

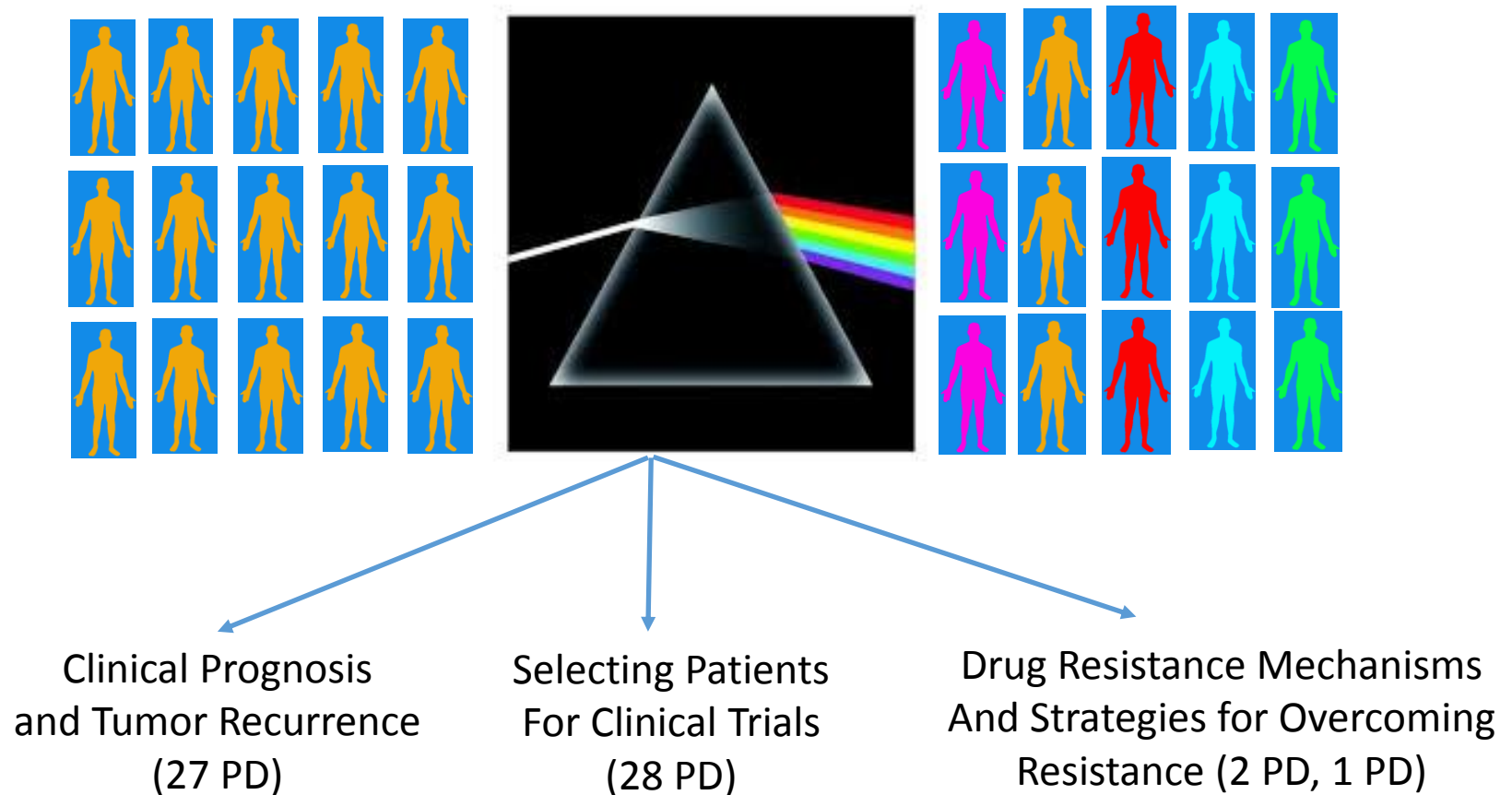
ESMO Asia 2015 Poster Discussion Session

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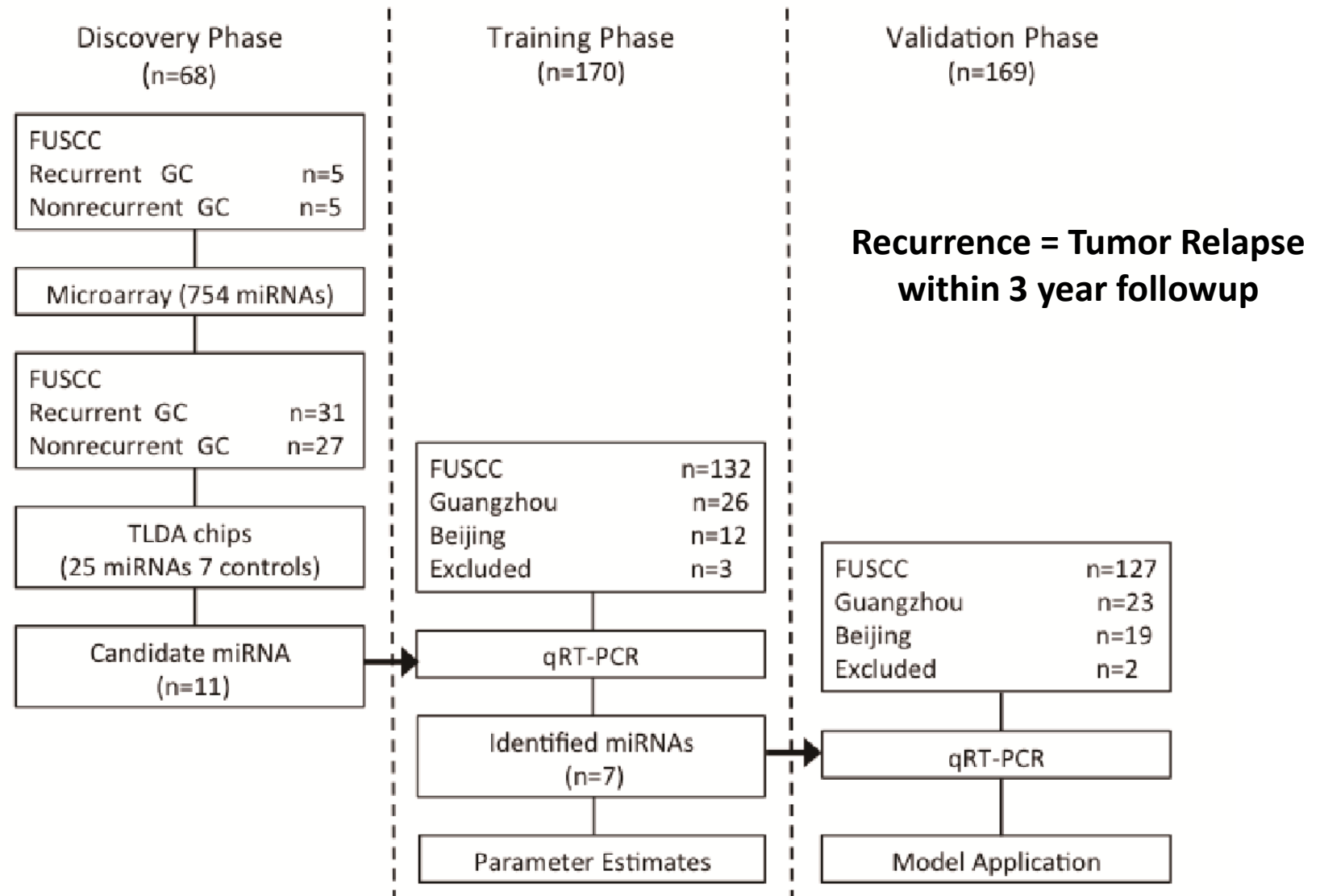
Overall Theme : Molecular Stratification of Patients



