

The genomic landscape of RAS-driven tumours

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DISCLOSURE

No conflicts of interest to declare

GLOBOCAN Projection for 2030 in Europe

Incidence: **4,000,000** new cancer cases

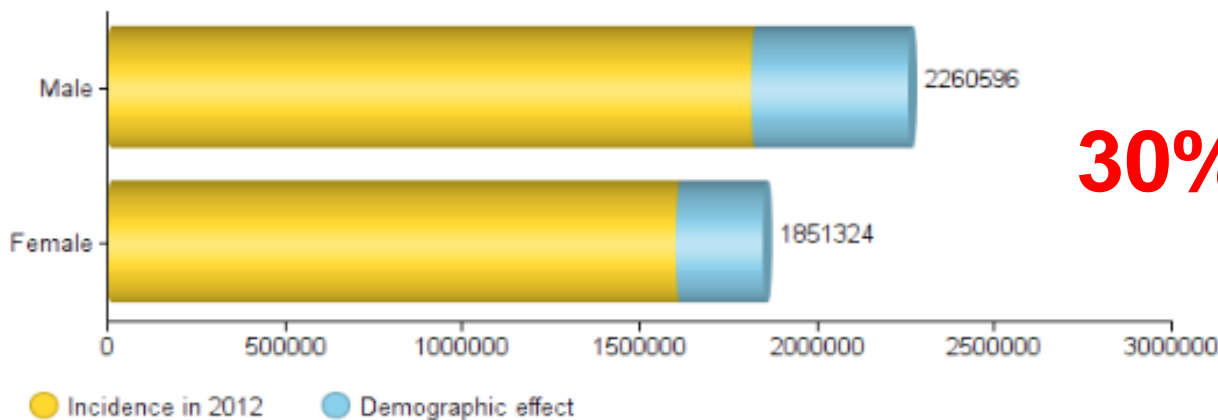


30% RAS-mutated



1,200,000 cases RAS-mutated

European Agency for Research on Cancer
Europe
All cancers excl. non-melanoma skin cancer
Number of new cancers in 2030 (all ages)



OUTLINE

1. *RAS* family members and their mutations
2. Prognostic and predictive role of *RAS* mutations
3. Downstream to *RAS*
4. *RAS* is guilty but he is not the only one

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RAS-oncogenic mutations

from COSMIC catalogue

Incidence per year in USA of RAS mutations in human cancers

Primary Tissue	<i>KRAS</i> (%)	<i>HRAS</i> (%)	<i>NRAS</i> (%)	Total (%)	
Pancreas	71	0	<1	71	95%
Colon	35	1	6	42	45%
Small intestine	35	0	<1	35	
Biliary tract	26	0	2	28	45%
Endometrium	17	<1	5	22	
Lung	19	<1	1	20	35%
Skin (melanoma)	1	1	18	20	
Cervix	8	9	2	19	
Urinary tract	5	10	1	16	

RAS family oncogenic mutations

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KRAS-oncogenic mutations

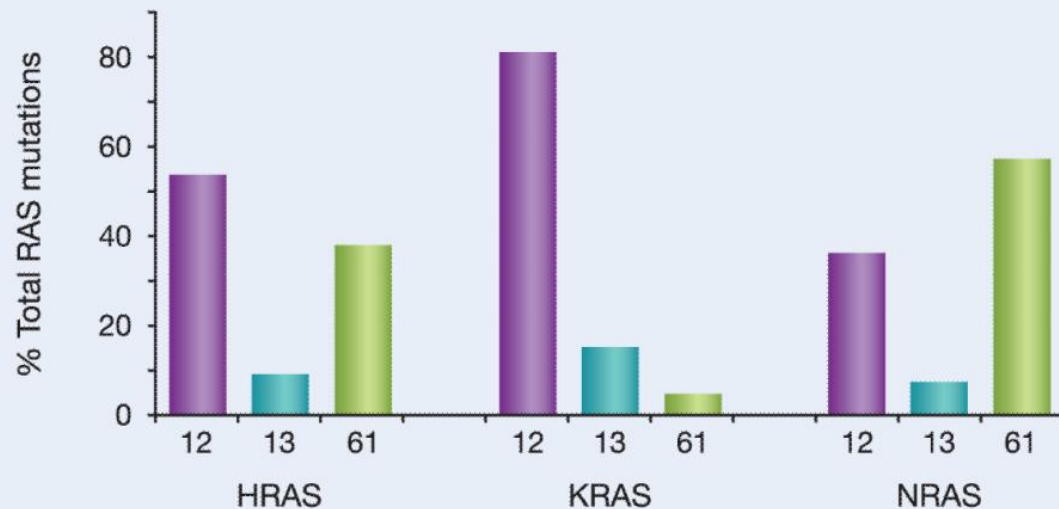
from COSMIC catalogue

Incidence per year in USA of **KRAS** mutations in human cancers

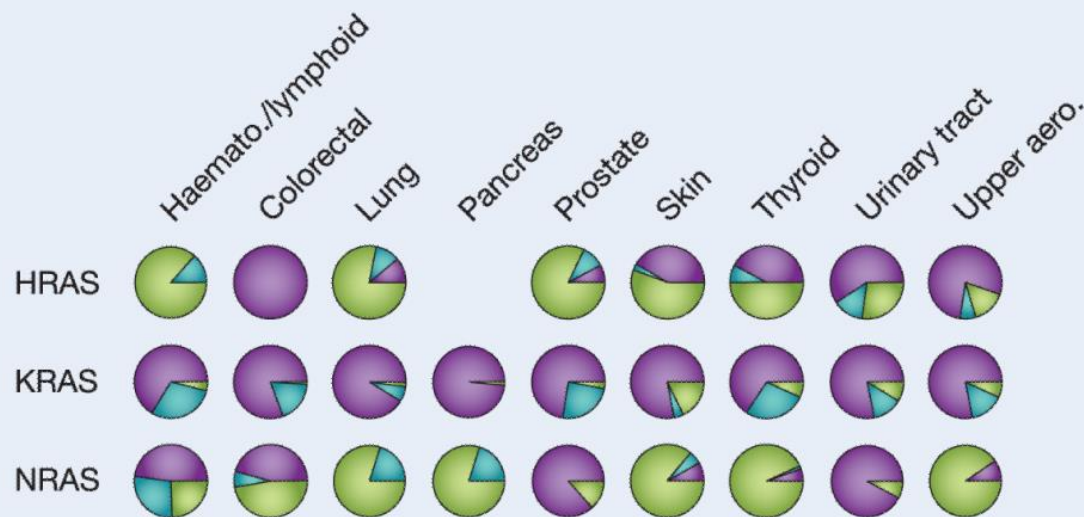
	All KRAS	G12C	G12D	G12V	G13D
Colorectal	60,000	5,700	25,000	15,700	13,600
Lung	45,600	23,000	9,200	11,900	1,500
Pancreas	32,200	1,000	19,500	11,500	200
Total new cases/year	137,800	29,700	53,700	39,100	15,300

RAS family codon mutations

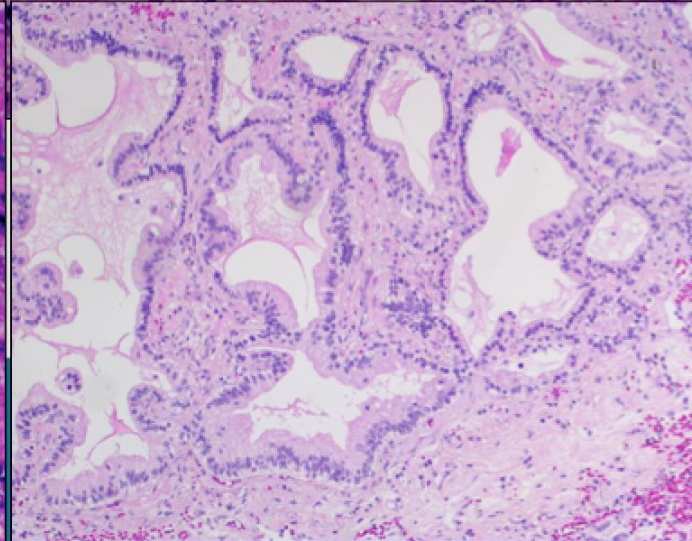
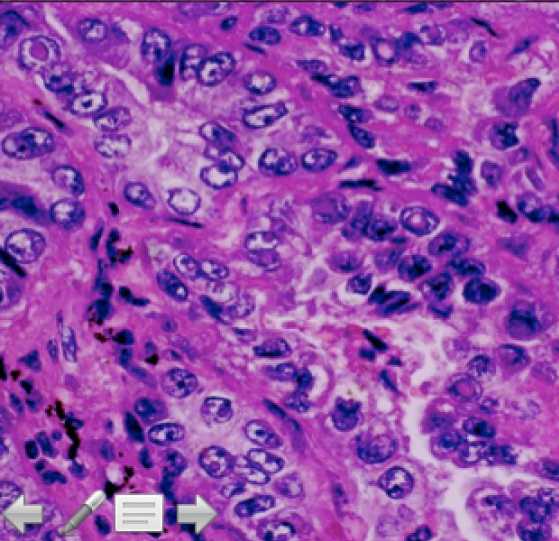
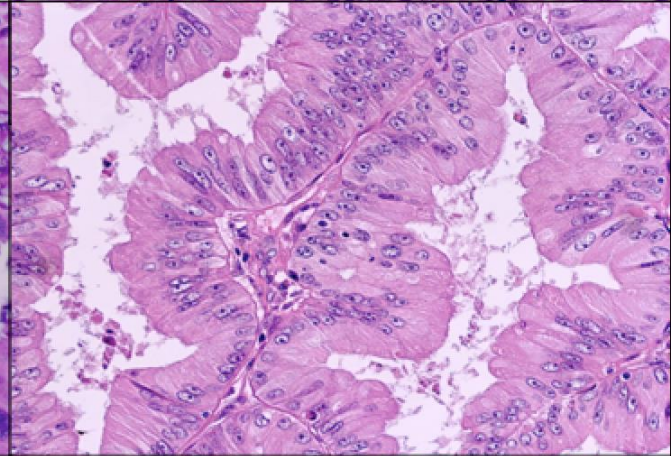
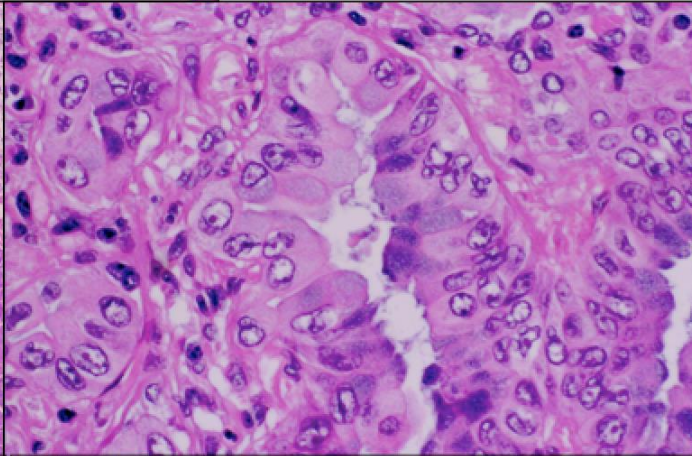
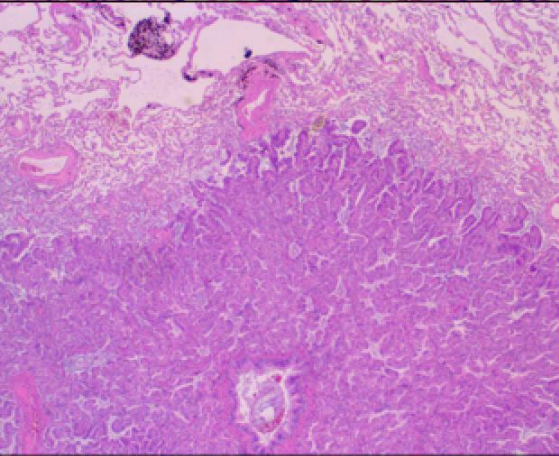
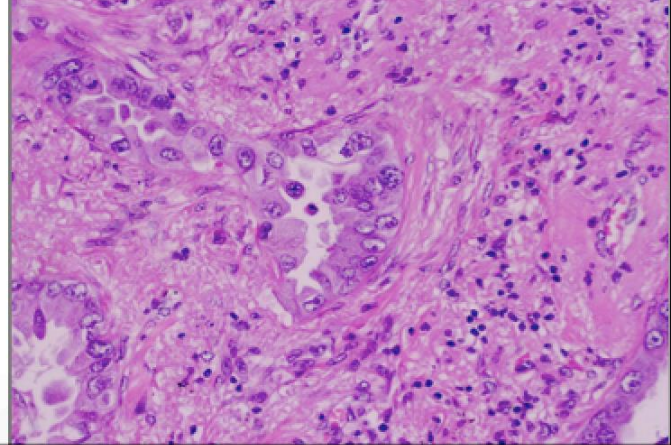
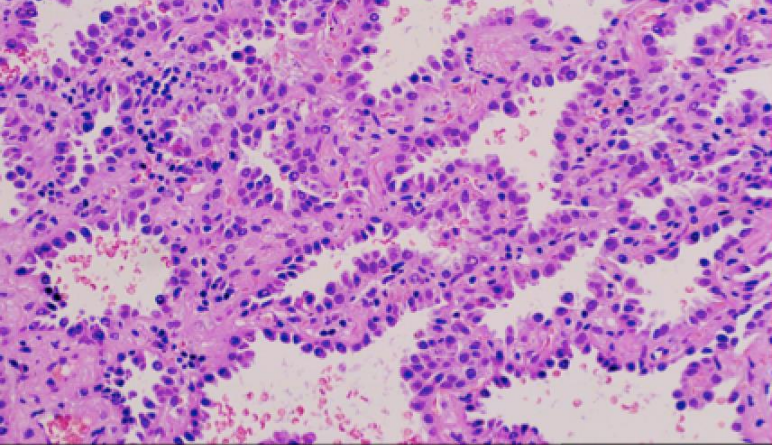
Isoform
specific pattern



