## Supporting Information:

Number of Patients	Susceptibility	Reference
HLA-A*01		
934 (278 EBV+)	Increased incidence of	[1]
516 (192 EBV+)	Increased incidence of	[2]
	EBV <sup>+</sup> cHL	
338 (78 EBV+ of 311	Increased incidence of	[3]
tested)	EBV <sup>+</sup> cHL	
HLA-A*02		
934 (278 EBV+)	Decreased incidence of	[1]
	EBV <sup>+</sup> cHL	
516 (192 EBV+)	Decreased incidence of	[2]
	EBV <sup>+</sup> cHL	
338 (78 EBV+ of 311	Decreased incidence of	[3]
tested)	EBV <sup>+</sup> cHL	
HLA-B*37		
338 (78 EBV+ of 311	Increased incidence of	[3]
tested)	EBV <sup>+</sup> cHL	

Table S1. Previously published HLA-class I associations with EBV<sup>+</sup>cHL.

 Table S2. LMP2A overlapping peptide pools.

Italics denotes a predicted epitope, bold a defined epitope.

MGSLEMVPMGAGPPSPGGTQDQSLYLGLQHDGNDLLLAAVASSYAAAQRKLPMGAGPPSPGGDPDGYDYLGLQHDGNDGLPPPPYSSYAAAQRKLLTPVTVLSPGGDPDGYDGGNNSQYGNDGLPPPPYSPRDDSSRKLLTPVTVLTAVVTFFGYDGGNNSQYPSASGSSPPYSPRDDSSQHIYEEATVLTAVVTFFAICLTWRSQYPSASGSGNTPTPPDSSQHIYEEAGRGSMNPTFFAICLTWRIEDPPFNGSSGNTPTPPNDEERESEEAGRGSMNPVCLPVIVTWRIEDPPFNSLLFALLTPPNDEERESNEEPPPPMNPVCLPVIVAPYLFWLPFNSLLFALLAAAGGLQRESNEEPPPPYEDPYWGVIVAPYLFWLAAIAASCALLAAAGGLQGIYVLVMPPYEDPYWGNGDRHSDFWLAAIAASCFTASVSTGLQGIYVLVMLVLLILAYWGNGDRHSDYQPLGTQASCFTASVSTVVTATGLLVMLVLLILAYRRRWRRHSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLILAYRRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVSMTLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	Pool #1	Pool #2	Pool #3		
PMGAGPPSPGGDPDGYDYLGLQHDGNDGLPPPPYSSYAAAQRKLLTPVTVLSPGGDPDGYDGGNNSQYGNDGLPPPPYSPRDDSSRKLLTPVTVLTAVVTFFGYDGGNNSQYPSASGSSPPYSPRDDSSQHIYEEATVLTAVVTFFAICLTWRSQYPSASGSSGNTPTPPDSSQHIYEEAGRGSMNPTFFAICLTWRIEDPPFNGSSGNTPTPPNDEERESEEAGRGSMNPVCLPVIVTWRIEDPPFNSLLFALLTPPNDEERESNEEPPPPMNPVCLPVIVAPYLFWLPFNSLLFALLAAAGGLQRESNEEPPPYEDPYWGVIVAPYLFWLAAIAASCALLAAAGGLQGIYVLVMPPYEDPYWGNGDRHSDFWLAAIAASCFTASVSTGLQGIYVLVMLVLLILAYWGNGDRHSDyQPLGTQASCFTASVSTVVTATGLLVMLVLLILAYRRRWRRHSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLILAYRRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGONRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALLCSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLIFLIGFA	<b>MGSLEMVPM</b> GAGPPSPG	GTQDQSLYLGLQHDGND	LLLAAVASSYAAAQRKL		
