

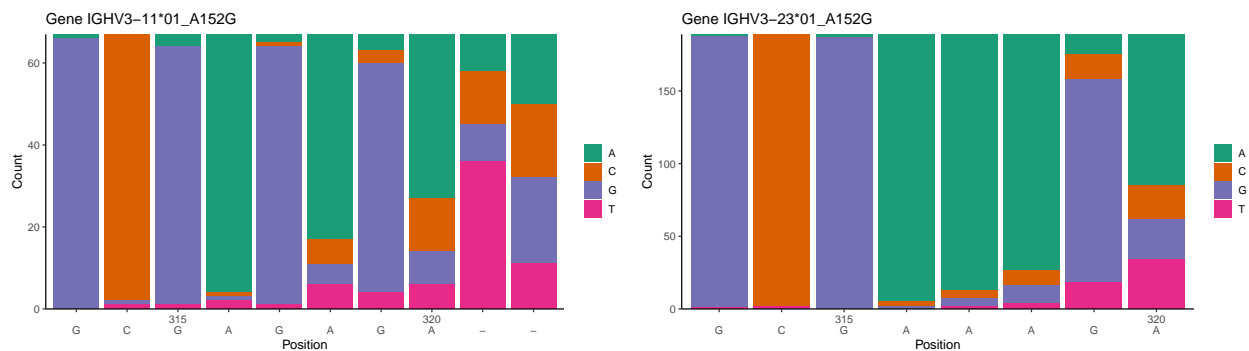
# OGRDBstats Report

## Contents

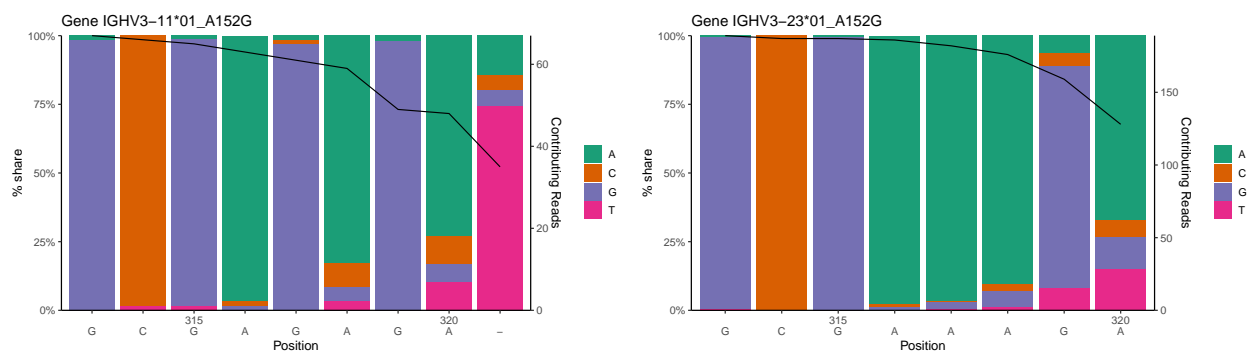
<b>1</b>	<b>Novel sequence analysis</b>	<b>2</b>
1.1	End-nucleotide composition . . . . .	2
1.2	Per-nucleotide consensus where previous nucleotides match the consensus . . . . .	2
1.3	Whole-sequence composition of each assigned read . . . . .	2
1.4	Final three nucleotides: frequency of each observed triplet . . . . .	2
1.5	CDR3 length distribution, in assignments to novel alleles . . . . .	3
<b>2</b>	<b>Variation from germline, in assignments to each allele</b>	<b>4</b>
<b>3</b>	<b>Allele usage in potential haplotype anchor genes</b>	<b>9</b>
<b>4</b>	<b>Haplotype plots</b>	<b>10</b>
<b>5</b>	<b>Configuration settings</b>	<b>11</b>

