# OGRDBstats Report

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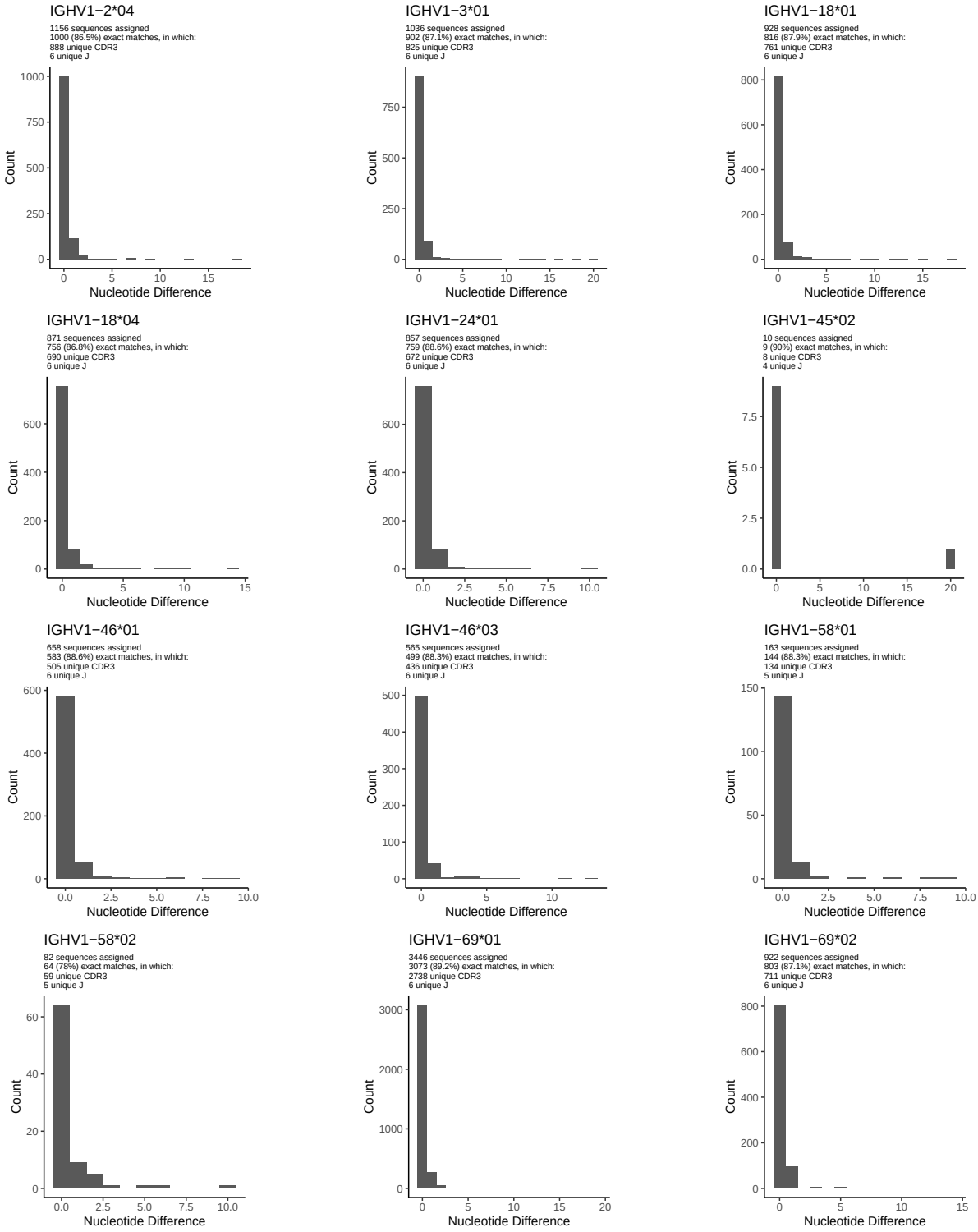
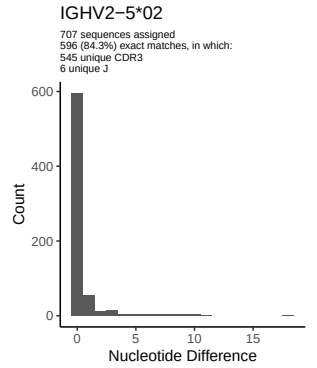
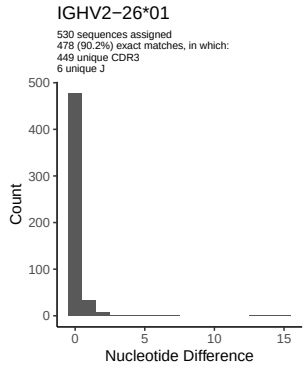
# 1 Novel sequence analysis