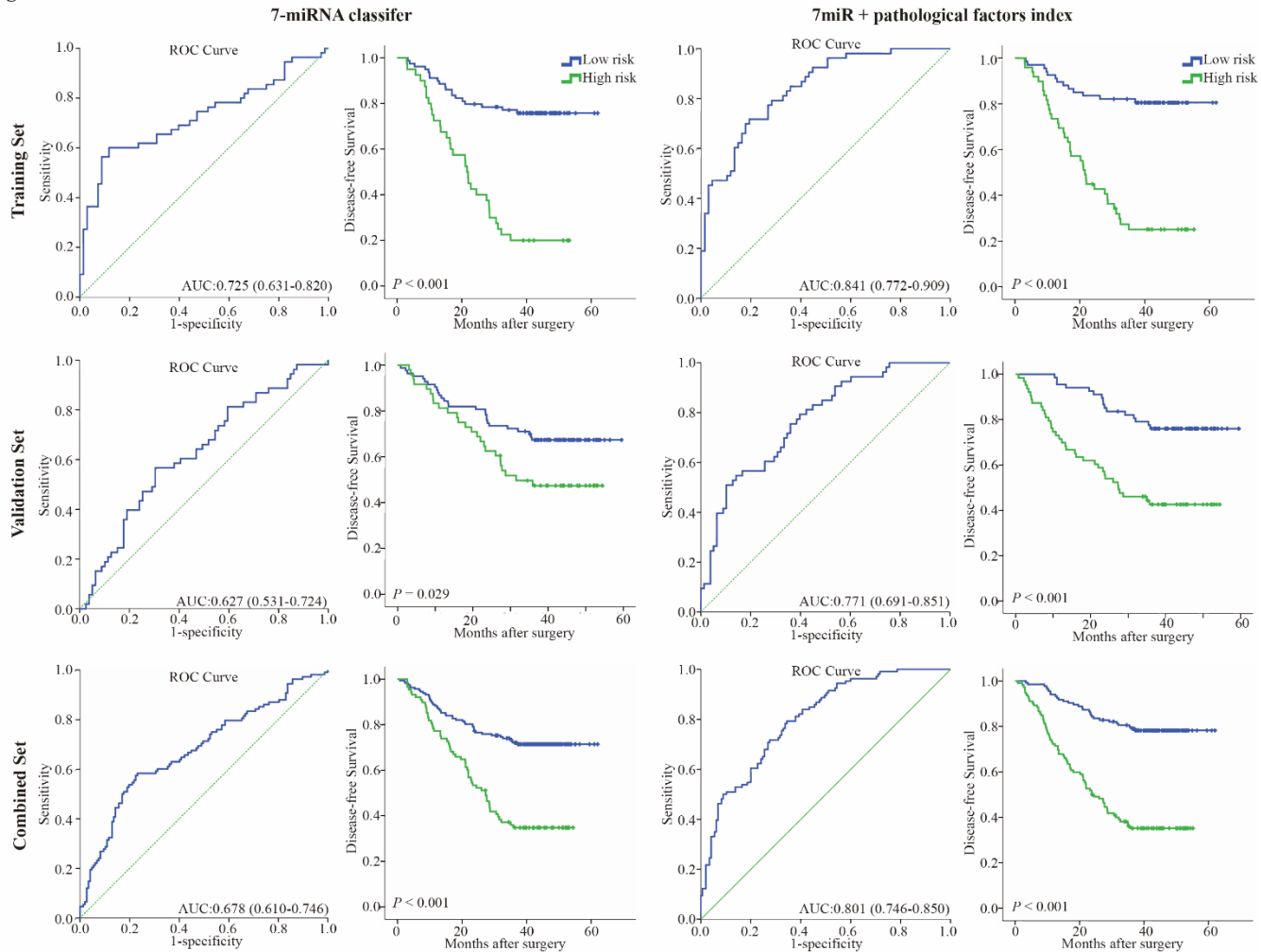
Plasma miRNA-based signatures to predict 3-year postoperative recurrence risk for patients with stage II and III Gastric cancer (PD27)

- Gastric cancer (GC) is a heterogeneous disease with large variability in disease outcome for patients with similar clinical features.
- Current TNM staging is the “gold standard” for predicting GC outcomes, but has limitations especially in stage II and III patients.
- Circulating miRNAs have been suggested as potential biomarkers for cancer diagnosis and prognosis
- Most current circulating miRNA studies in GC have focused on diagnosis, with only a few evaluating prognosis or recurrence. There is still no circulating miRNA panel for accurate prediction of GC recurrence or prognosis

Study Design (Total 407 patients with D2 Resection)



Results



The authors identified a **7 miRNA classifier** and 7miR+pathological factors that provided high predictive accuracy on GC recurrence.

miRNA stratified “High-risk” patients showed significantly shorter disease-free survival (DFS) and overall survival (OS).

