

Personalized treatment in NSCLC: fact or fiction?

Paul Germonpré



Personalized treatment in NSCLC

- Aims and challenges of biomarker driven treatment
- Treatment customized on histology or tumor biomarkers
 - Targeted therapies:
 - EGFR-TKIs
 - Anti-VEGF
 - Chemotherapy:
 - Pemetrexed
 - Cisplatin-based chemotherapy
- Treatment customized on patient genotype markers
 - Gemcitabine
 - Paclitaxel



Treatment selection in NSCLC

Tumor characteristics

- TNM-stage

Patient characteristics

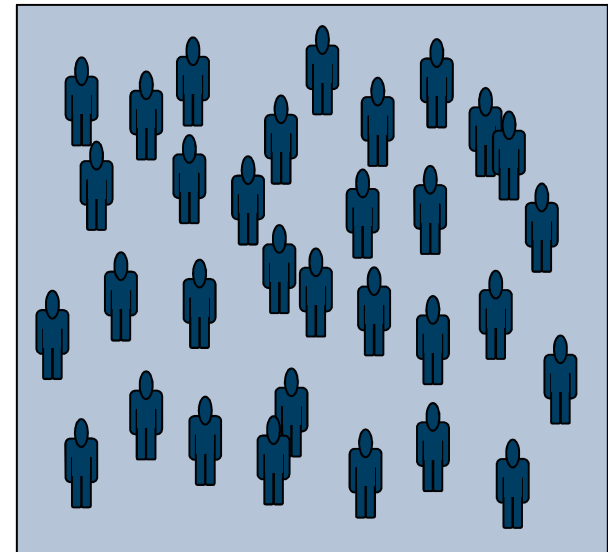
- Performance status
- Age and comorbidities

Patient preference

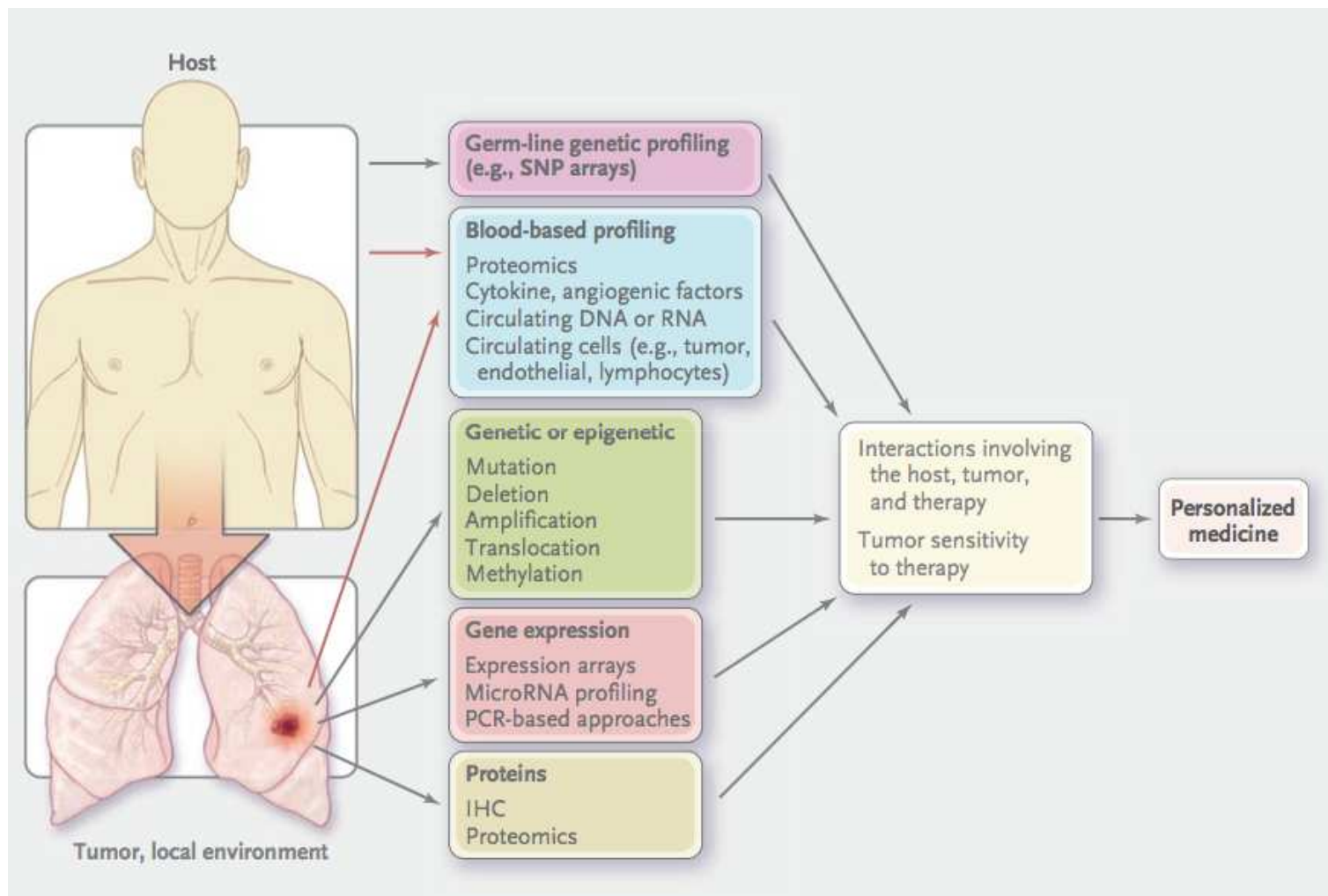
- Toxicities
- Treatment administration

Doctor preference

- Experience with drug



Development of Personalized Therapy for NSCLC



Aims of personalized cancer care

- Individual patient level
 - selection of treatment based on the biology and molecular characteristics of the patient as well as the tumor in order to:
 - improve the efficacy of the treatment and/or
 - avoid life threatening toxicity
- Society level
 - reduction of the cost of cancer care by
 - restricting the treatment to the patients most likely to benefit
 - avoiding ineffective treatments
 - reducing morbidity and complications



Prognostic versus predictive markers

Prognostic

Provides information on outcome, regardless of treatment

Predictive

Provides information on outcome with regards to a specific therapy

Many biomarkers have both prognostic and predictive value



Controlled trials or meta-analyses are required to determine the prognostic and predictive contributions made by a particular marker



Requirements on the trial design for identifying a predictive biomarker

Hypothesis
generating

Hypothesis
testing

Open label
Small numbers
Single arm



Retrospective
analysis
Non-stratified



Double-blind
randomized
Placebo-
controlled
Adequately
powered
Prospective
analysis
Stratified by
biomarker status



Moving towards customized treatment

Tumor characteristics

- TNM-stage
- **Tumor biomarkers**

Patient characteristics

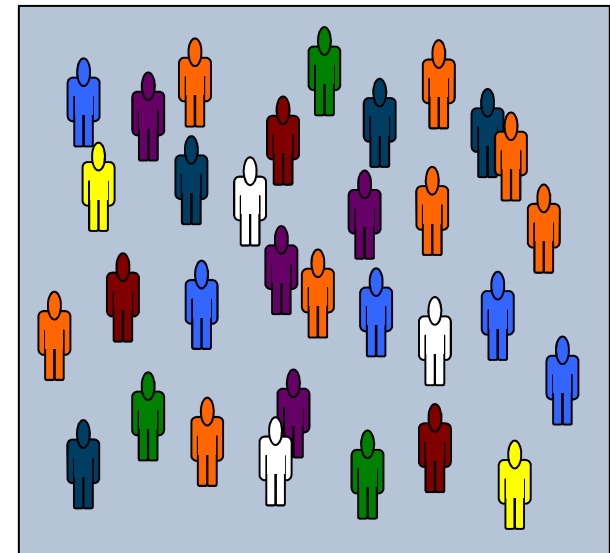
- Performance status
- Age and comorbidities
- **Patient biomarkers**

Patient preference

- Toxicities
- Treatment administration

Doctor preference

- Experience with drug

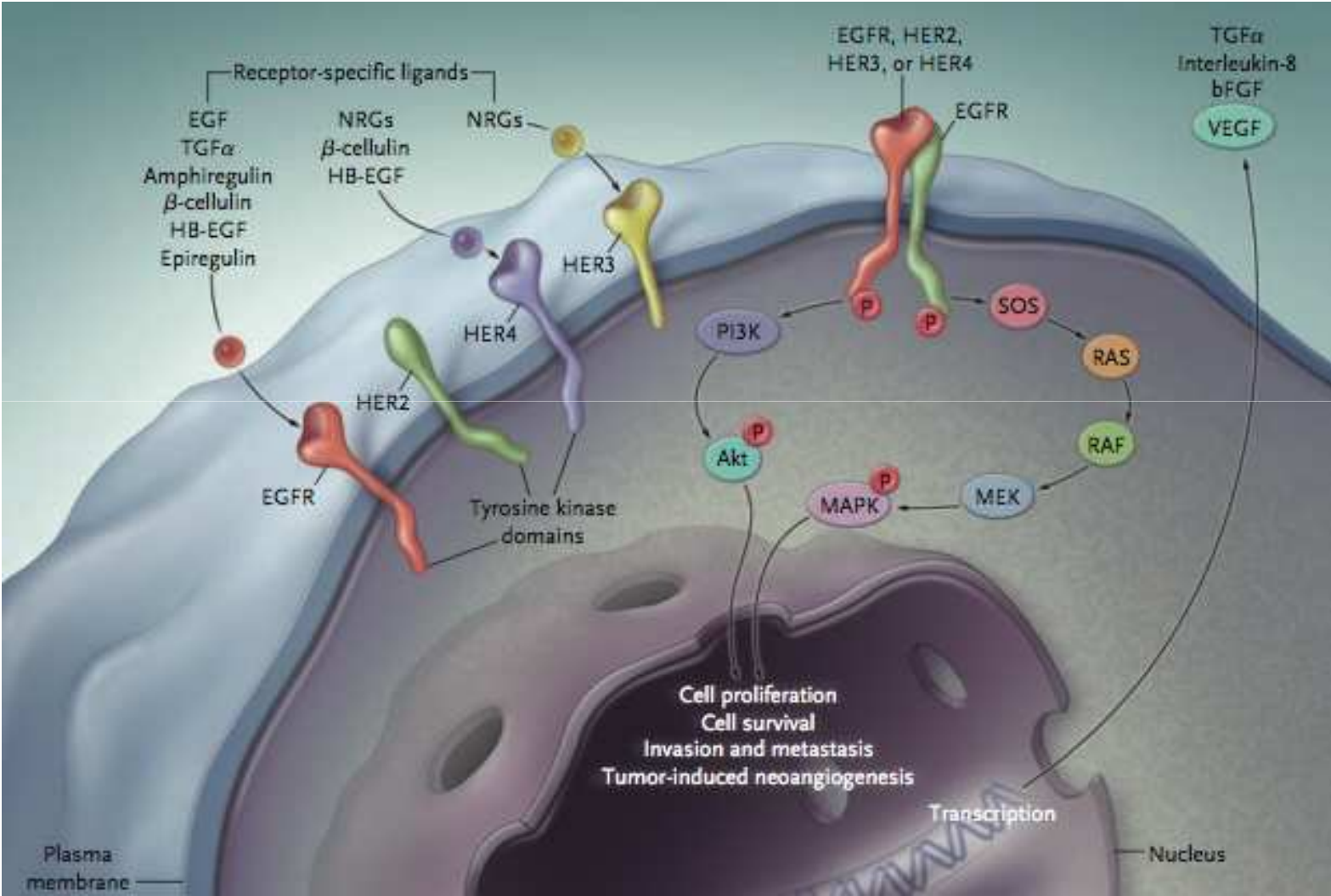


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Signal Transduction Pathways Controlled by the Activation of EGFR



BR.21: predictors of response

		Erlotinib Patients (%) (n=427)	p*
Gender	Female (146)	14.4	0.006
	Male (281)	6.1	
Histology	Adenocarcinoma (209)	13.9	<0.001
	Other (218)	4.1	
Ethnicity	Asian (53)	18.9	0.02
	Other (374)	7.5	
Ever smoked	Yes (311)	3.8	<0.001
	No (93)	24.7	
	Unknown (23)	13.0	

*Significance between subgroups

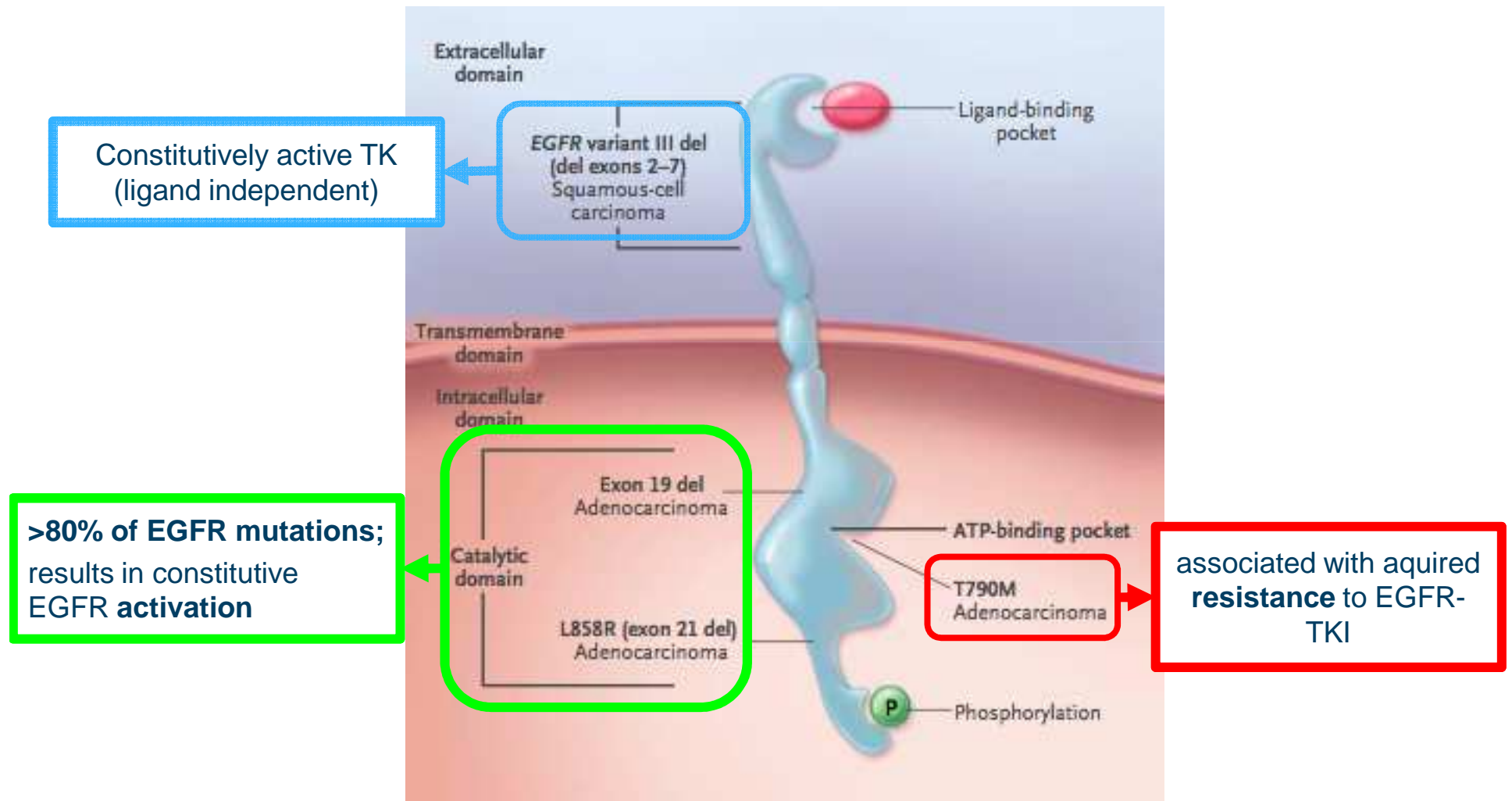


BR.21: overall survival ~ clinical predictors for response (EGFR mutation)