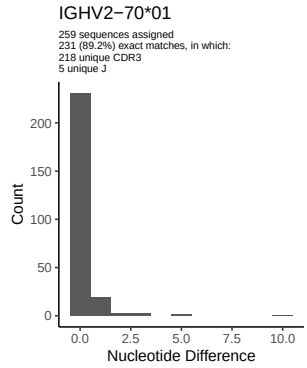
## 1.1 CDR3 length distribution, in assignments to novel alleles

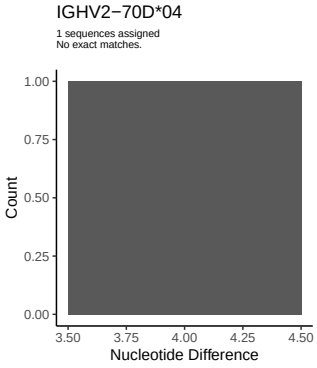
# 2 Variation from germline, in assignments to each allele

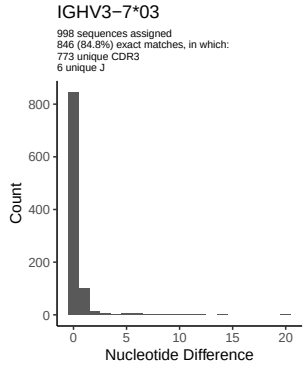


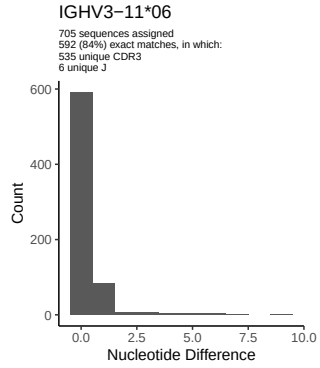

IGHV2−5*02
707 sequences assigned
596 (84.3%) exact matches, in which:
545 unique CDR3
6 unique J
Count
Nucleotide Difference

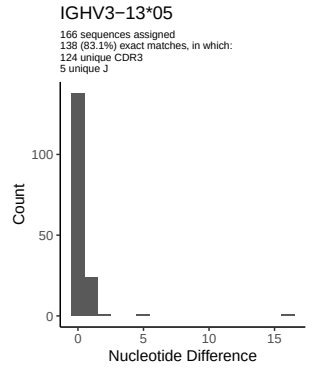

IGHV2−26*01
530 sequences assigned
478 (90.2%) exact matches, in which:
449 unique CDR3
6 unique J
Count
Nucleotide Difference

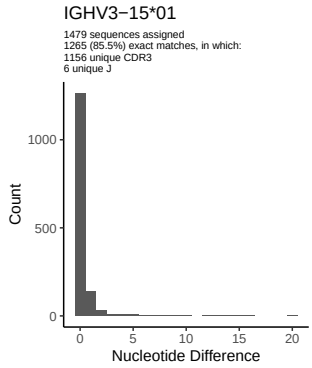

IGHV2−70*01
259 sequences assigned
231 (89.2%) exact matches, in which:
218 unique CDR3
5 unique J
Count
Nucleotide Difference

