7DUJHWHG FDQFHU JHQH VHTXHQFLQJ LGHQWL¿HV SRWHQWL
carcinogenesis

Colorectal cancer is the second cause of death in the world and genomic alteration plays an important role in this disease Much of the underlying genetic cancer driver mutations in sporadic colorectal cancer (CRC) have not been characterized by race. Here, we report the identi□cation of distinct novel variants from CRC patients in mismatch repair (MMR) genes *MHS3* and *MSH6* and *APC*. We developed a panel of 20 frequently altered colon cancer genes for targeted sequencing in 138 colon tissues using next generation sequencing to examine 98.8% of the targeted exons and splice junctions at a depth sequencing that allowed for high con□dence variant calling. A□er alignment and variant calling, we annotated the variants with infor6T EMC /SparoSld g(n)4 (cPd t)-6CID 92 (e jo)11 (7 (lo)12 (h)3 , C j)9.OS4 (d MI4 (d C,cPd32a)9 (n)1 (uena)9 (

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