

Supporting Evidence for Alleles Identified by TIgGER

This document contains supporting evidence for the novel V segment alleles identified by TIgGER and presented in Table 2 of:

"Automated analysis of high-throughput B cell sequencing data reveals a high frequency of novel immunoglobulin V gene segment alleles." Daniel Gadala-Maria, Gur Yaari, Mohamed Uduman, Steven H. Kleinstein (2014) Submitted.

For reference, this table is repeated below. For each predicted germline allele, a summary of the supporting evidence is provided, including: y-intercept detection, mutated-to nucleotide frequency, and J gene/junction length distribution. The complete nucleotide sequence of the proposed novel allele is also included. These data are analogous to Figure S3 in the manuscript. Equivalent data is also included for the six putative alleles excluded from Table 2 to support the conclusion that these are false positive results: IGHV3-21*01_T56C, IGHV3-23*01_T56C, IGHV3-48*02_T56C, IGHV3-66*02_T56C, IGHV3-74*01_T56C, IGHV4-39*01_C278T.

Table 2.

#	Nearest Allele(s)	Polymorphic Site(s)	Subject(s) (Tech.)	Perfect Matches
1	1-2*02, 1-2*05	T163C (vs *02) T299C (vs *05)	hu420143 (454)	629
			4106 (MiSeq)	736
			4014 (MiSeq)	283
2	1-8*02	G234T	PGP1 (454)	647
			PGP1 (MiSeq)	453
3	1-18*01	T111C	3928 (MiSeq)	1560
4	3-11*03	T13G	420IV (454)	866
5	3-11*03	C300T	3928 (MiSeq)	101
6	3-20*01	C307T	PGP1 (454)	187
			PGP1 (MiSeq)	85
7	1-69*06	C191T	3931 (MiSeq)	284
8	2-70*01, 2-70*11	T164G (vs *01)	PGP1 (454)	220
		G2A (vs *11)		
9	3-64*05	A210C & G265C	3928 (MiSeq)	251
10	3-43*01	A112G, C222T, & A286G	420IV (454)	192
11	3-9*01	C296T	PGP1 (454)	128
			PGP1 (MiSeq)	202

Inferred novel alleles are listed in order of prevalence. For each novel allele, the nearest allele(s) from IMGT is listed, along with the site(s) that differ(s) between the two. (The first letter represents the database nucleotide, the number is the IMGT-numbered nucleotide position, and the second letter represents the novel allele's nucleotide at that position). Allele 8 could not be detected in the PGP1 MiSeq data as the allele-differentiating position is in primer area. Excluded from this table are six alleles which were predicted by TIgGER but are believed to be artifacts (see text for further discussion). Novel alleles 3, 4, 9, and 11 have since been added to the IMGT database as *04, *05, D*06, and *03, respectively.

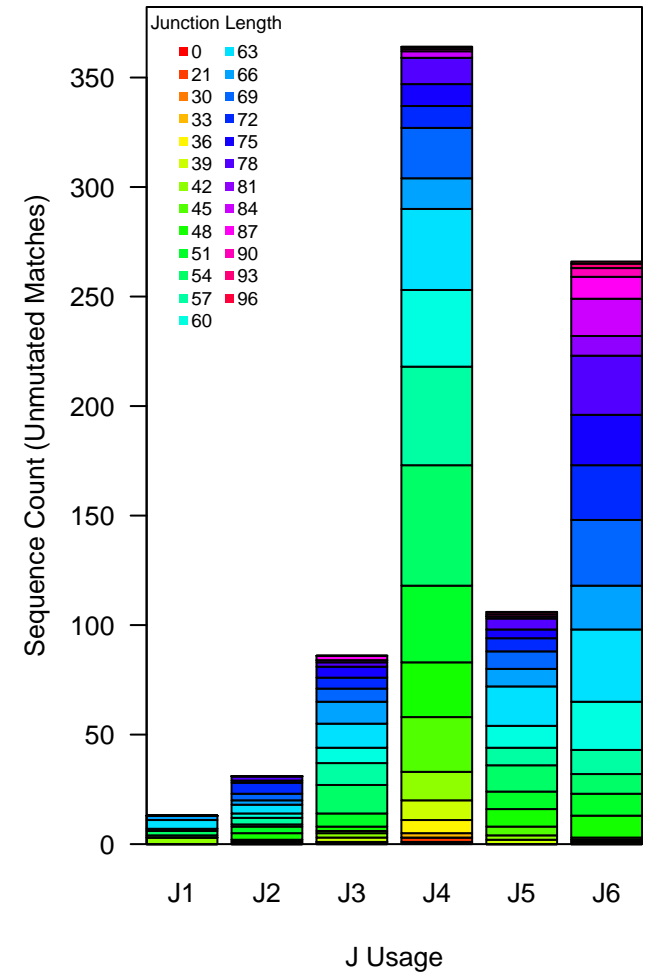
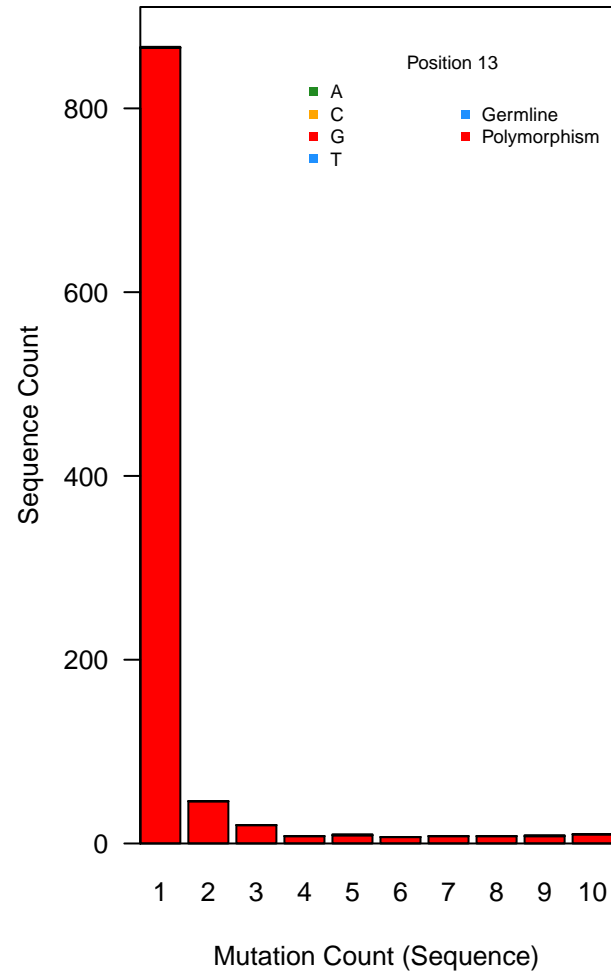
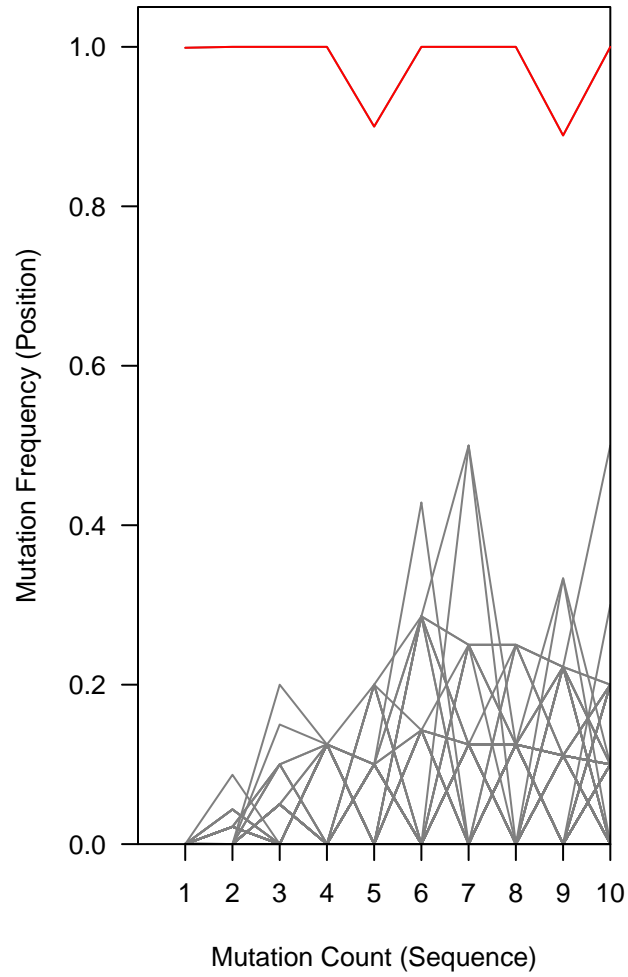
SUBJECT:

410IV

TECHNOLOGY:

454

IGHV3-11*03_T13G

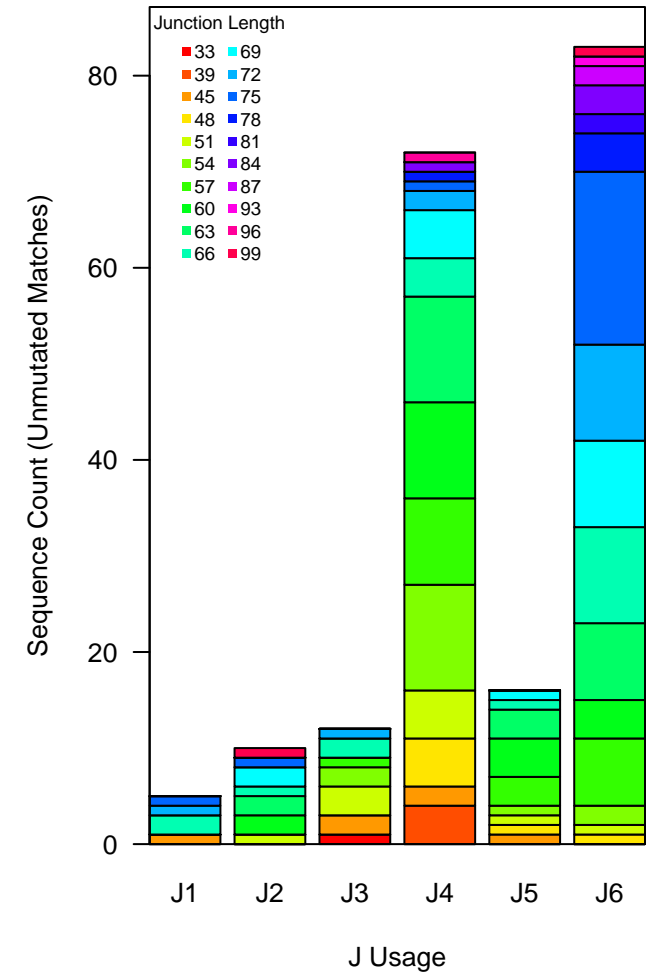
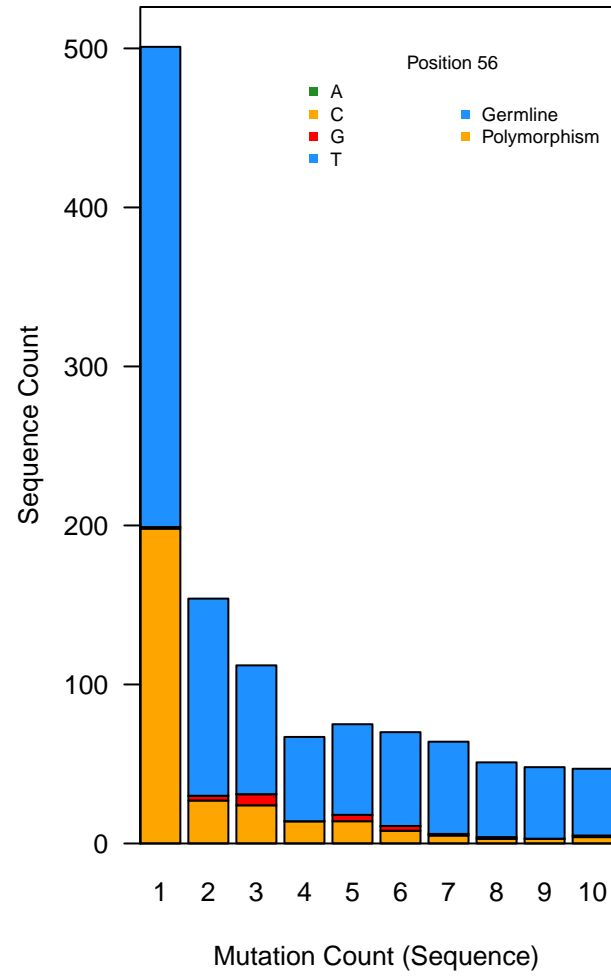
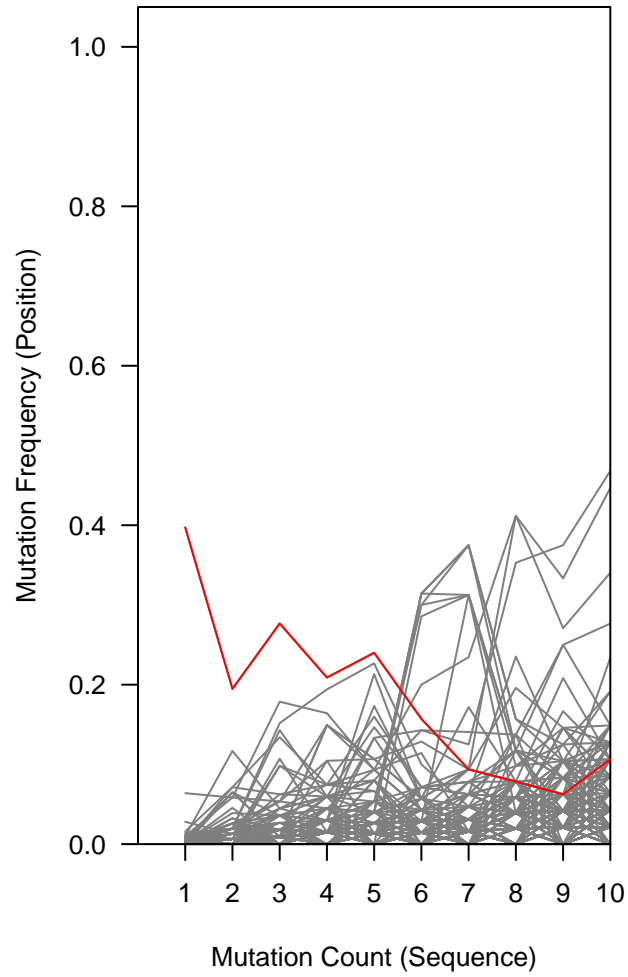


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IGHV3-21*01_T56C



IGHV3-21*01_T56C GAGGTGCAGCTGGTGGAGTCTGGGGGA---GGCC TGGTCAAGCCTGGGGGGTCCCCGAGACTCTCCTGTGCAGCCTCTGGATTACCTTC-----AGTAGCTATAGC

IGHV3-21*01T.....

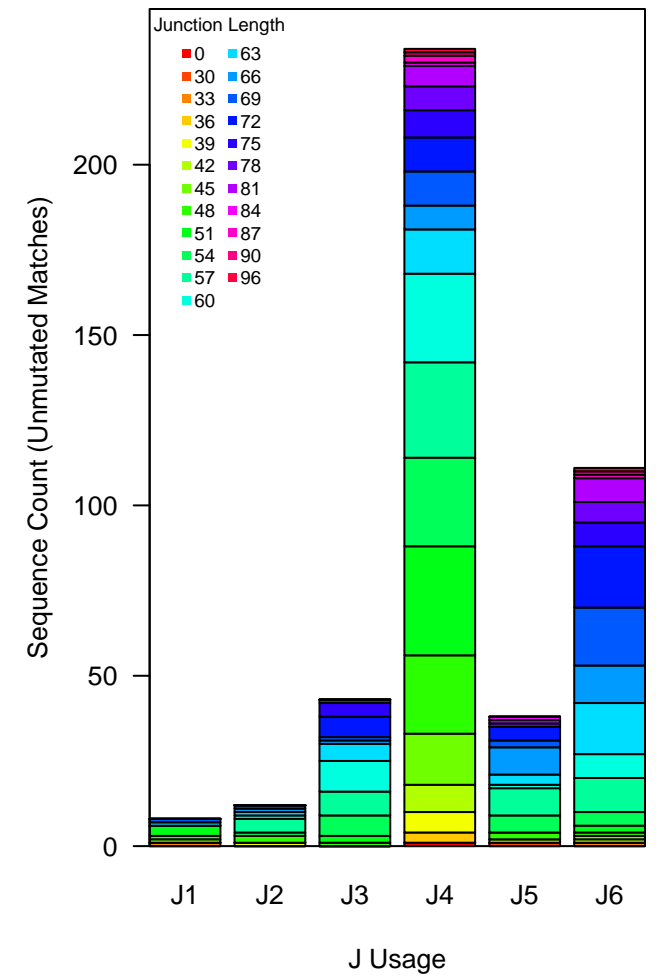
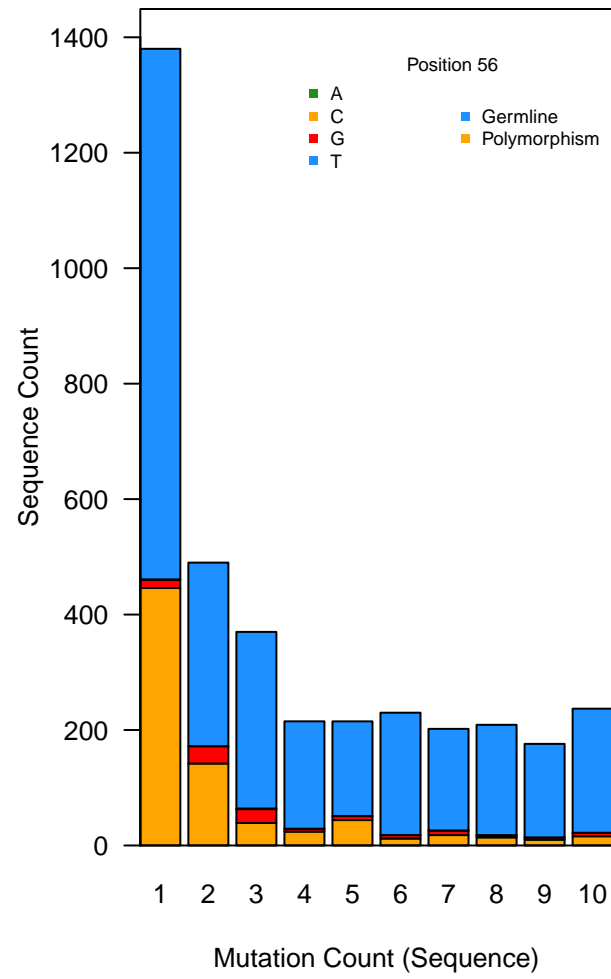
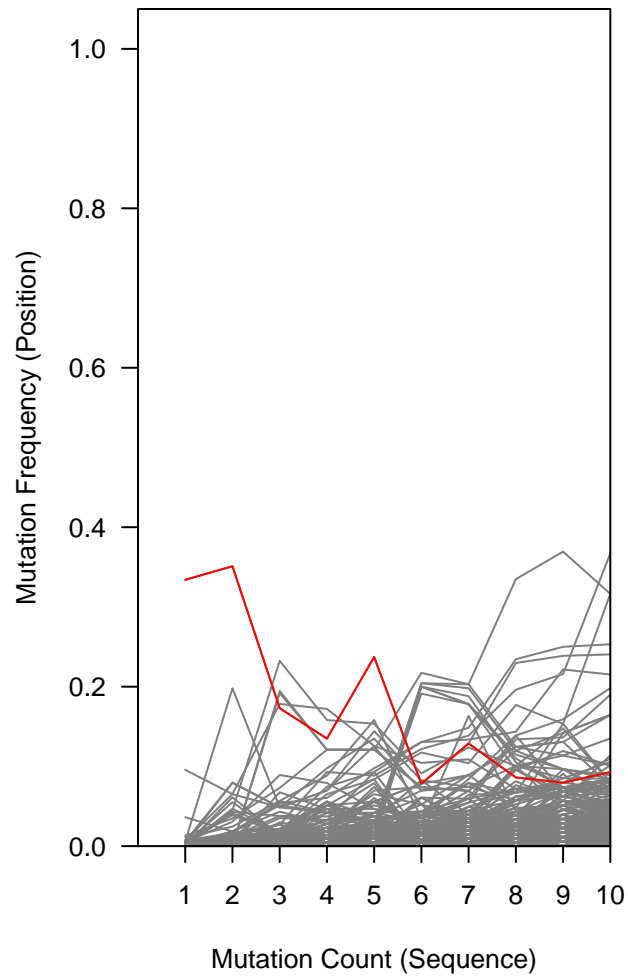
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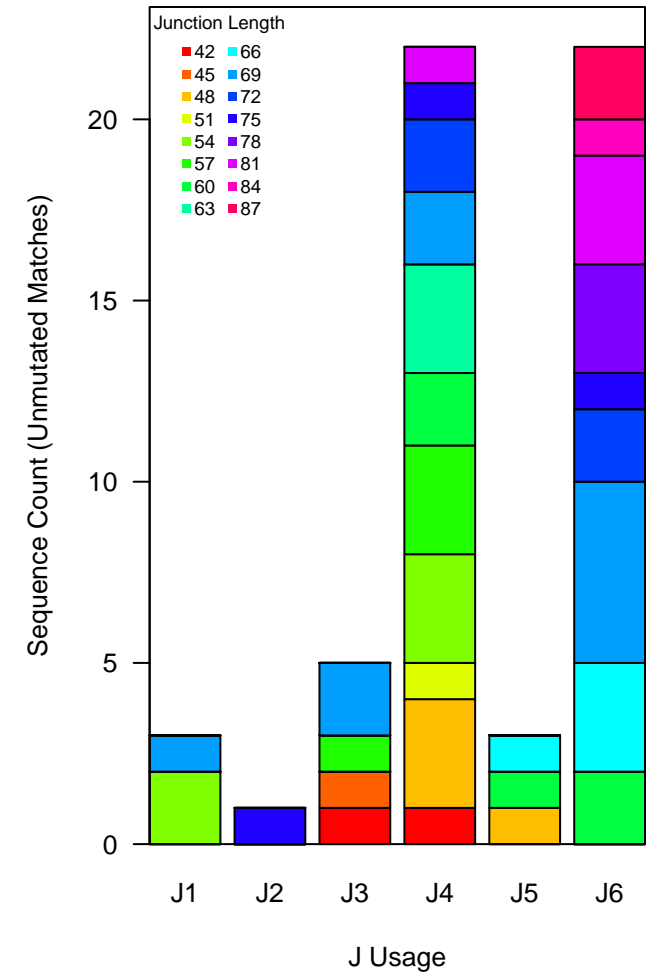
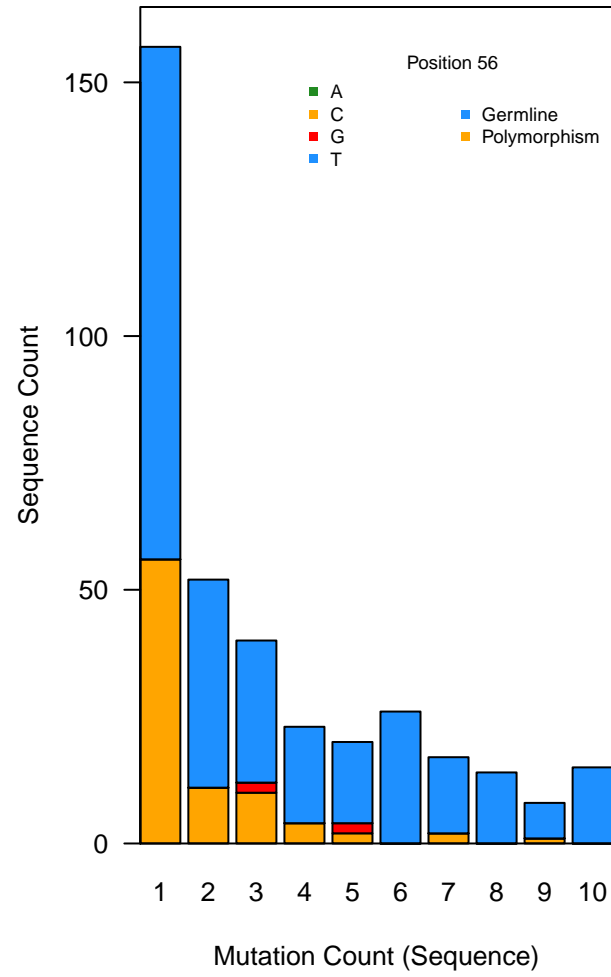
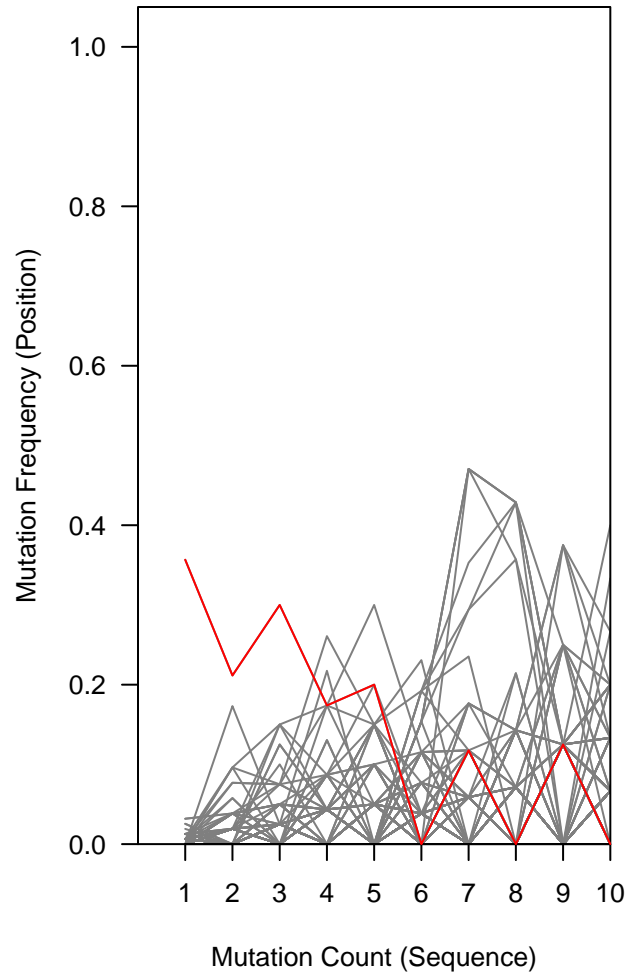
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IGHV3-48*02T.....

