



Induction of Resistances to Crizotinib in NSCLC Patient-Derived Xenograft Models Upon Treatment

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Poster #

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Introduction

Anaplastic lymphoma kinase (ALK) is a receptor tyrosine kinase, and its mutation, overexpression, and gene fusion have been associated with various forms of cancer. EML4-ALK fusion has been confirmed to be the oncogenic driver in a small subset of lung cancers (~4% of NSCLC)¹. ALK rapidly became an excellent drug target, leading to the development of crizotinib, an ALK tyrosine kinase inhibitor as the first effective therapy for this subset of NSCLC^{2,3}. However, like most cancer therapies so far, continuous crizotinib treatment over a prolonged period of time leads to the development of drug resistance, rendering the treatment ineffective⁴. Understanding the mechanisms causing drug resistance can potentially facilitate overcoming the problem and extend patients' life^{5,6}. However, lack of experimental model hinders research in this area.

Abstract

We recently established a large collection of lung cancer patient-derived xenografts (~350 PDXs)⁷, and we screened some of them for the presence of ALK gene fusion (by RT-PCR and RNAseq). The ALK fusion-positive models were tested for sensitivity to crizotinib. We kept these PDXs under crizotinib treatment pressure *in vivo* in order to induce acquired resistance, as seen in the clinic. The resistant models were genomically profiled to identify the changes that could potentially be responsible for the emergence of crizotinib resistance.

We identified the NSCLC-ADC LU1656 model as a candidate for our study since it displays EML4-ALK fusion and elevated ALK expression (type-1). This model initially responds well to crizotinib *in vivo*. Continuous treatment eventually leads to the development of resistance to crizotinib, a pattern already observed in patients undergoing the same treatment. We called the resistant model LU2445. We performed transcriptome sequencing of the tumor samples from the parental sensitive (LU1656) and the selected resistant (LU2445) models. So far, we found both models expressed similarly high levels ALK, but we could not detect additional mutations in ALK gene. Further data analysis is ongoing.

