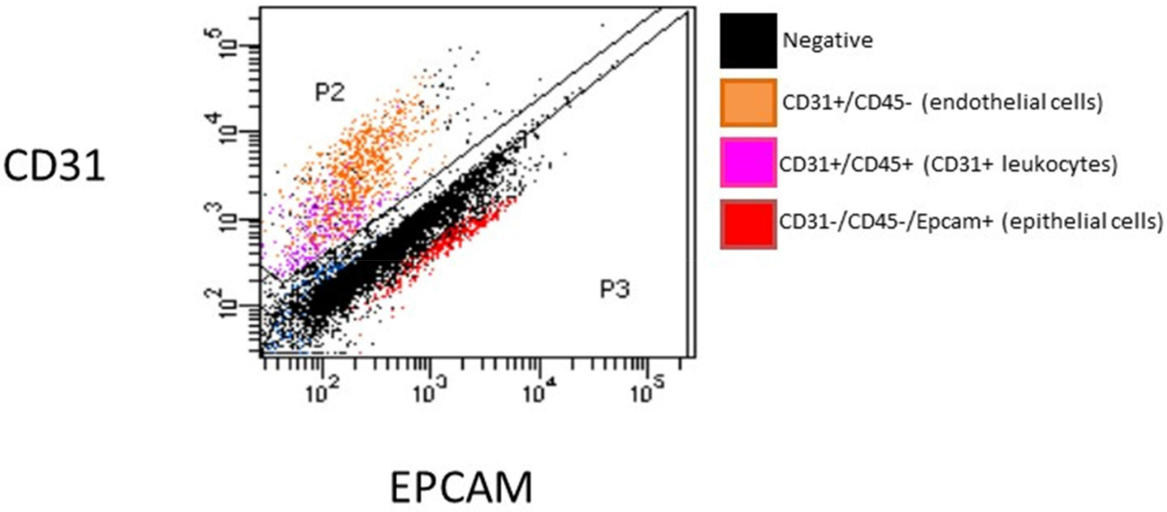
Apelin: A putative novel predictive biomarker for bevacizumab response in colorectal cancer

SUPPLEMENTARY MATERIALS

SUPPLEMENTARY FIGURE AND TABLES



Supplementary Figure 1: FACS plot showing different populations that were separated during sort procedure. EPCAM (Fitc) and CD31 (PE) are indicated on the x- and y-axis, respectively. The endothelial cells are depicted in orange, which were separated from CD31+ leukocytes (pink) based on CD45 expression. Epithelial cells (EPCAM+CD45-) are depicted in red and the black cloud mainly indicates autofluorescent cells.

Supplementary Table 1: Gene sets used to execute GSEA

GSEA data sets used for comparison	explanation
All 50 HALLMARK gene sets	Specific well-defined biological states or processes
BIOCARTA_VEGF_PATHWAY	Biocarta VEGF pathway gene set
ABE_VEGFA_TARGETS	Gene sets published by Abe et al, which reflects genes most profoundly induced in HUVEC cells by VEGFA treatment for max. 24 hours
ABE_VEGFA_TARGETS_30MIN	Gene sets published by Abe et al, which reflect genes most profoundly induced in HUVEC cells by VEGFA treatment for max 30 min.
ABE_VEGFA_TARGETS_2HRS	Gene sets published by Abe et al, which reflect genes upregulated in HUVEC cells by 2 hour VEGFA treatment
VEGF_A_UP_V1_UP	Gene sets published by Schoenfeld et al, which are the 200 most upregulated genes in HUVEC cells by treatment with VEGFA
VEGF_A_UP_V1_DN	Gene sets published by Schoenfeld et al, which are the 200 most downregulated genes in HUVEC cells by treatment with VEGFA

Supplementary Table 2: Top-10 "Hallmark gene sets" of GSEA

NAME	SIZE	NES	FDR q-val	RANK AT MAX	LEADING EDGE
HALLMARK_DNA_REPAIR	143	1.49	0.13	3662	Tags=41%, list=19%, signal=51%
HALLMARK_EPITHELIAL_ MESENCHYMAL_TRANSITION	199	1.46	0.14	2097	Tags=43%, list=11%, signal=48%
HALLMARK_ANGIOGENESIS	36	1.49	0.15	3089	Tags=58%, list=16%, signal=70%
HALLMARK_TGF_BETA_SIGNALING	54	1.46	0.15	3744	Tags=54%, list=20%, signal=67%
HALLMARK_COAGULATION	135	1.44	0.16	1130	Tags=30%, list=6%, signal=32%
HALLMARK_APICAL_SURFACE	44	1.42	0.16	2226	Tags=32%, list=12%, signal=36%
HALLMARK_MYC_TARGETS_V1	198	1.49	0.18	4180	Tags=61%, list=22%, signal=77%
HALLMARK_G2M_CHECKPOINT	200	1.39	0.20	3922	Tags=52%, list=21%, signal=65%
HALLMARK_MITOTIC_SPINDLE	199	1.50	0.23	2871	Tags=37%, list=15%, signal=43%
HALLMARK_E2F_TARGETS	198	1.36	0.23	3938	Tags=51%, list=21%, signal=64%

The top-10 gene sets are ranked on FDR. "Name" indicates the biological states or process represented by the gene set, "size" shows the number of genes included in the gene set, NES is the nominal enrichment score, FDR q-val is the *p*-value corrected for false discovery, "rank at max" means the position in the ranked list at which the maximum enrichment score occurred and the "leading edge" informs about the percentage of gene hits (tags) or genes in the ranked list (list) before the peak in the running enrichment score as well as the enrichment strength (signal).