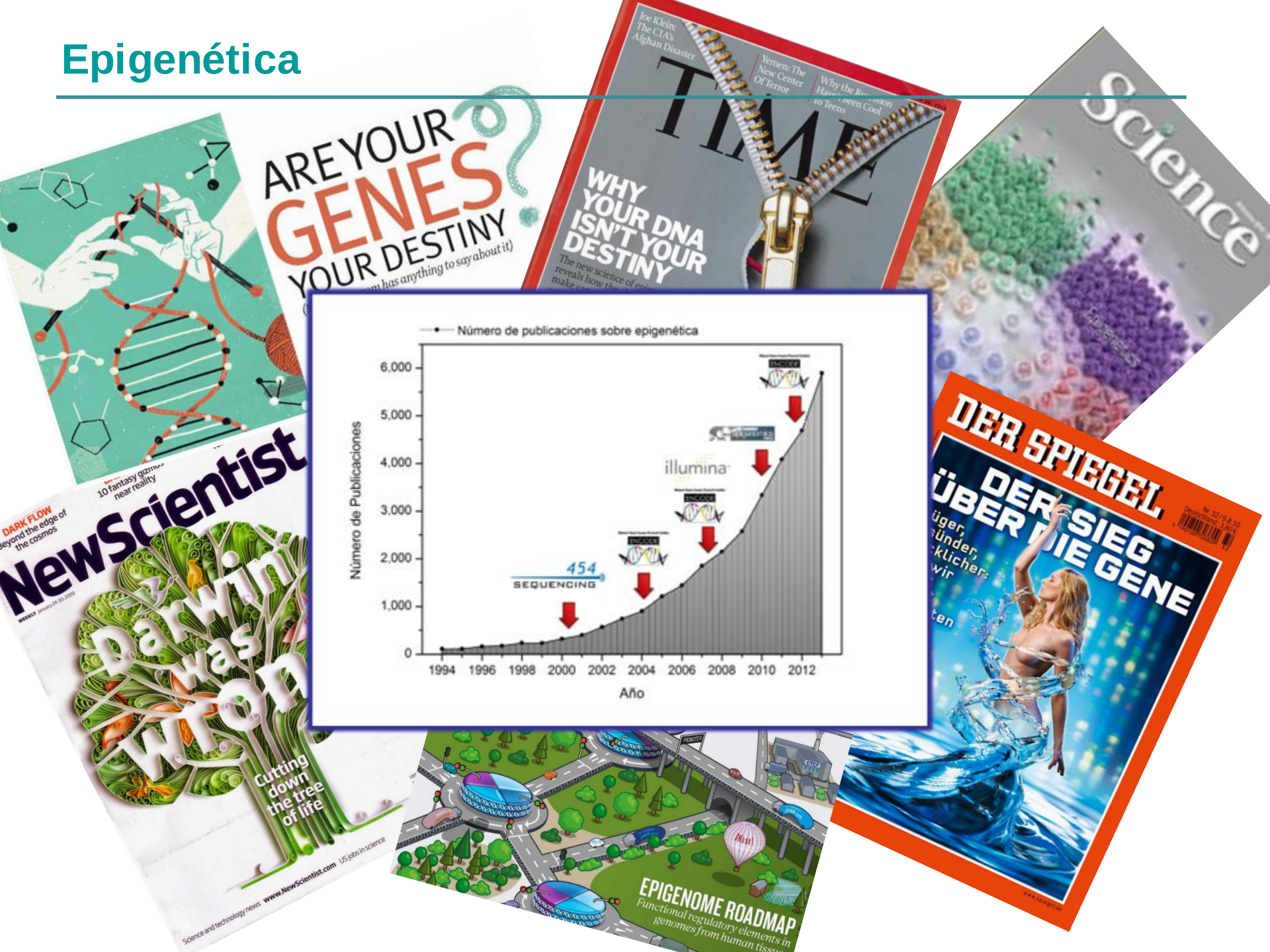


METILACIÓN DEL ADN

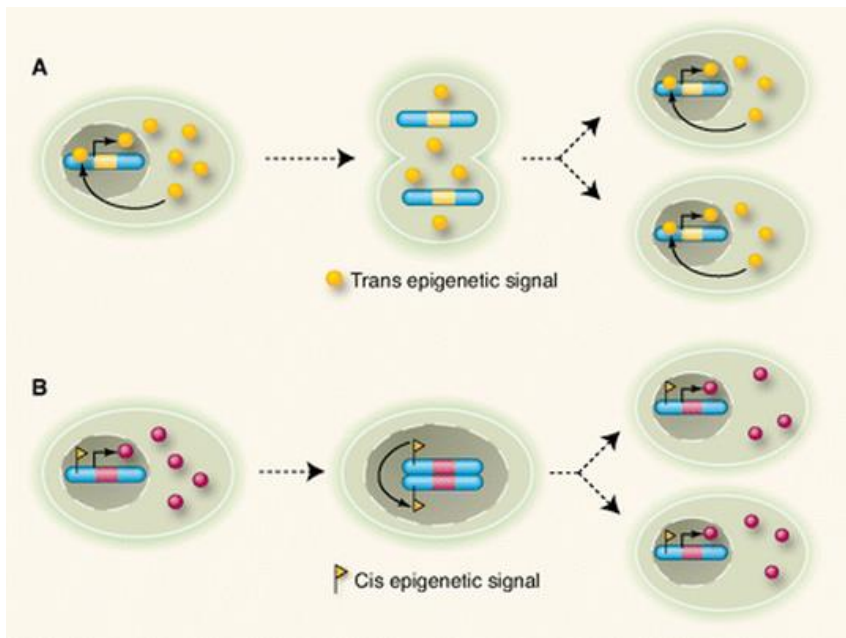
Epigenética



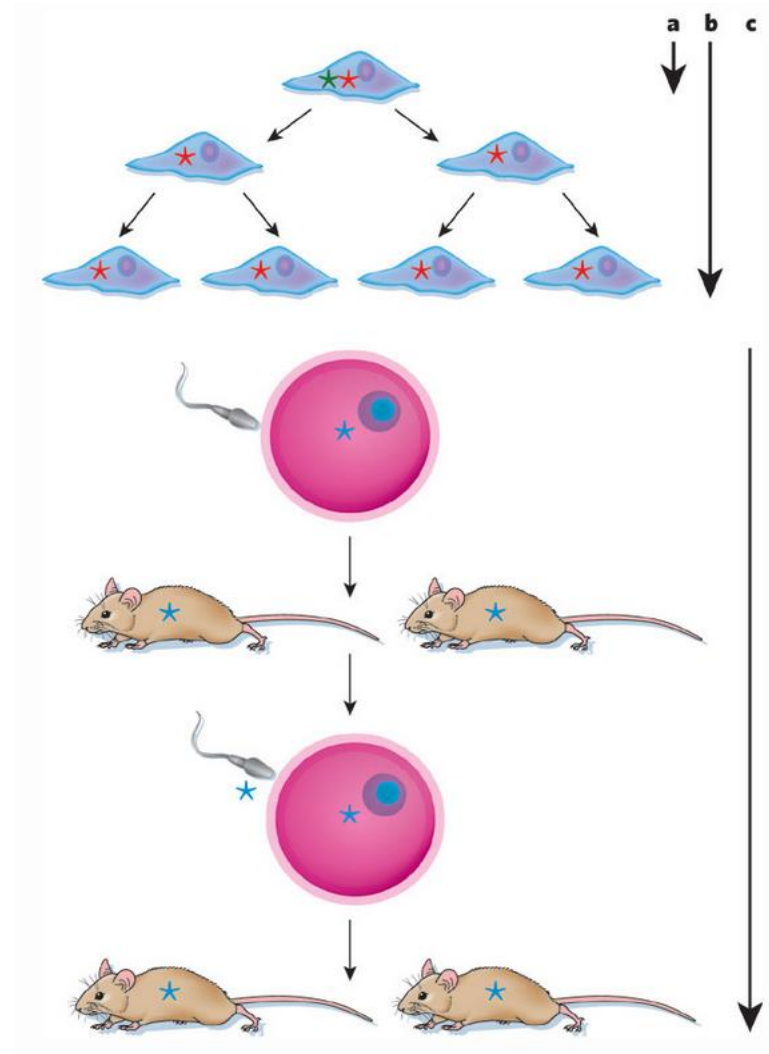
Factores epigenéticos

Características

