SUPPLEMENTAL TABLES

Supplemental Table 1. mRNAs whose translation was enriched upon HCMV infection and UL38 expression: DAVID Functional Analysis.

Supplemental Table 2. mRNAs whose translation was enriched upon HCMV infection but not UL38 Expression: David Functional Analysis.

Supplemental Table 3. mRNAs whose translation was suprressed upon HCMV infection or UL38 Expression: DAVID Functional Analysis.

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Supplemental Table 5. Subanalysis of *Cell cycle, mitochondrion, apoptosis, RNA processing stress-response* terms from Supplementary Table 1 & Table 2.

Supplementary Figure 6. 5' UTR analysis of mRNAs that are translationally regulated during HCMV infection.

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Supplementary Table 9. Overlap in translation signatures with other translateome studies.

Supplemental Table 1: mRNAs whose translation was enriched upon HCMV infection and UL38 expression: DAVID Functional Analysis

Category	GOTERM_BP_FAT		GOTERM_BP_FAT		GOTERM_BP_FAT		GOTERM_BP_FAT	GOTERM_BP_FAT		**Category**	GOTERM_BP_FAT
Term	**Cell Cycle**		**RNA Processing**		**Cytoskelton Organization**		**Translation**	**Apoptosis**		**Term**	**DNA Replication**
Counts	**56**		**39**		**31**		**25**	**48**		**Counts**	**15**
p*	**1.10E-04**		**3.40E-03**		**6.20E-03**		**7.40E-03**	**1.50E-02**		**p***	**3.10E-02**
Genes	ARL2	ILK	ARL6IP4	RPL35A	ARF6	TUBB	HBS1L	BAK1	MKL1	**Genes**	GINS3
	ARL3	ILF3	CD2BP2	HNRNPL	AGFG1		DHPS	BAX	MAPK1		GINS4
	CLIP1	KPNA2	EMG1	RNPS1	CKS2		EEF1A1	BNIP1	NME1, NME2		RAD1
	CDC14A	KRT18	FTSJ1	SNRPD1	FGFR1OP		EEF2	FAF1	NUDT2		RBM14
	CKS2	KIF22	ISY1	SNRPA	SEH1L		EIF2S3	FASTK	PPIF		CDT1
	DMC1	MAPRE3	LSM2	SNUPN	ABI2		EIF4E	PYCARD	PRDX5		CINP
	MAD2L2	MAPK1	LSM4	SIP1	ALDOA		EIF5A	ARHGDIA	PTENP1		CDKN2D
	PDS5B	NUP43	LSM6	TRA2A	ANK1		EIF6	ARHGEF12	PEA15		ING5
	RAD1	NDE1	LSM7		BIN3		MRPL12	SIVA1	PHLDA3		MCM5
	RASSF4	PIN1	PRPF18		CNN3		MRPL23	TIAL1	PML		RFC2
	S100A6	PML	RBM14		CAPZB		MRPL4	B4GALT1	PRKRA		RNASEH2A
	SEH1L	PSMD9	RBMS2		CDC42		MRPL9	ATF5	PPP3R1		TREX1
	SETD8	PSME2	RALY		CETN2		MRPS10	ASNS	RNF7		TK1
	UHMK1	PSMB8	TARBP2		CFL1		MRPS16	BTC	SOS2		TYMS
	AK1	PPP1CA	THOC4		CYTH2		PDF, COG8	CREB1	TGFB2		TBRG1
	BIN3	PPP2R3B	U2AF1		DLG1		RPL21	CASP2	TUBB		
	BUB3	SGOL1	WDR4		DYNC1H1		RPL34	CASP4	TP53I3		
	CALM1	RANBP1	WDR77		INF2		RPL35A	CASP6	YWHAB		
	CETN2	SUV39H1	CPSF4		MYH11		RPL36	C14orf153			
	CDT1	HAUS7	DUS2L		NDE1		RPS2	CFL1			
	CCNB1	TLK1	EXOSC3		OBSL1		RPS23	CDKN2D			
	CCND3	TBRG1	HNRNPH1		PAK1		RPS9	DAPK3			
	CDK10	TGFB2	HNRPLL		PFN1		RPLP1	DDAH2			
	CINP	TUBB	POLR2E		PPP4C		SARS2	EIF5A			
	CDKN2D	VPS24	POLR2F		RAC2		EIF1	FOXO3/B			
	DTYMK	VASH1	POLR2L		RAC3			GAS1			
	DYNC1H1		PRKRA		RANBP1			HSPB1			
	ERH		QTRT1		HAUS7			HDAC6			
	GAS1		RRP1		TPM1			ILK			
	HMG20B		RRP9		ARPC4			KRT18			

Supplemental Table 1: mRNAs whose translation was enriched upon HCMV infection and UL38 expression: DAVID Functional Analysis

GOTERM_CC_FAT			GOTERM_CC_FAT		GOTERM_CC_FAT	
Mitochondrion			**Nucleolus**		**Nucleoplasm**	
84			**44**		**59**	
1.40E-09			**1.90E-03**		**5.60E-05**	
ARL2BP	CREB1	PTENP1	EMG1	PITX1	CTBP1	HNRNPH1
ATP5G2	CLIC4	PEBP1	GPSM2	POLR2F	PDLIM1	HDAC6
ATP5S	C14orf153	PRKACA	ISY1	PML	PHF21A	HDAC9
ATP5O	COQ4	QTRT1	PRKRIP1	RRP1	PRPF18	ING5
ATP5D	COQ5	SHMT2	RBM14	RRP9	RBM14	KPNA2
BAK1	COQ7	SARS2	RRN3	RPL36	RRN3	MED20
BAX	CCDC123	GCSH	S100A4	RPS2	SIVA1	MED22
HAX1	CYB5B	SUCLG2	SAP30L	RPS9	SMAD9	MTA2
LYRM4	COX8A	SLC25A6	SENP3	STX17	SENP3	MBD1
MRS2	DGUOK	SLC25A10	UBAC1	STX5	TBX2	MBD2
MTERFD3	DCI	SLC25A30	APOBEC3F	TXN2	TAF6L	MCM5
ASAH2B	FIBP	SLC25A37	APOBEC3G	UBTF	TAF8	MAPK1
NDUFA7	GTF3C2	SLC25A40	APTX	ZNF174	TEAD2	POLR2E
NDUFAF3	GCAT	SAMM50	BUB3	ZNF3	TINF2	POLR2F
NDUFB7	HLCS	SPG7	CAMK4		THOC4	POLR2L
NDUFS6	HADH	TXN	CBX5		U2AF1	POLR3C
NFS1	HSD17B8	TXN2	EME1		WDR4	POLR3K
PRELID1	ILF3	TIMM10	EIF6		ATF5	PML
PARK7	IVD	TOMM22	EXOSC3		APTX	PRKAB2
SHC1	MSRB3	TMLHE	FGF22		CREB1	PPP1CA
SIVA1	MMAB	PDF, COG8	HNRNPH1		CAMK4	RFC2
ACOT7	MRPL12	PPIF	ILF3		CALM1	RPS2
AP2M1	MRPL23	PRDX5	MRTO4		CASP6	RFWD2
AK1	MRPL4	PEX11B	MTA2		CDT1	HNRNPL
AGMAT	MRPL54		MAPK1		CBX5	RNPS1
AKR7A2	MRPL9		MBNL3		CCNB1	SNRPD1
ANXA10	MRPS10		NLE1		ERCC8	SIP1
APOBEC3F	MRPS16		NFKBIE		GTF3C2	YWHAB
APOBEC3G	MAPK10		NIP7		GTF3C3	UBTF
BPHL	PANK2		NOL12		GTF3C4	

Category	GOTERM_CC_FAT		GOTERM_CC_FAT
Term	**Golgi Apparatus**		**Peroxisome**
Counts	**48**		**11**
p*	**1.40E-02**		**6.80E-03**
Genes	ARF6	GOSR2	ACOX3
	ARL2	LDLRAP1	AP2M1
	ARL3	MGAT2	GTF3C2
	AGFG1	MAP6	PRDX5
	GPSM2	MBNL3	PEX11B
	GNAS	NFKBIE	PEX13
	RAB34	PAK1	PEX7
	RAB38	PDF, COG8	PMVK
	RAB6A	PEBP1	SERHL2
	RAB7A	PRKACA	TRIM37
	RRAGB	PHTF1	XDH
	SYS1	SPPL2B	
	B4GALT1	SLC35C1	
	B4GALT6	STX5	
	AP1S3	STX6	
	AP3D1	VTI1B	
	AKR7A2	VAMP5	
	ACER3	ZFPL1	
	ARRB1		
	B3GALNT2		
	CREB3		
	CHST3		
	C11orf2		
	COPA		
	COPB2		
	COPE		
	DYNC1H1		
	ENTPD6		
	FGF22		
	FLOT1		

