

Supplementary Figures

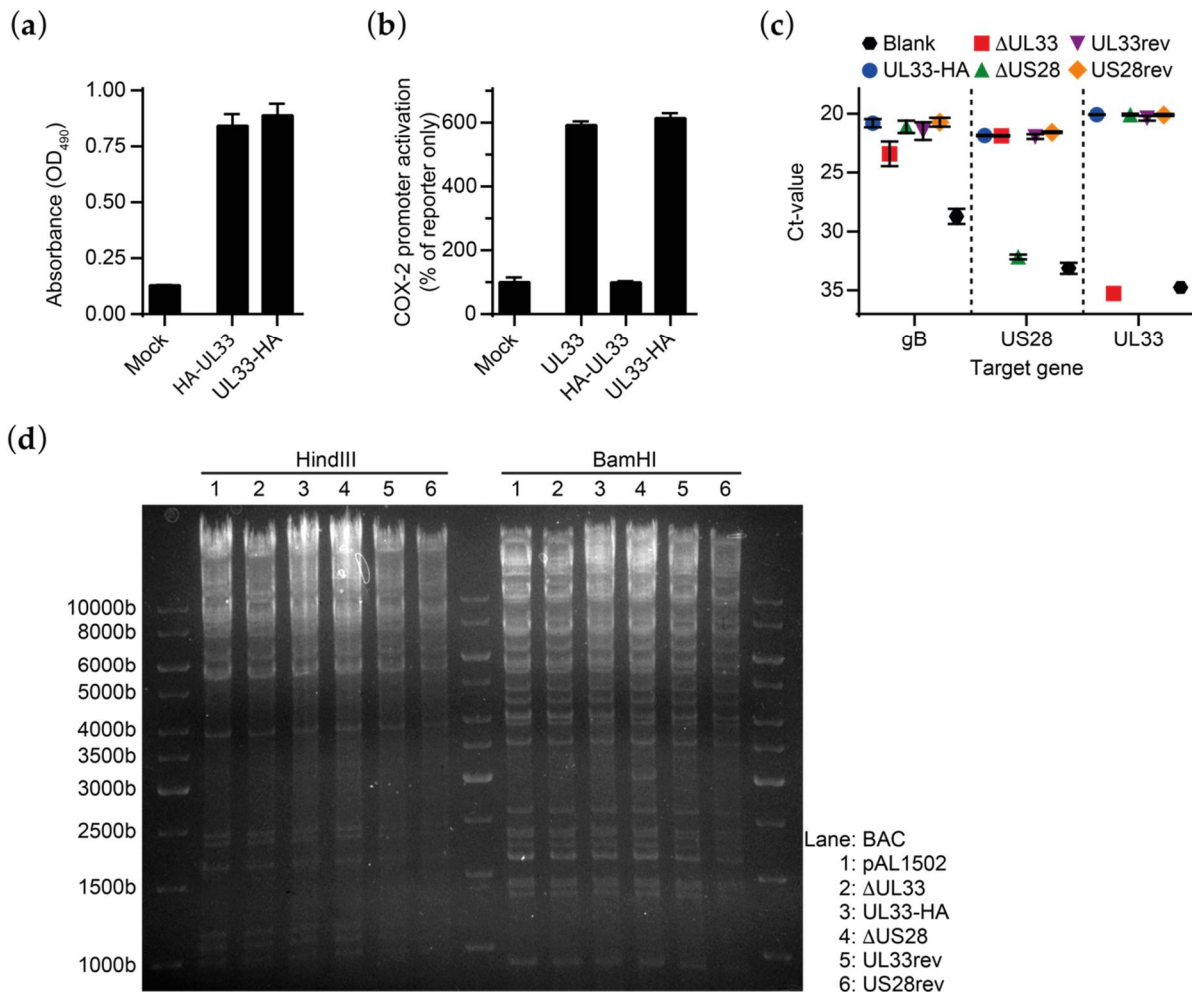


Figure S1. Validation of recombineering strategy and genomic integrity of HCMV Merlin BAC variants. Functionality check of N- or C-terminally HA-tagged UL33 receptors. HEK293T cells were transfected with receptor DNA and/or COX-2 promoter-driven reporter gene. The next day, receptor expression (a) and receptor signaling (b) were determined. Quality control of HCMV Merlin BAC derivatives as assessed by qRT-PCR of US28 and UL33 genes (c) and HindIII and BamHI endonuclease digestion pattern analysis (d).

