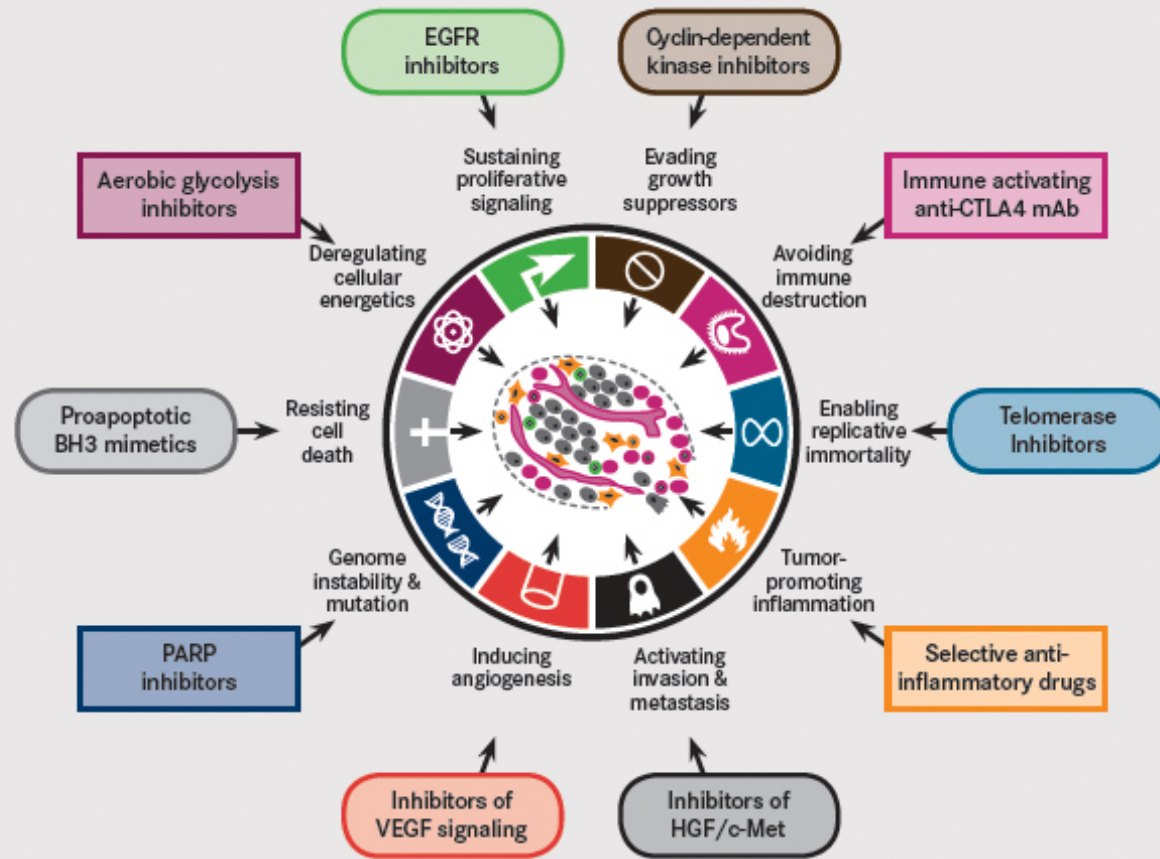


The Epigenetics of human cancer

Hallmarks of human cancer

Cancer cells show Defined key features

Alterations in central biological pathways that Ensure immortality and invasiveness



This figure illustrates some of the many approaches employed in developing therapeutics targeted to the known and emerging hallmarks of cancer.

EGFR indicates epidermal growth factor receptor; CTLA4, cytotoxic T lymphocyte-associated antigen 4; mAb, monoclonal antibody; HGF, hepatocyte growth factor; VEGF, vascular endothelial growth factor; PARP, poly-(ADP ribose) polymerase.

Source: Hanahan D, Weinberg RA. Hallmarks of cancer: the next generation. *Cell*. 2011; 144: 646-674. Reprinted with permission.

GENETIC AND EPIGENETIC ALTERATIONS IN HUMAN CANCER

Classic genetic basis of cancer

Knudsen hypothesis (1971): Two-hit or multiple hit hypothesis:

Genetic model: Both alleles of a gene or multiple gene mutations are required for cancer formation

The *extended* (epi)-genetic basis of cancer

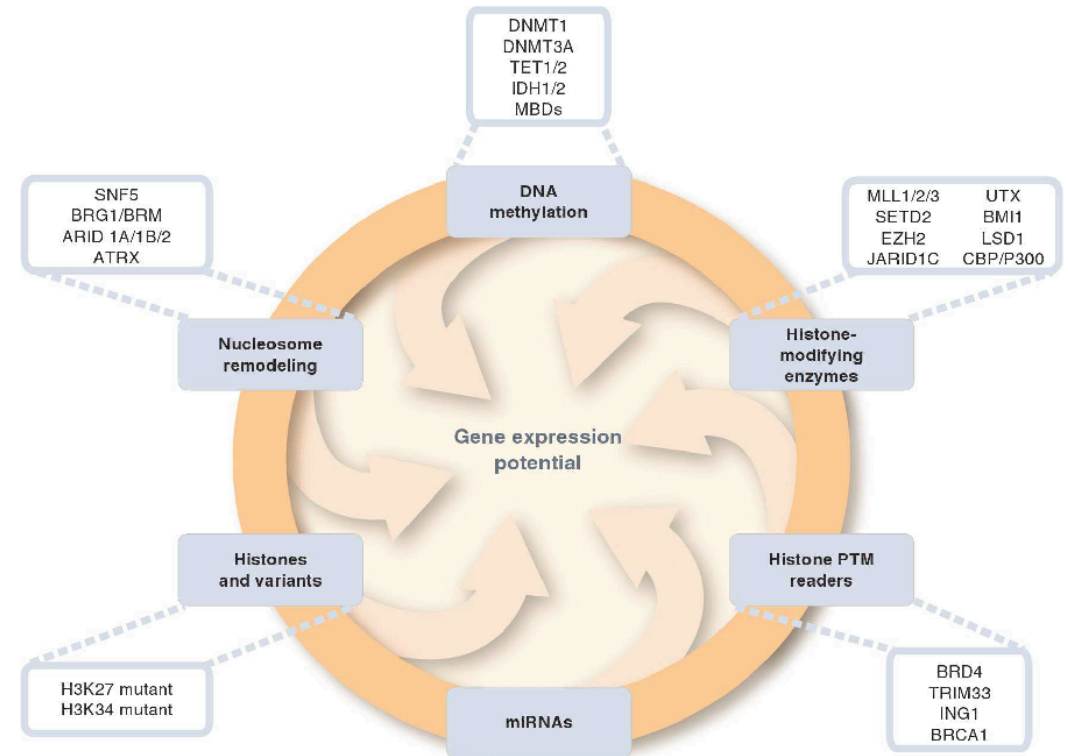
- Mutations in single alleles
- Loss of parts or entire genes
- Loss of one allele; second allele silenced by epigenetic alterations
- Epigenetic silencing of both alleles

Epigenetic alterations:

- Mutations in epigenetic writers/chromatin components
- Reduced expression of epigenetic regulators
- Increased expression of epigenetic regulators

Relevance of Epigenetic alterations

- Multiple direct and indirect effects on gene expression (silencing of DNA repair gene MLH1 mediates further mutations, etc)
- **Genome instability**
- **Important to understand immortalization and transformation**
- **Targets for chemotherapeutic approaches → effect on multiple genes**



The epigenetic machinery

Figure 1. Genetic mutations of epigenetic modifiers in cancer. The drawing shows the input of epigenetic processes in specifying gene expression patterns. Recent whole-exome sequencing studies show that mutations in various classes of epigenetic modifiers are frequently observed in many types of cancers, further highlighting the cross talk between genetics and epigenetics. Examples of some, but not all, of these mutations are illustrated here and listed in [Table 2](#). The mutations of epigenetic modifiers potentially cause genome-wide epigenetic alterations in cancer, but, save for isocitrate dehydrogenase (IDH) mutations as discussed in the text, these have yet to be shown on a genome-wide scale. Understanding the relationship of genetic and epigenetic changes in cancer will offer novel insights for cancer therapies. MBDs, methylcytosine-binding proteins; PTM, posttranslational modification. (Adapted from [You and Jones 2012](#).)

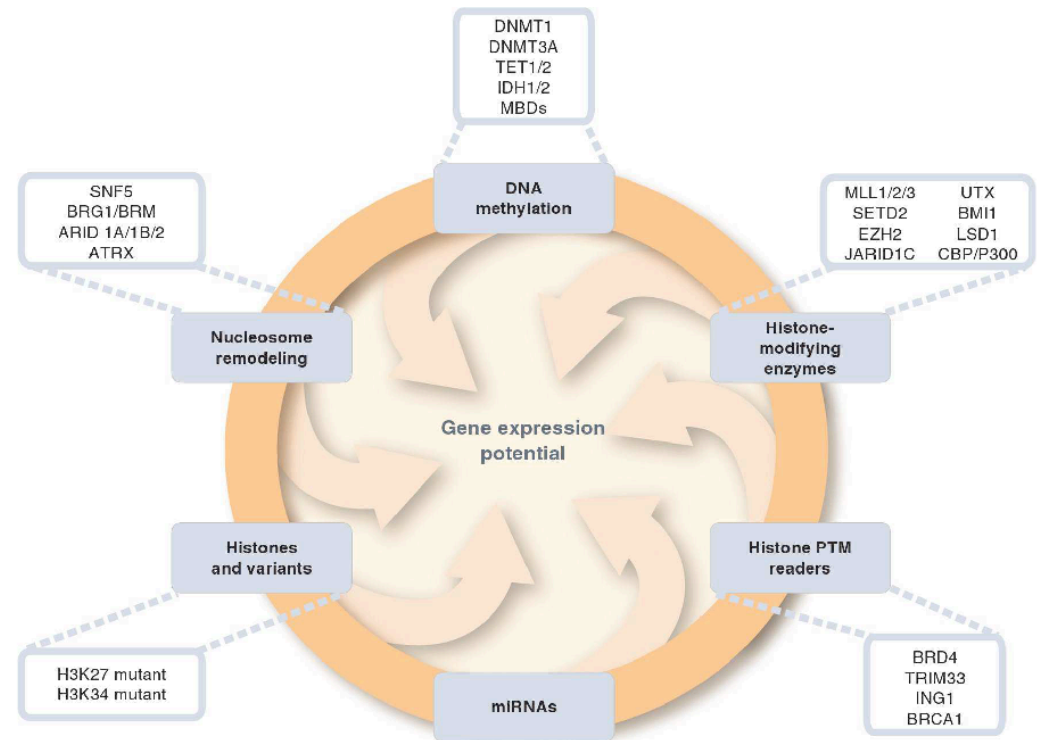
Hallmarks of human cancer – the epigenetics

ALTERATION OF EPIGENETIC REGULATORS (Mutation/altered expression) CAN SET UP CANCER ASSOCIATED GENE EXPRESSION SIGNATURES

THE CANCER EPIGENOME

Epigenetic alterations:

- Can be causal for the alteration of gene expression → epigenetic writer or epigenetic readers are altered (mutated or changed expression)
- Can also be a indirect consequence → another mechanism not directly related to epigenetics alters gene expression, epigenetic modifications change as a consequence
- Genome instability generates novel mutations



The epigenetic machinery

Figure 1. Genetic mutations of epigenetic modifiers in cancer. The drawing shows the input of epigenetic processes in specifying gene expression patterns. Recent whole-exome sequencing studies show that mutations in various classes of epigenetic modifiers are frequently observed in many types of cancers, further highlighting the cross talk between genetics and epigenetics. Examples of some, but not all, of these mutations are illustrated here and listed in [Table 2](#). The mutations of epigenetic modifiers potentially cause genome-wide epigenetic alterations in cancer, but, save for isocitrate dehydrogenase (IDH) mutations as discussed in the text, these have yet to be shown on a genome-wide scale. Understanding the relationship of genetic and epigenetic changes in cancer will offer novel insights for cancer therapies. MBDs, methylcytosine-binding proteins; PTM, posttranslational modification. (Adapted from [You and Jones 2012](#).)

Hallmarks of human cancer – the genetics

Genetics and Epigenetics impacts on hallmarks of human cancer

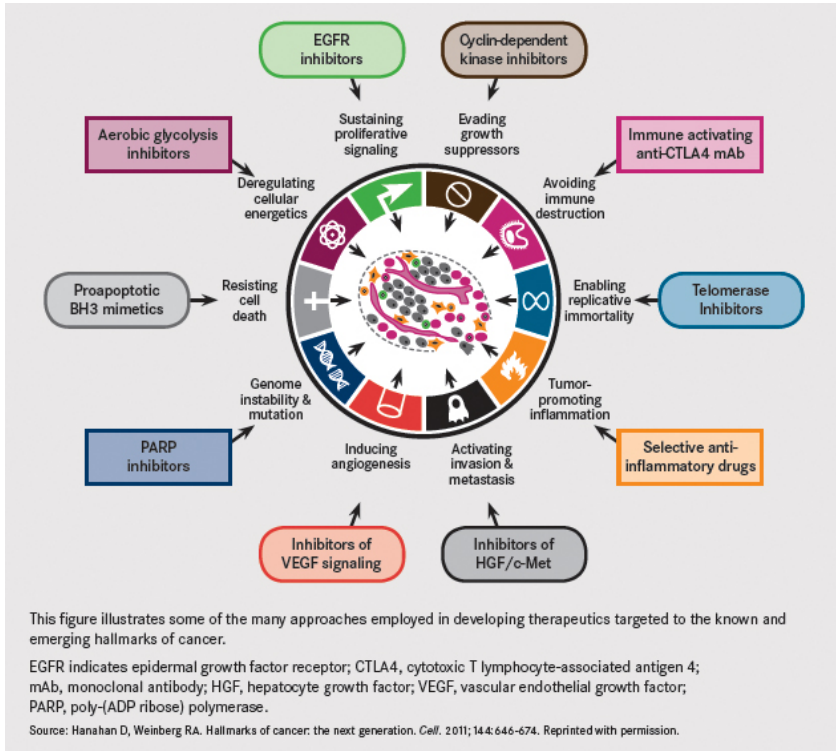


Table 1. Examples of key cellular pathways disrupted in human cancers by genetic and epigenetic mechanisms

Pathway	Example of genetic alteration	Example of epigenetic alteration
Self sufficiency in growth signals	Mutations in <i>Ras</i> gene	Methylation of <i>RASSF1A</i> gene
Insensitivity to antigrowth signals	Mutation in <i>TGF-β</i> receptors	Down-regulation of <i>TGF-β</i> receptors
Tissue invasion and metastasis	Mutation in <i>E-cadherin</i> gene	Methylation of <i>E-cadherin</i> promoter
Limitless replicative potential	Mutation in <i>p16</i> and <i>pRb</i> genes	Silencing of <i>p16</i> or <i>pRb</i> genes by promoter methylation
Sustained angiogenesis		Silencing of thrombospondin-1
Evading apoptosis	Mutation in <i>p53</i>	Methylation of <i>DAPK</i> , <i>ASC/TMS1</i> , and <i>HIC1</i>
DNA repair capacity	Mutations in <i>MLH1</i> , <i>MSH2</i>	Methylation of <i>GST Pi</i> , <i>O6-MGMT</i> , <i>MLH1</i>
Monitoring genomic stability	Mutations in <i>Chfr</i>	Methylation of <i>Chfr</i>
Protein ubiquitination functions regulating mitotic control genes	Mutations in <i>Chfr</i>	Methylation of <i>Chfr</i>

TGF-β, transforming growth factor β; *DAPK*, death-associated protein kinase.

Hallmarks of human cancer – the genetics

Alterations in central biological pathways that ensure immortality and invasiveness

Cancer is caused by key oncogene activation and/or loss of tumorsuppression (driver mutation) and paralleled by the acquisition of hundreds of mutations in different genes (passanger mutations) and also altered gene expression of mutated/non-mutated genes

Together this results up a cancer gene expression pattern/genomic instability

Genetics - Epigenetics

Table 1. Examples of key cellular pathways disrupted in human cancers by genetic and epigenetic mechanisms

Pathway	Example of genetic alteration	Example of epigenetic alteration
Self sufficiency in growth signals	Mutations in <i>Ras</i> gene	Methylation of <i>RASSF1A</i> gene
Insensitivity to antigrowth signals	Mutation in TGF- β receptors	Down-regulation of TGF- β receptors
Tissue invasion and metastasis	Mutation in <i>E-cadherin</i> gene	Methylation of <i>E-cadherin</i> promoter
Limitless replicative potential	Mutation in <i>p16</i> and <i>pRb</i> genes	Silencing of <i>p16</i> or <i>pRb</i> genes by promoter methylation
Sustained angiogenesis		Silencing of thrombospondin-1
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TGF- β , transforming growth factor β ; *DAPK*, death-associated protein kinase.

CHROMATIN STRUCTURE IS DIFFERENT IN CANCER CELLS

Staining of chromatin by hematoxylin → standard procedure in pathology

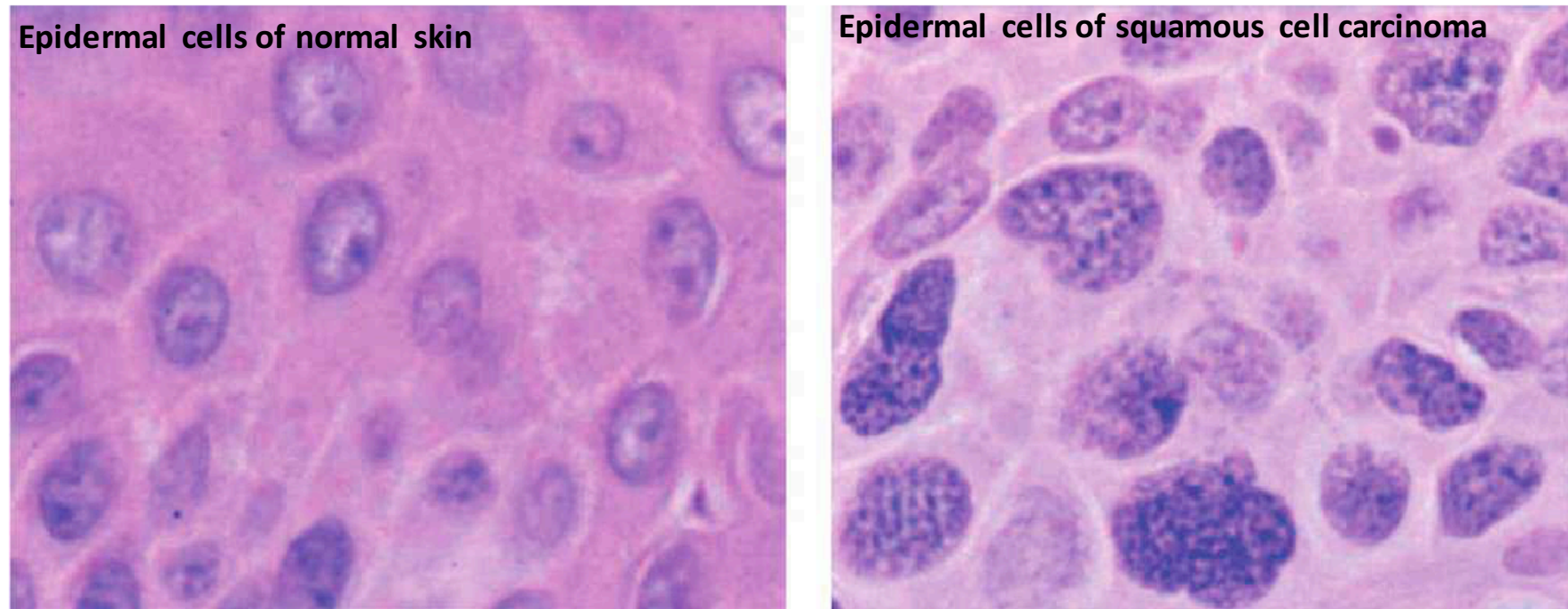
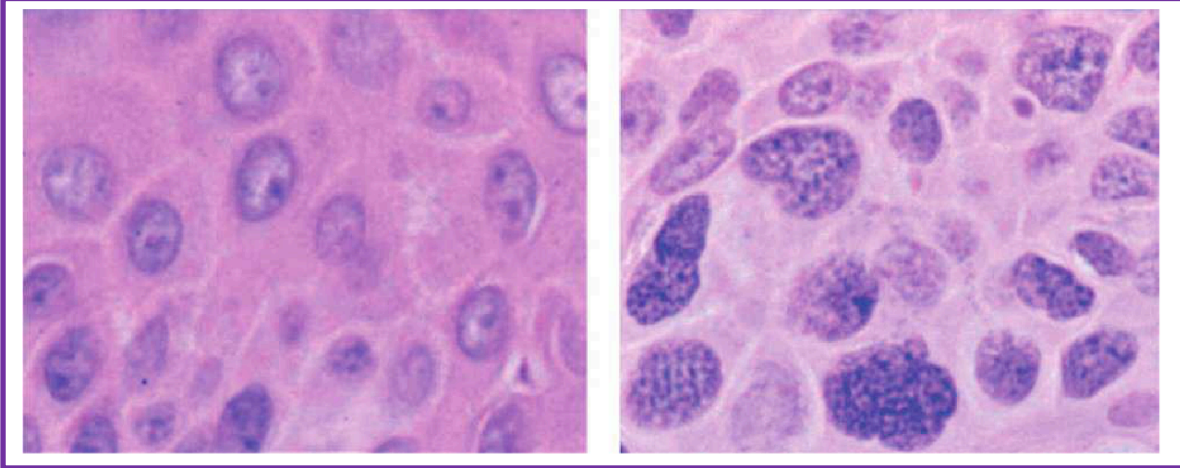


Figure 2. Chromatin structural changes in cancer cells. These two photomicrographs were taken from a patient with a squamous cell carcinoma of the skin. The *left* panel shows normal epidermal cells within one millimeter of the contiguous tumor shown at the same magnification on the *right*. The chromatin, which stains purple as a result of its affinity to hematoxylin, appears much more coarse and granular in the cancer cells than in normal epidermis. Such changes in the staining characteristics of chromatin are used by pathologists as diagnostic criteria for cancer.

Definition of epigenetic determinants in human cancer

Classic visual inspection



Changes in chromatin conformation

Detailed molecular analysis

Genome-wide epigenetic mapping
Chromosome conformation capture
RNA seq (lncRNA, siRNA, miRNA, etc)
DNA methylation profiling
Genome sequencing
Proteomics
Metabolomics

High resolution information on
Epigenetic alterations on the
single nucleotide level

Detailed understanding of pathological processes
in human cancer

Alteration of epigenetic modifiers in human cancer

DNA methylation

Genes in selected epigenetic modifiers in human cancers

Gene	Function	Tumor type	Alteration
<i>DNMT1</i>	DNA methyltransferase	Colorectal, Non-small cell lung, pancreatic, gastric, breast cancer	Mutation (Kanai et al. 2003) Overexpression (Wu et al. 2007)
<i>DNMT3A</i>	DNA methyltransferase	MDS; AML	Mutation (Ley et al. 2010; Yamashita et al. 2010; Yan et al. 2011)
<i>DNMT3B</i>	DNA methyltransferase	ICF syndrome, SNPs in breast and lung adenoma	Mutation (Wijmenga et al. 2000) Mutation (Shen et al. 2002)
<i>MBD1/2</i>	Methyl-binding protein	Lung and breast cancer	Mutation (Sansom et al. 2007)
<i>TET1</i>	5'-Methylcytosine hydroxylase	AML	Chromosome translocation (De Carvalho et al. 2010; Wu and Zhang 2010)
<i>TET2</i>	5'-Methylcytosine hydroxylase	MDS, myeloid malignancies, gliomas	Mutation/silencing (Araki et al. 2009)
<i>IDH1/2</i>	Isocitrate dehydrogenase	Glioma, AML	Mutation (Figuroa et al. 2010; Lu et al. 2012; Turcan et al. 2012)
<i>AID</i>	5'-Cytidine deaminase	CML	Aberrant expression (De Carvalho et al. 2010)
<i>MLL1/2/3</i>	Histone methyltransferase H3K4	Bladder hematopoietic, non-Hodgkin lymphoma, B-cell lymphoma, prostate (primary)	TCC, Translocation, mutation, aberrant expression (Cui et al. 2011; Morin et al. 2011)

Histone modifying complexes

<i>EZH2</i>	Histone methyltransferase H3K27	Breast, prostate, bladder, colon, pancreas, liver, gastric, uterine tumors, melanoma, lymphoma, myeloma, and Ewing's sarcoma	Mutation, aberrant expression (Chase and Cross 2011; Tsang and Cheng 2011)
<i>BMI-1</i>	PRC1 subunit	Ovarian, mantle cell lymphomas, and Merkel cell carcinomas	Overexpression (Jiang and Song 2009; Lukacs et al. 2010)
<i>G9a</i>	Histone methyltransferase H3K9	HCC, cervical, uterine, ovarian, and breast cancer	Aberrant expression (Varier and Timmers 2011)
<i>PRMT1/5</i>	Protein arginine methyltransferase	Breast/gastric	Aberrant expression (Miremedi et al. 2007)
<i> LSD1</i>	Histone demethyltransferase H3K4/H3K9	Prostate	Mutation (Rotili and Mai 2011)
<i>UTX (KDM6A)</i>	Histone demethyltransferase H3K27	Bladder, breast, kidney, lung, pancreas, esophagus, colon, uterus, brain, hematological malignancies	Mutation (Rotili and Mai 2011)
<i>JARID1B/C (KDM5C)</i>	Histone demethyltransferase H3K4/H3K9	Testicular and breast, RCC	Overexpression (Rotili and Mai 2011)
<i>EP300 (P300/KAT3B)</i>	Histone acetyltransferase	Breast, colorectal, pancreatic cancer	Mutation (Miremedi et al. 2007)
<i>CREBBP (CBP/KAT3A)</i>	Histone acetyltransferase	Gastric and colorectal, epithelial, ovarian, lung, esophageal cancer	Mutation, overexpression (Miremedi et al. 2007)
<i>PCAF</i>	Histone acetyltransferase	Epithelial	Mutation (Miremedi et al. 2007)
<i>HDAC2</i>	Histone deacetyltransferase	Colonic, gastric, endometrial cancer	Mutation (Ropero et al. 2006)
<i>SIRT1, HDAC5/7A</i>	Histone deacetyltransferase	Breast, colorectal, prostate cancer	Mutation, aberrant expression (Miremedi et al. 2007)

Chromatin remodeling complexes

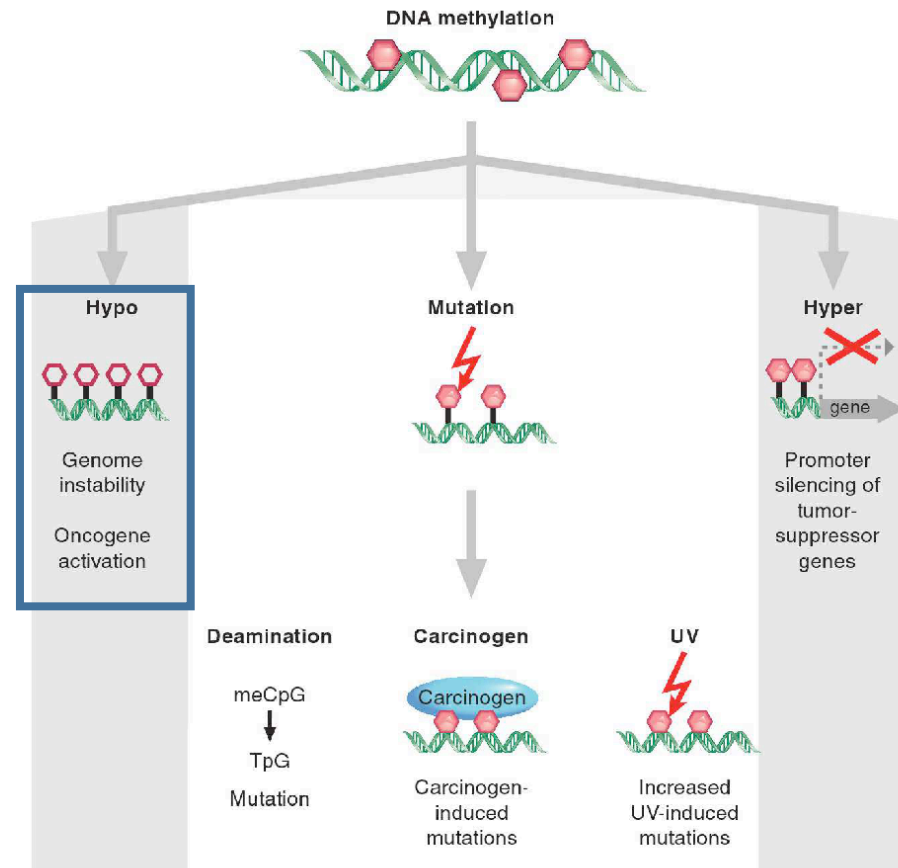
Chromatin-remodeling enzymes	<i>SMARCB1, INI1</i>	Kidney malignant rhabdoid tumors, atypical rhabdoid/teratoid tumors (extrarenal), epithelioid sarcomas, small cell hepatoblastomas, extraskelletal myxoid chondrosarcomas, and undifferentiated sarcomas	Mutation, silencing, loss of expression (Wilson and Roberts 2011)
	<i>BRG1, SMARCA4</i>	Lung, rhabdoid, medulloblastoma	Mutation, low expression (Wilson and Roberts 2011)
	<i>BRM, SMARCA2</i>	Prostate, basal cell carcinoma	Mutation, low expression (Sun et al. 2007; de Zwaan and Haas 2010)
	<i>BAF250A</i>	Ovarian clear cell carcinomas, 30% of endometrioid carcinomas, endometrial carcinomas	Mutation, genomic rearrangement, low expression (Jones et al. 2010; Guan et al. 2011)
	<i>BAF200</i>	Primary pancreatic adenocarcinomas	Mutation (Li et al. 2011)
	<i>BRD7</i>	Bladder TCC	Mutation (Drost et al. 2010)
	<i>BAF180</i>	Breast tumors	Mutation (Varela et al. 2011)
	<i>SRCAF</i>	Prostate	Aberrant expression (Balakrishnan et al. 2007)
	<i>Tip60</i>	Colon, lymphomas, head and neck, breast	Mutation, aberrant expression (Mattera et al. 2009)
	<i>CHD4/5</i>	Colorectal and gastric cancer, ovarian, prostate, neuroblastoma, hematopoietic	Mutation (Bagchi et al. 2007; Kim et al. 2011; Wang et al. 2011)
	<i>CHD7</i>	Gastric and colorectal	Mutation (Wessels et al. 2010)

Adapted from You and Jones 2012.