SPGGDPD <i>GYDGGNNSQY</i> GNDGLPPPPYSPRDDSSRKLLTPVTVLTAVVTFF <i>GYDGGNNSQYPSASGSS</i> PPYS <i>PRDDSSQHIYEEA</i> TVLTAVVTFFAICLTWRSQYPSASGSSGNTPTPPDSSQHIYEEAGRGSMNPTFFAICLTWRIEDPPFNGSSGNTPTPPNDEERESEEAGRGSMNPVCLPVIVTWRIEDPPFNSLLFALLTPPNDEERESNEEPPPPMNPVCLPVIVAPYLFWLPFNSLLFALLAAAGGLQRESNEEPPPYEDPYWGVIVA <b>PYLFWLAA</b> IAASCALLAAAGGLQGIYVLVMPPYEDPYWGNGDRHSDFWLAAIAASCFTASVSTGLQGIYVLVMLVLLILAYWGNGDRHSDYQPLGTQASCFTASVSTVVTATGLLVMLVLLILAYRRWRRHSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLILAYRRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGS/LQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	PMGAGPPSPGGDPDGYD	YLGLQHDGNDGLPPPPY	SSYAAAQRKLLTPVTVL		
GYDGGNNSQYPSASGSSPPYSPRDDSSQHIYEEATVLTAVVTFFAICLTWRSQYPSASGSSGNTPTPPDSSQHIYEEAGRGSMNPTFFAICLTWRIEDPPFNGSSGNTPTPPNDEERESEEAGRGSMNPVCLPVIVTWRIEDPPFNSLLFALLTPPNDEERESNEEPPPPMNPVCLPVIVAPYLFWLPFNSLLFALLAAAGGLQRESNEEPPPPYEDPYWGVIVAPYLFWLAAIAASCALLAAAGGLQGIYVLVMPPYEDPYWGNGDRHSDFWLAAIAASCFTASVSTGLQGIYVLVMLVLLILAYWGNGDRHSDYQPLGTQASCFTASVSTVVTATGLLVMLVLLILAYRRRWRRHSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLILAYRRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLIGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIGFA	SPGGDPD <i>GYDGGNN</i> SQY	GNDGLPPPPYSPRDDSS	RKLLTPVTVLTAVVTFF		
SQYPSASGSSGNTPTPPDSSQHIYEEAGRGSMNPTFFAICLTWRIEDPPFNGSSGNTPTPPNDEERESEEAGRGSMNPVCLPVIVTWRIEDPPFNSLLFALLTPPNDEERESNEEPPPPMNPVCLPVIVAPYLFWLPFNSLLFALLAAAGGLQRESNEEPPPPYEDPYWGVIVAPYLFWLAAIAASCALLAAAGGLQGIYVLVMPPPYEDPYWGNGDRHSDFWLAAIAASCFTASVSTGLQGIYVLVMLVLLILAYWGNGDRHSDYQPLGTQASCFTASVSTVVTATGLLVMLVLLILAYRRRWRRHSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLILAYRRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLIGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIGFA	GYDGGNNSQYPSASGSS	PPYS <i>PRDDSSQHIY</i> EEA	TVLTAVVTFFAICLTWR		
GSSGNTPTPPNDEERESEEAGRGSMNPVCLPVIVTWRIEDPPFNSLLFALLTPPNDEERESNEEPPPPMNPVCLPVIVAPYLFWLPFNSLLFALLAAAGGLQRESNEEPPPPYEDPYWGVIVAPYLFWLAAIAASCALLAAAGGLQGIYVLVMPPPYEDPYWGNGDRHSDFWLAAIAASCFTASVSTGLQGIYVLVMLVLLILAYWGNGDRHSDYQPLGTQASCFTASVSTVVTATGLLVMLVLLILAYRRRWRRHSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLILAYRRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	SQYPSASGSSGNTPTPP	DSSQHIYEEAGRGSMNP	TFFAICLTWRIEDPPFN		