Results

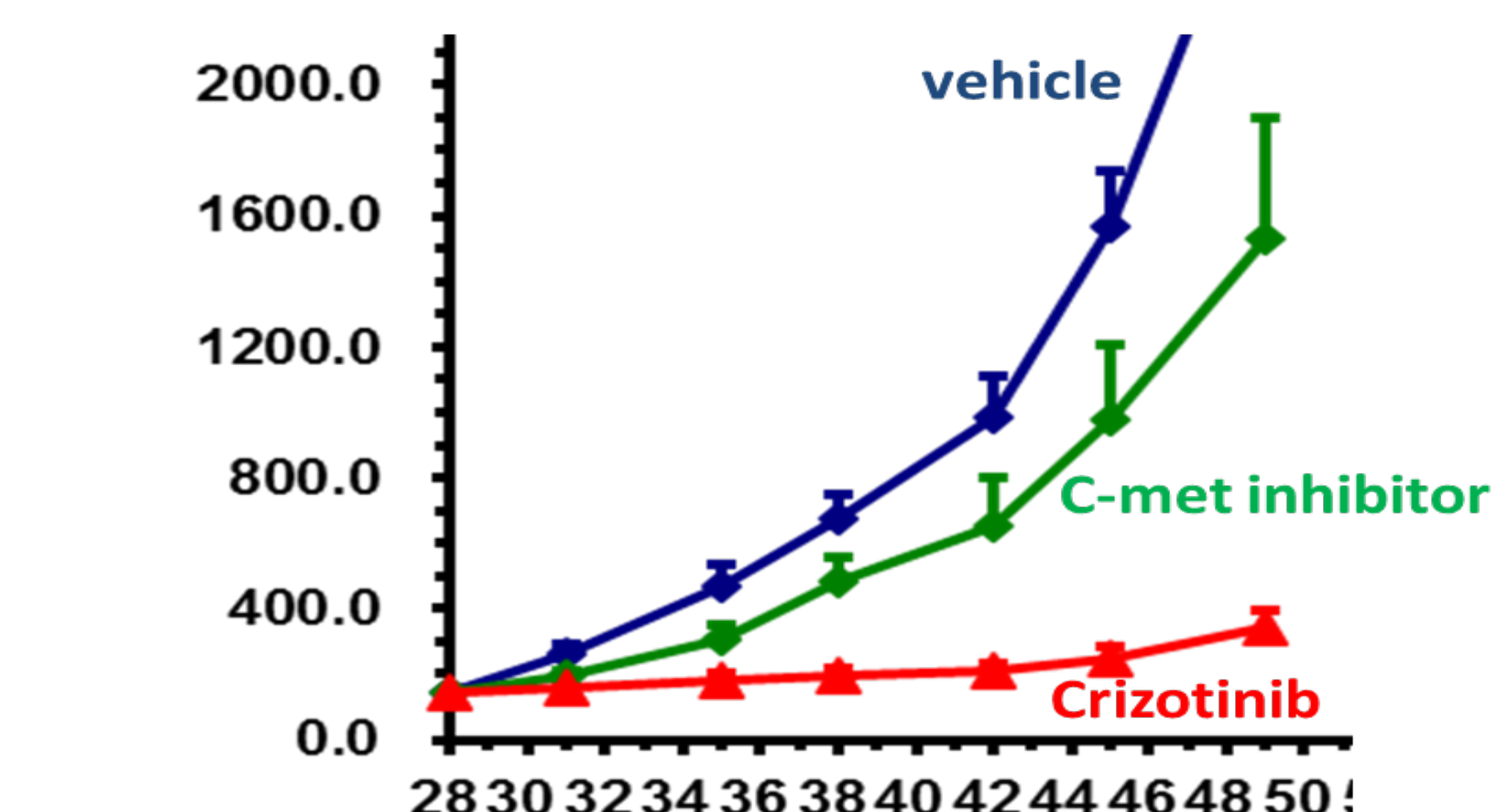


Figure 1: The LU1656 NSCLC PDX model is sensitive to crizotinib but not to MET inhibitors

ID	Ethnicity	Gender	Hospital pathology	Pathology QC
LU1656	Asian	Female	NSCLC, Carcinosarcoma; CK (+), Vim (+), Act(-), NSE(-), Syn (-), CD56 (±), Chr-A (-).	Moderately differentiated squamous cell carcinoma (P5).
LU2445	Asian	Female	Carcinosarcoma	Poorly differentiated tumor, giant cells, spindle cells and clear cells observed.

