

# OGRDBstats Report

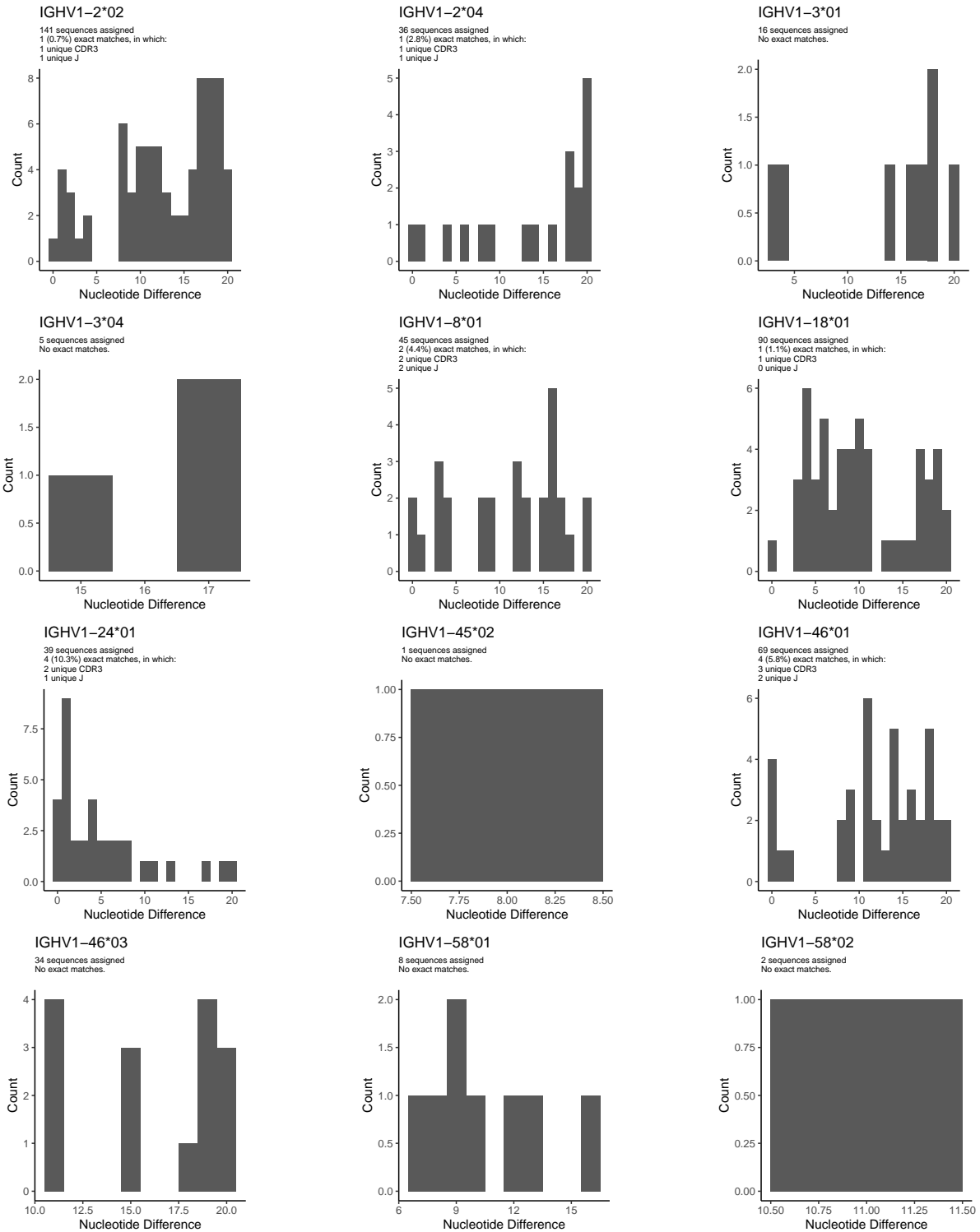
## Contents

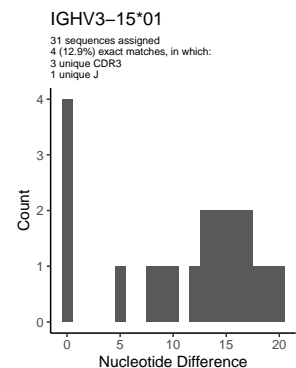
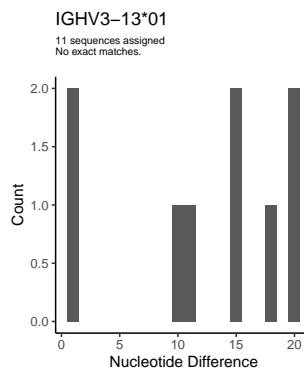
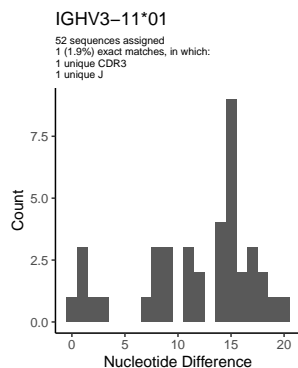
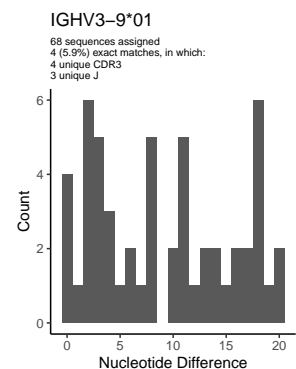
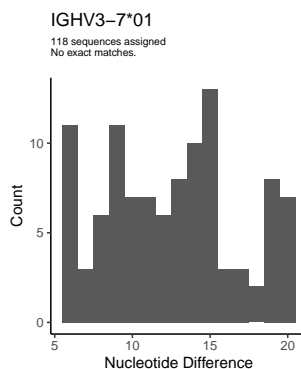
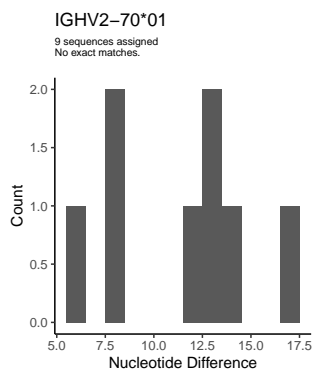
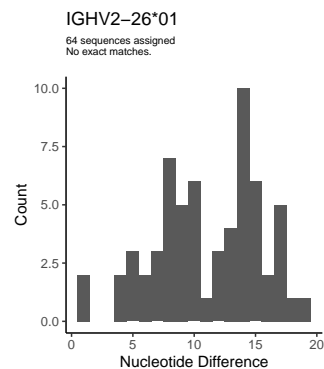
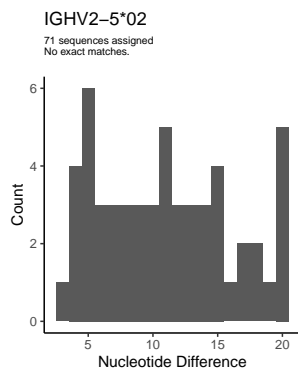
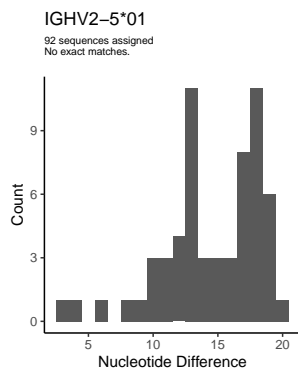
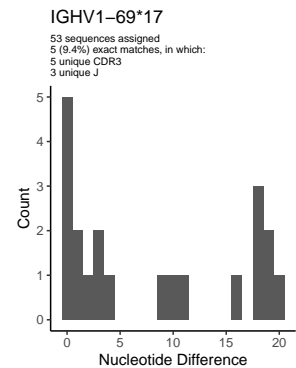
