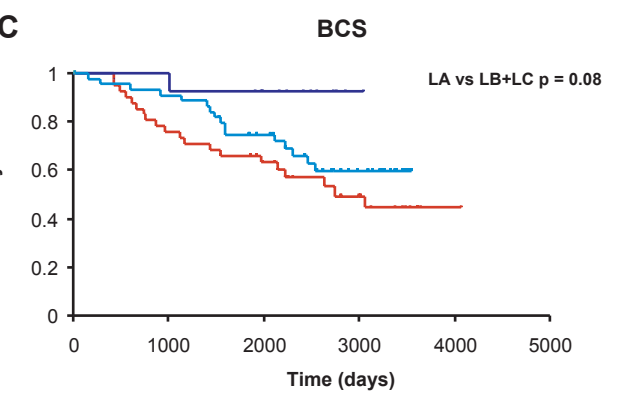
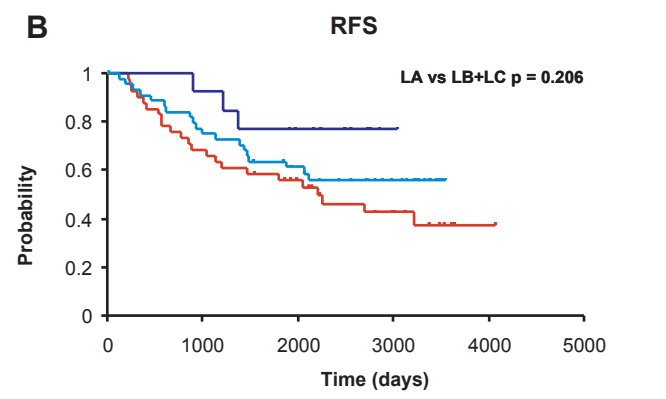
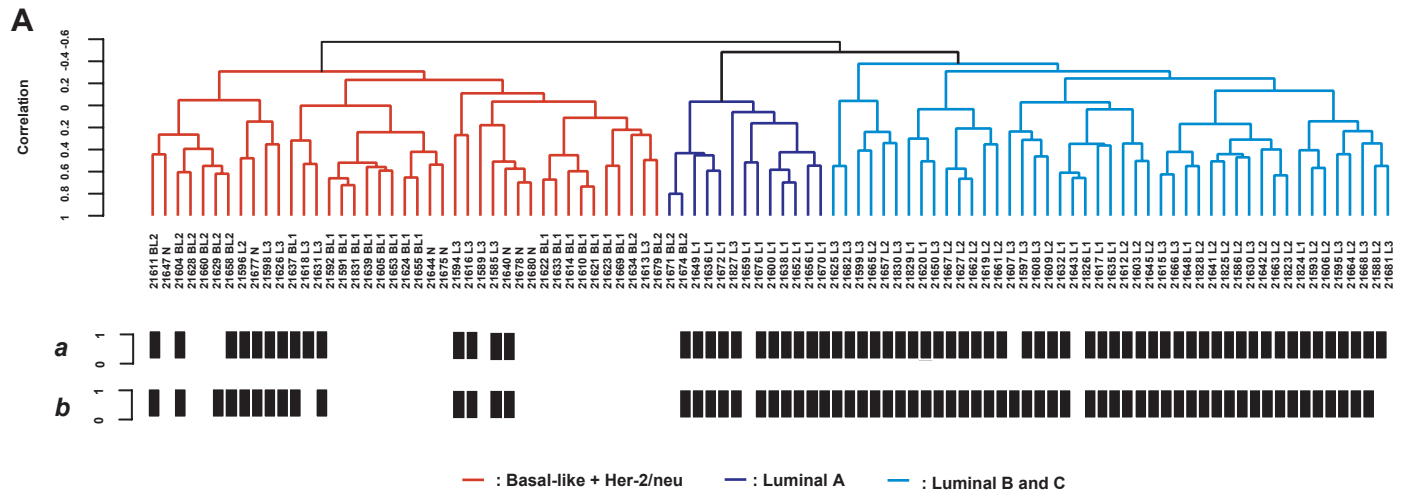


Figure 6. Hierarchical clustering analysis of 105 probes elements overlapping between the "intrinsic" list of Sorlie et al. and the NCI 706 gene list.



(A) Dendrogram of 99 breast cancer specimens analyzed by hierarchical clustering analysis using 105 overlapping probes elements between the intrinsic gene list of Sorlie et al, and our 706 survival list. The tumors were separated into two main groups mainly associated with ER status as determined by the ligand-binding assay. The dendrogram further branched into smaller subgroups within the ER+ and ER- classes based on their basal and luminal characteristics colored as: Her-2/neu subgroup and basal-like subgroup, red; luminal A subgroup, dark bleu; luminal B and C subgroups, light bleu. BL1: basal-like1; BL2 : basal-like2; NEU : Her-2/neu; L1: luminal-like 1; L2: luminal-like 2; L3: luminal-like3.

(B) Relapse-free survival of the 99 breast cancer patients based on the 3 expression-based tumor subtypes (luminal B and C were considered one group) assessed by Kaplan-Meier analysis. (C) Breast cancer survival of the 99 breast cancer patients based on the 3 expression-based tumor subtypes (luminal B and C were considered one group).