

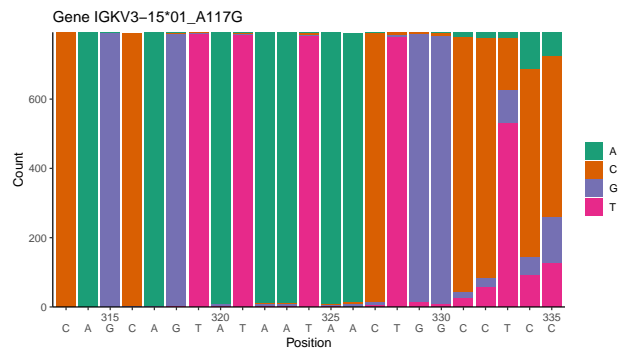
OGRDBstats Report

Contents

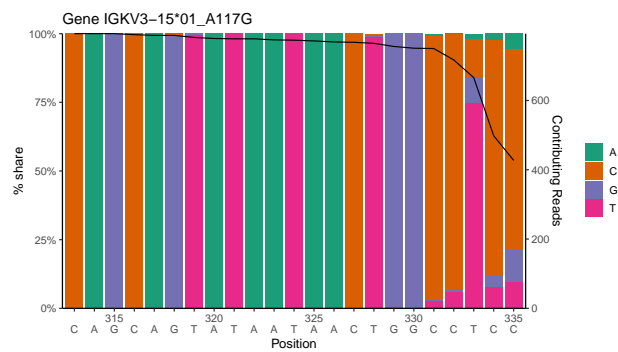
1	Novel sequence analysis	2
1.1	End-nucleotide composition	2
1.2	Per-nucleotide consensus where previous nucleotides match the consensus	2
1.3	Whole-sequence composition of each assigned read	2
1.4	Final three nucleotides: frequency of each observed triplet	2
1.5	CDR3 length distribution, in assignments to novel alleles	3
2	Variation from germline, in assignments to each allele	4
3	Allele usage in potential haplotype anchor genes	8
4	Haplotype plots	9
5	Configuration settings	10

1 Novel sequence analysis

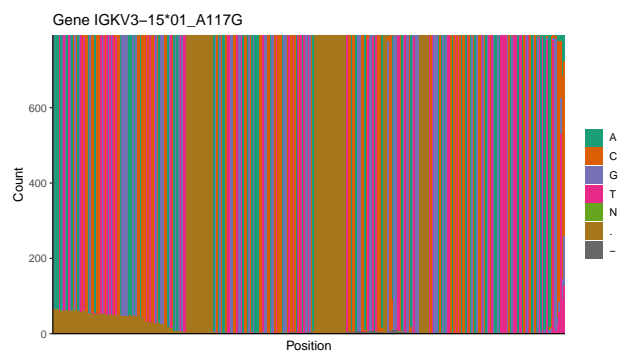
1.1 End-nucleotide composition



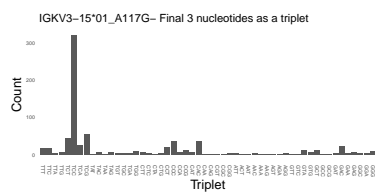
1.2 Per-nucleotide consensus where previous nucleotides match the consensus



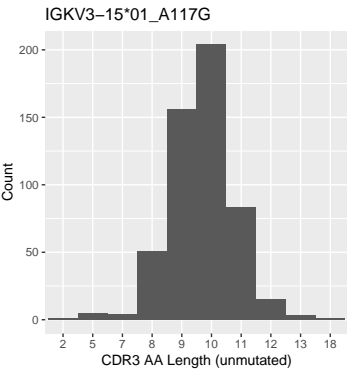
1.3 Whole-sequence composition of each assigned read



