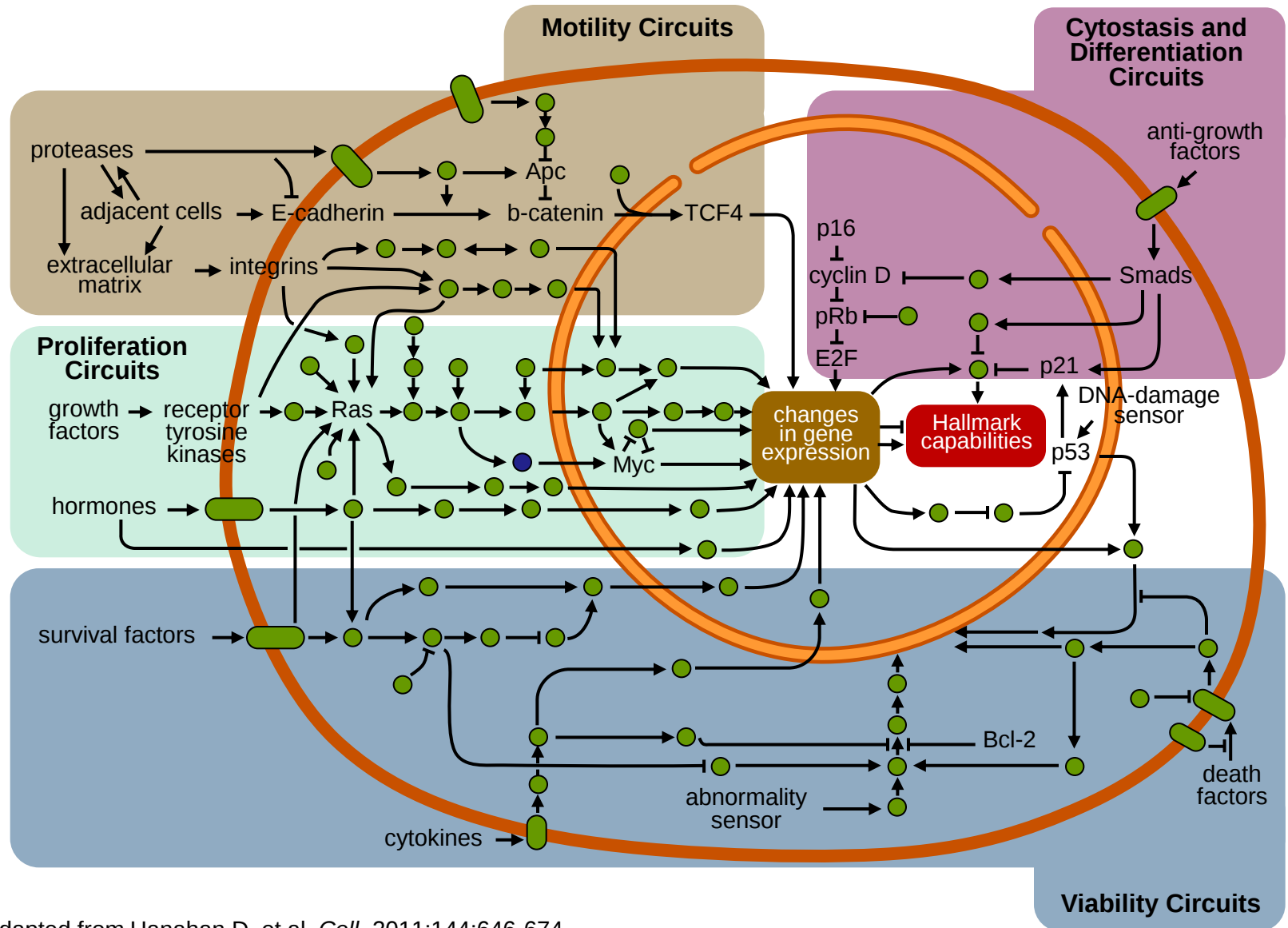


# Genomic Landscape of mCRC and GIST

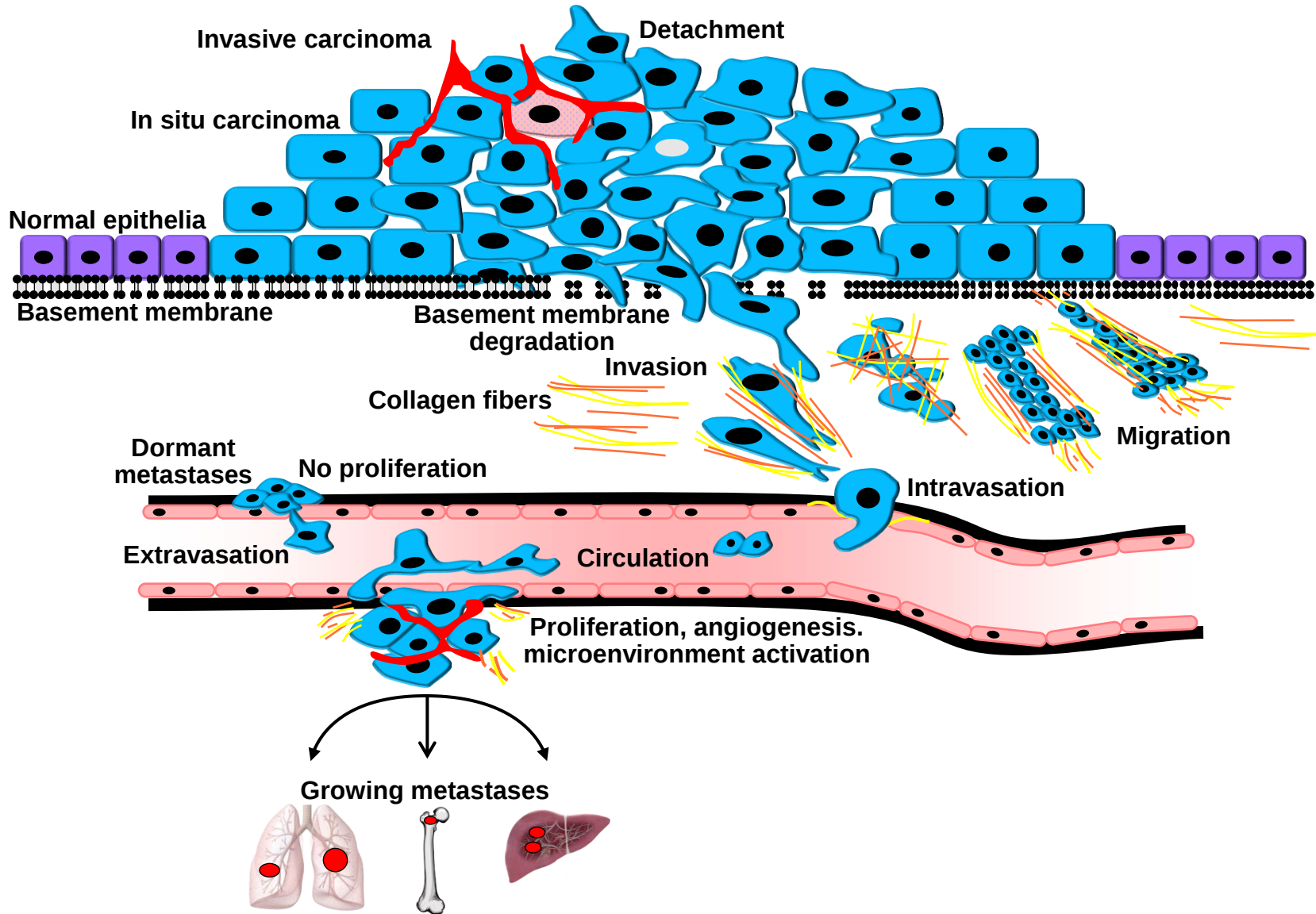
**Heinz-Josef Lenz, MD**

University of Southern California  
Norris Comprehensive Cancer Center  
Los Angeles, California

