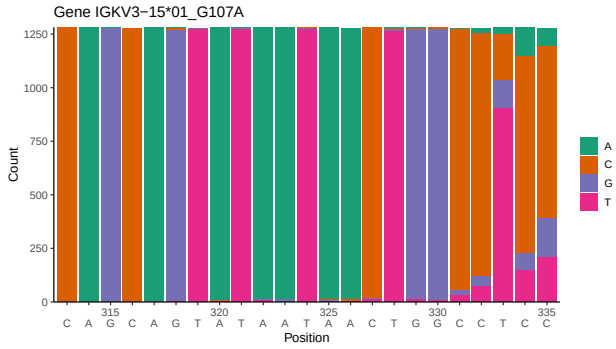
OGRDBstats Report

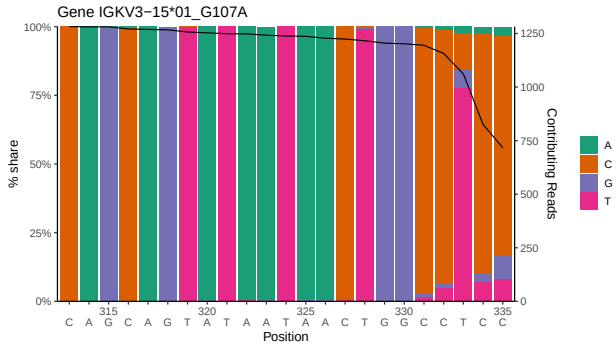
Contents

1 Novel sequence analysis

1.1 End-nucleotide composition

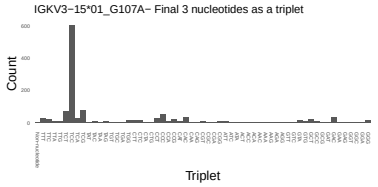


1.2 Per-nucleotide consensus where previous nucleotides match the consensus

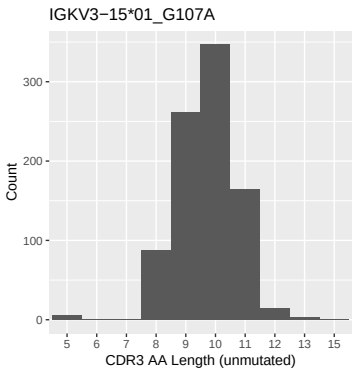


1.3 Whole-sequence composition of each assigned read

