Figure S1

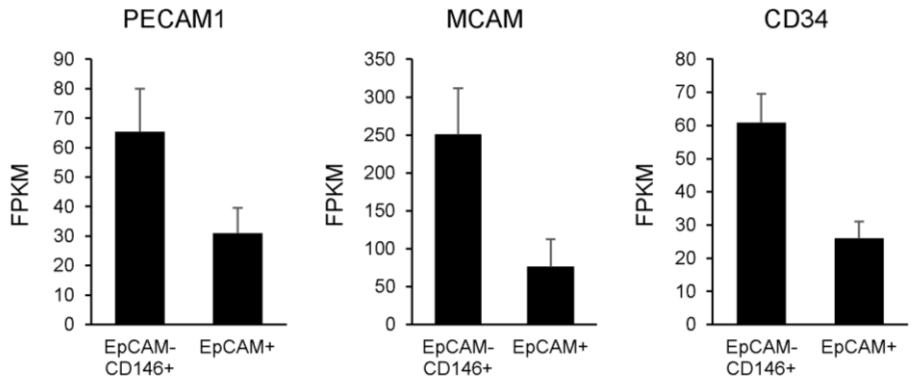

Figure S1

Expression of endothelial markers detected using RNA-seq. Results of *PECAM1*, (CD31), *MCAM* (CD146) and *CD34* expression in endothelial (EpCAM-, CD146+; n = 6) and epithelial (EpCAM+; n = 17) cells are shown.

Figure S2

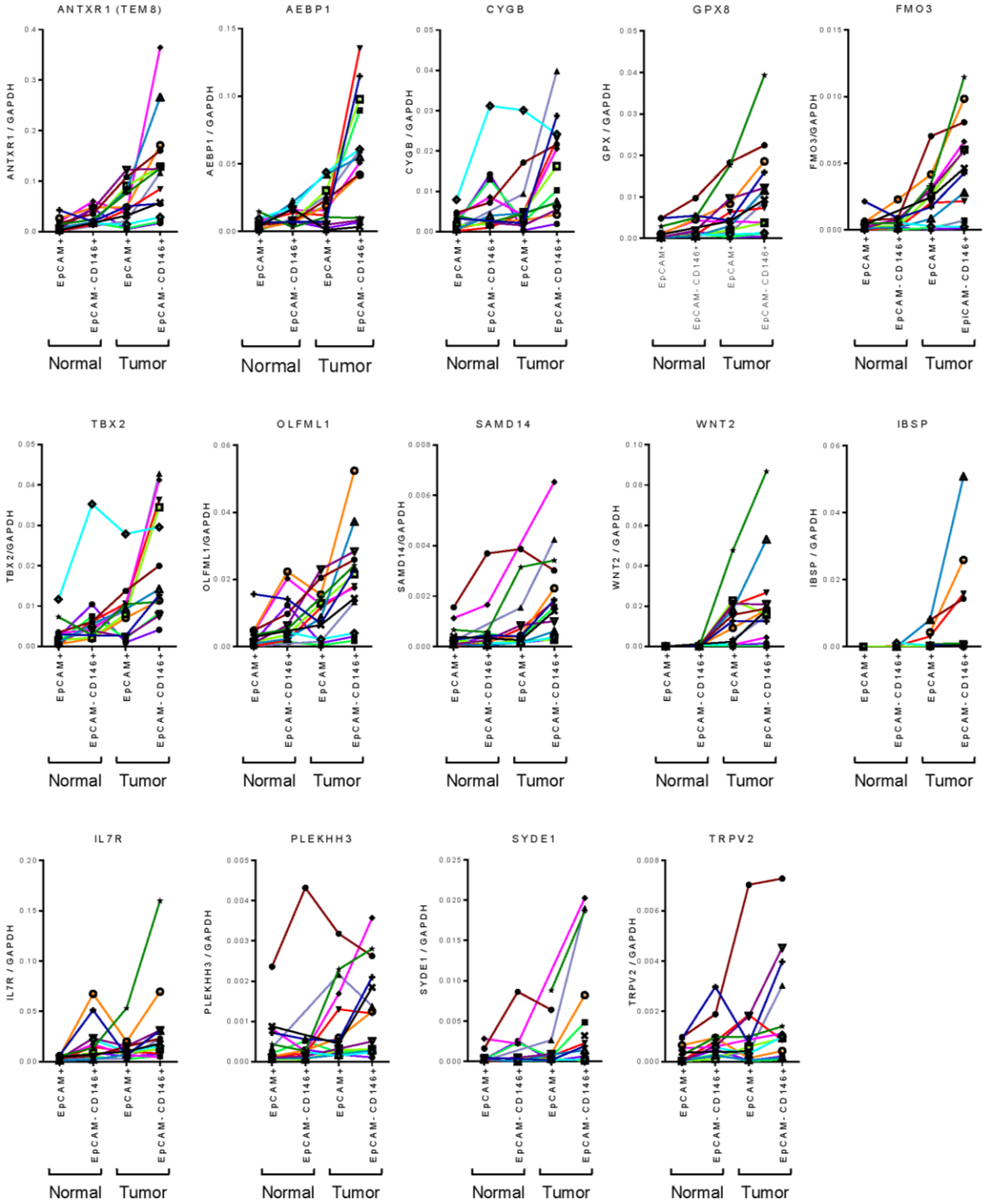
ANTXR1 (TEM8)
ANTXR1 / GAPDH
AEBP1
AEBP1 / GAPDH
CYGB
CYGB / GAPDH
GPX8
GPX / GAPDH
FMO3
FMO3/GAPDH
TBX2
TBX2/GAPDH
OLFML1
OLFML1/GAPDH
SAMD14
SAMD14/GAPDH
WNT2
WNT2 /GAPDH
IBSP
IBSP / GAPDH
IL7R
IL7R /GAPDH
PLEKHH3
PLEKHH3 / GAPDH
SYDE1
SYDE1 / GAPDH
TRPV2
TRPV2 / GAPDH
EpCAM+
EpCAM- CD146+
Normal
Tumor

