

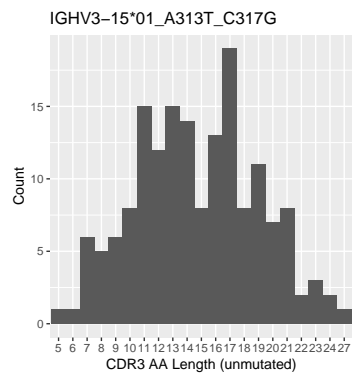
# OGRDBstats Report

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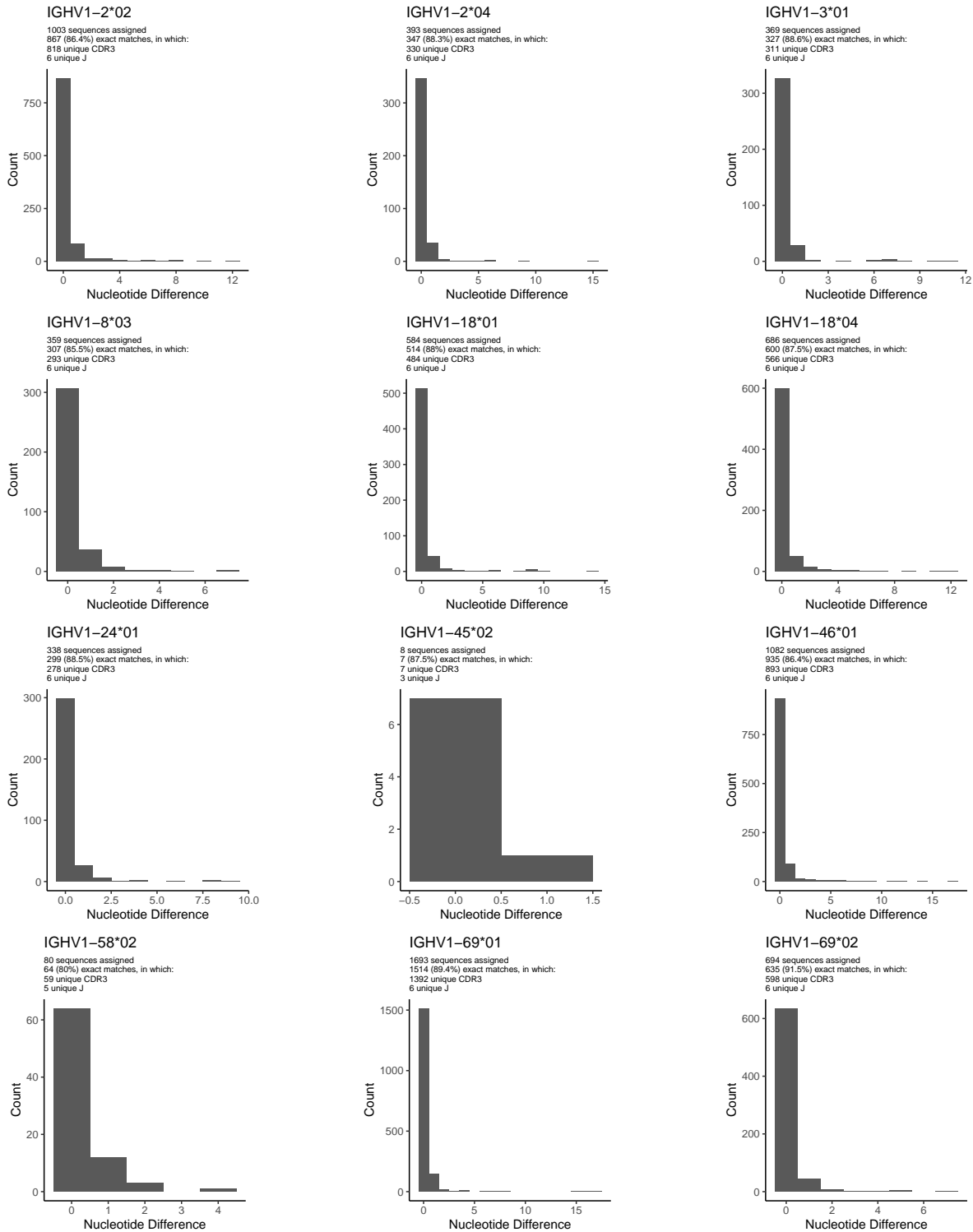
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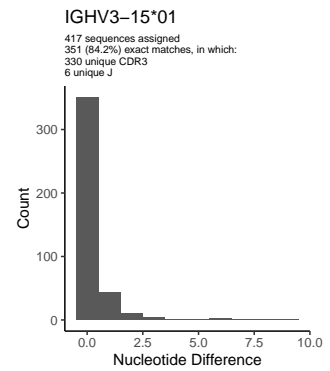
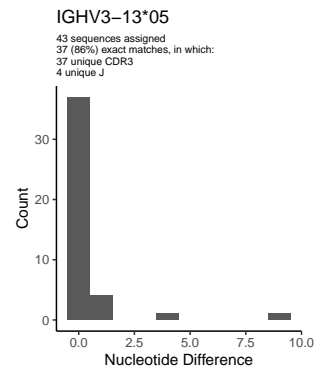
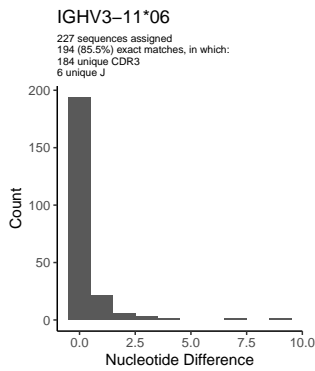
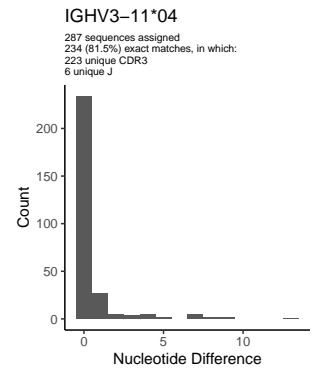
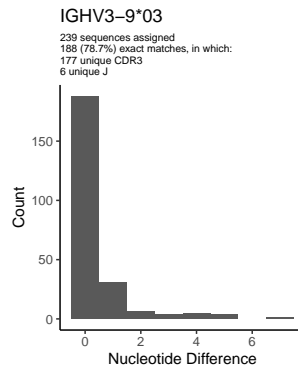
