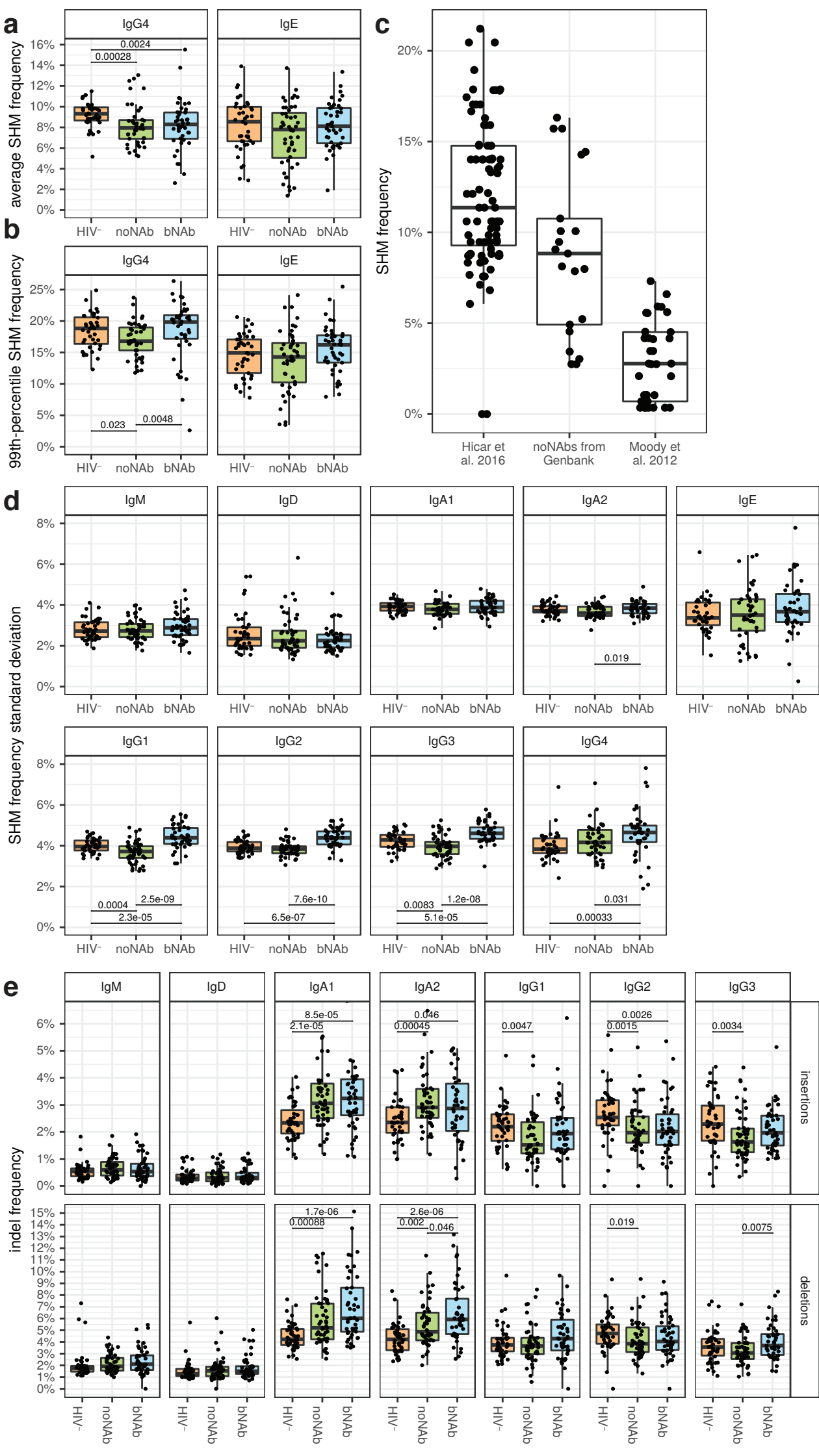


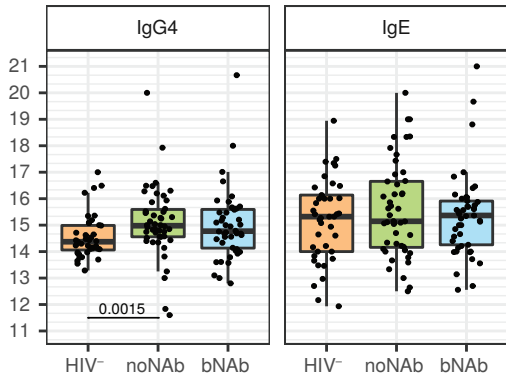
## Supplementary Figures



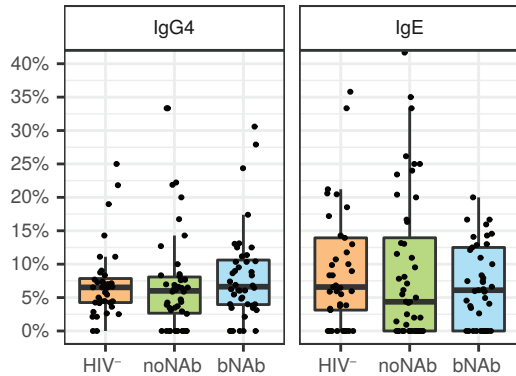
**Fig. S1: Additional SHM and macromutation data: SHM frequencies for rare isotypes IgG4 and IgE; reference SHM frequencies of HIV gp120-binding antibodies; frequencies of indels in IGHV genes in HIV-uninfected individuals, HIV-infected noNAb and bNAb individuals; standard deviation of SHM values.** (a) The mean per clone SHM frequency of rearrangements with IgG4 and IgE isotypes. Results for the other isotypes are shown in Fig. 1a. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46. (b) The 99<sup>th</sup>-percentile SHM frequency in the IgG4 and IgE isotypes. Results for the other isotypes are shown in Fig. 1b. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46. (c) Reported SHM frequencies for HIV gp120-binding antibodies elicited by virus-like particle vaccination, which bind quaternary HIV epitopes (Hicar et al., 2016); non-neutralizing gp120-binding antibodies from Genbank; and gp120-binding antibodies with antibody-dependent cellular cytotoxicity activity elicited in participants in the ALVAC-HIV/AIDS VAX-B/E RV144 vaccine trial (Moody et al. 2012). Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). (d) The standard deviation of SHM in IGHV of members of clones expressed as the indicated isotypes is shown. bNAb individuals had higher standard deviations of SHM in IgG isotype antibodies compared to noNAb and HIV-uninfected individuals. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46. (e) Frequency of insertions and deletions in the IGHV genes of antibodies expressed as IgM, IgD, IgG and IgA. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46.

**a**

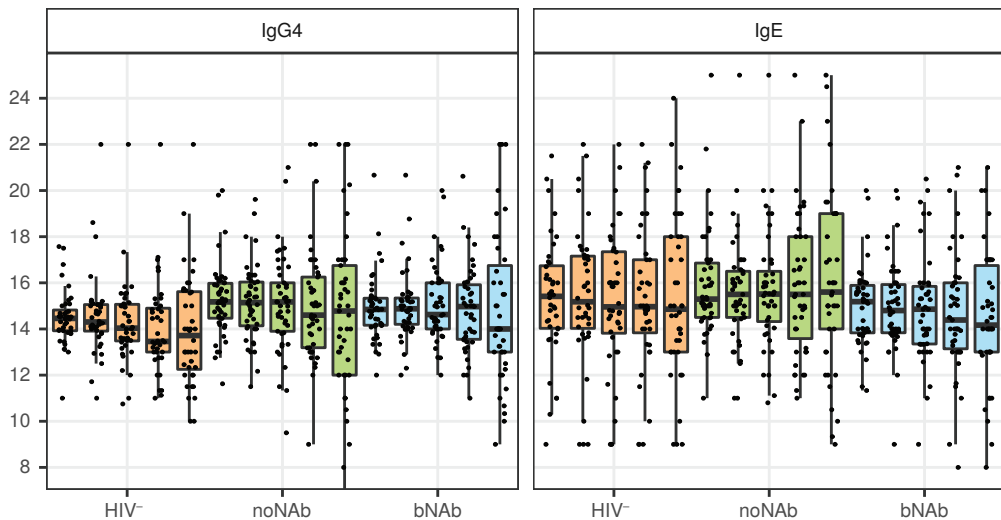
average CDR-H3 length (a.a.)

**b**

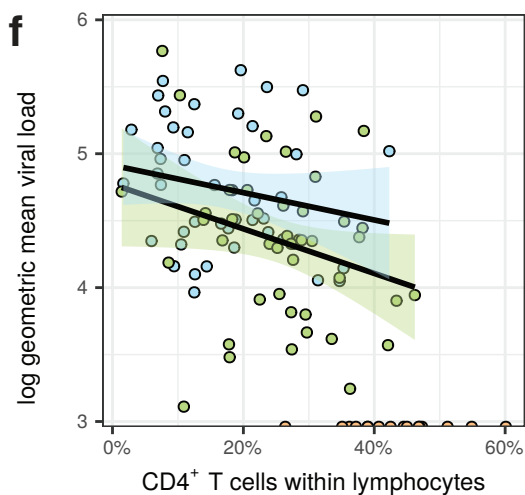
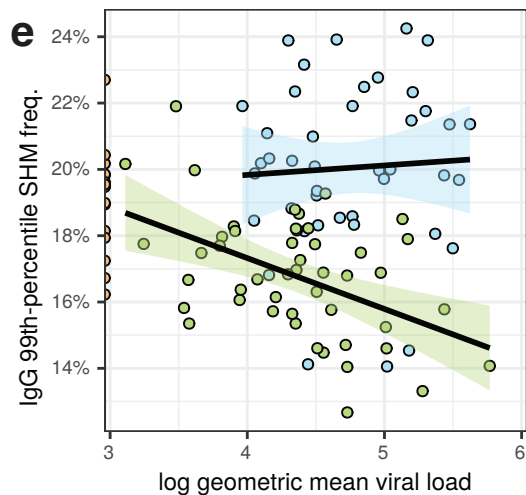
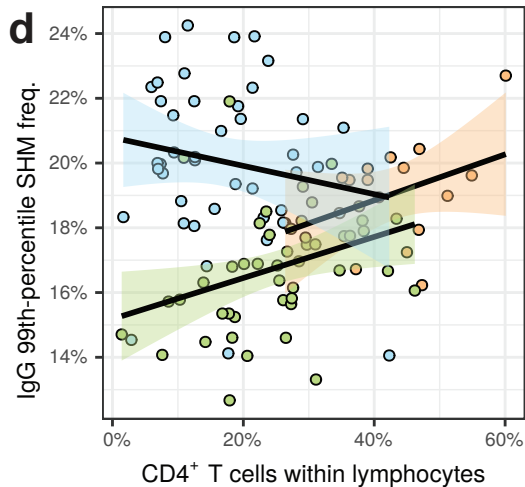
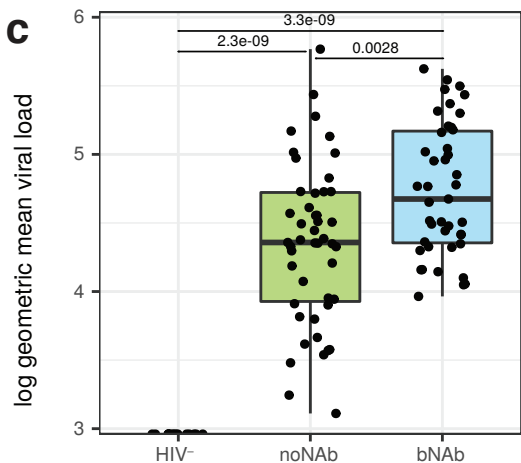
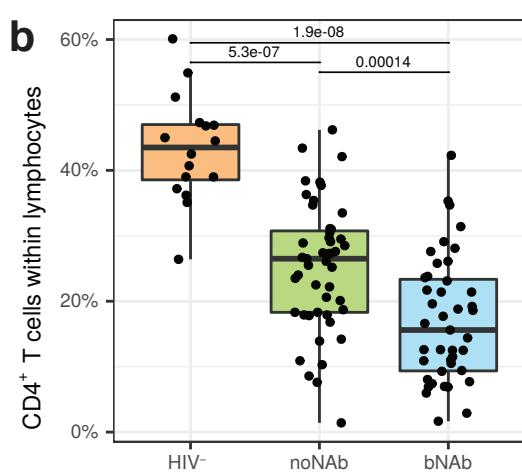
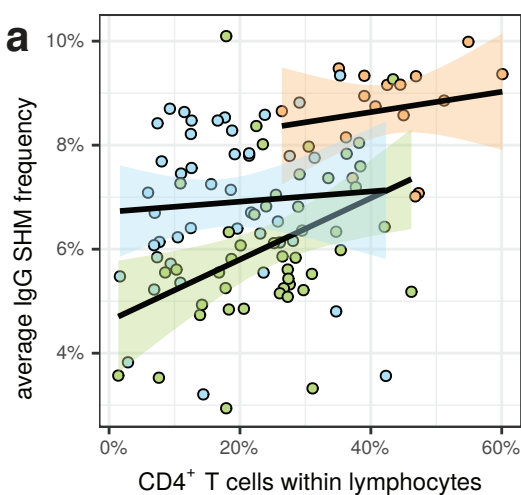
fraction CDR-H3 &gt; 19 a.a.

