Understanding Oncogenes and Tumor Suppressors

Pablo Sánchez Vela, MD.

HOPP ResTep/SEP

February 8th, 2023

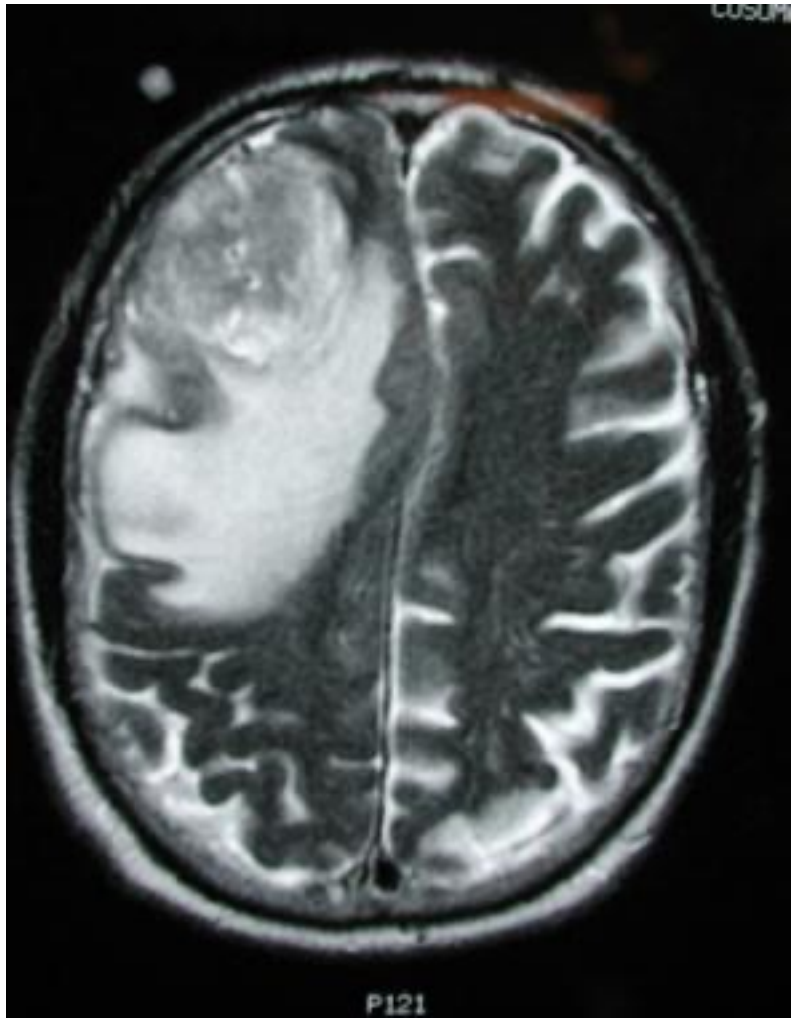
sanchezp@mskcc.org

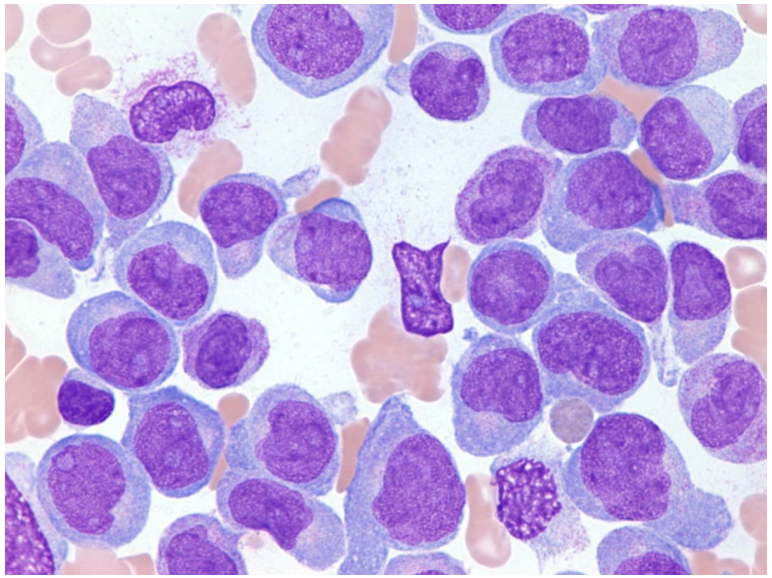
Recommended reads:

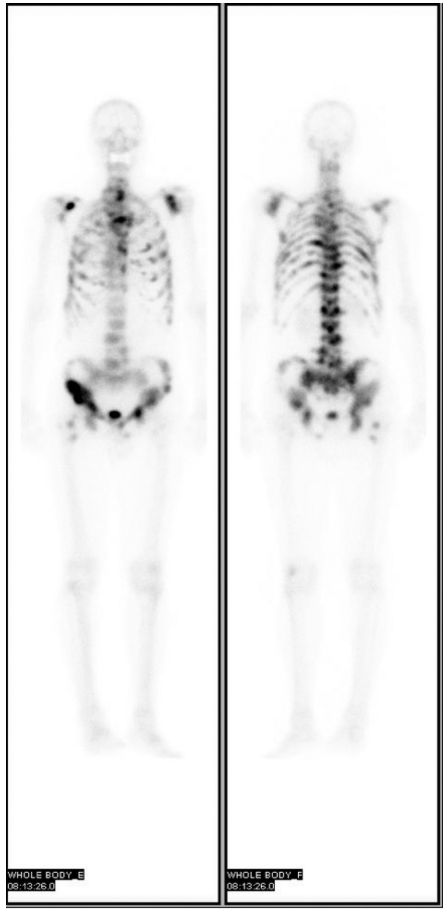
The Biology of Cancer. 2nd edition. Weinberg 2014.

Primer of the Molecular Biology of Cancer. DeVita 2021.

Available through MSK library.

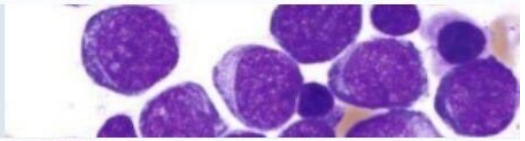
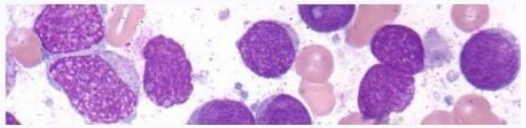
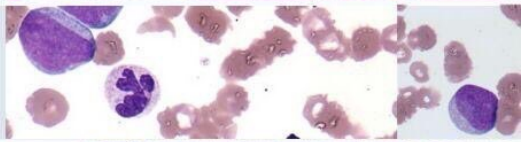
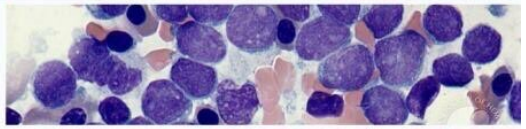
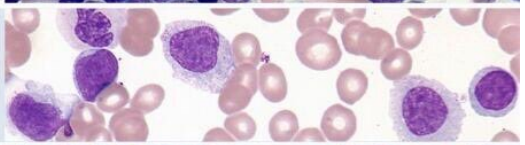
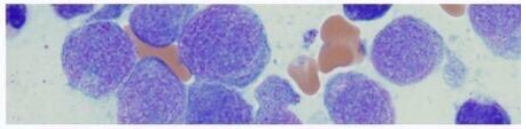
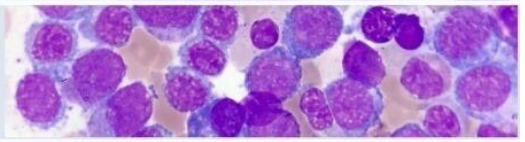
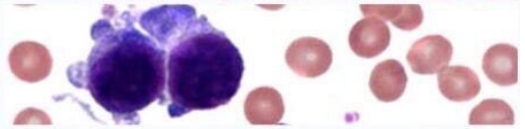






