

HVTN 302 BCR Sequencing Figures and Tables for Manuscript

Kellie MacPhee, Michael Duff, Zoe Moodie, Ollivier Hyrien

Document rendered on June 11, 2025

Table 1: Number of paired heavy and light chain BCR sequences

Group	UID	Non-base binder			Base binder			Antigen negative		
		Week 0	Week 10	Week 26	Week 0	Week 10	Week 26	Week 0	Week 10	Week 26
T2: 100 mcg of BG505 MD39.3 gp151 mRNA	177		20	66	9	39	93	225	151	146
	256	2		25	42		134	185		303
	325	2	11	9	1	19	31	222	132	153
	567		3	20	17	32	34			273
T3: 100 mcg of BG505 MD39.3 gp151 CD4KO mRNA	28	1	3	3	4	8	6	398	378	449
	54		42	3	5	18	3	184	339	79
	485		15	25	6	17	23	105	79	49
	618		41	15	9	34	15	451	494	252
	682	1		17	16	12	29			375
	840		5	58	20	16	126			400
	953	1	24	39	16	25	27		193	270
T5: 250 mcg of BG505 MD39.3 gp151 mRNA	380	1	37	30	10	41	35	543	306	85
	503	1	9	10	62	64	50		192	127
	556	2	12	12	8	16	8	326	68	88
	873	91	12	15	26	24	15		399	69
T6: 250 mcg of BG505 MD39.3 gp151 CD4KO mRNA	151		2	18	8	7	24	169	90	171
	291	1	13	26	48	57	81			152
	321		20	14	51	77	47		408	404
	787		3	15	3	3	13	227	37	64
	821	1	11	104	11	20	78	60	58	128
Total	9668	104	283	524	372	529	872	3095	3324	4037

Table 2: Median percent mutation in the V segment

Chain	Group	UID	Non-base binder			Base binder		
			Week 0	Week 10	Week 26	Week 0	Week 10	Week 26
Heavy	T2: 100 mcg of BG505 MD39.3 gp151 mRNA	177		2.8	5.2	6.9	2.5	5.2
		256	6.6		5.2	6.1		5.3
		325	9.7	2.8	4.5	13	2.8	4.2
		567		2.8	4.2	5.2	3.1	4.8
	T3: 100 mcg of BG505 MD39.3 gp151 CD4KO mRNA	28	0	3.1	4.5	5.9	7.2	3.1
		485		2.8	4.5	3.8	4.2	5.5
		54		2.4	2.1	3.1	2.4	5.6
		618		1.7	3.5	5.6	1.7	4.2
		682	0		4.5	6.8	3.1	4.8
		840		2	5.2	2.3	3.8	4.5
		953	3.5	3.5	4.5	5	4.2	5.2
	T5: 250 mcg of BG505 MD39.3 gp151 mRNA	380	0	2.4	4.5	5	2.4	4.5
		503	13	2.8	4.2	4.8	5.6	4.5
		556	1.6	2.9	4.9	3.3	2.6	5
		873	0	3.5	4.8	6.6	4.2	4.9
	T6: 250 mcg of BG505 MD39.3 gp151 CD4KO mRNA	151		1.2	4.2	10	3.2	4.2
		291	0	2.4	3.3	5.4	4.5	4.8
		321		3.1	5.1	4.2	3.5	4.5
		787		2.4	5.5	3.2	2.1	3.9
		821	1	1.7	4.6	6.2	3.5	4.5
	Median		1	2.8	4.5	5.3	3.2	4.65
Kappa	T2: 100 mcg of BG505 MD39.3 gp151 mRNA	177		1.1	2.5	4.2	1.1	2.5
		256	4.4		2.7	3.9		3.2
		325	4.2	1.7	2.5		1.7	2.1
		567		1.6	2.3	3.4	1.1	2.9
	T3: 100 mcg of BG505 MD39.3 gp151 CD4KO mRNA	28	0	1.4	1.8	5.7	3.2	1.4
		485		2.1	2.2	1.6	2.9	2.7
		54		0.72	0	1.8	2	3.9
		618		1.1	2.5	3.9	1.1	2.5
		682			2.7	4.1	1.8	2.3
		840		3.2	2.5	1.8	1.8	2.2
		953	5	1.4	2.3	3.6	1.7	3.4
	T5: 250 mcg of BG505 MD39.3 gp151 mRNA	380	0	0.87	2.5	4	1	1.6
		503	7.1	2.5	3.2	3.2	3.2	2.4
		556	0	0.68	2.7	2.5	0.71	2.9
		873	0	1.4	2.9	3.9	2.2	2.2
	T6: 250 mcg of BG505 MD39.3 gp151 CD4KO mRNA	151		1.4	2.1	7.7	1.3	1.9
		291	0	1.1	2.7	3.6	2.3	3.5
		321		2	3.2	2.6	2.5	2.4
		787		0.71	3	4.4	0.68	2
		821	1.4	1.1	2.9	3	1.4	2
	Median		0.7	1.4	2.5	3.6	1.7	2.4
Lambda	T2: 100 mcg of BG505 MD39.3 gp151 mRNA	177		1	3.1	1.4	1.7	2.8
		256	1		3.8	3.6		3
		325		2.1	2.5	3.8	1.8	2.8
		567		2.2	2.3	4.7	2.7	3.1
	T3: 100 mcg of BG505 MD39.3 gp151 CD4KO mRNA	28		2.5	4.2	3.4	4.8	1.9
		485		2.5	2.2	2.3	3.2	2.5
		54		1.4	3	1.7	1.4	
		618		0.72	1.4	1.7	1.4	2.4
		682	0		2.5	3.2	1.6	3.1
		840		1.9	2.8	1	1.8	2.8
		953		2.1	2.1	3.9	2.5	2.8
	T5: 250 mcg of BG505 MD39.3 gp151 mRNA	380		1	3.8	3.7	0.84	1.9
		503		1.4	3.9	2.5	4.5	2.3
		556	3.1	0.71	3.6	1	1.7	2.5
		873	0	1.4	3	3.5	3.2	4.5
	T6: 250 mcg of BG505 MD39.3 gp151 CD4KO mRNA	151			2.5	6.5	3.6	2.2
		291		1.4	1.1	3.9	2.4	3.7
		321		2.5	4.7	2.1	1.9	2.4
		787		0.88	3	3.9		2.1
		821		0.53	2.5	5.7	2.2	2.8
	Median		0.5	1.4	2.9	3.45	2.05	2.8