# 1 Novel sequence analysis

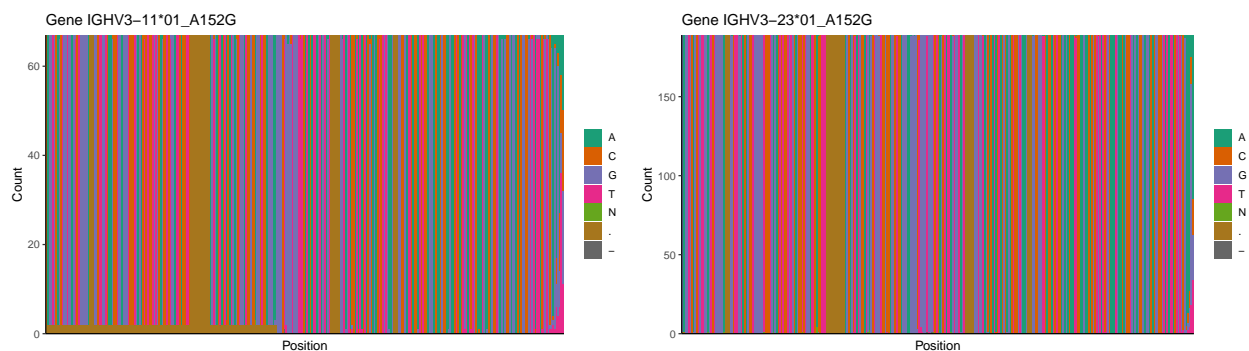
## 1.1 End-nucleotide composition



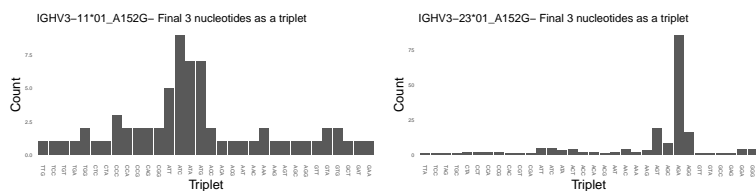
## 1.2 Per-nucleotide consensus where previous nucleotides match the consensus



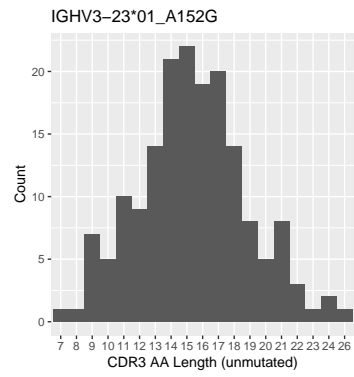
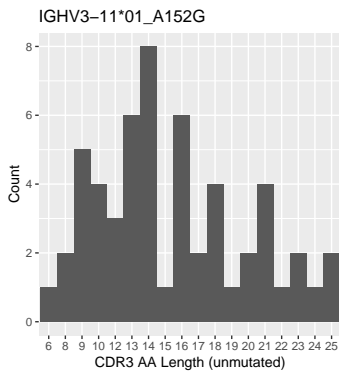
## 1.3 Whole-sequence composition of each assigned read