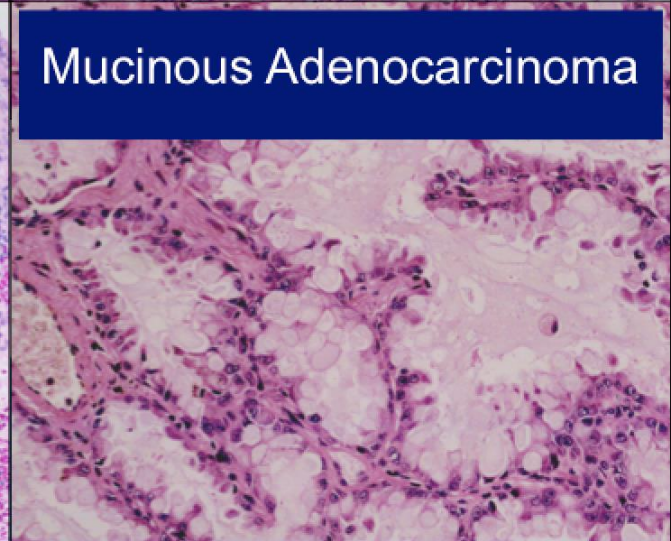
Cancer
specific pattern



Lung Carcinoma

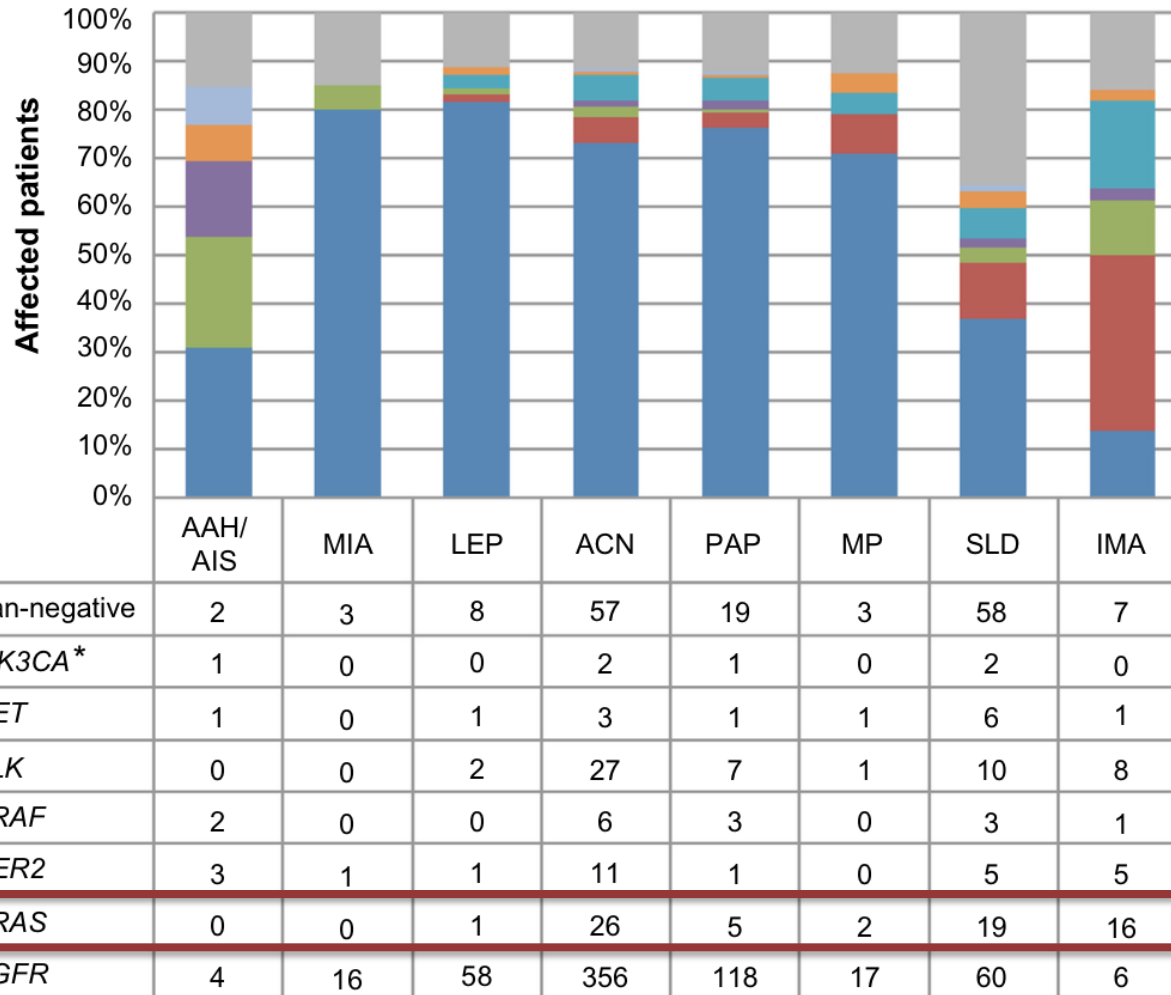


Mucinous Adenocarcinoma



KRAS mutation: histotype association

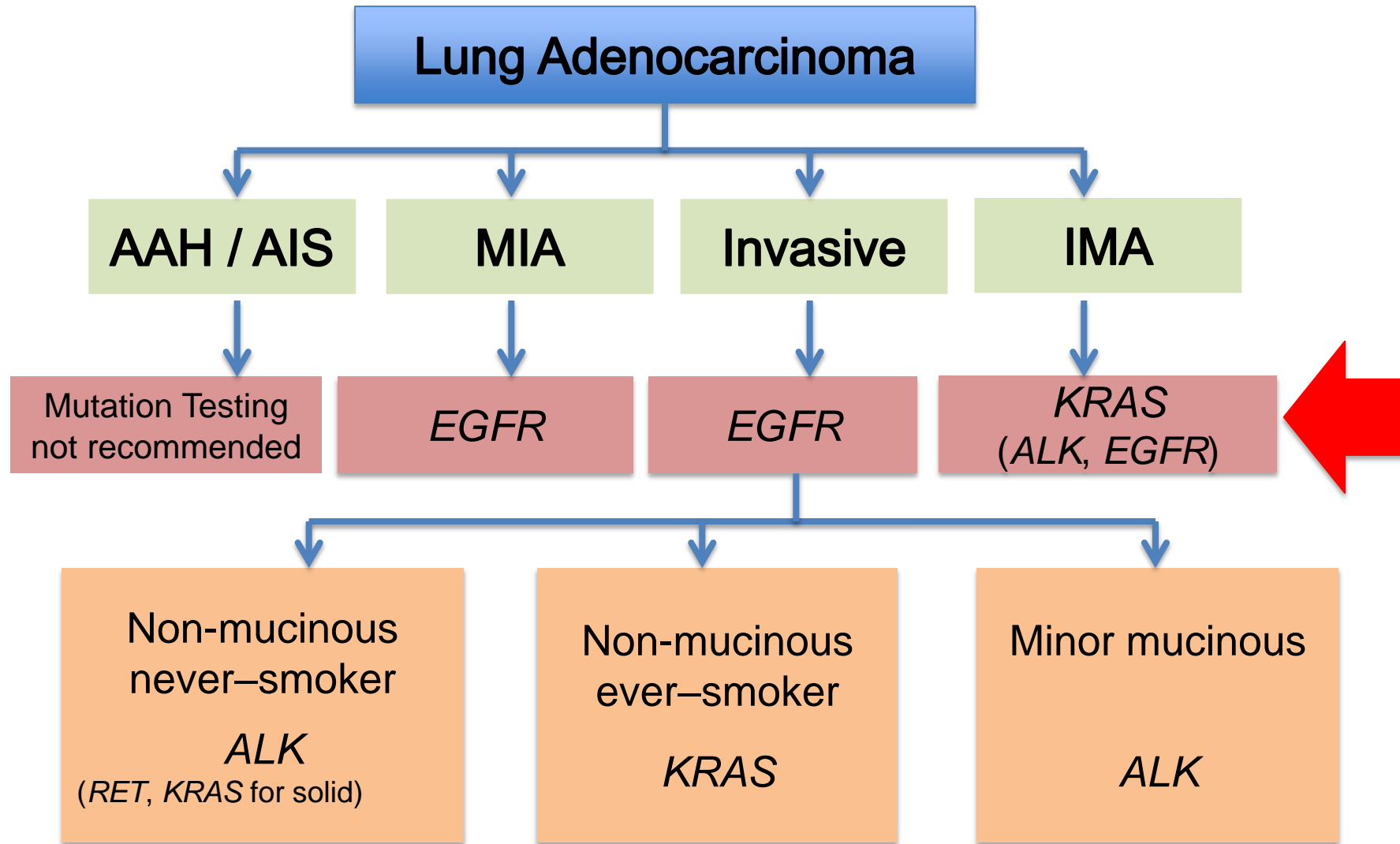
East Asian Lung Carcinoma



AAH/AIS: preinvasive lesions
MIAs: minimally invasive adenocarcinomas

Invasive Carcinoma
LEP: lepidic
ACN: acinar
PAP: papillary
MP: micropapillary
SLD: solid
IMA: invasive mucinous adenocarcinoma

KRAS mutation: histotype drives diagnostic workflow

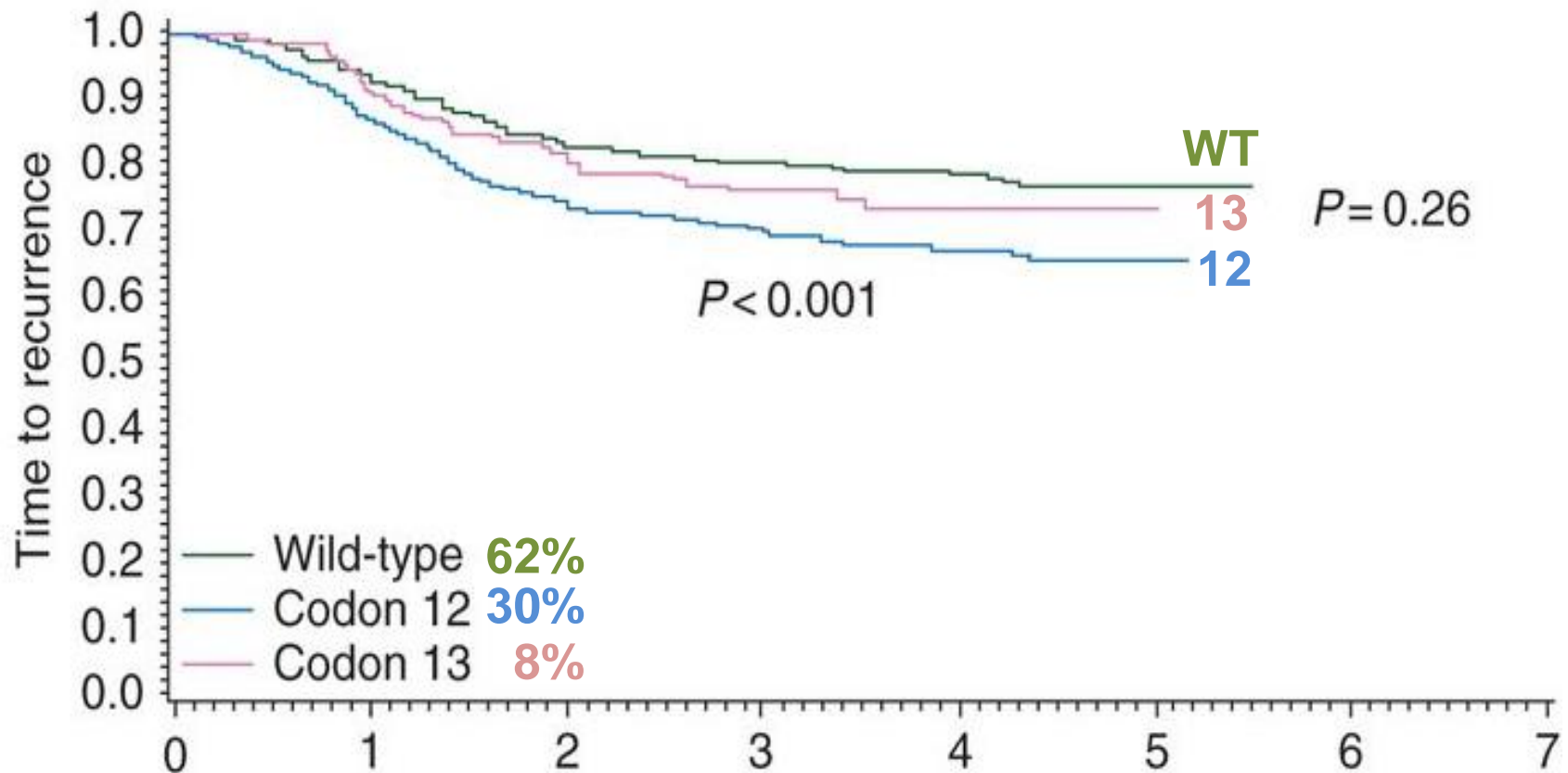


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KRAS mutations: Prognostic significance Colorectal Cancer

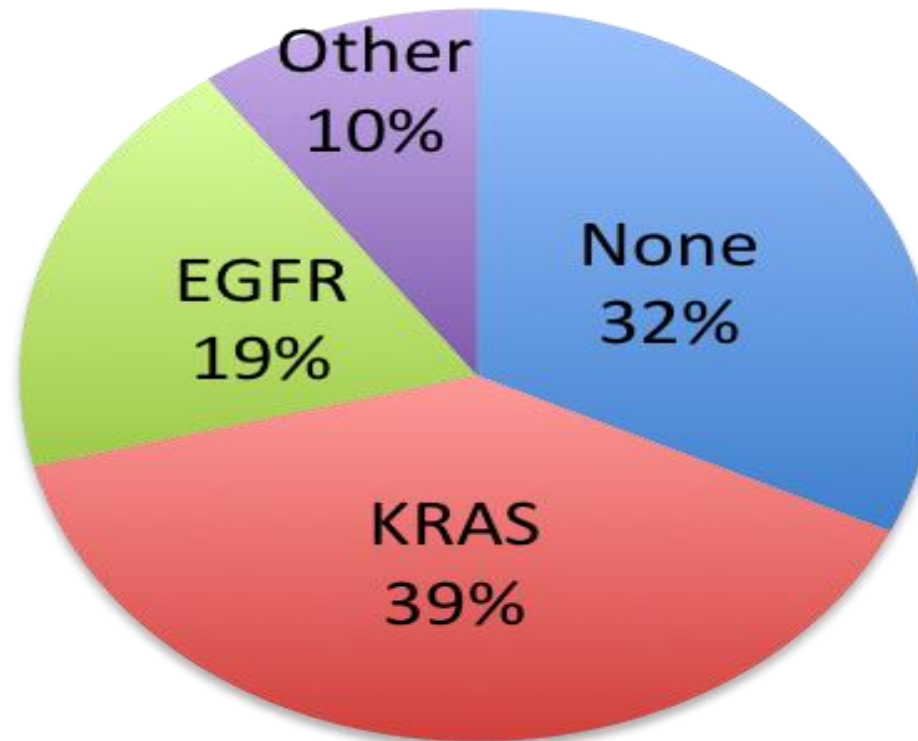
Codon 12 mutations associated with shorter TTP



KRAS mutations: Prognostic significance

Lung Cancer

312 resected stage I cancers



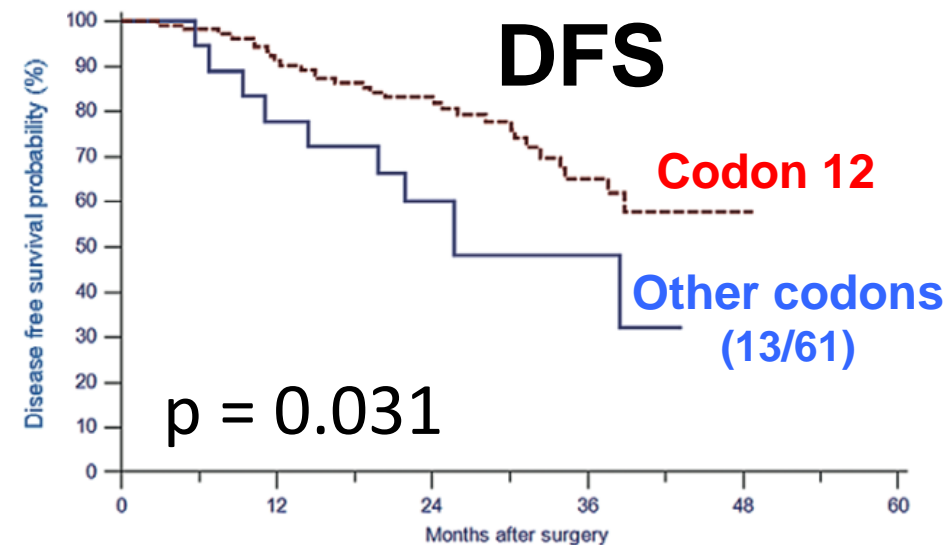
KRAS mutations: Prognostic significance Lung Cancer

312 resected stage I cancers

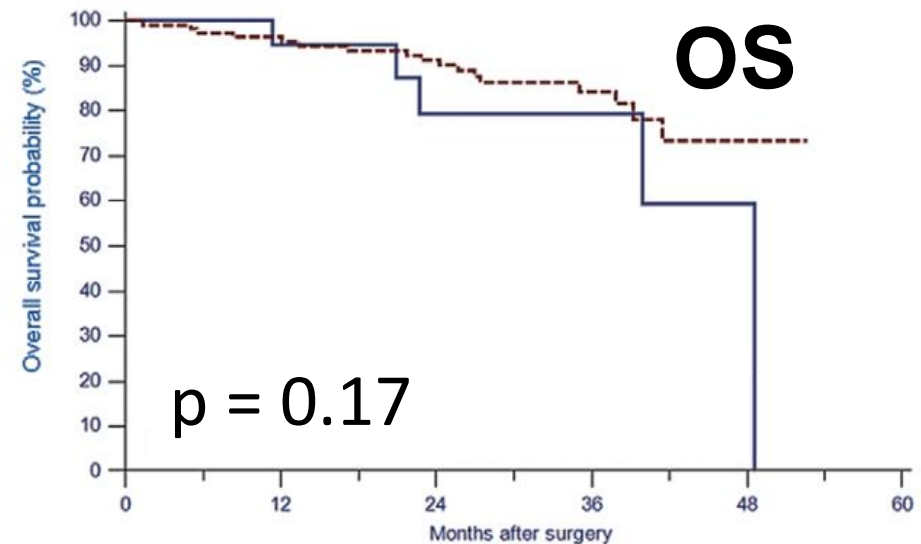
KRAS mutation: the only independent predictor of shorter OS ($p = 0.001$) and DFS ($p < 0.0001$) at multivariate analysis.

KRAS mutations: Prognostic significance Lung Cancer

312 resected stage I cancers



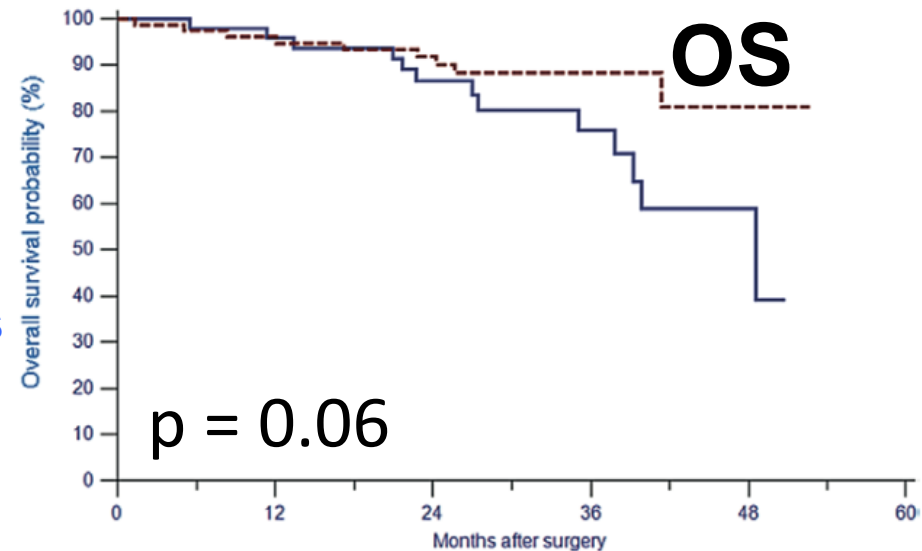
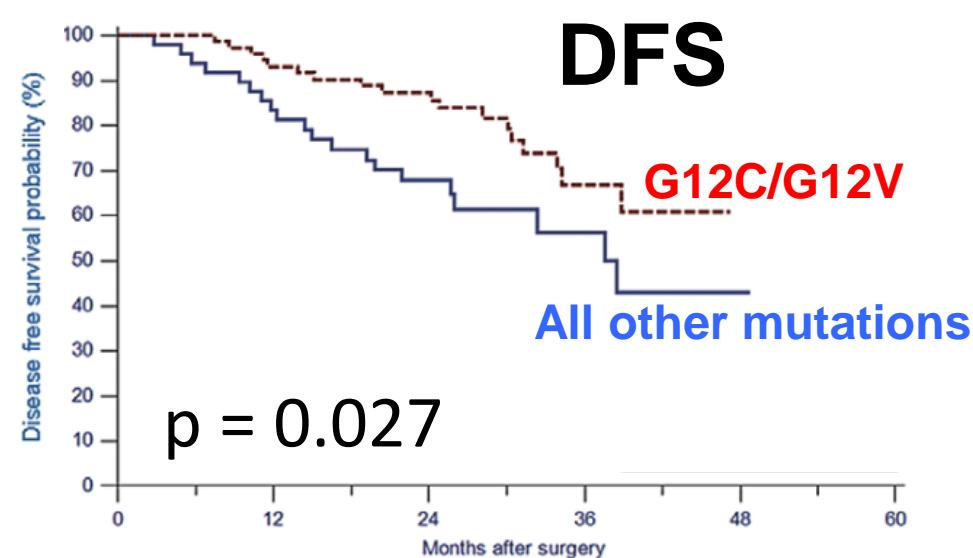
Other codon mutations	18	14	7	4	0	0
Codon 12 mutations	109	91	69	24	1	0



