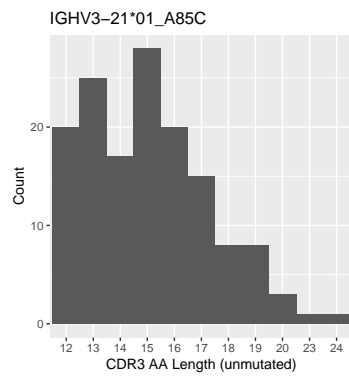


OGRDBstats Report

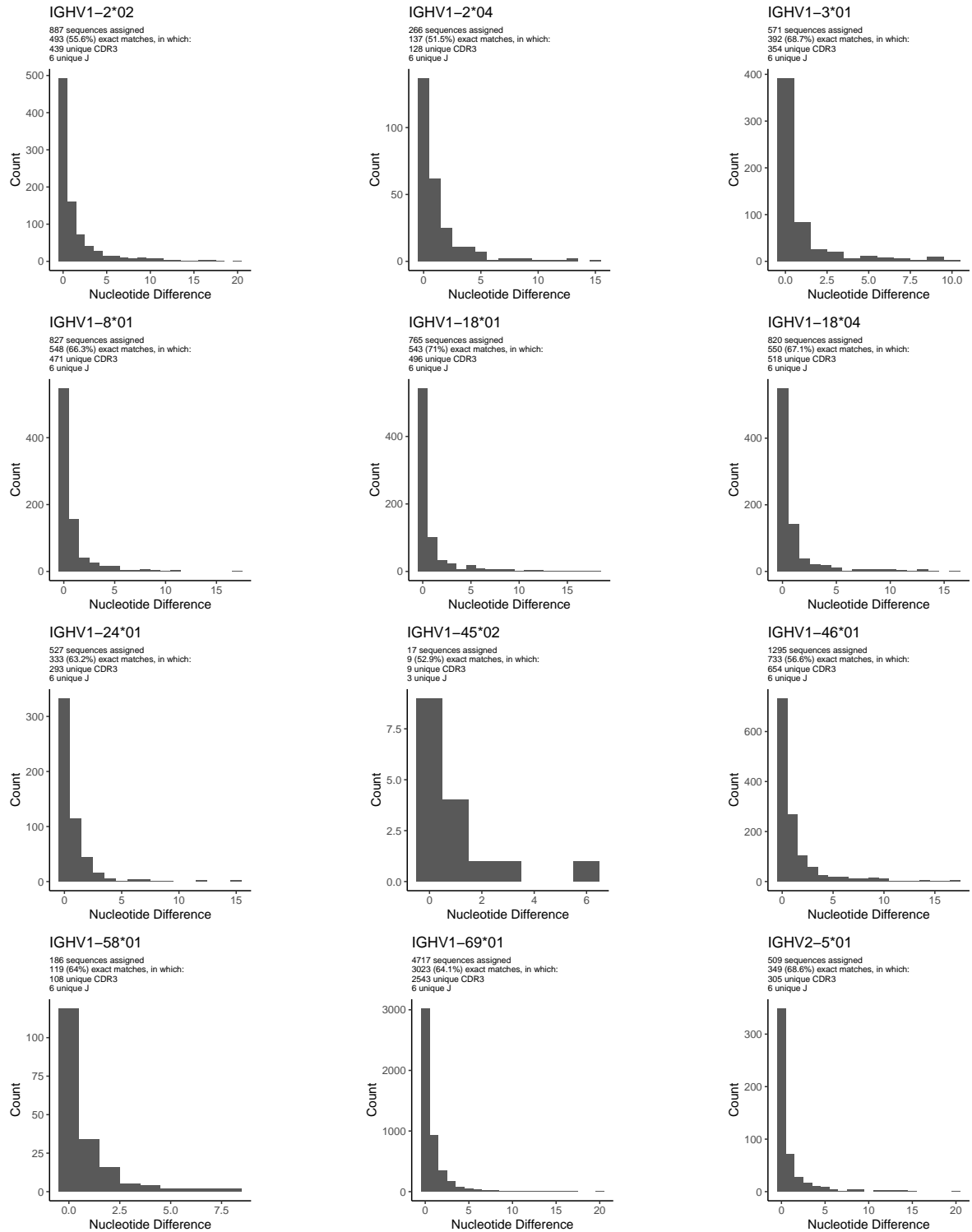
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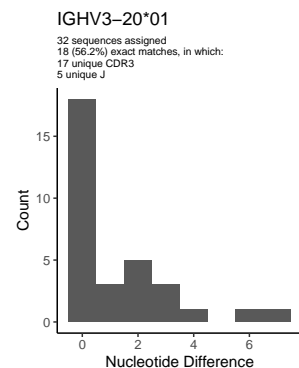
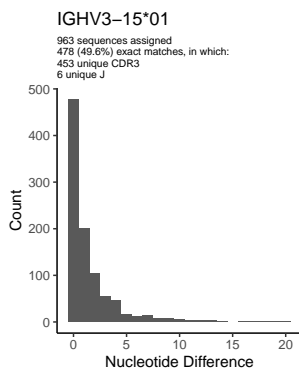
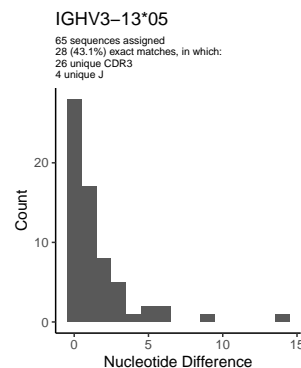
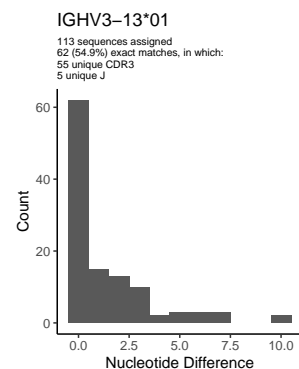
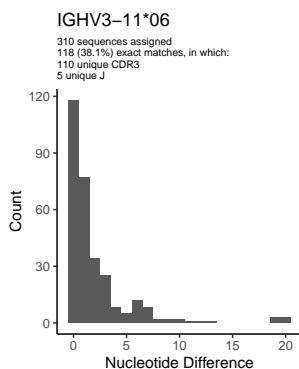
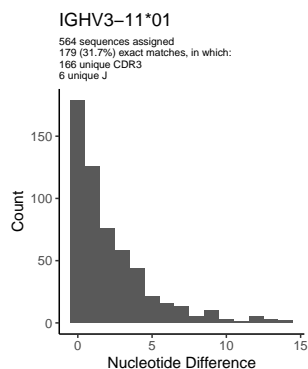