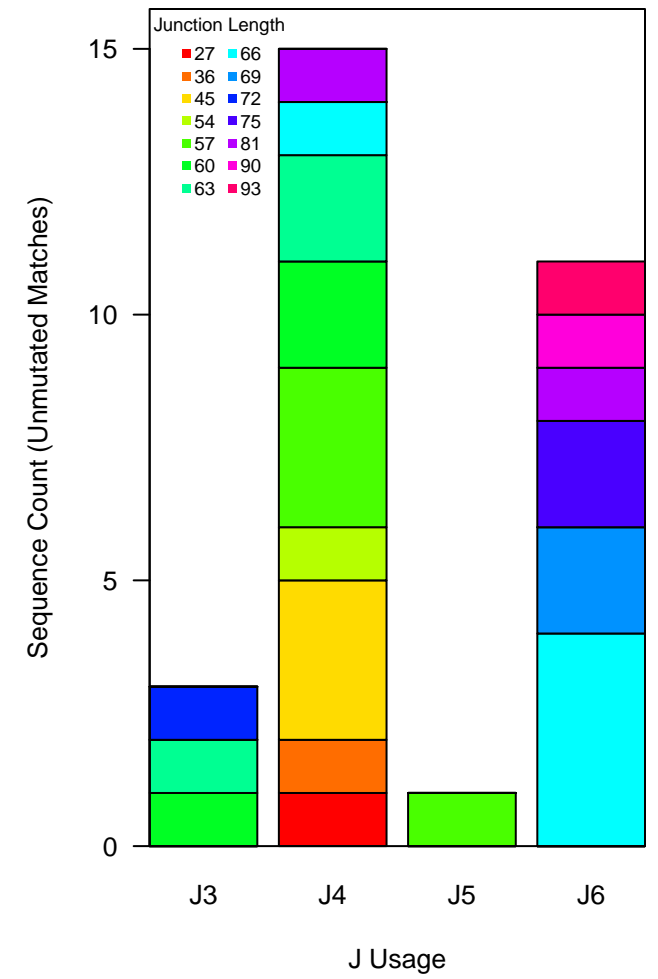
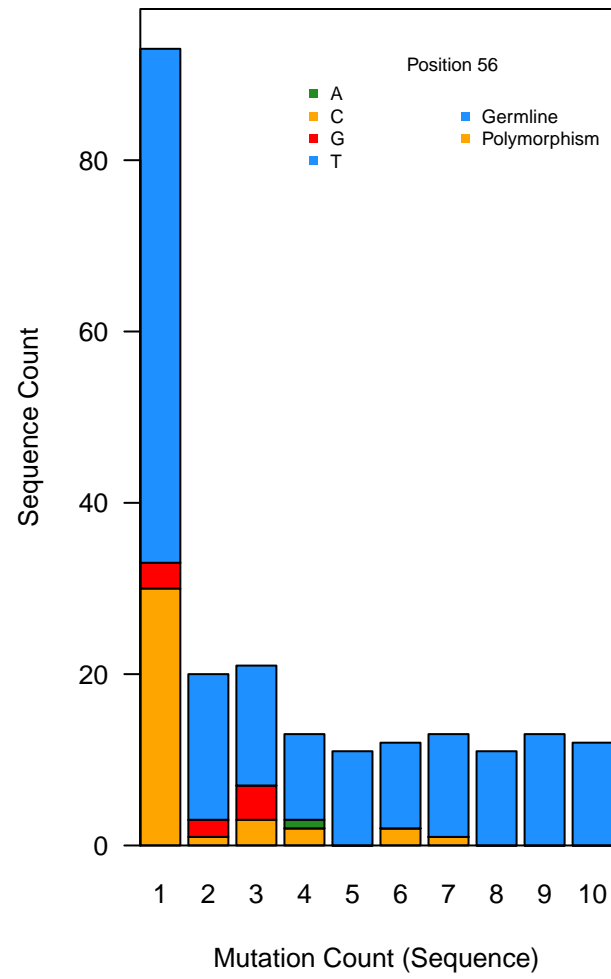
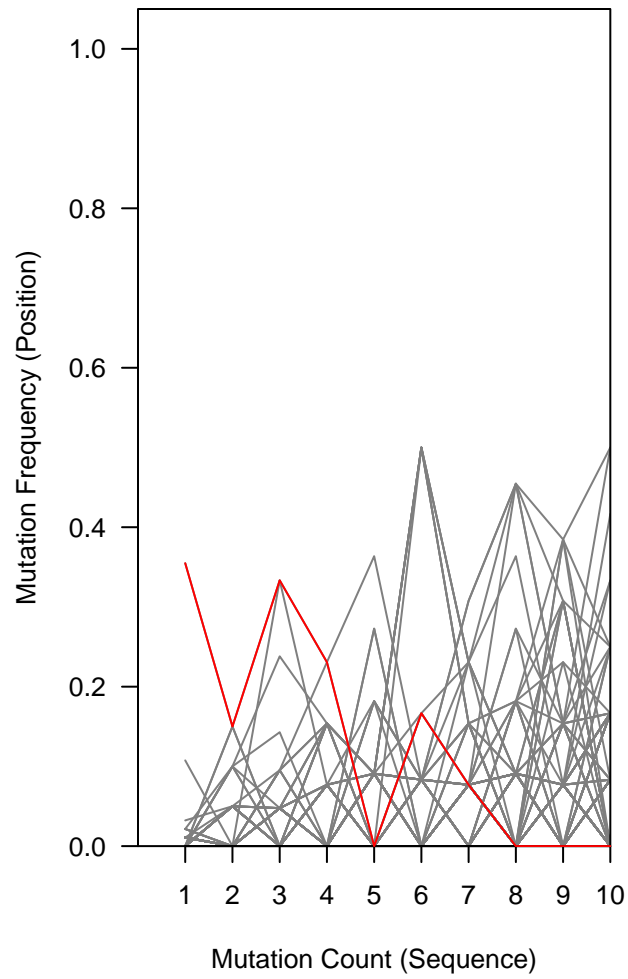
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IGHV3-66*02_T56C GAGGTGCAGCTGGTGGAGTCTGGGGGA---GGCTTGGTCCAGCCTGGGGGGTCCCCGAGACTCTCCTGTGCAGCCTCTGGATTCCACCGTC-----AGTAGCAACTAC

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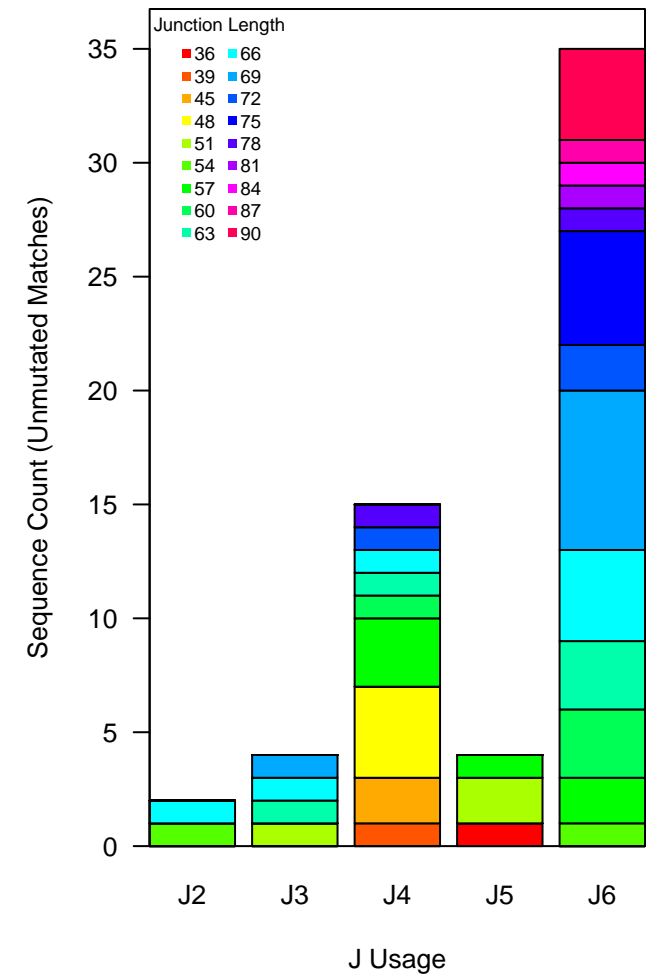
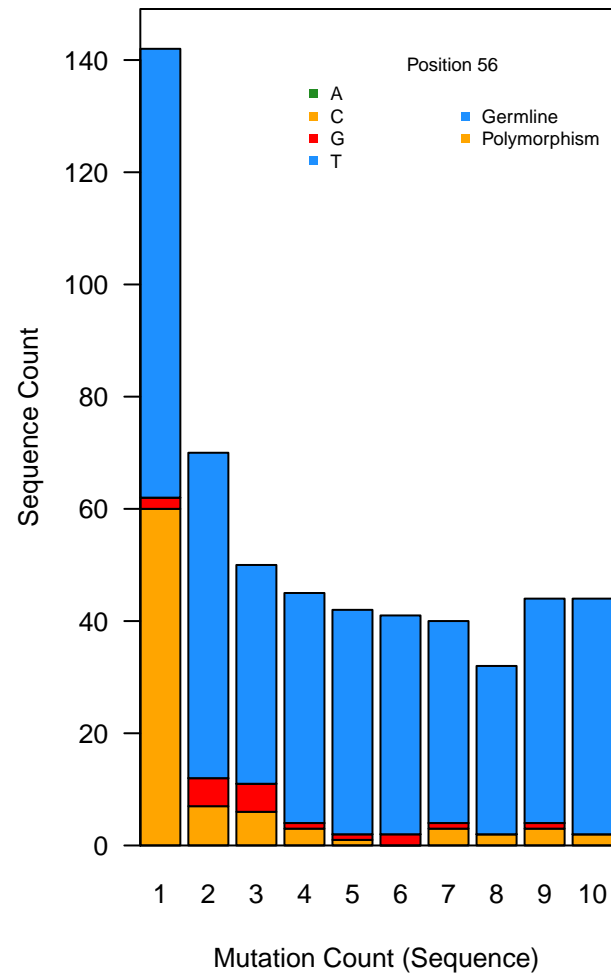
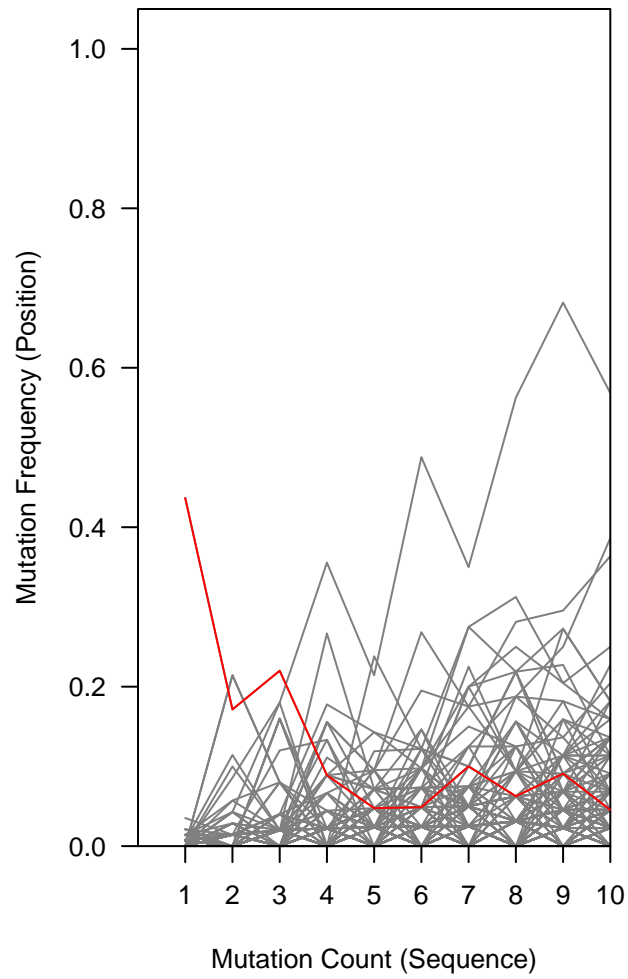
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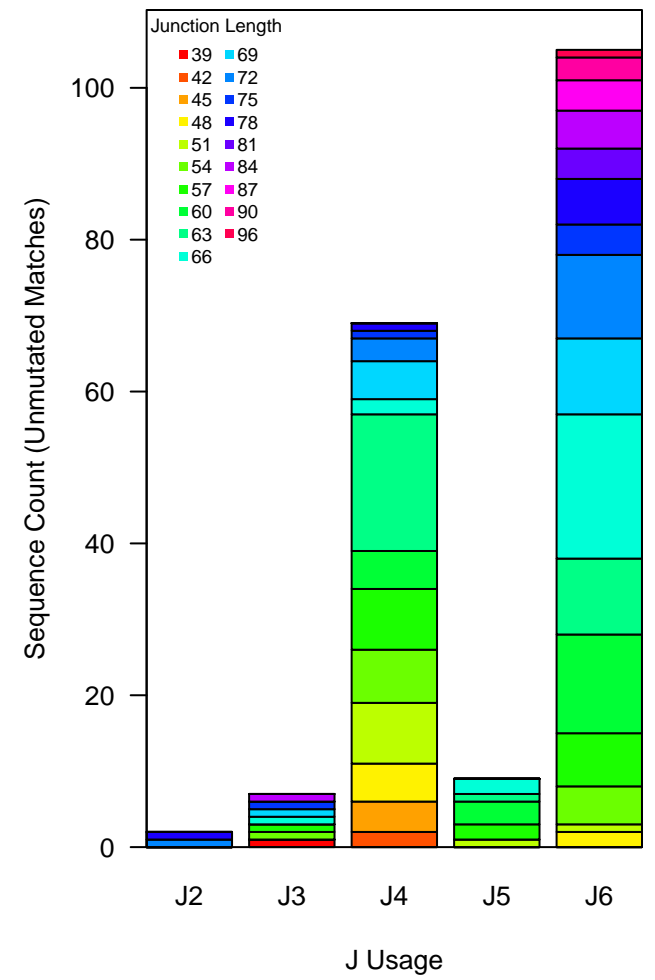
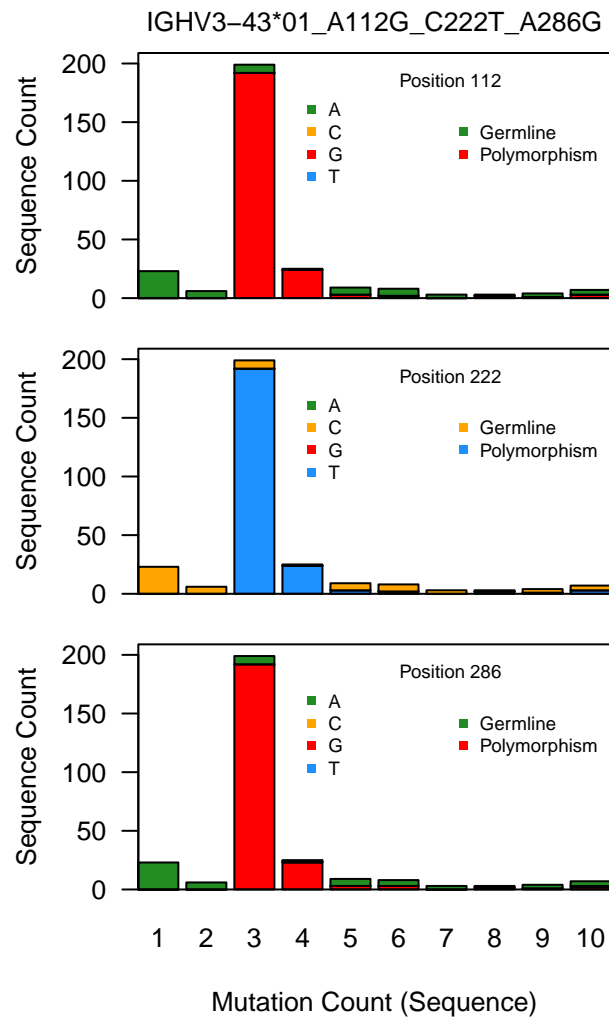
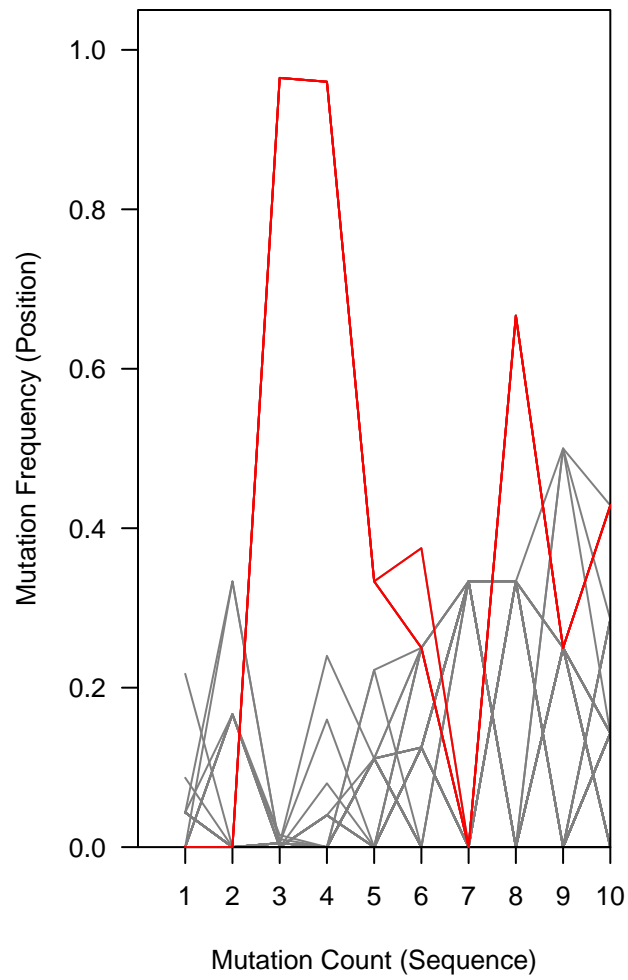
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IV3-43*01_A112G_C222T_A286G GAAGTGCAGCTGGTGGAGTCTGGGGGA---GTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTT-----GATGATTATGCC

IGHV3-43*01A..

