FIG. 1A

>gi|27886610|ref|NM_002821.3| Homo sapiens PTK7 protein tyrosine kinase 7 (PTK7), transcript variant PTK7-1, mRNA

(SEQ ID NO: 1)

GCGGCGCGCGGGGACTCGGAGGTACTGGGCGCGCGCGGCTCCGGCTCGGGACGCCTCGGGACGCCTCGGG
GTCGGGCTCCGGCTGCGGCTGCTGCTGCGGCGCCCGCGCTCCGGTGCGCTCCGCCTCCTGTGCCCGCCGC
GGAGCGCAGTCTGCGCGCCCGCCGTGCGCCCTCAGCTCCTTTTCCTGAGCCCGCCGCGATGGGAGCTGCG
CGGGGATCCCCGGCCAGACCCCGCCGGTTGCCTCTGCTCAGCGTCCTGCTGCTGCCGCTGCTGGGCGGTA
CCCAGACAGCCATTGTCTTCATCAAGCAGCCGTCCTCCCAGGATGCACTGCAGGGGCGCCGGGCGCTGCT
TCGCTGTGAGGTTGAGGCTCCGGGCCCGGTACATGTGTACTGGCTGCTCGATGGGGCCCCTGTCCAGGAC
ACGGAGCGGCGTTTCGCCCAGGGCAGCAGCCTGAGCTTTGCAGCTGTGGACCGGCTGCAGGACTCTGGCA
CCTTCCAGTGTGTGGCTCGGGATGATGTCACTGGAGAAGAAGCCCGCAGTGCCAACGCCTCCTTCAACAT
CAAATGGATTGAGGCAGGTCCTGTGGTCCTGAAGCATCCAGCCTCGGAAGCTGAGATCCAGCCACAGACC
CAGGTCACACTTCGTTGCCACATTGATGGGCACCCTCGGCCCACCTACCAATGGTTCCGAGATGGGACCC
CCCTTTCTGATGGTCAGAGCAACCACACAGTCAGCAGCAAGGAGCGGAACCTGACGCTCCGGCCAGCTGG
TCCTGAGCATAGTGGGCTGTATTCCTGCTGCGCCCACAGTGCTTTTGGCCAGGCTTGCAGCAGCCAGAAC
TTCACCTTGAGCATTGCTGATGAAAGCTTTGCCAGGGTGGTGCTGGCACCCCAGGACGTGGTAGTAGCGA
GGTATGAGGAGGCCATGTTCCATTGCCAGTTCTCAGCCCAGCCACCCCCGAGCCTGCAGTGGCTCTTTGA
GGATGAGACTCCCATCACTAACCGCAGTCGCCCCCCACACCTCCGCAGAGCCACAGTGTTTGCCAACGGG
TCTCTGCTGCTGACCCAGGTCCGGCCACGCAATGCAGGGATCTACCGCTGCATTGGCCAGGGGCAGAGGG
GCCCACCCATCATCCTGGAAGCCACACTTCACCTAGCAGAGATTGAAGACATGCCGCTATTTGAGCCACG
GGTGTTTACAGCTGGCAGCGAGGAGCGTGTGACCTGCCTTCCCCCCAAGGGTCTGCCAGAGCCCAGCGTG
TGGTGGGAGCACGCGGGAGTCCGGCTGCCCACCCATGGCAGGGTCTACCAGAAGGGCCACGAGCTGGTGT
TGGCCAATATTGCTGAAAGTGATGCTGGTGTCTACACCTGCCACGCGGCCAACCTGGCTGGTCAGCGGAG
ACAGGATGTCAACATCACTGTGGCCACTGTGCCCTCCTGGCTGAAGAAGCCCCAAGACAGCCAGCTGGAG
GAGGGCAAACCCGGCTACTTGGATTGCCTGACCCAGGCCACACCAAAACCTACAGTTGTCTGGTACAGAA
ACCAGATGCTCATCTCAGAGGACTCACGGTTCGAGGTCTTCAAGAATGGGACCTTGCGCATCAACAGCGT
GGAGGTGTATGATGGGACATGGTACCGTTGTATGAGCAGCACCCCAGCCGGCAGCATCGAGGCGCAAGCC
CGTGTCCAAGTGCTGGAAAAGCTCAAGTTCACACCACCACCCCAGCCACAGCAGTGCATGGAGTTTGACA
AGGAGGCCACGGTGCCCTGTTCAGCCACAGGCCGAGAGAAGCCCACTATTAAGTGGGAACGGGCAGATGG
GAGCAGCCTCCCAGAGTGGGTGACAGACAACGCTGGGACCCTGCATTTTGCCCGGGTGACTCGAGATGAC
GCTGGCAACTACACTTGCATTGCCTCCAACGGGCCGCAGGGCCAGATTCGTGCCCATGTCCAGCTCACTG
TGGCAGTTTTTATCACCTTCAAAGTGGAACCAGAGCGTACGACTGTGTACCAGGGCCACACAGCCCTACT
GCAGTGCGAGGCCCAGGGGGACCCCAAGCCGCTGATTCAGTGGAAAGGCAAGGACCGCATCCTGGACCCC
ACCAAGCTGGGACCCAGGATGCACATCTTCCAGAATGGCTCCCTGGTGATCCATGACGTGGCCCCTGAGG
ACTCAGGCCGCTACACCTGCATTGCAGGCAACAGCTGCAACATCAAGCACACGGAGGCCCCCCTCTATGT
CGTGGACAAGCCTGTGCCGGAGGAGTCGGAGGGCCCTGGCAGCCCTCCCCCCTACAAGATGATCCAGACC

FIG. 1A (CONT.)

(SEQ ID NO: 1) Cont.

ATTGGGTTGTCGGTGGGTGCCGCTGTGGCCTACATCATTGCCGTGCTGGGCCTCATGTTCTACTGCAAGA
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TGGGCCTTTGCAGAACGGGCAGCCCTCAGCAGAGATCCAAGAAGAAGTGGCCTTGACCAGCTTGGGCTCC
GGCCCCGCGGCCACCAACAAACGCCACAGCACAAGTGATAAGATGCACTTCCCACGGTCTAGCCTGCAGC
CCATCACCACGCTGGGGAAGAGTGAGTTTGGGGAGGTGTTCCTGGCAAAGGCTCAGGGCTTGGAGGAGGG
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CTGAGCCCCACTACATGGTGCTGGAATATGTGGATCTGGGAGACCTCAAGCAGTTCCTGAGGATTTCCAA
GAGCAAGGATGAAAAATTGAAGTCACAGCCCCTCAGCACCAAGCAGAAGGTGGCCCTATGCACCCAGGTA
GCCCTGGGCATGGAGCACCTGTCCAACAACCGCTTTGTGCATAAGGACTTGGCTGCGCGTAACTGCCTGG
TCAGTGCCCAGAGACAAGTGAAGGTGTCTGCCCTGGGCCTCAGCAAGGATGTGTACAACAGTGAGTACTA
CCACTTCCGCCAGGCCTGGGTGCCGCTGCGCTGGATGTCCCCCGAGGCCATCCTGGAGGGTGACTTCTCT
ACCAAGTCTGATGTCTGGGCCTTCGGTGTGCTGATGTGGGAAGTGTTTACACATGGAGAGATGCCCCATG
GTGGGCAGGCAGATGATGAAGTACTGGCAGATTTGCAGGCTGGGAAGGCTAGACTTCCTCAGCCCGAGGG
CTGCCCTTCCAAACTCTATCGGCTGATGCAGCGCTGCTGGGCCCTCAGCCCCAAGGACCGGCCCTCCTTC
AGTGAGATTGCCAGCGCCCTGGGAGACAGCACCGTGGACAGCAAGCCGTGAGGAGGGAGCCCGCTCAGGA
TGGCCTGGGCAGGGGAGGACATCTCTAGAGGGAAGCTCACAGCATGATGGGCAAGATCCCTGTCCTCCTG
GGCCCTGAGGCCCCTGCCCTAGTGCAACAGGCATTGCTGAGGTCTGAGCAGGGCCTGGCCTTTCCTCCTC
TTCCTCACCCTCATCCTTTGGGAGGCTGACTTGGACCCAAACTGGGCGACTAGGGCTTTGAGCTGGGCAG
TTTTCCCTGCCACCTCTTCCTCTATCAGGGACAGTGTGGGTGCCACAGGTAACCCCAATTTCTGGCCTTC
AACTTCTCCCCTTGACCGGGTCCAACTCTGCCACTCATCTGCCAACTTTGCCTGGGGAGGGCTAGGCTTG
GGATGAGCTGGGTTTGTGGGGAGTTCCTTAATATTCTCAAGTTCTGGGCACACAGGGTTAATGAGTCTCT
TGGCCCACTGGTCCCACTTGGGGGTCTAGACCAGGATTATAGAGGACACAGCAAGTGAGTCCTCCCCACT
CTGGGCTTGTGCACACTGACCCAGACCCACGTCTTCCCCACCCTTCTCTCCTTTCCTCATCCTAAGTGCC
TGGCAGATGAAGGAGTTTTCAGGAGCTTTTGACACTATATAAACCGCCCTTTTTGTATGCACCACGGGCG
GCTTTTATATGTAATTGCAGCGTGGGGTGGGTGGGCATGGGAGGTAGGGGTGGGCCCTGGAGATGAGGAG
GGTGGGCCATCCTTACCCCACACTTTTATTGTTGTCGTTTTTTGTTTGTTTTGTTTTTTTGTTTTTGTTT
TTGTTTTTACACTCGCTGCTCTCAATAAATAAGCCTTTTTTACAACCTG

>gi|47938093|gb|AAH71557.1| PTK7 protein tyrosine kinase 7 [Homo sapiens]

(SEQ ID NO:2)

MGAARGSPARPRRLPLLSVLLLPLLGGTQTAIVFIKQPSSQDALQGRRALLRCEVEAPGPVHVYWLLDGA
PVQDTERRFAQGSSLSFAAVDRPQDSGTFQCVARDDVTGEEARSANASFNIKWIEAGPVVLKHPASEAEI
QPQTQVTLRCHIDGHPRPTYQWFRDGTPLSDGQSNHTVSSKERNLTLRPAGPEHSGLYSCCAHSAFGQAC
SSQNFTLSIADESFARVVLAPQDVVVARYEEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLRRATV
FANGSLLLTQVRPRNAGIYRCIGQGQRGPPIILEATLHLAEIEDMPLFEPRVFTAGSEERVTCLPPKGLP
EPSVWWEHAGVRLPTHGRVYQKGHELVLANIAESDAGVYTCHAANLAGQRRQDVNITVATVPSWLKKPQD
SQLEEGKPGYLDCLTQATPKPTVVWYRNQMLISEDSRFEVFKNGTLRINSVEVYDGTWYRCMSSTPAGSI
EAQARVQVLEKLKFTPPPQPQQCMEFDKEATVPCSATGREKPTIKWERADGSSLPEWVTDNAGTLHFARV
TRDDAGNYTCIASNGPQGQIRAHVQLTVAVFITFKVEPERTTVYQGHTALLQCEAQGDPKPLIQWKGKDR
ILDPTKLGPRMHIFQNGSLVIHDVAPEDSGRYTCIAGNSCNIKHTEAPLYVVDKPVPEESEGPGSPPPYK
MIQTIGLSVGAAVAYIIAVLGLMFYCKKRCKAKRLQKQPEGEEPEMECLNGGPLQNGQPSAEIQEEVALT
SLGSGPAATNKRHSTSDKMHFPRSSLQPITTLGKSEFGEVFLAKAQGLEEGVAETLVLVKSLQSKDEQQQ
LDFRRELEMFGKLNHANVVRLLGLCREAEPHYMVLEYVDLGDLKQFLRISKSKDEKLKSQPLSTKQKVAL
CTQVALGMEHLSNNRFVHKDLAARNCLVSAQRQVKVSALGLSKDVYNSEYYHFRQAWVPLRWMSPEAILE
GDFSTKSDVWAFGVLMWEVFTHGEMPHGGQADDEVLADLQAGKARLPQPEGCPSKLYRLMQRCWALSPKD
RPSFSEIASALGDSTVDSKP

