

Supplemental Information

**Rhesus and cynomolgus macaque immunoglobulin
heavy-chain genotyping yields comprehensive
databases of germline VDJ alleles**

Néstor Vázquez Bernat, Martin Corcoran, Izabela Nowak, Mateusz Kaduk, Xaquín Castro Dopico, Sanjana Narang, Pauline Maisonasse, Nathalie Dereuddre-Bosquet, Ben Murrell, and Gunilla B. Karlsson Hedestam

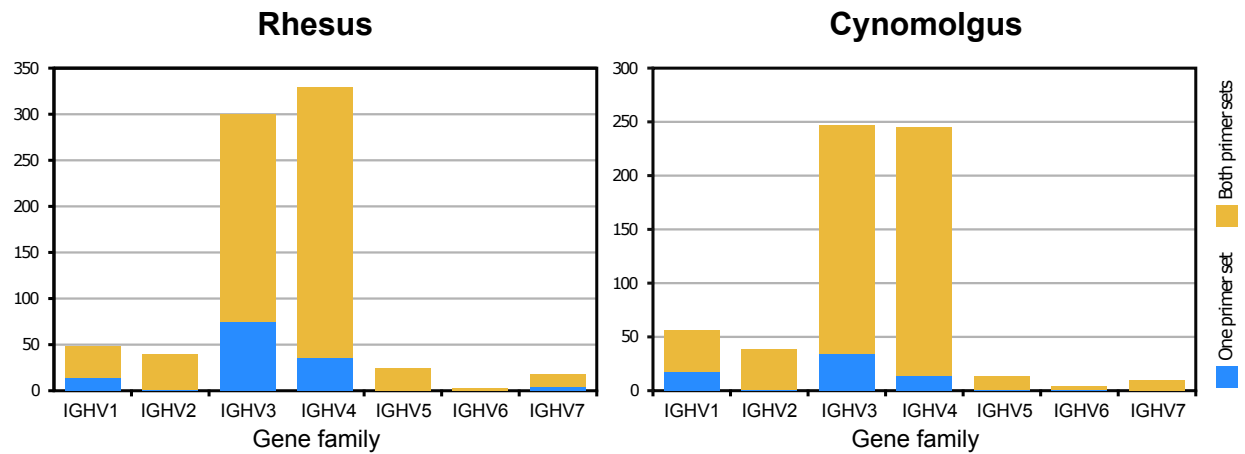


Figure S1. Number of alleles per gene family, related to Figure 1. Number of alleles per gene family in rhesus macaques (left) and cynomolgus macaques (right). IGHV alleles identified in libraries generated with both the upstream and leader primer sets are shown in orange, while IGHV alleles identified with only one of the primer sets are shown in blue.

Cynomolgus V alleles	
IGHV1	56
IGHV2	39
IGHV3	247
IGHV4	245
IGHV5	14
IGHV6	4
IGHV7	10
Total	615

