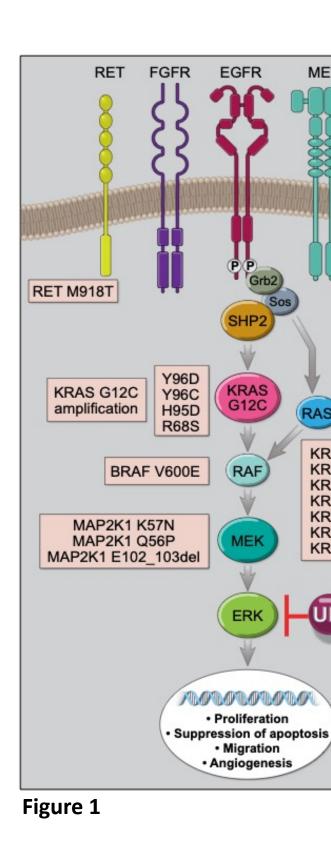
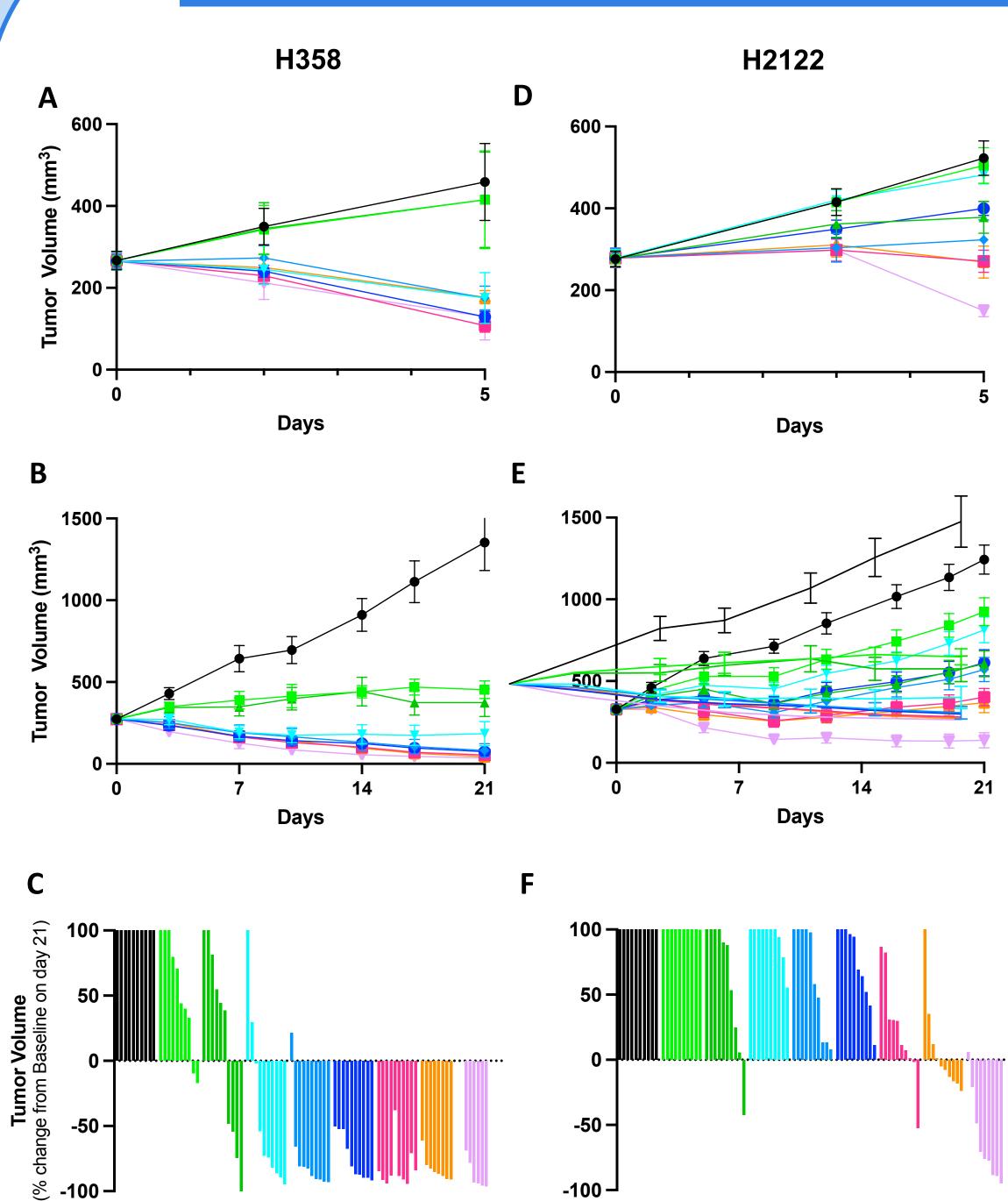
# BIOMEDVALLEY D I S C O V E R I E S