**c**

average CDR-H3 length (a.a.)

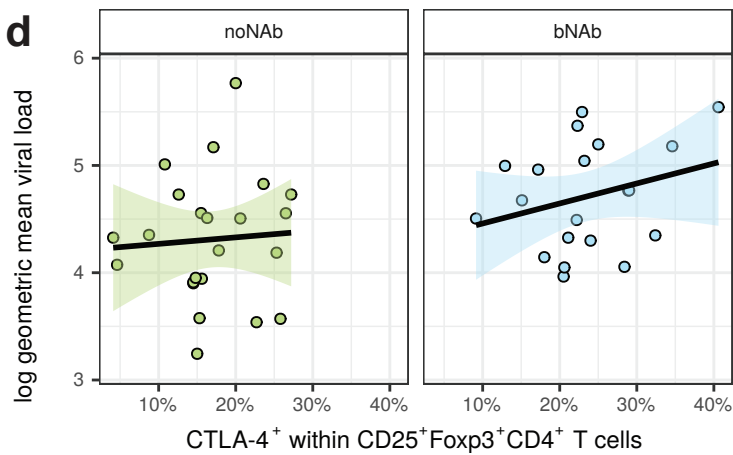
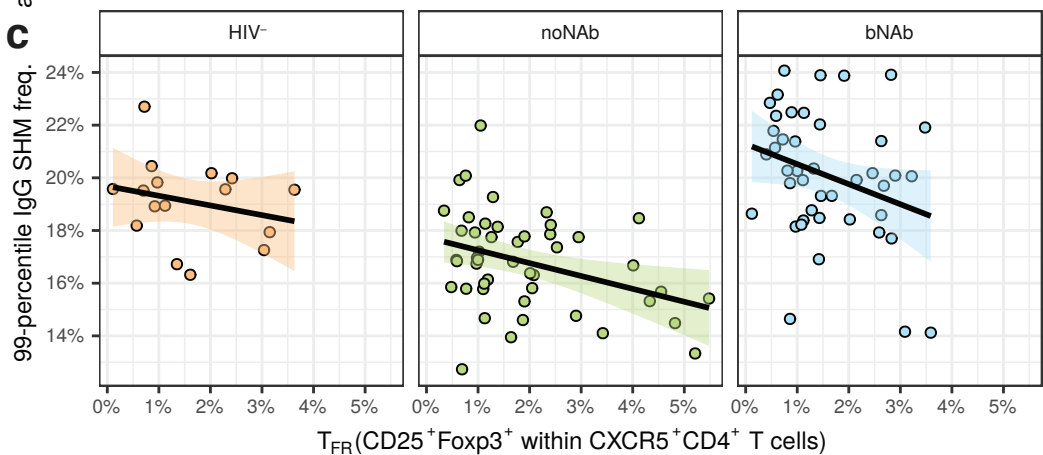
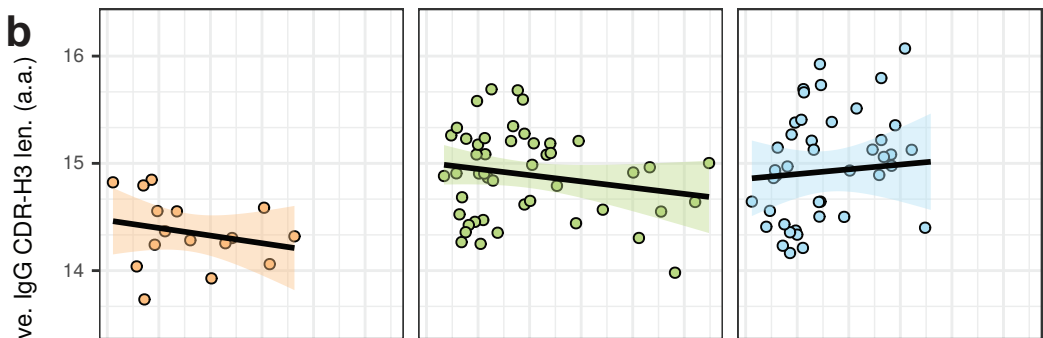
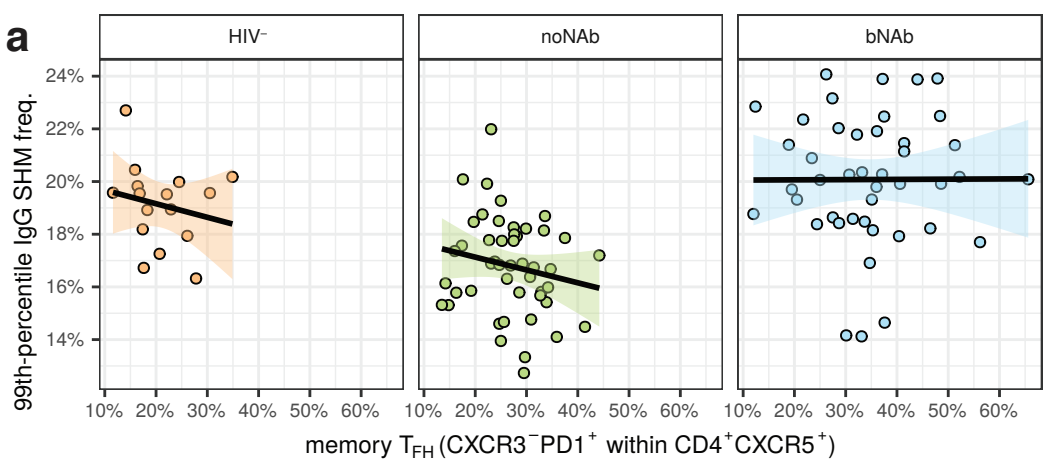


**Fig. S2: CDR-H3 lengths for rare isotypes IgG4 and IgE.** (a) Average CDR-H3 lengths in the IgG4 and IgE compartments. Results for the other isotypes are shown in Fig. 2a. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46. (b) Fraction of clones with CDR-H3s longer than 19 amino acids in the IgG4 and IgE isotypes. Results for the other isotypes are shown in Fig. 2b. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46. (c) Average heavy chain CDR-H3 lengths in IgG4 and IgE isotype fractions with increasing frequencies of SHM. Within each subject group, the columns from left to right indicate the mean CDR-H3 lengths in the 30%, 20%, 10%, 5%, or 1% most mutated sequences in each subject, respectively. Results for the other isotypes are shown in Fig. 3. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46.



**Fig: S3. Relationships between CD4<sup>+</sup> T cell frequencies or HIV viral load and IgG SHM**

**frequencies.** (a) Correlation between CD4 T helper cell frequencies within lymphocytes, and average IgG mutation frequencies. Correlation was statistically significant for HIV-infected noNAb subjects (green color,  $p=0.0066$ ) and not significant for HIV-infected bNAb subjects or HIV-uninfected controls. P-values are for the fit of the linear model. Shaded regions represent the 95% confidence interval of the linear regression model. (b) CD4<sup>+</sup> T cell frequencies within lymphocytes in HIV-infected and uninfected participants. HIV-uninfected subjects had higher CD4<sup>+</sup> T cell frequencies than all HIV-infected subjects, while HIV-infected noNAb subjects had higher CD4<sup>+</sup> T cell frequencies than bNAb individuals. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). (c) HIV viral loads in HIV-infected and uninfected subjects, as previously reported (Moody et al., 2016). P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). (d) The correlation between CD4<sup>+</sup> T cell frequencies within lymphocytes and IgG 99<sup>th</sup> percentile SHM level was only significant for HIV-infected noNAb subjects (green color,  $p=0.02065$ ). Shaded regions represent the 95% confidence interval of the linear regression model. (e) The negative correlation between viral load and IgG 99<sup>th</sup> percentile SHM level was significant for HIV-infected noNAb subjects (green color,  $p=0.00098$ ), but not significant for HIV-infected bNAb subjects (blue color). P-values are for the fit of the linear model. Shaded regions represent the 95% confidence interval of the linear regression model. (f) Correlation between CD4<sup>+</sup> T cell frequency within lymphocytes, and viral load. P-values are for the fit of the linear model. Shaded regions represent the 95% confidence interval of the linear regression model.

