Supplementary Tables:

Supplementary Table 1: TFPI2 Primers used for MSP, BSS, RT and Stool DNA methylation assay TFPI2 Size Strand Sense Antisense MSP1 U GTGGTGGGGGTGATAGTTTTTG CCAAACAACCCAAATACCCACTTTATACA 109 1 MSP1 M CGGCGGGGTGATAGTTTTC CAAACGACCCGAATACCCGCTTTATACG 106 1 93 2 MSP2* U CCCACATAAAACAAACACCCAAACCA TGGTTTGTTGGGTAAGGTGTTTG MSP2* M GTTCGTTGGGTAAGGCGTTC CATAAAACGAACACCCGAACCG 86 2 * Primer set used for MSP in FFPE and frozen samples. MSP3 U AAGTTGTGTATTTTTTTTTTGTTAGGTGTTTTTTTG ΑΑCAAACAAAATCCATAATACAAAAAATCAAACA 88 1 MSP3 M CGTATTTTTTTCGTTAGGCGTTTTTTC CGAAATCCATAATACAAAAAATCGAACG 75 1 MSP4 U GGGTTTTGTGTAGGTGTTTTTTAAGTTTTG CCCCCTACCAACAAAACACA 70 1 MSP4 M GGGTTTCGTGTAGGCGTTTTTTAAGTTTC CCCTACCAACGAAACGCG 67 1 BSS GGTTTATGGTGTAGGGG 2 CAATCACTAACAAATCATTTCC GGGCCCTACTTCTCCGTTAC **RT TFPI2** CACACTGGTCGTCCACACTC 183 213 ACTB CATCCACGAAACTACCTTCAACTCC GAGCCGCCGATCCACACG HPRT CTTTGCTGACCTGCTGGATT GTTGAGAGATCATCTCCACC 150

Stool DNA methylation assay

Nested primers used for pilot feasibility study

#Flank MSP 5	GTGTATGAATTAGTTATTTTTAGGTTT	CTAAACAAAACRTCCRAAAAAAC	144	1
MSP5# U	TTAGTTATTTTTAGGTTTTGTTTTGGT	ΑΑΑΑΑCACCTAACAAAAAAAAAAAAAAAAAAAAAAAAAA	118	1
MSP5# M	ATTTTTTAGGTTTCGTTTCGGC	GCCTAACGAAAAAAAAAACGCG	106	1

Primers for quantitative MSP (qMSP)

TFPI2_qMSP	GTTCGTTGGGTAAGGCGTTC	CATAAAACGAACACCCGAACCG	87	2
Molecular				
beacon	FAM—CGACATGCACCGCGCACCTCCTCCCGCCAAGCATGTCG—DABCYL			

Supplementary Figure 1: Epigenetic inactivation of TFPI2 in DKO. Gene expression changes are plotted by fold change (log scale) in DKO (Y-axis) compared to its parental cell line Hct116 (X-axis) treatment. TFPI2 expression increases 4.47 in log2 ratio (=22.12 fold) in DKO compared to HCT116 Mock. □ indicates the location of TFPI2 in the scatter plot.

Supplementary Figure 2: Bar graph showing methylation frequency of TFPI2 in various cultured cancer cell lines. U=unmethylated; PM = partially methylated; DM=methylated

Supplementary Figure 3: Line diagram (A) and bar graph (B) showing cell growth in mock, empty vector and *TFPI2* transfected HCT116 cells. There is no difference in cell survival between mock and empty vector transfected cells. *TFPI2* transfected cells show a 20% decrease in cell survival.

Supplementary Figure 4: Graphic representation of overlap between hypermethylation of HCT116 as determined by Schuebel *et. al.* (10) with PcG-targeted genes according to Bracken *et. al.* (22) in gene pool represented on Agilent 4x44k array platform.



Supplementary Figure 1 Glockner et al.



Supplementary Figure 2 Glockner et al.



3B

3A



Supplementary Figure 3 Glockner et al.



Supplementary Figure 4 Glockner et al.