Other codon mutations	18	17	9	5	1	0
Codon 12 mutations	109	99	81	37	5	0

KRAS mutations: Prognostic significance Lung Cancer

312 resected stage I cancers

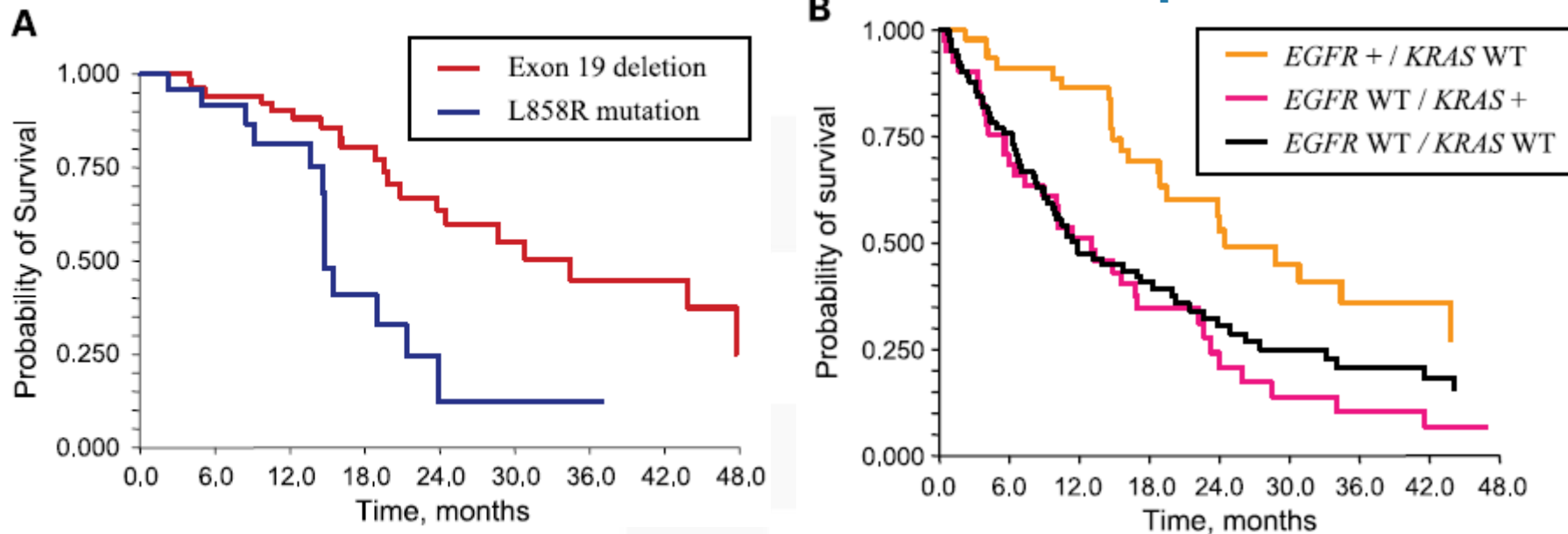


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Advanced Lung Cancer: anti EGFR prediction

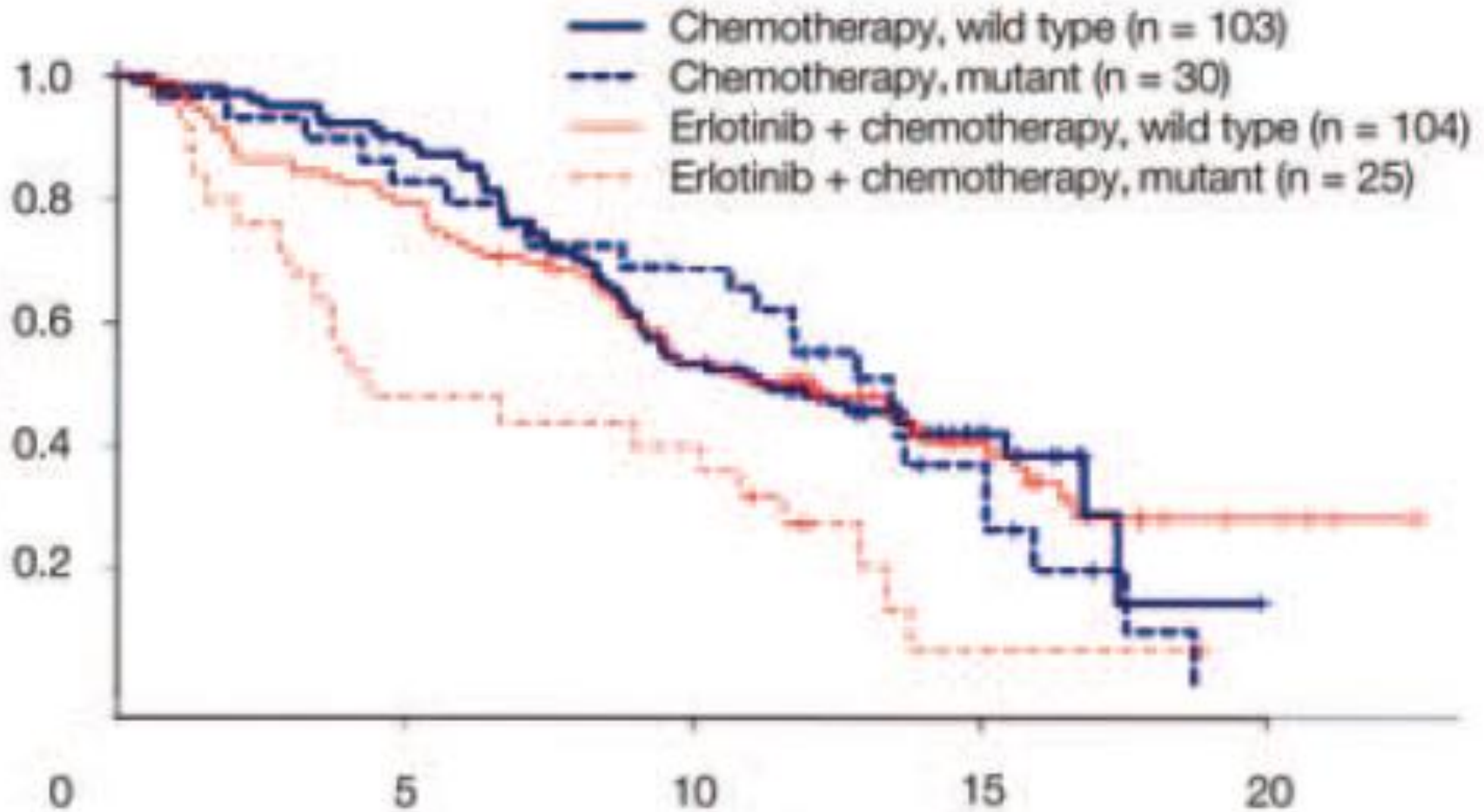
KRAS status does not affect response



	<i>EGFR</i> + / <i>KRAS</i> WT	<i>EGFR</i> WT / <i>KRAS</i> +	<i>EGFR</i> WT / <i>KRAS</i> WT	
N	47	41	83	P
RR	68%	0	5%	< .001
Median TTP (months)	13.1	3.3	3.1	< ,0001
Median OS	24,5	13,0	11,8	,002

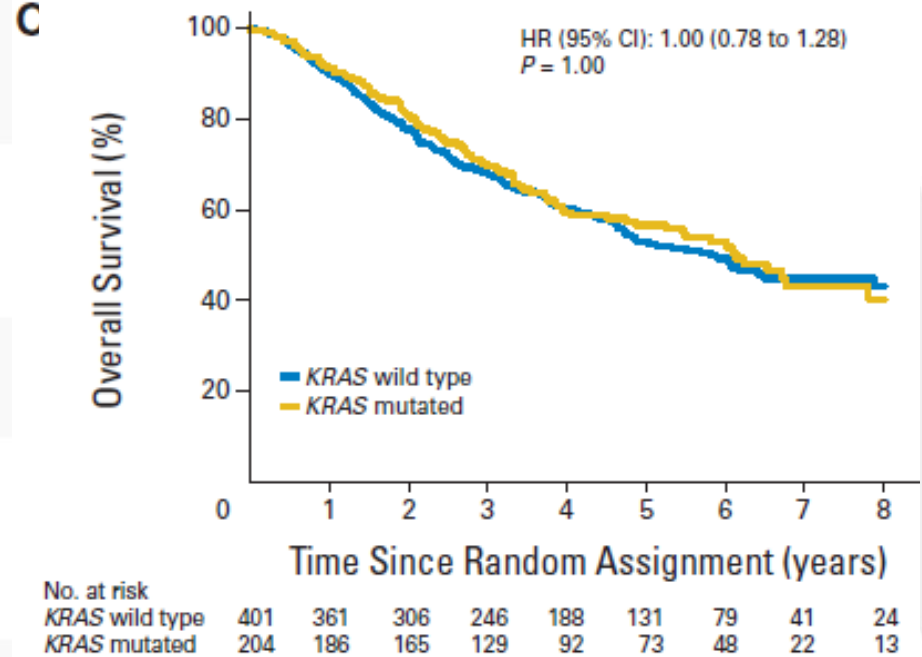
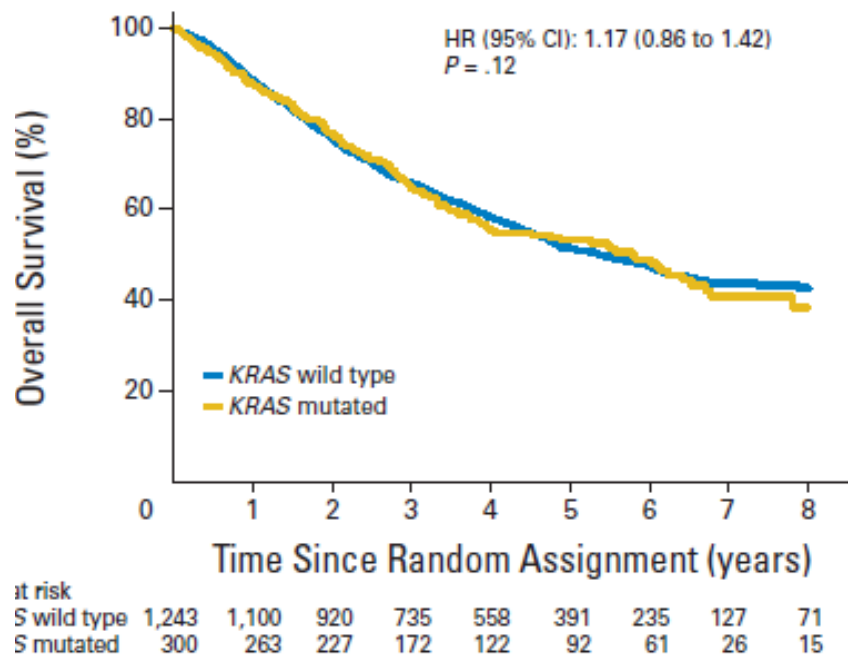
Locally Advanced Lung Cancer: anti EGFR prediction

Erlotinib is detrimental in KRAS mutated



Early Stage Resected Lung Cancer: anti EGFR prediction

KRAS status cannot be recommended to select patients for adjuvant chemotherapy



Colorectal Cancer: molecular classification

- *KRAS* mutated
- *NRAS* mutated
- *PIK3CA* mutated
- *RAF* mutated
- **Quadruple-negative**

New scenarios in EGFR targeting in

CRC THE LANCET Oncology

Effects of *KRAS*, *BRAF*, *NRAS*, and *PIK3CA* mutations on the efficacy of cetuximab plus chemotherapy in chemotherapy-refractory metastatic colorectal cancer: a retrospective consortium analysis

[Wendy De Roock MD a](#), [Bart Claes MSc b](#), [David Bernasconi MSc c](#), [Jef De Schutter MSc a](#), [Bart Biesmans MSc a](#), Prof [George](#)

**1022 tumours
treated with cetuximab**

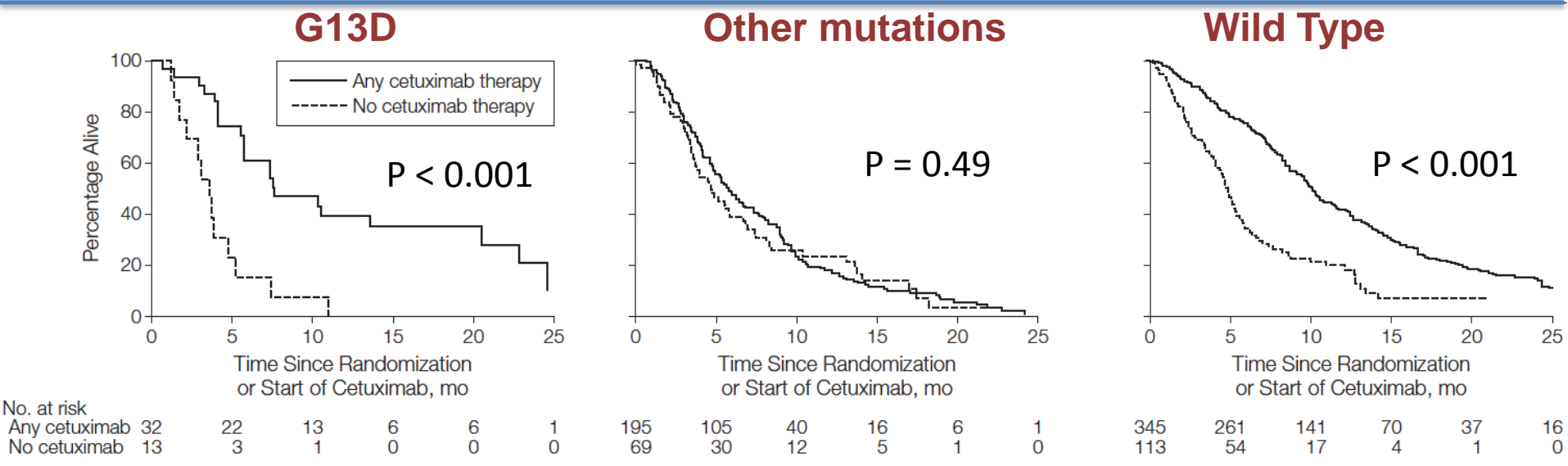
<i>KRAS</i>	40%
<i>BRAF</i>	5%
<i>NRAS</i>	3%
<i>PIK3CA</i>	15% (4% <i>ex 20</i>)

**are significantly associated with a
low response rate**

Colorectal Cancer: anti EGFR prediction

KRAS-G13D respond to Cetuximab as Wild Type tumors

Figure 1. Overall Survival: Predictive Analysis by *KRAS* Status for Patients Receiving Any Cetuximab-Based Therapy vs No Cetuximab



The no cetuximab group for all patients from the pooled data set is the best supportive care group from the CO.17 trial.