- Regular procesos genómicos
- No alteran la secuencia de ADN
- Heredables
- Auto-perpetuables
- Reversibles

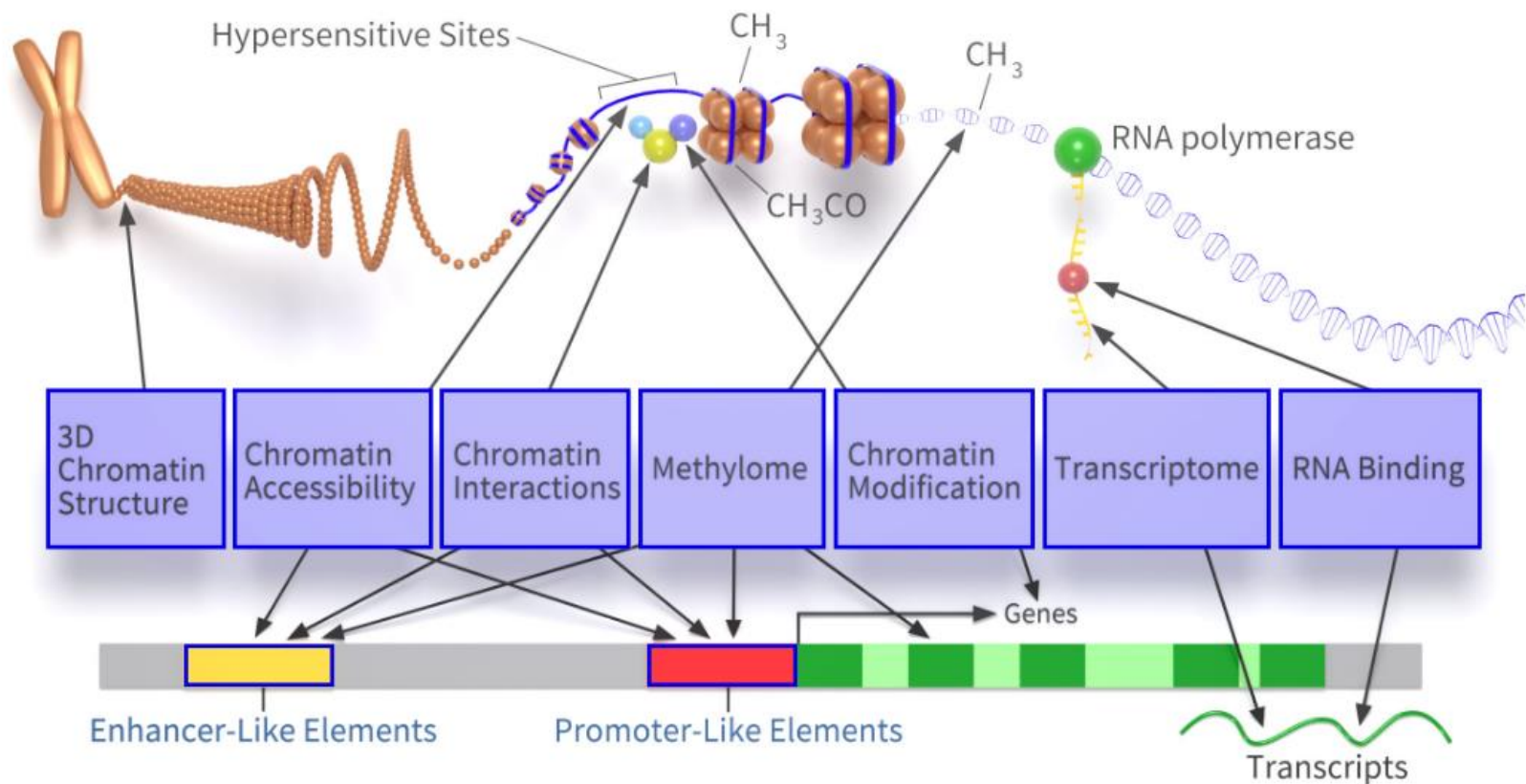
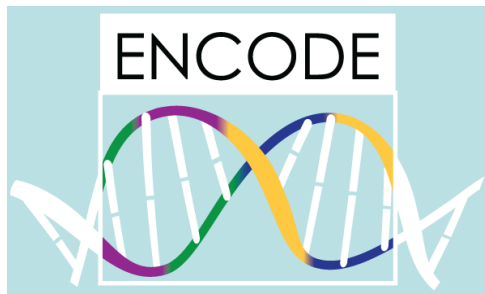


