

# **Detección de aberraciones cromosómicas que afectan a genes codificantes de proteínas con actividad tirosina-quinasa en tumores sólidos**

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Comunicación Oral (O10)

XXV Congreso Nacional de Genética Humana. 17-19 de junio de 2009, Santiago de Compostela



## **Aberraciones cromosómicas en cáncer (translocaciones y fusiones)**

### **Hematológicos vs. sólidos (mesenquimales/epiteliales)**

- próstata (ETS)
- pulmón (EML-ALK)

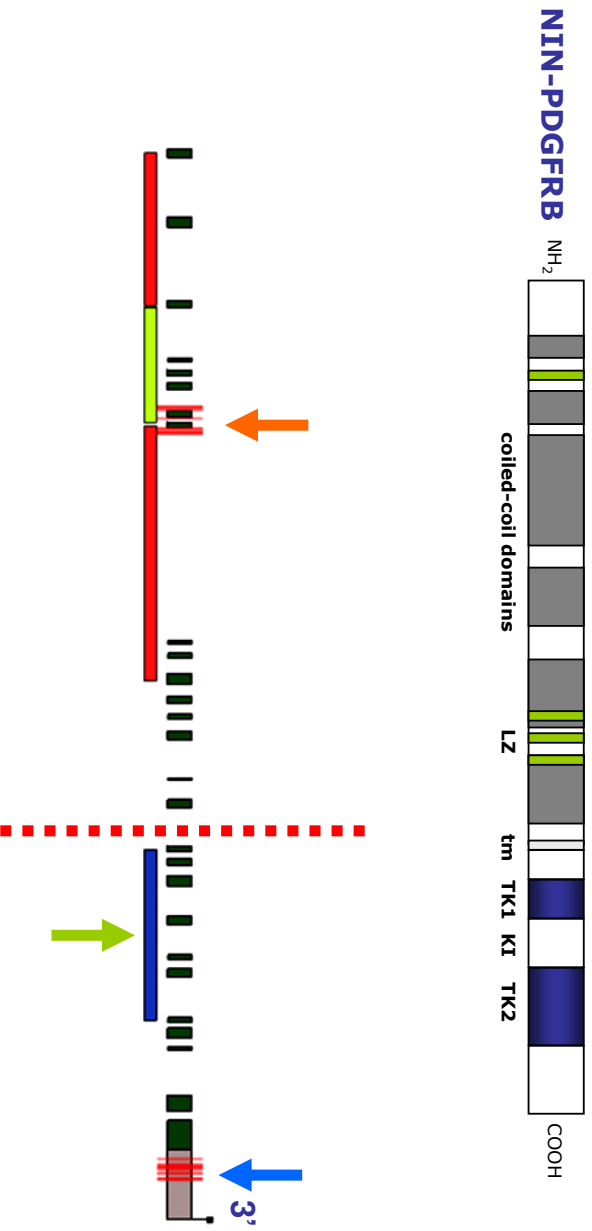
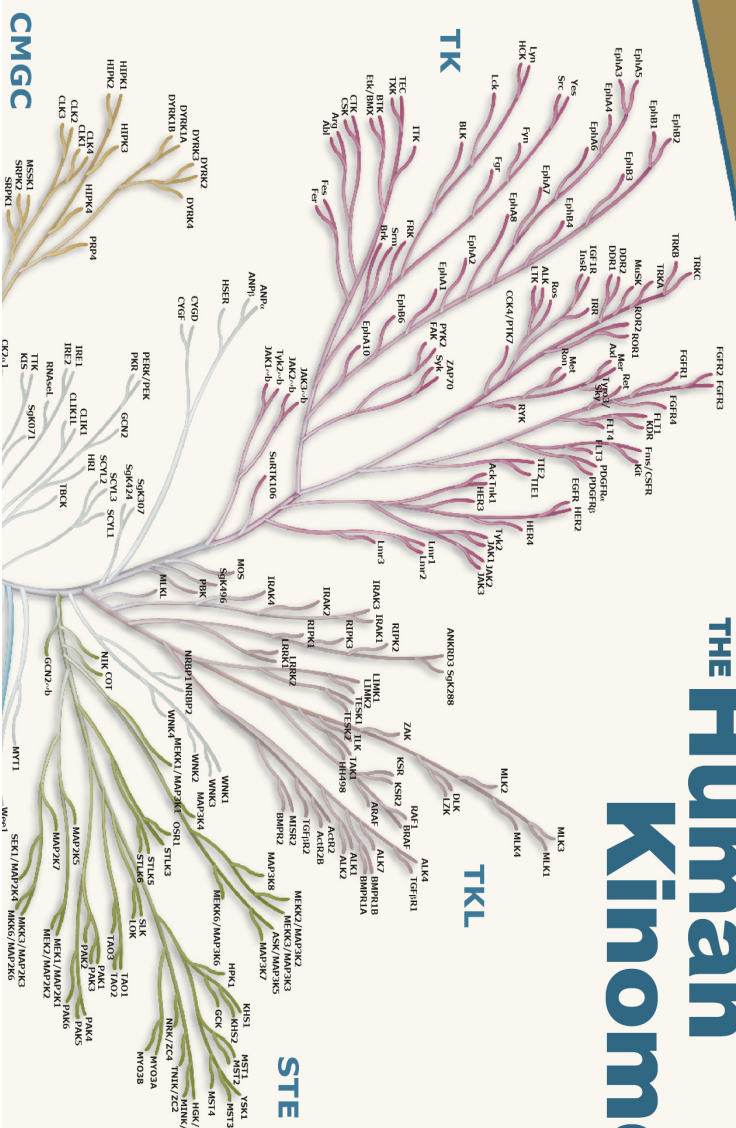
This phylogenetic tree depicts the relationships between members of the complete human protein kinase families and are key regulators of cell function. The 518 human protein kinases control protein activity by catalyzing the addition of a negatively charged phosphate group to other proteins. Protein kinases modulate a wide variety of biological processes, from cell division to cell movement to intracellular targets and coordinate complex biological functions.