FIG. 1B

PTK7 isoforms

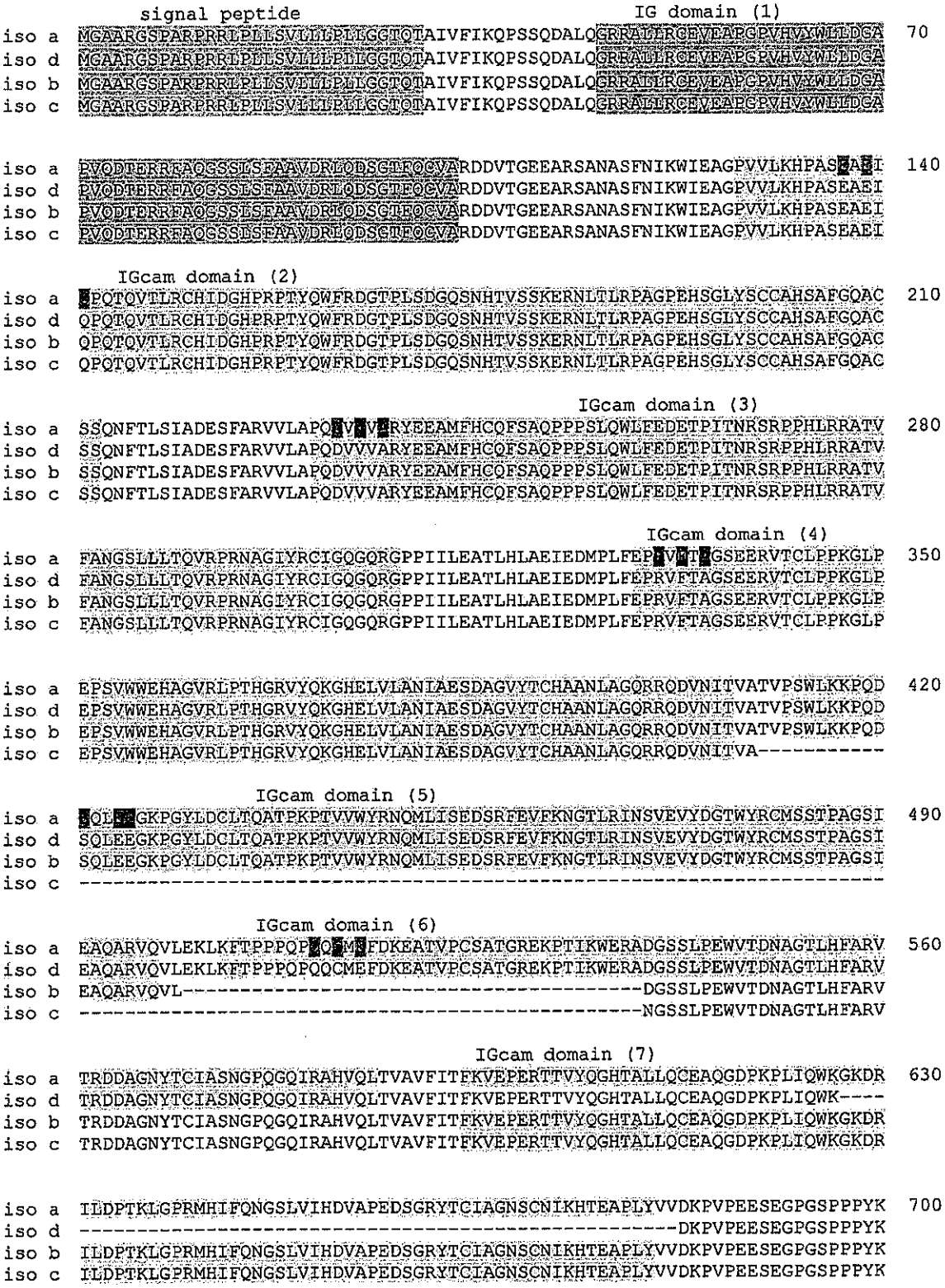


FIG. 1C

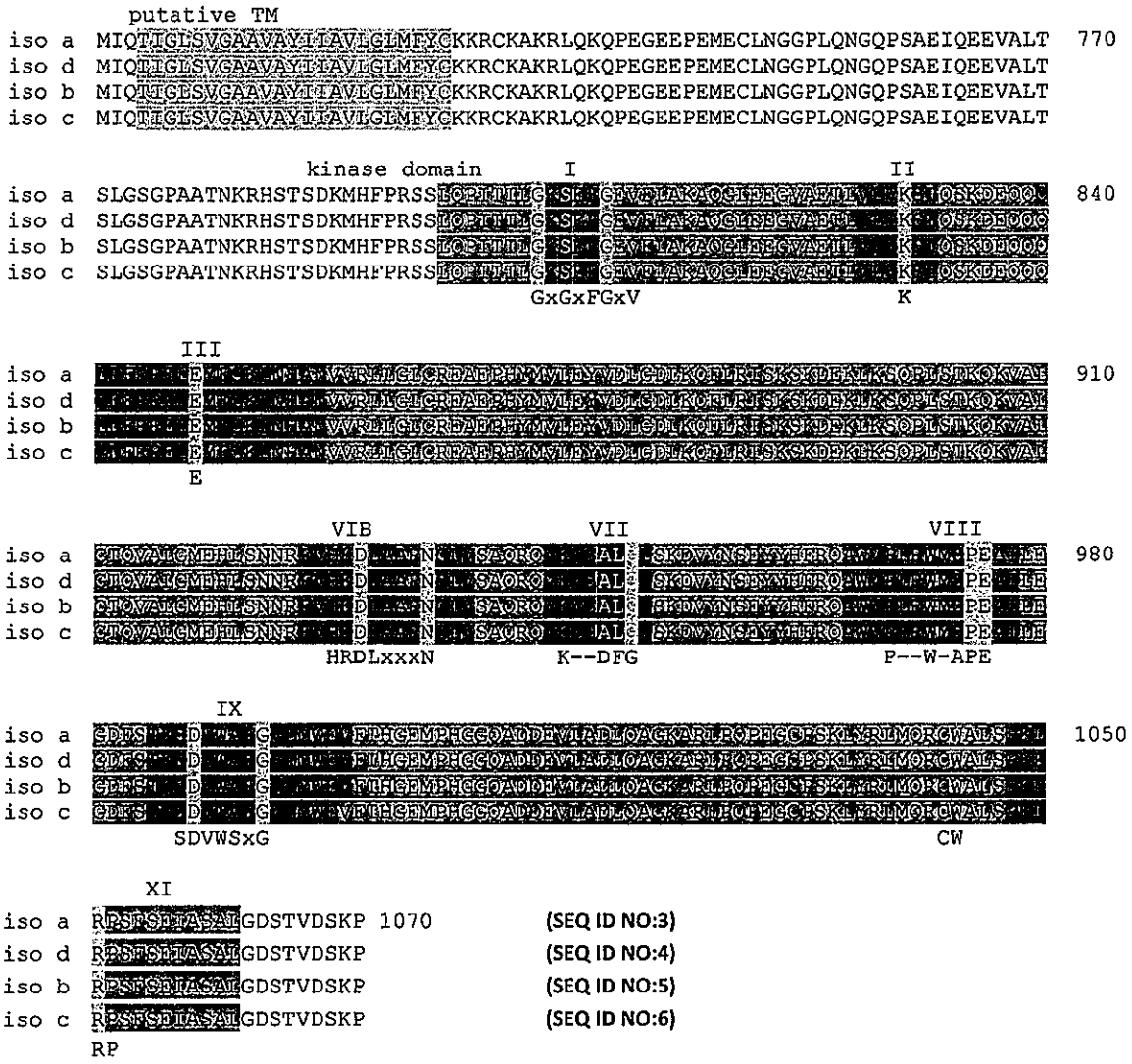

putative TM
iso a MIQTIGLSVGAAVAVIIAVLGIMFYCKKRCKAKRLQKQPEGEEPEMECLNGGPLQNGQPSAEIQEEVALT 770
iso d MIQTIGLSVGAAVAYIIAVLGIMFYCKKRCKAKRLQKQPEGEEPEMECLNGGPLQNGQPSAEIQEEVALT
iso b MIQTIGLSVGAAVAYIIAVLGIMFYCKKRCKAKRLQKQPEGEEPEMECLNGGPLQNGQPSAEIQEEVALT
iso c MIQTIGLSVGAAVAYIIAVLGIMFYCKKRCKAKRLQKQPEGEEPEMECLNGGPLQNGQPSAEIQEEVALT
kinase domain
I
II
iso a SLGSGPAATNKRHSTSDKMHFPRSS 840
iso d SLGSGPAATNKRHSTSDKMHFPRSS
iso b SLGSGPAATNKRHSTSDKMHFPRSS
iso c SLGSGPAATNKRHSTSDKMHFPRSS
GxGxFGxV
K
III
iso a 910
iso d
iso b
iso c
E
VIB
VII
VIII
iso a 980
iso d
iso b
iso c
HRDLxxxN
K--DFG
P--W-APE
IX
iso a 1050
iso d
iso b
iso c
SDVWSxG
CW
XI
iso a GDSTVDSKP 1070 (SEQ ID NO:3)
iso d GDSTVDSKP (SEQ ID NO:4)
iso b GDSTVDSKP (SEQ ID NO:5)
iso c GDSTVDSKP (SEQ ID NO:6)
RP

FIG. 1C (CONT.)

PTK7 Gene Expression is Elevated in Colorectal Cancer TPC

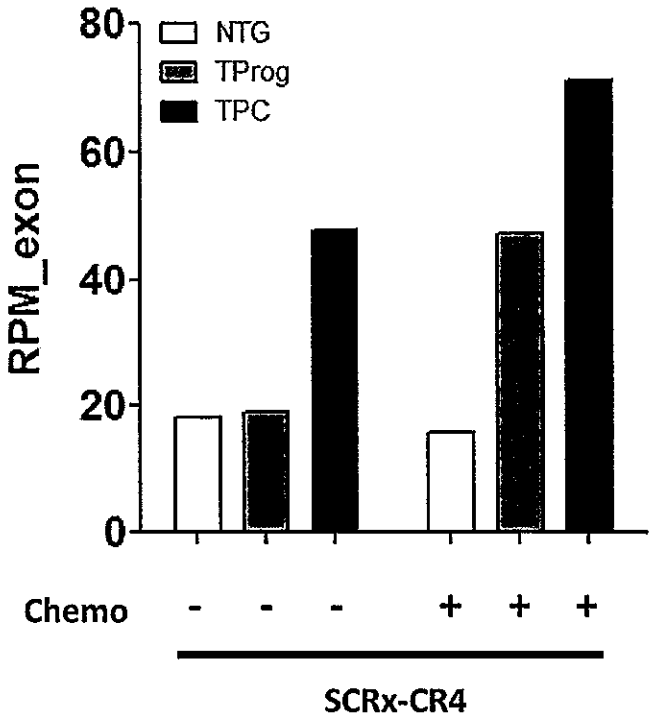


FIG. 2

Taqman PCR Confirms PTK7
Overexpression in Colorectal & Pancreatic TPC

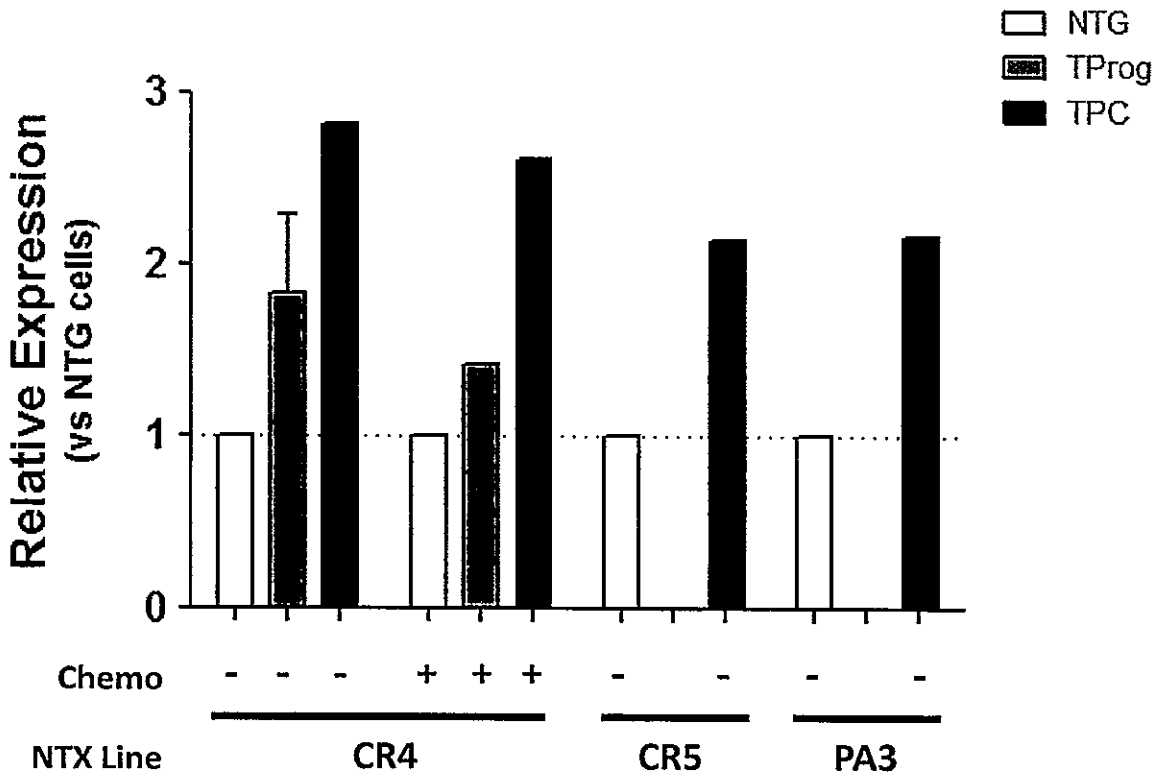


FIG. 3

Taqman PCR Confirms Elevated PTK7 Overexpression in Colorectal Tumor Specimens at Different Stages of Disease