- Strengths

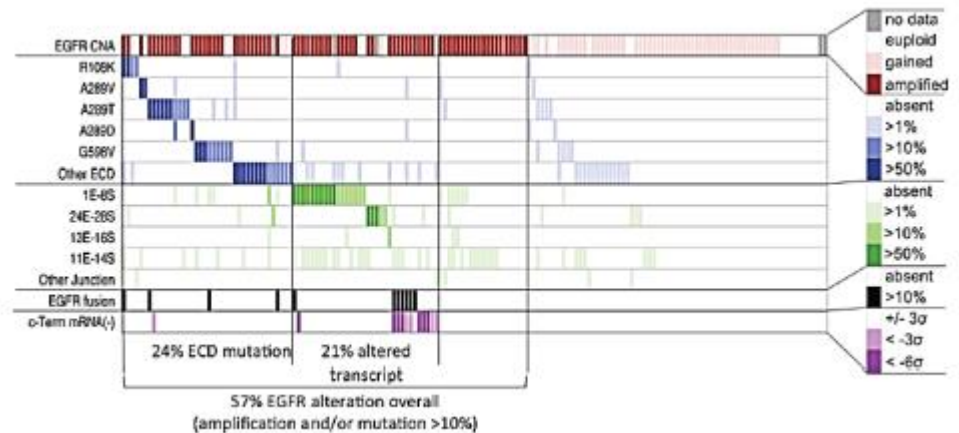
- Multi-centre Study involving a fairly large cohort of GC patients
- Circulating miRNAs represent an attractive platform, due to ease of accessibility
- Prognostic separation appears to hold even for Stage IIA patients, raising implications for treating patients with adjuvant chemotherapy

- Limitations

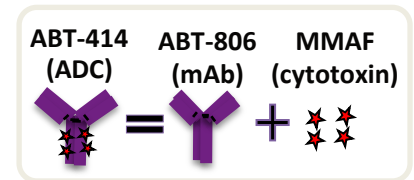
- Little details regarding origin or identity of miRNAs
- Exact thresholds for defining “high risk” and “low risk” are not described
- Ability to stratify Western GC populations and impact of chemotherapy is not clear
- These promising results should be validated in additional cohorts

Identifying the Correct Patient Population for ABT-414: Biomarker Assays for Epidermal Growth Factor Receptor in Patients with Glioblastoma (PD28)

- *EGFR* alterations are common in glioblastoma (mutation, amplification, expression)

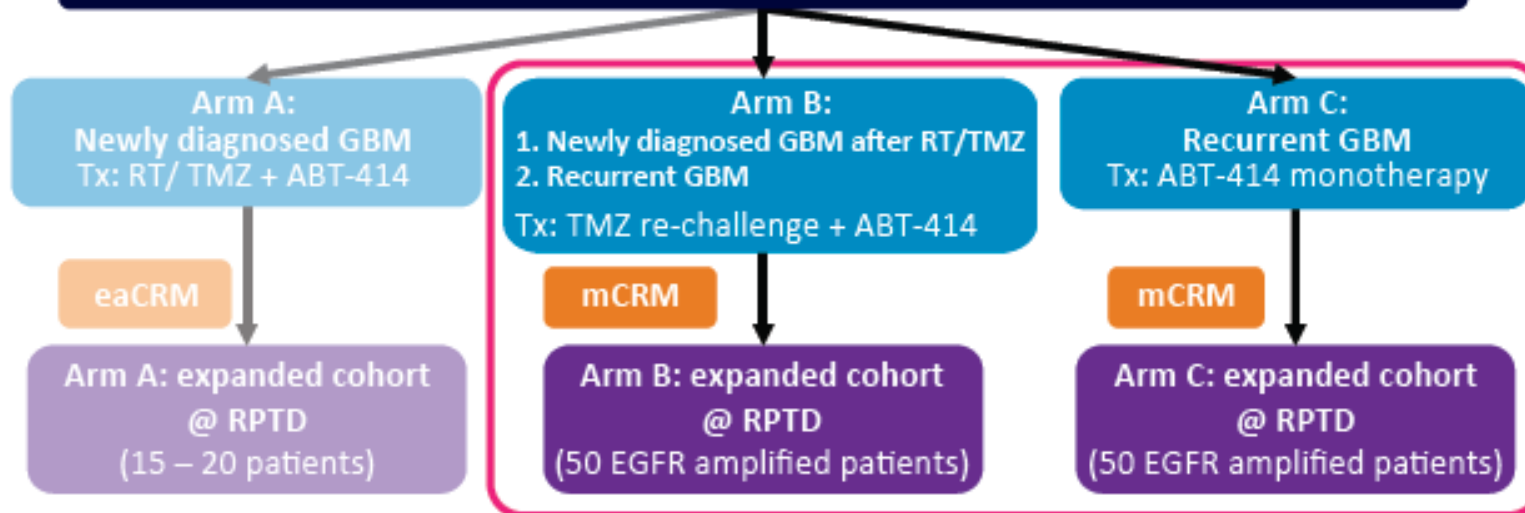


- ABT-414 is an antibody-drug conjugate that targets activated EGFR when EGFR is amplified (including EGFRvIII ECD mutation)

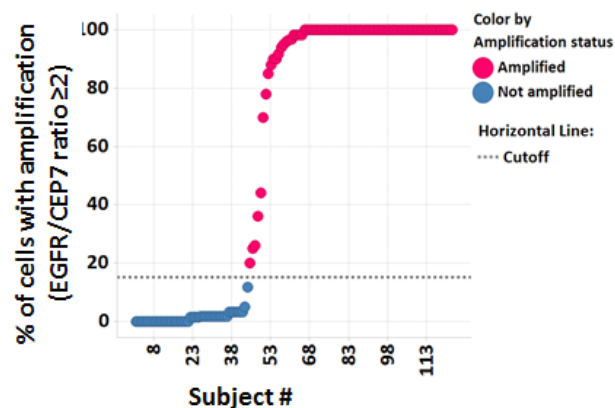


- Phase I trial M12-356 : Phase I dose escalation study, including efforts to identify patient population most likely to respond to ABT-414

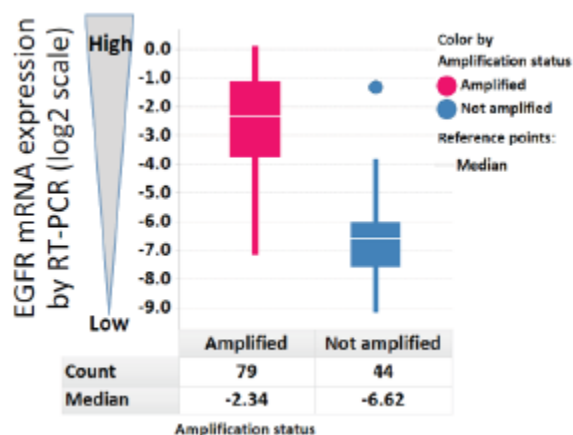
Phase 1b: Safety and PK of ABT-414 for patients with GBM



