Clone #	H1									
	26	27	28	29	30	31	32	33	34	35
184.6	G	F	T	F	T	S	T	G	I	S
184.6.1	G	F	T	F	T	S	T	G	I	S
184.6.58	G	F	T	F	T	S	T	G	I	S
184.6.62	G	F	T	F	S	T	T	G	I	S
184.6.21	G	F	T	F	T	S	T	G	I	S
184.6.49	G	F	T	F	T	S	T	G	I	S
184.6.51	G	F	S	F	T	G	T	G	I	S
184.6.52	G	F	T	F	Y	T	T	G	I	S
184.6.92	G	F	S	F	W	S	T	G	I	S
184.6.1.N54S	G	F	T	F	T	S	T	G	I	S
184.6.1.N54G	G	F	T	F	T	S	T	G	I	S
184.6.1.N54A	G	F	T	F	T	S	T	G	I	S
184.6.1.N54Q	G	F	T	F	T	S	T	G	I	S
184.6.58.N54S	G	F	T	F	T	S	T	G	I	S
184.6.58.N54G	G	F	T	F	T	S	T	G	I	S
184.6.58.N54A	G	F	T	F	T	S	T	G	I	S
184.6.58.N54Q	G	F	T	F	T	S	T	G	I	S
184.6.1.NS D30E	G	F	T	F	T	S	T	G	I	S

Clone #	H2																	
	49	50	51	52	52a	53	54	55	56	57	58	59	60	61	62	63	64	65
184.6	G	R	I	Y	P	T	N	G	S	T	N	Y	A	D	S	V	K	G
184.6.1	G	R	I	Y	P	T	N	G	S	T	N	Y	A	D	S	V	K	G
184.6.58	G	R	I	Y	P	T	N	G	S	T	N	Y	A	D	S	V	K	G
184.6.62	G	R	I	Y	P	L	Y	G	S	T	H	Y	A	D	S	V	K	G
184.6.21	G	R	I	Y	P	Y	D	D	S	F	Y	Y	A	D	S	V	K	G
184.6.49	G	R	I	Y	P	T	N	G	S	T	N	Y	A	D	S	V	K	G
184.6.51	G	S	I	Y	P	Y	F	A	T	K	N	Y	A	D	S	V	K	G
184.6.52	G	R	I	Y	P	A	F	G	S	S	I	Y	A	D	S	V	K	G
184.6.92	G	R	I	Y	P	S	S	A	T	T	N	Y	A	D	S	V	K	G
184.6.1.N54S	G	R	I	Y	P	T	S	G	S	T	N	Y	A	D	S	V	K	G
184.6.1.N54G	G	R	I	Y	P	T	G	G	S	T	N	Y	A	D	S	V	K	G
184.6.1.N54A	G	R	I	Y	P	T	A	G	S	T	N	Y	A	D	S	V	K	G
184.6.1.N54Q	G	R	I	Y	P	T	Q	G	S	T	N	Y	A	D	S	V	K	G
184.6.58.N54S	G	R	I	Y	P	T	S	G	S	T	N	Y	A	D	S	V	K	G
184.6.58.N54G	G	R	I	Y	P	T	G	G	S	T	N	Y	A	D	S	V	K	G
184.6.58.N54A	G	R	I	Y	P	T	A	G	S	T	N	Y	A	D	S	V	K	G
184.6.58.N54Q	G	R	I	Y	P	T	Q	G	S	T	N	Y	A	D	S	V	K	G
184.6.1.NS D30E	G	R	I	Y	P	T	S	G	S	T	N	Y	A	D	S	V	K	G

FIG. 1A

Clone #	H3																			
	93	94	95	96	97	98	99	100	A	B	C	D						M	101	102
184.6	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.1	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.58	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.62	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.21	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.49	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.51	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.52	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.92	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.1.N54S	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.1.N54G	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.1.N54A	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.1.N54Q	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.58.N54S	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.58.N54G	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.58.N54A	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.58.N54Q	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y
184.6.1.NS D30E	A	R	T	Y	G	I	Y	D	L	Y	V	D	Y	T	E	Y	V	M	D	Y

Clone #	L1										
	24	25	26	27	28	29	30	31	32	33	34
184.6	R	A	S	Q	D	V	S	T	A	V	A
184.6.1	R	A	S	Q	D	V	D	T	S	L	A
184.6.58	R	A	S	Q	D	V	D	I	S	L	A
184.6.62	R	A	S	Q	D	V	S	T	A	V	A
184.6.21	R	A	S	Q	D	V	S	T	A	V	A
184.6.49	R	A	S	Q	V	I	D	I	S	L	A
184.6.51	R	A	S	Q	D	V	S	T	A	V	A
184.6.52	R	A	S	Q	D	V	S	T	A	V	A
184.6.92	R	A	S	Q	D	V	S	T	A	V	A
184.6.1.N54S	R	A	S	Q	D	V	D	T	S	L	A
184.6.1.N54G	R	A	S	Q	D	V	D	T	S	L	A
184.6.1.N54A	R	A	S	Q	D	V	D	T	S	L	A
184.6.1.N54Q	R	A	S	Q	D	V	D	T	S	L	A
184.6.58.N54S	R	A	S	Q	V	V	D	T	S	L	A
184.6.58.N54G	R	A	S	Q	V	V	D	T	S	L	A
184.6.58.N54A	R	A	S	Q	V	V	D	T	S	L	A
184.6.58.N54Q	R	A	S	Q	V	V	D	T	S	L	A
184.6.1.NS D30E	R	A	S	Q	D	V	E	T	S	L	A

FIG. 1B

Clone #	L2						
	50	51	52	53	54	55	56
184.6	S	A	S	F	L	Y	S
184.6.1	S	A	S	F	L	Y	S
184.6.58	S	A	S	S	L	A	S
184.6.62	S	A	S	F	L	Y	S
184.6.21	S	A	S	F	L	Y	S
184.6.49	G	A	S	T	L	A	S
184.6.51	S	A	S	F	L	Y	S
184.6.52	S	A	S	F	L	Y	S
184.6.92	S	A	S	F	L	Y	S
184.6.1.N54S	S	A	S	F	L	Y	S
184.6.1.N54G	S	A	S	F	L	Y	S
184.6.1.N54A	S	A	S	F	L	Y	S
184.6.1.N54Q	S	A	S	F	L	Y	S
184.6.58.N54S	S	A	S	S	L	A	S
184.6.58.N54G	S	A	S	S	L	A	S
184.6.58.N54A	S	A	S	S	L	A	S
184.6.58.N54Q	S	A	S	S	L	A	S
184.6.1.NS D30E	S	A	S	F	L	Y	S

Clone #	L3								
	89	90	91	92	93	94	95	96	97
184.6	Q	Q	S	Y	T	T	P	P	T
184.6.1	Q	Q	S	T	G	H	P	Q	T
184.6.58	Q	Q	G	A	G	N	P	Y	T
184.6.62	Q	Q	T	Y	T	T	S	L	T
184.6.21	Q	Q	S	Y	T	T	P	L	T
184.6.49	Q	Q	S	A	A	D	P	Y	T
184.6.51	Q	Q	S	Y	T	T	P	P	T
184.6.52	Q	Q	T	Y	S	A	Q	P	T
184.6.92	Q	Q	S	Y	S	H	Q	S	T
184.6.1.N54S	Q	Q	S	T	G	H	P	Q	T
184.6.1.N54G	Q	Q	S	T	G	H	P	Q	T
184.6.1.N54A	Q	Q	S	T	G	H	P	Q	T
184.6.1.N54Q	Q	Q	S	T	G	H	P	Q	T
184.6.58.N54S	Q	Q	G	A	G	N	P	Y	T
184.6.58.N54G	Q	Q	G	A	G	N	P	Y	T
184.6.58.N54A	Q	Q	G	A	G	N	P	Y	T
184.6.58.N54Q	Q	Q	G	A	G	N	P	Y	T
184.6.1.NS D30E	Q	Q	S	T	G	H	P	Q	T

FIG. 1C

Clone 184.6.1.N54S

VH
EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTGISWVRQAPGKGLEWV
GRIYPTSGSTNYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAR
ARTYGIYDLYVDYTEYVMDYWGQGTLV (SEQ ID NO: 132)

VL
DIQMTQSPSSLSASVGDRVTITCRASQDVDTSLAWYQQKPGKAPKLLIYSASFLYS
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSTGHPQTFGQGTKVEIKR (SEQ ID NO:133)

Clone 184.6.58

VH
EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTGISWVRQAPGKGLEWV
ARIYPTNGSTNYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAR
ARTYGIYDLYVDYTEYVMDYWGQGTLV (SEQ ID NO:134)

VL
DIQMTQSPSSLSASVGDRVTITCRASQDVDISLAWYQQKPGKAPKLLIYSASFLYS
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGAGNPYTFGQGTKVEIKR (SEQ ID NO:135)

Clone 184.6.62

VH
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTTGISWVRQAPGKGLEWV
ARIYPLYGSTHYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAR
ARTYGIYDLYVDYTEYVMDYWGQGTLV (SEQ ID NO:136)

VL
DIQMTQSPSSLSASVGDRVTITCRASQDVSTAVAWYQQKPGKAPKLLIYSASFLYS
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQTYTTSLTFGQGTKVEIKR (SEQ ID NO:137)

Clone 184.6.1.NS D30E

VH
EVQLVESGGGLVQPGGSLRLSCAASGFTFTSTGISWVRQAPGKGLEWV
GRIYPTSGSTNYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCAR
ARTYGIYDLYVDYTEYVMDYWGQGTLV (SEQ ID NO:138)

VL
DIQMTQSPSSLSASVGDRVTITCRASQDVETSLAWYQQKPGKAPKLLIYSASFLYS
GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSTGHPQTFGQGTKVEIKR (SEQ ID NO:139)

FIG. 2A

Clone 1G6

HVR-H1: GYSFTDYNMY (SEQ ID NO:164)

HVR-H2: WIGYIEPYNGGTSYNQKFKG (SEQ ID NO:167)

HVR-H3: ASPNYYDSSPFAY (SEQ ID NO:170)

HVR-L1: SASSSVSYMH (SEQ ID NO:155)

HVR-L2: TWIYDTSILAS (SEQ ID NO:158)

HVR-L3: QQWTSNPLT (SEQ ID NO:161)

Clone 6G1

HVR-H1: GYVFTHYNMY (SEQ ID NO:165)

HVR-H2: WIGYIEPYNGGTSYNQKFKG (SEQ ID NO:168)

HVR-H3: ARGQGPDFDV (SEQ ID NO:171)

HVR-L1: SASSSVSYMH (SEQ ID NO:156)

HVR-L2: RWIYDTSKLAS (SEQ ID NO:159)

HVR-L3: QQWSSYPPT (SEQ ID NO:162)

Clone 15B2

HVR-H1: GYAFTSYNMY (SEQ ID NO:166)

HVR-H2: WIGYIDPYIGGTSYNQKFKG (SEQ ID NO:169)

HVR-H3: ARWGDYDVGAMDY (SEQ ID NO:172)

HVR-L1: LASQTIGTWLA (SEQ ID NO:157)

HVR-L2: LLIYAATSLAD (SEQ ID NO:160)

HVR-L3: QQLYSPPWT (SEQ ID NO:163)

FIG. 2B

I
A QVQLVQSGAEVKKPGASVKVSCKASGYTFT -H1- WVRQAPGQGLEWMG -H2-
B QVQLVQSGAEVKKPGASVKVSCKAS -H1- WVRQAPGQGLEWM -H2-
C QVQLVQSGAEVKKPGASVKVSCKAS -H1~ WVRQAPGQGLEWM ~H2~
D QVQLVQSGAEVKKPGASVKVSCKAS ~H1~ WVRQAPGQGLEWM ~H2~
II
A QVQLQESGPGLVKPSQTLSLTCTVSGGSVS -H1- WIRQPPGKGLEWIG -H2-
B QVQLQESGPGLVKPSQTLSLTCTVS -H1- WIRQPPGKGLEWI ~H2~
C QVQLQESGPGLVKPSQTLSLTCTVS ~H1~ WIRQPPGKGLEWI ~H2~
D QVQLQESGPGLVKPSQTLSLTCTVS ~H1~ WIRQPPGKGLEWI ~H2~
III
A EVQLVESGGGLVQPGGSLRLSCAASGFTFS -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS -H1- WVRQAPGKGLEWV ~H2~
C EVQLVESGGGLVQPGGSLRLSCAAS ~H1~ WVRQAPGKGLEWV ~H2~
D EVQLVESGGGLVQPGGSLRLSCAAS ~H1~ WVRQAPGKGLEWV ~H2~
Acceptor
A EVQLVESGGGLVQPGGSLRLSCAASGFNIK -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS ~H1~ WVRQAPGKGLEWV ~H2~
C EVQLVESGGGLVQPGGSLRLSCAAS ~H1~ WVRQAPGKGLEWV ~H2~
Second Acceptor
A EVQLVESGGGLVQPGGSLRLSCAASGFNIK -H1- WVRQAPGKGLEWVS -H2-
B EVQLVESGGGLVQPGGSLRLSCAAS ~H1~ WVRQAPGKGLEWV ~H2~
C EVQLVESGGGLVQPGGSLRLSCAAS ~H1~ WVRQAPGKGLEWV ~H2~
D EVQLVESGGGLVQPGGSLRLSCAAS ~H1~ WVRQAPGKGLEWV ~H2~

FIG. 3A

I

A RVTITADTSTSTAYMELSSLRSEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 19, 203-205
B RVTITADTSTSTAYMELSSLRSEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 20, 206-208
C RVTITADTSTSTAYMELSSLRSEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.: 21, 209-211
D RVTITADTSTSTAYMELSSLRSEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.: 22, 212-214

II

A RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 23, 215-217
B RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 24, 218-220
C RVTISVDTSKNQFSLKLSSVTAADTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.: 25, 221-223
D RVTISVDTSKNQFSLKLSSVTAADTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.: 26, 224-226

III

A RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 27, 227-229
B RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 28, 230-232
C RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.: 29, 233-235
D RFTISRDNSKNTLYLQMNSLRAEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.: 30, 236-238

Acceptor

A RFTISADTSKNTAYLQMNSLRAEDTAVYYCSR -H3- WGQGTLVTVSS SEQ ID NO.: 31, 239-241
B RFTISADTSKNTAYLQMNSLRAEDTAVYYCSR -H3- WGQGTLVTVSS SEQ ID NO.: 32, 242-244
C RFTISADTSKNTAYLQMNSLRAEDTAVYYCS -H3- WGQGTLVTVSS SEQ ID NO.: 33, 245-247

Second Acceptor

A RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 34, 248-250
B RFTISADTSKNTAYLQMNSLRAEDTAVYYCAR -H3- WGQGTLVTVSS SEQ ID NO.: 35, 251-253
C RFTISADTSKNTAYLQMNSLRAEDTAVYYCA -H3- WGQGTLVTVSS SEQ ID NO.: 36, 254-256
D RFTISADTSKNTAYLQMNSLRAEDTAVYYC -H3- WGQGTLVTVSS SEQ ID NO.: 37, 257-259

FIG. 3B

kV1 DIQMTQSPSSLSASVGDRVTITC -L1- WYQQKPGKAPKLLIY -L2- GVPSRFSGSGSGTDFTLTISSLQP
kV2 DIVMTQSPLSLPVTPGEPASISC -L1- WYLQKPGQSPQLLIY -L2- GVPDRFSGSGSGTDFTLKISRVEA
kV3 EIVLTQSPGTLSLSPGERATLSC -L1- WYQQKPGQAPRLLIY -L2- GIPDRFSGSGSGTDFTLTISRLEP
kV4 DIVMTQSPDSLAVSLGERATINC -L1- WYQQKPGQPPKLLIY -L2- GVPDRFSGSGSGTDFTLTISSLQA
EDFATYYC -L3- FGQGTKVEIK SEQ ID NO.: 38, 260-262
EDVGVYYC -L3- FGQGTKVEIK SEQ ID NO.: 39, 263-265
EDFAVYYC -L3- FGQGTKVEIK SEQ ID NO.: 40, 266-268
EDVAVYYC -L3- FGQGTKVEIK SEQ ID NO.: 41, 269-271

