OGRDBstats Report

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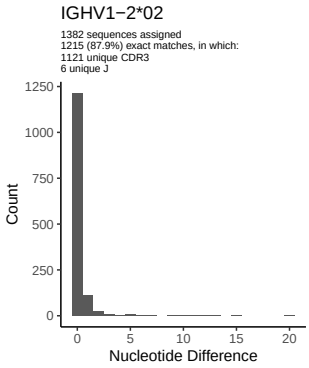
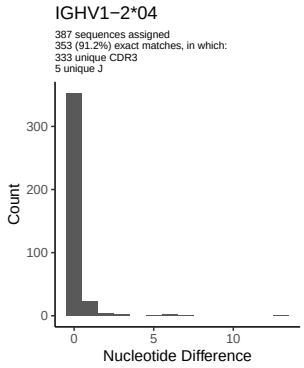
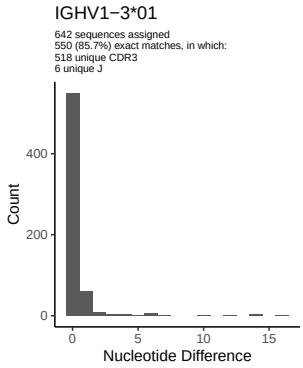
1 Novel sequence analysis

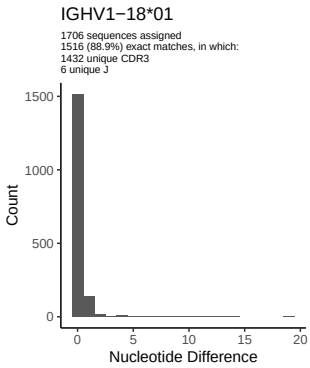
1.1 CDR3 length distribution, in assignments to novel alleles

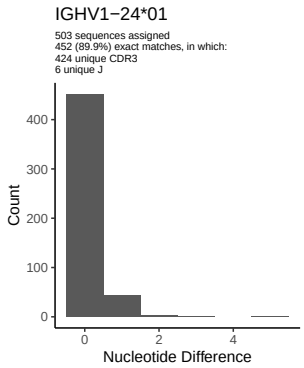
2 Variation from germline, in assignments to each allele

