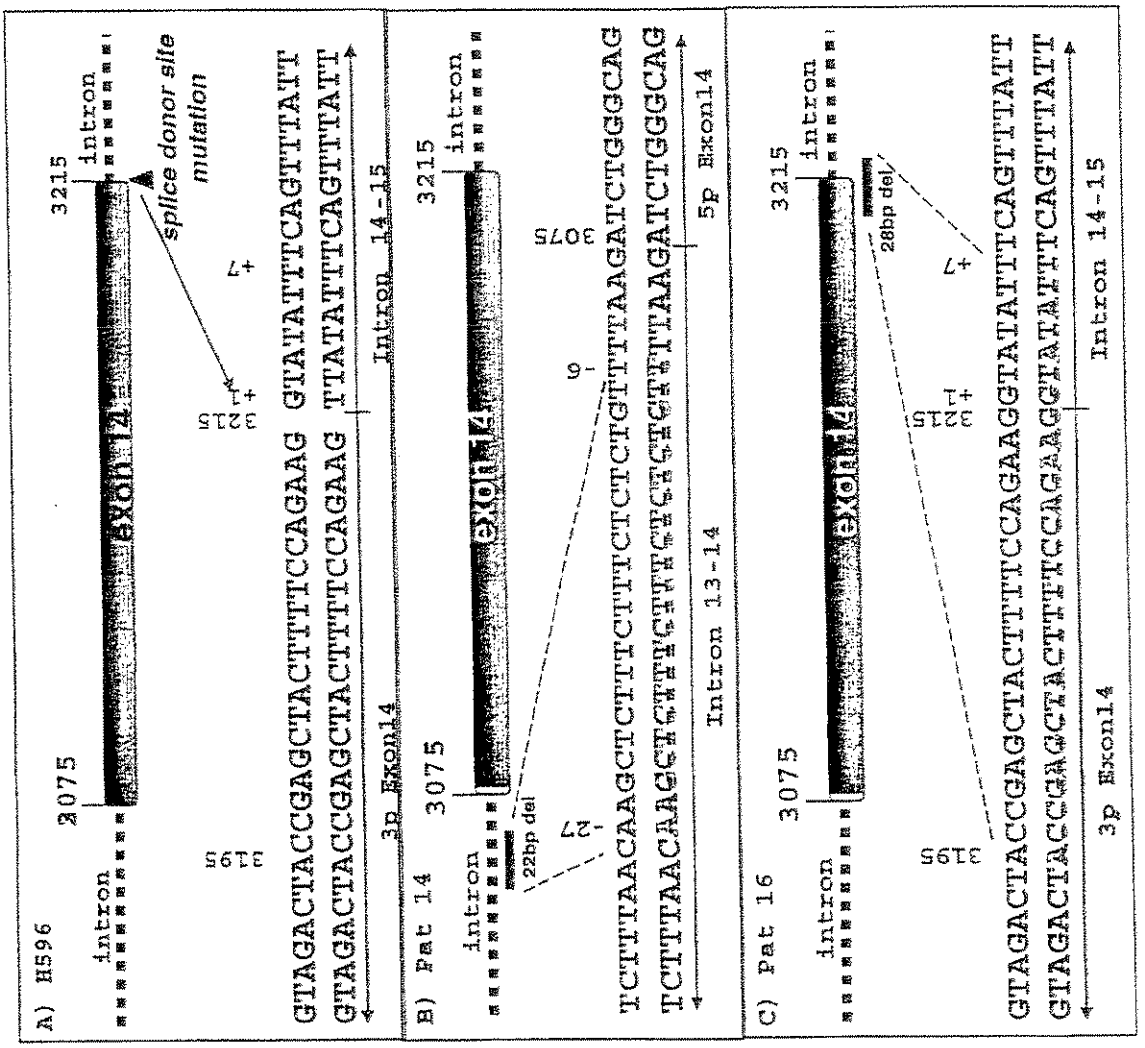

A) H596
2075
3215
Intron
exon 14
splice donor site mutation
3p Exon14
Intron 14-15
B) Pat 14
3075
22bp del
5p Exon14
Intron 13-14
C) Pat 16
28bp del
GTAGACTACCGAGCTACTTTTTCCAGAAG GTATATTTCAGTTTATT
GTAGACTACCGAGCTACTTTTTCCAGAAG TTATATTTCAGTTTATT
TCTTTAACAAGCTCTTTTCTTTTCTCTCTGTTTTTTAAGATCTGGGCAG
TCTTTAACAAGCTCTTTTCTTTTCTCTCTGTTTTTTAAGATCTGGGCAG
GTAGACTACCGAGCTACTTTTTCCAGAAGGTATATTTCAGTTTATT
GTAGACTACCGAGCTACTTTTTCCAGAAGGTATATTTCAGTTTATT

