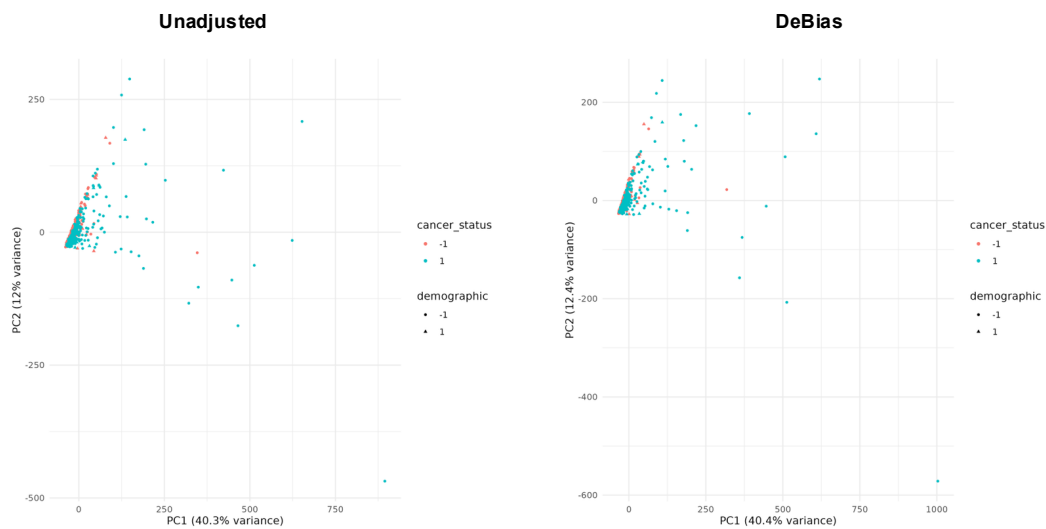
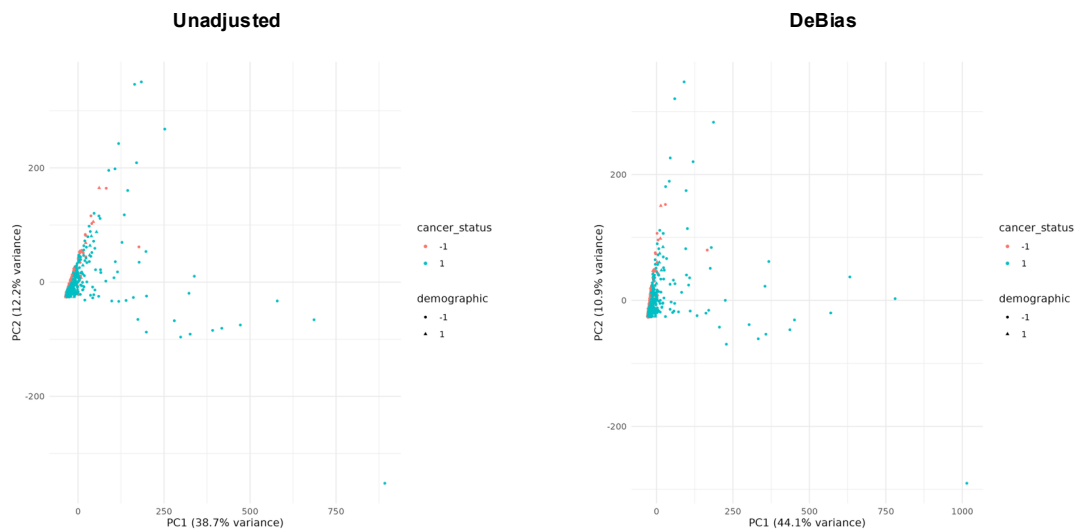


# Supplementary Figures

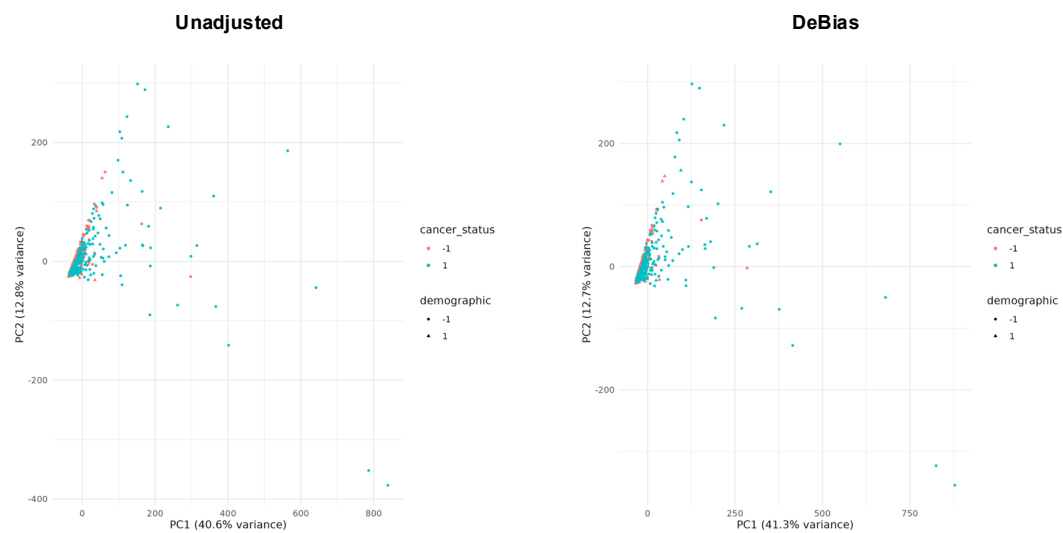
**Fig S1.** Scatter plots of training samples before and after DeBias correction for cross-validation Fold 1 in the racial bias removal analysis of multi-cancer detection. In the demographic variable, “-1” denotes the minority population and “1” denotes the majority population. In the cancer status variable, “-1” represents noncancer samples and “1” represents cancer samples.



