ColoTect Testing Report

1. INFORMATION

Sample and Referring Information

Project Name:	Sentis ColoTect CRC Screening	Sample ID:	22S03997366
Sample Type:	Stool	Sample Collection Date:	20220321
Sample Received Date:	20220322	Sample Report Date:	20220323
Clinical/Hospital:	Zentya a.s.	Referring Doctor:	NA

Patient Information

Patient Name: [redacted] Date of Birth: 19520414
Gender: Female
Clinical Symptoms and Disease History:
NA
Family History:
NA

2. RESULT

High RISK

Interpretation and Suggestion

A high-risk result indicates that the abnormal methylation level in the stool sample, and the chance that a person has colorectal cancer (CRC) or an advanced adenoma is high.

It is recommended that you should contact your doctor for further examination such as diagnostic colonoscopy, and the pathological changes of your colon need to be confirmed.

BGI Europe: COBIS, Ole Maaløesvej 3, Copenhagen N 2200, Denmark
Email: info@bgi.com Web: www.bgi.com Tel: +45 70260806

TEST APPROVED BY

Laboratory Director, BGI

Date:20220323

3. COLOTECH DESCRIPTIVE INFORMATION

Method

ColoTect is a non-invasive, highly sensitive screening test method for colorectal cancer (CRC) and precancerous lesions. Human DNA is extracted from self-collected stool sample and used for the multiplex methylation specific qPCR to detect the methylation level of CRC gene markers——SDC2, ADHFE1, and PPP2R5C.

SDC2: SDC2 encodes a kind of intracellular membrane protein, which has important biological functions in cell division and migration [1]. Multiple studies by comparing the patients with colorectal carcinoma tissues and adjacent tissues of methylation modify status, have discovered significant difference of SDC2 gene methylation in tissue adjacent to carcinoma tissues and an obvious decreasing detection rate in the cancer tissue, adenoma tissue, polyp tissues and normal tissues, so it can be used as an effective marker of colorectal cancer detection [2-3].

ADHFE1: ADHFE1 encodes a transhydrogenase, and the abnormal regulation caused by hypermethylation of this gene can shorten the cell cycle of colorectal cancer and promote the proliferation of cancer cells [4]. Compared with the normal tissue of large intestine, ADHFE1 gene showed high methylation level in both cancer tissues and advanced adenoma tissues [5]. Its methylation level is significantly different in normal tissues, colorectal cancer tissues and adenoma tissues, which is an ideal marker for colorectal cancer detection [6,7].

PPP2R5C: PPP2R5C encodes a regulatory subunit of PP2A phosphatase and is a negative regulator of cell growth and proliferation [8]. There is evidence that its encoding protein can regulate the dephosphorylation of p53 protein in response to DNA damage, thus inhibiting the growth of colorectal

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cancer cells [9]. Hypermethylation of PPP2R5C gene is closely related to the occurrence and development of colorectal cancer and can be used as a potential marker for colorectal cancer detection [10].

Limitations and Declaration

This report is specific to the tested sample. The false positive result and false negative result may present, due to individual differences among subjects and technical limitations. The test result is for clinical reference and cannot be used as the evidence for clinical diagnosis. If you have any doubt about the results, please contact us by email info@bgi.com within 7 days after receiving the report.

Reference

[1] Kim JH, Park SC. Syndecan-2 Methylation as a New Biomarker for Early Detection of Colorectal Neoplasm. Gut Liver. 2018;12(5):479-480.

[2] Oh TJ, Oh HI, Seo YY, Jeong D, Kim C, Kang HW, et al. Feasibility of quantifying SDC2 methylation in stool DNA for early detection of colorectal cancer. Clin Epigenetics. 2017;9:126.

[3] Han YD, Oh TJ, Chung TH, Jang HW, Kim YN, An S, et al. Early detection of colorectal cancer based on presence of methylated syndecan-2 (SDC2) in stool DNA. Clin Epigenetics. 2019;11(1):51.

[4] Hu YH, Ma S, Zhang XN, et al. Hypermethylation Of ADHFE1 Promotes The Proliferation Of Colorectal Cancer Cell Via Modulating Cell Cycle Progression. Onco Targets Ther. 2019;12:8105-8115. Published 2019 Oct 4. doi:10.2147/OTT.S223423

[5] Tae CH, Ryu KJ, Kim SH, Kim HC, Chun HK, Min BH, et al. Alcohol dehydrogenase, iron containing, 1 promoter hypermethylation associated with colorectal cancer differentiation. BMC Cancer. 2013;13:142.

[6] Naumov VA, Generozov EV, Zaharjevskaya NB, Matushkina DS, Larin AK, Chernyshov SV, et al. Genome-scale analysis of DNA methylation in colorectal cancer using Infinium HumanMethylation450 BeadChips. Epigenetics. 2013;8(9):921-34.

[7] Fan, J., Li, J., Guo, S. et al. Genome-wide DNA methylation profiles of low- and high-grade adenoma reveals potential biomarkers for early detection of colorectal carcinoma. Clin Epigenet, 2020, 12, 56

[8] Veerle JANSSENS, Jozef GORIS; Protein phosphatase 2A: a highly regulated family of serine/threonine phosphatases implicated in cell growth and signalling. Biochem J 1 February 2001; 353 (3): 417–439.

[9] Li HH, Cai X, Shouse GP, Piluso LG, Liu X. A specific PP2A regulatory subunit, B56gamma, mediates DNA damage-induced dephosphorylation of p53 at Thr55. EMBO J. 2007;26(2):402-411.

[10] Galamb O, Kalmar A, Peterfia B, Csabai I, Bodor A, Ribli D, et al. Aberrant DNA methylation of WNT pathway genes in the development and progression of CIMP-negative colorectal cancer. Epigenetics. 2016;11(8):588-602.

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