

Principles and pathology of cancer

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Lecture outline

- Review the “hallmarks” of cancer
- Discuss current views about how cancer starts and progresses
- Introduce the concept of “cancer stem cells” and how they relate to cancer heterogeneity
- Discuss what make cancers lethal – metastasis and other factors
- Goal: to set the stage for the other lectures

Definitions

- Oncogenes: normal genes that promote cancer when they are mutated, translocated, or amplified. They affect proliferative signal transduction pathways
- Tumor suppressor genes: normal genes that promote cancer when they are lost. Most regulate DNA repair and/or cell cycle progression

More definitions

- Amplification: occurs when a region of a chromosome containing an oncogene is multiplied (can be up to 20-fold or more)
- Deletion: occurs when a region of a chromosome containing a tumor suppressor is lost
- Translocation: occurs when part of one chromosome is fused to part of another
- Epigenetic: a change in mRNA expression caused by reversible mechanisms (usually DNA methylation or post-translational modifications of histones)

More definitions

- Tumor progression: occurs as cancers acquire more genetic and epigenetic defects and become clinically aggressive.
- Metastasis: when cancers leave their tissues of origin to colonize other sites within the body. Almost always used when describing solid tumors and not hematopoietic malignancies.
- Grade: appearance of a tumor under a microscope, linked to proliferation.
- Stage: measure of how disseminated a tumor is.

Cancer is a genetic and epigenetic disease

- Defined by the accumulation of “hard-wired” DNA alterations, including mutations, copy number variations (CNVs: amplifications and deletions), and translocations
- Probably occur in punctuated “bursts”
- Nevertheless, tumors are like “wounds that do not heal”, and as is true in wound healing, signals from the tumor microenvironment are critical for the development and progression of cancer

A Genetic Model for Colorectal Tumorigenesis

Review

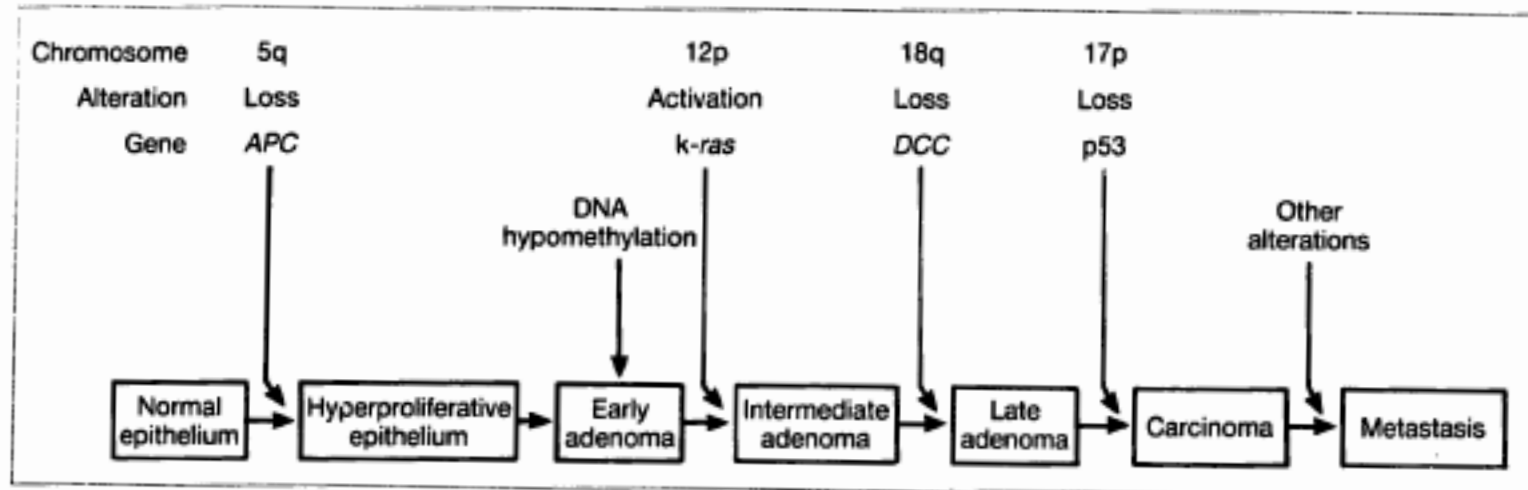
Eric R. Fearon and Bert Vogelstein

The Oncology Center

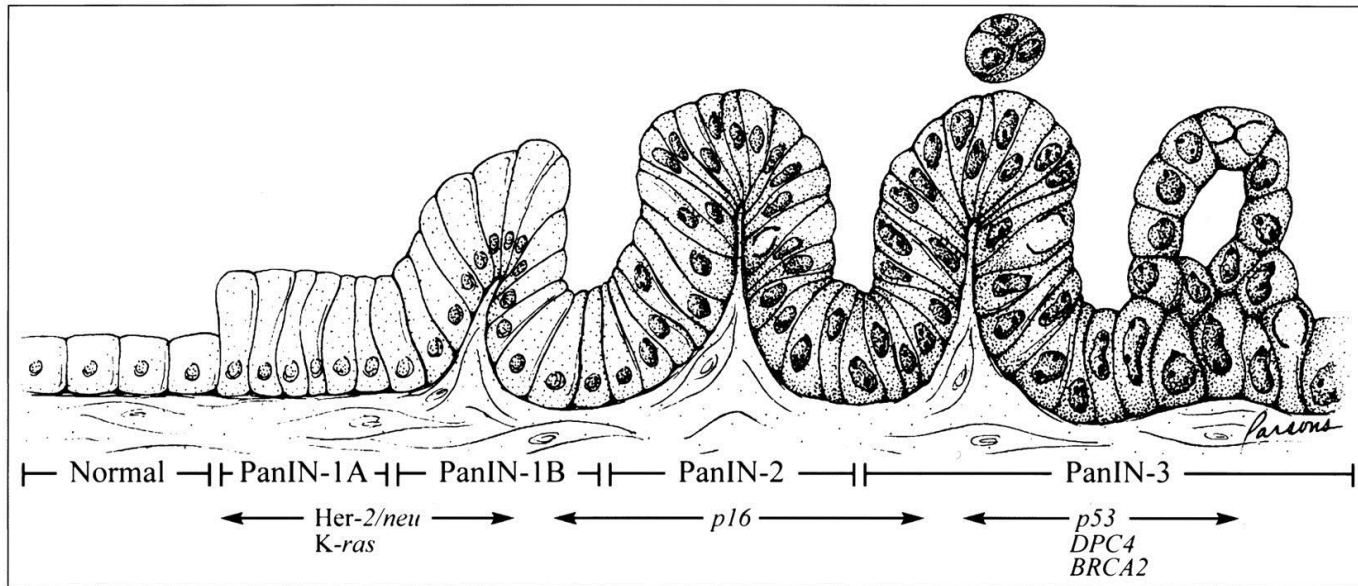
Program in Human Genetics

The Johns Hopkins University School of Medicine

Baltimore, Maryland 21231



Pancreatic cancer progression



Hruban, R. H. et al. Clin Cancer Res 2000;6:2969-2972

Factors that cause cancer

- Familial predisposition (inherited mutations)
- Ageing
- Exposure to viral and bacterial pathogens (chronic inflammation)
- Exposure to natural and man-made toxicants in the environment (UV, certain metals, cigarette smoke carcinogens)
- Oxidative stress

Cell, Vol. 100, 57–70, January 7, 2000, Copyright ©2000 by Cell Press

The Hallmarks of Cancer

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Massachusetts Institute of Technology
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Leading Edge
Review

Hallmarks of Cancer: The Next Generation

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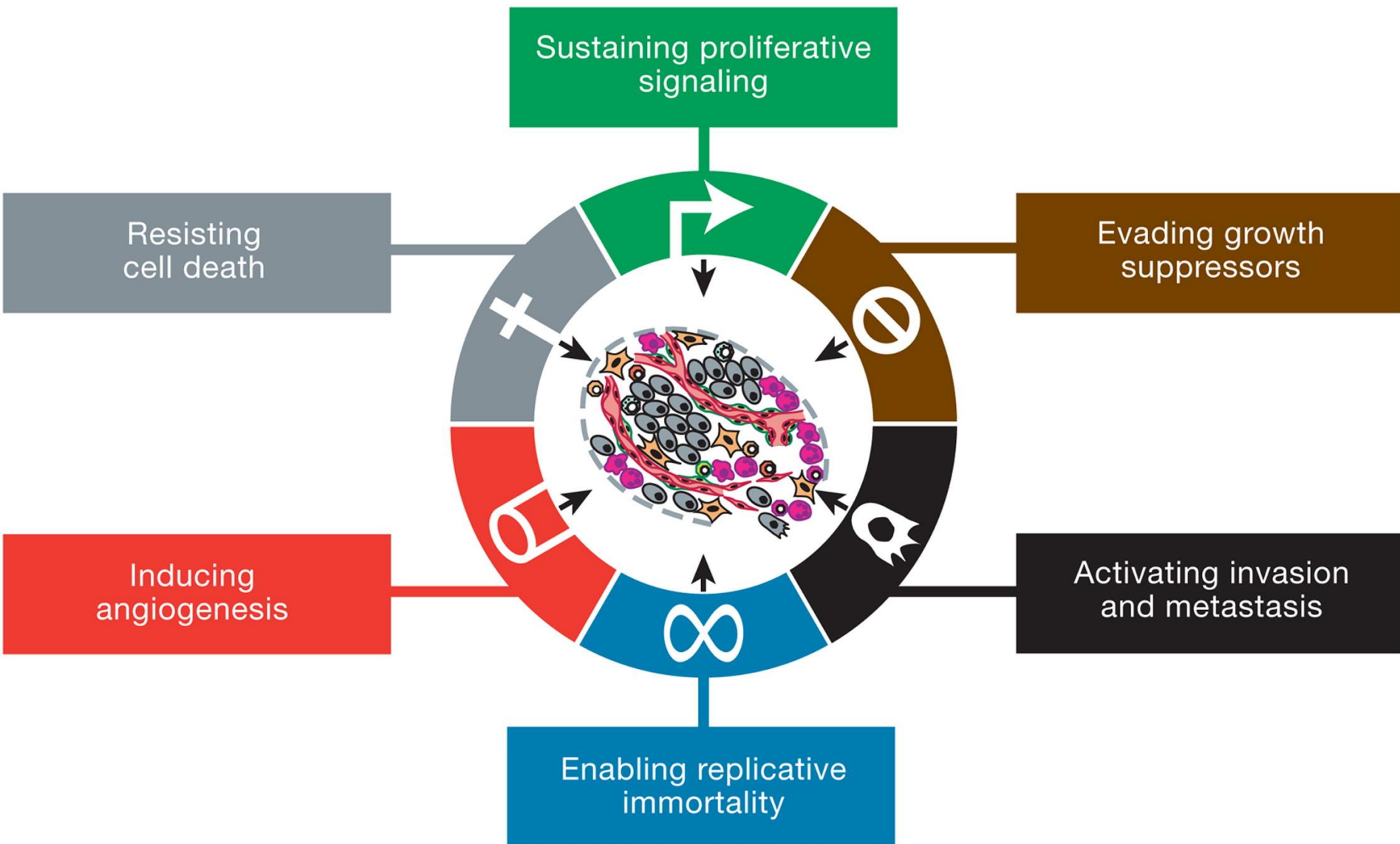
¹The Swiss Institute for Experimental Cancer Research (ISREC), School of Life Sciences, EPFL, Lausanne CH-1015, Switzerland

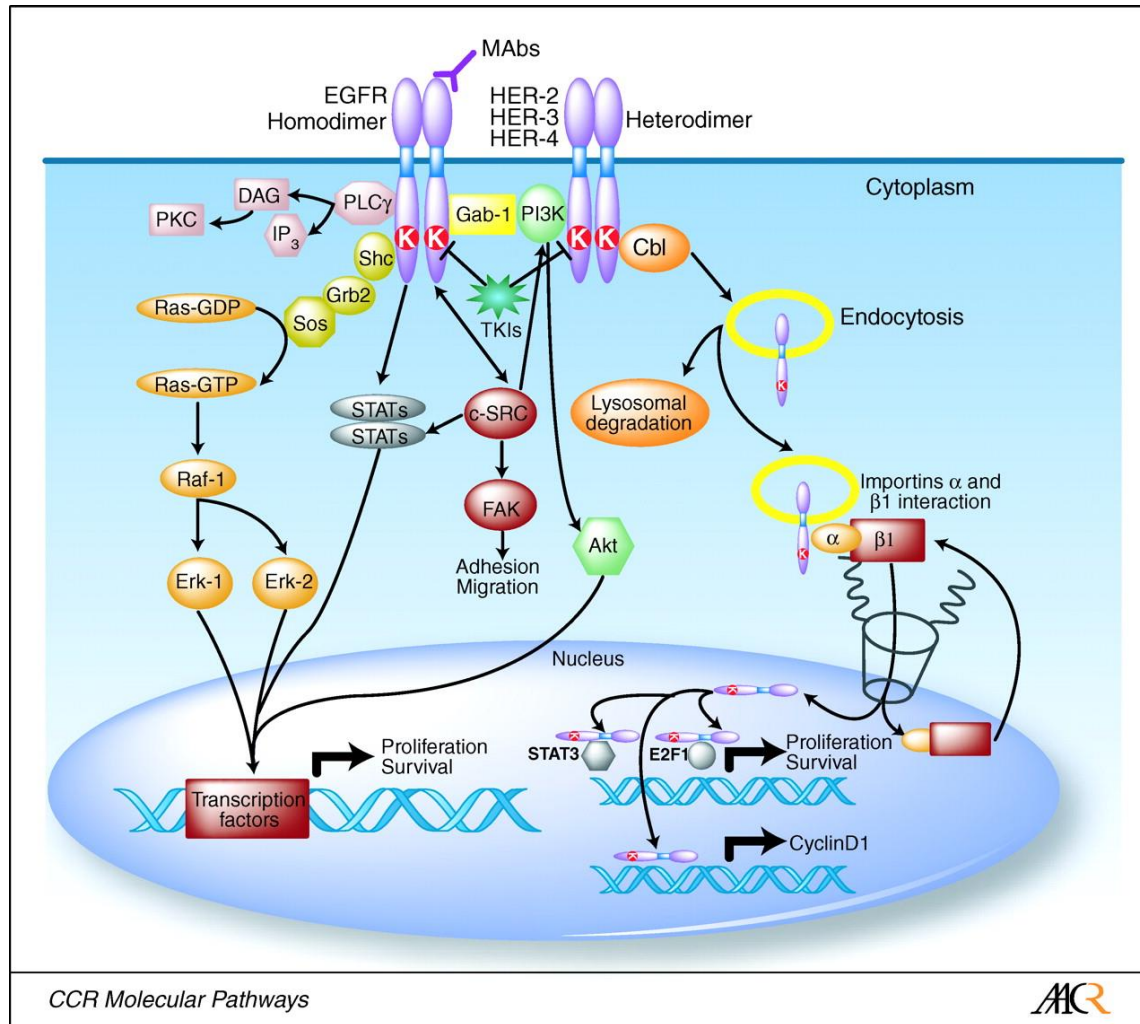
²The Department of Biochemistry & Biophysics, UCSF, San Francisco, CA 94158, USA

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Scaltriti, M. et al. Clin Cancer Res 2006;12:5268-5272

Sustained proliferative signaling

- Caused by inappropriate activation of growth factor receptors and/or their downstream signal transduction pathways.
- Tumors often make their own growth factors (ex: TGF α -EGFR)
- Growth factor receptors are often amplified (EGFR, HER2, MET, FGFR3, etc)
- Growth factor receptors can be constitutively activated by mutation or chromosomal translocation (EGFR, FGFRs, HER2)
- Downstream signal transduction genes are often mutated or amplified (Ras, PIK3CA, AKT, TSC-1, mTOR, PTEN).
- Genes that promote cell cycle progression are often amplified (Myc, cyclin D, aurora A, etc)

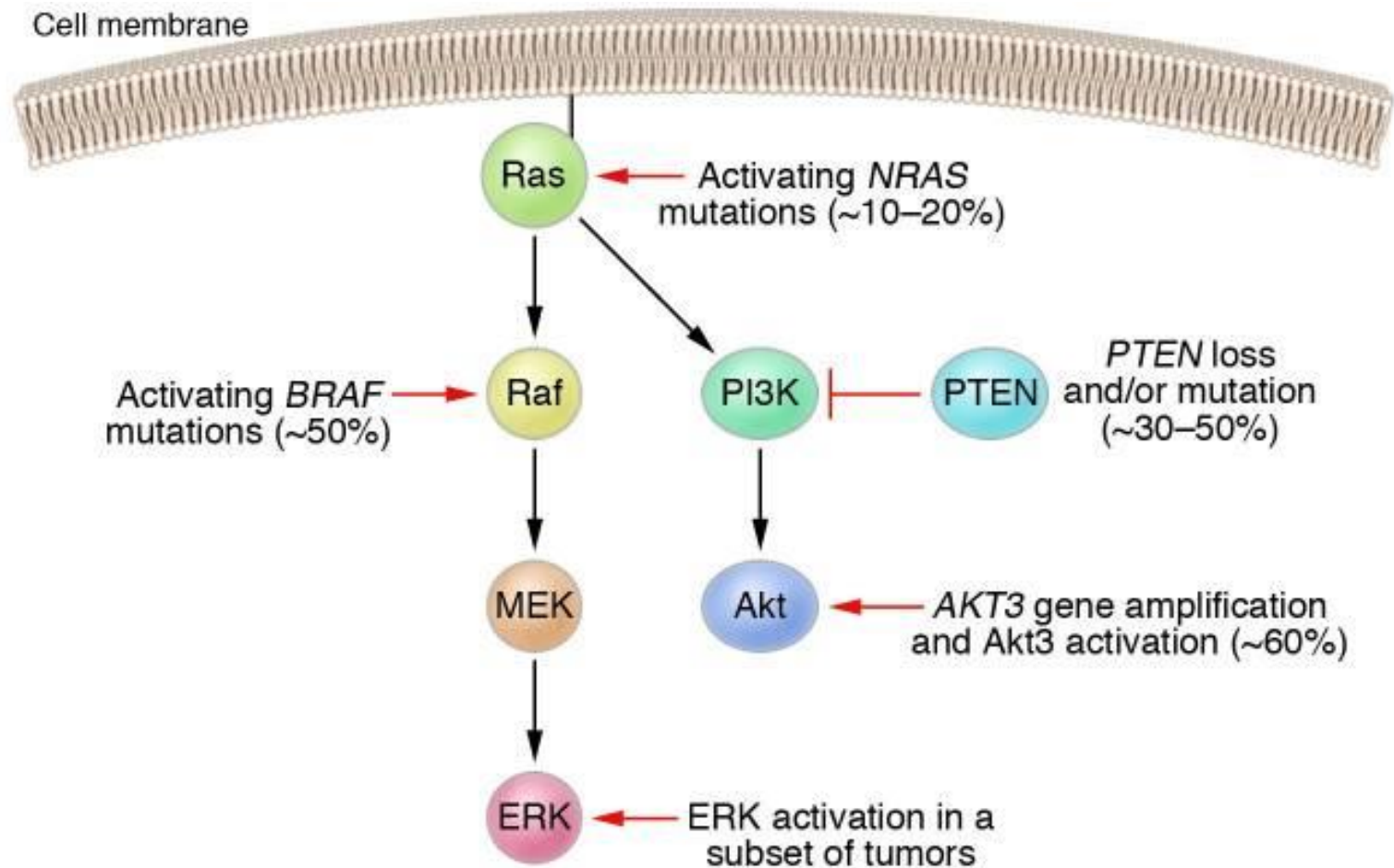


Melanoma genetics and the development of rational therapeutics

Yakov Chudnovsky, Paul A. Khavari, and Amy E. Adams

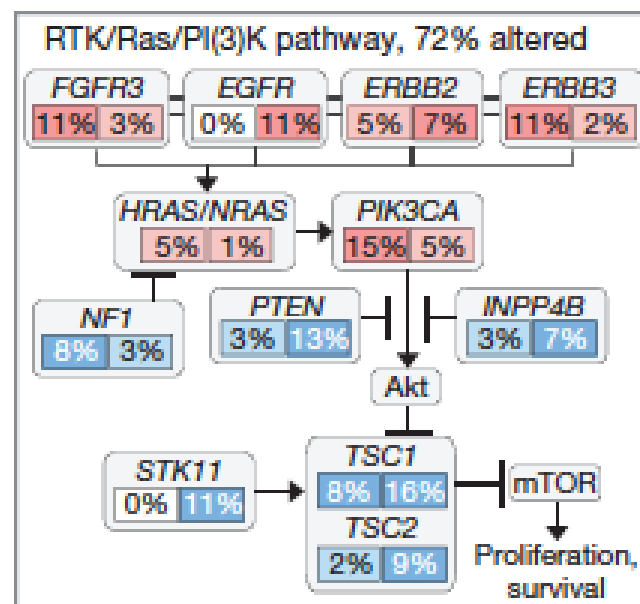
Veterans Affairs Palo Alto Healthcare System, Palo Alto, California. Program in Epithelial Biology, Stanford University School of Medicine, Stanford, California, USA.

Ras pathway activation in melanoma



Comprehensive molecular characterization of urothelial bladder carcinoma

The Cancer Genome Atlas Research Network*



Evading growth suppressors

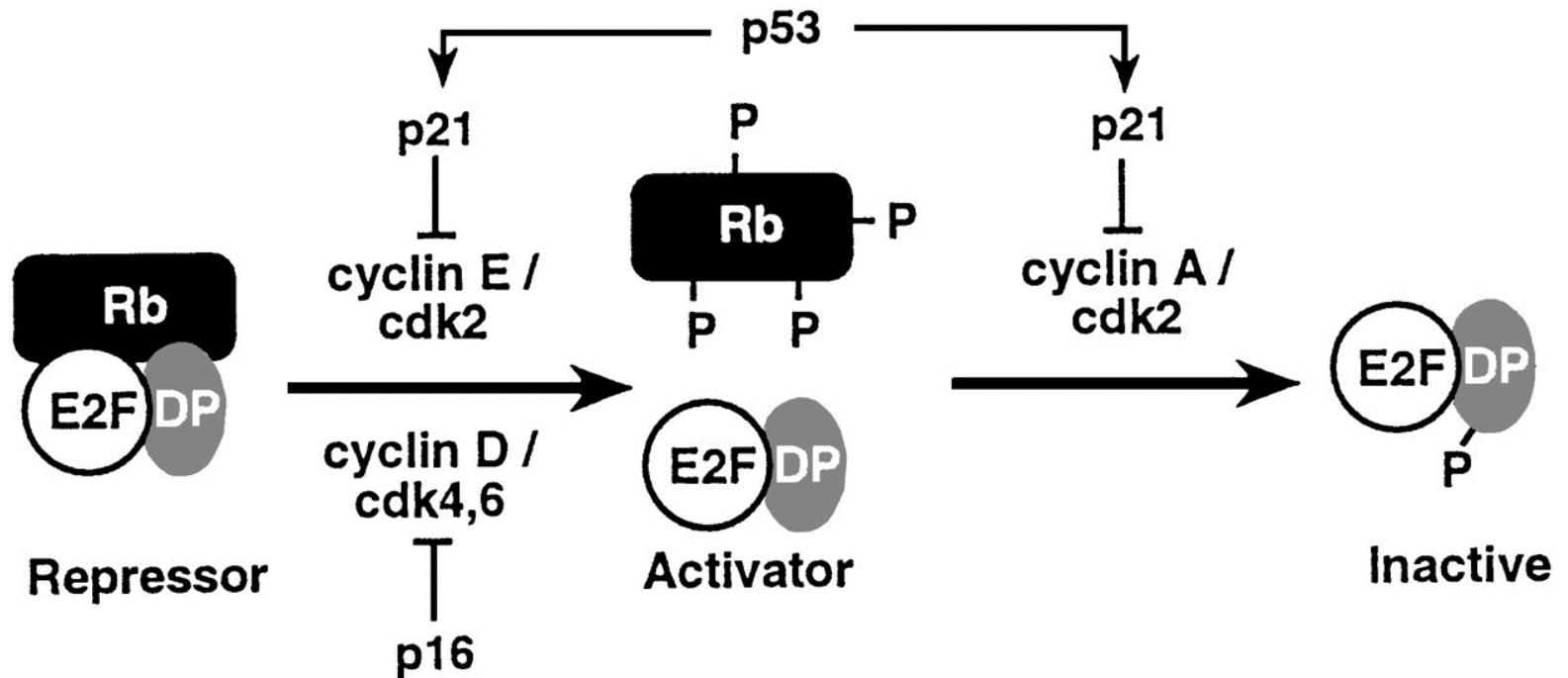
- Cancers typically inactivate the Rb and p53 pathways
- In normal cells, the Rb pathway is inhibited by growth factor receptors and activated by certain growth-inhibitory cytokines (TGF β)
- Cancers lose TGF β responsiveness by acquiring mutations in TGF β receptors, downstream signal transduction components (SMAD4), or the Rb pathway itself (p16, Rb)
- Cancers lose p53 function by inactivating p53 itself (point mutations, deletions), by amplifying its inhibitor (MDM2), and by silencing p53's effector, p21 (DNA methylation)

Control of Rb function

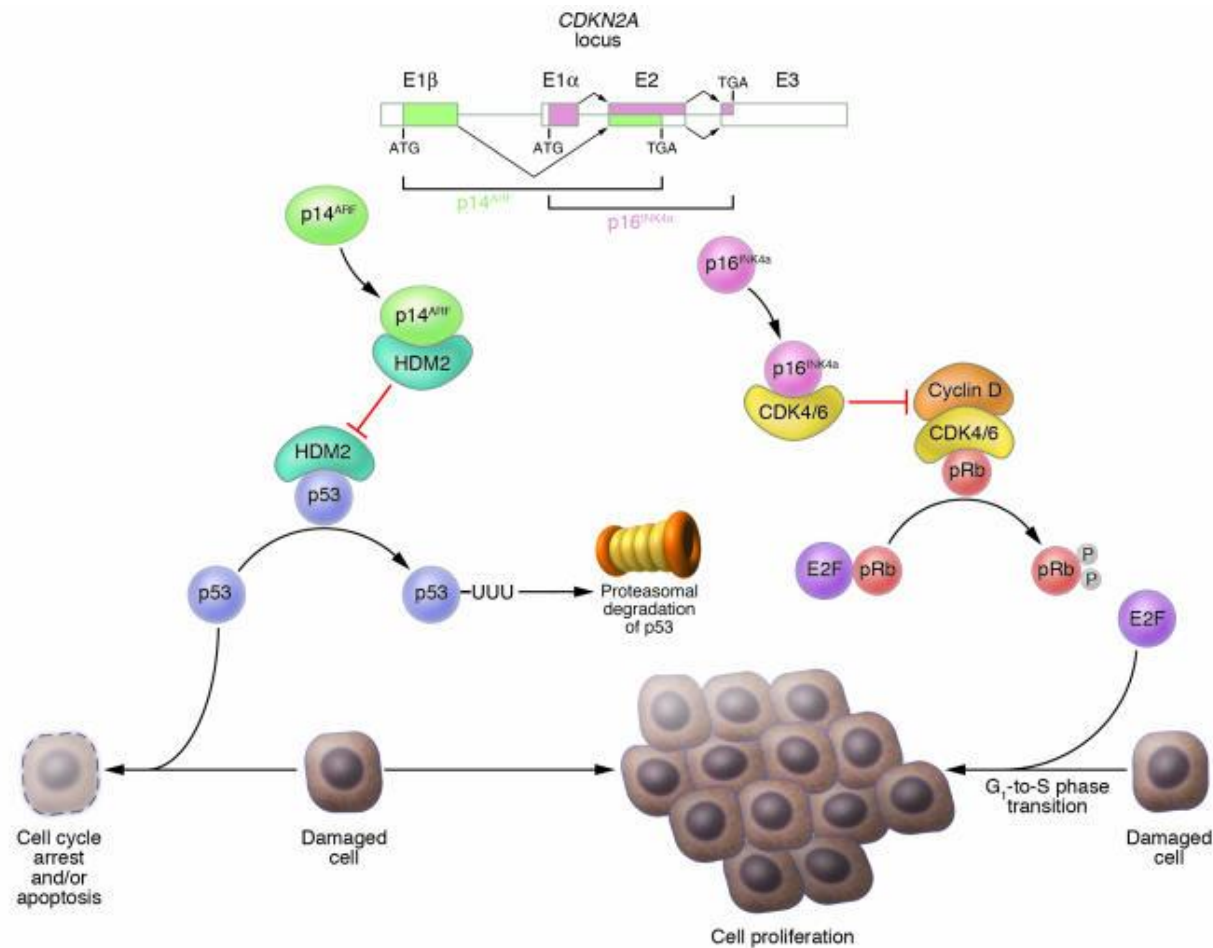
G0 / early G1

Late G1 / early S

S, G2, M



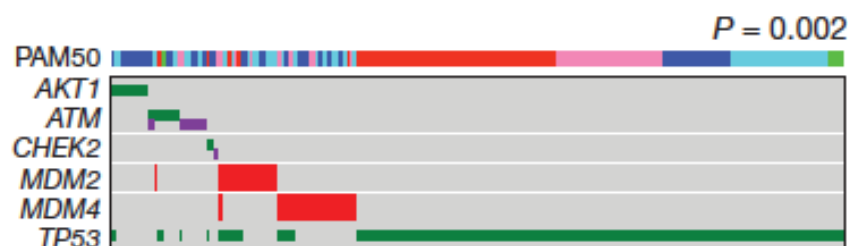
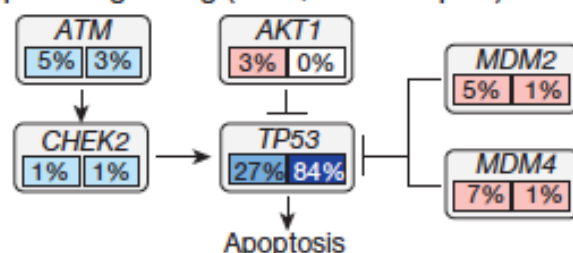
Functions of p14ARF and p16