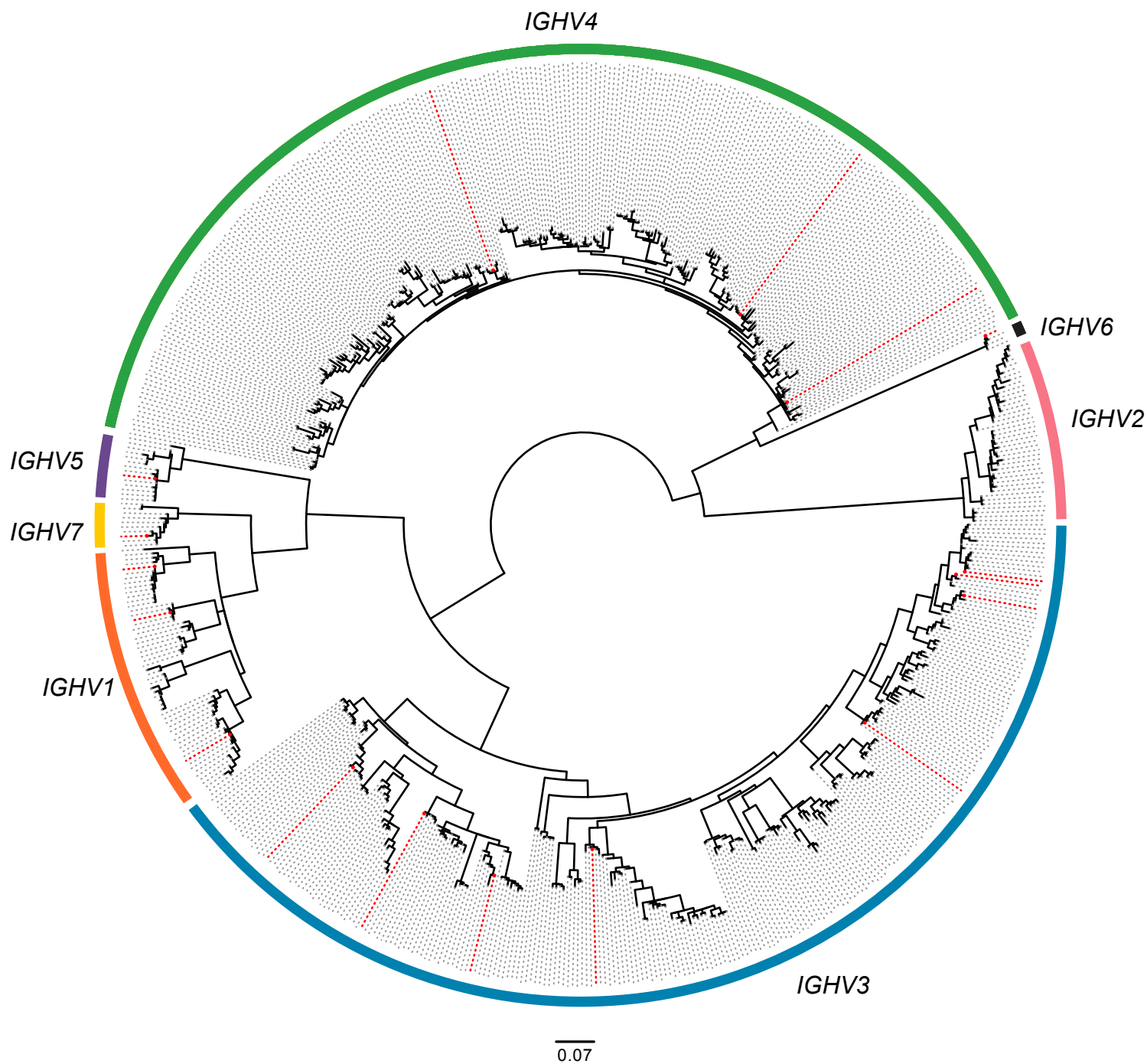
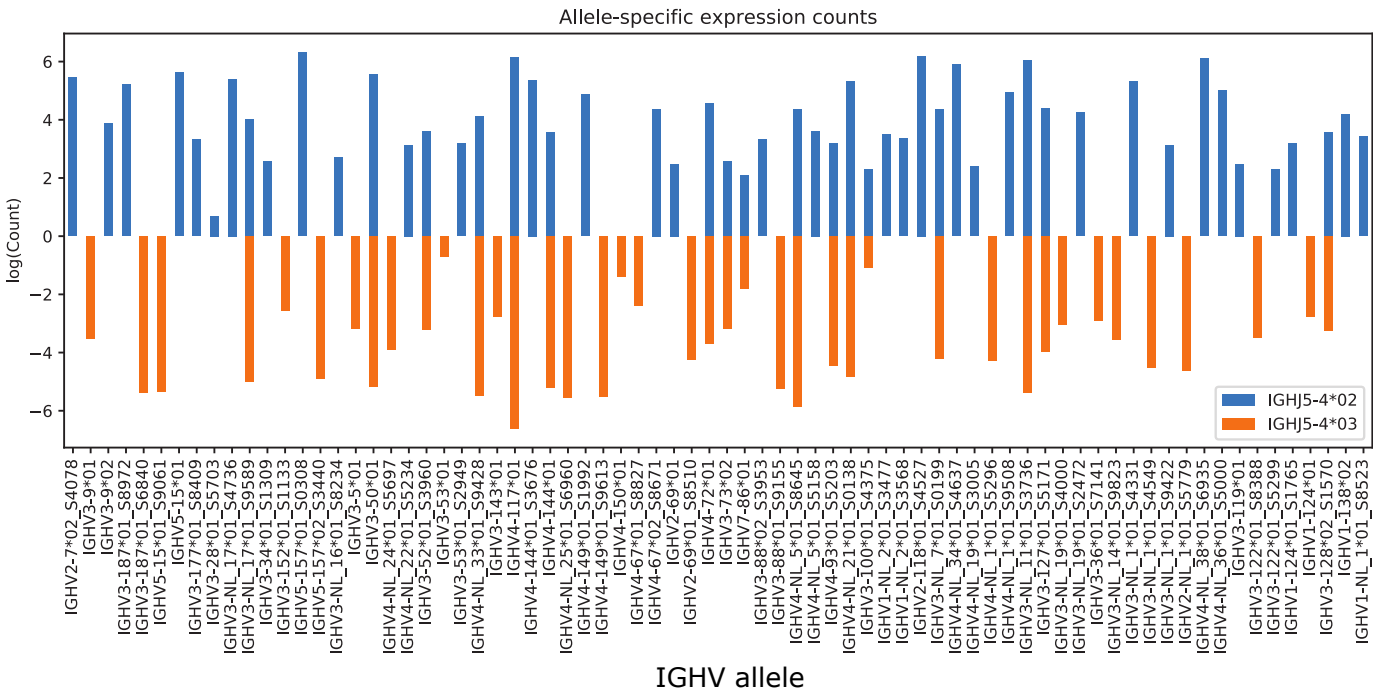


Figure S2. IGHV alleles in cynomolgus macaques inferred by IgDiscover, related to Figure 2. Phylogenetic analysis of IGHV alleles identified by IgDiscover in 12 Mauritian and 6 Indonesian cynomolgus macaques. IGHV families are indicated by arcs in different colors and alleles identical to those present in the IMGT cynomolgus IGHV database (downloaded May 2020) are shown in red dashed lines. A total of 615 IGHV alleles were identified in the 18 animals and the number of alleles in each IGHV family is indicated in the table.