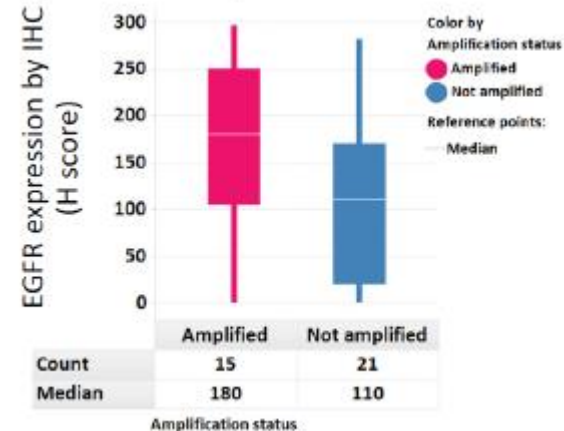
EGFR copy number (FISH)



EGFR copy number vs mRNA (RT-PCR)

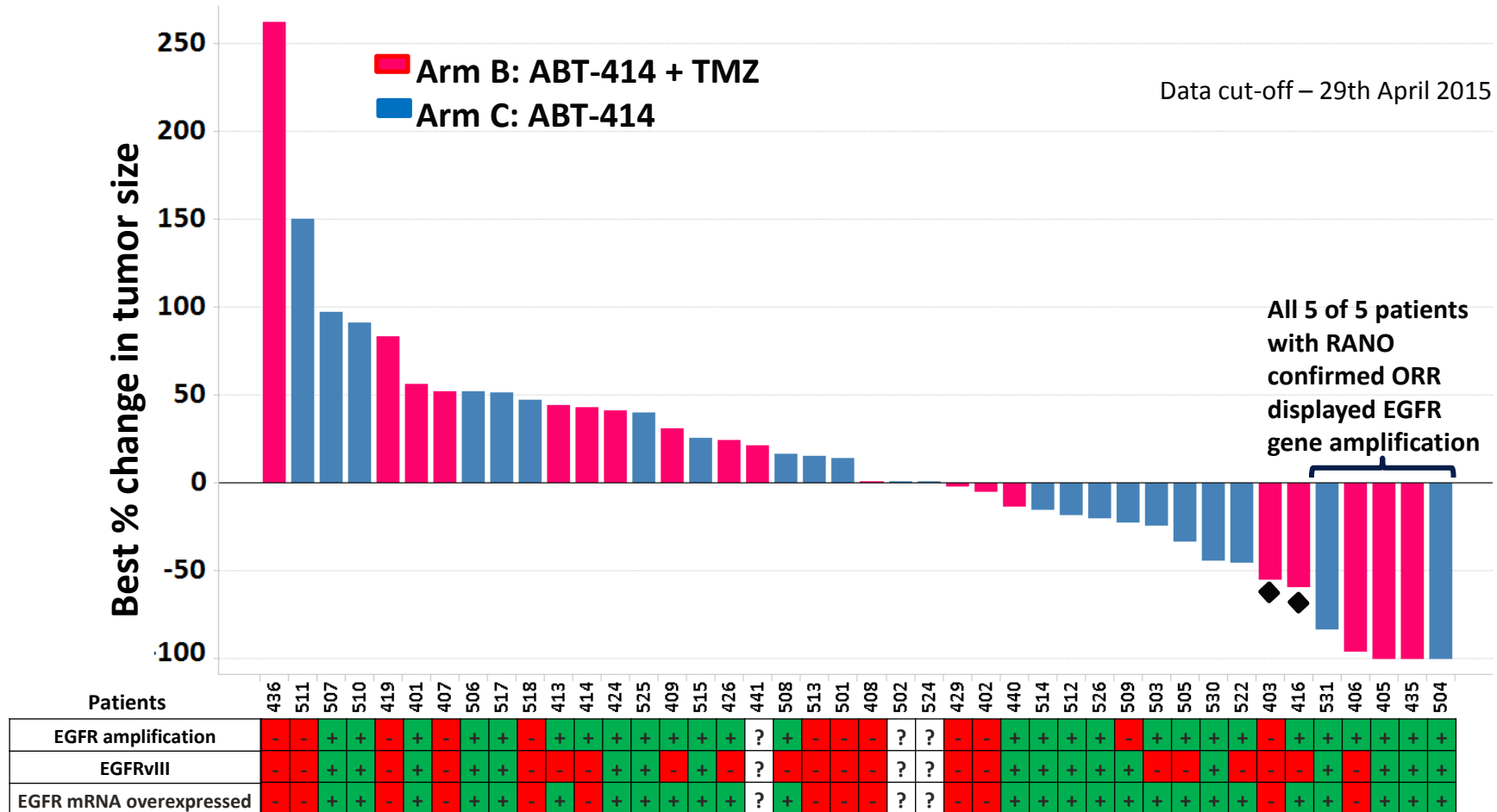


EGFR copy number vs Protein (IHC)



Response of ABT-414-treated Recurrent GBM patients

Only EGFR gene amplification identified all patients with RANO response



◆ Patient responses were not confirmed upon follow up scan.

- Strengths

- Phase I study involving a novel anti-EGFR/drug conjugate in a malignancy where *EGFR* alterations are frequent
- Assessment of EGFR status at multiple levels (Copy Number, mRNA, Protein)
- Responses were observed and associated with *EGFR* amplification, which appears binary
- *EGFR* amplification may be a selection criteria for enrolling patients into Phase II/III trials

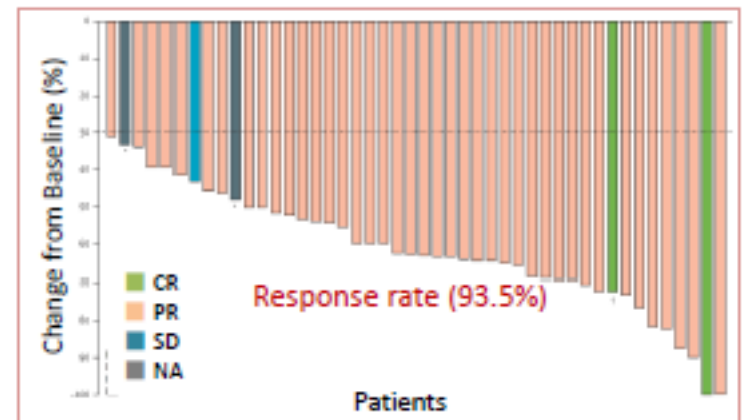
- Limitations

- Only *EGFR* was measured and other RTKs were not tested
- Formal statistical assessment of correlations between *EGFR* amplification and response were not reported
- Many *EGFR* amplified patients did not respond (22/27), suggesting the presence of additional predictive factors