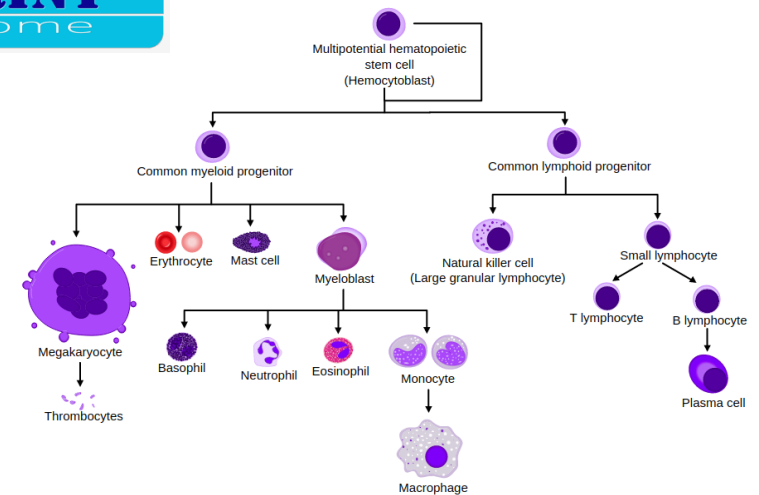
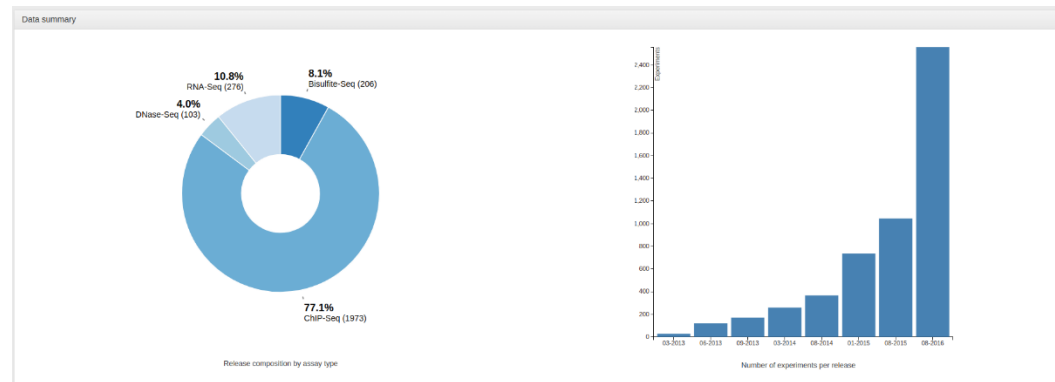
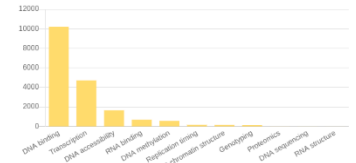
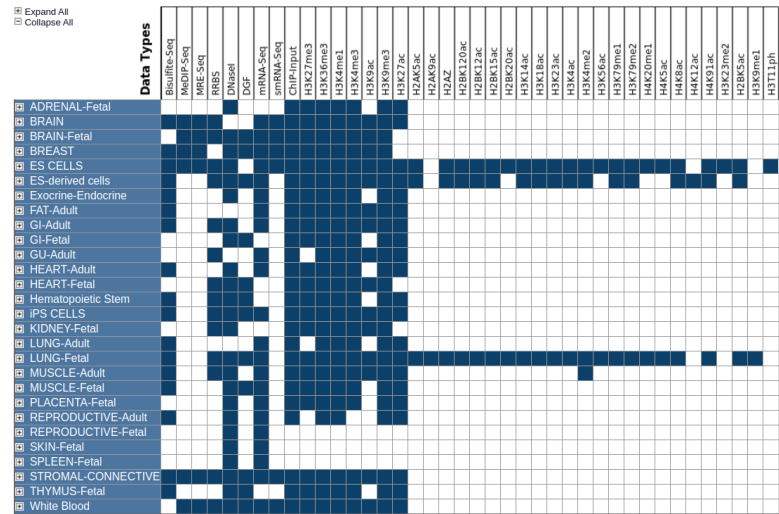
Auto-Perpetuables



Heredables

Proyectos Epigenoma





Proyectos Epigenoma

[Home](#)[Data Grid](#)[Download](#)[Community](#)[Help](#)[About](#)[IHEC Main Site](#)

About this site

The International Human Epigenome Consortium (IHEC) makes available comprehensive sets of reference epigenomes relevant to health and disease. The IHEC Data Portal can be used to view, search and download the data already released by the different IHEC-associated projects. Please [click here](#) to return to the main IHEC website.