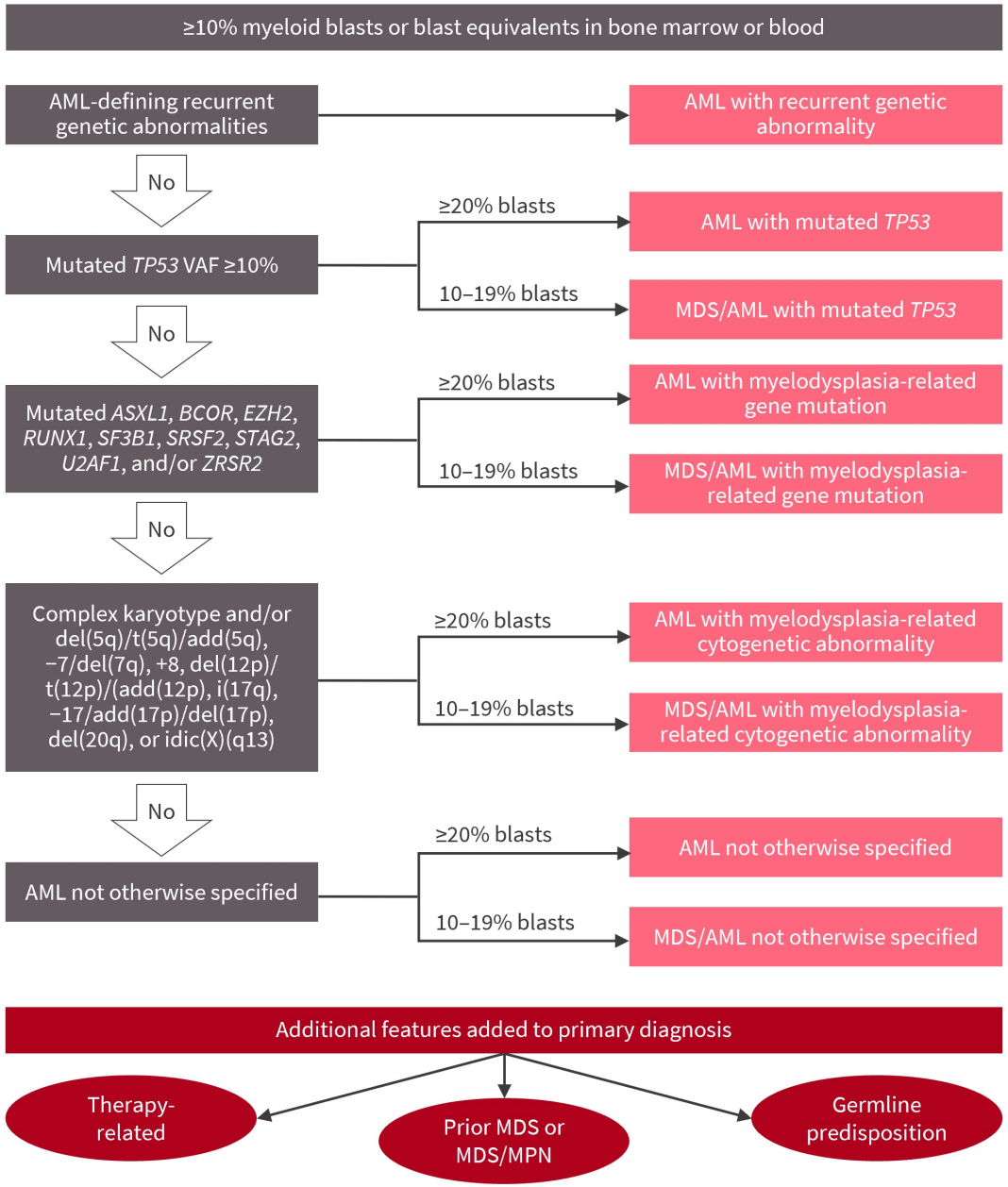
Medscape
SJCH
Wostnizer RCR 2010

FAB CLASSIFICATION SYSTEM OF ACUTE MYELOID LEUKAEMIA

M0	AML with minimal differentiation	
M1	AML without maturation	
M2	AML with maturation	
M3	Acute promyelocytic leukaemia	
M4	Acute myelomonocytic leukaemia	
M5	Acute monoblastic and monocytic leukaemia	
M6	Pure erythroid leukaemia	
M7	Acute megakaryoblastic leukemia	

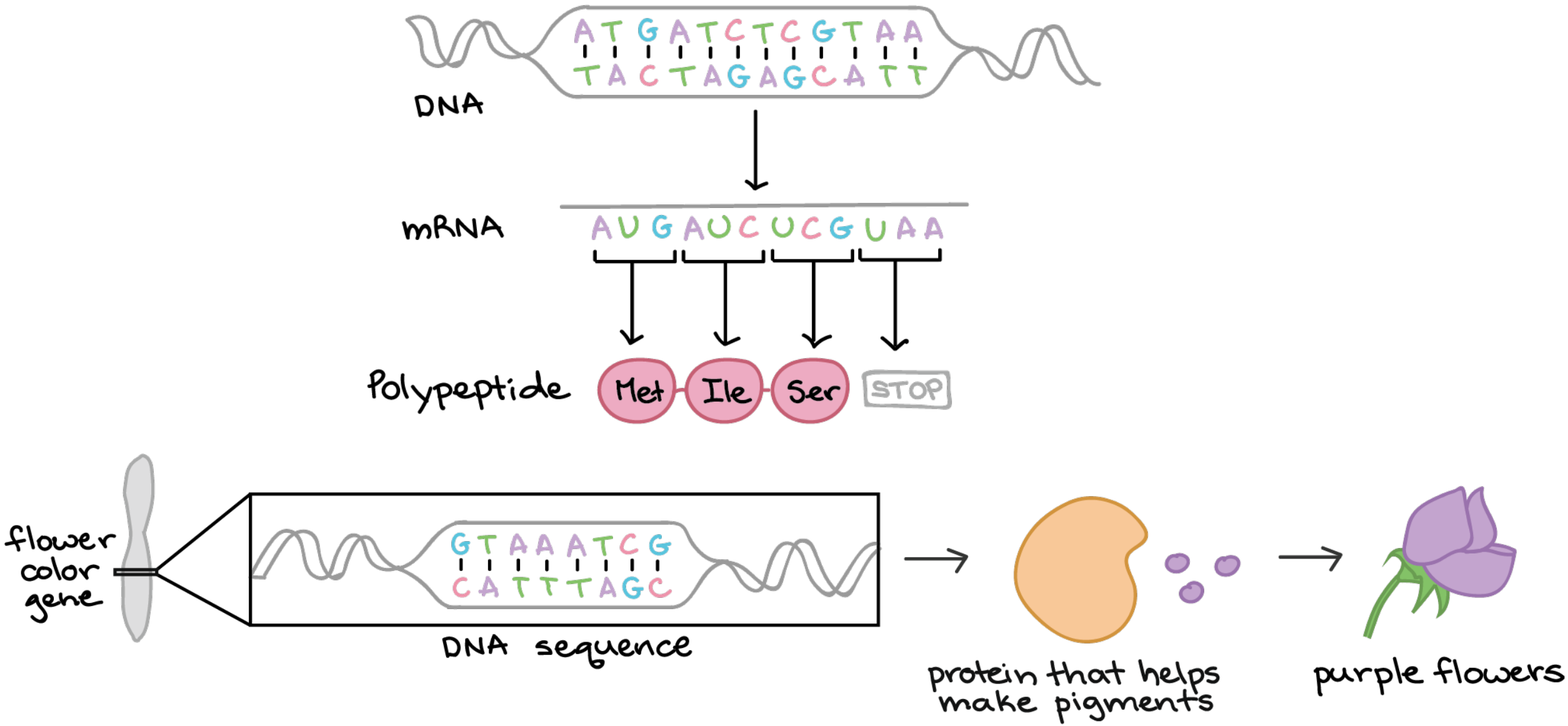
Blood Academy

WWW.BLOOD-ACADEMY.COM



ELN 2022

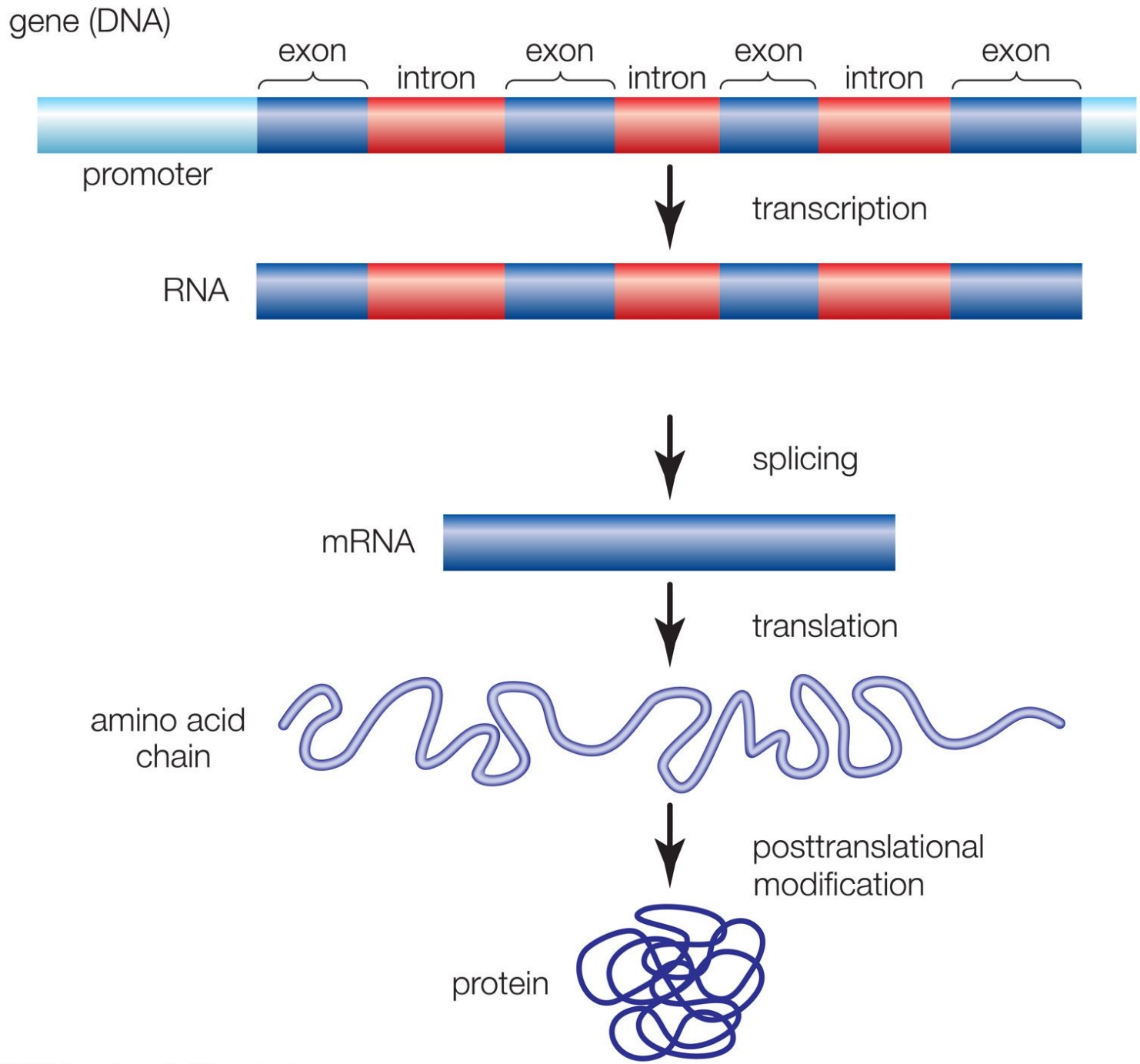
THE CENTRAL DOGMA



KhanAcademy

What are the differences between:

