

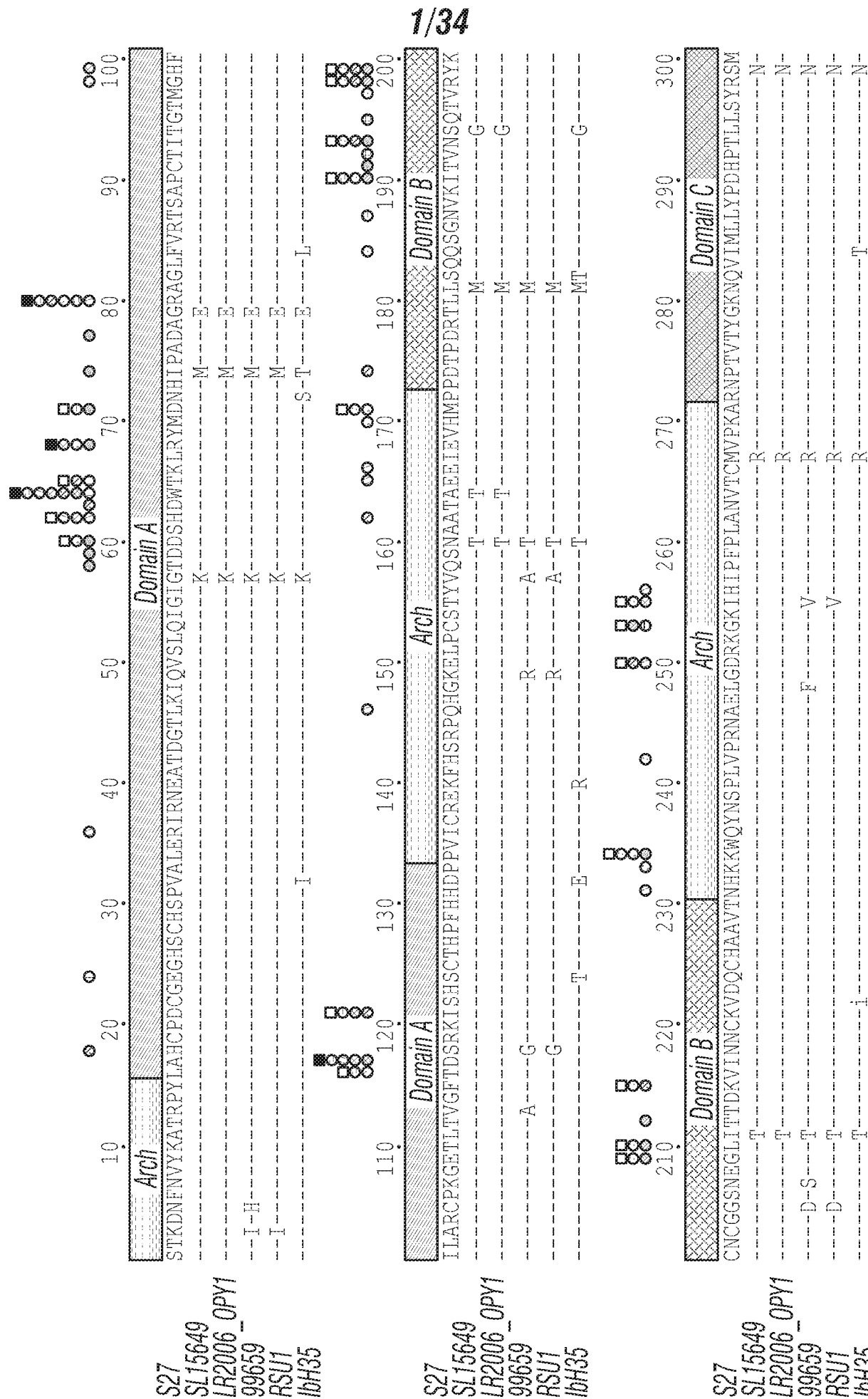


FIG. 1A

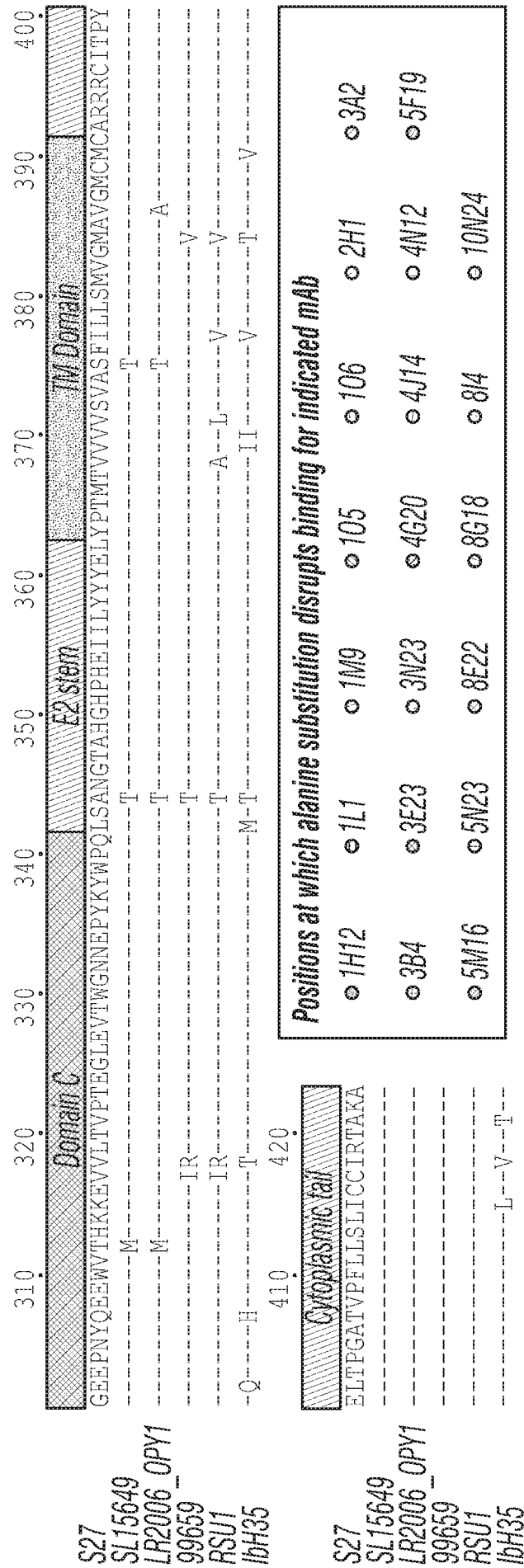


FIG. 1A
(Cont'd)



FIG. 1C



FIG. 1B

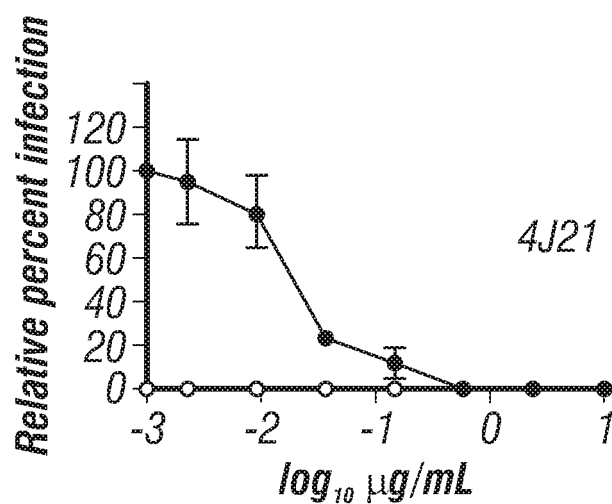
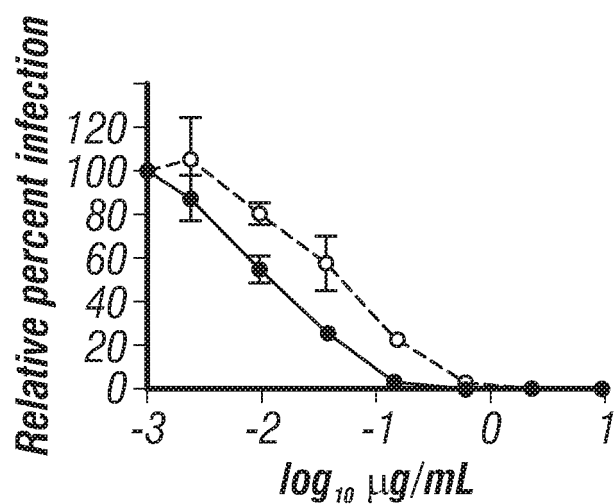
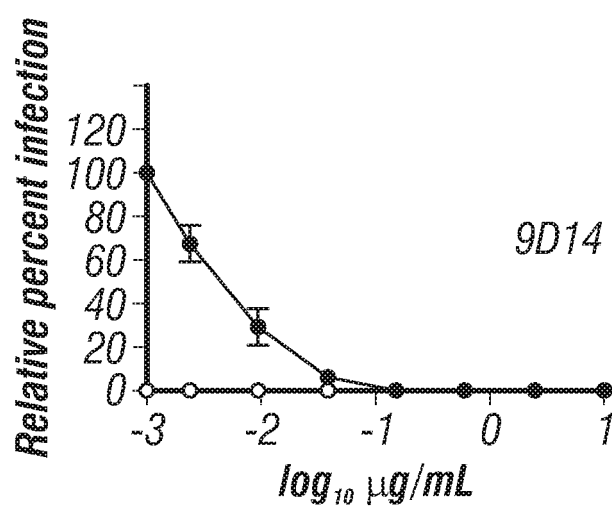
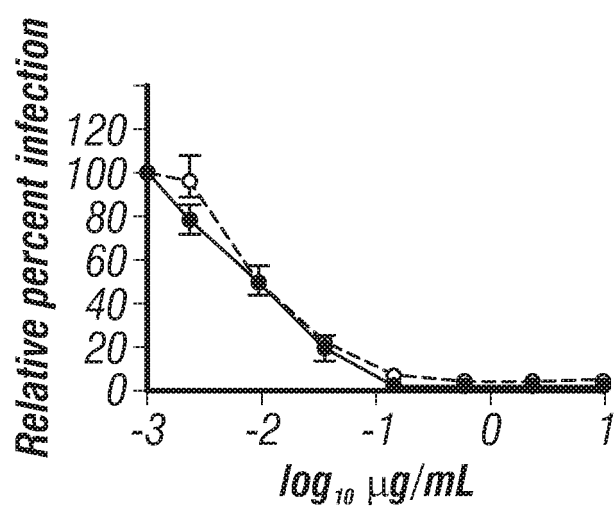
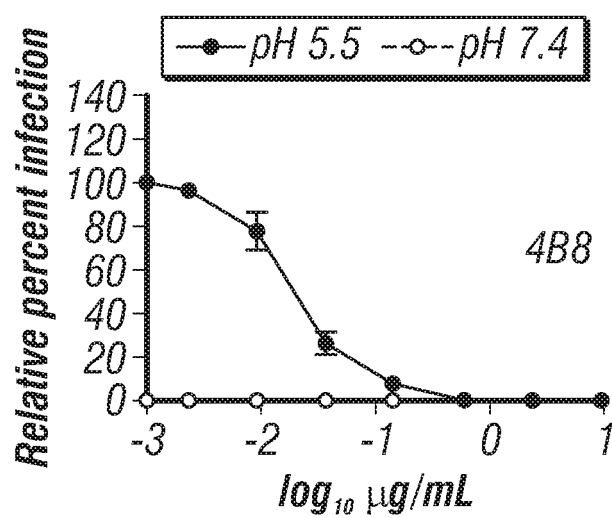
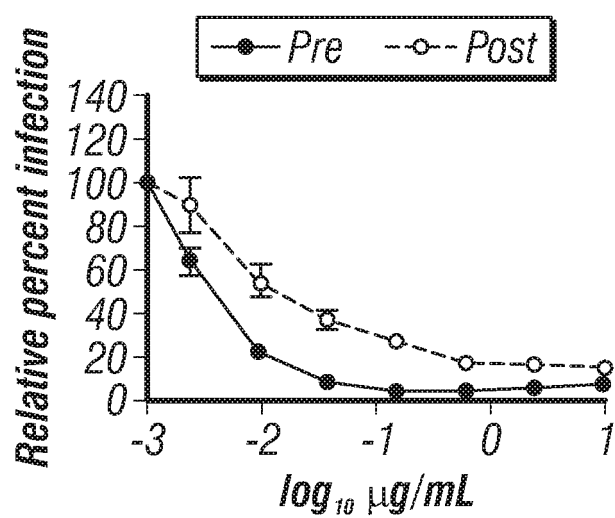
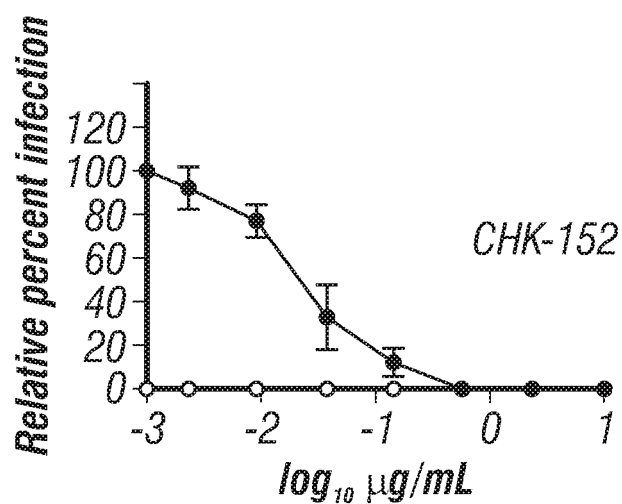
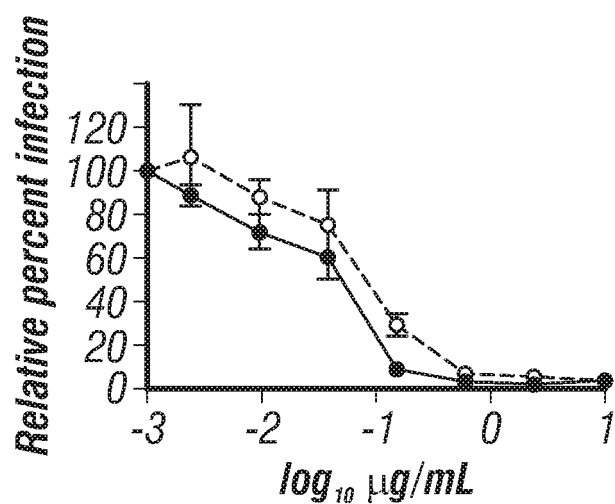
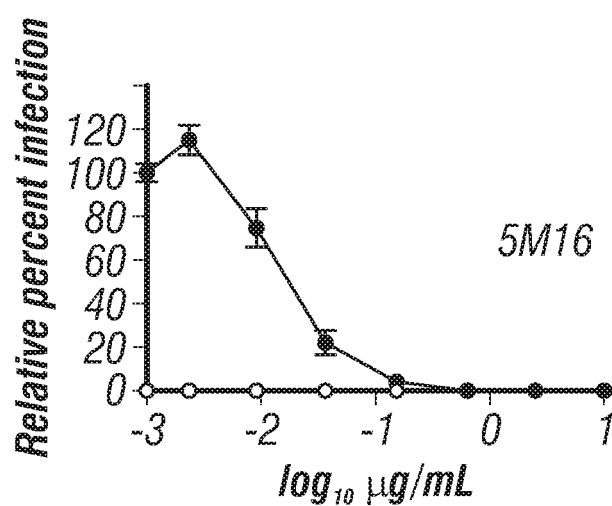
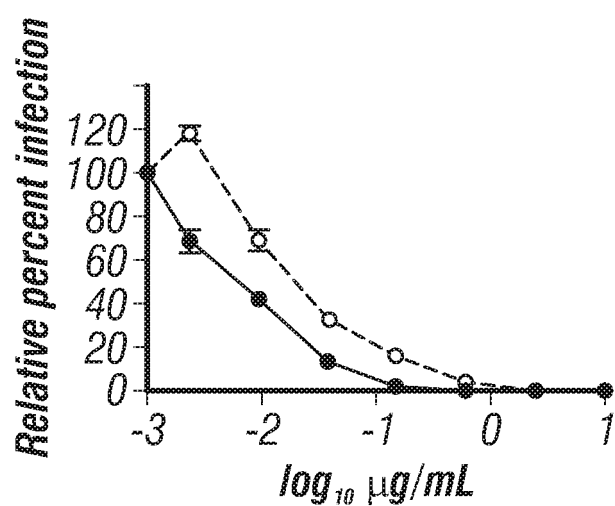
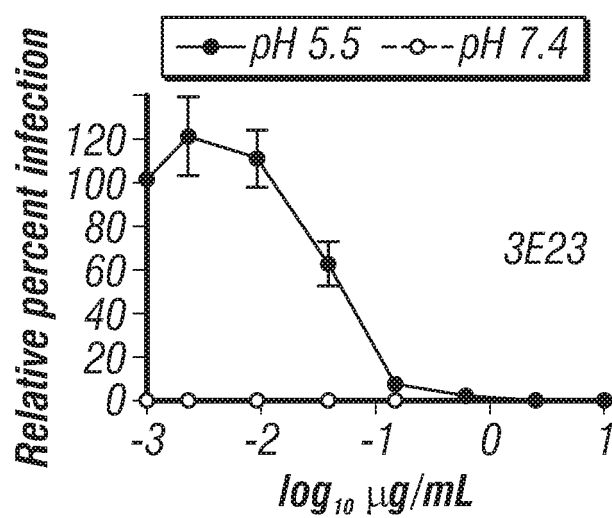
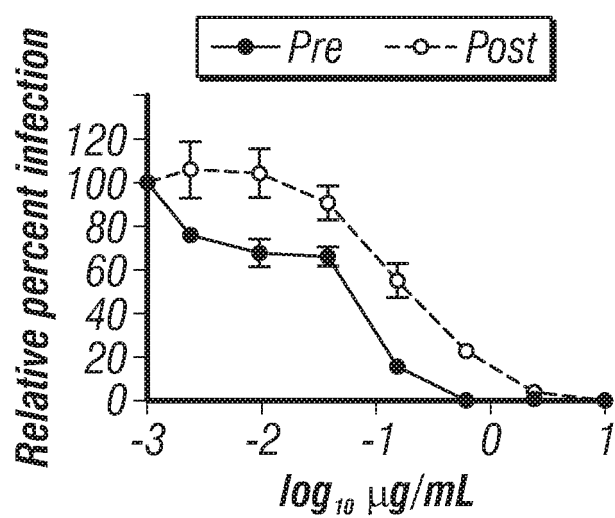