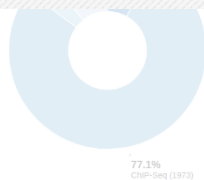
The Portal has been developed and is maintained by the McGill Epigenomics Data Coordination Centre (EDCC) and the McGill Epigenomics Mapping Centre (EMC). These two centres were established in 2012 at the McGill University and Genome Quebec Innovation Centre (Montreal, Canada) to support large-scale human epigenome mapping for a broad spectrum of cell types and diseases. Previous epigenetic studies have provided profiles of specific chromatin marks in relation to basic biological processes, and future studies of molecular mechanisms must build upon these proofs-of-concept by integrating sequence-based variation with multiple levels of epigenetic and transcriptional regulation across the genome of human tissues and animal disease models. This project leverages the high-throughput sequencing infrastructure and expertise in genomics and transcriptomics at the McGill Innovation Centre to carry out this research. Controlled access to the data by collaborators and the greater scientific community is gained via a portal, which takes advantage of Compute Canada high-performance computing cluster resources to manage the large volume of data associated from the generation of reference epigenome maps.

This project is funded under the Canadian Epigenetics, Environment, and Health Research Consortium (CEEHRC) by the Canadian Institutes of Health Research and by Genome Quebec, with additional support from Genome Canada. The computing and networking infrastructure, and part of the software development, are provided by Compute Canada and CANARIE as part of the [GenAP project](#).

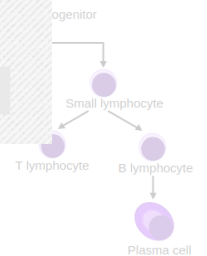
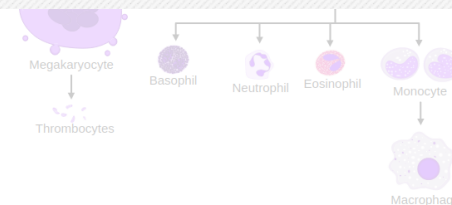
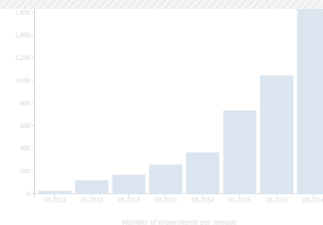
How to Cite

If you use the IHEC Data Portal to identify, download, visualize or analyze data in your research project, please cite:

Bujold et al. "The International Human Epigenome Consortium Data Portal." *Cell Systems* 3.5 (2016): 496-499. ([Link](#))



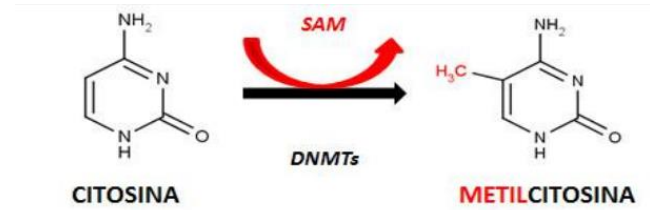
Release composition by assay type



¿Qué es la metilación del ADN?

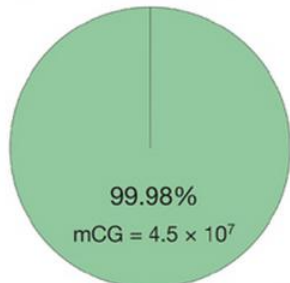
La metilación es la adición de grupos metilo ($-\text{CH}_3$) a una molécula

En eucariotas mayormente en las citosinas
Mediado por metiltransferasas específicas

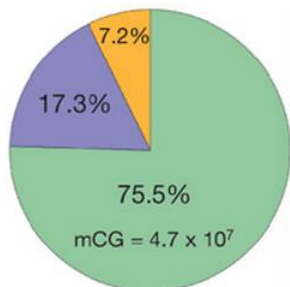


Humano

mCG mCHG mCHH



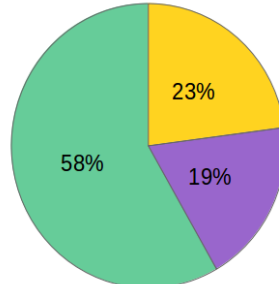
IMR90 mC = 4.5×10^7



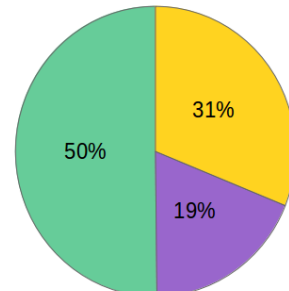
H1 mC = 6.2×10^7

Arabidopsis

mCG mCHG mCHH



Leaves mC = 5.7×10^7



Embryo mC = 1.8×10^7

En genomas de mamíferos el dinucleótido
CpG es la principal diana de metilación

Article

Nature 462, 315–322 (19 November 2009) | doi:10.1038/nature08514; Received 19 June 2009; Accepted 21 September 2009; Published online 14 October 2009

Human DNA methylomes at base resolution show widespread epigenomic differences

Ryan Lister^{1,9}, Mattia Pelizzola^{1,9}, Robert H. Dowen¹, R. David Hawkins², Gary Hon², Julian Tonti-Filippini⁴, Joseph R. Nery¹, Leonard Lee², Zhen Ye², Que-Minh Ngo², Lee Edsall², Jessica Antosiewicz-Bourget^{5,6}, Ron Stewart^{5,6}, Victor Ruotti^{5,6}, A. Harvey Millar⁴, James A. Thomson^{5,6,7,8}, Bing Ren^{2,3} & Joseph R. Ecker¹

Cell

Volume 133, Issue 3, 2 May 2008, Pages 523–536

Resource

Highly Integrated Single-Base Resolution Maps of the Epigenome in *Arabidopsis*

Ryan Lister^{1,2,5}, Ronan C. O'Malley^{1,2,5}, Julian Tonti-Filippini^{4,5}, Brian D. Gregory^{1,2}, Charles C. Berry³, A. Harvey Millar⁴, Joseph R. Ecker^{1,2}  

¿Qué es la metilación del ADN?

