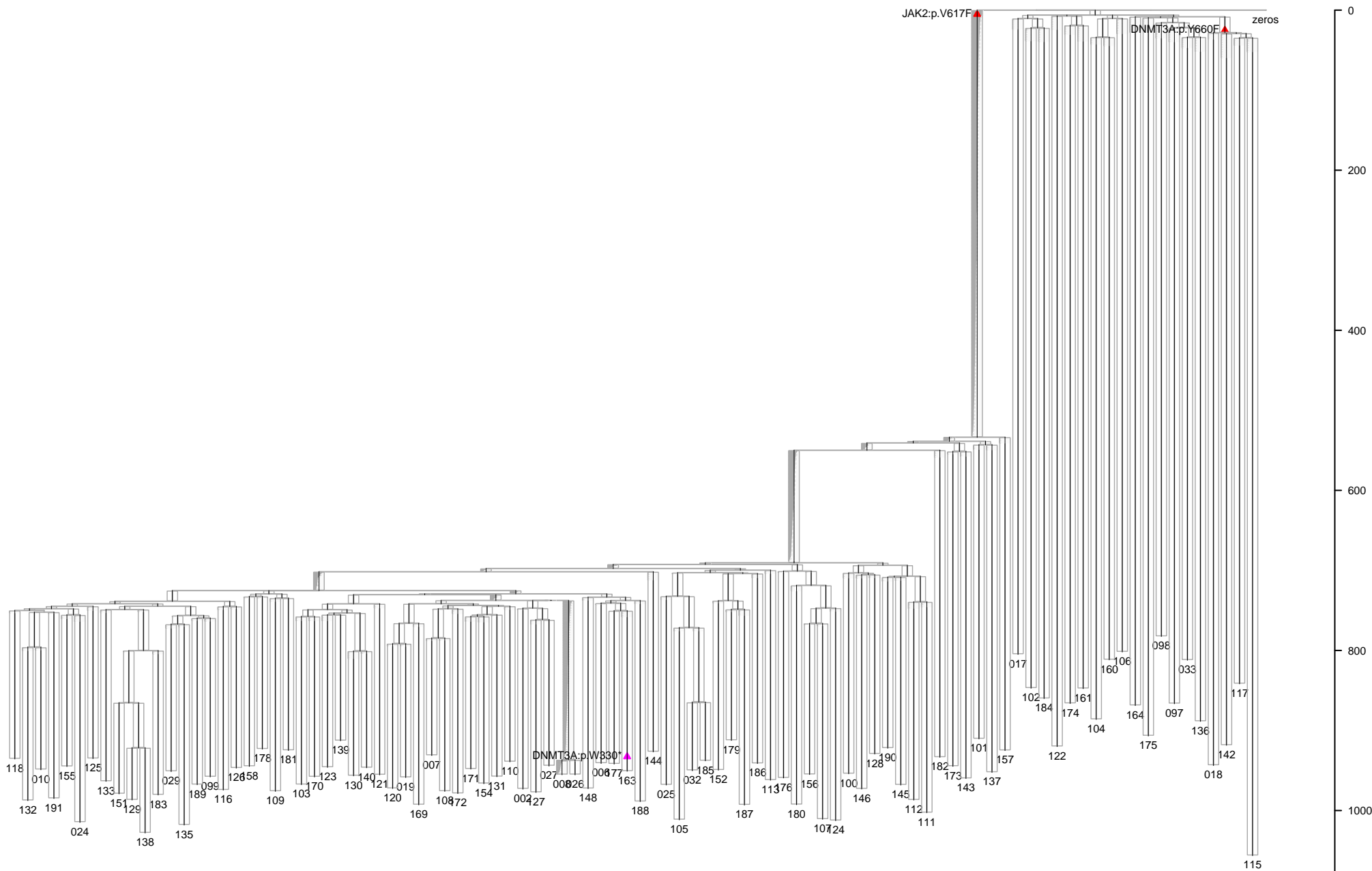


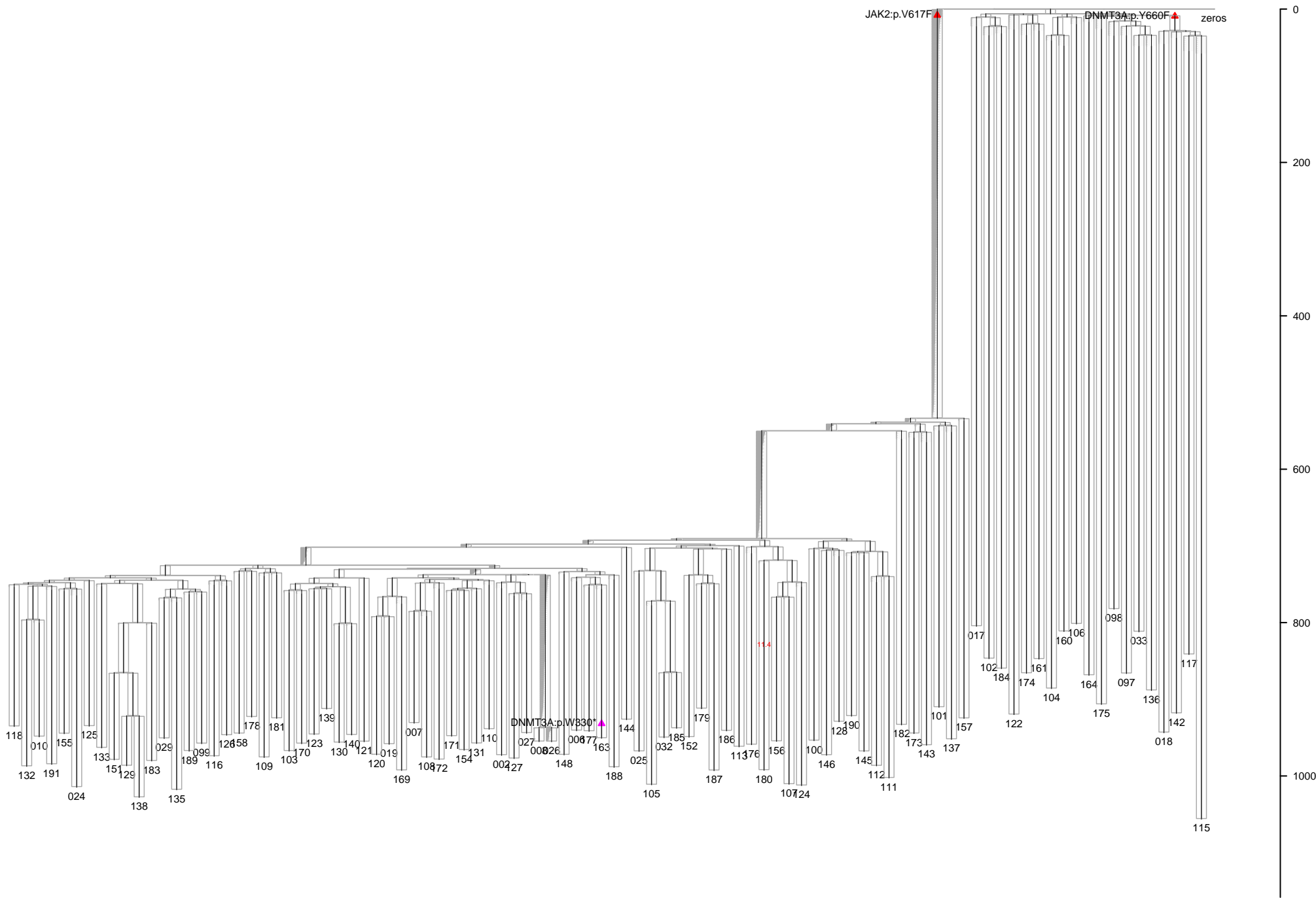


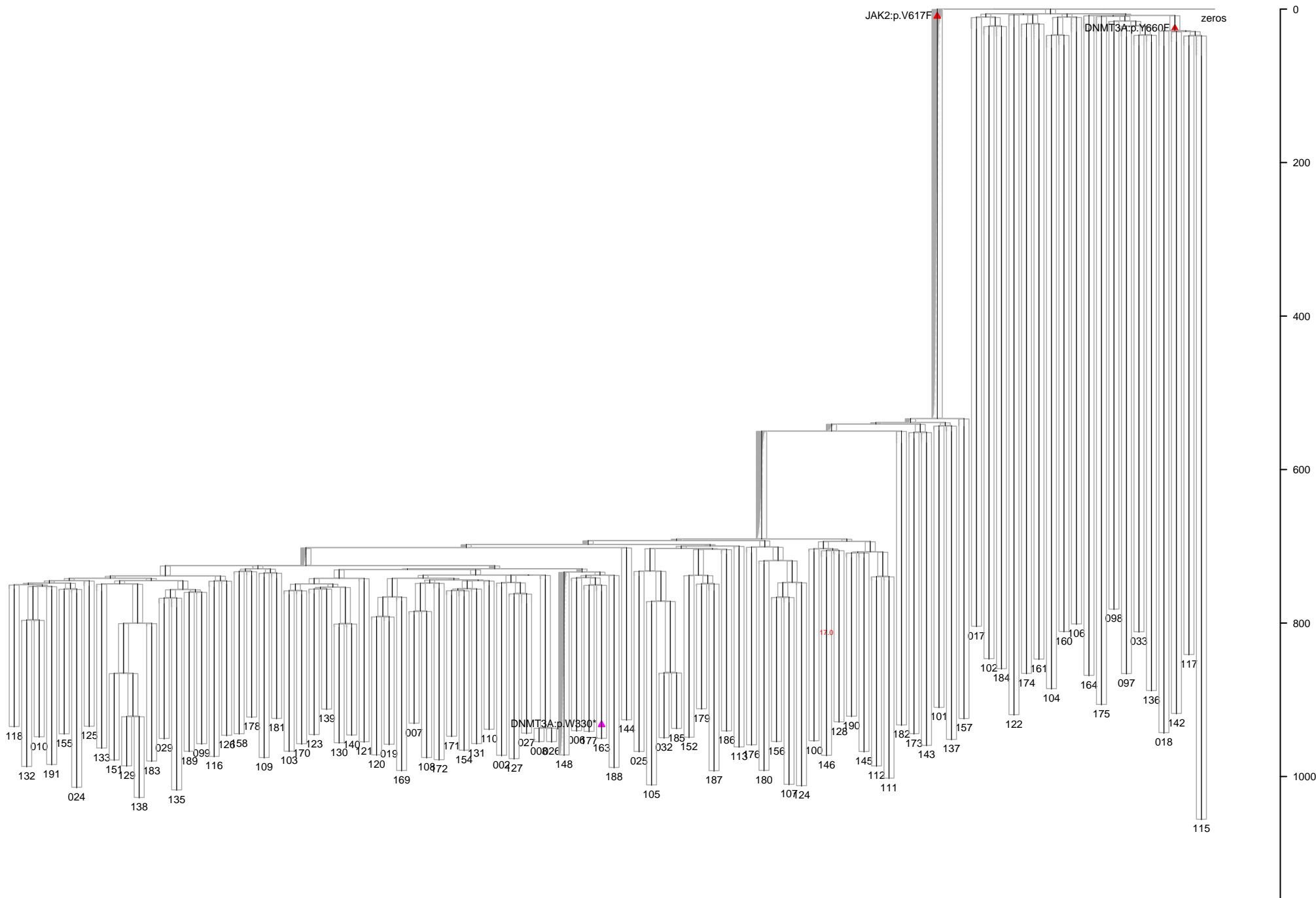
PD5847: Annotated with VAF from 027  
Mean Depth=12.53



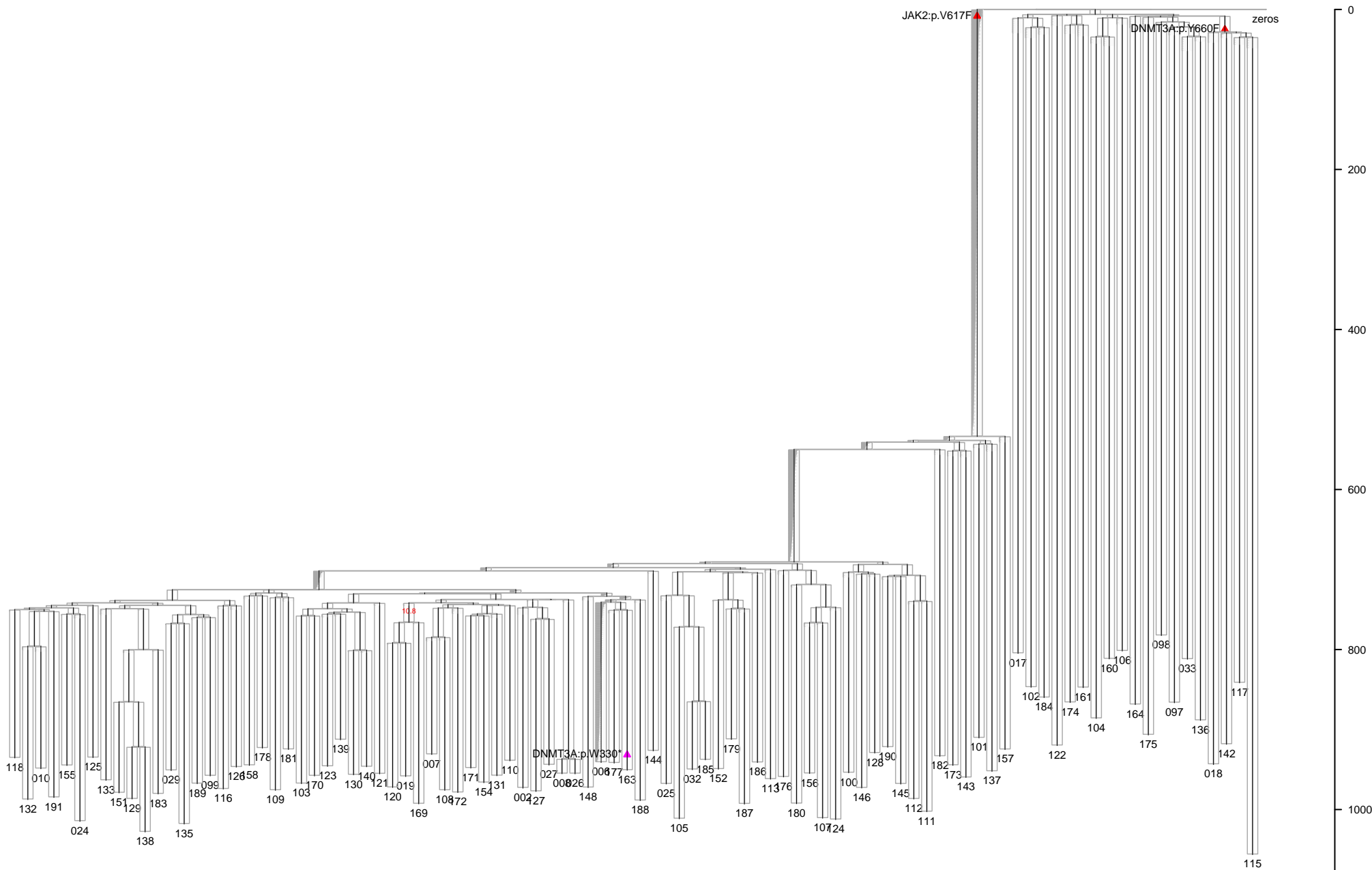
PD5847: Annotated with VAF from 008  
Mean Depth=13.00

