

OGRDBstats Report

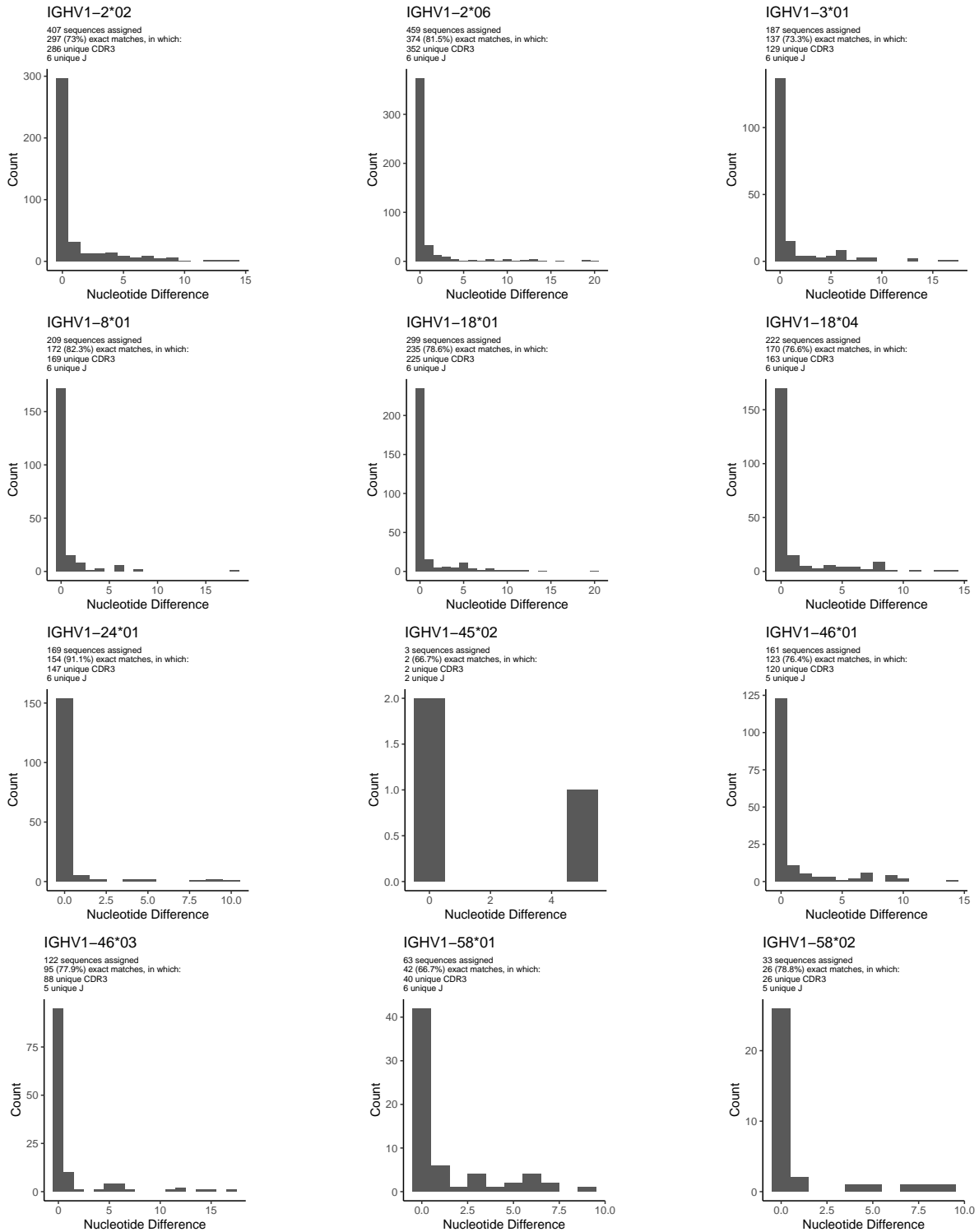
Contents

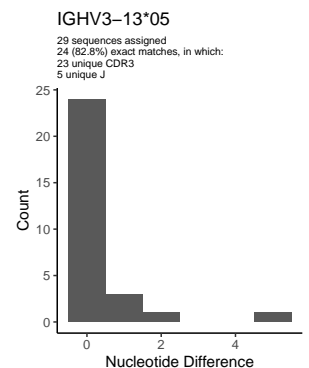
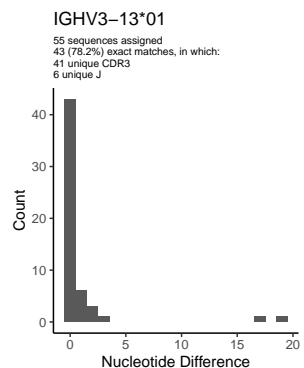
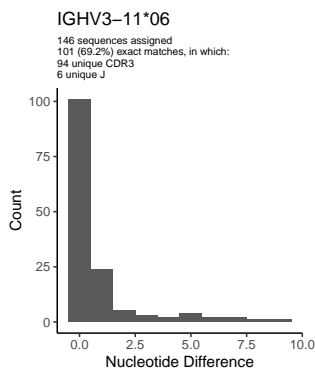
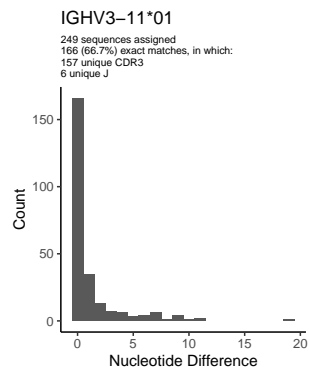
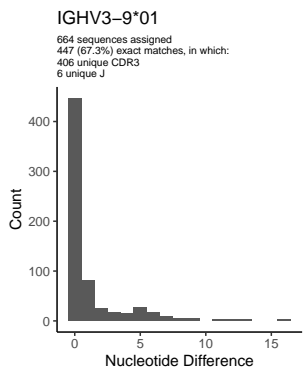
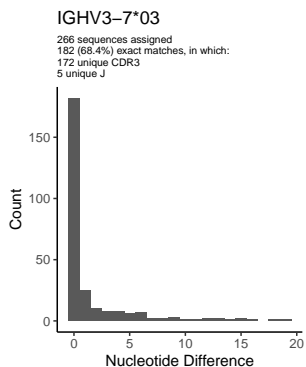
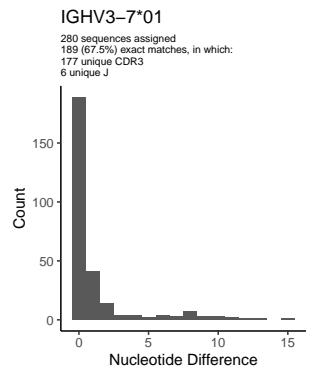
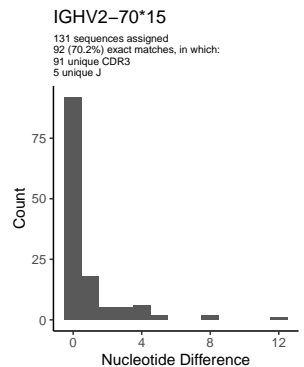
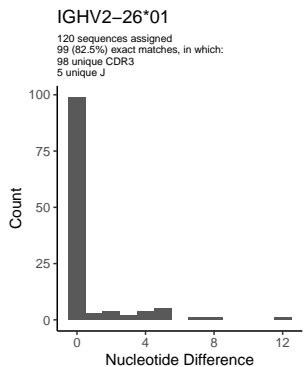
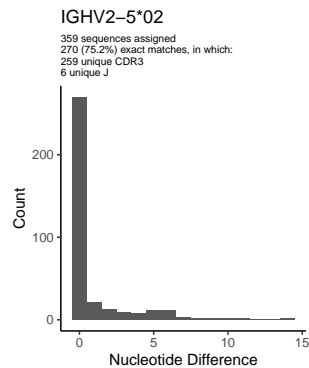
