

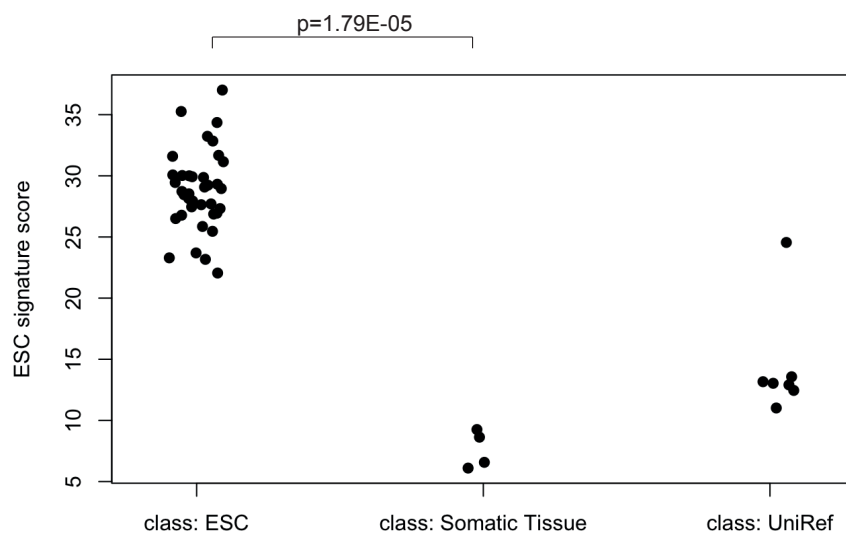
SUPPLEMENTAL FIGURES

In silico discovery of a FOXM1 driven embryonal signaling pathway in therapy resistant neuroblastoma tumors

Authors: Suzanne Vanhauwaert, Bieke Decaestecker, Sara De Brouwer, Carina Leonelli, Kaat Durinck, Pieter Mestdagh, Jo Vandesompele, Karen Sermon, Geertrui Denecker, Christophe Vanneste, Frank Speleman, Katleen De Preter

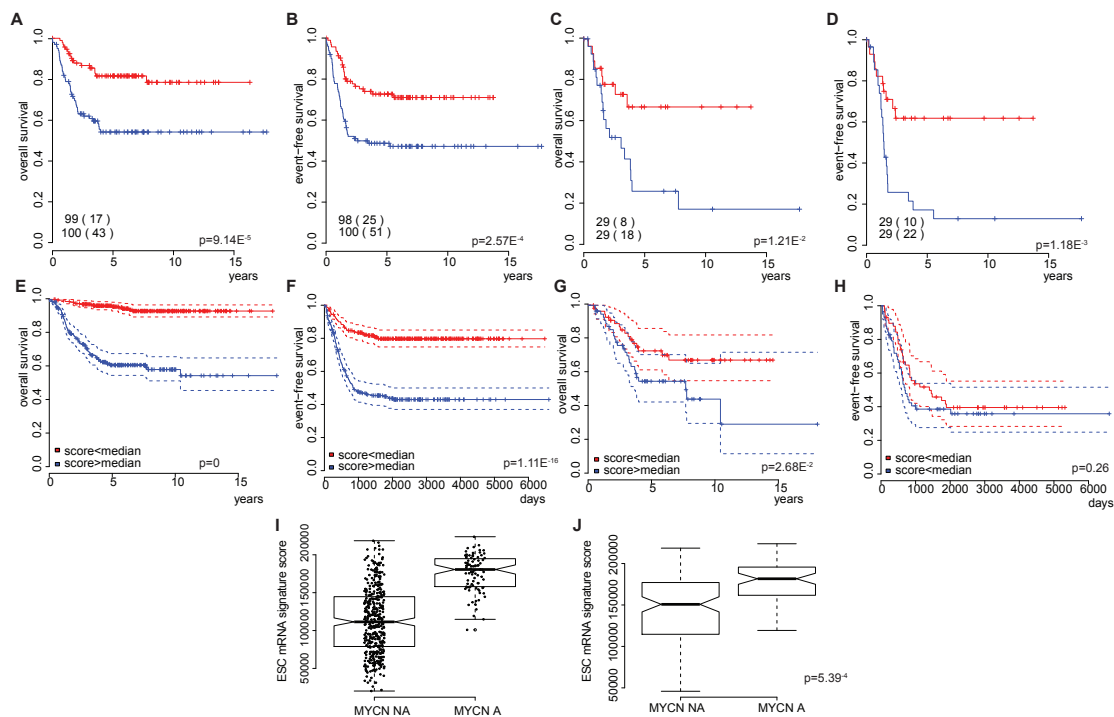
Supplemental figure 1: Validation of the miRNA ESC signature in an independent dataset