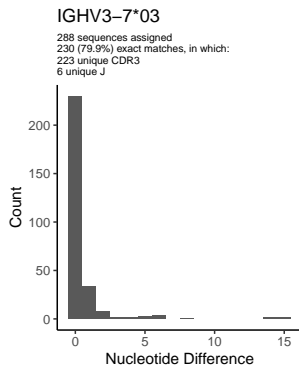
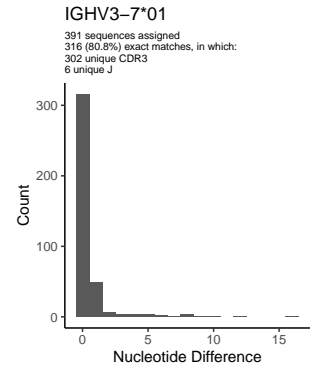
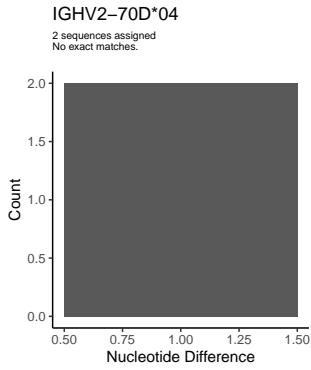
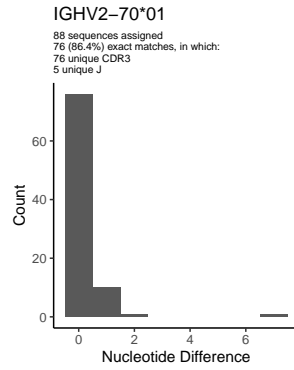
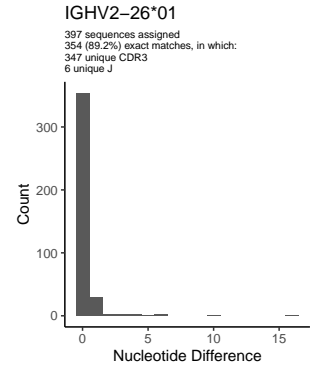
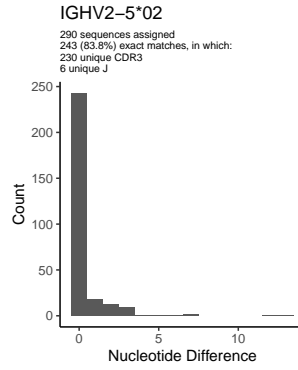
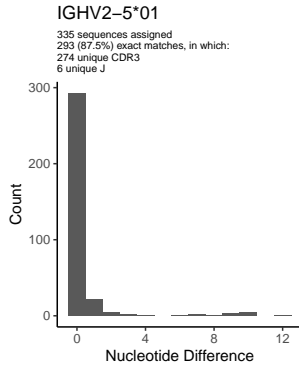


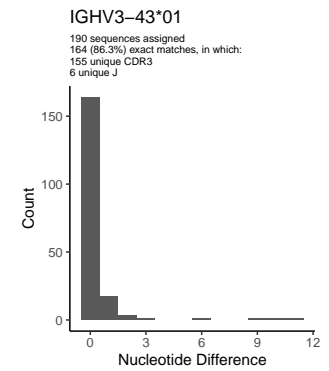
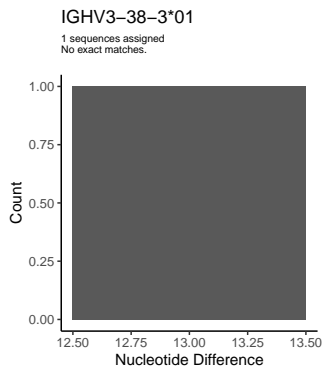
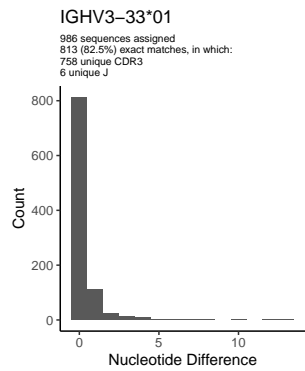
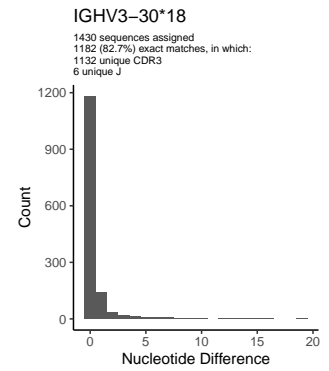