MDS, myelodysplastic syndromes; AML, acute myeloid leukemia; ICF, immunodeficiency, centromere instability, and facial anomalies; SNPs, single-nucleotide polymorphisms; TCC, transitional cell carcinoma; HCC, hepatocellular carcinoma; RCC, renal clear cell carcinoma; TET, ten-eleven translocation; NuRD, nucleosome remodeling and deacetylation.

1. Alteration of DNA methylation in human cancer

**CANCER IS ASSOCIATED
with
GLOBAL DNA
HYPOMETHYLATION
and
LOCAL DNA
HYPERMETHYLATION**



Normal tissue: 80% of CpG methylated
Cancer: 40-60% of CpG methylated

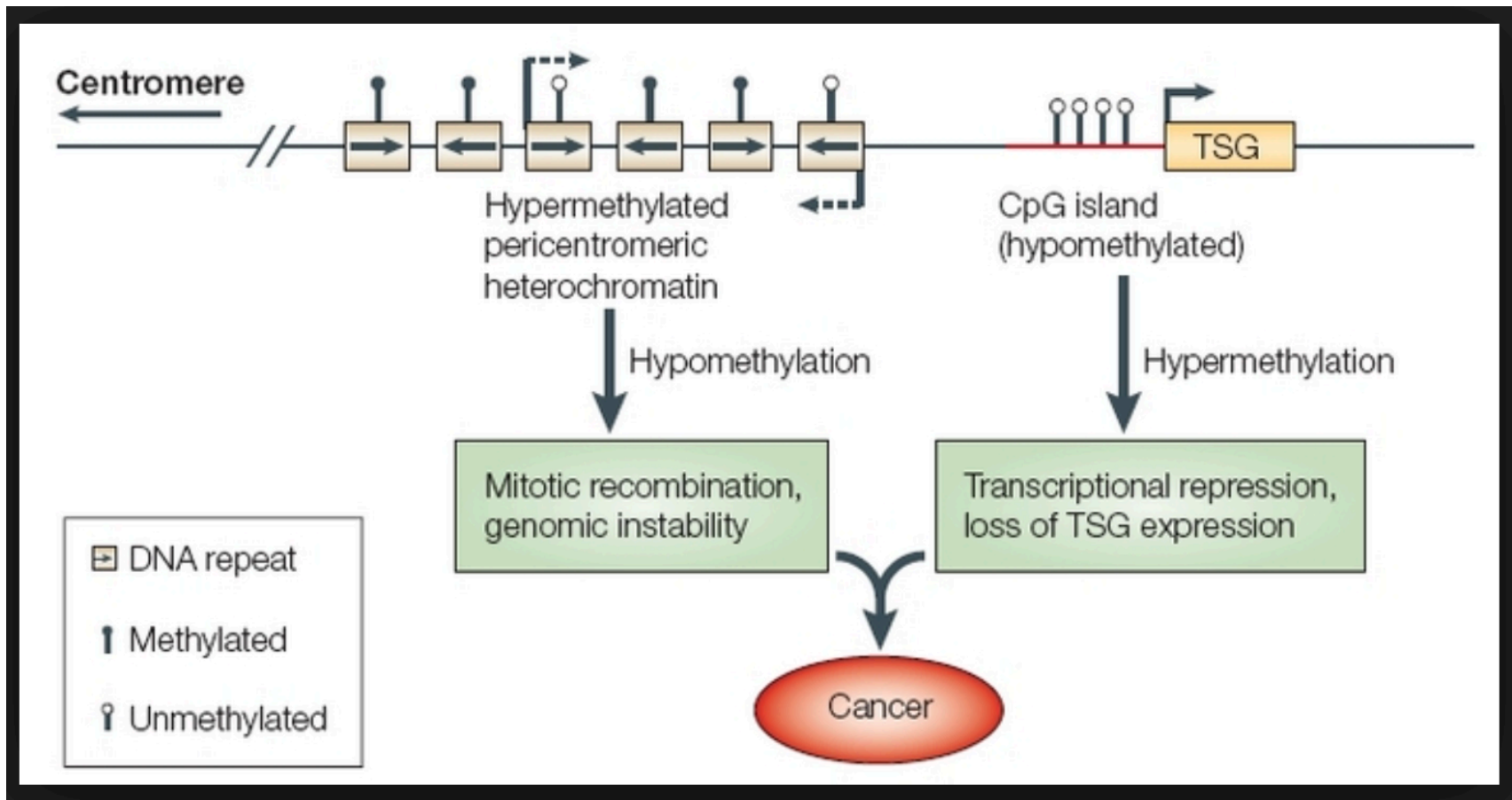
Global DNA methylation is lost from large blocks (28kb – 10Mb)

Local hypermethylation at specific locations such as tumor suppressors

Figure 3. Epigenetic alterations involving DNA methylation can lead to cancer by various mechanisms. Loss of DNA cytosine methylation (white hexagons) illustrated in the hypo column results in genome instability. Focal hypermethylation (pink hexagons) at gene promoters shown in the hyper column causes heritable silencing and, therefore, inactivation of tumor suppressors and other genes. Additionally, methylated CpG sites (pink hexagons) are prone to mutation: They are hot spots for C to T transition mutations caused by spontaneous hydrolytic deamination; or methylation of CpG sites can increase the binding of some chemical carcinogens to DNA; and it increases the rate of UV-induced mutations.

1. The role of DNA methylation in human cancer

A. HYPOMETHYLATION



1. The role of DNA methylation in human cancer

A. HYPOMETHYLATION

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LETTERS TO

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Hypomethylation distinguishes genes of some human cancers from their normal counterparts

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It has been suggested that cancer represents an alteration in DNA, heritable by progeny cells, that leads to abnormally regulated expression of normal cellular genes; DNA alterations such as mutations^{1,2}, rearrangements^{3–5} and changes in methylation^{6–8} have been proposed to have such a role. Because of increasing evidence that DNA methylation is important in gene expression (for review see refs 7, 9–11), several investigators have studied DNA methylation in animal tumours, transformed cells and leukaemia cells in culture^{8,12–30}. The results of these studies have varied; depending on the techniques and systems used, an increase^{12–19}, decrease^{20–24}, or no change^{25–29} in the degree of methylation has been reported. To our knowledge, however, primary human tumour tissues have not been used in such studies. We have now examined DNA methylation in human cancer with three considerations in mind: (1) the methylation pattern of specific genes, rather than total levels of methylation, was determined; (2) human cancers and adjacent analogous normal tissues, unconditioned by culture media, were analysed; and (3) the cancers were taken from patients who had received neither radiation nor chemotherapy. In four of five patients studied, representing two histological types of cancer, substantial hypomethylation was found in genes of cancer cells compared with their normal counterparts. This hypomethylation was progressive in a metastasis from one of the patients.

Landmark paper introducing differential DNA methylation in cancer research

Prepare DNA from healthy and tumor tissue

Digest with methylation sensitive restriction enzyme (does not cut methylated DNA)

Probe southern blot with probes generate from cDNA of different genes

Cancer tissue: smaller fragments → methylation lost

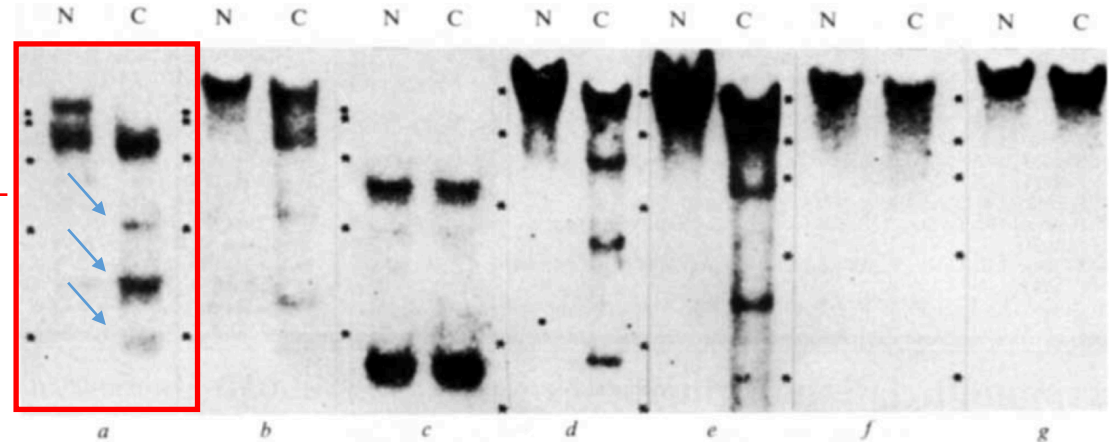
90

LETTERS TO NATURE

NATURE VOL. 301 6 JANUARY 1983

Fig. 1 Methylation pattern of adenocarcinoma of the colon and normal colonic mucosa from patient 1. Lanes C and N were prepared from DNA digests of the colon carcinoma and normal colonic mucosa, respectively. *a*, *Hpa*II digest, HGH probe; *b*, *Hha*I digest, HGH probe; *c*, *Msp*I digest, HGH probe; *d*, *Hpa*II digest, γ -globin probe; *e*, *Hha*I digest, γ -globin probe; *f*, *Hpa*II digest, α -globin probe; *g*, *Hha*I digest, α -globin probe. The asterisks on the left of *a–g* indicate molecular weight markers (*Hind*III-digested bacteriophage λ DNA, of sizes 9,500, 6,700, 4,400, 2,000 and 570 bp from top to bottom, respectively).

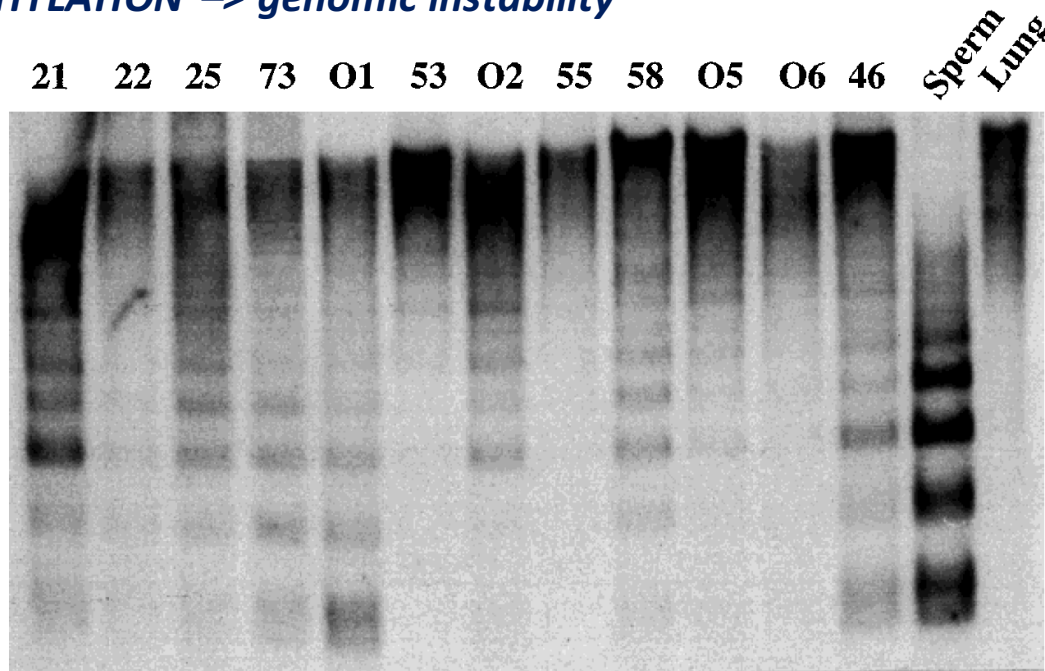
Methods: Tissues were frozen in liquid nitrogen, then pulverized and the DNA extracted essentially as described elsewhere⁵¹. The DNA was cleaved with 50-fold excess of restriction endonuclease, as assessed by the amount of restriction endonuclease required to digest pBR322 DNA included in a matched duplicate digest of the human DNA. DNA digests (5 μ g per lane as assessed by a fluorimetric assay⁵²) were electrophoresed on 0.8–1.5% agarose gels at 70 V for 4 h, then transferred to nitrocellulose by the modification of Southern's⁵³ procedure described by Wahl *et al.*⁴⁰. pBR322 plasmids containing cDNA inserts of human growth hormone (chGH800/pBR322; ref. 41), human γ -globin (JW101; ref. 42) and human α -globin (JW101; ref. 42), were grown in L-broth, and plasmid DNA was isolated by standard techniques^{53,54}. The inserts from these plasmids were purified and the DNA labelled with ³²P-dCTP to a specific activity of 10⁹ d.p.m. μ g⁻¹ using a technique described elsewhere⁵⁵. The blots obtained by this method were identical to those obtained when probes were labelled by nick-translation, but exposure times were significantly reduced. The probes were hybridized to the filters for 36–60 h and then washed according to a protocol supplied by K. Peden⁵⁶. The autoradiographs shown were exposed for 2–4 days using pre-exposed Kodak XAR-5 film with DuPont Lightning Plus intensifying screens⁵⁷.



In cancer tissues, genes are subjected to reduced DNA methylation (HGH and globin genes – randomly selected)

1. The role of DNA methylation in human cancer

A. HYPOMETHYLATION → genomic instability



Prepare genomic DNA from

- healthy tissue (lung)
- tumor tissue (breast cancer)
- Sperm

Digest with methylation sensitive restriction enzyme (does not cut methylated DNA) and run southern blot

Probe southern blot with probes for human, centromere satellite DNA

Cancer tissue: smaller fragments → methylation lost

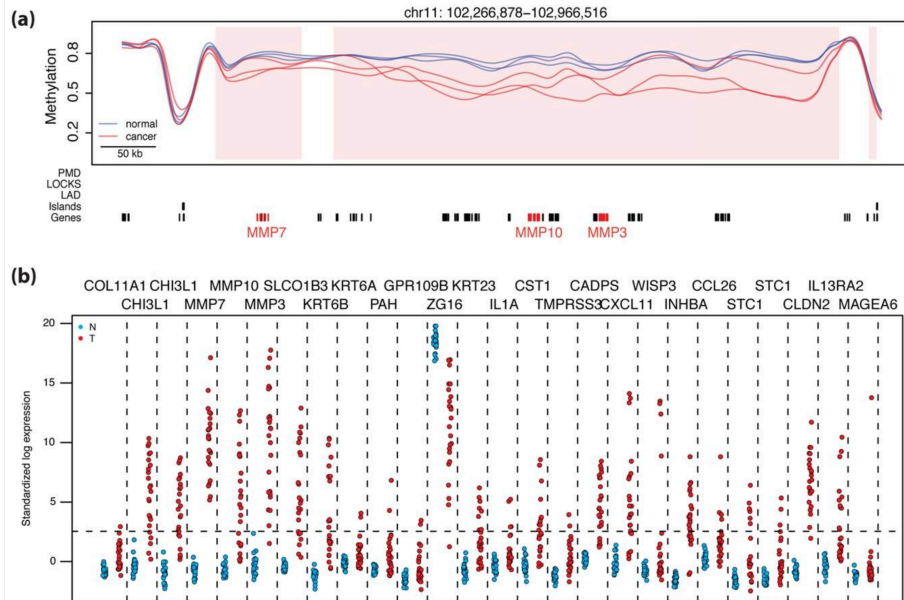
FIGURE 4 – Analysis of methylation of Chr1 Sat2 DNA sequences in malignant breast tissue samples. Breast adenocarcinoma DNA samples, in the first 12 lanes, and sperm and lung DNA samples, in the last 2 lanes, were analyzed for Chr1 Sat2 DNA hypomethylation. The 5 lowest bands in the sperm DNA samples, which were also seen in the breast cancer samples showing considerable hypomethylation (21, 25, 73, O1, 46), had DNA fragments of about 0.8, 1.3, 1.8, 2.2 and 2.7 kb. In addition, a hybridizing fragment migrating at the position for 4.0-kb DNA is seen above the 2.7-kb fragment in samples 21, 25, O2 and 46.

In cancer tissues, also repeat elements are subjected to reduced DNA methylation (HGH and globin genes – randomly selected)

Narayan et al 1998

1. The role of DNA methylation in human cancer

A. HYPOMETHYLATION → alteration in gene expression



(a) An example of hypervariably expressed genes contained within a block; note genes *MMP7*, *MMP10*, and *MMP3* highlighted in red. Methylation values for cancer samples (red) and normal samples (blue) with hypomethylated block locations highlighted (pink shading) are plotted against genomic location. Grey bars are as in Fig. 2. (b) Standardized log expression values for 26 hypervariable genes in cancer located within hypomethylated block regions (normal samples in blue, cancer samples in red). Standardization was performed using the gene expression barcode. Genes with standardized expression values below 2.54, or the 99.5th percentile of a normal distribution (horizontal dashed line) are determined to be silenced by the barcode method²⁶. Vertical dashed lines separate the values for the different genes. Note there is consistent expression silencing in normal samples compared to hypervariable expression in cancer samples. A similar plot drawn from an alternative GEO dataset is shown in Supplementary Figure 18.

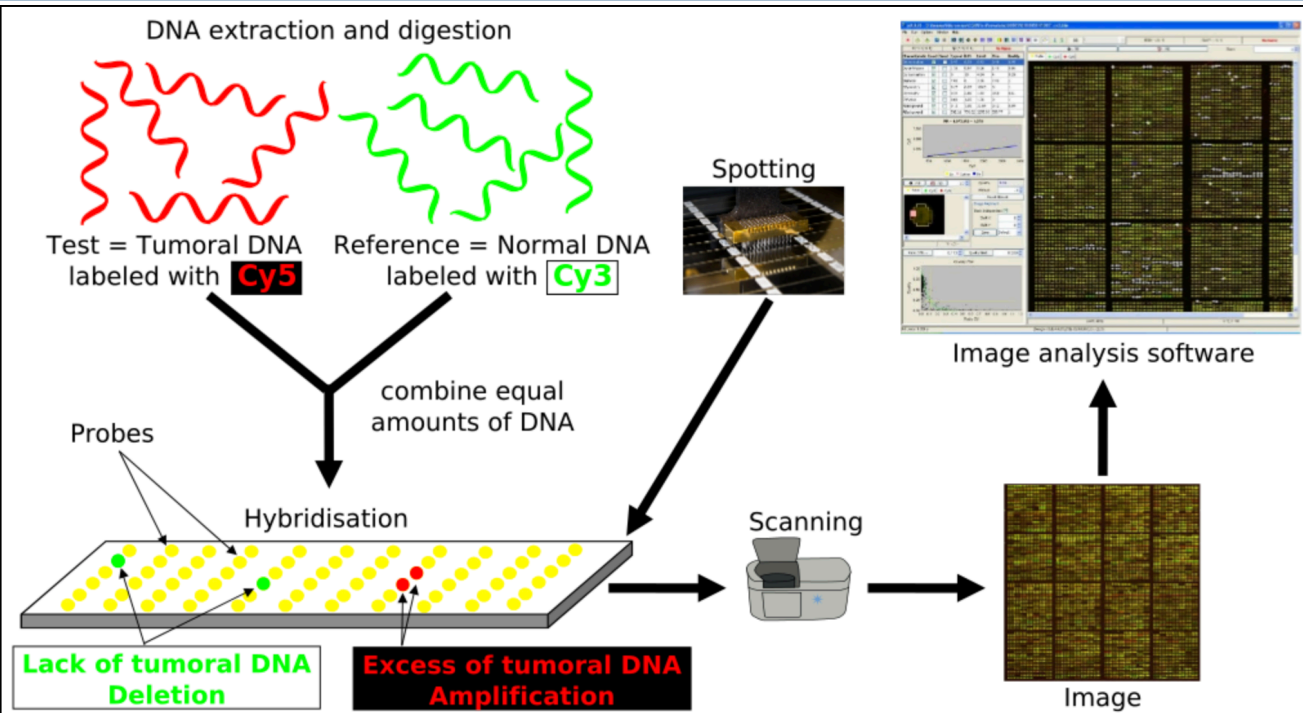
Stochastic methylation variation of differentially methylated regions, distinguishing cancer from normal tissue, in colon, lung, breast, thyroid and Wilms' tumors.

Whole-genome bisulfite sequencing shows these variable DMRs are related to loss of sharply delimited methylation boundaries at CpG islands.

Furthermore, we find hypomethylation of discrete blocks encompassing half the genome, with extreme gene expression variability.

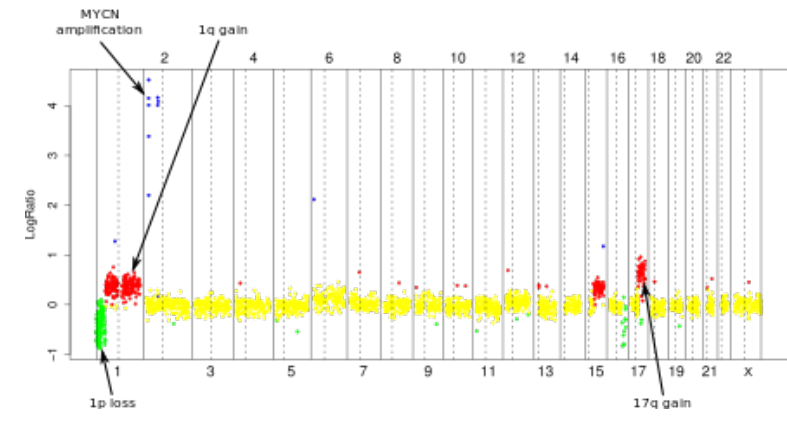
«We suggest a model for cancer involving loss of epigenetic stability of well-defined genomic domains that underlies increased methylation variability in cancer that may contribute to tumor heterogeneity.»

Comparative genomic hybridization (CGH)



Methodology

Array CGH is based on the same principle as conventional CGH. In both techniques, DNA from a reference (or control) sample and DNA from a test (or patient) sample are differentially labelled with two different fluorophores and used as probes that are cohybridized competitively onto nucleic acid targets. ((In conventional CGH, the target is a reference metaphase spread)). In array CGH, these targets can be genomic fragments cloned in a variety of vectors (such as BACs or plasmids), cDNAs, or oligonucleotides.[18] Figure 2.[15] is a schematic overview of the array CGH technique. DNA from the sample to be tested is labeled with a red fluorophore (Cyanine 5) and a reference DNA sample is labeled with green fluorophore (Cyanine 3). Equal quantities of the two DNA samples are mixed and cohybridized to a DNA microarray of several thousand evenly spaced cloned DNA fragments or oligonucleotides, which have been spotted in triplicate on the array. After hybridization, digital imaging systems are used to capture and quantify the relative fluorescence intensities of each of the hybridized fluorophores.[18] The resulting ratio of the fluorescence intensities is proportional to the ratio of the copy numbers of DNA sequences in the test and reference genomes. If the intensities of the fluorochromes are equal on one probe, this region of the patient's genome is interpreted as having equal quantity of DNA in the test and reference samples; if there is an altered Cy3: Cy5 ratio this indicates a loss or a gain of the patient DNA at that specific genomic region.[19]



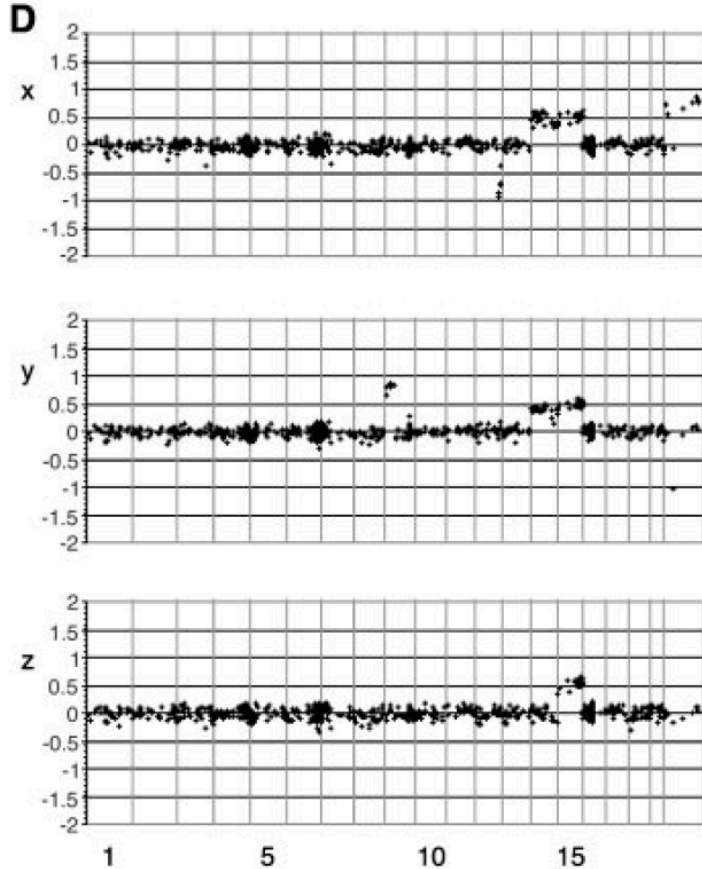
ACGH profile of the IMR32 neuroblastoma cell line

Technological approaches to array CGH

Array CGH has been implemented using a wide variety of techniques. Therefore, some of the advantages and limitations of array CGH are dependent on the technique chosen. The initial approaches used arrays produced from large insert genomic DNA clones, such as BACs. The use of BACs provides sufficient intense signals to detect single-copy changes and to locate aberration boundaries accurately. However, initial DNA yields of isolated BAC clones are low and DNA amplification techniques are necessary. These techniques include ligation-mediated polymerase chain reaction (PCR), degenerate primer PCR using one or several sets of primers, and rolling circle amplification.[20] Arrays can also be constructed using cDNA. These arrays currently yield a high spatial resolution, but the number of cDNAs is limited by the genes that are encoded on the chromosomes, and their sensitivity is low due to cross-hybridization.[15] This results in the inability to detect single copy changes on a genome wide scale.[21] The latest approach is spotting the arrays with short oligonucleotides. The amount of oligos is almost infinite, and the processing is rapid, cost-effective, and easy. Although oligonucleotides do not have the sensitivity to detect single copy changes, averaging of ratios from oligos that map next to each other on the chromosome can compensate for the reduced sensitivity.[22] It is also possible to use arrays which have overlapping probes so that specific breakpoints may be uncovered.