Figure S2

TaqMan assays validating the RNA-seq results. Shown are relative expression levels of the indicated genes in epithelial (EpCAM+) and endothelial (EpCAM-, CD146) cells isolated from normal and tumor tissues. Each line represents specimens from a single patient. Expression levels are normalized to *GAPDH* expression.

Figure S3

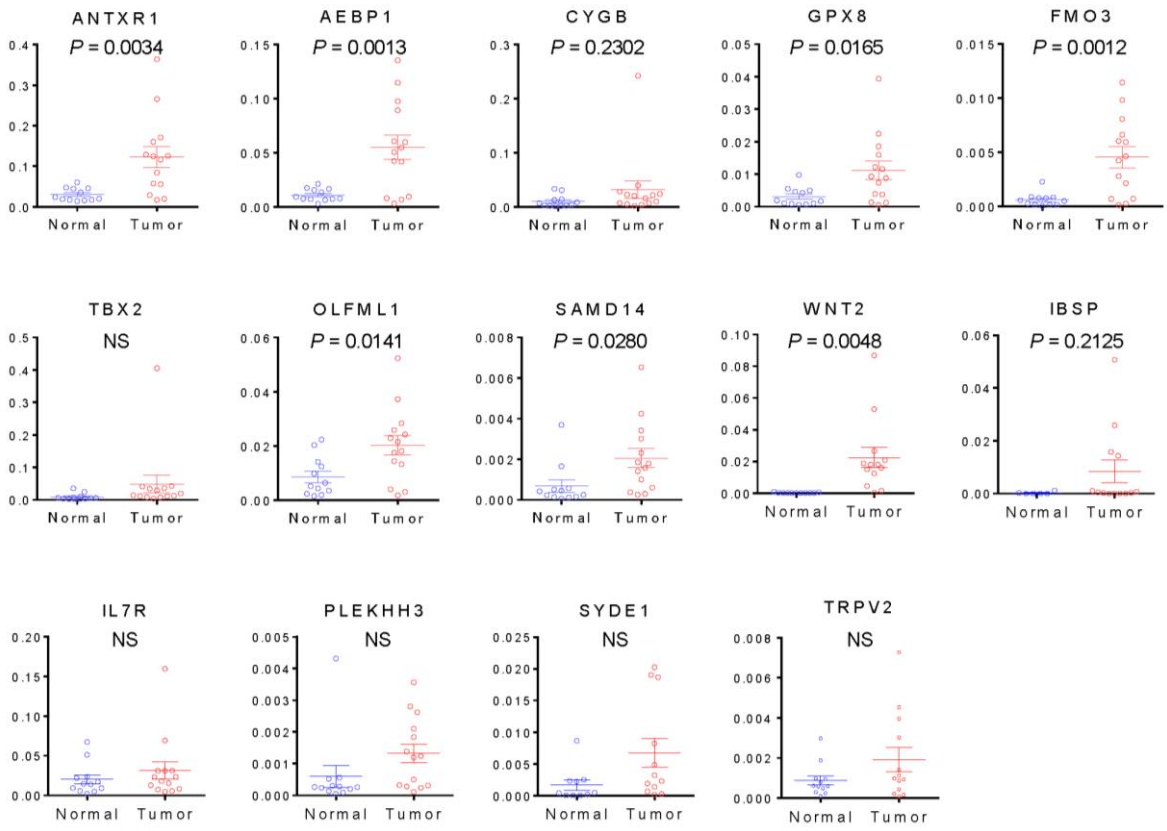

Figure S3

TaqMan assays validating the RNA-seq results. Assay results using endothelial cells were selected from Figure S2. Shown are relative expression levels of the indicated genes in endothelial cells isolated from normal (n = 12) and tumor tissues (n = 14). Expression levels are normalized to *GAPDH* expression. NS, not significant.

Figure S4

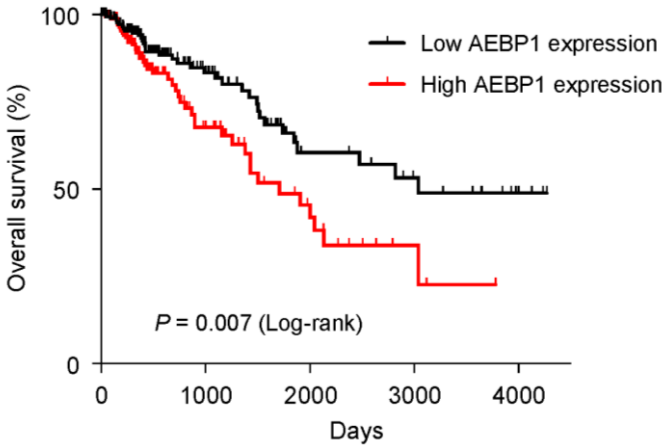

Figure S4

Kaplan-Meier curves showing the effect of *AEBP1* expression on overall survival of CRC patients in TCGA dataset (n = 411).

