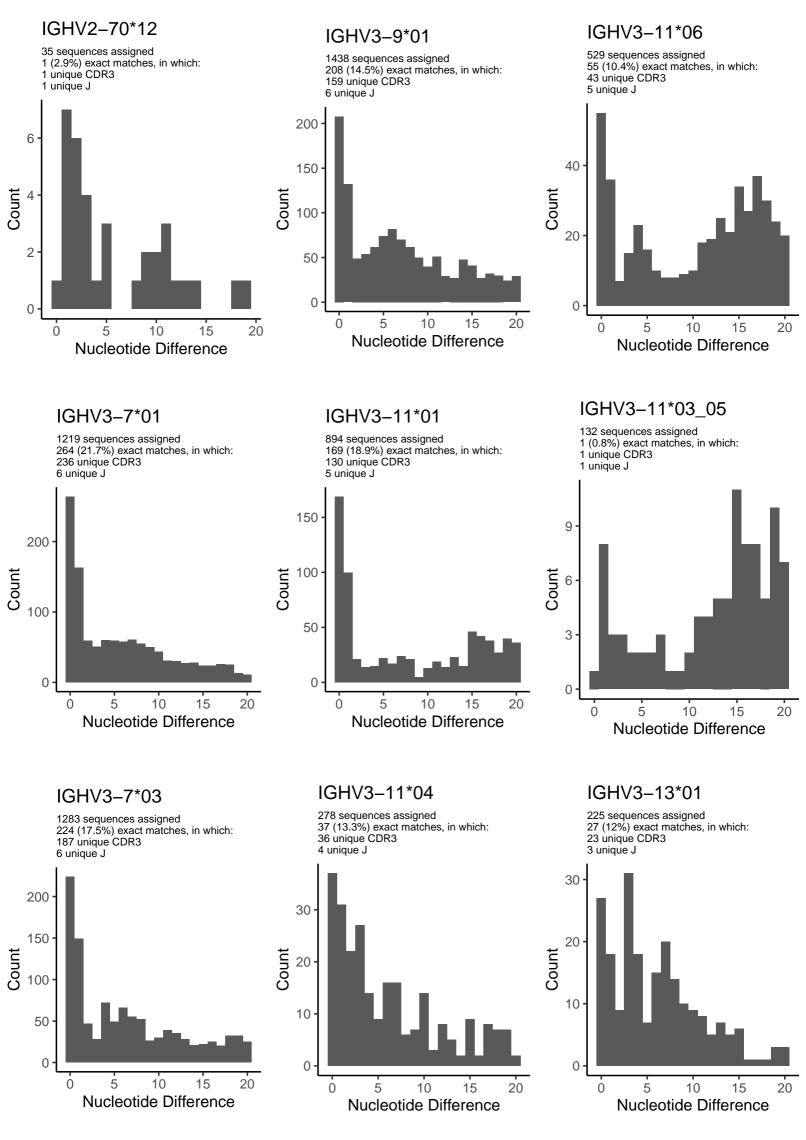