Table 1: Summary of patient and PDX model information

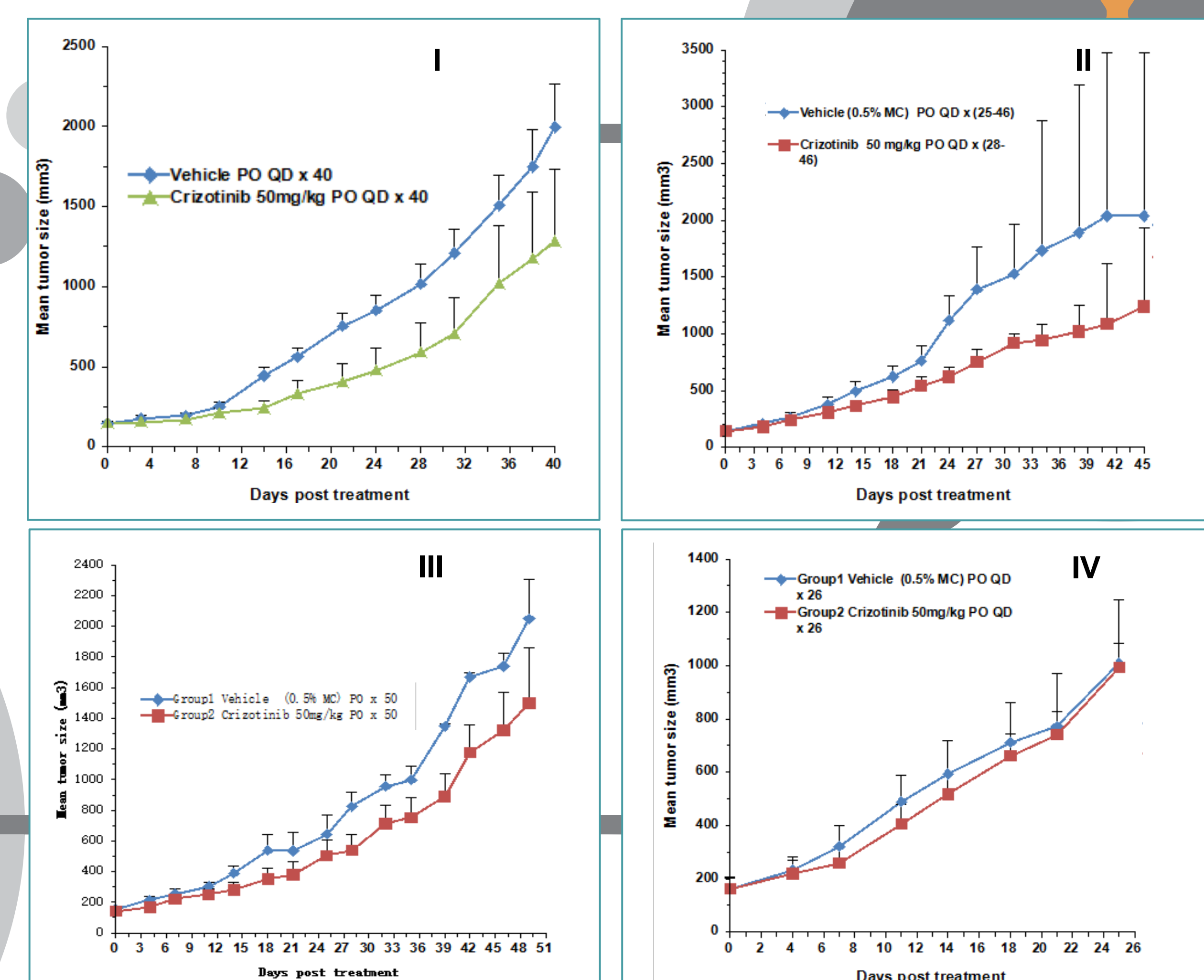


Figure 2: Generation of crizotinib resistant model LU2445 by repetitive exposure of LU1656 sensitive model