Most protein kinases belong to a single superfamily of enzymes whose catalytic domains are related in sequence and structure. The main diagram illustrates the similarity between the protein kinase families and their relationships to other kinases. The similarity between various kinases is inversely related to the distance between their positions on the tree diagram. Most kinases fall into small families of highly related sequences, and most

families are part of larger groups. The seven major groups are labeled and colored distinctly. The tree can be used to predict protein substrates and biological function for many of the over 100 uncharacterized kinases presented here.

The inset diagram shows trees for seven atypical protein kinase families. These proteins have unique catalytic domains and are not related to the other protein kinase families. The members of the protein kinase superfamily. A further eight atypical protein kinases in small families of one or two genes are not shown.

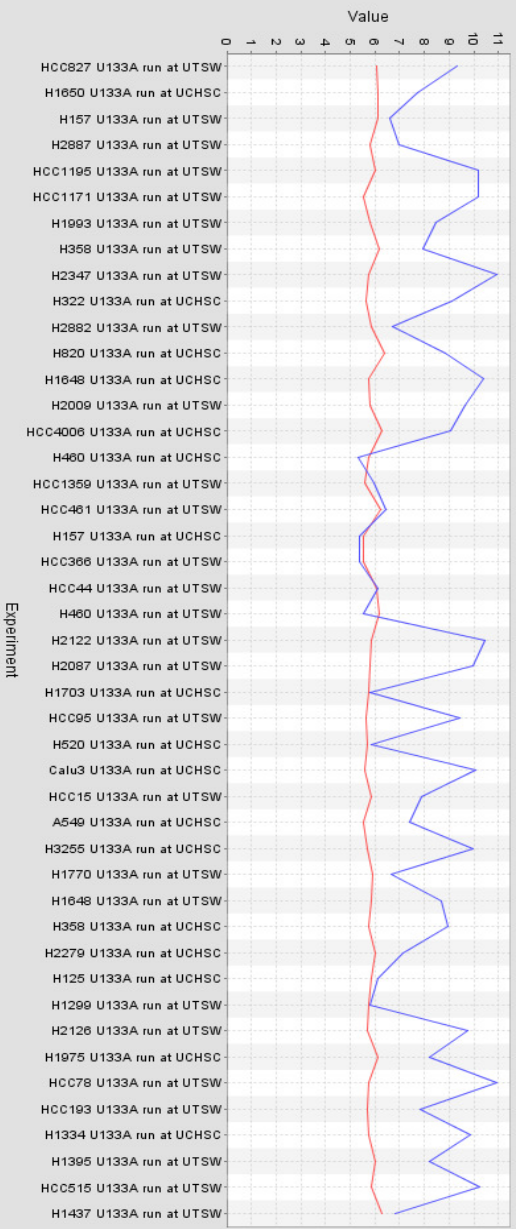
# THE Human Kinome



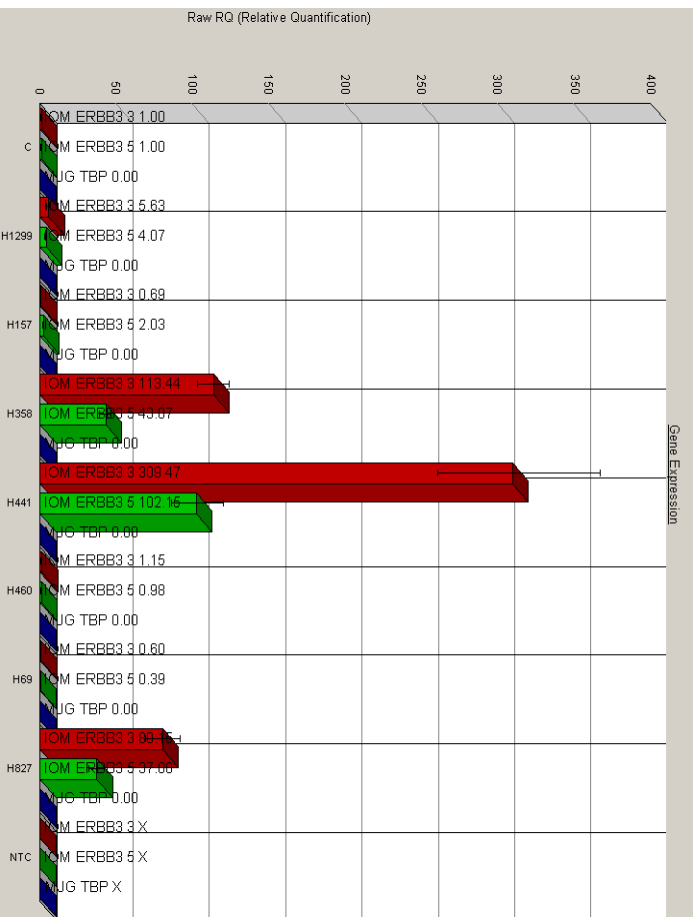
# U133A

- E-GEOD-7670 Transcription profiling of human lung cancer samples
- E-GEOD-4824 Transcription profiling of human lung cancer cell lines
- E-GEOD-4127 Transcription profiling of human lung cancer cell lines
- E-GEOD-4342 Transcription profiling of non squamous cell lung cancer cell lines to investigate sensitivity to gefitinib and predict this in previously untested cell lines

