Generation of mouse models for the identification of new driver pathways of drug resistance in human breast cancer

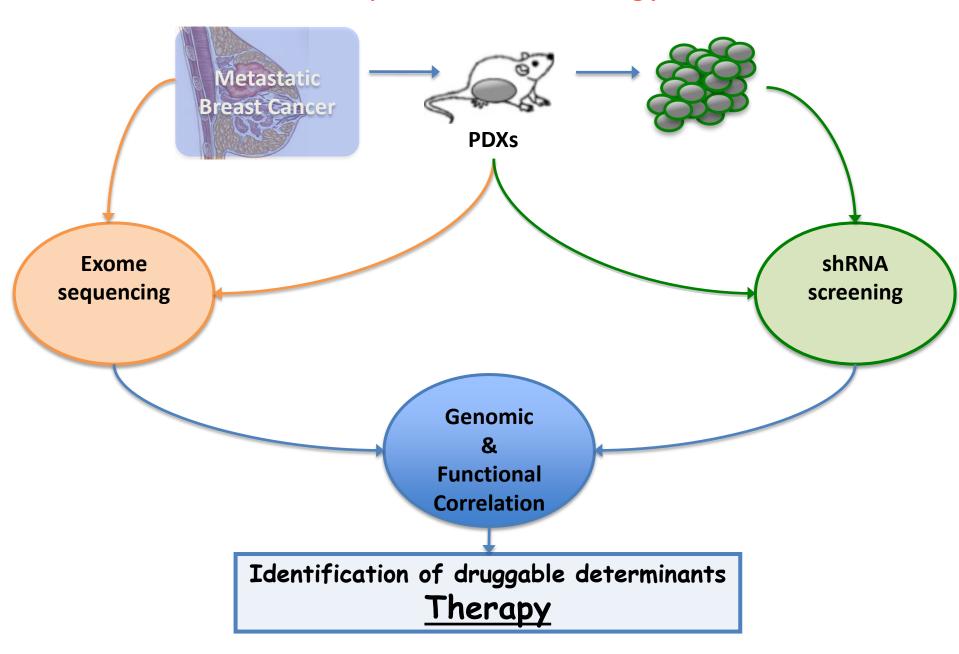
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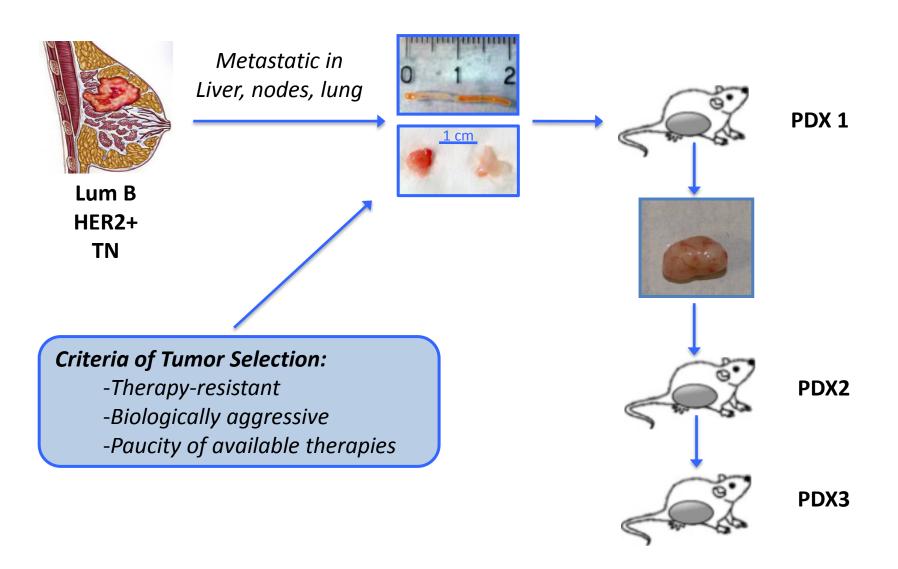
Aims of the study

- To generate patient derived xenograft (PDX) from metastatic breast cancer
- To perform exome sequencing in PDX model in order to identify potential driver pathways of resistance
- To set up an in vivo shRNA screening in PDX in order to identify druggable targets involved in tumor growth and drug resistance.

