

Identification of FURIN as a tumor maintenance gene in solid tumors by *in vivo* Retroviral Mutagenesis and Directed Complementation

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Abstract

To identify tumor maintenance genes and pathways, we applied a genome-wide, large-scale functional screening using retrovirus-mediated mutagenesis on a number of inducible murine solid tumor models, including a HER2-driven breast tumor model and KRAS-driven breast and lung cancer models, in which viral integration could maintain established tumors in the absence of the initiating oncogene.

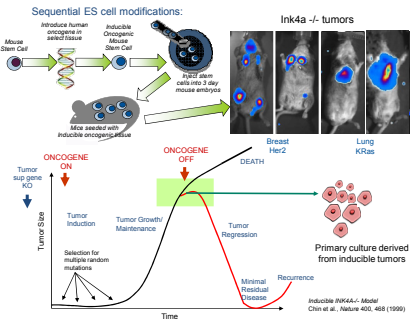
We identified more than 3,000 recurrent viral integration sites in a collection of about 400 tumors. Whereas some genes were targeted by viral integration in specific tumor models, others were prominently hit in all the models. For example, insertions targeting the *Furin* locus were detected in tumors from all three models. In such tumors, viral integrations mapped to the *Furin* promoter consistent with the notion that activation of this gene and/or pathway may represent a common mechanism of tumor maintenance.

Using our inducible directed complementation (DC) platform, we show that introduction of a wild type *Furin* cDNA can maintain primary tumors *in vivo* in the absence of the initial driving oncogene. The *Furin* DC tumors provide a useful pre-clinical model with which we can examine the effects of *Furin* antagonists on tumor maintenance. Next, we sought to extend the utility of these validated DC tumor models to drug discovery by establishing *Furin*-dependent cell lines for high-throughput screening.

Here we describe detailed molecular characterization of the *Furin* DC tumor models as well as from the cell lines derived from these tumor models. Furthermore, *Furin* DC Tumor Models as well as cell lines serve as a unique experimental tools, with which response to novel targeted therapies and other cancer agents can be studied.

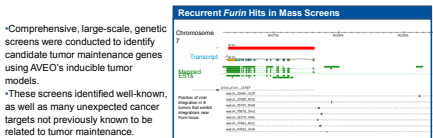
Inducible Tumor Models

Complex Models Can Be Generated Rapidly Inducible Breast and Lung Tumors (Kras, HER2)



Insertional Mutagenesis Genetic Screens in AVEO's Inducible Tumor Models

In vivo Moloney insertional mutagenesis screens in multiple inducible tumor models



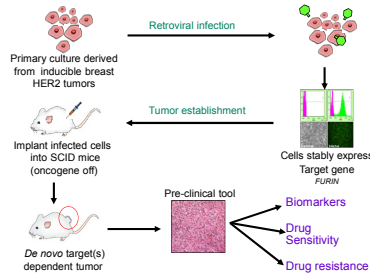
*Comprehensive, large-scale, genetic screens were conducted to identify candidate tumor maintenance genes using AVEO's inducible tumor models.

*These screens identified well-known, as well as many unexpected cancer targets not previously known to be related to tumor maintenance.

Generation of *Furin* Tumor Models

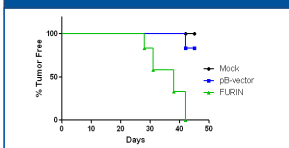
Directed Complementation Technology

- Creation of tumors driven by chosen target (directed complementation):
 - Allows for study of target biology in an *in vivo* tumor context
 - Allows for correlation between mutational variants and drug response

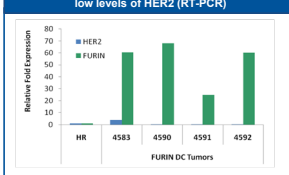


FURIN DC Tumor Models

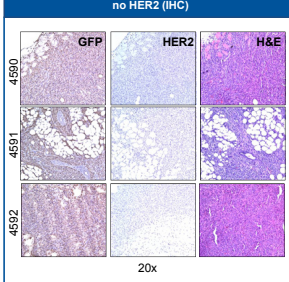
Latency and Penetrance of *Furin* DC Tumor Models



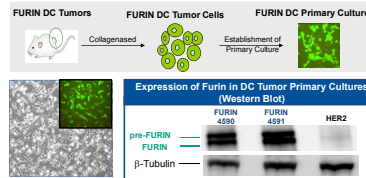
Furin DC Tumors Express high levels of *FURIN* and low levels of *HER2* (RT-PCR)



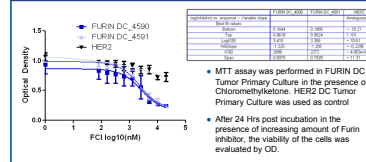
Furin DC Tumors Express high levels of GFP and no *HER2* (IHC)



Generation and Validation of *FURIN* DC Tumor Primary Cultures

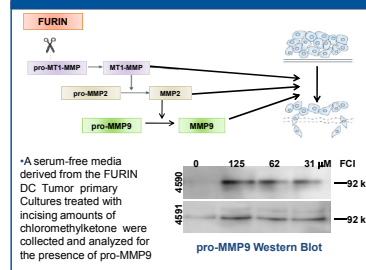


Furin DC Tumor Primary Cultures are sensitive to a *Furin* Convertase Inhibitor (Chloromethylketone)



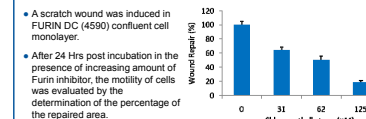
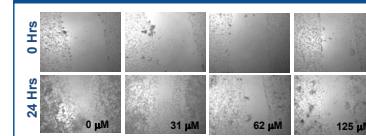
- MTT assay was performed in *FURIN* DC Tumor Primary Culture in the presence of Chloromethylketone. *HER2* DC Tumor Primary Culture was used as control
- After 24 Hrs post incubation in the presence of increasing amount of *Furin* inhibitor, the viability of the cells was evaluated by OD.

Endoprotease Activity in *Furin* DC Tumor Primary Cultures



*A serum-free media derived from the *FURIN* DC Tumor primary Cultures treated with increasing amounts of chloromethylketone were collected and analyzed for the presence of pro-MMP9

Regulation of *Furin* DC Tumor Primary Culture cell motility by *Furin* Convertase Inhibitor (Chloromethylketone)



- A scratch wound was induced in *FURIN* DC (4590) confluent cell monolayer.
- After 24 Hrs post incubation in the presence of increasing amount of *Furin* inhibitor, the motility of cells was evaluated by the determination of the percentage of the repaired area.

Summary

- Comprehensive, large-scale, genetic screens were conducted to identify candidate tumor maintenance genes in multiple AVEO's inducible Tumor Models. Several tumors carried retroviral insertions targeting the endogenous *Furin* locus.
- Introduction of defined cDNAs into inducible tumor background (Directed Complementation or DC) allows for creation of target-dependent tumor models. Using this approach, we created *Furin*-directed complemented tumor models, validating this endoprotease as a tumor maintenance candidate target.
- Cell primary cultures were established from *Furin* DC Tumor Models which show sensitive to Chloromethylketone treatment, a well established *Furin* Convertase Inhibitor (FCI).
- Furin* endoprotease activity and its role in cell motility were measured in *Furin* DC Tumor Primary Cultures in the presence of FCI.
- Together both *in vivo* and *in vitro* models provide ideal preclinical settings for the development of targeted anti-*Furin* therapies, as well as a tool for dissecting their accompanying molecular correlates of response.

Acknowledgments
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