Figure S18. Low smRNA content regions are hypermethylated, while high smRNA content regions are hypomethylated. DNA methylation of CpGs in BRCA patients at locations with different exon1 smRNA content are depicted. The heatmap depicts DNA methylation at CpGs (each CpG a different row) in different BRCA patients (columns). The upper panel of the heatmap corresponds to CpGs at locations overlapping the 1000 smRNA features with the lowest exon1 smRNA content while the lower panel the 1000 smRNA features with the highest smRNA content. Hypermethylation (value 100%) is represented as red, while hypomethylation (value 0%) is represented as blue, with the colour range between them reflecting values from 0 (blue) to 1 (red). The different number of rows between high and low content genes is attributed to the different number of CpGs (more than one) per feature for this specific gene list. In order the DNA methylation results between the two different smRNA content regions to be comparable we have applied a global color normalization. As shown in the heatmap, smRNA content is negative correlated with DNA methylation.