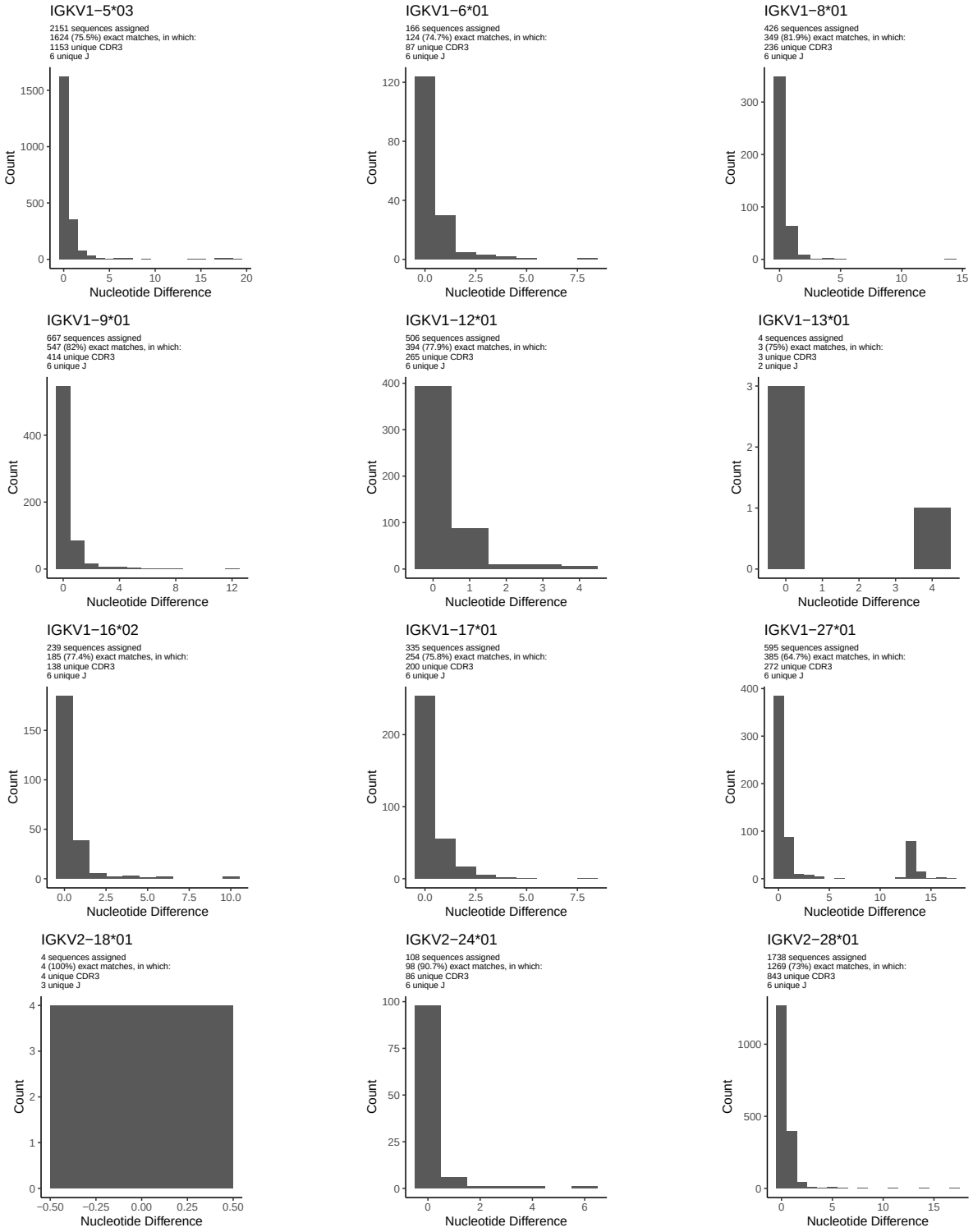
1.4 Final three nucleotides: frequency of each observed triplet

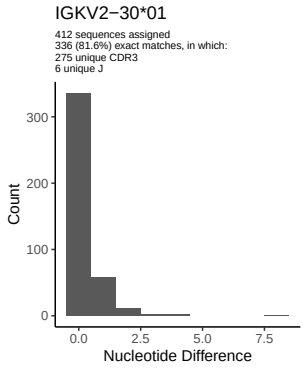


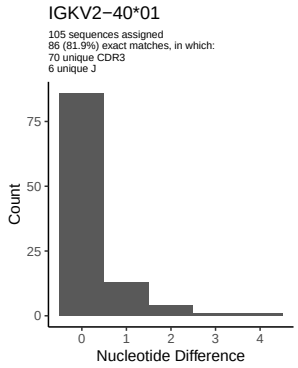
1.5 CDR3 length distribution, in assignments to novel alleles

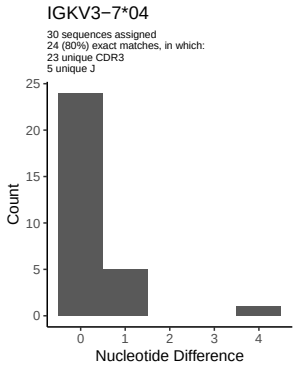


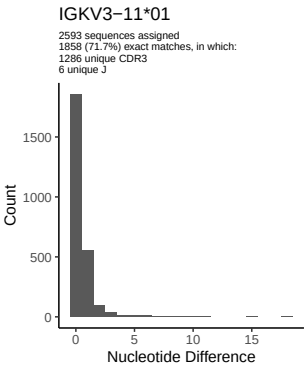
2 Variation from germline, in assignments to each allele

