

Supplementary Materials: High Intra- and Inter-Tumoral Heterogeneity of RAS Mutations in Colorectal Cancer

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Case 18

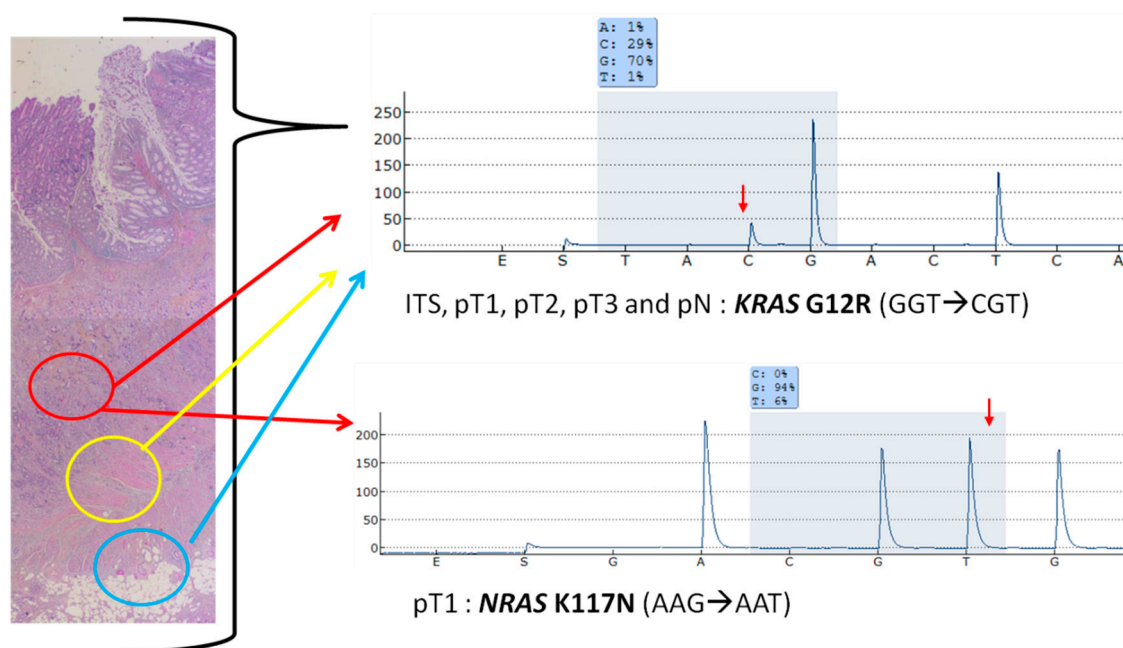


Figure S1. RAS subclones distribution for patient 18: Tumoral selection was performed according to pathological tumor node metastasis staging (pTNM) 2009 in submucosa (pT1, red arrow), in the muscular layer (pT2, yellow arrow) for pT2 tumors, selection in submucosa, in the muscular layer and in subserosa (pT3, blue arrow) for pT3 and pT4 tumors. Presence of *KRAS* MUT (p.G12R) in all selections and *NRAS* PLLM (potential low level mutation) (p.K117N) only in pT1.

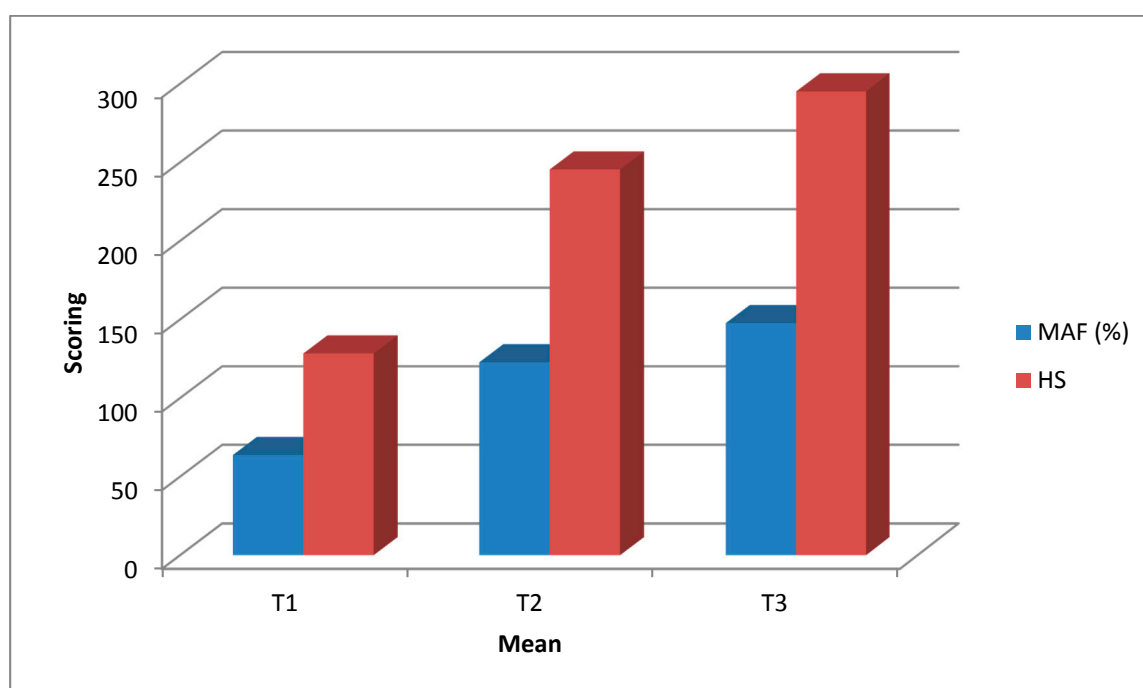


Figure S2. Mean heterogeneity score (HS) calculated from cases 7–9 and 13–18, which harbored the same mutation from pT1 to pT3 (Figure 1).

Table S1. Description of five colorectal cancers with WT mutational profile in the initial transperietal sections and spatially separated tumor areas.

	Patients	pTNM	%TC	KRAS	Other Genes
No Mutation	1	ITS	40	WT	WT
		pT1	90	WT	WT
		pT2	40	WT	WT
		pT3	30	WT	WT
		N	70	WT	WT
	3	ITS	80	WT	WT
		pT1	60	WT	WT
		pT2	40	WT	WT
		pT3	10	WT	WT
		N	5	WT	WT
	5	ITS	80	WT	WT
		pT1	90	WT	WT
		pT2	75	WT	WT
		pT3	25	WT	WT
	10	ITS	30	WT	WT
		pT1	20	WT	WT
		pT2	25	WT	WT
		pT3	30	WT	WT
		N	30	WT	WT
	6	ITS	90	WT	WT
		pT1	60	WT	WT
		pT2	30	WT	WT

%TC: percentage of tumoral cells; ITS: initial transperietal section; N: metastatic lymph node; WT: wild-type; pTNM: pathological tumor node metastasis staging.

Table S2. Sequences of primers for *BRAF* V600E mutation detection.

Nucleic Acid	Genomic	cDNA	Proteic	LOD	LOD + 3	Primers	Sequences	Dispensation Order	Sequence to Analyze
<i>BRAF</i> (V600E)						F	5'-Biotin-TTCATGAAGACCTCACAGTA-3'	TCGTATCTGTAG	CWCTGTAGC
GAG	g.140453136	c.1799T>A	p.V600E (Glu)	2.3	5.3	R	5'-CTTACCATCCACAAAATGGA-3'		
						S	5'-CCACTCCATCGAGATTT-3'		