(p-value from Mann-Whitney test)



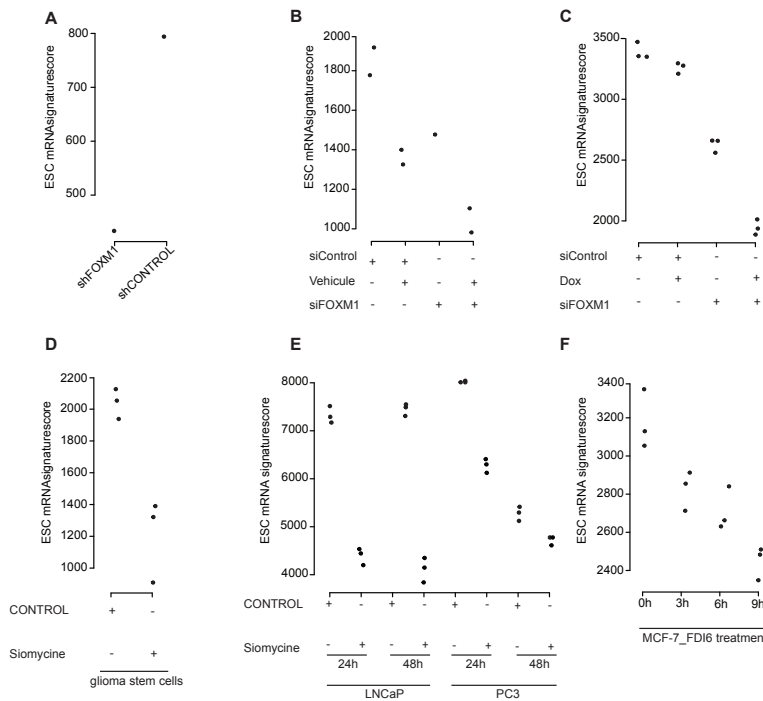
Supplemental figure 2: ESC mRNA signature score is related to survival

(A-B) Kaplan-Meier and log rank analysis on 200 neuroblastoma patients with a high or low ESC mRNA signature score. (C-D) Kaplan-Meier and log rank analysis within the subset of stage 4 neuroblastoma without MYCN amplification. Kaplan-Meier and log rank analysis of 498 neuroblastoma patients with high or low ESC mRNA signature score (independent validation), in the global cohort (E-F) and with the subset of stage 4 neuroblastoma without MYCN amplification (G-H). (I-J) ESC mRNA signature score in neuroblastoma patients with or without MYCN amplification in the global cohort and stage 4 neuroblastomas only.



Supplemental figure 4: FOXM1 also drives the ESC mRNA signature score in other cancer entities

A) ESC mRNA signature score upon lentiviral inhibition of FOXM1 in glioma cells, (B-C) upon siRNA FOXM1 inhibition in breast cancer cells, (D) upon inhibition of FOXM1 with siomycin A in glioma stem cells, (E) upon inhibition of FOXM1 with siomycin A in prostate cancer cells and (F) in breast cancer cells treated with FDI-6 to inhibit FOXM1.



Supplemental figure 5: ESC mRNA signature scores in other cancer entities with or without *MYCN* amplification

A) CCLE database analysis of the ESC mRNA signatures in *MYCN* non-amplified and *MYCN* amplified cancer cell lines. (B) ESC mRNA signature scores in medulloblastoma samples with and without *MYCN* amplification (p-values from t-tests).