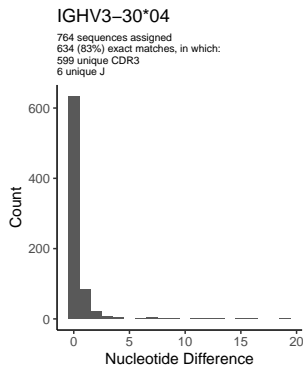
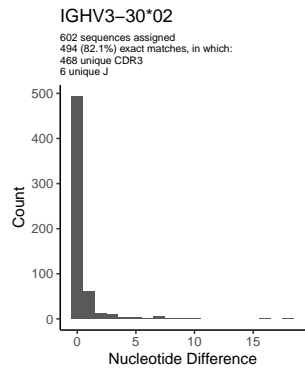
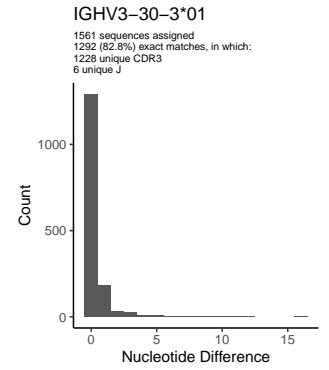
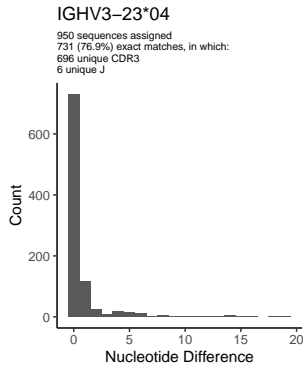
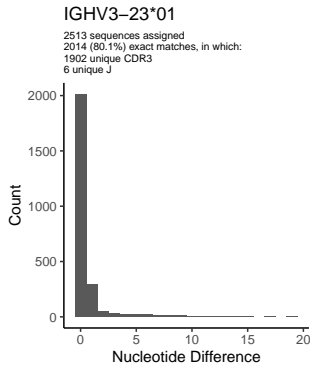
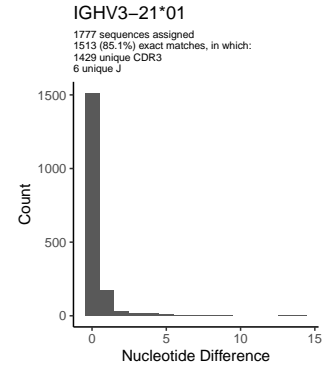
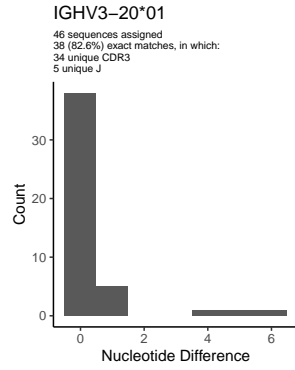
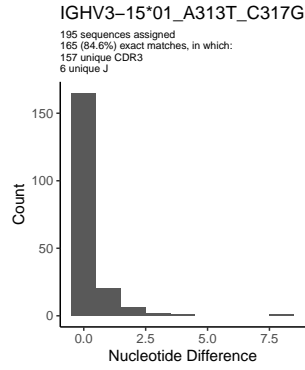
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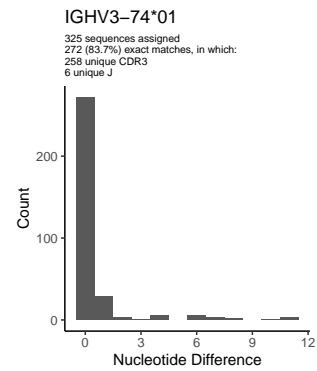