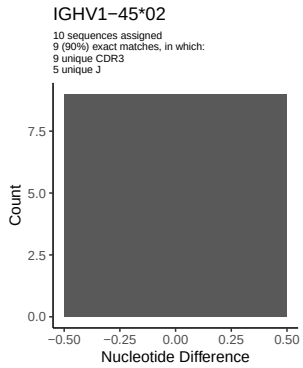


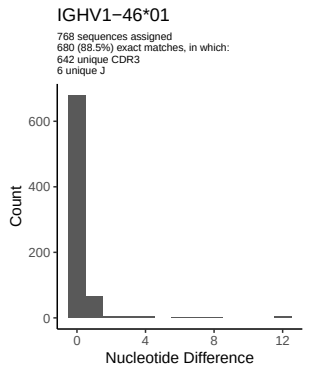


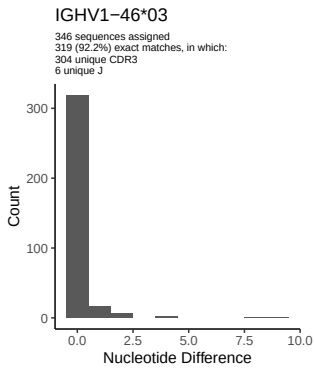


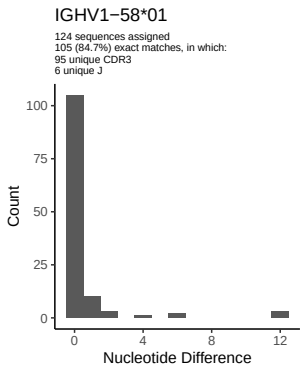


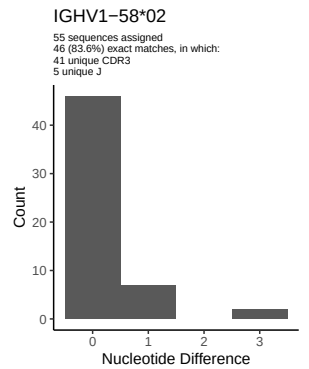


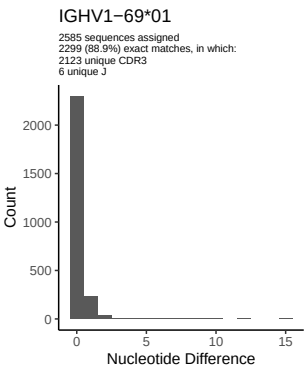


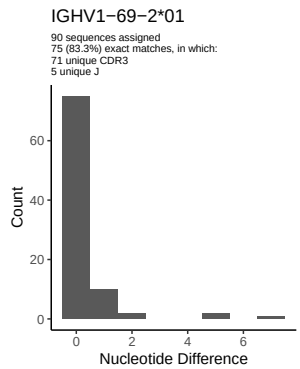


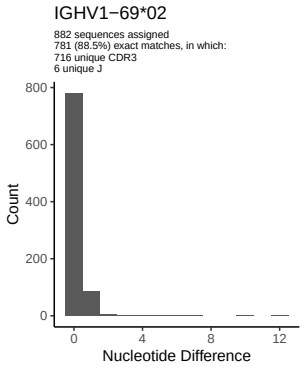


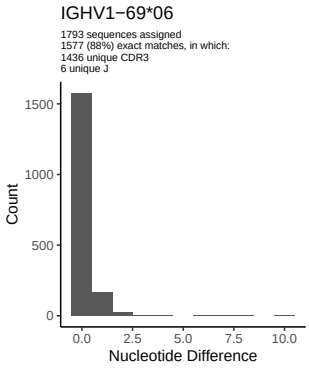


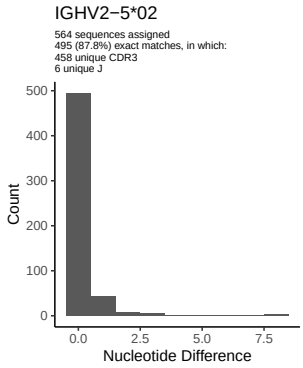


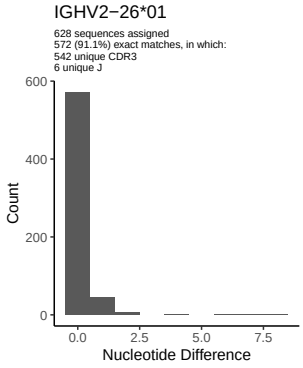


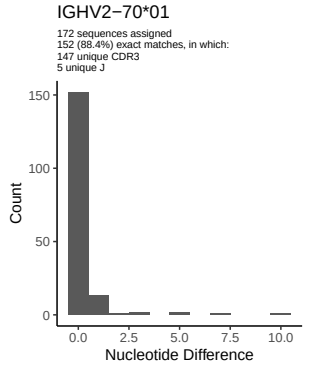


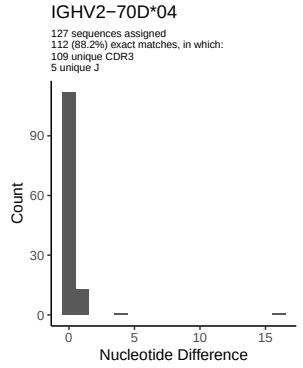

IGHV1−69*02
882 sequences assigned
781 (88.5%) exact matches, in which:
716 unique CDR3
6 unique J
Count
Nucleotide Difference

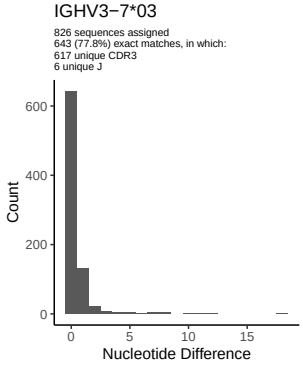

IGHV1−69*06
1793 sequences assigned
1577 (88%) exact matches, in which:
1436 unique CDR3
6 unique J
Count
Nucleotide Difference

