Epigenetics Makes You Healthy

EpiSure16

Cancer Gene Methylation Test

Early Diagnosis, Dynamic monitoring

Testing Report

EpiSure16

Patient Info.

Name	
Birthday	
Gender	
Pt. No.	
Spl. No.	

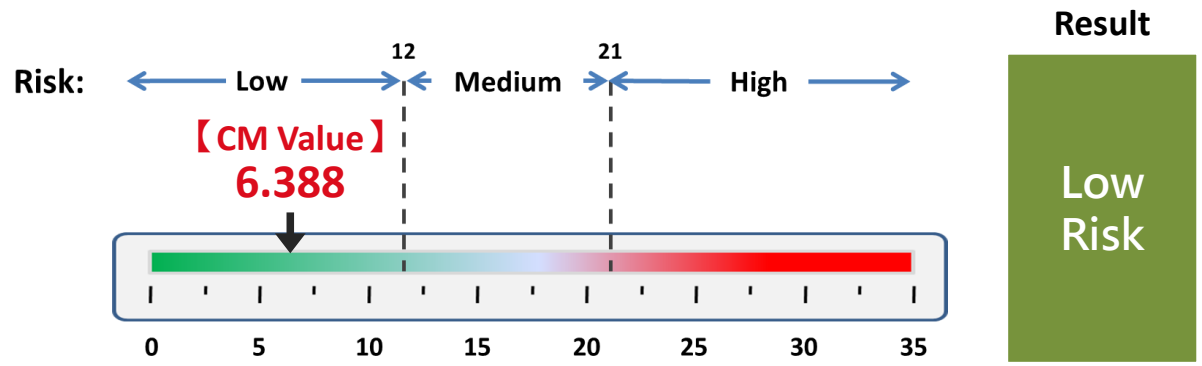
Sample Info.

Type	Blood
Coll. Tube	cfDNA Tube
Sal. Date	2026/03/05
Recv. Date	2026/03/11
Rept. Date	2026/03/14

Service Provider

Provider	
Tel.	
E-Mail	

Results



Gene: RASSF1A
Function: Tumor suppressor
Ct Value: ND
Common in Cancer: Lung, Breast, Prostate, Colon, Bladder, Head-neck, Ovary, Thyroid, Kidney, Liver, Cervix

Gene: APC
Function: Tumor suppressor
Ct Value: ND
Common in Cancer: Prostate, Breast, Colon, Stomach, pancreas, Kidney , Cervix

Gene: DAB2IP
Function: Tumor suppressor
Ct Value: ND
Common in Cancer: Prostate, Breast, Colon, Bladder, Stomach, Kidney

Gene: TSPYL5
Function: Tumor suppressor
Ct Value: ND
Common in Cancer: Prostate, Liver, Stomach, Lung, Glioma, Endometrium, Esophagus

Gene: GSTP1
Function: DNA Repair
Ct Value: 39.4
Common in Cancer: Prostate, Breast, Colon, Bladder, Lung, Liver , Cervix

Gene: SOCS2
Function: Immune Regulation
Ct Value: ND
Common in Cancer: Breast, Colon, Prostate, Stomach, Liver, Ovary , Cervix

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Conclusion

Your EpiSure16 testing result is

- [x] **Low risk**
  The methylation level of your tumor suppressor genes is lower than normal, suggesting a reduced risk of cancer.
- [ ] **Medium risk**
  The methylation level of your tumor suppressor genes is a slightly elevated, suggesting a moderate risk of cancer.
- [ ] **High risk**
  your tumor suppressor genes have a higher-than-normal level of methylation, suggesting an increased risk of cancer.

