OGRDBstats Report

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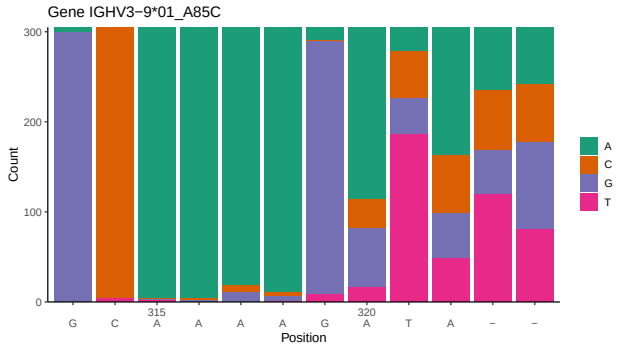
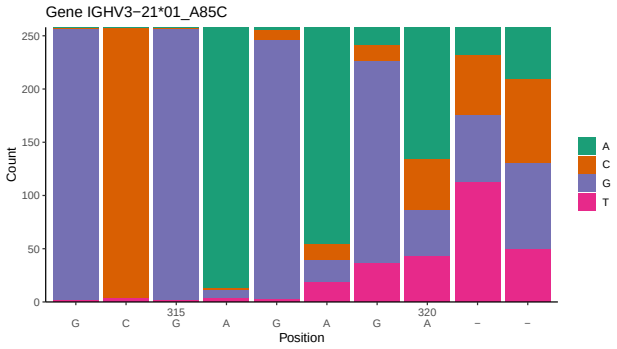
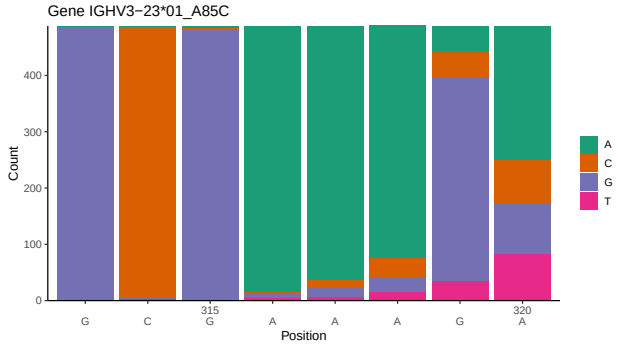
1 Novel sequence analysis