FIG. 4

Framework Sequences of huMAb4D5-8 Light Chain

LC-FR1 ^{1}Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys^{23} (SEQ ID NO: 42)

LC-FR2 ^{35}Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr^{49} (SEQ ID NO: 43)

LC-FR3 ^{57}Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys^{88} (SEQ ID NO: 44)

LC-FR4 ^{98}Phe Gly Gln Gly Thr Lys Val Glu Ile Lys^{107} (SEQ ID NO: 45)

Framework Sequences of huMAb4D5-8 Heavy Chain

HC-FR1 ^{1}Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser^{25} (SEQ ID NO: 46)

HC-FR2 ^{36}Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val^{48} (SEQ ID NO: 47)

HC-FR3 ^{66}Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn^{83} Ser^{83a} Leu^{83b} Arg^{83c} Ala Glu Asp Thr Ala Val Tyr Tyr Cys^{92} (SEQ ID NO: 175)

HC-FR4 ^{103}Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser^{113} (SEQ ID NO: 176)

FIG. 5

Framework Sequences of huMAb4D5-8 Light Chain Modified at Position 66 (Underlined)

LC-FR1 ^{1}Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys^{23} (SEQ ID NO: 42)

LC-FR2 ^{35}Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr^{49} (SEQ ID NO: 43)

LC-FR3 ^{57}Gly Val Pro Ser Arg Phe Ser Gly Ser <u>Gly</u> Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys^{88} (SEQ ID NO: 177)

LC-FR4 ^{98}Phe Gly Gln Gly Thr Lys Val Glu Ile Lys^{107} (SEQ ID NO: 45)

Framework Sequences of huMAb4D5-8 Heavy Chain Modified at Postions 71, 73 and 78 (Underlined)

HC-FR1 ^{1}Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser^{25} (SEQ ID NO: 46)

HC-FR2 ^{36}Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val^{48} (SEQ ID NO: 47)

HC-FR3 ^{66}Arg Phe Thr Ile Ser <u>Arg</u> Asp <u>Asn</u> Ser Lys Asn Thr <u>Leu</u> Tyr Leu Gln Met Asn83 Ser83a Leu83b Arg83c Ala Glu Asp Thr Ala Val Tyr Tyr Cys^{92} (SEQ ID NO: 178)

HC-FR4 ^{103}Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser^{113} (SEQ ID NO: 176)

FIG. 6

FIG. 7A

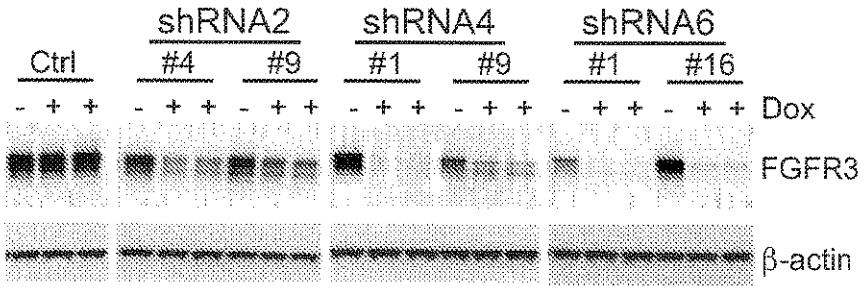


FIG. 7B

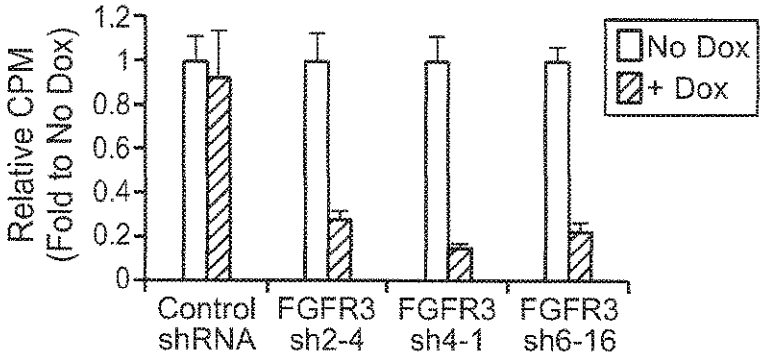
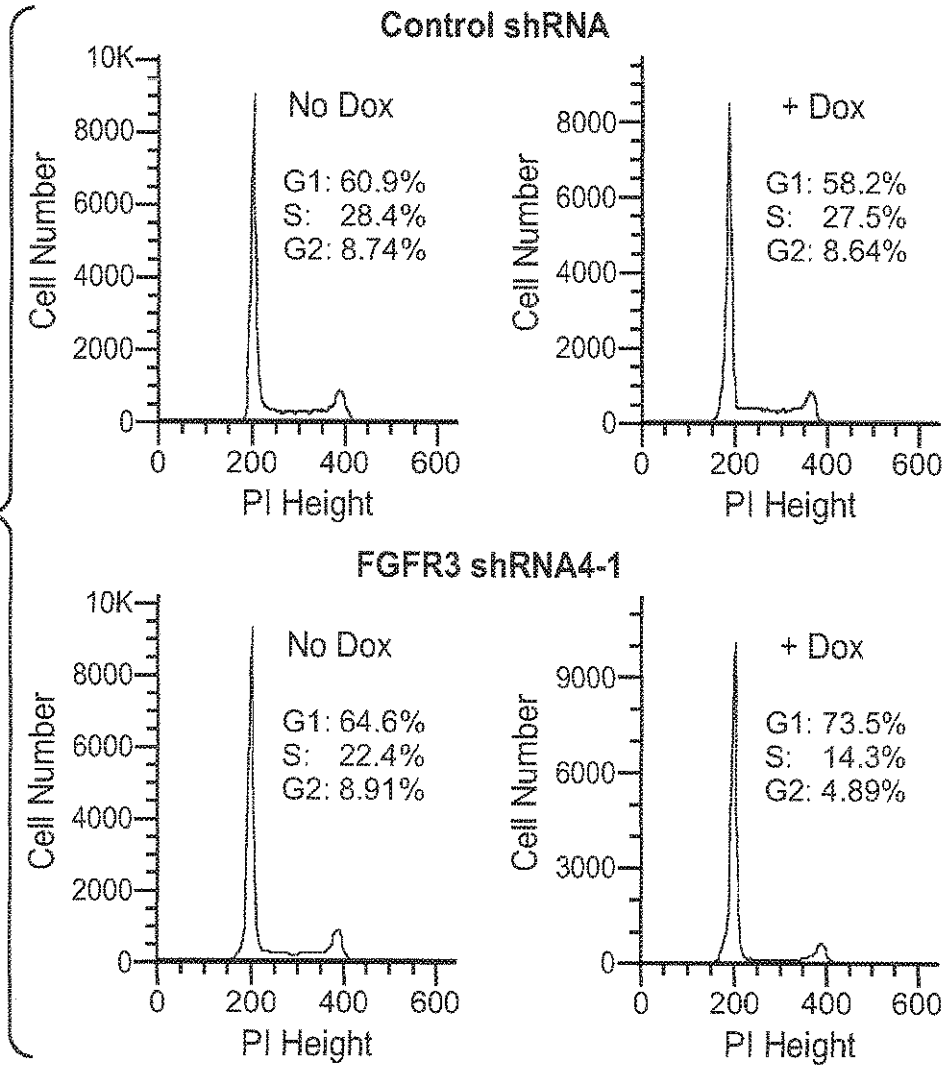


FIG. 7C



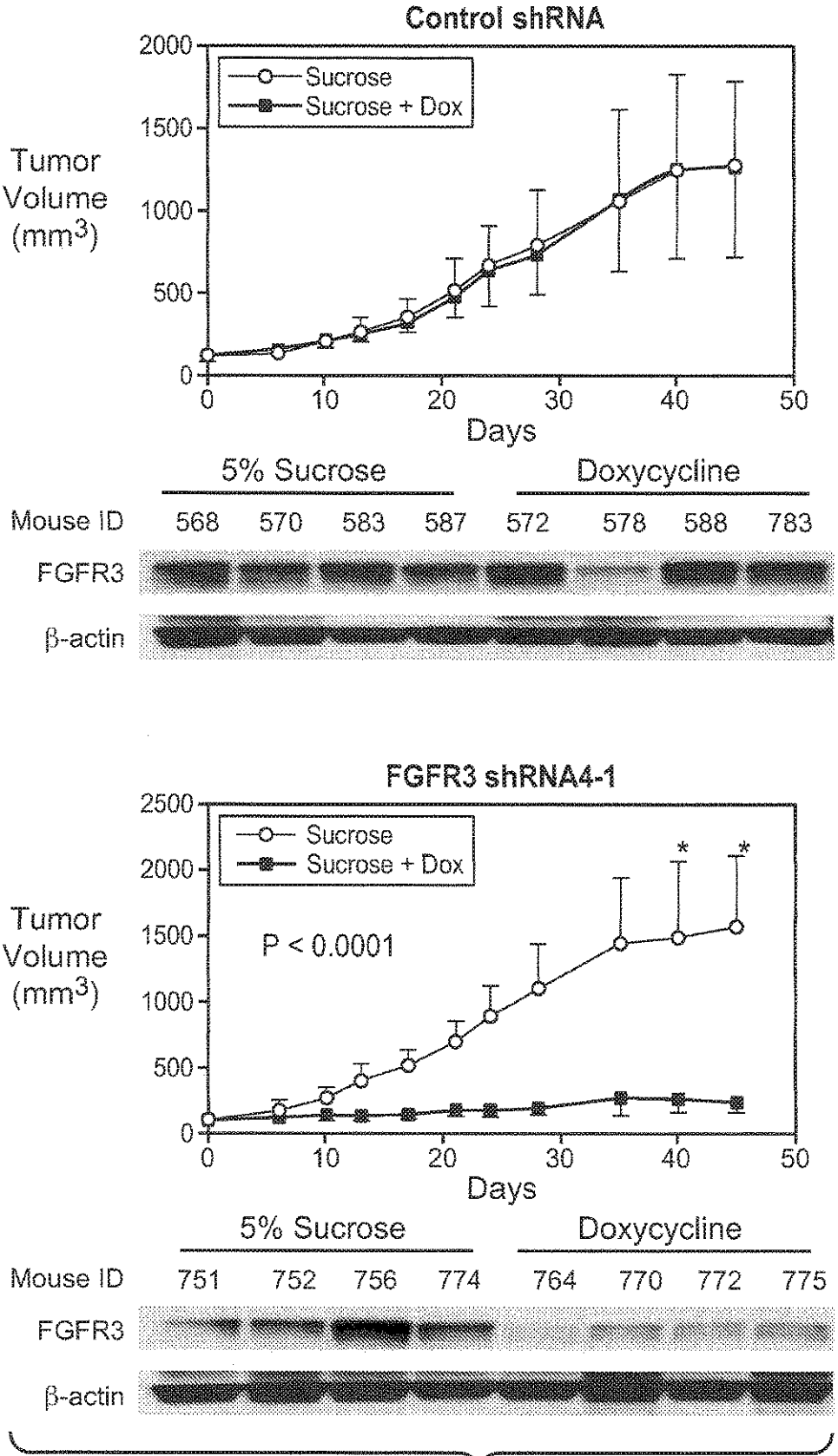

Control shRNA
Tumor Volume (mm3)
Sucrose
Sucrose + Dox
Days
5% Sucrose
Doxycycline
Mouse ID
568 570 583 587 572 578 588 783
FGFR3
β-actin
FGFR3 shRNA4-1
P < 0.0001
751 752 756 774 764 770 772 775

