

Can the tumor genome help us to better select patients for antiangiogenic therapy ?

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# Modest succes of bevacizumab in common cancers



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**Table 1. Randomized Phase III Studies Comparing Chemotherapy With or Without Bevacizumab As First-Line Chemotherapy for Advanced Epithelial Cancers**

Tumor Site and Study Name	Primary End Point	Sample Size	Design	PFS			OS			Reported As
				Diff (months)	HR	P	Diff (months)	HR	P	
Breast										
ECOG E2100 <sup>5</sup>	PFS	722	P ± B	+ 5.9	0.60	.0001	+ 1.5	0.88	.16	Positive
AVADO <sup>6</sup>	PFS	736	D ± B7.5	+ 0.8	0.86	.116	− 1.1	1.05	.72	Positive
			D ± B15	+ 1.9	0.77	.006	− 1.7	1.03	.85	
RIBBON-1 <sup>7</sup>	PFS	1,237	C ± B	+ 2.9	0.69	.0002	+ 7.8	0.85	.27	Positive
			A/T ± B	+ 1.2	0.64	< .001	+ 1.4	1.03	.83	
Meta-analysis <sup>8</sup>	—	2,447	Ch ± B	+ 2.5	0.64	.0001	+ 0.3	0.97	.56	—
Prostate										
CALGB 90401 <sup>10</sup>	OS	1,050	DP ± B	+ 2.4	0.77	.0001	+ 1.1	0.91	.18	Negative
Ovarian										
GOG-0218 <sup>11</sup>	OS→PFS	1,873	CT ± B	+ 0.9	0.91	.080	− 0.6	1.04	.36	Positive
			CT + B + mB	+ 3.8	0.72	.0001	+ 0.4	0.92	.25	
Lung										
ECOG E4599 <sup>12</sup>	OS	878	CP ± B	+ 1.7	0.66	< .001	+ 2.0	0.79	.003	Positive
AVAIL <sup>13,14</sup>	OS→PFS	1,043	CG ± B7.5	+ 0.6	0.75	.0003	+ 0.5	0.93	.42	Positive
			CG ± B15	+ 0.4	0.85	.046	+ 0.3	1.03	.76	
Pooled analysis*	—	1,921	Ch ± B	+ 1.1	0.73	< .001	+ 1.0	0.91	.22	—
Gastric										
AVAGAST <sup>15</sup>	OS	774	XELP ± B	+ 1.4	0.80	.0037	+2	0.87	.1002	Negative
Pancreas										
CALGB 80303 <sup>16</sup>	OS	602	G ± B	+ 0.9	1.00	.07	− 0.1	1.09	.95	Negative
Van Cutsem et al <sup>17</sup>	OS	607	GE ± B	+ 1.0	0.73	.0002	+ 1.1	0.89	.21	Negative
Colorectal										
Hurwitz <sup>18</sup>	OS	813	IFL ± B	+ 4.4	0.54	< .001	+ 4.7	0.66	< .001	Positive
Saltz <sup>19</sup>	PFS	1,401	FOLFOX4 or XELOX ± B	+ 1.4	0.83	.0023	+ 1.4	0.89	.0769	Positive

# Can we afford to develop drugs the way we used to ?



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## How Much Is Life Worth: Cetuximab, Non–Small Cell Lung Cancer, and the \$440 Billion Question

Tito Fojo and Christine Grady

J Natl Cancer Inst 2009; 101:1044-1048

# Discrepancy between preclinical models and patients



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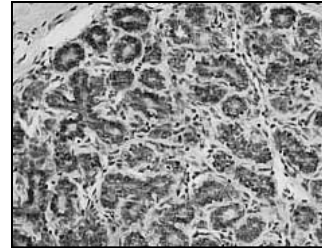
- In vitro models commonly use cell lines that have been maintained in culture for years
- Investigations focus on knock down of genes by siRNA, but functional consequences of mutations are rarely studied in preclinical models
- In vitro sensitivity to agents does not accurately predict their activity in vivo
- Mouse models employ xenografts of selected cell lines
- Transgenic mouse models have a defined genetic initiator of cancer
- Therefore: huge gap between preclinical models and our patients!!

# The patient as readout: Personalized Cancer Treatment



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Patient's  
tissue sample



pathology  
grade, size, IHC



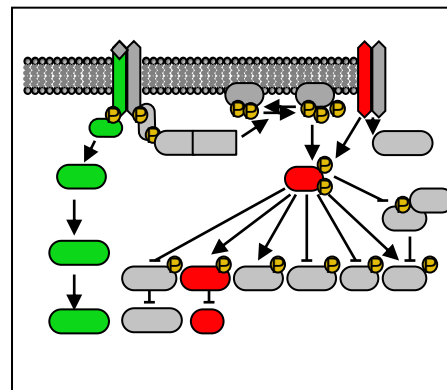
Chemotherapy

## Tailored therapy

Patient's  
tissue sample



Molecular  
diagnostics



Targeted therapy

Which pathways are active?

# Proof of concept !



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- After screening tumor samples from approximately **1500** patients with non–small-cell lung cancer for the presence of *ALK* rearrangement, **82** patients with advanced *ALK*-positive disease were identified
- Mean treatment duration of 6.4 months
- Overall response rate : 57% (47 of 82 patients);
- 27 patients (33%) had stable disease.
- The estimated probability of 6-month progression-free survival was 72%, with no median for the study reached.

## EML4-ALK Mutations in Lung Cancer That Confer Resistance to ALK Inhibitors

- Two secondary mutations within the kinase domain of EML4-ALK in tumor cells isolated from a patient developed during the relapse phase of treatment with an ALK inhibitor.
- Each mutation developed independently in subclones of the tumor and conferred marked resistance to two different ALK inhibitors.

# Can we achieve the same success for anti-angiogenic therapy ?

Question that needs to be addressed:

How to determine genetic dependency  
or “*angiogene addiction*” ?



