		Genes		
ABL1	EGFR	GNAS	MLH1	RET
AKT1	ERBB2	HNF1A	MPL	SMAD4
ALK	ERBB4	HRAS	NOTCH1	SMARCB1
APC	FBXW7	IDH1	NPM1	SMO
ATM	FGFR1	JAK2	NRAS	SRC
BRAF	FGFR2	JAK3	PDGFRA	STK11
CDH1	FGFR3	KDR	РІКЗСА	<i>TP53</i>
CDKN2A	FLT3	KIT	PTEN	VHL
CSF1R	GNA11	KRAS	PTPN1	
CTNNB1	GNAQ	MET	RB1	

Table S1. Cancer-related genes represented in the TruSeq Amplicon Cancer Panel (Illumina)

Gene mutation	Samples	%	Samples with	%	<i>P</i> -value
	with gene		gene		
	mutation:		mutation:		
	Colon		Rectum		
	(n=51)		(n=34)		
ABL1	4	7.8	0	0.0	0.15
$AKT1^{1}$	1	2.0	1	2.9	1.00
ALK	2	3.9	1	2.9	1.00
APC^{l}	24	47.1	20	58.8	0.37
ATM	4	7.8	3	8.8	1.00
ATM, C110RF65	39	76.5	25	73.5	0.80
$BRAF^{l}$	16	31.4	1	2.9	0.0016
CSF1R	1	2.0	0	0.0	1.00
$CTNNB1^{1}$	4	7.8	1	2.9	0.65
$EGFR^{1}$	3	5.9	3	8.8	1.00
ERBB2	0	0.0	1	2.9	1.00
ERBB4	5	9.8	1	2.9	0.39
$FBXW7^{1}$	7	13.7	5	14.7	1.00
FGFR1	8	15.7	9	26.5	0.27
FGFR3	10	19.6	3	8.8	0.23
FLT3	47	92.2	33	97.1	0.64
GNA11	7	13.7	8	23.5	0.26
GNAQ	40	78.4	26	76.5	1.00
GNAS	1	2.0	1	2.9	1.00
HNF1A	7	13.7	7	20.6	0.55
HRAS	4	7.8	1	2.9	0.64
JAK3	1	2.0	2	5.9	1.00
KDR	51	100.0	34	100.0	-
KIT	47	92.2	32	94.1	1.00
KRAS ¹	14	27.5	11	32.4	0.64
MET ¹	2	3.9	2	5.9	1.00
Chr22 rs35893428 ²	27	52.9	13	38.2	0.26
Chr2 rs1059524 ²	19	37.3	17	50.0	1.00
Chr7 rs3735146 ²	1	2.0	2	5.9	1.00
NPM1	1	2.0	0	0.0	1.00
NRAS ¹	1	2.0	2	5.9	1.00
PIK3CA ¹	47	92.2	30	88.2	0.70
$PTEN^{1}$	29	56.9	19	55.9	1.00
RB1	11	21.6	8	23.5	1.00
RET	1	2.0	2	5.9	1.00
SMO	49	96.1	32	94.1	1.00
$TP53^{1}$	51	100.0	34	100.0	-
VHL	3	5.9	2	5.9	1.00

Table S2. Distribution of gene mutations in the studied population, stratified according to tumor location; colon or rectum