		HR	CI	p*
Gender	Male (475)	0.8	0.6–0.9	0.76
	Female (256)	0.8	0.6–1.1	
Histology	Adenocarcinoma (365)	0.7	0.6–0.9	0.37
	Other (366)	0.8	0.6–1.0	
Ethnicity	Asian (91)	0.6	0.4–1.0	0.44
	Other (640)	0.8	0.7–0.9	
Smoking history	Ever (545)	0.9	0.7–1.0	0.02
	Never (146)	0.4	0.3–0.6	
	Unknown (40)	1.1	0.5–2.6	

*p value for interaction between erlotinib and clinical variables

Effect of Deletions and Mutations in EGFR on Disease Development and Drug Targeting



IPASS : 1st line EGFR-TKI vs chemotherapy

Inclusion criteria:

- Chemonaive Asian pts
- Adenocarcinoma
- Never or light ex-smokers

R

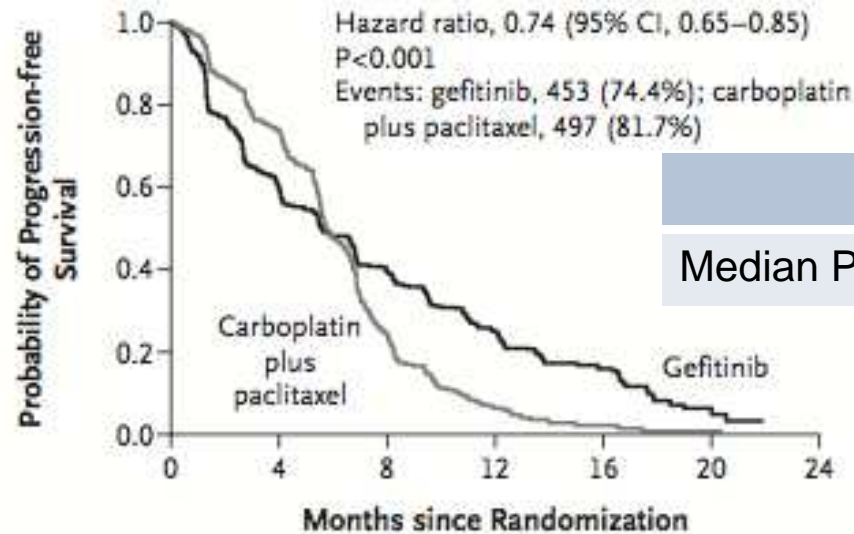
Gefitinib arm:

Gefitinib 250 mg/d until PD

Chemotherapy arm:

Carboplatin + Paclitaxel (6 cycles)

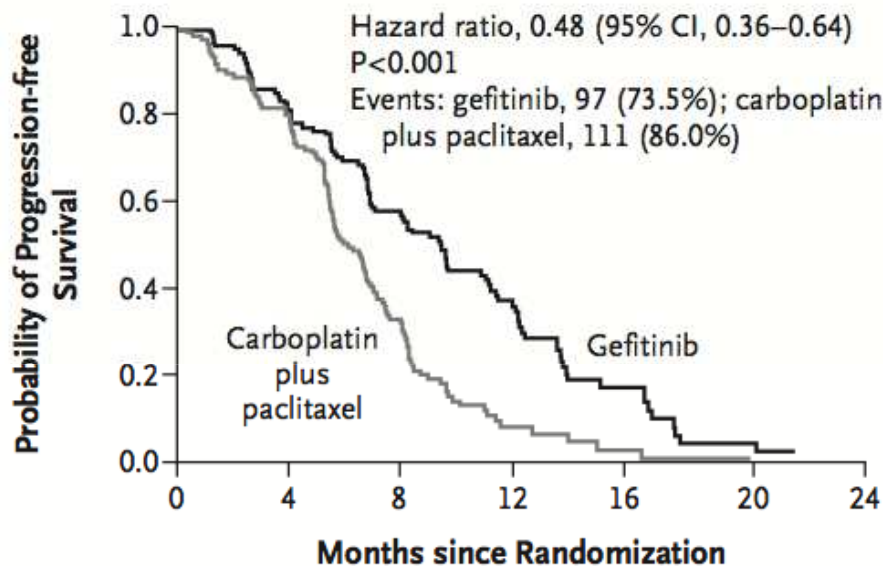
Statistics : PFS as primary endpoint



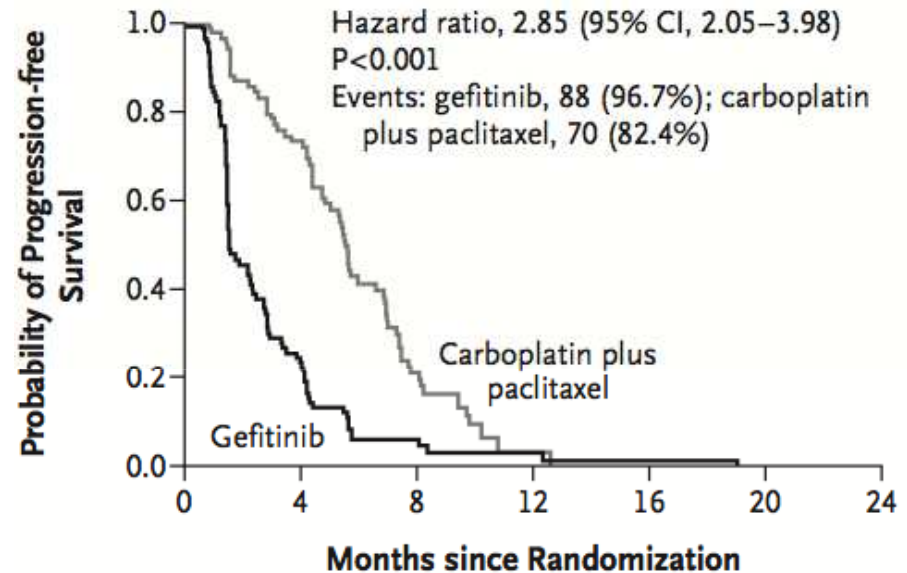
	Gefit	Chemo
Median PFS	5.7 m	5.8 m

IPASS: Progression-free survival

EGFR-mutation positive



EGFR-mutation negative



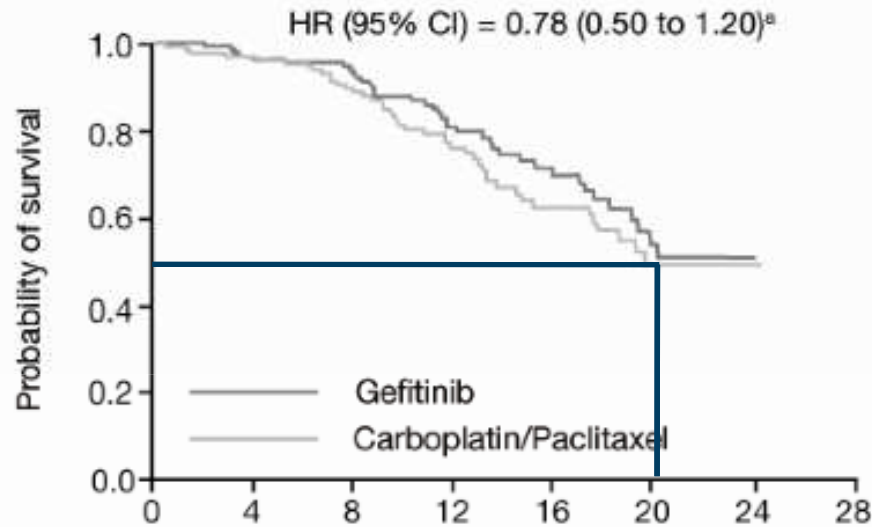
	EGFR-mutation pos.		EGFR-mutation neg.	
	Gefitinib	Carbo/Pacli	Gefitinib	Carbo/Pacli
Response rate	71%*	47%	1%	23%*
Median PFS	9.6 m*	6.3 m	1.5 m	5.5 m*

* $P < 0.05$

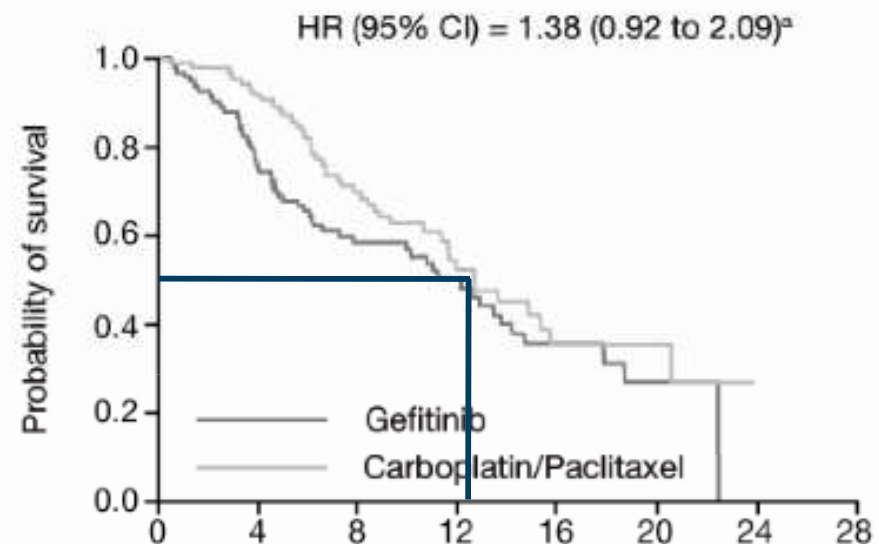


IPASS: Overall survival

EGFR-mutation positive



EGFR-mutation negative



At progression ~40% of patients in each arm crossed over to other treatment modality

The presence of an EGFR mutation:

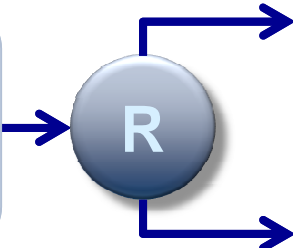
- is a strong predictive biomarker for ↗ response rate (both to chemotherapy and EGFR-TKI)
- is a strong predictive biomarker for ↗ PFS with EGFR-TKI *versus* chemotherapy
- is a favourable prognostic factor



WJTOG3405 : 1st line gefitinib vs chemotherapy

Inclusion criteria:

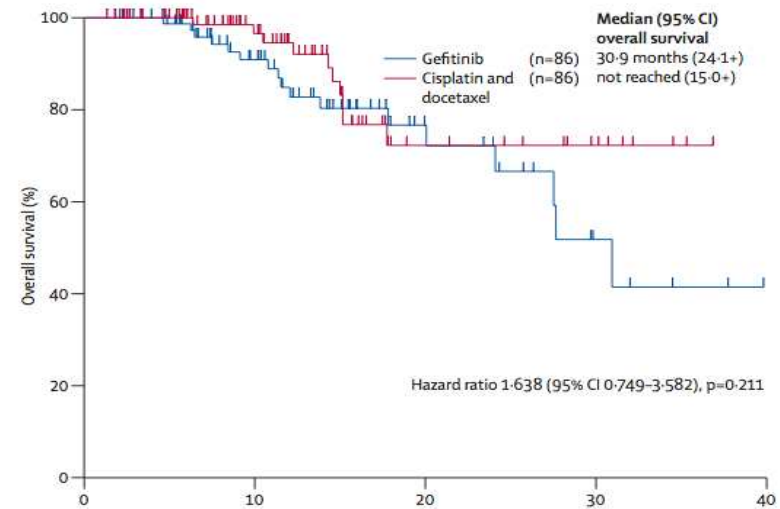
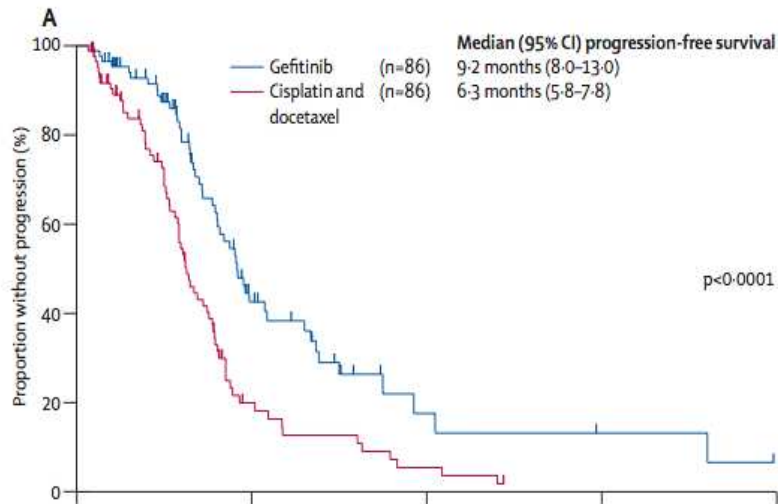
- Chemonaive Asian pts
- EGFR activating mutation



