Follow**ER**

Molecular follow up of delayed relapse in high risk luminal breast cancer

Primary objective:

Observational Prospective study

Aim:

Definition of the prevalence and the timing of the ctDNA mutations in luminal breast cancer node positive (high risk) obtaining data for a power calculation for a future randomized trial comparing observation vs active treatment for molecular relapse (proof of concept study)

Background

- Previous studies have described the presence of ctDNA in early malignancies in different types of cancer (Bettegowda et al Sci-Trasl-Med; 2014)

- Mutation tracking in serial samples increased sensitivity for the prediction of relapse, estimated with a median lead time of 7.9 months over clinical relapse but with a wide confidence interval due to sampling errors (Garcia-Murillas –Sci-Trasl-Med; 2015)

- There is no evidence that Circulating ESR1 mutation detection at the end of AI-based adjuvant treatment could be clinically useful. (Allouchery et al Breast Cancer Res; 2018)

Materials and methods (1)

- NGS primary tumor tissue for the detection of clonal drivers

- Designed of personalized ddPCR probes to identify minimal residual disease

Mateeials and method (2)

- Type of samples: Blood and urine collected at the same time point

- Timing of collection: start at the end of ET adjuvant (5° year of treatment) every 2 months for 3 years

Prospective and further applications

Luminal breast cancer high risk of relapse (pN+)

Molecular follow up to stratify in MDR+ and MDR-

MDR+ Randomization

Observation

Extended adjuvant treatment on a molecular basis