Explanation

1. The EpiSure16 test evaluates the methylation levels of six tumor suppressor genes (RASSF1A, APC, DAB2IP, TSPYL5, GSTP1, and SOCS2).
2. The CM score is calculated based on the quantitative methylation-specific PCR (qMSP) results (Ct values) of these six tumor suppressor genes. A CM score of 12 or below indicates a low risk, a score between 12 and 21 indicates a moderate risk, and a score of 21 or above indicates a high risk.
3. The Ct value of a methylated gene: 30-40 indicates high methylation, a Ct value > 40 indicates moderate methylation, and a Ct value of N.D. (not detected) indicates low methylation.

Recommendations & Notices

1. A high or moderate risk assessment does not mean you have cancer. It is recommended that you consult with a specialist to arrange further testing and a comprehensive evaluation.
2. A low-risk assessment does not guarantee that you will never develop cancer. Individuals with a low risk should still undergo regular check-ups as part of their annual health examination.

Declaration

1. This test is intended for cancer risk assessment only and is not a diagnostic tool for cancer.
2. This test cannot replace routine clinical cancer screening.
3. The results of this test are for informational purposes only and should be discussed with your doctor.

EpiSante Molecular Medicine Lab

Operator:	Supervisor:	Signatory:
Shing-Yi Tsai	*Pei-Jr Peng*	*Dr. Chang-Yi Lu*

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Recommendation

Low or Moderate Risk: undergo regular annual check-ups

1. Maintain a regular lifestyle: Pay attention to a balanced diet and avoid staying up late. Reduce your intake of foods high in triglycerides, such as fried foods, and limit your consumption of high-starch foods like flour, rice, potatoes, and corn.
2. Avoid smoking, chewing betel nuts, and excessive alcohol consumption.
3. Avoid consuming foods with artificial additives, pickled foods, or those that may be contaminated with aflatoxin, such as peanut products, soybean paste, and fermented tofu.
4. Avoid taking medications or remedies with unknown ingredients.
5. Engage in moderate exercise: Aim for at least 20-60 minutes of physical activity each day. The intensity and type of exercise should be adjusted based on your individual fitness level.
6. Individuals with diabetes should pay close attention to blood glucose control.

High Risk : undergo further testing for a comprehensive evaluation

1. Please follow your specialist's advice and undergo further evaluation tests for a comprehensive assessment.
2. If other serological and imaging tests are normal, it is recommended to increase the screening frequency to every six months using the EpiSure16 cancer gene methylation test. As DNA methylation occurs in the early stages of cell carcinogenesis and can be influenced by diet, environment, and other factors, it is well-suited for long-term monitoring of methylation gene changes.
3. If a diagnosis of cancer is confirmed by computed tomography (CT) or magnetic resonance imaging (MRI), there is no need to panic. Early-stage cancers, due to their smaller tumor size, have a high cure rate after surgical resection or ablation. Please discuss the most appropriate treatment plan with your doctor.
4. Cancer has a high recurrence rate. After treatment, it is necessary to closely monitor for any signs of recurrence. For example, due to the limitations of liver cancer detection tools, smaller recurrent tumors in the early stages are difficult to detect. Our company offers two additional testing products that can provide more accurate auxiliary testing tools for post-surgical resection and ablation prognosis and recurrence monitoring, enabling physicians to provide more effective intervention treatment in the early stages of recurrence. For more detailed information, please visit the EpiSante Biomedical website (www.episante-biomed.com)."

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Explanation of gene methylation function

RASSF1A Gene
Function: Tumor Suppressor

RASSF1A is a tumor suppressor gene that regulates critical physiological processes such as cell growth, apoptosis, and cell cycle. DNA methylation in the promoter region of the RASSF1A gene is a common epigenetic alteration in various cancers. When abnormal DNA methylation silences RASSF1A gene expression, it leads to uncontrolled cell growth and division, resulting in tumor formation, and interferes with apoptosis, allowing tumor cells to survive and accumulate further mutations. RASSF1A methylation has also been linked to cancer cell metastasis, enabling cancer cells to spread to distant parts of the body. Due to the prevalence of RASSF1A methylation in many types of cancer, it can serve as a biomarker for early detection and prognosis. Detection of RASSF1A methylation in blood or tissue samples can indicate the occurrence of cancer or the likelihood of having an aggressive disease.