Figure S5

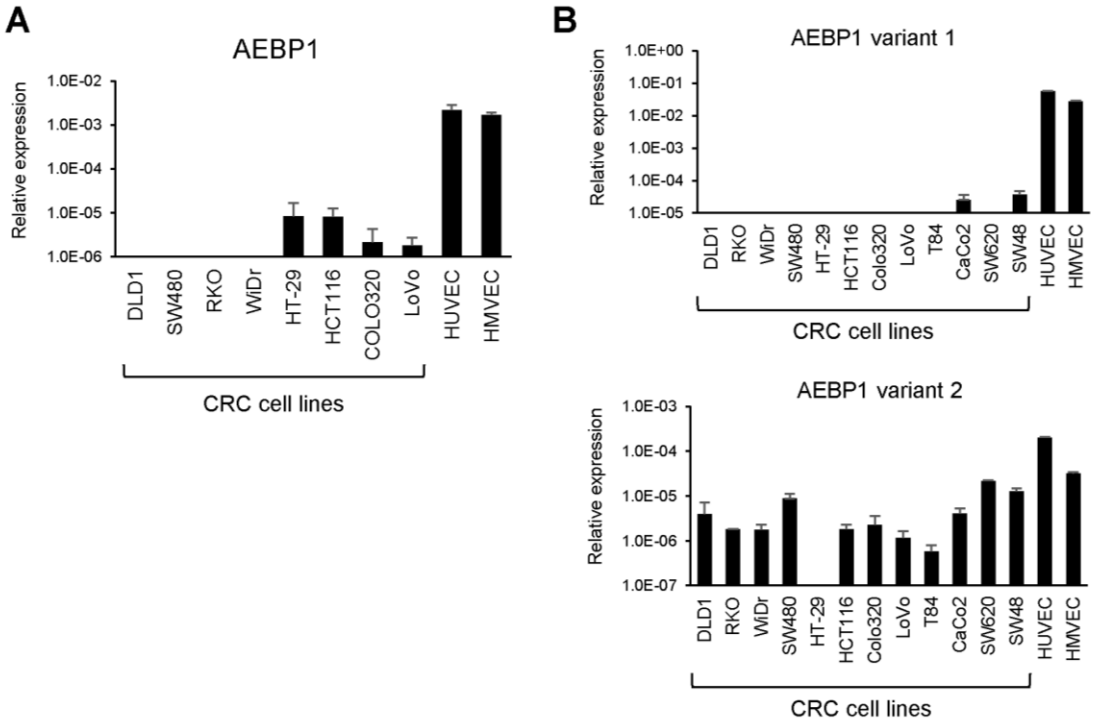

Figure S5

(A) TaqMan assays of *AEBP1* in CRC cell lines and endothelial cells. Results are normalized to *GAPDH* expression. Shown are means of 3 replications; error bars depict standard errors of the mean (SEMs). (B) qRT-PCR analysis of AEBP1 variants in CRC cell lines and endothelial cells. Results are normalized to *ACTB* expression. Shown are means of 3 replications; error bars depict SEMs.

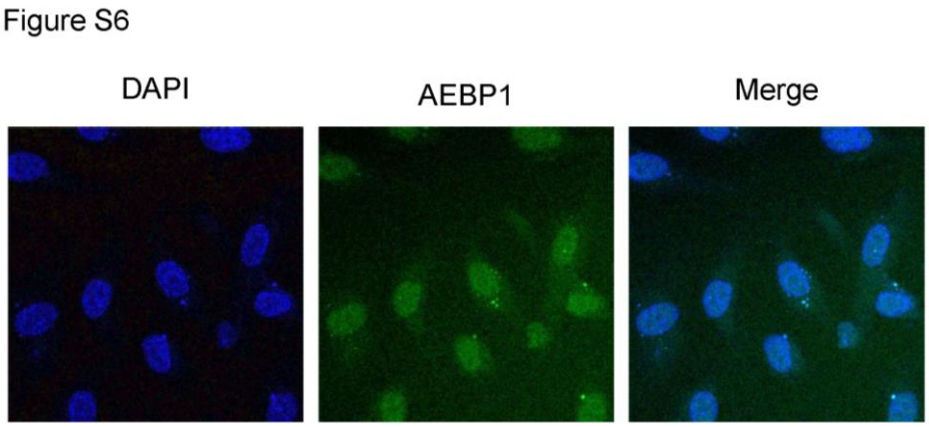