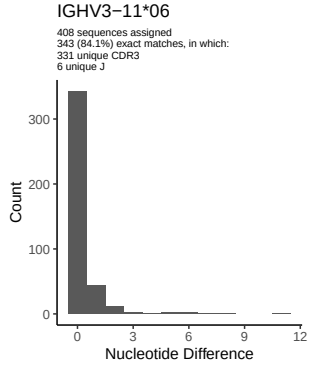

IGHV2−5*02
564 sequences assigned
495 (87.8%) exact matches, in which:
458 unique CDR3
6 unique J
Count
Nucleotide Difference

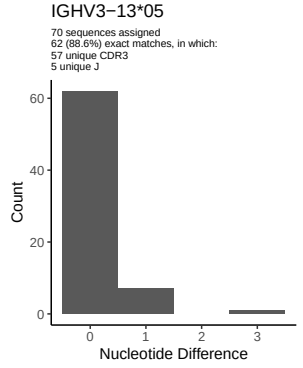

IGHV2−26*01
628 sequences assigned
572 (91.1%) exact matches, in which:
542 unique CDR3
6 unique J
Count
Nucleotide Difference

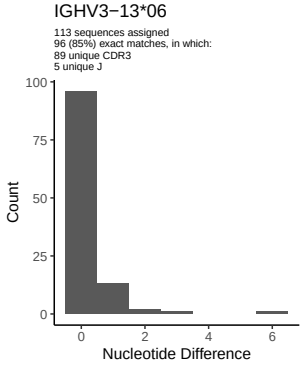

IGHV2−70*01
172 sequences assigned
152 (88.4%) exact matches, in which:
147 unique CDR3
5 unique J
Count
Nucleotide Difference

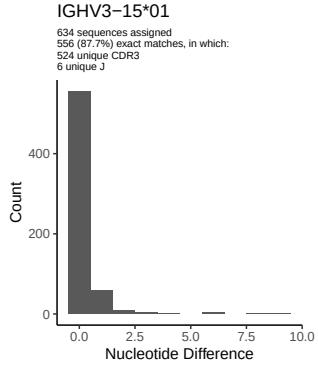

IGHV2−70D*04
127 sequences assigned
112 (88.2%) exact matches, in which:
109 unique CDR3
5 unique J
Count
Nucleotide Difference

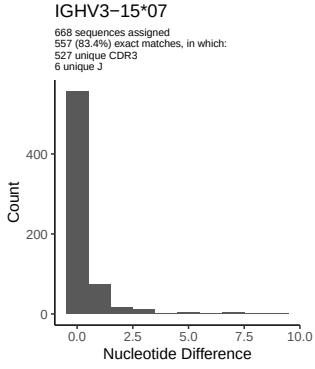

IGHV3−7*03
826 sequences assigned
643 (77.8%) exact matches, in which:
617 unique CDR3
6 unique J
Count
Nucleotide Difference