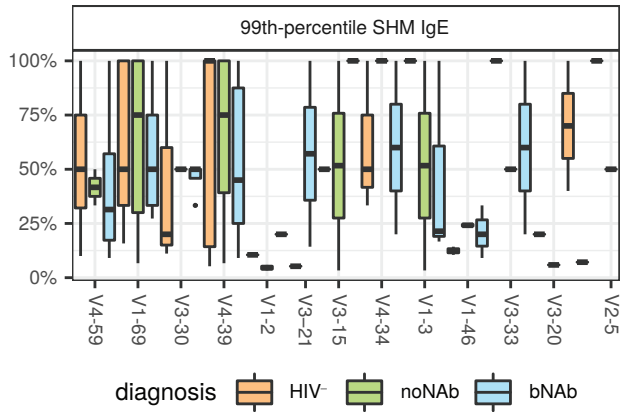




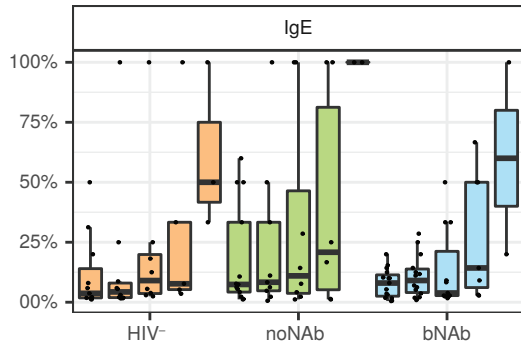
**Fig. S4: Correlation of IGH features and circulating memory CD4<sup>+</sup> T<sub>FH</sub> or T<sub>FR</sub> cell frequencies.** (a) IgG 99<sup>th</sup>-percentile SHM frequencies in relation to circulating resting memory T<sub>FH</sub> frequency (percent of CXCR3<sup>neg</sup> PD1<sup>+</sup> T cells within the CD4<sup>+</sup>CXCR5<sup>+</sup> population). Shaded regions represent the 95% confidence interval of the linear regression model. (b) Average CDR-H3 lengths showed no significant relationship with T<sub>FR</sub> subset phenotypic data as previously published in Moody et al., 2016. Shaded regions represent the 95% confidence interval of the linear regression model. (c) IgG 99<sup>th</sup>-percentile SHM frequencies in relation to T<sub>FR</sub> frequencies (CD25<sup>+</sup>FOXP3<sup>+</sup> within CXCR5<sup>+</sup>CD4<sup>+</sup> T cells) in HIV-uninfected, noNAbs and bNAbs individuals (p-values for linear model are 0.03668 for HIV-uninfected, 0.04789 for noNAbs, and 0.0344 for bNAbs). Shaded regions represent the 95% confidence interval of the linear regression model. (d) The geometric mean of HIV viral load was not correlated with the proportion of CTLA-4<sup>+</sup> cells within CD25<sup>+</sup> FOXP3<sup>+</sup> CD4<sup>+</sup> T cell populations in bNAbs participants. Shaded regions represent the 95% confidence interval of the linear regression model.

**a**

V segment usage

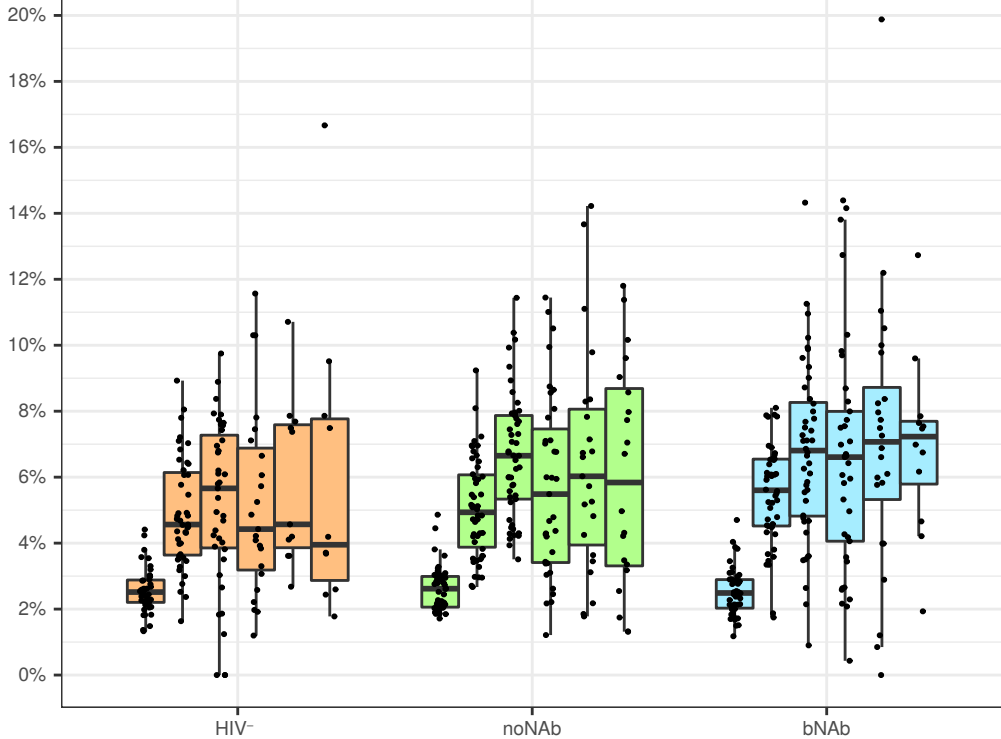
**b**

V4-34 segment usage

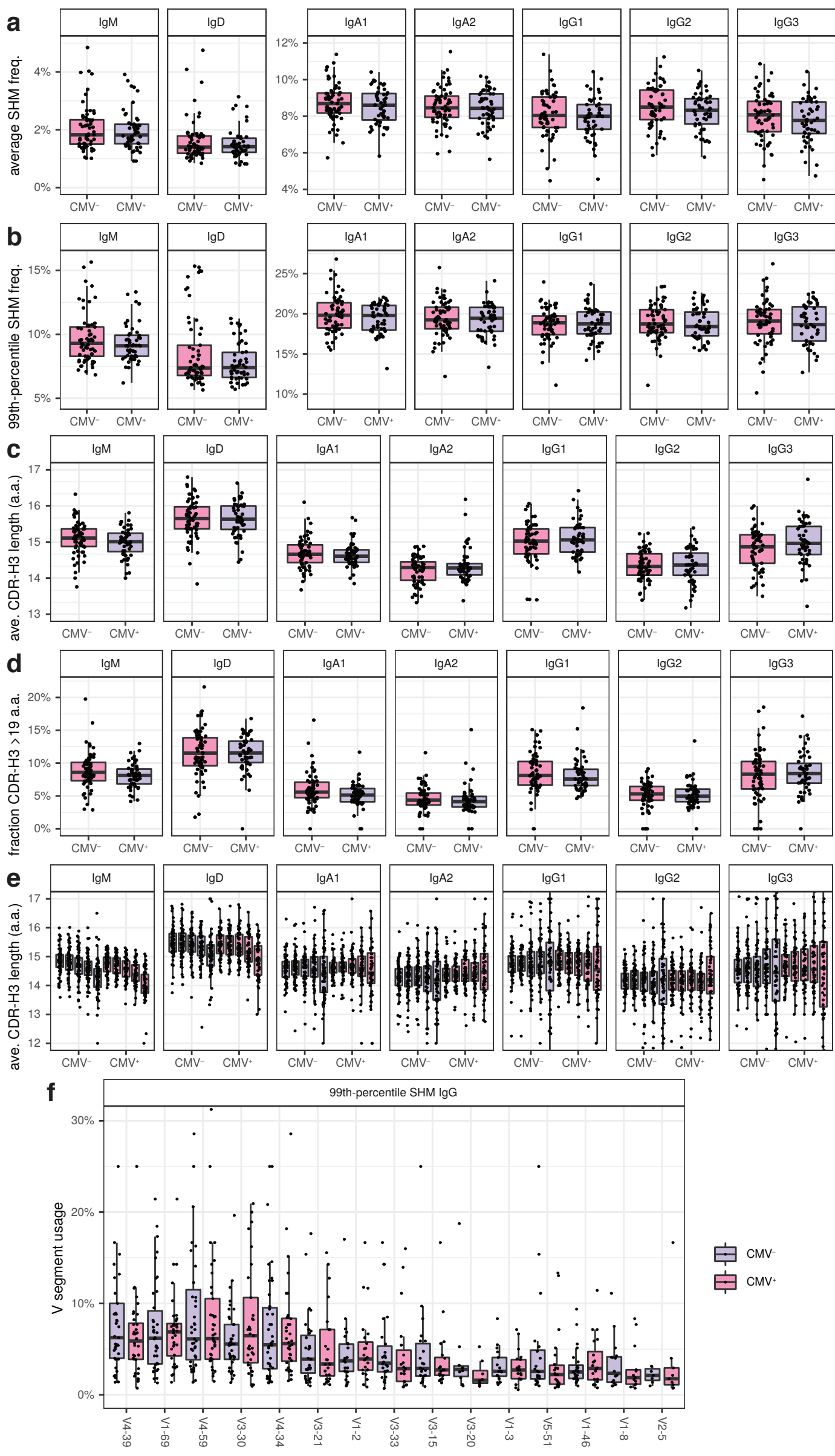


**Fig. S5: IGHV-segment usage and *IGHV4-34* usage in IgE isotype sequences at different SHM frequencies.** (a) Differences in IGHV-segment usage in the 1% most mutated IgE sequences. IGHV-segments used by many of the known broadly neutralizing HIV antibodies, including the known autoreactivity-associated *IGHV4-34* gene segment, are shown. Results for the other isotypes are shown in Fig. 5a. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46. (b) From left to right, for each patient group, usage of segment *IGHV4-34* in the 30%, 20%, 10%, 5%, or 1% most mutated IgE clones in each subject. Results for the other isotypes are shown in Fig. 5c. P-values for comparisons between groups are for the two-sided Wilcoxon-Mann-Whitney test. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46.

average SHM frequency



**Fig. S6: SHM of IGH amplified from genomic DNA template in replicate libraries.** IGH rearrangements were amplified from genomic DNA template of HIV-uninfected, noNAb and bNAb participants, with six libraries amplified from independent template aliquots from each participant's PBMC specimen. For each participant category, mean SHM percentages are shown for the IGHV gene segments in rearrangements present in clones detected in one, two, three, four, five or all six replicate libraries (from the left-most box-whisker in each set to the right-most box-whisker in each set). Highly expanded B cell clones are expected to be detected in multiple independent gDNA-templated IGH sequence libraries in this experimental design. Rare clones are expected to be detected in only a single replicate IGH library. SHM frequencies are lowest for the clones found in only a single replicate IGH library in all patient categories, and are increased in clones detected in two or more replicate libraries. The isotype is not known for these rearrangements, as the constant regions are located too far downstream in the genome for amplification with the V(D)J rearrangements from gDNA template. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was HIV-uninfected, n=43; noNAb, n=50; bNAb, n=46.



**Fig. S7: IGH repertoire characteristics of a cohort of healthy control individuals seronegative or seropositive for CMV (CMV<sup>-</sup> or CMV<sup>+</sup>).**

The individuals in this cohort are distinct from the HIV-uninfected or HIV-infected individuals in Figures 1-8 and Supplementary Figures S1-S6. (a) SHM frequencies of IGH sequences in individuals seronegative or seropositive for CMV (CMV<sup>-</sup> or CMV<sup>+</sup>). Each dot represents the mean SHM frequency of the IGHV gene segments for members of clones expressing the indicated isotype within a subject. The SHM frequencies did not differ with CMV status for any isotype. No significant differences between CMV<sup>-</sup> and CMV<sup>+</sup> individuals were seen for any isotype with two-sided Wilcoxon-Mann-Whitney testing. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was seropositive, n=52; seronegative, n=61. (b) The 99<sup>th</sup>-percentile SHM frequency for members of clones expressed as the indicated isotype in each subject. No significant differences between CMV<sup>-</sup> and CMV<sup>+</sup> individuals were seen for any isotype with two-sided Wilcoxon-Mann-Whitney testing. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was seropositive, n=52; seronegative, n=61. (c) Mean CDR-H3 lengths in the CMV<sup>-</sup> or CMV<sup>+</sup> individuals. No differences in mean CDR-H3 length were seen between CMV<sup>-</sup> and CMV<sup>+</sup> individuals in clones expressed as the indicated isotypes, with two-sided Wilcoxon-Mann-Whitney testing. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was seropositive, n=52; seronegative, n=61. (d) The fraction of CDR-H3s with length greater than 19 amino acids. No differences were seen between CMV<sup>-</sup> and CMV<sup>+</sup> individuals with two-sided Wilcoxon-Mann-Whitney testing. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was seropositive, n=52; seronegative, n=61. (e) Average heavy chain CDR-H3 lengths in IGH repertoire fractions with increasing frequencies of SHM in CMV<sup>-</sup> or CMV<sup>+</sup> subjects. Within each group (CMV<sup>-</sup> or CMV<sup>+</sup>), the columns from left to right indicate the mean CDR-H3 lengths in the 30%, 20%, 10%, 5% or 1% most mutated sequences in each subject, respectively. In contrast to the HIV bNAbs individuals (Fig. 3) no significant evidence for selection favoring longer CDR-H3s at increasing SHM frequencies in IgG isotypes in the CMV<sup>+</sup> individuals compared to CMV<sup>-</sup> individuals was seen with two-sided Wilcoxon-Mann-Whitney testing. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was seropositive, n=52; seronegative, n=61. (f) IGHV-segment usage and characterization of clones in the 1% most-mutated fraction of IgG sequences in CMV<sup>-</sup> or CMV<sup>+</sup> individuals. The CMV<sup>-</sup> and CMV<sup>+</sup> subjects show similar IGHV segment usage frequencies in IgG isotype antibodies, with a trend toward increased usage of *IGHV1-69* and *IGHV1-2* in CMV<sup>+</sup> individuals compared to CMV<sup>-</sup> individuals that did not reach statistical significance using two-sided Wilcoxon-Mann-Whitney testing. In contrast to the HIV-uninfected and HIV-infected individuals (Fig. 5), there is no evidence of an association between chronic CMV infection and increased usage of *IGHV4-34*. Box-whisker plots show median (horizontal line), interquartile range (box), and 1.5 times the interquartile range (whiskers). The number of participants analyzed was seropositive, n=52; seronegative, n=61.