# Intracellular Signaling Networks Within Cancer Cells

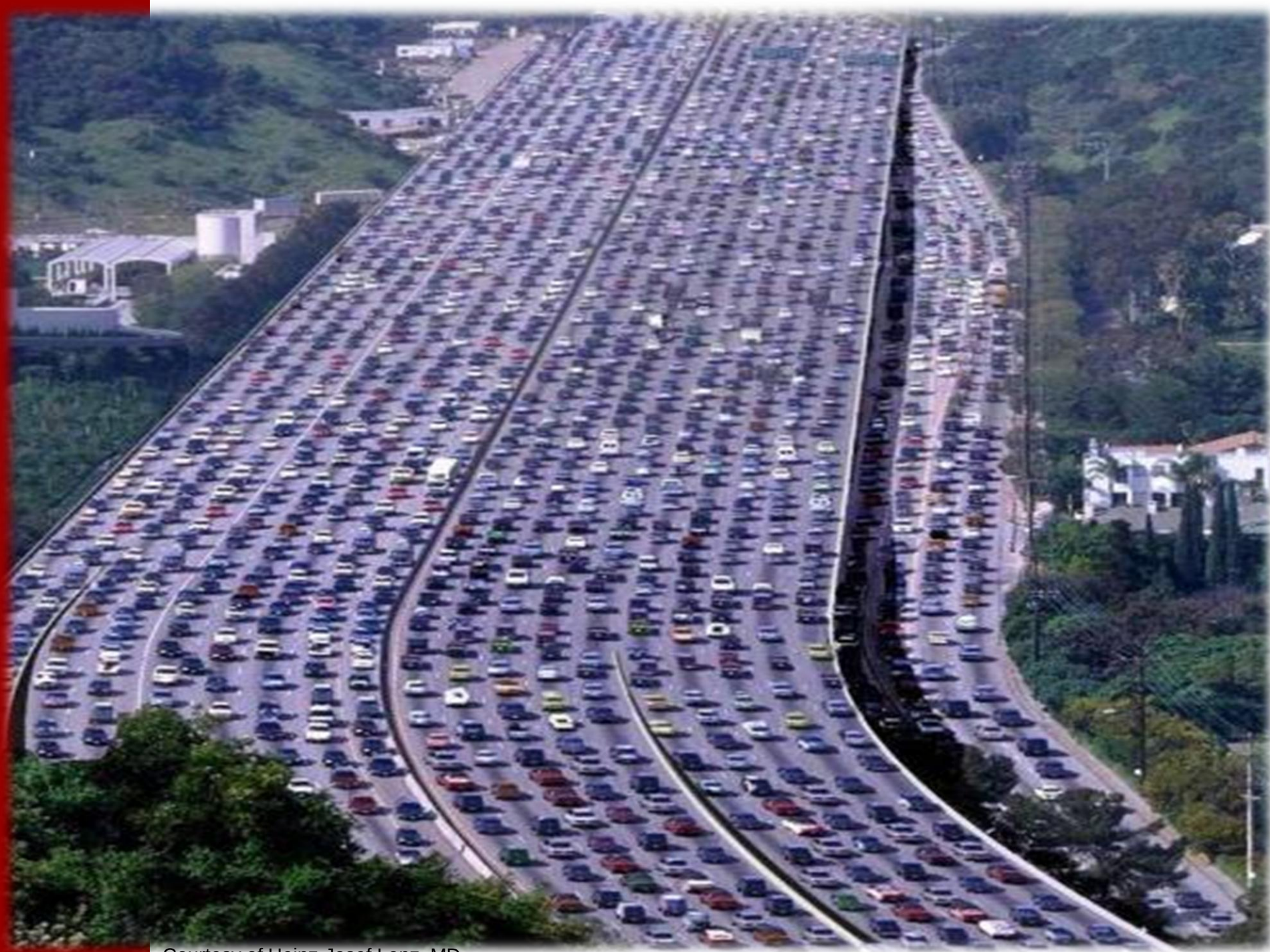


# Metastatic Cancer Cell



# The Driver and the Passenger



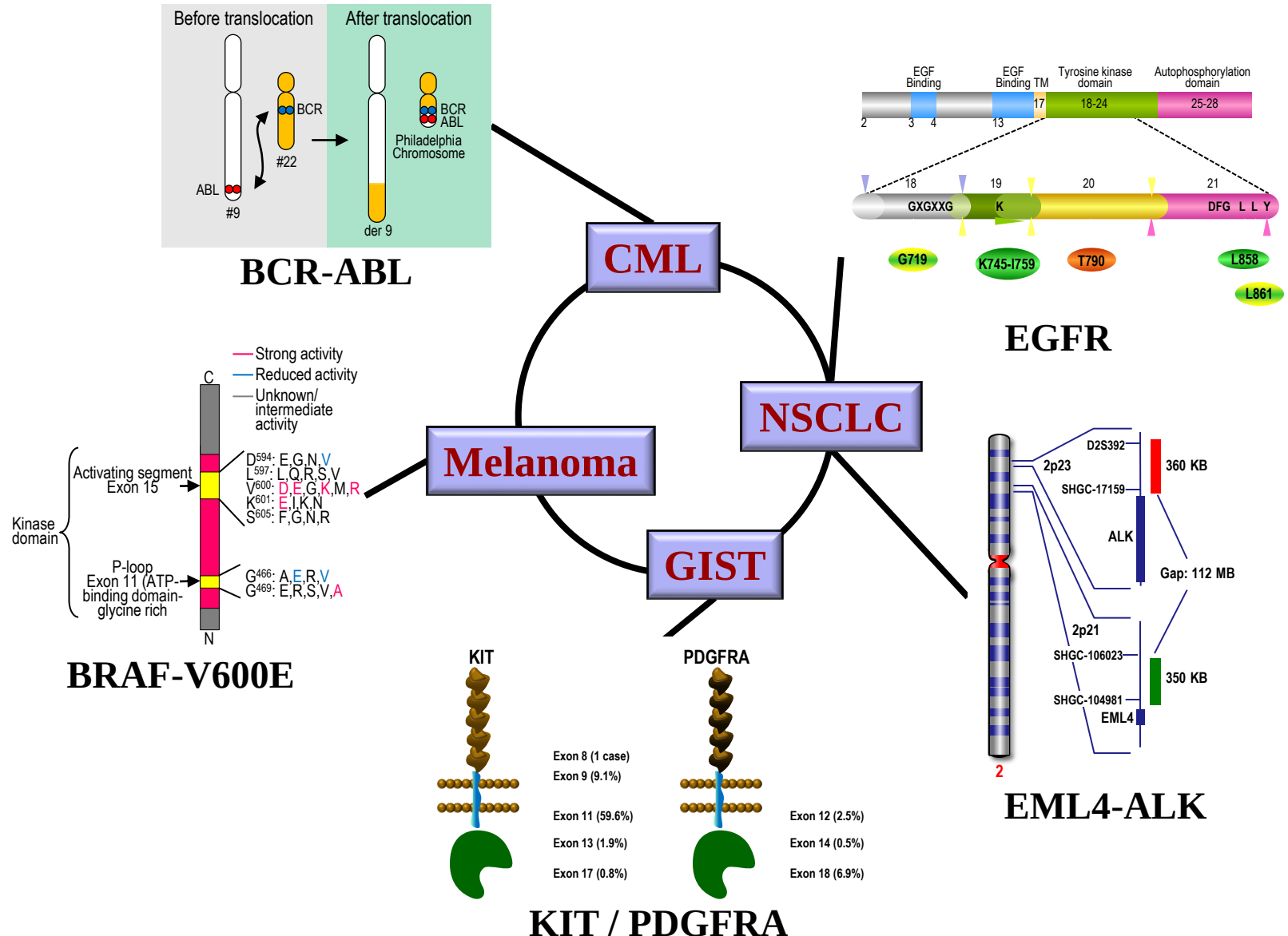


Courtesy of Heinz-Josef Lenz, MD.



Courtesy of Heinz-Josef Lenz, MD.

# The Drivers We Know Well

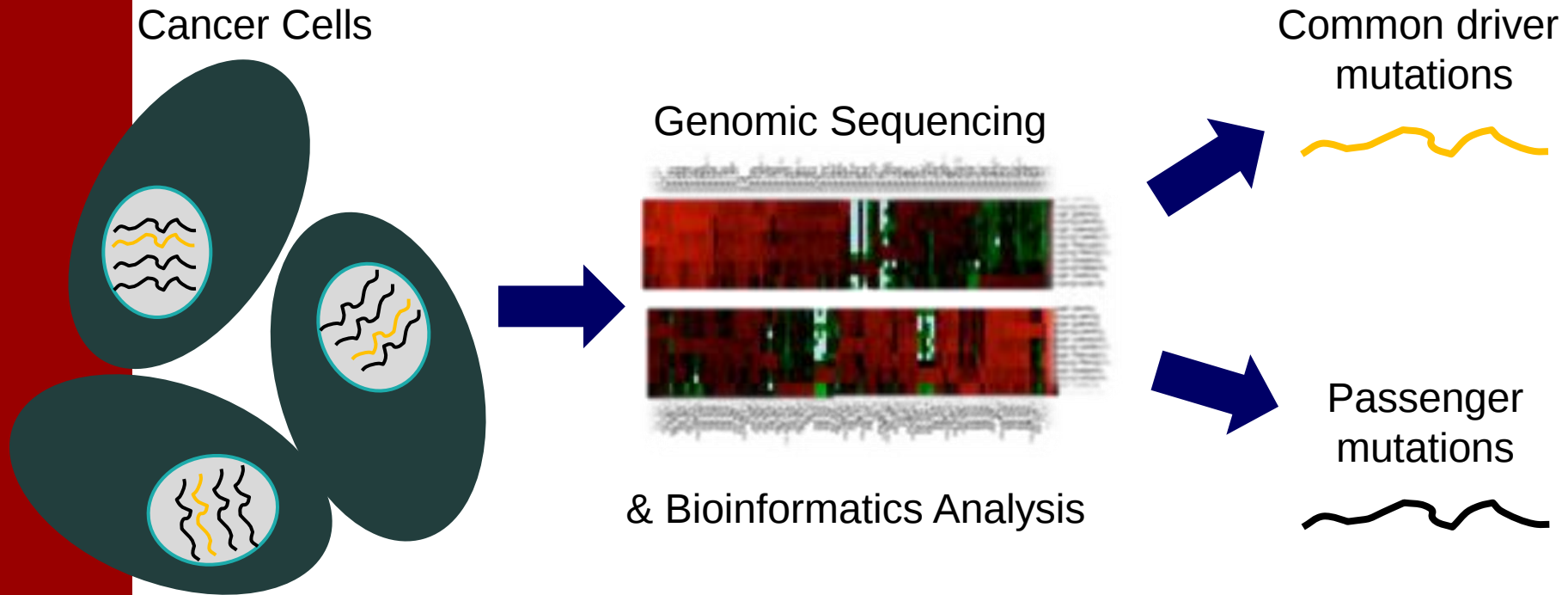


Adapted from: 1. Arkenau H-T, et al. *Br J Cancer*. 2011;104:392-398; 2. Haslam S. *Core Evid*. 2005;1:1-12; 3. SM-EGFR-DB. <http://www.somaticmutations-egfr.info/NSCLC.html>. Accessed September 11, 2012; 4. GIST Support International. <http://www.gistsupport.org/ask-the-professional/gist-with-pdgrf-alpha-mutations.php>. Accessed September 11, 2012; 5. KREATECH Diagnostics. <http://www.kreatech.com/?id=368>. Accessed September 11, 2012.

# Difference Between mCRC and GIST Driver vs Passenger Mutations

- Somatic mutations found in cancers are either “drivers” or “passengers”
  - Driver mutations are causally involved in the neoplastic process and are positively selected for during tumorigenesis (cKIT in GIST)
  - Passenger mutations provide no positive or negative selective advantage to the tumor but are retained by chance during repeated rounds of cell division and clonal expansion (Kras mutation in mCRC)

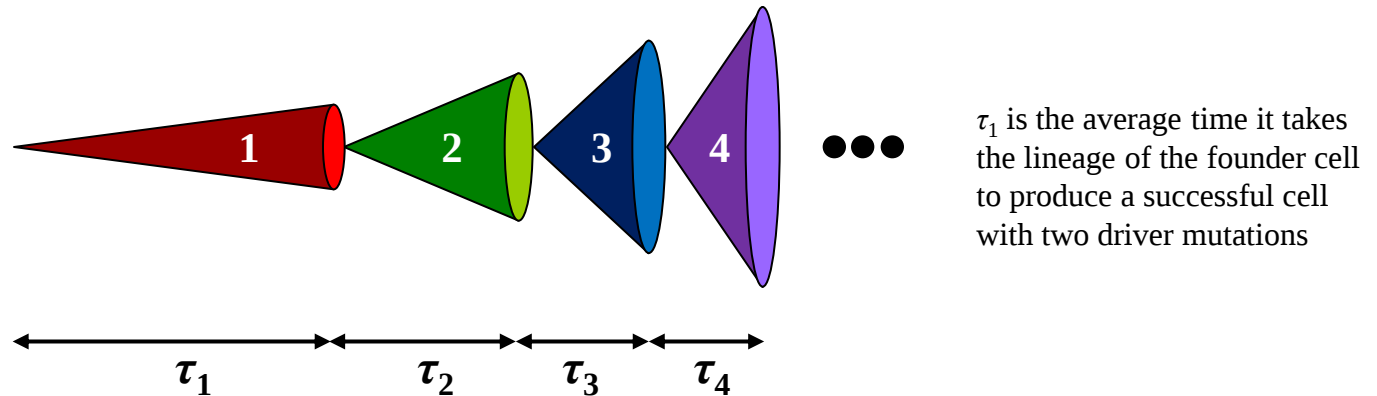
# Identification of Driver Mutations



# Distinguishing the Drivers from the Passengers

- Largely driven by modeling<sup>1,2</sup>
- Solid tumors typically contain 40-100 coding gene alterations, including 5-10 driver mutations<sup>2</sup>
- Driver mutations promote tumor expansion and similarly arise in a tumor of growing size<sup>2</sup>