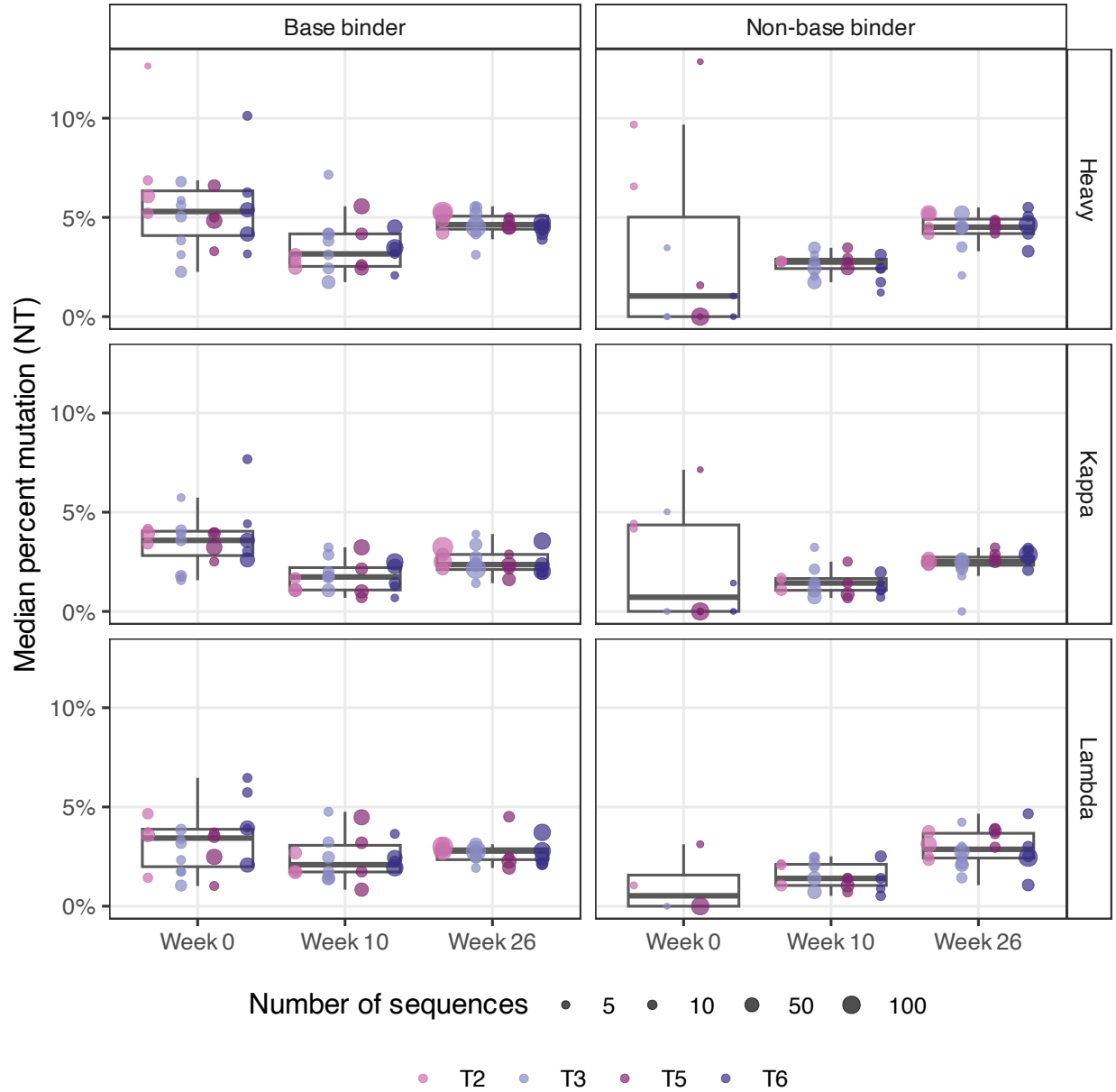


Figure 1: Median percent mutation in heavy, kappa, and lambda chain V genes, by sort population (antigen negative, base binder, and non-base binder) and study visit (Weeks 0, 10, and 26) in study participants from all treatment groups (T2, T3, T5, T6). Each dot represents one study participant, sized according to the number of sequences used to compute the median (note that the legend only shows example dot sizes for reference; dot size can take on more values than are shown).

Table 3: Percent mutation comparisons between base and non-base binders at a given study visit, performed using the Wilcoxon signed-rank test (two-sided) to account for paired data. Paired observations from at least 3 participants were required in order to run the test.

Comparison	Chain	Week	p-value	SampleSizes	Median (Range)
Base binder vs. Non-base binder	Heavy	Week 0	0.067	11	5.900 [3.300, 13.000] vs. 1.000 [0.000, 13.000]
		Week 10	**0.004**	18	3.350 [1.700, 7.200] vs. 2.800 [1.200, 3.500]
		Week 26	0.332	20	4.650 [3.100, 5.600] vs. 4.500 [2.100, 5.500]
	Kappa	Week 0	0.129	9	3.600 [2.500, 5.700] vs. 0.000 [0.000, 7.100]
		Week 10	0.052	18	1.700 [0.680, 3.200] vs. 1.400 [0.680, 3.200]
		Week 26	0.503	20	2.400 [1.400, 3.900] vs. 2.500 [0.000, 3.200]
	Lambda	Week 0	0.250	4	3.350 [1.000, 3.600] vs. 0.500 [0.000, 3.100]
		Week 10	**0.006**	16	2.050 [0.840, 4.800] vs. 1.400 [0.530, 2.500]
		Week 26	0.588	19	2.800 [1.900, 4.500] vs. 2.800 [1.100, 4.700]

Table 4: Percent mutation comparisons between study visits within base or non-base binders, performed using the Wilcoxon signed-rank test (two-sided) to account for paired data. Paired observations from at least 3 participants were required in order to run the test.