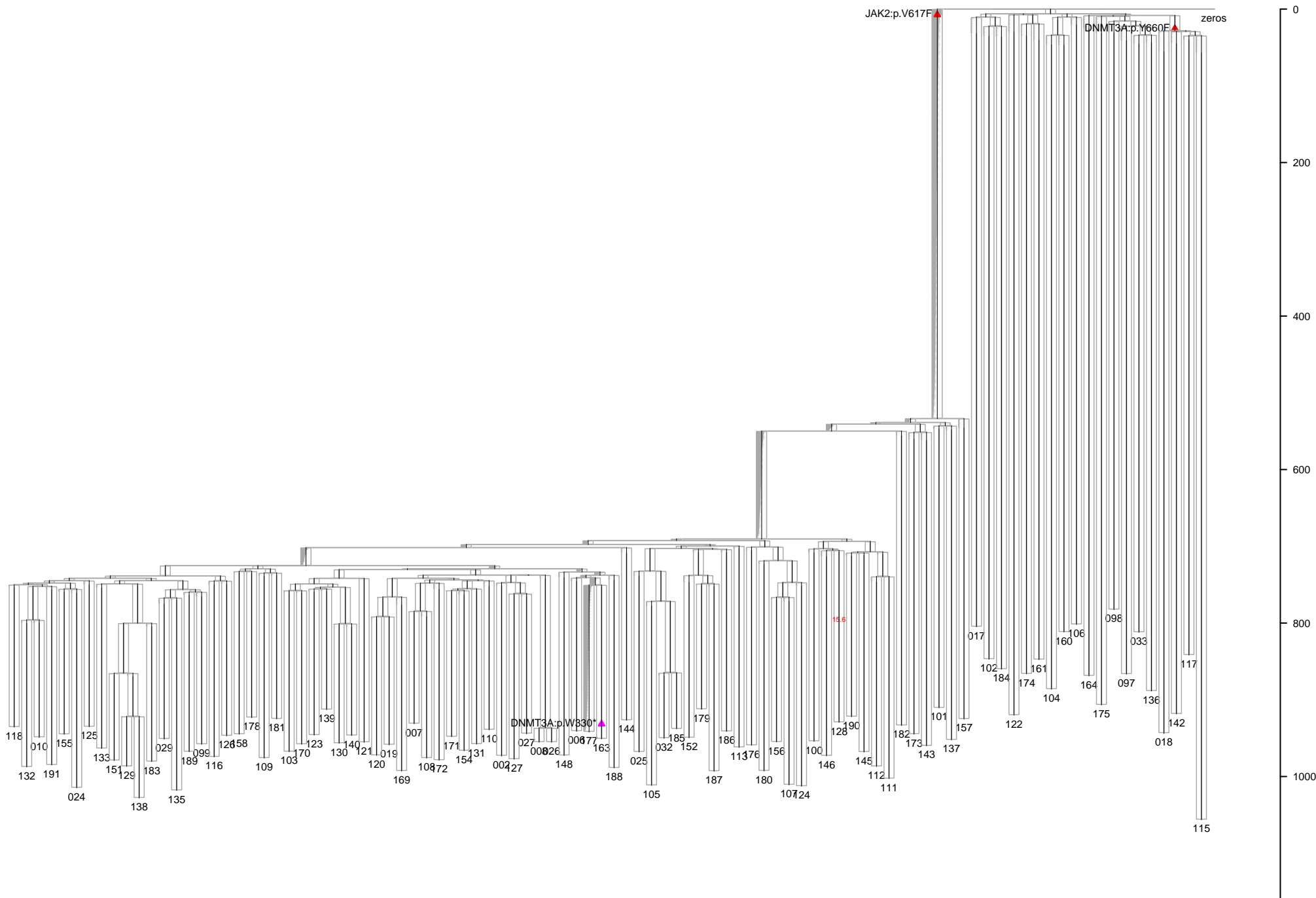




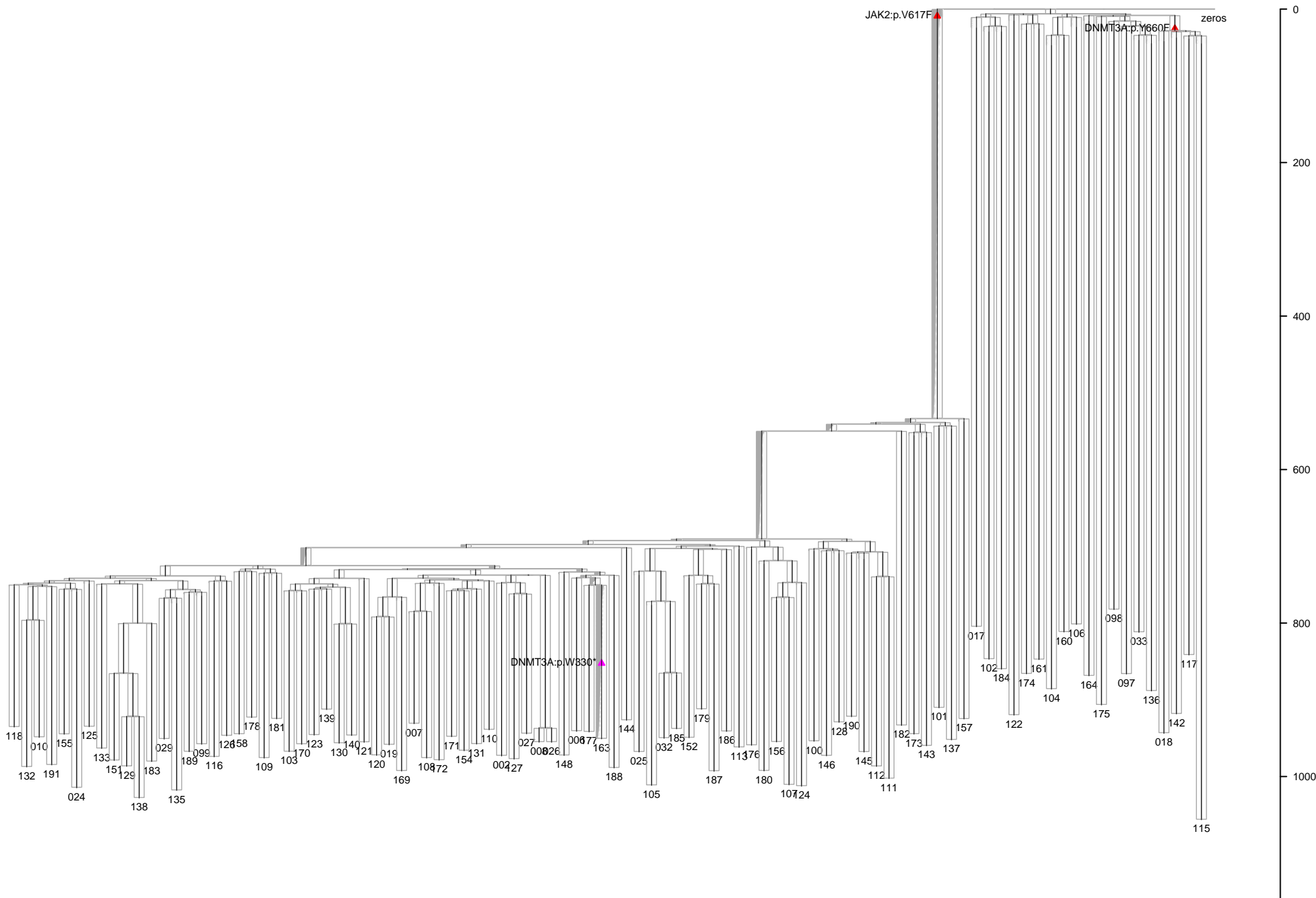


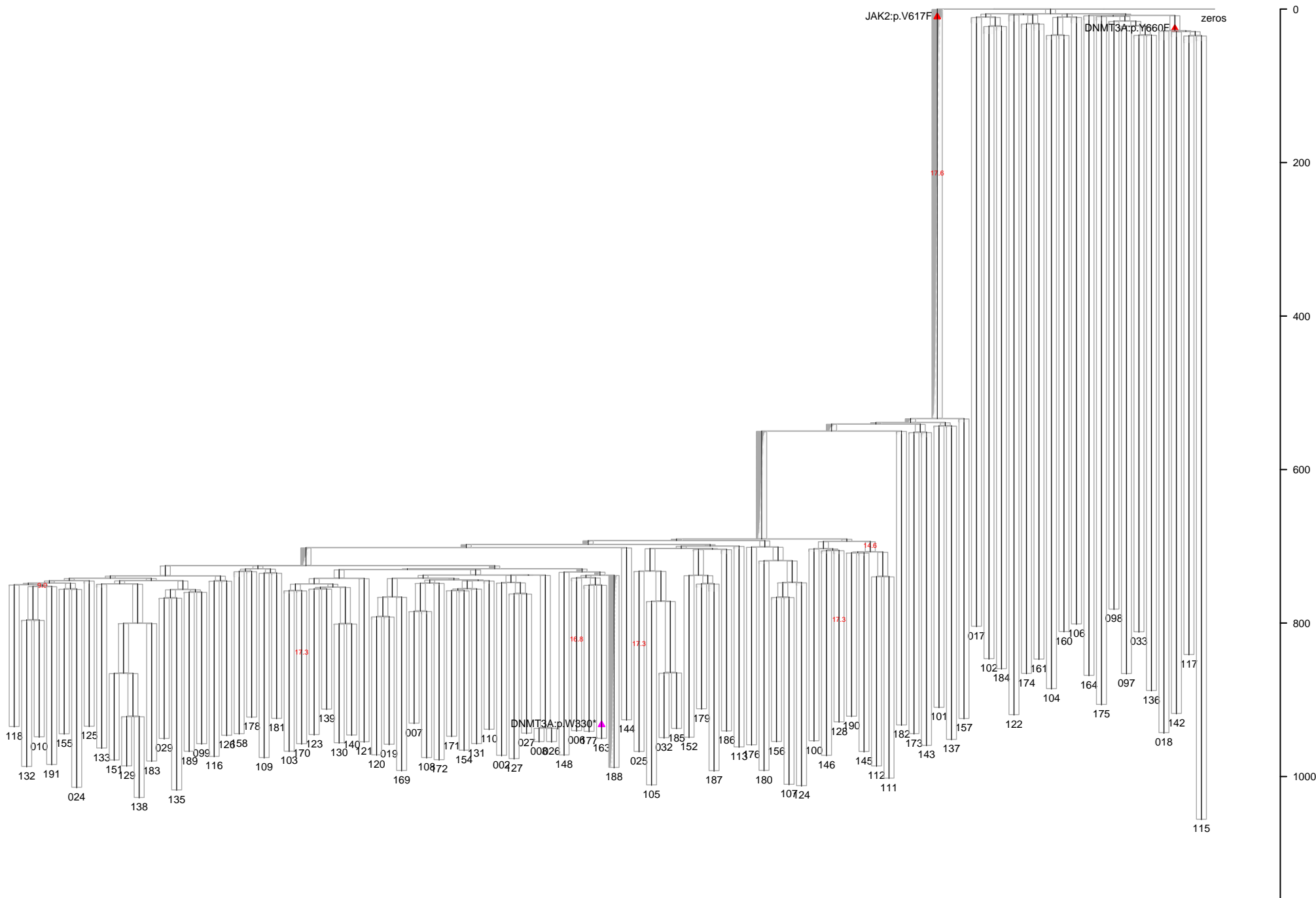
PD5847: Annotated with VAF from 006  
Mean Depth=13.30