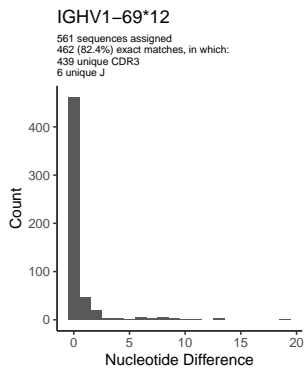
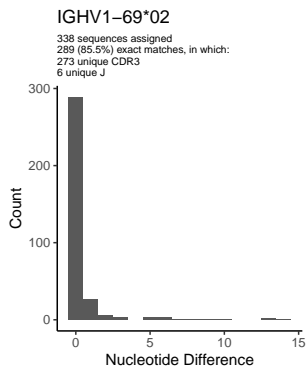
1	Novel sequence analysis	2
1.1	CDR3 length distribution, in assignments to novel alleles	2
2	Variation from germline, in assignments to each allele	3
3	Allele usage in potential haplotype anchor genes	8
4	Haplotype plots	9
5	Configuration settings	10

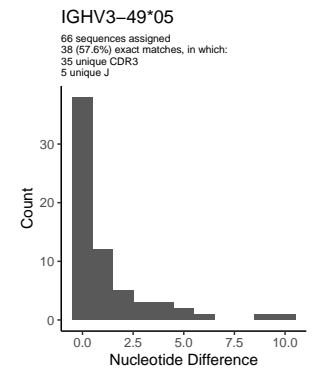
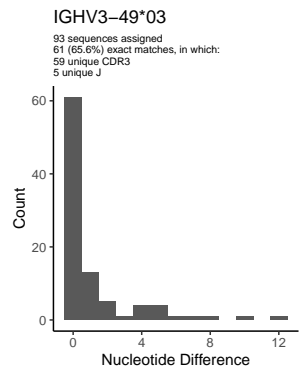
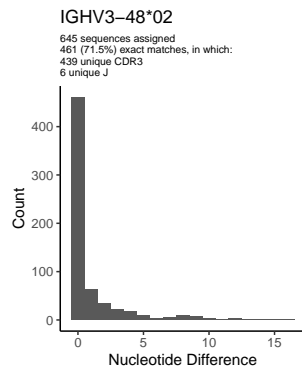