Gene Promoter and Exon

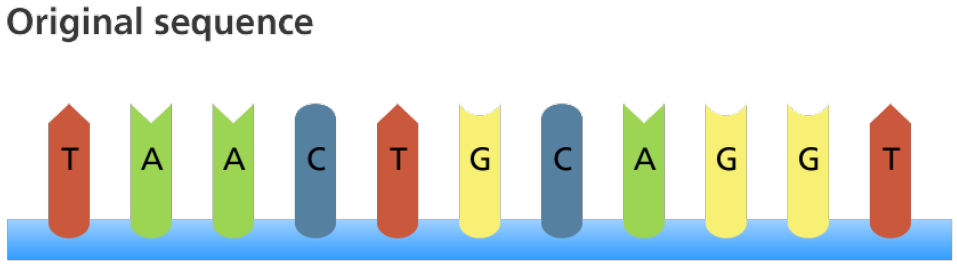


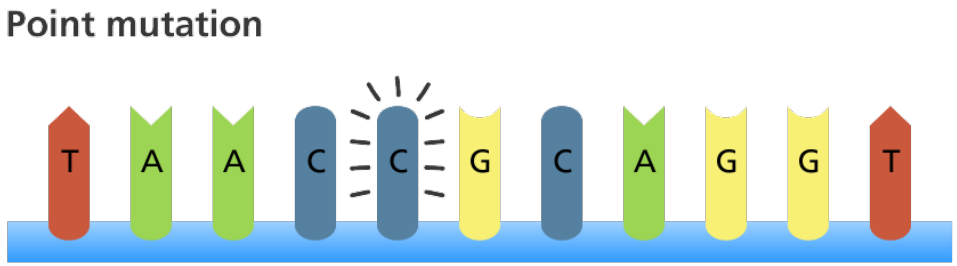
© 2013 Encyclopædia Britannica, Inc.

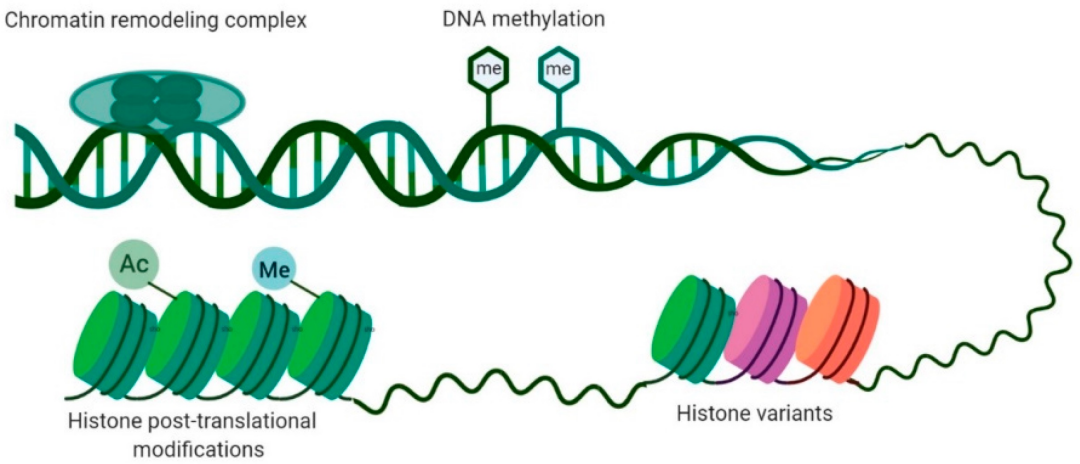
What are the differences between:

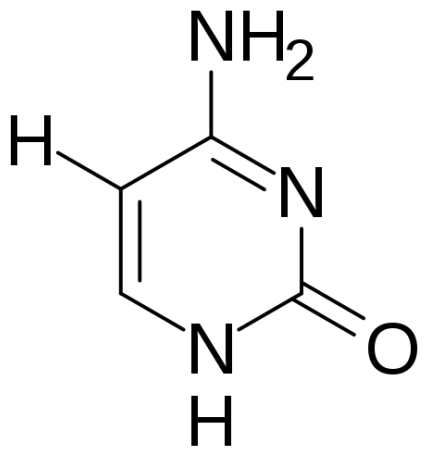
Mutation of the DNA and Methylation of the DNA

DNA mutation vs DNA methylation:

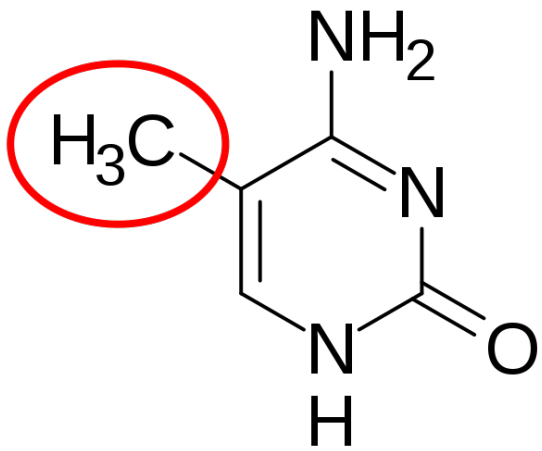








cytosine



methylated cytosine

Genome Research Limited
MDPI

What are the differences between:

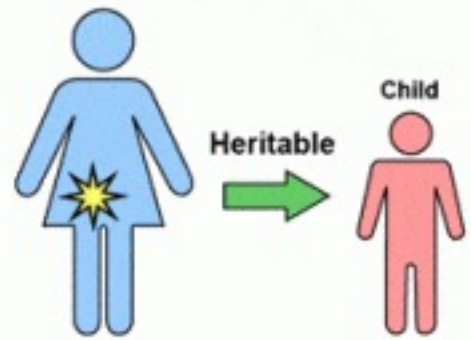
Somatic and Germline mutations

Somatic mutations
- Occur in ***nongermline*** tissues
- Cannot be inherited

Nonheritable

Mutation in tumor only
(for example, breast)

Germline mutations
- Present in egg or sperm
- Can be inherited
- Cause cancer family syndrome



Mutation in
egg or sperm

All cells
affected in
offspring

Adapted from the National Cancer Institute and the American Society of Clinical Oncology

What are the differences between:

Oncogenes and Tumor Suppressors

Normal Cell Cycle

Proto-oncogene (gas) | Tumor Suppressor Gene (brakes)

As part of your project, you are interested in modelling mutations that frequently occur in cancer patients. For this purpose, you are reviewing MSK-IMPACT clinical sequencing results using the cBioPortal platform. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known tumor suppressor gene. What are the characteristics of these types of genes?

A) In cancer patients, inactivating mutations are the most frequent type of mutations occurring in tumor suppressors genes.
B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like promoter methylation.
C) Loss of tumor suppressors decreases the likelihood of malignant transformation.
D) Mutation in tumor suppressors genes can only be somatic, and they don’t occur in the germline.

As part of your project, you are interested in **modelling** mutations that frequently occur in **cancer patients**. For this purpose, you are reviewing **MSK-IMPACT** clinical sequencing results using the **cBioPortal** platform. One of the genes that most commonly is found to be mutated in this dataset is **TP53**, a known **tumor suppressor** gene. What are the characteristics of these types of genes?

A) In cancer patients, **inactivating mutations** are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like **promoter methylation**.

C) Loss of tumor suppressors decreases the likelihood of **malignant transformation.**

D) Mutation in tumor suppressors genes can only be **somatic**, and they don’t occur in the **germline**.

As part of your project, you are interested in modelling mutations that frequently occur in **cancer patients**. For this purpose, you are reviewing MSK-IMPACT clinical sequencing results using the cBioPortal platform. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known tumor suppressor gene. What are the characteristics of these types of genes?

A) In cancer patients, inactivating mutations are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like promoter methylation.

C) Loss of tumor suppressors decreases the likelihood of malignant transformation.

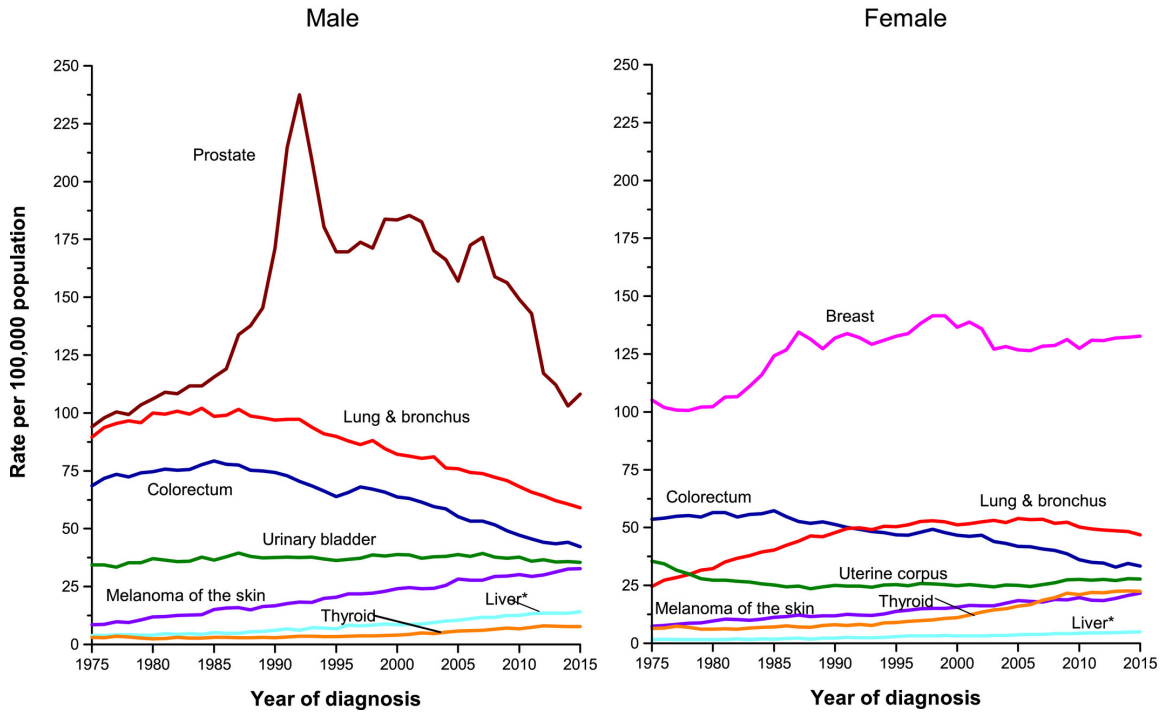
D) Mutation in tumor suppressors genes can only be somatic, and they don’t occur in the germline.