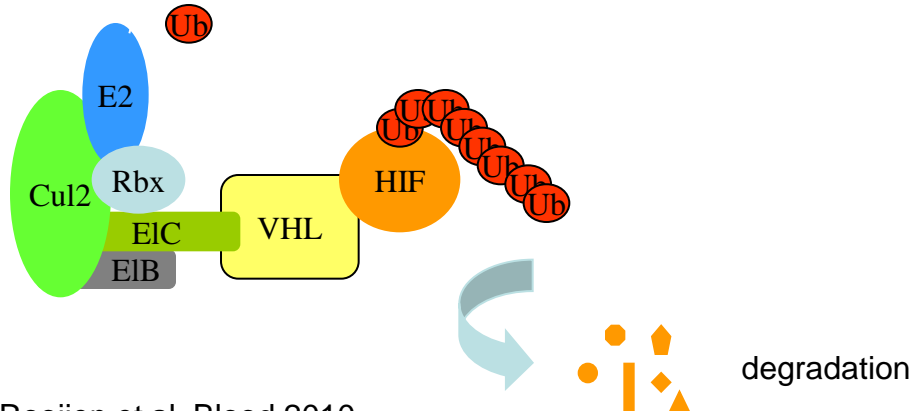
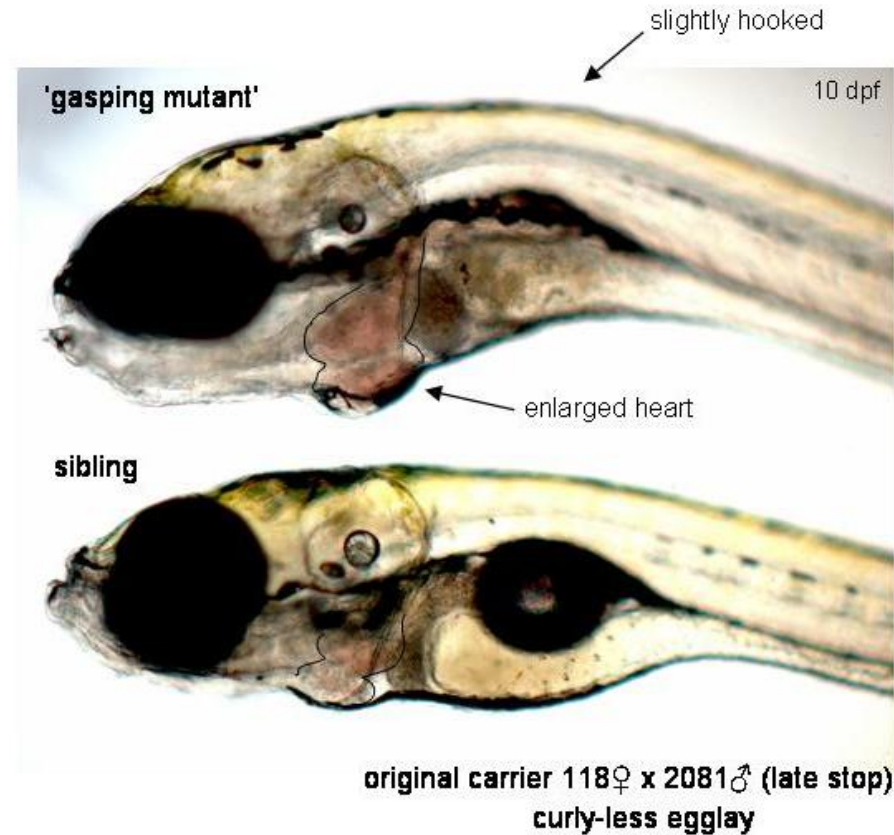
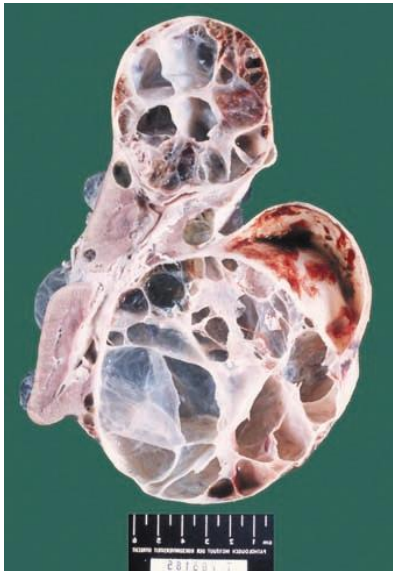
# *“Angiogene addiction”*



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- Tumor acquires genetic changes in growth factor pathways early in tumorigenesis that facilitate tumor growth
- Short time between initial mutagenesis and clinical manifestations ?
- Examples: clear cell renal cell cancer; pancreatic NET, PEComa