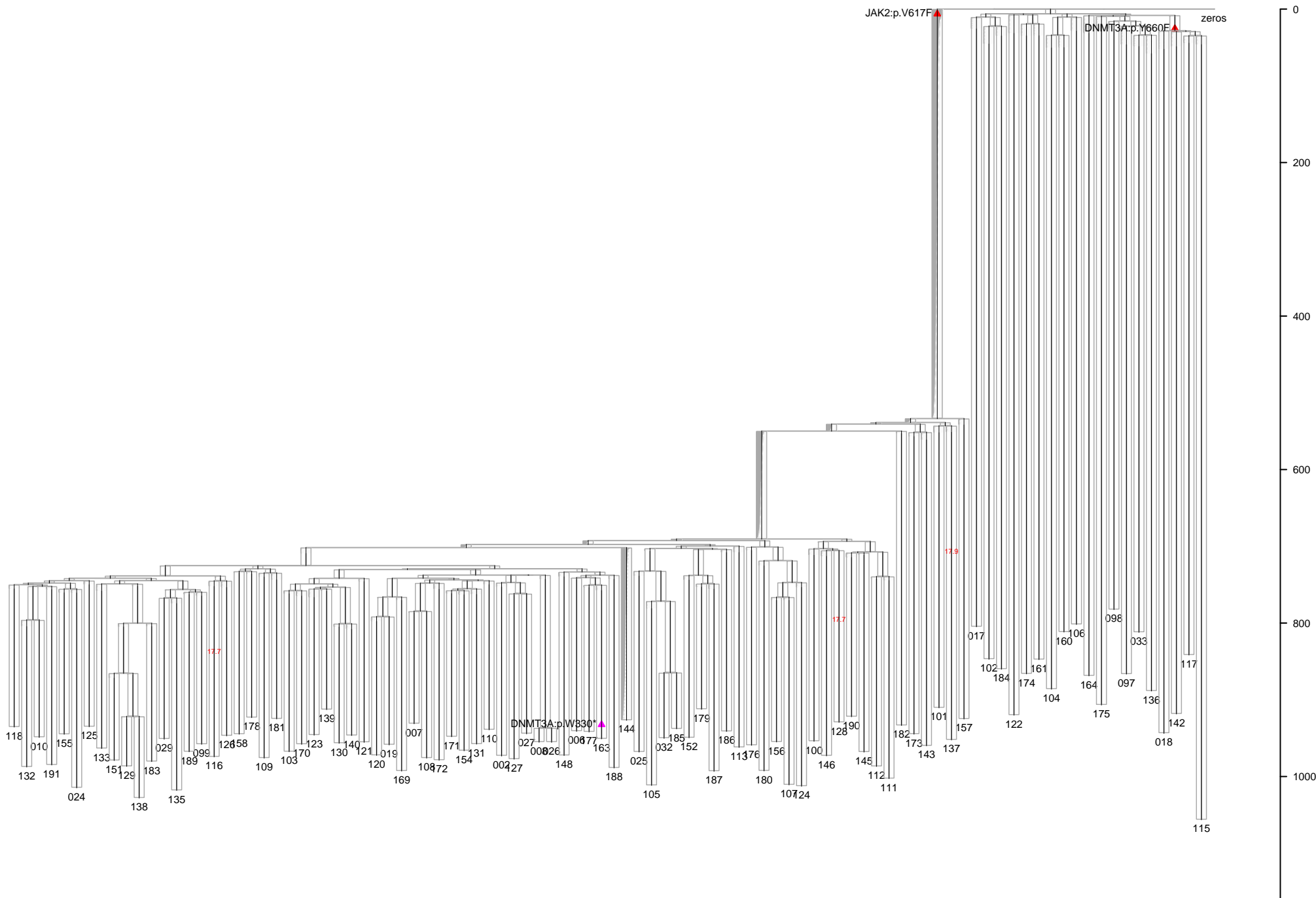


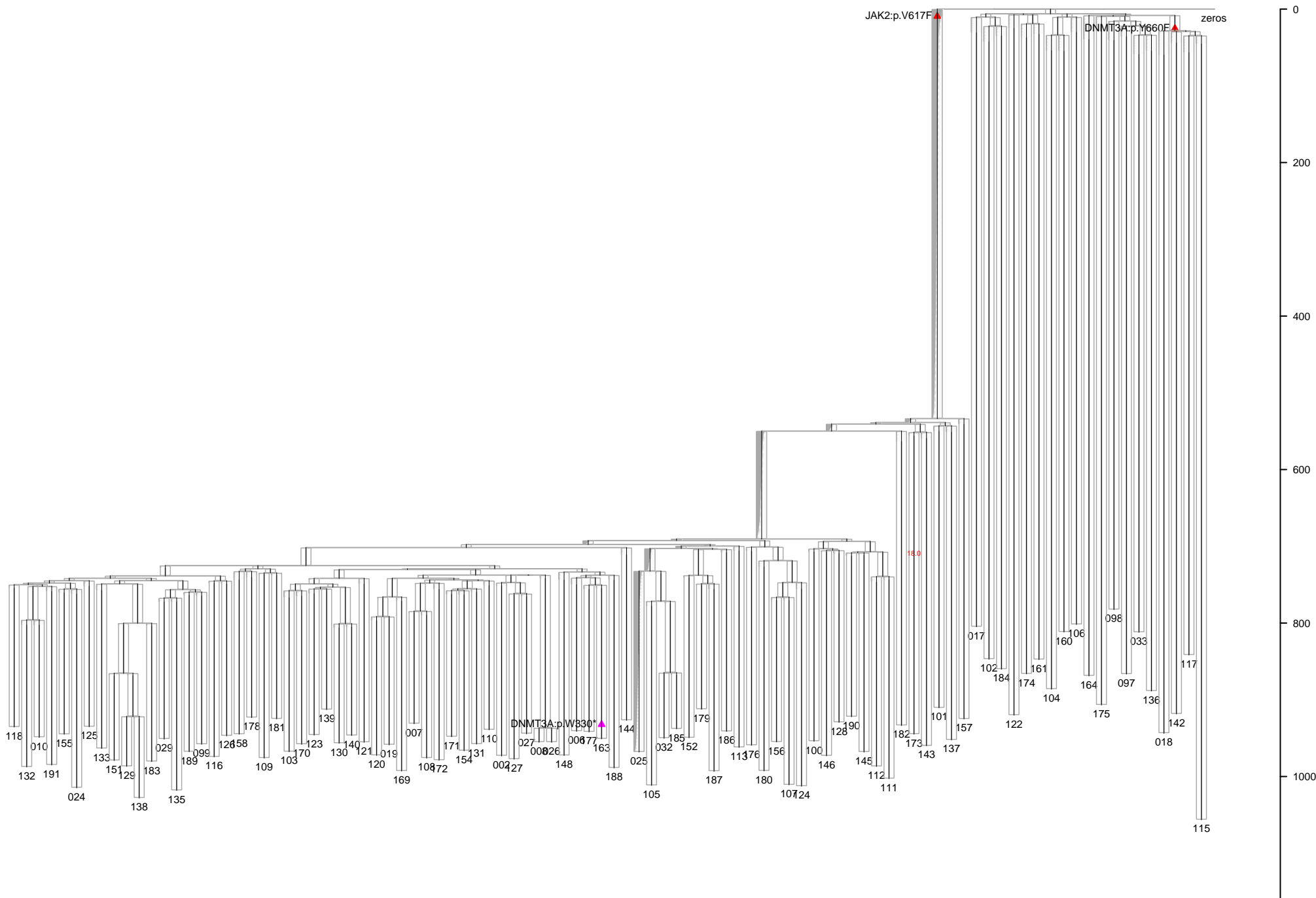


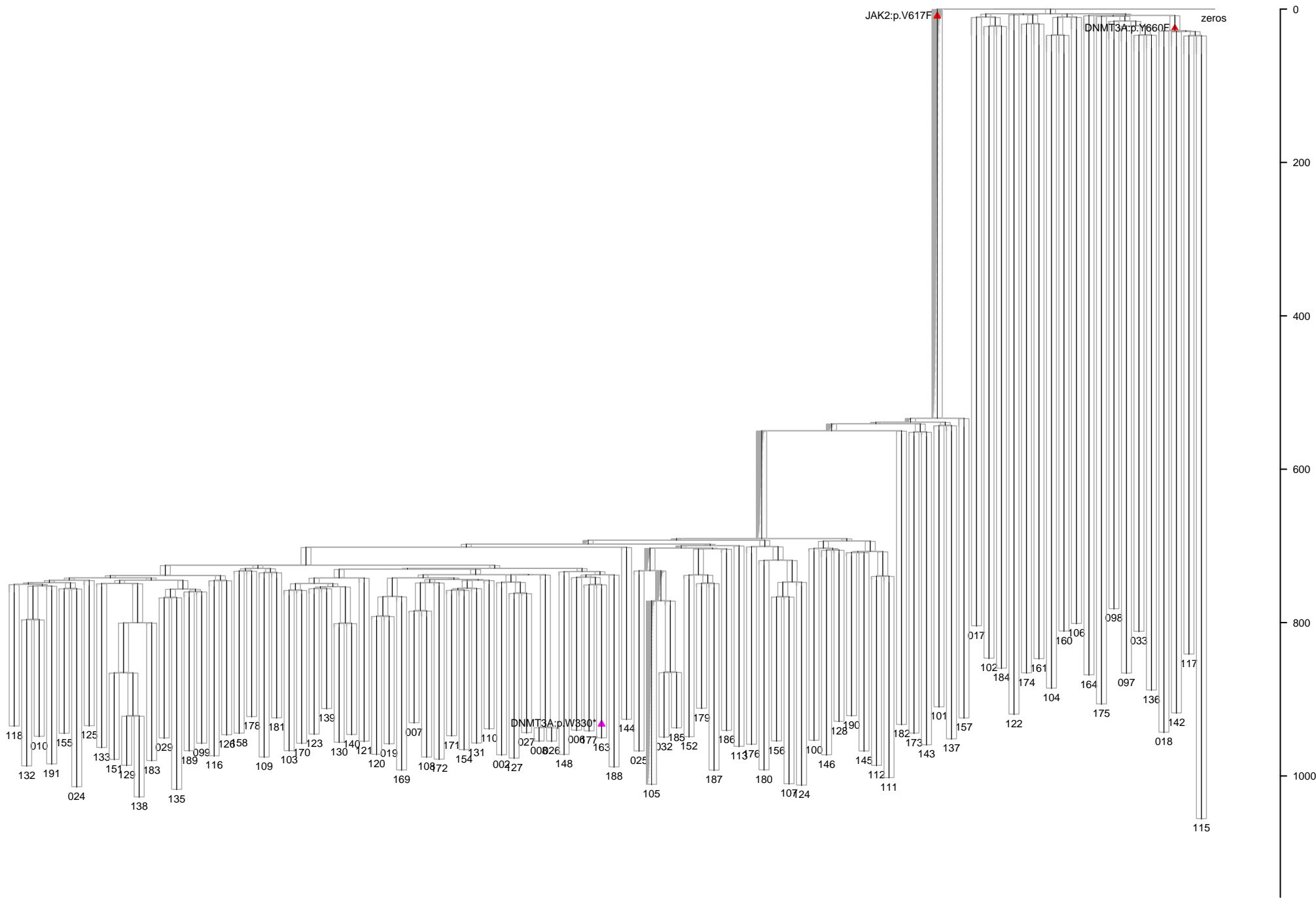


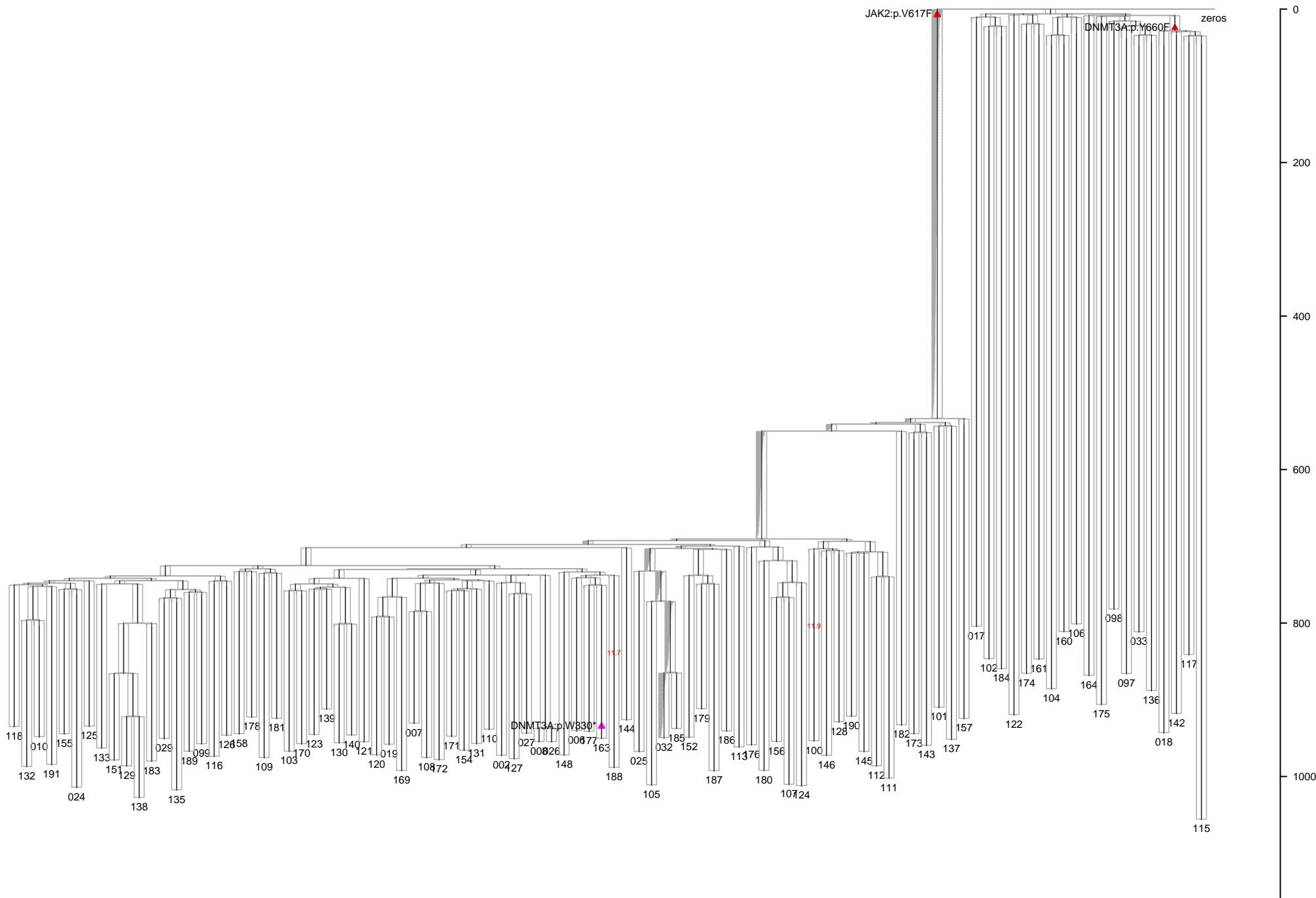


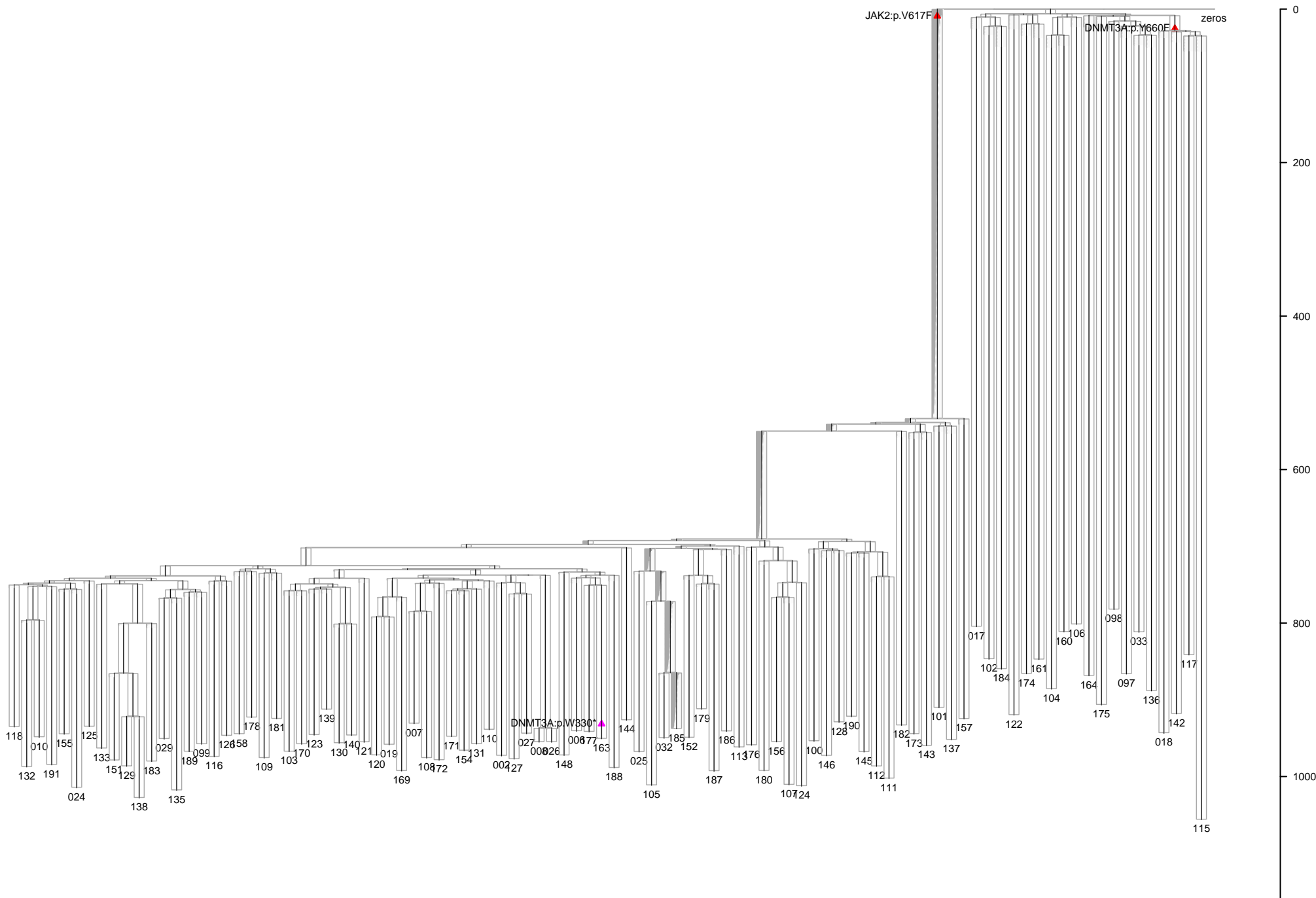


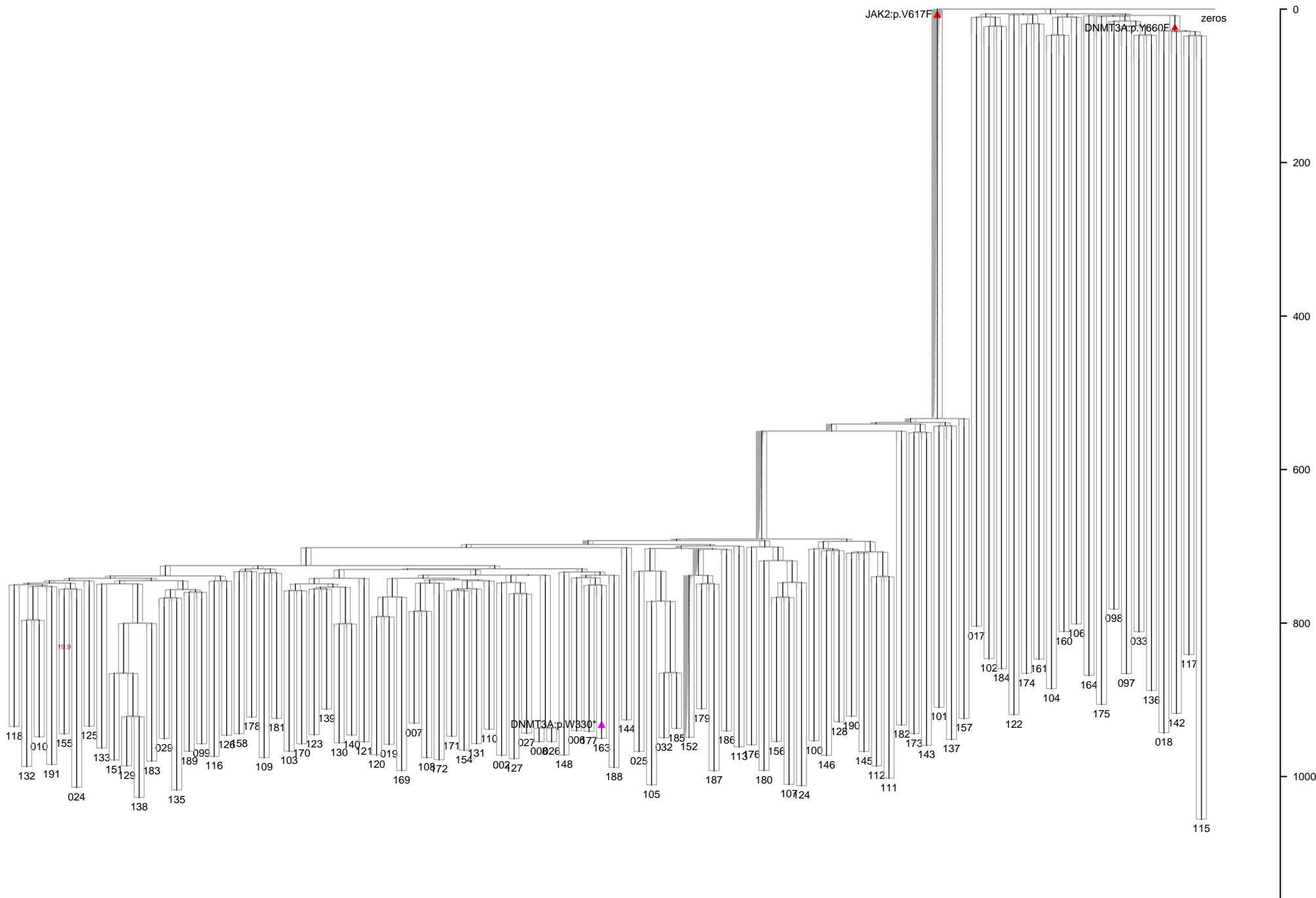






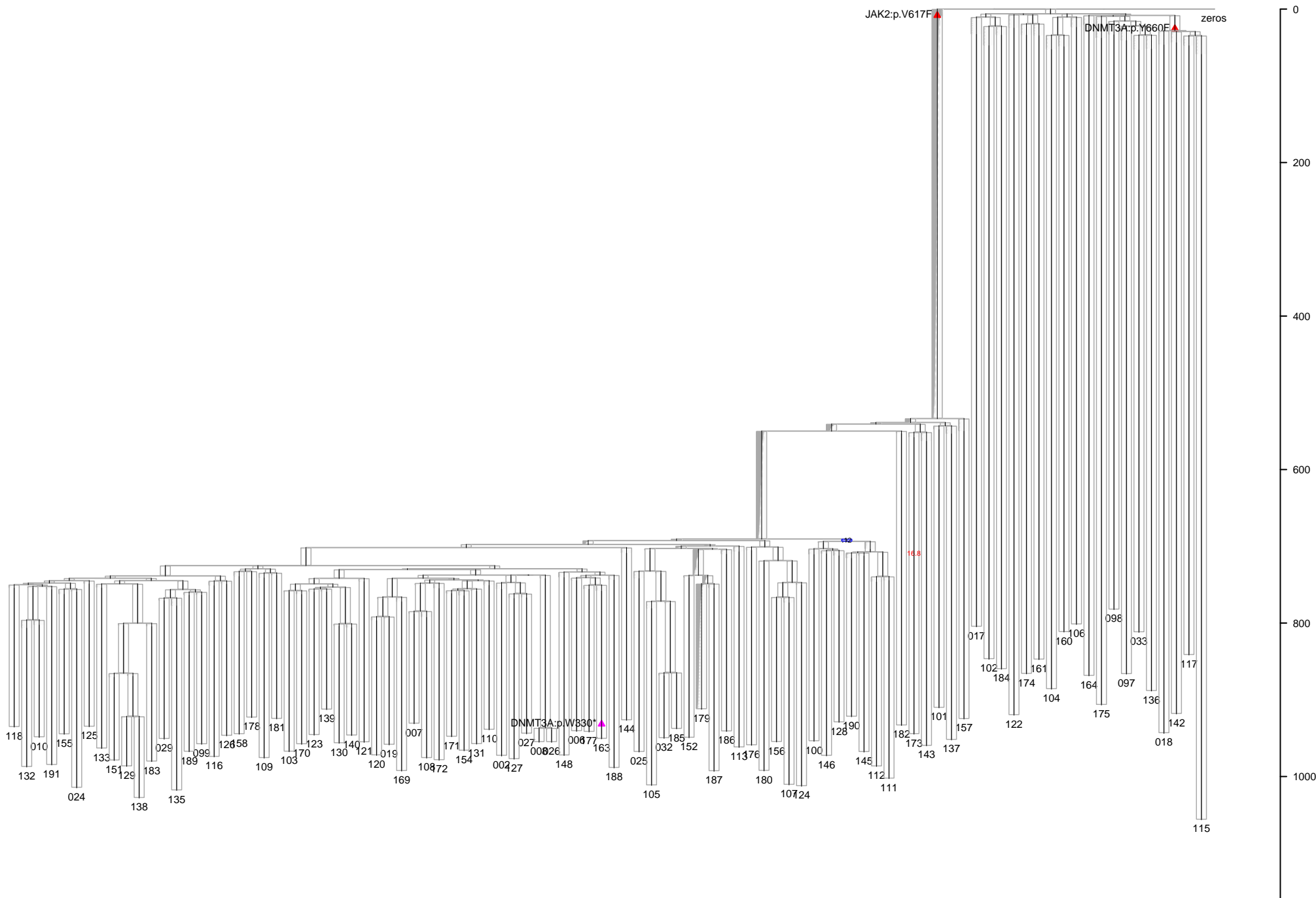


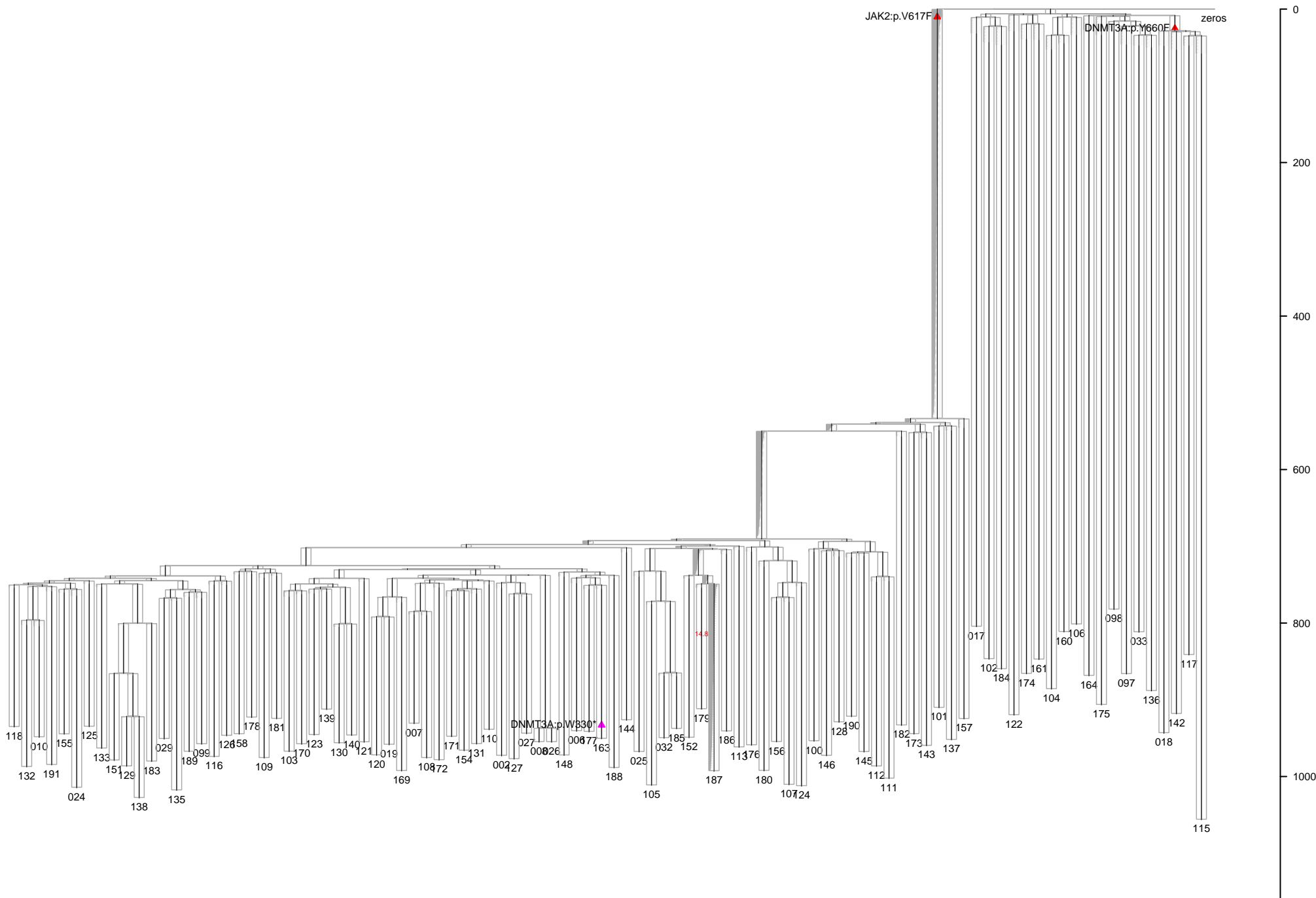