Rh4



D07

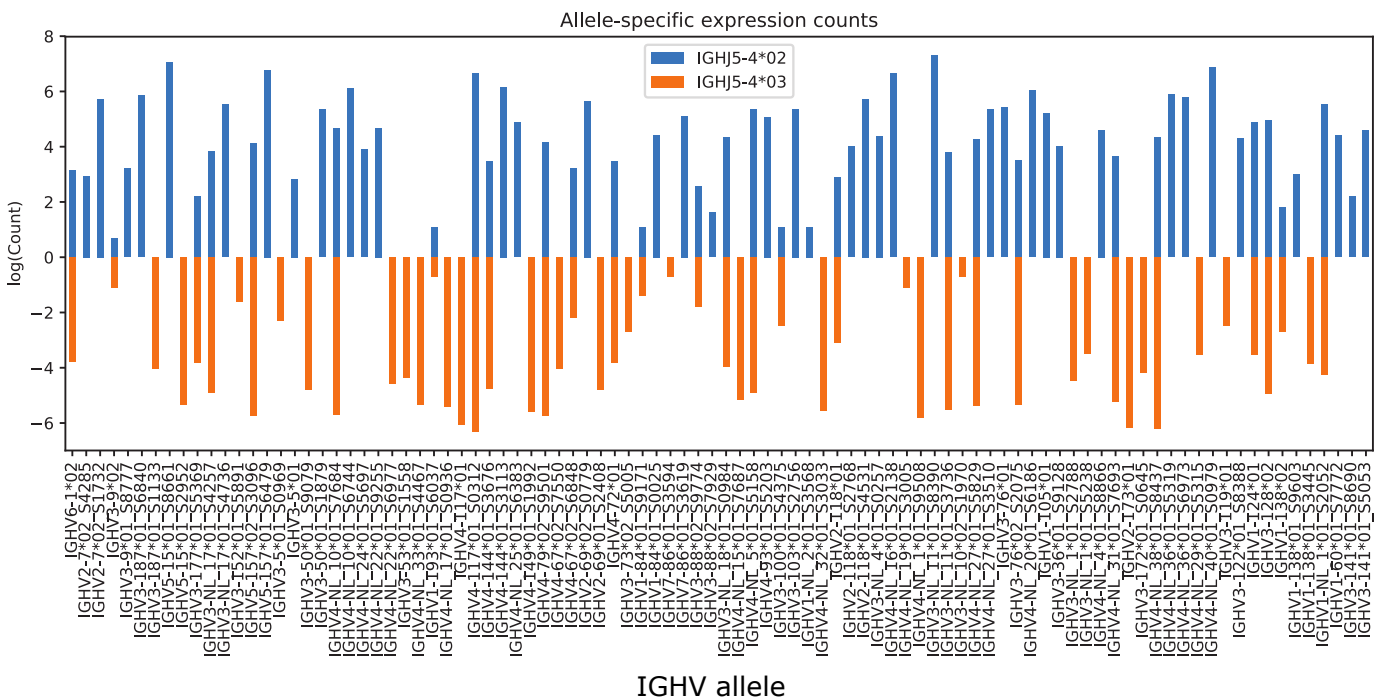