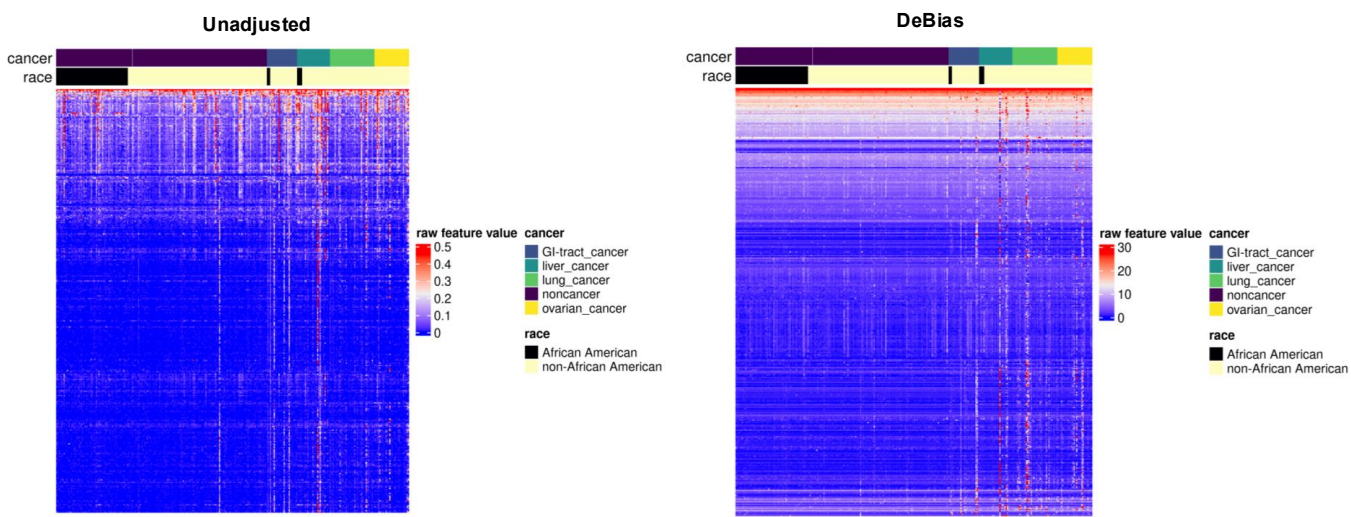
**Fig S2.** Scatter plots of training samples before and after DeBias correction for cross-validation Fold 2 in the racial bias removal analysis of multi-cancer detection. In the demographic variable, “-1” denotes the minority population and “1” denotes the majority population. In the cancer status variable, “-1” represents noncancer samples and “1” represents cancer samples.



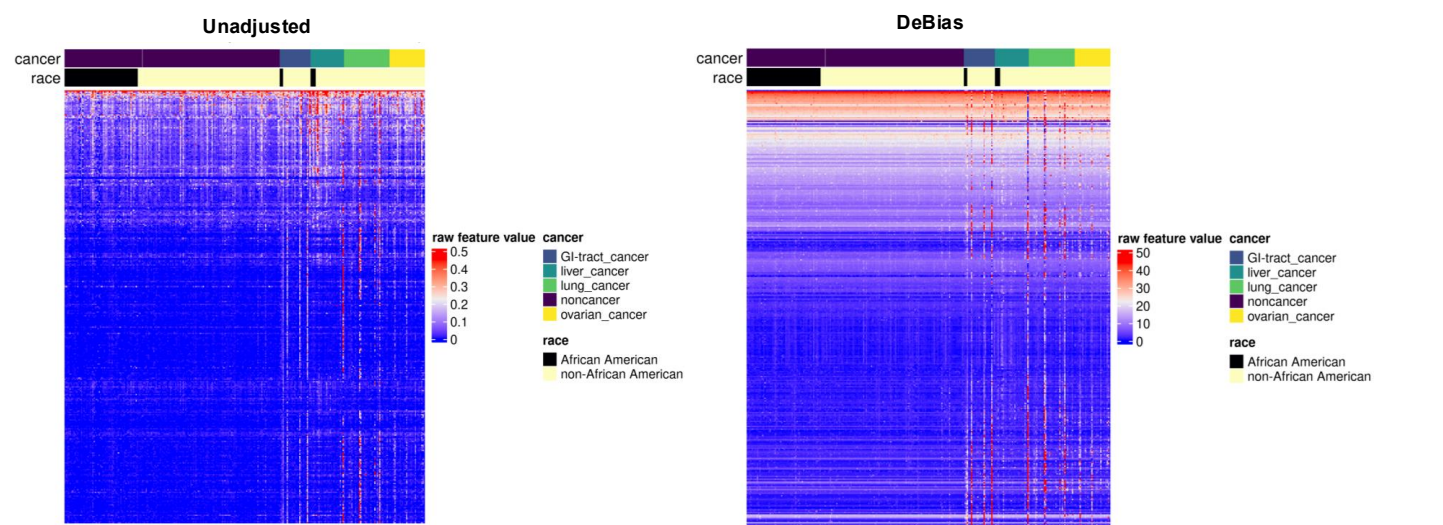
**Fig S3.** Scatter plots of training samples before and after DeBias correction for cross-validation Fold 3 in the racial bias removal analysis of multi-cancer detection. In the demographic variable, “-1” denotes the minority population and “1” denotes the majority population. In the cancer status variable, “-1” represents noncancer samples and “1” represents cancer samples.