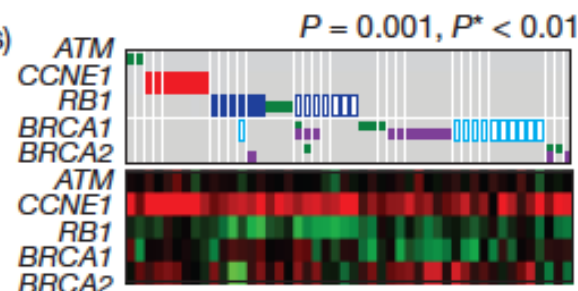
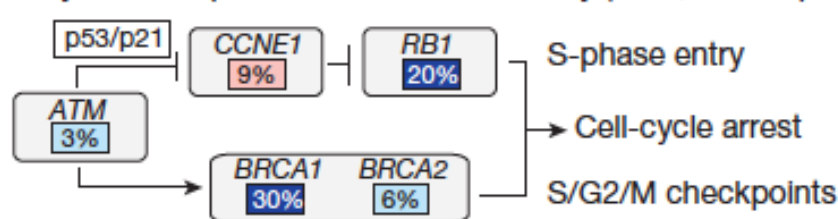
Comprehensive molecular portraits of human breast tumours

The Cancer Genome Atlas Network*

b p53 - signalling (49%, 227 samples)



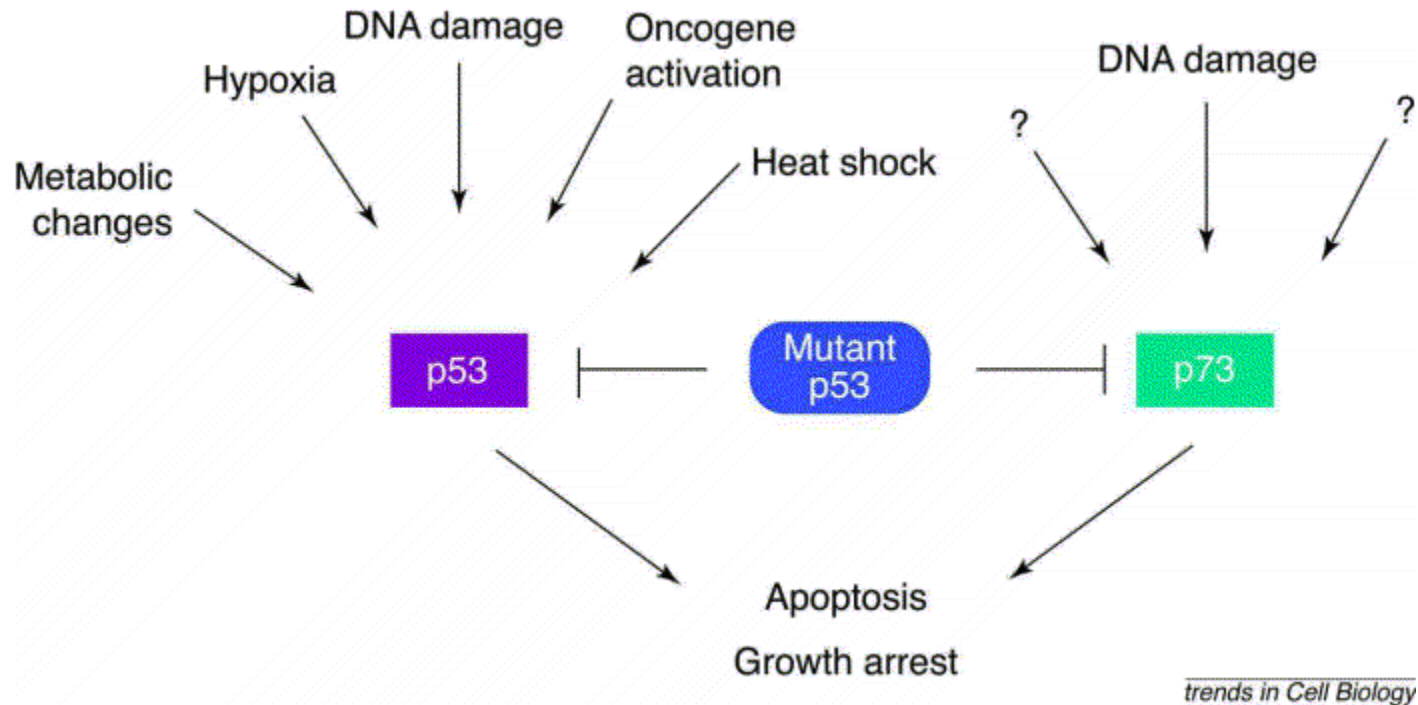
c Cell cycle checkpoints - Basal tumours only (57%, 46 samples)



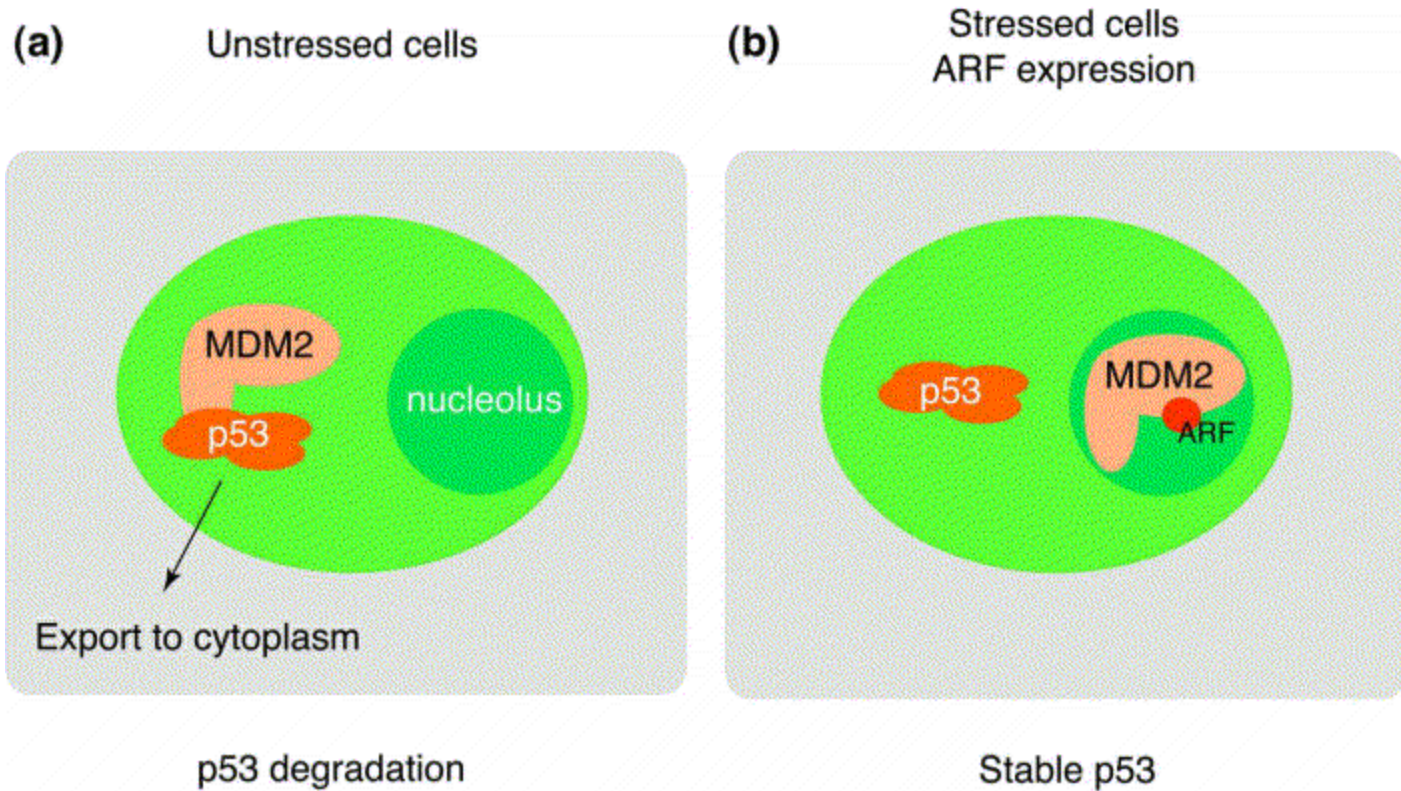
Evading apoptosis

- p53 promotes apoptosis in some normal (especially hematopoietic) cells
- Loss of p53 allows for evasion of apoptosis
- AKT pathway activation – blocks apoptosis induced by growth factor withdrawal
- Exiting the cell cycle (***quiescence***) also promotes apoptosis resistance
- ***Autophagy***: can sustain quiescent cells for long periods when nutrients and oxygen are scarce

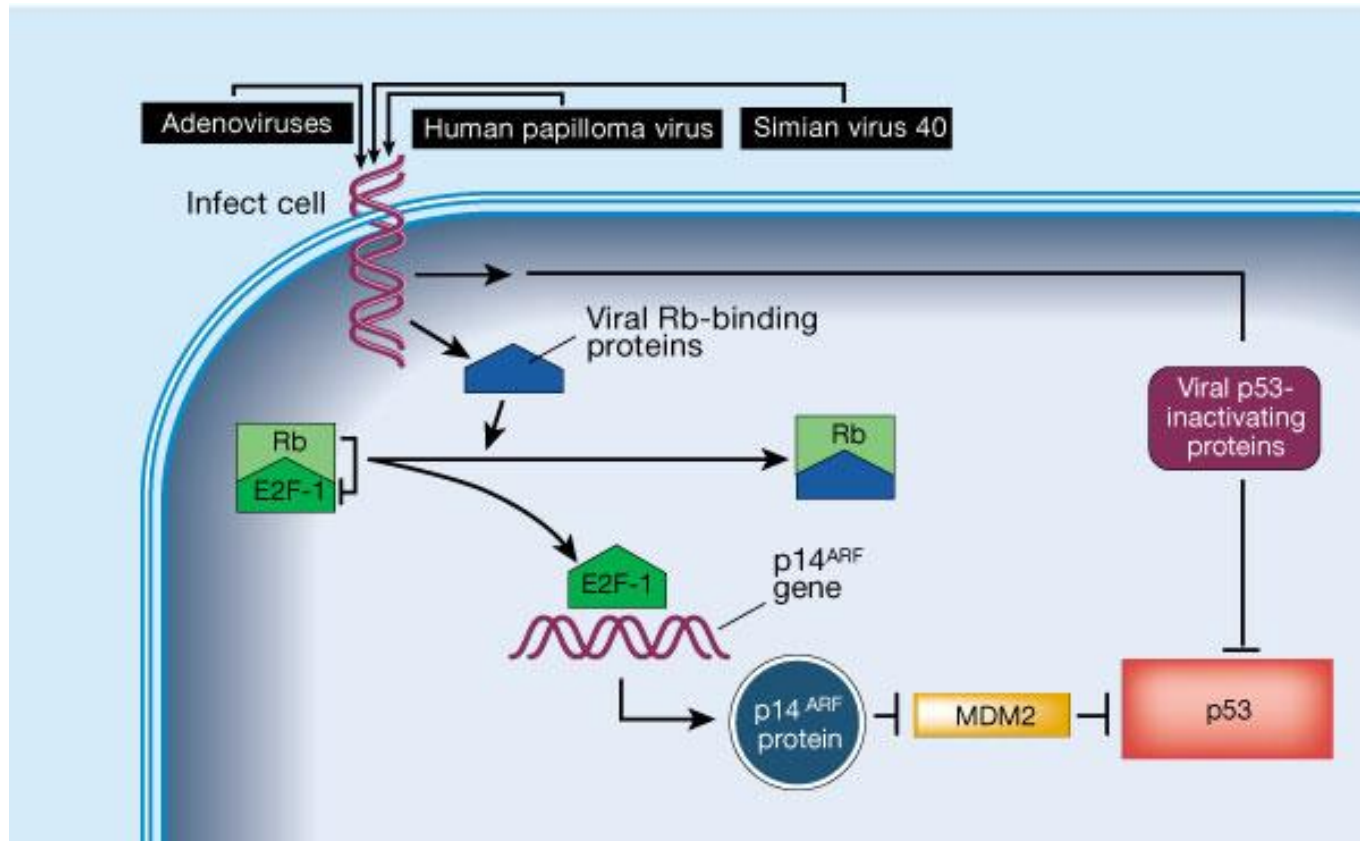
Many stimuli activate p53



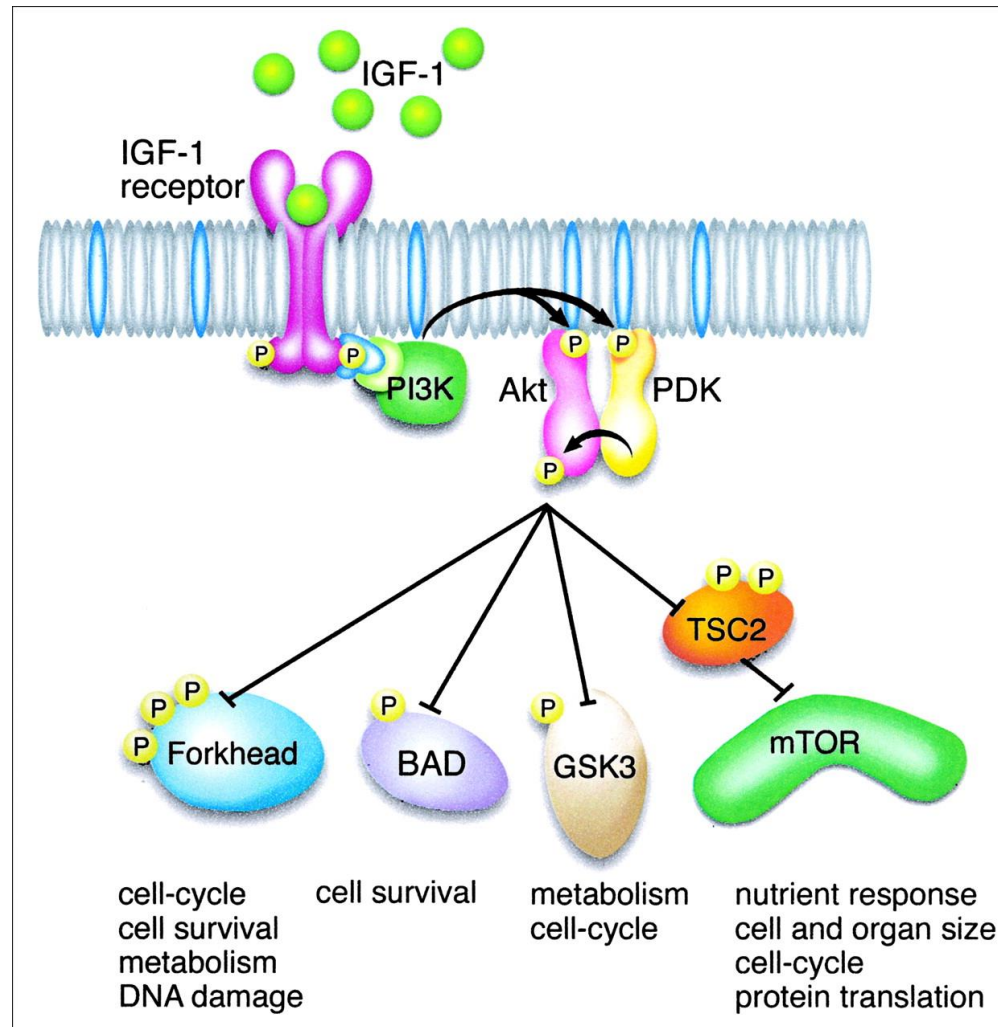
Control of p53 by MDM-2 and p14ARF



Viral disruption of p53 pathway regulation



Binding of growth factor ligands activates kinase receptors leading to recruitment of PI3K to receptor complex

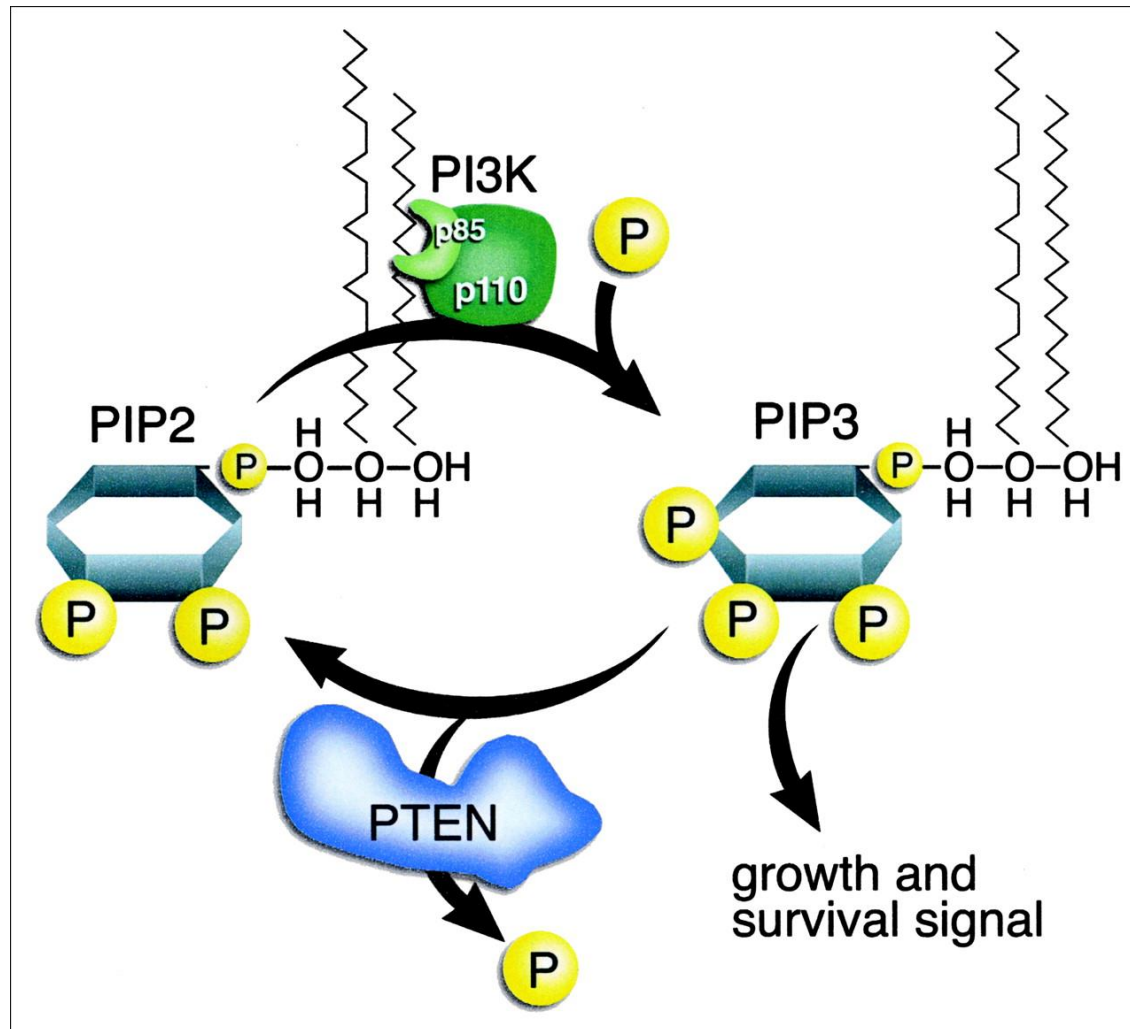


Sansal, I. et al. J Clin Oncol; 22:2954-2963 2004

The AKT pathway is negatively regulated by PTEN

- PTEN = phosphatase on chromosome 10
- Also known as MMAC = mutated in multiple adenocarcinomas
- Lipid phosphatase

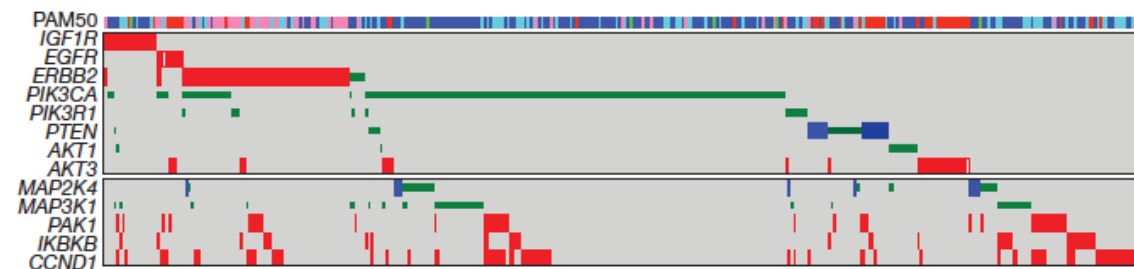
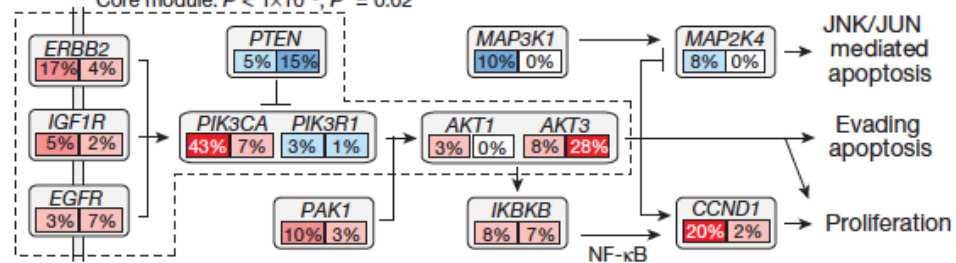
PTEN (blue), a lipid phosphatase



Sansal, I. et al. J Clin Oncol; 22:2954-2963 2004

a PI(3)K/Akt - signalling (77%, 357 samples)

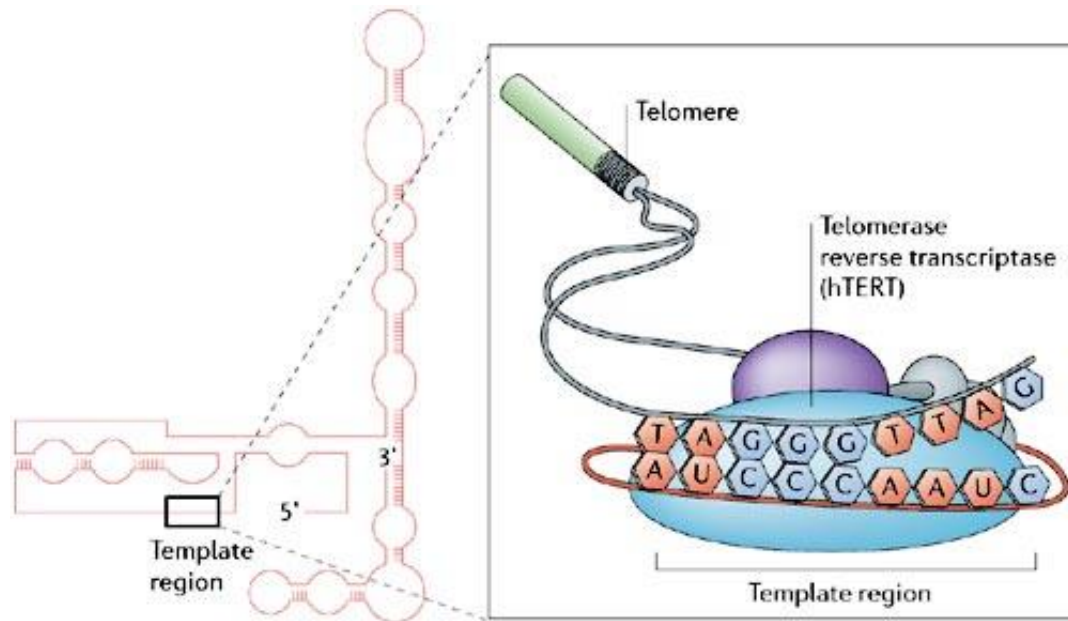
Core module: $P < 1 \times 10^{-3}$, $P^* = 0.02$



Limitless replicative potential

- Hayflick: First recognized that mammalian cells contain an in-built mechanism to limit proliferative potential
- It is now known that the erosion of telomeres is responsible for this phenomenon
- Tumor cells ultimately reach a stage of “crisis” and will undergo mitotic catastrophe if telomere length is not maintained
- Strategies: increase expression of telomerase (85-90%), acquire ALT/recombination-based mechanism

Structure of telomerase



***TERT* promoter mutations occur frequently in gliomas and a subset of tumors derived from cells with low rates of self-renewal**

Patrick J. Killela^{a,1}, Zachary J. Reitman^{a,1}, Yuchen Jiao^{b,1}, Chetan Bettegowda^{b,c,1}, Nishant Agrawal^{b,d}, Luis A. Diaz, Jr.^b, Allan H. Friedman^a, Henry Friedman^a, Gary L. Gallia^{c,d}, Beppino C. Giovanella^e, Arthur P. Grollman^f, Tong-Chuan He^g, Yiping He^a, Ralph H. Hruban^h, George I. Jallo^c, Nils Mandahlⁱ, Alan K. Meeker^{h,m}, Fredrik Mertensⁱ, George J. Netto^{h,i}, B. Ahmed Rasheed^a, Gregory J. Riggins^c, Thomas A. Rosenquist^f, Mark Schiffman^j, Ie-Ming Shih^h, Dan Theodorescu^k, Michael S. Torbenson^h, Victor E. Velculescu^b, Tian-Li Wang^h, Nicolas Wentzensen^j, Laura D. Wood^h, Ming Zhang^b, Roger E. McLendon^a, Darell D. Bigner^a, Kenneth W. Kinzler^b, Bert Vogelstein^{b,2}, Nickolas Papadopoulos^b, and Hai Yan^{a,2}

Table 1. Frequency of *TERT* promoter mutations

Tumor type*	No. tumors	No. tumors mutated (%)
Chondrosarcoma	2	1 (50)
Dysembryoplastic neuroepithelial tumor	3	1 (33.3)
Endometrial cancer	19	2 (10.5)
Ependymoma	36	1 (2.7)
Fibrosarcoma	3	1 (33.3)
Glioma [†]	223	114 (51.1)
Hepatocellular carcinoma	61	27 (44.2)
Medulloblastoma	91	19 (20.8)
Myxofibrosarcoma	10	1 (10.0)
Myxoid liposarcoma	24	19 (79.1)
Neuroblastoma	22	2 (9)
Osteosarcoma	23	1 (4.3)
Ovarian, clear cell carcinoma	12	2 (16.6)
Ovarian, low grade serous	8	1 (12.5)
Solitary fibrous tumor (SFT)	10	2 (20.0)
Squamous cell carcinoma of head and neck	70	12 (17.1)
Squamous cell carcinoma of the cervix	22	1 (4.5)
Squamous cell carcinoma of the skin	5	1 (20)
Urothelial carcinoma of bladder	21	14 (66.6)
Urothelial carcinoma of upper urinary epithelium	19	9 (47.3)