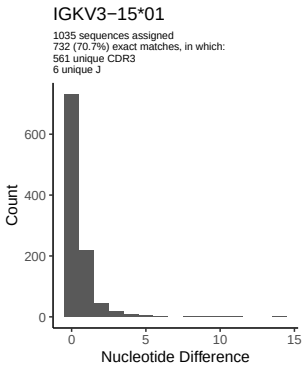


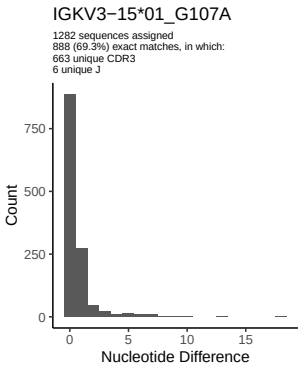

IGKV2−30*01
412 sequences assigned
336 (81.6%) exact matches, in which:
275 unique CDR3
6 unique J
Count
Nucleotide Difference

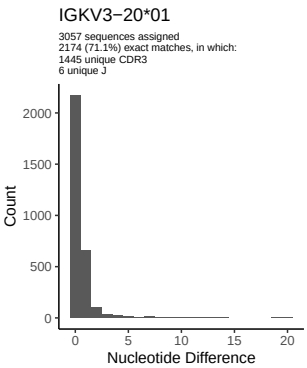

IGKV2−40*01
105 sequences assigned
86 (81.9%) exact matches, in which:
70 unique CDR3
6 unique J
Count
Nucleotide Difference

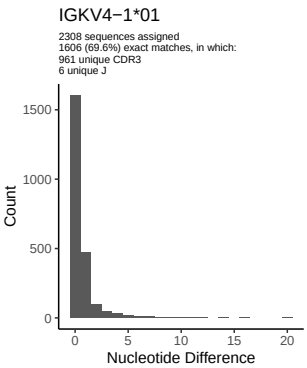

IGKV3−7*04
30 sequences assigned
24 (80%) exact matches, in which:
23 unique CDR3
5 unique J
Count
Nucleotide Difference

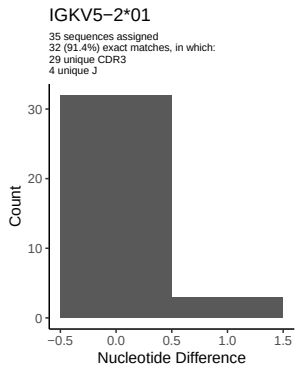

IGKV3−11*01
2593 sequences assigned
1858 (71.7%) exact matches, in which:
1286 unique CDR3
6 unique J
Count
Nucleotide Difference

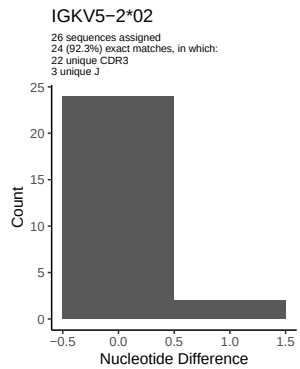

IGKV3−15*01
1035 sequences assigned
732 (70.7%) exact matches, in which:
561 unique CDR3
6 unique J
Count
Nucleotide Difference

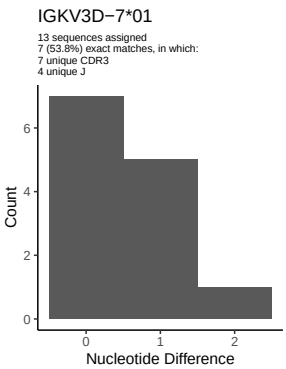

IGKV3−15*01_G107A
1282 sequences assigned
888 (69.3%) exact matches, in which:
663 unique CDR3
6 unique J
Count
Nucleotide Difference

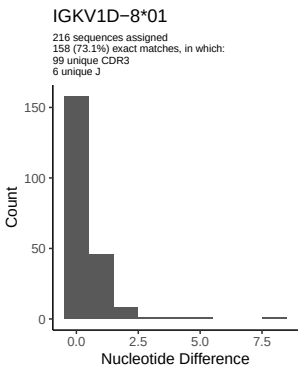

IGKV3−20*01
3057 sequences assigned
2174 (71.1%) exact matches, in which:
1445 unique CDR3
6 unique J
Count
Nucleotide Difference

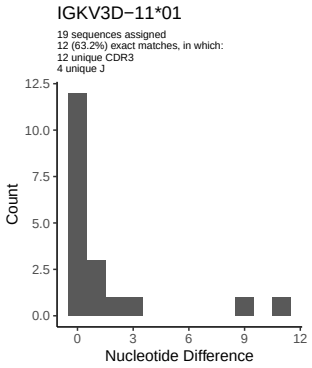

IGKV4−1*01
2308 sequences assigned
1606 (69.6%) exact matches, in which:
961 unique CDR3
6 unique J
Count
Nucleotide Difference