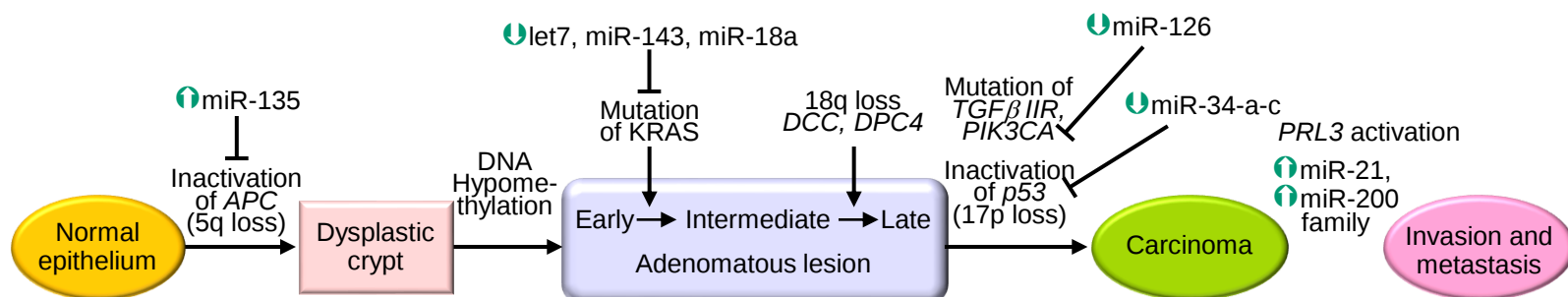
## Clonal Expansion with Cumulative Driver Mutations<sup>2</sup>



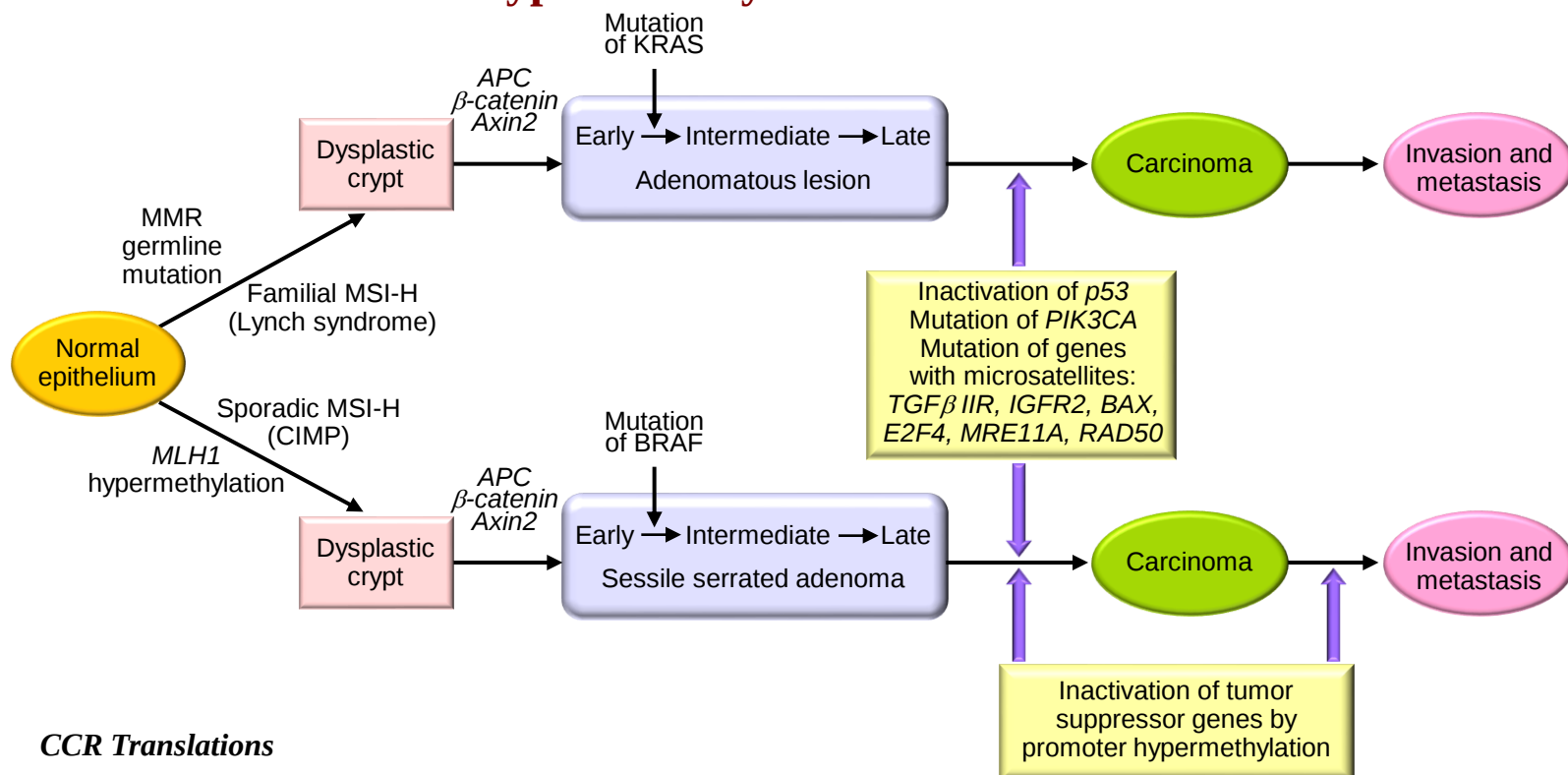
- Analysis of growth rate, average cell division time in a given tumor, expected number of driver versus passenger mutations, and validation screening of identified mutations  $\longrightarrow$  isolation of probable drivers<sup>2</sup>