FIG._1

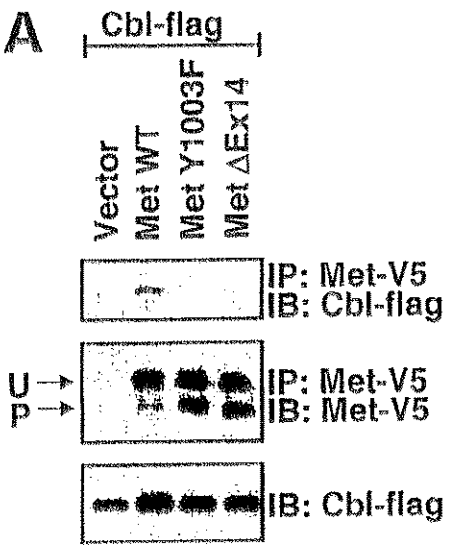
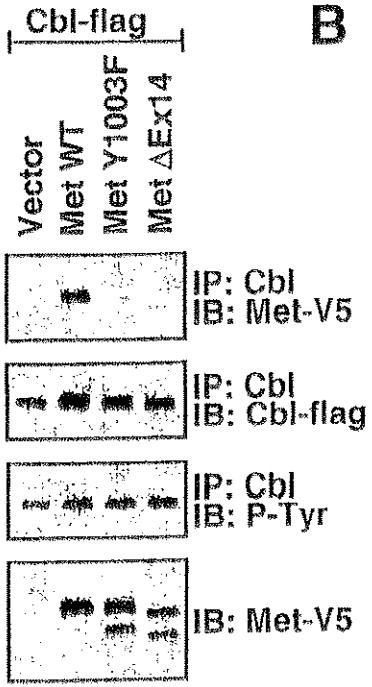

A
Cbl-flag
Vector
Met WT
Met Y1003F
Met ΔEx14
IP: Met-V5
IB: Cbl-flag
U
P
IP: Met-V5
IB: Met-V5
IB: Cbl-flag

FIG._2A


Cbl-flag
Vector
Met WT
Met Y1003F
Met ΔEx14
IP: Cbl
IB: Met-V5
IP: Cbl
IB: Cbl-flag
IP: Cbl
IB: P-Tyr
IB: Met-V5

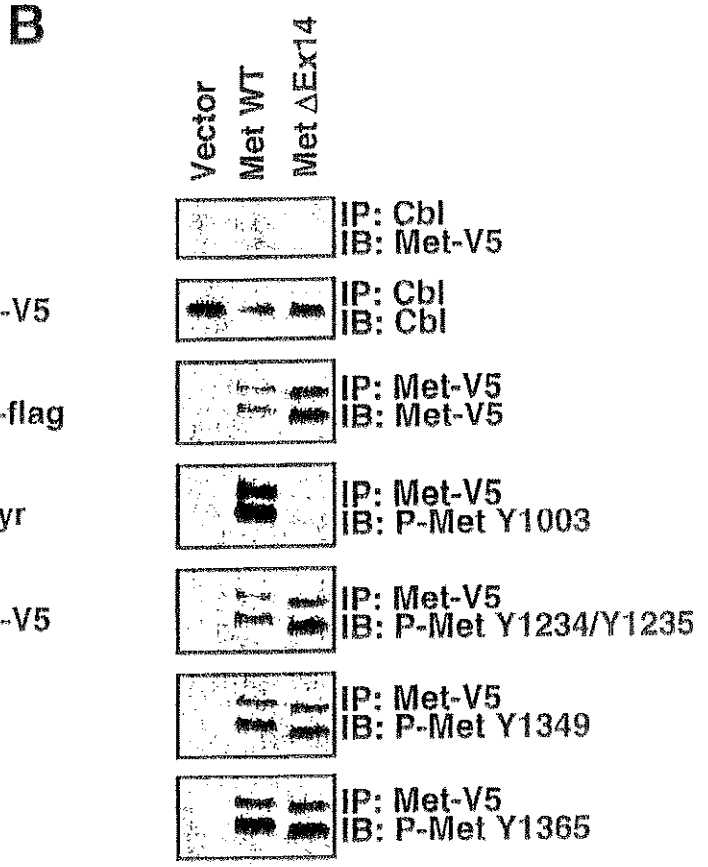

B
Vector
Met WT
Met ΔEx14
IP: Cbl
IB: Met-V5
IP: Cbl
IB: Cbl
IP: Met-V5
IB: Met-V5
IP: Met-V5
IB: P-Met Y1003
IP: Met-V5
IB: P-Met Y1234/Y1235
IP: Met-V5
IB: P-Met Y1349
IP: Met-V5
IB: P-Met Y1365

