Supplementary Table S1

| Features | No. of CRC patients (%) | No. of HC individuals (%) |
|---------------|-------------------------------|---------------------------------|
| Age (years) | | |
| <50 | 16 (36) | 10 (33) |
| ≥50 | 29 (64) | 20 (67) |
| Gender | | |
| Male | 36 (80) | 22 (73) |
| Female | 9 (20) | 8 (27) |
| Position | | |
| Colon | 18 (40) | |
| Rectal | 27 (60) | |
| Tumor size | | |
| <2 cm | 19 (42) | |
| ≥2 cm | 26 (58) | |
| LNM | | |
| Metastasis | 18 (40) | |
| No metastasis | 27 (60) | |
| Tumor stage | | |
| I+II | 28 (62) | |
| III | 17 (38) | |

Supplementary Table S1. The clinicopathological characteristics of CRC patients

Abbreviations: CRC, Colorectal cancer; HC, Healthy controls; LNM, Lymph node metastasis



Supplementary Figure S1. Diagnostic value of the expression of six candidate circRNAs. ROC curves were used to compare the diagnostic accuracy of each circRNA in discriminating CRC patients from healthy individuals. ROC curve was also generated to assess the combined analysis of six circRNAs, aiming to discriminate between CRC patients and healthy individuals.



Supplementary Figure S2. Transfer of circ_0084043 was determined by qRT-PCR in HUVECs incubated with both CAF Exo (100 μ g/ml) and α -amanitin (Sigma, 50 μ g/ml) compared to α -amanitin only treated cells (Neg. control) at time points 0, 12 and 24 h. Columns represent means of three different experiments, and bars represent standard deviation (SD). * *p*-value < 0.05, ** *p*-value < 0.01.



Supplementary Figure S3. *In silico* analysis. A. Circinteractome was used to predict miRNAs with binding potential to circ_0084043. B. CancerMIRNome was used to evaluate if the expression of miR-140 is changed in CRC or not. The gene expression analysis using CancerMIRNome suggested low expression of miR-140-3p in CRC patients.



Supplementary Figure S4. The transcript expression of HIF-1 α decreased when HUVECs were transfected with the miR-140-3p mimic, suggesting an inhibitory effect of this miRNA on HIF-1 α expression. Columns represent means of three different experiments, and bars represent standard deviation (SD). ** *p*-value < 0.01.

Supplementary Figs. S5-10





Supplementary Figure S5. Western blots raw data. The full-length blots of Calnexin and CD9.



Supplementary Figure S8. Western blots raw data. The full-length blots of VEGF and β -actin.



β-actin

Supplementary Figure S6. Western blots raw data. The full-length blots of VEGF and β -actin.



Supplementary Figure S9. Western blots raw data. The full-length blots of VEGF and β -actin.



P-VEGFR2

Supplementary Figure S7. Western blots raw data. The full-length blots of p-VEGFR2 and $\beta\text{-}$ actin.