NATURE | ARTICLE



[日本語要約](#)

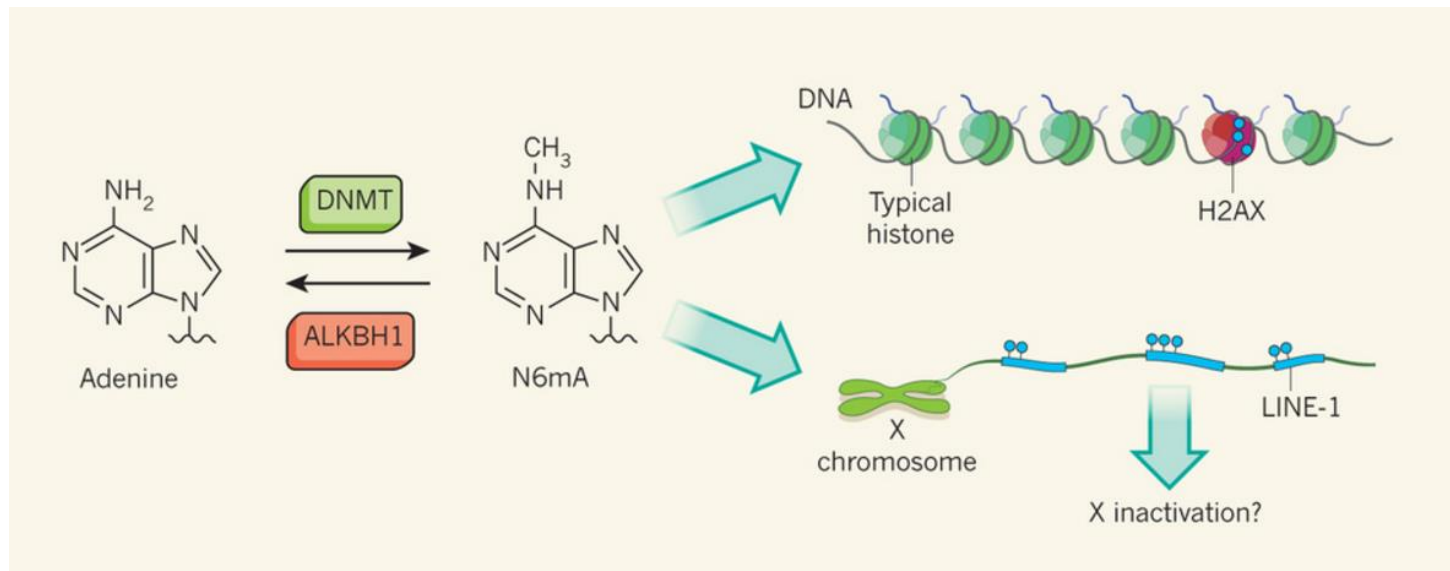
DNA methylation on N^6 -adenine in mammalian embryonic stem cells

Tao P. Wu, Tao Wang, Matthew G. Seetin, Yongquan Lai, Shijia Zhu, Kaixuan Lin, Yifei Liu, Stephanie D. Byrum, Samuel G. Mackintosh, Mei Zhong, Alan Tackett, Guilin Wang, Lawrence S. Hon, Gang Fang, James A. Swenberg & Andrew Z. Xiao

[Affiliations](#) | [Contributions](#) | [Corresponding author](#)

Nature **532**, 329–333 (21 April 2016) | doi:10.1038/nature17640

Received 16 August 2015 | Accepted 07 March 2016 | Published online 30 March 2016



Patrones de metilación

Review

Nature Reviews Genetics 9, 465-476 (June 2008) | doi:10.1038/nrg2341

DNA methylation landscapes: provocative insights from epigenomics

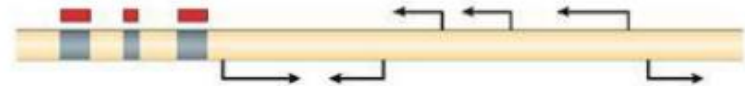
Miho M. Suzuki¹ & Adrian Bird¹ [About the authors](#)

Los patrones de metilación (distribución a lo largo de la secuencia) no son iguales en distintos eucariotas

- Genes
- Regiones metiladas
- Regiones no metiladas
- Elementos transponibles

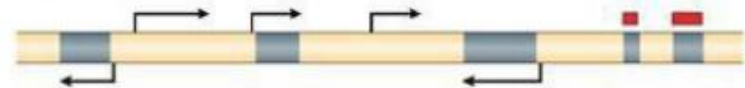
a Mosaic DNA methylation

(fungi, for example, *Neurospora crassa*)



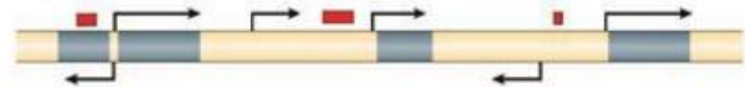
b Mosaic DNA methylation

(plants, for example, *Arabidopsis thaliana*)