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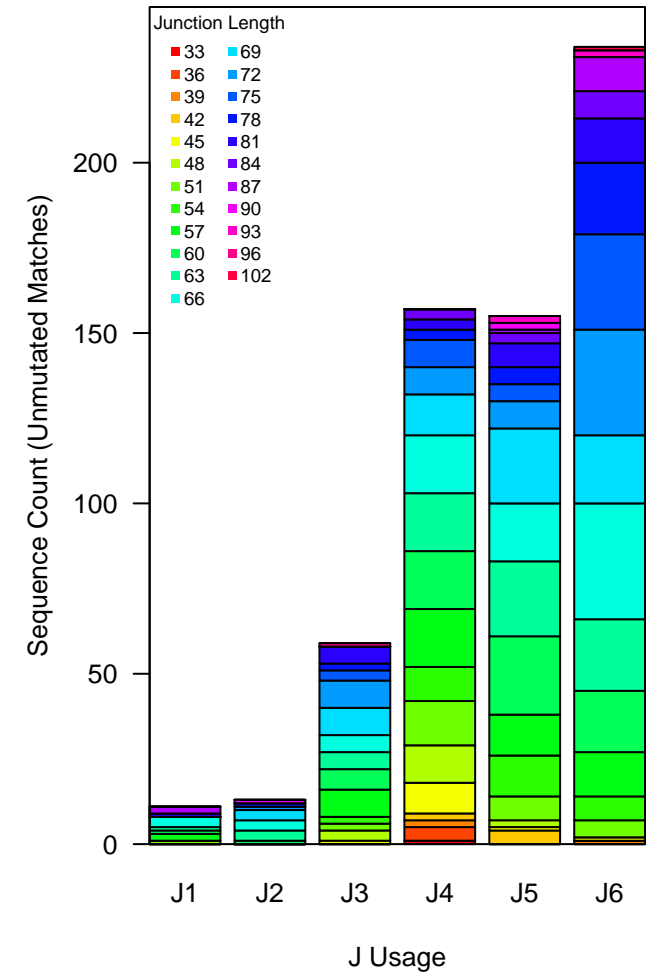
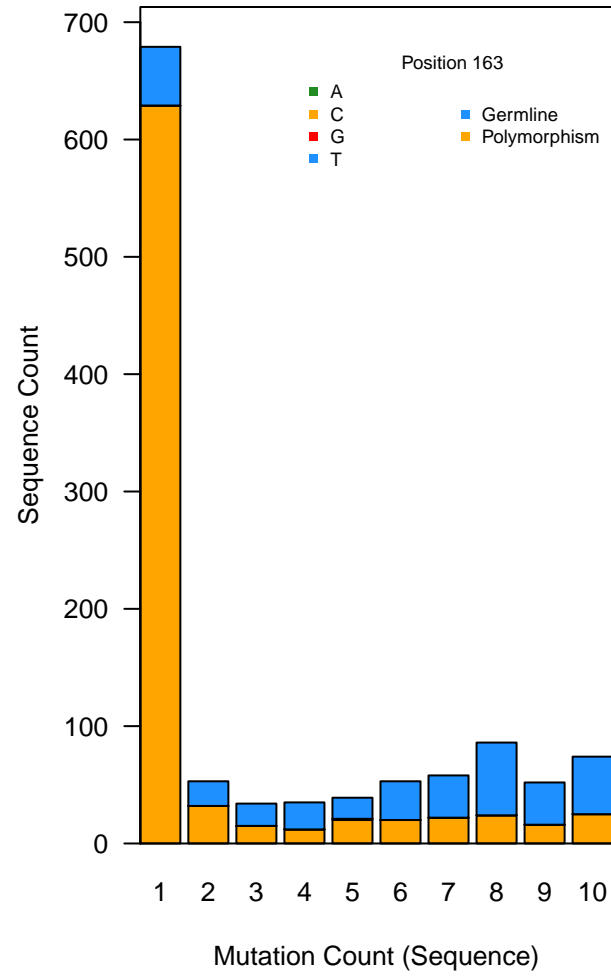
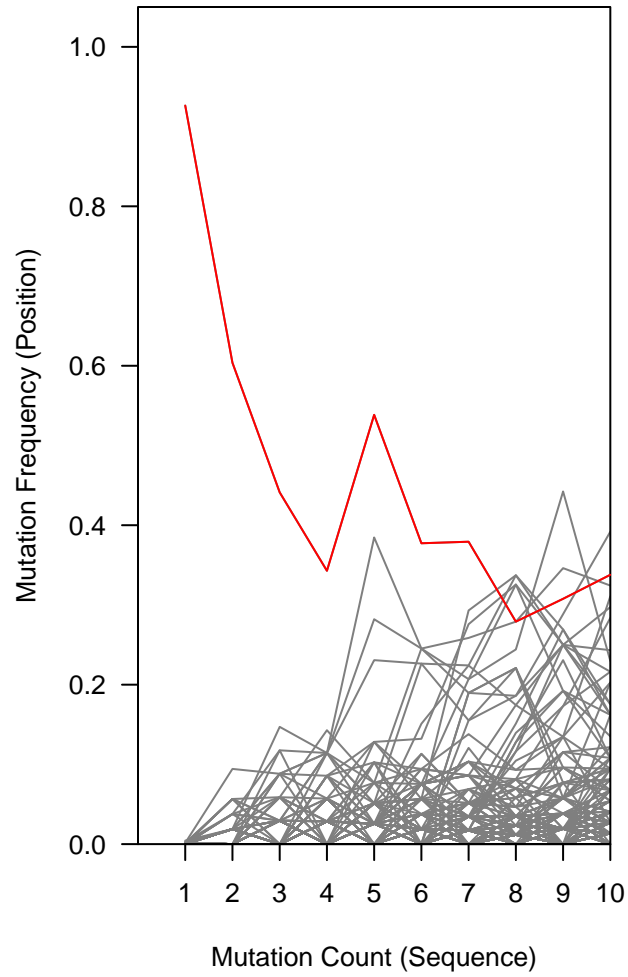
SUBJECT:

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454

IGHV1-2*02_T163C

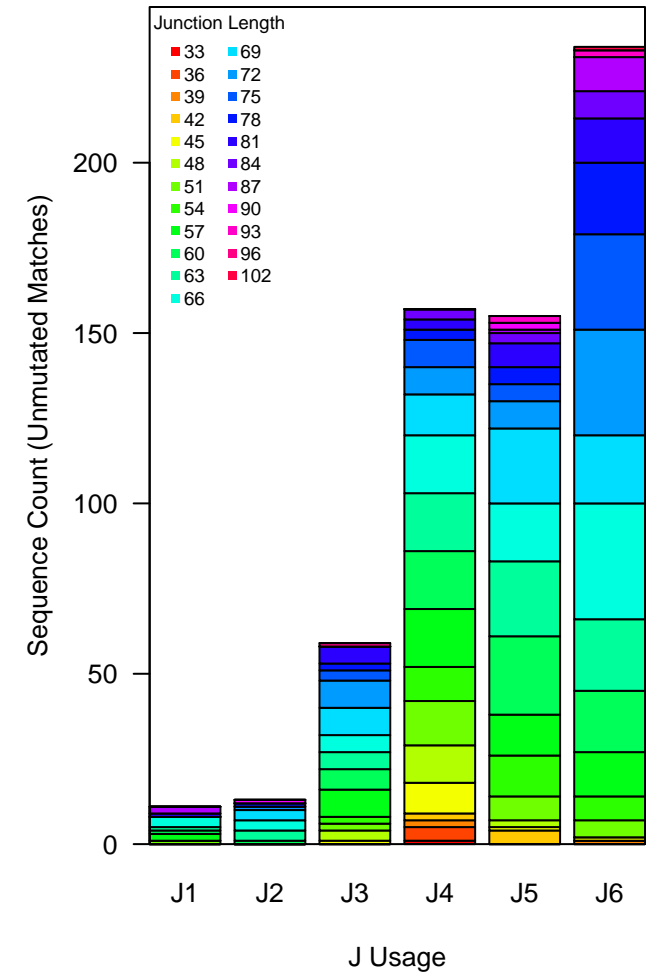
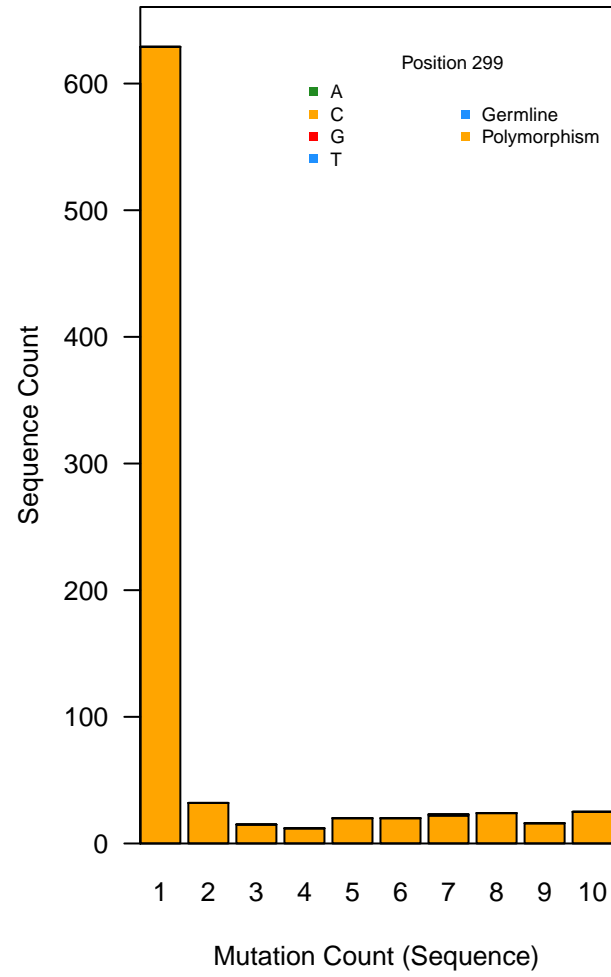
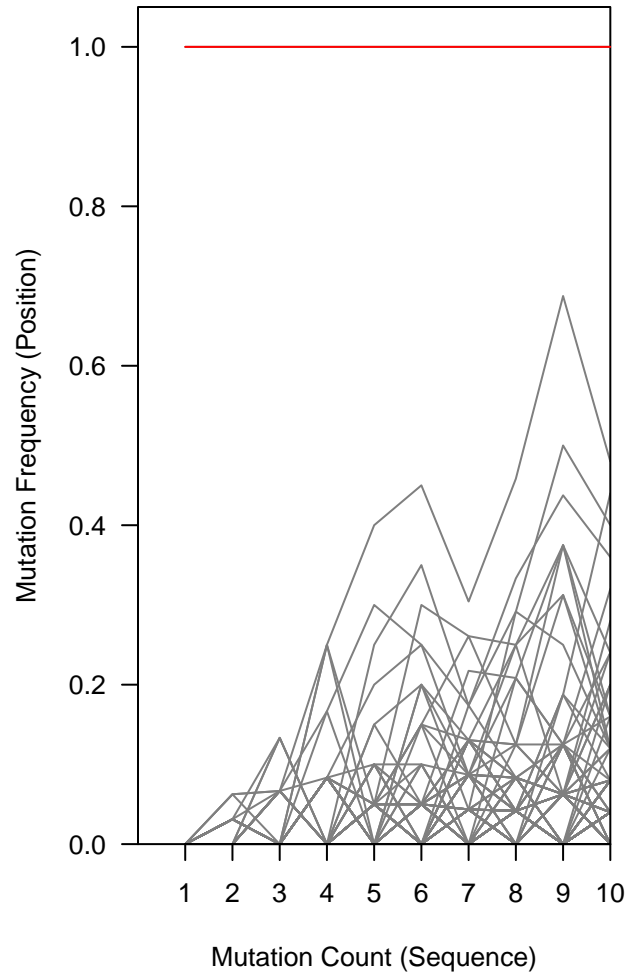


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 IGHV1-2*02

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IGHV1-2*05_T299C



IGHV1-2*05_T299C CAGGTGCAGCTGGTGCAGTCTGGGGCT---GAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGC TTCTGGATACACCTTC-----ACCGGCTACTAT
 IGHV1-2*05

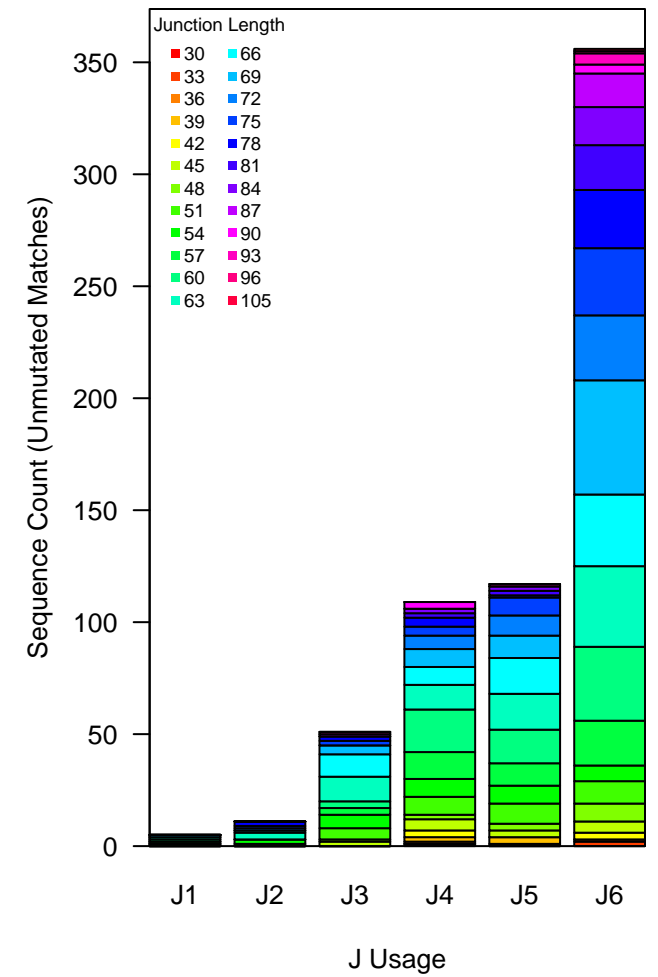
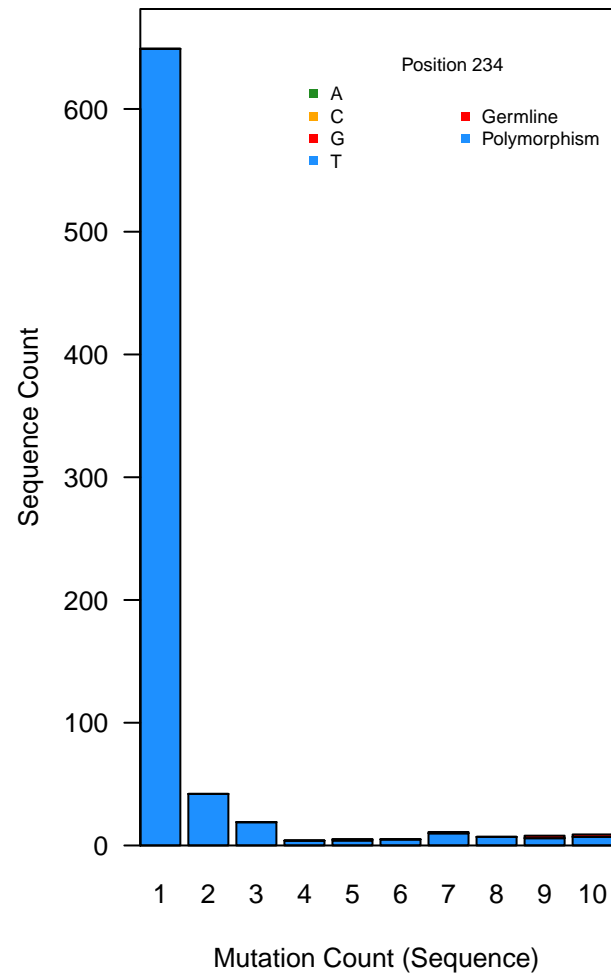
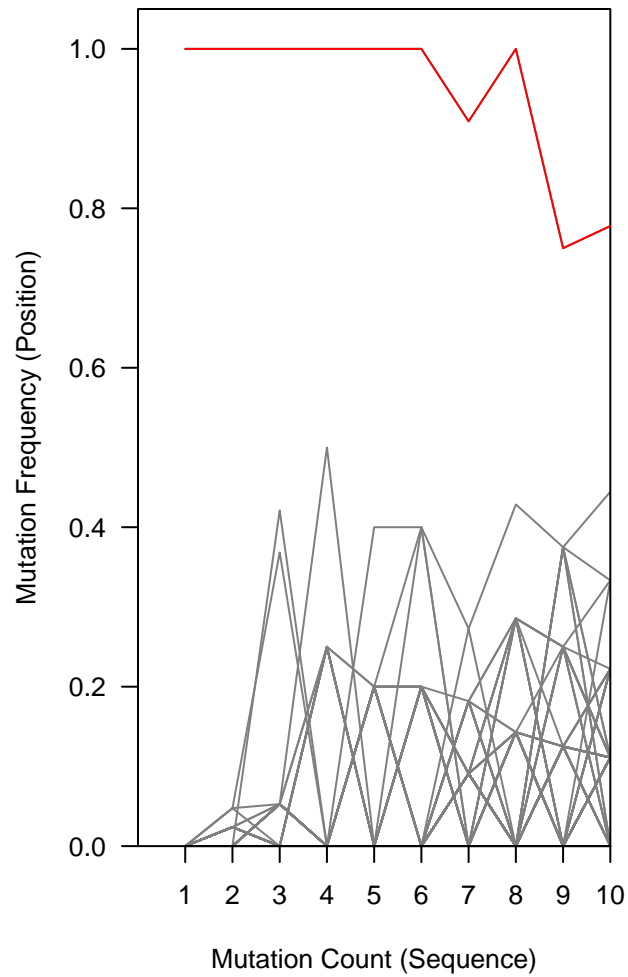
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SUBJECT:
PGP1