FIG. 2A

FIG. 2B

FIG. 2A
(Cont'd)FIG. 2B
(Cont'd)

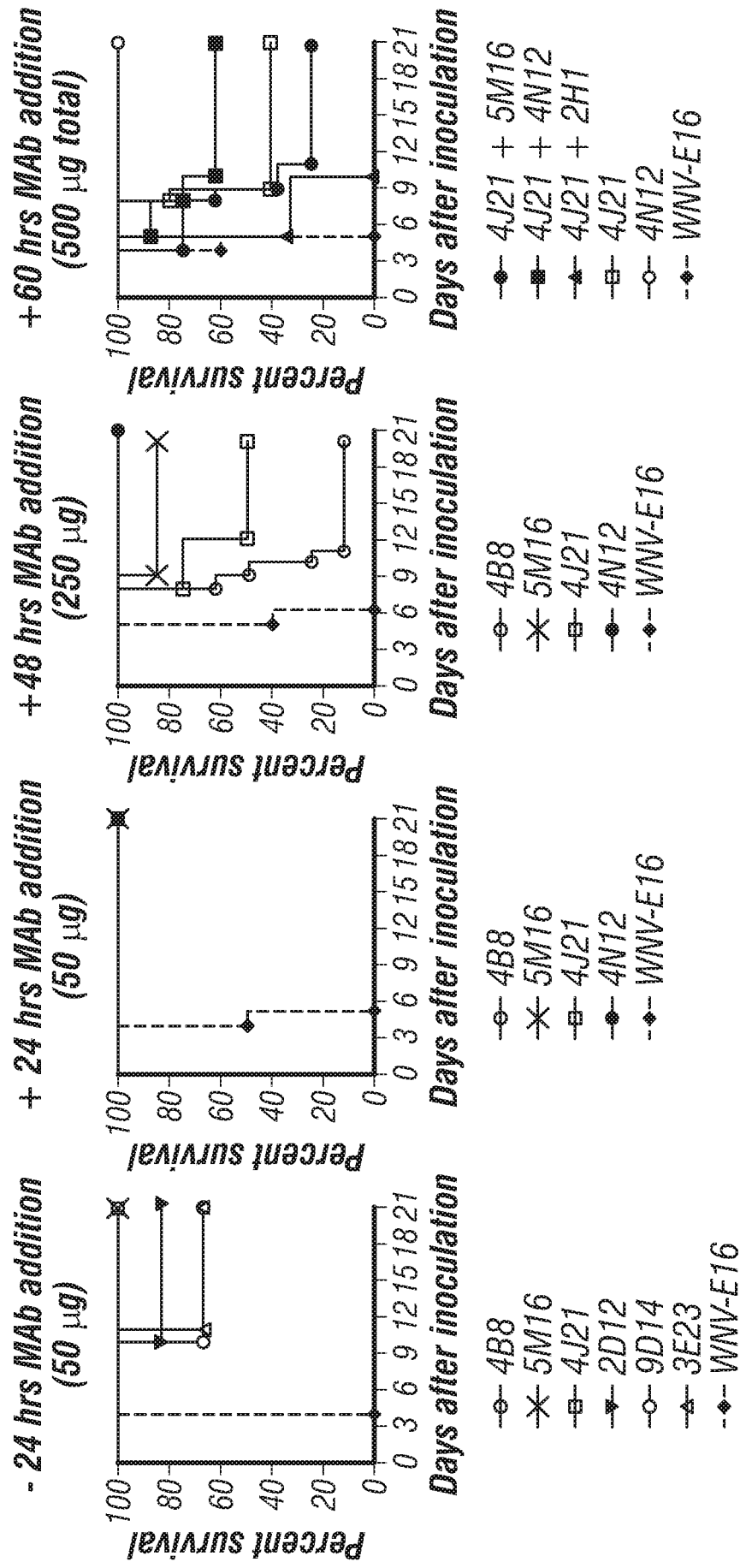


FIG. 3A

FIG. 3B

FIG. 3C

FIG. 3D

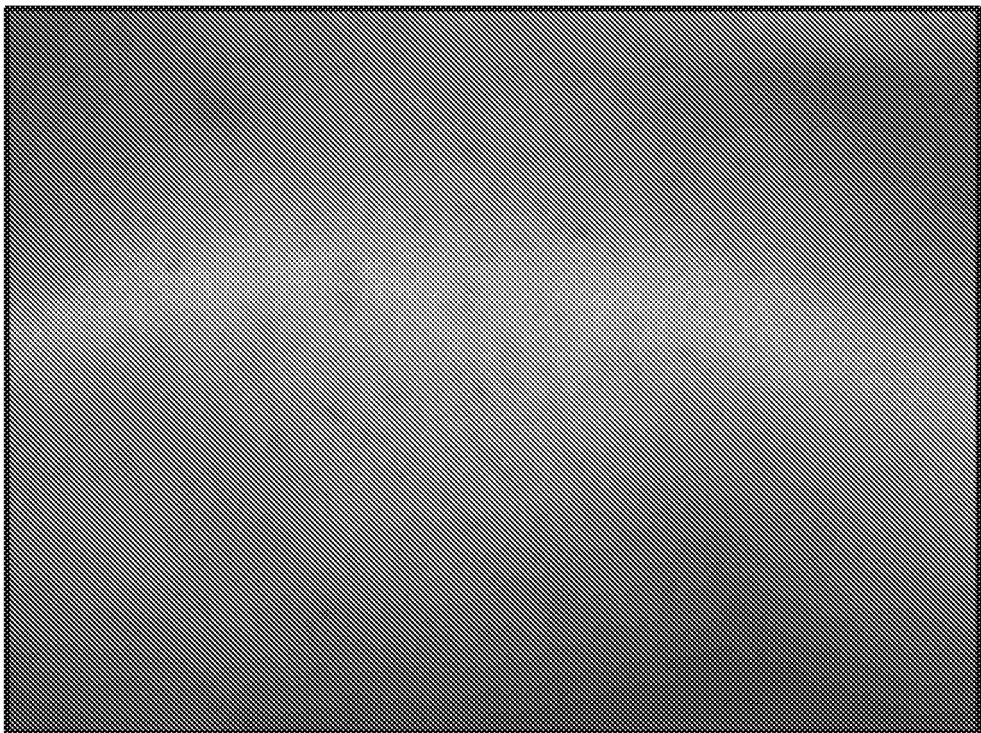


FIG. 4

Domain(s)
identified by
mutagenesis
studies

Competing antibody

mAb	5N23	CHK-84	CHK-141	5014	5M16	106	9D14	4B8	1H12	5F10	CHK-265	CHK-88	3A2	5F19
5N23	0	-1	-3	82	92	111	79	96	-2	103	98	96	108	96
CHK-84	5	2	4	5	-2	48	103	102	-4	100	92	90	99	81
CHK-141	5	5	-1	-9	38	65	97	101	30	96	86	85	92	80
5014	77	47	49	-1	27	15	44	33	1	89	85	89	15	91
5M16	93	21	34	-10	5	-3	20	18	-2	96	84	87	64	88
106	89	68	79	-20	-12	-7	34	3	-4	82	85	110	86	87
9D14	98	105	98	26	25	30	23	27	24	118	105	116	114	94
4B8	92	88	94	-1	6	4	4	6	4	96	92	91	112	103
1H12	31	38	54	5	26	19	48	36	-10	52	52	49	56	91
5F10	92	94	101	86	95	97	84	90	45	-3	-3	5	93	99
CHK-265	100	94	100	77	90	79	80	88	45	2	2	10	101	96
CHK-88	97	85	101	77	91	108	89	91	38	3	3	8	53	97
3A2	92	95	94	37	72	89	71	92	44	88	95	44	3	103