Estimated New Cases

	Males			Females		
Prostate	174,650	20%		Breast	268,600	30%
Lung & bronchus	116,440	13%		Lung & bronchus	111,710	13%
Colon & rectum	78,500	9%		Colon & rectum	67,100	8%
Urinary bladder	61,700	7%		Uterine corpus	61,880	7%
Melanoma of the skin	57,220	7%		Melanoma of the skin	39,260	4%
Kidney & renal pelvis	44,120	5%		Thyroid	37,810	4%
Non-Hodgkin lymphoma	41,090	5%		Non-Hodgkin lymphoma	33,110	4%
Oral cavity & pharynx	38,140	4%		Kidney & renal pelvis	29,700	3%
Leukemia	35,920	4%		Pancreas	26,830	3%
Pancreas	29,940	3%		Leukemia	25,860	3%
All Sites	**870,970**	**100%**		**All Sites**	**891,480**	**100%**

Estimated Deaths

	Males			Females		
Lung & bronchus	76,650	24%		Lung & bronchus	66,020	23%
Prostate	31,620	10%		Breast	41,760	15%
Colon & rectum	27,640	9%		Colon & rectum	23,380	8%
Pancreas	23,800	7%		Pancreas	21,950	8%
Liver & intrahepatic bile duct	21,600	7%		Ovary	13,980	5%
Leukemia	13,150	4%		Uterine corpus	12,160	4%
Esophagus	13,020	4%		Liver & intrahepatic bile duct	10,180	4%
Urinary bladder	12,870	4%		Leukemia	9,690	3%
Non-Hodgkin lymphoma	11,510	4%		Non-Hodgkin lymphoma	8,460	3%
Brain & other nervous system	9,910	3%		Brain & other nervous system	7,850	3%
All Sites	**321,670**	**100%**		**All Sites**	**285,210**	**100%**



Siegel. CA 2019

As part of your project, you are interested in modelling mutations that frequently occur in cancer patients. For this purpose, you are reviewing **MSK-IMPACT** clinical sequencing results using the **cBioPortal** platform. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known tumor suppressor gene. What are the characteristics of these types of genes?

A) In cancer patients, inactivating mutations are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like promoter methylation.

C) Loss of tumor suppressors decreases the likelihood of malignant transformation.

D) Mutation in tumor suppressors genes can only be somatic, and they don’t occur in the germline.

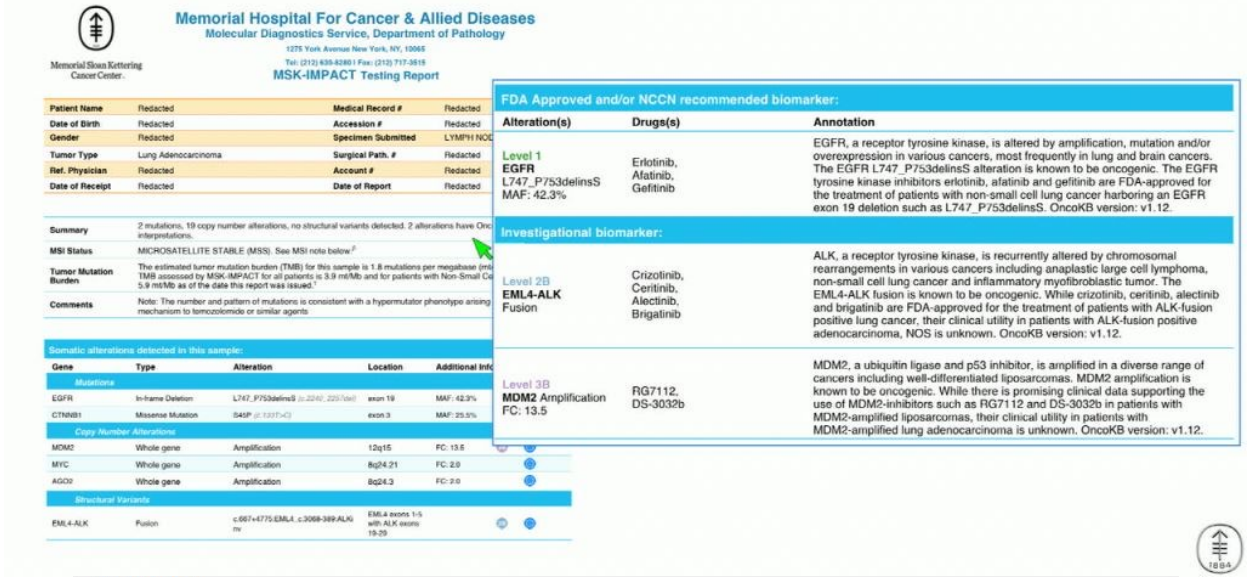
MSK-IMPACT

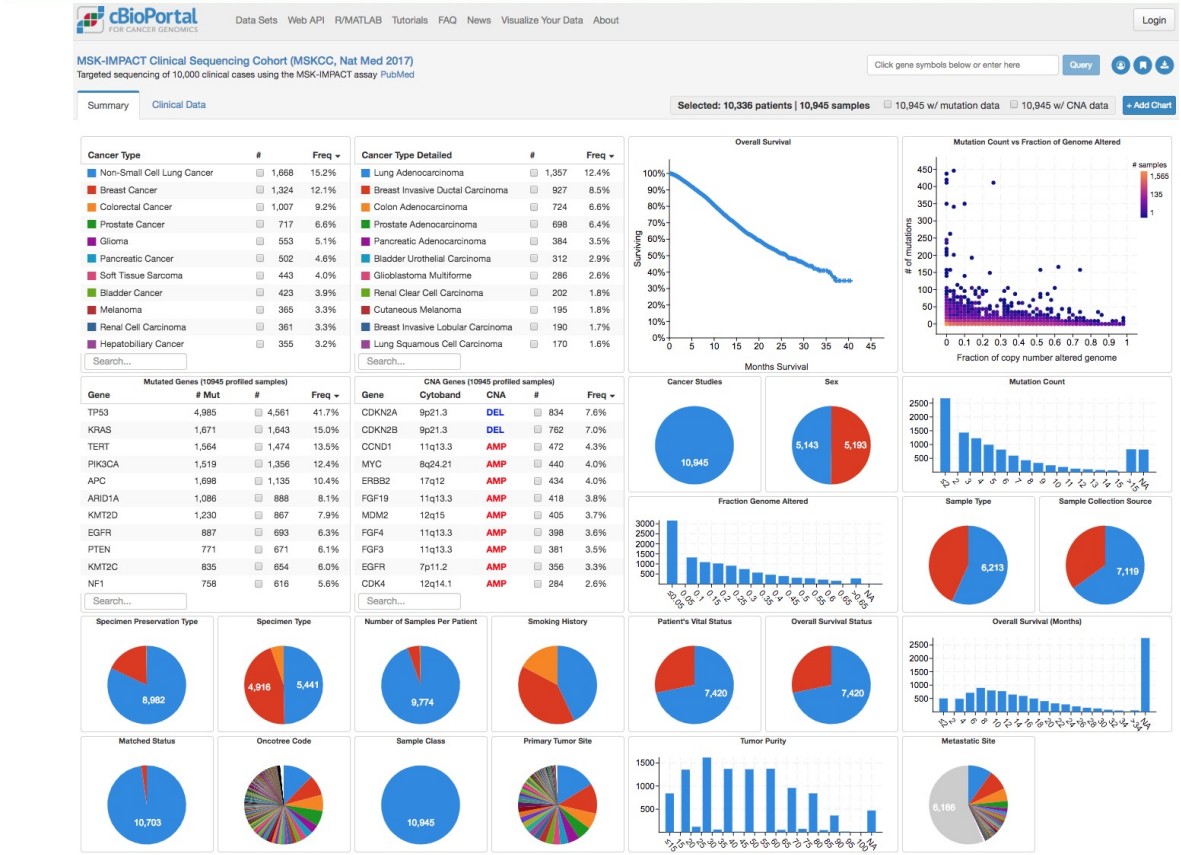
(Integrated Mutation Profiling of Actionable Cancer Targets)