Crizotinib could overcome acquired resistance to alectinib caused by HGF autocrine in ALK rearranged non-small cell lung cancer (PD2)

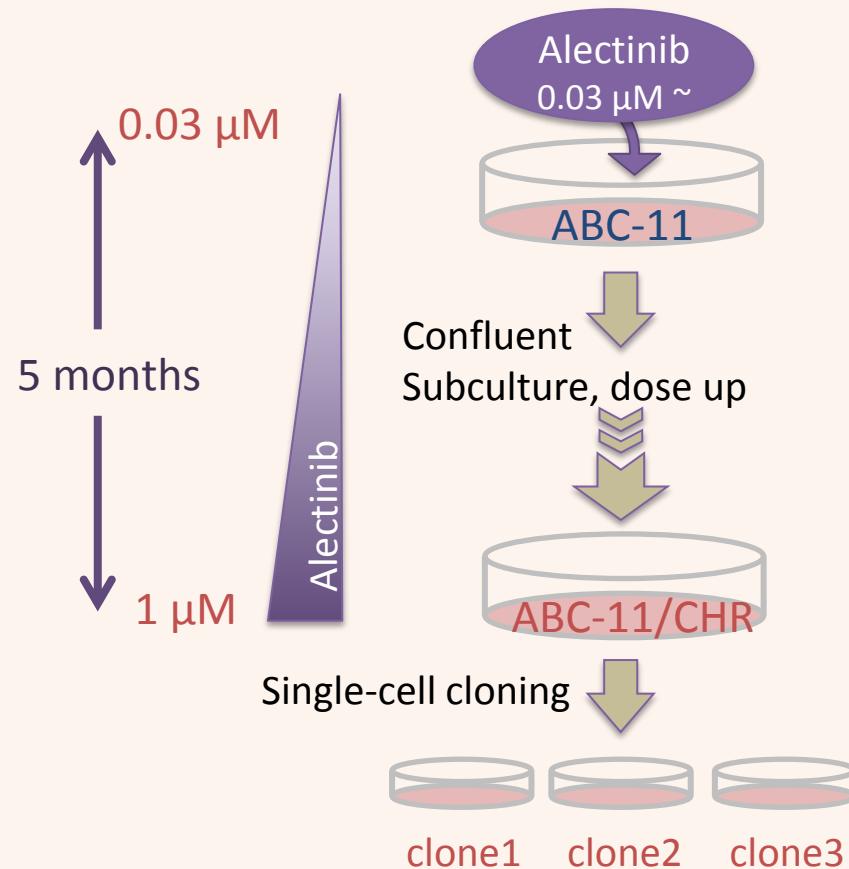
- ALK rearrangements are a major genetic driver in certain subtypes of non-small cell lung cancer (NSCLC)
- Crizotinib, which targets ALK, MET, and ROS1, is an effective therapy for ALK-positive NSCLC, but resistance can develop
- Alectinib is a new-generation selective ALK-TKI that can partially overcome acquired resistance to crizotinib (Cancer Cell 19, 2011: 679-90)
- Phase II study of alectinib demonstrated a 93.5% response rate (Lancet Oncol 14, 2013: 590-98);. However, acquired resistance is also a limitation

Waterfall plot of the best percentage change in target lesions from baseline based on Independent Review Facility assessment (N=46).



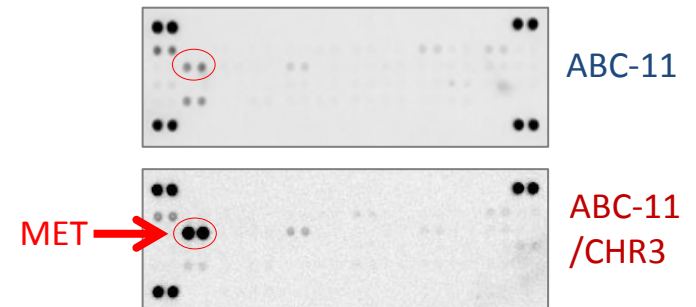
Preclinical Studies : Alectinib-resistance *in vitro* associated with increased MET activation

Establishment of alectinib-resistant cells (Stepwise manner)

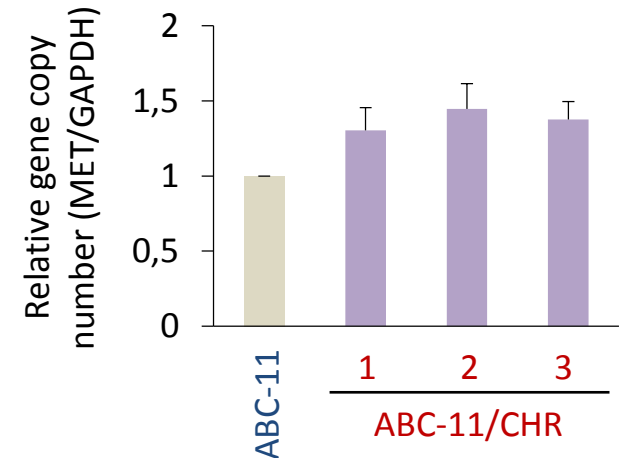


ABC-11: (EML4-ALK variant 3b E6;A20)

Survival signaling (p-RTK array)