1. The role of DNA methylation in human cancer

A. HYPOMETHYLATION → genomic instability



**Studying DNA methylation using cancer models with impaired DNMT1 function:
(→ FORCED LOSS OF DNA METHYLATION → CANCER)**

Mouse model for cancer:

Hypermorph of DNMT1 ($DNMT1^{chip}$) reduced DNA methylation
 $DNMT1^{-/Chip}$ mice are viable; 80% develop aggressive lymphoma

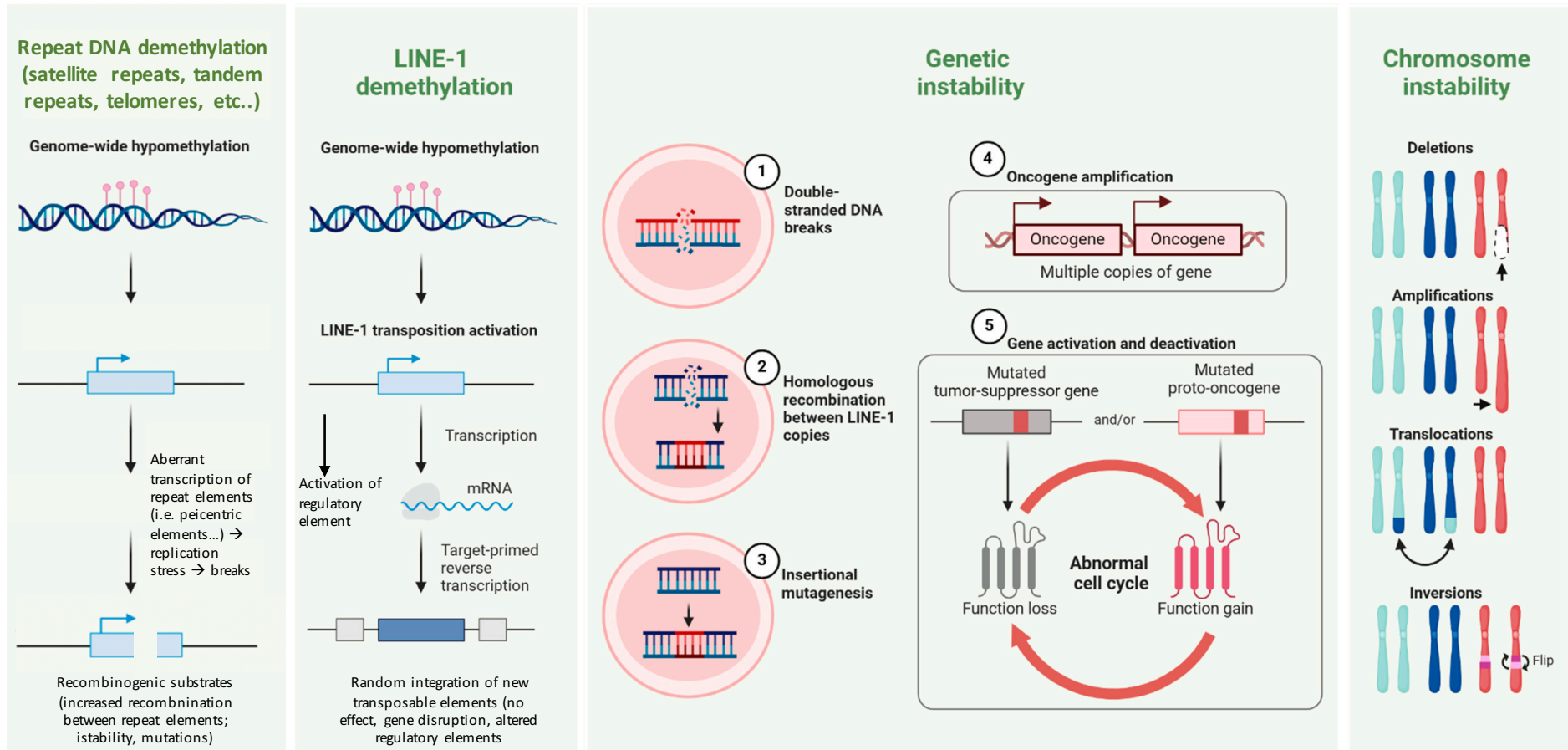
QUESTION: Does global loss of dna methylation select for cancer driving genome instability (positive selection for cancer driving mutations)

CGH array shows genomic instability:

- The increased fluorescence ratios observed for chromosomes 14 and 15 are consistent with single copy whole-chromosome gains throughout the tumor → amplification
- Observed independently in multiple animals → directed process (selected)

(D) Array comparative genome hybridization (CGH) analyses of three $Dnmt1^{chip/-}$ tumors, showing clear single-copy, whole-chromosome gain of chromosome 15 (x, y, and z), whole-chromosome gains of 14 and loss on distal 12 (x), and gains of chromosome 14 and proximal 9 (y). The X gain (x) reflects a sex difference between tumor and control. Array CGH was performed as in (26). Fluorescence ratios (average of quadruplicate measurements) for each bacterial artificial chromosome are plotted as a function of genome location based on the February 2002 freeze of the assembled mouse genome sequence (<http://genome.ucsc.edu>). Vertical lines delimit chromosome boundaries.

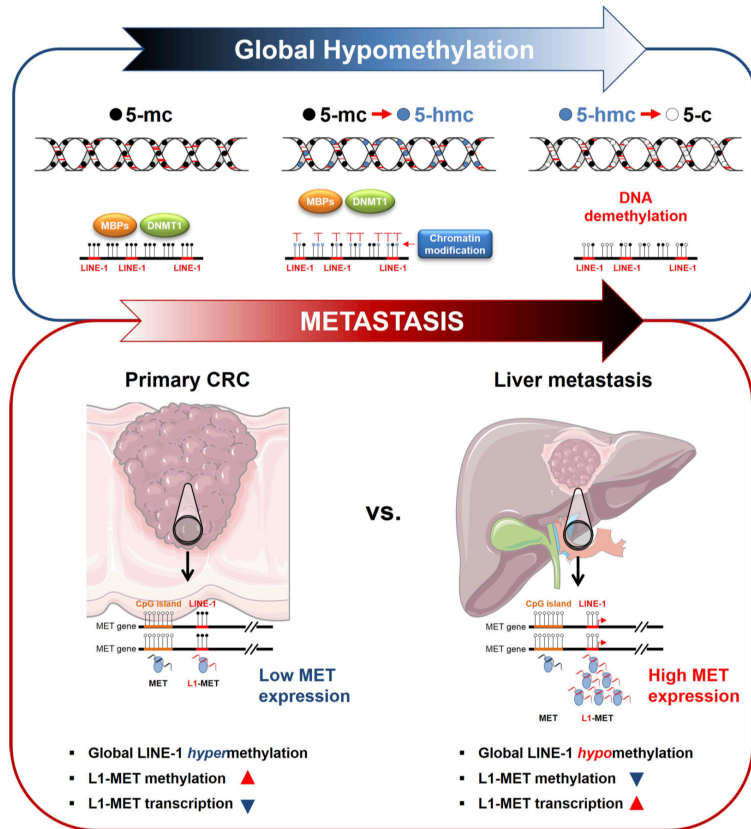
1. Global hypomethylation drives the formation of mutations



Loss of DNA methylation: Ectopic expression of RNAs from repeat DNA and/or transposable elements (such as LINE-1). The role of LINE-1 demethylation in cancer. Genome-wide hypomethylation activates LINE-1 transposition, leading to double-stranded DNA breaks. Alternatively, suppressive regulatory elements in LINE-1 elements get activated. Homologous recombination between repeat elements or LINE-1 copies with similar base composition, and insertional mutagenesis by LINE elements. These events cause genetic instability, including oncogene amplification (4), gene activation or deactivation (5), and an abnormal cell cycle. Chromosome instability results in structural alterations such as deletions, amplifications, translocations, and inversions, further promoting tumorigenesis.

1. The role of DNA methylation in human cancer

A. HYPOMETHYLATION → genomic instability, altered gene expression



Colorectal cancer + liver metastasis:

LINE-1 element controls the expression of the MET oncogene

The MET oncogene encodes the receptor tyrosine kinase known as the hepatocyte growth factor receptor (HGFR). This receptor plays a crucial role in various cellular processes, including:

1. Cell Proliferation: It promotes the growth and division of cells.
 2. Migration: It aids in the movement of cells, which is essential for processes like wound healing.
 3. Survival: It helps cells resist apoptosis (programmed cell death).
 4. Angiogenesis: It supports the formation of new blood vessels
- Upregulation or amplification of MET drives cancer formation, metastasis and therapy resistance

Reduced DNA methylation in LINE1 retrotransposons

LINE1 elements contain normal promoter but also an additional promoters (cryptic promoter) that can activate downstream located oncogenes (i.e. MET oncogene)

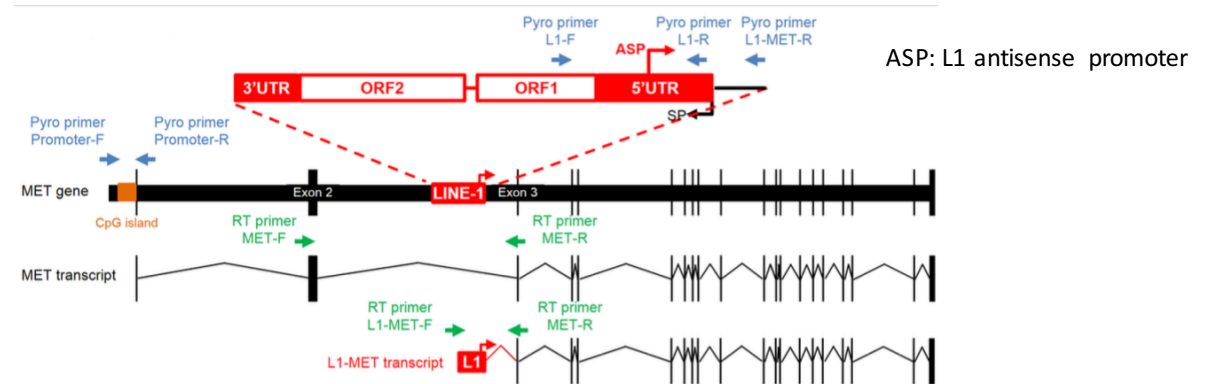
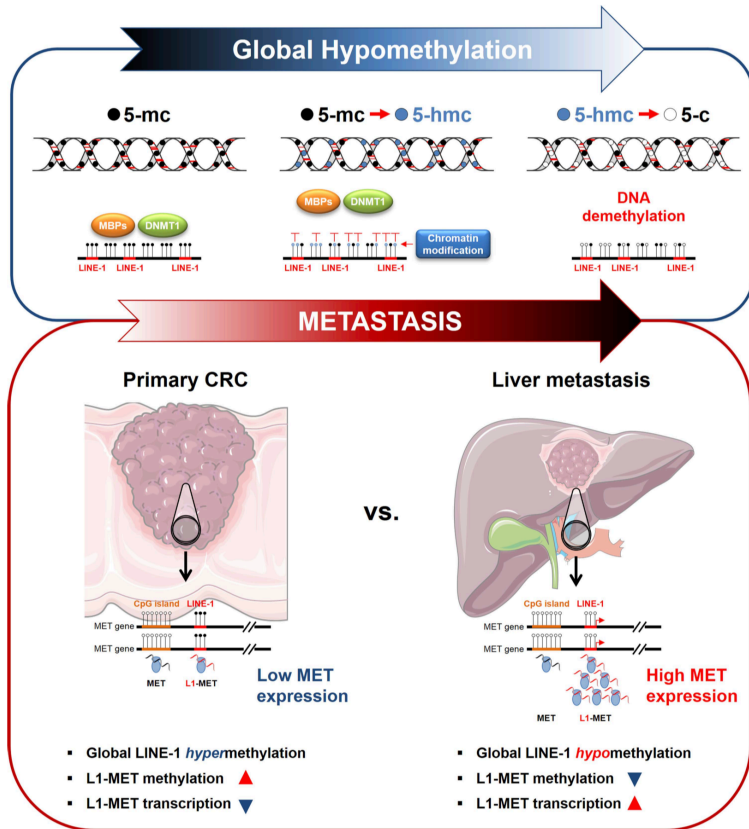
LINE1 elements are normally epigenetically silenced by DNA methylation

Metastasis → loss of LINE1 methylation → increases expression of MET oncogene.

A consolidated model for the activation mechanism of the MET proto-oncogene by LINE-1 hypomethylation in colorectal cancer (CRC) metastasis. In this model, hypomethylation of CpG sites is characterised by enhanced conversion of 5-mc (5-methylcytosine) to 5-c (5-cytosine), with an intermediary generation of 5-hmc (5-hydroxylated methylcytosine). Enhanced CpG demethylation with consequent accumulation of 5-hmc prevents the binding of various DNA methyltransferases (DNMTs) and methyl binding proteins (MBPs) to CpG sites, triggering a cascade of events that favour DNA hypomethylation. Occurrence of DNA hypomethylation events in the context of LINE-1 elements can potentially permit activation of certain oncogenes, including the MET proto-oncogene which may result in accelerated CRC metastasis.

1. The role of DNA methylation in human cancer

A. HYPOMETHYLATION → genomic instability, altered gene expression

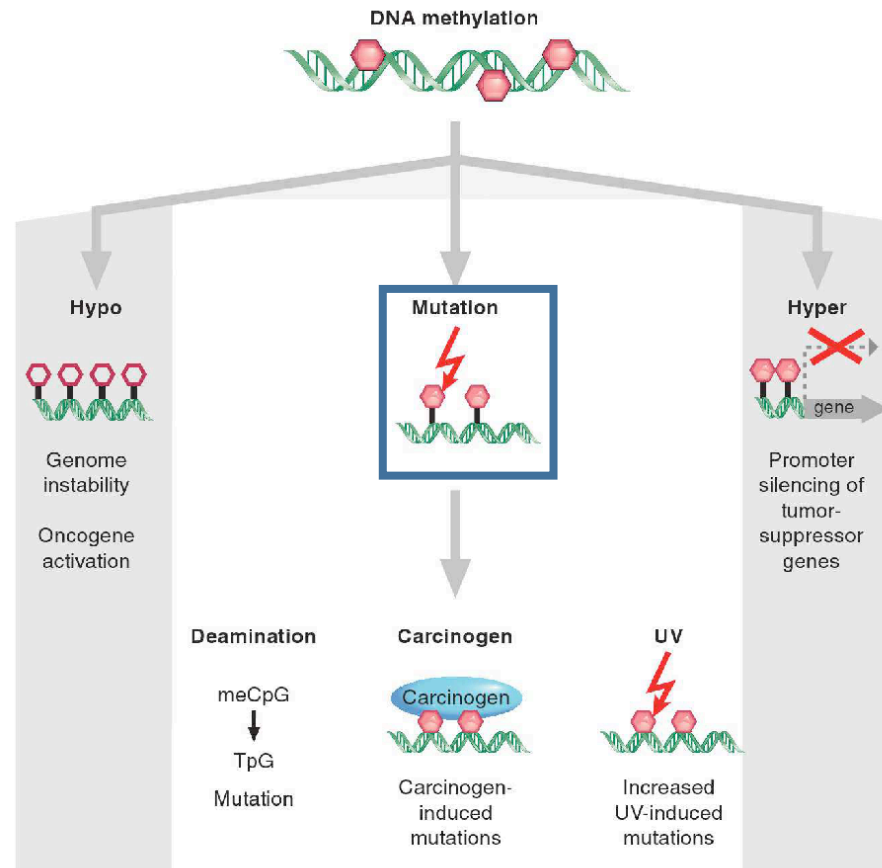


- Loss of DNA in LINE-1 element allows expression of MET variants from promoter element in LINE-1 element
- High MET expression
- Metastasis

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1. Alteration of DNA methylation in human cancer

CANCER IS ASSOCIATED WITH GLOBAL DNA HYPOMETHYLATION and LOCAL DNA HYPERMETHYLATION



Normal tissue: 80% of CpG methylated
Cancer: 40-60% of CpG methylated

Global DNA methylation is lost from large blocks (28kb – 10Mb)

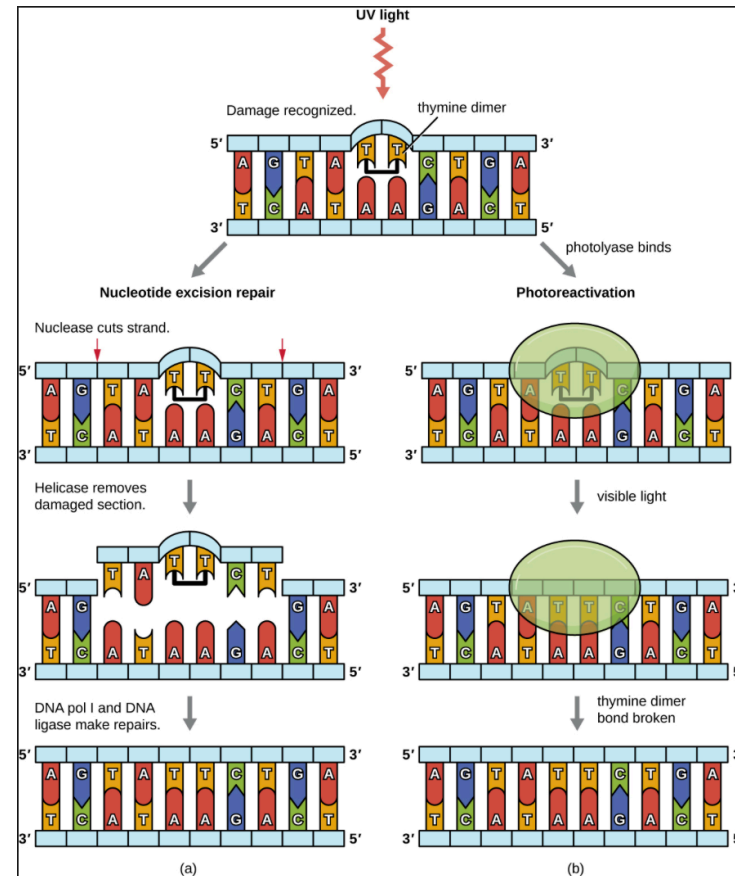
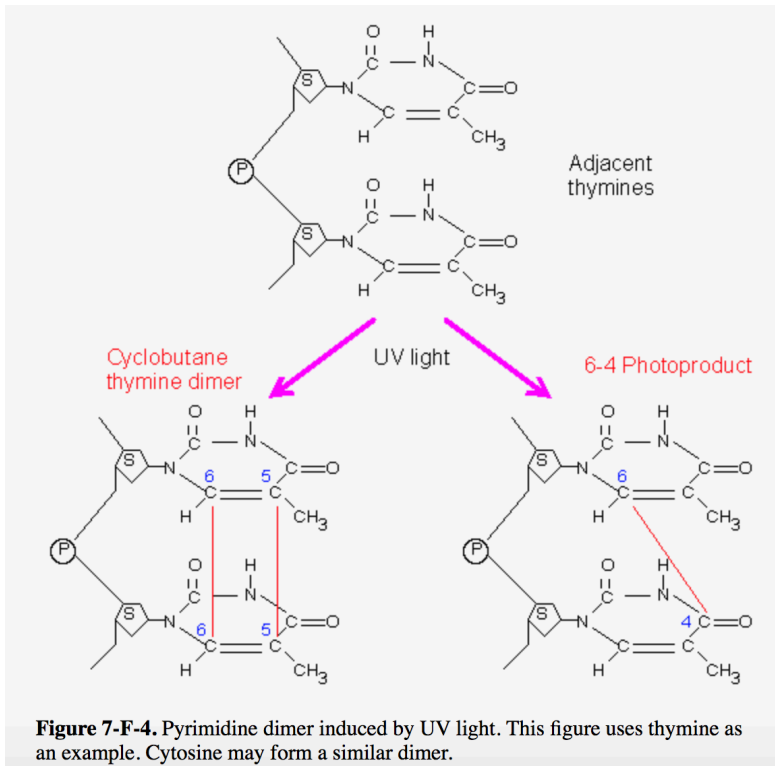
Local hypermethylation at specific locations such as tumor suppressors

Figure 3. Epigenetic alterations involving DNA methylation can lead to cancer by various mechanisms. Loss of DNA cytosine methylation (white hexagons) illustrated in the hypo column results in genome instability. Focal hypermethylation (pink hexagons) at gene promoters shown in the hyper column causes heritable silencing and, therefore, inactivation of tumor suppressors and other genes. Additionally, methylated CpG sites (pink hexagons) are prone to mutation: They are hot spots for C to T transition mutations caused by spontaneous hydrolytic deamination; or methylation of CpG sites can increase the binding of some chemical carcinogens to DNA; and it increases the rate of UV-induced mutations.

1. The role of DNA methylation in human cancer

B. UV damage at 5mC

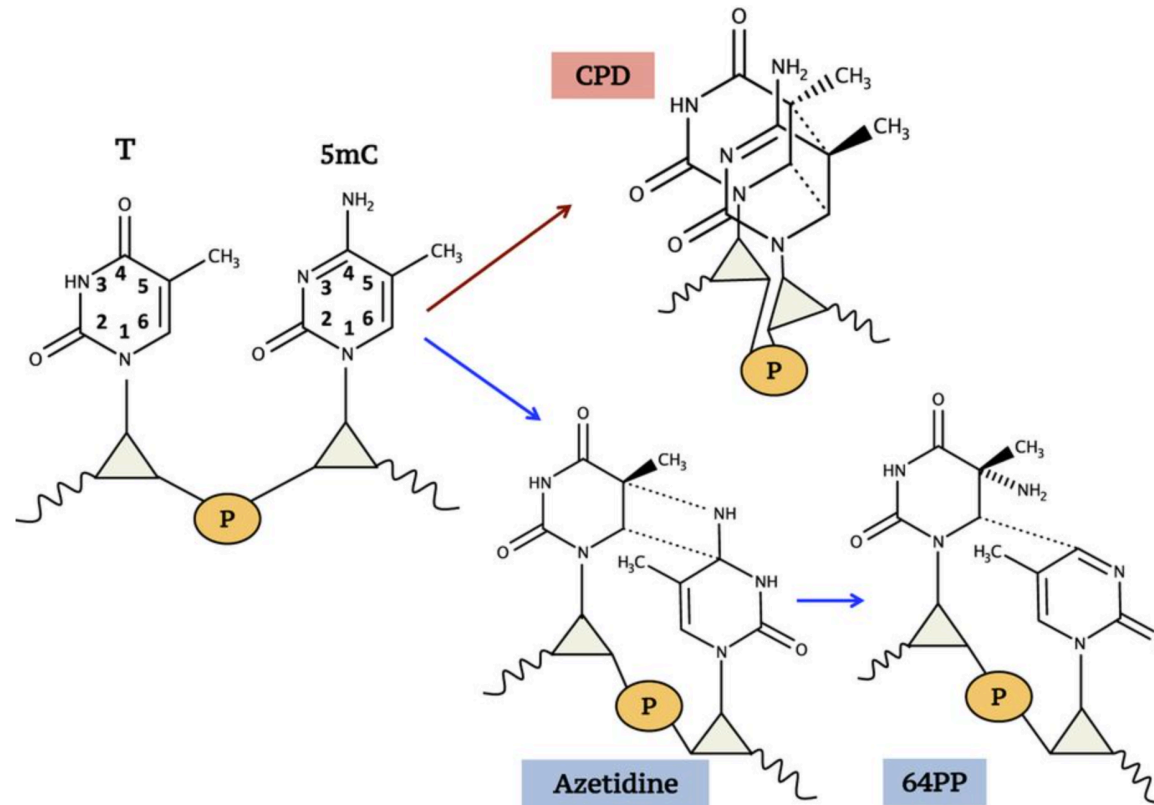
Thymidine dimers



Not in placental mammals

1. The role of DNA methylation in human cancer

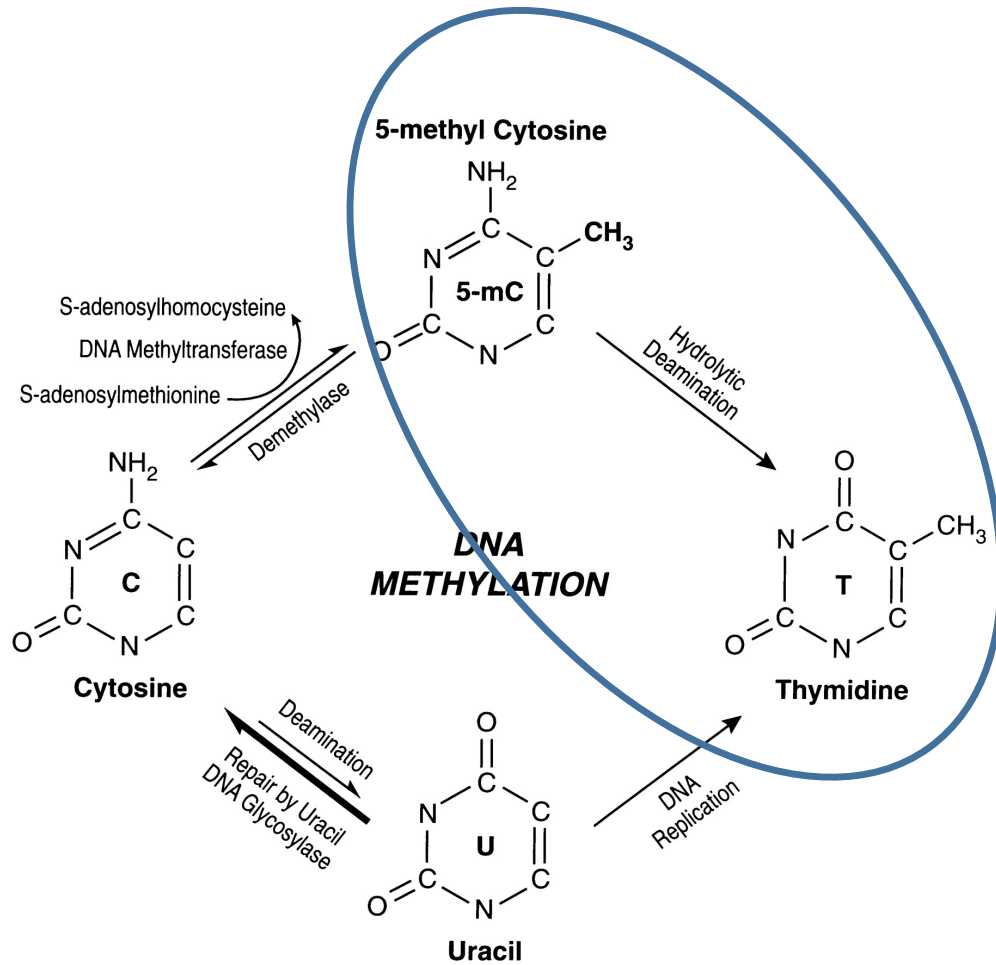
B. UV damage at 5mC



Formation of T5mC dimeric photoproducts. CPD, cyclobutane pyrimidine dimers (c,s stereo isomers); 64PP, pyrimidine (6-4) pyrimidone photoproducts, sugars are represented by triangles, phosphate groups by a circle.

