Pasi A. Jänne, M.D., Ph.D. Lowe Center for Thoracic Oncology Dana Farber Cancer Institute

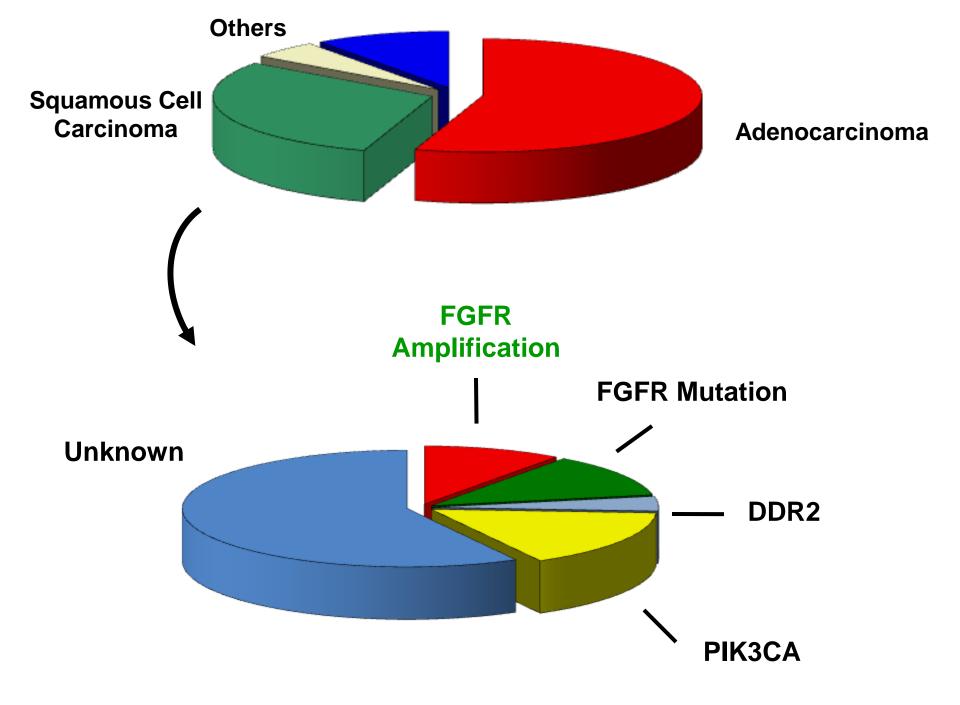




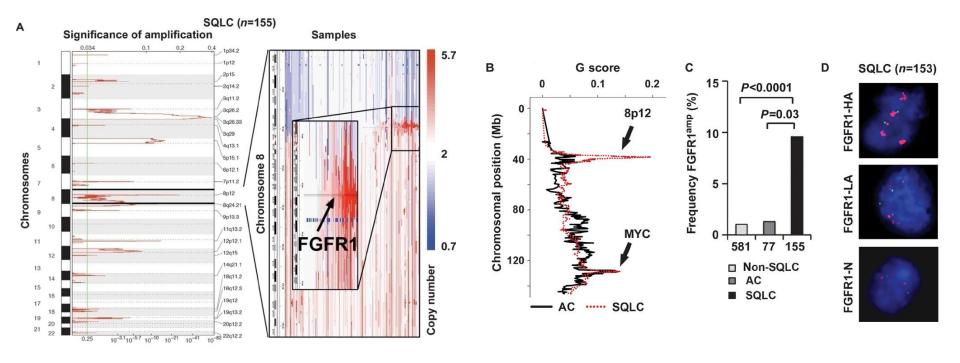


- Squamous Cell Lung Cancer
- New Oncogenes in adenocarcinoma
- Co-clinical trials to guide clinical drug development

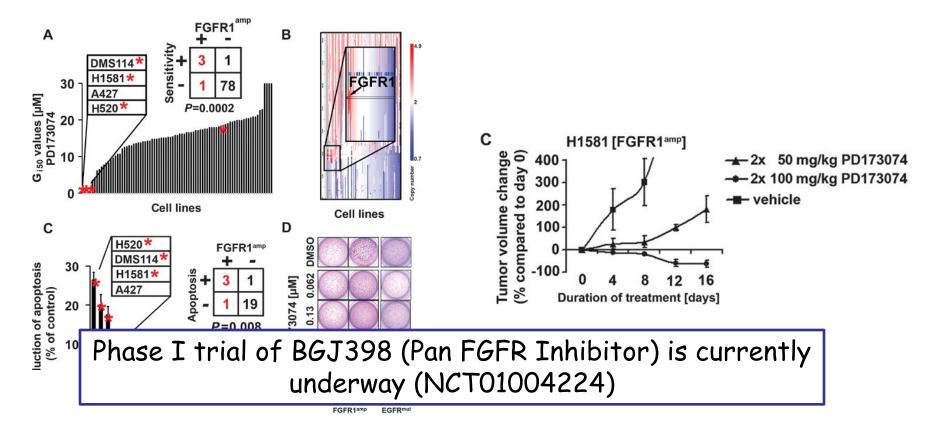
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FGFR1 Amplification in a Subset of Squamous Cell Cancers



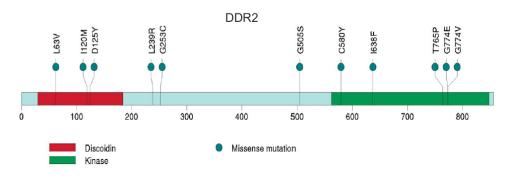
FGFR1 Inhibitor is Effective in FGFR1 Amplified Cells

