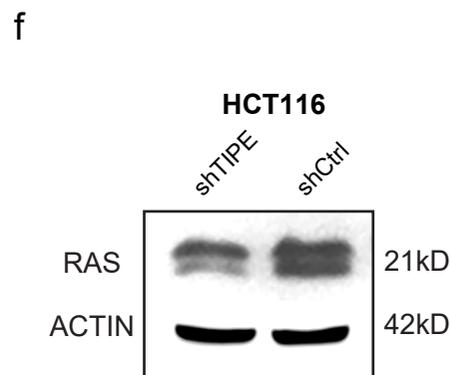
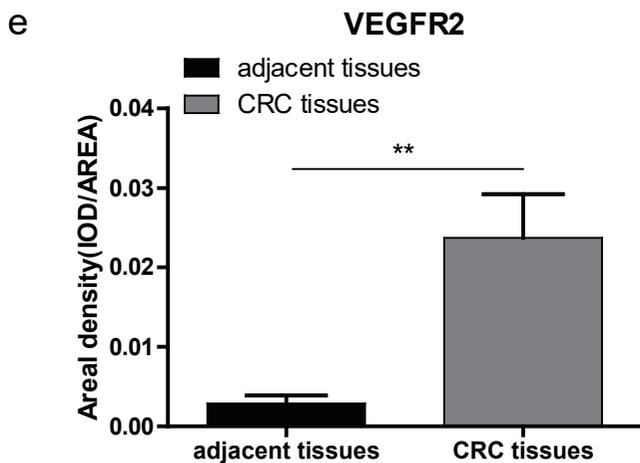
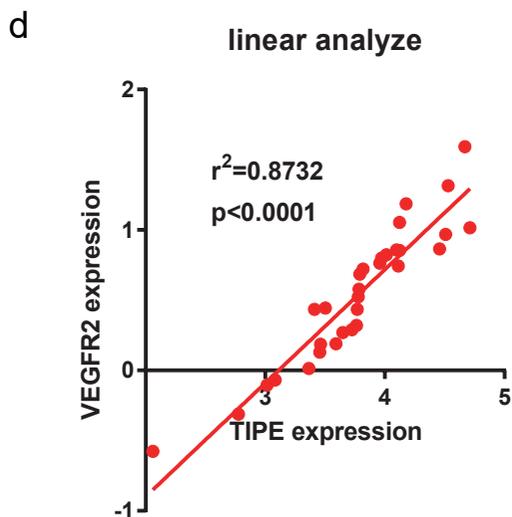
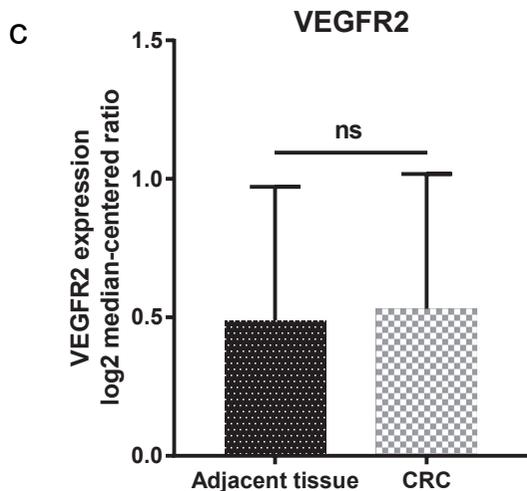
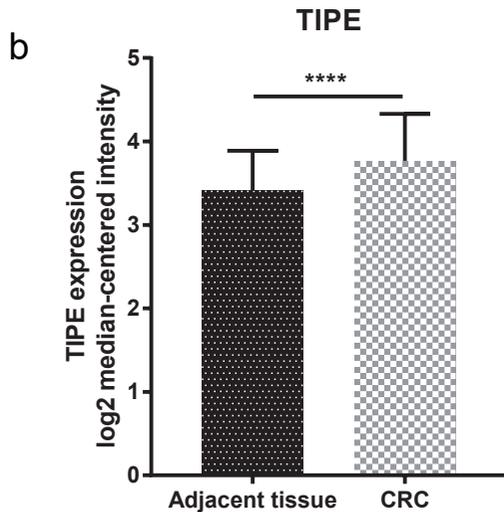
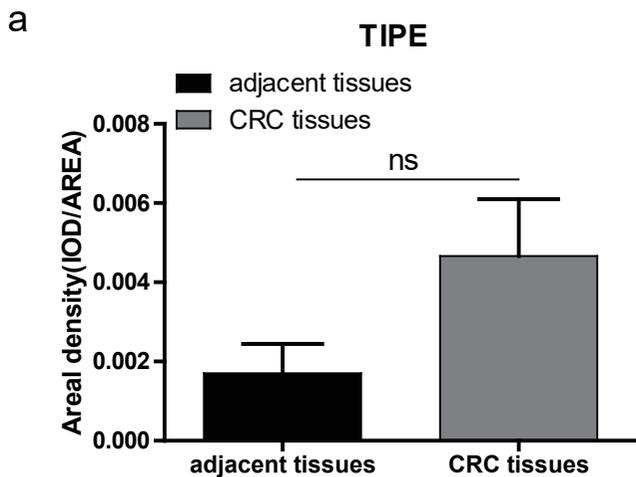


Supplementary Material

Supplementary Figure 1. Histograms demonstrate mRNA upregulation in CRC samples relative to that in normal samples (data downloaded from Oncomine). **(a)** The immunohistochemical density of TIPE expression as assessed by statistical analysis. **(b)** Relative TIPE mRNA expression in Sabates-Bellver datasets, which include 32 matched pairs of colorectal carcinoma and normal colon samples. **(c)** Detection of relative VEGFR2 mRNA expression in the same database. **(d)** The linear analysis relationship was positively correlated. **(e)** The immunohistochemical density of VEGFR2 expression as assessed by statistical analysis. **(f)** The expression levels of RAS in shTIPE and shRNA control HCT116 cells were determined by Western blot analysis. ns: no significance, **p <0.01, ****p<0.0001.

Supplementary Table 1. Difference between TIPE and VEGFR2 overexpression in colorectal cancer.



Supplementary Table 1. Difference between TIPE and VEGFR2 overexpression in colorectal cancer.

| | | TIPE | | sum |
|---------------|-----|-------------|----|-----|
| | | + | - | |
| VEGFR2 | + | 24 | 7 | 31 |
| | - | 5 | 19 | 24 |
| | sum | 29 | 26 | 55 |

$$\chi^2 = 17.3773, P < 0.001$$