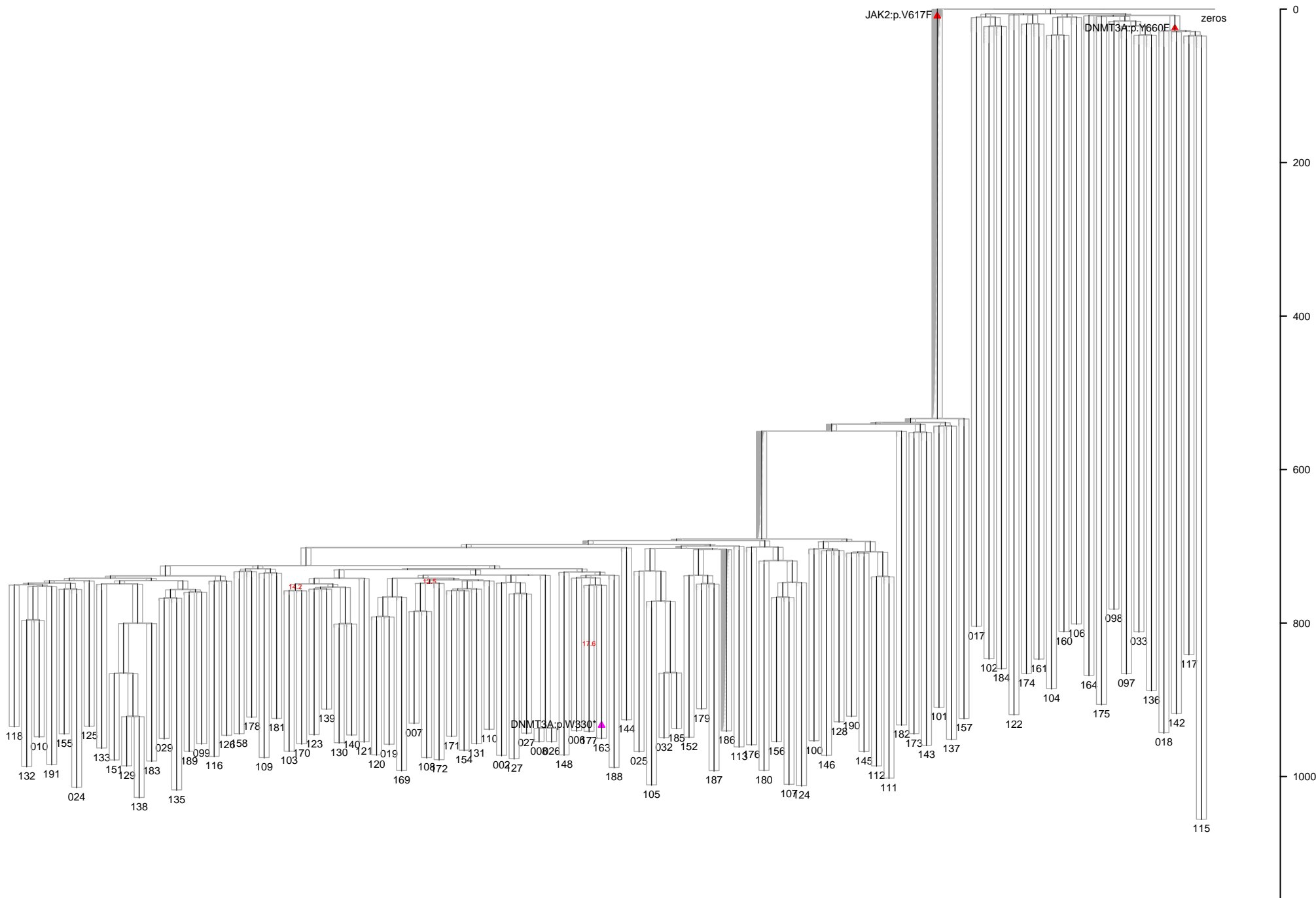


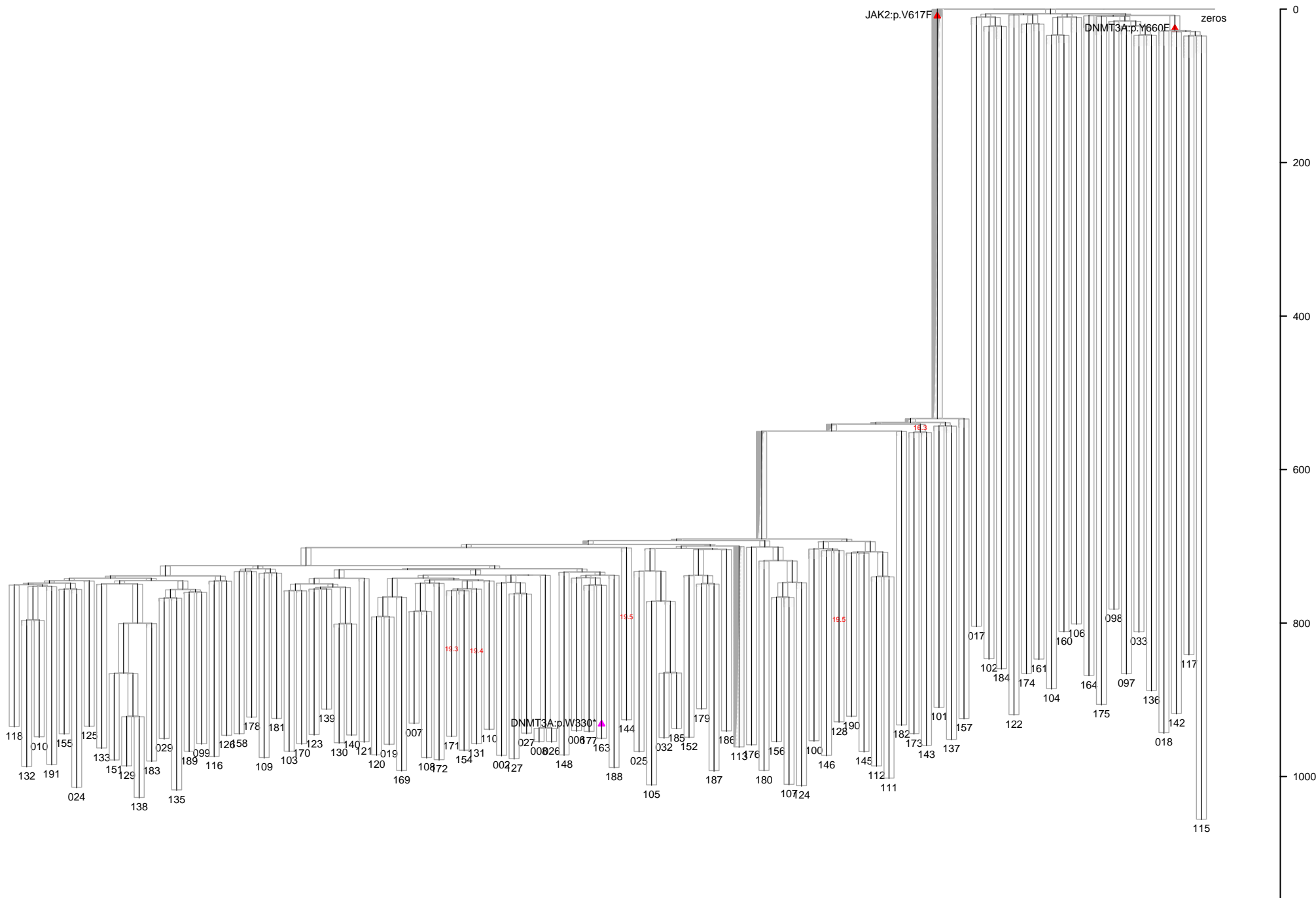


PD5847: Annotated with VAF from 179  
Mean Depth=17.89

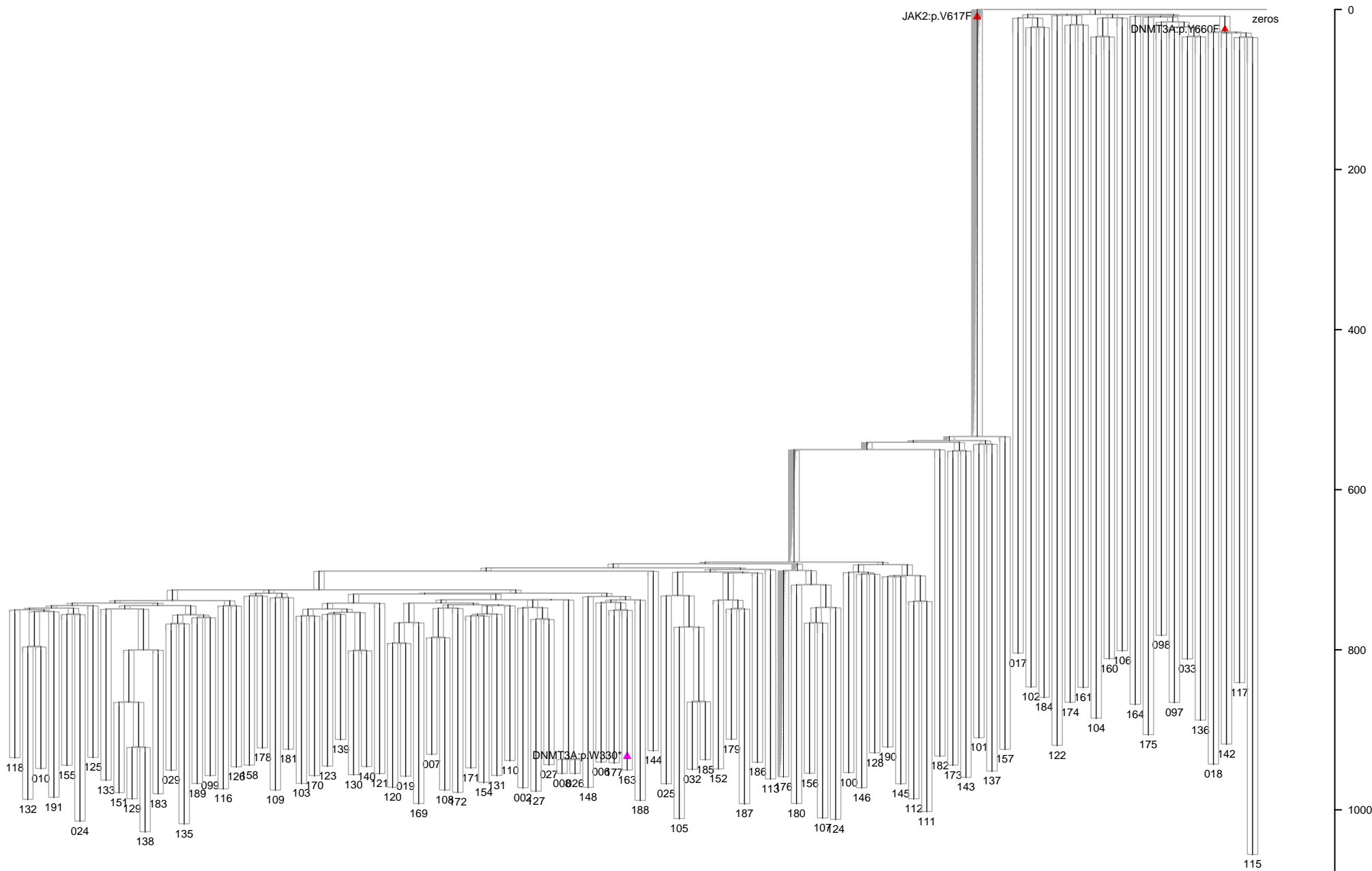


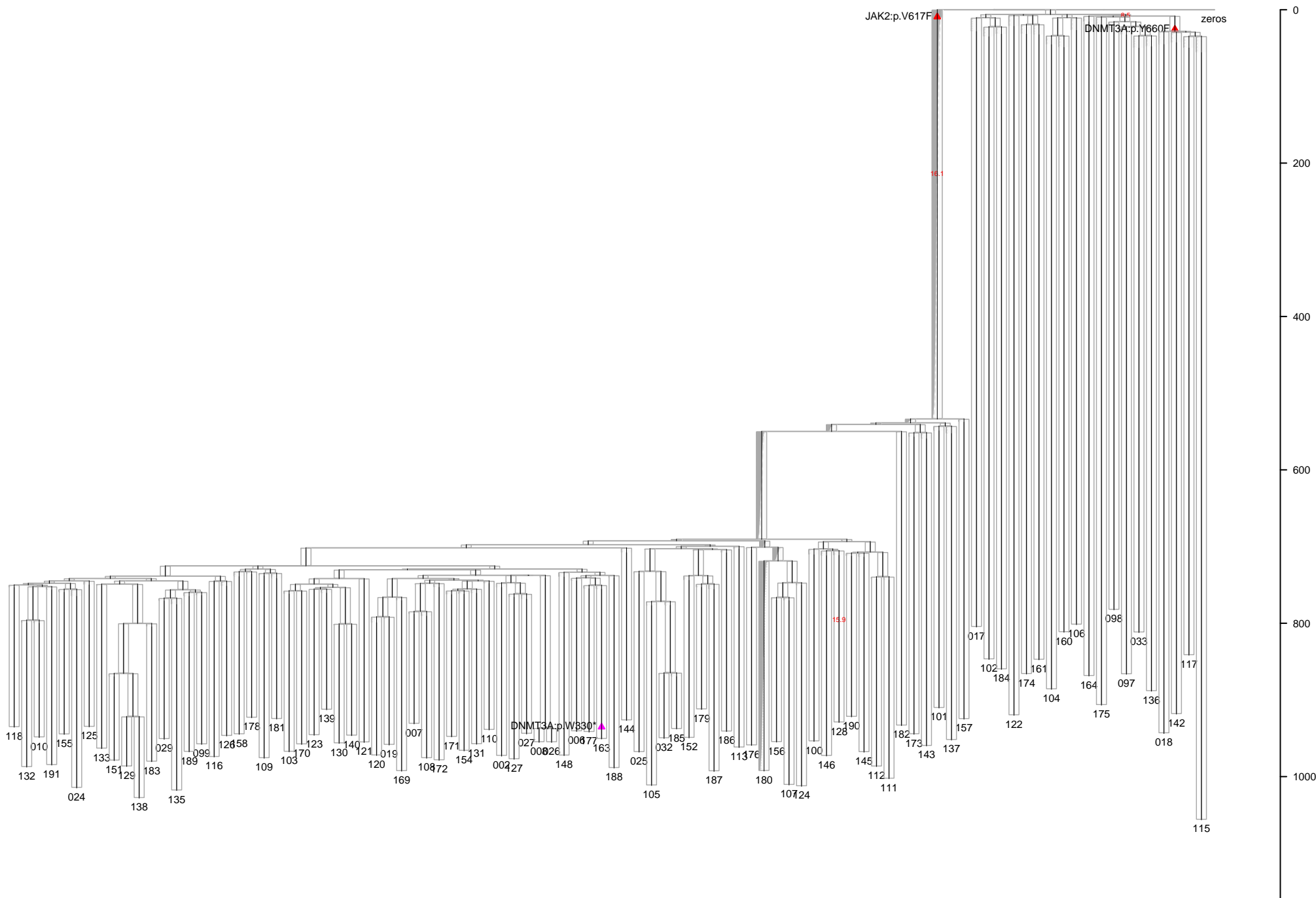


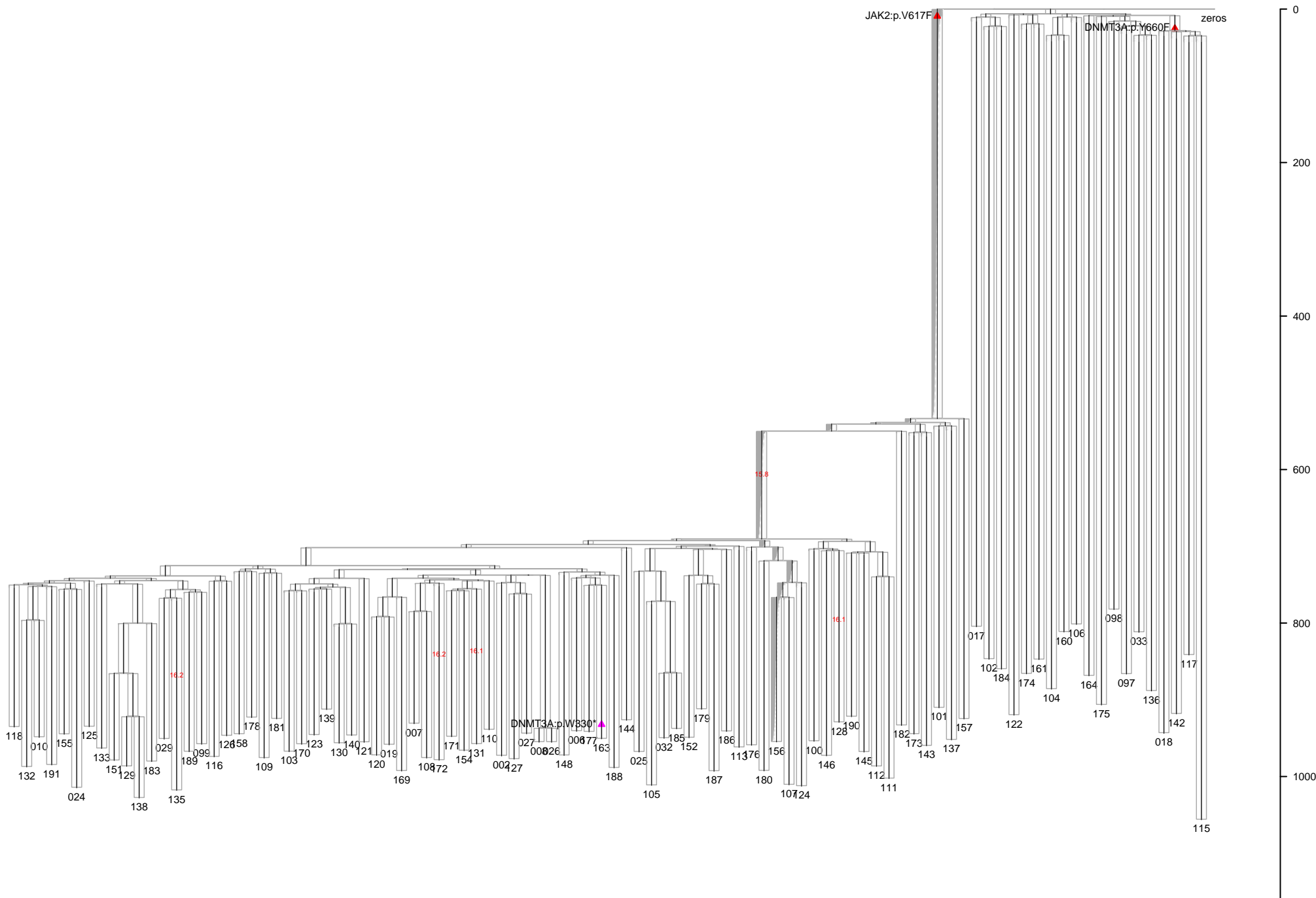




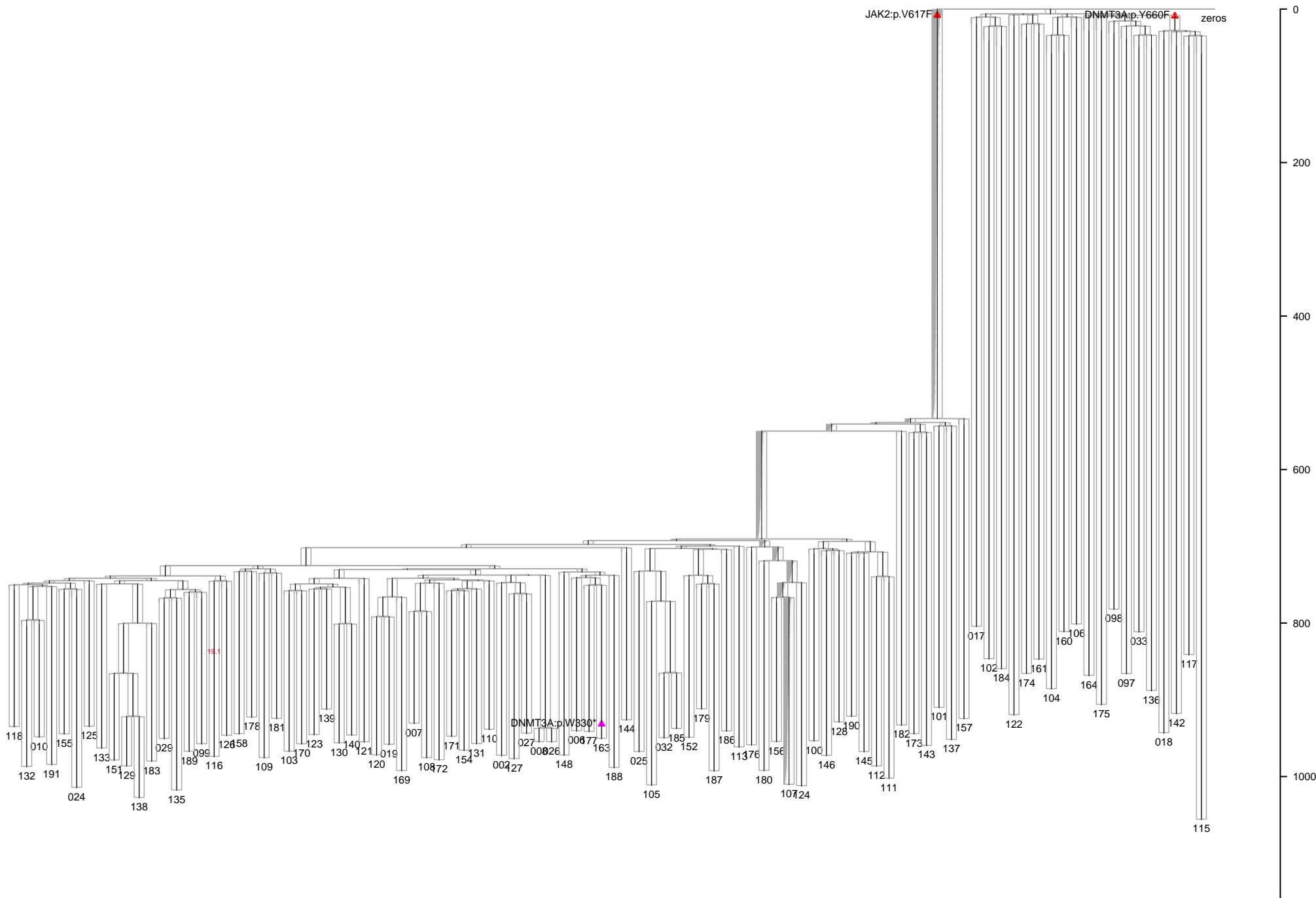
PD5847: Annotated with VAF from 176  
Mean Depth=17.45