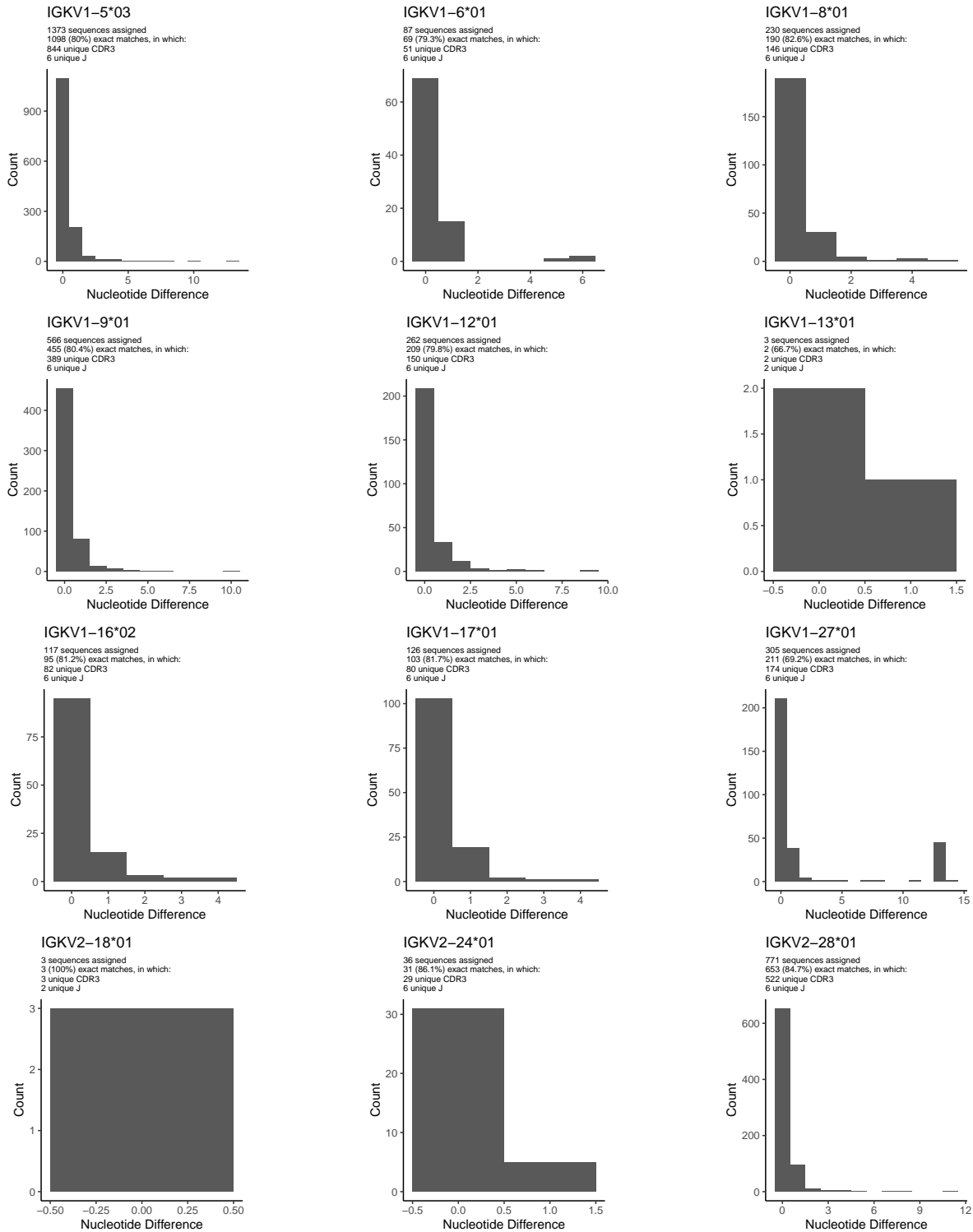
1.4 Final three nucleotides: frequency of each observed triplet