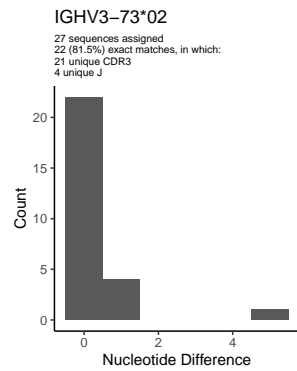
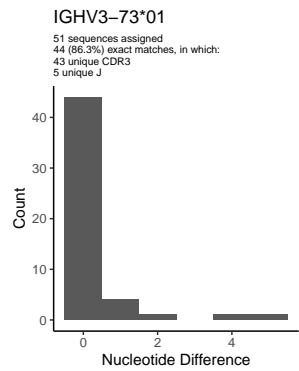
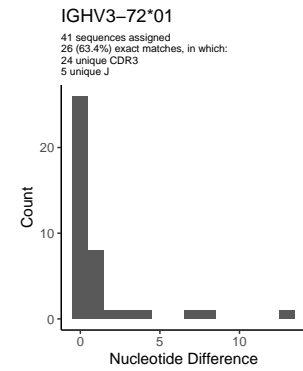
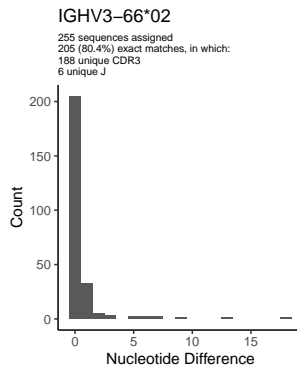
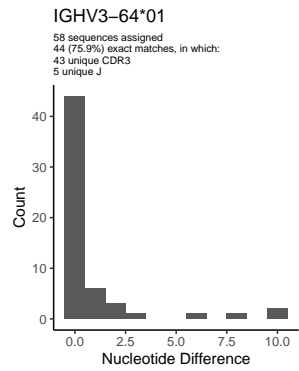
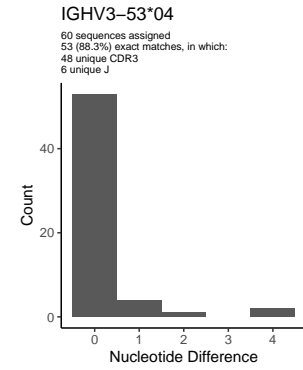
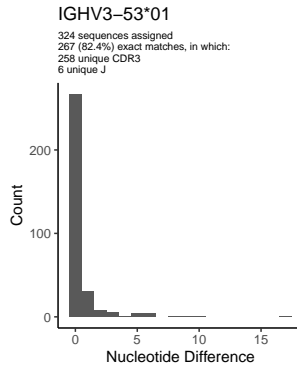
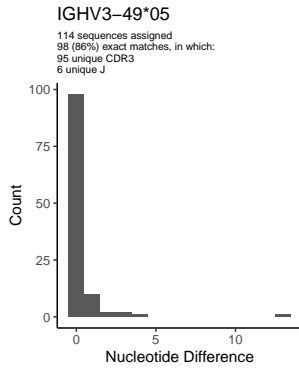
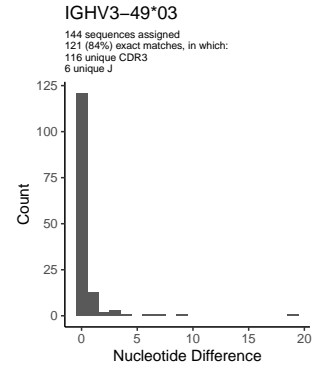
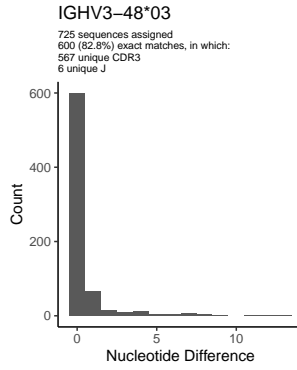
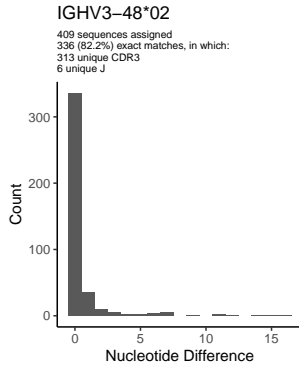


