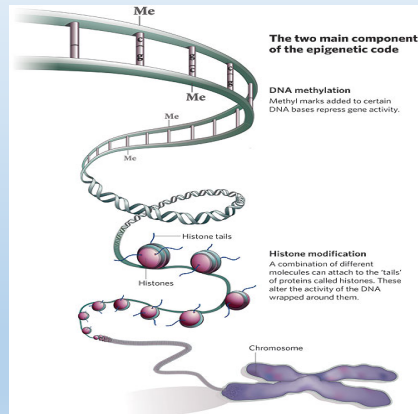
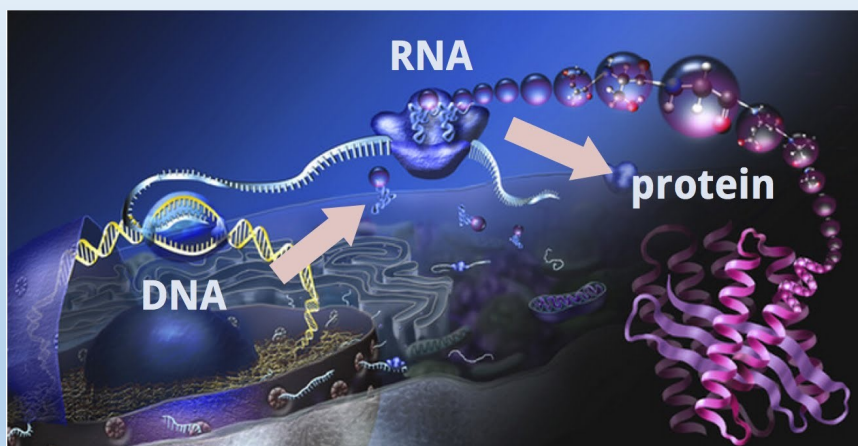
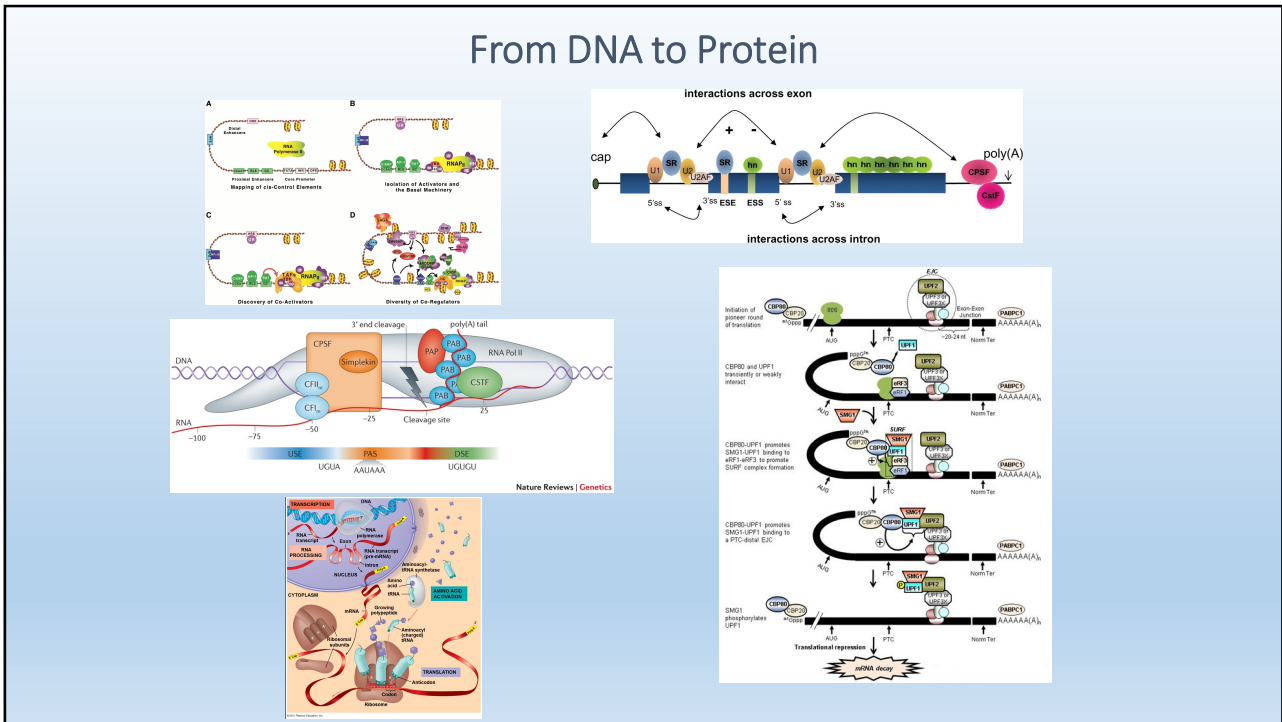


Marcadores epigenéticos: A nova era da genética molecular



From DNA to Protein





Epigenetics

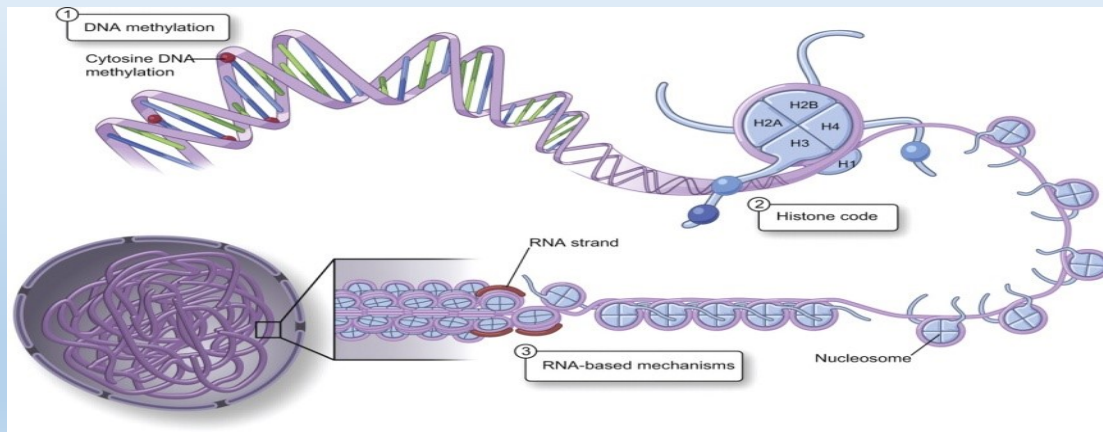
from mechanisms to disease

Environmentally-mediated and widespread changes that **affect gene expression** without **modifying the DNA sequence**

Epigenetic modifications includes:

- DNA methylation
- Histone modification
- Small non-coding RNAs

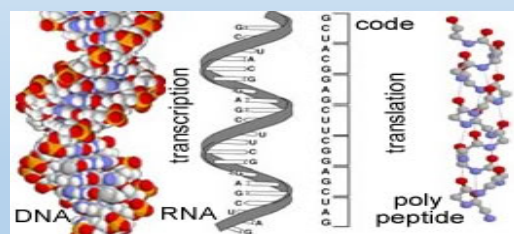
Epigenetic changes



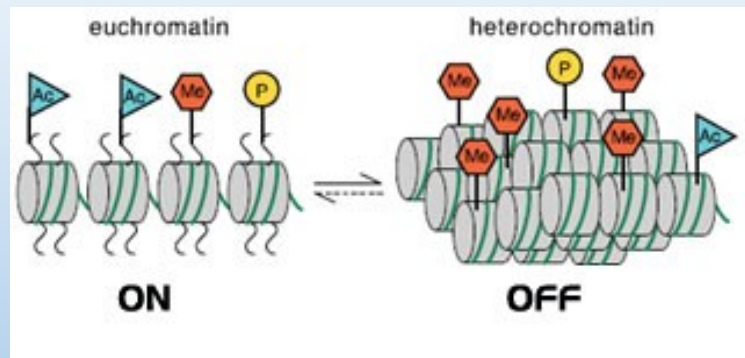
<http://www.intechopen.com/source/html/44560/media/image1.jpeg>

Chromatin Structure

- Every cell in our body contains exactly the **same genome**, however, inside the individual cells **some genes are activated while others are silenced**.



