

Abstract #3079: In silico approaches to patient selection: Credentialing elraglusib as a novel treatment in metastatic melanoma resistant to checkpoint inhibitors



MAYO CLINIC

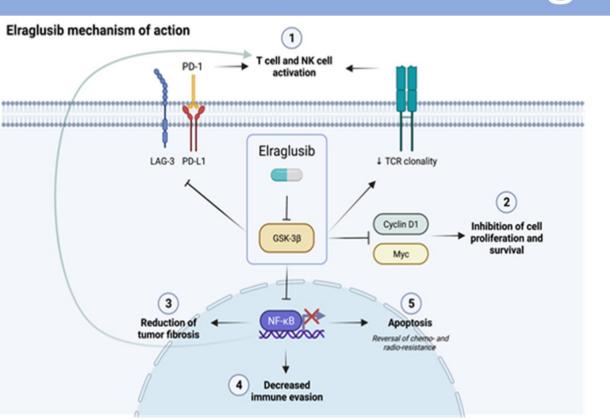


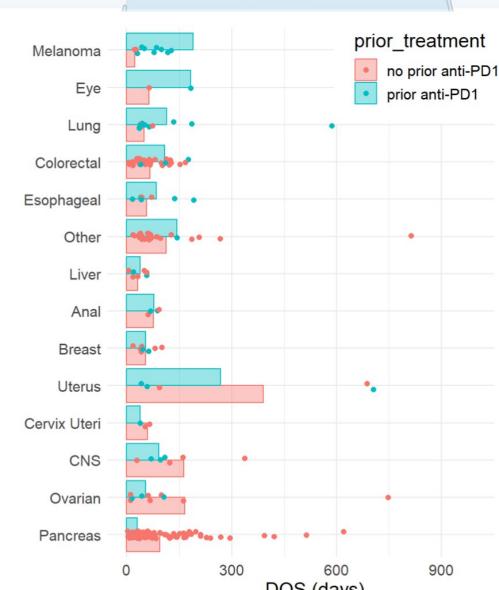


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## Background





- Elraglusib (9-ING-41), a novel inhibitor of GSK-3β, has been evaluated in >230 patients (pts) with advanced malignancies, including metastatic melanoma 1801 phase 1/2 trial (NCT03678883).
- 12 metastatic pts with advanced melanoma were treated elraglusib
- Elraglusib showed clinical benefit with multiple prior lines of therapy including checkpoint inhibitors (CPI)
- 5 pts demonstrated durable clinical benefit with 1 CR (ongoing, >1400 days) and prolonged OS of 107, 256, 357, and 556 days.

#### Figure 1. 1801 Patient Days on Study (DOS) Across **Tumor Types and Prior Lines of Treatment**

Among tumor types with at least one patient having had anti-PD-1 and one not having had having αPD-1 in prior lines of treatment have DOS shown.

### Methods

- We collected pt omic data from the 1801 trial to characterize markers of elraglusib response with bioinformatics and machine learning (ML).
- Pts were treated with elraglusib as a single agent or in combination with chemotherapy
- Genomic panels were available for 106 pts
  - The most frequent tumor types included colorectal cancer (n=35), pancreas (n=31), lung (n=15), and metastatic melanoma (n=12).
- Pathway-based features were generated by quantifying the percent of each Reactome pathway that was mutated
  - Pathway features were iteratively evaluated in a training set of 80 pts for performance in shallow neural networks predicting patient RECIST, with each model using 5-15 randomly suggested features at a time
- Publicly available genomics data from an  $\alpha PD-1$  trial in pts with metastatic melanoma (Hugo et al., Cell 2017) were transformed into pathway-based features and input into the final model to predict elraglusib response in this population
- RNA-seq of Pts given anti-PD-1 (without other CPI) was taken from public data (Hugo et al., Cell 2017; Gide et al., Cancer Cell 2019), with log2(fpkm+1) GSK3B values standardized before merging the datasets
  - Kaplain-Meier plots were made with the survminer and survival R packages