# Mutations in the VHL gene to select patients for anti-angiogenic therapy



Rooijen et al. Blood 2010

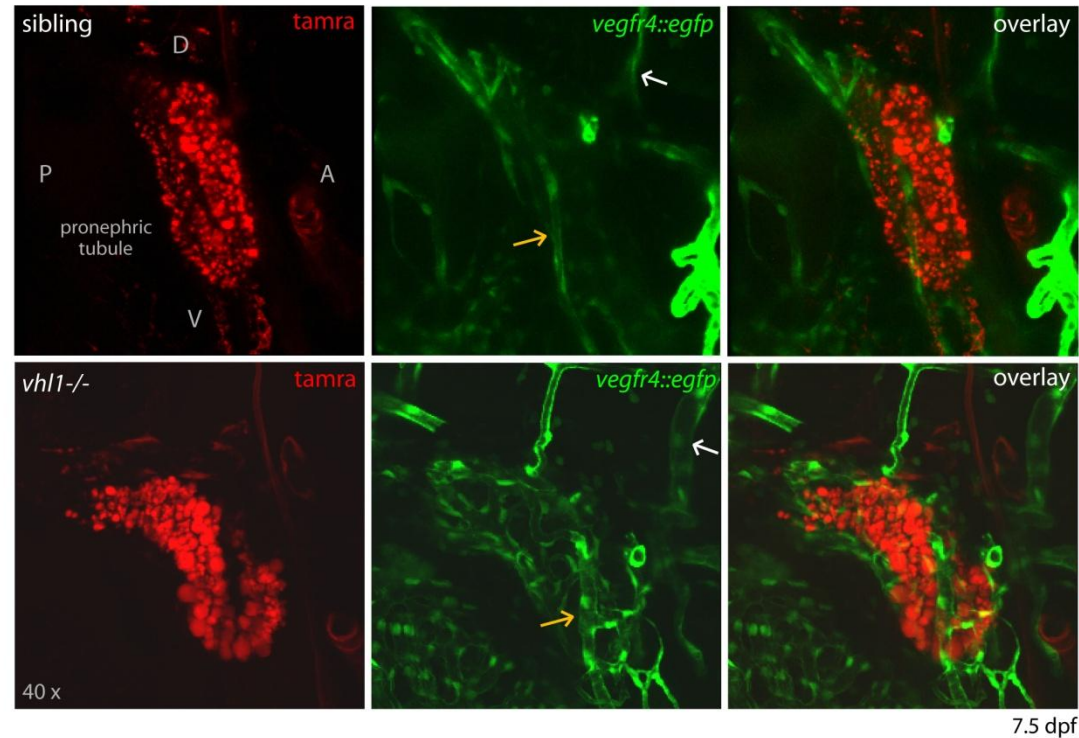
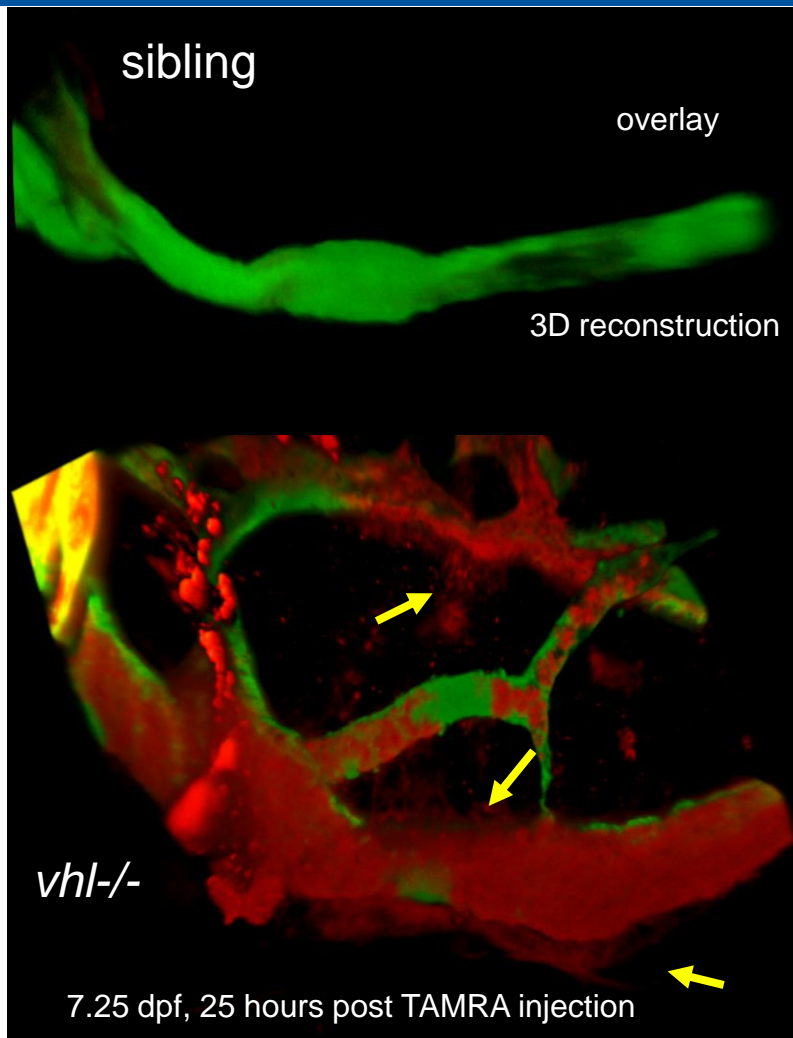
Nordstrom-O'Brien et al., Human Mutations 2010

Rooijen et al., Dis Models Mech 2010

# Mutations in the VHL gene to select patients for anti-angiogenic therapy



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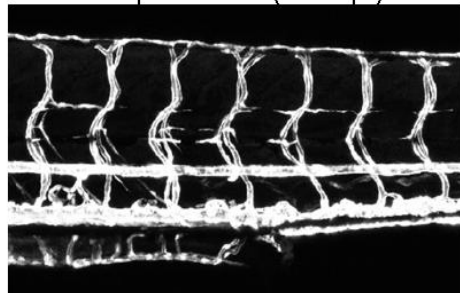


Rooijen et al. Blood 2010

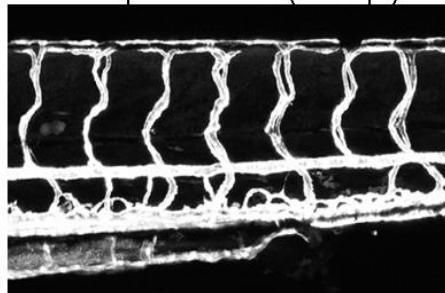
Nordstrom-O'Brien et al., Human Mutations 2010

Rooijen et al., Dis Models Mech 2010

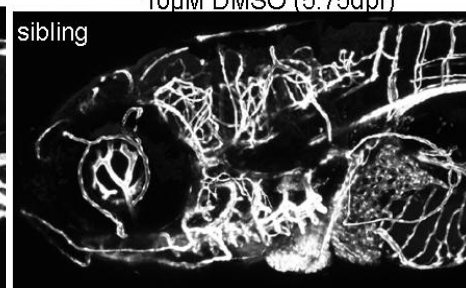
10μM DMSO (5.75dpf)