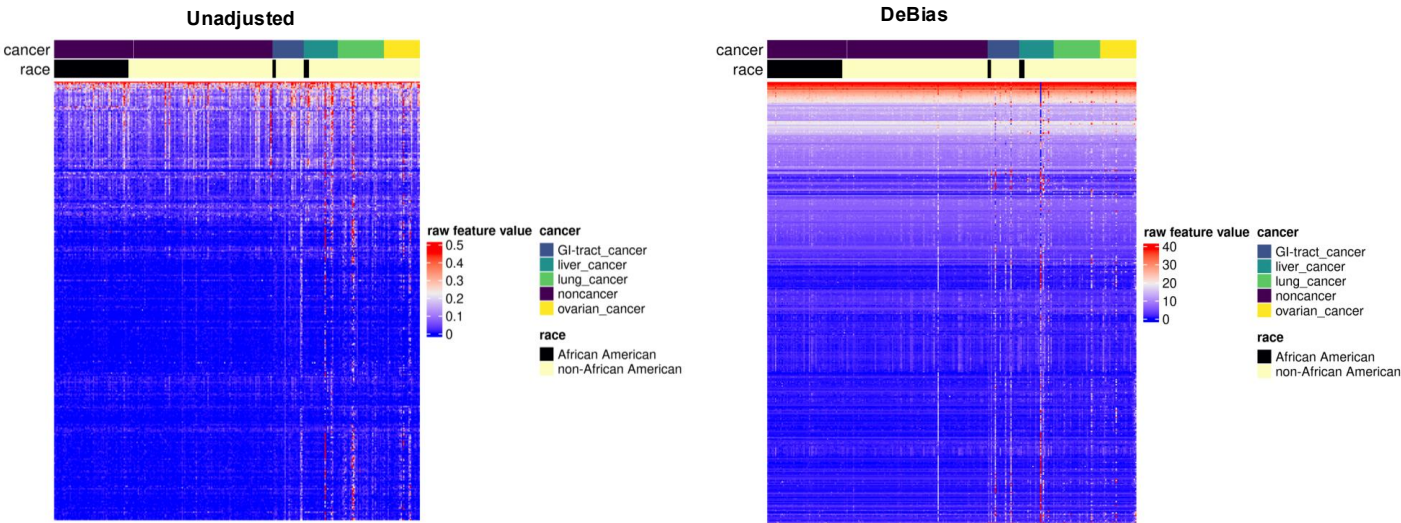
**Fig S4.** Heatmaps of training samples before and after DeBias correction for cross-validation Fold 1 in the racial bias removal analysis of multi-cancer detection.



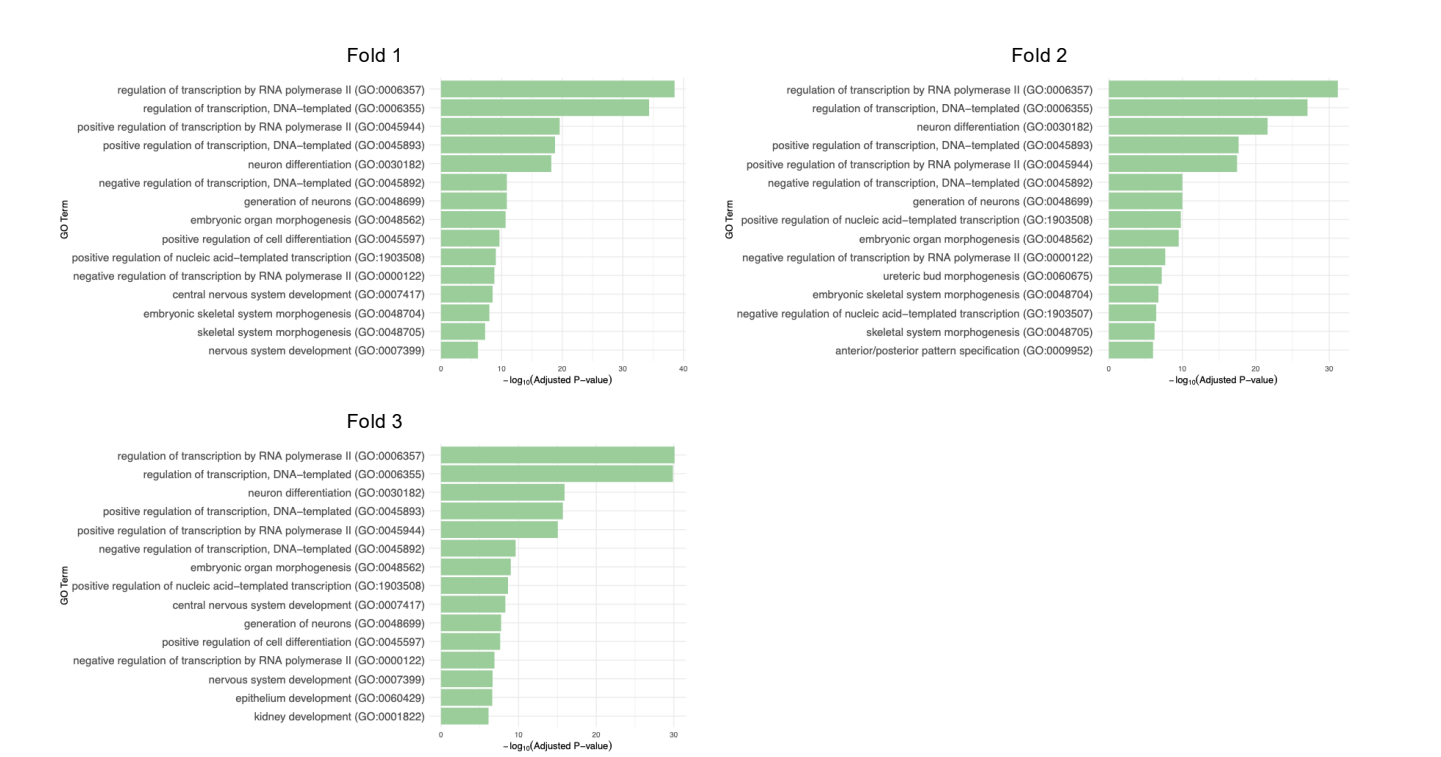
**Fig S5.** Heatmaps of training samples before and after DeBias correction for cross-validation Fold 2 in the racial bias removal analysis of multi-cancer detection.