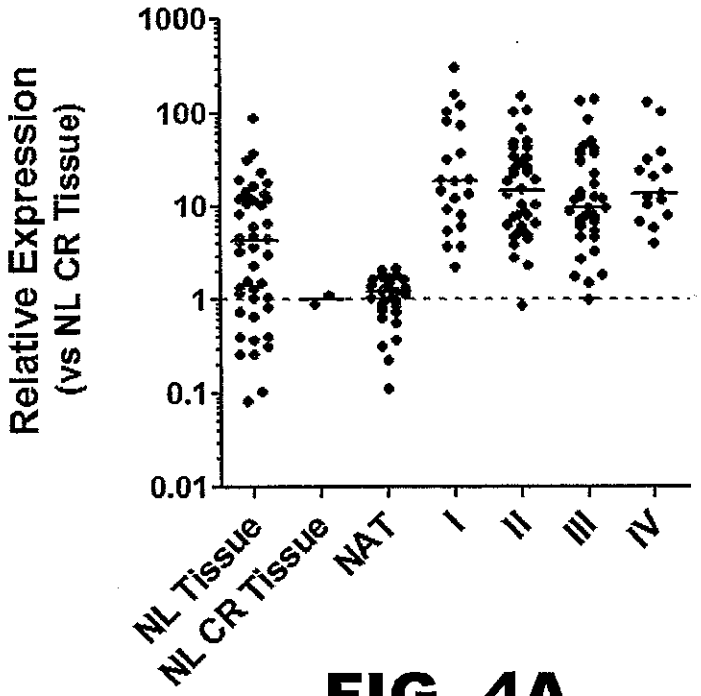


FIG. 4A

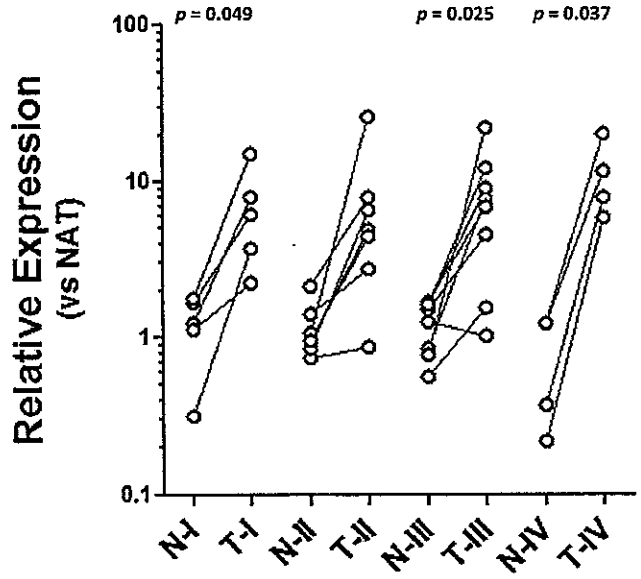


FIG. 4B

Taqman PCR Demonstrates PTK7 Overexpression in Adrenal, Colorectal, Endometrial, Esophageal, Liver & Bladder Cancer

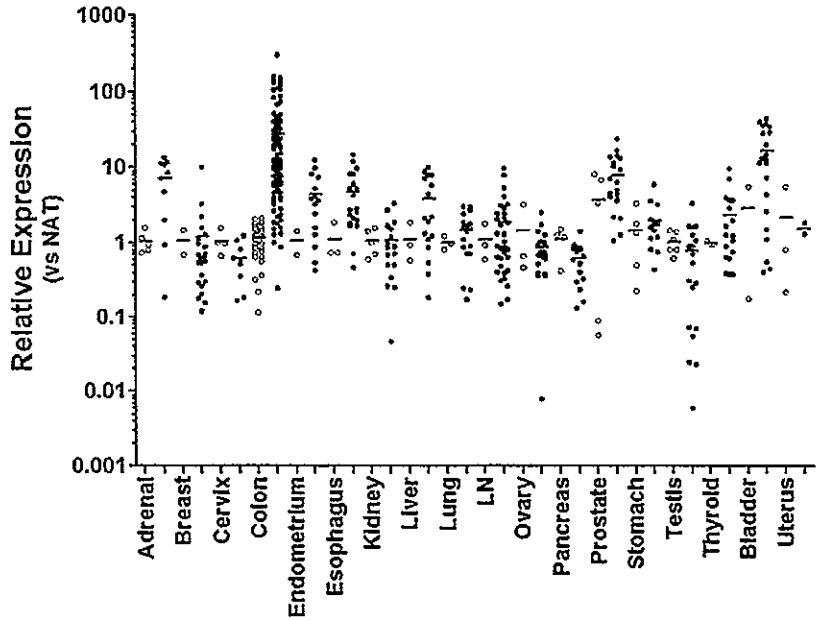


FIG. 5A

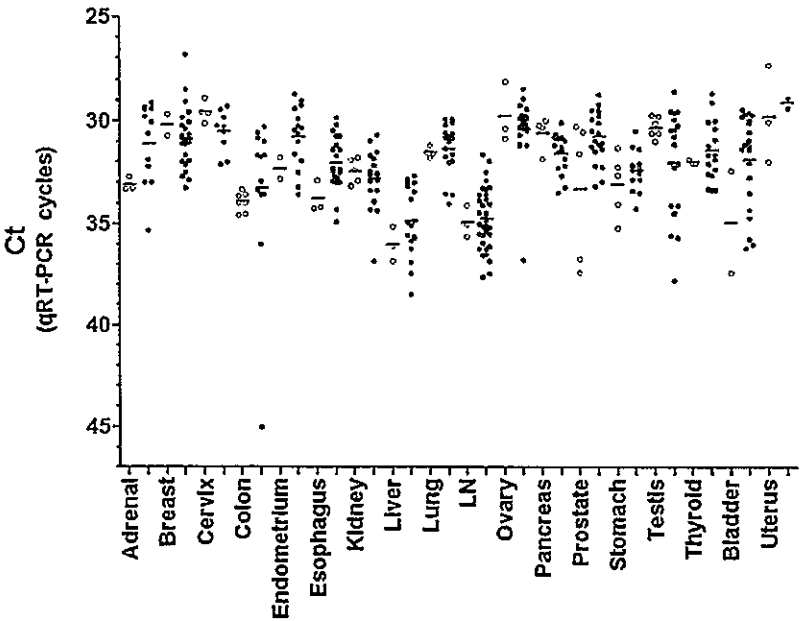


FIG. 5B

Protein Sequences of Exemplary Murine and Humanized PTK7 Modulator Light Chain Variable Regions

Murine Light Chain Variable Regions

mAb	FW1	CDRL1	FW2	CDRL2	FW3	CDRL3	SEQ ID NO
SC6.2.35	DIVLTQSPASLAVSLGQRATISC	RASESVDSFGNSF	MHWYQQKPGQPPKLLIY	AASNLGS	GVPARFSGSGSGTDFSLNIHPVEEDDSAMYFC	QQSKEVPRTFGGGSRLEIKR	20
SC6.10.2	DIVMTQSQKFMSTSVGDRVNVTC	KASQNVGTN	VVWYQQKTGQSPKALIH	SASYRYS	GVPDRFTGSGSGTDFTLTLSNVQSEDLAEYFC	QHYNSFPYTFGGGTKLEIKR	22
SC6.4.1	LGGRVTITC	KASDHINNW	LAWYQQKPGNAPRLLIS	GATTLET	GVPSRFSGSGSGKDYTLSITSLQTEDVATYYC	QQYWSIPYTFGGGTKLEIKR	24
SC6.50.1	DIVLTQSPATLSVTPGDSVSLSC	RASQSVSNN	LHWYQQKSHASPRLLIK	YASQSIS	GIPSRFSGSGSGTDFTLSINSVETEDFGMYFC	QQSYSWPRTFGGGTKLEIKR	26
SC6.3	DIVMTQSPSSLSVSAGEKVTMSC	KSSQSLLNGGNQQNS	LAWYQQKPGQPPKLLIY	GASTRES	GVPDRFTGSGSGTDFALTISSVQAEDLAVYYC	QNDHTYPYTFGGGTELEIKR	28
SC6.4	DIQMTQSPASLSASVGETVTITC	RTSENIYSYLAWYQQKQ	LAWYQQKQGKSPQLLVH	NANTLAE	GVPSRFSGSGSGTQFSLRINSLQPEDFGSYYC	QHHYGIPFTFGGGTKLEVER	30
SC6.6	DIVLTQSPASLAVSLGQRATVFC	RASQTVDYNGMSY	MHWFQQKPGQPPKLLIY	AASNLDS	GIPARFSGSGSGTDFTLNIHPVEEEDAATYYC	QQCIEDPLTFGAGTMLEVK	32
SC6.7	DIQMTQSPASLSVSVGETVTITC	RASENIYSN	LAWYQQKQGKSPQLLVN	AATNLAD	GVSSRFRGSGSGTQYSLKINSLQSEDFGSYYC	QHFWITPFTFGSGTKLERK	34
SC6.13	DIVLTQSPASLAVSLGQRATISC	RASESVDNYGISF	MHWFQQKPGQPPKLLIY	AASNLGS	GVPARFSGSGSGTDFSLNIHPLEEADTAMYFC	QQSKEVPRTFGGGTKLEIK	36
SC6.14	SIVLTQSLKFLLVSAGDRVTMTC	KASQSVTND	VAWYQQKPGQSPKLLIY	YASKHYT	GVPDRFTGSGYGTDFTFTISTVQAEDLAVYFC	QQDYSSPYTFGGGTKLEIKR	38
SC6.15	DIVLTQSPASLAVSLGQRATISC	RASQSVSTSTSIY	MHWYQQKPGQPPKLLIK	YASNLES	GVPARFSGSGSGTEITLNIHPVEEEDTATYYC	QHSWEIPWTFGGGTKLEIK	40
SC6.19	DIVMTQSPSSLSVSAGEKVTMSC	KSSQSLLNSGNPKNY	LAWYQQKPGQPPKLLIY	GASTRGS	GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC	QNDHTFPYTFGGGTKLEIKR	42
SC6.20	DIQMTQTPSSLSASLGDRVTINC	RASQGLSNY	LNWYQQKPDGTVKLLIY	YASILHS	GVPSRFTGSGSGTDYSLTISTLEQEDIGTYFC	QQGNTLPWTFGGGTKLEIK	44
SC6.21	DIVMSQSPSSLAVSVGEKVTLSC	KSSQSLLYSSTQNNY	LAWYQQTPGQSPKLLIY	WASTRES	GVPDRFTGSGSGTDFTLTISSVKAEDLAVYYC	QQYYSYPWTFGGGTKLEIK	46
SC6.23	DIKMTQSPSSMYASLGERVTITC	KASQDIYPY	LNWFQQKPGKSPKTLIY	RTNRLLD	GVPSRFSGSGSGQDYSLTISSLDYEDMGIYYC	LQYDEFPLTFGAGTKLELK	48
SC6.24	DIVLTQSPASLAVSLGQRATISC	RASESVDSYGKSF	MHWYQQRPGQPPKLLIY	RASNLES	GIPARFSGSGSRTDFTLTINPVEADDVATYYC	QQSNEDPWTFGGGTKLEIK	50
SC6.26	DIALTQSPASLAVSLGQRATISC	RASESVDNSGICF	VNWFQQKPGQPPKLLIY	AASNQGS	GVPARFSGSGSGTDFSLNIHPMEKDDTAMYFC	QQSKEVPWTFGGGTKLEIK	52
SC6.29	DIVLTQSPASLTVSLGQRATISC	RASQSVSTSTFNY	MNWYQQKLGQPPKLLIK	YASNLES	GVPARFSGSGSGTDFTLNIHPVEEEDIATYYC	QHSWEIPWTFGGGTKLEIK	54
SC6.41	DIVLTQATPSVPVTPGESVSISC	RSSKSLLHTKGDTY	LYWFLQRPGQSPQLLIY	RMSNLAS	GVPDRFSGSGSGTVFTLRISRVEAEDVGVYYC	MQHLEYPFTFGSGTKLEIKR	56
SC6.58	ETTVTQSPASLSMAIGEKVTIRC	ITNTDIDDD	MNWYQQKPGEPPKLLIS	EGNGLRP	GVPSRFSSSGYGTDFVFTIENMLSEDVADYYC	LQSDNLPLTFGSGTKLEIK	58
SC6.59	DIVMTQSPSSLTVTAGVKVTMSC	KSSQSLLNSGDQKNC	LTWYQQKPGQPPKLLIY	WASTRES	GVPDRFTGSGSGTDFTLTISSVQAEDLAVYYC	QNDYSYPLTFGAGTKLELK	60