FIG. 7D

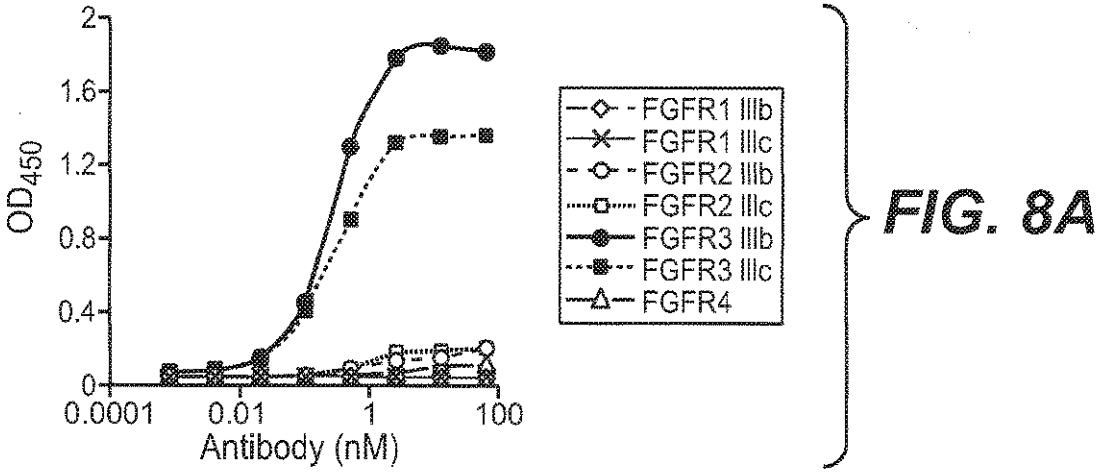


FIG. 8A

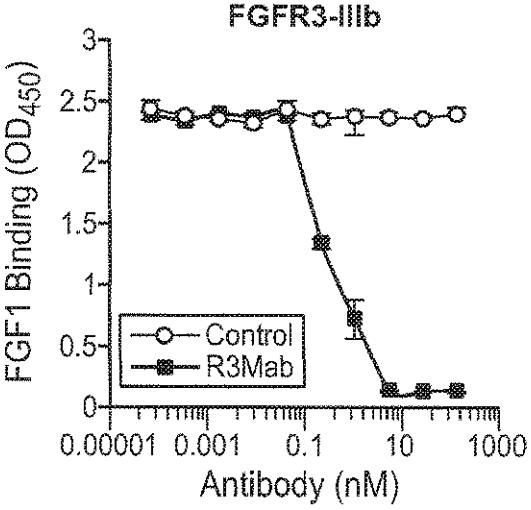


FIG. 8B

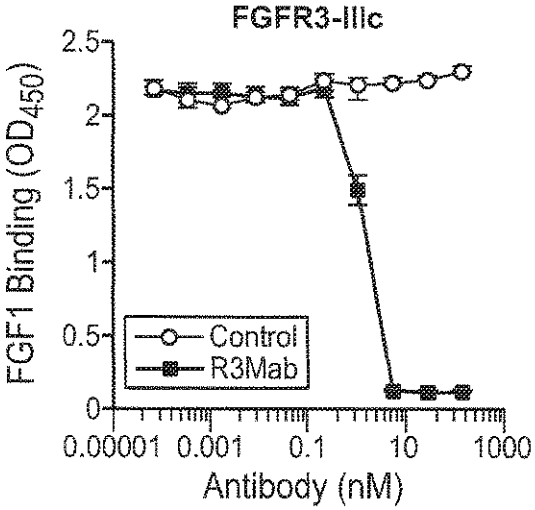


FIG. 8C

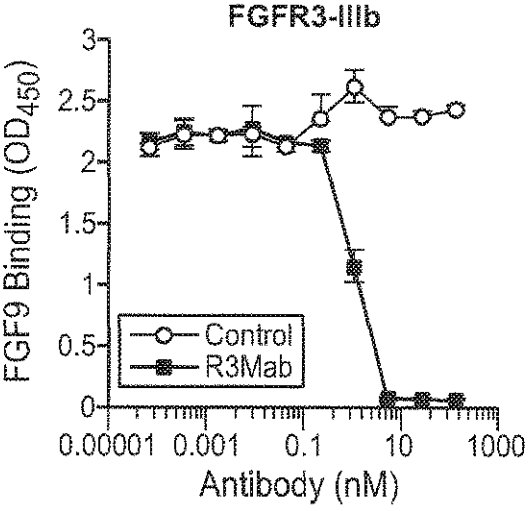


FIG. 8D

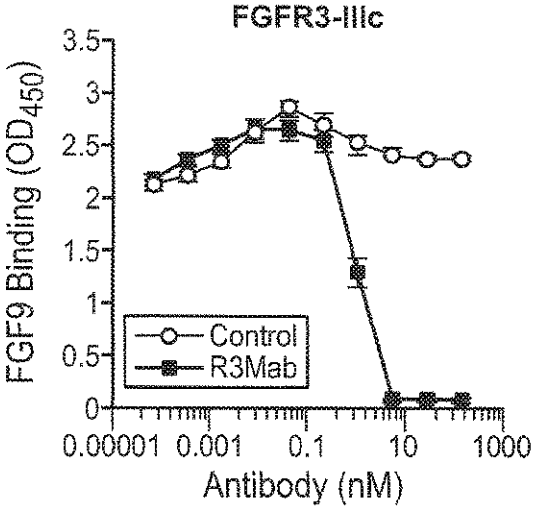


FIG. 8E

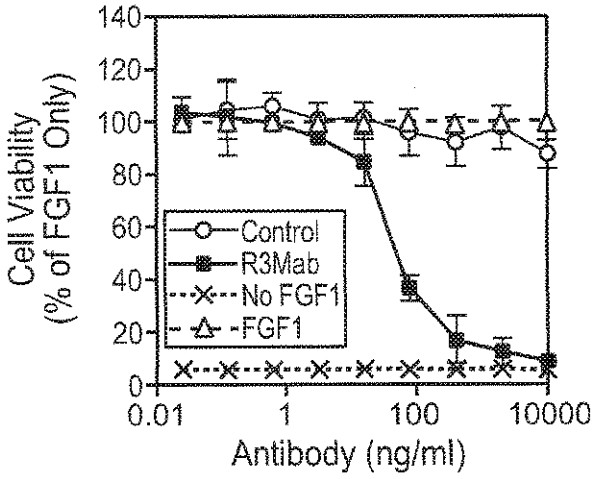


FIG. 9A

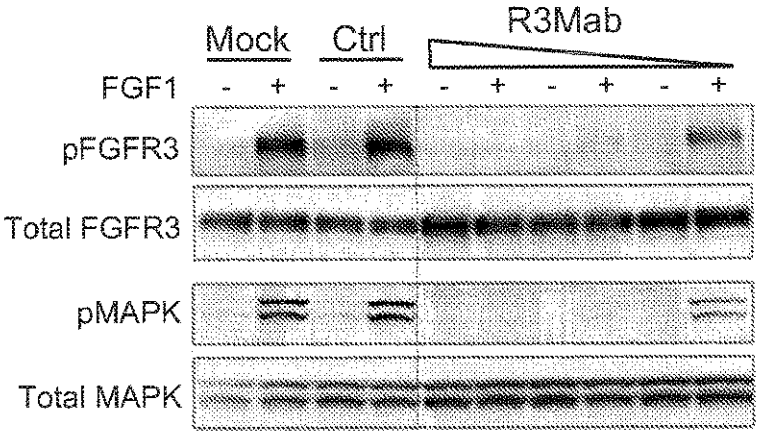


FIG. 9B

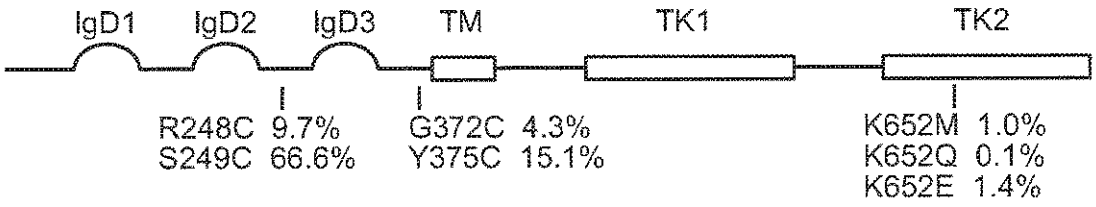


FIG. 9C

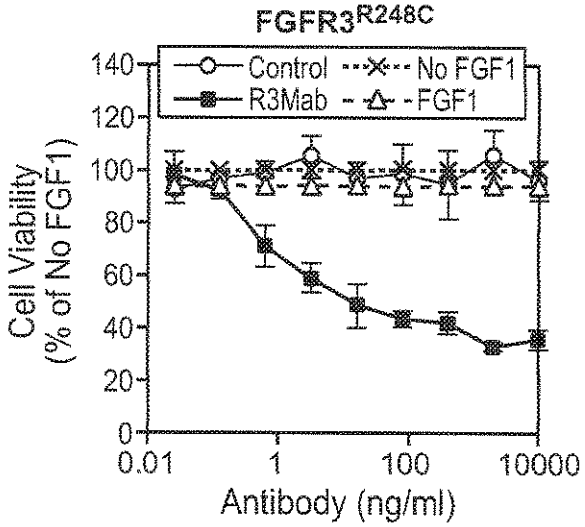


FIG. 9D

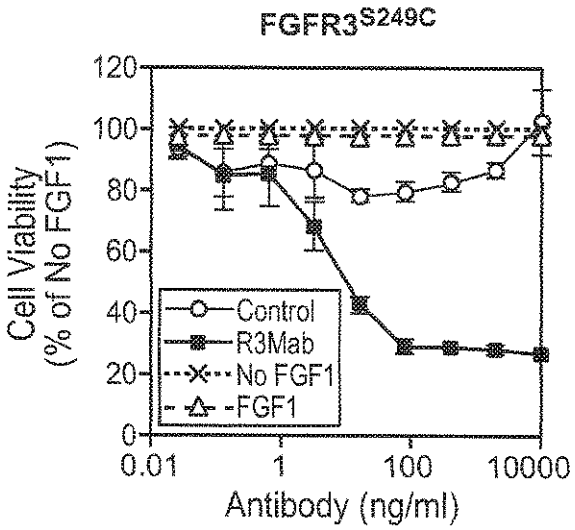


FIG. 9E

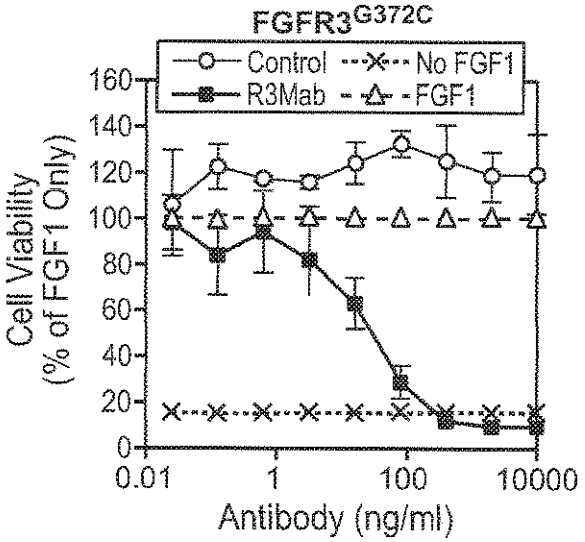


FIG. 9F

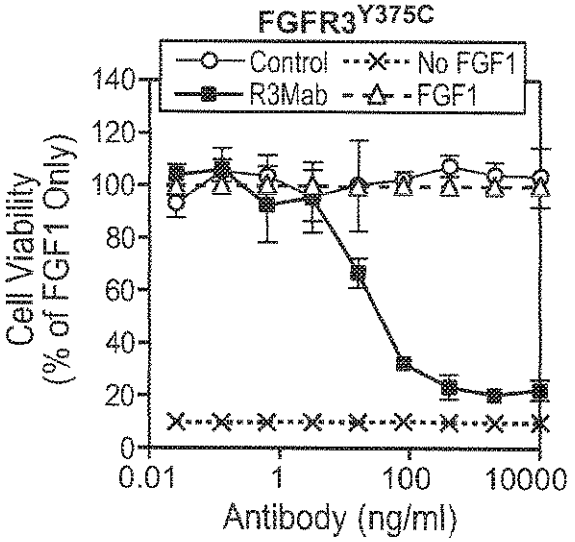


FIG. 9G

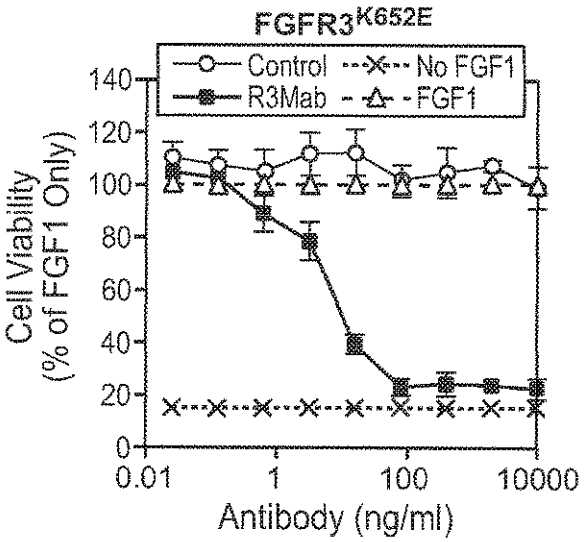


FIG. 9H

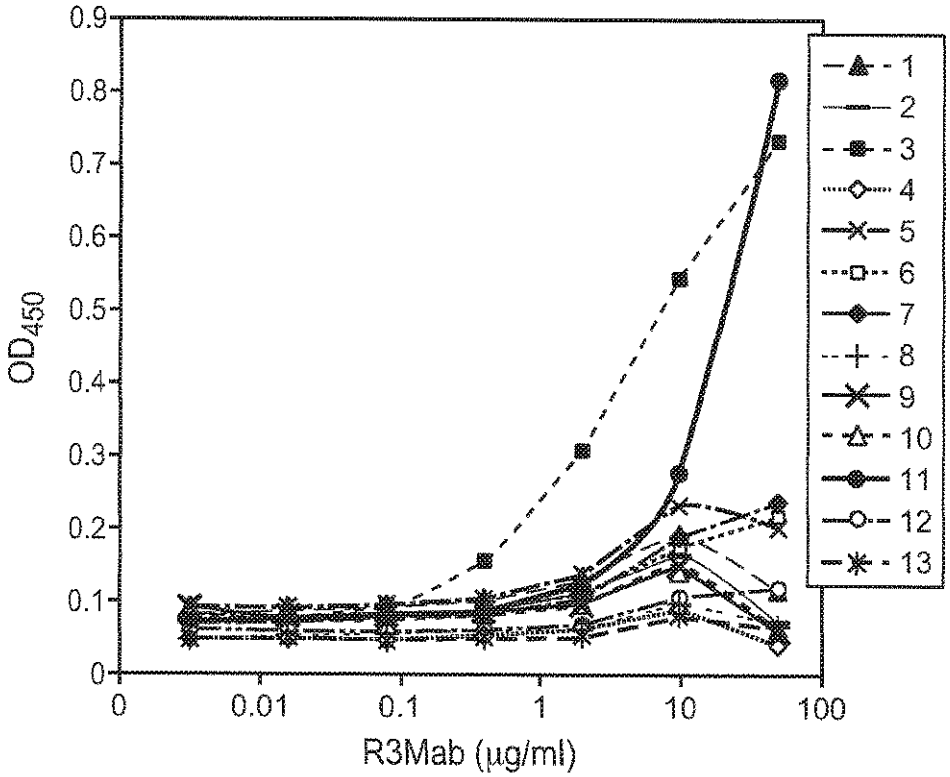
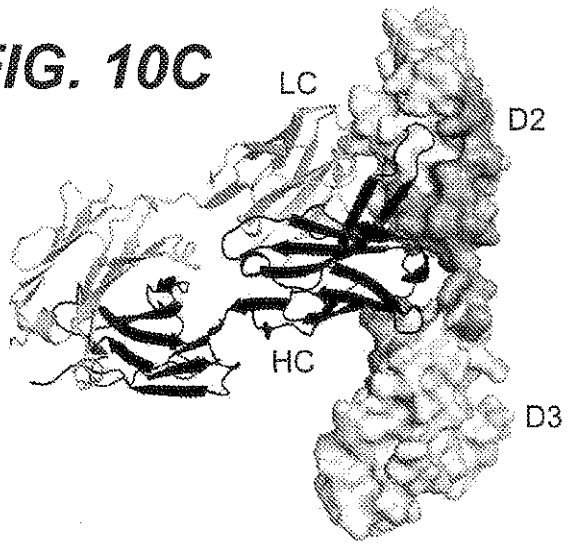


FIG. 10A

164 178		
FGFR3	**LAVP**AA**N**TVR**F**RCPA	Peptide 3
FGFR1	**HAVP**AA**K**TVK**F**KCPS	
269 283		
FGFR3	SDVEFHCK**VYSDAQP**	Peptide 11
FGFR1	SNVEFMCK**VYSDPQP**	