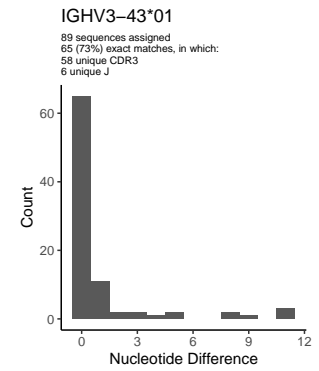
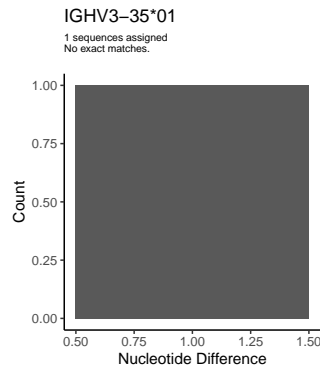
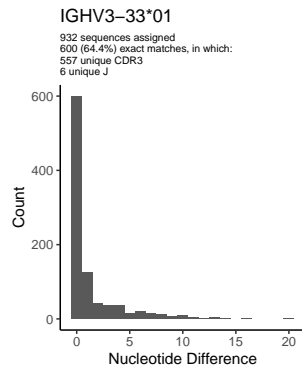
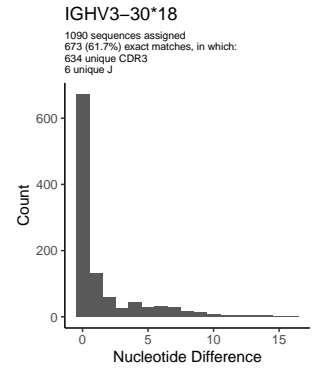
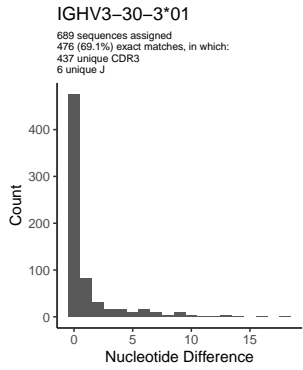
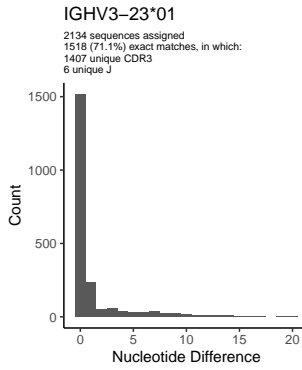
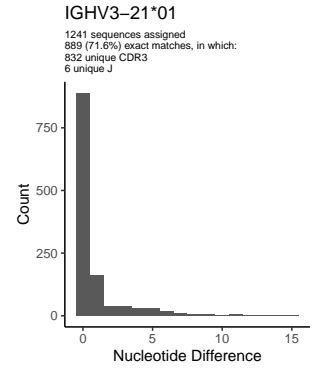
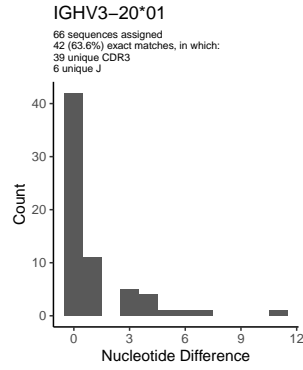
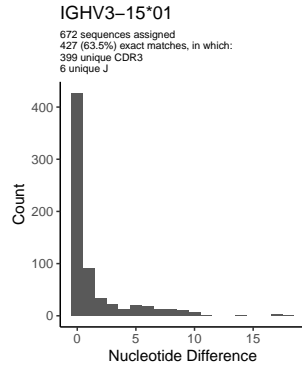
1 Novel sequence analysis

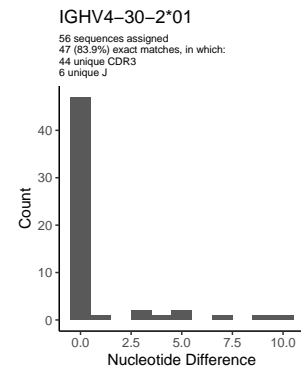
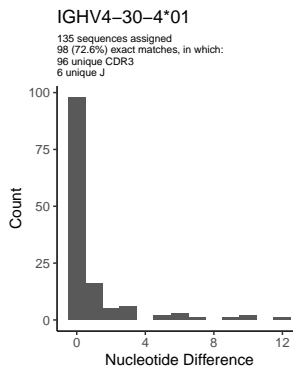