Colorectal Cancer: anti EGFR prediction

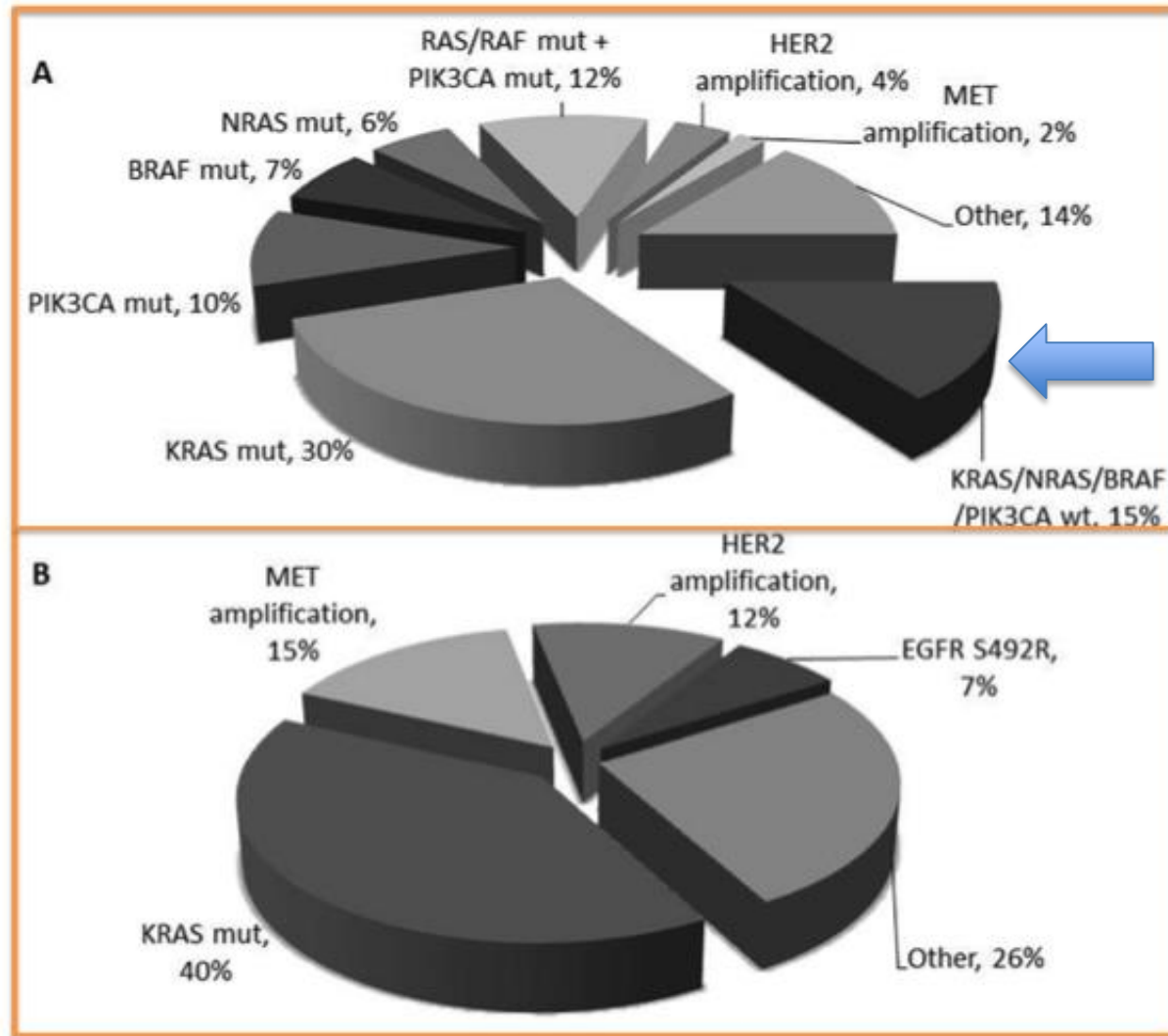
Resistance

Primary

Response

Quadruple-negative

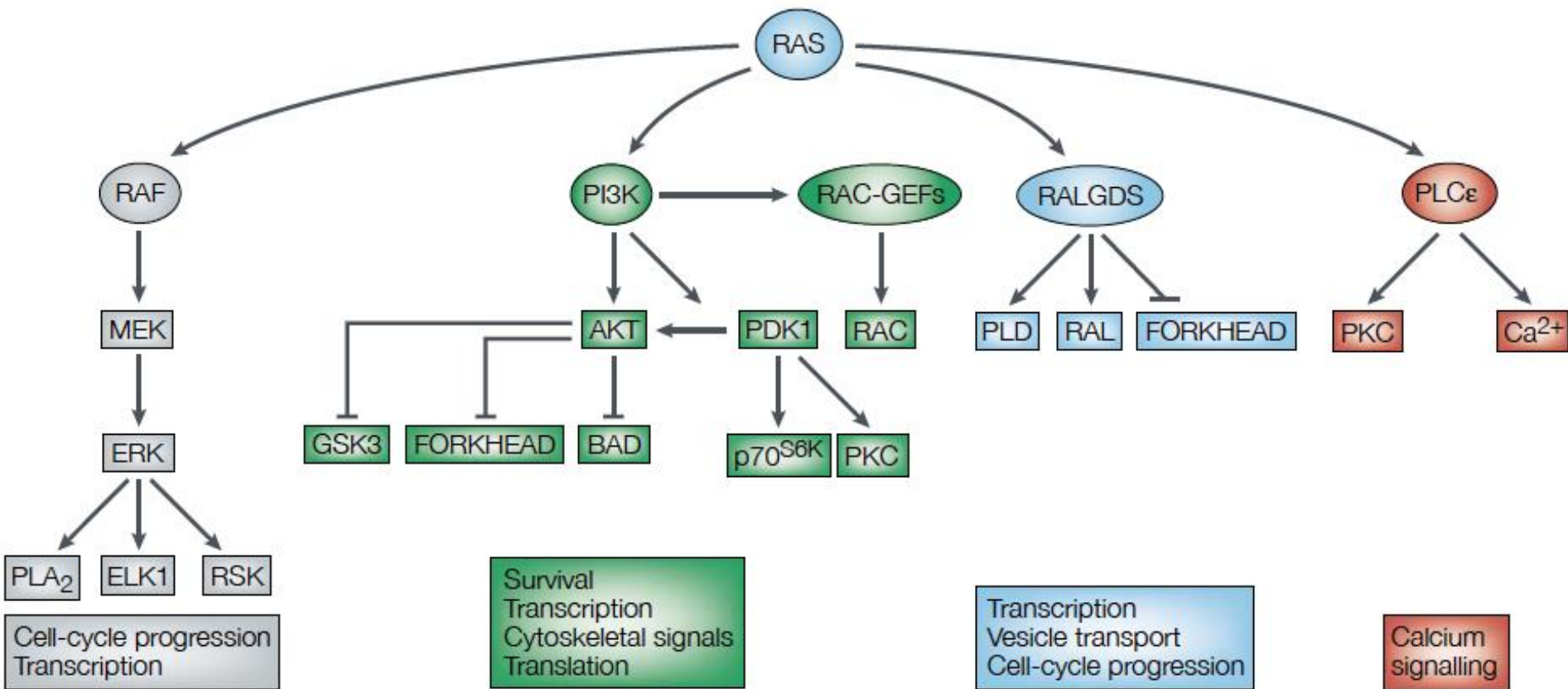
Acquired



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The landscape of RAS-driven pathway

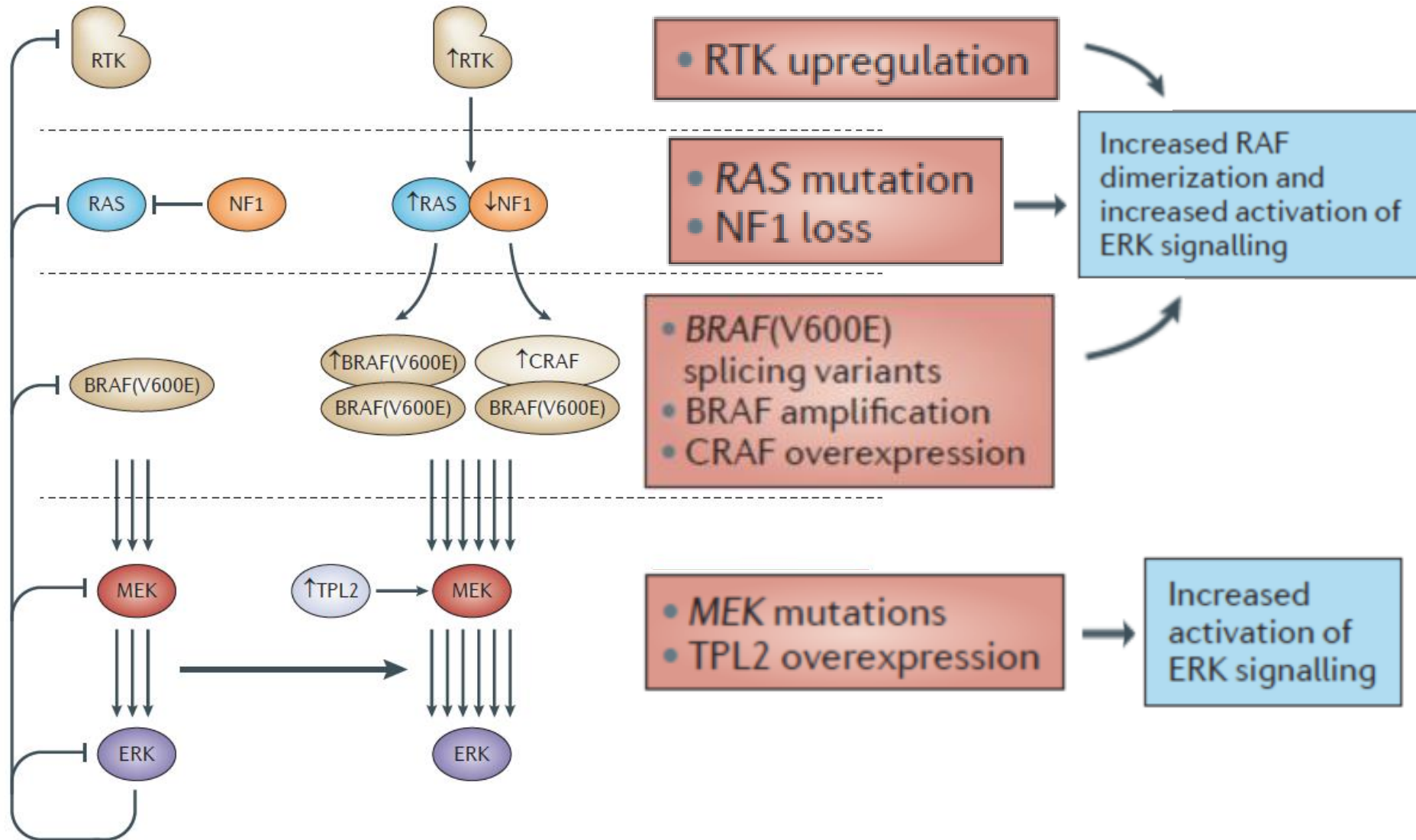


Mechanism of resistance

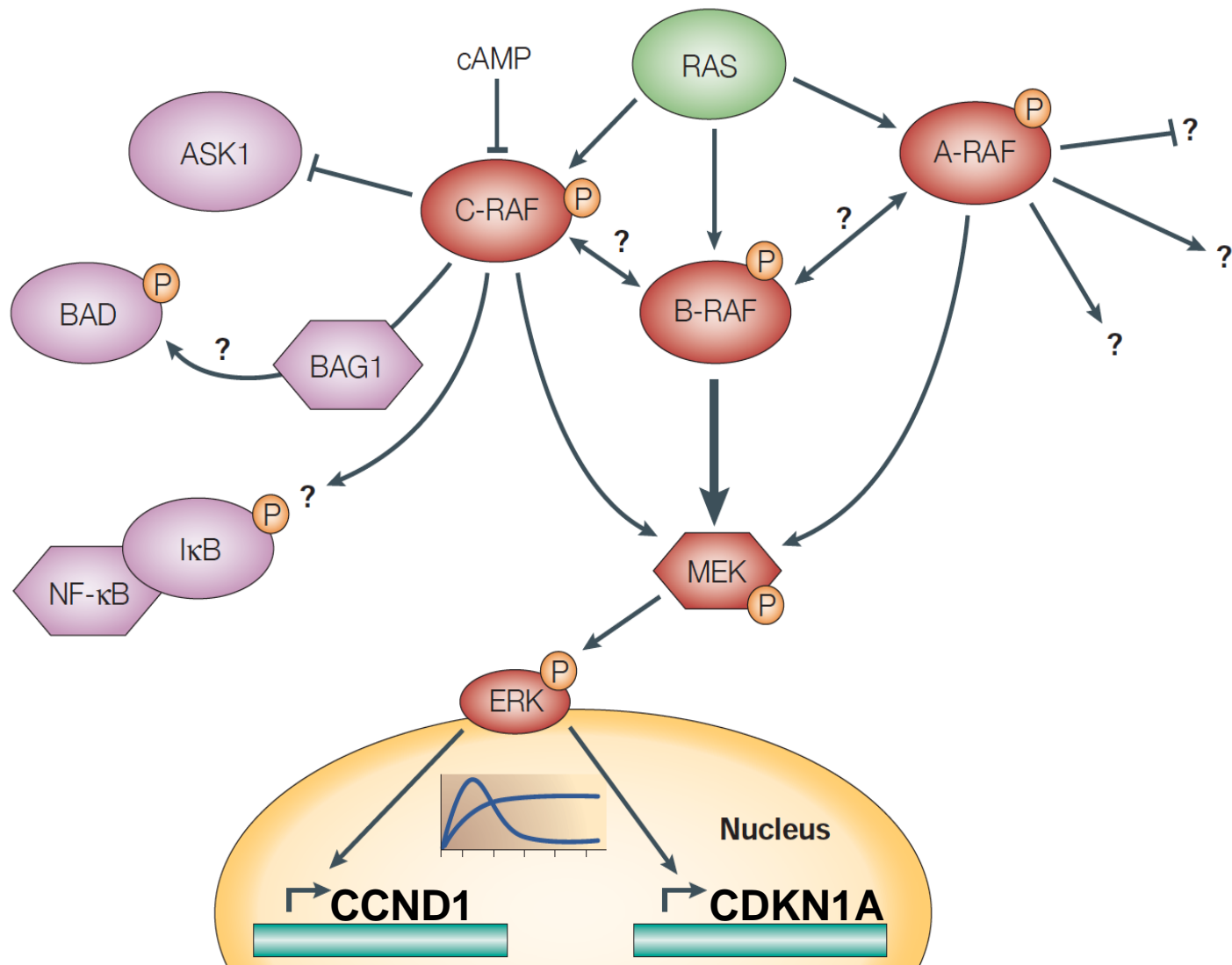
Sensitive state

Resistant state

Mechanism



RAF FAMILY



BRAF mutations:

- Melanoma
- Non-small cell lung cancer
- Colorectal cancer
- Bile duct cancer
- Hairy-cell leukemia

V600

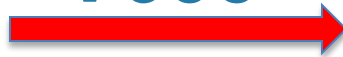


Table 1 | **Correct numbering of the important amino acids in B-RAF**

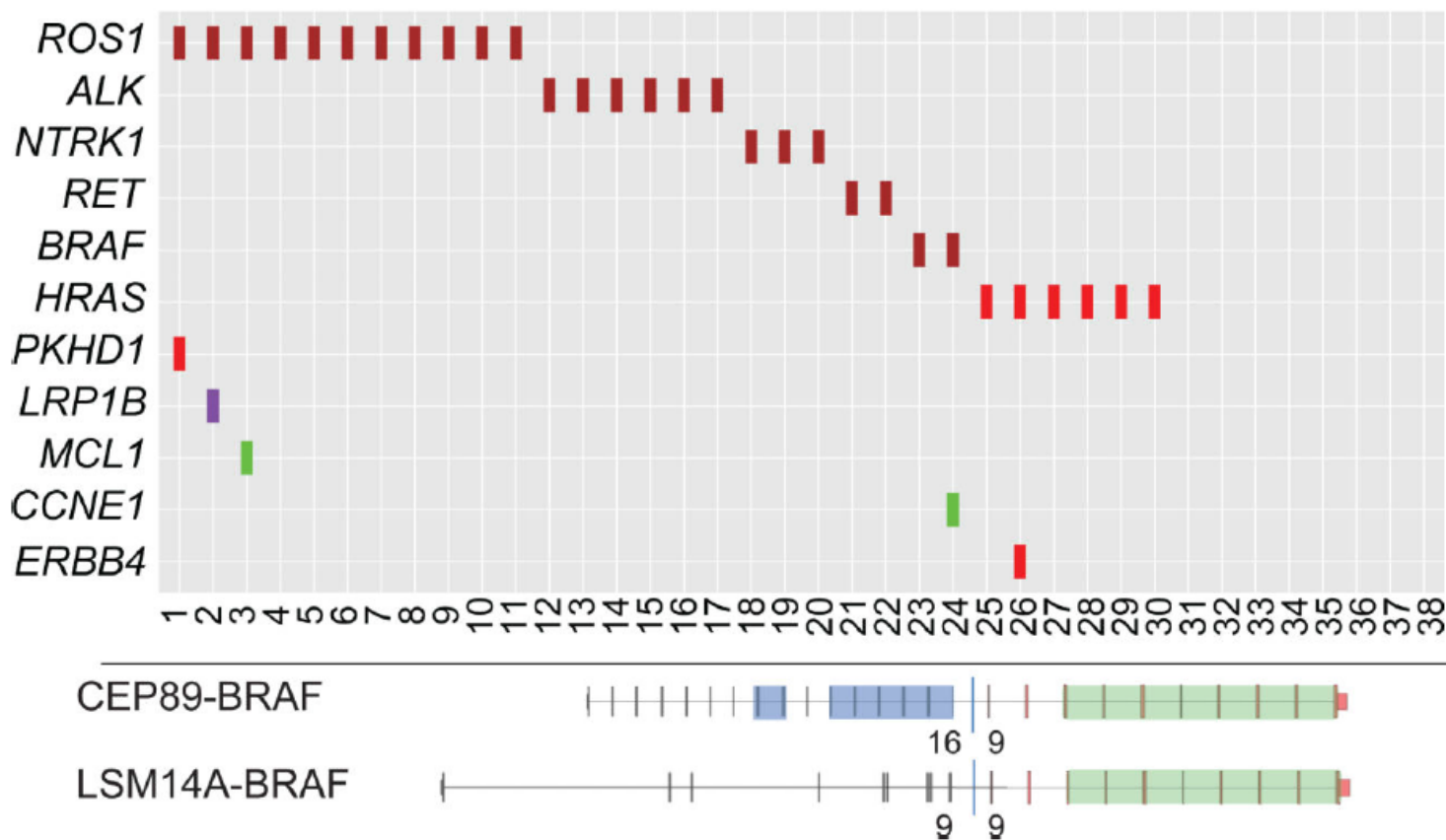
Original assignment	Correct assignment	Comments
M116	M117	Mutated in cancer
R187	R188	Equivalent of R89 in C-RAF where it is required for RAS binding
I325	I326	Mutated in cancer
S364	S365	Phosphorylation site, possibly by AKT/PKB and PKA; forms core of 14-3-3 binding motif
S428	S429	AKT/PKB phosphorylation site
K438	K439	Mutated in cancer
T439	T440	AKT/PKB phosphorylation site; mutated in cancer
S445	S446	N-region phosphorylation site; equivalent to S338 of C-RAF
D448	D449	Equivalent of Y341 of C-RAF
V458	V459	Mutated in cancer
R461	R462	Mutated in cancer
I462	I463	Mutated in cancer
G463	G464	First glycine of the glycine-rich loop; mutated in cancer
G465	G466	Second glycine of the glycine-rich loop; mutated in cancer
F467	F468	Mutated in cancer
G468	G469	Third glycine of the glycine-rich loop; mutated in cancer
K474	K475	Mutated in cancer
N580	N581	Catalytic asparagine; mutated in cancer
E585	E586	Mutated in cancer
D586	D587	Mutated in cancer
D593	D594	Aspartic acid of the 'DFG' motif; mutated in cancer
F594	F595	Phenylalanine of the 'DFG' motif; mutated in cancer
G595	G596	Glycine of the 'DFG' motif; mutated in cancer
L596	L597	Mutated in cancer
T598	T599	Activation segment phosphorylation site; mutated in cancer
V599	V600	Most commonly mutated residue in cancer
K600	K601	Mutated in cancer
S601	S602	Activation segment phosphorylation site
R681	R682	Mutated in cancer
A727	A728	Located within C-terminal 14-3-3 binding motif; mutated in cancer
S728	S729	Phosphorylation site and core of 14-3-3 binding motif

PKA, protein kinase A; PKB, protein kinase B.