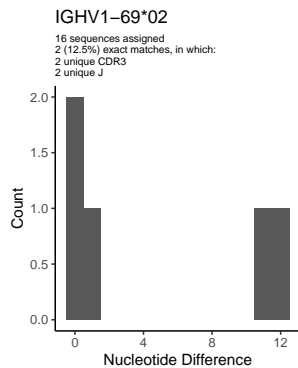
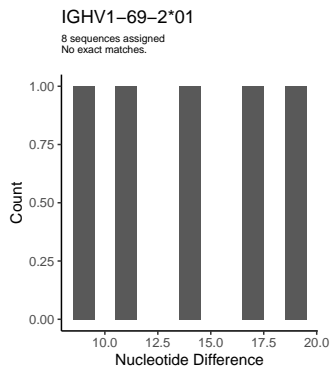
<b>1</b>	<b>Novel sequence analysis</b>	<b>2</b>
1.1	CDR3 length distribution, in assignments to novel alleles . . . . .	2
<b>2</b>	<b>Variation from germline, in assignments to each allele</b>	<b>3</b>
<b>3</b>	<b>Allele usage in potential haplotype anchor genes</b>	<b>8</b>
<b>4</b>	<b>Haplotype plots</b>	<b>9</b>
<b>5</b>	<b>Configuration settings</b>	<b>10</b>