1. The role of DNA methylation in human cancer

B. INCREASED MUTATION RATE RELATED TO 5mC



5mC transition mutation to T is most frequent type of transition mutation (for example 50% of p53 mutations in colorectal cancer occur at sites of DNA methylation)
→ **CpG transition**

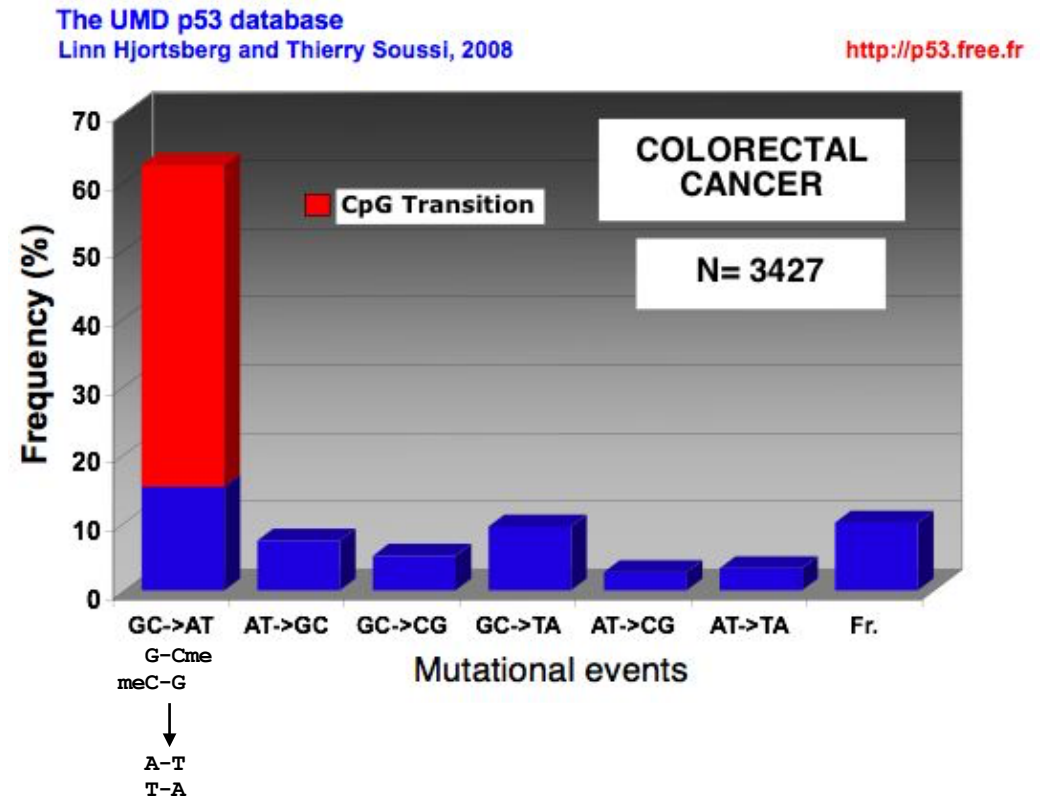
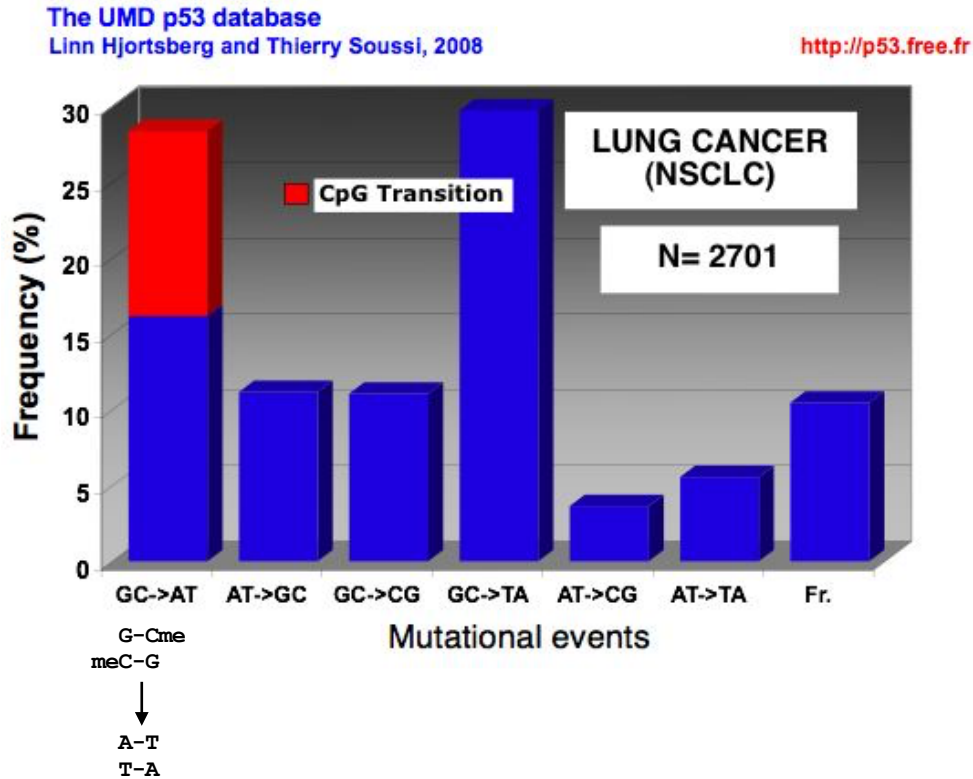
5mC → T is frequent in exons of tumorsuppressor gene bodies

5mC → promotes the formation of adducts with benzo(a)pyrene diol epoxide → increased mutation rate in smokers

1. The role of DNA methylation in human cancer

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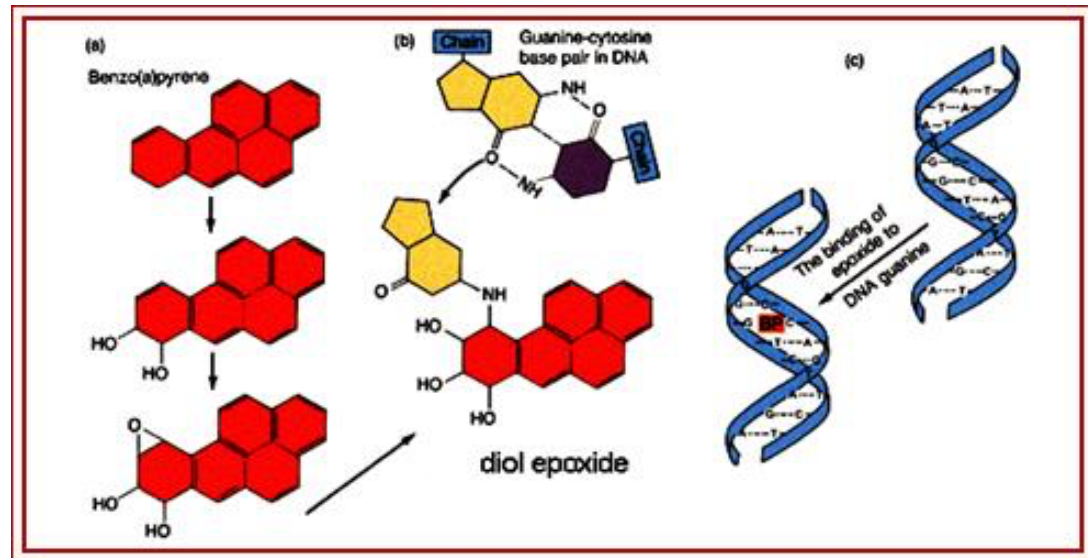
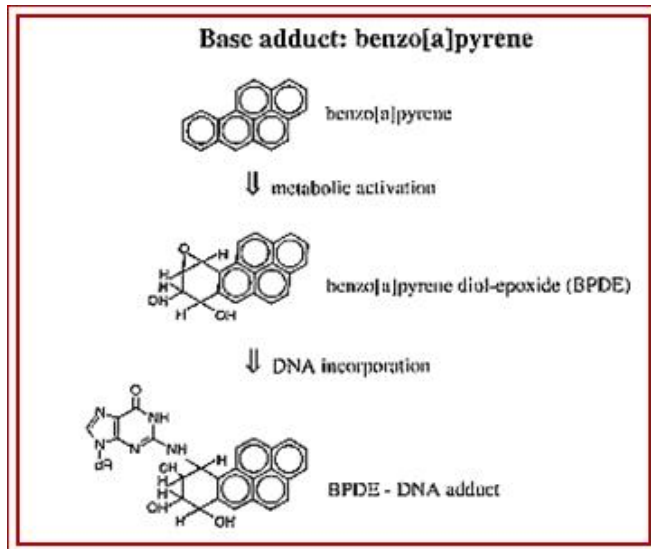
5mC → T is frequent in exons of the tumorsuppressor gene p53 in colorectal cancer and lung cancer



1. The role of DNA methylation in human cancer

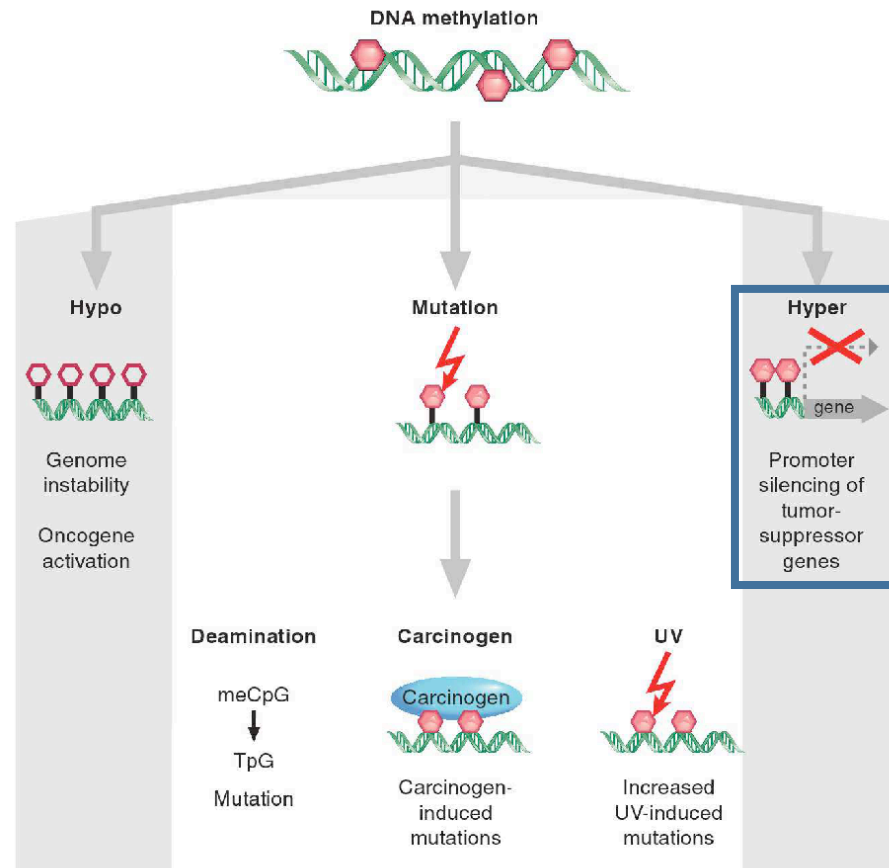
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1. The role of DNA methylation in human cancer

C. HYPERMETHYLATION

In human cancer, DNA methylation occurs at CpG islands that are located in and around the transcriptional start site of abnormally silenced genes (in cancer cells)

Typically 5-10% of these CpG island promoters are methylated in cancer.

In an individual tumor hundreds of genes can be subjected to this type of epigenetic alteration.

The number of genes with hypermethylated promoters outnumbers the number of genes mutated in the same cancer.

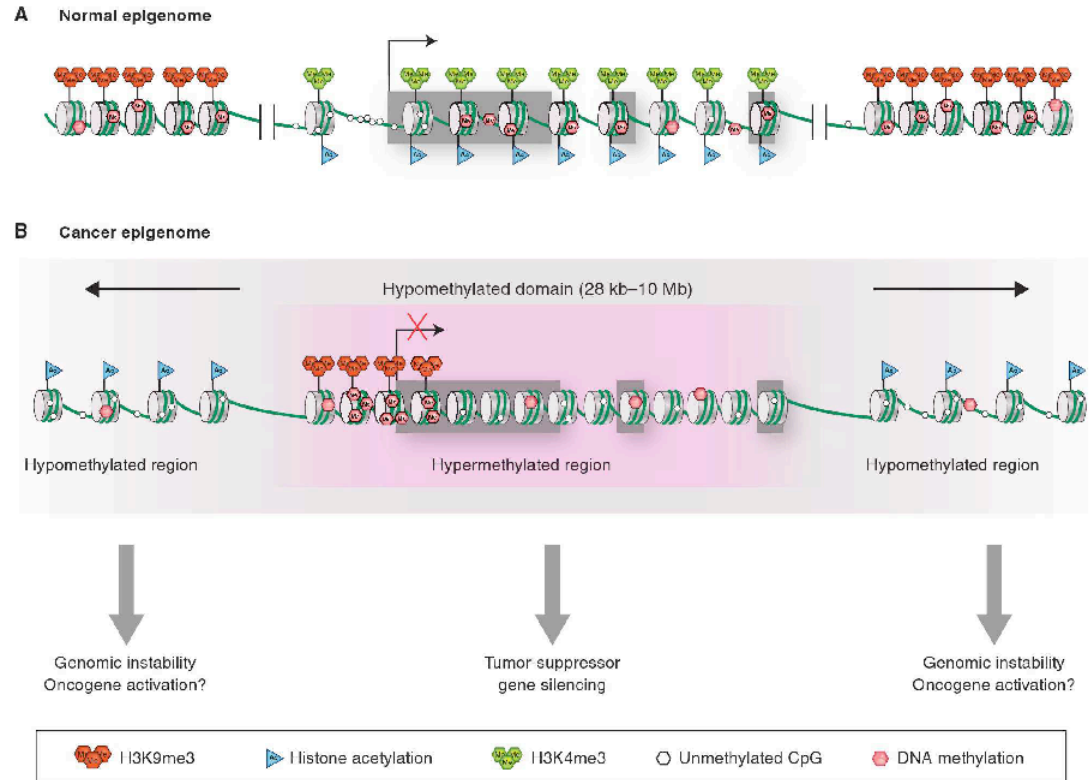


Figure 4. Chromatin structural changes in cancer cells. (A) In a typical cell, a CpG-island-containing active gene can be recognized by virtue of a nucleosome-depleted promoter, absence of promoter DNA methylation, but marked by H3K4me3 surrounding the promoter and histone acetylation along the locus. Gene body CpG methylation often can be observed. Nongenic regions flanking an active gene are frequently marked by repressive epigenetic marks, such as H3K9me3 and 5mC. (B) The cancer epigenome is characterized by simultaneous global losses in DNA methylation (gray shading), interspersed with silenced genes that have abnormal gains of DNA methylation and repressive histone modifications in CpG island promoter regions. These silenced genes may be hypomethylated in their gene body, similar to surrounding chromatin. The hypomethylated regions can have an abnormally open nucleosome configuration and acetylated histone lysines. Conversely, abnormal DNA hypermethylation in promoter CpG islands of silenced genes is associated with nucleosomes positioned over the transcription start sites.

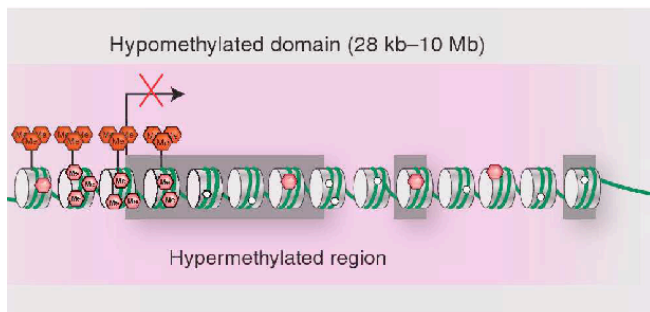
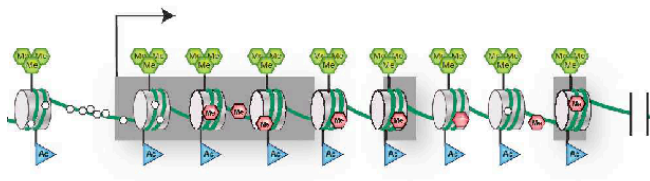
→ Gene silencing of tumorsuppressors

2. HYPERMETHYLATION OF GENE PROMOTERS of TSGs (tumor suppressor genes) IN CANCER

NORMAL DEVELOPMENT: Promoters of 60% of genes contain CpG islands → majority is never DNA methylated during development

CANCER: 5–10% of the thousands of promoter CpG islands that never normally contain DNA methylation from embryonic development onwards show increased methylation in human cancer

Silencing of tumor suppressors (“driver”) but also potential “passengers”



Class of hypermethylated gene	Examples
Known TSG ^a	<i>VHL</i> <i>E-cadherin</i> <i>P16Ink4a</i> <i>MLH1</i> <i>APC</i> <i>Stk4</i> <i>Rb</i>
Candidate TSG	<i>FHIT</i> <i>Rassf1a</i> <i>O6-MGMT</i> <i>Gst-Pi</i> <i>GATA4/5</i> <i>DAP-kinase</i>
Gene discovered through random screens for hypermethylated genes	<i>HIC-1</i> <i>SFRP1, -2, -4, -5</i> <i>BMP-3</i> <i>SLC5A8</i> <i>SSI1</i>

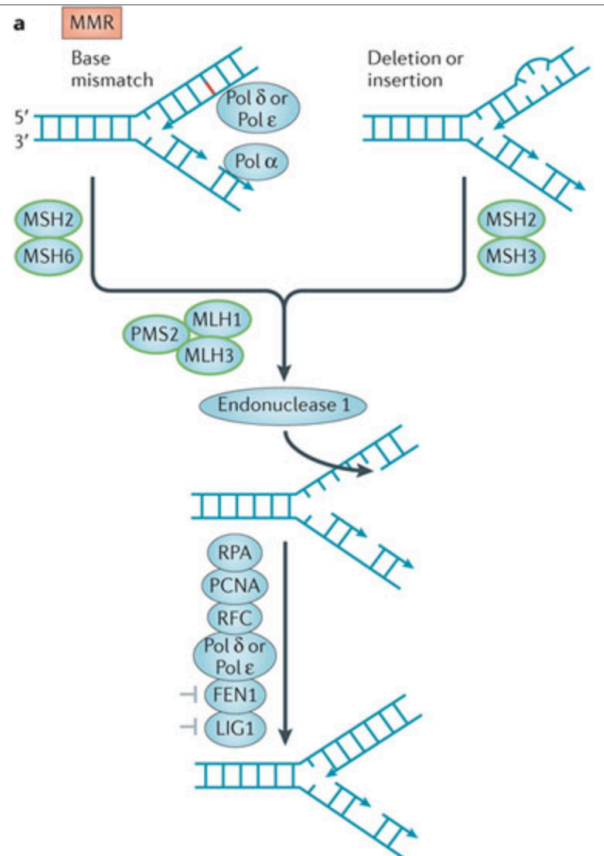
Also frequently mutated = driver mutations

Have role in tumorsuppression, but are not frequently mutated

Identified in screens for DNA methylation, but function of gene is not clear

^a A classic tumor-suppressor gene (TSG) is known to be mutated in the germline of families with hereditary cancer syndromes.

2. HYPERMETHYLATION OF GENE PROMOTERS OF TSGs: MLH1 in colorectal cancer

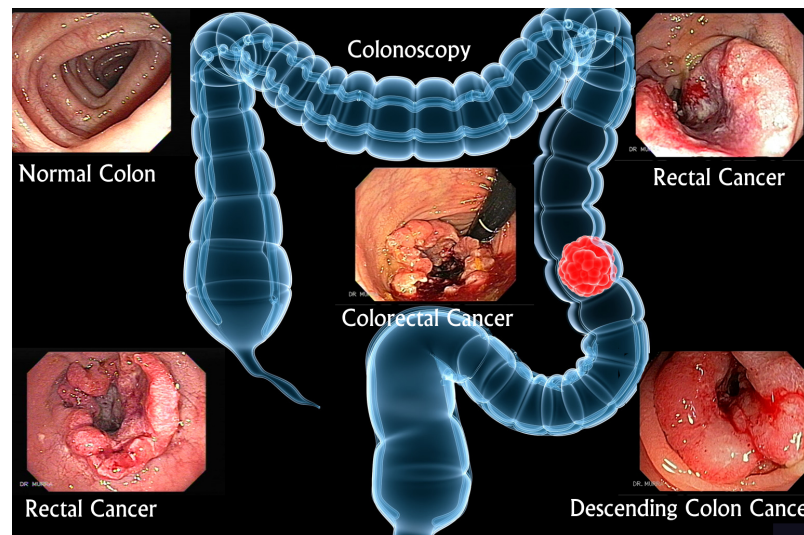


DNA mismatch repair

MLH1: DNA mismatch repair pathway

- Defect in DNA damage repair
- Accumulation of mutation
- Genomic instability (microsatellite instability)
- Driver mutation for colon cancer

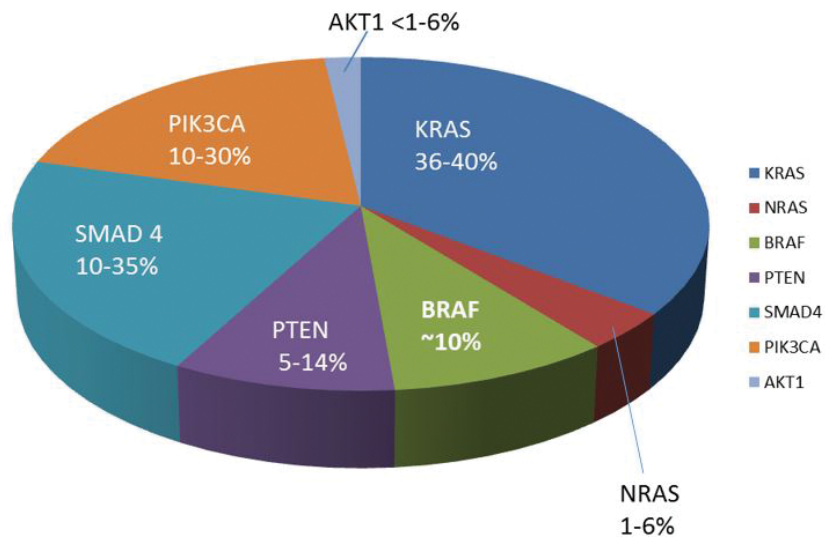
A subclass of colorectal cancer is characterized by a hypermethylation of CpG islands at the MLH1 promoter



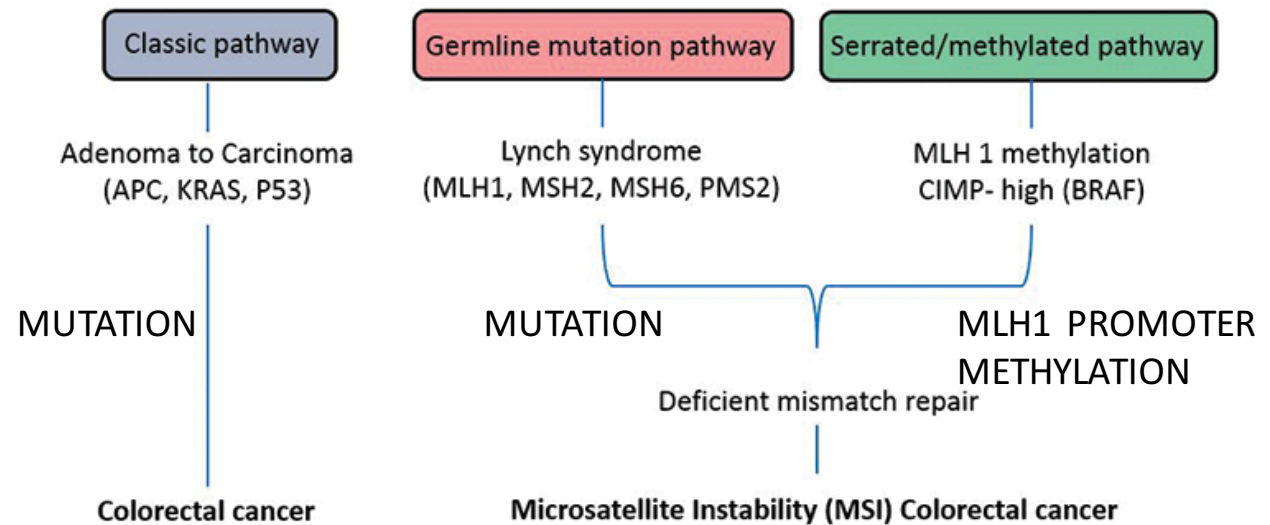
2. HYPERMETHYLATION OF GENE PROMOTERS OF TSGs: MLH1 in colorectal cancer

MLH1 is not frequently mutated

Somatic Mutation Frequencies in Colorectal Cancer



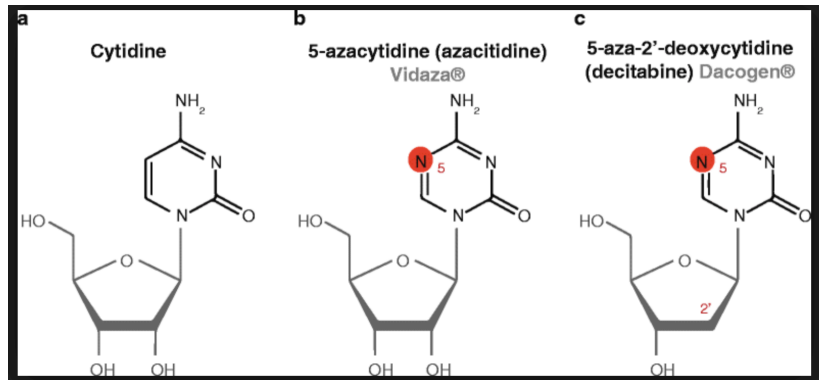
Pathways to tumorigenesis in Colorectal cancer



Lynch syndrome (HNPCC or hereditary nonpolyposis colorectal cancer) is an autosomal dominant genetic condition that has a high risk of colon cancer[1] as well as other cancers including endometrial cancer (second most common), ovary, stomach, small intestine, hepatobiliary tract, upper urinary tract, brain, and skin. The increased risk for these cancers is due to inherited mutations that impair DNA mismatch repair. **It is a type of cancer syndrome.** MUTATIONS in MLH1, MSH2, MSH6, PMS2

Serrated adenocarcinoma is a recently described subset of colorectal cancer (CRC), which account for about 10% of all CRCs and follows an alternative pathway in which serrated polyps replace the traditional adenoma as the precursor lesion to CRC. Serrated polyps form a heterogeneous group of colorectal lesions that includes hyperplastic polyps (HPs), sessile serrated adenoma (SSA), traditional serrated adenoma (TSA) and mixed polyps.

EPIGENETIC DRUGS: DNMT INHIBITORS → loss of DNA methylation



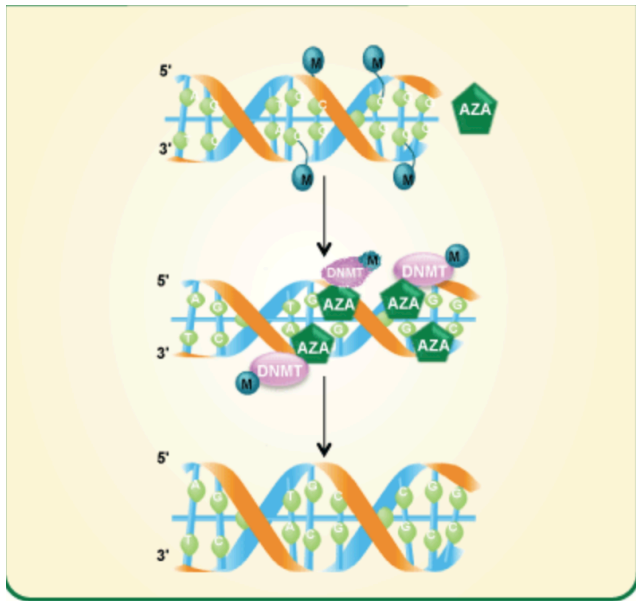
Azacitidine is a **chemical analogue of the nucleoside cytidine**, which is present in DNA and RNA. It is thought to have antineoplastic activity via two mechanisms – at low doses, by **inhibiting of DNA methyltransferase, causing hypomethylation of DNA**, and at high doses, by **its direct cytotoxicity to abnormal hematopoietic cells** in the bone marrow through its incorporation into DNA and RNA, resulting in cell death. Azacitidine is a ribonucleoside, so it is incorporated into RNA to a larger extent than into DNA. Azacitidine's incorporation into RNA leads to the disassembly of polyribosomes, defective methylation and acceptor function of transfer RNA, and inhibition of the production of proteins

Decitabine (5-aza-2'-deoxycytidine) is a deoxyribonucleoside, so it can only incorporate into DNA. Its incorporation into DNA leads to covalent binding with DNA methyltransferases, which prevents DNA synthesis and subsequent leads to cytotoxicity.

When entered the cells a nucleosides such as **azacitidine** is also metabolized to **5-aza-2'-deoxycytidine-triphosphate** (aka, decitabine-triphosphate), and can be incorporated into DNA, **substituting for cytosine**. Azacytosine-guanine dinucleotides are recognized as substrate by the DNA methyltransferases, which catalyze the methylation reaction by a nucleophilic attack.

This results in a **covalent bond between the carbon-6 atom of the cytosine ring and the enzyme**. The bond is normally resolved by beta-elimination through the carbon-5 atom, but this latter reaction does not occur with azacytosine because its carbon-5 is substituted by nitrogen, leaving the enzyme remains covalently bound to DNA and blocking its DNA methyltransferase function.

In addition, the **covalent protein adduction also compromises the functionality of DNA and triggers DNA damage signaling, resulting in the degradation of trapped DNA methyltransferases**. As a consequence, methylation marks become lost during DNA replication.

