

Figure 1

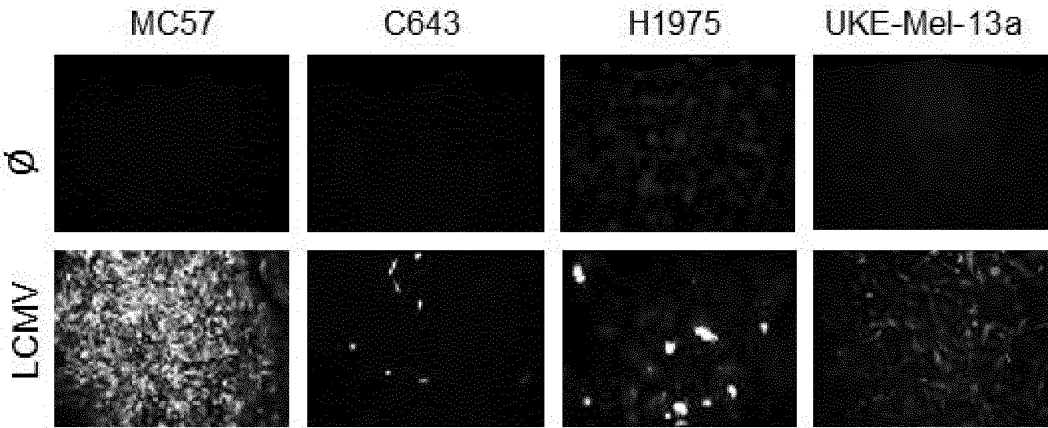


Figure 2

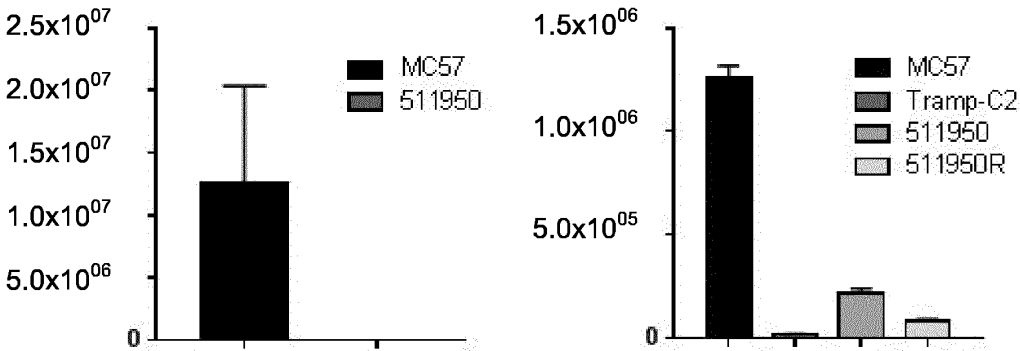


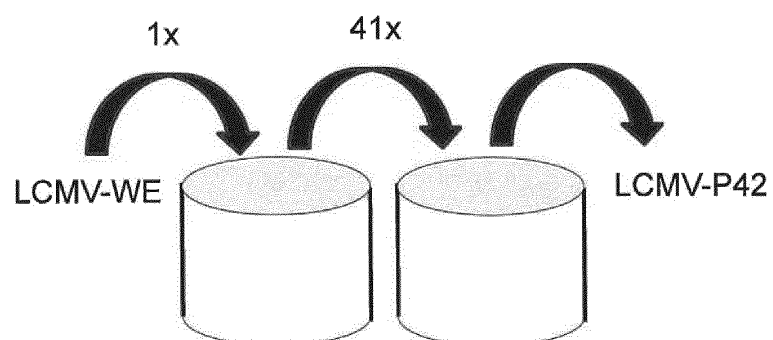
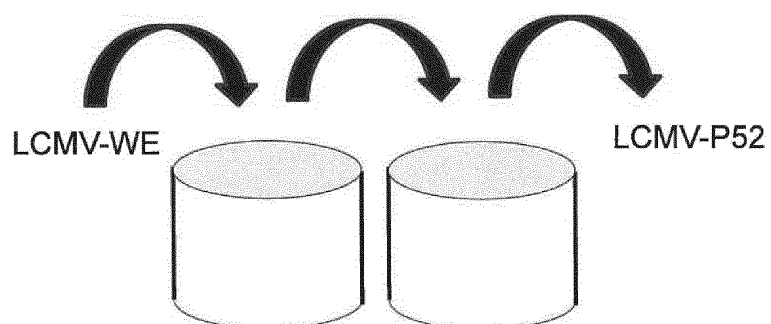
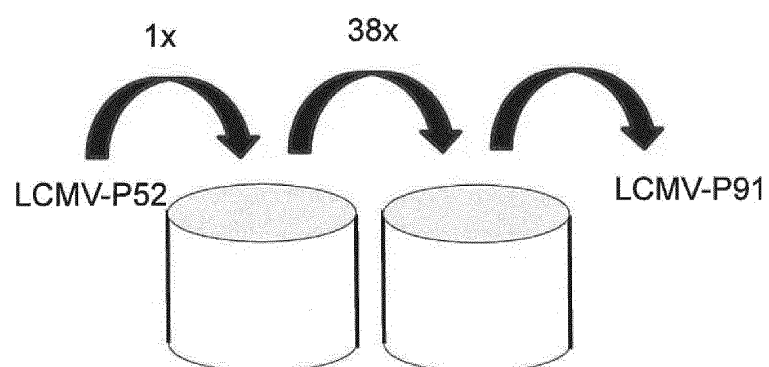
Figure 3**Figure 4****Figure 5**

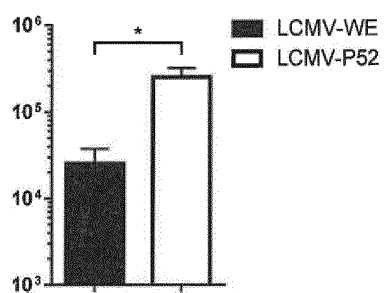
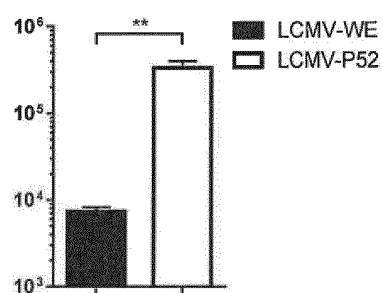
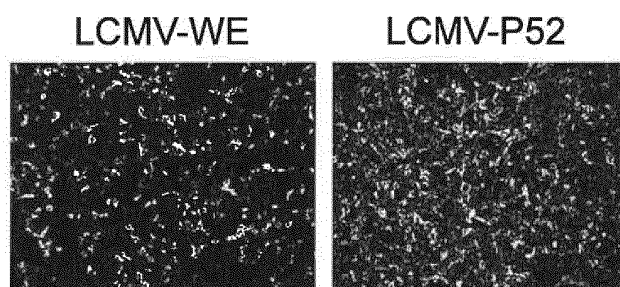
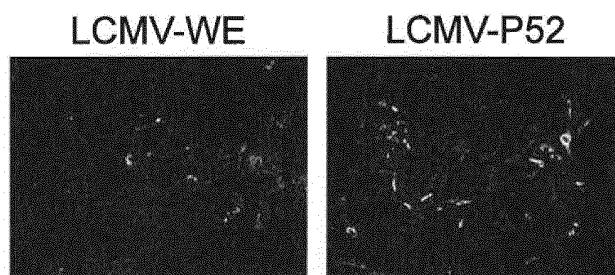
Figure 6**Figure 7****Figure 8****Figure 9**

Figure 10

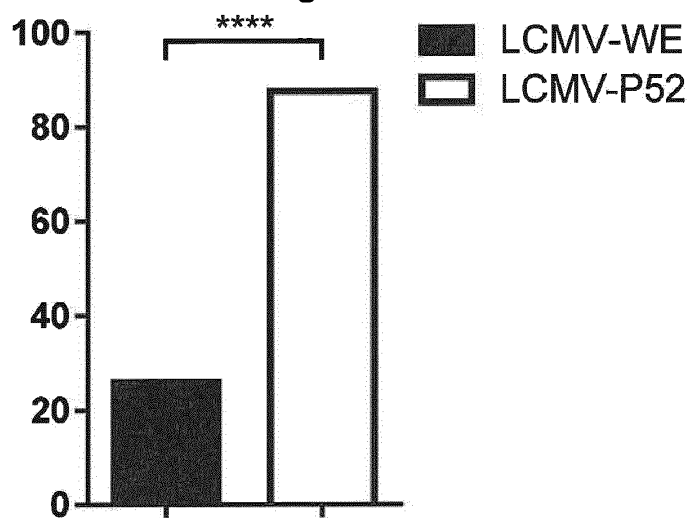


Figure 11

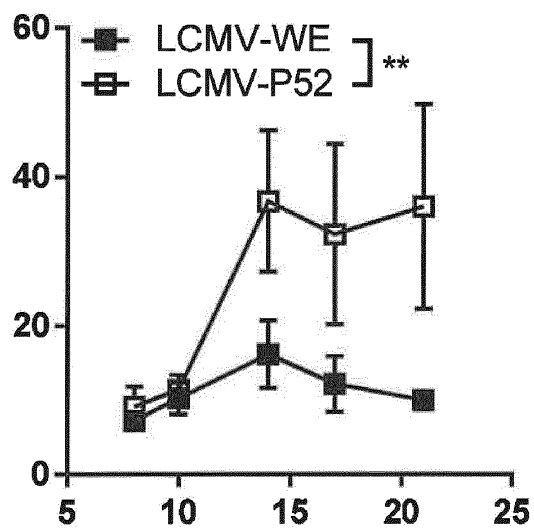


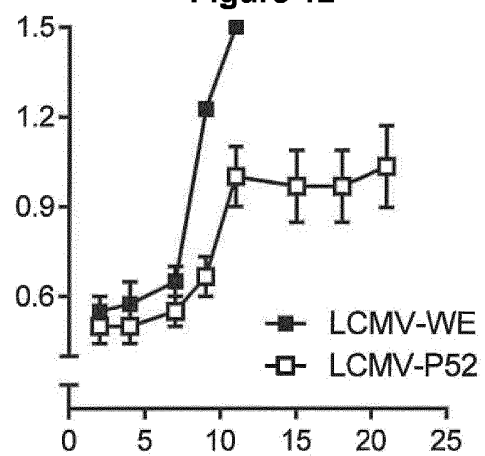
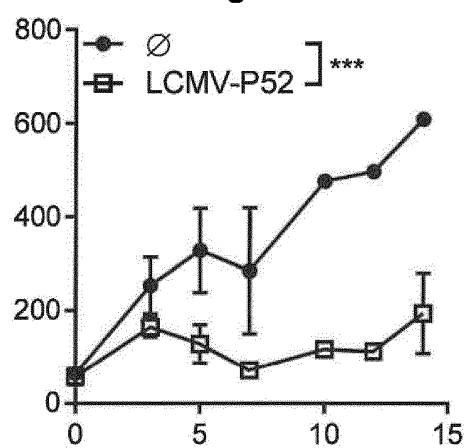
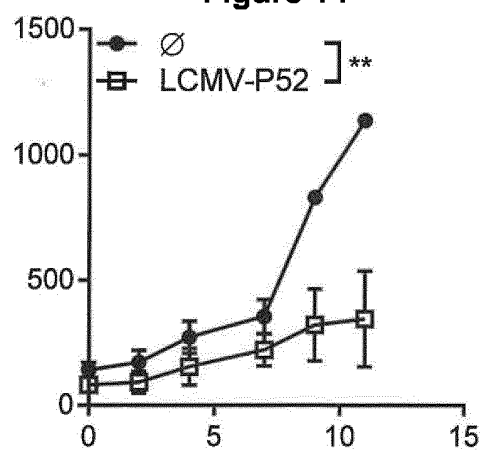
Figure 12**Figure 13****Figure 14**

Figure 15

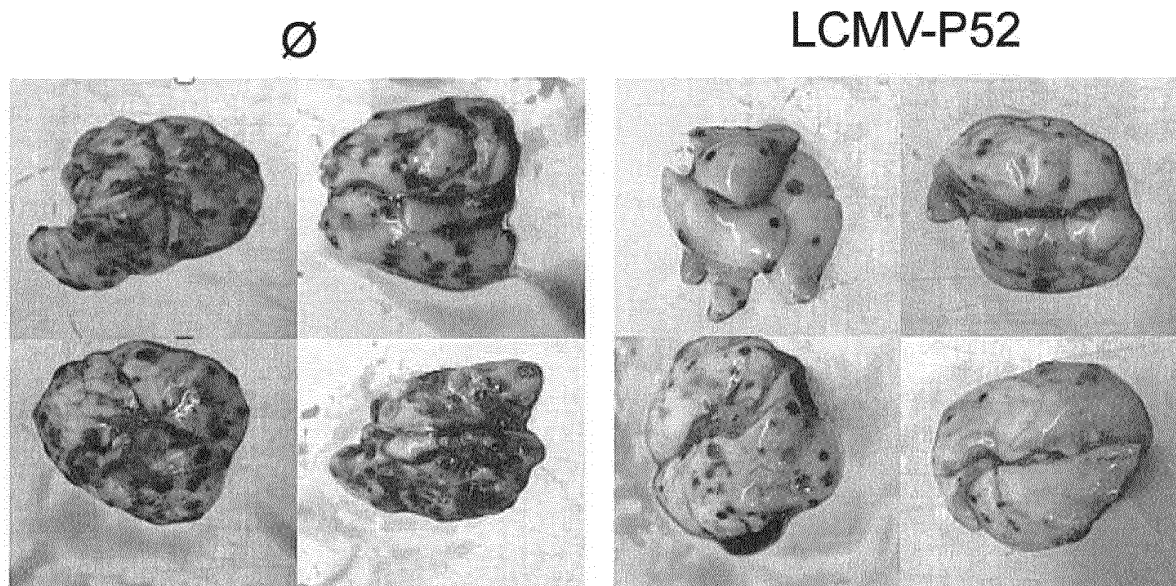


Figure 16

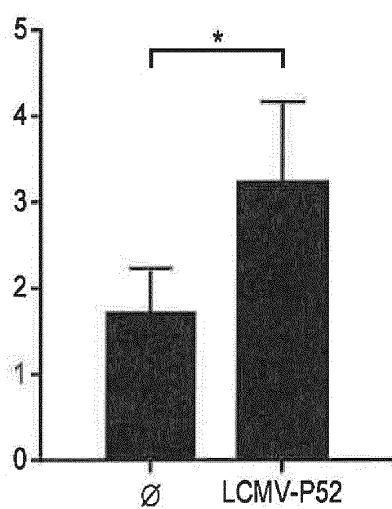


Figure 17

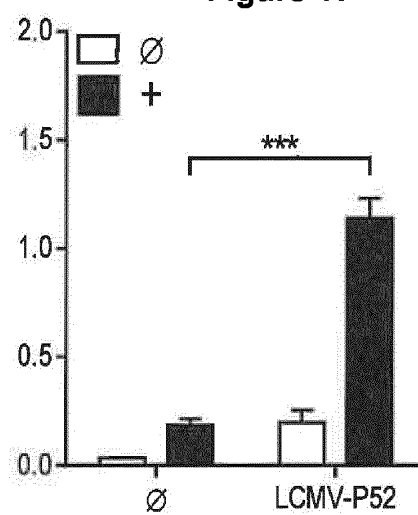


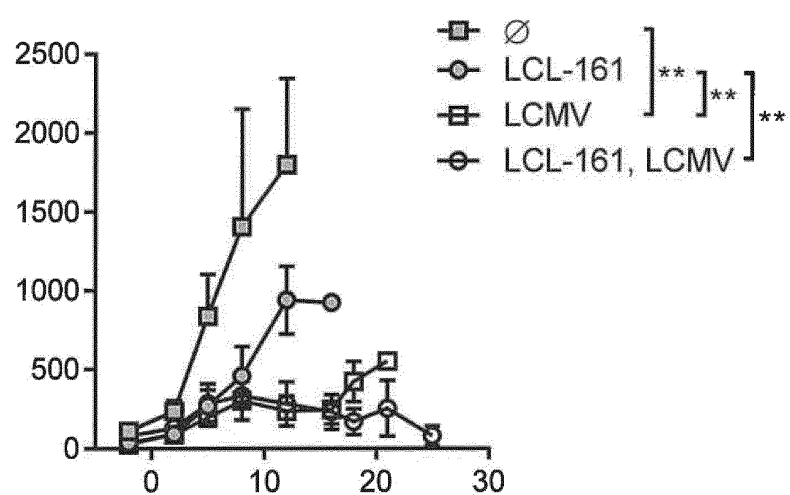
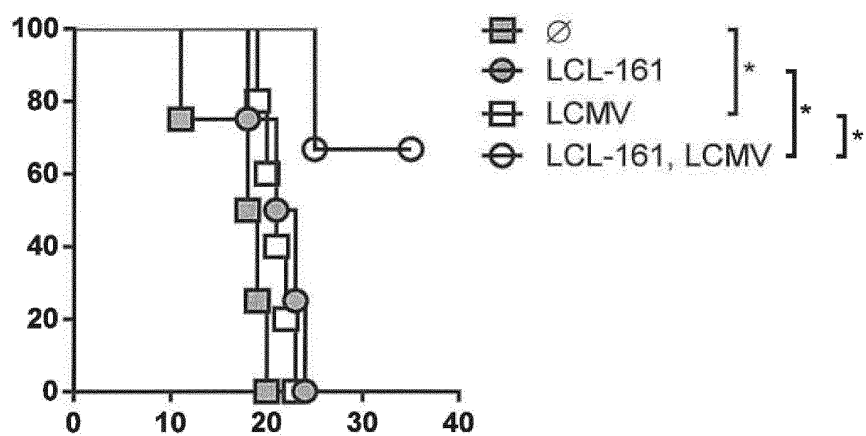
Figure 18**Figure 19**

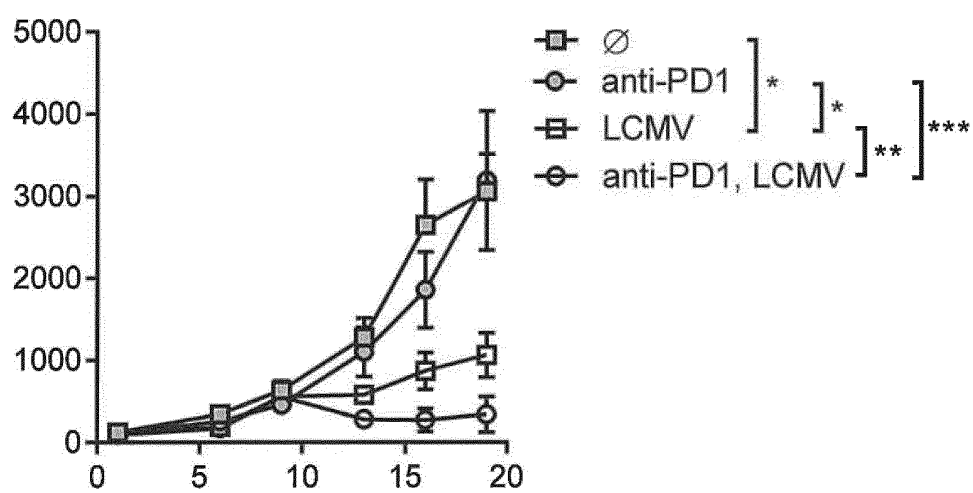
Figure 20

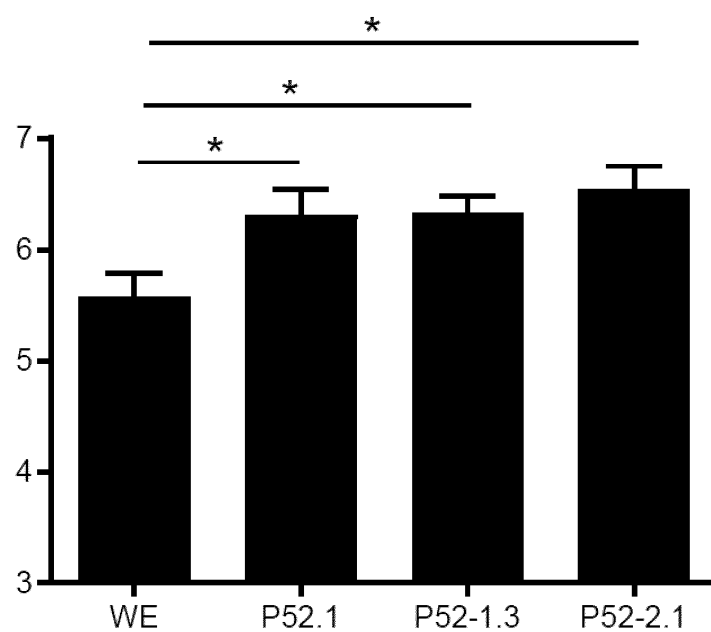
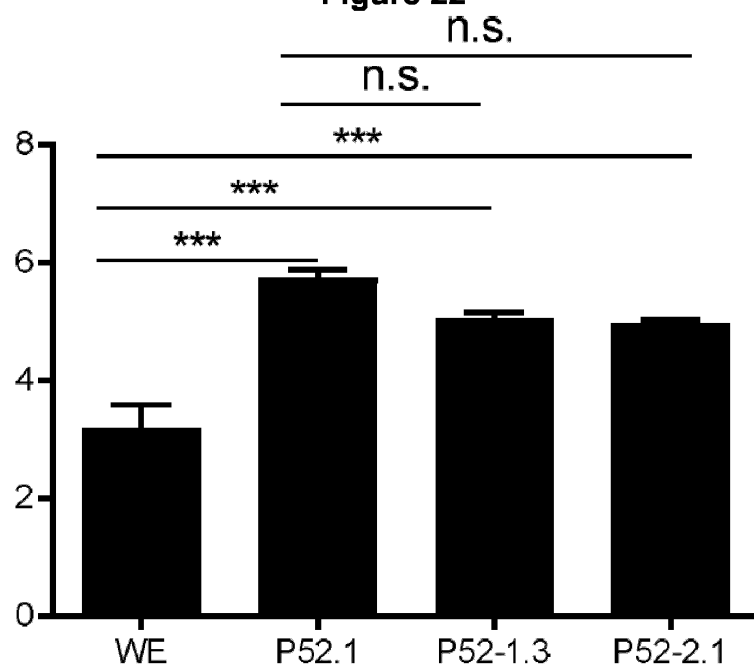
Figure 21**Figure 22**

Figure 23

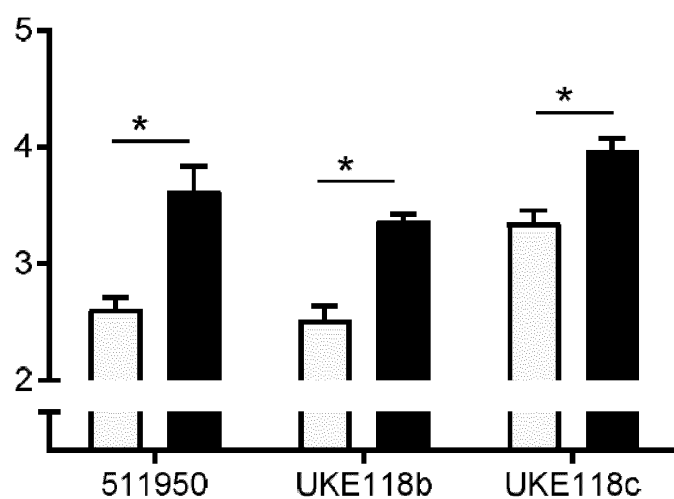


Figure 24

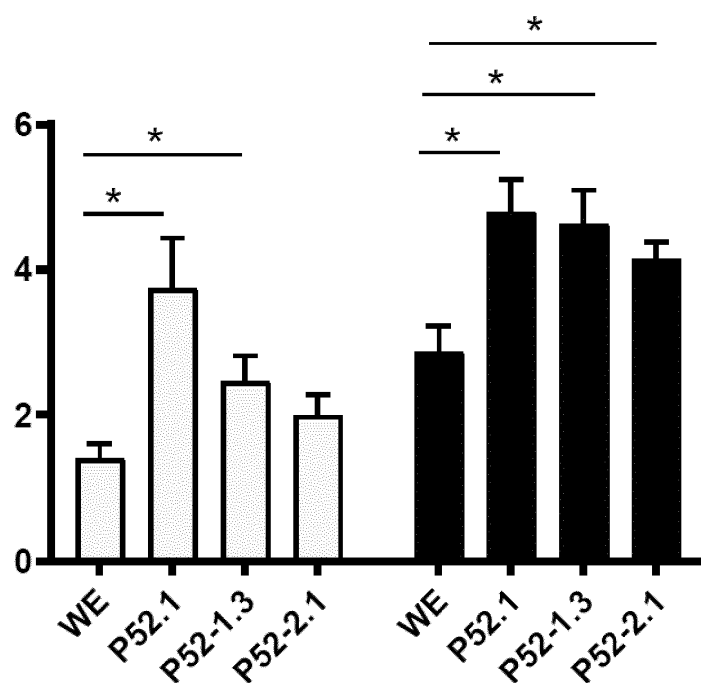


Figure 25**A. Lymphocytic choriomeningitis virus (LCMV) strain WE**

Source: 1-3376 Segment = S
Protein: Pre-glycoprotein polyprotein GP complex
Gene: GPC
Gene: 79-1575

>LCMV-WE-DUE_GP
ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTCAATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTGCCACC
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GGCCTTAATGGTCCCACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTTGACCATACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT
GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCATTTTTCGGACCCACAGAGCGCT
ATAAGCCAGTGTAGGACTTTTCAGAGGTAGAGTCTTGGACATGTTTAGAAGTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCTAGTGGCAAGACCACTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCCTGACCAAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTTAGTGATCAAATCGAACAAGAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
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(SEQ ID NO: 9)

CDS: 79-1575
Codon Start = 1; Codons 1-498
Chain: 1-498 *Pre-glycoprotein polyprotein GP complex*
Chain: 1-58 *Stable signal peptide*
Chain: 59-265 *Glycoprotein G1*
Chain: 266-498 *Glycoprotein G2*

Translation=

>LCMV-WE-DUE_GP
MGQIVTMFEALPHIIDVINIVIIIVLIITSIKAVYNFATCGILALVSFLFLAGRSCGMY
GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMSSGLELFTTNDLSILNH
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
ISQCRFTFRGRVLDMFRTAFGGKYMRSWCWAGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO:10)

Figure 25 (continued)

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

```
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GCCAAGTCACTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC
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ATGCACACTGGGGTAGTGAGAGACAAAAGAAGAAAGAGATCACCCACACTGTCCACTC
ATGGACTGCATCATTTTTGAGAGTGTCCAAGGCAAGACTCCCTCATCTAAAAACCGTT
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(SEQ ID NO: 11)
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CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558

Translation=

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>LCMV-WE-DUE_NP
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ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY
NFSLGA AVKAGAAALDGGNMLESILIKPSNSEDLKAVLGAKKKLNMFVSDQVGDNPYE
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SQTMLLKDLMGIDPNAPT WIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPLGTSSVIGALPQGMVLSCQGSDDIRKLLDSQNRDRIKLIDVEMT
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(SEQ ID NO: 12)
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Figure 25 (continued)

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

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AGCTTGGTTAGATGCCATGACCACTATCTTTCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 13)

CDS: 90-362
Codon Start = 1; Codons 1-91

Translation=

>LCMV-WE-DUE_ZP
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VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

```
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ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTATTCTT
CTTGAATGTTTTGTTAGAAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGCTTCCAATA
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AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAAGTTTTGAGGAG
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TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAAATCC
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Figure 25 (cont'd)

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TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCTACAAAGAGCAGGTTGGG
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GATTATTTTGAATCCTTTCTAGTTTCTTTTCAGGATCTTGTTTTAAACAATGACAAAGAG
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TTGACTTGGCATATGCATAAACTTGTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG
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CATGTACAAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA
CAGGAGAGGCTCACCCTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT
TGCATCTCATTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTACGAGAACCCTGTGAAA
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GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCTGATGTG
AGCTCAAAAATATGAGATGGAGTCCAGGATTAATTCCTTGACCTTTGTGTCTGATT
GACATCAACTCAGAGTCTTTGTCACTCATTCTCATGTTGTCAAATGGAAGAGGGACGAA
CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCACCGTCAGACTCAAGTTTA
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TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCCTTCCAA
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CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGATGTTGTGTGTAATGCCGCTATG
TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTGTGGGAT
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AACCAGAACAACACTGACTGCTTGAAGAAATTTTCATTGATCTTTGTGTTAAATGCCAA
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CCAGATTGGTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAACCTGGGGGAGGTTGAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

Figure 25 (cont'd)

CGCGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 15)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-WE-DUE_LP
MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC
IHNHDDKSIVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTIVDKRSGMDSMKILKDARSFHNDIEMKMCHDGVNPNMSCDDVVFINS
FFGRFRDLLNGKLRNFQKVSPPGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSLLKLNTRRRQLLNLDVLCSSLIKQSIKGL
ENDKHVWGCCYSSVNDRLVSLQSTKEEFMRLLNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRKLSSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIKLDSEEH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPISFDEVLHNMTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKCLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMNLVSYLCHLITKETPDRLTDQIKCFEKEFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMVSSFNNG
TLILKGEKRLNLDPMNTNSGCATALDLASNKSVVNKHNGERLLEYDFNKLIVSAVSQI
TEGFMRKQYKLRHSDYKYSKLVSRVLVIGSRKTEVDKLEDDPVDVCFEGEEETSSFRS
LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPYFTSAVKEQCGLDEMARNLCRKFSEGDWFS
CMKMILLQMANAYSGKYRHMQRQSLNFKFDWDKLEEDVRIERESNSSELSKALSLTKC
MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLNYSMDHSHKWPMMCPFLFLMLLQ
NLKLDDQYVRSGKDHVSTLLTWHMHKLVEVPPVNVAMMKSYYKSKLKLKGSCTTVTE
RIFREYFEMGVVPSHISLIDMQGILHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVSDPEEVLVLLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKEVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDDLKY
ANFPLDPFLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFLDLFRNREKKEAILQLGEILGLEDDLNELASINWLNLMEMFLRMVLRQKVVPVSM
TFQEEKIPSLIKTLQNKLCSEKFTTRGAQKLLSEAINKSAFQSCVSSCGFIGLCKTLGSRV
NKNRENMYIRKVLDELTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGNESNSAVRHLNPCDYVARKPESSRLLEDKVS LNHVQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLISHVVKWRDE
HYTVLFSDLVNSHQSDSSLVDEFVSTRDVCKNFKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEGDGAELGPFQSFIKVVNKKIERPMFRNDLQFGFGWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCHSHFFKGEVDRLLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRIILNEIKSTDFERIGPEWEPVPLTIRKGALEGRNFVNISVKLET
KDMRVFLAELEGCGKIGDVLGSLLLHFRFTGEHLMSEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFRSKNTVMYETTGGFRFLKKGKSCDDWLAERVAEEID
(SEQ ID NO: 16)

Figure 25 (cont'd)**B. Lymphocytic choriomeningitis virus (LCMV) P42 mutant**

Source: 1-3376 Segment = S
Protein: Pre-glycoprotein polyprotein GP complex
Gene: GPC
Gene: 79-1575

>LCMV-P42_GP

ATGGGTGAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTTCATTATTGTGCTCATTATAATCAGGAGCATCAAAGCTGTGTACAATTTCCGCCACC
TGTGGGATATTAGCACTGGTCAGCTTCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT
GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCATTTTTCGGACCCACAGAGCGCT
ATGAGCCAGTGTAGGACTTTGAGAGGTAGAGTCTTGGACATGTTTAGAAGTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTGAGATGGCAAGACCACTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGGCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTCAAAACAACAGTAAATTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCAAGTGCTGGCTTGTCACATAATGGCTCCTACTTG
AATGAGAGCCCACTTTAGTGATCAAATCGAACAAGAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAAGTTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAGACGCTGA
(SEQ ID NO: 17)

CDS: 79-1575

Codon Start = 1; Codons 1-498

Chain: 1-498 *Pre-glycoprotein polyprotein GP complex*
Chain: 1-58 *Stable signal peptide*
Chain: 59-265 *Glycoprotein G1*
Chain: 266-498 *Glycoprotein G2*

Translation=**>LCMV-P42_GP**

MGQIVTMFEALPHIIDEVINIVIIIVLIITSIKAVYNFATCGILALVSFLFLAGRSCGM
GLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSHHYISMSSGLELFTTND
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQ
MSQCRFTFRGRVLDMFRTAFGGKYMRSWGWAGSDGKTTWCSQTSYQYLI IQNRTW
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELK
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSFKQDVESALHVFKTTVNSLISDQLLMR
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQADNMITE
LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 18)

Figure 25 (cont'd)

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-P42_NP

ATGTCCTTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG
CAGAGTTTTACATCAGATGTAAAGGCTGCCGTATCAAGGACGCAACCAGTCTTCTAAAT
GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCCTCAA
GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACTTGATCAAAGATCCCAAATA
CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTCGTCTAGTAAGCGTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAAATGCCAAGCCTGACAATG
GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC
CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTCAAAGGCTAAAGGAT
AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT
AATTTAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG
GCCAAGAAGAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAACTTGTT
GCCAATCTATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAAT
GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAACTCATTCATGTTGACATGACC
AAGGAGGCCCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAAATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 19)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558