Humanized Light Chain Variable Regions

mAb	FW1	CDRL1	FW2	CDRL2	FW3	CDRL3	SEQ ID NO
hSC6.23	DIQMTQSPSSLSASVGDRVTITC	KASQDIYPY	LNWFQQKPGKAPKTLIY	RTNRLLD	GVPSRFSGSGSGTDFTFTISSLQPYYC	LQYDEFPLTFGAGTKLEIKR	62
hSC6.24	EIVLTQSPATLSLSPGERATLSC	RASESVDSYGKSF	MHWYQQKPGQAPRLLIY	RASNLES	GIPARFSGSGSGTDFTLTISSLEPEDFAVYYC	QQSNEDPWTFGGGTKLEIKR	64
hSC6.41	DIVMTQSPLSLPVTPGEPASISC	RSSKSLLHTKGDTY	LYWFLQKPGQSPQLLIY	RMSNRAS	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	MQHLEYPFTFGQGTKLEIKR	66
hSC6.58	ETTLTQSPAFMSATPGDKVNISC	ITNTDIDDD	MNWYQQKPGEAAILLIS	EGNGLRP	GIPPRFSGSGYGTDFTLTINNIESEDAAYYFC	LQSDNLPLTFGSGTKLEIKR	68

FIG. 6A

Protein Sequences of Exemplary Murine and Humanized PTK7 Modulator Heavy Chain Variable Regions

Murine Heavy Chain Variable Regions

mAb	FR1	CDRH1	FR2	CDRH2	FR3	CDR3	SEQ ID NO
SC6.2.35	QVQMQQSGAELMKPGASVKLSCKAT	GYTFTGYW	IEWVKQRPGHGLEWIGE	ILPGSGRS	NSNEKFKGKATFTADTSSNTAYMQLSSLTTEDSAIYYC	ARGKLSWGQGTLVTVSA	21
SC6.10.2	QVQLQQSGAELVRPGVSVKISCKGS	GYRFTDYP	IHWVKQSHAKSLEWIGI	ISTYYGDV	TNNPKFRGKATMTVDKSSTTAYMELARLTSEDSAIYYC	ARNDLFAYWGQGTLVTVSA	23
SC6.4.1	SDVQLQESGPGLVKPSQSLSLTCTVT	GYSITSDYA	WNWIRQFPGNKLEWMV	SYSGYT	NYNPSLKSRISITRDTSKNQFFLQLSVTTEDTATYYC	ARGDAYDVRRSTYYFDYWGQGTTLTVSS	25
SC6.50.1	QLEESGAELMQPGASVKVSCKAT	LEEGYTFTVYW	IEWVKQRPGHGLEWIGE	ILPGSGSTD	YNEKFKGKATFTADSSSNTAYMQLSSLTTEDSAI YYC	ARGKLHWGQGTLVTVSA	27
SC6.3	EVKLLESGGGLVQPGGSLKLSCAAS	GFDFSKDW	MSWVRQAPGKGLEWIGE	INPDSRTI	NYAPSLKDKFIISRENAKNTLYLQMSKVRSEDTALYYC	ARWDYDGGMDYWGQGTSVTVSS	29
SC6.4	EVKLLESGGGLVQPGGSLKLSCAAS	GFDFSRYW	MSWVRQAPGKGLEWIGE	INPDSSTI	NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYC	ARPGYGNLFAYWGQGTLVTVSA	31
SC6.6	EVQLQQSGPELVKPGASVKMSCKAS	GYTFTSY	VIHWVKQKPGQGLEWIGYI	INPFSDGT	KFTEKFKGKASLTSDKSSSTAYMELNSLTSEDSAVYYC	ARRGPYYYGTAMDYWGQGTSVTVSS	33
SC6.7	QVQLQQSGAELGRPGASVKLSCKDS	GYTITIYW	MQWVKQRPGQGLEWIGA	IYPGDGDT	RYPQKFKGKSTLSADKSSNTASMHLSSLASDDSAVYYC	SRGGSTNYDYDGFAYWGQGTLVTVSA	35
SC6.13	QVQLQQSGAELMKPGASVKISCKAT	GYTFSNYW	IEWVKQRPGHGLEWIGE	ILPGRGST	NYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYC	ARGKQYWGQGTTLTVSS	37
SC6.14	QVQLQQPGAELVKPGASVKLSCKAS	GYTFTSYW	MHWVKQRPGQGLEWIGE	INPSNGRS	NYNEKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYFC	AHYYDGSYGFFDYWGQGTTLTVSS	39
SC6.15	EVKLLESGGGLVQPGGSLKVSCTAS	GFDFSRYW	MSWVRQAPGKGLEWIGE	INPDSSTI	NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYC	ARPGYGNLFVYWGQGTLVTVSS	41
SC6.19	EVKLLESGGGLVQPGGSLRLSCAAS	GFDFSKDW	MSWVRQAPGKGLEWIGE	INPDSSTI	NYAPALKDKFIISRENAKNTLYLQMNKVRSEDTALYYC	ARWSTGLDYWGQGTTLTVSS	43
SC6.20	QVQLQQSGPELVKPGASVKISCKAS	GYPFSTSW	MNWVKQRPGKGLEWIGR	IYLGDGDT	NYNGKFTGKATLTADKSSSTVYMQLSSLTSEDSAVYFC	ARWRGDYDYWGQGTTLTVSS	45
SC6.21	SDVQLQESGPGLVKPSQTLSLTCSVP	DYSITSDYH	WHWIRQFPGNKLEWMG	YISSRGST	NYNPSLKNRISITHDTSENQFFLKLTSVTTEDSATYYC	AGLSQLALDYWGQGTTLTVSS	47
SC6.23	QVTLKESGPGILKPSQTLSLTCSFS	GFSLSTSNMG	VGWIRQPSGKGLEWLAH	IWWDDDK	YYNPSLKSQLTISKDTSRNQVFLKITSVDTEDTATYYC	VRSNYGYAWFAYWGQGTLVTVSA	49
SC6.24	QVQLQQSGPEVVRPGVSVKISCKGS	GYTFTDYA	VHWVKLSHAKSLEWIGV	ISTYNDYT	YNNQDFKGKATMTVDKSSSTAYMELARLTSEDSAIYYC	ARGNSYFYALDYWGQGTSVTVSS	51
SC6.26	QVQLQQSGAELASPGTSVKLSCKAS	GYTFTFYG	ISWVKQKTGQGLEWIGE	IYPGSYNA	YYNDKFKGKATLTADRSSSTAYMQLSSLTSEDSAVYFC	ARDYGDPYYYAMDYWGQGTSVTVSS	53
SC6.29	EVKLLESGGGLVQPGGSQKLSCAAS	GFDFSRYW	MSWVRQAPGKGLEWIGE	INPDSSTV	NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYC	ARPGYGNLFVYWGQGTLVTVSA	55
SC6.41	EVQLQQSGAESVRSGASVKLSCTAS	GLNIKDYY	MHWVNLRPEQGLEWIGW	IDPENGDT	EYAPEFQGKATMTADTSSNTAYLQLSSLTSEDTAVYYC	NACNYGSAYGYWGQGTTLTVSS	57
SC6.58	EVKLLESGGGLVQPGGSLKLSCAAS	GFDFSRYW	MSWVRQAPGKGLEWIGD	LNPDSSAI	NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYC	TLITTLVPYTMDFWGQGTSVTVSS	59
SC6.59	EIHLVESGGGLVKPGGSLKVSCAAS	GFTFSRYA	MSWVRQTPEKRLEWVAT	ISGGGRYT	YYPDLVKGRFTISRDIARTTLYLQMSSLRSEDTAMYYC	ARTARASNYAMDYWGQGTSVTVSS	61

Humanized Heavy Chain Variable Regions

mAb	FR1	CDRH1	FR2	CDRH2	FR3	CDR3	SEQ ID NO
hSC6.23	QITLKESGPTLVKPTQTLTLTCTFS	GFSLSTSNMG	VGWIRQPPGKALEWLAH	IWWDDDK	YYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYC	VRSNYGYAWFAYWGQGTLVTVSS	63
hSC6.24	QVQLVQSGPEVKKPGASVKVSCKAS	GYTFTDYA	VHWVRQAPGKRLEWIGV	ISTYNDYT	YNNQDFKGRVTMTRDTSASTAYMELSRLRSEDTAVYYC	ARGNSYFYALDYWGQGTSVTVSS	65
hSC6.41	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFKDYY	MHWVRQAPGQGLEWMGW	IDPENGDT	EYAPEFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC	NACNYGSAYGYWGQGTTLTVSS	67
hSC6.58	EVQLVESGGGLVQPGGSLRLSCAAS	GFDFSRYW	MSWVRQAPGKGLEWIGD	LNPDSSAI	NYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYC	TLITTLVPYTMDFWGQGTSVTVSS	69

FIG. 6B

Binning and Cross-Reactivity Analysis for Selected PTK7 Modulators

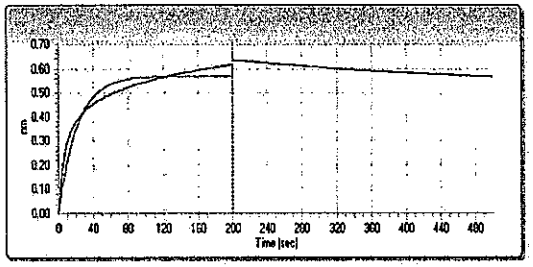
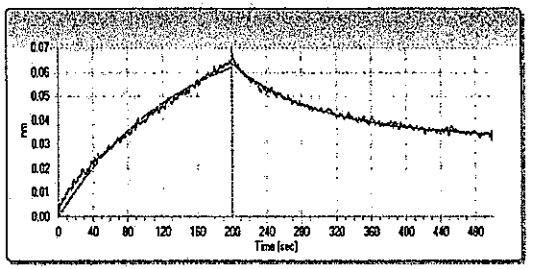
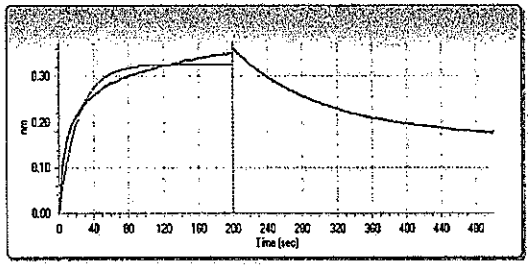
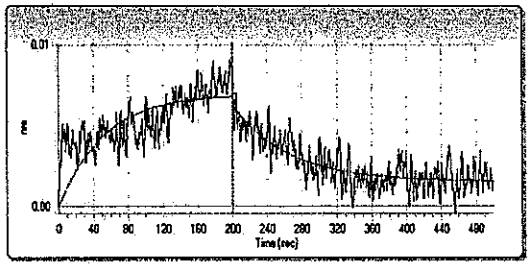
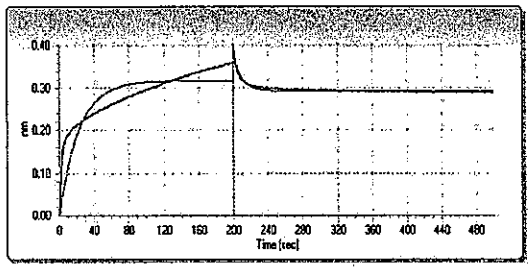
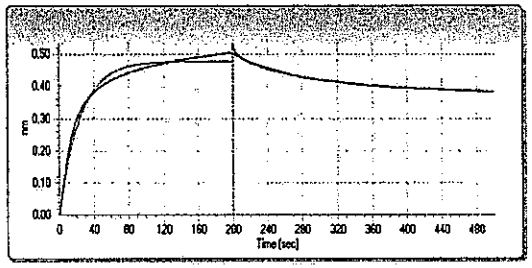
Clone	400nM Human PTK7	400nM Mouse PTK7	Bin
H2.35			B
H10.2			A
H25.1			C