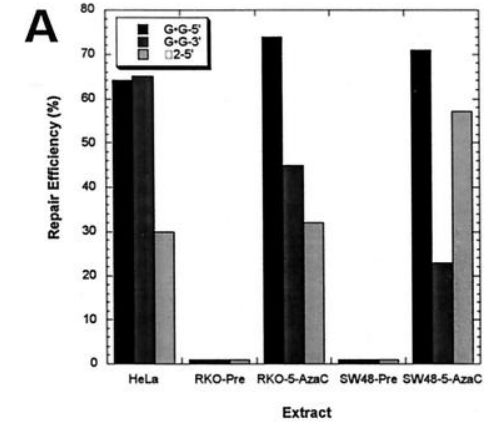
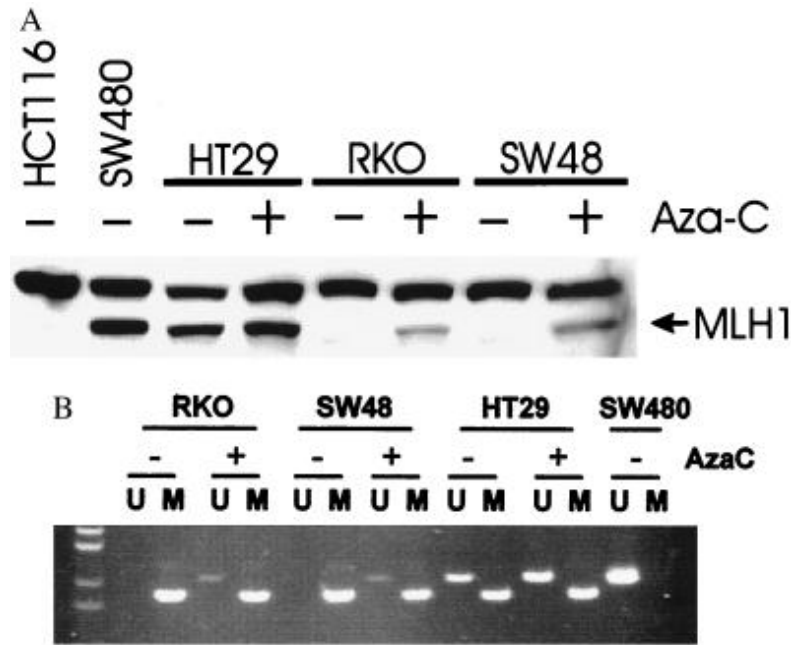


2. HYPERMETHYLATION OF GENE PROMOTERS OF TSGs: MLH1 in colorectal cancer

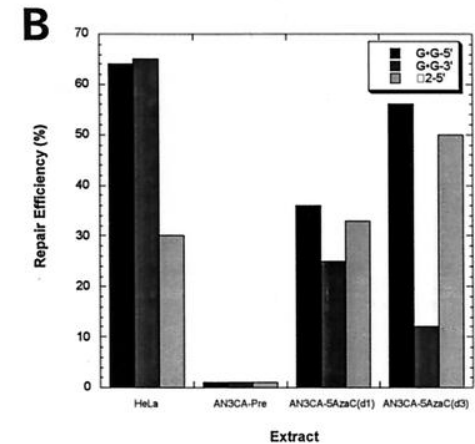
Reversibly of DNA damage repair defect caused by MLH1 silencing

Treatment of colon cancer cell line (with silenced MLH1) with 5-Aza-2'-deoxycytidine

Re-expression of MLH1 and rescue of DNA damage repair



DNA damage repair assay



DNA damage repair assay

2. HYPERMETHYLATION OF GENE PROMOTERS OF TSGs: WHAT ARE THE IMPORTANT GENES?

Class of hypermethylated gene	Examples	
Known TSG ^a	<i>VHL</i> <i>E-cadherin</i> <i>P16Ink4a</i> <i>MLH1</i> <i>APC</i> <i>Stk4</i> <i>Rb</i>	<i>Also frequently mutated = clear driver mutations</i>
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Gene discovered through random screens for hypermethylated genes	<i>HIC-1</i> <i>SFRP1, -2, -4, -5</i> <i>BMP-3</i> <i>SLC5A8</i> <i>SSI1</i>	

^a A classic tumor-suppressor gene (TSG) is known to be mutated in the germline of families with hereditary cancer syndromes.

Drivers: genes that are causal for tumor formation

Passengers: genes that are not causal for tumor formation, but support the tumorformation and progression

2. HYPERMETHYLATION OF GENE PROMOTERS OF TSGs: WHAT ARE THE IMPORTANT GENES?

Approaches to identify relevance of potential TSG silenced in human cancer

Table 5. Steps in documenting the importance of a hypermethylated gene for tumorigenesis

1. Document CpG island promoter methylation and correlate with transcriptional silencing of the gene and ability to reverse the silencing with demethylating drugs in culture.
2. Document correlation of promoter hypermethylation with specificity for this change in tumor cells (cell culture and primary tumors) versus normal cell counterparts and incidence for the hypermethylation change in primary tumors.
3. Document the position of the hypermethylation change for tumor progression of given cancer types.
4. Document the potential significance for the gene silencing in tumorigenesis through gene reinsertion studies in culture and effects on soft agar cloning, growth of tumor cells in nude mouse explants, etc.
5. Establish function of the protein encoded by the silenced gene, through either known characteristics of the gene or testing for activity of recognized protein motifs in culture systems, etc.
6. Document tumor-suppressor activity and functions of the gene for cell renewal, etc., especially for totally unknown genes, through mouse knockout studies.

First observation in a commercially available cancer cell line (Hela,...)
→ Bisulfite sequencing, gene expression, 5-aza-2'-deoxycytidine treatment

Validation of first observation in different type of cancer cells

- Use primary cell line or primary tumor cells (grown in cell culture plate)
- Bisulfite sequencing, gene expression, 5-aza-2'-deoxycytidine treatment
- Use large datasets of methylation mapping and RNA seq (patient tissue)

Fine mapping of critical position and dynamic change of DNA methylation in tumor progression

- More detailed methylation analysis using cancer progression models (in vitro models for cancer progression (EMT, oncogenes...))
- Datasets for different tumor stages, metastasis, therapy resistance

Functional experiments related to central cancer features

- Reconstitute the expression of the silenced gene (cell models, mouse models)
- Does proliferation, apoptosis, anchorage independent growth, EMT features change

Dissect functional pathways

- Identify the biological pathways the gene is involved
- Interacting factors, eventual target genes

(for example: RNAseq, proteomics – try to understand alteration in gene expression – highlight pathways)

More complex model systems

- Animal models (transgene, knock-out)
- Patient derived cell models (patient derived xenografts, tumor-organoids)

3. THE IMPORTANCE OF EPIGENETIC GENE REGULATION IN **EARLY** TUMORPROGRESSION

Early phases in colon cancer

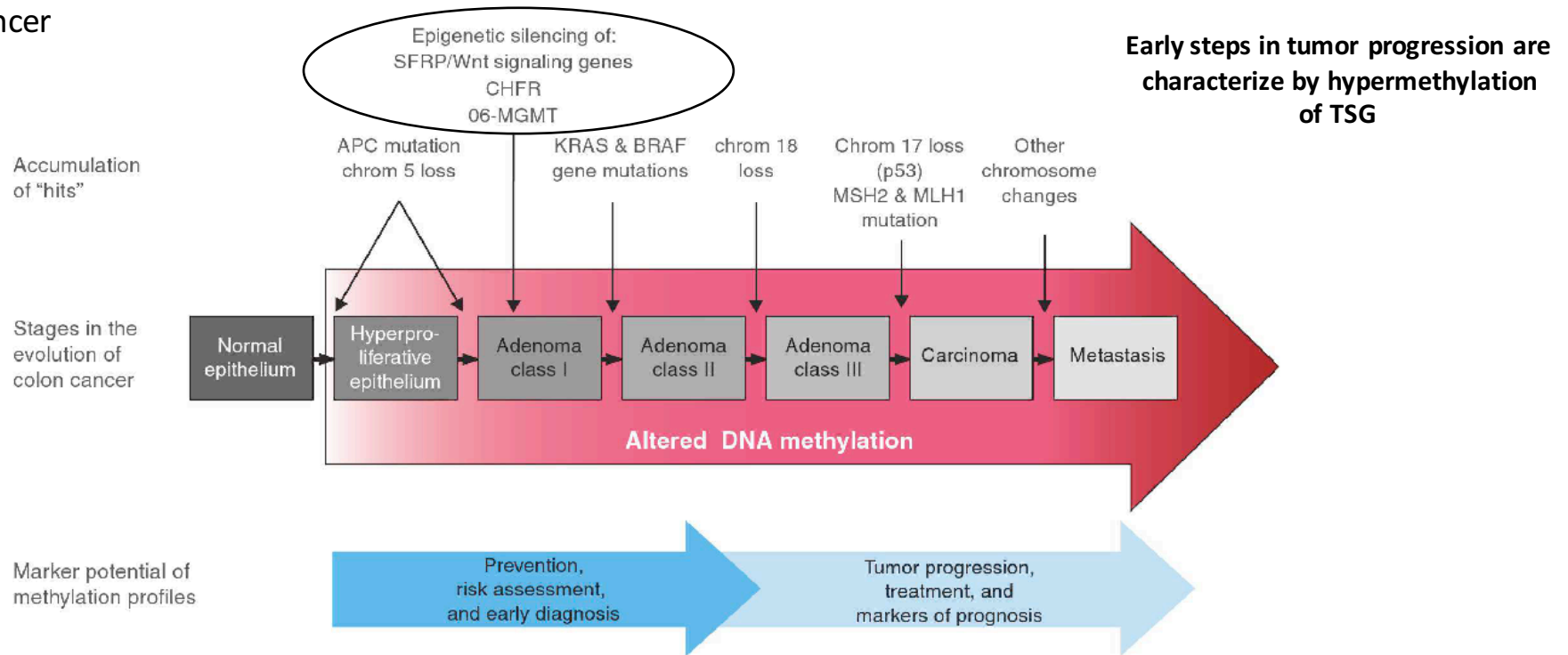


Figure 5. The position of abnormal DNA methylation in tumor progression. This is depicted in the classic model ([Kinzler and Vogelstein 1997](#)) for genetic alterations during the evolution of colon cancer. Altered DNA methylation is shown to occur from very early on in tumorigenesis (red arrow), as discussed in the text, during the conversion of normal to hyperplastic epithelium, accruing during the progression from noninvasive to invasive and, ultimately, metastatic tumors. This places it in a strategic position for channeling stem cells into abnormal clonal expansion (illustrated in [Fig. 6](#)) by cooperating with key genetic alterations. These epigenetic abnormalities also have connotations for cancer treatment and markers of prognosis.

3. THE IMPORTANCE OF EPIGENETIC GENE REGULATION IN EARLY TUMORPROGRESSION

Experiments have specifically shown that this leads to the buildup of repressive histone marks in gene promoter regions and, subsequently, DNA hyper-methylation.

Alterations promote molecular progression

What is happening:

Inflammation, aging or chronic injury may program an epigenetic pattern that leads to gene expression that promotes clonal expansion of progenitor cells (instead of differentiation)

Expanded cell population are subjected to subsequent mutations or epigenetic alterations promoting tumor formation.

Experiments:

Engineering the mutations/epigenetic alterations into mice or cells, in vitro, appears to trap stem progenitor cells in states of abnormal self-renewal and/or diminishes their capacity for lineage commitment and differentiation.

Inducing DNA de-methylation can partially restore the capacity of cells with the mutations to respond to differentiation cues

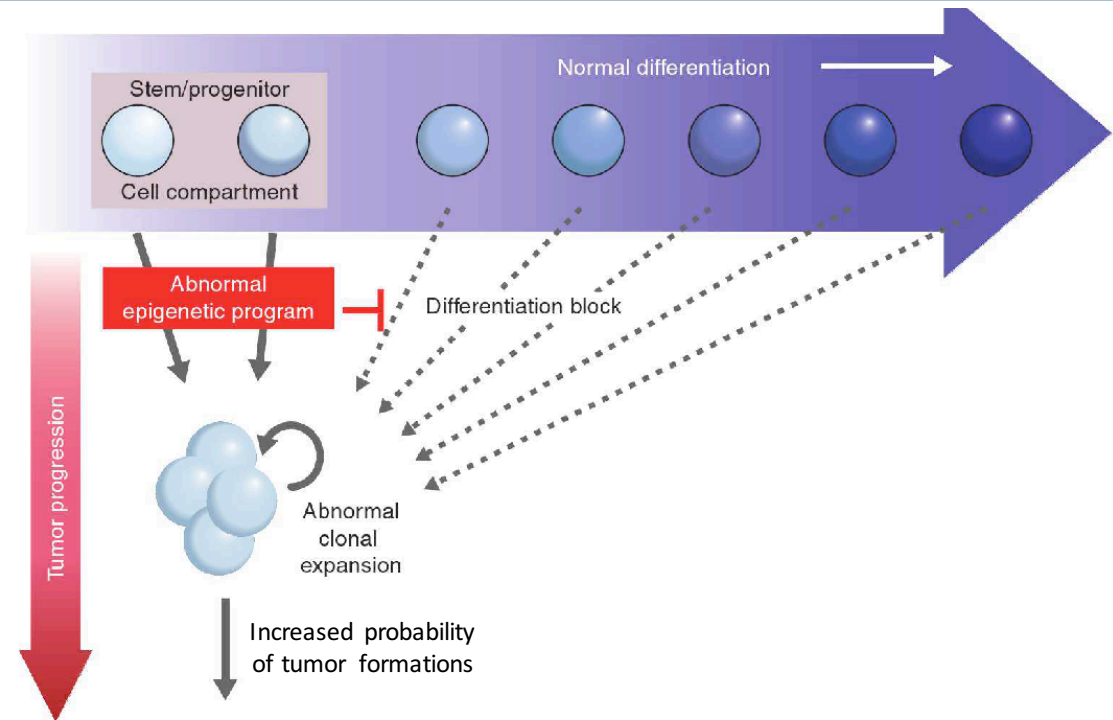
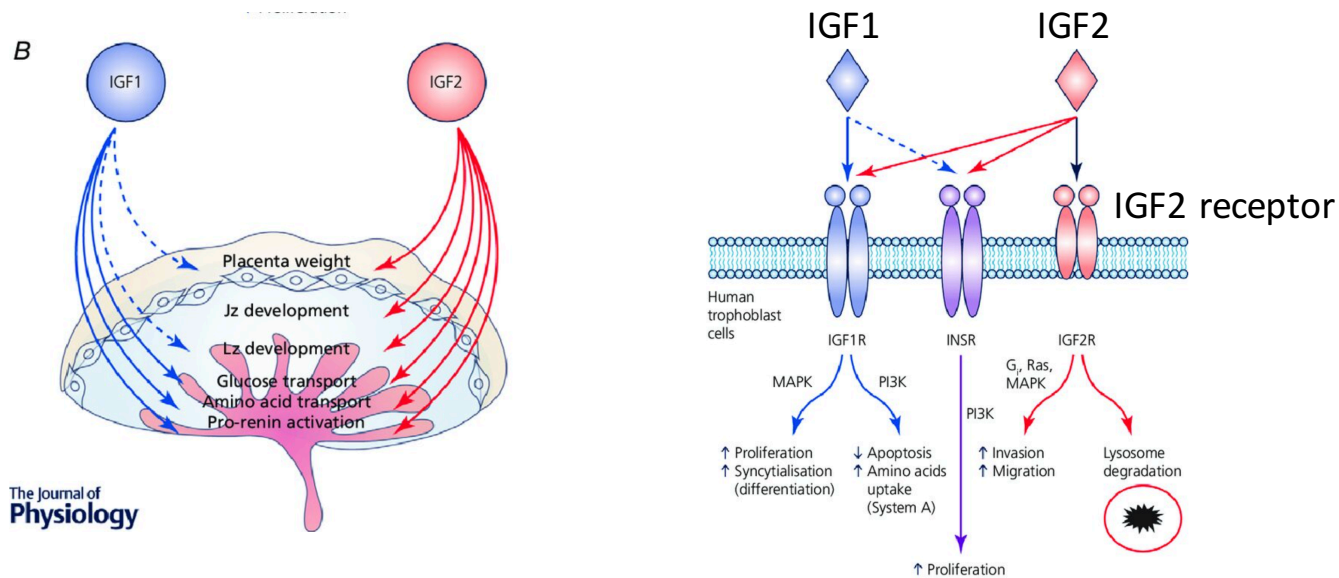


Figure 6. Epigenetic gene-silencing events and tumorigenesis. The earliest steps in tumorigenesis are depicted as abnormal clonal expansion, which evolves during the stress of cell renewal. This is caused by factors, such as aging and chronic injury from, for example, inflammation. These cell clones are those at risk of subsequent genetic and epigenetic events that could drive tumor progression. Abnormal epigenetic events, such as the aberrant gene silencing focused on in this chapter, could be the earliest heritable causes, in many instances, for a potential role in inducing the abnormal clonal expansion from within stem/progenitor cell compartments in a renewing adult cell system. The gene silencing is triggered by chromatin modifications that repress transcription, and the DNA hypermethylation of this chromatin serves as the tight lock to stabilize the heritable silencing. The gene silencing, in turn, disrupts normal homeostasis, preventing stem and progenitor cells from moving properly along the differentiation pathway for a given epithelial cell system (blue arrow) and channels them into the abnormal clonal expansion (red arrow).

3. THE IMPORTANCE OF EPIGENETIC GENE REGULATION IN **EARLY** TUMORPROGRESSION

IGF2 levels determine IGF2R signaling, IGF2 is an imprinted gene



IGF2 receptor signalling plays a role in development and cancer

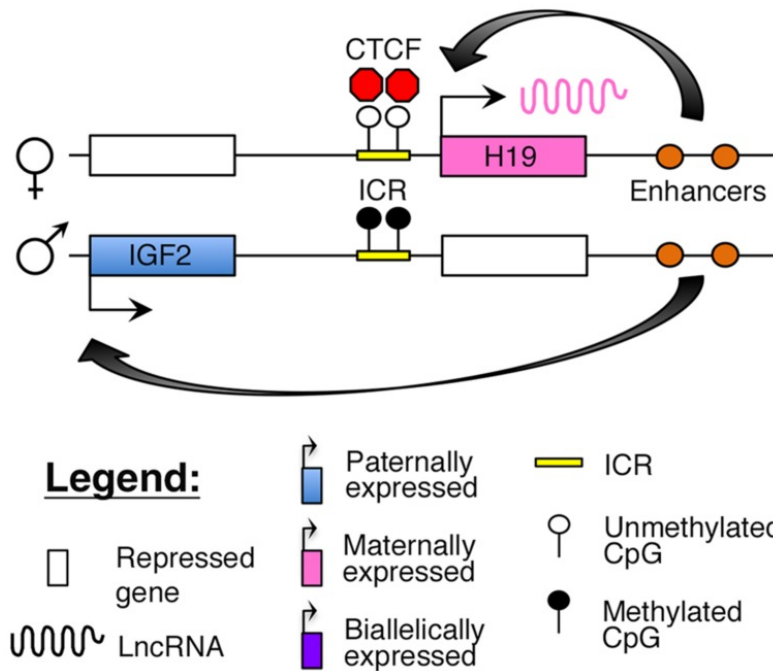
→ Proliferation

→ Growth

IGF2R knock-out mice are smaller

3. THE IMPORTANCE OF EPIGENETIC GENE REGULATION IN **EARLY** TUMORPROGRESSION

Loss of imprinting (LOI): EXAMPLE H19-IGF2 locus



Proposed model of imprinting at the H19-IGF2 locus: the H19-IGF2 locus consists of a paternally methylated ICR (Imprinting Control Region). On the maternal allele, this ICR is unmethylated and is bound by the insulator protein CTCF that prevents access of the IGF2 promoter to downstream enhancers.

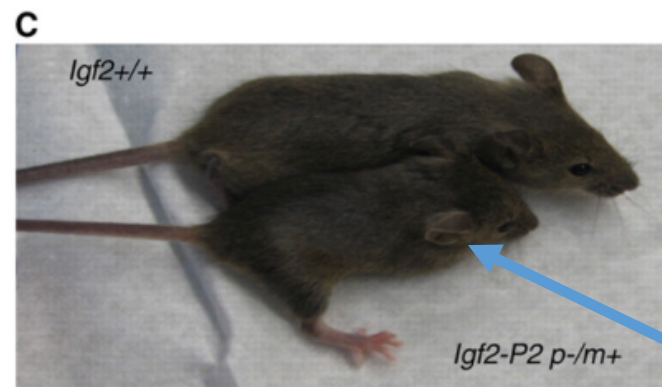
The imprinted H19-IGF2 LOCUS

The *H19-IGF2* locus resides adjacent to the *KCNQ1* region on human Chr. 1p15.5.

- paternally expressed *insulin-like growth factor 2 (IGF2)* gene
- maternally expressed *H19* lncRNA.

The *IGF2* protein functions as a growth factor essential for embryonic development, whereas *H19* may function as a tumor suppressor. Imprinting at this locus is maintained by an ICR, which is selectively methylated on the paternal allele. The insulator protein, CCCTC-binding factor (*CTCF*), binds to critical regulatory regions in the unmethylated ICR (Imprinting control region) on the maternal allele, thus blocking access of downstream enhancers to the *IGF2* promoter.

Loss of methylation at the *H19/IGF2* ICR results in short body length and low birth weight, both in rodent models as well as in humans

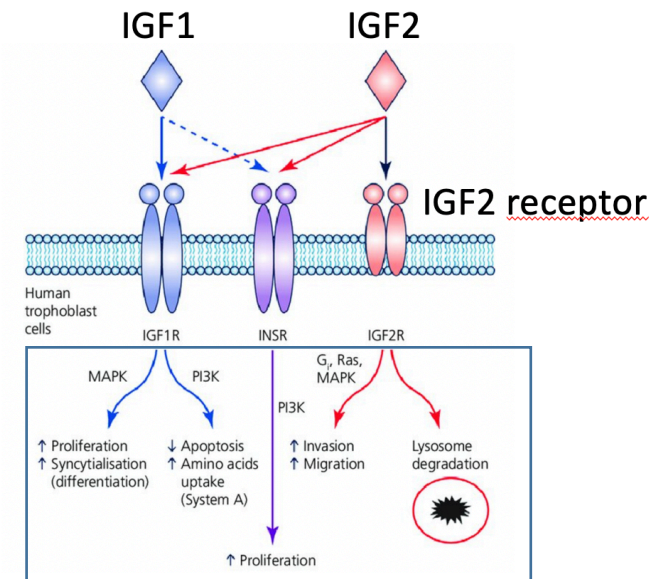
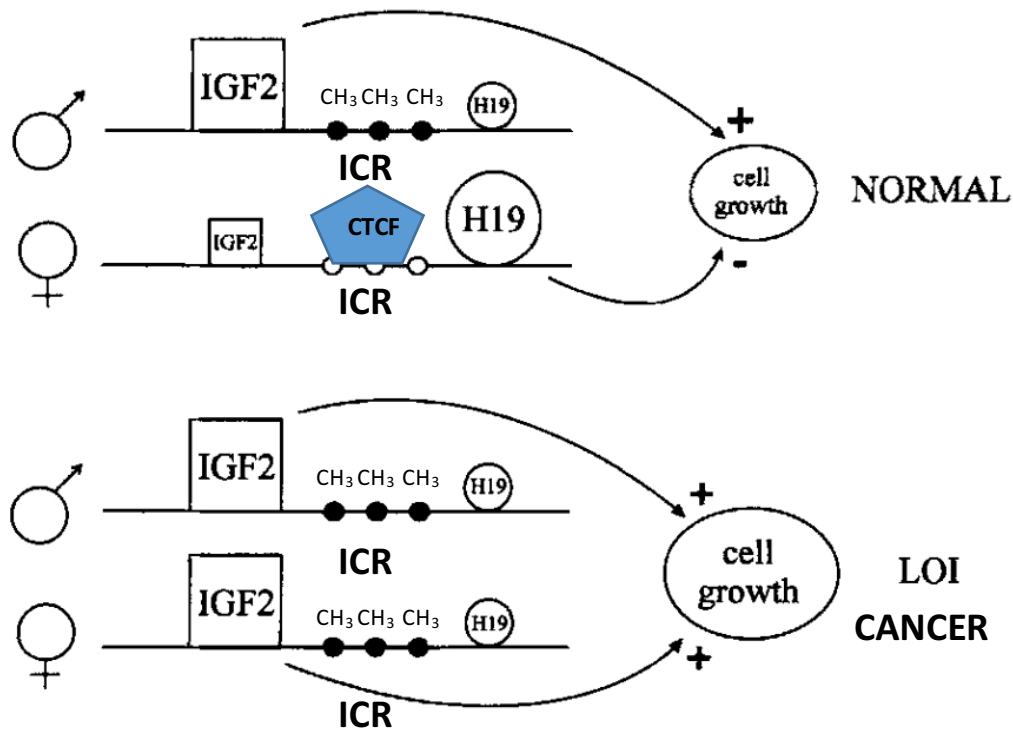


IGF2 knock-out allele was inherited from the father of the mouse

3. THE IMPORTANCE OF EPIGENETIC GENE REGULATION IN EARLY TUMORPROGRESSION

Loss of imprinting (LOI) is a early event in cancer formation

In tumors (colon) : HYPER-methylation of ICR on maternal allele; increased IGF2 expression; increased proliferation potential



In mouse loss of IGF2 imprinting may be sufficient to **initiate** tumorigenesis

3. THE IMPORTANCE OF EPIGENETIC GENE REGULATION IN EARLY TUMORPROGRESSION

IDH1 mutations in glioblastoma lead to epigenetic deregulation in oncogenesis

Classic oncogenic driver mutations in glioblastoma

Gene symbol	Gene name	Function of encoded protein	Point of mutation (%)
EGFR	Epidermal growth factor receptor	Regulator of cell signaling involved in cell proliferation and survival	14–15
ERBB2	V-erb-b2-erythroblastic leukemia viral oncogene homolog 2	Regulator of cell signaling involved in cell proliferation and survival	0–7
IDH1	Isocitrate dehydrogenase 1	NADPH production	12–20
NF1	Neurofibromin 1	Regulator of cell signaling involved in cell proliferation and survival	15–17
PIK3CA	Phosphoinositide-3-kinase catalytic alpha	Regulator of cell signaling involved in cell proliferation and survival	7–10
PIK3R1	Phosphoinositide-3-kinase regulatory 1	Regulator of cell signaling involved in cell proliferation and survival	7–8
PTEN	Phosphatase and tensin homolog	Regulator of cell signaling involved in cell proliferation and survival	24–37
PTPRD	Protein tyrosine phosphatase receptor type D	Regulator of cell signaling involved in cell proliferation and survival	0–6
RB1	Retinoblastoma 1	Regulator of cell cycle	8–13
TP53	Tumor protein p53	Apoptosis	31–38

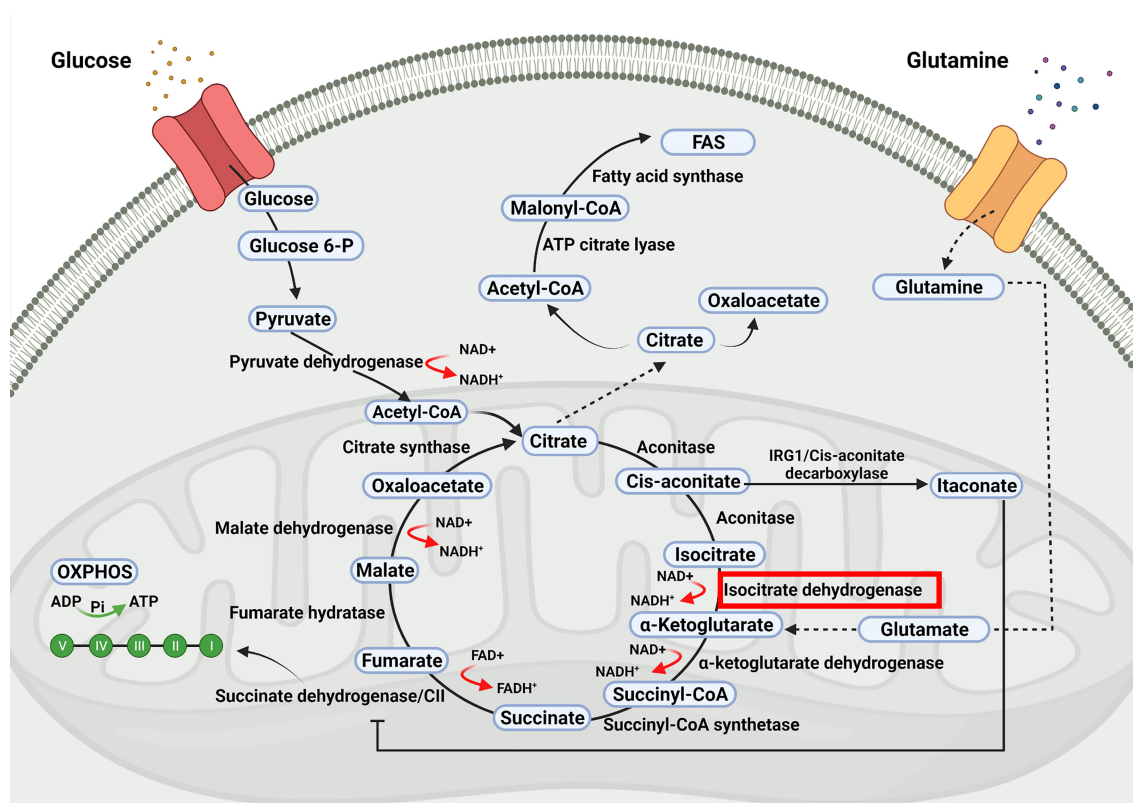
IDH1 mutations are highly frequent in glioblastoma

Tumor types	IDH1 mutation frequency (%)
Astrocytoma pilocytic (WHO Grade I)	0.01
Diffuse glioma (WHO Grade II)	76
Astrocytoma anaplastic (WHO Grade III)	62.2
Primary glioblastoma (WHO Grade IV)	5.6
Secondary glioblastoma (WHO Grade IV)	76.4
Oligodendroglioma	
WHO Grade II	78.8
WHO Grade III	67.5
Oligoastrocytoma	
WHO Grade II	79.8
WHO Grade III	69.7

CNS, central nervous system; WHO, World Health Organisation; AML, acute myeloid leukemia; D-2-HGA, D-2-hydroxyglutaric aciduria; MDS, myelodysplastic syndrome; MPN, myeloproliferative neoplasms.