Translation=

>LCMV-P42_NP

MSLSKEVKSFQWTQALRRELQSFTSDVKA AVIKDATSLNLGLDFSEVSNVQRIMRKERRD
DKDLQRLRLSNQTVHSLVDLKSTS KKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ
ASGVYMGNLTAQQLDQRSQILQVMGMRRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKD KHPVLGVITEQQSSINISGY
NFSLGA AVKAGAAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGD RNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDL TNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGIDPNAPT WIDIEGRFNDPVEIAIFQPONGQFIH FYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLLDSQNR RDIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNNVTL
(SEQ ID NO: 20)

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-P42_ZP

ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT
TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 21)

CDS: 90-362
Codon Start = 1; Codons 1-91

Translation=**>LCMV-P42_ZP**

MGQGKSKEERDTSTNGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 22)

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-P42_LP

ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG
AGGCTGTCAAGGCAAACTCAACTTCCTGGGACAAAGAGAACCAGAATGGTGCTAATT
GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTATTCTT
CTTGAATGTTTGTAGAAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATCGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAAGTTTTTGAGGAG
TCTGAATACCTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAAAGTTCGGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAGGAATTTCCAAAAG
GTCAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTCAAT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTGAACAAGGTGAAAAGTTTAAATATTAAACACTAGAAGGAGACAGCTG
CTGAACCTTAGATGTCTTATGTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC
CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAAGAACAGAAGAAAATCAAGAGTG
CACAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA
ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
CTCGTGCAAGAATGCCATATACCATTGCTGAATTTGAGAATTTATGAGAGCCGGGACT
CATCCTGTATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA
TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGTGTTGGCTCTAACAAACAGC
ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA
GTGGTGGAGTGCAAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT
CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATTCATACAAGTCCGGATGGT
CACTTGATTTCCCTTTTACGCAGATCCAAAAGGTTCTTTTACCATTATTTTTCAGATGAG
GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTATGCCCTGACTTAAAA
GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC
CCAACAAGAGGAAATCAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGCT
TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC
GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTGGTACTGGTGAA
AAGGTGTTATTGAGTGCAAAATTCAGTTTATGTTGAATGTGTATACCTGTGTCAATTTG
ATCACAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTCTTT
GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG
GAATGTGTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTGAGCAT
TCAACCCCTGGTGTAAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC
ACCTTAATTTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCATGACCAACTCTGGA
TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT
GGAGAACGGCTTTTGGAGTATGATTTTAACAAATGCTTGTAGTGCTGTGAGCCAAAT
ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG
GTCTCAAAGCTTGCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAAATTC
GAAGATGATCCGGTAGATCTGTGTTTCCAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT
TTAGAAGATAAGGTCAGTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA
GGGCAAGGGGAGGGGAGAAATCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG
TCAGGTAAGAGAGCTTATCTGAGGAAAGTCAATTTATCAGAAATTCATTTTCATCTAGTA
GAGGACTTTGATCCATCTGTCTCACCATTGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAAGTGTCAACATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA
TGATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC

Figure 25 (cont'd)

ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
ATTAGTGAAAGGGAAAGCAATCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCACATCATACACT
TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG
GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCAAGATTGGTAGAA
GATTATTTTGAATCCTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG
TTTGAAATGCAATCTTGCAATGACTATCAATGTGAGAGAAGGGTTGTTAACTACAGC
ATGGATCACAGCAAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTCTCCAA
AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG
TTGACTTGGCATATGCATAAACTTGTGTAAGTCCCTTTCCCTGTTGTGAATGCAATGATG
AAATCATATGTTAAATCAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG
AGAATCTTTAGAGAGTATTTTGAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT
GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG
TTTATCAATTATTGTATTGCTGTCAATTTTGGAGAGAGGCCAGAACCTATACATCAAGT
GATGATCAGATCACTTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA
GAAGTCCTTGCTTGTGCTGGAATCCACTCTCACTTAAAGTGGTTTGTGAACAAGTTTCATC
AGTCCAAAAAGTGTTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG
GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACACACAATGTTAAGTGT
AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT
GGAGTTCCAGTTTTTTTTAGTAACTGTATCCAGAGGAGGACACGATCTCTTGAATATAT
GCTAATTTCCCTTTAGATCCATTTCTTGTAAACACTCACACTGATGTAAAGGATTGGTTA
GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA
AAGATCATGAGAAAATCTGTAAGAAGACTACATCACAACTCAAGAACGGTGAATGTAAC
GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA
GAGATTCCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTCAATCTG
AATGAAATGTTCCCATTTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCACTATG
ACCTTTCAAGAGGAAAAGATCCCTCATTTGATTAAACACTCCAAAATAAGCTTTGTAGT
AAGTTCACAAGAGGTGCACAGAAGCTGTGTGTCAGAGGCAATCAACAAATCAGCTTTTCAG
AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA
AATAAAACAGGGAAAATATGTATATCAGAAAGGTCTTGAAGATCTGACCATCGCATGAA
CATGTCAAAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTCCGACAAACGAGAGA
CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT
TGCATCTCATTTGAGCAACTCTTTTGAGCTGGGTGTTGGGTTTTAGCAGAACCCTGTGAAA
GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTCATTATGTAGCAAGA
AAACCTGAGAGTTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATCAATCT
GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTTTCATGTC
AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT
GACATCAACTCAGAGTCTTGTCACTCATTCTCATGTTGTCAAATGGAAGAGGGACGAA
CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA
GTTGATGAATTTGTTGTGTCAGCACAAAGGATGTCTGCAAGAATTTTTGAAGCAAGTGTAT
TTCGAATCATTTGTACGAGAGTTTGTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG
TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCTTCCAA
TCATTTATTTTGAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG
CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGATGTTGTGTGTAATGCCGCTATG
TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTCTGCGGAT
TACATGCTCAGCAGCACAGAGGGATATTGGAGTTCTCAATCACACTGGATTTACACAC
AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA
TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCTTCAAAGGTGAGGTT
GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG
AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCCTTG
ACACTTGGTGATTCACTAGAACTTGAACATAAGGTTCTAGAAGCATTCTGAATGAGATC
AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAAGATATCTCTGTGAAATGGAGACA
AAGGACATGAGGCTCTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATTTGGTGATGTCTC
GGCAGCCTCCTCTGCACCGATTGAGAACTGGTGAGCACTTGATGAGTCAAGAAATAAGT
ACAGTTCTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTTATCTTTGTG
CCAGATTGGTTACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGT
ATGTATGAGACAACCTGGGGCAGGTTCAAGGGGAAATCCTGTGACGATTGGCTG

Figure 25 (cont'd)

CGCGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 23)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210

Translation=

>LCMV-P42_LP

MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIIEGLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPDIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTIVDKRSGMDSMKILKDARSFHNDIMKMHDCVNPNMSCDDVVFINS
FFGRFRDLLNGKLKRNFKQVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSILKLLNTRRRQLLNLDVLCSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLKNNRKS RVHKKASLDELFRVSINEFIK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRLKSSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPISDEVLHNMIDTMI SWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNI RYLVMAIVSDFSSTSLMDKCLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKF FMLNVSYLCHLITKETPDRLTDQIKCFEKKF
EPKSEFGFFVNPKETITPEEECVFYE QMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMNTNSGCATALDLASNKSVVKNHNGERLLEYDFNKLIVSAVSQI
TEGFMRKQKYKLRHSDYKYVSKLVSR LVIGSRKTEVDKLEDDPVDVCFEGEEETSFERS
LEDKVSSTITRYNRGTRLNEGQGEFKN TKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSP LYFTSAVKEQCGLDEMARNLCRKFSEGDWFS
CMKMILLQMNANAYS GKYRHMQRQSLNFKFDWDKLEEDVRI SERESNSESLSKALS LTKC
MSAALKNLCFYSEESPTSYTSVGPDSGR LKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAIL SMTINVREGLNYSMDHSHKWCPPMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEV PFPVNNAMKSYVSKLKLKSGSTTVTE
RIFREYFEMGVVPSHISSLIDMGQGI LHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDS DPEEVLVLLEFHS HSLGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLC ETIDTIADQAIANGVPVFLVNCIQRRTLDDLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRI QRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFDLDFNREKKEAILQLGEILGLEDDL NELASINWLNLMFPLRMVLRQKVYPSVM
TFQEEKIPSLIKTLQNKLC SKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSR CVR
NKNRENMYIRKVL EDLTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGNESNSA VRHLNPCDYVARKPESSRLLEDKVS LNHHVQS
VRRLYPKIFEDQLLPFMFDVSSKNMRWSPRIKF LDCVLIDINSESLISHVVKWRDE
HYTVLFSDLVNSHQRS DSSLVDEFVVS TRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAELGPFQSFILKVVNKKIERP MFRNDLQFGCWFYSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCHSHFFKGEVDRRLLECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRI LNEIKSTDFERICPEWEPVPLTIRKALFEGRN FVNISVKLET
KDMRVFLAELEGCGKIGDVLGSLLLH RFTGEHLMSEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFRSRKN TVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 24)

Figure 25 (cont'd)**C. Lymphocytic choriomeningitis virus (LCMV) P52 mutant**

Source: 1-3376 Segment = S
 Protein: Pre-glycoprotein polyprotein GP complex
 Gene: GPC
 Gene: 79-1575

>LCMV-P52_GP

ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
 ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTCGCCACC
 TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
 GGCCTTAATGGTCCCACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
 ATGTCTCAGTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC
 ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACCTAACGACTCCATCCTTAATCAC
 AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACTCATGAGT
 ATAGTCTCGAGTCTGCAGCTCAGTATTAGAGGGAATTCCAACCACAAAGCAGTGTCTTGT
 GATTTTAAACAATGGCATCACCATTCAATACAACCTGTCATTTTCGGACCCACAGAGCGCT
 ATGAGCCAGTGTGGACTTTAGAGGTAGAGTCTTGGACATGTTTAGAATGCCTTTGGA
 GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCAGATGGCAAGACCCTTGGTGC
 AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
 TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTGTCTCAGGAAAAGACAAAGTTTCTC
 ACTAGGAGACTTGCAGGCACATTCACCTGGACCCCTGTCAGACTCCTCAGGAGTAGAAAAAT
 CCAGGTGGTTATTGCCGACCAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
 AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
 CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
 CATGTATTCAAAACAACAGTAAATCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
 CTAAGAGATCTAATGGGGTACCATACTGTAATTACTCAAAGTTCTGCTATCTGGAACAT
 CCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCATAATGGCTCCTACTTG
 AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
 TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
 ATGTTTTCAACATCAGCATATCTAATCAGCATCTTCTGCATCTGTGAAGATACCAACA
 CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
 TGTAGTTGTGGTGATTCAAGGTGCCTGGTGTAAAACTATCTGCAAAAGACGCTGA
 (SEQ ID NO: 25)

CDS: 79-1575

Codon Start = 1; Codons 1-498

Chain: 1-498 Pre-glycoprotein polyprotein GP complex

Chain: 1-58 Stable signal peptide

Chain: 59-265 Glycoprotein G1

Chain: 266-498 Glycoprotein G2

Translation=**>LCMV-P52_GP**

MGQIVTMFEALPHIIDVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGMY
 GLNGPDIYKGVYQFKSVEFDMSHLNLMPNACSANNSHHYISMSSGLELFTNDSILNH
 NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
 MSQCWTFRGRVLDMFRTAFGGKYMRSWGWSGDKTTWCSQTSYQYLIQNRTWENHCR
 YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
 NTAVAKCNVNHDEEFCMDLRLIDYNKAALSFKQDVESALHVFKTTVNSLISDQLLMRNH
 LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
 LRKDYIKRQGSTPLALMDLLMFST SAYLISIFLHLVKIPTHRIKGCSCPKPHRLTNKGI
 CSCGAFKVPGVKTIWKRR
 (SEQ ID NO: 26)

Figure 25 (cont'd)

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-P52_NP

```
ATGTCCTTTTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG
CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT
GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCCTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA
GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACTTGATCAAAGATCCCAAATA
CTGCAAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTCGTCTAGTAAGCGTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAAATGCCAAGCCTGACAATG
GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC
CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTCAAAGGCTAAAGGAT
AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT
AATTTAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG
GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAACTTGTT
GCCAATCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAAAGAGGGACATAAACTCATGATGTTGACATGACC
AAGGAGGCCCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAAATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 27)
```

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-P52_NP

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DKDLQRLRLSNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ
ASGVYMGNLTAQQLDQRSQILQVMGMRRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKD KHPVLGVITEQQSSINISGY
NFSLGA AVKAGAAALLDGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVCDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDL TNEKLVANS SRPVGAAGPPQVGLSY
SQTMLLKDLMGIDPNAPT WIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLS CQGSDDIRKLLDSQNRDRIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 28)
```

Figure 25 (cont'd)

Organism: Lymphocytic choriomeningitis virus (LCMV strain WE)
Subtype: P52
Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-P52_ZP

ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT
TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAAATTGAC
AGCTTGGTTAGATGCCATGACCACTATCTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCTCTCTGTAAGTATCCACTGCCAACCAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 29)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-P52_ZP

MGQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHLYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 30)

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-P52_LP

```
ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG
AGGCTGTCAAGGCAAACTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGCTAATT
GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTATTCTT
CTTGAATGTTTTGTTAGAACACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATCGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAATTTTTGAGGAG
TCTGAATACCTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAAACGTTCCGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAGGAATTTCCAAAAG
GTCAGCCCTGGGGGCTTAATCAAGGAATTCCTCTGAACTTTATGAAACCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTGAACAAGGTGAAAAGTTTAAATATTAAACACTAGAAGGAGACAGCTG
CTGAACTTAGATGTCTTATGTCTTTCTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTTGGGTTGGTTGTTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC
CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAAGAACAGAAGAAAATCAAGAGTG
CACAAAAGGCATCTCTTGATGAGCTTTTATAGGTTATCCATAAATGAGTTCATAGCAAAA
ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
CTCGTGCAAGAATGCCATATACCATTGCTGAATTTGAGAATTTATGAGAGCCGGGACT
CATCCTGTATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA
TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGTGTTGGCTCTAACAAACAGC
ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA
GTGGTGGAGTGCAAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT
CTACTATATCAGAAAACGTGAGAATCATCGAGGTGTTATTCATACAAGTCCGGATGGT
CACTTGATTTCCTTTTACGCAGATCCAAAAGGTTCTTTTTACCAATTTTTTTCAGATGAG
GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTATGCCCTGACTTAAAA
GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC
CCAACAAGAGGAAATCAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGCT
TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC
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ATCACAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCTTT
GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG
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GAAGATGATCCGGTAGATCTGTGTTTTCCAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT
TTAGAAGATAAGGTGAGTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA
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TCAGGTAAGAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCAATTCATCTAGTA
GAGGACTTTGATCCATCTGTCTCACCATTGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAATCTGACCATTTGATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA
TGATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC
```

Figure 25 (cont'd)

ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
ATTAGTGAAAGGGAAAGCAATCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCACATCATACACT
TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG
GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCAAGATTGGTAGAA
GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG
TTTGAAATGCAATCTTGTCATGACTATCAATGTGAGAGAAGGGTTGTTAACTACAGC
ATGGATCACAGCAAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA
AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG
TTGACTTGGCATATGCATAAACTTGTGTAAGTCCCTTTCCCTGTTGTGAATGCAATGATG
AAATCATATGTTAAATCAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG
AGAATCTTTAGAGAGTATTTTGAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT
GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG
TTTATCAATTATTGTATTGCTGTCATTTTTGGAGAGAGGCCAGAACCTATACATCAAGT
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GAAGTCCTTGCTTGTGCTGGAATTCCTCTCACTTAAAGTGGTTTGTGAACAAGTTCATC
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CATGTCAAAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTCCGACAAAGCAGAGA
CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT
TGCATCTCATTTGAGCAACTCTTTTGAGCTGGGTGTTTGGGTTTTAGCAGAACCCTGTGAAA
GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTCATTATGTAGCAAGA
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TTCGAATCATTTGTACGAGAGTTTGTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG
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TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTCTGCGGAT
TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACACTGGATTTACACAC
AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA
TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCCTTCAAAGGTGAGGTT
GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG
AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCCTTTG
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AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
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GGCAGCCTCCTCTGCACCGATTGAGAACTGGTGAGCACTTGATGAGTACAGAAATAAGT
TCAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTTCTTTGTG
CCAGATTGGTTACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAACCTGGGGCAGGTTGAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

Figure 25 (cont'd)

CGCGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 31)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-P52_LP

MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLEIQLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPDIVDGRCDYDNSFMPPEWVNFKFRDLLFKLLEYSSQDEKVFE
SEYFRLCESLKTIVDKRSGMDSMKILKDARSFHNDIMKMHDCVNPNMSCDDVVFINS
FFGRFRDLLNGKLKRNFKQVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSILKLLNTRRRQLLNLDVLCSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLKNRRKSRVHKKASLDELFRVSINEFIAK
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LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFSEGDWFS
CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRI SERESNSESLKALSITKC
MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLNYSMDHSHKWCPPMCPFLFLMLLQ
NLKLGDDQYVRSKGDHVSSTLLTWHMHKLVEVFPVNVAMMKS YVSKLKLKSGSTTVTE
RIFREYFEMGVVPSHISLIDMGQGIHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPPEVLVLLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFDLDFNREKKEAILQLGEILGLEDDLNELASINWLNLMFMFLRMVLRQKVVPVSM
TFQEEKIPSLIKTLQNKLCSEKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRV
NKNRENMYIRKVLDTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGNESNSAVRHLNPCDYVARKPESSRLLEDKVSINHVQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVIDINSESLISHVVKWRDE
HYTVLFSDLVNSHQSDSSSLVDEFVVSSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAALGPFSFILKVVNKKIERPMFRNDLQFGCFWFSYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
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TLGDSLELELIGSRRIINEIKSTDFERIGPEWEPVPLTIRKCALFEGRNFVQN~~X~~SVKLET
KDMRVFLAELEGCGKIGDVLGSLLLHRTGEHLMSEIS~~X~~VLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 32)

X=I/V

X=T/A

Figure 25 (cont'd)**D. Lymphocytic choriomeningitis virus (LCMV) P91 mutant**

Source: 1-3376 Segment = S
 Protein: Pre-glycoprotein polyprotein GP complex
 Gene: GPC
 Gene: 79-1575

>LCMV-P91_GP

ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
 ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTGCCACC
 TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
 GGCCTTAATGGTCCCACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
 ATGTCTCATTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC
 ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACCTAACGACTCCATCCTTAATCAC
 AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACTCATGAGT
 ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATTCCAACCACAAAGCAGTGTCTTGT
 GATTTTAAACAATGGCATCACCATTCAATACAACCTTGTCATTTTCGGACCCACAGAGCGCT
 ATGAGCCAGTGTGGACTTTAGAGGTAGAGTCTTGGACATGTTTAGAATGCCTTTGGA
 GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCAGATGGCAAGACCCTTGGTGC
 AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
 TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
 ACTAGGAGACTTGCAGGCACATTCACCTGGACCTGTCAGACTCCTCAGGAGTAGAAAAAT
 CCAGGTGGTTATTGCCGACCAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
 AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
 CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
 CATGTATTCAAAACAACAGTAAATCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
 CTAAGAGATCTAATGGGGTACCATACTGTAATTACTCAAAGTTCTGCTATCTGGAACAT
 CCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTTGCTCACTAATGGCTCCTACTTG
 AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
 TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
 ATGTTTTCAACATCAGCATATCTAATCAGCATCTTCTGCATCTGTGAAGATACCAACA
 CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
 TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAGACGCTGA
 (SEQ ID NO: 33)

CDS: 79-1575

Codon Start = 1; Codons 1-498

Chain: 1-498 Pre-glycoprotein polyprotein GP complex
 Chain: 1-58 Stable signal peptide
 Chain: 59-265 Glycoprotein G1
 Chain: 266-498 Glycoprotein G2

Translation=**>LCMV-P91_GP**

MGQIVTMFEALPHIIDEVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLACRSCGMY
 GLNGPDIYKGVYQFKSVFEFDMSHLNLTPNACSANNSSHYYISMSSGLELFTNDSILNH
 NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
 MSQCWTFRGRVLDMFRTAFGGKYMRSWGWSGDKTTWCSQTSYQYLIIQNRTWENHCR
 YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
 NTAVAKCNVNHDEEFCDMLRLIDYNKAALSFKQDVESALHVFKTTVNSLISDQLLMRNH
 LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
 LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
 CSCGAFKVPGVKTIWKRR
 (SEQ ID NO: 34)

Figure 25 (cont'd)

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-P91_NP

```
ATGTCCTTTTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG
CAGAGTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCCAACCAGTCTTCTAAAT
GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA
GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACTTGATCAAAGATCCCAAATA
CTGCAAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTCGCTAGTAAGCGTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAAATGCCAAGCCTGACAATG
GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC
CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTCAAAGGCTAAAGGAT
AAACACCCAGTTCTGGGGTCAATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT
AATTTAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG
GCCAAGAAGAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAACTTGTT
GCCAATCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCACACCAAAAAAT
GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCAGAAAATAGAAAGGGACATAAACTCATTCATGTTGACATGACC
AAGGAGGCCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAAATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 35)
```

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-P91_NP

```
MSLSKEVKSFQWTQALRRELQSFTSDVKA AVIKDATSLNGLDFSEVSNVQRIMRKERRD
DKDLQRLRLSNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ
ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY
NFSLGA AVKAGAAALLDGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVCDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDL TNEKLVANS SRPVGAAGPPQVGLSY
SQTMLLKDLMGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKL LDSQNRD IKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNVVTL
(SEQ ID NO: 36)
```

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-P91_ZP

ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT
TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 37)

CDS: 90-362
Codon Start = 1; Codons 1-91

Translation=

>LCMV-P91_ZP

MQQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 38)

Source: 1-7235 Segment = L

Figure 25 (cont'd)

Protein: RNA-directed RNA polymerase L

Gene: LP

Gene: 574-7203 complement

>LCMV-P91_LP

ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG
AGGCTGTCAAGGCAAACTCAACTTCTGGGACAAAGAGAACCAGAATGGTGCTAATT
GAGGGACTCAAATTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTATTCTT
CTTGAATGTTTGTAGAAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATCGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAAGTTTTTGAGGAG
TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAAAGTTCGGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAAACTCAAAAGGAATTTCCAAAAG
GTCAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTCAAT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTGAACAAGGTGAAAAGTTTAAATATTATAACACTAGAAGGAGACAGCTG
CTGAACTTAGATGTCTTATGTCTTTCTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTTGGGTTGGTTGCTGCTACAGTAGTGTGAATCATAGGCTTGTGAGC
CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAAGAACAGAAGAAAATCAAGAGTG
CACAAAAGGCATCTCTTGATGAGCTTTTAGGGTATCCATAAATGAGTTCATAGCAAAA
ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
CTCGTGCAAGAATGCCATATACCATTGCTGAATTTGAGAATTTATGAGAGCCGGGACT
CATCCTGTATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA
TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGGTCTTAACAAACAGC
ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA
GTGGTGGAGTGCAAAAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT
CTACTATATCAGAAAACGTGAGAATCATCGAGGTGTTATTCATACAAGTCCGGATGGT
CACTTGATTTCCTTTTACGCAGATCCAAAAGGTTCTTTTTACCAATTTTTTCAGATGAG
GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTATGCCCTGACTTAAAA
GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC
CCAACAAGAGAAATCAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGCT
TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC
GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA
AAGGTGTTATTGAGTGCAAAATTCAGTTTATGTTGAATGTGTATACCTGTGTCAATTTG
ATCACAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTCTTT
GAGCCCAAGAGTGAGTTTGGTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG
GAATGTGTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATTTGATTGTGAGCAT
TCAACCCCTGGTGTAAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC
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TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT
GGAGAACGGCTTTTGGAGTATGATTTTAACAAATGCTTGTAGTGCTGTGAGCCAAAT
ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG
GTCTCAAAGCTTGCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAAATG
GAAGATGATCCGGTAGATCTGTGTTTTCCAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT
TTAGAAGATAAGGTCAGTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA
GGGCAAGGGGAGGGGAGAAATCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG
TCAGGTAAGAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTTCAATTCATCTAGTA
GAGGACTTTGATCCATCTGTCTCACCATTGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAACTGTCAACATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTCTCA
TGATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC

Figure 25 (cont'd)

ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
ATTAGTGAAAGGGAAAGCAATCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCACATCATACACT
TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG
GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCAAGATTGGTAGAA
GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGATAAAGAG
TTTGAAATGCAATCTTGTCATGACTATCAATGTGAGAGAAGGGTTGTTAACTACAGC
ATGGATCACAGCAAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA
AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG
TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG
AAATCATATGTTAAATCAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG
AGAATCTTTAGAGAGTATTTTGAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT
GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG
TTTATCAATTATTGTATTGCTGTCATTTTTGGAGAGAGGCCAGAACCTATACATCAAGT
GATGATCAGATCACTTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA
GAAGTCCTTGCTTGTGCTGGAATTCCTCTCACTTAAAGTGGTTTGTGAACAACCTTCATC
AGTCCAAAAAGTGTGGTTGGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG
GGGGAGGAGGTCCTCTCCTCACGAAATTTGTGTCTGCGGCACACACAATGTTAAGTGT
AAAGAACC GCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT
GGAGTTCCAGTTTTTTTTAGTAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATAT
GCTAATTTCCCTTTAGATCCATTCCTTGTAAACACTCACACTGATGTAAGGATTGGTTA
GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA
AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAACTCAAGAACGGTGAATGTAAC
GAGGAATTTTTCTAGACCTCTTCAACAGGGAAAAGGAAGAGGCCATCCTTCAATTGGGA
GAGATTCCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTCAATCTG
AATGAAATGTTCCCATTTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG
ACCTTTCAAGAGGAAAAGATCCCTCATTTGATTAAACACTCCAAAATAAGCTTTGTAGT
AAGTTCACAAGAGGTGCACAGAAGCTGTGTGTCAGAGGCAATCAACAAATCAGCTTTTCAG
AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA
AATAAAACAGGGAAAATATGTATATCAGAAAGGTCTTGAAGATCTGACCATCGCATGAA
CATGTCAAAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTCCGACAAAGCAGAGA
CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT
TGCATCTCATTTGAGCAACTCTTTTGAGCTGGGTGTTGGGTTTTAGCAGAACCCTGTGAAA
GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTCATTATGTAGCAAGA
AAACCTGAGAGTTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATCAATCT
GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCGATGTG
AGCTCAAAAAATAGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT
GACATCAACTCAGAGTCTTTGTCACTCATTCTCATGTTGTCAAATGGAAGAGGGACGAA
CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCACACTCAAGTTTA
GTTGATGAATTTGTTGTGTCAGCACAAAGGGATGTCTGCAAGAATTTTTGAAGCAAGTGTAT
TTCGAATCATTTGTACGAGAGTTTGTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG
TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCCTCCAA
TCATTTATTTTGAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG
CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGATGTTGTGTGTAATGCCGCTATG
TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTCTGCGGAT
TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACACTGGATTTACACAC
AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA
TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCCTTCAAAGGTGAGGTT
GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG
AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCCTTG
ACACTTGGTGATTCACTAGAACTTGAACATAAGGTTCTAGAAGGATTCTGAATGAGATC
AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAAGATATCTCTGTGAAATGGAGACA
AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATGGTGATGTCTC
GGCAGCCTCCTCTGCACCGATTGAGAACTGGTGAGCACTTGATGAGTCAAGAAATAAGT
ACAGTTCTCAGGAGCTGTGCATGGACAGATCCGTGATGCTGACACCATTTATCTTTGTG
CCAGATTGGTTACCTTCAGAGATTGTAGGCTCTGCTTCAGCAAGTCAAAGAACACTGTA
ATGTATGAGACAACCTGGGGCAGGTTGAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

Figure 25 (cont'd)

CGCGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 39)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210

Translation=

>LCMV-P91_LP

MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPDIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFE
SEYFRLCESLKTIVDKRSGMDSMKILKDARSFHNDIMKMHGCVNPNMSCDDVVFINS
FFGRFRDLLNGKLKRNFKQVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSILKLLNTRRRQLLNLDVLCSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLKNNRKRVRHKKASLDELFRVSINEFIK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPMHYTKFEDYTFQPNIEQ
LRGLQSLRLKSSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPD
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIIRYLVMIAIVSDFSSLSMDKLEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMLNVSYLCHLITKETPDRLTDQIKCFEKF
EPKSEFGFFVNPKEITITPEEECVFYEQMKKFTGKDIDCQHSTPCVNLEIFSMMVSSF
NNGTLILKGEKRLNNLDPMNTNSGCATALDLASNKSVVKNHNGERLLEYDFNKLIVSAV
SQITEGFMKQKYKLRHSDYKYVSKLVSRVIGSRKTEVDKLEDDPVDVCFEGEEETSF
FRSLEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHL
VEDFDPSCLTNDDMRFICEAVEGSTELSPYFTSAVKEQCGLDEMARNLCRKFSEGDWFS
CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALS
LTKCMSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTK
MFTRLVEDYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLNYSMDHSGKWP
MMPFLFLMLLQNLKLGDDQYVRSKGDHVSSTLLTWHMHKLVEVFPVNVAMMKS
YVKSCLKLKGSGTTVTE RIFREYFEMGVVPSHISLIDMGQGIHNASDFYGLISER
FINYCIGVIFGERPEAYTSSDDQITLFDKRLSDLVDSDPPEVLVLLFESHLSGL
LNKFISPKSVVGRFAAEFKSRFYVWGEEVPLLTKFVSAALHNVKCKEPHQLCET
IDTIADQAIANGVPVFLVNCIQRRITLDLLKYANFPLDPFLLNTHTDVKDWL
DGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECNEEFFDLDFNREKEE
AILQLGEILGLEDDLNELASINWLNLMFPLRMVLRQKVYPVMTFQEEKIPSLIK
TLQNKLCSEKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRVNRKNREN
MYIRKVLDTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDYI
CISLSNSFELGVWVLAEPVKGNESNSAVRHLNPCDYVARKPESSRLLEDKVS
LNHVIQSVRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVIDINSE
SLISHVVKWRDEHYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFLKQVYFES
FVREFVATARTLGNFSWFPHKDMMPSEDGAALGPFQSFILKVNNKIERPMFRNDLQ
FGCFWFSYRVGDVVCNAAMLIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITV
DFTHNQNNTDCLRKFSLIFVVKCQLQSPGVADYLSCHSFKGEVDRRLLECLN
LLRTDPIFKANDGVFDIRSEEFEDYMEDPLTLGDSLELELIGSRRI
LNEIKSTDFERICPEWEPVPLTIRKCALFEGRNQNFVNISVKLET
KDMRVFLAELEGCGKIGDVLGSLLLHRTGEHLMSEISTVLQELCMDRSV
MLTPLSFVPDWFTFRDRCRLCFSXSKNTVMYETTGGRFRLKKGSCDDWLAERVA
EEID (SEQ ID NO: 40)

X=R/K

Figure 25 (cont'd)

E. Lymphocytic choriomeningitis virus (LCMV) P52-1 mutant

Source: 1-3376 Segment = S
 Protein: Pre-glycoprotein polyprotein GP complex
 Gene: GPC
 Gene: 79-1575

```
>LCMV-P52-1
ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTCATTATTGTGCTCATTATAATCAGAGCATCAAAGCTGTGTACAATTCGCCACC
TGTGGGATATTAGCACCTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTCAATGGTCCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTCGACTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCCTAAGGACTCCATCCTTAATCAC
AATTTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATAACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTCTCTTGT
GATTTTAAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGCT
ATGAGCCAGTGTGGACTTTTCAGAGGTAGAGTCTTGACATGTTTAGAAGTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCAGATGGCAAGACCCTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTCACCTGGACCCGTGCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCTGACCAAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG
CATGTATTTAAAACAACAGTAAATTTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATGACACATAAAAGGGCGTTTCTATGTTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAAGTTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAGACGCTGA
(SEQ ID NO: 41)
```

CDS: 79-1575
 Codon Start = 1; Codons 1-498

Chain:	1-498	Pre-glycoprotein polyprotein GP complex
Chain:	1-58	Stable signal peptide
Chain:	59-265	Glycoprotein G1
Chain:	266-498	Glycoprotein G2

Translation=

```
>LCMV-P52-1
MCQIVTMFEALPHIIDEVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGM
GLNGPDIYKGVYQFKSVEFDMSHLNLTMFNACSNANSHHYISMSSGLELFTTNDLSILNH
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
MSQCWTFGRVLDMFRTAFGGKYMRSWGWAGSDGKTTWCSQTSYQYLI IQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPGGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAAYLISIFLHLVKIPTHRIKGGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 42)
```

Figure 25 (cont'd)

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

```
>LCMV-P52-1_NP
ATGTCCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG
CAGAGTTTTTACATCAGATGTAAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT
GGGTTGGACTTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCCTCAA
GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA
CTGCAAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGCTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG
GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC
CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT
AAACACCCAGTTCTGGGGGTCAATTACTGAACAGCAATCTAGTATCAATATCTCTGTTAT
AATTTTCAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCTCTCGG
GCCAAGAAGAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAACTTGTT
GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTCAGTTAC
AGTCAGACAATGCTGTGAAAGACTTGATGGGAGGATTGATCCCAATGCTCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTATACATTTTTTACAGGGAACCTACGGACCAGAAGCAATCAAGCAGGACTCA
AAGTATTACACGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCACAAAGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAACTCATTGATGTTGACATGACC
AAGGAGGCCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAA
ATGCACACTGGGGTAGTGAGAGACAAAAGAAGAAAGAGATCACCCACACTGTGCACTC
ATGGACTGCATCATTTTTTGAAGTGTCTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAAATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 43)
```

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