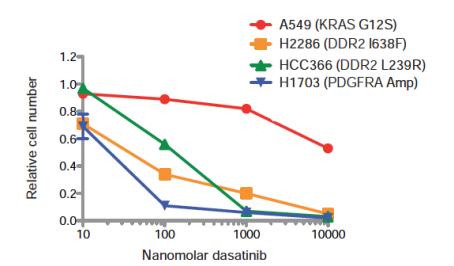


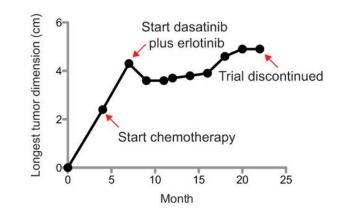
In Vitro

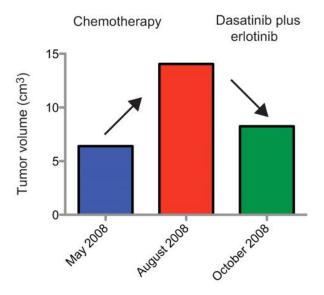
In Vivo

Sanger sequencing of the tyrosine kinome of lung SqCCs identifies recurrent mutations in DDR2





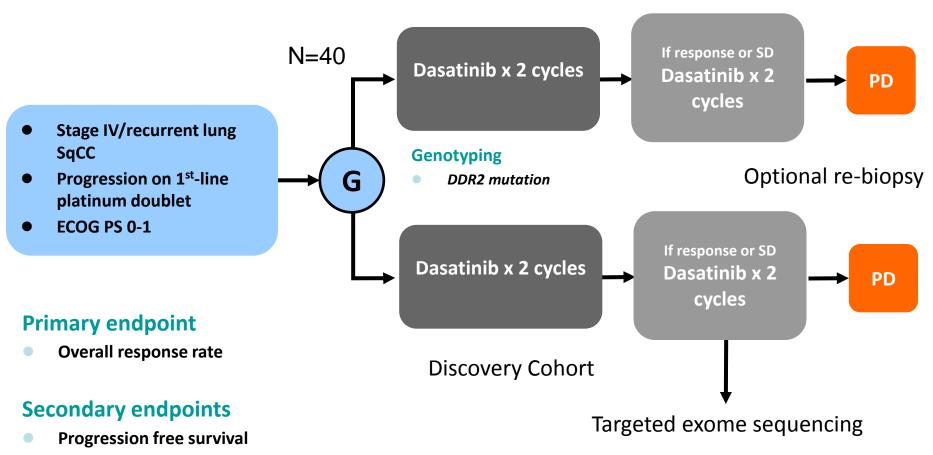




Hammerman et al. Cancer Discovery 2011

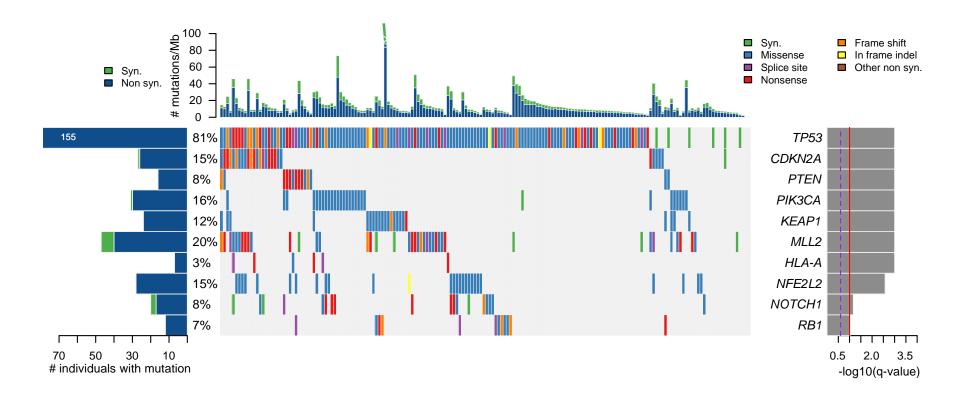
A phase II study of dasatinib in lung SqCC

Biomarker cohort



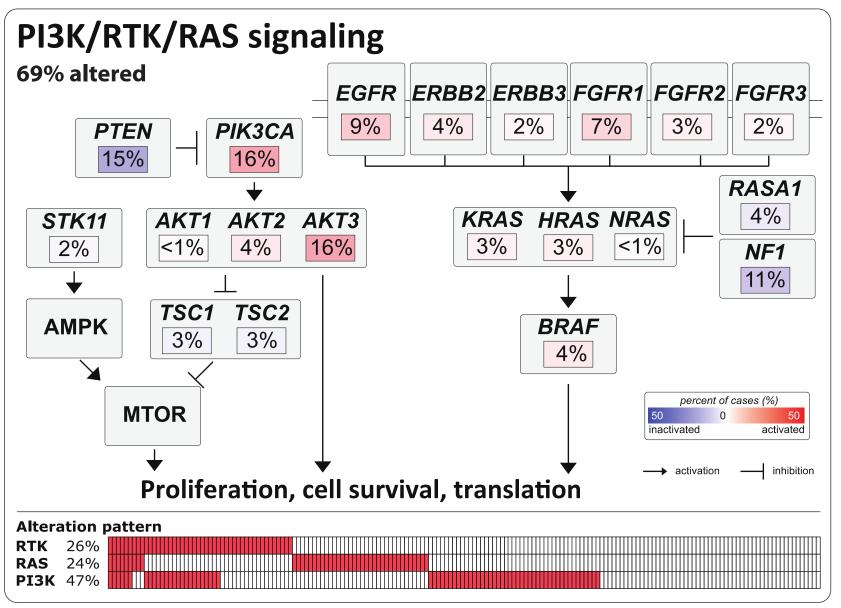
- Overall survival
- Safety
- DDR2 genotype subset analysis

Squamous Cell NSCLC - TCGA



TCGA (Hammerman) Nature. 2012 Sep 9.