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IGHV1-8*02_G234T

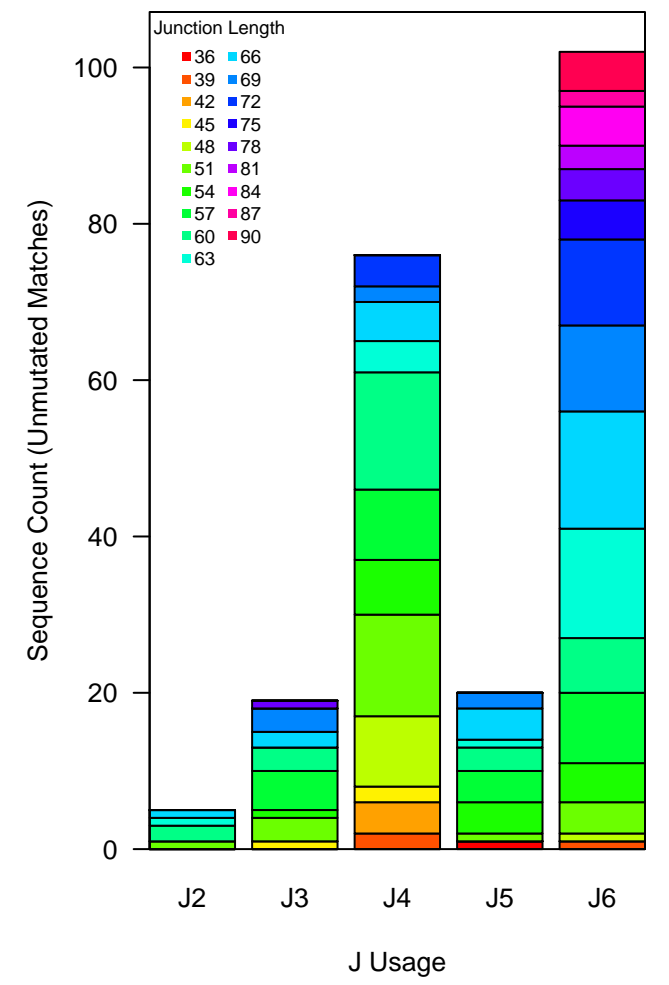
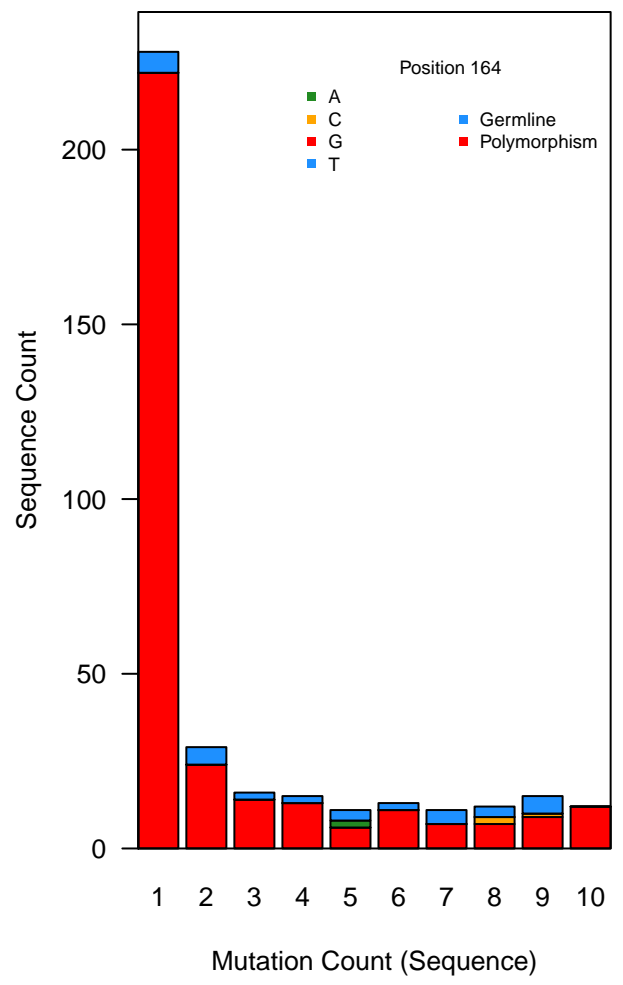
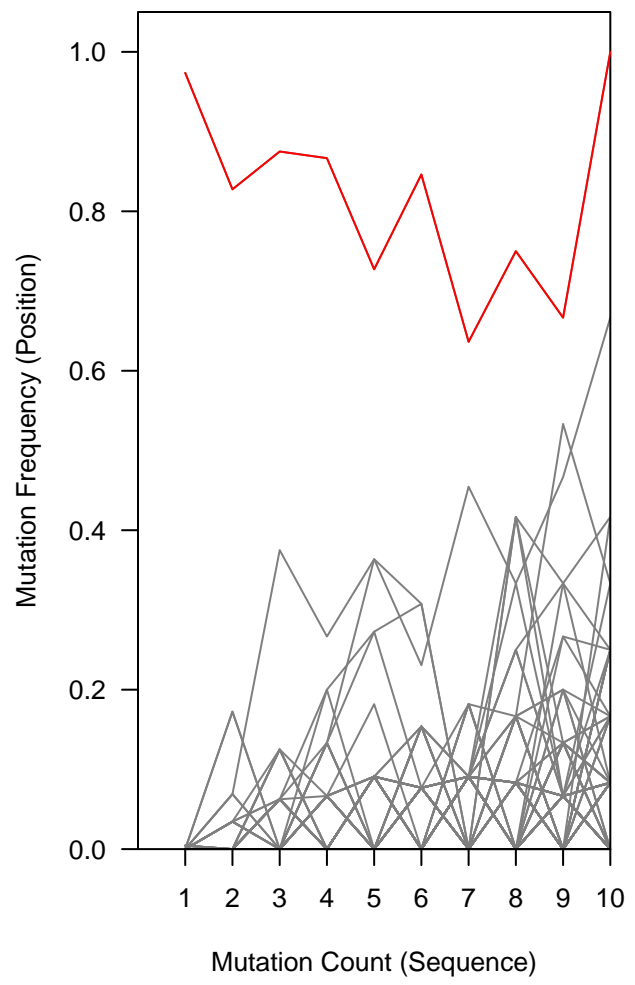


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 IGHV1-8*02

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G.....

IGHV2-70*01_T164G



IGHV2-70*01_T164G CAGGTCA CCTTGAGGGAGTCTGGTCC T---GCGCTGGTGAAACCCACACAGACCC TCACACTGACCTGCACCTTCTCTGGGTTCTCACTCAGC-----ACTAGTGAATGTGT

IGHV2-70*01

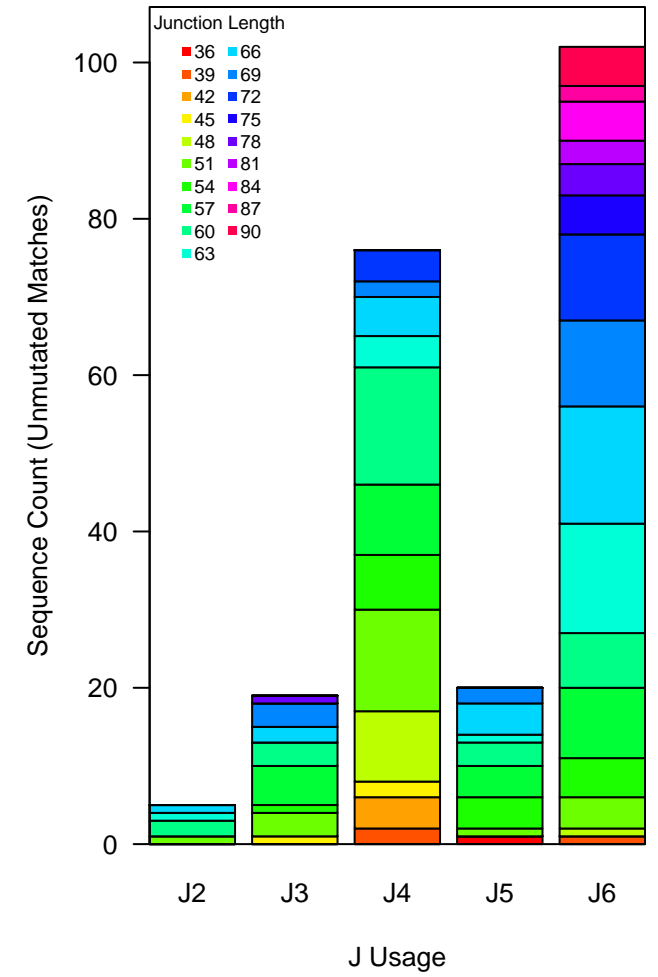
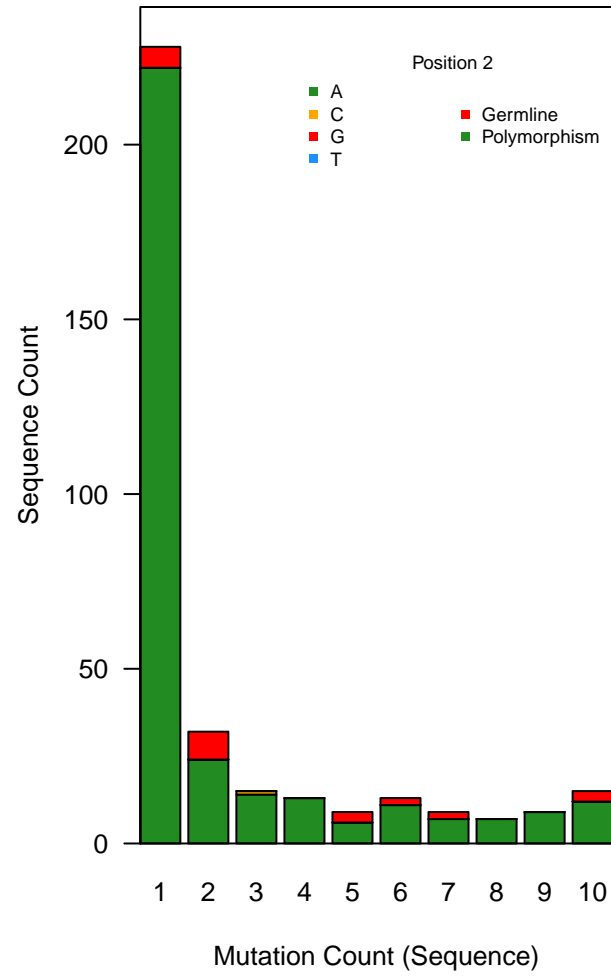
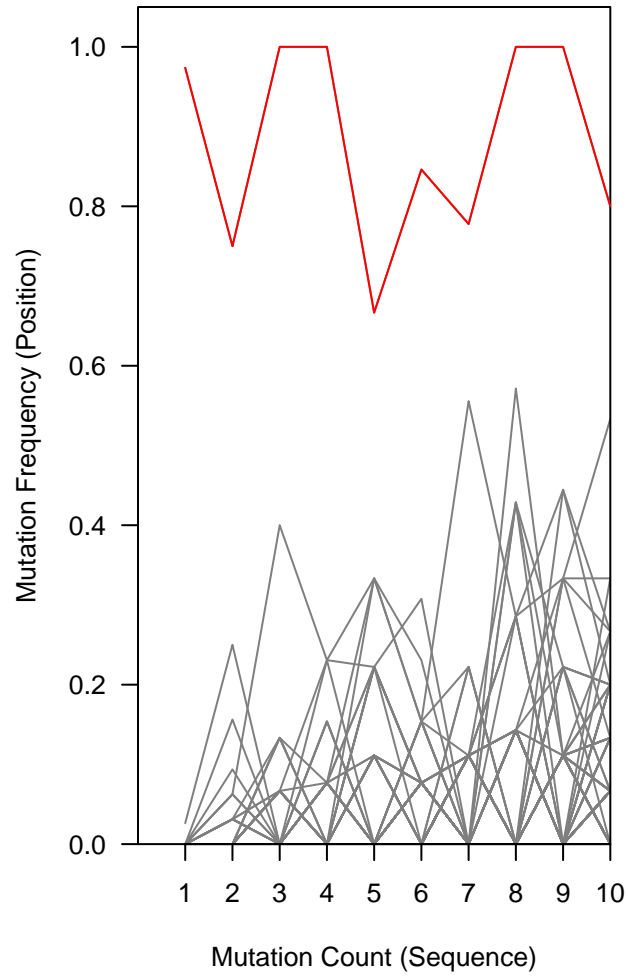
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IGHV2-70*11_G2A

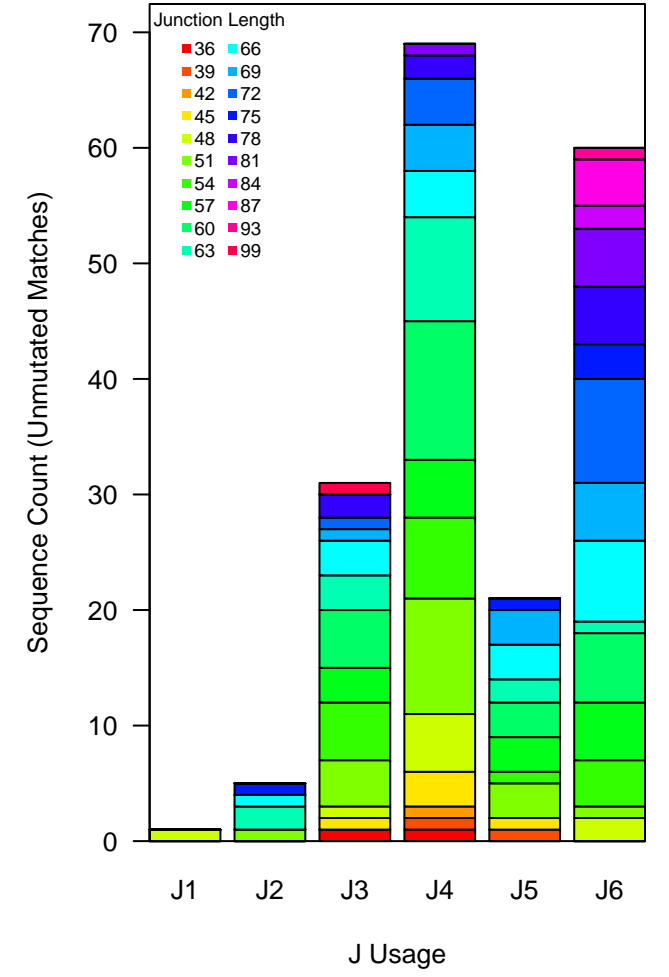
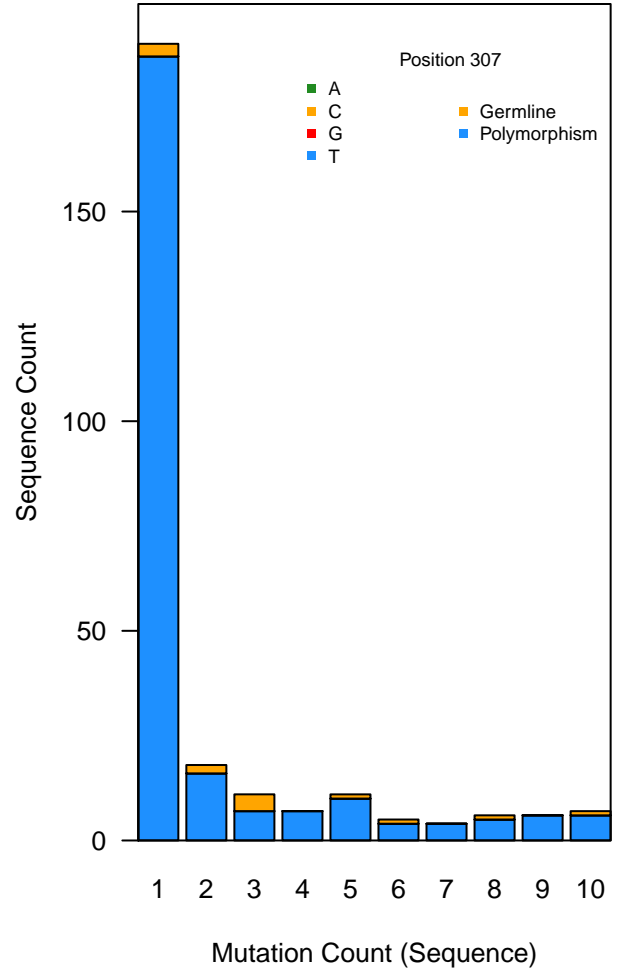
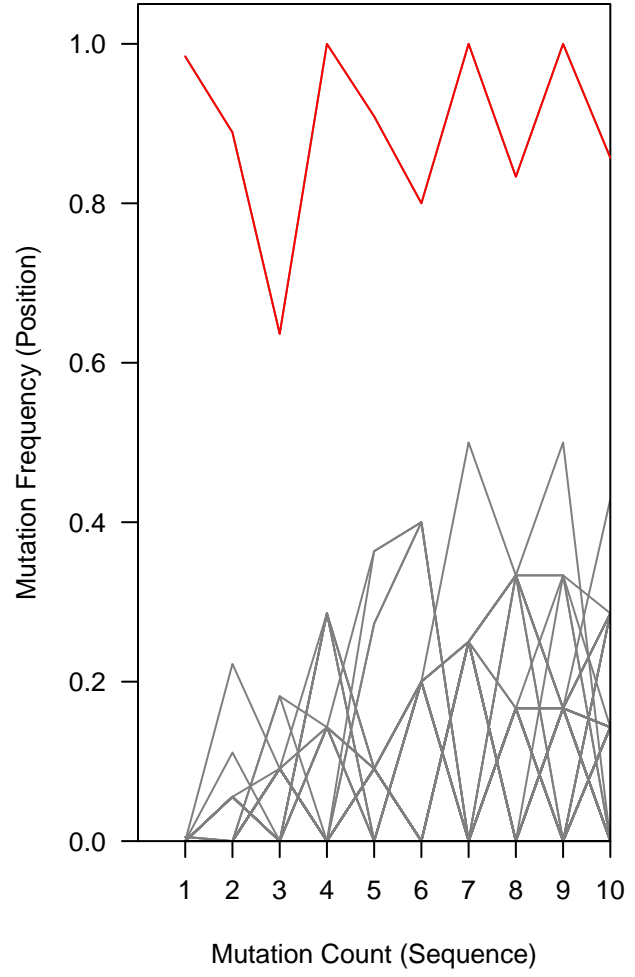


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 IGHV2-70*11 ·G·

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IGHV3-20*01_C307T



IGHV3-20*01_C307T GAGGTGCAGCTGGTGGAGTCTGGGGGA---GGTGTGGTACGGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACACCTTT-----GATGATTATGGC

IGHV3-20*01

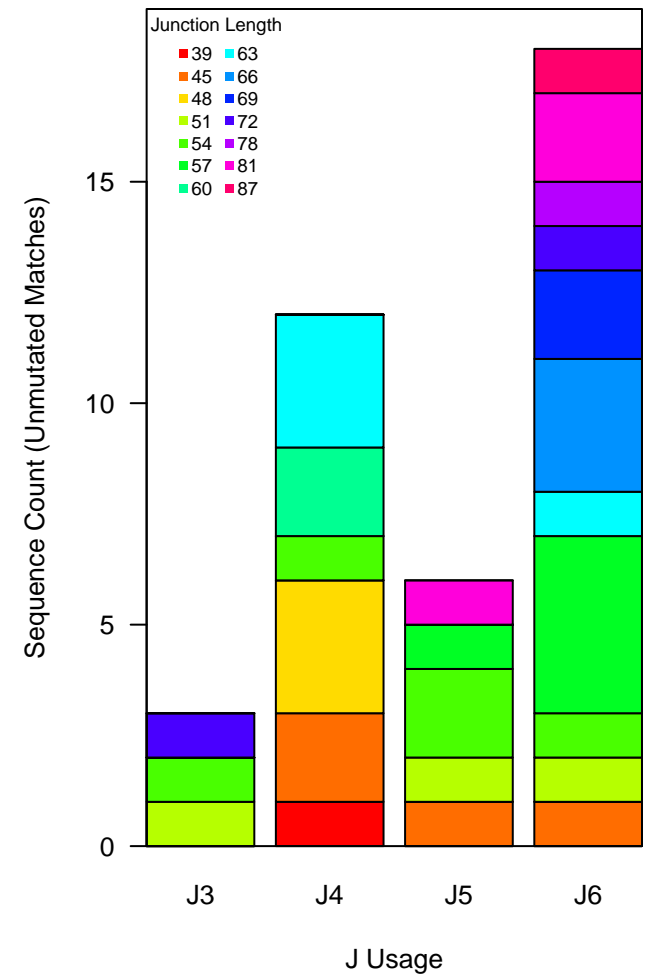
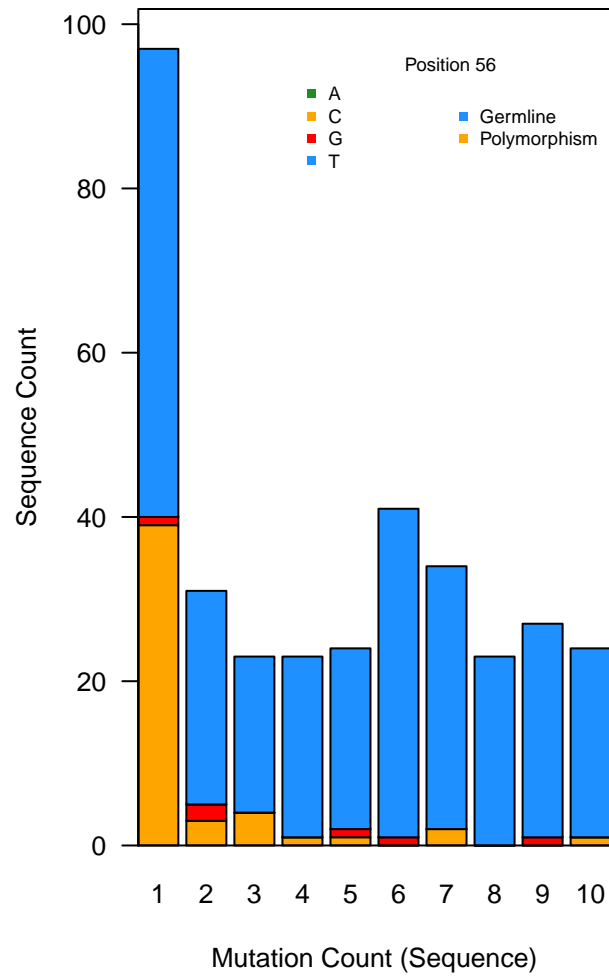
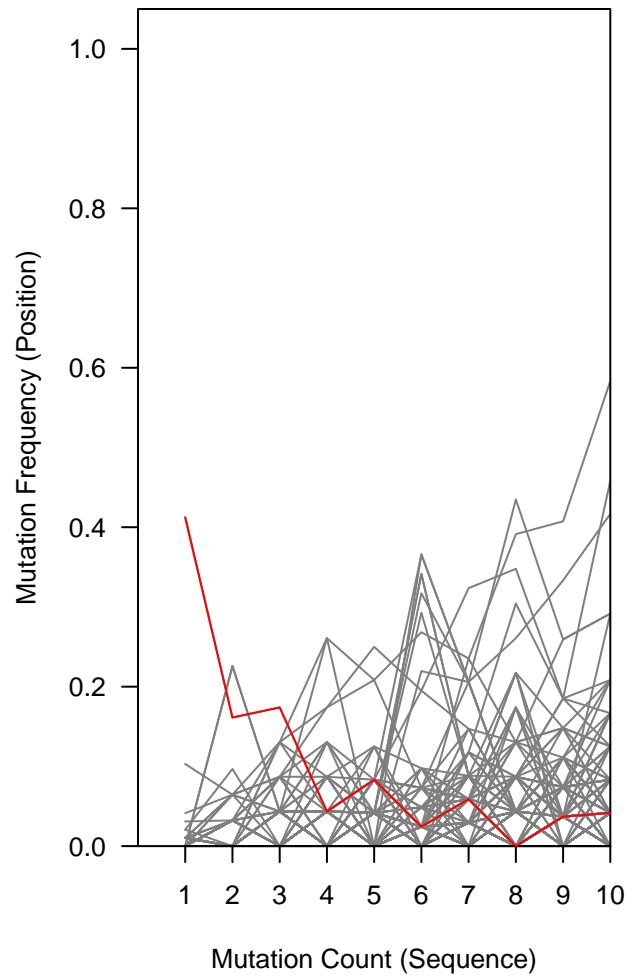
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IGHV3-21*01_T56C