Figure S6

Fluorescent immunostaining of AEBP1 in HUVECs.

Figure S7

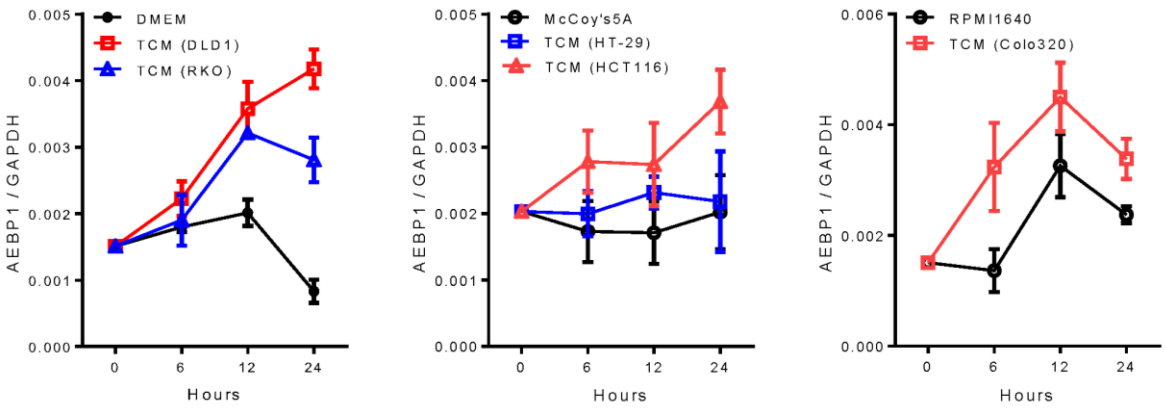

Figure S7

Induction of *AEBP1* in HUVECs treated with tumor-conditioned medium (TCM). Shown are relative expression levels of *AEBP1* in HUVECs treated with control medium or TCM derived from the indicated CRC cell lines. Expression levels are normalized to *GAPDH* expression. Symbols depict means of 3 replications; error bars depict SEMs.