```
>LCMV-P52-1_NP
MSLSKEVKSFQWTQALRRELQSFTSDVKA AVIKDATSLNGLDFSEVSNVQRIMRKERRD
DKDLQRLRLSNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ
ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM
ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY
NFSLGA AVKAGAAALDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGNPNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDL TNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSCQGSDDIRKLDSQNRDRIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRD KKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGNPVVTL
(SEQ ID NO: 44)
```

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-P52-1_ZP
ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT
TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 45)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-P52-1_ZP
MGQGKSKEERDTSTNGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 46)

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-P52-1_LP
ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG
AGGCTGTCAAGGCAAACTCAACTTCTGGGACAAAGAGAACCAGAATGGTGCTAATT
GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTATTCTT
CTTGAATGTTTGTAGAACACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATCGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAAGTTTTTGAGGAG
TCTGAATACCTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAAAGTTCGGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAGACTCAAAAGGAATTTCCAAAAG
GTCAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTCAAT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTGAACAAGGTGAAAAGTTTAAATATTAAACACTAGAAGGAGACAGCTG
CTGAACCTTAGATGTCTTATGTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTTGGGTTGGTTGTTGCTACAGTAGTGTGAATCATAGGCTTGTGAGC
CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAAGAACAGAAGAAAATCAAGAGTG
CACAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA
ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
CTCGTGCAAGAATGCCATATACCATTGCTGAATTTGAGAATTTATGAGAGCCGGGACT
CATCCTGTATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA
TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGTGTTGGCTCTAACAAACAGC
ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA
GTGGTGGAGTGCAAAAGAGGTGTTTTGCCAGATAATAAACTGGATTCCGAAGAGTATCAT
CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATTCATACAAGTCCGGATGGT
CACTTGATTTTCTTTTACGCAGATCCAAAAGGTTCTTTTACCAATTTTTTTCAGATGAG
GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTATGCCCTGACTTAAAA
GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC
CCAACAAAAGAGAAATCAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGTC
TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC
GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGTATTAGGACAATTTTTGGTACTGGTGAA
AAGGTGTTATTGAGTGCAAAATTCAGTTTATGTTGAATGTGTATACCTGTGTCAATTTG
ATCACAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTCTTT
GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG
GAATGTGTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTGAGCAT
TCAACCCCTGGTGTAAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC
ACCTTAATTTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCATGACCAACTCTGGA
TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT
GGAGAACGGCTTTTGGAGTATGATTTTAACAAATGCTTGTAGTCTGTGAGCCAAAT
ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG
GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCTAGGAAAACAGAAGTAGACAAAATG
GAAGATGATCCGGTAGATCTGTGTTTCCAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT
TTAGAAGATAAGGTCAGTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA
GGGCAAGGGGAGGGGAGAAATCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG
TCAGGTAAGAGAGCTTATCTGAGGAAAGTCAATTTATCAGAAATTTCAATTCATCTAGTA
GAGGACTTTGATCCATCTGTCTCACCATTGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAATCTGACCATTTGATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTTCTTCTCAGAGGGTGATTGGTTCTCA
TGTATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC

Figure 25 (cont'd)

ATGCAGAGGCAGAGTTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
ATTAGTGAAAGGGAAAGCAATCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCACATCATACACT
TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG
GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCAAGATTGGTAGAA
GATTATTTTGAATCCTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG
TTTGAAATGCAATCTTGCAATGACTATCAATGTGAGAGAAGGGTTGTTAACTACAGC
ATGGATCACAGCAAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA
AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGGAAAGATCATGTTAGCACCTTG
TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG
AAATCATATGTTAAATCAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG
AGAATCTTTAGAGAGTATTTTGAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT
GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG
TTTATCAATTATTGTATTGCTGTCATTTTTGGAGAGAGGCCAGAACCTATACATCAAGT
GATGATCAGATCACTTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA
GAAGTCCTTGCTTGTGCTGGAATCCACTCTCACTTAAAGTGGTTTGTGAACAACCTTCATC
AGTCCAAAAAGTGTTGGTTGGGCGGTTTGCAGCGGAATCAAATCCAGATTTTATGTGTGG
GGGGAGGAGGTCCTCTCCTCACGAAATTTGTGTCTGCGGCACACACAATGTTAAGTGT
AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT
GGAGTTCCAGTTTTTTTTAGTAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATATAT
GCTAATTTCCCTTTAGATCCATTCCTTGTAAACACTCACACTGATGTAAAGGATTGGTTA
GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA
AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAACTCAAGAACGGTGAATGTAAC
GAGGAATTTTTCTAGACCTCTTCAACAGGGAAATGAAAGAGGCCATCCTTCAATTGGGA
GAGATTCCTTGGTCTTGAGGATGATCTCAATGAGTTGGCAAGCATCAATTTGGTTCAATCTG
AATGAAATGTTCCCATTTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG
ACCTTTCAAGAGGAAAAGATCCCTCATTTGATTAAACACTCCAAAATAAGCTTTGTAGT
AAGTTCACAAGAGGTGCACAGAAGCTGTTGTGAGAGGCAATCAACAAATCAGCTTTTCAG
AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA
AATAAAACAGGGAAAATATGTATATCAGAAAGGTCTTGAAGATCTGACCATCGCATGAA
CATGTCAAAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTCCGACAAAGCAGAGA
CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT
TGCATCTCATTTGAGCAACTCTTTTGAGCTGGGTGTTGGGTTTTAGCAGAACCCTGTGAAA
GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTCATTATGTAGCAAGA
AAACCTGAGAGTTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATCAATCT
GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCGATGTG
AGCTCAAAAAATAGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT
GACATCAACTCAGAGTCTTTGTCACTCATTCTCATGTTGTCAAATGGAAGAGGGACGAA
CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA
GTTGATGAATTTGTTGTGTCAGCACAAAGGATGTCTGCAAGAATTTTTGAAGCAAGTGTAT
TTCGAATCATTTGTACGAGAGTTTGTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG
TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCTTCCAA
TCATTTATTTTGAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG
CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGATGTTGTGTGTAATGCCGCTATG
TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTCTGCGGAT
TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACACTGGATTTACACAC
AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA
TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCTTCAAAGGTGAGGTT
GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG
AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCCTTG
ACACTTGGTGATTCACTAGAACTTGAACATAAGGTTCTAGAAGCATTCTGAATGAGATC
AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAAGATATCTCTGTGAAATGGAGACA
AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAGAAATGGTGATGTCTC
GGCAGCCTCCTCTGCACCGATTGAGAACTGGTGAGCACTTGATGAGTACAGAAATAAGT
RCAGTTCTTCAGGAGCTGTGCATGGACAGATCCGTGATGCTGACACCATTATCTTTGTG
CCAGATTGGTTACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAGCTGGGGCAGGTTGAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

Figure 25 (cont'd)

CGCGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 47)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-P52-1_LP
MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIIEGLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPDIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTIVDKRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFINS
FFGRFRDLLNGRLKRNFKQVSPGGLIKEFSELYETLTDNDDIIMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSILKLLNTRRRQLLNLDVLCSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLKNRRKSRVHKKASLDELFRVSINEFIK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPMHYTKFEDYTFQPNIEQ
LRGLQSLRLKSSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIIRYLVMIAIVSDFSSTSLMDKCLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMNLVSYLCHLITKETPDRLTDQIKCFEKFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPCVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMNTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLIVSAVSQI
TEGFMKQKYKLRHSDYKYVSKLVSRVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFSEGDWFS
CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRI SERESNSESLKALSITKC
MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLNYSMDHSHKWPMMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVFPVNVAMMKSIVKSKLKLKSGSTTVTE
RIFREYFEMGVVPSHISLIDMGQGIHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPPEVLVLLFEHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRITLDLLKY
ANFPLDPFLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFDLDFNREMKEAILQLGEILGLEDDLNELASINWNLNEMFPLRMVLRQKVVPVSM
TFQEEKIPSLIKTLQNKLCSEKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRV
NKNRENMYIRKVLDTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDYI
CISLSNSFELGVWVLAEPVKGNESNSAVRHLNPCDYVARKPESSRLLEDKVSINHVQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVIDINSESLISHVVKWRDE
HYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAALGPFQSFILKVVNKKIERPMFRNDLQFGCWFESYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCHSHFFKGEVDRRLLECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRIINEIKSTDFERICPEWEPVPLTIRKCALFEGRNQVQNISVKLET
KDMRVFLAELEGCEIGDVLGSLLLHRTGEHLMESEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFRSKNTVMYETAGGRFRLKKGKSCDDWLAERVAEEID
(SEQ ID NO: 48)

Figure 25 (cont'd)

F. Lymphocytic choriomeningitis virus (LCMV) p52-1.3

Source: 1-3376 Segment = S
 Protein: Pre-glycoprotein polyprotein GP complex
 Gene: GPC
 Gene: 79-1575

```
>LCMV-p52-1.3_GP
ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTTGCCACC
TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT
GATTTTAAACAATGGCATCACCATTCAATACAACCTTGTCATTTTCGGACCCACAGAGCGCT
ATAAGCCAGTGTGGACTTTGAGAGGTAGAGTCTTGACATGTTTAGAAGTGCCTTTGGA
GGAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTGAGATGGCAAGACCACTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAAACAGGACTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAT
CCAGGTGGTTATTGCCCTGACCAATGGATGATCCTTGCTGCAGAGCTCAAATGTTTTGGG
AAACACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCCTTG
CATGTATTTCAAAACAACAGTAAATTTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGCTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAGTTGTGGTGCATTCAGGTGCCCTGGTGTAAAAACTATCTGCAAAAGACGCTGA
(SEQ ID NO: 49)
```

CDS: 79-1575
 Codon Start = 1; Codons 1-498

Chain:	1-498	Pre-glycoprotein polyprotein GP complex
Chain:	1-58	Stable signal peptide
Chain:	59-265	Glycoprotein G1
Chain:	266-498	Glycoprotein G2

Translation=

```
>LCMV-p52-1.3_GP
MGQIVTMFEALPHIIDDEVINIVIIIVLIITSIKAVYNFATCGILALVSFLFLAGRSCGM
YGLNGPDIYKGVYQFKSVEFDMSHLNLTMPNACSANNSSHYYISMGSSGLELFTTND
SILNHNFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLS
FSDPQSAISQCWTFRGRVLDMFRTAFGGKYMRSWGWAGSDGKTTWCSQTSYQYLI
IQNRTWENHCRYAGPFGMSRILFAQEKTKEFLTRRLAGTFTWTLSDSSGVENPGGY
CLTKWMILAAELKCFGNTAVAKCNVNHDEEFCDMLRLIDYNKAALSKEFKQDVESAL
HVFKTTVNSLISDQLLMRNHLRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGS
YLNETHFSDQIEQEAADNMITEMLRKDYIKRQGSTPLALMDLLMFSTSA
YLISIFLHLVKIPTHRIHKGSCPKPHRLTNKGI
CSCGAFKVPGVKTIWKRR
(SEQ ID NO: 50)
```

Figure 25 (cont'd)

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-p52-1.3_NP
ATGTCCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG
CAGAGTTTTTACATCAGATGTAAAGGCTGCCGTCAATCAAGGACGCAACCAGTCTTCTAAAT
GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAAGGATCATGAGAAAGGAAAGGAGGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCCTTGCAGCTGATCTCGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCCTCAA
GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA
CTGCAAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGCTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAATGCCAAGCCTGACAATG
GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC
CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGTCTTGAAAGGCTAAAGGAT
AAACACCCAGTCTTGGGGGTCAATTACTGAACAGCAATCTAGTATCAATATCTCTGTTAT
AATTTTCACTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCTCGGG
GCCAAGAAGAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAACTTGT
GCCAATCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTCACTTAC
AGTCAGACAATGCTGTGAAAGACTTGATGGGAGGATTGATCCCAATGCTCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT
GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATCAAGCAGGACTCA
AAGTATTACACGGCATGGATCTTGTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCACAAAGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAACTCATTGATGTTGACATGACC
AAGGAGGCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAGAAGAAAGAGATCACCCACACTGTGCACTC
ATGGACTGCATCATTTTTGAGAGTGCCTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 51)

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558
Translation=

>LCMV-p52-1.3_NP
MSLSKEVKSFQWTQALRRELQSFTSDVKA AVIKDATSLNGLDFSEVSNVQRIMRKERRD
DKDLQRLRLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ
ASGVYMGNLTAQQLDQRSQILQVMGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY
NFSLGA AVKAGAAALDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVQDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLNEKLVANSSRPVPGAAGPPQVGLSY
SQTMLLKDLMGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKLLDSQNRDRIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPVNVTL
(SEQ ID NO: 52)

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-p52-1.3_ZP
ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT
TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 53)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-p52-1.3_ZP
MGQGKSKEERDTISNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHLYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 54)

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-p52-1.3_LP

ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAG
AGGCTGTCAAGGCAAACTCAACTTCTGGGACAAAGAGAACCAGAATGGTGCTAATT
GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTATTCTT
CTTGAATGTTTTGTTAGAACACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATCGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAAGTTTTTGAGGAG
TCTGAATACCTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAAAGTTCGGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAACTCAAAGGAATTTCCAAAAG
GTCAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCAAT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTAAACAAGGTGAAAAGTTTAAATATTAAACACTAGAAGGAGACAGCTG
CTGAACCTTAGATGTCTTATGTCTTTCTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTTGGGTTGGTTGTTGCTACAGTAGTGTGAATCATAGGCTTGTGAGC
CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAAGAACAGAAGAAAATCAAGAGTG
CACAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA
ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAATGC
CTCGTGCAAGAATGCCATATACCATTGCTGAATTTGAGAATTTATGAGAGCCGGGACT
CATCCTGTATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA
TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGTGTTGGCTCTAACAAACAGC
ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA
GTGGTGGAGTGCAAGAGAGGTGTTTTGCCAGATAATAAACTGGATTCCGAAGAGTATCAT
CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATTCATACAAGTCCGGATGGT
CACTTGATTTTCTTTTACGCAGATCCAAAAGGTTCTTTTACCAATTTTTTTCAGATGAG
GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTATGCCCTGACTTAAAA
GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC
CCAACAAGAGGAAATCAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGCT
TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC
GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGATTAGGACAATTTTTGGTACTGGTGAA
AAGGTGTTATTGAGTGCAAAAATTCAGTTTATGTTGAATGTGTATACCTGTGTCAATTTG
ATCACAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTCTTTT
GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG
GAATGTGTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTGAGCAT
TCAACCCCTGGTGTAAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC
ACCTTAATTTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCATGACCAACTCTGGA
TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT
GGAGAACGGCTTTTGGAGTATGATTTTAACAAATGCTTGTAGTGCTGTGAGCCAAAT
ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG
GTCTCAAAGCTTGCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAAATTA
GAAGATGATCCGGTAGATCTGTGTTTTCCAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT
TTAGAAGATAAGGTGAGTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA
GGGCAAGGGGAGGGGAGAAATCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG
TCAGGTAAGAGAGCTTATCTGAGGAAAGTCAATTTATCAGAAATTTCAATTCATCTAGTA
GAGGACTTTGATCCATCTGTCTCACCATTGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAACCTGTCAACATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA
TGATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC

Figure 25 (cont'd)

ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
ATTAGTGAAAGGGGAAAGCAATCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCACATCATACACT
TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG
GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCAAGATTGGTAGAA
GATTACTTTGAATCCTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG
TTTGAAATGCAATCTTGCAATGACTATCAATGTGAGAGAAGGGTTGTTAACTACAGC
ATGGATCACAGCAAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA
AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG
TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG
AAATCATATGTTAAATCAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG
AGAATCTTTAGAGAGTATTTTGAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT
GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG
TTTATCAATTATTGTATTGCTGTCATTTTTGGAGAGAGGCCAGAACCTATACATCAAGT
GATGATCAGATCACTTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA
GAAGTCCTTGCTTGTGCTGGAATTCCTCTCACTTAAAGTGGTTTGTGAACAAGTTCATC
AGTCCAAAAAGTGTTGGTTGGGCGGTTTGCAGCGGAATCAAATCCAGATTTTATGTGTGG
GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACACACAATGTTAAGTGT
AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT
GGAGTTCAGTTTTTTTTAGTAACTGTATCCAGAGGAGGACACGGATCTCTTGAATATAT
GCTAATTTCCCTTTAGATCCATTCCTTGTAAACACTCACACTGATGTAAAGGATTGGTTA
GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA
AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAACTCAAGAACGGTGAATGTAAC
GAGGAATTTTTTCTAGACCTCTTCAACAGGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA
GAGATTCCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTCAATCTG
AATGAAATGTTCCCATTTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG
ACCTTTCAAGAGGAAAAGATCCCTCATTTGATTAAACACTCCAAAATAAGCTTTGTAGT
AAGTTCACAAGAGGTGCACAGAAGCTGTGTGTCAGAGGCAATCAACAAATCAGCTTTTCAG
AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA
AATAAAACAGGGAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATCGCATGAA
CATGTCAAAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTCCGACAAAGCAGAGA
CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT
TGCATCTCATTTGAGCAACTCTTTTGAGCTGGGTGTTGGGTTTTAGCAGAACCCTGTGAAA
GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTGATTATGTAGCAAGA
AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATCAATCT
GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCATGCTG
AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT
GACATCAACTCAGAGTCTTGTCACTCATTCTCATGTTGTCAAATGGAAGAGGGACGAA
CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA
GTTGATGAATTTGTTGTGTCAGCACAAAGGATGTCTGCAAGAATTTTTGAAGCAAGTGTAT
TTCGAATCATTTGTACGAGAGTTTGTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG
TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCCTCCAA
TCATTTATTTTGAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG
CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGATGTTGTGTGTAATGCCGCTATG
TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTCTGTTGGAT
TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACACTGGATTTACACAC
AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA
TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCCTTCAAAGGTGAGGTT
GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG
AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCCTTG
ACACTTGGTGATTCACTAGAACTTGAACATAAGGTTCTAGAAGGATTCTGAATGAGATC
AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAAGATATCTCTGTGAAATGGAGACA
AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAAAAATGGTGATGTCTC
GGCAGCCTCCTCTGCACCGATTGAGAACTGGTGAGCACTTGATGAGTCAAGAAATAGT
ACAGTTCTCAGGAGCTGTGCATGGACAGATCCGTATGCTGACACCATTATCTTTGTG
CCAGATTGGTTACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAACCTGGGGCAGGTTGAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

Figure 25 (cont'd)

CGGGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 55)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210

Translation=

>LCMV-p52-1.3_LP

MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIIEGLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPDIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTIVDKRSGMDSMKILKDARSFHNDIMKMHDCVNPNMSCDDVVFINS
FFGRFRDLLNGKLKRNFKQVSPGGLIKEFSELYETLTDNDDIIMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSILKLLNTRRRQLLNLDVLCSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLKNNRRKSRVHKKASLDELFRVSINEFIAK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRLKSSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPISDEVLHNMIDTMI SWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMAIVSDFSSTSLMDKCLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMNLVSYLCHLITKETPDRLTDQIKCFEKFF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMNTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLIVSAVSQI
TEGFMRKQKYKLRHSDYKYVSKLVSRVIGSRKTEVDKLEDDPVDVCFEGEEETSFFRS
LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFSEGDWFS
CMKMILLQMNANAYS GK YRHMQRS LNFKFDWDKLEEDVRI SERESNSESLKALSLTKC
MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLNYSMDHSHKWCPPMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVFPVNVAMMKS YVSKLKLKSGSTTVTE
RIFREYFEMGVVPSHISSLIDMGQGI LHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDS DPEEVLVLLFEHSHLSGLLNKFI SPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFDLDFNREKKEAILQLGEILGLEDDLNELASINWLNLMFMFLRMVLRQKVVPVSM
TFQEEKIPSLIKTLQNKLC SKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRCVR
NKNRENMYIRKVLDTMDEHVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGNESNSAVRHLNPCDYVARKPESSRLLEDKVS LN HVIQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCVLIDINSESLISHVVKWRDE
HYTVLFSDLVNSHQRS DSSLVDEFVVS TRDVCKNFLKQVYFESFVREFVATARTLGNFSW
FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGCWF SYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFSLIFVVKCQ
LQSPGVADYLSCHSHFKGEVDRRLLECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRI LNEIKSTDFERICPEWEPVPLTIRKCALFEGRN FVNISVKLET
KDMRVFLAELEGCGKIGDVLGSLLLHRTGEHLMSEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 56)

Figure 25 (cont'd)**G. Lymphocytic choriomeningitis virus (LCMV) P52-2.1**

Source: 1-3376 Segment = S
Protein: Pre-glycoprotein polyprotein GP complex
Gene: GPC
Gene: 79-1575

```
>LCMV-p52-2.1_GP
ATGGGTCAGATTGTGACAAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC
ATTGTTATTATTATTGTGCTCATTATAATCAGCAGCATCAAAGCTGTGTACAATTTGCCACC
TGTGGGATATTAGCACCTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC
GGCCTTAATGGTCCCAGCATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT
ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC
ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTCACTAACGACTCCATCCTTAATCAC
AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATAACACTCATGAGT
ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATFCCAACCACAAAGCAGTCTCTTGT
GATTTTAAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGCT
ATGAGCCAGTGTAGGACTTTTCAAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA
GGAAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCAAGATGGCAAGACCCTTGGTGC
AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTTGGGAAAACCACTGTAGA
TATGCAGGCCCTTTTGGGATGTCTAGAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC
ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAAT
CCAGGTGGTTATTGCCTGACCAATGGATGATCCTTGTGTCAGAGCTCAAATGTTTGGG
AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA
CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATCTAGAGTCTGCCTTG
CATGTATTTAAAACAACAGTAAATTTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT
CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT
GCTAAGACTGGTGAGACTAGTGTACCCAAGTGTGGCTTGTCACTAATGGCTCCTACTTG
AATGAGACCCACTTTAGTGATCAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG
TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG
ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA
CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC
TGTAGTTGTGGTGCAATCAAGGTGCCTGGTGTAAAAACTATCTGAAAAAGACGCTGA
(SEQ ID NO: 57)
```

CDS: 79-1575
Codon Start = 1; Codons 1-498

Chain:	1-498	Pre-glycoprotein polyprotein GP complex
Chain:	1-58	Stable signal peptide
Chain:	59-265	Glycoprotein G1
Chain:	266-498	Glycoprotein G2

Translation=

```
>LCMV-p52-2.1_GP
MGQIVTMFEALPHIIDEVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLACRSCGMY
GLNGPDIYKGVYQFKSVFEFDMSHLNLTMPNACSANNHHYISMSSGLELFTFTNDSILNH
NFCNLTSAFNKKTFDHTLMSIVSSLHLSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA
MSQCRTRFRGRVLDMFRTAFGGKYMRSWGWSGSDGKTTWCSQTSYQYLIIQNRTWENHCR
YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSSGVENPCGYCLTKWMILAAELKCFG
NTAVAKCNVNHDEEFCDMLRLIDYNKAALSKFKQDVESALHVFKTTVNSLISDQLLMRNH
LRDLMGVPYCNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQEADNMITEM
LRKDYIKRQGSTPLALMDLLMFSTSAAYLISIFLHLVKIPTHRHIKGGSCPKPHRLTNKGI
CSCGAFKVPKVKTWKRR
(SEQ ID NO: 58)
```

Figure 25 (cont'd)

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement

>LCMV-p52-2.1_NP

```
ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG
CAGAGTTTTACATCAGATGTAAAGGCTGCCGTATCAAGGACGCAACCAGTCTTCTAAAT
GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGAT
GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG
AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG
ACCCTTGCAGCTGATCTTGAGAAGCTGAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA
GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACTTGATCAAAGATCCCAAATA
CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTCGTCTAGTAAGCGTTTGG
GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGCACAAATGCCAAGCCTGACAATG
GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACTCACAGAC
CTTGGCTTACTTTACACAGTCAAATACCCGAATCTCAGTGATCTTCAAAGGCTAAAGGAT
AAACACCCAGTTCTGGGGGTCATTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT
AATTTAGTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG
CTGGAATCTATCTTGATCAAACCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG
GCCAAAAAGAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA
AACATCCTTTATAAAGTCTGTCTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG
TCAGTTGTGGGAGAGCATGGGAGAACACAACAATTGATCTCACAAATGAAAACTTGTT
GCCAATCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC
AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCACATGG
ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAAT
GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA
AAGTATTCACACGGCATGGATCTTGCTGATCTCTCAATGCACAGCCTGGGCTGACCTCA
TCAGTTATAGGTGCTCTCCACAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC
AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAACTCATTGATGTTGACATGACC
AAGGAGGCCCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA
ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCACTC
ATGGACTGCATCTTTTGAAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT
CACAAATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA
(SEQ ID NO: 59)
```

CDS: 1640-3316 complement
Codon Start = 1; Codons 1-558

Translation=

>LCMV-p52-2.1_NP