# **mCRC and GIST: Transformation Process and Therapeutic Targeting**

## MSS – Chromosomal Instability Pathway

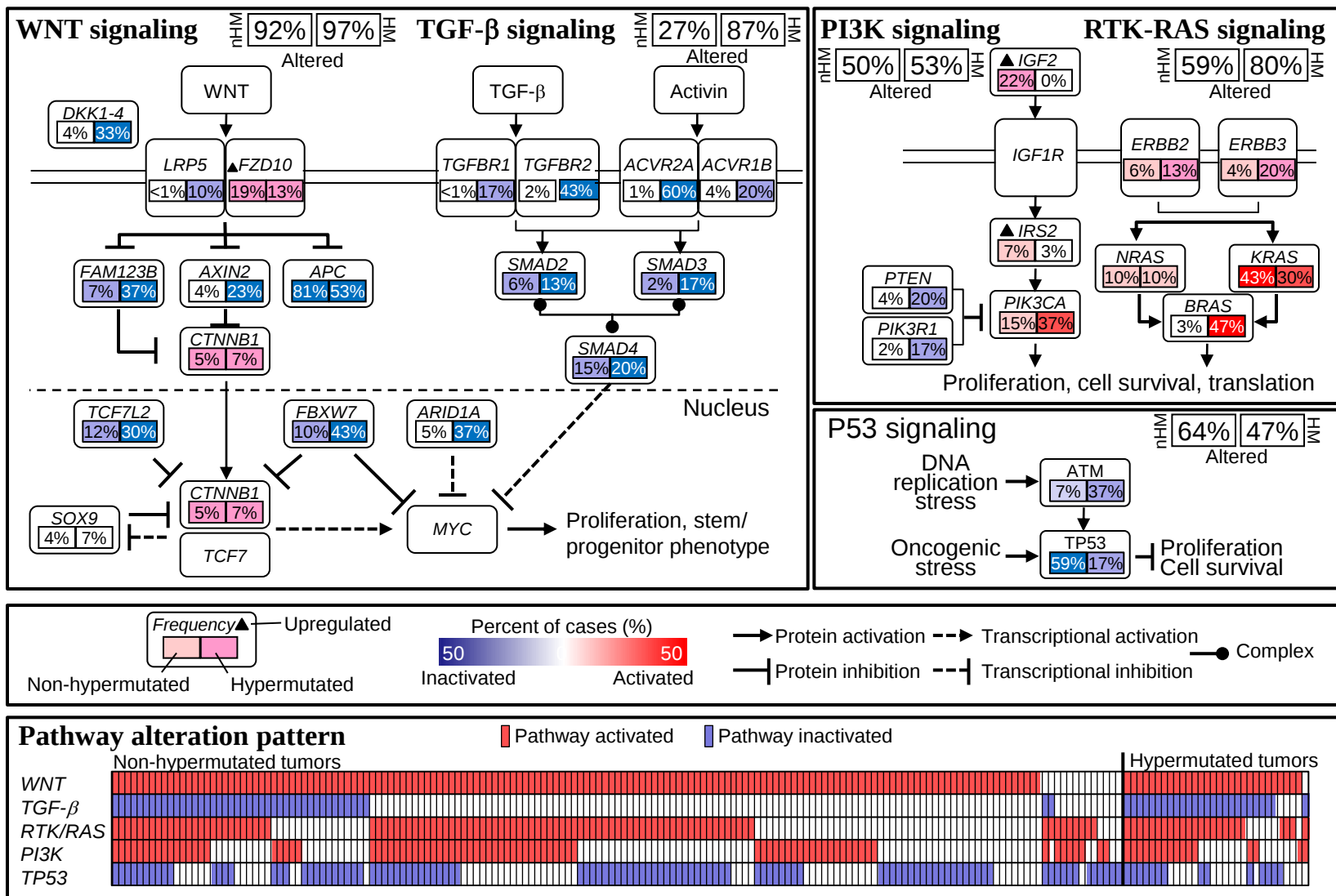


## MSI – Mutator Phenotype Pathway



### CCR Translations

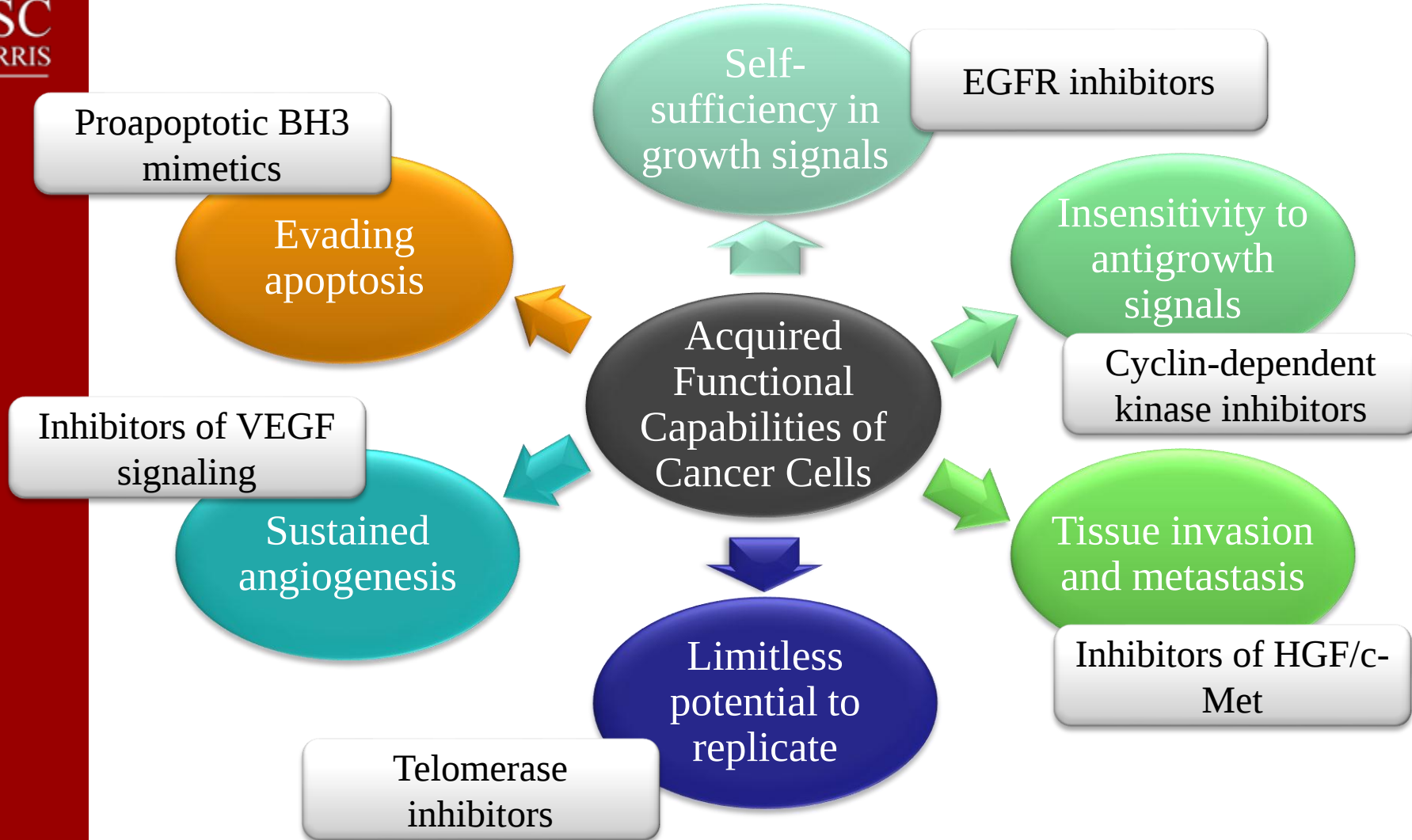
# Genetic Changes in CRC

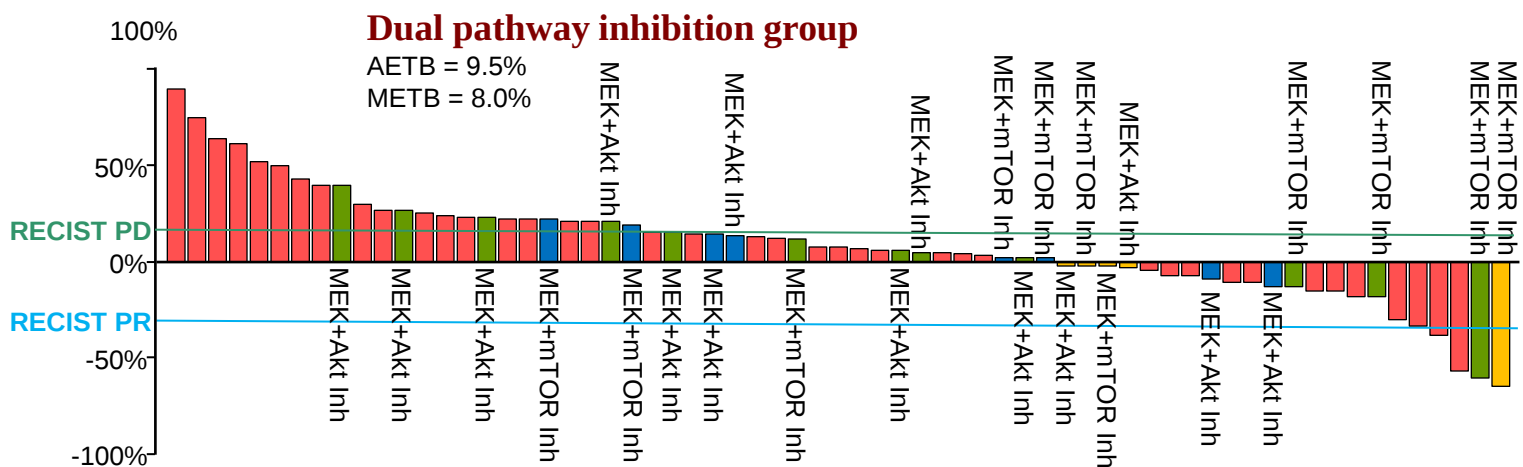
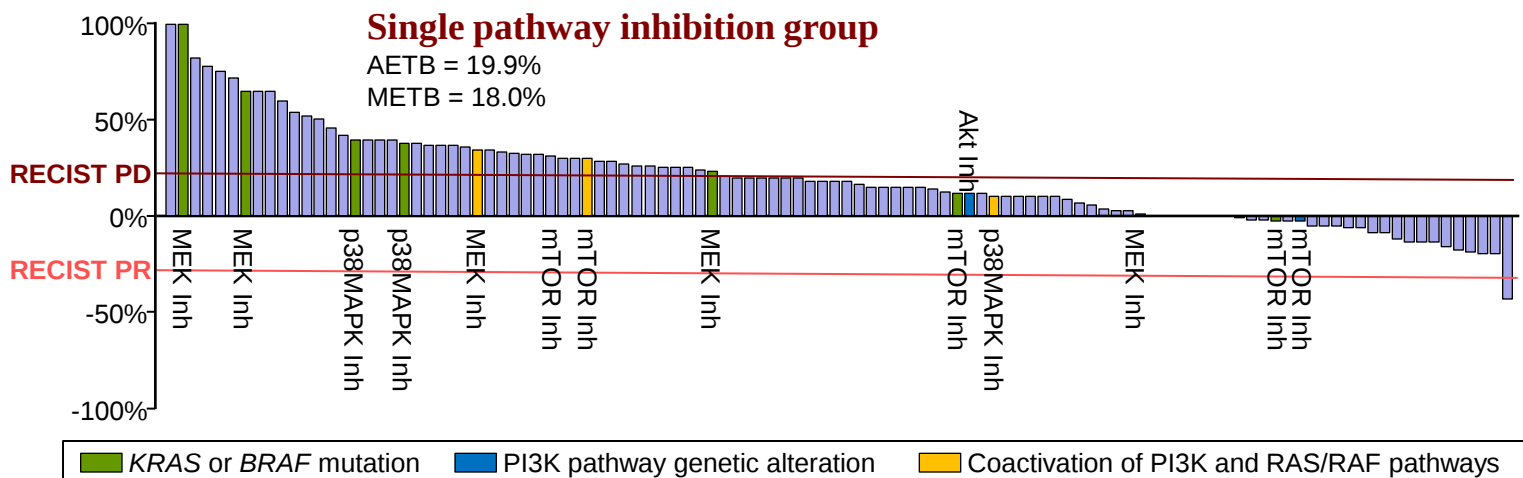




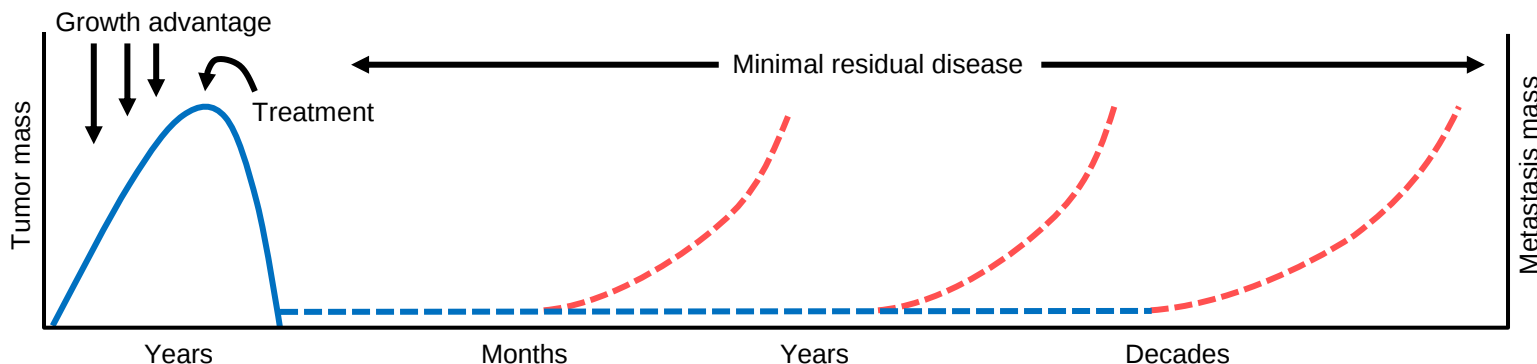
Courtesy of Axel Grothey, MD.

# Hallmarks of Cancer – Therapeutic Targeting



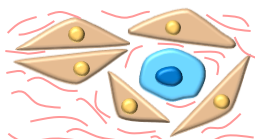


## Genetic/Epigenetic Changes

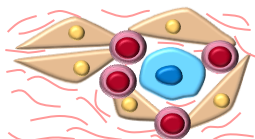


## Cellular Dormancy

Quiescent solitary tumor cell  
Microenvironment-dependent

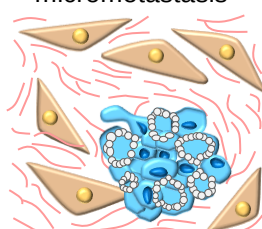


Evasion of the immune system  
by quiescent tumor cells



## Angiogenic Dormancy

Dormant micrometastasis



Pro-angiogenic factors

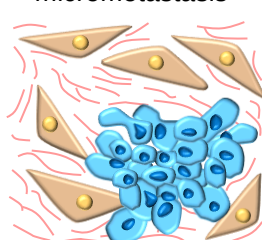
Ras → VEGF  
Ras → TSP  
Low O<sub>2</sub>

Anti-angiogenic factors

p38 → VEGF  
p38 → TSP  
p53 → TSP

Angiogenic switch  
Exogenous angiogenic "spike"

Growing micrometastasis



Pro-angiogenic factors

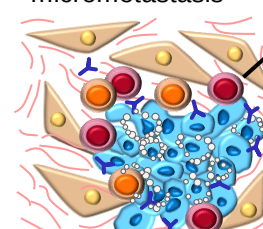
Ras → VEGF  
Ras → TSP  
Low O<sub>2</sub>