FIG._2B

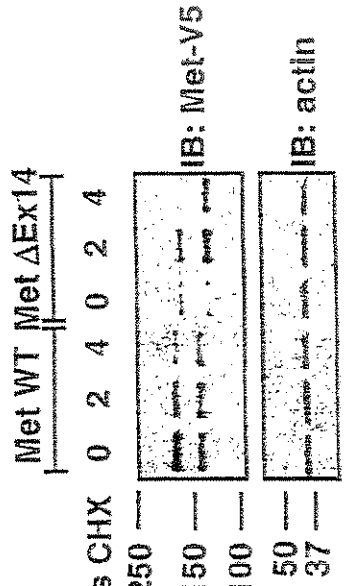

D
Met WT Met ΔEx14
Hrs CHX 0 2 4 0 2 4
250
150
100
50
37
IB: Met-V5
IB: actin

FIG._2D

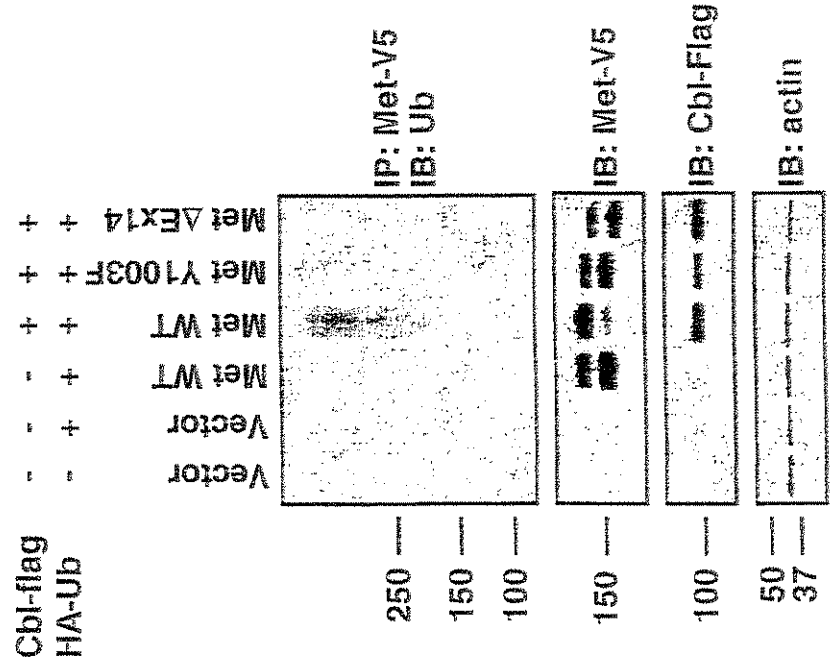

C
Cbl-flag
HA-Ub
- - + + + +
- - + - + +
Vector
Vector
Met WT
Met WT
Met Y1003F
Met ΔEx14
250
150
100
150
100
50
37
IP: Met-V5
IB: Ub
IB: Met-V5
IB: Cbl-Flag
IB: actin