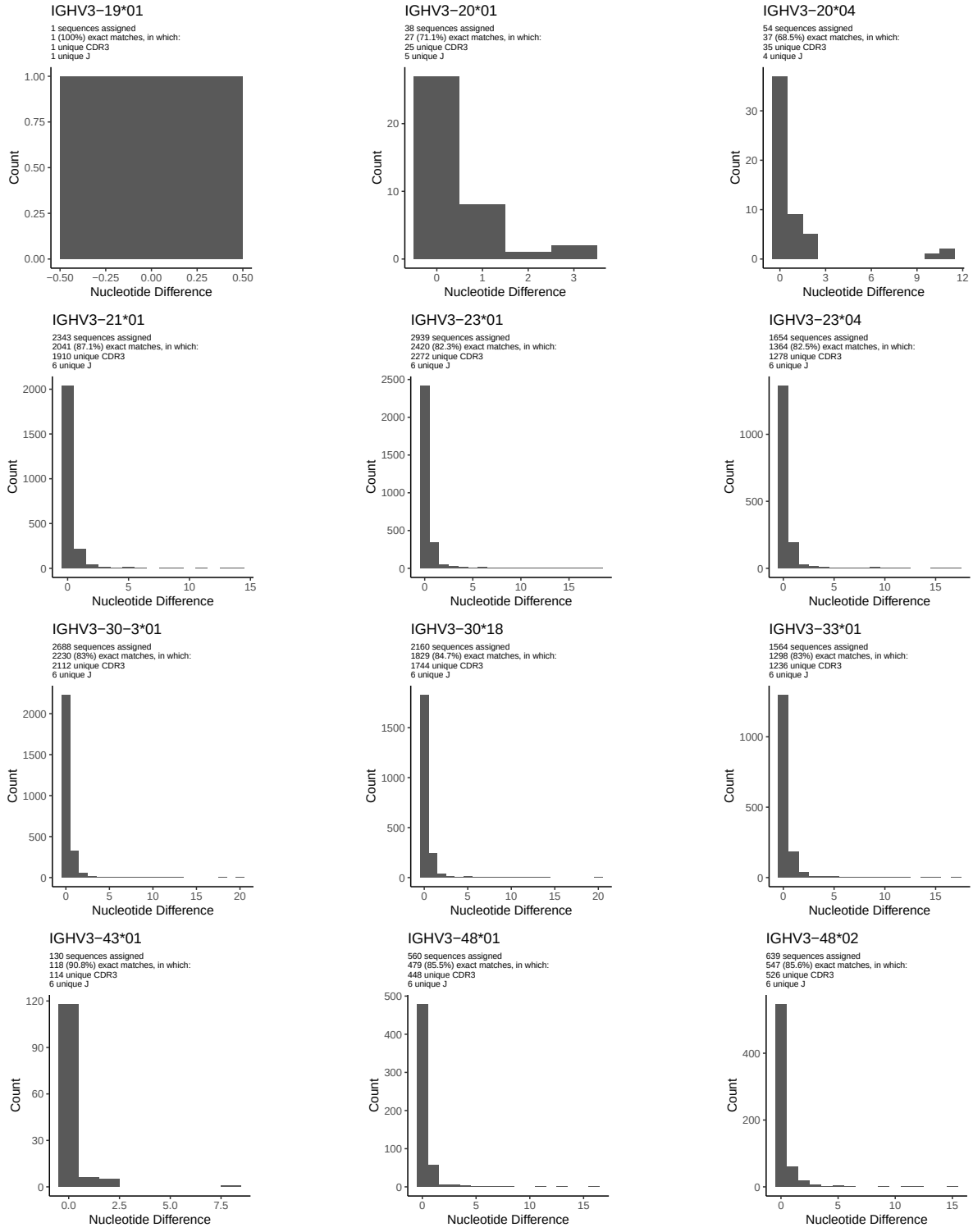

IGHV3−11*06
408 sequences assigned
343 (84.1%) exact matches, in which:
331 unique CDR3
6 unique J
Count
Nucleotide Difference