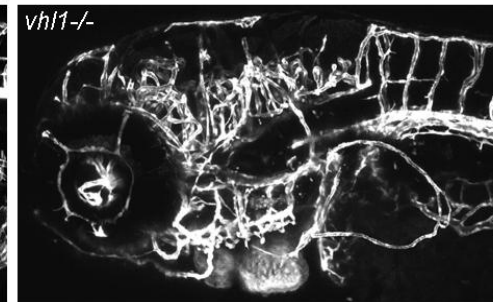
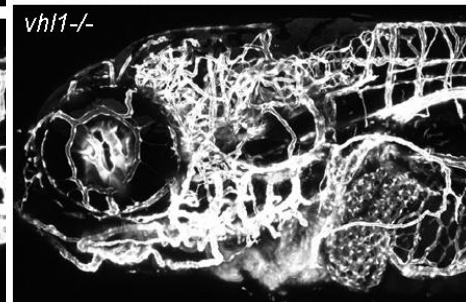
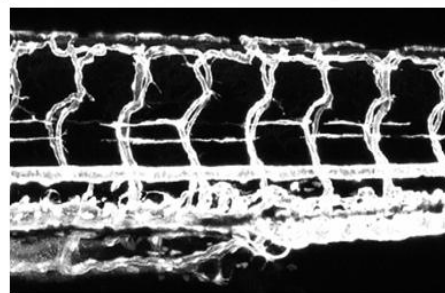
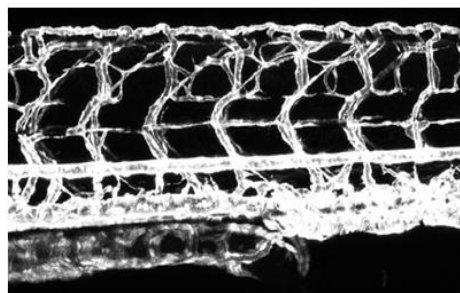
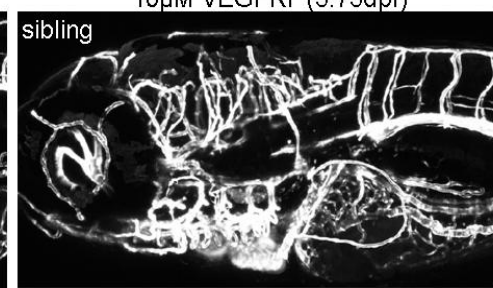
10μM VEGFRi (5.75dpf)



10μM DMSO (5.75dpf)



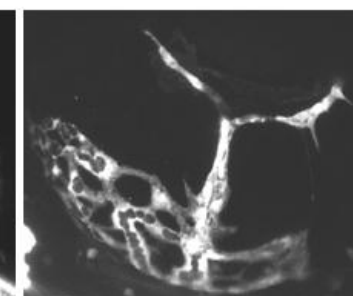
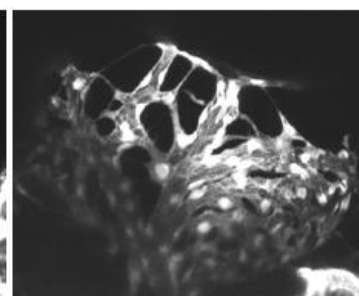
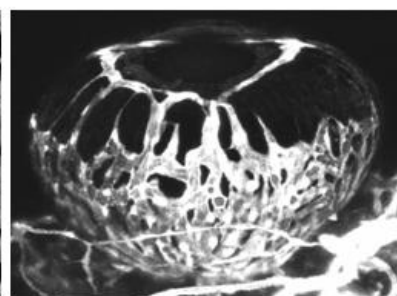
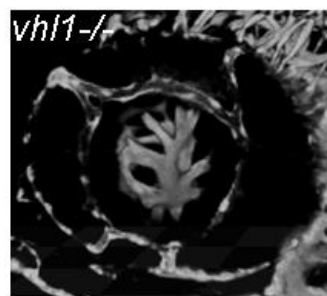
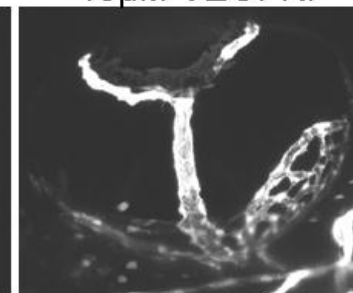
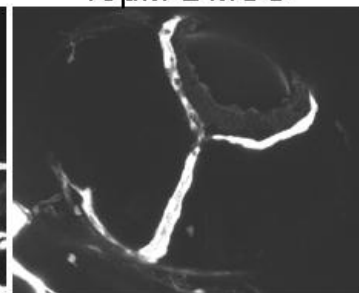
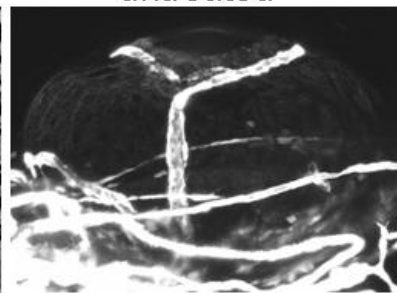
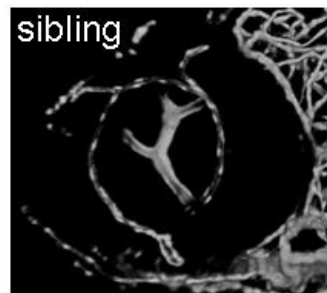
10μM VEGFRi (5.75dpf)