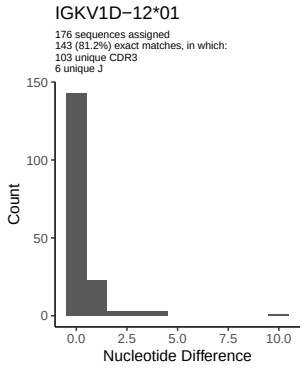

IGKV5−2*01
35 sequences assigned
32 (91.4%) exact matches, in which:
29 unique CDR3
4 unique J
Count
Nucleotide Difference

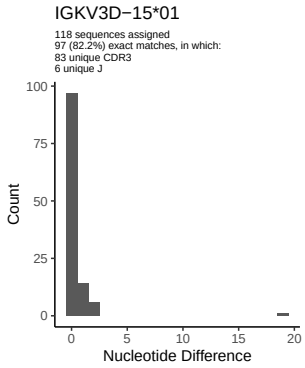

IGKV5−2*02
26 sequences assigned
24 (92.3%) exact matches, in which:
22 unique CDR3
3 unique J
Count
Nucleotide Difference

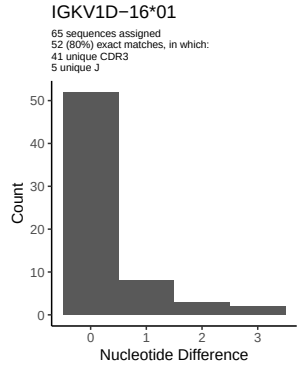

IGKV3D−7*01
13 sequences assigned
7 (53.8%) exact matches, in which:
7 unique CDR3
4 unique J
Count
Nucleotide Difference

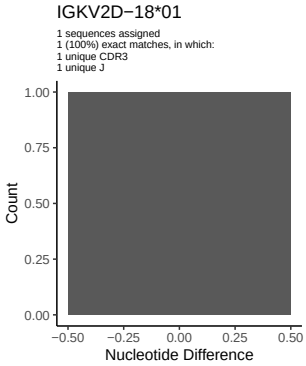

IGKV1D−8*01
216 sequences assigned
158 (73.1%) exact matches, in which:
99 unique CDR3
6 unique J
Count
Nucleotide Difference

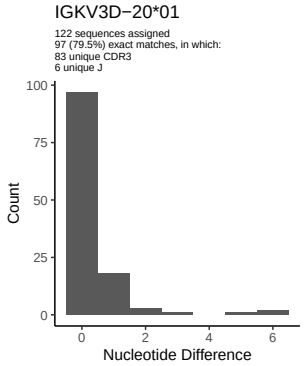

IGKV3D−11*01
19 sequences assigned
12 (63.2%) exact matches, in which:
12 unique CDR3
4 unique J
Count
Nucleotide Difference

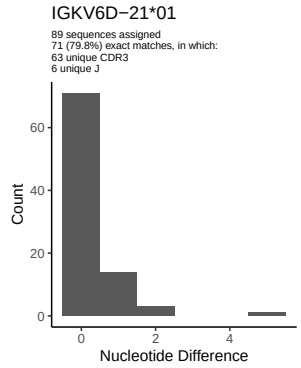

IGKV1D−12*01
176 sequences assigned
143 (81.2%) exact matches, in which:
103 unique CDR3
6 unique J
Count
Nucleotide Difference

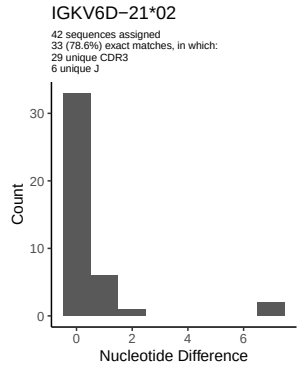

IGKV3D−15*01
118 sequences assigned
97 (82.2%) exact matches, in which:
83 unique CDR3
6 unique J
Count
Nucleotide Difference

