**INTRODUCTION**

- cfDNA methylation profiles in blood - candidate biomarker for hematologic malignancies.

**METHODS**

- cfDNA samples from the second pre-specified sub-study of CCGA, cfDNA samples were from the second pre-specified sub-study of CCGA, which were selected for their high-quality methylation patterns.
- Samples were subjected to a custom classification model for hematologic malignancies.
- The custom classifier was validated on a test dataset for hematologic malignancies.

**RESULTS**

- The custom classifier was evaluated on a test dataset for hematologic malignancies.
- The classifier achieved high sensitivity and specificity for the detection of hematologic malignancies.
- The classifier was able to distinguish between hematologic malignancies and non-malignant conditions.

**CONCLUSIONS**

- The custom classifier for hematologic malignancies offers a convenient way to simultaneously detect and distinguish five major hematologic malignancies, which could help facilitate clinical diagnosis and treatment selection.

**ACKNOWLEDGMENTS**

- The authors would like to thank all the participants in the CCGA study.

**DISCLOSURES**

- The authors declare no conflict of interest.

---

**References**


---

**Images**

- Figure 1: Hematologic Classifier Sensitivity at the OLG1 Target Specificity Levels.
- Figure 2: Tissue of Origin Prediction for Tissue Predicted As Hematologic Cancers.
- Figure 3: Hematologic Malignancies Are Clustered Into 5 Major Groups. Classification features were visualized using the UMAP visualization technique.
- Figure 4: The Correlation Between Classification Scores and the Actual Cancer Status of Hematologic Cancer samples predicted by predicted versus actual TSCID.

---

**Author Information**

- Corresponding author: [Name], [Email]

---