untreated

10μM DMSO

10μM VEGFRi



5.75 dpf, *kdra::egfp*



# von Hippel-Lindau gene status and response to VEGF targeted therapy for metastatic ccRCC

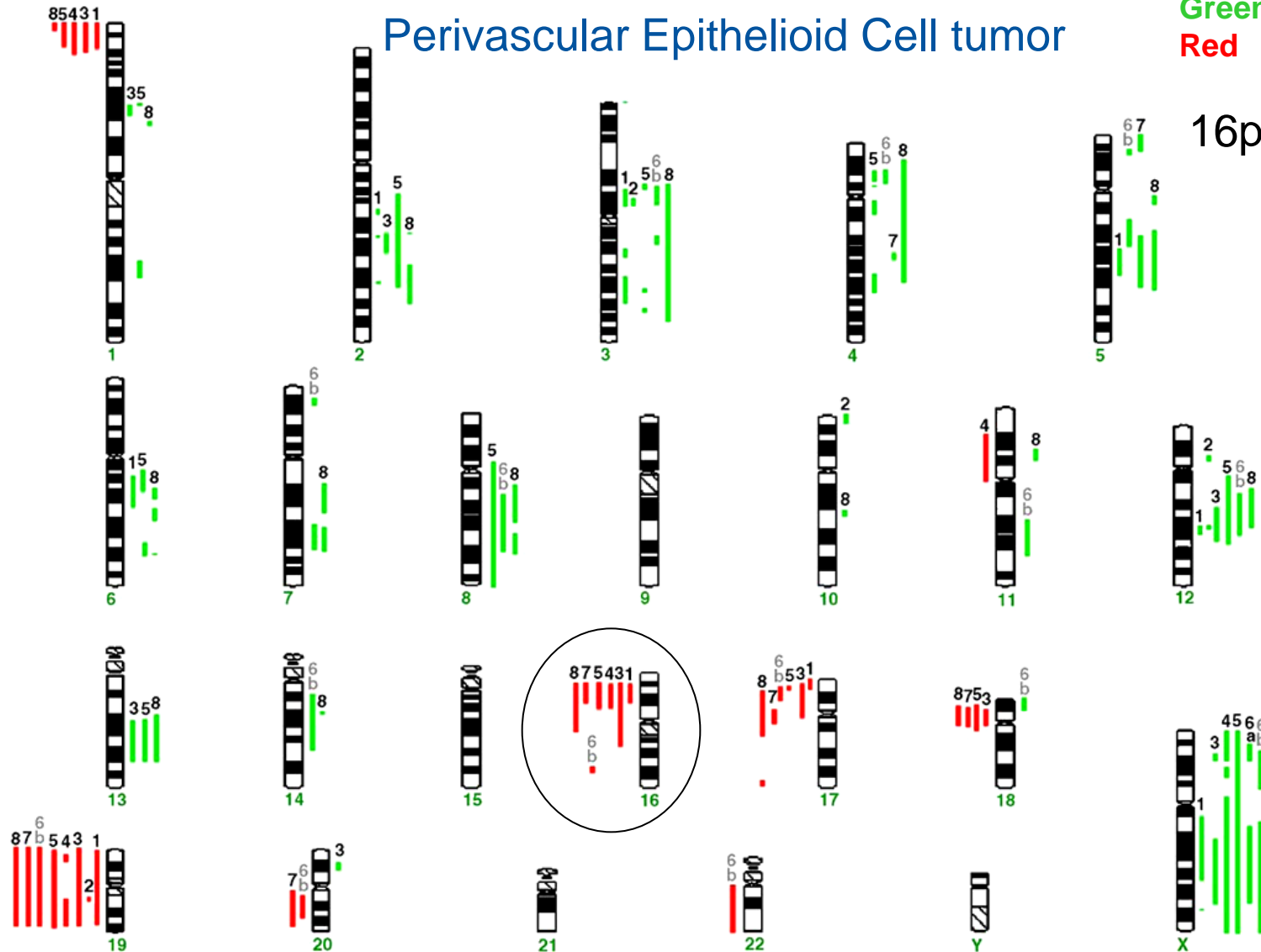


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- 700 different types of mutations, derived from this protein of only 213 amino acids.
- Retrospective analysis in 123 ccRCC patients. Patients with VHL inactivation had a response rate of 41% vs 31% for those with wild-type VHL ( $p = 0.34$ ). Patients with loss of function mutations had a 52% response rate vs 31% with wild-type VHL ( $p = 0.04$ ).
- On multivariate analysis the presence of a loss of function mutation remained an independent prognostic factor associated with improved response.
- In VHL disease, clear evidence supports strong genotype-phenotype correlations, but the situation in sporadic ccRCC is less clear.

Choueiri TK et al, J Urol 2008, Gossage L, Eisen T. Nat Rev Clin Oncol. 2010, Nordstrom-O'Brien, et al. Human Mutations 2010