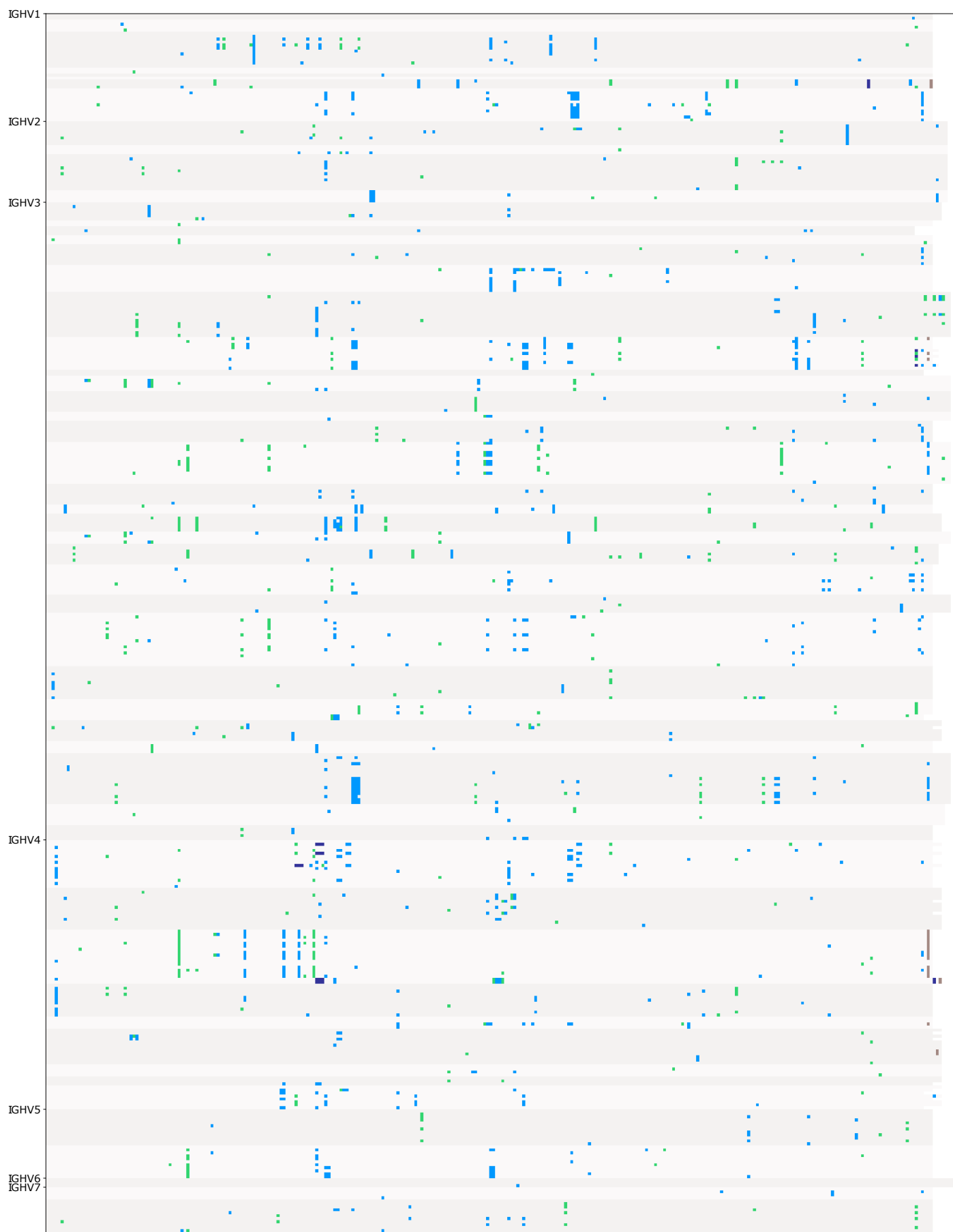
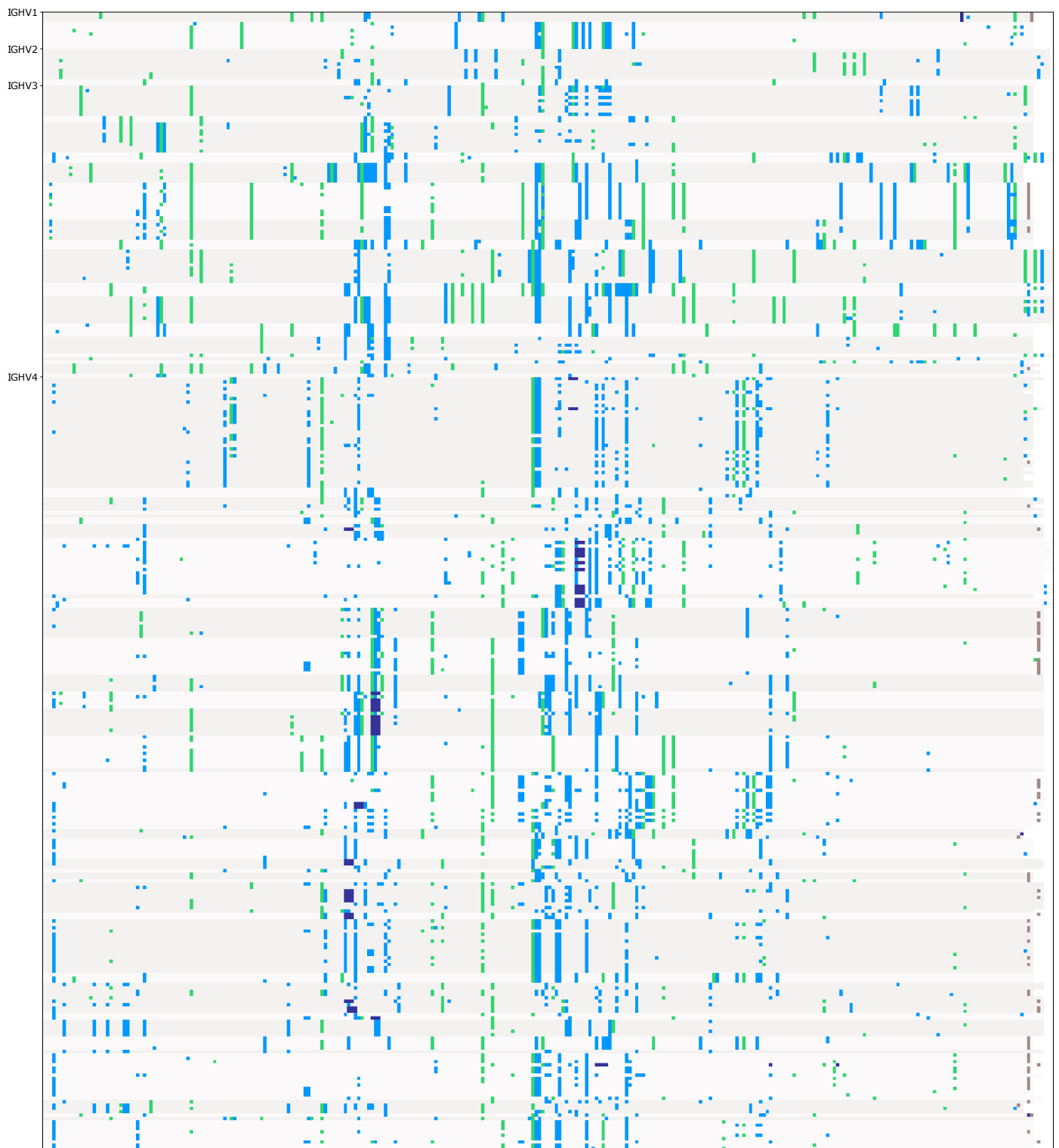