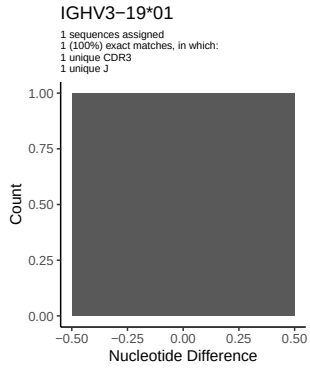

IGHV2−70D*04
1 sequences assigned
No exact matches.
Count
Nucleotide Difference

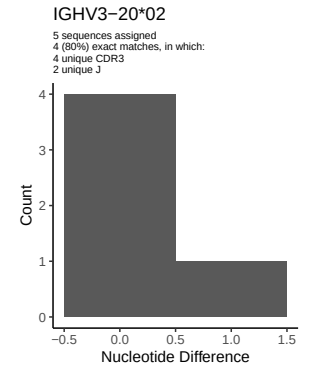

IGHV3−7*03
998 sequences assigned
846 (84.8%) exact matches, in which:
773 unique CDR3
6 unique J
Count
Nucleotide Difference

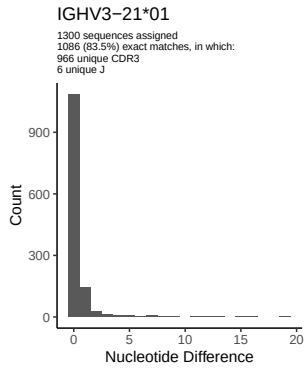

IGHV3−11*06
705 sequences assigned
592 (84%) exact matches, in which:
535 unique CDR3
6 unique J
Count
Nucleotide Difference

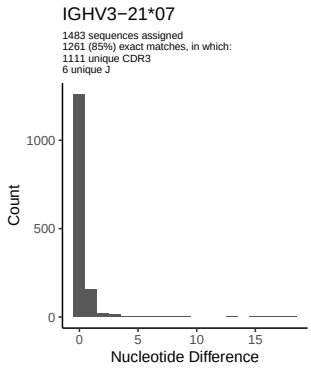

IGHV3−13*05
166 sequences assigned
138 (83.1%) exact matches, in which:
124 unique CDR3
5 unique J
Count
Nucleotide Difference

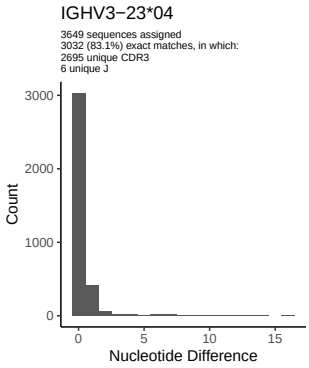

IGHV3−15*01
1479 sequences assigned
1265 (85.5%) exact matches, in which:
1156 unique CDR3
6 unique J
Count
Nucleotide Difference

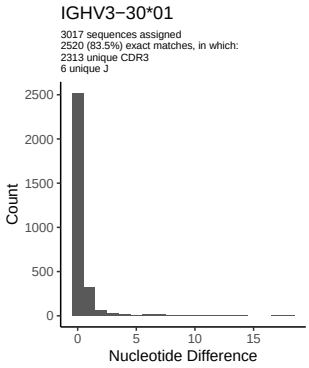

IGHV3−19*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

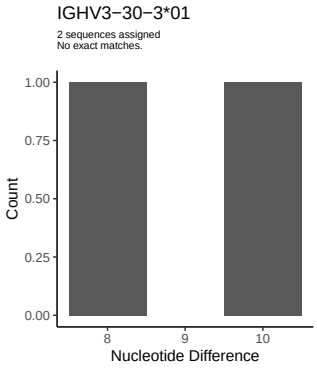

IGHV3−20*02
5 sequences assigned
4 (80%) exact matches, in which:
4 unique CDR3
2 unique J
Count
Nucleotide Difference

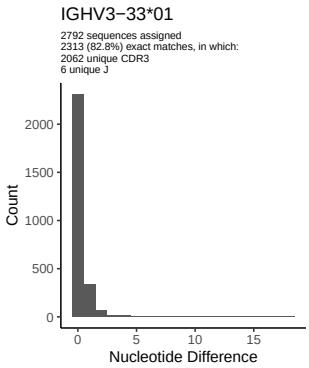

IGHV3−21*01
1300 sequences assigned
1086 (83.5%) exact matches, in which:
966 unique CDR3
6 unique J
Count
Nucleotide Difference