Experimental strategy



Feasibility of transplantation



Patients' characteristics

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Patients included in the study: 21

✓ 14 Luminal B

✓ 3 HER2+

✓ 4 Triple-negative
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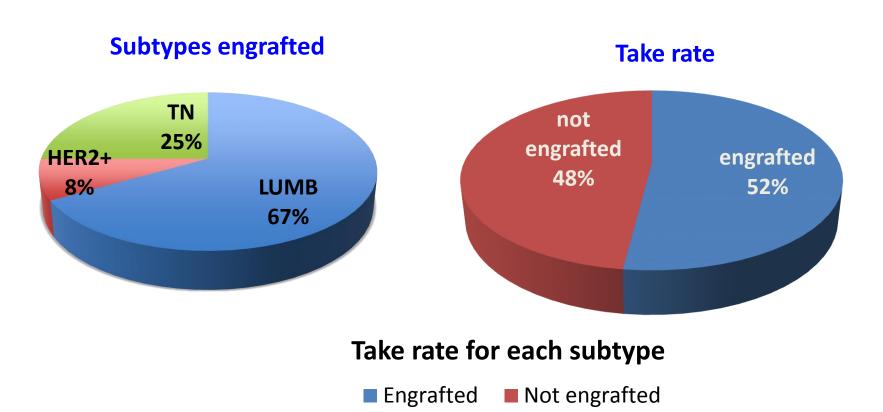
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Biopsied site:

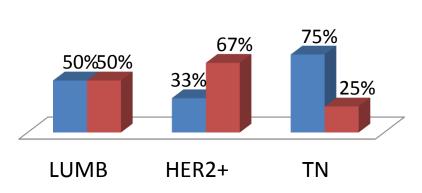
✓ 14 liver

✓ 1 lymph-node

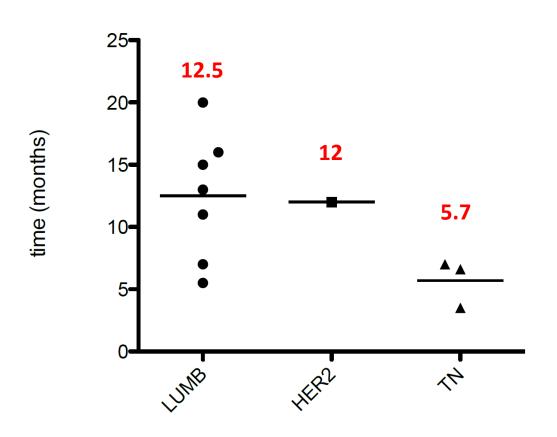
✓ 6 lung
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Engraftment