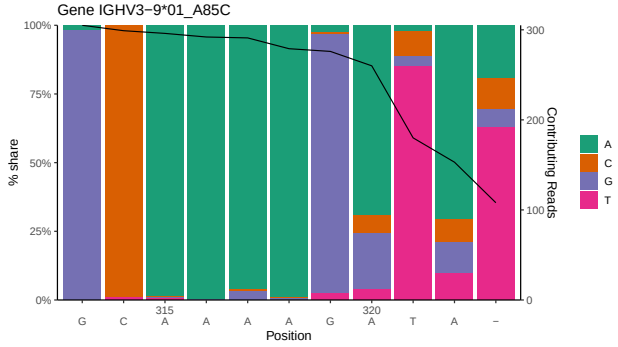
1.1 End-nucleotide composition

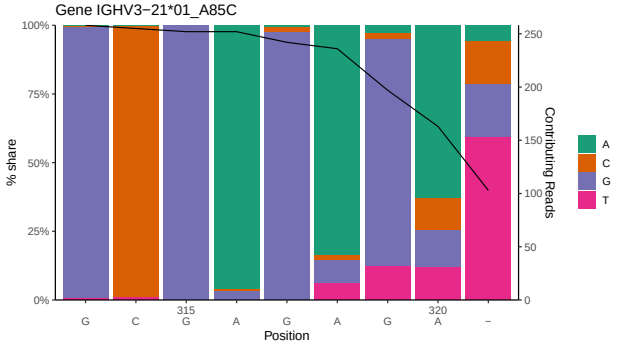


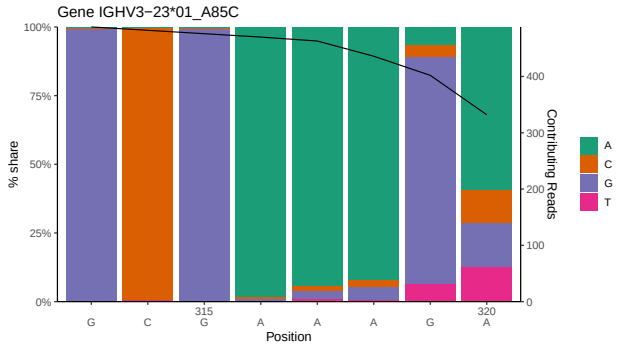




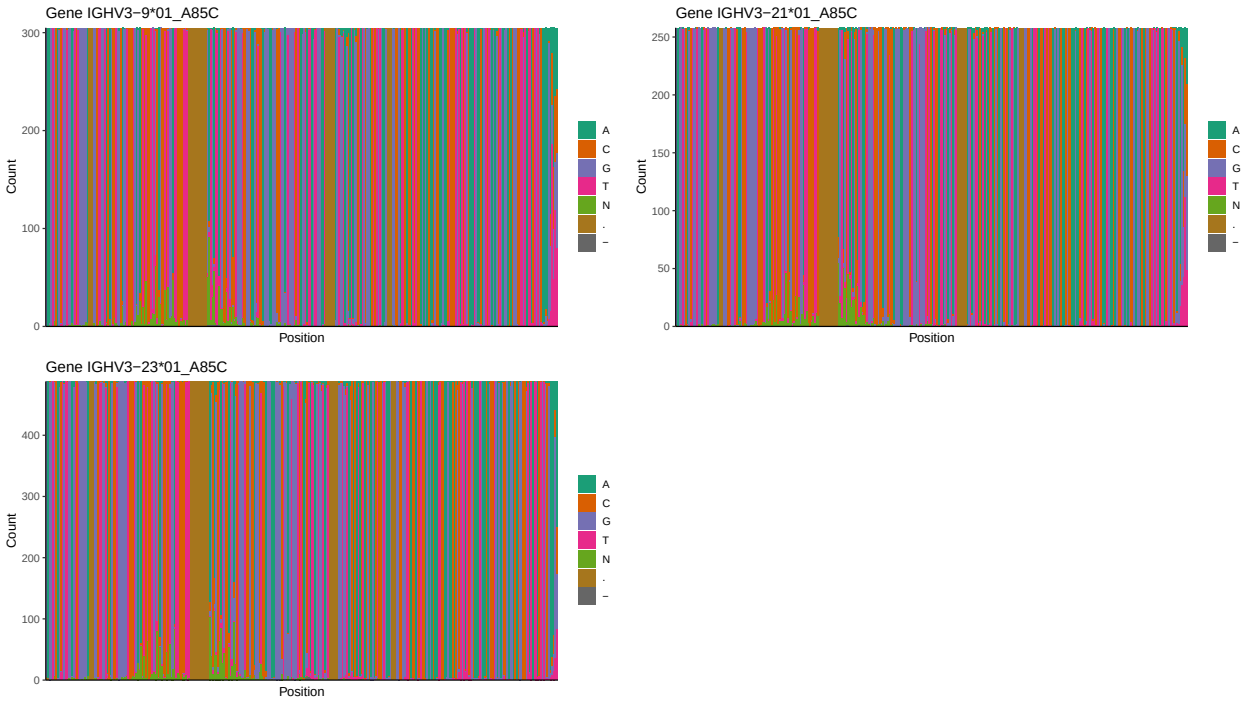
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



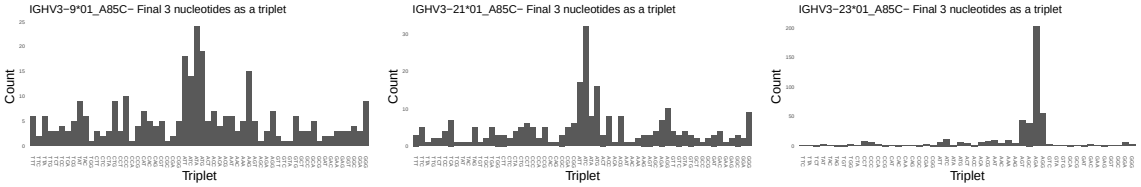




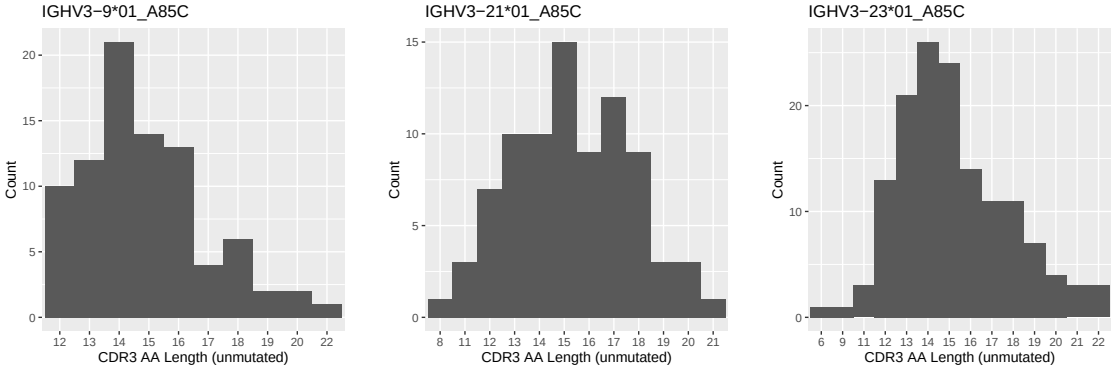
1.3 Whole-sequence composition of each assigned read