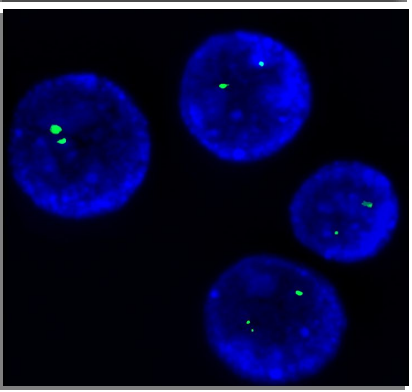
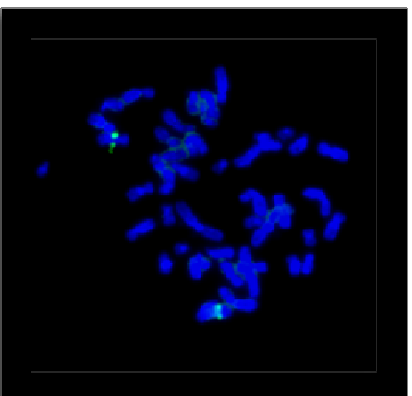
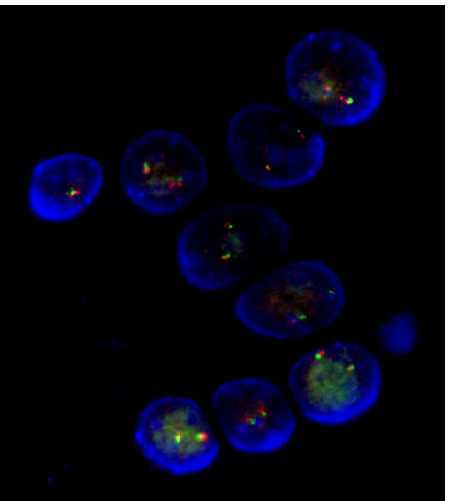
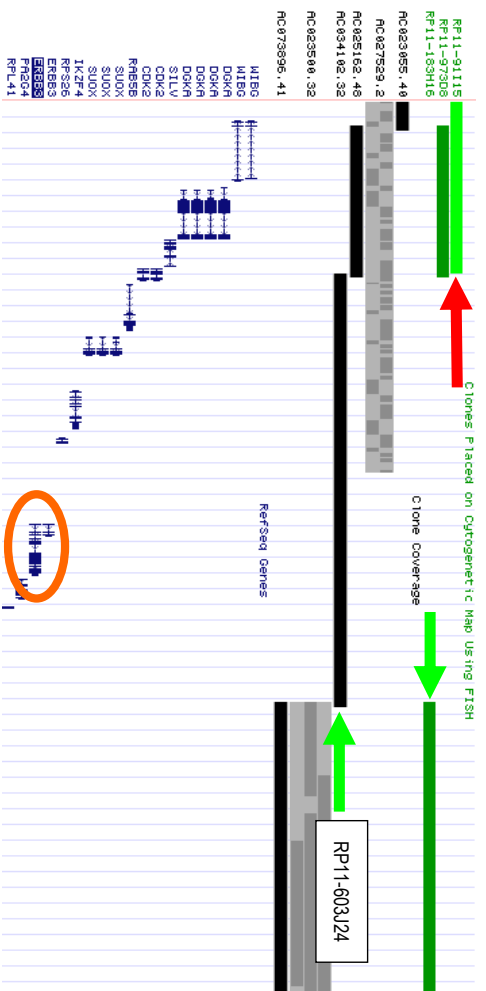
## GEOD-4342 ERBB3



ENST00000267101



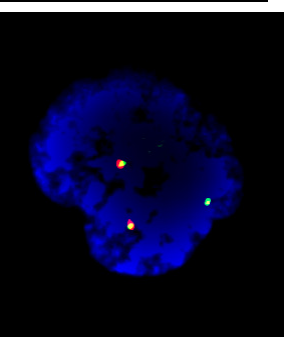
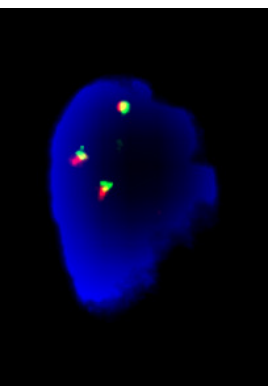
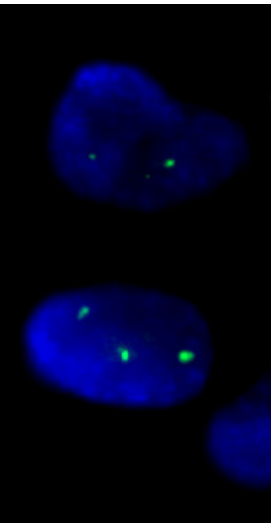
Linea celular	NCI-H1299	NCI-H157	NCI-H460	NCI-H69	NCI-H358	NCI-H441	NCI-H827
Cociente 3' 5'	1,38	0,35	1,17	1,50	2,63	3,02	2,38



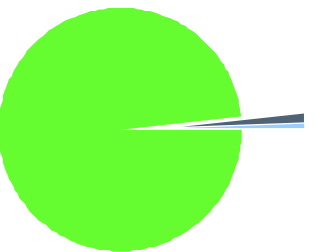
**RP11-603J24**  
(internal)