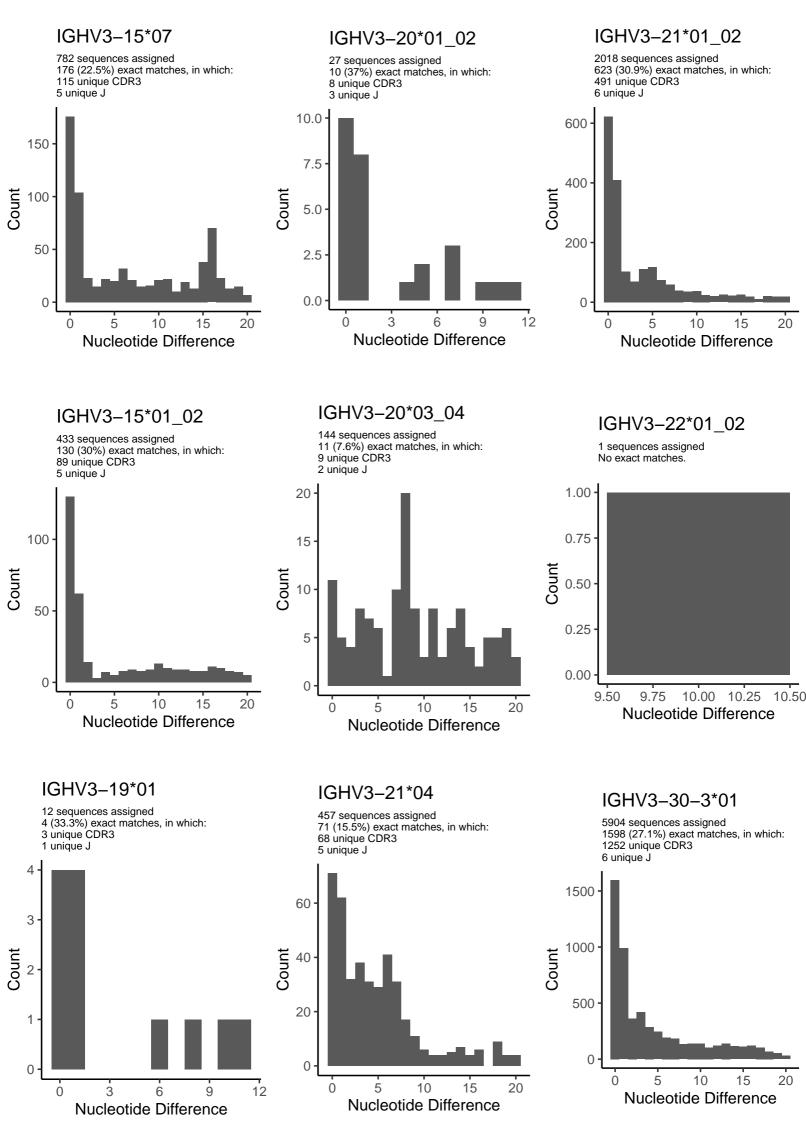
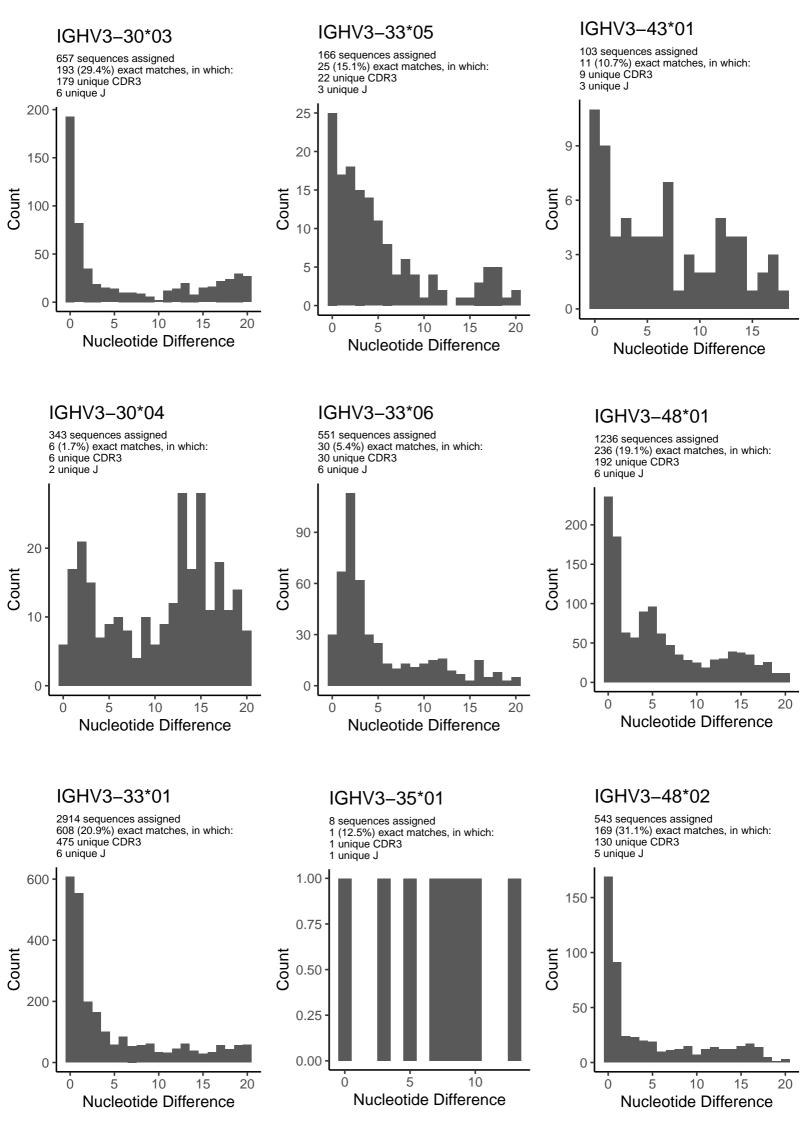