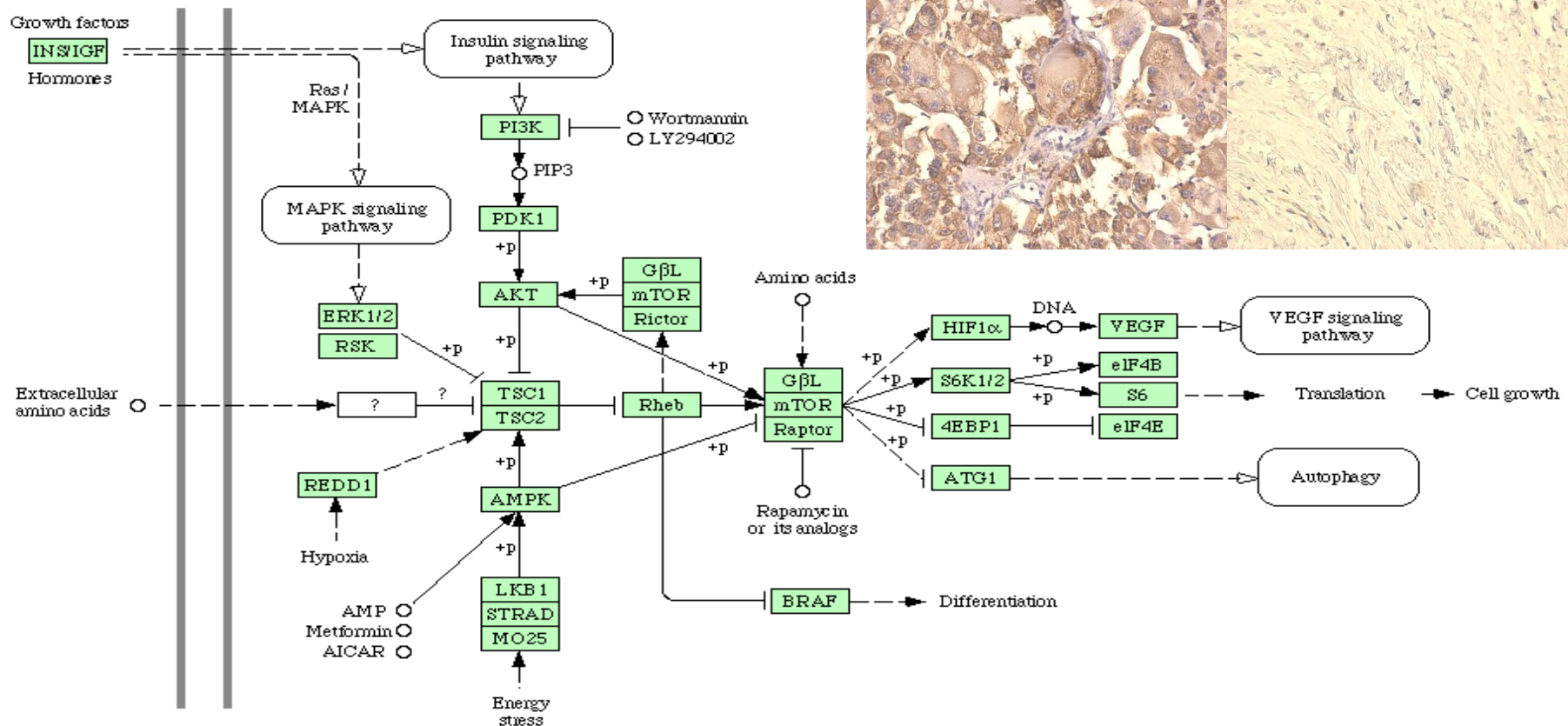
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# Proof of concept...

- Clinical Activity of mTOR Inhibition With Sirolimus in Malignant Perivascular Epithelioid Cell Tumors: Targeting the Pathogenic Activation of mTORC1 in Tumors. Wagner et al. J Clin Oncol Feb 2010