Figure S8

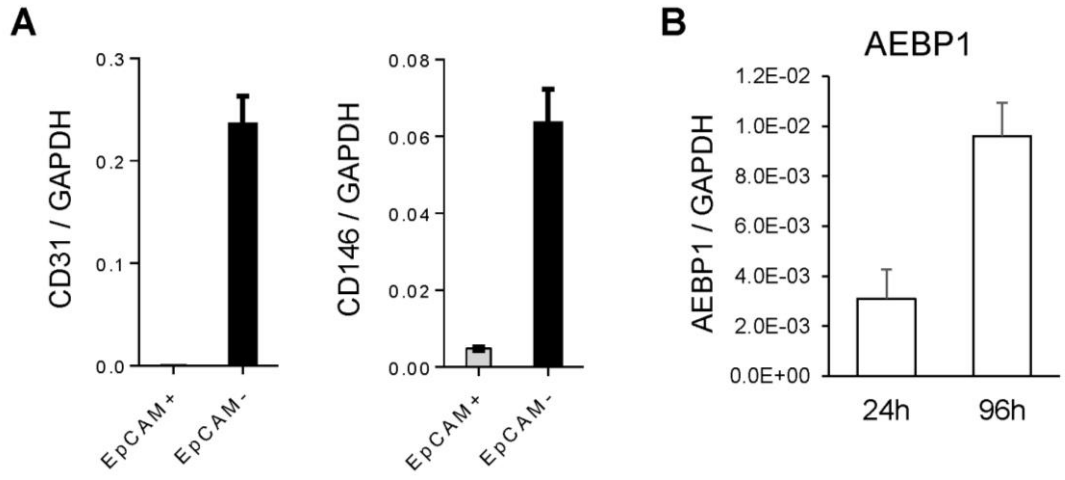

Figure S8

Induction of *AEBP1* in HUVECs co-cultured with CRC cells. HUVECs (1×10^6) and DLD1 cells (2.5×10^5) were co-cultured in EGM-2 medium for 24 or 96 h, after which EpCAM-positive (DLD1) and EpCAM-negative (HUVECs) cells were isolated. (A) Isolation of DLD1 and HUVECs was confirmed by TaqMan assays of CD31 and CD146 in the EpCAM-positive and -negative fractions. Expression levels are normalized to *GAPDH* expression. Shown are means of 3 replications, error bars depict SEMs. (B) TaqMan assays of *AEBP1* in HUVECs co-cultured with DLD1 for 24 h or 96 h. Expression levels are normalized to *GAPDH* expression. Shown are means of 3 replications; error bars depict SEMs.

Figure S9

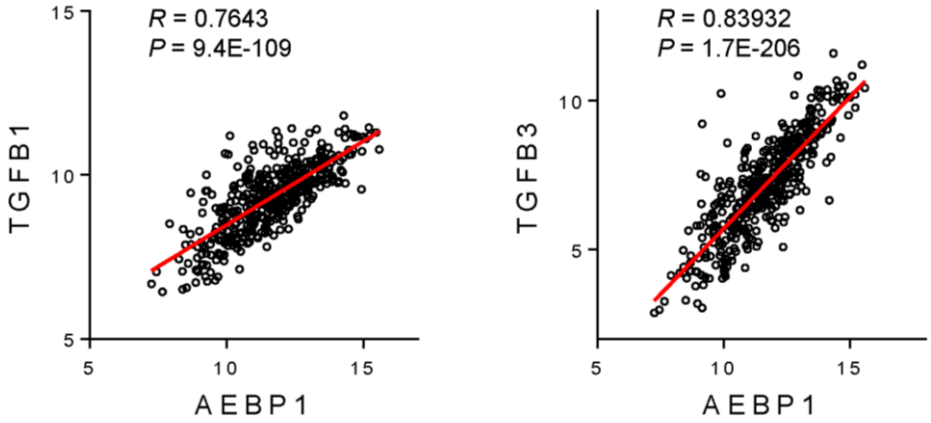

Figure S9

Correlations between expression levels of *AEBP1* and those of *TGFB1* or *TGFB3* in primary CRC in a dataset from TCGA. Pearson's correlation coefficients and *P* values are shown.