Gefitinib arm:
Gefitinib 250 mg/d until PD

Chemotherapy arm:
Cisplatin + Docetaxel (6 cycles)

Statistics : PFS as primary endpoint

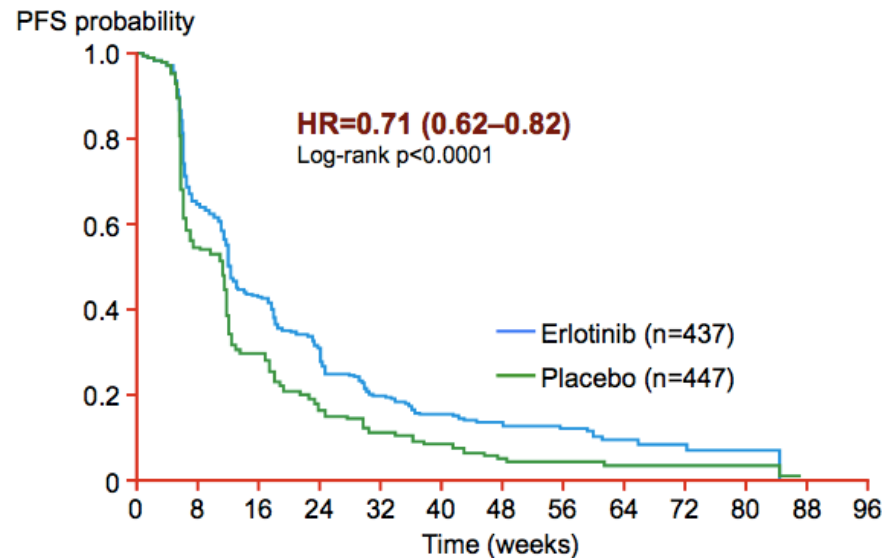


SATURN: erlotinib as maintenance in 1st-line treatment of advanced NSCLC

Inclusion criteria:

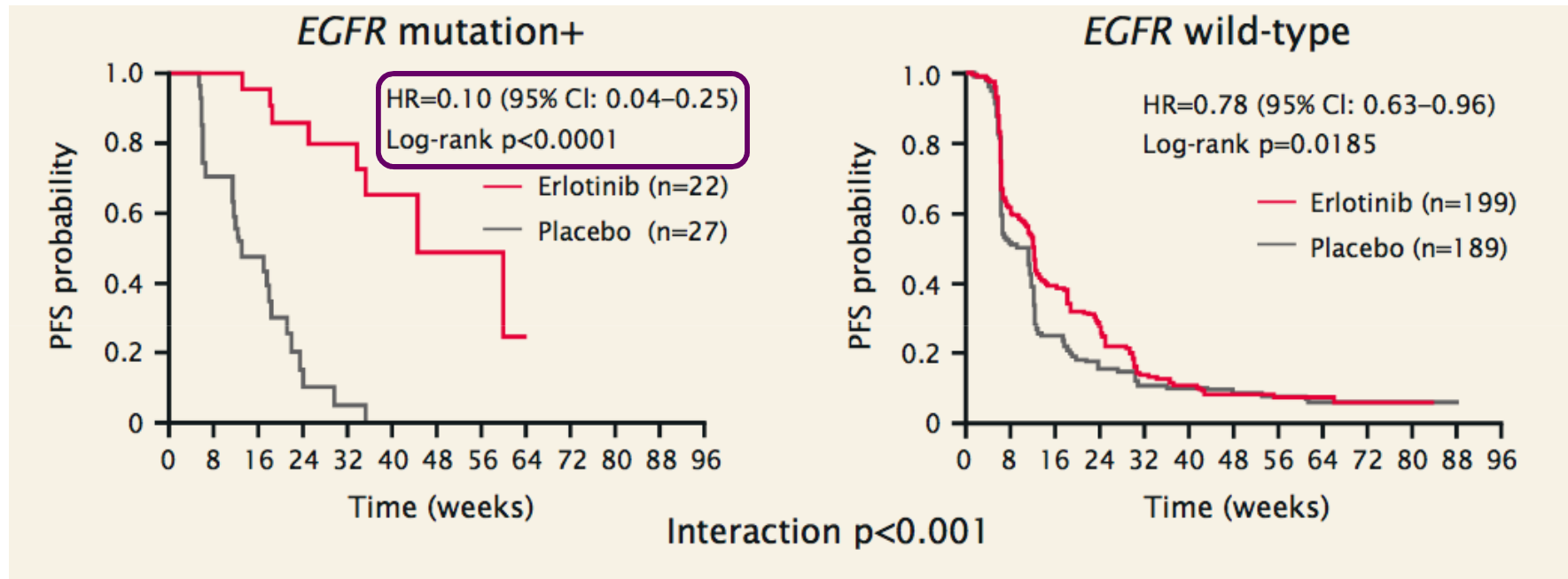
- Stage IIIB/IV NSCLC
- PS 0-1
- Non-PD following 4 cycles of platinum-based chemotherapy*

Statistics : PFS as primary endpoint



* 1st line chemotherapy: Cisplatin/Carboplatin + Docetaxel/Paclitaxel/Gemcitabine/Vinorelbine

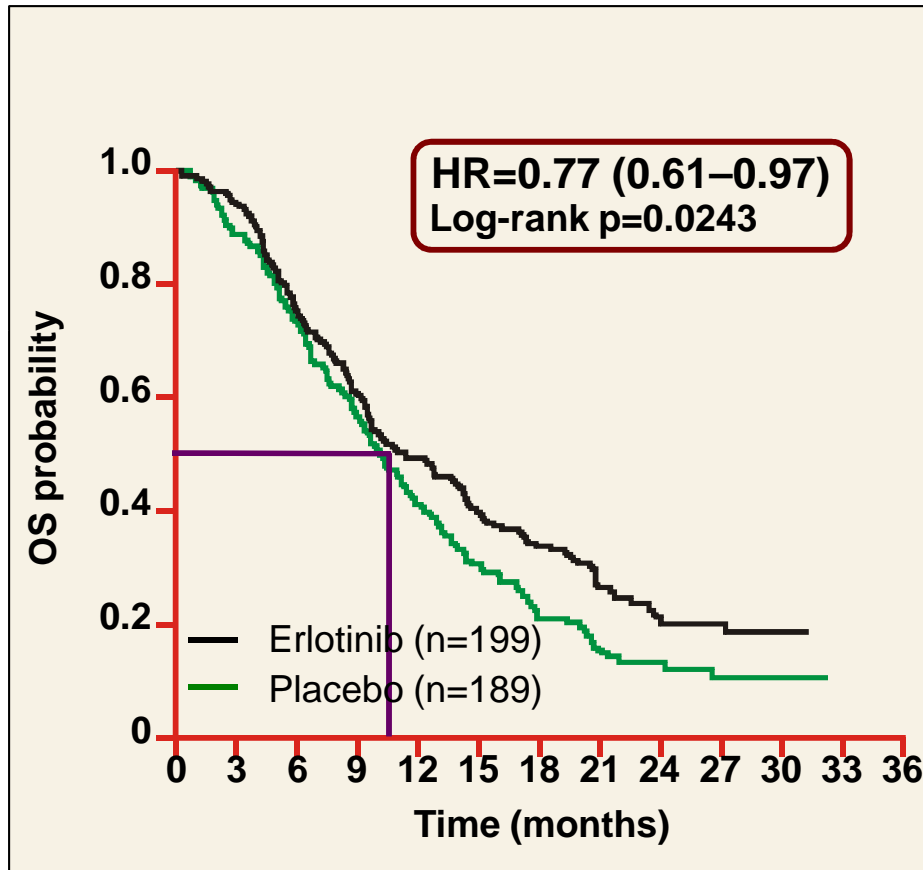
SATURN: PFS by biomarkers



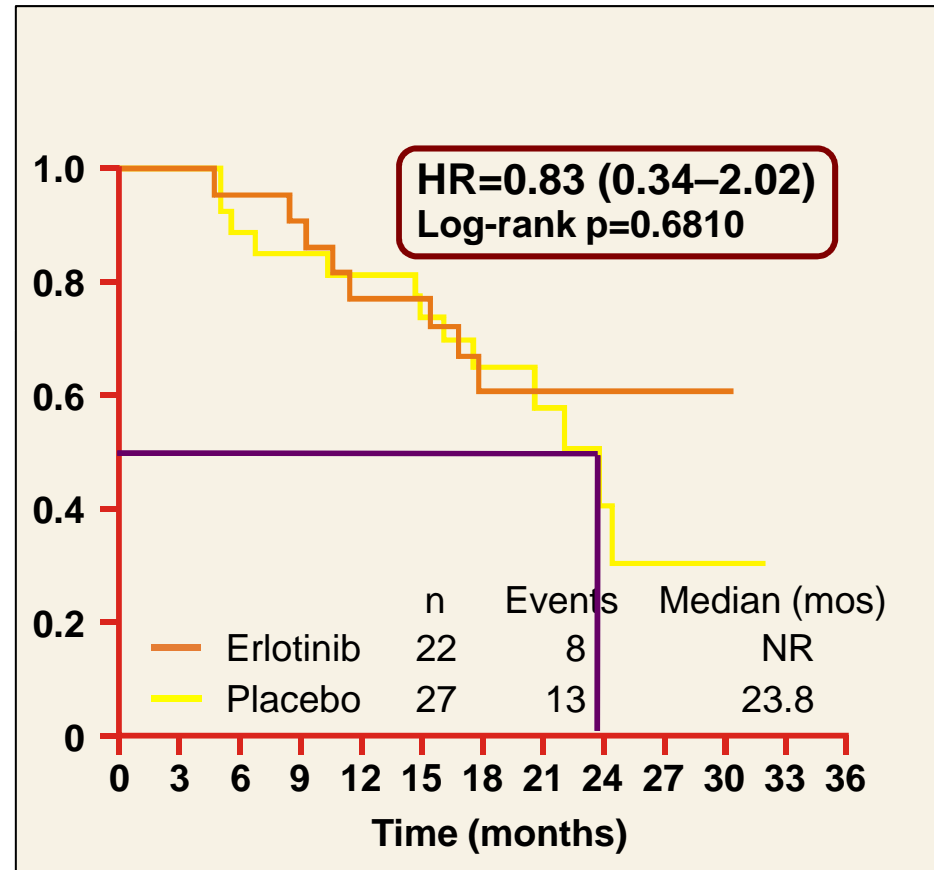
EGFR mutations identify patients who derive a great PFS-benefit from erlotinib maintenance (median PFS 45 wks vs 13 wks).

