Figure S1. a) Distribution of smRNA locations around Transcription Initiation Site (TSS) of protein coding genes for samples of Fig. 1. b) smRNA expression profiles in Normal vs Tumor samples at exon 1, and at regions 1kb upstream and downstream of gene borders (protein coding genes). Figure depicts smRNA expression fold changes (log2) between all Tumor and Normal samples in composite profiles of 20 bins for the above regions for all protein coding genes. Initial smRNA values are mean values from all samples normalized per number of read counts/sample, per feature number and length (see methods). The vertical arrows on the left depict whether expression of smRNAs favors the Normal or Tumor samples.