#### Results

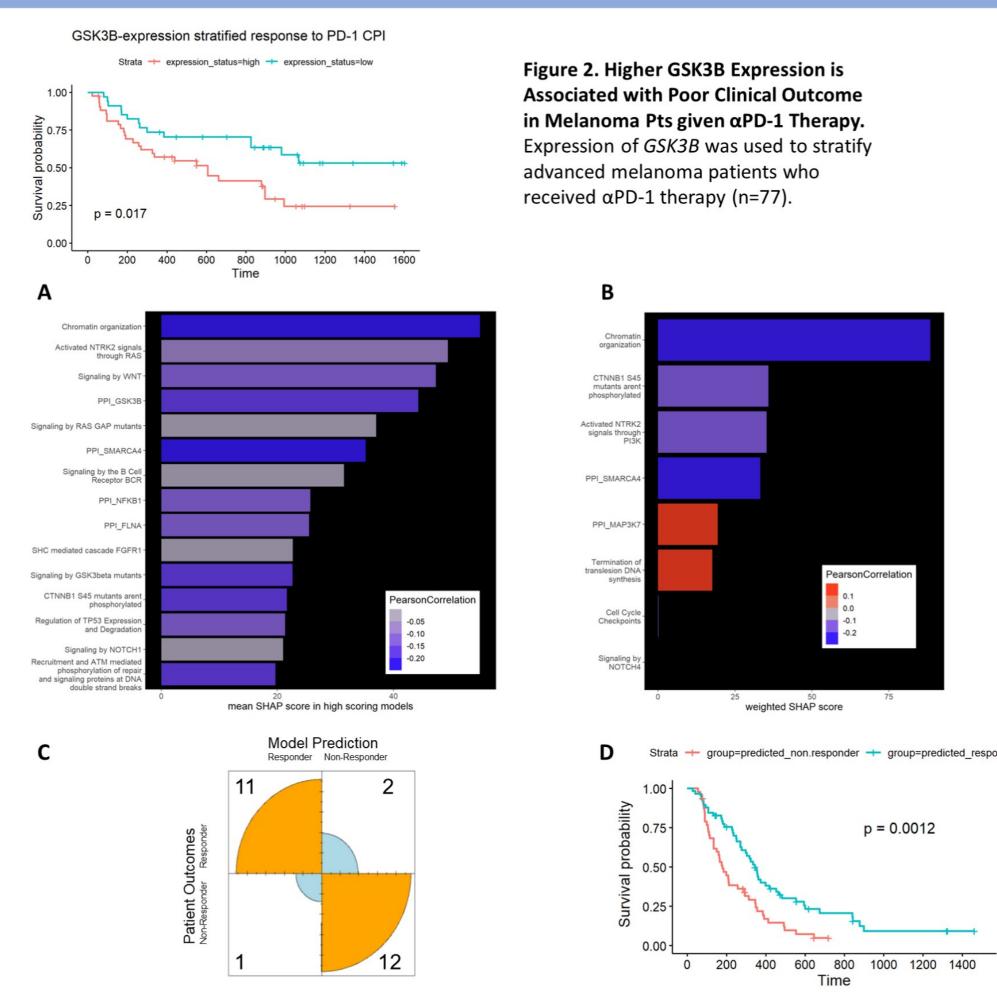


Figure 3. A) Feature impact on model prediction based on mean weighted SHAP scores of thousands of models. Red color indicates a positive feature association to Pt response, blue indicates a negative association. B) Feature SHAP contributions in a top-performing model. C) Confusion matrix of top model predictions on a test set of 26 pts with >88% accuracy. The upper left indicates true negatives, and the bottom right true positives. D) Kaplain-Meier plot of 1801 patient overall survival days for predicted responder or non-responder groups.