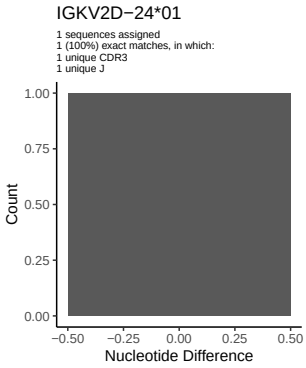

IGKV1D−16*01
65 sequences assigned
52 (80%) exact matches, in which:
41 unique CDR3
5 unique J
Count
Nucleotide Difference

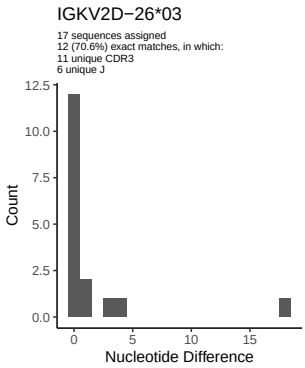

IGKV2D−18*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

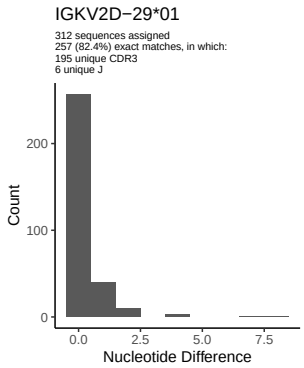

IGKV3D−20*01
122 sequences assigned
97 (79.5%) exact matches, in which:
83 unique CDR3
6 unique J
Count
Nucleotide Difference

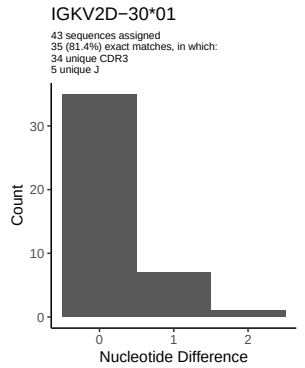

IGKV6D−21*01
89 sequences assigned
71 (79.8%) exact matches, in which:
63 unique CDR3
6 unique J
Count
Nucleotide Difference

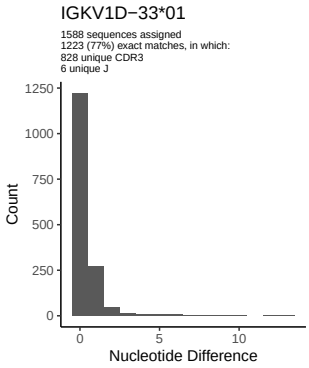

IGKV6D−21*02
42 sequences assigned
33 (78.6%) exact matches, in which:
29 unique CDR3
6 unique J
Count
Nucleotide Difference

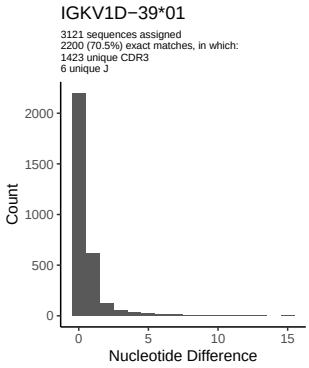

IGKV2D−24*01
1 sequences assigned
1 (100%) exact matches, in which:
1 unique CDR3
1 unique J
Count
Nucleotide Difference

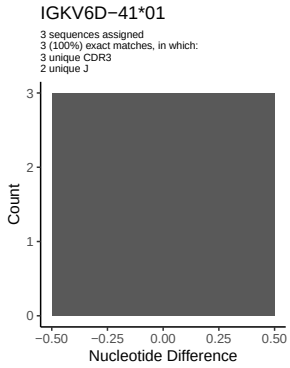

IGKV2D−26*03
17 sequences assigned
12 (70.6%) exact matches, in which:
11 unique CDR3
6 unique J
Count
Nucleotide Difference

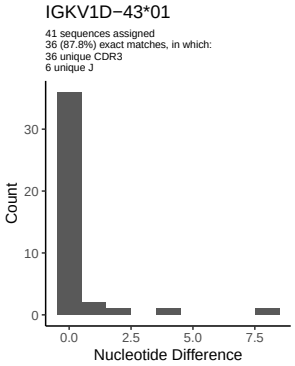

IGKV2D−29*01
312 sequences assigned
257 (82.4%) exact matches, in which:
195 unique CDR3
6 unique J
Count
Nucleotide Difference