FIG._2C

E

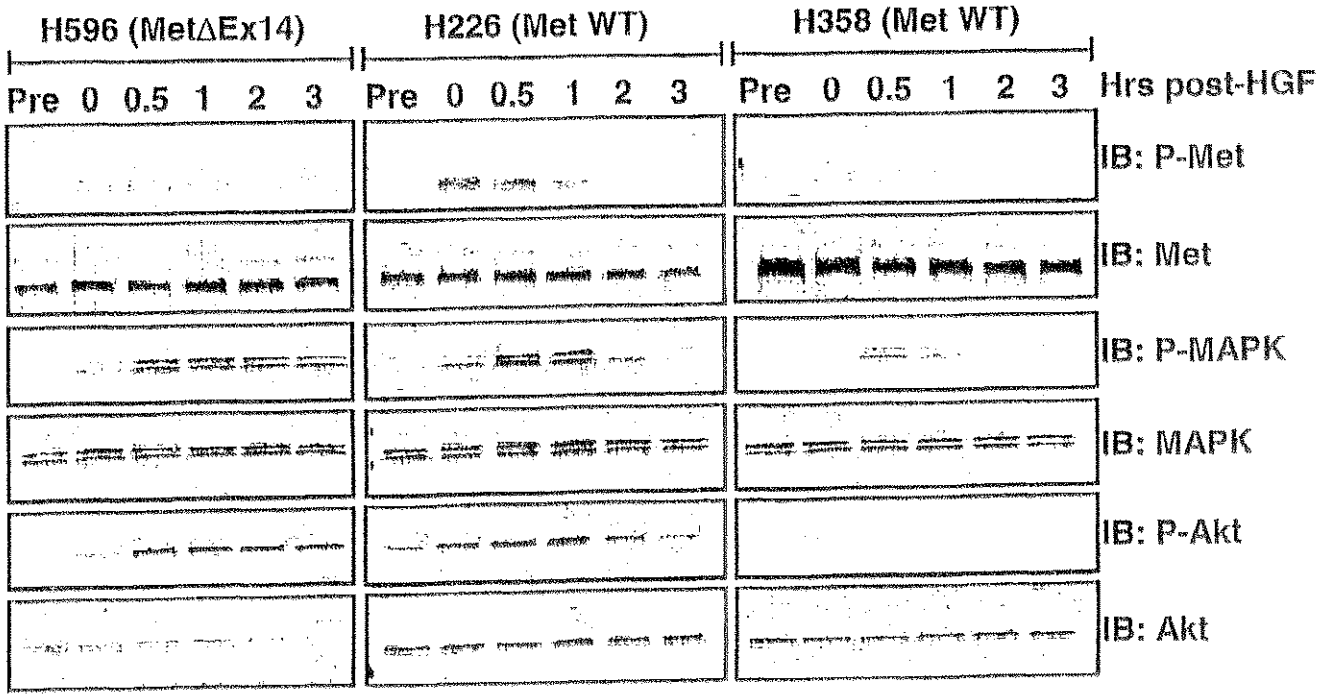


FIG. 2E

F

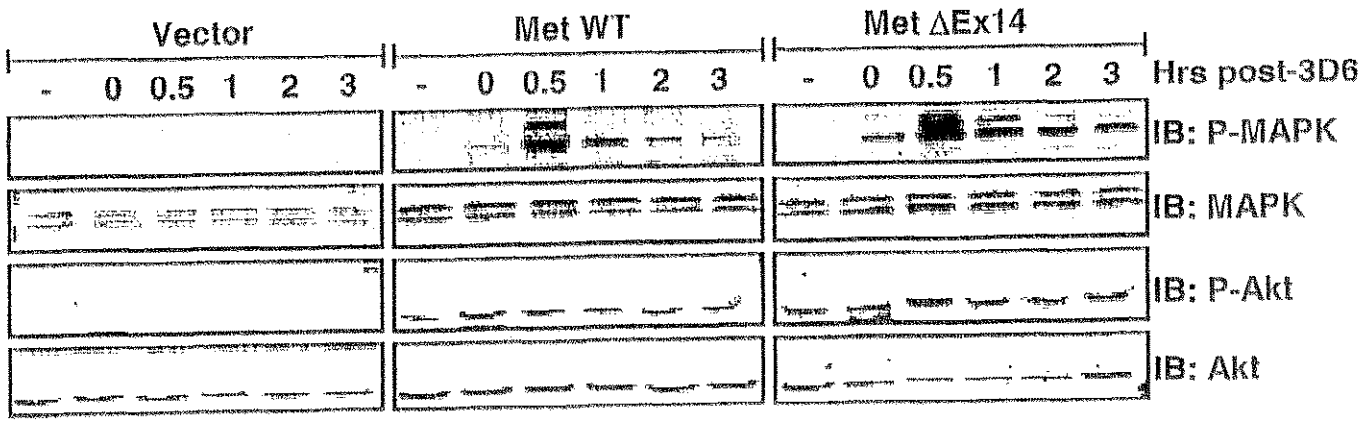
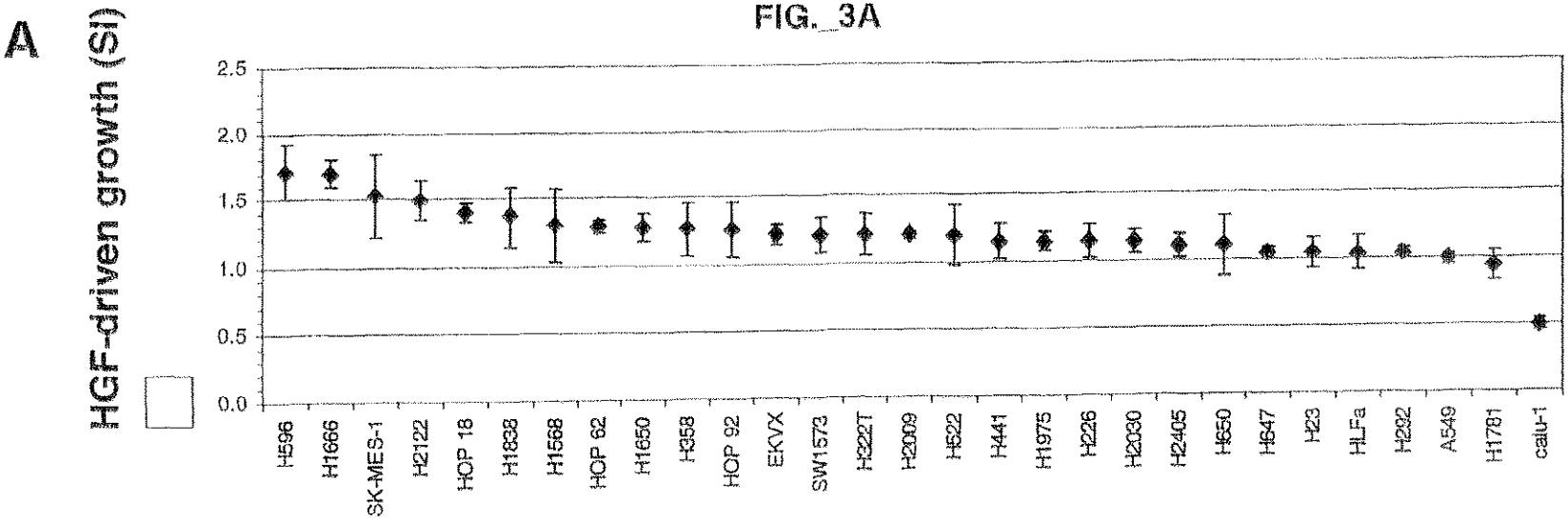


FIG. 2F

FIG. 3A


A
HGF-driven growth (SI)
2.5
2.0
1.5
1.0
0.5
0.0
H596
H1666
SK-MES-1
H2122
HOP 18
H1838
H1568
HOP 62
H1650
H358
HOP 92
EKVX
SW1573
H322T
H2009
H522
H441
H1975
H226
H2030
H2405
H650
H647
H23
HLFa
H292
A549
H1781
calu-1

