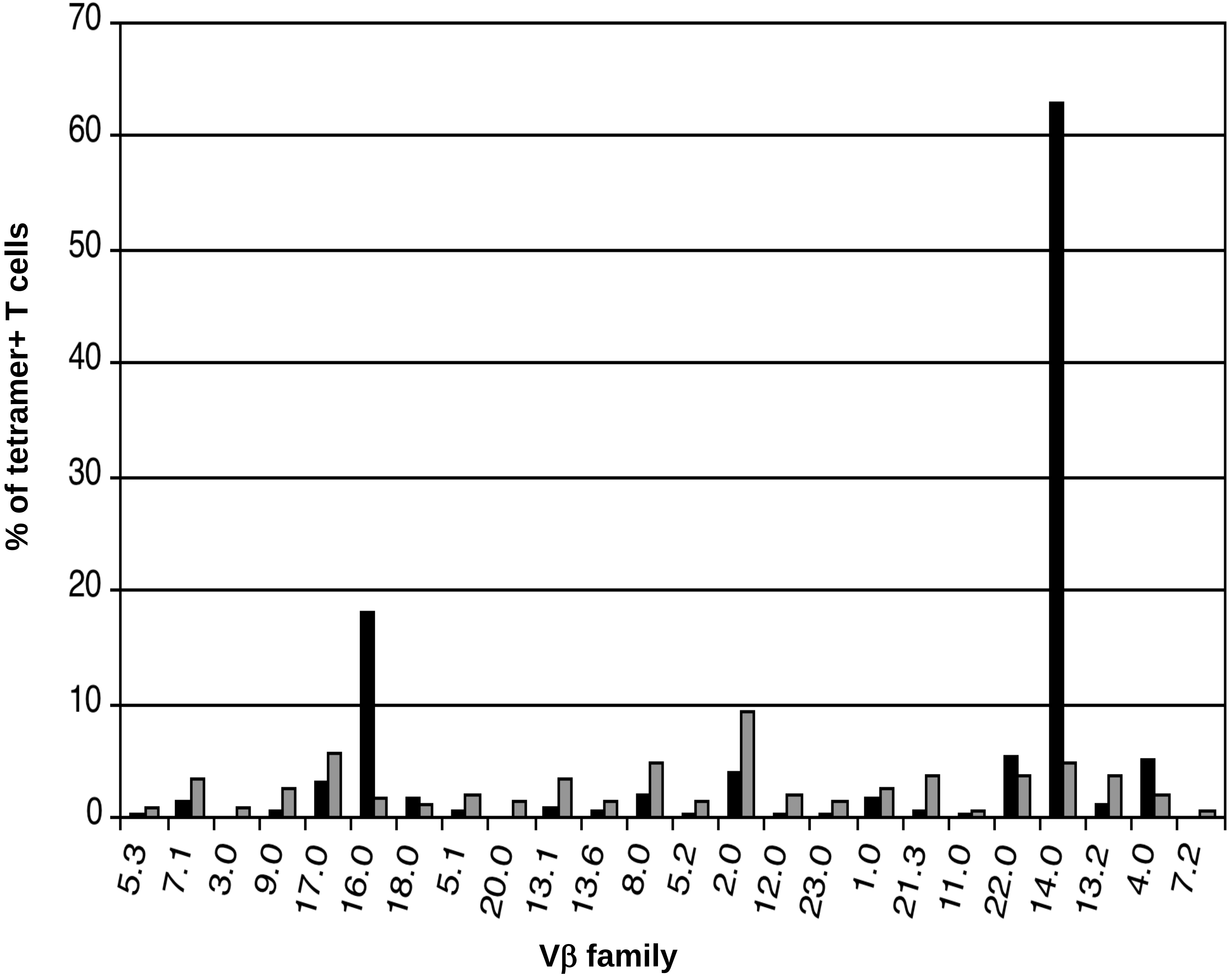
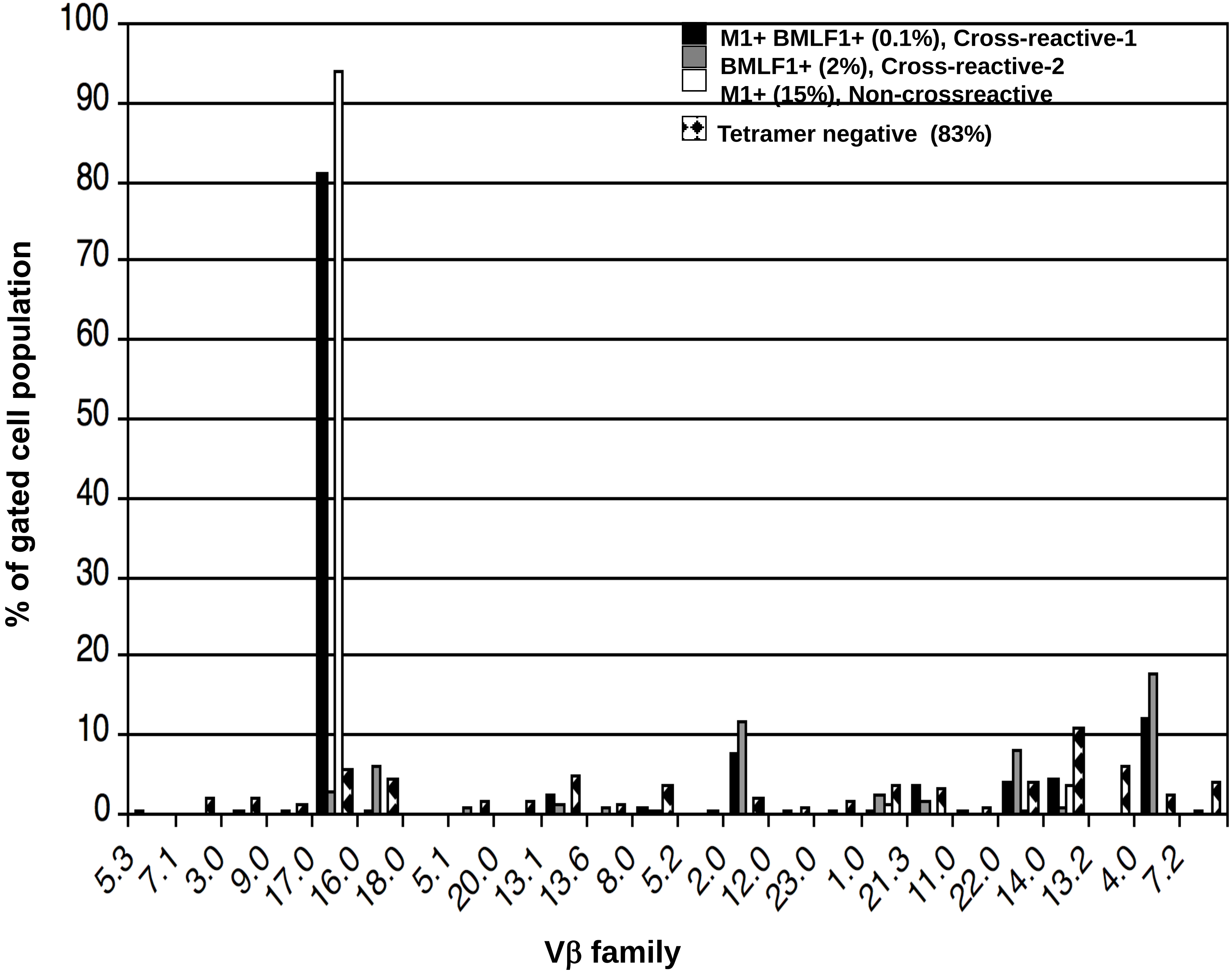