## Supplementary Tables

**Table S1: DNA sequence read-pair counts and clonotypes identified from each participant**

Participant	Group	Clone Count	Read Count
BFI-0000254	bNAbs	83269	231831
BFI-0000255	bNAbs	50682	238270
BFI-0000256	bNAbs	91716	312315
BFI-0002855	bNAbs	107104	424578
BFI-0002857	bNAbs	125831	414811
BFI-0002859	bNAbs	56307	242782
BFI-0002864	bNAbs	136099	380953
BFI-0002865	bNAbs	120782	335906
BFI-0002870	bNAbs	63231	248208
BFI-0002871	bNAbs	62653	299415
BFI-0002875	bNAbs	84092	442460
BFI-0002877	bNAbs	58263	296058
BFI-0002879	bNAbs	69954	302627
BFI-0003450	bNAbs	105202	332604
BFI-0003451	bNAbs	70317	275989
BFI-0003452	bNAbs	128020	351286
BFI-0003453	bNAbs	119244	414702
BFI-0003454	bNAbs	63067	249998
BFI-0003455	bNAbs	68773	221087
BFI-0003456	bNAbs	67115	306086
BFI-0003457	bNAbs	65601	276476
BFI-0003458	bNAbs	62620	280207
BFI-0003459	bNAbs	79103	259521
BFI-0003460	bNAbs	113201	476295
BFI-0003461	bNAbs	104661	401961
BFI-0003462	bNAbs	139042	398449
BFI-0003463	bNAbs	98730	441444
BFI-0003464	bNAbs	68061	159624
BFI-0003465	bNAbs	54822	268249
BFI-0003466	bNAbs	131276	366489
BFI-0003467	bNAbs	91191	305322
BFI-0003468	bNAbs	90131	264580
BFI-0003469	bNAbs	54868	400769
BFI-0003470	bNAbs	81602	230639
BFI-0003471	bNAbs	95282	382522
BFI-0003472	bNAbs	88320	456019
BFI-0003733	bNAbs	28710	126391



BFI-0003735	bNAb	49826	173136
BFI-0003736	bNAb	40061	163248
BFI-0003738	bNAb	37913	138470
BFI-0003739	bNAb	41420	184916
BFI-0003740	bNAb	36693	155166
BFI-0003741	bNAb	60139	191232
BFI-0003742	bNAb	35961	175808
BFI-0003766	bNAb	78937	177275
BFI-0003768	bNAb	76672	182860
BFI-0000258	noNAb	160406	435188
BFI-0002854	noNAb	44404	262734
BFI-0002856	noNAb	65929	223120
BFI-0003473	noNAb	77654	359713
BFI-0003474	noNAb	126268	394302
BFI-0003475	noNAb	66633	552293
BFI-0003476	noNAb	115944	261523
BFI-0003477	noNAb	109395	595134
BFI-0003478	noNAb	75502	378278
BFI-0003479	noNAb	87710	415930
BFI-0003480	noNAb	74259	367374
BFI-0003481	noNAb	116707	494841
BFI-0003482	noNAb	84931	276322
BFI-0003483	noNAb	83040	366495
BFI-0003484	noNAb	68160	302511
BFI-0003485	noNAb	41520	205983
BFI-0003486	noNAb	80129	266253
BFI-0003487	noNAb	67552	280564
BFI-0003488	noNAb	88109	323094
BFI-0003734	noNAb	49649	167973
BFI-0003737	noNAb	51821	160531
BFI-0003743	noNAb	42232	160350
BFI-0003745	noNAb	25297	140988
BFI-0003746	noNAb	48215	167252
BFI-0003747	noNAb	22253	156013
BFI-0003748	noNAb	26810	146561
BFI-0003749	noNAb	67494	182317
BFI-0003750	noNAb	34236	124377
BFI-0003751	noNAb	46895	169427
BFI-0003752	noNAb	44458	152066
BFI-0003754	noNAb	49499	183266
BFI-0003755	noNAb	48126	154154

BFI-0003756	noNAb	35414	137527
BFI-0003757	noNAb	34427	160364
BFI-0003758	noNAb	67846	168660
BFI-0003759	noNAb	51611	182245
BFI-0003760	noNAb	48088	168523
BFI-0003761	noNAb	32336	179262
BFI-0003762	noNAb	58921	194407
BFI-0003763	noNAb	66243	190934
BFI-0003764	noNAb	65129	204833
BFI-0003765	noNAb	52812	165212
BFI-0003767	noNAb	60196	196681
BFI-0003769	noNAb	63577	187275
BFI-0003770	noNAb	75464	202232
BFI-0003771	noNAb	58354	161179
BFI-0003772	noNAb	35732	146765
BFI-0003773	noNAb	67799	205734
BFI-0003774	noNAb	48759	219515
BFI-0003775	noNAb	71058	250475
BFI-0000234	HIV-	71206	189823
BFI-0002850	HIV-	47375	170111
BFI-0002851	HIV-	52505	183211
BFI-0002852	HIV-	70890	187601
BFI-0002861	HIV-	13931	119126
BFI-0002862	HIV-	55221	176417
BFI-0002863	HIV-	50966	176265
BFI-0002866	HIV-	34054	146228
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BFI-0002868	HIV-	56158	189137
BFI-0003700	HIV-	54164	190165
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BFI-0003727	HIV-	36735	156103
BFI-0003728	HIV-	61440	164968
BFI-0003729	HIV-	35180	172466
BFI-0003730	HIV-	25316	135095
BFI-0003731	HIV-	23396	135496
BFI-0003732	HIV-	51128	173529
BFI-0003053	CMV+	45305	774226
BFI-0003054	CMV+	55798	751021
BFI-0003055	CMV+	56656	466351
BFI-0003056	CMV+	6096	35384
BFI-0003059	CMV+	86044	823205
BFI-0003060	CMV+	19199	730957
BFI-0003062	CMV+	45733	992512
BFI-0003063	CMV+	24413	362902
BFI-0003074	CMV+	3143	75170
BFI-0003075	CMV+	35147	153561
BFI-0003076	CMV+	34902	206515
BFI-0003081	CMV+	32092	150033
BFI-0003082	CMV+	68519	687395
BFI-0003084	CMV+	72534	637598
BFI-0003085	CMV+	65019	528500
BFI-0003093	CMV+	108760	712586
BFI-0003099	CMV+	59207	835038
BFI-0003101	CMV+	117915	485401
BFI-0003102	CMV+	56167	852291
BFI-0003103	CMV+	125514	631471
BFI-0003106	CMV+	14554	408144

BFI-0003107	CMV+	56946	907102
BFI-0003109	CMV+	33994	553093
BFI-0003110	CMV+	35996	812025
BFI-0003111	CMV+	68084	697954
BFI-0003112	CMV+	11999	1046616
BFI-0003117	CMV+	91237	610905
BFI-0003120	CMV+	48155	180898
BFI-0003124	CMV+	68992	858116
BFI-0003125	CMV+	50730	953509
BFI-0003126	CMV+	88577	896301
BFI-0003129	CMV+	122008	535550
BFI-0003132	CMV+	279667	997464
BFI-0003134	CMV+	174485	864414
BFI-0003135	CMV+	200009	618078
BFI-0003136	CMV+	116935	381859
BFI-0003137	CMV+	181888	1113004
BFI-0003140	CMV+	200869	1303351
BFI-0003145	CMV+	37202	811798
BFI-0003146	CMV+	212204	939661
BFI-0003147	CMV+	181879	1033633
BFI-0003149	CMV+	108548	1413606
BFI-0003150	CMV+	77085	784096
BFI-0003151	CMV+	22212	858133
BFI-0003152	CMV+	245063	1081590
BFI-0003153	CMV+	57829	920150
BFI-0003154	CMV+	319834	1148969
BFI-0003155	CMV+	61755	244683
BFI-0003156	CMV+	69220	698946
BFI-0003159	CMV+	98649	678074
BFI-0003160	CMV+	25784	769570
BFI-0003162	CMV+	287031	706668
BFI-0003050	CMV-	18338	81849
BFI-0003051	CMV-	217879	939608
BFI-0003052	CMV-	7884	655023
BFI-0003057	CMV-	28763	1057068
BFI-0003058	CMV-	57901	675993
BFI-0003061	CMV-	100809	829714
BFI-0003064	CMV-	1443	184925
BFI-0003065	CMV-	5159	1248653
BFI-0003066	CMV-	120286	1567808
BFI-0003067	CMV-	22551	787862

BFI-0003068	CMV-	24482	303592
BFI-0003069	CMV-	27504	81826
BFI-0003070	CMV-	35947	1094580
BFI-0003071	CMV-	39085	983146
BFI-0003072	CMV-	2233	75630
BFI-0003073	CMV-	916	22088
BFI-0003077	CMV-	50528	182182
BFI-0003078	CMV-	31778	159403
BFI-0003079	CMV-	31413	116766
BFI-0003080	CMV-	34552	215492
BFI-0003083	CMV-	7362	906732
BFI-0003086	CMV-	27355	782972
BFI-0003087	CMV-	157832	1003915
BFI-0003088	CMV-	57332	737017
BFI-0003089	CMV-	47516	924752
BFI-0003090	CMV-	74364	927854
BFI-0003091	CMV-	18667	1040034
BFI-0003092	CMV-	77538	871501
BFI-0003094	CMV-	135741	531130
BFI-0003095	CMV-	236626	1472124
BFI-0003096	CMV-	79517	978736
BFI-0003097	CMV-	96242	841592
BFI-0003098	CMV-	85753	913225
BFI-0003100	CMV-	35916	470822
BFI-0003104	CMV-	62949	586123
BFI-0003105	CMV-	2454	637303
BFI-0003108	CMV-	26938	200753
BFI-0003113	CMV-	57867	746604
BFI-0003114	CMV-	115994	1207393
BFI-0003115	CMV-	914	203417
BFI-0003116	CMV-	45626	212816
BFI-0003118	CMV-	130821	615102
BFI-0003119	CMV-	163662	487270
BFI-0003121	CMV-	83670	866685
BFI-0003122	CMV-	86079	415545
BFI-0003123	CMV-	82538	1441519
BFI-0003127	CMV-	95760	1264737
BFI-0003128	CMV-	146223	958734
BFI-0003130	CMV-	279266	1414938
BFI-0003131	CMV-	169233	816825
BFI-0003133	CMV-	121502	575332

BFI-0003138	CMV-	135882	869016
BFI-0003139	CMV-	256347	1295677
BFI-0003141	CMV-	56744	199245
BFI-0003142	CMV-	85802	916853
BFI-0003143	CMV-	7646	547320
BFI-0003148	CMV-	148366	1910305
BFI-0003157	CMV-	135110	889294
BFI-0003158	CMV-	85120	1009907
BFI-0003161	CMV-	35396	641849
BFI-0003163	CMV-	236247	833417

**Table S2: Isotype-specific primers used to construct sequencing libraries derived from cDNA.** Abbreviations: iso.: the target isotype; BC: label of the barcode used for sample multiplexing; P5: read 1 Illumina sequencing adapter; and DBs: random bases added to increase library diversity. All primers are listed 5' to 3'.