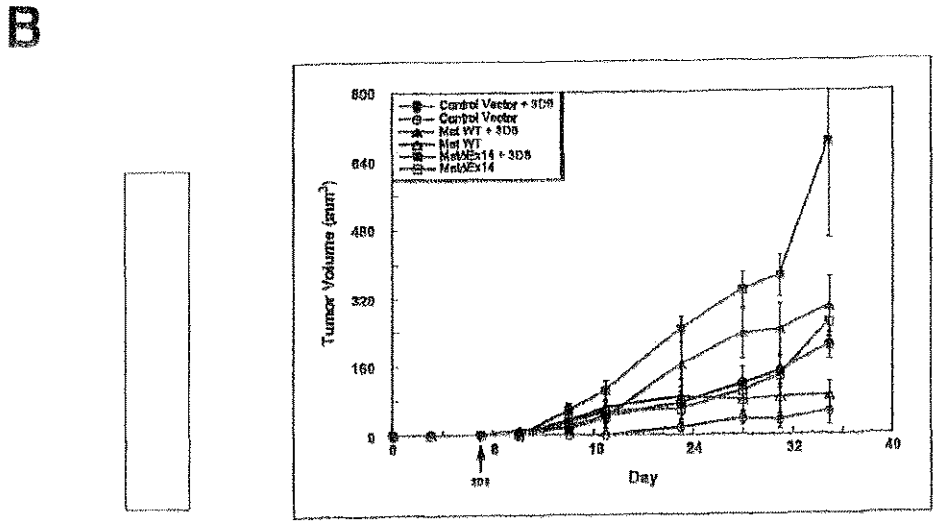

B
Control Vector + 3D8
Control Vector
Met WT + 3D8
Met WT
MetΔEx14 + 3D8
MetΔEx14
Tumor Volume (mm³)
800
640
480
320
160
0
0
8
16
24
32
40
3D8
Day

FIG. 3B

FIG._4

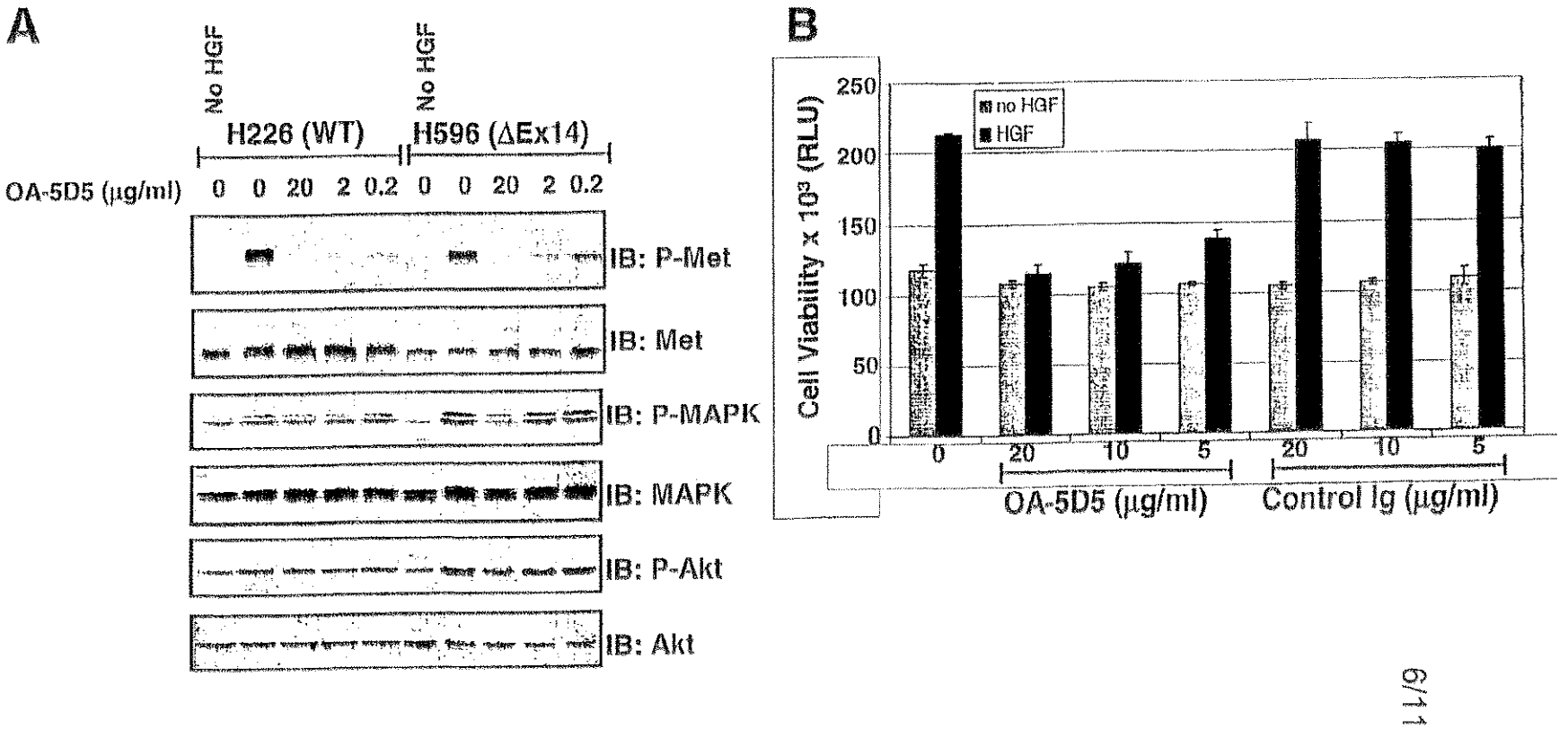

A
No HGF
No HGF
H226 (WT)
H596 (ΔEx14)
OA-5D5 (μg/ml) 0 0 20 2 0.2 0 0 20 2 0.2
IB: P-Met
IB: Met
IB: P-MAPK
IB: MAPK
IB: P-Akt
IB: Akt
B
Cell Viability x 10³ (RLU)
250
200
150
100
50
0
no HGF
HGF
0
20
10
5
20
10
5
OA-5D5 (μg/ml)
Control Ig (μg/ml)