ABL1	CALR	DICER1	FGFR1	HLA-C	MALT1	NOTCH1	PPP4R2	RXRA	SUZ12
ACVR1	CARD11	DIS3	FGFR2	HNF1A	MAP2K1	NOTCH2	PPP6C	RYBP	SYK
AGO1	CARM1	DNAJB1	FGFR3	HOXB13	MAP2K2	NOTCH3	PRDM1	SCG5	TAP1
AGO2	CASP8	DNMT1	FGFR4	HRAS	MAP2K4	NOTCH4	PRDM14	SDHA	TAP2
AKT1	CBFB	DNMT3A	FH	ICOSLG	MAP3K1	NPM1	PREX2	SDHAF2	TBX3
AKT2	CBL	DNMT3B	FLCN	ID3	MAP3K13	NRAS	PRKAR1A	SDHB	TCEB1
AKT3	CCND1	DOT1L	FLT1	IDH1	MAP3K14	NSD1	PRKCI	SDHC	TCF3
ALB	CCND2	DROSHA	FLT3	IDH2	MAPK1	NTHL1	PRKD1	SDHD	TCF7L2
ALK	CCND3	DUSP4	FLT4	IFNGR1	MAPK3	NTRK1	PTCH1	SERPINB3	TEK
ALOX12B	CCNE1	E2F3	FOXA1	IGF1	MAPKAP1	NTRK2	PTEN	SERPINB4	TERT
ANKRD11	CD274	EED	FOXF1	IGF1R	MAX	NTRK3	PTP4A1	SESN1	TET1
APC	CD276	EGFL7	FOXL2	IGF2	MCL1	NUF2	PTPN11	SESN2	TET2
APLNR	CD79A	EGFR	FOXO1	IKBKE	MDC1	NUP93	PTPRD	SESN3	TGFBR1
AR	CD79B	EIF1AX	FOXP1	IKZF1	MDM2	PAK1	PTPRS	SETD2	TGFBR2
ARAF	CDC42	EIF4A2	FUBP1	IL10	MDM4	PAK7	PTPRT	SETDB1	TMEM127
ARHGAP35	CDC73	EIF4E	FYN	IL7R	MED12	PALB2	RAB35	SF3B1	TMPRSS2
ARID1A	CDH1	ELF3	GAB1	INHA	MEF2B	PARK2	RAC1	SH2B3	TNFAIP3
ARID1B	CDK12	EP300	GAB2	INHBA	MEN1	PARP1	RAC2	SH2D1A	TNFRSF14
ARID2	CDK4	EPAS1	GATA1	INPP4A	MET	PAX5	RAD21	SHOC2	TOP1
ARID5B	CDK6	EPCAM	GATA2	INPP4B	MGA	PBRM1	RAD50	SHQ1	TP53
ASXL1	CDK8	EPHA3	GATA3	INPPL1	MITF	PDCD1	RAD51	SLFN11	TP53BP1
ASXL2	CDKN1A	EPHA5	GLI1	INSR	MLH1	PDCD1LG2	RAD51C	SLX4	TP63
ATM	CDKN1B	EPHA7	GNA11	IRF4	MLLT1	PDGFRA	RAD51L1	SMAD2	TRAF2
ATR	CDKN2A	EPHB1	GNAQ	IRS1	MPL	PDGFRB	RAD51L3	SMAD3	TRAF7
ATRX	CDKN2B	ERBB2	GNAS	IRS2	MRE11A	PDPK1	RAD52	SMAD4	TRIP13
ATXN7	CDKN2C	ERBB3	GNB1	JAK1	MSH2	PGBD5	RAD54L	SMARCA2	TSC1
AURKA	CEBPA	ERBB4	GPS2	JAK2	MSH3	PGR	RAF1	SMARCA4	TSC2
AURKB	CENPA	ERCC2	GREM1	JAK3	MSH6	PHF6	RARA	SMARCB1	TSHR
AXIN1	CHEK1	ERCC3	GRIN2A	JUN	MSI1	PHOX2B	RASA1	SMARCD1	U2AF1
AXIN2	CHEK2	ERCC4	GSK3B	KBTBD4	MSI2	PIK3C2G	RB1	SMARCE1	UPF1
AXL	CIC	ERCC5	H3F3A	KDM5A	MST1	PIK3C3	RBM10	SMO	USP8
B2M	CMTR2	ERF	H3F3B	KDM5C	MST1R	PIK3CA	RECQL	SMYD3	VEGFA
BABAM1	CREBBP	ERG	H3F3C	KDM6A	MTAP	PIK3CB	RECQL4	SOCS1	VHL
BAP1	CRKL	ERRFI1	HGF	KDR	MTOR	PIK3CD	REL	SOS1	VTCN1
BARD1	CRLF2	ESR1	HIST1H1C	KEAP1	MUTYH	PIK3CG	REST	SOX17	WHSC1
BBC3	CSDE1	ETAA1	HIST1H2BD	KIT	MYC	PIK3R1	RET	SOX2	WHSC1L1
BCL10	CSF1R	ETV1	HIST1H3A	KLF4	MYCL1	PIK3R2	RFWD2	SOX9	WT1
BCL2	CSF3R	ETV6	HIST1H3B	KLF5	MYCN	PIK3R3	RHEB	SPEN	WWTR1
BCL2L1	CTCF	EZH1	HIST1H3C	KMT2A	MYD88	PIM1	RHOA	SPOP	XIAP
BCL2L11	CTLA4	EZH2	HIST1H3D	KMT2B	MYOD1	PLCG2	RICTOR	SPRED1	XPO1
BCL6	CTNNB1	FAM123B	HIST1H3E	KMT2C	NADK	PLK2	RIT1	SPRTN	XRCC2
BCOR	CTR9	FAM175A	HIST1H3F	KMT2D	NBN	PMAIP1	RNF43	SRC	YAP1
BIRC3	CUL3	FAM46C	HIST1H3G	KMT5A	NCOA3	PMS1	ROS1	SRSF2	YES1
BLM	CXCR4	FAM58A	HIST1H3H	KNSTRN	NCOR1	PMS2	RPS6KA4	STAG2	ZFHX3
BMPR1A	CXORF67	FANCA	HIST1H3I	KRAS	NEGR1	PNRC1	RPS6KB2	STAT3	ZNRF3
BRAF	CYLD	FANCC	HIST1H3J	LATS1	NF1	POLD1	RPTOR	STAT5A	ZRSR2
BRCA1	CYP19A1	FAT1	HIST2H3C	LATS2	NF2	POLE	RRAGC	STAT5B	
BRCA2	CYSLTR2	FBXW7	HIST2H3D	LMO1	NFE2L2	POT1	RRAS	STK11	
BRD4	DAXX	FGF19	HIST3H3	LYN	NFKBIA	PPARG	RRAS2	STK19	
BRIP1	DCUN1D1	FGF3	HLA-A	LZTR1	NKX2-1	PPM1D	RTEL1	STK40	
BTK	DDR2	FGF4	HLA-B	MAD2L2	NKX3-1	PPP2R1A	RUNX1	SUFU	

cBioPortal for Cancer Genomics -->

https://www.cbioportal.org





As part of your project, you are interested in modelling mutations that frequently occur in cancer patients. For this purpose, you are reviewing MSK-IMPACT clinical sequencing results using the cBioPortal platform. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known **tumor suppressor gene**. What are the characteristics of these types of genes?

A) In cancer patients, inactivating mutations are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like promoter methylation.

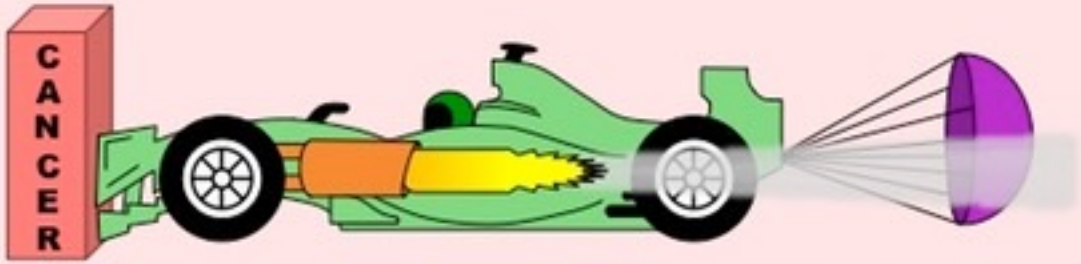
C) Loss of tumor suppressors decreases the likelihood of malignant transformation.

D) Mutation in tumor suppressors genes can only be somatic, and they don’t occur in the germline.

Normal Cell Cycle

Proto-oncogene (gas) | Tumor Suppressor Gene (brakes)

Mutations leading to Cancer



Proto-oncogene → Oncogene = *Too much gas!*

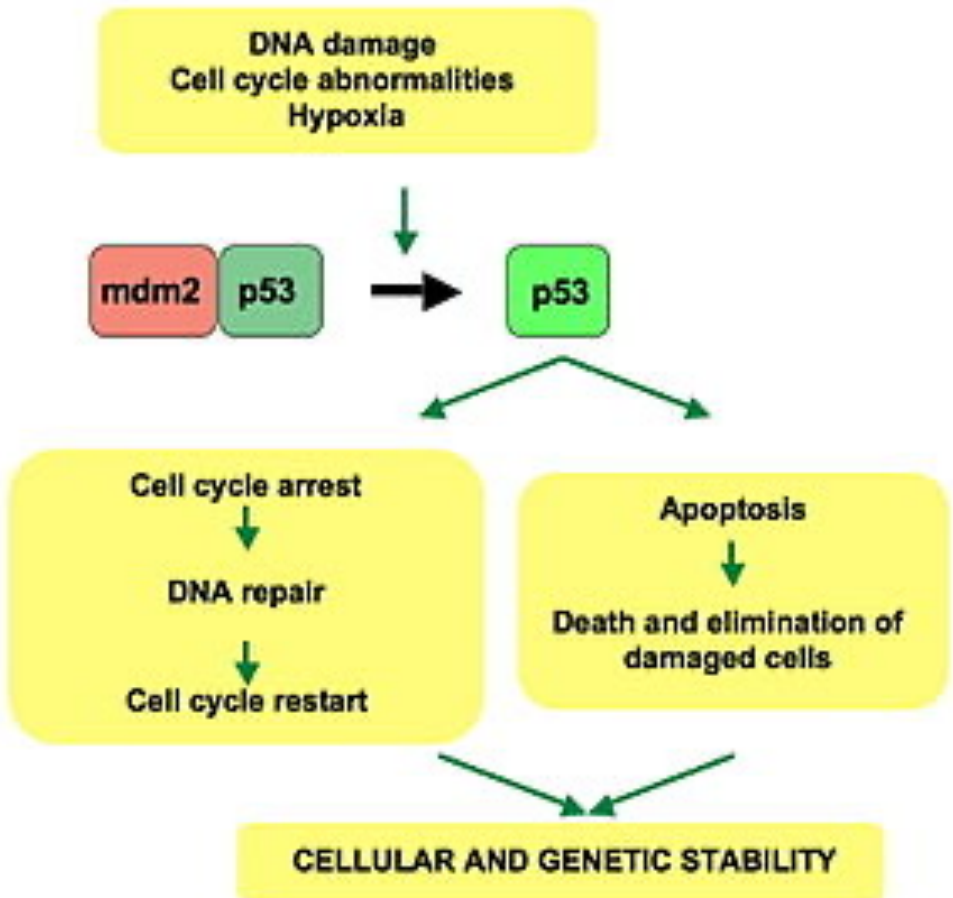
Tumor Suppressor Gene Inactivated = *No brake!*

Bioninja.com

As part of your project, you are interested in modelling mutations that frequently occur in cancer patients. For this purpose, you are reviewing MSK-IMPACT clinical sequencing results using the cBioPortal platform. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known tumor suppressor gene. What are the characteristics of these types of genes?