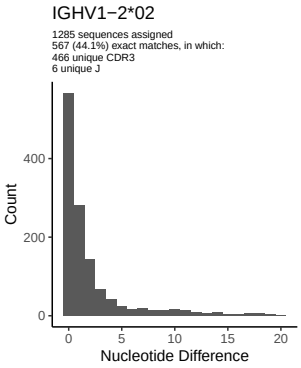
1.4 Final three nucleotides: frequency of each observed triplet

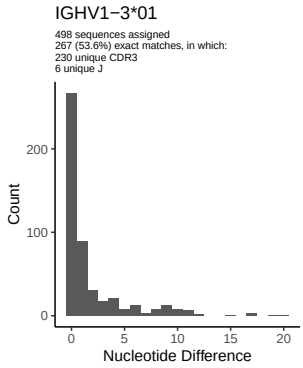


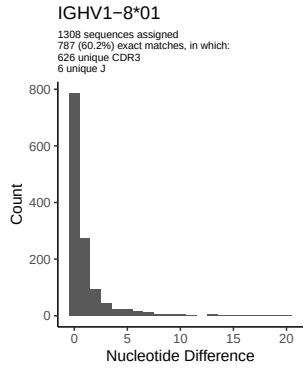
1.5 CDR3 length distribution, in assignments to novel alleles

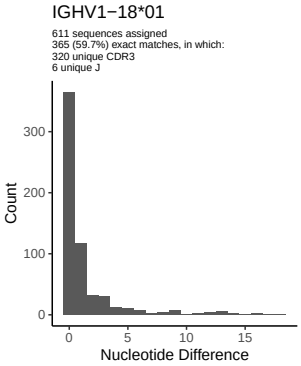


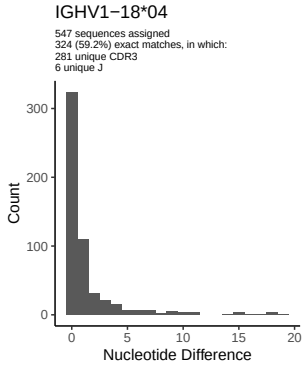
2 Variation from germline, in assignments to each allele