3. THE IMPORTANCE OF EPIGENETIC GENE REGULATION IN EARLY TUMORPROGRESSION

Altered TCA cycle (tricarboxylic acid cycle) drives epigenetic deregulation in oncogenesis



Wild-type Isocitrate dehydrogenase (IDH) converts Isocitrate to alpha-ketoglutarate

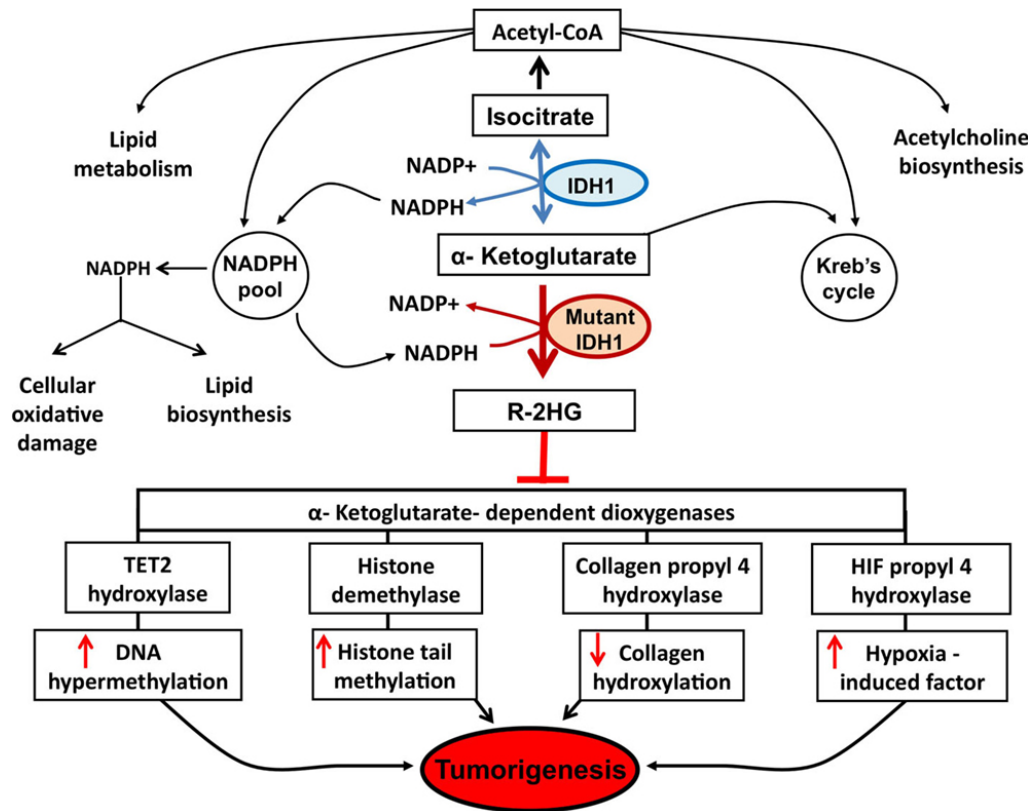
IDH1 mutations results result the aberrant production of high levels of **2-hydroxyglutarate (2-HG)**, a possible oncometabolite that is thought to influence a range of cellular programs involved in epigenetic control and various processes leading to tumor development.

Mutant IDH drives a neomorphogenic reaction

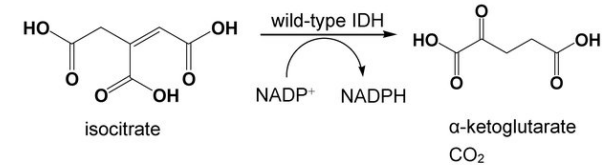
Neomorphic reactions, in the context of mutations, describe a change in a gene's product that results in a novel function or expression pattern. Essentially, a mutation that gives the mutated gene product a completely new ability, beyond the original function of the gene

3. THE IMPORTANCE OF EPIGENETIC GENE REGULATION IN EARLY TUMORPROGRESSION

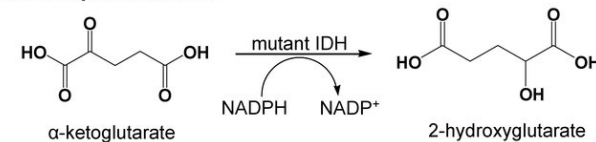
IDH1 mutations in glioblastoma lead to epigenetic deregulation in oncogenesis



Normal reaction:



Neomorphic reaction:



IDH1 mutations are **heterozygous**, typically involving an amino acid substitution in the active site of the enzyme in codon 132. The mutation results in a loss of normal enzymatic function and the abnormal production of 2-hydroxyglutarate (2-HG)

This abnormal **2-hydroxy-glutarate** metabolite, which increases to mM levels in cells with the IDH mutations, constituting a biomarker. On the mechanistic level 2-HG competes with the necessary α -ketoglutarate metabolite needed by the TET and lysine (K) demethylase (KDM) enzymes, which regulate either chromatin demethylase function or levels of DNA methylation.

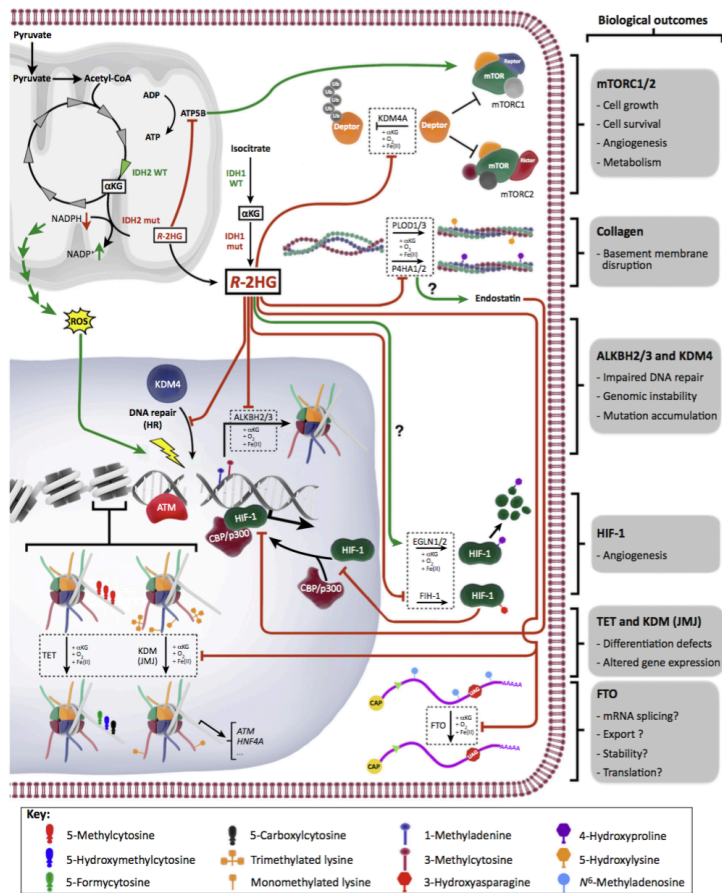


Figure 2. Multiple α KG-dependent dioxygenases family are dependent on α KG for their enzymatic activities to modify gene expression. When associated with α KG, ten-eleven translocation (TET) family catalyze the conversion of the modified DNA base 5-methylcytosine to 5-hydroxymethylcytosine, which can then be further oxidized to form derivatives 5-formylcytosine and 5-carboxylcytosine. While this activity requires α KG, TET methylcytosine hydroxylation is strongly inhibited by *R*-2HG production following *IDH1/2* mutation. Similarly, the activity of Jumong (JmJ) lysine demethylases, which normally demethylate specific regulatory lysines on histones H3 and H4, is abrogated upon *R*-2HG production, and the ensuing major changes in gene expression impair cell differentiation. (RNA methylation) FTO (fat mass and obesity-associated protein) catalyzes the demethylation of N^6 -methyladenosine (m^6A), an abundant modification present in mRNAs. m^6A regulates several aspects of RNA metabolism such as RNA splicing, transport, stability, and translation. FTO may be inhibited by *R*-2HG, but the consequences of reduced FTO activity in mutant IDH tumors are largely unknown. (DNA damage response and repair) ALKBH2 and ALKBH3 (α -KG-dependent dioxygenase homologs 2 and 3) are involved in repair of alkylated DNA lesions containing 1-methyladenine and 3-methylcytosine by oxidative demethylation. *R*-2HG production inhibits ALKBH2/3 activity, thus interfering with normal DNA repair processes. Inhibition of KDM4A and KDM4B by *R*-2HG leads to DNA repair defects by impairing homologous recombination (HR). In addition, IDH mutations cause accumulation of the repressive H3K9me3 histone mark at the promoter of genes inhibited by *R*-2HG. ALKBH2/3 may be activated by HIF-1, thus decreasing the levels of ATM and altering DNA repair. (mTOR Signaling) KDM4A and ATP5B modulate mTOR activation in the presence of α KG or *R*-2HG. KDM4A stabilizes DEPTOR, the endogenous negative regulator of mTOR, by inhibiting its polyubiquitylation, thus decreasing both mTORC1 and mTORC2 activation. In presence of *R*-2HG, DEPTOR is rapidly degraded, resulting in a massive increase in mTORC1/2 activation in a PI3K/PTEN-independent fashion, thus favoring the proliferation and survival of cancer cells harboring *IDH1/2* mutations. In addition, *R*-2HG inhibits ATP synthase activity, leading to reduced ATP content and thus causing mTOR inhibition. *R*-2HG production by *IDH1/2* mutations engages a complex network that likely regulates mTOR activity through regulatory feedback loops. (HIF-1 Signaling) Hypoxia-inducible factor 1 α (HIF-1 α) is a major regulator of cell proliferation, cell survival, and a promoter of angiogenesis. HIF-1 α is a highly unstable protein regulated by O_2 availability. EGLN1/2 and FIH are potent regulators of HIF-1 α stability and activity, respectively. While FIH is inhibited by *R*-2HG, EGLN1/2 may be activated by the oncometabolite, resulting in a complex modulation of HIF-1 α functions in tumors carrying *IDH1/2* mutations. (Collagen maturation) Both prolyl 4-hydroxylases (P4H-A1/3) and procollagen-lysine 2-oxoglutarate 5-dioxygenases (PLOD1/3) are enzymes that stabilize the collagen triple helix through hydroxylation of lysine and proline within each collagen chain. Because these enzymes are α KG-dependent, reduced availability of α KG and accumulation of *R*-2HG in *IDH1/2* mutated tumors affect collagen maturation.

Table 1. Enzymes Regulated by Mutated *IDH1/2* and the Associated Oncometabolite *R*-2HG

Enzyme	Enzymatic function	Type of regulation by <i>R</i> -2HG	Consequence of <i>R</i> -2HG-mediated regulation
TET1	Methylcytosine dioxygenase	Inhibition [39]	Inhibition of TET1 and TET2 by <i>IDH1/2</i> mutations caused downregulation of 5-hydroxymethylcytosine (5hmC) [39]
TET2	Methylcytosine dioxygenase	Inhibition [39]	Inhibition of TET1 and TET2 by <i>IDH1/2</i> mutations caused downregulation of 5hmC [39]; impaired hematopoietic differentiation [47]
KDM2A	H3K36me1/2 demethylase	Inhibition (IC ₅₀ = 106 μ M [39])	Not determined
KDM4A	H3K9me2/3, H1.4K26me2/3, and H3K36me2/3 demethylase	Inhibition (IC ₅₀ from 2.1 μ M [97] to 24 μ M [38])	Global increase of H3K9me3 [38]; increased mTOR activity through destabilization of DEPTOR [97]; DNA repair defects [82]
KDM4C	H3K9me2/3, H1.4K26me2/3, and H3K36me2/3 demethylase	Inhibition [23]	Global increase of H3K9me3 [38]; differentiation defects [23]
KDM4D	H3K9me2/3, H1.4K26me2/3, and H3K36me2/3 demethylase	Inhibition (IC ₅₀ = 79 μ M [38])	Global increase of H3K9me3 [38]
KDM5B	H3K4me2/3 demethylase	Weak inhibition (IC ₅₀ = 10.9 mM [38])	Not determined
HIF1AN/FIH	HIF asparaginyl hydroxylase	Inhibition (IC ₅₀ from ~1 mM [123] to 1.5 mM [38])	HIF-1 α accumulation in <i>R</i> -2HG-treated cells [39] as well as in <i>IDH1</i> ^{R132H} -expressing cells and gliomas [116]
EGLN1/2	HIF prolyl 4-hydroxylase	Activation [123]	Activation of EGLN1/2 in <i>IDH</i> ^{R132H} mutated cells diminished HIF activity [123]
Collagen prolyl hydroxylases (P4HA1/2) and lysine hydroxylases (PLOD1/3)	Collagen prolyl hydroxylases; Collagen lysine hydroxylases	Inhibition (IC ₅₀ ~2 mM; C-P4H-I [123])	Defective collagen maturation, impairment of basal membrane structure and function, activation of the ER stress response [92]
ALKBH2	Repair of methylated DNA bases, such as 1-methyladenine and 3-methylcytosine	Inhibition (IC ₅₀ from 424 μ M [38] to ~500 μ M [83])	Accumulation of DNA damage, decreased DNA repair kinetics, and increased sensitivity to alkylating agents of IDH mutated cells [83]
ALKBH3	Repair of methylated DNA bases such as 1-methyladenine and 3-methylcytosine	Inhibition (IC ₅₀ ~500 μ M [83])	Accumulation of DNA damage, decreased DNA repair kinetics, and increased sensitivity to alkylating agents of IDH mutated cells [83]
FTO	N^6 -methyladenosine and $N^6,2'$ -O-dimethyladenosine RNA demethylase	Inhibition [70]	Accumulation of m^6A RNAs [70]
ATP5B	ATP synthase β subunit	Inhibition [104]	Increased ratio of ADP to ATP, inhibition of mTOR signaling [104]

4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

Table 1. Examples of key cellular pathways disrupted in human cancers by genetic and epigenetic mechanisms

Pathway	Example of genetic alteration	Example of epigenetic alteration
Self sufficiency in growth signals	Mutations in <i>Ras</i> gene	Methylation of <i>RASSF1A</i> gene
Insensitivity to antigrowth signals	Mutation in TGF- β receptors	Down-regulation of TGF- β receptors
Tissue invasion and metastasis	Mutation in <i>E-cadherin</i> gene	Methylation of <i>E-cadherin</i> promoter
Limitless replicative potential	Mutation in <i>p16</i> and <i>pRb</i> genes	Silencing of <i>p16</i> or <i>pRb</i> genes by promoter methylation
Sustained angiogenesis		Silencing of thrombospondin-1
Evading apoptosis	Mutation in <i>p53</i>	Methylation of <i>DAPK</i> , <i>ASC/TMS1</i> , and <i>HIC1</i>
DNA repair capacity	Mutations in <i>MLH1</i> , <i>MSH2</i>	Methylation of <i>GST Pi</i> , <i>O6-MGMT</i> , <i>MLH1</i>
Monitoring genomic stability	Mutations in <i>Chfr</i>	Methylation of <i>Chfr</i>
Protein ubiquitination functions regulating mitotic control genes	Mutations in <i>Chfr</i>	Methylation of <i>Chfr</i>

TGF- β , transforming growth factor β ; *DAPK*, death-associated protein kinase.

4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

SILENCING OF p16

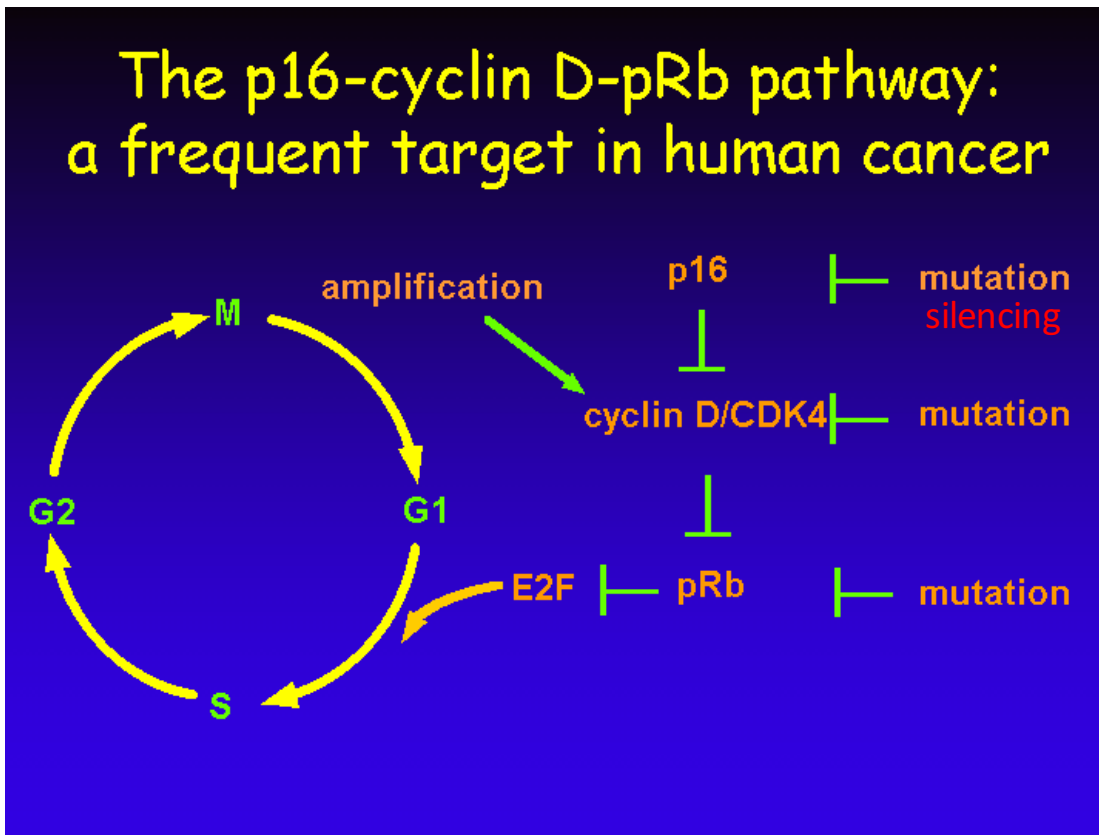
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TGF- β , transforming growth factor β ; *DAPK*, death-associated protein kinase.

3. The importance of epigenetic gene regulation in early tumor progression

SILENCING OF p16



Because of its importance in cell proliferation, the human INK4 gene locus, encoding p16, is a frequent target of inactivation by deletion or aberrant DNA methylation in a wide variety of human cancers

p16 silencing is an early event in tumorformation

→ Increased activity of cyclinD/CDK4

→ pRB hyperphosphorylation

→ E2F activates genes required for the induction of S-Phase

4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

SILENCING OF MLH1

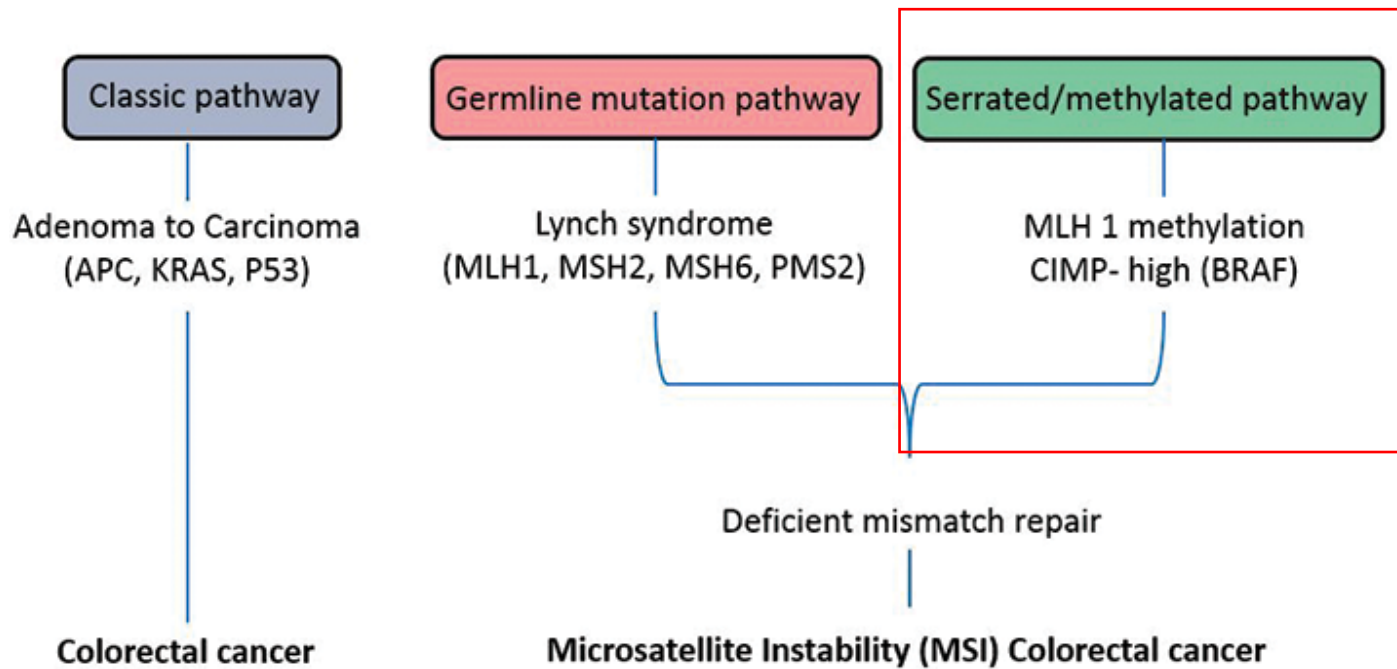
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4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

Pathways to tumorigenesis in Colorectal cancer



4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

SILENCING OF *Chfr*

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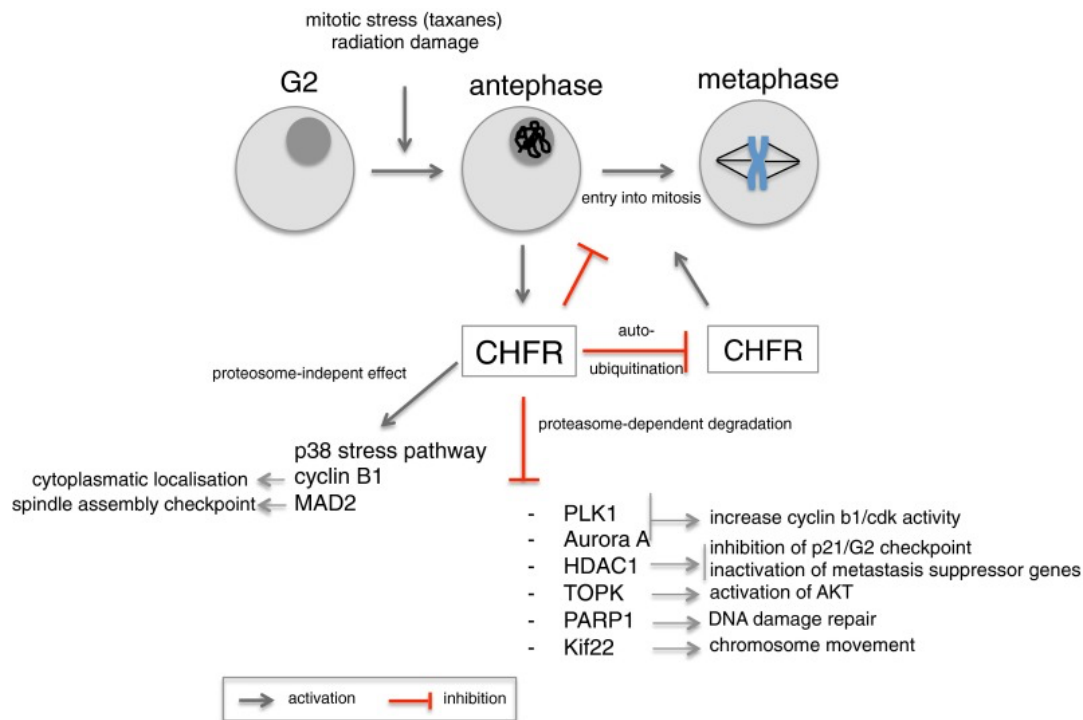
Silencing of *Chfr* in different tumor types

	No. methylated (%)
Cell lines	
Colorectal	11/13 (85)
Head and neck	4/10 (40)
ALL	4/8 (50)
Myeloma	4/7 (57)
Other hematopoietic	2/5 (40)
Hepatocellular	0/5 (0)
Other tumors	0/8 (0)
Primary tumors	
Colorectal cancer	25/63 (40)
Colorectal adenoma	27/51 (53)
Head and neck	16/54 (30)
Hepatocellular	0/20 (0)

...note: early event in CRC

4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

Chfr function



CHFR is an early mitotic checkpoint gene that functions as a key player in controlling chromosomal integrity.

CHFR is expressed in the cytoplasm of all normal tissues and accumulates in the nucleus in response to **microtubule poisoning, carcinogen or radiation damaging stress**.

After localization into the nucleus, CHFR becomes phosphorylated by protein kinase B (PKB/AKT), a member of the PI3K signaling pathway.

Microtubule stress/Radiation leads to an elevation of CHFR expression levels and a mitotic arrest.

→ In conditions with increased risk of genomic instability CHFR blocks mitotic progression to allow damage repair

→ **Absence of CHFR: mitosis precedes, DNA damage will not be repaired → accumulation of mutations → genomic instability/cancer.**

CHFR is a E3 ubiquitin-protein ligase that delays entry into metaphase in response to microtubular stress/radiation by effecting target proteins in a proteasome-dependent and a proteasome-independent manner → maintains genomic stability

4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

Chfr knock out mouse model

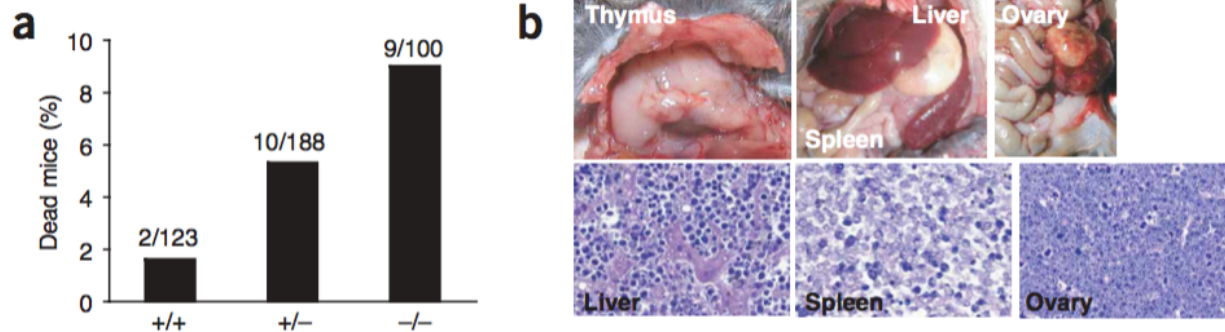
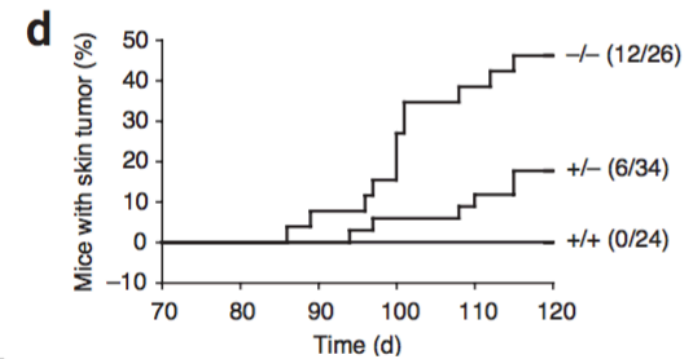
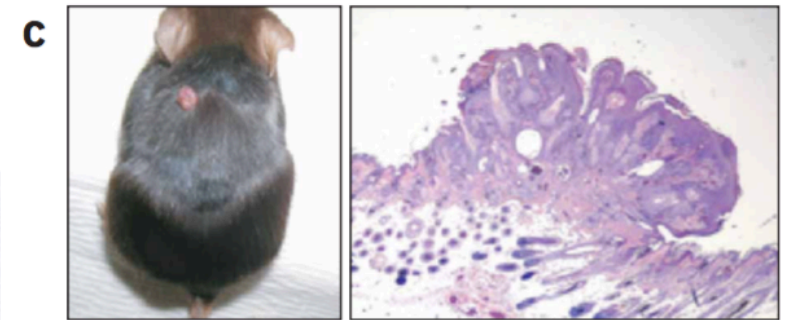


Figure 2 Chfr deficiency increases tumor incidence in mice. **(a)** Death rates of wild-type and Chfr-deficient mice (0–40 weeks). **(b)** Tumors derived from *Chfr*^{-/-} mice. We included examples of spontaneous lymphomas obtained from *Chfr*^{-/-} mice and the hematoxylin and eosin–stained sections. **(c)** DMBA treatment induced skin tumor formation in *Chfr*^{-/-} mice. A hematoxylin and eosin–stained skin tumor observed in *Chfr*^{-/-} mice is shown. **(d)** Incidences of DMBA-induced skin tumors in wild-type and Chfr-deficient mice.