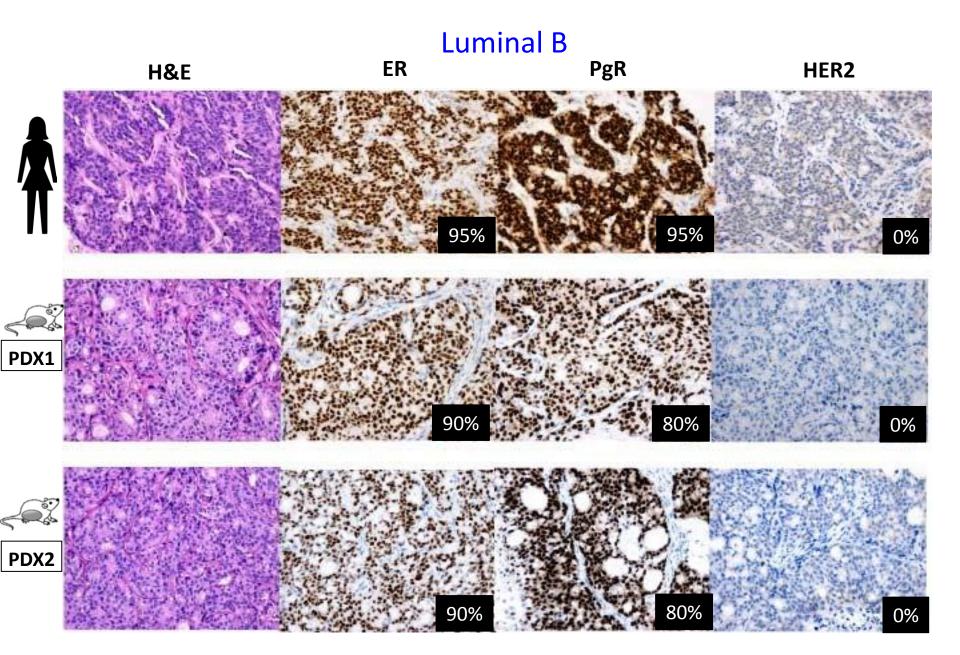




Median time to xenograft generation

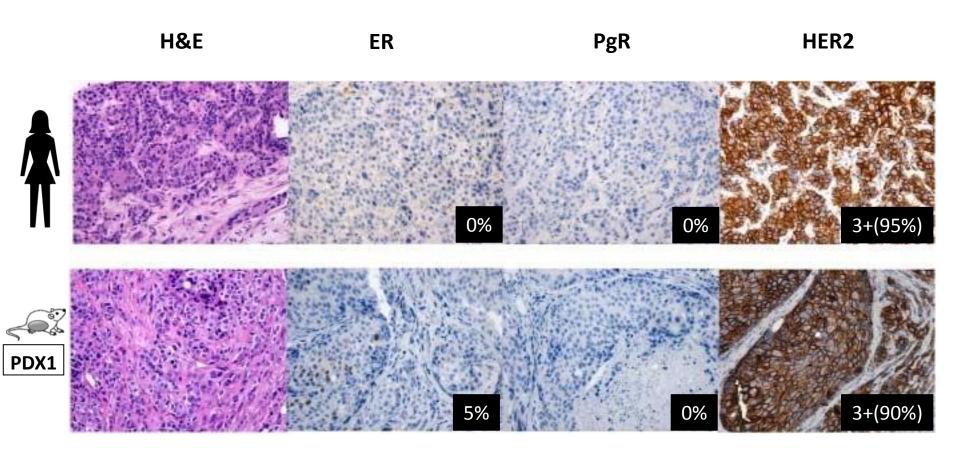


PDXs recapitulate human tumors



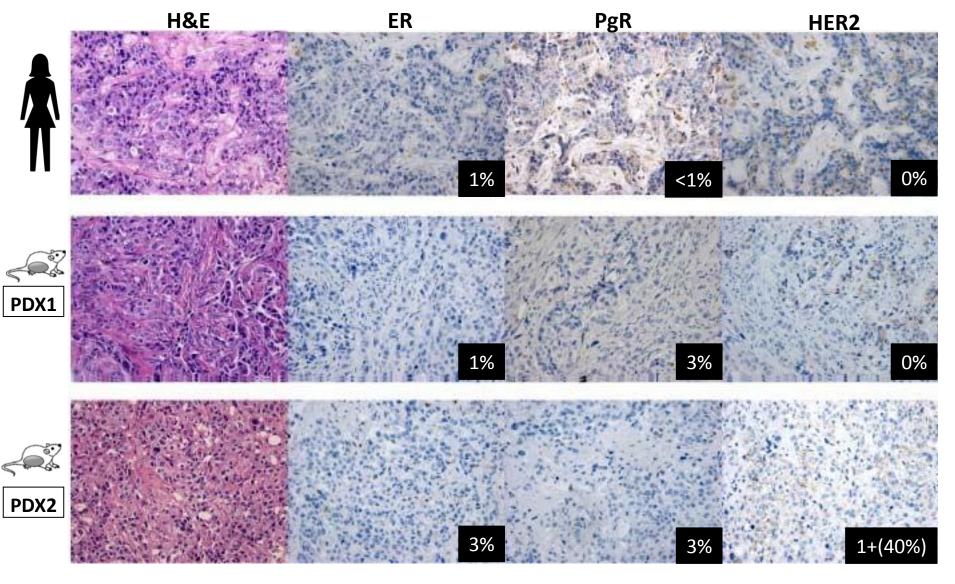
PDXs recapitulate human tumors

HER2+



PDXs recapitulate human tumors

Triple Negative



Study Steps

PDX generation

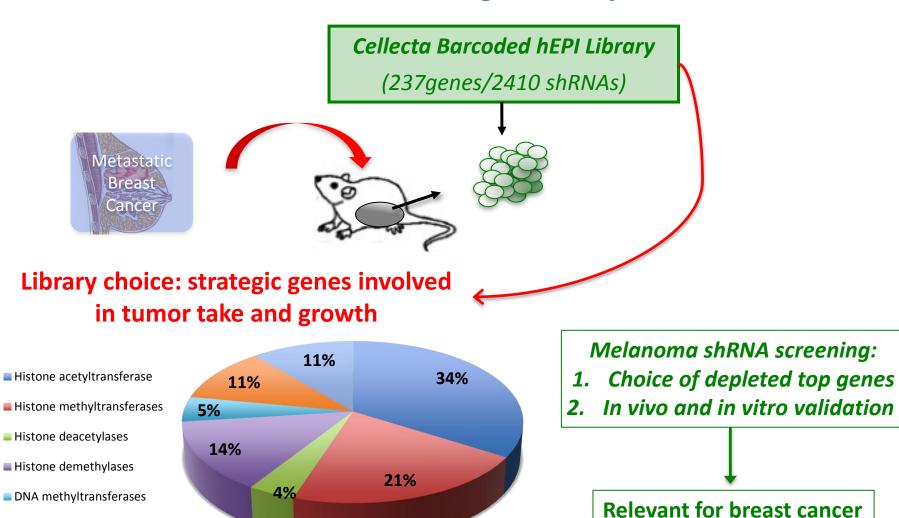
shRNA screening

PDX2 generation

Metastatic
Breast
Cancer

- What we did: Generation of PDXs
- What we're doing: Culture, Infection and Selection
- What we'll do: Transplantation of Transduced Cells

shRNA screening- The way we do it



Identification of novel druggable hits

Chromating remodelling complexes

Others

Conclusions

- We generated human PDXs from patients with metastatic breast cancer progressing on standard of care.
- The xenograft model recapitulates the characteristics of the originating human tumor, maintaining the histologic and immunophenotipic features, thus confirming to be a reliable phenocopy.
- In vivo shRNA screening may allow to identify new determinants of tumor progression in a preclinical setting.
- The exome seq will integrate the *in vivo* functional analysis with the identification of activating mutations in breast cancer progression.

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