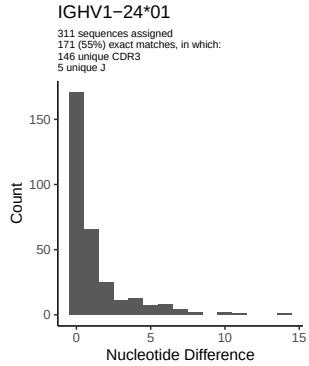


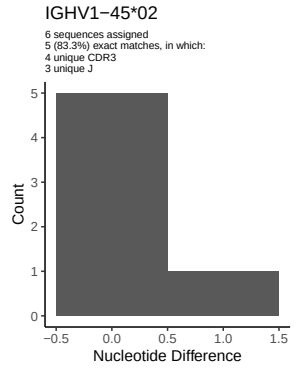


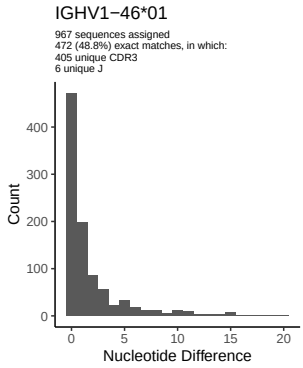


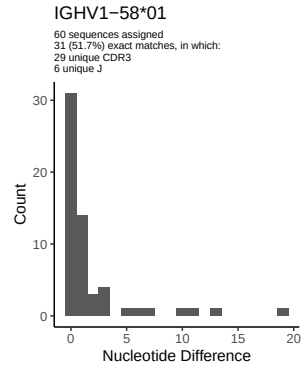


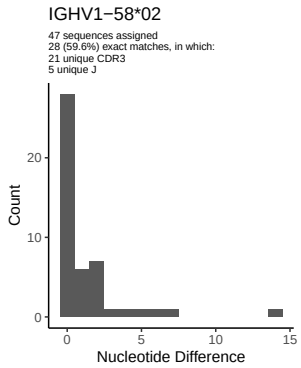


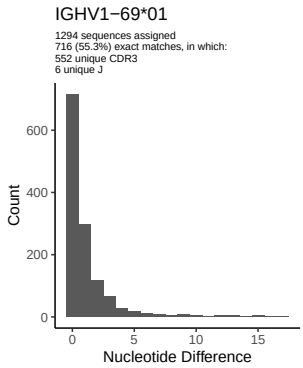


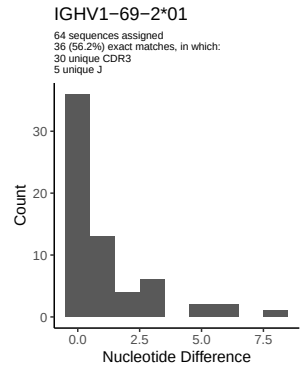


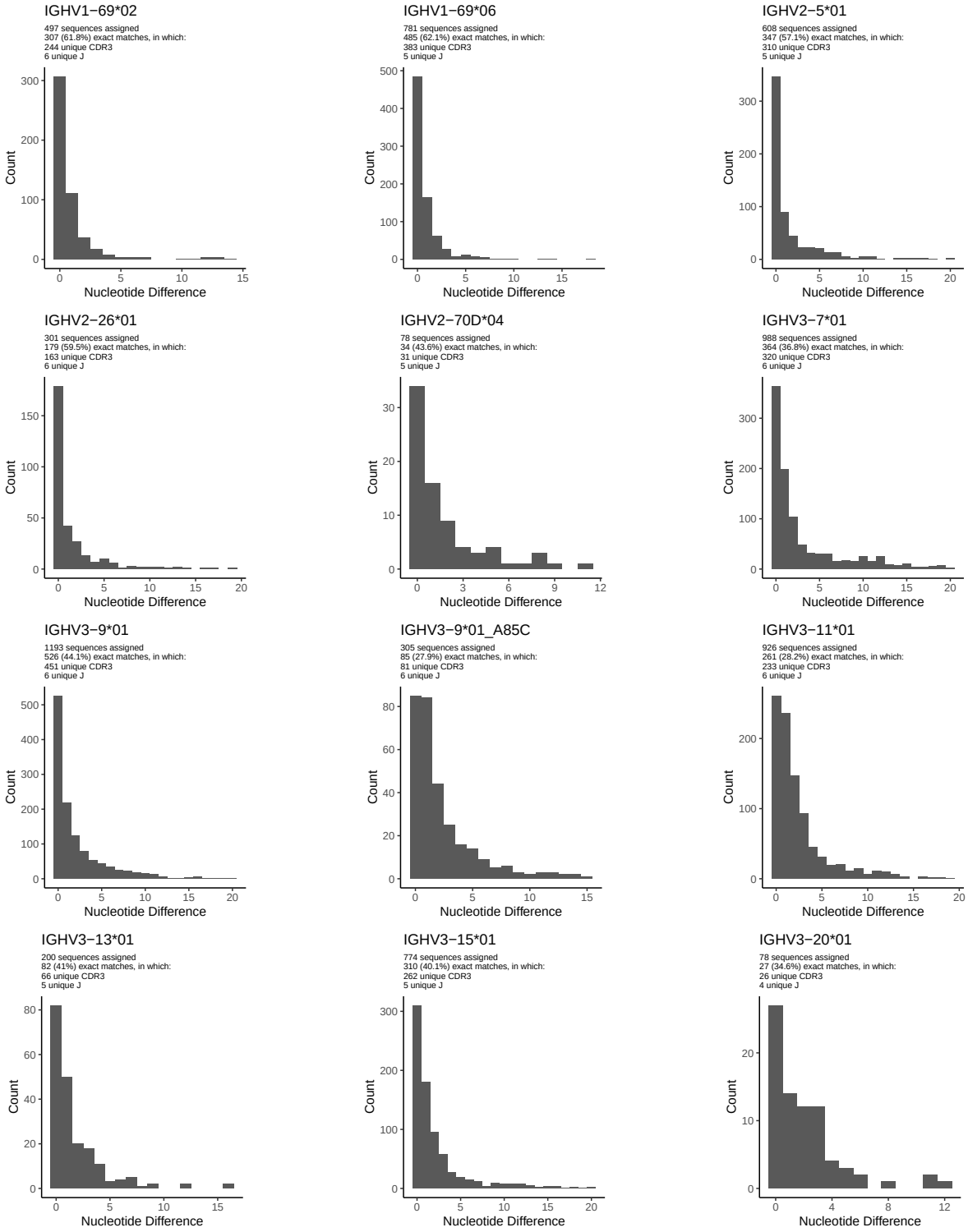


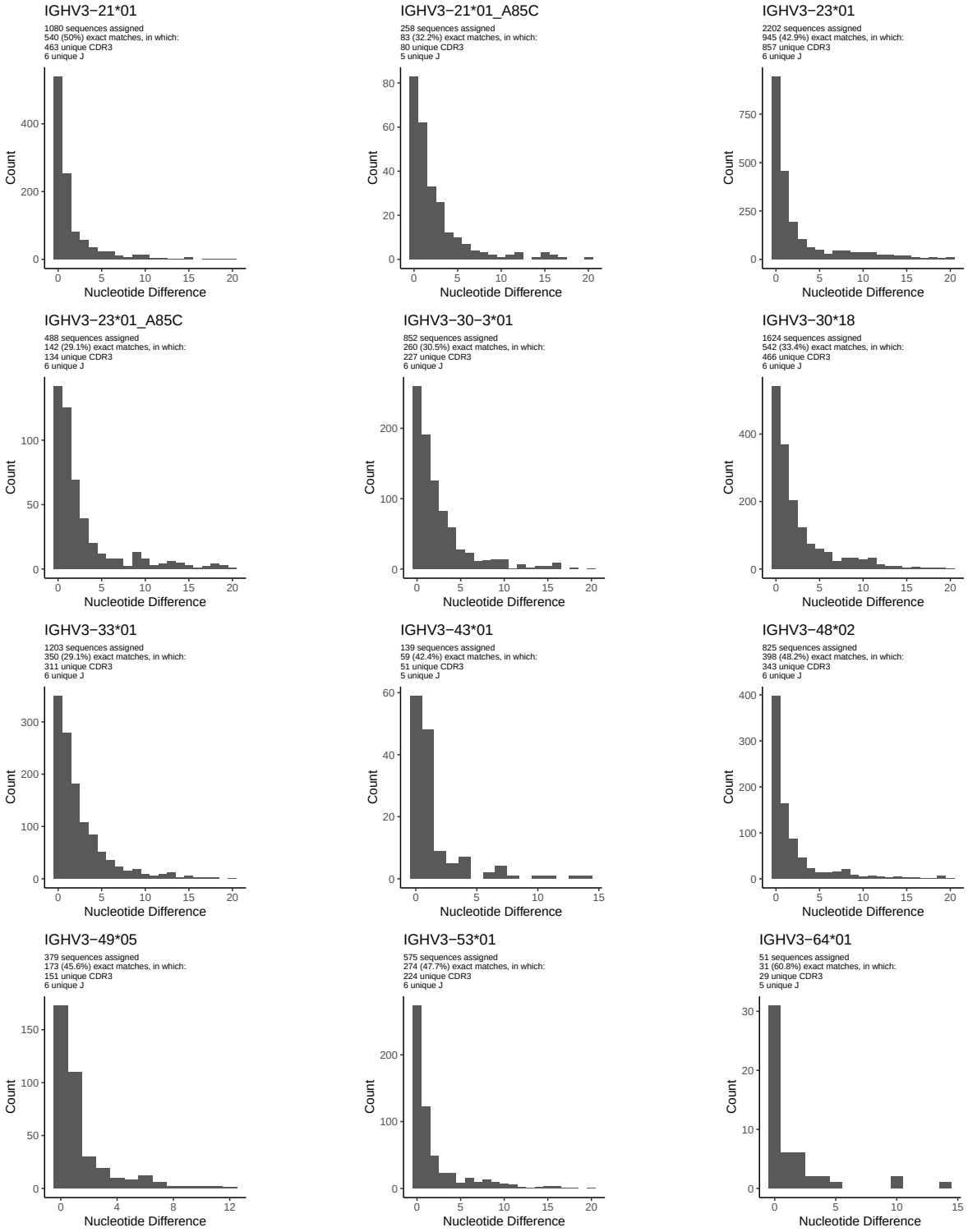


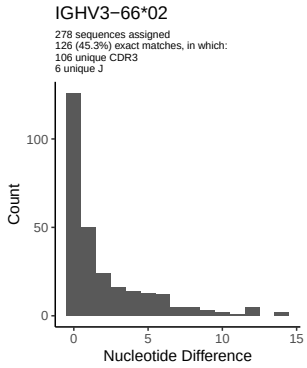


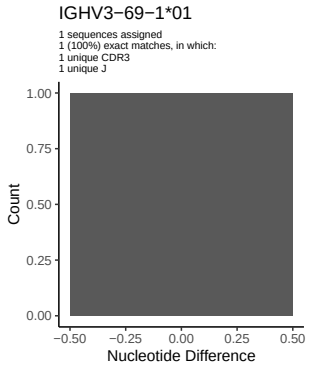


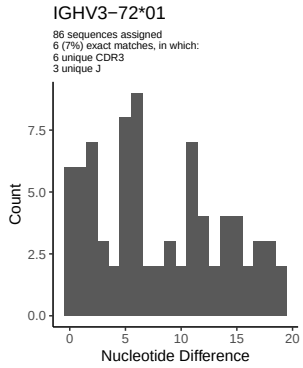


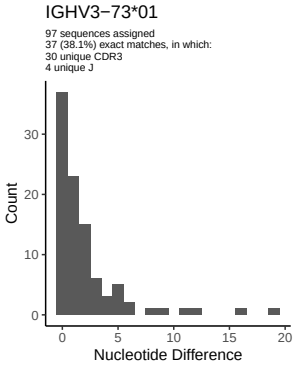

IGHV1−69*02
497 sequences assigned
307 (61.8%) exact matches, in which:
244 unique CDR3
6 unique J
IGHV1−69*06
781 sequences assigned
485 (62.1%) exact matches, in which:
383 unique CDR3
5 unique J
IGHV2−5*01
608 sequences assigned
347 (57.1%) exact matches, in which:
310 unique CDR3
5 unique J
IGHV2−26*01
301 sequences assigned
179 (59.5%) exact matches, in which:
163 unique CDR3
6 unique J
IGHV2−70D*04
78 sequences assigned
34 (43.6%) exact matches, in which:
31 unique CDR3
5 unique J
IGHV3−7*01
988 sequences assigned
364 (36.8%) exact matches, in which:
320 unique CDR3
6 unique J
IGHV3−9*01