Chromatin Structure



Chromatin and Condensed Chromosome Structure

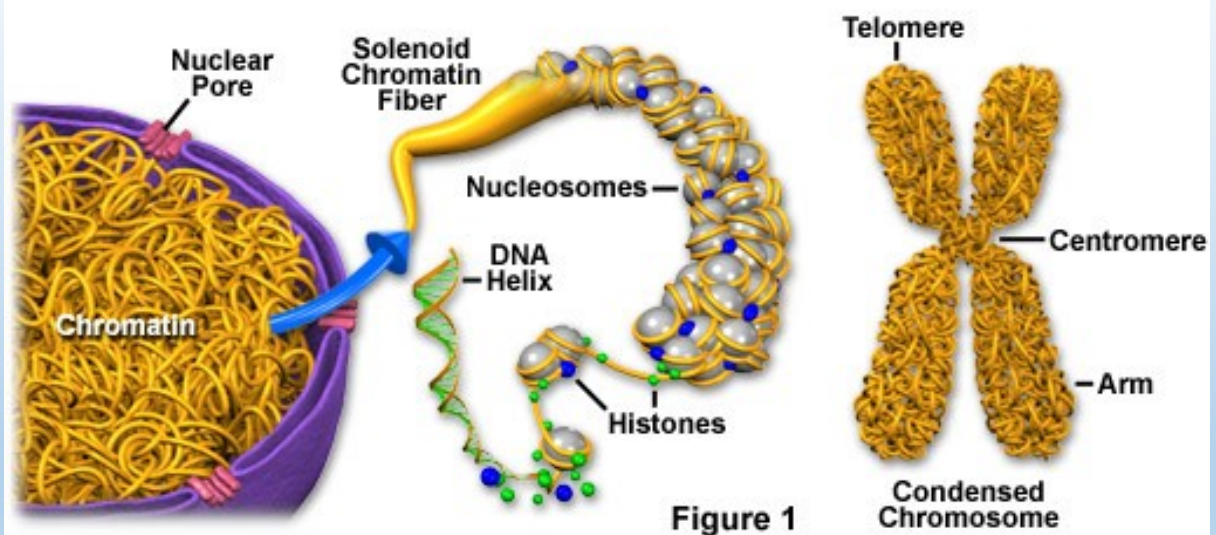
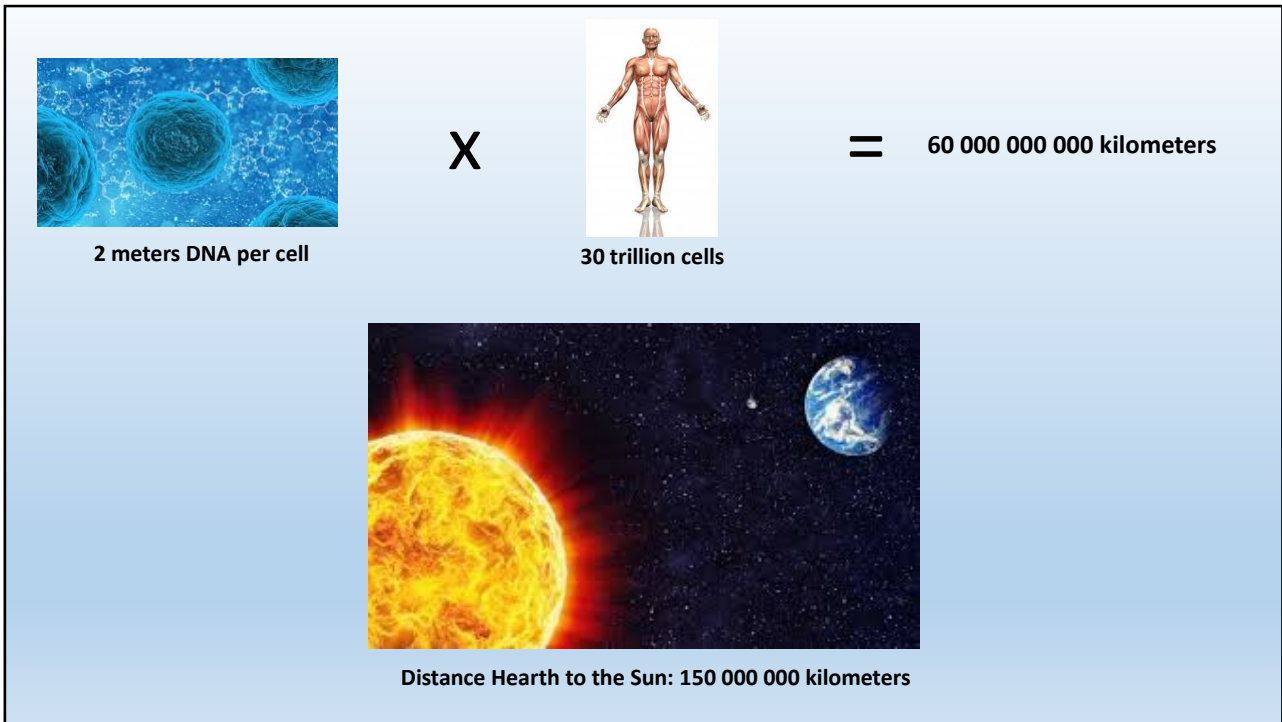


Figure 1

micro.magnet.fsu.edu



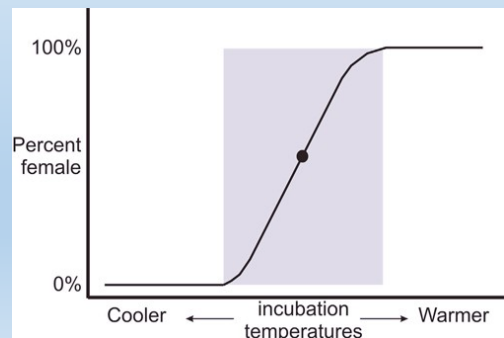
Epigenetics: Sex determination

- Turtles

Sex phenotype determined by environmental conditions – **temperature**



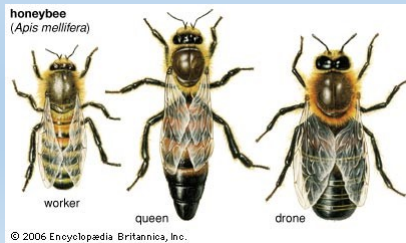
Differences in temperature alter the percentage of **DNA methylation** of the *aromatase (estrogen synthetase)* promoter



Diaz-Hernandez, et al. Developmental Biology, volume 408, Issue 1

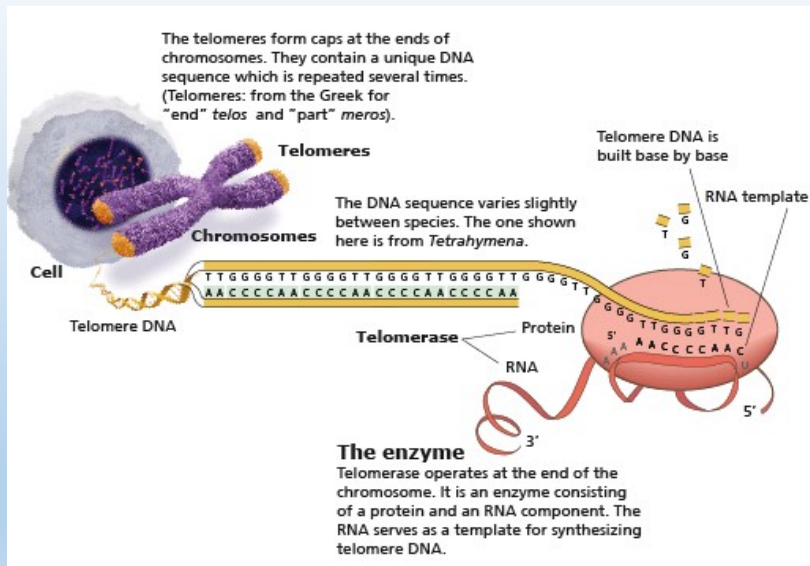
Epigenetics: Phenotype / Longevity

- When ***Dnmt3*** is turned "on," the queen genes are epigenetically silenced, and the larvae develop into the default "worker" variety.
- But when royal jelly turns ***Dnmt3*** "off," the queen genes jump into action, turning the larvae into queens.

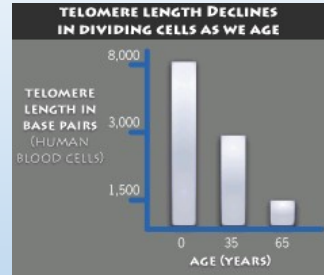
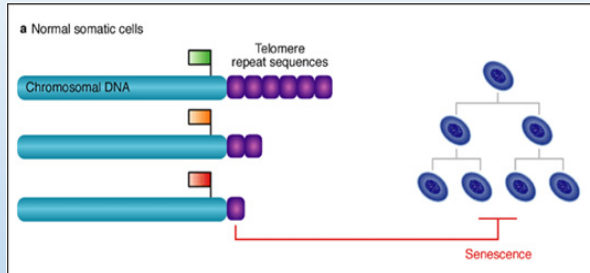


Queen bees live
10x longer
than worker bees!!!!

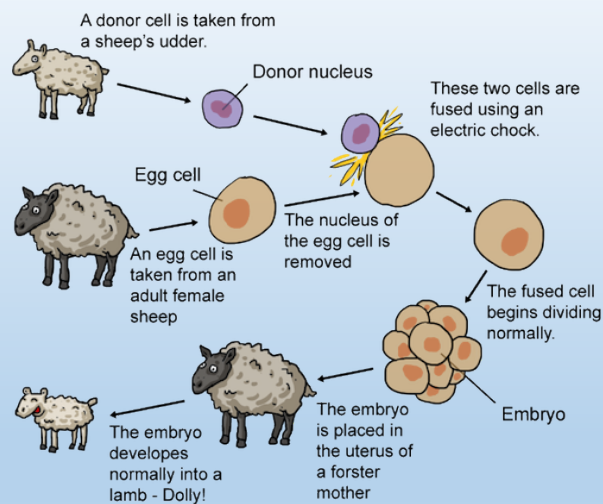
Telomeres and Telomerase



Aging



Aging – The Dolly story



Aging – The Dolly story

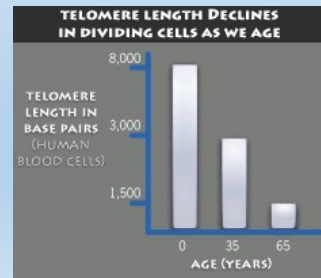


Dolly (5 July 1996 – 14 February 2003)

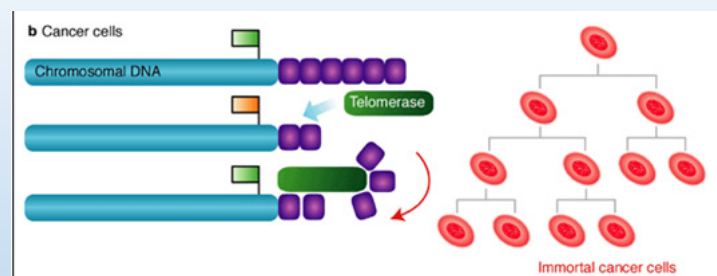
“Em 1999 foi divulgado na revista *Nature* que Dolly poderia tender a desenvolver formas de envelhecimento precoce, uma vez que os seus telómeros eram mais curtos que os das ovelhas normais.”

Fact: Sheep's life expectancy – 15 years.

Fact: Dolly's "Mother" Age – 6 years.



Telomerase activation in cancer



Telomerase is active in 90% of cancers

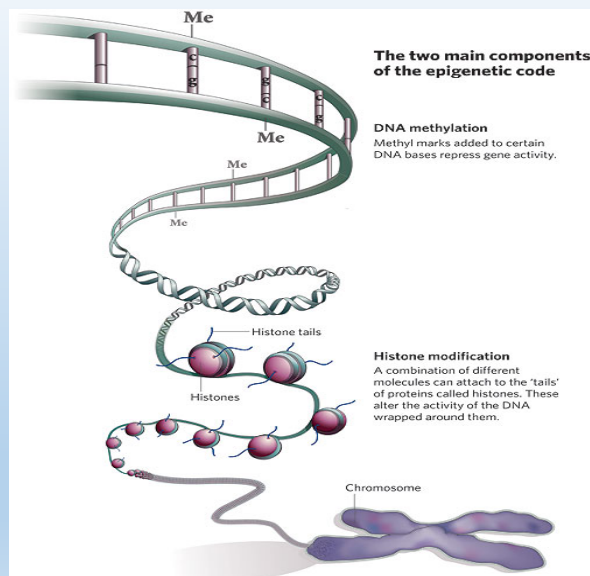
Prognostic Factor in Cancer

Telomerase activity is also found in normal cells – embryonic stem cells, germ lines, lymphocytes.