TPPNDEERESNEEPPPPMNPVCLPVIVAPYLFWLPFNSLLFALLAAAGGLQRESNEEPPPPYEDPYWGVIVAPYLFWLAAIAASCALLAAAGGLQGIYVLVMPPPYEDPYWGNGDRHSDFWLAAIAASCFTASVSTGLQGIYVLVMLVLLILAYWGNGDRHSDYQPLGTQASCFTASVSTVVTATGLLVMLVLLILAYRRRWRRHSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLILAYRRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGS/LQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	GSSGNTPTPPNDEERES	EEAGRGSMNPVCLPVIV	TWR <b>IEDPPFNSL</b> LFALL		
RESNEEPPPPYEDPYWGVIVAPYLFWLAAIAASCALLAAAGGLQGIYVLVMPPPYEDPYWGNGDRHSDFWLAAIAASCFTASVSTGLQGIYVLVMLVLLILAYWGNGDRHSDYQPLGTQASCFTASVSTVVTATGLLVMLVLLILAYRRRWRRHSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLLVMLVLLILAYRRRWRRBool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGS/LQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	TPPNDEERESNEEPPPP	MNPVCLPVIVAPYLFWL	PFNSLLFALLAAAGGLQ		
PPPYEDPYWGNGDRHSD YWGNGDRHSDYQPLGTQ HSDYQPLGTQDQSLYLGFWLAAIAASCFTASVST ASCFTASVSTVVTATGL VSTVVTATGLALSLLLLGLQGIYVLVMLVLLILA LVMLVLLILAYRRWRR ILAYRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVL GGIMFLACVLVLIVDAVLGTLNLTTMFLLMLLWT TMFLLMLLWTLVVLLICVAGILFILAILTEWGSGGGIMFLACVLVLIVDAV DAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLIGAVTVVSMTLLLLA LVSMTLLLLAFVLWLSSLICSSCSSCPLSKILLA SCPLSKILLARLFLYALGPVFMCLGGLLTMVAGAVVSMTLLLAFVLWLSSSCPLSKILLARLFLYAL LASALIAGGS/LQTNFKGGULTMVASNTLLSAWLSSPGGLGTLGAALLTL GTLGAALLTLAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	RESNEEPPPPYEDPYWG	VIVA <b>PYLFWLAAI</b> AASC	ALLAAAGGLQGIYVLVM		
YWGNGDRHSDYQPLGTQ HSDYQPLGTQDQSLYLGASCFTASVSTVVTATGL VSTVVTATGLALSLLLLVMLVLLILAYRRRWRR ILAYRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVL GGIMFLACVLVLIVDAVLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLIC TMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLA LICSSCSSCPLSKILLARLFLYALGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYAL LLARLFLYALALLLLASGGLLTMVAGAVWLTVMSLSSPGGLGTLGAALLTL GTLGAALLTLAAALALLLASALIAGGS/LQTNFK GSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	PPPYEDPYWGNGDRHSD	FWLAAIAASCFTASVST	GLQGIYVLVMLVLLILA		