SATURN: overall survival

EGFR-wild type

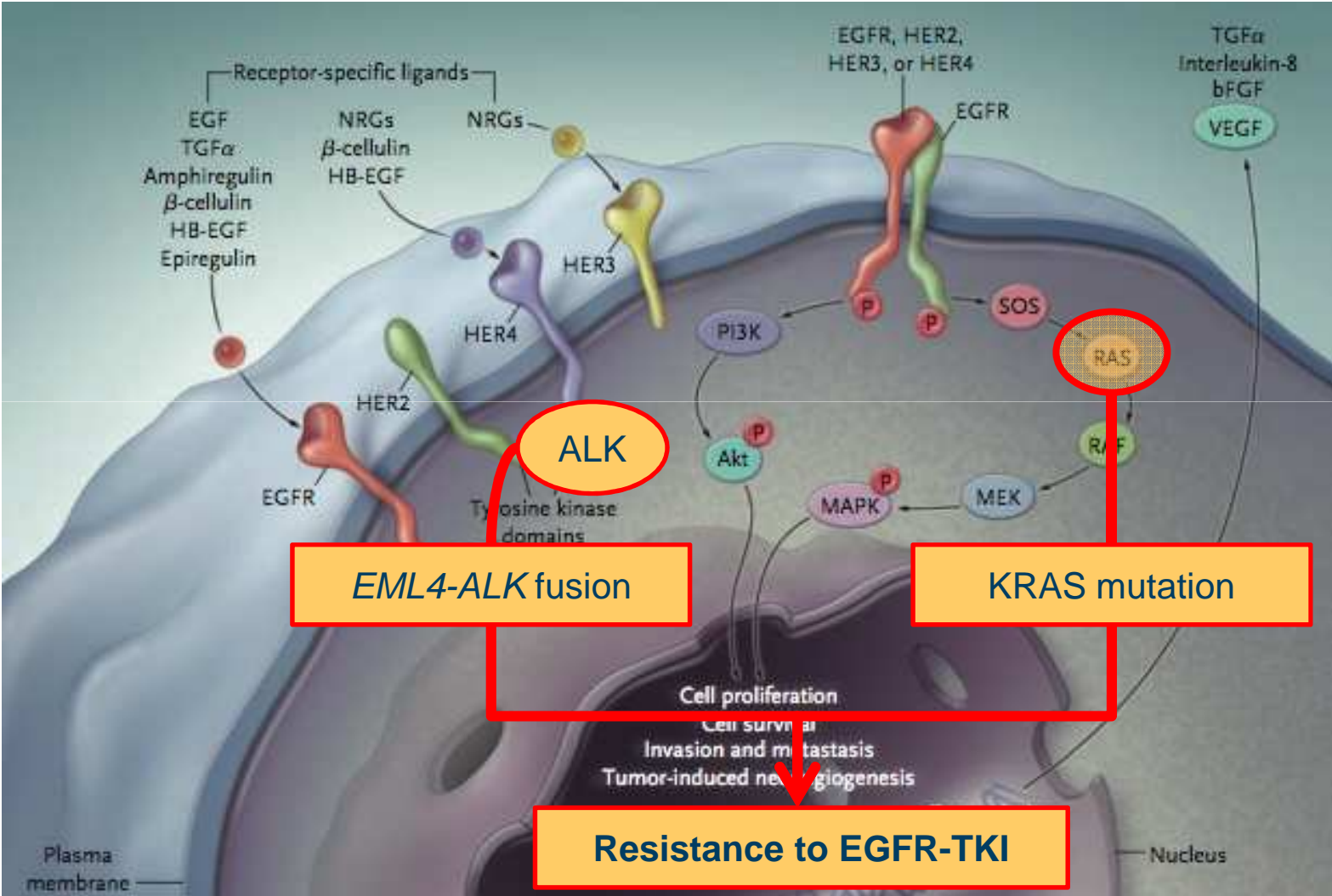


EGFR-mutation positive *



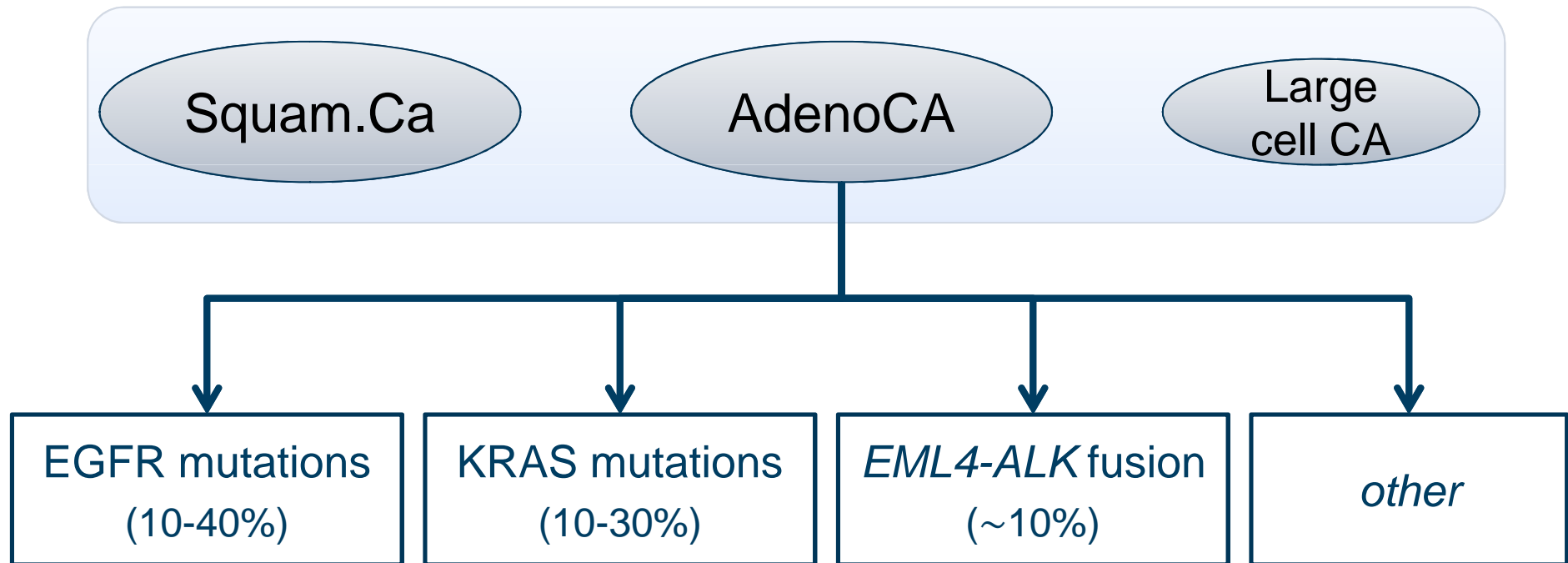
*67% of patients with *EGFR* mutation+ disease in the placebo arm received a second-line *EGFR* TKI

Signal Transduction Pathways Controlled by the Activation of EGFR



NSCLC: driver mutations

Genetic alterations responsible for initiating and maintaining lung cancer:



ALK gene rearrangements and crizotinib in NSCLC

- ALK gene rearrangements:
 - occur in 3-5% of unselected NSCLC
 - higher frequency in adenoCA in light or never smokers
- Crizotinib (PF-02341066):
 - potent oral inhibitor of ALK and MET
- Phase I-II trial of crizotinib :
 - heavily pre-treated NSCLC with proven FISH-positive ALK rearrangement
 - symptomatic improvements occur within 3 days
 - in 50 evaluable pts:
 - objective response rate 64%
 - disease control rate 90%

→ Phase III initiated



Bevacizumab and NSCLC

- Randomized phase 2 trial of carbo-pacli ± bevacizumab:
 - incidence of life-threatening pulmonary hemorrhage:
 - 9% in all bevacizumab-treated patients
 - 31% in pts with squamous cell cancer
 - 4% in pts with adenocarcinoma
 - the phase 3 studies enrolled only **non-squamous-cell NSCLC**.
- EMA label:
bevacizumab, in addition to platinum-based chemotherapy, is indicated for 1st-line treatment of patients with unresectable advanced, metastatic or recurrent **NSCLC other than predominantly squamous cell histology**.



Personalized treatment in NSCLC

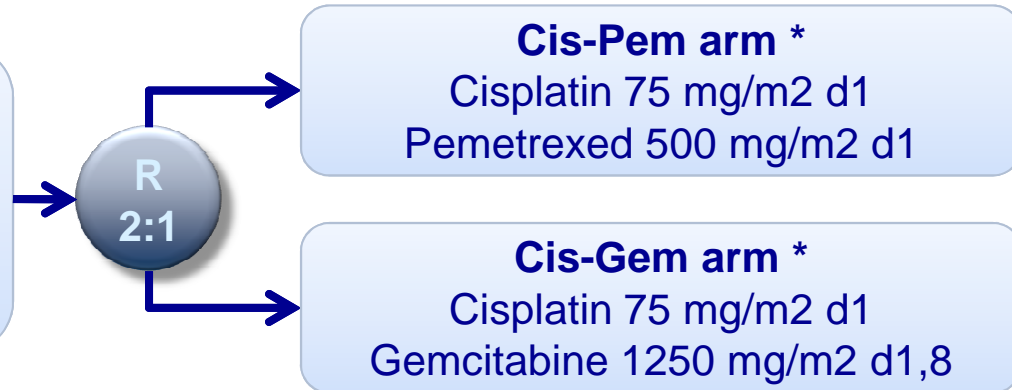
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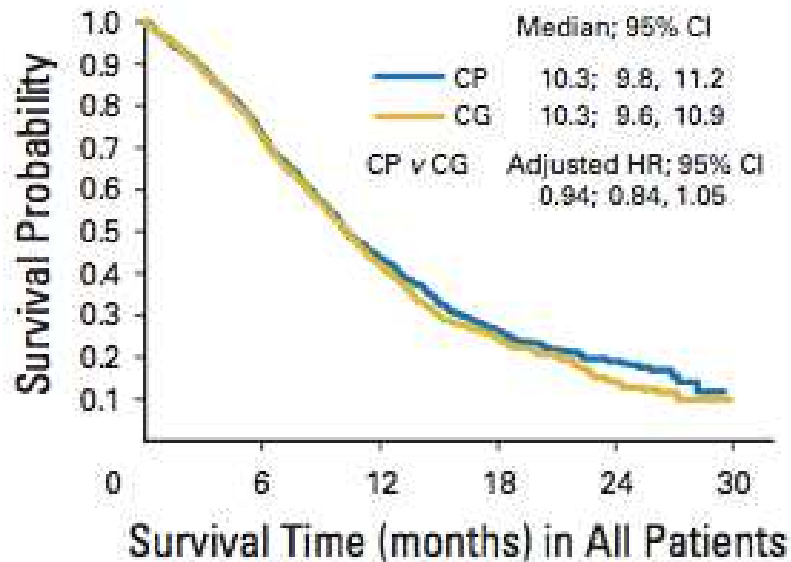
Cisplatin+Pemetrexed vs Cisplatin+Gemcitabine in 1st-line treatment of advanced NSCLC

Inclusion criteria:

- Chemo-naïve advanced NSCLC
- PS 0-2
- No CNS metastasis



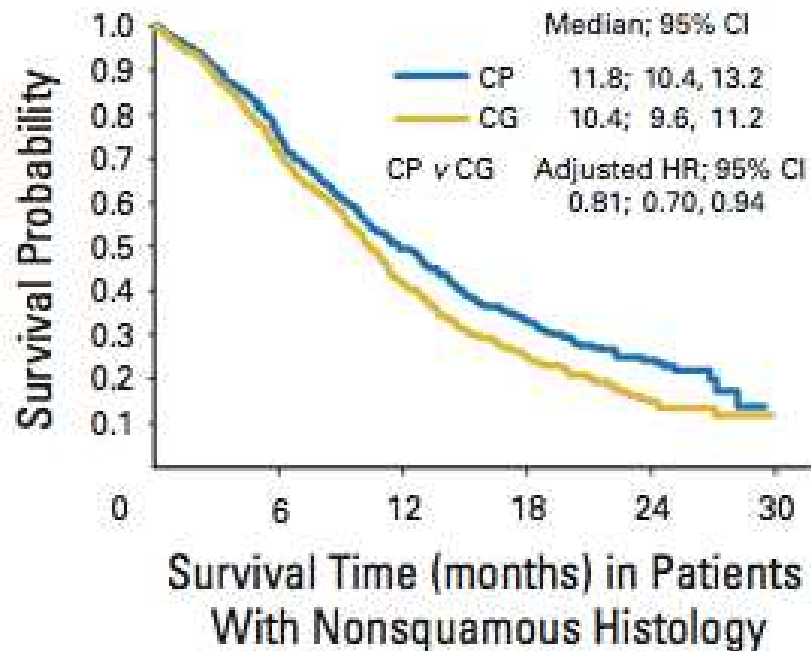
* every 3 weeks for 6 cycles



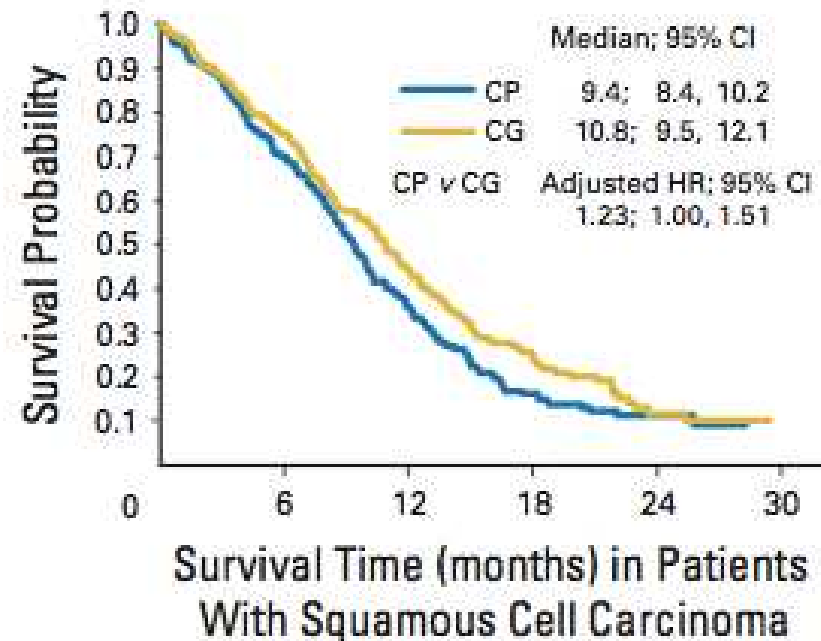
ITT population	C-P	C-G	HR
Median OS (m)	10.3	10.3	0.94

Cisplatin+Pemetrexed vs Cisplatin+Gemcitabine in 1st-line treatment of advanced NSCLC

Non-squamous patients



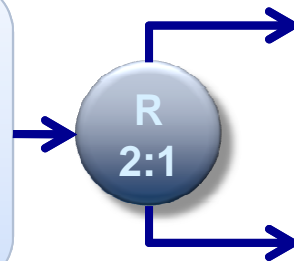
Squamous patients



Pemetrexed as maintenance in 1st-line treatment of advanced NSCLC

Inclusion criteria:

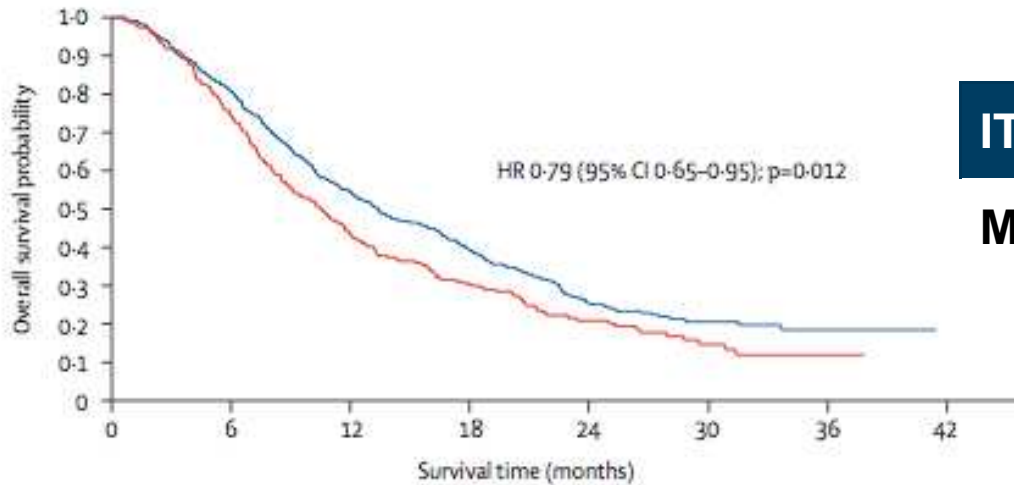
- PS 0-1
- Non-progressing following 4 cycles of platinum + gemci, doc or pacli



Maintenance arm:
Pemetrexed 500 mg/m² Q3wks*
until PD (n=441)

Control arm:
Placebo d1 Q3wks*
until PD (n=222)