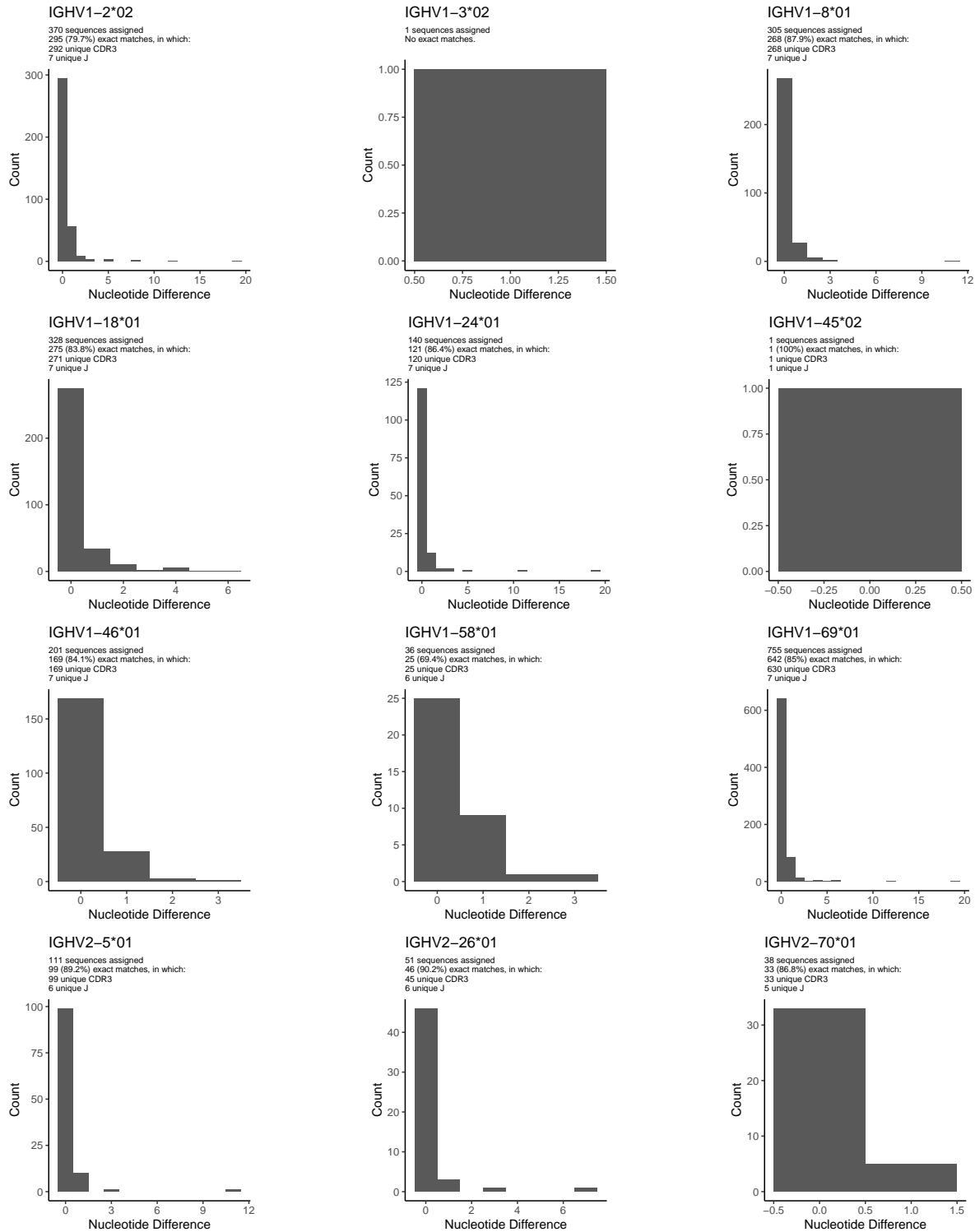
## 1.4 Final three nucleotides: frequency of each observed triplet

