





Supplementary Figure S6 DNA methylation levels and mRNA expression levels for the 70 genes, for which the 80 probes listed in Supplementary Table S8 had been designed, examined in The Cancer Genome Atlas (TCGA) database using MethHC pipeline (<http://MethHC.mbc.nctu.edu.tw>). Inverse correlations ($r < -0.2$) between DNA methylation and mRNA expression levels were observed for 22 of the 70 genes: the DNA methylation levels of the *ACOT7*, *ARF4*, *DHX36*, *FLCN*, *FOXN3*, *FYTTD1*, *MAML3*, *MICAL3*, *MRPS24*, *NQO2*, *PCNT*, *PKP4*, *PLAG1*, *PMPCA*, *PROSER3*, *RASA2*, *SPG7*, *TRAPPC10*, *WDR6*, *WHSC1*, *ZC3H14* and *ZZEF1* genes were inversely correlated with levels of expression in samples of human pancreas, kidney, kidney, uterine cervix, uterine corpus, urinary bladder, pancreas, skin, liver, urinary bladder, prostate, pancreas, kidney, uterine cervix, urinary bladder, pancreas, breast, pancreas, rectum, colon, breast and kidney tissue, respectively. Red circles: cancerous tissue; green circles: non-cancerous tissue. These correlations were examined using the DNA methylation levels for the individual CpG sites, i.e. Infinium probe CpG sites shown in parentheses above, and were not examined for nine of the 80 probes annotated to the intergenic regions and not to any gene.