Anti-angiogenic factors

p38  
p53

## Immunosurveillance

Dormant micrometastasis

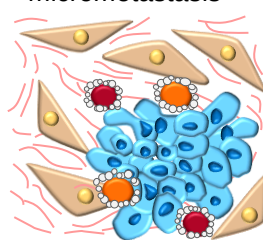


Immunity coordinated by CD8<sup>+</sup> T-cells and memory T cells

Humoral response

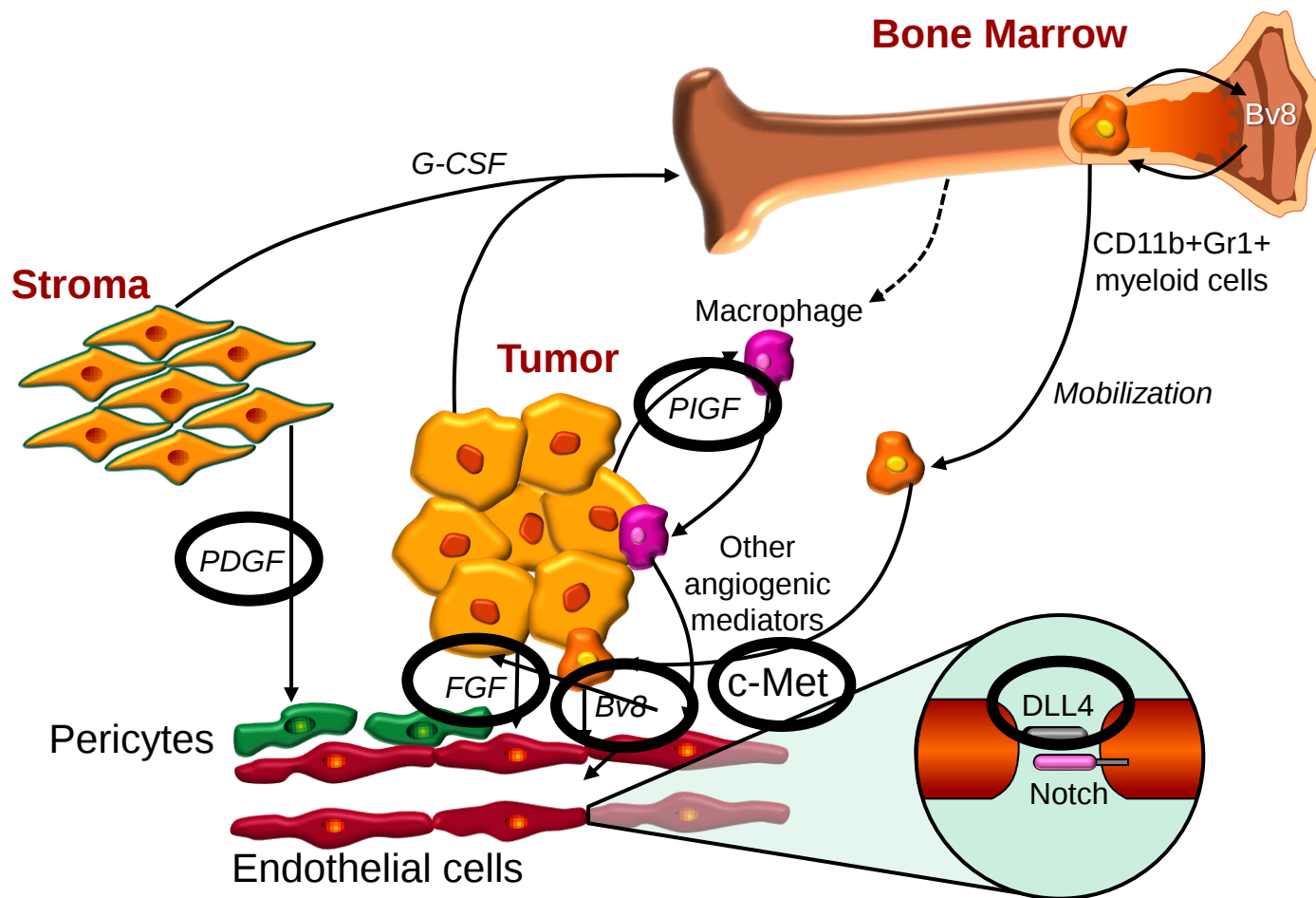
Cellular escape mechanisms  
Immunosuppression?

Growing micrometastasis



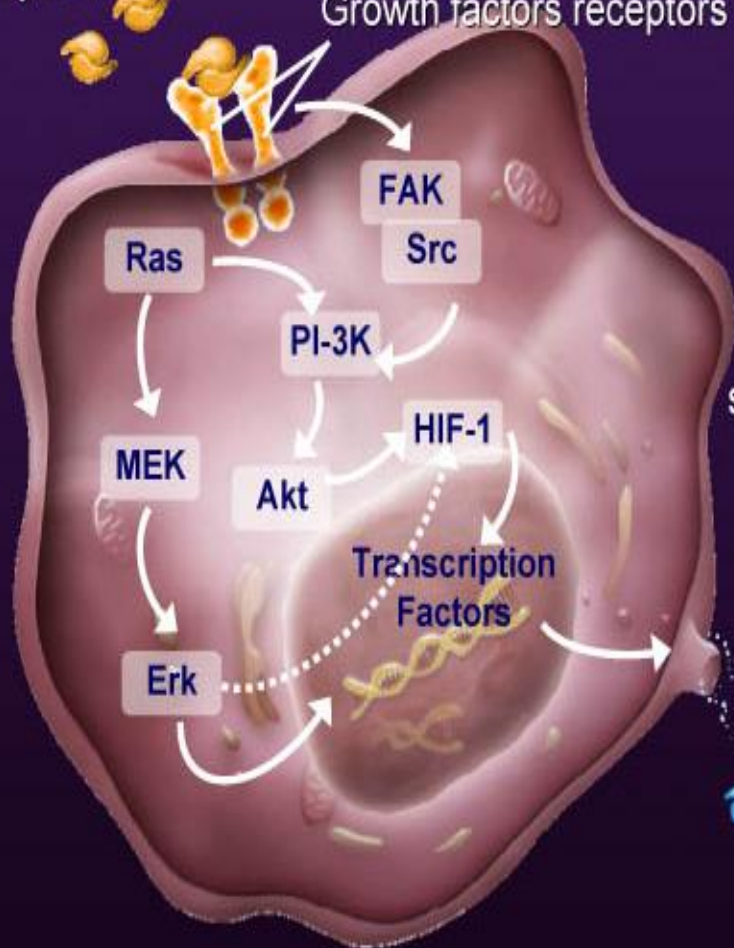
Evasion of the immune system causes tumor mass expansion