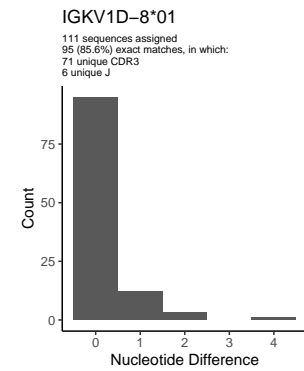
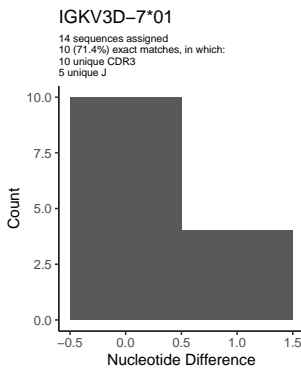
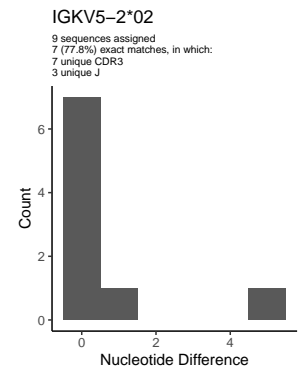
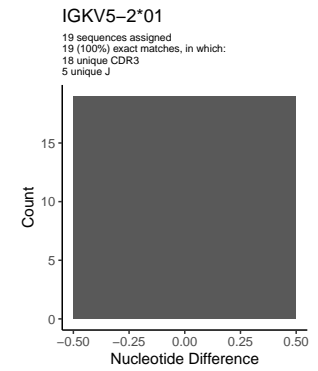
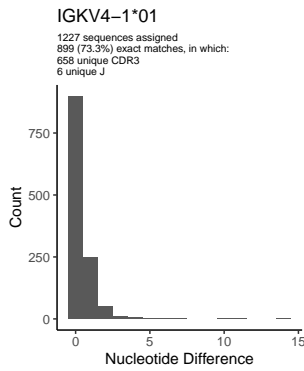
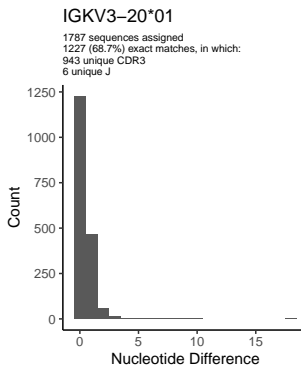
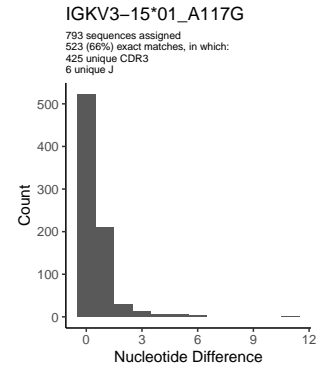
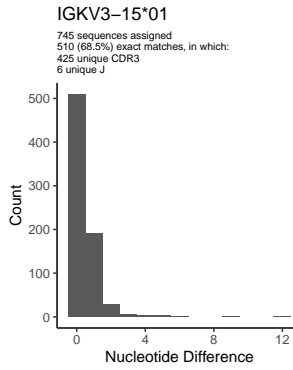
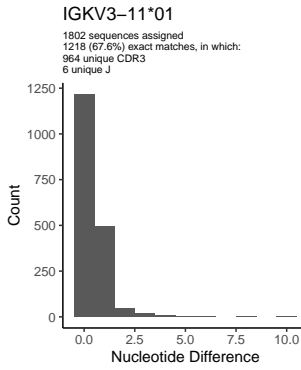
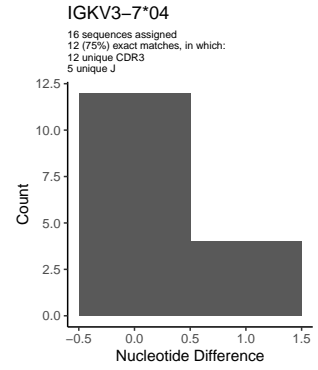
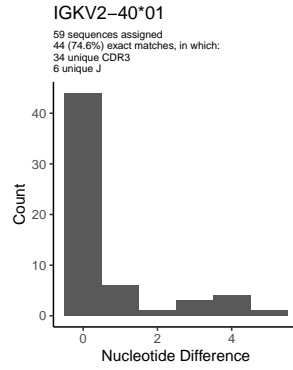
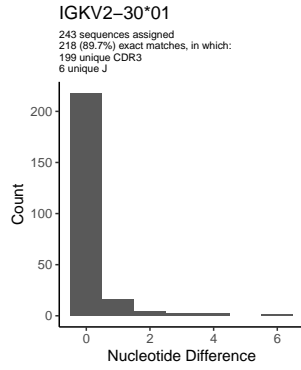


