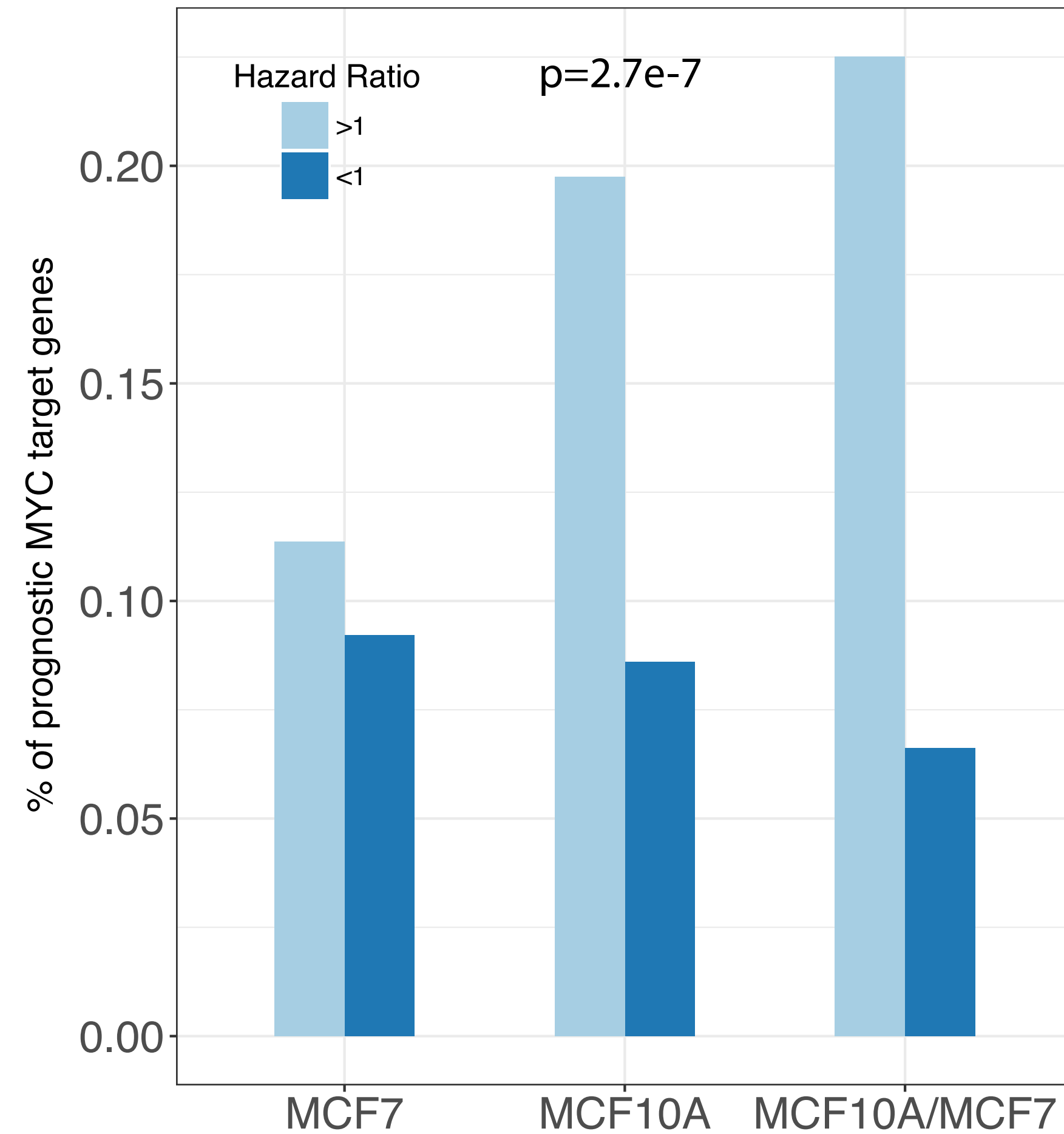


Survival Analysis

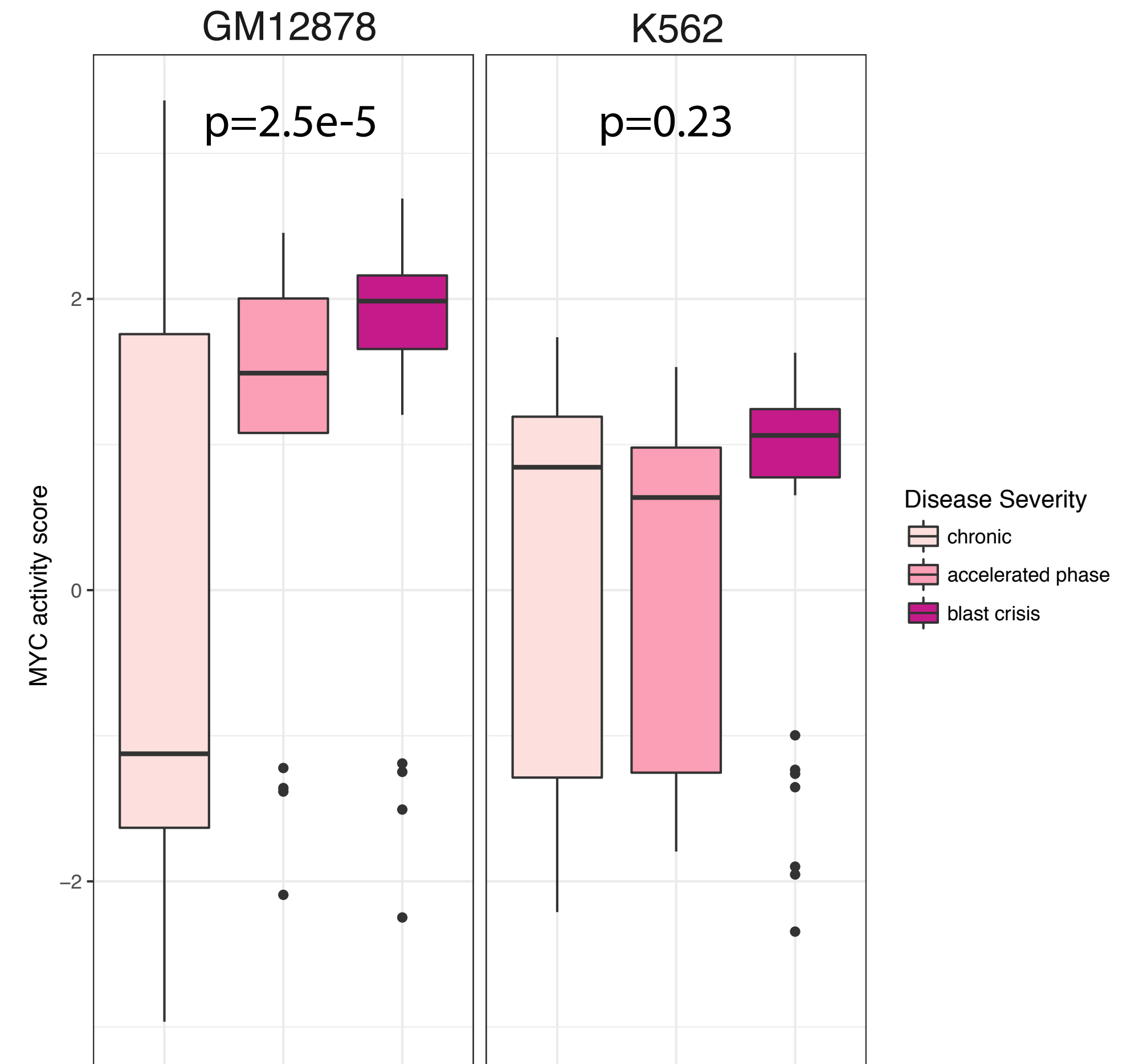
Matt Ung from Chao's lab

DL

Target genes conserved in both normal and cancer cell lines tended to be more associated with poor prognosis. (i.e., core target genes that are essential for proliferation and growth are retained)



METABRIC breast cancer cohort
HQ survival data (n=2509)



Independent CML dataset by Radich et al
MYC activity scores ~ 3 diff severity lvls

1. Expand the target gene analysis (tumor-specific, normal-specific, shared) to AML dataset. We hope to see the similar pattern in leukemia dataset.
2. Survival analysis on key regulator candidates (MCF-7), focusing on two TFs, FOSL2 and JUN, which have ENCODE ChIP-seq data.