# Most Resistance Manuscripts and Reviews Focus on Redundant Angiogenic Pathways



Growth factors/  
cytokines

Growth factors receptors



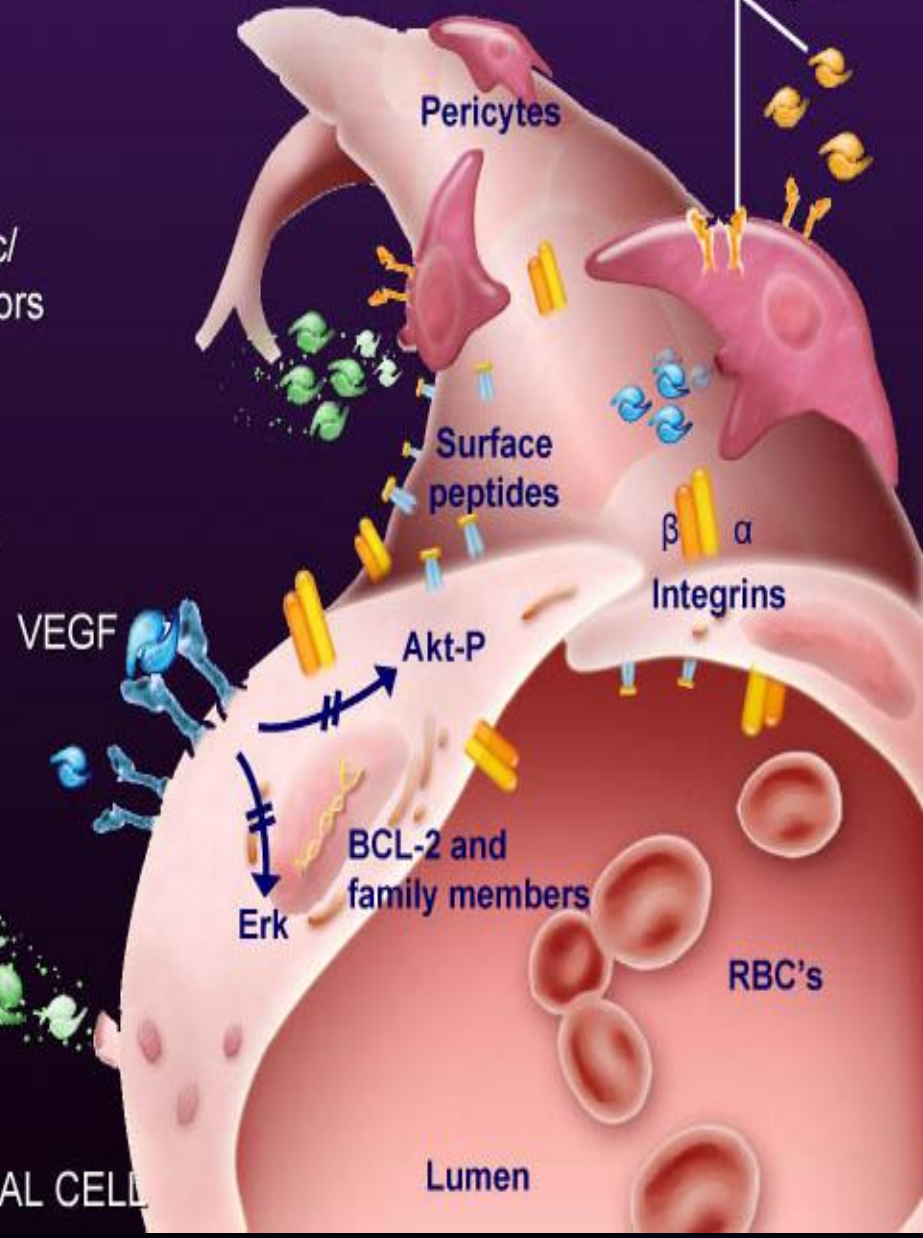
TUMOR CELL

Angiogenic/  
survival factors  
VEGF  
IL-8  
B-FGF  
Ang-1, -2

VEGF, Ang-1, -2

VEGF

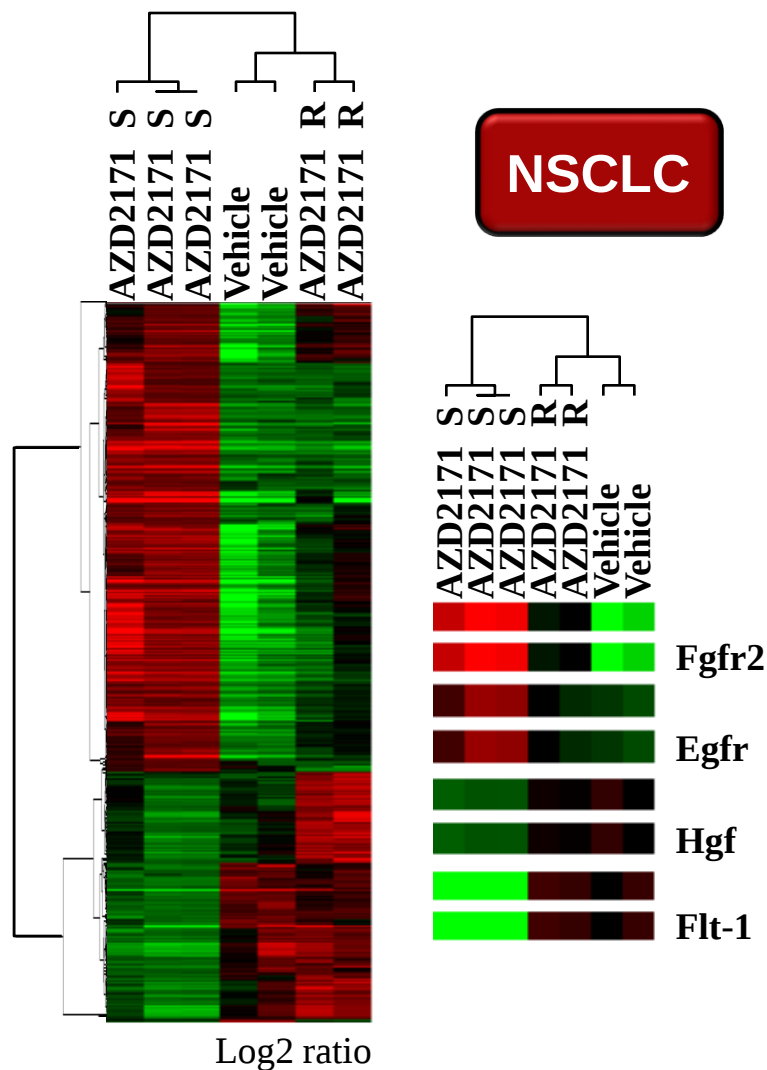
Growth factors  
and receptor



Lumen

ENDOTHELIAL CELL

## Stromal VEGFR1 (Flt-1) and VEGFR TKI Resistance



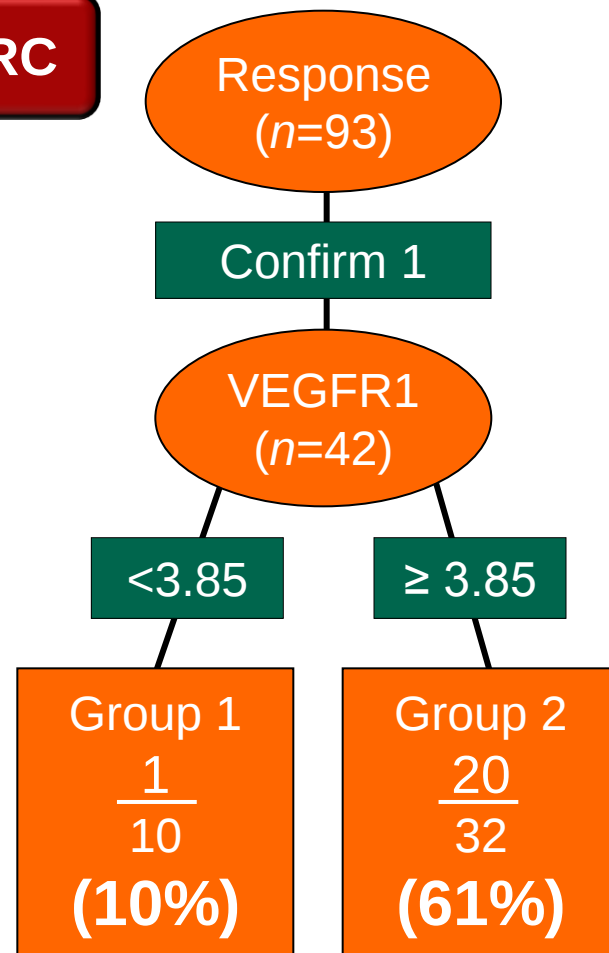
( $p < 0.005$ )

Cascone et al. In preparation.  
Lenz, ASCO 2011.

## VEGFR1 (Flt-1) mRNA and VEGFR TKI Resistance

NSCLC

mCRC

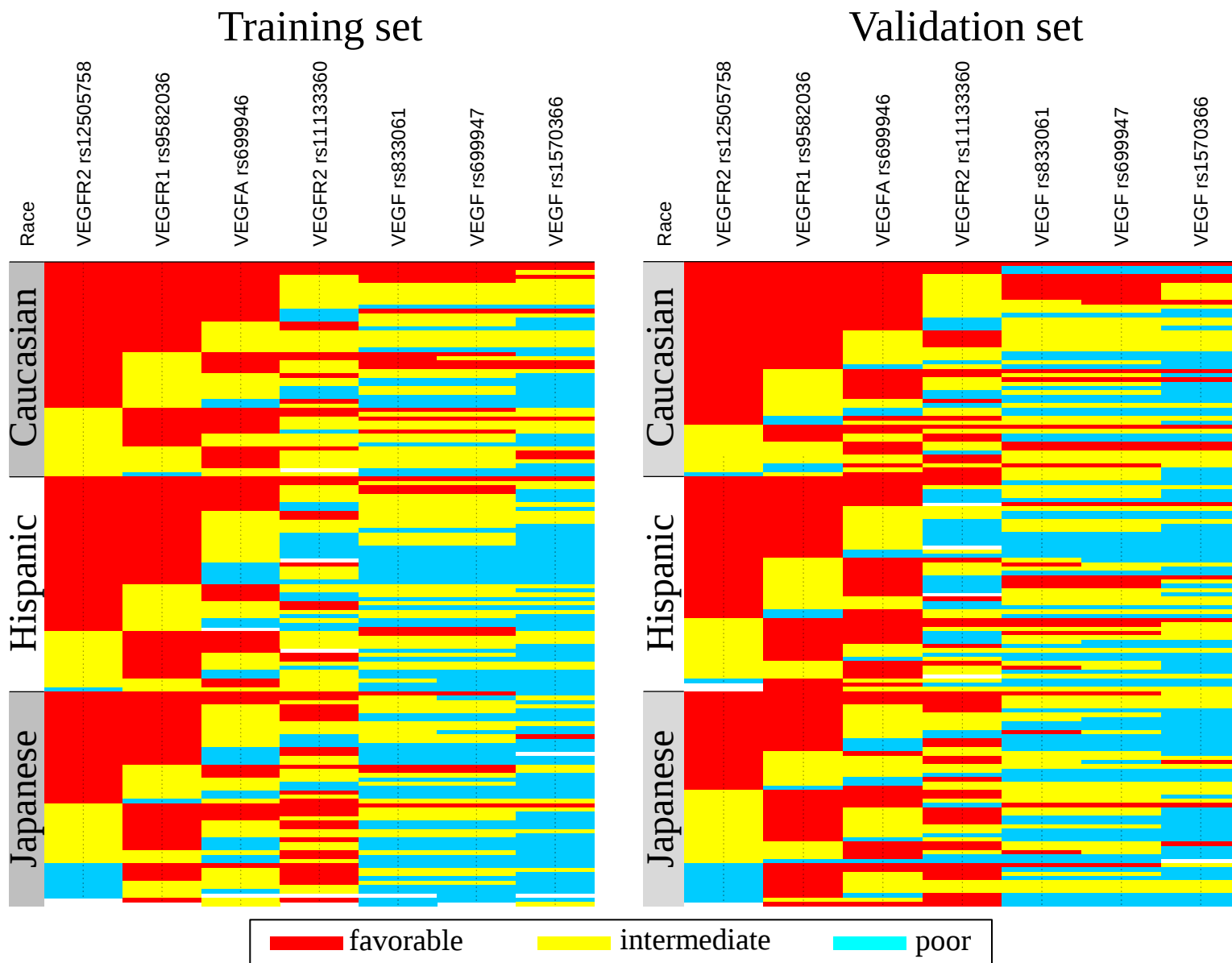


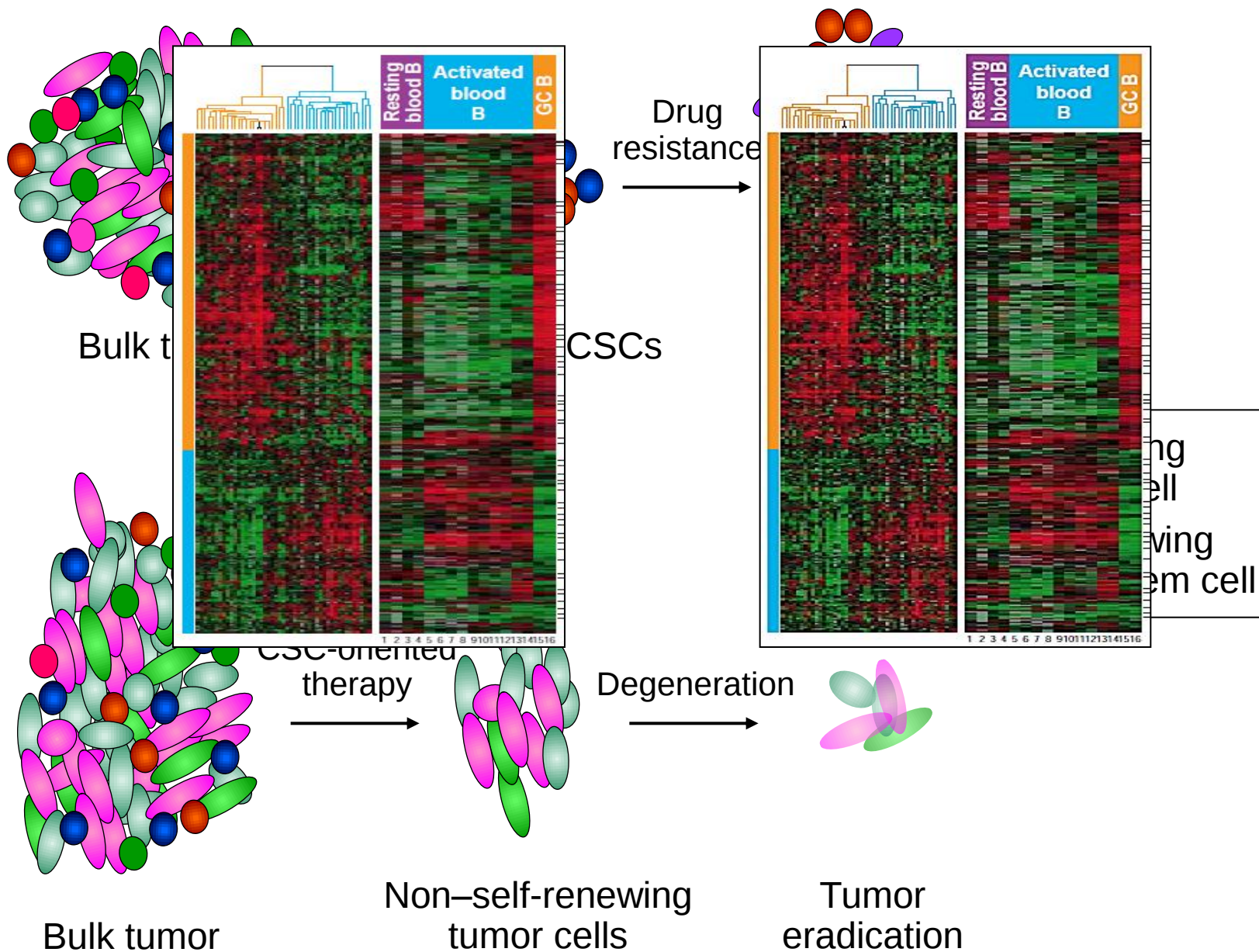
Unsupervised clustering analysis in control and AZD2171 sensitive and resistant H1975 tumors



Courtesy of Heinz-Josef Lenz, MD.