BRAF

Beyond BRAF mutations: translocations

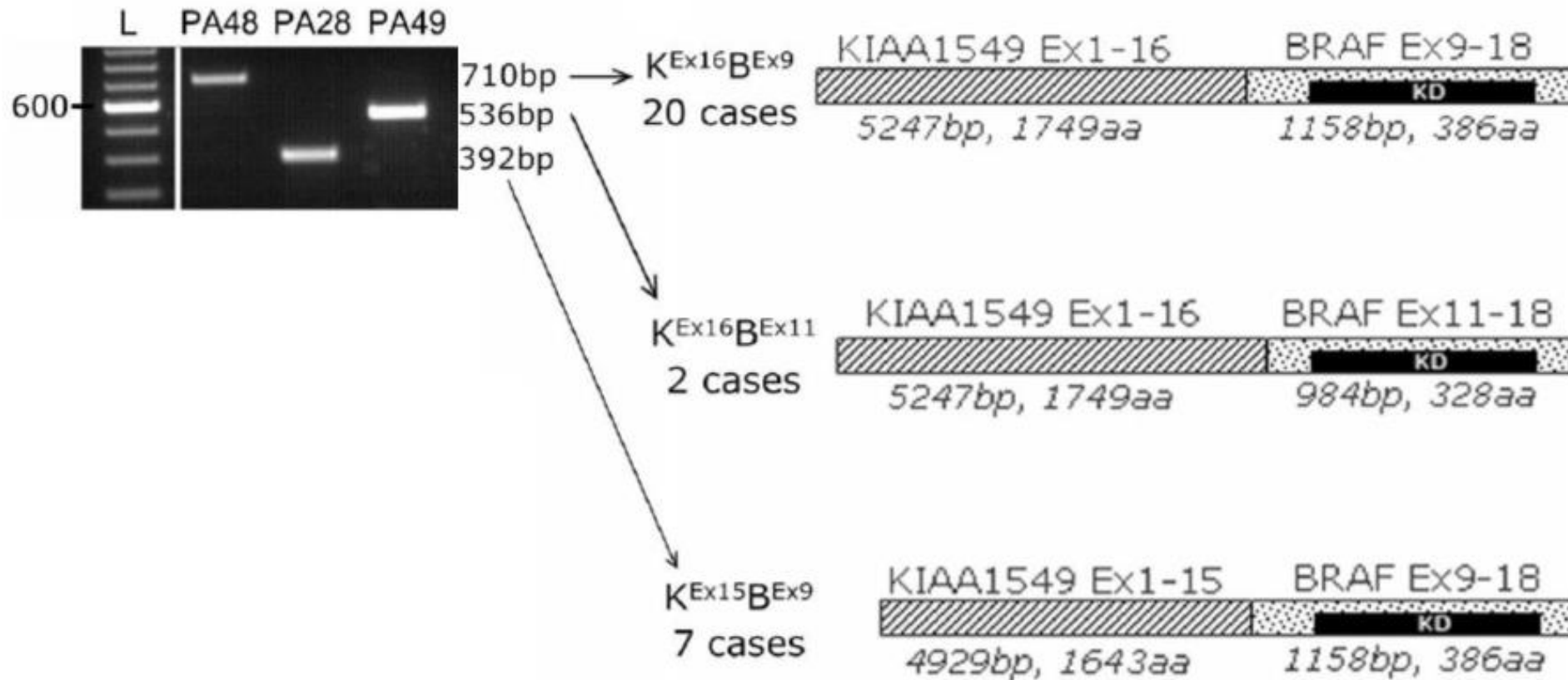
38 cutaneous spitzoid lesions



BRAF

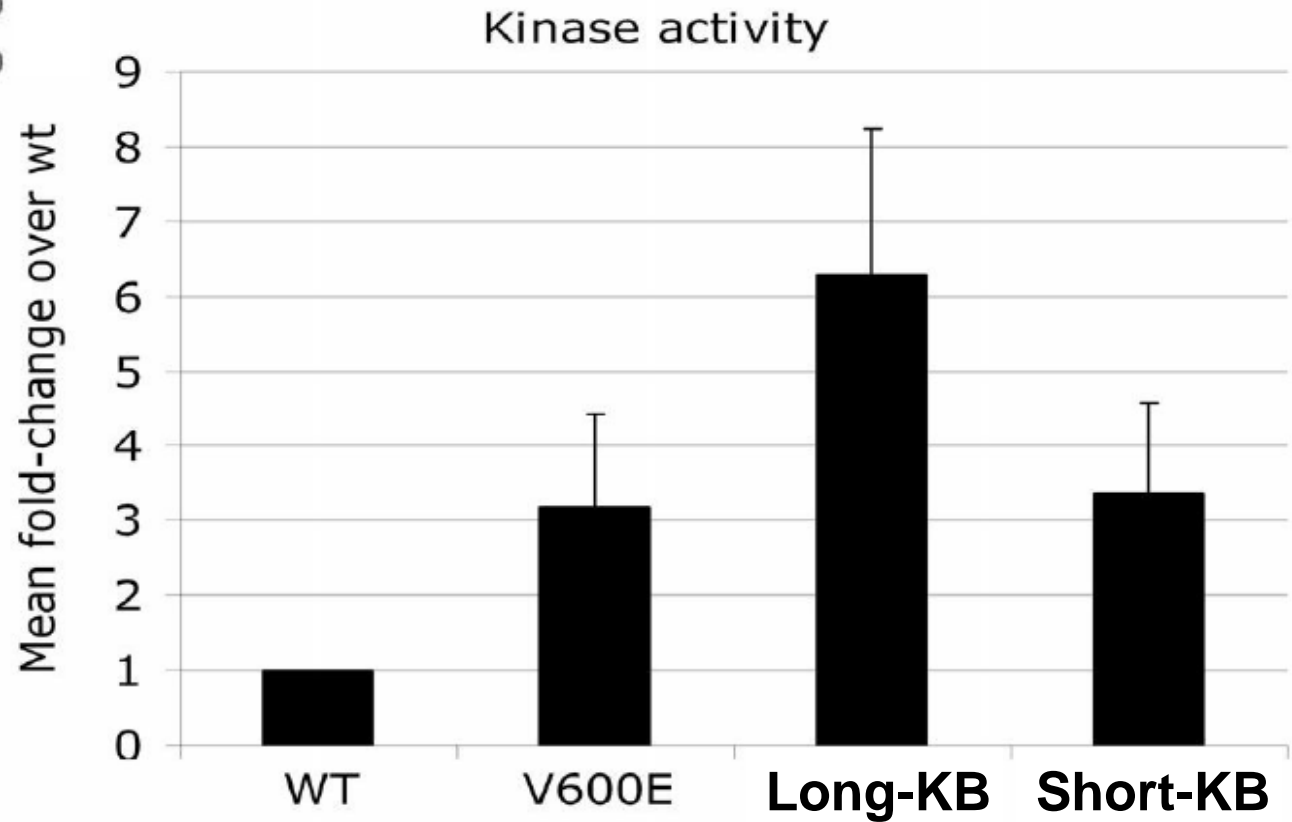
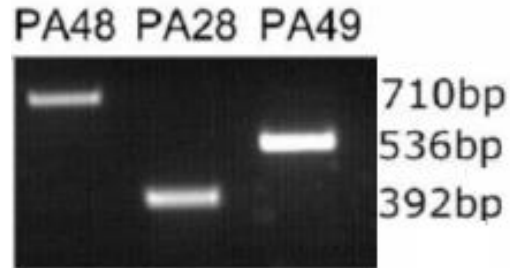
Beyond BRAF mutations: amplification/fusion genes

44 pilocytic astrocytomas

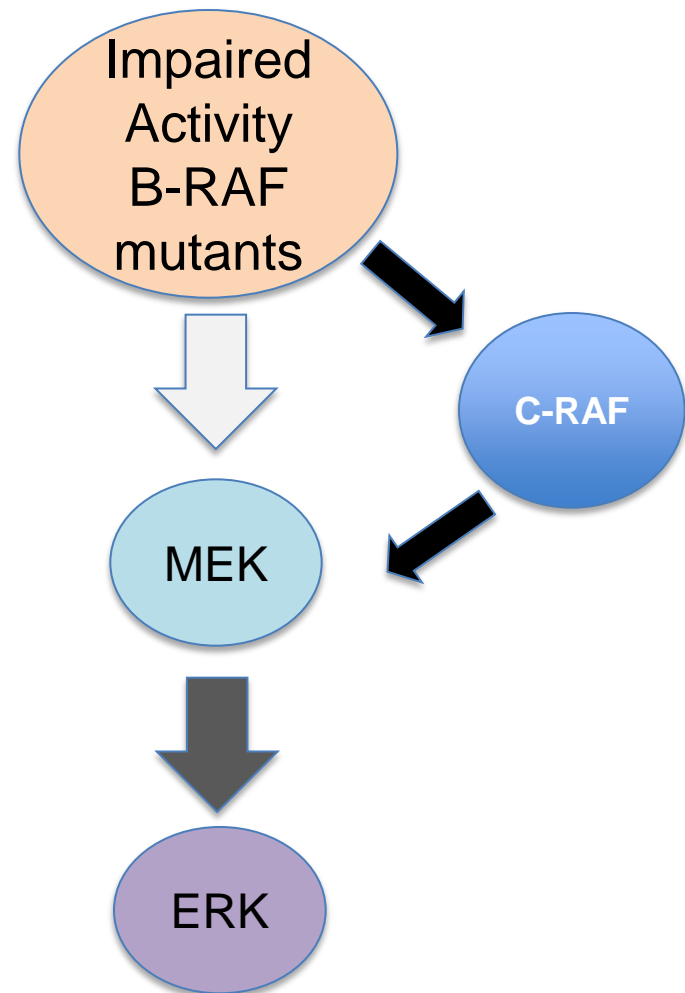
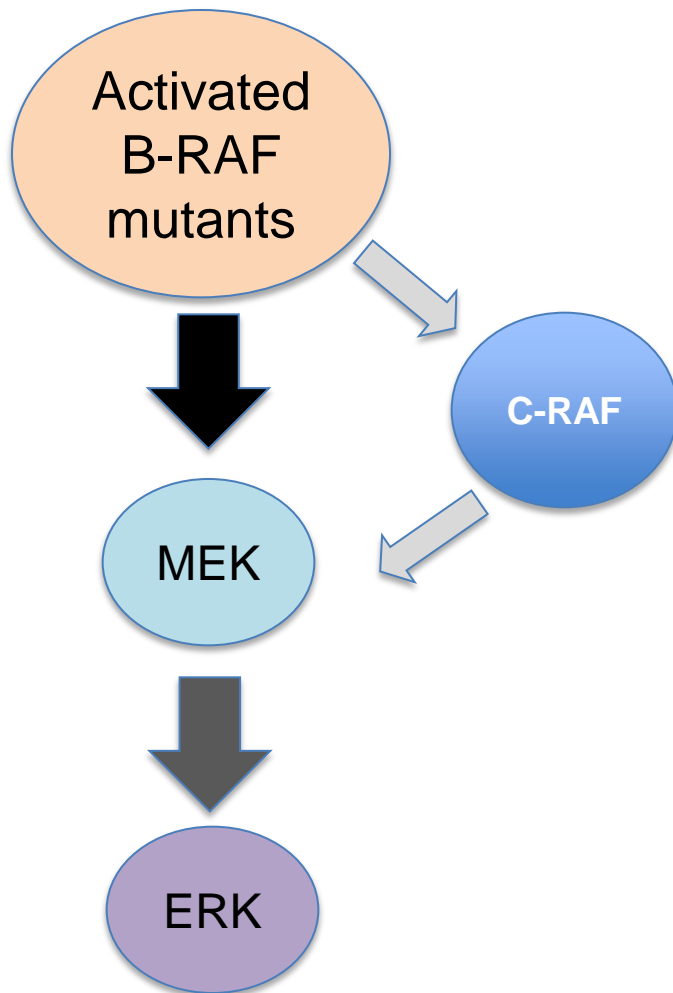