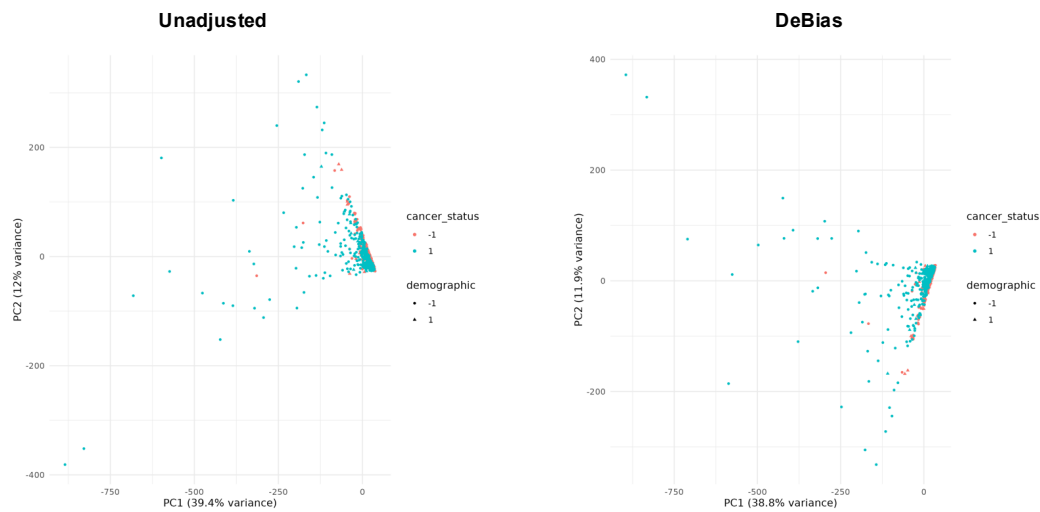
**Fig S6.** Heatmaps of training samples before and after DeBias correction for cross-validation Fold 3 in the racial bias removal analysis of multi-cancer detection.



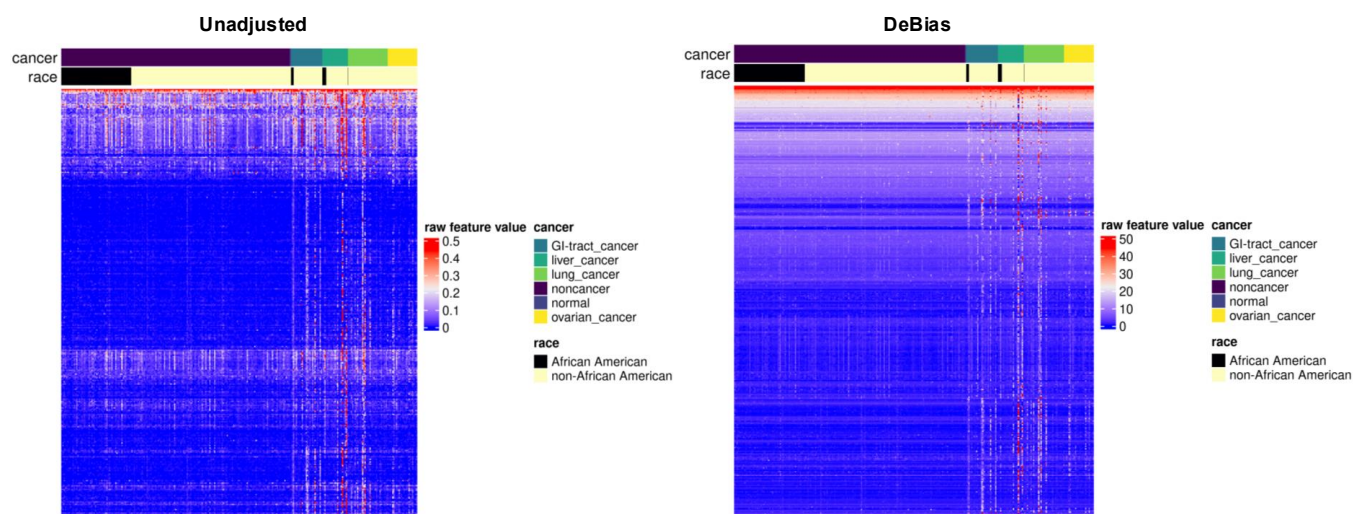
**Fig S7.** Top 15 enriched Gene Ontology (GO) terms (adjusted p-value < 0.001) of the nearest genes corresponding to the most affected features following bias removal across the three cross-validation folds in the multi-cancer detection analysis.



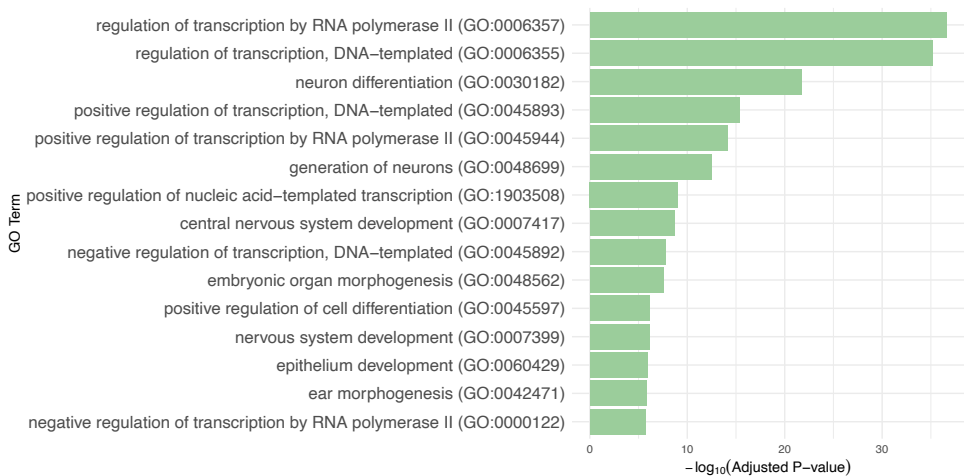
**Fig S8.** Scatter plots of training samples before and after DeBias correction for independent test in the racial bias removal analysis of multi-cancer detection. In the demographic variable, “-1” denotes the minority population and “1” denotes the majority population. In the cancer status variable, “-1” represents noncancer samples and “1” represents cancer samples.