Common in Cancer

Lung, Breast, Prostate, Colon, Bladder, Head-neck, Ovary, Thyroid, Kidney, Liver

APC Gene
Function: Tumor suppressor

APC is a tumor suppressor gene that helps regulate cell growth and prevents tumor development. Gene silencing caused by APC methylation results in the loss of its tumor suppressive function, leading to uncontrolled cell growth and division, thereby promoting cancer initiation and progression. As a critical negative regulator of the Wnt signaling pathway, APC methylation-induced silencing results in aberrant activation of the Wnt pathway, which promotes cell proliferation, survival, and tumor growth, contributing to cancer progression.

Common in Cancer:

Prostate, Breast, Colon, Stomach, pancreas, Kidney

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Explanation of gene methylation function

DAB2IP Gene
Function: Tumor Suppressor

DAB2IP is a tumor suppressor gene that plays a crucial role in regulating cancer development and progression. DAB2IP exerts its tumor suppressive function by modulating cell proliferation, apoptosis, and inhibiting tumor invasion and metastasis through signaling pathways such as PI3K/Akt and NF-κB. DAB2IP methylation has also been linked to the induction of epithelial-mesenchymal transition (EMT), a cellular process that endows cancer cells with migratory and invasive properties, allowing them to detach from the primary tumor and metastasize to distant sites.

Common in Cancer:

Prostate, Breast, Colon, Bladder, Stomach, Kidney

TSPYL5 Gene
Function: Tumor Suppressor

The TSPYL5 protein, which is produced from the TSPYL5 gene, can bind to chromatin and histones, which are important components of chromosomes. This protein plays a role in many bodily processes, including how cells respond to radiation, and it helps regulate certain signaling pathways that are important for cell growth and survival. In cancer, TSPYL5 often behaves like a tumor suppressor gene. When TSPYL5 is not working properly, it can contribute to the development and progression of cancer. For example, in prostate cancer, low levels of TSPYL5 protein can be a sign that the cancer is becoming more aggressive. Additionally, changes to the TSPYL5 gene, such as methylation, can make cancer cells less sensitive to treatment.

Common in Cancer:

Prostate, Liver, Stomach, Lung, Glioma, Endometrium, Esophagus

Explanation of gene methylation function

GSTP1 Gene
Function: DNA Repair, Anti-oxidant

GSTP1 normally functions in antioxidant activity and detoxification, helping to protect cells from damage caused by carcinogens and oxidative stress. When the GSTP1 gene is methylated, it leads to decreased expression of the GSTP1 protein, making cells more susceptible to oxidative damage and carcinogens, thereby increasing the risk of tumor formation. GSTP1 methylation may also affect DNA repair processes, increasing cellular sensitivity, and preventing the effective repair of damaged DNA.

Common in Cancer:

Prostate, Breast, Colon, Bladder, Lung, Liver

SOCS2 Gene
Function: Immune Regulation

SOCS2 is involved in the negative regulation of cellular signaling pathways, such as those induced by growth hormone and insulin-like growth factor-1 (IGF-1). Methylation of the SOCS2 gene promoter can lead to dysregulation of cellular signaling pathways and abnormal cell growth and proliferation. Moreover, SOCS2 is involved in regulating immune responses. Methylation-induced suppression of SOCS2 expression alters immune cell function, allowing cancer cells to evade immune surveillance and promote tumor growth.

