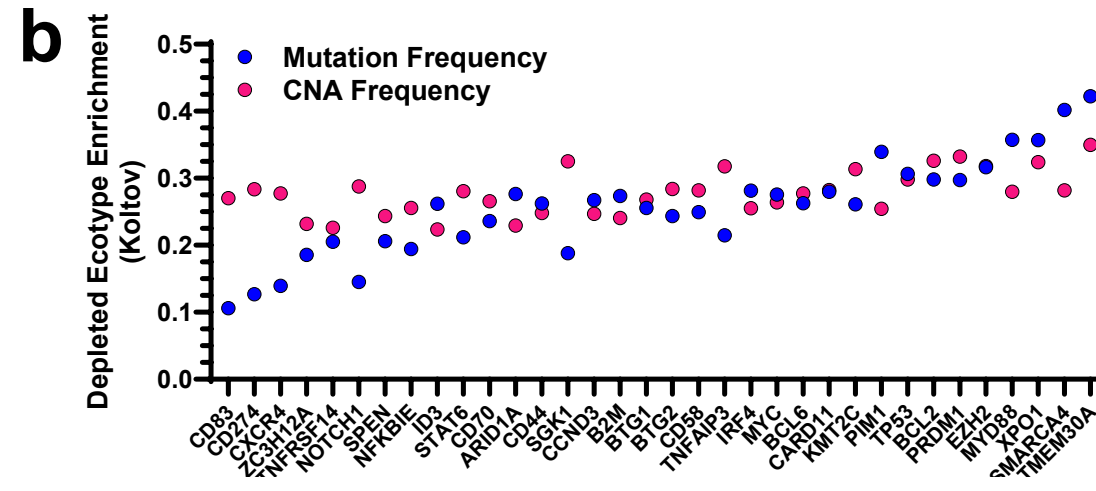
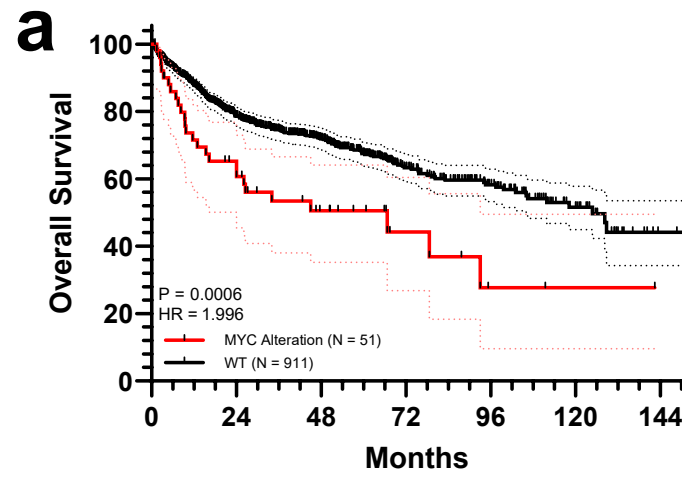
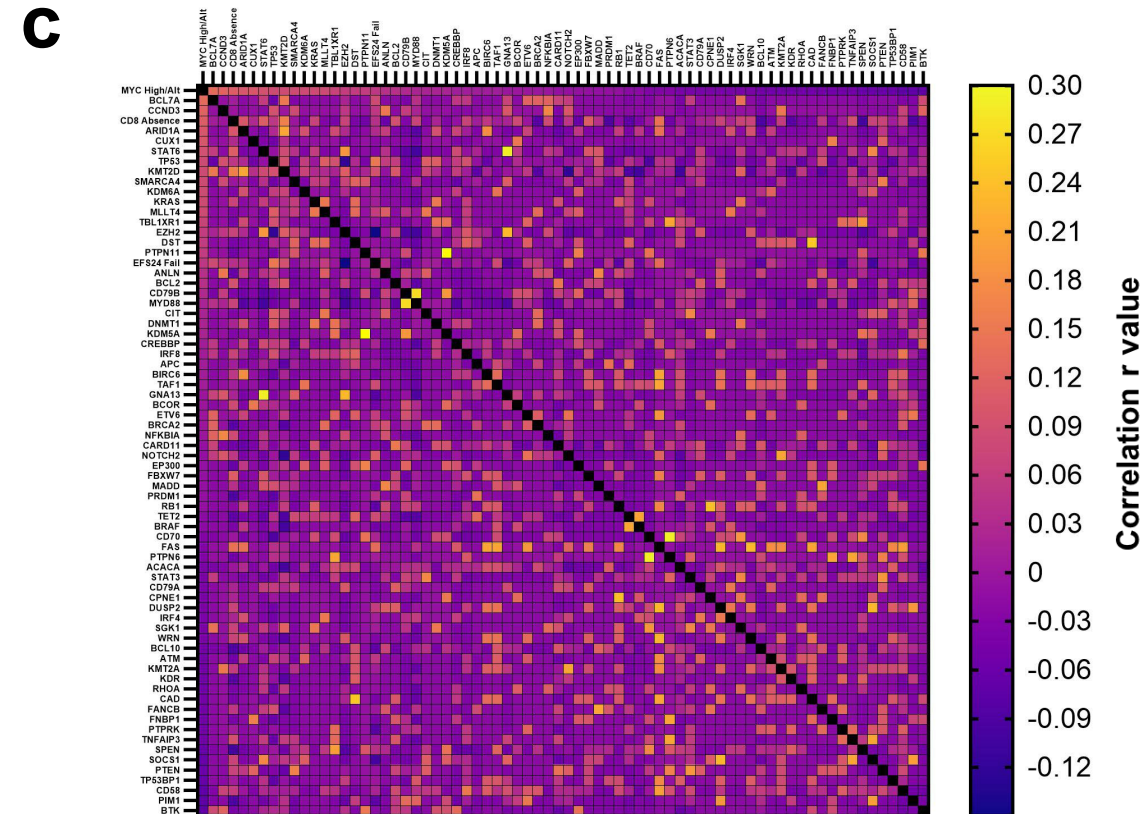
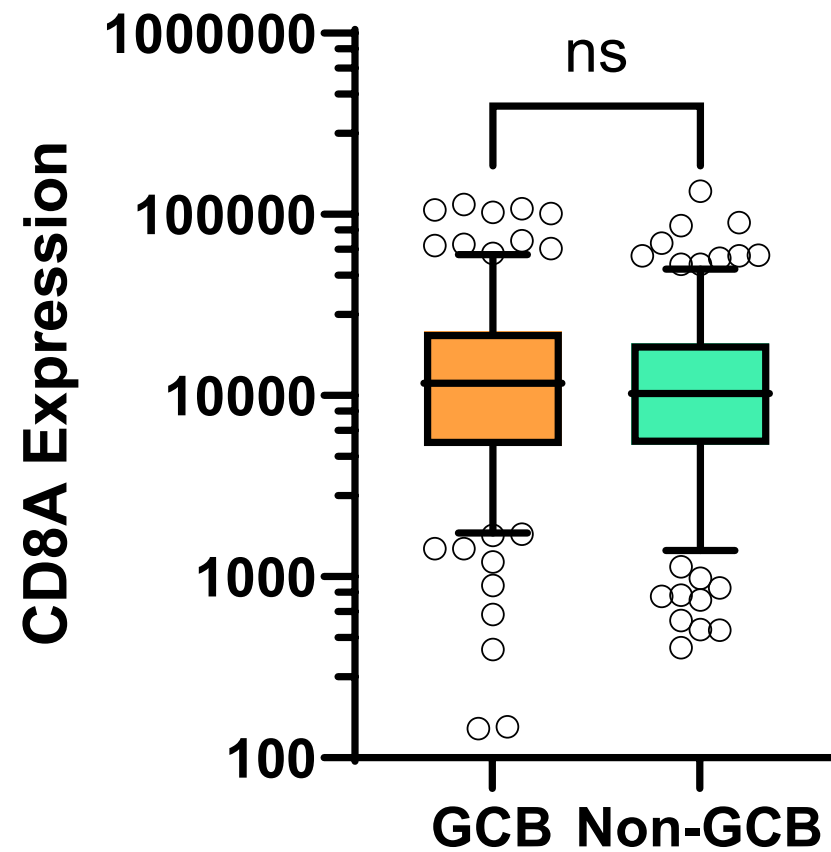
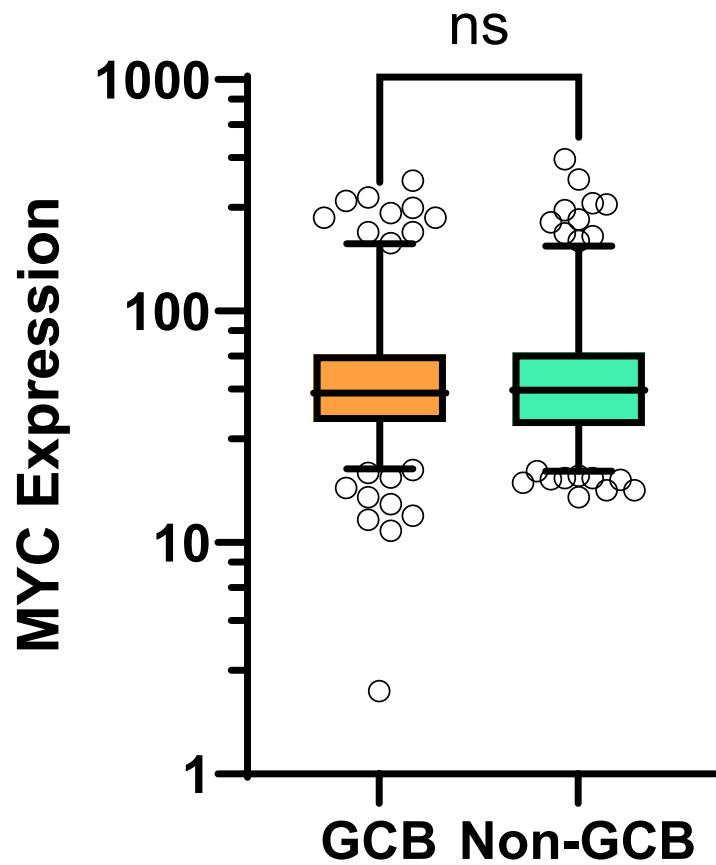


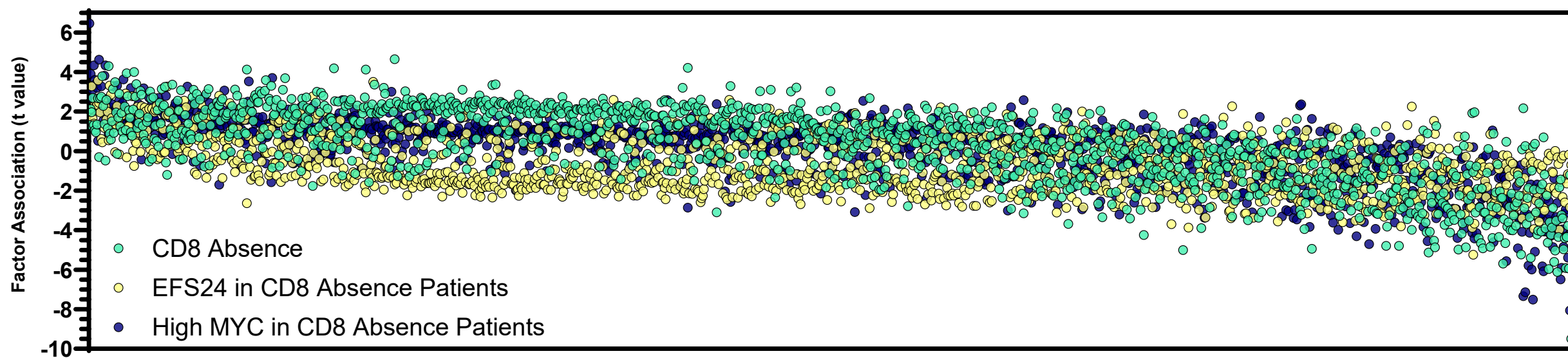


Supp Fig. 1 MYC gene aberrations are associated with inferior survival, enriched within the depleted ecotype (DPE), and co-occur with other DNA alterations. (A) Patients with MYC alterations within the Reddy et. al. study face an inferior de-novo survival prognosis. Significance was determined using Logrank Kaplan-Meier survival analysis. Dotted lines represent 95% confidence intervals. (B) MYC and XPO1 gene alterations are among those enriched in the Depleted tumor microenvironment. Data from the Koltov et. al. 2021 analysis are compared on the differential basis of their DPE subtype for both mutation and Copy Number Alteration (CNA) frequency of each gene. (C) High/Altered MYC co-occurs with notable genomic mutation drivers of lymphomagenesis.