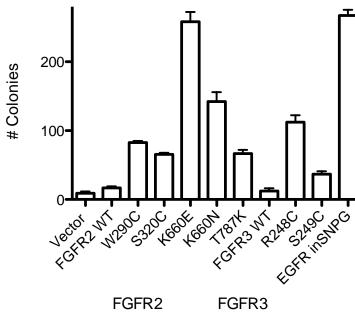
Revisiting the kinome by exome sequencing

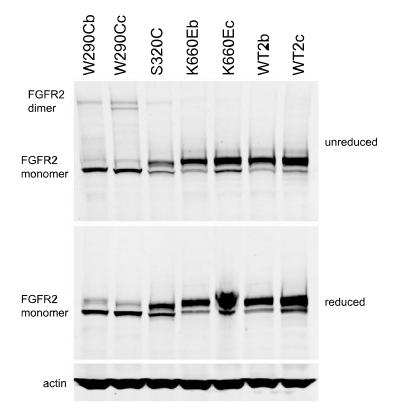


FGFR Mutations in TCGA lung squamous cancer

Extrac	ellular domain			Kinas	e domain	C-termir	nal tail
FGFR1 P25Q FGFR1 W471L FGFR1 R445W	FGFR3 FGFR3 FGFR3				K660E K660N G584W K717M	FGFR1 FGFR3 FGFR2 FGFR2	R623S T787K
FGFR2 R190G FGFR2 W290C	FGFR3	S249C		FGFR4	Q738K		N/JON
FGFR2 G302W FGFR2 S320C FGFR3 S435C	FGFR4	Q144E					
FGFR2 E471Q FGFR4 R434Q Note: Recurrent mutations at FGFR2 K660 (kinase domain) and FGFR3 aa 248-249 (extracellular domain).							

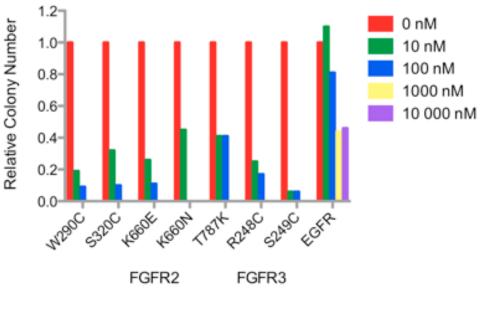
FGFR mutations are oncogenic





Peter Hammerman

FGFR-driven transformation is blocked by multiple FGFR kinase inhibitors



AP24534 (uM):	0	.01	.1	0	.01	.1	0	.01	.1	0	.01	.1	0	.01	.1	
FGFR2	-	-	_	_	_	-	-	-	-	-	-	-	=	-	-	
pFGFR	-						-									
FRS2	-	-	-	-		-	-	-	-		-	-	-	-		
pFRS2	-			111			11			-	111		-	111		
Erk 1/2	=	=	=	=	=	=	=	=	=	=	=	=	=	=	=	
pErk 1/2	-	4		-	-		-	-	-					-		
actin	-	-	-	-	-	-	-	-	-	-	-	_	-	-	-	

S320C

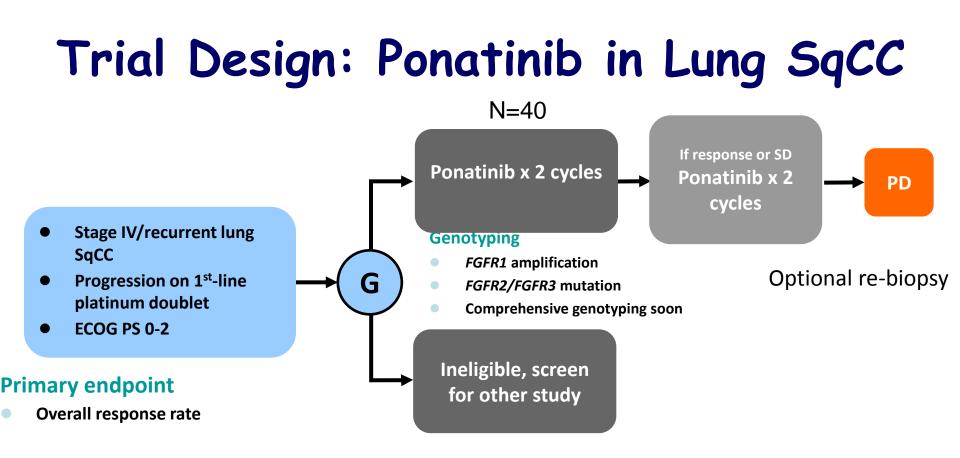
K660Eb

K660Ec

Ponatinib

BGJ398

Peter Hammerman



Secondary endpoints

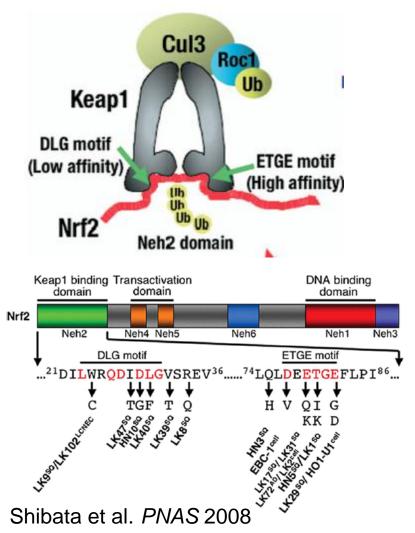
- Progression free survival
- Overall survival
- Safety
- FGFR genotype subset analysis

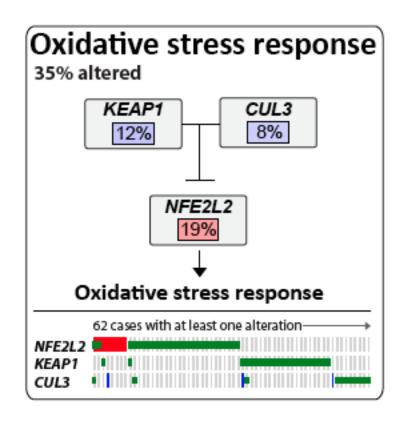
Correlatives

- Primary xenografts for shRNA and inhibitor profiling
- Tumor IHC (p-FRS2, p-FGFR), FGFR1 expression
- Comprehensive genomics for resistance