Table S2: First Round Isotype Primers

iso.	BC	partial P5 adapter	DBs	barcode	constant region sequence
IgG	A01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATGATACA	CAGGCAGCCCAGGGC
IgA	A01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATGATACA	AGCCCTGGACCAGGCA
IgD	A01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATGATACA	CCCTGATATGATGGGGAACA
IgM	A01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATGATACA	GGGAATTCTCACAGGAGACG
IgE	A01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATGATACA	GAAGACGGATGGGCTCTGT
IgG	A02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CATGTCAT	CAGGCAGCCCAGGGC
IgA	A02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CATGTCAT	AGCCCTGGACCAGGCA
IgD	A02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CATGTCAT	CCCTGATATGATGGGGAACA
IgM	A02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CATGTCAT	GGGAATTCTCACAGGAGACG
IgE	A02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CATGTCAT	GAAGACGGATGGGCTCTGT
IgG	A03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CACGCACT	CAGGCAGCCCAGGGC
IgA	A03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CACGCACT	AGCCCTGGACCAGGCA
IgD	A03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CACGCACT	CCCTGATATGATGGGGAACA
IgM	A03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CACGCACT	GGGAATTCTCACAGGAGACG
IgE	A03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CACGCACT	GAAGACGGATGGGCTCTGT
IgG	A04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGTGAGCG	CAGGCAGCCCAGGGC
IgA	A04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGTGAGCG	AGCCCTGGACCAGGCA
IgD	A04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGTGAGCG	CCCTGATATGATGGGGAACA
IgM	A04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGTGAGCG	GGGAATTCTCACAGGAGACG
IgE	A04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGTGAGCG	GAAGACGGATGGGCTCTGT
IgG	A05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCGCATGC	CAGGCAGCCCAGGGC
IgA	A05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCGCATGC	AGCCCTGGACCAGGCA
IgD	A05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCGCATGC	CCCTGATATGATGGGGAACA
IgM	A05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCGCATGC	GGGAATTCTCACAGGAGACG
IgE	A05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCGCATGC	GAAGACGGATGGGCTCTGT
IgG	A06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACACGACG	CAGGCAGCCCAGGGC
IgA	A06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACACGACG	AGCCCTGGACCAGGCA
IgD	A06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACACGACG	CCCTGATATGATGGGGAACA
IgM	A06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACACGACG	GGGAATTCTCACAGGAGACG
IgE	A06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACACGACG	GAAGACGGATGGGCTCTGT
IgG	A07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGTCGTC	CAGGCAGCCCAGGGC
IgA	A07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGTCGTC	AGCCCTGGACCAGGCA
IgD	A07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGTCGTC	CCCTGATATGATGGGGAACA
IgM	A07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGTCGTC	GGGAATTCTCACAGGAGACG
IgE	A07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGTCGTC	GAAGACGGATGGGCTCTGT
IgG	A08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGTATGCA	CAGGCAGCCCAGGGC

IgA	A08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGTATGCA	AGCCCTGGACCAGGCA
IgD	A08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGTATGCA	CCCTGATATGATGGGGAACA
IgM	A08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGTATGCA	GGGAATTCTCACAGGAGACG
IgE	A08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGTATGCA	GAAGACGGATGGGCTCTGT
IgG	A09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGAGCAGA	CAGGCAGCCCAGGGC
IgA	A09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGAGCAGA	AGCCCTGGACCAGGCA
IgD	A09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGAGCAGA	CCCTGATATGATGGGGAACA
IgM	A09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGAGCAGA	GGGAATTCTCACAGGAGACG
IgE	A09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGAGCAGA	GAAGACGGATGGGCTCTGT
IgG	A10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCGAGC	CAGGCAGCCCAGGGC
IgA	A10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCGAGC	AGCCCTGGACCAGGCA
IgD	A10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCGAGC	CCCTGATATGATGGGGAACA
IgM	A10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCGAGC	GGGAATTCTCACAGGAGACG
IgE	A10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCGAGC	GAAGACGGATGGGCTCTGT
IgG	A11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCATGCAC	CAGGCAGCCCAGGGC
IgA	A11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCATGCAC	AGCCCTGGACCAGGCA
IgD	A11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCATGCAC	CCCTGATATGATGGGGAACA
IgM	A11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCATGCAC	GGGAATTCTCACAGGAGACG
IgE	A11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCATGCAC	GAAGACGGATGGGCTCTGT
IgG	A12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACGATGC	CAGGCAGCCCAGGGC
IgA	A12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACGATGC	AGCCCTGGACCAGGCA
IgD	A12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACGATGC	CCCTGATATGATGGGGAACA
IgM	A12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACGATGC	GGGAATTCTCACAGGAGACG
IgE	A12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACGATGC	GAAGACGGATGGGCTCTGT
IgG	B01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTATAGAG	CAGGCAGCCCAGGGC
IgA	B01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTATAGAG	AGCCCTGGACCAGGCA
IgD	B01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTATAGAG	CCCTGATATGATGGGGAACA
IgM	B01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTATAGAG	GGGAATTCTCACAGGAGACG
IgE	B01	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTATAGAG	GAAGACGGATGGGCTCTGT
IgG	B02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTATCTG	CAGGCAGCCCAGGGC
IgA	B02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTATCTG	AGCCCTGGACCAGGCA
IgD	B02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTATCTG	CCCTGATATGATGGGGAACA
IgM	B02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTATCTG	GGGAATTCTCACAGGAGACG
IgE	B02	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTATCTG	GAAGACGGATGGGCTCTGT
IgG	B03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTCATA	CAGGCAGCCCAGGGC
IgA	B03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTCATA	AGCCCTGGACCAGGCA
IgD	B03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTCATA	CCCTGATATGATGGGGAACA
IgM	B03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTCATA	GGGAATTCTCACAGGAGACG
IgE	B03	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTCATA	GAAGACGGATGGGCTCTGT
IgG	B04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGCAGAT	CAGGCAGCCCAGGGC
IgA	B04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGCAGAT	AGCCCTGGACCAGGCA
IgD	B04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGCAGAT	CCCTGATATGATGGGGAACA
IgM	B04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGCAGAT	GGGAATTCTCACAGGAGACG



IgE	B04	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGCAGAT	GAAGACGGATGGGCTCTGT
IgG	B05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCATAG	CAGGCAGCCCAGGGC
IgA	B05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCATAG	AGCCCTGGACCAGGCA
IgD	B05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCATAG	CCCTGATATGATGGGGAACA
IgM	B05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCATAG	GGGAATTCTCACAGGAGACG
IgE	B05	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCATAG	GAAGACGGATGGGCTCTGT
IgG	B06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGTGTCA	CAGGCAGCCCAGGGC
IgA	B06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGTGTCA	AGCCCTGGACCAGGCA
IgD	B06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGTGTCA	CCCTGATATGATGGGGAACA
IgM	B06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGTGTCA	GGGAATTCTCACAGGAGACG
IgE	B06	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGTGTCA	GAAGACGGATGGGCTCTGT
IgG	B07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTGTAT	CAGGCAGCCCAGGGC
IgA	B07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTGTAT	AGCCCTGGACCAGGCA
IgD	B07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTGTAT	CCCTGATATGATGGGGAACA
IgM	B07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTGTAT	GGGAATTCTCACAGGAGACG
IgE	B07	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTGTAT	GAAGACGGATGGGCTCTGT
IgG	B08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATCTGAGC	CAGGCAGCCCAGGGC
IgA	B08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATCTGAGC	AGCCCTGGACCAGGCA
IgD	B08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATCTGAGC	CCCTGATATGATGGGGAACA
IgM	B08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATCTGAGC	GGGAATTCTCACAGGAGACG
IgE	B08	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATCTGAGC	GAAGACGGATGGGCTCTGT
IgG	B09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TATACGCT	CAGGCAGCCCAGGGC
IgA	B09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TATACGCT	AGCCCTGGACCAGGCA
IgD	B09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TATACGCT	CCCTGATATGATGGGGAACA
IgM	B09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TATACGCT	GGGAATTCTCACAGGAGACG
IgE	B09	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TATACGCT	GAAGACGGATGGGCTCTGT
IgG	B10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACATAGT	CAGGCAGCCCAGGGC
IgA	B10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACATAGT	AGCCCTGGACCAGGCA
IgD	B10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACATAGT	CCCTGATATGATGGGGAACA
IgM	B10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACATAGT	GGGAATTCTCACAGGAGACG
IgE	B10	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACATAGT	GAAGACGGATGGGCTCTGT
IgG	B11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGATGATC	CAGGCAGCCCAGGGC
IgA	B11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGATGATC	AGCCCTGGACCAGGCA
IgD	B11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGATGATC	CCCTGATATGATGGGGAACA
IgM	B11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGATGATC	GGGAATTCTCACAGGAGACG
IgE	B11	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGATGATC	GAAGACGGATGGGCTCTGT
IgG	B12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGAGTAG	CAGGCAGCCCAGGGC
IgA	B12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGAGTAG	AGCCCTGGACCAGGCA
IgD	B12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGAGTAG	CCCTGATATGATGGGGAACA
IgM	B12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGAGTAG	GGGAATTCTCACAGGAGACG
IgE	B12	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGAGTAG	GAAGACGGATGGGCTCTGT

**Table S3. IGHJ-segment specific primers used to construct sequencing libraries derived from genomic DNA.** Abbreviations: BC: label of the barcode used for sample multiplexing; P5: read 1 Illumina sequencing adapter; and DBs: random bases added to increase library diversity. All primers are listed 5' to 3'.