FIG. 10B

FIG. 10C



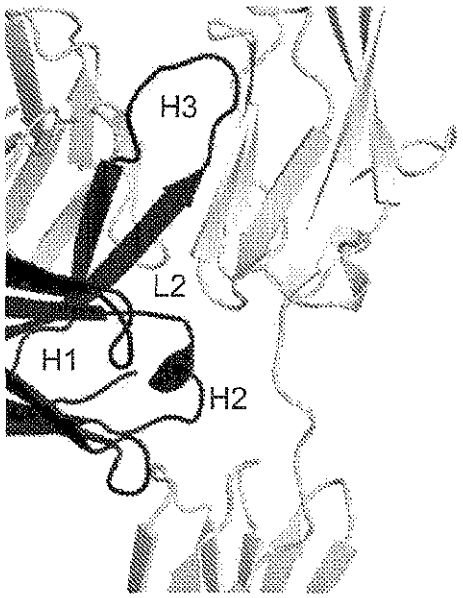


FIG. 10D

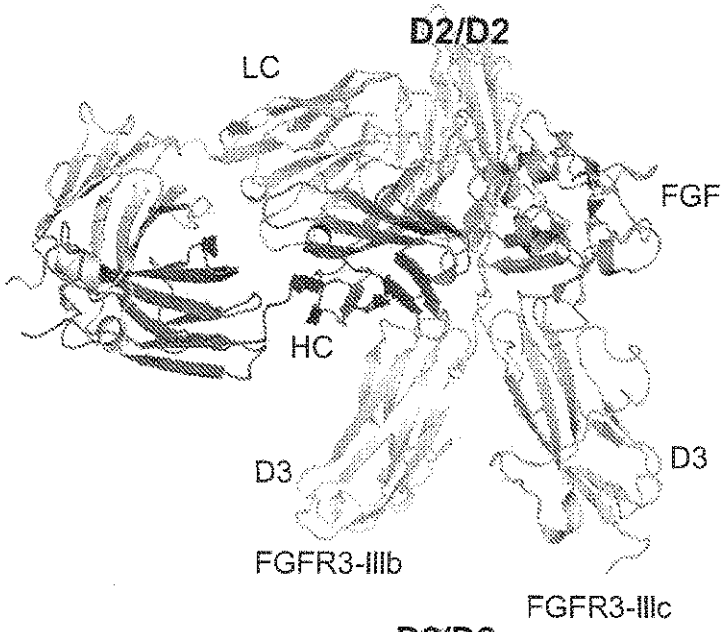


FIG. 10E

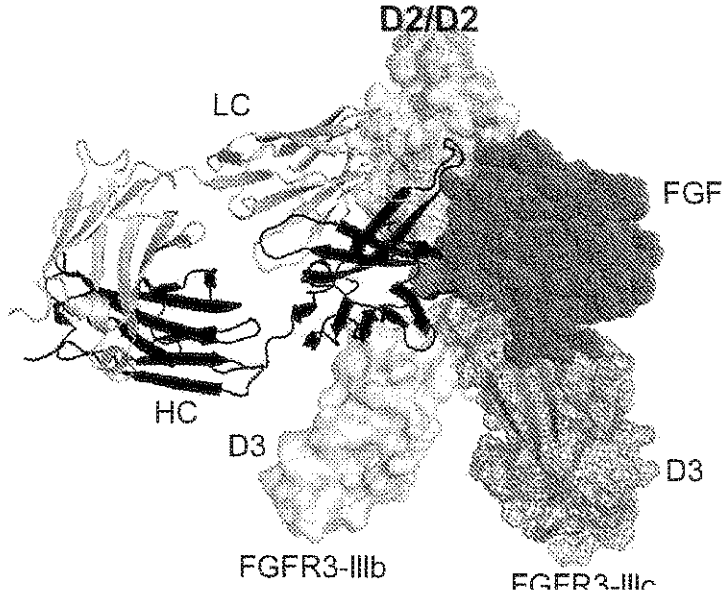


FIG. 10F

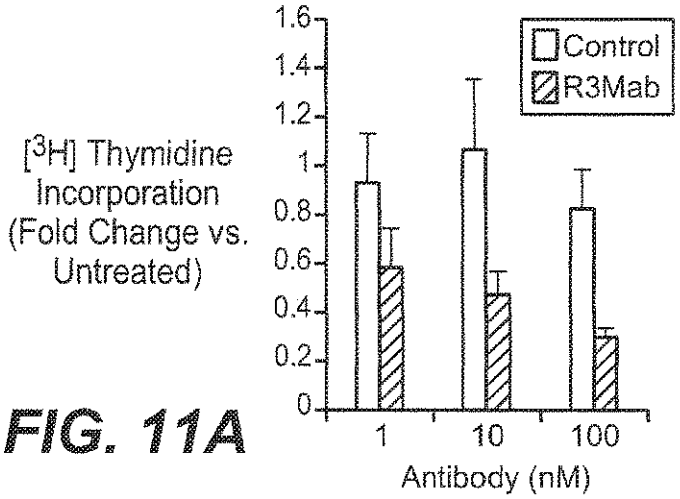


FIG. 11A

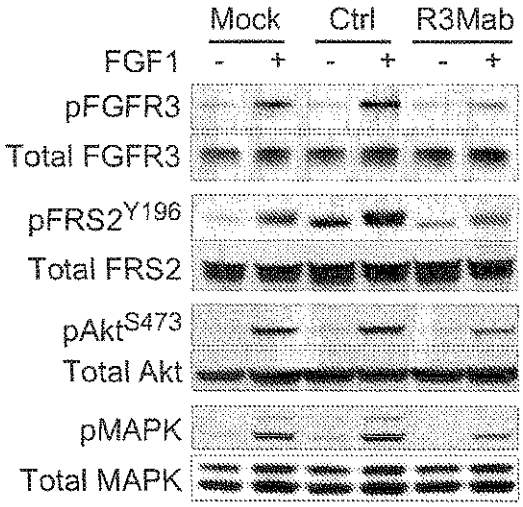


FIG. 11B

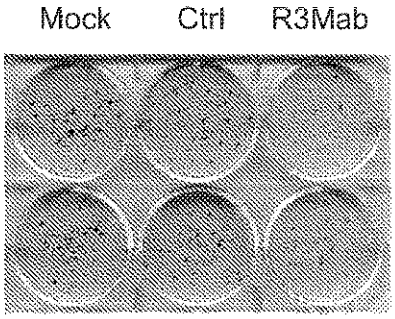


FIG. 11C

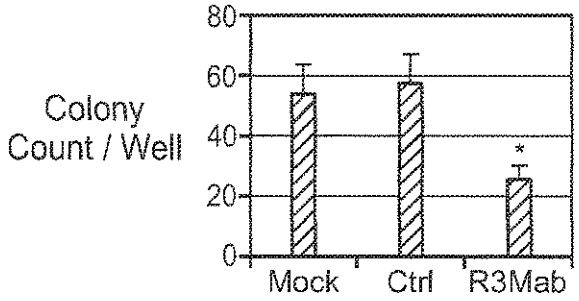


FIG. 11D

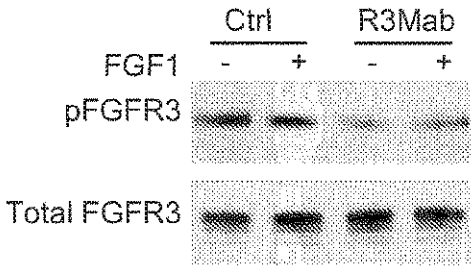


FIG. 11E

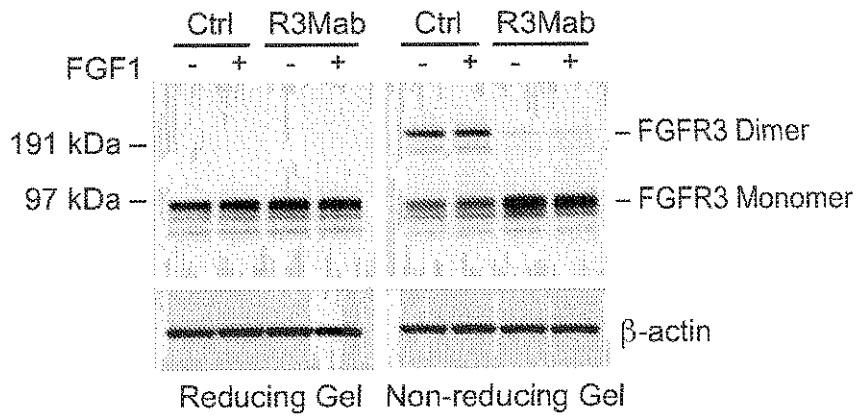


FIG. 12A

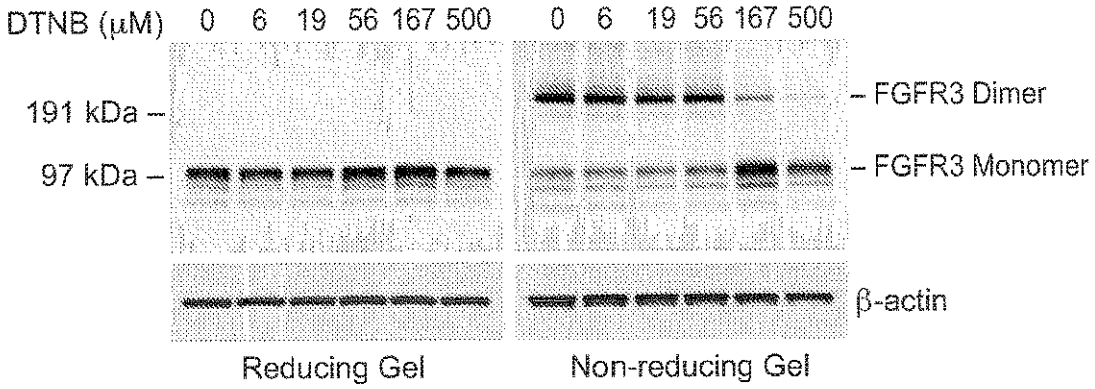


FIG. 12B

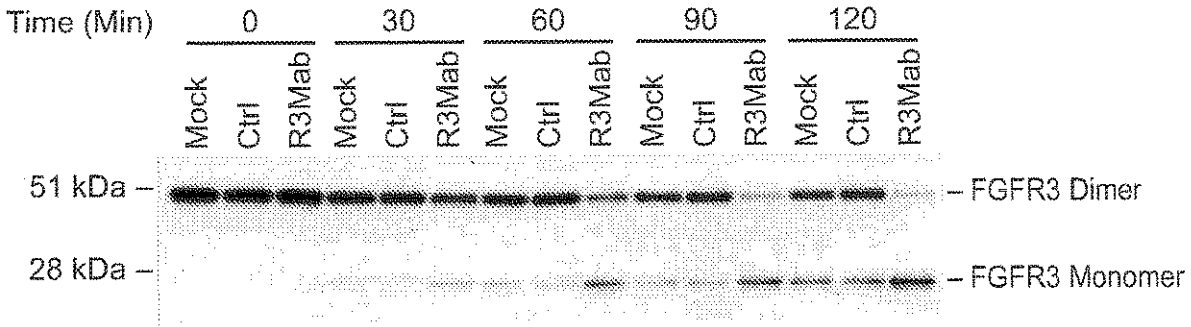


FIG. 12C

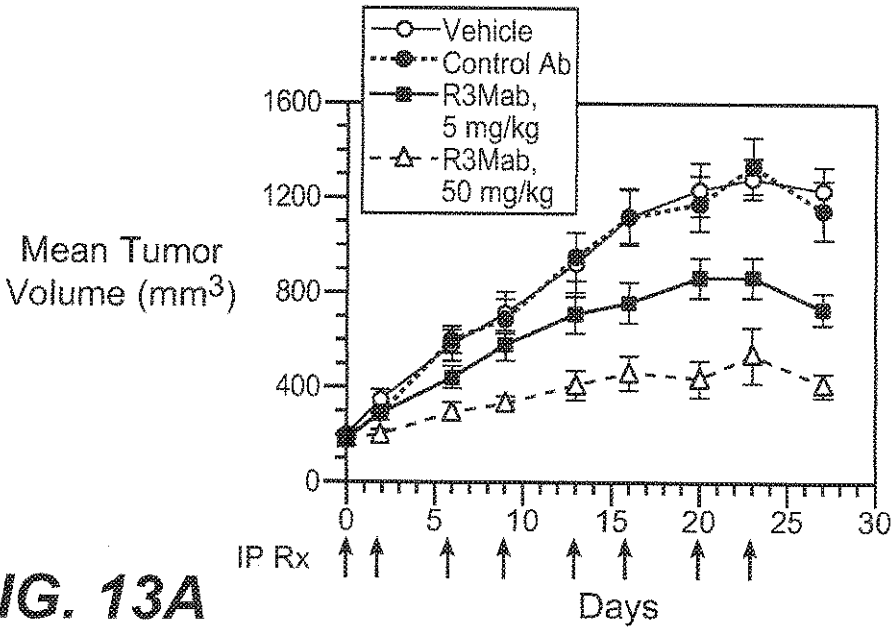


FIG. 13A

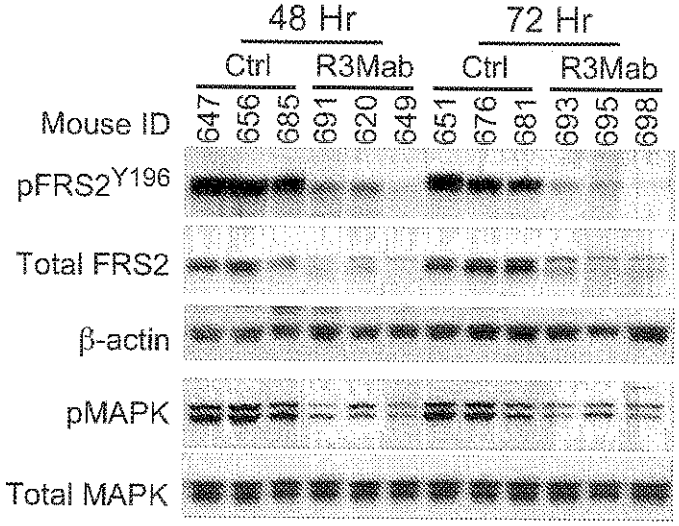


FIG. 13B

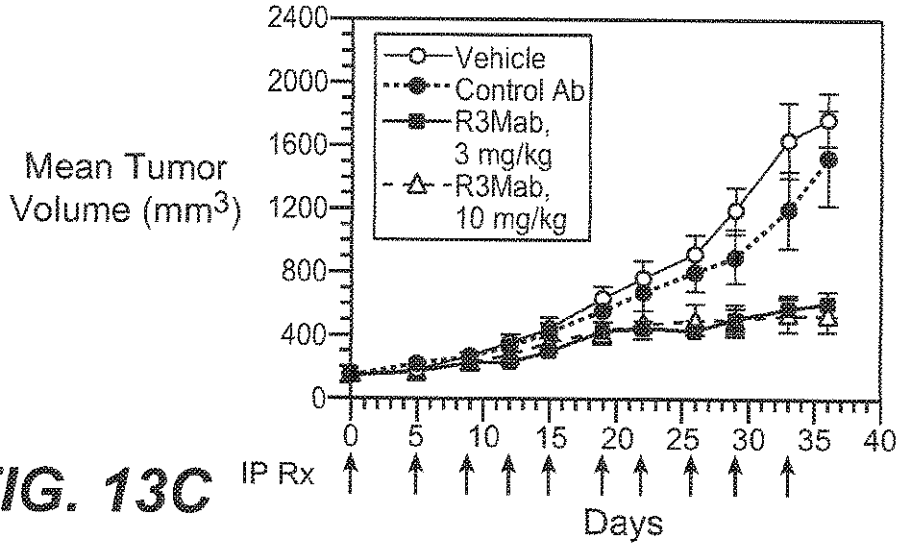


FIG. 13C