FIG._5

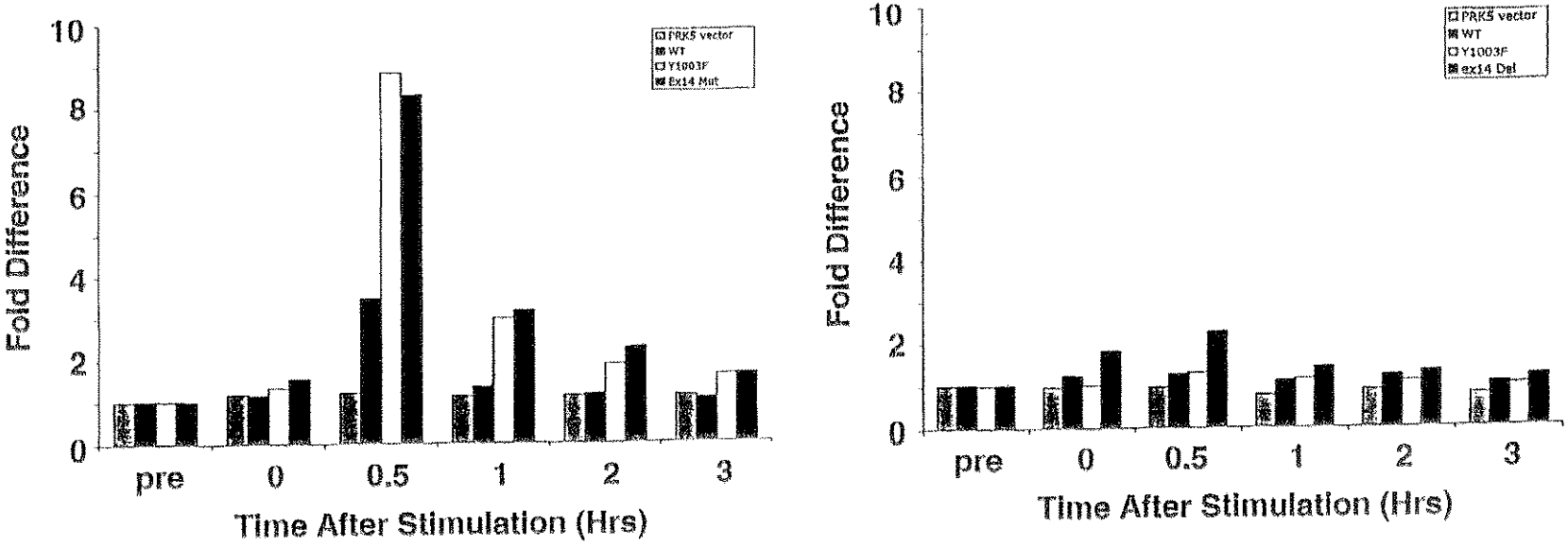

Fold Difference
10
8
6
4
2
0
pre
0
0.5
1
2
3
Time After Stimulation (Hrs)
PRK5 vector
WT
Y1003F
Ex14 Mut
Fold Difference
10
8
6
4
2
0
pre
0
0.5
1
2
3
Time After Stimulation (Hrs)
PRK5 vector
WT
Y1003F
ex14 Del

