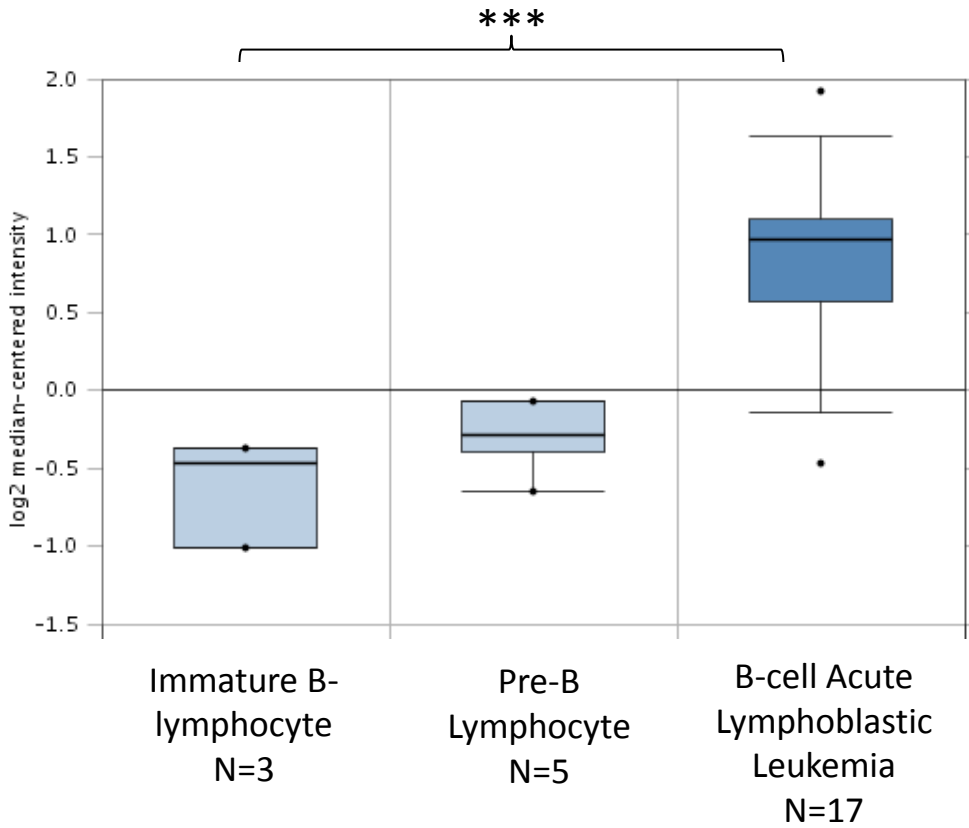
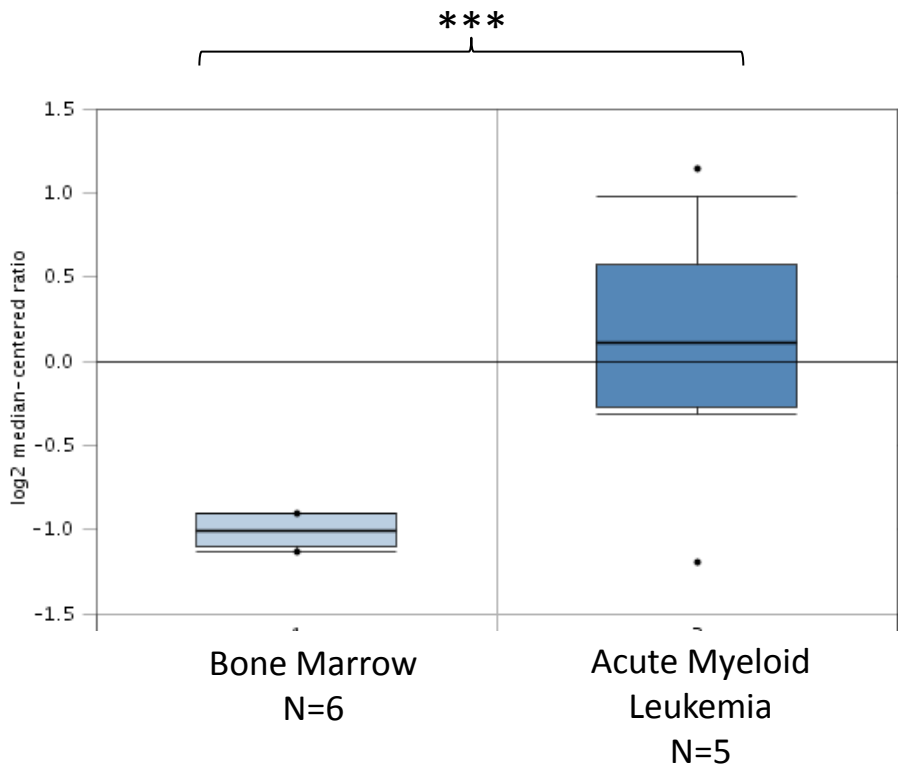


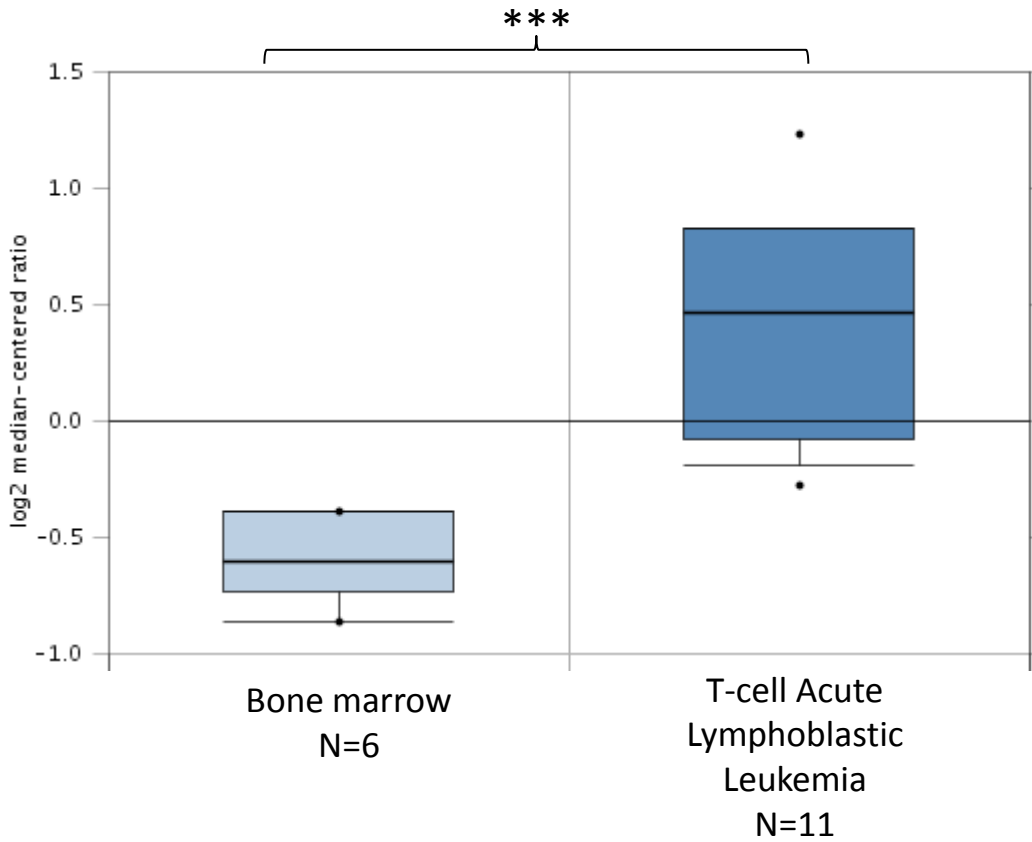