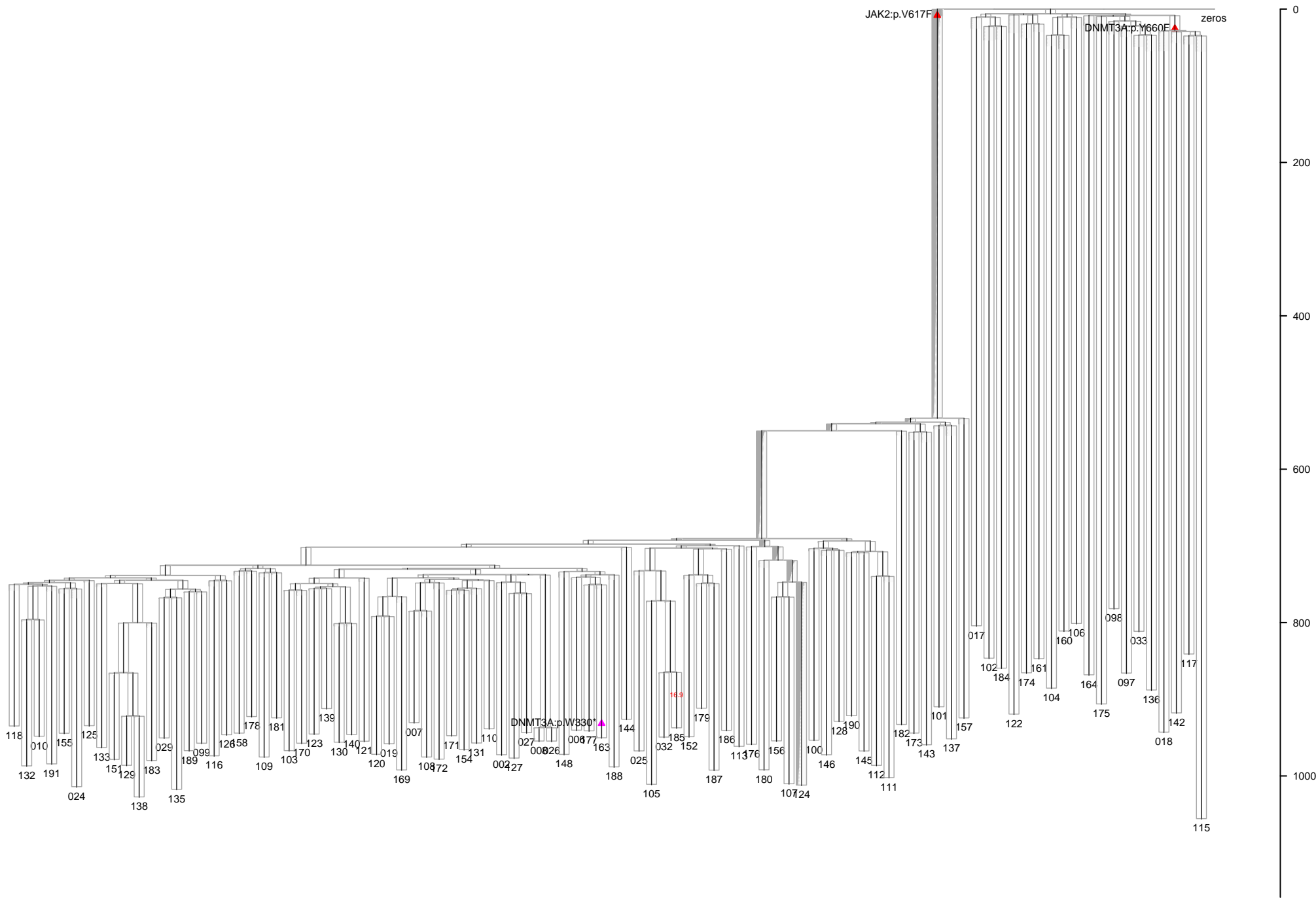


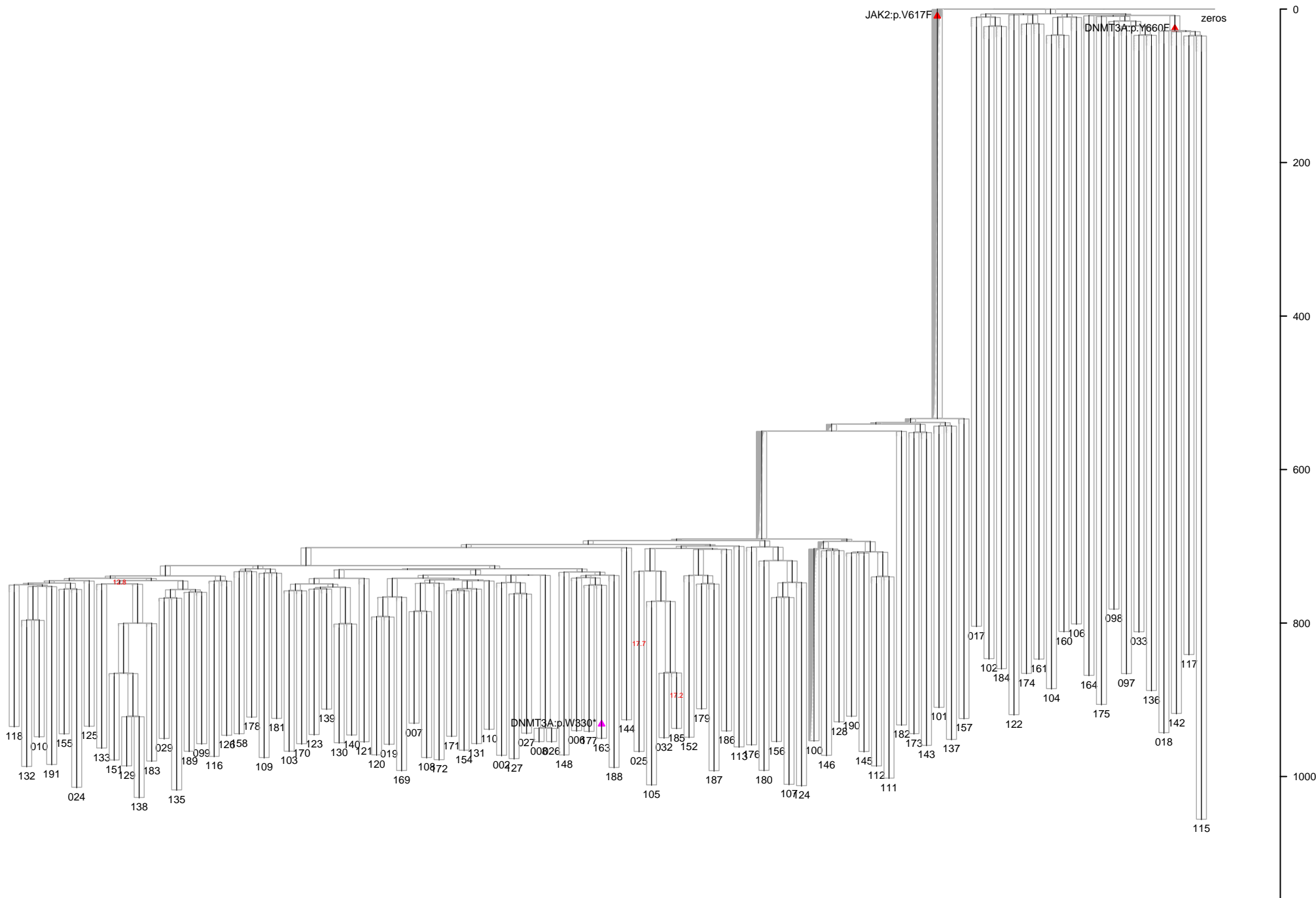


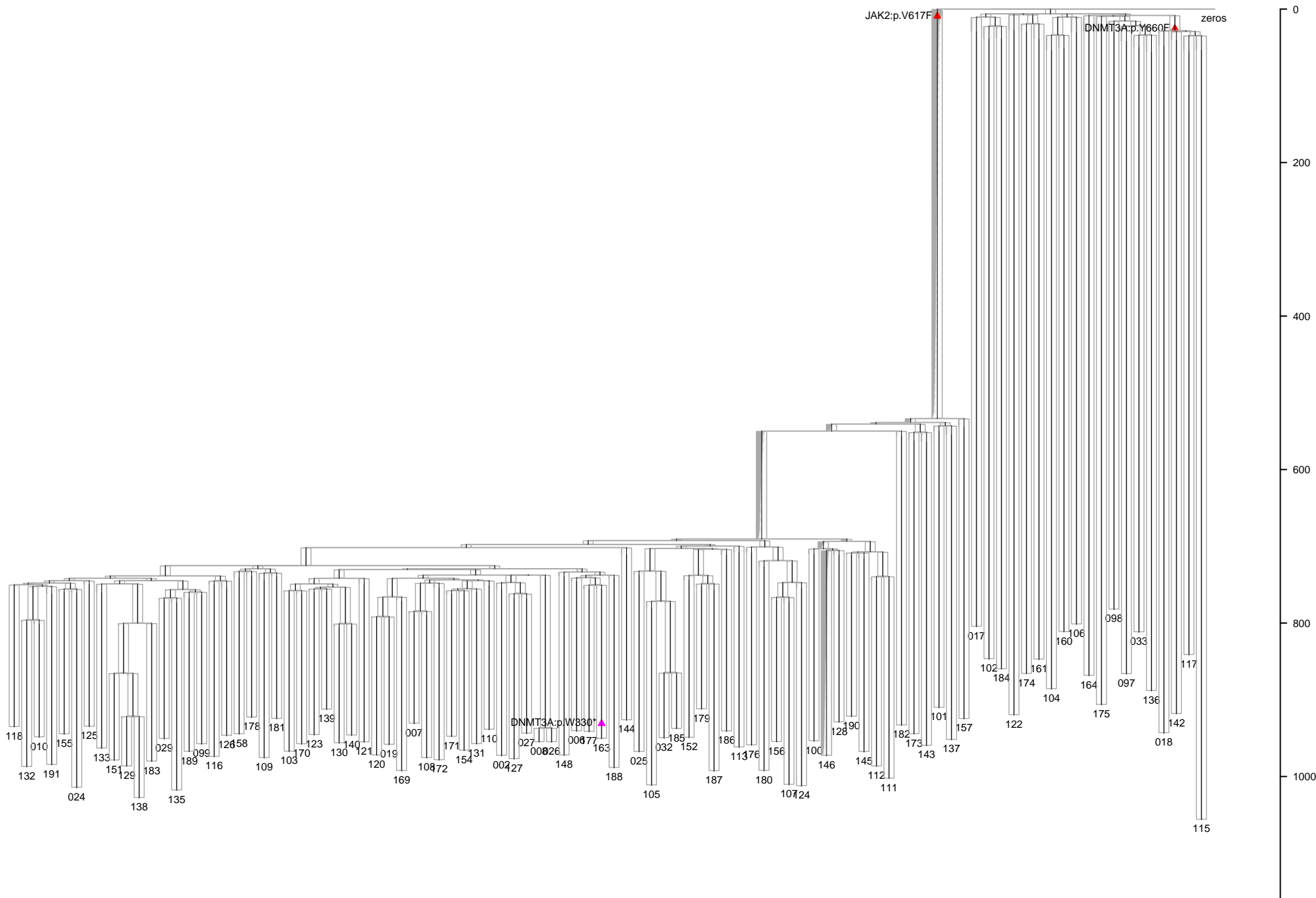
PD5847: Annotated with VAF from 107  
Mean Depth=20.23

