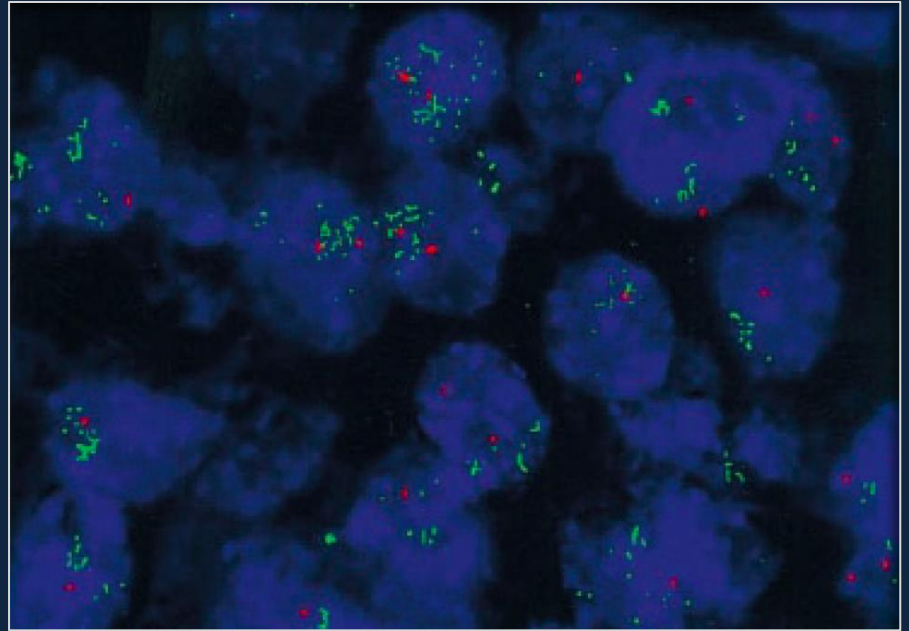


Solange Peters, MD-PhD
Cancer Center, Lausanne
Switzerland

HER2

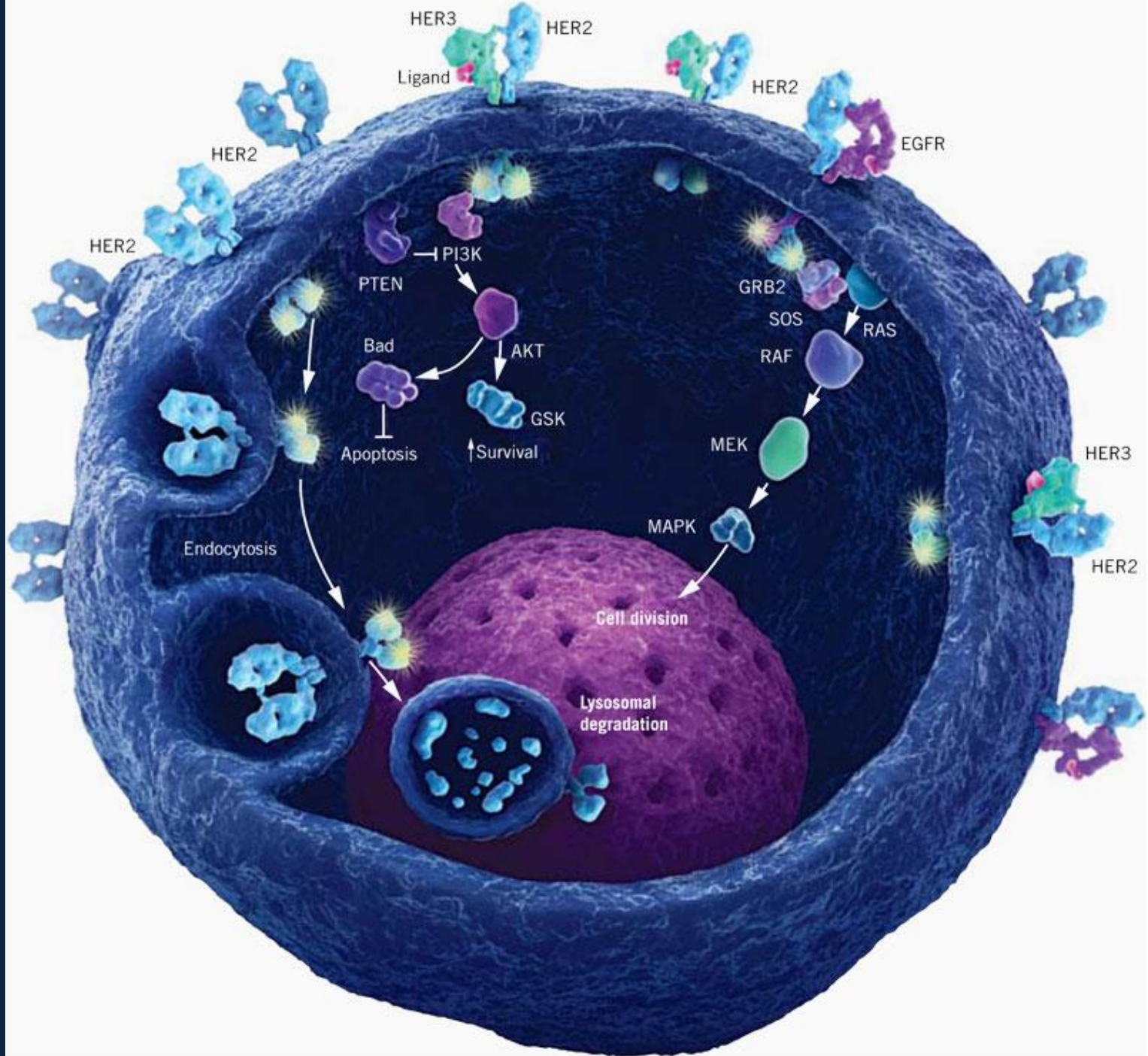


Disclosures

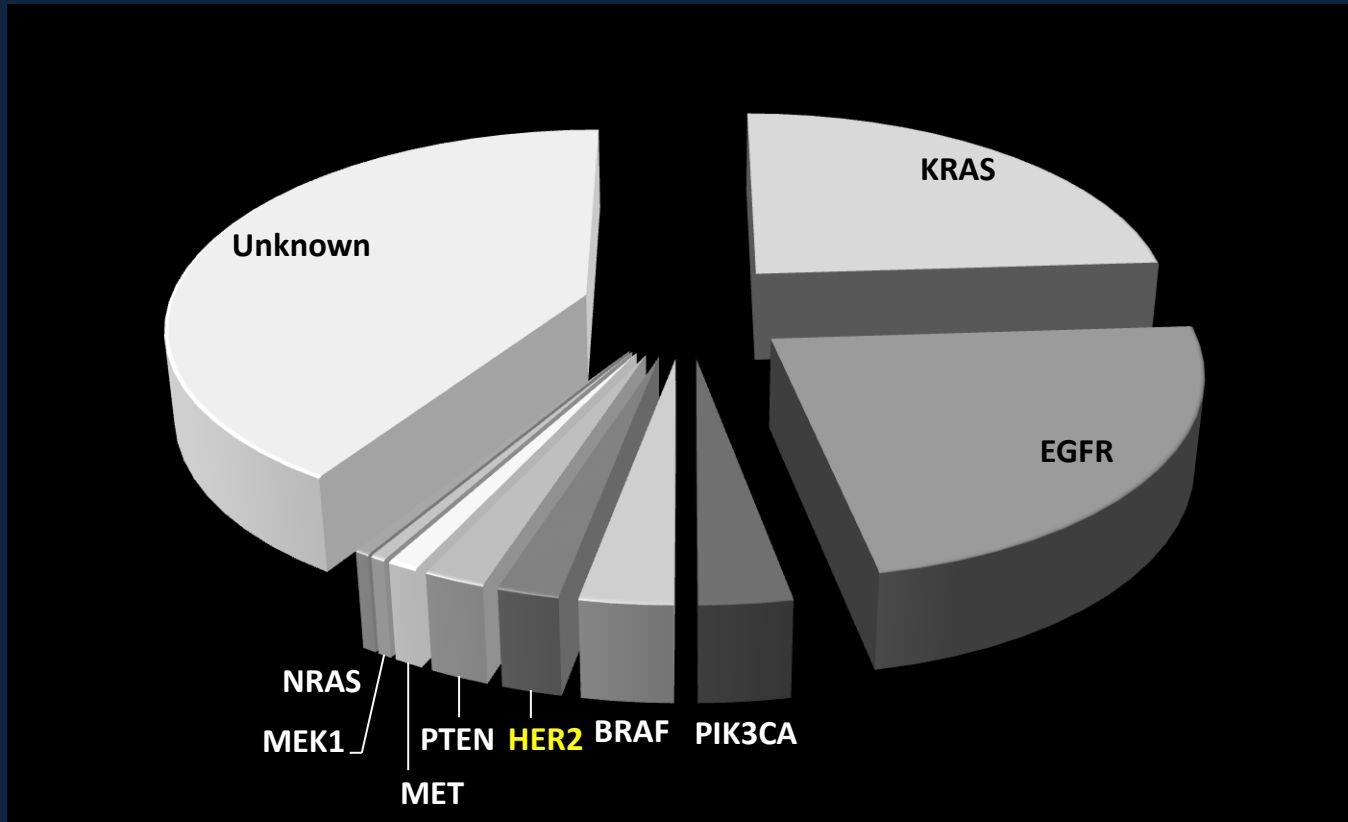
I have provided consultation, attended advisory boards and/or provided lectures for:

F. Hoffmann–La Roche, Ltd; Eli Lilly and Company Oncology, AstraZeneca, Pfizer, Boehringer-Ingelheim, BMS, Daiichi-Sankyo, Morphotek, Merrimack , Merck Serono and Tesaro, for which I received honoraria.