Supplemental Table 2: mRNAs whose translation was enriched upon HCMV infection but not UL38 Expression: David Functional Analysis

Category	**GOTERM_BP_FAT**		**GOTERM_BP_FAT**			**GOTERM_BP_FAT**		
Term	**DNA Repair**		**Cell Cycle**			**Translation**		
Counts	45		74			39		
p*	6.60E-05		5.80E-04			3.40E-04		
Genes	APEX1	MORF4	ARL2	IRF6	CDK11A, CDK11B	COPS5	RPL11	
	ASF1A	MLH3	CDC5L	MAPRE3	STAG2	DPH1	RPL19	
	FBXO6	MYO6	FANCI	MAPK1	SMC3	FAU	RPL35A	
	FANCI	NONO	NIPBL	MAPK13	TERF2	GFM2	RPS10	
	FANCM	NHEJ1	RAD21	MLH3	TLK1	PET112L	RPS19	
	KAT5	PARP2	RAD51C	MLL	TLK2	C12orf65	RPLP1	
	PRPF19	PSEN1	RAD51L1	NUDC	TBRG1	DHPS	SELT	
	RAD21	RFC1	RIF1	PES1	TBRG4	EEF1G	EIF4A1	
	RAD51C	SFPQ	PRR5	PSMC1	TUBB2A	EIF1AD	UBB	
	RAD51L1	SMC3	ARHGEF2	PSMC2	TUBB2B	EIF2B2	UBC	
	RIF1	SOD1	SKP1	PSMC3	TPD52L1	EIF3I		
	REV1	TERF2	WEE1	PSMD1	UBB	EIF4G3		
	RECQL	TLK1	BTRC	PSMD11	UBC	EIF4E2		
	XRCC4	TLK2	BIN3	PSMD12	UBE2I	EIF4H		
	XRCC5	UIMC1	BUB1	PSMD13	ZNF830	EIF5A		
	XRCC6	UBE2A	CDC123	PSMD3	ZC3HC1	EIF5B		
	ANKRD17		CUL2	PSMD4		QRSL1		
	AATF		CUL3	PSMD6		HARS		
	AIFM1		CCNDBP1	PSMD7		ICT1		
	CIB1		CDK7	PSMF1		MRPL22		
	CASP9		CDKN1B	PSMA1		MRPL27		
	C11orf30		DCTN2	PSMA3		MRPL28		
	CDK7		GSK3B	PSMA5		MRPL35		
	FOXO3/B		GADD45GIP1	PSMB1		MRPL37		
	FLJ35220		HHEX	PSMB4		MRPL43		
	ING4		RBBP4	PSMB5		MRPL45		
	MBD4		ID4	PPP1CA		MRPS18A		
	MAPK1		ING1	PPP5C		FARSA		
	MAPK14		ING4	PPP6C		RSL1D1		

Supplemental Table 2: mRNAs whose translation was enriched upon HCMV infection but not UL38 Expression: David Functional Analysis

GOTERM_BP_FAT		Category	GOTERM_BP_FAT	GOTERM_BP_FAT		
Chromatin Organization		Term	Ribosome Biogenesis	RNA Processing		
42		Counts	18	82		
6.80E-04		p*	2.00E-03	8.30E-13		
ASF1A	MORF4	Genes	BMS1	XRN2	CPSF3L	PPP2CA
ARID2	MLL		GTPBP5	CD2BP2	CSTF1	PPP2R1A
ARID4B	MLL3		GTPBP10	CDC5L	CSTF2T	QKI
BNIP3	NAP1L2		IMP3	DDX1	EXOSC10	RPP30
CTR9	PHB		SDAD1	DDX20	EXOSC4	RSL1D1
DMAP1	RSF1		TSR1	DDX46	EXOSC6	RPL11
H2AFJ	TERF2		UTP15	DHX15	FUS	RPL35A
H2AFY	TLK1		DCAF13	DHX38	GEMIN6	RPS19
KAT5	TLK2		AATF	DGCR14	GTF2F1	SRRM1
PHF15	TTF1		RPF1	GRSF1	HNRNPC	RBM39
RCOR1	TADA1		EXOSC10	IMP3	HNRNPH1	SNRNP40
SETDB1	UIMC1		EXOSC4	PRPF19	HNRNPU	SNRPA1
SMARCA1	UBE2A		EXOSC6	PRPF40A	INTS4	SNRPC
SMARCA5			PES1	RNMT	LIN28B	SNRPB
SMARCC1			RPL11	RBM22	WDR83	SF3A1
SAP130			RPL35A	RBM25	MOCS3	SF3B1
RERE			RPS19	RBMS2	NOVA1	SF3B2
C11orf30			TFB1M	RNGTT	NONO	SFPQ
DAPK3				SRPK2	NUDT21	SART3
HP1BP3				SNW1	PPIE	SKIV2L2
HAT1				THOC2	PES1	SYNCRIP
HIST1H3A				TRUB2	PNN	TRMU
HIST2H4A/4B				UTP15	PLRG1	TFB1M
HDAC6				DCAF13	PABPN1	ZNF638
RBBP4				WBP4	PCBP1	
ING4				YBX1	PCBP2	
JMJD1C				RSRC1	PUF60	
L3MBTL2				RPF1	POLR2J	
KDM4D				C1orf25	PTBP1	

Supplemental Table 2: mRNAs whose translation was enriched upon HCMV infection but not UL38 Expression: David Functional Analysis

GOTERM_BP_FAT		Category	GOTERM_BP_FAT	GOTERM_BP_FAT		
Stress Response		**Term**	**Protein Folding**	**Apoptosis**		
55		**Counts**	**22**	78		
2.20E-03		**p***	**4.80E-03**	2.40E-04		
APEX1	ING4	**Genes**	CLPX	API5	CSDA	PHB
ASF1A	MBD4		DNAJA1	BAD	CUL2	PROC
FBXO6	MAPK1		DNAJB6	BNIP1	CUL3	PRKCI
FANCI	MAPK14		DNAJC5	BNIP3	CDKN1B	PPP2CA
FANCM	MORF4L1, MORF4		FKBP15	BNIP3L	DEDD	PPP2R1A
KAT5	MLH3		HSPBP1	DDX20	DAPK3	PPP3R1
MBIP	MYO6		RANBP2	DNAJB6	DAD1	RHOA
PRPF19	NONO		AIP	DNAJC5	DIABLO	RIPK1
RAD21	NHEJ1		CANX	NDUFA13	EIF5A	RPL11
RAD51C	NFE2L2		CCT2	NDUFS3	FOXO3/B	YWHAE
RAD51L1	PRDX1		HSPD1	ARHGEF2	GSTP1	BCLAF1
RIF1	PRDX2		HSPA8	SAP30BP	GSK3B	TPT1
REV1	PRDX5		HSPA9	SCAND1	HSPD1	SPHK2
RECQL	PARP2		HSP90AA1	SON	HSPA9	SOD1
XRCC4	PSEN1		HSP90AB1	TRAF4	HDAC6	TMBIM6
XRCC5	PTPLAD1		MPDU1	WWOX	ING4	YWHAB
XRCC6	RIPK1		NFYC	XRCC4	LCK	YWHAZ
ANKRD17	RFC1		PPIB	XRCC5	MBD4	UBB
AATF	SFPQ		PPIE	ABR	MAPK1	UBC
AIFM1	SMC3		PFDN6	ANXA4	MAP3K7	ZC3HC1
CIB1	SOD1		TTC1	APH1A	NME6	
CASP9	TERF2		TBCE	AATF	NAIF1	
C11orf30	TLK1			AIFM1	PAK7	
C12orf44	TLK2			CREB1	PRDX1	
CDK7	UIMC1			CASP2	PRDX2	
FOXO3/B	UBE2A			CASP8	PRDX5	
GSK3B				CASP9	PRAME	
HDAC6				CADM1	PSEN1	
FLJ35220				CLN8	PSENEN	

Supplemental Table 2: mRNAs whose translation was enriched upon HCMV infection but not UL38 Expression: David Functional Analysis

