

**Table S1.** Characteristics of the *KRAS* assays used by ddPCR.

Gene	Assay ID	COSMIC ID	Expected variant	
			AA mutation	CDS mutation
<i>KRAS</i>	dHsaMDV2010001	COSM521	p.G12D	c.35G>A
	dHsaMDV2510588	COSM517	p.G12S	c.34G>A
	dHsaMDV2510598	COSM532	p.G13D	c.38G>A

AA, aminoacid; CDS, coding sequence.

**Table S2.** List of genes analyzed in DNA by the TST170 panel.

<b>SNVs and Indels</b>									
<i>AKT1</i>	<i>BRIP1</i>	<i>CREBBP</i>	<i>FANCI</i>	<i>FGFR2</i>	<i>JAK3</i>	<i>MSH3</i>	<i>PALB2</i>	<i>RAD51D</i>	<i>TSC1</i>
<i>AKT2</i>	<i>BTK</i>	<i>CSF1R</i>	<i>FANCL</i>	<i>FGFR3</i>	<i>KDR</i>	<i>MSH6</i>	<i>PDGFRA</i>	<i>RAD54L</i>	<i>TSC2</i>
<i>AKT3</i>	<i>CARD11</i>	<i>CTNNB1</i>	<i>FBXW7</i>	<i>FGFR4</i>	<i>KIT</i>	<i>MTOR</i>	<i>PDGFRB</i>	<i>RB1</i>	<i>VHL</i>
<i>ALK</i>	<i>CCND1</i>	<i>DDR2</i>	<i>FGF1</i>	<i>FLT1</i>	<i>KMT2A</i>	<i>MUTYH</i>	<i>PIK3CA</i>	<i>RET</i>	<i>XRCC2</i>
<i>APC</i>	<i>CCND2</i>	<i>DNMT3A</i>	<i>FGF10</i>	<i>FLT3</i>	<i>KRAS</i>	<i>MYC</i>	<i>PIK3CB</i>	<i>RICTOR</i>	<i>TSC1</i>
<i>AR</i>	<i>CCNE1</i>	<i>EGFR</i>	<i>FGF14</i>	<i>FOXL2</i>	<i>MAP2K1</i>	<i>MYCL1</i>	<i>PIK3CD</i>	<i>ROS1</i>	<i>TSC2</i>
<i>ARID1A</i>	<i>CD79A</i>	<i>EP300</i>	<i>FGF2</i>	<i>GEN1</i>	<i>MAP2K2</i>	<i>MYCN</i>	<i>PIK3CG</i>	<i>RPS6KB1</i>	
<i>ATM</i>	<i>CD79B</i>	<i>ERBB2</i>	<i>FGF23</i>	<i>GNA11</i>	<i>MCL1</i>	<i>MYD88</i>	<i>PIK3R1</i>	<i>SLX4</i>	
<i>ATR</i>	<i>CDH1</i>	<i>ERBB3</i>	<i>FGF3</i>	<i>GNAQ</i>	<i>MDM2</i>	<i>NBN</i>	<i>PMS2</i>	<i>SMAD4</i>	
<i>BAP1</i>	<i>CDK12</i>	<i>ERBB4</i>	<i>FGF4</i>	<i>GNAS</i>	<i>MDM4</i>	<i>NF1</i>	<i>PPP2R2A</i>	<i>SMARCB1</i>	
<i>BARD1</i>	<i>CDK4</i>	<i>ERCC1</i>	<i>FGF5</i>	<i>HNF1A</i>	<i>MET</i>	<i>NOTCH1</i>	<i>PTCH1</i>	<i>SMO</i>	
<i>BCL2</i>	<i>CDK6</i>	<i>ERCC2</i>	<i>FGF6</i>	<i>HRAS</i>	<i>MLH1</i>	<i>NOTCH2</i>	<i>PTEN</i>	<i>SRC</i>	
<i>BCL6</i>	<i>CDKN2A</i>	<i>ERG</i>	<i>FGF7</i>	<i>IDH1</i>	<i>MLLT3</i>	<i>NOTCH3</i>	<i>PTPN11</i>	<i>STK11</i>	
<i>BRAF</i>	<i>CEBPA</i>	<i>ESR1</i>	<i>FGF8</i>	<i>IDH2</i>	<i>MPL</i>	<i>NPM1</i>	<i>RAD51</i>	<i>TERT</i>	
<i>BRCA1</i>	<i>CHEK1</i>	<i>EZH2</i>	<i>FGF9</i>	<i>INPP4B</i>	<i>MRE11A</i>	<i>NRAS</i>	<i>RAD51B</i>	<i>TET2</i>	
<i>BRCA2</i>	<i>CHEK2</i>	<i>FAM175A</i>	<i>FGFR1</i>	<i>JAK2</i>	<i>MSH2</i>	<i>NRG1</i>	<i>RAD51C</i>	<i>TP53</i>	
<b>CNVs</b>									
<i>AKT2</i>	<i>BRCA2</i>	<i>CHEK1</i>	<i>ERCC2</i>	<i>FGF2</i>	<i>FGF7</i>	<i>FGFR4</i>	<i>MDM4</i>	<i>NRG1</i>	<i>RAF1</i>
<i>ALK</i>	<i>CCND1</i>	<i>CHEK2</i>	<i>ESR1</i>	<i>FGF23</i>	<i>FGF8</i>	<i>JAK2</i>	<i>MET</i>	<i>PDGFRA</i>	<i>RET</i>
<i>AR</i>	<i>CCND3</i>	<i>EGFR</i>	<i>FGF1</i>	<i>FGF3</i>	<i>FGF9</i>	<i>KIT</i>	<i>MYC</i>	<i>PDGFRB</i>	<i>RICTOR</i>
<i>ATM</i>	<i>CCNE1</i>	<i>ERBB2</i>	<i>FGF10</i>	<i>FGF4</i>	<i>FGFR1</i>	<i>KRAS</i>	<i>MYCL1</i>	<i>PIK3CA</i>	<i>RPS6KB1</i>
<i>BRAF</i>	<i>CDK4</i>	<i>ERBB3</i>	<i>FGF14</i>	<i>FGF5</i>	<i>FGFR2</i>	<i>LAMP1</i>	<i>MYCN</i>	<i>PIK3CB</i>	<i>TFRC</i>
<i>BRCA1</i>	<i>CDK6</i>	<i>ERCC1</i>	<i>FGF19</i>	<i>FGF6</i>	<i>FGFR3</i>	<i>MDM2</i>	<i>NRAS</i>	<i>PTEN</i>	