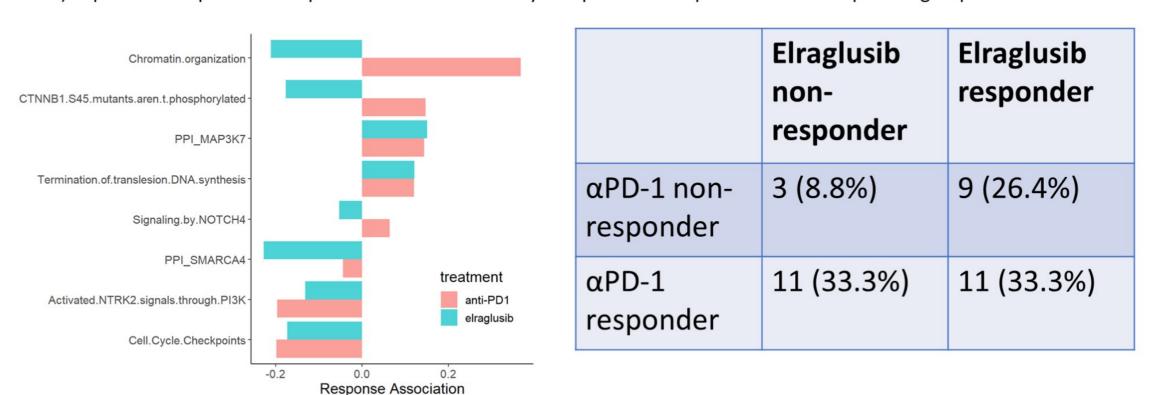


Figure 4. Predicted Elraglusib Response Analysis in Metastatic Melanoma Patients Treated with αPD-1 A) Comparison of feature associations to elraglusib response and αPD-1 response. B) Most Metastatic Melanoma Pts are Predicted Elra Responders (66%) with selectivity in  $\alpha PD-1$  non-Responders (78.5% of all  $\alpha PD-1$  non-responders).

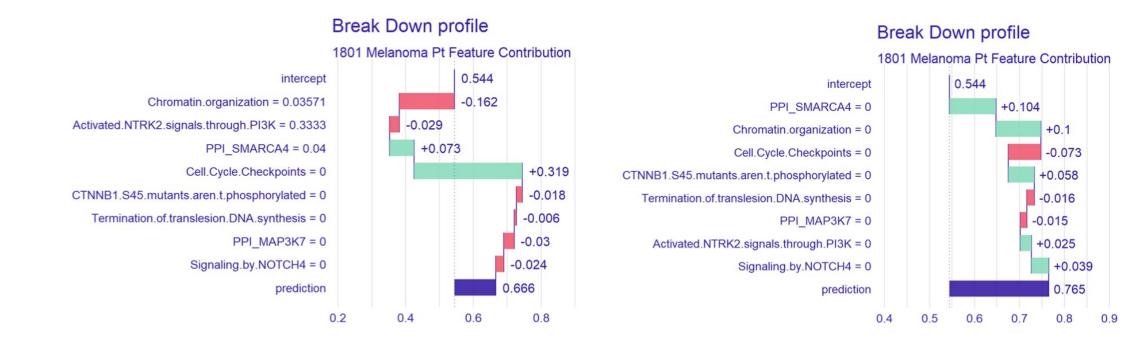


Figure 5. Explanation of Model Response Predictions on Individual Patients SHAPley break-down plots calculate the importance of model input features by their contribution to model predictions at given values.

# Major Take Aways

- Elraglusib showed strong responses in metastatic melanoma patients.
- Al modeling predicts that checkpoint resistant metastatic melanoma patients will benefit from elraglusib therapy, particularly CPI failures

#### **Future Directions**

- Exploration of Elraglusib and  $\alpha PD-1$  combination in select indications
- Use ML model to select patient populations, such as advanced melanoma
- Develop clinical applications of ML model to inform clinical decision making