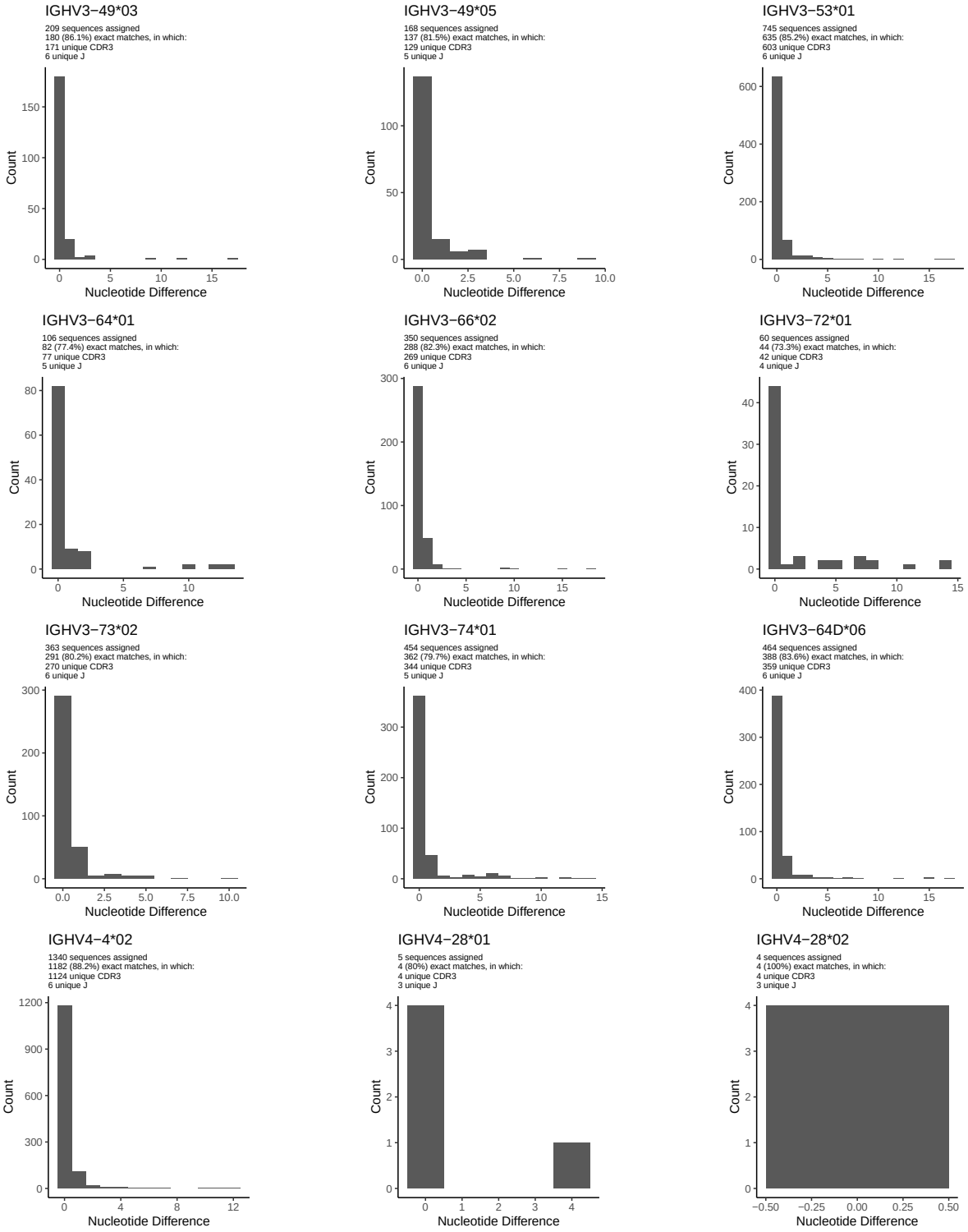

IGHV3−13*05
70 sequences assigned
62 (88.6%) exact matches, in which:
57 unique CDR3
5 unique J
Count
Nucleotide Difference

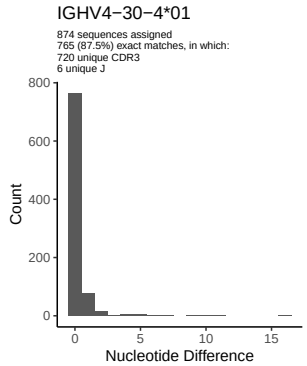

IGHV3−13*06
113 sequences assigned
96 (85%) exact matches, in which:
89 unique CDR3
5 unique J
Count
Nucleotide Difference