SNVs, single nucleotide variants; indels, insertion/deletion; CNVs, copy number variants.

**Table S3.** Quantity of cfDNA used for TST170 assay.

Sample ID	cfDNA (ng)
CRC032	40
CRC035	50
CRC062	100
CRC095	35
CRC100	40
CRC106	35
CRC112	100
CRC116	100
CRC131	100
CRC133	100
CRC137	40
CRC142	40
CRC145	35
CRC152	40
CRC154	40
CRC158	40
CRC160	40
CRC164	40
CRC168	40

**Table S4.** Tumor location of mCRC patients included in the study.

Sample ID	Primary tumor location	Metastasis location				Tissue biopsy location
		Liver	Lung	Peritoneal	Lymph Node	
CRC032	Right Colon	Yes	No	No	No	Primary
CRC035	Right Colon	No	No	Yes	No	Primary
CRC062	Left Colon/rectum	Yes	Yes	No	No	Primary
CRC095	Left Colon/rectum	Yes	Yes	No	No	Primary
CRC100	Right Colon	No	Yes	Yes	Yes	Metastasis (lymph node)
CRC106	Right Colon	No	Yes	No	Yes	Primary
CRC112	Right Colon	Yes	No	No	No	Unknown
CRC116	Left Colon/rectum	Yes	No	No	No	Primary
CRC131	Left Colon/rectum	Yes	Yes	No	No	Primary
CRC133	Right Colon	Yes	No	No	No	Unknown
CRC137	Left Colon/rectum	No	No	Yes	No	Primary
CRC142	Left Colon/rectum	No	Yes	No	Yes	Metastasis (lung)
CRC145	Left Colon/rectum	No	No	Yes	No	Unknown
CRC152	Left Colon/rectum	No	Yes	No	Yes	Primary
CRC154	Left Colon/rectum	Yes	Yes	No	No	Primary
CRC158	Left Colon/rectum	Yes	Yes	No	No	Primary
CRC160	Left Colon/rectum	No	No	No	Yes	Primary
CRC164	Right Colon	No	Yes	Yes	Yes	Primary
CRC168	Right Colon	Yes	No	No	Yes	Primary

