

Targeted molecular profiling of genetic alterations in colorectal cancer using next-generation sequencing

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Abstract. Colorectal cancer (CRC) is a major contributor to cancer-associated mortality in China and remains a vast challenge worldwide. Although the genetic basis of CRC has been investigated, the uncommonly mutated genes in CRC remain unknown, in particular in the Asian population. In the present study, targeted region sequencing on 22 CRC and 10 paired non-cancerous tissues was performed to determine the genetic pattern of CRC samples in the Chinese population. Driver genes were detected by three distinct softwares, including MutSigCV, oncodriveFM and iCAGES. A total of 1,335 reliable somatic mutations were identified in tumour samples compared with normal samples. Furthermore, mismatch repair (MMR) mutant patients presented significantly higher mutation density compared with MMR wild-type patients. The results from MutSigCV, oncodriveFM and iCAGES analyses simultaneously detected 29 unique driver genes. In addition, the genes *APC* regulator of WNT signaling pathway, *SMAD* family member 4, neurofibromin 1, AT-rich interaction domain 5B and nuclear receptor corepressor 1 were the top five most frequently mutated genes in CRC samples, with mutation rates of 68, 36, 36, 32 and 27%, respectively. The findings from the present study may therefore serve as a basis for future investigation on the diagnosis and oncogenesis of CRC.

Introduction

Colorectal cancer (CRC) is the fourth most frequently diagnosed cancer and the second leading cause of cancer-associated mortality worldwide according to the global cancer statistics from 2018 (1). In the United States, approximately 135,430 new cases are diagnosed each year and approximately 50,260 patients die of CRC, which accounts for approximately 9% of all cancer-associated mortalities (2). In 2015, CRC was considered as the fifth most common type of cancer in terms of occurrence and mortality in China (3). Cancer stage is a major factor contributing to the overall survival of patients with CRC. The 3-year survival rate is 80-90% for patients with CRC who are diagnosed with stages I or II, whereas the 3-year survival rate is reduced to 20% for patients with CRC diagnosed with stage IV (4).

Over the past decade, large-scale sequencing studies have investigated the genetic basis of CRC and uncovered key pathways involved in the pathogenesis of CRC, including WNT, RAS-MAPK, PI3K, TGF- β , P53 and DNA mismatch repair pathways (5-8). The Cancer Genome Atlas program conducted a genome-scale analysis of 276 CRC samples using multi-omics sequencing results and discovered that 16% of hypermutated CRC samples are characterized by high microsatellite instability, hypermethylation, *mutL* homolog 1 (*MLH1*) silencing or somatic mutations in mismatch repair genes and polymerases. In addition to the known mutations in the genes *APC* regulator of WNT signaling pathway (*APC*), tumor protein 53 (*TP53*), *SMAD* family member 4 (*SMAD4*), phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha and *KRAS* proto-oncogene GTPase, 19 new recurrently mutated genes have been detected, including AT-rich interaction domain 1A (*ARID1A*), SRY-box transcription factor 9 (*SOX9*) and *APC* membrane recruitment protein 1, and amplifications of the genes *erb-b2* receptor tyrosine kinase 2 and insulin like growth factor 2 have been identified (9).

Although our understanding of genomic alterations of oncology has rapidly improved (5-9), the uncommonly mutated genes in CRC, especially in the Asian population, remain unknown. In the present study, targeted region sequencing (508 genes) on 22 CRC and 10 paired non-cancerous samples from patients with CRC was performed to study genetic

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Abbreviations: CNV, copy number variation; CRC, colorectal cancer; GO, Gene ontology; iCAGES, Integrated CAnCER GEnome Score; KEGG, Kyoto Encyclopedia of Genes and Genomes; MMR, mismatch repair

Key words: colorectal cancer, driver gene, Gene Ontology, Kyoto Encyclopedia of Genes and Genomes

changes. The conclusion of this study may provide further insight into genomic changes in CRC and determine potential therapeutic targets in CRC.

Materials and methods

Patients and samples. A total of 22 primary CRC and 10 paired normal colorectal tissues were surgically resected at Sanming Hospital between May 2014 and August 2015 and immediately frozen. Patients with secondary CRC were excluded from the present study. The mean age of patients at diagnosis was 66.7 ± 10.3 years and ranged between 35 and 80 years old. Written informed consent was obtained from all patients and the study was approved by the Ethics Review Board of the Sanming First Hospital. The clinical characteristics of patients are presented in Table I.