NFE2L2/KEAP1/CUL3

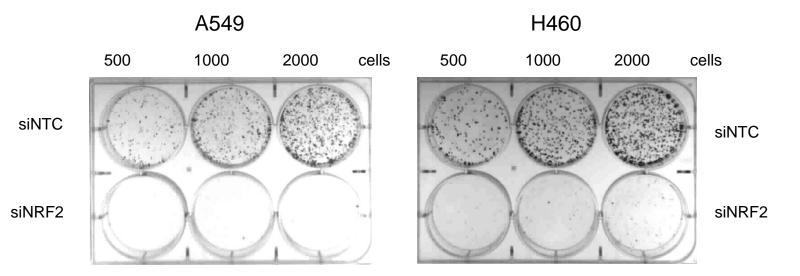
- Mutations in KEAP1 are lof (frequent LOH of second allele)
- Mutations in NRF2 cluster in DLG and ETGE motif -> prevent KEAP1 interaction -> results in NRF2 stabilization and nuclear entry



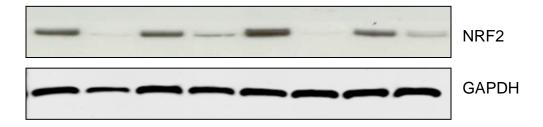


In head and neck cancer mutations in *NFE2L2/KEAP1/CUL3* are mutually exclusive with HPV+ (p<0.02); *TP53* (p=0), *CDKN2A* (p<0.001)

2 KEAP1 mutant lung cancer lines are sensitive to siRNA targeting NFE2L2

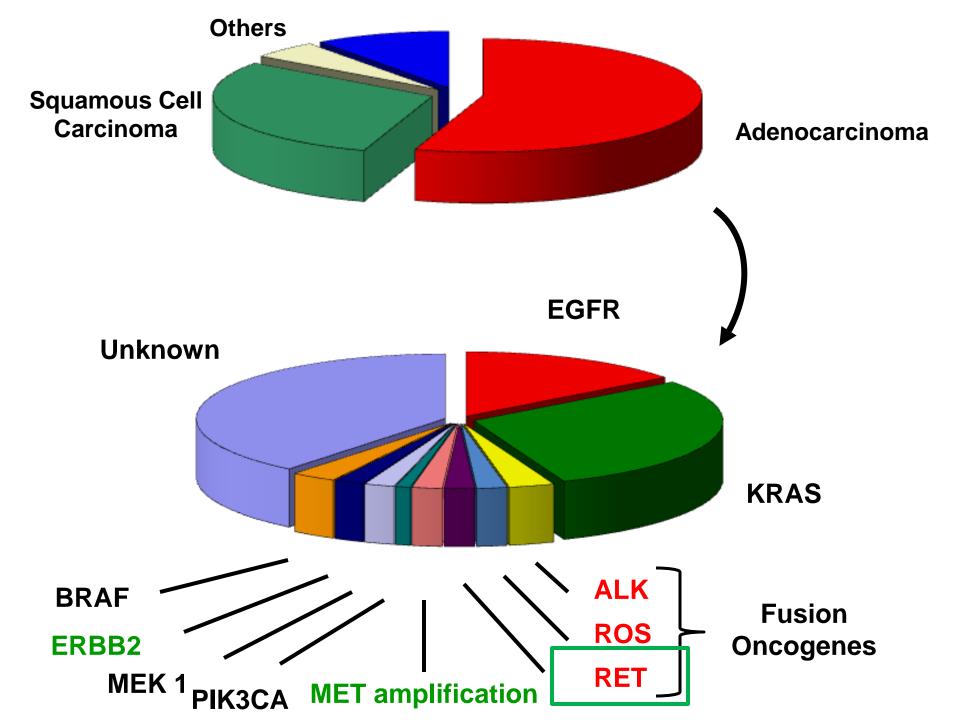


	A5	49		H460				
siNTC-	siNRF2-	siNTC-	siNRF2-	siNTC-	siNRF2-	siNTC-	siNRF2-	
D3	D3	D7	D7	D3	D3	D7	D7	