**Table S5. Analysis of variants in the reference standard cfDNA by TST170.**

Gene	Variant type	Expected variant	Expected VAF (%)	Detected variant		Detected VAF (%)	
				40 ng DNA	100 ng DNA	40 ng DNA	100 ng DNA
<i>GNA11</i>	SNV	p.Q209L	5.6	p.Q209L		5.5	4.6
<i>AKT1</i>	SNV	p.E17K	5.0	p.E17K		4.2	3.6
<i>PIK3CA</i>	SNV	p.E545K	5.6	p.E545K		5.0	4.3
<i>EGFR</i>	Indel	p.V769_D770insASV	5.6	p.V769_D770insASV		2.9	2.8
<i>EGFR</i>	Indel	p.E746_A750	5.3	p.E746_A750		4.4	4.1
<i>MET</i>	CNV	Amplification	4.5*	Amplification		1.8*	1.8*
<i>MYCN</i>	CNV	Amplification	9.5*	Amplification		4.0*	3.6*

\*Fold change; SNV, single nucleotide variant; Indel, insertion/deletion; CNV, copy number variant; VAF, variant allele fraction; ng, nanograms.

**Table S6.** List of genes with variants (frameshift, inframe, missense, stop gain) detected in cfDNA of mCRC patients by TST170.

[illegible]

									<i>ROS1</i>
									<i>SMAD4</i>
									<i>TET2</i>
									<i>TP53</i>
									<i>TSC2</i>

CRC, colorectal cancer patient.

**Table S7.** List of genes with variants (frameshift, inframe, missense, stop gain) detected in cfDNA of mCRC patients by TST170.