A) In cancer patients, **inactivating mutations** are the most frequent type of mutations occurring in tumor suppressors genes.
B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like promoter methylation.
C) Loss of tumor suppressors decreases the likelihood of malignant transformation.
D) Mutation in tumor suppressors genes can only be somatic, and they don’t occur in the germline.

TP53 as an example of a tumor suppressor



Wikicommons

As part of your project, you are interested in modelling mutations that frequently occur in cancer patients. For this purpose, you are reviewing MSK-IMPACT clinical sequencing results using the cBioPortal platform. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known tumor suppressor gene. What are the characteristics of these types of genes?

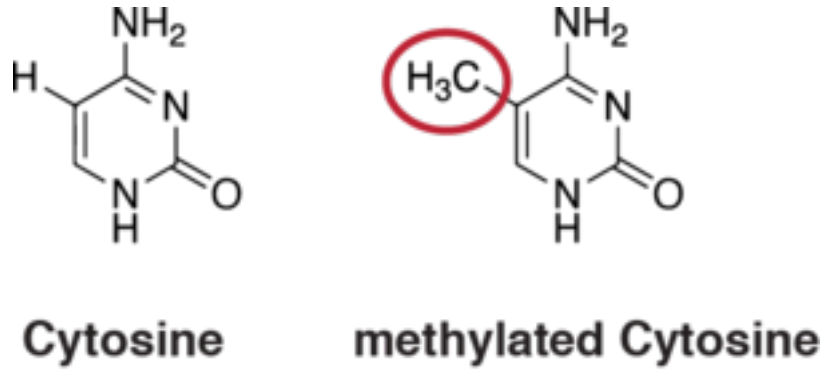
A) In cancer patients, inactivating mutations are the most frequent type of mutations occurring in tumor suppressors genes.

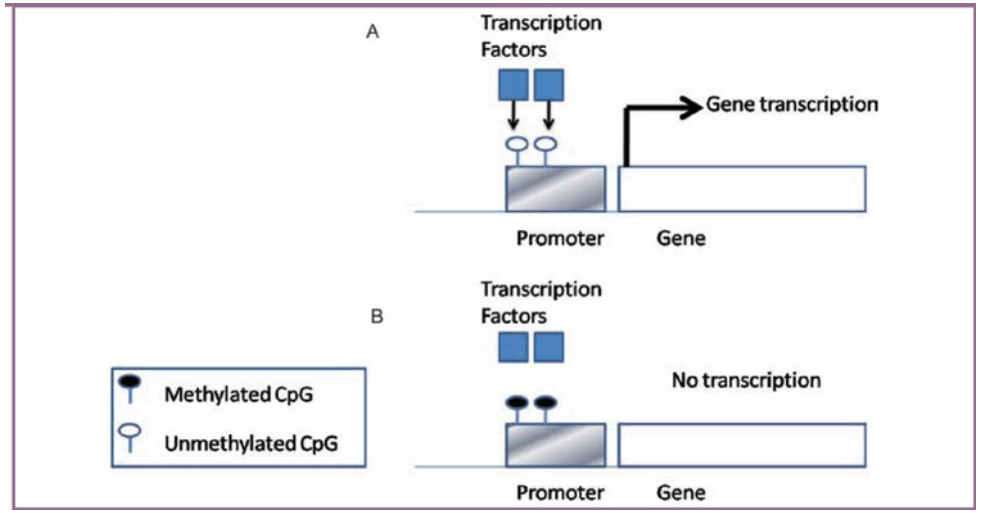
B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like **promoter methylation**.

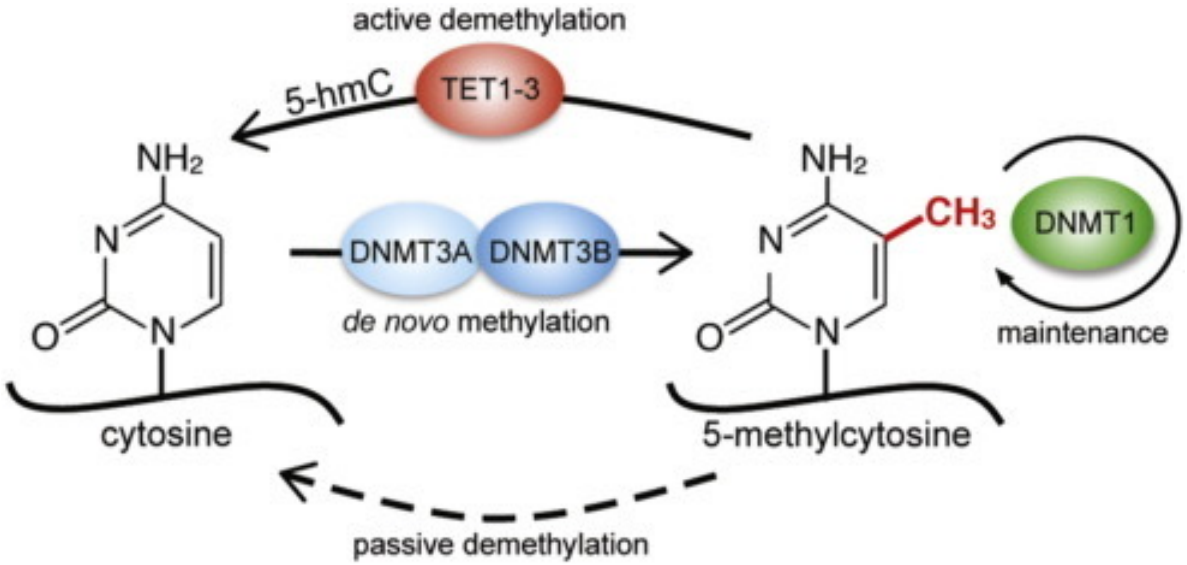
C) Loss of tumor suppressors decreases the likelihood of malignant transformation.

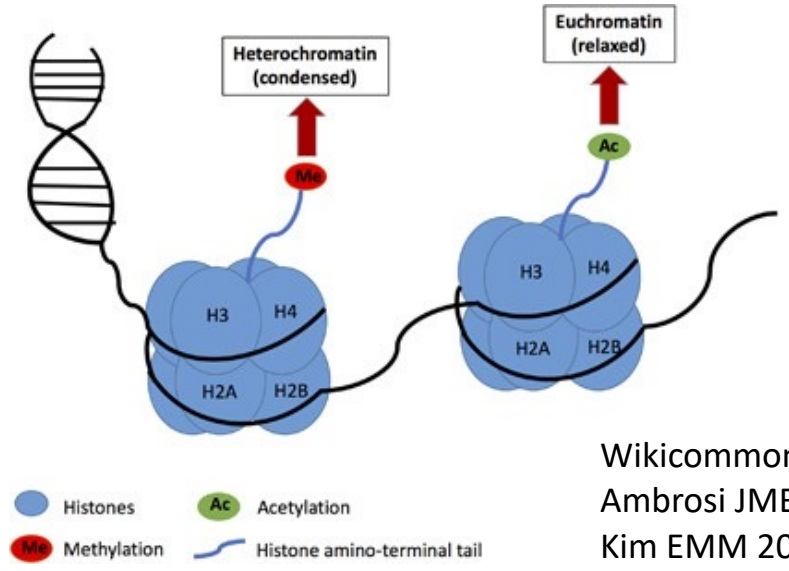
D) Mutation in tumor suppressors genes can only be somatic, and they don’t occur in the germline.