Table S3: First Round J-Segment Primers

BC	partial P5 adapter	DBs	barcode	J-consensus sequence
BC001	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGTAACG	CTTACCTGAGGAGACGGTGACC
BC002	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGTCGTA	CTTACCTGAGGAGACGGTGACC
BC003	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGAGACG	CTTACCTGAGGAGACGGTGACC
BC004	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTGTACG	CTTACCTGAGGAGACGGTGACC
BC005	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTCCGTA	CTTACCTGAGGAGACGGTGACC
BC006	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGCATCGT	CTTACCTGAGGAGACGGTGACC
BC007	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGAACTAC	CTTACCTGAGGAGACGGTGACC
BC008	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGAAGCGT	CTTACCTGAGGAGACGGTGACC
BC009	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTCCACGT	CTTACCTGAGGAGACGGTGACC
BC010	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTCCATAC	CTTACCTGAGGAGACGGTGACC
BC011	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTGGTGTA	CTTACCTGAGGAGACGGTGACC
BC012	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTGTAACG	CTTACCTGAGGAGACGGTGACC
BC013	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTTTCGTA	CTTACCTGAGGAGACGGTGACC
BC014	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATGTGTA	CTTACCTGAGGAGACGGTGACC
BC015	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATGGACG	CTTACCTGAGGAGACGGTGACC
BC016	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TAAGGTAC	CTTACCTGAGGAGACGGTGACC
BC017	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TAATGCGT	CTTACCTGAGGAGACGGTGACC
BC018	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TAAATTAC	CTTACCTGAGGAGACGGTGACC
BC019	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCCCATAC	CTTACCTGAGGAGACGGTGACC
BC020	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCCCCCGT	CTTACCTGAGGAGACGGTGACC
BC021	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGTCCGT	CTTACCTGAGGAGACGGTGACC
BC022	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGACTAC	CTTACCTGAGGAGACGGTGACC
BC023	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACGAGCGT	CTTACCTGAGGAGACGGTGACC
BC024	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTCTCGT	CTTACCTGAGGAGACGGTGACC
BC025	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTGCTAC	CTTACCTGAGGAGACGGTGACC
BC026	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGAAGACG	CTTACCTGAGGAGACGGTGACC
BC027	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGCAGGTA	CTTACCTGAGGAGACGGTGACC
BC028	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGCCTGTA	CTTACCTGAGGAGACGGTGACC
BC029	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTCCAGTA	CTTACCTGAGGAGACGGTGACC
BC030	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTACAACG	CTTACCTGAGGAGACGGTGACC
BC031	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTGTATAC	CTTACCTGAGGAGACGGTGACC
BC032	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTGTTCTG	CTTACCTGAGGAGACGGTGACC
BC033	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTTATTAC	CTTACCTGAGGAGACGGTGACC
BC034	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATGTTAC	CTTACCTGAGGAGACGGTGACC
BC035	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATGGAGT	CTTACCTGAGGAGACGGTGACC
BC036	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TAATACCG	CTTACCTGAGGAGACGGTGACC

BC037	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TAATCGTA	CTTACCTGAGGAGACGGTGACC
BC038	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACGGACG	CTTACCTGAGGAGACGGTGACC
BC039	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCAGAACG	CTTACCTGAGGAGACGGTGACC
BC040	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCCCCGTA	CTTACCTGAGGAGACGGTGACC
BC041	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACTAGGTA	CTTACCTGAGGAGACGGTGACC
BC042	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACATTACG	CTTACCTGAGGAGACGGTGACC
BC043	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACTCAGTA	CTTACCTGAGGAGACGGTGACC
BC044	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGGGCACG	CTTACCTGAGGAGACGGTGACC
BC045	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGATAGTA	CTTACCTGAGGAGACGGTGACC
BC046	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGGGGCGT	CTTACCTGAGGAGACGGTGACC
BC047	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGCAGTAC	CTTACCTGAGGAGACGGTGACC
BC048	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGCCTTAC	CTTACCTGAGGAGACGGTGACC
BC049	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTCGCCGT	CTTACCTGAGGAGACGGTGACC
BC050	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTGGCTAC	CTTACCTGAGGAGACGGTGACC
BC051	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTATCACG	CTTACCTGAGGAGACGGTGACC
BC052	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTTAGGTA	CTTACCTGAGGAGACGGTGACC
BC053	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTTATACG	CTTACCTGAGGAGACGGTGACC
BC054	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCAGTA	CTTACCTGAGGAGACGGTGACC
BC055	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAATAACG	CTTACCTGAGGAGACGGTGACC
BC056	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TAATCGT	CTTACCTGAGGAGACGGTGACC
BC057	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACAGCGT	CTTACCTGAGGAGACGGTGACC
BC058	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TAGCTTAC	CTTACCTGAGGAGACGGTGACC
BC059	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCCGCTAC	CTTACCTGAGGAGACGGTGACC
BC060	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCGTACGT	CTTACCTGAGGAGACGGTGACC
BC061	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACTGTAAG	CTTACCTGAGGAGACGGTGACC
BC062	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGATCCGT	CTTACCTGAGGAGACGGTGACC
BC063	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTGCATCC	CTTACCTGAGGAGACGGTGACC
BC064	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TACAGGTA	CTTACCTGAGGAGACGGTGACC
BC081	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATGAGCAG	CTTACCTGAGGAGACGGTGACC
BC082	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATGACCTC	CTTACCTGAGGAGACGGTGACC
BC083	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATGACTGT	CTTACCTGAGGAGACGGTGACC
BC084	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGCACTCA	CTTACCTGAGGAGACGGTGACC
BC085	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGCGTTAG	CTTACCTGAGGAGACGGTGACC
BC086	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGCGCTTC	CTTACCTGAGGAGACGGTGACC
BC087	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGCGTTGT	CTTACCTGAGGAGACGGTGACC
BC088	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CGCGTACA	CTTACCTGAGGAGACGGTGACC
BC089	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CATGTAAG	CTTACCTGAGGAGACGGTGACC
BC090	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CATCTATC	CTTACCTGAGGAGACGGTGACC
BC091	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCCAGT	CTTACCTGAGGAGACGGTGACC
BC092	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCAACA	CTTACCTGAGGAGACGGTGACC
BC093	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GATCAGAG	CTTACCTGAGGAGACGGTGACC
BC094	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCACAGTC	CTTACCTGAGGAGACGGTGACC
BC095	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCATAGGT	CTTACCTGAGGAGACGGTGACC

BC096	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCATAGCA	CTTACCTGAGGAGACGGTGACC
BC097	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCATGGAG	CTTACCTGAGGAGACGGTGACC
BC098	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCATGCTC	CTTACCTGAGGAGACGGTGACC
BC099	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TTGTGCGT	CTTACCTGAGGAGACGGTGACC
BC100	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TTGAGCCA	CTTACCTGAGGAGACGGTGACC
BC101	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACTGACGT	CTTACCTGAGGAGACGGTGACC
BC102	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACTAATCG	CTTACCTGAGGAGACGGTGACC
BC103	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACCAGTAG	CTTACCTGAGGAGACGGTGACC
BC104	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATCAGGTC	CTTACCTGAGGAGACGGTGACC
BC105	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATCAGTGC	CTTACCTGAGGAGACGGTGACC
BC106	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTCAGTCA	CTTACCTGAGGAGACGGTGACC
BC107	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTCCGAAT	CTTACCTGAGGAGACGGTGACC
BC108	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTGCCGTA	CTTACCTGAGGAGACGGTGACC
BC109	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCCTGA	CTTACCTGAGGAGACGGTGACC
BC110	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCCGCA	CTTACCTGAGGAGACGGTGACC
BC111	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGCCGAC	CTTACCTGAGGAGACGGTGACC
BC112	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAGTCATG	CTTACCTGAGGAGACGGTGACC
BC113	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GAATTAGC	CTTACCTGAGGAGACGGTGACC
BC114	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GGATTACT	CTTACCTGAGGAGACGGTGACC
BC115	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GGATTGAC	CTTACCTGAGGAGACGGTGACC
BC116	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGATTATG	CTTACCTGAGGAGACGGTGACC
BC117	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGAGTCGT	CTTACCTGAGGAGACGGTGACC
BC118	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGTGACCA	CTTACCTGAGGAGACGGTGACC
BC119	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCTGACAT	CTTACCTGAGGAGACGGTGACC
BC120	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TCTGACTG	CTTACCTGAGGAGACGGTGACC
BC121	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTTCAGC	CTTACCTGAGGAGACGGTGACC
BC122	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	AGTACGTT	CTTACCTGAGGAGACGGTGACC
BC123	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACTGTGCA	CTTACCTGAGGAGACGGTGACC
BC124	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ACCGCTAG	CTTACCTGAGGAGACGGTGACC
BC125	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	ATCGCAGC	CTTACCTGAGGAGACGGTGACC
BC126	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CTCGTGAA	CTTACCTGAGGAGACGGTGACC
BC127	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCGCTT	CTTACCTGAGGAGACGGTGACC
BC128	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CATCTTCG	CTTACCTGAGGAGACGGTGACC
BC129	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAGCTAGC	CTTACCTGAGGAGACGGTGACC
BC130	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	CAACTGAA	CTTACCTGAGGAGACGGTGACC
BC131	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTGAGCTT	CTTACCTGAGGAGACGGTGACC
BC132	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTAAGTCG	CTTACCTGAGGAGACGGTGACC
BC133	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCTAGAGC	CTTACCTGAGGAGACGGTGACC
BC134	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GCATCCTA	CTTACCTGAGGAGACGGTGACC
BC135	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	GTCAGCAT	CTTACCTGAGGAGACGGTGACC
BC136	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGCTATCG	CTTACCTGAGGAGACGGTGACC
BC137	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TAGTAAGC	CTTACCTGAGGAGACGGTGACC
BC138	ACACTCTTTCCCTACACGACGCTCTTCCGATCT	NNNN	TGGTAGTA	CTTACCTGAGGAGACGGTGACC

BC139	ACACTCTTCCCTACACGACGCTCTCCGATCT	NNNN	TCAGACCT	CTTACCTGAGGAGACGGTGACC
BC140	ACACTCTTCCCTACACGACGCTCTCCGATCT	NNNN	TGACATAG	CTTACCTGAGGAGACGGTGACC

**Table S4: Framework 1 and Framework 2 IGHV-segment specific primers used to construct sequencing libraries.** Abbreviations: BC: label of the barcode used for sample multiplexing; V: IGHV gene family; fwk: framework region of primer target; and P7: read 2 Illumina sequencing adapter. All primers are listed 5' to 3'.