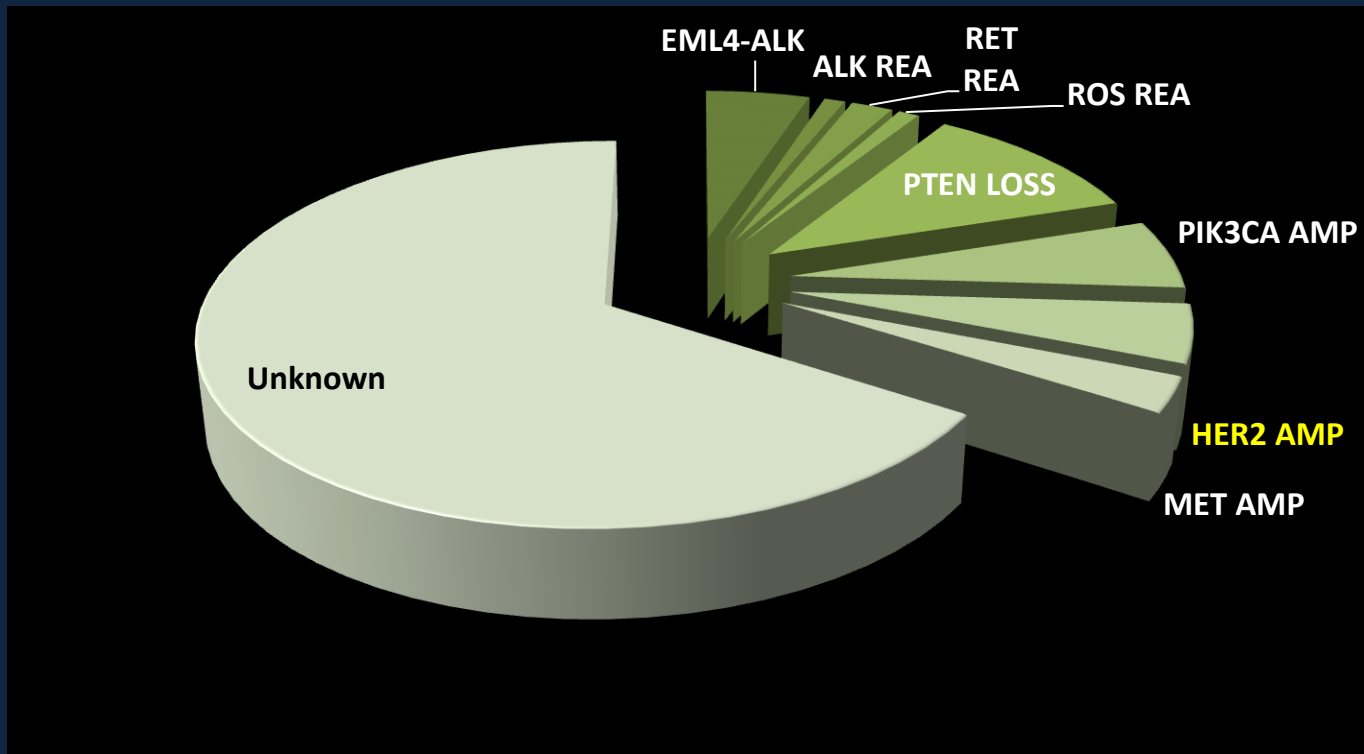
I declare no conflict of interest.



2012 update on adenocarcinoma driver mutations



2012 update on adenocarcinoma driver gene alterations



Definition of drivers?

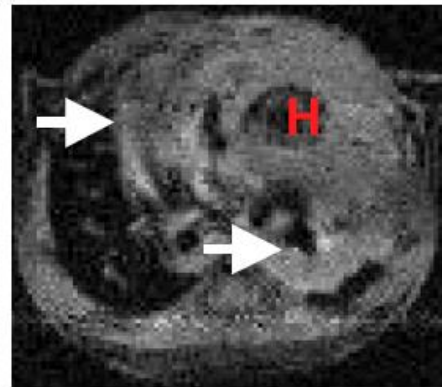
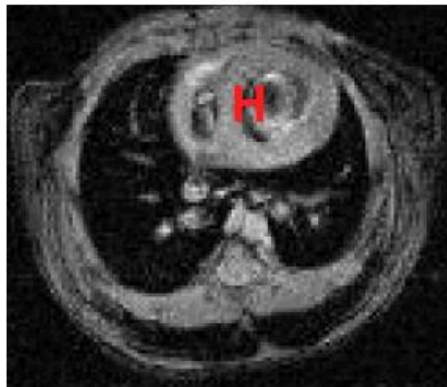
Inducible expression of mutated HER2 (HER2YVMA):
Rapid development/maintenance of adenosquamous lung tumors
in mice