DNA extraction, library preparation and sequencing. Genomic DNA was extracted from the 22 CRC and 10 paired normal colorectal tissues using the QIAamp DNA Blood Midi Kit (Qiagen GmbH) according to the manufacturer's protocol. A NanoDrop 2000 (NanoDrop Technologies; Thermo Fisher Scientific, Inc.) was used to assess DNA quality and concentration. Total DNA samples (400 ng) were used to construct sequencing libraries following the improved protocols for Illumina sequencing (10). In brief, genomic DNA samples were fragmented and ligated with Illumina standard adapters to both fragments ends. Adapter-ligated fragments are then PCR-amplified and gel-purified. Libraries were pooled (11) and hybridized using the Oseq-T panel (508 genes; BGI Genomics Co. Ltd.) for capturing. The process of hybridization was performed as previously described (12). The hybridized product was sequenced using the Illumina MiSeq platform (Illumina, Inc.) using a 100 paired-end (PE) sequencing strategy.

Variant calling and filtering. High-quality reads were aligned to the human reference genome 19 (<http://hgdownload.soe.ucsc.edu/goldenPath/hg19/chromosomes/>) using MEM algorithms of Burrows-Wheeler-Aligner v.0.7.17 (<http://bio-bwa.sourceforge.net>) with default parameters, except that the number of threads was set to 2 to accelerate this mapping process (-t 2) (13). Read deduplication was performed utilizing Picard v.1.98 software (<http://picard.sourceforge.net/>), using the main parameters as follows: ASSUME_SORTED=true and VALIDATION_STRINGENCY=LENIENT. Local realignment around insertion-deletions were performed using GATK v3.3.0 RealignerTargetCreator and IndelRealigner model (<https://software.broadinstitute.org/gatk/>) (14). Base quality score recalibration was also performed by GATK v3.3.0 BaseRecalibrator and PrintReads model (<https://software.broadinstitute.org/gatk/>) (13). Single nucleotide variant and insertion-deletion (indel) mutations were detected by 3.3.0 HaplotypeCaller of GATK (<https://software.broadinstitute.org/gatk/>). New variants and variants with maximum allele frequency <1% reported in the 1000 genome project (15) and dbSNP v141 database (16) were considered as high confidence variants. High confidence variants that were detected specifically in CRC samples but not in normal colon tissues were regarded as somatic mutations. The SnpEff tool ([http://snpeff.](http://snpeff.sourceforge.net/SnpEff_manual.html)

[sourceforge.net/SnpEff_manual.html](http://snpeff.sourceforge.net/SnpEff_manual.html)) was applied to annotate somatic mutations (17). The final somatic variants and annotation results were used in the downstream analysis.

Driver gene prediction and functional annotation. Driver genes were predicted using three distinct computational tools, including MutSigCV (v1.0) (<https://cloud.genepattern.org/gp/pages/index.jsf>) (18), oncodriveFM (v0.0.1) (<https://www.intogen.org>) (19) and Integrated Cancer Genome Score (iCAGES) (<http://icages.wglab.org>) (20). All parameters were set to default values. Driver genes were determined according to the following criteria: i) Genes with q-value <0.1 in the MutSigCV analysis (21); ii) genes with q-value less <0.05 in the oncodriveFM analysis (19); and iii) genes predicted to be drivers by iCAGES, with icages-GeneScores of predicted drivers >0.5 (22). To functionally annotate these driver genes, the Database for Annotation, Visualization and Integrated Discovery (<https://david.ncifcrf.gov>) (23) was applied to analyse the significant Gene Ontology (GO; <https://david.ncifcrf.gov>) terms and Kyoto Encyclopedia of Genes and Genomes (KEGG; <https://david.ncifcrf.gov>) (24) pathways in which driver genes were enriched. Bonferroni adjusted P-value <0.05 indicated a statistical significance.