**NCI-H441**

**RP11-91115**  
**RP11-973D8**

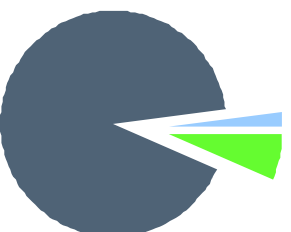


**H441**



RV RV RV 97,6%  
RV RV RV RV 1,2%  
Otros 0,6%

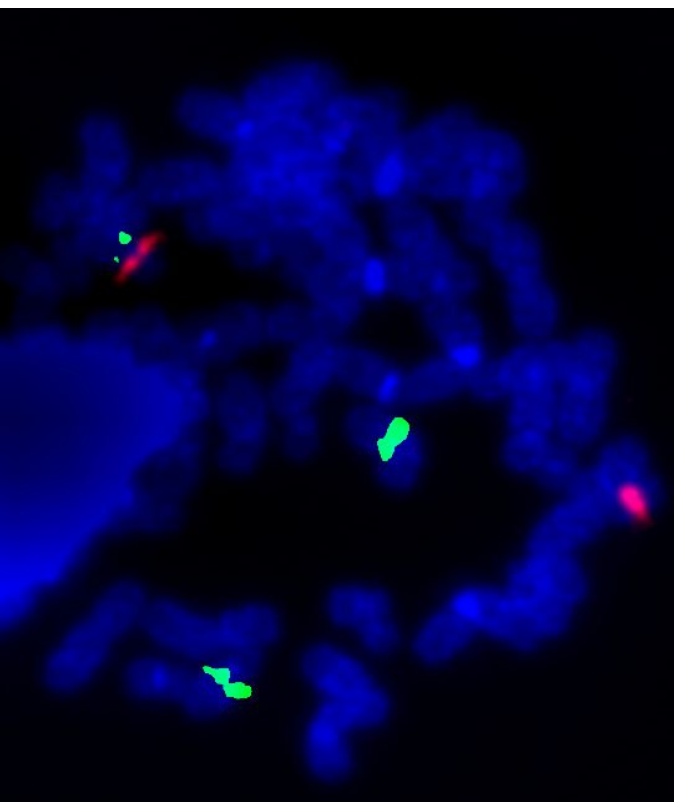
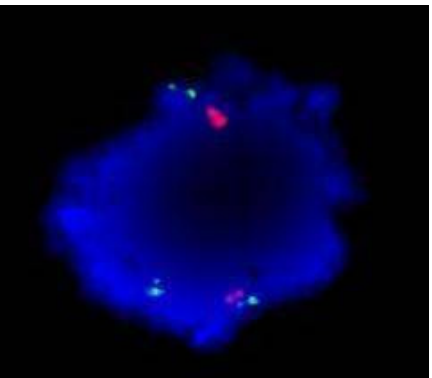
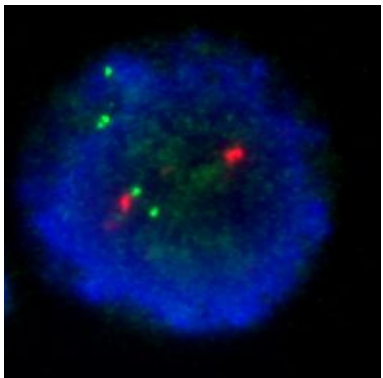
**H441**



V V 6,8%  
V V V 92,3%  
V V V V 2,1%

NCI-H441

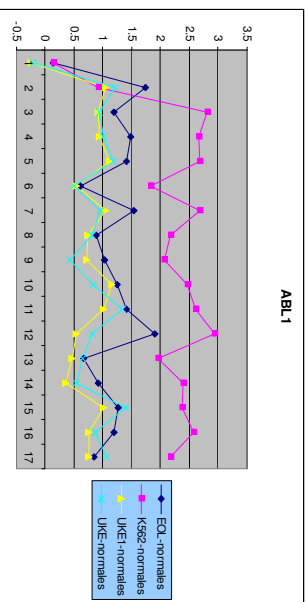
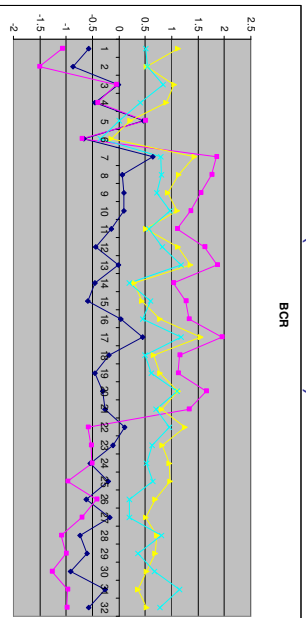
**CEP 12**  
**RP11-973D8**



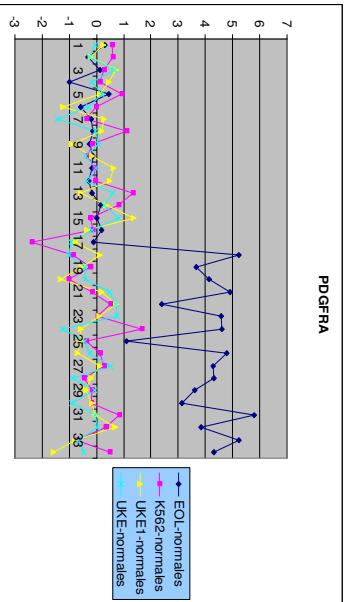
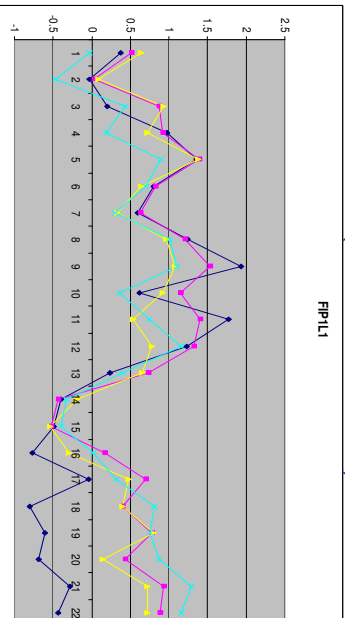
## Human Exon Array 1.0