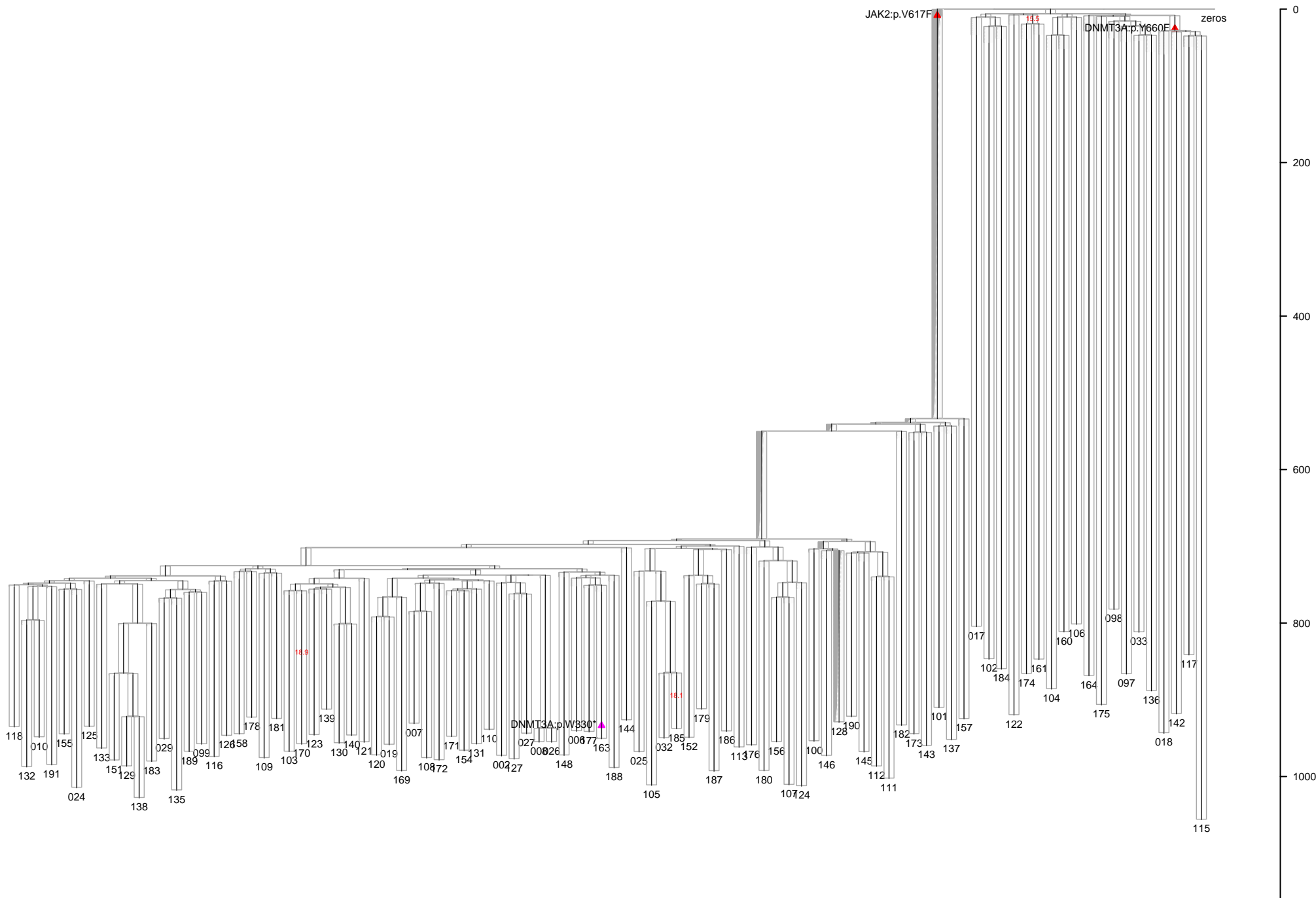




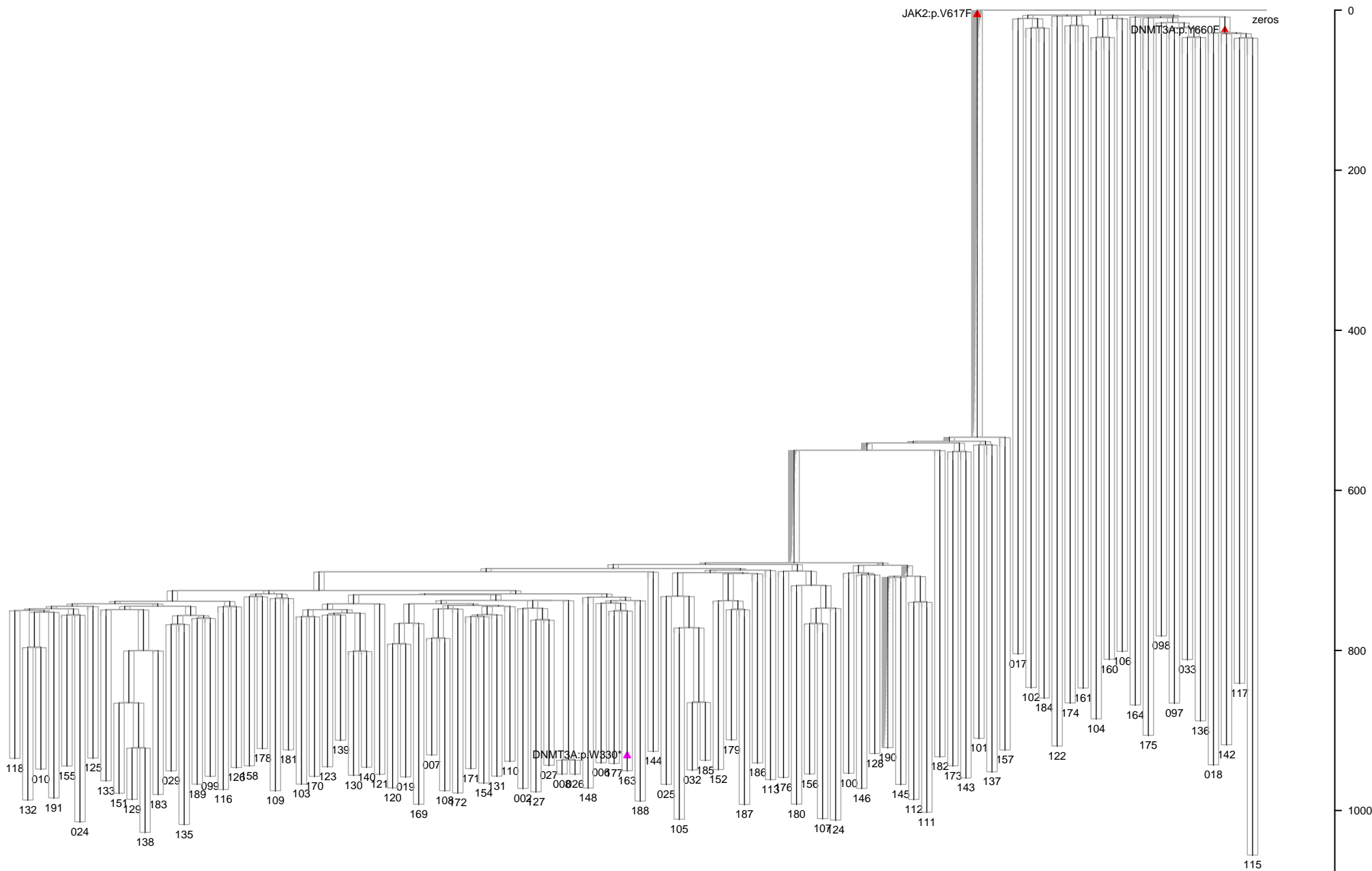


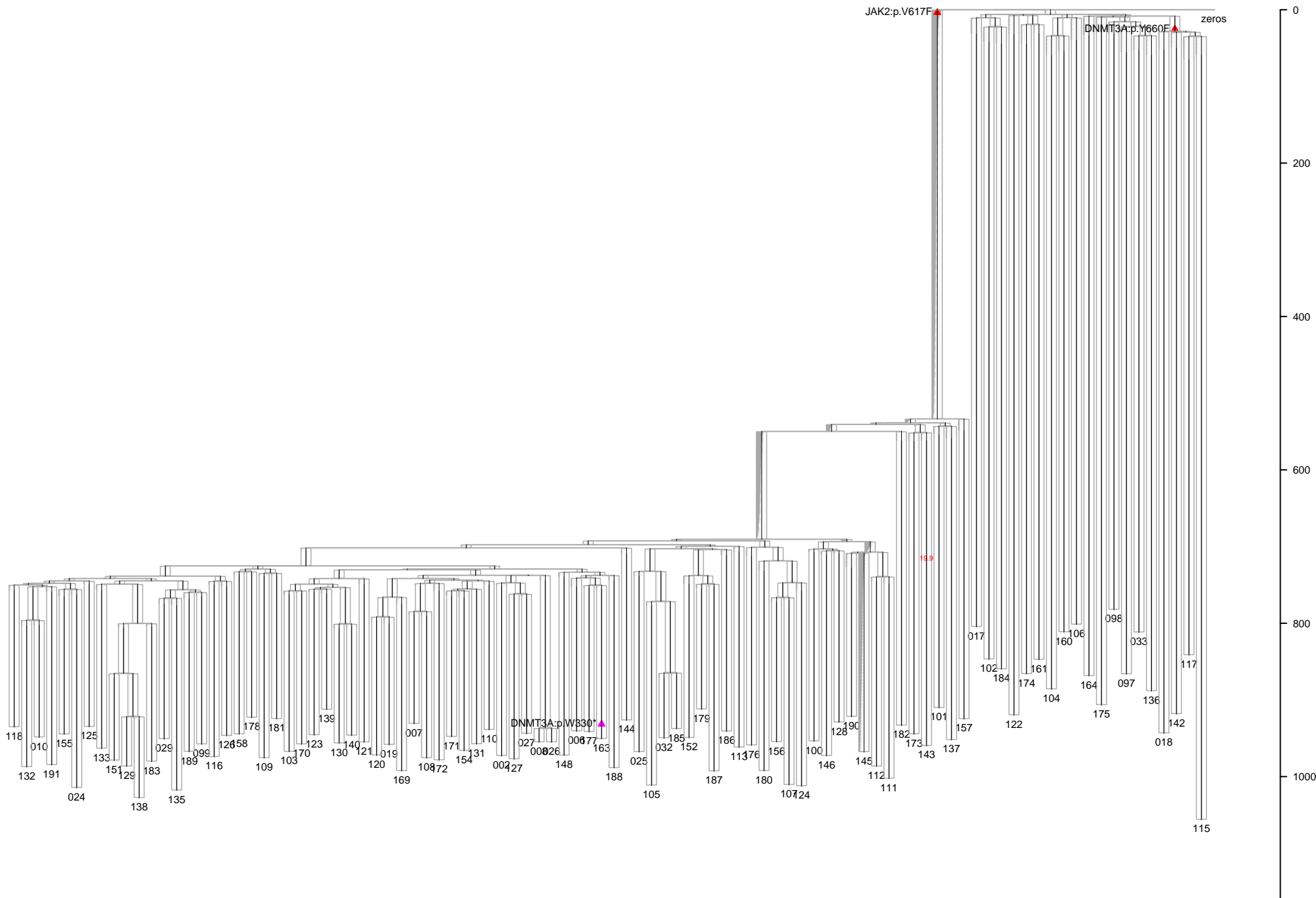


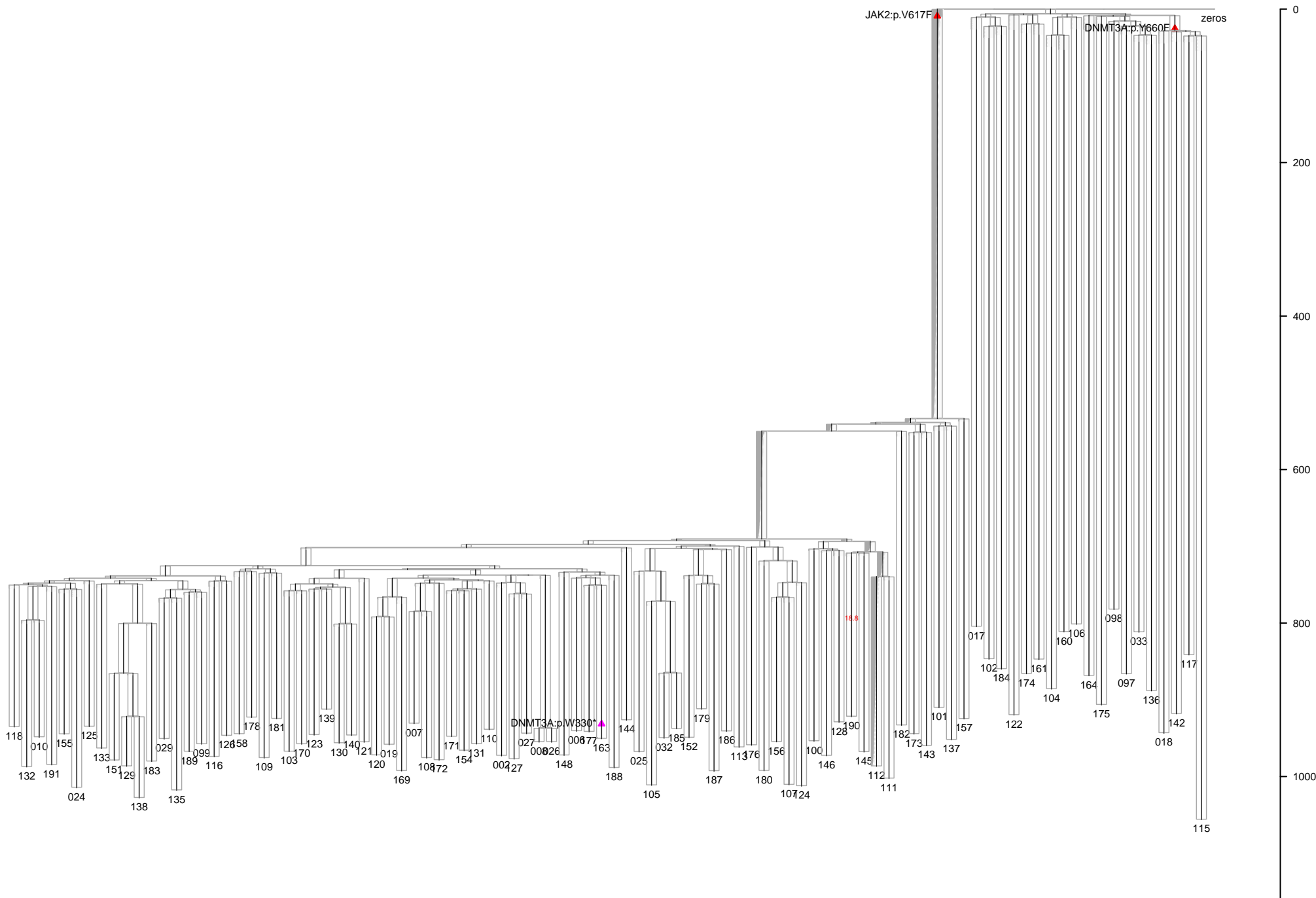




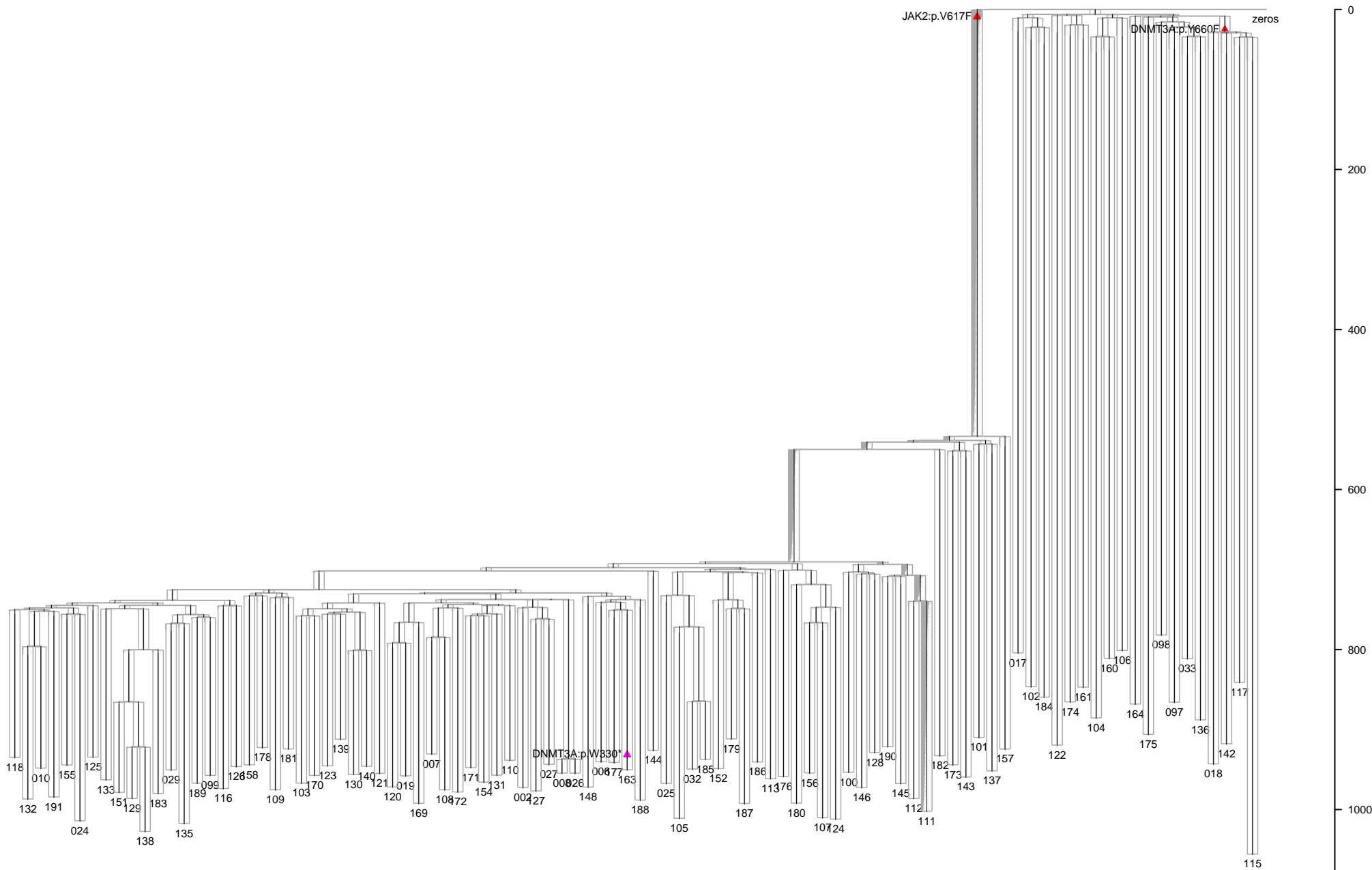
PD5847: Annotated with VAF from 190  
Mean Depth=17.88



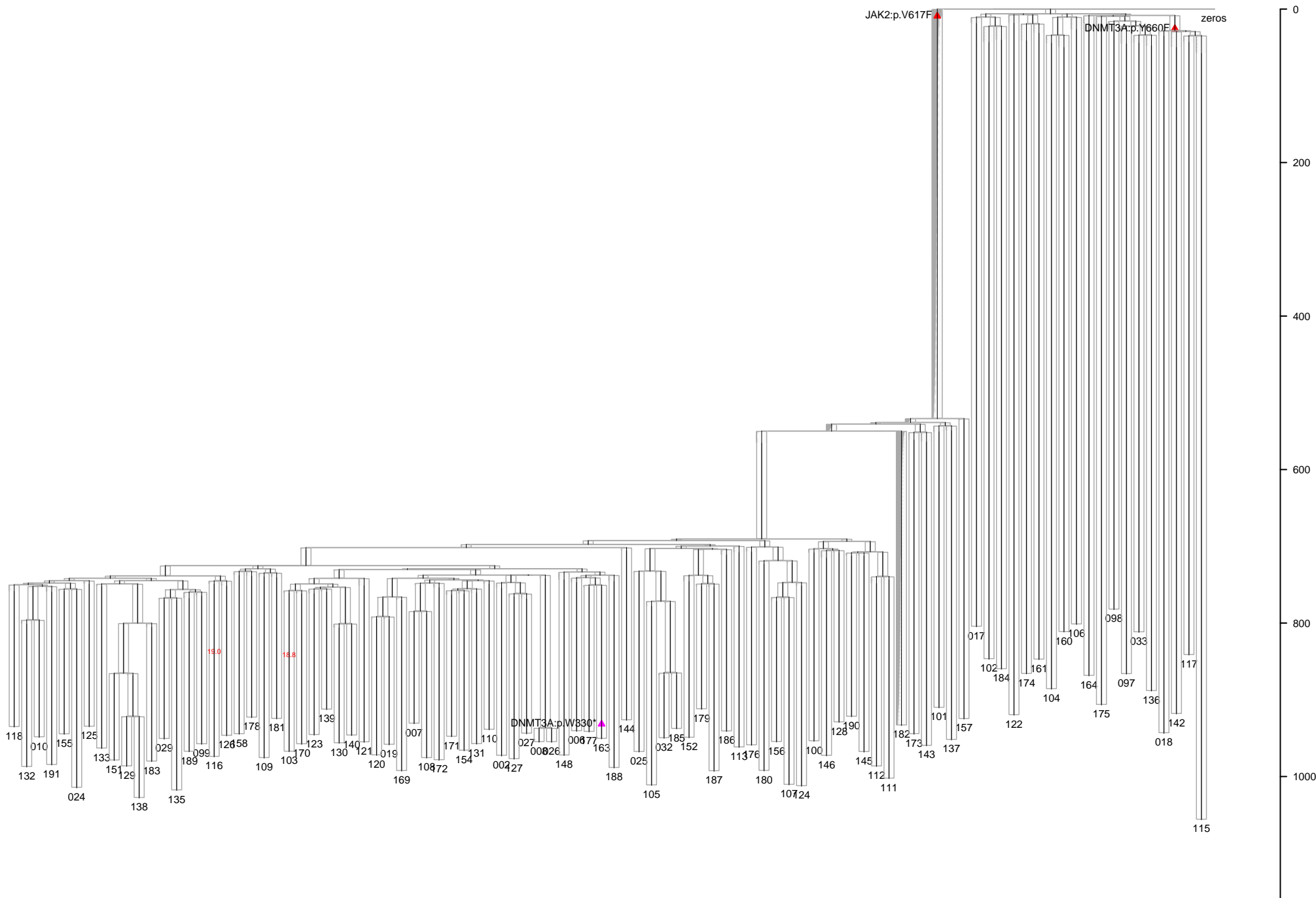


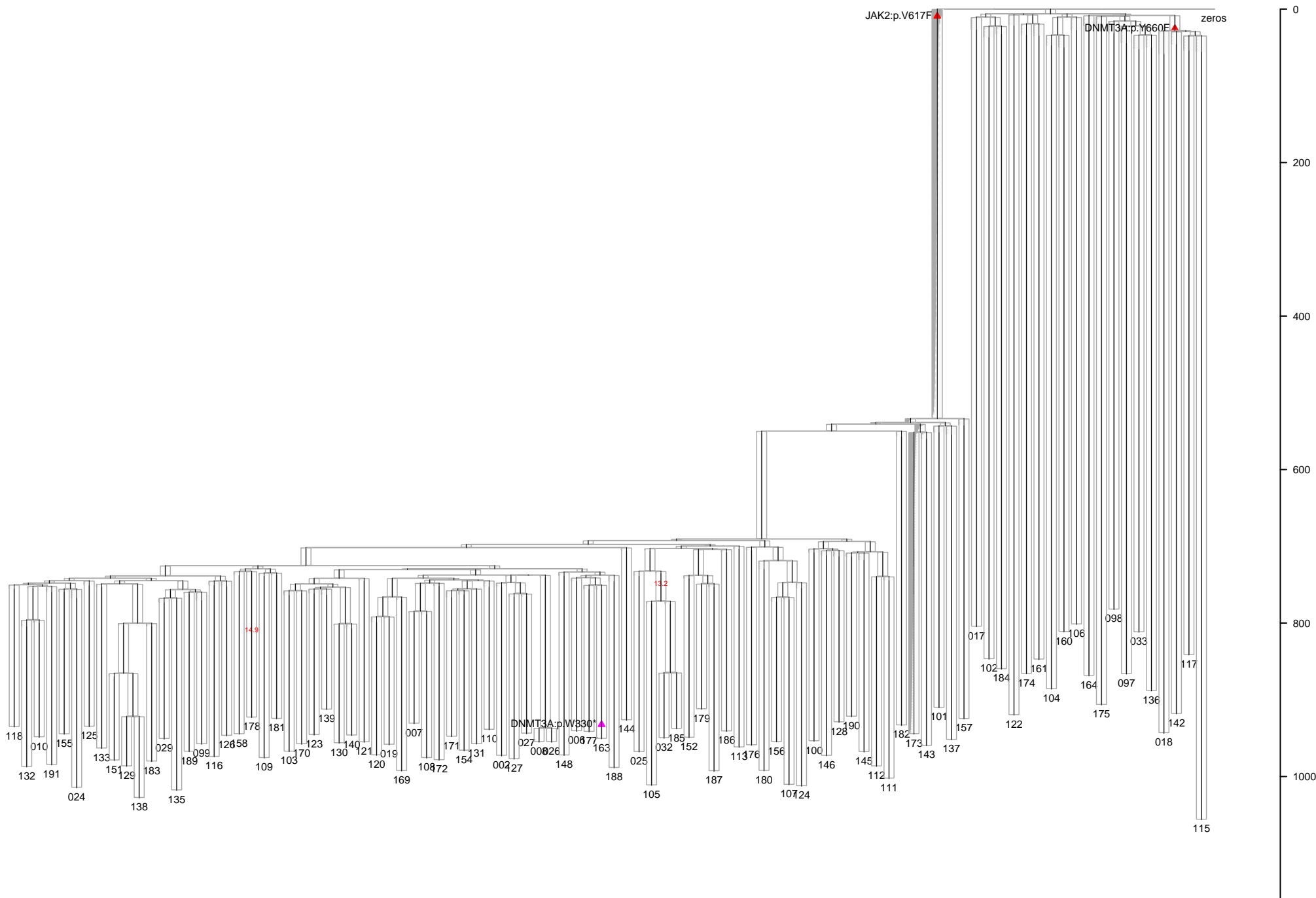


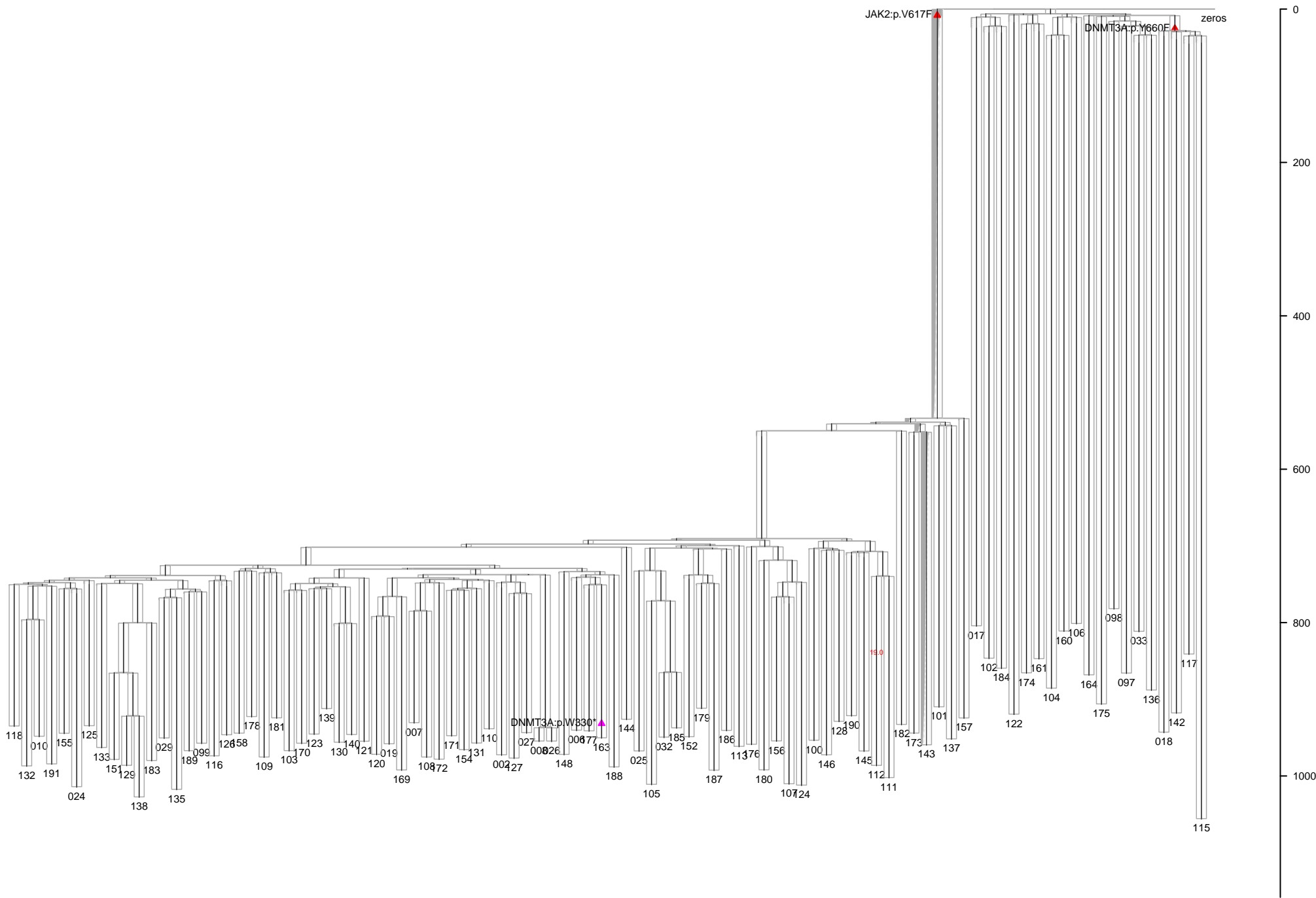
PD5847: Annotated with VAF from 111  
Mean Depth=18.84