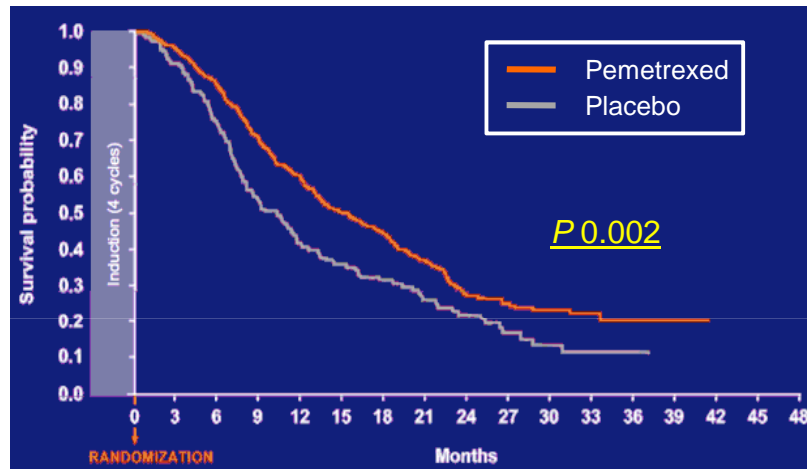
*Vitamin B12, folate and dexamethasone given in both arms



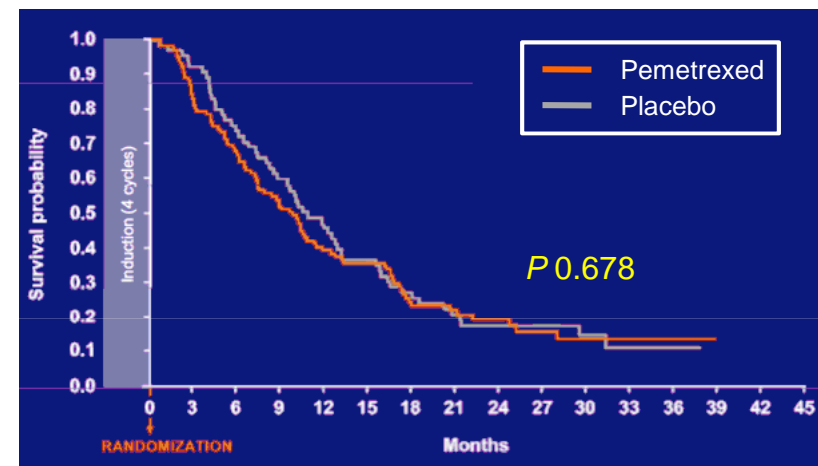
ITT population	Pem	Plac	P
Median OS (m)	15.5	10.3	.012

Pemetrexed maintenance trial: preplanned analysis of OS by histology

Non-squamous patients



Squamous patients



Median OS (months)

	Pem	Plac	HR
Nonsquamous	15.5	10.3	0.70
Squamous	9.9	10.8	1.07

Pemetrexed and NSCLC histology: hazard ratios for overall survival

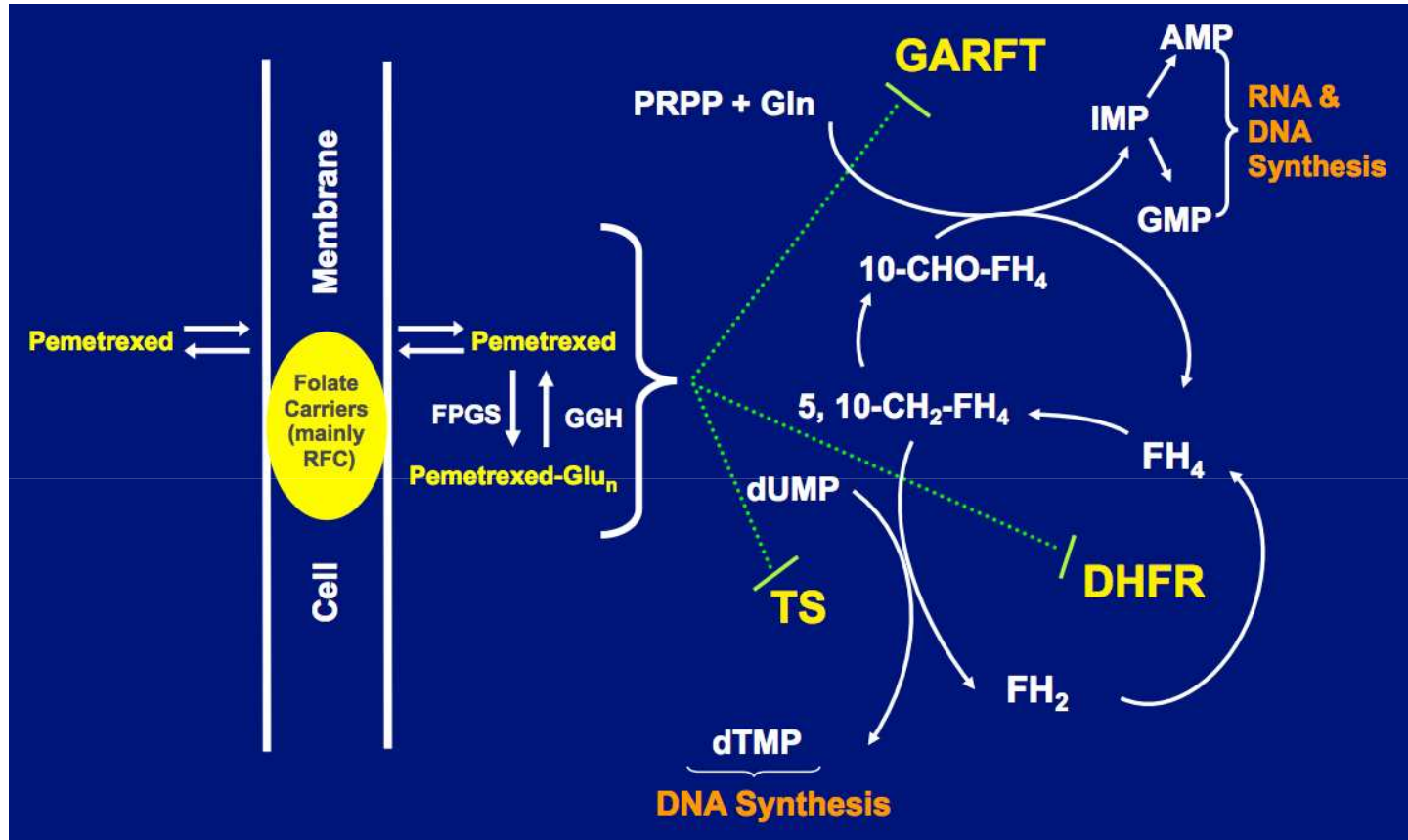
Histology	1 st line: Cis-Pem vs Cis-Gem	2 nd line: Pem vs Doc	Maintenance: Pem vs Plac
Non-squamous	0.81 *	0.78 *	0.70 *
Squamous	1.23	1.56 *	1.07

Conclusion:

- Pemetrexed is superior compared to gemcitabine (and placebo) in patients with non-squamous NSCLC and/or
- Pemetrexed has no anti-tumoral activity in squamous cell NSCLC



Pemetrexed: mechanism of action



Resistance to pemetrexed in cancer cell line is solely due to upregulation of thymidylate synthase (TS)

Thymidylate expression in lung cancer

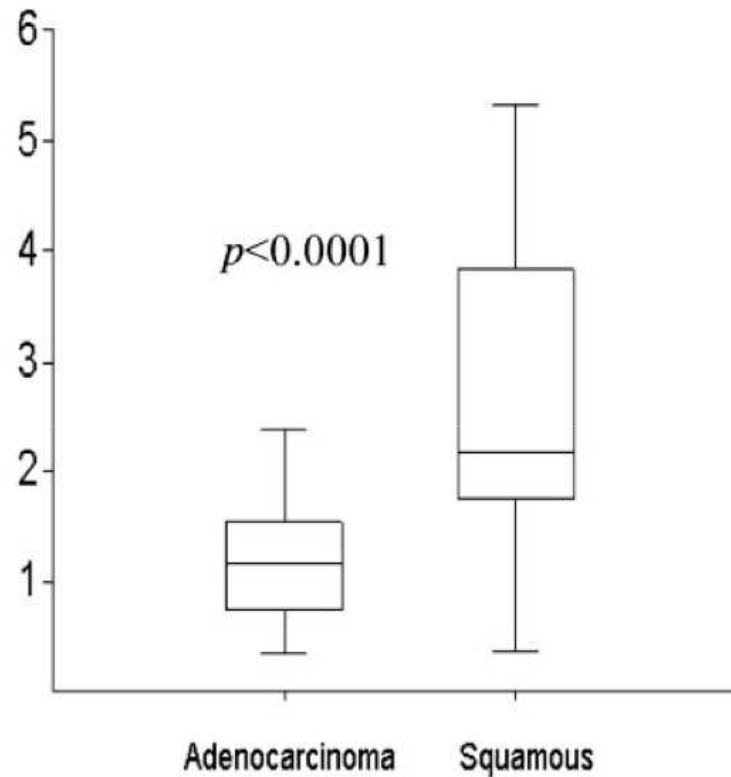
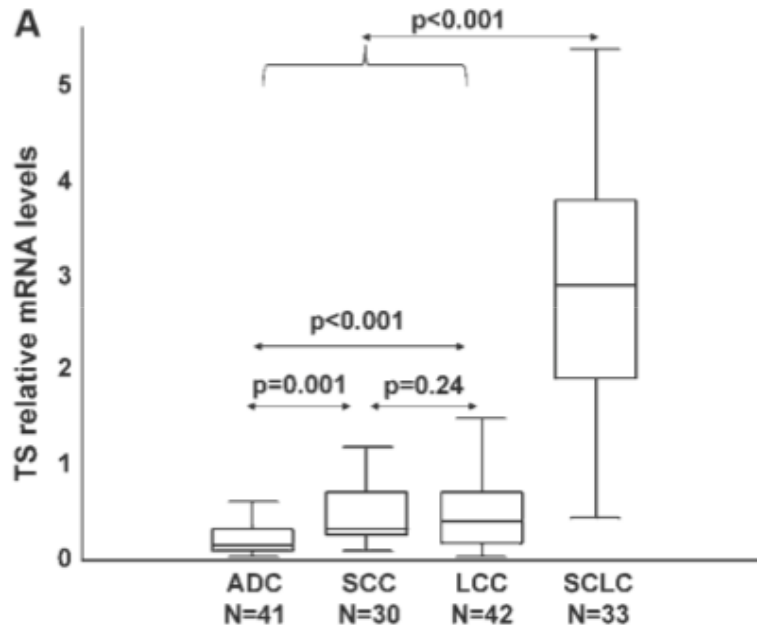


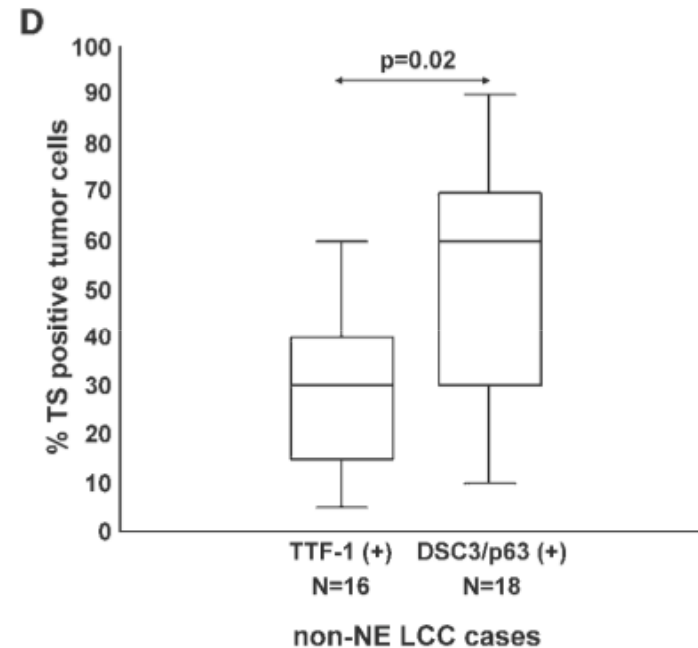
FIGURE 1. Thymidylate synthase messenger RNA levels are illustrated in adenocarcinoma compared with squamous cell carcinoma. Horizontal lines in the middle represent median values, and upper and lower bars represent the distance from the 10th to 90th percentile from the median, respectively.

