Figure S12. NMF consensus clustering of all 94 BRCA samples (Normal and Tumor) and features of Fig 1 based on smRNA sense expression profiles of each sample at a) 1kb upstream TSS, b) exon 1, c) other exons of protein coding genes. Differences in the allocation of misclassified samples between Normal and Tumor cannot be assessed due to the unsupervised nature of this clustering.