FIG. 7A

Exemplary PTK7 Modulator Characteristics

Clone	Bin	Affinity (nM)	Western Reactivity	Cynomolgus XR	Mouse XR
SC6.2.35	B	<0.1[B]	NR	Yes	No
SC6.10.2	A	5.6[B]	ND	Yes	No
SC6.25.1	C	21[B]	NR	Yes	Yes
SC6.18	D	2[F]	ND	Yes	Yes
SC6.21	E	<0.1[F]	ND	Yes	Yes
SC6.23	F	2.3[B]	ND	Yes	Yes
SC6.24	A	0.6[B]	ND	Yes	Yes
SC6.30	A	<0.1[F]	ND	Yes	No
SC6.41	H	1.0[B]	ND	Yes	Yes
SC6.55	A	2[F]	ND	Yes	Yes
SC6.57	ND	0.2[F]	ND	Yes	Yes
SC6.58	B	0.5[B]	ND	Yes	Yes

[B] - Biacore
[F] - ForteBio

FIG. 7B

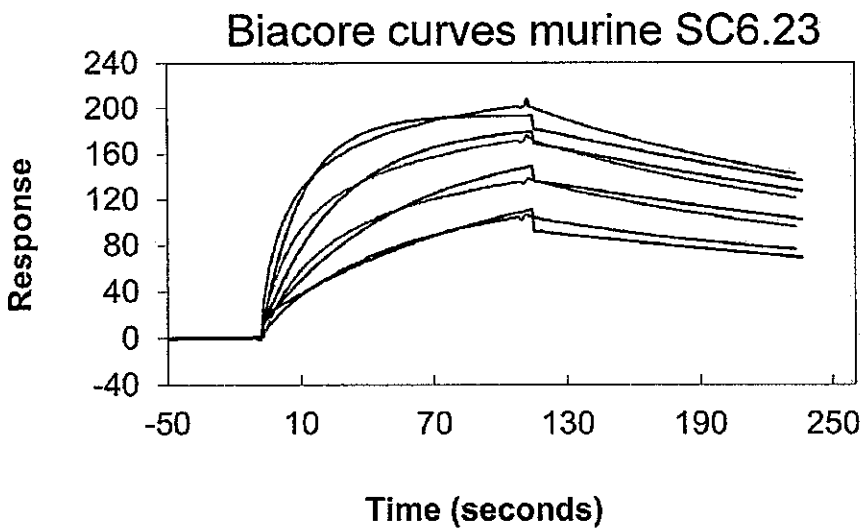


FIG.7C

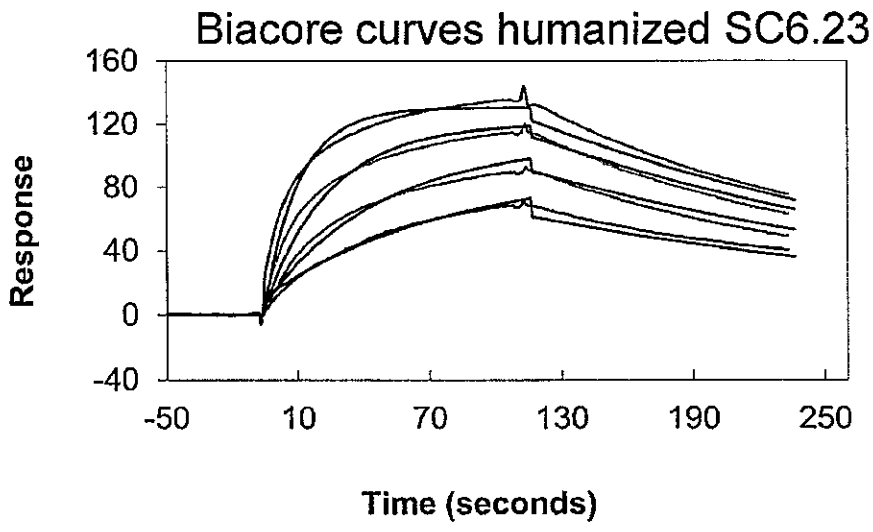


FIG. 7D

hClone	Bin	Hu Ag Affinity (Murine mAb)	Hu Ag Affinity (Human mAb)
SC6.23	F	2.3 nM	3.9 nM
SC6.24	A	0.6 nM	1.2 nM
SC6.41	H	1.0 nM	2.1 nM
SC6.58	B	0.5 nM	1.0 nM

FIG. 7E

Translation of pEE12.4_ScRx6_2IgGs::IgG2Fc (Ig domains 1 & 2)

FIG. 8A

(SEQ ID NO: 70)

```
  1    AIVFIKQPSS QDALQGRRAL LRCEVEAPGP VHVYWLLDGA PVQDTERRFA
 51    QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN IKWIEAGPVV
101    LKHPASEAEI QPQTQVTLRC HIDGHPRPTY QWFRDGTPLS DGQSNHTVSS
151    KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SSQNFTLSIA DESFARVVLA
201    PQDVVVHPVR SVECPPCPAP PVAGPSVFLF PPKPKDTLMI SRTPEVTCVV
251    VDVSHEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTFRVV SVLTVVHQDW
301    LNGKEYKCKV SNKGLPAPIE KTISKTKGQP REPQVYTLPP SREEMTKNQV
351    SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPMLDSDGS FFLYSKLTVD
401    KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK
```

Translation of pEE12.4_ScRx6_IgG3to7_IgG2Fc (Ig domains 3 to 7)

FIG. 8B

(SEQ ID NO: 71

```
  1    APQDVVVARY EEAMFHCQFS AQPPPSLQWL FEDETPITNR SRPPHLRRAT
 51    VFANGSLLLT QVRPRNAGIY RCIGQGQRGP PIILEATLHL AEIEDMPLFE
101    PRVFTAGSEE RVTCLPPKGL PEPSVWWEHA GVRLPTHGRV YQKGHELVLA
151    NIAESDAGVY TCHAANLAGQ RRQDVNITVA TVPSWLKKPQ DSQLEEGKPG
201    YLDCLTQATP KPTVVWYRNQ MLISEDSRFE VFKNGTLRIN SVEVYDGTWY
251    RCMSSTPAGS IEAQARVQVL EKLKFTPPPQ PQQCMEFDKE ATVPCSATGR
301    EKPTIKWERA DGSSLPEWVT DNAGTLHFAR VTRDDAGNYT CIASNGPQGQ
351    IRAHVQLTVA VFITFKVEPE RTTVYQGHTA LLQCEAQGDP KPLIQWKGKD
401    RILDPTKLGP RMHIFQNGSL VIHDVAPEDS GRYTCIAGNS CNIKHTEAPL
451    YVVDKPVPEE SEGPGSPPPY KMIQHPVRSV ECPPCPAPPV AGPSVFLFPP
501    KPKDTLMISR TPEVTCVVVD VSHEDPEVQF NWYVDGVEVH NAKTKPREEQ
551    FNSTFRVVSV LTVVHQDWLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE
601    PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP
651    PMLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP
701    GK*
```

pEE12.4_ScRx6_5IgGs::IgG2Fc (Ig domains 1 to 5)

FIG. 8C

(SEQ ID NO: 72

```
  1    AIVFIKQPSS QDALQGRRAL LRCEVEAPGP VHVYWLLDGA PVQDTERRFA
 51    QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN IKWIEAGPVV
101    LKHPASEAEI QPQTQVTLRC HIDGHPRPTY QWFRDGTPLS DGQSNHTVSS
151    KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SSQNFTLSIA DESFARVVLA
201    PQDVVVARYE EAMFHCQFSA QPPPSLQWLF EDETPITNRS RPPHLRRATV
251    FANGSLLLTQ VRPRNAGIYR CIGQGQRGPP IILEATLHLA EIEDMPLFEP
301    RVFTAGSEER VTCLPPKGLP EPSVWWEHAG VRLPTHGRVY QKGHELVLAN
351    IAESDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKKPQD SQLEEGKPGY
401    LDCLTQATPK PTVVWYRNQM LISEDSRFEV FKNGTLRINS VEVYDGTWYR
451    CMSSTPAGSI EAQARVQVLE KLKFTPPPQP HPVRSVECPP CPAPPVAGPS
501    VFLFPPKPKD TLMISRTPEV TCVVVDVSHE DPEVQFNWYV DGVEVHNAKT
551    KPREEQFNST FRVVSVLTVV HQDWLNGKEY KCKVSNKGLP APIEKTISKT
601    KGQPREPQVY TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN
651    NYKTTPPMLD SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK
701    SLSLSPGK
```

Translation of pEE12.4 ScRx6 IgG6&7 IgG2Fc (Ig domains 6 & 7)

FIG. 8D

(SEQ ID NO: 7

```
  1    KFTPPPQPQQ CMEFDKEATV PCSATGREKP TIKWERADGS SLPEWVTDNA
 51    GTLHFARVTR DDAGNYTCIA SNGPQGQIRA HVQLTVAVFI TFKVEPERTT
101    VYQGHTALLQ CEAQGDPKPL IQWKGKDRIL DPTKLGPRMH IFQNGSLVIH
151    DVAPEDSGRY TCIAGNSCNI KHTEAPLYVV DKPVPEESEG PGSPPPYKMI
201    QHPVRSVECP PCPAPPVAGP SVFLFPPKPK DTLMISRTPE VTCVVVDVSH
251    EDPEVQFNWY VDGVEVHNAK TKPREEQFNS TFRVVSVLTV VHQDWLNGKE
301    YKCKVSNKGL PAPIEKTISK TKGQPREPQV YTLPPSREEM TKNQVSLTCL
351    VKGFYPSDIA VEWESNGQPE NNYKTTPPML DSDGSFFLYS KLTVDKSRWQ
401    QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
```

Translation of pEE12.4 ScRx6 IgG2&3 IgG2Fc (Ig domains 2 & 3)

FIG. 8E

(SEQ ID NO: 7

```
  1    EEARSANASF NIKWIEAGPV VLKHPASEAE IQPQTQVTLR CHIDGHPRPT
 51    YQWFRDGTPL SDGQSNHTVS SKERNLTLRP AGPEHSGLYS CCAHSAFGQA
101    CSSQNFTLSI ADESFARVVL APQDVVVARY EEAMFHCQFS AQPPPSLQWL
151    FEDETPITNR SRPPHLRRAT VFANGSLLLT QVRPRNAGIY RCIGQGQRGP
201    PIILEATLHL AEHPVRSVEC PPCPAPPVAG PSVFLFPPKP KDTLMISRTP
251    EVTCVVVDVS HEDPEVQFNW YVDGVEVHNA KTKPREEQFN STFRVVSVLT
301    VVHQDWLNGK EYKCKVSNKG LPAPIEKTIS KTKGQPREPQ VYTLPPSREE
351    MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPM LDSDGSFFLY
401    SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK
```

Translation of pEE12.4 ScRx6 4IgGs IgG2Fc (Ig domains 1 to 4)

FIG. 8F

(SEQ ID NO: 7

```
  1    AIVFIKQPSS QDALQGRRAL LRCEVEAPGP VHVYWLLDGA PVQDTERRFA
 51    QGSSLSFAAV DRLQDSGTFQ CVARDDVTGE EARSANASFN IKWIEAGPVV
101    LKHPASEAEI QPQTQVTLRC HIDGHPRPTY QWFRDGTPLS DGQSNHTVSS
151    KERNLTLRPA GPEHSGLYSC CAHSAFGQAC SSQNFTLSIA DESFARVVLA
201    PQDVVVARYE EAMFHCQFSA QPPPSLQWLF EDETPITNRS RPPHLRRATV
251    FANGSLLLTQ VRPRNAGIYR CIGQGQRGPP IILEATLHLA EIEDMPLFEP
301    RVFTAGSEER VTCLPPKGLP EPSVWWEHAG VRLPTHGRVY QKGHELVLAN
351    IAESDAGVYT CHAANLAGQR RQDVNITVAH PVRSVECPPC PAPPVAGPSV
401    FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVQFNWYVD GVEVHNAKTK
451    PREEQFNSTF RVVSVLTVVH QDWLNGKEYK CKVSNKGLPA PIEKTISKTK
501    GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN
551    YKTTPPMLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS
601    LSLSPGK
```