BRAF

Beyond BRAF mutations: amplification/fusion genes



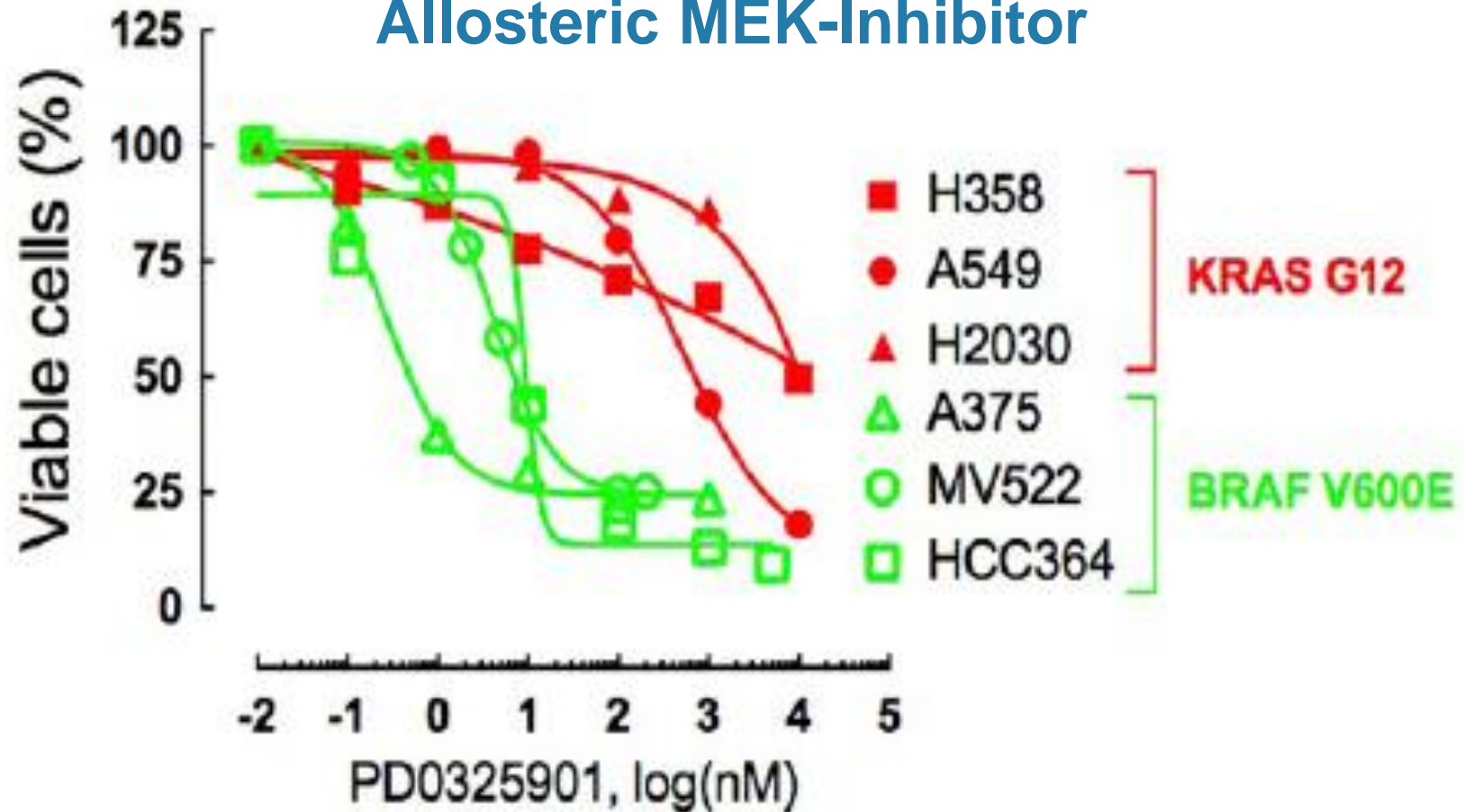
BRAF



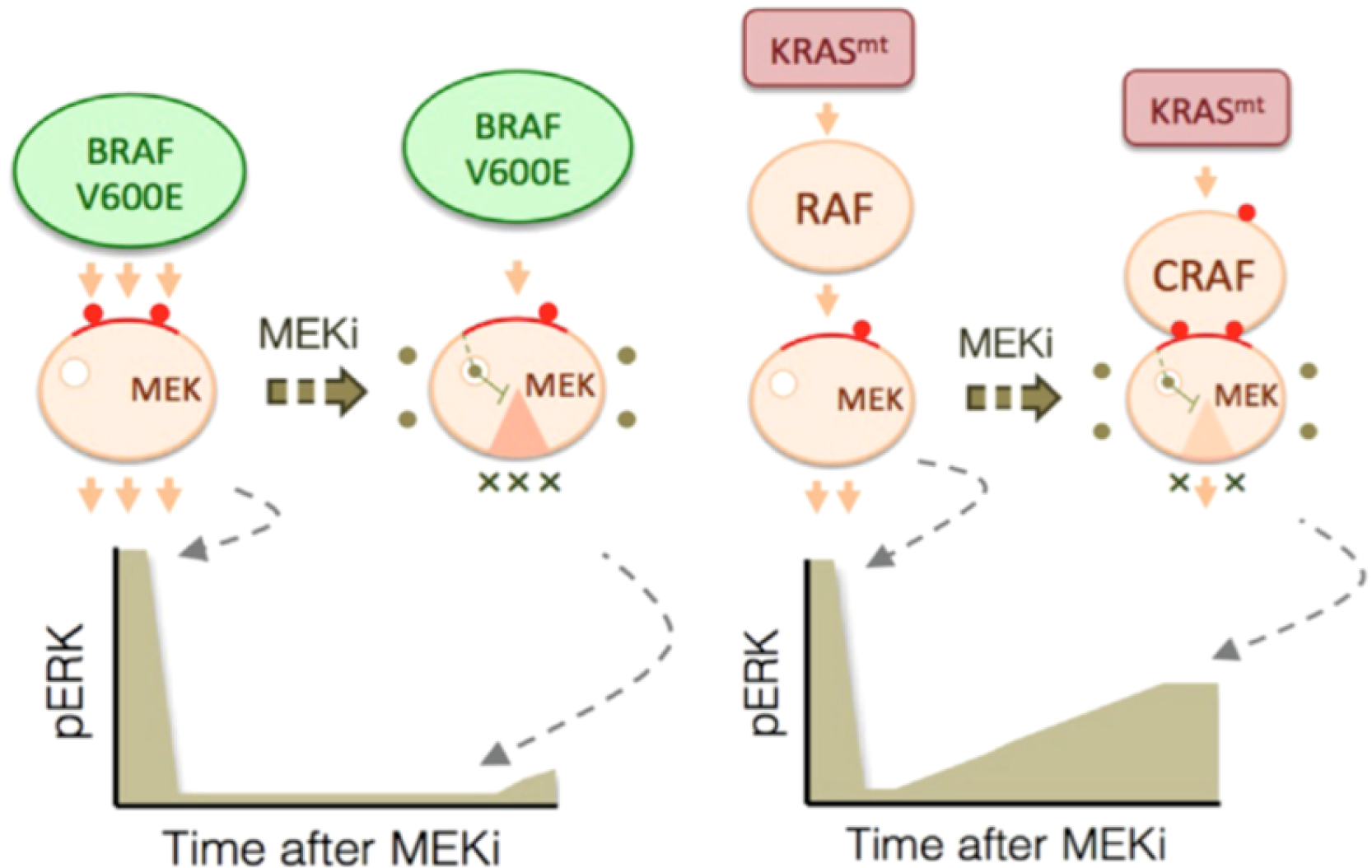
BRAF

C-RAF (Raf-1): there is more than MEK activation

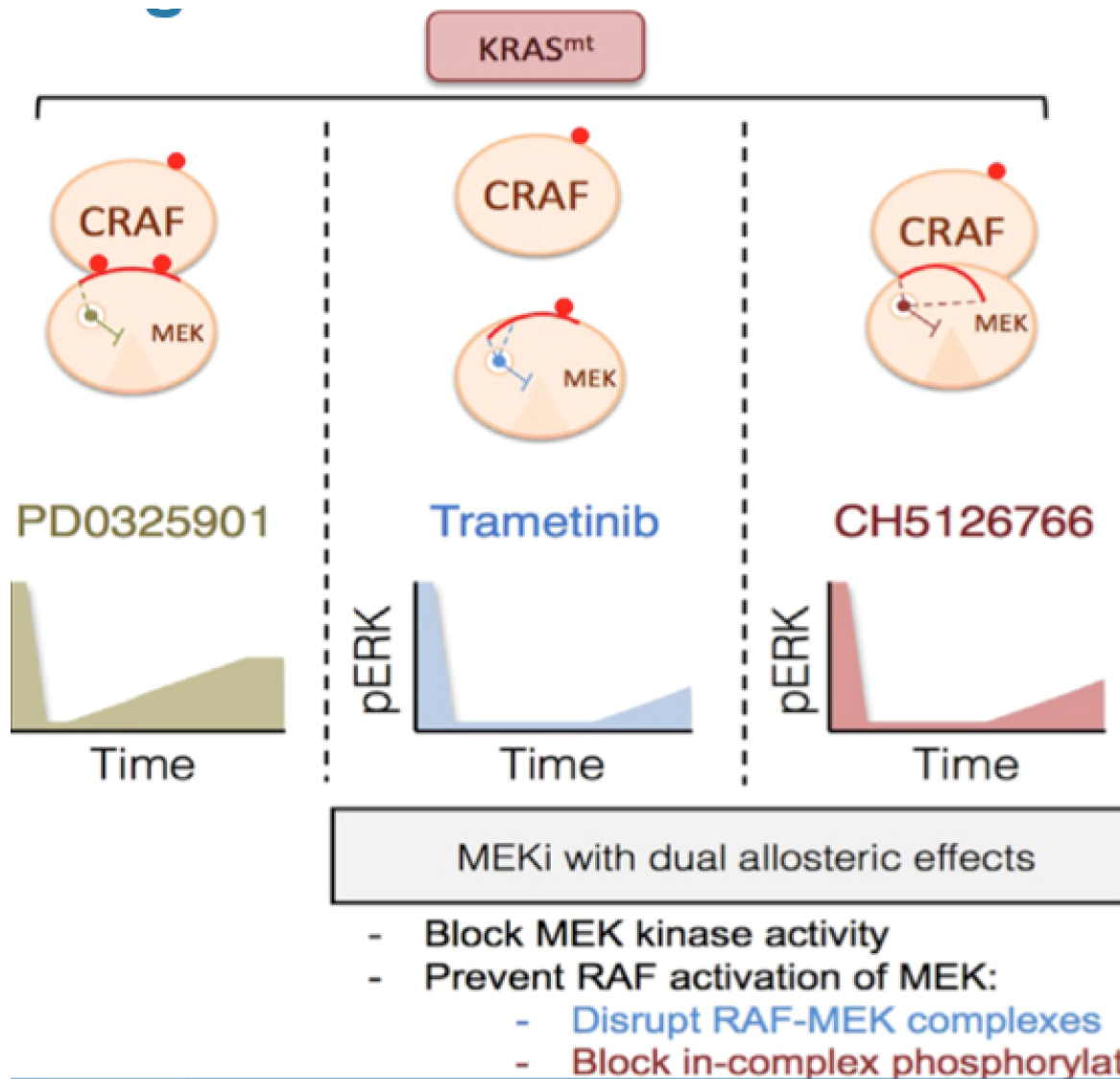
Allosteric MEK-Inhibitor



Allosteric MEK-Inhibitor

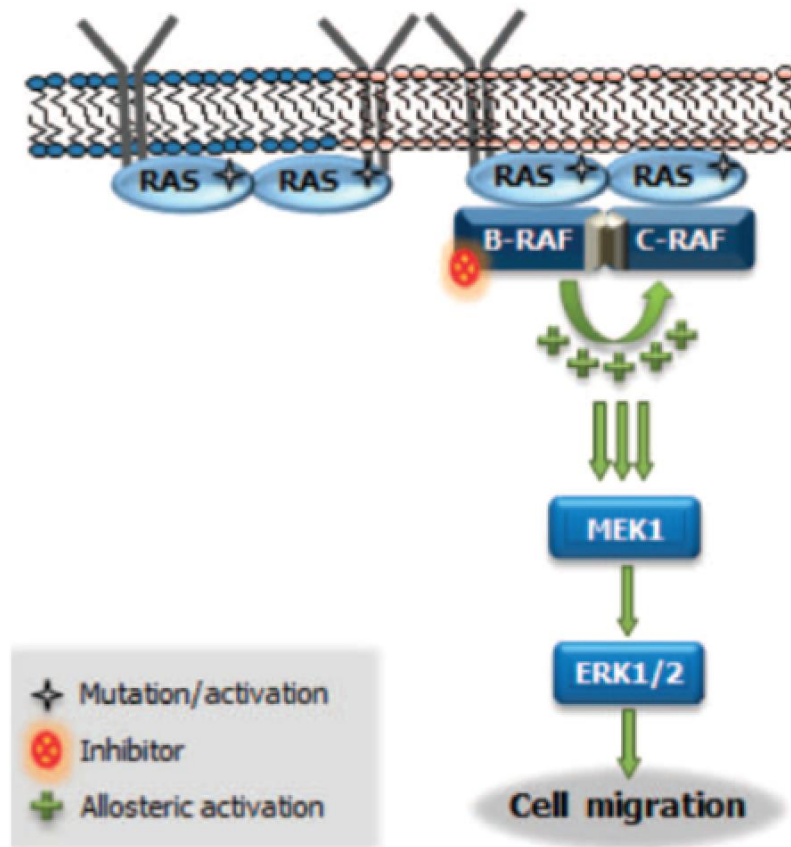


Stronger Allosteric MEK-Inhibitor



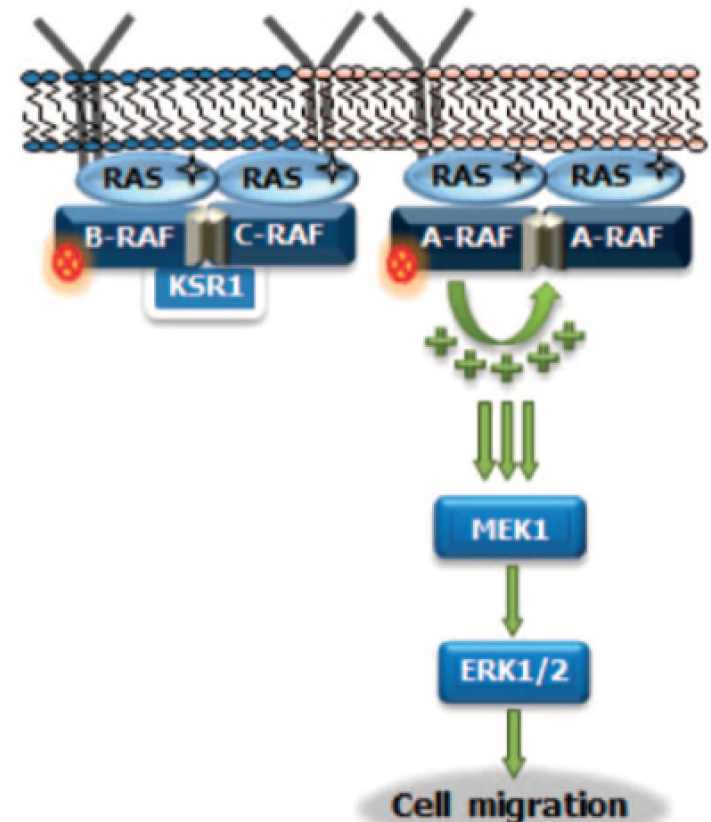
ARAF independent

RAFi-mediated ERK1/2 activation needs CRAF in RAS mutated cells



ARAF dependent

RAFi-mediated ERK1/2 activation needs ARAF in a cell type-dependent manner



OUTLINE

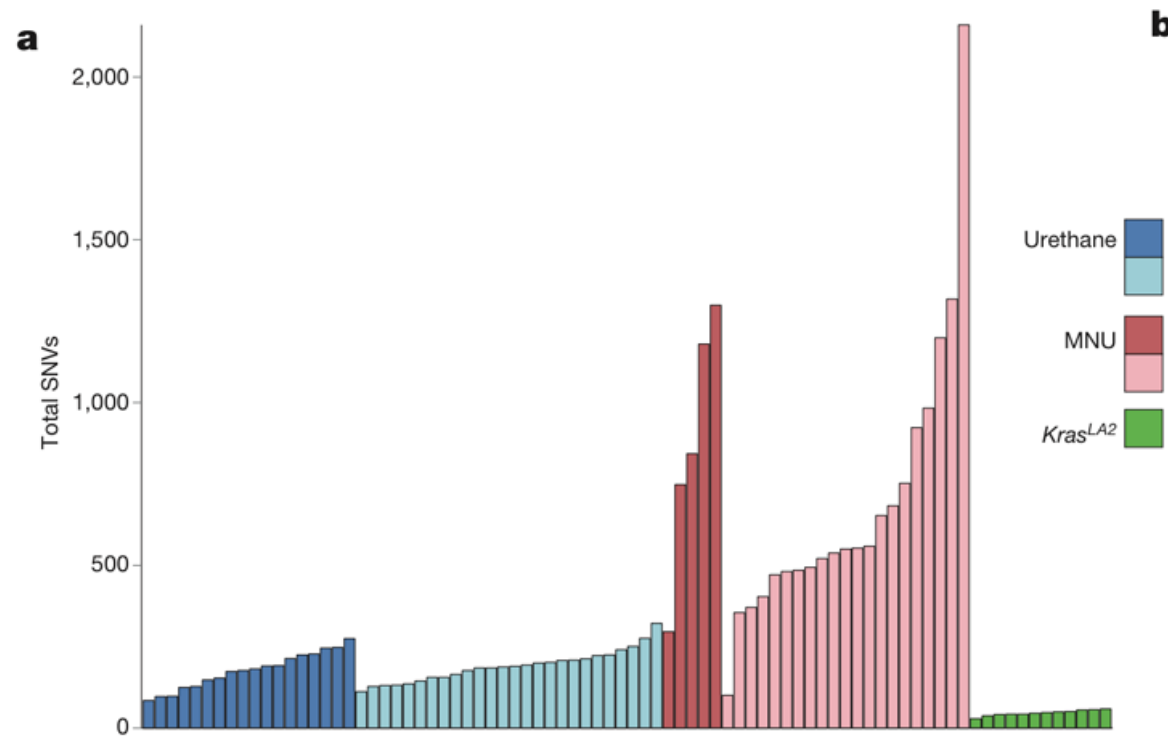
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Not a “one man band”



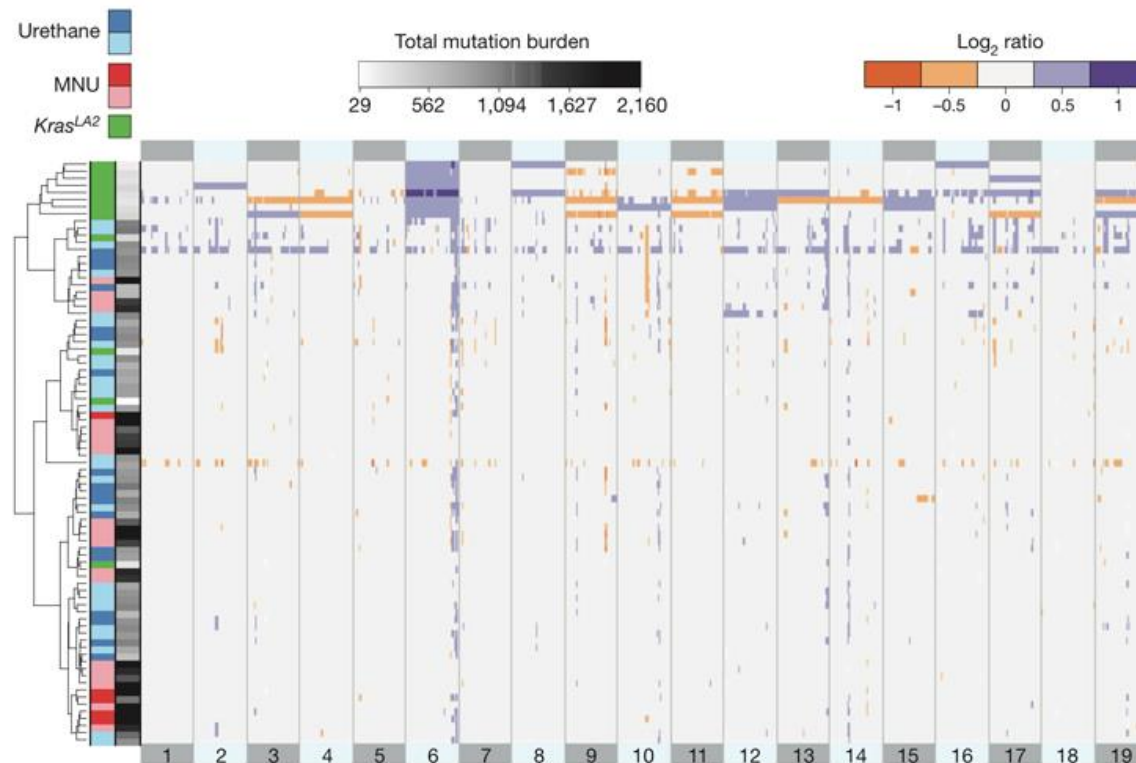
The mutational landscapes of genetic and chemical models of *Kras*-driven lung cancer

Peter M. K. Westcott^{1,2}, Kyle D. Halliwill^{1,2}, Minh D. To¹, Mamunur Rashid³, Alistair G. Rust³, Thomas M. Keane³, Reyno Delrosario¹, Kuang-Yu Jen⁴, Kay E. Gurley⁵, Christopher J. Kemp⁵, Erik Fredlund⁶, David A. Quigley¹, David J. Adams³ & Allan Balmain^{1,7}



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Lung cancer

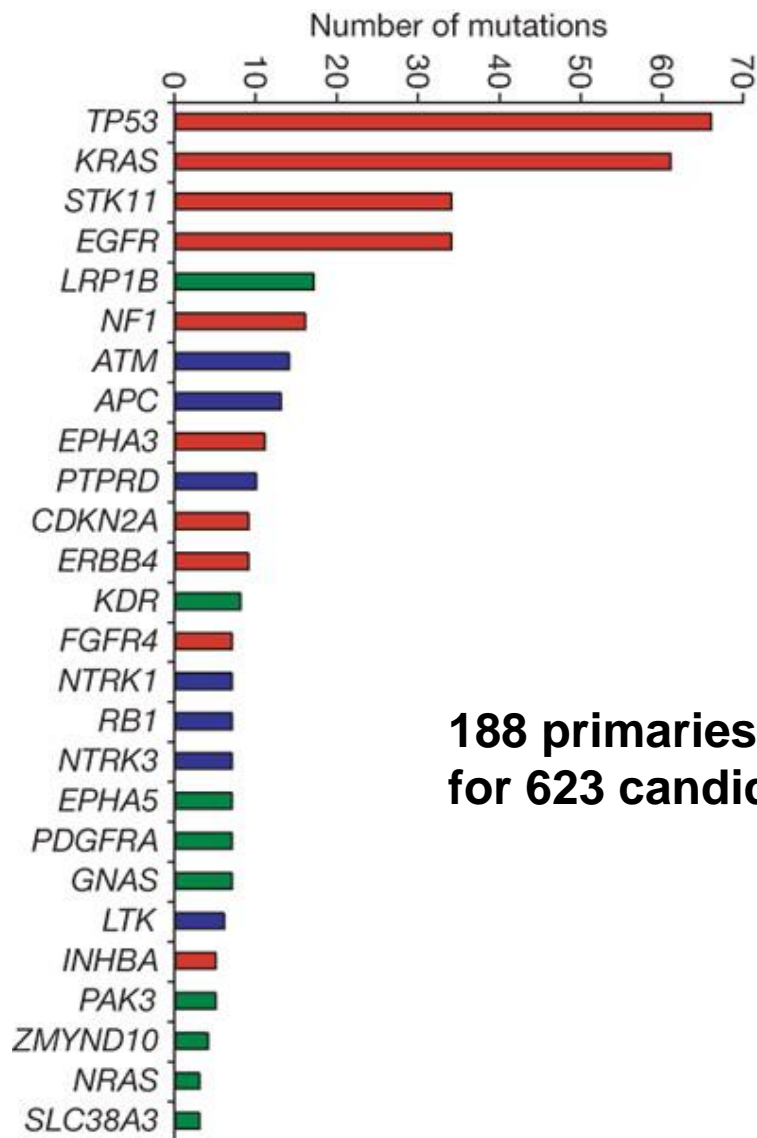
Nature. 2008 October 23; 455(7216): 1069–1075. doi:10.1038/nature07423.