APP expression in B-cell Acute Lymphoblastic Leukemia, *Maia et al., Cancer Res 2005*



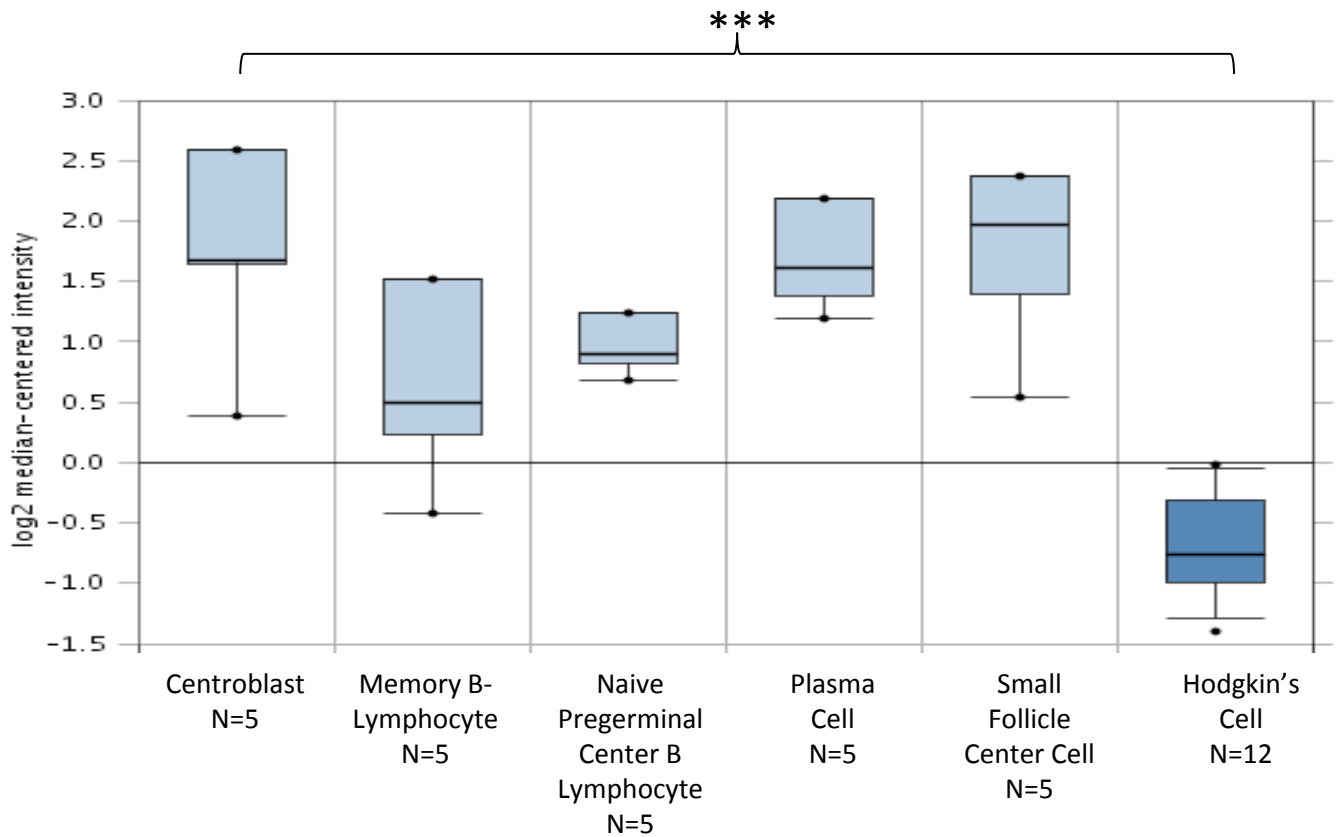
ASCC3 expression in Acute Myeloid