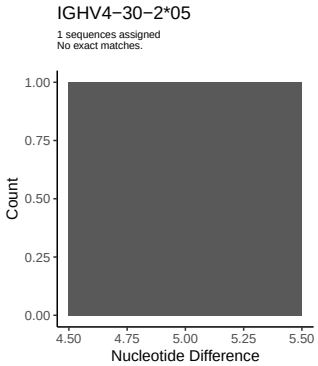

IGHV3−15*01
634 sequences assigned
556 (87.7%) exact matches, in which:
524 unique CDR3
6 unique J
Count
Nucleotide Difference

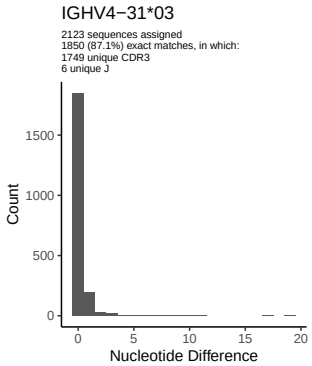

IGHV3−15*07
668 sequences assigned
557 (83.4%) exact matches, in which:
527 unique CDR3
6 unique J
Count
Nucleotide Difference

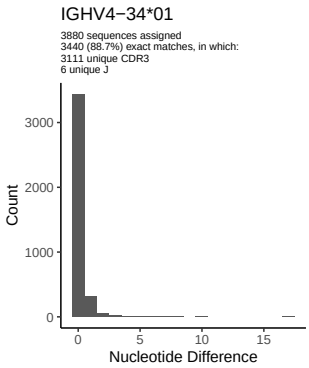

IGHV3−19*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
IGHV3−20*01
38 sequences assigned
27 (71.1%) exact matches, in which:
25 unique CDR3
5 unique J
IGHV3−20*04
54 sequences assigned
37 (68.5%) exact matches, in which:
35 unique CDR3
4 unique J
IGHV3−21*01
2343 sequences assigned
2041 (87.1%) exact matches, in which:
1910 unique CDR3
6 unique J
IGHV3−23*01
2939 sequences assigned
2420 (82.3%) exact matches, in which:
2272 unique CDR3
6 unique J
IGHV3−23*04
1654 sequences assigned
1364 (82.5%) exact matches, in which:
1278 unique CDR3
6 unique J
IGHV3−30−3*01
2688 sequences assigned
2230 (83%) exact matches, in which:
2112 unique CDR3
6 unique J
IGHV3−30*18
2160 sequences assigned
1829 (84.7%) exact matches, in which:
1744 unique CDR3
6 unique J
IGHV3−33*01
1564 sequences assigned
1298 (83%) exact matches, in which:
1236 unique CDR3
6 unique J
IGHV3−43*01
130 sequences assigned
118 (90.8%) exact matches, in which:
114 unique CDR3
6 unique J
IGHV3−48*01
560 sequences assigned
479 (85.5%) exact matches, in which:
448 unique CDR3
6 unique J
IGHV3−48*02
639 sequences assigned
547 (85.6%) exact matches, in which:
526 unique CDR3
6 unique J
Count
Nucleotide Difference