Comparison	Chain	Sort Population	p-value	SampleSizes	Median (Range)
Week 0 vs. Week 10	Heavy	Base binder	**0.003**	19	5.200 [2.300, 13.000] vs. 3.200 [1.700, 7.200]
		Non-base binder	0.594	9	1.000 [0.000, 13.000] vs. 2.800 [1.700, 3.500]
	Kappa	Base binder	**<0.001**	18	3.600 [1.600, 7.700] vs. 1.750 [0.680, 3.200]
		Non-base binder	0.797	9	0.000 [0.000, 7.100] vs. 1.400 [0.680, 2.500]
	Lambda	Base binder	0.116	18	3.300 [1.000, 6.500] vs. 2.050 [0.840, 4.800]
		Non-base binder	—	2	1.550 [0.000, 3.100] vs. 1.055 [0.710, 1.400]
Week 0 vs. Week 26	Heavy	Base binder	0.180	20	5.300 [2.300, 13.000] vs. 4.650 [3.100, 5.600]
		Non-base binder	0.412	11	1.000 [0.000, 13.000] vs. 4.500 [3.300, 5.200]
	Kappa	Base binder	**0.012**	19	3.600 [1.600, 7.700] vs. 2.400 [1.400, 3.900]
		Non-base binder	0.609	10	0.700 [0.000, 7.100] vs. 2.700 [1.800, 3.200]
	Lambda	Base binder	0.206	19	3.500 [1.000, 6.500] vs. 2.800 [1.900, 4.500]
		Non-base binder	0.125	4	0.500 [0.000, 3.100] vs. 3.300 [2.500, 3.800]
Week 10 vs. Week 26	Heavy	Base binder	**0.004**	19	3.200 [1.700, 7.200] vs. 4.500 [3.100, 5.600]
		Non-base binder	**<0.001**	18	2.800 [1.200, 3.500] vs. 4.500 [2.100, 5.500]
	Kappa	Base binder	**0.010**	19	1.700 [0.680, 3.200] vs. 2.400 [1.400, 3.900]
		Non-base binder	**<0.001**	18	1.400 [0.680, 3.200] vs. 2.500 [0.000, 3.200]
	Lambda	Base binder	0.258	17	2.200 [0.840, 4.800] vs. 2.800 [1.900, 4.500]
		Non-base binder	**<0.001**	17	1.400 [0.530, 2.500] vs. 3.000 [1.100, 4.700]

Table 5: Germline V gene usage in each sort population, with 95 percent confidence interval indicated in parentheses, estimated across all study participants and time points. Pseudo-likelihood method is used to obtain the point estimates and confidence intervals.

