

# DCIS Study Design

## Sample Selection:

**Patient Registries:** JHU, UAB, SEER RTR (U.Iowa, USC, U.Hawaii)

**Progressors (n = 93):** DCIS with later progression to IBC

**Non-progressors (n = 93):** DCIS with no progression to IBC > 10y

**Normals (n = 11):** 7 DCIS-adjacent benign breast tissues, 4 normal breast tissues

**Transcriptome:** n = 123  
Illumina RNA Access Sequencing

Transcriptome Analysis  
P = 59; NP = 64

PAM-50 classification  
P = 59; NP = 64

RNA Splicing analysis  
P = 58; NP = 64

**Methylome:** n = 196  
Illumina 450K Methylation array

Methylome Analysis  
P = 93; NP = 92; N = 11

CNV analysis  
P = 93; NP = 92

**Multi-Omic analyses:** P = 59; NP = 63.

A total of 122 samples for which there is both transcriptome and methylome data.