1193 sequences assigned
526 (44.1%) exact matches, in which:
451 unique CDR3
6 unique J
IGHV3−9*01_A85C
305 sequences assigned
85 (27.9%) exact matches, in which:
81 unique CDR3
6 unique J
IGHV3−11*01
926 sequences assigned
261 (28.2%) exact matches, in which:
233 unique CDR3
6 unique J
IGHV3−13*01
200 sequences assigned
82 (41%) exact matches, in which:
66 unique CDR3
5 unique J
IGHV3−15*01
774 sequences assigned
310 (40.1%) exact matches, in which:
262 unique CDR3
5 unique J
IGHV3−20*01
78 sequences assigned
27 (34.6%) exact matches, in which:
26 unique CDR3
4 unique J
Count
Nucleotide Difference

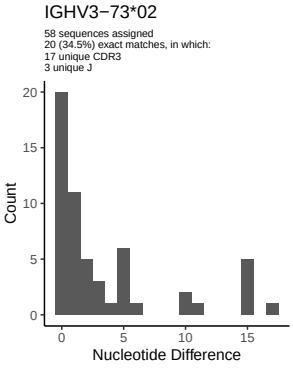

IGHV3−21*01
1080 sequences assigned
540 (50%) exact matches, in which:
463 unique CDR3
6 unique J
IGHV3−21*01_A85C
258 sequences assigned
83 (32.2%) exact matches, in which:
80 unique CDR3
5 unique J
IGHV3−23*01
2202 sequences assigned
945 (42.9%) exact matches, in which:
857 unique CDR3
6 unique J
IGHV3−23*01_A85C
488 sequences assigned
142 (29.1%) exact matches, in which:
134 unique CDR3
6 unique J
IGHV3−30−3*01
852 sequences assigned
260 (30.5%) exact matches, in which:
227 unique CDR3
6 unique J