CRC137	CRC142	CRC145	CRC152	CRC154	CRC158	CRC160	CRC164	CRC168
FAM175A	FAM175A	FAM175A	FAM175A	FAM175A	ALK	ALK	FAM175A	FAM175A
ALK	ALK	ALK	ALK	ALK	APC	APC	ALK	AKT2
APC	APC	APC	APC	APC	ARID1A	ATM	APC	ALK
AR	ATM	AR	ARID1A	ATM	ATM	ATR	AR	APC
ATM	ATR	ARID1A	ATM	ATR	ATR	BARD1	ATM	AR
ATR	BARD1	ATM	ATR	BARD1	BARD1	BRCA1	ATR	ATM
BARD1	BCL6	ATR	BARD1	BCL6	BRCA2	BRCA2	BARD1	ATR
BRCA1	BRCA1	BARD1	BRCA1	BRCA1	BRIP1	BRIP1	BRCA2	BARD1
BRCA2	BRCA2	BRCA1	BRCA2	BRCA2	CCNE1	CDKN2A	CHEK1	BRCA1
CCNE1	BRIP1	BRCA2	BRIP1	BRIP1	CD79A	CHEK1	EP300	BRCA2
CHEK1	CHEK1	BRIP1	CHEK1	CARD11	CDK12	EP300	ERBB2	CEBPA
DNMT3A	DNMT3A	CARD11	EP300	CEBPA	CHEK1	ERBB2	ERBB3	CHEK1
ERBB2	ERBB2	CHEK1	ERBB2	CHEK1	CSF1R	FANCI	ERCC2	CSF1R
ERCC2	ERCC2	DDR2	FANCI	CSF1R	DDR2	FGFR4	FANCI	EGFR
FANCI	FANCI	EP300	FGF23	EGFR	DNMT3A	FLT3	FGF23	ERBB2
FGF6	FGF2	ERBB2	FGFR4	ERBB2	EP300	FOXL2	FGFR4	FGF1
FGFR4	FGFR4	FANCI	FLT3	ERBB4	ERBB2	GEN1	FLT3	FGF23
FLT3	FLT3	FGF6	GEN1	ERCC2	ERCC2	HNF1A	GEN1	FGF6
GEN1	GEN1	FGFR4	GNAS	FANCI	EZH2	KDR	GNAS	FGFR4
KMT2A	HNF1A	FLT3	HNF1A	FGF6	FANCI	KRAS	HNF1A	FLT3
MET	JAK3	GEN1	KDR	FGFR4	FGF6	MLLT3	JAK2	GEN1
MLLT3	KDR	KDR	KIT	FLT3	FGFR4	MSH2	KDR	GNAS
MSH3	KIT	MAP2K2	KRAS	GEN1	FLT3	MSH3	KIT	HNF1A
MUTYH	MLH1	MLH1	MLLT3	HNF1A	GEN1	MSH6	KRAS	KDR
MYCL1	MSH3	MLLT3	MSH2	KDR	HNF1A	MUTYH	MLH1	KIT
NRG1	MUTYH	MSH2	MSH3	KIT	IDH1	MYCL1	MLLT3	KRAS
RAD51B	MYCL1	MSH3	MSH6	KMT2A	KRAS	NBN	MSH3	MLLT3
RAD51D	NOTCH3	MUTYH	MYCL1	KRAS	MLH1	NF1	MSH6	MRE11A
RAD54L	NRG1	MYCL1	NBN	MLLT3	MRE11A	NOTCH3	MYC	MSH3
RET	PALB2	NOTCH3	NF1	MRE11A	MSH3	NRG1	MYCL1	MSH6
RICTOR	PIK3CG	PIK3CG	NOTCH1	MSH3	MYCL1	PALB2	NBN	MUTYH
ROS1	PTCH1	PIK3R1	NOTCH2	MSH6	NBN	PDGFRB	NOTCH2	MYCL1
TET2	RAD51B	PTCH1	NOTCH3	MUTYH	NF1	PIK3CA	NOTCH3	NBN
TP53	RAD51D	RAD51B	NRG1	MYCL1	NOTCH3	PIK3R1	NRG1	NOTCH1
XRCC2	RET	RAD51D	PTCH1	NBN	NRG1	PTEN	PTCH1	NOTCH3
	RICTOR	TET2	PTEN	NOTCH3	PDGFRB	RET	PTEN	NRG1
	ROS1	TP53	RAD51D	NRG1	PIK3CA	RICTOR	RET	PIK3CA
	TET2	TSC1	RET	PALB2	PIK3R1	ROS1	RICTOR	PTCH1
	TP53		RICTOR	PIK3CG	PTCH1	TET2	ROS1	PTEN
	TSC1		SMAD4	PTCH1	PTEN	TP53	TET2	RET
	XRCC2		TET2	PTEN	RAD51D	XRCC2	TP53	RICTOR
			TP53	RICTOR	RET		TSC1	ROS1
			VHL	ROS1	RICTOR			SMAD4
				TET2	SLX4			TP53
				TP53	TET2			
				XRCC2	TP53			

CRC, colorectal cancer patient.



**Table S8.** CNVs detected in cfDNA of patient CRC100 by TST170

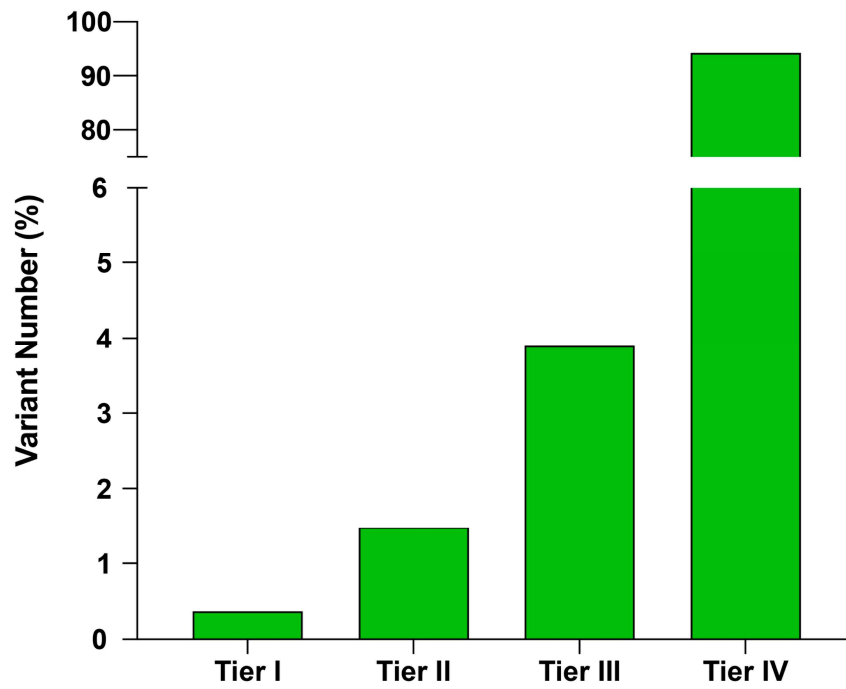
Gene	Variant type	Alteration	FC
<i>FGF6</i>	CNV	Amplification	4.59
<i>FGF23</i>	CNV	Amplification	4.93