MRI

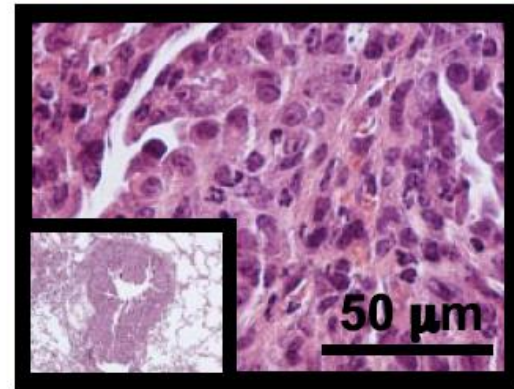
No Doxy

1 week

2 weeks



Histology

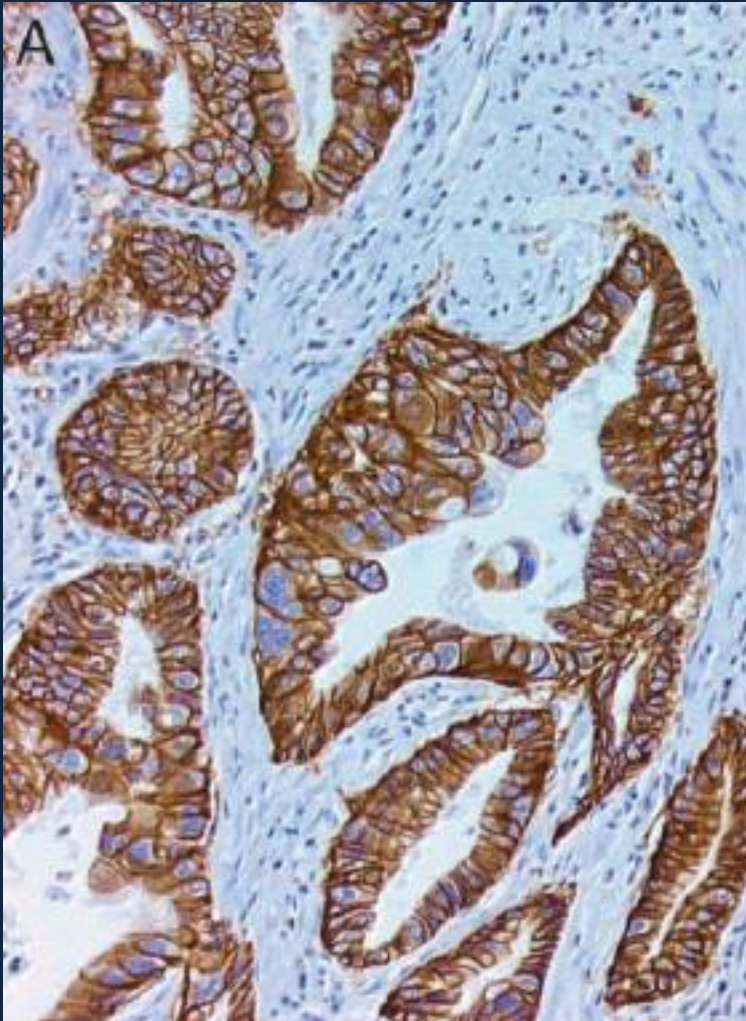


Epidemiology IHC/FISH (1)

- HER2 overexpression by IHC in 20% (83 of 410) of stage IIIB-IV NSCLC, whereas 2% (7 of 378) positive by FISH
- Concordance between FISH and IHC 3+

Carcinoma type	Total	Positive	IHC 2+	IHC 3+	FISH
Adenocarcinoma	143	42 (29%)	33 (23%)	4 (3%)	5 (4%)
Squamous cell carcinoma	80	14 (18%)	11 (14%)	2 (3%)	1 (1%)

Epidemiology IHC/FISH/RT-PCR (2)



115 stage I-III NSCLC.

- IHC positive in 23%, with 5 NSCLC (4%) showing intense staining
- RT-PCR with HER2 mRNA levels above normal in 54 of 115 of carcinomas (47%)
- FISH positive in 9 of 41 NSCLC (22%)

Lung cancer

Intragenic ERBB2 kinase mutations in tumours

Table 1 ERBB2 mutations in primary tumours

Sample	Tumour/histology	Nucleotide*	Amino acid*
PD1353a	NSCLC adenocarcinoma	2322 ins/dup(GCATACGTGATG)	ins774(AYVM)
PD0258a	NSCLC adenocarcinoma	2322 ins/dup(GCATACGTGATG)	ins774(AYVM)
PD0317a	NSCLC adenocarcinoma	2322 ins/dup(GCATACGTGATG)	ins774(AYVM)
PD0319a	NSCLC adenocarcinoma	2335 ins(CTGTGGGCT)	ins779(VGS)
PD0270a	NSCLC adenocarcinoma	TT2263-4CC	L755P

- 120 primary NSCLC, 4.2% with mutations in HER2 kinase domain, 9.8% (5/51) in adenocarcinomas
- Overexpression probably does not accompany the mutation

Epidemiology HER2 mutation (2)

- 403 stage I-III adenocarcinomas in caucasian patients: mutation in 9 (2.2%).
- Seven (78%) of the mutations were in frame duplications/ insertions at codons 776–779 (YVMA)
- Frequency higher in females (4.1% vs 1.8%) and in never smokers (3.1% vs 1.9%)

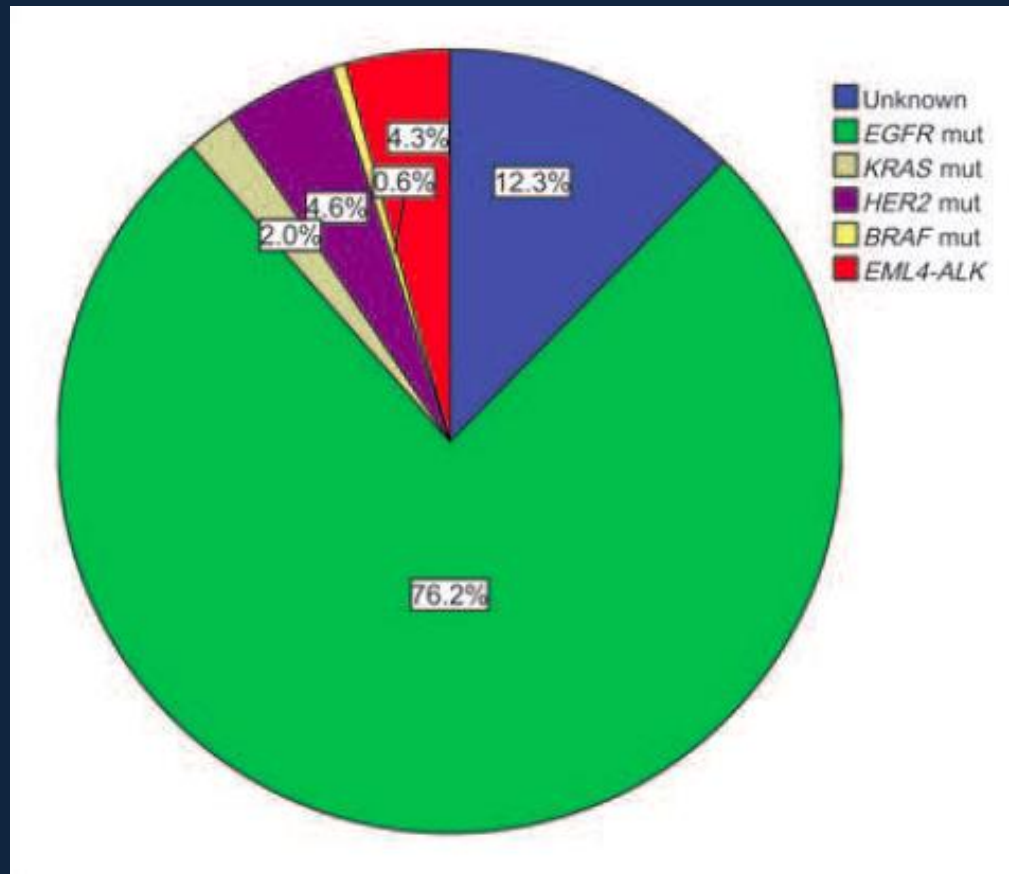
Buttitta, Int J Cancer 2006

- 394 adenocarcinoma, HER2 mutations preferentially in oriental ethnicity (3.9% vs 0.7%)
- All HER2 mutations were in-frame insertions in exon 20
- HER2 mutations significantly more frequent in never smokers (3.2%; $P = 0.02$) and adenocarcinoma histology (2.8%, $P = 0.003$)