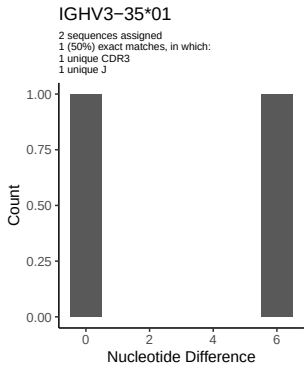

IGHV3−21*07
1483 sequences assigned
1261 (85%) exact matches, in which:
1111 unique CDR3
6 unique J
Count
Nucleotide Difference

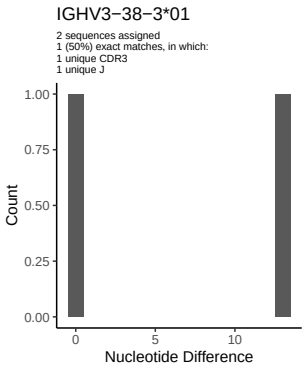

IGHV3−23*04
3649 sequences assigned
3032 (83.1%) exact matches, in which:
2695 unique CDR3
6 unique J
Count
Nucleotide Difference

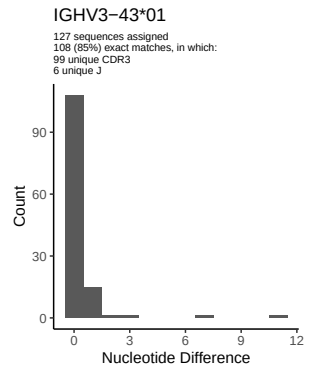

IGHV3−30*01
3017 sequences assigned
2520 (83.5%) exact matches, in which:
2313 unique CDR3
6 unique J
Count
Nucleotide Difference

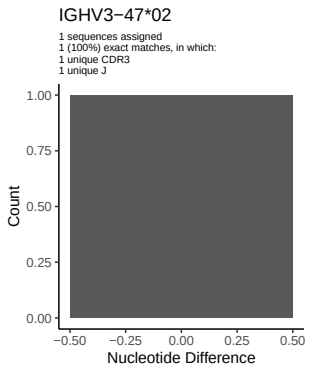

IGHV3−30−3*01
2 sequences assigned
No exact matches.
Count
Nucleotide Difference

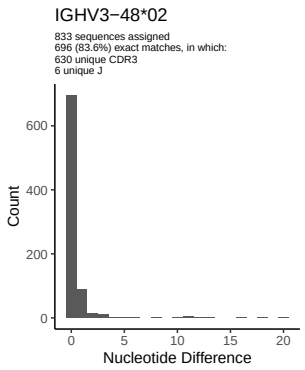

IGHV3−33*01
2792 sequences assigned
2313 (82.8%) exact matches, in which:
2062 unique CDR3
6 unique J
Count
Nucleotide Difference

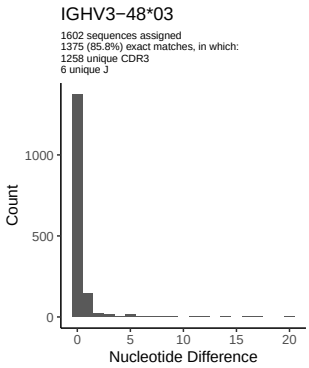

IGHV3−35*01
2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

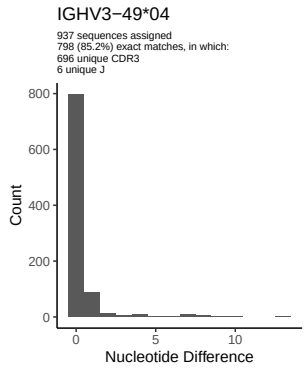

IGHV3−38−3*01
2 sequences assigned
1 (50%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

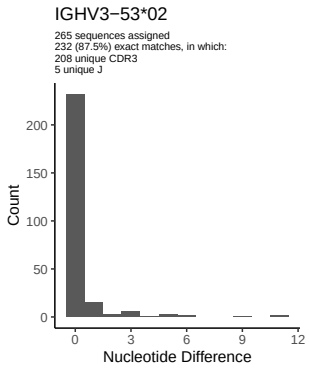

IGHV3−43*01
127 sequences assigned
108 (85%) exact matches, in which:
99 unique CDR3
6 unique J
Count
Nucleotide Difference