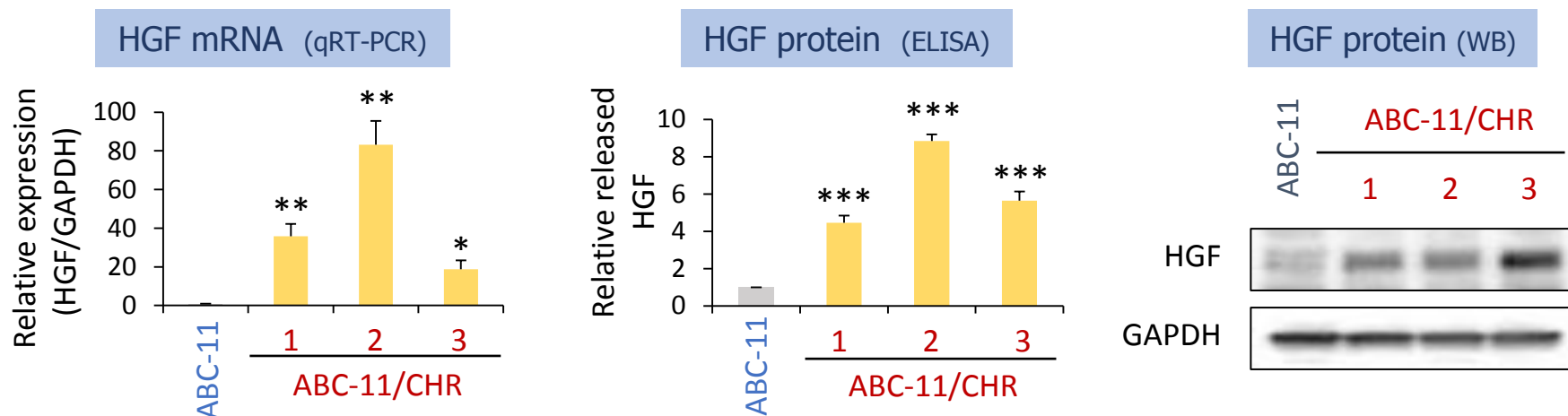


Genomic MET (qPCR)

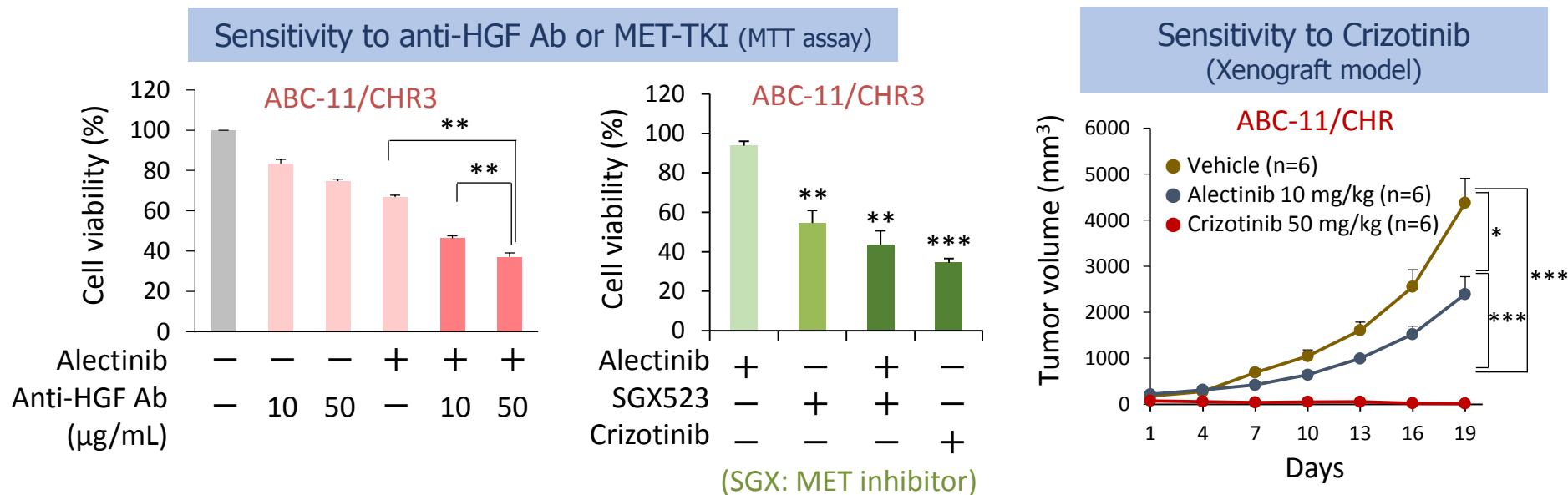


t test : not significance Bars : SE

HGF mRNA and protein are overexpressed in ABC-11/CHR

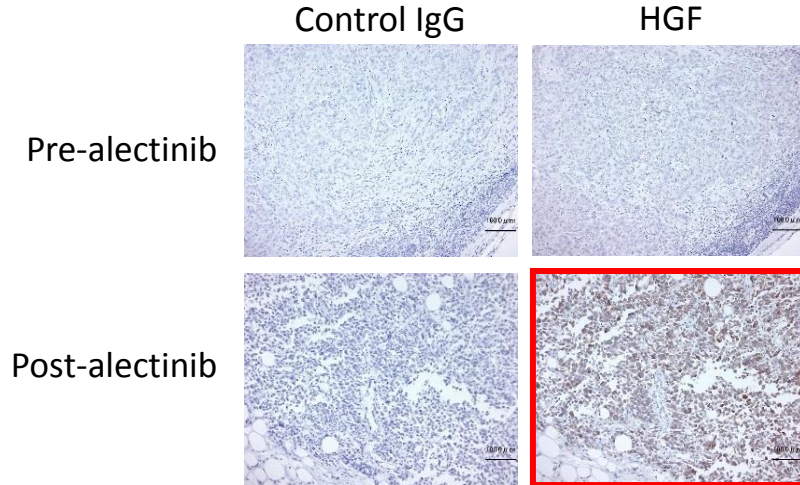


Inhibition of HGF/MET and ALK was effective on ABC-11/CHR

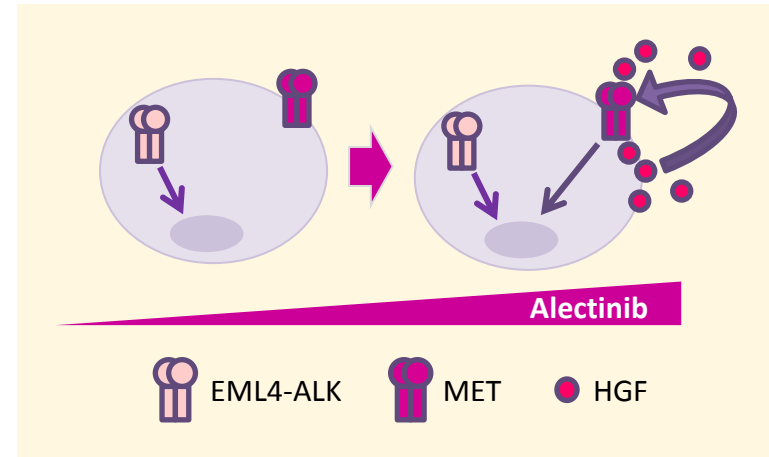


t test : *** $p < 0.001$ ** $p < 0.01$ * $p < 0.05$ Bars: SE

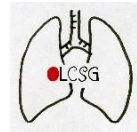
Expression of HGF in an alectinib-refractory patient (IHC)