Thymidylate expression in lung cancer

TS mRNA expression



TS protein expression



- The LCC immunoprofile may resemble that of SCCs or ADCs.
- This immunoprofile is associated with differential TS expression levels

LCC: large cell carcinoma
SCLC: small cell lung cancer

Pemetrexed and NSCLC histology: hazard ratios for overall survival

Histology	1 st line: Cis-Pem vs Cis-Gem	2 nd line: Pem vs Doc	Maintenance: Pem vs Plac
Non-squamous	0.81 *	0.78 *	0.70 *
<i>Adenocarcinoma</i>	<i>0.84 *</i>	<i>0.92</i>	<i>0.73 *</i>
<i>Large cell</i>	<i>0.67</i>	<i>0.27 *</i>	<i>0.98</i>
<i>NOS</i>	<i>1.08</i>	<i>0.57</i>	<i>0.61 *</i>
Squamous	1.23	1.56 *	1.07

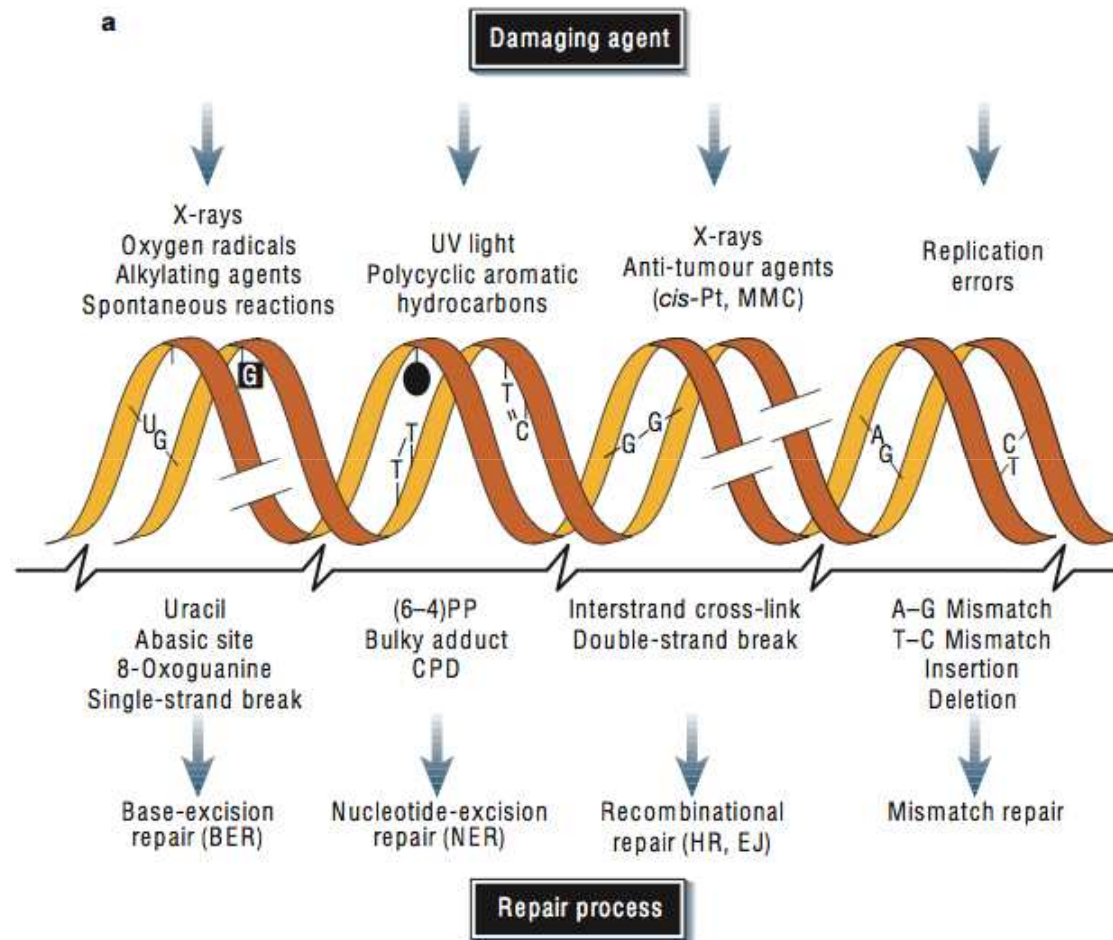


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DNA Damage and DNA repair mechanisms



Cisplatin-based chemotherapy and DNA repair mechanisms

Excision repair cross-complementation group 1 (ERCC1)

- ERCC1 is a rate-limiting protein in the NER and ICL-R pathways, which works by recognising and removing platinum adducts and by repairing interstrand DNA cross-links

Ribonucleotide reductase messenger 1 (RRM1)

- RRM1 is the regulatory component of ribonucleotide reductase, which assists with DNA synthesis and repair.
- RRM1 is the predominant target of the nucleoside analogue gemcitabine.
- RRM1 mediates suppression of cell migration and tumour metastasis by inducing *PTEN*, a prominent tumour-suppressor gene responsible for attenuation of growth-factor pathway signalling.



Cisplatin-based chemotherapy and DNA repair mechanisms

Breast cancer type 1 susceptibility protein (BRCA1)

- BRCA1 is a component of multiple repair pathways and plays a central role in DNA repair:
 - is involved in the repair of double-strand DNA breaks by the HR and NH-EJ pathways
 - is implicated in the transcription-coupled NER and the ICL-R pathway.
 - is a component of the BRCA1-associated genome surveillance complex, suggesting a role for BRCA1 in mismatch repair
- BRCA1 and β -tubulin co-localise to the microtubules of the mitotic spindle → potential regulator of mitotic spindle assembly.
- BRCA1 has been implicated BRCA1 in apoptosis via the c-Jun N-terminal kinase pathway.



Biomarkers and cisplatin-based chemotherapy in NSCLC

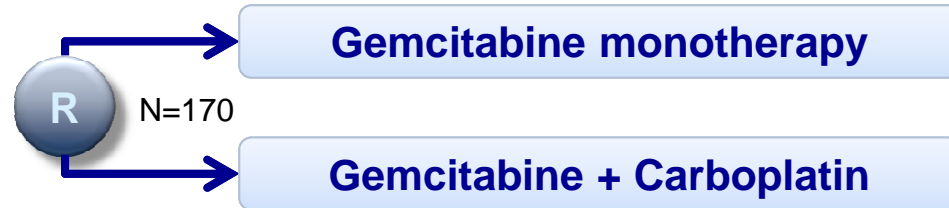
	Prognostic significance	Predictive significance
ERCC1 overexpression	conflicting results	resistance to cisplatin
RRM1 overexpression	better prognosis	resistance to cisplatin
BRCA1 overexpression	worse prognosis	resistance to cisplatin sensitivity taxane/vinca

Based on surgical series of untreated pts

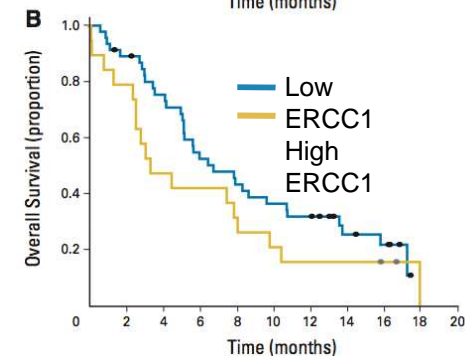
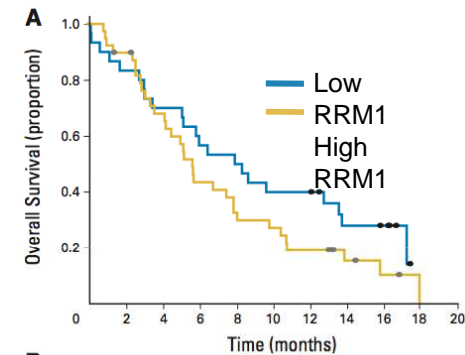
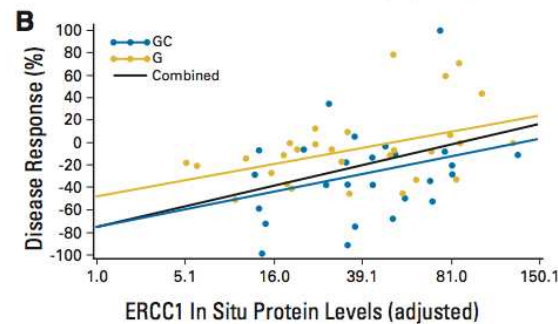
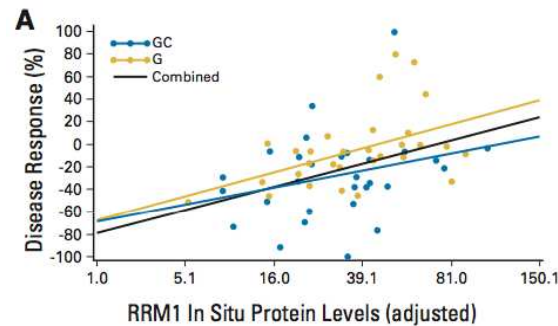
Based on preclinical data, retrospective analyses, uncontrolled phase 2 trials and IALT



RRM1 and ERCC1 in Gemcitabine treated NSCLC



	G	G+C
Median OS	5.1 m	6.7 m



RRM1 (and ERCC1) overexpression is correlated with resistance to gemcitabine (and carboplatin) chemotherapy in NSCLC



Molecular Analysis-Directed Therapy in NSCLC

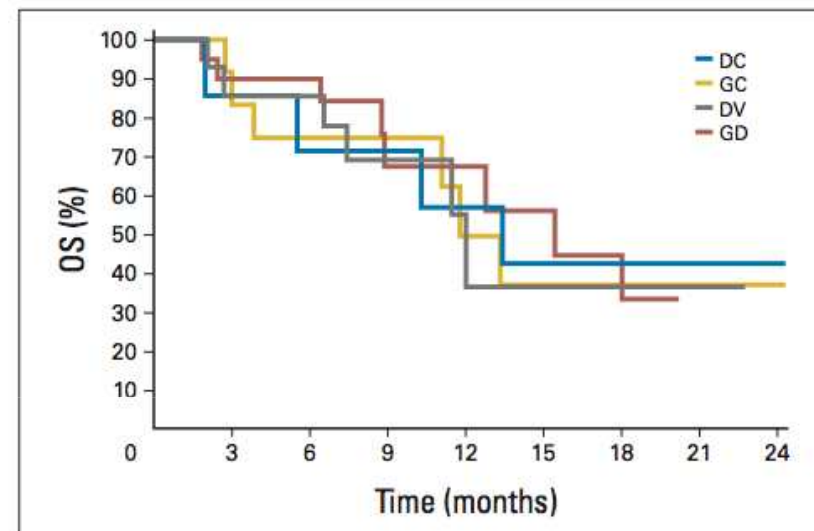
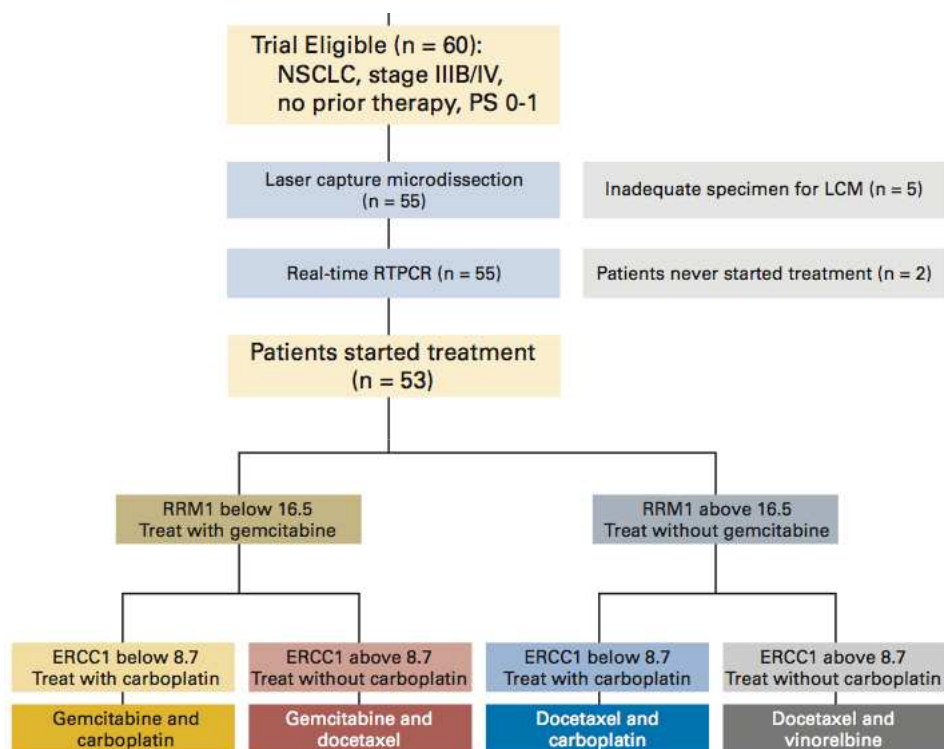
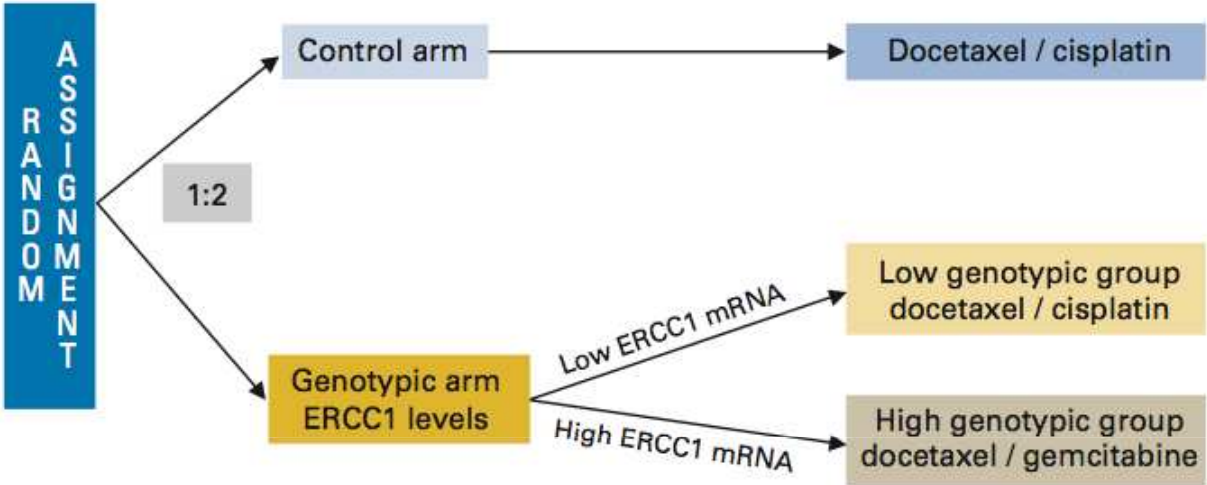


Fig 3. Overall survival (OS) by assigned chemotherapy. DC, docetaxel and carboplatin; GC, gemcitabine and carboplatin; DV, docetaxel and vinorelbine; GD, gemcitabine and docetaxel.