### Validación K562 (BCR-ABL1)

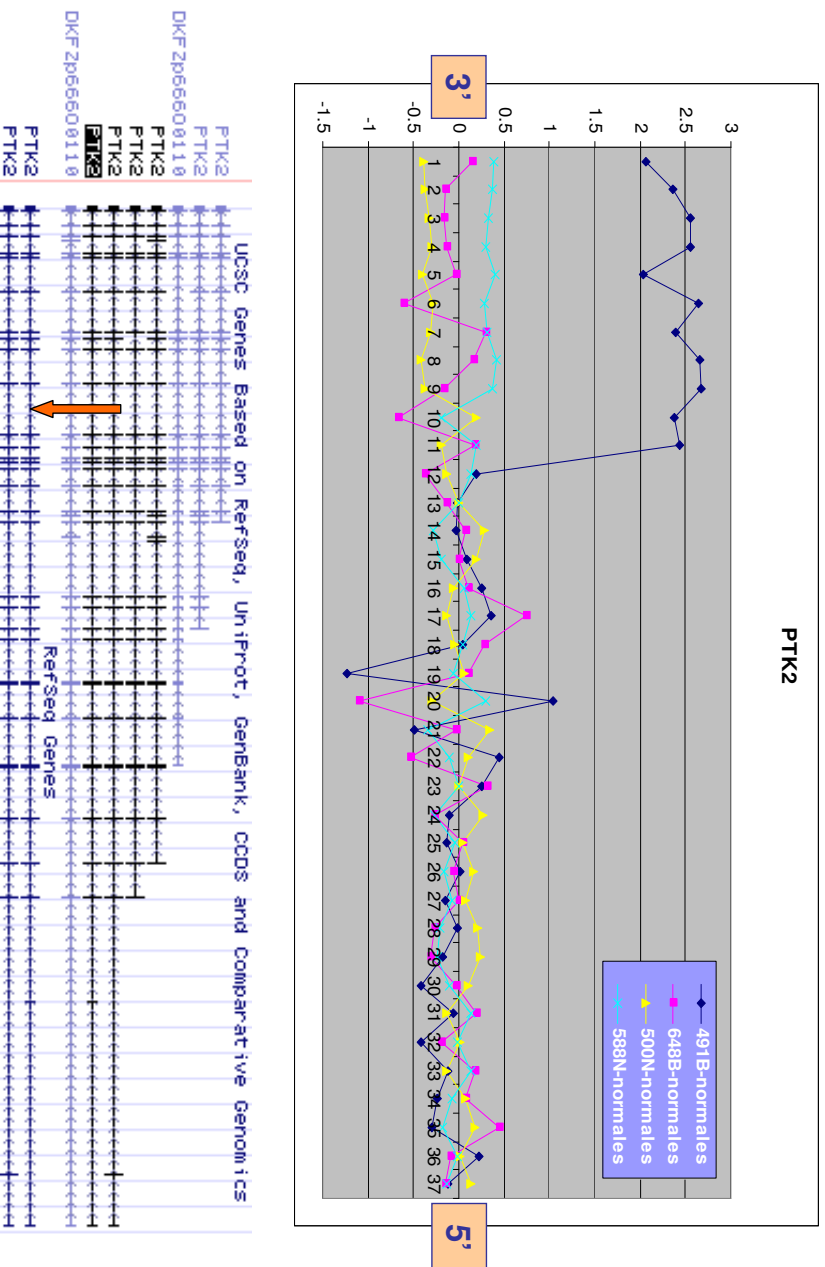
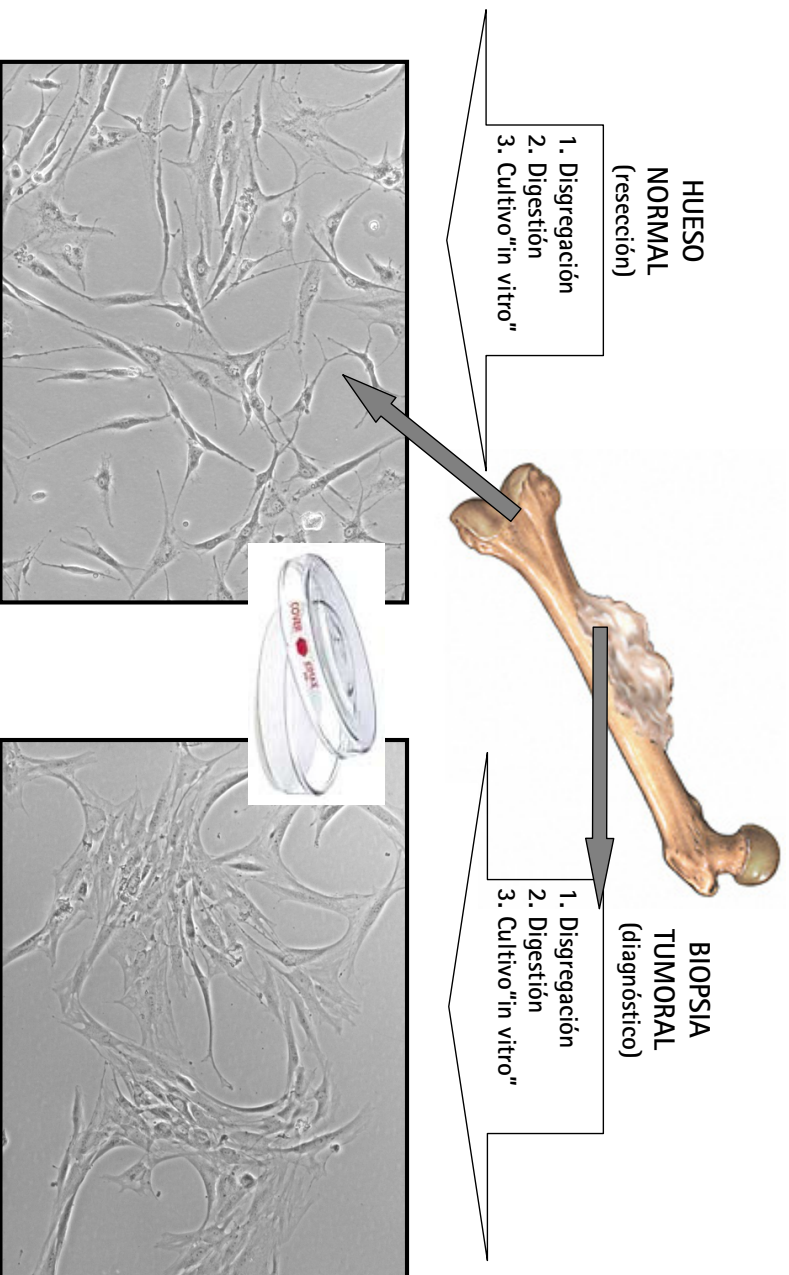