Copy number variation analysis. Focal copy number variations (CNVs) were detected using CONTRA v2.0.8 software (25) between CRC and paired normal samples using default parameters, (eg: `contra.py -t *.bed -s *tumor.bam -c *normal.bam -f hg19.fasta -o output-removeDups`), except for '-removeDups'. For CRC samples without paired normal tissues, deduplicated bam files of 10 normal samples were merged to form one bam file. Focal CNVs were detected between deduplicated bam files of CRC samples and the merged bam file of 10 normal samples. All parameters were set to default values. Focal CNVs with P-values <0.05 were considered statistically significant. Fraction of CNV (FCNV) was computed as follows: $FCNV = (\text{size of significant CNVs}) / (\text{size of exons})$.

Statistical analyses. In the MutSigCV analysis, P-value was calculated for the gene by convoluting the background distributions of all the mutation types, and determining the probability of meeting or exceeding that score by background mutation alone. Benjamini-Hochberg false discovery rate procedure was used to correct for P-values of multiple tests. In the oncodriveFM analysis, the method randomly sampled one million groups of the same number of observed mutations. P-value referred to the fraction of functional impact scores equal to or greater than the observed average functional impact score of the gene. Bonferroni correction was applied to calculate the q-value for each gene. The Bonferroni correction was used to adjust the P-values computed by Fisher's exact test in the GO and KEGG pathway enrichment analyses. Difference of quantitative values was compared between two groups using Wilcoxon rank-sum test in R 3.2.0 (www.r-project.org).

Results

Clinical and demographic characteristics of the 22 patients with CRC. The 22 patients with CRC comprised 13 female and 9 male patients. The primary sites of CRC included rectum

(7 cases), sigmoideum (1 case), ascending colon (7 cases), transverse colon (1 case), rectosigmoid (1 case) and descending colon (5 cases). The pathological types of the 22 patients comprised 14 cases of protruding adenocarcinoma, 7 cases of protruding and mucinous adenocarcinoma and 1 case of protruding moderately differentiated adenocarcinoma. In addition, 6, 11, 3 and 2 patients with CRC were diagnosed with stages I, II, III and IV, respectively. Furthermore, 2 and 4 patients presented positive metastasis in lymph nodes and distant organs, respectively (Table I).

Summary statistics of alignment to target regions. A 3.65 Mb target region comprising 508 genes was captured from genomic DNA and used to perform variant calling. On average, 98.87% reads were mapped successfully. The duplicated reads were removed, resulting in an average of 4,312,287 (425.73 Mb) effective reads. Of the total effective bases, 69.95% was mapped to target regions (capture specificity), and the mean sequencing depth in the target regions was 81.57-fold. On average, 99.37% of targeted bases had at least 1x coverage, and 97.15% of the targeted bases had at least 10x coverage (Table SI). In addition, the distributions of per-base sequencing depth, cumulative sequencing depth and insert size are presented in Fig. 1. The density of sequencing depth on the target region followed normal distribution, with a mean of 100X. As expected, the peak of the insertion size distribution of the sequencing library was ~200 bp.

Somatic mutations in colorectal cancer. To characterize the mutational spectrum, a targeted region sequencing (3.65 Mb) on the 22 CRC and 10 paired normal tissues was performed. A total of 1,335 somatic mutations were identified, including 122 missense mutations, 48 silent variants, 48 splicing site variants, 13 inframe deletions and 8 inframe insertions. Furthermore, 513, 404 and 113 variants were located in the untranslated region, intron and noncoding regions, respectively. In total, 52 variants caused a frame shift and 15 variants led to stop gain (Fig. 2A). The somatic mutation rates varied considerably among the samples. The average mutation density was 16.63 mutations/Mb in the 508-gene panel (range, 4.38-69.04 mutations/Mb). To analyse the cause for the different mutation densities, the mutation statuses in DNA mismatch repair (MMR) pathway genes was assessed, including *MLH1*, *MLH3*, mutS homolog 2 (*MSH2*), *MSH3*, *MSH6* and PMS1 homolog 2. Five patients with CRC had mutations in any of the MMR genes, and the average mutation density in MMR mutant patients was significantly higher compared with MMR wild-type patients (31.73 vs. 12.18 mutations/Mb; $P=0.01$; Wilcoxon rank sum test; Fig. 2B). In addition, indels, C>T/G>A and A>G/T>C were the three most prevalent mutation types with mutation rates of 48, 18.8, and 12.8%, respectively (Fig. 2C).