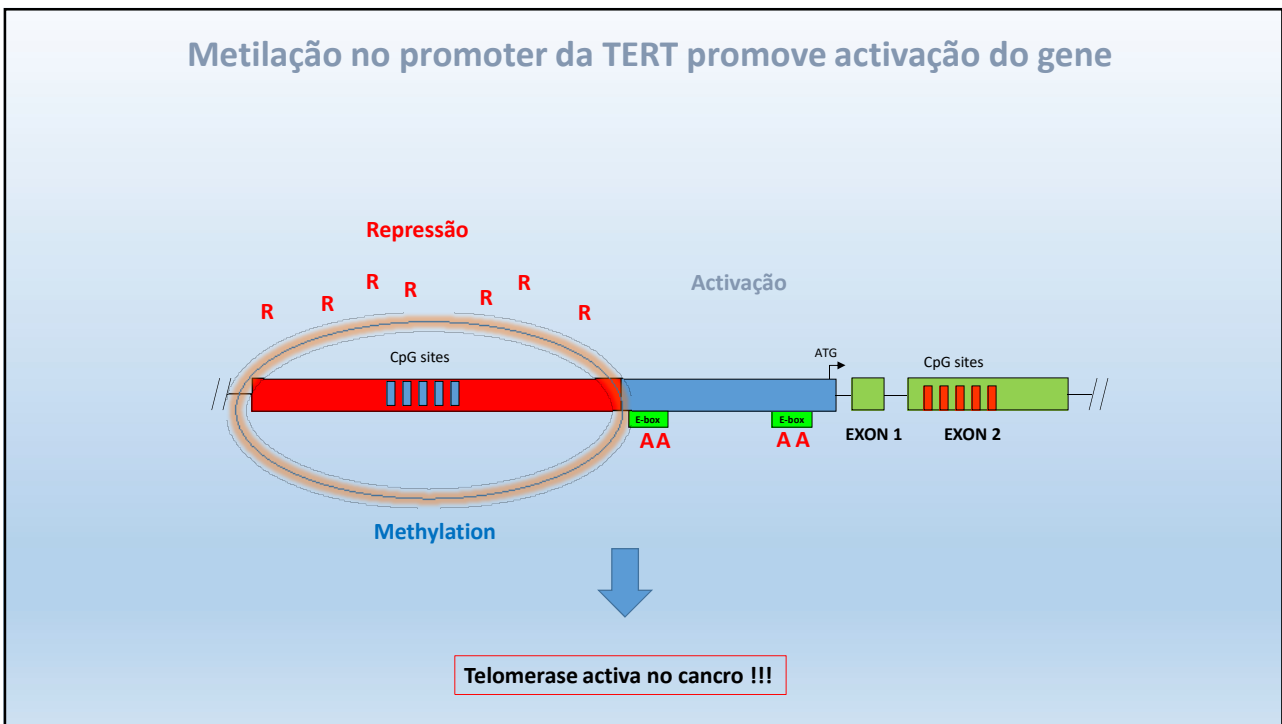
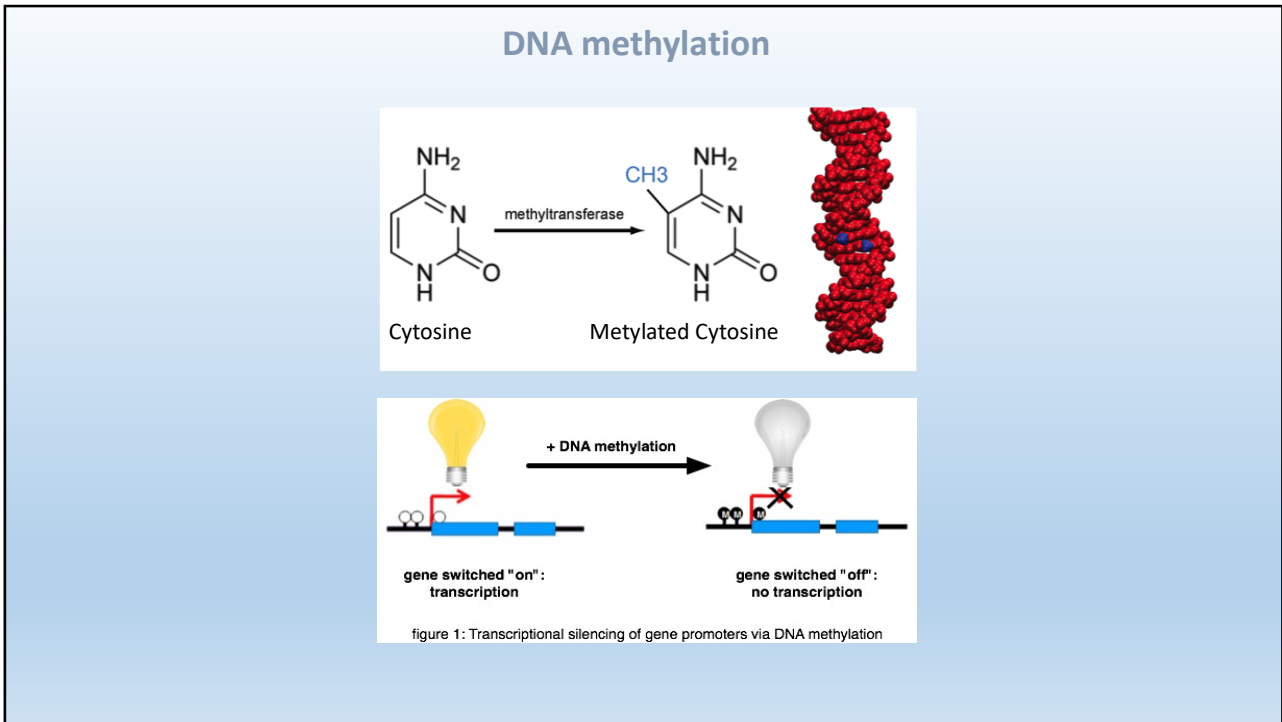
Pergunta: Como é que as células cancerígenas activam a telomerase?



Mecanismo Epigenético



Qiu, Nature, 2006



Implicações no diagnóstico e prognóstico do cancro

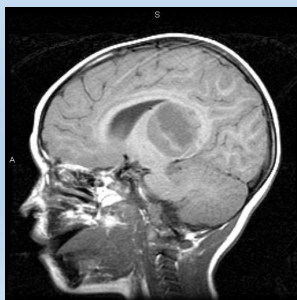
Articles

Lancet Oncol 2013; 14: 534-42

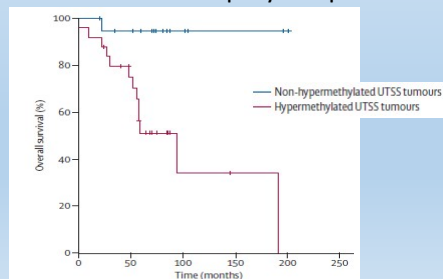


Methylation of the TERT promoter and risk stratification of childhood brain tumours: an integrative genomic and molecular study

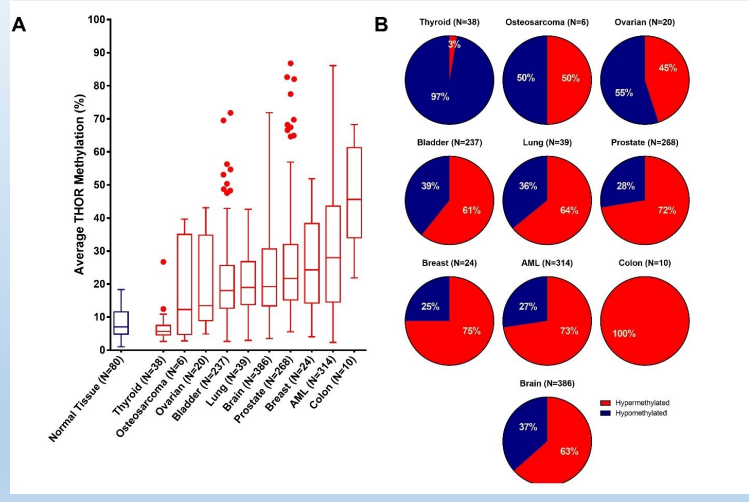
Pedro Castelo-Branco, Sanaa Choufani, Stephen Mack, Denis Gallagher, Cindy Zhang, Tatiana Lipman, Nataliya Zhukova, Erin J Walker, Dianna Martin, Diana Merino, Jonathan D Wasserman, Cynthia Elizabeth, Noa Alon, Libo Zhang, Volker Hovestadt, Marcel Kool, David TW Jones, Gelareh Zadeh, Sidney Croul, Cynthia Hawkins, Johann Hitzler, Jean CY Wang, Sylvain Baruchel, Peter B Dirks, David Malkin, Stefan Pfister, Michael D Taylor, Rosanna Weksberg, Uri Tabori