DA, Arch

DA

DA

NR

DA

DA

NotR

NR

DA/DB Arch

DB

DB

DB

FIG. 5

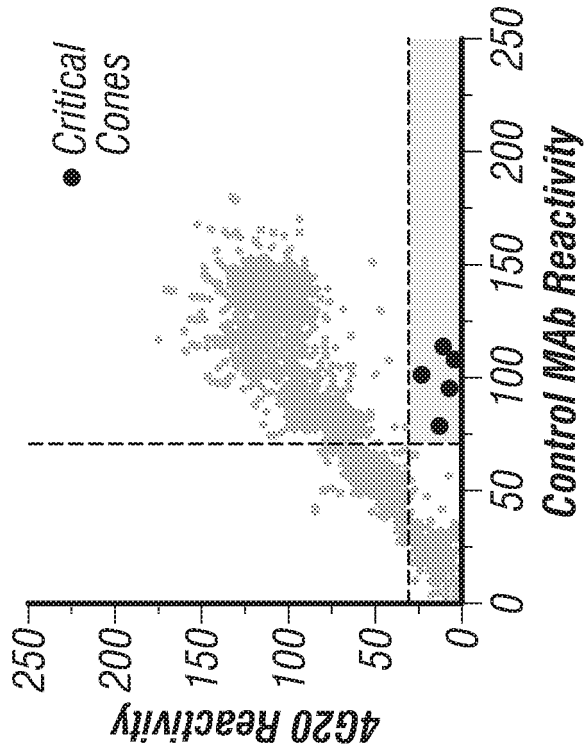


FIG. 6B

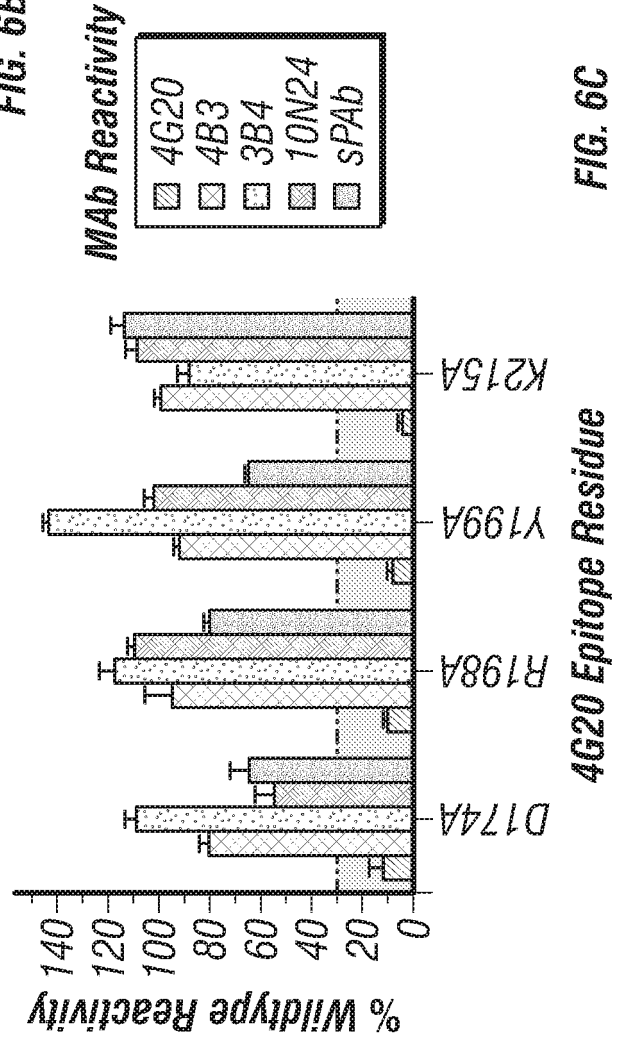


FIG. 6C

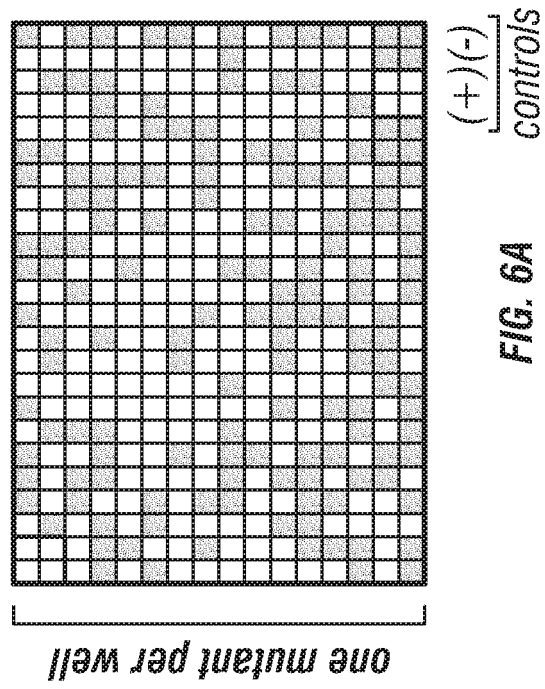


FIG. 6A

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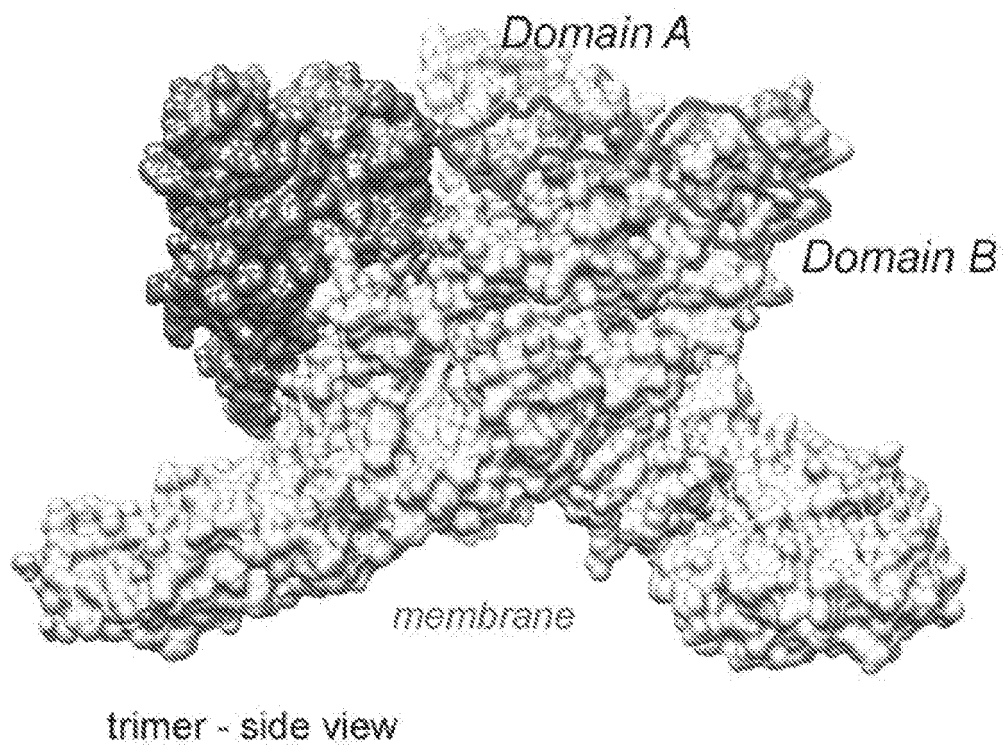


FIG. 6E

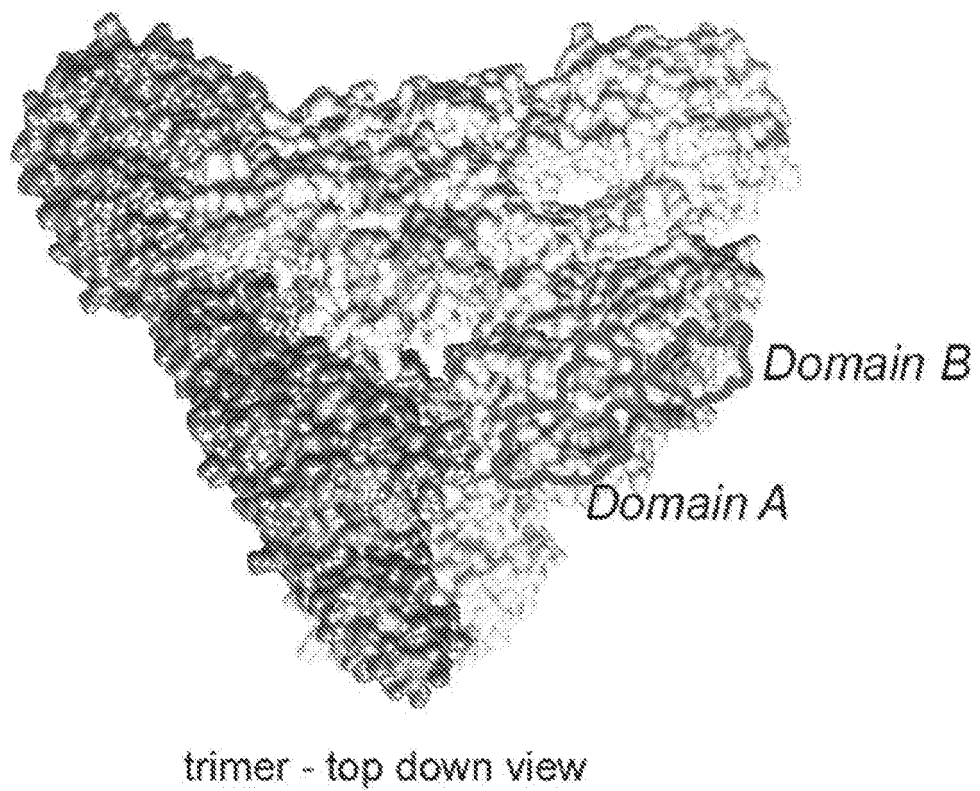


FIG. 6F

- Group 1
- Group 2
- Group 3
- Group 4
- Groups 1 and 2
- Groups 2 and 3
- Groups 1, 2, and 3
- Putative RBD

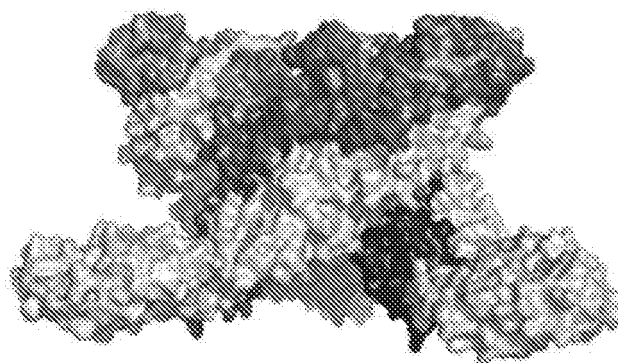
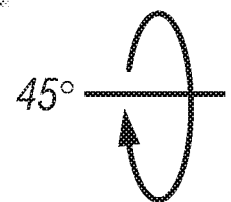
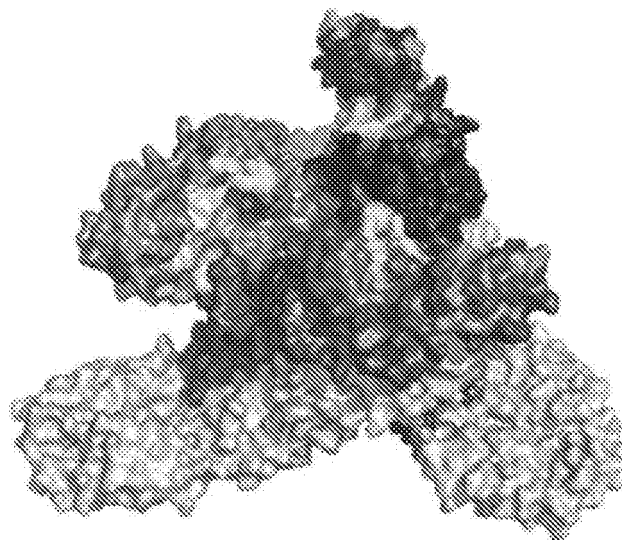
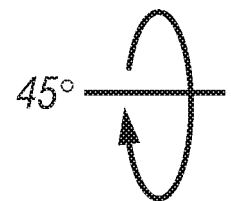
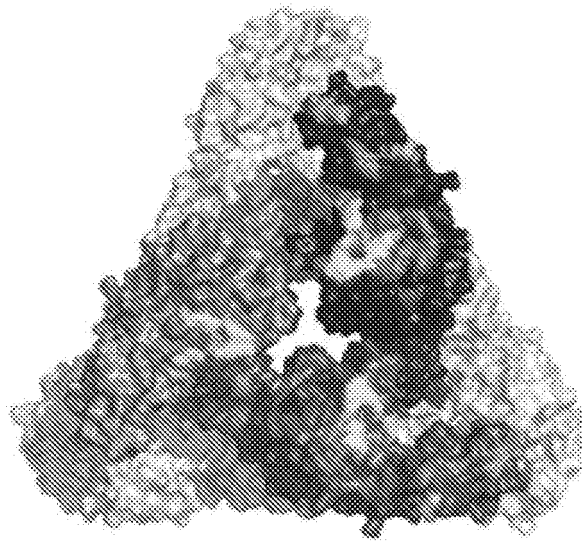