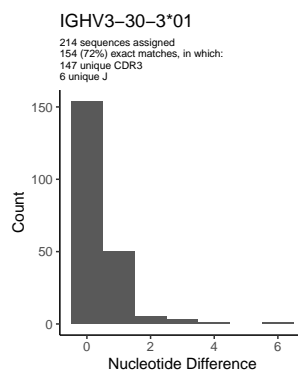
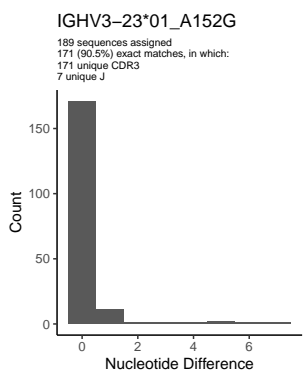
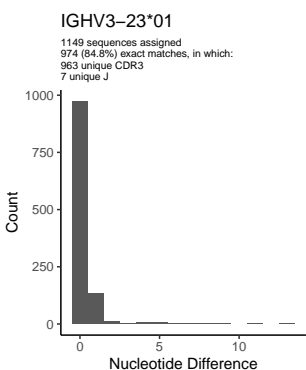
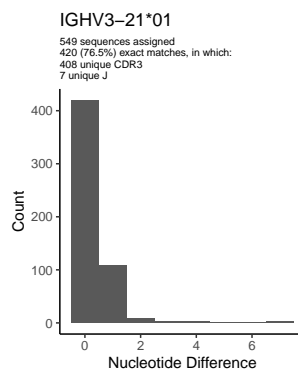
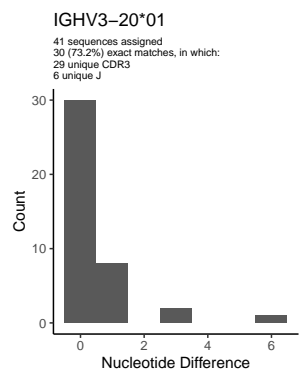
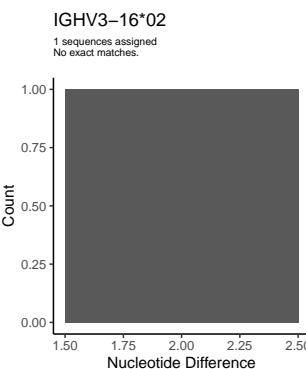
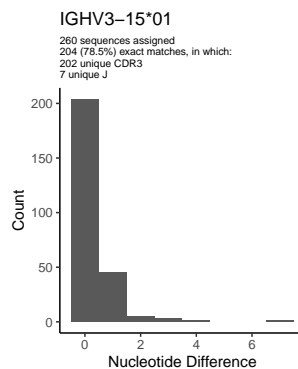
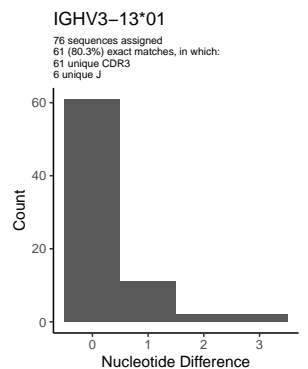
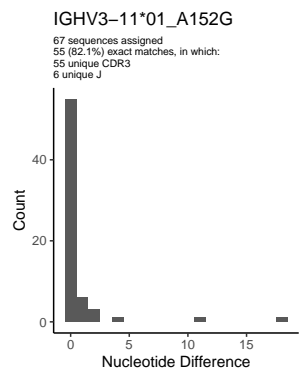
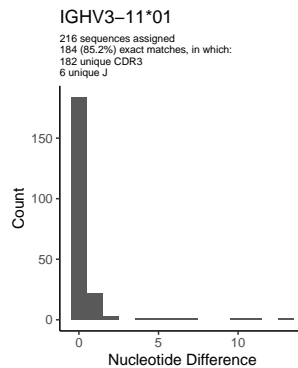
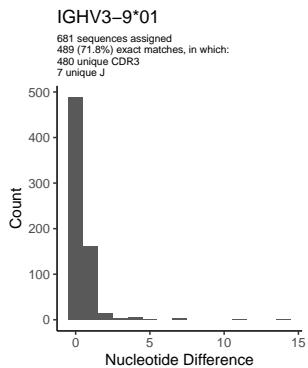
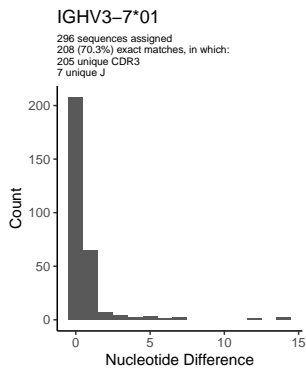