Overall Survival – ependymoma patients

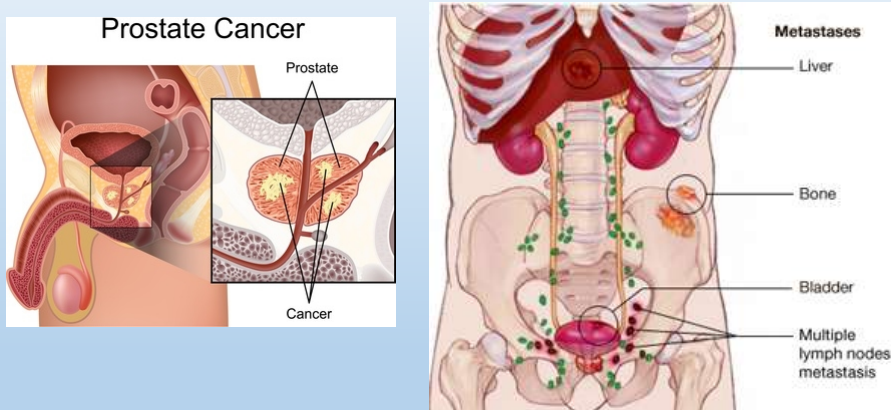


THOR is a pan-cancer biomarker



Dave Lee, et al. *Jour. Clin. Investigation* 2018

Prostate cancer – primary and metastatic



Prostate cancer – pathological grading

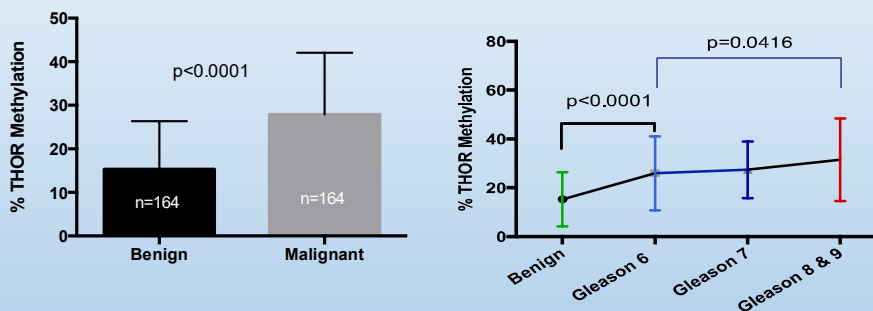
Gleason Sum of Primary and secondary histological patterns (such as Cell morphology and invasion) ex: Gleason 7 (4+3 or 3+4)

Gleason Score 2, 3, 4	Gleason Score 5, 6, 7	Gleason Score 8, 9, 10
Low-grade tumor	Medium-grade tumor	High-grade tumor
Slow Growth	Unpredictable Growth	Aggressive Growth
Least dangerous. Cells look most like normal prostate cells and are described as being "well-differentiated". Tends to be slow growing.	Intermediate cancers may behave like low-grade or high-grade cancers. The cells' behavior may depend on the volume of the cancer and the PSA level. This is the most common grade of prostate cancer.	High-grade cancers are usually very aggressive and quick to spread to the tissue surrounding the prostate. These cancer cells look least like normal prostate cells and are usually described as "poorly-differentiated".

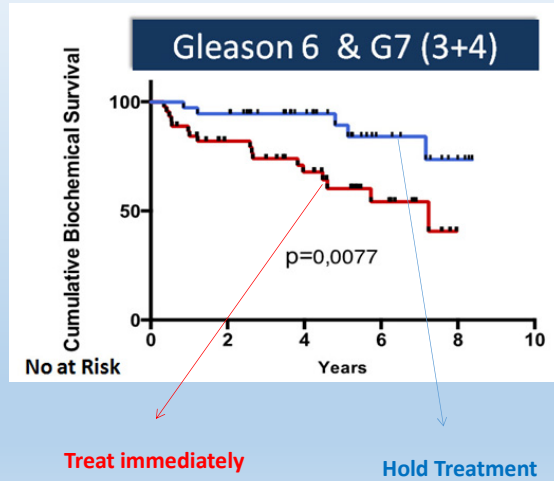


Grey Area

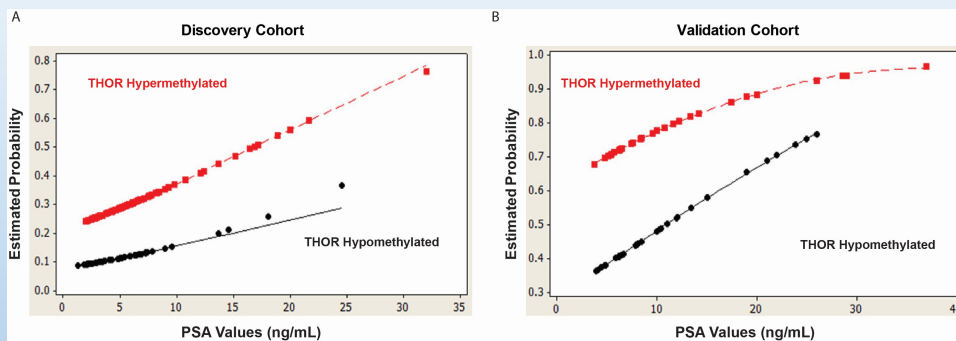
THOR distinguishes benign and malignant prostate samples



THOR defines two different populations of patients amongst lower Gleason scores

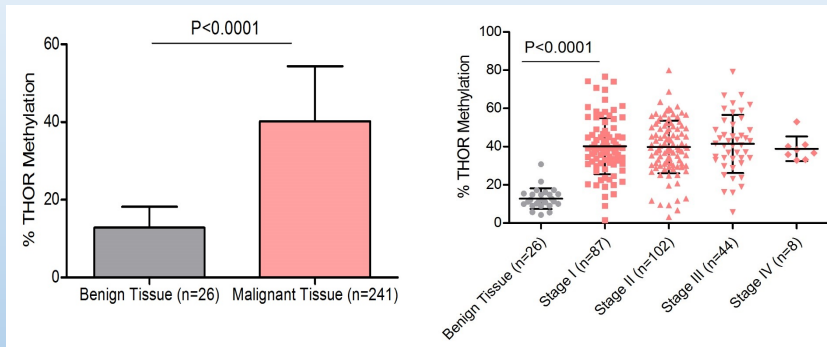


THOR significantly adds predictive value to Prostate Cancer recurrence.

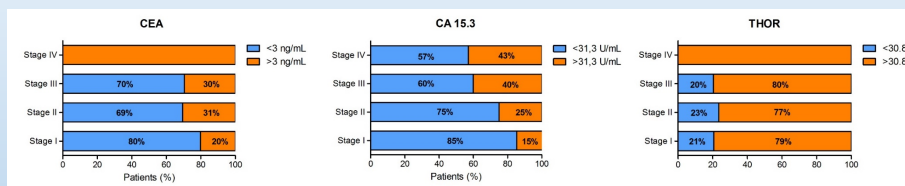


Ricardo Leão et al *Oncotarget*, 2016

THOR is Diagnostic Biomarker in Breast Cancer



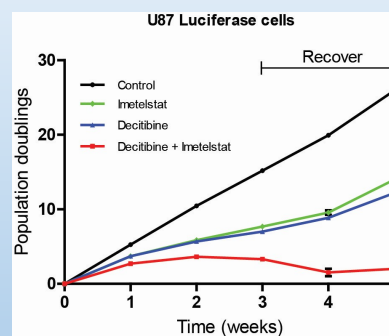
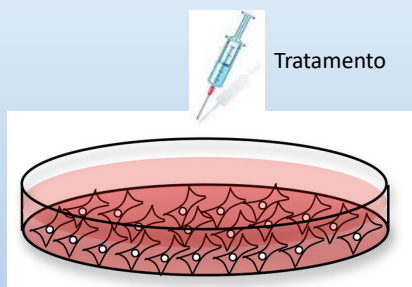
THOR compared to other biomarker for breast cancer diagnosis



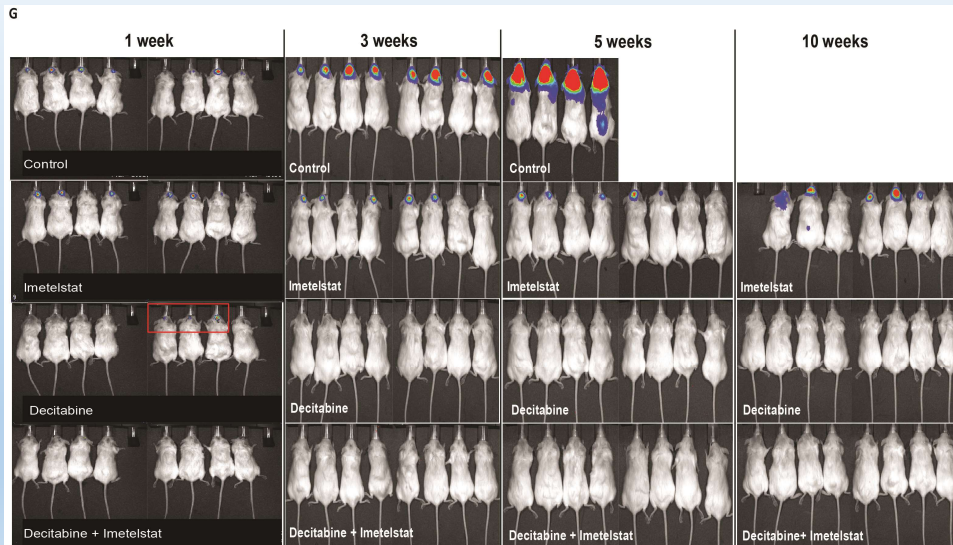
✓ A high percentage of patients with invasive disease had normal values of CA 15.3 and CEA, but had pathological levels of THOR.