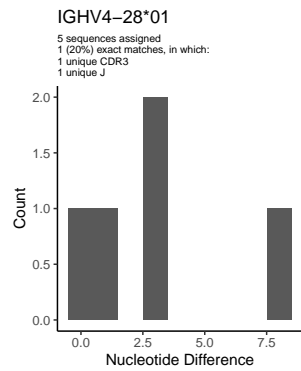
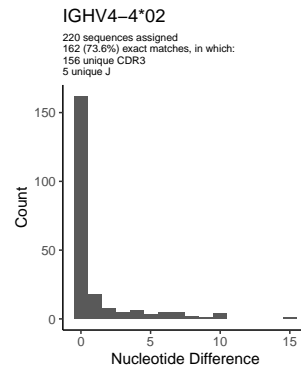
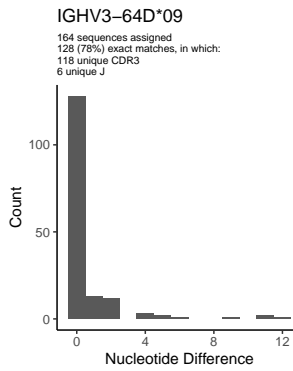
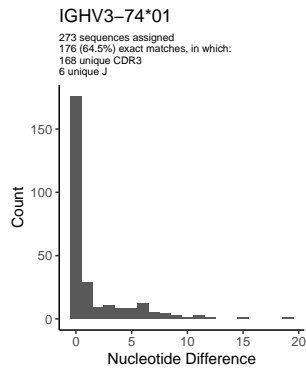
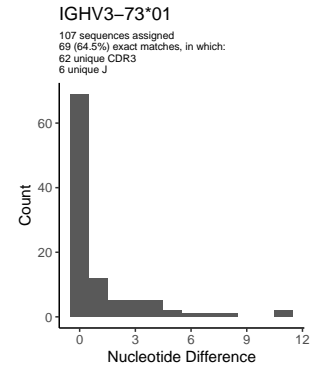
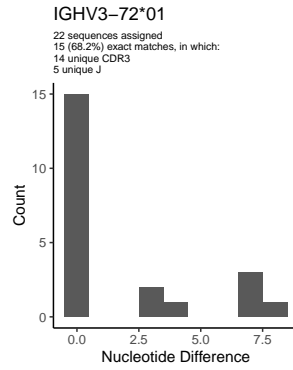
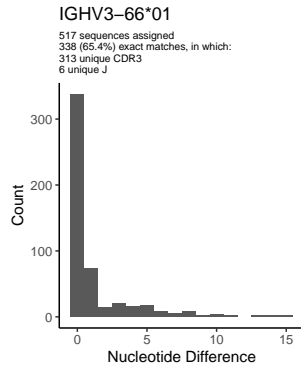
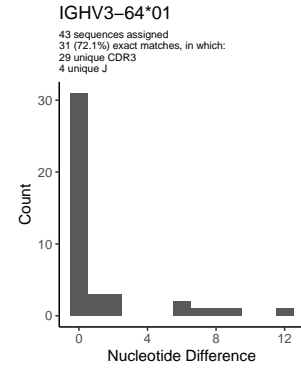
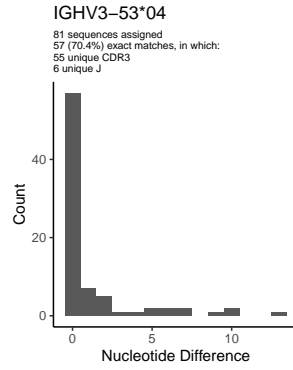
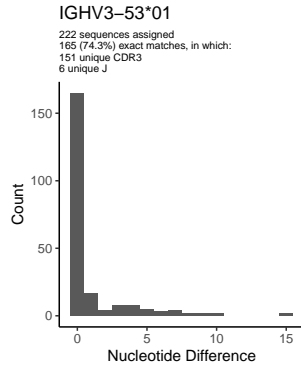
1.1 CDR3 length distribution, in assignments to novel alleles

