

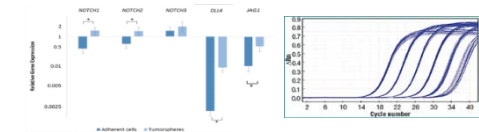
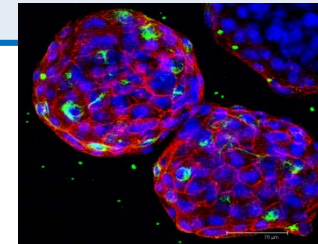
ANALYSIS OF CANCER STEM CELLS IN HUMAN NON-SMALL CELL LUNG CANCER

A. Herreros Pomares PhD student

OBJECTIVES:

- To isolate CSCs from lung cancer cell lines and tumor-tissue from resectable NSCLC.
- To establish potential prognostic or therapeutic biomarkers.

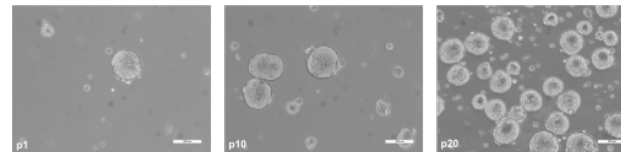
RESULTS (I): Primary cultures



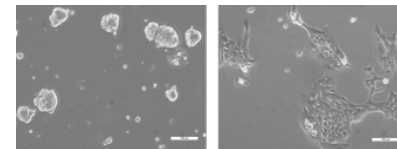
5. Gene expression



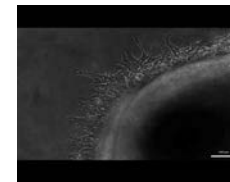
8 NSCLC tumor samples



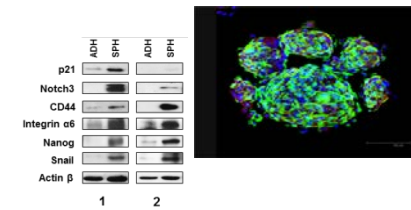
1. Growth ability



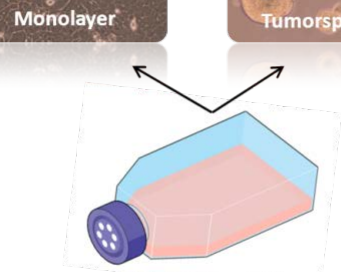
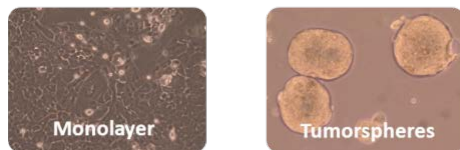
2. Differentiation capacity



3. Invasion capacity

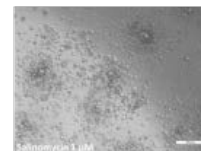
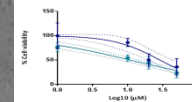
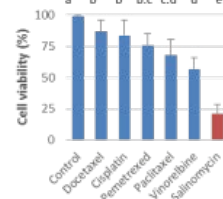
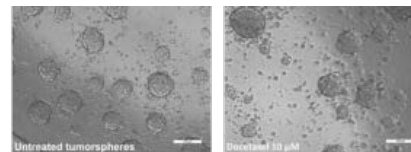


6. WB & IF

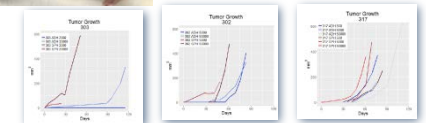


12 NSCLC cell lines

(H1650, H1993, A549, H2228, H23, H358, H460, H1395, H1975, HCC827, PC9, SW900)