GOTERM_BP_FAT			**Category**	GOTERM_BP_FAT			GOTERM_BP_FAT	
Proteolysis			**Term**	**Vesicle Mediated Transport**			**Transcription**	
88			**Counts**	**60**			**35**	
8.70E-03			**p***	**2.40E-04**			**5.50E-04**	
ATP6AP2	CUL2	PSMB4	**Genes**	ARF1	CHMP5	YWHAZ	XRN2	SNAPC3
BRAP	CUL3	PROC		ARF3	VIPAR	USE1	AFF4	TRIP4
CLPX	CUL7	PIAS4		ARF4	COPG		APEX1	THRB
DZIP3	DLD	RFFL		ARF5	COPG2		BRF2	TCEA3
FBXO6	GAN	RNF25		ARF6	DTNBP1		COPS5	TCEB2
FBXO7	HDAC6	SPCS2		ARFGEF1	ELMO2		GABPA	TTF1
OTUD5	NPEPPS	TOM1L1		ACTR1A	GOSR2		MAX	
OTUB1	LAP3	TRIP12		ATP5B	GGA2		SMARCA5	
RANBP2	LRRC41	TCEB2		ATP6V1H	GNAI3		TAF11	
SKP1	PMPCA	TRIM5		BNIP1	HSPA8		TAF7L	
SMURF1	PMPCB	UQCRC1		ERGIC3	HOOK3		YBX1	
SUMO2	PSEN1	UQCRC2		KDELR1	M6PR		BTF3	
SENP8	PSENEN	UBB		KDELR3	MYO6		CREB1	
UFSP2	PSMC1	UBC		NAPG	NRBP1		CDK7	
VPRBP	PSMC2	UBE3B		RAB14	PI4KB		CDK9	
WSB1	PSMC3	USP28		RAB1A	PICALM		FUBP1	
WDR48	PSMD1	USP47		RAB2A	PSEN1		GTF2I	
WWP2	PSMD11	USP9Y		RAB5A	PACSIN3		GTF2F1	
XPNPEP1	PSMD12	UBE2V1		SAR1B	PRKCI		GTF3C3	
YME1L1	PSMD13	UBE2J2		SNAPIN	PUM1		HSF2	
APH1A	PSMD3	UBE2A		AP1G1	SCAMP1		MED16	
RNPEP	PSMD4	UBE2I		AP1S1	SCAMP3		MED23	
ARIH1	PSMD6	UBE2L3		AP2B1	SNX1		MED7	
BTRC	PSMD7	UBE2M		AP4M1	SNX3		MYEF2	
CAPN7	PSMF1	UBL7		ALS2	SNX4		MLL	
CASP2	PSMA1	UBA6		ARCN1	STX18		NFE2L2	
CASP8	PSMA3	UBE4B		ARRB1	STX4		POLR2J	
CASP9	PSMA5	ZER1		ATL2	TRIP10		RSF1	
CRBN	PSMB1	ZC3HC1		ATL3	TRAPPC5		SNAPC2	

Supplemental Table 2: mRNAs whose translation was enriched upon HCMV infection but not UL38 Expression: David Functional Analysis

GOTERM_BP_FAT	
Metabolism	
58	
5.30E-13	
ADPGK	CYBA
ATP5F1	CYB561
ATP5G2	CYB561D2
ATP5H	COX4I1
ATP5A1	CYC1
ATP5B	DLST
ATP5C1	DLD
ATP6V1D	ETFDH
ATP6V0D1	ENO1
ATP6V1C1	EPM2A
ATP6V1H	GAPDH
ATP6V1B2	GSK3B
ATP6V1A	IDH3A
ATP6V0E1	IDH3B
COX15	IDH3G
NDUFA1	LDHB
NDUFA10	LEPR
NDUFA11	NNT
NDUFA13	NRF1
NDUFS2	OXA1L
NDUFS3	PGK1
NDUFS7	PYGL
SCO1	PPP1CA
TPI1	PDHA1
ACOX1	SLC25A13
ALDOA	SDHC
ALDOC	TXN2
SDHAF2	UQCRC1
CYBRD1	UQCRC2

Supplemental Table 3: mRNAs whose translation was suprressed upon HCMV infection or UL38 Expression: DAVID Functional Analysis

Category	**GOTERM_BP_FAT**		**GOTERM_BP_FAT**					**GOTERM_BP_FAT**
Term	**Differentiation**		**Transcription**					**Negative Regulator of Apoptosis**
Counts	**39**		**124**					**25**
p*	**1.30E-03**		**1.00E-03**					**3.10E-02**
Genes	ELAVL3	TSSK6	AEBP2	ATF5	MLL4	ZFHX3	ZNF80	BCL6
	MDGA1	TNP2	BCL11A	ASXL2	NPAS1	ZNF131	ZNF805	BAG1
	NAA15	ZBTB7B	BCL6	APOBEC3G	NPAT	ZNF221	ZNF844	CFLAR
	PDLIM7	ZNF281	BCOR	ASH1L	PPARA	ZNF224	ZMYM2	GIMAP1
	RASGRP1	ZNF3	CNOT4	BPTF	POLR2J2	ZNF230	XBP1	SON
	TNFSF13	SQSTM1	GABPB2	BRWD1	PTGER3	ZNF235	MYT1	SOX4
	UTP14C		ZGLP1	CDC73	PIAS1	ZNF264	ZBTB7B	STAMBP
	BMP1		KHSRP	CHD9	RBPJ	ZNF281	ZNF791	TBX3
	BMP5		KCNIP3	CUX1	RSF1	ZNF286A		ATF5
	CTNNA2		MXD1	CSRNP3	SHOX	ZNF292		ERCC5
	C11orf9		MYST3	EGR4	SNAPC4	ZNF3		GCLC
	CCDC85B		MYST4	EREG	STON1	ZNF396		HIPK2
	DAZ1,2,3,4		NAB1	EIF2C2	SUV420H1	ZNF432		HIPK3
	EREG		NAA15	FOXN1	SSX3	ZNF440		APOE
	FXR1		POU2F1	FOXN3	TCEANC	ZNF493		IER3
	FRZB		POU3F4	FOXP4	TBL1XR1	ZNF529		IL3
	GPM6B		RORA	GMEB1	TRPS1	ZNF540		ITSN1
	HEMGN		RBM16	GMEB2	TRIM24	ZNF558		NEFL
	INSC		SERTAD2	HNF4A	TTLL5	ZNF585A		NUP62
	JMJD6		SIX5	HOXB1	TP63	ZNF585B		PTEN
	LGALS3		SOX2	HOXB3	UTF1	ZNF592		PTCRA
	MYT1		SOX4	HIPK2	UBTF	ZNF594		PCSK6
	NTRK2		SOX5	HIPK3	ERG	ZNF618		SQSTM1
	ODF3		SMARCC1	JMJD6	ZBTB10	ZNF626		RTEL1
	PPP1R9A		SMARCD3	JUNB	ZBTB11	ZNF653		TP63
	RNF151		SP3	LRRFIP1	ZBTB33	ZNF701		
	SIK1		SPIC	KDM1A	ZBTB34	ZNF703		
	SFRP4		TBX3	KDM2A	ZBTB38	ZNF718		
	SEMA6D		TAF4	MED13	ZBTB44	ZNF780B		

Supplemental Table 3: mRNAs whose translation was suprressed upon HCMV infection or UL38 Expression: DAVID Functional Analysis

GOTERM_BP_FAT	**Category**	**KEGG_PATHWAY**	**SP_PIR_KEYWORDS**	**GOTERM_CC_FAT**	
Chromatin Organization	**Term**	**Antigen Processing and Presentation**	**Immunoglobulin Domain**	**Golgi Apparatus**	
27	**Counts**	**8**	**29**	57	
2.10E-02	**p***	**3.70E-02**	**4.50E-02**	6.70E-04	
AEBP2	**Genes**	IFNA1	BOC	ARFGEF2	CUX1
BCOR		IFNA13	CD2	ARL3	CLASP1
INO80		IFNA2	CD200	ABCA1	DSE
MPHOSPH8		KIR2DL4	CD22	EMID2	DPP4
MYST3		KIR2DL5A	FCRL2	FGD6	ENTPD4
MYST4		HLA-DOB	MDGA1	GCC2	FTCD
SATB1		HLA-DQB1	VSIG1	JAKMIP3	FUT7
SATB2		HLA-DQA1	CEACAM7	KCNIP3	GAD2
SOX2			IGHA1	MFNG	GGA2
SMARCC1			IGHA2	NAPB	GOLGA2
SMARCD3			IGHD	NAB1	GOLGA4
ASH1L			IGHG3	RAB2A	GOLIM4
BPTF			IGHG2	RASGRP1	HS2ST1
CDC73			IGSF9B	SAR1B	APOE
CHD9			JAM3	SEC16A	FGF7
HIST1H1B			KIR2DL4	SEC24A	KGFLP2
HIST1H3I			KIR2DL5A	ST8SIA1	MAN1A2
JMJD6			LRIG2	ST8SIA4	NUFIP2
KDM1A			LILRA1	B3GNT8	PAQR3
KDM2A			LILRA2	GALNT1	PCSK6
MLL4			MFAP3L	GALNTL1	SERINC3
RSF1			MPZL2	AIMP1	SLC30A7
SUV420H1			NTRK2	AVPR2	SLC35A1
SYCP3			VPREB1	ARSB	SYNE1
TSSK6			PRTG	BICD1	STX12
TLK2			SEMA3F	C16orf70	VPS53
TBL1XR1			SIGLEC11	CLTB	VCPIP1
			TMEM25	COG6	ZDHHC17
			UNC5C	CUL3	