FIG. 7

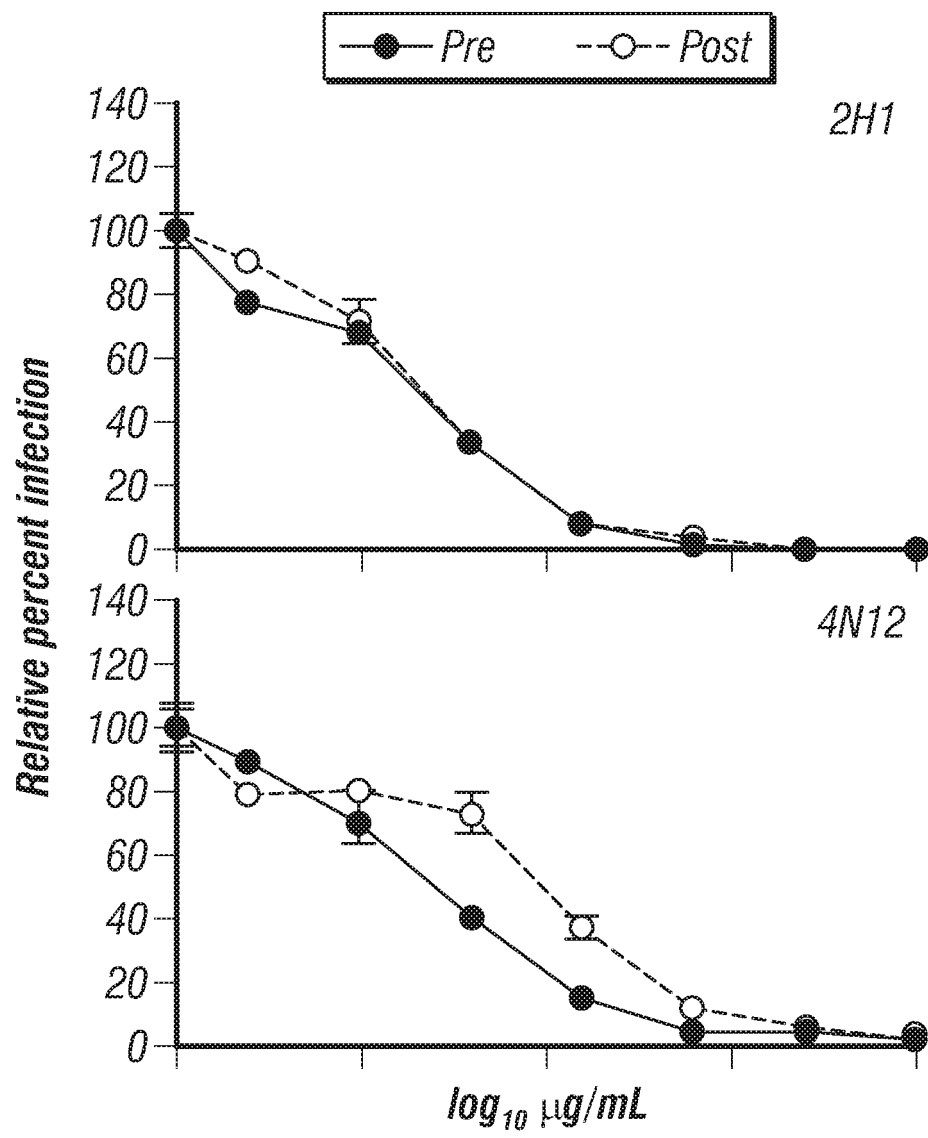
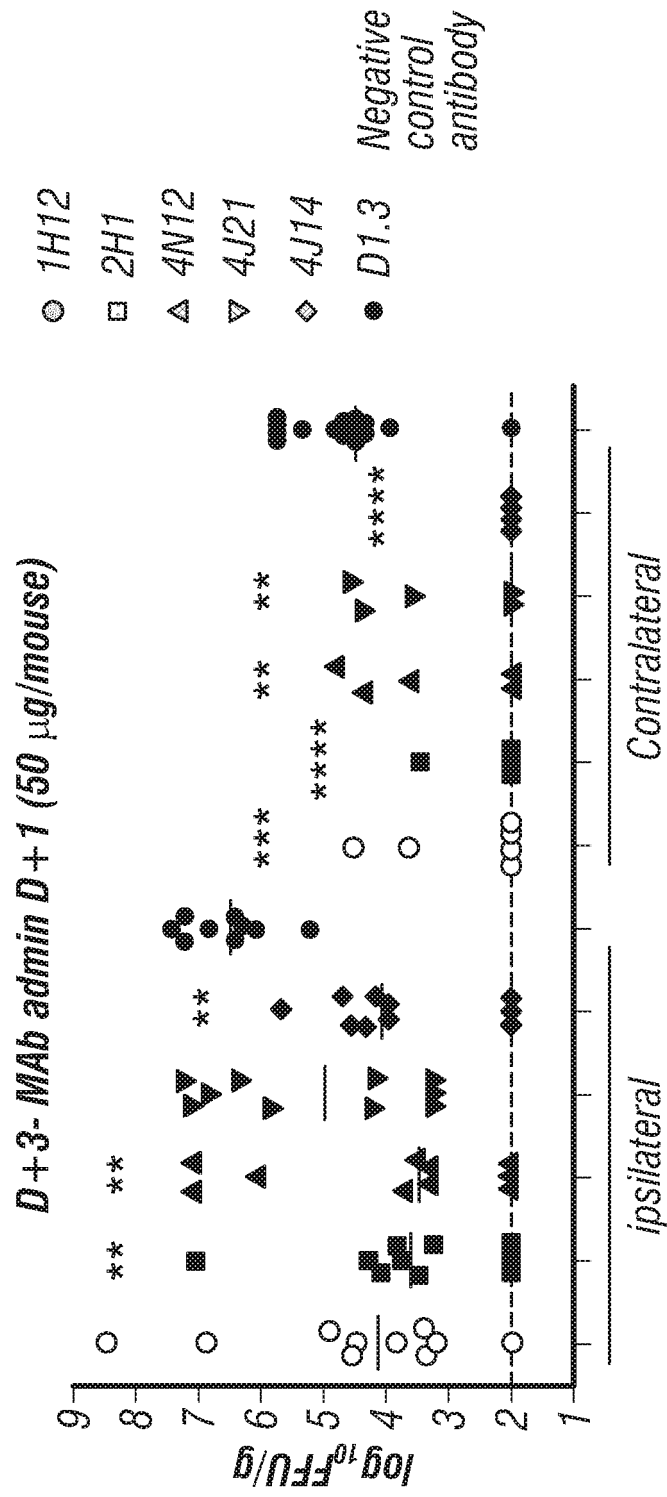


FIG. 8

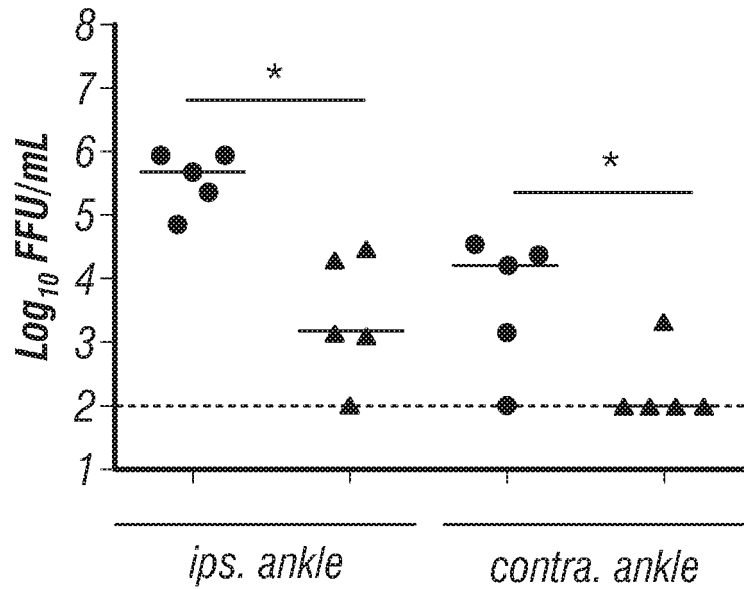


Kruskal-Wallis test for each tissue compared to D1.3

FIG. 9

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*MAbs: 50 μ g/mouse on D+3
(Analyze on D+5)*