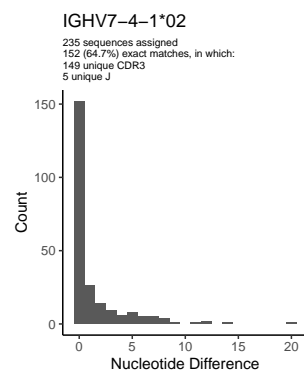
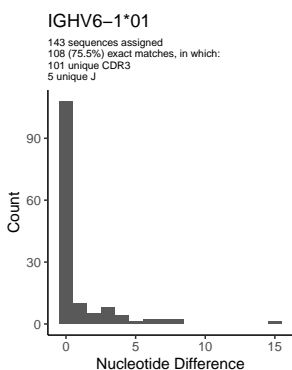
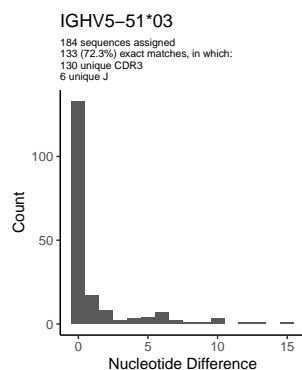
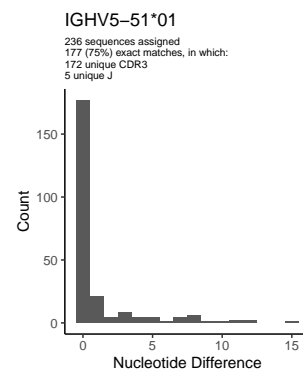
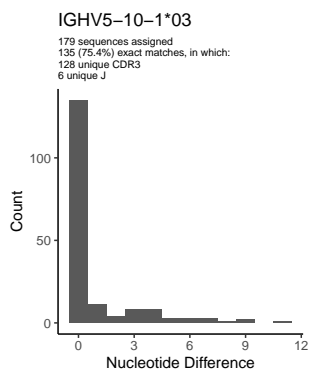
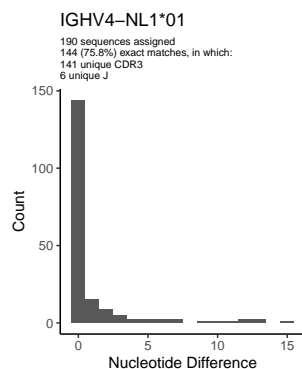
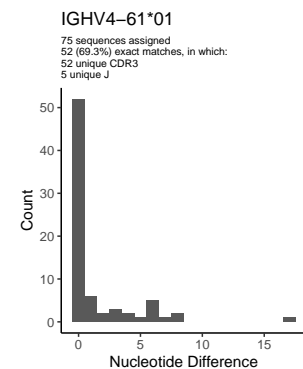
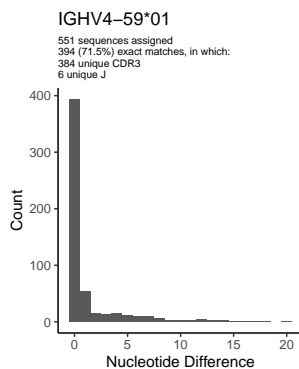
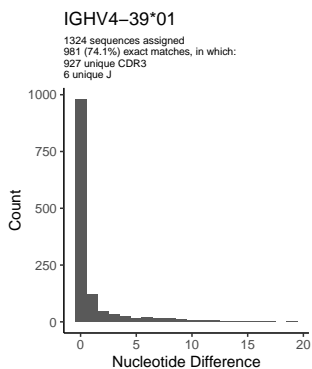
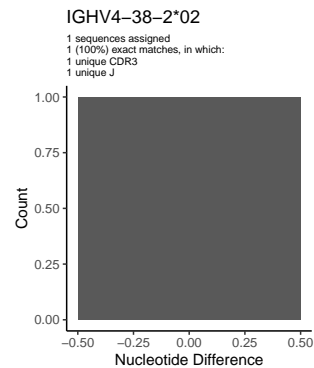
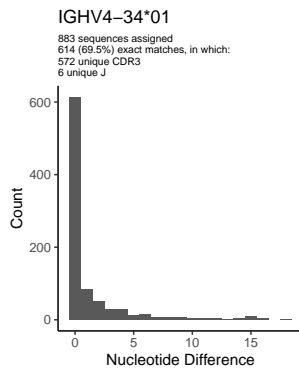
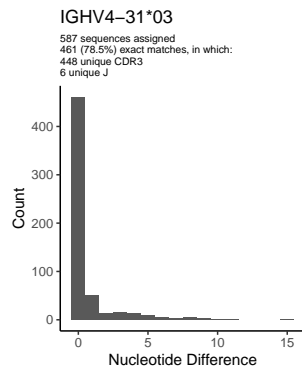
2 Variation from germline, in assignments to each allele











3 Allele usage in potential haplotype anchor genes



4 Haplotype plots

5 Configuration settings

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##
## Germline reference file: /misc/work/jenkins/PRJEB26509/S78/S78/82/82/7e/afc120b048709abc20afdb03d23e
##
## Novel allele file:
##
## Species: Homosapiens
##
## Chain: IGHV
##
## Segment: V
##
## Warning    no inferred sequences found.
```