HSDYQPLGTQDQSLYLGVSTVVTATGLALSLLLLILAYRRWRRLTVCGGIPool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	YWGNGDRHSDYQPLGTQ	ASCFTASVSTVVTATGL	LVMLVLLILAYRRRWRR		
Pool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLARGPVFMCLGGLLTMVAGAVVSMTLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	HSDYQPLGTQDQSLYLG	VSTVVTATGLALSLLLL	ILAYRRRWRRLTVCGGI		
Pool #4Pool #5Pool #6WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA					
WRRLTVCGGIMFLACVLLGTLNLTTMFLLMLLWTVAGILFILAILTEWGSGGGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	Pool #4	Pool #5	Pool #6		
GGIMFLACVLVLIVDAVTMFLLMLLWTLVVLLICLAILTEWGSGNRTYGPVDAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	WRRLTVCGGIMFLACVL	LGTLNLTTMFLLMLLWT	VAGILFILAILTEWGSG		
DAVLQLSPLLGAVTVVSLWTLVVLLICSSCSSCPGSGNRTYGPVFMCLGGLPLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	GGIMFLACVLVLIVDAV	TMFLLM <b>LLWTLVVL</b> LIC	LAI <i>LTEWGSGNRTY</i> GPV		
PLLGAVTVVSMTLLLLALICSSCSSCPLSKILLAGPVFMCLGGLLTMVAGAVVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	DAVL <i>QLSPLLGAVT</i> VVS	LWTLVVLLICSSCSSCP	GSGNR <b>TYGPVFMCL</b> GGL		
VVSMTLLLLAFVLWLSSSCPLSKILLARLFLYALGGLLTMVAGAVWLTVMSLLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	PLLGAVTVVSMTLLLLA	LIC <b>SSCSSCPLSKILL</b> A	GPVFM <b>CLGGLLTMV</b> AGA		
LLAFVLWLSSPGGLGTLLLARLFLYALALLLLASAGAVWLTVMSNTLLSAWLSSPGGLGTLGAALLTLLASALIAGGSILQTNFKVMSNTLLSAWILTAGFLGTLGAALLTLAAALALLGGSILQTNFKSLSSTEFSAWILTAGFLIFLIGFA	VVSMTLLLLAFVLWLSS	S <b>CPLSKILL</b> ARLFLYAL	GGLLTMVAGAVWLTVMS		
LSSPG <b>GLGTLGAAL</b> LTL LAS <i>ALIAGGSIL</i> QTNFK VMSNT <b>LLSAWILTA</b> GFL GTLGAALLTLAAALALL GGSILQTNFKSLSSTEF SAWI <b>LTAGFLIFL</b> IGFA	LLAFVLWLSSPGGLGTL	LLARL <b>FLYALALLL</b> LAS	AGAVWLTVMSNTLLSAW		
GTLGAALLTLAAALALL GGSILQTNFKSLSSTEF SAWI <b>LTAGFLIFL</b> IGFA	LSSPG <b>GLGTLGAAL</b> LTL	LAS <i>ALIAGGSIL</i> QTNFK	VMSNT <b>LLSAWILTA</b> GFL		
	GTLGAALLTLAAALALL	GGSILQTNFKSLSSTEF	SAWI <b>LTAGFLIFL</b> IGFA		
LTLAAALALLASLILGT NFKSLSSTEFIPNLFCM GFLIFLIGFALFGVIRC	LTLAAALALLASLILGT	NFKSLSSTEFIPNLFCM	GFLIFLIGFALFGVIRC		
ALLASLILGTLNLTTMF TEFIPNLFCMLLLIVAG CYYCLTLESEERPPTPY	ALLASLILGTLNLTTMF	ASLILGTLNLTTMF TEFIPNLFCMLLLIVAG CYYCLTL <i>ESEEI</i>			
FCMLLLIVAGILFILAI ESEERPPTPYRNTV		FCMLLLIVAGILFILAI	<b>ESEERPPTPYRNTV</b>		