	RR	MST	1-yr OS
Individualized chemo	44 %	13.3 m	59%

Customizing Cisplatin-chemotherapy based on ERCC1 mRNA expression in NSCLC



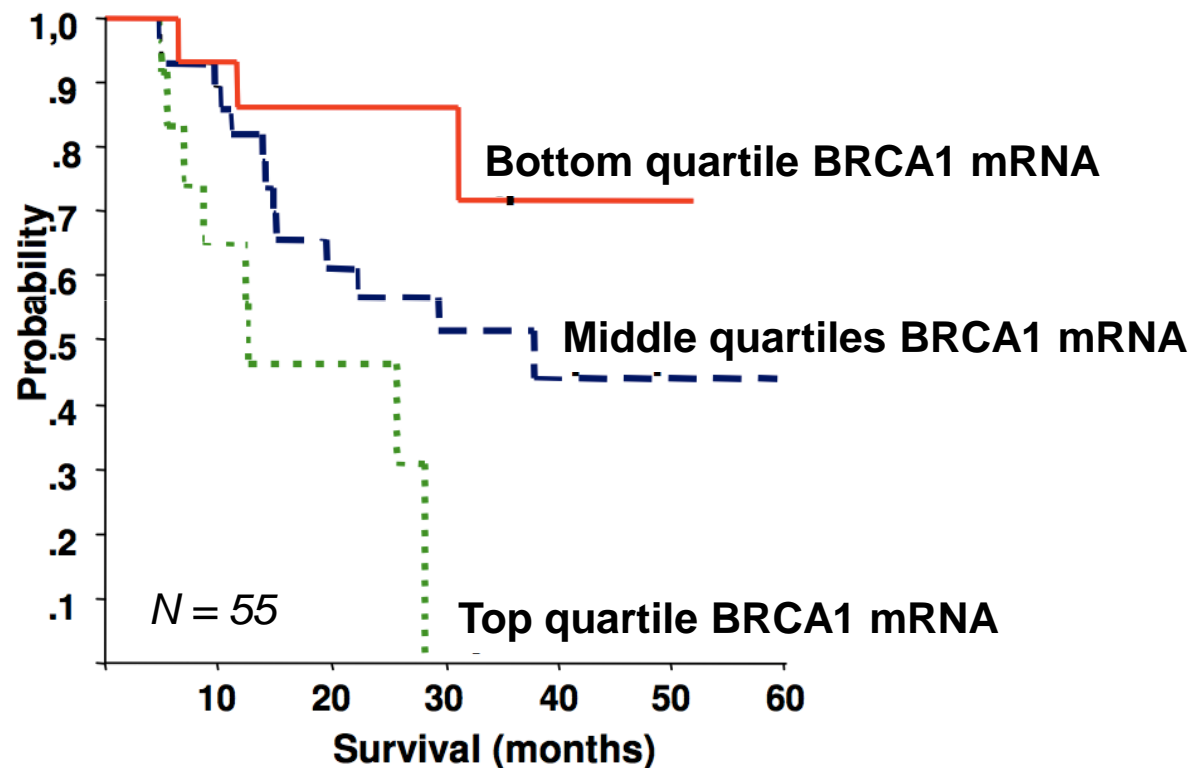
	RR	PFS	MST	1-yr OS	2-yr OS
Control arm	40%	5.2 m	9.8 m	39%	19%
Genotypic arm	51%	6.1 m	9.9 m	41%	20%

Customizing chemo based on tumor ERCC1 mRNA expression:

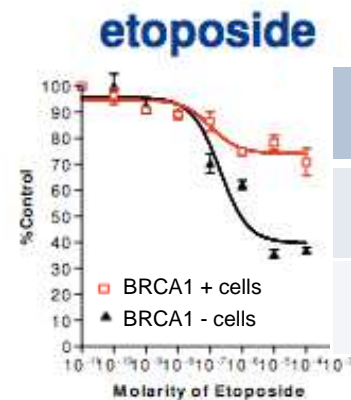
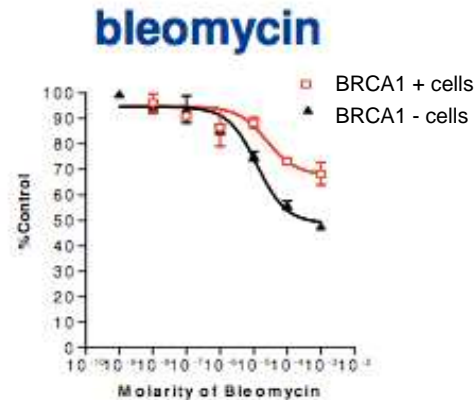
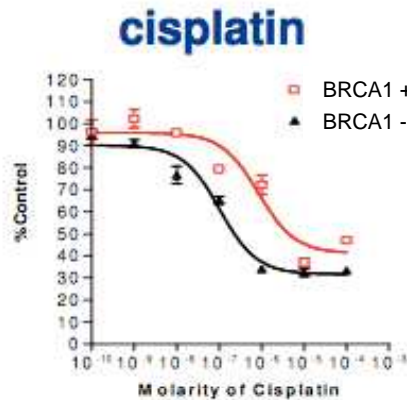
- is feasible in the clinical setting
- improves response rate (but not overall survival)



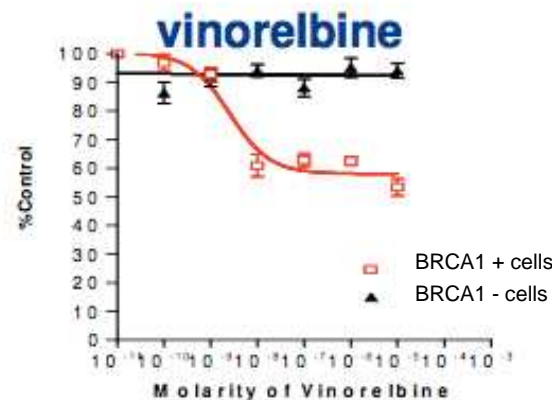
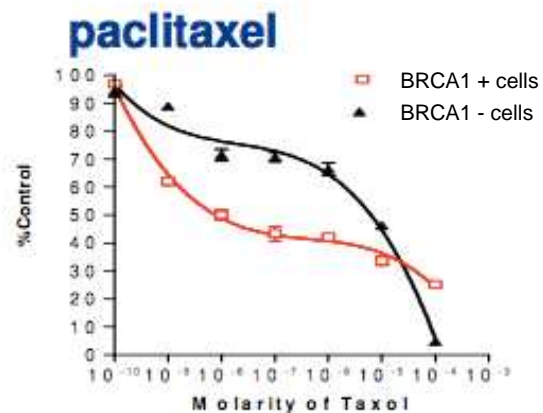
BRCA1 as predictor of survival in patients with resected NSCLC treated with induction cis + gemci



BRCA1 has differential modulating effect on chemotherapy



IC 50	BRCA1 -	BRCA1 +
Cispl	0,2 μ M	4,1 μ M
Etop	0,9 μ M	>100 μ M

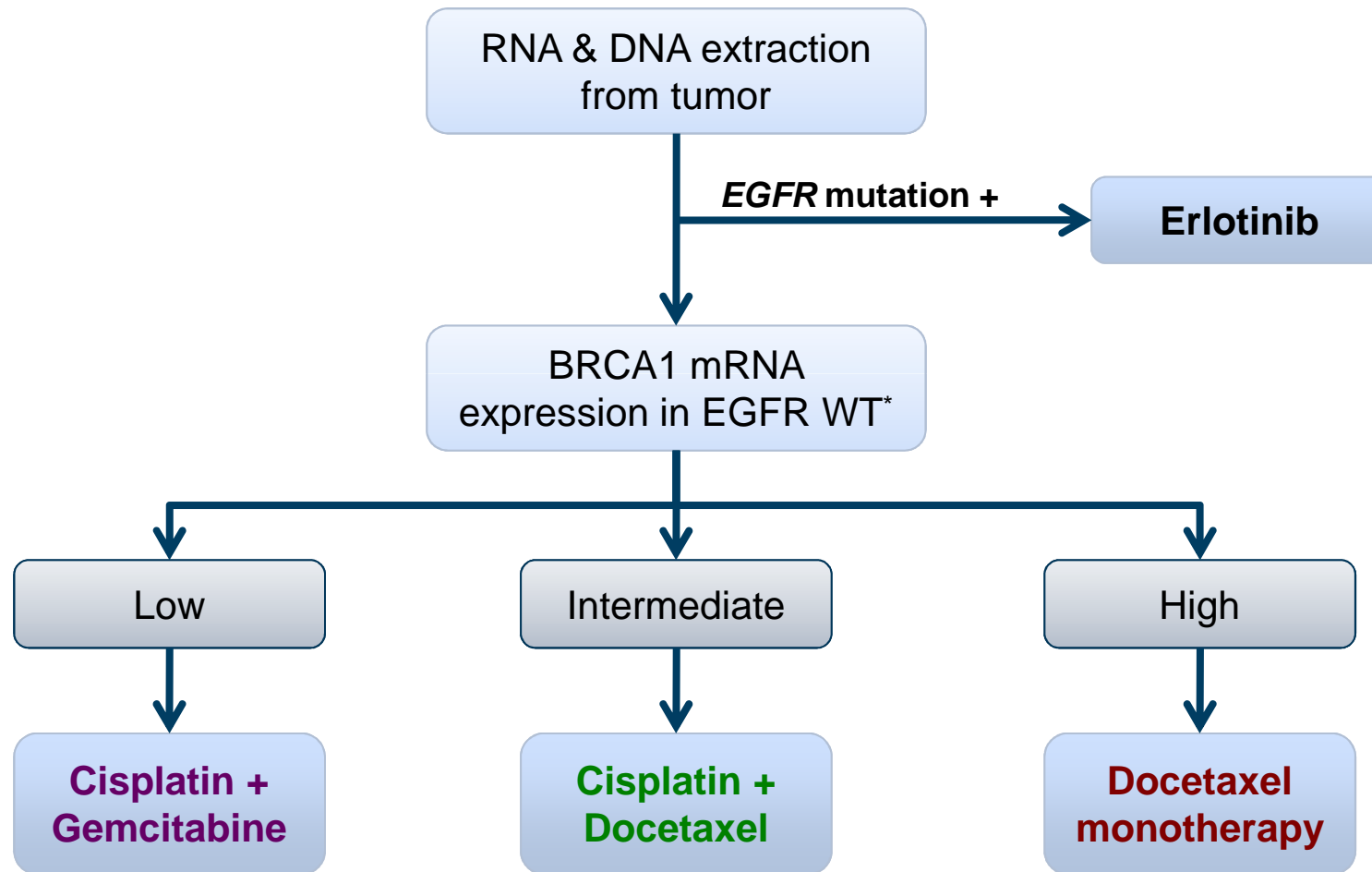


IC 50	BRCA1 -	BRCA1 +
Pacli	6,2 μ M	7,2 nM
VRB	17 μ M	1,9 nM

BRCA1 expression induces resistance to cisplatin and sensitivity to paclitaxel and vinorelbine.

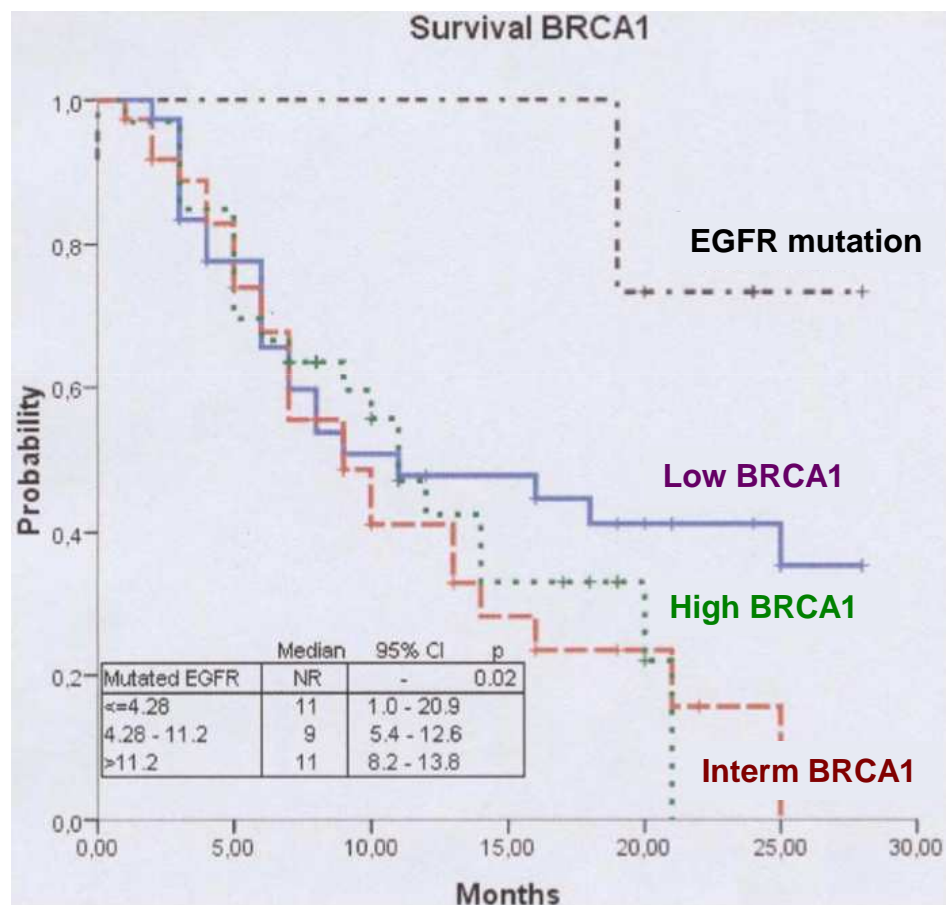


Customized treatment of NSCLC based on EGFR mutations and BRCA1 mRNA expression



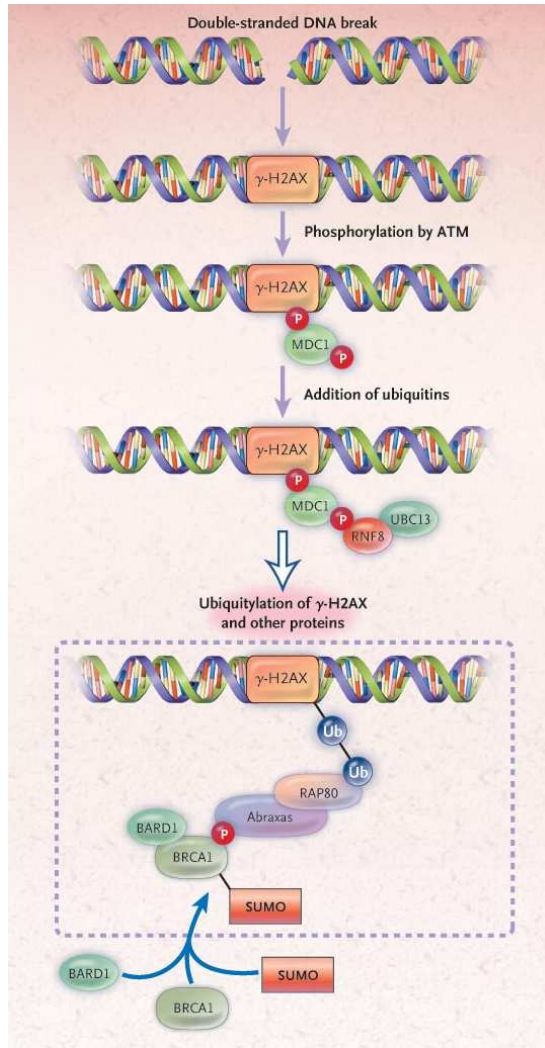
* exploratory analysis of RAP80 and Abraxas expression

