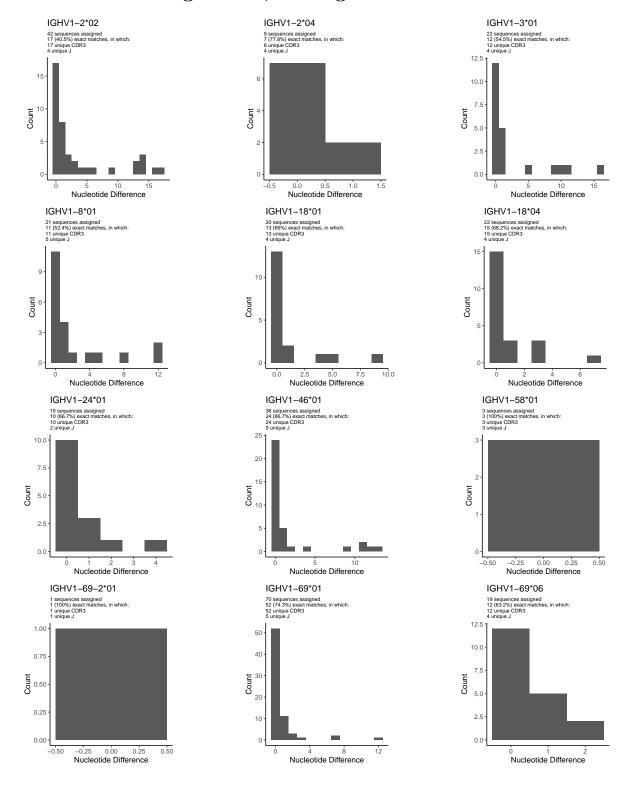
# OGRDBstats Report

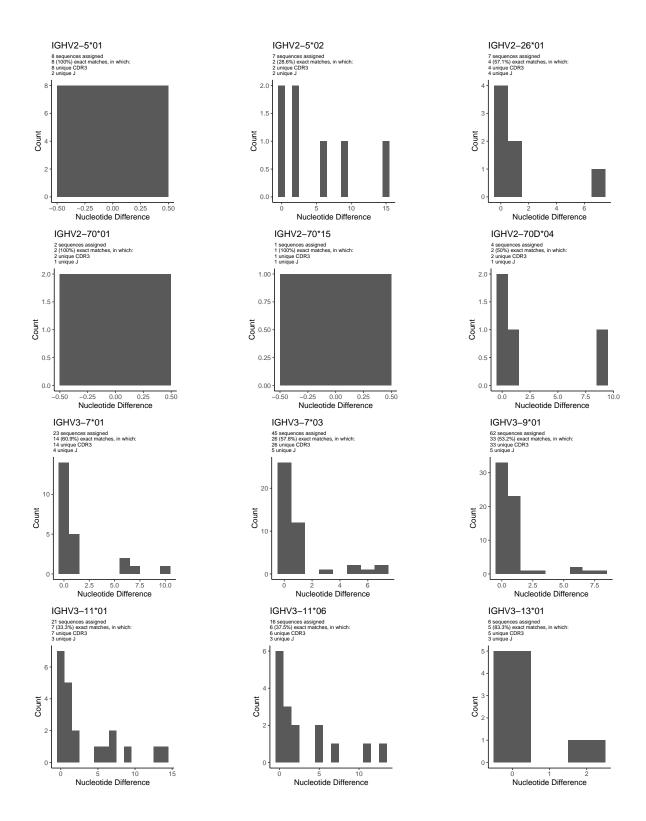
### Contents

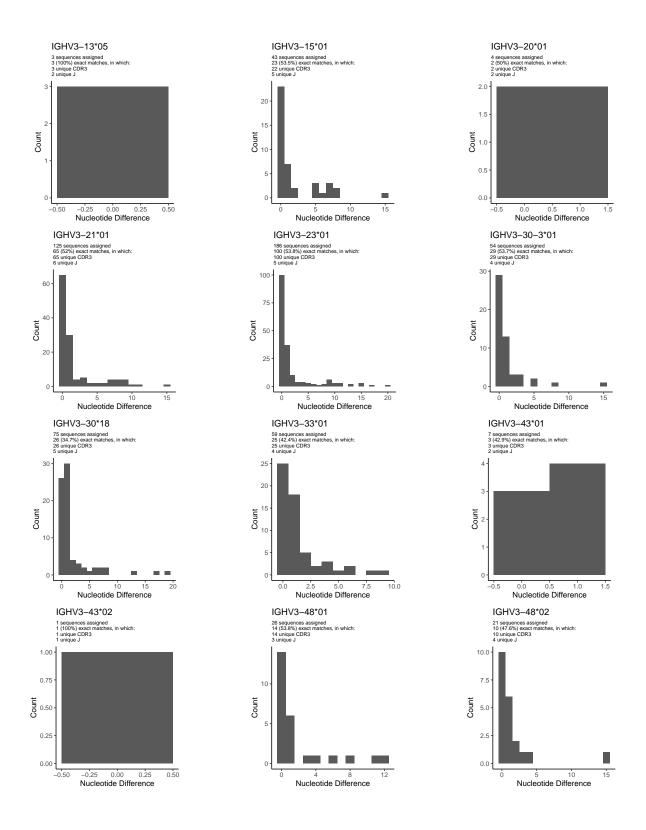
1	Novel sequence analysis 1.1 CDR3 length distribution, in assignments to novel alleles	<b>2</b> 2
2	Variation from germline, in assignments to each allele	3
3	Allele usage in potential haplotype anchor genes	8
4	Haplotype plots	9
5	Configuration settings	10