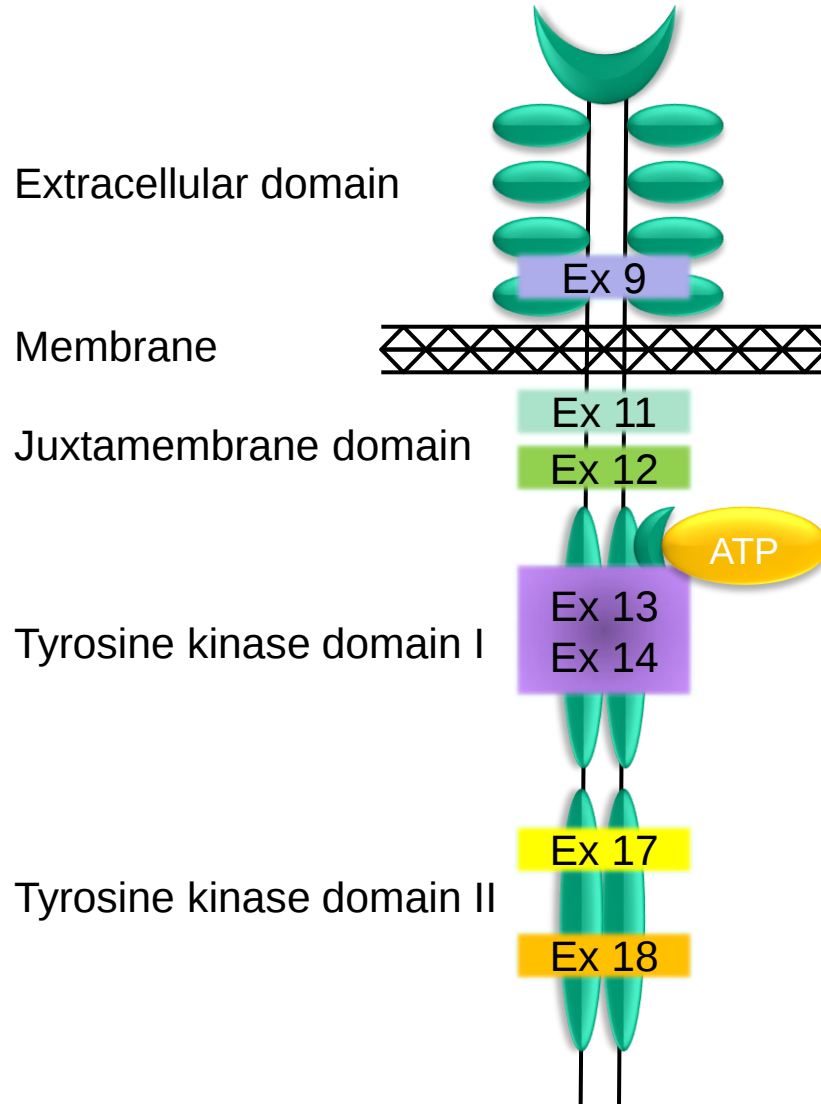
# Heatmaps in 7 Favorable Polymorphisms in Bevacizumab





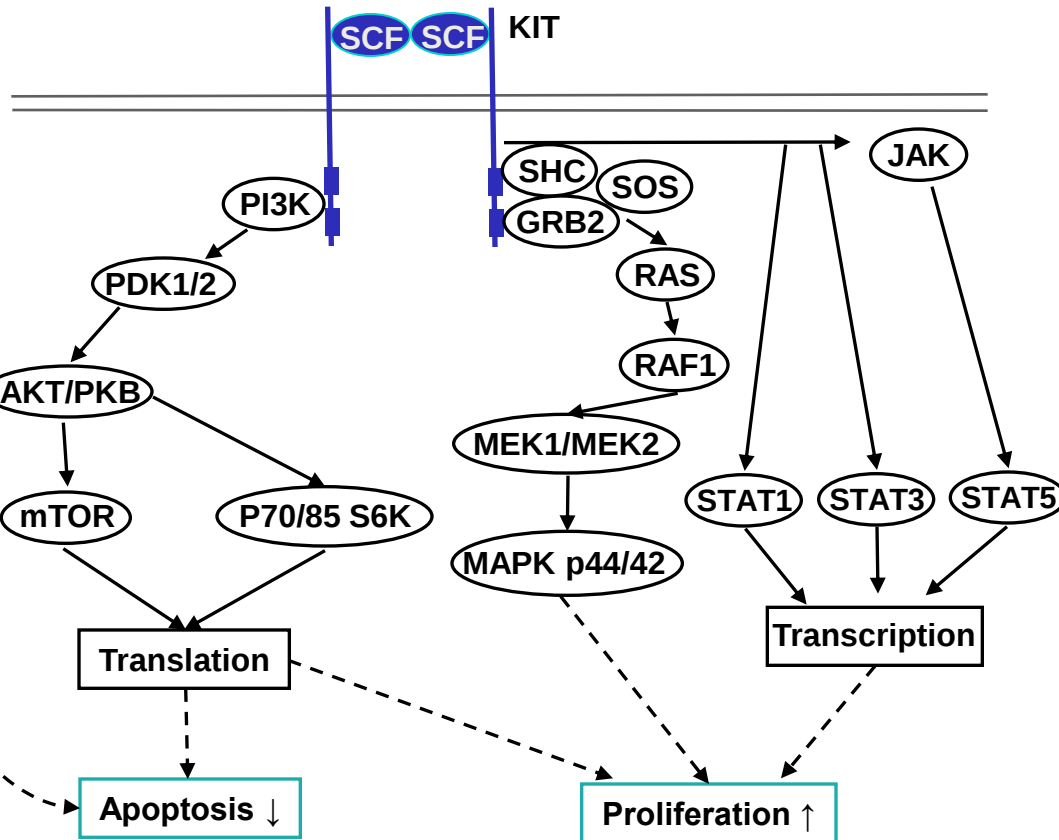


# Oncogenetic Activation in the Pathogenesis of GIST



| Gene   | Exon | Prevalence |
|--------|------|------------|
| KIT    | 9    | 18%        |
|        | 11   | 67%        |
|        | 13   | 2%         |
|        | 17   | 2%         |
| PDGFRA | 12   | 1%         |
|        | 18   | 4%         |

# Constitutive Activation of KIT and PDGFR Promotes Tumor Growth



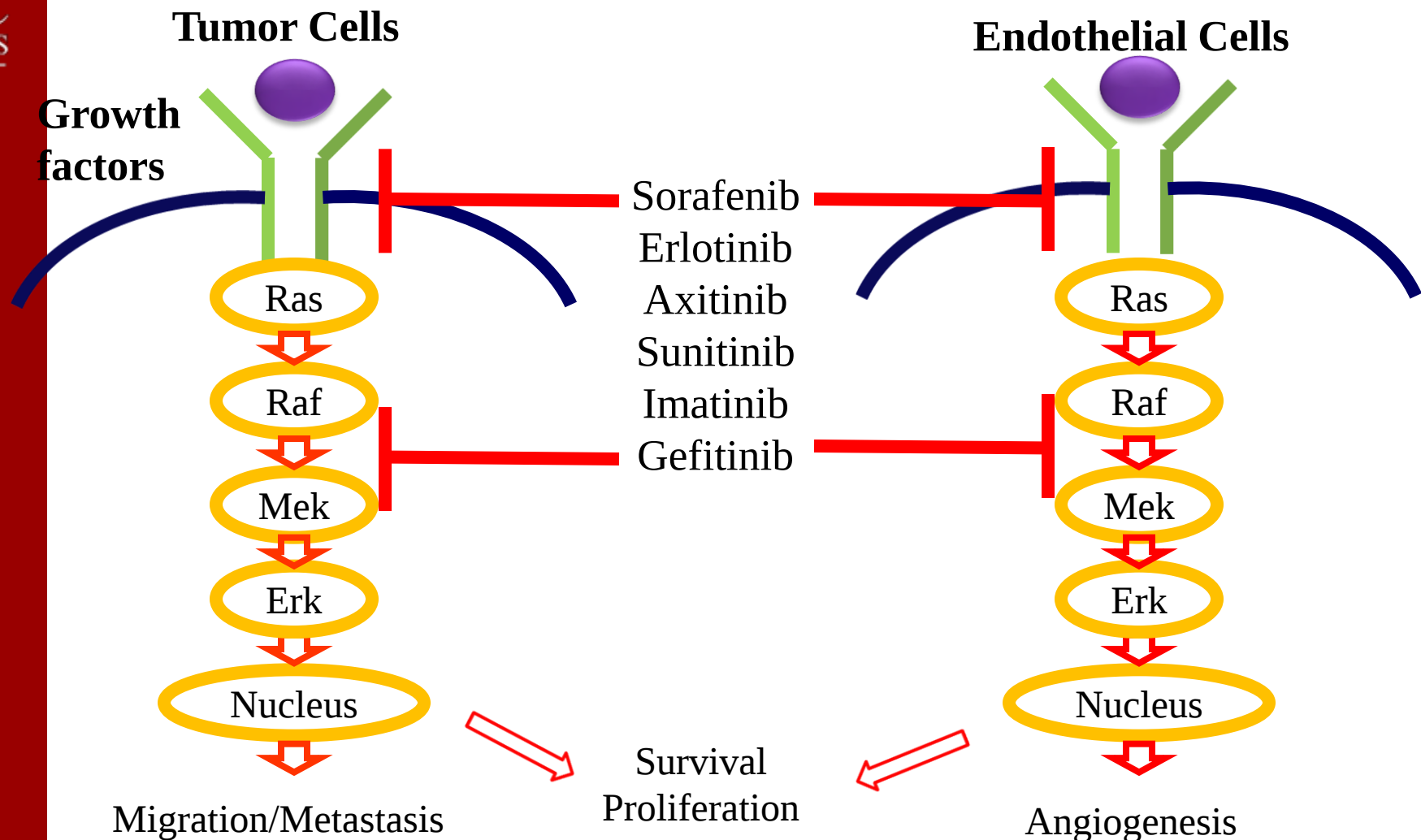
- Mutations of KIT and PDGFRA RTKs increase cell proliferation while decreasing apoptosis

• Downstream signaling pathways of mutant KIT or PDGFRA are thought to be similar, although specific gene expression differs

