

Supplementary Information

Digital polymerase chain reaction for detecting *c-MYC* copy number gain in tissue and cell-free plasma samples of colorectal cancer patients

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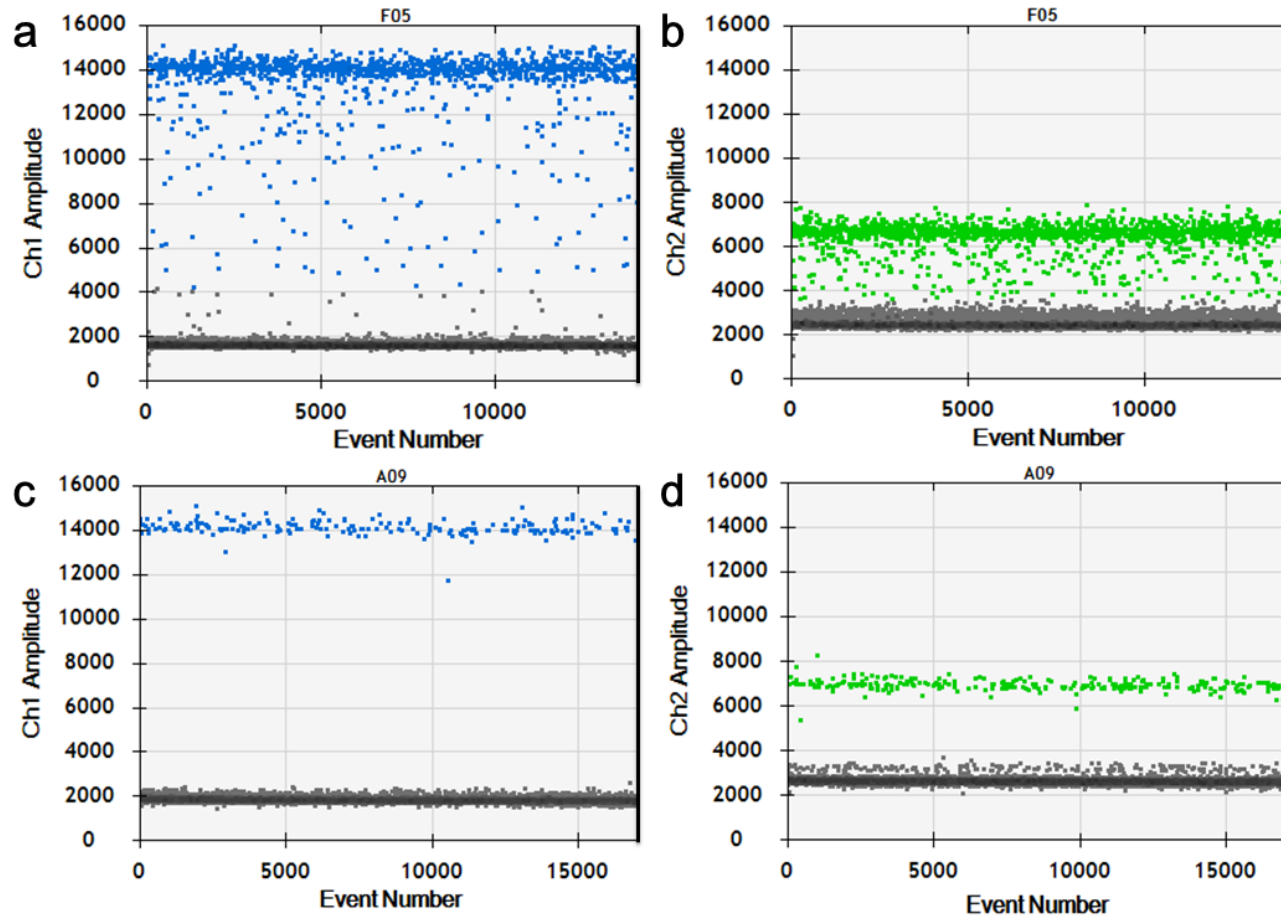
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Supplementary Table 1. The correlation between concordance of SISH and ddPCR result, and intratumoral genetic and regional heterogeneity in 64 CRC patients of cohort 2

		Concordance of SISH and tissue ddPCR result				Concordance of SISH and tissue plasma ddPCR result			
		Concordance	Discordance	Total	P value	Concordance	Discordance	Total	P value
Intratumoral genetic heterogeneity	Homogeneous	30 (46.9%)	5 (7.8%)	35 (54.7%)	0.139	28 (43.8%)	7 (10.9%)	35 (54.7%)	0.133
	Heterogeneous	28 (43.8%)	1 (1.6%)	29 (45.3%)		27 (42.2%)	2 (3.1%)	29 (45.3%)	
Regional (central and peripheral) heterogeneity	Homogeneous	50 (78.1%)	6 (9.4%)	56 (87.5%)	0.331	48 (75.0%)	8 (12.5%)	56 (87.5%)	0.892
	Heterogeneous	8 (12.5%)	0 (0%)	8 (12.5%)		7 (10.9%)	1 (1.6%)	8 (12.5%)	

p values are from the χ^2 or Fisher's exact test and were significant at less than 0.05.



Supplementary Figure 1. Experimental positive and negative ddPCR results according to Digital MIQE Guideline. (a) Tissue distinction between positive and negative partitions FAM(MYC). (b) Tissue distinction between positive and negative partitions HEX(EIF2C1). (c) Plasma distinction between positive and negative partitions FAM(MYC). (d) Plasma distinction between positive and negative partitions HEX(EIF2C1).