Shigematsu, CCR 2005

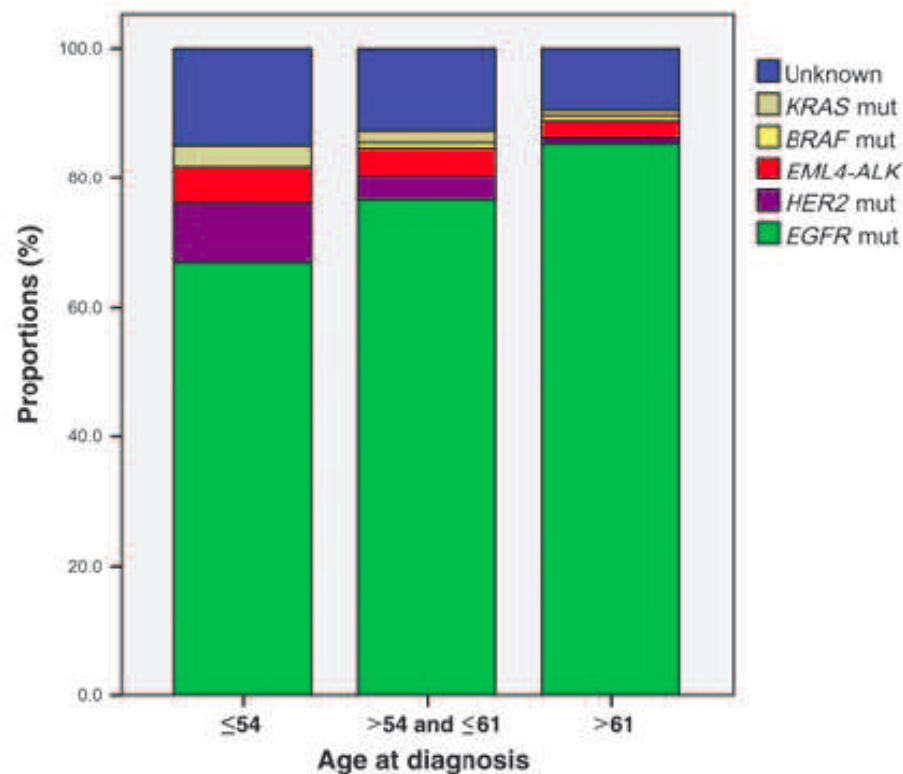
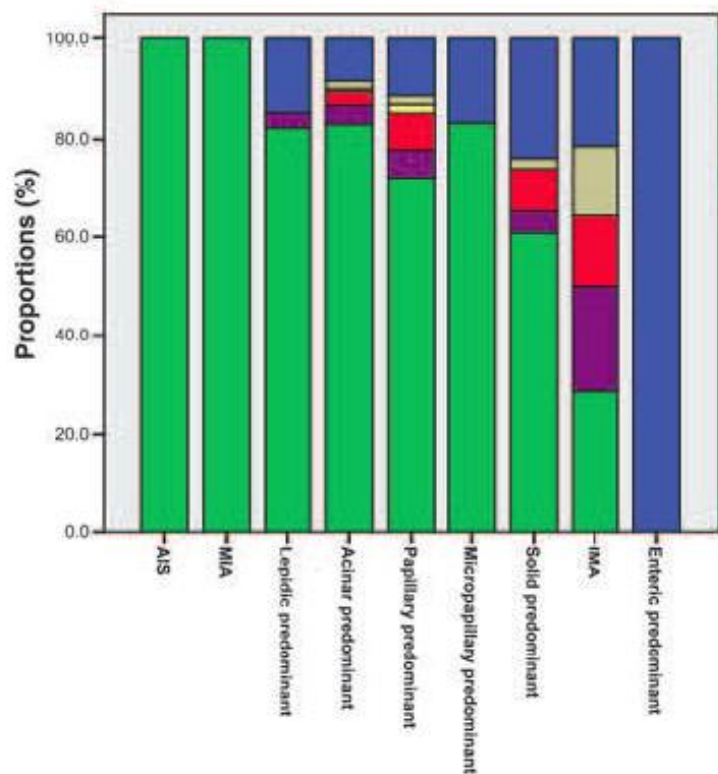
HER-2 mutation prevalence variability?

Frequency of Mutations in Lung Adenocarcinoma from Female Never-Smokers ...



HER-2 prevalence variability (2)?

Frequency of Mutations in Lung Adenocarcinoma from Female Never-Smokers ... varies with age, and histologic subtype