Common in Cancer:
Breast, Colon, Prostate, Stomach, Liver, Ovary

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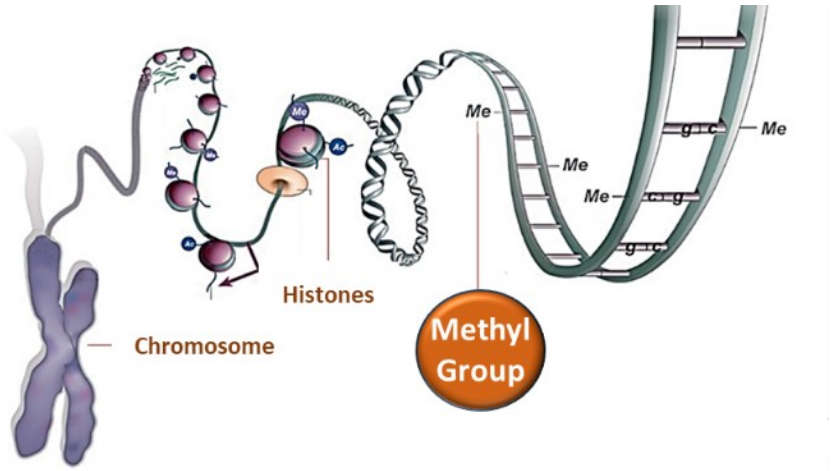
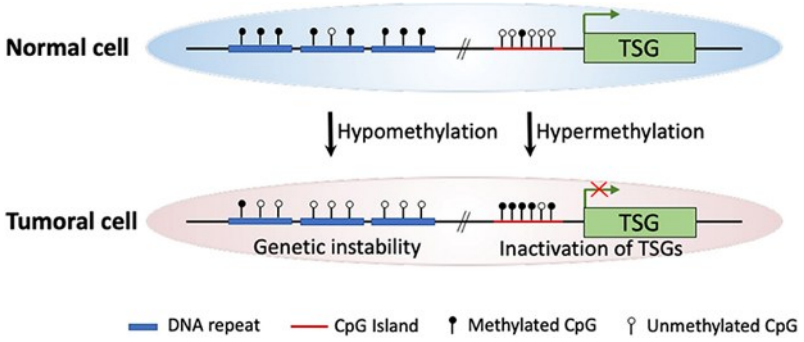
DNA Methylation Regulates Gene Expression

DNA methylation is a chemical modification process that occurs on DNA. A methyl group (CH3) attaches to cytosine bases in DNA. When DNA is excessively methylated, it can suppress gene expression, leading to a loss of function. This alteration of gene expression, without changing the underlying DNA sequence, is known as epigenetics. In simpler terms, epigenetics refers to changes in gene activity that do not involve alterations to the genetic code itself.



In the early stages of cancer development, many genes undergo abnormal methylation. For instance, tumor suppressor genes, which normally help to prevent cancer, become highly methylated when normal cells transform into cancer cells. Consequently, detecting methylated cell-free tumor DNA (ctDNA) in the blood can aid in early cancer detection and disease monitoring.



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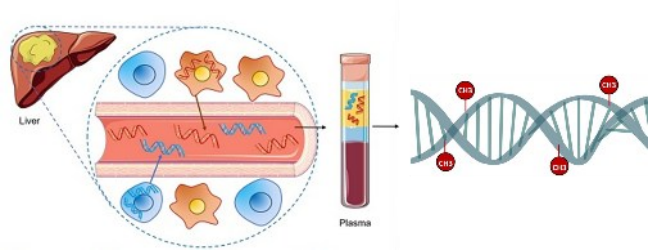
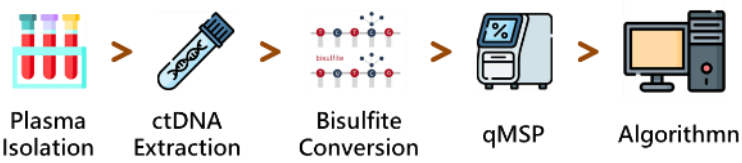
Liquid Biopsy ctDNA Methylation Test

Recent studies have shown that tumor cells release short fragments of DNA into the bloodstream at an early stage of cancer. EpiSure16 is a testing technique that detects methylation markers on circulating tumor DNA (ctDNA) released by tumor cells into the blood. As a type of liquid biopsy, this non-invasive test can provide a more comprehensive representation of the tumor than traditional tissue biopsies, avoiding sampling bias and allowing for repeated sampling and real-time monitoring. It is currently a mainstream testing method in precision medicine, used for early cancer screening, prognosis, monitoring recurrence, and evaluating treatment response.