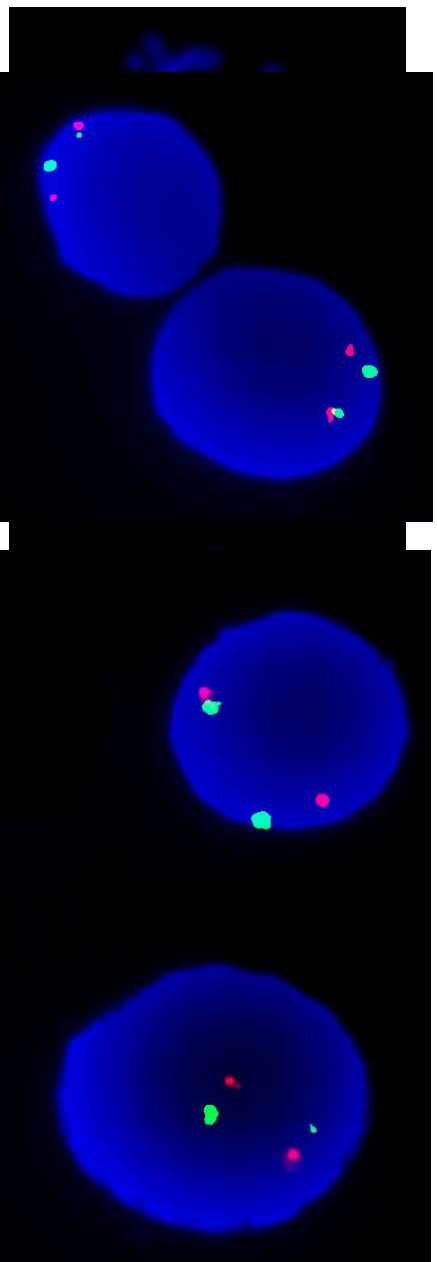
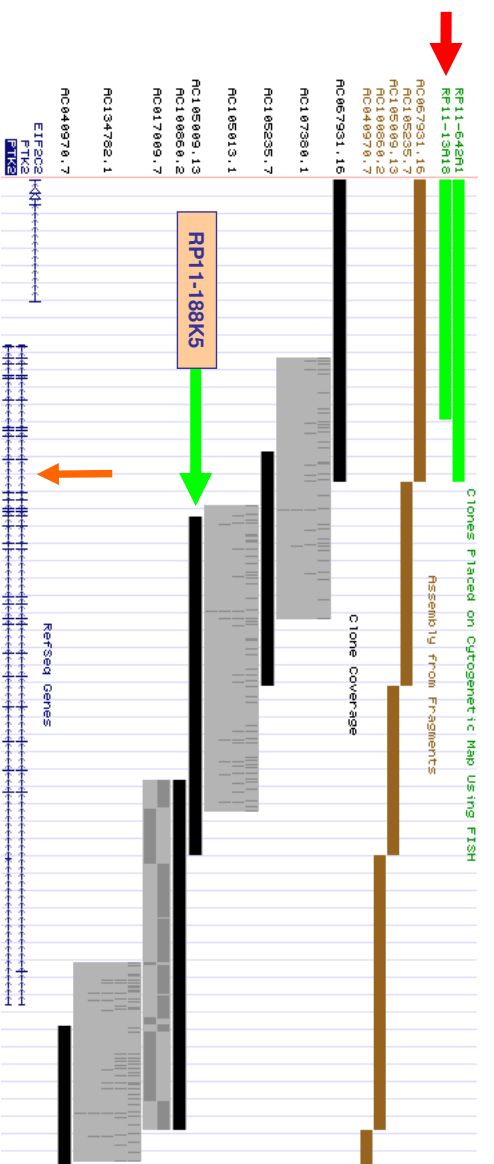
### Validación EOL1 (FIP1L1-PDGFRFA)