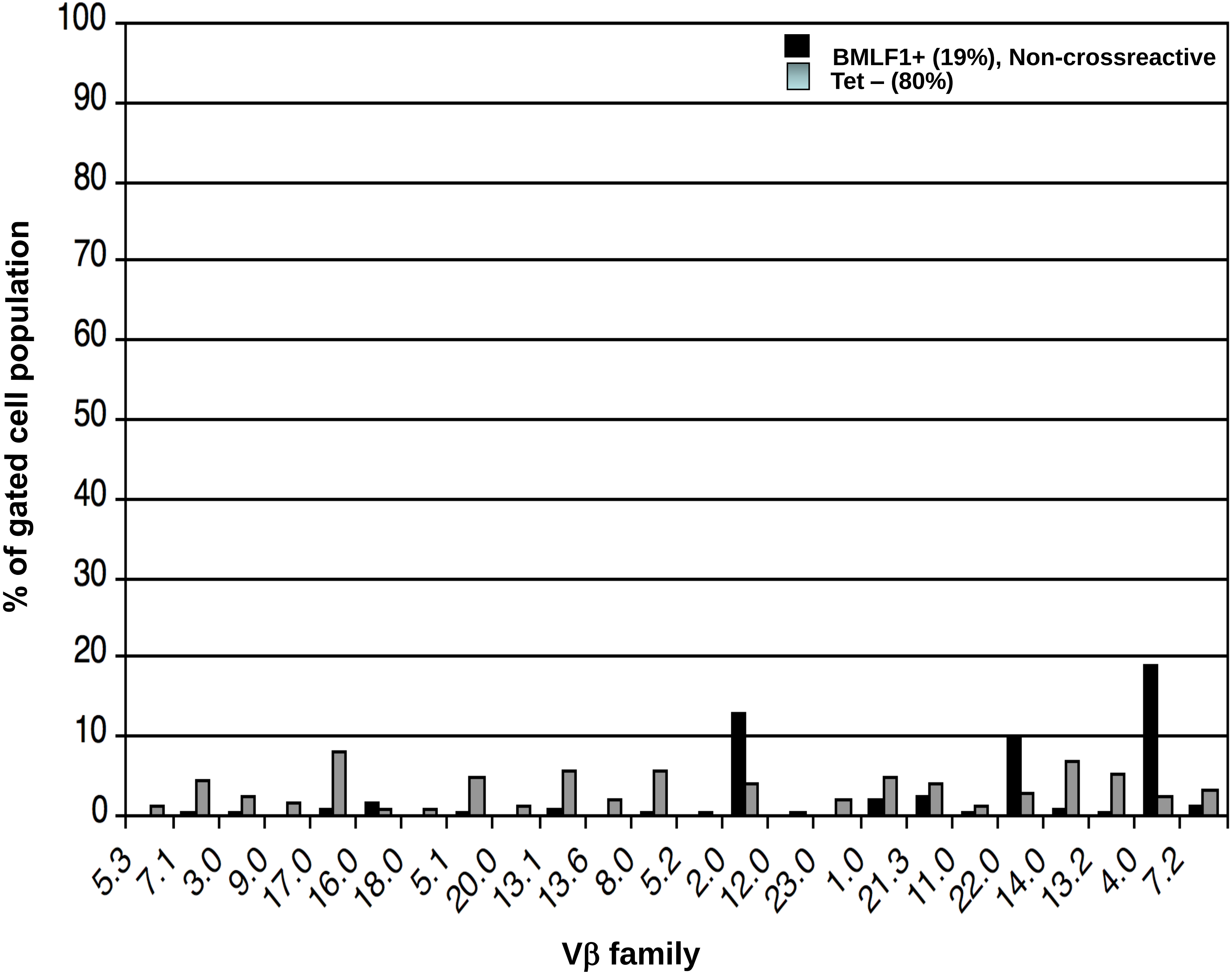
Supplemental Figure 1