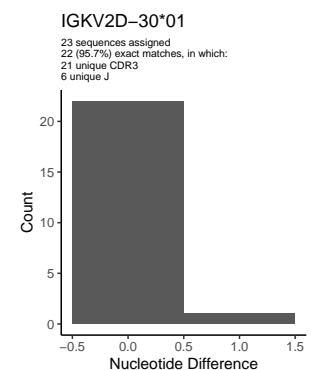
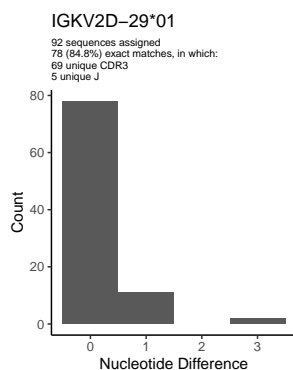
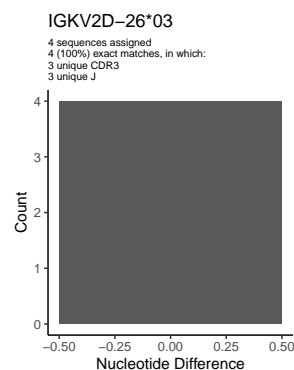
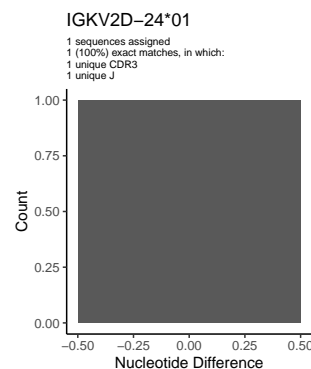
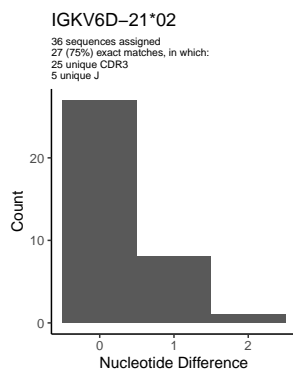
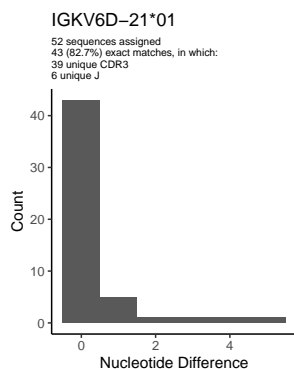
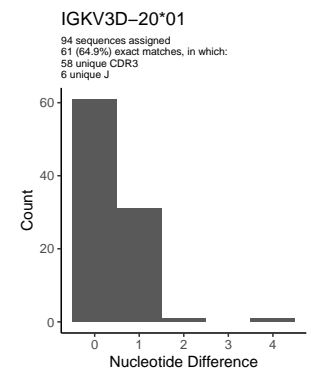
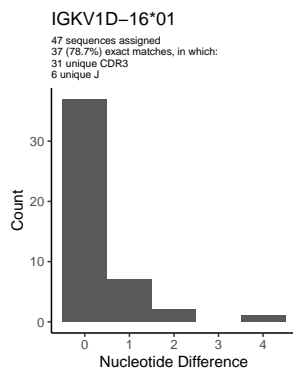
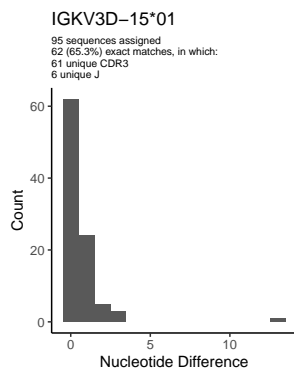
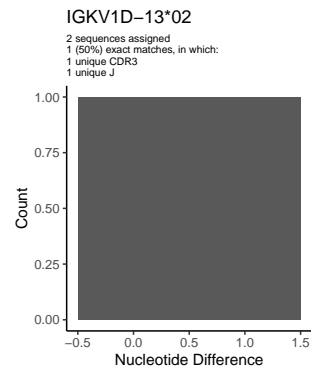
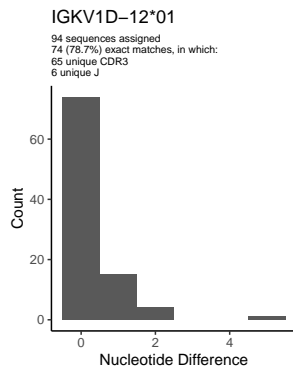
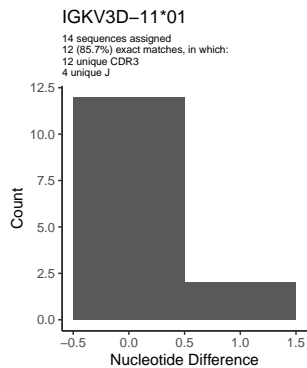
1.5 CDR3 length distribution, in assignments to novel alleles