Strain	UL33 receptor amino acid sequence	Residue
Merlin	MDTIIHNTNRSTDTPHVNTCNITEPLSAIRTTEAVINTFIIIFVGGPLNAIVLTQLLT	60
Towne	MDTIIHNTNRSTSTPHVNSTCNMTETLSAIRTTEAVINTFIIIFVGGPLNAIVLTQLLT	60
Toledo	MDTIIHNST-RNTTTPHINDTCNMTGPLFAIRTTEAVLNTLIIIFVGGPLNAIVLTQLLT	59
TB40/E	MDTIIHNST-RNNTTPHINDTCNMTGPLFAIRTTEAVLNTFIIIFVGGPLNAIVLTQLLT	59
AD169	MDTIIHNST-RNNTTPHINDTCNMTGPLFAIRTTEAVLNTFIIIFVGGPLNAIVLTQLLT	59
FIX/PH/TR	MDTIIHNST-RNNTTPHINDTCNMTGPLFAIRTTEAVLNTFIIIFVGGPLNAIVLTQLLT *****:*..**:***:* * *****:***:*****:*****:*****	59
Merlin	NRVLGYSTPTIYMTNLYSTNFLTTLTVLPFIVLSNQWLLPASVASCFLSVIYYSSCTVGF	120
Towne	NRVLG STPTIYMTNLYSTNFLTTLTVLPFIVLSNQWLLPASVASCFLSVIYYSSCTVGF	120
Toledo	NRVLGYSTPTIYMTNLYSTNFLTTLTVLPFIVLSNQWLLPAGVASCKFLSVIYYSSCTVGF	119
TB40/E	NRVLGYSTPTIYMTNLYSTNFLTTLTVLPFIVLSNQWLLPAGVASCKFLSVIYYSSCTVGF	119
AD169	NRVLGYSTPTIYMTNLYSTNFLTTLTVLPFIVLSNQWLLPAGVASCKFLSVIYYSSCTVGF	119
FIX/PH/TR	NRVLGYSTPTIYMTNLYSTNFLTTLTVLPFIVLSNQWLLPAGVASCKFLSVIYYSSCTVGF *****:*****:*****:*****:*****	119
Merlin	ATVALIAADRYRVLHKRTYARQSYRSTYIILLTWFAGLIFSPAAVYTTVVTHNGTNG-	179
Towne	ATVALIAADRYRVLHKRTYARQSYRSTYIILLTWFAGLIFSPAAVYTTVVTHNGTDE-	179
Toledo	ATVALIAADRYRVLHKRIYARQSYRSTYIILLTWLAGLIFSPAAVYTTVVMHHEANDT	179
TB40/E	ATVALIAADRYRVLHKRTYARQSYRSTYIILLTWLAGLIFSPAAVYTTVVMHHDANDT	179
AD169	ATVALIAADRYRVLHKRTYARQSYRSTYIILLTWLAGLIFSPAAVYTTVVMHHDANDT	179
FIX/PH/TR	ATVALIAADRYRVLHKRTYARQSYRSTYIILLTWLAGLIFSPAAVYTTVVMHHDANDT *****:*****:*****:*****:*****:*****:*****:*****:*****	179
Merlin	QSSNGHATCVLYFIADEVYTVLLSWKVLLTLVWGAAPVIMMTWFYAFFYSTVQRASQKQR	239
Towne	-NTNGHATCVLYFIADEVYTVLLSWKVLLTLVWGAAPVIMMTWFYAFFYSTVQRASQKQR	238
Toledo	TNATGHATCVLYFVADEVHTVLLSWKVLLTLVWGAAPVIMMTWFYAFFYSTVQRASQKQR	239
TB40/E	NNTNGHATCVLYFVAEEVHTVLLSWKVLLTLVWGAAPVIMMTWFYAFFYSTVQRASQKQR	239
AD169	NNTNGHATCVLYFVAEEVHTVLLSWKVLLTLVWGAAPVIMMTWFYAFFYSTVQRASQKQR	239