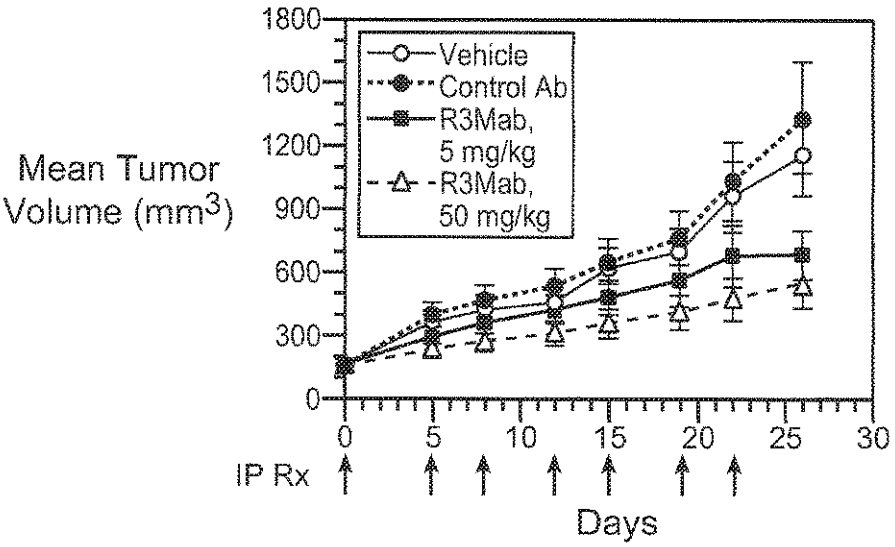


FIG. 13D

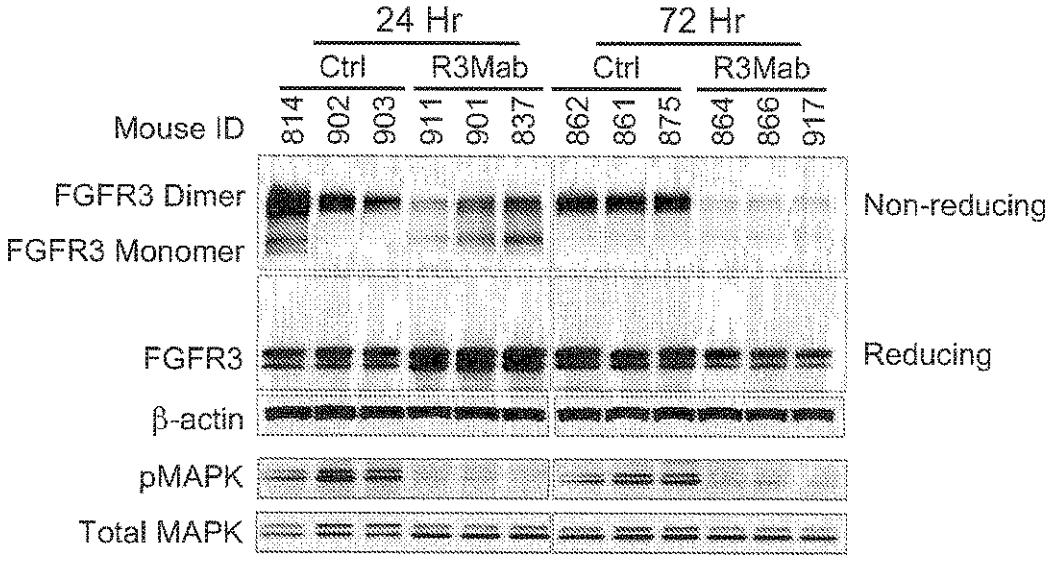


FIG. 13E

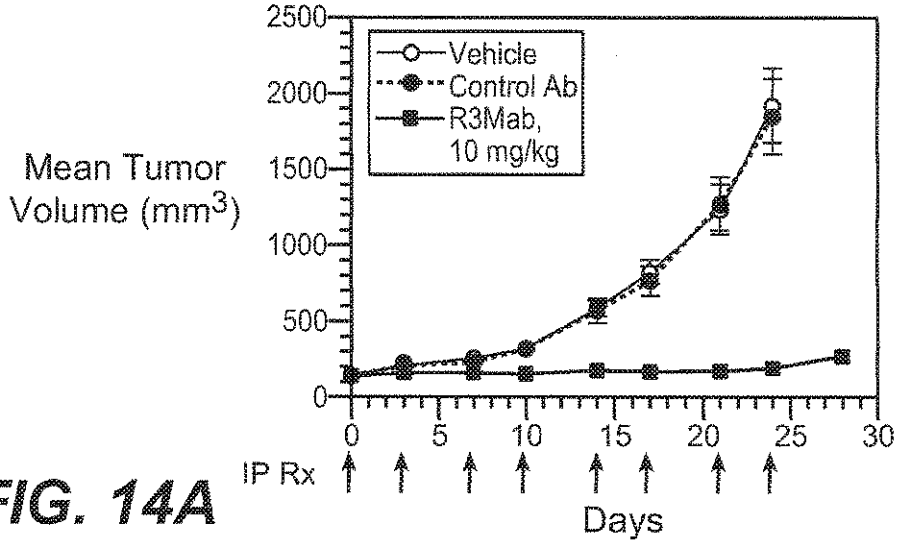


FIG. 14A

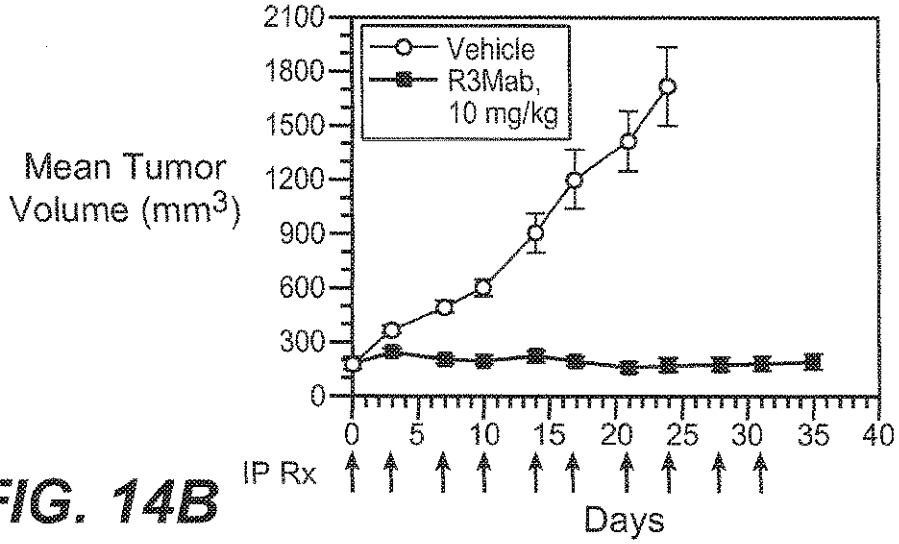


FIG. 14B

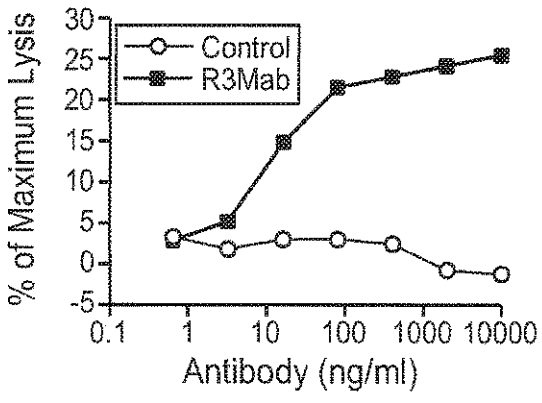


FIG. 14C

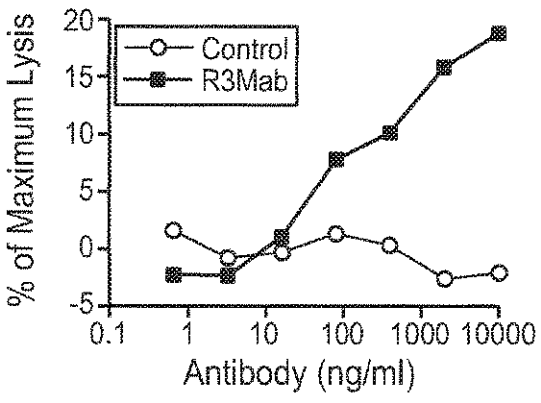


FIG. 14D

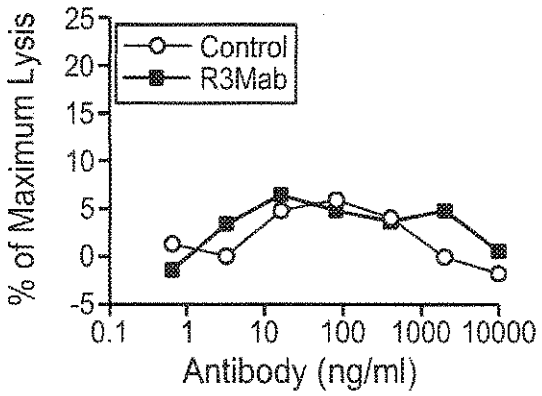


FIG. 14E

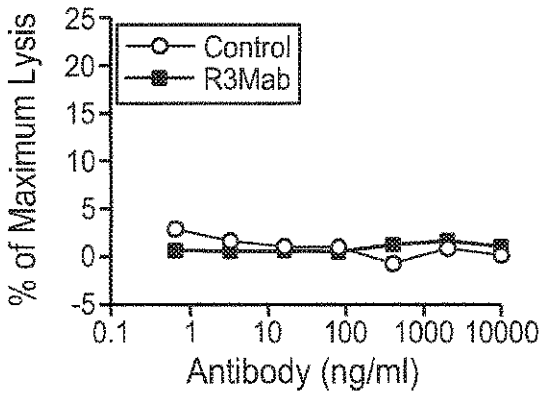


FIG. 14F

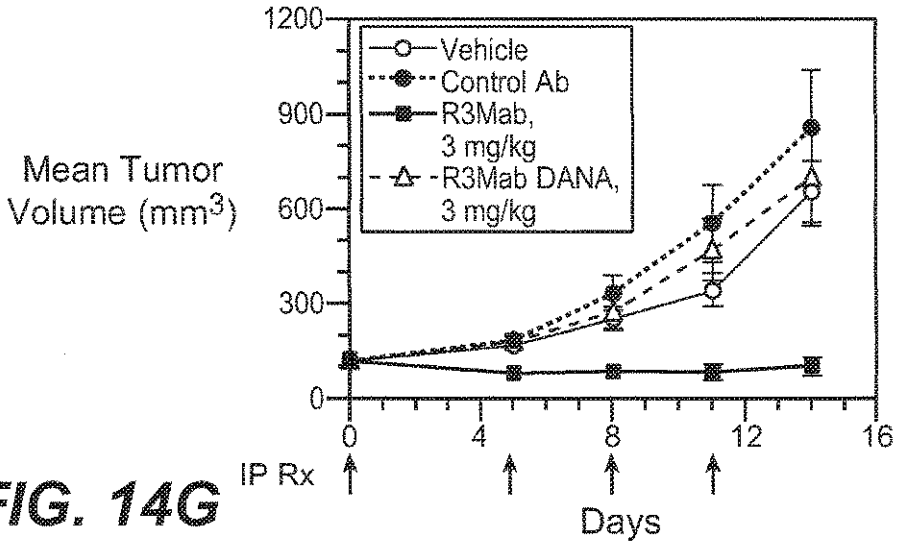


FIG. 14G

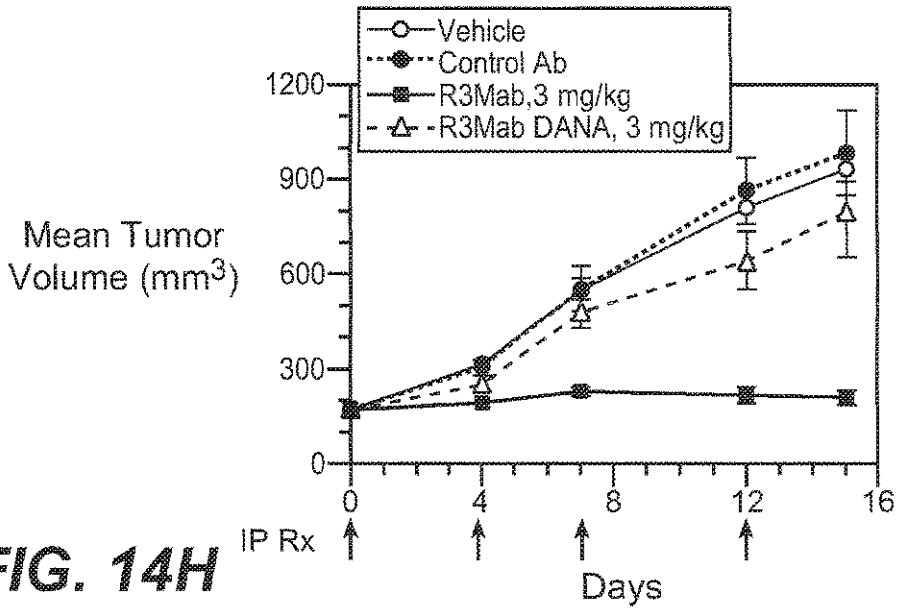


FIG. 14H

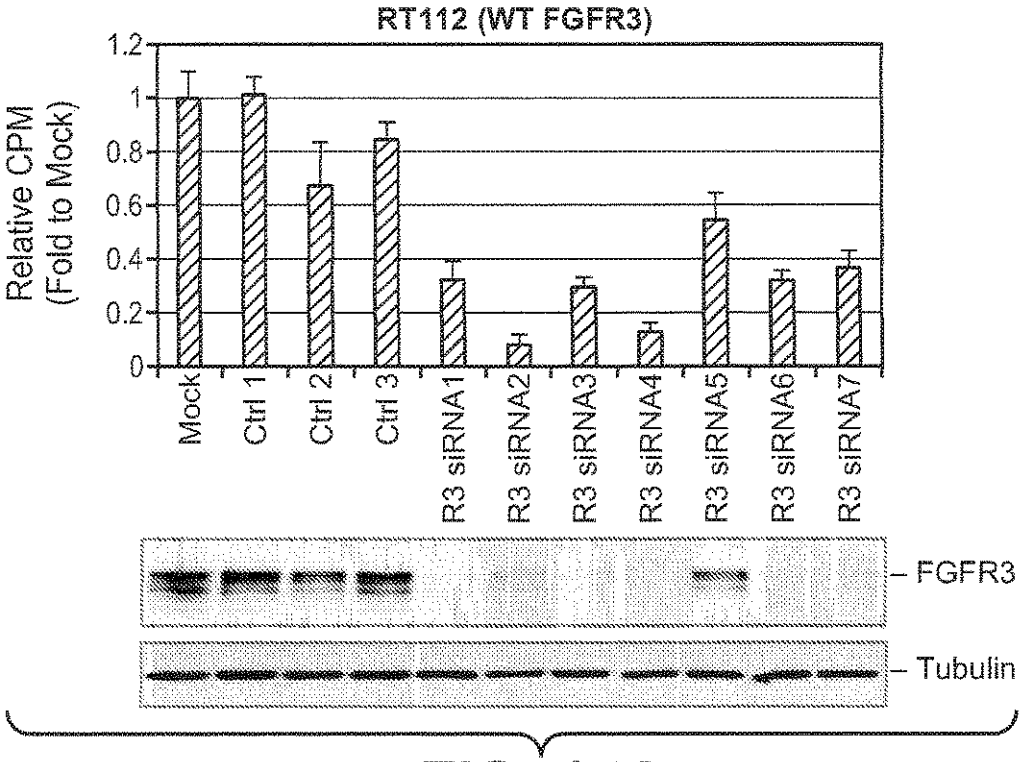


FIG. 15A

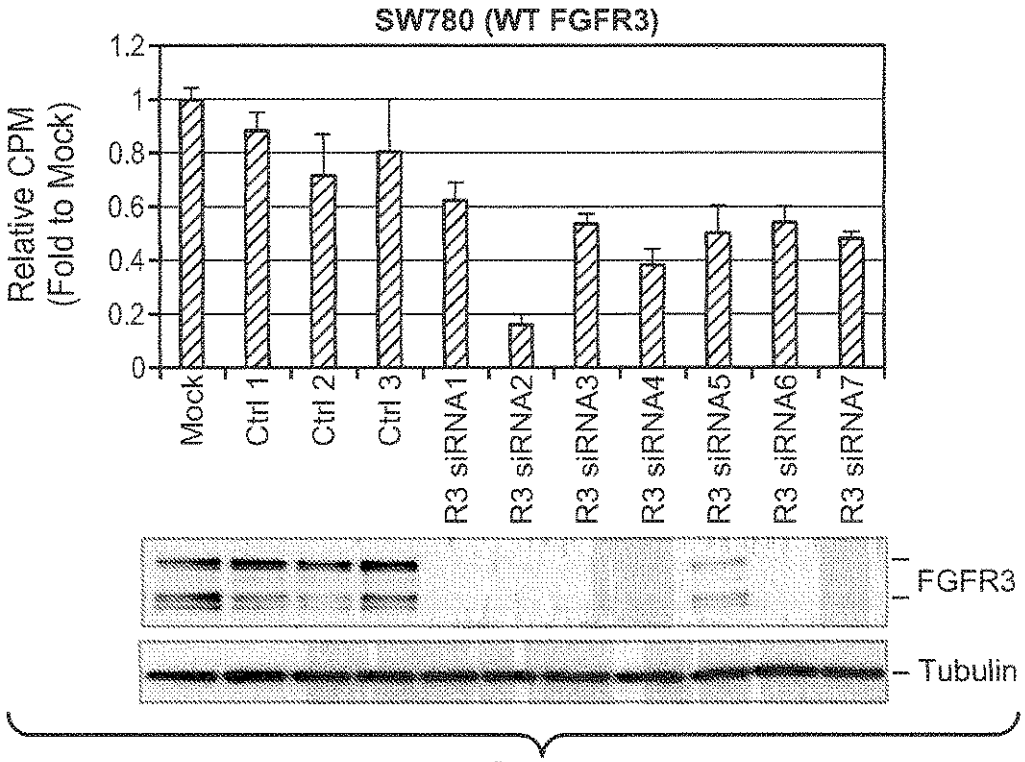


FIG. 15B

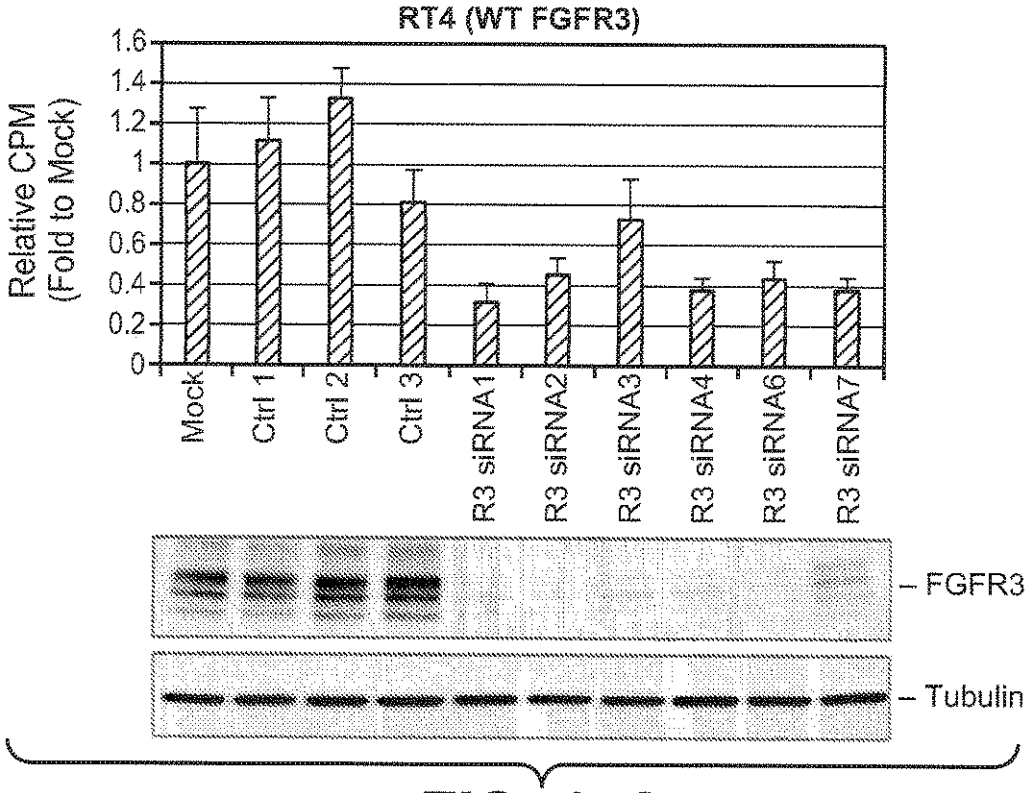


FIG. 15C

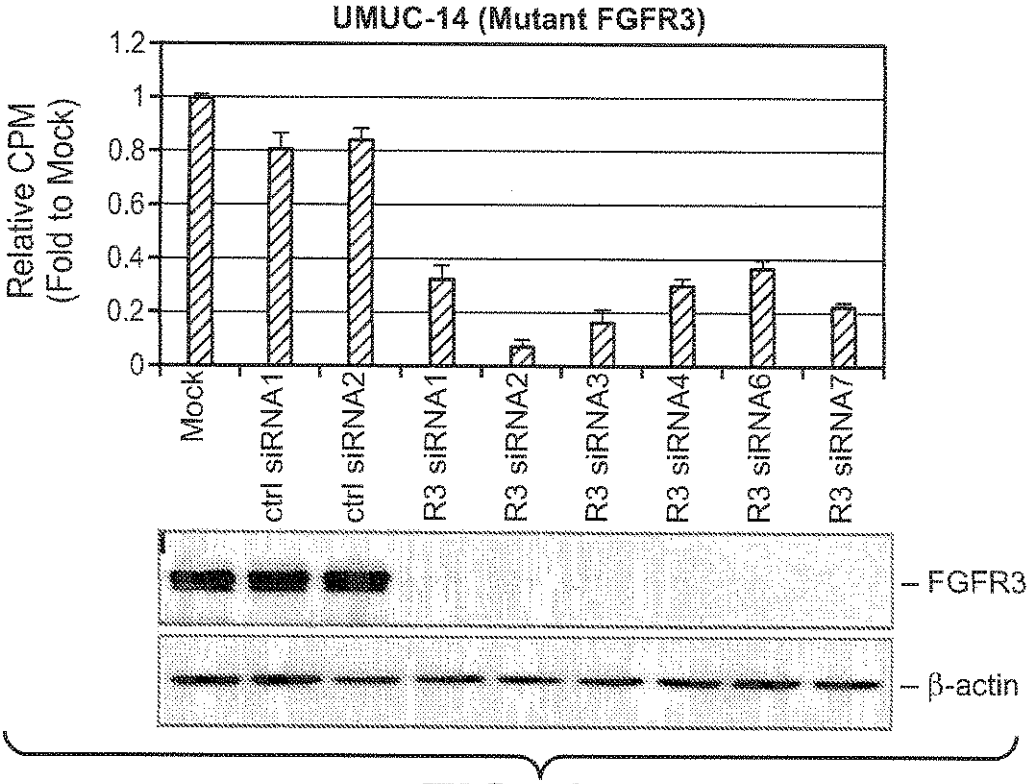


FIG. 15D

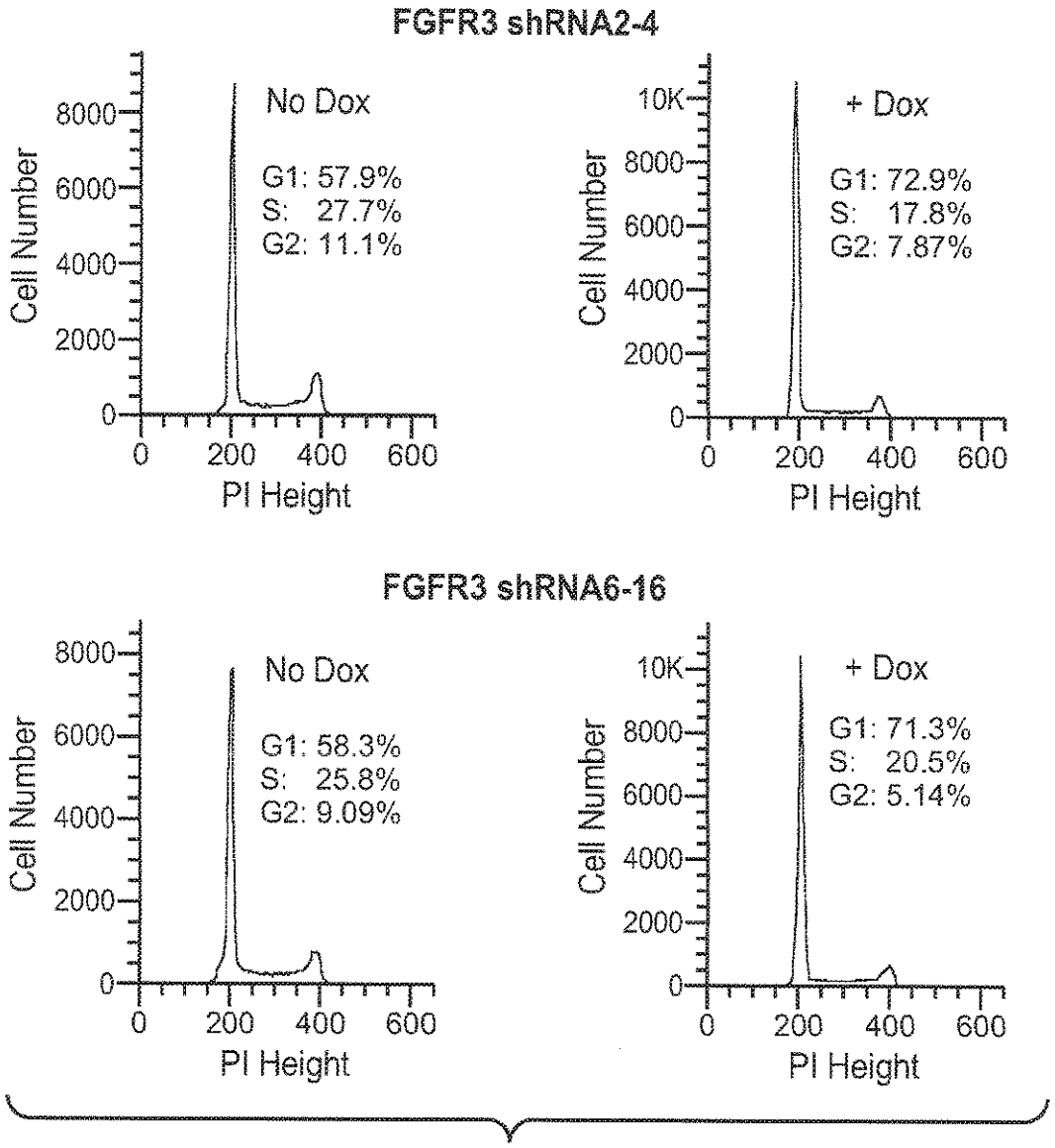