Supplemental Table 3: mRNAs whose translation was suprressed upon HCMV infection or UL38 Expression: DAVID Functional Analysis

GOTERM_BP_FAT		Category	GOTERM_CC_FAT	GOTERM_BP_FAT	COG_ONTOLOGY
Calcium		**Term**	**Proteinaceous Extracellular Matrix**	**Lipid Transport**	**Cell Division**
47		**Counts**	**21**	**16**	**15**
2.40E-02		**p***	**4.50E-02**	**2.30E-03**	**1.60E-03**
ADAMTS13	MAN1A2	**Genes**	ADAMTS13	ABCA1	CTAGE5
EFHB	MMP11		ADAMTS8	ATP9B	DAB2IP
EHD4	MMP16		EMID2	APOL2	FKBP15
GPR98	PON1		AGRN	APOL4	IQCE
KCNIP3	PON2		CHI3L1	FABP2	RAB11FIP4
RAB11FIP4	PTHLH		COL1A1	APOE	RASAL3
RASGRP1	PLA2G12B		COL9A2	LDLR	CEP350
S100A14	PCSK6		COL27A1	MTTP	CCDC144A
GALNT1	PRKCB		ENTPD2	OSBP2	DSP
GALNTL1	PPEF2		EPYC	OSBPL11	KIF13A
ABP1	PCDHB3		ERBB2IP	OSBPL8	NINL
ARSB	SRL		FLRT3	PNLIP	SYNE1
ARSD	SLC25A24		GPLD1	PPARA	STAG1
BEST1	SPOCK3		HMCN2	PITPNC1	STAG2
BMP1	SPATA21		LGALS3	PLEKHA8	TLK2
CDH10	TRPM3		MMP11	STX12	
CDH12	TRPV6		MMP16		
CDH4	TPCN2		SERPINA1		
CDH26			SPOCK3		
CLTB			TNXB		
DMD			WNT9A		
ENTPD2					
ENTPD4					
FLG2					
GRIN2A					
GRIN2B					
GRIN3A					
ITPR2					
ITSN1					

Supplemental Table 4: mRNAs whose translation are enriched during UL38 expression but not HCMV infection

Category	**GOTERM_BP_FAT**			**GOTERM_BP_FAT**	**GOTERM_BP_FAT**	**GOTERM_BP_FAT**
Term	**Transcription**			**Regulation of Cellular Response To Stress**	**DNA Metabolic Process**	**Regulation of JNK Cascade**
Counts	**71**			**7**	**3.9**	**5**
p*	**0.02**			**0.023**	**0.044**	**0.05**
Genes	BCL11A	HMG20B	ZNF329	EDN1	DFFA	EDN1
	BRF1	HIPK2	ZNF493	HIPK2	FBXO4	HIPK2
	DPF3	HIF3A	ZNF548	MAPK8IP3	GATAD2A	MAPK8IP3
	GABPB2	IFT57	ZNF558	PAK1	PMS1	PAK1
	GATAD2A	NR2F2	ZNF562	RNF168	PMS2CL	AKT2
	KLF7	NFYB	ZNF575	TMEM189	PMS2	
	LIMD1	NACC1	ZNF587	AKT2	RAD18	
	LHX9	PPARA	ZNF599		RAD52	
	MXD1	PBX3	ZNF611		RECQL4	
	MAMSTR	PKIA	ZNF618		CEP164	
	MLXIP	RUNX1T1	ZNF621		CYCS	
	MDM4	SQSTM1	ZNF677		ESCO2	
	PKNOX1	ZNF605	ZNF710		KRT7	
	SLC2A4RG	TCEB3	ZNF765		RNASEH1	
	SOX11	TFAP2A	ZNF791		RPS27L	
	SOX4	TCFL5	ANP32A		RNF168	
	TSC22D2	TMEM189	HMGA2		TTC5	
	BNC1	UBP1	ZFP30		TOP3A	
	CAMKK2	MYB	ZNF320			
	CTNNBIP1	VAX2				
	CDYL	VDR				
	CCDC85B	ZBTB8B				
	DGKQ	ZNF783				
	EGR1	ZNF100				
	EGR2	ZNF17				
	EGR3	ZNF197				

Supplemental Table 4: mRNAs whose translation are enriched during UL38 expression but not HCMV infection

Category	**GOTERM_BP_FAT**	**GOTERM_BP_FAT**	**GOTERM_CC_FAT**	
Term	**Cellular Macromolecule Catabolic Process**	**Response to DNA Damage Stimulus**	**Cytoskeleton**	
Counts	**24**	**14**	**36**	
p*	**0.038**	**0.057**	**0.02**	
Genes	ADAM9	PMS1	ACTR3B	KIF1C
	ATG10	PMS2CL	CDK5RAP2	MYO3B
	DFFA	PMS2	FRMD4A	OPHN1
	FBXL17	RAD18	FRMD8	SHROOM2
	FBXO4	RAD52	ARHGAP24	STX1A
	FBXO46	RECQL4	ARHGAP32	TMSB15B
	HECTD2	XIAP	SH3KBP1	TTN
	RAB40B	CEP164	WIPF1	TBCD
	RAD18	DYRK2	ANXA11	KRTAP4-7
	XIAP	ESCO2	CEP164	KRTAP4-9
	ARIH2	HIPK2	CCDC85B	
	CLN8	RPS27L	CYLC1	
	CYCS	RNF168	DGKQ	
	EIF2C4	TTC5	DVL1	
	KLHL3		EML3	
	MIB2		FEZ1	
	RNASEH1		FERMT1	
	RNF168		FHL3	
	SQSTM1		GAS2L1	
	CACYBP		HIPK2	
	USP42		IFT57	
	USP7		IFT80	
	TMEM189		KLHL2	
	UBE2D4		KLHL3	
			KRT19	
			KRT7	

Supplemental Table 5: Subanalysis of *Cell cycle, mitochondrion, apoptosis, RNA processing stress-response* terms from Supplementary Table 1 and Table 2

Cell Cycle

Category	Term	Counts	%	Pvalue	Genes					
GOTERM_BP_FAT	Mitosis	32	26	9.70E-29	CLIP1	SEH1L	CCNB1	NDE1	SMC3	ZC3HC1
					MAD2L2	SETD8	DCTN2	PES1	HAUS7	ZNF830
					NIPBL	WEE1	KIF22	PPP5C	TUBB2A	TGFB2
					PDS5B	BUB1	MAPRE3	SGOL1	TUBB2B	
					RAD21	BUB3	NUDC	CDK11A/B	TUBB	
					ARHGEF2	CETN2	NUP43	STAG2	UBE2I	
GOTERM_BP_FAT	Cell Cycle Arrest	17	13.8	7.80E-16	UHMK1	AK1	CDC123	CUL2	CUL3	VASH1
					CDKN1B	CDKN2D	GAS1	ING4	ILK	
					IRF6	PML	PPP2R3B	TBRG1	TBRG4	
GOTERM_BP_FAT	Interphase	13	10.6	1.80E-10	CDC123	CUL2	CUL3	CCNB1	CDK10	PPP6C
					CDKN1B	CDKN2D	ID4	KPNA2	PPP2R3B	TBRG4
										TPD52L1
GOTERM_BP_FAT	Meiosis	11	8.9	1.80E-08	CKS2	DMC1	RAD1	RAD21	RAD51C	SMC3
					RAD51L1	MLH3	PSMD13	SGOL1	STAG2	
GOTERM_BP_FAT	Response to DNA Damage	18	14.6	3.90E-08	FANCI	RAD1	RAD21	RAD51C	RAD51L1	HAUS7
					RIF1	CDK7	CDKN2D	ING4	KIF22	TLK1
					MAPK1	MLH3	PML	SMC3	TERF2	TLK2
GOTERM_BP_FAT	Chromosome Segregation	11	8.9	2.70E-09	NIPBL	PDS5B	RAD21	RAD51C	SEH1L	BUB3
					NUP43	SGOL1	STAG2	SMC3	UBE2I	
GOTERM_BP_FAT	G1/S transition of the mitotic cell cycle	6	4.9	1.50E-04	CUL2	CUL3	CDKN1B	CDKN2D	ID4	PPP6C
					DCTN2	DYNC1H1	NDE1	RANBP1	SMC3	HAUS7
						TUBB				
GOTERM_BP_FAT	Cytoskeletal Organization	13	10.6	5.70E-04	CKS2	PRR5	ARHGEF2	SEH1L	BIN3	CETN2
GOTERM_BP_FAT	DNA Replication	8	6.5	1.70E-03	RAD1	CDT1	CINP	CDKN2D	RBBP4	ING4
						TERF2	TBRG1			
GOTERM_BP_FAT	Regulation of Apoptosis	17	13.8	2.30E-03	ARHGEF2	CUL2	CUL3	CDKN1B	CDKN2D	GSK3B
					GAS1	ING4	ILK	KRT18	MAPK1	ZC3HC1
					PML	TGFB2	TUBB	UBB	UBC	