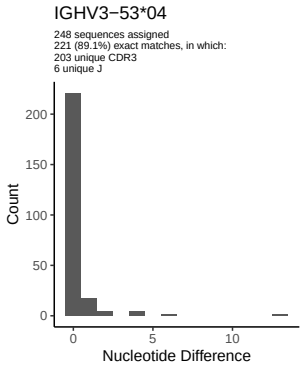

IGHV3−47*02
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

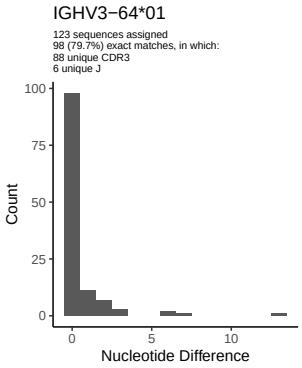

IGHV3−48*02
833 sequences assigned
696 (83.6%) exact matches, in which:
630 unique CDR3
6 unique J
Count
Nucleotide Difference

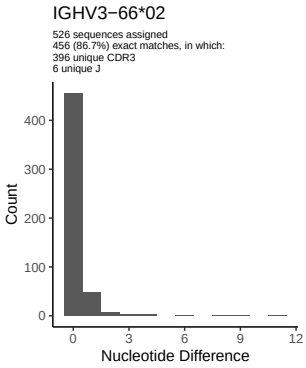

IGHV3−48*03
1602 sequences assigned
1375 (85.8%) exact matches, in which:
1258 unique CDR3
6 unique J
Count
Nucleotide Difference

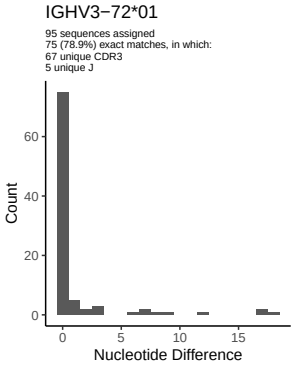

IGHV3−49*04
937 sequences assigned
798 (85.2%) exact matches, in which:
696 unique CDR3
6 unique J
Count
Nucleotide Difference

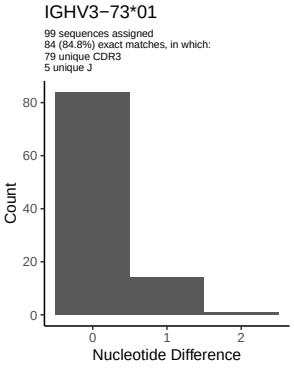

IGHV3−53*02
265 sequences assigned
232 (87.5%) exact matches, in which:
208 unique CDR3
5 unique J
Count
Nucleotide Difference

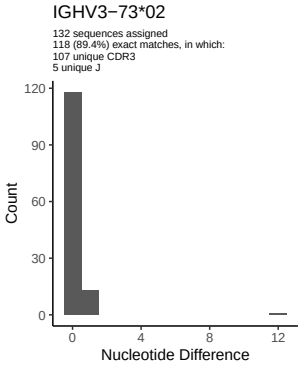

IGHV3−53*04
248 sequences assigned
221 (89.1%) exact matches, in which:
203 unique CDR3
6 unique J
Count
Nucleotide Difference

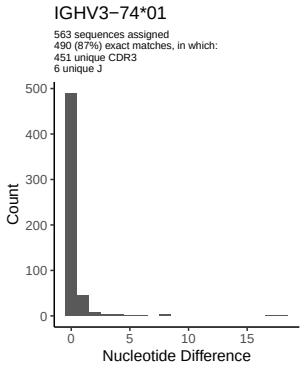

IGHV3−64*01
123 sequences assigned
98 (79.7%) exact matches, in which:
88 unique CDR3
6 unique J
Count
Nucleotide Difference