Chain	V Gene	Antigen negative	Base binder	Non-base binder
Heavy	IGHV1-18	3.9 (3.2, 4.4)	3.5 (2.1, 5.3)	4.4 (1.8, 6.9)
	IGHV1-2	3.5 (2.5, 4.6)	3.1 (1.8, 4.9)	0.8 (0, 2.2)
	IGHV1-24	0.8 (0.5, 1.1)	0.9 (0.6, 2.4)	0.1 (0, 0.4)
	IGHV1-3	1.7 (1.1, 2.3)	0.6 (0, 1.5)	1.1 (0, 4.6)
	IGHV1-46	2.8 (2.3, 3.4)	4.1 (2.5, 6.4)	1.8 (0, 3.5)
	IGHV1-69	5.1 (4.1, 6.2)	23.8 (18.6, 29.7)	11.3 (7.3, 15.7)
	IGHV2-5	2.2 (1.8, 2.9)	1.4 (0.3, 2.2)	0.4 (0, 1.8)
	IGHV2-70	1.1 (0.8, 1.4)	1 (0, 2)	2.1 (0.6, 3.7)
	IGHV3-11	2.8 (2.3, 3.3)	1.5 (0.5, 2.3)	2.2 (0.7, 5.1)
	IGHV3-15	2.9 (2.3, 3.3)	2.6 (1.5, 3.8)	2.7 (1, 5.3)
	IGHV3-21	3.7 (3.2, 4.2)	2.2 (0.9, 3.2)	10.3 (6.6, 14.9)
	IGHV3-23	9.4 (8.1, 10.9)	7.3 (5.8, 9.2)	17.9 (12.9, 23.6)
	IGHV3-30	7.1 (5.9, 8.2)	6.1 (4, 7.6)	6.9 (4, 10.4)
	IGHV3-30-3	1.7 (1.1, 2.4)	1.7 (0.5, 3.4)	0.7 (0, 2.1)
	IGHV3-33	2.9 (2, 3.7)	2 (1, 3.8)	1.5 (0.1, 3.2)
	IGHV3-48	3.5 (2.9, 4.2)	2.2 (1.5, 3.6)	3.7 (1.8, 6.6)
	IGHV3-49	1.1 (0.7, 1.5)	1.1 (0, 1.8)	2 (0, 4.4)
	IGHV3-7	4.2 (3.5, 5.1)	1.7 (0.8, 3)	1.3 (0, 2.5)
	IGHV3-74	2.4 (2, 2.9)	1.3 (0.1, 2.1)	1.6 (0.2, 3.5)
	IGHV3-9	2.2 (1.5, 2.9)	1.1 (0.1, 2)	2 (0.4, 3.3)
	IGHV4-30-4	2.7 (1.8, 3.8)	3.1 (1.7, 4.4)	4.8 (2.3, 7.9)
	IGHV4-34	2.4 (2, 3.1)	3.9 (2.3, 5.5)	1.6 (0.3, 3.1)
	IGHV4-39	5.5 (4.5, 6.5)	5.8 (3.6, 8.1)	4.3 (1.9, 6.5)
	IGHV4-4	2.4 (2, 3)	1.8 (0.8, 3)	1.4 (0.3, 3)
	IGHV4-59	4.8 (3.8, 6)	4 (1.8, 6.3)	2.6 (1, 4.6)
	IGHV4-61	1.5 (1, 2.1)	1.8 (0.6, 2.6)	1 (0.2, 2.9)
	IGHV5-10-1	1.1 (0.6, 1.6)	0.5 (0, 1.4)	0.8 (0, 2.1)
	IGHV5-51	3.7 (3, 4.1)	2.5 (1.4, 3.8)	2.1 (0.7, 4.2)
Kappa	IGKV1-12	2.8 (2.1, 3.3)	1.9 (0.4, 3.4)	4.2 (0.9, 6.8)
	IGKV1-16	1.7 (1.4, 2.2)	0.9 (0, 1.8)	0.9 (0, 2.3)
	IGKV1-17	1.8 (1.4, 2.3)	1.6 (0, 2.6)	2.7 (0.7, 6.1)