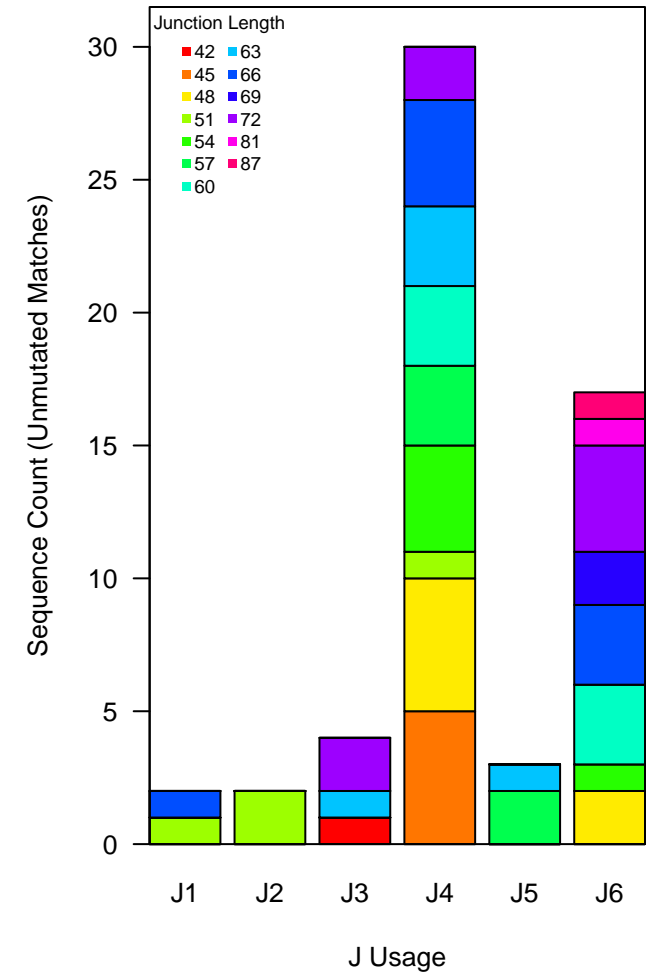
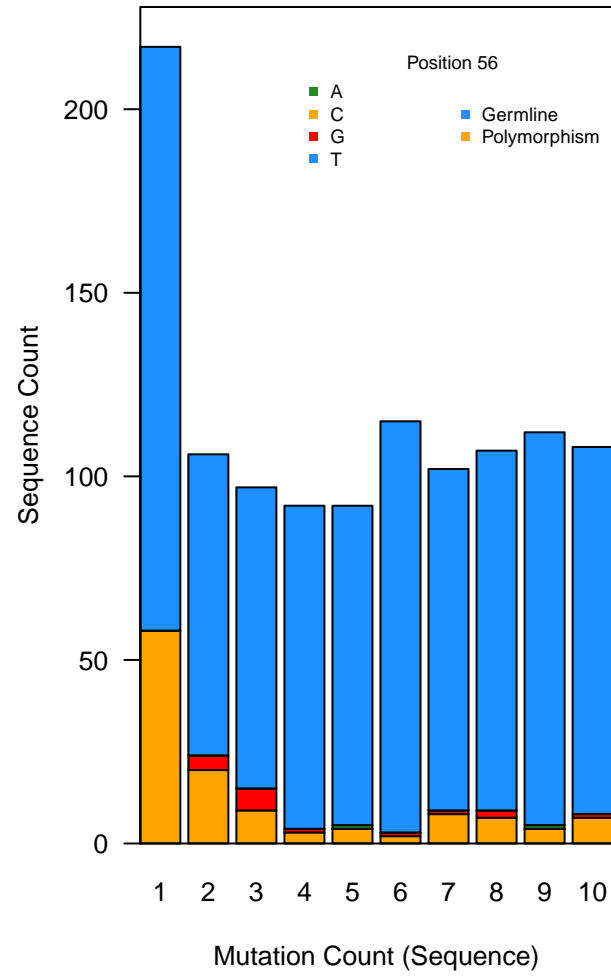
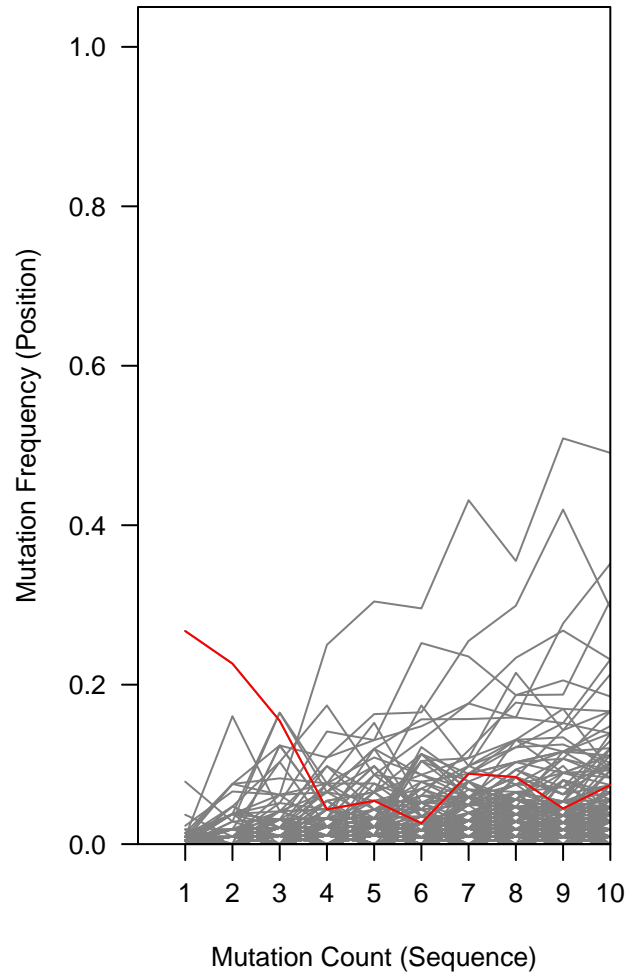


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 IGHV3-21*01T.....

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IGHV3-23*01_T56C



IGHV3-23*01_T56C GAGGTGCAGCTGTTGGAGTCTGGGGGA---GGCTTGGTACAGCCTGGGGGGTCCCCGAGACTCTCCTGTGCAGCCTCTGGATTTCACCTTT-----AGCAGCTATGCC

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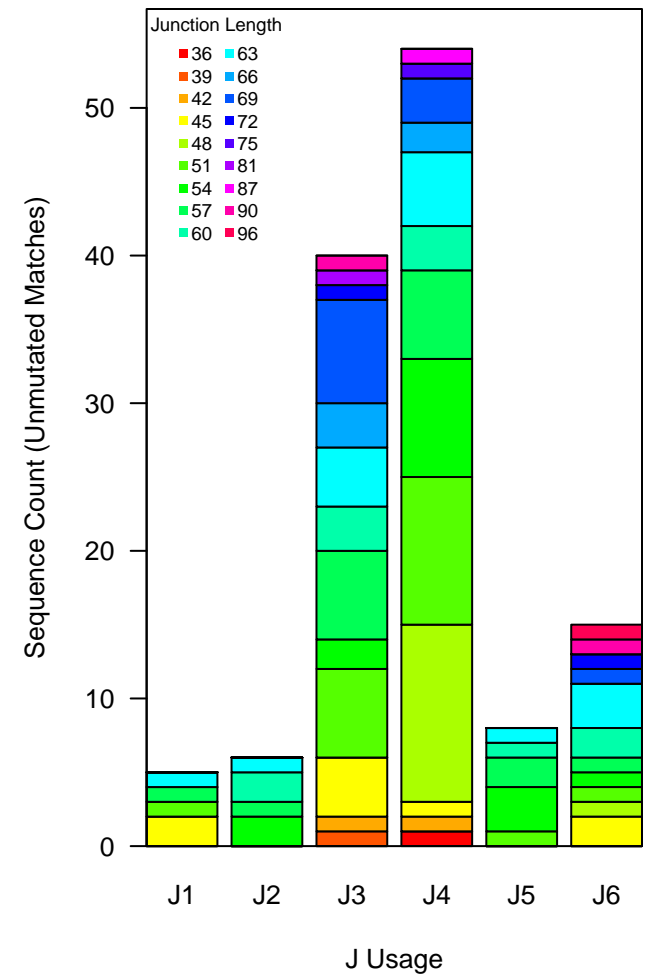
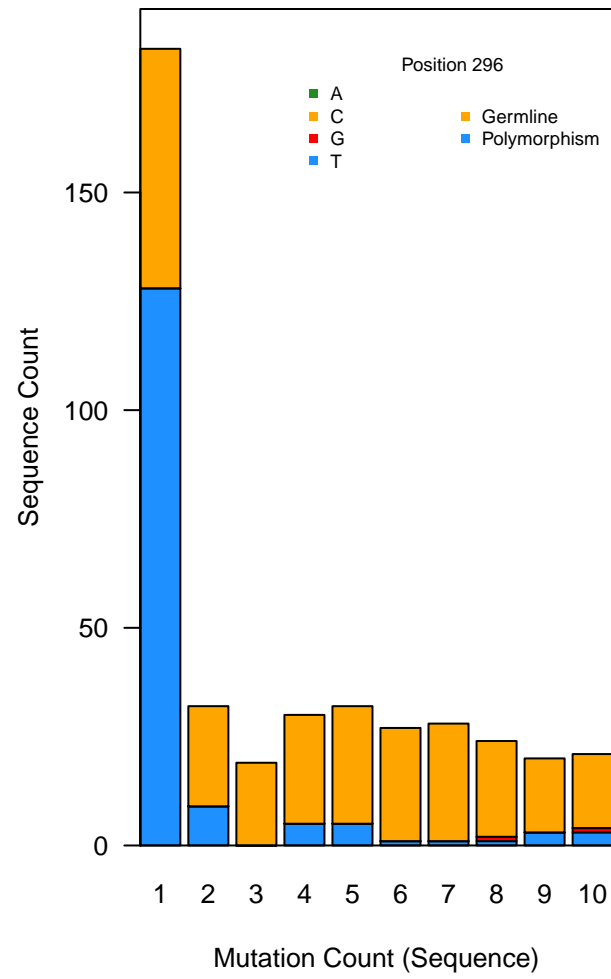
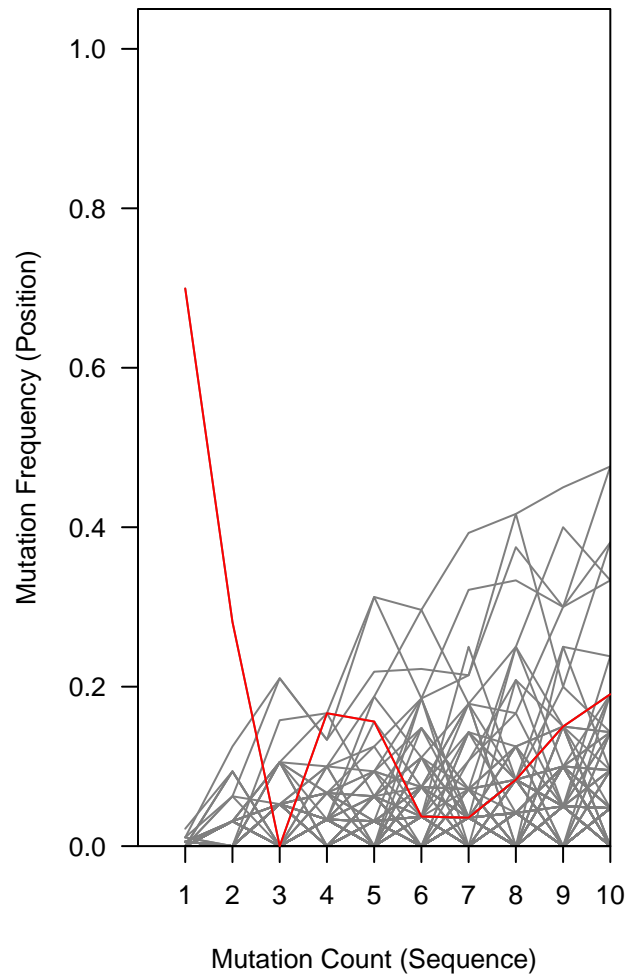
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IGHV3-9*01_C296T GAAGTGCAGCTGGTGGAGTCTGGGGGA---GGCTTGGTACAGCCTGGCAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACACCTTT-----GATGATTATGCC

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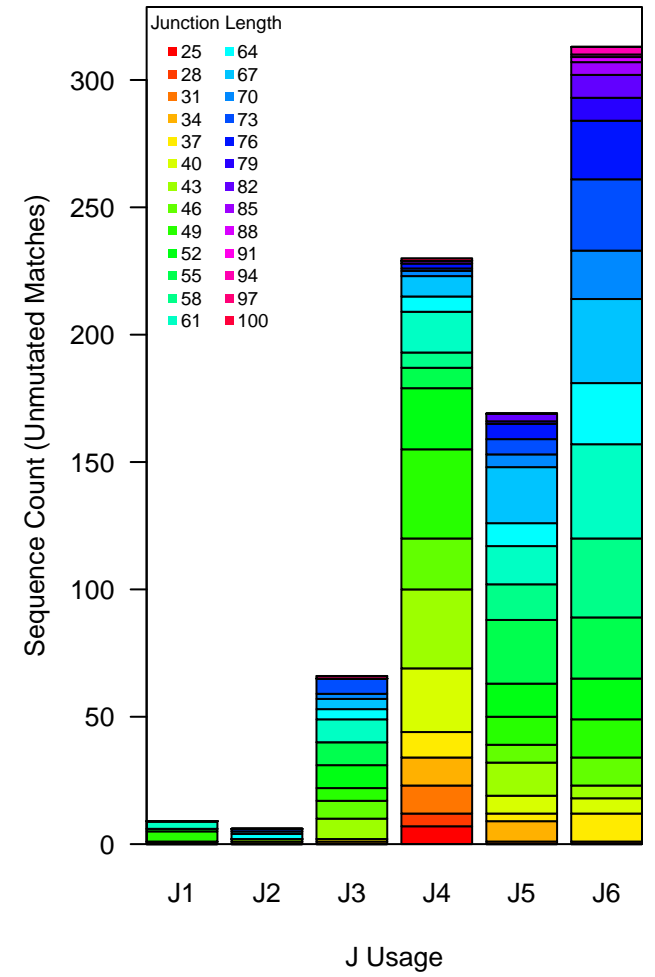
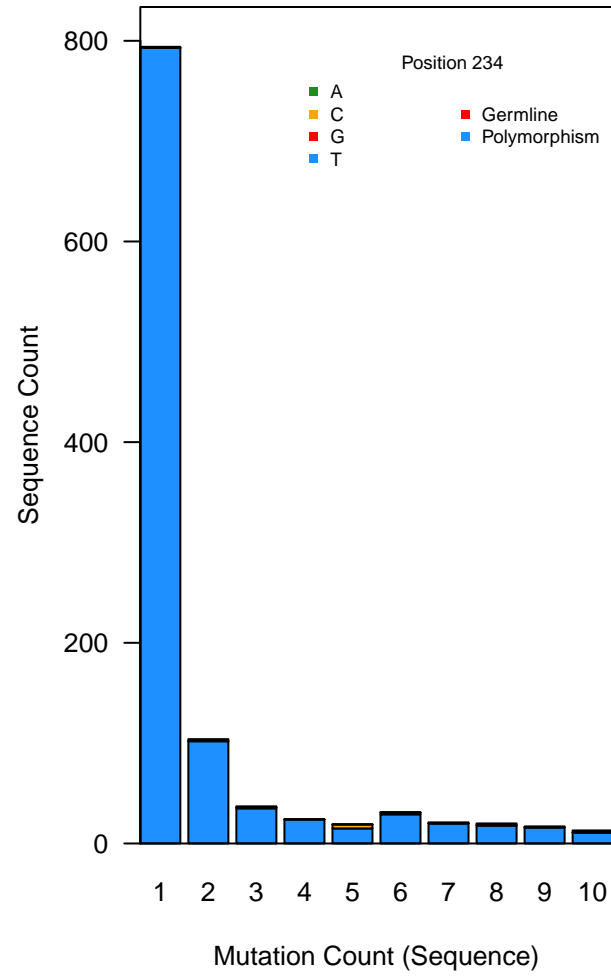
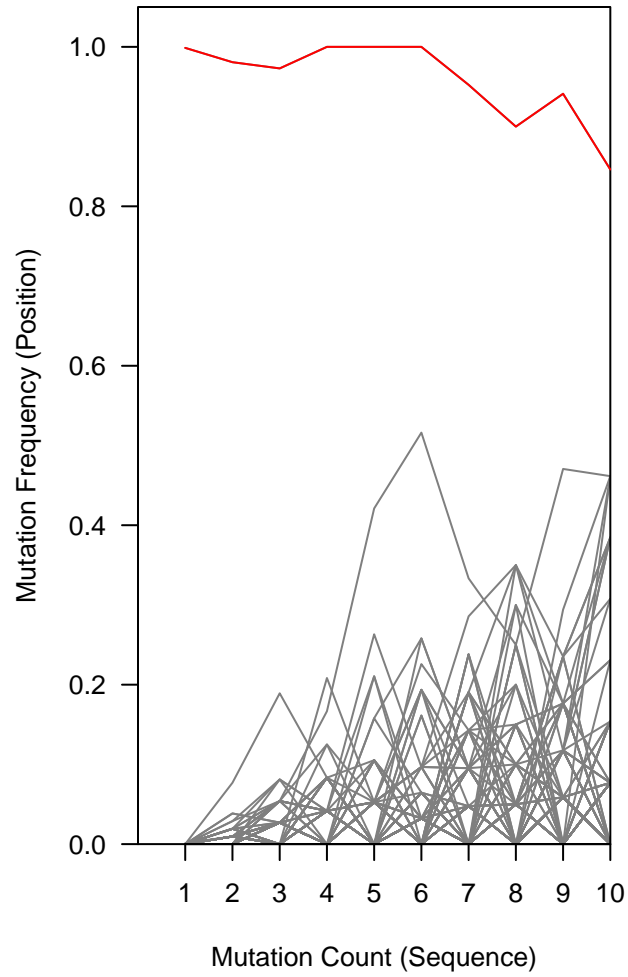
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SUBJECT:
PGP1