Figure S3. Inferred haplotype analysis of animals Rh4 and D07, related to Figure 2. Illustration of the inferred chromosomally phased allelic content of Rh4 and D07 was produced using the IgDiscover plotalleles function. In both animals the IGHJ5-4 gene is heterozygous enabling the identification of the set of V alleles involved in VDJ recombinations with each of the J alleles. The set of V alleles is plotted in the estimated chromosomal order based on similarity to the closest match on the RheMAC10 assembly.



- Nonsynonymous
- Synonymous
- Insertion
- Unclassified

Figure S4. Rhesus macaque IGHV alleles of genes described in the Cirelli et al. DB aligned to the closest allele in that DB, related to Figure 7. Each allele is displayed as a single row of pixels, sorted vertically by gene family, gene grouping and allelic variant, aligned to the nearest sequence (by edit distance) in the Cirelli et al. database. Each nucleotide that did not map identically to the aligned sequence was categorized as Nonsynonymous, Synonymous, or Insertion, based on its coding change considered in isolation (ie. the effect that each nucleotide would have if it were the only change in that codon). Differences near the end of the sequence, without the full codon context, were marked "Unclassified".



- Nonsynonymous
- Synonymous
- Insertion
- Unclassified

Figure S5. Rhesus macaque IGHV-NL alleles aligned to the closest allele in the Cirelli et al. DB, related to Figure 7. Each allele is displayed as a single row of pixels, sorted vertically by gene family, gene grouping and allelic variant, aligned to the nearest sequence (by edit distance) in the Cirelli et al. database. Each nucleotide that did not map identically to the aligned sequence was categorized as Nonsynonymous, Synonymous, or Insertion, based on its coding change considered in isolation (ie. the effect that each nucleotide would have if it were the only change in that codon). Differences near the end of the sequence, without the full codon context, were marked "Unclassified".

Table S1. Primers employed for library construction, related to Figure 1. (A) 5'RACE primers and (B) 5'MTPX primers for library construction for rhesus and cynomolgus macaques.

A

5'RACE	
5' primers	
Read1_TS	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTNNNNNNNNNNNrGrGrGrG
Read1U	CTACACTCTTTCCCTACACGACGCTCTTCCGATCT
3' primers	
Ma_IgM_RACE_in	CAGACGTGTGCTCTTCCGATCTAACGGGGCATTCTCACAGGAGACGAGGGGGAAAAG
Ma_IgM_RACE_out	GCCAACGGCCACTTCGTTTGTATCAA