Driver genes in colorectal cancer. MutSigCV analysis identified four recurrently mutated genes, named *APC*, *TP53*, *SUZ12* polycomb repressive complex 2 subunit (*SUZ12*) and AT-rich interaction domain 5B (*ARID5B*), with significant statistical evidence (q -value <0.2). Furthermore, OncodriveFM and iCAGES detected five and 24 driver genes, respectively. In total, 29 unique driver genes were detected using these three computational tools. *TP53* was the overlapping gene among the three sets of driver genes. *APC*, *SMAD4*, neurofibromin 1 (*NFI*),

Table I. Clinical and demographic characteristics of the 22 patients with CRC.

Variable	CRC (n=22)
Sex	
Male	9
Female	13
Tumor/adenoma/Polyp location	
Rectum	7
Sigmoideum	1
Ascending colon	7
Transverse colon	1
Rectosigmoid	1
Descending colon	5
Pathologic diagnosis	
Protruding adenocarcinoma	14
Protruding and mucinous adenocarcinoma	7
Protruding moderately differentiated adenocarcinoma	1
Pathologic stage	
I	6
II	11
III	3
IV	2
Tumor stage	
T1	6
T2	12
T3	2
T4	2
Nodal stage	
N0	18
N1	1
N2	3
Metastasis stage	
M0	20
M1	2

ARID5B and nuclear receptor corepressor 1 (*NCOR1*) were the top five most frequently mutated genes in patients with CRC with mutation rates of 68, 36, 36, 32 and 27%, respectively (Fig. 3). In addition, the tumour-suppressor genes *APC* and *SMAD4* had an excessively high number of frameshift or nonsense mutations. The average mutation rate was 18% in the 29 driver genes (Table SII). Certain driver genes, including mitogen-activated protein kinase kinase kinase 1 (*MAP3K1*), *FGFR4* and *PDGFR-β*, were mutated at low frequencies (5% for all three genes), and firstly reported as driver genes in CRC samples.

To functionally annotate the 29 driver genes, GO term and KEGG pathway enrichment analyses were performed. The results from GO enrichment analysis demonstrated that the 29 driver genes were significantly enriched in 152 GO terms, including 'positive regulation of cell proliferation', 'phosphatidylinositol-mediated signalling', 'cellular response to DNA