Leukemia, *Andersson et al., Leukemia 2007*



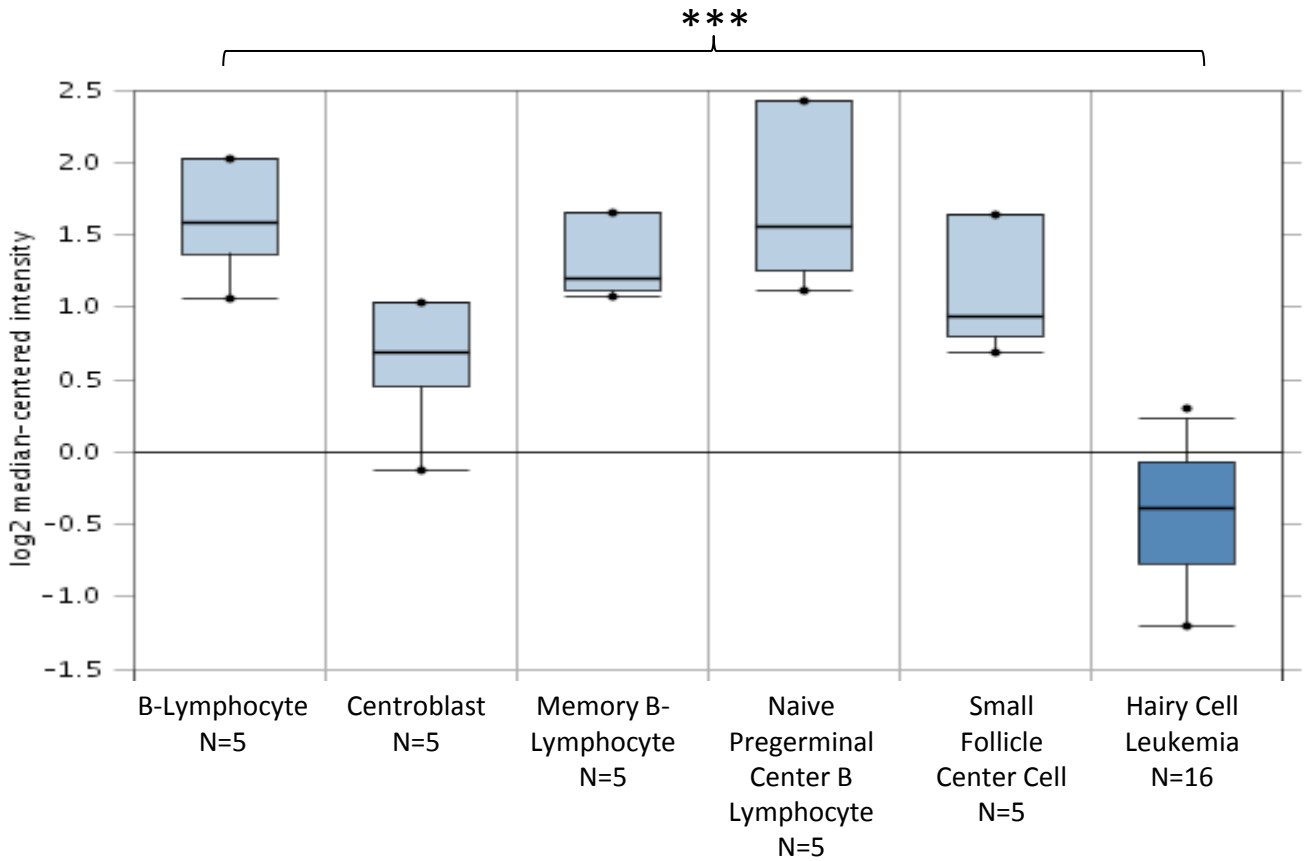
CLCN3 expression in T-cell Acute Lymphoblastic Leukemia, *Andersson