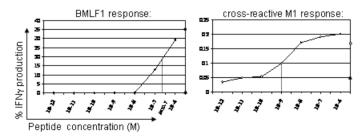
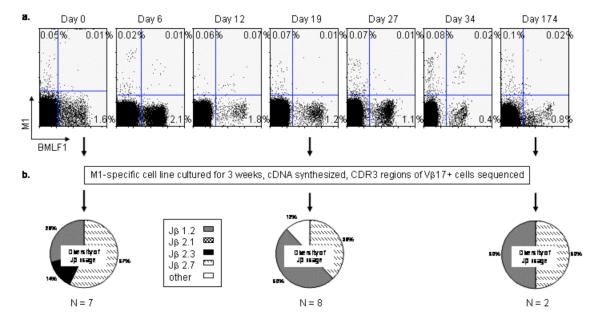
(EBV) BMLF1-stimulated T cell line



Supplementary Figure 1

A BMLF1-specific T cell line demonstrates a difference in avidity for the BMLF1 versus the M1 peptide. A preserved T cell line derived from healthy donor D-002 had been cultured for 4 weeks in the presence of BMLF1 peptide-pulsed T2 cells and was used in a standard intracellular IFNγ assay that included a titration of peptide concentrations. (▲ tyrosinase, O M1, ◆ BMLF1 stimulation)



Supplementary Figure 2

Acute EBV infection selectively expands cross-reactive M1-specific memory cells that can recognize BMLF1. CD8 T cells were isolated ex vivo from patient E1178 at various time points post-presentation with symptoms of acute infectious mononucleosis. (a) The percentages of CD8 T cells staining positive when co-stained with M1- and BMLF1-loaded tetramers are shown. The number of events shown is variable because the maximum number possible was collected for each sample. (b) CD8 T cells isolated at days 0, 19 and 174 were cultured for 3 weeks in the presence of M1 peptide-pulsed T2 cells. Following the RNA isolation and cDNA synthesis of those T cell lines, the CDR3\$ region of V\$17+ sub-clones was sequenced. The pie charts illustrate the percentage of unique V\$17+ sub-clones using each J\$ family, where N = the total number of unique sub-clones. The complete CDR3 sequences of all the sub-clones analyzed are displayed in Supplementary Table 1, structured according to Chothia et al. (57).

