

Supplementary Report Intrinsic molecular signature of breast cancer
in a population-based cohort of 412 patients
S Calza et al.

Figure 1S: Hierarchical clustering of Stanford/Norway data based on 516 genes. Dendrogram labels and colors correspond to subtype clusters.

Figure 2S: Gene profile for the five subtypes in the Stanford/Norway data.

Figure 3S: Stockholm hierarchical clustering based on 465 genes in common with the “Intrinsic set” in Sorlie et al¹. Labels and colors correspond to centroid-predicted assignment of tumor subtype.

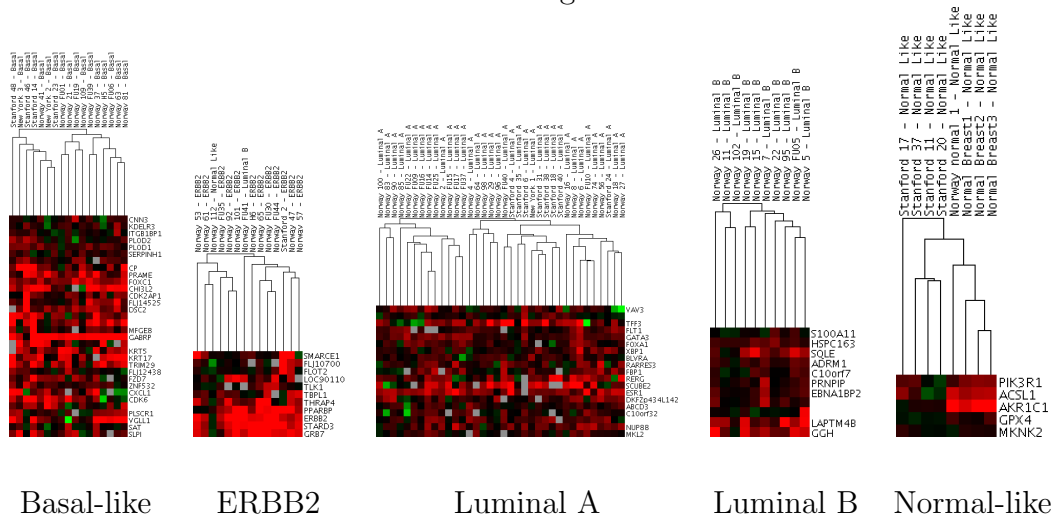
Figure 4S Uppsala hierarchical clustering based on 465 genes in common with the “Intrinsic set” in Sorlie et al¹. Colors correspond to centroid-predicted assignment of tumor subtype.

Figure 5S: Gene profile for some subtypes in the Stockholm cohort. Labels indicate the centroid label whose the sample is more correlated to and the Estrogen Receptor status.

Figure 6S: Gene profile for some subtypes in the Uppsala cohort. Labels indicate the centroid label whose the sample is more correlated to and the Estrogen Receptor status.

Figure 7S: Kaplan-Meier breast-cancer specific survival curves of the tumor subtypes in (a) Sweden with endocrine therapy, (b) Uppsala without any adjuvant therapy. The P-value, computed in a Cox regression, is for simultaneous comparison of all the curves.

Figure 2S:



Basal-like

ERBB2

Luminal A

Luminal B

Normal-like

Figure 4S:

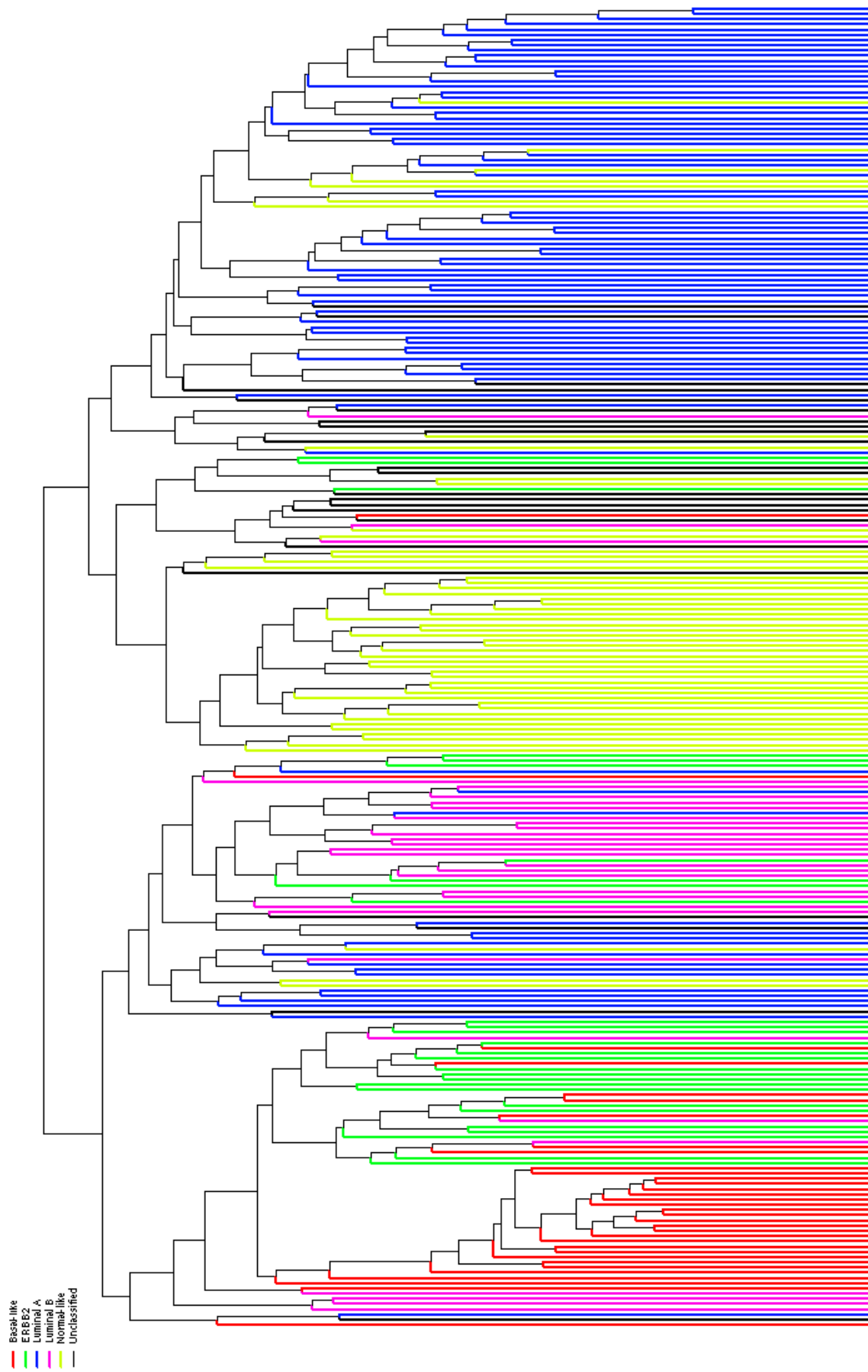
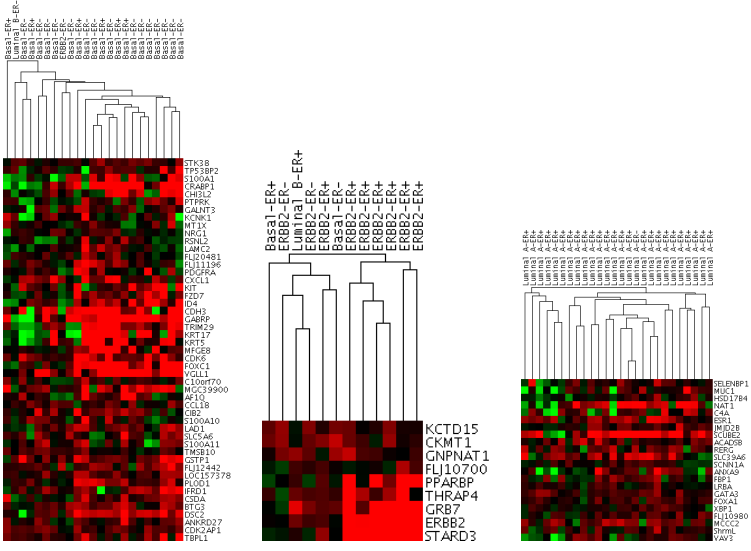


Figure 5S:

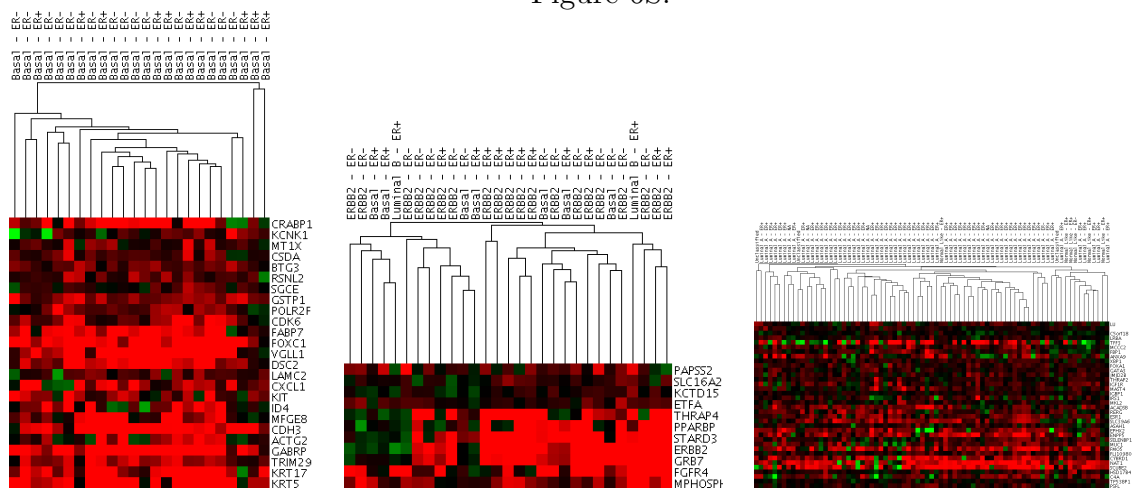


(a) Basal-like

(b) ERBB2

(c) Luminal A

Figure 6S:



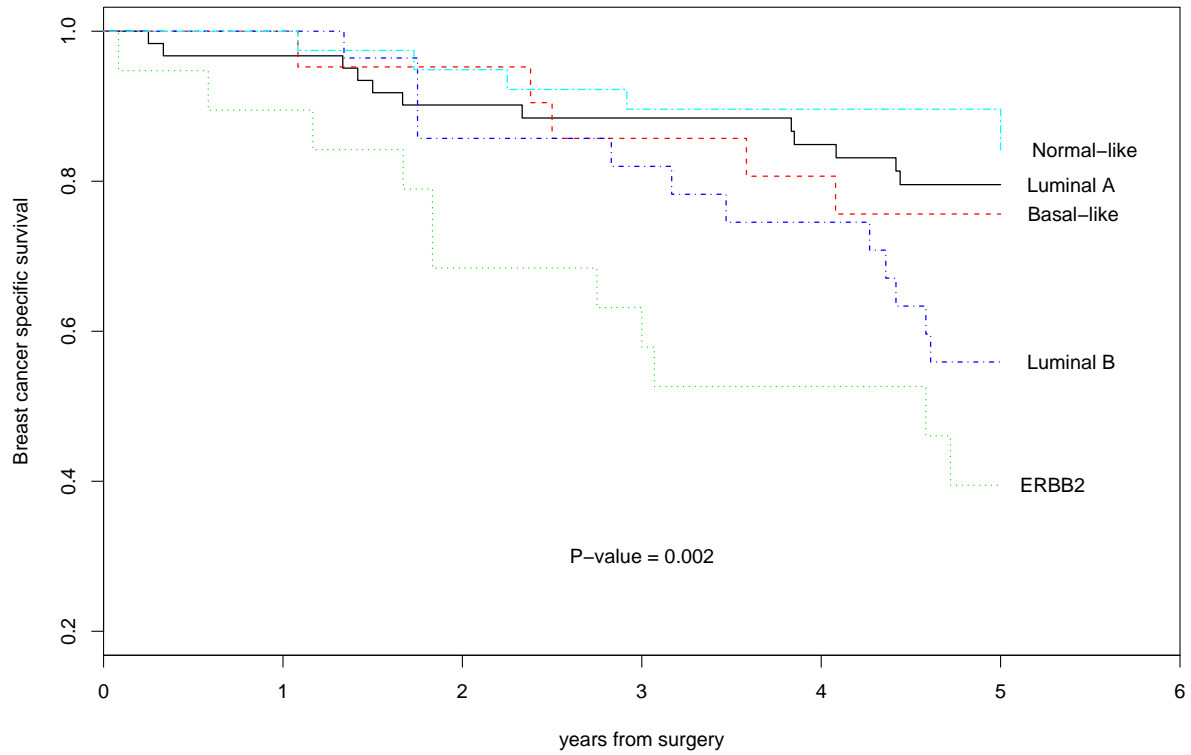
(a) Basal-like

(b) ERBB2

(c) Luminal A

Figure 7S:

(a) Patients treated with endocrine adjuvant therapy (N = 171)



(b) Patients without any adjuvant therapy (N = 130)