	IGKV1-27	2.2 (1.5, 2.6)	1.4 (0, 2.7)	1 (0, 3.9)
	IGKV1-33	5.3 (4.4, 6.1)	8.4 (5.6, 12.6)	8.5 (4.8, 13.5)
	IGKV1-39	14 (12.9, 15.3)	18.7 (14.3, 23.2)	14.3 (8.8, 19.3)
	IGKV1-5	10.2 (9.1, 11.9)	8.4 (5.3, 12.2)	12 (5.7, 19.2)
	IGKV1-9	2.8 (2.1, 3.4)	2.4 (1.1, 4.2)	1.6 (0, 4.1)
	IGKV2-24	1.5 (1.2, 2)	1.1 (0, 2.7)	1.7 (0, 3.7)
	IGKV2-28	7.3 (6.1, 8.2)	7.8 (5.3, 10.9)	4 (1.1, 8)
	IGKV2-30	3 (2.3, 4)	1.8 (0.5, 3.5)	2.1 (0.4, 4.4)
	IGKV3-11	7.7 (6.6, 8.6)	6.1 (3.7, 8.8)	8.9 (4.5, 14)
	IGKV3-15	9.8 (8.8, 10.7)	8.8 (6.3, 11.3)	15.6 (10.5, 22.1)
	IGKV3-20	16.9 (15.2, 18.7)	18.3 (14.9, 23.1)	12.3 (7.1, 17)
	IGKV4-1	10 (8.9, 11.5)	9.9 (6.8, 12.3)	8.5 (5.3, 12)
Lambda	IGLV1-36	0.7 (0.4, 1.1)	0.4 (0, 1.3)	0 (0, 2.4)
	IGLV1-40	8.1 (7.2, 9.3)	11.7 (7.9, 16.1)	10.8 (4, 15.7)
	IGLV1-44	9 (7.7, 10.5)	9 (6, 12.2)	10.5 (3.7, 16.9)
	IGLV1-47	5.8 (4.9, 6.8)	5.8 (2.1, 11)	12.4 (7.3, 20.9)
	IGLV1-51	7 (5.7, 8.6)	10.9 (7.2, 15.4)	5.5 (0, 9.5)
	IGLV2-11	3.6 (3.1, 4.4)	2.4 (0.8, 5.2)	3.9 (0, 9.4)
	IGLV2-14	13.2 (11.4, 15.3)	11.2 (8.1, 15.3)	8.8 (0, 16.1)
	IGLV2-23	5.2 (4.1, 5.9)	6.1 (2.2, 10.1)	2.4 (0, 7.7)
	IGLV2-8	4.8 (3.7, 6.1)	2.5 (0.5, 4.6)	0 (0, 2.5)
	IGLV3-1	7.2 (5.8, 8.8)	6.5 (2.9, 9.6)	1.4 (0, 5.1)
	IGLV3-10	1.9 (1.3, 2.5)	0.9 (0, 3.4)	0.4 (0, 1.2)
	IGLV3-19	4.1 (3.1, 4.9)	3.8 (1.4, 7.4)	3.4 (0, 8.6)
	IGLV3-21	10 (8.3, 11.9)	11.9 (8.2, 16.3)	21.3 (13.6, 32.4)
	IGLV3-25	4.1 (3.3, 5.2)	4.5 (1.8, 7.4)	2.2 (0, 8.6)
	IGLV3-9	1.2 (0.7, 1.6)	0.9 (0, 2)	0 (0, 3.5)
	IGLV4-69	2.2 (1.8, 3)	2.3 (0.1, 6.8)	0.3 (0, 1.4)
	IGLV6-57	2.9 (1.9, 3.8)	2.4 (0, 4.3)	5.8 (0, 12.1)
	IGLV7-43	1.4 (0.8, 2.1)	2 (0.1, 4.6)	0.1 (0, 0.7)
	IGLV7-46	1.4 (0.9, 2.1)	1.1 (0, 3.8)	1.5 (0, 6.6)