Epigenetics: Methylation as an example of an epigenetic modification









Wikicommons
Ambrosi JMB 2017
Kim EMM 2017
Lim TOG 2011

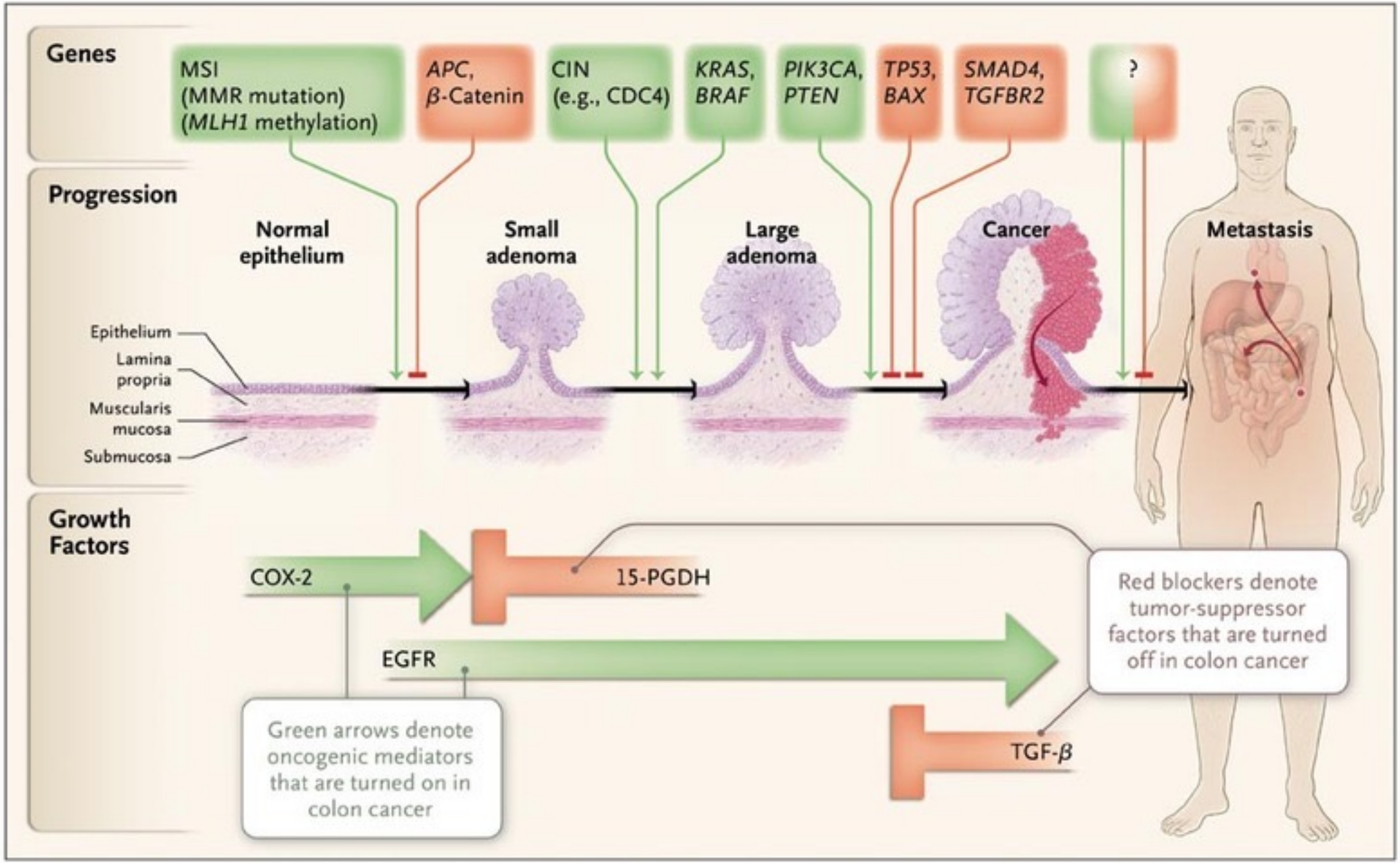
As part of your project, you are interested in modelling mutations that frequently occur in cancer patients. For this purpose, you are reviewing MSK-IMPACT clinical sequencing results using the cBioPortal platform. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known tumor suppressor gene. What are the characteristics of these types of genes?

A) In cancer patients, inactivating mutations are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like promoter methylation.

C) Loss of tumor suppressors decreases the likelihood of **malignant transformation**.

D) Mutation in tumor suppressors genes can only be somatic, and they don't occur in the germline.



Markowitz NEJM 2009

As part of your project, you are interested in modelling mutations that frequently occur in cancer patients. For this purpose, you are reviewing MSK-IMPACT clinical sequencing results using the cBioPortal platform. One of the genes that most commonly is found to be mutated in this dataset is TP53, a known tumor suppressor gene. What are the characteristics of these types of genes?

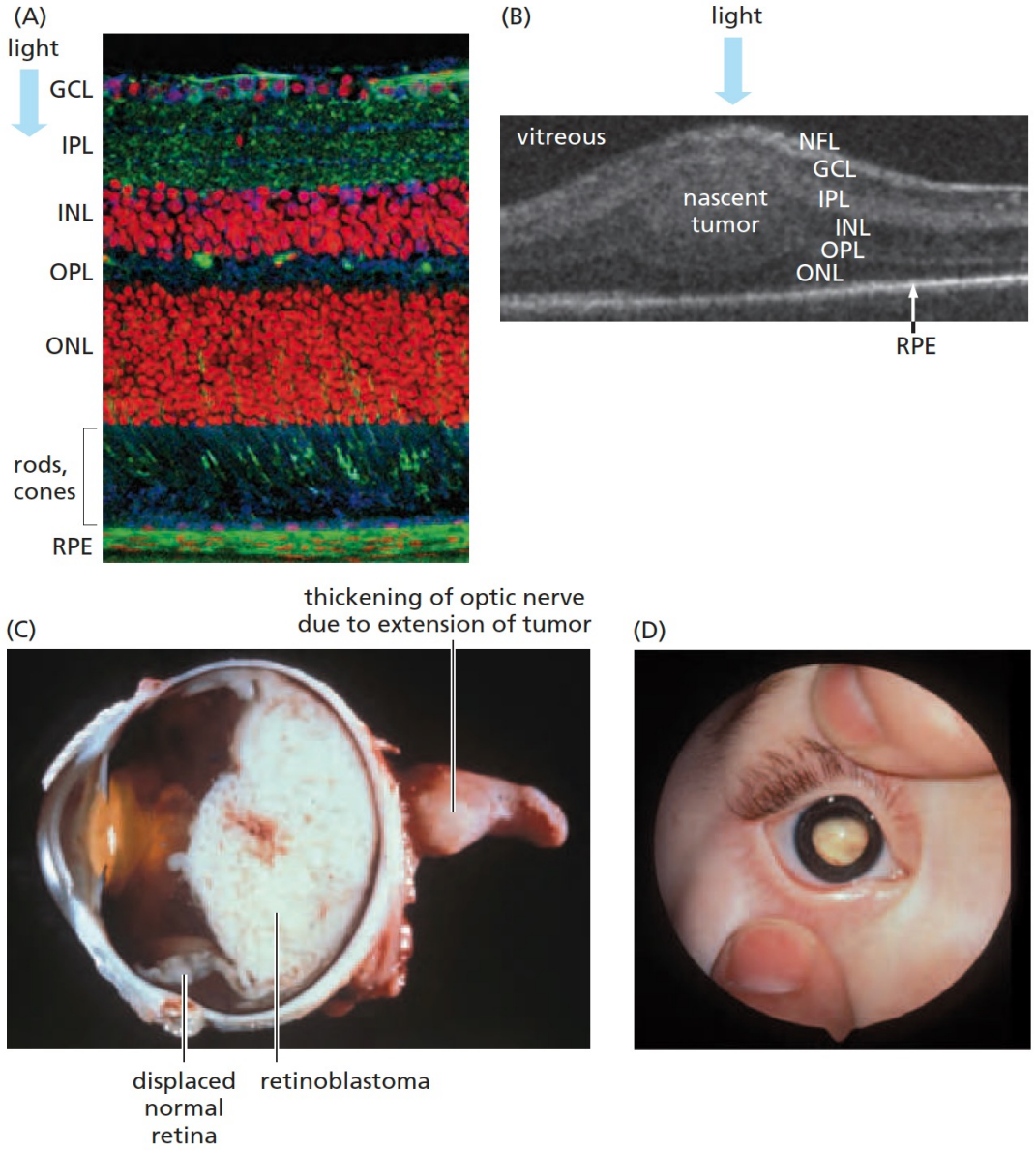
A) In cancer patients, inactivating mutations are the most frequent type of mutations occurring in tumor suppressors genes.

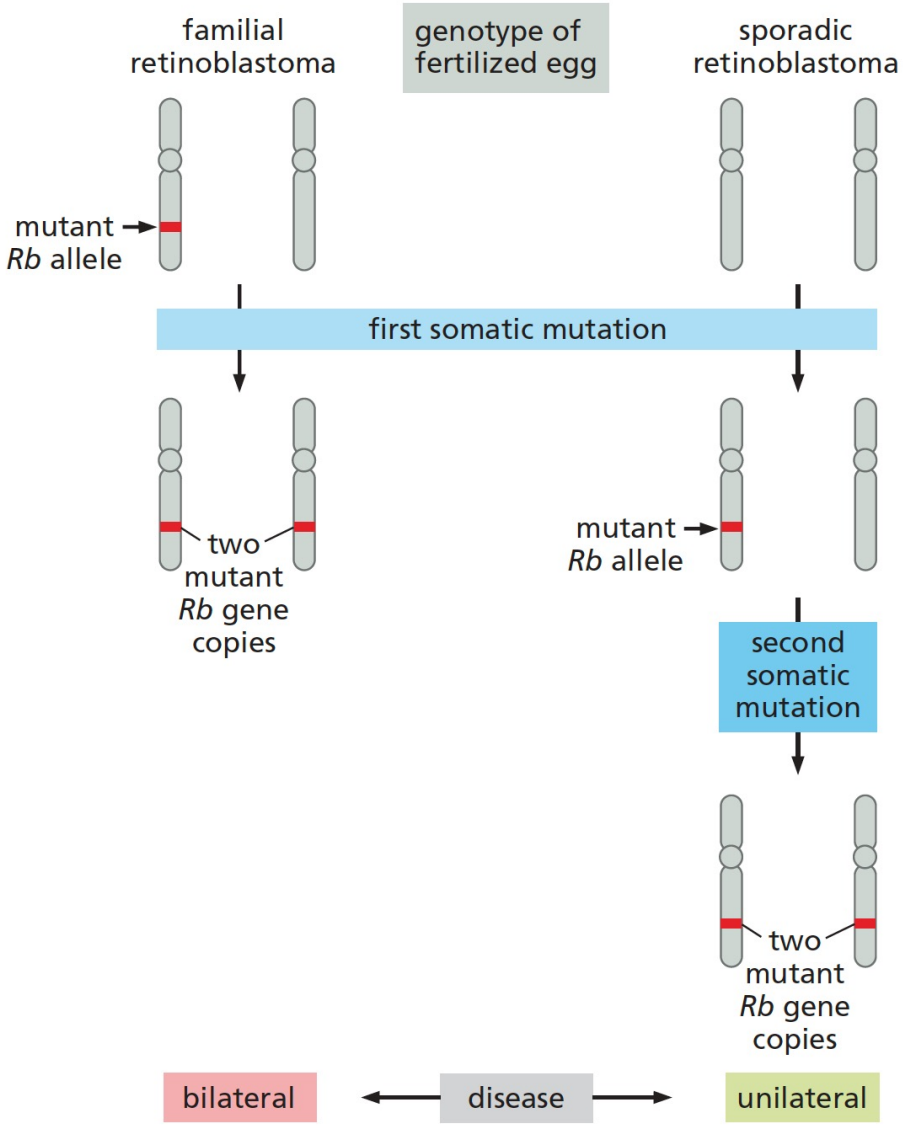
B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like promoter methylation.