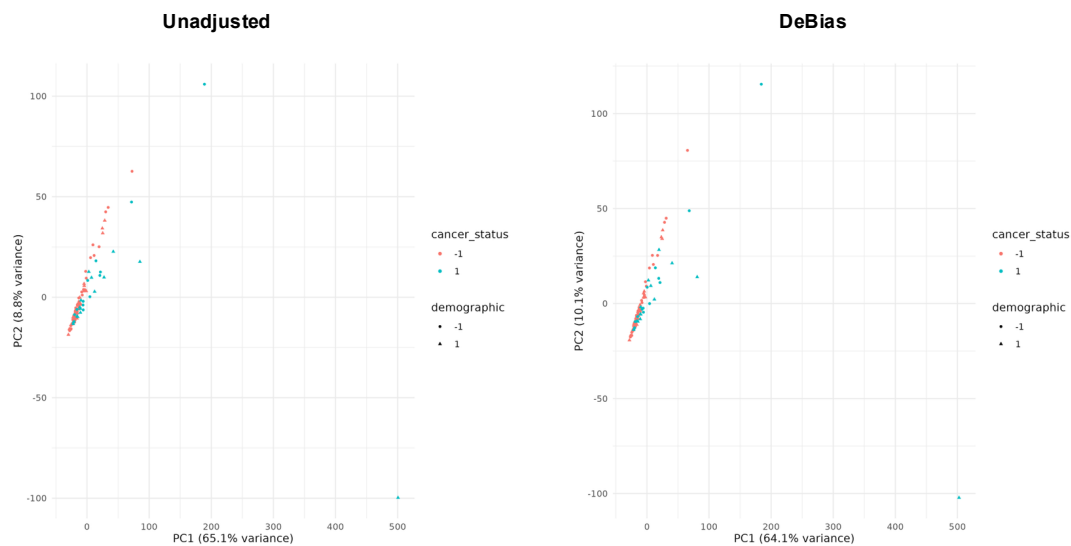
**Fig S9.** Heatmaps of training samples before and after DeBias correction for independent test in the racial bias removal analysis of multi-cancer detection.



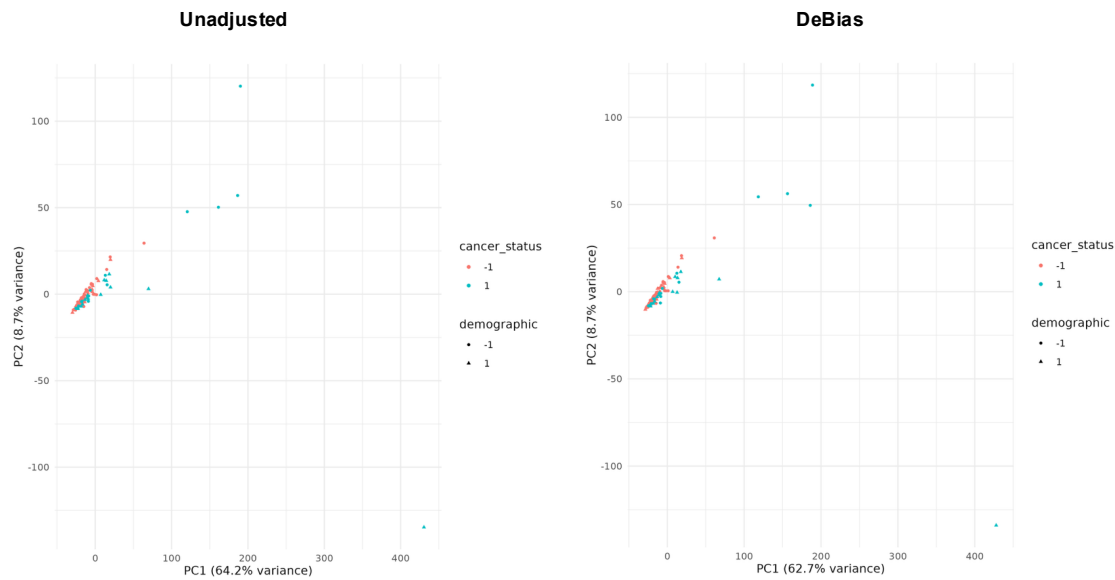
**Fig S10.** Top 15 enriched Gene Ontology (GO) terms (adjusted p-value < 0.001) of the nearest genes corresponding to the most affected features following bias removal across the independent test in the multi-cancer detection analysis.



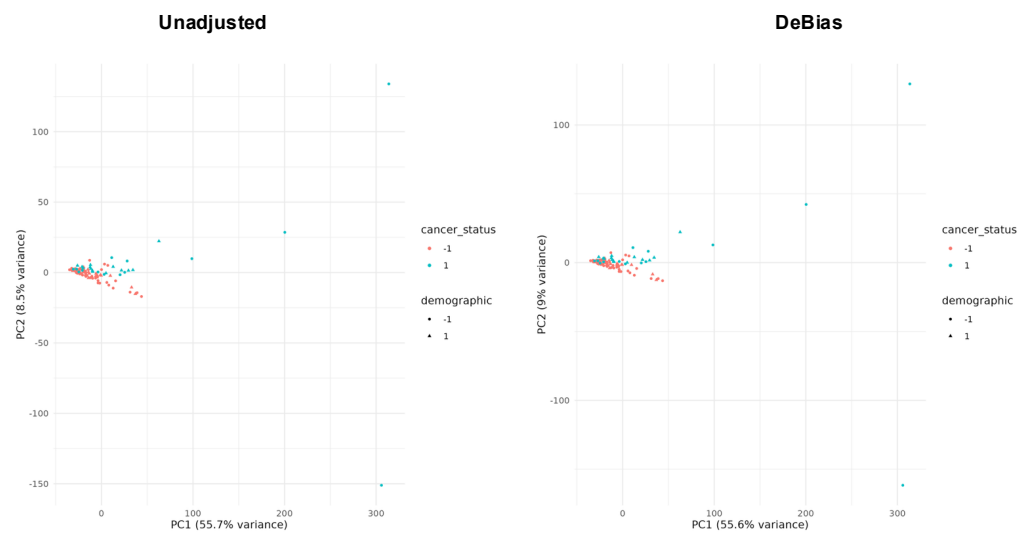
**Fig S11.** Scatter plots of training samples before and after DeBias correction for cross-validation Fold 1 in the ethnicity-related bias removal in liver cancer detection. In the demographic variable, “-1” denotes the minority population and “1” denotes the majority population. In the cancer status variable, “-1” represents noncancer samples and “1” represents cancer samples.