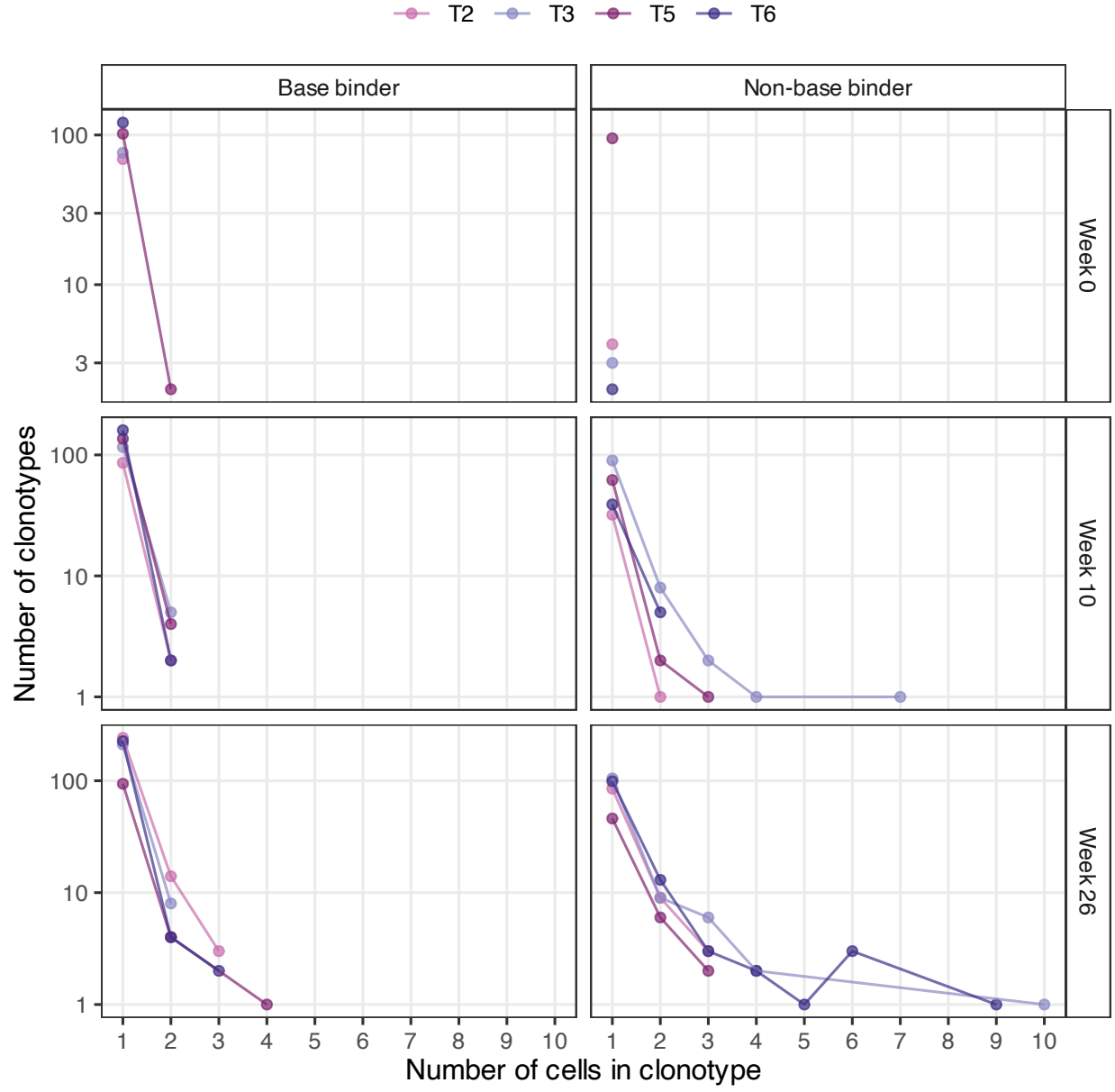


Figure 2: Observed clonotype sizes for each treatment group, time point, and sort population. Each line corresponds to one treatment group. Clonotypes containing B cells from multiple sort populations or treatment groups have been excluded.