				Binding/					Binding/
Epitope	Protein	Score	Source	Reference	Epitope	Protein	Score	Source	Reference
HLA-A*01					HLA-A*11				
VLEKARGSTY	EBNA3A	25	Predicted	Confirmed	SSCSSCPLSK	LMP2A	29	Defined	[4]
TNEEIDLAY	EBNA3B	26	Predicted	Confirmed	HLA-A*24				
CDEGTRHATTY	EBNA3B	23	Predicted	Confirmed	TYGPVFMCL	LMP2A	24	Defined	[5]
PKDAKQTDY	EBNA3C	25	Predicted	Confirmed	PYLFWLAAI	LMP2A	22	Defined	[6]
ASERLVPEESY	EBNA3C	27	Predicted	Confirmed	HLA-B*07				
ELESSDDELPY	EBNA3C	27	Predicted	Confirmed	RPPIFIRRL	EBNA3A	21	Defined	[7]
YQEPPAPQAPY	EBNA3C	25	Predicted	Confirmed	QPRAPIRPI	EBNA3C	23	Defined	[7]
YQEPPPPQAPY	EBNA3C	25	Predicted	Confirmed	VPAPAGPIV	EBNA3A	20	Defined	[8]
LLALLFWLY	LMP1	21	Predicted	Confirmed	HLA-B*08				
WTGGALLVLY	LMP1	24	Predicted	Confirmed	CPLSKILL	LMP2A	26	Defined	[9]
ESEERPPTPY	LMP2A	27	Predicted	Confirmed	QAKWRLQTL	EBNA3A	32	Defined	[10]
GYDGGNNSQY	LMP2A	25	Predicted	Confirmed	FLRGRAYGL	EBNA3A	31	Defined	[10]
PRDDSSQHIY	LMP2A	25	Predicted	Confirmed	HLA-B*35				
LTEWGSGNRTY	LMP2A	29	Predicted	Confirmed	MGSLEMVPM	LMP2A	8	Defined	[11]
HLA-A*03					YPLHEQHGM	EBNA3A	17	Defined	[10]
ALFLGIVLF	LMP1	24	Predicted	Confirmed	AVLLHEESM	EBNA3B	7	Defined	[8]
MLWRLGATI	LMP1	23	Predicted	Confirmed	HLA-B*37				
QLTEEVENK	LMP1	23	Predicted	Confirmed	VDLLWLLLF	LMP1	28	Predicted	Unconfirmed
ALIAGGSIL	LMP2A	26	Predicted	Confirmed	DEHHHDDSL	LMP1	25	Predicted	Unconfirmed
LLLAAVASSY	LMP2A	28	Predicted	Confirmed	TEFIPNLF	LMP2A	24	Predicted	Unconfirmed
QLSPLLGAVT	LMP2A	25	Predicted	Confirmed	TDLSYIKSF	EBNA3A	27	Predicted	Unconfirmed
RLLLMRAGK	EBNA3A	31	Predicted	Confirmed	SDLRPLGSL	EBNA3B	28	Predicted	Unconfirmed
RVVVSAVVH	EBNA3A	29	Predicted	Confirmed	LDTQHILCF	EBNA3C	28	Predicted	Unconfirmed
IVSRGGPKVK	EBNA3A	30	Predicted	Confirmed	PDAPLDLSL	EBNA3C	27	Predicted	Unconfirmed
HLEPAQKGTK	EBNA3A	28	Predicted	Confirmed	LDFVRFMGV	EBNA3C	17	Defined	[12]
RLRAEAQVK	EBNA3A	36	Defined	[13]	HLA-B*44				
HLA-A*02					VEITPYKPTW	EBNA3B	25	Defined	[8]
LLWTLVVLL	LMP2A	30	Defined	[4]	EGGVGWRHW	EBNA3C	13	Defined	[14]
FLYALALLL	LMP2A	24	Defined	[15]	EENLLDFVRF	EBNA3C	25	Defined	[16]
CLGGLLTMV	LMP2A	27	Defined	[17]	KEHVIQNAF	EBNA3C	25	Defined	[18]
LTAGFLIFL	LMP2A	25	Defined	[5]	HLA-B*60 (HLA-B*40.01)				
YLLEMLWRL	LMP1	30	Defined	[19]	IEDPPFNSL	LMP2A	22	Defined	[5]
YLQQNWWTL	LMP1	24	Defined	[19]					
TLLVDLLWL	LMP1	27	Defined	[19]					
LLLIALWNL	LMP1	28	Defined	[19]					
ALLVLYSFA	LMP1	19	Defined	[20]					
SVRDRLARL	EBNA3A	23	Defined	[10]					
LLDFVRFMGV	EBNA3C	22	Defined	[21]					

