Results for Signature

579 patients

85 genes

**Method**

Predictive mean matching imputed five complete datasets using multiple imputations with chained equations in the *mice* package. LASSO with an optimized L2 regularization deciphered a molecular signature in each imputed dataset. If a gene appears in at least three of the five signatures for a particular subset determined by ER/PR status, then the gene is included in the final signature.

**Results**