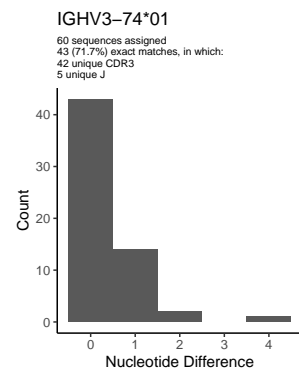
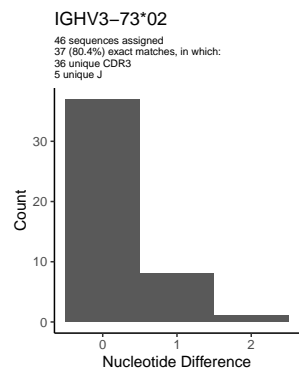
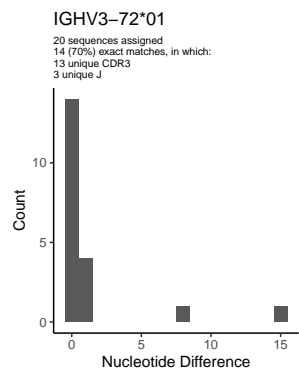
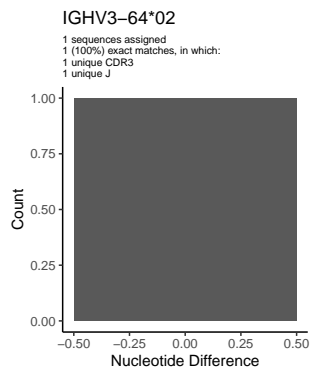
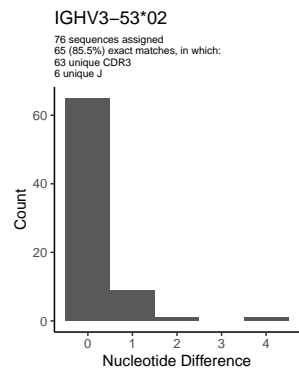
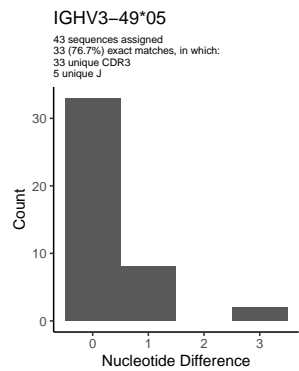
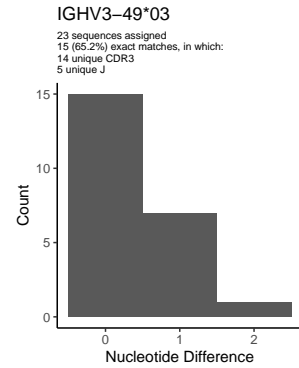
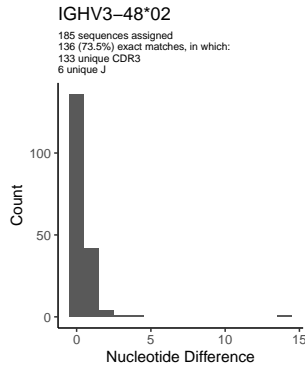
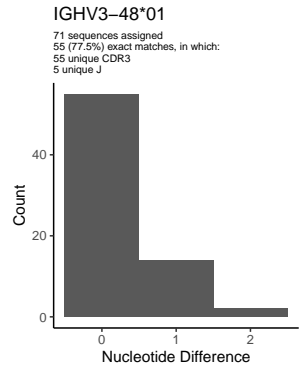
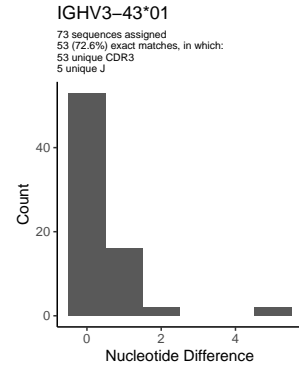
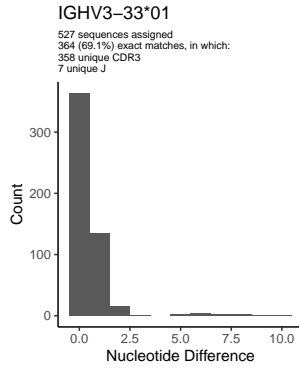
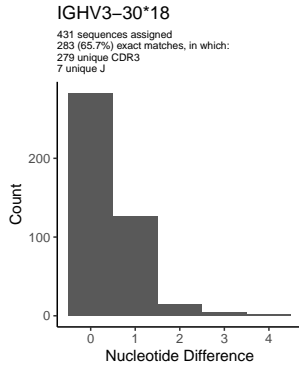
## 1.5 CDR3 length distribution, in assignments to novel alleles