FIX/PH/TR	NNTNGHATCVLYFVAEEVHTVLLSWKVLLTLVWGAAPVIMMTWFYAFFYSTVQRASQKQR .:*****:***:*****:*****:*****:*****:*****:*****	239
Merlin	SRTLTFVSVLLISFVALQTPYVSLIMFNSYATAAWPMDCEHLTLRRTIGTLSRLVPHLHC	299
Towne	SRTLTFVSVLLISFVALQTPYVSLIMFNSYATAAWPMDCEHLTLRRTIGTLSRLVPHLHC	298
Toledo	SRTLTFVSVLLISFVALQTPYISLMIFNSYATTAWSTKCEHLTLRRTIGTLARLVPHLHC	299
TB40/E	SRTLTFVSVLLISFVALQTPYVSLIMFNSYATTAWPMQCEHLTLRRTIGTLARLVPHLHC	299
AD169	SRTLTFVSVLLISFVALQTPYVSLIMFNSYATTAWPMQCEHLTLRRTIGTLARLVPHLHC	299
FIX/PH/TR	SRTLTFVSVLLISFVALQTPYVSLIMFNSYATTAWPMQCEHLTLRRTIGTLARLVPHLHC *****:*****:*****:*****:*****:*****:*****:*****	299
Merlin	LINPILYALLGHDFLQMRQCFRGQLDRAFLRSQQNQQRATAETNLAAGNNSQSVATSLS	359
Towne	LINPILYALLGHDFLQMRQCFRGQLDRAFLRSQQNQQRATAETNLAAGNNSQSVATSLS	358
Toledo	LINPILYALLGHDFLQMRQCFRGQLDRAFLRSQQNQQRATAETNLAAGNNSQSVATSLS	359
TB40/E	LINPILYALLGHDFLQMRQCFRGQLDRAFLRSQQNQQRATAETNLAAGNNSQSVATSLS	359
AD169	LINPILYALLGHDFLQMRQCFRGQLDRAFLRSQQNQQRATAETNLAAGNNSQSVATSLS	359
FIX/PH/TR	LINPILYALLGHDFLQMRQCFRGQLDRAFLRSQQNQQRATAETNLAAGNNSQSVATSLS *****:*****:*****:*****:*****:*****:*****:*****	359
Merlin	DTSSKNCNQHAKRSVSFNFPSTGWTGGQKTASNDTSTKIPHRLSQSHHNLSGV	412
Towne	DTNSKNCNQHAKRSVSFNFPSTGWTGGQKTASNDTSTKIPHRLSQSHHNLSGV	411
Toledo	DNPSKNCNQHAKRSVSFNFPSTGWTGGQKTASNDTSTKIPHRLSQSHHNLSGV	412
TB40/E	DTNSKNCNQHAKRSVSFNFPSTGWTGGQKTASNDTSTKIPHRLSQSHHNLSGV	412
AD169	DTNSKNYNQHAKRSVSFNFPSTGWTGGQKTASNDTSTKIPHRLSQSHHNLSGV	412
FIX/PH/TR	DNPSKNCNQHAKRSVSFNFPSTGWTGGQKTASNDTSTKIPHRLSQSHHNLSGV *..*** *****:*****:*****:*****:*****:*****:*****	412

Figure S2. Multiple sequence alignment of HCMV UL33 orthologs. Sequence variability is highlighted in yellow. (*) fully conserved residue; (:) conservation between groups of strongly similar properties; (.) conservation between groups of weakly similar properties.