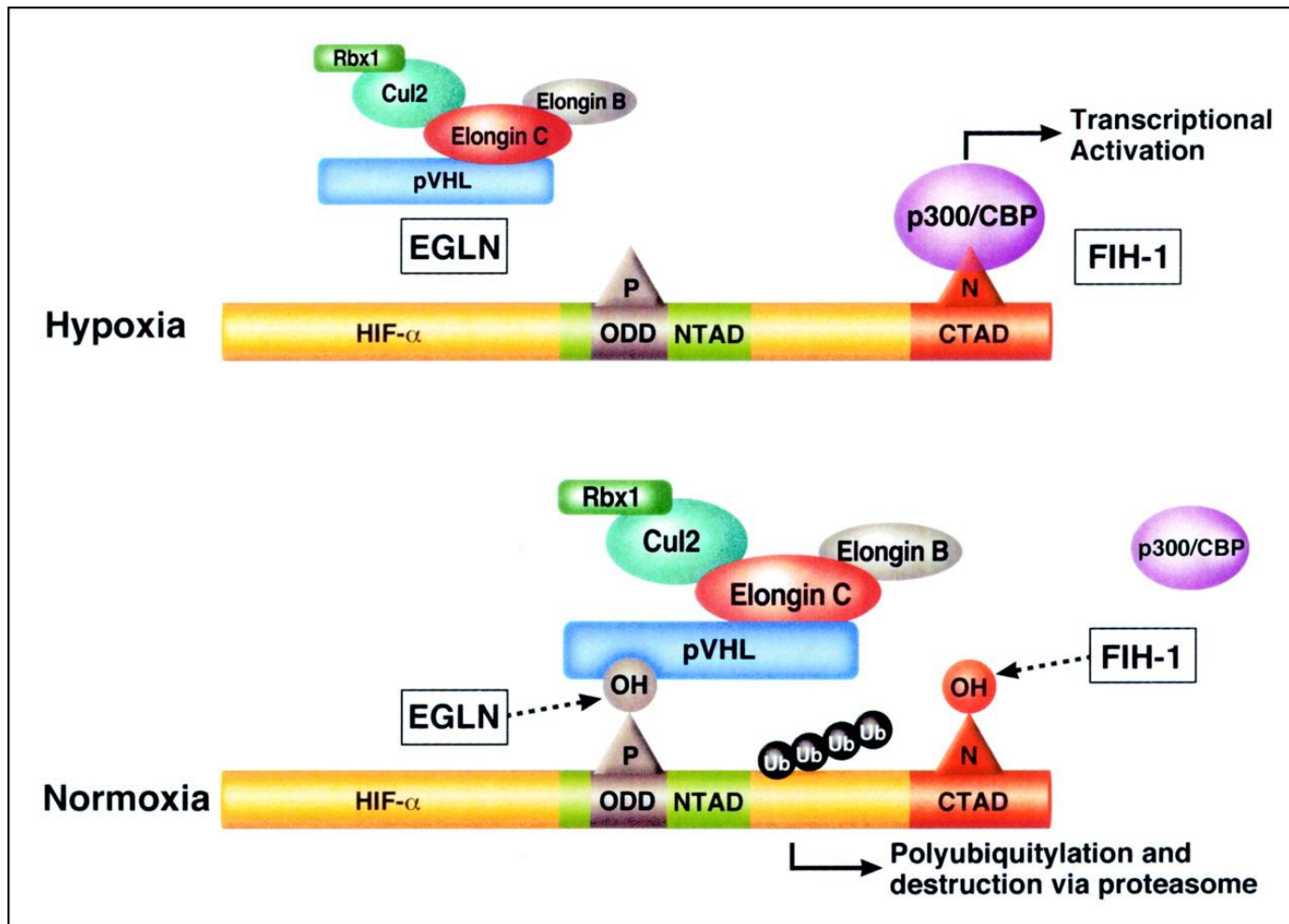
Sustained angiogenesis

- Tumors cannot grow beyond the diffusion distance of oxygen (100 μm)
- Tumor progression therefore involves an “angiogenic switch” (Hanahan), whereby tumors acquire the capacity to stimulate angiogenesis in a malregulated fashion
- Mechanisms: oncogene/growth factor activation, Von Hippel Lindau (VHL) gene inactivation in kidney cancers

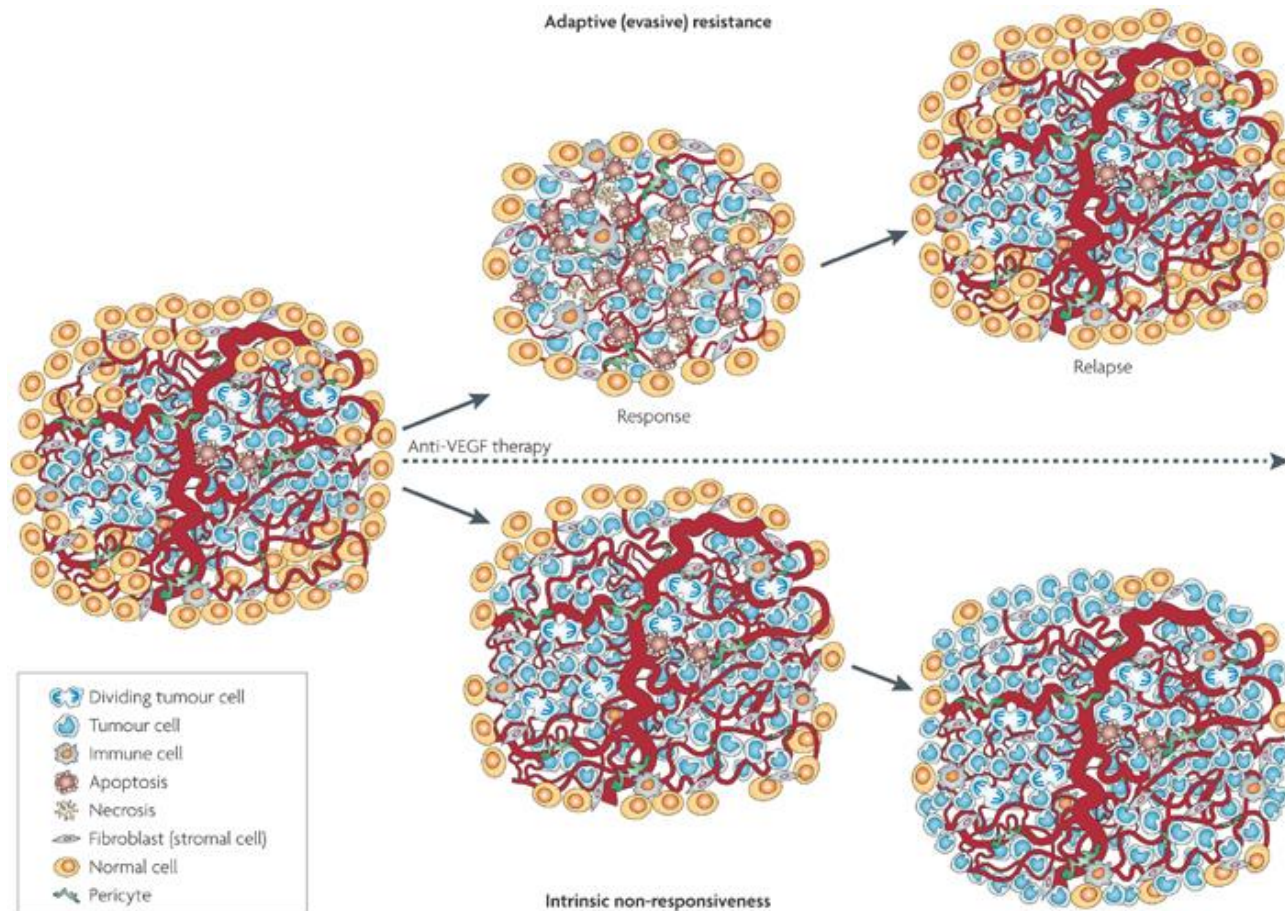
HIF-1 α : A key regulator of tumor angiogenesis

- Dimerizes with another protein (ARNT) to form a hypoxia-sensitive transcription factor
- Drives expression of VEGF, TGF α , PDGF, erythropoietin
- Targeted for degradation by the VHL protein
- Kidney cancers are highly angiogenic and sensitive to inhibitors of the VEGF-VEGF receptor pathway

Fig 1. Regulation of hypoxia-inducible factor alpha (HIF{alpha}) by the von Hippel-Lindau tumor suppressor protein (pVHL)

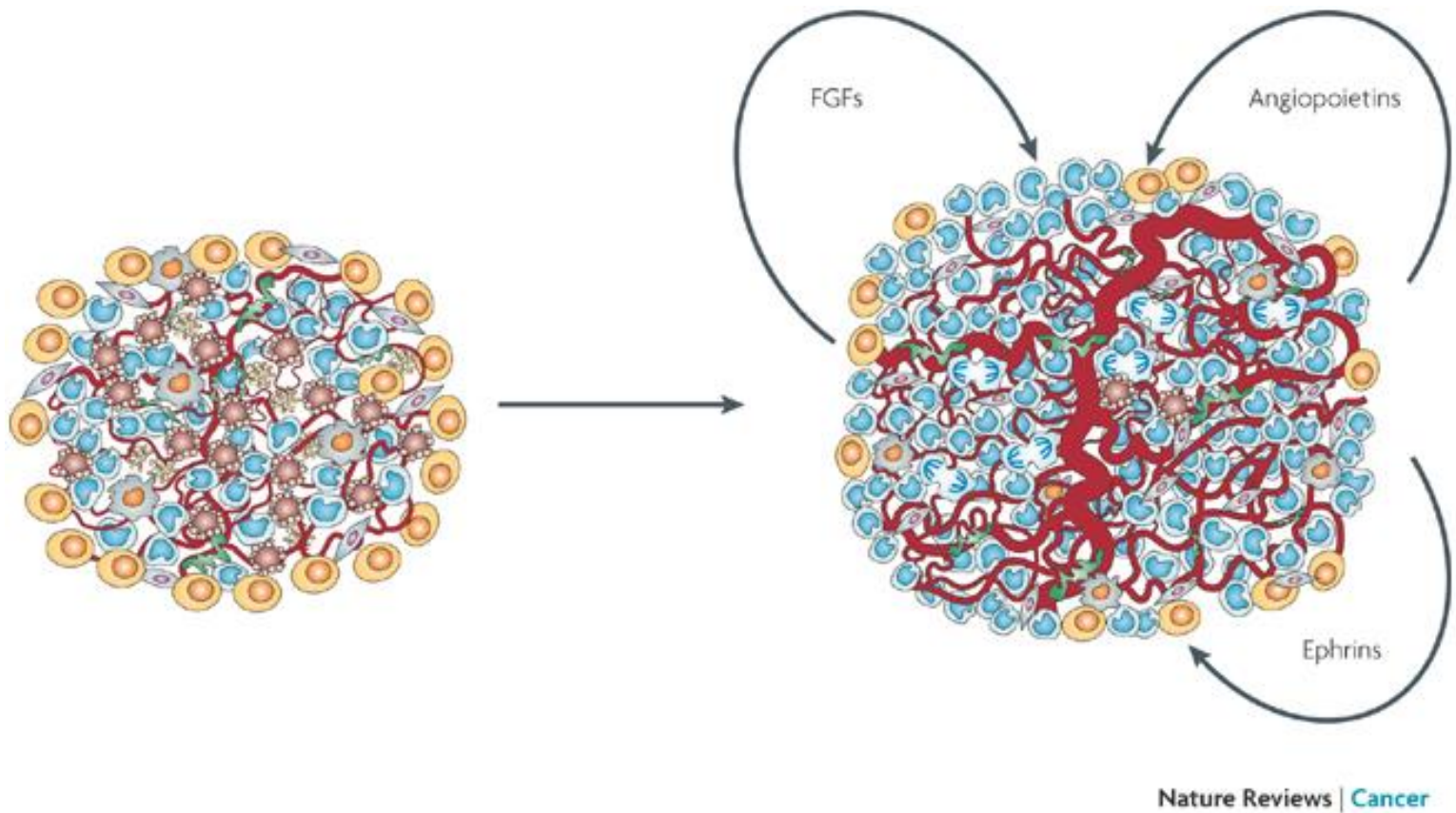


Kim, W. Y. et al. J Clin Oncol; 22:4991-5004 2004



Nature Reviews | Cancer

Nature Reviews Cancer **8**, 592-603 (August 2008)



Nature Reviews Cancer 8, 592-603 (August 2008)

Tissue invasion and metastasis

- Shares many similarities with the process of wound healing (“tumors are wounds that don’t heal”)
- Associated with changes in the expression of adhesion molecules (E-cadherin and integrins) and cell polarity proteins
- Increased motility and invasiveness
- Involves a process known as “epithelial-to-mesenchymal transition” (EMT)

Physiological and pathological roles of EMT

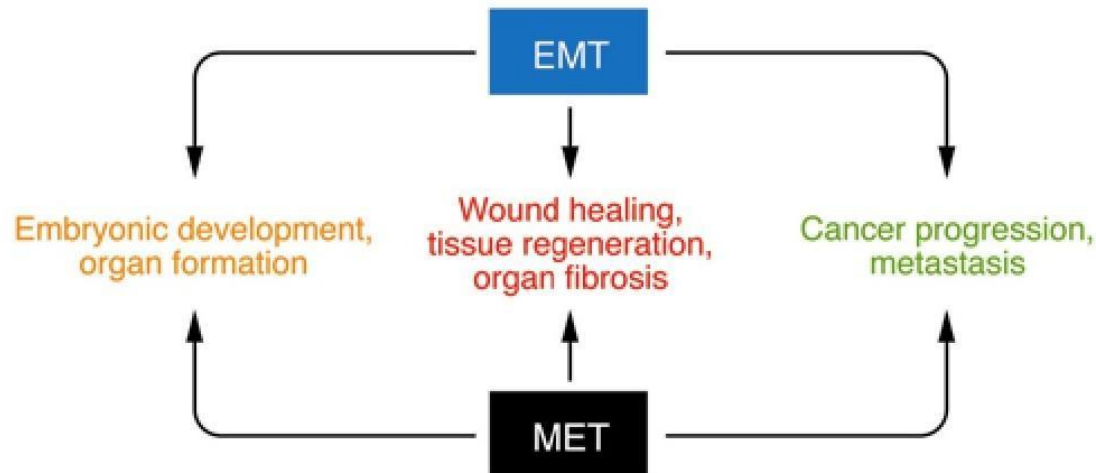


Figure 1

EMT and MET in health and disease. The evidence for EMT is compelling in embryonic development, organ formation, wound healing, tissue regeneration, organ fibrosis, cancer progression, and metastasis. The role for MET in wound healing, tissue regeneration, organ fibrosis, cancer progression, and metastasis is only speculated and rigorous evidence is still lacking.

Epithelial-to-mesenchymal transition

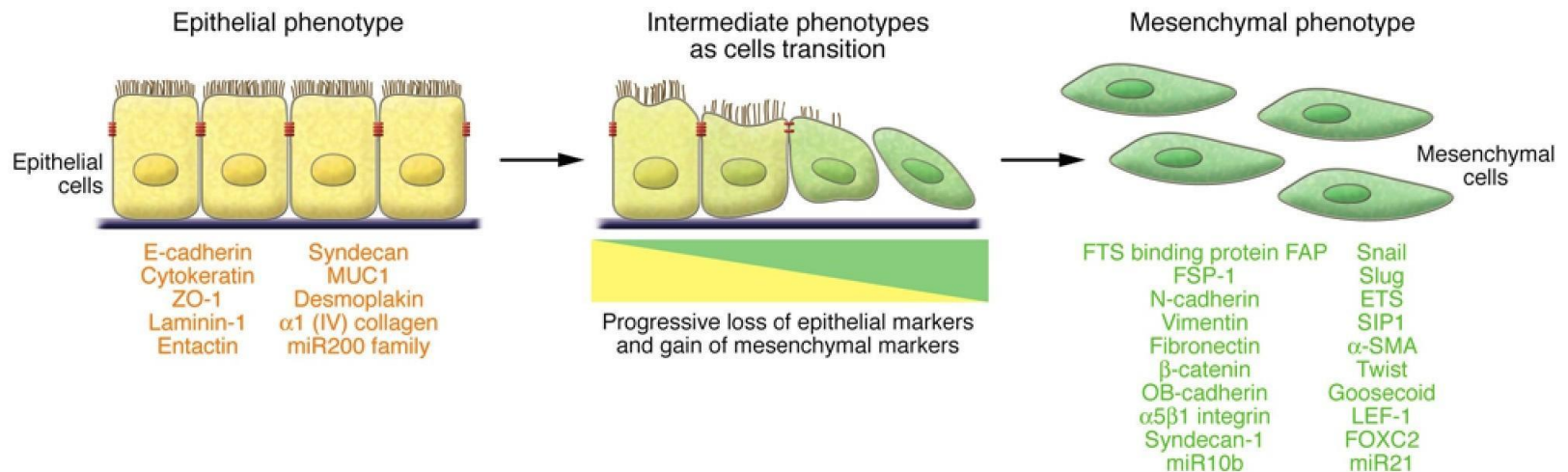


Figure 1

EMT. An EMT involves a functional transition of polarized epithelial cells into mobile and ECM component-secreting mesenchymal cells. The epithelial and mesenchymal cell markers commonly used by EMT researchers are listed. Colocalization of these two sets of distinct markers defines an intermediate phenotype of EMT, indicating cells that have passed only partly through an EMT. Detection of cells expressing both sets of markers makes it impossible to identify all mesenchymal cells that originate from the epithelia via EMT, as many mesenchymal cells likely shed all epithelial markers once a transition is completed. For this reason, most studies in mice use irreversible epithelial cell-lineage tagging to address the full range of EMT-induced changes. ZO-1, zona occludens 1; MUC1, mucin 1, cell surface associated; miR200, microRNA 200; SIP1, survival of motor neuron protein interacting protein 1; FOXC2, forkhead box C2.

Spatiotemporal Regulation of Epithelial-Mesenchymal Transition Is Essential for Squamous Cell Carcinoma Metastasis

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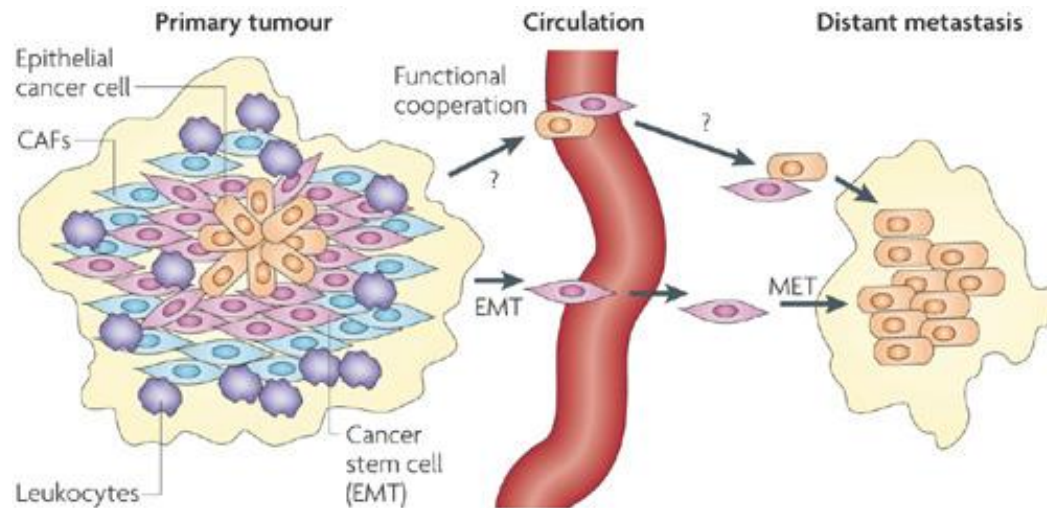
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<http://dx.doi.org/10.1016/j.ccr.2012.09.022>

SUMMARY

Epithelial-mesenchymal transition (EMT) is implicated in converting stationary epithelial tumor cells into motile mesenchymal cells during metastasis. However, the involvement of EMT in metastasis is still controversial, due to the lack of a mesenchymal phenotype in human carcinoma metastases. Using a spontaneous squamous cell carcinoma mouse model, we show that activation of the EMT-inducing transcription factor Twist1 is sufficient to promote carcinoma cells to undergo EMT and disseminate into blood circulation. Importantly, in distant sites, turning off Twist1 to allow reversion of EMT is essential for disseminated tumor cells to proliferate and form metastases. Our study demonstrates *in vivo* the requirement of “reversible EMT” in tumor metastasis and may resolve the controversy on the importance of EMT in carcinoma metastasis.

EMT-MET in metastasis

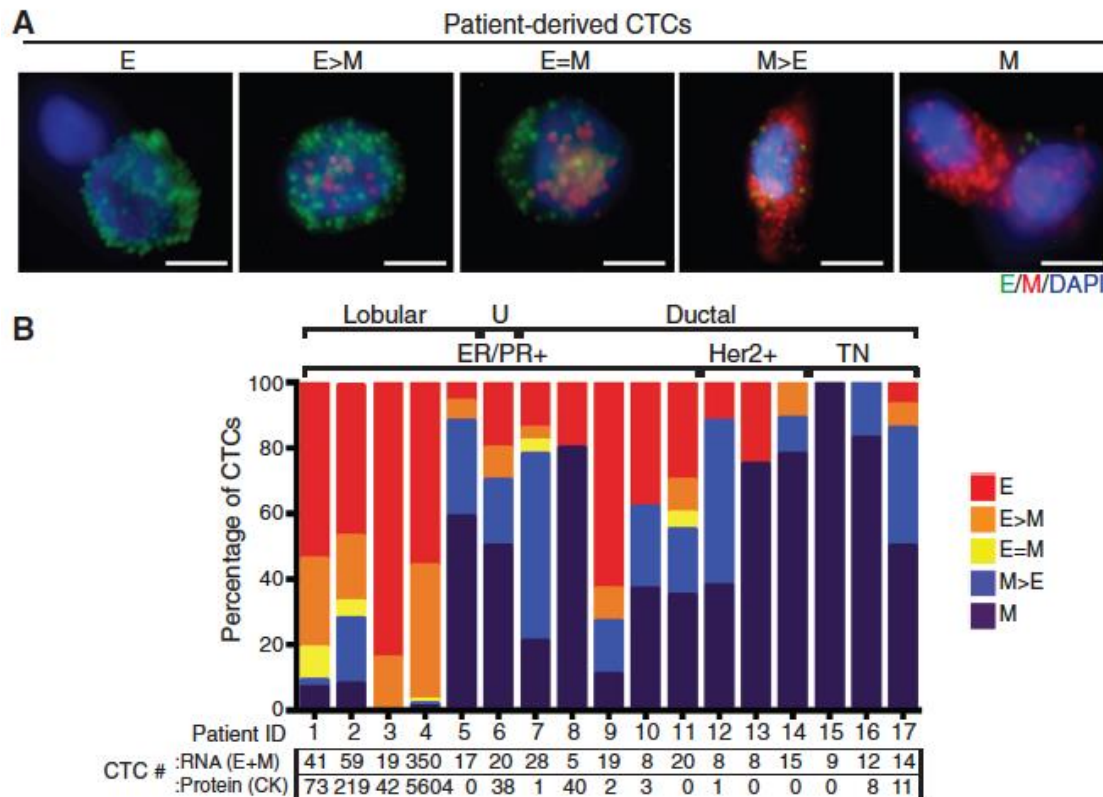


Nature Reviews | Cancer

Polyak and Weinberg, Nat Rev Cancer, 2007

Circulating Breast Tumor Cells Exhibit Dynamic Changes in Epithelial and Mesenchymal Composition

Min Yu,^{1,6*} Aditya Bardia,^{1,3*} Ben S. Wittner,¹ Shannon L. Stott,^{1,2} Malgorzata E. Smas,¹ David T. Ting,¹ Steven J. Isakoff,^{1,3} Jordan C. Ciciliano,¹ Marissa N. Wells,¹ Ajay M. Shah,² Kyle F. Concannon,¹ Maria C. Donaldson,¹ Lecia V. Sequist,^{1,3} Elena Brachtel,^{1,4} Dennis Sgroi,^{1,4} Jose Baselga,^{1,3} Sridhar Ramaswamy,^{1,3} Mehmet Toner,^{2,5} Daniel A. Haber,^{1,3,6†} Shyamala Maheswaran^{1,5†}



Direct Signaling between Platelets and Cancer Cells Induces an Epithelial-Mesenchymal-Like Transition and Promotes Metastasis

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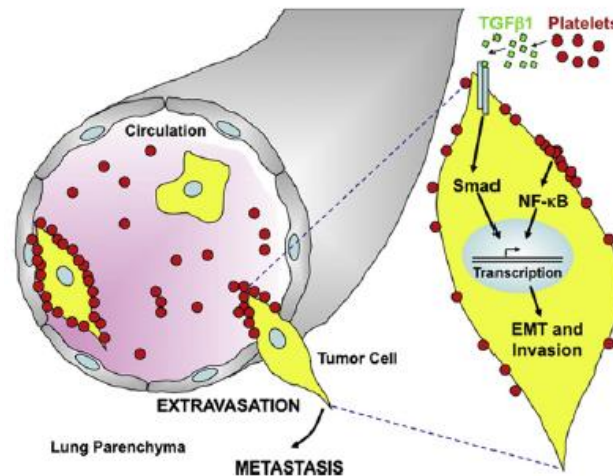
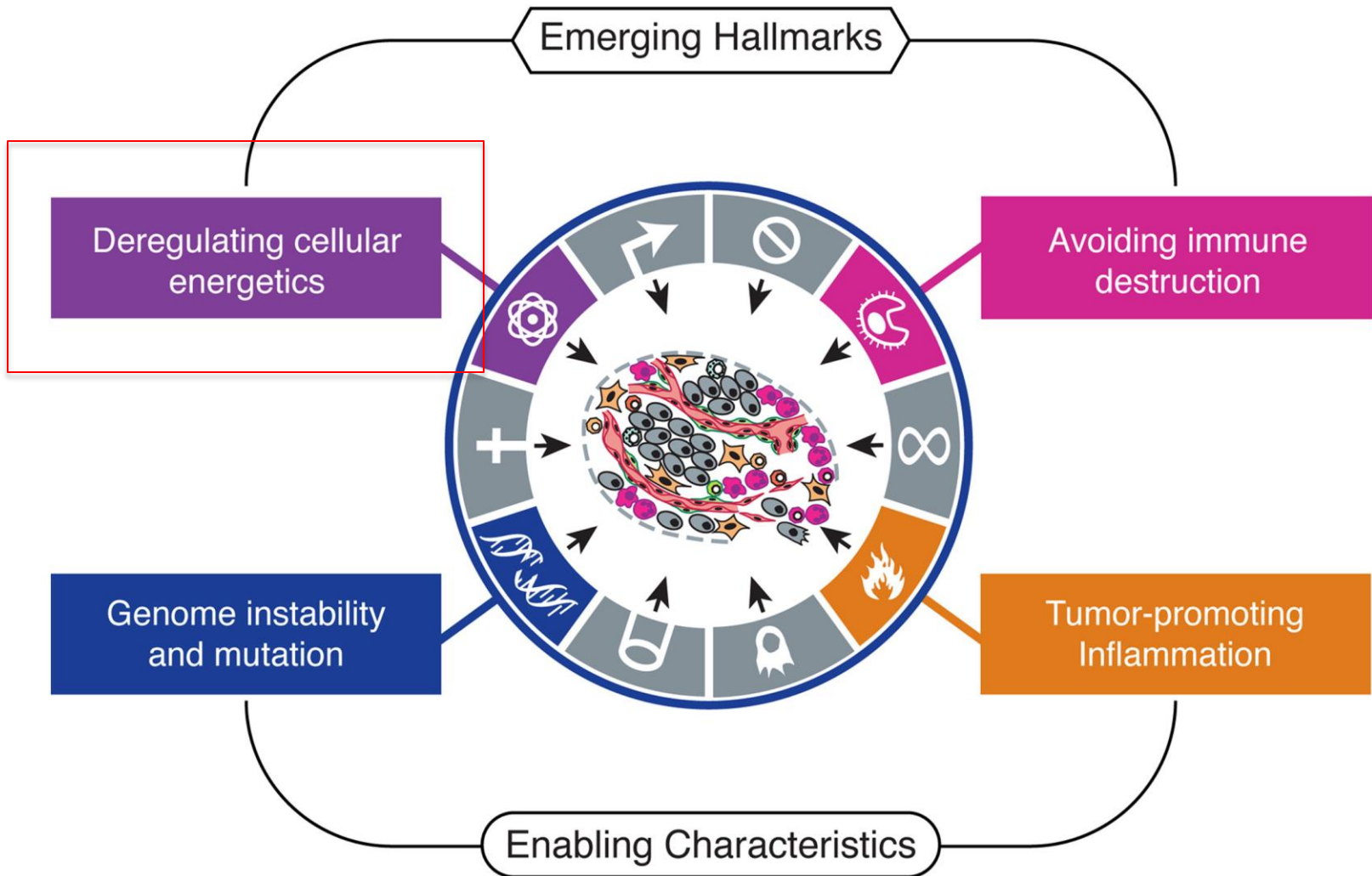


Figure 7. Platelet-Tumor Cell Contact and Platelet-Derived TGFβ1 Synergize to Promote an EMT-Like Transition and Metastasis

Platelets secrete TGFβ1, which activates the TGFβ/Smad pathway in tumor cells. Upon direct platelet-tumor cell contact, the NF-κB pathway is also activated in tumor cells and synergizes with TGFβ/Smad signaling to induce a rapid EMT, enhance invasiveness and promote metastasis. Activation of neither the TGFβ/Smad nor the NF-κB pathway alone is sufficient to promote metastasis. Thus, platelet-tumor cell contact triggers a synergistic interaction between TGFβ/Smad and NF-κB pathways that is necessary for efficient metastasis. The metastatic potential of tumor cells therefore continues to evolve outside of the primary tumor site in response to platelet-to-tumor cell signaling.