TECHNOLOGY:
MiSeq

IGHV1-8*02_G234T

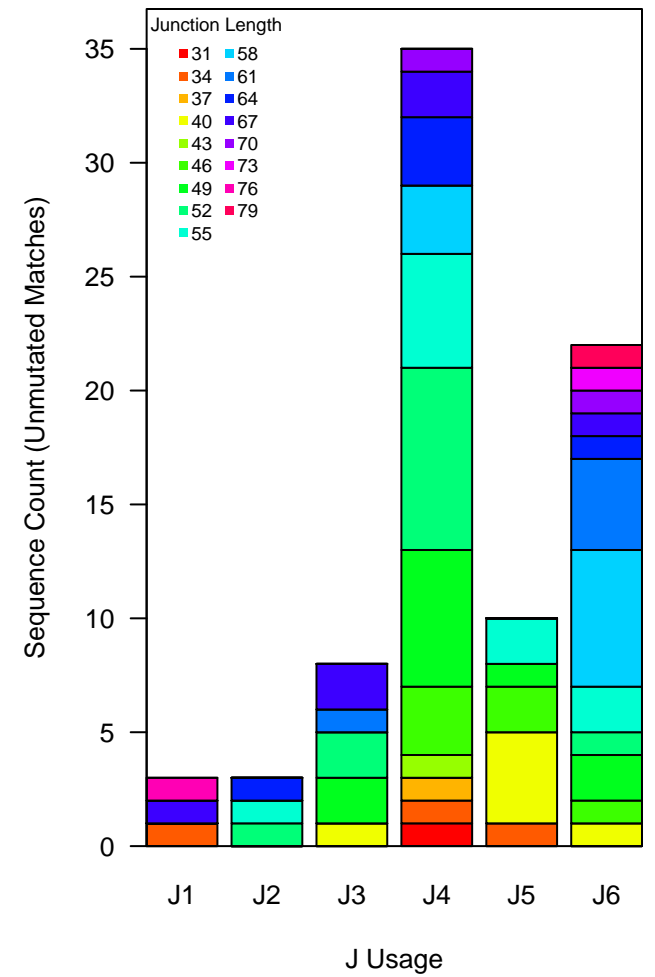
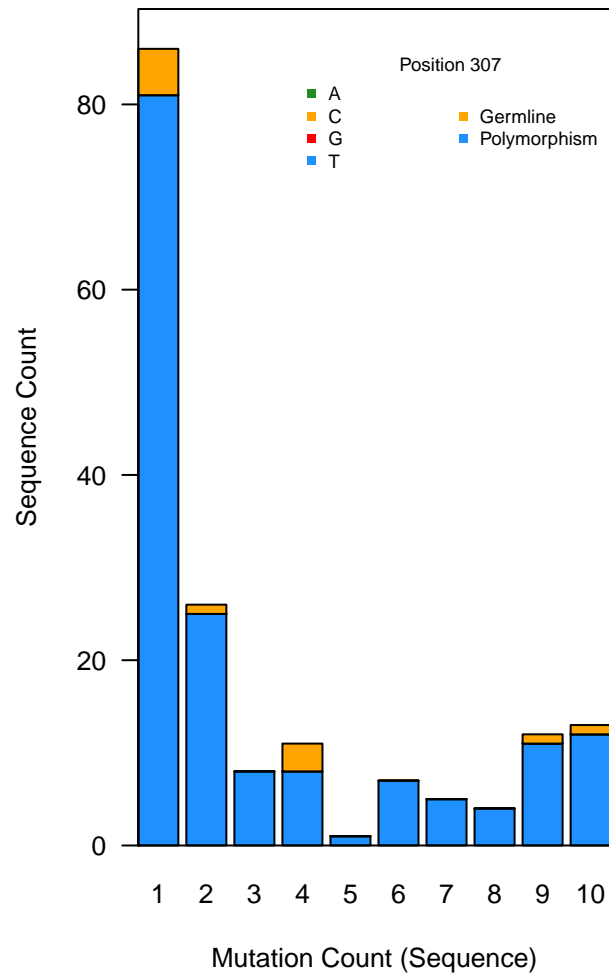
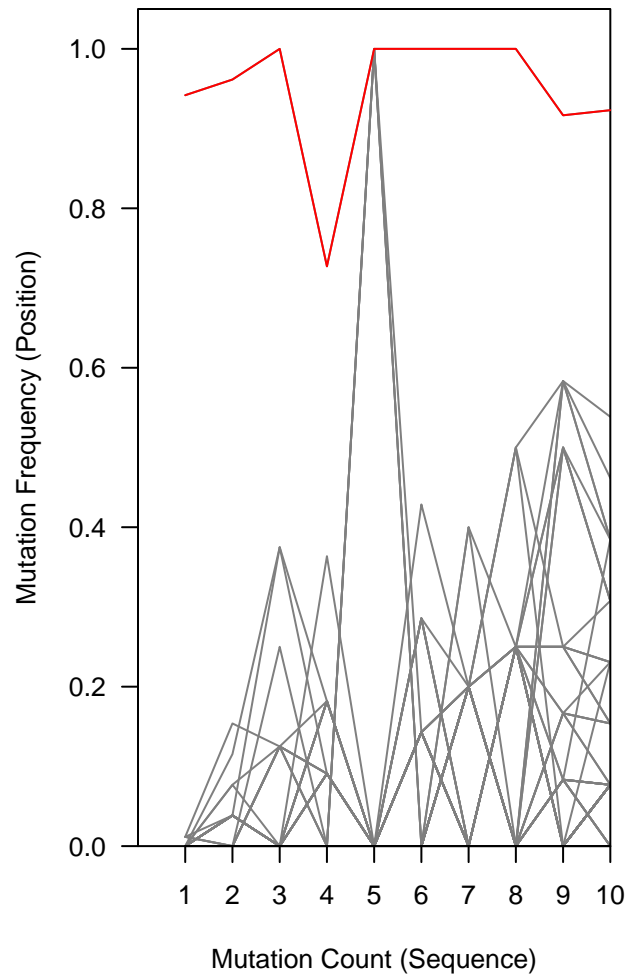


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IGHV3-20*01_C307T



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IGHV3-20*01

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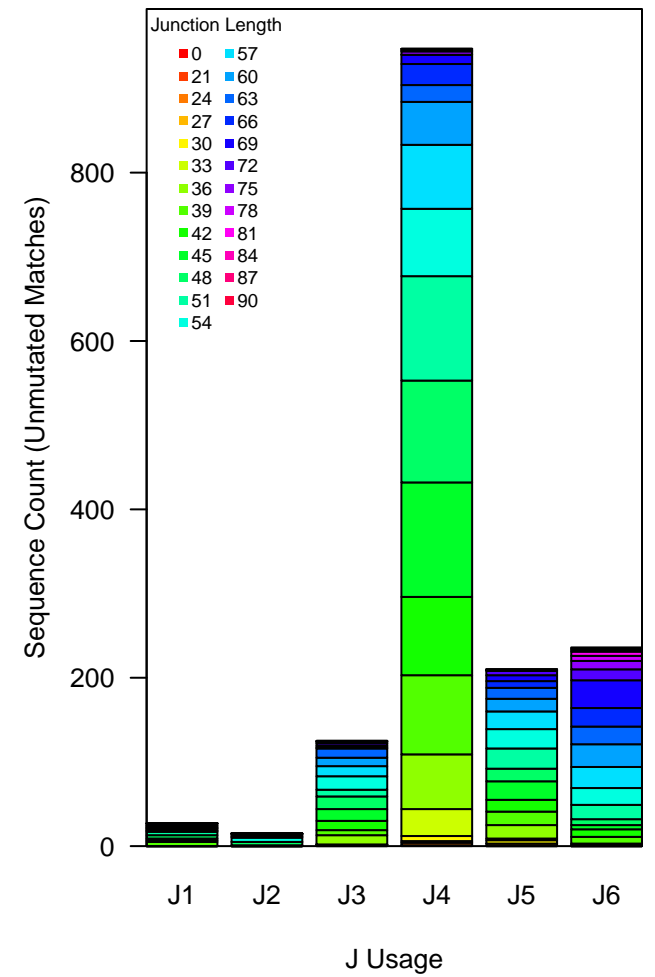
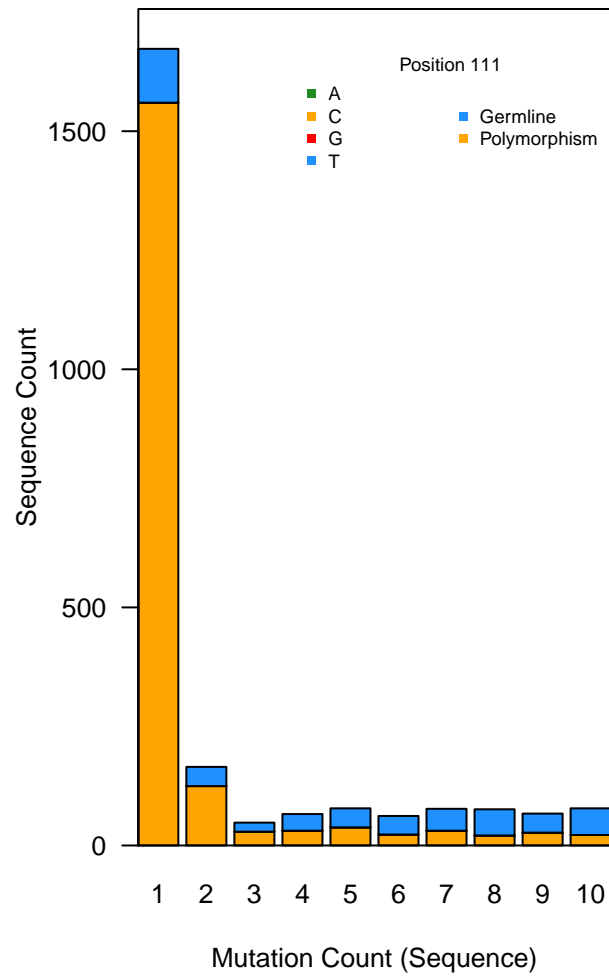
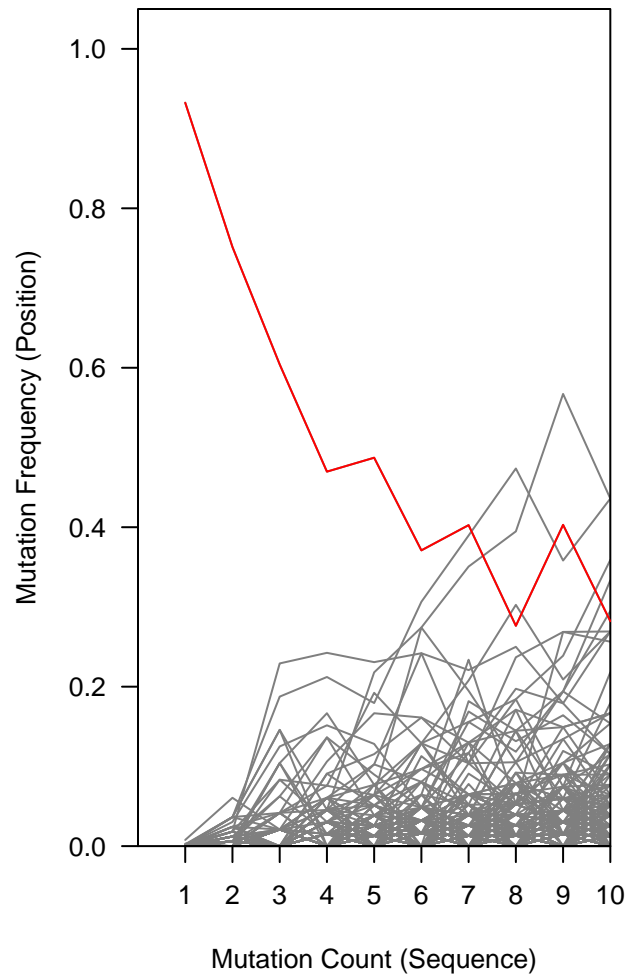
SUBJECT:

M2

TECHNOLOGY:

MiSeq

IGHV1-18*01_T111C

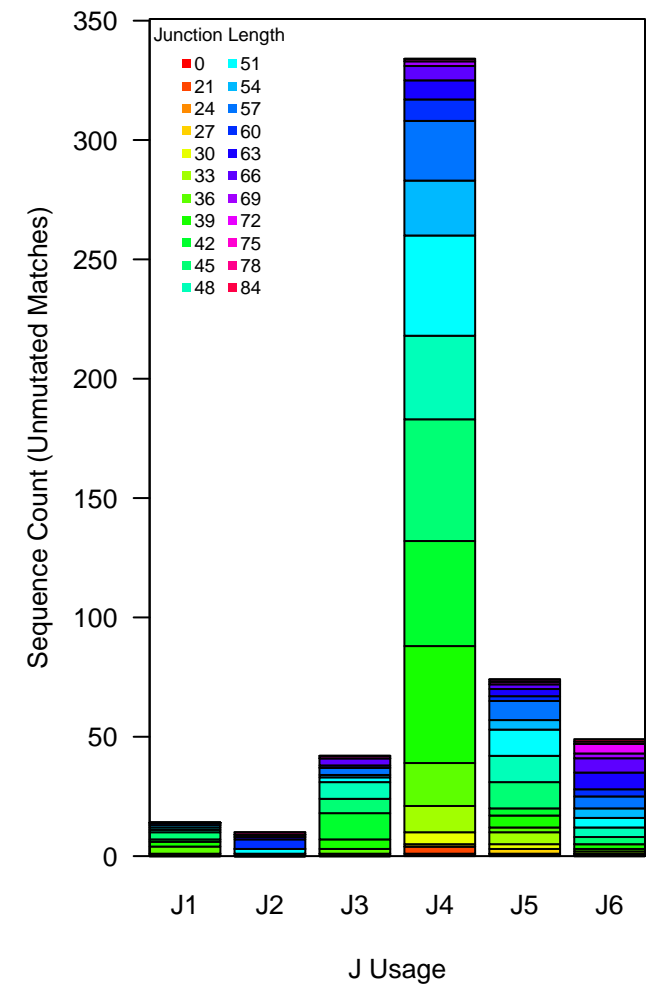
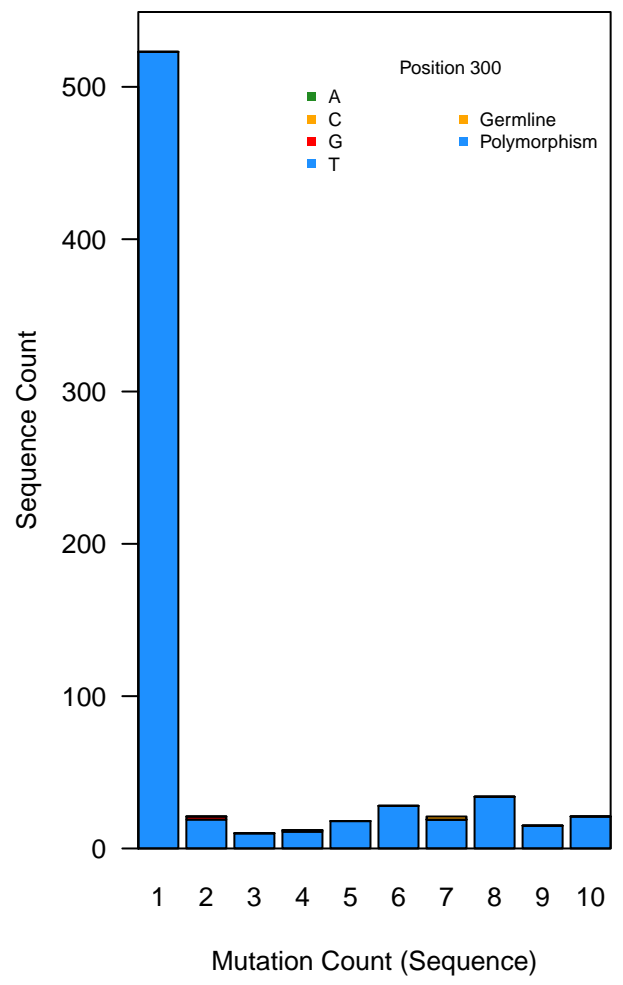
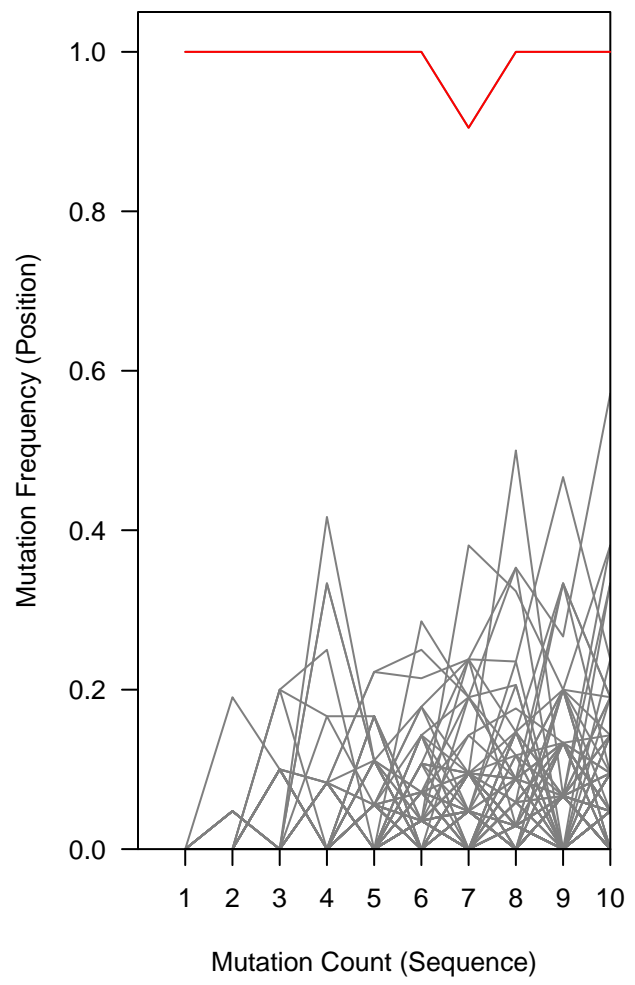


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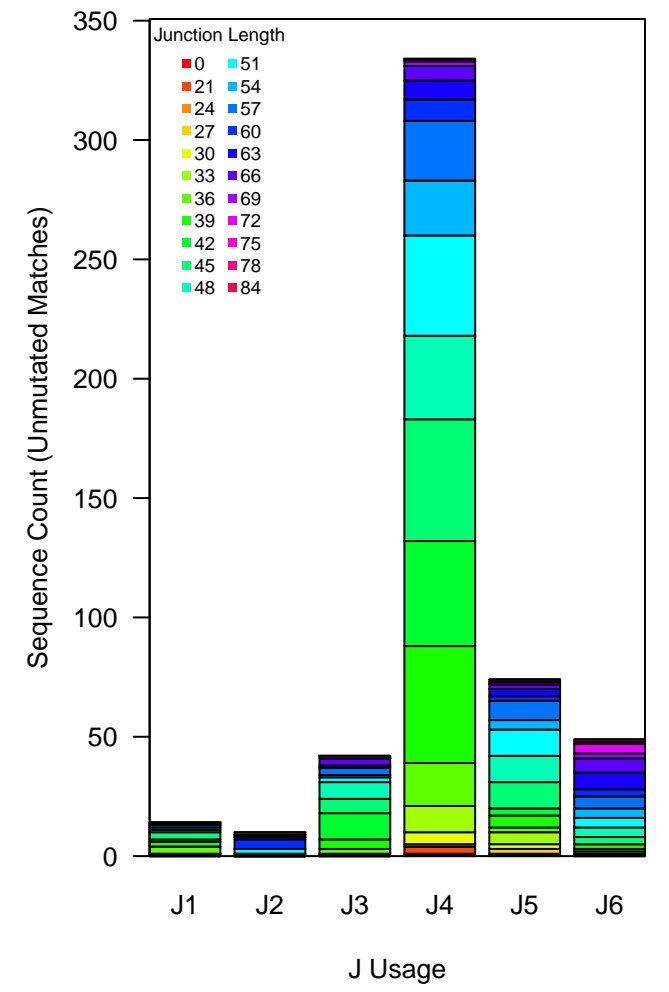
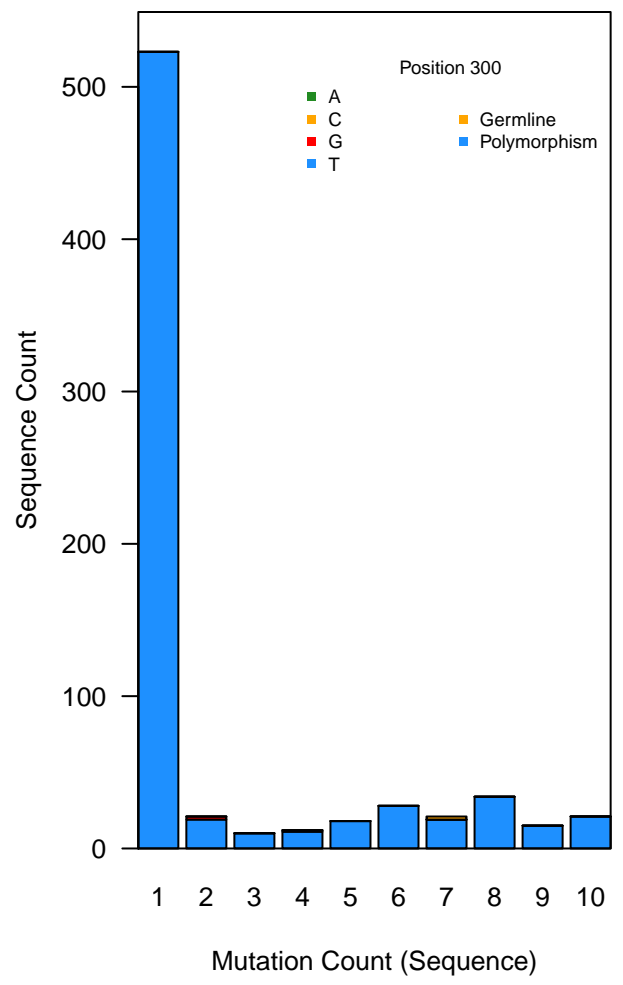
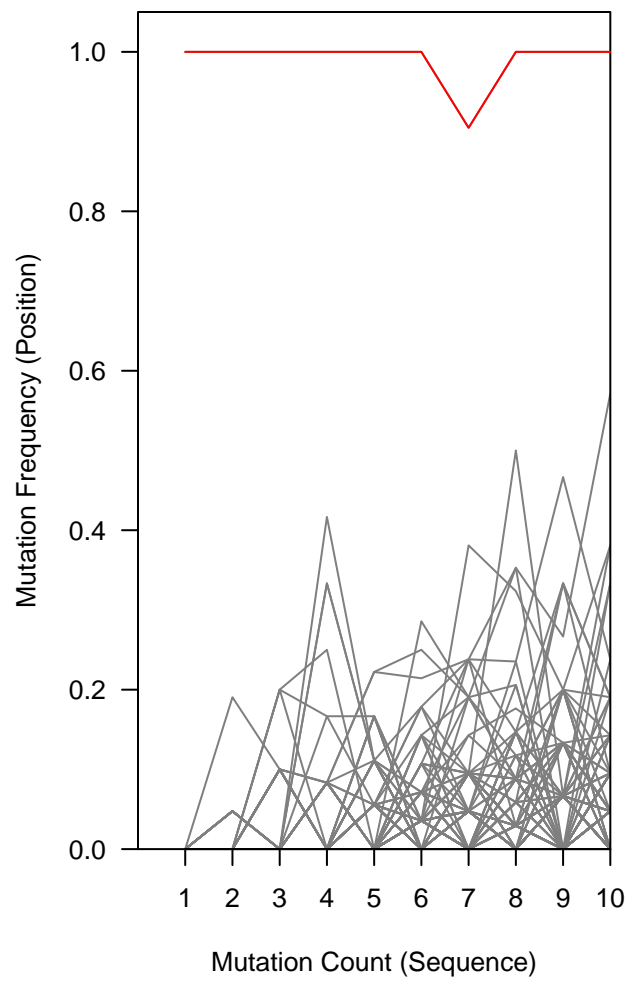
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IGHV3-11*05_C300T