Similarity with EGFR insertions

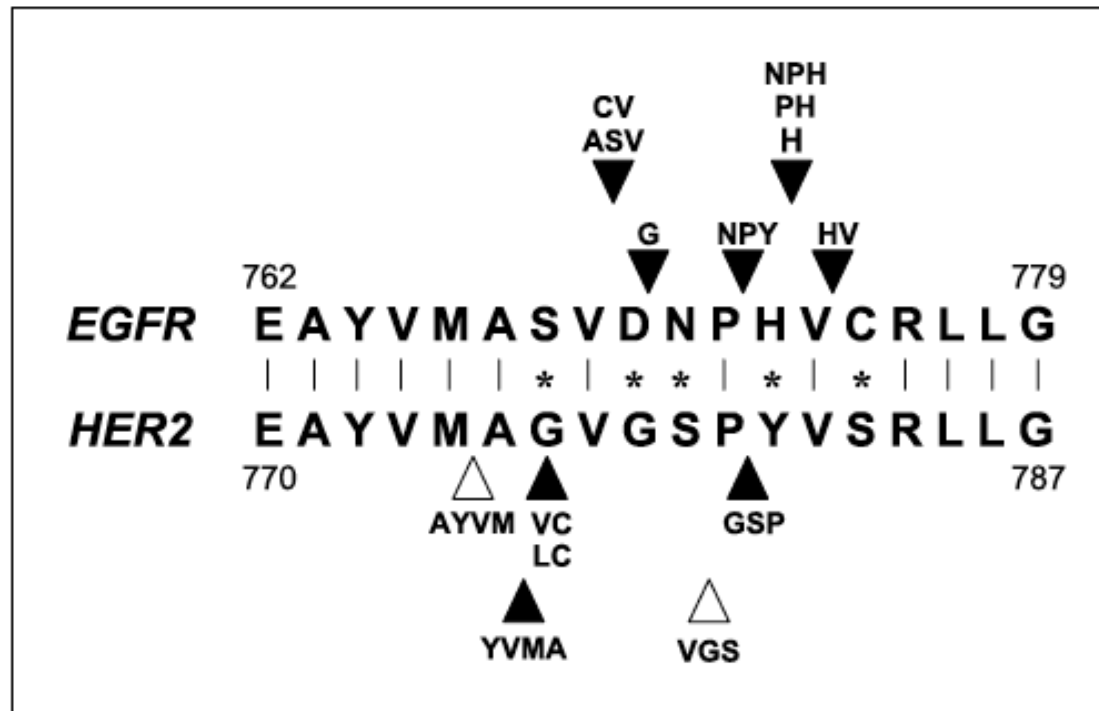
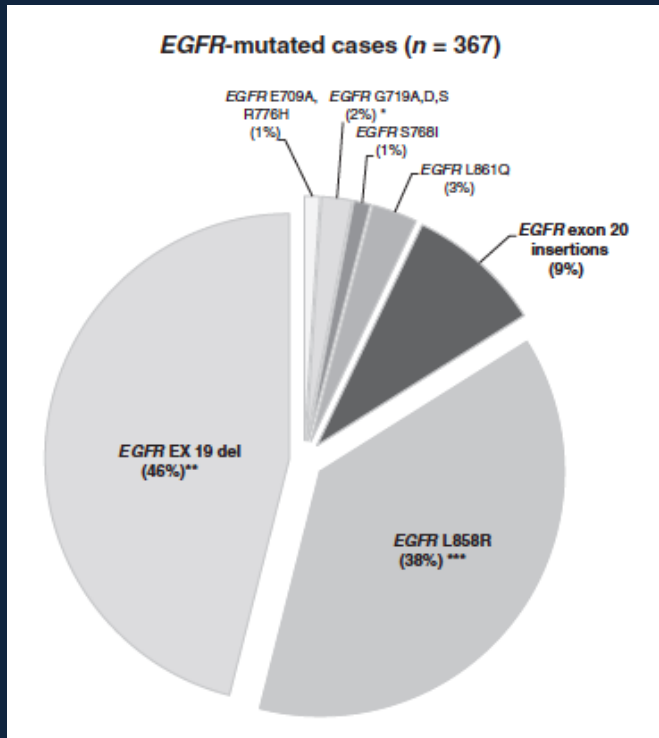
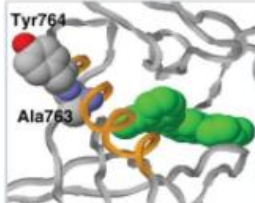
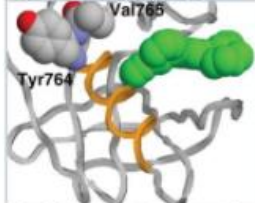
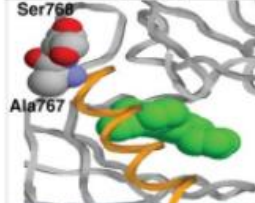
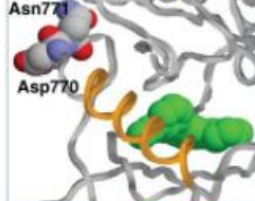
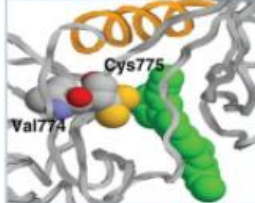


Figure 2. Amino acid alignments of the tyrosine kinase domain in EGFR and HER2. ▲ and ▼, duplications/insertions in this study (for HER2) or previously reported by us for EGFR (23). △, HER2 duplications/insertions described by Stephens et al. (22). *, nonconserved amino acid.

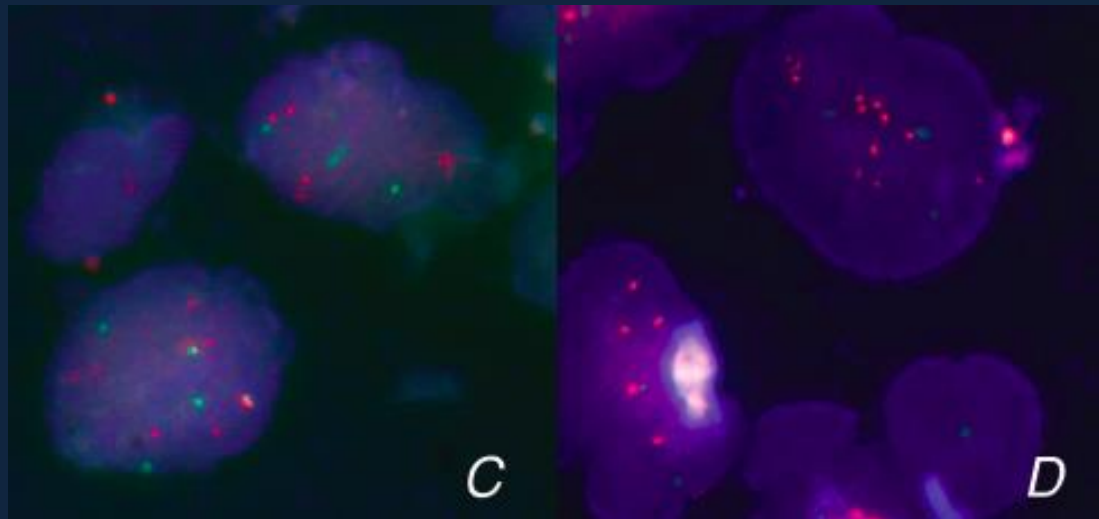
EGFR exon 20 insertions



	Predicted effect of insertion	Response data
 <p>Tyr764 Ala763</p>	A763_Y764insFQEA: likely to cause significant rearrangement of the C helix 753-766 (orange). The insertion does not affect the drug-binding pocket directly but the disturbance of the helix may reduce drug-binding affinity.	None reported.
 <p>Val765 Tyr764</p>	Y764_V765insHH: affects C-terminus of the C helix 753-766 helix (orange). The insertion does not affect the drug-binding pocket directly but the disturbance of the helix may reduce drug-binding affinity.	None reported. One patient reported with prolonged stable disease for 10 mo on gefitinib (ref. 33).
 <p>Ser768 Ala767</p>	A767_S768insTLA: affects the loop region after the C helix 753-766 (orange) and does not affect the drug-binding pocket directly. Effect on drug binding may be less significant.	None reported.
 <p>Asn771 Asp770</p>	D770ins_N771insSVD: affects a loop region after the C helix 753-766 (orange) and does not affect directly the drug-binding pocket. The effect on drug binding may be less significant.	Resistance reported but some responders. One patient with partial response to gefitinib for 24 mo (ref. 8).
 <p>Cys775 Val774</p>	V774_C775insHV: directly affects a loop region that forms a drug-binding pocket. This is likely to result in a significant reduction of the drug-binding affinity.	None reported. Two patients in our study showed no response (1 treated with single agent erlotinib, 1 patient treated with neratinib).