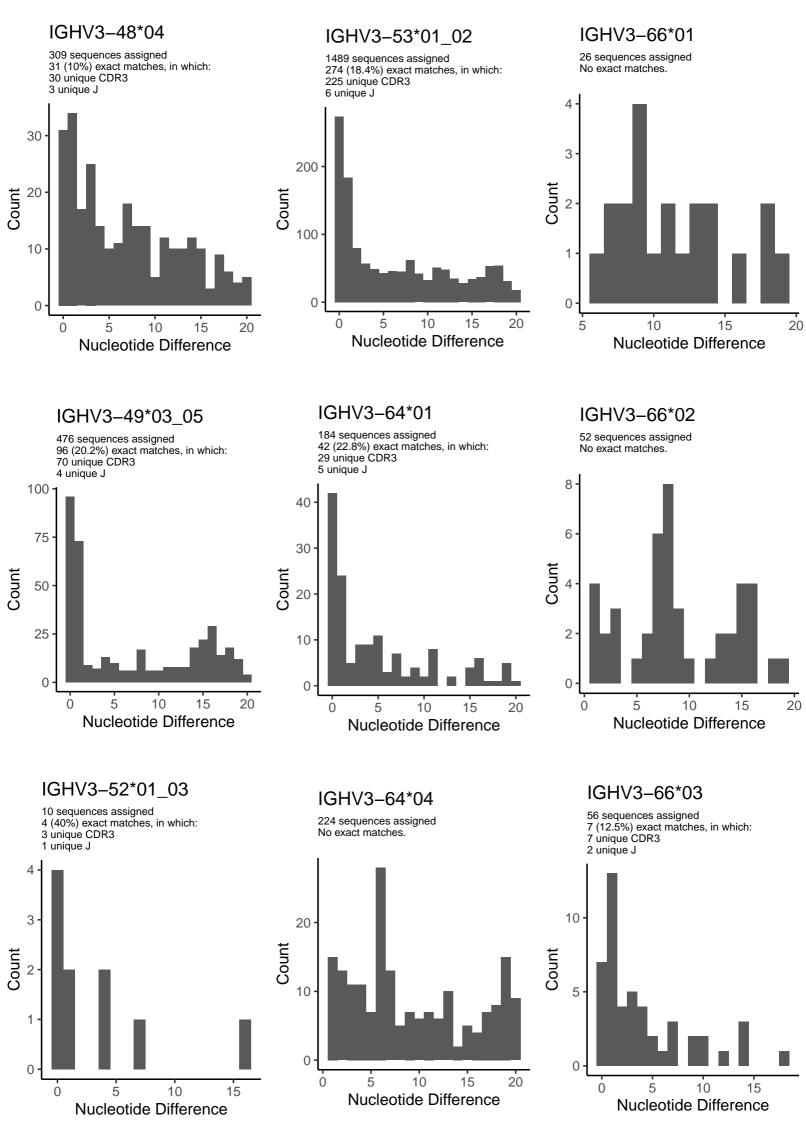