Summary Alectinib-resistant mechanism



Efficacy of crizotinib in alectinib-refractory patients in NSCLC harboring EML4-ALK; phaseII trial (OLCSG1405)



Alectinib-refractory patients (n=9)

UMIN 000015984

EML4-ALK +
IIIB/IV NSCLC
Age ≥ 20
ECOG PS 0-2



Crizotinib 250mg
Oral twice per day
Until PD

Primary endpoint: objective response rate

Secondary endpoint: PFS, OS, AE, QOL

Expression of HGF, MET, EML4-ALK ... using re-biopsy samples

- Strengths

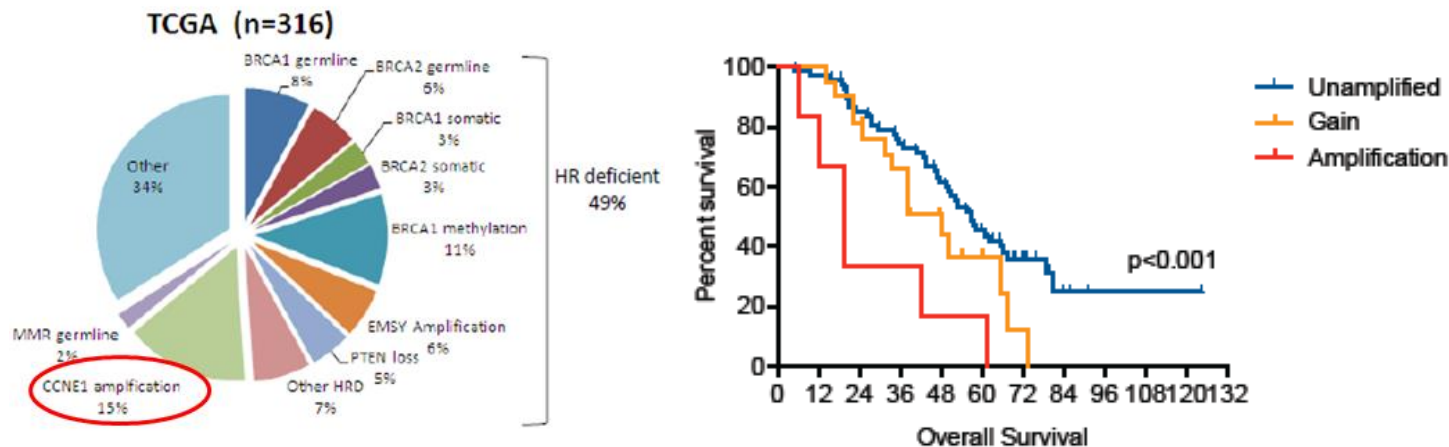
- Studying resistance mechanisms *in vitro* can provide powerful insights into similar *in vivo* mechanisms
- One of the few studies investigating resistance mechanisms for alectinib, with supporting data from human samples
- Identified HGF upregulation and MET activation as a resistance mechanism
- HGF blockade or MET inhibition via crizotinib may have potential for overcoming alectinib resistance

- Limitations

- Contribution of HGF upregulation vs other mechanisms (eg ALK mutations) remains to be established
- May not be applicable to crizotinib-resistant patients
- Results are based on a single cell line

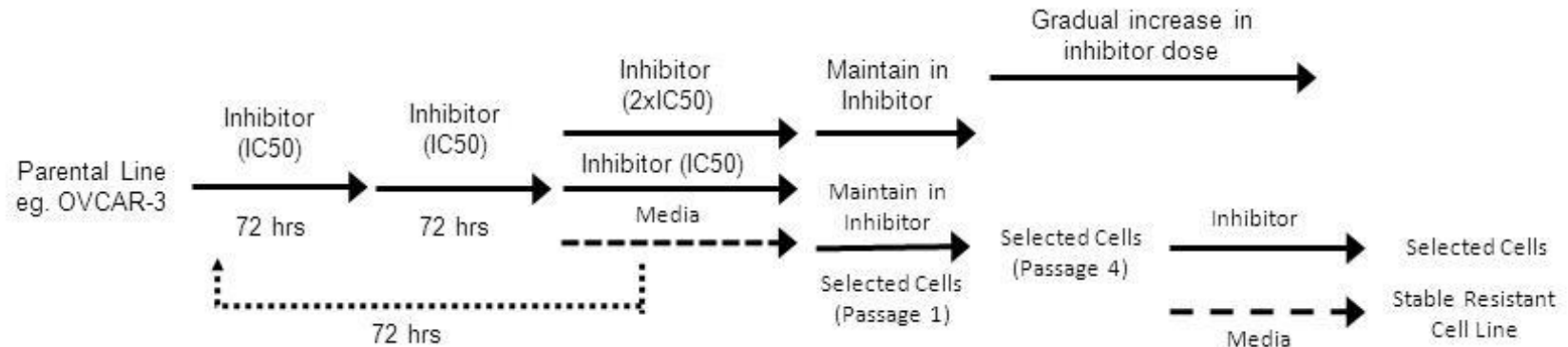
A HIGH THROUGHPUT COMPOUND SCREEN IDENTIFIES POTENTIAL COMBINATIONS TO CDK2 INHIBITOR RESISTANCE IN *CYCLIN E1* AMPLIFIED HIGH GRADE SEROUS OVARIAN CANCER (PD1)

- High grade serous ovarian cancer (HGSOC) is the most common histological subtype of epithelial ovarian cancer
- Cyclin E1 (*CCNE1*) amplification is detected in 15% of HGSOC, and associated with primary treatment resistance and poor outcome

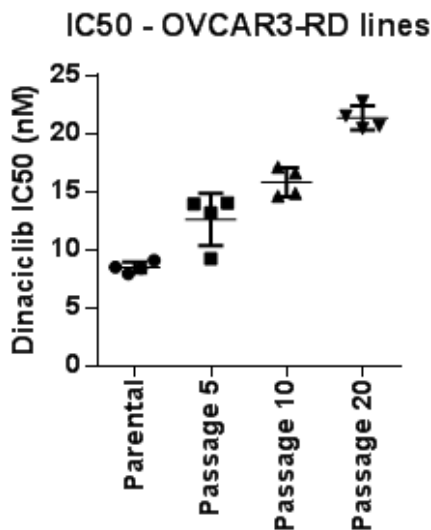


- Ovarian cancer cell lines with CCNE1 amplification are selectively sensitive to Cdk2 inhibitors (Etemadmoghadam et al, Clinical Cancer Research, 2013)