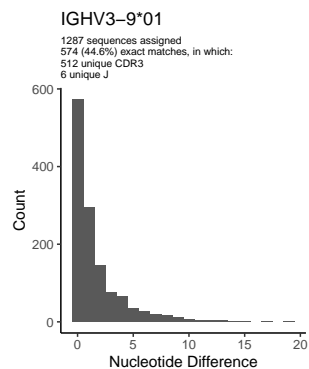
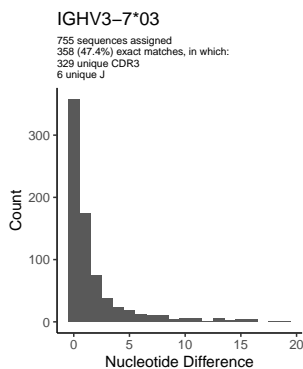
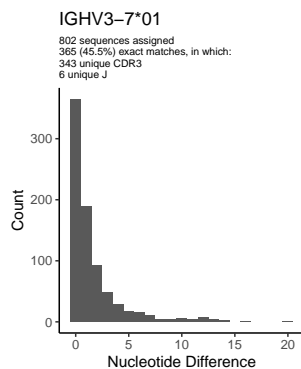
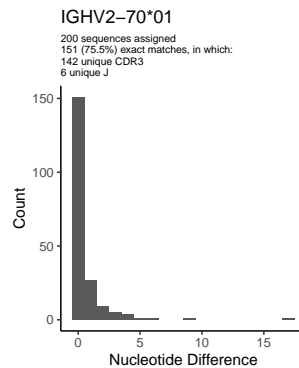
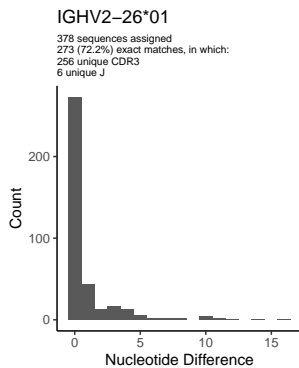
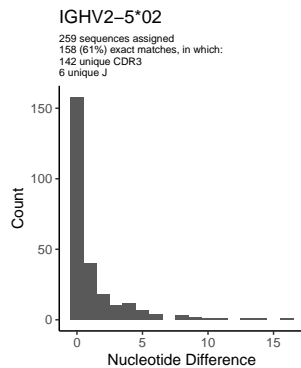
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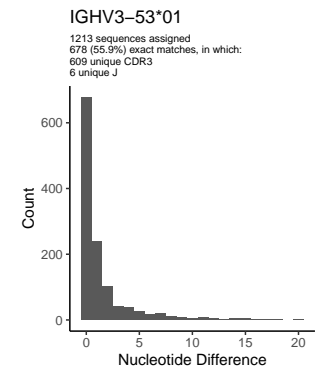
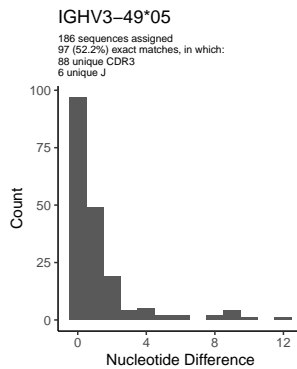
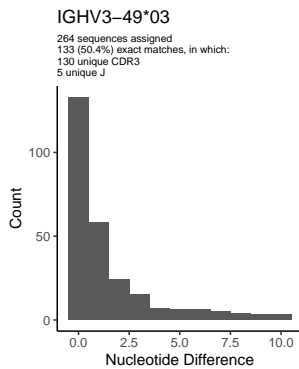