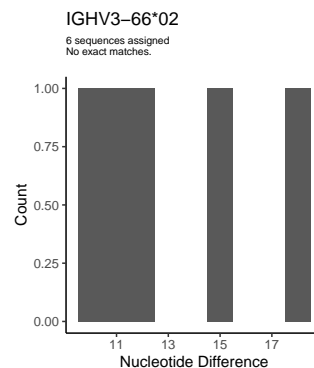
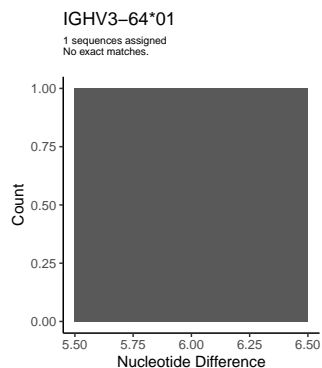
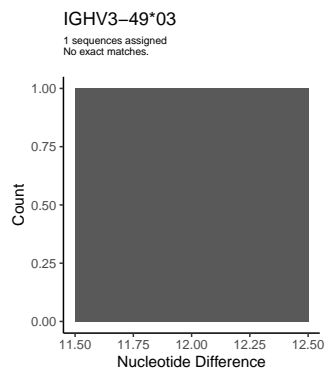
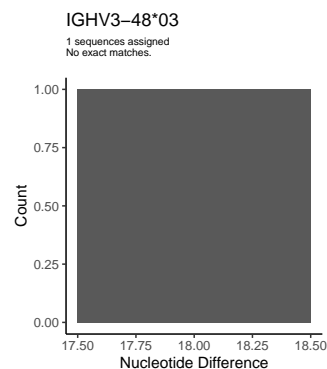
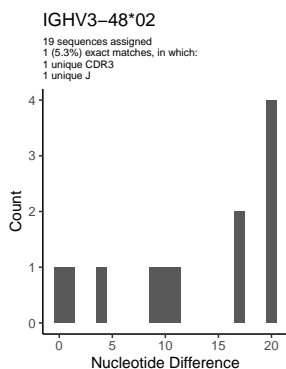
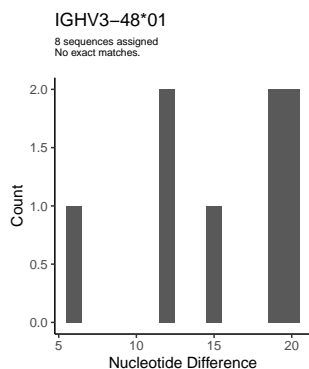
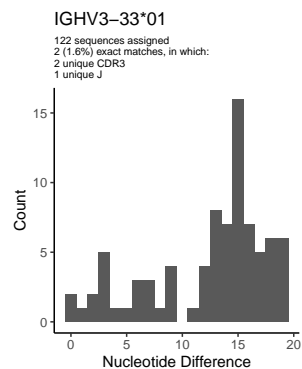
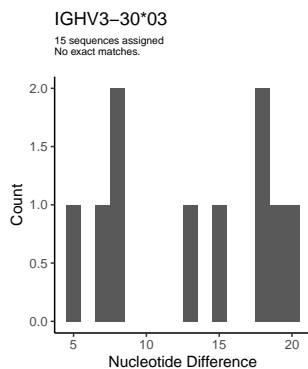
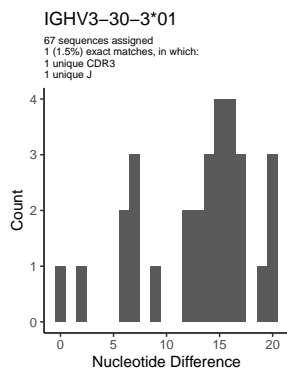
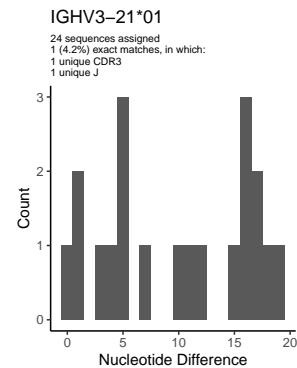
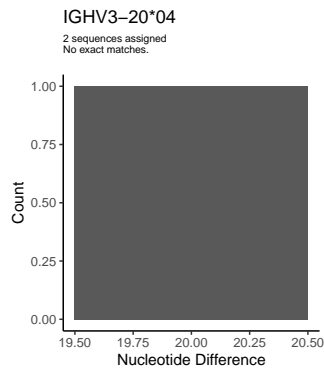
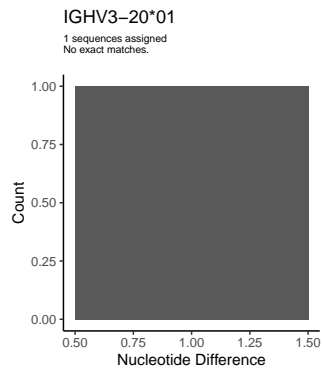
# 1 Novel sequence analysis

