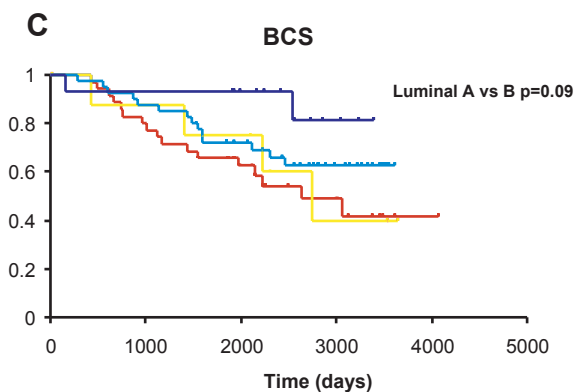
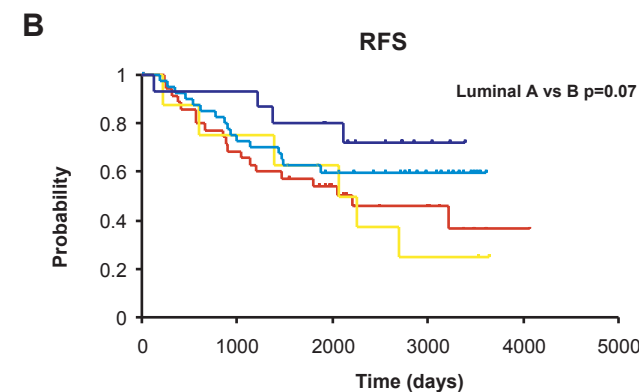
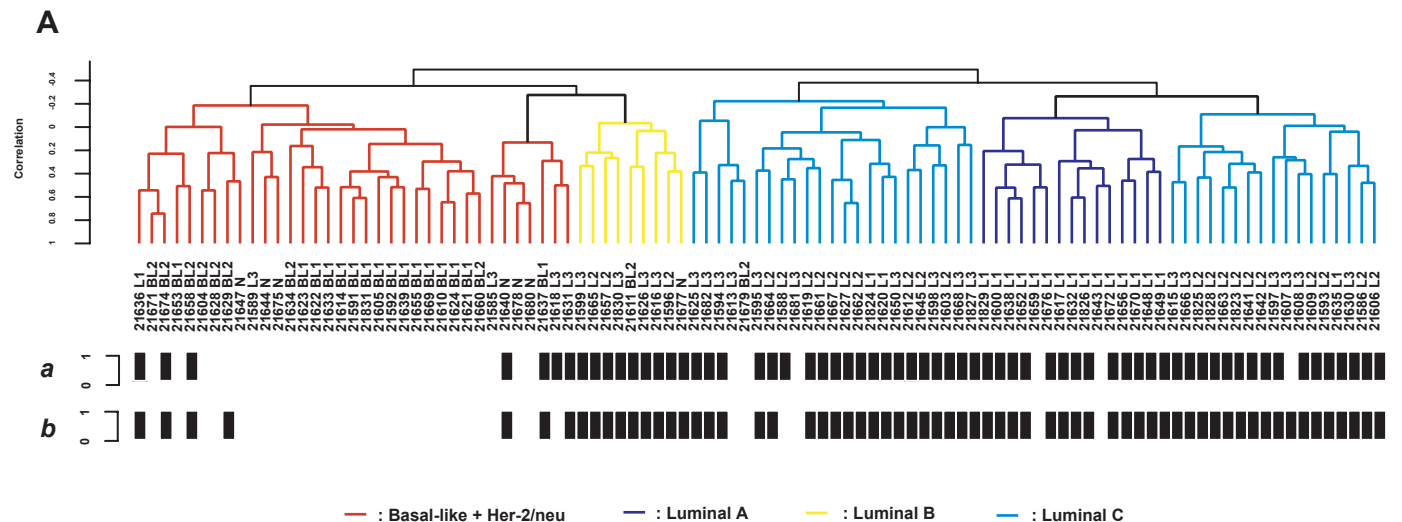


Figure 5. Hierarchical clustering analysis of 332 probes elements overlapping between the "intrinsic" list of Sorlie et al. and the NCI cDNA microarray.



(A) Dendrogram of 99 breast cancer specimens analyzed by hierarchical clustering analysis using 332 overlapping probes elements between the intrinsic gene list of Sorlie et al. and our 7,650-elements array. The tumors were separated into two main groups mainly associated with ER status as determined by the ligand-binding assay (LBA). Black bars represent (a) ER-positive tumors assessed by IHC, (b) ER-positive tumors assessed by LBA. 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 blue; luminal B subgroup, yellow; and luminal C subgroup, light blue. BL1: basal-like1; BL2: basal-like2; N: 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 4 expression-based tumor subtypes assessed by Kaplan-Meier analysis.
 (C) Breast cancer survival of the 99 breast cancer patients based on the 4 expression-based tumor subtypes.