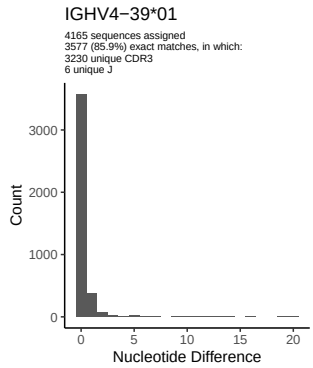

IGHV3−49*03
209 sequences assigned
180 (86.1%) exact matches, in which:
171 unique CDR3
6 unique J
IGHV3−49*05
168 sequences assigned
137 (81.5%) exact matches, in which:
129 unique CDR3
5 unique J
IGHV3−53*01
745 sequences assigned
635 (85.2%) exact matches, in which:
603 unique CDR3
6 unique J
IGHV3−64*01
106 sequences assigned
82 (77.4%) exact matches, in which:
77 unique CDR3
5 unique J
IGHV3−66*02
350 sequences assigned
288 (82.3%) exact matches, in which:
269 unique CDR3
6 unique J
IGHV3−72*01
60 sequences assigned
44 (73.3%) exact matches, in which:
42 unique CDR3
4 unique J
IGHV3−73*02
363 sequences assigned
291 (80.2%) exact matches, in which:
270 unique CDR3
6 unique J
IGHV3−74*01
454 sequences assigned
362 (79.7%) exact matches, in which:
344 unique CDR3
5 unique J
IGHV3−64D*06
464 sequences assigned
388 (83.6%) exact matches, in which:
359 unique CDR3
6 unique J
IGHV4−4*02
1340 sequences assigned
1182 (88.2%) exact matches, in which:
1124 unique CDR3
6 unique J
IGHV4−28*01
5 sequences assigned
4 (80%) exact matches, in which:
4 unique CDR3
3 unique J
IGHV4−28*02
4 sequences assigned
4 (100%) exact matches, in which:
4 unique CDR3
3 unique J
Count
Nucleotide Difference

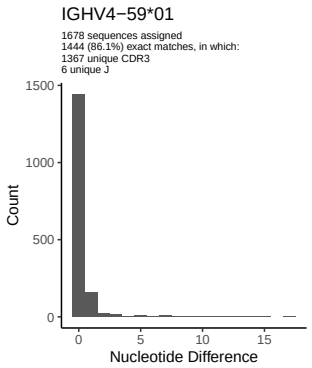

IGHV4−30−4*01
874 sequences assigned
765 (87.5%) exact matches, in which:
720 unique CDR3
6 unique J
Count
Nucleotide Difference

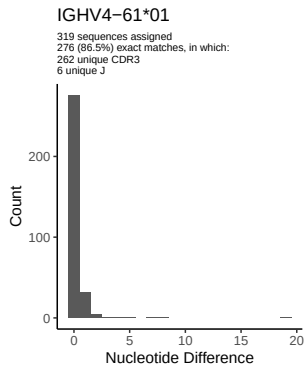

IGHV4−30−2*05
1 sequences assigned
No exact matches.
Count
Nucleotide Difference

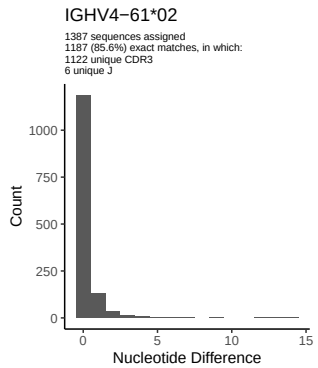

IGHV4−31*03
2123 sequences assigned
1850 (87.1%) exact matches, in which:
1749 unique CDR3
6 unique J
Count
Nucleotide Difference

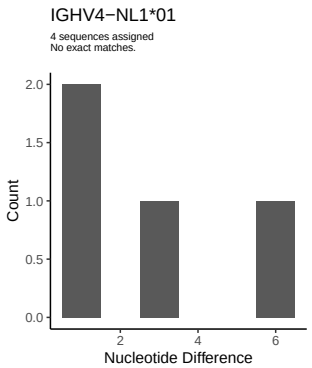

IGHV4−34*01
3880 sequences assigned
3440 (88.7%) exact matches, in which:
3111 unique CDR3
6 unique J
Count
Nucleotide Difference

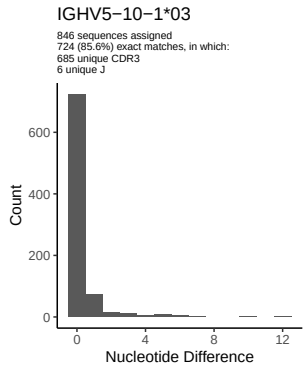

IGHV4−39*01
4165 sequences assigned
3577 (85.9%) exact matches, in which:
3230 unique CDR3
6 unique J
Count
Nucleotide Difference