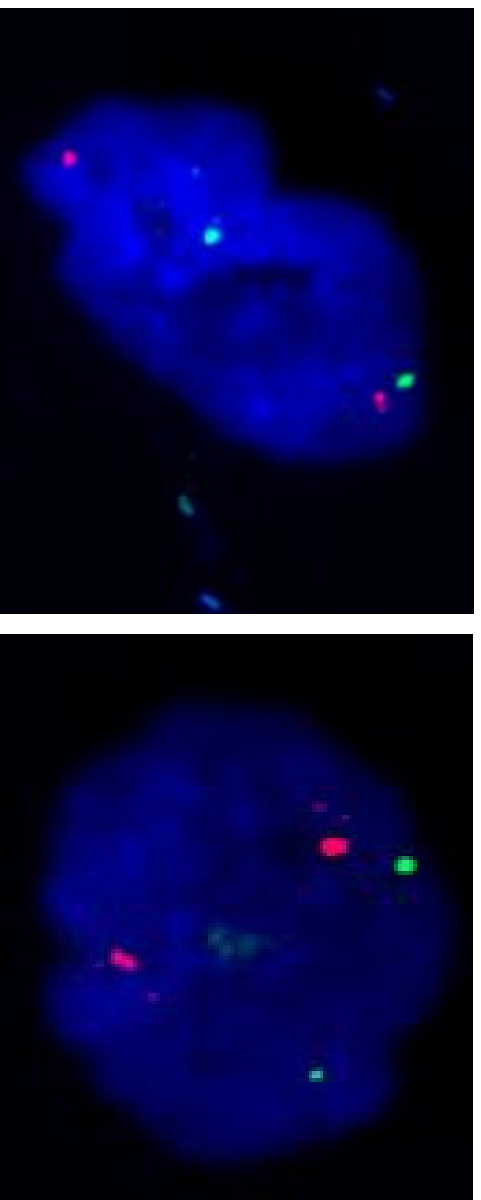
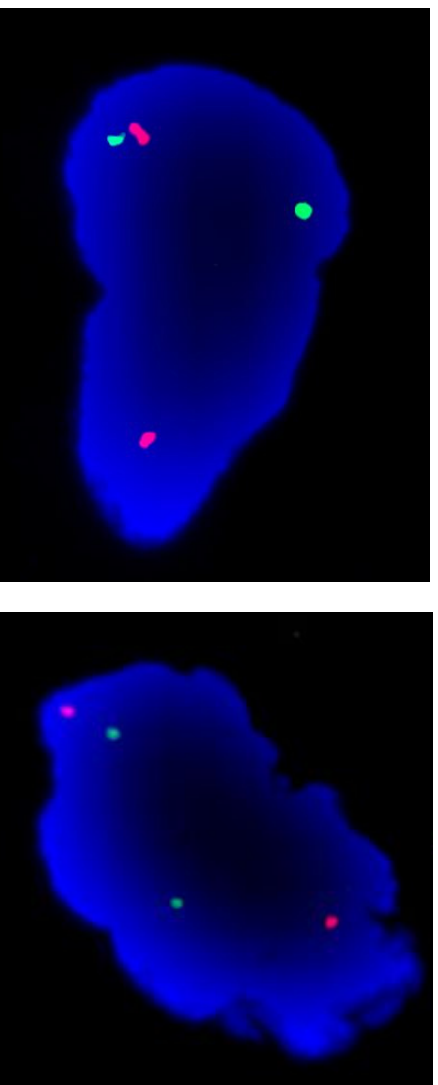


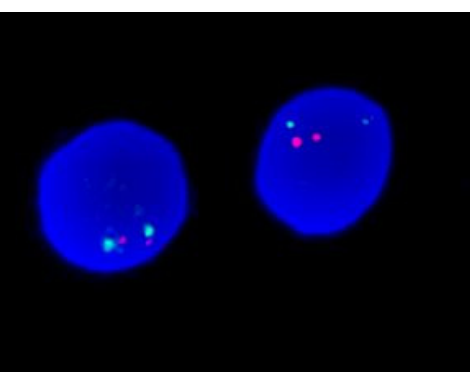
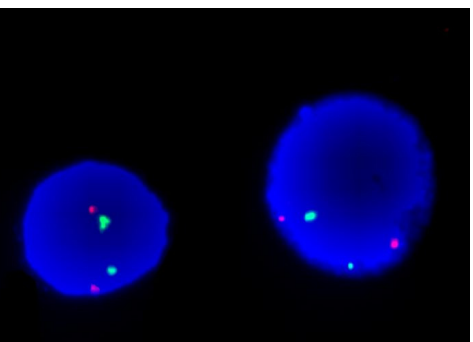
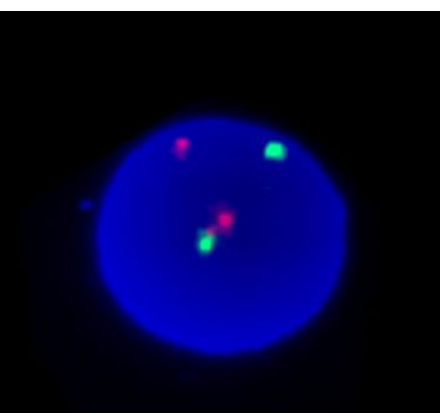
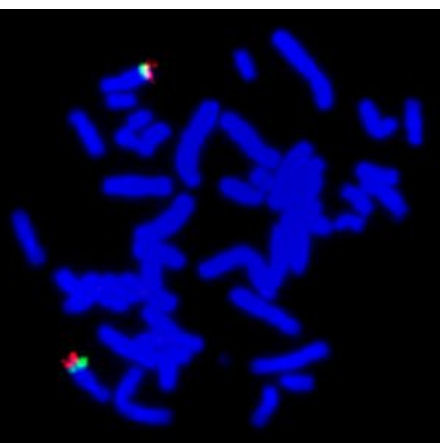
# Líneas primarias de pacientes con osteosarcoma