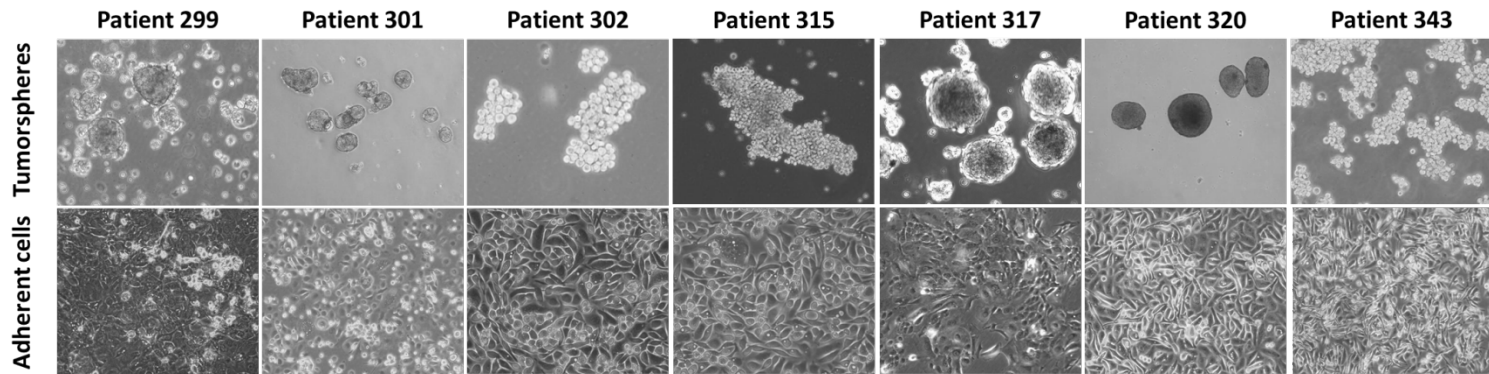


4. Drug Screening



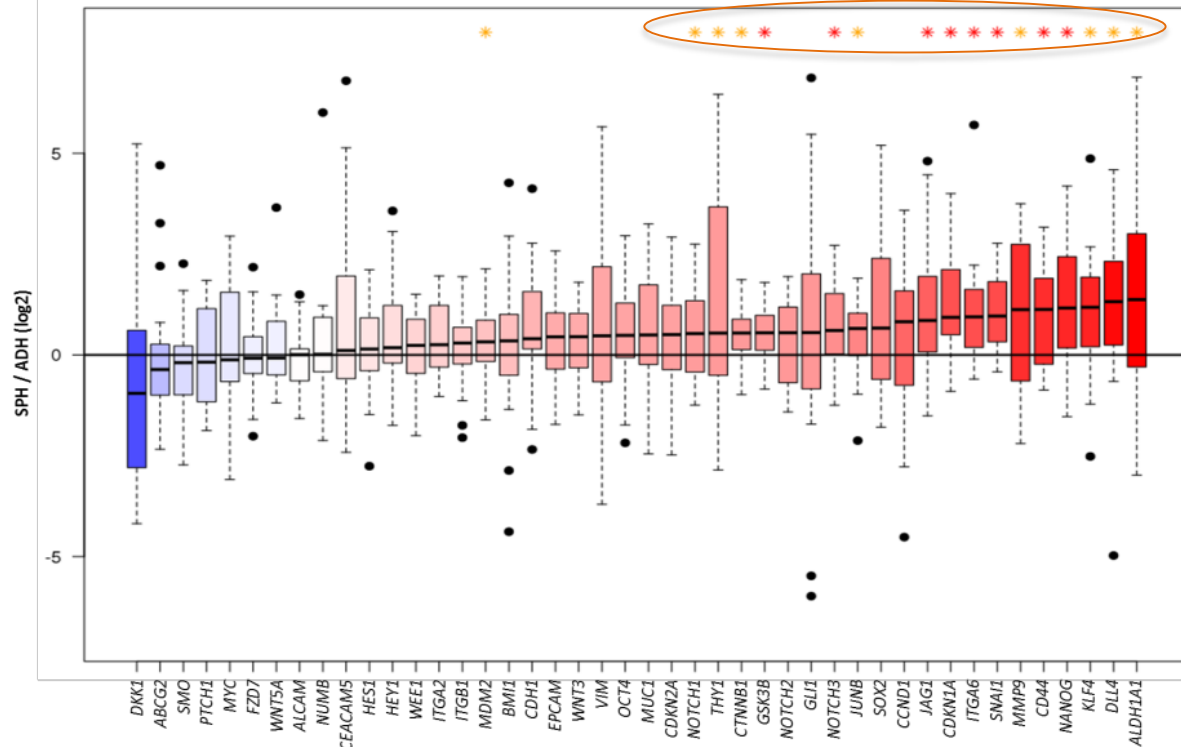
7. In vivo model

RESULTS (I): Primary cultures



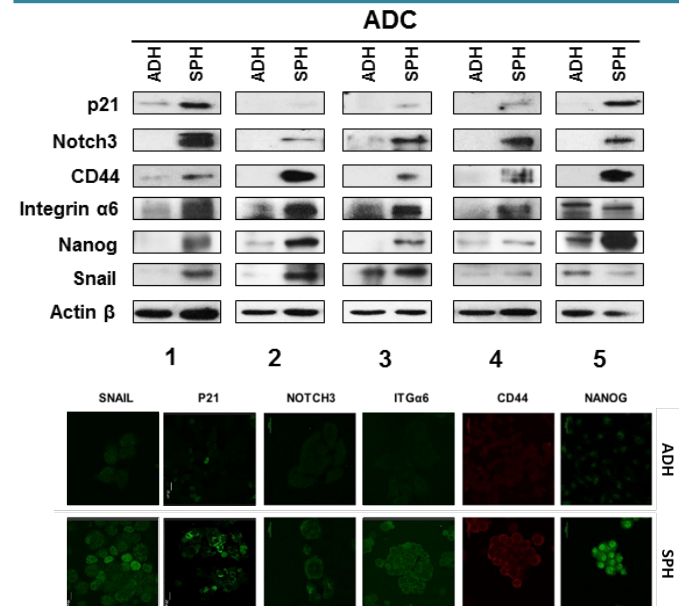
RESULTS (II): mRNA and protein expression