Figure S10

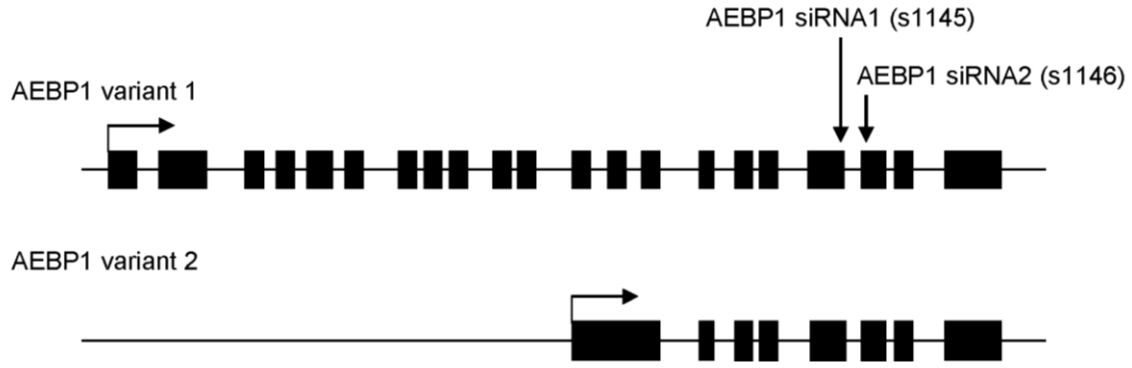

Figure S10

Locations of the target sites of the *AEBP1* siRNAs used in this study.

Figure S11

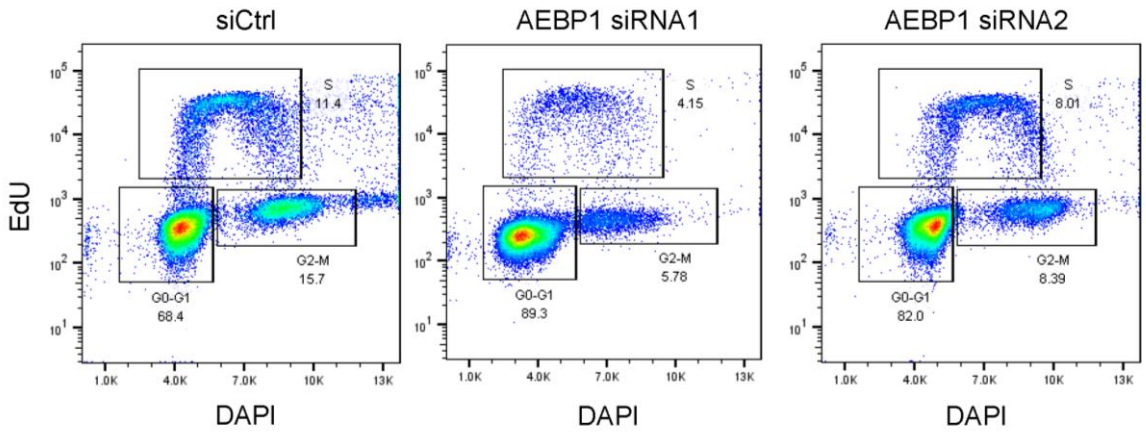

Figure S11

Effects of *AEBP1* knockdown on the cell cycle in HUVECs. Shown are representative results from a cell cycle analysis of HUVECs transfected with the indicated siRNAs.

Figure S12

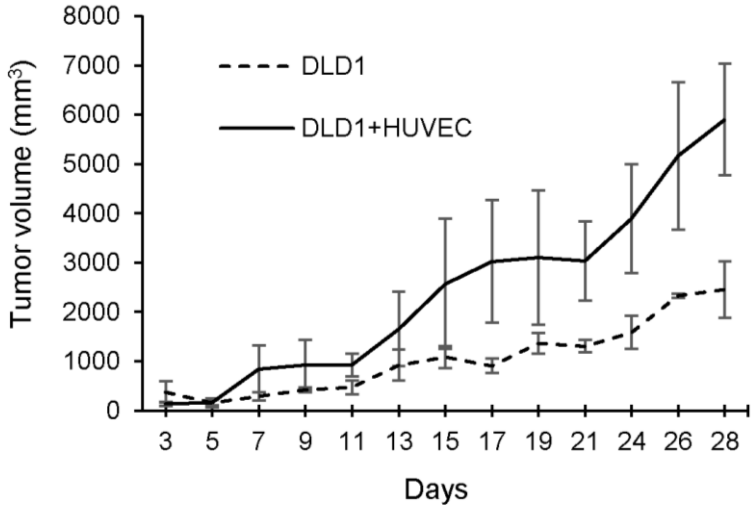

Figure S12

HUVECs promote xenograft formation by CRC cells. Mice were injected with DLD1 cells alone or with DLD1 cells plus HUVECs, after which growth of tumor xenografts were analyzed at the indicated times. Shown are means of 3 replications; error bars depict SEMs.