FGFR3 shRNA2-4
No Dox
G1: 57.9%
S: 27.7%
G2: 11.1%
+ Dox
G1: 72.9%
S: 17.8%
G2: 7.87%
FGFR3 shRNA6-16
No Dox
G1: 58.3%
S: 25.8%
G2: 9.09%
+ Dox
G1: 71.3%
S: 20.5%
G2: 5.14%
Cell Number
PI Height
0
2000
4000
6000
8000
10K
200
400
600

FIG. 16A

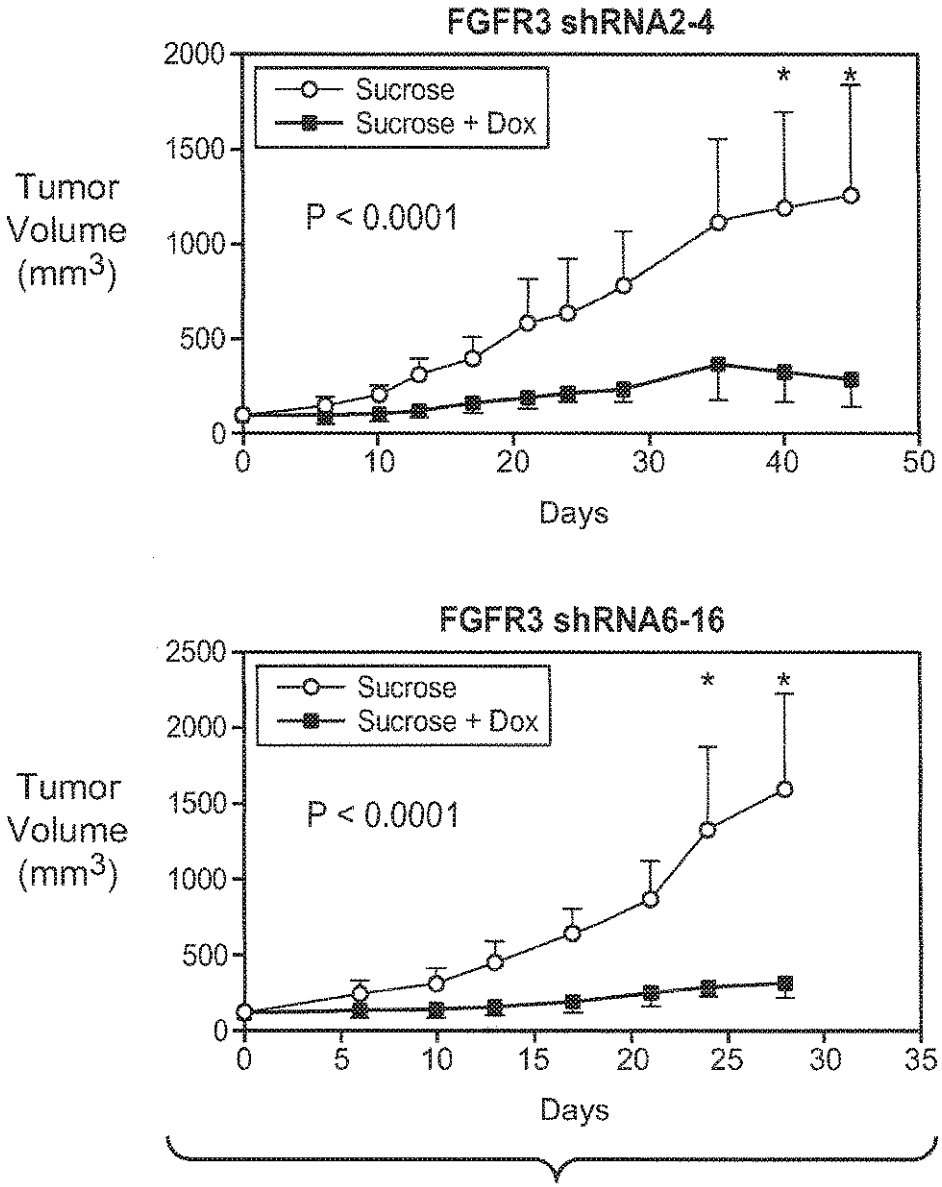

FGFR3 shRNA2-4
Tumor Volume (mm3)
Sucrose
Sucrose + Dox
P < 0.0001
*
*
2000
1500
1000
500
0
0
10
20
30
40
50
Days
FGFR3 shRNA6-16
Tumor Volume (mm3)
Sucrose
Sucrose + Dox
P < 0.0001
*
*
2500
2000
1500
1000
500
0
0
5
10
15
20
25
30
35
Days

FIG. 16B

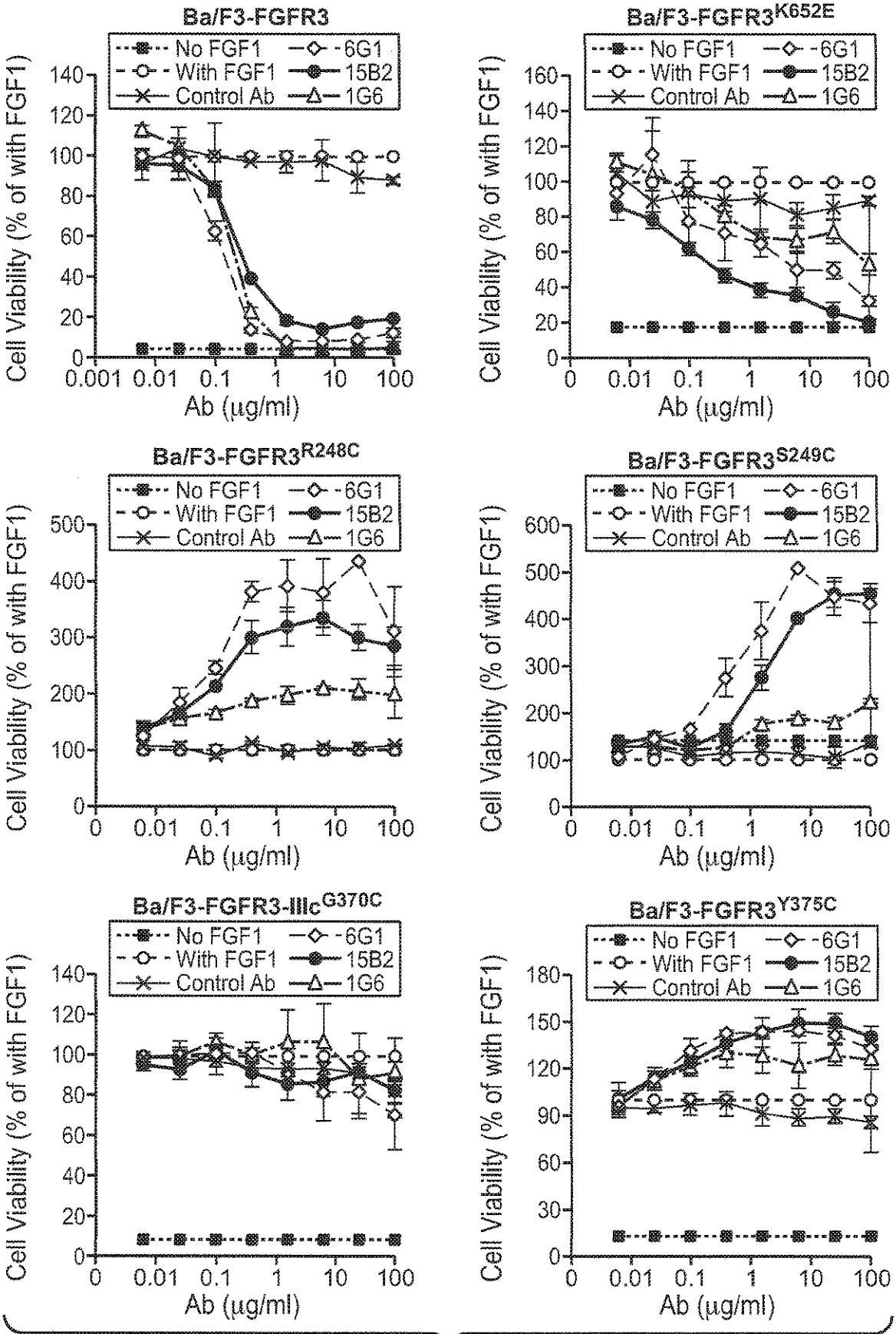

Ba/F3-FGFR3
Ba/F3-FGFR3K652E
Ba/F3-FGFR3R248C
Ba/F3-FGFR3S249C
Ba/F3-FGFR3-IIIcG370C
Ba/F3-FGFR3Y375C
No FGF1
With FGF1
Control Ab
6G1
15B2
1G6
Cell Viability (% of with FGF1)
Ab (μg/ml)