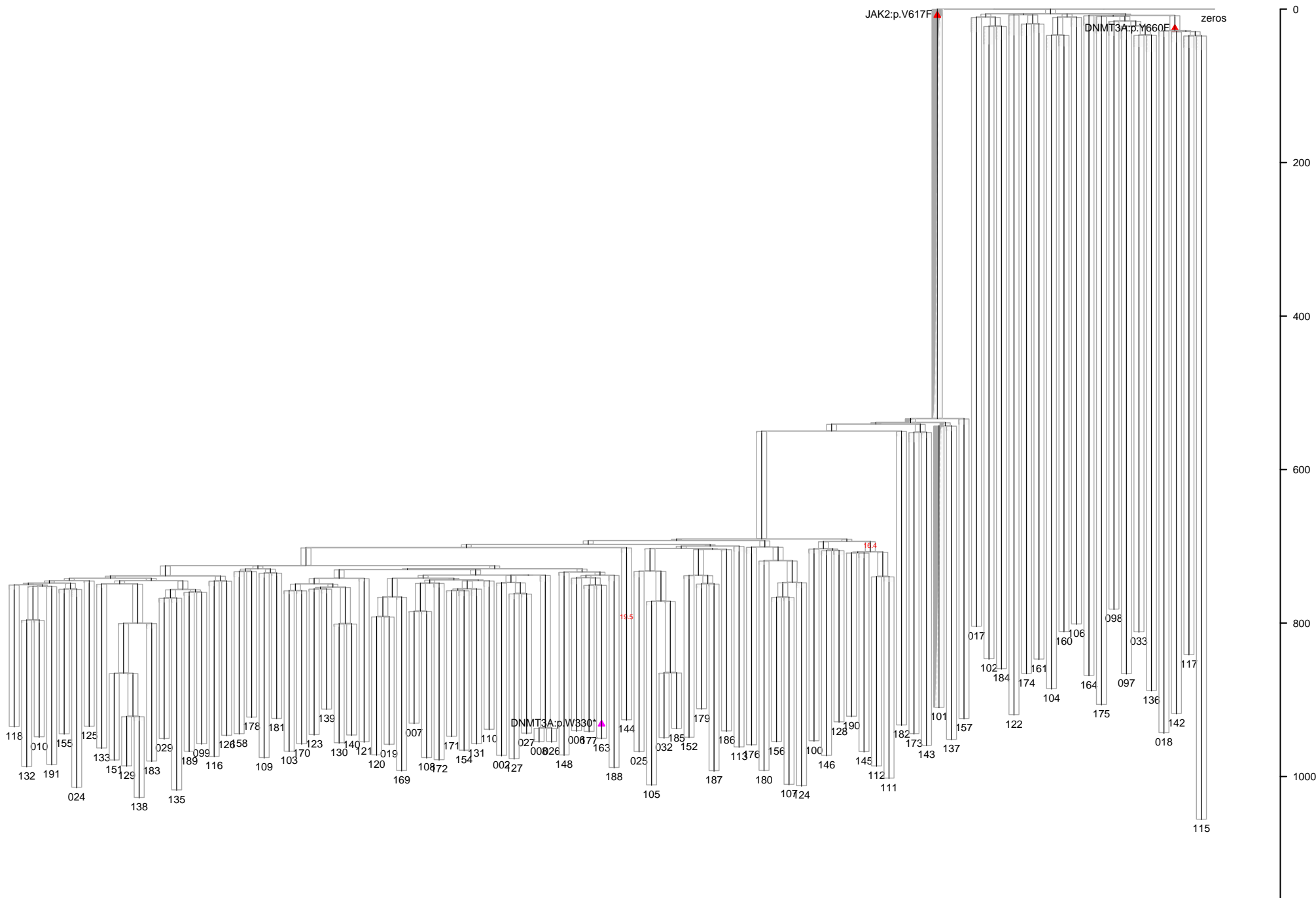


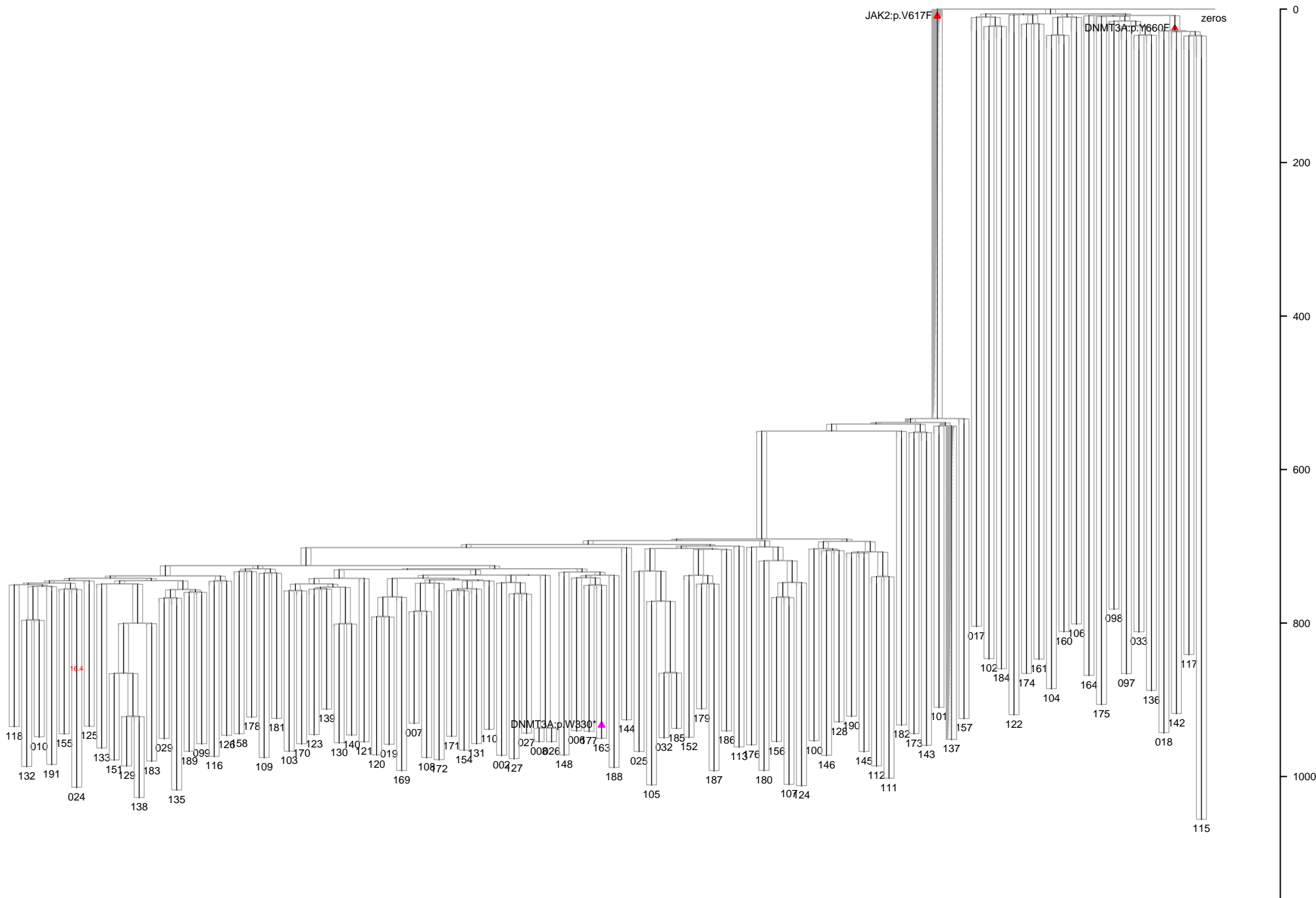


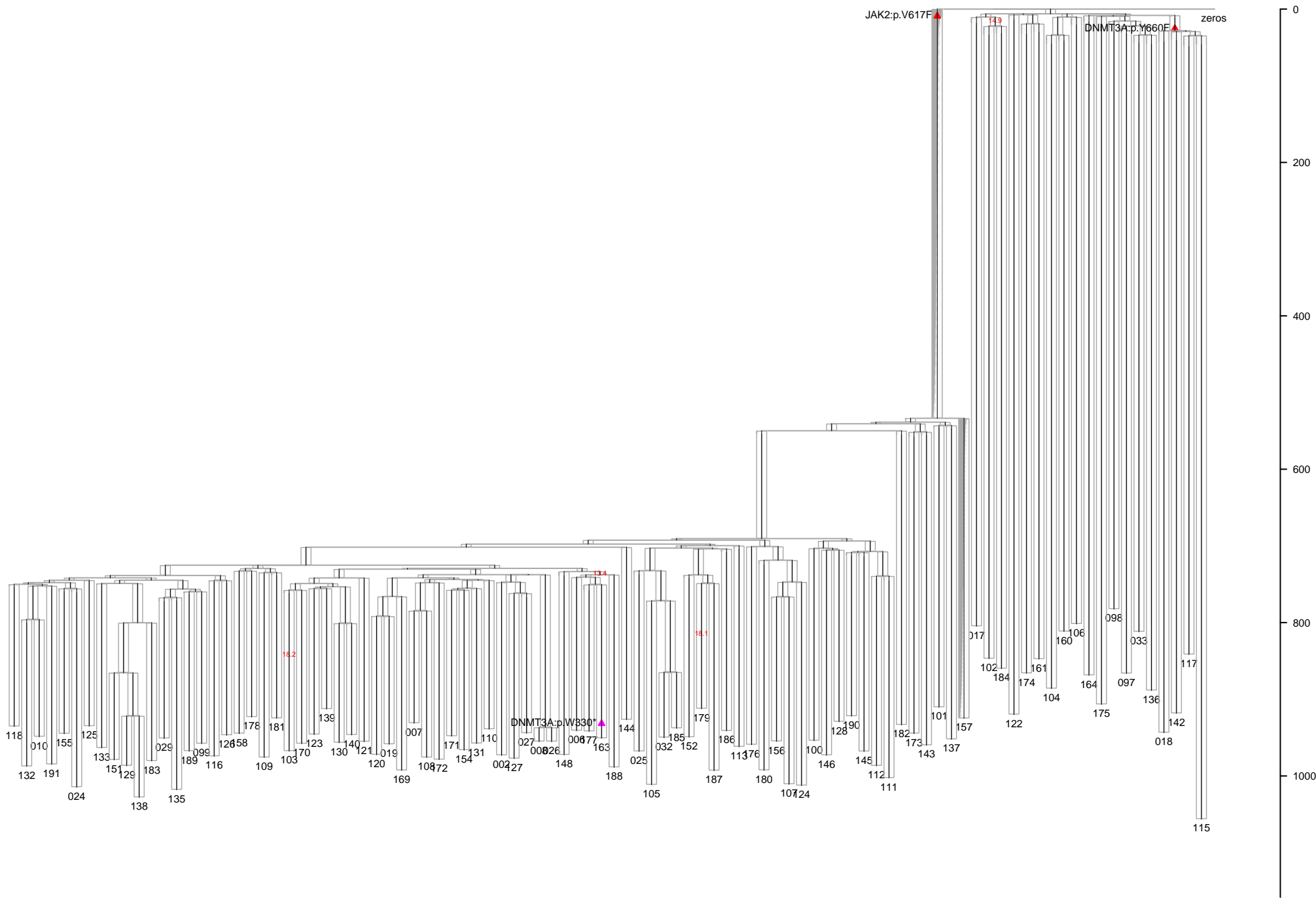




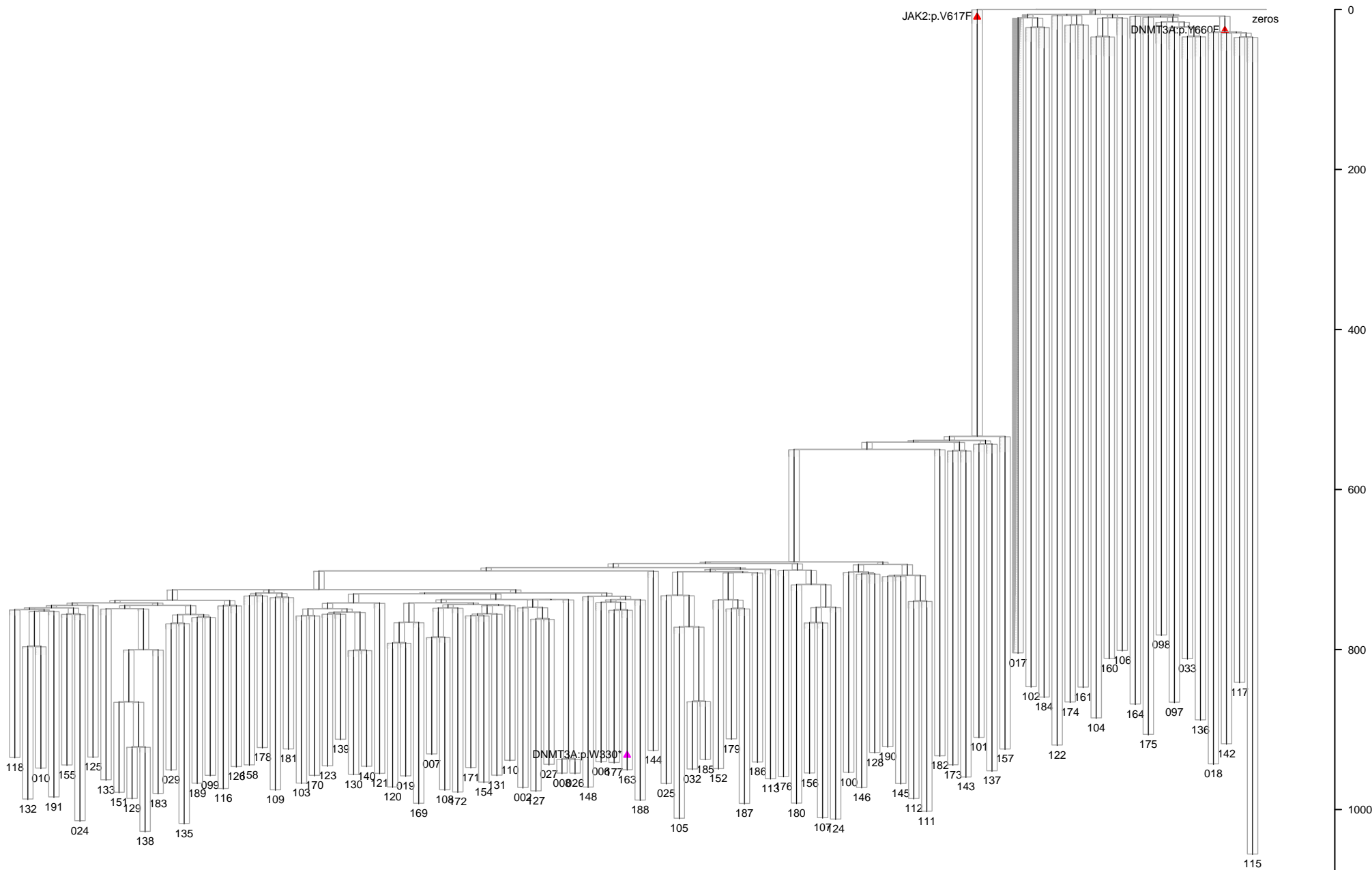


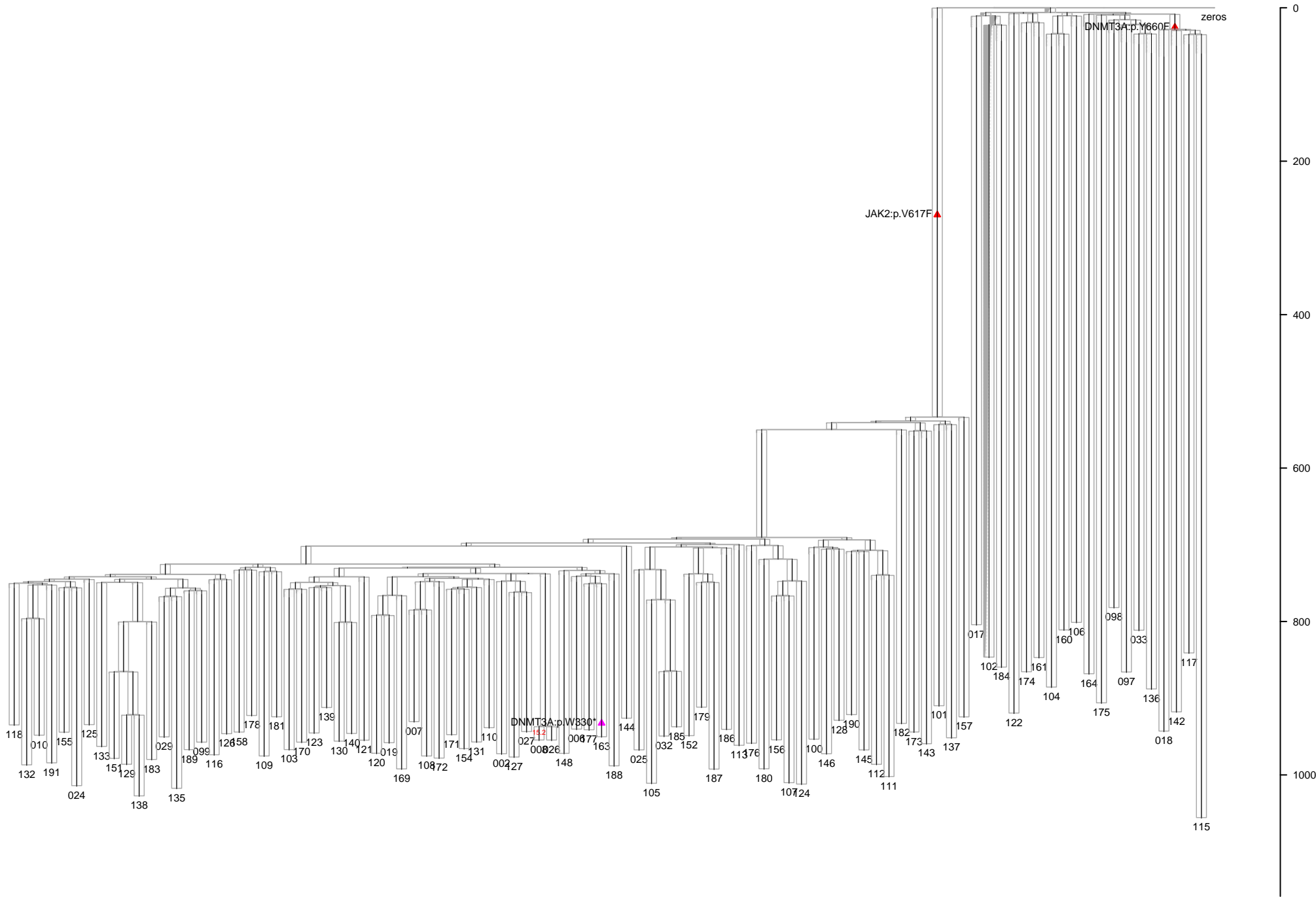




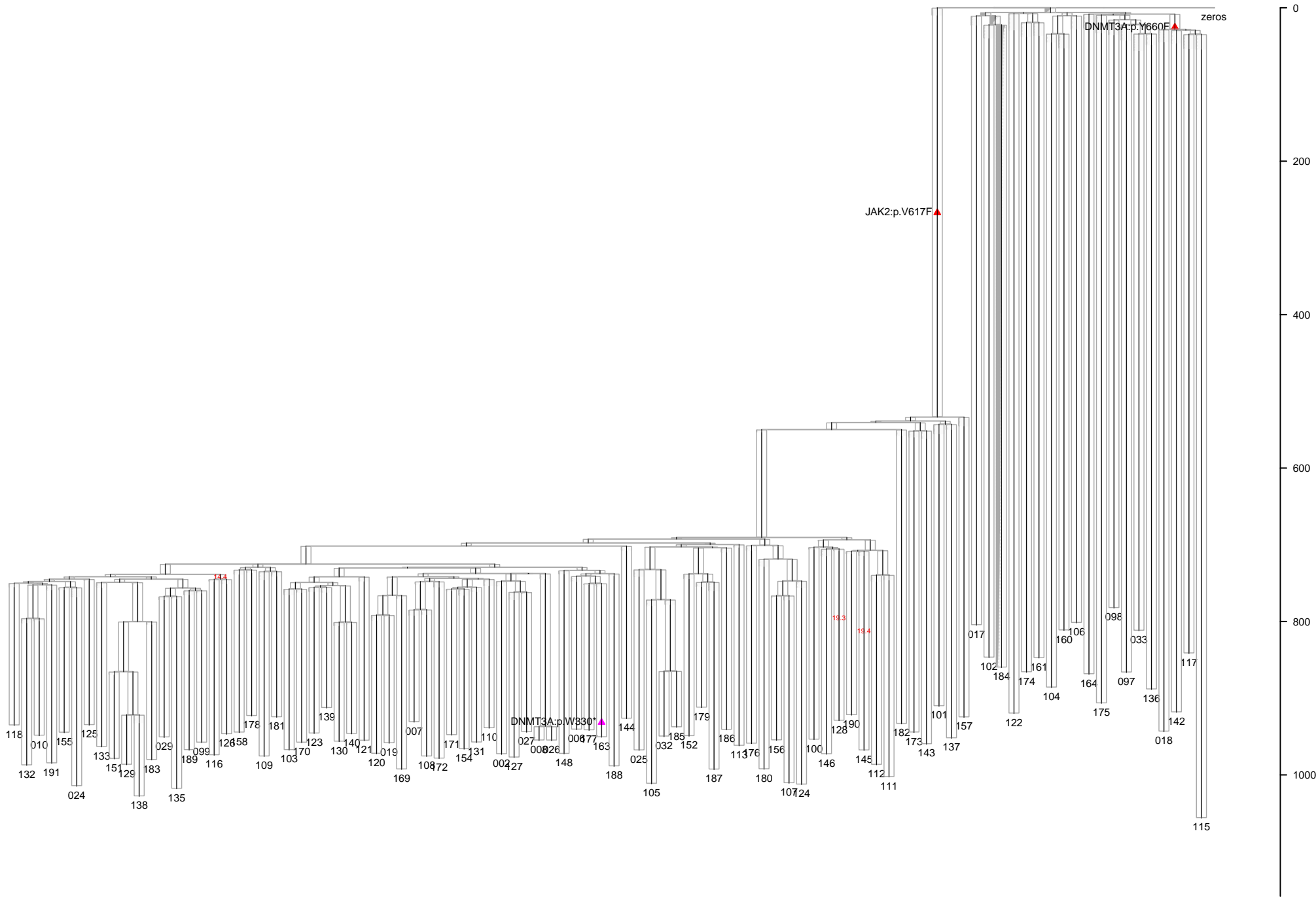


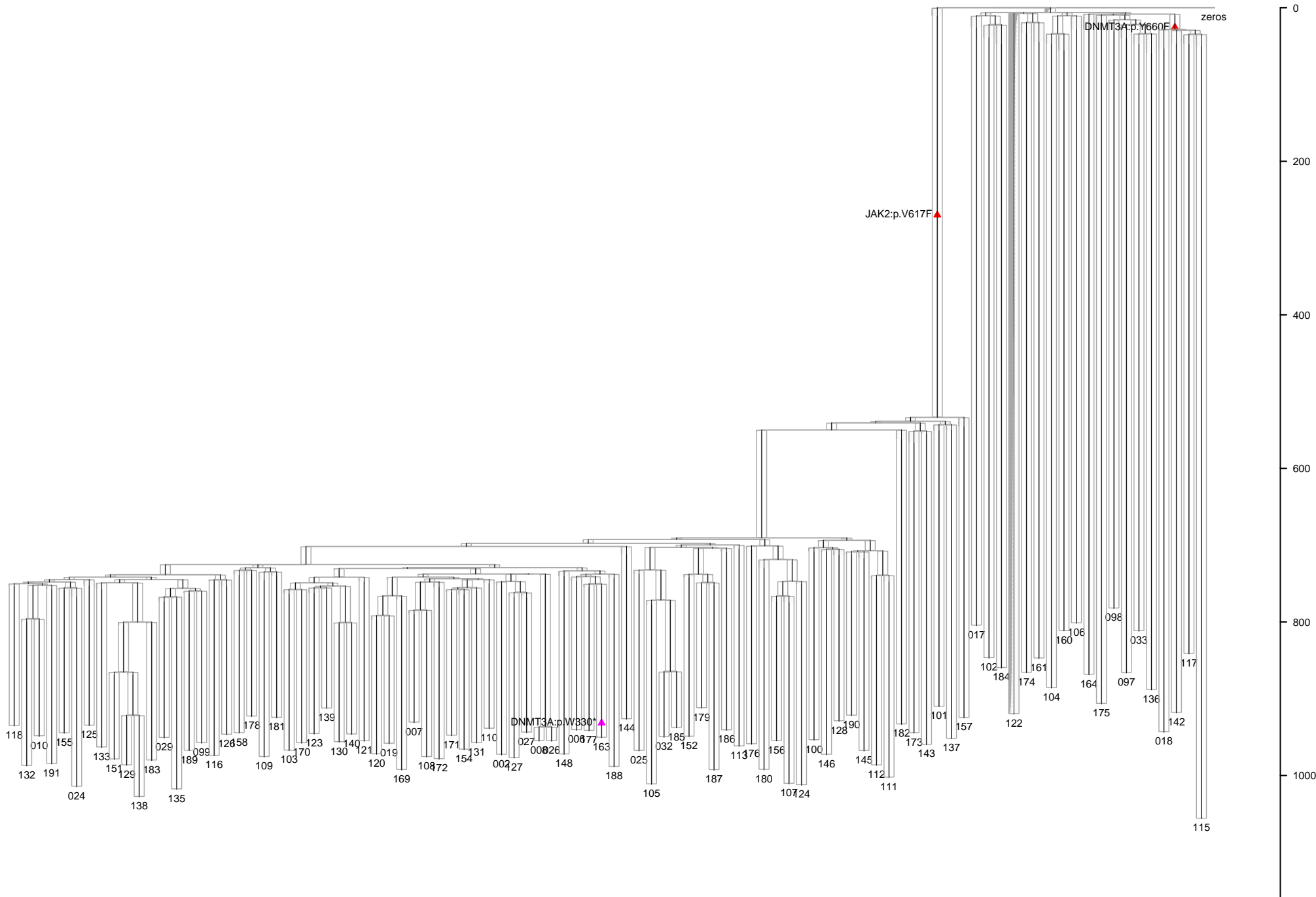