- Control antibody
- ▲ CHO cell produced recombinant 4N12 antibody

FIG. 10

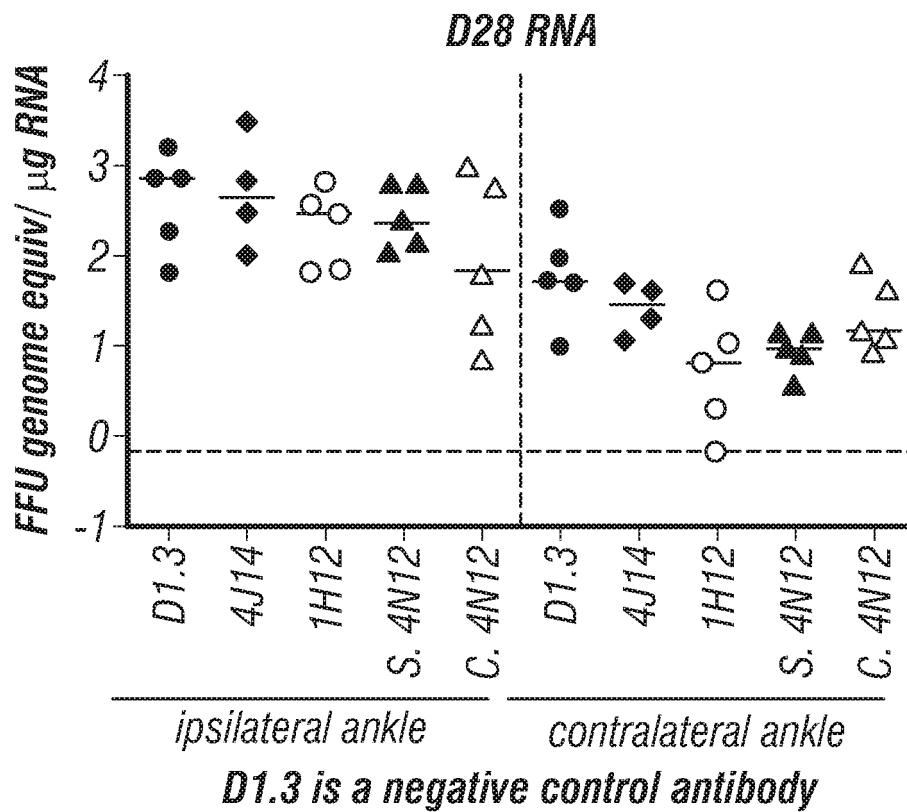


FIG. 11

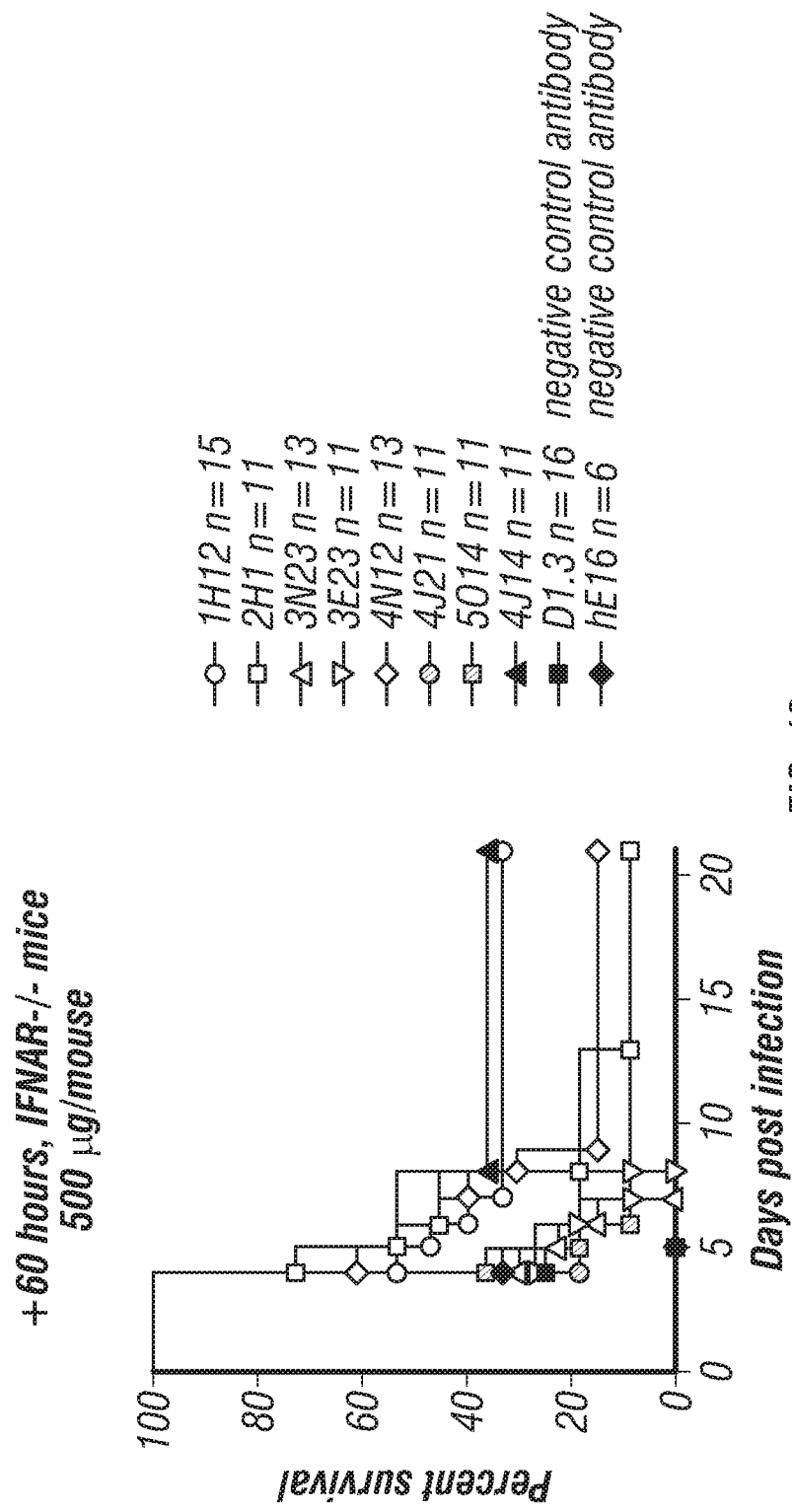


FIG. 12

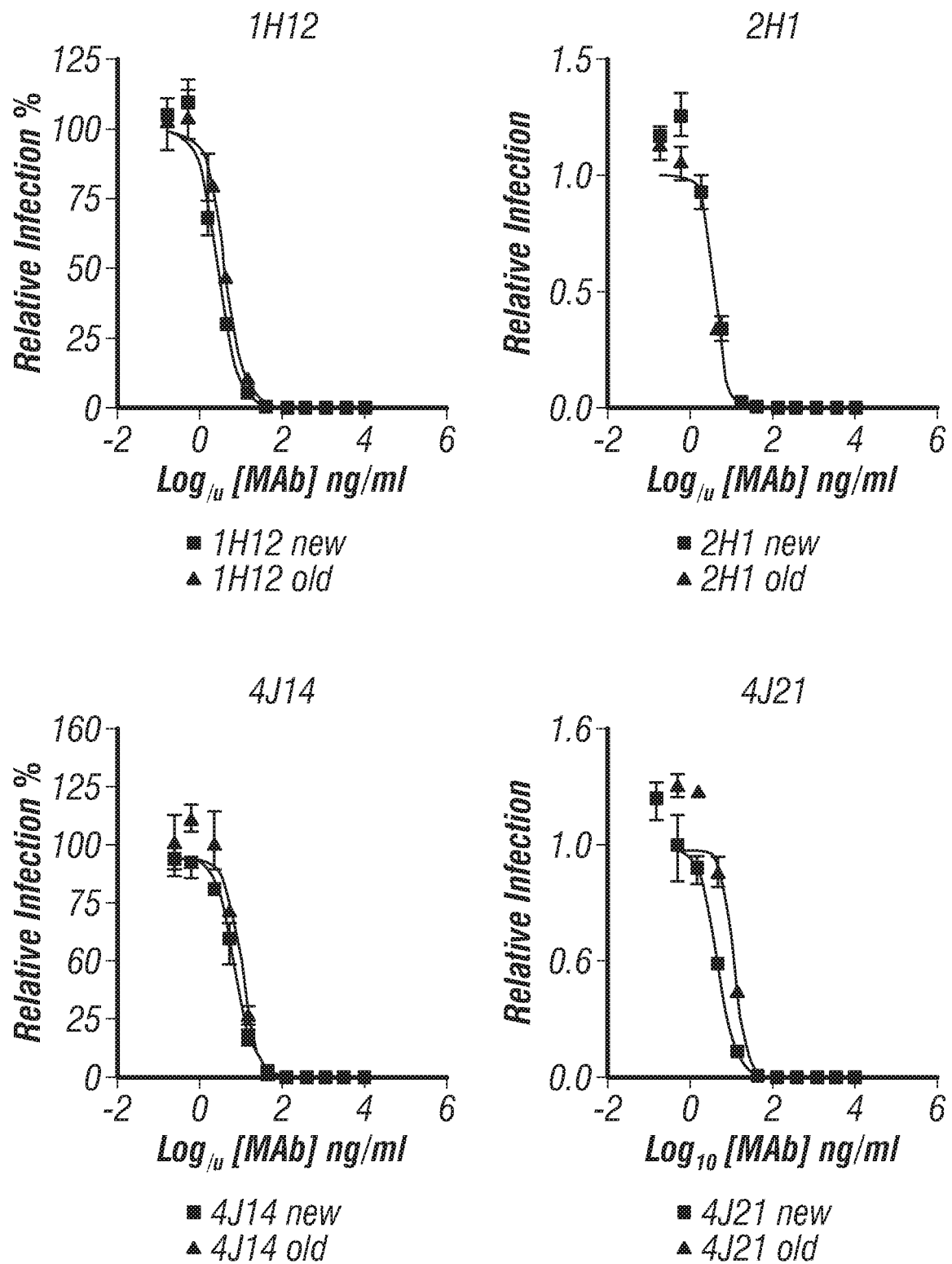


FIG. 13

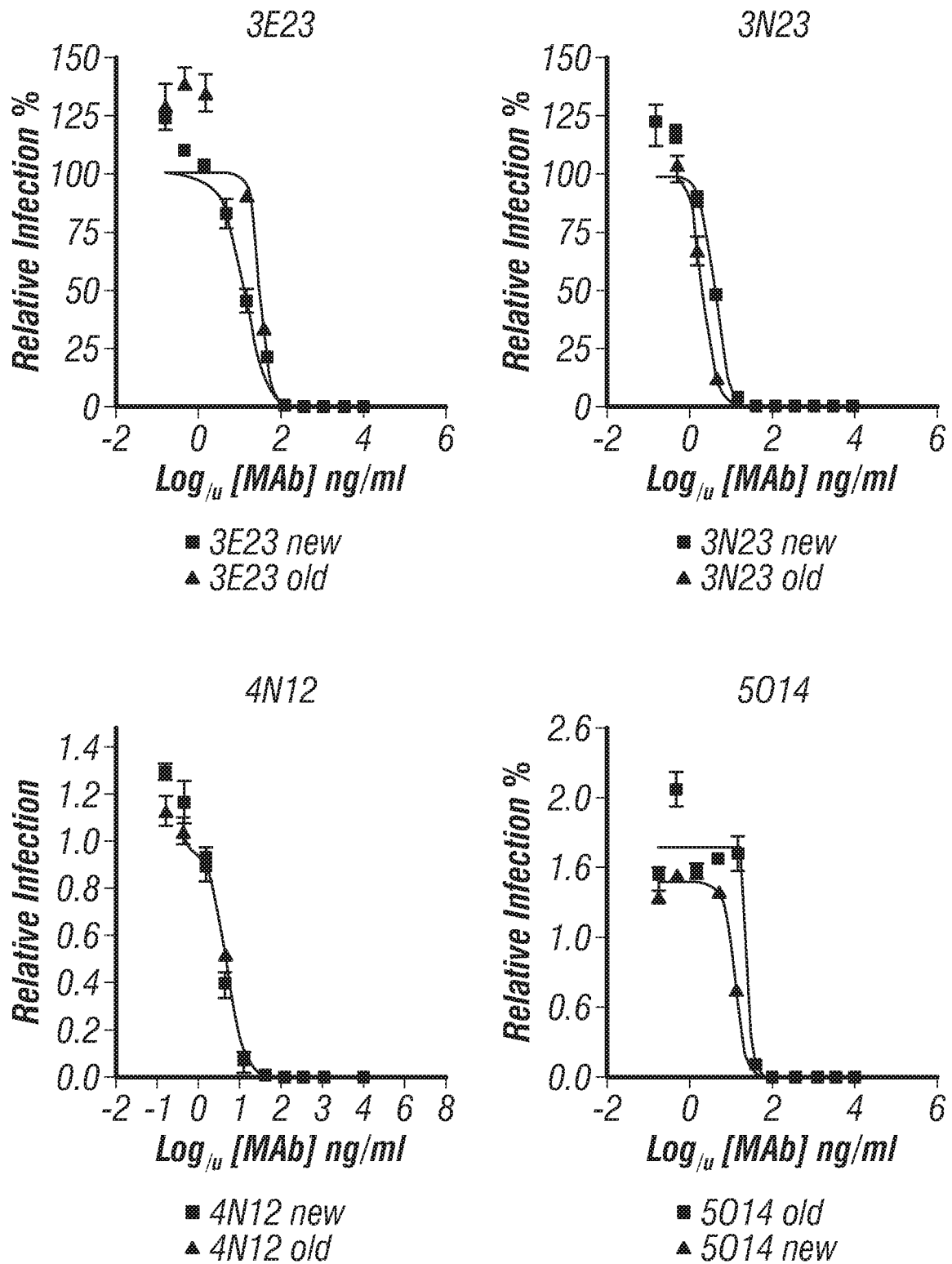


FIG. 13
(Cont'd)

<i>Clone</i>	<i>Hybridoma- produced mAb (old)</i>	<i>Recombinant CHO cell- produced mAb (new)</i>
1H12	4.2	2.7
2H1	4	3.8
(3E)23	34	13.8
3N23	2.1	4.5
4J14	8.6	5.7
4J21	11.4	4.8
4N12	4.8	5
5M16	5.9	1,094
5(O)14	14.3	34.8

FIG. 14*Chikungunya virus E1/E2 alignment:*

ECSA Genotypes: LR2006
 S27
 SL15649

Asian Genotypes: 181/25
 99659

West African Genotype: IbH35

Aligned sequences are shown as Protein_Strain_Genbank accession number

FIG. 15

CLUSTAL O(1.2.1) multiple sequence alignment

```

E1_S27_NC004162.2
E1_SL15649_GU189061.1
E1_LR2006_KT449801.1
E1_181/25_L37661.3
E1_99659_KJ451624.1
E1_IbH35_HM045786.1

E1_S27_NC004162.2
E1_SL15649_GU189061.1
E1_LR2006_KT449801.1
E1_181/25_L37661.3
E1_99659_KJ451624.1
E1_IbH35_HM045786.1

E1_S27_NC004162.2
E1_SL15649_GU189061.1
E1_LR2006_KT449801.1
E1_181/25_L37661.3
E1_99659_KJ451624.1
E1_IbH35_HM045786.1

E1_S27_NC004162.2
E1_SL15649_GU189061.1
E1_LR2006_KT449801.1
E1_181/25_L37661.3
E1_99659_KJ451624.1
E1_IbH35_HM045786.1

TACGAACACGTAACAGTGATCCCGAACACACGGTGGAGTACCGTATAAGACTCTAGTCAAC
TACGAACACGTAACAGTGATCCCGAACACACGGTGGAGTACCGTATAAGACTCTAGTCAAT
TACGAACACGTAACAGTGATCCCGAACACACGGTGGAGTACCGTATAAGACTCTAGTCAAT
TACGAACACGTAACAGTGATCCCGAACACACGGTGGAGTACCGTATAAGACTCTAGTCAAC
TACGAACACGTAACAGTGATCCCGAACACACGGTGGAGTACCGTATAAGACTCTAGTCAAC
TACGAACACGTAACAGTGATCCCGAACACACGGTGGAGTACCGTATAAGACTCTAGTCAAC
TACGAACACGTAACAGTGATCCCGAACACACGGTGGAGTACCGTATAAGACTCTAGTCAAC
*****
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AGACCTGGCTACAGCCCCCATGGTATTGGAGATGGAACTACTGTCAGTCACTTTGGAGCCA
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AGACCGGGCTACAGCCCCCATGGTATTGGAGATGGAGCTTCTGTCAGTCACTTTGGAACCA
AGACCGGGTTACAGCCCCCATGGTATTGGAGATGGAGCTACAACTCGGTCACTTTGGAACCA
*****
ACGCTATCGCTTGATTACATCACGTGCGGAATACAAAACCGTCATCCCGTCTCCGTACGTG
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ACACTATCGCTTGATTACATCACGTGCGGAGTACAAAACCGTCATCCCGTCTCCGTACGTG
ACGCTATCGCTTGATTACATCACGTGCGGAGTATAAAAACCGTCATCCCGTCTCCGTACGTG
ACGCTATCGCTTGATTACATCACGTGCGGAGTATAAAAACCGTTATCCCGTCTCCGTACGTG
ACACTGTCACTTGACTACATCACGTGCGGAGTACAAAACCTGTCACTCCCGTCCCGTACGTG
**..**..*****
AAATGCTGCGGTACAGCAGAGTGCAAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
AAGTGCTGCGGTACAGCAGAGTGCAAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
AAGTGCTGCGGTACAGCAGAGTGCAAGGACAAAAACCTACCTGACTACAGCTGTAAGGTC
AAATGCTGCGGTACAGCAGAGTGCAAGGACAAAGAGCCTACCTGATTACAGCTGTAAGGTC
AAATGCTGCGGTACAGCAGAGTGTAAGGACAAAGAGCCTACCTGATTACAGCTGTAAGGTC
AAGTGCTGTTGTTACAGCAGAGTGCAAGGACAAAGAGCCTACCACTACAGCTGCAAGGTC
**..*****

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FIG. 15 (Cont'd)

E1_S27_NC004162.2	TTCACCGGCGTCTACCCATTATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAAC
E1_SL15649_GU189061.1	TTCACCGGCGTCTACCCATTATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAAC
E1_LR2006_KT449801.1	TTCACCGGCGTCTACCCATTATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAAC
E1_181/25_L37661.3	TTCACCGGCGTCTACCCATTATGTGGGGCGGCCCTACTGCTTCTGCGACGCTGAAAAAT
E1_99659_KJ451624.1	TTCACCGGCGTCTACCCATTATGTGGGGCGGCCCTACTGCTTCTGCGACGCGAAAAAT
E1_IbH35_HM045786.1	TTTACTGGAGTCTACCCATTATGTGGGGCGGCCCTACTGCTTCTGCGACGCGCGAAAAAT
	** ** *
	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAAACAGAAATTGCAATCA
E1_S27_NC004162.2	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAAACAGAAATTGCAATCA
E1_SL15649_GU189061.1	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAAACAGAAATTGCAATCA
E1_LR2006_KT449801.1	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAAACAGAAATTGCAATCA
E1_181/25_L37661.3	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAAACAGAAATTGCAATCA
E1_99659_KJ451624.1	ACGCAATTGAGCGAAGCACATGTGGAGAAAGTCCGAATCATGCAAAAACAGAAATTGCAATCA
E1_IbH35_HM045786.1	ACGCAATTGAGCGAAGCACATGTAGAGAAATCTGAATCTTGCAAAAACAGAGTTTGCAATCG
	*****.*****.*****.*****.*****.*****.*****.*****.
	GCATACAGGGCTCATACCGCATCCGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_S27_NC004162.2	GCATACAGGGCTCATACCGCATCTGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_SL15649_GU189061.1	GCATACAGGGCTCATACCGCATCTGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_LR2006_KT449801.1	GCATACAGGGCTCATACCGCATCTGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_181/25_L37661.3	GCATACAGGGCTCATACCGCATCTGCATCAGCTAAGCTCCGCGTCCTTTACCAAGGAAAT
E1_99659_KJ451624.1	GCCTACAGAGCCCCACACCGCATCCGCGTCGGGAAAGTCCGCGTCCTTTACCAAGGAAAC
E1_IbH35_HM045786.1	** ** *
	AACATCACTGTAAGTGCCTATGCAAAACGGGACCATGCCGTCACAGTTAAGGACGCCAA
E1_S27_NC004162.2	

FIG. 15 (Cont'd)