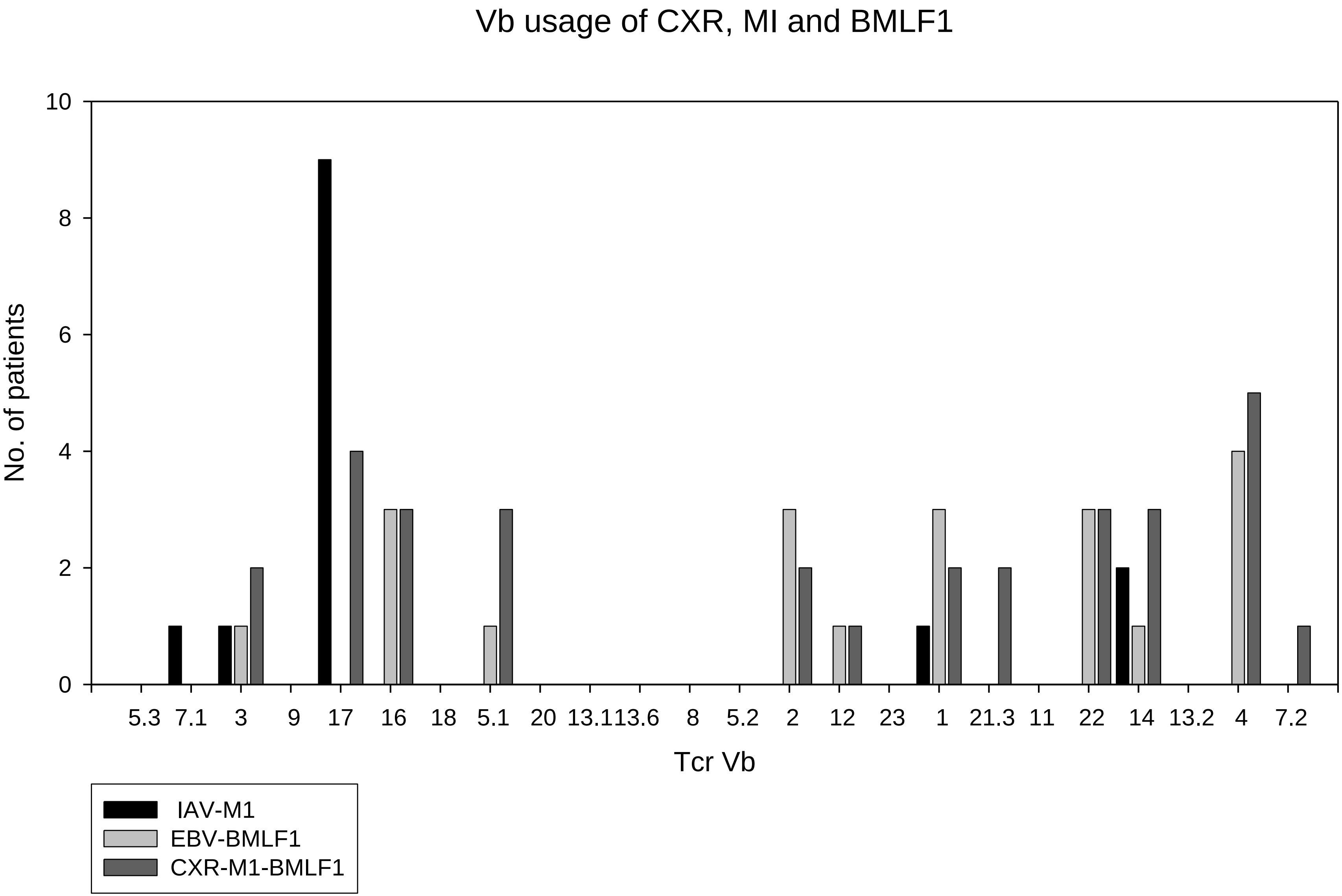
Supplemental Figure 2A



Supplemental Figure 2B



Supplemental Figure 3



Supplemental Table 1.

Full sequences of the CDR3 of Vβ and Vα clonotypes

Figure 2:

A. Donor D-002 ex vivo BMLF1+ sequences.

*Vβ	Jβ	Clonotype ID	Frequency	aa sequence CDR3β loop	**Length (aa)	Nucleotide sequence of V/N/D/N/J region
14	1.1	B14.1	42	AS-GRTNTEA-FF	7	gccagcggtcggacgaacactgaagctttcttt
		Total unique clonotypes:	*1*			
		Total sequences analyzed:	*42*			
16	2.5	B16.2	19	AS-SQSPGGTQ-YF	8	gccagcagccagagtccagggggggacccagtacttc
	2.5	B16.86	11	AS-SQSPGGTQ-YF	8	gccagcagccaaagcccagggggggacccagtacttc
	2.5	B16.85	7	AS-SQSPGATQ-YF	8	gccagcagccaaagtccgggagcgacccagtacttc
	2.5	B16.4	3	AS-SQSPGGTQ-YF	8	gccagcagccagtcccccggcgggacccagtacttc
	2.5	B16.5	1	AS-SQTPGGTQ-YF	8	gccagcagccagacccccgggggggacccagtacttc
	2.5	B16.6	1	AS-SQSPGGTQ-YF	8	gccagcagccaatctcctggggggacccagtacttc
	1.2	B16.3	1	AS-SQSPGGLE-TF	8	gccagcagccaatctccggggggcctcgagaccttc
