Figure S7

The image shows a Kaplan-Meier survival curve for 47 BRCA patients from Figs. 1 and 3a,b, separated into two groups based on mRNA expression data from TCGA for these patients. Gene sets tested overlap the top 100 smRNA features of Fig. 3a that are differentially expressed in Tumor (regarding the mRNA expression values used see materials and methods). The gene sets correspond to the mRNAs (and not the smRNAs) regarding expression values of genes compared to the rest of the genes in these patients (z-score values). Classification between the two groups was done solely based on the above mentioned mRNA z-score values and no smRNA expression value was taken into account as in case of Fig. 3. Figure shows that for genes overlapping smRNAs, the differences on mRNA expression (gene set altered vs gene set not altered) corresponds also to differences in survival outcome. This finding is an indication of the biological significance of the mRNAs that overlap these smRNA locations. Our finding that smRNAs “are prognostic in the patients” is based on the survival curves of Fig 3 and not these of this figure. These curves do not refer to clustering based on smRNA data but to an automatic clustering created by the cancer genome bio portal on RNA data and shows that the identified locations where smRNAs reside have indeed a clear connection with cancer with regards to RNA levels.