Customized treatment of NSCLC based on EGFR mutations and BRCA1 mRNA expression



	N	MST	1y OS	2y OS
EGFR mut +	12	NR	92%	73%
BRCA1 low	38	11m	48%	41%
BRCA1 inter	40	9m	41%	16%
BRCA1 high	33	11m	42%	0%

Bringing BRCA1 to Sites of DNA Damage



- Histone γ -H2AX and MDC1 are recruited to site of DNA damage
- ↓
- Ubiquitylation of γ -H2AX and MDC1 complex occurs
- ↓
- RAP80 (and Abraxas) are attracted to the site
- ↓
- RAP80 transfers BRCA1 to the site of DNA-damage

MDC1: mediator of DNA-damage checkpoint 1
BRCA1: breast cancer susceptibility gene 1
RAP80: receptor associated protein 80

RAP80 and DNA repair mechanisms

Receptor associated protein 80 (RAP80):

- acts upstream of BRCA1
- is required for accumulation of BRCA1 to sites of double strand DNA breaks
 - *RAP80 is required for DNA damage repair*
- is able to translocate to DNA-damage foci in cells which express a truncated BRCA1 that is unable to migrate to nuclear foci
 - *RAP 80 could replace the BRCA1 DNA repair function in cells lacking BRCA1*



Customized treatment of NSCLC based on EGFR mutations and BRCA1 mRNA expression

Median survival ~ BRCA1 and RAP80 expression

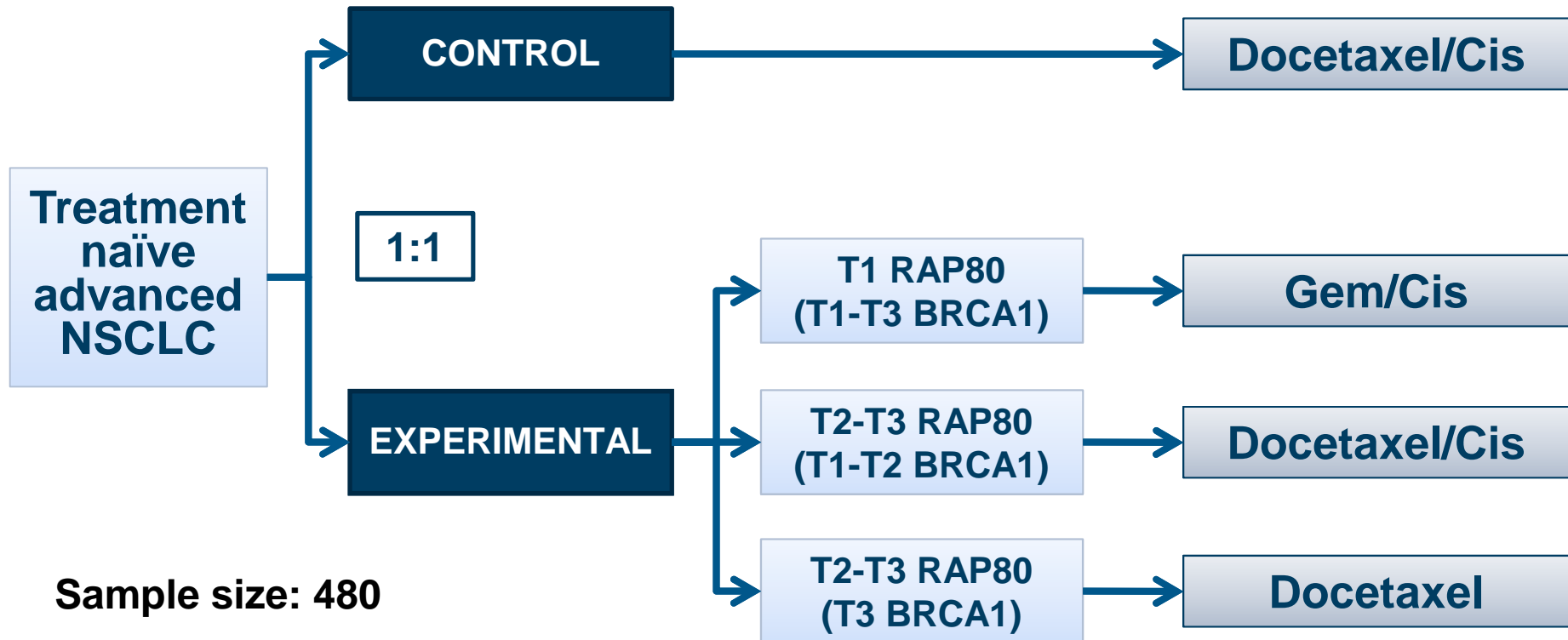
		RAP80 mRNA		
		Low	Intermediate	High
BRCA1 mRNA	Low	NR	8 m	7 m
	Intermediate	5 m	13 m	16 m
	High	6 m	12 m	11 m

Phase III trial

Cisplatin + Gemcitabine
 Cisplatin + Docetaxel
 Docetaxel monotherapy



BREC trial: design



Primary endpoint:

- Time to progression between the standard non-customized first-line chemotherapy group and the 3 customized chemotherapy subgroups



Selection factors for customizing systemic treatment for NSCLC

Category	Drug	Selection factor	Effect
Tumor histology	EGFR-TKI	Adeno	Improved response rate
	Pemetrexed	Non-Squamous	Exclusion non-benefiting pts
	Bevacizumab	Non-Squamous	Safety
Molecular tumor biomarkers	EGFR-TKI	EGFR-mutation	Improved PFS
	Pemetrexed	Low TS expression	Selection benefiting pts
	Gemcitabine	Low RRM1	Selection benefiting pts
	Platinum	ERCC1, BRCA1 or RAP80 expression	Improved RR, PFS and/or OS

Data from adequately powered RCTs with prospective biomarker analysis



Personalized treatment in NSCLC

- Aims and challenges of biomarker driven treatment
- Treatment customized on histology or tumor biomarkers
 - Targeted therapies:
 - EGFR-TKIs
 - Anti-VEGF
 - Chemotherapy:
 - Pemetrexed
 - Cisplatin-based chemotherapy
- Treatment customized on patient genotype markers
 - Gemcitabine
 - Paclitaxel



Correlation of CDA Polymorphisms with Outcome in Gemcitabine/Cisplatin Treated NSCLC

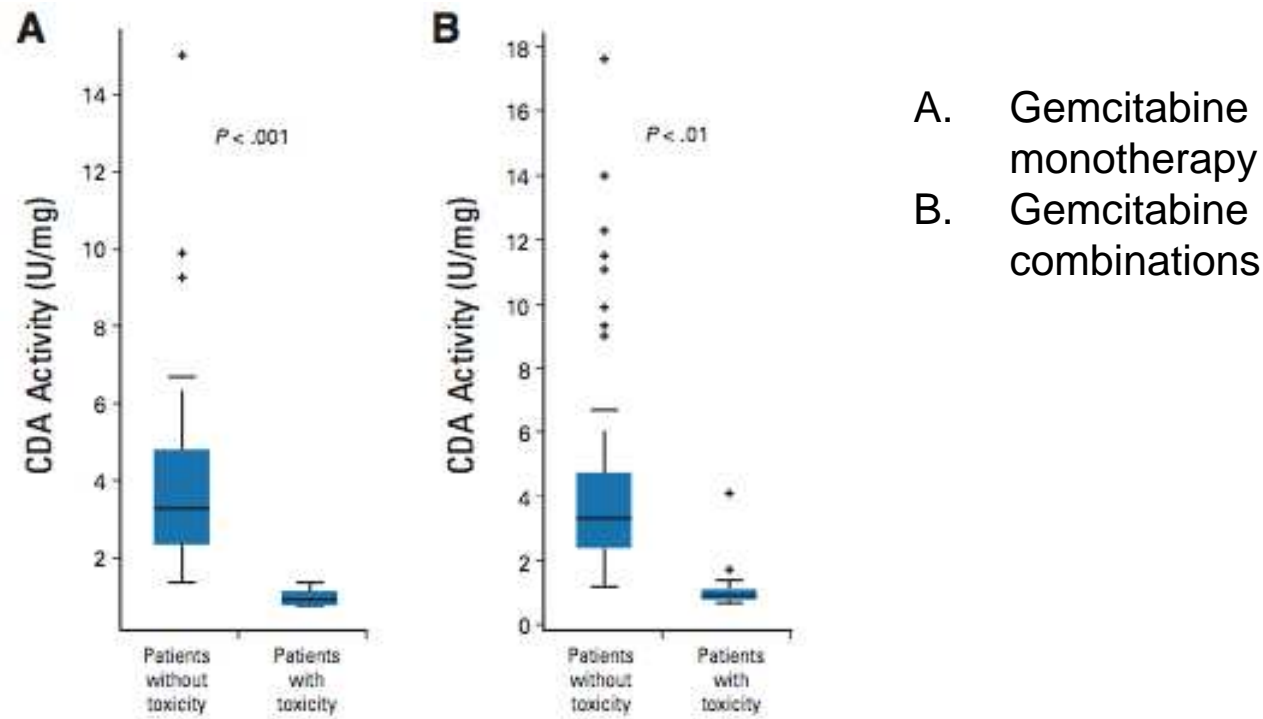
- The metabolic inactivation of gemcitabine is catalyzed by cytidine deaminase (CDA).
- CDA polymorphisms were analyzed in 65 chemo-naïve NSCLC pts treated with cisplatin + gemcitabine:
 - mean enzymatic activity in carriers of Lys/Gln and Gln/Gln genotypes was 1.7-fold higher compared to the wild-type CDA²⁷ Lys/Lys (P = 0.048)

CDA Lys ²⁷ Gln	Incidence	RR	MST	Gr 3-4 Neutropenia	Gr 3-4 Thrombopenia
Lys/Lys	38%	52%	17 m	48%	33%
Lys/Gln	47%	31%	14 m	10%	7%
Gln/Gln	15%	11%	4 m	22%	11%



Cytidine deaminase (CDA) activity in serum and severe toxicities with gemcitabine

- Gemcitabine is primarily detoxified by cytidine deaminase



→ CDA deficiency is associated with a maximum risk of developing early severe toxicities with gemcitabine

Pharmacogenomic analysis of the common carboplatin-paclitaxel arm in US-Japanese trials

- Genomic DNA was prospectively collected in three phase III trials in advanced NSCLC, each with a common arm of paclitaxel plus carboplatin.
- Population-based pharmacogenomic analysis of genotypic variants of CYP3A4, CYP3A5, CYP2C8, NR1I2-206, ABCB1, ERCC1, and ERCC2 was performed.
- The CYP3A isozymes account for 45% to 60% of paclitaxel metabolism.
- An association was observed between occurrence of the CYP3A4*1B allele and PFS (P = .04)
(this association should be interpreted in the context that only African American patients harbored this allele)



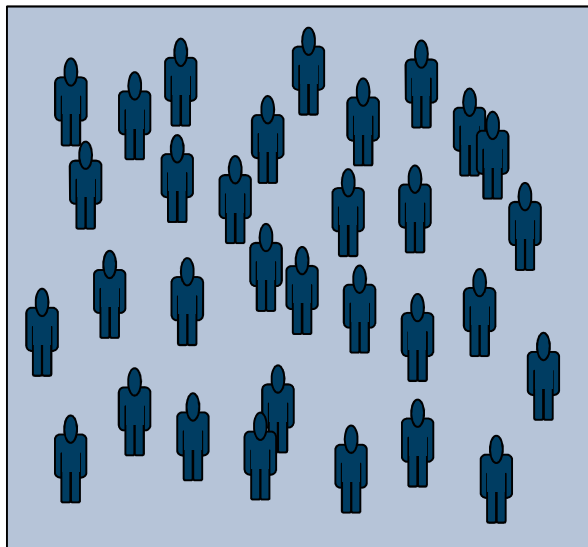
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	Pemetrexed	Non-Squamous	Exclusion non-benefiting pts
	Bevacizumab	Non-Squamous	Safety concerns in squamous
Molecular tumor biomarkers	EGFR-TKI	EGFR-mutation	Improved PFS
	Pemetrexed	Low TS expression	Selection of benefiting pts
	Gemcitabine	Low RRM1	Selection of benefiting pts
	Platinum	ERCC1, BRCA1, RAP80	Improved RR, PFS and/or OS
Patient genotype	Gemcitabine	CDA ²⁷ Lys/Lys	Improved OS(worse toxicity)
	Paclitaxel	CYP3A4 SNP	Improved PFS

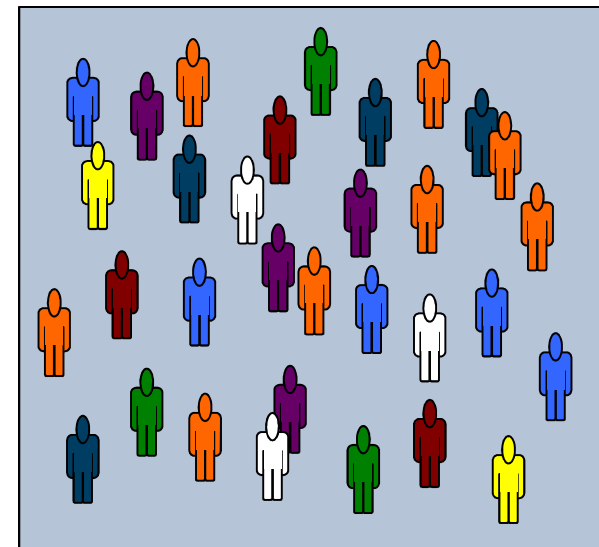
Data from adequately powered RCTs with prospective biomarker analysis



Personalized treatment of NSCLC



**“NSCLC is a
common cancer”**



**“NSCLC is a collection
of rare cancers”**