Supplemental Table 5: Subanalysis of *Cell cycle, mitochondrion, apoptosis, RNA processing stress-response* terms from Supplementary Table 1 and Table 2

Mitochondrion

Category	Term	Counts	%	Pvalue	Genes					
GOTERM_BP_FAT	mitochondrial transport	11	13.1	3.40E-12	ATP5O	ATP5D	BAK1	BAX	PPIF	SLC25A6
					SLC25A10	SLC25A30	SLC25A37	TIMM10	TOMM22	
GOTERM_BP_FAT	mitochondrial membrane organization	6	7.1	7.70E-07	BAK1	BAX	PPIF	SAMM50	TIMM10	TOMM22
GOTERM_BP_FAT	Oxidative Phosphorylation	6	7.1	2.00E-04	ATP5G2	ATP5O	ATP5D	NDUFA7	NDUFB7	NDUFS6
GOTERM_BP_FAT	Translation	8	9.5	2.20E-03	MRPL12	MRPL23	MRPL4	MRPL9	MRPS10	MRPS16
					COG8, PDF	SARS2				
GOTERM_BP_FAT	regulation of defense response to virus	3	3.6	4.80E-03	AP2M1	APOBEC3F	APOBEC3G			

Apoptosis

Category	Term	Counts	%	Pvalue	Genes					
GOTERM_BP_FAT	Cell cycle arrest	9	8	2.40E-06	CUL2	CUL3	CDKN1B	CDKN2D	GAS1	ING4
					ILK	PML	TGFB2			
GOTERM_BP_FAT	Response to DNA damage stimulus	15	13	3.00E-06	BAX	XRCC4	XRCC5	AATF	AIFM1	CASP9
					CDKN2D	FOXO3B, F	ING4	MBD4	MAPK1	SOD1
					PHLDA3	PSEN1	PML			
GOTERM_BP_FAT	Immune system development	13	11	3.60E-06	BAK1	BAX	SCAND1	XRCC4	XRCC5	CASP8
					HSPD1	LCK	PRDX2	PSEN1	PML	TGFB2
					SOD1					
GOTERM_BP_FAT	Regulation of cell size	11	10	9.30E-06	NDUFA13	NDUFS3	CREB1	CLN8	CDKN1B	CDKN2D
					ILK	PML	PPP2CA	PPP2R1A	TGFB2	
GOTERM_BP_FAT	DNA fragmentation involved in apoptosis	4	4	5.10E-04	BAX	BNIP3	AIFM1	SOD1		
GOTERM_BP_FAT	Response to nutrient levels	8	7	1.40E-03	ASNS	CDKN2D	DAD1	DDAH2	HDAC6	PTENP1
					PSEN1	SOD1				
GOTERM_BP_FAT	Response to radiation	8	7	1.50E-03	BAK1	BAX	XRCC4	CASP6	CASP9	CDKN2D
					MBD4	PML				
GOTERM_BP_FAT	posttranscriptional regulation of gene expression	8	7	2.00E-03	NDUFA13	EIF5A	HSPB1	HSPD1	MAPK1	PTENP1
					PML	PRKRA				

Supplemental Table 5: Subanalysis of *Cell cycle, mitochondrion, apoptosis, RNA processing stress-response* terms from Supplementary Table 1 and Table 2

RNA Processing

Category	Term	Counts	%	Pvalue	Genes					
	nuclear mRNA splicing, via spliceosome	32	39	2.60E-40	CD2BP2	DDX1	DDX20	DHX38	RBM25	SRPK2
					SNW1	YBX1	RSRC1	CSTF1	FUS	GEMIN6
					GTF2F1	HNRNPC	HNRNPH1	HNRNPU	WDR83	NOVA1
					NUDT21	PABPN1	PCBP1	PCBP2	POLR2J	PTBP1
					SRRM1	SNRNP40	SNRPA1	SNRPC	SNRPB	SF3A1
					SF3B1	SF3B2				
GOTERM_BP_FAT	rRNA processing	12	14.6	1.00E-11	IMP3	UTP15	DCAF13	RPF1	EXOSC10	EXOSC4
					EXOSC6	PES1	RPL11	RPL35A	RPS19	TFB1M
GOTERM_BP_FAT	tRNA processing	5	6.1	1.10E-03	TRUB2	C1orf25	MOCS3	RPP30	TRMU	
GOTERM_BP_FAT	RNA stabilization	3	3.7	3.50E-03	YBX1	HNRNPU	SYNCRIP			
GOTERM_BP_FAT	posttranscriptional regulation of gene expression	6	7.3	8.70E-03	DDX1	YBX1	HNRNPU	LIN28B	QKI	SYNCRIP
GOTERM_BP_FAT	mRNA capping	2	2.4	2.40E-02	RNMT	RNGTT				

Stress Response

Category	Term	Counts	%	Pvalue	Genes					
GOTERM_BP_FAT	DNA recombination	10	18.2	2.90E-10	RAD21	RAD51C	RAD51L1	RECQL	XRCC4	XRCC5
					XRCC6	MLH3	NONO	SFPQ		
GOTERM_BP_FAT	DSB repair via nonhomologous end joining	4	7.3	7.10E-06	XRCC4	XRCC5	XRCC6	NHEJ1		
GOTERM_BP_FAT	cell cycle	14	25.5	8.20E-06	FANCI	RAD21	RAD51C	RAD51L1	RIF1	CDK7
					GSK3B	ING4	MAPK1	MLH3	SMC3	TERF2
					TLK1	TLK2				
GOTERM_BP_FAT	cellular response to oxidative stress	5	9.1	2.50E-05	HDAC6	PRDX1	PRDX2	PRDX5	SOD1	
GOTERM_BP_FAT	telomere maintenance	4	7.3	1.80E-04	XRCC5	XRCC6	RFC1	TERF2		
GOTERM_BP_FAT	induction of apoptosis	8	14.5	2.60E-04	AATF	AIFM1	FOXO3B, F	MBD4	MAPK1	PRDX1
					PSEN1	RIPK1				
GOTERM_BP_FAT	response to ionizing radiation	4	7.3	1.80E-03	XRCC4	XRCC6	NHEJ1	UIMC1		
GOTERM_BP_FAT	base-excision repair	3	5.5	5.10E-03	APEX1	MBD4	PARP2			
GOTERM_BP_FAT	cellular response to starvation	3	5.5	7.20E-03	C12orf44	HDAC6	PSEN1			
GOTERM_BP_FAT	anti-apoptosis	5	9.1	9.10E-03	AATF	GSK3B	PRDX2	PSEN1	SOD1	
GOTERM_BP_FAT	autophagy	3	5.5	1.00E-02	C12orf44	HDAC6	PSEN1			

Supplementary Figure 6: 5' UTR analysis of mRNAs that are translationally regulated during HCMV infection

	Avg 5'UTR length	**%GC**
HCMV/UL38 Upregulated	311	0.64
HCMV Upregulated	346	0.63
HCMV/UL38 Downregulated	382	0.62

Supplemental Table 7: TOP motif-bearing mRNAs recruited to polysomes during UL38 stimulation and/or HCMV infection