Implicações terapêuticas

Tratamento com agentes demetilantes inibe a divisão celular (in vitro)



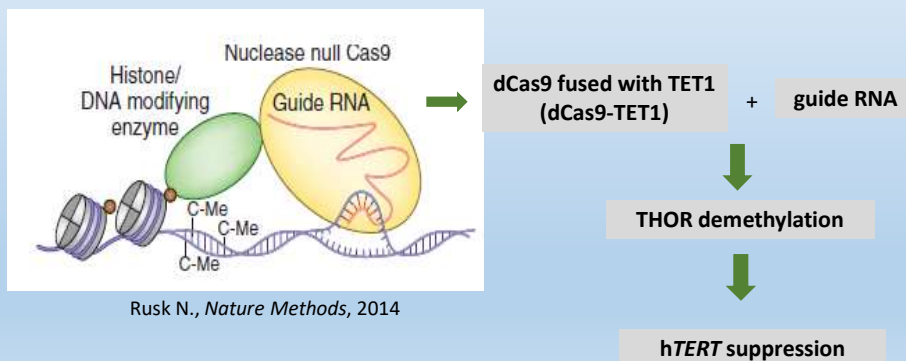
Tratamento com agentes demetilantes previne a recorrência tumoral (in vivo)



Targeted THOR demethylation using CRISPR/dCas9 system

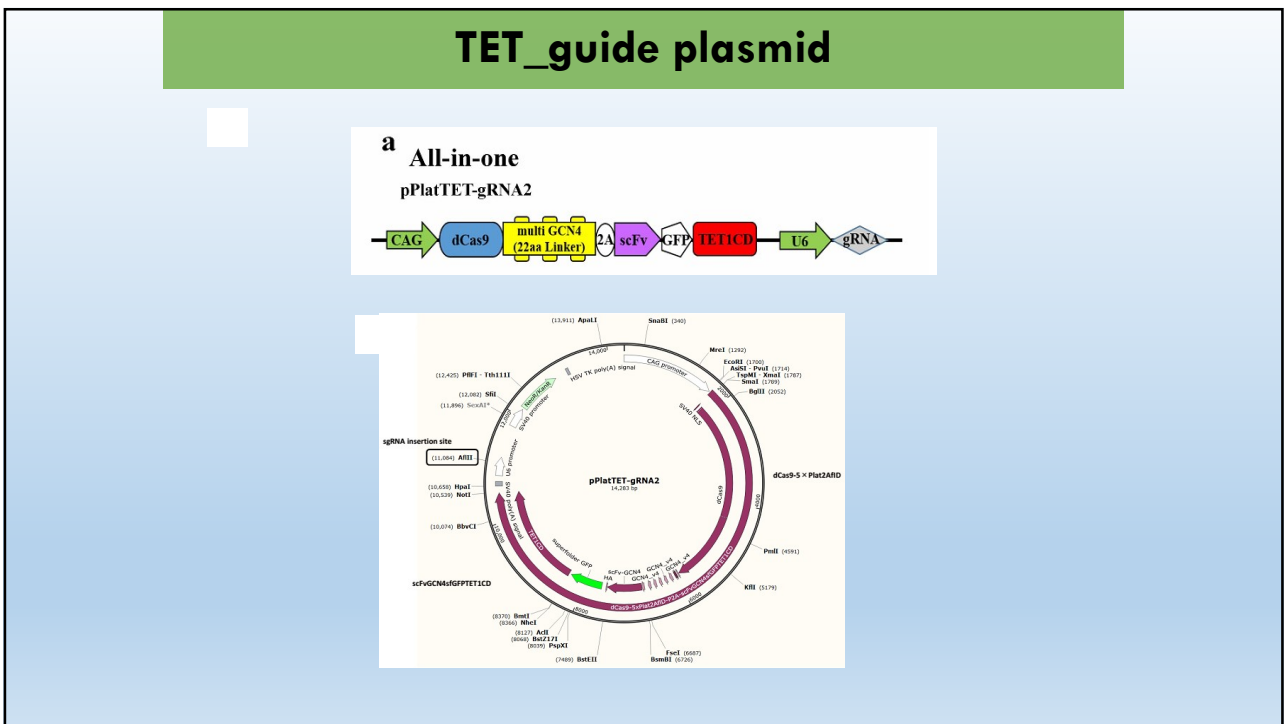
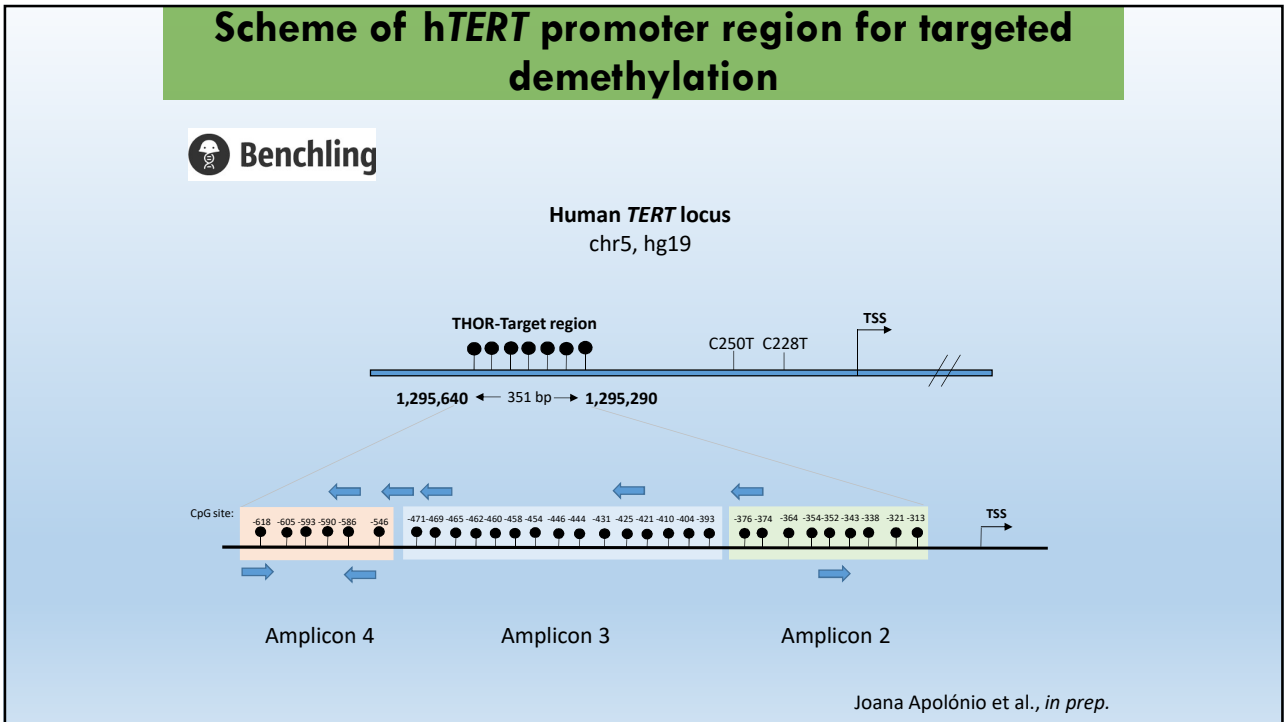
CRISPR/dCas9 system

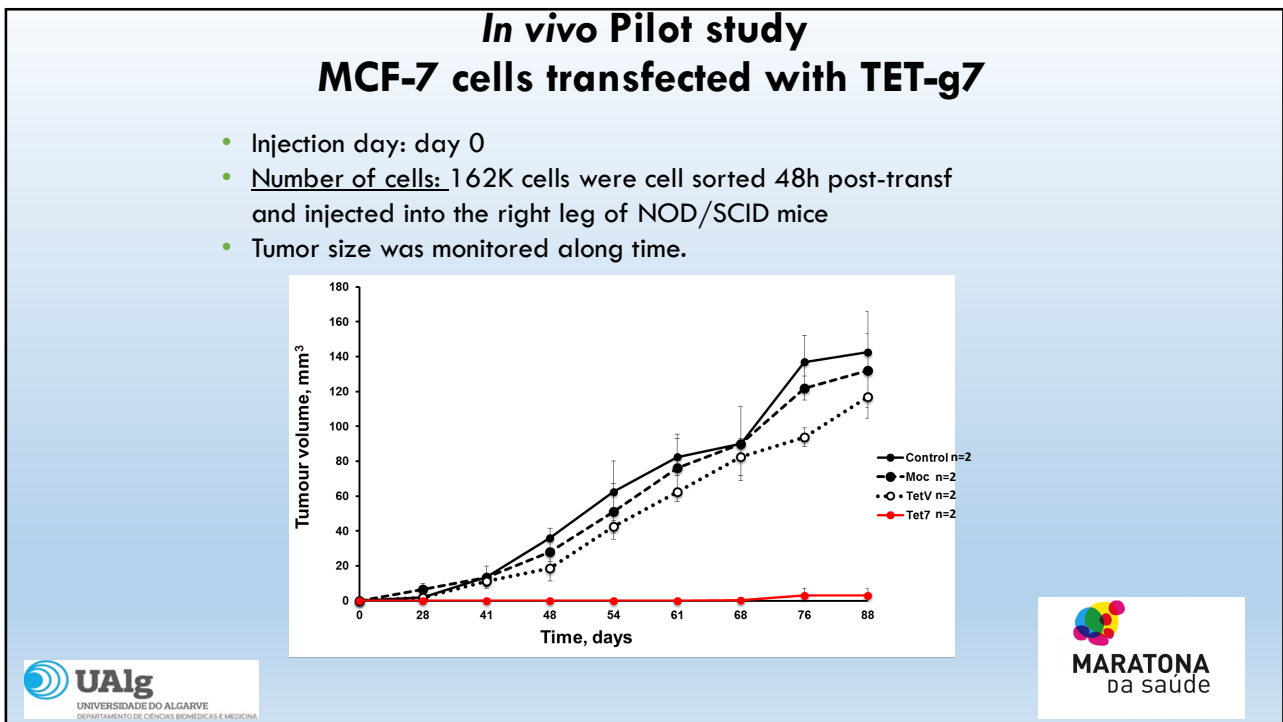
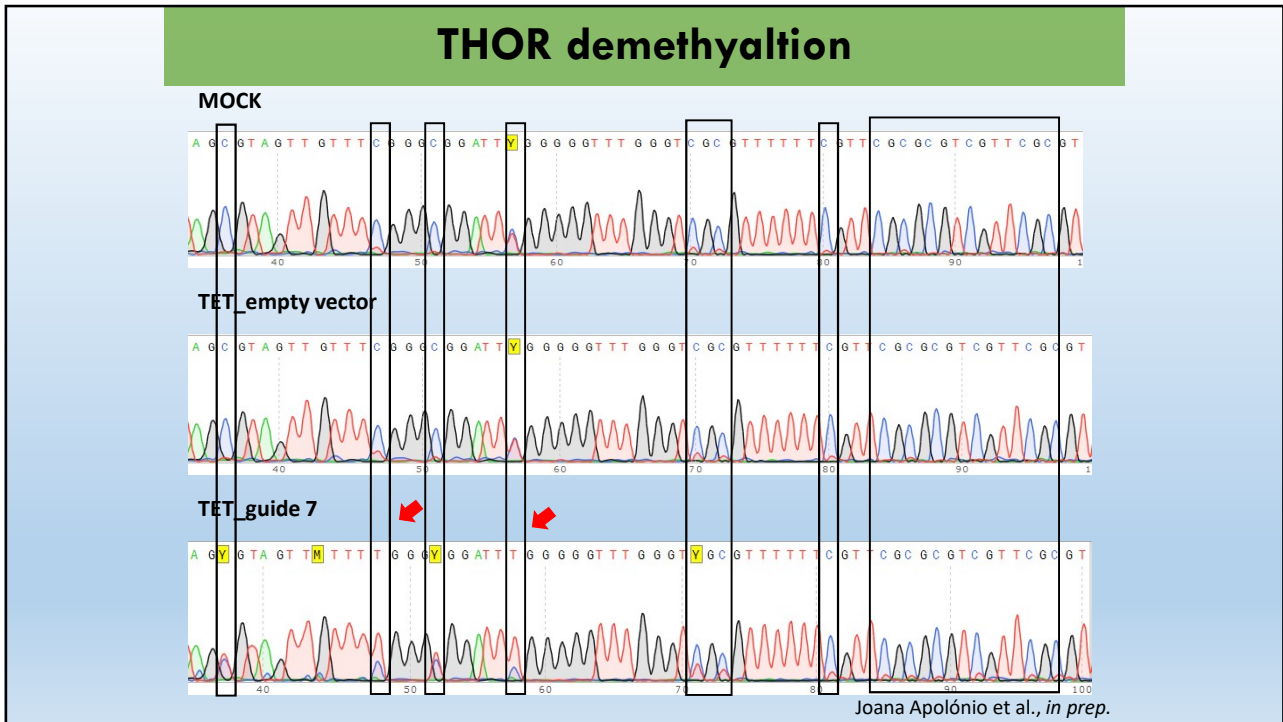
- Cas9 catalytic domain inactivated (dCas9) and function conferred by fusion to a novel effector domain, the catalytic component of TET1 demethylase enzyme.