B

5'MTPX	
3' primers	
Ma_IgM_MTPX	GGAGTTCAGACGTGTGCTCTTCCGATCTHHHHHACAHHHHHCAHHHHNCACTTCGTTTGTATCCAACGGGGCATTCTC
Read2U	GGAGTTCAGACGTGTGCTCTTCCGATCT
5' primers	
Leader	
Ma_VHL_MTPX_1	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGACTGGACCTGGAGGCTCCTC
Ma_VHL_MTPX_2	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGACTTGACCTGGAAGATCCTC
Ma_VHL_MTPX_3	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGACTGGACCTGGAGGATCCTC
Ma_VHL_MTPX_4	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGACACGCTYTGCTCCACGCTCCTGC
Ma_VHL_MTPX_5	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGACACGCTTTGCTACACACTCCTGC
Ma_VHL_MTPX_6	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCTGTGCCCCACCATGGACACG
Ma_VHL_MTPX_7	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGACACGCTTTGCTYACGCTCCTGC
Ma_VHL_MTPX_8	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGAGTTTGKSCTGAGCTGGGTTTTCT
Ma_VHL_MTPX_9	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTGAGACGCACCATGGAGTTTGTGCTGAG
Ma_VHL_MTPX_10	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGAATTTTGGCYGAGCTGGGTTTTCT
Ma_VHL_MTPX_11	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGARTTTGTGCTGAGCTKGGTTTTCT
Ma_VHL_MTPX_12	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGAATTTAGGCTGAGCTGGGTTTTCT
Ma_VHL_MTPX_13	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGMGTGGGGCTGAGCTGGGTTTTCT
Ma_VHL_MTPX_14	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGAGTCTGGGCTGAGCTGGGTTTTCT
Ma_VHL_MTPX_15	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGAAGCACCTGTGGTTCTTCTCCTCCTG
Ma_VHL_MTPX_16	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGAAGCACCTGTGGTTCTTCTCCTCCTG
Ma_VHL_MTPX_17	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGAAGCACCTGTGGKTCTTCTCCTCCTG
Ma_VHL_MTPX_18	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGAAGCATCTGTGGTTCTTCTCCTCCTG
Ma_VHL_MTPX_19	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGGGTCAACTGCCATCCTCGCCCTC
Ma_VHL_MTPX_20	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGGGTCAACTGCCATCCTCACCCCTC
Ma_VHL_MTPX_21	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGCTGTCTCCTTCTCATCGTCTCCTC
Ma_VHL_MTPX_22	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCAGGCAATGTCTGTCTCCTTCTCCTC
Ma_VHL_MTPX_23	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTGGCAGTCAGCAGAGCTCCAGGC
Ma_VHL_MTPX_24	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGACTGGACCTGGAGGATCCTTCTTG
Ma_VHL_MTPX_25	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTATGGACCTCACCTGGAGCATCCTTTTCTTG
UTR	
Ma_VHU_MTPX_1	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCCCAGAGCACAGCACCTCAYC
Ma_VHU_MTPX_2	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCCTGGAAGTCAGCTCCTCACC
Ma_VHU_MTPX_3	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCCTGGGARCACAGCTCATCACC
Ma_VHU_MTPX_4	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCCCCTGAGAGGAAAGCTCTTACC
Ma_VHU_MTPX_5	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCCCCTGAGAGCACAGTTTCTCACC
Ma_VHU_MTPX_6	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCTGTGCCCCACCATGGACACG
Ma_VHU_MTPX_7	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCACAGARGACCCACCATGGAGTTGG
Ma_VHU_MTPX_8	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCACARAGGACTACCATGGAGTTGG
Ma_VHU_MTPX_9	CTTTCCCTACACGACGCTCTTCCGATCTCCATTGCGGTGATCAGCACWGAACACAG
Ma_VHU_MTPX_10	CTTTCCCTACACGACGCTCTTCCGATCTGATTYCCAGCYGTCTCCACTTGGTGATC
Ma_VHU_MTPX_11	CTTTCCCTACACGACGCTCTTCCGATCTGATCAGCACTGAACACARAACCTCACCTGG
Ma_VHU_MTPX_12	CTTTCCCTACACGACGCTCTTCCGATCTGATCAGCACTGAASACAGARGACTCACC
Ma_VHU_MTPX_13	CTTTCCCTACACGACGCTCTTCCGATCTGATCAGCACTGAACACAGAAGACTCATCATGG
Ma_VHU_MTPX_14	CTTTCCCTACACGACGCTCTTCCGATCTGTTTCCACTTGGTGAYCAGCACTGAACAC
Ma_VHU_MTPX_15	CTTTCCCTACACGACGCTCTTCCGATCTGCAGCAGTTTCCACYTGGTGACCAGC
Ma_VHU_MTPX_16	CTTTCCCTACACGACGCTCTTCCGATCTCCAGKAGTTTCCACTTGGTGACCAGC
Ma_VHU_MTPX_17	CTTTCCCTACACGACGCTCTTCCGATCTGATCAGCACTAAACACAGAACAYACCATGGAG
Ma_VHU_MTPX_18	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTGAGCACAGAGGACGCAYCATGGAG
Ma_VHU_MTPX_19	CTTTCCCTACACGACGCTCTTCCGATCTGGAGACCCAGACCTGGCATTTTCAGG
Ma_VHU_MTPX_20	CTTTCCCTACACGACGCTCTTCCGATCTGATCAGGACTGCACACAGGACTCACC
Ma_VHU_MTPX_21	CTTTCCCTACACGACGCTCTTCCGATCTGGTGATCAGCACCAACACAGAAGACTCAC
Ma_VHU_MTPX_22	CTTTCCCTACACGACGCTCTTCCGATCTGATCAGSACTGAACACACAGGACTCACC
Ma_VHU_MTPX_23	CTTTCCCTACACGACGCTCTTCCGATCTGCACTGAACACAGACCACCAACCATGG
Ma_VHU_MTPX_24	CTTTCCCTACACGACGCTCTTCCGATCTCCCAGACCTGGSATTTTCAGGTGTTTTT
Ma_VHU_MTPX_25	CTTTCCCTACACGACGCTCTTCCGATCTGGATTCCCAGGCGTTTCCACTCAGTG
Ma_VHU_MTPX_26	CTTTCCCTACACGACGCTCTTCCGATCTTCCACTTGGTCATGAACACTGAACWCAG
Ma_VHU_MTPX_27	CTTTCCCTACACGACGCTCTTCCGATCTGAGAGTCACGGACATCCTGTGCAAGAAC
Ma_VHU_MTPX_28	CTTTCCCTACACGACGCTCTTCCGATCTGAGAGTCAYGGACCTCCTGTGCAAGAAC
Ma_VHU_MTPX_29	CTTTCCCTACACGACGCTCTTCCGATCTGAGAGTYAYGGACATCCTGTGCAAGAAC
Ma_VHU_MTPX_30	CTTTCCCTACACGACGCTCTTCCGATCTGAGAGTCATGGACCTWCTGTGCAAGAAC
Ma_VHU_MTPX_31	CTTTCCCTACACGACGCTCTTCCGATCTCAGTGCTTCATTCTGTCTCCTCCACCACG
Ma_VHU_MTPX_32	CTTTCCCTACACGACGCTCTTCCGATCTGTGCTTCTTTCTGTCTCCTCCACCACG
Ma_VHU_MTPX_33	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTGGCAGTCAGCAGAGCTCCAGRC
Ma_VHU_MTPX_34	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTGCCCCCTAGATCACAGCTCCTTGCC
Ma_VHU_MTPX_35	CTACACTCTTTCCCTACACGACGCTCTTCCGATCTCCCCTAGTGACAGCTCCTCACC

Table S2. Library sequence numbers for total, assembled and unique reads for the 45 macaques, related to Figure 1.

