GCATCTGGTTTGTCAGATCCGAGAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGA
GCAGGTAGCAGC**ATG**CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTG
CCTGCGGCCTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCT
TTTGCAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC
AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGC
CACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACAT
CAACACGGTTGTGTCCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACTCCACACTTCTGAGA
ATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGG
GAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTG
GCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACT
GTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTA
AAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGT
TCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAGGAAGTTATCTG
CGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAG
ATTGGTGGCTGTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACT
AATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAG
CAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTC
CCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGA
ACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC
ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACTGCTTTAAGTCATGCTTAT
GCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTT
CAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCT**TGA**AAG
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:1)

*FIG. 1*

MQPPPSLCGRALVALVLACGLSRIWGEERGFPPDRATPLLQTAEIMTPPTKTLWPKGSNASLAR
SLAPAEVPKGDRTAGSPPRTISPPPCQGPIEIKETFKYINTVVSCLVFVLGIIGNSTLLRIIYK
NKCMRNGPNILIASLALGDLLHIVIDIPINVYKLLAEDWPFGAEMCKLVPFIQKASVGITVLSL
CALSIDRYRAVASWSRIKGIGVPKWTAVEIVLIWVVSVVLAVPEAIGFDIITMDYKGSYLRICL
LHPVQKTAFMQFYKTAKDWWLFSFYFCLPLAITAFFYTLMTCEMLRKKSGMQIALNDHLKQRRE
VAKTVFCLVLVFALCWLPLHLSRILKLTLYNQNDPNRCELLSFLLVLDYIGINMASLNSCINPI
ALYLVSKRFKNCFKSCLCCWCQSFEEKQSLEEKQSCLKFKANDHGYDNFRSSNKYSSS
(SEQ ID NO:2)

Signal sequence.

amino acids 1-26

Transmembrane domains.

amino acids 101-121, 137-157, 177-197, 216-236, 275-295, 323-343, 362-382

N-glycosylation sites.

amino acids 59-62, 119-122

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 302-305

Tyrosine kinase phosphorylation site.

amino acids 424-430

N-myristoylation sites.

amino acids 57-62, 115-120, 170-175, 306-311, 371-376

7 transmembrane receptor homology.

amino acids 118-386

***FIG. 2***

Full-Length Light Chain of Murine 5E9

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVP
DRFTGSGSGTDFTLKITRVEAEDLGVYYCWQGTHFPYTFGGGTKLEIKRADAAPTVSIFPPSSE
QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYE
RHNSYTCEATHKTSTSPIVKSFNRNEC (SEQ ID NO:3)

VL of Murine 5E9

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVP
DRFTGSGSGTDFTLKITRVEAEDLGVYYCWQGTHFPYTFGGGTKLEIK (SEQ ID NO:5)

FIG. 3

Full-Length Heavy Chain of Murine 5E9

QVQLLQSGAELARPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGTIYPGDGDTSYAQKF
KGKATLTTDKYSSTAYMQLSSLASEDSAVYYCARWGYAYDIDNWGQGTTVTVSSASTKGPSVYP
LAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSST
WPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISL
SPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEF
KCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTN
NGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
(SEQ ID NO:4)

VH of Murine 5E9

QVQLLQSGAELARPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGTIYPGDGDTSYAQKF
KGKATLTTDKYSSTAYMQLSSLASEDSAVYYCARWGYAYDIDNWG (SEQ ID NO:6)

FIG. 4

Full-Length Light Chain of hu5E9.v1

DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWLQQKPGKAPKRLIYLVSKLDSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCWQGTHFPYTFGQGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:13)

VL of hu5E9.v1

DIQMTQSPSSLSASVGDRVTITCKSSQSLLDSDGKTYLNWLQQKPGKAPKRLIYLVSKLDSGVP
SRFSGSGSGTDFTLTISSLQPEDFATYYCWQGTHFPYTFGQGTKVEIK (SEQ ID NO:15)