Correlation between HER2 mutation and amplification (1)

- HER2 mutation in 3.6% (8/224) = 11.1% without EGFR and KRAS mutations
- **Seven of eight HER2-mutated tumors showed HER2 copy number gains (CNGs)**

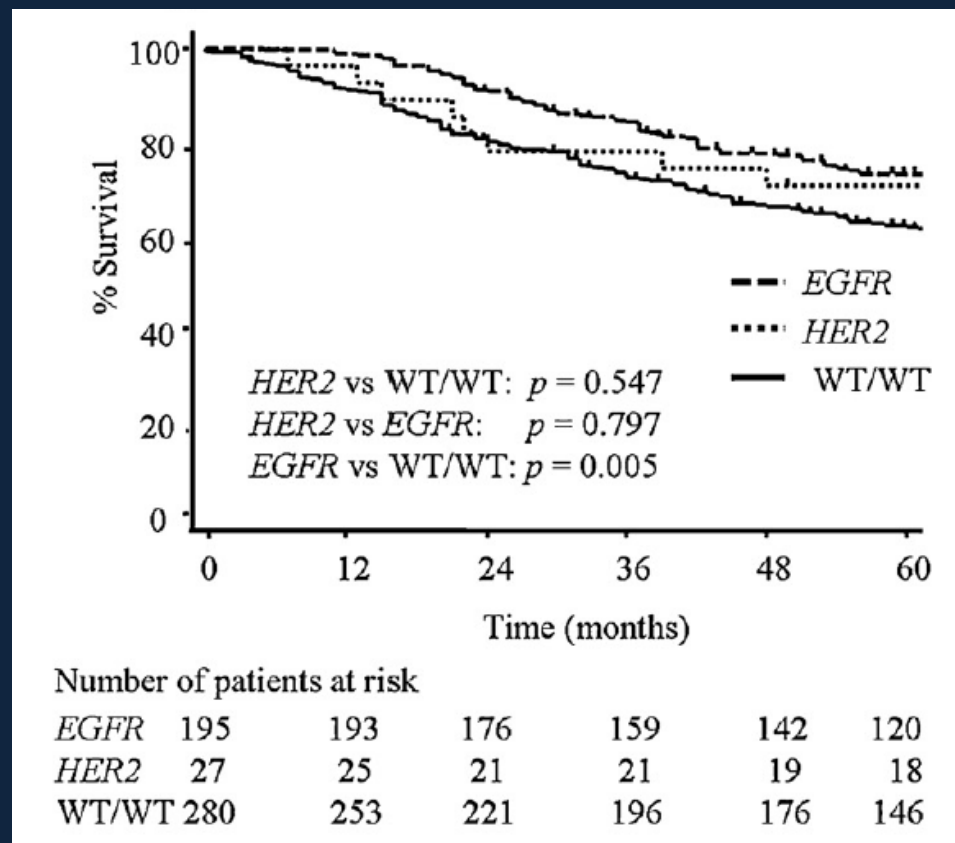


Correlation between HER2 mutation and amplification (2)

- Identification of 25 cases with HER2 mutations, representing 6% of EGFR/KRAS/ALK-negative specimens
- HER2 mutations were more frequent among never-smokers ($P < 0.0001$) but there were no associations with sex, race, or stage
- **HER2 mutation was not associated with concurrent HER2 amplification in 11 cases tested for both**

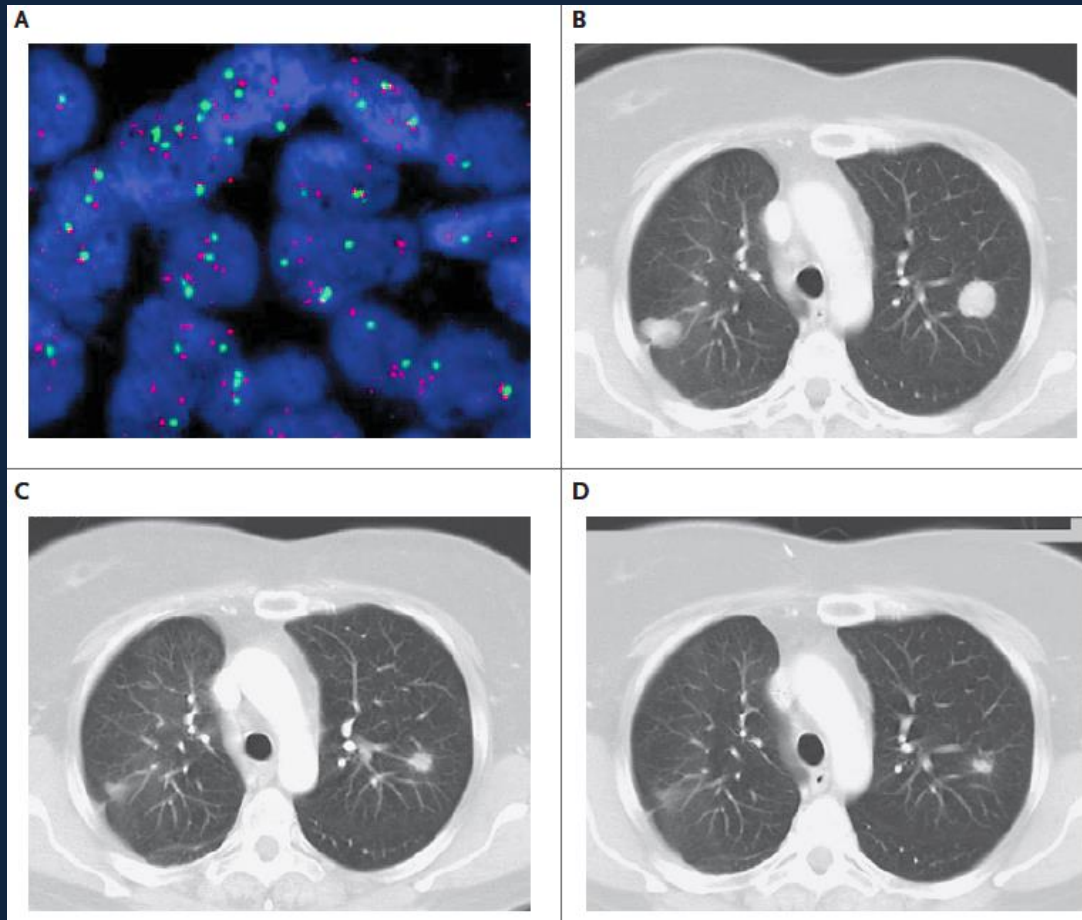
Pronostic impact of HER2 mutations

- HER2 mutations in 13 of 504 japanese patients (2.6%) undergoing surgery for NSCLC
- No difference in the overall survival of patients with HER2 mutations, compared with patients harboring EGFR mutations and patients harboring wild types for both EGFR and HER2



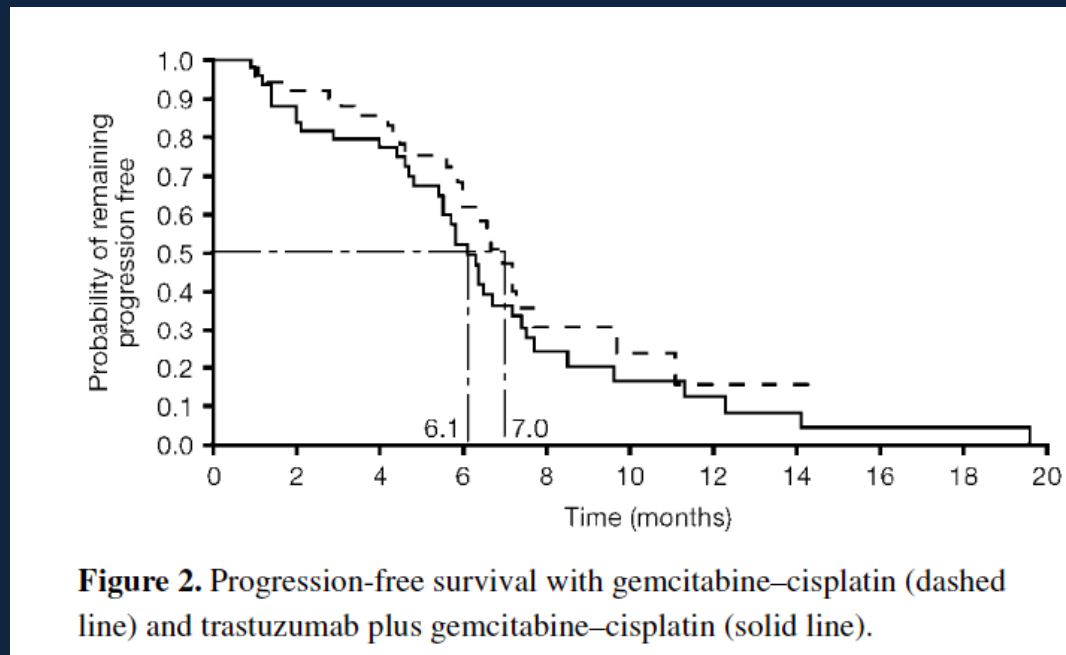
The case report

HER2 mutation and response to trastuzumab (+ paclitaxel) therapy in non-small-cell lung cancer (increased HER2 and EGFR GCN and HER2 exon 20 mut+)