### Background

- Ulixertinib (BVD-523) is a first-in-class and best-in-class small molecule inhibitor of ERK1/2 currently being investigated in oncology clinical trials, both as a single agent and in combination with other therapeutics.
- Ulixertinib has demonstrated efficacy in patients with tumors harboring alterations within the RAS-MAPK pathway<sup>1</sup>.
- The *KRAS*<sup>G12C</sup> mutation occurs in approximately 10% of nonsmall cell lung cancer (NSCLC), 3% of colorectal cancer, and 1-2% across all other tumor types<sup>2</sup>.
- KRAS<sup>G12C</sup> mutant-inhibitors, including AMG-510 (sotorasib), MRTX849 (adagrasib), and JDQ443 have demonstrated efficacy in *KRAS*<sup>G12C</sup>-mutant cancers, including NSCLC.
- Clinically described mechanisms of acquired resistance to KRAS<sup>G12C</sup> inhibitors converge on reactivation of the RAS-MAPK pathway (Figure 1)<sup>3-6</sup>.
- We hypothesized combining ulixertinib with a KRAS<sup>G12C</sup> inhibitor would circumvent resistance to single agent KRAS<sup>G12C</sup> inhibition, generating increased magnitude and duration of response compared to either single agent alone.



### **1.** Ulixertinib in combination with *KRAS*<sup>G12C</sup> inhibition is efficacious



• The efficacy of ERK1/2 inhibitor, ulixertinib (uli), in combination with KRAS<sup>G12C</sup> inhibitor, adagrasib (MRTX849), was assessed in cell line-derived xenograft models harboring *KRAS*<sup>G12C</sup> mutations. Models were selected based on response to single agent adagrasib, ranging from sensitive (H358) to partially responsive (H2122)<sup>7</sup>.

