**Figure S2.** Optimization of the number of predictive reporter genes to be included in the basal *BRCA1* signature (A) and lumB *BRCA2* signature (B). For *BRCA1* classification 110 genes were found to be the lowest number of genes providing the highest mean balanced accuracy, while 100 genes were the most optimal for *BRCA2* classification. See Materials and methods section for more details.