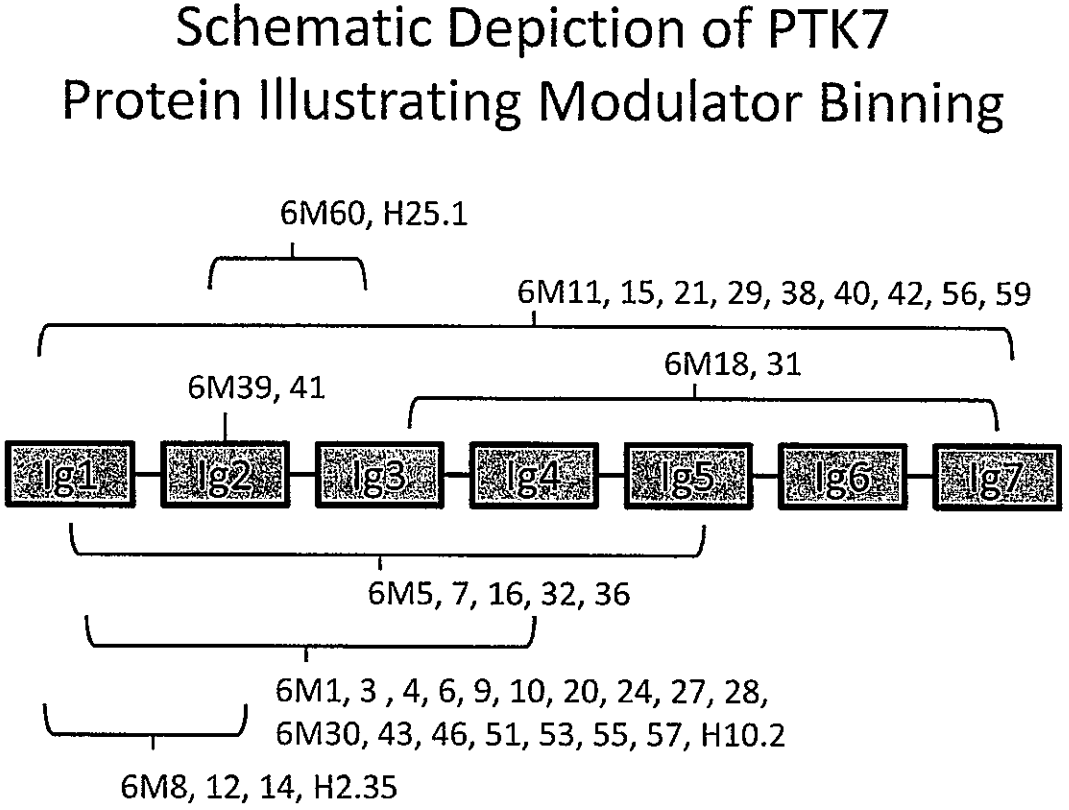

Schematic Depiction of PTK7
Protein Illustrating Modulator Binning
6M60, H25.1
6M11, 15, 21, 29, 38, 40, 42, 56, 59
6M18, 31
6M39, 41
Ig1
Ig2
Ig3
Ig4
Ig5
Ig6
Ig7
6M5, 7, 16, 32, 36
6M1, 3 , 4, 6, 9, 10, 20, 24, 27, 28,
6M30, 43, 46, 51, 53, 55, 57, H10.2
6M8, 12, 14, H2.35

FIG. 8G

PTK7 Protein Expression is Elevated in a Subset of Colorectal and Pancreatic Cancer Tumor Lysates

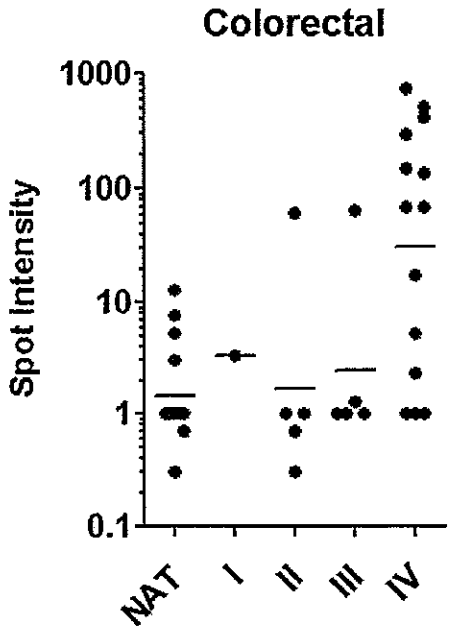


FIG. 9A

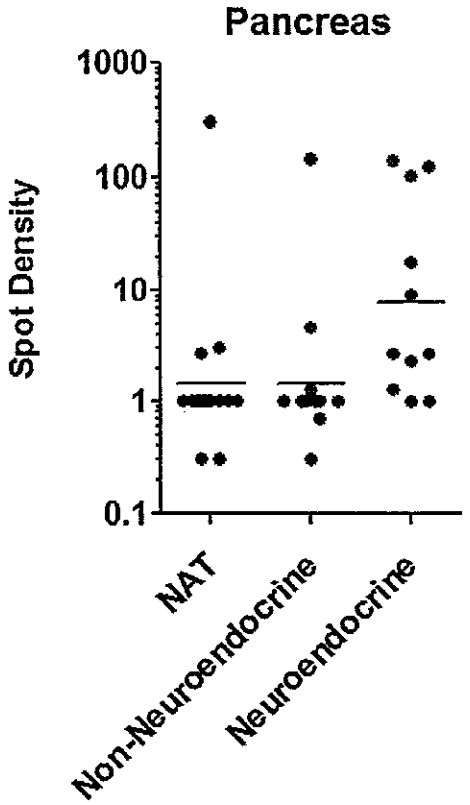


FIG. 9B

PTK7 Protein Expression is Elevated in a Subset of Breast and Ovarian Cancer Tumor Lysates