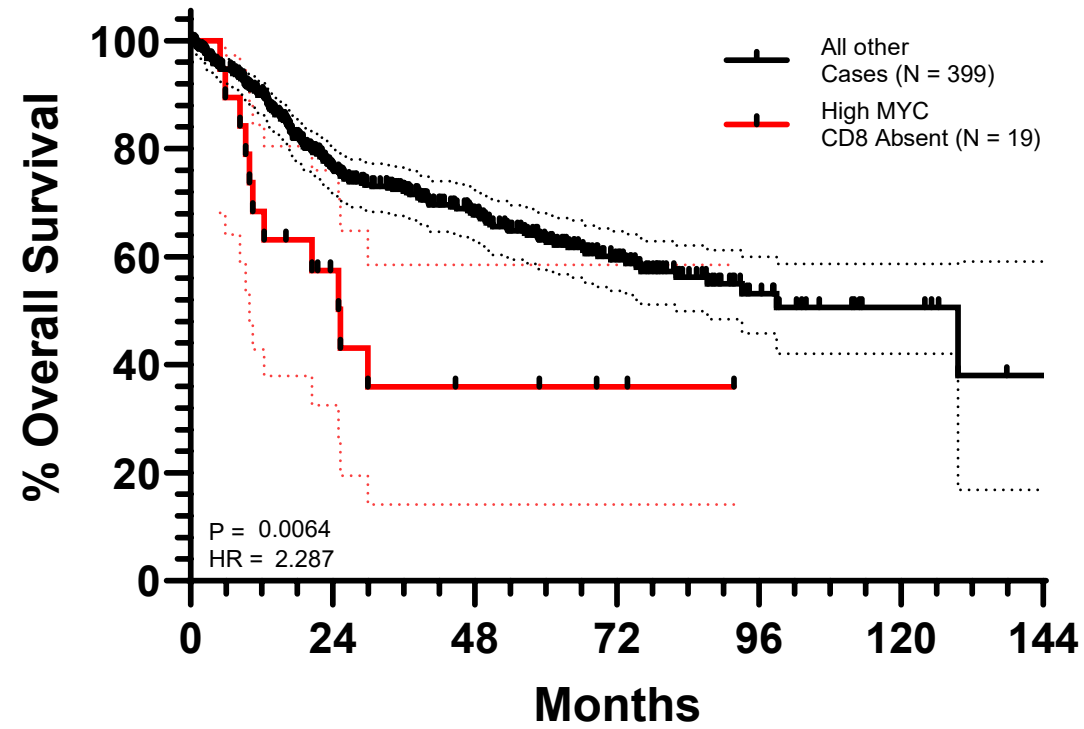
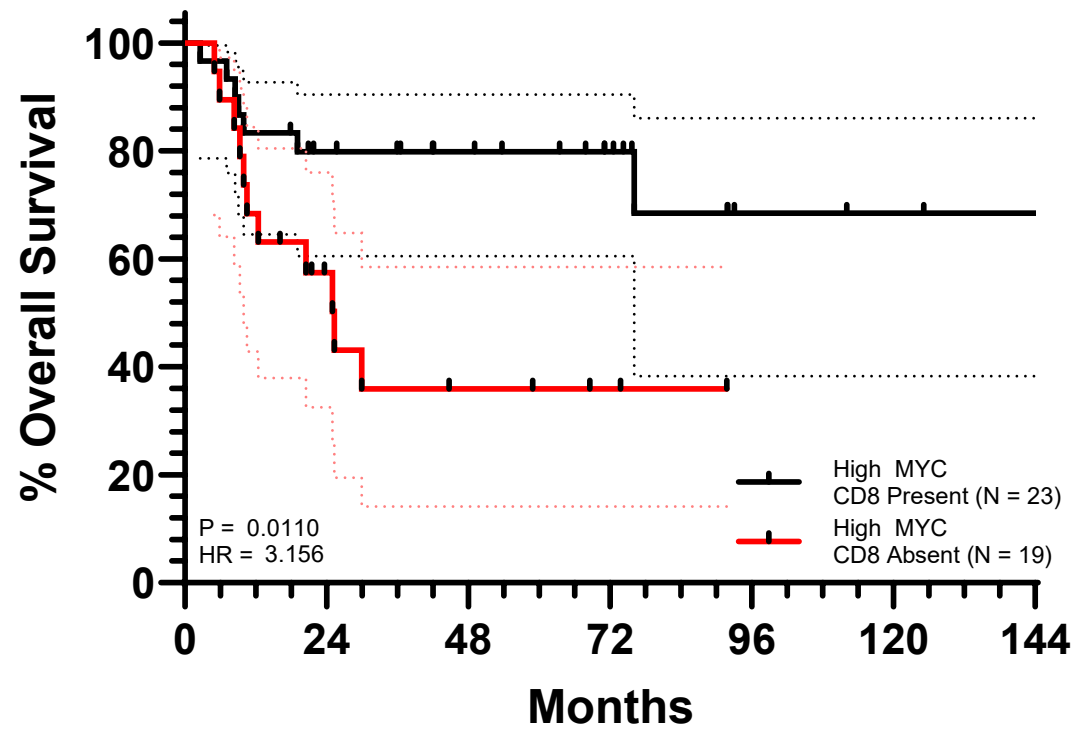




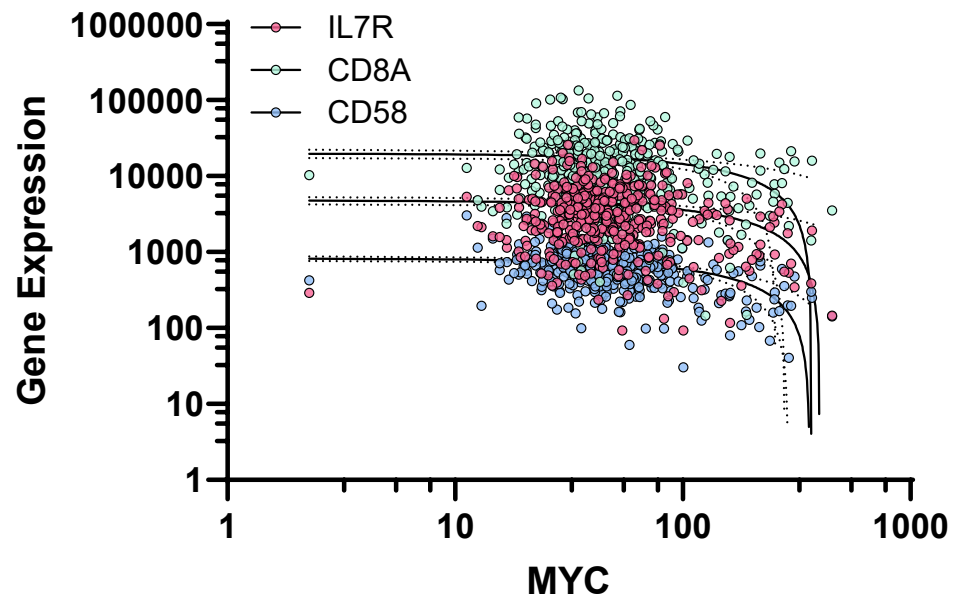
Supp Fig. 2 MYC and CD8A gene expression levels are not associated with Cell of Origin (COO). Median and quartiles are displayed in each box. The top 5% values in either direction are displayed individually. Significance was determined using a Welch's t test.



Supp Fig. 3 CD8, MYC and EFS24 status associations across all genes. Data are descending based on the average t value association of each gene to the 3 factors. 1398 genes with expression data are displayed across 418 patients. Among the total, 109 patients were absent CD8 T-cells, and of these, 35 failed to achieve EFS24 and 19 bore High/Altered MYC.



Supp Fig. 4 Patients with High/Altered MYC and absence of CD8 T-cells face an inferior de-novo survival prognosis. Significance was determined using Logrank Kaplan-Meier survival analysis. Dotted lines represent 95% confidence intervals.



	MYC vs. IL7R	MYC vs. CD8A	MYC vs. CD58
Pearson r			
r	-0.1780	-0.1705	-0.3070
95% confidence interval	-0.2693 to -0.08352	-0.2621 to -0.07579	-0.3914 to -0.2175
R squared	0.03169	0.02906	0.09424
P value			
P (two-tailed)	0.0003	0.0005	<0.0001

Supp Fig. 5 MYC expression is significantly inversely correlated with IL7R, CD8A, and CD58 gene expression.