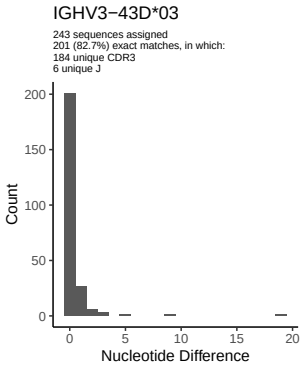

IGHV3−66*02
526 sequences assigned
456 (86.7%) exact matches, in which:
396 unique CDR3
6 unique J
Count
Nucleotide Difference

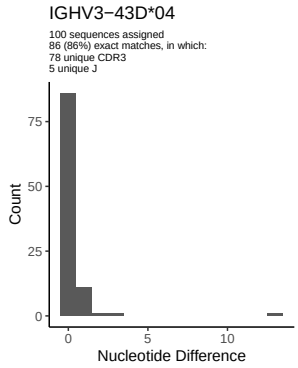

IGHV3−72*01
95 sequences assigned
75 (78.9%) exact matches, in which:
67 unique CDR3
5 unique J
Count
Nucleotide Difference

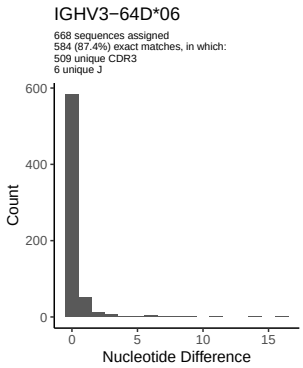

IGHV3−73*01
99 sequences assigned
84 (84.8%) exact matches, in which:
79 unique CDR3
5 unique J
Count
Nucleotide Difference

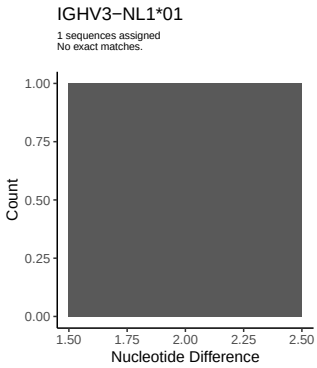

IGHV3−73*02
132 sequences assigned
118 (89.4%) exact matches, in which:
107 unique CDR3
5 unique J
Count
Nucleotide Difference

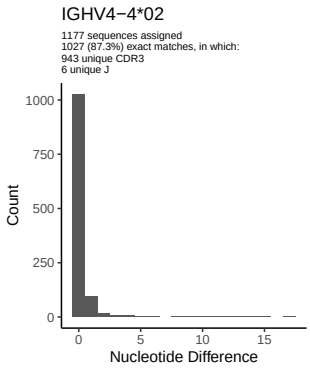

IGHV3−74*01
563 sequences assigned
490 (87%) exact matches, in which:
451 unique CDR3
6 unique J
Count
Nucleotide Difference