¹CRC-associated gene as defined by the gene panel ²No gene assigned

Gene mutation	Samples with gene mutation: Poor differentiation	%	Samples with gene mutation: Moderate/well differentiation	%	<i>P</i> -value
	(n=20)		(n=65)		
ABL1	3	15.0	1	1.5	0.039
$AKT1^{1}$	1	5.0	1	1.5	0.42
ALK	1	5.0	2	3.1	0.56
APC^{I}	5	25.0	39	60.0	0.01
ATM	2	10.0	5	7.7	0.67
ATM, C110RF65	14	70.0	50	76.9	0.56
$BRAF^{I}$	13	65.0	4	6.2	< 0.0001
CSF1R	0	0.0	1	1.5	1.00
CTNNB1 ¹	0	0.0	5	7.7	0.33
$EGFR^{1}$	1	5.0	5	7.7	1.00
ERBB2	0	0.0	1	1.5	1.00
ERBB4	2	10.0	4	6.2	0.62
$FBXW7^{1}$	3	15.0	9	13.8	1.00
FGFR1	6	30.0	11	16.9	0.21
FGFR3	5	25.0	8	12.3	0.17
FLT3	18	90.0	62	95.4	0.59
GNA11	3	15.0	12	18.5	1.00
GNAQ	16	80.0	50	76.9	1.00
GNAS	2	10.0	0	0.0	1.00
HNF1A	4	20.0	10	15.4	0.73
HRAS	3	15.0	2	3.1	0.08
JAK3	1	5.0	2	3.1	0.56
KDR	20	100.0	65	100.0	-
KIT	18	90.0	61	93.8	0.62
KRAS ¹	2	10.0	23	35.4	0.047
MET^{1}	0	0.0	4	6.2	0.57
Chr22 rs35893428 ²	9	45.0	31	47.7	1.00
Chr2 rs1059524 ²	10	50.0	25	38.5	0.30
Chr7 rs3735146 ²	0	0.0	3	4.6	1.00
NPM1	1	5.0	0	0.0	0.24
NRAS ¹	1	5.0	2	3.1	0.56
PIK3CA ¹	16	80.0	61	93.8	0.08
$PTEN^{1}$	14	70.0	34	52.3	0.20
RB1	3	15.0	16	24.6	0.54
RET	0	0.0	3	4.6	1.00
SMO	19	95.0	62	95.4	1.00
$TP53^{1}$	20	100.0	65	100.0	-
VHL	1	5.0	4	6.2	1.00

Table S3. Distribution of gene mutations in the studied population, stratified according to tumor differentiation grade; poor differentiation or moderate/well differentiation grade

¹CRC-associated gene as defined by the gene panel

²No gene assigned

Gene mutation	Samples	%	Samples	%	<i>P</i> -	Total	%
	with gene		with gene		value	number	
	mutation:		mutation:			of	
	Cancer		No cancer			samples	
	recurrence		recurrence			with gene	
	(n=12)		(n=73)			mutation	
ABL1	0	0.0	4	5.5	1.00	4	4.7
$AKT1^{1}$	0	0.0	2	2.7	1.00	2	2.4
ALK	2	16.7	1	1.4	1.00	3	3.5
APC^{l}	7	58.3	37	50.7	0.76	44	51.8
ATM	2	16.7	5	6.8	0.26	7	8.2
ATM, C110RF65	5	41.7	59	80.8	0.007	64	75.3
$BRAF^{1}$	4	33.3	13	17.8	0.25	17	20.0
CSF1R	0	0.0	1	1.4	1.00	1	1.2
CTNNB1 ¹	1	8.3	4	5.5	0.54	5	5.9
$EGFR^{1}$	0	0.0	6	8.2	0.59	6	7.1
ERBB2	0	0.0	1	1.4	1.00	1	1.2
ERBB4	0	0.0	6	8.2	0.59	6	7.1
$FBXW7^{1}$	1	8.3	11	15.1	1.00	12	14.1
FGFR1	4	33.3	13	17.8	0.24	17	20.0
FGFR3	1	8.3	12	16.4	0.68	13	15.3
FLT3	11	91.7	69	94.5	0.54	80	94.1
GNA11	2	16.7	13	17.8	1.00	15	17.6
GNAQ	8	66.7	58	79.5	0.45	66	77.6
GNAS	0	0.0	2	2.7	1.00	2	2.4
HNF1A	2	16.7	12	16.4	1.00	14	16.5
HRAS	2	16.7	3	4.1	0.14	5	5.9
JAK3	0	0.0	3	4.1	1.00	3	3.5
KDR	12	100.0	73	100.0	-	85	100.0
KIT	12	100.0	67	91.8	0.59	79	92.9
KRAS ¹	3	25.0	22	30.1	1.00	25	29.4
MET'	0	0.0	4	5.5	1.00	4	4.7
Chr22 rs35893428 ²	5	41.7	35	47.9	0.76	40	47.1
Chr2 rs1059524 ²	7	58.3	29	39.7	0.34	36	42.4
Chr7 rs3735146 ²	0	0.0	3	4.1	1.00	3	3.5
NPM1	0	0.0	1	1.4	1.00	1	1.2
NRAS	0	0.0	3	4.1	1.00	3	3.5
PIK3CA ¹	10	83.3	67	91.8	0.31	77	90.6
$PTEN^{I}$	4	33.3	44	60.3	0.12	48	56.5
RB1	4	33.3	15	20.5	0.45	19	22.4
RET	0	0.0	3	4.1	1.00	3	3.5
SMO	12	100.0	69	94.5	1.00	81	95.3
$TP53^{1}$	12	100.0	73	100.0	-	85	100.0
VHL	0	0.0	5	6.8	1.00	5	5.9