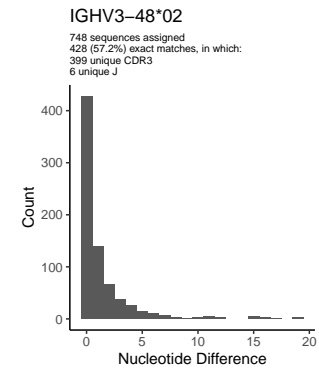
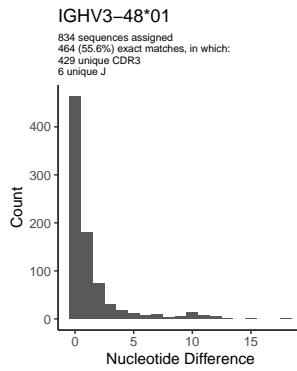
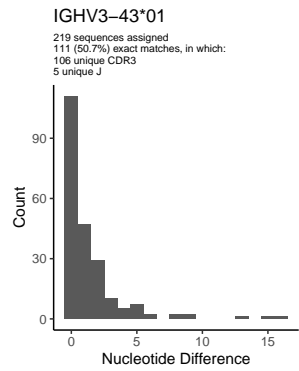
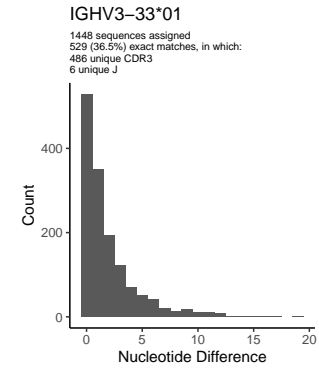
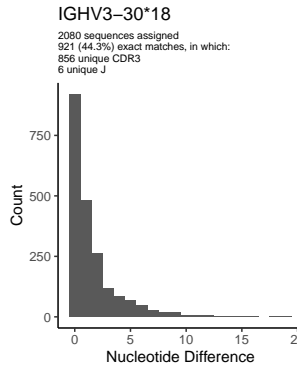
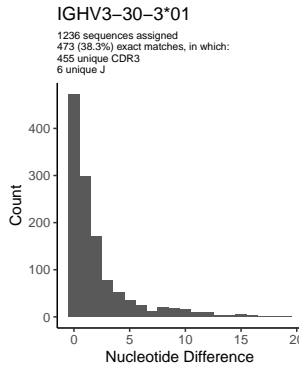
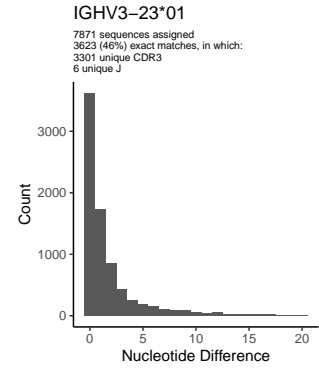
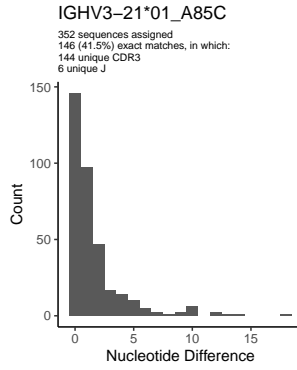
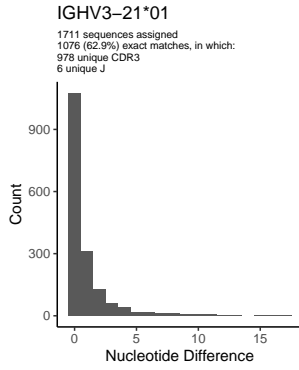
1.5 CDR3 length distribution, in assignments to novel alleles