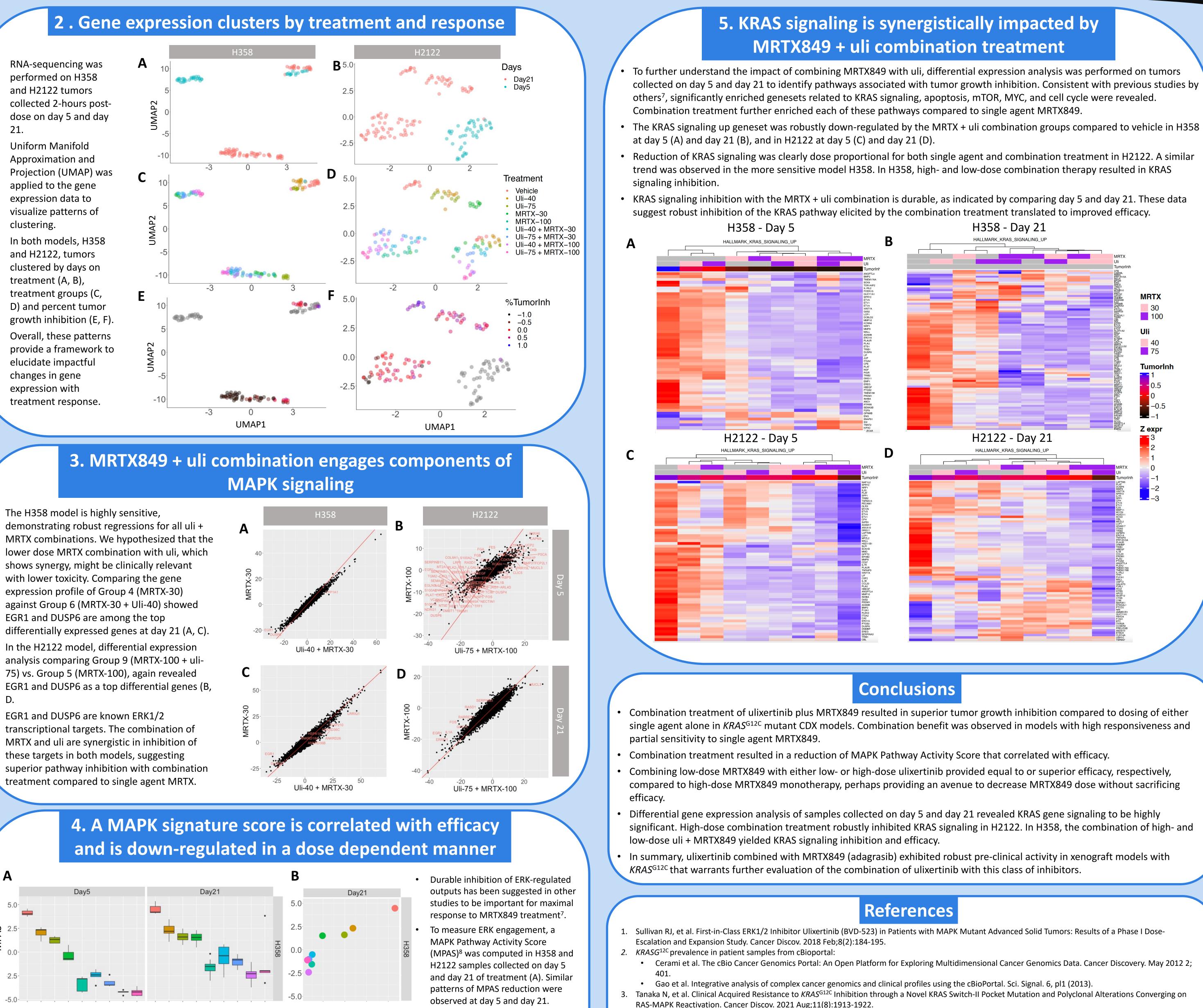
• Combining uli with MRTX849 (MRTX) resulted in superior tumor growth inhibition compared to dosing of either single agent alone in both models. In the highly sensitive model, H358, high- and low-dose combination was efficacious. In H2122, the addition of low- or high-dose ulixertinib to 30mg MRTX849 resulted in equal or improved efficacy, respectively, compared to 100mg MRTX849 monotherapy. High-dose combination treatment (Groups 8 and 9) yielded robust regression compared to all other treatment groups.

• Tumor volume over time is shown for groups dosed to day 5 and day 21 for H359 (A, B) and H2122 (D, E). Tumor volume percent change from baseline at day 21 is shown for H359 (C) and H2122 (F). Visualization of growth is capped at 100% (C, F).

# The combination of ulixertinib (ERK1/2 inhibitor) and KRAS<sup>G12C</sup> inhibition demonstrates significant efficacy in preclinical models