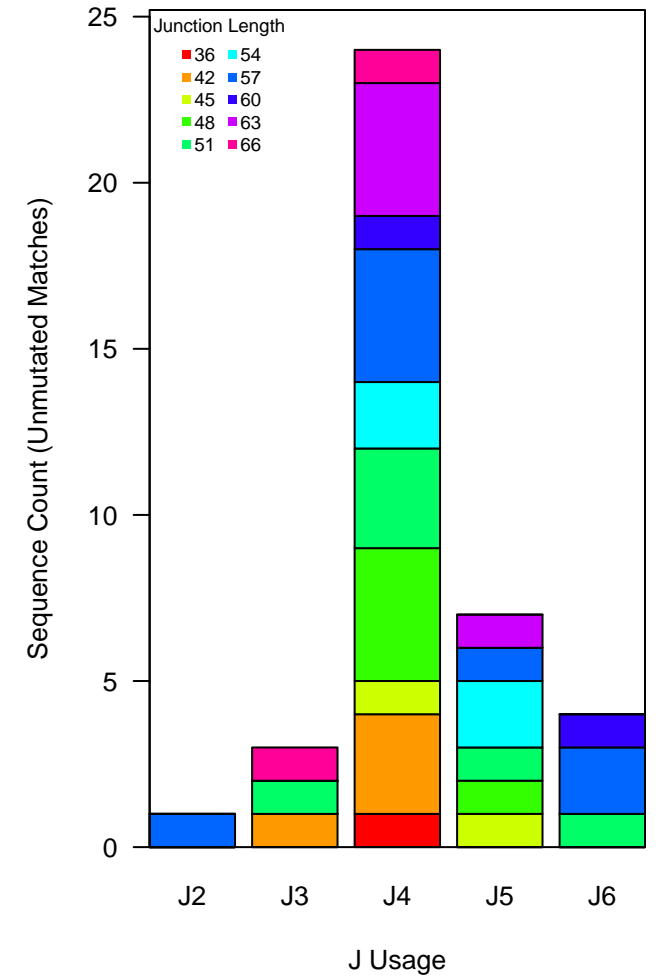
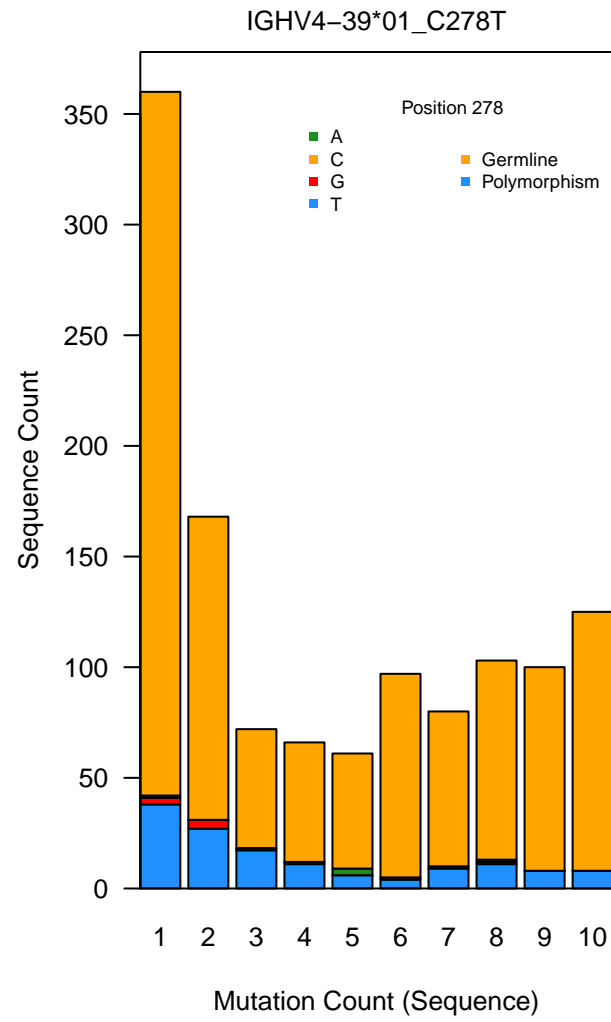
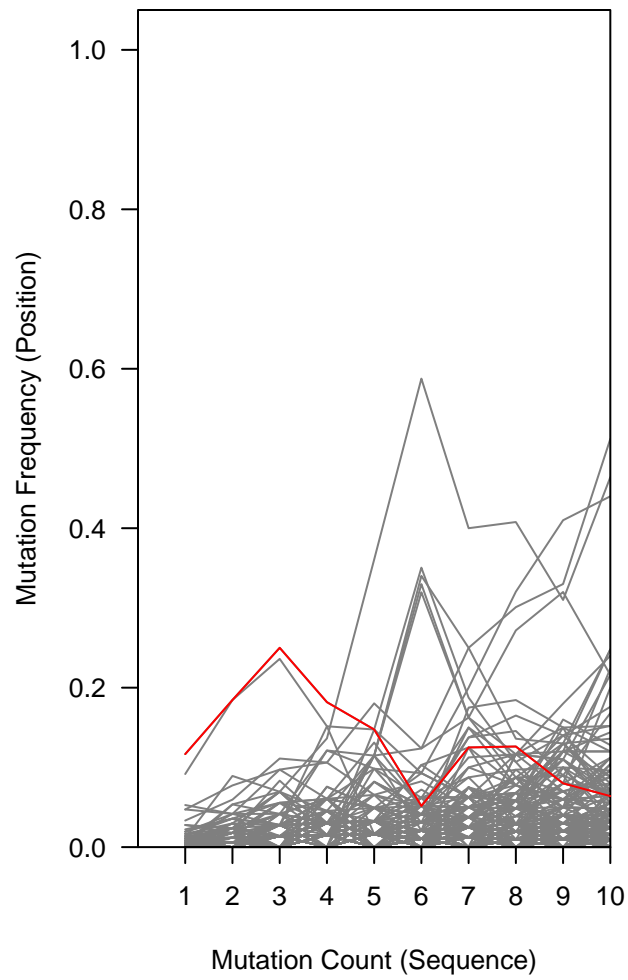


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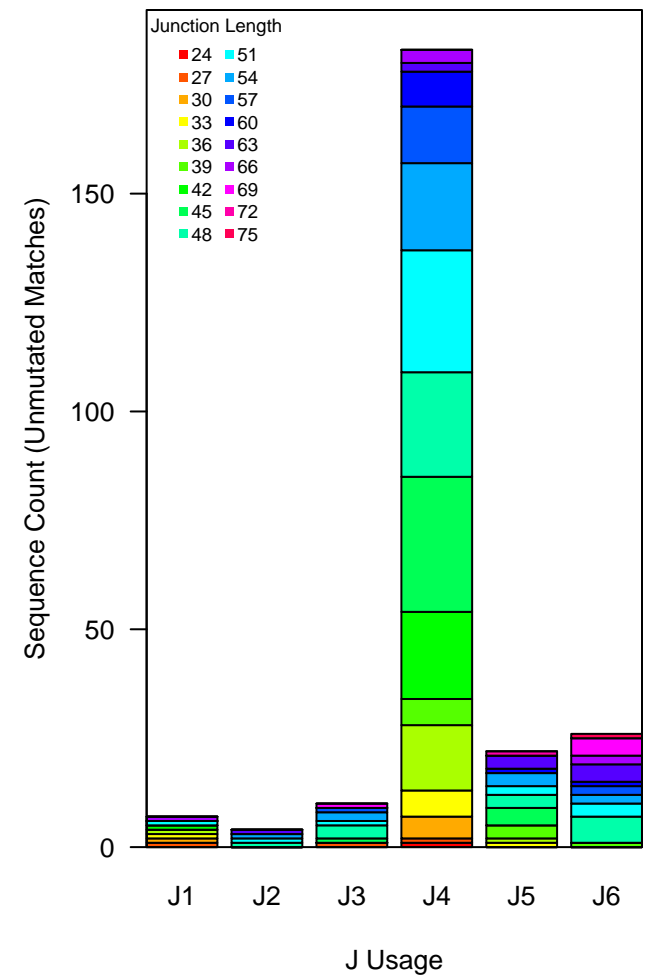
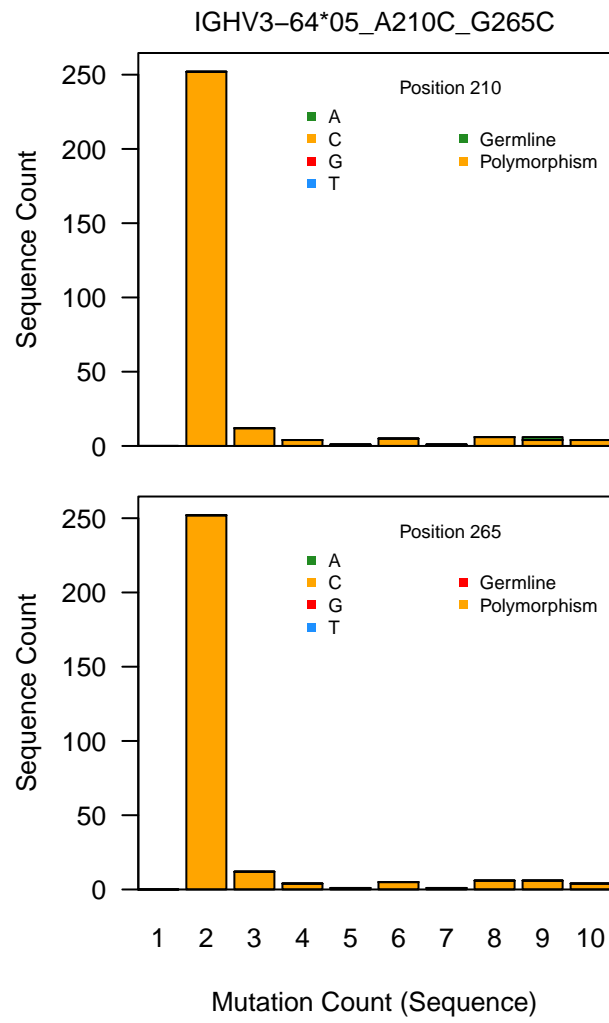
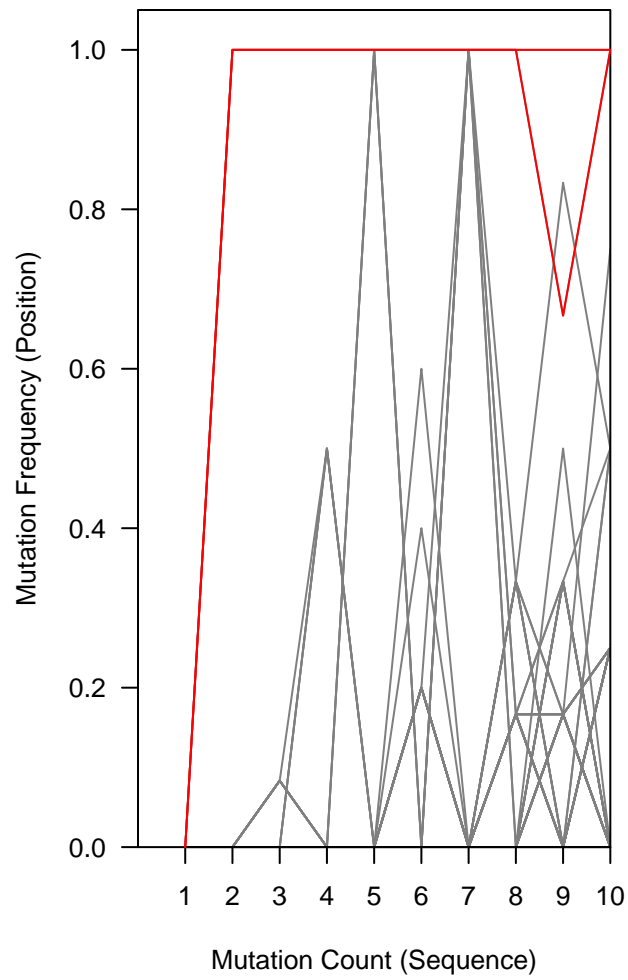


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IGHV3-64*05_A210C_G265C GAGGTGCAGCTGGTGGAGTCTGGGGGA---GGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTTTCAGCCTCTGGATTTCACCTTC-----AGTAGCTATGCT
 IGHV3-64*05

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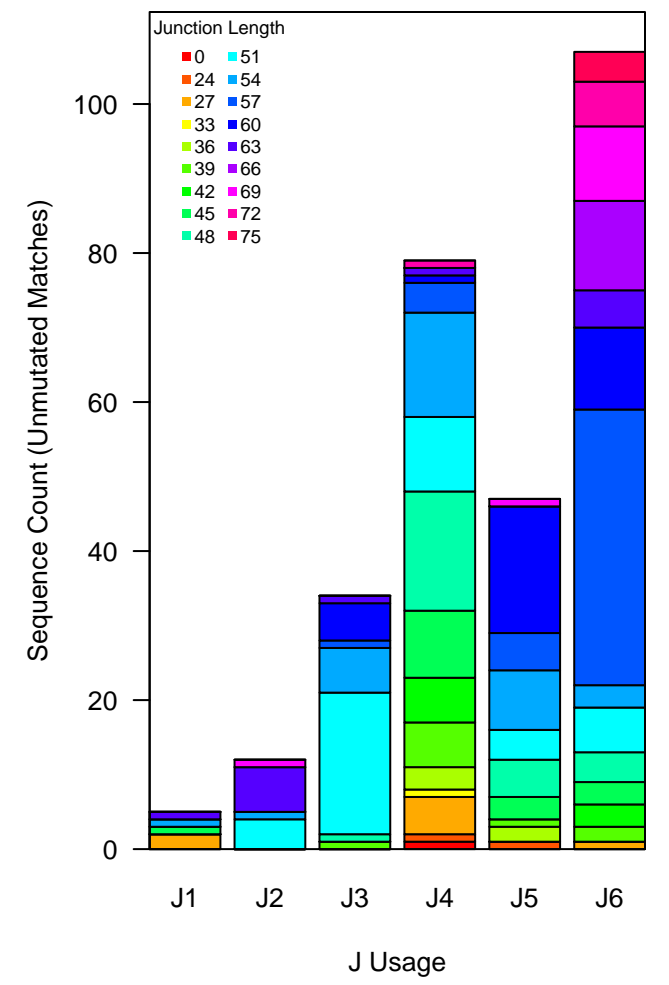
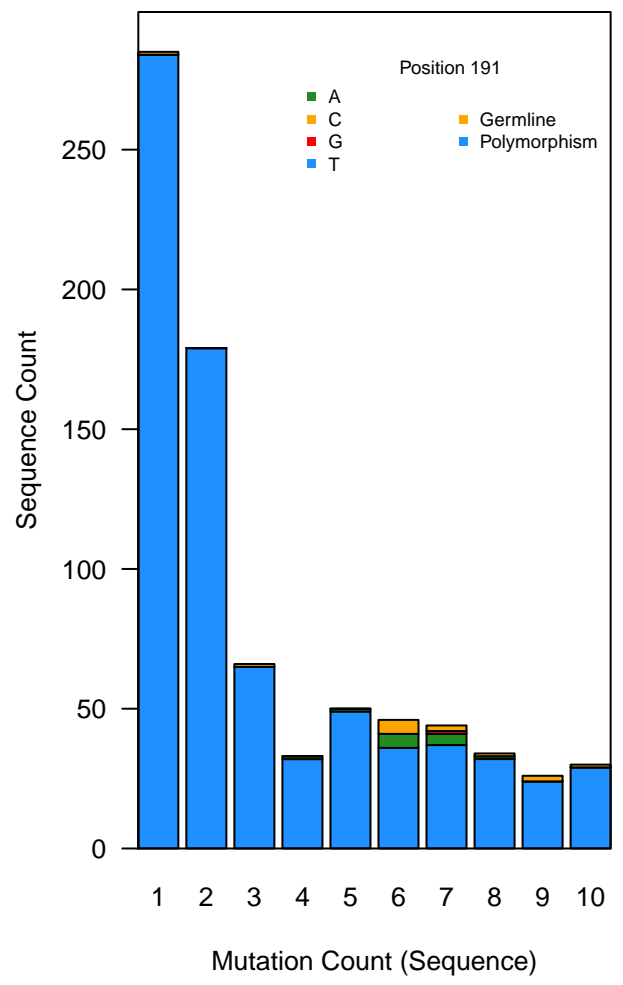
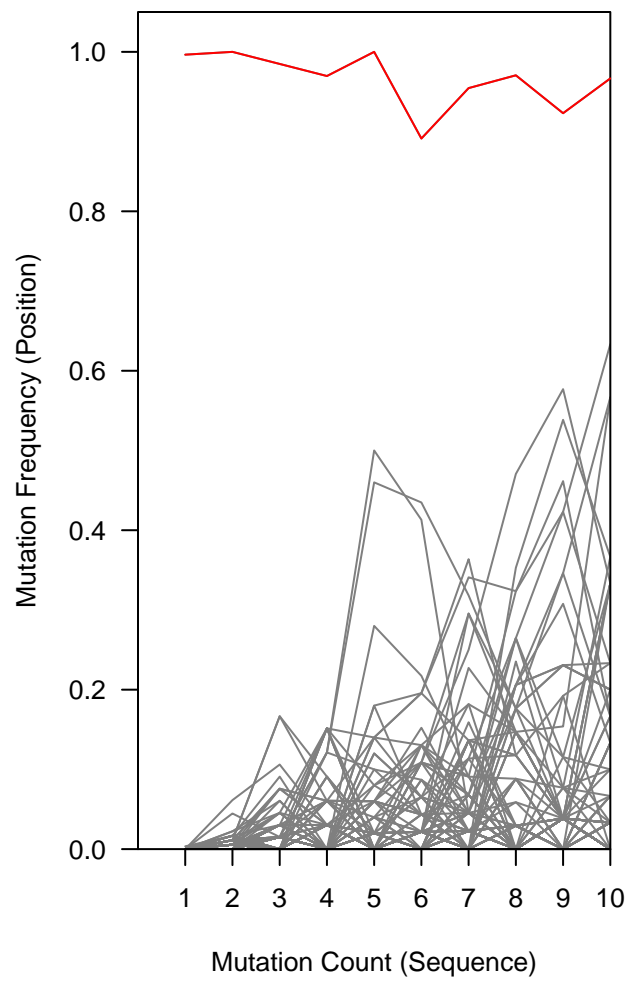
SUBJECT:

M3

TECHNOLOGY:

MiSeq

IGHV1-69*06_C191T



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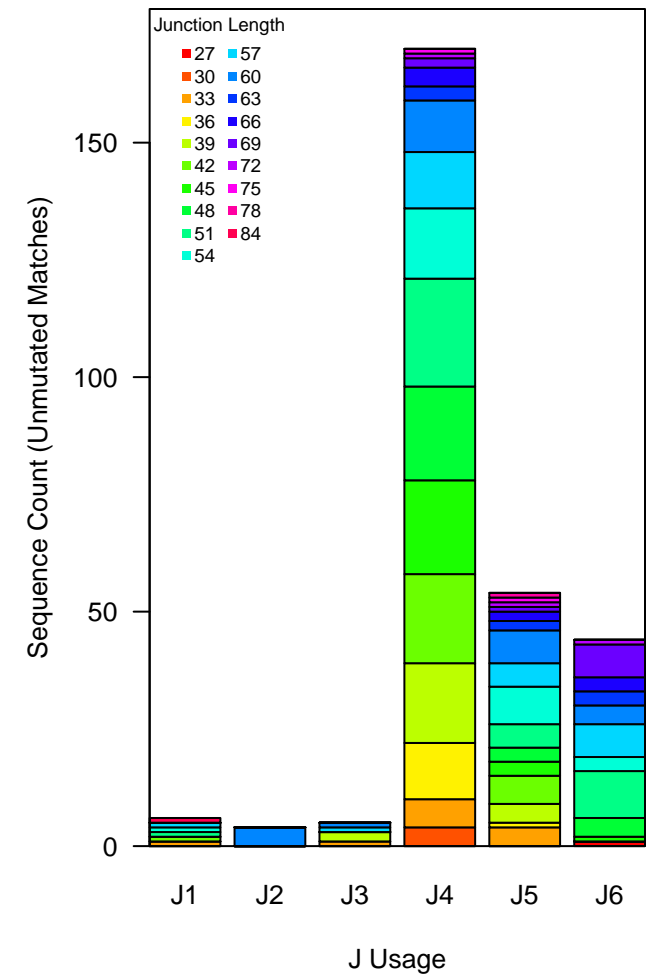
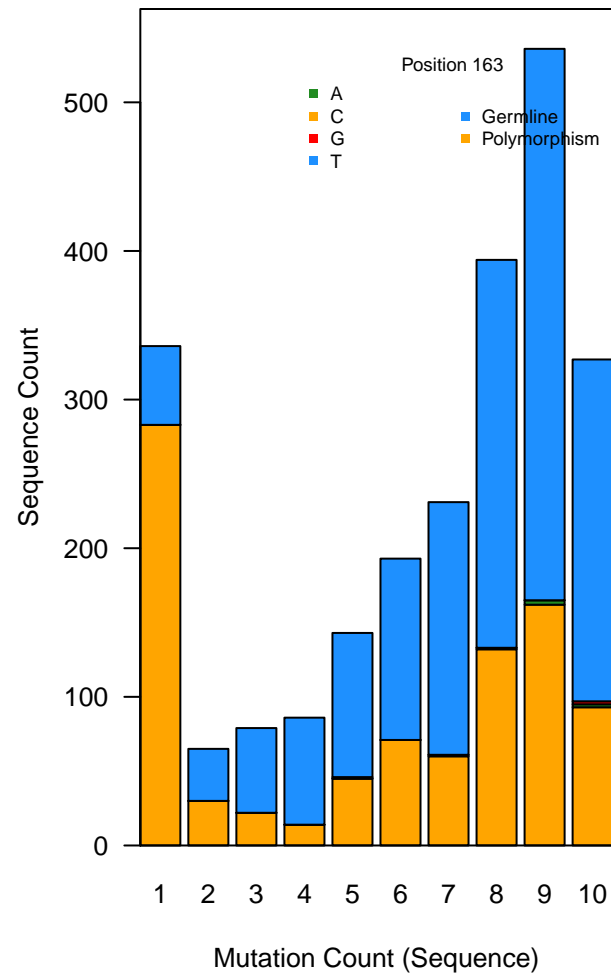
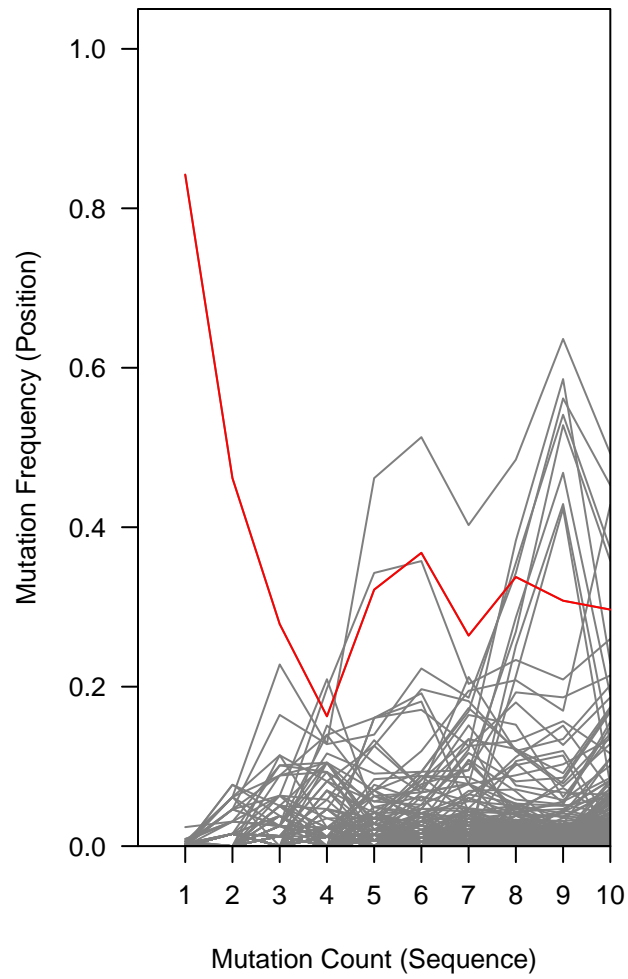
SUBJECT:

M4

TECHNOLOGY:

MiSeq

IGHV1-2*02_T163C

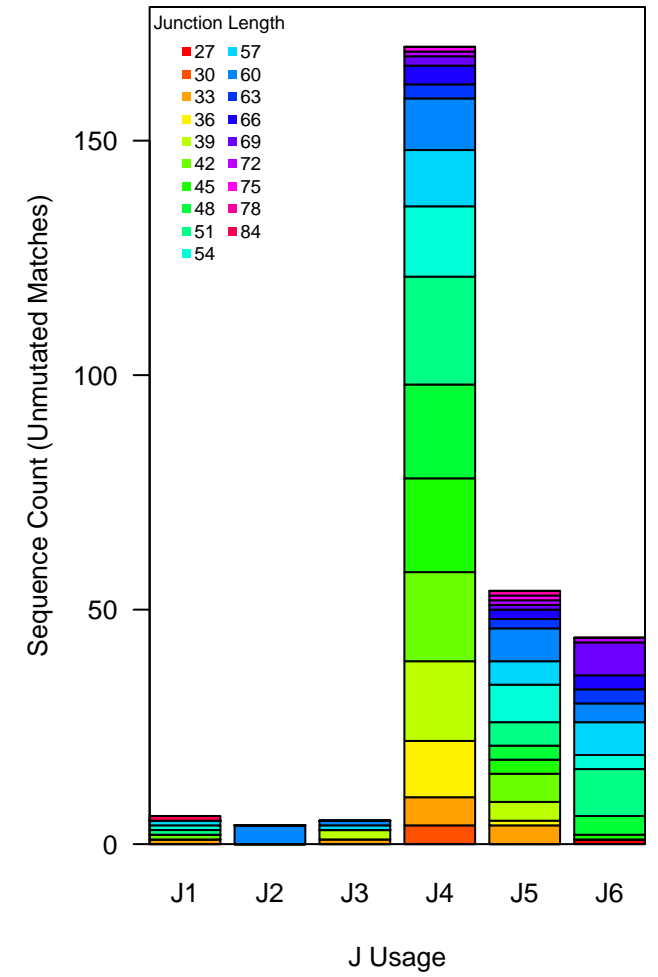
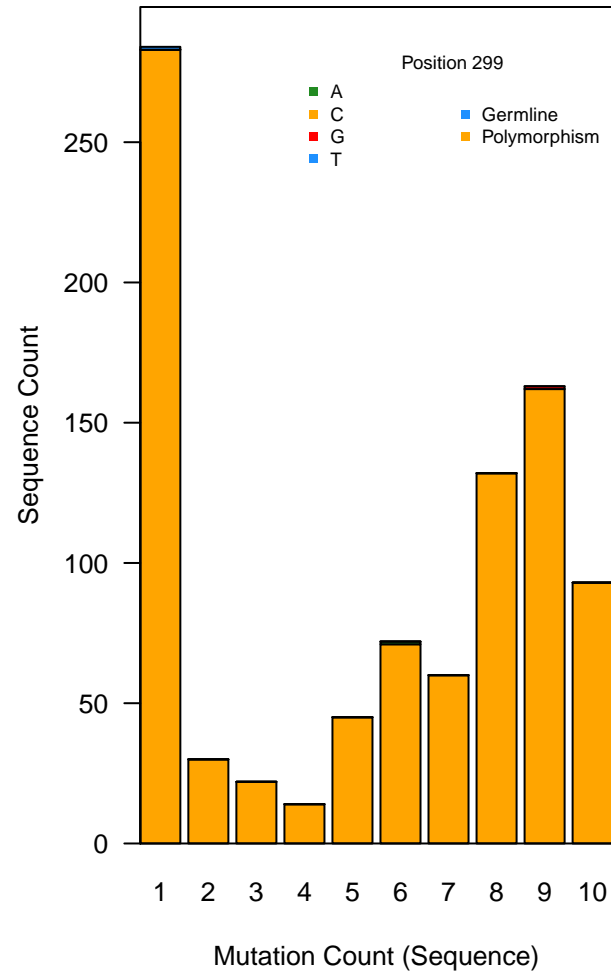
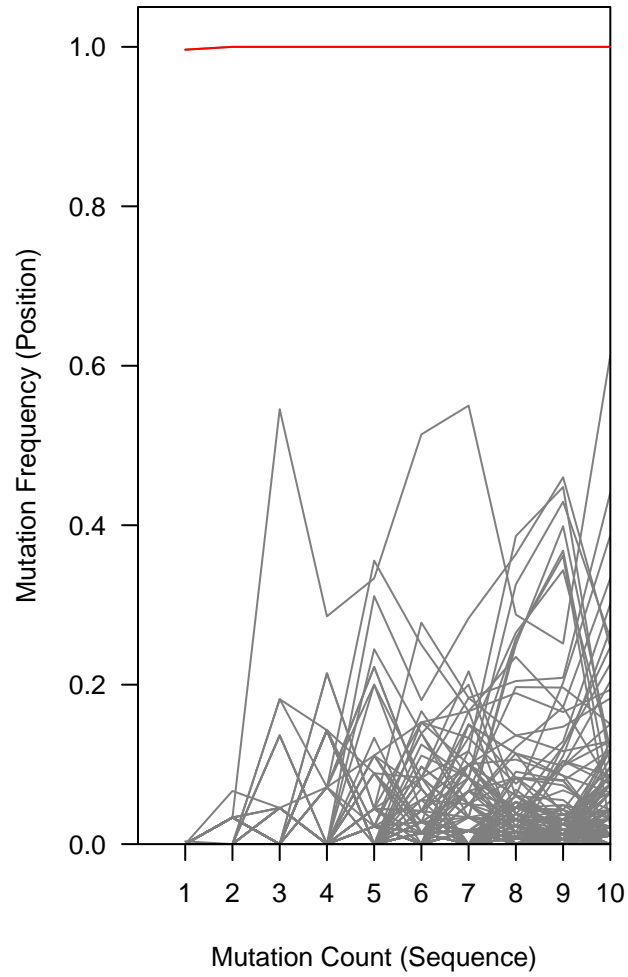


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IGHV1-2*05_T299C



IGHV1-2*05_T299C CAGGTGCAGCTGGTGCAGTCTGGGGCT---GAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTC-----ACCGGCTACTAT

IGHV1-2*05

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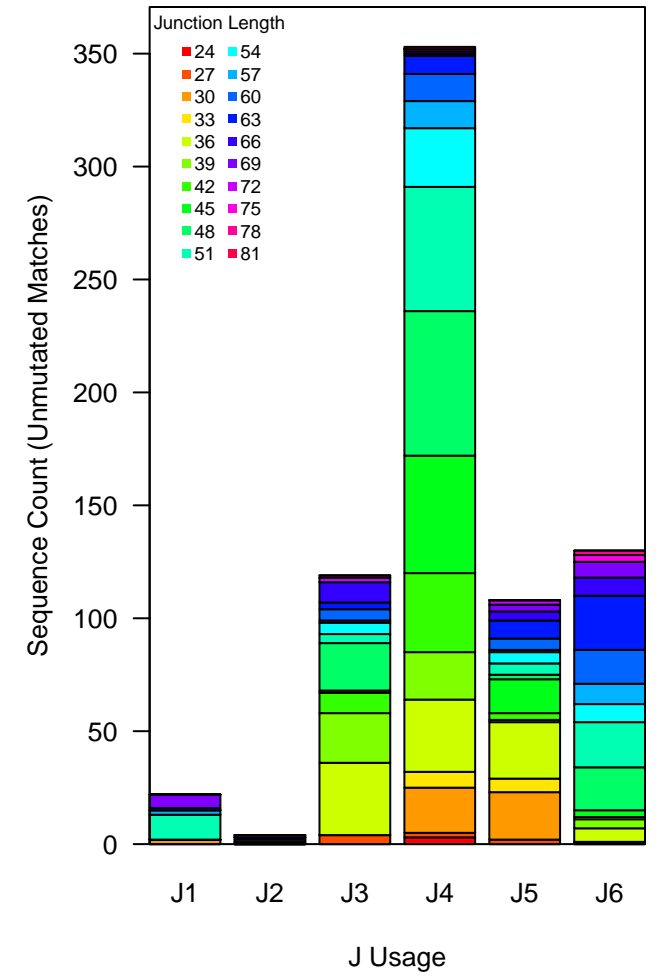
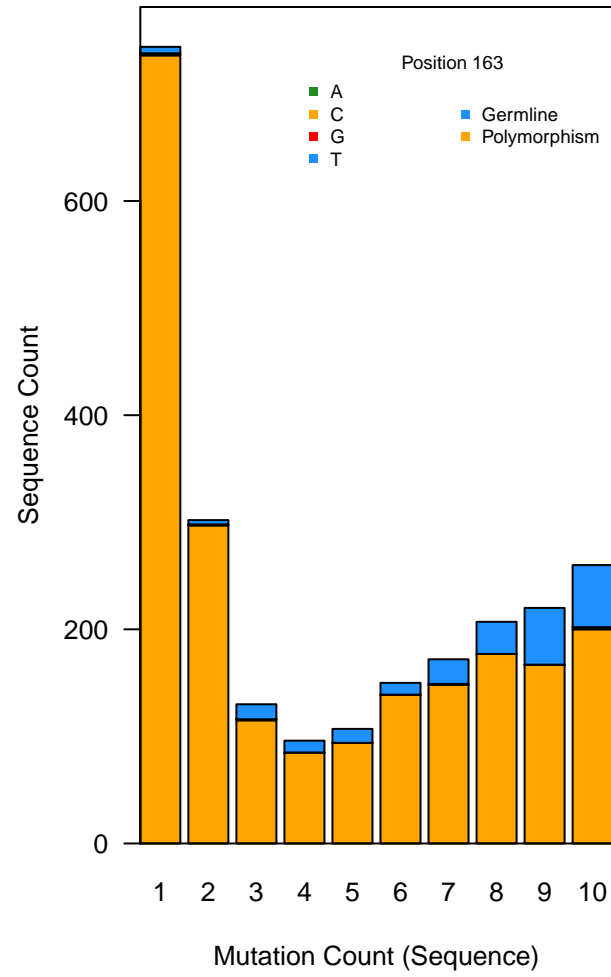
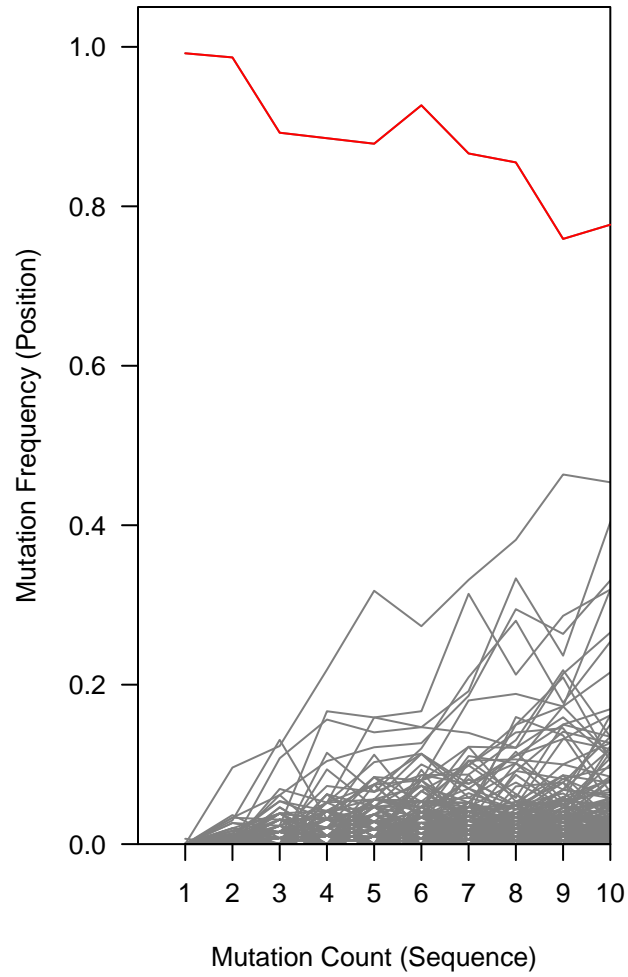
SUBJECT:

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TECHNOLOGY:

MiSeq

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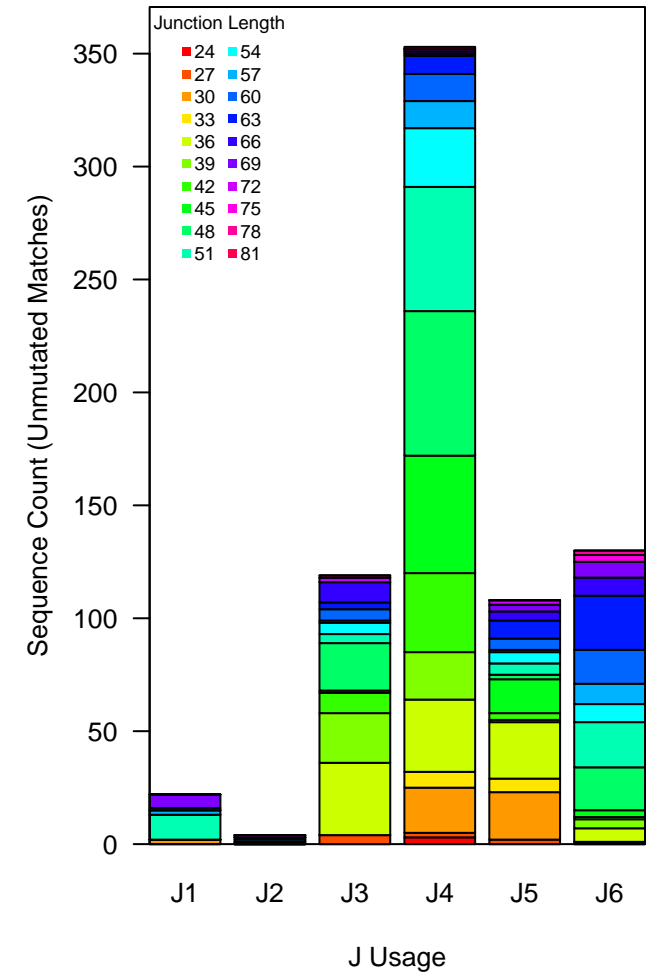
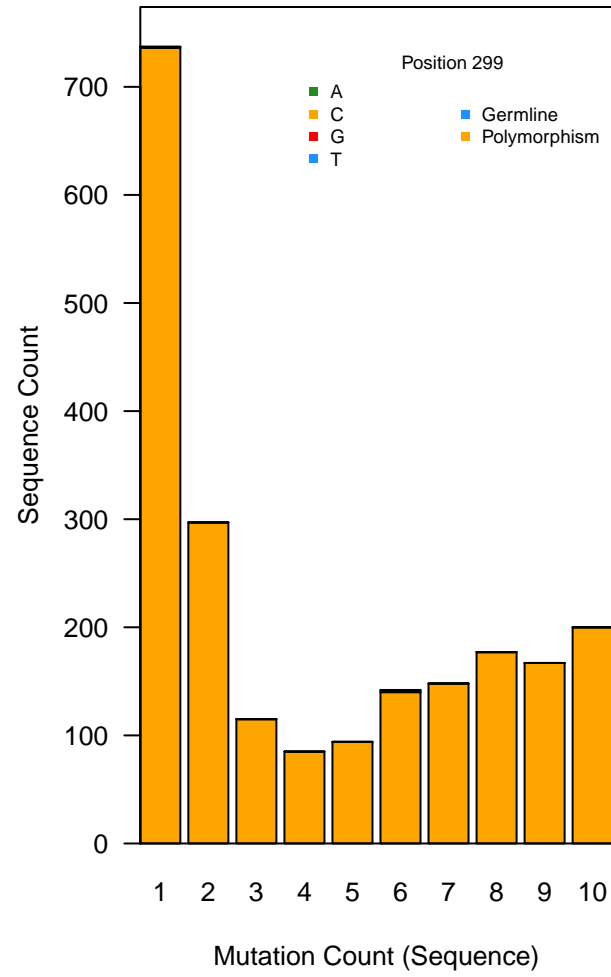
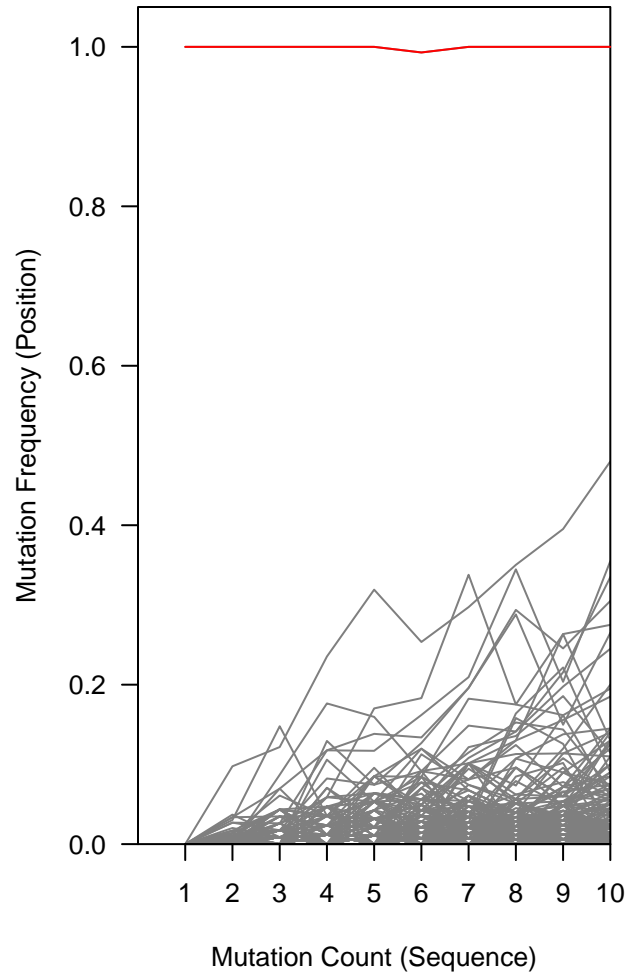


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IGHV1-2*05_T299C



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IGHV1-2*05

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