Cancers use “aerobic glycolysis”

- In terminally differentiated cells, glycolysis is used to generate ATP in response to hypoxia
- Warburg: noted that glycolysis is active in cancer cells even when oxygen is present (“Warburg effect”)
- This property of cancer is exploited in PET imaging (using fluoro-deoxyglucose, or FdG)
- Aerobic glycolysis allows cancers to upregulate biosynthetic pathways (anabolic metabolism)

Metabolic Reprogramming: A Cancer Hallmark Even Warburg Did Not Anticipate

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DOI 10.1016/j.ccr.2012.02.014

Cancer metabolism has long been equated with aerobic glycolysis, seen by early biochemists as primitive and inefficient. Despite these early beliefs, the metabolic signatures of cancer cells are not passive responses to damaged mitochondria but result from oncogene-directed metabolic reprogramming required to support anabolic growth. Recent evidence suggests that metabolites themselves can be oncogenic by altering cell signaling and blocking cellular differentiation. No longer can cancer-associated alterations in metabolism be viewed as an indirect response to cell proliferation and survival signals. We contend that altered metabolism has attained the status of a core hallmark of cancer.

Metabolic reprogramming in cancer is an active process

- Anabolic metabolism: redirecting energy to building biomolecules (DNA, proteins, lipids)
- The PI3 kinase/AKT/mTOR pathway plays a central role in this “switch”
- Cancer cells still use mitochondria for a significant fraction of their ATP production

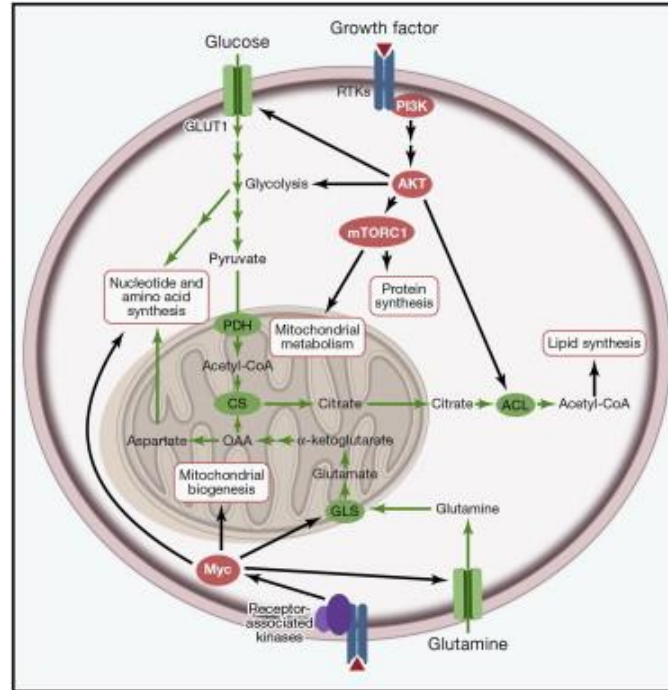


Figure 3 Alterations in Classic Oncogenes Directly Reprogram Cell Metabolism to Increase Nutrient Uptake and Biosynthesis PI3K/Akt signaling downstream of receptor tyrosine kinase (RTK) activation increases glucose uptake through the transporter GLUT1, an...

Patrick S. Ward , Craig B. Thompson

Metabolic Reprogramming: A Cancer Hallmark Even Warburg Did Not Anticipate

Cancer Cell, Volume 21, Issue 3, 2012, 297 - 308

<http://dx.doi.org/10.1016/j.ccr.2012.02.014>

Cancer cells display altered expression of metabolic enzymes

- Pyruvate kinase: quiescent cells express the M1 isoform, whereas proliferating cells express M2, promoting anabolic metabolism
- Isocitrate dehydrogenase-1 and -2: mutated to versions that produce a novel metabolite (2HG) that inhibits the TET family of enzymes, thereby producing epigenetic changes (i.e., histone modifications) that block differentiation

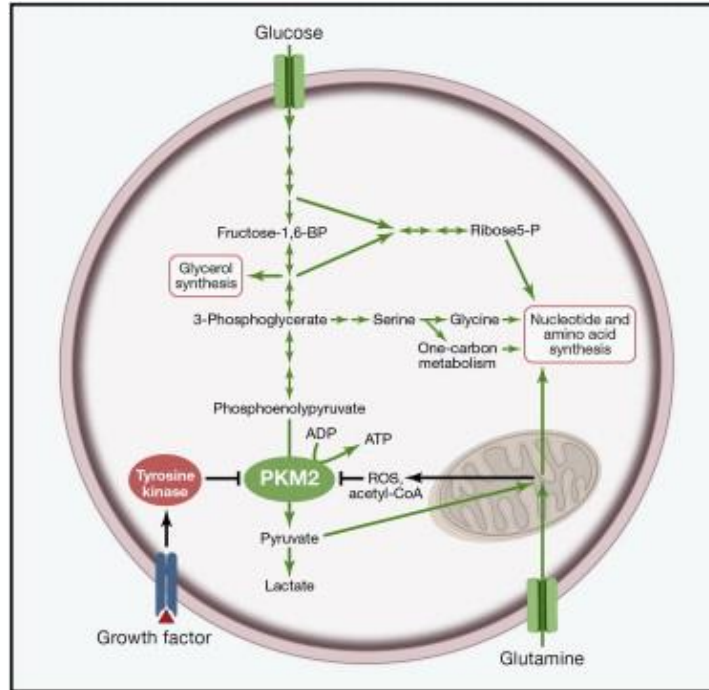


Figure 4 Pyruvate Kinase M2 Expression in Proliferating Cells Is Regulated by Signaling and Mitochondrial Metabolism to Facilitate Macromolecular Synthesis Pyruvate kinase M2 (PKM2) is a less active isoform of the terminal glycolytic enzyme pyruvate kinas...

Patrick S. Ward , Craig B. Thompson

Metabolic Reprogramming: A Cancer Hallmark Even Warburg Did Not Anticipate

Cancer Cell, Volume 21, Issue 3, 2012, 297 - 308

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Acetate Dependence of Tumors

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<http://dx.doi.org/10.1016/j.cell.2014.11.020>

Acetate Is a Bioenergetic Substrate for Human Glioblastoma and Brain Metastases

Tomoyuki Mashimo,^{1,2,3,11} Kumar Pichumani,^{4,11} Vamsidhara Vemireddy,^{1,2,3} Kimmo J. Hatanpaa,^{2,3,5} Dinesh Kumar Singh,^{2,3,6} Shyam Sirasanagandla,^{1,2,3} Suraj Nannepaga,^{2,3,6} Sara G. Piccirillo,^{3,6} Zoltan Kovacs,⁴ Chan Foong,⁵ Zhiguang Huang,⁷ Samuel Barnett,⁸ Bruce E. Mickey,^{2,3,8} Ralph J. DeBerardinis,^{2,9,10} Benjamin P. Tu,⁷ Elizabeth A. Maher,^{1,2,3,6,12,*} and Robert M. Bachoo^{1,2,3,6,12,*}

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<http://dx.doi.org/10.1016/j.cell.2014.11.025>

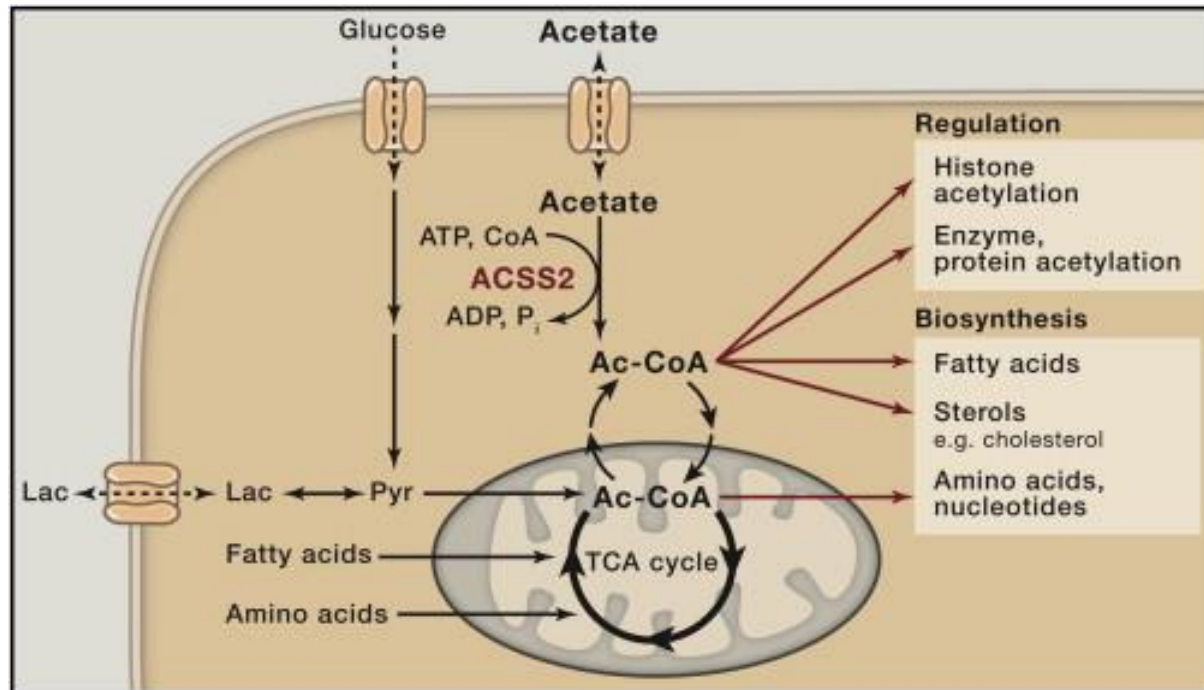


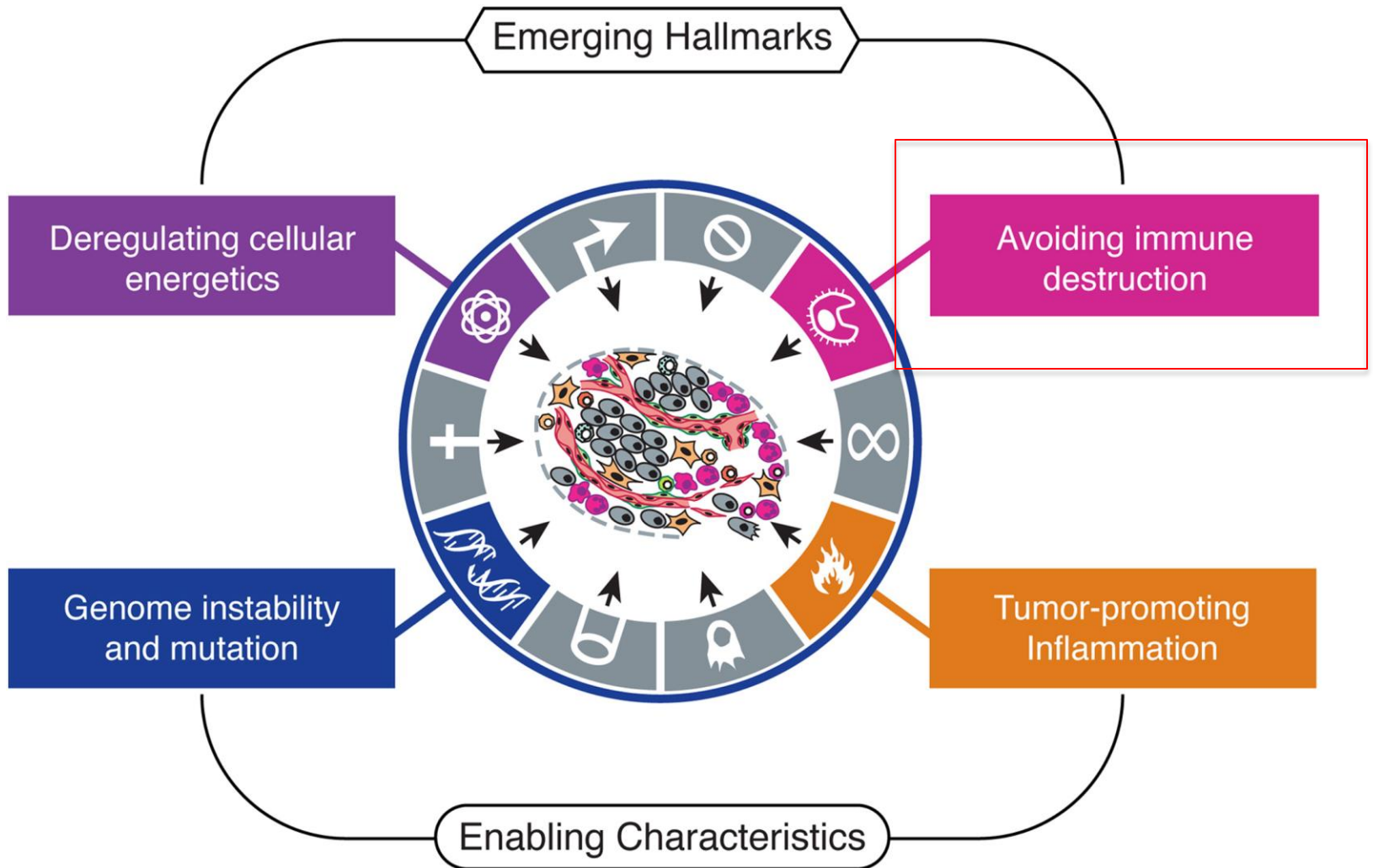
Figure 1 Acetyl-CoA Is a Central Node in Carbon Metabolism Acetyl-CoA plays numerous roles in both regulatory and biosynthetic processes. It can be added in a posttranslational fashion to histone proteins to regulate gene expression or to other proteins a...

Costas A. Lyssiotis , Lewis C. Cantley

Acetate Fuels the Cancer Engine

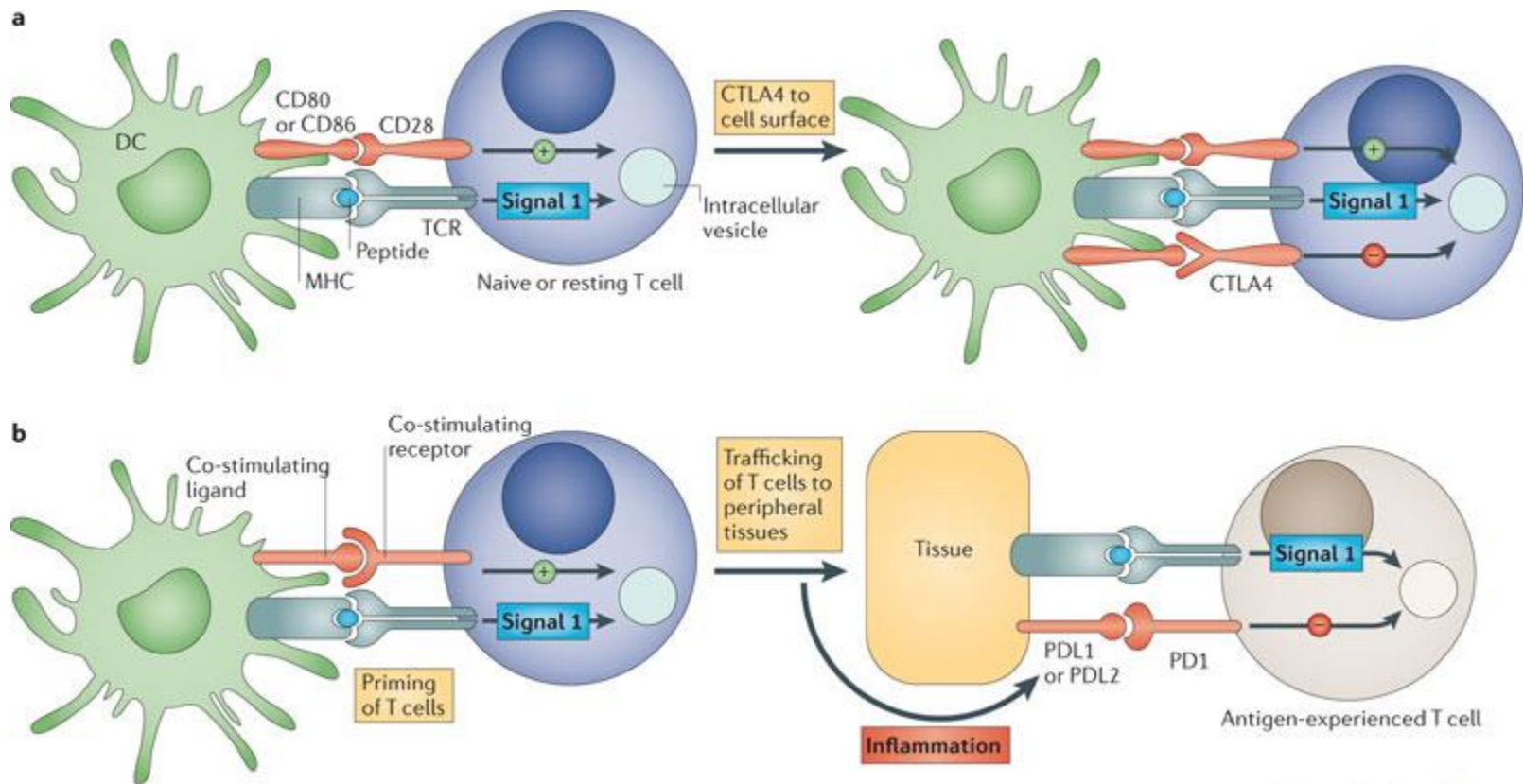
Cell, Volume 159, Issue 7, 2014, 1492 - 1494

<http://dx.doi.org/10.1016/j.cell.2014.12.009>

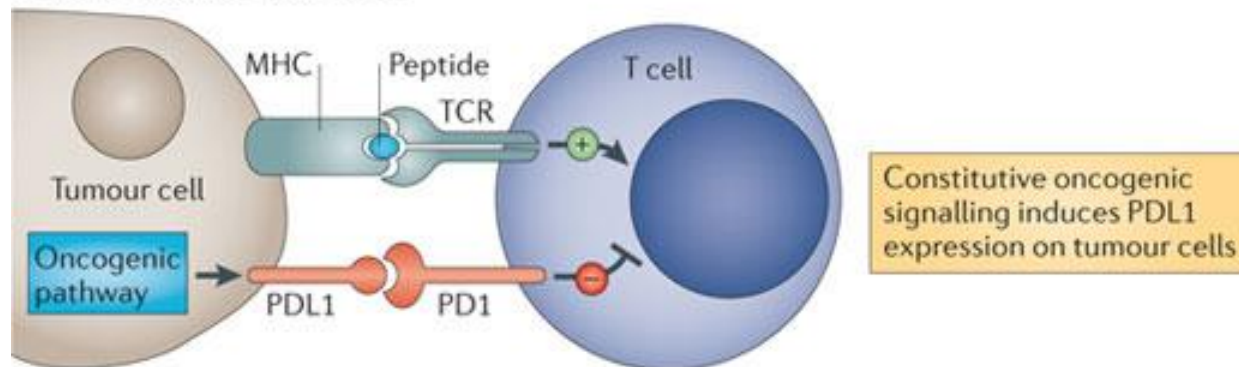


Avoiding immune destruction

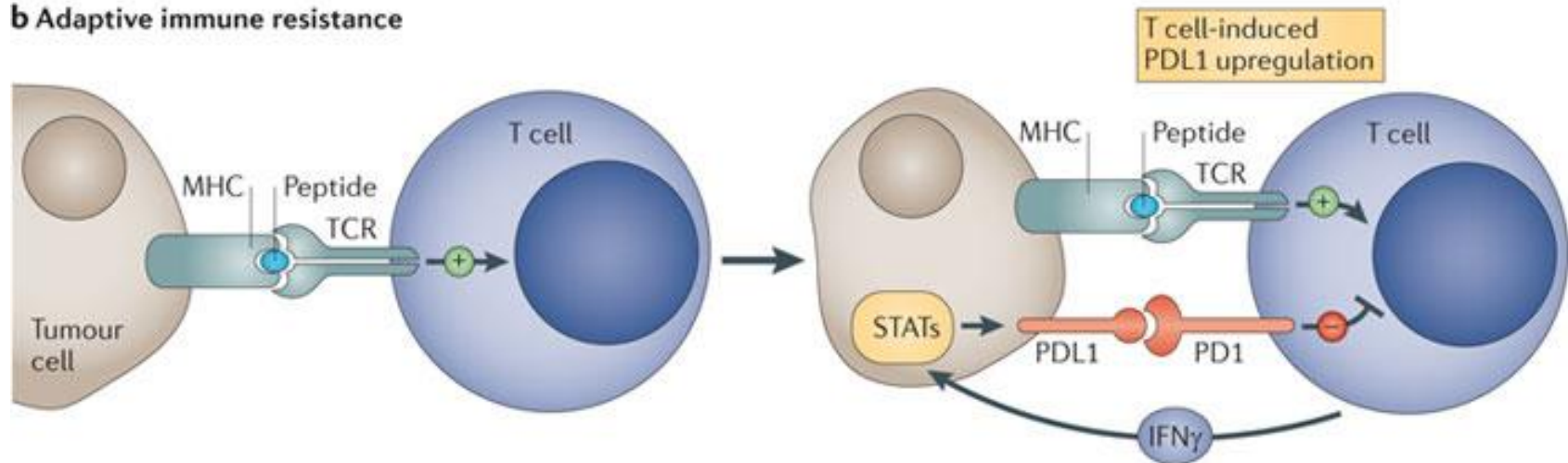
- Tumors co-opt physiological mechanisms that have evolved to dampen the immune response
- Involve specialized subsets of immune cells (T regulatory cells, myeloid-derived suppressor cells)
- Tumor-induced immune suppression is being aggressively targeted with novel therapies



a Innate immune resistance



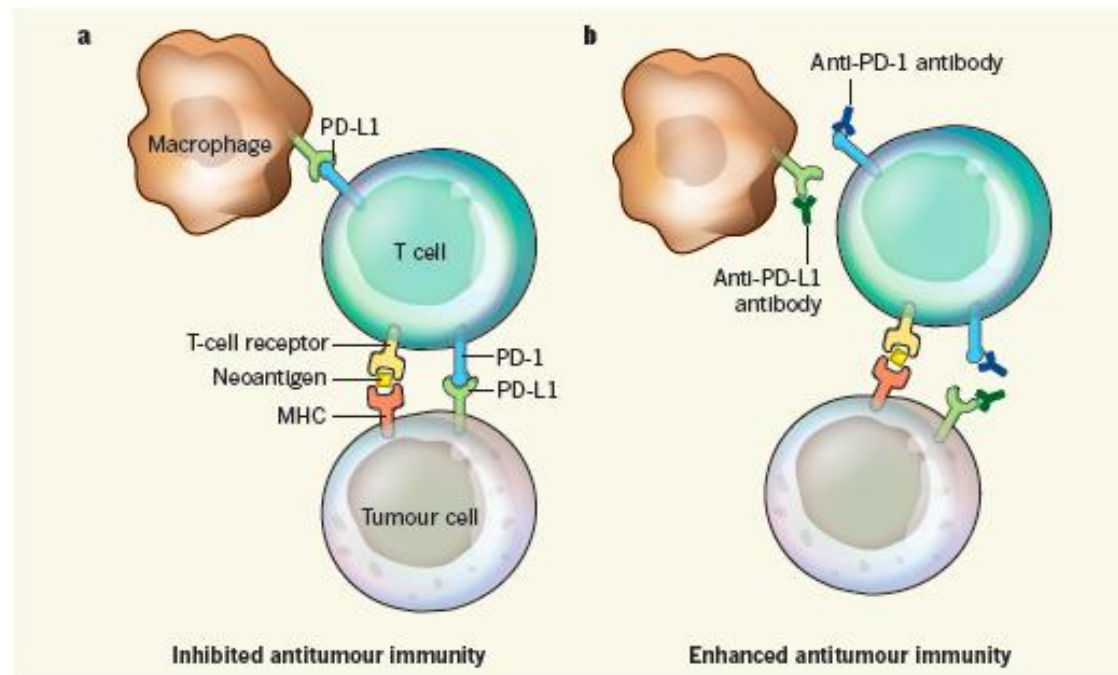
b Adaptive immune resistance

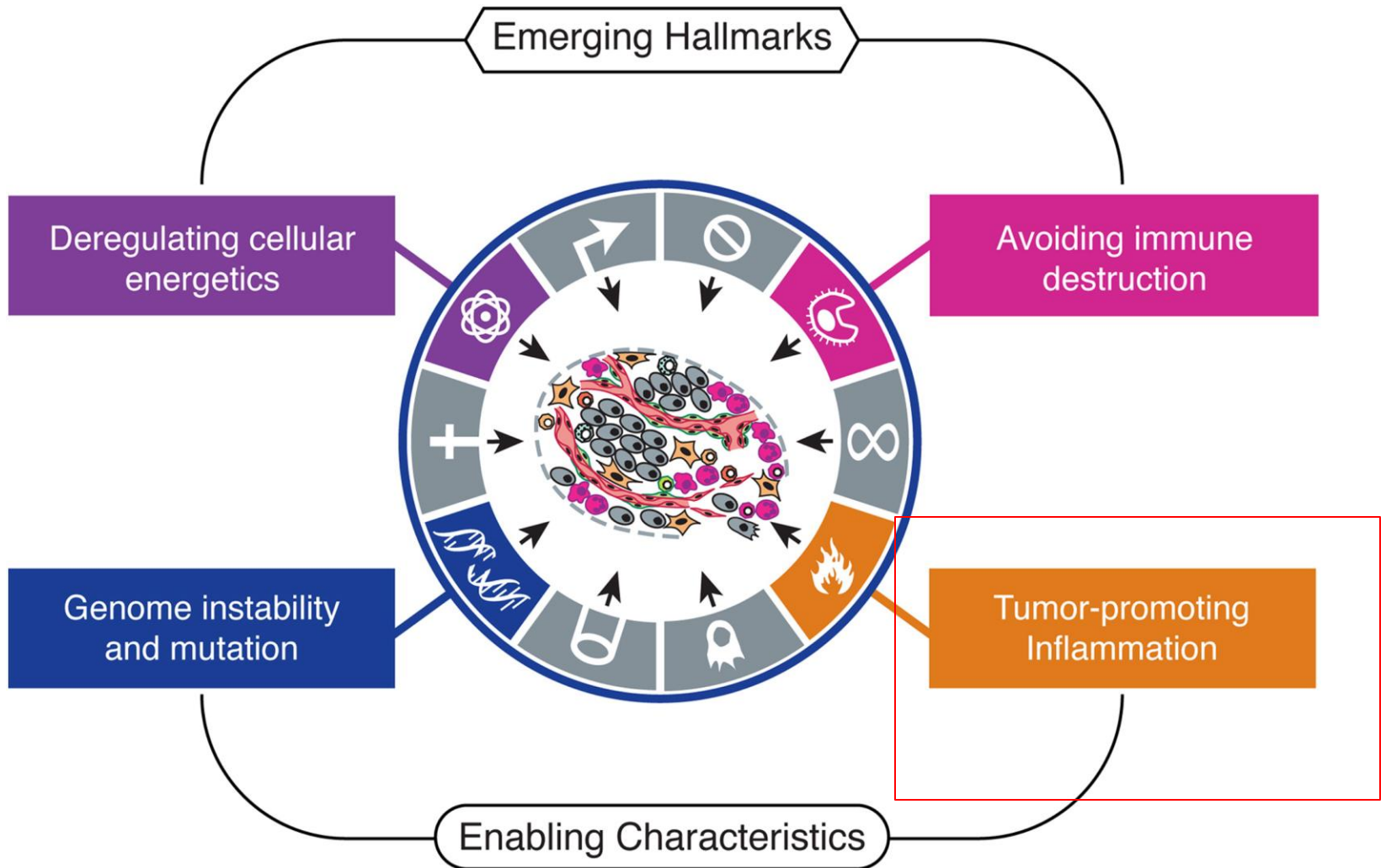


Antitumour immunity gets a boost

Five papers extend the list of cancers that respond to therapies that restore antitumour immunity by blocking the PD-1 pathway, and characterize those patients who respond best. [SEE LETTERS P.558, P.563, P.568, P.572 & P.577](#)

JEDD D. WOLCHOK & TIMOTHY A. CHAN





Tumor-stromal interactions play a crucial role in cancer progression

- Cancer resembles the complex architecture of a tissue, containing many different types of cell
- Cancer cells co-opt the cells in their environments to promote aspects of all of the hallmarks



Tumors as Organs: Complex Tissues that Interface with the Entire Organism

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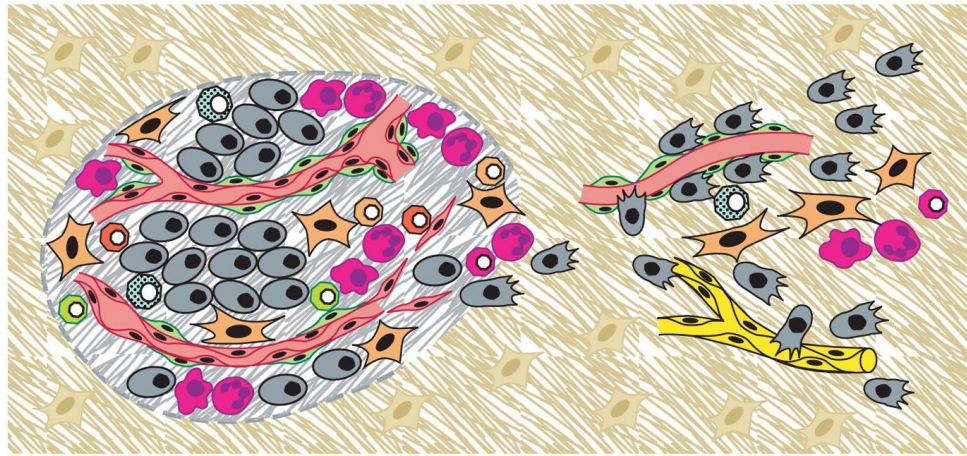
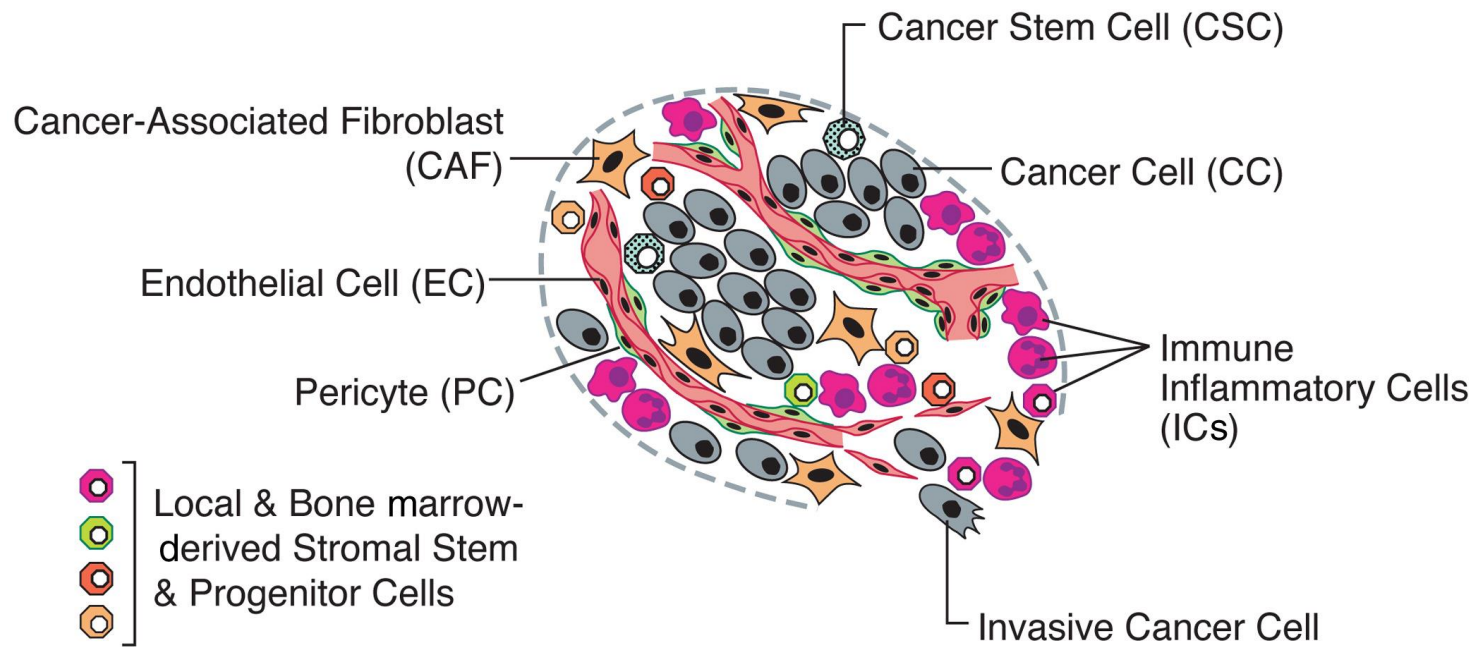
³Department of Anatomy, University of California, 513 Parnassus Avenue, Box 0452, San Francisco, CA 94143, USA

*Correspondence: egeblad@cshl.edu (M.E.), zena.werb@ucsf.edu (Z.W.)