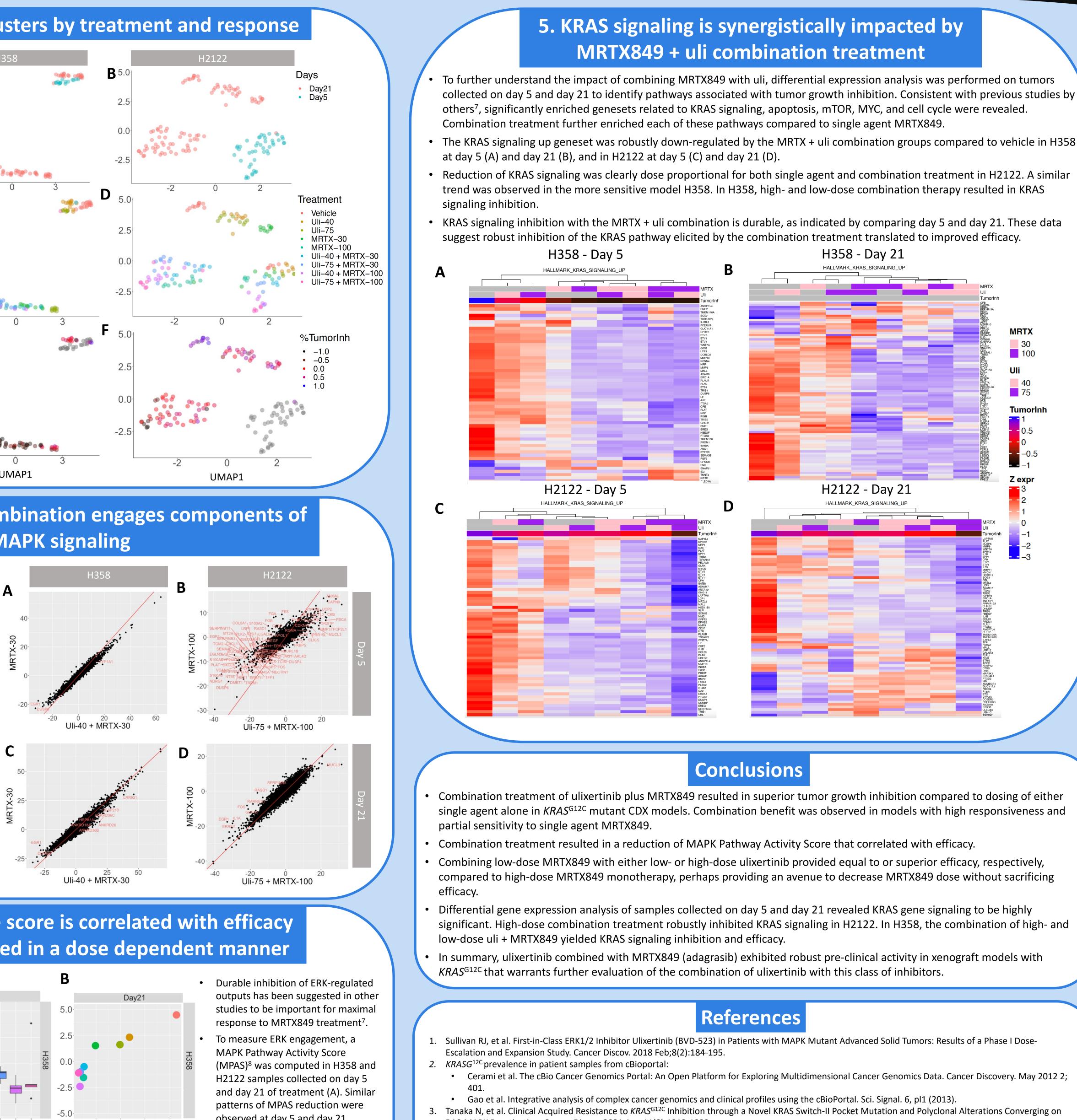
Deborah Knoerzer<sup>1</sup>, Anupama Reddy<sup>2</sup>, Jessica A. Box<sup>1</sup>, Anna Groover<sup>1</sup>, Brent Kreider<sup>1</sup>, Martin Teresk<sup>1</sup>, Caroline M. Emery<sup>1</sup> <sup>1</sup>BioMed Valley Discoveries, Kansas City, MO <sup>2</sup>Vindhya Data Science Inc., Morrisville, NC

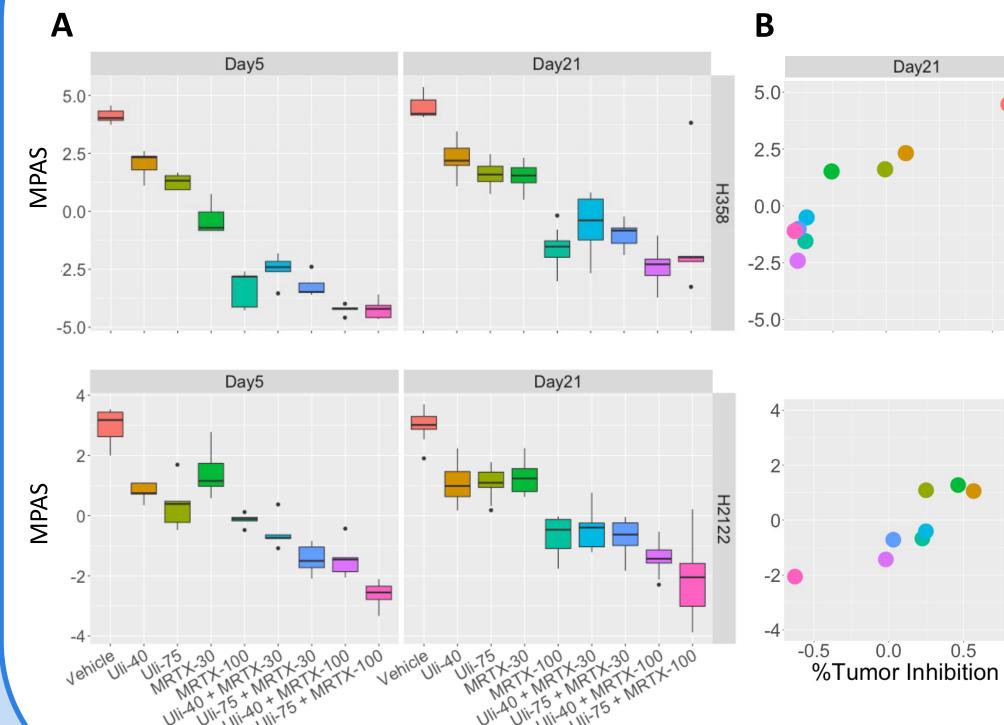
- RNA-sequencing was performed on H358 and H2122 tumors collected 2-hours postdose on day 5 and day
- Uniform Manifold Approximation and Projection (UMAP) was applied to the gene expression data to visualize patterns of clustering.
- In both models, H358 and H2122, tumors clustered by days on treatment (A, B), treatment groups (C D) and percent tumor growth inhibition (E, F).
- Overall, these patterns provide a framework to elucidate impactful changes in gene expression with treatment response.



