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Discovery Of Methylated Circulating DNA Biomarkers For Comprehensive Non-Invasive Monitoring Of Treatment Response In Metastatic Colorectal Cancer

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Contributions:

LB, AB, ASB and FDN participated in the design of the study. AA, AP, AC, ABi, CCr, SB, KB, PR, KBM, SS and ASB contributed to the collection and retrieval of clinical data of blood samples. AA, AC, AV, MT, SS and ASB contributed to the collection and retrieval of tissue samples. LB, AP, CF, CCr, AC, BM, GS and DO contributed to blood sample preparation and processing. LB, SMO, SMA, WG and ME contributed to the genome wide methylation experiments. PZ contributed to establishing the pipeline for in silico and wet validation of GRIA4. LB performed the bioinformatics analyses of the genome wide methylation experiments. LB, CF and DO performed methylation analyses in cfDNA samples. BM and GS performed genetic alteration analyses in cfDNA samples. LB, BM and GS interpreted the results in cfDNA. LB and FDN wrote the manuscript. All authors critically reviewed and commented the manuscript.