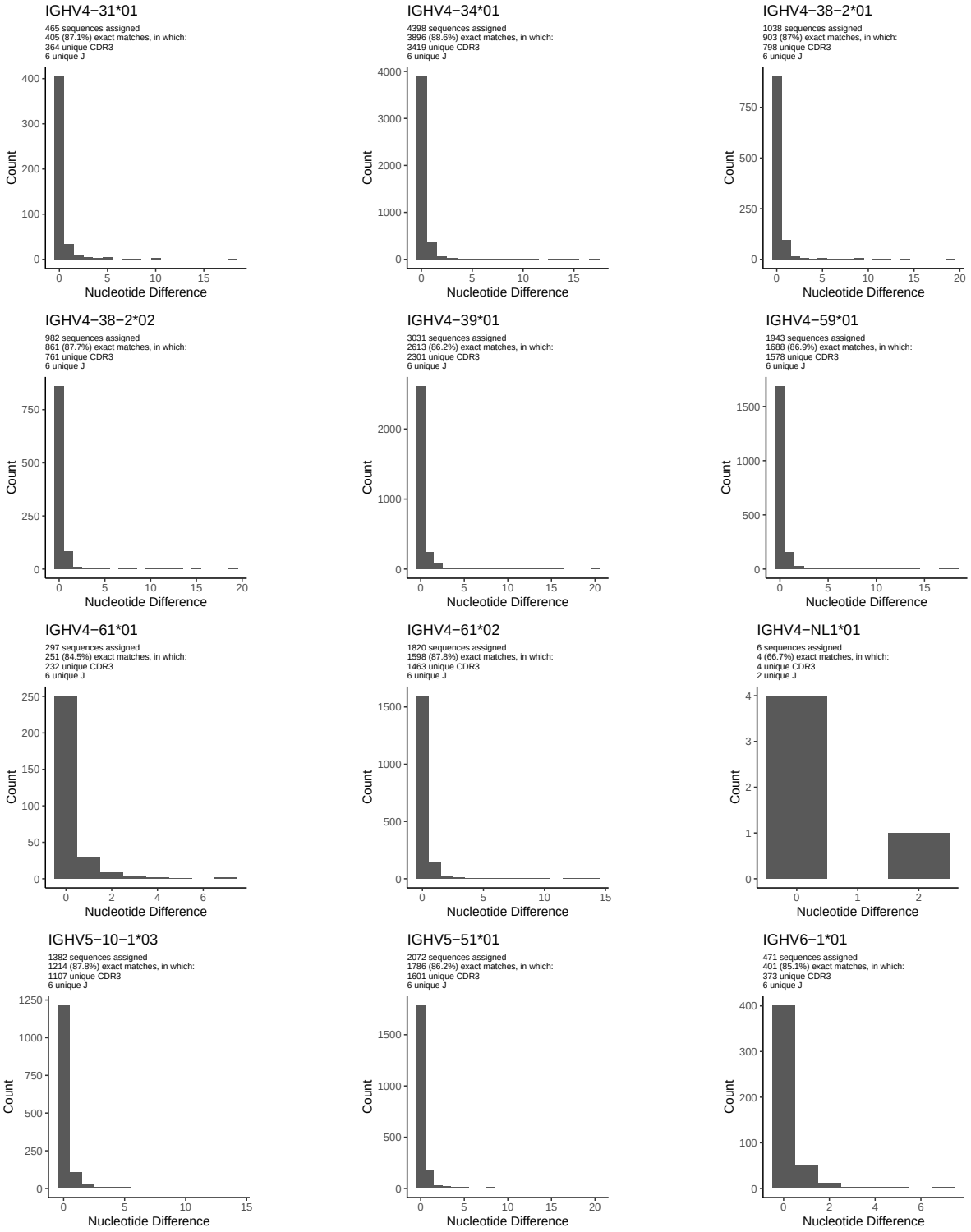

IGHV3−43D*03
243 sequences assigned
201 (82.7%) exact matches, in which:
184 unique CDR3
6 unique J
Count
Nucleotide Difference

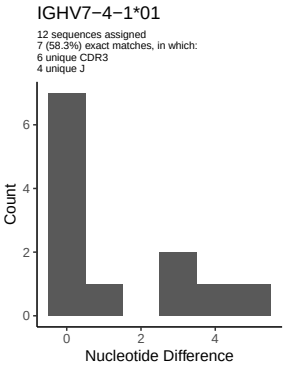

IGHV3−43D*04
100 sequences assigned
86 (86%) exact matches, in which:
78 unique CDR3
5 unique J
Count
Nucleotide Difference

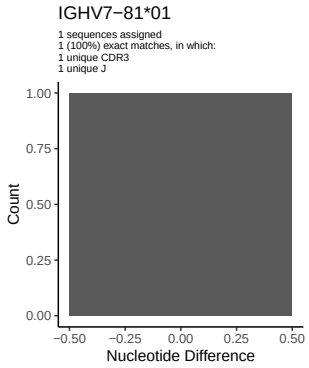

IGHV3−64D*06
668 sequences assigned
584 (87.4%) exact matches, in which:
509 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV3−NL1*01
1 sequences assigned
No exact matches.
Count
Nucleotide Difference