**Table S3.** Predicted and defined peptide epitopes from EBV-latent proteins.



**Figure S1.** Flow Cytometry analysis gating strategy. Gating on patient sample with positive control stimulation. Arrows indicate order from parent gate. Gating strategy follows previously published standard practice [22].



**Figure S2.** *Ex vivo* EBV-specific CD8<sup>+</sup> T-cell responses in healthy controls and comparison between responses against EBV-latency-II proteins. Error bars represent SEM. (**A**) Summed percentages of *ex vivo* LMP1/2A-specific CD8<sup>+</sup> T-cell responses defined by IFN $\gamma$ , TNF $\alpha$  and CD107a in healthy EBV-seropositive controls. (**B-C**) Comparison of EBV-latency-II antigenspecific CD8<sup>+</sup> T-cells. Summed percentages of IFN $\gamma$ , TNF $\alpha$  and CD107a responses in (**B**) cHL patients and (**C**) healthy EBV-seropositive controls.



**Fig. S3.** *In vitro* LMP2A-specific CD8<sup>+</sup> T-cell cytotoxicity compared between HLA-A\*02<sup>+</sup> and HLA-A\*02<sup>-ve</sup> healthy control donors. EBV-specific T-cells were expanded in four EBV-seropositive healthy control donors (Donors 1-4, HLA-A\*02/A\*02/B\*07/B\*44; HLA-A\*03/A\*23/B\*35/B\*44; HLA-A\*02/A\*02/B\*35/B\*57; HLA-A\*03/A\*32/B\*8/B\*47 respectively). (A) LMP2A-specific cytotoxicity was quantified using autologous CFSE labeled PHA blasts (target cells) incubated with each of six LMP2A overlapping peptide pools (Table S2). LMP2A-specific lysis was calculated for each well relative to the unpulsed control sample. (B) Representative intracellular cytokine and CD107ab mobilization by CD8<sup>+</sup> T-cells (gated on CD3<sup>+</sup>) in response to 6 hours stimulation by LMP2A peptide pool #1 pulsed PHA blasts in donor 3 (top panel) compared with unpulsed PHA blasts (bottom panel).

## **Supporting Information References**

- Hjalgrim H, Rostgaard K, Johnson PC, Lake A, Shield L, Little AM, Ekstrom-Smedby K, Adami HO, Glimelius B, Hamilton-Dutoit S, Kane E, Taylor GM, McConnachie A, Ryder LP, Sundstrom C, Andersen PS, Chang ET, Alexander FE, Melbye M, Jarrett RF. HLA-A alleles and infectious mononucleosis suggest a critical role for cytotoxic T-cell response in EBV-related Hodgkin lymphoma. Proc Natl Acad Sci U S A 2010; **107**:6400-5.
- Niens M, Jarrett RF, Hepkema B, Nolte IM, Diepstra A, Platteel M, Kouprie N, Delury CP, Gallagher A, Visser L, Poppema S, te Meerman GJ, van den Berg A. HLA-A\*02 is associated with a reduced risk and HLA-A\*01 with an increased risk of developing EBV+ Hodgkin lymphoma. Blood 2007; 110:3310-5.
- 3. Huang X, Kushekhar K, Nolte I, Kooistra W, Visser L, Bouwman I, Kouprie N, Veenstra R, van Imhoff G, Olver B, Houlston RS, Poppema S, Diepstra A, Hepkema B, van den Berg A. HLA associations in classical Hodgkin lymphoma: EBV status matters. PLoS One 2012; 7:e39986.
- 4. Lee SP, Thomas WA, Blake NW, Rickinson AB. Transporter (TAP)-independent processing of a multiple membrane-spanning protein, the Epstein-Barr virus latent membrane protein 2. Eur J Immunol 1996; **26**:1875-83.
- 5. Lee SP, Tierney RJ, Thomas WA, Brooks JM, Rickinson AB. Conserved CTL epitopes within EBV latent membrane protein 2: a potential target for CTL-based tumor therapy. J Immunol 1997; **158**:3325-34.
- 6. Burrows SR, Elkington RA, Miles JJ, Green KJ, Walker S, Haryana SM, Moss DJ, Dunckley H, Burrows JM, Khanna R. Promiscuous CTL recognition of viral epitopes on multiple human leukocyte antigens: biological validation of the proposed HLA A24 supertype. J Immunol 2003; **171**:1407-12.
- Hill A, Worth A, Elliott T, Rowland-Jones S, Brooks J, Rickinson A, McMichael A. Characterization of two Epstein-Barr virus epitopes restricted by HLA-B7. Eur J Immunol 1995; 25:18-24.
- 8. Rickinson AB, Moss DJ. Human cytotoxic T lymphocyte responses to Epstein-Barr virus infection. Annu Rev Immunol 1997; **15**:405-31.
- 9. Tsang ML, Munz C. Cytolytic T lymphocytes from HLA-B8+ donors frequently recognize the Hodgkin's lymphoma associated latent membrane protein 2 of Epstein Barr virus. Herpesviridae 2011; **2**:4.
- 10. Burrows SR, Gardner J, Khanna R, Steward T, Moss DJ, Rodda S, Suhrbier A. Five new cytotoxic T cell epitopes identified within Epstein-Barr virus nuclear antigen 3. J Gen Virol 1994; **75** ( **Pt 9**):2489-93.
- 11. Straathof KC, Leen AM, Buza EL, Taylor G, Huls MH, Heslop HE, Rooney CM, Bollard CM. Characterization of latent membrane protein 2 specificity in CTL lines from patients with EBV-positive nasopharyngeal carcinoma and lymphoma. J Immunol 2005; **175**:4137-47.
- 12. Shi Y, Smith KD, Kurilla MG, Lutz CT. Cytotoxic CD8+ T cells recognize EBV antigen but poorly kill autologous EBV-infected B lymphoblasts: immunodominance is elicited by a peptide epitope that is presented at low levels in vitro. J Immunol 1997; **159**:1844-52.
- 13. Hill AB, Lee SP, Haurum JS, Murray N, Yao QY, Rowe M, Signoret N, Rickinson AB, McMichael AJ. Class I major histocompatibility complex-restricted cytotoxic T lymphocytes specific for Epstein-Barr virus (EBV)-transformed B lymphoblastoid cell lines against which they were raised. J Exp Med 1995; **181**:2221-8.