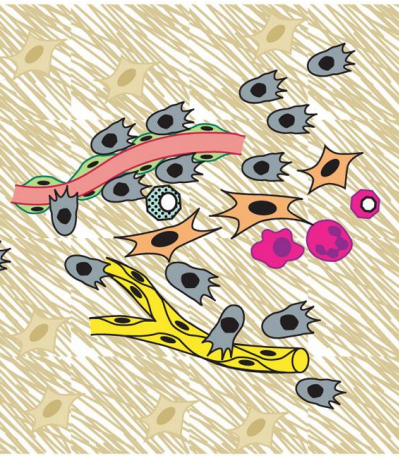
DOI 10.1016/j.devcel.2010.05.012

Stromal cells in cancer

- Endothelial cells
- Lymphocytes
- Macrophages and other cells of the innate immune system (mast cells, neutrophils, etc)
- Smooth muscle cells (pericytes, etc)
- Adipocytes (fat cells)
- Fibroblasts



Core of Primary Tumor
microenvironment



Invasive Tumor
microenvironment

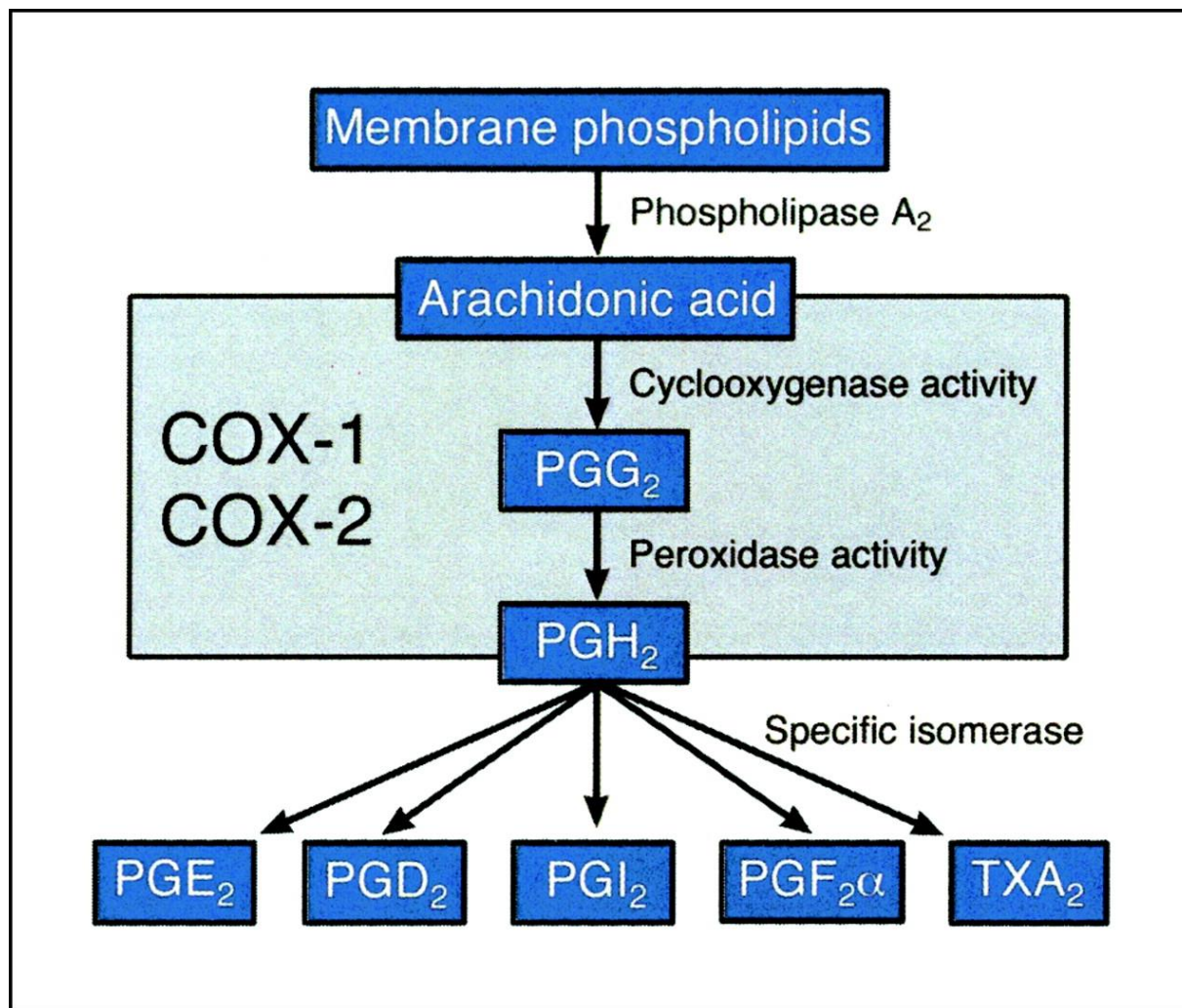


Metastatic Tumor
microenvironment

Inflammation

- Acute response to injury and/or infection
- Mediated by innate immune cells (macrophages, neutrophils, etc) and fibroblasts
- Can lead to scarring or fibrosis
- Long-term (chronic) inflammation – strongly associated with cancer
- Nuclear factor kappa B (NF κ B) and cyclooxygenase-2 (COX2) are key regulators

Fig 1. The arachidonic acid cascade

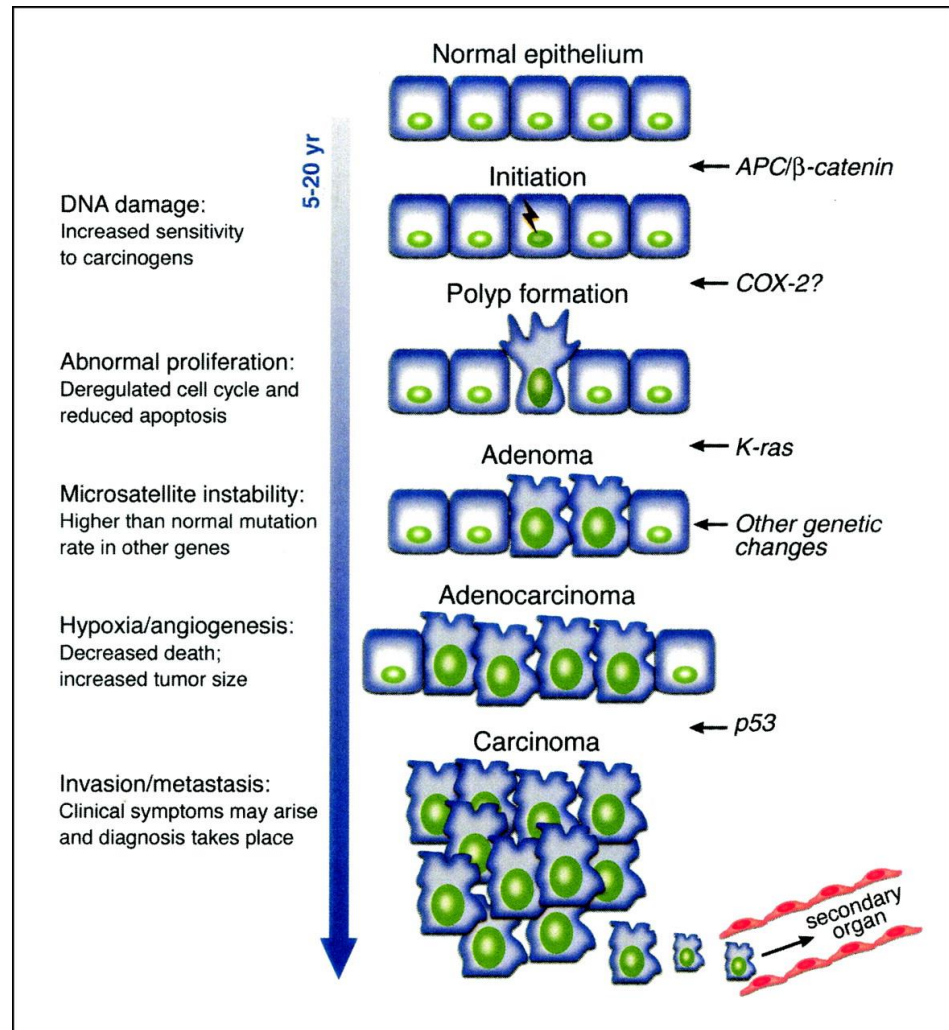


Brown, J. R. et al. J Clin Oncol; 23:2840-2855 2005

Inflammation in colon cancer

- Somatic mutations in APC cause familial predisposition to colon cancer (FAP)
- APC mutations: cause activation of beta-catenin, which drives activation of the Wnt and NF κ B pathways
- Alterations in the microbiome
- These effects lead to upregulation of COX2
- Non-steroidal anti-inflammatory drugs (NSAIDs): prevent cancer in animal models and FAP patients

Fig 2. A genetic model for colorectal tumorigenesis illustrating the accumulation of mutations in oncogenes and tumor suppressor genes, which is thought to contribute to tumor progression and the propensity to metastasize



Brown, J. R. et al. J Clin Oncol; 23:2840-2855 2005

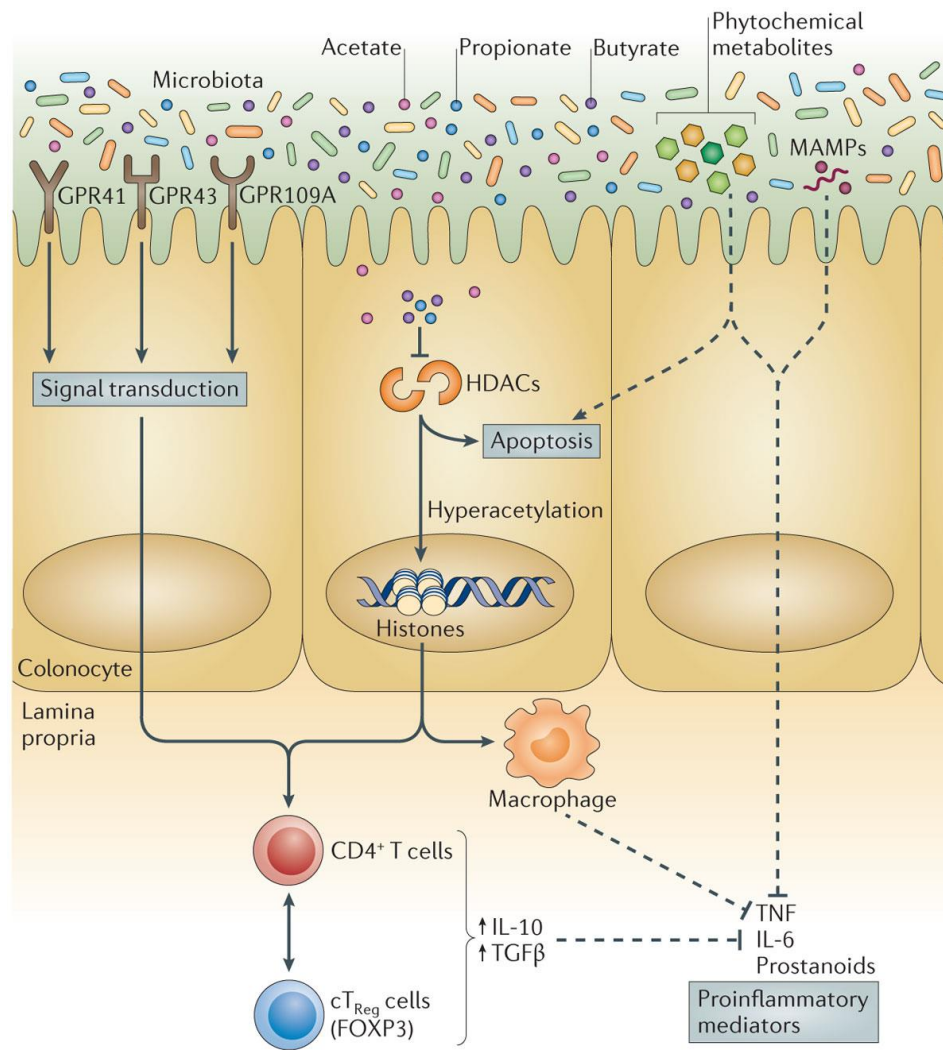
Potential role of the “microbiome”

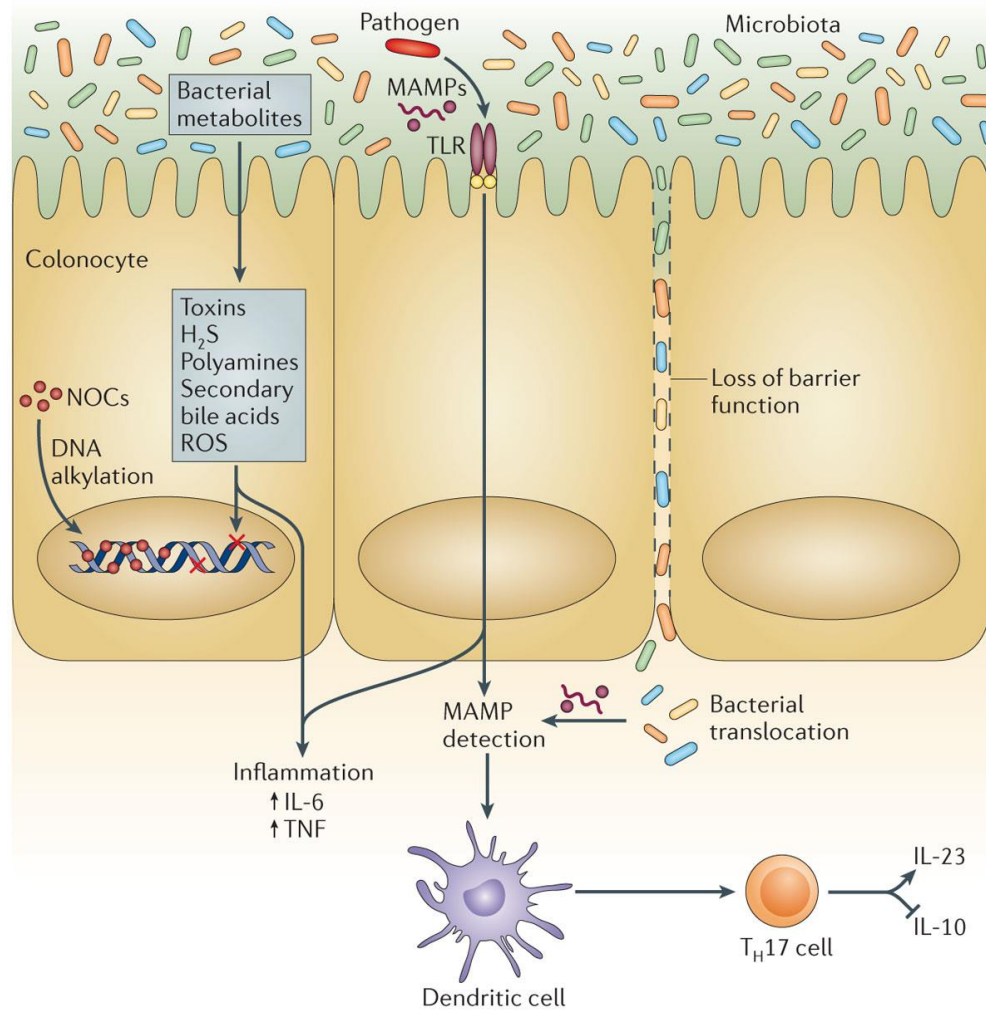
- Recent work indicates that the bacteria that colonize the colon (and other surface-exposed areas of the body) have important effects on many aspects of human health, including obesity, metabolism, and immunity
- Disruption of homeostasis is linked to chronic inflammation and may promote cancer

The gut microbiota, bacterial metabolites and colorectal cancer

Petra Louis¹, Georgina L. Hold² and Harry J. Flint¹

Abstract | Accumulating evidence suggests that the human intestinal microbiota contributes to the aetiology of colorectal cancer (CRC), not only via the pro-carcinogenic activities of specific pathogens but also via the influence of the wider microbial community, particularly its metabolome. Recent data have shown that the short-chain fatty acids acetate, propionate and butyrate function in the suppression of inflammation and cancer, whereas other microbial metabolites, such as secondary bile acids, promote carcinogenesis. In this Review, we discuss the relationship between diet, microbial metabolism and CRC and argue that the cumulative effects of microbial metabolites should be considered in order to better predict and prevent cancer progression.



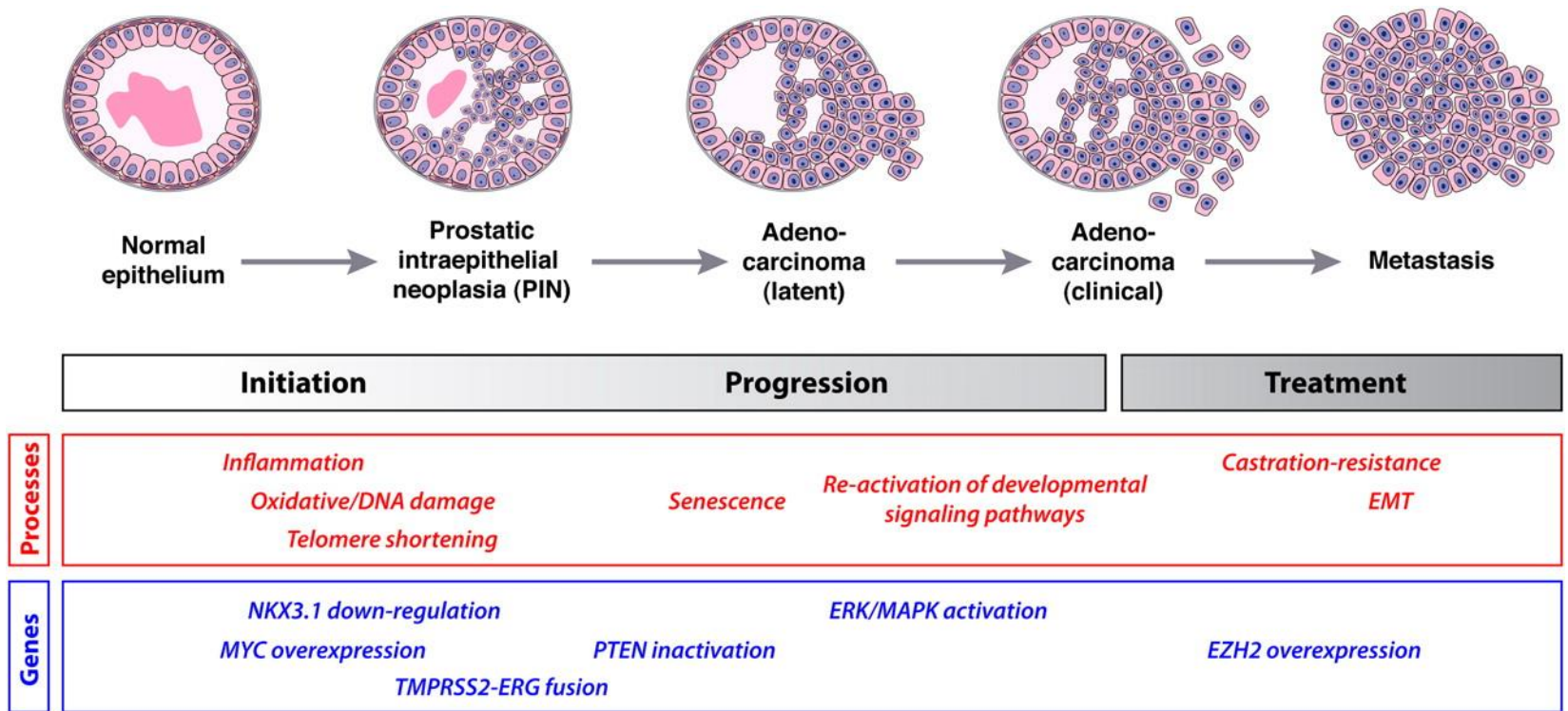


Dietary and enviromental compounds	Microbial products	Known effect on host
Non-digestible carbohydrates →	SCFAs	• Microbiota modulation • Cellular differentiation; apoptosis • Inflammation
Phytochemicals →	Phenolic acids; isothiocyanates	• Xenobiotic detoxification • Microbiota modulation • Cellular differentiation; apoptosis • Inflammation
Protein →	NOCs; ammonia	• ROS production; genotoxicity
	Polyamines	• Inflammation • ROS production; genotoxicity
	Hydrogen sulphide	• Inflammation • ROS production; genotoxicity
Fat → Bile acids →	Taurine	• Microbiota modulation
	Secondary bile acids	• Microbiota modulation • Cellular differentiation; apoptosis • ROS production; genotoxicity
Xenobiotics →	Carcinogens	• ROS production; genotoxicity
Ethanol →	Acetaldehyde	• ROS production; genotoxicity

Inflammation and prostate cancer

- The emergence of cancer precursor lesions (prostatic intraepithelial neoplasia, or PIN) is strongly associated with inflammation
- Also associated with focal atrophy
- Referred to as “proliferative inflammatory atrophy” (PIA)

Progression pathway for human prostate cancer.



Shen M M , and Abate-Shen C Genes Dev. 2010;24:1967-2000

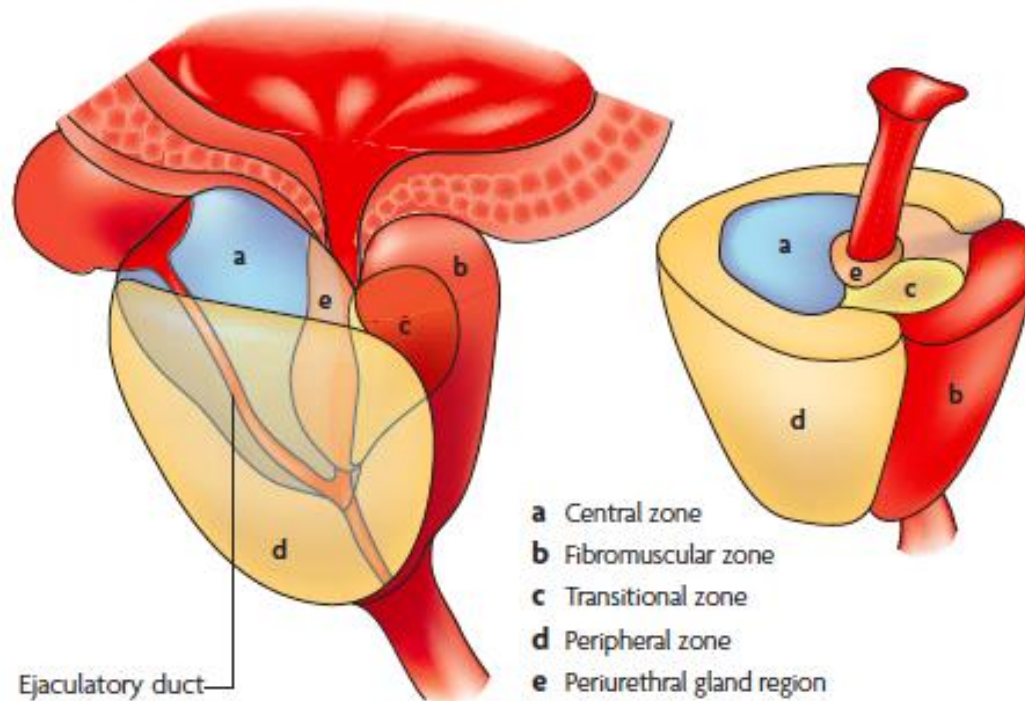


Inflammation in prostate carcinogenesis

Angelo M. De Marzo^{†}, Elizabeth A. Platz[§], Siobhan Sutcliffe[§], Jianfeng Xu^{||}, Henrik Grönberg[†], Charles G. Drake[†], Yasutomo Nakai[#], William B. Isaacs^{**} and William G. Nelson[†]*

Abstract | About 20% of all human cancers are caused by chronic infection or chronic inflammatory states. Recently, a new hypothesis has been proposed for prostate carcinogenesis. It proposes that exposure to environmental factors such as infectious agents and dietary carcinogens, and hormonal imbalances lead to injury of the prostate and to the development of chronic inflammation and regenerative 'risk factor' lesions, referred to as proliferative inflammatory atrophy (PIA). By developing new experimental animal models coupled with classical epidemiological studies, genetic epidemiological studies and molecular pathological approaches, we should be able to determine whether prostate cancer is driven by inflammation, and if so, to develop new strategies to prevent the disease.