Table S4. Distribution of gene mutations in the studied population, stratified according to cancer
 recurrence at follow-up

¹Classified as CRC-associated gene according to the gene panel ²No gene assigned

Gene mutation	HR (95% CI)	HR P-value
APC^{1}	1.63 (0.39 - 6.84)	0.50
ATM, C110RF65	0.31 (0.08 - 1.25)	0.10
$BRAF^{I}$	1.57 (0.32 - 7.80)	0.58
$CTNNB1^{1,3}$	2.68 (0.33 - 21.96)	0.36
$FBXW7^{1}$	0.79(0.10-6.41)	0.82
FGFR1	2.23(0.53 - 9.32)	0.27
FGFR3	0.87 (0.11 - 7.10)	0.90
GNA11	0.58(0.07 - 4.79)	0.61
GNAQ	0.48 (0.11 – 1.99)	0.31
$HNF1A^4$	-	-
$HRAS^{3}$	5.78 (1.17 – 28.71)	0.031
KRAS ¹	1.48 (0.35 - 6.19)	0.59
Chr22 rs35893428 ²	1.13 (0.28 – 4.53)	0.86
Chr2 rs1059524 ²	2.34 (0.56 - 9.81)	0.24
PIK3CA ¹	0.72(0.09 - 5.84)	0.76
$PTEN^{1}$	0.49 (0.12 - 2.04)	0.32
RB1	3.36 (0.84 - 13.46)	0.09
APC or CTNNB1 ¹	1.37 (0.33 – 5.76)	0.67
KRAS, BRAF, NRAS ¹	1.60 (0.38 - 6.69)	0.52
KRAS, BRAF, NRAS, APC^{1}	2.48 (0.30 - 20.18)	0.40

Table S5. Association between cancer specific survival and gene mutation status, described in terms of hazard ratios, HR

Genes with mutation present in at least ten patients were included in the analysis. ¹Classified as CRCassociated gene according to the gene panel, ²No gene assigned, ³Five patients with gene mutation, *CTNNB1* included based on its involvement in the Wnt signaling pathway, *HRAS* based on the significant result, although few patients with gene mutation, ⁴HNF1A; no gene mutation detected in uncensored patients. HR; hazard ratio, CI; confidence interval. **Table S6a.** Association between recurrence free survival and the total number of gene mutations and total mutation count per patient, expressed in terms of hazard ratios

	HR	95% CI	<i>P</i> -value
Gene mutation CRC	0.77	0.49 - 1.20	0.25
Gene mutation (tot)	0.83	0.63 - 1.09	0.18
Mutation count CRC	0.96	0.68 - 1.34	0.80
Mutation count (tot)	0.91	0.76 - 1.09	0.32

HR; hazard ratio, CI; confidence interval, CRC; colorectal cancer

Table S6b. Logistic regression analysis for the association of the number of gene mutations and mutation count with poor tumor differentiation grade

	OR: Poor	95% CI	<i>P</i> -value
	differentiation		
Gene mutation CRC	0.86	0.57 - 1.30	0.47
Gene mutation (tot)	1.05	0.81 - 1.36	0.71
Mutation count CRC	0.84	0.61 - 1.15	0.28
Mutation count (tot)	1.00	0.84 - 1.18	0.96

OR; odds ratio, CI; confidence interval, CRC; colorectal cancer

Table S6c. Logistic regression analysis for the association of the number of gene mutations and mutation count with the risk of colon cancer compared with rectal cancer

	OR: Colon cancer	95% CI	<i>P</i> -value
Gene mutation CRC	1.09	0.76 - 1.56	0.64
Gene mutation (tot)	1.01	0.81 - 1.27	0.91
Mutation count CRC	1.06	0.81 - 1.38	0.67
Mutation count (tot)	1.03	0.89 - 1.19	0.71

OR; odds ratio, CI; confidence interval, CRC; colorectal cancer