Supplementary Figure 1: Application of the Gaussian mixture model to ESR1- and ERBB2-expression data
Supplementary Figure 2: Normalization

Kruskal-Wallis test: P<0.0001
Supplementary Figure 3: Silhouette Analysis

A) Silhouette Analysis On IBC

B) Silhouette Analysis On NIBC

C) Silhouette Analysis On BC

D) Silhouette Analysis

- IBC
- NIBC
- BC
- NIBC (N=137)
Supplementary Figure 4: Silhouette Analysis (P-Values)

Significance Analysis Of Clustering

Comparison
Supplementary Figure 5: Validation of Limma-corrected IBC/nIBC signature

A

CONSORTIUM DATA SET (N=389, 137 IBC and 252 nIBC samples)

TRAINING SET (N=250, 84 IBC and 166 nIBC samples)

Regression Analysis

491 Probe sets; 443 Unique genes
(Up IBC: 231; Up nIBC: 260)

412 Probe sets with IBC- and molecular-subtype-specific expression components

79 Uniquely IBC-specific probe sets

VALIDATION SET (N=139, 53 IBC and 86 nIBC samples)

Global Test + PAM

B

79 Gene Signature

491 Gene Signature
Supplementary Figure 6: Networks overrepresented in IBC
Supplementary Figure 7: Networks overrepresented in nIBC
Supplementary Figure 8: Prognostic value of the IBC/nIBC signature in nIBC

Distant metastasis-free survival

nIBC-like, N=728

IBC-like, N=143

N = 871
Log-rank, P=0.002

Months after diagnosis