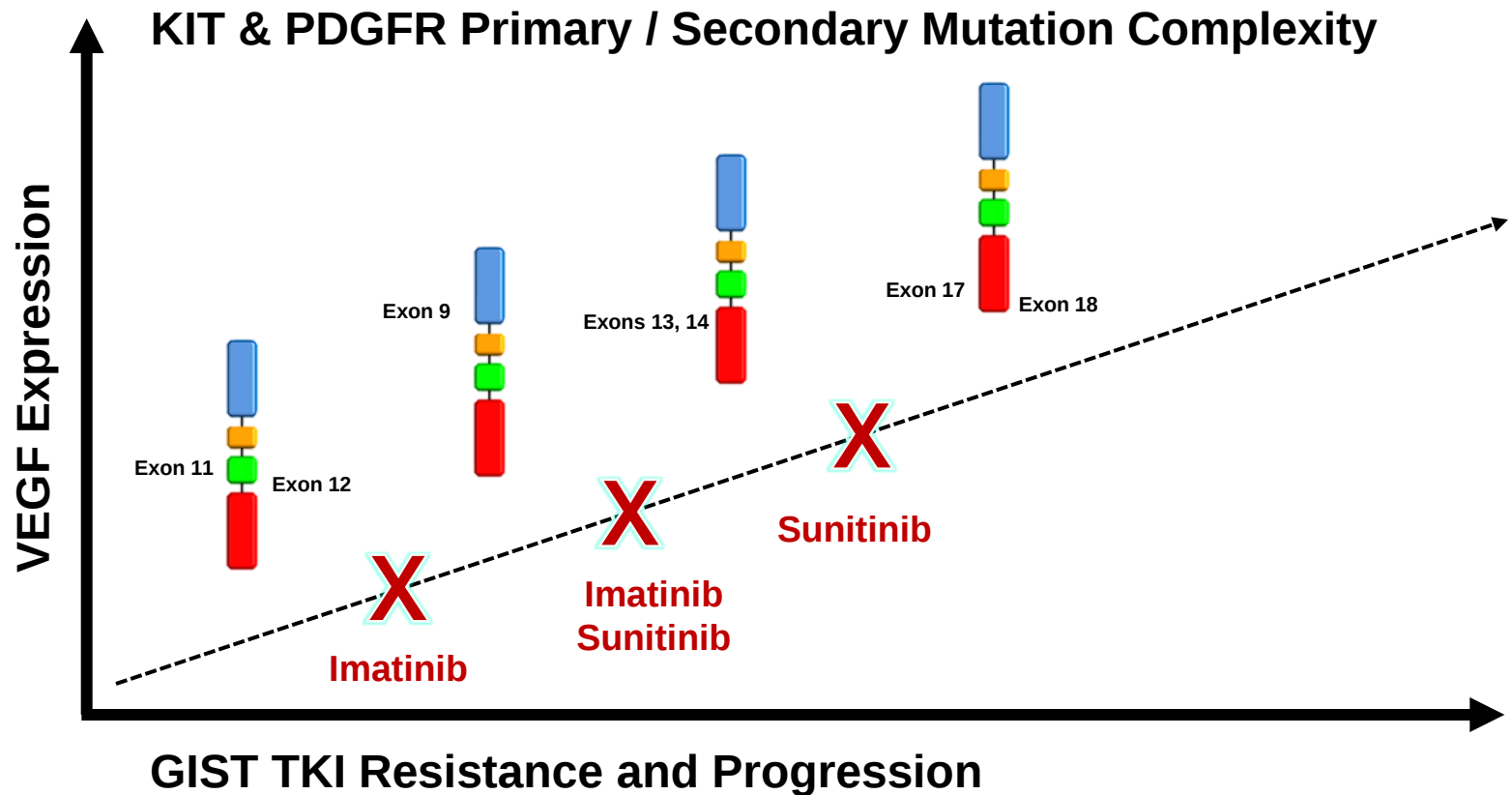
PDGFRA, platelet-derived growth factor receptor- $\alpha$ ; PI3K, phosphoinositide 3-kinase; RTK, receptor tyrosine kinase; SCF, stem cell factor.

GIST Support International website. [www.gistsupport.org/about-gist/mutation-analysis-kit-and-pdgfra.php](http://www.gistsupport.org/about-gist/mutation-analysis-kit-and-pdgfra.php). Accessed September 11, 2012.

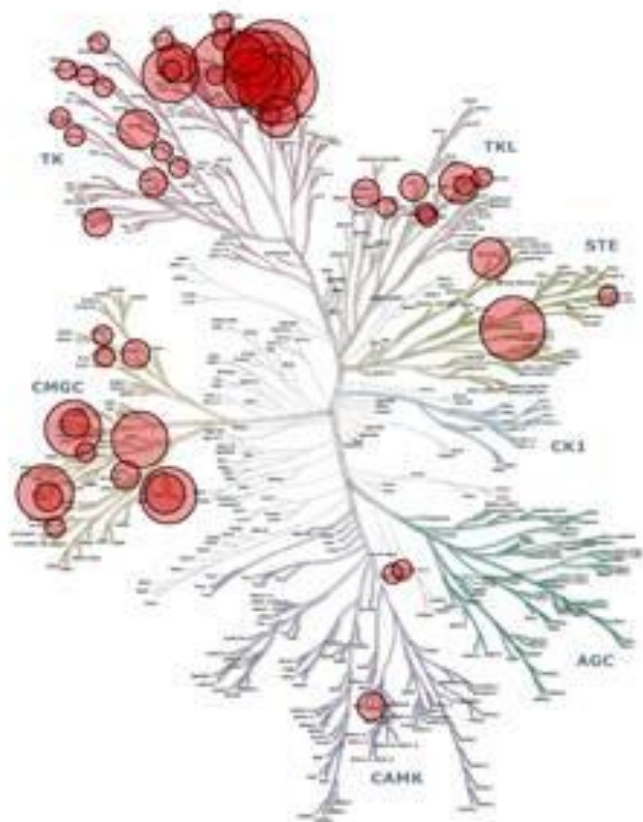
# Benefits of Multikinase Inhibitors as Therapeutic Agents



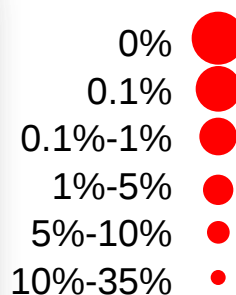
# Therapeutic Disruption of Oncogene Addiction



# Regorafenib (BAY 73-4506) Is a Structurally Distinct Oral Inhibitor of Multiple Kinases



Percent control

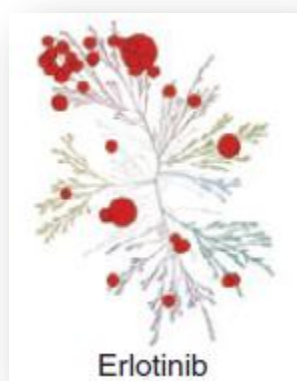
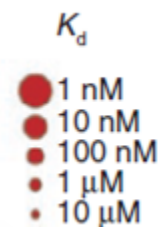


## Biochemical Activity

| IC <sub>50</sub> (nmol/l) |     |
|---------------------------|-----|
| KIT                       | 7   |
| VEGFR-1                   | 13  |
| Murine VEGFR-2            | 4   |
| PDGFR-β                   | 22  |
| RET                       | 1.5 |
| B-RAF                     | 28  |
| FGFR1                     | 202 |

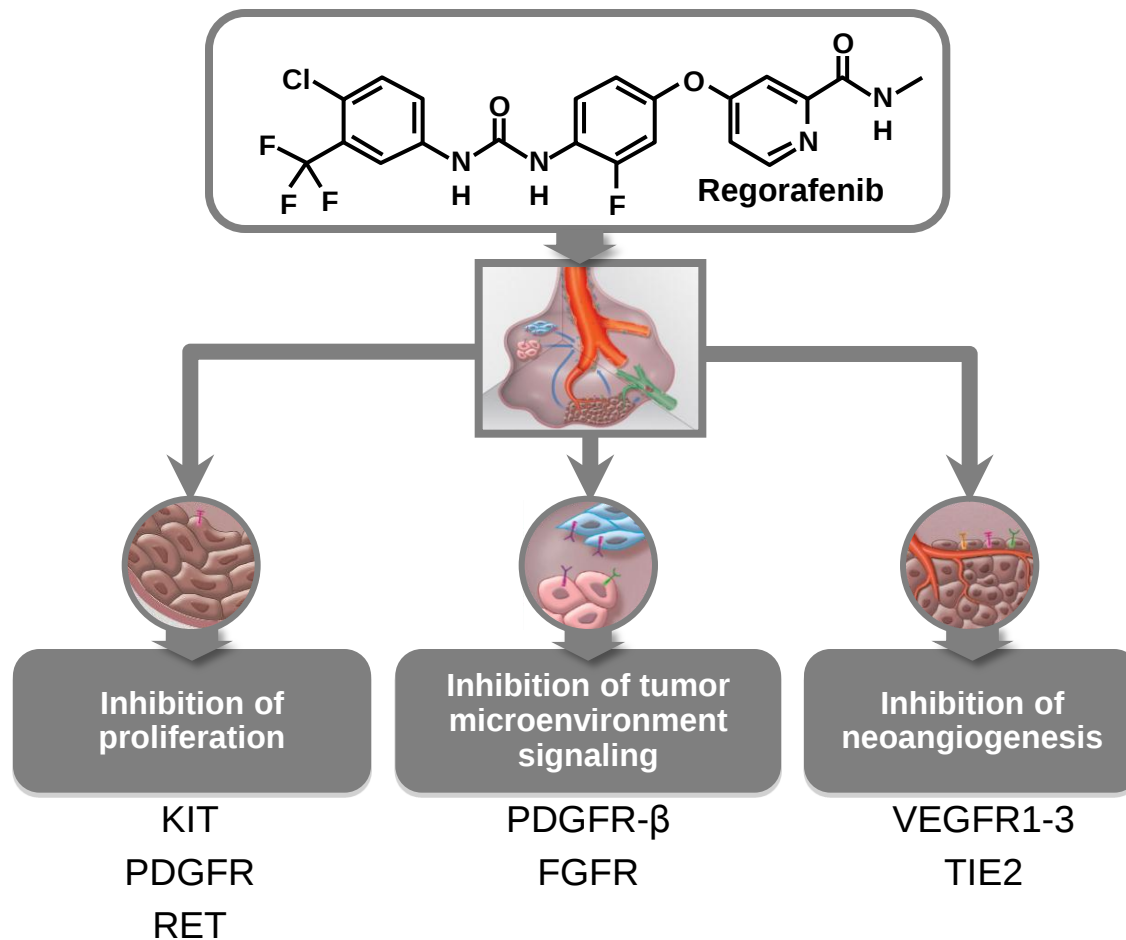
# Biologic Specificity and Potency of Diverse Multikinase Inhibitors

## *Comparative Kinome Mapping*



Promiscuity and affinity drives tolerability and efficacy

# Regorafenib (BAY 73-4506), an Oral Multikinase Inhibitor Targeting Multiple Tumor Pathways<sup>1-3</sup>



# Summary

- Mutations identified in an individual cancer, whether driver or passenger, can be used as a specific biomarker to guide patient management<sup>1</sup>
- Selective co-targeting of multiple hallmark capabilities in mechanism-guided combinations will result in more effective and durable therapies for cancer<sup>2</sup>
- Signaling pathways controlled by tyrosine kinases offer unique opportunities for pharmacological intervention<sup>3-5</sup>
- Regorafenib is potentially a new approach in the management of patients with mCRC and refractory GIST<sup>6-7</sup>

1. Sjoblom T, et al. *Science*. 2006;314:268-274; 2. Hanahan D, et al. *Cell*. 2011;144:646-674; 3. Wilhelm S, et al. *Cancer Res*. 2004;64:7099-7109; 4. Carlomagno F, et al. *J Natl Cancer Inst*. 2006;98:326-334; 5. Heath VL, et al. *Nat Rev Clin Oncol*. 2009;6(7):395-404; 6. Van Cutsem E, et al. Oral abstract presented at ASCO 2012. *J Clin Oncol*. 2012;30: (suppl). Abstract 3502; 7. Demetri G, et al. Oral abstract presented at ASCO 2012. *J Clin Oncol*. 2012;30:(suppl). Abstract LBA10008.