PD5847: Annotated with VAF from 017  
Mean Depth=18.12

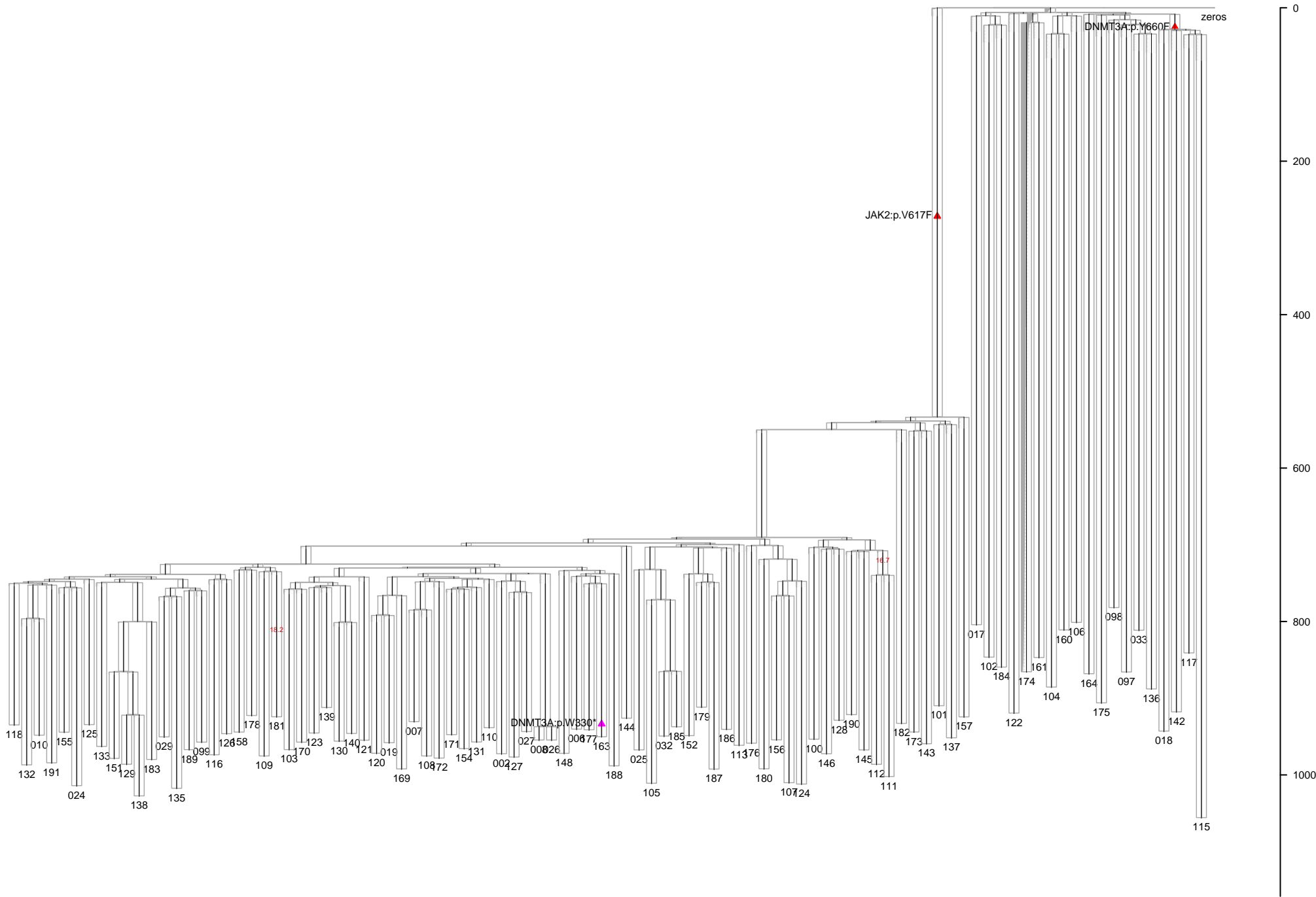


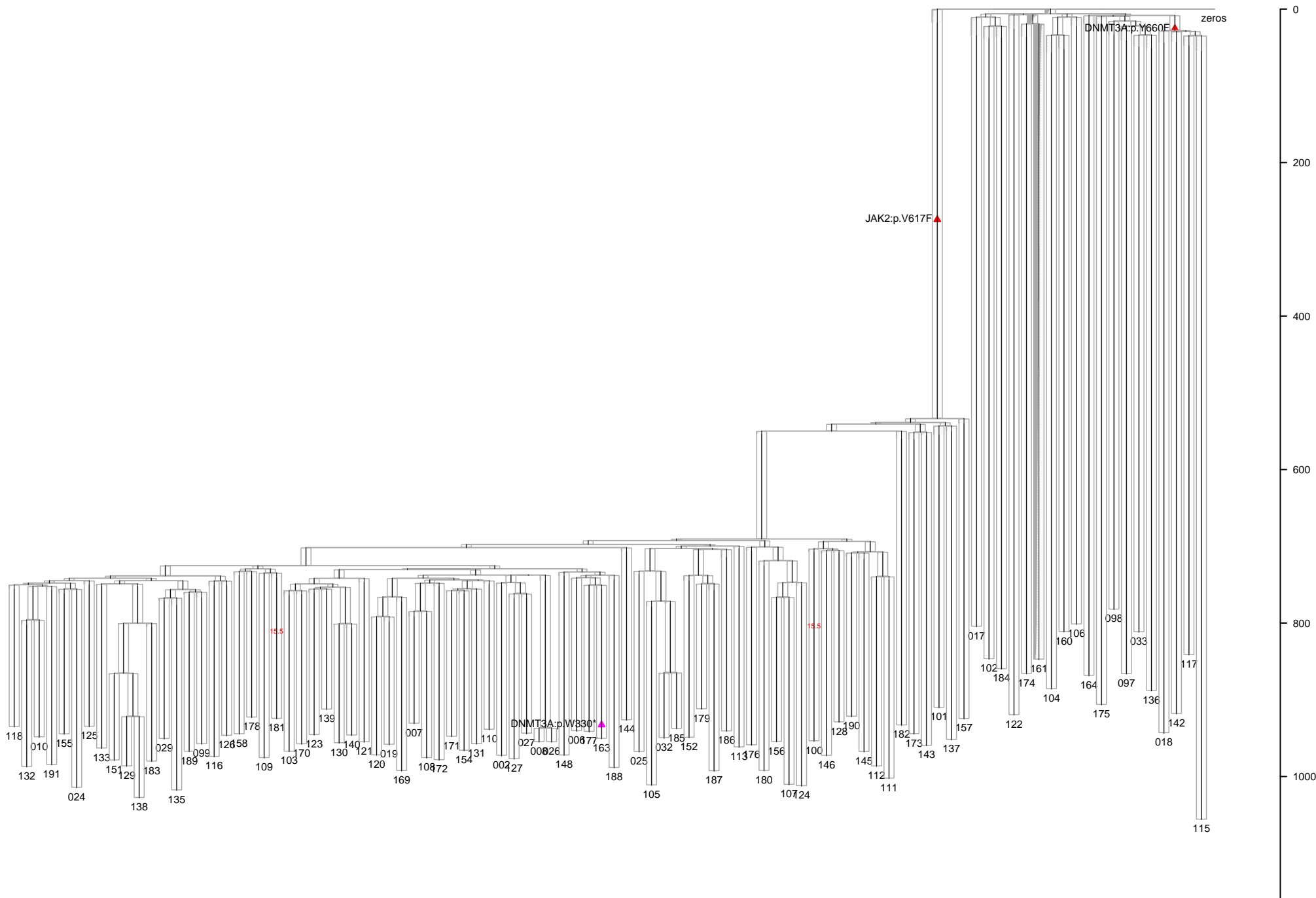


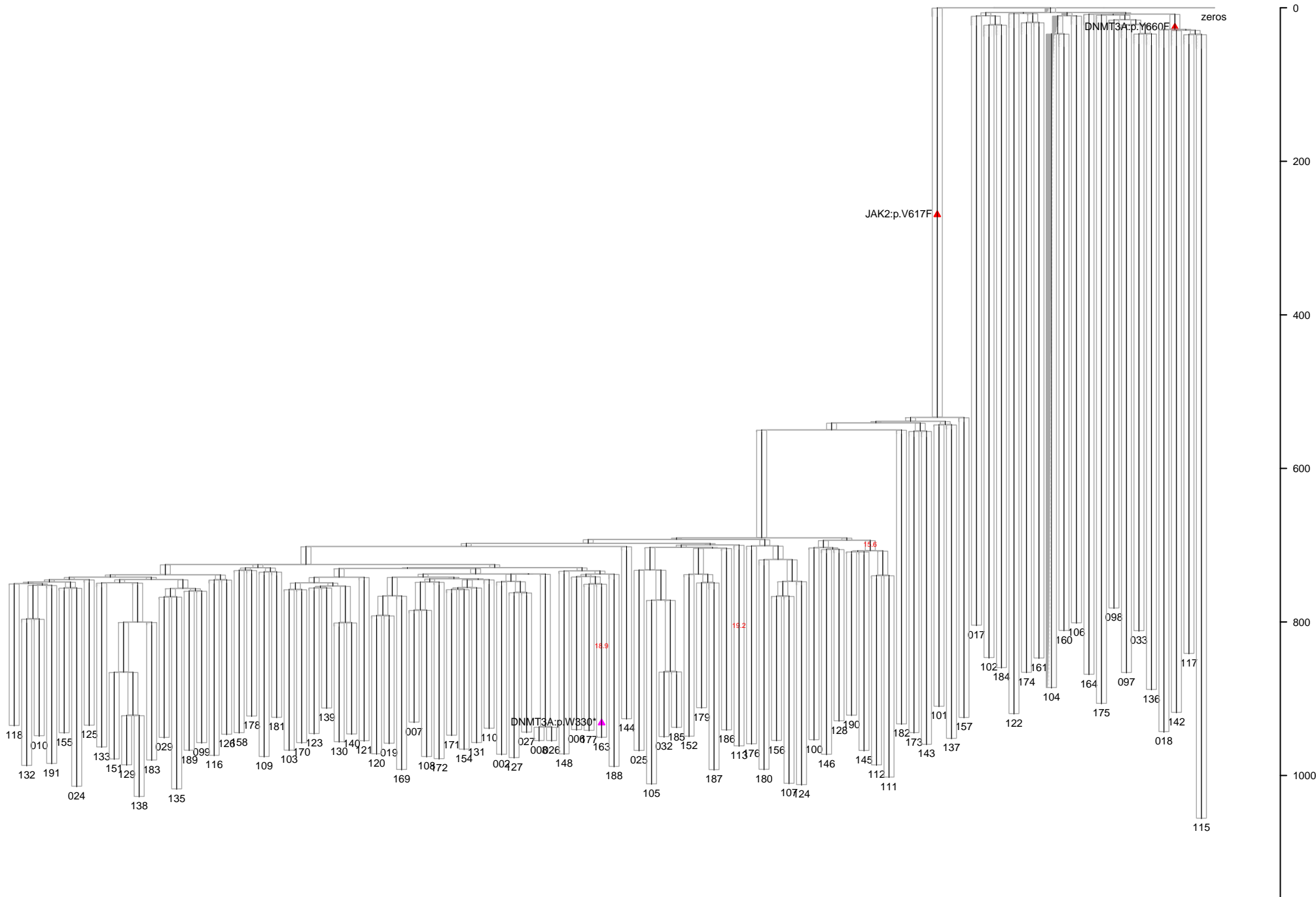


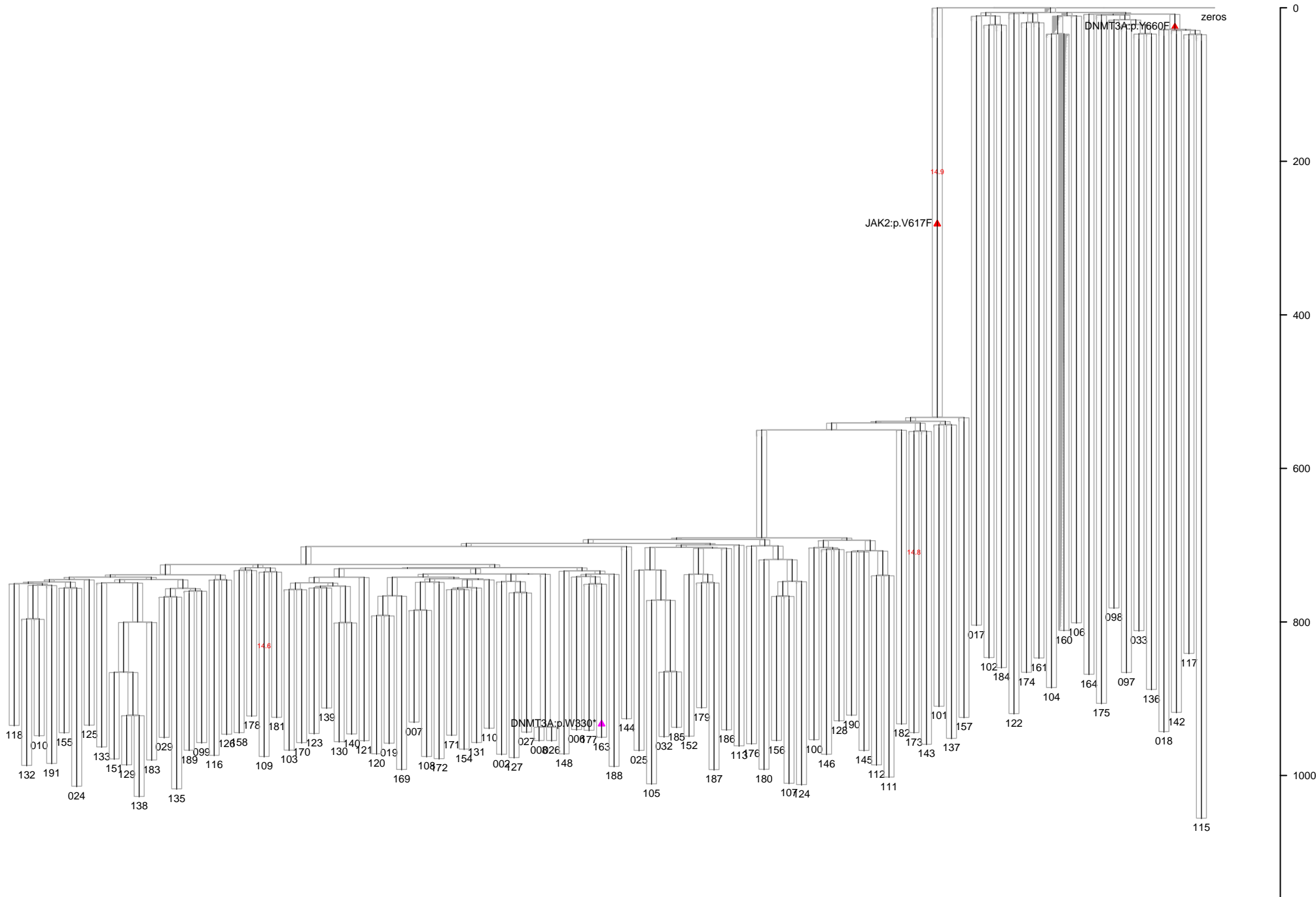












PD5847: Annotated with VAF from 106  
Mean Depth=21.03