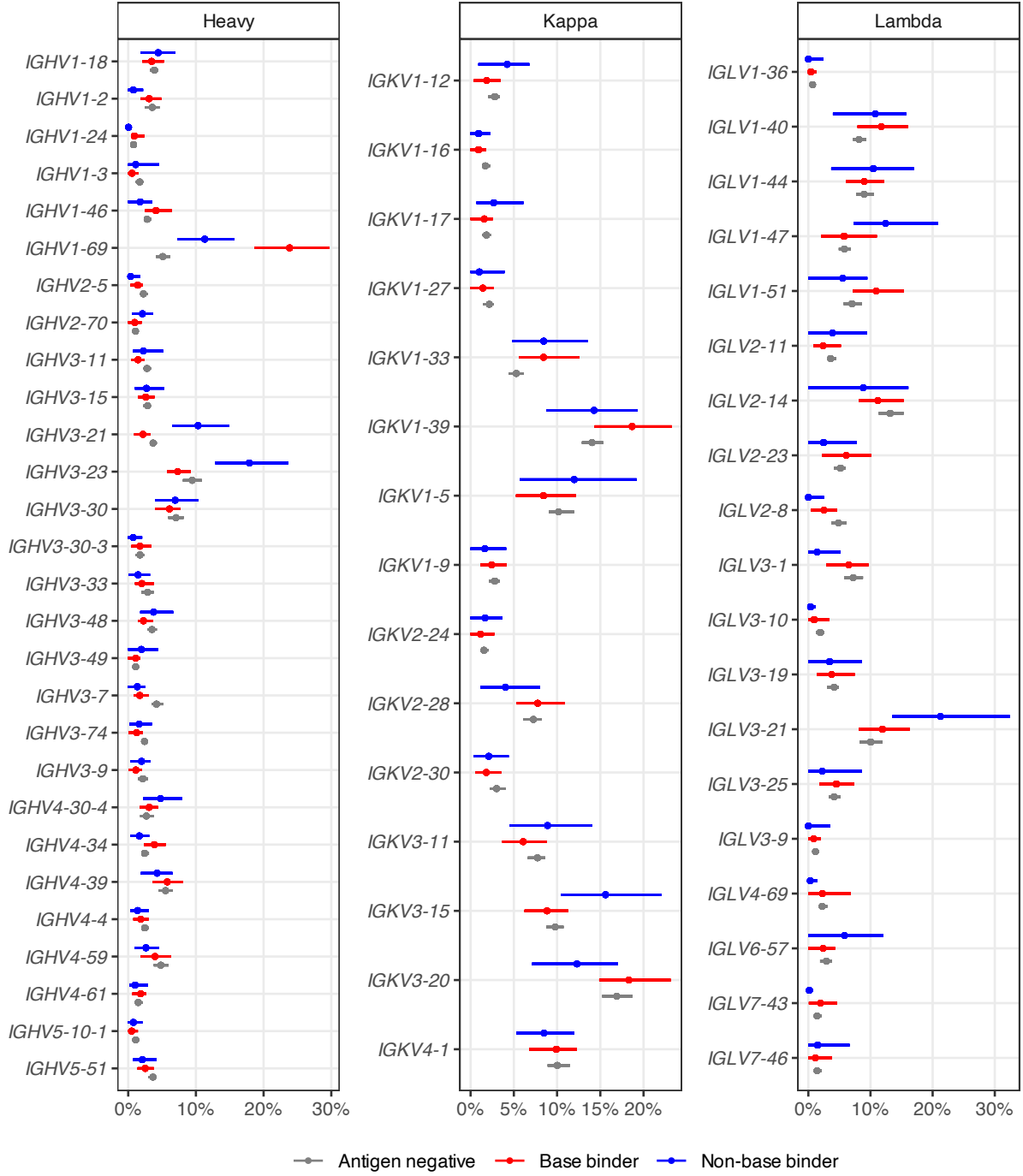


Figure 3: Germline V gene usage in each sort population, with 95 percent confidence intervals, estimated across all study participants and time points. Pseudo-likelihood method is used to obtain the point estimates and confidence intervals. V genes observed less than one percent of the time in the non-base binder and base binder repertoires are grouped together in the Other category.

Table 6: Summary of clonotypes containing at least 4 cells. Numbers in parentheses indicate the number of cells in the clonotype with the listed feature.