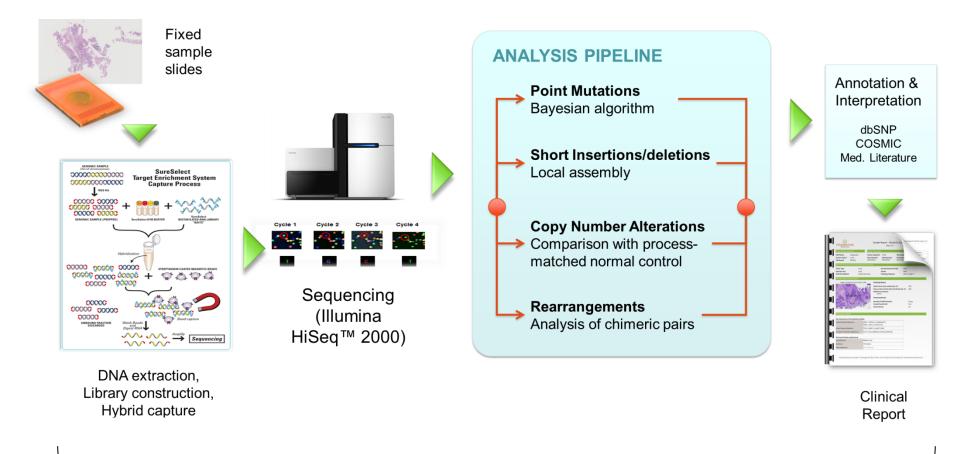


Mohamed Abazeed

- Squamous Cell Lung Cancer
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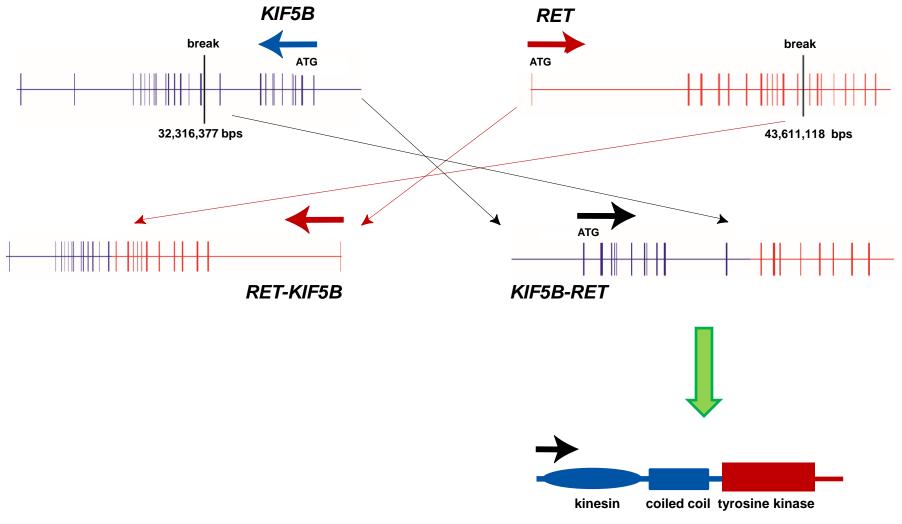


Foundation Medicine Cancer Genotyping Platform



< 21 days

Identification of a pericentric inversion on chromosome 10 leading to KIF5B-RET

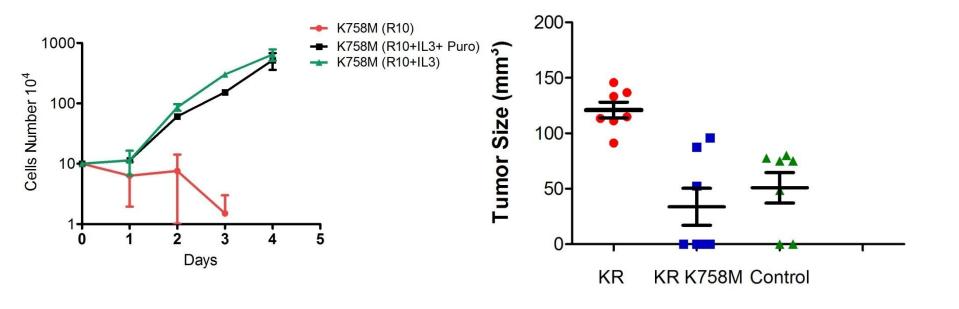


KIF5B (exons 1-15)

RET (exons 12-20)

Lipson, Capelletti et al. Nature Medicine 2012

KIF5B-RET is oncogenic in vitro and in vivo and requires kinase activity



Ba/F3 cells

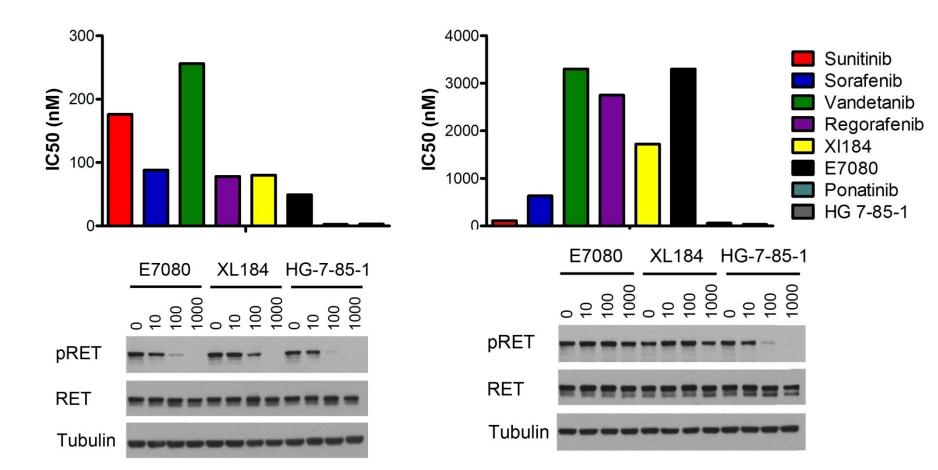
BEAS2B cells

Marzia Capelletti

Efficacy of kinase inhibitors against KIF5B-RET and KIF5B-RET V804M Ba/F3 cells

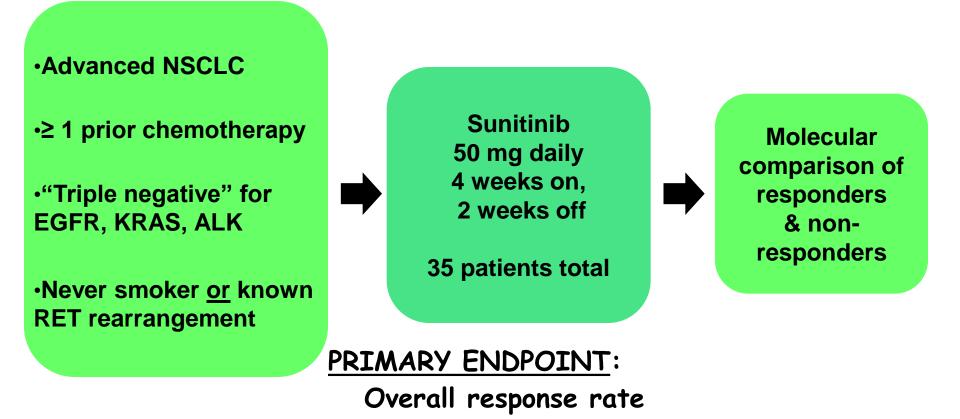
KIF5B-RET

KIF5B-RET V804M



Marzia Capelletti

Sunitinib in Never-Smokers with NSCLC



PI: Geoff Oxnard

SECONDARY ENDPOINT:

Activity in subset with RET rearrangements

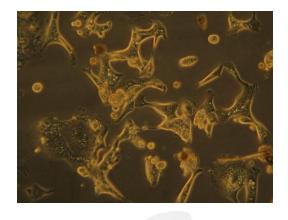
- Squamous Cell Lung Cancer
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Co-Clinical Trial

- Perform analogous study in model system at the same time as human clinical trial
 - Genetically engineered mouse models that can recapitulate human cancer
- Findings can inform development and/or interpretation of findings from human trial

Preclinical model systems

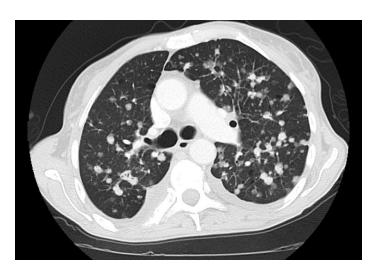
NSCLC patients





Guide clinical drug development

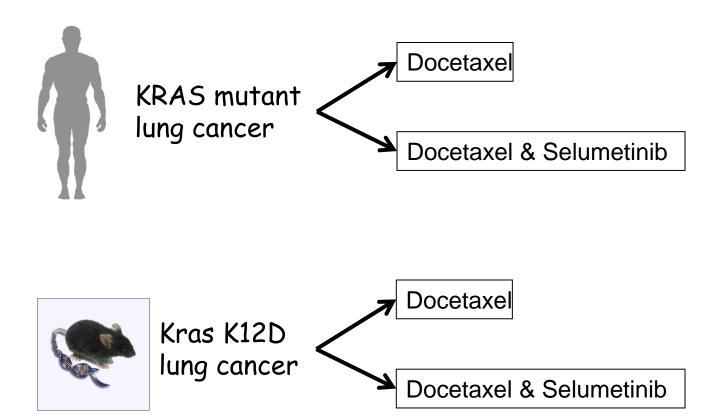
> Inform preclinical studies



Prioritize clinical therapies
Identify resistance mechanisms
Test novel combination therapies

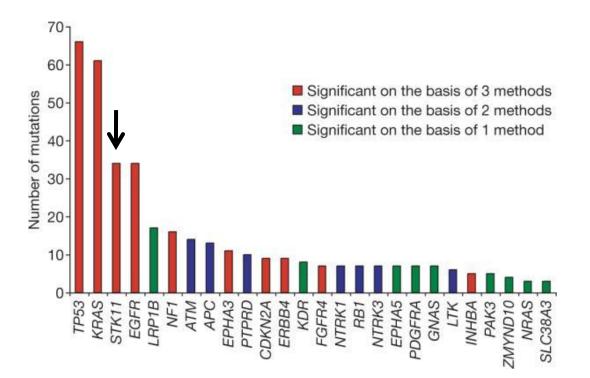
Evaluate targeted therapies
Determine biomarker modulation
Study clinical drug resistance

Co-clinical trials: mouse studies to mimic ongoing human clinical studies



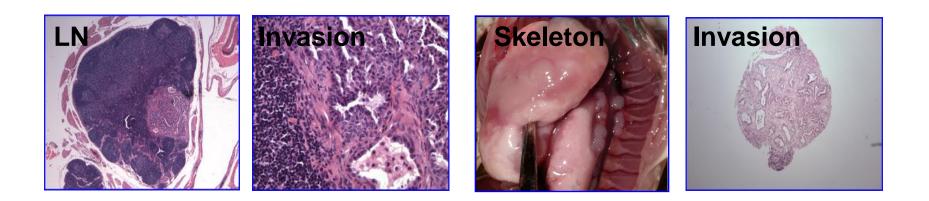
LKB1 in NSCLC

Common in NSCLC Associated with KRAS (~ 30%) mutations; not with EGFR mutations



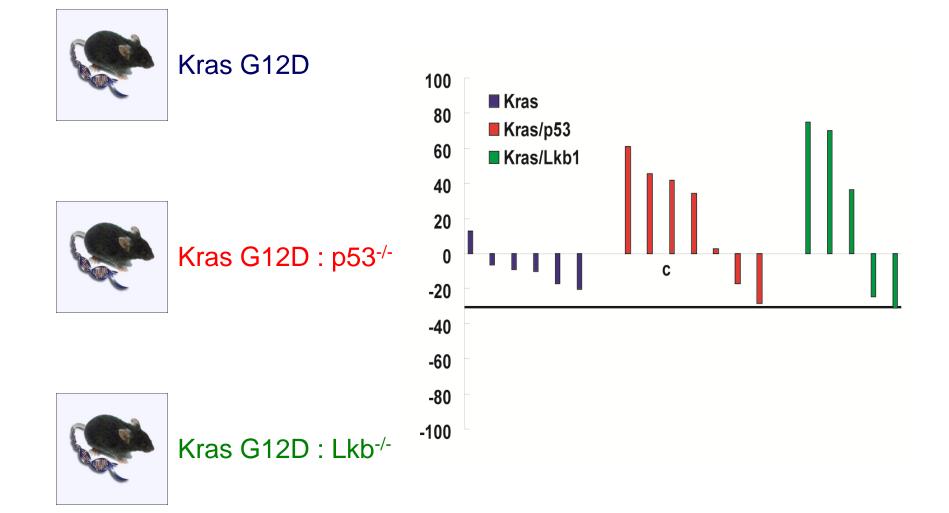
Kras G12D/Lkb1^{-/-} mice have a more aggressive phenotype than *Kras* G12D alone