FIG. 17

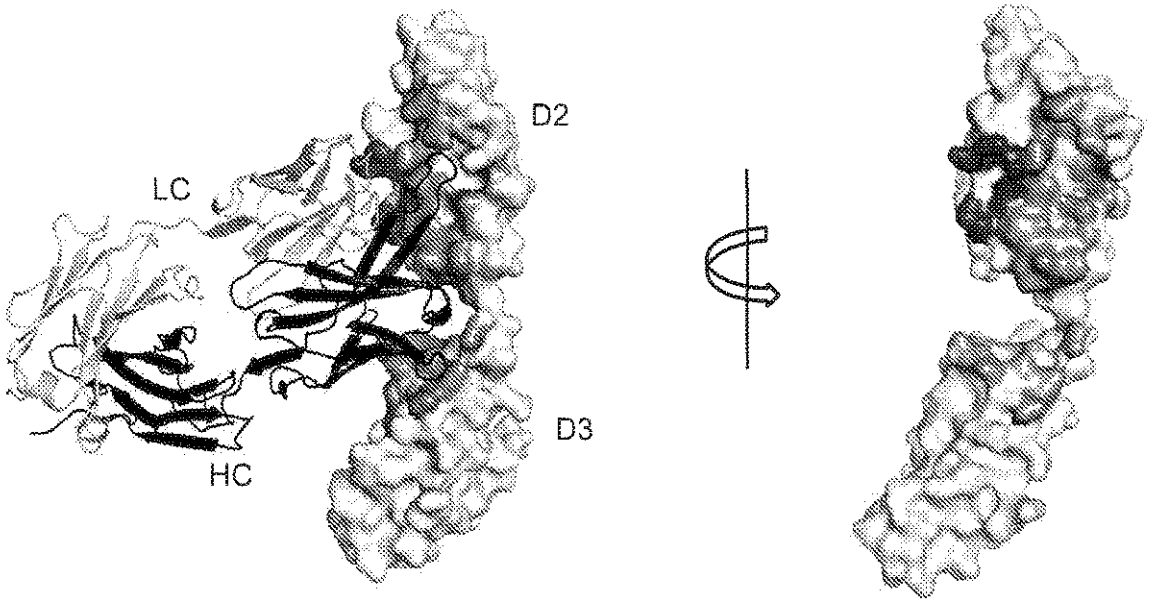


FIG. 18A

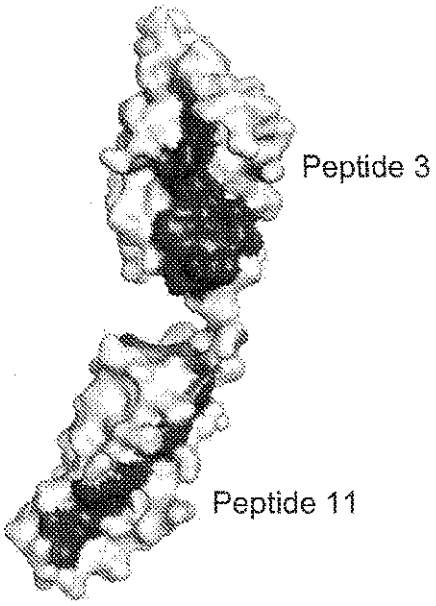


FIG. 18B

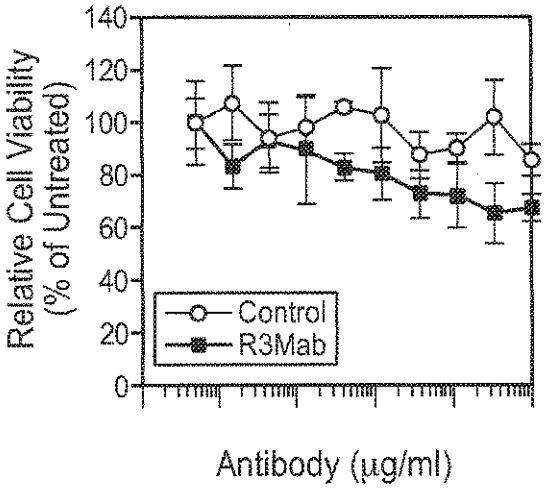


FIG. 19A

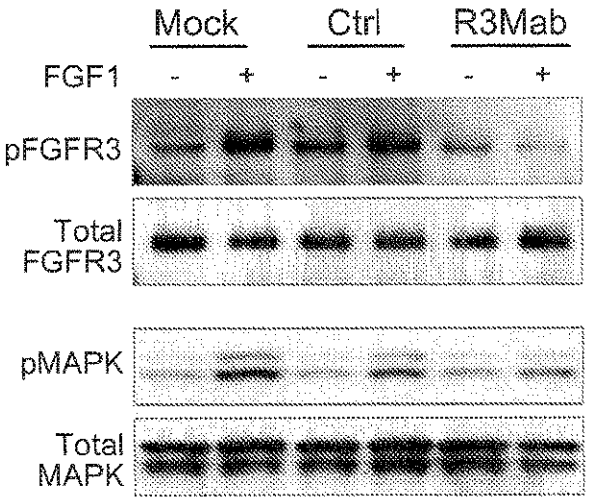


FIG. 19B

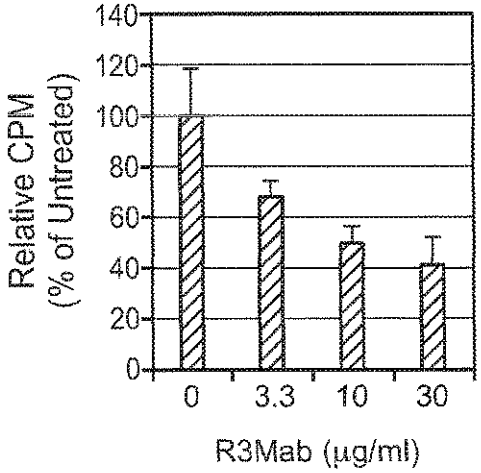


FIG. 19C

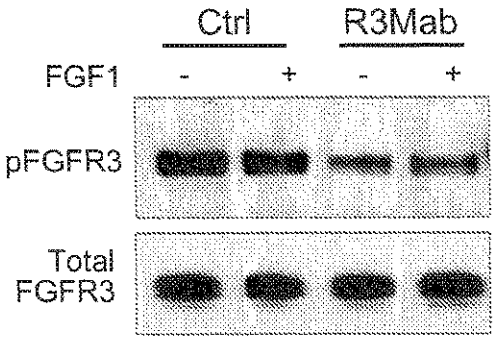


FIG. 19D

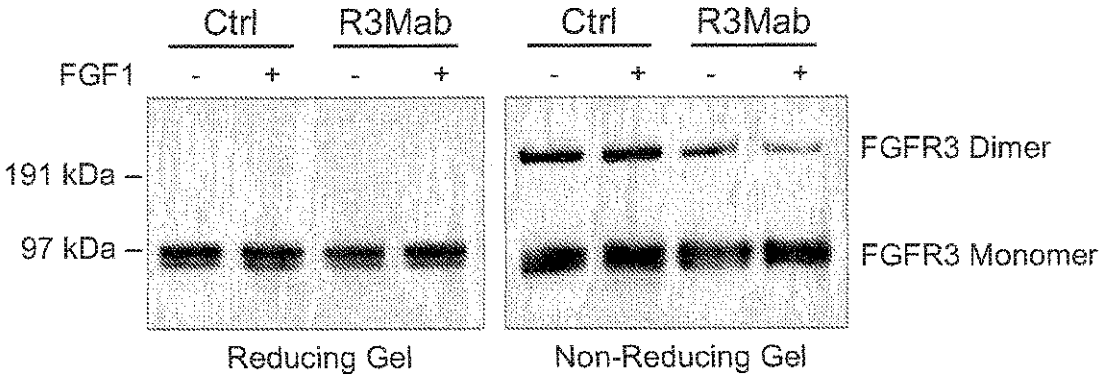


FIG. 19E

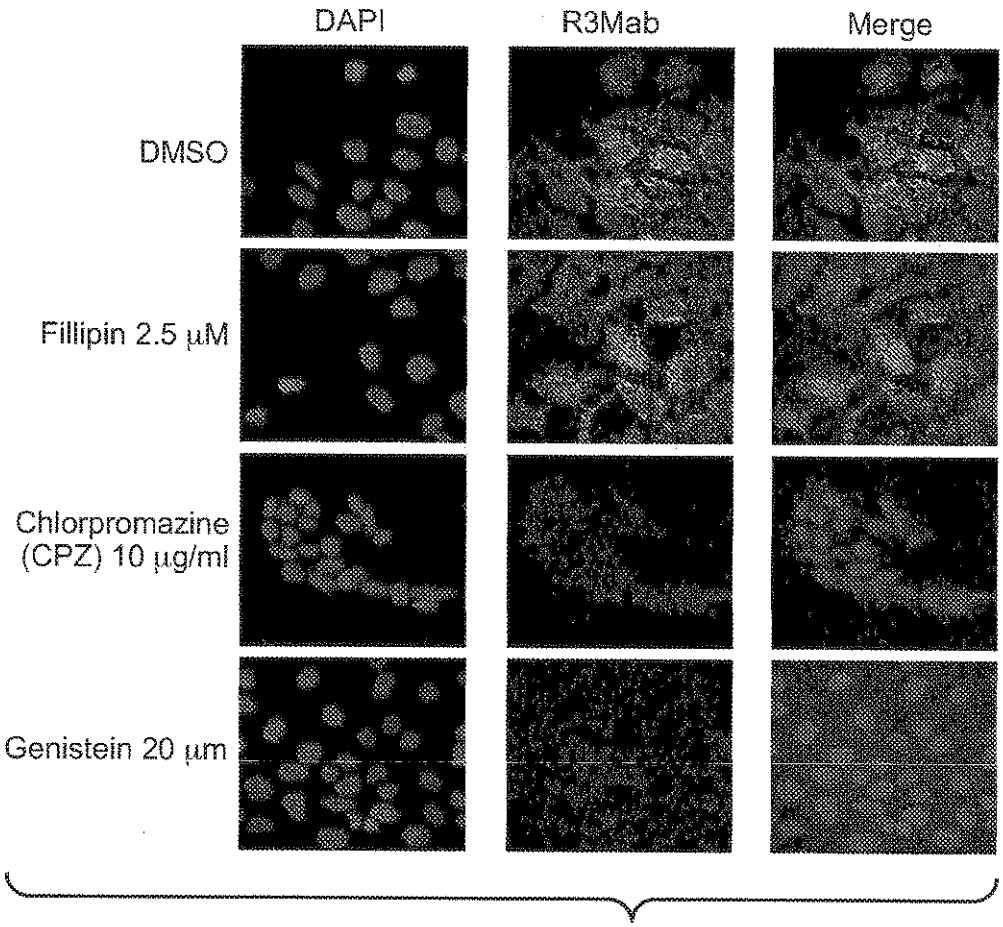


FIG. 20A

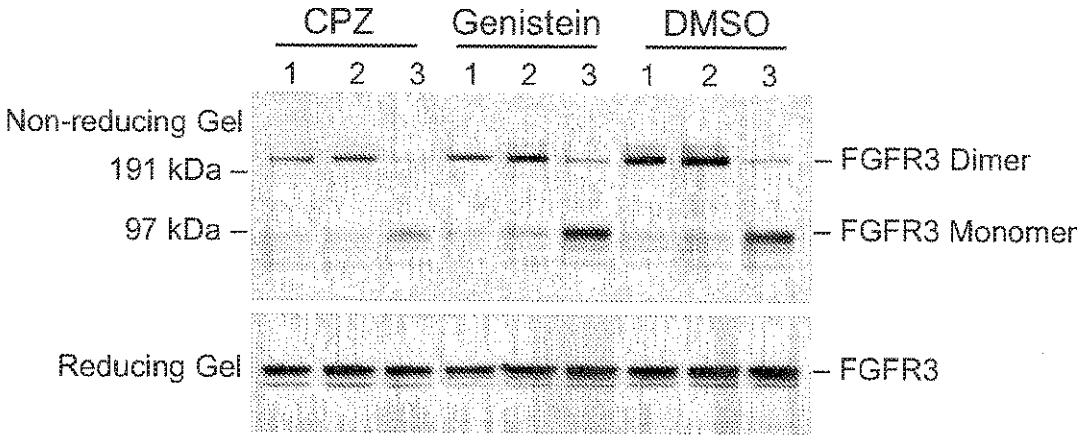


FIG. 20B

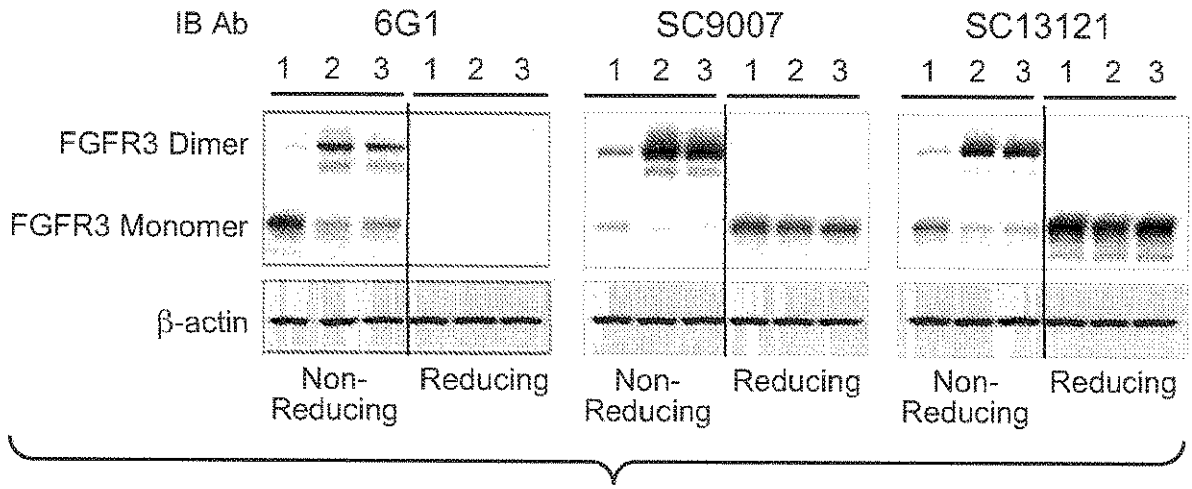

IB Ab
6G1
SC9007
SC13121
1 2 3 1 2 3
1 2 3 1 2 3
1 2 3 1 2 3
FGFR3 Dimer
FGFR3 Monomer
β-actin
Non-Reducing
Reducing
Non-Reducing
Reducing
Non-Reducing
Reducing