FIG_6

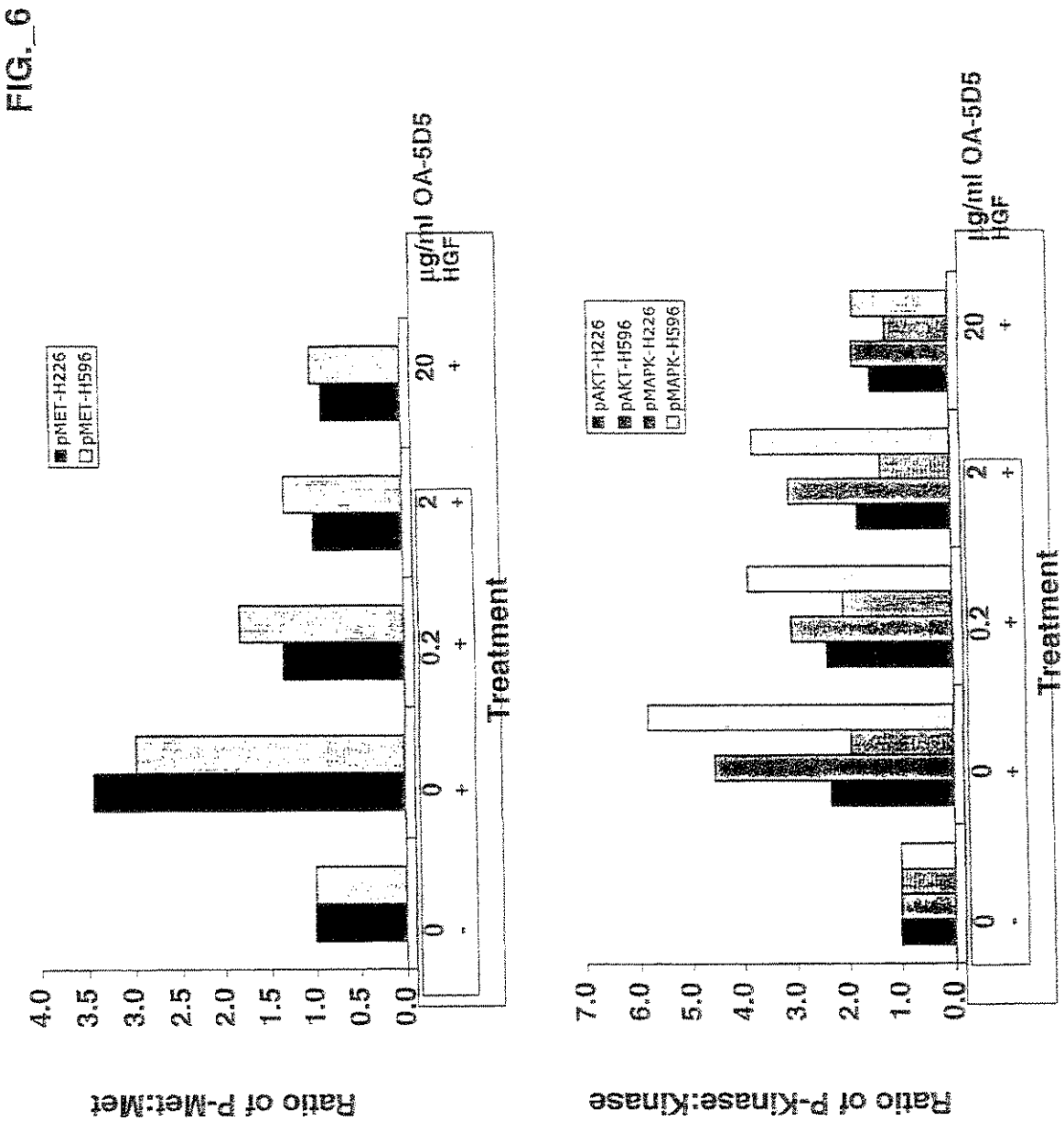

Ratio of P-Met:Met
pMET-H226
pMET-H596
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
0
0.2
2
20
-
+
+
+
µg/ml OA-5D5
HGF
Treatment
Ratio of P-Kinase:Kinase
pAKT-H226
pAKT-H596
pMAPK-H226
pMAPK-H596
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
0
0
0.2
2
20
-
+
+
+
µg/ml OA-5D5
HGF
Treatment

FIG._7

Illustrative splicing structures encompassing the intron/exon boundaries of human c-met exon 14