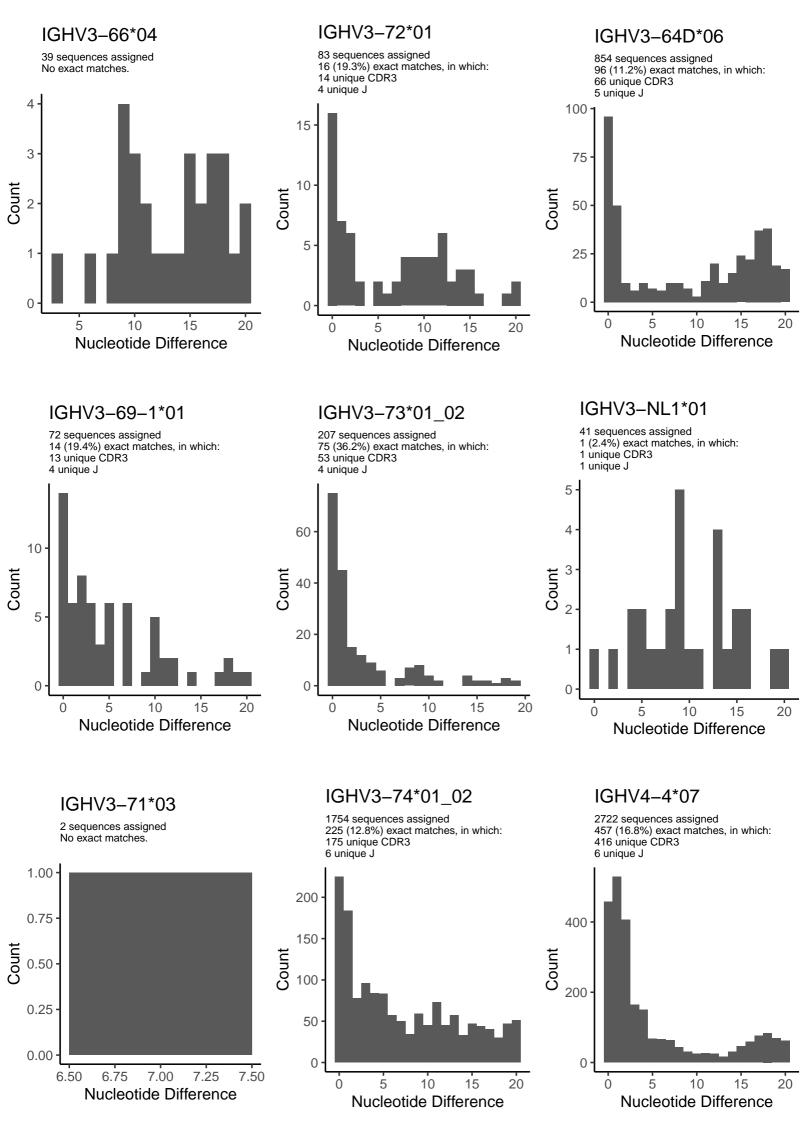
IGHV1-58*02 IGHV1-69*10 IGHV2-5*02 88 sequences assigned 4012 sequences assigned 778 sequences assigned 95 (12.2%) exact matches, in which: 17 (19.3%) exact matches, in which: 676 (16.8%) exact matches, in which: 17 unique CDR3 646 unique CDR3 85 unique CDR3 4 unique J 6 unique J 5 unique J 150 600 20 15 100 400 Count Count Count 10 50 200 5 0 0 0 5 10 15 20 5 10 15 0 0 10 0 15 Nucleotide Difference Nucleotide Difference Nucleotide Difference IGHV1-58*01_03 IGHV2-26*01 IGHV1-69*06_14 115 sequences assigned 35 (30.4%) exact matches, in which: 140 sequences assigned 43 (30.7%) exact matches, in which: 745 sequences assigned 155 (20.8%) exact matches, in which: 34 unique CDR3 39 unique CDR3 153 unique CDR3 5 unique J 5 unique J 5 unique J 40 150 40 30 30 100 Count Count 20 20 50 10 10 0 0 0 10 15 20 0 5 10 15 20 10 15 0 0 Nucleotide Difference Nucleotide Difference Nucleotide Difference IGHV1-69-2*01 IGHV2-70*01 IGHV1-NL1*01 34 sequences assigned 308 sequences assigned 12 sequences assigned 8 (23.5%) exact matches, in which: No exact matches. 38 (12.3%) exact matches, in which: 8 unique CDR3 34 unique CDR3 2 unique J 4 unique J 5 80 4 60 6 Count Count 40 20 2 1 0 0 9 10 11 12 0 10 15 20 0 10 15 20 Nucleotide Difference **Nucleotide Difference** Nucleotide Difference

