Suppl. Fig. 2. Significant correlation between *SFRP1* (r= -0.688, p=0.001) and *SFRP2* (r= -0.657, p=0.002) mRNA expression and methylation. Tissue origin of cell lines is specified in Suppl. table 4. NC, normal colon; NE, normal endometrium; T, 5-aza-CdR and TSA treated cell line (without T, untreated).