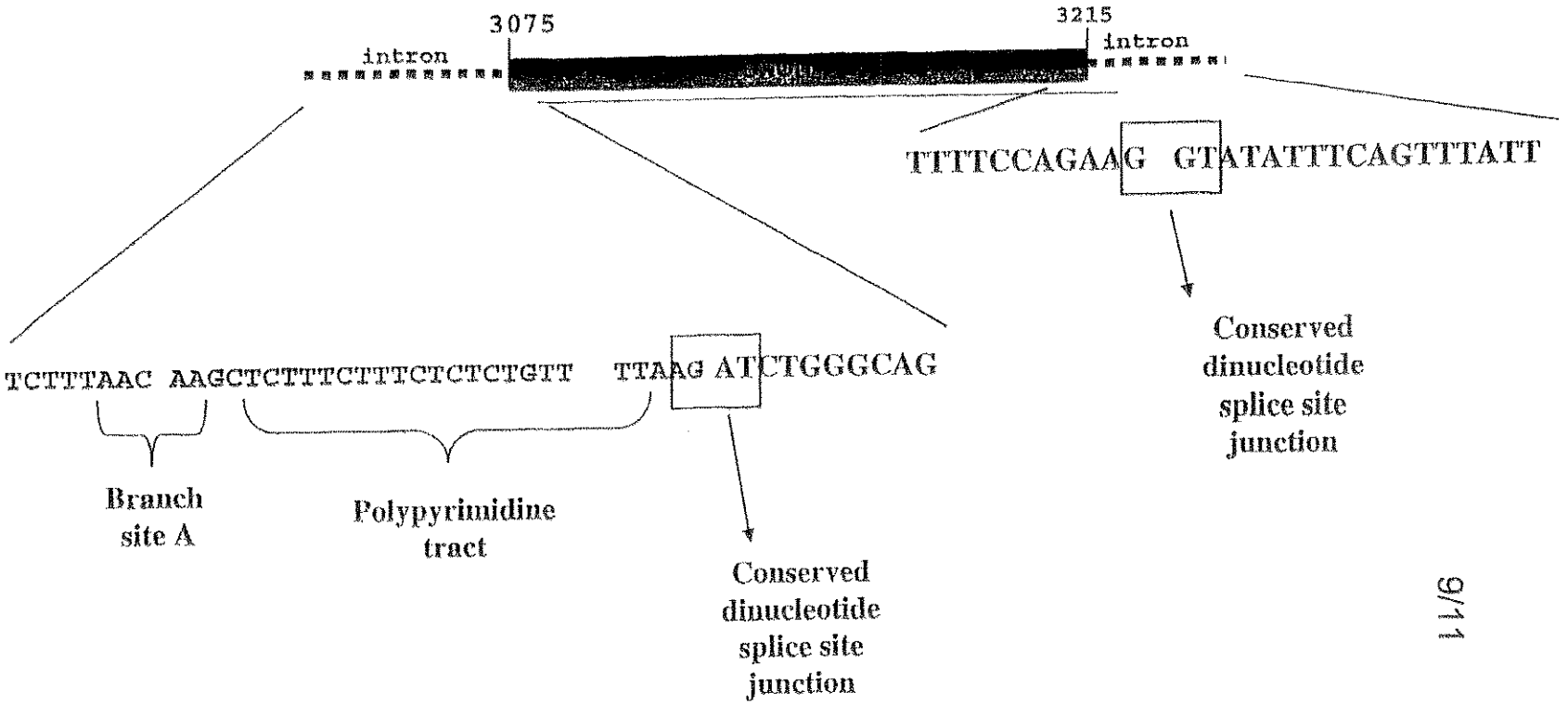


FIG._8

```
1     MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAET
51    PIQNVILHEHHIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFPCQD
101   CSSKANLSGGVWKDNINMALVVDTYYDDQLISCGSVNRGTCQRHVFPHNH
151   TADIQSEVHCIFSPQIEEPSQCPDCVVSALGAKVLSSVKDRFINFFVGNT
201   INSSYFPDHPLHSISVRRLKETKDGFMFLTDQSYIDVLPEFRDSYPIKYV
251   HAFESNNFIYFLTVQRETLDAQTFHTRIIRFCSINSGLHSYMEMPLECIL
301   TEKRKKRSTKKEVFNILQAAYVSKPGAQLARQIGASLNDDILFGVFAQSK
351   PDSAEPMDRSAMCAFPIKYVNDFFNKIVNKNNVRCLQHFYGPNHEHCFNR
401   TLLRNSSGCEARRDEYRTEFTTALQRVDLFMGQFSEVLLTSISTFIKGDL
451   TIANLGTSEGRFMQVVVSRSGPSTPHVNFLLDSHPVSPEVIVEHTLNQNG
501   YTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCGWCHDKCVRSEE
551   CLSGTWTQQICLPAIYKVFPNSAPLEGGTRLTICGWDFGFRRNNKFDLKK
601   TRVLLGNESCTLTLSESTMNTLKCTVGPAMNKHFNMSIIISNGHGTTQYS
651   TFSYVDPVITSISPKYGPMAGGTLLTLTGNYLNSGNSRHISIGGKTCTLK
701   SVSNSILECYTPAQTISTEFAVKLKIDLANRETSIFSYREDPIVYEIHPT
751   KSFISGGSTITGVGKNLNSVSVPRMVINVHEAGRNFTVACQHRSNSEIIC
801   CTTPSLQQLNLQLPLKTKAFFMLDGILSKYFDLIYVHNPVFKPFEKPVMI
851   SMGNENVLEIKGNDIDPEAVKGEVLKVGNKSCENIHLHSEAVLCTVPNDL
901   LKLNSELNIEWKQAISSTVLGKVIVQPDQNFTGLIAGVVSISTALLLLLG
951   FFLWLKKRKQIKDLGSELVRYDARVHTPHLDRLVSARSVSPTTEMVSNES
1001  VDYRATFPEDQFPNSSQNGSCRQVQYPLTDMSPILTSGDSDISSPLLQNT
1051  VHIDLSALNPELVQAVQHVVIGPSSLIVHFNEVIGRGHFGCVYHGTLLDN
1101  DGKKIHCAVKSLNRITDIGEVSQFLTEGIIMKDFSHPNVLSLLGICLRSE
1151  GSPLVVLPYMKHGDLRNFIRNETHNPTVKDLIGFGLQVAKAMKYLASKKF
1201  VHRDLAARNCMLDEKFTVKVADFGLARDMYDKEYYSVHNKTGAKLPVKWM
1251  ALESLQTQKFTTKSDVWSFGVVLWELMTRGAPPYPDVNTFDITVYLLQGR
1301  RLLQPEYCPDPLYEVMLKCWHPKAEMRPSFSELVSRISAIFSTFIGEHYV
1351  HVNATYVNVKCVAPYPSLLSSEDNADDEVDTRPASFWETS
```

(SEQ ID NO: ____)

FIG. 9

Light chain variable domain sequence of anti-c-met OA-5D5

DIQMTQSPSSLSASVGDRVTITCKSSQSLLYTSSQKNYLAWYQQKPGKAPKLLIYWASTRESGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQYYAYPWTFGQGTKVEIK

Heavy chain variable domain sequence of anti-c-met OA-5D5

EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWLHWVRQAPGKGLEWVGMIDPSNSDTRFNPNFKDRF
TISADTSKNTAYLQMNSLRAEDTAVYYCATYRSYVTPLDYWGQGTLVTVSS