```
MSLSKEVKSFQWTQALRRELQSFTSDVKA AVIKDATSLNLGLDFSEVSNVQIRIMRKERRD
DKDLQRLRLSNQTVHSLVDLKSTS KKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ
ASGVYMGNLTAQQLDQRSQILQVMGMRRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM
ACMAKQSQTPLNDVVQALTDLGLLYTVKYPNLSDLERLKD KHPVLGVITEQQSSINISGY
NFSLGA AVKAGAAALLDGGNMLESILIKPSNSEDLLKAVLGAKKKLNMFVSDQVGDRNPYE
NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDL TNEKLVANSRPPVPGAAGPPQVGLSY
SQTMLLKDLMGIDPNAPT WIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS
KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLS CQGSDDIRKLLDSQNRDRIKLIDVEMT
KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV
HNILPHDLIFRGPNNVTL
(SEQ ID NO: 60)
```

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362

>LCMV-p52-2.1_ZP
ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT
TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC
AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA
GTTTCCGACAGATGTCTCTCTGTAAGTATCCACTGCCAACCAAACTGAAGGTGTCAACA
GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA
(SEQ ID NO: 61)

CDS: 90-362
Codon Start = 1; Codons 1-91
Translation=

>LCMV-p52-2.1_ZP
MGQGKSKEERDTISNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS
VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE
(SEQ ID NO: 62)

Figure 25 (cont'd)

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement

>LCMV-p52-2.1_LP

ATGGATGAACTATTGCAGATTTGAGAGAGTTGTGTCTAAATTACATAGAACAGGACGAA
AGGCTGTCAAGGCAAACTCAACTTCTGGGACAAAGAGAACCAGAATGGTGCTAATT
GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC
ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT
CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTATTCTT
CTTGAATGTTTGTAGAAAGCACACCAGCTAGTTTTGAAAAGAAGTTCATTGAGGACACC
AACAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA
GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATCGGTGAATTTTAAGTTC
AGAGACCTCCTATTTAAACTCCTGGAGTATTCTAGTCAAGATGAGAAAAGTTTTTGAGGAG
TCTGAATACCTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAAAGTTCGGGCATG
GACTCAATGAAAATTTTGAAAGACGCAAGATCATTTCAACGATGAGATTATGAAAATG
TGCCACGATGGTGTCAACCCCAACATGAGTTGCGATGATGTGGTCTTTGGCATAAATTCC
TTTTTTGGCAGGTTTAGGAGGGACCTGTTAAATGGGAACTCAAAGGAATTTCCAAAAG
GTCAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCTTACTGATAAT
GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT
ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA
CTCTCTATGTTGAACAAGGTGAAAAGTTTAAATATTAAACACTAGAAGGAGACAGCTG
CTGAACCTTAGATGTCTTATGTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG
GAAAATGATAAACATTTGGGTTGGTTGTTGCTACAGTAGTGTGAATCATAGGCTTGTGAGC
CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAAGAACAGAAGAAAATCAAGAGTG
CACAAAAGGCATCTCTTGATGAGCTTTTATAGGTTATCCATAAATGAGTTCATAGCAAAA
ATCCAGAAATGCCTATCAACAGTGGGACTTAGTTTTGAGCATTACGGACTATCAGAAATGC
CTCGTGCAAGAATGCCATATACCATTGCTGAATTTGAGAATTTATGAGAGCCGGGACT
CATCCTGTATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA
TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGTGTTGGCTCTAACAAACAGC
ATGAAAACAAGCTCAGTTGCAAGGTTGAGACAGAACCAACTGGGGTCTGTGAGATATCAA
GTGGTGGAGTGCAAGAGAGGTGTTTTGCCAGATAATAAAACTGGATTCCGAAGAGTATCAT
CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATTCATACAAAGTCCGGATGGT
CACTTGATTTCCCTTTTACGCAGATCCAAAAGGTTCTTTTACCATTATTTTTCAGATGAG
GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTTCATGCCCTGACTTAAAA
GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAAC
CCAACAAGAGGAAATCAAAGCAGGTTCAAAATATTAGGTATTTAGTGATGGCCATCGCT
TCAGACTTTTCATCGACCTCATTAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC
GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTGTATTAGGACAATTTTGGTACTGGTGAA
AAGGTGTTATTGAGTGCAAAAATTTAAGTTTATGTTGAATGTGTCTACCTGTGTCAATTTG
ATCACAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTCTTTT
GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG
GAATGTGTTTTTTATGAACAAATGAAGAAGTTCACCGGTAAAGATATTGATTGTGAGCAT
TCAACCCCTGGTGTAAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC
ACCTTAATTTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCATGACCAACTCTGGA
TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT
GGAGAACGGCTTTTGGAGTATGATTTTAAACAAATGCTTGTAGTCTGTGAGCCAAAT
ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG
GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAAATG
GAAGATGATCCGGTAGATCTGTGTTTTCCAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT
TTAGAAGATAAGGTCAGTCCACAATAACACGGTATAATAGAGGCACTAGGCTTAATGAA
GGGCAAGGGGAGGGGAGAAATCAAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG
TCAGGTAAGAGAGCTTATCTGAGGAAAGTCAATTTATCAGAAATTTCAATTCATCTAGTA
GAGGACTTTGATCCATCTGTCTCACCATTGACGACATGAGGTTTATTTGTGAGGCTGTT
GAAGGTTCAACAGAAGTGTCAACATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT
CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA
TGATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC

Figure 25 (cont'd)

ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA
ATTAGTGAAAGGGAAAGCAATCTGAATCTCTAAGTAAGGCCCTTTCATTGACAAAATGC
ATGAGTGCTGCTCTAAAGAATCTGTGTTTTTACTCAGAAGAATCACCACATCATACACT
TCAGTTGGCCCTGACTCTGGGAGACTAAAATTTGCATTGTCATACAAAGAGCAGGTTGGG
GGAAATAGAGAGCTTTACATTGGGGATTTGAGGACAAAAATGTTCAAGATTGGTAGAA
GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG
TTTGAAATGCAATCTTGTCATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC
ATGGATCACAGCAAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA
AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG
TTGACTTGGCATATGCATAAACTTGTTGAAGTCCCTTTCCCTGTTGTGAATGCAATGATG
AAATCATATGTTAAATCAAACTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG
AGAATCTTTAGAGAGTATTTTGAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT
GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAAGG
TTTATCAATTATTGTATTGCTGTCATTTTTGGAGAGAGGCCAGAAGCCTATACATCAAGT
GATGATCAGATCACTTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA
GAAGTCCTTGCTTGTGCTGGAATCCACTCTCACTTAAAGTGGTTTGTGAACAAGTTCATC
AGTCCAAAAGTGTTGGTTGGGCGGTTTGCAGCGGAATCAAATCCAGATTTTATGTGTGG
GGGGAGGAGGTCCCTCTCCTCACGAAATTTGTGTCTGCGGCACACACAATGTTAAGTGT
AAAGAACC GCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT
GGAGTTCCAGTTTTTTTTAGTAACTGTATCCAGAGGAGGACACGATCTCTTGAATATAT
GCTAATTTCCCTTTAGATCCATTCCTTGTAAACACTCACACTGATGTAAAGGATTGGTTA
GATGGTTCTAGAGGTTATAGAATCCAAAGACTCATTGAAGAATTGTGTCCCAGTGAAACA
AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAACTCAAGAACGGTGAATGTAAC
GAGGAATTTTTTCTAGACCTCTTCAACAGGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA
GAGATTCCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTTGGTTCAATCTG
AATGAAATGTTCCCATTTGAGGATGGTTCTGAGACAAAAAGTGGTTTACCCATCAGTAATG
ACCTTTCAAGAGGAAAAGATCCCTCATTTGATTAAACACTCCAAAATAAGCTTTGTAGT
AAGTTCACAAGAGGTGCACAGAAGCTGTTGTGAGAGGCAATCAACAAATCAGCTTTTCAG
AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA
AATAAAACAGGGGAAAATATGTATATCAGAAAGGTCTTGAAGATCTGACCATCGCATGAA
CATGTCAAAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTCCGACAAAGCAGAGA
CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT
TGCATCTCATTTGAGCAACTCTTTTGAGCTGGGTGTTGGGTTTTAGCAGAACCCTGTGAAA
GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACTTAAATCCATGTCATTATGTAGCAAGA
AAACCTGAGAGTTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATCAATCT
GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGTCGATGTG
AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT
GACATCAACTCAGAGTCTTGTCACTCATTCTCATGTTGTGCAATGGAAGAGGGACGAA
CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCAACGGTCAGACTCAAGTTTA
GTTGATGAATTTGTTGTGTCAGCACAAAGGATGTCTGCAAGAATTTTTGAAGCAAGTGAT
TTCGAATCATTTGTACGAGAGTTTGTGCAACAGCTAGGACCTTAGGTAACTTTTCATGG
TTCCCCCATAAGGACATGATGCCATCTGAAGATGGCGCTGAAGCACTGGGACCCCTCCAA
TCATTTATTTTGAAGTGGTGAACAAGAAAATAGAGAGGCCCATGTTTAGGAATGACTTG
CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGATGTTGTGTGTAATGCCGCTATG
TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTTAAATCTTTAAGAGATTCTGTTGGAT
TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACACTGGATTTACACAC
AACCAGAACAACACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA
TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTCTTCAAAGGTGAGGTT
GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG
AATGATGGAGTCTTTGACATTAGGTCTGAAGAGTTTGAAGATTACATGGAAGACCCCTTG
ACACTTGGTGATTCACTAGAACTTGAACATAAGGTTCTAGAAGGATTCTGAATGAGATC
AAATCTACTGACTTTGAGAGGATAGGGCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG
AAGGGTGCCCTCTTTGAGGGGAGGAACTTTGTTCAAGATATCTCTGTGAAATGGAGACA
AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGGAGAAATGGTGATGTCTC
GGCAGCCTCCTCTGCACCGATTGAGAACTGGTGAGCACTTGATGAGTCAAGAAATAAGT
ACAGTTCTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTGTG
CCAGATTGGTTACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA
ATGTATGAGACAACCTGGGGCAGGTTGAGACTCAAGGGGAAATCCTGTGACGATTGGCTG

Figure 25 (cont'd)

CGCGAGCGGGTGGCCGAGGAGATCGACTAG
(SEQ ID NO: 63)

CDS: 574-7203 complement
Codon Start = 1; Codons 1-2210
Translation=

>LCMV-p52-2.1_LP
MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLEI GLKLLSRCIEIDSADKSGC
IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT
NKLACIKEDLAVAGITLVPDIVDGRCDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE
SEYFRLCESLKTIVDKRSGMDSMKILKDARSFHNDIMKMHDCVNPNMSCDDVVFINS
FFGRFRDLLNGKLKRNFKQVSPGGLIKEFSELYETLTDNDDILMLSKEAVESCPLMRFI
TAETHGHERGSDANTEYERLLSMLNKVKSILKLLNTRRRQLLNLDVLCSSLIKQSISKGL
ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLKNNRKRVRHKKASLDELFRVSINEFIK
IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRAGTHPVMHYTKFEDYTFQPNIEQ
LRGLQSLRLKSSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH
LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPISDEVLHNMIDTMISWIRSCPDLK
DSLIDIETALRTLILLMLTNPTKRNQKQVQNIIRYLVMIAIVSDFSSTSLMDKCLKEDLITPA
EKVVYRLLRFLIRTIFGTGEKVLLSAKFKFMNLVSYLCHLITKETPDRLTDQIKCFEKKF
EPKSEFGFFVNPKETITPEEECVFYEQMKKFTGKDIDCQHSTPCVNLEIFSMMVSSFNNG
TLILKGEKRLNNLDPMNTNSGCATALDLASNKSVVVNKHLNGERLLEYDFNKLIVSAVSQI
TEGFMRKQKYKLRHSDYKYVSKLVSRVIGSRKTEVDKLEDDPVDVCFEGEEETSFERS
LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV
EDFDPSCLTNDDMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFSEGDWFS
CMKMILLQMNANAYS GK YRHMQRQSLNFKFDWDKLEEDVRISERESNSESLKALS LTKC
MSAALKNLCFYSEESPTSYTSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE
DYFESFSSFFSGSCLNNDKEFENAILSMTINVREGLNYSMDHSHKWCPPMCPFLFLMLLQ
NLKLGDDQYVRSGKDHVSTLLTWHMHKLVEVFPVNVAMMKS YVKS LKLLKGS GTTVTE
RIFREYFEMGVVPSHISSLIDMGQILHNASDFYGLISERFINYCIGVIFGERPEAYTSS
DDQITLFDKRLSDLVDSDPPEVLVLLFEHSHLSGLLNKFISPKSVVGRFAAEFKSRFYVW
GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIADQAIANGVPVFLVNCIQRRTLDLLKY
ANFPLDPFLNTHTDVKDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHHKLKNGECN
EEFFDLDFNREKKEAILQLGEILGLEDDLNELASINWLNLMFMFLRMVLRQKVVPVSM
TFQEEKIPSLIKTLQNKLC SKFTRGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRV
NKNRENMYIRKVLDTLMDHEVTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLWDYI
CISLSNSFELGVWVLAEPVKGNESNSAVRHLNPCDYVARKPESSRLLEDKVS LNHVIQS
VRRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDL CVLIDINSESLISHVVKWRDE
HYTVLFSDLVNSHQSDSSSLVDEFVVS TRDVCKNFLKQVYFESFVREFVATARTLG NFSW
FPHKDMMPSEDGAEALGPFSFILKVVNKKIERPMFRNDLQFGCWF SYRVGDVVCNAAM
LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNNTDCLRKFS LIFVVKCQ
LQSPGVADYLSCHSHFFKGEVDRRLLECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL
TLGDSLELELIGSRRI LNEIKSTDFERICPEWEPVPLTIRKCALFEGRN FVNISVKLET
KDMRVFLAELEGCEIGDVLGSLLLHRTGEHLMSEISTVLQELCMDRSVMLTPLSFV
PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID
(SEQ ID NO: 64)

Figure 26

A.

Source: 1-3376 Segment = S

Protein: Pre-glycoprotein polyprotein GP complex

Gene: GPC

Gene: 79-1575

Sequence Alignment: Nucleotide

LCMV-WE_GP	ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC	60
LCMV-P42_GP	ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC	60
LCMV-P52_GP	ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC	60
LCMV-P91_GP	ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC	60
LCMV-P52-1	ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC	60
LCMV-P52-1.3_GP	ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC	60
LCMV-P52-2.1_GP	ATGGGTCAGATTGTGACAATGTTTGAGGCTTTGCCTCACATCATTGATGAGGTCATCAAC	60

LCMV-WE_GP	ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTCGCCACC	120
LCMV-P42_GP	ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTCGCCACC	120
LCMV-P52_GP	ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTCGCCACC	120
LCMV-P91_GP	ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTCGCCACC	120
LCMV-P52-1	ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTCGCCACC	120
LCMV-P52-1.3_GP	ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTCGCCACC	120
LCMV-P52-2.1_GP	ATTGTCATTATTGTGCTCATTATAATCACGAGCATCAAAGCTGTGTACAATTCGCCACC	120

LCMV-WE_GP	TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC	180
LCMV-P42_GP	TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC	180
LCMV-P52_GP	TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC	180
LCMV-P91_GP	TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC	180
LCMV-P52-1	TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC	180
LCMV-P52-1.3_GP	TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC	180
LCMV-P52-2.1_GP	TGTGGGATATTAGCACTGGTCAGCTTCCTTTTTTTGGCTGGTAGGTCCTGTGGCATGTAC	180

LCMV-WE_GP	GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT	240
LCMV-P42_GP	GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT	240
LCMV-P52_GP	GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT	240
LCMV-P91_GP	GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT	240
LCMV-P52-1	GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT	240
LCMV-P52-1.3_GP	GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT	240
LCMV-P52-2.1_GP	GGCCTTAATGGTCCCGACATCTATAAAGGGGTTTACCAGTTCAAATCAGTGGAGTTTGAT	240

LCMV-WE_GP	ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC	300
LCMV-P42_GP	ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC	300
LCMV-P52_GP	ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC	300
LCMV-P91_GP	ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC	300
LCMV-P52-1	ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC	300
LCMV-P52-1.3_GP	ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC	300
LCMV-P52-2.1_GP	ATGTCTCACTTAAATCTGACGATGCCCAATGCGTGCTCAGCCAACAACCTCTCATCACTAC	300

LCMV-WE_GP	ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC	360
LCMV-P42_GP	ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC	360
LCMV-P52_GP	ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC	360
LCMV-P91_GP	ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC	360
LCMV-P52-1	ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC	360
LCMV-P52-1.3_GP	ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC	360
LCMV-P52-2.1_GP	ATCAGTATGGGAAGCTCTGGACTGGAGCTAACTTTCACTAACGACTCCATCCTTAATCAC	360

LCMV-WE_GP	AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT	420
LCMV-P42_GP	AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT	420
LCMV-P52_GP	AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT	420
LCMV-P91_GP	AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT	420
LCMV-P52-1	AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT	420
LCMV-P52-1.3_GP	AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT	420
LCMV-P52-2.1_GP	AATTTTTGCAACTTAACCTCCGCTTTCAACAAAAAGACTTTTGACCATACACTCATGAGT	420

Figure 26 (cont'd)

LCMV-WE_GP	ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT	480
LCMV-P42_GP	ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT	480
LCMV-P52_GP	ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT	480
LCMV-P91_GP	ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT	480
LCMV-P52-1	ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT	480
LCMV-P52-1.3_GP	ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT	480
LCMV-P52-2.1_GP	ATAGTCTCGAGTCTGCACCTCAGTATTAGAGGGAATCCAACCACAAAGCAGTGTCTTGT	480

LCMV-WE_GP	GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGGT	540
LCMV-P42_GP	GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGGT	540
LCMV-P52_GP	GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGGT	540
LCMV-P91_GP	GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGGT	540
LCMV-P52-1	GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGGT	540
LCMV-P52-1.3_GP	GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGGT	540
LCMV-P52-2.1_GP	GATTTTAACAATGGCATCACCATTCAATACAACCTTGTCAATTTTCGGACCCACAGAGCGGT	540

LCMV-WE_GP	ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA	600
LCMV-P42_GP	ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA	600
LCMV-P52_GP	ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA	600
LCMV-P91_GP	ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA	600
LCMV-P52-1	ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA	600
LCMV-P52-1.3_GP	ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA	600
LCMV-P52-2.1_GP	ATAAGCCAGTGTAGGACTTTCAGAGGTAGAGTCTTGGACATGTTTAGAACTGCCTTTGGA	600
** *****		
LCMV-WE_GP	GGAAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCCAGATGGCAAGACCACCTTGGTGC	660
LCMV-P42_GP	GGAAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCCAGATGGCAAGACCACCTTGGTGC	660
LCMV-P52_GP	GGAAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCCAGATGGCAAGACCACCTTGGTGC	660
LCMV-P91_GP	GGAAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCCAGATGGCAAGACCACCTTGGTGC	660
LCMV-P52-1	GGAAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCCAGATGGCAAGACCACCTTGGTGC	660
LCMV-P52-1.3_GP	GGAAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCCAGATGGCAAGACCACCTTGGTGC	660
LCMV-P52-2.1_GP	GGAAAAATACATGAGAAGTGGCTGGGGCTGGGCAGGTTTCCAGATGGCAAGACCACCTTGGTGC	660

LCMV-WE_GP	AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA	720
LCMV-P42_GP	AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA	720
LCMV-P52_GP	AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA	720
LCMV-P91_GP	AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA	720
LCMV-P52-1	AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA	720
LCMV-P52-1.3_GP	AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA	720
LCMV-P52-2.1_GP	AGCCAAACAAGCTATCAGTACCTAATCATACAAAACAGGACTTGGGAAAACCACTGTAGA	720

LCMV-WE_GP	TATGCAGGCCCTTTTGGGATGCTCAGAAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC	780
LCMV-P42_GP	TATGCAGGCCCTTTTGGGATGCTCAGAAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC	780
LCMV-P52_GP	TATGCAGGCCCTTTTGGGATGCTCAGAAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC	780
LCMV-P91_GP	TATGCAGGCCCTTTTGGGATGCTCAGAAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC	780
LCMV-P52-1	TATGCAGGCCCTTTTGGGATGCTCAGAAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC	780
LCMV-P52-1.3_GP	TATGCAGGCCCTTTTGGGATGCTCAGAAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC	780
LCMV-P52-2.1_GP	TATGCAGGCCCTTTTGGGATGCTCAGAAATCCTCTTTGCTCAGGAAAAGACAAAGTTTCTC	780

LCMV-WE_GP	ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAAT	840
LCMV-P42_GP	ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAAT	840
LCMV-P52_GP	ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAAT	840
LCMV-P91_GP	ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAAT	840
LCMV-P52-1	ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAAT	840
LCMV-P52-1.3_GP	ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAAT	840
LCMV-P52-2.1_GP	ACTAGGAGACTTGCAGGCACATTACCTGGACCCTGTCAGACTCCTCAGGAGTAGAAAAAT	840

LCMV-WE_GP	CCAGGTGGTTATTGCCTGACCAAAATGGATGATCCTTGCTGCAGAGCTCAAAATGTTTTGGG	900
LCMV-P42_GP	CCAGGTGGTTATTGCCTGACCAAAATGGATGATCCTTGCTGCAGAGCTCAAAATGTTTTGGG	900
LCMV-P52_GP	CCAGGTGGTTATTGCCTGACCAAAATGGATGATCCTTGCTGCAGAGCTCAAAATGTTTTGGG	900
LCMV-P91_GP	CCAGGTGGTTATTGCCTGACCAAAATGGATGATCCTTGCTGCAGAGCTCAAAATGTTTTGGG	900
LCMV-P52-1	CCAGGTGGTTATTGCCTGACCAAAATGGATGATCCTTGCTGCAGAGCTCAAAATGTTTTGGG	900
LCMV-P52-1.3_GP	CCAGGTGGTTATTGCCTGACCAAAATGGATGATCCTTGCTGCAGAGCTCAAAATGTTTTGGG	900
LCMV-P52-2.1_GP	CCAGGTGGTTATTGCCTGACCAAAATGGATGATCCTTGCTGCAGAGCTCAAAATGTTTTGGG	900

Figure 26 (cont'd)

LCMV-WE_GP	AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA	960
LCMV-P42_GP	AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA	960
LCMV-P52_GP	AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA	960
LCMV-P91_GP	AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA	960
LCMV-P52-1	AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA	960
LCMV-P52-1.3_GP	AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA	960
LCMV-P52-2.1_GP	AATACAGCTGTTGCAAAATGTAATGTCAATCATGATGAAGAGTTCTGTGACATGCTACGA	960

LCMV-WE_GP	CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG	1020
LCMV-P42_GP	CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG	1020
LCMV-P52_GP	CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG	1020
LCMV-P91_GP	CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG	1020
LCMV-P52-1	CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG	1020
LCMV-P52-1.3_GP	CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG	1020
LCMV-P52-2.1_GP	CTAATTGATTACAACAAGGCCGCCCTGAGTAAGTTCAAGCAAGATGTAGAGTCTGCCTTG	1020

LCMV-WE_GP	CATGTATTCAAAACAACAGTAAATTTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT	1080
LCMV-P42_GP	CATGTATTCAAAACAACAGTAAATTTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT	1080
LCMV-P52_GP	CATGTATTCAAAACAACAGTAAATTTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT	1080
LCMV-P91_GP	CATGTATTCAAAACAACAGTAAATTTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT	1080
LCMV-P52-1	CATGTATTCAAAACAACAGTAAATTTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT	1080
LCMV-P52-1.3_GP	CATGTATTCAAAACAACAGTAAATTTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT	1080
LCMV-P52-2.1_GP	CATGTATTCAAAACAACAGTAAATTTCTCTGATTTCCGATCAGCTGTTGATGAGGAATCAT	1080

LCMV-WE_GP	CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT	1140
LCMV-P42_GP	CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT	1140
LCMV-P52_GP	CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT	1140
LCMV-P91_GP	CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT	1140
LCMV-P52-1	CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT	1140
LCMV-P52-1.3_GP	CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT	1140
LCMV-P52-2.1_GP	CTAAGAGATCTAATGGGGGTACCATACTGTAATTACTCAAAGTTCTGGTATCTGGAACAT	1140

LCMV-WE_GP	GCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTTGTGCTACTAATGGCTCCTACTTG	1200
LCMV-P42_GP	GCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTTGTGCTACTAATGGCTCCTACTTG	1200
LCMV-P52_GP	GCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTTGTGCTACTAATGGCTCCTACTTG	1200
LCMV-P91_GP	GCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTTGTGCTACTAATGGCTCCTACTTG	1200
LCMV-P52-1	GCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTTGTGCTACTAATGGCTCCTACTTG	1200
LCMV-P52-1.3_GP	GCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTTGTGCTACTAATGGCTCCTACTTG	1200
LCMV-P52-2.1_GP	GCTAAGACTGGTGAGACTAGTGTACCCAAGTGGCTTGTGCTACTAATGGCTCCTACTTG	1200

LCMV-WE_GP	AATGAGACCCACTTTAGTGATCAAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG	1260
LCMV-P42_GP	AATGAGACCCACTTTAGTGATCAAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG	1260
LCMV-P52_GP	AATGAGACCCACTTTAGTGATCAAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG	1260
LCMV-P91_GP	AATGAGACCCACTTTAGTGATCAAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG	1260
LCMV-P52-1	AATGAGACCCACTTTAGTGATCAAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG	1260
LCMV-P52-1.3_GP	AATGAGACCCACTTTAGTGATCAAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG	1260
LCMV-P52-2.1_GP	AATGAGACCCACTTTAGTGATCAAAATCGAACAAGAAGCAGATAACATGATCACAGAGATG	1260

LCMV-WE_GP	TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG	1320
LCMV-P42_GP	TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG	1320
LCMV-P52_GP	TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG	1320
LCMV-P91_GP	TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG	1320
LCMV-P52-1	TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG	1320
LCMV-P52-1.3_GP	TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG	1320
LCMV-P52-2.1_GP	TTGAGGAAGGACTACATAAAAAGACAAGGGAGTACTCCTTTAGCCTTAATGGATCTTTTG	1320

LCMV-WE_GP	ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA	1380
LCMV-P42_GP	ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA	1380
LCMV-P52_GP	ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA	1380
LCMV-P91_GP	ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA	1380
LCMV-P52-1	ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA	1380
LCMV-P52-1.3_GP	ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA	1380
LCMV-P52-2.1_GP	ATGTTTTCAACATCAGCATATCTAATCAGCATCTTTCTGCATCTTGTGAAGATACCAACA	1380

Figure 26 (cont'd)

LCMV-WE_GP	CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC	1440
LCMV-P42_GP	CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC	1440
LCMV-P52_GP	CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC	1440
LCMV-P91_GP	CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC	1440
LCMV-P52-1	CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC	1440
LCMV-P52-1.3_GP	CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC	1440
LCMV-P52-2.1_GP	CATAGACACATAAAGGGCGGTTTCATGTCCAAAGCCACACCGCTTGACCAACAAGGGGATC	1440

LCMV-WE_GP	TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAAAGACGCTGA	1497
LCMV-P42_GP	TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAAAGACGCTGA	1497
LCMV-P52_GP	TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAAAGACGCTGA	1497
LCMV-P91_GP	TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAAAGACGCTGA	1497
LCMV-P52-1	TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAAAGACGCTGA	1497
LCMV-P52-1.3_GP	TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAAAGACGCTGA	1497
LCMV-P52-2.1_GP	TGTAGTTGTGGTGCATTCAAGGTGCCTGGTGTAAAACTATCTGGAAAAGACGCTGA	1497

LCMV-WE_GP:	SEQ ID NO: 9
LCMV-P42_GP:	SEQ ID NO: 17
LCMV-P52_GP:	SEQ ID NO: 25
LCMV-P91_GP:	SEQ ID NO: 33
LCMV-P52-1:	SEQ ID NO: 41
LCMV-P52-1.3_GP:	SEQ ID NO: 49
LCMV-P52-2.1_GP:	SEQ ID NO: 57

Figure 26 (cont'd)

B.

Source: 1-3376 Segment = S

Protein: Pre-glycoprotein polypeptide GP complex

Gene: GPC

Gene: 79-1575

Sequence Alignment: Aminoacid

LCMV-WE_GP	MGQIVTMFEALPHIIDVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGM	60
LCMV-P42_GP	MGQIVTMFEALPHIIDVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGM	60
LCMV-P52_GP	MGQIVTMFEALPHIIDVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGM	60
LCMV-P91_GP	MGQIVTMFEALPHIIDVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGM	60
LCMV-P52-1	MGQIVTMFEALPHIIDVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGM	60
LCMV-P52-1.3_GP	MGQIVTMFEALPHIIDVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGM	60
LCMV-P52-2.1_GP	MGQIVTMFEALPHIIDVINIVIIIVLIIITSIKAVYNFATCGILALVSFLFLAGRSCGM	60

LCMV-WE_GP	GLNGPDIYKGVYQFKSVEFDMSHLNLTPNACSAANSHHYISMGSSGLELFTFNDLSILNH	120
LCMV-P42_GP	GLNGPDIYKGVYQFKSVEFDMSHLNLTPNACSAANSHHYISMGSSGLELFTFNDLSILNH	120
LCMV-P52_GP	GLNGPDIYKGVYQFKSVEFDMSHLNLTPNACSAANSHHYISMGSSGLELFTFNDLSILNH	120
LCMV-P91_GP	GLNGPDIYKGVYQFKSVEFDMSHLNLTPNACSAANSHHYISMGSSGLELFTFNDLSILNH	120
LCMV-P52-1	GLNGPDIYKGVYQFKSVEFDMSHLNLTPNACSAANSHHYISMGSSGLELFTFNDLSILNH	120
LCMV-P52-1.3_GP	GLNGPDIYKGVYQFKSVEFDMSHLNLTPNACSAANSHHYISMGSSGLELFTFNDLSILNH	120
LCMV-P52-2.1_GP	GLNGPDIYKGVYQFKSVEFDMSHLNLTPNACSAANSHHYISMGSSGLELFTFNDLSILNH	120

LCMV-WE_GP	NFCNLTSAPFNKKTDFHTLMSIVSSLHLHSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA	180
LCMV-P42_GP	NFCNLTSAPFNKKTDFHTLMSIVSSLHLHSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA	180
LCMV-P52_GP	NFCNLTSAPFNKKTDFHTLMSIVSSLHLHSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA	180
LCMV-P91_GP	NFCNLTSAPFNKKTDFHTLMSIVSSLHLHSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA	180
LCMV-P52-1	NFCNLTSAPFNKKTDFHTLMSIVSSLHLHSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA	180
LCMV-P52-1.3_GP	NFCNLTSAPFNKKTDFHTLMSIVSSLHLHSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA	180
LCMV-P52-2.1_GP	NFCNLTSAPFNKKTDFHTLMSIVSSLHLHSIRGNSNHKAVSCDFNNGITIQYNLSFSDPQSA	180

LCMV-WE_GP	ISQCRTPFRGRVLDMFRTAFGCKYMRSGWAGSDGKTTWCSQTSYQYLIQNRWENHCR	240
LCMV-P42_GP	MSQCRTPFRGRVLDMFRTAFGCKYMRSGWAGSDGKTTWCSQTSYQYLIQNRWENHCR	240
LCMV-P52_GP	MSQCRTPFRGRVLDMFRTAFGCKYMRSGWAGSDGKTTWCSQTSYQYLIQNRWENHCR	240
LCMV-P91_GP	MSQCRTPFRGRVLDMFRTAFGCKYMRSGWAGSDGKTTWCSQTSYQYLIQNRWENHCR	240
LCMV-P52-1	MSQCRTPFRGRVLDMFRTAFGCKYMRSGWAGSDGKTTWCSQTSYQYLIQNRWENHCR	240
LCMV-P52-1.3_GP	ISQCRTPFRGRVLDMFRTAFGCKYMRSGWAGSDGKTTWCSQTSYQYLIQNRWENHCR	240
LCMV-P52-2.1_GP	MSQCRTPFRGRVLDMFRTAFGCKYMRSGWAGSDGKTTWCSQTSYQYLIQNRWENHCR	240
*** *****		
LCMV-WE_GP	YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSGSGVENPGGYCLTKWMILAAELKCFG	300
LCMV-P42_GP	YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSGSGVENPGGYCLTKWMILAAELKCFG	300
LCMV-P52_GP	YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSGSGVENPGGYCLTKWMILAAELKCFG	300
LCMV-P91_GP	YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSGSGVENPGGYCLTKWMILAAELKCFG	300
LCMV-P52-1	YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSGSGVENPGGYCLTKWMILAAELKCFG	300
LCMV-P52-1.3_GP	YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSGSGVENPGGYCLTKWMILAAELKCFG	300