Prostate zones



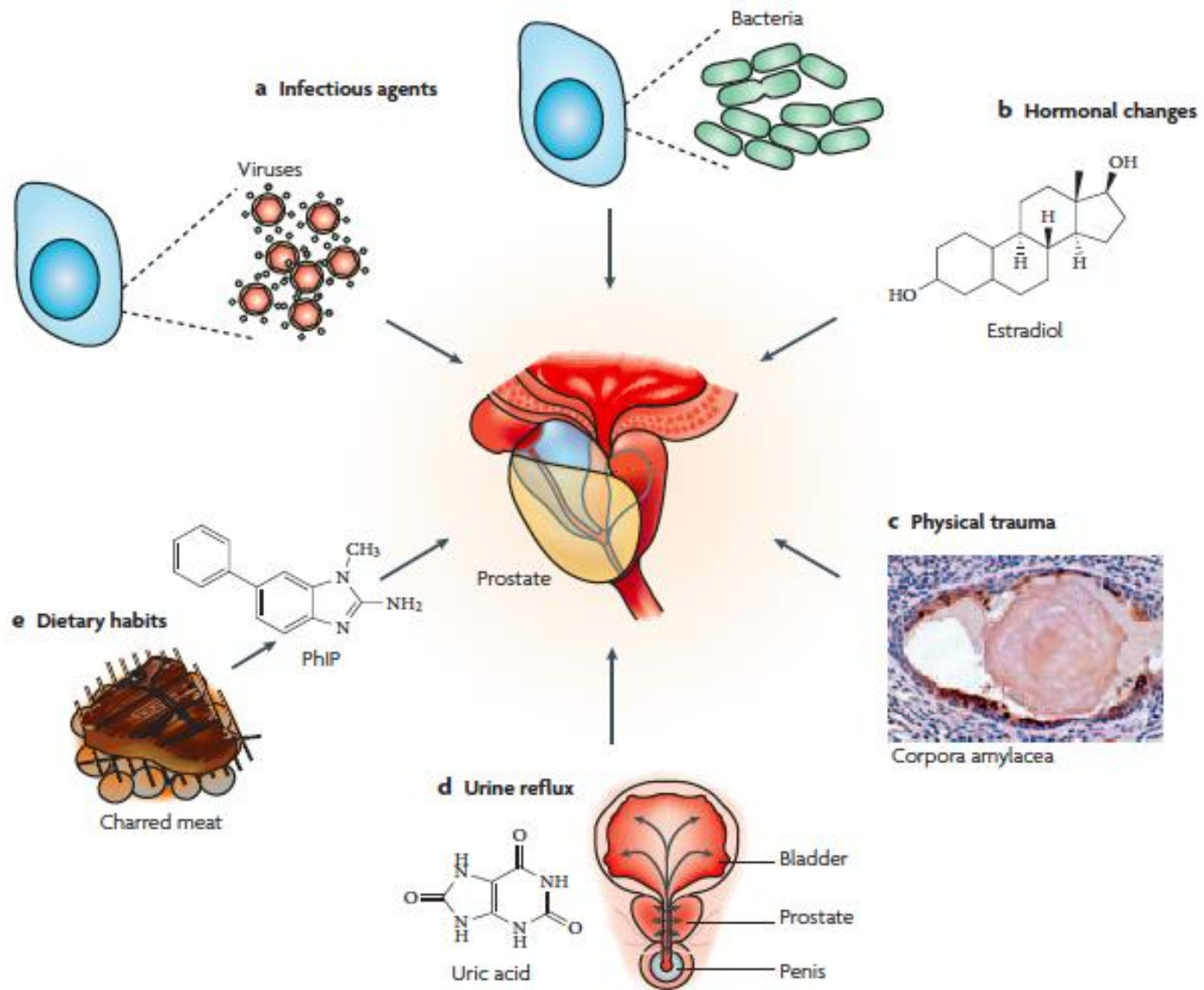
	Prostate zone		
	Peripheral	Transition	Central
Focal atrophy	High prevalence	Medium-high prevalence	Low prevalence
Acute inflammation	Low prevalence	Low prevalence	None
Chronic inflammation	Medium-high prevalence	Medium-high prevalence	Low prevalence
Benign prostatic hyperplasia	None	High prevalence	Low prevalence
High-grade PIN	Medium-high prevalence	Medium-high prevalence	Low prevalence
Carcinoma	Medium-high prevalence	Medium-high prevalence	Low prevalence

High prevalence

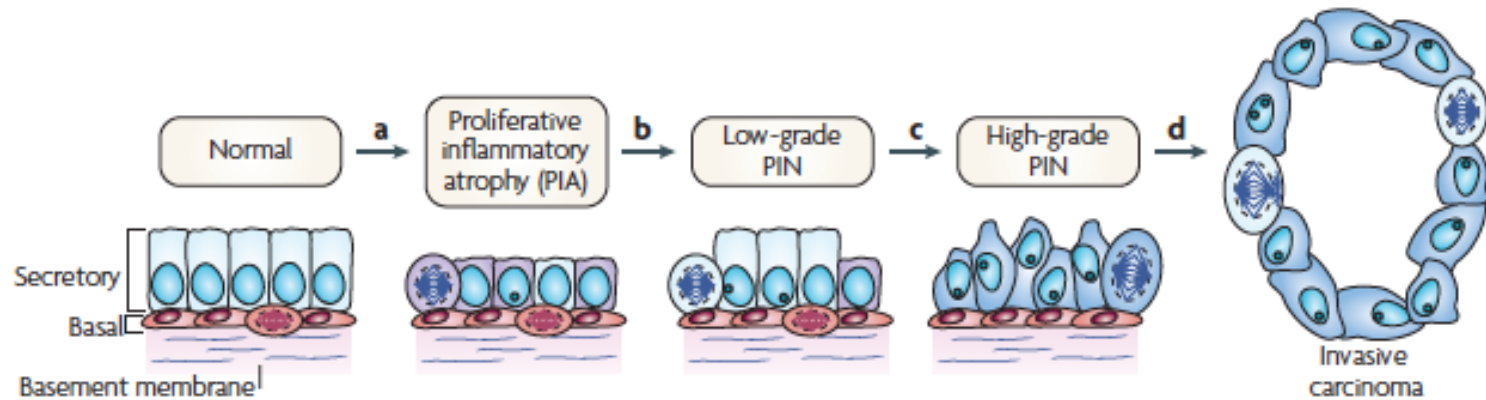
Medium-high prevalence

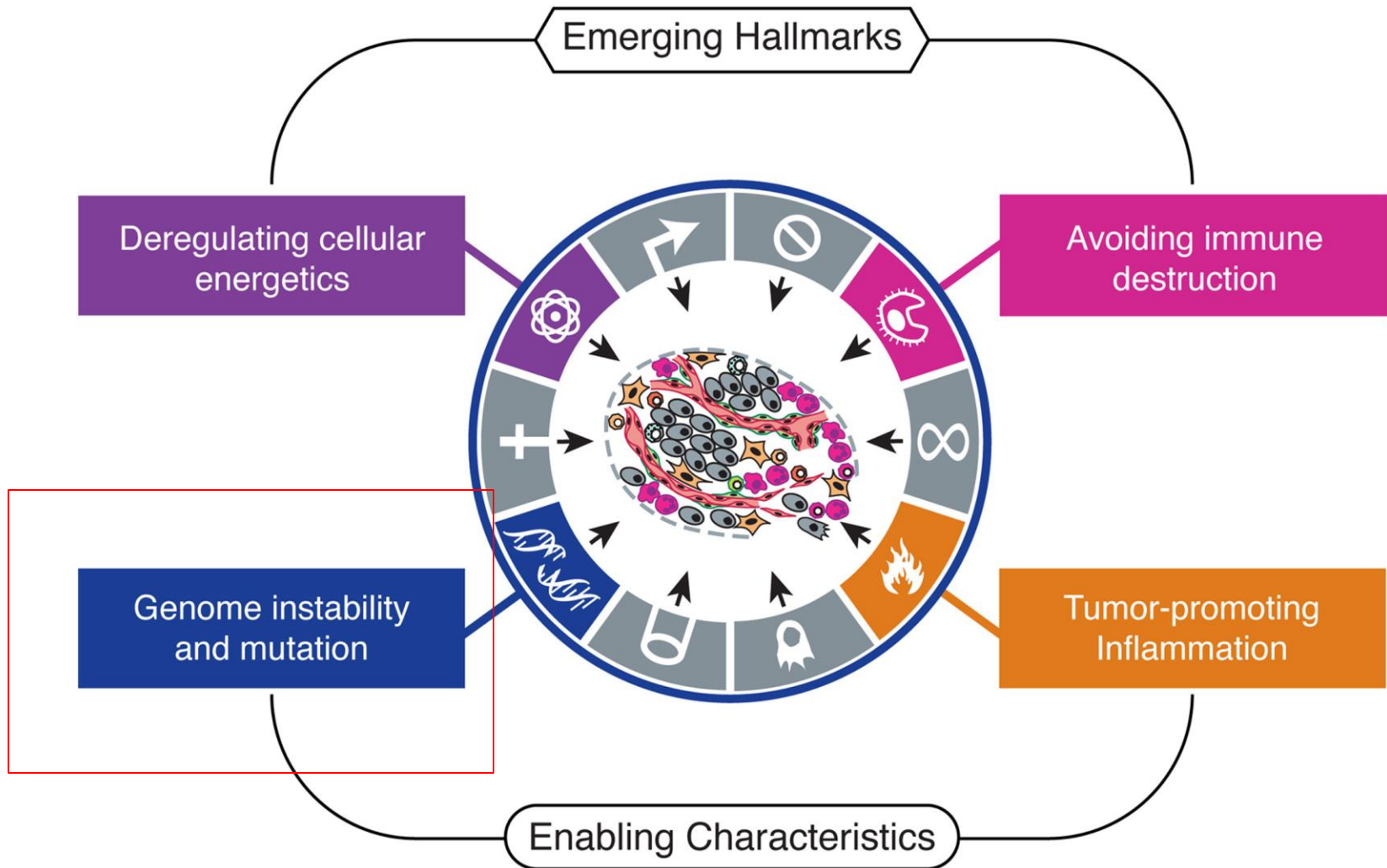
Low prevalence

None



“Proliferative inflammatory atrophy” (PIA)

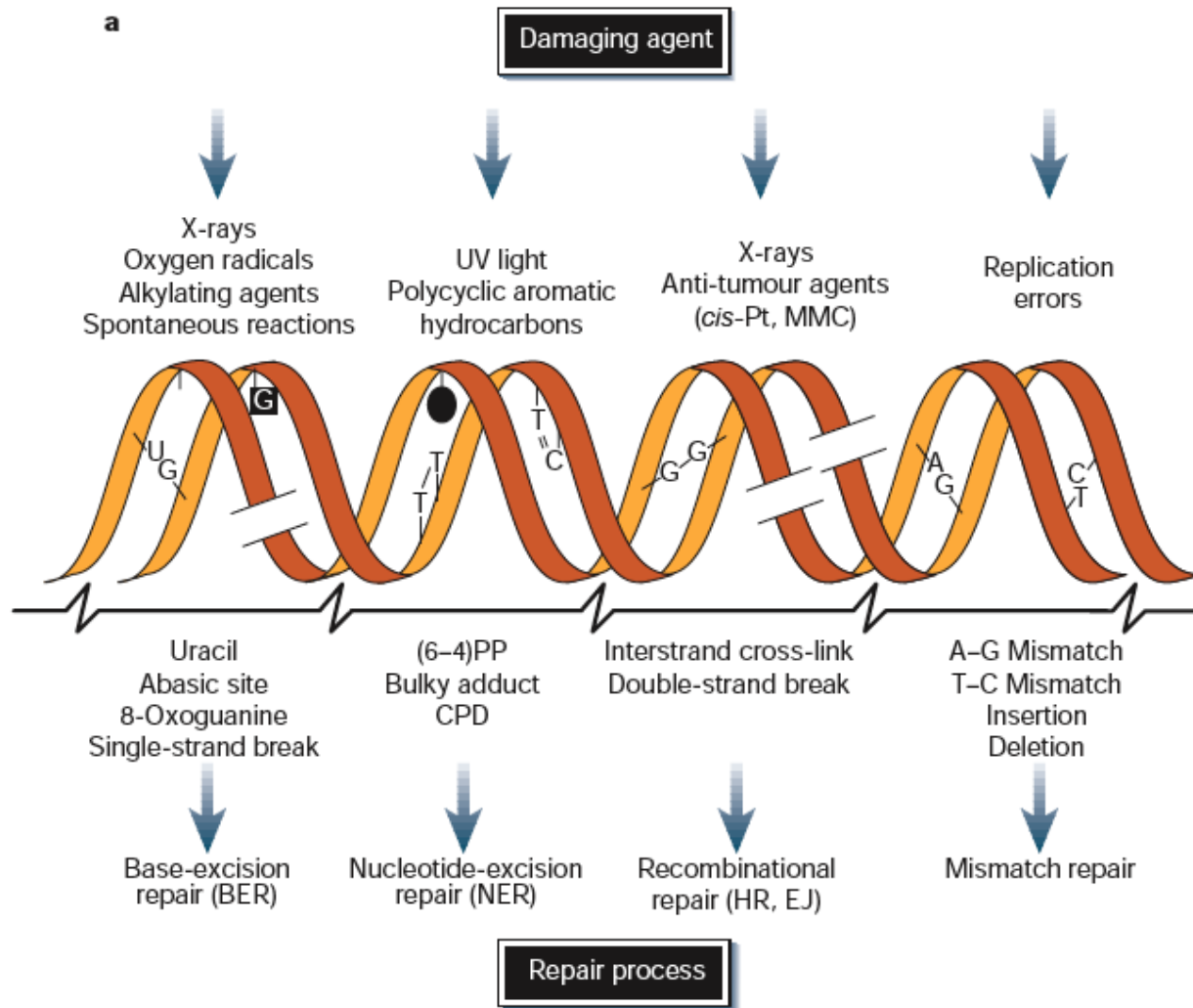




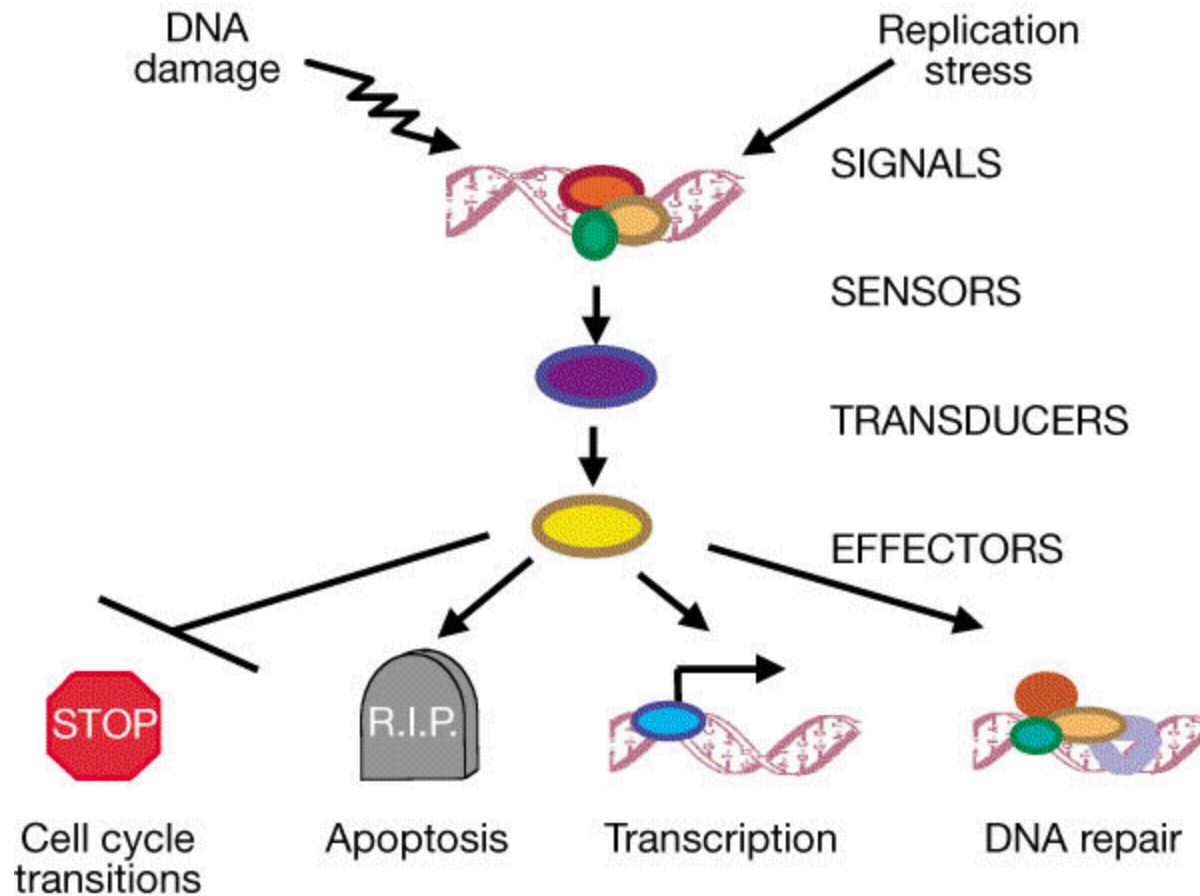
Familial cancer syndromes are caused by DNA repair defects

- Hereditary breast, ovarian, and pancreatic cancers: BRCA1/2
- Hereditary non-polyposis colon cancer/HNPCC: DNA mismatch repair genes
- Li-Fraumeni syndrome: p53
- Ataxia telangectasia: ATM

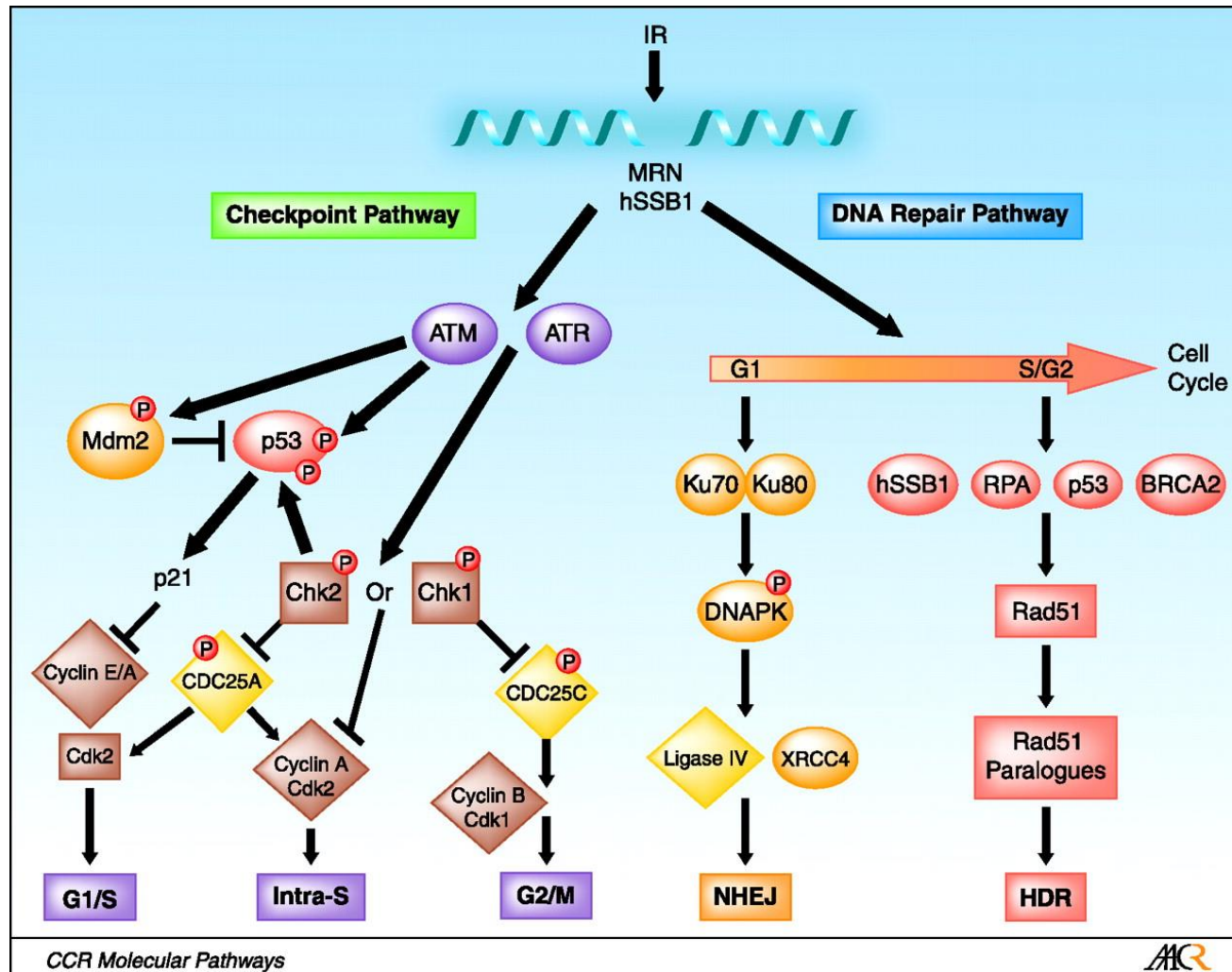
DNA repair pathways



The DNA damage response



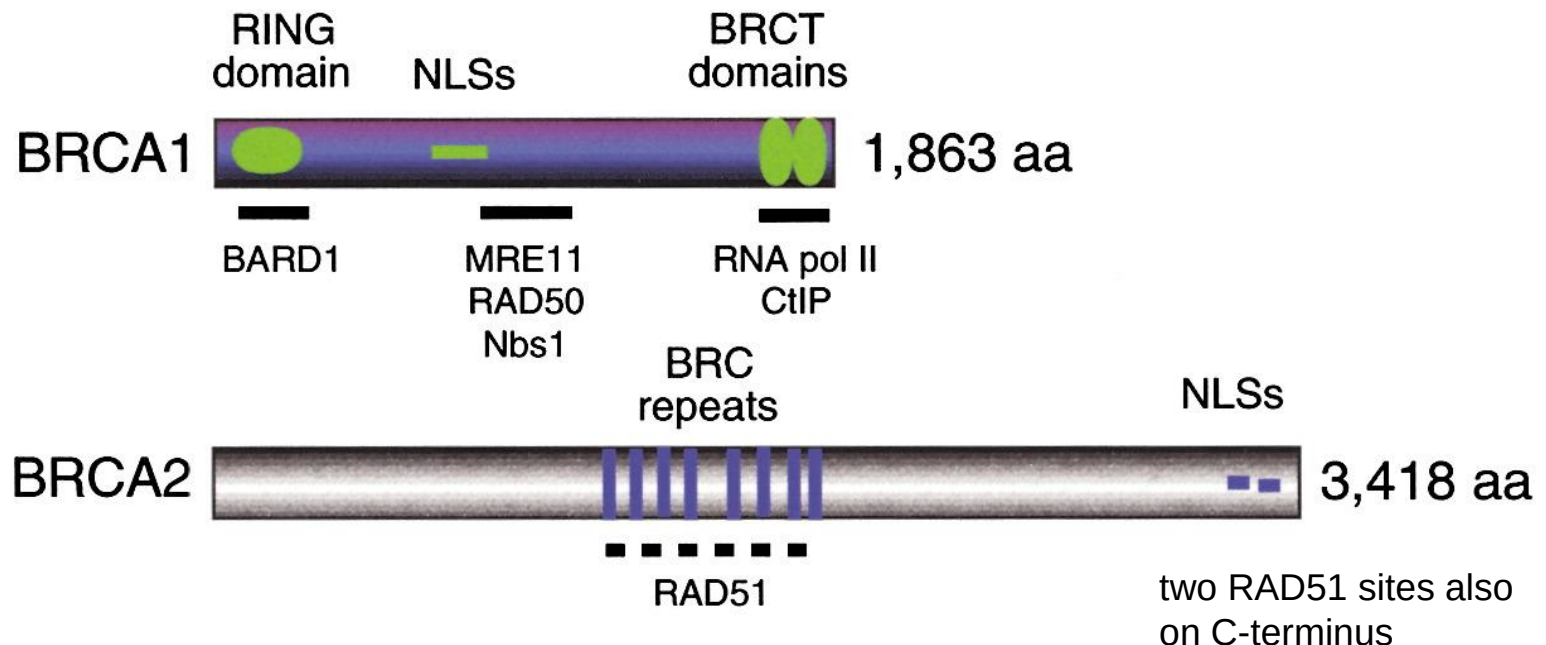
DNA DSB-induced activation of checkpoint and repair pathways



Bolderson E et al. Clin Cancer Res 2009;15:6314-6320

BRCA1 and BRCA2

- Breast cancer susceptibility genes
- Localize to sites of damage (damage foci)
- Both phosphorylated in response to damage
- Defects associated with breast, ovarian, and pancreatic cancer



A Synthetic Lethal Therapeutic Approach: Poly(ADP) Ribose Polymerase Inhibitors for the Treatment of Cancers Deficient in DNA Double-Strand Break Repair

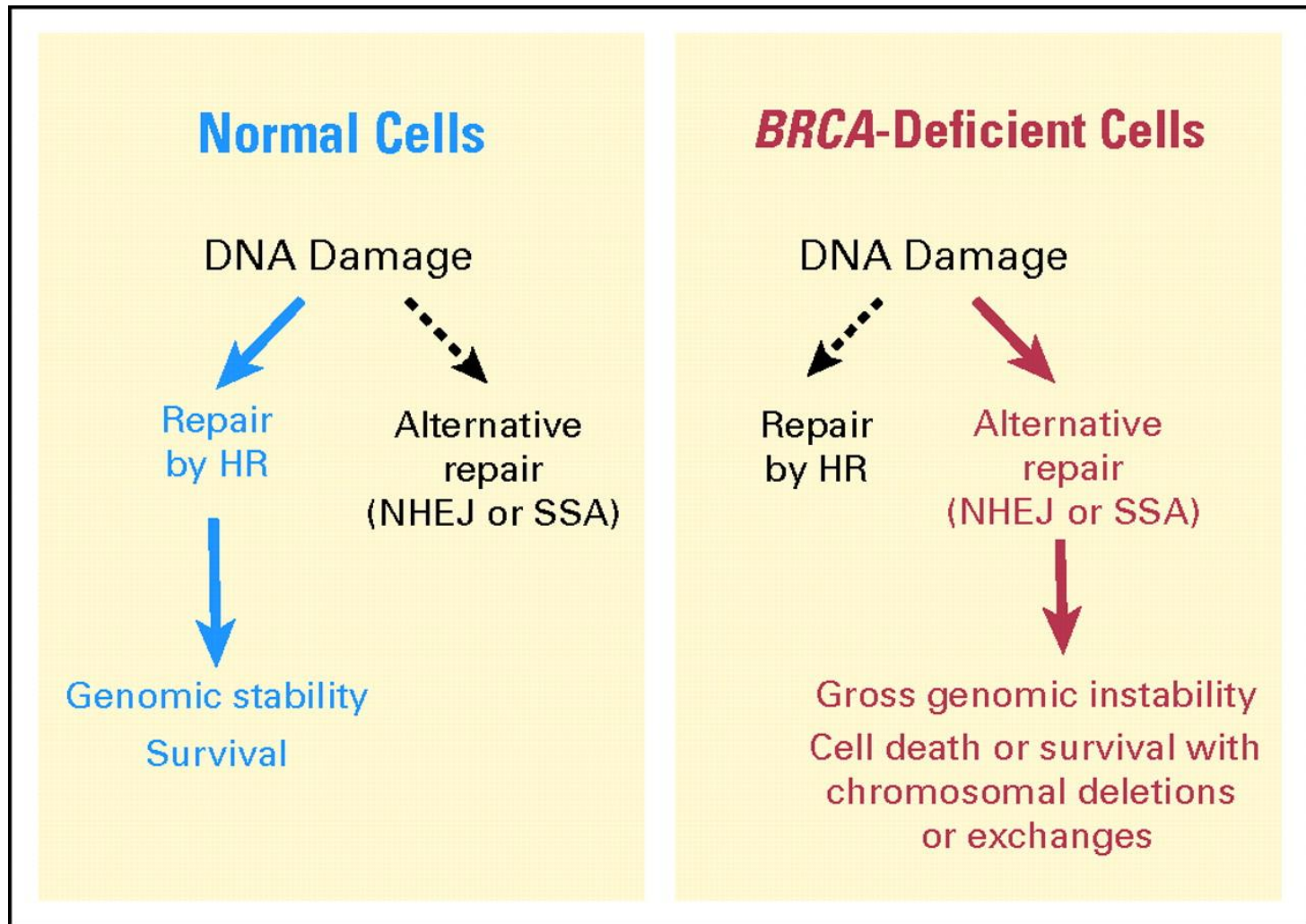
Alan Ashworth

A B S T R A C T

Cancer cells frequently harbor defects in DNA repair pathways, leading to genomic instability. This can foster tumorigenesis but also provides a weakness in the tumor that can be exploited therapeutically. Tumors with compromised ability to repair double-strand DNA breaks by homologous recombination, including those with defects in *BRCA1* and *BRCA2*, are highly sensitive to blockade of the repair of DNA single-strand breaks via the inhibition of the enzyme poly(ADP) ribose polymerase. This provides the basis for a novel synthetic lethal approach to cancer therapy.