HCMV/UL38 stimulated

	Refseq_mRNA	Gene Symbol		Refseq_mRNA	Gene Symbol
1	NM_001001396	ATP2B4	**32**	NM_032873	UBASH3B
2	NM_001146310	C1orf86	**33**	NM_014312	VSIG2
3	NM_001185094	NIT1	**34**	NM_006331	EMG1
4	NM_001277223	TAGLN2	**35**	NM_012461	TINF2
5	NM_001684	ATP2B4	**36**	NM_001099274	TINF2
6	NM_003564	TAGLN2	**37**	NM_033250	PML
7	NM_006608	PHTF1	**38**	NM_033249	PML
8	NM_001135659	NRXN1	**39**	NM_002675	PML
9	NM_004801	NRXN1	**40**	NM_033246	PML
10	NM_138735	NRXN1	**41**	NM_033244	PML
11	NM_001035521	GTF3C2	**42**	NM_033240	PML
12	NM_001521	GTF3C2	**43**	NM_033239	PML
13	NM_001381	DOK1	**44**	NM_033238	PML
14	NM_002823	PTMA	**45**	NM_033247	PML
15	NM_001099285	PTMA	**46**	NM_001003	RPLP1
16	NM_020701	ISY1	**47**	NM_213725	RPLP1
17	NM_001199469	ISY1	**48**	NM_002952	RPS2
18	NM_000995	RPL34	**49**	NM_001128827	DLG4
19	NM_021177	LSM2	**50**	NM_018096	NLE1
20	NM_001402	EEF1A1	**51**	NM_001014445	NLE1
21	NM_001199464	PDCD2	**52**	NM_001961	EEF2
22	NM_001199463	PDCD2	**53**	NM_001005335	HNRNPL
23	NM_001199462	PDCD2	**54**	NM_001013	RPS9
24	NM_032983	CASP2	**55**	NM_014501	UBE2S
25	NM_032982	CASP2	**56**	NM_007367	RALY
26	NM_015878	AZIN1	**57**	NM_016732	RALY
27	NM_148174	AZIN1	**58**	NM_203417	RCAN1
28	NM_032928	TMEM141	**59**	NM_013327	PARVB
29	NM_001171689	AMMECR1	**60**	NM_001084392	DDT
30	NM_006201	CDK16			
31	NM_001177660	HABP2			

HCMV stimulated

	Refseq_mRNA	Gene Symbol		Refseq_mRNA	Gene Symbol
61	NM_014873	LPGAT1	**97**	NM_152713	STT3A
62	NM_001277223	TAGLN2	**98**	NM_001190977	YAF2
63	NM_003564	TAGLN2	**99**	NM_001769	CD9
64	NM_001177665	RIF1	**100**	NM_004064	CDKN1B
65	NM_001037631	CTLA4	**101**	NM_002300	LDHB
66	NM_005214	CTLA4	**102**	NM_001206710	PRKAG1
67	NM_004622	TSN	**103**	NM_005967	NAB2
68	NM_001261401	TSN	**104**	NM_001009894	C12orf29
69	NM_001690	ATP6V1A	**105**	NM_003295	TPT1
70	NM_001005474	NFKBIZ	**106**	NM_002515	NOVA1
71	NM_015173	TBC1D1	**107**	NM_006491	NOVA1
72	NM_001253912	TBC1D1	**108**	NM_006489	NOVA1
73	NM_001104631	PDE4D	**109**	NM_001164814	ACIN1
74	NM_012343	NNT	**110**	NM_014977	ACIN1
75	NM_024337	IRX1	**111**	NM_001164815	ACIN1
76	NM_015288	PHF15	**112**	NM_012461	TINF2
77	NM_003447	ZNF165	**113**	NM_001099274	TINF2
78	NM_175061	JAZF1	**114**	NM_182758	WDR72
79	NM_032983	CASP2	**115**	NM_144598	LRRC28
80	NM_032982	CASP2	**116**	NM_171846	LACTB
81	NM_018941	CLN8	**117**	NM_032857	LACTB
82	NM_003406	YWHAZ	**118**	NM_001003	RPLP1
83	NM_152786	C9orf43	**119**	NM_213725	RPLP1
84	NM_006603	STAG2	**120**	NM_007014	WWP2
85	NM_001042750	STAG2	**121**	NM_001270455	WWP2
86	NM_001042751	STAG2	**122**	NM_001270454	WWP2
87	NM_001193417	DDX3X	**123**	NM_000196	HSD11B2
88	NM_001193416	DDX3X	**124**	NM_014003	DHX38
89	NM_001356	DDX3X	**125**	NM_001002841	MYL4
90	NM_014456	PDCD4	**126**	NM_006801	KDELR1
91	NM_145341	PDCD4	**127**	NM_004461	FARSA
92	NM_001199492	PDCD4	**128**	NM_006814	PSMF1
93	NM_018259	TTC17	**129**	NM_144703	LSM14B
94	NM_015231	NUP160	**130**	NM_001135161	COMT
95	NM_006597	HSPA8			
96	NM_153201	HSPA8			

Supplemental Table 8: DAVID functional analysis of TOP bearing mRNAs in Supplentary Table 6

Category	Term	Counts	%	p-val	Genes
GOTERM_BP_FAT	Translational elongation	6	7.3	1.40E-04	eEF1A1,EEF2,RPL34,RPS2,RPS9, RPLP1
GOTERM_BP_FAT	Translation	7	8.5	5.80E-03	eEF1A1,EEF2,FARSA, RPL34,RPS2,RPS9,RPLP1
GOTERM_BP_FAT	Transmission of Nerve Impulse	7	8.5	7.60E-03	CD9,NAB2COMT,CLN8,DLG4,NRXN1, NOVA1
GOTERM_BP_FAT	Negative Regulation of Macromolecule Metabolic Process	10	12	9.90E-03	JAZF1,NAB2,TINF2,WWP2,YAF2,CLN8,CDKN1B,PDCD4,PML,PSMF1
GOTERM_BP_FAT	RNA splicing	6	7.3	1.30E-02	DHX38,ISY1,LSM2,RALY,NOVA1, HNRNPL
GOTERM_BP_FAT	Negative Reg. of Nitrogen Compound Metabolic Process	8	9.8	1.40E-02	JAZF1,NAB2,TINF2,YAF2,COMT, CDKN1B,PDCD4,PML
GOTERM_BP_FAT	mRNA Processing	6	7.3	2.10E-02	DHX38,ISY1,LSM2,RALY,NOVA1, HNRNPL
GOTERM_BP_FAT	Neg. Reg. of Cell Proliferation	6	7.3	3.30E-02	CD9,TINF2,COMT,CDKN1B,CTLA4,PML
GOTERM_BP_FAT	learning	3	3.7	3.60E-02	COMT,CLN8,DLG4
GOTERM_BP_FAT	mRNA metabolic process	6	7.3	3.60E-02	DHX38,ISY1,LSM2,RALY,NOVA1, HNRNPL
GOTERM_BP_FAT	Neg. Reg. of Gene Expression	7	8.5	3.80E-02	JAZF1,NAB2,WWP2,YAF2,CDKN1B, PDCD4,PML
GOTERM_BP_FAT	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	4	4.9	4.00E-02	DHX38,LSM2,NOVA1,HNRNPL
GOTERM_BP_FAT	Nuclear mRNA splicing, via spliceosome	4	4.9	4.00E-02	DHX38,LSM2,NOVA1,HNRNPL

Supplementary Table 9: Overlap in translation signatures with other translateome studies

Badura et al

Query List: Translationally upregulated mRNAs in IR treated MCF10a cells where eIF4G1 is upregulated

Target List: HCMV induced translationally upregulated genes

p= 0

Overlapping Genes:

ACADSB	BBX	DDX46	GNPDA2	MLH3	PEX13	RAB3GAP2	SLC41A2	TAB3
ACOX1	BCLAF1	DDX6	HNRNPU	MLL	PGK1	RANBP9	SLC4A1AP	TBC1D12
ACTR2	BNIP3L	DIAPH2	HOOK3	MR1	PGM3	RBBP4	SMARCA1	TBC1D8B
AFF4	BRAP	DZIP3	HP1BP3	MYEF2	PICALM	RBM25	SMARCA5	THOC2
AKAP12	BUB1	EIF4G3	HSPA4	MYO6	PIK3C2A	RECQL	SMC3	TLK1
ANKHD1	C11orf30	EIF5B	IFNGR1	NAMPT	PLAA	REV1	SMEK1	TLK2
API5	C1orf25	EPB41L2	INPP4A	NAPG	PLEKHA1	RFC1	SNX1	TMOD3
APPBP2	C3orf38	EPB41L4A	IRF6	NDFIP2	PLRG1	RIF1	SNX4	TOR1AIP2
ARFGEF1	CANX	EPM2AIP1	JAZF1	NFKBIZ	PNN	RIOK3	SPG20	TTF1
ARIH1	CAPN7	FANCM	JMJD1C	NIPBL	PRKAA1	RIPK1	SRPK2	UBA6
ARL6IP5	CASK	FNDC3B	KIF3A	NPEPPS	PRKCI	RNGTT	SS18	UBE4B
ASF1A	CDC5L	FUBP1	KRIT1	NRP2	PRPF40A	RSF1	SSH2	UBXN4
ATL2	CDK8	FXR1	LARP4	NT5DC1	PSMC2	RSL1D1	SSR1	USP28
ATP6AP2	CHMP2B	G3BP1	LPGAT1	NUMB	PSMD12	RSRC1	STAG2	USP47
ATP6V1A	CTNNA1	GABPA	LRRFIP1	ORMDL1	PSPC1	SCAMP1	STAM2	UTP15
ATP6V1C1	CUL2	GALNT7	MAP3K7	PCM1	QKI	SGCB	STK38	VPS53
BAZ2B	CUL3	GAN	MATR3	PDCD4	QRSL1	SKAP2	STXBP4	WAC
BBS9	DDX18	GFM2	MFN1	PDE4D	RAB2A	SKIV2L2	SYNCRIP	WAPAL
WBP4	WDR48	YLPM1	YTHDC2	ZBTB44	ZFR	ZNF165	ZNF638	ZNF654