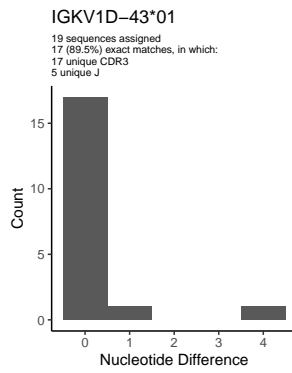
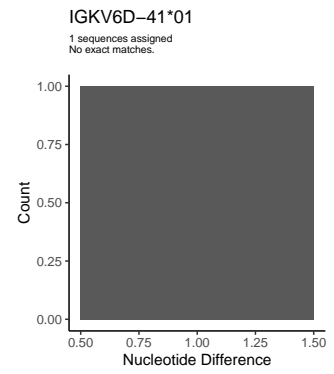
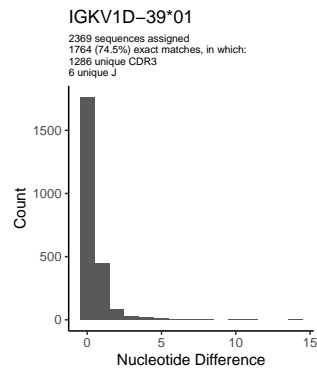
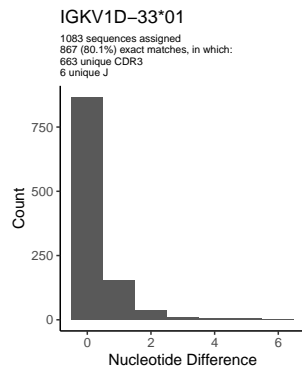


2 Variation from germline, in assignments to each allele

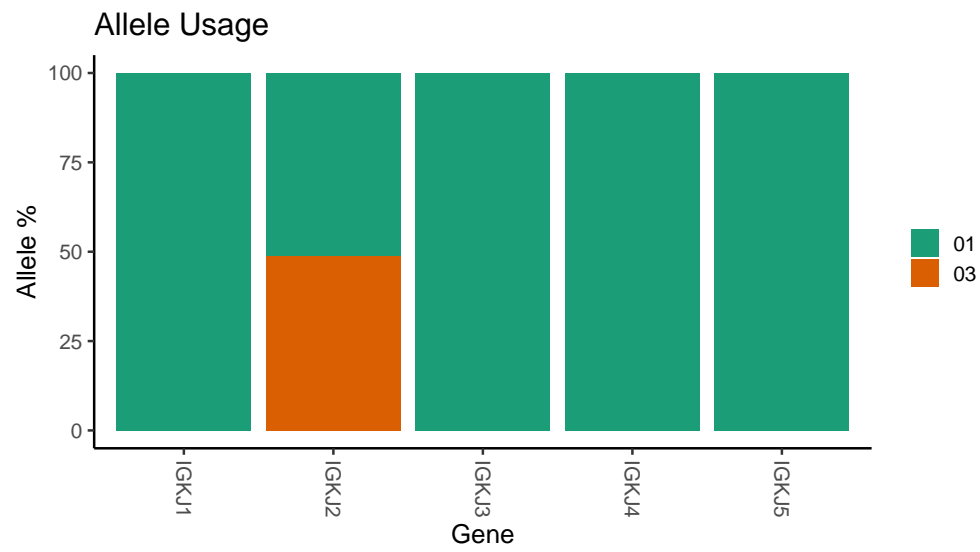




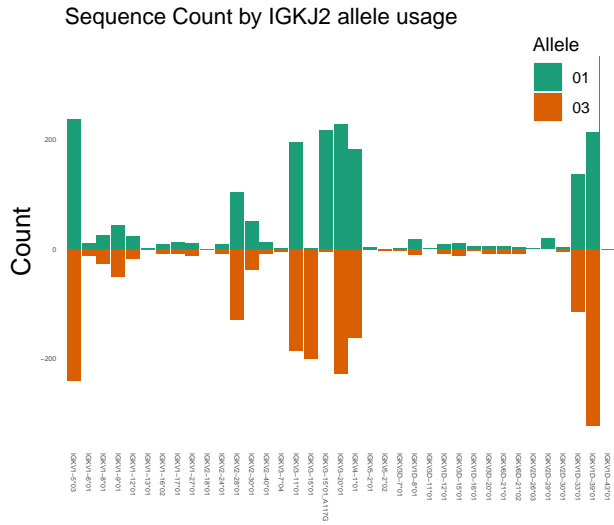




3 Allele usage in potential haplotype anchor genes



4 Haplotype plots



5 Configuration settings

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##
## Germline reference file: /misc/work/dolphinnext/PRJEB26509/run172/work/26/947665155ac5eadbd825906ec4
##
## Novel allele file: /misc/work/dolphinnext/PRJEB26509/run172/work/26/947665155ac5eadbd825906ec45882/n
##
## Species: Homosapiens
##
## Chain: IGKV
##
## Segment: V
```