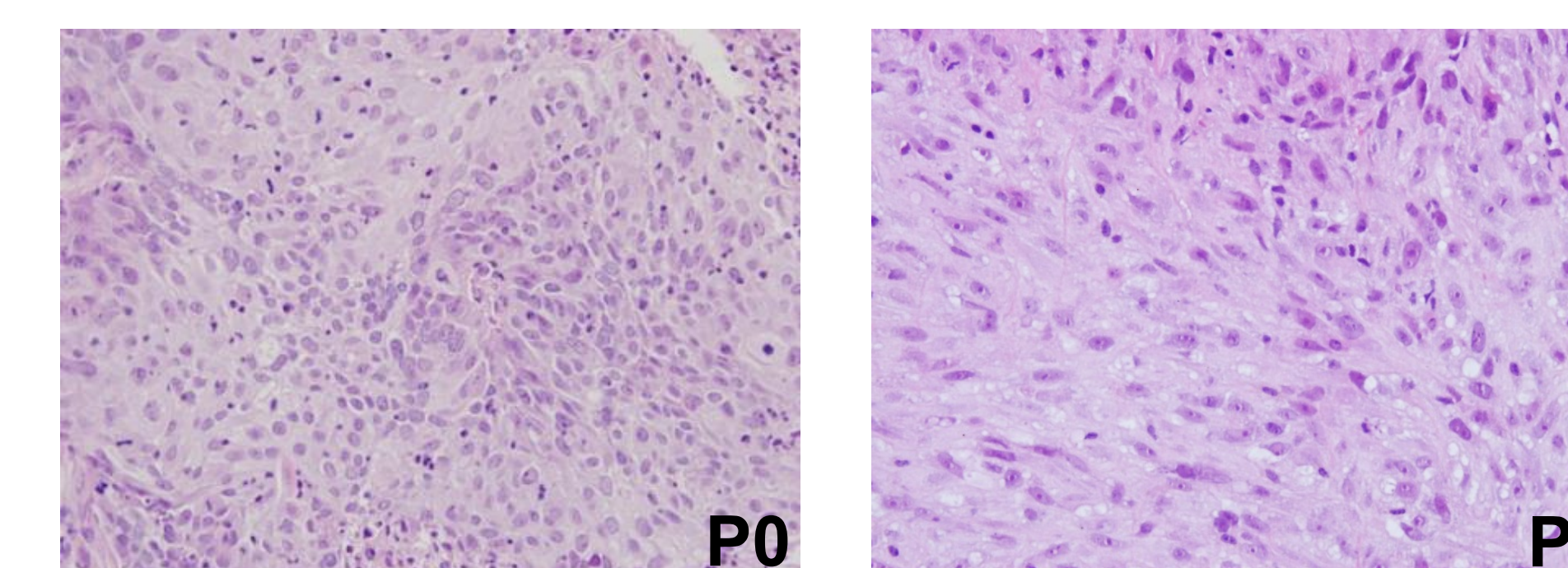


Figure 3: H&E Stain of LU1656

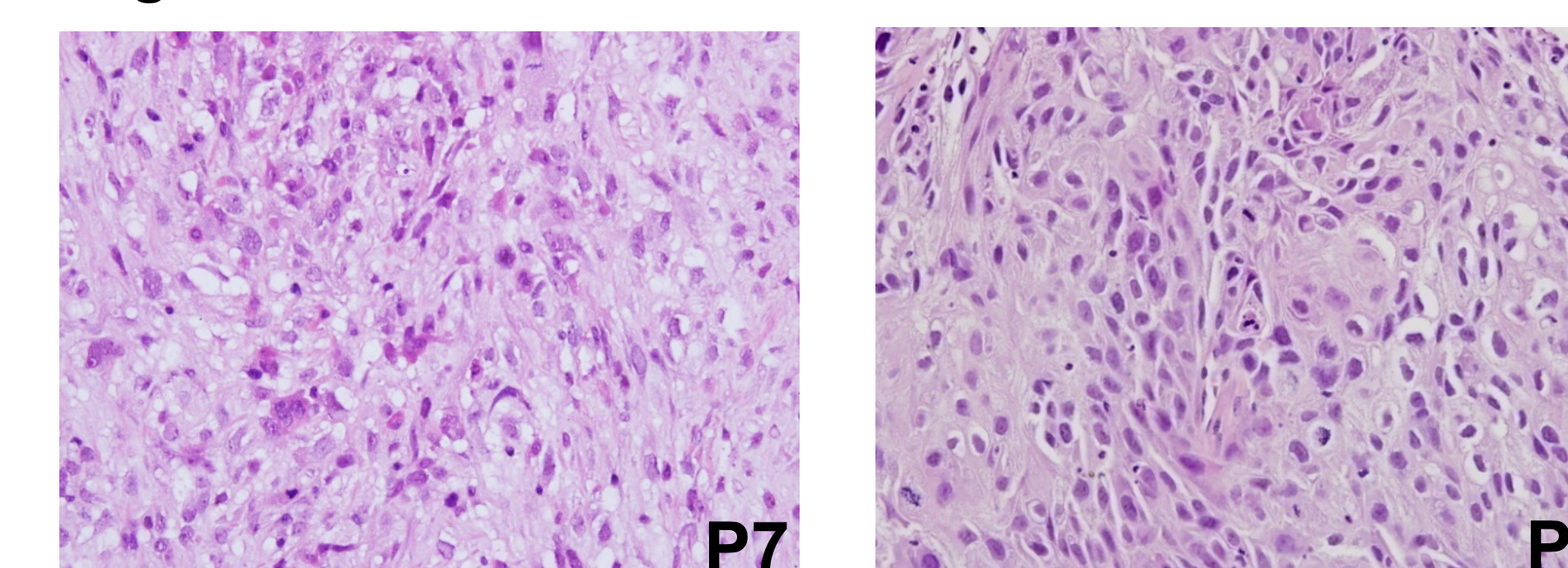


Figure 4: H&E Stain of LU2445

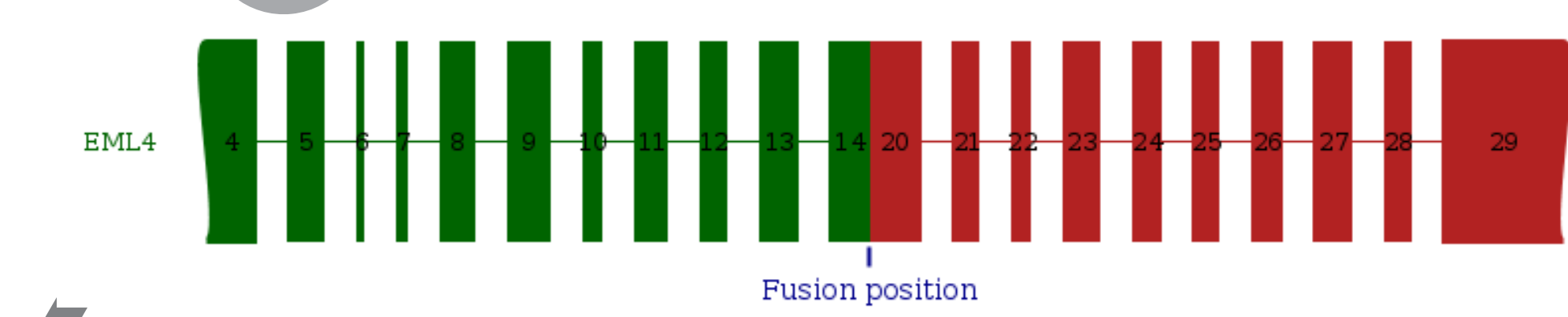


Figure 5: EML4-ALK fusion in LU1656

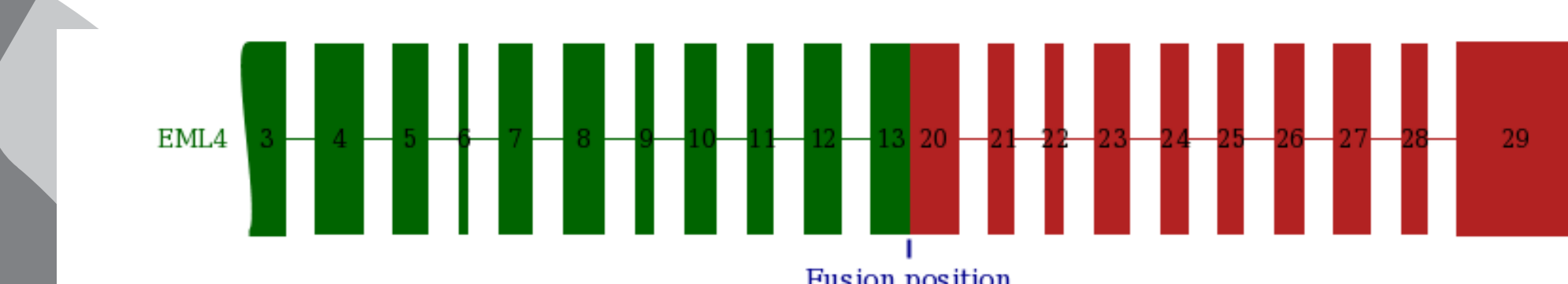