Badura et al

Query List: Translationally downregulated mRNAs in IR treated MCF10a cells where eIF4G1 is depleted

Target List: HCMV/UL38 induced translationally upregulated genes

p= 0 .00927

Overlapping Genes:

AP1S3	CASP2	CENPO	GINS3	KPNA2	NUP43	RFC2	TMPO	NFKBIL2
ARHGDIA	CBX5	CKS2	GINS4	MCM5	OBSL1	S100A4	TYMS	RAD1
B4GALT6	CCNB1	CYB5B	H2AFZ	MYBL2	PHTF1	SAP30L	UBE2S	TK1
CALM1	CDT1	EIF4E	H3F3B	MYO19	PPIL5	SGOL1	UBE2T	VTI1B
CAMK4	CENPM	G3BP1	HADH					

Mamame et al

Query List: Translationally upregulated mRNAs in eIF4E overexpressing 3T3 cells

Target List: HCMV induced translationally upregulated genes

p= 0.0421

Overlapping Genes:

COPE	PMM1	RGS12	DCTD	PSPH	SSNA1	GNAI2	RBBP9	TREX1
COX8A	PRKRA	SEH1L	EIF1	QDPR	STX17	H2AFZ	RGS12	TROAP

Supplementary Table 9: Overlap in translation signatures with other translateome studies

Larsson et al

Query List: Translationally down-regulated mRNAs in metformin treated MCF7 cells
Target List: HCMV/UL38 induced translationally upregulated genes
p= 0
Overlapping Genes:

ACAT2	ATP5O	CENPW	EIF1	GINS4	MRPL12	PARVB	PSPH	SLC25A10
ACER3	C10orf140	CLN6	EIF6	GPN2	MRPL23	PFDN6	RANBP1	SRSF1
ACOT7	C11orf1	CYB5B	EMG1	HAUS7	MRPL54	PIR	RFC2	SRSF6
ADK	C12orf48	DMC1	ETNK1	LUC7L	MRTO4	POLR3C	RFXANK	TIMM10
ALG13	C3orf75	DNLZ	FAH	MCM5	NDUFS6	POLR3K	RQCD1	TK1
ASNS	C7orf44	DOHH	GALE	MED22	NUDT1	PPIF	S100A4	TMEM138
ATP5D	CCND3	DTYMK	GINS3	METTL11A	ORC5	PSME2	SIP1	TMPO
TUBB	TYMS	UBE2T	UEVLD	WDR4				

Larsson et al

Query List: Translationally down-regulated mRNAs in metformin treated MCF7 cells
Target List: HCMV induced translationally upregulated genes
p= 0.00000008
Overlapping Genes:

AP1S1	CUL2	GPATCH2	MRPS31	PRKAB1	RIF1	SPG20	CRBN	COPS3
ARMC6	DIAPH2	HAT1	NAA15	PSMA3	RIPK1	SRPRB	GLRX3	GEMIN6
ATL3	DNAJA1	HHEX	NFKBIZ	PSMD3	RNF25	TIMM44	MRPL27	MED6
C12orf44	EXOSC4	HSD11B2	ORC5	PSPC1	RPAP3	TIMM50	PRAME	PNN
C12orf60	EXOSC6	HSPA4	OSBPL11	RAD51L1	S100A4	TRMU	RBM45	RBM39
CCDC58	G3BP2	ICT1	PCYT1A	RBBP4	SENP8	WSB1	SNRNP40	SMC3
CDKAL1	GADD45GI	MED21	PFDN6	RBM25	SFPQ	YBX1	ZNF654	

Hsieh et al

Query List: Translationally down-regulated mRNAs in pp242 treated PC3 cells
Target List: HCMV/UL38 induced translationally upregulated genes
p= 0.000386
Overlapping Genes:

EEF2	ALKBH7	EEF1A1	PGLS	RPL36	RPS2	RPS9	RPS23	SIGMAR1
AHCY	ATP5G2	EIF2S3	RPL34	RPLP1				

Bilanges et al

Query List: Translationally up-regulated mRNAs in TSC2 knockout MEFs
Target List: HCMV induced translationally upregulated genes
p= 0.000963
Overlapping Genes:

ACBD6	BTF3	CCT2	FXR1	HSPA8	KDELR1	NUDT21	PPIB	RPL35A
ATP5A1	SSR4							

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Antibodies and quantitative immunoblotting

Antibodies were acquired from the following vendors/individuals: PABP1 (*S. Morley, Univ. Sussex, UK*), Akt (*Cell Signaling #9272*), Actin (*Calbiochem #CP01*), pp28 (*Abcam # ab6502*), UL44 (*Virusys # CA006*), IE1/2 (*Millipore #MAB810*), UL38 (*gift from T. Shenk-Princeton Univ.*), PP1α (*Cell Signaling #2582*), STAT3 (*Cell Signaling #4904*), eEF2 (*Cell Signaling #2332*), Gsk3β (*Cell Signaling #5676*), eIF4H (*Cell Signaling #2444*), anti- Vaccinia Virus (*Virostat #8101*), ICP0 (*Goodwin Inst. #1114*), VP16 (*gift from A. Wilson, NYU*), Us11 (*gift from Rich Roller, Univ. Iowa*). For quantitative immunoblotting, a secondary antibody covalently linked to an infrared fluorophore was used (#'s 827-08364, 926-68171 *Li-Cor Biosciences*) and the membrane was scanned using an Odyssey infrared imager (*Li-Cor Biosciences*).

Cells, Viruses and Chemicals

Normal Human Diploid Fibroblasts (NHDFs; purchased from *Clonetics*) were routinely sub-cultured by a 1:3 split and maintained until passage 20 in complete media (DMEM supplemented with 5% FBS, 1% L-glutamine, and 1% Penicillin/Streptomycin [v/v]). GFP-expressing HCMV (AD169 strain) Wild-type (WT) virus was propagated as described (*Terhune et al., 2007*). Doxycycline-inducible, UL38-expressing NHDFs were generated as described *(McKinney et al., 2013*). To produce lentiviruses, 293 FT cells were transfected at 70%

confluency with equimolar amounts of the pSLIK hygro-UL38 recombined plasmid produced above, Δ8.9 packaging vector, and pMO2G VSV-G envelope protein containing vector. Supernatants were collected 48 and 72 hrs post transfection and used to infect early passage NHDFs twice for 18 hours each. A Tet-inducible UL38-expressing population of transduced cells was then selected using 50 μg/ml hygromycin B (*Life Technologies*).

Preparation of cell-free extracts for polysome isolation

NHDFs (1 x10^7 mock or HCMV-infected (MOI=3); or stably-transduced with a dox-inducible (-/+ 1 μg/ml dox) UL38-expression vector (*McKinney et al., 2013*) were cycloheximide (CHX)-treated (100 μg/ml) for 10 min. in complete media, washed with PBS, trypsinized to detach the cells, and resuspended in an equal volume buffer 1 [PBS + 1x EDTA-protease inhibitor (Roche)+ CHX]. Cells were pelleted at 1250 RPM for 4 min. and the resulting pellet rinsed with buffer 1, resuspended in 750 μl of polysome isolation buffer (200mM Tris-HCl, pH 7.5, 100 mM NaCl, 30 mM $MgCl_2$, 100 μg/ml CHX) and cooled on ice for 5 min. Detergent lysis buffer [1.2% triton X-100, 0.2M sucrose in polysome isolation buffer) was added (250 μl) to the suspended cells and the mixture homogenized gently with 10 strokes using a dounce. Lysates were clarified by centrifugation (10,000 x g) for 10 min. at 4°C. Supernatants were transferred to a fresh tube containing 100 μl of heparin sulfate (10 mg/ml; *Sigma*) in polysome isolation buffer + CHX (100 μg/ml).

