

Name of Journal: *World Journal of Gastroenterology*

Manuscript NO: 47414

Manuscript Type: ORIGINAL ARTICLE

Basic Study

Identification of differentially-expressed genes regulated by methylation in colon cancer based on bioinformatics analysis

Liang Y *et al.* Identification of methylation-regulated differentially-expressed genes

Match Overview

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gene expression of colon cancer systemically, and acquire candidate genes potentially regulated by altered methylation for this disease. Data were downloaded from The Cancer Genome ...

Identification of differentially-expressed genes by DNA ...

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In the present study, **genome-wide DNA methylation** was examined, RNA expression profiles were analyzed and an integrated analysis of these two profiles was conducted to **identify differentially-expressed DNA methylation-regulated genes** that are involved in **cervical cancer**.

Cited by: 8

Author: Heun-Sik Lee, Jun Ho Yun, Junghee Jung...

Publish Year: 2015

Identification of biomarkers associated with diagnosis and ...

<https://www.sciencedirect.com/science/article/pii/S0378111919300137>

For example, **Huang et al.** (2018) identified hundreds of CRC associated **differentially expressed genes** (DEGs) based on the **Gene Expression Omnibus** (GEO) and The **Cancer Genome Atlas** (TCGA) database, and five genes of which can used as diagnostic **biomarkers** for CRC patients.

Author: Linbo Chen, Dewen Lu, Keke Sun, Yu...

Publish Year: 2019

Identification of metastasis-associated genes in ...

www.ncbi.nlm.nih.gov › Journal List › Oncol Lett

Nov 23, 2015 · In the present study, **gene expression** data were initially analyzed using the metaDE package in R language, in order to **identify** the DEGs in CRC samples, and a total of 370 **genes** were **identified** as DEGs between primary and **metastatic cancer** samples.

Cited by: 5

Author: Chong Qi, Liang Hong, Zhijian Cheng, Qin...

Publish Year: 2016



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Identification of differentially-expressed genes by DNA ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4356325>

In the present study, **genome-wide DNA methylation** was examined, **RNA expression profiles** were analyzed and an integrated analysis of these two profiles was conducted to **identify differentially-expressed DNA methylation-regulated genes** that are involved in **cervical cancer**.

Cited by: 9

Author: Heun-Sik Lee, Jun Ho Yun, Junghee Jung...

Publish Year: 2015

Identification of regulatory role of DNA methylation in ...

https://www.researchgate.net/publication/321233630_Identification_of_regulatory_role...

Identification of regulatory role of DNA methylation in colon cancer gene expression via systematic bioinformatics analysis Article (PDF Available) in *Medicine* 96(47):e8487 · November 2017 with ...

Identification of Differentially-expressed Genes in ...

<https://www.sciencedirect.com/science/article/pii/S1672022914001338>

A total of 1519 genes were recognized to be differentially expressed in **intestinal GC** when compared to **normal gastric mucosa tissue** (Figure S1). These included 593 **upregulated** and 926 **downregulated genes**.

Cited by: 5

Author: Shizhu Zang, Ruifang Guo, Rui Xing, Lian...

Publish Year: 2014

Identification of gene-specific DNA methylation signature ...

<https://www.sciencedirect.com/science/article/pii/S2210776218300802>

Screening of differentially expressed gene-specific DNA methylation. The **gene-specific DNA methylation expression levels** between **tumor** and adjacent **non-tumor tissues** were ascertained with SAMR in R language.

Author: Kaixue Li, Li Zeng, Hong Wei, Jingjing... Publish Year: 2018

The Identification of Specific Methylation Patterns across ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4361543>

Background. **BRCA1/2** are the most cancer-related genes in breast cancer, they involve in **DNA repair, regulation** of transcriptional activation and apoptosis. The hypermethylation of **BRCA1/2** in promoter regions results in the inactivation of function and increases the risk of **breast cancer** [11, 12].

Cited by: 16

Author: Chunlong Zhang, Hongyan Zhao, Jie Li, H...

Publish Year: 2015

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作者: G Sun - 2019 - 被引用次数: 2 - 相关文章

2019年1月16日 - Identification of differentially expressed genes and biological characteristics of colorectal cancer by integrated bioinformatics analysis. ... The module analysis was performed by the MCODE plug-in of Cytoscape based on the ...

缺少字词: methylation

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作者: Y Yang - 2017 - 被引用次数: 1 - 相关文章

2017年11月27日 - Differentially expressed genes (DEGs) were identified by DESeq2. ... network analysis of genes is increasingly used in bioinformatics analysis. ... Based on the differential methylation analysis of colon cancer, we obtained ...

Identification of differentially expressed genes in cervical cancer by ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6036588/> - 翻译此页

作者: Y Ge - 2018 - 被引用次数: 2 - 相关文章

Keywords: bioinformatics analysis, differentially expressed gene, cervical cancer WGCNA uses a soft threshold based on the determination method. First, the enrichment aspect of 'aldosterone-regulated sodium reabsorption' included 4 DEGs that were from the methylation of polycomb target genes in colon cancer.

Identification of differentially-expressed genes by DNA methylation in ...

<https://www.spandidos-publications.com/10.3892/ol.2015.2917> - 翻译此页

作者: HS Lee - 2015 - 被引用次数: 11 - 相关文章