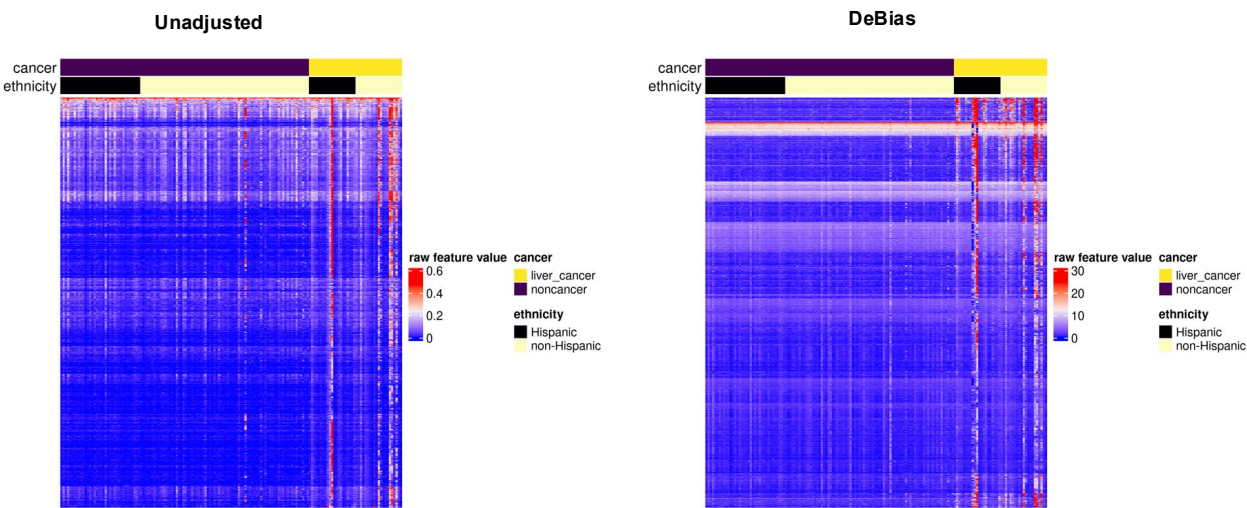
**Fig S12.** Scatter plots of training samples before and after DeBias correction for cross-validation Fold 2 in the ethnicity-related bias removal in liver cancer detection. In the demographic variable, “−1” denotes the minority population and “1” denotes the majority population. In the cancer status variable, “−1” represents noncancer samples and “1” represents cancer samples.



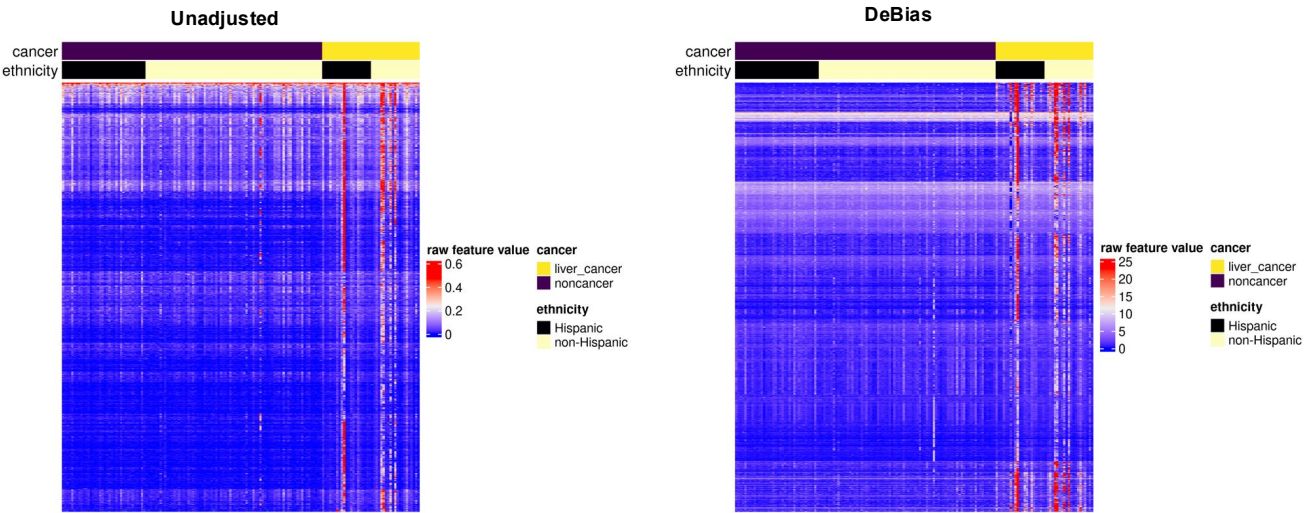
**Fig S13.** Scatter plots of training samples before and after DeBias correction for cross-validation Fold 3 in the ethnicity-related bias removal in liver cancer detection. In the demographic variable, “-1” denotes the minority population and “1” denotes the majority population. In the cancer status variable, “-1” represents noncancer samples and “1” represents cancer samples.