IGKV2D−30*01
43 sequences assigned
35 (81.4%) exact matches, in which:
34 unique CDR3
5 unique J
Count
Nucleotide Difference

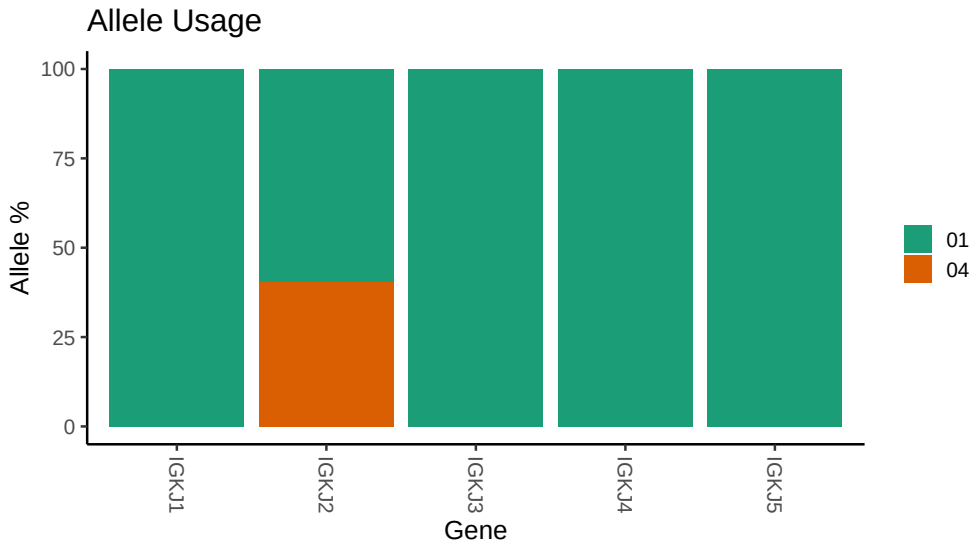

IGKV1D−33*01
1588 sequences assigned
1223 (77%) exact matches, in which:
828 unique CDR3
6 unique J
Count
Nucleotide Difference


IGKV1D−39*01
3121 sequences assigned
2200 (70.5%) exact matches, in which:
1423 unique CDR3
6 unique J
Count
Nucleotide Difference

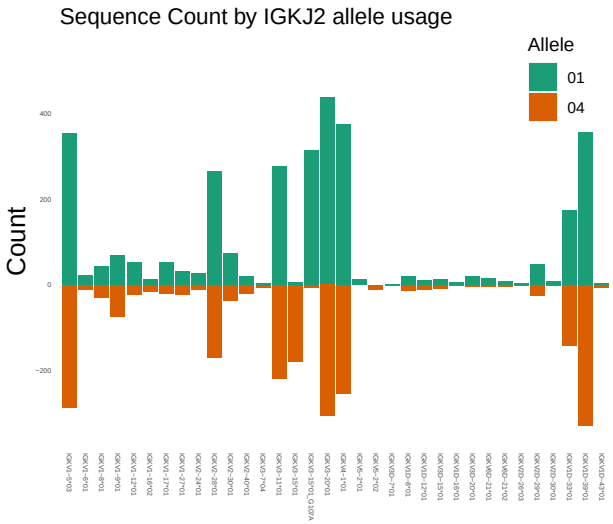

IGKV6D−41*01
3 sequences assigned
3 (100%) exact matches, in which:
3 unique CDR3
2 unique J
Count
Nucleotide Difference


IGKV1D−43*01
41 sequences assigned
36 (87.8%) exact matches, in which:
36 unique CDR3
6 unique J
Count
Nucleotide Difference

3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

```
## Repertoire file: /misc/work/dolphinnext/PRJEB26509/run172/work/6f/bea822831f9a49f3ed0208e99f938f/P1_
##
## Germline reference file: /misc/work/dolphinnext/PRJEB26509/run172/work/6f/bea822831f9a49f3ed0208e99f
##
## Novel allele file: /misc/work/dolphinnext/PRJEB26509/run172/work/6f/bea822831f9a49f3ed0208e99f938f/n
##
## Species: Homosapiens
##
## Chain: IGKV
##
## Segment: V
```