Skin carcinogenesis

(mice are treated with carcinogen (DMBA = DNA damaging agent, TPA cell cycle stimulator)



4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

Chfr knock out mouse model

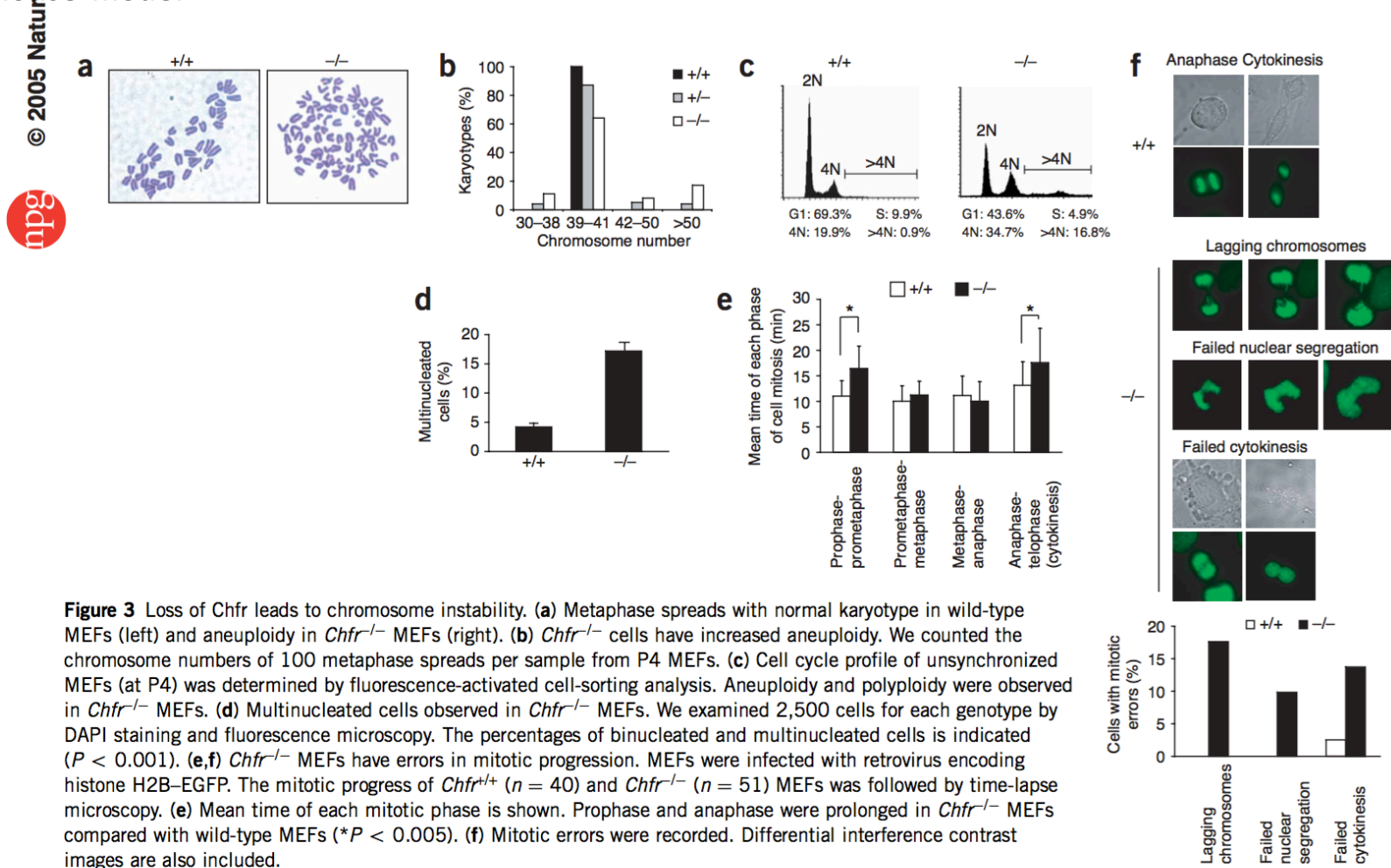


Figure 3 Loss of *Chfr* leads to chromosome instability. (a) Metaphase spreads with normal karyotype in wild-type MEFs (left) and aneuploidy in *Chfr*^{-/-} MEFs (right). (b) *Chfr*^{-/-} cells have increased aneuploidy. We counted the chromosome numbers of 100 metaphase spreads per sample from P4 MEFs. (c) Cell cycle profile of unsynchronized MEFs (at P4) was determined by fluorescence-activated cell-sorting analysis. Aneuploidy and polyploidy were observed in *Chfr*^{-/-} MEFs. (d) Multinucleated cells observed in *Chfr*^{-/-} MEFs. We examined 2,500 cells for each genotype by DAPI staining and fluorescence microscopy. The percentages of binucleated and multinucleated cells is indicated ($P < 0.001$). (e,f) *Chfr*^{-/-} MEFs have errors in mitotic progression. MEFs were infected with retrovirus encoding histone H2B-EGFP. The mitotic progress of *Chfr*^{+/+} ($n = 40$) and *Chfr*^{-/-} ($n = 51$) MEFs was followed by time-lapse microscopy. (e) Mean time of each mitotic phase is shown. Prophase and anaphase were prolonged in *Chfr*^{-/-} MEFs compared with wild-type MEFs ($*P < 0.005$). (f) Mitotic errors were recorded. Differential interference contrast images are also included.

4. EXAMPLES OF TSG EPIGENETIC SILENCING IN ONCOGENESIS

Chfr is frequently inactivated in human cancer

CHFR inactivation in multiple cancers

Cancer	Aberration	Method, region analyzed	Percentage of methylation	Ref
Breast cancer	Reduced expression	IHC	36 % (51/142)	[70]
	Methylation	demethylation and northern blot	8 % (2/24) (cell lines)	[71]
Bladder cancer	Methylation	MLPA	18.7 % (17/91)	[72]
Colorectal cancer	Methylation	COBRA	40 % (25/63)	[73]
		MSP, -281 to +51 bp	37 % (11/30)	[74]
		COBRA	53 % (27/51) (adenomas)	[71]
		MSP, -240 to -73 bp	41 % (29/71)	[75]
		MSP, -226 to -82 bp	26% (25/98)	[76]
		qMSP, +221 to +325 bp	24 % (217/888)	[77]
Gastric cancer	Methylation	MSP, -240 to -73 bp	31 % (19/61)	[67]
		COBRA	39 % (24/61)	[56]
		MSP, -9 to +98 bp	35 % (25/71)	[78]
		COBRA	44 % (19/43)	[79]
		MSP, -163 to -8 bp	52 % (24/46)	[57]
Nasopharyngeal cancer	Methylation	MSP, -220 bp to -14 bp	61 % (22/36)	[80]
		MSP, -220 to -14 bp	59 % (31/53)	[81]
Non-small cell lung cancer	Reduces expression	IHC	39 % (16/41)	[63]
	Methylation	MSP, -220 to -14 bp	19 % (7/37)	[42]
	Mutation	MSP, -220 to -14 bp	10 % (2/20)	[74]
		MSP, -220 to -14 bp/IHC	15 % (3/20)/39 % (69/157)	[53]
		MSP -195 to -99 bpm	32.4 % (100/308) (serum)	[47]
		MSP, -220 to -14 bp	10 % (16/165)	[52]
Esophageal cancer	Methylation	MSP, -220 to -14 bp	3.1 % (1/32)	[63]
			6 % 3/53	[44]
		MSP, -163 to -8 bp	16.3 % (7/43)	[46]
		Copy number loss	MSP, -227 to -86 bp	24 % (9/38)
		bisulfite pyrosequencing	31 % (18/58)	[45]
		qPCR	59 % (16/27)	[45]
Cervical cancer	Methylation	MSP, +168 to 318	12 % (2/14)	[59]
Hepatocellular cancer	Methylation	MSP, -225 to -85 bp	35 % (22/62)	[83]
Biliary tract carcinoma	Methylation	MSP, -9 to +98 bp	16 % (6/37)	[84]
Oral squamous cell cancer	Methylation	MSP, -220 bp -14 bp	31 % (4/13)	[85]
			34.7 % (17/49)	[86]
Cutaneous T-cell lymphoma	Methylation	CpG island microarray	19 % (5/28)	[87]
Head and neck cancer		COBRA	30 % (16/54)	[73]
		MS-MLPA	25 % (7/28)	[88]
Endometrial cancer	Methylation	MSP, +168 to 318 bp	12 % (6/50)	[60]

IHC, immunohistochemistry; (MS)-MLPA, (methylation-specific) multiplex ligation-dependent probe amplification; MSP, methylation-specific PCR; COBRA, combined bisulfite restriction analysis

CHFR is more frequently inactivated in cancer than all other mitotic checkpoint control genes together.

Absence of CHFR in these cell lines resulted in a **high mitotic index** when exposed to microtubule stress compared to wild-type cancer cells, which was restored by reintroduction of functional CHFR.

In a breast cancer cell line model, **decreased CHFR expression resulted in an accelerated growth rate, enhanced invasiveness and amplified colony formation.**

In order to study the physiological role of CHFR and its function in tumorigenesis, Chfr knockout mice have been generated.

Chfr knockout mice develop invasive lymphomas and solid tumors (lung, liver, gastrointestinal) after 40 weeks and have an increased susceptibility to chemical carcinogenesis.

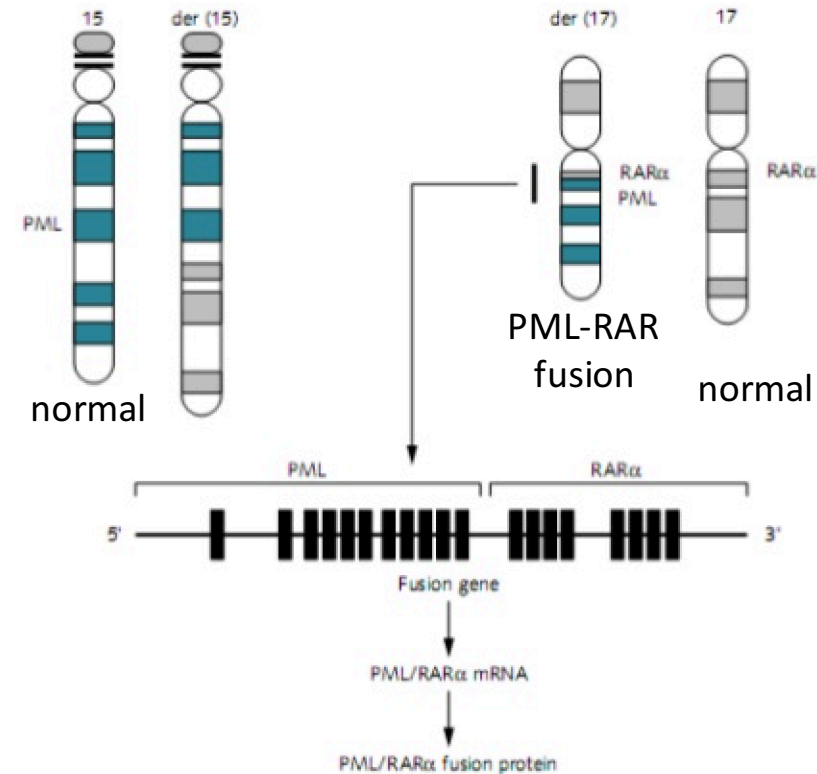
Embryonic fibroblasts from Chfr-deficient mice show substantial aneuploidy and polyploidy.

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION/USE OF EPIGENETIC REGULATORS

PML – RAR fusion and aberrant use of HDAC

Acute promyelocytic leukemia (APML, APL) is the M3 subtype of acute myelogenous leukemia (AML), a cancer of the white blood cells. In APL, there is an abnormal accumulation of immature granulocytes called promyelocytes.

The disease is characterized by a chromosomal translocation involving the retinoic acid receptor alpha (RAR α or RARA) gene and is distinguished from other forms of AML by its responsiveness to all-trans retinoic acid (ATRA; also known as tretinoin) therapy.



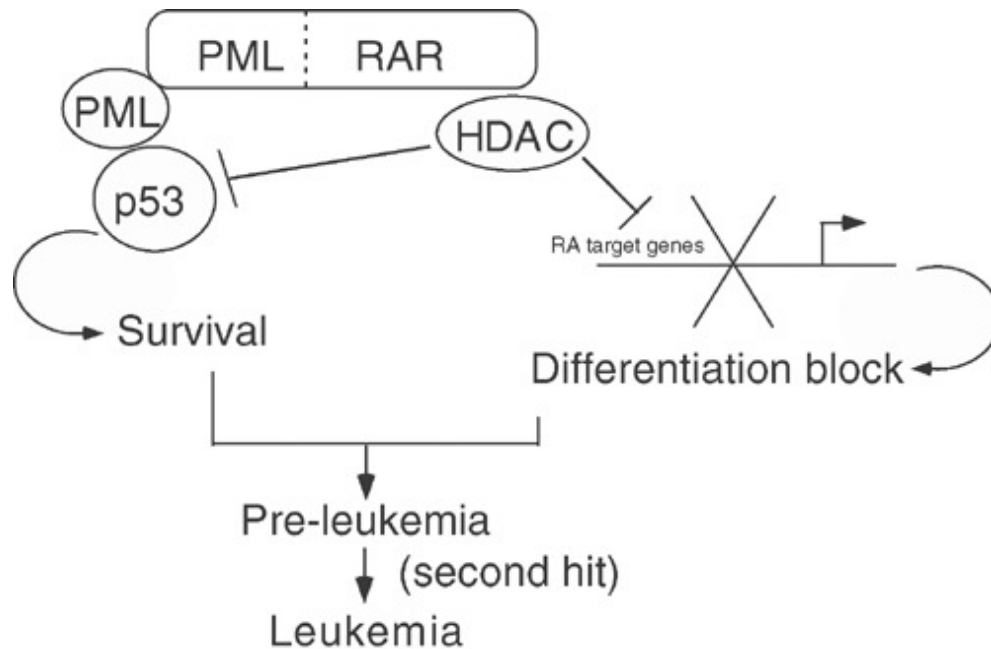
FUSION OF PML WITH RETINOIC ACID RECEPTOR GENE

Note: retinoic acid receptor activation by retinoic acid drives differentiation

Acute promyelocytic leukemia

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION OF EPIGENETIC REGULATORS

PML – RAR fusion and aberrant use of HDAC



PML–RAR acts as an HDAC-dependent inhibitor of pathways regulated by wild-type PML and RAR.

PML–RAR acts as a bifunctional protein:

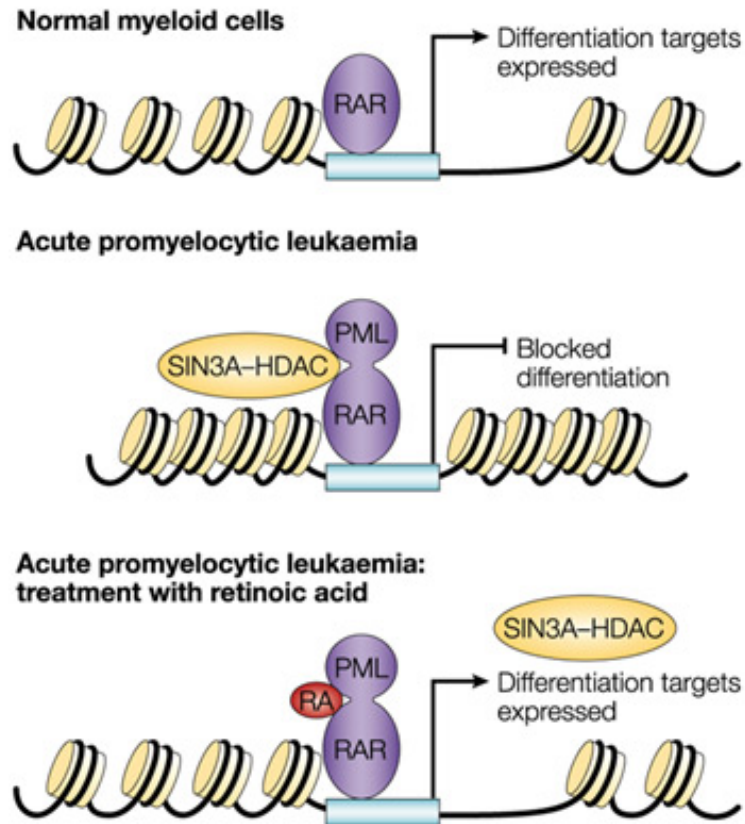
- (i) it inhibits the transcription of RA target genes in the presence of physiological concentrations of ligand, thus blocking myeloid differentiation; and
- (ii) it inhibits p53 function (in a manner requiring wild-type PML), allowing enhanced survival of APL blasts.

Both differentiation block and enhanced survival are mediated by recruitment of HDAC by the fusion protein.

Acute promyelocytic leukemia

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION OF EPIGENETIC REGULATORS

PML – RAR fusion and aberrant use of HDAC



Histone deacetylase (HDAC) complexes have been implicated in oncogenesis. In acute promyelocytic leukaemia, a recurrent chromosomal translocation results in fusion of the promyelocytic leukaemia gene product (PML), which directly recruits SIN3A-HDAC, to the retinoic-acid receptor (RAR). During normal development of myeloid cells, the RAR transcriptionally activates target genes that promote differentiation into mature myeloid cells. In acute promyelocytic leukaemia, the PML-RAR fusion protein recruits SIN3A-HDAC to RAR targets (see figure). SIN3A-HDAC deacetylates histones, leading to transcriptional repression and to a block in differentiation that contributes to leukaemic growth.

Treatment of these patients with high-dose retinoic acid (RA) causes dissociation of SIN3A-HDAC and differentiation of immature leukemic blast cells into mature, and benign, myeloid cells.

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION OF EPIGENETIC REGULATORS

MLL fusion with other genes:

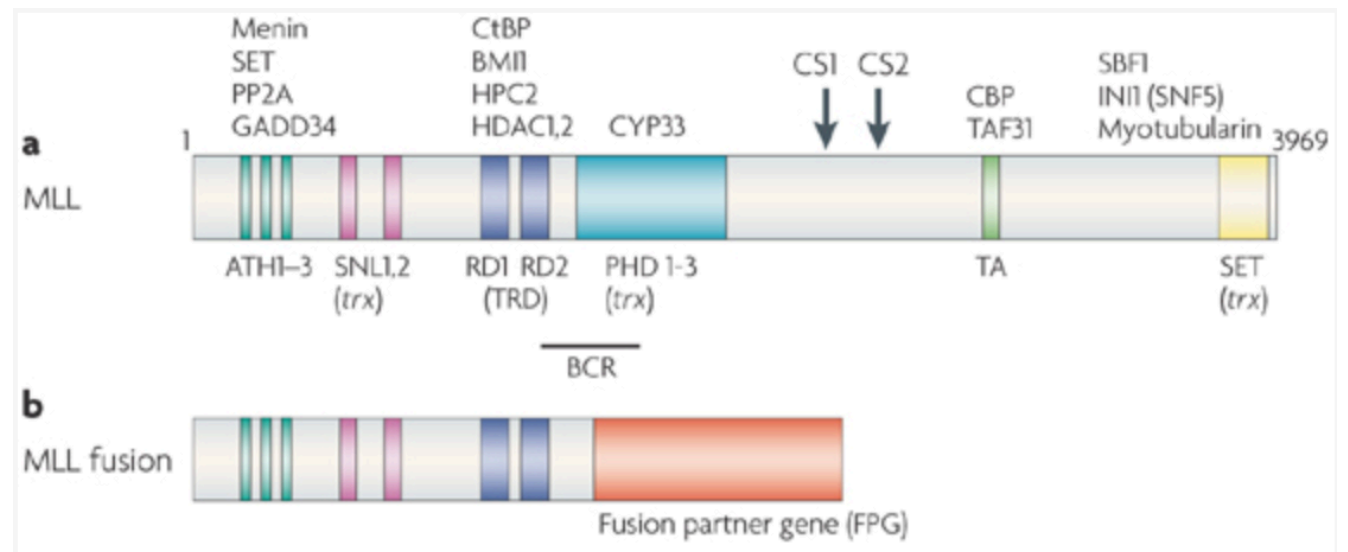
MLL gene on 11q23 is often rearranged with other partner genes in ALL (Acute lymphoblastic leukemia) and AML (Adult Acute Myeloid Leukemia):
 accounting for 8% of pediatric and 10% of adult ALL, 15-20% of pediatric AML and <3% of adult AML

Chromosomal translocations lead to the fusion of 5'-end portion of MLL to one of >60 different partner genes, resulting in the formation of different fusion genes, such as

MLL-AF4 (4q21),
 MLL-AF9 (9p22),
 MLL-ENL (19p13.3),
 MLL-AF10 (10p12),
 MLL-AF6 (6q27),
 MLL-ELL (19p13.1).

All MLL fusion proteins retain N-terminal AT-hooks, DNA methyltransferase homology domain, thus preserving DNA binding activity whereas the **trithorax PHD domains, TAD and SET domains** are always replaced by the partners.

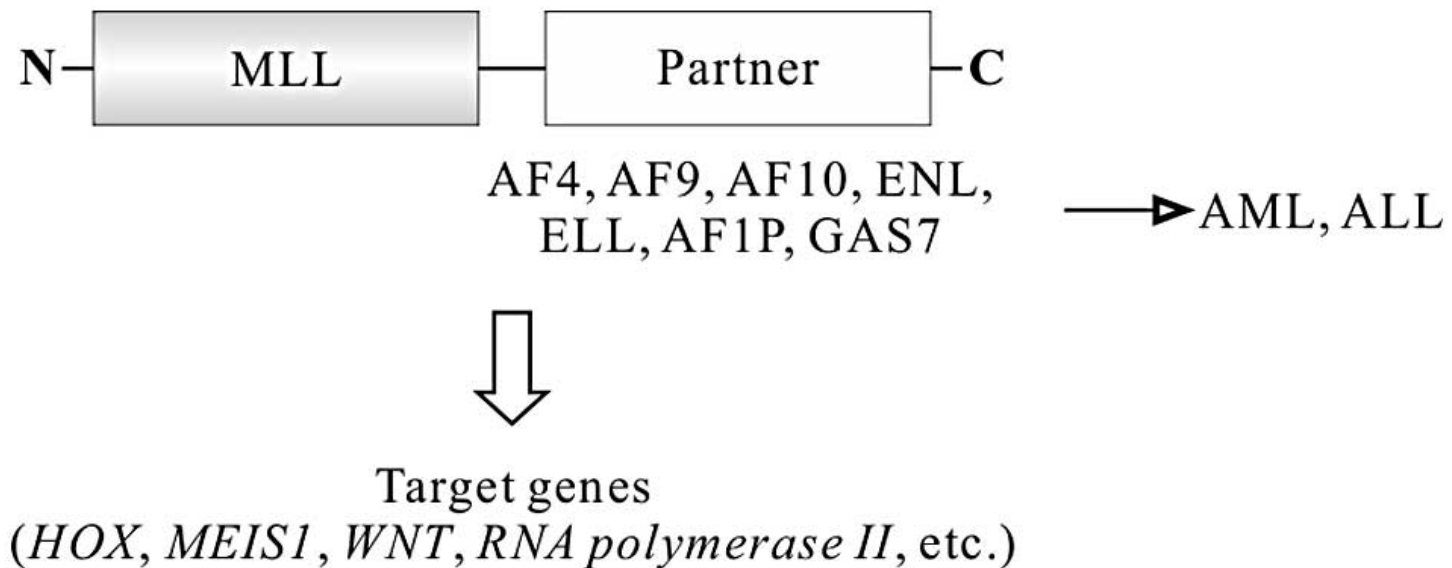
In these fusions, the original MLL H3K4 methyltransferase activity is replaced by the partners which play a critical role in MLL oncoproteins



Adult Acute Myeloid Leukemia

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION OF EPIGENETIC REGULATORS

MLL fusion with other genes:



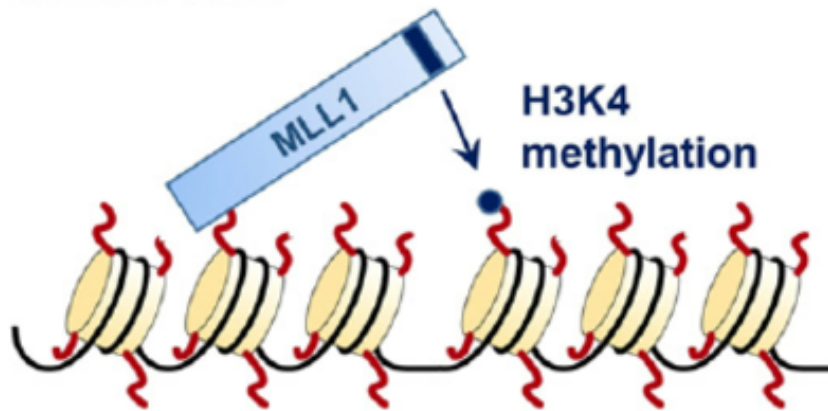
**Aberrant expression of genes that promote cancer formation
...classic example: MLL-AF9 (9p22)**

Adult Acute Myeloid Leukemia

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION OF EPIGENETIC REGULATORS

MLL—AF9 fusion:

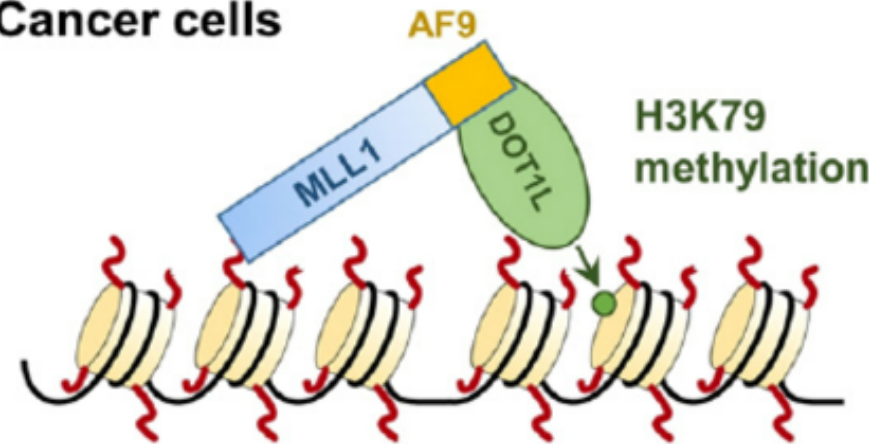
Normal cells



Schematic picture showing the tumor promoting effect of MLL translocations via recruitment of DOT1L. In normal cells, the MLL1 protein binds to its target genes and introduces H3K4 methylation via its catalytic SET domain (highlighted in dark blue).

In the tumor cells MLL1 forms fusions with other protein like AF9, which leads to the loss of the SET domain.