EpiSure16 Technology

This test involves isolating plasma from a blood sample and extracting circulating tumor DNA (ctDNA) from the plasma. The extracted ctDNA is then treated with sodium bisulfite, which converts unmethylated cytosine bases to uracil, while leaving methylated cytosines unchanged. Subsequently, cancer-specific primers and probes are employed in quantitative methylation-specific PCR (qMSP) to detect the methylation levels of six genes: RASSF1A, APC, DAB2IP, IGFBP7, GSTP1, and SOCS2 within the ctDNA. An algorithm is then used to evaluate the individual's cancer risk based on the methylation profiles of these genes. qMSP offers exceptionally high sensitivity, capable of detecting as little as $1/10^5$ methylated DNA molecules in the plasma. Moreover, the procedure is straightforward, making it highly suitable for the analysis of minute quantities of liquid biopsy samples like ctDNA.



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Strength of EpiSure16

Non-invasive testing

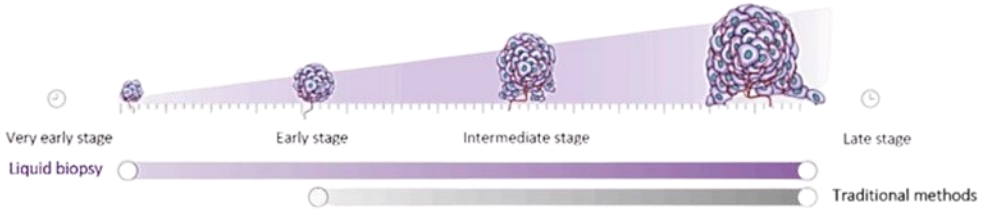
Detects ctDNA (circulating tumor DNA) released from tumor cells into the bloodstream. It requires only a blood draw, is non-invasive, low-risk, and convenient, making it suitable for long-term monitoring and real-time detection. As a type of liquid biopsy, it is a mainstream testing method in precision medicine. Moreover, since tumors are composed of multiple cancer cells with different genetic mutations, liquid biopsies can represent the overall tumor status, avoiding sampling bias.

Dynamic DNA Methylation Tracking

Recent studies have shown that 80-90% of cancers are linked to environmental factors. DNA methylation, which regulates gene expression in response to environmental influences, exhibits dynamic changes in its levels and patterns according to cellular physiological states and environmental factors. This dynamic nature of DNA methylation provides a unique perspective for examining the complex processes of carcinogenesis. Consequently, DNA methylation has emerged as a powerful diagnostic tool for early cancer detection, disease prognosis, and guiding and monitoring the efficacy of cancer treatments. Methylation markers have thus become one of the hottest biomarker molecules in cancer research.

Early Detection

A vast body of literature has demonstrated that alterations in DNA methylation occur very early in the process of cellular carcinogenesis. Compared to all current cancer screening tools, whether they are serum protein markers or imaging modalities such as abdominal ultrasound, computed tomography (CT), or magnetic resonance imaging (MRI), methylation markers can detect early-stage cancers more accurately and at an earlier stage. This can complement the limitations of existing cancer screening tools and achieve the goal of "early detection and early treatment," thereby increasing patient survival rates and reducing medical and societal costs.



Half of cancers can be prevented, the WHO urges a focus on cancer prevention

One in every six people worldwide dies from cancer, and in developed countries, this figure rises to one in four. Approximately 20 million people are diagnosed with cancer annually, and the World Health Organization (WHO) predicts that this number will exceed 35 million by 2050, resulting in a global economic loss of $25.2 trillion. The WHO urges countries to prioritize cancer prevention, emphasizing that it can reduce unnecessary pain, premature death, and healthcare costs while extending patients' lives.