PhosphoS6 staining

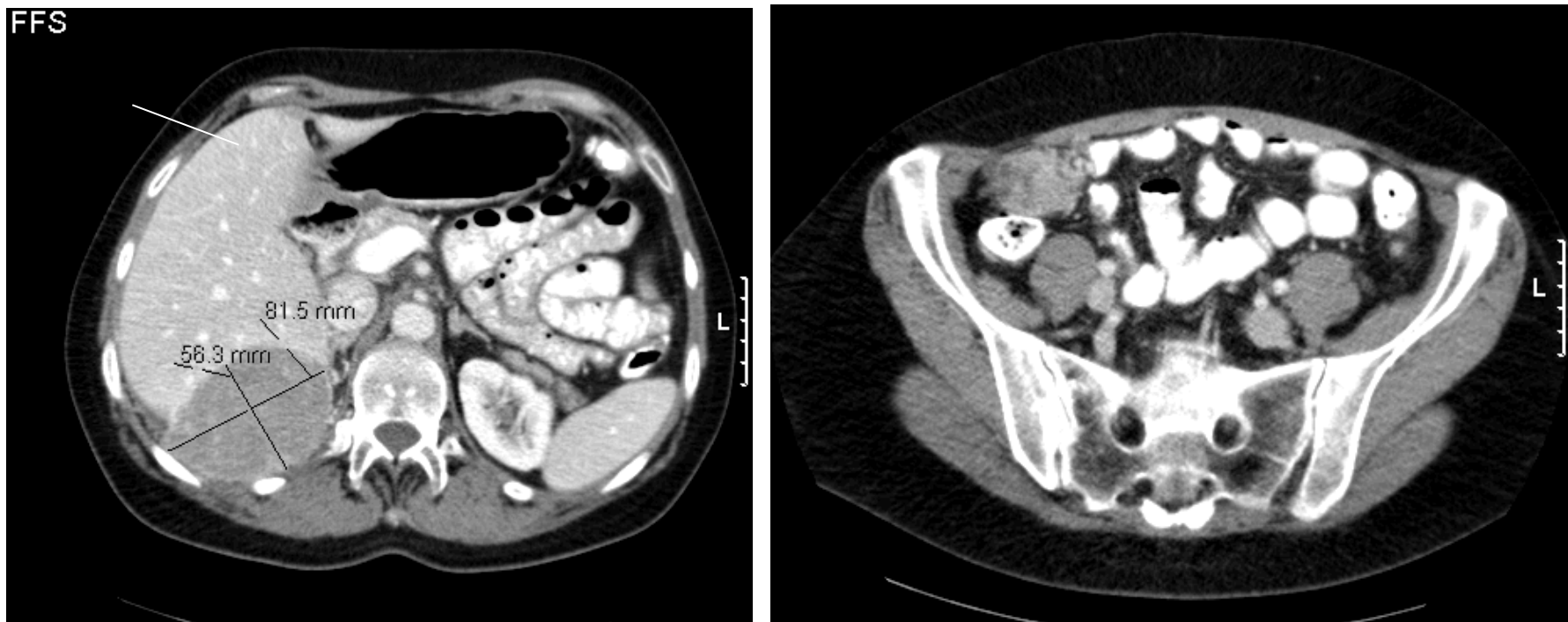


# A clinical example of a successful DNA guided anti-angiogenic treatment



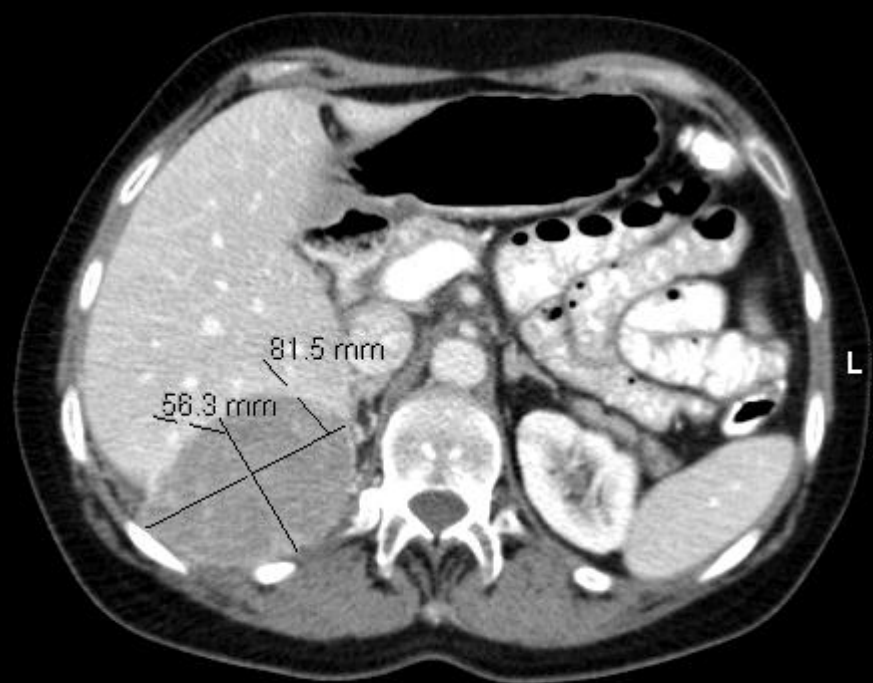
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- Patient with a perivascular epithelioid cell tumor (PEComa) with liver and intraperitoneal metastases
- Initial response on doxorubicin but progressive disease within 6 months, no other treatment options





FFS



January 2010

FFS



February 2011



# “*Angiogene addiction*” in common cancer?



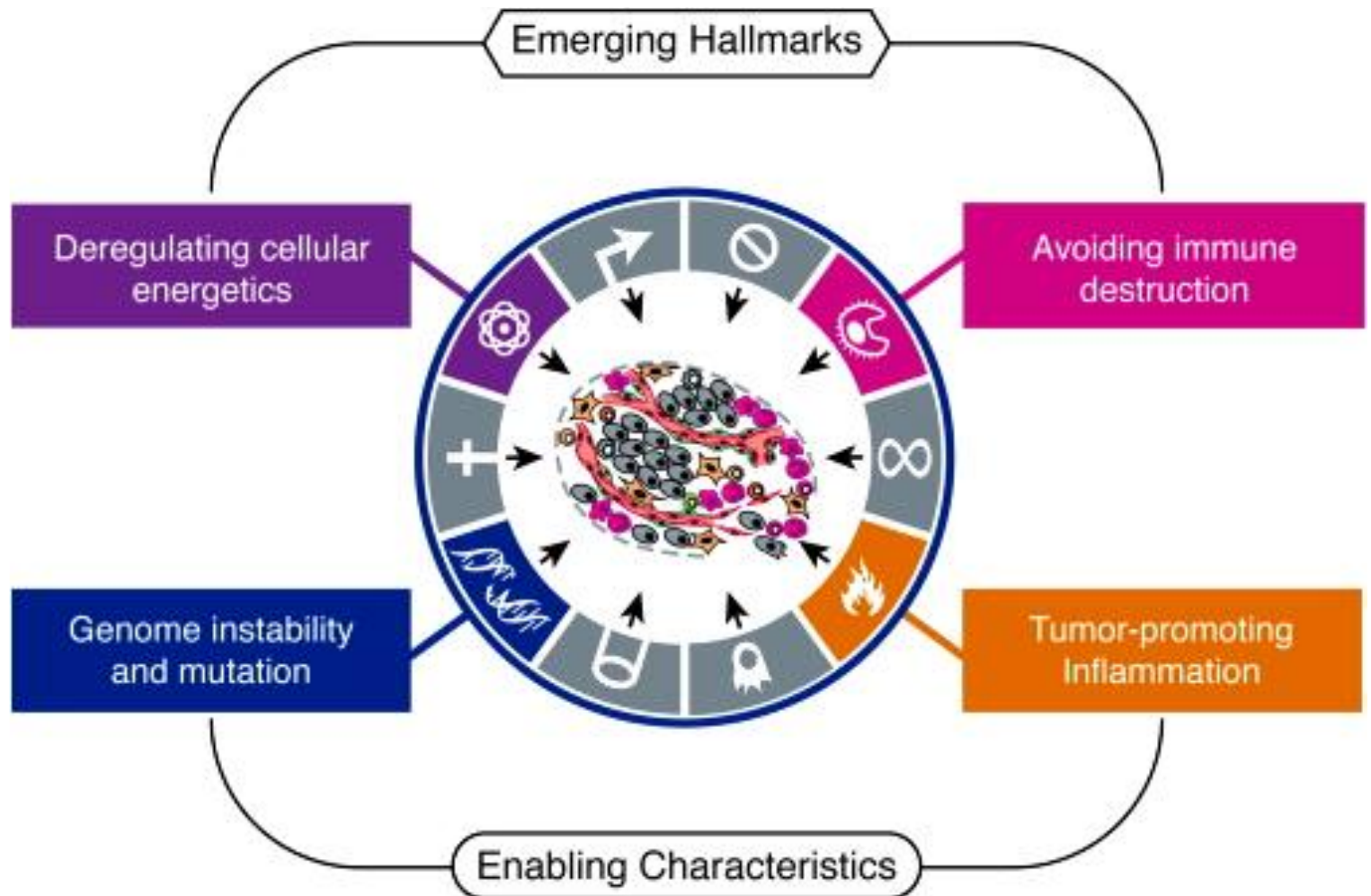
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- Potential examples of “*angiogene addiction*” : ccRCC, GIST, PEComa, pancreatic NET
- Better selection of patients with common cancers is essential
- Can tumor DNA provide answers ?