LCMV-P52-2.1_GP	YAGPFGMSRILFAQEKTKFLTRRLAGTFTWTLSDSGSGVENPGGYCLTKWMILAAELKCFG	300

LCMV-WE_GP	NTAVAKCNVNHEEFCDMLRLIDYNKAALSXFKQDVEGALHVFKTTVNSLISDQLLMRNH	360
LCMV-P42_GP	NTAVAKCNVNHEEFCDMLRLIDYNKAALSXFKQDVEGALHVFKTTVNSLISDQLLMRNH	360
LCMV-P52_GP	NTAVAKCNVNHEEFCDMLRLIDYNKAALSXFKQDVEGALHVFKTTVNSLISDQLLMRNH	360
LCMV-P91_GP	NTAVAKCNVNHEEFCDMLRLIDYNKAALSXFKQDVEGALHVFKTTVNSLISDQLLMRNH	360
LCMV-P52-1	NTAVAKCNVNHEEFCDMLRLIDYNKAALSXFKQDVEGALHVFKTTVNSLISDQLLMRNH	360
LCMV-P52-1.3_GP	NTAVAKCNVNHEEFCDMLRLIDYNKAALSXFKQDVEGALHVFKTTVNSLISDQLLMRNH	360
LCMV-P52-2.1_GP	NTAVAKCNVNHEEFCDMLRLIDYNKAALSXFKQDVEGALHVFKTTVNSLISDQLLMRNH	360

LCMV-WE_GP	LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQADNMITEM	420
LCMV-P42_GP	LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQADNMITEM	420
LCMV-P52_GP	LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQADNMITEM	420
LCMV-P91_GP	LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQADNMITEM	420
LCMV-P52-1	LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQADNMITEM	420
LCMV-P52-1.3_GP	LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQADNMITEM	420
LCMV-P52-2.1_GP	LRDLMGVPCYNYSKFWYLEHAKTGETSVPKCWLVTNGSYLNETHFSDQIEQADNMITEM	420

Figure 26 (cont'd)

LCMV-WE_GP	LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHKGGSCPKPHRLTNKGI	480
LCMV-P42_GP	LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHKGGSCPKPHRLTNKGI	480
LCMV-P52_GP	LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHKGGSCPKPHRLTNKGI	480
LCMV-P91_GP	LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHKGGSCPKPHRLTNKGI	480
LCMV-P52-1	LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHKGGSCPKPHRLTNKGI	480
LCMV-P52-1.3_GP	LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHKGGSCPKPHRLTNKGI	480
LCMV-P52-2.1_GP	LRKDYIKRQGSTPLALMDLLMFSTSAYLISIFLHLVKIPTHRHKGGSCPKPHRLTNKGI	480

LCMV-WE_GP	CSCGAFKVPGVKTIWKRR	498
LCMV-P42_GP	CSCGAFKVPGVKTIWKRR	498
LCMV-P52_GP	CSCGAFKVPGVKTIWKRR	498
LCMV-P91_GP	CSCGAFKVPGVKTIWKRR	498
LCMV-P52-1	CSCGAFKVPGVKTIWKRR	498
LCMV-P52-1.3_GP	CSCGAFKVPGVKTIWKRR	498
LCMV-P52-2.1_GP	CSCGAFKVPGVKTIWKRR	498

LCMV-WE_GP:	SEQ ID NO: 10
LCMV-P42_GP:	SEQ ID NO: 18
LCMV-P52_GP:	SEQ ID NO: 26
LCMV-P91_GP:	SEQ ID NO: 34
LCMV-P52-1:	SEQ ID NO: 42
LCMV-P52-1.3_GP:	SEQ ID NO: 50
LCMV-P52-2.1_GP:	SEQ ID NO: 58

Figure 26 (cont'd)

C.

Source: 1-3376 Segment = S
Protein: Nucleoprotein
Gene: NP
Gene: 1640-3316 complement
Sequence Alignment: Nucleotide

LCMV-WE_NP	ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG	60
LCMV-P42_NP	ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG	60
LCMV-P52_NP	ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG	60
LCMV-P91_NP	ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG	60
LCMV-P52-1_NP	ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG	60
LCMV-P52-1.3_NP	ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG	60
LCMV-P52-2.1_NP	ATGTCTTTGTCCAAAGAAGTCAAAAGCTTTTCAGTGGACACAGGCGTTGAGGAGGGAGTTG	60

LCMV-WE_NP	CAGAGTTTTACATCAGATGTAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT	120
LCMV-P42_NP	CAGAGTTTTACATCAGATGTAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT	120
LCMV-P52_NP	CAGAGTTTTACATCAGATGTAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT	120
LCMV-P91_NP	CAGAGTTTTACATCAGATGTAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT	120
LCMV-P52-1_NP	CAGAGTTTTACATCAGATGTAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT	120
LCMV-P52-1.3_NP	CAGAGTTTTACATCAGATGTAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT	120
LCMV-P52-2.1_NP	CAGAGTTTTACATCAGATGTAAGGCTGCCGTCATCAAGGACGCAACCAGTCTTCTAAAT	120

LCMV-WE_NP	GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT	180
LCMV-P42_NP	GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT	180
LCMV-P52_NP	GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT	180
LCMV-P91_NP	GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT	180
LCMV-P52-1_NP	GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT	180
LCMV-P52-1.3_NP	GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT	180
LCMV-P52-2.1_NP	GGGTTGGACTTTTCTGAAGTCAGCAACGTTTCAGAGGATCATGAGAAAGGAAAGGAGGGAT	180

LCMV-WE_NP	GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG	240
LCMV-P42_NP	GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG	240
LCMV-P52_NP	GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG	240
LCMV-P91_NP	GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG	240
LCMV-P52-1_NP	GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG	240
LCMV-P52-1.3_NP	GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG	240
LCMV-P52-2.1_NP	GATAAAGACTTGCAGAGACTCAGGAGTCTTAACCAGACTGTGCATTCTCTTGTGATCTG	240

LCMV-WE_NP	AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG	300
LCMV-P42_NP	AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG	300
LCMV-P52_NP	AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG	300
LCMV-P91_NP	AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG	300
LCMV-P52-1_NP	AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG	300
LCMV-P52-1.3_NP	AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG	300
LCMV-P52-2.1_NP	AAGTCTACATCAAAGAAAAATGTTCTGAAAGTGGGAAGACTTAGTGCAGAGGAATTGATG	300

LCMV-WE_NP	ACCCTTGCAGCTGATCTTGACAAGCTCAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA	360
LCMV-P42_NP	ACCCTTGCAGCTGATCTTGACAAGCTCAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA	360
LCMV-P52_NP	ACCCTTGCAGCTGATCTTGACAAGCTCAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA	360
LCMV-P91_NP	ACCCTTGCAGCTGATCTTGACAAGCTCAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA	360
LCMV-P52-1_NP	ACCCTTGCAGCTGATCTTGACAAGCTCAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA	360
LCMV-P52-1.3_NP	ACCCTTGCAGCTGATCTTGACAAGCTCAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA	360
LCMV-P52-2.1_NP	ACCCTTGCAGCTGATCTTGACAAGCTCAAGGCCAAAATTATGAGAACTGAGAGGCCTCAA	360

LCMV-WE_NP	GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA	420
LCMV-P42_NP	GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA	420
LCMV-P52_NP	GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA	420
LCMV-P91_NP	GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA	420
LCMV-P52-1_NP	GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA	420
LCMV-P52-1.3_NP	GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA	420
LCMV-P52-2.1_NP	GCTTCTGGAGTCTACATGGGAAATTTGACAGCACAACAACCTTGATCAAAGATCCCAAATA	420

Figure 26 (cont'd)

LCMV-WE_NP	CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG	480
LCMV-P42_NP	CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG	480
LCMV-P52_NP	CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG	480
LCMV-P91_NP	CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG	480
LCMV-P52-1_NP	CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG	480
LCMV-P52-1.3_NP	CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG	480
LCMV-P52-2.1_NP	CTGCAAATGGTTGGGATGAGAAGACCTCAGCAGGGTGCAAGTGGTGTAGTAAGGGTTTGG	480

LCMV-WE_NP	GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGGCACAATGCCAAGCCTGACAATG	540
LCMV-P42_NP	GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGGCACAATGCCAAGCCTGACAATG	540
LCMV-P52_NP	GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGGCACAATGCCAAGCCTGACAATG	540
LCMV-P91_NP	GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGGCACAATGCCAAGCCTGACAATG	540
LCMV-P52-1_NP	GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGGCACAATGCCAAGCCTGACAATG	540
LCMV-P52-1.3_NP	GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGGCACAATGCCAAGCCTGACAATG	540
LCMV-P52-2.1_NP	GATGTGAAGGACTCATCACTTCTGAACAATCAGTTCGGGCACAATGCCAAGCCTGACAATG	540

LCMV-WE_NP	GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACCTCACAGAC	600
LCMV-P42_NP	GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACCTCACAGAC	600
LCMV-P52_NP	GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACCTCACAGAC	600
LCMV-P91_NP	GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACCTCACAGAC	600
LCMV-P52-1_NP	GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACCTCACAGAC	600
LCMV-P52-1.3_NP	GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACCTCACAGAC	600
LCMV-P52-2.1_NP	GCTTGCATGGCAAAACAGTCACAGACCCCACTCAATGATGTTGTGCAGGCACCTCACAGAC	600

LCMV-WE_NP	CTTGGCTTACTTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT	660
LCMV-P42_NP	CTTGGCTTACTTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT	660
LCMV-P52_NP	CTTGGCTTACTTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT	660
LCMV-P91_NP	CTTGGCTTACTTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT	660
LCMV-P52-1_NP	CTTGGCTTACTTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT	660
LCMV-P52-1.3_NP	CTTGGCTTACTTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT	660
LCMV-P52-2.1_NP	CTTGGCTTACTTTTACACAGTCAAATACCCGAATCTCAGTGATCTTGAAAGGCTAAAGGAT	660

LCMV-WE_NP	AAACACCCAGTTCCTGGGGTCACTTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT	720
LCMV-P42_NP	AAACACCCAGTTCCTGGGGTCACTTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT	720
LCMV-P52_NP	AAACACCCAGTTCCTGGGGTCACTTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT	720
LCMV-P91_NP	AAACACCCAGTTCCTGGGGTCACTTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT	720
LCMV-P52-1_NP	AAACACCCAGTTCCTGGGGTCACTTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT	720
LCMV-P52-1.3_NP	AAACACCCAGTTCCTGGGGTCACTTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT	720
LCMV-P52-2.1_NP	AAACACCCAGTTCCTGGGGTCACTTACTGAACAGCAATCTAGTATCAATATCTCTGGTTAT	720

LCMV-WE_NP	AATTTCACTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG	780
LCMV-P42_NP	AATTTCACTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG	780
LCMV-P52_NP	AATTTCACTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG	780
LCMV-P91_NP	AATTTCACTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG	780
LCMV-P52-1_NP	AATTTCACTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG	780
LCMV-P52-1.3_NP	AATTTCACTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG	780
LCMV-P52-2.1_NP	AATTTCACTCTTGGTGCAGCTGTGAAAGCGGGGGCAGCTCTGCTAGATGGAGGGAACATG	780

LCMV-WE_NP	CTGGAATCTATCTTGATCAAACCCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG	840
LCMV-P42_NP	CTGGAATCTATCTTGATCAAACCCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG	840
LCMV-P52_NP	CTGGAATCTATCTTGATCAAACCCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG	840
LCMV-P91_NP	CTGGAATCTATCTTGATCAAACCCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG	840
LCMV-P52-1_NP	CTGGAATCTATCTTGATCAAACCCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG	840
LCMV-P52-1.3_NP	CTGGAATCTATCTTGATCAAACCCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG	840
LCMV-P52-2.1_NP	CTGGAATCTATCTTGATCAAACCCGAGCAACAGTGAGGATCTCCTAAAAGCAGTCCTCGGG	840

LCMV-WE_NP	GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA	900
LCMV-P42_NP	GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA	900
LCMV-P52_NP	GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA	900
LCMV-P91_NP	GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA	900
LCMV-P52-1_NP	GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA	900
LCMV-P52-1.3_NP	GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA	900
LCMV-P52-2.1_NP	GCCAAGAAGAAACTCAACATGTTTGTCTCAGATCAAGTTGGAGATAGAAATCCCTATGAA	900

Figure 26 (cont'd)

LCMV-WE_NP	AACATCCTTTATAAAGTCTGTCTTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG	960
LCMV-P42_NP	AACATCCTTTATAAAGTCTGTCTTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG	960
LCMV-P52_NP	AACATCCTTTATAAAGTCTGTCTTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG	960
LCMV-P91_NP	AACATCCTTTATAAAGTCTGTCTTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG	960
LCMV-P52-1_NP	AACATCCTTTATAAAGTCTGTCTTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG	960
LCMV-P52-1.3_NP	AACATCCTTTATAAAGTCTGTCTTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG	960
LCMV-P52-2.1_NP	AACATCCTTTATAAAGTCTGTCTTTTCAGGTGAAGGATGGCCATACATAGCCTGTAGAACG	960

LCMV-WE_NP	TCAGTTGTGGGGAGAGCATGGGAGAACAACAATTGATCTCACAAATGAAAACTTGTT	1020
LCMV-P42_NP	TCAGTTGTGGGGAGAGCATGGGAGAACAACAATTGATCTCACAAATGAAAACTTGTT	1020
LCMV-P52_NP	TCAGTTGTGGGGAGAGCATGGGAGAACAACAATTGATCTCACAAATGAAAACTTGTT	1020
LCMV-P91_NP	TCAGTTGTGGGGAGAGCATGGGAGAACAACAATTGATCTCACAAATGAAAACTTGTT	1020
LCMV-P52-1_NP	TCAGTTGTGGGGAGAGCATGGGAGAACAACAATTGATCTCACAAATGAAAACTTGTT	1020
LCMV-P52-1.3_NP	TCAGTTGTGGGGAGAGCATGGGAGAACAACAATTGATCTCACAAATGAAAACTTGTT	1020
LCMV-P52-2.1_NP	TCAGTTGTGGGGAGAGCATGGGAGAACAACAATTGATCTCACAAATGAAAACTTGTT	1020

LCMV-WE_NP	GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC	1080
LCMV-P42_NP	GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC	1080
LCMV-P52_NP	GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC	1080
LCMV-P91_NP	GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC	1080
LCMV-P52-1_NP	GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC	1080
LCMV-P52-1.3_NP	GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC	1080
LCMV-P52-2.1_NP	GCCAACTCATCTAGGCCAGTGCCTGGAGCAGCAGGCCACCTCAGGTGGGCTTGAGTTAC	1080

LCMV-WE_NP	AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG	1140
LCMV-P42_NP	AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG	1140
LCMV-P52_NP	AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG	1140
LCMV-P91_NP	AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG	1140
LCMV-P52-1_NP	AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG	1140
LCMV-P52-1.3_NP	AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG	1140
LCMV-P52-2.1_NP	AGTCAGACAATGCTGTTGAAAGACTTGATGGGAGGGATTGATCCCAATGCTCCCACATGG	1140

LCMV-WE_NP	ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT	1200
LCMV-P42_NP	ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT	1200
LCMV-P52_NP	ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT	1200
LCMV-P91_NP	ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT	1200
LCMV-P52-1_NP	ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT	1200
LCMV-P52-1.3_NP	ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT	1200
LCMV-P52-2.1_NP	ATTGACATTGAGGGCAGGTTCAATGATCCAGTGGAGATAGCAATATTCCAACCACAAAAT	1200

LCMV-WE_NP	GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA	1260
LCMV-P42_NP	GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA	1260
LCMV-P52_NP	GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA	1260
LCMV-P91_NP	GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA	1260
LCMV-P52-1_NP	GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA	1260
LCMV-P52-1.3_NP	GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA	1260
LCMV-P52-2.1_NP	GGGCAATTCATACATTTTACAGGGAACCTACGGACCAGAAGCAATTCAAGCAGGACTCA	1260

LCMV-WE_NP	AAGTATTACACAGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA	1320
LCMV-P42_NP	AAGTATTACACAGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA	1320
LCMV-P52_NP	AAGTATTACACAGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA	1320
LCMV-P91_NP	AAGTATTACACAGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA	1320
LCMV-P52-1_NP	AAGTATTACACAGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA	1320
LCMV-P52-1.3_NP	AAGTATTACACAGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA	1320
LCMV-P52-2.1_NP	AAGTATTACACAGGCATGGATCTTGCTGATCTCTTCAATGCACAGCCTGGGCTGACCTCA	1320

LCMV-WE_NP	TCAGTTATAGGTGCTCTCCACAAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC	1380
LCMV-P42_NP	TCAGTTATAGGTGCTCTCCACAAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC	1380
LCMV-P52_NP	TCAGTTATAGGTGCTCTCCACAAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC	1380
LCMV-P91_NP	TCAGTTATAGGTGCTCTCCACAAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC	1380
LCMV-P52-1_NP	TCAGTTATAGGTGCTCTCCACAAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC	1380
LCMV-P52-1.3_NP	TCAGTTATAGGTGCTCTCCACAAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC	1380
LCMV-P52-2.1_NP	TCAGTTATAGGTGCTCTCCACAAAGGGATGGTTTTGAGCTGTCAAGGTTCTGATGACATC	1380

Figure 26 (cont'd)

LCMV-WE_NP	AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC	1440
LCMV-P42_NP	AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC	1440
LCMV-P52_NP	AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC	1440
LCMV-P91_NP	AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC	1440
LCMV-P52-1_NP	AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC	1440
LCMV-P52-2.1_NP	AGAAAGCTTCTGGACTCACAAAATAGAAGGGACATAAAACTCATTGATGTTGAGATGACC	1440

LCMV-WE_NP	AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA	1500
LCMV-P42_NP	AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA	1500
LCMV-P52_NP	AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA	1500
LCMV-P91_NP	AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA	1500
LCMV-P52-1_NP	AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA	1500
LCMV-P52-2.1_NP	AAGGAGGCCTCAAGAGAATATGAAGATAAAGTGTGGGACAAATATGGCTGGCTATGCAAA	1500

LCMV-WE_NP	ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCATC	1560
LCMV-P42_NP	ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCATC	1560
LCMV-P52_NP	ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCATC	1560
LCMV-P91_NP	ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCATC	1560
LCMV-P52-1_NP	ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCATC	1560
LCMV-P52-2.1_NP	ATGCACACTGGGGTAGTGAGAGACAAAAAGAAGAAAGAGATCACCCACACTGTGCATC	1560

LCMV-WE_NP	ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT	1620
LCMV-P42_NP	ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT	1620
LCMV-P52_NP	ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT	1620
LCMV-P91_NP	ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT	1620
LCMV-P52-1_NP	ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT	1620
LCMV-P52-2.1_NP	ATGGACTGCATCATTTTTGAGAGTGCTTCCAAGGCAAGACTCCCTGATCTAAAAACCGTT	1620

LCMV-WE_NP	CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA	1677
LCMV-P42_NP	CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA	1677
LCMV-P52_NP	CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA	1677
LCMV-P91_NP	CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA	1677
LCMV-P52-1_NP	CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA	1677
LCMV-P52-2.1_NP	CACAACATCCTGCCACATGATTTAATCTTCAGAGGACCCAATGTTGTGACACTCTAA	1677

LCMV-WE_NP:	SEQ ID NO: 11	
LCMV-P42_NP:	SEQ ID NO: 19	
LCMV-P52_NP:	SEQ ID NO: 27	
LCMV-P91_NP:	SEQ ID NO: 35	
LCMV-P52-1_NP:	SEQ ID NO: 43	
LCMV-P52-1.3_NP:	SEQ ID NO: 51	
LCMV-P52-2.1_NP:	SEQ ID NO: 59	

Figure 26 (cont'd)

D.

Source: 1-3376 Segment = S
 Protein: Nucleoprotein
 Gene: NP
 Gene: 1640-3316 complement
 Sequence Alignment: Aminoacid

LCMV-WE_NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAIVKDATSLLNGLDFSEVSNVQIRIMRKERRD	60
LCMV-P42_NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAIVKDATSLLNGLDFSEVSNVQIRIMRKERRD	60
LCMV-P52_NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAIVKDATSLLNGLDFSEVSNVQIRIMRKERRD	60
LCMV-P91_NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAIVKDATSLLNGLDFSEVSNVQIRIMRKERRD	60
LCMV-P52-1_NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAIVKDATSLLNGLDFSEVSNVQIRIMRKERRD	60
LCMV-P52-1.3_NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAIVKDATSLLNGLDFSEVSNVQIRIMRKERRD	60
LCMV-P52-2.1_NP	MSLSKEVKSFQWTQALRRELQSFTSDVKAIVKDATSLLNGLDFSEVSNVQIRIMRKERRD	60

LCMV-WE_NP	DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ	120
LCMV-P42_NP	DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ	120
LCMV-P52_NP	DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ	120
LCMV-P91_NP	DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ	120
LCMV-P52-1_NP	DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ	120
LCMV-P52-1.3_NP	DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ	120
LCMV-P52-2.1_NP	DKDLQRLRSLNQTVHSLVDLKSTSKKNVLKVGRLSAEELMTLAADLEKLKAKIMRTERPQ	120

LCMV-WE_NP	ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM	180
LCMV-P42_NP	ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM	180
LCMV-P52_NP	ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM	180
LCMV-P91_NP	ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM	180
LCMV-P52-1_NP	ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM	180
LCMV-P52-1.3_NP	ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM	180
LCMV-P52-2.1_NP	ASGVYMGNLTAQQLDQRSQILQMVGMRPQQGASGVVRVWDVKDSSLNNQFGTMPSLTM	180

LCMV-WE_NP	ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY	240
LCMV-P42_NP	ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY	240
LCMV-P52_NP	ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY	240
LCMV-P91_NP	ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY	240
LCMV-P52-1_NP	ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY	240
LCMV-P52-1.3_NP	ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY	240
LCMV-P52-2.1_NP	ACMAKQSQTPLNDDVVQALTDLGLLYTVKYPNLSDLERLKDHPVLGVITEQQSSINISGY	240

LCMV-WE_NP	NFSLGAAVKAGAAILLDGCNMLESILIKPSNSEDLLKAVLGAKKKLNMVSDQVGDNRNPE	300
LCMV-P42_NP	NFSLGAAVKAGAAILLDGCNMLESILIKPSNSEDLLKAVLGAKKKLNMVSDQVGDNRNPE	300
LCMV-P52_NP	NFSLGAAVKAGAAILLDGCNMLESILIKPSNSEDLLKAVLGAKKKLNMVSDQVGDNRNPE	300
LCMV-P91_NP	NFSLGAAVKAGAAILLDGCNMLESILIKPSNSEDLLKAVLGAKKKLNMVSDQVGDNRNPE	300
LCMV-P52-1_NP	NFSLGAAVKAGAAILLDGCNMLESILIKPSNSEDLLKAVLGAKKKLNMVSDQVGDNRNPE	300
LCMV-P52-1.3_NP	NFSLGAAVKAGAAILLDGCNMLESILIKPSNSEDLLKAVLGAKKKLNMVSDQVGDNRNPE	300
LCMV-P52-2.1_NP	NFSLGAAVKAGAAILLDGCNMLESILIKPSNSEDLLKAVLGAKKKLNMVSDQVGDNRNPE	300

LCMV-WE_NP	NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPCAAGPPQVGLSY	360
LCMV-P42_NP	NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPCAAGPPQVGLSY	360
LCMV-P52_NP	NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPCAAGPPQVGLSY	360
LCMV-P91_NP	NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPCAAGPPQVGLSY	360
LCMV-P52-1_NP	NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPCAAGPPQVGLSY	360
LCMV-P52-1.3_NP	NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPCAAGPPQVGLSY	360
LCMV-P52-2.1_NP	NILYKVCLSGEGWPYIACRTSVVGRAWENTTIDLTNEKLVANSSRPVPCAAGPPQVGLSY	360

LCMV-WE_NP	SQTMLLKDLGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS	420
LCMV-P42_NP	SQTMLLKDLGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS	420
LCMV-P52_NP	SQTMLLKDLGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS	420
LCMV-P91_NP	SQTMLLKDLGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS	420
LCMV-P52-1_NP	SQTMLLKDLGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS	420
LCMV-P52-1.3_NP	SQTMLLKDLGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS	420
LCMV-P52-2.1_NP	SQTMLLKDLGGIDPNAPTWIDIEGRFNDPVEIAIFQPQNGQFIHFYREPTDQKQFKQDS	420

Figure 26 (cont'd)

LCMV-WE_NP	KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKLLDSQNRRDIKLIDVEMT	480
LCMV-P42_NP	KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKLLDSQNRRDIKLIDVEMT	480
LCMV-P52_NP	KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKLLDSQNRRDIKLIDVEMT	480
LCMV-P91_NP	KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKLLDSQNRRDIKLIDVEMT	480
LCMV-P52-1_NP	KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKLLDSQNRRDIKLIDVEMT	480
LCMV-P52-1.3_NP	KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKLLDSQNRRDIKLIDVEMT	480
LCMV-P52-2.1_NP	KYSHGMDLADLFNAQPGLTSSVIGALPQGMVLSQGSDDIRKLLDSQNRRDIKLIDVEMT	480

LCMV-WE_NP	KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV	540
LCMV-P42_NP	KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV	540
LCMV-P52_NP	KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV	540
LCMV-P91_NP	KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV	540
LCMV-P52-1_NP	KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV	540
LCMV-P52-1.3_NP	KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV	540
LCMV-P52-2.1_NP	KEASREYEDKVWDKYGWLCKMHTGVVRDKKKKEITPHCALMDCIIFESASKARLPDLKTV	540

LCMV-WE_NP	HNILPHDLIFRGPNVVTL	558
LCMV-P42_NP	HNILPHDLIFRGPNVVTL	558
LCMV-P52_NP	HNILPHDLIFRGPNVVTL	558
LCMV-P91_NP	HNILPHDLIFRGPNVVTL	558
LCMV-P52-1_NP	HNILPHDLIFRGPNVVTL	558
LCMV-P52-1.3_NP	HNILPHDLIFRGPNVVTL	558
LCMV-P52-2.1_NP	HNILPHDLIFRGPNVVTL	558

LCMV-WE_NP:	SEQ ID NO: 12	
LCMV-P42_NP:	SEQ ID NO: 20	
LCMV-P52_NP:	SEQ ID NO: 28	
LCMV-P91_NP:	SEQ ID NO: 36	
LCMV-P52-1_NP:	SEQ ID NO: 44	
LCMV-P52-1.3_NP:	SEQ ID NO: 52	
LCMV-P52-2.1_NP:	SEQ ID NO: 60	

Figure 26 (cont'd)

E.

Source: 1-7235 Segment = L
 Protein: RING finger protein Z
 Gene: ZP
 Gene: 90-362
 Sequence Alignment: Nucleotide

LCMV-WE_ZP	ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT	60
LCMV-P42_ZP	ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT	60
LCMV-P52_ZP	ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT	60
LCMV-P91_ZP	ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT	60
LCMV-P52-1_ZP	ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT	60
LCMV-P52-1.3_ZP	ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT	60
LCMV-P52-2.1_ZP	ATGGGCCAAGGCAAGTCCAAAGAAGAAAGGGACACCAGCAATACAGGCAGAGCAGAGCTT	60

LCMV-WE_ZP	TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC	120
LCMV-P42_ZP	TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC	120
LCMV-P52_ZP	TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC	120
LCMV-P91_ZP	TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC	120
LCMV-P52-1_ZP	TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC	120
LCMV-P52-1.3_ZP	TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC	120
LCMV-P52-2.1_ZP	TTGCCAGACACCACCTATCTTGGTCCTCTAAATTGTAAATCATGTTGGCAGAAATTTGAC	120

LCMV-WE_ZP	AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA	180
LCMV-P42_ZP	AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA	180
LCMV-P52_ZP	AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA	180
LCMV-P91_ZP	AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA	180
LCMV-P52-1_ZP	AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA	180
LCMV-P52-1.3_ZP	AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA	180
LCMV-P52-2.1_ZP	AGCTTGGTTAGATGCCATGACCACCTATCTTTGCAGACACTGTCTGAATCTCCTGCTGTCA	180

LCMV-WE_ZP	GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACCTGAAGGTGTCAACA	240
LCMV-P42_ZP	GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACCTGAAGGTGTCAACA	240
LCMV-P52_ZP	GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACCTGAAGGTGTCAACA	240
LCMV-P91_ZP	GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACCTGAAGGTGTCAACA	240
LCMV-P52-1_ZP	GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACCTGAAGGTGTCAACA	240
LCMV-P52-1.3_ZP	GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACCTGAAGGTGTCAACA	240
LCMV-P52-2.1_ZP	GTTTCCGACAGATGTCCTCTCTGTAAGTATCCACTGCCAACCAAACCTGAAGGTGTCAACA	240

LCMV-WE_ZP	GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA	273
LCMV-P42_ZP	GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA	273
LCMV-P52_ZP	GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA	273
LCMV-P91_ZP	GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA	273
LCMV-P52-1_ZP	GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA	273
LCMV-P52-1.3_ZP	GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA	273
LCMV-P52-2.1_ZP	GTCCCAAGCTCCCCACCTCCCTATGAGGAGTGA	273

LCMV-WE_ZP:	SEQ ID NO: 13	
LCMV-P42_ZP:	SEQ ID NO: 21	
LCMV-P52_ZP:	SEQ ID NO: 29	
LCMV-P91_ZP:	SEQ ID NO: 37	
LCMV-P52-1_ZP:	SEQ ID NO: 45	
LCMV-P52-1.3_ZP:	SEQ ID NO: 53	
LCMV-P52-2.1_ZP:	SEQ ID NO: 61	

Figure 26 (cont'd)

F.

Source: 1-7235 Segment = L
Protein: RING finger protein Z
Gene: ZP
Gene: 90-362
Sequence Alignment: Aminoacid

LCMV-WE_ZP	MGQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS	60
LCMV-P42_ZP	MGQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS	60
LCMV-P52_ZP	MGQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS	60
LCMV-P91_ZP	MGQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS	60
LCMV-P52-1_ZP	MGQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS	60
LCMV-P52-1.3_ZP	MGQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS	60
LCMV-P52-2.1_ZP	MGQGSKEERDTSNTGRAELLPDTTYLGPLNCKSCWQKFDSLVRCHDHYLCRHCLNLLLS	60

LCMV-WE_ZP	VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE	90
LCMV-P42_ZP	VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE	90
LCMV-P52_ZP	VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE	90
LCMV-P91_ZP	VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE	90
LCMV-P52-1_ZP	VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE	90
LCMV-P52-1.3_ZP	VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE	90
LCMV-P52-2.1_ZP	VSDRCPLCKYPLPTKLKVSTVPSSPPPYEE	90

LCMV-WE_ZP:	SEQ ID NO: 14
LCMV-P42_ZP:	SEQ ID NO: 22
LCMV-P52_ZP:	SEQ ID NO: 30
LCMV-P91_ZP:	SEQ ID NO: 38
LCMV-P52-1_ZP:	SEQ ID NO: 46
LCMV-P52-1.3_ZP:	SEQ ID NO: 54
LCMV-P52-2.1_ZP:	SEQ ID NO: 62

Figure 26 (cont'd)

G.

Source: 1-7235 Segment = L
Protein: RNA-directed RNA polymerase L
Gene: LP
Gene: 574-7203 complement
Sequence Alignment: Nucleotide

LCMV-WE_LP	ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGCTAAATTACATAGAACAGGACGAG	60
LCMV-P42_LP	ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGCTAAATTACATAGAACAGGACGAG	60
LCMV-P52_LP	ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGCTAAATTACATAGAACAGGACGAG	60