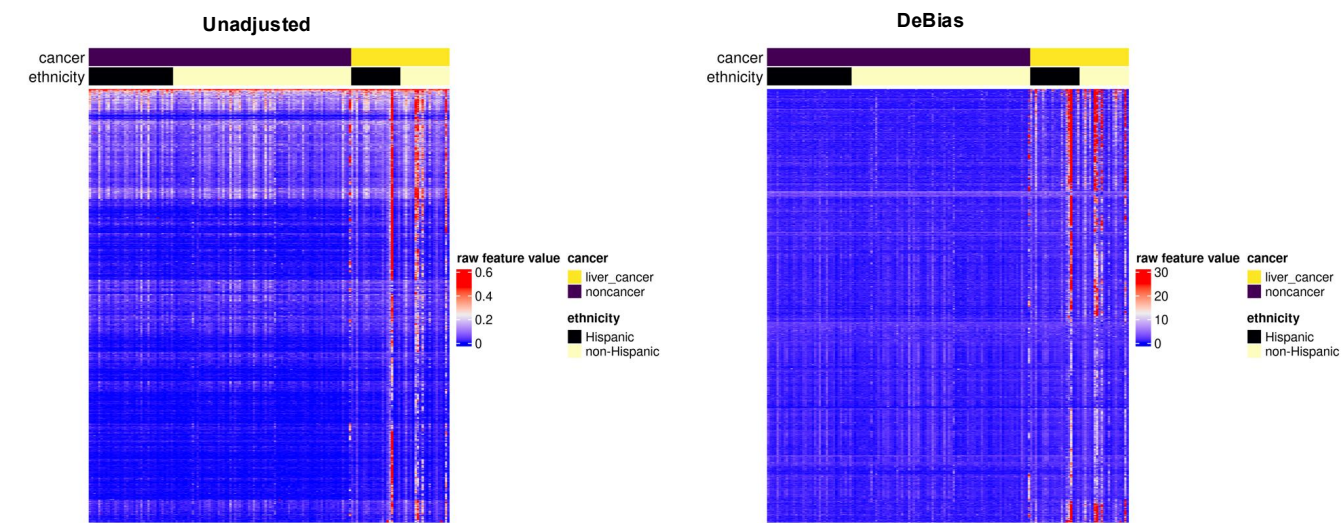
**Fig S14.** Heatmaps of training samples before and after DeBias correction for cross-validation Fold 1 in the ethnicity-related bias removal in liver cancer detection.



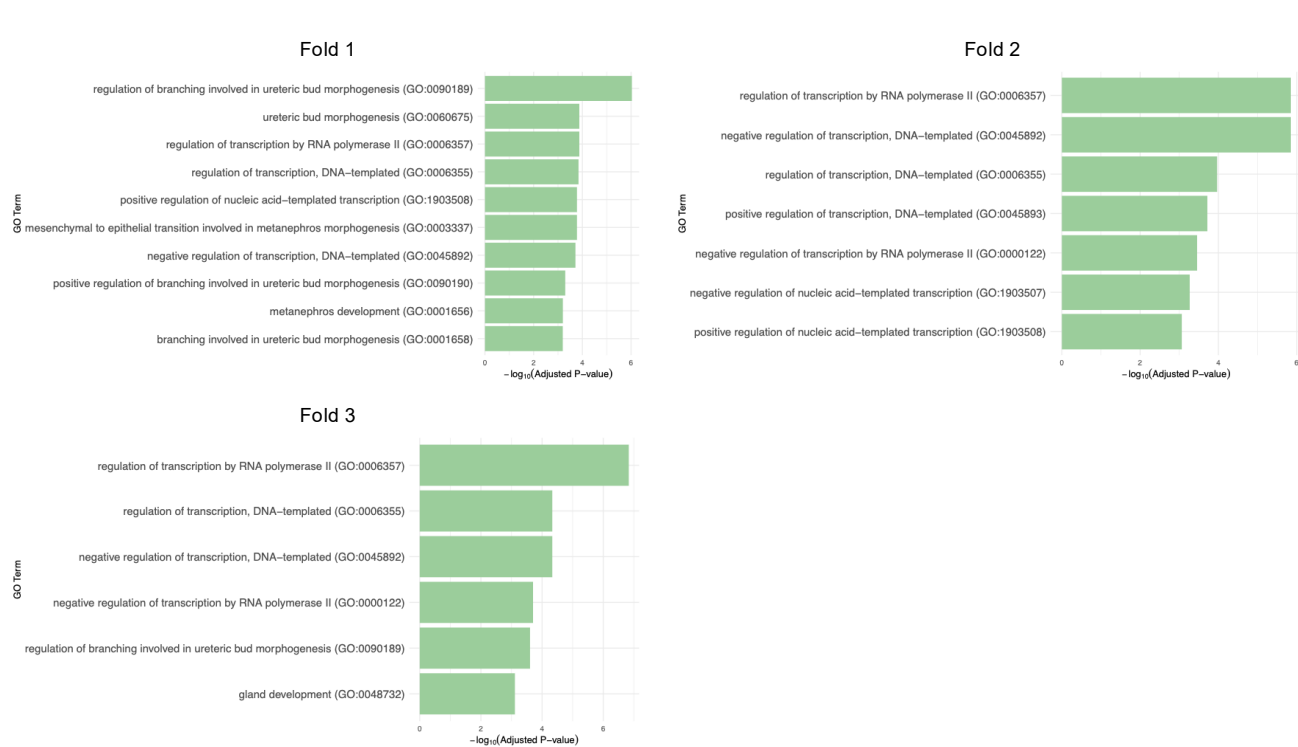
**Fig S15.** Heatmaps of training samples before and after DeBias correction for cross-validation Fold 2 in the ethnicity-related bias removal in liver cancer detection.