```

E1 SL15649 GU189061.1
E1 LR2006 KT449801.1
E1 181/25 L37661.3
E1 99659 KJ451624.1
E1 1bH35 HM045786.1

E1 S27 NC004162.2
E1 SL15649 GU189061.1
E1 LR2006 KT449801.1
E1 181/25 L37661.3
E1 99659 KJ451624.1
E1 1bH35 HM045786.1

E1 S27 NC004162.2
E1 SL15649 GU189061.1
E1 LR2006 KT449801.1
E1 181/25 L37661.3
E1 99659 KJ451624.1
E1 1bH35 HM045786.1

E1 S27 NC004162.2
E1 SL15649 GU189061.1
E1 LR2006 KT449801.1
E1 181/25 L37661.3
E1 99659 KJ451624.1
E1 1bH35 HM045786.1

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AATGTTACTGTATCTGCTTATGC AAAACGGCGATCATGCCGTACAGTTAAGGACGCTAAA
AATATCACTGTGGCTGCTTATGC AAAACGGCGACCATGCCGTACAGTTAAGGACGCTAAA
AACATTACTGTAGCTGCCTACGCTAAACGGCGACCATGCCGTACAGTTAAGGACGCCAAG
** . * ****. **** ** **;*****;***** **
TTCATTGTGGGGCCAAATGTCTTCAGCCTGGACACCTTTTGACAAACAAAATCGTGGTGATAC
TTCATTGTGGGGCCAAATGTCTTCAGCCTGGACACCTTTTCGACAAACAAAATGTGGTGATAC
TTCATTGTGGGGCCAAATGTCTTCAGCCTGGACACCTTTTCGACAAACAAAATGTGGTGATAC
TTCATTGTGGGGCCAAATGTCTTCAGCCTGGACACCTTTTGACAAATAAAATCGTGGTGATAC
TTCATAGTGGGGCCAAATGTCTTCAGCCTGGACACCTTTTCGACAAATAAAATCGTGGTGATAC
TTTGTCGTGGGACCAATGTCTCCTCCGCTGGACACCTTTTGACAAACAAAATCGTGGTGATAC
** . * ****. ***** **;***** ***** ***** *****
AAAGGTGACGTTTACAACATGGACTACCCGCCCTTTGGCGCAGGAAGACCAGGACAATTT
AAAGGTGACGTCATAACATGGACTACCCGCCCTTTGGCGCAGGAAGACCAGGACAATTT
AAAGGTGACGCTATAACATGGACTACCCGCCCTTTGGCGCAGGAAGACCAGGACAATTT
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AAAGGCGACGCTACAACATGGACTACCCGCCCTTCGCGCAGGAAGACCAGGACAATTT
AAAGGCGACGCTACAACATGGACTACCCACCTTTTGCGCGCAGGAAGACCAGGACAATTT
***** ***** ** *****. ** ** ***** ***** *****
GGCGATATCCAAAGTCGCACGCCCTGAGAGCAAAGACGTCATATGCTAACACACAACCTGGTA
GGCGATATCCAAAGTCGCACACCTGAGAGTAAAGACGTCATATGCTAATACACAACCTGGTA
GGCGATATCCAAAGTCGCACACCTGAGAGTAAAGACGTCATATGCTAATACACAACCTGGTA
GGCGACATCCAAAGTCGCACGCCCTGAGAGCGGAAGACGTCATATGCTAACACACAACCTGGTA
GGCGACATCCAAAGTCGCACGCCCTGAGAGCGGAAGACGTCATATGCTAATACACAACCTGGTA
GGTGACATTCAAAGTCGTACACCCGGAAAGTAAAGACGTTTATGCCAACACTCAGTTGGTA
** ** ***** ** ** **;***** ***** ***** *****

```

FIG. 15 (Cont'd)

[illegible]

FIG. 15 (Cont'd)

E1_S27_NC004162.2	TGCGAGGTACCAAGCCCTGCACCCATTCCCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
E1_SL15649_GU189061.1	TGCGAGGTACTAGCCTGCACCCATTCCCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
E1_LR2006_KT449801.1	TGCGAGGTACCAAGCCCTGCACCCATTCCCTCAGACTTTGGGGCGTCGCCATTATTAAATAT
E1_181/25_L37661.3	TGTGAGGTACCAAGCCCTGCACCCACTCCCTCAGACTTTGGGGCGTAGCCATCATFAAATAT
E1_99659_KJ451624.1	TGTGAGGTATCAGCCCTGCACCCATTCCCTCAGACTTTGGGGCGTAGCCATCATFAAATAT
E1_IbH35_HM045786.1	TGCGAAGTACCAAGCCCTGCACCTCACTCCCTCCGACTTTGGGGCGTCGCCATCATCAAAATAT
	** ** ** . **** ** ** ** . **** ** ** ** . **** ** ** **
E1_S27_NC004162.2	GCAGTCAGCAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACCAACGCCGTCACATATCCGG
E1_SL15649_GU189061.1	GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACTAACGCCGTCACATATCCGG
E1_LR2006_KT449801.1	GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACTAACGCCGTCACATATCCGG
E1_181/25_L37661.3	GCAGCCAGCAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACTAACGCCGTCACATATCCGG
E1_99659_KJ451624.1	GCAGCCAGTAAGAAAGGCAAGTGTGCGGTGCATTTCGATGACTAACGCCGTCACATATCCGG
E1_IbH35_HM045786.1	ACAGCTAGCAAGAAAGGTAATGTGCAGTACATTTCGATGACCAACGCCGTTACCATTCGA
	. *** ** **** ** . *** ** . *** ** . *** ** . *** ** .
E1_S27_NC004162.2	GAAAGCTGAGATAGAAGTTGAAGGGAATTCAGCTGCAAAATCTCTTTCTCGACGGCCTTG
E1_SL15649_GU189061.1	GAAAGCTGAGATAGAAGTTGAAGGGAATTCAGCTGCAAAATCTCTTTCTCGACGGCCTTA
E1_LR2006_KT449801.1	GAAAGCTGAGATAGAAGTTGAAGGGAATTCAGCTGCAAAATCTCTTTCTCGACGGCCTTA
E1_181/25_L37661.3	GAAAGCTGAAATAGAAGTAGAAGGGAACCTCTCAGTTGCAAAATCTCTTTCTCGACGGCCTA
E1_99659_KJ451624.1	GAAAGCTGAAATAGAAGTAGAAGGGAACCTCTCAGTTGCAAAATCTCTTTCTCGACGGCCTA
E1_IbH35_HM045786.1	GAAAGCCGACGTAGAAGTAGAGGGGAATTCAGCTGCAAAATATCCTTCTCAACAGCCTTG
	***** ** . *****:***. ***** ** *** *****. ** ** . *** ** .
E1_S27_NC004162.2	GCCAGCGCCGAATTCCGCGTACAAGTCTGTTCACACAAGTACACTGTGCAGCCGAGTGC
E1_SL15649_GU189061.1	GCCAGCGCCGAATTCCGCGTACAAGTCTGTTCACACAAGTACACTGTGCAGCTGAGTGC
E1_LR2006_KT449801.1	GCCAGCGCCGAATTCCGCGTACAAGTCTGTTCACACAAGTACACTGTGCAGCCGAGTGC
E1_181/25_L37661.3	GCCAGCGCCGAATTCCGCGTACAAGTCTGTTCACACAAGTACACTGTGCAGCCGAGTGC
E1_99659_KJ451624.1	GCCAGCGCCGAATTCCGCGTACAAGTCTGTTCACACAAGTACACTGTGCAGCCGAGTGC
E1_IbH35_HM045786.1	GCAAGCGCCGAGTTTCGCGTGCAAGTGTGCTCCACACAAGTACACTGCGCAGCCGATGC
	** . ***** ** ** ***** . ***** ** ** ***** ** . ***

FIG. 15 (Contd)

E1_S27_NC004162.2	CACCCCTCCGAAGGACCACATAGTCAACTACCCGGCGTCACATACCACCCCTCGGGGTCCAG
E1_SL15649_GU189061.1	CACCCCTCCGAAGGACCACATAGTCAACTACCCGGCGTCACATACCACCCCTCGGGGTCCAG
E1_LR2006_KT449801.1	CACCCCTCCGAAGGACCACATAGTCAACTACCCGGCGTCACATACCACCCCTCGGGGTCCAG
E1_181/25_L37661.3	CATCCACCCGAAAGACCATAATAGTCAATTACCCGGCGTCACACACCCCTCGGGGTCCAA
E1_99659_KJ451624.1	CATCCACCCGAAAGACCATAATAGTCAATTACCCGGCGTCACACACCCCTCGGGGTCCAA
E1_IbH35_HM045786.1	CACCCCTCCAAAGGACCACATAGTCAATTACCCAGCATCACACACCCCTTGGGGTCCAG
	** ** ** . ** . ** . ** . ** . ** . ** . ** . ** . ** . ** . ** . ** . ** .
E1_S27_NC004162.2	GACATTTCCGCTACGGCGATGTCTATGGGTGCAGAAAGATCACGGGAGGTGTGGGACTGGTT
E1_SL15649_GU189061.1	GACATCTCCGCTACGGCGATGTCTATGGGTGCAGAAAGATCACGGGAGGTGTGGGACTGGTT
E1_LR2006_KT449801.1	GACATCTCCGCTACGGCGATGTCTATGGGTGCAGAAAGATCACGGGAGGTGTGGGACTGGTT
E1_181/25_L37661.3	GACATTTCCGTTACGGCGATGTCTATGGGTGCAGAAAGATCACGGGAGGTGTGGGACTGGTT
E1_99659_KJ451624.1	GACATTTCCGCTACGGCGATGTCTATGGGTGCAGAAAGATCACGGGAGGTGTGGGACTGGTT
E1_IbH35_HM045786.1	GATATATCCACAACGGCAATGTCTTGGGTGCAGAAAGATTACGGGAGGAGTAGGATTAAAT
	** ** ** . ; ** ** . ** ** . ** ** . ** ** . ** ** . ** ** . ** ** . ** . ** .
E1_S27_NC004162.2	GTCGCTGTTGCAGCACTGATTCTAATCGTGGTGTCTATGCCGTGTCGTTTCAGCAGGCAC
E1_SL15649_GU189061.1	GTTGCTGTTGCCGCACTGATTCTAATCGTGGTGTCTATGCCGTGTCGTTTCAGCAGGCAC
E1_LR2006_KT449801.1	GTTGCTGTTGCCGCACTGATTCTAATCGTGGTGTCTATGCCGTGTCGTTTCAGCAGGCAC
E1_181/25_L37661.3	GTCGCTGTTGCAGCACTGATCCTAATCGTGGTGTCTATGCCGTGTCGTTTCAGCAGGCAC
E1_99659_KJ451624.1	GTCGCTGTTGCAGCACTGATCCTAATCGTGGTGTCTATGCCGTGTCGTTTCAGCAGGCAC
E1_IbH35_HM045786.1	GTTGCTGTTGCTGCCCTTAATTTTAATTGTGGTGTCTATGCCGTGTCGTTTCAGCAGGCAC
	** ** ** ** ** . ** . ** . ** . ** . ** . ** . ** . ** . ** . ** . ** .

FIG. 15 (Cont'd)

CLUSTAL O(1.2.1) multiple sequence alignment

E1_IbH35_HM045786.1	YEHTVIPNTVGVVPYKTLVNRRPGYSMPVMLEMLQSVTLEPTLSLDYITCEYKTVIPSPYV
E1_S27_NC004162.2	YEHTVIPNTVGVVPYKTLVNRRPGYSMPVMLEMLLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_SL15649_GUI89061.1	YEHTVIPNTVGVVPYKTLVNRRPGYSMPVMLEMLLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_LR2006_KT449801.1	YEHTVIPNTVGVVPYKTLVNRRPGYSMPVMLEMLLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_99659_KJ451624.1	YEHTVIPNTVGVVPYKTLVNRRPGYSMPVMLEMLLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_181/25_L37661.3	YEHTVIPNTVGVVPYKTLVNRRPGYSMPVMLEMLLSVTLEPTLSLDYITCEYKTVIPSPYV
E1_IbH35_HM045786.1	KCCGTAECKDKSLPDYSCKVFVTGVYPFMWGGAYCFCDAENTQLSEAHVEKSESCKTEEFAS
E1_S27_NC004162.2	KCCGTAECKDKNLPDYSCKVFVTGVYPFMWGGAYCFCDAENTQLSEAHVEKSESCKTEEFAS
E1_SL15649_GUI89061.1	KCCGTAECKDKNLPDYSCKVFVTGVYPFMWGGAYCFCDAENTQLSEAHVEKSESCKTEEFAS