Number of Cells	Clone ID	V Genes (Heavy, Light)	CDR3 Lengths (Heavy, Light)	mAbs Ordered	Sort Populations	UIDs	Weeks	Isotypes	Median V % Mutation (Heavy, Light)	Max V % Mutation (Heavy, Light)
10	3448	IGHV3-21, IGKV1-5	17, 9	FH_302_14	Non-base binder (10)	485 (10)	Week 26 (10)	IGHG1 (9), IGHG2 (1)	4.7, 3.8	6.2, 6.8
9	5973	IGHV3-30, IGKV3D-15	14, 9	FH_302_15	Non-base binder (9)	821 (9)	Week 0 (1), Week 10 (2), Week 26 (6)	IGHA1 (1), IGHG1 (8)	1, 1.8	3.5, 6.1
9	8971	IGHV3-7, IGKV1-16	17, 9	FH_302_16	Non-base binder (9)	821 (9)	Week 26 (9)	IGHA1 (3), IGHG1 (6)	2.4, 3.2	4.2, 5.7
8	3528	IGHV3-21, IGKV1-33	11, 9	FH_302_17	Non-base binder (8)	54 (2), 556 (1), 787 (1), 840 (4)	Week 10 (3), Week 26 (5)	IGHA1 (3), IGHG1 (5)	5.9, 4.5	7.6, 5.4
7	3549	IGHV3-21, IGKV1-39	17, 9	FH_302_18	Non-base binder (7)	953 (7)	Week 10 (3), Week 26 (4)	IGHG1 (6), IGHG3 (1)	3.5, 2.2	5.6, 7.2
7	3988	IGHV3-23, IGKV1-33	12, 9	FH_302_19	Non-base binder (7)	54 (7)	Week 10 (7)	IGHG1 (7)	2.4, 2.9	4.6, 3.2
6	2418	IGHV2-70, IGKV1-12	20, 9	FH_302_22	Non-base binder (6)	821 (6)	Week 26 (6)	IGHG1 (6)	4.5, 4.3	5.2, 6.1
6	2580	IGHV1-46, IGLV1-40	19, 11	FH_302_20	Non-base binder (6)	821 (6)	Week 26 (6)	IGHA1 (3), IGHG2 (3)	12.5, 4.2	13.2, 4.5
6	6928	IGHV1-69, IGLV2-23	20, 11	FH_302_21, FH_302_4	Base binder (1), Non-base binder (5)	380 (6)	Week 10 (2), Week 26 (4)	IGHA1 (1), IGHG1 (5)	5.9, 3.6	8, 4.2
5	6347	IGHV3-30-3, IGKV2-28	14, 8	FH_302_23	Non-base binder (5)	821 (5)	Week 10 (1), Week 26 (4)	IGHG2 (5)	7.6, 3.7	8.7, 4.4
5	7305	IGHV1-69, IGKV1-39	14, 10	FH_302_8	Base binder (1), Non-base binder (4)	54 (5)	Week 10 (4), Week 26 (1)	IGHG1 (5)	2.1, 0.4	5.6, 1.8
5	7815	IGHV3-48, IGKV3-11	14, 10		Non-base binder (5)	380 (5)	Week 10 (3), Week 26 (2)	IGHG1 (5)	1.7, 1.1	4.9, 2.5
5	10696	IGHV1-18, IGKV3-11	13, 9		Non-base binder (5)	821 (5)	Week 26 (5)	IGHG1 (5)	6.1, 3.2	6.5, 3.2
5	10973	IGHV4-34, IGKV1-33	14, 9	FH_302_7	Base binder (5)	380 (4), 873 (1)	Week 10 (1), Week 26 (4)	IGHG1 (5)	3.2, 1.8	4.6, 3.6
5	11281	IGHV4-34, IGKV2-28	18, 9	FH_302_1, FH_302_5	Antigen negative (1), Base binder (4)	503 (5)	Week 0 (1), Week 10 (2), Week 26 (2)	IGHG3 (5)	7, 3.1	11.6, 6.5
5	12125	IGHV4-39, IGKV1-39	16, 9	FH_302_6	Base binder (3), Non-base binder (2)	177 (5)	Week 26 (5)	IGHG3 (5)	4.5, 5.4	6.9, 5.4

Table 6: Summary of clonotypes containing at least 4 cells. Numbers in parentheses indicate the number of cells in the clonotype with the listed feature. *(continued)*

Number of Cells	Clone ID	V Genes (Heavy, Light)	CDR3 Lengths (Heavy, Light)	mAbs Ordered	Sort Populations	UIDs	Weeks	Isotypes	Median V % Mutation (Heavy, Light)	Max V % Mutation (Heavy, Light)
4	1593	IGHV5-10-1, IGLV1-47	19, 13	FH_302_12	Antigen negative (1), Base binder (3)	256 (4)	Week 26 (4)	IGHG3 (4)	2.4, 1.4	2.4, 1.8
4	2557	IGHV1-46, IGKV3-11	25, 10		Non-base binder (4)	821 (4)	Week 26 (4)	IGHA1 (2), IGHG1 (2)	4.5, 2	5.2, 3.2
4	3441	IGHV3-21, IGKV1-5	17, 9		Non-base binder (4)	873 (4)	Week 10 (1), Week 26 (3)	IGHG1 (3), IGHG3 (1)	4.5, 2.2	6.2, 5.4
4	3554	IGHV3-21, IGKV1-39	17, 9		Non-base binder (4)	291 (4)	Week 10 (2), Week 26 (2)	IGHG1 (4)	2.6, 1.4	2.8, 2.9
4	4774	IGHV3-23, IGKV3-15	16, 9		Non-base binder (4)	953 (4)	Week 10 (2), Week 26 (2)	IGHG1 (4)	3.6, 1.6	5.9, 1.8
4	4843	IGHV3-23, IGKV3-20	14, 8	FH_302_10	Base binder (1), Non-base binder (3)	485 (4)	Week 10 (3), Week 26 (1)	IGHG1 (4)	4.2, 2.1	6.2, 2.5
4	7192	IGHV1-69, IGKV4-1	23, 9	FH_302_11	Base binder (4)	325 (4)	Week 10 (1), Week 26 (3)	IGHG1 (4)	3.7, 2.4	5, 3
4	8252	IGHV1-69, IGKV3-20	19, 11	FH_302_13	Base binder (1), Non-base binder (3)	618 (4)	Week 10 (4)	IGHG1 (4)	1.7, 1.2	2.4, 2.1
4	8496	IGHV1-69, IGLV1-40	17, 10	FH_302_9	Base binder (4)	177 (4)	Week 10 (1), Week 26 (3)	IGHG1 (4)	5.7, 2.3	8.3, 3.5