	2.1	B16.1	1	AS-SQSPGGQQ-FF	8	gccagcagccaatccccggggggtcagcagttcttc
	2.4	B16.7	1	AS-SQSPGGIQ-YF	8	gccagcagccaatcgcccggcgggattcagtacttc
		Total unique clonotypes:	*9*			
		Total sequences analyzed:	*45*			
17	2.7	B17.1	36	AS-SIDGTAYEQ-YF	9	gccagtagtatagacgggacagcctacgagcagtacttc
	2.1	B17.12	1	AS-SIDRGLINEQ-FF	10	gccagtagtatagatagaggacttatcaatgagcagttcttc
		Total unique clonotypes:	*2*			
		Total sequences analyzed:	*37*			
18	2.7	B18.1	38	AS-SPPAESYEQ-YF	9	gccagctcaccaccggccgagagctacgagcagtacttc
		Total unique clonotypes:	*1*			
		Total sequences analyzed:	*38*			
22	2.2	B22.1	17	AS-SDGKLAPGEL-FF	10	gccagcagcgacggaaaactagcccccggggagctgtttttt
	2.1	B22.4	12	AS-SDGELLPNEQ-FF	10	gccagcagtgacggtgaactcctacccaatgagcagttcttt
	2.2	B22.2	7	AS-SEGQVAPGEL-FF	10	gccagcagtgaaggtcaggtggcccccggggagctgtttttt
	2.2	B22.5	2	AS-SAGEVFPGEL-FF	10	gccagcagtgcaggggaagtttttcccggggagctgtttttt
	2.2	B22.6	1	AS-SDGRVAPGEL-FF	10	gccagcagtgacggcagggtagctcccggggagctgtttttt
		Total unique clonotypes:	*5*			
		Total sequences analyzed:	*39*			