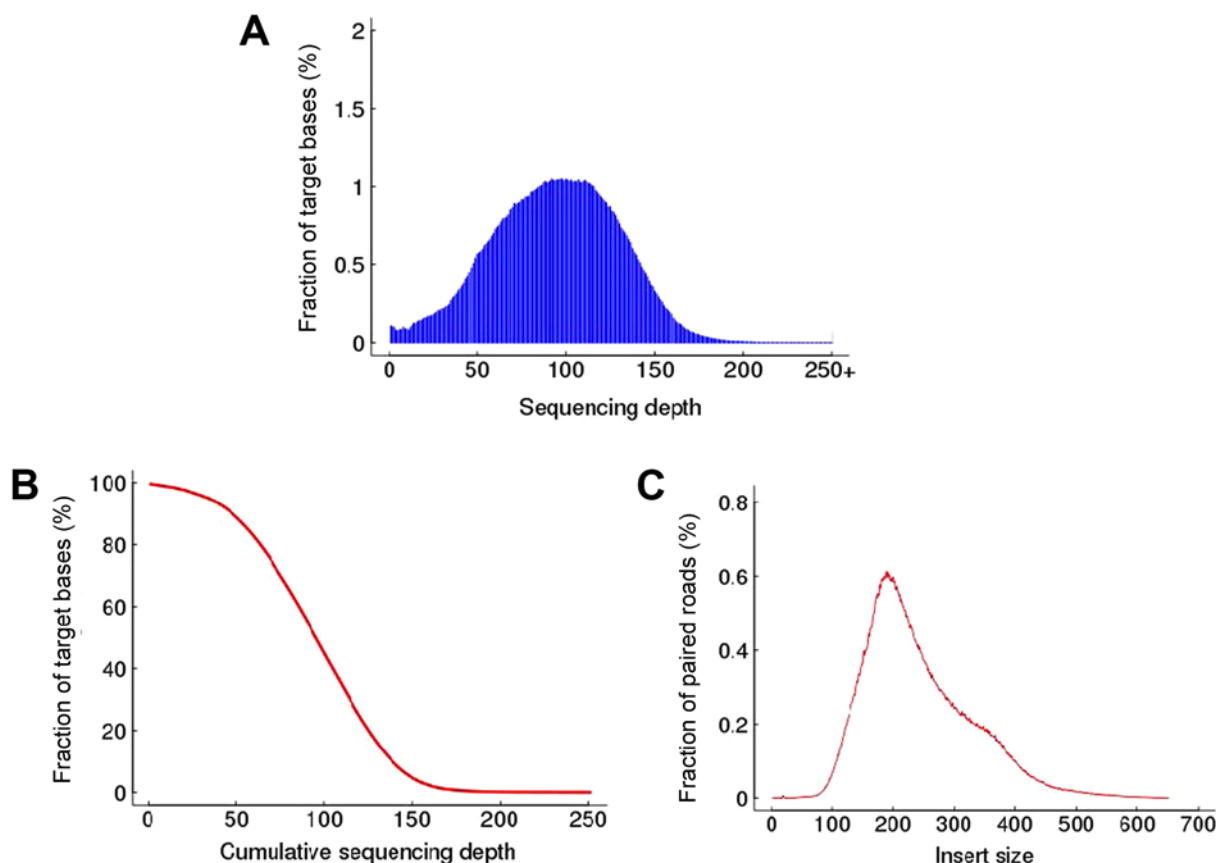


Figure 1. Distributions of per-base sequencing depth, cumulative depth and insert size of 22 colorectal cancer and 10 paired normal colon tissues. (A) Distribution of per-base sequencing depth in targeted regions. (B) Cumulative depth distribution in target regions. (C) Insert size distribution of paired reads.

damage stimulus' and 'MAPK cascade' (Bonferroni-adjusted $P < 0.05$; data not shown). Furthermore, the driver genes were significantly enriched in 9 KEGG pathways, including 'Wnt signalling pathways', 'cell cycle', 'colorectal cancer', 'melanoma, glioma', 'pancreatic and endometrial cancer' (Bonferroni-adjusted $P < 0.05$; Table SIII).

Copy number variation analysis in CRC samples. To further analyse the copy number variation in driver genes, CONTRA was used to detect focal CNVs at the exon level. The results demonstrated that 12 driver genes had FCNV $> 20\%$ in all CRC sample, including *GNAS* complex locus (*GNAS*), *BRCA2* DNA repair associated (*BRCA2*), *SOX9*, fibroblast growth factor receptor 4 (*FGFR4*), *SMAD4*, *SUZ12*, *FGFR3*, epidermal growth factor receptor (*EGFR*), E1A binding protein p300, *NCOR1*, *TP53* and insulin like growth factor 1 receptor. In particular, *GNAS* presented a significant focal gain $> 20\%$ in 45% (10/22) of CRC samples compared with normal samples. In addition, tumour suppressor genes, including *TP53*, presented a significant focal loss $> 20\%$ in 22.7 (5/22) and 4.5% (1/22) of CRC samples compared with normal samples. The *EGFR* oncogene exhibited a significant focal gain $> 20\%$ in 9.1% (2/22) of CRC samples compared with normal samples (Table II).

Discussion

The activation of driver mutations might serve a crucial role in cancer development (26). Genes that carry these driver

mutations are considered as driver genes and are essential to tumorigenesis (27-31). The most common approach to predict driver genes in numerous cancer samples is the identification of genes that present significantly higher mutation frequencies compared with the background mutation rate (18,32), via the MutSigCV model for example. However, many driver genes may occur at a low frequency. ($< 1\%$) in tumours (8). Novel computational tools have therefore been developed to detect driver genes with middle or low mutation frequencies. OncodriveFM first evaluates the functional impact of a somatic mutation using the three different tools SIFT (33), PolyPhen2 (34) and MutationAssessor (35), and applies the transFIC method (<http://bg.upf.edu/transfic>) to transform the three functional scores into a uniform score (36). To identify driver genes, oncodriveFM (19) compares the actual functional impact with a null distribution model generated by 1,000,000 permutations and computes the bias towards the accumulation of variants with high functional impact.