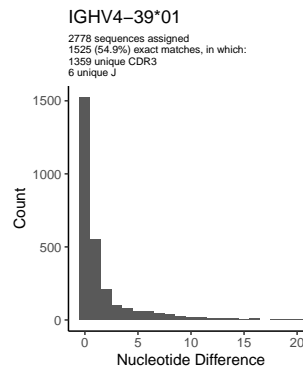
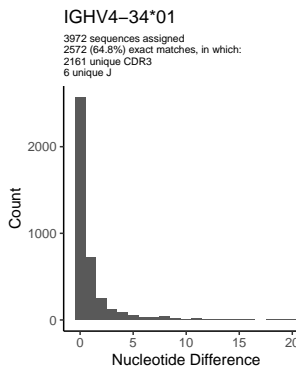
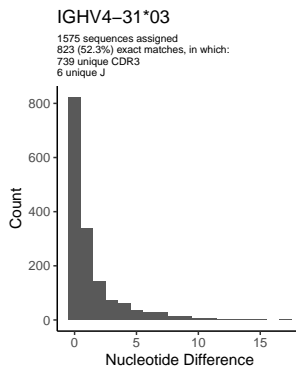
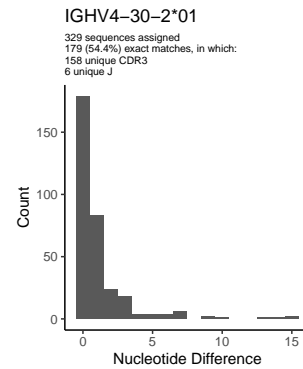
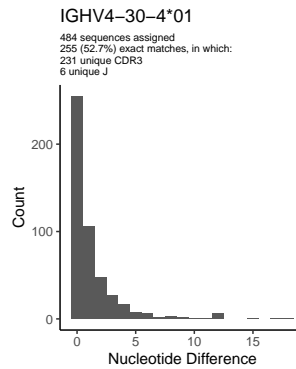
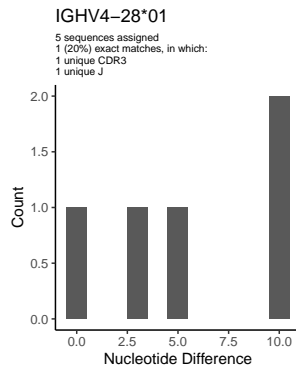
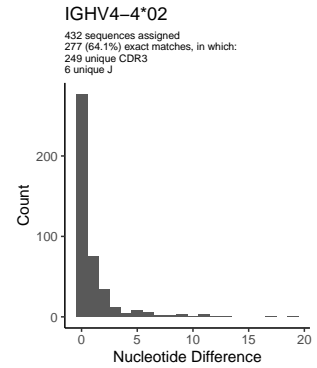
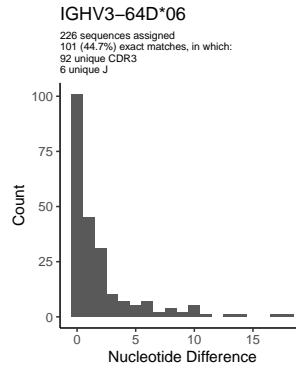
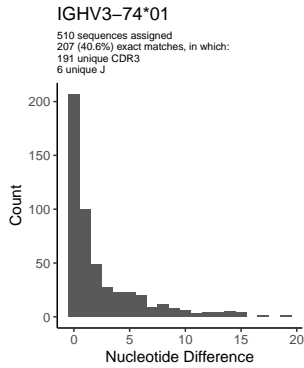
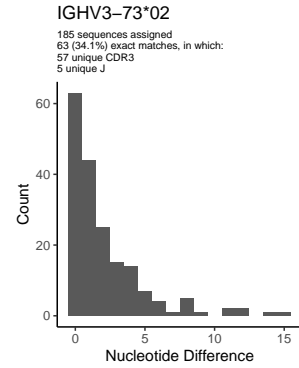