Cancer cells



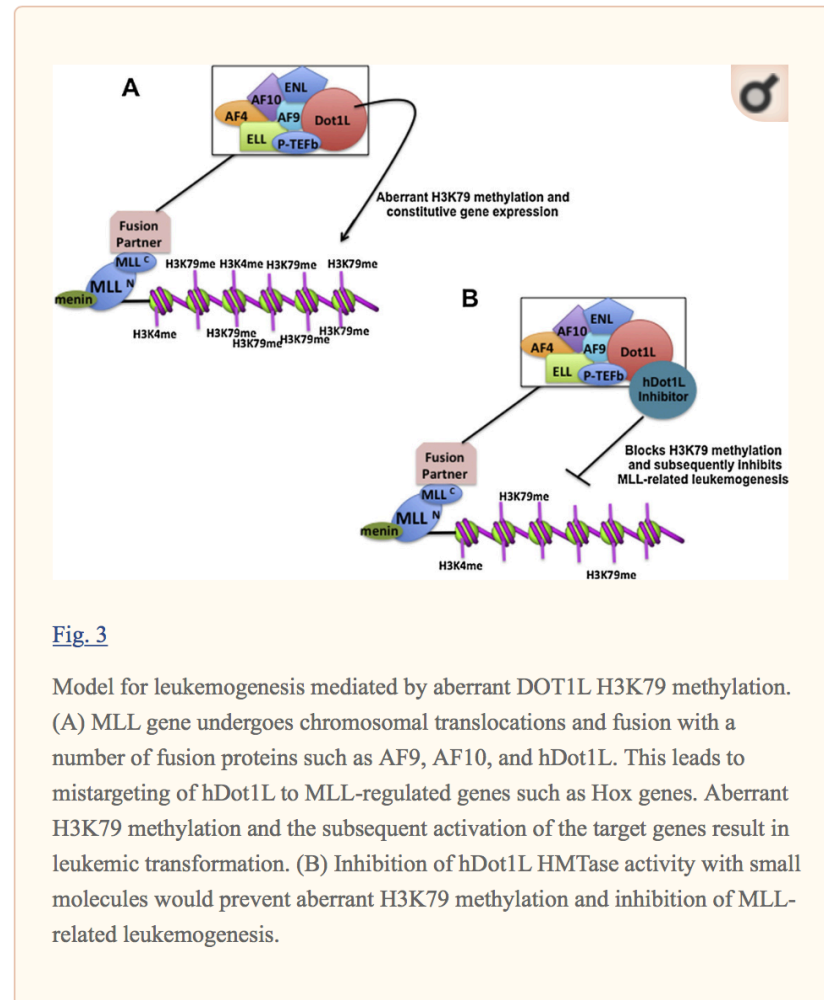
DOT1-mediated H3K79 methylation is linked to euchromatic gene transcription and transcription elongation.

Although MLL fusion proteins lose the activity of H3K4 methylation, these fusion proteins gain the activity of H3K79 methylation via recruiting the H3K79 methyltransferase hDOT1L which can cause dysregulation of whole genomic expression and is associated with MLL leukemogenesis. Since hDOT1L plays a key role in the development of MLL leukemia, hDOT1L is an ideal target for MLL leukemia. Several hDOT1L inhibitors are underdeveloped. In particular, **EPZ004777, a special hDOT1L inhibitor, seems to be a promising drug for leukemia with MLL gene translocation**

Adult Acute Myeloid Leukemia

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION OF EPIGENETIC REGULATORS

MLL—AF9 fusion:



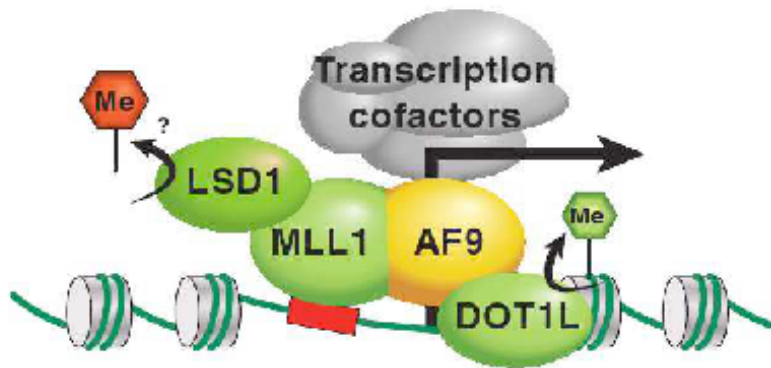
[Fig. 3](#)

Model for leukemogenesis mediated by aberrant DOT1L H3K79 methylation. (A) MLL gene undergoes chromosomal translocations and fusion with a number of fusion proteins such as AF9, AF10, and hDot1L. This leads to mistargeting of hDot1L to MLL-regulated genes such as Hox genes. Aberrant H3K79 methylation and the subsequent activation of the target genes result in leukemic transformation. (B) Inhibition of hDot1L HMTase activity with small molecules would prevent aberrant H3K79 methylation and inhibition of MLL-related leukemogenesis.

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION OF EPIGENETIC REGULATORS

MLL—AF9 fusion:

A



LSD1: H3K4 de-methylase

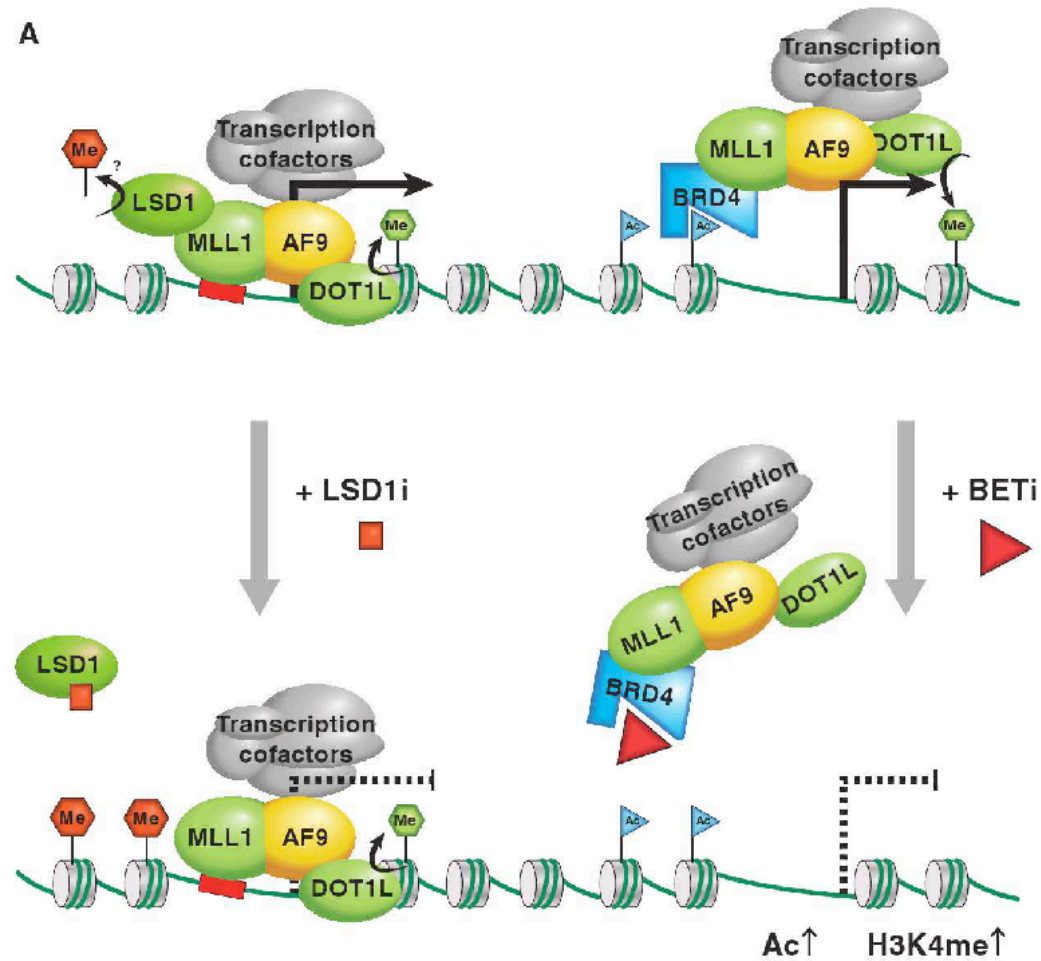
Interaction of LSD1 with MLL-AR9 ensures leukemia stem cells features → oncogenic function

LSD1 inhibitors work in MLL-AR9 fusions models

Adult Acute Myeloid Leukemia

5. EXAMPLES OF MUTATIONS THAT CHANGE THE FUNCTION OF EPIGENETIC REGULATORS

MLL—AF9 fusion:



Adult Acute Myeloid Leukemia

6. MAJOR EPIGENETIC DRUGS IN CURRENTLY IN DEVELOPMENT

Development status of drugs targeting histone modifications and histone modifiers in oncology			
Research	Preclinical development	Clinical development	Approved
KDMI; KMTi; HATi; HDACi Bromodomain inhibitors; other chromatin readers			
	BETi; EZH2i (CPI-1205); KDMI (KDM5i)		
		BETi (iBET762, CPI-0610, OTX-015, Ten010, RVX-208); EZH2i (EPZ6438, GSK126); LSD1 (OG98, GSK2879552, SP2577) DOT1Li (EPZ5676); selective HDACi, DNMTi	
			DNMTi (Azacitidine, Decitabine); HDACi (vorinostat, romidepsin)

Figure 5. The development status of epigenetic drugs. KDMI, lysine demethylase inhibitor; KMTi, lysine methyltransferase inhibitor; HATi, histone acetyltransferase inhibitor; HDACi, histone deacetylase inhibitor; BETi, bromodomain and extracardio terminal domain inhibitor; DNMTi, DNA methyltransferase inhibitor.

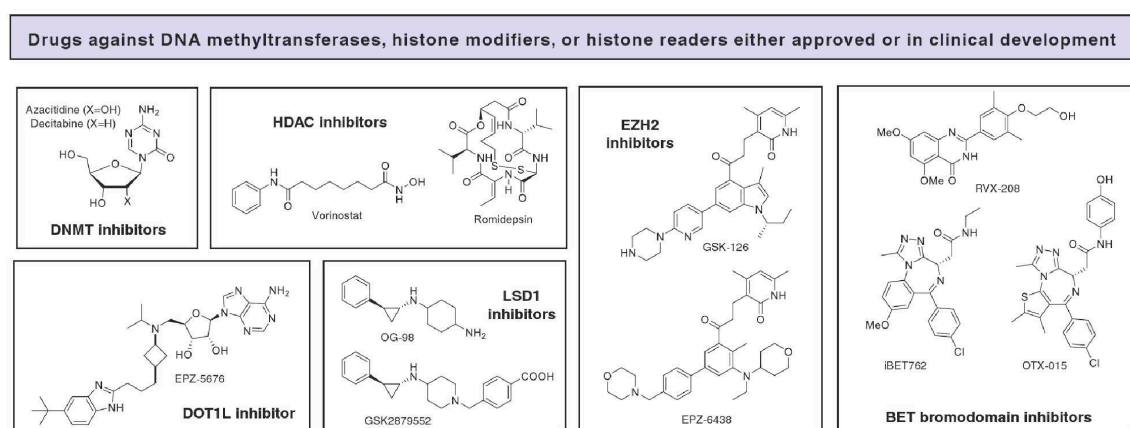
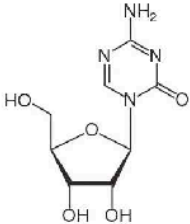
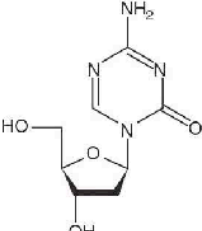
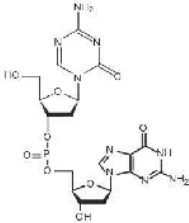


Figure 6. Representative structures of drugs targeting DNA methylation, histone modifications, and histone readers in oncology.

EPIGENETIC DRUGS: DNMT INHIBITORS

Compound	Structure	Cancer type	Clinical trial status
DNA methylation inhibitors			
5-Azacytidine 5-Aza-CR (Vidaza)		Myelodysplastic syndrome; AML	FDA-approved for MDS in 2004
5-Aza-2'-deoxycytidine 5-Aza-CdR Decitabine (Dacogen)		Myelodysplastic syndrome; AML	FDA-approved for MDS in 2006
SGI-110		Acute myeloid leukemia; AML	Phase 2

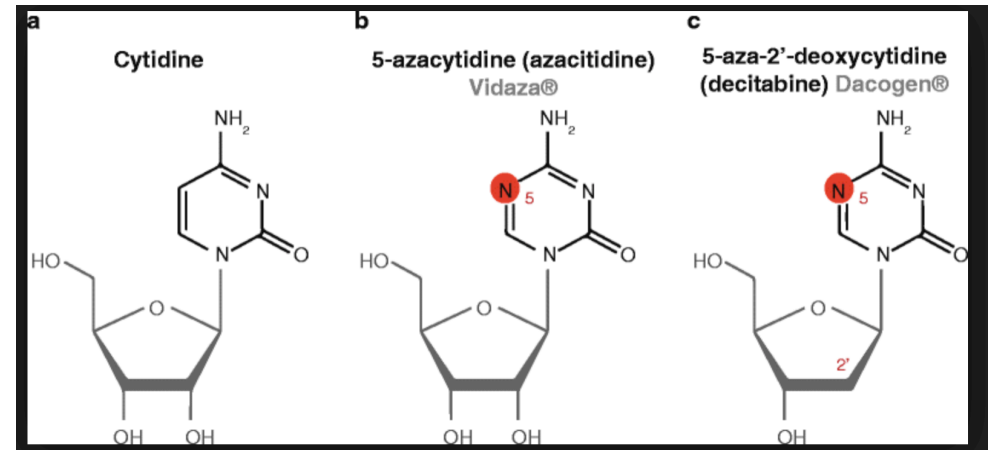
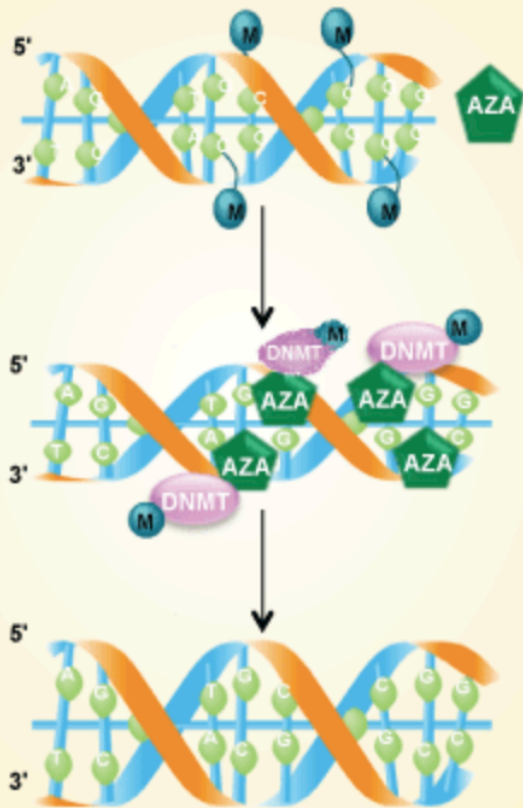


Figure 8. Structures of selected epigenetic drugs. Three nucleoside analogs are known that can inhibit DNA methylation after incorporation into DNA. 5-aza-CR (Vidaza) and 5-aza-CdR (decitabine) have been FDA approved for the treatment of the preleukemic disorder, myelodysplasia. Two HDAC inhibitors are also FDA approved for cutaneous T-cell lymphoma and several others are in clinical trials.

EPIGENETIC DRUGS: DNMT INHIBITORS

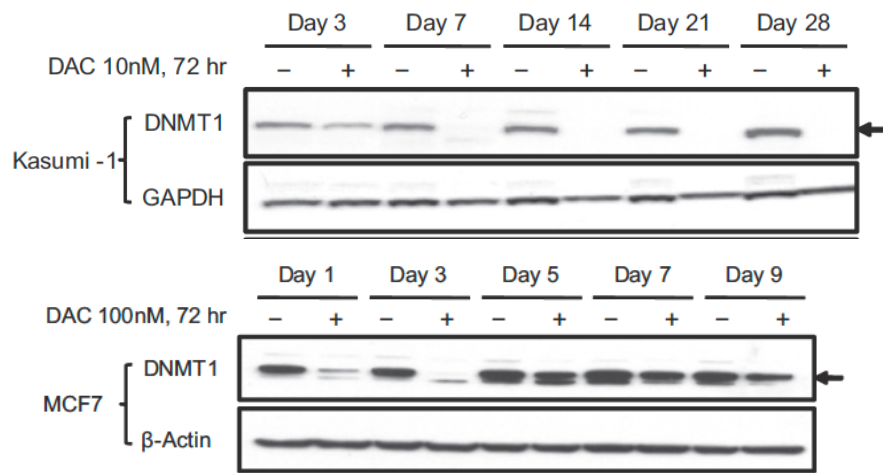


Azacitidine is a chemical analogue of the nucleoside cytidine, which is present in DNA and RNA. It is thought to have antineoplastic activity via two mechanisms – at low doses, by **inhibiting of DNA methyltransferase, causing hypomethylation of DNA**, and at high doses, by **its direct cytotoxicity to abnormal hematopoietic cells** in the bone marrow through its incorporation into DNA and RNA, resulting in cell death. Azacitidine is a ribonucleoside, so it is incorporated into RNA to a larger extent than into DNA. In contrast, **decitabine (5-aza-2'-deoxycytidine) is a deoxyribonucleoside, so it can only incorporate into DNA**. Azacitidine's incorporation into RNA leads to the disassembly of polyribosomes, defective methylation and acceptor function of transfer RNA, and inhibition of the production of proteins. Its incorporation into DNA leads to covalent binding with DNA methyltransferases, which prevents DNA synthesis and subsequently leads to cytotoxicity.

After azanucleosides such as azacitidine have been metabolized to **5-aza-2'-deoxycytidine-triphosphate** (aka, decitabine-triphosphate), they can be incorporated into DNA and azacytosine can be **substituted for cytosine**. Azacytosine-guanine dinucleotides are recognized as substrate by the DNA methyltransferases, which catalyze the methylation reaction by a nucleophilic attack. This results in a **covalent bond between the carbon-6 atom of the cytosine ring and the enzyme**. The bond is normally resolved by beta-elimination through the carbon-5 atom, but this latter reaction does not occur with azacytosine because its carbon-5 is substituted by nitrogen, leaving the enzyme remains covalently bound to DNA and **blocking its DNA methyltransferase function**.

In addition, the **covalent protein adduction also compromises the functionality of DNA and triggers DNA damage signaling, resulting in the degradation of trapped DNA methyltransferases**. As a consequence, methylation marks become lost during DNA replication.

EPIGENETIC DRUGS: DNMT INHIBITORS



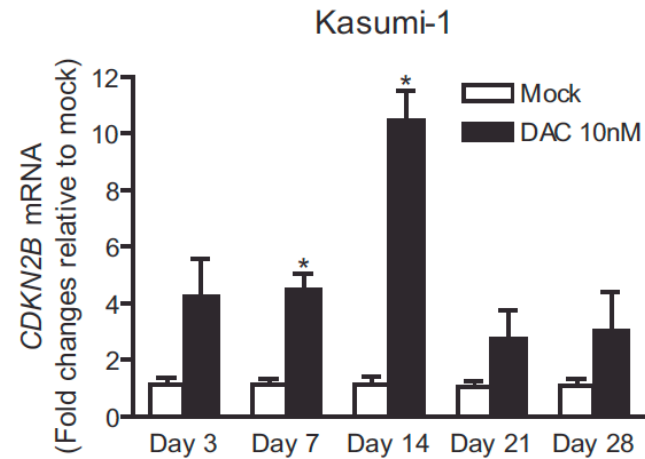
Western blot of DNMT1 expression levels in human leukemia cells (Kasumi-1) and breast cancer cell lines (MCF7) after 72 hr daily treatment of 10 nM (leukemia) DACOGEN.

Special effect in leukemia:

Treatment with DAC for 72hrs → then DAC removal → loss of DNMT1 is maintained
 → Memory effect «reprogramming of cancer cell

Effect of azanucleosides:

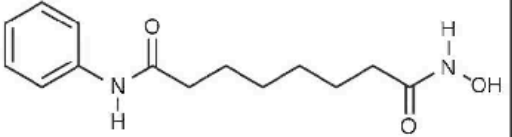
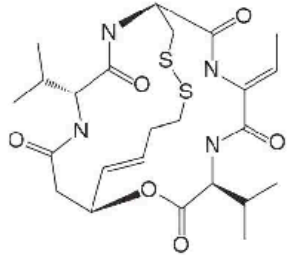
- de-repression of genes
- Other effects: immuneresponse → important anti-tumor effect!



Quantitative real-time PCR analyses of CDKN2B gene expression over time in Kasumi-1 after 72 hr daily treatment of 10 nM DAC. Expression levels are adjusted to GAPDH for each sample and graphed as fold changes relative to mock.

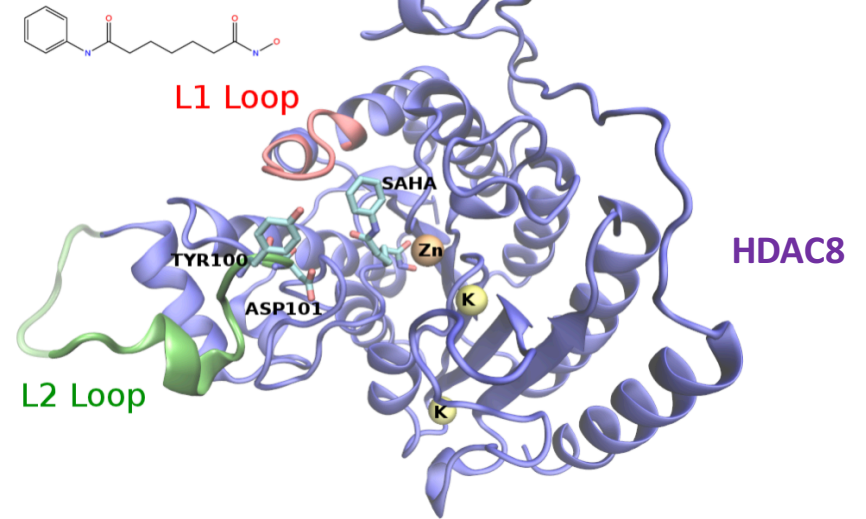
CDKN2B: This gene encodes a cyclin-dependent kinase inhibitor, which forms a complex with CDK4 or CDK6, and prevents the activation of the CDK kinases, thus the encoded protein functions as a cell growth regulator that controls cell cycle G1 progression

EPIGENETIC DRUGS: HDAC INHIBITORS

Histone deacetylase inhibitors			
Suberoylanilide hydroxamic acid (SAHA) Vorinostat (Zolinza)		T-cell lymphoma	FDA-approved in 2006
Depsipeptide FK-229 FR901228 Romidepsin (Istodax)		T-cell lymphoma	FDA-approved in 2009

Two HDAC inhibitors are also FDA approved for cutaneous T-cell lymphoma and several others are in clinical trials. Drugs targeting other epigenetic processes are in earlier stages of clinical development (see also [Figs. 5 and 6 of Ch. 35 \[Audia and Campbell 2014\]](#)).

SAHA - chemical structure



Vorinostat has been shown to bind to the active site of histone deacetylases and act as a chelator for zinc ions also found in the active site of histone deacetylases. Vorinostat's inhibition of histone deacetylases results in the accumulation of acetylated histones and acetylated proteins, including transcription factors crucial for the expression of genes needed to induce cell differentiation. It acts on class I, II and IV of histone deacetylase.



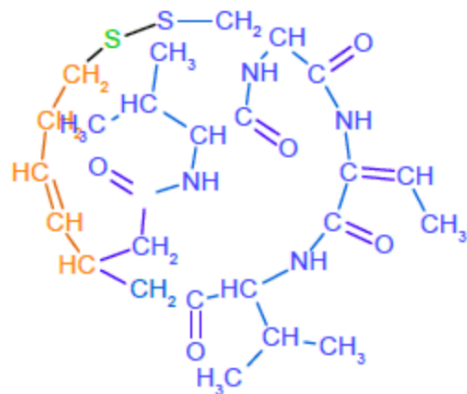
Surface Recognition

Linker

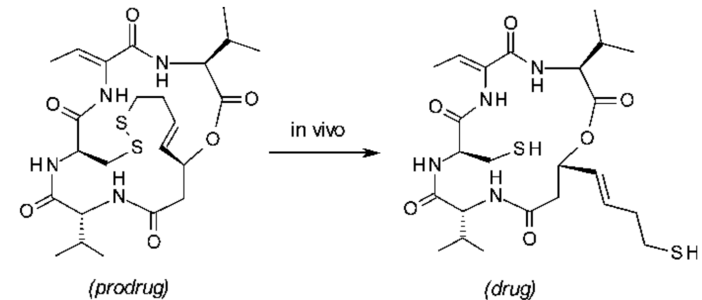
Metal Binding

EPIGENETIC DRUGS: HDAC INHIBITORS

Romidepsin acts as a prodrug with the disulfide bond undergoing reduction within the cell to release a **zinc-binding thiol**. The thiol **binds to a zinc atom in the binding pocket of Zn-dependent histone deacetylase to block its activity**.



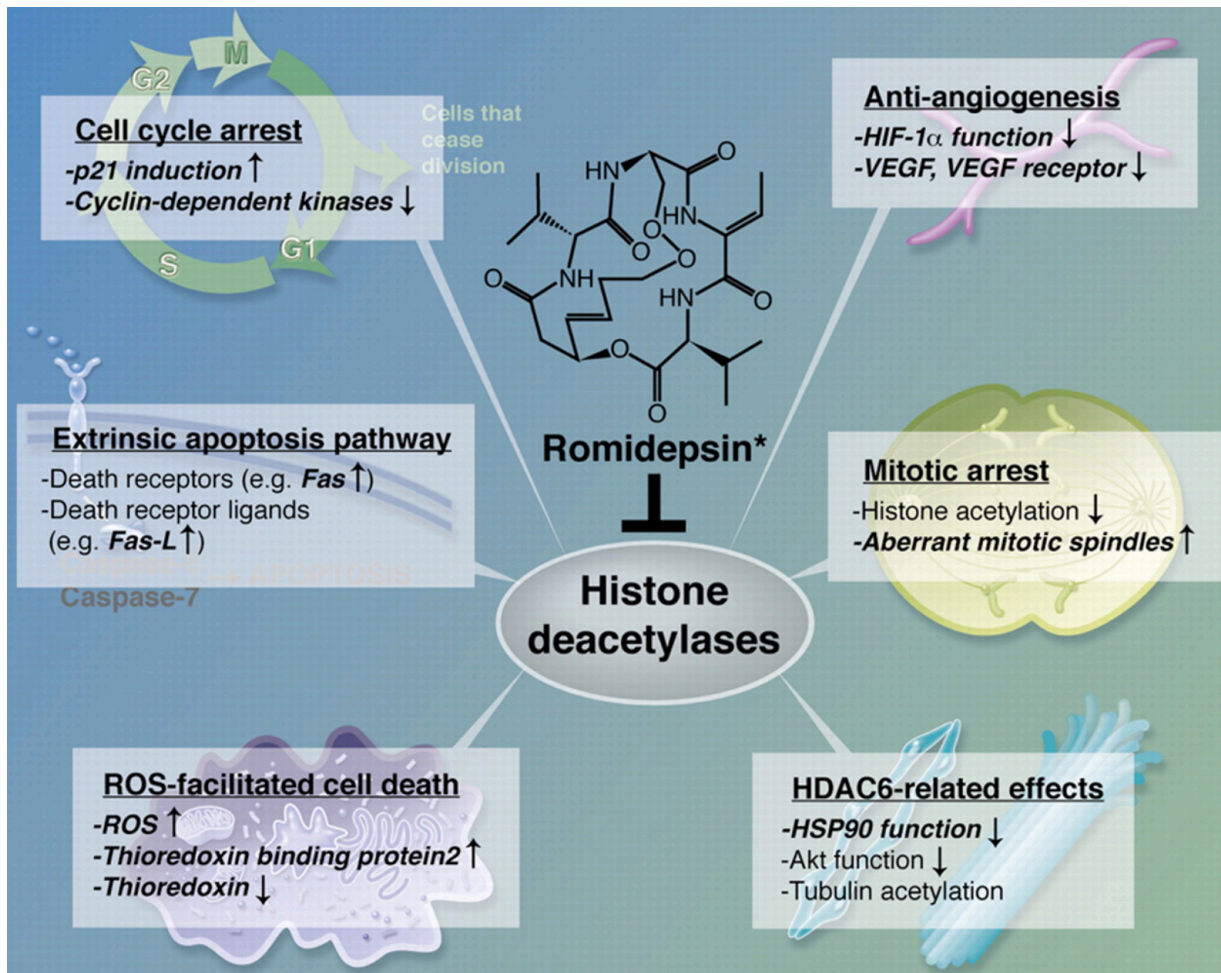
Romidepsin (Istodax*)



2
Romidepsin; Istodax
Gloucester Pharmaceuticals, Inc.; now: Celgene Corporation

Romidepsin (2) is a prodrug, with a disulfide bridge reduced by glutathione upon uptake into the

EPIGENETIC DRUGS: HDAC INHIBITORS



Work well in lymphoma (T cells) ì but low efficiency in solid tumors when given alone.

Tests: HDAC treatment sensitizes tumors to conventional chemotherapy and newer targeted therapies
 i.e. NSCLC: HDACi (entinostat) + EGFRi
 i.e. NSCLC: HDACi (vorionostat) + carboplatin and paxitaxel

HDAC inhibitors increase acetylation levels of genes and cause altered gene expression

→ Hypothesis: TSG re-expressed (to be validated)

Many pathways altered → difficult to identify a DIRECT contribution of HDACi