The iCAGES is a novel statistical framework that can predict driver variants by integrating contributions from coding, noncoding and structural variants. iCAGES can therefore identify driver genes by combining genomic information and biological knowledge to generate prioritized drug treatments (20). iCAGES consists of three consecutive layers. The first layer prioritizes personalized cancer driver coding, noncoding and structural variations. The second layer associates these mutations to genes using a statistical model with prior biological knowledge of cancer driver genes

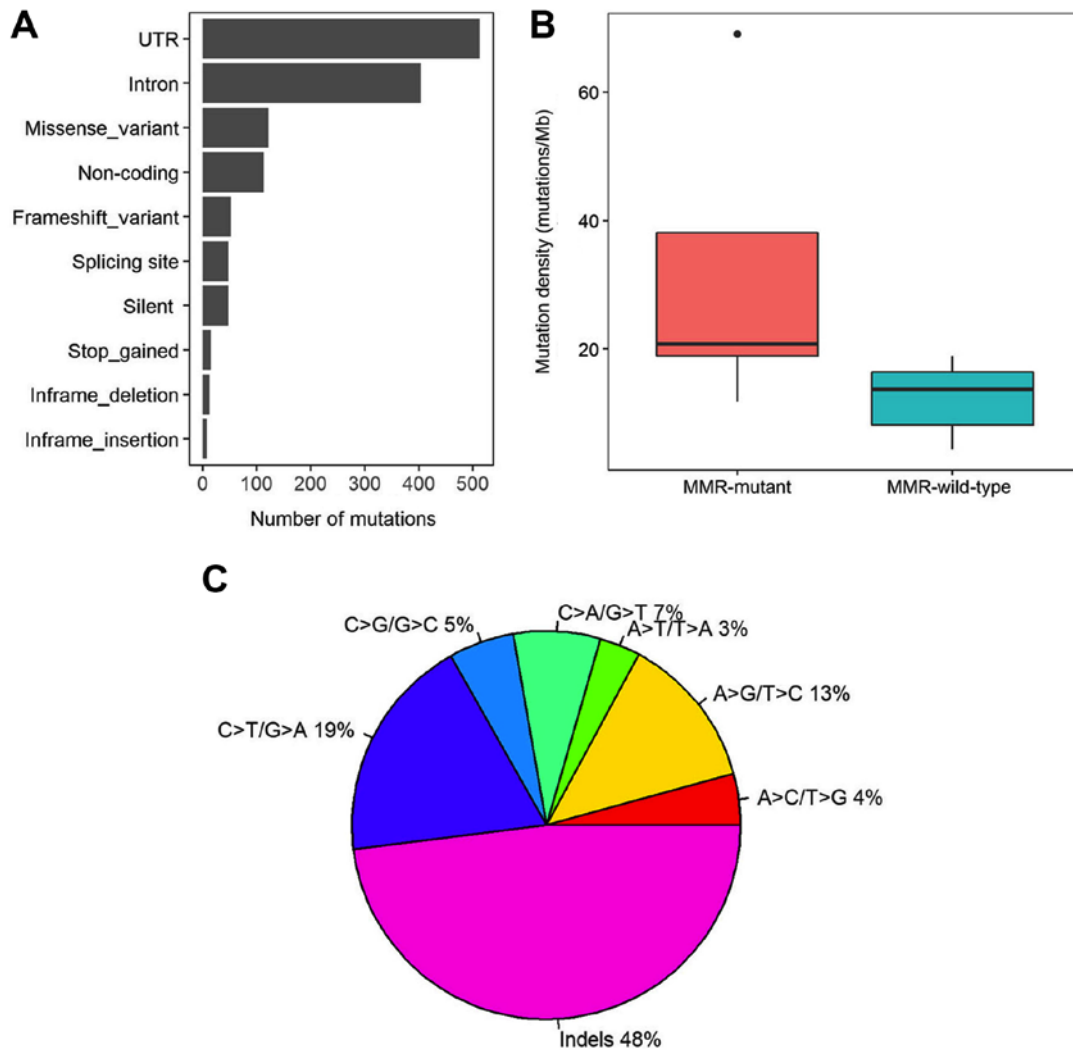


Figure 2. Characterization of somatic mutations in CRC samples. (A) Numbers of 10 different mutation classes with various functional impacts in CRC samples. (B) Differences in mutation densities between MMR mutant and MMR wild-type CRC samples. (C) Somatic mutation signatures in CRC samples. CRC, colorectal cancer; MMR, mismatch repair; UTR, untranslated region.