C) Loss of tumor suppressors decreases the likelihood of malignant transformation.

D) Mutation in tumor suppressors genes can only be **somatic**, and they don't occur in the **germline**.

RB (Retinoblastoma) as an example of a tumor suppressor with somatic and germline mutations





Weinberg. 2014

Understanding Cancer Classification and Modelling of Tumor Suppressors

Pablo Sánchez Vela, MD.

HOPP SEP

03/02/22

Recommended reads:

- Primer of the Molecular Biology of Cancer. DeVita 2021.

- The Biology of Cancer. 2nd edition. Weinberg 2014.

Available through MSK library (print and online formats).

sanchezp@mskcc.org

As part of your project, you are interested in **modelling** mutations that frequently occur in **cancer patients**. For this purpose, you are reviewing **MSK-IMPACT** clinical sequencing results using the **cBioPortal** platform. One of the genes that most commonly is found to be mutated in this dataset is **TP53**, a known **tumor suppressor** gene. What are the characteristics of these types of genes?

A) In cancer patients, **inactivating mutations** are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like **promoter methylation**.

C) Loss of tumor suppressors decreases the likelihood of **malignant transformation.**

D) Mutation in tumor suppressors genes can only be somatic, and they don’t occur in the **germline**.

As part of your project, you are interested in **modelling** mutations that frequently occur in **cancer patients**. For this purpose, you are reviewing **MSK-IMPACT** clinical sequencing results using the **cBioPortal** platform. One of the genes that most commonly is found to be mutated in this dataset is **TP53**, a known **tumor suppressor** gene. What are the characteristics of these types of genes?

A) In cancer patients, **inactivating mutations** are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like **promoter methylation**.

C) Loss of tumor suppressors decreases the likelihood of **malignant transformation.**

D) Mutation in tumor suppressors genes can ~~only~~ be **somatic**, and ~~they don't~~ occur in the **germline**.

As part of your project, you are interested in **modelling** mutations that frequently occur in **cancer patients**. For this purpose, you are reviewing **MSK-IMPACT** clinical sequencing results using the **cBioPortal** platform. One of the genes that most commonly is found to be mutated in this dataset is **TP53**, a known **tumor suppressor** gene. What are the characteristics of these types of genes?

A) In cancer patients, **inactivating mutations** are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes cannot occur due to non-mutational processes like **promoter methylation**.

C) Loss of tumor suppressors ~~decreases~~ INCREASE the likelihood of **malignant transformation.**

D) Mutation in tumor suppressors genes can ~~only~~ be **somatic**, and ~~they don't~~ occur in the **germline**.

As part of your project, you are interested in **modelling** mutations that frequently occur in **cancer patients**. For this purpose, you are reviewing **MSK-IMPACT** clinical sequencing results using the **cBioPortal** platform. One of the genes that most commonly is found to be mutated in this dataset is **TP53**, a known **tumor suppressor** gene. What are the characteristics of these types of genes?

A) In cancer patients, **inactivating mutations** are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes ~~cannot~~ CAN occur due to non-mutational processes like **promoter methylation**.

C) Loss of tumor suppressors ~~decreases~~ INCREASE the likelihood of **malignant transformation.**

D) Mutation in tumor suppressors genes can ~~only~~ be **somatic**, and ~~they don't~~ occur in the **germline**.

As part of your project, you are interested in **modelling** mutations that frequently occur in **cancer patients**. For this purpose, you are reviewing **MSK-IMPACT** clinical sequencing results using the **cBioPortal** platform. One of the genes that most commonly is found to be mutated in this dataset is **TP53**, a known **tumor suppressor** gene. What are the characteristics of these types of genes?

A) In cancer patients, **inactivating mutations** are the most frequent type of mutations occurring in tumor suppressors genes.

B) Loss of function in tumor suppressors genes ~~cannot~~ CAN occur due to non-mutational processes like **promoter methylation**.

C) Loss of tumor suppressors ~~decreases~~ INCREASE the likelihood of **malignant transformation.**

D) Mutation in tumor suppressors genes can ~~only~~ be **somatic**, and ~~they don't~~ occur in the **germline**.

After acknowledging the importance of TP53 as a tumor suppressor, you are interested in understanding the effect of other tumor suppressors. Which of the following genes is not a tumor suppressor?

A) RB, a gene involved in controlling the pass through a cell cycle checkpoint..
B) APC, a gene involved in downregulating the expression of beta-catenin, a known proto-oncogene.
C) BRCA, a gene responsible for the reparation of DNA.
D) RAS, a gene involved in promoting cell growth.

After acknowledging the importance of TP53 as a tumor suppressor, you are interested in understanding the effect of other tumor suppressors. Which of the following genes is **NOT** a tumor suppressor?

A) RB, a gene involved in controlling the pass through a cell cycle checkpoint.
B) APC, a gene involved in downregulating the expression of beta-catenin, a known proto-oncogene.
C) BRCA, a gene responsible for the reparation of DNA.
D) RAS, a gene involved in promoting cell growth.

After acknowledging the importance of TP53 as a tumor suppressor, you are interested in understanding the effect of other tumor suppressors. Which of the following genes is **NOT** a tumor suppressor?

A) RB, a gene involved in controlling the pass through a cell cycle checkpoint.

B) APC, a gene involved in downregulating the expression of beta-catenin, a known proto-oncogene.

C) BRCA, a gene responsible for the reparation of DNA.

D) RAS, a gene involved in promoting cell growth.

- X + = -

After acknowledging the importance of TP53 as a tumor suppressor, you are interested in understanding the effect of other tumor suppressors. Which of the following genes is **NOT** a tumor suppressor?

A) RB, a gene involved in controlling the pass through a cell cycle checkpoint.

B) APC, a gene involved in downregulating the expression of beta-catenin, a known proto-oncogene.

C) BRCA, a gene responsible for the reparation of DNA.

D) RAS, a gene involved in promoting cell growth.

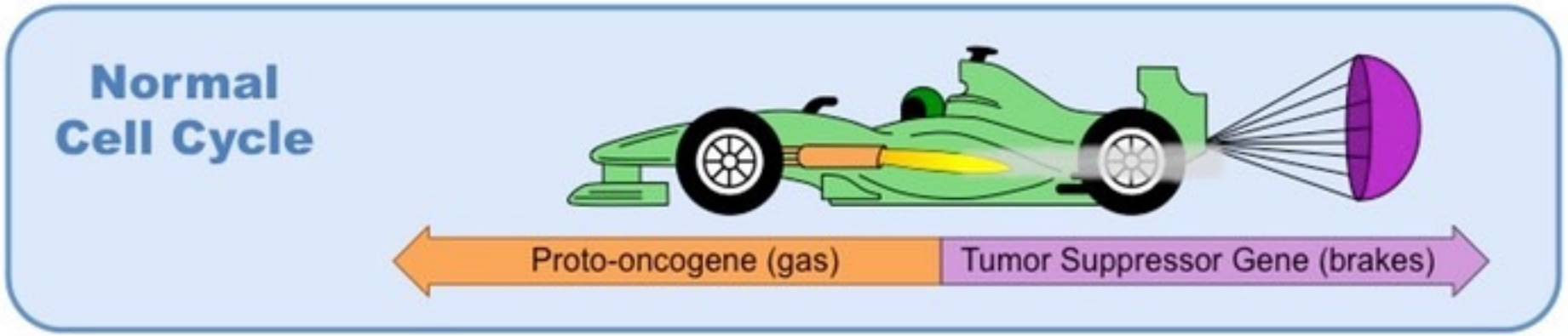
After acknowledging the importance of TP53 as a tumor suppressor, you are interested in understanding the effect of other tumor suppressors. Which of the following genes is **NOT** a tumor suppressor?

A) RB, a gene involved in controlling the pass through a cell cycle checkpoint.

B) APC, a gene involved in downregulating the expression of beta-catenin, a known proto-oncogene.

C) BRCA, a gene responsible for the reparation of DNA.

D) RAS, a gene involved in promoting cell growth.



After acknowledging the importance of TP53 as a tumor suppressor, you are interested in understanding the effect of other tumor suppressors. Which of the following genes is **NOT** a tumor suppressor?

A) RB, a gene involved in controlling the pass through a cell cycle checkpoint.

B) APC, a gene involved in downregulating the expression of beta-catenin, a known proto-oncogene.

C) BRCA, a gene responsible for the reparation of DNA.

D) RAS, a gene involved in promoting cell growth.

Understanding Cancer Classification and Modelling of Tumor Suppressors

Pablo Sánchez Vela, MD.

HOPP SEP

03/02/22

Recommended reads:

- Primer of the Molecular Biology of Cancer. DeVita 2021.

- The Biology of Cancer. 2nd edition. Weinberg 2014.

Available through MSK library (print and online formats).

sanchezp@mskcc.org