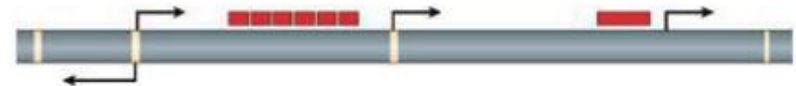
c Mosaic DNA methylation

(animals, for example, *Ciona intestinalis*)



d Global DNA methylation

(animals, for example, *Homo sapiens*)



e Global DNA methylation

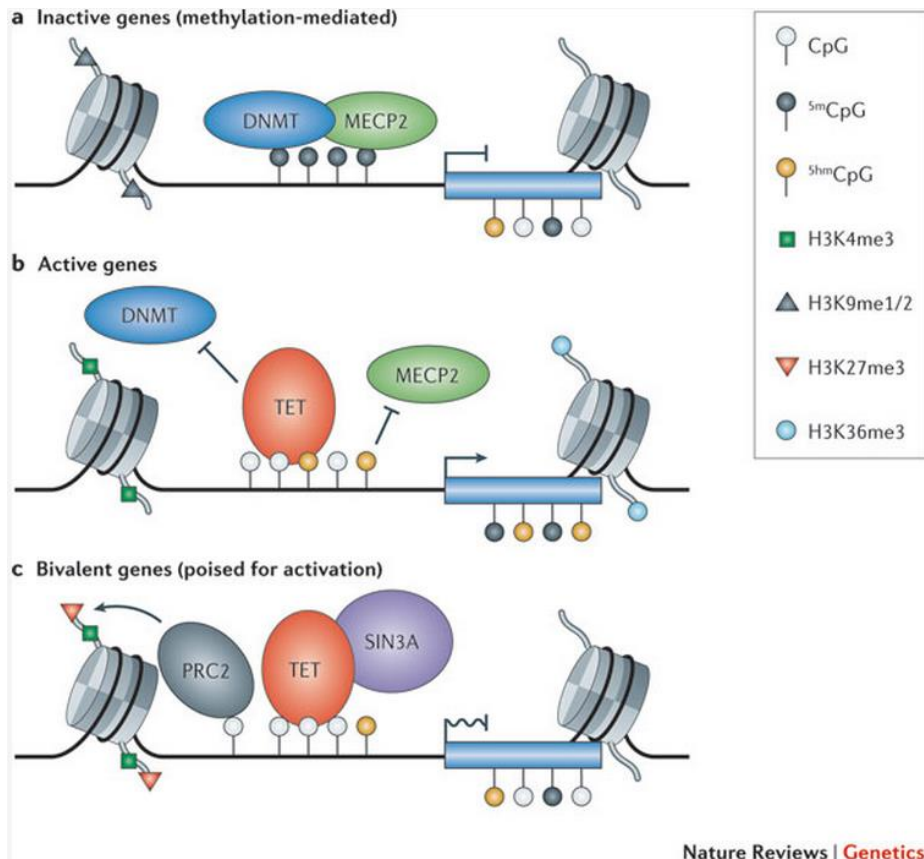
(plants, for example, *Zea mays*)



Función e impacto de la metilación

Funciones más importantes

- Desarrollo embrionario
- Impronta génica e inactivación del cromosoma X
- En el cuerpo génico estabiliza la transcripción
- En promotores inhibe la transcripción



Review

Nature Reviews Genetics **13**, 484-492 (July 2012) | doi:10.1038/nrg3230

Functions of DNA methylation: islands, start sites, gene bodies and beyond

Peter A. Jones¹ [About the author](#)

Progress

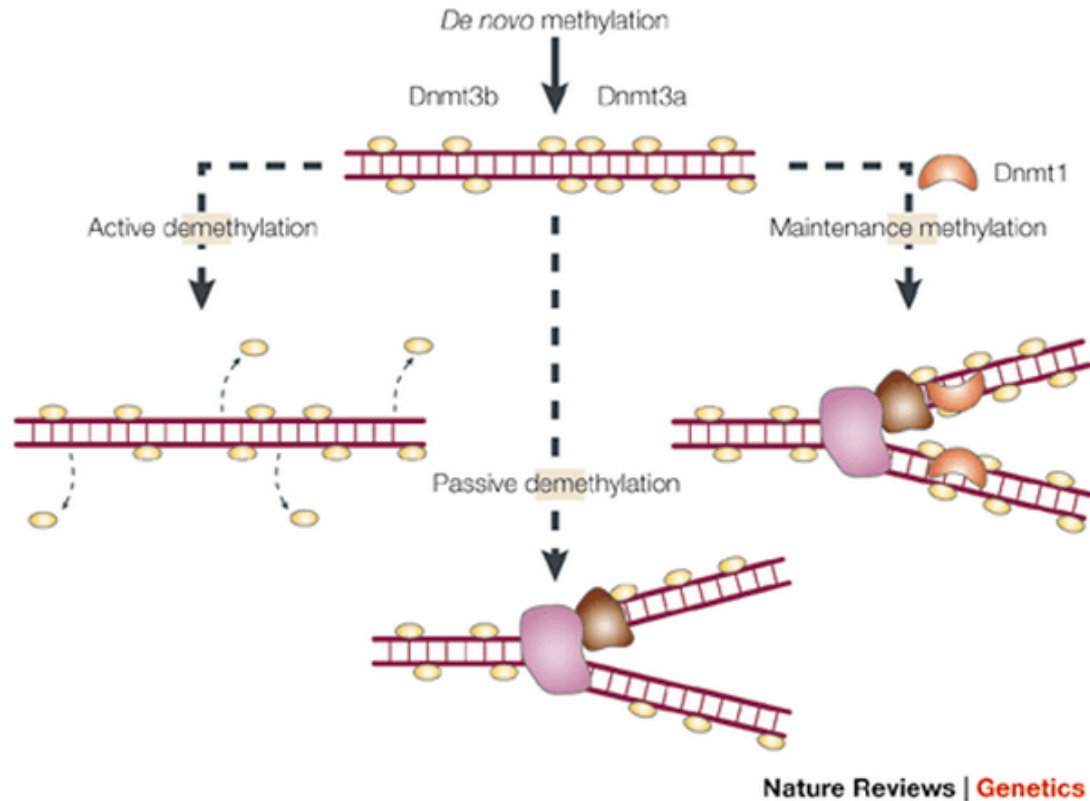
Nature Reviews Genetics **13**, 7-13 (January 2012) | doi:10.1038/nrg3080