E1_LR2006_KT449801.1	KCCGTAECKDKNLPDYSCKVFVTGVYPFMWGGAYCFCDAENTQLSEAHVEKSESCKTEEFAS
E1_99659_KJ451624.1	KCCGTAECKDKSLPDYSCKVFVTGVYPFMWGGAYCFCDTENTQLSEAHVEKSESCKTEEFAS
E1_181/25_L37661.3	KCCGTAECKDKSLPDYSCKVFVTGVYPFMWGGAYCFCDTENTQLSEAHVEKSESCKTEEFAS
E1_IbH35_HM045786.1	AYRAHTASAKLRVLVLYQGNNITVAAYANGDHAVTVKDAKFVVGPMSSAWTPFDNKIIVVY
E1_S27_NC004162.2	AYRAHTASAKLRVLVLYQGNNITVTAYANGDHAVTVKDAKFI VGPMSAWTPFDNKIIVVY
E1_SL15649_GUI89061.1	AYRAHTASAKLRVLVLYQGNNITVTAYANGDHAVTVKDAKFI VGPMSAWTPFDNKIIVVY
E1_LR2006_KT449801.1	AYRAHTASAKLRVLVLYQGNNITVTAYANGDHAVTVKDAKFI VGPMSAWTPFDNKIIVVY
E1_99659_KJ451624.1	AYRAHTASAKLRVLVLYQGNNITVAAYANGDHAVTVKDAKFI VGPMSAWTPFDNKIIVVY
E1_181/25_L37661.3	AYRAHTASAKLRVLVLYQGNNITVSAYANGDHAVTVKDAKFI VGPMSAWTPFDNKIIVVY
E1_IbH35_HM045786.1	KGDVYNMDYPPFFAGRPGQFGDI QSRTPESKDVIYANTQLVLQRPAAGTVHVHPYSQAPSGF
E1_S27_NC004162.2	KGDVYNMDYPPFFAGRPGQFGDI QSRTPESKDVIYANTQLVLQRPAAGTVHVHPYSQAPSGF
E1_SL15649_GUI89061.1	KGDVYNMDYPPFFAGRPGQFGDI QSRTPESKDVIYANTQLVLQRPAAGTVHVHPYSQAPSGF
E1_LR2006_KT449801.1	KGDVYNMDYPPFFAGRPGQFGDI QSRTPESKDVIYANTQLVLQRPAAGTVHVHPYSQAPSGF
E1_99659_KJ451624.1	KGDVYNMDYPPFFAGRPGQFGDI QSRTPESKDVIYANTQLVLQRPSAGTVHVHPYSQAPSGF
E1_181/25_L37661.3	KGDVYNMDYPPFFAGRPGQFGDI QSRTPESKDVIYANTQLVLQRPSAGTVHVHPYSQAPSGF

FIG. 15 (Cont'd)

EE2_181/25_L37661.3	AGTATTAAGGACAACTTCAATGTC	TATAAAGCCATAAGACCGTACCTAGCTCACTGTCTCC
EE2_IbH35_HM045786.1	AGTACTAAGGACAAATTTTAATGTC	TATAAAGCTACAAGACCATAATCTAGCTCATTTGTCCT
EE2_LR2006_KT449801.1	AGCACCAAGGACAACTTCAATGTC	TATAAAGCCACAAGACCATACTTAGCTCACTGTCTCC
EE2_SL15649_GU189061.1	AGCACCAAGGACAACTTCAATGTC	TATAAAGCCACAAGACCATACTTAGCTCACTGTCTCC
EE2_S27_NC004162.2	AGCACCAAGGACAACTTCAATGTC	TATAAAGCCACAAGACCATACTTAGCTCACTGTCTCC
EE2_99659_KJ451624.1	AGTATTAAGGACCACCTTCAATGTC	TATAAAGCCACAAGACCCTACCTAGCTCACTGTCTCC
	** * **** * * * **** * * **** * * **** * * **** *	
EE2_181/25_L37661.3	GACTGTGGAGAAAGGCACCTCGTGCCATAGTCCG	TAGTCCGTAGCGCTAGAACGCATCAGAAAACGAA
EE2_IbH35_HM045786.1	GACTGCGGAGAAAGGCATTCGTGCCACAGCCCTATCGCAT	TGGAGCGCATCAGAAAATGAA
EE2_LR2006_KT449801.1	GACTGTGGAGAAAGGCACCTCGTGCCATAGTCCG	TAGTCCGTAGCACTAGAACGCATCAGAAAATGAA
EE2_SL15649_GU189061.1	GACTGTGGAGAAAGGCACCTCGTGCCATAGTCCG	TAGTCCGTAGCACTAGAACGCATCAGAAAATGAA
EE2_S27_NC004162.2	GACTGTGGAGAAAGGCACCTCGTGCCATAGTCCG	TAGTCCGTAGCACTAGAACGCATCAGAAAATGAA
EE2_99659_KJ451624.1	GACTGTGGAGAAAGGCACCTCGTGCCATAGTCCG	TAGTCCGTAGCACTAGAACGCATCAGAAAACGAA
	**** * **** * * **** * * **** * * **** * * **** *	
EE2_181/25_L37661.3	GCGACAGACGGGACGCTGAAAATCCAGGTTTCCTTGCAAA	TCGGAATAAAGACGGATGAT
EE2_IbH35_HM045786.1	GCAACGGACGGAAACGCTGAAAATCCAGGTCCTCTTTGCAGAT	CGGGAATAAAGACAGATGAC
EE2_LR2006_KT449801.1	GCGACAGACGGGACGCTGAAAATCCAGGTCCTCTTTGCAAA	TCGGAATAAAGACGGATGAC
EE2_SL15649_GU189061.1	GCGACAGACGGGACGCTGAAAATCCAGGTCCTCTTTGCAAA	TCGGAATAAAGACGGACGAC
EE2_S27_NC004162.2	GCGACAGACGGGACGCTGAAAATCCAGGTCCTCTTTGCAAA	TCGGAATAAGGACGGATGAT
EE2_99659_KJ451624.1	GCGACAGACGGGACGCTGAAAATCCAGGTTTCCTTGCAAA	TCGGAATAAAGACGGATGAT
	** . ** . **** * * * * **** * * **** * * **** * * **** *	
EE2_181/25_L37661.3	AGCCATGATTGGACCAAGCTGCGTTACATGGACAATCATATGCCAGCAGACGCAGAGAGG	
EE2_IbH35_HM045786.1	AGCCACGATTGGACCAAGCTGCGCTATATGGATAGCCATACGCCAGCGGACCGCGAGCGGA	
EE2_LR2006_KT449801.1	AGCCACGATTGGACCAAGCTGCGTTATATGGACAACCCACATGCCAGCAGACGCAGAGAGG	
EE2_SL15649_GU189061.1	AGCCACGATTGGACCAAGCTGCGTTATATGGACAACCCACATGCCAGCAGACGCAGAGAGG	
EE2_S27_NC004162.2	AGCCATGATTGGACCAAGCTGCGTTACATGGACAATCACATACCAGCAGACGCAGGGAGG	
EE2_99659_KJ451624.1	AGCCATGATTGGACCAAGCTGCGTTATATGGACAATCACATGCCAGCAGACGCAGAGCGG	
	**** * **** * * **** * * **** * * **** * * **** * * **** *	

FIG. 15 (Cont'd)

E2_181/25_L37661.3	GCCAGGCTATTTGTAAGAACGTCAGCACCGTGCACGATTACTGGAACAATGGGACACTTC
E2_IbH35_HM045786.1	GCCGGATTGCTTTGTAAGGACTTCAGCACCGTGCACGATCACCGGGACCATGGGACACTTT
E2_LR2006_KT449801.1	GCCGGCTATTTGTAAGAACATCAGCACCGTGTACGATTACTGGAACAATGGGACACTTC
E2_SL15649_GU189061.1	GCCGGCTATTTGTAAGAACATCAGCACCGTGTACGATTACTGGAACAATGGGACACTTC
E2_S27_NC004162.2	GCCGGCTATTTGTAAGAACATCAGCACCGTGTACGATTACTGGAACAATGGGACACTTC
E2_99659_KJ451624.1	GCCGGCTATTTGTAAGAACGTCAGCACCGTGCACGATTACTGGAACAATGGGACACTTC
	** . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
E2_181/25_L37661.3	ATCCTGGCCCCGATGTCGAAAGGAGAAACTCTGACGGTGGGATTCACTGACGGTAGGAAG
E2_IbH35_HM045786.1	ATTCTGGCCCCGATGCCCGAAAGGAGAGACGCTGACAGTGGGATTTACGGACAGCAGAAAG
E2_LR2006_KT449801.1	ATCCTGGCCCCGATGTCCAAAAGGGGAAACTCTGACGGTGGGATTCCTGACAGTAGGAAG
E2_SL15649_GU189061.1	ATCCTGGCCCCGATGTCCAAAAGGGGAAACTCTGACGGTGGGATTCCTGACAGTAGGAAG
E2_S27_NC004162.2	ATCCTGGCCCCGATGTCGAAAGGAGAAACTCTGACGGTGGGATTCCTGACAGTAGGAAG
E2_99659_KJ451624.1	ATTCTGGCCCCGATGTCGAAAGGAGAAACTCTGACGGCGGGGTTCACTGACGGTAGGAAG
	** *
E2_181/25_L37661.3	ATCAGTCACATCATGTACGCACCCCATTTACACACGACCCTCCTGTGATAGCCGGGAAAAA
E2_IbH35_HM045786.1	ATCAGCCACACATGCACACACCCCGTTCCATCATGAACCACTGTGATAGTAGGGAGAGG
E2_LR2006_KT449801.1	ATTAGTCACTCATGTACGCACCCCATTTACACACGACCCTCCTGTGATAGTGGGAAAAA
E2_SL15649_GU189061.1	ATTAGTCATTTCATGTACGCACCCCATTTACACACGACCCTCCTGTGATAGTGGGAAAAA
E2_S27_NC004162.2	ATTAGTCACTCATGTACGCACCCCATTTACACACGACCCTCCTGTGATAGCCGGGAAAAA
E2_99659_KJ451624.1	ATCAGTCACATCATGTACGCACCCCATTTACACCATGACCCTCCTGTGATAGCCGGGAAAAA
	** *
E2_181/25_L37661.3	TTTCATTCCCGACCGCAGCACGGTAGAGAACTACCTTGCAGCACGTACGGCAGAGCACCC
E2_IbH35_HM045786.1	TTCCCACTCTCGACCACAACATGGTAAAGAGTTACCTTGCAGCACGTACGTGCAGAGCACCC
E2_LR2006_KT449801.1	TTCCCATTTCCGACCGCAGCACGGTAAAGAGCTACCTTGCAGCACGTACGTGCAGAGCACCC
E2_SL15649_GU189061.1	TTCCCATTTCCGACCGCAGCACGGTAAAGAGCTACCTTGCAGCACGTACGTGCAGAGCACCC
E2_S27_NC004162.2	TTCCCATTTCCGACCGCAGCACGGTAAAGAGCTACCTTGCAGCACGTACGTGCAGAGCAAC
E2_99659_KJ451624.1	TTCCCATTTCCGACCGCAGCACGGTAGGGAACCTTGCAGCACGTACGTGCAGAGCACCC
	** *

FIG. 15 (Cont'd)

E2_181/25_L37661.3	GCTGCAACTGCCGAGGAGATAGAGGTACATATGCCCCCAGACACCCAGATCGCACATTG
E2_IbH35_HM045786.1	GCTGCCACTGCCGAGGAGATAGAGGTGCATATGCCCCCAGATCTCTGACCGCACGCTG
E2_LR2006_KT449801.1	GCCGCAACTACCGAGGAGATAGAGGTACACATGCCCCCAGACACCCCTGATCGCACATTA
E2_SL15649_GU189061.1	GCCGCAACTACCGAGGAGATAGAGGTACACATGCCCCCAGACACCCCTGATCGCACATTA
E2_S27_NC004162.2	GCCGCAACTGCCGAGGAGATAGAGGTACACATGCCCCCAGACACCCCTGATCGCACATTG
E2_99659_KJ451624.1	GCTGCAACTGCCGAGGAGATAGAGGTACACATGCCCCCAGACACCCAGATCGCACATTA
	** ** ** ** **
E2_181/25_L37661.3	ATGTCACAACAGTCCGGTAATGTAAAGATCACAGTCAATAGTCAGACGGTGCGGTACAAAG
E2_IbH35_HM045786.1	ATGACGCAGCAGTCTGGCAACGTGAAGATCACAGTTAATGGCAGACGGTGCGGTACAAAG
E2_LR2006_KT449801.1	ATGTCACAACAGTCCGGCAACGTAAAGATCACAGTCAATGGCCAGACGGTGCGGTACAAAG
E2_SL15649_GU189061.1	ATGTCACAACAGTCCGGCAACGTAAAGATCACAGTCAATGGCCAGACGGTGCGGTACAAAG
E2_S27_NC004162.2	CTGTCACAACAGTCCGGCAACGTAAAGATCACAGTCAATAGTCAGACGGTGCGGTATAAAG
E2_99659_KJ451624.1	ATGTCACAACAGTCCGGCAATGTAAAGATCACAGTCAATAGTCAGACGGTGCGGTACAAAG
	. ** ** ** **
E2_181/25_L37661.3	TGTAATTGCGGTGACTCAAATGAAGGACTAACCCACTACAGACAAAGTGATTAAATAACTGC
E2_IbH35_HM045786.1	TGCAACTGCGGGGCTCAAACGAGGGACTGACAAACCACAGACAAAGTGATCAATAACTGC
E2_LR2006_KT449801.1	TGTAATTGCGGTGGCTCAAATGAAGGACTAACCACTACAGACAAAGTGATTAAATAACTGC
E2_SL15649_GU189061.1	TGTAATTGCGGTGGCTCAAATGAAGGACTAACCACTACAGACAAAGTGATTAAATAACTGC
E2_S27_NC004162.2	TGTAATTGCGGTGGCTCAAATGAAGGACTAAATACTACAGATAAAGTGATTAAATAACTGC
E2_99659_KJ451624.1	TGCAATTGTGGTGACTCAAAGTGAAGGATTAAACCCTACAGATAAAGTGATTAAATAACTGC