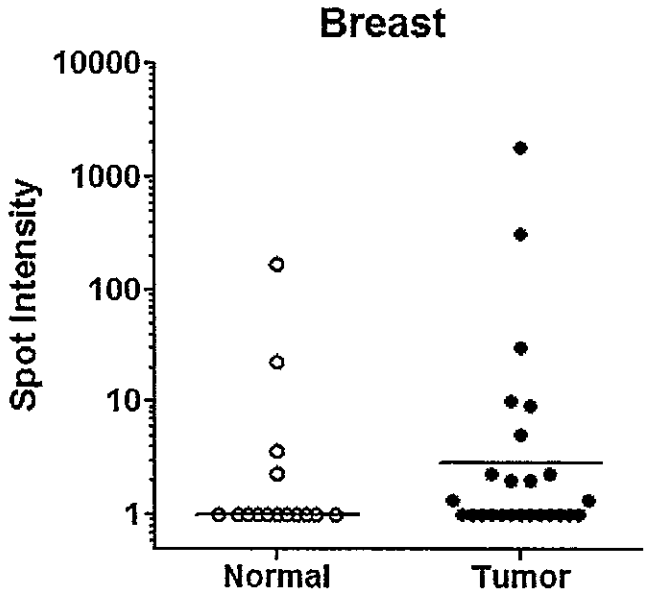


FIG. 9C

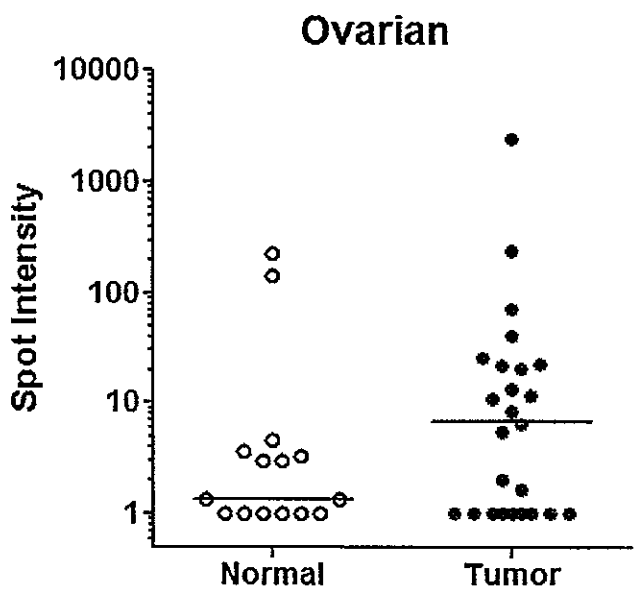


FIG. 9D

PTK7 Protein Expression is Elevated in NTX Samples

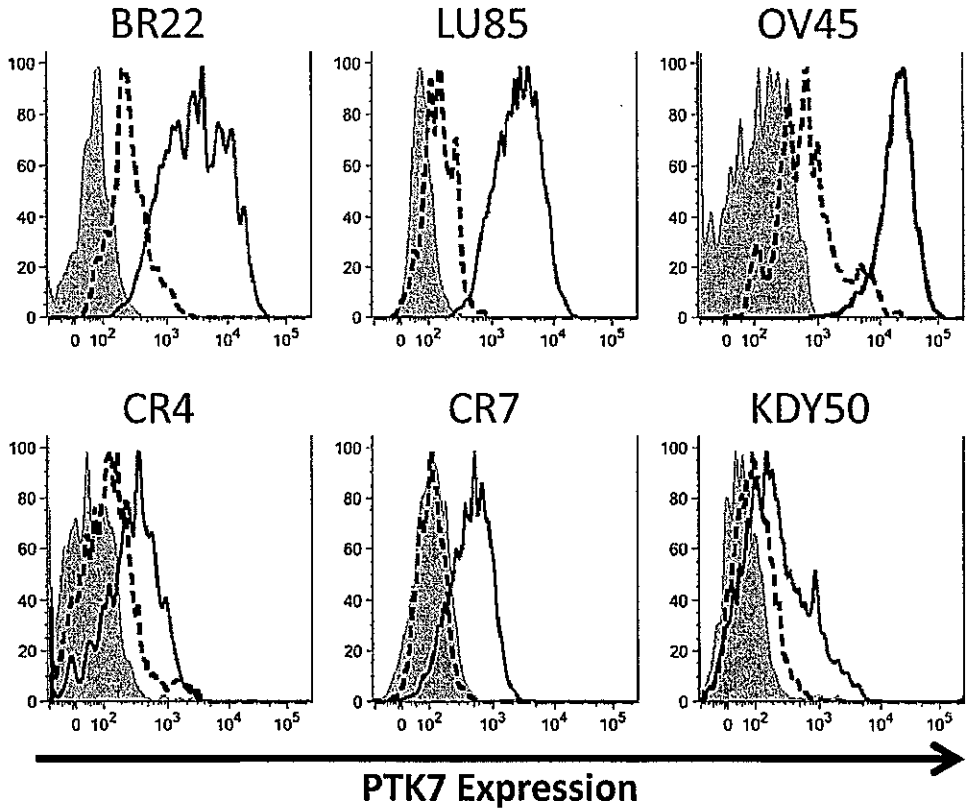


FIG. 9E

PTK7 Modulators Associate With K562 Cells and Internalize

FIG. 10A

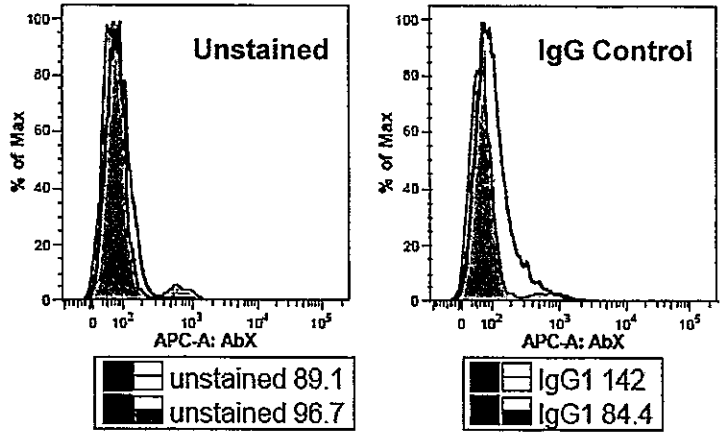


FIG. 10B

FIG. 10C

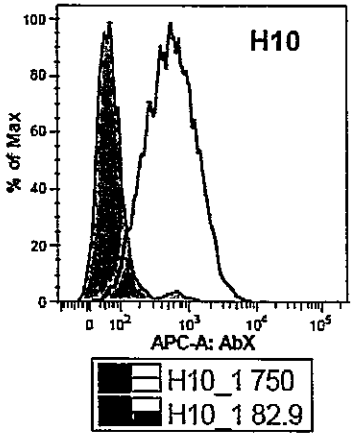
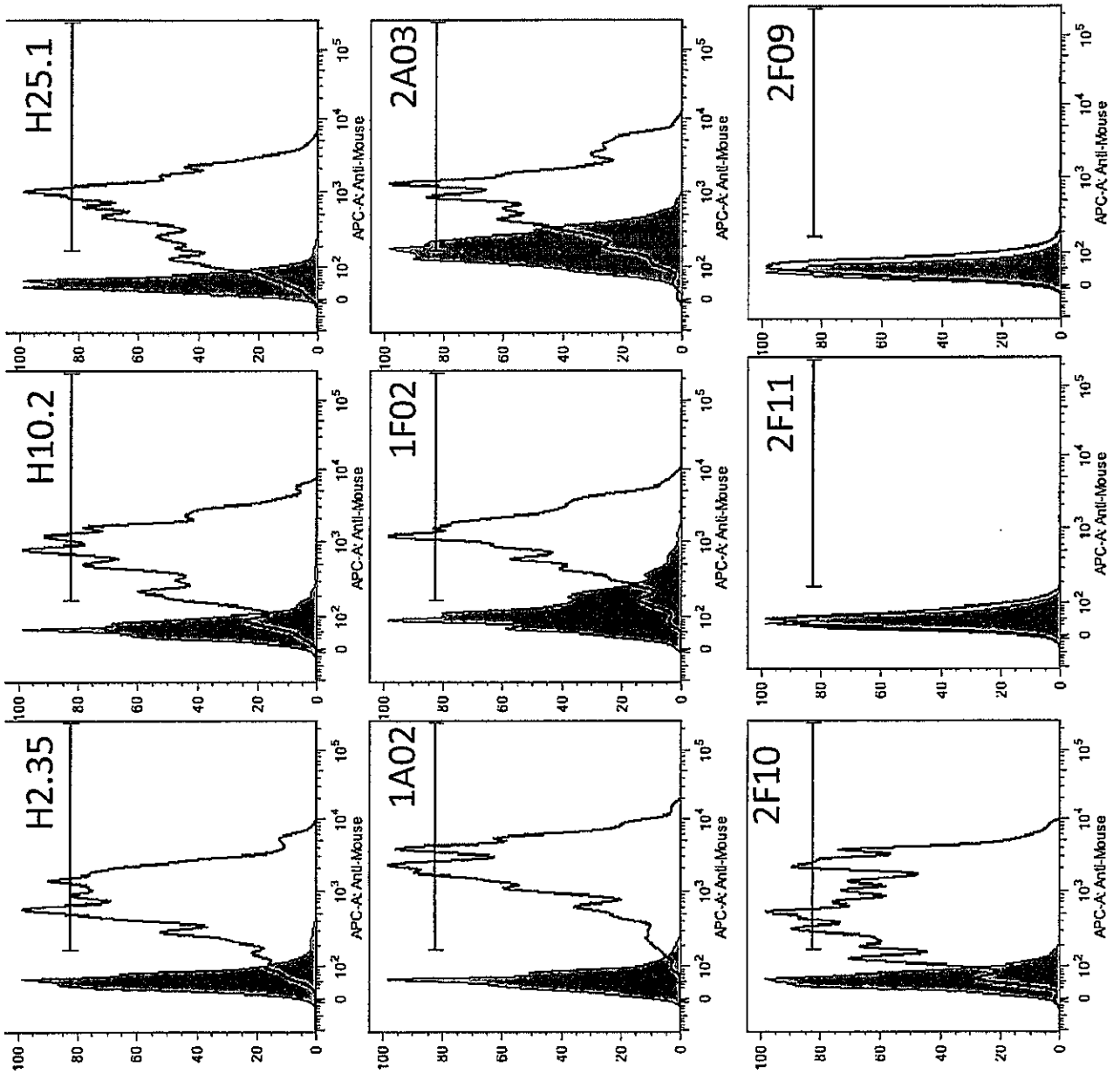