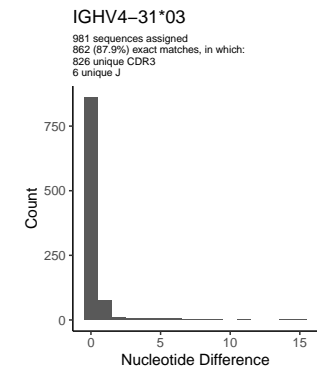
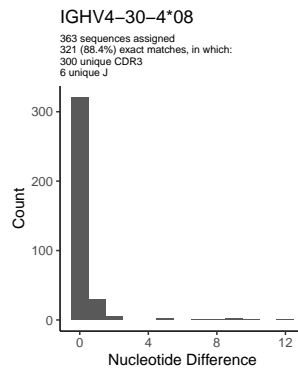
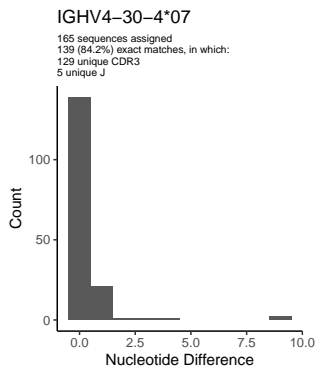
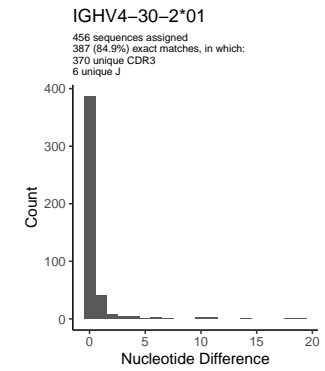
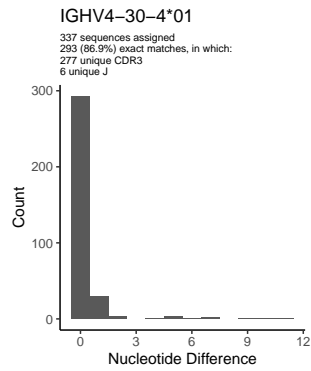
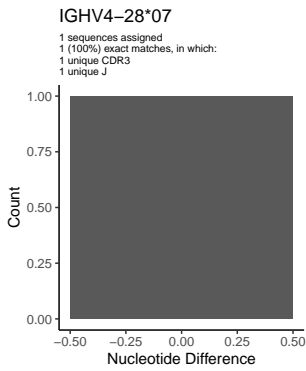
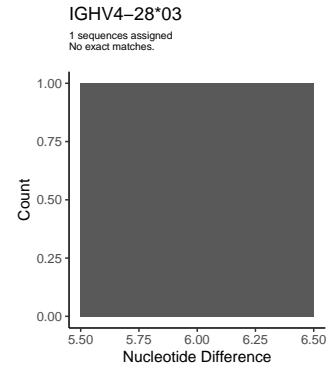
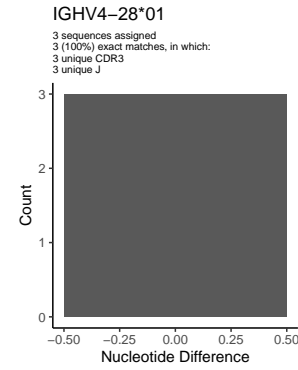
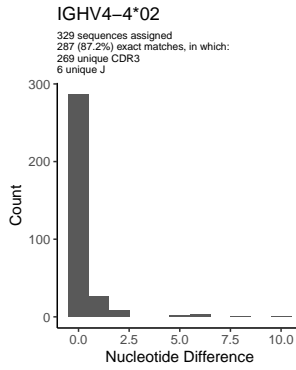
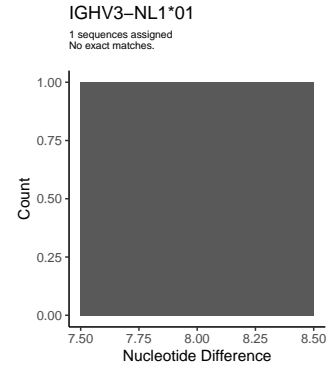