Gradient fractionation and polysome isolation

Cell free lysates supplemented with heparin sulfate prepared as described in the preceding section were layered onto 11 ml 15-50% linear sucrose gradients (in polysome isolation buffer supplemented with 100 μg/ml CHX), sedimented at 36,000 RPM for 1.5 hours, at 4°in an SW40 rotor and allowed to stop without use of the brake. Gradients were fractionated using an ISCO fraction collector by pushing >50% sucrose from the bottom and collecting 750 μl fractions from the top while monitoring the RNA absorbance at 254 nM. EDTA was added to 20 mM and RNA extracted with 1 volume of acid phenol-$CHCl_3$ followed by $CHCl_3$-extraction and precipitated overnight with 1 volume of isopropanol and 0.1 volume of sodium acetate. RNA was pelleted at 13000 x g for 10 min at 4^{o}C, rinsed with 75% ethanol, and resuspended in 100 μl of nuclease-free H_2O. Fractions 5-12, representing polysome fractions were pooled, phenol-$CHCl_3$ extracted, precipitated with isopropanol, washed with ethanol as described and resuspended in 30 μl nuclease-free H_2O.

Microarray analysis

DNA array analysis was performed at the NYU Genome Technology Center. Samples were processed in duplicate for each experimental condition. RNA quantity and quality was analyzed using Agilent 2100 Bioanalyzer and Nanodrop-2000. Preparation of biotinylated cRNA probes using 100 ng of pooled polysome RNA and hybridization to GeneChip HGU133A 2.0 arrays followed the recommendations of the manufacturer (Affymetrix). Raw data were normalized by Robust Multichip Average (RMA) involving a background adjustment, quantile normalization and summarization performed by the GeneSpring (*Agilent*) software version GX11 (*Irizarry et al., 2003*). Differentially abundant mRNAs were identified by t-test with the p-value cut-off of 0.05 at alpha level. Individual differential abundance data obtained from independent, duplicate samples were extensively validated by qPCR and immunoblotting in lieu of applying corrections for multiple testing due to the investigative, rather than corroborative nature of the microarray experiment. We used the Pavlidis Template Matching algorithm available in the open source TM4 analytical suite and fold-change thresholding to define specific types of profiles of mRNA abundance across experimental conditions (*Saeed et al., 2003*). The complete set of microarray data was deposited for public access to the NCBI Gene Expression Omnibus database.

RNA interference, Viral Replication Assay, and Microscopy

The eIF6 siRNA smartpool was purchased from *Dharmacon* (*M-010096-01-0005*). PP1α siRNA # 5 and 6 were purchased from *Qiagen (SI02225748 and SI02225755,* respectfully). AllStars Negative Control siRNA, a synthetic 21-nucleotide complementary RNA with 2 nucleotide overhangs was used as a nonsilencing control (*Qiagen 102728*). NHDFs were grown to 70-80% confluence on a 12 well plate and transfected with 20 nM of siRNA + 2ul of RNAi Max according to the manufacturer's instructions (*Life Technologies*). 48 hours after transfection, cells were infected with AD169 WT HCMV-GFP (MOI= 0.1) for 4 days. EGFP-expression was used to measure HCMV spread and visualized under 5x magnification using a Zeiss Axiovert 200 fluorescent microscope. To quantify viral replication, supernatants were collected and viral progeny quantified by $TCID_{50}$ as previously described (*Kudchodkar et al., 2004*).

RNA Isolation and qPCR

RNA was extracted from cell free lysates using Trizol according the manufacturer's instructions. 250 ng of RNA was reverse transcribed using qScript cDNA Supermix (*Quanta Biosciences* -#95048) according to manufacturer instructions. PCR amplifications were performed using a BIO-RAD iQ iCycler. The following primer sets were used for qPCR analysis: 18s (fw: AGGAATTGAC GGAAGGGCACCA and rev: TTATCGGAATTAACCAGACAAATCG); STAT3, eIF6, Ago3 (eIF2S3), eIF4H, GSK3β, PP1α and eEF2 were purchased commercially (*Origene)*. mRNA induction was approximated using the –ΔΔCT relative quantification method (*Perez et al., 2011*).

Comparison of polysome profile signatures with other genome-wide studies on translationally-controlled genes

Comparisons between lists of genes with polysome signatures (*target list*) and lists of translationally-controlled genes from previously published studies (*query list*), were evaluated with the Chi-squared test, assuming as an expected value (*null hypothesis*) an equivalent number of genes randomly drawn from the genome.

$Chi(x) = (observed - expected)^2/expected.$

expected = (# genes in target list / # genes in genome) x genes in query list.

observed = actual number of matches between lookup list and target list.

RNA signature analysis

5'-UTR sequences for each human gene were extracted from the UCSC refGene table using standard HUGO gene names. If multiple RefSeq transcripts exist for a single gene, all unique 5'-UTR sequences were used and indexed by RefSeq transcript ID. 5'-UTR length is the count of bases from the transcription start site (TSS) to the start codon of the protein-coding region. G+C content of each 5' sequence was calculated with the EMBOSS geecee program. Gibbs free energy of folding was calculated with the Quickfold method of the DINAMelt Web Server (m-fold; *Zuker & Markham, 2013*) with the RNA 3.0 default settings. Statistical significance of differences between G+C content, 5'-UTR length, and free energy were computed with students t-test. To discover motifs in the 5'-UTR, the EMBOSS fuzznuc program (*Rice et al., 2000*) was used with the following regular expressions. For the TOP motif (*Meyuhas, 2000*): <C[TC][TC][TC][TC] (5' UTR must start with C at TSS, followed by 4 T/C). For the PRTE motif (*Hsieh et al., 2012*): [TC][TC][TC][TC][TC]T[TC][TC][TC] (5 T/C, one required T, 3 more T/C located anywhere in 5' UTR).

SUPPLEMENTAL REFERENCES

Hsieh, A.C., Liu, Y., Edlind, M.P., Ingolia, N.T., Janes, M.R., Sher, A., Shi, E.Y., Stumpf, C.R., Christensen, C., Bonham, M.J. et al. (2012). The translational landscape of mTOR signaling steers cancer initiation and metastasis. *Nature* **485**, 55-61.

Kobayashi, M., Wilson, A.C., Chao, M.V., and Mohr, I. (2012). Control of viral latency in neurons by axonal mTOR signaling and the 4E-BP translation repressor. *Genes Dev*. **14**, 1527-1532.

Kudchodkar, S.B., Yu, Y., Maguire, T.G., and Alwine, J.C. (2004). Human cytomegalovirus infection induces rapamycin-insensitive phosphorylation of downstream effectors of mTOR kinase. *J. Virol*. **78**,11030-11039.

McKinney, C., Yu, D., and Mohr I. (2013). A new role for the cellular PABP repressor Paip2 as an innate restriction factor capable of limiting productive cytomegalovirus replication. *Genes Dev*. **27,** 1809-1820.

Meyuhas, O. (2000). Synthesis of the translational apparatus is regulated at the translational level. *Eur. J. Biochem*. **267**, 6321-6330.

Moorman, N.J., Cristea, I.M., Terhune, S.S., Rout, M.P., Chait, B.T., and Shenk, T. (2008). Human cytomegalovirus protein UL38 inhibits host cell stress responses by antagonizing the tuberous sclerosis protein complex. *Cell Host Mic*robe **3**, 253-262.

Perez, C., McKinney, C., Chuluunbaatar, U., and Mohr, I. (2011). Translational control of cytoplasmic poly A binding protein (PABP) abundance in HCMV-infected cells. *J. Virol.* **85**, 156 -164.

Rice, P., Longden, I., and Bleasby, A. (2000). EMBOSS: the European Molecular Biology Open Software Suite. *Trends Genetics* **16**, 276-277.

Saeed, A.I., Sharov, V., White, J., Li, J., Liang, W., Bhagabati, N., Braisted, J., Klapa, M., Currier, T., Thiagarajan, M. et al., (2003). TM4: a free, open-source system for microarray data management and analysis. *Biotechniques*. **34**, 374-378.

Terhune, S., Torigoi, E., Moorman, N., Silva, M., Qian, Z., Shenk, T., and Yu, D. (2007). Human cytomegalovirus UL38 protein blocks apoptosis. *J. Virol*. **81**, 3109-3123.

Zuker, M., and Markham, N. m-fold web server: © Rensselaer Polytechnic Institute, hosted by The RNA Institute, College of Arts and Sciences, State

University of New York at Albany. 1995-2013.
http://mfold.rit.albany.edu/?q=DINAMelt/Quickfold