LCMV-P91_LP	ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGCTAAATTACATAGAACAGGACGAG	60
LCMV-P52-1_LP	ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGCTAAATTACATAGAACAGGACGAG	60
LCMV-P52-1.3_LP	ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGCTAAATTACATAGAACAGGACGAG	60
LCMV-P52-2.1_LP	ATGGATGAAACTATTGCAGATTTGAGAGAGTTGTGCTAAATTACATAGAACAGGACGAG	60

LCMV-WE_LP	AGGCTGTCAAGGCAAAAACCTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGTAAATT	120
LCMV-P42_LP	AGGCTGTCAAGGCAAAAACCTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGTAAATT	120
LCMV-P52_LP	AGGCTGTCAAGGCAAAAACCTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGTAAATT	120
LCMV-P91_LP	AGGCTGTCAAGGCAAAAACCTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGTAAATT	120
LCMV-P52-1_LP	AGGCTGTCAAGGCAAAAACCTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGTAAATT	120
LCMV-P52-1.3_LP	AGGCTGTCAAGGCAAAAACCTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGTAAATT	120
LCMV-P52-2.1_LP	AGGCTGTCAAGGCAAAAACCTCAACTTCCTGGGACAAAGAGAACCCAGAATGGTGTAAATT	120

LCMV-WE_LP	GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC	180
LCMV-P42_LP	GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC	180
LCMV-P52_LP	GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC	180
LCMV-P91_LP	GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC	180
LCMV-P52-1_LP	GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC	180
LCMV-P52-1.3_LP	GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC	180
LCMV-P52-2.1_LP	GAGGGACTCAAATTTGTTATCACGCTGTATAGAGATAGACAGTGCAGACAAAAGTGGTTGC	180

LCMV-WE_LP	ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT	240
LCMV-P42_LP	ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT	240
LCMV-P52_LP	ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT	240
LCMV-P91_LP	ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT	240
LCMV-P52-1_LP	ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT	240
LCMV-P52-1.3_LP	ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT	240
LCMV-P52-2.1_LP	ATACACAACCACGATGACAAATCTGTTGAAACAATCCTAATAGACTCTGGGATTGTGTGT	240

LCMV-WE_LP	CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTTATTCCTT	300
LCMV-P42_LP	CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTTATTCCTT	300
LCMV-P52_LP	CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTTATTCCTT	300
LCMV-P91_LP	CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTTATTCCTT	300
LCMV-P52-1_LP	CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTTATTCCTT	300
LCMV-P52-1.3_LP	CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTTATTCCTT	300
LCMV-P52-2.1_LP	CCAGGACTGCCACTCATCATCCCTGATGGTTATAAGTTGATTGACAATTCCTTTATTCCTT	300

LCMV-WE_LP	CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTGAAGAAGTTTCATTGAGGACACC	360
LCMV-P42_LP	CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTGAAGAAGTTTCATTGAGGACACC	360
LCMV-P52_LP	CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTGAAGAAGTTTCATTGAGGACACC	360
LCMV-P91_LP	CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTGAAGAAGTTTCATTGAGGACACC	360
LCMV-P52-1_LP	CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTGAAGAAGTTTCATTGAGGACACC	360
LCMV-P52-1.3_LP	CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTGAAGAAGTTTCATTGAGGACACC	360
LCMV-P52-2.1_LP	CTTGAATGTTTTGTTAGAAGCACACCAGCTAGTTTGAAGAAGTTTCATTGAGGACACC	360

LCMV-WE_LP	AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA	420
LCMV-P42_LP	AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA	420
LCMV-P52_LP	AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA	420
LCMV-P91_LP	AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA	420
LCMV-P52-1_LP	AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA	420
LCMV-P52-1.3_LP	AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA	420
LCMV-P52-2.1_LP	AACAAACTAGCATGCATCAAAGAAGATCTTGCTGTTGCAGGCATCACACTGGTTCCAATA	420

Figure 26 (cont'd)

LCMV-WE_LP	GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC	480
LCMV-P42_LP	GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC	480
LCMV-P52_LP	GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC	480
LCMV-P91_LP	GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC	480
LCMV-P52-1_LP	GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC	480
LCMV-P52-1.3_LP	GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC	480
LCMV-P52-2.1_LP	GTGGATGGTCGTTGTGATTATGATAACAGTTTCATGCCAGAATGGGTGAATTTTAAGTTC	480

LCMV-WE_LP	AGAGACCTCCTATTTTAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG	540
LCMV-P42_LP	AGAGACCTCCTATTTTAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG	540
LCMV-P52_LP	AGAGACCTCCTATTTTAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG	540
LCMV-P91_LP	AGAGACCTCCTATTTTAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG	540
LCMV-P52-1_LP	AGAGACCTCCTATTTTAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG	540
LCMV-P52-1.3_LP	AGAGACCTCCTATTTTAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG	540
LCMV-P52-2.1_LP	AGAGACCTCCTATTTTAACTCCTGGAGTATTCTAGTCAAGATGAGAAAGTTTTTGAGGAG	540

LCMV-WE_LP	TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG	600
LCMV-P42_LP	TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG	600
LCMV-P52_LP	TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG	600
LCMV-P91_LP	TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG	600
LCMV-P52-1_LP	TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG	600
LCMV-P52-1.3_LP	TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG	600
LCMV-P52-2.1_LP	TCTGAATACTTCAGGCTCTGTGAGTCTCTTAAGACCACTGTTGACAAACGTTCCGGCATG	600

LCMV-WE_LP	GACTCAATGAAAAATTTTGAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAAATG	660
LCMV-P42_LP	GACTCAATGAAAAATTTTGAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAAATG	660
LCMV-P52_LP	GACTCAATGAAAAATTTTGAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAAATG	660
LCMV-P91_LP	GACTCAATGAAAAATTTTGAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAAATG	660
LCMV-P52-1_LP	GACTCAATGAAAAATTTTGAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAAATG	660
LCMV-P52-1.3_LP	GACTCAATGAAAAATTTTGAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAAATG	660
LCMV-P52-2.1_LP	GACTCAATGAAAAATTTTGAAGACGCAAGATCATTTCATAACGATGAGATTATGAAAAATG	660

LCMV-WE_LP	TGCCACGATGGTGTCAACCCCAACATGAGTTGCCGATGATGTGGTCTTTGGCATAAATTC	720
LCMV-P42_LP	TGCCACGATGGTGTCAACCCCAACATGAGTTGCCGATGATGTGGTCTTTGGCATAAATTC	720
LCMV-P52_LP	TGCCACGATGGTGTCAACCCCAACATGAGTTGCCGATGATGTGGTCTTTGGCATAAATTC	720
LCMV-P91_LP	TGCCACGATGGTGTCAACCCCAACATGAGTTGCCGATGATGTGGTCTTTGGCATAAATTC	720
LCMV-P52-1_LP	TGCCACGATGGTGTCAACCCCAACATGAGTTGCCGATGATGTGGTCTTTGGCATAAATTC	720
LCMV-P52-1.3_LP	TGCCACGATGGTGTCAACCCCAACATGAGTTGCCGATGATGTGGTCTTTGGCATAAATTC	720
LCMV-P52-2.1_LP	TGCCACGATGGTGTCAACCCCAACATGAGTTGCCGATGATGTGGTCTTTGGCATAAATTC	720

LCMV-WE_LP	TTTTTTGGCAGGTTTAGGAGGGACCTGTAAATGGGAAACTCAAAGGAATTTCCAAAAG	780
LCMV-P42_LP	TTTTTTGGCAGGTTTAGGAGGGACCTGTAAATGGGAAACTCAAAGGAATTTCCAAAAG	780
LCMV-P52_LP	TTTTTTGGCAGGTTTAGGAGGGACCTGTAAATGGGAAACTCAAAGGAATTTCCAAAAG	780
LCMV-P91_LP	TTTTTTGGCAGGTTTAGGAGGGACCTGTAAATGGGAAACTCAAAGGAATTTCCAAAAG	780
LCMV-P52-1_LP	TTTTTTGGCAGGTTTAGGAGGGACCTGTAAATGGGAAACTCAAAGGAATTTCCAAAAG	780
LCMV-P52-1.3_LP	TTTTTTGGCAGGTTTAGGAGGGACCTGTAAATGGGAAACTCAAAGGAATTTCCAAAAG	780
LCMV-P52-2.1_LP	TTTTTTGGCAGGTTTAGGAGGGACCTGTAAATGGGAAACTCAAAGGAATTTCCAAAAG	780

LCMV-WE_LP	GTGAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCCCTTACTGATAAT	840
LCMV-P42_LP	GTGAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCCCTTACTGATAAT	840
LCMV-P52_LP	GTGAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCCCTTACTGATAAT	840
LCMV-P91_LP	GTGAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCCCTTACTGATAAT	840
LCMV-P52-1_LP	GTGAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCCCTTACTGATAAT	840
LCMV-P52-1.3_LP	GTGAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCCCTTACTGATAAT	840
LCMV-P52-2.1_LP	GTGAGCCCTGGGGGCTTAATCAAGGAATTCCTGAACTTTATGAAACCCCTTACTGATAAT	840

LCMV-WE_LP	GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT	900
LCMV-P42_LP	GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT	900
LCMV-P52_LP	GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT	900
LCMV-P91_LP	GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT	900
LCMV-P52-1_LP	GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT	900
LCMV-P52-1.3_LP	GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT	900
LCMV-P52-2.1_LP	GATGACATATTAATGTTGAGCAAAGAGGCAGTTGAATCCTGCCCTTAATGAGGTTTCATT	900

Figure 26 (cont'd)

LCMV-WE_LP	ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA	960
LCMV-P42_LP	ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA	960
LCMV-P52_LP	ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA	960
LCMV-P91_LP	ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA	960
LCMV-P52-1_LP	ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA	960
LCMV-P52-1.3_LP	ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA	960
LCMV-P52-2.1_LP	ACAGCAGAGACCCATGGGCATGAGAGAGGAAGCGATGCTAACACTGAGTATGAAAGGCTA	960

LCMV-WE_LP	CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAAATTATTAACACTAGAAGGAGACAGCTG	1020
LCMV-P42_LP	CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAAATTATTAACACTAGAAGGAGACAGCTG	1020
LCMV-P52_LP	CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAAATTATTAACACTAGAAGGAGACAGCTG	1020
LCMV-P91_LP	CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAAATTATTAACACTAGAAGGAGACAGCTG	1020
LCMV-P52-1_LP	CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAAATTATTAACACTAGAAGGAGACAGCTG	1020
LCMV-P52-1.3_LP	CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAAATTATTAACACTAGAAGGAGACAGCTG	1020
LCMV-P52-2.1_LP	CTCTCTATGTTGAACAAGGTGAAAAGTTTAAAAATTATTAACACTAGAAGGAGACAGCTG	1020

LCMV-WE_LP	CTGAACCTAGATGCTTATGCTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG	1080
LCMV-P42_LP	CTGAACCTAGATGCTTATGCTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG	1080
LCMV-P52_LP	CTGAACCTAGATGCTTATGCTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG	1080
LCMV-P91_LP	CTGAACCTAGATGCTTATGCTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG	1080
LCMV-P52-1_LP	CTGAACCTAGATGCTTATGCTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG	1080
LCMV-P52-1.3_LP	CTGAACCTAGATGCTTATGCTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG	1080
LCMV-P52-2.1_LP	CTGAACCTAGATGCTTATGCTCTTCTTCACTTATTAAGCAGTCAATTTCCAAAGGGTTG	1080

LCMV-WE_LP	GAAAATGATAAACATTGGGTTGGTTGGTGTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC	1140
LCMV-P42_LP	GAAAATGATAAACATTGGGTTGGTTGGTGTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC	1140
LCMV-P52_LP	GAAAATGATAAACATTGGGTTGGTTGGTGTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC	1140
LCMV-P91_LP	GAAAATGATAAACATTGGGTTGGTTGGTGTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC	1140
LCMV-P52-1_LP	GAAAATGATAAACATTGGGTTGGTTGGTGTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC	1140
LCMV-P52-1.3_LP	GAAAATGATAAACATTGGGTTGGTTGGTGTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC	1140
LCMV-P52-2.1_LP	GAAAATGATAAACATTGGGTTGGTTGGTGTGCTACAGTAGTGTGAATGATAGGCTTGTGAGC	1140

LCMV-WE_LP	CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAGAAGAAATCAAGAGTG	1200
LCMV-P42_LP	CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAGAAGAAATCAAGAGTG	1200
LCMV-P52_LP	CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAGAAGAAATCAAGAGTG	1200
LCMV-P91_LP	CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAGAAGAAATCAAGAGTG	1200
LCMV-P52-1_LP	CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAGAAGAAATCAAGAGTG	1200
LCMV-P52-1.3_LP	CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAGAAGAAATCAAGAGTG	1200
LCMV-P52-2.1_LP	CTTCAAAGTACCAAAGAAGAATTCATGAGACTTTTGAAGAACAGAGAAGAAATCAAGAGTG	1200

LCMV-WE_LP	CACAAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA	1260
LCMV-P42_LP	CACAAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA	1260
LCMV-P52_LP	CACAAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA	1260
LCMV-P91_LP	CACAAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA	1260
LCMV-P52-1_LP	CACAAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA	1260
LCMV-P52-1.3_LP	CACAAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA	1260
LCMV-P52-2.1_LP	CACAAAAAGGCATCTCTTGATGAGCTTTTATAGGGTATCCATAAATGAGTTCATAGCAAAA	1260

LCMV-WE_LP	ATCCAGAAATGCCATATCAACAGTGGGACTTAGTTTGGAGCATTACGGACTATCAGAATGC	1320
LCMV-P42_LP	ATCCAGAAATGCCATATCAACAGTGGGACTTAGTTTGGAGCATTACGGACTATCAGAATGC	1320
LCMV-P52_LP	ATCCAGAAATGCCATATCAACAGTGGGACTTAGTTTGGAGCATTACGGACTATCAGAATGC	1320
LCMV-P91_LP	ATCCAGAAATGCCATATCAACAGTGGGACTTAGTTTGGAGCATTACGGACTATCAGAATGC	1320
LCMV-P52-1_LP	ATCCAGAAATGCCATATCAACAGTGGGACTTAGTTTGGAGCATTACGGACTATCAGAATGC	1320
LCMV-P52-1.3_LP	ATCCAGAAATGCCATATCAACAGTGGGACTTAGTTTGGAGCATTACGGACTATCAGAATGC	1320
LCMV-P52-2.1_LP	ATCCAGAAATGCCATATCAACAGTGGGACTTAGTTTGGAGCATTACGGACTATCAGAATGC	1320

LCMV-WE_LP	CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAAGTTTATGAGAGCCGGGACT	1380
LCMV-P42_LP	CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAAGTTTATGAGAGCCGGGACT	1380
LCMV-P52_LP	CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAAGTTTATGAGAGCCGGGACT	1380
LCMV-P91_LP	CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAAGTTTATGAGAGCCGGGACT	1380
LCMV-P52-1_LP	CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAAGTTTATGAGAGCCGGGACT	1380
LCMV-P52-1.3_LP	CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAAGTTTATGAGAGCCGGGACT	1380
LCMV-P52-2.1_LP	CTCGTGCAAGAATGCCATATACCATTTGCTGAATTTGAGAAGTTTATGAGAGCCGGGACT	1380

Figure 26 (cont'd)

LCMV-WE_LP	CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA	1440
LCMV-P42_LP	CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA	1440
LCMV-P52_LP	CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA	1440
LCMV-P91_LP	CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA	1440
LCMV-P52-1_LP	CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA	1440
LCMV-P52-1.3_LP	CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA	1440
LCMV-P52-2.1_LP	CATCCTGTAATGCATTACACAAAATTTGAAGATTACACTTTCCAGCCTAACATAGAGCAA	1440

LCMV-WE_LP	TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGGCTCTAACAAACAGC	1500
LCMV-P42_LP	TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGGCTCTAACAAACAGC	1500
LCMV-P52_LP	TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGGCTCTAACAAACAGC	1500
LCMV-P91_LP	TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGGCTCTAACAAACAGC	1500
LCMV-P52-1_LP	TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGGCTCTAACAAACAGC	1500
LCMV-P52-1.3_LP	TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGGCTCTAACAAACAGC	1500
LCMV-P52-2.1_LP	TTGAGGGGTTTACAGAGTTTGAGAAAACGTGCATCTGTTTGGCTCTAACAAACAGC	1500

LCMV-WE_LP	ATGAAAACAAGCTCAGTTGCAAGGTTGACACAGAACCACCTGGGCTCTGTGAGATATCAA	1560
LCMV-P42_LP	ATGAAAACAAGCTCAGTTGCAAGGTTGACACAGAACCACCTGGGCTCTGTGAGATATCAA	1560
LCMV-P52_LP	ATGAAAACAAGCTCAGTTGCAAGGTTGACACAGAACCACCTGGGCTCTGTGAGATATCAA	1560
LCMV-P91_LP	ATGAAAACAAGCTCAGTTGCAAGGTTGACACAGAACCACCTGGGCTCTGTGAGATATCAA	1560
LCMV-P52-1_LP	ATGAAAACAAGCTCAGTTGCAAGGTTGACACAGAACCACCTGGGCTCTGTGAGATATCAA	1560
LCMV-P52-1.3_LP	ATGAAAACAAGCTCAGTTGCAAGGTTGACACAGAACCACCTGGGCTCTGTGAGATATCAA	1560
LCMV-P52-2.1_LP	ATGAAAACAAGCTCAGTTGCAAGGTTGACACAGAACCACCTGGGCTCTGTGAGATATCAA	1560

LCMV-WE_LP	GTGGTGGAGTGCAAAGAGGTGTTTGGCAGATAATAAACTGGATTCCGAAGAGTATCAT	1620
LCMV-P42_LP	GTGGTGGAGTGCAAAGAGGTGTTTGGCAGATAATAAACTGGATTCCGAAGAGTATCAT	1620
LCMV-P52_LP	GTGGTGGAGTGCAAAGAGGTGTTTGGCAGATAATAAACTGGATTCCGAAGAGTATCAT	1620
LCMV-P91_LP	GTGGTGGAGTGCAAAGAGGTGTTTGGCAGATAATAAACTGGATTCCGAAGAGTATCAT	1620
LCMV-P52-1_LP	GTGGTGGAGTGCAAAGAGGTGTTTGGCAGATAATAAACTGGATTCCGAAGAGTATCAT	1620
LCMV-P52-1.3_LP	GTGGTGGAGTGCAAAGAGGTGTTTGGCAGATAATAAACTGGATTCCGAAGAGTATCAT	1620
LCMV-P52-2.1_LP	GTGGTGGAGTGCAAAGAGGTGTTTGGCAGATAATAAACTGGATTCCGAAGAGTATCAT	1620

LCMV-WE_LP	CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATCCATACAAGGTCGGATGGT	1680
LCMV-P42_LP	CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATCCATACAAGGTCGGATGGT	1680
LCMV-P52_LP	CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATCCATACAAGGTCGGATGGT	1680
LCMV-P91_LP	CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATCCATACAAGGTCGGATGGT	1680
LCMV-P52-1_LP	CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATCCATACAAGGTCGGATGGT	1680
LCMV-P52-1.3_LP	CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATCCATACAAGGTCGGATGGT	1680
LCMV-P52-2.1_LP	CTACTATATCAGAAAACCTGGAGAATCATCGAGGTGTTATCCATACAAGGTCGGATGGT	1680

LCMV-WE_LP	CACCTTGATTTCCCTTTTACGCAGATCCAAAAAGGTTCTTTTACCAATTTTTTCAGATGAG	1740
LCMV-P42_LP	CACCTTGATTTCCCTTTTACGCAGATCCAAAAAGGTTCTTTTACCAATTTTTTCAGATGAG	1740
LCMV-P52_LP	CACCTTGATTTCCCTTTTACGCAGATCCAAAAAGGTTCTTTTACCAATTTTTTCAGATGAG	1740
LCMV-P91_LP	CACCTTGATTTCCCTTTTACGCAGATCCAAAAAGGTTCTTTTACCAATTTTTTCAGATGAG	1740
LCMV-P52-1_LP	CACCTTGATTTCCCTTTTACGCAGATCCAAAAAGGTTCTTTTACCAATTTTTTCAGATGAG	1740
LCMV-P52-1.3_LP	CACCTTGATTTCCCTTTTACGCAGATCCAAAAAGGTTCTTTTACCAATTTTTTCAGATGAG	1740
LCMV-P52-2.1_LP	CACCTTGATTTCCCTTTTACGCAGATCCAAAAAGGTTCTTTTACCAATTTTTTCAGATGAG	1740

LCMV-WE_LP	GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTCATGCCCTGACTTAAAA	1800
LCMV-P42_LP	GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTCATGCCCTGACTTAAAA	1800
LCMV-P52_LP	GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTCATGCCCTGACTTAAAA	1800
LCMV-P91_LP	GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTCATGCCCTGACTTAAAA	1800
LCMV-P52-1_LP	GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTCATGCCCTGACTTAAAA	1800
LCMV-P52-1.3_LP	GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTCATGCCCTGACTTAAAA	1800
LCMV-P52-2.1_LP	GTGTTGCACAACATGATAGACACAATGATTTTCATGGATTAGGTCATGCCCTGACTTAAAA	1800

LCMV-WE_LP	GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAC	1860
LCMV-P42_LP	GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAC	1860
LCMV-P52_LP	GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAC	1860
LCMV-P91_LP	GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAC	1860
LCMV-P52-1_LP	GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAC	1860
LCMV-P52-1.3_LP	GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAC	1860
LCMV-P52-2.1_LP	GATTCTCTTATTGACATTGAGACTGCACTAAGGACATTGATCCTACTGATGCTCACCAC	1860

Figure 26 (cont'd)

LCMV-WE_LP	CCAACAAAGAGAAATCAAAGCAGGTTCAAATATTAGGTATTTAGTGATGGCCATCGTC	1920
LCMV-P42_LP	CCAACAAAGAGAAATCAAAGCAGGTTCAAATATTAGGTATTTAGTGATGGCCATCGTC	1920
LCMV-P52_LP	CCAACAAAGAGAAATCAAAGCAGGTTCAAATATTAGGTATTTAGTGATGGCCATCGTC	1920
LCMV-P91_LP	CCAACAAAGAGAAATCAAAGCAGGTTCAAATATTAGGTATTTAGTGATGGCCATCGTC	1920
LCMV-P52-1_LP	CCAACAAAGAGAAATCAAAGCAGGTTCAAATATTAGGTATTTAGTGATGGCCATCGTC	1920
LCMV-P52-1.3_LP	CCAACAAAGAGAAATCAAAGCAGGTTCAAATATTAGGTATTTAGTGATGGCCATCGTC	1920
LCMV-P52-2.1_LP	CCAACAAAGAGAAATCAAAGCAGGTTCAAATATTAGGTATTTAGTGATGGCCATCGTC	1920

LCMV-WE_LP	TCAGACTTTTCATCGACCTCATTAAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC	1980
LCMV-P42_LP	TCAGACTTTTCATCGACCTCATTAAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC	1980
LCMV-P52_LP	TCAGACTTTTCATCGACCTCATTAAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC	1980
LCMV-P91_LP	TCAGACTTTTCATCGACCTCATTAAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC	1980
LCMV-P52-1_LP	TCAGACTTTTCATCGACCTCATTAAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC	1980
LCMV-P52-1.3_LP	TCAGACTTTTCATCGACCTCATTAAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC	1980
LCMV-P52-2.1_LP	TCAGACTTTTCATCGACCTCATTAAATGGATAAGTTGAAGGAGGATCTAATCACACCTGCC	1980

LCMV-WE_LP	GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTTCATTAGGACAATTTTTGGTACTGGTGAA	2040
LCMV-P42_LP	GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTTCATTAGGACAATTTTTGGTACTGGTGAA	2040
LCMV-P52_LP	GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTTCATTAGGACAATTTTTGGTACTGGTGAA	2040
LCMV-P91_LP	GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTTCATTAGGACAATTTTTGGTACTGGTGAA	2040
LCMV-P52-1_LP	GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTTCATTAGGACAATTTTTGGTACTGGTGAA	2040
LCMV-P52-1.3_LP	GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTTCATTAGGACAATTTTTGGTACTGGTGAA	2040
LCMV-P52-2.1_LP	GAGAAAGTGGTGTACAGGCTGCTTCGGTTTTTTCATTAGGACAATTTTTGGTACTGGTGAA	2040

LCMV-WE_LP	AAGGTGTTATTGAGTGCAAAATTCAGTTTTATGTTGAATGTGTCATACCTGTGTCAATTTG	2100
LCMV-P42_LP	AAGGTGTTATTGAGTGCAAAATTCAGTTTTATGTTGAATGTGTCATACCTGTGTCAATTTG	2100
LCMV-P52_LP	AAGGTGTTATTGAGTGCAAAATTCAGTTTTATGTTGAATGTGTCATACCTGTGTCAATTTG	2100
LCMV-P91_LP	AAGGTGTTATTGAGTGCAAAATTCAGTTTTATGTTGAATGTGTCATACCTGTGTCAATTTG	2100
LCMV-P52-1_LP	AAGGTGTTATTGAGTGCAAAATTCAGTTTTATGTTGAATGTGTCATACCTGTGTCAATTTG	2100
LCMV-P52-1.3_LP	AAGGTGTTATTGAGTGCAAAATTCAGTTTTATGTTGAATGTGTCATACCTGTGTCAATTTG	2100
LCMV-P52-2.1_LP	AAGGTGTTATTGAGTGCAAAATTCAGTTTTATGTTGAATGTGTCATACCTGTGTCAATTTG	2100

LCMV-WE_LP	ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCCTTT	2160
LCMV-P42_LP	ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCCTTT	2160
LCMV-P52_LP	ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCCTTT	2160
LCMV-P91_LP	ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCCTTT	2160
LCMV-P52-1_LP	ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCCTTT	2160
LCMV-P52-1.3_LP	ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCCTTT	2160
LCMV-P52-2.1_LP	ATCACAAAGGAGACCCCTGATAGATTGACAGATCAGATAAAATGTTTTGAAAAGTTCCTTT	2160

LCMV-WE_LP	GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG	2220
LCMV-P42_LP	GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG	2220
LCMV-P52_LP	GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG	2220
LCMV-P91_LP	GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG	2220
LCMV-P52-1_LP	GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG	2220
LCMV-P52-1.3_LP	GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG	2220
LCMV-P52-2.1_LP	GAGCCCAAGAGTGAGTTTGGTTTCTTTGTCAACCCTAAGGAAACAATCACACCCGAAGAG	2220

LCMV-WE_LP	GAATGTGTTTTTTATGAACAAATCAAGAAGTTCACCGGTAAGATATTGATTGTGTCAGCAT	2280
LCMV-P42_LP	GAATGTGTTTTTTATGAACAAATCAAGAAGTTCACCGGTAAGATATTGATTGTGTCAGCAT	2280
LCMV-P52_LP	GAATGTGTTTTTTATGAACAAATCAAGAAGTTCACCGGTAAGATATTGATTGTGTCAGCAT	2280
LCMV-P91_LP	GAATGTGTTTTTTATGAACAAATCAAGAAGTTCACCGGTAAGATATTGATTGTGTCAGCAT	2280
LCMV-P52-1_LP	GAATGTGTTTTTTATGAACAAATCAAGAAGTTCACCGGTAAGATATTGATTGTGTCAGCAT	2280
LCMV-P52-1.3_LP	GAATGTGTTTTTTATGAACAAATCAAGAAGTTCACCGGTAAGATATTGATTGTGTCAGCAT	2280
LCMV-P52-2.1_LP	GAATGTGTTTTTTATGAACAAATCAAGAAGTTCACCGGTAAGATATTGATTGTGTCAGCAT	2280

LCMV-WE_LP	TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC	2340
LCMV-P42_LP	TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC	2340
LCMV-P52_LP	TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC	2340
LCMV-P91_LP	TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC	2340
LCMV-P52-1_LP	TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC	2340
LCMV-P52-1.3_LP	TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC	2340
LCMV-P52-2.1_LP	TCAACCCCTGGTGTTAATTTAGAGATCTTTAGCATGATGGTATCTTCATTCAACAATGGC	2340

Figure 26 (cont'd)

LCMV-WE_LP	ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA	2400
LCMV-P42_LP	ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA	2400
LCMV-P52_LP	ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA	2400
LCMV-P91_LP	ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA	2400
LCMV-P52-1_LP	ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA	2400
LCMV-P52-2.1_LP	ACCTTAATTCTAAAAGGGGAGAAAAGGCTCAACAATCTGGACCCCATGACCAACTCTGGA	2400

LCMV-WE_LP	TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT	2460
LCMV-P42_LP	TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT	2460
LCMV-P52_LP	TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT	2460
LCMV-P91_LP	TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT	2460
LCMV-P52-1_LP	TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT	2460
LCMV-P52-2.1_LP	TGTGCGACAGCATTAGATCTCGCAAGCAACAAAAGTGTGGTTGTCAATAAACATCTGAAT	2460

LCMV-WE_LP	GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTAGTCTGTGAGCCAAATT	2520
LCMV-P42_LP	GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTAGTCTGTGAGCCAAATT	2520
LCMV-P52_LP	GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTAGTCTGTGAGCCAAATT	2520
LCMV-P91_LP	GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTAGTCTGTGAGCCAAATT	2520
LCMV-P52-1_LP	GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTAGTCTGTGAGCCAAATT	2520
LCMV-P52-2.1_LP	GGAGAACGGCTTTTGGAGTATGATTTTAACAAATTGCTTGTAGTCTGTGAGCCAAATT	2520

LCMV-WE_LP	ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG	2580
LCMV-P42_LP	ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG	2580
LCMV-P52_LP	ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG	2580
LCMV-P91_LP	ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG	2580
LCMV-P52-1_LP	ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG	2580
LCMV-P52-2.1_LP	ACAGAGGGCTTCATGAGGAAACAAAAGTATAAGCTGAGACACTCAGATTACGAATATAAG	2580

LCMV-WE_LP	GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG	2640
LCMV-P42_LP	GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG	2640
LCMV-P52_LP	GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG	2640
LCMV-P91_LP	GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG	2640
LCMV-P52-1_LP	GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG	2640
LCMV-P52-2.1_LP	GTCTCAAAGCTTGTCTCTAGATTAGTCATCGGTTCCAGGAAAACAGAAGTAGACAAATTG	2640

LCMV-WE_LP	GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT	2700
LCMV-P42_LP	GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT	2700
LCMV-P52_LP	GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT	2700
LCMV-P91_LP	GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT	2700
LCMV-P52-1_LP	GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT	2700
LCMV-P52-2.1_LP	GAAGATGATCCGGTAGATGTGTGTTTCGAGGGGGAGGAGGAGACAAGTTTTTTCAGGAGT	2700

LCMV-WE_LP	TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCAC TAGGCTTAATGAA	2760
LCMV-P42_LP	TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCAC TAGGCTTAATGAA	2760
LCMV-P52_LP	TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCAC TAGGCTTAATGAA	2760
LCMV-P91_LP	TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCAC TAGGCTTAATGAA	2760
LCMV-P52-1_LP	TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCAC TAGGCTTAATGAA	2760
LCMV-P52-2.1_LP	TTAGAAGATAAGGTCAGCTCCACAATAACACGGTATAATAGAGGCAC TAGGCTTAATGAA	2760

LCMV-WE_LP	GGGCAAGGGGAGGGAGAAATTCAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG	2820
LCMV-P42_LP	GGGCAAGGGGAGGGAGAAATTCAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG	2820
LCMV-P52_LP	GGGCAAGGGGAGGGAGAAATTCAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG	2820
LCMV-P91_LP	GGGCAAGGGGAGGGAGAAATTCAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG	2820
LCMV-P52-1_LP	GGGCAAGGGGAGGGAGAAATTCAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG	2820
LCMV-P52-2.1_LP	GGGCAAGGGGAGGGAGAAATTCAGAACACAAAAGGACTACACCACCTTCAGATTATTTTG	2820

Figure 26 (cont'd)

LCMV-WE_LP	TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTCATTTTCATCTAGTA	2880
LCMV-P42_LP	TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTCATTTTCATCTAGTA	2880
LCMV-P52_LP	TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTCATTTTCATCTAGTA	2880
LCMV-P91_LP	TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTCATTTTCATCTAGTA	2880
LCMV-P52-1_LP	TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTCATTTTCATCTAGTA	2880
LCMV-P52-1.3_LP	TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTCATTTTCATCTAGTA	2880
LCMV-P52-2.1_LP	TCAGGTAAAAGAGCTTATCTGAGGAAAGTCATTTTATCAGAAATTCATTTTCATCTAGTA	2880

LCMV-WE_LP	GAGGACTTTGATCCATCCTGTCTCACC AATGACGACATGAGGTTTATTTGTGAGGCTGTT	2940
LCMV-P42_LP	GAGGACTTTGATCCATCCTGTCTCACC AATGACGACATGAGGTTTATTTGTGAGGCTGTT	2940
LCMV-P52_LP	GAGGACTTTGATCCATCCTGTCTCACC AATGACGACATGAGGTTTATTTGTGAGGCTGTT	2940
LCMV-P91_LP	GAGGACTTTGATCCATCCTGTCTCACC AATGACGACATGAGGTTTATTTGTGAGGCTGTT	2940
LCMV-P52-1_LP	GAGGACTTTGATCCATCCTGTCTCACC AATGACGACATGAGGTTTATTTGTGAGGCTGTT	2940
LCMV-P52-1.3_LP	GAGGACTTTGATCCATCCTGTCTCACC AATGACGACATGAGGTTTATTTGTGAGGCTGTT	2940
LCMV-P52-2.1_LP	GAGGACTTTGATCCATCCTGTCTCACC AATGACGACATGAGGTTTATTTGTGAGGCTGTT	2940

LCMV-WE_LP	GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT	3000
LCMV-P42_LP	GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT	3000
LCMV-P52_LP	GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT	3000
LCMV-P91_LP	GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT	3000
LCMV-P52-1_LP	GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT	3000
LCMV-P52-1.3_LP	GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT	3000
LCMV-P52-2.1_LP	GAAGGTTCAACAGAACTGTCACCATTGTATTTTACATCAGCTGTCAAAGAACAATGTGGT	3000

LCMV-WE_LP	CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA	3060
LCMV-P42_LP	CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA	3060
LCMV-P52_LP	CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA	3060
LCMV-P91_LP	CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA	3060
LCMV-P52-1_LP	CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA	3060
LCMV-P52-1.3_LP	CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA	3060