BC	V	fwk	partial P7 adapter	barcode	IGHV-segment specific sequence
A01	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	GGCCTCAGTGAAGGTCTCCTGCAAG
A01	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	CTGGGTGCGACAGGCCCTGGACAA
A01	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	GTCTGGTCTACGCTGGTGAACCC
A01	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	TGGATCCGTAGCCCCAGGGAAGG
A01	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	CTGGGGGGTCCCTGAGACTCTCTG
A01	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	GGTCCGCCAGGCTCCAGGGAA
A01	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	CTTCGGAGACCCTGTCCCTCACCTG
A01	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	TGGATCCGCCAGCCCCAGGGAAGG
A01	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	CGGGGAGTCTCTGAAGATCTCCTGT
A01	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	GGGTGCGCCAGATGCCCGGAAAGG
A01	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	TCGAGACCCTCTACTCACCTGTG
A01	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	TGGATCAGGCAGTCCCATCGAGAG
A01	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ATGATACA	TTGGGTGCGACAGGCCCTGGACAA
A02	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	GGCCTCAGTGAAGGTCTCCTGCAAG
A02	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	CTGGGTGCGACAGGCCCTGGACAA
A02	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	GTCTGGTCTACGCTGGTGAACCC
A02	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	TGGATCCGTAGCCCCAGGGAAGG
A02	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	CTGGGGGGTCCCTGAGACTCTCTG
A02	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	GGTCCGCCAGGCTCCAGGGAA
A02	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	CTTCGGAGACCCTGTCCCTCACCTG
A02	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	TGGATCCGCCAGCCCCAGGGAAGG
A02	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	CGGGGAGTCTCTGAAGATCTCCTGT
A02	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	GGGTGCGCCAGATGCCCGGAAAGG
A02	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	TCGAGACCCTCTACTCACCTGTG
A02	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	TGGATCAGGCAGTCCCATCGAGAG
A02	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CATGTCAT	TTGGGTGCGACAGGCCCTGGACAA
A03	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	GGCCTCAGTGAAGGTCTCCTGCAAG
A03	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	CTGGGTGCGACAGGCCCTGGACAA
A03	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	GTCTGGTCTACGCTGGTGAACCC
A03	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	TGGATCCGTAGCCCCAGGGAAGG
A03	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	CTGGGGGGTCCCTGAGACTCTCTG
A03	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	GGTCCGCCAGGCTCCAGGGAA
A03	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	CTTCGGAGACCCTGTCCCTCACCTG
A03	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	TGGATCCGCCAGCCCCAGGGAAGG
A03	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	CGGGGAGTCTCTGAAGATCTCCTGT
A03	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	GGGTGCGCCAGATGCCCGGAAAGG
A03	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	TCGAGACCCTCTACTCACCTGTG
A03	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	TGGATCAGGCAGTCCCATCGAGAG
A03	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CACGCACT	TTGGGTGCGACAGGCCCTGGACAA
A04	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	GGCCTCAGTGAAGGTCTCCTGCAAG
A04	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	CTGGGTGCGACAGGCCCTGGACAA
A04	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	GTCTGGTCTACGCTGGTGAACCC
A04	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	TGGATCCGTAGCCCCAGGGAAGG
A04	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	CTGGGGGGTCCCTGAGACTCTCTG
A04	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	GGTCCGCCAGGCTCCAGGGAA

A04	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	CTTCGGAGACCCTGTCCCTCACCTG
A04	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	TGGATCCGCCAGCCCCAGGGAAGG
A04	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	CGGGGAGTCTCTGAAGATCTCCTGT
A04	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	GGGTGCGCCAGATGCCCGGAAAGG
A04	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	TCGAGACCCTCTCACTACCTGTG
A04	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	TGGATCAGGCAGTCCCCATCGAGAG
A04	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TGTGAGCG	TTGGGTGCGACAGGCCCTGGACAA
A05	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	GGCCTCAGTGAAGGTCTCCTGCAAG
A05	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	CTGGGTGCGACAGGCCCTGGACAA
A05	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	GTCTGGTCTACGCTGGTGAACCC
A05	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	TGGATCCGTAGCCCCAGGGAAGG
A05	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	CTGGGGGGTCCCTGAGACTCTCCTG
A05	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	GGTCCGCCAGGCTCCAGGGAA
A05	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	CTTCGGAGACCCTGTCCCTCACCTG
A05	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	TGGATCCGCCAGCCCCAGGGAAGG
A05	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	CGGGGAGTCTCTGAAGATCTCCTGT
A05	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	GGGTGCGCCAGATGCCCGGAAAGG
A05	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	TCGAGACCCTCTCACTACCTGTG
A05	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	TGGATCAGGCAGTCCCCATCGAGAG
A05	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GCGCATGC	TTGGGTGCGACAGGCCCTGGACAA
A06	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	GGCCTCAGTGAAGGTCTCCTGCAAG
A06	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	CTGGGTGCGACAGGCCCTGGACAA
A06	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	GTCTGGTCTACGCTGGTGAACCC
A06	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	TGGATCCGTAGCCCCAGGGAAGG
A06	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	CTGGGGGGTCCCTGAGACTCTCCTG
A06	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	GGTCCGCCAGGCTCCAGGGAA
A06	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	CTTCGGAGACCCTGTCCCTCACCTG
A06	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	TGGATCCGCCAGCCCCAGGGAAGG
A06	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	CGGGGAGTCTCTGAAGATCTCCTGT
A06	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	GGGTGCGCCAGATGCCCGGAAAGG
A06	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	TCGAGACCCTCTCACTACCTGTG
A06	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	TGGATCAGGCAGTCCCCATCGAGAG
A06	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACACGACG	TTGGGTGCGACAGGCCCTGGACAA
A07	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	GGCCTCAGTGAAGGTCTCCTGCAAG
A07	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	CTGGGTGCGACAGGCCCTGGACAA
A07	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	GTCTGGTCTACGCTGGTGAACCC
A07	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	TGGATCCGTAGCCCCAGGGAAGG
A07	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	CTGGGGGGTCCCTGAGACTCTCCTG
A07	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	GGTCCGCCAGGCTCCAGGGAA
A07	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	CTTCGGAGACCCTGTCCCTCACCTG
A07	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	TGGATCCGCCAGCCCCAGGGAAGG
A07	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	CGGGGAGTCTCTGAAGATCTCCTGT
A07	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	GGGTGCGCCAGATGCCCGGAAAGG
A07	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	TCGAGACCCTCTCACTACCTGTG
A07	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	TGGATCAGGCAGTCCCCATCGAGAG
A07	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	TCGTCGTC	TTGGGTGCGACAGGCCCTGGACAA
A08	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CGTATGCA	GGCCTCAGTGAAGGTCTCCTGCAAG
A08	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CGTATGCA	CTGGGTGCGACAGGCCCTGGACAA
A08	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CGTATGCA	GTCTGGTCTACGCTGGTGAACCC
A08	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CGTATGCA	TGGATCCGTAGCCCCAGGGAAGG
A08	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CGTATGCA	CTGGGGGGTCCCTGAGACTCTCCTG

A08	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGTATGCA	GGTCCGCCAGGCTCCAGGGAA
A08	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGTATGCA	CTTCGAGACCCTGTCCCTCACCTG
A08	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGTATGCA	TGGATCCGCCAGCCCCAGGGAAGG
A08	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGTATGCA	CGGGGAGTCTCTGAAGATCTCCTGT
A08	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGTATGCA	GGGTGCGCCAGATGCCCGGAAAGG
A08	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGTATGCA	TCGAGACCCTCTCACTACCTGTG
A08	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGTATGCA	TGGATCAGGCAGTCCCCATCGAGAG
A08	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGTATGCA	TTGGGTGCGACAGGCCCTGGACAA
A09	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	GGCCTCAGTGAAGGTCTCTGCAAG
A09	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	CTGGGTGCGACAGGCCCTGGACAA
A09	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	GTCTGGTCTACGCTGGTGAACCC
A09	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	TGGATCCGTAGCCCCAGGGAAGG
A09	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	CTGGGGGGTCCCTGAGACTCTCCTG
A09	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	GGTCCGCCAGGCTCCAGGGAA
A09	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	CTTCGAGACCCTGTCCCTCACCTG
A09	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	TGGATCCGCCAGCCCCAGGGAAGG
A09	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	CGGGGAGTCTCTGAAGATCTCCTGT
A09	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	GGGTGCGCCAGATGCCCGGAAAGG
A09	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	TCGAGACCCTCTCACTACCTGTG
A09	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	TGGATCAGGCAGTCCCCATCGAGAG
A09	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGAGCAGA	TTGGGTGCGACAGGCCCTGGACAA
A10	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	GGCCTCAGTGAAGGTCTCTGCAAG
A10	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	CTGGGTGCGACAGGCCCTGGACAA
A10	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	GTCTGGTCTACGCTGGTGAACCC
A10	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	TGGATCCGTAGCCCCAGGGAAGG
A10	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	CTGGGGGGTCCCTGAGACTCTCCTG
A10	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	GGTCCGCCAGGCTCCAGGGAA
A10	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	CTTCGAGACCCTGTCCCTCACCTG
A10	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	TGGATCCGCCAGCCCCAGGGAAGG
A10	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	CGGGGAGTCTCTGAAGATCTCCTGT
A10	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	GGGTGCGCCAGATGCCCGGAAAGG
A10	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	TCGAGACCCTCTCACTACCTGTG
A10	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	TGGATCAGGCAGTCCCCATCGAGAG
A10	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GATCGAGC	TTGGGTGCGACAGGCCCTGGACAA
A11	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	GGCCTCAGTGAAGGTCTCTGCAAG
A11	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	CTGGGTGCGACAGGCCCTGGACAA
A11	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	GTCTGGTCTACGCTGGTGAACCC
A11	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	TGGATCCGTAGCCCCAGGGAAGG
A11	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	CTGGGGGGTCCCTGAGACTCTCCTG
A11	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	GGTCCGCCAGGCTCCAGGGAA
A11	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	CTTCGAGACCCTGTCCCTCACCTG
A11	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	TGGATCCGCCAGCCCCAGGGAAGG
A11	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	CGGGGAGTCTCTGAAGATCTCCTGT
A11	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	GGGTGCGCCAGATGCCCGGAAAGG
A11	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	TCGAGACCCTCTCACTACCTGTG
A11	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	TGGATCAGGCAGTCCCCATCGAGAG
A11	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GCATGCAC	TTGGGTGCGACAGGCCCTGGACAA
A12	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	GGCCTCAGTGAAGGTCTCTGCAAG
A12	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	CTGGGTGCGACAGGCCCTGGACAA
A12	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	GTCTGGTCTACGCTGGTGAACCC
A12	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	TGGATCCGTAGCCCCAGGGAAGG



A12	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	CTGGGGGGTCCCTGAGACTCTCCTG
A12	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	GGTCCGCCAGGCTCCAGGGAA
A12	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	CTTCGGAGACCCTGTCCCTCACCTG
A12	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	TGGATCCGCCAGCCCCAGGGAAGG
A12	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	CGGGGAGTCTCTGAAGATCTCCTGT
A12	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	GGGTGCGCCAGATGCCCGGAAAGG
A12	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	TCGCAGACCCTCTACTCACCTGTG
A12	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	TGGATCAGGCAGTCCCCATCGAGAG
A12	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACGATGC	TTGGGTGCGACAGGCCCTGGACAA
B01	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	GGCCTCAGTGAAGGTCTCTGCAAG
B01	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	CTGGGTGCGACAGGCCCTGGACAA
B01	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	GTCTGGTCTACGCTGGTGAACCC
B01	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	TGGATCCGTAGCCCCAGGGAAGG
B01	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	CTGGGGGGTCCCTGAGACTCTCCTG
B01	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	GGTCCGCCAGGCTCCAGGGAA
B01	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	CTTCGGAGACCCTGTCCCTCACCTG
B01	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	TGGATCCGCCAGCCCCAGGGAAGG
B01	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	CGGGGAGTCTCTGAAGATCTCCTGT
B01	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	GGGTGCGCCAGATGCCCGGAAAGG
B01	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	TCGCAGACCCTCTACTCACCTGTG
B01	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	TGGATCAGGCAGTCCCCATCGAGAG
B01	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CTATAGAG	TTGGGTGCGACAGGCCCTGGACAA
B02	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	GGCCTCAGTGAAGGTCTCTGCAAG
B02	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	CTGGGTGCGACAGGCCCTGGACAA
B02	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	GTCTGGTCTACGCTGGTGAACCC
B02	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	TGGATCCGTAGCCCCAGGGAAGG
B02	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	CTGGGGGGTCCCTGAGACTCTCCTG
B02	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	GGTCCGCCAGGCTCCAGGGAA
B02	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	CTTCGGAGACCCTGTCCCTCACCTG
B02	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	TGGATCCGCCAGCCCCAGGGAAGG
B02	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	CGGGGAGTCTCTGAAGATCTCCTGT
B02	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	GGGTGCGCCAGATGCCCGGAAAGG
B02	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	TCGCAGACCCTCTACTCACCTGTG
B02	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	TGGATCAGGCAGTCCCCATCGAGAG
B02	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	AGTATCTG	TTGGGTGCGACAGGCCCTGGACAA
B03	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	GGCCTCAGTGAAGGTCTCTGCAAG
B03	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	CTGGGTGCGACAGGCCCTGGACAA
B03	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	GTCTGGTCTACGCTGGTGAACCC
B03	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	TGGATCCGTAGCCCCAGGGAAGG
B03	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	CTGGGGGGTCCCTGAGACTCTCCTG
B03	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	GGTCCGCCAGGCTCCAGGGAA
B03	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	CTTCGGAGACCCTGTCCCTCACCTG
B03	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	TGGATCCGCCAGCCCCAGGGAAGG
B03	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	CGGGGAGTCTCTGAAGATCTCCTGT
B03	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	GGGTGCGCCAGATGCCCGGAAAGG
B03	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	TCGCAGACCCTCTACTCACCTGTG
B03	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	TGGATCAGGCAGTCCCCATCGAGAG
B03	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	GAGTCATA	TTGGGTGCGACAGGCCCTGGACAA
B04	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	ACGCAGAT	GGCCTCAGTGAAGGTCTCTGCAAG
B04	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	ACGCAGAT	CTGGGTGCGACAGGCCCTGGACAA
B04	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	ACGCAGAT	GTCTGGTCTACGCTGGTGAACCC