# Can we achieve the same success in common cancers ?



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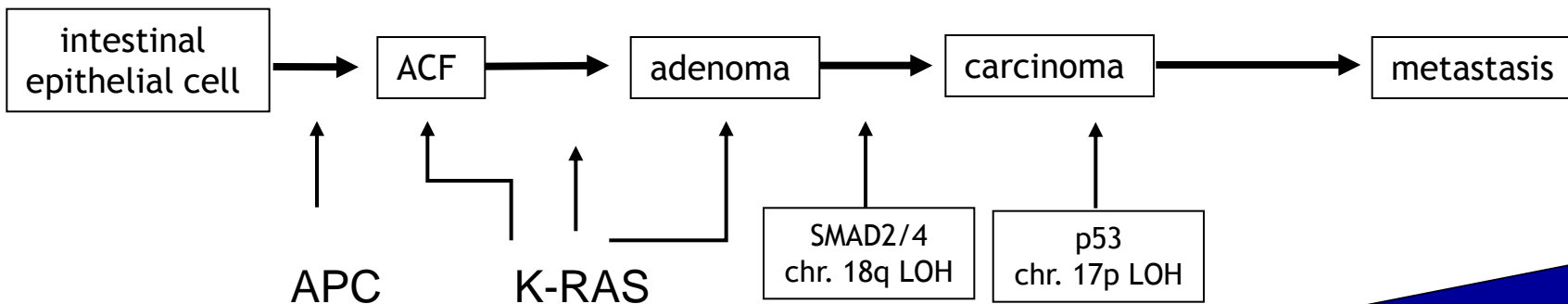
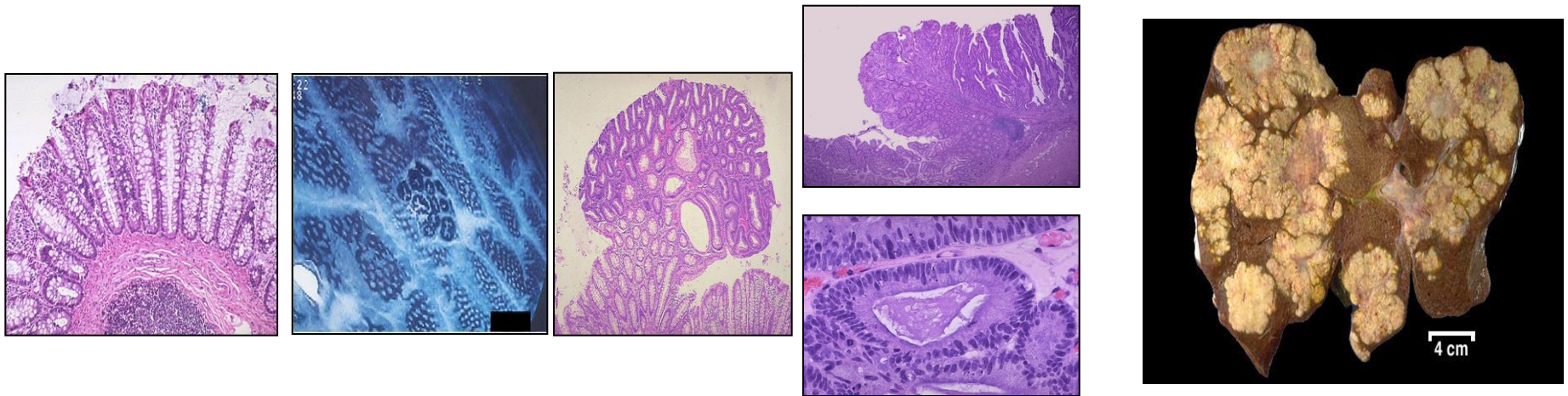


Hanahan and Weinberg, Cell, april 2011

# The Adenoma-Carcinoma Sequence in Colorectal Cancer: tumor initiation, progression, and metastasis



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Genetic alterations



# Are we sure that the target is present in metastatic disease ?

## Primary tumors are not the same as metastases



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- Paired colorectal tumors and metastasis of 21 patients were selected (42 tumor samples)
- Tumor DNA was isolated by microdissection and sequenced for 1263 genes covering all major pathways and kinases
- Looking for function altering genetic changes
- Very stringent SNP calling
- **On average a metastasis gains 89 relevant mutations and loses 70 mutations present in the primary**

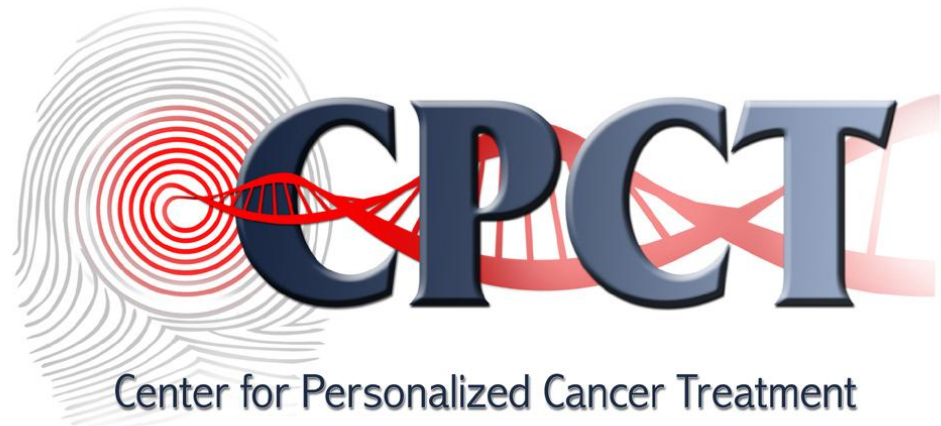
- Molecular diagnostics (sequencing, molecular imaging) will improve patient selection for targeted therapy
- Single agent activity of anti-angiogenics is most likely seen in tumors addicted to mutations in growth factor pathways
- Mutations, copy number variations, structural variance all contribute
- Next generation sequencing data within clinical trials need to be connected through data sharing (open source !!!)
- Biopsies of tumor at start of and at progression under treatment are essential

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