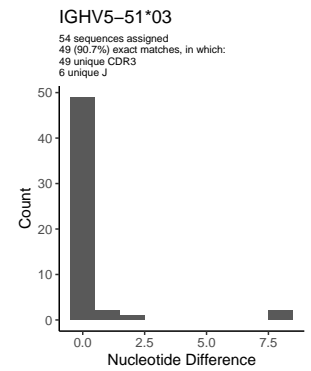
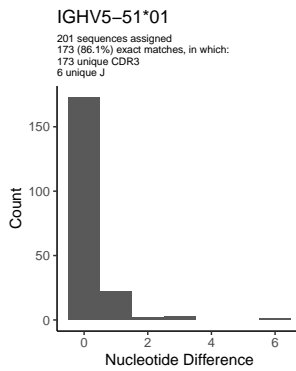
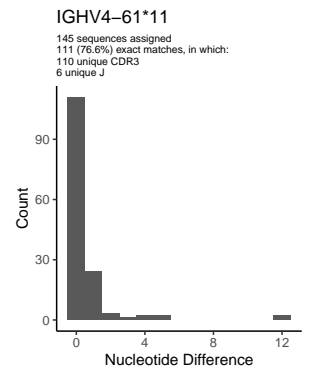
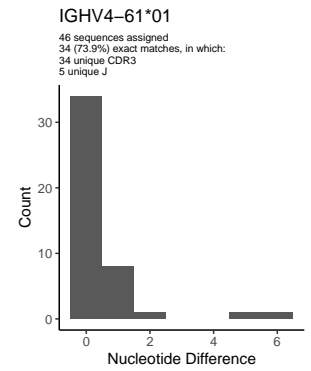
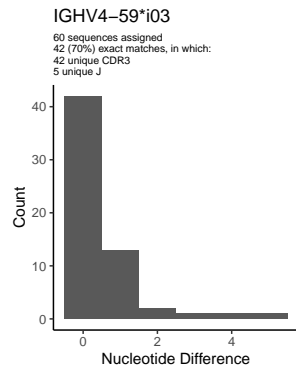
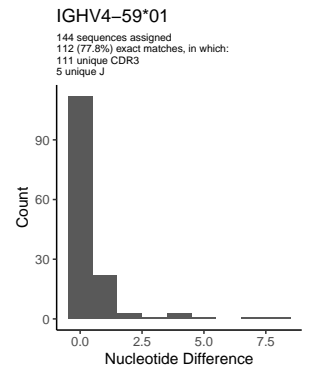
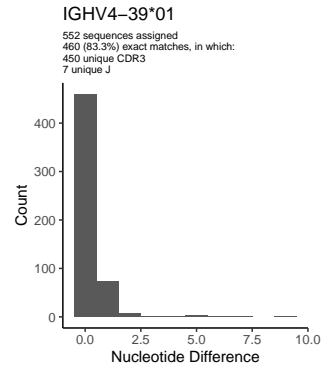
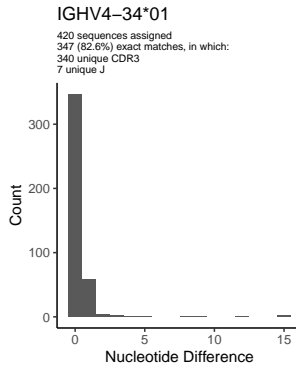
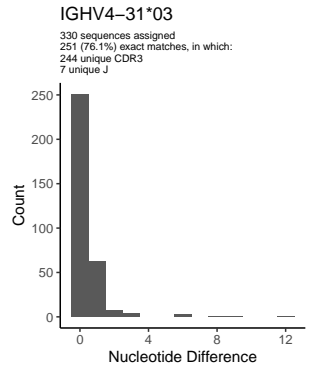
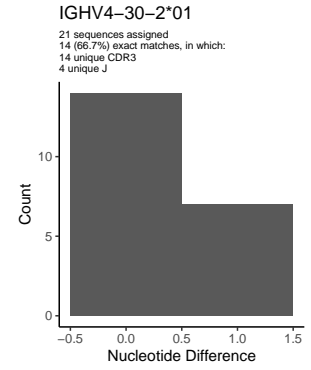
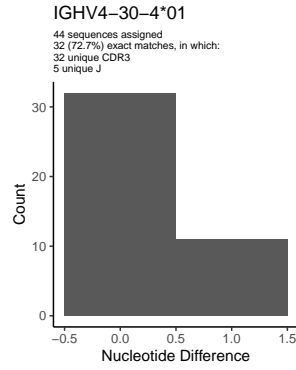
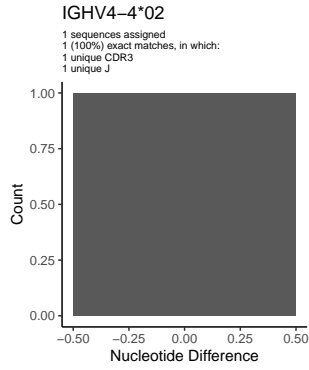