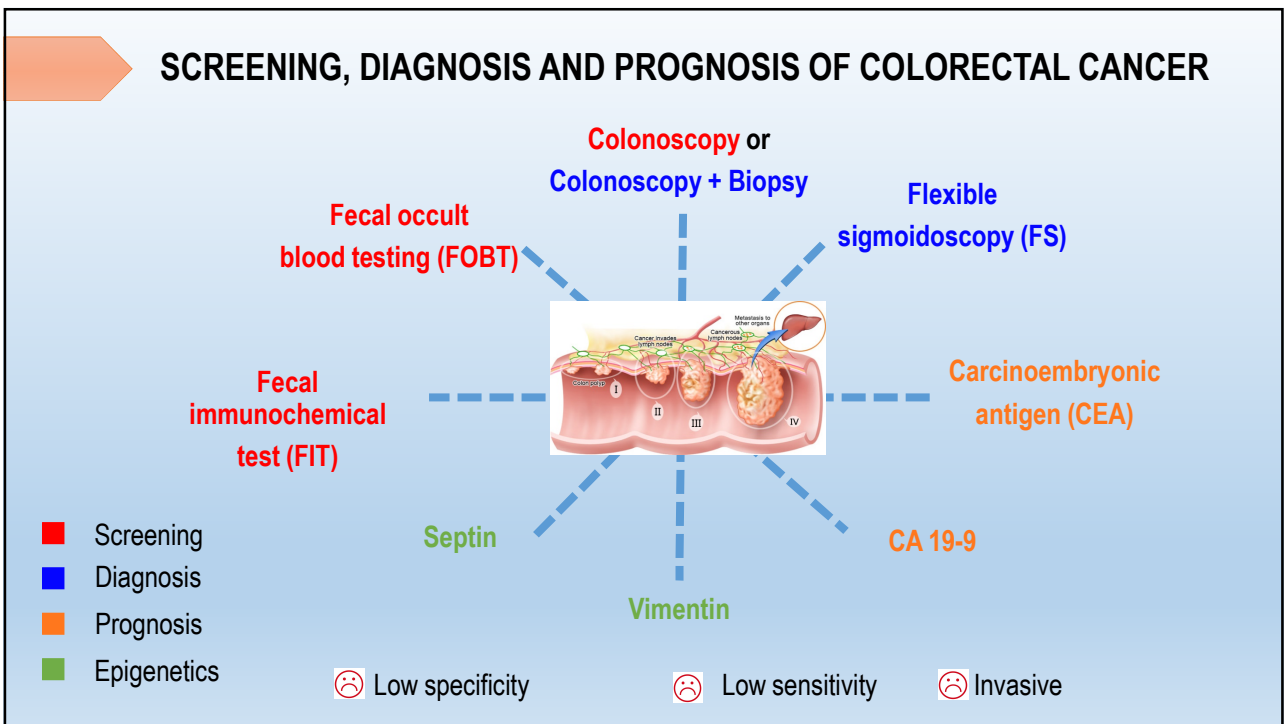
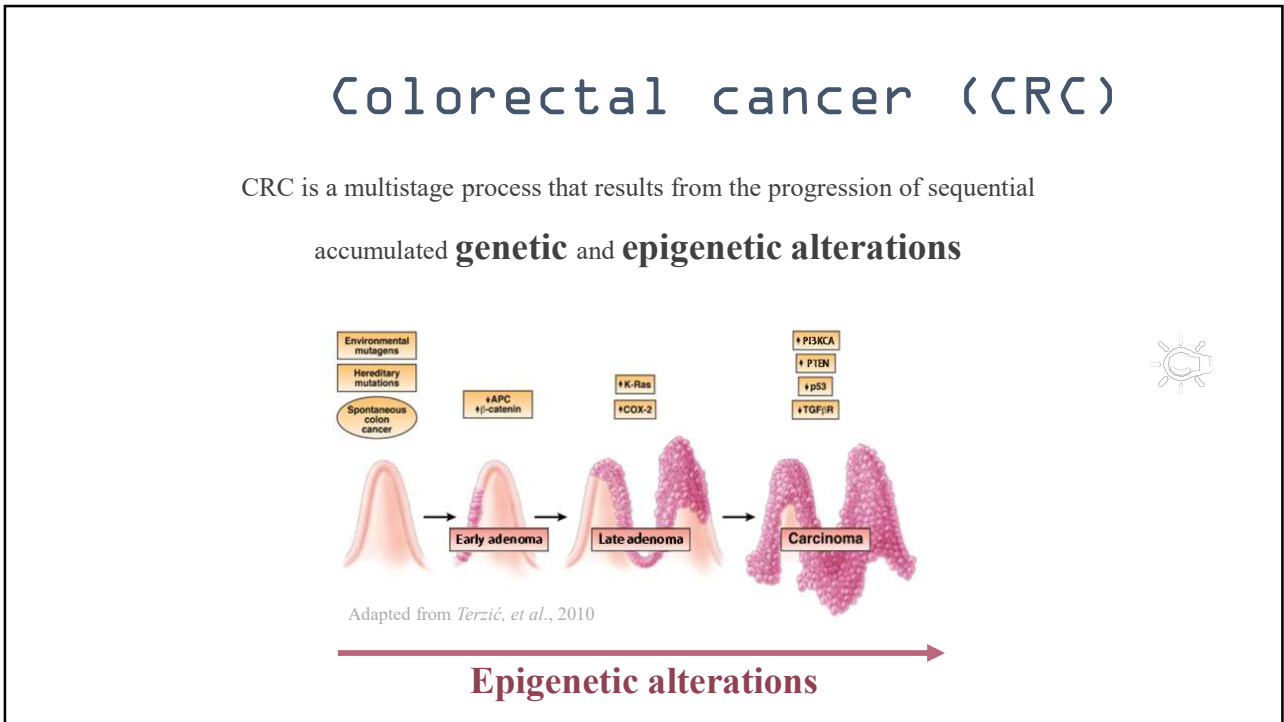


Rusk N., *Nature Methods*, 2014

Joana Apolónio et al., *in prep.*

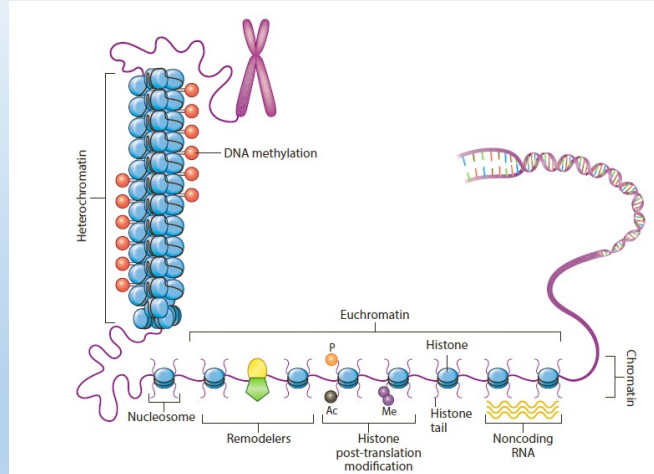






THERE IS A NEED OF NEW TOOLS: EPIGENETIC MECHANISMS

- DNA methylation
- Micro RNAs
- Histone Modifications



from Ahuja et al. 2016

DATA ANALYSIS

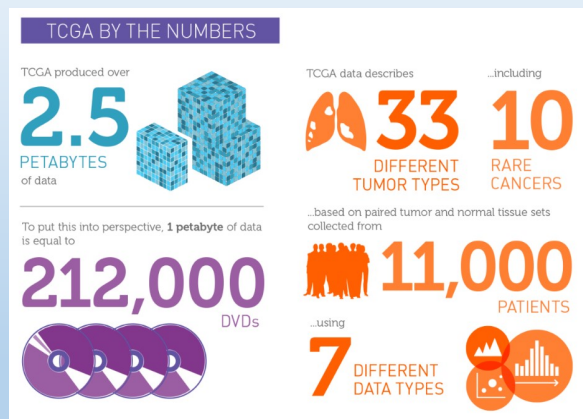
Whole genome analysis DNA methylation and gene expression