Uncovering the role of 5-hydroxymethylcytosine in the epigenome

Miguel R. Branco¹, Gabriella Ficz¹ & Wolf Reik¹ [About the authors](#)

La interacción entre la metilación del DNA y varias proteínas modifican las cadenas de las histonas determinando el estado de la cromatina

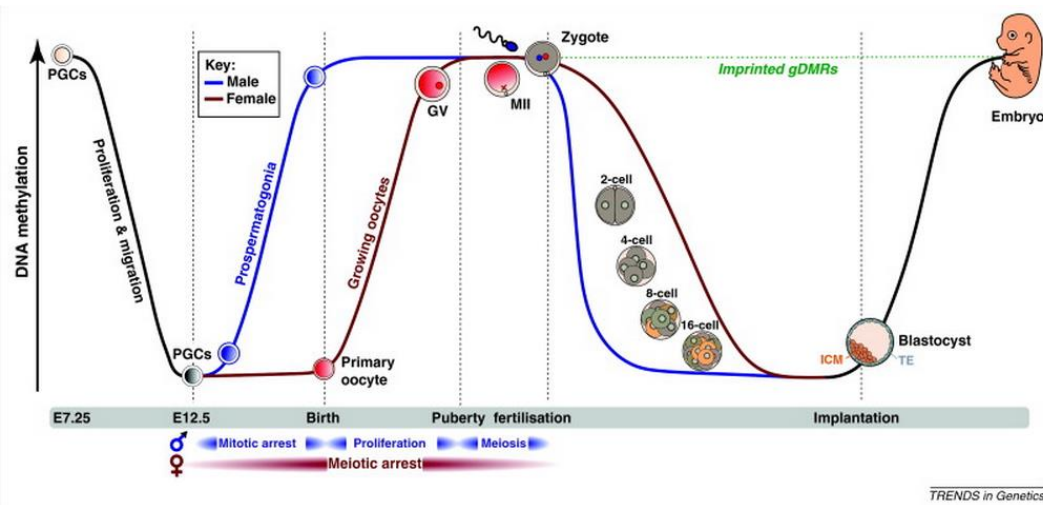
Dinámica de la metilación



Metilación 'de novo'
Metilación de mantenimiento
Desmetilación activa y/o pasiva

Dinámica de la metilación

- Metilación 'de novo'



Trends in
Genetics

Volume 28, Issue 1, January 2012, Pages 33–42

Review

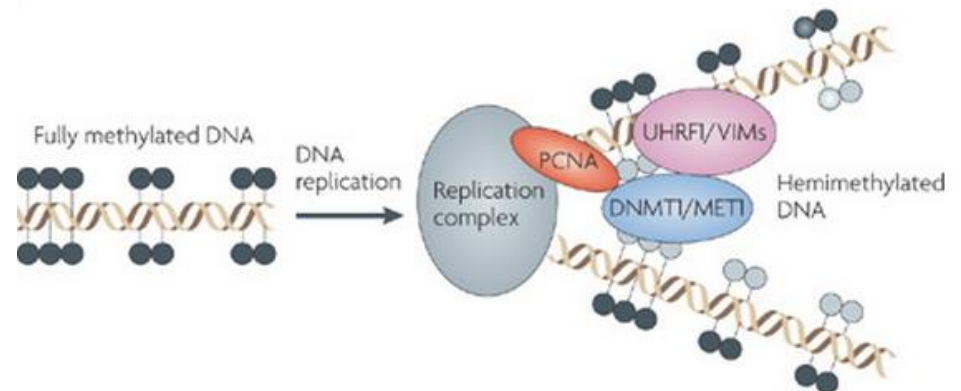
De novo DNA methylation: a germ cell perspective

Sébastien A. Smallwood, Gavin Kelsey

Las regiones improntadas se establecen previa fertilización

- Metilación de mantenimiento

DNMT1 reconoce las regiones hemimetiladas y copia el patrón en la hebra complementaria