Genotype	Survival	Histology	Metastases
Kras G12D	24 weeks	100% Adeno ca	0% (0/19)
LKb1-/-	> 40 weeks	No tumors	N/A
Kras G12D/Lkb1-/-	9 weeks	56% mixed	61% (27/44)
<i>Kras</i> G12D/ <i>p53</i> -/-	14 weeks	100% Adeno ca	44% (4/9)

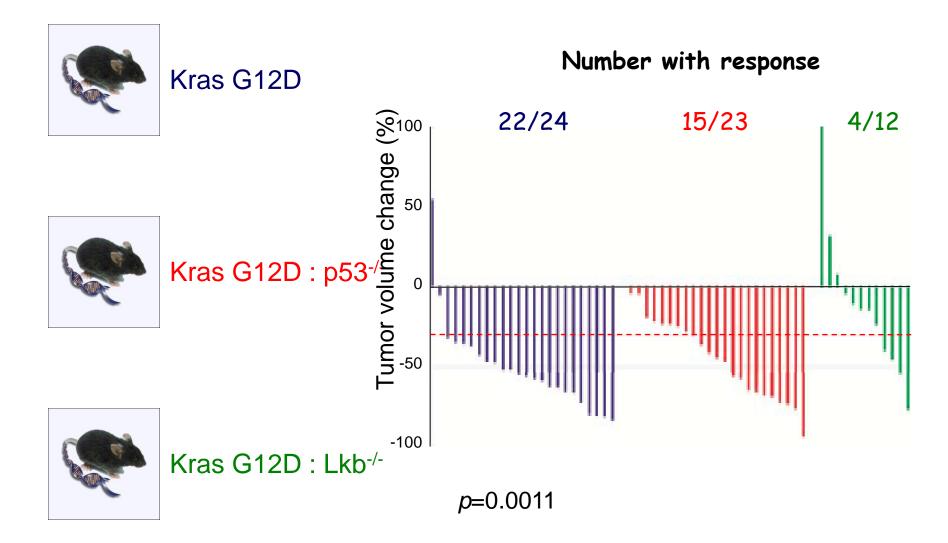


Li et al. Nature 2007

Impact of genotype on treatment with selumetinib

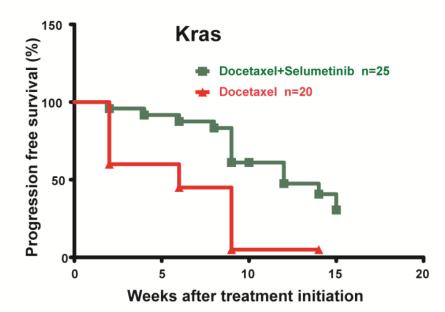


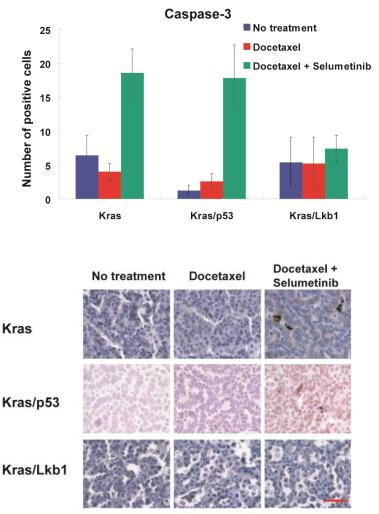
Impact of genotype on treatment with selumetinib/docetaxel



Chen et al. Nature 2012

Improved PFS with Docetaxel/Selumetinib compared with docetaxel in *Kras* G12D murine model of NSCLC

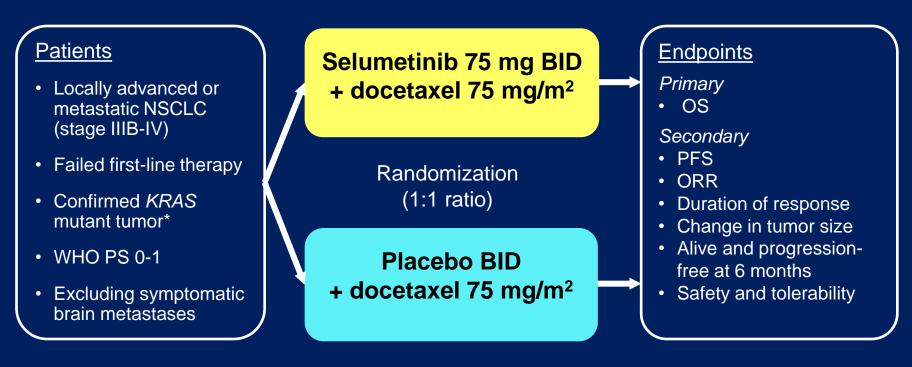




Caspase-3

Chen et al. Nature 2012

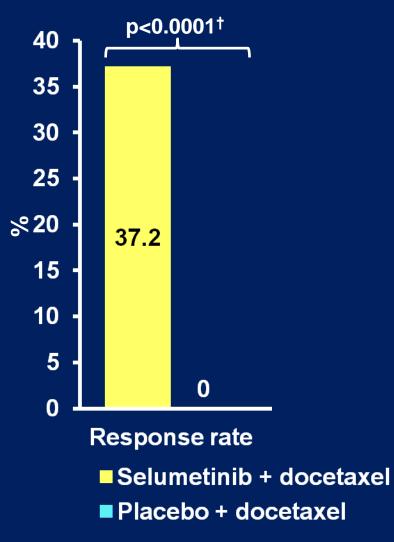
Phase II, double-blind, randomised, placebocontrolled, multi-centre trial; NCT00890825



- Docetaxel was administered every 21 days for a maximum of 6 cycles followed by SEL/PBO
- Following completion of patient enrollment, the primary endpoint was changed from PFS to OS, without changing the sample size[‡]
 - OS analysis was planned for after approximately 58 events; HR 0.57, 80% power assuming a 1-sided 10% significance level