FIG. 21

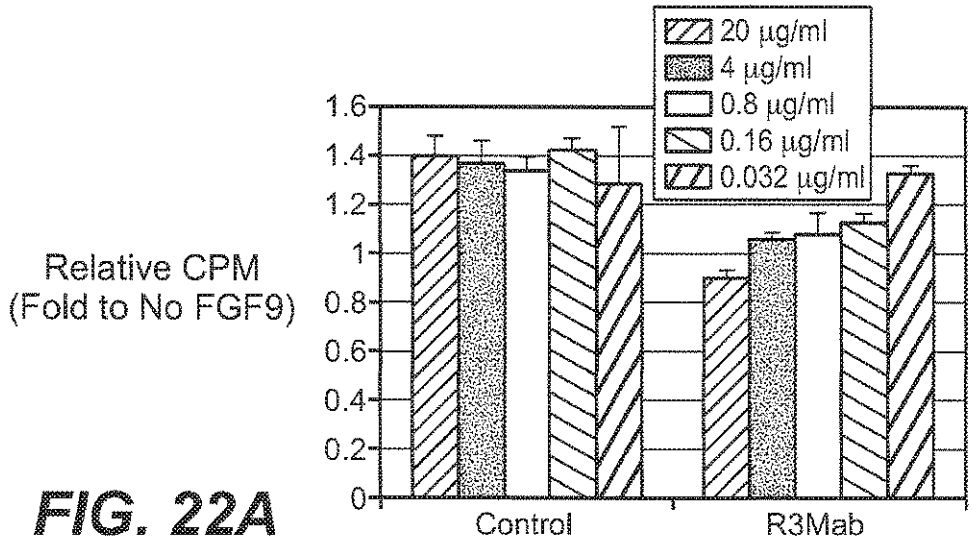


FIG. 22A

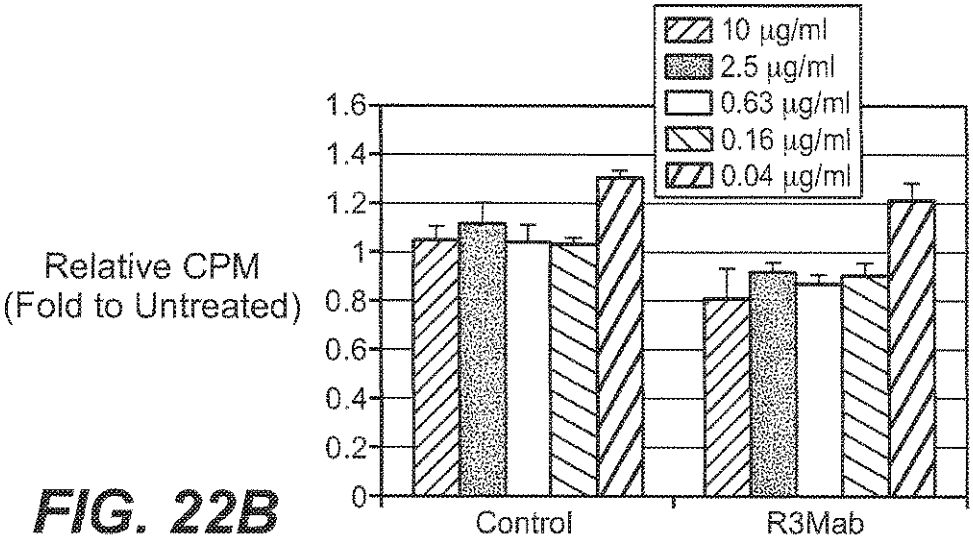


FIG. 22B

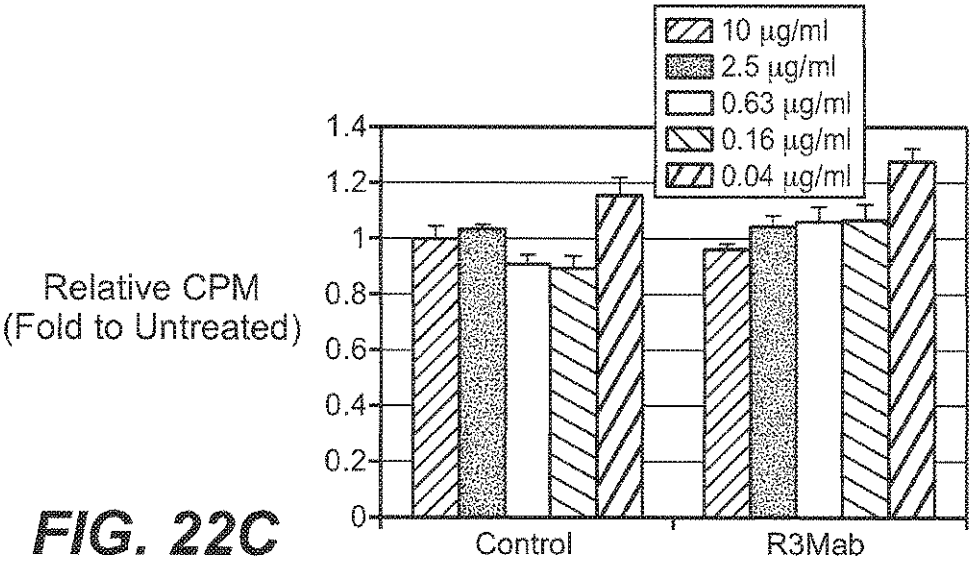


FIG. 22C

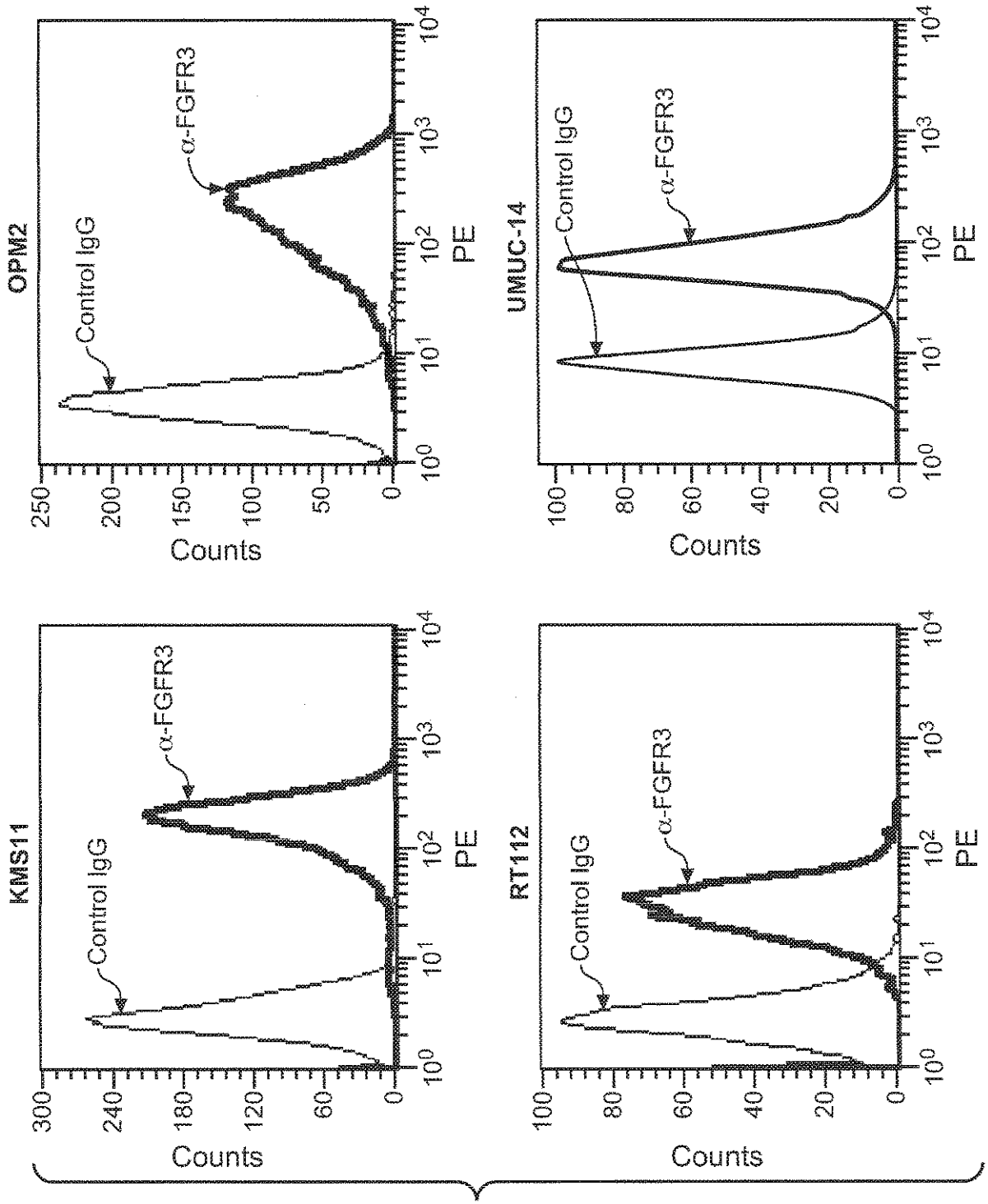


FIG. 23A

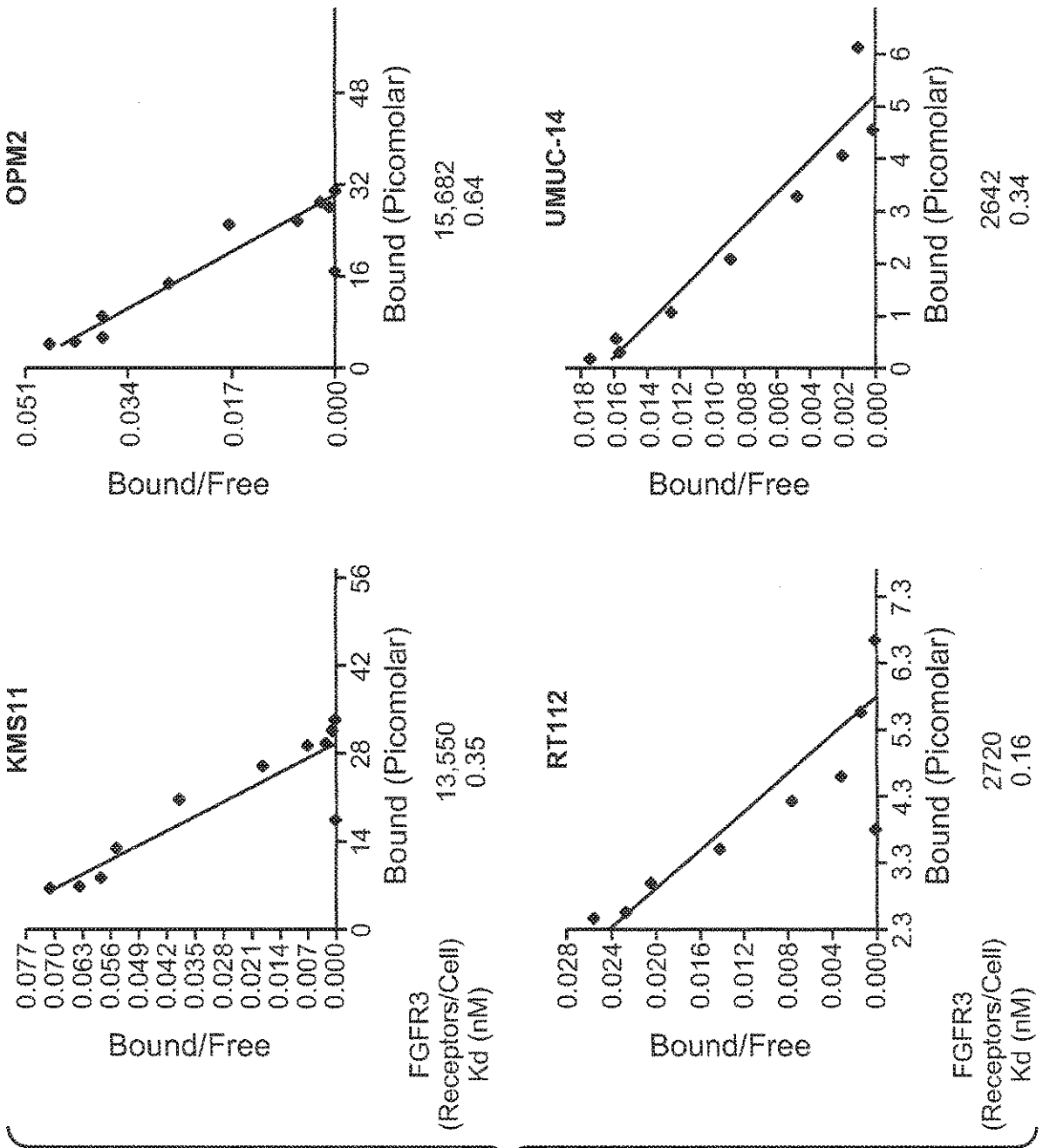

OPM2
Bound/Free
Bound (Picomolar)
0.051
0.034
0.017
0.000
0
16
32
48
15,682
0.64
UMUC-14
Bound/Free
Bound (Picomolar)
0.018
0.016
0.014
0.012
0.010
0.008
0.006
0.004
0.002
0.000
0
1
2
3
4
5
6
2642
0.34
KMS11
Bound/Free
Bound (Picomolar)
0.077
0.070
0.063
0.056
0.049
0.042
0.035
0.028
0.021
0.014
0.007
0.000
0
14
28
42
56
FGFR3
(Receptors/Cell)
13,550
Kd (nM)
0.35
RT112
Bound/Free
Bound (Picomolar)
0.028
0.024
0.020
0.016
0.012
0.008
0.004
0.000
2.3
3.3
4.3
5.3
6.3
7.3
FGFR3
(Receptors/Cell)
2720
Kd (nM)
0.16

FIG. 23B

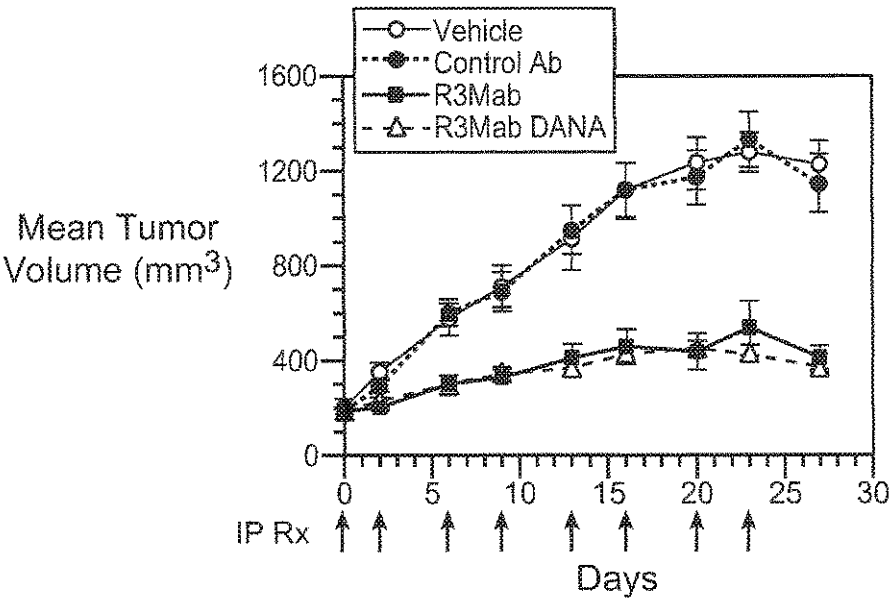


FIG. 24A

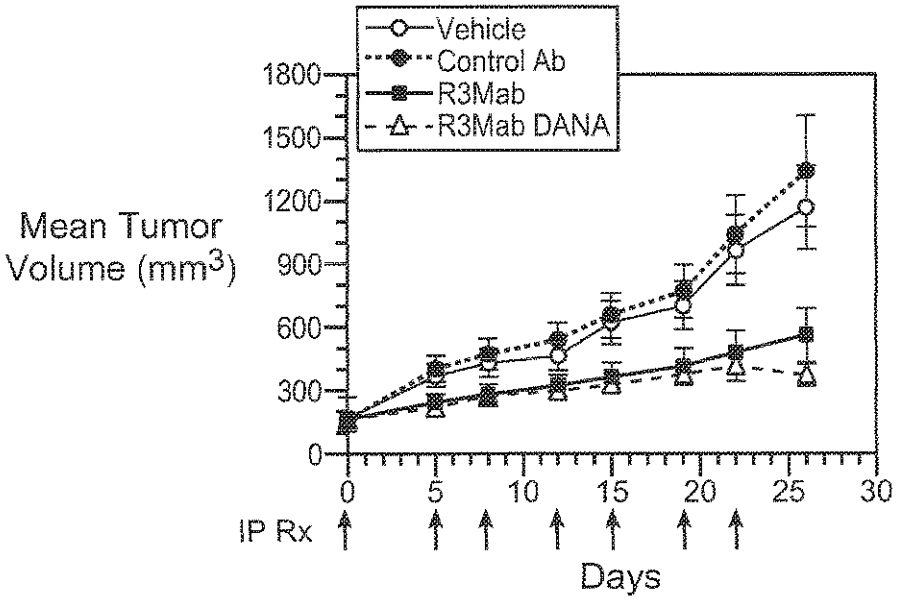


FIG. 24B