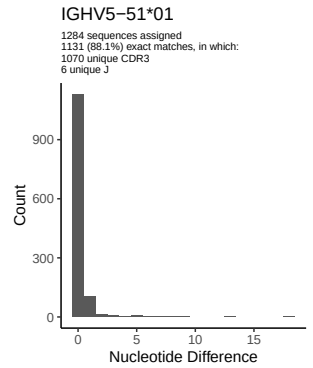

IGHV4−59*01
1678 sequences assigned
1444 (86.1%) exact matches, in which:
1367 unique CDR3
6 unique J
Count
Nucleotide Difference

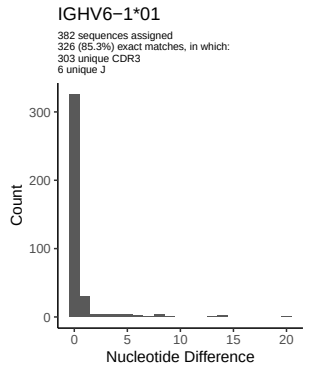

IGHV4−61*01
319 sequences assigned
276 (86.5%) exact matches, in which:
262 unique CDR3
6 unique J
Count
Nucleotide Difference

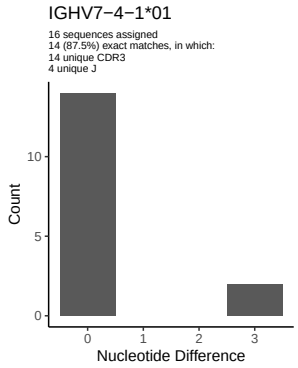

IGHV4−61*02
1387 sequences assigned
1187 (85.6%) exact matches, in which:
1122 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV4−NL1*01
4 sequences assigned
No exact matches.
Count
Nucleotide Difference

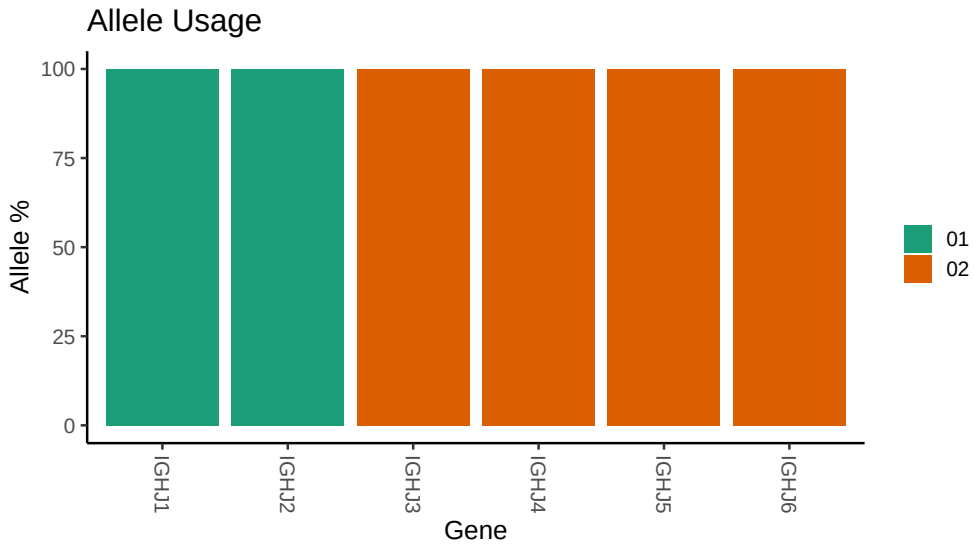

IGHV5−10−1*03
846 sequences assigned
724 (85.6%) exact matches, in which:
685 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV5−51*01
1284 sequences assigned
1131 (88.1%) exact matches, in which:
1070 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV6−1*01
382 sequences assigned
326 (85.3%) exact matches, in which:
303 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV7−4−1*01
16 sequences assigned
14 (87.5%) exact matches, in which:
14 unique CDR3
4 unique J
Count
10
5
0
0
1
2
3
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

```
## Repertoire file: /misc/work/jenkins/PRJEB26509/S50/S50/53/53/f3/7dded3b87c6c53586109fec6da453b/53_Fi
##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S50/S50/53/53/61/77ce7944ec401ff41cdf7d50c4b5
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```