

Supplemental File 2. Nucleotide sequence of cDNA clone L29 (2A), Translation of sequence obtained for L29 (2B), and Blast analysis of translated sequence for L29 against predicted MCMV M116 protein sequence (accession # YP_214111) (2C).

Supplemental File 2A. Nucleotide sequence of cDNA clone L29 (sequence from 5' end—Vector sequence is bold; splice junction in red and underlined)

>clone L29

NNNNNNNNNNNNNTTAGCTTGGTACCGAGCTCGGATCCACTAGTCCAGTGTGGTGGGAATCCCGCGGGTTTAAAC~~GAGAACGGCAACGAG
ACGACGGTCGCCGCGCCGGCTCCGCCCGCGCACCAGCGCCAGCAGCCGCTTCTGCCCTCCGAGCTAGCACTCGGGCCGAGACGCCCCGTGTCGC
CGCCGCCGCGCTGCCACCACCGCCGCTAAAAAACGGGTTTCGACCATACTATCTCGAGCGAGCGACGGGACGAAGATCTTAACCCACCGACG
GGACGAAGATCTTAATCTACGCCTCTTCGTCATCGGACTCTTCGGATATCTCTCAGACGACTCGGATAGCGAAACGAACTCGTCGCAAGCGAAC
GTCTAACTCGTCCTTACCACCGGGATCGGAGACCGAACCCCTTTCATCATCTCATATTCATCTTCATCATCTTCATCATCTCTCCATCTCTCCGAC
TCAGAGGATGAACCATCATCATCATCATCATCGTCATCTACCAGCTCGGACGGCGCTTCATCGGATTCGGAGGCCATCTTCGGATTCTGGATCCG
AATCCATAGGCTCGACGTCGCCAAATCGGAATCGGAGTCTCAGACTCAGAAAAAGATCAAGAGAAGAATAAGAAAACATCGACACCCGCATCT
ACTCGCGGAGTTCGCCGCAACCAGGAGCAGCACCAGCAGCCCCCGGAACACAGAACCAGCCCGAGACGCGTCGACGGAGCTGTCGTCGAAGA
TGTTATCCGCTCGATCGTGGACAAGCCGACGAAGCTCGCCGACGCTGCCAAGACTACTCCTCAGCAGGT~CAACACAGAGTGCGACAACGGTCC
AGACGAAAAGCGGTCACGCCGGTCTACAGAAAGAGACGCCGAAGAAATCGACGTCCTATCGACCTTGAAGAGAGCGGGTTCGACAGACCAGAGA
ACTGCAGCAGAGCTCGGAGACGGCGACGATCACTGACGCGTCGCGGGTTCGAGCAGGTCACGGCNGTCCCGCCGACGAGCATCCCGTACCTG
ACNNCTAACGACAGCCCCGCCAGCACCCACATCAGACGTCGACAACAACACCAACACANATCACCGCCATCACCACCAAGGACCCGCTACCAC
AGCNGTANNTTCGANAGNATNTNNGANCGTNACTCNCNNTNCCAGCAGNANTAGNACCNATCTCNCCTCNCNCCGTCGAANNCCAGACNN
NACTGNNGNCNCACAGAANGCTACTAATAANNNNANGANNNNNAAAAANANANNNNNNGCNNATNNCCNCNACNNNNNNNTANNTNCN
NCNTCTGGNNNNNNCCNNNCCNNNNNNNNNGNNNNNNNTNCNNNNNNNTNCCTNANANNNNNAANNNNNTNCNNNGNNNN
NNGNNGAN

Supplemental File 2B. Translation of sequence obtained for L29. The italicized sequence diverges from published sequence because of change in open reading frame and introduction of stop codon caused by splicing (altered residues due to reading frame shift in red). The 5' end of the transcript has not been unambiguously determined. While current genome annotation indicates M116 is predicted to be 645 AA, These findings provide evidence of a novel truncated protein product that diverges from the predicted protein sequence at residue 350 and introduction of a new stop codon at position 401.

>clone L29: 16 to 984: Frame 1 323 aa

SLVPSSDPLVQCGGIPAGLNENGNETTVAAPAPPAAPAPAAASASAASTRAETPAVAAAAAATTAAKKRVSTIL
SRASDGTKILTPTDGTKILYASSSSDSSDISSDDSDSETNSSSSEPSNSSLPPGSETEPSSSSSYSSSSSSSS
PSSSDSEDEPSSSSSSSSTSSDGASSDSEAPSSDSGSESIGSTSPKSESESSDSEKDQEKNKKTSTPASTRAS
SPQPGAAPAAPANTEPARDASTELESKMLSASIVDKPTKLADAAKTTPQQV**NTECDNGPDGKRSRRSTERDA**
EEIDVPIDLEESGSTDQRTAELGDGDHSTOP

Supplemental File 2C. Blast of our translated sequence for L29 against MCMV M116 protein sequence (accession # YP_214111). Note that the spliced clones in the cDNA library are also truncated at the 5' end relative to current gene annotation. While current genome annotation indicates M116 is predicted to be 645 AA, These findings provide evidence of a novel product predicted to be approx. 401 AA.

[GENE ID: 3293866 MuHV1 gp103](#) | UL116 [Murid herpesvirus 1]

(10 or fewer PubMed links)

Score = 160 bits (405), Expect = 3e-48, Method: Compositional matrix adjust.
Identities = 252/255 (99%), Positives = 253/255 (99%), Gaps = 2/255 (1%)

Query	21	ENGNETTVAAPAPPAAPAPAAAASASAASTRAETPAVAAAAAATTAAKKRVSTILSRASDG	80
		+NGNETTVAAPAPPAAPAPAAAASASAASTRAETPAVAAAAAATTAAKKRVSTILSRASDG	
Sbjct	98	KNGNETTVAAPAPPAAPAPAAAASASAASTRAETPAVAAAAAATTAAKKRVSTILSRASDG	157
Query	81	TKILTPTDGTKILIIYASSSSDSSDISSDDSDSETNSSSSEPSNSSLPPGSETEPSSSSSY	140
		TKILTPTDGTKILIIYASSSSDSSDISSDDSDSETNSSSSEPSNSSLPPGSETEPSSSSSY	
Sbjct	158	TKILTPTDGTKILIIYASSSSDSSDISSDDSDSETNSSSSEPSNSSLPPGSETEPSSSSSY	217
Query	141	SSSSSSSSSPSSSDSEDEPSSSSSSSSTSSDGASSDSEAPSSDSGSESIGSTSPKSESES	200
		SSSSSSSSSPSSSDSEDEPSSSSSSSSTSSDGASSDSEAPSSDSGSESIGSTSPKSESES	
Sbjct	218	SSSSSSSSSPSSSDSEDEPSSSSSSSSTSSDGASSDSEAPSSDSGSESIGSTSPKSESES	277
Query	201	SDSEKDQEKNNKTSTPASTRASSPQPGAAPAAPANTEPARDASTELSSKMETLSASIVDK	260
		SDSEKDQEKNNKTSTPASTRASSPQPGAAPAAPANTEPARDASTELSSK LSASIVDK	
Sbjct	278	SDSEKDQEKNNKTSTPASTRASSPQPGAAPAAPANTEPARDASTELSSK--LSASIVDK	335
Query	261	PTKLADAAKTTTPQQV	275
		PTKLADAAKTTTPQQV	
Sbjct	336	PTKLADAAKTTTPQQV	350