## 2 Variation from germline, in assignments to each allele



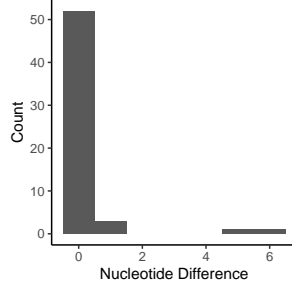






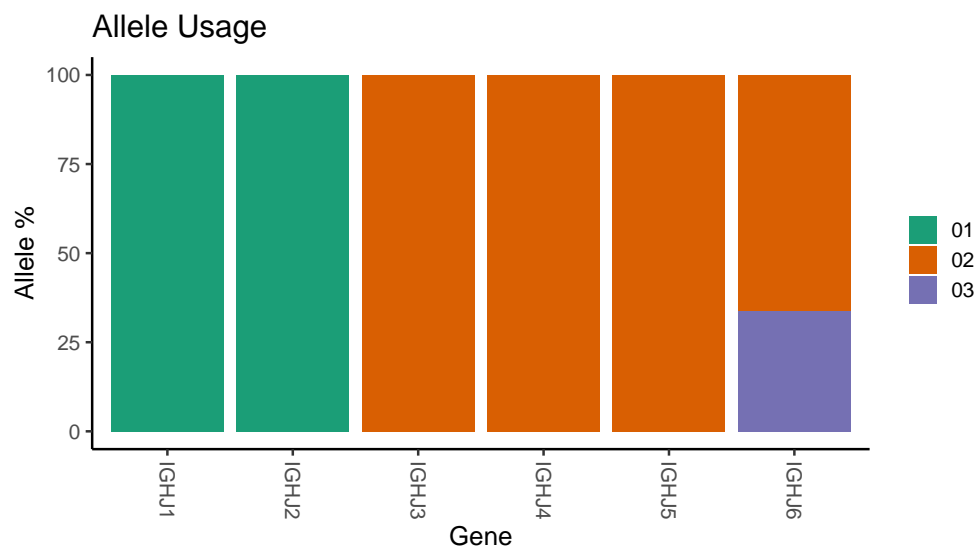
# IGHV6-1\*01

57 sequences assigned  
52 (91.2%) exact matches, in which:  
52 unique CDR3  
6 unique J

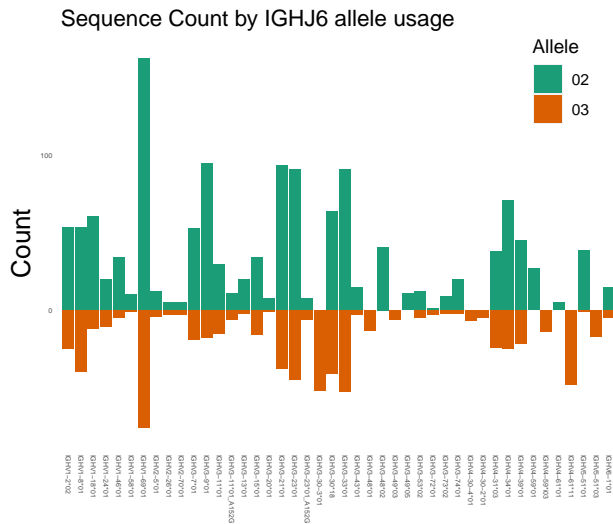




### 3 Allele usage in potential haplotype anchor genes



# 4 Haplotype plots



## 5 Configuration settings

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## Germline reference file: /misc/work/jenkins/PRJEB26509/S36/S36/38/38/6d/5ac8c29dddeb4c1625ad040b4fbcd
##
## Novel allele file: /misc/work/jenkins/PRJEB26509/S36/S36/38/38/6d/5ac8c29dddeb4c1625ad040b4fbcd9/nov
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## warning: non codon aligned gaps were found in novel sequence IGHV3 11 01_A152G
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