LCMV-P52-2.1_LP	CTGGATGAGATGGCAAGAAACCTCTGTAGAAAGTCTTCTCAGAGGGTGATTGGTTCTCA	3060

LCMV-WE_LP	TGTATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC	3120
LCMV-P42_LP	TGTATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC	3120
LCMV-P52_LP	TGTATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC	3120
LCMV-P91_LP	TGTATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC	3120
LCMV-P52-1_LP	TGTATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC	3120
LCMV-P52-1.3_LP	TGTATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC	3120
LCMV-P52-2.1_LP	TGTATGAAGATGATCTTGTACAGATGAATGCAAAATGCGTATTCAGGGAAGTACAGACAC	3120

LCMV-WE_LP	ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA	3180
LCMV-P42_LP	ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA	3180
LCMV-P52_LP	ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA	3180
LCMV-P91_LP	ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA	3180
LCMV-P52-1_LP	ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA	3180
LCMV-P52-1.3_LP	ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA	3180
LCMV-P52-2.1_LP	ATGCAGAGGCAGAGCTTAAATTTTAAATTTGACTGGGACAAATTGGAAGAAGATGTAAGA	3180

LCMV-WE_LP	ATTAGTCAAAGGGAAAGCAATTCGAACTCTAAGTAAGGCCCTTTCATTGACAAAATGC	3240
LCMV-P42_LP	ATTAGTCAAAGGGAAAGCAATTCGAACTCTAAGTAAGGCCCTTTCATTGACAAAATGC	3240
LCMV-P52_LP	ATTAGTCAAAGGGAAAGCAATTCGAACTCTAAGTAAGGCCCTTTCATTGACAAAATGC	3240
LCMV-P91_LP	ATTAGTCAAAGGGAAAGCAATTCGAACTCTAAGTAAGGCCCTTTCATTGACAAAATGC	3240
LCMV-P52-1_LP	ATTAGTCAAAGGGAAAGCAATTCGAACTCTAAGTAAGGCCCTTTCATTGACAAAATGC	3240
LCMV-P52-1.3_LP	ATTAGTCAAAGGGAAAGCAATTCGAACTCTAAGTAAGGCCCTTTCATTGACAAAATGC	3240
LCMV-P52-2.1_LP	ATTAGTCAAAGGGAAAGCAATTCGAACTCTAAGTAAGGCCCTTTCATTGACAAAATGC	3240

LCMV-WE_LP	ATGAGTGCTGCTCTAAAGAATCTGTGTTTTACTCAGAAGAATCACC AATCATACACT	3300
LCMV-P42_LP	ATGAGTGCTGCTCTAAAGAATCTGTGTTTTACTCAGAAGAATCACC AATCATACACT	3300
LCMV-P52_LP	ATGAGTGCTGCTCTAAAGAATCTGTGTTTTACTCAGAAGAATCACC AATCATACACT	3300
LCMV-P91_LP	ATGAGTGCTGCTCTAAAGAATCTGTGTTTTACTCAGAAGAATCACC AATCATACACT	3300
LCMV-P52-1_LP	ATGAGTGCTGCTCTAAAGAATCTGTGTTTTACTCAGAAGAATCACC AATCATACACT	3300
LCMV-P52-1.3_LP	ATGAGTGCTGCTCTAAAGAATCTGTGTTTTACTCAGAAGAATCACC AATCATACACT	3300
LCMV-P52-2.1_LP	ATGAGTGCTGCTCTAAAGAATCTGTGTTTTACTCAGAAGAATCACC AATCATACACT	3300

Figure 26 (cont'd)

LCMV-WE_LP	TCAGTTGGCCCTGACTCTGGGAGACTAAAAATTTGCATTGTGCATACAAAGAGCAGGTTGGG	3360
LCMV-P42_LP	TCAGTTGGCCCTGACTCTGGGAGACTAAAAATTTGCATTGTGCATACAAAGAGCAGGTTGGG	3360
LCMV-P52_LP	TCAGTTGGCCCTGACTCTGGGAGACTAAAAATTTGCATTGTGCATACAAAGAGCAGGTTGGG	3360
LCMV-P91_LP	TCAGTTGGCCCTGACTCTGGGAGACTAAAAATTTGCATTGTGCATACAAAGAGCAGGTTGGG	3360
LCMV-P52-1_LP	TCAGTTGGCCCTGACTCTGGGAGACTAAAAATTTGCATTGTGCATACAAAGAGCAGGTTGGG	3360
LCMV-P52-1.3_LP	TCAGTTGGCCCTGACTCTGGGAGACTAAAAATTTGCATTGTGCATACAAAGAGCAGGTTGGG	3360
LCMV-P52-2.1_LP	TCAGTTGGCCCTGACTCTGGGAGACTAAAAATTTGCATTGTGCATACAAAGAGCAGGTTGGG	3360

LCMV-WE_LP	GGAAATAGAGAGCTTTACATTGGGGATTGAGGACAAAAATGTTACACAAGATTGGTAGAA	3420
LCMV-P42_LP	GGAAATAGAGAGCTTTACATTGGGGATTGAGGACAAAAATGTTACACAAGATTGGTAGAA	3420
LCMV-P52_LP	GGAAATAGAGAGCTTTACATTGGGGATTGAGGACAAAAATGTTACACAAGATTGGTAGAA	3420
LCMV-P91_LP	GGAAATAGAGAGCTTTACATTGGGGATTGAGGACAAAAATGTTACACAAGATTGGTAGAA	3420
LCMV-P52-1_LP	GGAAATAGAGAGCTTTACATTGGGGATTGAGGACAAAAATGTTACACAAGATTGGTAGAA	3420
LCMV-P52-1.3_LP	GGAAATAGAGAGCTTTACATTGGGGATTGAGGACAAAAATGTTACACAAGATTGGTAGAA	3420
LCMV-P52-2.1_LP	GGAAATAGAGAGCTTTACATTGGGGATTGAGGACAAAAATGTTACACAAGATTGGTAGAA	3420

LCMV-WE_LP	GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG	3480
LCMV-P42_LP	GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG	3480
LCMV-P52_LP	GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG	3480
LCMV-P91_LP	GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG	3480
LCMV-P52-1_LP	GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG	3480
LCMV-P52-1.3_LP	GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG	3480
LCMV-P52-2.1_LP	GATTATTTTGAATCCTTTTCTAGTTTCTTTTCAGGATCTTGTTTAAACAATGACAAAGAG	3480
**** *****		
LCMV-WE_LP	TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC	3540
LCMV-P42_LP	TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC	3540
LCMV-P52_LP	TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC	3540
LCMV-P91_LP	TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC	3540
LCMV-P52-1_LP	TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC	3540
LCMV-P52-1.3_LP	TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC	3540
LCMV-P52-2.1_LP	TTTGAAAATGCAATCTTGTCAATGACTATCAATGTGAGAGAAGGGTTGTTAAACTACAGC	3540

LCMV-WE_LP	ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA	3600
LCMV-P42_LP	ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA	3600
LCMV-P52_LP	ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA	3600
LCMV-P91_LP	ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA	3600
LCMV-P52-1_LP	ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA	3600
LCMV-P52-1.3_LP	ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA	3600
LCMV-P52-2.1_LP	ATGGATCACAGCAAATGGGGACCAATGATGTGCCCATTCCTATTCTTAATGCTTCTCCAA	3600

LCMV-WE_LP	AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG	3660
LCMV-P42_LP	AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG	3660
LCMV-P52_LP	AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG	3660
LCMV-P91_LP	AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG	3660
LCMV-P52-1_LP	AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG	3660
LCMV-P52-1.3_LP	AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG	3660
LCMV-P52-2.1_LP	AATCTCAAACCTGGGTGATGATCAGTACGTGCGTTCTGGAAAAGATCATGTTAGCACCTTG	3660

LCMV-WE_LP	TTGACTTGGCATAATGCATAAACTTGTTCGAAGTCCCTTCCCTGTTGTGAATGCAATGATG	3720
LCMV-P42_LP	TTGACTTGGCATAATGCATAAACTTGTTCGAAGTCCCTTCCCTGTTGTGAATGCAATGATG	3720
LCMV-P52_LP	TTGACTTGGCATAATGCATAAACTTGTTCGAAGTCCCTTCCCTGTTGTGAATGCAATGATG	3720
LCMV-P91_LP	TTGACTTGGCATAATGCATAAACTTGTTCGAAGTCCCTTCCCTGTTGTGAATGCAATGATG	3720
LCMV-P52-1_LP	TTGACTTGGCATAATGCATAAACTTGTTCGAAGTCCCTTCCCTGTTGTGAATGCAATGATG	3720
LCMV-P52-1.3_LP	TTGACTTGGCATAATGCATAAACTTGTTCGAAGTCCCTTCCCTGTTGTGAATGCAATGATG	3720
LCMV-P52-2.1_LP	TTGACTTGGCATAATGCATAAACTTGTTCGAAGTCCCTTCCCTGTTGTGAATGCAATGATG	3720

LCMV-WE_LP	AAATCATATGTTAAATCAAACCTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG	3780
LCMV-P42_LP	AAATCATATGTTAAATCAAACCTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG	3780
LCMV-P52_LP	AAATCATATGTTAAATCAAACCTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG	3780
LCMV-P91_LP	AAATCATATGTTAAATCAAACCTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG	3780
LCMV-P52-1_LP	AAATCATATGTTAAATCAAACCTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG	3780
LCMV-P52-1.3_LP	AAATCATATGTTAAATCAAACCTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG	3780
LCMV-P52-2.1_LP	AAATCATATGTTAAATCAAACCTCAAGCTTCTCAAAGGGTCAGGAACGACTGTTACGGAG	3780

Figure 26 (cont'd)

LCMV-WE_LP	AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT	3840
LCMV-P42_LP	AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT	3840
LCMV-P52_LP	AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT	3840
LCMV-P91_LP	AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT	3840
LCMV-P52-1_LP	AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT	3840
LCMV-P52-1.3_LP	AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT	3840
LCMV-P52-2.1_LP	AGAATCTTTAGAGAGTATTTTGAAATGGGGGTGGTGCCATCTCACATATCTAGTCTCATT	3840

LCMV-WE_LP	GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAGG	3900
LCMV-P42_LP	GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAGG	3900
LCMV-P52_LP	GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAGG	3900
LCMV-P91_LP	GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAGG	3900
LCMV-P52-1_LP	GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAGG	3900
LCMV-P52-1.3_LP	GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAGG	3900
LCMV-P52-2.1_LP	GACATGGGACAGGGGATCCTACACAATGCTTCTGATTTTTACGGTTTAATTAGTGAAGG	3900

LCMV-WE_LP	TTTATCAATTATTGTATTGGTGTCTATTTTGGAGAGAGGCCAGAACCTATACATCAAGT	3960
LCMV-P42_LP	TTTATCAATTATTGTATTGGTGTCTATTTTGGAGAGAGGCCAGAACCTATACATCAAGT	3960
LCMV-P52_LP	TTTATCAATTATTGTATTGGTGTCTATTTTGGAGAGAGGCCAGAACCTATACATCAAGT	3960
LCMV-P91_LP	TTTATCAATTATTGTATTGGTGTCTATTTTGGAGAGAGGCCAGAACCTATACATCAAGT	3960
LCMV-P52-1_LP	TTTATCAATTATTGTATTGGTGTCTATTTTGGAGAGAGGCCAGAACCTATACATCAAGT	3960
LCMV-P52-1.3_LP	TTTATCAATTATTGTATTGGTGTCTATTTTGGAGAGAGGCCAGAACCTATACATCAAGT	3960
LCMV-P52-2.1_LP	TTTATCAATTATTGTATTGGTGTCTATTTTGGAGAGAGGCCAGAACCTATACATCAAGT	3960

LCMV-WE_LP	GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA	4020
LCMV-P42_LP	GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA	4020
LCMV-P52_LP	GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA	4020
LCMV-P91_LP	GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA	4020
LCMV-P52-1_LP	GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA	4020
LCMV-P52-1.3_LP	GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA	4020
LCMV-P52-2.1_LP	GATGATCAGATCACTTTATTTGACAAGAGATTGAGTGACTTAGTTGATAGTGACCCAGAA	4020

LCMV-WE_LP	GAAGTCCTTGTCTTGTCTGGAATTCCACTCTCACTTAAGTGGTTTGTGTAACAAGTTCATC	4080
LCMV-P42_LP	GAAGTCCTTGTCTTGTCTGGAATTCCACTCTCACTTAAGTGGTTTGTGTAACAAGTTCATC	4080
LCMV-P52_LP	GAAGTCCTTGTCTTGTCTGGAATTCCACTCTCACTTAAGTGGTTTGTGTAACAAGTTCATC	4080
LCMV-P91_LP	GAAGTCCTTGTCTTGTCTGGAATTCCACTCTCACTTAAGTGGTTTGTGTAACAAGTTCATC	4080
LCMV-P52-1_LP	GAAGTCCTTGTCTTGTCTGGAATTCCACTCTCACTTAAGTGGTTTGTGTAACAAGTTCATC	4080
LCMV-P52-1.3_LP	GAAGTCCTTGTCTTGTCTGGAATTCCACTCTCACTTAAGTGGTTTGTGTAACAAGTTCATC	4080
LCMV-P52-2.1_LP	GAAGTCCTTGTCTTGTCTGGAATTCCACTCTCACTTAAGTGGTTTGTGTAACAAGTTCATC	4080

LCMV-WE_LP	AGTCCAAAAAGTGTGGTTGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG	4140
LCMV-P42_LP	AGTCCAAAAAGTGTGGTTGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG	4140
LCMV-P52_LP	AGTCCAAAAAGTGTGGTTGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG	4140
LCMV-P91_LP	AGTCCAAAAAGTGTGGTTGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG	4140
LCMV-P52-1_LP	AGTCCAAAAAGTGTGGTTGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG	4140
LCMV-P52-1.3_LP	AGTCCAAAAAGTGTGGTTGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG	4140
LCMV-P52-2.1_LP	AGTCCAAAAAGTGTGGTTGGCGGTTTGCAGCGGAATTCAAATCCAGATTTTATGTGTGG	4140

LCMV-WE_LP	GGGAGGAGGTCCCTCTCCTCACGAAATTTGTGCTCGCGGCACTACACAATGTTAAGTGT	4200
LCMV-P42_LP	GGGAGGAGGTCCCTCTCCTCACGAAATTTGTGCTCGCGGCACTACACAATGTTAAGTGT	4200
LCMV-P52_LP	GGGAGGAGGTCCCTCTCCTCACGAAATTTGTGCTCGCGGCACTACACAATGTTAAGTGT	4200
LCMV-P91_LP	GGGAGGAGGTCCCTCTCCTCACGAAATTTGTGCTCGCGGCACTACACAATGTTAAGTGT	4200
LCMV-P52-1_LP	GGGAGGAGGTCCCTCTCCTCACGAAATTTGTGCTCGCGGCACTACACAATGTTAAGTGT	4200
LCMV-P52-1.3_LP	GGGAGGAGGTCCCTCTCCTCACGAAATTTGTGCTCGCGGCACTACACAATGTTAAGTGT	4200
LCMV-P52-2.1_LP	GGGAGGAGGTCCCTCTCCTCACGAAATTTGTGCTCGCGGCACTACACAATGTTAAGTGT	4200

LCMV-WE_LP	AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT	4260
LCMV-P42_LP	AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT	4260
LCMV-P52_LP	AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT	4260
LCMV-P91_LP	AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT	4260
LCMV-P52-1_LP	AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT	4260
LCMV-P52-1.3_LP	AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT	4260
LCMV-P52-2.1_LP	AAAGAACCGCATCAACTTTGTGAGACAATAGATACGATTGCTGATCAAGCTATAGCAAAAT	4260

Figure 26 (cont'd)

LCMV-WE_LP	GGAGTTCACAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATAT	4320
LCMV-P42_LP	GGAGTTCACAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATAT	4320
LCMV-P52_LP	GGAGTTCACAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATAT	4320
LCMV-P91_LP	GGAGTTCACAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATAT	4320
LCMV-P52-1_LP	GGAGTTCACAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATAT	4320
LCMV-P52-1.3_LP	GGAGTTCACAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATAT	4320
LCMV-P52-2.1_LP	GGAGTTCACAGTTTTTTTAGTAAACTGTATCCAGAGGAGGACACTGGATCTCTTGAATAT	4320

LCMV-WE_LP	GCTAATTTCCCTTTAGATCCATTCTTGTAAACACTCACACTGATGTAAGGATTGGTTA	4380
LCMV-P42_LP	GCTAATTTCCCTTTAGATCCATTCTTGTAAACACTCACACTGATGTAAGGATTGGTTA	4380
LCMV-P52_LP	GCTAATTTCCCTTTAGATCCATTCTTGTAAACACTCACACTGATGTAAGGATTGGTTA	4380
LCMV-P91_LP	GCTAATTTCCCTTTAGATCCATTCTTGTAAACACTCACACTGATGTAAGGATTGGTTA	4380
LCMV-P52-1_LP	GCTAATTTCCCTTTAGATCCATTCTTGTAAACACTCACACTGATGTAAGGATTGGTTA	4380
LCMV-P52-1.3_LP	GCTAATTTCCCTTTAGATCCATTCTTGTAAACACTCACACTGATGTAAGGATTGGTTA	4380
LCMV-P52-2.1_LP	GCTAATTTCCCTTTAGATCCATTCTTGTAAACACTCACACTGATGTAAGGATTGGTTA	4380

LCMV-WE_LP	GATGGTCTAGAGGTTATAGAATCCAAGACTCATGGAAGAAATGTTGCCAGTGAAACA	4440
LCMV-P42_LP	GATGGTCTAGAGGTTATAGAATCCAAGACTCATGGAAGAAATGTTGCCAGTGAAACA	4440
LCMV-P52_LP	GATGGTCTAGAGGTTATAGAATCCAAGACTCATGGAAGAAATGTTGCCAGTGAAACA	4440
LCMV-P91_LP	GATGGTCTAGAGGTTATAGAATCCAAGACTCATGGAAGAAATGTTGCCAGTGAAACA	4440
LCMV-P52-1_LP	GATGGTCTAGAGGTTATAGAATCCAAGACTCATGGAAGAAATGTTGCCAGTGAAACA	4440
LCMV-P52-1.3_LP	GATGGTCTAGAGGTTATAGAATCCAAGACTCATGGAAGAAATGTTGCCAGTGAAACA	4440
LCMV-P52-2.1_LP	GATGGTCTAGAGGTTATAGAATCCAAGACTCATGGAAGAAATGTTGCCAGTGAAACA	4440

LCMV-WE_LP	AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC	4500
LCMV-P42_LP	AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC	4500
LCMV-P52_LP	AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC	4500
LCMV-P91_LP	AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC	4500
LCMV-P52-1_LP	AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC	4500
LCMV-P52-1.3_LP	AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC	4500
LCMV-P52-2.1_LP	AAGATCATGAGAAAACCTGTAAGAAGACTACATCACAAACTCAAGAACGGTGAATGTAAC	4500

LCMV-WE_LP	GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA	4560
LCMV-P42_LP	GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA	4560
LCMV-P52_LP	GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA	4560
LCMV-P91_LP	GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA	4560
LCMV-P52-1_LP	GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA	4560
LCMV-P52-1.3_LP	GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA	4560
LCMV-P52-2.1_LP	GAGGAATTTTTTCTAGACCTCTTCAACAGGGAAAAGAAAGAGGCCATCCTTCAATTGGGA	4560

LCMV-WE_LP	GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG	4620
LCMV-P42_LP	GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG	4620
LCMV-P52_LP	GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG	4620
LCMV-P91_LP	GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG	4620
LCMV-P52-1_LP	GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG	4620
LCMV-P52-1.3_LP	GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG	4620
LCMV-P52-2.1_LP	GAGATTCTTGGTCTTGAGGATGATCTTAATGAGTTGGCAAGCATCAATTGGTTGAATCTG	4620

LCMV-WE_LP	AATGAAATGTTCCCATTCAGGATGTTCTGAGACAAAAAGTGGTTACCCATCAGTAATG	4680
LCMV-P42_LP	AATGAAATGTTCCCATTCAGGATGTTCTGAGACAAAAAGTGGTTACCCATCAGTAATG	4680
LCMV-P52_LP	AATGAAATGTTCCCATTCAGGATGTTCTGAGACAAAAAGTGGTTACCCATCAGTAATG	4680
LCMV-P91_LP	AATGAAATGTTCCCATTCAGGATGTTCTGAGACAAAAAGTGGTTACCCATCAGTAATG	4680
LCMV-P52-1_LP	AATGAAATGTTCCCATTCAGGATGTTCTGAGACAAAAAGTGGTTACCCATCAGTAATG	4680
LCMV-P52-1.3_LP	AATGAAATGTTCCCATTCAGGATGTTCTGAGACAAAAAGTGGTTACCCATCAGTAATG	4680
LCMV-P52-2.1_LP	AATGAAATGTTCCCATTCAGGATGTTCTGAGACAAAAAGTGGTTACCCATCAGTAATG	4680

LCMV-WE_LP	ACCTTTCAAGAGGAAAAGATCCCCTCATTTGATTAACACTCCAAAATAAGCTTTGTAGT	4740
LCMV-P42_LP	ACCTTTCAAGAGGAAAAGATCCCCTCATTTGATTAACACTCCAAAATAAGCTTTGTAGT	4740
LCMV-P52_LP	ACCTTTCAAGAGGAAAAGATCCCCTCATTTGATTAACACTCCAAAATAAGCTTTGTAGT	4740
LCMV-P91_LP	ACCTTTCAAGAGGAAAAGATCCCCTCATTTGATTAACACTCCAAAATAAGCTTTGTAGT	4740
LCMV-P52-1_LP	ACCTTTCAAGAGGAAAAGATCCCCTCATTTGATTAACACTCCAAAATAAGCTTTGTAGT	4740
LCMV-P52-1.3_LP	ACCTTTCAAGAGGAAAAGATCCCCTCATTTGATTAACACTCCAAAATAAGCTTTGTAGT	4740
LCMV-P52-2.1_LP	ACCTTTCAAGAGGAAAAGATCCCCTCATTTGATTAACACTCCAAAATAAGCTTTGTAGT	4740

Figure 26 (cont'd)

LCMV-WE_LP	AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG	4800
LCMV-P42_LP	AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG	4800
LCMV-P52_LP	AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG	4800
LCMV-P91_LP	AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG	4800
LCMV-P52-1_LP	AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG	4800
LCMV-P52-1.3_LP	AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG	4800
LCMV-P52-2.1_LP	AAGTTCACAAGAGGTGCACAGAAGCTGTTGTCAGAGGCAATCAACAAATCAGCTTTTCAG	4800

LCMV-WE_LP	AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA	4860
LCMV-P42_LP	AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA	4860
LCMV-P52_LP	AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA	4860
LCMV-P91_LP	AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA	4860
LCMV-P52-1_LP	AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA	4860
LCMV-P52-1.3_LP	AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA	4860
LCMV-P52-2.1_LP	AGTTGTGTCTCATCCGGCTTTATAGGTCTCTGTAAGACTTTAGGAAGTAGGTGTGTGAGA	4860

LCMV-WE_LP	AATAAAAACAGGGAAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA	4920
LCMV-P42_LP	AATAAAAACAGGGAAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA	4920
LCMV-P52_LP	AATAAAAACAGGGAAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA	4920
LCMV-P91_LP	AATAAAAACAGGGAAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA	4920
LCMV-P52-1_LP	AATAAAAACAGGGAAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA	4920
LCMV-P52-1.3_LP	AATAAAAACAGGGAAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA	4920
LCMV-P52-2.1_LP	AATAAAAACAGGGAAAAATATGTATATCAGAAAGGTGCTTGAAGATCTGACCATGGATGAA	4920

LCMV-WE_LP	CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA	4980
LCMV-P42_LP	CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA	4980
LCMV-P52_LP	CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA	4980
LCMV-P91_LP	CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA	4980
LCMV-P52-1_LP	CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA	4980
LCMV-P52-1.3_LP	CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA	4980
LCMV-P52-2.1_LP	CATGTCACAAGGGTTCACAAACAAGATGGTGTGATGTTGTACATTTGCGACAAGCAGAGA	4980

LCMV-WE_LP	CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT	5040
LCMV-P42_LP	CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT	5040
LCMV-P52_LP	CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT	5040
LCMV-P91_LP	CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT	5040
LCMV-P52-1_LP	CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT	5040
LCMV-P52-1.3_LP	CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT	5040
LCMV-P52-2.1_LP	CACCCAGAGGCTCACCGTGACCACATCAACCTTTTGAGGCCCTTCTCTGGGACTACATT	5040

LCMV-WE_LP	TGCATCTCATTTAGCAACTCTTTTGGAGCTGGGTGTTTGGGTTTACGAGAACCCTGTGAAA	5100
LCMV-P42_LP	TGCATCTCATTTAGCAACTCTTTTGGAGCTGGGTGTTTGGGTTTACGAGAACCCTGTGAAA	5100
LCMV-P52_LP	TGCATCTCATTTAGCAACTCTTTTGGAGCTGGGTGTTTGGGTTTACGAGAACCCTGTGAAA	5100
LCMV-P91_LP	TGCATCTCATTTAGCAACTCTTTTGGAGCTGGGTGTTTGGGTTTACGAGAACCCTGTGAAA	5100
LCMV-P52-1_LP	TGCATCTCATTTAGCAACTCTTTTGGAGCTGGGTGTTTGGGTTTACGAGAACCCTGTGAAA	5100
LCMV-P52-1.3_LP	TGCATCTCATTTAGCAACTCTTTTGGAGCTGGGTGTTTGGGTTTACGAGAACCCTGTGAAA	5100
LCMV-P52-2.1_LP	TGCATCTCATTTAGCAACTCTTTTGGAGCTGGGTGTTTGGGTTTACGAGAACCCTGTGAAA	5100

LCMV-WE_LP	GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACCTAAATCCATGTGATTATGTAGCAAGA	5160
LCMV-P42_LP	GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACCTAAATCCATGTGATTATGTAGCAAGA	5160
LCMV-P52_LP	GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACCTAAATCCATGTGATTATGTAGCAAGA	5160
LCMV-P91_LP	GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACCTAAATCCATGTGATTATGTAGCAAGA	5160
LCMV-P52-1_LP	GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACCTAAATCCATGTGATTATGTAGCAAGA	5160
LCMV-P52-1.3_LP	GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACCTAAATCCATGTGATTATGTAGCAAGA	5160
LCMV-P52-2.1_LP	GGAAAGAACGAGAGTAATTCGGCTGTTAGGCACCTAAATCCATGTGATTATGTAGCAAGA	5160

LCMV-WE_LP	AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCATCT	5220
LCMV-P42_LP	AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCATCT	5220
LCMV-P52_LP	AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCATCT	5220
LCMV-P91_LP	AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCATCT	5220
LCMV-P52-1_LP	AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCATCT	5220
LCMV-P52-1.3_LP	AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCATCT	5220
LCMV-P52-2.1_LP	AAACCTGAGAGTTCGAGACTACTAGAGGATAAAGTGAGTTTGAATCATGTAATTCATCT	5220

Figure 26 (cont'd)

LCMV-WE_LP	GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGCTCTGATGTG	5280
LCMV-P42_LP	GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGCTCTGATGTG	5280
LCMV-P52_LP	GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGCTCTGATGTG	5280
LCMV-P91_LP	GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGCTCTGATGTG	5280
LCMV-P52-1_LP	GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGCTCTGATGTG	5280
LCMV-P52-1.3_LP	GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGCTCTGATGTG	5280
LCMV-P52-2.1_LP	GTGAGGCGACTGTACCCCAAAATCTTTGAGGATCAGTTGCTCCCATTCATGCTCTGATGTG	5280

LCMV-WE_LP	AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT	5340
LCMV-P42_LP	AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT	5340
LCMV-P52_LP	AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT	5340
LCMV-P91_LP	AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT	5340
LCMV-P52-1_LP	AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT	5340
LCMV-P52-1.3_LP	AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT	5340
LCMV-P52-2.1_LP	AGCTCAAAAAATATGAGATGGAGTCCCAGGATTAATTCCTTGACCTTTGTGTGCTGATT	5340

LCMV-WE_LP	GACATCAACTCAGAGTCTTTGTCACCTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA	5400
LCMV-P42_LP	GACATCAACTCAGAGTCTTTGTCACCTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA	5400
LCMV-P52_LP	GACATCAACTCAGAGTCTTTGTCACCTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA	5400
LCMV-P91_LP	GACATCAACTCAGAGTCTTTGTCACCTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA	5400
LCMV-P52-1_LP	GACATCAACTCAGAGTCTTTGTCACCTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA	5400
LCMV-P52-1.3_LP	GACATCAACTCAGAGTCTTTGTCACCTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA	5400
LCMV-P52-2.1_LP	GACATCAACTCAGAGTCTTTGTCACCTCATTTCTCATGTTGTCAAATGGAAGAGGGACGAA	5400

LCMV-WE_LP	CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCACGGTCAGACTCAAGTTTA	5460
LCMV-P42_LP	CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCACGGTCAGACTCAAGTTTA	5460
LCMV-P52_LP	CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCACGGTCAGACTCAAGTTTA	5460
LCMV-P91_LP	CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCACGGTCAGACTCAAGTTTA	5460
LCMV-P52-1_LP	CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCACGGTCAGACTCAAGTTTA	5460
LCMV-P52-1.3_LP	CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCACGGTCAGACTCAAGTTTA	5460
LCMV-P52-2.1_LP	CATTACACTGTGCTGTTTTCTGATCTCGTCAACTCTCACCACGGTCAGACTCAAGTTTA	5460

LCMV-WE_LP	GTTGATGAATTTGTTGTGTCAGCACAAAGGGATGTCGCAAGAACTTTTTGAAGCAAGTGAT	5520
LCMV-P42_LP	GTTGATGAATTTGTTGTGTCAGCACAAAGGGATGTCGCAAGAACTTTTTGAAGCAAGTGAT	5520
LCMV-P52_LP	GTTGATGAATTTGTTGTGTCAGCACAAAGGGATGTCGCAAGAACTTTTTGAAGCAAGTGAT	5520
LCMV-P91_LP	GTTGATGAATTTGTTGTGTCAGCACAAAGGGATGTCGCAAGAACTTTTTGAAGCAAGTGAT	5520
LCMV-P52-1_LP	GTTGATGAATTTGTTGTGTCAGCACAAAGGGATGTCGCAAGAACTTTTTGAAGCAAGTGAT	5520
LCMV-P52-1.3_LP	GTTGATGAATTTGTTGTGTCAGCACAAAGGGATGTCGCAAGAACTTTTTGAAGCAAGTGAT	5520
LCMV-P52-2.1_LP	GTTGATGAATTTGTTGTGTCAGCACAAAGGGATGTCGCAAGAACTTTTTGAAGCAAGTGAT	5520

LCMV-WE_LP	TTCGAATCATTGTACGAGAGTTTGTTCGAACAGCTAGGACCTTAGGTAACTTTTTCATGG	5580
LCMV-P42_LP	TTCGAATCATTGTACGAGAGTTTGTTCGAACAGCTAGGACCTTAGGTAACTTTTTCATGG	5580
LCMV-P52_LP	TTCGAATCATTGTACGAGAGTTTGTTCGAACAGCTAGGACCTTAGGTAACTTTTTCATGG	5580
LCMV-P91_LP	TTCGAATCATTGTACGAGAGTTTGTTCGAACAGCTAGGACCTTAGGTAACTTTTTCATGG	5580
LCMV-P52-1_LP	TTCGAATCATTGTACGAGAGTTTGTTCGAACAGCTAGGACCTTAGGTAACTTTTTCATGG	5580
LCMV-P52-1.3_LP	TTCGAATCATTGTACGAGAGTTTGTTCGAACAGCTAGGACCTTAGGTAACTTTTTCATGG	5580
LCMV-P52-2.1_LP	TTCGAATCATTGTACGAGAGTTTGTTCGAACAGCTAGGACCTTAGGTAACTTTTTCATGG	5580

LCMV-WE_LP	TTCCCCATAAGGACATGATGCCATCTCAAGATGGCGCTGAAGCACTGGGACCCCTCCAA	5640
LCMV-P42_LP	TTCCCCATAAGGACATGATGCCATCTCAAGATGGCGCTGAAGCACTGGGACCCCTCCAA	5640
LCMV-P52_LP	TTCCCCATAAGGACATGATGCCATCTCAAGATGGCGCTGAAGCACTGGGACCCCTCCAA	5640
LCMV-P91_LP	TTCCCCATAAGGACATGATGCCATCTCAAGATGGCGCTGAAGCACTGGGACCCCTCCAA	5640
LCMV-P52-1_LP	TTCCCCATAAGGACATGATGCCATCTCAAGATGGCGCTGAAGCACTGGGACCCCTCCAA	5640
LCMV-P52-1.3_LP	TTCCCCATAAGGACATGATGCCATCTCAAGATGGCGCTGAAGCACTGGGACCCCTCCAA	5640
LCMV-P52-2.1_LP	TTCCCCATAAGGACATGATGCCATCTCAAGATGGCGCTGAAGCACTGGGACCCCTCCAA	5640

LCMV-WE_LP	TCATTTATTTTGAAGTGGTCAACAAGAAAAATAGAGAGGCCCATGTTTAGGAATGACTTG	5700
LCMV-P42_LP	TCATTTATTTTGAAGTGGTCAACAAGAAAAATAGAGAGGCCCATGTTTAGGAATGACTTG	5700
LCMV-P52_LP	TCATTTATTTTGAAGTGGTCAACAAGAAAAATAGAGAGGCCCATGTTTAGGAATGACTTG	5700
LCMV-P91_LP	TCATTTATTTTGAAGTGGTCAACAAGAAAAATAGAGAGGCCCATGTTTAGGAATGACTTG	5700
LCMV-P52-1_LP	TCATTTATTTTGAAGTGGTCAACAAGAAAAATAGAGAGGCCCATGTTTAGGAATGACTTG	5700
LCMV-P52-1.3_LP	TCATTTATTTTGAAGTGGTCAACAAGAAAAATAGAGAGGCCCATGTTTAGGAATGACTTG	5700
LCMV-P52-2.1_LP	TCATTTATTTTGAAGTGGTCAACAAGAAAAATAGAGAGGCCCATGTTTAGGAATGACTTG	5700

Figure 26 (cont'd)

LCMV-WE_LP	CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG	5760
LCMV-P42_LP	CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG	5760
LCMV-P52_LP	CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG	5760
LCMV-P91_LP	CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG	5760
LCMV-P52-1_LP	CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG	5760
LCMV-P52-1.3_LP	CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG	5760
LCMV-P52-2.1_LP	CAGTTTGGTTTTGGTTGGTTCTCTTATCGTGTGGGGGATGTTGTGTGTAATGCCGCTATG	5760

LCMV-WE_LP	TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTAAATCTTTAAGAGATTGTGGGAT	5820
LCMV-P42_LP	TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTAAATCTTTAAGAGATTGTGGGAT	5820
LCMV-P52_LP	TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTAAATCTTTAAGAGATTGTGGGAT	5820
LCMV-P91_LP	TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTAAATCTTTAAGAGATTGTGGGAT	5820
LCMV-P52-1_LP	TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTAAATCTTTAAGAGATTGTGGGAT	5820
LCMV-P52-1.3_LP	TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTAAATCTTTAAGAGATTGTGGGAT	5820
LCMV-P52-2.1_LP	TTAATTAAGCAGGGTTTGACAGATCCAAAAGCATTAAATCTTTAAGAGATTGTGGGAT	5820

LCMV-WE_LP	TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC	5880
LCMV-P42_LP	TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC	5880
LCMV-P52_LP	TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC	5880
LCMV-P91_LP	TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC	5880
LCMV-P52-1_LP	TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC	5880
LCMV-P52-1.3_LP	TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC	5880
LCMV-P52-2.1_LP	TACATGCTCAGCAGCACAGAGGGGATATTGGAGTTCTCAATCACAGTGGATTTCACACAC	5880

LCMV-WE_LP	AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA	5940
LCMV-P42_LP	AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA	5940
LCMV-P52_LP	AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA	5940
LCMV-P91_LP	AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA	5940
LCMV-P52-1_LP	AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA	5940
LCMV-P52-1.3_LP	AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA	5940
LCMV-P52-2.1_LP	AACCAGAACAACTGACTGCTTGAGGAAATTTTCATTGATCTTTGTGGTTAAATGCCAA	5940

LCMV-WE_LP	TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCCTCAAAGGTGAGGTT	6000
LCMV-P42_LP	TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCCTCAAAGGTGAGGTT	6000
LCMV-P52_LP	TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCCTCAAAGGTGAGGTT	6000
LCMV-P91_LP	TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCCTCAAAGGTGAGGTT	6000
LCMV-P52-1_LP	TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCCTCAAAGGTGAGGTT	6000
LCMV-P52-1.3_LP	TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCCTCAAAGGTGAGGTT	6000
LCMV-P52-2.1_LP	TTACAGAGTCCAGGTGTAGCTGATTACTTATCGTGCTCTCATTTCCTCAAAGGTGAGGTT	6000

LCMV-WE_LP	GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG	6060
LCMV-P42_LP	GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG	6060
LCMV-P52_LP	GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG	6060
LCMV-P91_LP	GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG	6060
LCMV-P52-1_LP	GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG	6060
LCMV-P52-1.3_LP	GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG	6060
LCMV-P52-2.1_LP	GACAGGAGATTATTAGATGAGTGTCTCAATCTGTTGAGGACAGACCCCATCTTTAAAGCG	6060

LCMV-WE_LP	AATGATGGAGTCTTTGACATTAGGTCTCAAGAGTTTGAAGATTACATGGAAGACCCCTTTG	6120
LCMV-P42_LP	AATGATGGAGTCTTTGACATTAGGTCTCAAGAGTTTGAAGATTACATGGAAGACCCCTTTG	6120
LCMV-P52_LP	AATGATGGAGTCTTTGACATTAGGTCTCAAGAGTTTGAAGATTACATGGAAGACCCCTTTG	6120
LCMV-P91_LP	AATGATGGAGTCTTTGACATTAGGTCTCAAGAGTTTGAAGATTACATGGAAGACCCCTTTG	6120
LCMV-P52-1_LP	AATGATGGAGTCTTTGACATTAGGTCTCAAGAGTTTGAAGATTACATGGAAGACCCCTTTG	6120
LCMV-P52-1.3_LP	AATGATGGAGTCTTTGACATTAGGTCTCAAGAGTTTGAAGATTACATGGAAGACCCCTTTG	6120
LCMV-P52-2.1_LP	AATGATGGAGTCTTTGACATTAGGTCTCAAGAGTTTGAAGATTACATGGAAGACCCCTTTG	6120