B. Donor D-002 in vitro BMLF1+ sequences.

*Vβ	Jβ	Clonotype ID	Frequency	aa sequence CDR3β loop	**Length (aa)	Nucleotide sequence of V/N/D/N/J region
14	1.1	B14.1	10	AS-GRTNTEA-FF	7	gccagcggtcggacgaacactgaagctttcttt
		Total unique clonotypes:	*1*			
		Total sequences analyzed:	*10*			
16	2.1	B16.1	7	AS-S QSPG GQQ-FF	8	gccagcagccaatccccggggggtcagcagttcttc
	2.5	B16.2	3	AS-S QSPG GTQ-YF	8	gccagcagccagagtccagggggggacccagtacttc
	1.2	B16.3	1	AS-S QSPG GLE-TF	8	gccagcagccaatctccggggggcctcgagaccttc
		Total unique clonotypes:	*3*			
		Total sequences analyzed:	*11*			
17	2.7	B17.1	88	AS-SIDGTAYEQ-YF	9	gccagtagtatagacgggacagcctacgagcagtacttc
	2.1	B17.9	6	AS-SIMGGNYEQ-YF	9	gccagtagtataatgggggggcaataatgagcagttcttc
	2.7	B17.2	1	AS-SIDGTAYEQ-YF	9	gccagtagtatcgacgggacagcctacgagcagtacttc
	2.7	B17.3	1	AS-SIDGTAYEQ-YF	9	gccagtagtatagatgggacagcctacgagcagtacttc
	2.7	B17.4	1	AS-SIDGTAYEQ-YF	9	gccagtagtatagacgggacggcctacgagcagtacttc
	2.7	B17.5	1	AS-SVDGTAYEQ-YF	9	gccagtagtgtagacgggacagcctacgagcagtacttc
	2.7	B17.6	1	AS-SIDGAAYEQ-YF	9	gccagtagtatagacggggcagcctacgagcagtacttc
	2.7	B17.8	1	AS-SINGTAYEQ-YF	9	gccagtagtataaacgggacagcctacgagcagtacttc
	1.3	B17.10	1	AS-SQSDSGYEQ-YF	9	gccagtagtcagtccgactctggaaacaccatatatttt
	1.2	B17.11	1	AS-SSGTARYEQ-YF	9	gccagtagttccgggacagcccgctatggctacaccttc
	2.7	B17.12	1	AS-SISGTGYEQ-YF	9	gccagtagtatctccgggacagggcctacgagcagtacttc
	2.7	B17.7	2	AS-SIPRTGTAYEQ-YF	11	gccagtagtattcctcggacagggacagcctacgagcagtacttc
		Total unique clonotypes:	*12*			
		Total sequences analyzed:	*105*			
18	2.7	B18.1	14	AS-SPPAESYEQ-YF	9	gccagctcaccaccggccgagagctacgagcagtacttc
		Total unique clonotypes:	*1*			
		Total sequences analyzed:	*14*			
22	2.2	B22.1	9	AS-SDGKLAPGEL-FF	10	gccagcagcgacggaaaactagcccccggggagctgtttttt
	2.2	B22.2	8	AS-SEGQVAPGEL-FF	10	gccagcagtgaaggtcaggtggcccccggggagctgtttttt
	1.2	B22.3	2	AS-NEGAGFNYGY-TF	10	gccagcaacgaaggggccggatttaactatggctacaccttc
	2.1	B22.4	1	AS-SDGELLPNEQ-FF	10	gccagcagtgacggtgaactcctacccaatgagcagttcttc
		Total unique clonotypes:	*4*			
		Total sequences analyzed:	*20*			

Figure 5:

A. Donor D-002 cross-reactive sequences in an M1-specific T cell line.

*Vβ	Jβ	Clonotype ID	Frequency	aa sequence CDR3β loop	**Length (aa)	Nucleotide sequence of V/N/D/N/J region
14	1.1	B14.1	16	AS-GRTNTEA-FF	7	gccagcggtcggacgaacactgaagctttcttt
	2.1	14.6	4	AS-SSGSSGYYNEQ-FF	11	gccagcagttccgggtcctcgggttactacaatgagcagttcttc
	2.1	14.15	1	AS-SLGTSGSYNEQ-FF	11	gccagcagtttaggtactagcgggagttacaatgagcagttcttc
	1.1	14.24	1	AS-GRTNIEA-FF	7	gccagcggtcggacgaacattgaagctttcttt
	2.1	14.28	1	AS-SFGTSPYNEQ-FF	10	gccagcagtttcgggactagtccctacaatgagcagttcttc
		Total unique clonotypes:	*5*			
		Total sequences analyzed:	*23*			
17	2.7	17.3	4	AS-SIRSSYEQ-YF	8	gccagtagtataaggagctcctacgagcagtacttc
		17.27	3	AS-SIDGTAYEQ-YF	9	gccagtagtatagacgggacagcctacgagcagtacttc
		17.13	2	AS-SIRSSYEQ-YF	8	gccagtagtatacggtcgtcttacgagcagtacttc
		17.16	2	AS-SVRSSYEQ-YF	8	gccagtagtgttagaagctcctacgagcagtacttc
		17.26	2	AS-STRSSYEQ-YF	8	gccagtagtacgcgaagctcctacgagcagtacttc
		17.21	2	AS-SMRSAYEQ-YF	8	gccagtagtatgcggagcgcctacgagcagtacttc
		17.6	1	AS-SIRSSYEQ-YF	8	gccagtagtatacgaagctcctacgagcagtacttc
		17.12	1	AS-S IRSS YEQ-YF	8	gccagtagtatccgaagctcctacgagcagtacttc
		17.20	1	AS-SIRSSYEQ-YF	8	gccagtagtattcgaagtagttacgagcagtacttc
		17.5	1	AS-SIRSSYEQ-YF	8	gccagtagtataaggtcttcctacgagcagtacttc
		17.28	1	AS-SIRSSYEQ-YF	8	gccagtagtattaggagttcctacgagcagtacttc
		17.32	1	AS-SIRSSYEQ-YF	8	gccagtagtattcgttcctcctacgagcagtacttc
		17.36	1	AS-SIRSSYEQ-YF	8	gccagtagtattagaagctcctacgagcagtacttc
		17.39	1	AS-SIRSSYEQ-YF	8	gccagtagtattcggtcatcctacgagcagtacttc
		17.49	1	AS-SIRSSYEQ-YF	8	gccagtagtatacgtagctcctacgagcagtacttc
		17.57	1	AS-SIRSSYEQ-YF	8	gccagtagtatcaggagttcctacgagcagtacttc
		17.62	1	AS-SIRSSYEQ-YF	8	gccagtagtatcaggagctcctacgagcagtacttc
		17.8	1	AS-SVRSSYEQ-YF	8	gccagtagtgtcagaagctcctacgagcagtacttc
		17.30	1	AS-SVRSSYEQ-YF	8	gccagtagtgtcaggagctcctacgagcagtacttc
		17.37	1	AS-SVRSSYEQ-XF	8	gccagtagtgtacggagctcctacgagcagtanttc
		17.38	1	AS-SVRSSYEQ-YF	8	gccagtagtgttaggtcctcctacgagcagtacttc
		17.43	1	AS-SVRSSYEQ-YF	8	gccagtagtgtacgtagctcctacgagcagtacttc
		17.54	1	AS-STRSSYEQ-YF	8	gccagtagtacacgatcttcctacgagcagtacttc
		17.64	1	AS-SLRSSYEQ-YF	8	gccagtagtttgagaagctcctacgagcagtacttc
		17.11	1	AS-SMRSSYEQ-YF	8	gccagtagtatgaggagctcctacgagcagtacttc
		17.19	1	AS-SSRSSYEQ-YF	8	gccagtagtagtcggagctcctacgagcagtacttc
		17.56	1	AS-SSRSAYEQ-YF	8	gccagtagttctcgatccgcctacgagcagtacttc
		17.40	1	AS-SMRAAYEQ-YF	8	gccagtagtatgcgggcagcctacgagcagtacttc

Supplemental Table 1 continued

	2.3	17.2	2	AS-SKRSTDTQ-YF	8	gccagtagcaaaaggagcacagatacgcagtatttt
		17.15	2	AS-SQRSTDTQ-YF	8	gccagtagtcagagaagcacagatacgcagtatttt
		17.10	1	AS-SPRSTDTQ-YF	8	gccagtagtccccggagcacagatacgcagtatttt
		17.29	1	AS-SPRSTDTQ-YF	8	gccagtagtccccggtccacagatacgcagtatttt
		17.24	1	AG-SGRSTDTQ-YF	8	gccggtagcggacggagcacagatacgcagtatttt
		17.55	1	AS-SGRSTDTQ-YF	8	gccagtagcgggagaagcacagatacgcagtatttt
		17.50	1	AS-STRSSDTQ-YF	8	gccagtagtacccgatcgtcagatacgcagtatttt
		17.60	1	AS-SIRSADTQ-YF	8	gccagtagtataaggtcggcggatacgcagtatttt
		17.33	1	AS-SIRPADTQ-YF	8	gccagtagtataaggccggcggatacgcagtatttt
	2.1	17.41	2	AS-SALAGPTYNEQ-FF	11	gccagttccgcgctagcgggaccaacctacaatgagcagttcttc
		17.31	1	AS-SIGTGEQ-FF	7	gccagtagtatcggtacaggggagcagttcttc
		17.65	1	AS-S IETTSGSSYNEQ-FF	13	gccagtagtatcgagacgactagcggaagctcctacaatgagcagttcttc
	1.2	17.48	2	AS-S IGIYGY-TF	7	gccagtagtatcgggatctatggctacaccttcggttcg
		17.52	1	AS-SSGSYGY-TF	7	gccagtagttcgggcagttatggctacaccttcggttcg
		Total unique clonotypes:	*42*			
		Total sequences analyzed:	*55*			