B04	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	TGGATCCGTAGCCCCAGGGAAGG
B04	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	CTGGGGGGTCCCTGAGACTCTCTG
B04	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	GGTCCGCCAGGCTCCAGGGAA
B04	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	CTTCGAGACCCTGTCCCTCACCTG
B04	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	TGGATCCGCCAGCCCCAGGGAAGG
B04	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	CGGGGAGTCTCTGAAGATCTCTGT
B04	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	GGGTGCGCCAGATGCCCGGAAAGG
B04	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	TCGCAGACCCTCTACTCACCTGTG
B04	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	TGGATCAGGCAGTCCCCATCGAGAG
B04	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGCAGAT	TTGGGTGCGACAGGCCCTGGACAA
B05	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	GGCCTCAGTGAAGGTCTCTGCAAG
B05	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	CTGGGTGCGACAGGCCCTGGACAA
B05	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	GTCTGGTCTACGCTGGTGAACCC
B05	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	TGGATCCGTAGCCCCAGGGAAGG
B05	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	CTGGGGGGTCCCTGAGACTCTCTG
B05	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	GGTCCGCCAGGCTCCAGGGAA
B05	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	CTTCGAGACCCTGTCCCTCACCTG
B05	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	TGGATCCGCCAGCCCCAGGGAAGG
B05	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	CGGGGAGTCTCTGAAGATCTCTGT
B05	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	GGGTGCGCCAGATGCCCGGAAAGG
B05	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	TCGCAGACCCTCTACTCACCTGTG
B05	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	TGGATCAGGCAGTCCCCATCGAGAG
B05	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	CAGCATAG	TTGGGTGCGACAGGCCCTGGACAA
B06	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	GGCCTCAGTGAAGGTCTCTGCAAG
B06	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	CTGGGTGCGACAGGCCCTGGACAA
B06	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	GTCTGGTCTACGCTGGTGAACCC
B06	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	TGGATCCGTAGCCCCAGGGAAGG
B06	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	CTGGGGGGTCCCTGAGACTCTCTG
B06	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	GGTCCGCCAGGCTCCAGGGAA
B06	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	CTTCGAGACCCTGTCCCTCACCTG
B06	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	TGGATCCGCCAGCCCCAGGGAAGG
B06	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	CGGGGAGTCTCTGAAGATCTCTGT
B06	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	GGGTGCGCCAGATGCCCGGAAAGG
B06	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	TCGCAGACCCTCTACTCACCTGTG
B06	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	TGGATCAGGCAGTCCCCATCGAGAG
B06	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ACGTGTCA	TTGGGTGCGACAGGCCCTGGACAA
B07	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	GGCCTCAGTGAAGGTCTCTGCAAG
B07	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	CTGGGTGCGACAGGCCCTGGACAA
B07	VH2	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	GTCTGGTCTACGCTGGTGAACCC
B07	VH2	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	TGGATCCGTAGCCCCAGGGAAGG
B07	VH3	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	CTGGGGGGTCCCTGAGACTCTCTG
B07	VH3	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	GGTCCGCCAGGCTCCAGGGAA
B07	VH4	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	CTTCGAGACCCTGTCCCTCACCTG
B07	VH4	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	TGGATCCGCCAGCCCCAGGGAAGG
B07	VH5	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	CGGGGAGTCTCTGAAGATCTCTGT
B07	VH5	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	GGGTGCGCCAGATGCCCGGAAAGG
B07	VH6	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	TCGCAGACCCTCTACTCACCTGTG
B07	VH6	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	TGGATCAGGCAGTCCCCATCGAGAG
B07	VH7	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	GAGTGTAT	TTGGGTGCGACAGGCCCTGGACAA
B08	VH1	FR1	GGCATTCTGCTGAACCGCTCTCCGATCT	ATCTGAGC	GGCCTCAGTGAAGGTCTCTGCAAG
B08	VH1	FR2	GGCATTCTGCTGAACCGCTCTCCGATCT	ATCTGAGC	CTGGGTGCGACAGGCCCTGGACAA

B08	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	GTCTGGTCTACGCTGGTGAAACCC
B08	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	TGGATCCGTAGCCCCAGGGAAGG
B08	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	CTGGGGGGTCCCTGAGACTCTCTTG
B08	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	GGTCCGCCAGGCTCCAGGGAA
B08	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	CTTCGAGACCCTGTCCCTCACCTG
B08	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	TGGATCCGCCAGCCCCAGGGAAGG
B08	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	CGGGGAGTCTCTGAAGATCTCCTGT
B08	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	GGGTGCGCCAGATGCCCGGGAAGG
B08	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	TCGAGACCCTCTCACTCACCTGTG
B08	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	TGGATCAGGCAGTCCCCATCGAGAG
B08	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	ATCTGAGC	TTGGGTGCGACAGGCCCTGGACAA
B09	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	GGCCTCAGTGAAGGTCTCTGCAAG
B09	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	CTGGGTGCGACAGGCCCTGGACAA
B09	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	GTCTGGTCTACGCTGGTGAAACCC
B09	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	TGGATCCGTAGCCCCAGGGAAGG
B09	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	CTGGGGGGTCCCTGAGACTCTCTTG
B09	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	GGTCCGCCAGGCTCCAGGGAA
B09	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	CTTCGAGACCCTGTCCCTCACCTG
B09	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	TGGATCCGCCAGCCCCAGGGAAGG
B09	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	CGGGGAGTCTCTGAAGATCTCCTGT
B09	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	GGGTGCGCCAGATGCCCGGGAAGG
B09	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	TCGAGACCCTCTCACTCACCTGTG
B09	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	TGGATCAGGCAGTCCCCATCGAGAG
B09	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TATACGCT	TTGGGTGCGACAGGCCCTGGACAA
B10	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	GGCCTCAGTGAAGGTCTCTGCAAG
B10	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	CTGGGTGCGACAGGCCCTGGACAA
B10	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	GTCTGGTCTACGCTGGTGAAACCC
B10	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	TGGATCCGTAGCCCCAGGGAAGG
B10	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	CTGGGGGGTCCCTGAGACTCTCTTG
B10	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	GGTCCGCCAGGCTCCAGGGAA
B10	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	CTTCGAGACCCTGTCCCTCACCTG
B10	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	TGGATCCGCCAGCCCCAGGGAAGG
B10	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	CGGGGAGTCTCTGAAGATCTCCTGT
B10	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	GGGTGCGCCAGATGCCCGGGAAGG
B10	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	TCGAGACCCTCTCACTCACCTGTG
B10	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	TGGATCAGGCAGTCCCCATCGAGAG
B10	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TACATAGT	TTGGGTGCGACAGGCCCTGGACAA
B11	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	GGCCTCAGTGAAGGTCTCTGCAAG
B11	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	CTGGGTGCGACAGGCCCTGGACAA
B11	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	GTCTGGTCTACGCTGGTGAAACCC
B11	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	TGGATCCGTAGCCCCAGGGAAGG
B11	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	CTGGGGGGTCCCTGAGACTCTCTTG
B11	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	GGTCCGCCAGGCTCCAGGGAA
B11	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	CTTCGAGACCCTGTCCCTCACCTG
B11	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	TGGATCCGCCAGCCCCAGGGAAGG
B11	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	CGGGGAGTCTCTGAAGATCTCCTGT
B11	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	GGGTGCGCCAGATGCCCGGGAAGG
B11	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	TCGAGACCCTCTCACTCACCTGTG
B11	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	TGGATCAGGCAGTCCCCATCGAGAG
B11	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	CGATGATC	TTGGGTGCGACAGGCCCTGGACAA
B12	VH1	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	GGCCTCAGTGAAGGTCTCTGCAAG

B12	VH1	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	CTGGGTGCGACAGGCCCTGGACAA
B12	VH2	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	GTCTGGTCTACGCTGGTGAACCC
B12	VH2	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	TGGATCCGTACGCCCCAGGGAAGG
B12	VH3	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	CTGGGGGGTCCCTGAGACTCTCTG
B12	VH3	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	GGTCCGCCAGGCTCCAGGGAA
B12	VH4	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	CTTCGAGACCCTGTCCCTCACCTG
B12	VH4	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	TGGATCCGCCAGCCCCAGGGAAGG
B12	VH5	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	CGGGGAGTCTCTGAAGATCTCTGT
B12	VH5	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	GGGTGCGCCAGATGCCCGGGAAGG
B12	VH6	FR1	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	TCGAGACCCTCTCACTCACCTGTG
B12	VH6	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	TGGATCAGGCAGTCCCCATCGAGAG
B12	VH7	FR2	GGCATTCTGCTGAACCGCTCTTCCGATCT	TCGAGTAG	TTGGGTGCGACAGGCCCTGGACAA

**Table S5: Second round PCR primers used to construct sequencing libraries.**  
Abbreviations: P5: read 1 Illumina sequencing adapter; and P7: read 2 Illumina sequencing adapter. Adapters are listed 5' to 3'.

Table S5: Second Round Primers

remainder of P5 adapter	partial P5 adapter
AATGATACGGCGACCAACCGAGATCT	ACACTCTTTCCCTACACGACGCTCTTCCGATC
remainder of P7 adapter	partial P7 adapter
CAAGCAGAAGACGGCATACGAGATCGGTCTC	GGCATTCTGCTGAACCGCTC

**Table S6: DNA sequencing libraries and protocols used for each Figure.**

Figure	Template	IGHV primers	Constant region or IGHJ primers	Notes
<b>Figs. 1-5, 7; Figs. S1-S5, S7</b>	cDNA	FR1 set	Constant region isotype	Each isotype library (IgM, IgD, IgG, IgA, IgE) was PCR amplified separately
<b>Fig. 6, Fig. S6</b>	genomic DNA	FR1 and FR2 sets	IGHJ	Six independent replicate libraries were amplified per sample, each from a different aliquot of genomic DNA template