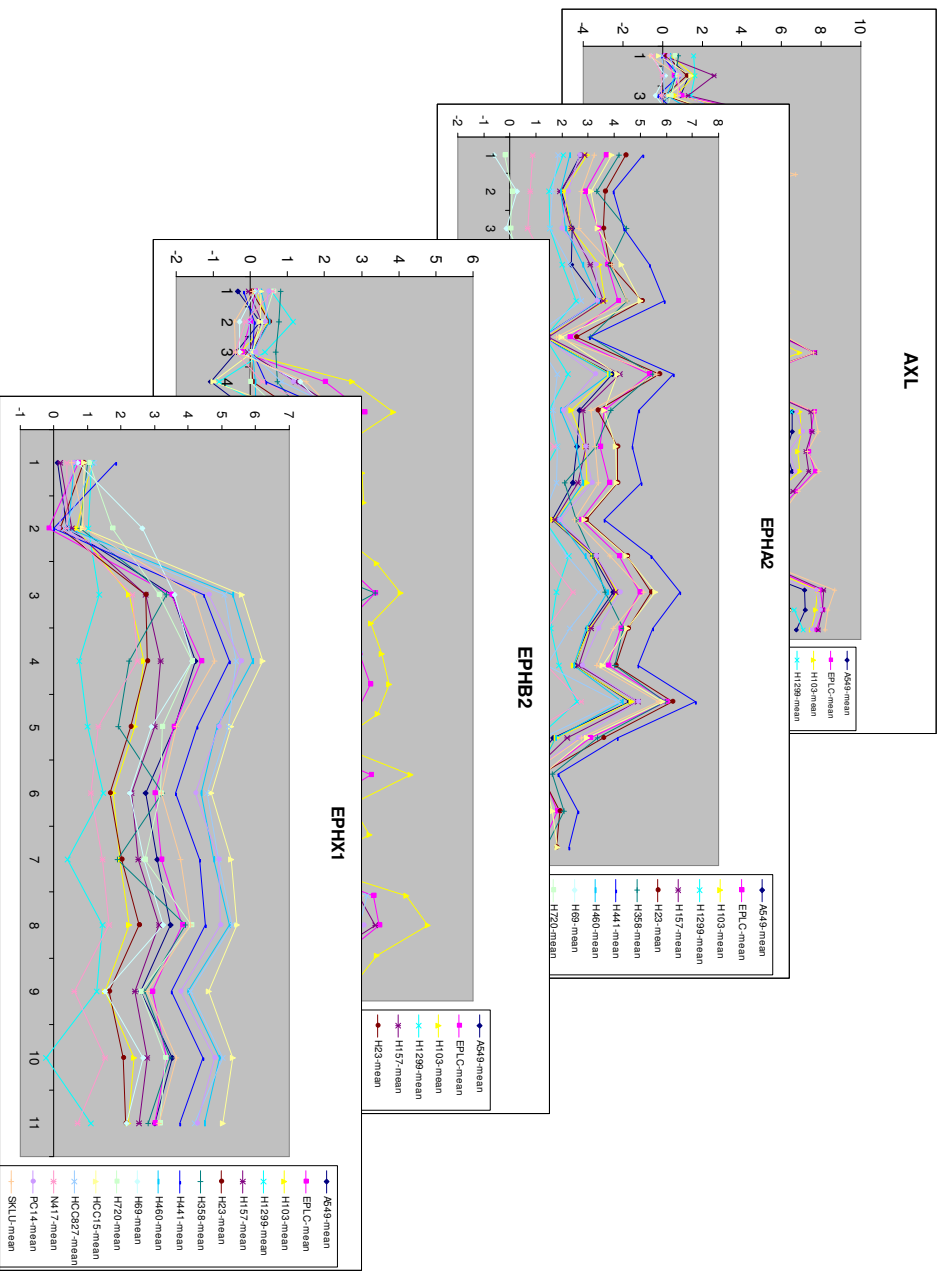
491B





NCI-N417	ATCC	Carcinoma de células pequeñas
NCI-H69	ATCC	Carcinoma de células pequeñas
NCI-H23	ATCC	Adenocarcinoma
NCI-H441	ATCC	Adenocarcinoma
HCC-827	DSMZ	Adenocarcinoma
SK-LU-1 (ATCC HTB 57)	EGACC	Adenocarcinoma
PC-14	EGACC	Adenocarcinoma
NCI-H358	ATCC	Adenocarcinoma bronquialveolar
A549	ATCC	Adenocarcinoma bronquialveolar
EPLC-272H	DSMZ	Carcinoma escamoso
HCC-15	DSMZ	Carcinoma escamoso
NCI-H157	ATCC	Carcinoma escamoso
NCI-H1299	ATCC	Carcinoma de células grandes
NCI-H460	ATCC	Carcinoma de células grandes
LCLC-103H	DSMZ	Carcinoma de células grandes
NCI-H720	ATCC	Carcinoma atípico





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