FIG. 10D

PTK7 Modulators Associate With G401 Cells and Internalize



Heterogeneous Internalization of PTK7 Modulators

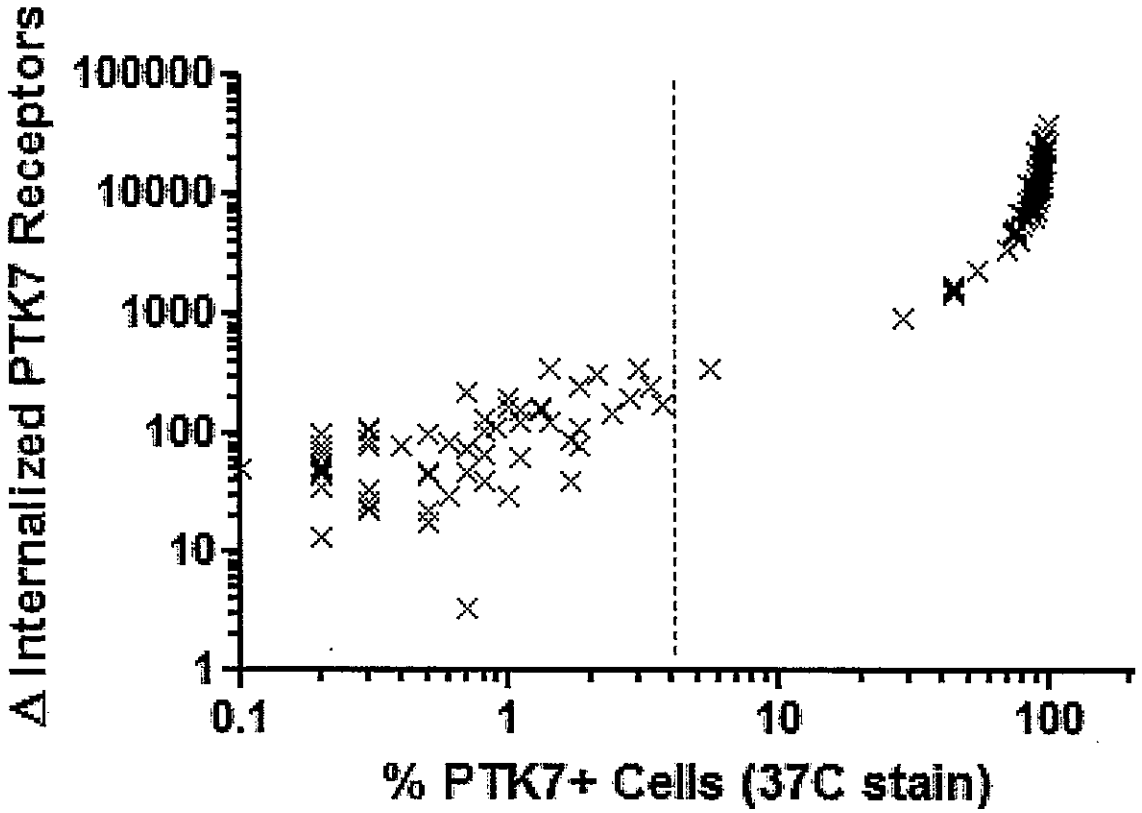


FIG. 10E

PTK7 Modulators Mediate Toxin Delivery *In Vitro*

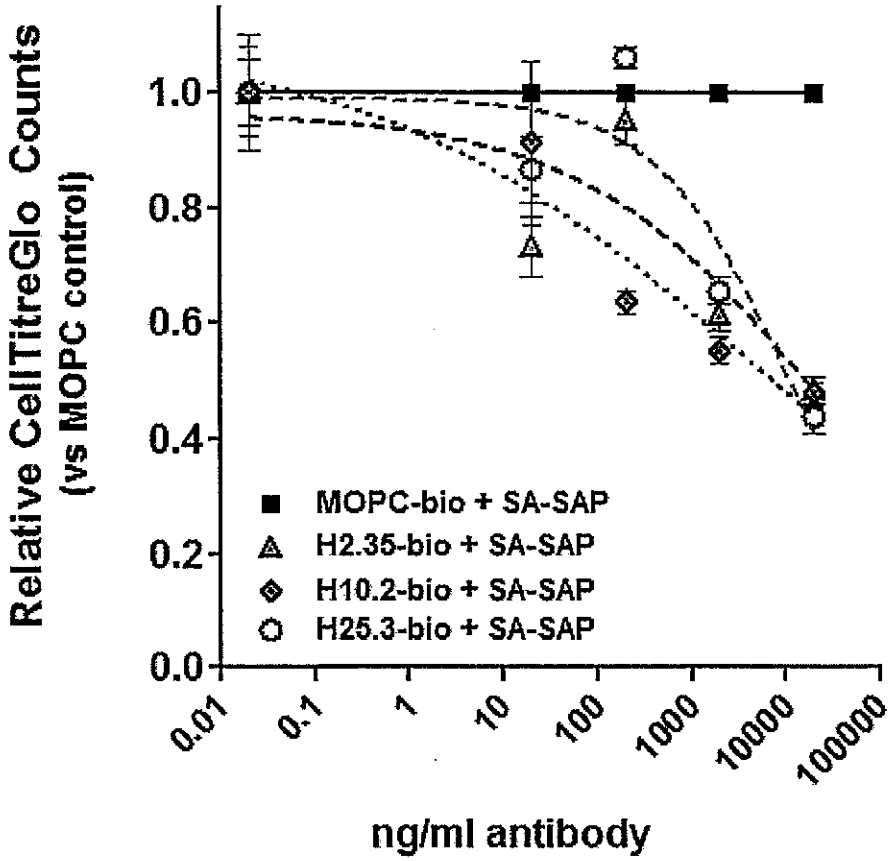


FIG. 11A

PTK7 Modulators Mediate Cell Killing

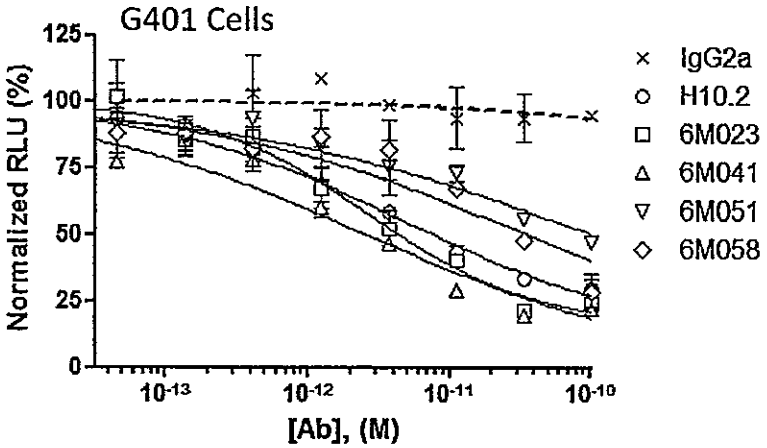


FIG. 11B

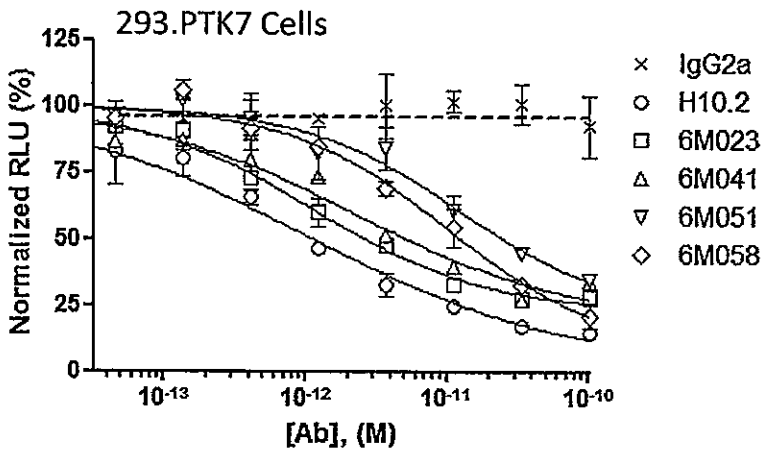


FIG. 11C

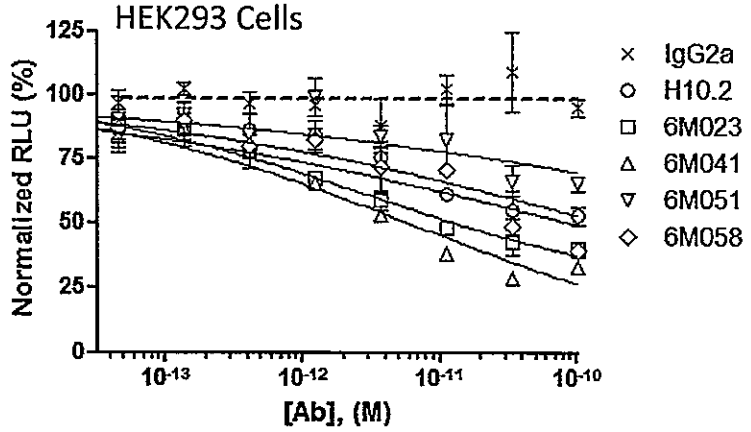


FIG. 11D

PTK7 Modulators Reduce Tumor Cell Viability

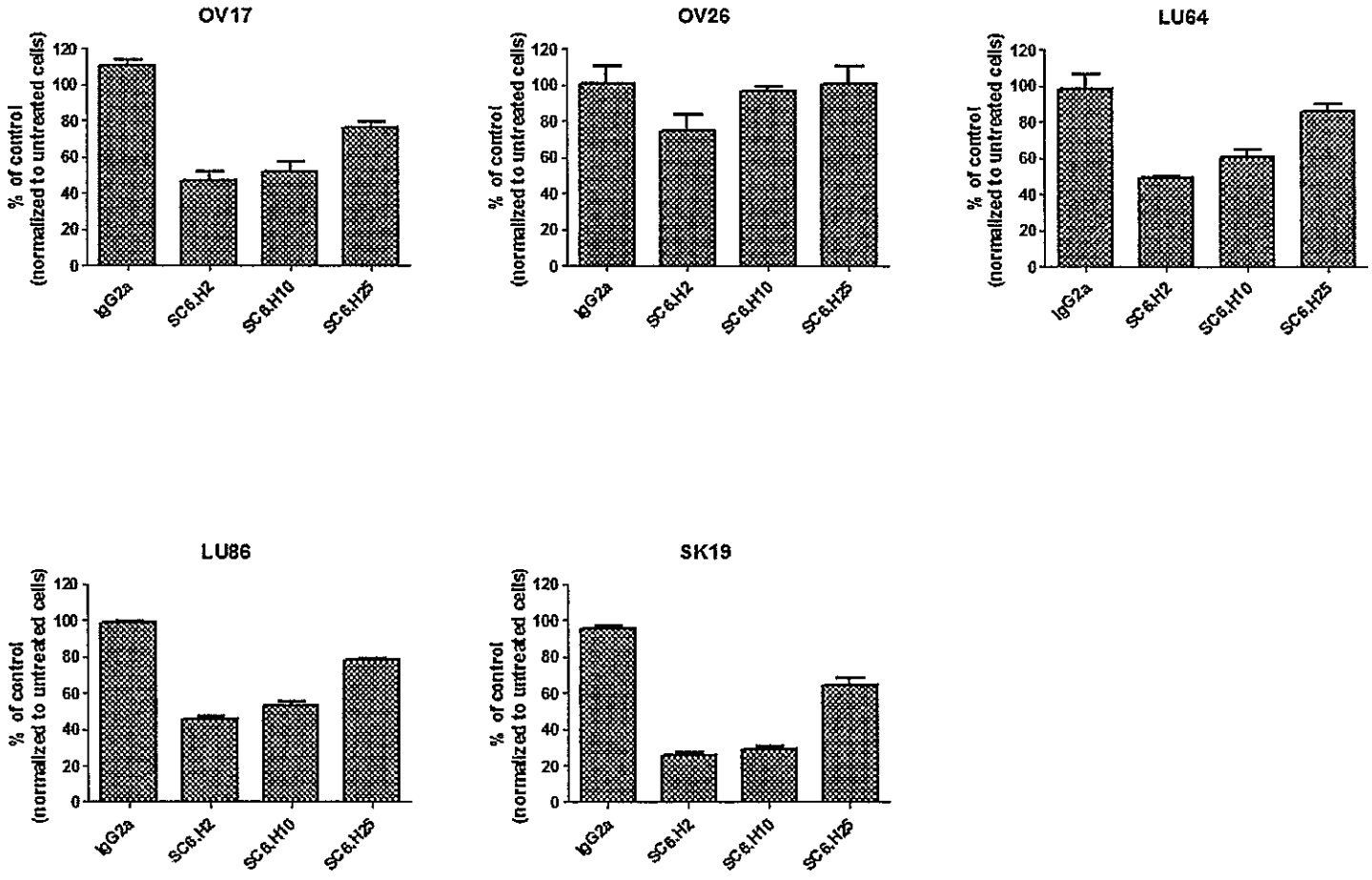


FIG. 12

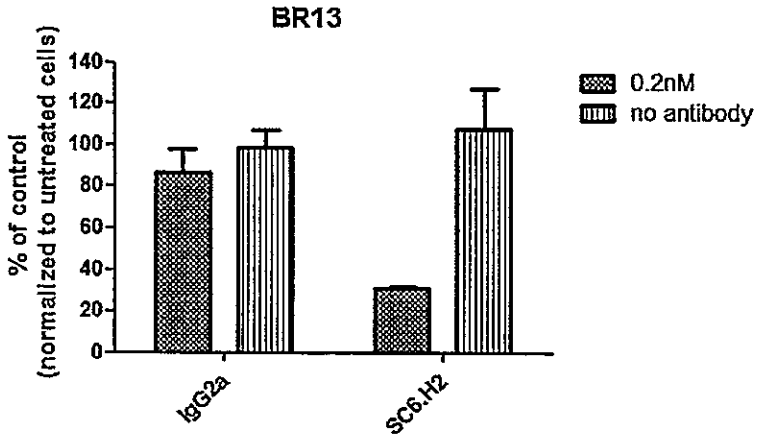


FIG. 13A

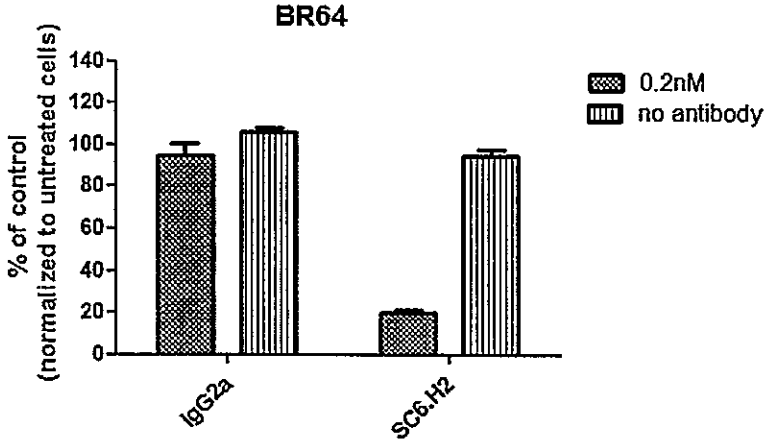


FIG. 13B

PTK7 Modulators Reduce Cell Tumorigenicity

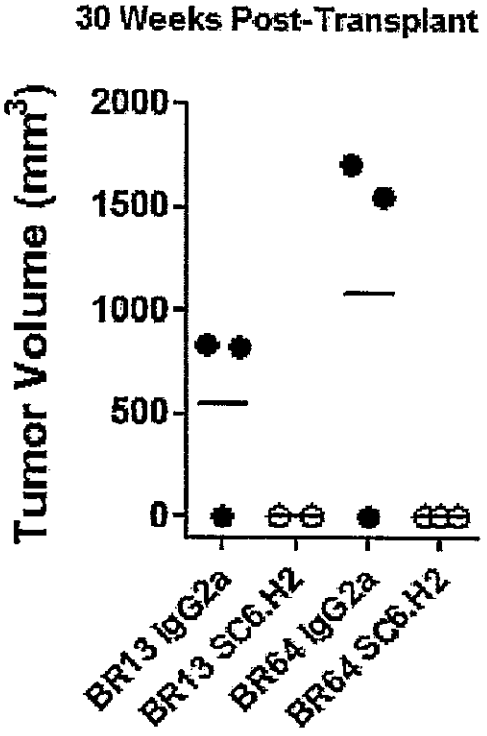


FIG. 13C

Humanized PTK7 Modulators Induce Cell Killing

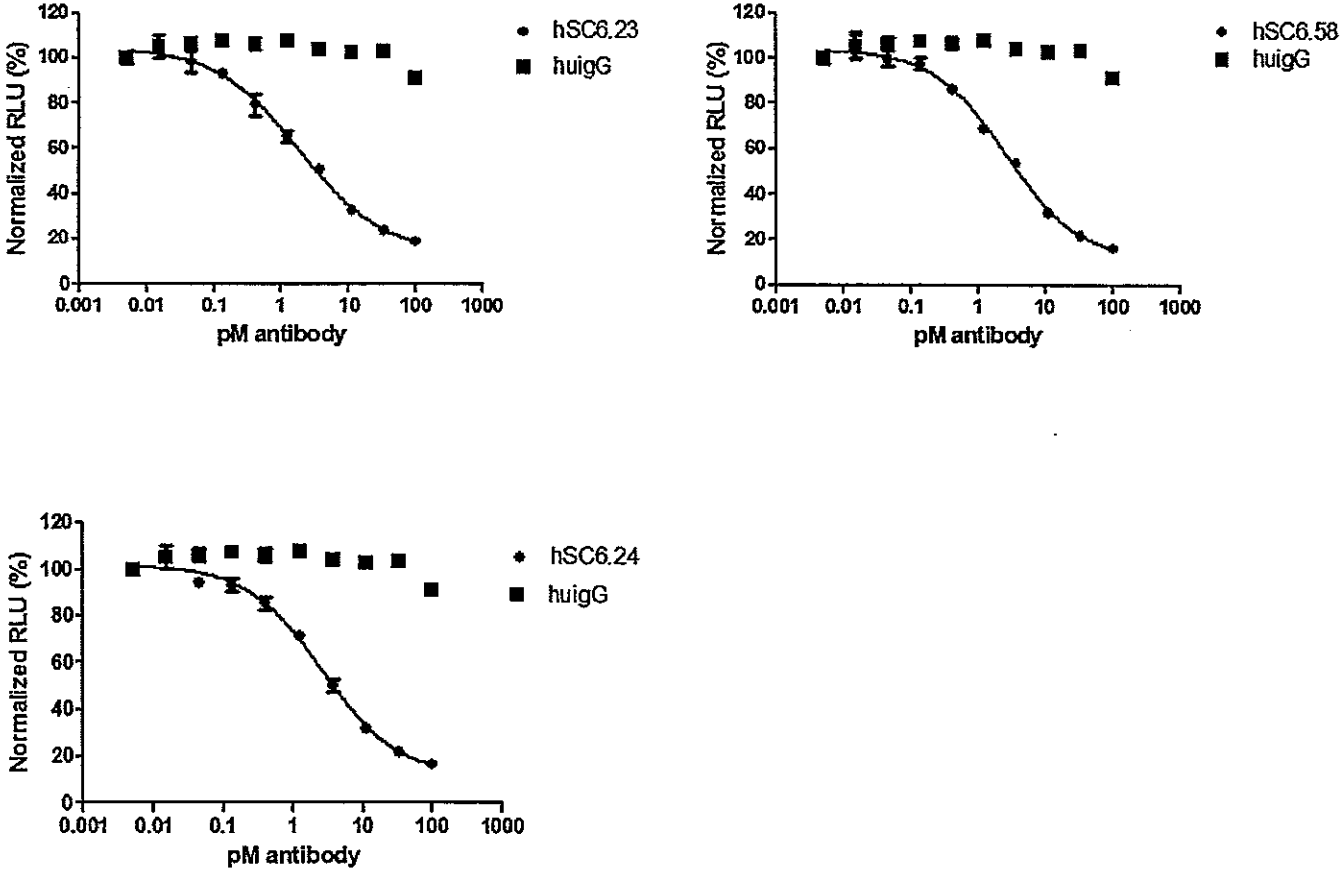


FIG. 14