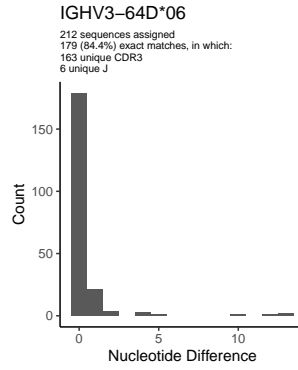
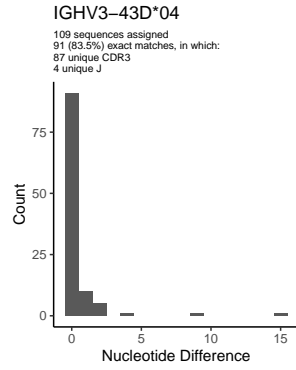
## 2 Variation from germline, in assignments to each allele



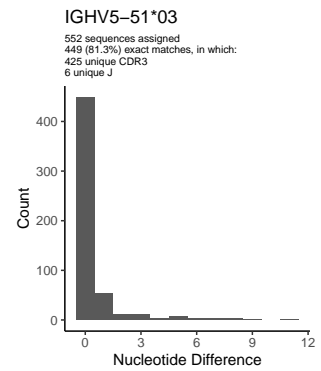
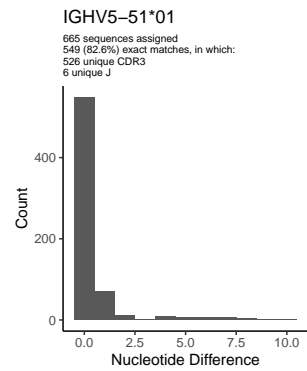
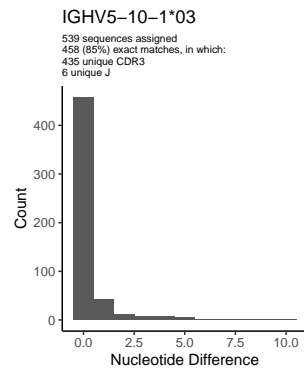
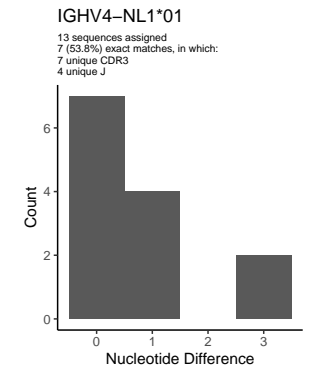
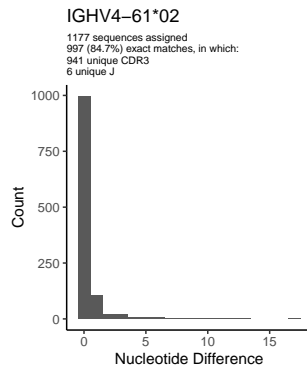
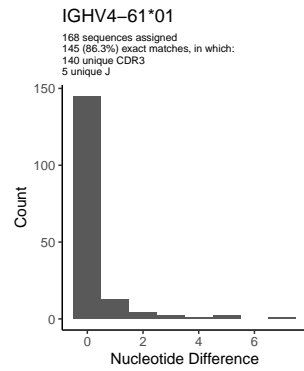
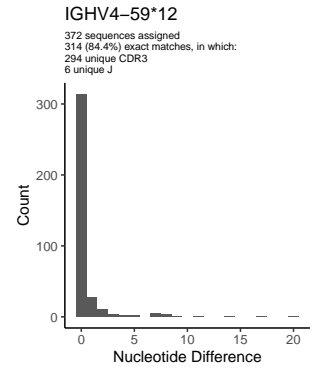