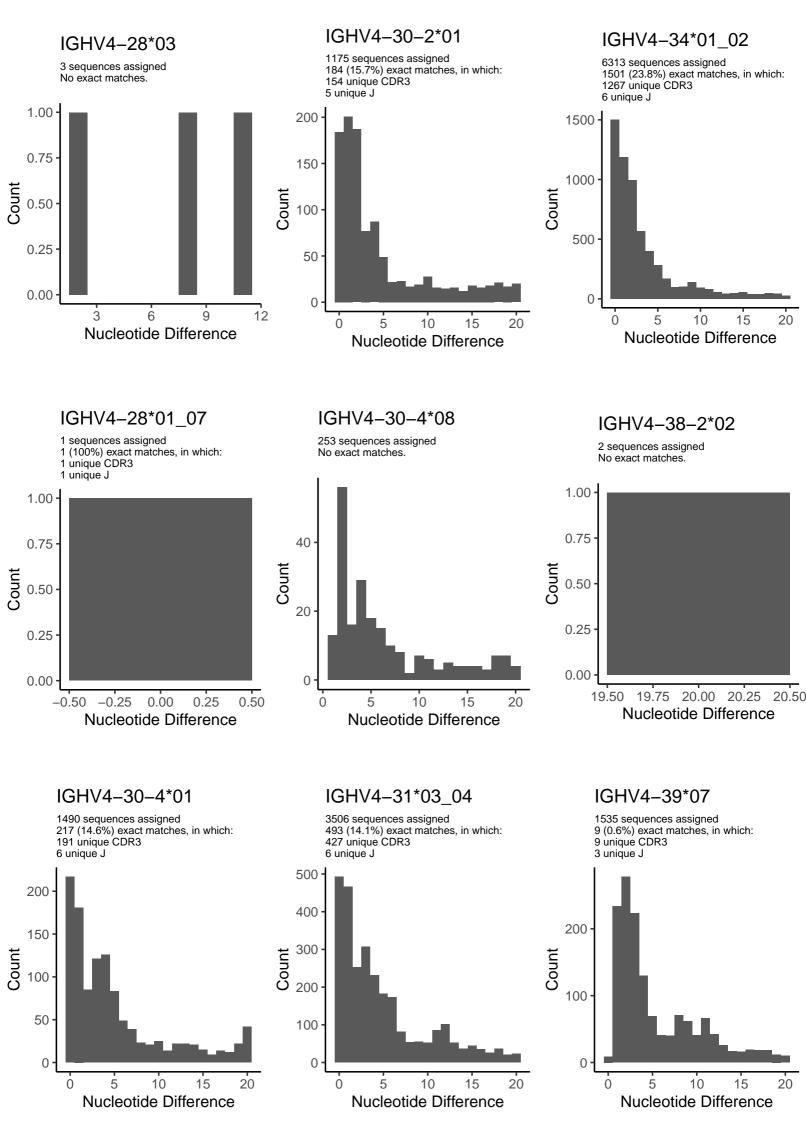


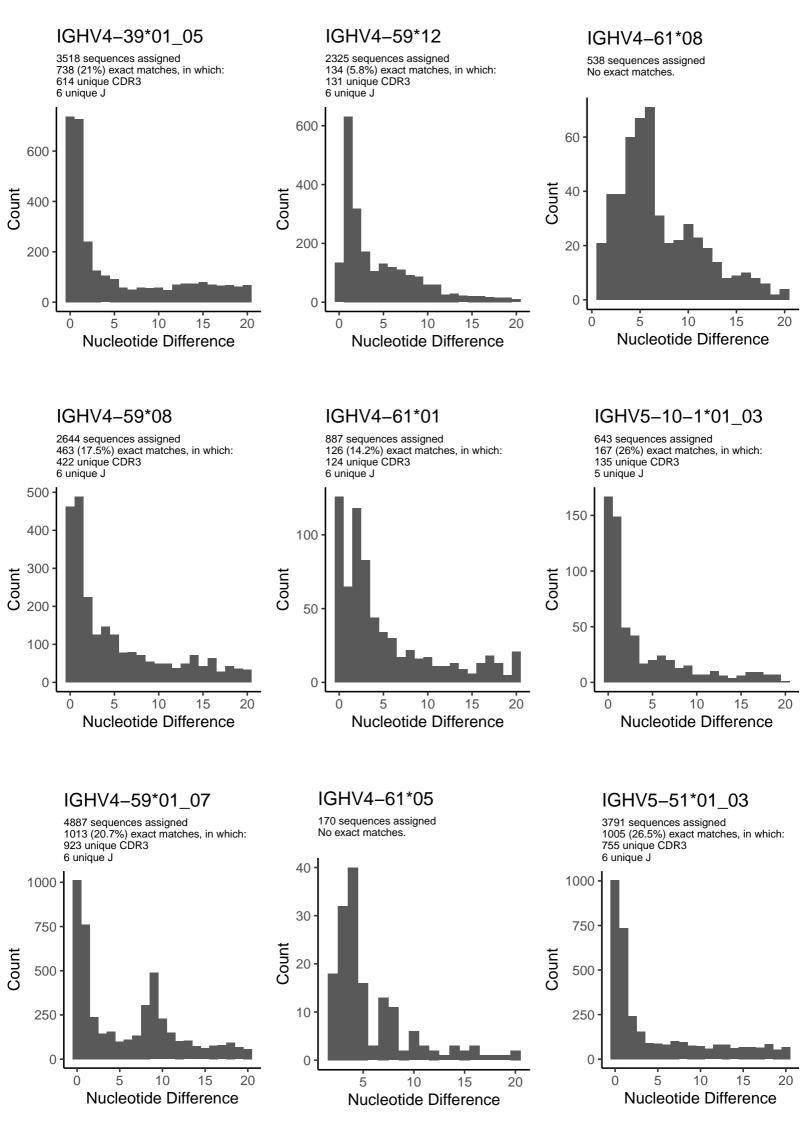






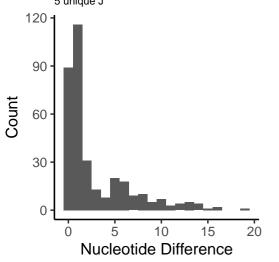






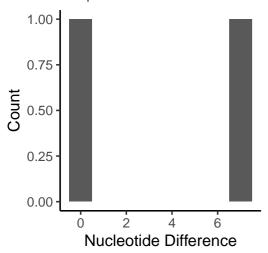
IGHV6-1*01_02

363 sequences assigned 89 (24.5%) exact matches, in which: 78 unique CDR3 5 unique J



IGHV7-4-1*01

2 sequences assigned 1 (50%) exact matches, in which: 1 unique CDR3 1 unique J





Warning – no inferred sequences found.

Novel sequence(s) IGHV1-69*08_C191T IGHV3-48*03_T303G IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Warning – no inferred sequences found.

Novel sequence(s) IGHV3-30*03_T288C IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning: IGHV4-31*02, IGHV4-31*03_04 have identical germline sequences.

Novel sequence(s) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV1-69*04_09_G112A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Novel sequence(s) IGHV1-69*08_C191T IGHV3-30*03_T288C IGHV3-30-3*02_G75C IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-4*02_03_C300T IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning – no inferred sequences found.

Novel sequence(s) IGHV4-59*02_G88A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV1-69*08_C191T IGHV3-11*06_T300C IGHV3-30*03_T288C IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-59*02_G88A IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Warning – no inferred sequences found.

Novel sequence(s) IGHV3-30*03_T288C IGHV3-30-3*01_T288C IGHV4-59*02_G88A IGHV5-10-1*01_03_T258C IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Warning - no inferred sequences found.

Novel sequence(s) IGHV3-48*04_A193T_C198T_A200C_C201T_T210A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV4-59*02_G88A are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV5-51*07_A128G are not listed in the genotype and will be ignored.

Novel sequence(s) IGHV3-33*01_C288T IGHV5-51*07_A128G are not listed in the genotype and will be ignored.