Macaque ID	Leader primer set			UTR primer set		
	Reads	Assembled	Unique	Reads	Assembled	Unique
ChinRhe_D7	642414	631180	244828	503618	488460	315234
ChinRhe_D8	793605	779648	469648	696775	677986	411195
ChinRhe_D11	668885	659206	380786	525504	510617	280639
ChinRhe_D15	1085483	1064162	561695	677312	649165	306198
ChinRhe_D16	917069	901053	514237	891052	861302	487808
ChinRhe_D19	967964	948339	316196	1025318	994811	523083
ChinRhe_Rh1	831675	813133	329789	696518	654298	246681
ChinRhe_Rh2	926876	911958	449487	790205	766370	380848
ChinRhe_Rh3	768135	756003	260118	767454	744213	419269
ChinRhe_Rh4	772641	756968	270873	652429	632029	357318
ChinRhe_Rh5	961622	942980	410847	861511	836068	376199
ChinRhe_Rh6	946192	932232	243204	787910	751742	79470
IndiRhe_A01	726070	712585	248692	542903	521138	296759
IndiRhe_A02	856121	839013	272528	701879	678069	369699
IndiRhe_A03	823737	806555	275381	615603	597925	329507
IndiRhe_A04	784394	769278	287834	601600	582161	355152
IndiRhe_A05	579985	566278	236908	871114	824203	287557
IndiRhe_E01	850289	829695	290282	876550	814159	201801
IndiRhe_E02	805112	793103	315363	778979	760162	244853
IndiRhe_E03	1991208	1972080	1085224	2002758	1978651	1259033
IndiRhe_E04	928816	913028	370719	906197	884746	301651
IndiRhe_E05	1439293	1424799	844938	1918525	1893956	1098689
IndiRhe_E06	883642	867962	290802	769942	750675	229753
IndiRhe_E07	821284	806084	286308	625042	603083	205227
IndiRhe_E08	918213	901777	323716	724009	696814	243167
IndiRhe_E09	1669440	1649882	873414	953088	917821	378000
IndiRhe_E10	592963	581009	299983	779454	752694	381930
IndoCyn_F135	802409	788308	256125	689756	671862	242204
IndoCyn_F136	852775	840535	288742	730914	713236	282223
IndoCyn_F137	751911	738140	259190	612329	600163	223619
IndoCyn_F138	815855	801561	279847	696403	685939	280855
IndoCyn_F139	832114	819831	311537	716380	704592	331253
IndoCyn_F140	863155	841522	272007	737446	724598	281339
MaurCyn_Cy1	876452	864275	488896	906341	870538	463341
MaurCyn_Cy2	881989	867266	428924	841964	809010	434686
MaurCyn_Cy3	1106870	1091487	642362	1028565	1001935	589133
MaurCyn_Cy4	916718	901969	476115	903139	879190	490277
MaurCyn_Cy5	1026966	1011002	580890	904767	885735	545959
MaurCyn_Cy6	1043524	1027159	588833	1030347	1004015	593271
MaurCyn_Cy7	1065202	1047624	512180	1061974	1031101	551095
MaurCyn_Cy8	1184324	1166150	695852	607535	594778	360120
MaurCyn_Cy9	1015192	999342	539286	988116	968836	535228
MaurCyn_Cy10	1097082	1079382	566428	1053806	1030662	557377
MaurCyn_Cy11	1091959	1077231	559386	925296	906564	471769
MaurCyn_Cy12	795204	779049	304459	591404	572208	358533

Table S3. Genomically validated and Sanger sequenced IGHD and IGHJ alleles, related to Figure 3.

Genomically validated alleles			
IGHD		IGHJ	
Rhesus	Cynomolgus	Rhesus	Cynomolgus
IGHD2-10*01	IGHD2-10*01_S8741	IGHJ1-1*01	IGHJ1-1*01_S0456
IGHD2-10*01_S295	IGHD2-14*02_S0040	IGHJ2*01	IGHJ1-1*01_S0488
IGHD2-11*01	IGHD2-9*01	IGHJ2*01_S5087	IGHJ4-3*01_S9191
IGHD2-11*01_S1259	IGHD3-41*01_S1308	IGHJ4-3*01	IGHJ6-6*01_S0171
IGHD2-12*01	IGHD3-41*01_S1524	IGHJ5-4*01	
IGHD2-13*01	IGHD5-28*01	IGHJ5-5*01	
IGHD2-14*02_S0100	IGHD6-33*01	IGHJ5-5*01_S6098	
IGHD2-14*02_S1717	IGHD6-33*01_S4467		
IGHD3-17*01	IGHD6-34*01		
IGHD3-19*02_S4720	IGHD6-38*01_S4618		
IGHD3-41*01_S4389	IGHD6-39*01		
IGHD3-41*01_S8240			
IGHD5-27*01			
IGHD5-28*01_S4021			
IGHD5-32*01			
IGHD5-32*01_S0263			
IGHD5-32*01_S0995			
IGHD5-32*01_S2987			
IGHD6-39*01_S0850			

Table S4. Genomically validated and Sanger sequenced IGHV alleles, related to Figure 3.