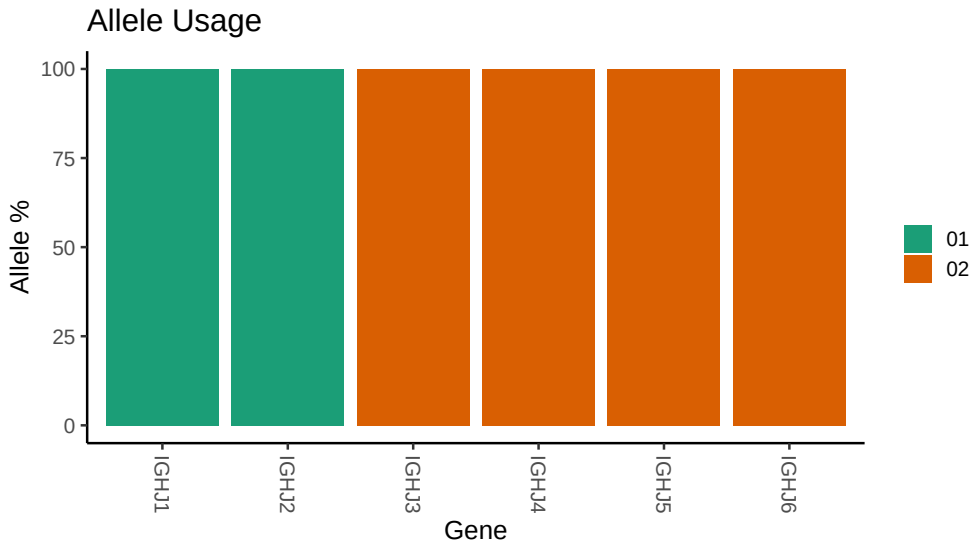

IGHV4−4*02
1177 sequences assigned
1027 (87.3%) exact matches, in which:
943 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV4−31*01
465 sequences assigned
405 (87.1%) exact matches, in which:
364 unique CDR3
6 unique J
IGHV4−34*01
4398 sequences assigned
3896 (88.6%) exact matches, in which:
3419 unique CDR3
6 unique J
IGHV4−38−2*01
1038 sequences assigned
903 (87%) exact matches, in which:
798 unique CDR3
6 unique J
IGHV4−38−2*02
982 sequences assigned
861 (87.7%) exact matches, in which:
761 unique CDR3
6 unique J
IGHV4−39*01
3031 sequences assigned
2613 (86.2%) exact matches, in which:
2301 unique CDR3
6 unique J
IGHV4−59*01
1943 sequences assigned
1688 (86.9%) exact matches, in which:
1578 unique CDR3
6 unique J
IGHV4−61*01
297 sequences assigned
251 (84.5%) exact matches, in which:
232 unique CDR3
6 unique J
IGHV4−61*02
1820 sequences assigned
1598 (87.8%) exact matches, in which:
1463 unique CDR3
6 unique J
IGHV4−NL1*01
6 sequences assigned
4 (66.7%) exact matches, in which:
4 unique CDR3
2 unique J
IGHV5−10−1*03
1382 sequences assigned
1214 (87.8%) exact matches, in which:
1107 unique CDR3
6 unique J
IGHV5−51*01
2072 sequences assigned
1786 (86.2%) exact matches, in which:
1601 unique CDR3
6 unique J
IGHV6−1*01
471 sequences assigned
401 (85.1%) exact matches, in which:
373 unique CDR3
6 unique J
Count
Nucleotide Difference


IGHV7−4−1*01
12 sequences assigned
7 (58.3%) exact matches, in which:
6 unique CDR3
4 unique J
Count
0
2
4
6
0
2
4
Nucleotide Difference


IGHV7−81*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
0.00
0.25
0.50
0.75
1.00
−0.50
−0.25
0.00
0.25
0.50
Nucleotide Difference

## 3 Allele usage in potential haplotype anchor genes



# 4 Haplotype plots

# 5 Configuration settings

```
## Repertoire file: /work/jenkins/PRJEB26509/S76/S76/80/80/82/55d4fb93c2e475e38223b38076f5fd/80_Finale_
##
## Germline reference file: /work/jenkins/PRJEB26509/S76/S76/80/80/14/9b9da5ab54e1081d0979facf22a65d/re
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning   no inferred sequences found.
```