

9

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Retrospective Study

A signature based on molecular subtypes of DNA methylation predicts overall survival in gastric cancer

A survival prediction model for GC

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Dec 31, 2019 · In this study, we explored the **prognostic value** of **subtypes based on DNA methylation status** in 424 colon adenocarcinoma samples from the Cancer Genome Atlas database. **Differences in DNA methylation levels** were associated with differences in T, N, and M category, age, stage, and prognosis.

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Jan 20, 2020 · The **DNA methylation signature** for **overall survival** (OS) prediction of **gastric cancer** (GC) patients. a Kaplan-Meier estimate of the OS using the identified **DNA methylation signature**. GC patients were divided into **low-risk** (N = 181) or **high-risk** (N = 182) **subgroup based** on the median of risk score. The difference between the two curves was determined by ...

**Cited by:** 1

**Author:** Yaojun Peng, Qiyan Wu, Lingxiong Wan...

**Publish Year:** 2020

## DNA methylation signatures define molecular subtypes of ...

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2993635>

Nov 18, 2010 · Array-**based methylation** analysis with the use of HELP. The HELP assay was performed as previously published. 18,19 One microgram of high-**molecular-weight DNA** was digested overnight with isoschizomer enzymes HpaII and MspI, respectively (New England Biolabs). **DNA** fragments were purified with phenol/chloroform, resuspended in 10mM Tris-HCl pH 8.0, ...

**Cited by:** 124

**Author:** Rita Shaknovich, Huimin Geng, Nathalie...

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## [Molecular subtypes based on DNA methylation predict ...](#)

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Dec 31, 2019 · In this study, we explored the prognostic value of **subtypes based on DNA methylation** status in 424 colon adenocarcinoma samples from the **Cancer** Genome Atlas database. Differences in **DNA methylation** levels were associated with differences in T, N, and M category, age, stage, and prognosis.

**Cited by:** 2**Author:** Changshun Yang, Yu Zhang, Xiaoqin Xu, ...**Publish Year:** 2019

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Jan 20, 2020 · The **DNA methylation signature** for **overall survival** (OS) prediction of **gastric cancer** (GC) patients. a Kaplan-Meier estimate of the OS using the identified **DNA methylation signature**. GC patients were divided into **low-risk** (N = 181) or **high-risk** (N = 182) **subgroup based** on the median of risk score. The difference between the two curves was determined by ...

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## [A methylation-based mRNA signature predicts survival in ...](#)

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Jul 06, 2020 · Evidence suggests that altered DNA methylation plays a causative role in the occurrence, progression and prognosis of **gastric cancer** (GC). Thus, **methyated-differentially expressed genes** (MDEGs) could potentially serve as biomarkers and therapeutic targets in GC.

**Cited by:** 1**Author:** Yang Li, Rongrong Sun, Youwei Zhang, Y...**Publish Year:** 2020





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## [Molecular Classification of Gastric Adenocarcinoma](#)

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6879029>

Nov 21, 2019 · Lei **Subtypes**. In 2013, Lei et al [] provided another **molecular** classification of GC which was reproducible and biologically and therapeutically meaningful. After comparing gene expression patterns among 248 **gastric** tumors (Singaporean patients from the National **Cancer** Centre and hospitals of the National Healthcare Group, Australian patients from the Peter MacCallum **Cancer** ...

**Cited by:** 1

**Author:** Qianqian Wang, Ganglei Liu, Chunhong Hu

**Publish Year:** 2019

## [A 19-Gene expression signature as a predictor of survival ...](#)

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5016995>

Sep 08, 2016 · The **overall survival** rate for CRC patients has increased, however, the individual **survival** rate for patients with Dukes' B and C is still low. A previous study developed a **molecular** classifier **based** on a core set of 43 genes to **predict** the 3-year **survival** for patients . The gene signatures were also validated on a different population using a ...

**Cited by:** 28

**Author:** Nurul Ainin Abdul Aziz, Norfilza Mohd Mo...

**Publish Year:** 2016

## [Parallel serial assessment of somatic mutation and ...](#)

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6976349>

The **methylation** status of genes such as APC, CDKN2A, RUNX3, RARB2, MSH2, and ESR1B in esophageal , liver , **gastric** , and breast **cancer** , respectively, has been associated with residual tumor after surgery and prognosis. In addition to its potential as a prognostic marker, monitoring of methylated ctDNA can also **predict** response to therapy.

**Cited by:** 1

**Author:** Shu Xia, Junyi Ye, Yu Chen, Analyn Lizas...

**Publish Year:** 2019

## [A two-gene epigenetic signature for the prediction of ...](#)

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6381754>

Triple-negative breast **cancer** has a high relapse rate after conventional chemotherapy treatment. To date, no predictors of treatment effectiveness have been identified. In this study, we propose an epigenetic **signature based** on the **methylation** levels of the FERD3L and TRIP10 genes. Our algorithm