Gene <i>X</i>	Gene <i>Y</i>	
+	+	No effect
—	+	No effect
+	—	No effect
—	—	Death

Ashworth A JCO 2008;26:3785-3790



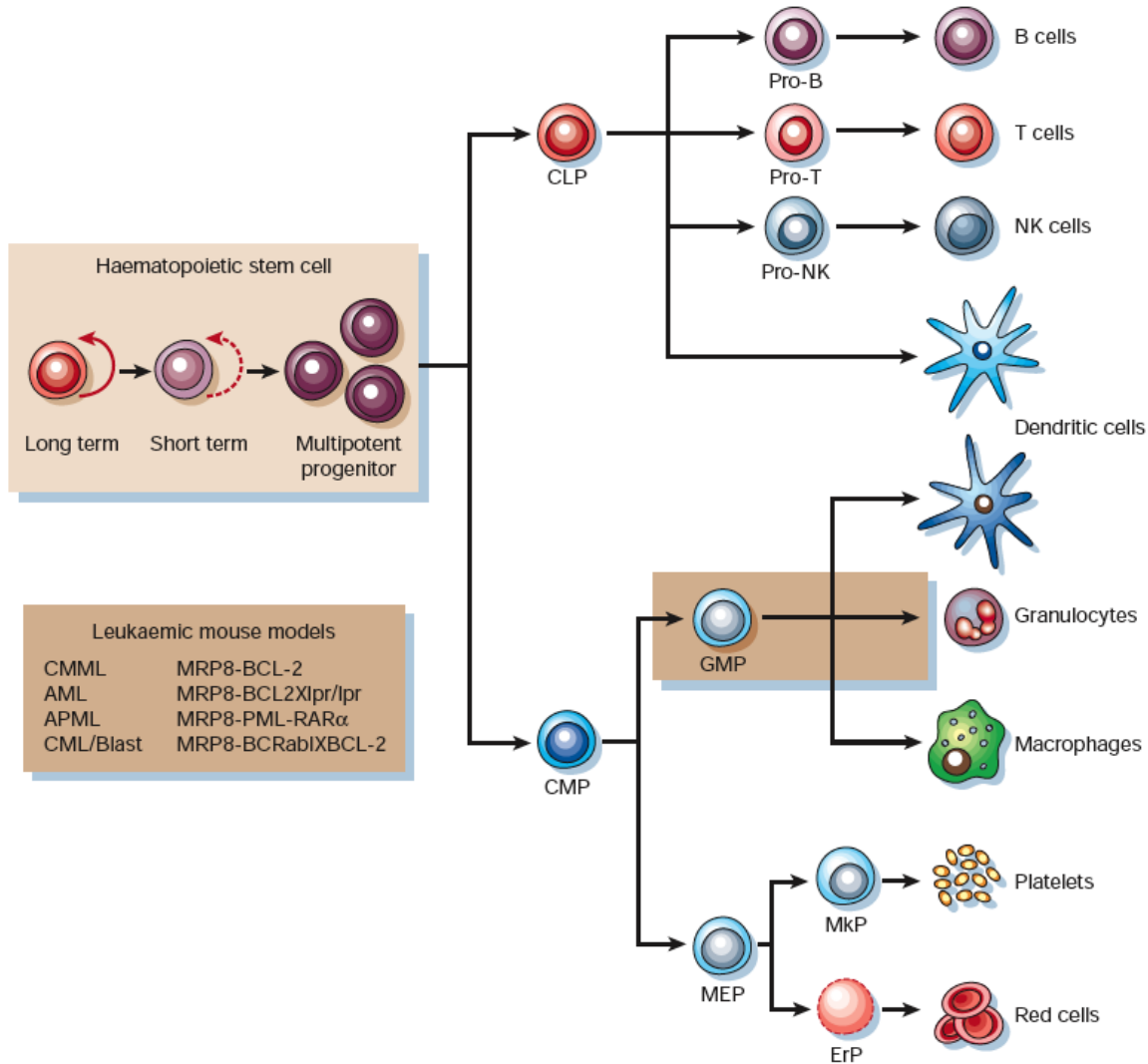
Ashworth A JCO 2008;26:3785-3790

Origins of cancer:

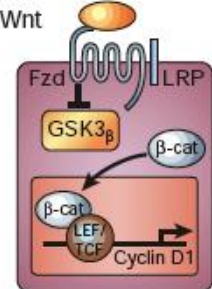
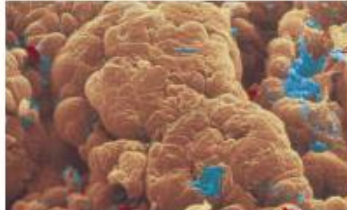
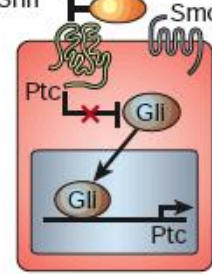
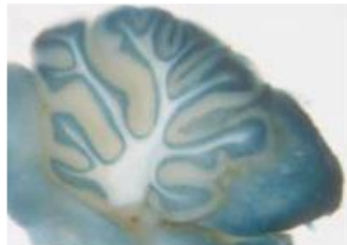
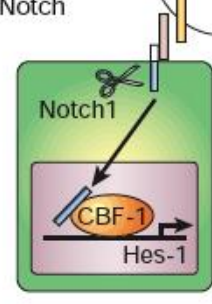
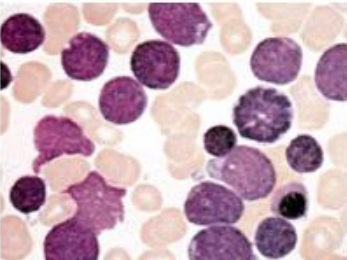
Stem cells

- Long-term capacity to repopulate tissues following injury
- Self-renewal: can reproduce themselves without undergoing differentiation
- Also produce “transit amplifying” cells that have high proliferative potential (but cannot repopulate the tissue permanently)
- Their biology is heavily influenced by epigenetic mechanisms

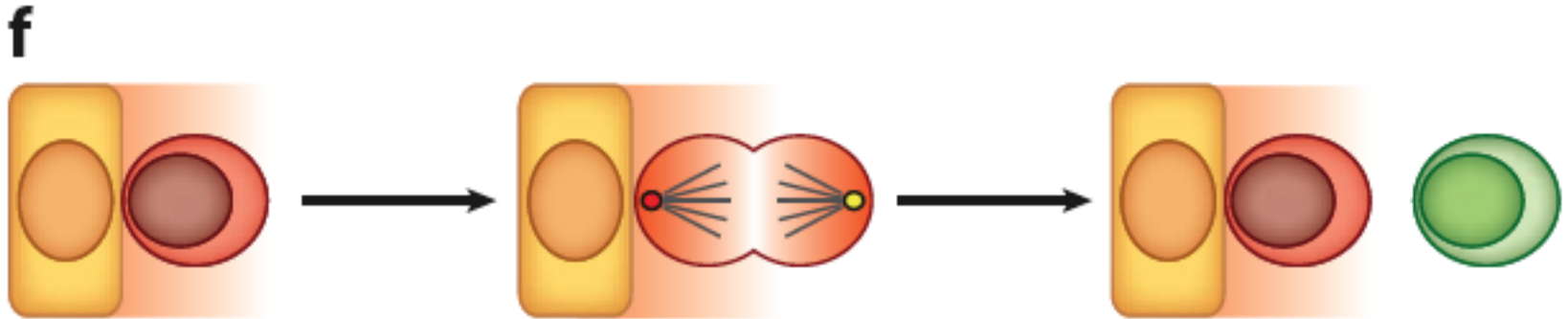
Hematopoietic stem cells



Developmental pathways regulate normal stem cells and cancer

 Wnt	Stem/progenitor cell self-renewal Haematopoietic Epidermal Gut 			Tumorigenesis Colon carcinoma Epidermal tumours 
 Shh	Haematopoietic Neural Germ line 			Medulloblastoma Basal cell carcinoma 
 Notch	Haematopoietic Neural Germ line 			Leukaemia Mammary tumours 

Asymmetric cell division: control by the stem cell niche

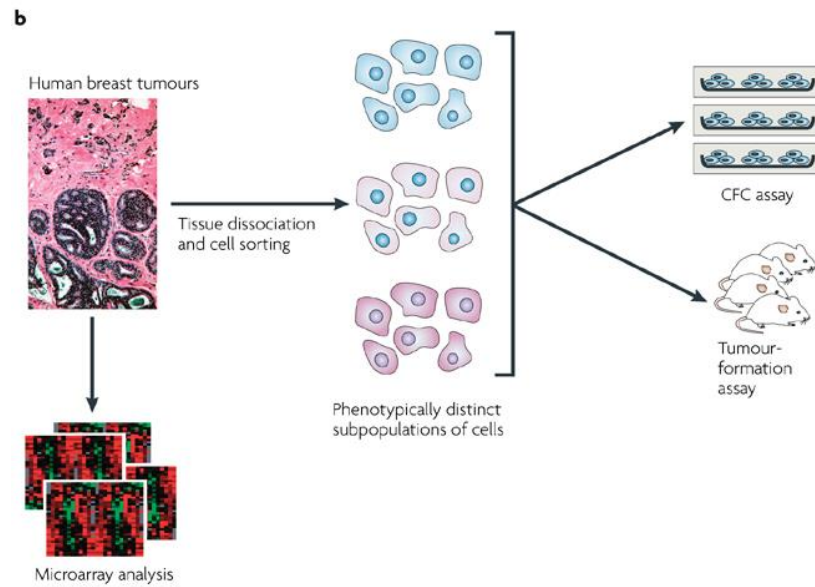
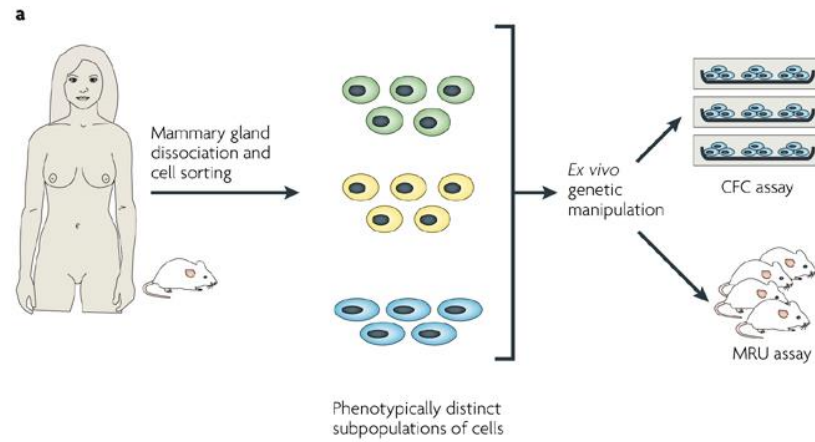


Red cell – daughter cell that remains within the niche.

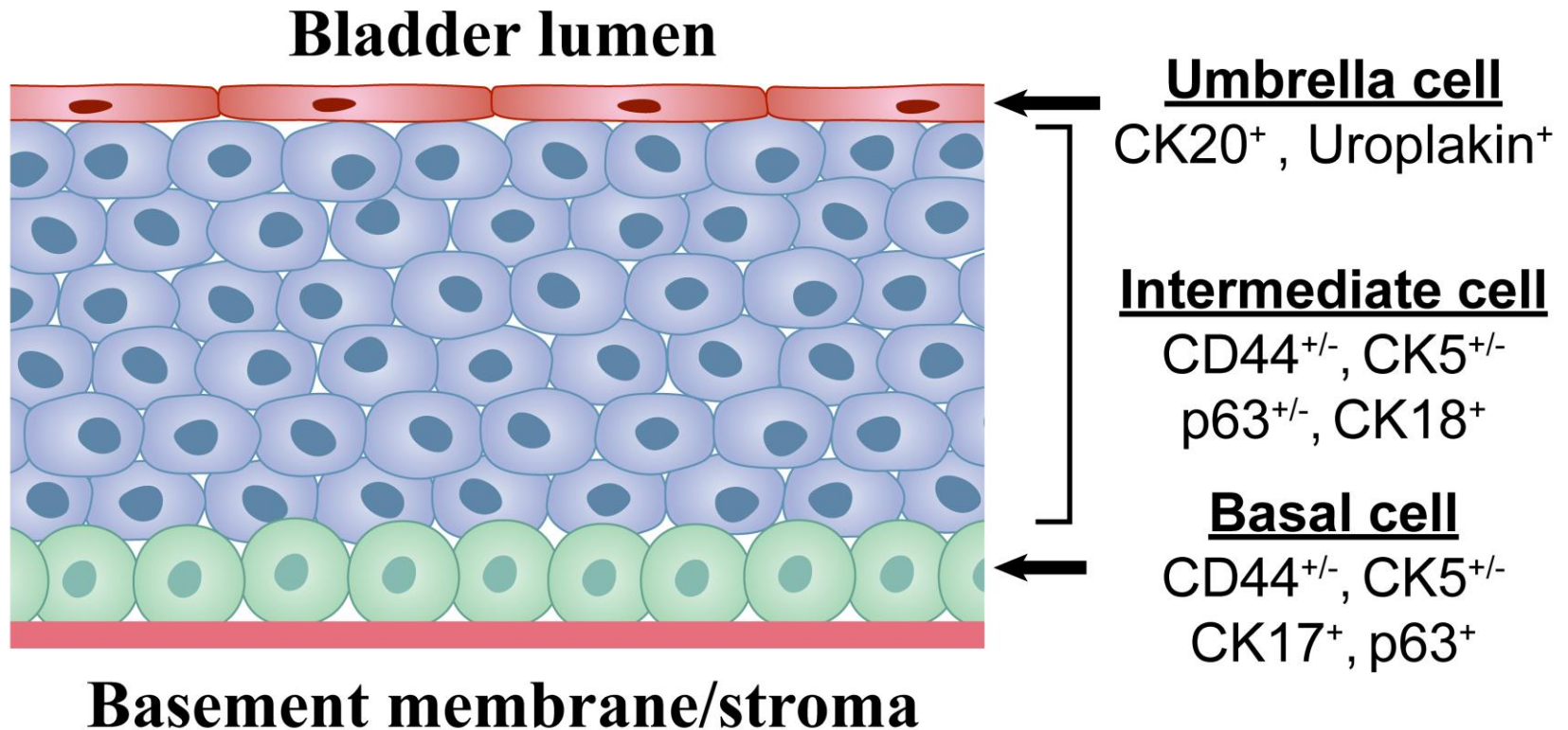
Stem cell niche: the microenvironment in which stem cells reside; promotes stem cell maintenance and regulates stem cell function

Cancers also appear to contain “stem cells”

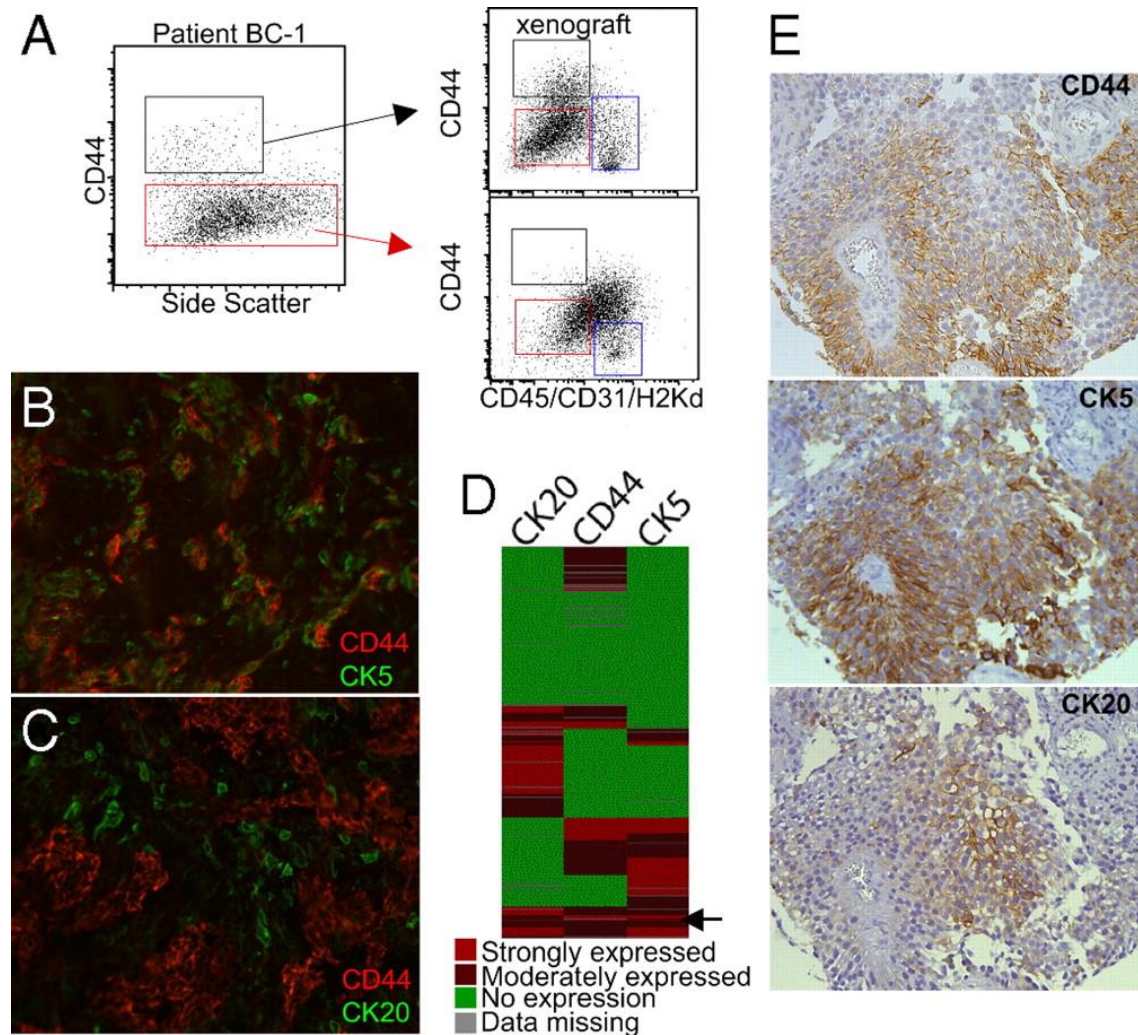
- Subpopulations of cells that can regenerate the whole tumor when transplanted in mice
- The cancer stem cells that have been isolated from different solid tumors and experimentally characterized in mice share biomarkers that are also expressed by the basal layers of surface epithelia
- However, cancers form “intrinsic subtypes” that suggest different cells of origin



Differentiation in the normal urothelium



Bladder tumor-initiating cells possess cell properties in common with bladder basal cells.



Chan K S et al. PNAS 2009;106:14016-14021

Molecular portraits of human breast tumours

Charles M. Perou^{*†}, Therese Sørlie^{†‡}, Michael B. Eisen^{*},
Matt van de Rijn[§], Stefanie S. Jeffrey^{||}, Christian A. Rees^{*},
Jonathan R. Pollack[§], Douglas T. Ross[§], Hilde Johnsen[‡],
Lars A. Akslen[#], Øystein Fluge[☆], Alexander Pergamenschikov^{*},
Cheryl Williams^{*}, Shirley X. Zhu[§], Per E. Lønning^{**},
Anne-Lise Børresen-Dale[‡], Patrick O. Brown^{††} & David Botstein^{*}

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[¶] Department of Biochemistry, Stanford University School of Medicine, Stanford, California 94305, USA

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^{**} Department of Oncology, Haukeland University Hospital, N-5021 Bergen, Norway

^{††} Howard Hughes Medical Institute, Stanford University School of Medicine, Stanford, California 94305, USA

[†] These authors contributed equally to this work

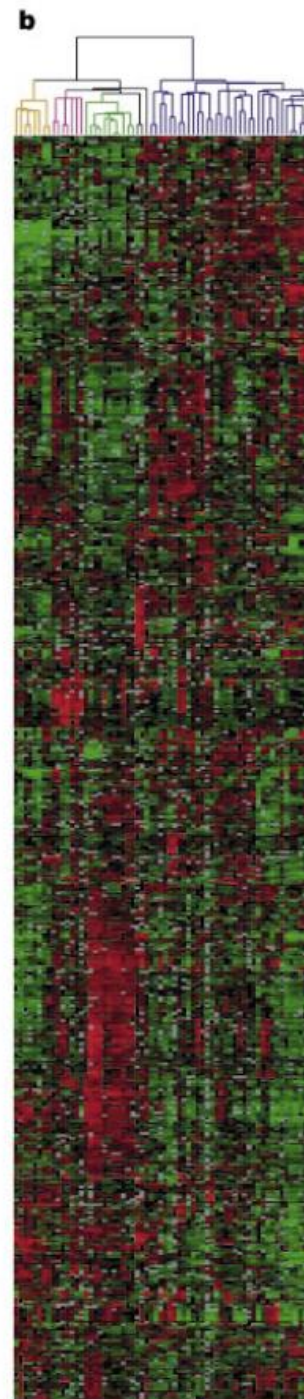
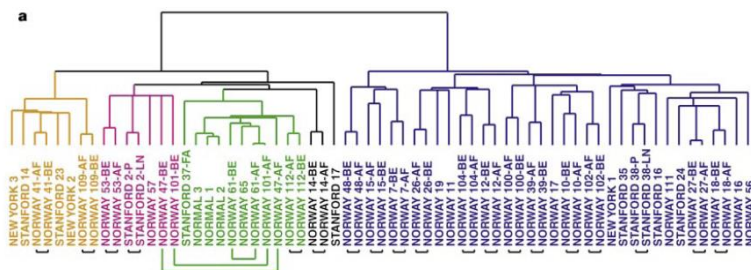
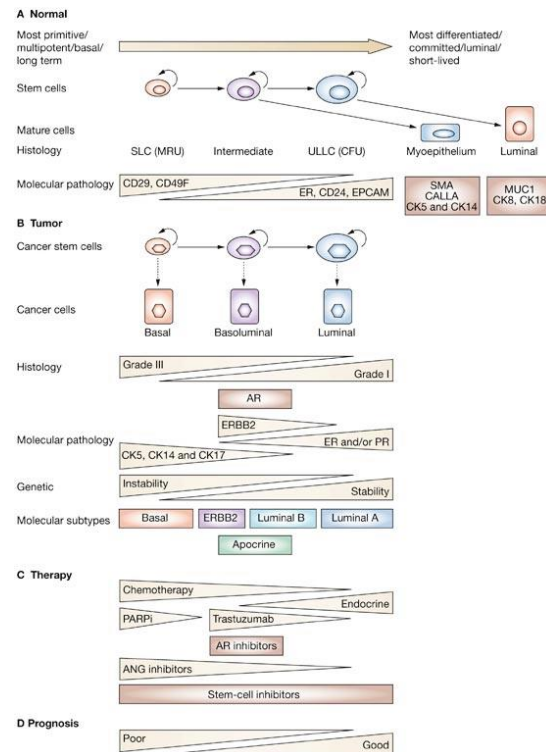
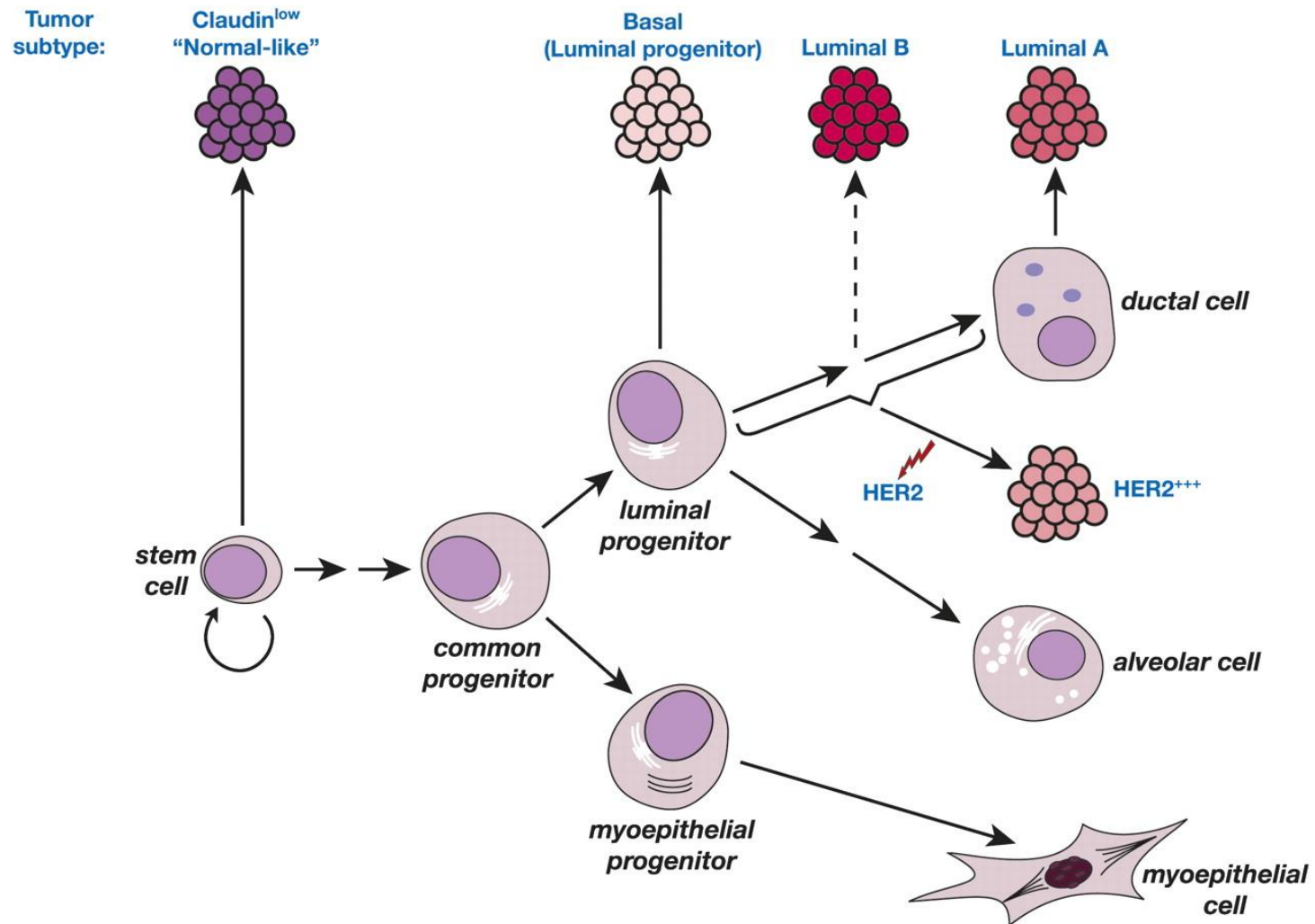


Figure 3 A model of stem-cell hierarchy and how it may account for the origins of different subtypes of breast cancer via cancer stem cells



Sims AH *et al.* (2007) Origins of breast cancer subtypes and therapeutic implications
Nat Clin Pract Oncol 4: 516–525 doi:10.1038/ncponc0908

Schematic model of the human breast epithelial hierarchy and potential relationships with breast tumor subtypes