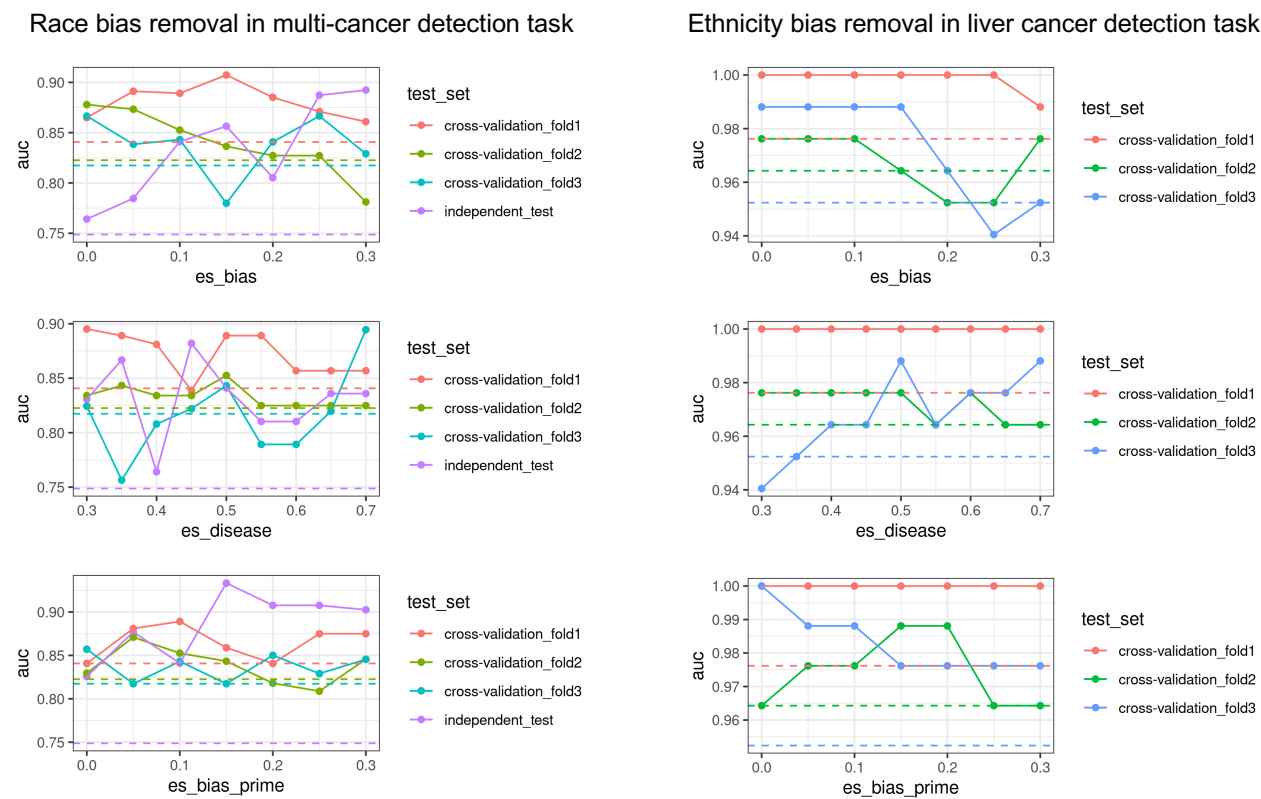
**Fig S16.** Heatmaps of training samples before and after DeBias correction for cross-validation Fold 3 in the ethnicity-related bias removal in liver cancer detection.



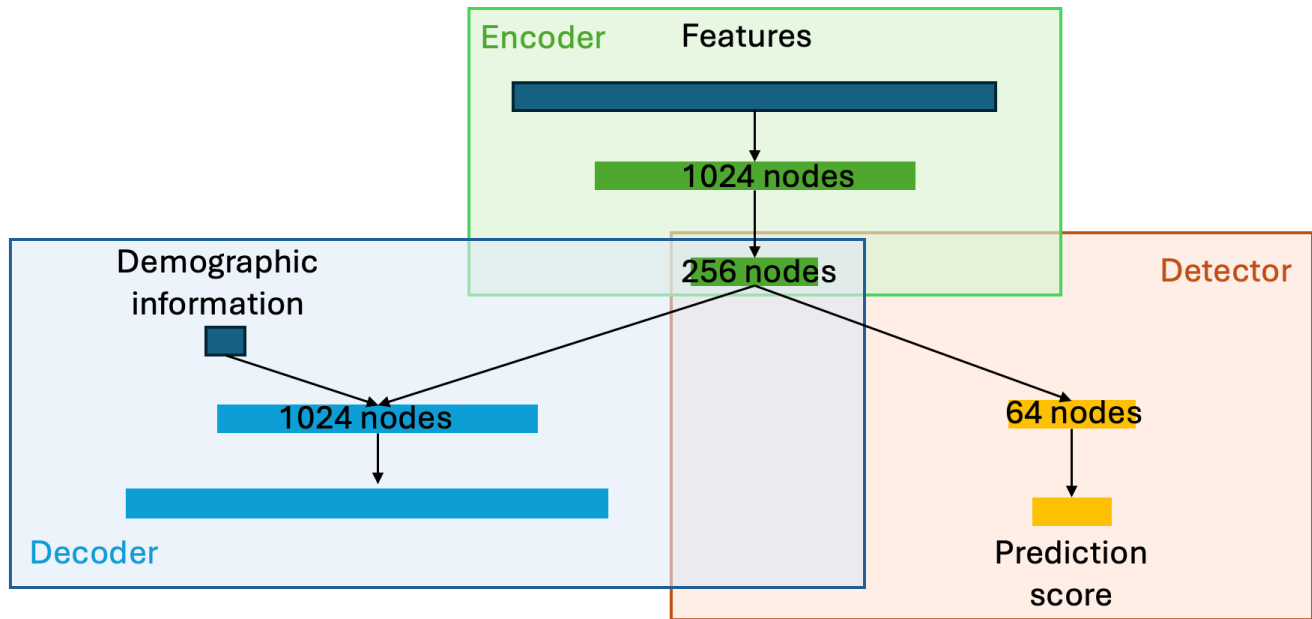
**Fig S17.** Top 15 enriched Gene Ontology (GO) terms (adjusted p-value < 0.001) of the nearest genes corresponding to the most affected features following bias removal across the three cross-validation folds in the liver cancer detection analysis.



**Fig S18.** Cancer detection AUC in the minority population after DeBias under different threshold settings. The dashed line indicates the performance before bias adjustment.



**Fig S19.** Structure Illustration of the variational auto-encoder (VAE).



$$\text{Loss} = w_{\text{decoder}} * \text{MSE}(\text{decoder output, input}) + w_{\text{detector}} * \text{BinaryCrossEntropy}(\text{detector output, true label})$$