*Mutation status determined either by central laboratory (Esoterix, ARMS) or an approved local laboratory [‡]To allow decisions to be made based on OS data without breaking study blinding at the earlier endpoint of PFS Jänne et al. ASCO 2012

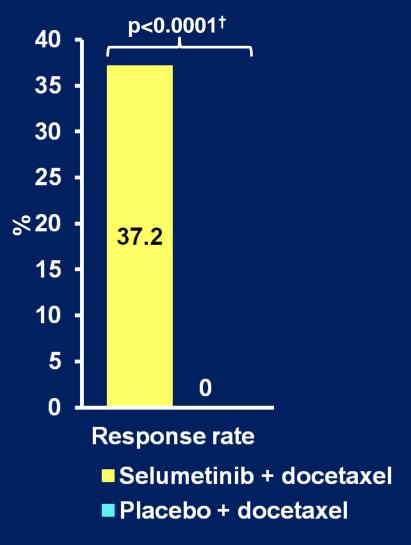
Response Rate and Alive and Progression Free at 6 months



†Fisher's exact 2-sided mid p value ‡1-sided p value

CR, complete response; PR, partial response; SD, stable disease PD, progressive disease; DoR, duration of response; APF6, alive and progression-free at 6 months

Response Rate and Alive and Progression Free at 6 months



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	Selumetinib + docetaxel N=44	Placebo + docetaxel N=43
Best objective re	esponse (RECIST	1.0), number (%)
CR	0	0
PR	16 (37.2)*	O§
SD ≥6 weeks	19 (44.2)	20 (50.0)
PD	8 (18.6)	18 (45.0)
Not evaluable	0	2 (5.0)
Median DoR, days	182	-

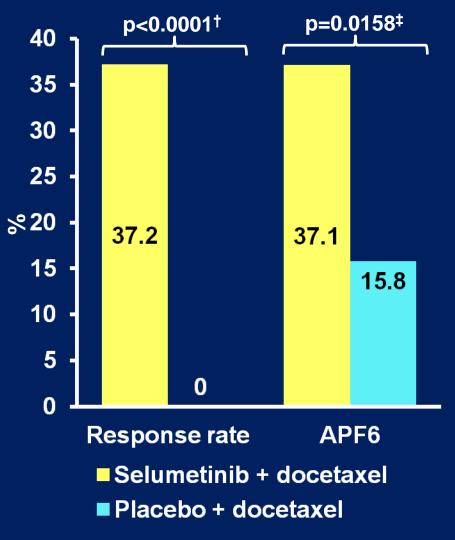
†Fisher's exact 2-sided mid p value

‡1-sided p value

*11 confirmed, 5 unconfirmed

[§]One patient was classed as non-evaluable due to non-evaluable non-target lesions and would have had a partial response according to RECIST 1.1 criteria

Response Rate and Alive and Progression Free at 6 months



CR, complete response; PR, partial response; SD, stable disease PD, progressive disease; DoR, duration of response; APF6, alive and progression-free at 6 months

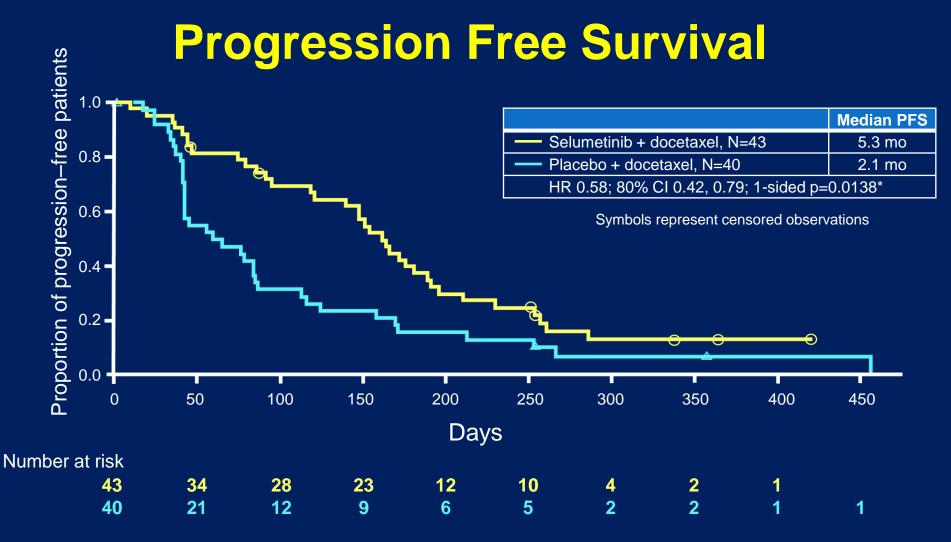
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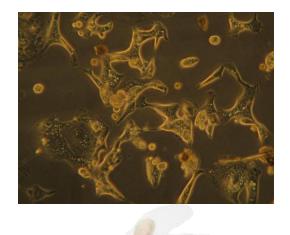


- There was a statistically and clinically significant improvement in PFS
 - 71/83 events (85.5%): selumetinib + docetaxel 35/43, placebo + docetaxel 36/40

*Analysis was performed using a Cox proportional hazards model; The model allows for the effect of treatment and included terms for WHO PS, gender, histology and smoking status.

Preclinical model systems

NSCLC patients



Guide clinical drug development





Efficacy of docetaxel/selumetinib
Impact of *Lkb1^{-/-}* on drug
treatment

•Efficacy of docetaxel/selumetinib
•? Impact of *LKB1*^{-/-}

Develop strategies to evaluate *LKB^{/-}* from human tumors Evaluate retrospectively or prospectively

Co-Clinical Trial

- Perform analogous study in model system at the same time as human clinical trial
- Findings can inform development and/or interpretation of findings from human trial
 - Predict outcome of human trials
 - Use model to prioritize most effective therapeutic strategy to study in humans
 - Biomarker discovery
 - Validate biomarker in human clinical trials

- Squamous Cell Lung Cancer
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