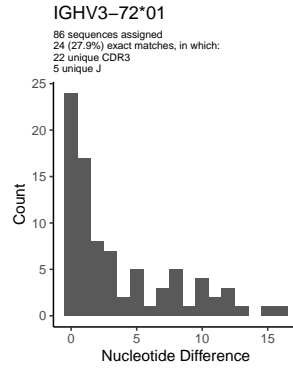
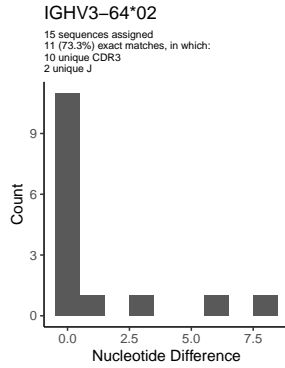


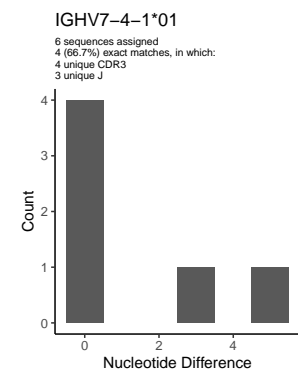
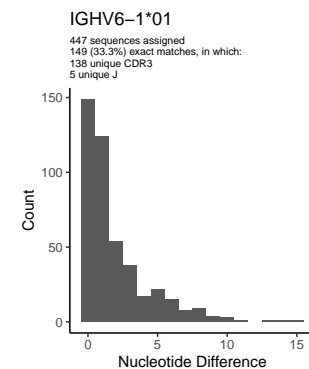
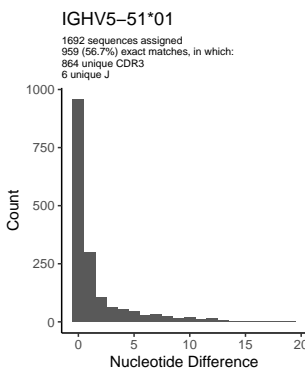
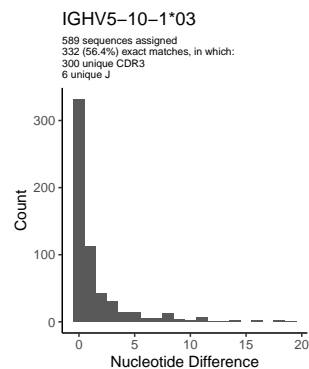
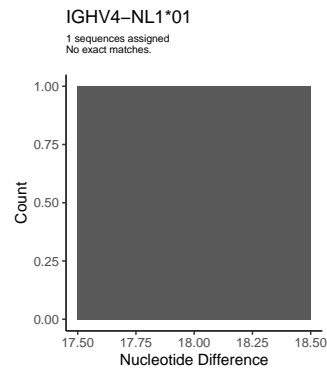
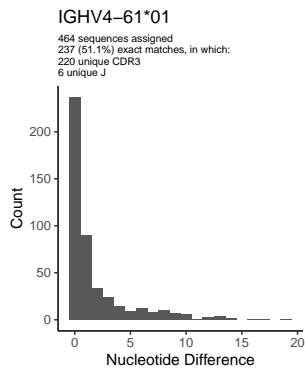
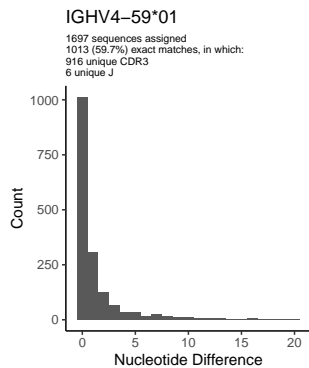
