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The original version of this Article contained errors in Table 1 where the data was listed incorrectly in the column 'M-*KRAS* patients'. The original Table 1 and accompanying legend appear below.

The original Article has been corrected.

Parameters (units)	Description	Typical values		Reference
		WT-*KRAS* patients	M-*KRAS* patients	
T_{s_0}(mm^2)	Baseline of T_s (clonal population that is sensitive to anti-EGFR inhibitor (D_1))	5500	100	Data/Estimated value; Mutation was assumed to be acquired during treatment
T_{R1_0}(mm^2)	Baseline of T_{R1} (clonal population that is resistance to D_1 but is sensitive to the second hypothetical treatment (D_2))	0	1700	Data/Estimated value; Mutation was assumed to be acquired during treatment
T_{R2_0}(mm^2)	Baseline of T_{R2} (clonal population that is resistance to both treatments)	0	0	Data/Estimated value; Mutation was assumed to be acquired during treatment
M_{ctDNA1_0}(fragments/ml)	Baseline of mutant *KRAS* (M_{ctDNA1}) in ctDNA	0	500	Data/Estimated value; Mutation was assumed to be acquired during treatment
M_{ctDNA2_0}(fragments/ml)	Baseline of a second hypothetical mutation (M_{ctDNA2}) in ctDNA	0	0	Data/Estimated value; Mutation was assumed to be acquired during treatment
k_{g1}(/week)	Growth rate constant of T_s	0.03		[40]
k_{g2}(/week)	Growth rate constant of T_{R1}	0.021		[43,44]
k_{g3}(/week)	Growth rate constant of T_{R2}	0.015		[43,44]
k_{s1}(/week)	Tumor shrinkage rate constant due to D_1	0.1		Estimated value
k_{s2}(/week)	Tumor shrinkage rate constant due to D_2	0.1		k_{s1}
k_{M1}(/week)	Mutation rate from T_s to T_{R1} when $D_1=1$	0.05		Estimated value
k_{M2}(/week)	Mutation rate from T_{R1} to T_s when $D_1=0$	0.03		Lower than k_{M1}[9]
k_{M3}(/week)	Mutation rate from T_{R1} to T_{R2} when $D_2=1$	0.05		k_{M1}
k_{M4}(/week)	Mutation rate from T_{R2} to T_{R1} when $D_2=0$	0.03		k_{M2}
H	Hill coefficient	5		Visually matching the slope of data and the detectable time of mutant *KRAS*
KT_{50}(mm^2)	The size of tumor that provide half-maximal shedding rate of ctDNA	3500		Visually matching the slope of data and the detectable time of mutant *KRAS*
k_{max_1}((fragments/ml)/(week*mm^2))	Maximum shedding rate of M_{ctDNA1}	0.015	1.5	Visually matching the slope of data and the detectable time of mutant *KRAS*
k_e(/week)	ctDNA eliminate rate constant	0.5		Visually matching the slope of data and the detectable time of mutant *KRAS*
k_{max_2}((fragments/ml)/(week*mm^2))	Maximum shedding rate of M_{ctDNA2}	0.015	1.5	k_{max_1}
IIV_ B (ω_1)	Standard deviation of IIV of baselines	0.6		Data
IIV_ k_g (ω_2)	Standard deviation of IIV of k_g	0.2		Data

Table 1. Parameters values of the developed model characterizing the dynamics of tumor size and mutation concentrations in metastatic colorectal cancer (mCRC) patients. ctDNA, circulating tumor DNA; IIV, interindividual variability; WT-KRAS patients, patients who were initially identifed as *KRAS* wild-type in ctDNA; M-KRAS patients, patients who had detectable mutant *KRAS* in ctDNA pre-treatment.