Visvader J E Genes Dev. 2009;23:2563-2577



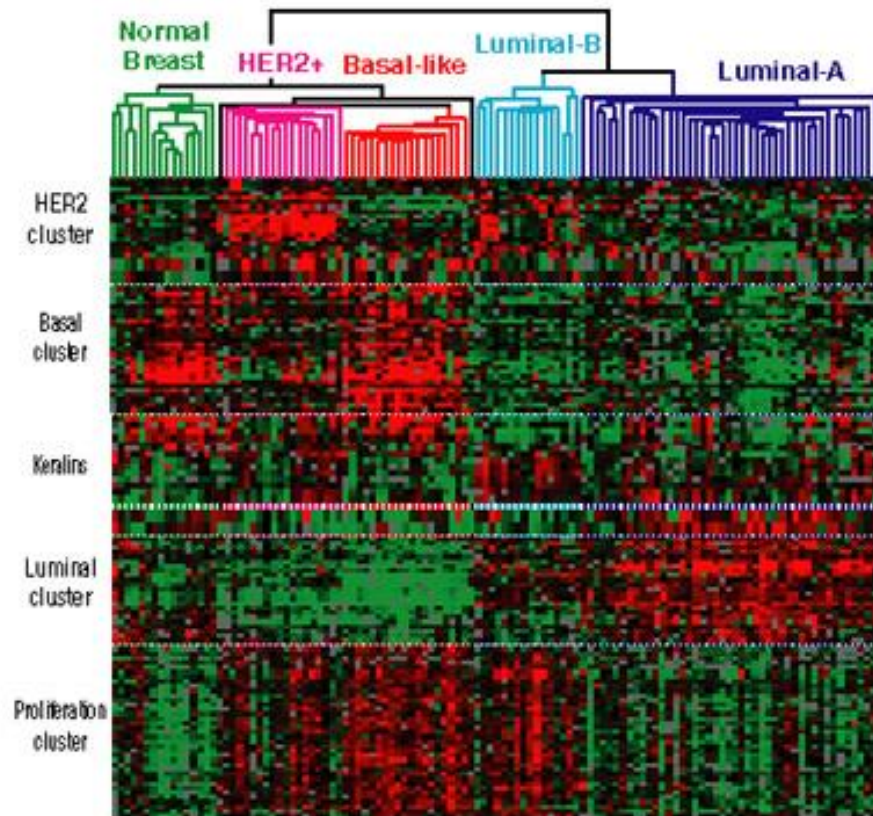
Subtype Implications

letters to nature

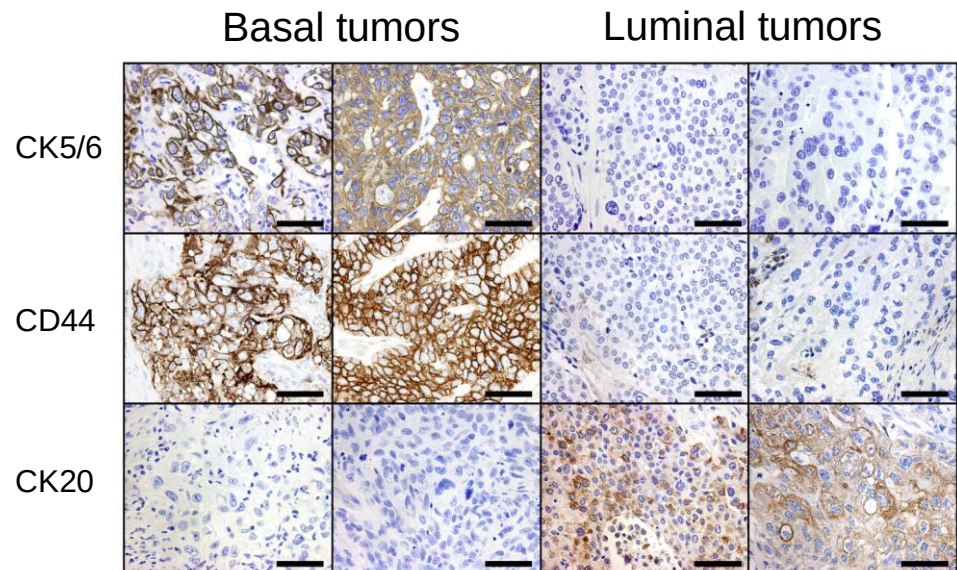
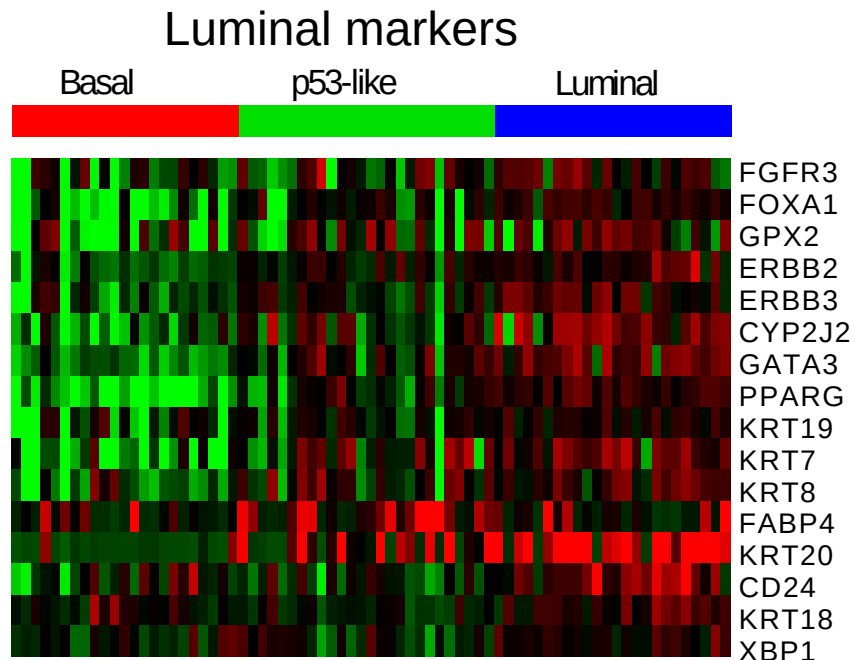
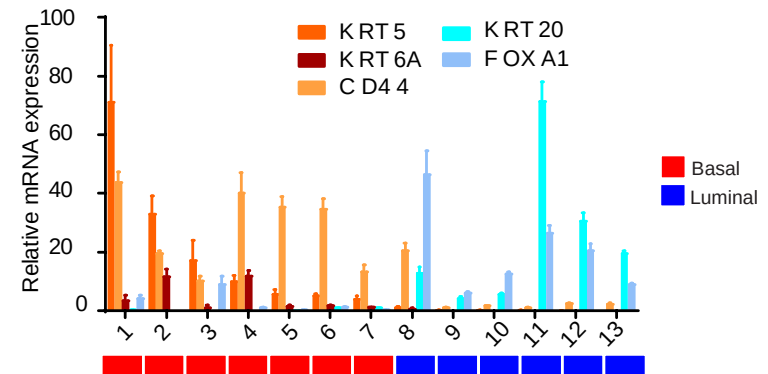
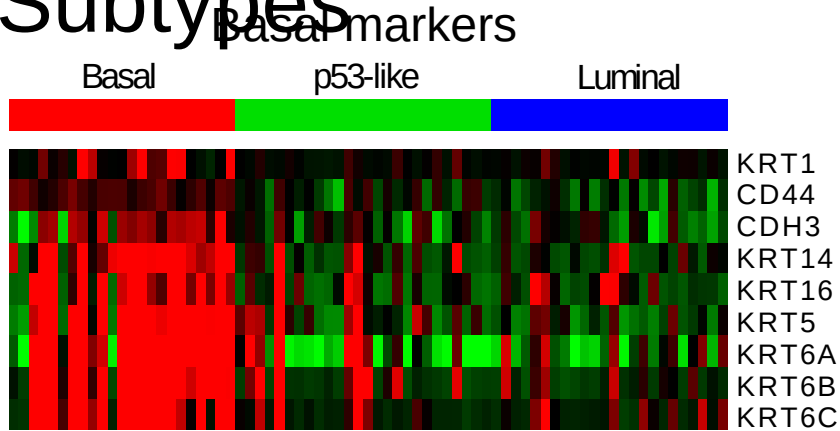
Molecular portraits of human breast tumours

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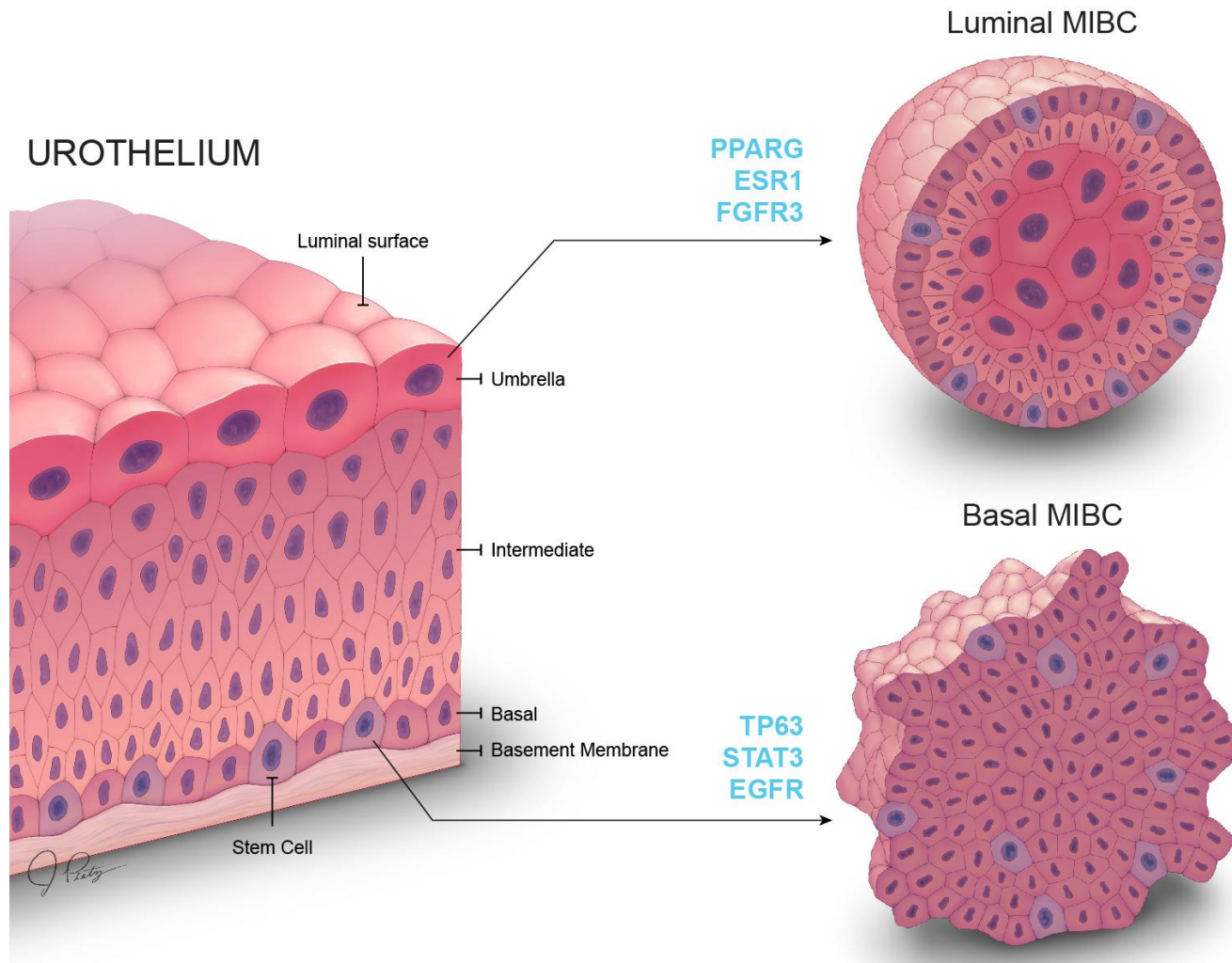
Diversity of Breast Tumor Subtypes



Expression of Basal and Luminal Markers in Subtypes

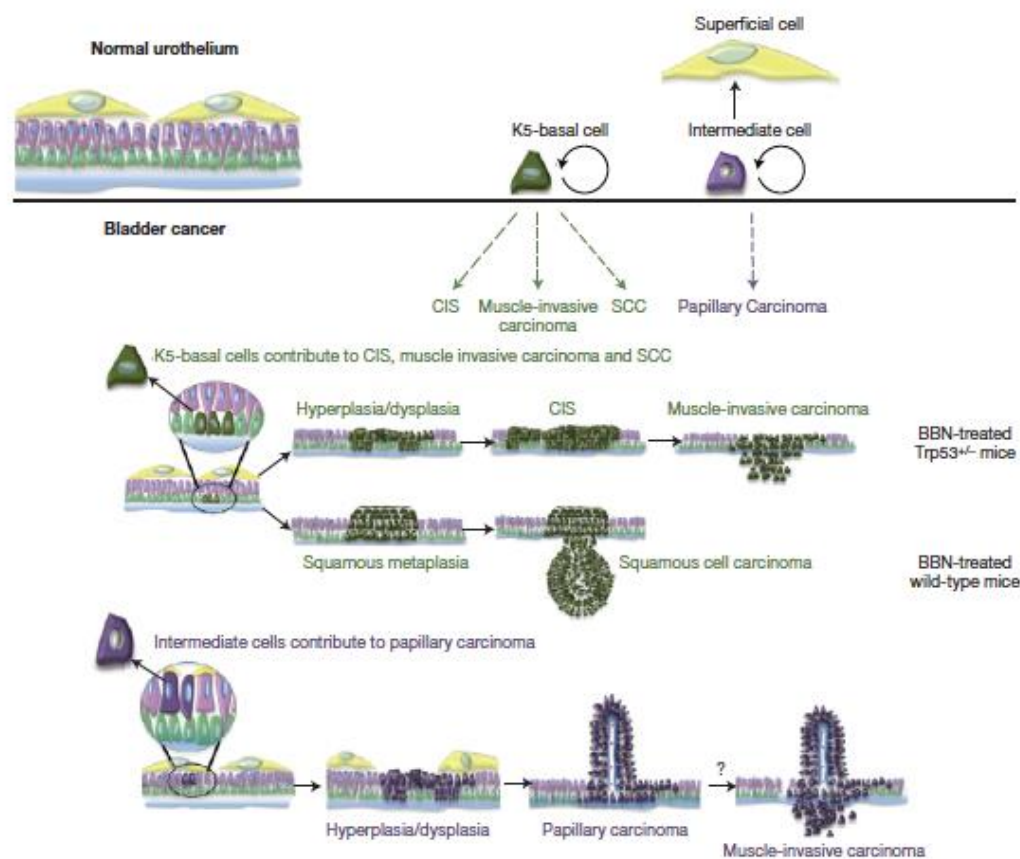


Potential origins of basal and luminal tumors



Bladder cancers arise from distinct urothelial sub-populations

Jason Van Batavia^{1,6}, Tammer Yamany^{1,6}, Andrei Molotkov^{1,6,7}, Hanbin Dan¹, Mahesh Mansukhani², Ekaterina Batourina¹, Kerry Schnelder¹, Daniel Oyon¹, Mark Dunlop¹, Xue-Ru Wu^{3,4}, Carlos Cordon-Cardo⁵ and Cathy Mendelsohn^{1,8}



ARTICLES

A luminal epithelial stem cell that is a cell of origin for prostate cancer

Xi Wang^{1,2,5,6}, Marianna Kruithof-de Julio^{1,2}, Kyriakos D. Economides^{5,7}†, David Walker^{5,6}†, Hailong Yu^{5,6}†, M. Vivienne Halili^{5,6}†, Ya-Ping Hu^{5,6}†, Sandy M. Price^{5,6}, Cory Abate-Shen^{3,4,5,7} & Michael M. Shen^{1,2,5,6}

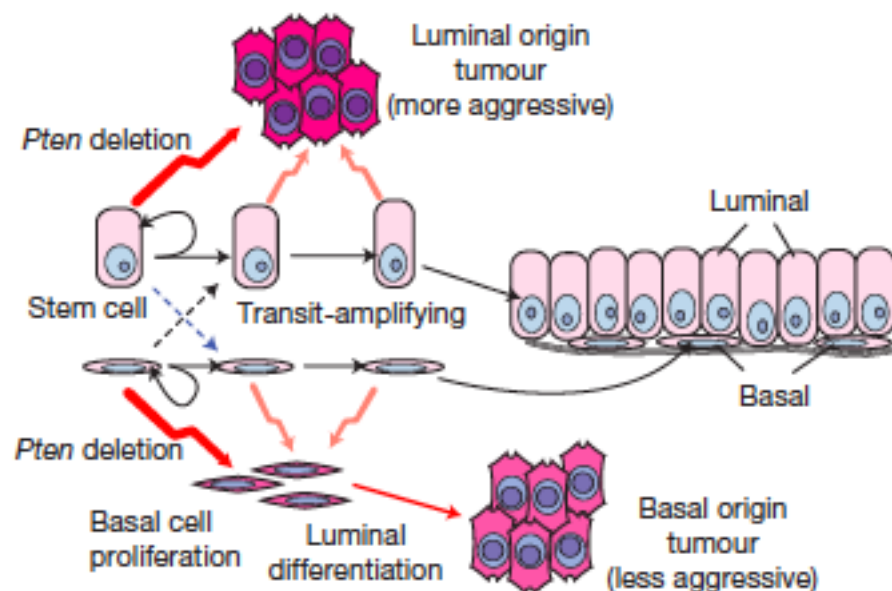
In epithelial tissues, the lineage relationship between normal progenitor cells and cell type(s) of origin for cancer has been poorly understood. Here we show that a known regulator of prostate epithelial differentiation, the homeobox gene *Nkx3-1*, marks a stem cell population that functions during prostate regeneration. Genetic lineage-marking demonstrates that rare luminal cells that express *Nkx3-1* in the absence of testicular androgens (castration-resistant *Nkx3-1*-expressing cells, CARNs) are bipotential and can self-renew *in vivo*, and single-cell transplantation assays show that CARNs can reconstitute prostate ducts in renal grafts. Functional assays of *Nkx3-1* mutant mice in serial prostate regeneration suggest that *Nkx3-1* is required for stem cell maintenance. Furthermore, targeted deletion of the *Pten* tumour suppressor gene in CARNs results in rapid carcinoma formation after androgen-mediated regeneration. These observations indicate that CARNs represent a new luminal stem cell population that is an efficient target for oncogenic transformation in prostate cancer.

Castration-resistant *Nkx3-1*-expressing cells (CARNs)

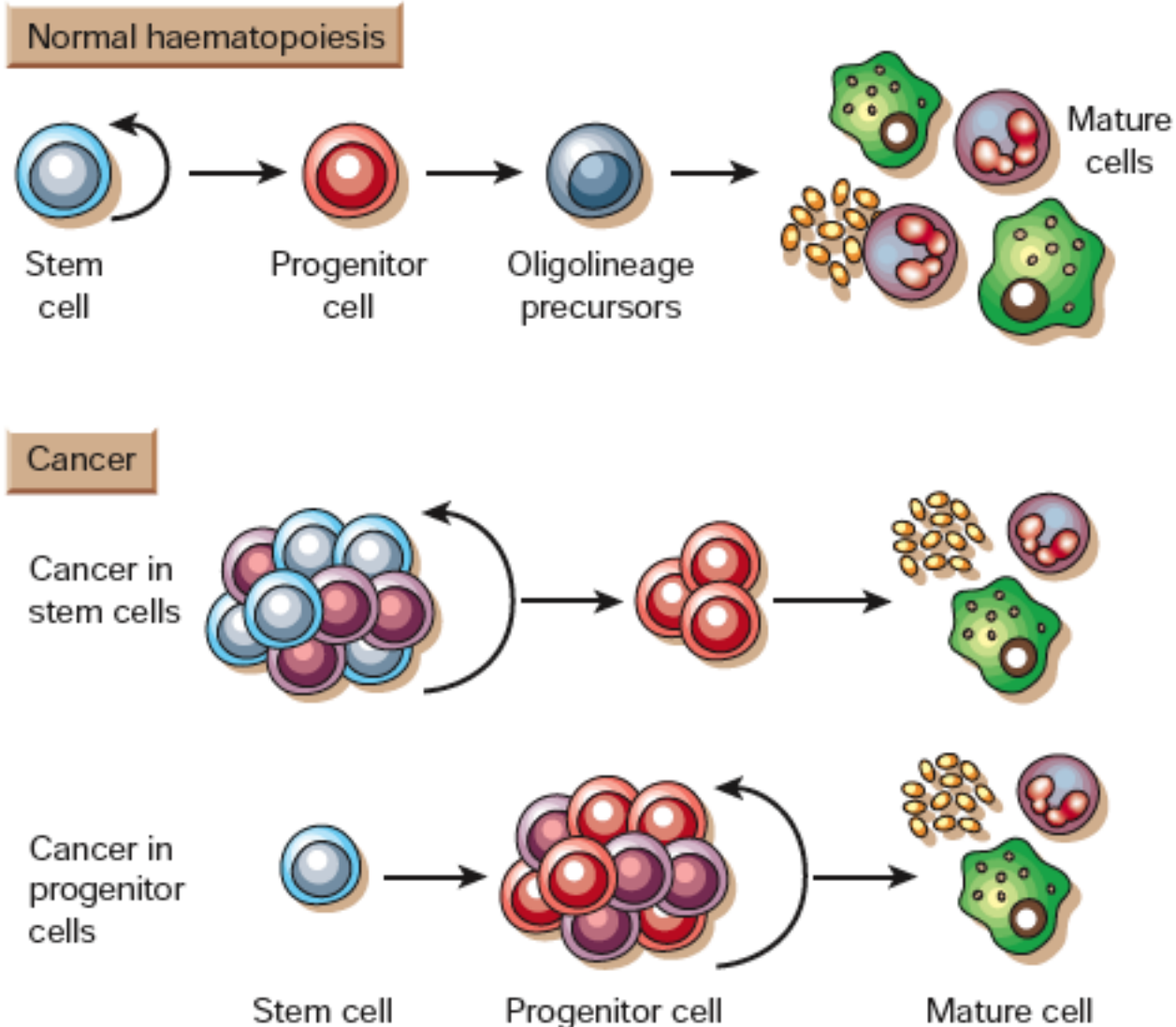
Lineage analysis of basal epithelial cells reveals their unexpected plasticity and supports a cell-of-origin model for prostate cancer heterogeneity

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a Lineage hierarchy



Stem and committed progenitor cells can both give rise to cancer



The Epithelial-Mesenchymal Transition Generates Cells with Properties of Stem Cells

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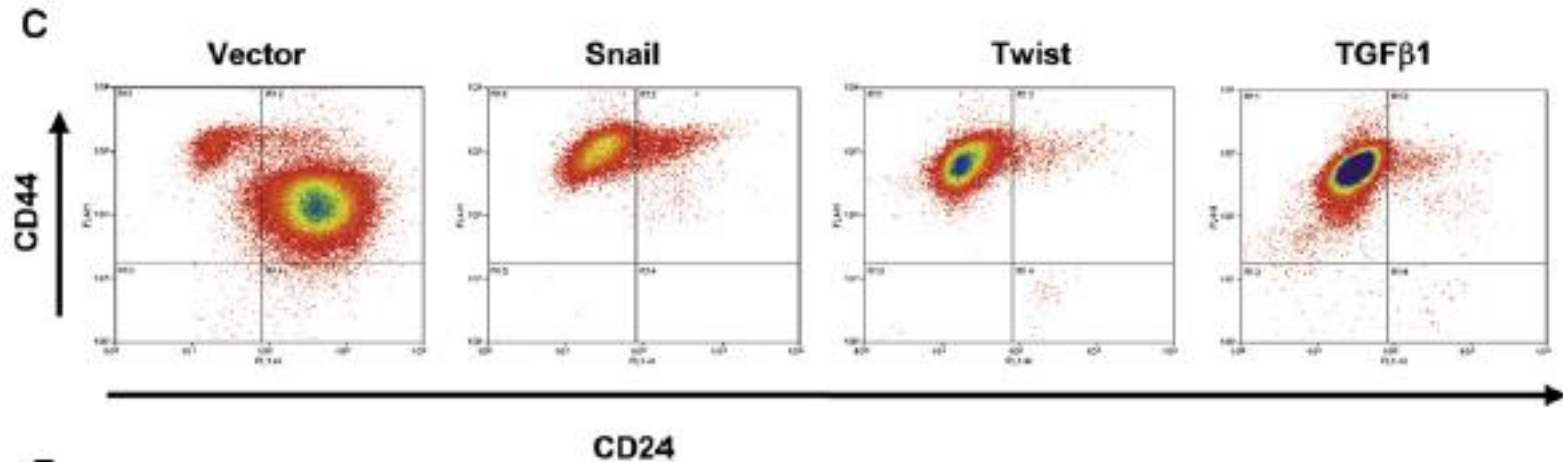
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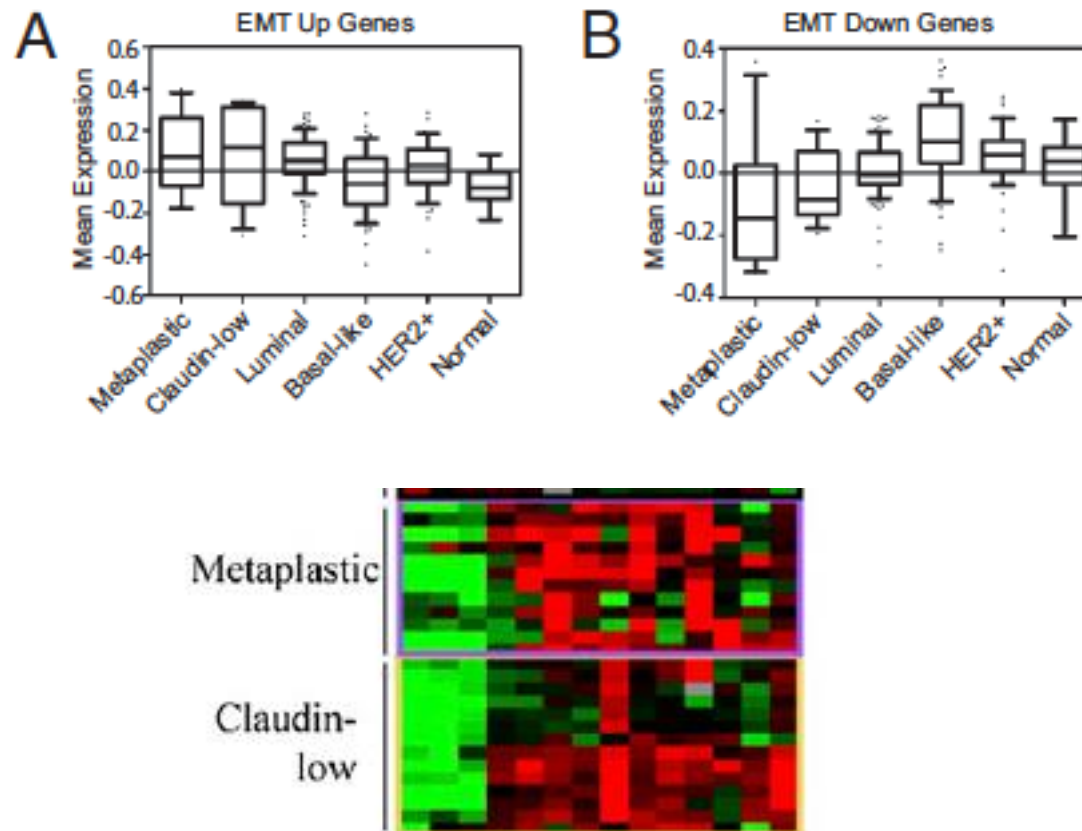
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Core epithelial-to-mesenchymal transition interactome gene-expression signature is associated with claudin-low and metaplastic breast cancer subtypes

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TCGA_Subtype David_Subtype

relative

-3 -1.5 0 1.5 3

TCGA_Subtype David_Subtype

TCGA_Subtype

miR 200 family

Epithelial markers

Mesenchymal markers

Gene ID

hsa-mir-141

hsa-mir-200c

hsa-mir-200a

hsa-mir-200b

hsa-mir-429

EPCAM

CDH1

CLDN4

MUC1

CLDN7

CLDN3

CD44

hsa-mir-205

KRT5

KRT14

KRT6A

TP63

EGFR

SNAI2

ALDH1A1

hsa-mir-155

MIR155HG

THY1

VIM

ZEB1

ZEB2

SNAI1

TWIST1

TCGA cluster IV = UNC “claudin-low”

Poised Chromatin at the ZEB1 Promoter Enables Breast Cancer Cell Plasticity and Enhances Tumorigenicity

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Basal tumor cells can easily switch between “epithelial” and “mesenchymal” states

Stem cell kinetics are associated with cancer incidence

- There is a linear relationship between the odds that a given tissue will produce a tumor and its kinetics of stem cell self-renewal
- In these tissues cancer may be caused by mistakes in the repair of the random DNA damage that occurs during self-renewal rather than to environmental exposures

Rethinking cancer etiology

NEWS | IN DEPTH

BIOMEDICINE

The bad luck of cancer

Analysis suggests most cases can't be prevented

By Jennifer Couzin-Frankel

Why? That's the first word on many lips after a cancer diagnosis. "It's a perfectly reasonable question," says Bert Vogelstein, a cancer geneticist at Johns Hopkins University in Baltimore, Maryland, who has spent a lifetime trying to answer it. Thanks to his friendship with a recently minted Ph.D. in applied mathematics, the two now propose a framework arguing that most cancer cases are the result of biological bad luck.

In a paper published on page 78 this week in *Science*, Vogelstein and Cristian Tomasetti,



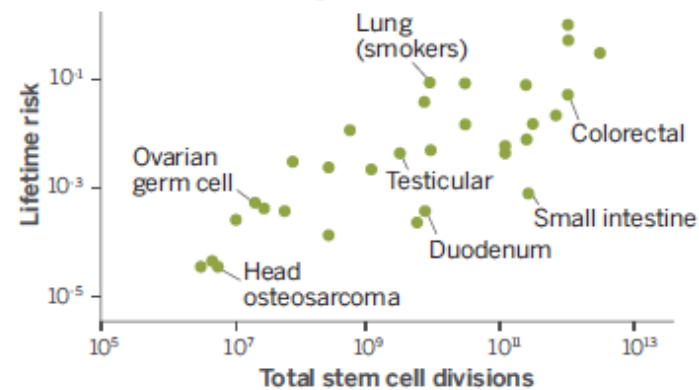
Random mutations in healthy cells may explain two-thirds of cancers, like this one in the colon.

who studies mathematics and biology at Harvard University and has worked with Tomasetti and Vogelstein. "It's a baseline risk of being an animal that has cells that need to divide."

The idea emerged during one of the pair's weekly brainstorming sessions in Vogelstein's office. They returned to an age-old question: How much of cancer is driven by environmental factors, and how much by genetics?

Charting cancer risk

As the number of stem cell divisions in a tissue rises, so does the chance of cancer striking that site.



Science,