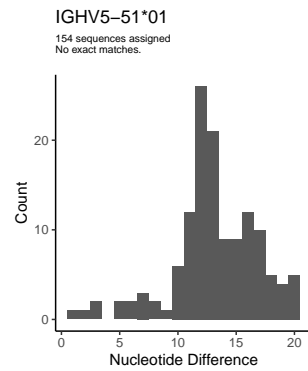
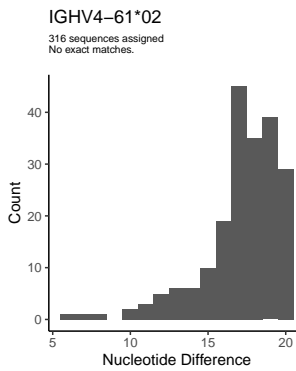
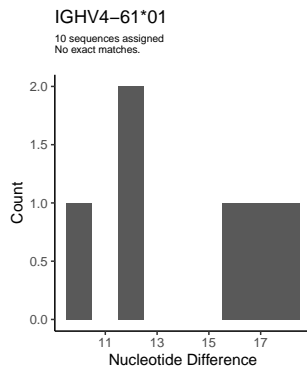
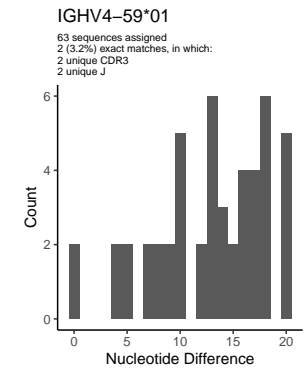
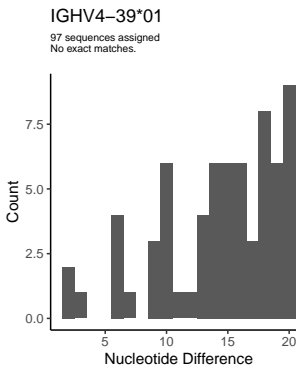
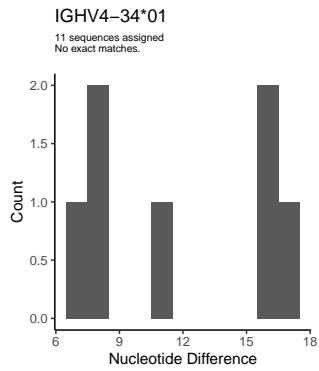
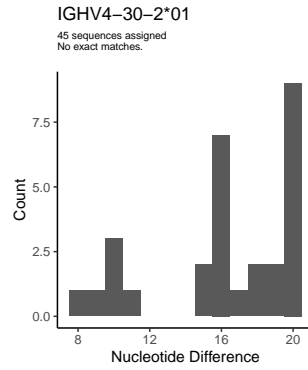
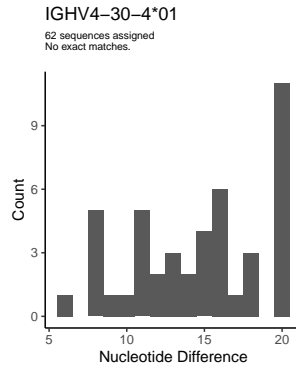
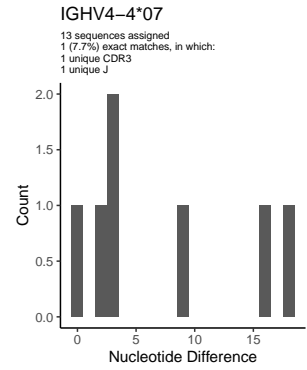
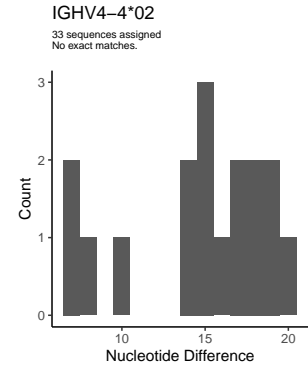
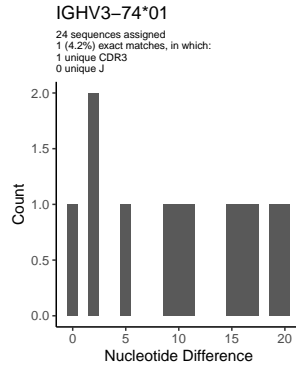
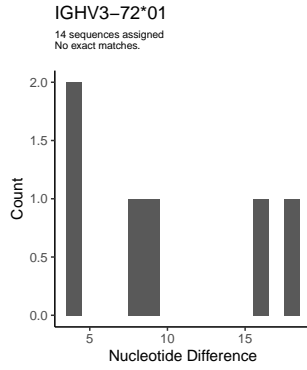