LCMV-WE_LP	ACACTTGGTGATTCACTAGAAGTTGAAGTAAAGTTCTAGAAGGATTCTGAATGAGATC	6180
LCMV-P42_LP	ACACTTGGTGATTCACTAGAAGTTGAAGTAAAGTTCTAGAAGGATTCTGAATGAGATC	6180
LCMV-P52_LP	ACACTTGGTGATTCACTAGAAGTTGAAGTAAAGTTCTAGAAGGATTCTGAATGAGATC	6180
LCMV-P91_LP	ACACTTGGTGATTCACTAGAAGTTGAAGTAAAGTTCTAGAAGGATTCTGAATGAGATC	6180
LCMV-P52-1_LP	ACACTTGGTGATTCACTAGAAGTTGAAGTAAAGTTCTAGAAGGATTCTGAATGAGATC	6180
LCMV-P52-1.3_LP	ACACTTGGTGATTCACTAGAAGTTGAAGTAAAGTTCTAGAAGGATTCTGAATGAGATC	6180
LCMV-P52-2.1_LP	ACACTTGGTGATTCACTAGAAGTTGAAGTAAAGTTCTAGAAGGATTCTGAATGAGATC	6180

Figure 26 (cont'd)

LCMV-WE_LP	AAATCTACTGACCTTTGAGAGGATAGGGCCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG	6240
LCMV-P42_LP	AAATCTACTGACCTTTGAGAGGATAGGGCCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG	6240
LCMV-P52_LP	AAATCTACTGACCTTTGAGAGGATAGGGCCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG	6240
LCMV-P91_LP	AAATCTACTGACCTTTGAGAGGATAGGGCCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG	6240
LCMV-P52-1_LP	AAATCTACTGACCTTTGAGAGGATAGGGCCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG	6240
LCMV-P52-1.3_LP	AAATCTACTGACCTTTGAGAGGATAGGGCCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG	6240
LCMV-P52-2.1_LP	AAATCTACTGACCTTTGAGAGGATAGGGCCCTGAGTGGGAACCTGTGCCTCTGACCATAAGG	6240

LCMV-WE_LP	AAGGGTGCCCTCTTTGAGGGGAGGAACCTTTGTTTTCAGAAATATCTCTGTGAAATTTGGAGACA	6300
LCMV-P42_LP	AAGGGTGCCCTCTTTGAGGGGAGGAACCTTTGTTTTCAGAAATATCTCTGTGAAATTTGGAGACA	6300
LCMV-P52_LP	AAGGGTGCCCTCTTTGAGGGGAGGAACCTTTGTTTTCAGAAATATCTCTGTGAAATTTGGAGACA	6300
LCMV-P91_LP	AAGGGTGCCCTCTTTGAGGGGAGGAACCTTTGTTTTCAGAAATATCTCTGTGAAATTTGGAGACA	6300
LCMV-P52-1_LP	AAGGGTGCCCTCTTTGAGGGGAGGAACCTTTGTTTTCAGAAATATCTCTGTGAAATTTGGAGACA	6300
LCMV-P52-1.3_LP	AAGGGTGCCCTCTTTGAGGGGAGGAACCTTTGTTTTCAGAAATATCTCTGTGAAATTTGGAGACA	6300
LCMV-P52-2.1_LP	AAGGGTGCCCTCTTTGAGGGGAGGAACCTTTGTTTTCAGAAATATCTCTGTGAAATTTGGAGACA	6300

LCMV-WE_LP	AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGAAAAATTTGGTGATGTCCCTC	6360
LCMV-P42_LP	AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGAAAAATTTGGTGATGTCCCTC	6360
LCMV-P52_LP	AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGAAAAATTTGGTGATGTCCCTC	6360
LCMV-P91_LP	AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGAAAAATTTGGTGATGTCCCTC	6360
LCMV-P52-1_LP	AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGAAAAATTTGGTGATGTCCCTC	6360
LCMV-P52-1.3_LP	AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGAAAAATTTGGTGATGTCCCTC	6360
LCMV-P52-2.1_LP	AAGGACATGAGGGTCTTTCTGGCAGAGCTCGAGGGCTGTGAAAAATTTGGTGATGTCCCTC	6360

LCMV-WE_LP	GGCAGCCTCCTCCTGCACCGATTGAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT	6420
LCMV-P42_LP	GGCAGCCTCCTCCTGCACCGATTGAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT	6420
LCMV-P52_LP	GGCAGCCTCCTCCTGCACCGATTGAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT	6420
LCMV-P91_LP	GGCAGCCTCCTCCTGCACCGATTGAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT	6420
LCMV-P52-1_LP	GGCAGCCTCCTCCTGCACCGATTGAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT	6420
LCMV-P52-1.3_LP	GGCAGCCTCCTCCTGCACCGATTGAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT	6420
LCMV-P52-2.1_LP	GGCAGCCTCCTCCTGCACCGATTGAGAACTGGTGAGCACTTGATGGAGTCAGAAATAAGT	6420

LCMV-WE_LP	ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG	6480
LCMV-P42_LP	ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG	6480
LCMV-P52_LP	ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG	6480
LCMV-P91_LP	ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG	6480
LCMV-P52-1_LP	ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG	6480
LCMV-P52-1.3_LP	ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG	6480
LCMV-P52-2.1_LP	ACAGTTCTTCAGGAGCTCTGCATGGACAGATCCGTCATGCTGACACCATTATCTTTTGTG	6480

LCMV-WE_LP	CCAGATTGGTTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA	6540
LCMV-P42_LP	CCAGATTGGTTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA	6540
LCMV-P52_LP	CCAGATTGGTTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA	6540
LCMV-P91_LP	CCAGATTGGTTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA	6540
LCMV-P52-1_LP	CCAGATTGGTTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA	6540
LCMV-P52-1.3_LP	CCAGATTGGTTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA	6540
LCMV-P52-2.1_LP	CCAGATTGGTTTCACCTTCAGAGATTGTAGGCTCTGCTTCAGCAGGTCAAAGAACACTGTA	6540

LCMV-WE_LP	ATGTATGAGACAACCTGGGGGAGGTTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG	6600
LCMV-P42_LP	ATGTATGAGACAACCTGGGGGAGGTTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG	6600
LCMV-P52_LP	ATGTATGAGACAACCTGGGGGAGGTTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG	6600
LCMV-P91_LP	ATGTATGAGACAACCTGGGGGAGGTTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG	6600
LCMV-P52-1_LP	ATGTATGAGACAACCTGGGGGAGGTTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG	6600
LCMV-P52-1.3_LP	ATGTATGAGACAACCTGGGGGAGGTTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG	6600
LCMV-P52-2.1_LP	ATGTATGAGACAACCTGGGGGAGGTTTCAGACTCAAGGGGAAATCCTGTGACGATTGGCTG	6600

LCMV-WE_LP	GCGGAGCGGGTGGCCGAGGAGATCGACTAG	6630
LCMV-P42_LP	GCGGAGCGGGTGGCCGAGGAGATCGACTAG	6630
LCMV-P52_LP	GCGGAGCGGGTGGCCGAGGAGATCGACTAG	6630
LCMV-P91_LP	GCGGAGCGGGTGGCCGAGGAGATCGACTAG	6630
LCMV-P52-1_LP	GCGGAGCGGGTGGCCGAGGAGATCGACTAG	6630
LCMV-P52-1.3_LP	GCGGAGCGGGTGGCCGAGGAGATCGACTAG	6630
LCMV-P52-2.1_LP	GCGGAGCGGGTGGCCGAGGAGATCGACTAG	6633

LCMV-WE_LP	SEQ ID NO: 15	
LCMV-P42_LP	SEQ ID NO: 23	
LCMV-P52_LP	SEQ ID NO: 31	
LCMV-P91_LP	SEQ ID NO: 39	
LCMV-P52-1_LP	SEQ ID NO: 47	
LCMV-P52-1.3_LP	SEQ ID NO: 55	
LCMV-P52-2.1_LP	SEQ ID NO: 63	

Figure 26 (cont'd)

H.

Source: 1-7235 Segment = L
 Protein: RNA-directed RNA polymerase L
 Gene: LP
 Gene: 574-7203 complement
 Sequence Alignment: Aminoacid

LCMV-WE_LP	MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC	60
LCMV-P42_LP	MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC	60
LCMV-P52_LP	MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC	60
LCMV-P91_LP:	MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC	60
LCMV-P52-1_LP	MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC	60
LCMV-P52-1.3_LP	MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC	60
LCMV-P52-2.1_LP	MDETIADLRELCLNYIEQDERLSRQKLNFLGQREPRMVLIEGLKLLSRCIEIDSADKSGC	60

LCMV-WE_LP	IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT	120
LCMV-P42_LP	IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT	120
LCMV-P52_LP	IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT	120
LCMV-P91_LP:	IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT	120
LCMV-P52-1_LP	IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT	120
LCMV-P52-1.3_LP	IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT	120
LCMV-P52-2.1_LP	IHNHDDKSVETILIDSGIVCPGLPLIIPDGYKLIDNSLILLECFVRSTPASFEKKFIEDT	120

LCMV-WE_LP	NKLACIKEDLAVAGITLVPIDGRCDDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE	180
LCMV-P42_LP	NKLACIKEDLAVAGITLVPIDGRCDDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE	180
LCMV-P52_LP	NKLACIKEDLAVAGITLVPIDGRCDDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE	180
LCMV-P91_LP:	NKLACIKEDLAVAGITLVPIDGRCDDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE	180
LCMV-P52-1_LP	NKLACIKEDLAVAGITLVPIDGRCDDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE	180
LCMV-P52-1.3_LP	NKLACIKEDLAVAGITLVPIDGRCDDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE	180
LCMV-P52-2.1_LP	NKLACIKEDLAVAGITLVPIDGRCDDYDNSFMPEWVNFKFRDLLFKLLEYSSQDEKVFEE	180

LCMV-WE_LP	SEYFRLCESLKTITVDDRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFEGINS	240
LCMV-P42_LP	SEYFRLCESLKTITVDDRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFEGINS	240
LCMV-P52_LP	SEYFRLCESLKTITVDDRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFEGINS	240
LCMV-P91_LP:	SEYFRLCESLKTITVDDRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFEGINS	240
LCMV-P52-1_LP	SEYFRLCESLKTITVDDRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFEGINS	240
LCMV-P52-1.3_LP	SEYFRLCESLKTITVDDRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFEGINS	240
LCMV-P52-2.1_LP	SEYFRLCESLKTITVDDRSGMDSMKILKDARSFHNDEIMKMCHDGVNPNMSCDDVVFEGINS	240

LCMV-WE_LP	FFGRFRDLLNGKIKRNFQKVPGGGLIKEFSELYETLTNDNDILMLSKEAVESCPLMRFI	300
LCMV-P42_LP	FFGRFRDLLNGKIKRNFQKVPGGGLIKEFSELYETLTNDNDILMLSKEAVESCPLMRFI	300
LCMV-P52_LP	FFGRFRDLLNGKIKRNFQKVPGGGLIKEFSELYETLTNDNDILMLSKEAVESCPLMRFI	300
LCMV-P91_LP:	FFGRFRDLLNGKIKRNFQKVPGGGLIKEFSELYETLTNDNDILMLSKEAVESCPLMRFI	300
LCMV-P52-1_LP	FFGRFRDLLNGKIKRNFQKVPGGGLIKEFSELYETLTNDNDILMLSKEAVESCPLMRFI	300
LCMV-P52-1.3_LP	FFGRFRDLLNGKIKRNFQKVPGGGLIKEFSELYETLTNDNDILMLSKEAVESCPLMRFI	300
LCMV-P52-2.1_LP	FFGRFRDLLNGKIKRNFQKVPGGGLIKEFSELYETLTNDNDILMLSKEAVESCPLMRFI	300

LCMV-WE_LP	TAETHGHERGSDANTEYERLLSMLNKVKSCLKLLNTRRRQLNLDVLCCLSSLIKQSI SKGL	360
LCMV-P42_LP	TAETHGHERGSDANTEYERLLSMLNKVKSCLKLLNTRRRQLNLDVLCCLSSLIKQSI SKGL	360
LCMV-P52_LP	TAETHGHERGSDANTEYERLLSMLNKVKSCLKLLNTRRRQLNLDVLCCLSSLIKQSI SKGL	360
LCMV-P91_LP:	TAETHGHERGSDANTEYERLLSMLNKVKSCLKLLNTRRRQLNLDVLCCLSSLIKQSI SKGL	360
LCMV-P52-1_LP	TAETHGHERGSDANTEYERLLSMLNKVKSCLKLLNTRRRQLNLDVLCCLSSLIKQSI SKGL	360
LCMV-P52-1.3_LP	TAETHGHERGSDANTEYERLLSMLNKVKSCLKLLNTRRRQLNLDVLCCLSSLIKQSI SKGL	360
LCMV-P52-2.1_LP	TAETHGHERGSDANTEYERLLSMLNKVKSCLKLLNTRRRQLNLDVLCCLSSLIKQSI SKGL	360

LCMV-WE_LP	ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLNRRKSRVHKKASLDELFRVSINEFIAK	420
LCMV-P42_LP	ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLNRRKSRVHKKASLDELFRVSINEFIAK	420
LCMV-P52_LP	ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLNRRKSRVHKKASLDELFRVSINEFIAK	420
LCMV-P91_LP:	ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLNRRKSRVHKKASLDELFRVSINEFIAK	420
LCMV-P52-1_LP	ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLNRRKSRVHKKASLDELFRVSINEFIAK	420
LCMV-P52-1.3_LP	ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLNRRKSRVHKKASLDELFRVSINEFIAK	420
LCMV-P52-2.1_LP	ENDKHWVGCCYSSVNDRLVSLQSTKEEFMRLLNRRKSRVHKKASLDELFRVSINEFIAK	420

Figure 26 (cont'd)

LCMV-WE_LP	IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRACTHPVMHYTKFEDYTFQPNIEQ	480
LCMV-P42_LP	IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRACTHPVMHYTKFEDYTFQPNIEQ	480
LCMV-P52_LP	IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRACTHPVMHYTKFEDYTFQPNIEQ	480
LCMV-P91_LP:	IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRACTHPVMHYTKFEDYTFQPNIEQ	480
LCMV-P52-1_LP	IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRACTHPVMHYTKFEDYTFQPNIEQ	480
LCMV-P52-1.3_LP	IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRACTHPVMHYTKFEDYTFQPNIEQ	480
LCMV-P52-2.1_LP	IQKCLSTVGLSFEHYGLSECLVQECHIPFAEFENFMRACTHPVMHYTKFEDYTFQPNIEQ	480

LCMV-WE_LP	LRGLQSLRKLSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH	540
LCMV-P42_LP	LRGLQSLRKLSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH	540
LCMV-P52_LP	LRGLQSLRKLSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH	540
LCMV-P91_LP:	LRGLQSLRKLSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH	540
LCMV-P52-1_LP	LRGLQSLRKLSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH	540
LCMV-P52-1.3_LP	LRGLQSLRKLSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH	540
LCMV-P52-2.1_LP	LRGLQSLRKLSVCLALTNMKTSSVARLRQNQLGSVRYQVVECKEVFCQIIKLDSEEH	540

LCMV-WE_LP	LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK	600
LCMV-P42_LP	LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK	600
LCMV-P52_LP	LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK	600
LCMV-P91_LP:	LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK	600
LCMV-P52-1_LP	LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK	600
LCMV-P52-1.3_LP	LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK	600
LCMV-P52-2.1_LP	LLYQKTGESSRCYSIQGPDGHLISFYADPKRFFLPIFSDEVLHNMIDTMISWIRSCPDLK	600

LCMV-WE_LP	DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMIAIVSDFSSTSLMDKLEDLITPA	660
LCMV-P42_LP	DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMIAIVSDFSSTSLMDKLEDLITPA	660
LCMV-P52_LP	DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMIAIVSDFSSTSLMDKLEDLITPA	660
LCMV-P91_LP:	DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMIAIVSDFSSTSLMDKLEDLITPA	660
LCMV-P52-1_LP	DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMIAIVSDFSSTSLMDKLEDLITPA	660
LCMV-P52-1.3_LP	DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMIAIVSDFSSTSLMDKLEDLITPA	660
LCMV-P52-2.1_LP	DSLIDIETALRTLILLMLTNPTKRNQKQVQNIRYLVMIAIVSDFSSTSLMDKLEDLITPA	660

LCMV-WE_LP	EKVYRLLRFLIRTI FGTGEKVLLSAKFKFMNLSYLCHELTKEPDRDLDQIKCFEKEFF	720
LCMV-P42_LP	EKVYRLLRFLIRTI FGTGEKVLLSAKFKFMNLSYLCHELTKEPDRDLDQIKCFEKEFF	720
LCMV-P52_LP	EKVYRLLRFLIRTI FGTGEKVLLSAKFKFMNLSYLCHELTKEPDRDLDQIKCFEKEFF	720
LCMV-P91_LP:	EKVYRLLRFLIRTI FGTGEKVLLSAKFKFMNLSYLCHELTKEPDRDLDQIKCFEKEFF	720
LCMV-P52-1_LP	EKVYRLLRFLIRTI FGTGEKVLLSAKFKFMNLSYLCHELTKEPDRDLDQIKCFEKEFF	720
LCMV-P52-1.3_LP	EKVYRLLRFLIRTI FGTGEKVLLSAKFKFMNLSYLCHELTKEPDRDLDQIKCFEKEFF	720
LCMV-P52-2.1_LP	EKVYRLLRFLIRTI FGTGEKVLLSAKFKFMNLSYLCHELTKEPDRDLDQIKCFEKEFF	720

LCMV-WE_LP	EPKSEFGFFVNPKEITITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMVVSFFNNG	780
LCMV-P42_LP	EPKSEFGFFVNPKEITITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMVVSFFNNG	780
LCMV-P52_LP	EPKSEFGFFVNPKEITITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMVVSFFNNG	780
LCMV-P91_LP:	EPKSEFGFFVNPKEITITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMVVSFFNNG	780
LCMV-P52-1_LP	EPKSEFGFFVNPKEITITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMVVSFFNNG	780
LCMV-P52-1.3_LP	EPKSEFGFFVNPKEITITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMVVSFFNNG	780
LCMV-P52-2.1_LP	EPKSEFGFFVNPKEITITPEEECVFYEQMKKFTGKDIDCQHSTPGVNLEIFSMVVSFFNNG	780

LCMV-WE_LP	TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVKHLNGERLLEYDFNKLLVSAVSQI	840
LCMV-P42_LP	TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVKHLNGERLLEYDFNKLLVSAVSQI	840
LCMV-P52_LP	TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVKHLNGERLLEYDFNKLLVSAVSQI	840
LCMV-P91_LP:	TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVKHLNGERLLEYDFNKLLVSAVSQI	840
LCMV-P52-1_LP	TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVKHLNGERLLEYDFNKLLVSAVSQI	840
LCMV-P52-1.3_LP	TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVKHLNGERLLEYDFNKLLVSAVSQI	840
LCMV-P52-2.1_LP	TLILKGEKRLNNLDPMTNSGCATALDLASNKSVVVKHLNGERLLEYDFNKLLVSAVSQI	840

LCMV-WE_LP	TEGFMRKQKYKLHSDYKYKSVKLSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFRRS	900
LCMV-P42_LP	TEGFMRKQKYKLHSDYKYKSVKLSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFRRS	900
LCMV-P52_LP	TEGFMRKQKYKLHSDYKYKSVKLSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFRRS	900
LCMV-P91_LP:	TEGFMRKQKYKLHSDYKYKSVKLSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFRRS	900
LCMV-P52-1_LP	TEGFMRKQKYKLHSDYKYKSVKLSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFRRS	900
LCMV-P52-1.3_LP	TEGFMRKQKYKLHSDYKYKSVKLSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFRRS	900
LCMV-P52-2.1_LP	TEGFMRKQKYKLHSDYKYKSVKLSRLVIGSRKTEVDKLEDDPVDVCFEGEEETSFRRS	900

Figure 26 (cont'd)

LCMV-WE_LP	LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV	960
LCMV-P42_LP	LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV	960
LCMV-P52_LP	LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV	960
LCMV-P91_LP:	LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV	960
LCMV-P52-1_LP	LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV	960
LCMV-P52-1.3_LP	LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV	960
LCMV-P52-2.1_LP	LEDKVSSTITRYNRGTRLNEGQGEFKNKGLHHLQIILSGKRAYLRKVILSEISFHLV	960

LCMV-WE_LP	EDFDPSCLTNDMMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS	1020
LCMV-P42_LP	EDFDPSCLTNDMMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS	1020
LCMV-P52_LP	EDFDPSCLTNDMMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS	1020
LCMV-P91_LP:	EDFDPSCLTNDMMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS	1020
LCMV-P52-1_LP	EDFDPSCLTNDMMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS	1020
LCMV-P52-1.3_LP	EDFDPSCLTNDMMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS	1020
LCMV-P52-2.1_LP	EDFDPSCLTNDMMRFICEAVEGSTELSPLYFTSAVKEQCGLDEMARNLCRKFFSEGDWFS	1020

LCMV-WE_LP	CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTTC	1080
LCMV-P42_LP	CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTTC	1080
LCMV-P52_LP	CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTTC	1080
LCMV-P91_LP:	CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTTC	1080
LCMV-P52-1_LP	CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTTC	1080
LCMV-P52-1.3_LP	CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTTC	1080
LCMV-P52-2.1_LP	CMKMILLQMNANAYSCKYRHMQRQSLNFKFDWDKLEEDVRISERESNSESLSKALSLTTC	1080

LCMV-WE_LP	MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE	1140
LCMV-P42_LP	MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE	1140
LCMV-P52_LP	MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE	1140
LCMV-P91_LP:	MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE	1140
LCMV-P52-1_LP	MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE	1140
LCMV-P52-1.3_LP	MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE	1140
LCMV-P52-2.1_LP	MSAALKNLCFYSEESPTSYSVGPDSGRLKFALSYKEQVGGNRELYIGDLRTKMFTRLVE	1140

LCMV-WE_LP	DYFESFSSFFSGSCLNNDKEFENAILSMITINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ	1200
LCMV-P42_LP	DYFESFSSFFSGSCLNNDKEFENAILSMITINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ	1200
LCMV-P52_LP	DYFESFSSFFSGSCLNNDKEFENAILSMITINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ	1200
LCMV-P91_LP:	DYFESFSSFFSGSCLNNDKEFENAILSMITINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ	1200
LCMV-P52-1_LP	DYFESFSSFFSGSCLNNDKEFENAILSMITINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ	1200
LCMV-P52-1.3_LP	DYFESFSSFFSGSCLNNDKEFENAILSMITINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ	1200
LCMV-P52-2.1_LP	DYFESFSSFFSGSCLNNDKEFENAILSMITINVREGLLNYSMDHSKWGPMMCPFLFLMLLQ	1200

LCMV-WE_LP	NLKLGDQYVRSRGKDHVSTLLTWHMHKLVEVFPFVNVNMMKSYVKSCLKLLKSGSTTVTE	1260
LCMV-P42_LP	NLKLGDQYVRSRGKDHVSTLLTWHMHKLVEVFPFVNVNMMKSYVKSCLKLLKSGSTTVTE	1260
LCMV-P52_LP	NLKLGDQYVRSRGKDHVSTLLTWHMHKLVEVFPFVNVNMMKSYVKSCLKLLKSGSTTVTE	1260
LCMV-P91_LP:	NLKLGDQYVRSRGKDHVSTLLTWHMHKLVEVFPFVNVNMMKSYVKSCLKLLKSGSTTVTE	1260
LCMV-P52-1_LP	NLKLGDQYVRSRGKDHVSTLLTWHMHKLVEVFPFVNVNMMKSYVKSCLKLLKSGSTTVTE	1260
LCMV-P52-1.3_LP	NLKLGDQYVRSRGKDHVSTLLTWHMHKLVEVFPFVNVNMMKSYVKSCLKLLKSGSTTVTE	1260
LCMV-P52-2.1_LP	NLKLGDQYVRSRGKDHVSTLLTWHMHKLVEVFPFVNVNMMKSYVKSCLKLLKSGSTTVTE	1260

LCMV-WE_LP	RIFREYFEMGVVPSHISSLIDMQGQILHNASDFYGLISERFINYCIGVIFGERPEAYTSS	1320
LCMV-P42_LP	RIFREYFEMGVVPSHISSLIDMQGQILHNASDFYGLISERFINYCIGVIFGERPEAYTSS	1320
LCMV-P52_LP	RIFREYFEMGVVPSHISSLIDMQGQILHNASDFYGLISERFINYCIGVIFGERPEAYTSS	1320
LCMV-P91_LP:	RIFREYFEMGVVPSHISSLIDMQGQILHNASDFYGLISERFINYCIGVIFGERPEAYTSS	1320
LCMV-P52-1_LP	RIFREYFEMGVVPSHISSLIDMQGQILHNASDFYGLISERFINYCIGVIFGERPEAYTSS	1320
LCMV-P52-1.3_LP	RIFREYFEMGVVPSHISSLIDMQGQILHNASDFYGLISERFINYCIGVIFGERPEAYTSS	1320
LCMV-P52-2.1_LP	RIFREYFEMGVVPSHISSLIDMQGQILHNASDFYGLISERFINYCIGVIFGERPEAYTSS	1320

LCMV-WE_LP	DDQITLFDKRLSDLVSDPPEEVLVLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW	1380
LCMV-P42_LP	DDQITLFDKRLSDLVSDPPEEVLVLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW	1380
LCMV-P52_LP	DDQITLFDKRLSDLVSDPPEEVLVLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW	1380
LCMV-P91_LP:	DDQITLFDKRLSDLVSDPPEEVLVLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW	1380
LCMV-P52-1_LP	DDQITLFDKRLSDLVSDPPEEVLVLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW	1380
LCMV-P52-1.3_LP	DDQITLFDKRLSDLVSDPPEEVLVLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW	1380
LCMV-P52-2.1_LP	DDQITLFDKRLSDLVSDPPEEVLVLEFHSLSGLLNKFISPKSVVGRFAAEFKSRFYVW	1380

Figure 26 (cont'd)

LCMV-WE_LP	GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIDQATANGVPVFLVNCIQRRITDLDLLKY	1440
LCMV-P42_LP	GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIDQATANGVPVFLVNCIQRRITDLDLLKY	1440
LCMV-P52_LP	GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIDQATANGVPVFLVNCIQRRITDLDLLKY	1440
LCMV-P91_LP:	GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIDQATANGVPVFLVNCIQRRITDLDLLKY	1440
LCMV-P52-1_LP	GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIDQATANGVPVFLVNCIQRRITDLDLLKY	1440
LCMV-P52-1.3_LP	GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIDQATANGVPVFLVNCIQRRITDLDLLKY	1440
LCMV-P52-2.1_LP	GEEVPLLTKFVSAALHNVKCKEPHQLCETIDTIDQATANGVPVFLVNCIQRRITDLDLLKY	1440

LCMV-WE_LP	ANFPLDPFLLNTHTDVVDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHKKLNGECN	1500
LCMV-P42_LP	ANFPLDPFLLNTHTDVVDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHKKLNGECN	1500
LCMV-P52_LP	ANFPLDPFLLNTHTDVVDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHKKLNGECN	1500
LCMV-P91_LP:	ANFPLDPFLLNTHTDVVDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHKKLNGECN	1500
LCMV-P52-1_LP	ANFPLDPFLLNTHTDVVDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHKKLNGECN	1500
LCMV-P52-1.3_LP	ANFPLDPFLLNTHTDVVDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHKKLNGECN	1500
LCMV-P52-2.1_LP	ANFPLDPFLLNTHTDVVDWLDGSRGYRIQRLIEELCPSETKIMRKLVRRLHKKLNGECN	1500

LCMV-WE_LP	EEFFLDLFNREKKKAILQLGEILGLEDDLNELASINWLNLMFPLRMVLRQKVVPVSM	1560
LCMV-P42_LP	EEFFLDLFNREKKKAILQLGEILGLEDDLNELASINWLNLMFPLRMVLRQKVVPVSM	1560
LCMV-P52_LP	EEFFLDLFNREKKKAILQLGEILGLEDDLNELASINWLNLMFPLRMVLRQKVVPVSM	1560
LCMV-P91_LP:	EEFFLDLFNREKKKAILQLGEILGLEDDLNELASINWLNLMFPLRMVLRQKVVPVSM	1560
LCMV-P52-1_LP	EEFFLDLFNREKKKAILQLGEILGLEDDLNELASINWLNLMFPLRMVLRQKVVPVSM	1560
LCMV-P52-1.3_LP	EEFFLDLFNREKKKAILQLGEILGLEDDLNELASINWLNLMFPLRMVLRQKVVPVSM	1560
LCMV-P52-2.1_LP	EEFFLDLFNREKKKAILQLGEILGLEDDLNELASINWLNLMFPLRMVLRQKVVPVSM	1560

LCMV-WE_LP	TFQEEKIPSLIKTLQNKLCCKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRGVR	1620
LCMV-P42_LP	TFQEEKIPSLIKTLQNKLCCKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRGVR	1620
LCMV-P52_LP	TFQEEKIPSLIKTLQNKLCCKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRGVR	1620
LCMV-P91_LP:	TFQEEKIPSLIKTLQNKLCCKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRGVR	1620
LCMV-P52-1_LP	TFQEEKIPSLIKTLQNKLCCKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRGVR	1620
LCMV-P52-1.3_LP	TFQEEKIPSLIKTLQNKLCCKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRGVR	1620
LCMV-P52-2.1_LP	TFQEEKIPSLIKTLQNKLCCKFTTGAQKLLSEAINKSAFQSCVSSGFIGLCKTLGSRGVR	1620

LCMV-WE_LP	NKNRENMYIRKVLDTMDEHVTTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDWYI	1680
LCMV-P42_LP	NKNRENMYIRKVLDTMDEHVTTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDWYI	1680
LCMV-P52_LP	NKNRENMYIRKVLDTMDEHVTTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDWYI	1680
LCMV-P91_LP:	NKNRENMYIRKVLDTMDEHVTTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDWYI	1680
LCMV-P52-1_LP	NKNRENMYIRKVLDTMDEHVTTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDWYI	1680
LCMV-P52-1.3_LP	NKNRENMYIRKVLDTMDEHVTTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDWYI	1680
LCMV-P52-2.1_LP	NKNRENMYIRKVLDTMDEHVTTRVHKQDGVMLYICDKQRHPEAHRDHINLLRPLLDWYI	1680

LCMV-WE_LP	CISLSNSFELGVVWLAEPVKCKNESNSAVRHLNCPDYVARKPESSRLLEDKVSLSNHVIQS	1740
LCMV-P42_LP	CISLSNSFELGVVWLAEPVKCKNESNSAVRHLNCPDYVARKPESSRLLEDKVSLSNHVIQS	1740
LCMV-P52_LP	CISLSNSFELGVVWLAEPVKCKNESNSAVRHLNCPDYVARKPESSRLLEDKVSLSNHVIQS	1740
LCMV-P91_LP:	CISLSNSFELGVVWLAEPVKCKNESNSAVRHLNCPDYVARKPESSRLLEDKVSLSNHVIQS	1740
LCMV-P52-1_LP	CISLSNSFELGVVWLAEPVKCKNESNSAVRHLNCPDYVARKPESSRLLEDKVSLSNHVIQS	1740
LCMV-P52-1.3_LP	CISLSNSFELGVVWLAEPVKCKNESNSAVRHLNCPDYVARKPESSRLLEDKVSLSNHVIQS	1740
LCMV-P52-2.1_LP	CISLSNSFELGVVWLAEPVKCKNESNSAVRHLNCPDYVARKPESSRLLEDKVSLSNHVIQS	1740

LCMV-WE_LP	VRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVLDINSESLSLISHVVVKWRDE	1800
LCMV-P42_LP	VRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVLDINSESLSLISHVVVKWRDE	1800
LCMV-P52_LP	VRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVLDINSESLSLISHVVVKWRDE	1800
LCMV-P91_LP:	VRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVLDINSESLSLISHVVVKWRDE	1800
LCMV-P52-1_LP	VRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVLDINSESLSLISHVVVKWRDE	1800
LCMV-P52-1.3_LP	VRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVLDINSESLSLISHVVVKWRDE	1800
LCMV-P52-2.1_LP	VRLYPKIFEDQLLPFMSDVSSKNMRWSPRIKFLDLCLVLDINSESLSLISHVVVKWRDE	1800

LCMV-WE_LP	HYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFKQVYFESFVREFVATARTLGNFSW	1860
LCMV-P42_LP	HYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFKQVYFESFVREFVATARTLGNFSW	1860
LCMV-P52_LP	HYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFKQVYFESFVREFVATARTLGNFSW	1860
LCMV-P91_LP:	HYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFKQVYFESFVREFVATARTLGNFSW	1860
LCMV-P52-1_LP	HYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFKQVYFESFVREFVATARTLGNFSW	1860
LCMV-P52-1.3_LP	HYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFKQVYFESFVREFVATARTLGNFSW	1860
LCMV-P52-2.1_LP	HYTVLFSDLVNSHQSDSSLVDEFVVSSTRDVCKNFKQVYFESFVREFVATARTLGNFSW	1860

Figure 26 (cont'd)

LCMV-WE_LP	FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGGWFSYRVGDVVCNAAM	1920
LCMV-P42_LP	FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGGWFSYRVGDVVCNAAM	1920
LCMV-P52_LP	FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGGWFSYRVGDVVCNAAM	1920
LCMV-P91_LP:	FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGGWFSYRVGDVVCNAAM	1920
LCMV-P52-1_LP	FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGGWFSYRVGDVVCNAAM	1920
LCMV-P52-1.3_LP	FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGGWFSYRVGDVVCNAAM	1920
LCMV-P52-2.1_LP	FPHKDMMPSEDGAEALGPFQSFILKVVNKKIERPMFRNDLQFGGWFSYRVGDVVCNAAM	1920

LCMV-WE_LP	LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNTDCLRKFSLIFVVKCQ	1980
LCMV-P42_LP	LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNTDCLRKFSLIFVVKCQ	1980
LCMV-P52_LP	LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNTDCLRKFSLIFVVKCQ	1980
LCMV-P91_LP:	LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNTDCLRKFSLIFVVKCQ	1980
LCMV-P52-1_LP	LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNTDCLRKFSLIFVVKCQ	1980
LCMV-P52-1.3_LP	LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNTDCLRKFSLIFVVKCQ	1980
LCMV-P52-2.1_LP	LIKQGLTDPKAFKSLRDLWDYMLSSTEGILEFSITVDFTHNQNTDCLRKFSLIFVVKCQ	1980

LCMV-WE_LP	LQSPGVADYLSCHFFKGEVDRRLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL	2040
LCMV-P42_LP	LQSPGVADYLSCHFFKGEVDRRLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL	2040
LCMV-P52_LP	LQSPGVADYLSCHSFKGEVDRRLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL	2040
LCMV-P91_LP:	LQSPGVADYLSCHSFKGEVDRRLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL	2040
LCMV-P52-1_LP	LQSPGVADYLSCHFFKGEVDRRLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL	2040
LCMV-P52-1.3_LP	LQSPGVADYLSCHSFKGEVDRRLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL	2040
LCMV-P52-2.1_LP	LQSPGVADYLSCHFFKGEVDRRLDECLNLLRTDPIFKANDGVFDIRSEEFEDYMEDPL	2040

$X=T/V$		
LCMV-WE_LP	TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKCALFEGRNQVQNISVKLET	2100
LCMV-P42_LP	TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKCALFEGRNQVQNISVKLET	2100
LCMV-P52_LP	TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKCALFEGRNQVQNXSVKLET	2100
LCMV-P91_LP:	TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKCALFEGRNQVQNISVKLET	2100
LCMV-P52-1_LP	TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKCALFEGRNQVQNISVKLET	2100
LCMV-P52-1.3_LP	TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKCALFEGRNQVQNISVKLET	2100
LCMV-P52-2.1_LP	TLGDSLELELIGSRRILNEIKSTDFERIGPEWEPVPLTIRKCALFEGRNQVQNISVKLET	2100

$X=T/A$		
LCMV-WE_LP	KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMSEISTVLQELCMDRSVMLTPLSFV	2160
LCMV-P42_LP	KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMSEISTVLQELCMDRSVMLTPLSFV	2160
LCMV-P52_LP	KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMSEISTVLQELCMDRSVMLTPLSFV	2160
LCMV-P91_LP:	KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMSEISTVLQELCMDRSVMLTPLSFV	2160
LCMV-P52-1_LP	KDMRVFLAELEGCGEIGDVLGSLLLHRFRTGEHLMSEISTVLQELCMDRSVMLTPLSFV	2160
LCMV-P52-1.3_LP	KDMRVFLAELEGCGKIGDVLGSLLLHRFRTGEHLMSEISTVLQELCMDRSVMLTPLSFV	2160
LCMV-P52-2.1_LP	KDMRVFLAELEGCGEIGDVLGSLLLHRFRTGEHLMSEISTVLQELCMDRSVMLTPLSFV	2160

$X=R/K$		
LCMV-WE_LP	PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID	2209
LCMV-P42_LP	PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID	2209
LCMV-P52_LP	PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID	2209
LCMV-P91_LP:	PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID	2209
LCMV-P52-1_LP	PDWFTFRDCRLCFRSKNTVMYETTAGGRFRLKGKSCDDWLAERVAEEID	2209
LCMV-P52-1.3_LP	PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID	2209
LCMV-P52-2.1_LP	PDWFTFRDCRLCFRSKNTVMYETTGGRFRLKGKSCDDWLAERVAEEID	2209

LCMV-WE_LP:	SEQ ID NO: 16	
LCMV-P42_LP:	SEQ ID NO: 24	
LCMV-P52_LP:	SEQ ID NO: 32	
LCMV-P91_LP:	SEQ ID NO: 40	
LCMV-P52-1_LP:	SEQ ID NO: 48	
LCMV-P52-1.3_LP:	SEQ ID NO: 56	
LCMV-P52-2.1_LP:	SEQ ID NO: 64	
LCMV-P52-1.3_LP:	SEQ ID NO: 56	