B. Donor D-002 non-crossreactive M1+ sequences in an M1-specific T cell line.

***Vβ**	**Jβ**	**Clonotype ID**	**Frequency**	**aa sequence CDR3β loop**	****Length (aa)**	**Nucleotide sequence of V/N/D/N/J region**
17	2.7	43.27	6	AS-SMRSSYEQ-YF	8	gccagtagtatgaggagttcctacgagctgtacttc
		17.27	5	AS-SIRSSYEQ-YF	8	gccagtagtataagaagctcctacgagcagtacttc
		23.27	3	AS-SIRSSYEQ-YF	8	gccagtagtatccgttcgtcctacgagcagtacttc
		28.27	3	AS-SIRSSYEQ-YF	8	gccagtagtatcaggagctcctacgagcagtacttc
		6.27	2	AS-SIRSSYEQ-YF	8	gccagtagtatccgaagctcctacgagcagtacttc
		25.27	2	AS-SIRSSYEQ-YF	8	gccagtagtatacgtagctcctacgagcagtacttc
		36.27	2	AS-STRSSYEQ-YF	8	gccagtagtaccaggagctcctacgagcagtacttc
		51.27	2	AS-SVRSSYEQ-YF	8	gccagtagtgtcagaagctcctacgagcagtacttc
		72.27	2	AS-ALRSSYEQ-YF	8	gccagtagtttgagaagctcctacgagcagtacttc
		73.27	2	AS-SIRAAYEQ-YF	8	gccagtagtaccgggcagcctacgagcagtacttc
		84.27	2	AS-SIRSGYEQ-YF	8	gccagtagtattcgatcagggtacgagcagtacttc
		86.27	2	AS-SFRSAYEQ-YF	8	gccagtagctttaggagtgcctacgagcagtacttc
		1.27	1	AS-SIRSSYEQ-YF	8	gccagtagtattaggagctcctacgagcagtacttc
		3.27	1	AS-SIRSSYEQ-YF	8	gccagtagtatcagaagctcctacgagcagtacttc
		19.27	1	AS-SIRSSYEQ-YF	8	gccagtagtattcggagctcctacgagcagtacttc
		22.27	1	AS-SIRSSYEQ-YF	8	gccagtagtattcgttcgtcctacgagcagtacttc
		29.27	1	AS-SIRSSYEQ-YF	8	gccagtagtatacggagctcctacgagcagtacttc
		35.27	1	AS-STRSSYEQ-YF	8	gccagtagtacgcgaagctcctacgagcagtacttc
		38.27	1	AS-STRSSYEQ-YF	8	gccagtagtaccaggtcttcctacgagcagtacttc
		39.27	1	AS-STRSSYER-YF	8	gccagtagtactaggagctcctacgagcagtacttc
		40.27	1	AS-STRSSYER-YF	8	gccagtagtacacgatcttcctacgagcagtacttc
		41.27	1	AS-STRSSYER-YF	8	gccagtagtaccaggagctcctacgagcagtacttc
		49.27	1	AS-SVRSSYEQ-YF	8	gccagtagtgttcggagctcctacgagcagtacttc
		59.27	1	AS-SSRSAYEQ-YF	8	gccagtagttccaggtccgcctacgagcagtacttc
		60.27	1	AS-SSRSAYEQ-YF	8	gccagtagttctcgatccgcctacgagcagtacttc
		85.27	1	AS-SMRSAYEQ-YF	8	gccagtagtatgcggagcgcctacgagcagtacttc
		91.27	1	AS-SIRSAYEQ-YF	8	gccagtagtatccgcagtgcctacgagcagtacttc
	2.3	1.23	3	AS-SGRSTDTQ-YF	8	gccagtagcgggagaagcacagatacgcagtatttt
		5.23	1	AS-SPRSGDTQ-YF	8	gccagttccccgcgcagtggggatacgcagtatttt
		10.23	1	AS-SSRSTDTQ-YF	8	gccagtagttcaagatccacagatacgcagtatttt
		16.23	1	AS-SQRSTDTQ-YF	8	gccagtagtcagagaagcacagatacgcagtatttt
		18.23	1	AS-SQRSTDTQ-YF	8	gccagttccgggaggagcacagatacgcagtatttt
		19.23	1	AS-SQRSTDTQ-YF	8	gccagtagcagagaagcacagatacgcagtatttt
		25.23	1	AS-STRSSDTQ-YF	8	gccagtagtacccgatcgtcagatacgcagtatttt
		30.23	1	AS-SIRSTDTQ-YF	8	gccagtagtataagaagcacagatacgcagtatttt
		32.23	1	AS-STRSADTQ-YF	8	gccagtagtactagaagcgcagatacgcagtatttt
		33.23	1	AS-SMRTGDTQ-YF	8	gccagtagtatgcggaccggtgatacccagtatttt
	2.1	1.21	1	AT-SGRAGVEQ-FF	8	gccacctccggccgggccggggt tgagcagttcttc
		7.21	1	AS-SYRSSNEQ-FF	8	gccagtagttacaggtcgtccaatgagcagttcttc
		2.21	2	AS-SIGTGEQ-FF	7	gccagtagtatcggtacaggggagcagttcttc
		Total unique clonotypes:	*40*			
		Total sequences analyzed:	*64*			