Somatic mutations affect key pathways in lung adenocarcinoma

Li Ding^{1,*}, Gad Getz^{2,*}, David A. Wheeler^{3,*}, Elaine R. Mardis¹, Michael D. McLellan¹, Kristian Cibulskis², Carrie Sougnez², Heidi Greulich^{2,4}, Donna M. Muzny³, Margaret B. Morgan³, Lucinda Fulton¹, Robert S. Fulton¹, Qunyan Zhang⁵, Michael C. Wendl¹, Michael S. Lawrence², David E. Larson¹, Ken Chen¹, David J. Dooling¹, Aniko Sabo³, Alicia C. Hawes³, Hua Shen³, Shalini N. Jhangiani³, Lora R. Lewis³, Otis Hall³, Yiming Zhu³, Tittu Mathew³, Yanru Ren³, Jiqiang Yao³, Steven E. Scherer³, Kerstin Clerc³, Ginger A. Metcalf³, Brian Ng³, Aleksandar Milosavljevic³, Manuel L. Gonzalez-Garay³, John R. Osborne¹, Rick Meyer¹, Xiaoqi Shi¹, Yuzhu Tang¹, Daniel C. Koboldt¹, Ling Lin¹, Rachel Abbott¹, Tracie L. Miner¹, Craig Pohl¹, Ginger Fewell¹, Carrie Haipek¹, Heather Schmidt¹, Brian H. Dunford-Shore¹, Aldi Kraja⁵, Seth D. Crosby¹, Christopher S. Sawyer¹, Tammi Vickery¹, Sacha Sander¹, Jody Robinson¹, Wendy Winckler^{2,4}, Jennifer Baldwin², Lucian R. Chirieac^{6,7}, Amit Dutt^{2,4}, Tim Fennell², Megan Hanna^{2,4}, Bruce E. Johnson⁴, Robert C. Onofrio², Roman K. Thomas^{8,9}, Giovanni Tonon⁴, Barbara A. Weir^{2,4}, Xiaojun Zhao^{2,4}, Liuda Ziaugra², Michael C. Zody², Thomas Giordano¹⁰, Mark B. Orringer¹¹, Jack A. Roth¹², Margaret R. Spitz¹³, Ignacio I. Wistuba^{12,14}, Bradley Ozenberger¹⁵, Peter J. Good¹⁵, Andrew C. Chang¹¹, David G. Beer¹¹, Mark A. Watson¹⁶, Marc Ladanyi^{17,18}, Stephen Broderick¹⁷, Akihiko Yoshizawa¹⁷, William D. Travis¹⁷, William Pao^{17,18}, Michael A. Province⁵, George M. Weinstock¹, Harold E. Varmus¹⁹, Stacey B. Gabriel², Eric S. Lander², Richard A. Gibbs³, Matthew Meyerson^{2,4}, and Richard K. Wilson¹

Lung cancer

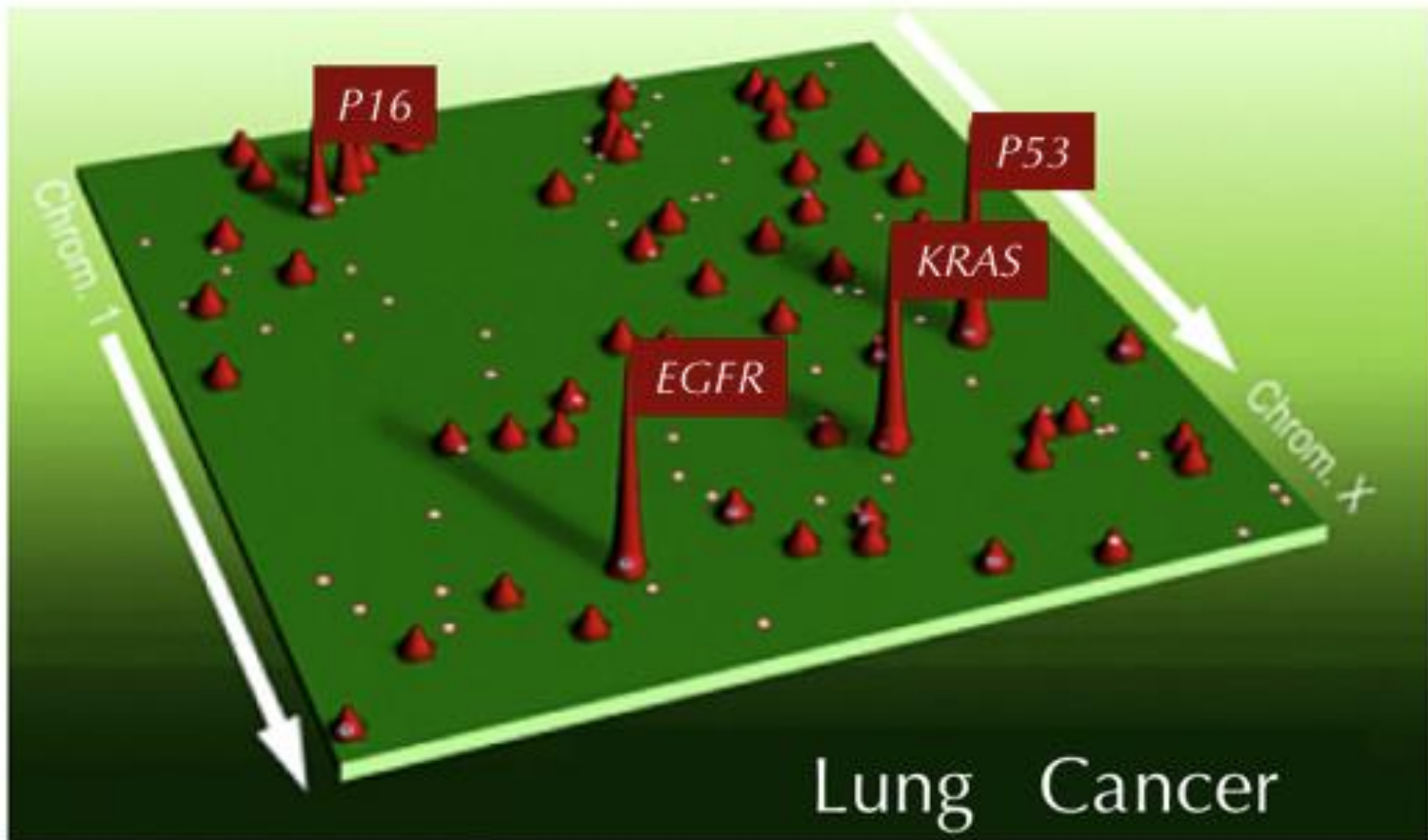
**26 significantly mutated genes
in lung adenocarcinomas**



**188 primaries screened
for 623 candidate genes**

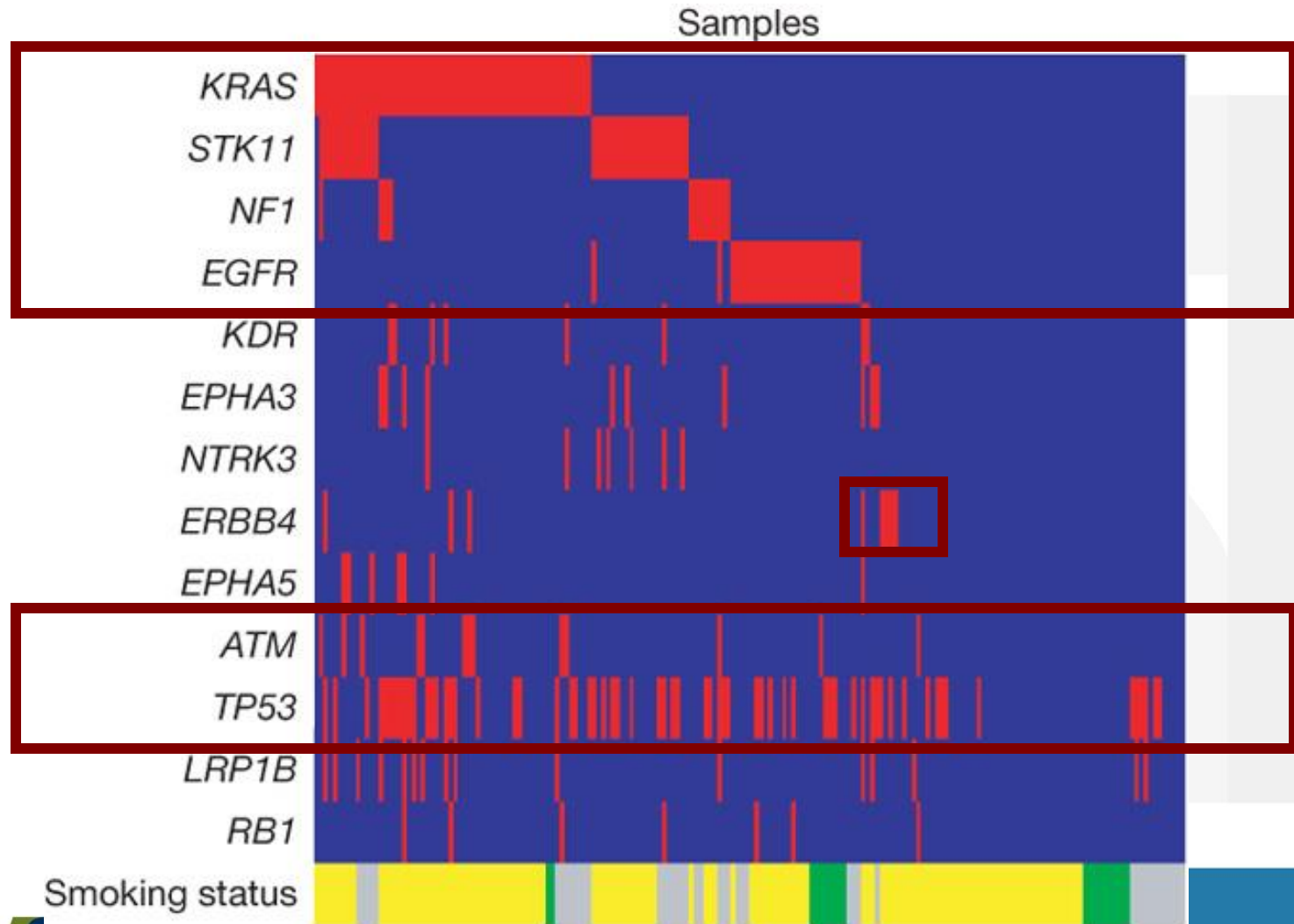
Lung cancer

Each cancer holds from 4 to 29 mutated genes



Lung cancer

Concurrent and mutual exclusion of mutations

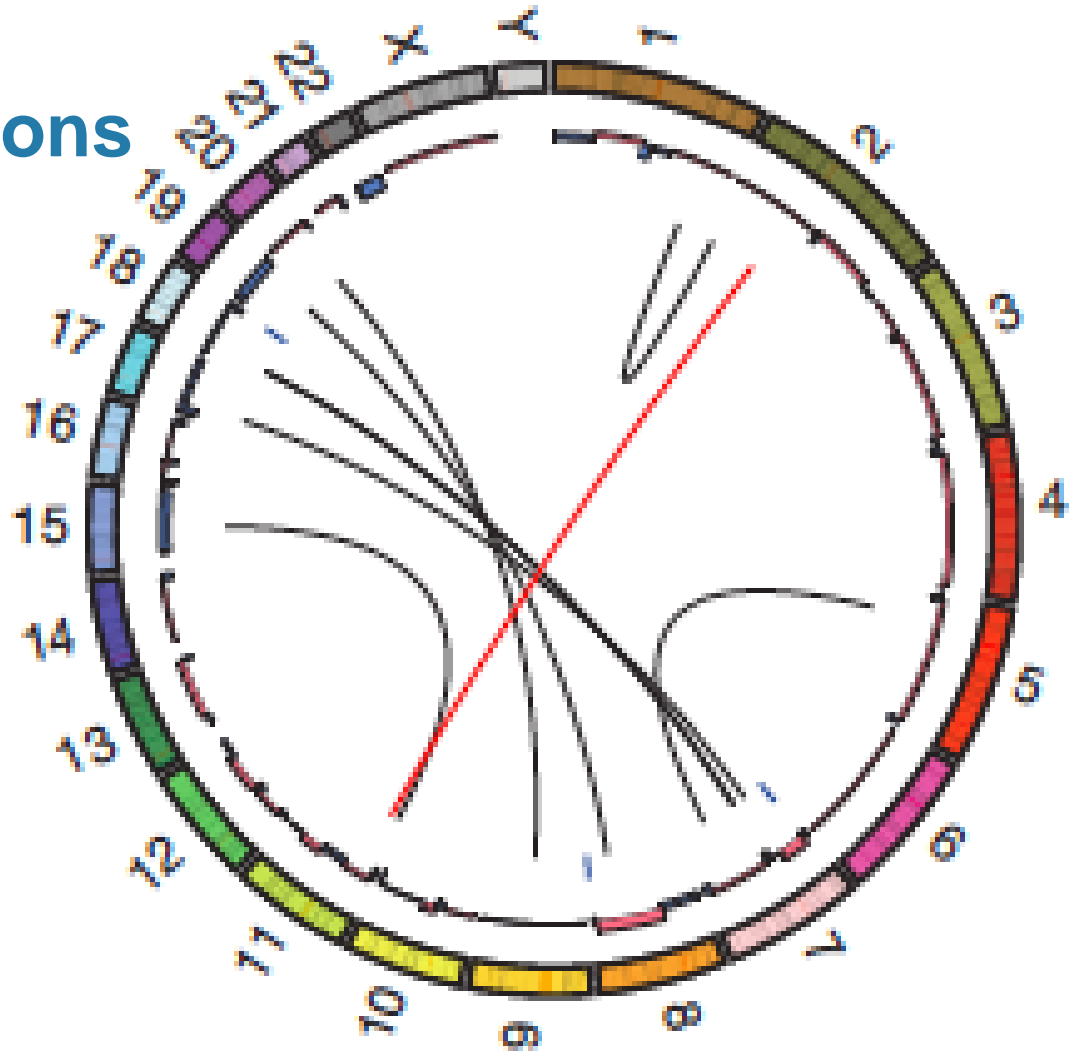


Mutations

Copy number alterations

Focal amplifications

Translocations

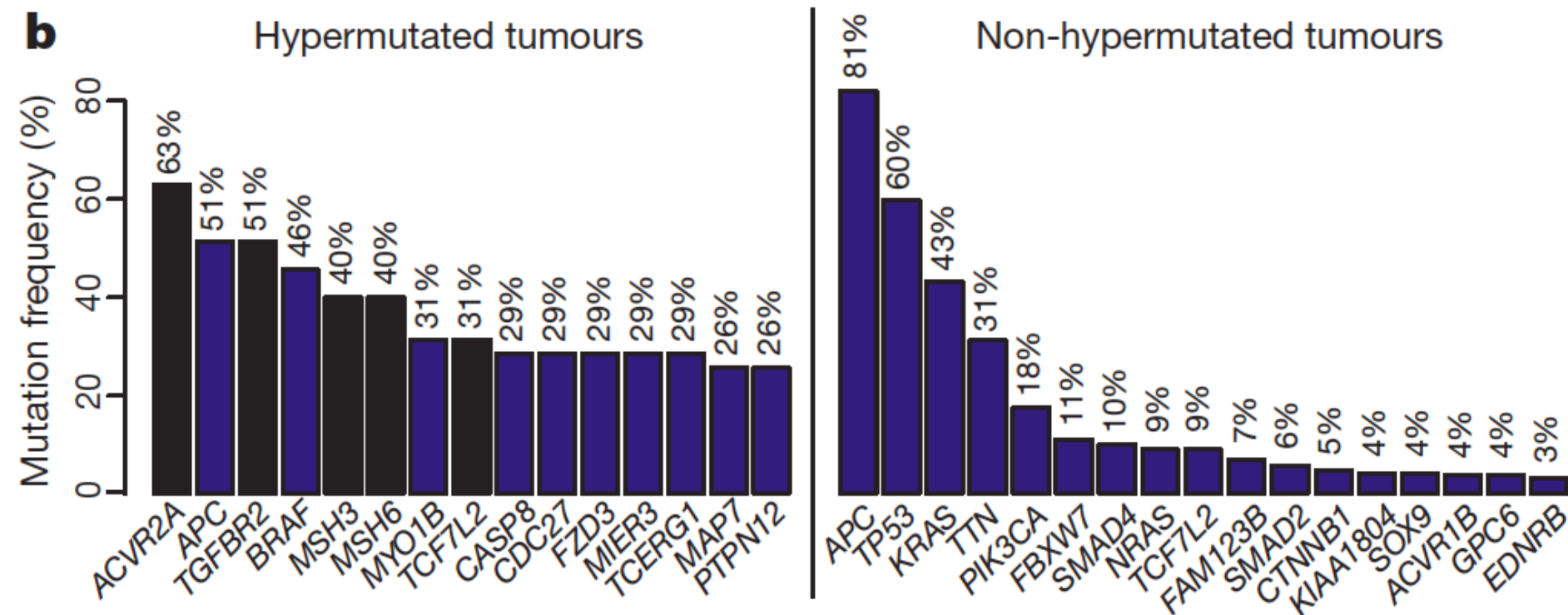


Colorectal cancer

32 somatic recurrently mutated genes

15

17



Lung cancer

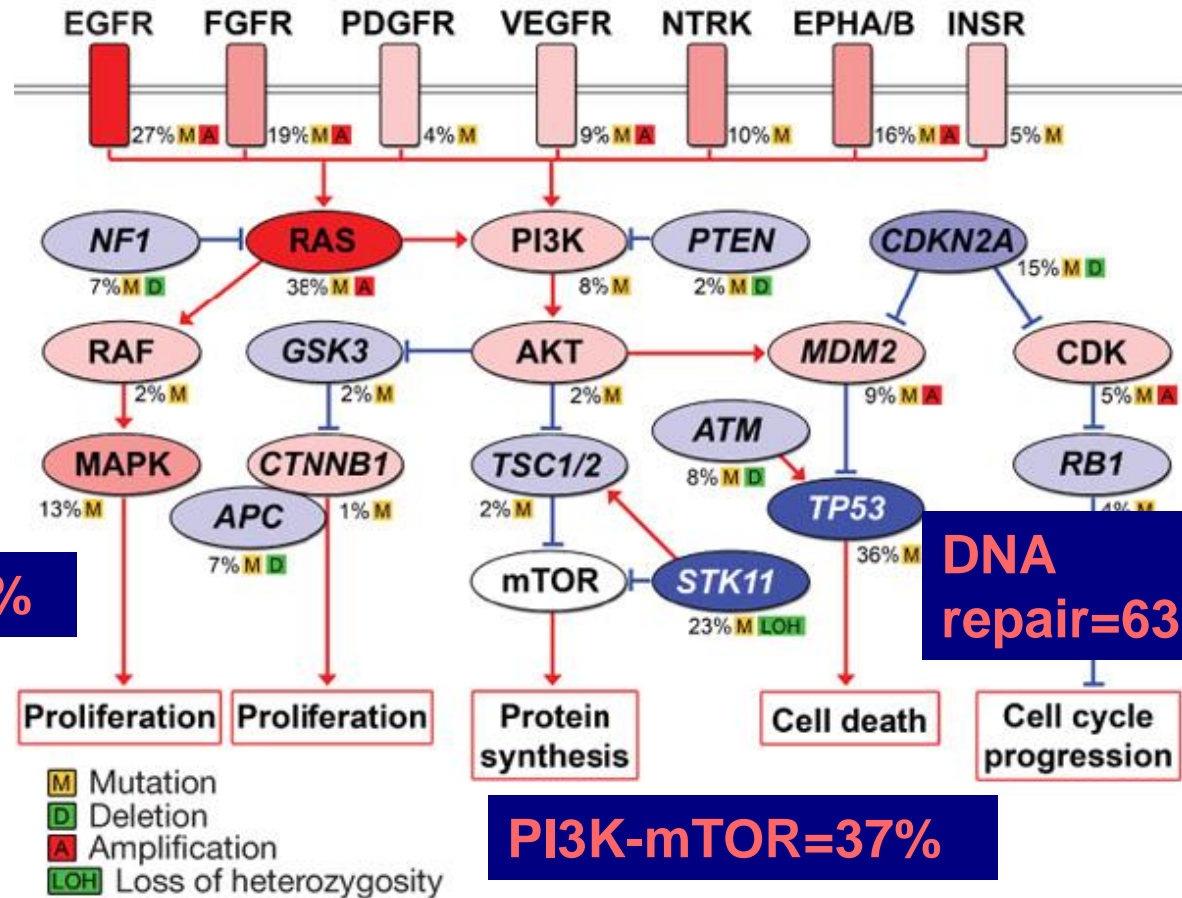
Mutated pathways in lung adenocarcinomas