The WHO has identified several preventable risk factors for cancer,

Tobacco

Tobacco smoke contains over 7,000 chemicals, of which at least 250 are harmful to humans, and at least 69 are known to cause cancer. Globally, tobacco is the leading preventable risk factor for cancer, causing over 8 million deaths annually. Smoking can lead to various types of cancer, including lung, liver, esophageal, laryngeal, oral, pharyngeal, kidney, bladder, pancreatic, stomach, and cervical cancer. Approximately 70% of lung cancer cases are attributable to smoking alone. Secondhand smoke has been proven to cause lung cancer in non-smokers. Smokeless tobacco can lead to oral, esophageal, and pancreatic cancer.

Alcohol

Alcohol is classified by the International Agency for Research on Cancer as a Group 1 carcinogen, meaning it is a substance that is known to cause cancer in humans. It is a toxic, psychoactive, and addictive substance linked to seven types of cancer, including esophageal, liver, colorectal, and breast cancer. Annually, 740,000 new cancer cases are attributed to alcohol consumption. Globally, one in every 20 breast cancer cases can be linked to alcohol. The risk of developing various cancers, including oral, pharyngeal, laryngeal, esophageal, liver, colorectal, and breast cancer, increases with increasing alcohol consumption. Alcohol-attributable cancers account for an estimated 400,000 deaths worldwide, primarily among men.

Overweight and obesity

Being overweight or obese is linked to many types of cancer, including esophageal, colorectal, breast, endometrial, and kidney cancer. Regular physical activity, maintaining a healthy weight, and following a balanced diet can reduce the risk of these cancers. Consuming a diet rich in fruits and vegetables can protect cells and help prevent various types of cancer. Conversely, excessive consumption of red and processed meat may increase the risk of colorectal cancer. Additionally, healthy eating habits that can prevent diet-related cancers can also reduce the risk of cardiovascular disease. Obesity is estimated to cause approximately 3.4% of all cancers, including 110,000 cases of breast cancer annually.

Infection

Cancers caused by infections, such as hepatitis viruses and human papillomavirus (HPV), account for approximately 25% of cancer cases in low- and middle-income countries. Hepatitis B and C viruses cause liver cancer; HPV infection leads to cervical cancer; and Helicobacter pylori increases the risk of stomach cancer. In some countries, parasitic infections like schistosomiasis increase the risk of bladder cancer, while in others, liver flukes increase the risk of bile duct cancer. Prevention measures include vaccination and prevention of transmission and infection.

Pollution

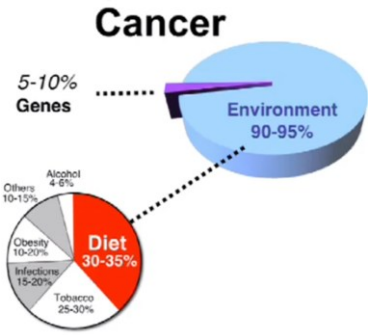
The World Health Organization (WHO) estimates that outdoor air pollution causes 4.2 million deaths globally. Of these deaths, 58% are due to ischemic heart disease and stroke, 18% to chronic obstructive pulmonary disease (COPD) and acute lower respiratory infections, and 6% to lung cancer. Additionally, household air pollution from the use of solid fuels and kerosene for cooking results in nearly 4 million deaths annually. Environmental pollution with carcinogenic chemicals in air, water, and soil accounts for 1-4% of all cancers. Exposure to environmental carcinogens can occur through contaminated drinking water or indoor and ambient air pollution. Exposure to carcinogens can also occur through chemical contamination of food, such as the accumulation of aflatoxin or dioxin in the food chain.