IGHV3−30*18
1624 sequences assigned
542 (33.4%) exact matches, in which:
466 unique CDR3
6 unique J
IGHV3−33*01
1203 sequences assigned
350 (29.1%) exact matches, in which:
311 unique CDR3
6 unique J
IGHV3−43*01
139 sequences assigned
59 (42.4%) exact matches, in which:
51 unique CDR3
5 unique J
IGHV3−48*02
825 sequences assigned
398 (48.2%) exact matches, in which:
343 unique CDR3
6 unique J
IGHV3−49*05
379 sequences assigned
173 (45.6%) exact matches, in which:
151 unique CDR3
6 unique J
IGHV3−53*01
575 sequences assigned
274 (47.7%) exact matches, in which:
224 unique CDR3
6 unique J
IGHV3−64*01
51 sequences assigned
31 (60.8%) exact matches, in which:
29 unique CDR3
5 unique J
Count
Nucleotide Difference

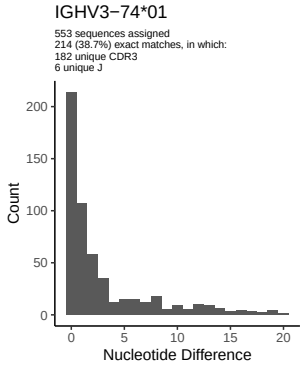

IGHV3−66*02
278 sequences assigned
126 (45.3%) exact matches, in which:
106 unique CDR3
6 unique J
Count
Nucleotide Difference

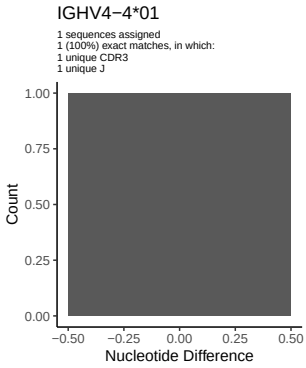

IGHV3−69−1*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

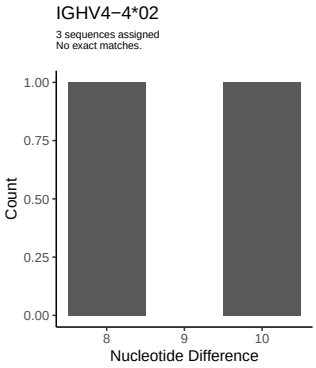

IGHV3−72*01
86 sequences assigned
6 (7%) exact matches, in which:
6 unique CDR3
3 unique J
Count
Nucleotide Difference