HER2 dedicated clinical trial in NSCLC (1)

Randomized phase II trial of gemcitabine-cisplatin with or without trastuzumab in HER2-positive non-small-cell lung cancer



- Clinical benefit was not observed
- Although HER2 3+/FISH-positive patients may benefit from trastuzumab, the subgroup was too small to provide definitive information

HER2 dedicated clinical trial in NSCLC (2)

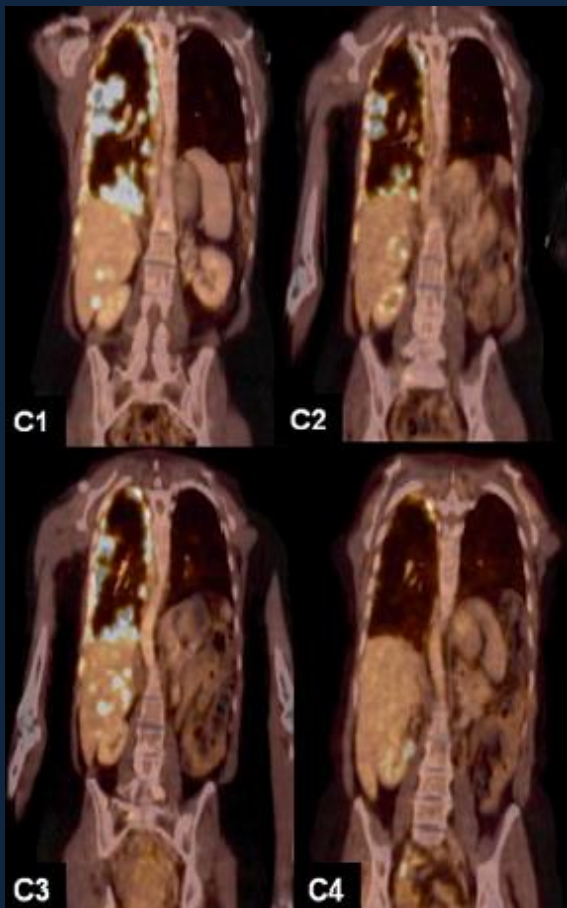
Trastuzumab + docetaxel in HER2 positive non-small-cell lung cancer

- Patients with HER2 2+ or 3+ randomized to either single-agent trastuzumab or docetaxel -> after 2 cycles, all receive the trastuzumab/docetaxel combination
- Only 13 patients (19%) had HER2-positive disease
- None responded to trastuzumab alone

« In view of the limited target population for HER2 inhibition, future efforts and resources should be directed toward molecular targets other than HER2 in NSCLC »

HER2 dedicated clinical trial in NSCLC (3)

Clinical activity of afatinib (BIBW 2992) in patients with lung adenocarcinoma with mutations in the kinase domain of HER2



Five patients with metastatic HER2 mutated adenocarcinomas were identified, three of which were evaluable for response

Objective response was observed in all three patients, even after failure of other EGFR- and/or HER2-targeted treatments

Our French/European experience (1)

- *HER2* mutation was identified in 65 patients out of 3800 patients (1.7%)
- Exclusive driver, except one single case with a concomitant *KRAS* mutation
- Median age of 60 years (31-86), high proportion of women (45 vs. 20 men, 69%), and of never smokers (34, 52.3%)
- All tumors were adenocarcinomas and 50% were stage IV at diagnosis

Our French/European experience (2)

22 anti-HER2 treatments were administered after conventional chemotherapy in 16 patients:

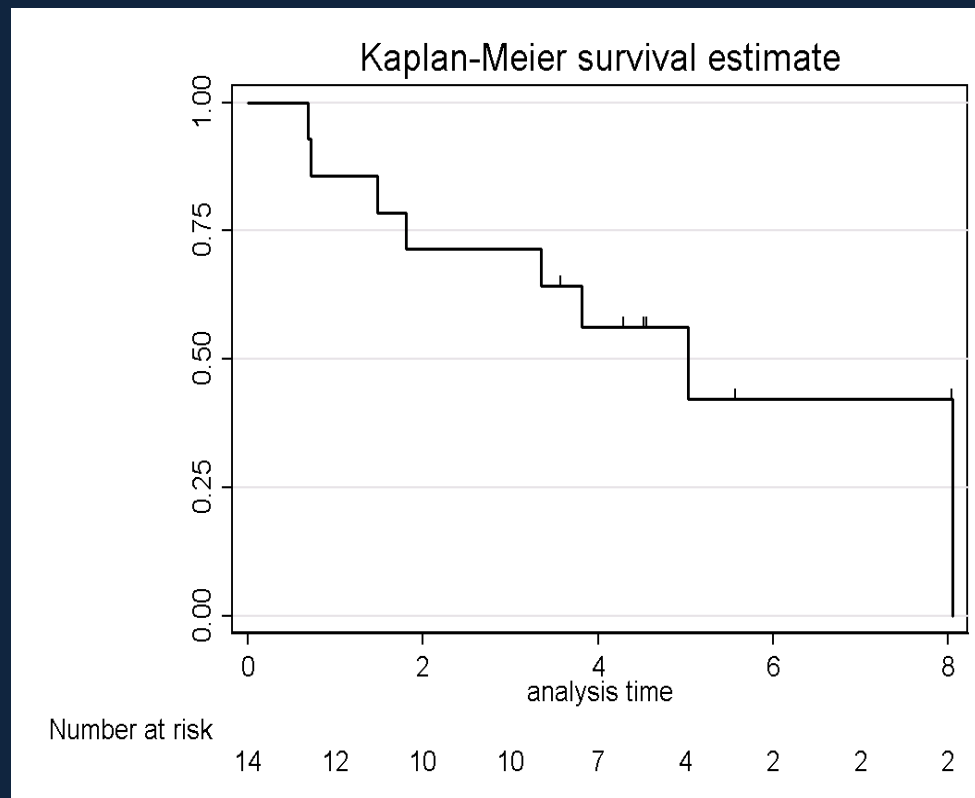
- 4 PD
- 7 SD
- 11 PR
- overall response rate ORR 50%; disease control rate DCR 82%
 - DCR of 93% for trastuzumab-based therapies (n = 15)
 - 100 % for afatinib (n = 3)
 - 0% to other HER2-targeted drugs (n = 3)