Figure 3. Mutation rates of 29 driver genes in 22 CRC samples. The left panel presents the mutation rates of 29 driver genes in CRC samples. The right panel represents the distribution of all mutations, which are coloured according to the mutation type. CRC, colorectal cancer.

Table II. Fraction of significant CNVs of driver genes in colorectal cancer samples.

Genes	Sample	Fraction of CNV	CNV type
<i>GNAS</i>	13CB	0.54	Gain
<i>GNAS</i>	15CB	0.55	Gain
<i>GNAS</i>	16CB	0.86	Gain
<i>GNAS</i>	18CB	0.56	Gain
<i>GNAS</i>	19CB	0.56	Gain
<i>GNAS</i>	20CB	0.23	Gain
<i>GNAS</i>	21CB	0.65	Gain
<i>GNAS</i>	31CB	0.33	Gain
<i>GNAS</i>	36CB	0.56	Gain
<i>GNAS</i>	41CB	0.93	Gain
<i>BRCA2</i>	17CB	0.58	Gain
<i>BRCA2</i>	28CB	0.88	Gain
<i>BRCA2</i>	30CB	0.56	Gain
<i>BRCA2</i>	32CB	0.49	Loss
<i>BRCA2</i>	35CB	0.48	Loss
<i>SMAD4</i>	19CB	0.31	Loss
<i>SMAD4</i>	30CB	0.27	Loss
<i>SMAD4</i>	31CB	0.22	Loss
<i>SMAD4</i>	40CD	0.22	Loss
<i>SOX9</i>	17CB	0.29	Loss
<i>SOX9</i>	18CB	0.83	Gain
<i>SUZ12</i>	19CB	0.23	Loss
<i>SUZ12</i>	30CB	0.22	Gain
<i>FGFR3</i>	11CB	0.20	Gain
<i>FGFR3</i>	18CB	0.22	Gain
<i>EGFR</i>	16CB	0.73	Gain
<i>EGFR</i>	31CB	0.33	Gain
<i>EP300</i>	16CB	0.42	Gain
<i>NCOR1</i>	19CB	0.23	Loss
<i>TP53</i>	39CB	0.27	Loss
<i>IGF1R</i>	42CB	0.25	Loss
<i>FGFR4</i>	19CB	0.20	Gain

BRCA2, *BRCA2* DNA repair associated; CNV, copy number variation; *EGFR*, epidermal growth factor receptor; *EP300*, E1A binding protein p300; *FGFR3*, fibroblast growth factor receptor 3; *FGFR4*, fibroblast growth factor receptor 4; *GNAS*, *GNAS* complex locus; *IGF1R*, insulin like growth factor 1 receptor; *NCOR1*, nuclear receptor corepressor 1; *SMAD4*, SMAD family member 4; *SOX9*, SRY-box transcription factor 9; *SUZ12*, *SUZ12* polycomb repressive complex 2 subunit; *TP53*, tumor protein p53.

for specific subtypes of cancer. The third layer generates a list of drugs targeting the repertoire of these potential driver genes. Three computational tools, including MutSigCV, oncodriveFM and iCAGES, were applied to detect driver genes based on complementary principles independently of somatic mutation recurrence. The combination of the three tools enables the detection of recurrently and rarely mutated driver genes in a more comprehensive manner than with MutSigCV alone (9).