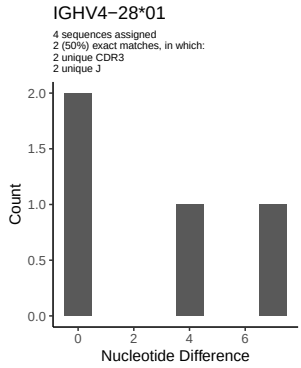

IGHV3−73*01
97 sequences assigned
37 (38.1%) exact matches, in which:
30 unique CDR3
4 unique J
Count
Nucleotide Difference

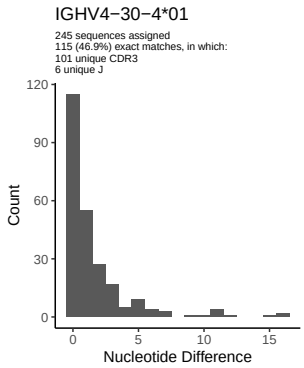

IGHV3−73*02
58 sequences assigned
20 (34.5%) exact matches, in which:
17 unique CDR3
3 unique J
Count
Nucleotide Difference

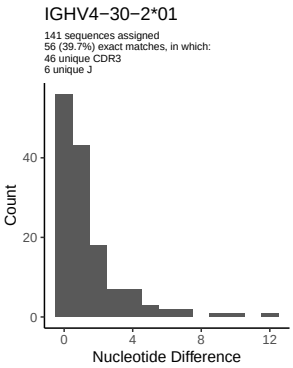

IGHV3−74*01
553 sequences assigned
214 (38.7%) exact matches, in which:
182 unique CDR3
6 unique J
Count
Nucleotide Difference

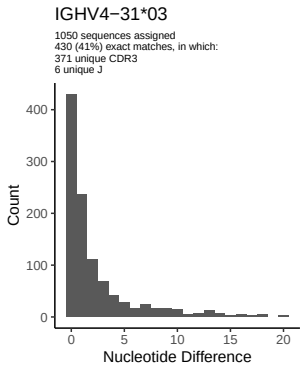

IGHV4−4*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

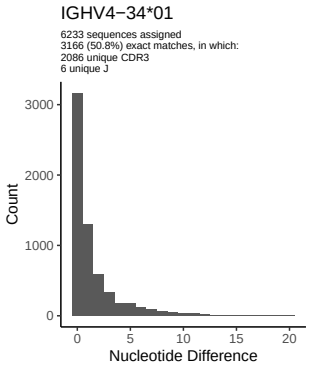

IGHV4−4*02
3 sequences assigned
No exact matches.
Count
Nucleotide Difference

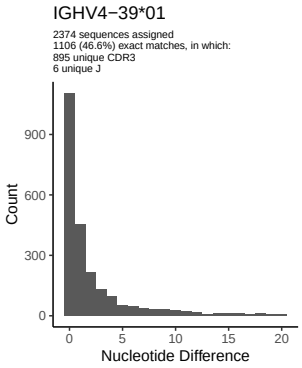

IGHV4−28*01
4 sequences assigned
2 (50%) exact matches, in which:
2 unique CDR3
2 unique J
Count
Nucleotide Difference

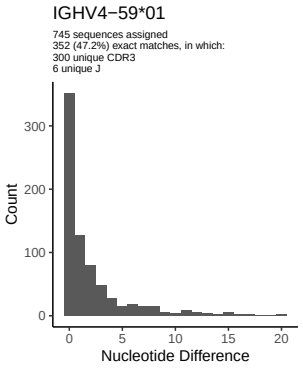

IGHV4−30−4*01
245 sequences assigned
115 (46.9%) exact matches, in which:
101 unique CDR3
6 unique J
Count
Nucleotide Difference

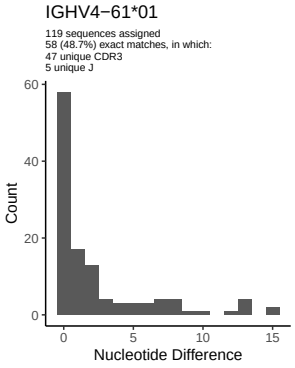

IGHV4−30−2*01
141 sequences assigned
56 (39.7%) exact matches, in which:
46 unique CDR3
6 unique J
Count
Nucleotide Difference

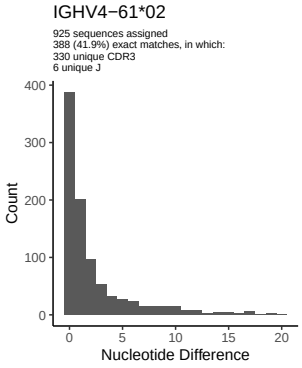

IGHV4−31*03
1050 sequences assigned
430 (41%) exact matches, in which:
371 unique CDR3
6 unique J
Count
Nucleotide Difference