## 1.1 CDR3 length distribution, in assignments to novel alleles

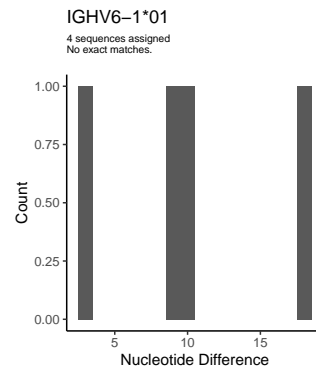
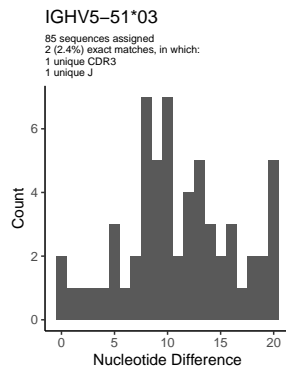
## 2 Variation from germline, in assignments to each allele











### 3 Allele usage in potential haplotype anchor genes





## 4 Haplotype plots

## 5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJNA248475/M3/M3_cln/M3_cln/M3_cln/40/ded1b84f090c69744049ecbff
##
## Germline reference file: /misc/work/jenkins/PRJNA248475/M3/M3_cln/M3_cln/M3_cln/1c/bff8c5ed46038562f
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```