Patient	1 st line treatment	Best disease response	2 nd line treatment	Best disease response	3rd line treatment	Best disease response	4th line treatment	Best disease response
11	VIN-HER	PR						
15	CAR-PAC-TRAS	SD						
19	TXT-MASA	PD						
24	VIN-TRAS	PR						
26	CAR-PAC-TRAS	PR						
27	VIN-TRAS	PR						
28	VIN-TRAS	SD						
30	LAP	PD						
31	NVB-HER	PR						
32	LAP	PD	TRAS-VIN	PR	AFA	SD	CAR-TRAS	SD
37	VIN-TRAS	PD						
41	DOC-TRAS	PR						
43	VIN-TRAS	PR	AFA	PR				
44	VIN-TRAS	PR	AFA	SD				
45	VIN-TRAS	SD	PAC-TRAS	SD				
47	TRAS	PR						

Mazieres and Peters, JCO in press

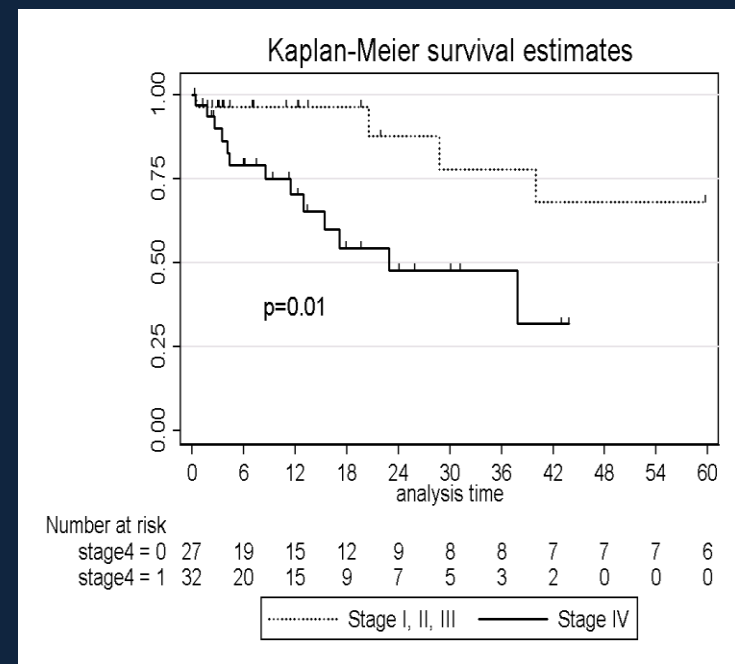
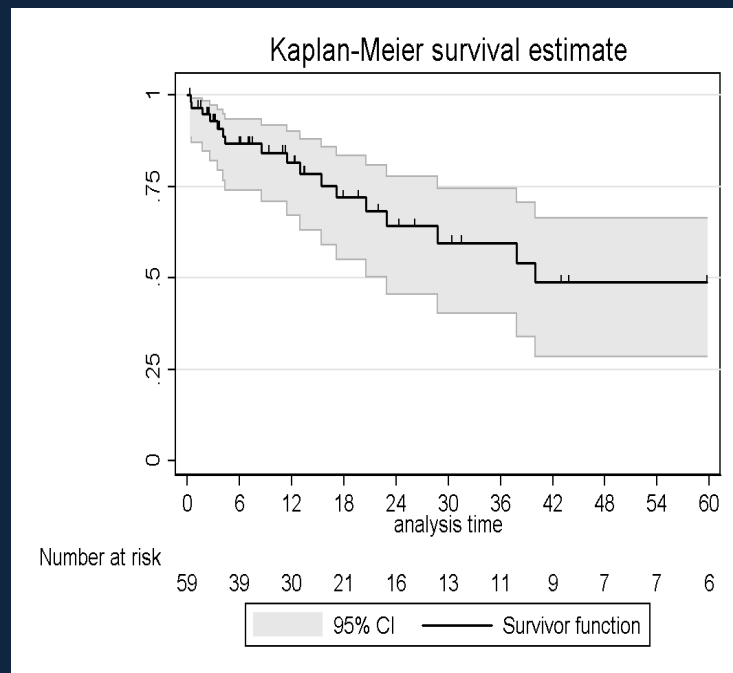
Our French/European experience (3)

Progression free survival for patients with HER2-therapies was 5.1 mos



Our French/European experience (4)

Median survival was of 89.6 and 22.9 months for early stage and stage IV patients, respectively



Conclusions (1)

HER2 mutated NSCLC represent a small distinct subgroup of oncogene addicted cancers with specific demographics and potentially outcomes

Prognostic features related to HER2 mutations remains to be studied in large cohorts of patient

NSCLC patients with mutated *HER2* are mainly female, non-smokers, exclusively suffering from adenocarcinoma subtype

We identified some men and heavy smokers (up to 60 packs-year) suggesting that *HER2* testing should not be restricted to clinically defined subgroups

Conclusions (2)

Trastuzumab is currently tested as a single-agent in patients with HER2-IHC positive, *HER2*-mutated or *HER2*-amplified NSCLC (NCT00004883 and NCT00758134), as well as in combination with carboplatin and paclitaxel

Pertuzumab is currently tested in a phase II trial in patients with advanced, pretreated NSCLC (NCT00063154)

The relative efficacy of trastuzumab as well as afatinib clearly deserves prospective evaluation in larger prospective international clinical trials

Such a prospective phase II trial is currently under preparation within European Thoracic Oncology Platform in collaboration with large national collaborative groups

Thanks for your attention



HER2 mutation description

TABLE II – HER2 MUTATIONS IN LUNG ADENOCARCINOMA

Case no.	Ethnicity (country)	Mutation (nucleotide)	Mutation (aminoacid)	Reference
60	Oriental (Japan)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	28
79	Oriental (Japan)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	28
438	Oriental (Taiwan)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	28
n.i.	Oriental (Japan)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	29
189	Oriental (Japan)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	28
276	Oriental (Japan)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	28
11	Oriental (Taiwan)	2327–2329 ins (TTT)	G776V, C ins	28
135	Oriental (Japan)	2327–2329 ins (TTT)	G776V, C ins	28
153	Oriental (Japan)	2327–2329 ins (TTT), 2326 (G>C)	G776L, C ins	28
154	Oriental (Japan)	2340–2348 ins (GGGCTCCCC)	GSP 781–783 ins	28
254	Oriental (Japan)	2341–2349 ins (GGCTCCCCA)	GSP 781–783 ins	28
23T	Caucasian (Italy)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	Current study
62T	Caucasian (Italy)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	Current study
157T	Caucasian (Italy)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	Current study
302T	Caucasian (Italy)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	Current study
375T	Caucasian (Italy)	2325–2336 ins (ATACGTGATGGC)	YVMA 776–779 ins	Current study
478	Caucasian (Australia)	2326–2337 ins (TACGTGATGGCT)	YVMA 776–779 ins	28
81T	Caucasian (Italy)	2326–2337 ins (TACGTGATGGCT)	YVMA 776–779 ins	Current study
391T	Caucasian (Italy)	2326–2337 ins (TACGTGATGGCT)	YVMA 776–779 ins	Current study
PD1353a	Not available	2323–2334 ins (GCATACGTGATG)	AYVM 775–778 ins	27
PD0258a	Not available	2323–2334 ins (GCATACGTGATG)	AYVM 775–778 ins	27
PD0317a	Not available	2323–2334 ins (GCATACGTGATG)	AYVM 775–778 ins	27
525T	Caucasian (Italy)	2329 (G>T)	V777L	Current study
PD0319a	Not available	2336–2344 (CTGTGGGCT)	VGS 779–781 ins	27
PD0270a	Not available	2263–2264 (TT>CC)	L755P	27
260T	Caucasian (Italy)	2263–2264 (TT>CC)	L755P	Current study