The Cancer Genome Atlas

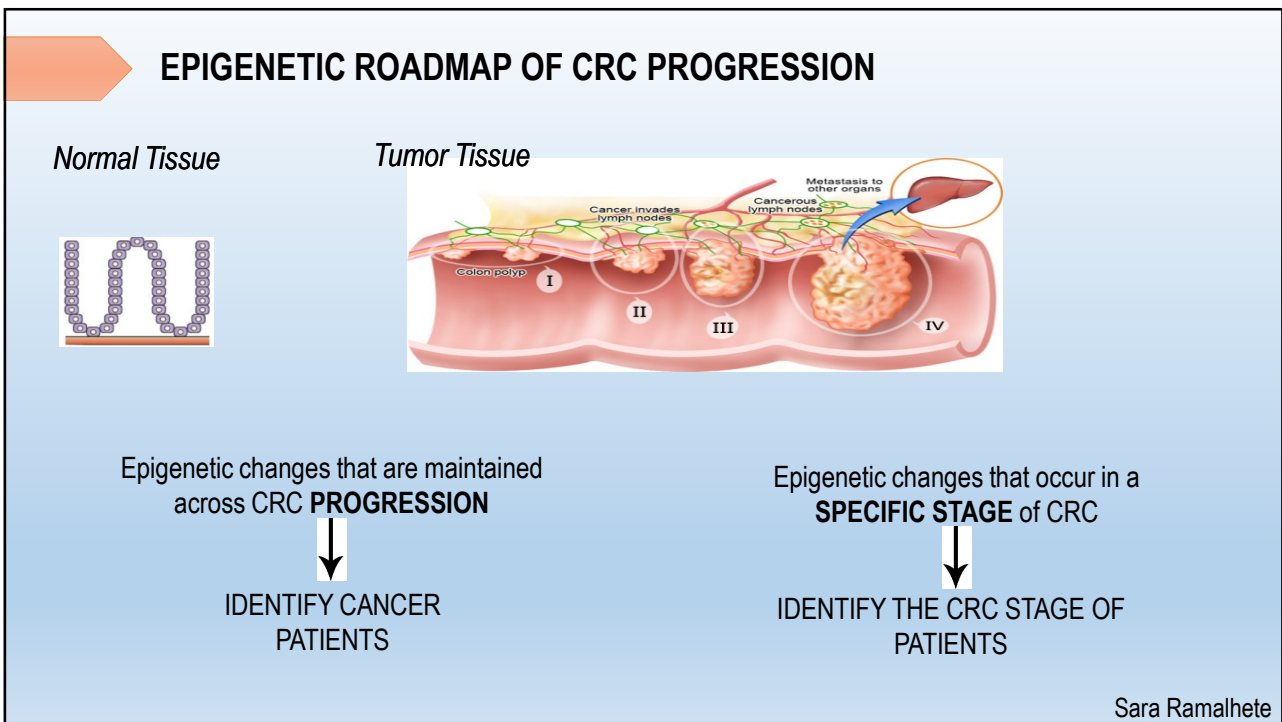
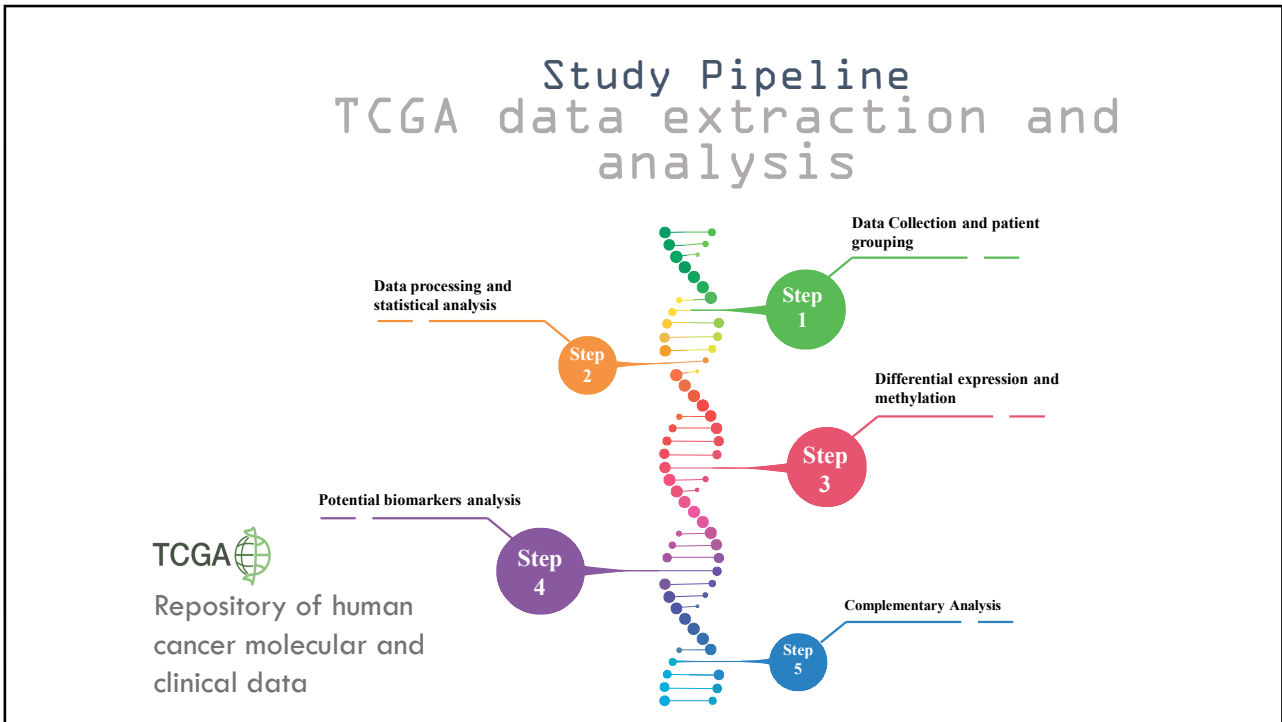
Colon and Rectum Cohorts
(n=351)

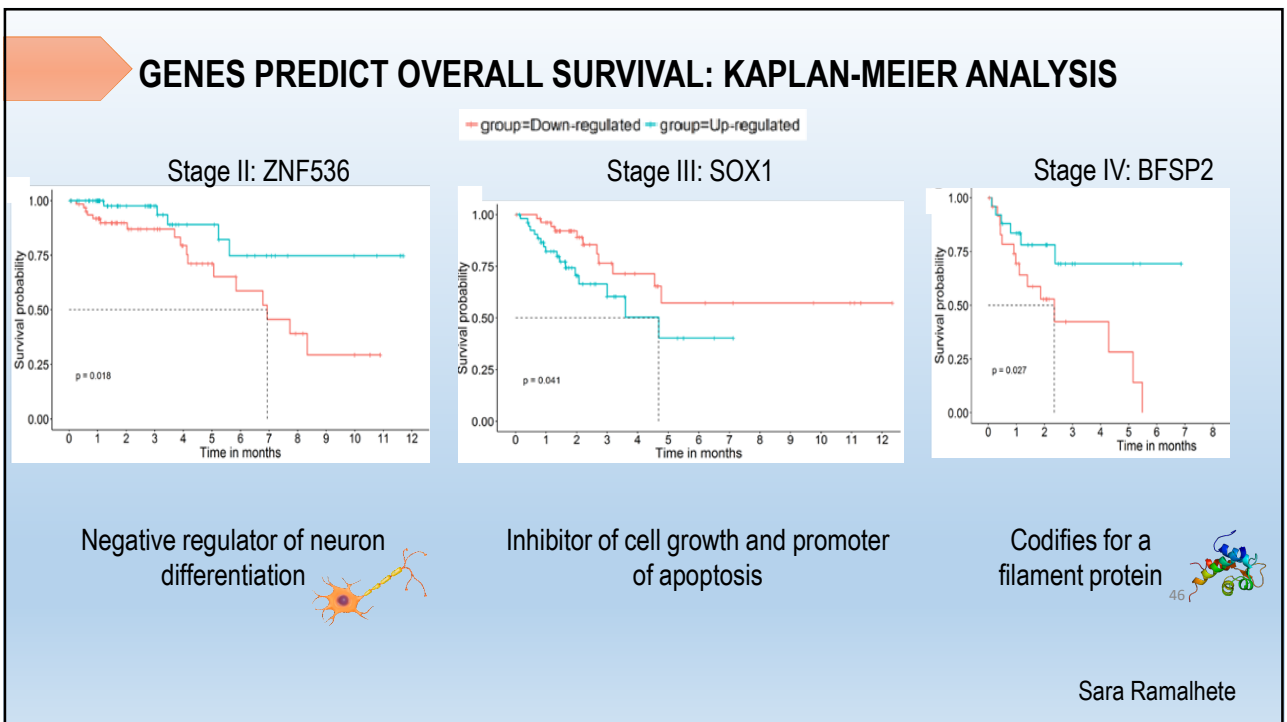
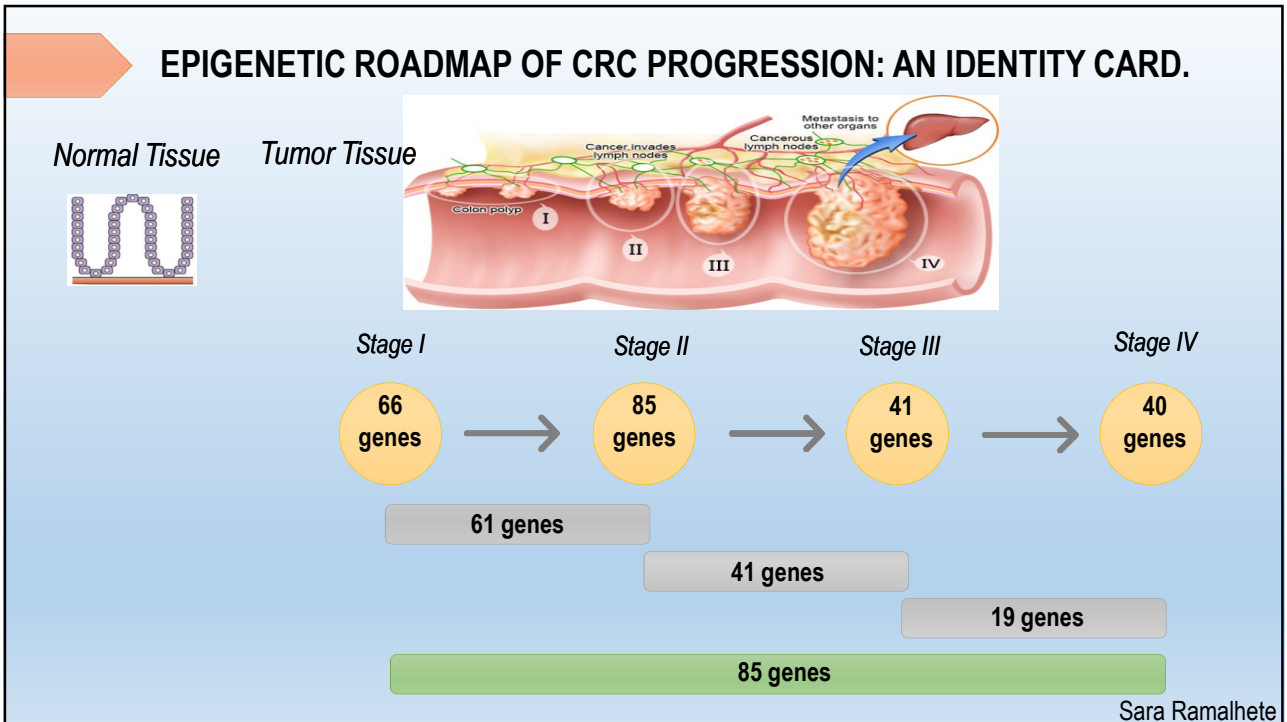
All stages of TNM classification

