

**Table S4.** Spliced transcripts of MCMV<sup>#</sup>

<b>Overlapping Gene(s) or Known Designation</b>	<b>Strand</b>	<b>Clone Name</b>	<b>Total No. of Clones Found in This Study</b>	<b>Genomic Position (only positions of longest clone shown)<sup>†</sup></b>	<b>First Report</b>
<b>#m15, m16</b>	+	E253	1	14635-15083 + 15622-15700	This Study
<b>m18</b>	+	L123	1	17079-17188 + 17853-17957 + 18351-19285	This Study
<b>M33</b>				41486-41519 + 41679-42780	Poynter et al. <sup>2</sup>
<b>M34</b>	+	E196	1	44012-44242 + 44304-44516	This Study
<b>M36</b>	-			49267-49036 + 48909-47621	Rawlinson et al. <sup>1</sup>
<b>m42, m41</b>	-	IE106	1	55312-55123 + 54218-53678	This Study
<b>M44, M43</b>	-	IE160		58976-58668 + 57157-56856 + 56667-56361	This Study
<b>m60</b>				94984-95063 + 105879-106093	Scalzo et al. <sup>6</sup>
<b>#M71, IGR m74-M75</b>	+	E180	1	102514-102830 +105879-106090	This Study
<b>#M73</b>	+	L33	1	103985-104548+ 105879-106093	Scalzo et al. <sup>6</sup> and this study
<b>M73.5</b>	+	L443	4	103985-104160+ 105879-106093	Scalzo et al. <sup>6</sup> and this study
<b>M73.5 long</b>	+			103700-104160+ 105879-106093	Scalzo et al. <sup>6</sup>
<b>M76(AS), M78(S)</b>	+	E139	1	108476-108714 + 111789----112593*	This Study
<b>M78</b>	+	E41	1	111280-111409 + 111444----112592*	This Study
<b>M80</b>	+	L116	1	114889-115148 + 115187-115396	This Study
<b>M92 , M93, M94</b>	+	L14	1	134691-135369 + 135956-137333*	This Study
<b>M93, M94</b>	+	L107	1	135978-136052 + 136181-136754	This Study
<b>M93, M94</b>	+	L172	1	135978-136524 + 136651-137227	This Study
<b>M89</b>	-			138283-137393 + 132771-131649	Rawlinson et al. <sup>1</sup>
<b>M102</b>	+	IE224	1	145586-145908 + 147011-147682	This Study
<b>Stable 7.2kb intron</b>				162090-161622 + 154365-153916	This Study and Kulesza and Shenk <sup>3</sup> .

<b>Stable 8.0kb intron</b>				162606-162415 + 154365-153916	Kulesza and Shenk <sup>3</sup>
<b>Stable 7.2kb intron IGR m106-m107, m106(S)</b>	-	E289 E206 L63	3	161905-161622 + 154368-153873, 161919-161622 + 154368-153886, 161904-161622 + 154368----153867*	This Study and Kulesza and Shenk <sup>3</sup>
<b>M112</b>	+			163097-163889 + 163983-164159 + 164486-164505	Rawlinson et al. <sup>1</sup> Ciocco-Schmitt et al. <sup>5</sup> demonstrate 4 transcripts (each with 3 exons) of 1.5, 1.4, 1.1 and 0.9kb, but genomic positions were not provided.
<b>M112 Ex1, M113, M112 Ex2</b>	+	E184	1	163778-163891 + 163983-164157	This Study
<b>M112 Ex1, M113, M112 Ex2, M112 Ex3 (last exon in IGR M112 Ex3-M114)</b>	+	L2	1	163779-163891 + 163983-164160 + 164485-164582 + 164871-165510*	This Study
<b>#M116</b>	-	E367, E263, L214, E110, L243, E231, E135, L29	8	168189-168091 + 168015-167555	This Study
<b>m119, M118</b>	-	E243		171957-171684 + 171585-171255	This Study and Rawlinson et al. <sup>1</sup>
<b>M102</b>		IE224		145586-145908 + 147011-147682	This Study
<b>m123 Ex2,3,4</b>				181766-181660 + 181562-181372 + 181249-179763	Rawlinson et al. <sup>1</sup>
<b>M122 Ex 5</b>				179517-177983	Rawlinson et al. <sup>1</sup>
<b>M128 Ex3</b>				186085-187296	Rawlinson et al. <sup>1</sup>
<b>m133 Ex1, m132 Ex2</b>	-			189795-188881 + 188601-188382 +	Lagenaur et al., <sup>4</sup> Rawlinson et al. <sup>1</sup> (Smith strains has alternate donor site at 188840)
<b>m133 Ex1, m132 Ex2, m131</b>	-	IE138	1	189808-189499 + 188602-188269	This Study
<b>IGR m124.1 - m125, m123Ex2, m123 Ex3, m122 Ex5</b>	-	E279	1	182798-182596 + 181770-181659 + 181562-181371 + 179520-179420	This Study
<b>m133 Ex1, m132 Ex2, m131</b>	-	L78 IE208	2	189791-188880 + 188602-188407*	This Study

<b>m132 Ex2 - m131</b>	-	E96 L102	2	188885-188695 + 188603-188292*	This Study
<b>m165, m164, m163</b>	-	IE197	1	223828-223662 + 223593----221832*	This Study
<b># m169(S) m168 (AS)</b>	-	E20, E125	139	229112-228325 +228247-227426	This Study

# The spliced MAT transcript [ m169(S) m168 (AS)], the spliced M116 transcript represented by clone L29, and the spliced transcripts in the M71-M75 region represented by clones L33 and E180 have been verified by other methods (see Results). The spliced transcript in the m15-16 region could not be validated by PCR (see Results). Other novel spliced transcripts isolated in the cDNA library of this study have not yet been validated by other methods.

\*Denotes 3' end of clone was successfully sequenced.

‡ Genomic positions determined by aligning sequences of the clones to target genome using MegaBLAST.

<sup>1</sup>Rawlinson WD, Farrell HE, Barrell BG. Analysis of the complete DNA sequence of murine cytomegalovirus. J Virol. 1996 Dec;70(12):8833-49.

<sup>2</sup> Identification and characterization of a G protein-coupled receptor homolog encoded by murine cytomegalovirus. Davis-Poynter NJ, Lynch DM, Vally H, Shellam GR, Rawlinson WD, Barrell BG, Farrell HE. J Virol. 1997 Feb;71(2):1521-9.

<sup>3</sup> Murine cytomegalovirus encodes a stable intron that facilitates persistent replication in the mouse. Kulesza CA, Shenk T. Proc Natl Acad Sci U S A. 2006 Nov 28;103(48):18302-7

<sup>4</sup>Lagenaur LA, Manning WC, Vieira J, Martens CL, Mocarski ES. Structure and function of the murine cytomegalovirus sgg1 gene: a determinant of viral growth in salivary gland acinar cells. J Virol. 1994 Dec;68(12):7717-27.

<sup>5</sup>Ciocco-Schmitt GM, Karabekian Z, Godfrey EW, Stenberg RM, Campbell AE, Kerry JA. Identification and characterization of novel murine cytomegalovirus M112-113 (e1) gene products. Virology. 2002 Mar 1;294(1):199-208.

<sup>6</sup>Scalzo AA, Dallas PB, Forbes CA, Mikosza AS, Fleming P, Lathbury LJ, Lyons PA, Laferté S, Craggs MM, Loh LC. The murine cytomegalovirus M73.5 gene, a member of a 3' co-terminal alternatively spliced gene family, encodes the gp24 virion glycoprotein. Virology. 2004 Nov 24;329(2):234-50.