RTK=90%

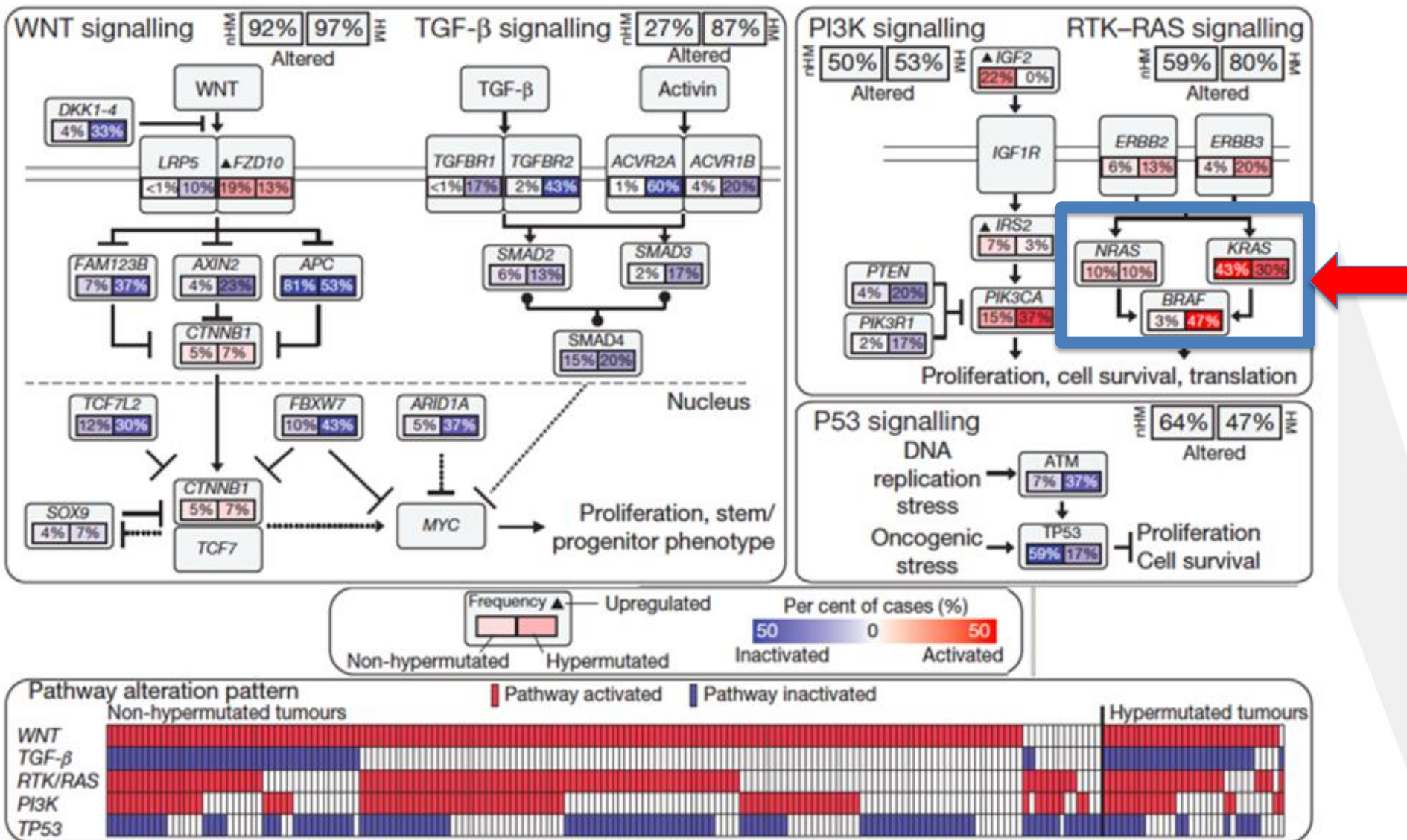
MAPK=60%

**DNA
repair=63%**

PI3K-mTOR=37%



Colorectal cancer

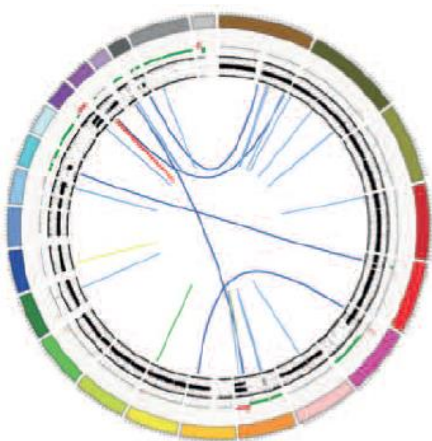


Pancreas cancer



Pancreas cancer

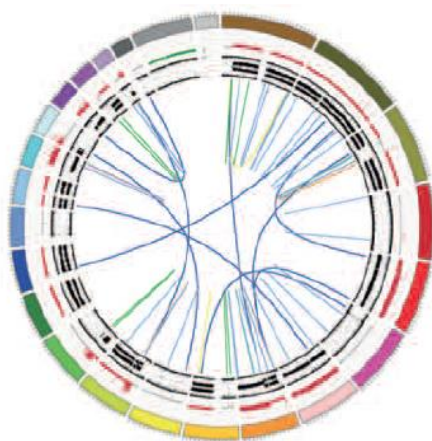
Stable



<50 events

18%

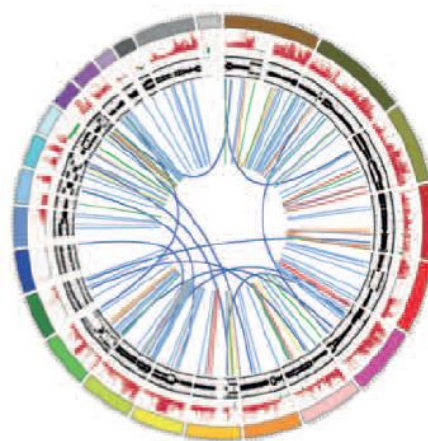
Scattered



50 – 200 events
widespread

39%

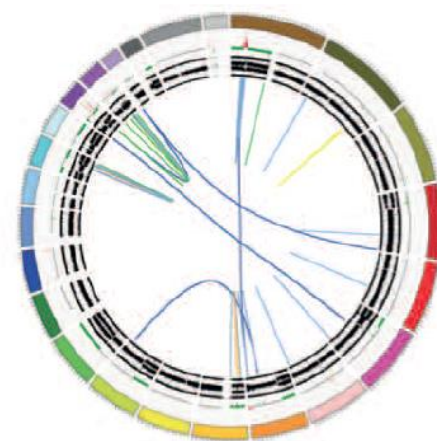
Unstable



>200 events
widespread

18%

Locally rearranged



50-200 events
50% on 1 Chr

25%

■ Intra-chromosomal
rearrangement

■ Inter-chromosomal
translocation

■ Duplication

■ Tandem duplication

■ Inversion

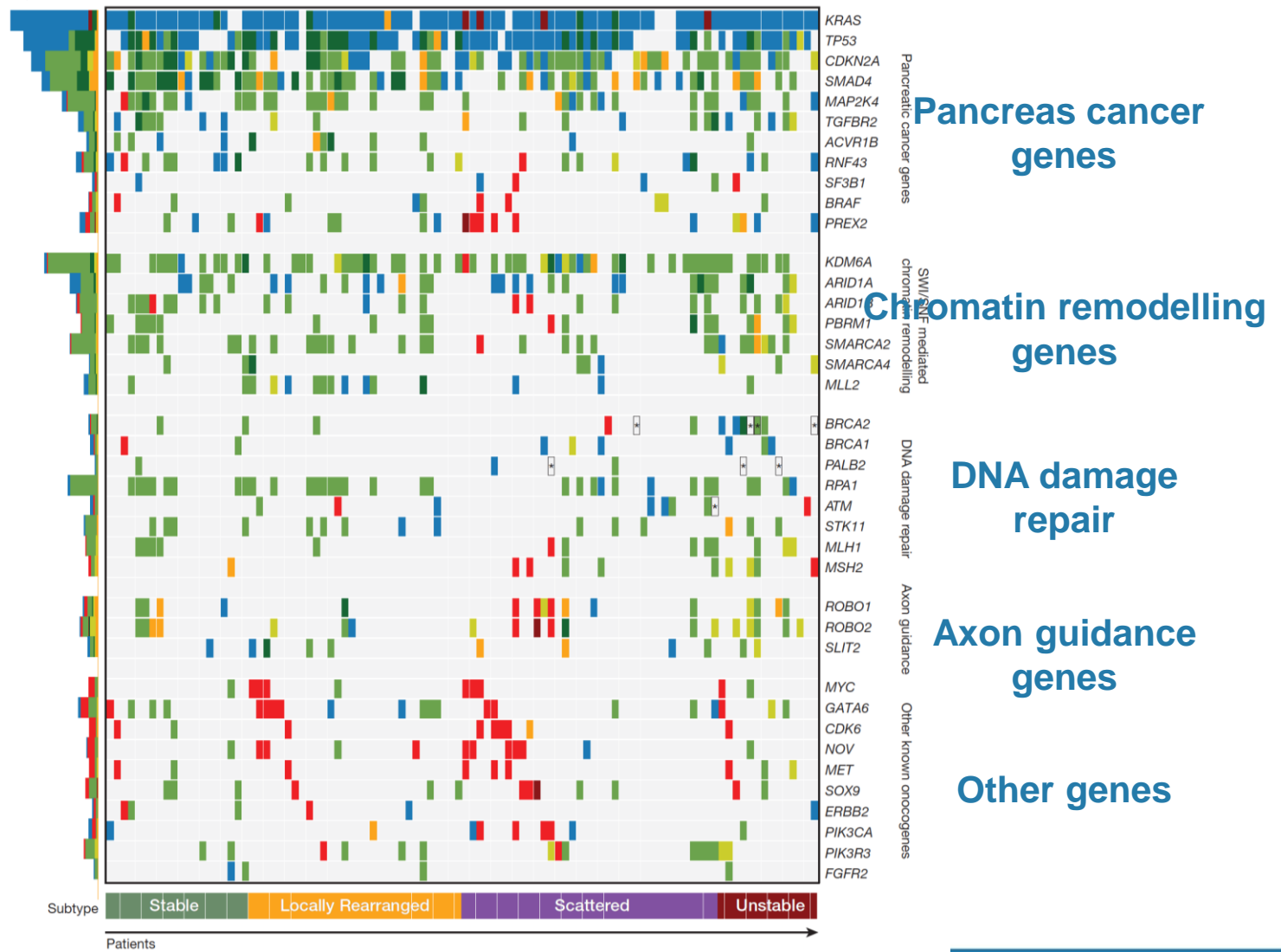
■ Foldback
inversion

■ Deletion

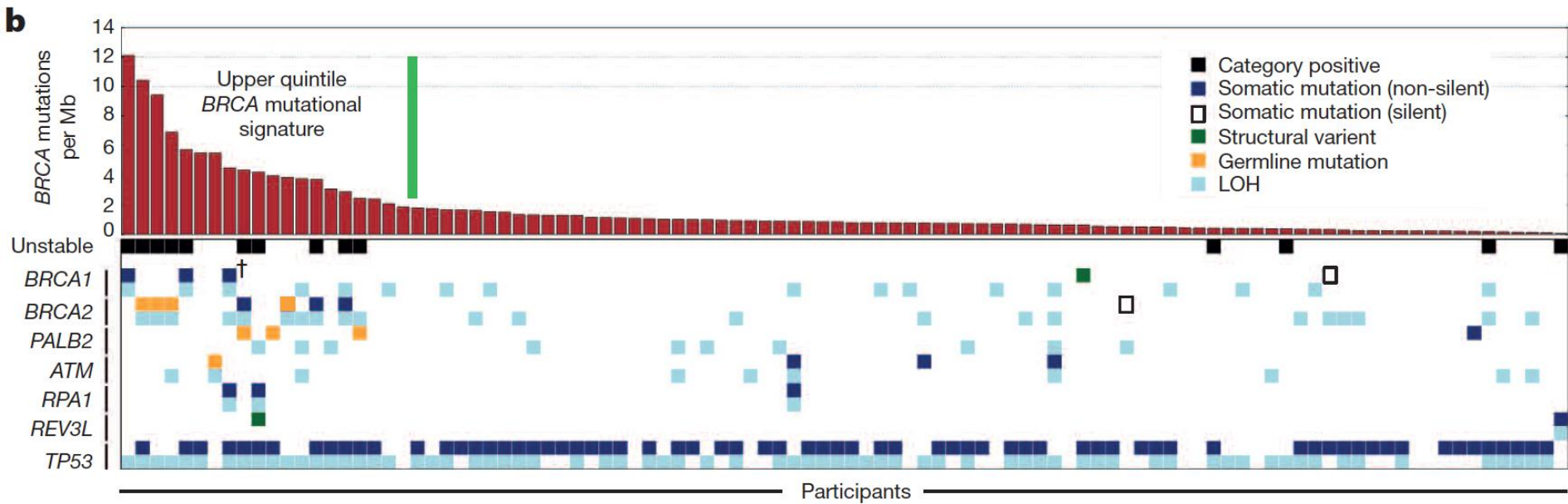
■ Amplified inversion

Pancreas

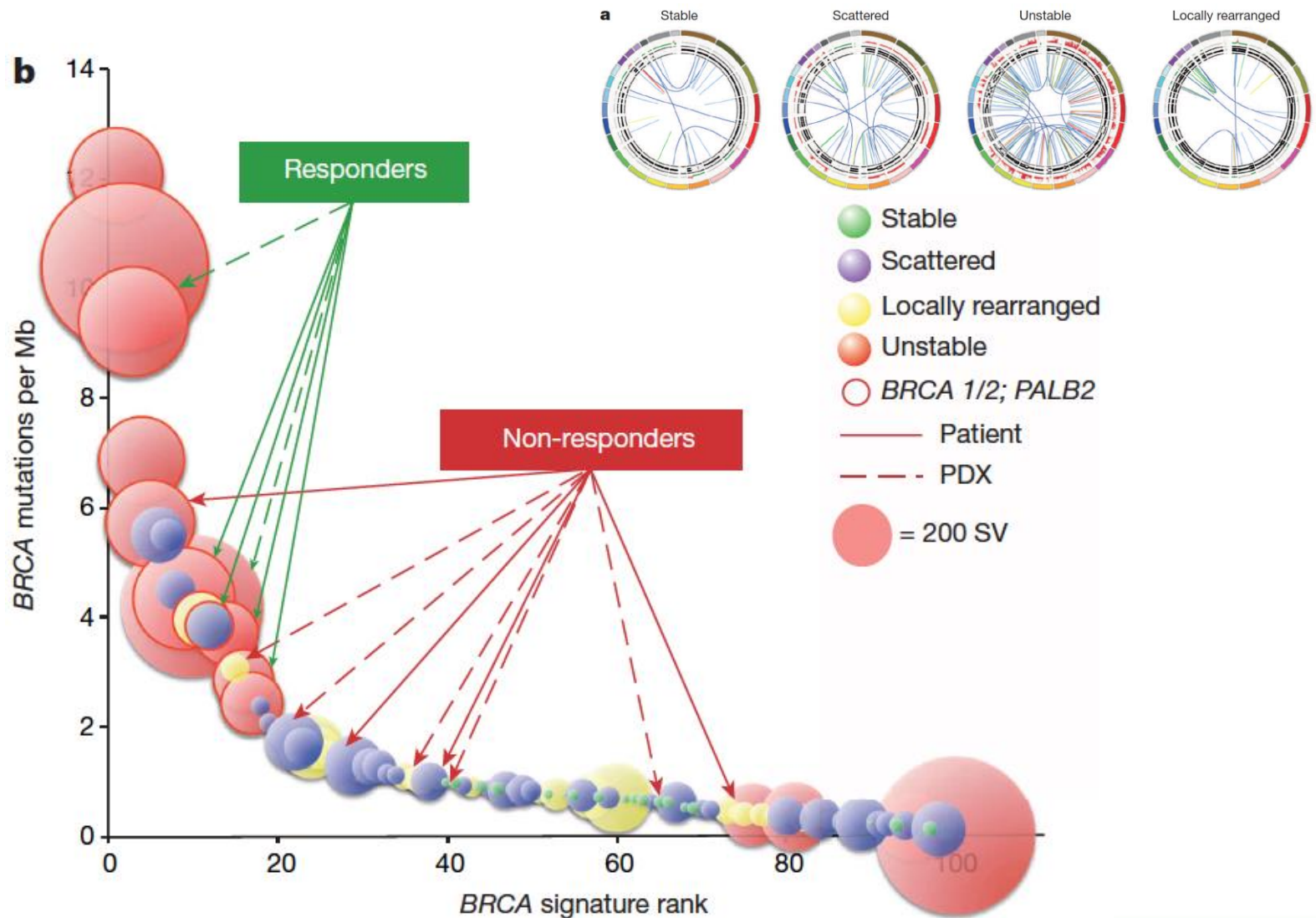
Stable Locally rearranged Scattered Unstable



Pancreas cancer



Pancreas cancer



Targetting-Ras...dream or reality?