	** ** ** ** *
E2_181/25_L37661.3	AAGGTTGATCAAATGCCATGCGCGGTCAACCAATCACAAAAAATGGCAGTATAATTCCCCCT
E2_IbH35_HM045786.1	AAAAATTGATCAGTGCCATGCTGCAGTCACCTAATCACAGAAGTGGCAATACAACTCCCCCT
E2_LR2006_KT449801.1	AAGGTTGATCAAATGTCATGCCCGGTCAACCAATCACAAAAAGTGGCAGTATAACTCCCCCT
E2_SL15649_GU189061.1	AAGGTTGATCAAATGTCATGCCCGGTCAACCAATCACAAAAAGTGGCAGTATAACTCCCCCT
E2_S27_NC004162.2	AAGGTTGATCAAATGTCATGCCCGGTCAACCAATCACAAAAAGTGGCAGTATAACTCCCCCT
E2_99659_KJ451624.1	AAGGTCGATCAAATGCCATGCGCGGTCAACCAATCACAAAAAATGGCAGTATAATTCCCCCT
	** ** * ** ** *

FIG. 15 (Cont'd)

E2 181/25 L37661.3	CTGGTCCCGCGTAATGCTGAACCTCGGGACCGGAAAGGAAAGTTACATTCCGTTTCCT
E2 IbH35 HM045786.1	TTAGTCCCGCGTAACGCTGAACCTCGGGACCGGTAAGGAAAGATTACATCCCATTCCCA
E2 LR2006 KT449801.1	CTGGTCCCGCGTAATGCTGAACCTTGGGACCGGAAAGGAAATTCACATCCCGTTCCG
E2 SL15649 GU189061.1	CTGGTCCCGCGTAATGCTGAACCTTGGGACCGGAAAGGAAATTCACATCCCGTTCCG
E2 S27 NC004162.2	CTGGTCCCGCGTAACGCTGAACCTCGGGACCGGAAAGGAAATTCACATCCCGTTCCG
E2 99659 KJ451624.1	CTGGTCCCGCGTAATGCTGAATTCGGGGACCGGAAAGGAAAGTTACATTCCATTTCCT
	*.***** *
E2 181/25 L37661.3	CTGGCAAAATGTGACATGCAGGGTGCCCTAAGGCAAGGAACCCACCGTGACGTACGGAAAA
E2 IbH35 HM045786.1	TTGGCAAAACGTGACTTGCAGAGTGCCAAAAGCAAGAAACCCACAGTAACGTACGGAAAA
E2 LR2006 KT449801.1	CTGGCAAAATGTAACATGCAGGGTGCCCTAAGCAAGGAACCCACCGTGACGTACGGGAAA
E2 SL15649 GU189061.1	CTGGCAAAATGTAACATGCAGGGTGCCCTAAGCAAGGAACCCACCGTGACGTACGGGAAA
E2 S27 NC004162.2	CTGGCAAAATGTAACATGCATGGTGCCCTAAGCAAGGAACCCACCGTGACGTACGGGAAA
E2 99659 KJ451624.1	CTGGCAAAATGTGACATGCAGGGTGCCCTAAGCAAGGAACCCACCGTGACGTACGGAAAA
	***** ** *
E2 181/25 L37661.3	AACCAAGTCATCATGCTGCTGTATCCTGACCACCCAAACGCTCCTGTCTACCGGAATATG
E2 IbH35 HM045786.1	AACCAAGTCACCATGCTGCTGTATCCTGACCATCCGACACTCTTGCTTATCGTAACATG
E2 LR2006 KT449801.1	AACCAAGTCATCATGCTACTGTATCCTGACCACCCAAACACTCCTGTCTACCGGAATATG
E2 SL15649 GU189061.1	AACCAAGTCATCATGCTACTGTATCCTGACCACCCAAACACTCCTGTCTACCGGAATATG
E2 S27 NC004162.2	AACCAAGTCATCATGCTACTGTATCCTGACCACCCAAACACTCCTGTCTACCGGAATATG
E2 99659 KJ451624.1	AACCAAGTCATCATGCTGTATCCTGACCACCCAAACGCTCCTGTCTACAGGAATATG
	***** *
E2 181/25 L37661.3	GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGACGCATAAGAAGGAGATCAGGTTAACC
E2 IbH35 HM045786.1	GGACAGGAACCAAAATTACCACGAGGAGTGGGTGACACACACAAGAGGAGTTACCTTGACC
E2 LR2006 KT449801.1	GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGATGCATAGAAGGAAGTCGTGCTAACC
E2 SL15649 GU189061.1	GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGATGCATAGAAGGAAGTCGTGCTAACC
E2 S27 NC004162.2	GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGACGCACAGAAGGAGTCGTGCTAACC
E2 99659 KJ451624.1	GGAGAAGAACCAAACTATCAAGAAGAGTGGGTGACGCATAAGAAGGAGATCAGGTTAACC
	*** *

FIG. 15 (Contd)

E2_181/25_L37661.3	GTGCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTACAAGTATTGGCCG
E2_IbH35_HM045786.1	GTGCCCTACTGAGGGTCTCGAGGTCACCTTGGGGCAACAACGAACCATACAAGTACTGGCCG
E2_LR2006_KT449801.1	GTGCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_SL15649_GU189061.1	GTGCCGACTGAAGGGCTCGAGGTCACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_S27_NC004162.2	GTGCCGACTGAAGGGCTCGAGGTTACGTGGGGCAACAACGAGCCGTATAAGTATTGGCCG
E2_99659_KJ451624.1	GTGCCGACTGAGGGGCTCGAGGTCACGTGGGGTAACAATGAGCCGTACAAGTATTGGCCG
	*****.*** ** ***** ** ***** ** ** ***** ***** *****
E2_181/25_L37661.3	CAGTTATCCACAACGGGTACAGCCCCACGGCCACCCCGCATGAGATAATTTTGTATTATTAT
E2_IbH35_HM045786.1	CAGATGTCTACGAACGGTACTGCTCATGTGTCACCCACATGAGATAATCTTGTACTATTAT
E2_LR2006_KT449801.1	CAGTTATCTACAACGGGTACAGCCCCATGGCCACCCCGCATGAGATAATCTGTATTATTAT
E2_SL15649_GU189061.1	CAGTTATCTACAACGGGTACAGCCCCATGGCCACCCCGCATGAGATAATCTGTATTATTAT
E2_S27_NC004162.2	CAGTTATCTGCAACGGGTACAGCCCCACGGCCACCCCGCATGAGATAATCTTGTACTATTAT
E2_99659_KJ451624.1	CAGTTATCCACAACGGGTACAGCCCCACGGCCACCCCGCATGAGATAATCTGTATTATTAT
	;*..*** *****;*** ** *****.***** ***** *****
E2_181/25_L37661.3	GAGCTGTACCCCTACTATGACTGTGGTAGTTGTGTCAGTGGCCCTCGTTCTGCTACTCCTGTGCG
E2_IbH35_HM045786.1	GAGCTGTACCCCACTATGACTGTAAATCATTTGTGTCGGTGGCCCTCGTTCTGCTTCTGTGCG
E2_LR2006_KT449801.1	GAGCTGTACCCCACTATGACTGTAGTAGTTGTGTCAGTGGCCACGTTTCATACTCCTGTGCG
E2_SL15649_GU189061.1	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTCAGTGGCCACGTTTCATACTCCTGTGCG
E2_S27_NC004162.2	GAGCTGTACCCCTACTATGACTGTAGTAGTTGTGTCAGTGGCCCTCGTTTCATACTCCTGTGCG
E2_99659_KJ451624.1	GAGCTGTACCCCACTATGACTGCGGTAGTTTGTGTCAGTGGCCCTCGTTTCATACTCCTGTGCG
	***** ***** ***** ..** ** *****.*****;*****.*** *****
E2_181/25_L37661.3	ATGCTGGGTGTGGCAGTGGGGATGTGCATGTGTGCACGACGACGATGCATTACACCGTAC
E2_IbH35_HM045786.1	ATGCTGGGCACAGCAGTGGGGATGTGTGTGCGCAGCGGCGCAGATGCATTACACCATAT
E2_LR2006_KT449801.1	ATGCTGGGTATGGCAGCGGGGATGTGCATGTGTGCACGACGACGATGCATCACACCGTAT
E2_SL15649_GU189061.1	ATGCTGGGTATGGCAGTGGGGATGTGCATGTGTGCACGACGACGATGCATCACACCGTAT
E2_S27_NC004162.2	ATGCTGGGTATGGCAGTGGGGATGTGCATGTGTGCACGACGACGATGCATCACACCATAC
E2_99659_KJ451624.1	ATGCTGGGTGTGGCAGTGGGGATGTGCATGTGTGCACGACGACGATGCATTACACCGTAC
	*****.*** ***** *****;*****.***** ***** *****

FIG. 15 (Cont'd)

E2_181/25_L37661.3	GCTAAAGCG
E2_IbH35_HM045786.1	ACCAAGCGG
E2_LR2006_KT449801.1	GCTAAAGCG
E2_SL15649_GU189061.1	GCTAAAGCG
E2_S27_NC004162.2	GCTAAAGCG
E2_99659_KJ451624.1	GCTAAAGCG
	* * * *

FIG. 15 (Cont'd)

E2_IbH35_HM045786.1	STKDNFNVYKATRPYLAHCPDCGEGHSCHSPIALERIRNEATDGTLKIQVSLQIGIKTDD
E2_99659_KJ451624.1	SIKDHFNVYKATRPYLAHCPDCGEGHSCHSVALERIRNEATDGTLKIQVSLQIGIKTDD
E2_181/25_L37661.3	SIKDNFNVYKAIRPYLAHCPDCGEGHSCHSVALERIRNEATDGTLKIQVSLQIGIKTDD
E2_S27_NC004162.2	STKDNFNVYKATRPYLAHCPDCGEGHSCHSVALERIRNEATDGTLKIQVSLQIGIGTDD
E2_SL15649_GU189061.1	STKDNFNVYKATRPYLAHCPDCGEGHSCHSVALERIRNEATDGTLKIQVSLQIGIKTDD
E2_LR2006_KT449801.1	STKDNFNVYKATRPYLAHCPDCGEGHSCHSVALERIRNEATDGTLKIQVSLQIGIKTDD
E2_IbH35_HM045786.1	SHDWTCLRMDSHTPADAERAGLLVRTSAPCTITGTMGHFILARCPKGETLTVGFTDSRK
E2_99659_KJ451624.1	SHDWTCLRMDNHMPADAERAGLFVRTSAPCTITGTMGHFILARCPKGETLTVAGTDSRK
E2_181/25_L37661.3	SHDWTCLRMDNHMPADAERARLFVRTSAPCTITGTMGHFILARCPKGETLTVGFTDGRK
E2_S27_NC004162.2	SHDWTCLRMDNHIADAGRAGLFVRTSAPCTITGTMGHFILARCPKGETLTVGFTDSRK
E2_SL15649_GU189061.1	SHDWTCLRMDNHMPADAERAGLFVRTSAPCTITGTMGHFILARCPKGETLTVGFTDSRK
E2_LR2006_KT449801.1	SHDWTCLRMDNHMPADAERAGLFVRTSAPCTITGTMGHFILARCPKGETLTVGFTDSRK
E2_IbH35_HM045786.1	ISHTCTHPFHHEPPVIGRERFHSRPQHKGELPCSTYVQSTAATAEEIEVHMPPDTPDRTL
E2_99659_KJ451624.1	ISHSCTHPFHHDPPVIGREKFHSRPQHGRELPSTYAQSTAATAEEIEVHMPPDTPDRTL
E2_181/25_L37661.3	ISHSCTHPFHHDPPVIGREKFHSRPQHGRELPSTYAQSTAATAEEIEVHMPPDTPDRTL
E2_S27_NC004162.2	ISHSCTHPFHHDPPVIGREKFHSRPQHGRELPSTYVQSNAAATAEEIEVHMPPDTPDRTL
E2_SL15649_GU189061.1	ISHSCTHPFHHDPPVIGREKFHSRPQHGRELPSTYVQSTAATAEEIEVHMPPDTPDRTL
E2_LR2006_KT449801.1	ISHSCTHPFHHDPPVIGREKFHSRPQHKGELPCSTYVQSTAATAEEIEVHMPPDTPDRTL
E2_IbH35_HM045786.1	MTQQSGNVKITVNGQTVRYKNCNCGGSNEGLTTTDKVINNCKIDQCHAAVTNHKKWQYNP
E2_99659_KJ451624.1	MSQQSGNVKITVNSQTVRYKNCNCGGSSEGLTTTDKVINNCKVDQCHAAVTNHKKWQYNP
E2_181/25_L37661.3	MSQQSGNVKITVNSQTVRYKNCNCGDSNEGLTTTDKVINNCKVDQCHAAVTNHKKWQYNP
E2_S27_NC004162.2	LSQQSGNVKITVNSQTVRYKNCNCGGSNEGLTTTDKVINNCKVDQCHAAVTNHKKWQYNP
E2_SL15649_GU189061.1	MSQQSGNVKITVNGQTVRYKNCNCGGSNEGLTTTDKVINNCKVDQCHAAVTNHKKWQYNP
E2_LR2006_KT449801.1	MSQQSGNVKITVNGQTVRYKNCNCGGSNEGLTTTDKVINNCKVDQCHAAVTNHKKWQYNP

FIG. 15 (Contd.)