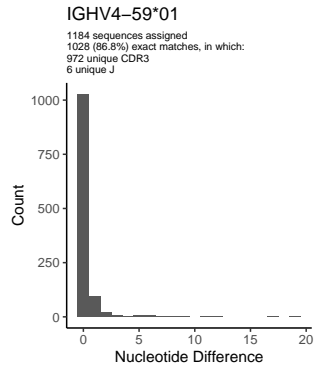
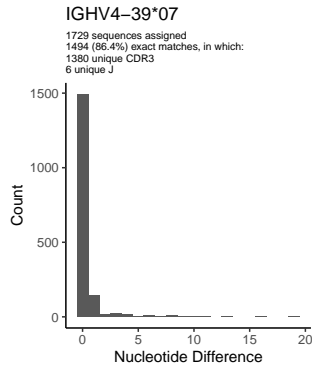
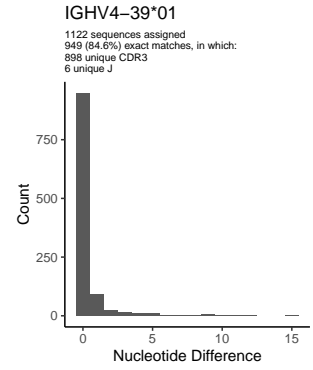
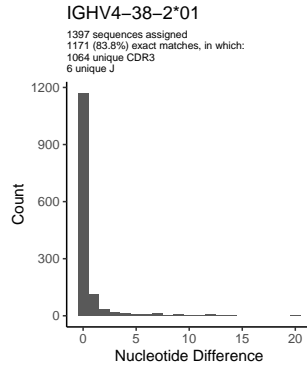
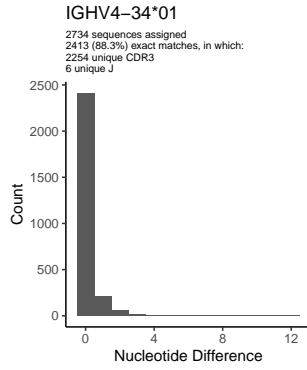


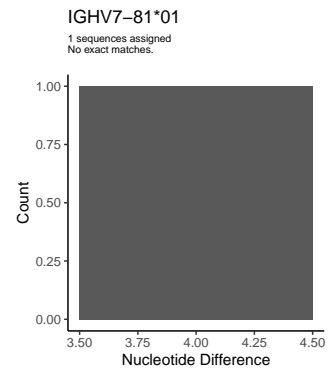
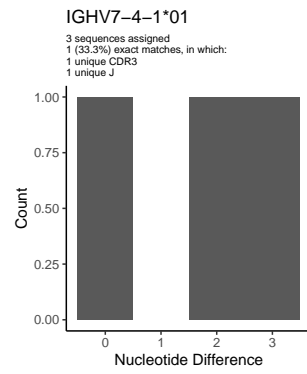
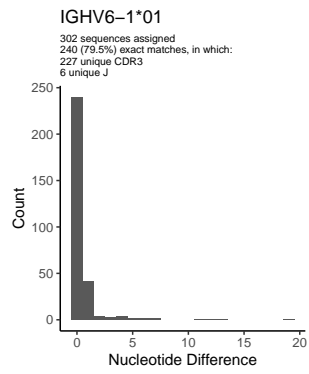




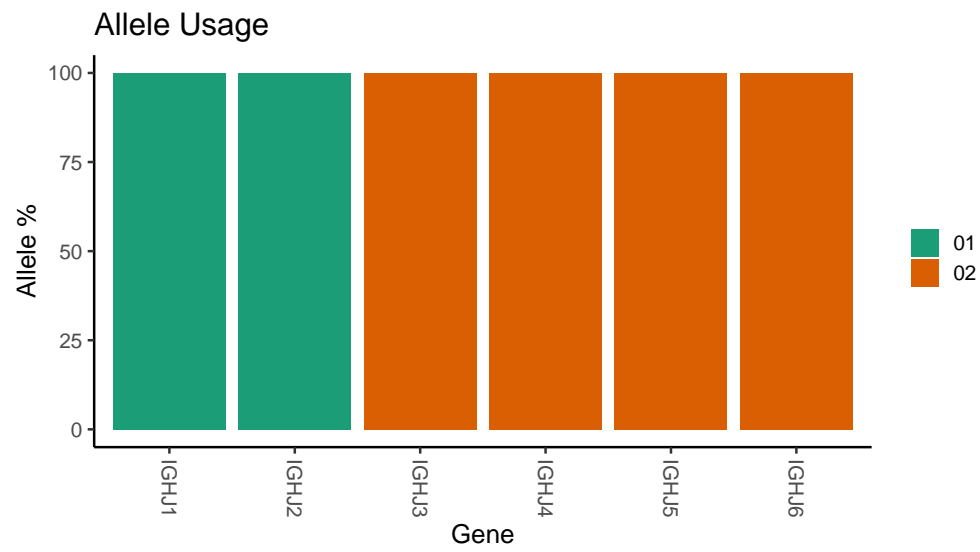








### 3 Allele usage in potential haplotype anchor genes



## 4 Haplotype plots

## 5 Configuration settings

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## Germline reference file: /work/jenkins/PRJEB26509/S60/S60/64/64/f9/9d3651f412791973777886658d7ede/pe.  
##  
## Novel allele file: /work/jenkins/PRJEB26509/S60/S60/64/64/f9/9d3651f412791973777886658d7ede/novel_se  
##  
## Species: Homosapiens  
##  
## Chain: IGHV  
##  
## Segment: V
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