• The H358 model is highly sensitive, demonstrating robust regressions for all uli + MRTX combinations. We hypothesized that the lower dose MRTX combination with uli, which shows synergy, might be clinically relevant with lower toxicity. Comparing the gene expression profile of Group 4 (MRTX-30) against Group 6 (MRTX-30 + Uli-40) showed EGR1 and DUSP6 are among the top

- In the H2122 model, differential expression analysis comparing Group 9 (MRTX-100 + uli-75) vs. Group 5 (MRTX-100), again revealed EGR1 and DUSP6 as a top differential genes (B,
- EGR1 and DUSP6 are known ERK1/2 transcriptional targets. The combination of MRTX and uli are synergistic in inhibition of these targets in both models, suggesting superior pathway inhibition with combination treatment compared to single agent MRTX.





Group 01, Vehicle

**RTKs** activation

**KRAS G13D** 

**KRAS Q61L** 

**KRAS Q61R** 

KRAS Q61K

Ulixertinib

MET amplification

- Group 02,
- Ulixertinib,40mg/kg → Group 03,
- Ulixertinib,75mg/kg
- Group 04, MRTX849,30mg/kg
- Group 05, MRTX849,100mg/kg
- Group 06, Ulixertinib,40mg/kg + MRTX849,30mg/kg
- Group 07, Ulixertinib,75mg/kg +
- MRTX849,30mg/kg Group 08, Ulixertinib,40mg/kg +
- MRTX849,100mg/kg Group 09, Ulixertinib,75mg/kg +
- MRTX849,100mg/kg

• In both models, a dose-dependent decrease in MPAS was observed in uli and MRTX treatment groups. In H2122, the benefit of adding ulixertinib to low dose MRTX849 monotherapy observed in panel 1 was also reflected in the MPAS score reduction.

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0.0 0.5

Combination treatment durably inhibited ERK activity, as indicated by decreased MPAS. MPAS score reduction is correlated with efficacy in both models at day 21 (B).

• Crown Bioscience for CDX experiments.

Cancer Discov. 2020 Jan;10(1):54-71.

7;2(1):7.

- Azenta Life Sciences for RNAseq.
- Mark Miller (Stowers Institute for Medical Research, Kansas City, MO) for pathway illustrations.



Abstract

4. Zhao Y et al. Diverse alterations associated with resistance to *KRAS*(G12C) inhibition. Nature. 2021 Nov;599(7886):679-683. Awad MM et al. Acquired Resistance to *KRAS*<sup>G12C</sup> Inhibition in Cancer. N Engl J Med. 2021 Jun 24;384(25):2382-2393.

5. Blaquier JB, Cardona AF, Recondo G. Resistance to KRAS<sup>G12C</sup> Inhibitors in Non-Small Cell Lung Cancer. Front Oncol. 2021 Dec 24;11:787585.

. Hallin J et al. The KRAS<sup>G12C</sup> Inhibitor MRTX849 Provides Insight toward Therapeutic Susceptibility of KRAS-Mutant Cancers in Mouse Models and Patients.

3. Wagle MC et al. A transcriptional MAPK Pathway Activity Score (MPAS) is a clinically relevant biomarker in multiple cancer types. NPJ Precis Oncol. 2018 Mar

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