FIG. 5

Full-Length Heavy Chain of hu5E9.v1

EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMQWVRQAPGKGLEWIGTIYPGDGDTSYAQKF
KGRATLSTDKSKNTAYLQMNSLRAEDTAVYYCARWGYAYDIDNWGQGTLVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
SLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO:14)

VH of hu5E9.v1

EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMQWVRQAPGKGLEWIGTIYPGDGDTSYAQKF
KGRATLSTDKSKNTAYLQMNSLRAEDTAVYYCARWGYAYDIDNWG (SEQ ID NO:16)

*FIG. 6*

VH of hu5E9.v2

EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWIGTIYPGDGDTSYAQKF
KGRVTITRDTSTSTAYLELSSLRSEDTAVYYCARWGYAYDIDNWG (SEQ ID NO:17)

*FIG. 7*

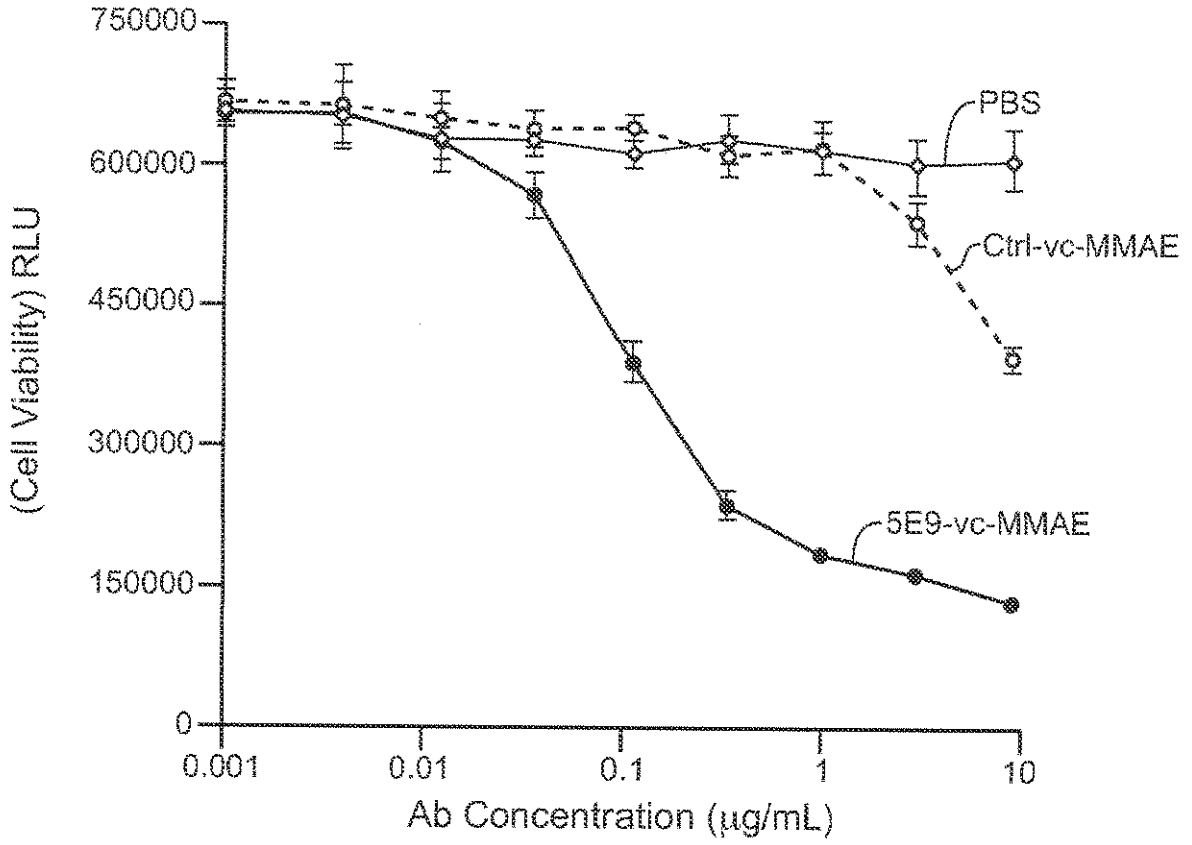

750000
600000
450000
300000
150000
0
(Cell Viability) RLU
PBS
Ctrl-vc-MMAE
5E9-vc-MMAE
0.001
0.01
0.1
1
10
Ab Concentration (μg/mL)