Supplementary Table 1

A.	IM patient: E1101						B. IM patient: E1178						
M1 line		i ido i	Freq:			Nucleotide sequence of the V/N/D/N/J junction:	M1 line	¹ Length					Nucleotide sequence of the V/N/D/N/J junction;
Day 22	7 AA	H2.1 H2.2	1	1.2	AS-SIGLYGY-TF AS-SIGYYGY-TF	gccagtagtattggtctctatggctacaccttc gccagtagtatcgggtactatggctacaccttc	Day 0	7 AA	v1mi v1mi				gccagtagtatagggagctatggctacaccttc gccagtagtataggtgtctatggctacaccttc
		H2.3	1	1.2	AS-STGVYGY-TF	gccagtagtaccggtgtctatggctacaccttc		8 AA	v1m	2 5	2.7	AS-SIRSSYEQ-YF	gocagtagtataaggagotoctacgagcagtacttc
	8 AA	H4.3 H4.10	7	1.2	AS-S MGS YGY-TF AS-SI R SGNTI-YF	gccagtagtatgggttcctatggctacaccttc gccagtagtattcgttccggaaacaccatatatttt			v1m		2.7	7 AS-S TRS SYEQ-YF B AS-SI R STDTQ-YF	gccagtagtaccaggagctcctacgagcagtacttc gccagtagtaccaggagcacagatacgcagtatttt
	OAN	H2.6	4	2.1	AS-STRAGVEQ-FF	gccagtagtacacgggcgggggttgagcagttcttc			v1m1	11 1	2.7	AS-SI RS SYEQ-YF	gocagtagtataaggagctoctacgagcagtacttc
		H4.24 H2.10	2	2.3	AS-S GRSA DTQ-YF AS-S RR STDTQ-YF	gccagtagcggacggagcgcagatacgcagtatttt gccagtagtcgacggagcacagatacgcagtatttt	Day 19	7.00	v1m1 v4m		2.7	AS-SIRSSYEQ-YF AS-SIGVYGY-TF	gocagtagtatcogcagttoctacgagcagtacttc gocagtagtataggggtctatggctacaccttc
		H2.4	1	1.6	AS-SI G YNSPL-HF	gocagtagtatoggctataattcacccctccacttt	Day 15	1.77	v4m	1 1	1.2	AS-SIGSYGY-TF	gccagtagtattgggagttatggctacaccttc
		H2.5	1	2.1	AS-SI RSGY EQ-FF AS-S AGLAS EQ-FF	gccagtagtataagatctgggtatgagcagttcttc gccagtagtgccggacttgctagtgagcagttcttc			v4m2		1.2		gccagtagtattgggagctatggctacaccttc gccagtagtattgggtgttatggctacaccttc
		H2.8	1	2.3	AS-SIRSTDTQ-YF	gccagtagtatacggagcacagatacgcagtatttt		8 AA	v4mi				gocagtagtatocgttocgcotagagcagtacttc
		H5.19	1	2.3	AS-SI R STDTQ-YF AS-S GR STDTQ-YF	gccagtagtataaggagcacagatacgcagtatttt		0.44	v4m				gocagtagtataagaagotootacgagcagtacttc
		H2.9 H2.11	1	2.5	AS-S NRAG ETQ-YF	gocagtaggggggggggggggggggggggggggggggggg		9 AA	v4m v4m		1.1		gccagtagtataactagcggggggcaactgaagcagtacttc gccagtagtctcggcagggtgcacactgaagctttcttt
		H2.12	1	2.7	AS-SI RSST EQ-YV	gccagtagtattaggtctagcaccgagcagtacgtc	Day 174	7 AA	v7mi	2 10	0 1.2	AS-SI GI YGY-TF	gccagtagtatcgggatctatggctacaccttc
	9 AA	H2.13 H2.14	1	2.7	AS-S VRSAYT Q-YF AS-S PR SGANVL-TF	gccagtagtgtccggagtgcttatacgcagtatttt gccagtagtccccgttctggggccaacgtcctgacttc		8 AA	v7m	11 9	2.7	7 AS-S TRS SYEQ-YF	gocagtagtacgaggagctoctacgagcagtacttc
		H2.15	1	2.3	SS-S SRSGE DTQ-YF	tocagtagtagccgatcgggagagaggatacgcagtatttt							
Day 165	11 AA 7 AA	H2.16 H4.1	6	12	AS-SIVMGSSYNEQ-FF AS-SIGSYGY-TF	gccagtagtatagtaatggggagctcctacaatgagcagttcttc gccagtagtatcggatcgtacggctacaccttc	1						
Day 100	,,,,	H4.3	5	1.2	AS-SMGSYGY-TF	gccagtagtatgggttcctatggctacaccttc							
		H4.2 H4.4	1	1.2	AS-SI GSN GY-TF AS-S MGS YGY-TF	gccagtagtateggategaaeggetacaeette gccagtagtateggategaaeggetacaeette							
		H4.5	1	1.2	AS-SI GLH GY-TF	gccagtagtataggccttcatggctacaccttc							