2 Variation from germline, in assignments to each allele



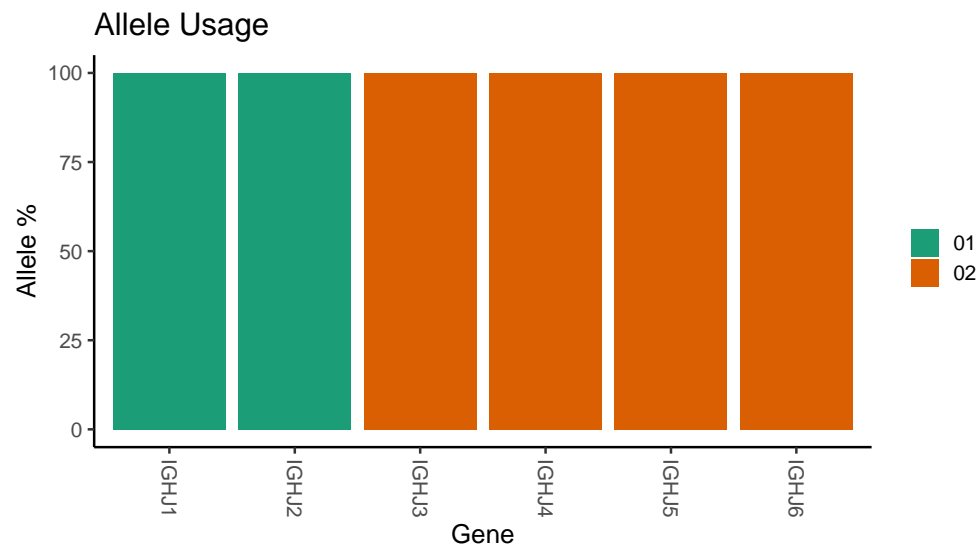








3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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##  
## Novel allele file: /work/jenkins/PRJEB26509/S2/S2/2/2/eb/3d7f7db82932ff99d59d4d9a253f66/novel_sequen  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V
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