- 14. Morgan SM, Wilkinson GW, Floettmann E, Blake N, Rickinson AB. A recombinant adenovirus expressing an Epstein-Barr virus (EBV) target antigen can selectively reactivate rare components of EBV cytotoxic T-lymphocyte memory in vitro. J Virol 1996; **70**:2394-402.
- 15. Lautscham G, Haigh T, Mayrhofer S, Taylor G, Croom-Carter D, Leese A, Gadola S, Cerundolo V, Rickinson A, Blake N. Identification of a TAP-independent, immunoproteasome-dependent CD8+ T-cell epitope in Epstein-Barr virus latent membrane protein 2. J Virol 2003; **77**:2757-61.
- 16. Burrows SR, Misko IS, Sculley TB, Schmidt C, Moss DJ. An Epstein-Barr virusspecific cytotoxic T-cell epitope present on A- and B-type transformants. J Virol 1990; **64**:3974-6.
- 17. Lee SP, Thomas WA, Murray RJ, Khanim F, Kaur S, Young LS, Rowe M, Kurilla M, Rickinson AB. HLA A2.1-restricted cytotoxic T cells recognizing a range of Epstein-Barr virus isolates through a defined epitope in latent membrane protein LMP2. J Virol 1993; **67**:7428-35.
- 18. Khanna R, Burrows SR, Kurilla MG, Jacob CA, Misko IS, Sculley TB, Kieff E, Moss DJ. Localization of Epstein-Barr virus cytotoxic T cell epitopes using recombinant vaccinia: implications for vaccine development. J Exp Med 1992; **176**:169-76.
- Khanna R, Burrows SR, Nicholls J, Poulsen LM. Identification of cytotoxic T cell epitopes within Epstein-Barr virus (EBV) oncogene latent membrane protein 1 (LMP1): evidence for HLA A2 supertype-restricted immune recognition of EBV-infected cells by LMP1-specific cytotoxic T lymphocytes. Eur J Immunol 1998; 28:451-8.
- 20. Duraiswamy J, Burrows JM, Bharadwaj M, Burrows SR, Cooper L, Pimtanothai N, Khanna R. Ex vivo analysis of T-cell responses to Epstein-Barr virus-encoded oncogene latent membrane protein 1 reveals highly conserved epitope sequences in virus isolates from diverse geographic regions. J Virol 2003; **77**:7401-10.
- 21. Kerr BM, Kienzle N, Burrows JM, Cross S, Silins SL, Buck M, Benson EM, Coupar B, Moss DJ, Sculley TB. Identification of type B-specific and cross-reactive cytotoxic T-lymphocyte responses to Epstein-Barr virus. J Virol 1996; **70**:8858-64.
- 22. Mahnke YD, Roederer M. OMIP-001: Quality and phenotype of Ag-responsive human T-cells. Cytometry A 2010; **77**:819-20.