Normal tissue Stage I Stage II Stage III Stage IV



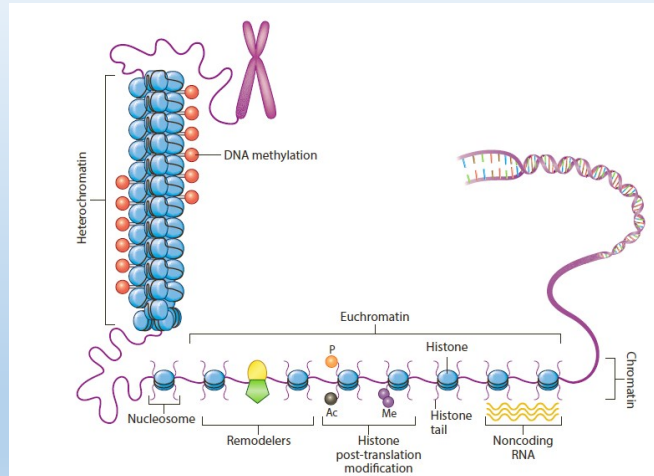
adapted from <https://cancergenome.nih.gov/abouttga>





THERE IS A NEED OF NEW TOOLS: EPIGENETIC MECHANISMS

- DNA methylation
- **Micro RNAs**
- Histone Modifications



from Ahuja et al. 2016

miRNA analysis

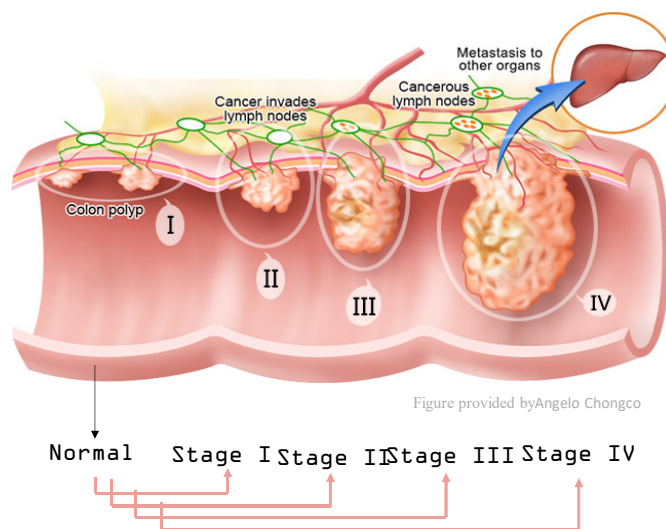
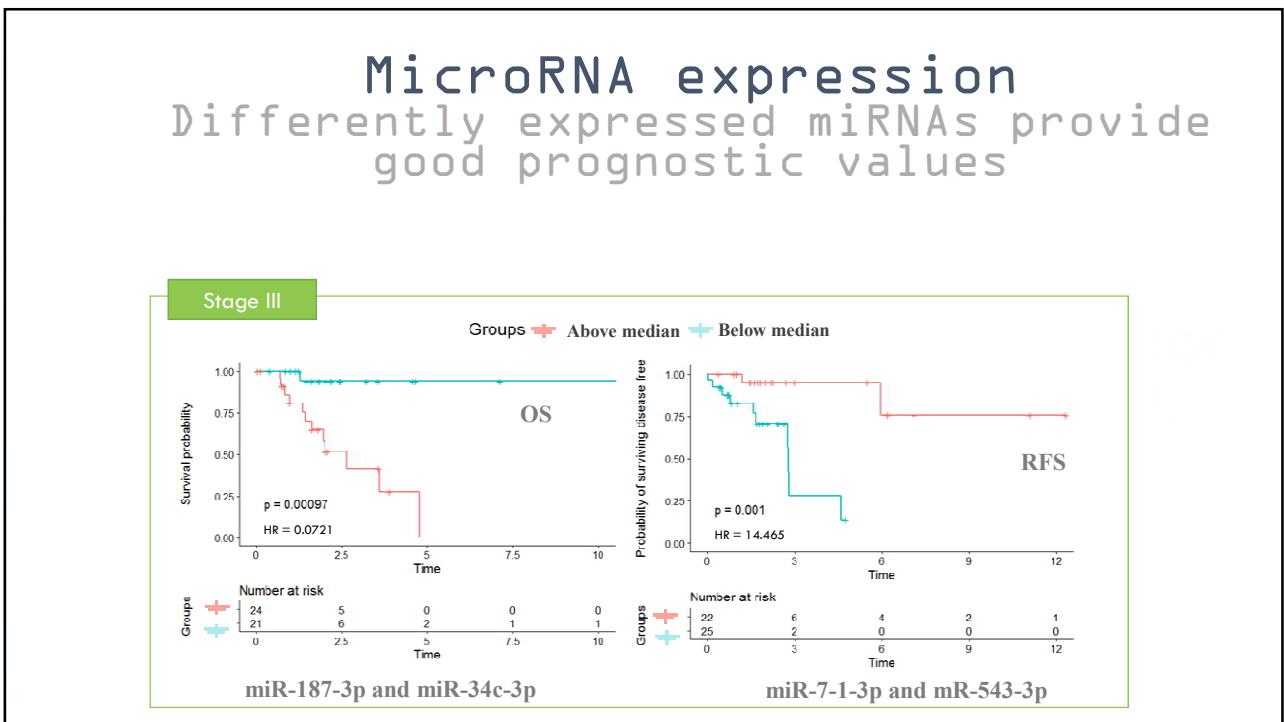
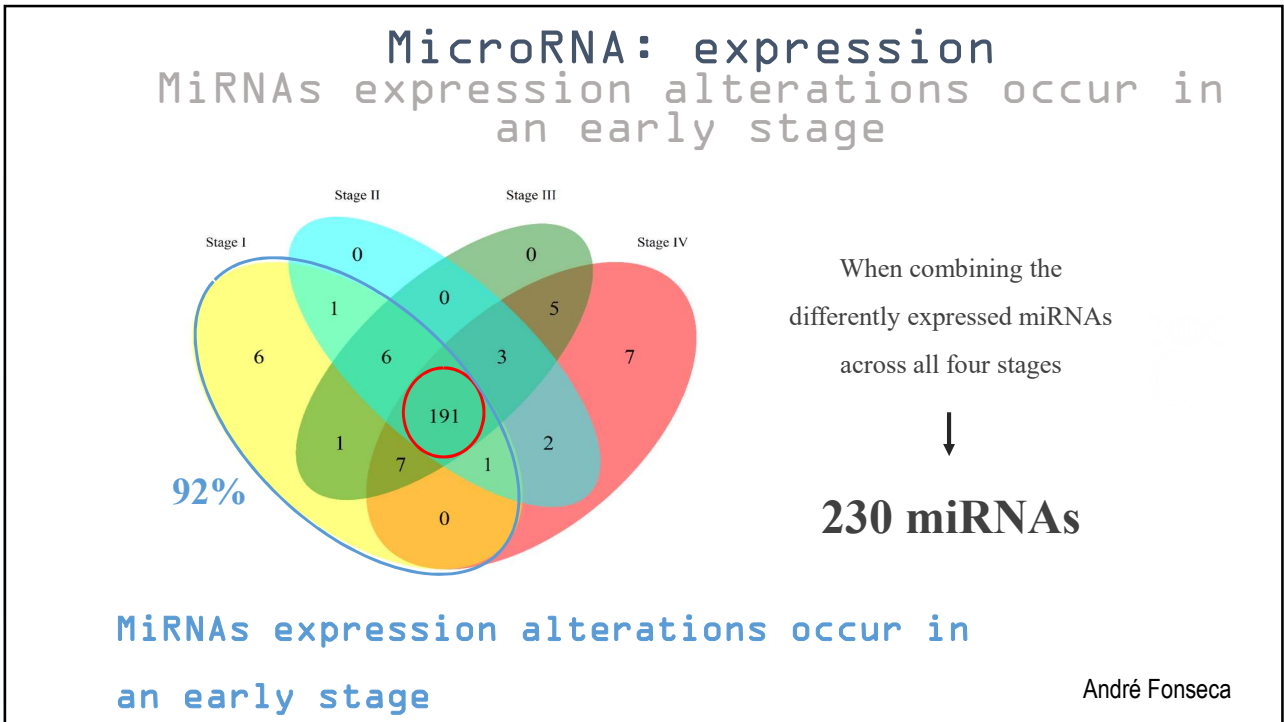


Figure provided by Angelo Chongco

André Fonseca



[J Mammary Gland Biol Neoplasia](#). 2010 Mar;15(1):101-12. doi: 10.1007/s10911-010-9164-2. Epub 2010 Feb 4.
Epigenetic regulation of milk production in dairy cows.

[BMC Genomics](#). 2018 Oct 11;19(1):744. doi: 10.1186/s12864-018-5124-9.

DNA methylation patterns in peripheral blood mononuclear cells from Holstein cattle with variable milk yield.

[Best Pract Res Clin Endocrinol Metab](#). 2017 Aug;31(4):427-442. doi: 10.1016/j.beem.2017.10.003. Epub 2017 Oct 20.

MicroRNAs: Milk's epigenetic regulators.

[J Dairy Sci](#). 2019 Jul;102(7):5853-5870. doi: 10.3168/jds.2018-16126. Epub 2019 Apr 25.

Advances and challenges in application of feedomics to improve dairy cow production and health.

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(DKFZ), Heidelberg,
Germany.
Holger Sultmann