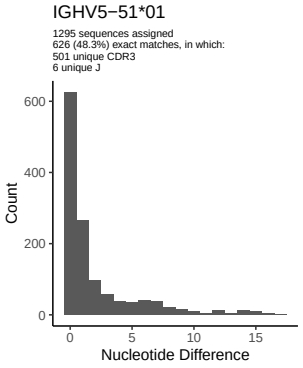

IGHV4−34*01
6233 sequences assigned
3166 (50.8%) exact matches, in which:
2086 unique CDR3
6 unique J
Count
Nucleotide Difference

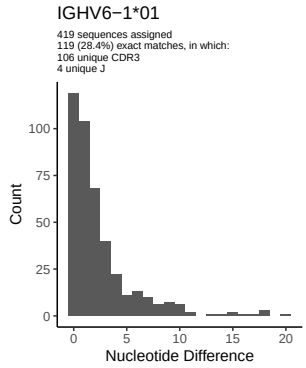

IGHV4−39*01
2374 sequences assigned
1106 (46.6%) exact matches, in which:
895 unique CDR3
6 unique J
Count
Nucleotide Difference

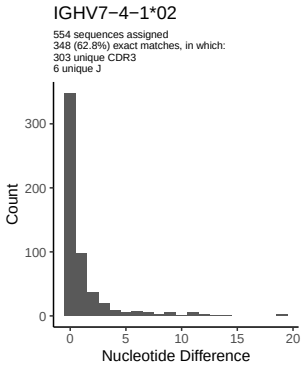

IGHV4−59*01
745 sequences assigned
352 (47.2%) exact matches, in which:
300 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV4−61*01
119 sequences assigned
58 (48.7%) exact matches, in which:
47 unique CDR3
5 unique J
Count
Nucleotide Difference

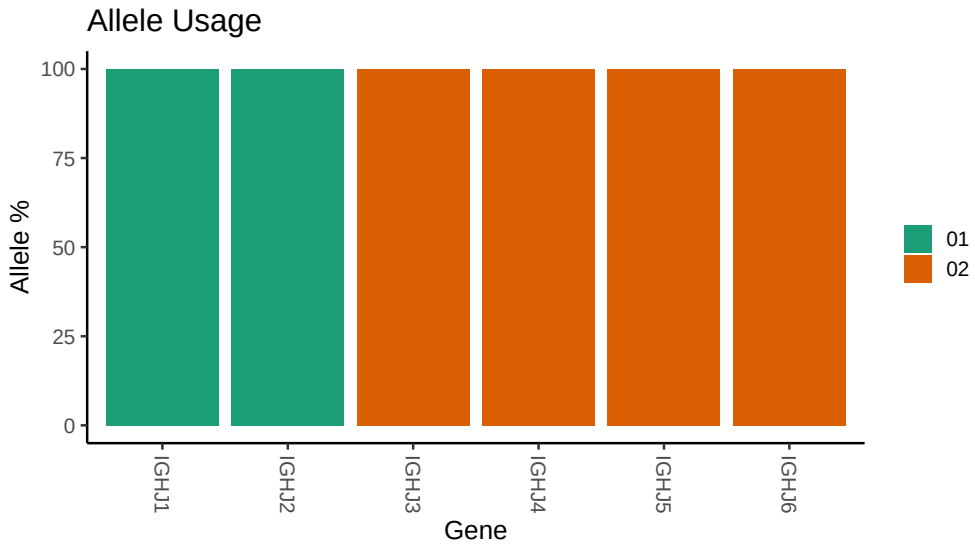

IGHV4−61*02
925 sequences assigned
388 (41.9%) exact matches, in which:
330 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV5−51*01
1295 sequences assigned
626 (48.3%) exact matches, in which:
501 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV6−1*01
419 sequences assigned
119 (28.4%) exact matches, in which:
106 unique CDR3
4 unique J
Count
Nucleotide Difference


IGHV7−4−1*02
554 sequences assigned
348 (62.8%) exact matches, in which:
303 unique CDR3
6 unique J
Count
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S3/S3/3/3/c5/3e70dbc1464751fb42edc164455501/3_Finale_genoty
##
## Germline reference file: /work/jenkins/PRJEB26509/S3/S3/3/3/c5/3e70dbc1464751fb42edc164455501/persona
##
## Novel allele file: /work/jenkins/PRJEB26509/S3/S3/3/3/c5/3e70dbc1464751fb42edc164455501/novel_sequen
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## warning: non codon aligned gaps were found in novel sequence IGHV3 9 01_A85C
##
##
## warning: non codon aligned gaps were found in novel sequence IGHV3 21 01_A85C
```