Figure 6: EML4-ALK fusion in LU2445

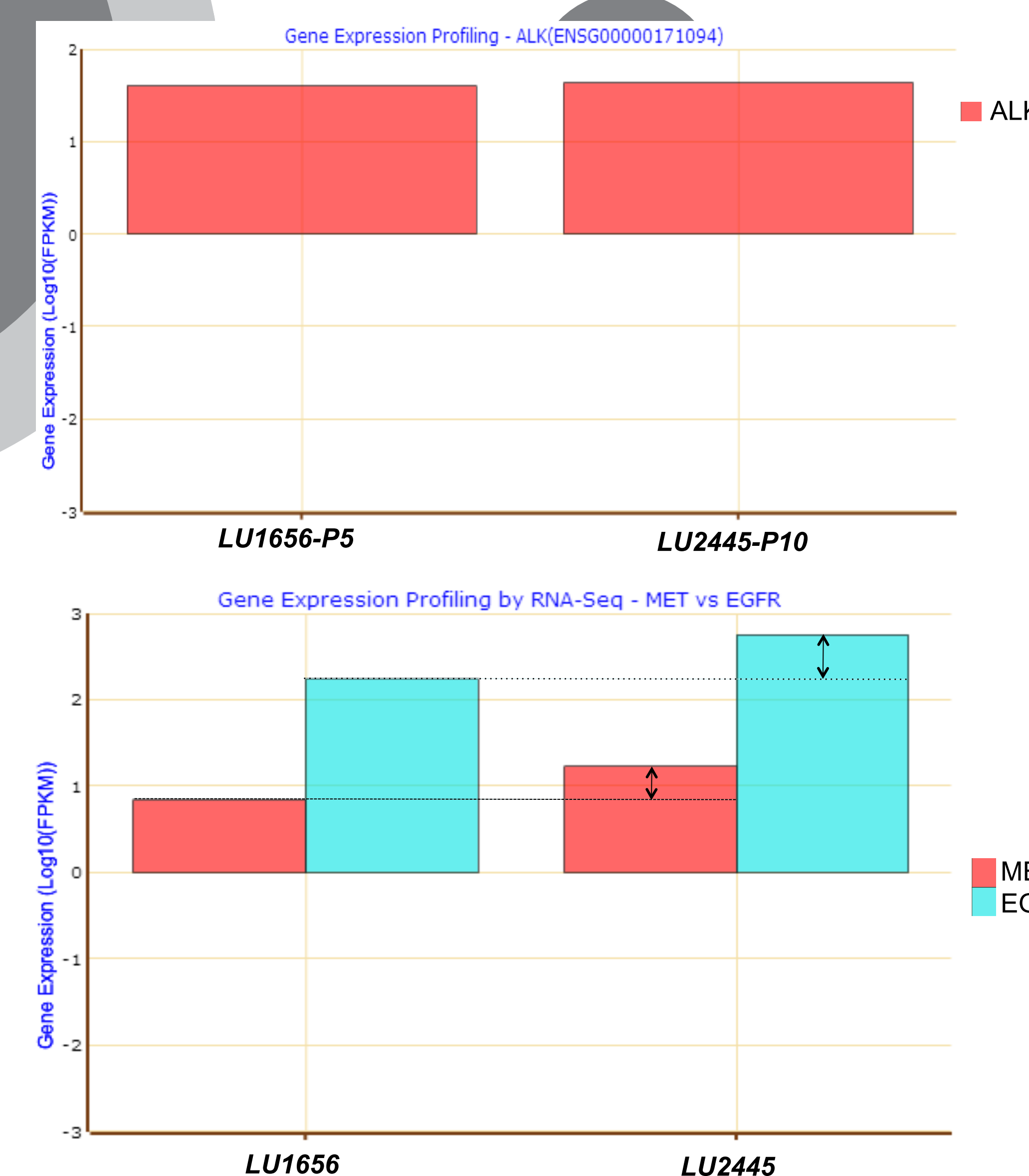


Figure 7: ALK, MET and EGFR expression in LU1656 vs. LU2445 NSCLC PDX models

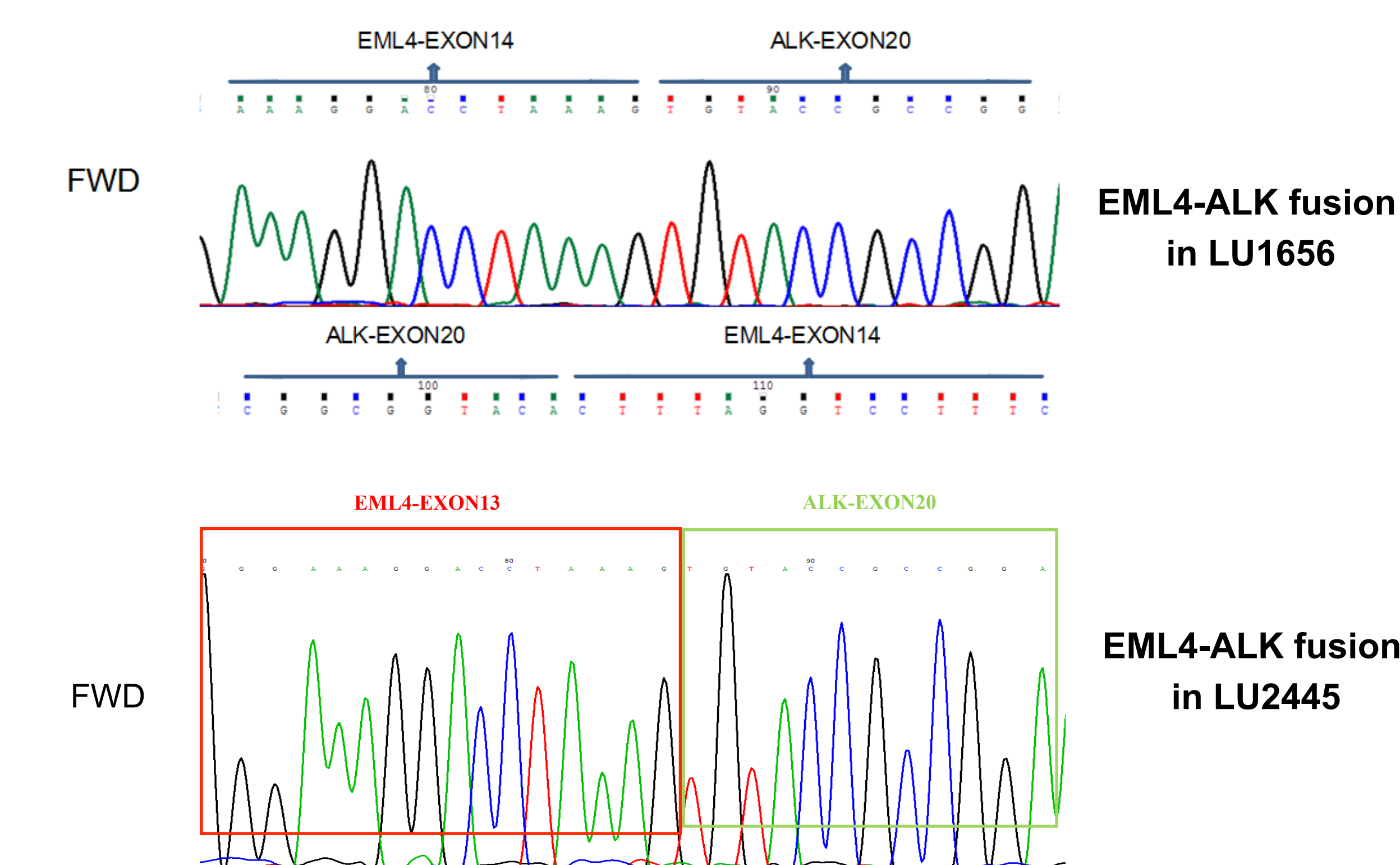


Figure 8: EML4-ALK fusion in LU1656 vs. LU2445

Conclusions

1. The NSCLC PDX model LU1656 carries a EML4-ALK fusion;
2. LU1656 is sensitive to crizotinib;
3. LU1656 has no c-MET activation, mutation or amplification, and is insensitive to c-MET inhibitors;
4. LU1656 partially responds to EGFR inhibitors (Erbix[®], erlotinib);
5. Prolonged exposure to crizotinib *in vivo* causes development of resistance in the LU1656 model;
6. No further ALK mutations or change in the level of expression were identified in the resistant model. The molecular mechanism underlying the observed resistance is still to be identified.

References

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