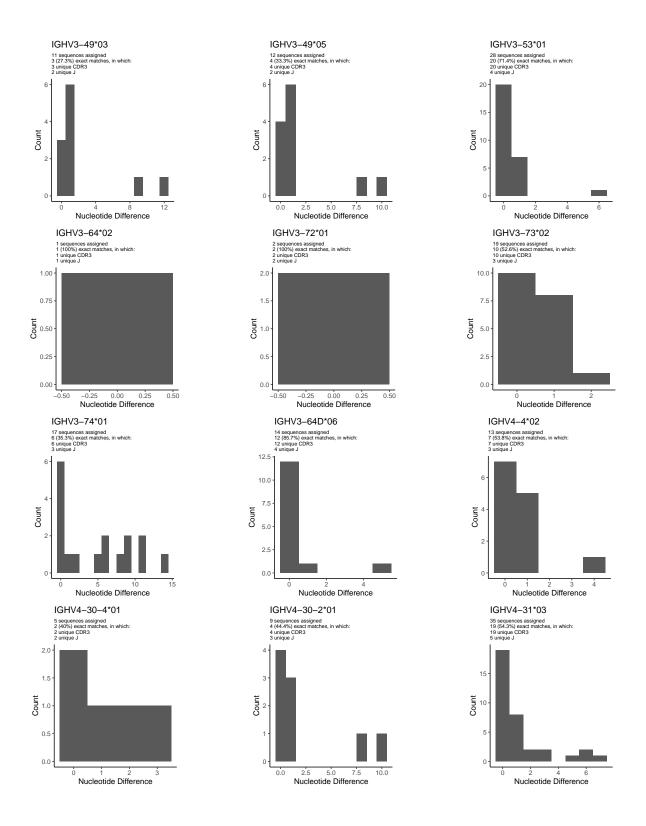
- 1 Novel sequence analysis
- 1.1 CDR3 length distribution, in assignments to novel alleles

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



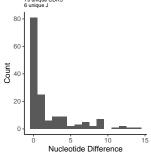






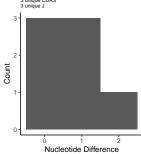


154 sequences assigned 81 (52.6%) exact matches, in which: 79 unique CDR3 6 unique J



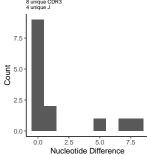
#### IGHV4-61\*01

7 sequences assigned 3 (42.9%) exact matches, in which: 3 unique CDR3 3 unique J



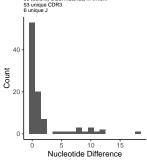
#### IGHV6-1\*01

14 sequences assigned 9 (64.3%) exact matches, in which: 8 unique CDR3 4 unique J



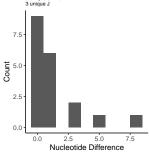
#### IGHV4-39\*01

95 sequences assigned 53 (55.8%) exact matches, in which: 53 unique CDR3 6 unique J



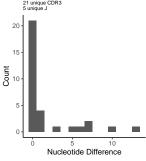
#### IGHV5-10-1\*03

19 sequences assigned 9 (47.4%) exact matches, in which: 9 unique CDR3 3 unique J



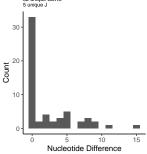
#### IGHV4-59\*01

32 sequences assigned 21 (65.6%) exact matches, in which: 21 unique CDR3 5 unique J



#### IGHV5-51\*01

58 sequences assigned 33 (56.9%) exact matches, in which: 32 unique CDR3 5 unique J



## 3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

### 5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S92/S92/96/00/a60aa4bd82ff57f8a1ac06e6a57801/96_Finale_
##
## Germline reference file: /work/jenkins/PRJEB26509/S92/S92/96/96/dc/5fc41c78c8757c909dba7cfad2c178/re
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning no inferred sequences found.
```