		H4.6 H4.7	1	1.2	AS-SIGIHGY-TF	gocagtagtatagggatccacggctacaccttc							
		H4.7 H4.8	1	1.2	AS-SI GVH GY-TF AS-S TGL YGY-TF	gocagtagtateggggteeatggetaeacette gocagtagtaeeggettatatggetaeaeette							
		H4.9	1	1.2	AS-STGVYGY-TF	gocagtagcacaggggtttatggctacacettc							
	8 AA	H4.13 H4.10	9	2.3	AS-SI RSG DTQ-YF AS-SI R SGNTI-YF	gccagtagtattacggagtggagatacgcagtatttt gccagtagtattcgttccggaaacaccatatatttt							
		H4.19	4	2.3	AS-SPRSTDTQ-YF	gccagtaqtccacqqaqcacaqatacqcaqtatttt							
		H4.11 H4.21	2	2.1	AS-S TFHS NEQ-FF AS-S QR STDTQ-YF	gocagtagtacettecacagcaatgagcagttette gccagtagccaaaagatecacagatacgcagtatttt							
		H4.12	1	2.1	AS-SILVSHNEQ-FF	gocagtagtotagtatcccacaatgagcagttottc							
		H4.20 H4.17	1	2.3	AS-S TR STDTQ-YI AS-S MR STDTQ-YF	gccagtagtactaggagcacagatacgcngtatntn gccagtagtatggagcacagatacgcagtatttt							
		H4.17	1	2.3	AS-SMRSTDTQ-YF	gccagtagtatgcggagcacagatacgcagtatttt							
		H4.14	1	2.3	AS-SI R STDTQ-YF	gocagtagtatcaggagcacagatacgcagtatttt							
		H4.16 H4.15	1	2.3	AS-S GR STDTQ-YF AS-S GR STDTQ-YF	gccagtagcggggggagcacagatacgcagtatttt gccagtagtggccggagcacagatacgcagtatttt							
		H4.22	1	2.3	AS-SLRSTDTQ-YF	gocagtagoctaagatocacagatacgcagtatttt							
		H4.23 H4.24	1	2.3	AS-SI V STDTQ-YF AS-S GRSA DTQ-YF	gccagtagtatagtcagcacagatacgcagtatttt gccagtagcggacgcagatacgcagtatttt							
		H4.25	1	2.3	AS-S VRSAY TQ-YF	gccagtagtgtccggagtgcttatacgcagtatttt							
		H4.26 H4.27	1	2.5	AS-S GRAS ETQ-YF AS-S MRSG ETQ-YF	gccagtaggggggggggagacccagtacttc gccagtagtatgcgatcggggggagacccagtacttc							
		H4.28	1	2.7	AS-SIRSSYEQ-YF	gocagtagtattaggagctoctacgagcagtacttc							
	9 AA	H4.29 H4.30	2	1.5	AS-SI FSGD QPQ-HF AS-S TVGG INFQ-FF	gccagtagtattttctcaggggaccagcccagcatttt							
		H4.31	1	2.4	AI-LRGSGVHIQ-YF	gccagtagtaggggggggggggggggggggggggggggg							
	10 AA	H4.32 H4.33	1	2.1	AS-SI GASD YNEQ-FF AS-S QGGNF YNEQ-FF	gccagtagtataggggctagcgactacaatgagcagttcttc gccagtagccagggggtaatttttacaatgagcagttcttc							
	11 AA	H4.33	1	2.1	AS-SIVGGRWGNEQ-FF	gocagtagtcaggggggaaggtgggggaatgagcagttcttc							
Day 349		H4.35	1	2.2	AS-SI EPSR NTGEL-FF	gccagtagtatagagcctagtcgaaacaccggggagctgtttttt	1						
Day 349	6 AA 7 AA	5.1 4.6	2	2.1 1.2	AS-SI WD EQ-FF AS-SI GIH GY-TF	gccagtagtatatgggatgaccagttcttc gccagtagtatagggatccacggctacaccttc							
		4.1	2	1.2	AS-SI GS YGY-TF AS-S MGS YGY-TF	gocagtagtatoggatogtacggotacaccttc							
		4.3 5.30	1	1.2	AS-SMGSYGY-TF AS-GMGSYGY-TF	gccagtagtatgggttcctatggctacaccttc gccagtggtatgggatcctatggctacaccttc							
		5.2	1	1.2	AS-SIGLYGY-TF	gocagtagtatoggoctotatggotacacotto							
		5.3 4.8	1	1.2	AS-SI GL YGY-TF AS-S TGL YGY-TF	gccagtagtatogggctctatggctacaccttc gccagtagtaccggcttatatggctacaccttc							
		5.4	1	1.2	AS-SIGSYGY-TF	gccagtagtataggctcttatggctacaccttc							
	8 AA	4.10 5.9	9	1.3	AS-SI R SGNTI-YF AS-S VRS SYEQ-YF	gccagtagtattcgttccggaaacaccatatatttt gccagtagtgtacggagctcctacgagcagtacttc							