Radiation

Exposure to various types of ionizing radiation increases the risk of developing multiple types of malignant tumors, including leukemia and solid tumors. The risk is higher when exposure occurs at a younger age or when the exposure dose is greater. It is estimated that radon exposure from soil and building materials accounts for 3-14% of all lung cancers, making it the second leading cause of lung cancer after tobacco. Ionizing radiation is an essential diagnostic and therapeutic tool. To ensure that the benefits outweigh the potential radiation risks, appropriate regulations should be in place for radiomedical procedures, and correct procedures should be followed to reduce unnecessary radiation doses, especially in children. Ultraviolet (UV) radiation, particularly from the sun, is carcinogenic to humans, causing various major skin cancers such as basal cell carcinoma (BCC), squamous cell carcinoma (SCC), and melanoma. Avoiding excessive exposure and using sunscreen and protective clothing are effective preventive measures.

Methylation Testing vs. Genetic Testing

Recent research suggests that only about 5-10% of cancers are linked to genetic mutations, while 90-95% are attributed to environmental factors such as diet, smoking, alcohol consumption, and obesity. These environmental factors influence gene expression through DNA methylation. Therefore, unlike genetic testing, which merely predicts the lifetime risk of cancer based on a specific gene mutation, DNA methylation profiles reflect an individual's health status as influenced by dietary habits and environmental factors. Furthermore, unlike genetic mutations, which are irreversible, the methylation levels of certain genes can be dynamic and reversible. Consequently, DNA methylation testing is well-suited for regular health monitoring and is currently the most popular biomarker.



Reference

(1) Luke B Hesson, Wendy N Cooper, Farida Latif. The role of RASSF1A methylation in cancer. Dis Markers. 2007;23(1-2):73-87.

(2) Giorgia Gurioli, Filippo Martignano, Samanta Salvi, Matteo Costantini, Roberta Gunelli, Valentina Casadio. GSTP1 methylation in cancer: a liquid biopsy biomarker? Clin Chem Lab Med. 2018 Apr 25;56(5):702-717.

(3) E Letellier, M Schmitz, K Baig, N Beaume, C Schwartz, S Frasquilho, L Antunes, N Marcon, P V Nazarov, L Vallar, J Even, S Haan. Identification of SOCS2 and SOCS6 as biomarkers in human colorectal cancer. Br J Cancer. 2014 Aug 12;111(4):726-35.

(4) Jin Kim, Woo Ho Kim, Sun-Ju Byeon, Byung Lan Lee, Min A Kim. Epigenetic Downregulation and Growth Inhibition of IGFBP7 in Gastric Cancer. Asian Pac J Cancer Prev. 2018 Mar 27;19(3):667-675.

(5) Yeonjoo Jung, Jinah Park, Yung-Jue Bang, Tae-You Kim. Gene silencing of TSPYL5 mediated by aberrant promoter methylation in gastric cancers. Lab Invest. 2008 Feb;88(2):153-60.

(6) H Dote, S Toyooka, K Tsukuda, M Yano, T Ota, M Murakami, M Naito, M Toyota, A F Gazdar, N Shimizu. Aberrant promoter methylation in human DAB2 interactive protein (hDAB2IP) gene in gastrointestinal tumour. Br J Cancer. 2005 Mar 28;92(6):1117-25.

(7) Fang Liu, Xiaoling Lu, Xiaoxi Zhou, He Huang. APC gene promoter methylation as a potential biomarker for lung cancer diagnosis: A meta-analysis. Thorac Cancer. 2021 Nov;12(21):2907-2913.

(8) Xueliang Zhou, Dechao Jiao, Mengmeng Dou, Weijie Zhang, Hao Hua, Jianjian Chen, Zhaonan Li, Lifeng Li, Xinwei Han. Association of APC gene promoter methylation and the risk of gastric cancer: A meta-analysis and bioinformatics study. Medicine (Baltimore). 2020 Apr;99(16):e19828.

(9) Keli He, Li Zhang, Xinghua Long. Quantitative assessment of the association between APC promoter methylation and breast cancer. Oncotarget. 2016 Jun 21;7(25):37920-37930.

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