FIG. 8

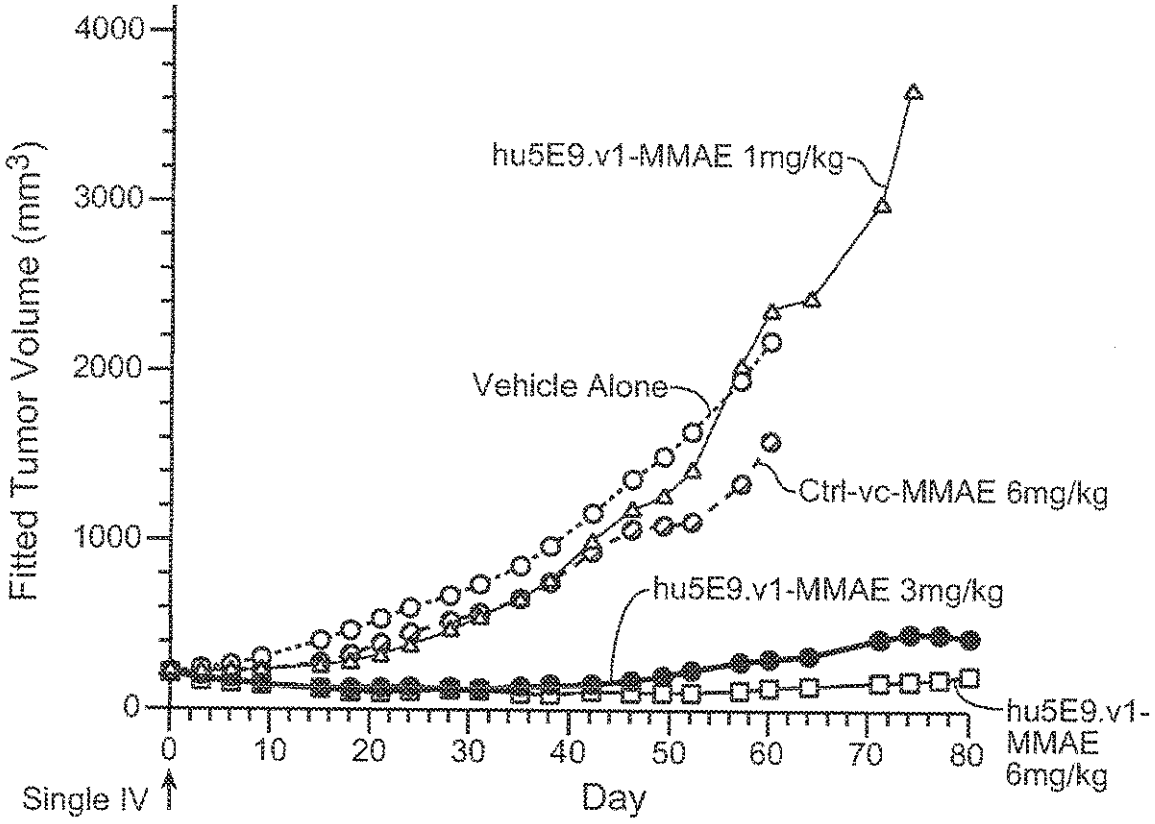

4000
3000
2000
1000
0
Fitted Tumor Volume (mm3)
hu5E9.v1-MMAE 1mg/kg
Vehicle Alone
Ctrl-vc-MMAE 6mg/kg
hu5E9.v1-MMAE 3mg/kg
hu5E9.v1-MMAE 6mg/kg
0
10
20
30
40
50
60
70
80
Day
Single IV

FIG. 9