Genomically validated IGHV alleles			
Rhesus		Cynomolgus	
IGHV1-105*01	IGHV4-144*01_S3008	IGHV1-105*01_S1228	IGHV4-117*01_S2181
IGHV1-138*01_S2593	IGHV4-149*01_S3418	IGHV1-105*01_S9006	IGHV4-117*01_S6852
IGHV1-138*01_S3445	IGHV4-149*02_S6878	IGHV1-138*01_S0032	IGHV4-144*01_S1446
IGHV1-170*01	IGHV4-174*02	IGHV1-138*01_S0851	IGHV4-144*01_S6192
IGHV1-84*01	IGHV4-174*02_S5400	IGHV1-138*01_S2054	IGHV4-150*01_S1575
IGHV1-84*01_S0025	IGHV4-67*02_S8878	IGHV1-138*01_S2734	IGHV4-67*02_S4494
IGHV1-84*01_S4663	IGHV4-72*01	IGHV1-138*01_S4144	IGHV4-NL_1*01_S7317
IGHV1-NL_2*01_S3568	IGHV4-72*01_S8261	IGHV1-138*01_S6073	IGHV4-NL_10*01_S8809
IGHV1-NL_2*01_S9896	IGHV4-79*02_S9501	IGHV1-138*01_S8860	IGHV4-NL_13*01_S9273
IGHV2-118*01	IGHV4-NL_1*01_S1456	IGHV1-138*02_S0669	IGHV4-NL_17*01_S8189
IGHV2-118*01_S6364	IGHV4-NL_1*01_S1593	IGHV1-84*01_S2078	IGHV4-NL_18*01_S3907
IGHV2-69*01_S4797	IGHV4-NL_1*01_S8621	IGHV1-NL_2*01_S2245	IGHV4-NL_22*01_S2393
IGHV2-69*02	IGHV4-NL_1*01_S8720	IGHV1-NL_2*01_S5862	IGHV4-NL_23*01_S3043
IGHV2-69*02_S8202	IGHV4-NL_1*01_S9508	IGHV1-NL_2*01_S8362	IGHV4-NL_25*01_S1514
IGHV3-100*01	IGHV4-NL_1*02_S1821	IGHV1-NL_2*01_S9602	IGHV4-NL_27*01_S0482
IGHV3-100*01_S4375	IGHV4-NL_1*02_S5113	IGHV2-118*01_S0293	IGHV4-NL_27*01_S1515
IGHV3-103*01	IGHV4-NL_10*01_S7684	IGHV2-118*01_S1355	IGHV4-NL_28*01_S8886
IGHV3-119*01	IGHV4-NL_10*02_S9348	IGHV2-69*01	IGHV4-NL_29*01_S7498
IGHV3-120*01	IGHV4-NL_15*01_S5717	IGHV2-69*01_S0230	IGHV4-NL_29*01_S9610
IGHV3-128*01	IGHV4-NL_16*01_S2138	IGHV2-69*01_S2648	IGHV4-NL_33*01_S9333
IGHV3-141*02_S6589	IGHV4-NL_16*01_S2324	IGHV2-NL_2*01_S2193	IGHV4-NL_36*01_S5766
IGHV3-187*01_S1387	IGHV4-NL_17*01_S2080	IGHV3-127*01	IGHV4-NL_37*01_S0825
IGHV3-187*02	IGHV4-NL_17*01_S2469	IGHV3-143*01	IGHV4-NL_37*01_S0997
IGHV3-28*01	IGHV4-NL_17*01_S3082	IGHV3-177*01_S8409	IGHV4-NL_5*01_S6960
IGHV3-5*01	IGHV4-NL_17*01_S4099	IGHV3-NL_1*01_S4850	IGHV4-NL_5*01_S8913
IGHV3-52*02_S4550	IGHV4-NL_17*01_S5431	IGHV3-NL_2*01_S9710	IGHV4-NL_8*02_S1704
IGHV3-73*02_S5005	IGHV4-NL_20*01_S3868	IGHV3-NL_5*01_S8361	
IGHV3-87*01	IGHV4-NL_20*01_S7244		
IGHV3-88*01	IGHV4-NL_21*01_S0138		
IGHV3-88*01_S9155	IGHV4-NL_21*01_S1118		
IGHV3-88*01_S9470	IGHV4-NL_22*01_S9255		
IGHV3-9*01_S8777	IGHV4-NL_23*01_S1296		
IGHV3-NL_1*01_S4331	IGHV4-NL_24*01_S7595		
IGHV3-NL_1*01_S9854	IGHV4-NL_24*01_S8809		
IGHV3-NL_11*01_S3736	IGHV4-NL_25*01_S6383		
IGHV3-NL_12*02_S5864	IGHV4-NL_25*01_S9955		
IGHV3-NL_13*01_S3277	IGHV4-NL_27*01_S7431		
IGHV3-NL_16*01_S5133	IGHV4-NL_27*01_S9596		
IGHV3-NL_17*01_S4250	IGHV4-NL_28*01_S2610		
IGHV3-NL_18*01_S3867	IGHV4-NL_29*01_S3761		
IGHV3-NL_2*01_S3900	IGHV4-NL_29*01_S9965		
IGHV3-NL_7*01_S0199	IGHV4-NL_33*01_S3086		
IGHV3-NL_8*01_S7474	IGHV4-NL_33*01_S4377		
IGHV3-NL_9*01_S6098	IGHV4-NL_36*01_S0848		
IGHV4-117*01	IGHV4-NL_36*01_S5847		
IGHV4-117*01_S0992	IGHV4-NL_36*01_S6474		
IGHV4-117*01_S1924	IGHV4-NL_36*01_S6687		
IGHV4-117*01_S2204	IGHV4-NL_40*01_S0979		
IGHV4-117*01_S2932	IGHV4-NL_5*01_S5158		
IGHV4-144*01			