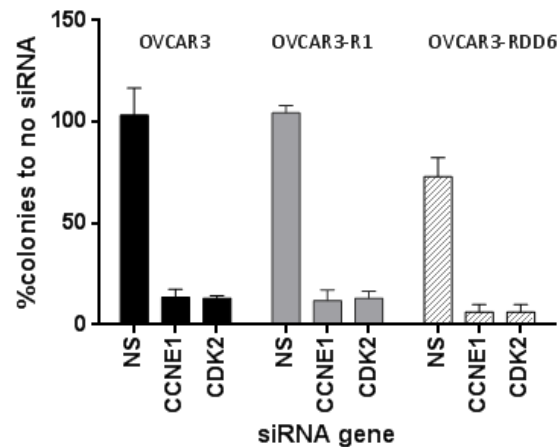
Understanding CDK inhibitor resistance *in vitro*



Resistance is Stable

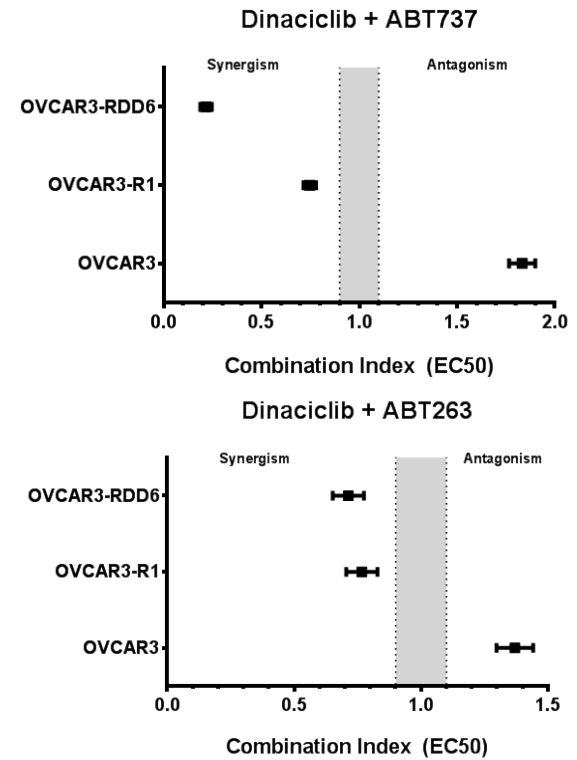
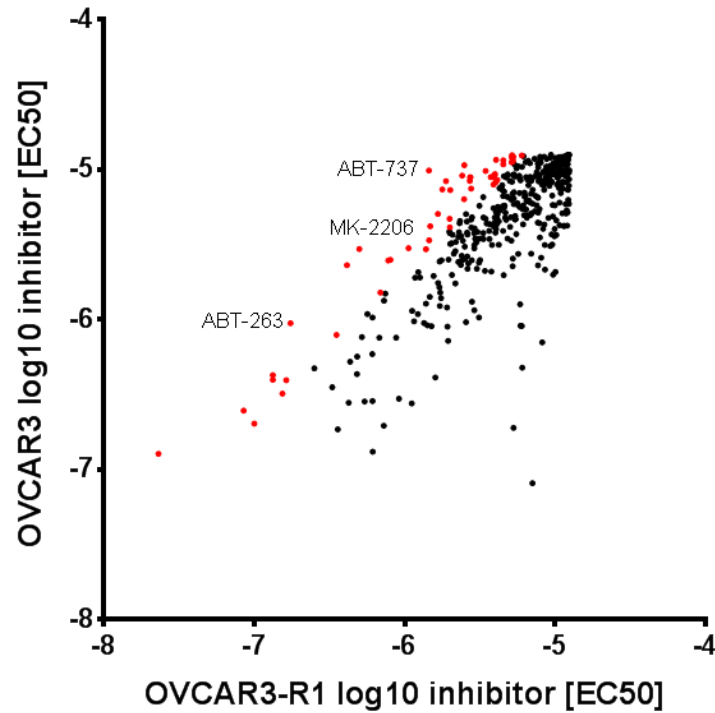


Resistant Lines still require CCNE1/CDK2

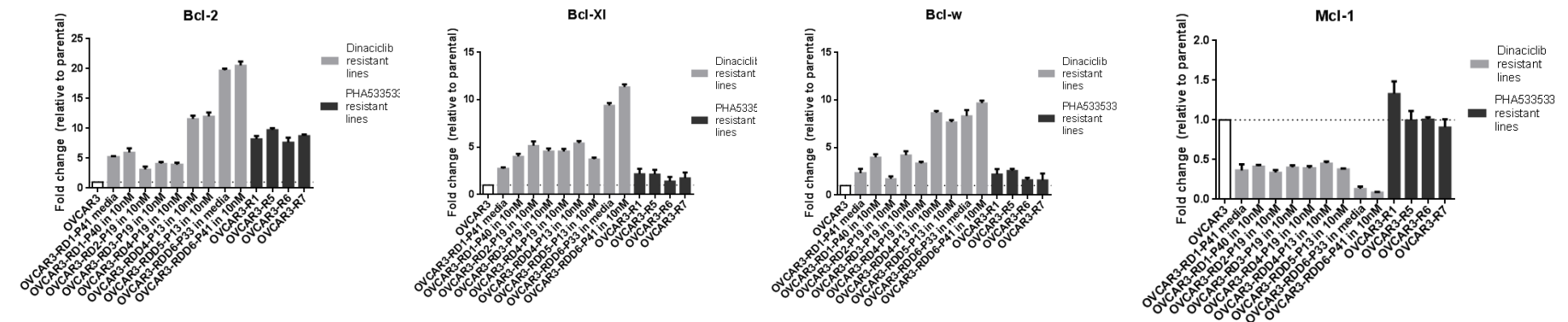


High throughput compound screening to identify drug combinations for overcoming Cdk2 inhibitor resistance

Non-selective BH3-mimetics show synergy



CDK2i Resistant Lines show upregulation of several anti-apoptotic genes



- Strengths

- Stable resistance to Cdk2 inhibitors can be generated by continuous drug exposure
- CDK2i-resistant lines are still dependent on CCNE1 and CDK
- A high throughput compound screen identifies potential drug combinations to overcome CDKi resistance
- Potential hits with non-selective BH3-mimetics provides evidence for upregulation of anti-apoptotic proteins

- Limitations

- Results are based on 1 parental cell line
- *In vivo* relevance of findings remain to be assessed
- Do OvCAs with baseline high expression of anti-apoptotic proteins exhibit primary resistance to CDK inhibitors?

Questions