Review

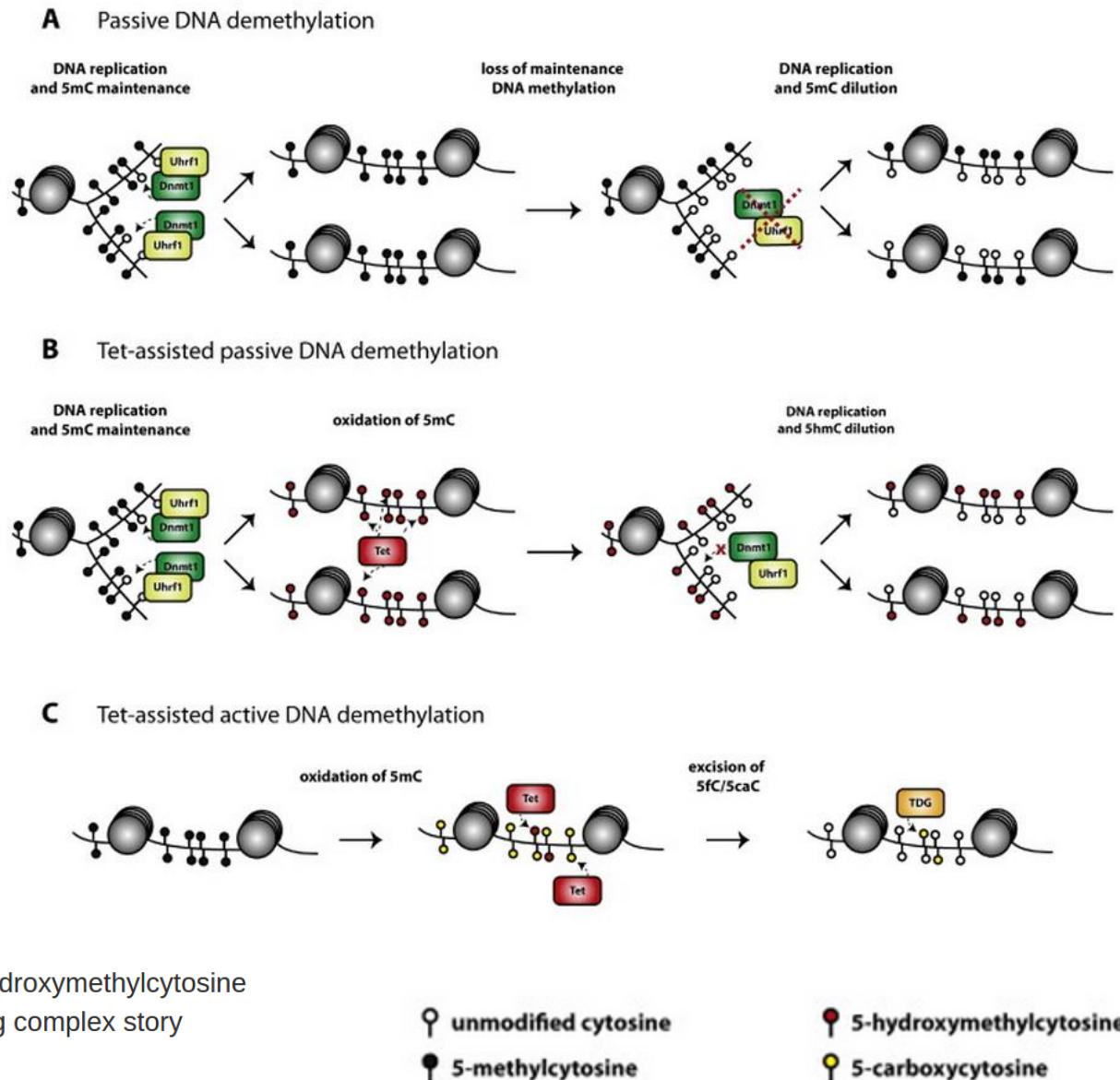
Nature Reviews Genetics 11, 204–220 | doi:10.1038/nrg2719

Establishing, maintaining and modifying DNA methylation patterns in plants and animals

Julie A. Law¹ & Steven E. Jacobsen² [About the authors](#)

Dinámica de la metilación

- Desmetilación



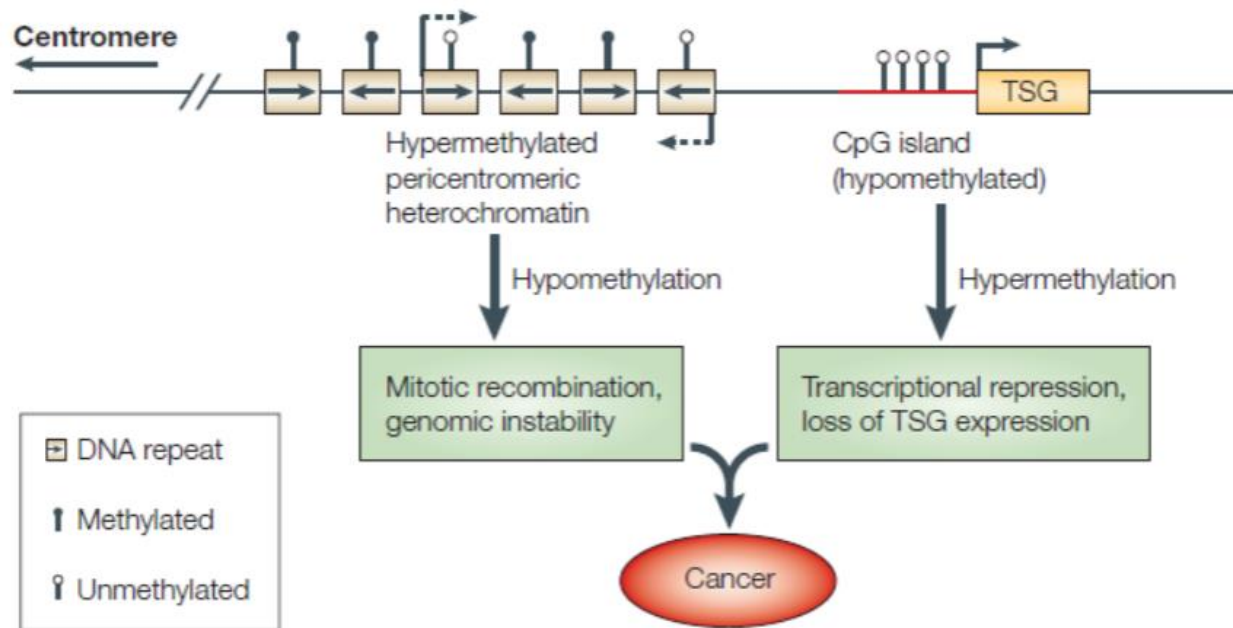
Las variantes de las metilcitosinas no son reconocidas por DNMT1, pero si por mecanismos de reparación que las cambian por citosinas no metiladas

Review

DNA demethylation, Tet proteins and 5-hydroxymethylcytosine in epigenetic reprogramming: An emerging complex story

Peter W.S. Hill, Rachel Amouroux, Petra Hajkova

Metilación y Enfermedad



Review

Nature Reviews Genetics 6, 597-610 (August 2005) | doi:10.1038/nrg1655

DNA methylation and human disease

Keith D. Robertson¹ [About the author](#)

Tanto el exceso como la ausencia de metilación pueden desembocar en situaciones patológicas