Figure 6.

A. Donor D-002 non-crossreactive BMLF1+ sequences in an BMLF1-specific T cell line.

***Vα**	**Jα**	**Clonotype ID**	**Frequency**	**aa sequence CDR3α loop**	****Length (aa)**	**Nucleotide sequence of V/N/D/N/J region**
15	45	B1	38	AE-RKGGADGL-TF	8	gcagagagaaaaggaggtgctgacggactcaccttt
	3	B2	5	AE-YSSASKI-IF	7	gcagagtacagcagtgcttccaagataatcttt
	37	B3	2	AE-STGKL-IF	5	gcagagtcaacaggcaaactaatcttt
	41	B47	2	AE-SKGAL-NF	5	gcagagagtaaaggcgcactcaacttc
	15	B16	1	AE-SEGTAP-IF	6	gcagagagtgaaggaactgctccgatcttt
	3	B31	1	AE-YSSAPKI-IF	7	gcagagtacagcagtgctcccaagataatcttt
	5	B38	1	AE-SRGAL-TF	5	gcagagagtcgaggagcacttactttt
		Total unique clonotypes:	*7*			
		Total sequences analyzed:	*50*			

B. Donor D-002 crossreactive sequences in an M1-specific T cell line.

***Vα**	**Jα**	**Clonotype ID**	**Frequency**	**aa sequence CDR3α loop**	****Length (aa)**	**Nucleotide sequence of V/N/D/N/J region**
15	45	B1	35	AE-RKGGADGL-TF	8	gcagagagaaaaggaggtgctgacggactcaccttt
	37	X5	5	AE-STGKL-IF	5	gcagagtcgacaggcaaactaatcttt
	13	X3	3	AE-LGYQKV-TF	6	gcagagttgggttaccagaaagttaccttt
	15	X12	3	AE-SEGTAL-IF	6	gcagagagtgaaggaactgctctgatcttt
	11	X45	2	AE-DRDSTL-TF	6	gcagaggaccgggacagcaccctcaccttt
	15	B16	1	AE-SEGTAP-IF	6	gcagagagtgaaggaactgctccgatcttt
	45	X23	1	AE-RKGGANGL-TF	8	gcagagagaaaaggaggtgctaacggactcaccttt
		Total unique clonotypes:	*7*			
		Total sequences analyzed:	*50*			

C. Donor D-002 non-crossreactive M1+ sequences in an M1-specific T cell line.

***Vα**	**Jα**	**Clonotype ID**	**Frequency**	**aa sequence CDR3α loop**	****Length (aa)**	**Nucleotide sequence of V/N/D/N/J region**
15	23	M2	19	AE-DNQGGKL-IF	7	gcagaggataaccagggaggaaagcttatcttc
	8	M1	6	AE-SPSLNTGFQKL-VF	11	gcagagagcccttccctgaacacaggctttcagaaacttgtattt
	43	M8	3	AE-SNNDM-RF	5	gcagagagtaacaatgacatgcgcttt
	42	M70	2	AE-PGSQGNL-IF	7	gcagagccgggaagccaaggaaatctcatcttt
	42	M25	1	AE-PGSQGNL-VF	7	gcagagccgggaagccaaggaaatctcgtcttt
		Total unique clonotypes:	*5*			
		Total sequences analyzed:	*31*			

Each unique clonotype is distinguished by its unique nucleotide sequence. * TCR variable (V) region nomenclature based on Arden et al., ** CDR3 loop length according to Chothia et al. shown flanked by two framework regions.