Over the last decade, large-scale sequencing projects have been completed to characterize the mutation profiling of CRC (9,37,38). Recurrent gene mutations, including *APC*, *KRAS* proto-oncogene, GTPase and titin genes, and dysregulated signalling pathways, including the Wnt, tumour growth factor- β , phosphoinositide 3-kinase and P53 signalling pathways, have been reported to contribute to CRC carcinogenesis (9,37,38). Giannakis *et al* (37) identified recurrently mutated genes in CRC, including *BCL9* like, RNA binding motif protein 10, CCCTC-binding factor and Kruppel like factor 5, which were not previously reported in CRC. R-spondin (*RSPO*) gene fusions are present in 10% of colon tumours and are mutually exclusive with *APC* mutations, which suggests that they might be involved in the activation of Wnt signalling pathway (38). In the present study, the use of three computational algorithms, including MutSigCV, oncodriveFM and iCAGES allowed the detection of 29 driver genes on 22 CRC samples using somatic mutations. The results demonstrated that *APC*, *SMAD4*, *NF1*, *ARID5B* and *TP53* genes were frequently mutated in patients with CRC, which was similar to results from a previous study (9). Among the 29 driver genes, *EGFR*, kinase insert domain receptor and platelet derived growth factor receptor beta (*PDGFR- β*) are oncogenes, whereas von Hippel-Lindau tumor suppressor, *NF1*, *SUZ12*, *BRCA1* and *BRCA2* are tumour suppressor genes, according to the curated oncogene (39) and tumour suppressor gene (40) databases. In particular, certain driver genes, including mitogen-activated protein kinase kinase kinase 1 (*MAP3K1*), *FGFR4* and *PDGFR- β* , had low mutation frequencies. To the best of our knowledge, these three genes were reported as driver genes in CRC samples for the first time. *MAP3K1* is a Ser/Thr protein kinase that belongs to the mitogen-activated protein kinase kinase kinase 1 (MEKK)/serine/threonine protein kinase subgroup of the MEKK family. Silencing *MAP3K1* expression significantly enhances paclitaxel-induced cell proliferation inhibition in breast cancer cells, (41) pancreatic cancer cells (42) and medulloblastoma cells (43) and inhibits the human pancreatic cancer cell invasive and migratory abilities (43). In accordance to previous studies (41-44), this study suggests that *MAP3K1* may have oncogenic role in cancers. It has been demonstrated that *FGFR4* serves the role of oncogene and regulator of drug or radiation resistance in CRC (45). Furthermore, *FGFR4* silencing can inhibit colon cancer cell line proliferation and induces caspase-dependent apoptosis (45). In addition, *FGFR4* can regulate FLICE-like inhibitory protein expression via Signal transducer and activator of transcription 3, conferring resistance to 5-fluorouracil (5-FU) and oxaliplatin chemotherapy in colon cancer cell lines (45). Furthermore, it has been reported that *FGFR* induces resistance to radiation therapy in CRC by downregulating *RAD51 recombinase* level and inhibiting cancer cell proliferation (46). *PDGFR- β* is a cell surface tyrosine kinase receptor for members of the PDGF family (47). It has been demonstrated that *PDGFR- β* high expression is positively correlated with lymphatic metastasis and advanced UICC stages, and that *PDGFR- β* high expression might be considered as a negative factor for the prognosis of patients with colon cancer (48-50). Decreased expression of *PDGFR- β* can inhibit the invasion and proliferation of CRC cell lines (HCT116 and DLD-1) in a dose-dependent manner (48). *PDGFR- β* expression may

therefore be considered as a risk factor for recurrence in CRC, suggesting that PDGFR inhibitor could represent a useful therapeutic agent for CRC (48). These newly identified driver genes may be considered as novel candidates that could be used for functional validation in future investigation.

In conclusion, the present study screened over 500 genes in order to analyse the genetic alterations present in 22 CRC samples. A total of 29 driver genes were identified. Driver genes with significant copy number variations, such as *GNAS* and *TP53*, may be crucial in CRC oncogenesis. These findings discoveries may serve as basis for further investigation on CRC diagnosis and oncogenesis.

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Availability of data and materials

The raw sequencing data that support the findings of this study have been deposited in the CNSA (<https://db.cngb.org/cnsa/>) of CNGBdb (accession number, CNP0000601: published on 2019/09/30).

Author's contributions

YH designed the entire study. HX, YT and SZ conducted library preparation and targeted region sequencing. JLuo, SZ, JLi and MT were responsible for the bioinformatics analyses, manuscript preparation and manuscript revision. All authors read and approved the final version of the manuscript.

Ethics approval and consent to participate

This study was approved by the Ethics Review Board of the Sanming First Hospital [SFHRB(2014) No 3] and all patients provided informed consent prior to the study.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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