## **SUPPLEMENTARY INFORMATION**

Parameter		Number (%)
Age	<65.8	28 (35)
ngc .	≥65.8	52 (65)
Gender	female	30 (38)
	male	50 (63)
	right colon (right colon and transverse)	34 (43)
Tumor site	left colon (left colon and sigmoid colon)	29 (36)
	rectum	13 (16)
	unknown	1 (1)
Grading	G1	4 (5)
	G2	60 (75)
	G3	9 (11)
	undefined	7 (9)
Progression (RECIST CRITERIA)	Not Progressed	35 (44)
	Progressed	45 (56)
Overall Survival	Alive	30 (38)
Overall July1901	Dead	50 (63)
	Complete Response	9 (11)
	Partial Response	18 (23)
Best Response (RECIST CRITERIA)	Stable disease	31 (39)
	Progression	16 (20)
	Unknown	6 (7)
	Wild type	26 (32)
KRAS status	Mutated	47 (59)
	undefined	7 (9)

**Table S1. Distribution of clinicopathological and molecular characteristics.** Absolute values and percentages are indicated. All the clinical data were collected by medical oncologists of the hospitals involved in the study.

MARKER	NEGATIVE/INACTIVE SAMPLE	POSITIVE/ACTIVE SAMPLE	References	
hERG1	0-49%	0-49% ≥50%		
B1-Integrin	0-49%	6 ≥50% N/A		
рАКТ	0-10%	≥10%	N/A	
NFkB	0-100% cytoplasm 0% nucleus	1-100% nucleus	N/A	
HIF-1α	0-100% cytoplasm 0% nucleus	1-100% nucleus	N/A	
HIF-2α	0-100% cytoplasm 0% nucleus	1-100% nucleus N/A		
p53	0-10%	>10%	Lastraioli et al, 2012	
VEGF-A	0-10%	>10% Lastraioli et al, 2012		
GLUT-1	0-10%	>10%	Lastraioli et al, 2012	
CA-IX	0-10%	>10%	Lastraioli et al, 2012	

**Table S2**. Scoring system. The applied scoring system for each marker is reported, it is indicated the percentage and/or the localization of labelled tumour cells.

	Log-Rank test	Comparison	Pr>Chi	Hazard Ratio	95% Wald
	Pr>Chi square		square		Confidence
hERG1-pAKT	0.032	+- VS	0.023	0.277	0.092-0.835
		++ vs	0.012	0.259	0.100-0.702
hERG1-NFkB	0.021	+- VS	0.015	0.347	0.149-0.807
		++ vs	0.001	0.270	0.112-0.649
hERG1-HIF-1α	0.011	+- VS	0.022	0.305	0.113-0.819
		++ vs	0.013	0.297	0.114-0.769
hERG1-HIF-2α	0.012	++ vs	0.001	0.235	0.090-0.613
hERG1-VEGF-A	0.001	++ vs	0.044	0.358	0.135-0.947
KRAS-hERG1	0.008	-+ VS +-	0.021	0.310	0.113-0-850
		++ VS +-	0.001	0.210	0.080-0.551

**Table S3. PFS analysis of combined markers expression**. Only statistically significant results are reported in the table. Negative/inactive marker is indicated with – and positive/active marker with +. For *KRAS* status, - indicates Wild type *KRAS* and + identifies mutated *KRAS* samples.

	Number In	P Value
hERG1	0	0.002
HIF-2α	1	0.219
GLUT-1	2	0.265
KRAS status	3	0.238
NFkB	4	0.365
β1-Integrin	5	0.481
HIF-1α	6	0.527
рАКТ	7	0.547
VEGF-A	8	0.718
p53	9	0.838
CA-IX	10	0.974

**Table S4. Multivariate PFS analysis.** Significant P values are in bold. A) Multivariate PFS analysis with all markers of proangiogenic pathway and *KRAS* status. Multivariate analysis was performed as described in Materials and Methods section. P values of Log Rank test, Median PFS: 11.2 months. Significant P values are in bold and underlined.

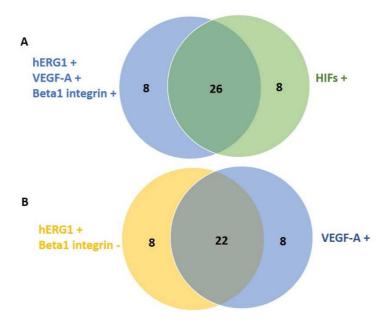


Figure S1. Venn diagram showing the distribution and overlapping of some of the markers evaluated in the patients enrolled in the study. A) Patients expressing hERG1,  $\beta$ 1-integrin and VEGF-A (34/80) were positive also for aHIF-1 $\alpha$  and/or aHIF-2 $\alpha$  (26/34). B) 30/80 samples were positive for hERG1 and negative for  $\beta$ 1-Integrin, 22/30 of them were positive also for VEGF-A.

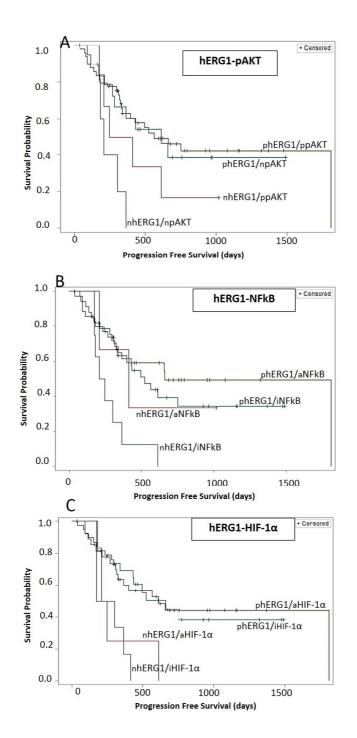


Figure S2. Kaplan-Meier curves of significant progression free survival obtained from the risk analysis with combined markers. A) hERG1 and pAKT combination; B) hERG1 and NFkB; C) hERG1 and HIF-1 $\alpha$ . Combinations are defined as follows: 00: hERG1 negative- other marker negative/inactive; 01: hERG1 negative- other marker positive/active; 10: hERG1 positive-other marker negative/inactive; 11: both hERG1 and other marker positive/active. Number of patients: hERG1 and pAKT (00: 5, 10: 20); (00: 5, 11: 49); hERG1 and NFkB (00: 8, 10: 34); (00: 8, 11: 35); hERG1 and HIF-1 $\alpha$  (00: 6, 10: 27); (00: 6, 11: 39). Only statistically significant curves are reported. "n": Negative samples; "p": positive samples; "a": samples with active protein; "I": samples with inactive protein.