Gene expression in Tumorspheres vs. Monolayers



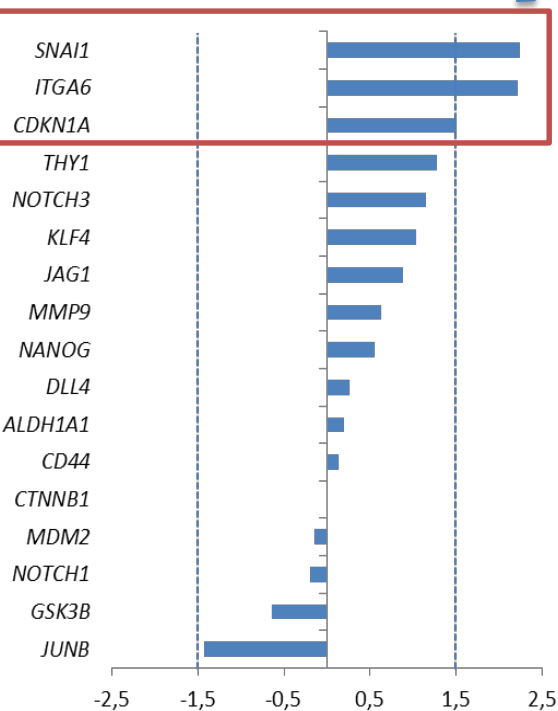
17 genes were differentially expressed $p < 0.05$. Selection was done: logistic regression stepwise & Akaike information criterion (AIC).

CD44/NANOG/ITGA6/SNAI1/CDKN1A/NOTCH3



RESULTS (III): Prognostic impact

Z score



Multivariate model

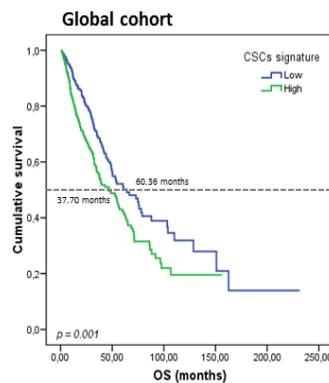
Variable	Regression coefficient	SE	p-value	HR	95% CI
CDKN1A	0.123	0.164	0.452	1.131	0.821-1.559
ITGA6	0.196	0.102	0.054	1.217	0.997-1.486
SNAI1	0.255	0.133	0.056	1.290	0.994-1.674

$$(CDKN1A \times 0.123) + (ITGA6 \times 0.196) + (SNAI1 \times 0.255)$$

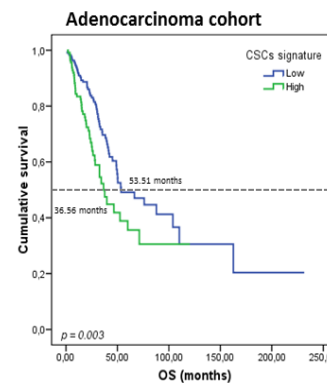
In silico set (N = 661)

Validation set (N = 114)

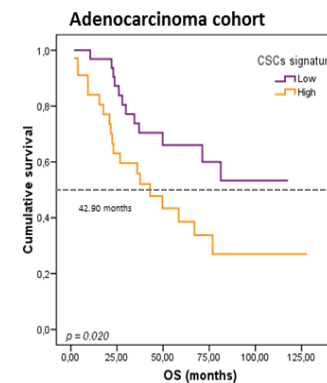
A.



B.



C.



CONCLUSIONS:

Sphere-forming assays can be used for CSCs enrichment in a simple and cost-effective way. A CSCs score based on the gene expression of *ITGA6*, *SNAI1* and *CDKN1A* is an independent prognostic biomarker of overall survival in lung adenocarcinoma.

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UNIVERSIDAD POLITÈCNICA DE VALÈNCIA



THANK YOU!

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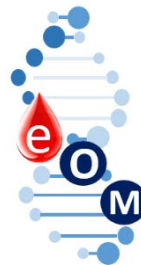
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