		5.19	5	2.3	AS-SIRSTDTQ-YF	gccagtagtataaggagcacagatacgcagtatttt							
		4.28 4.24	4	2.7	AS-SIRSSYEQ-YF AS-SGRSADTQ-YF	gccagtagtattaggagctcctacgagcagtacttc gccagtagcggacggagcagatacgcagtatttt							
		5.11	2	1.5	AS-SIRSNQPQ-HF	gccagtagtattcgctctaatcagccccagcatttt							
		4.13 5.9	2	2.3	AS-SI RSG DTQ-YF AS-SI RS SYEQ-YF	gccagtagtatacggagtggagatacgcagtatttt gccagtagtattaggagctcctacgagcagtatttc							
		5.5	1	1.3	AS-SIRSGNTI-YF	gocagtagtattogttooggaaacaccatatatttt							
		5.6 5.20	1	1.6	AS-SIRSSNPL-HF AS-SIMSLDEQ-FF	gccagtagtattaggtcgtcgaatcccctccacttt gccagtagtataatgagcttggatgagcagttcttc							
		5.17	1	2.2	AS-SIRSTGEL-FF	gocagtagtatacggagcaccggggagctgttttt							
		4.25	1	2.3	AS-SVRSAYTQ-YF	gocagtagtgtccggagtgcttatacgcagtatttt							
		5.14 5.15	1	2.3	AS-S GR STDTQ-YF AS-S TR STDTQ-YF	gccagtagtggtagaagcacagatacgcagtatttt gccagtagtacccgtagcacagatacgcagtatttt							
		5.16	1	2.3	AS-STRSTDTQ-YF	gocagtagtactaggtccacagatacgcagtatttt							
		4.19 5.18	1	2.3	AS-S PR STDTQ-YF AS-SI R STDTQ-YF	gccagtagtccacggagcacagatacgcagtatttt gccagtagtattcggagcacagatacgcagtatttt							
		4.21	1	2.3	AS-SQRSTDTQ-YF	gocagtagocaaagatocacagatacgcagtatttt							
		4.27 4.26	1	2.5	AS-S MRSG ETQ-YF AS-S GRAS ETQ-YF	gccagtagtatgcgatcgggggggagacccagtacttc gccagtagcgggagggcctcagagacccagtacttc							
		5.7	i	2.7	AS-SIRSSYEQ-YF	gccagtagtattaggagctcctacgggcagtacttc							
		5.8 5.12	1	2.7	AS-SI RS SYEQ-YF AS-SI RA SYEQ-YV	gocagtagtatocgaagctoctacgggcagtacttc gocagtagtatocgggcttcatacgagcagtacgtc	l						
	9 AA	5.21	2	1.1	AS-S ATIG NTEA-FF	gccagtagtgcgacgattgggaacactgaagctttcttt	l						
		4.30 5.24	2	2.1	AS-S TVGGI NEQ-FF AS-SI R SGNTK-YL	gccagtagtacggtgggtggaatcaatgagcagttcttc gccagtagtattcgttccggaaacaccanatatttgga							
		5.22	1	2.1	AS-SSSTSNEQ-FF	gocagtagtagcagtacctcctacaatgagcagttcttc	l						
	40.47	5.23	1	2.2	AS-S ARASL GEL-FF	gocagtagtgocaggggaggotgggggggggggggggggg	l						
	10 AA	5.27 4.33	1	1.1	AS-SI HGGG NTEA-FF AS-S QGGNF YNEQ-FF	gccagtagtatocacggaggtggaaacactgaagctttcttt gccagtagccaggggggaaatttttacaatgagcagttcttc							
		5.25	1	2.2	AS-RVLAGPAGEL-FF	gccagtagggttctagcgggccggccgggagctgttttt	l						
	12 AA	5.26 5.28	1	2.3	AS-SI TRL STDTQ-YF AS-S RLAGDAW YNEQ-FF	gccagtagtataacccgattaagcacagatacgcagtatttt gccagtagtagactagcgggagatgcctggtacaatgagcagttcttc	l						
	13 AA	5.29	2	2.5	AS-SISPSVFREEETQ-YF	gccagtagtattagcccatcggtcttccgcgaggaagagacccagtacttc							

¹ Length of CDR3β loop according to Chothia et al., shown supported by 2 flanking framework regions 2 Each donotype is distinguished by a unique nucleotide sequence at the V/NVD/NVJ

All of the V β 17+ sub-clones analyzed in this study are shown. ^{1,2} Each sub-clone is distinguished by the unique nucleotide sequence of the CDR3 loop of the TCR β -chain with length according to Chothia et al. (57). ³ Bolded residues represent the N/D/N region of the CDR3 β loop.