FC, fold change; CNV, copy number variant.

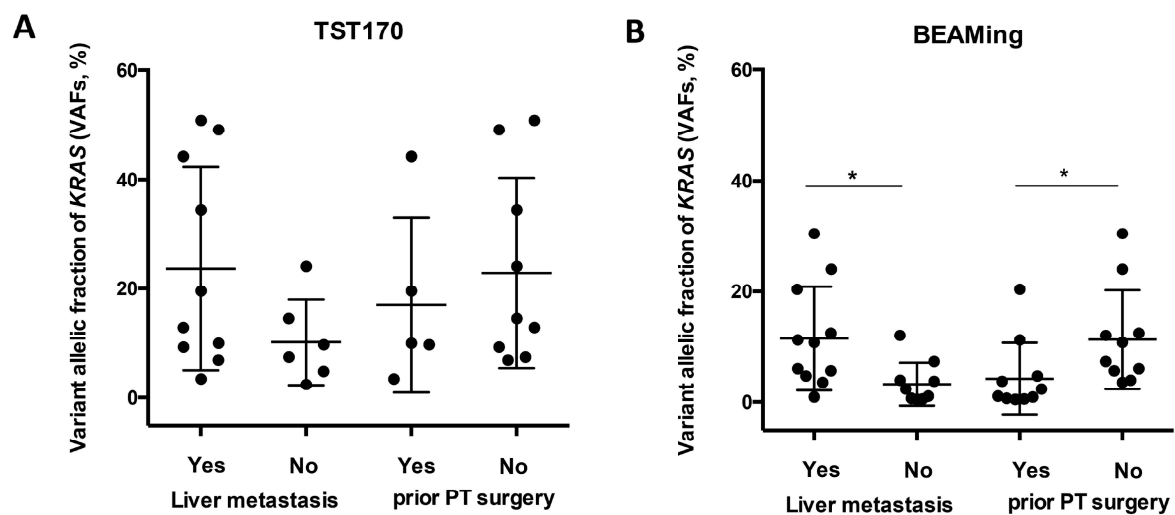
**Table S9.** *NRAS* status in cfDNA of mCRC patients analyzed by BEAMing and TST170.

Sample ID	<i>NRAS</i>	
	BEAMing	TST170
CRC032	WT	WT
CRC035	NA	WT
CRC062	NA	WT
CRC095	WT	WT
CRC100	WT	WT
CRC106	WT	WT
CRC112	NA	WT
CRC116	WT	WT
CRC131	WT	WT
CRC133	WT	WT
CRC137	WT	WT
CRC142	WT	WT
CRC145	WT	WT
CRC152	WT	WT
CRC154	WT	WT
CRC158	WT	WT
CRC160	WT	WT
CRC164	M	ND
	(VAF: 0.12%)	
CRC168	WT	WT

WT, wild type; M, Mutated; VAF, variant allele fraction; NA, not available.



**Figure S1.** Distribution of variants detected by TST170 in cfDNA of mCRC patients according to their clinical impact. Tier I, variants with strong clinical significance; tier II, variants with potential clinical significance; tier III, variants with unknown clinical significance; and tier IV, benign or likely benign variants.



**Figure S2.** Impact of KRAS VAFs detected by TST170 and BEAMing on patient clinical-pathological characteristics. (A) Levels of KRAS VAFs obtained with TST170 according to metastasis location and previous surgery of primary tumor (PT). (B) KRAS VAFs obtained by BEAMing according to metastasis location and previous surgery for primary tumor (PT). P-values were calculated using Student's t-test. \*p<0.05.