et al., Leukemia 2007*



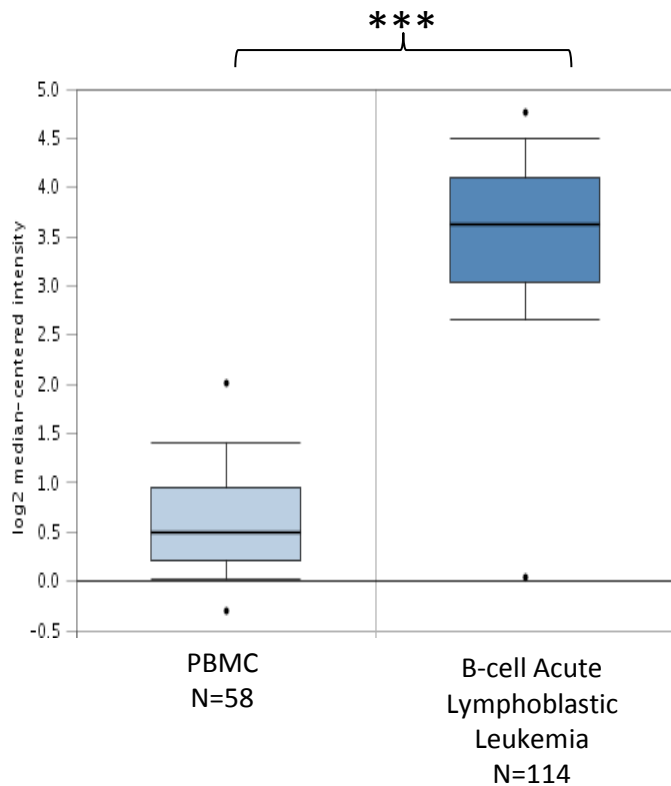
FAM3C expression in Hodgkin's Lymphoma, *Brune et al., J Exp Med 2008*



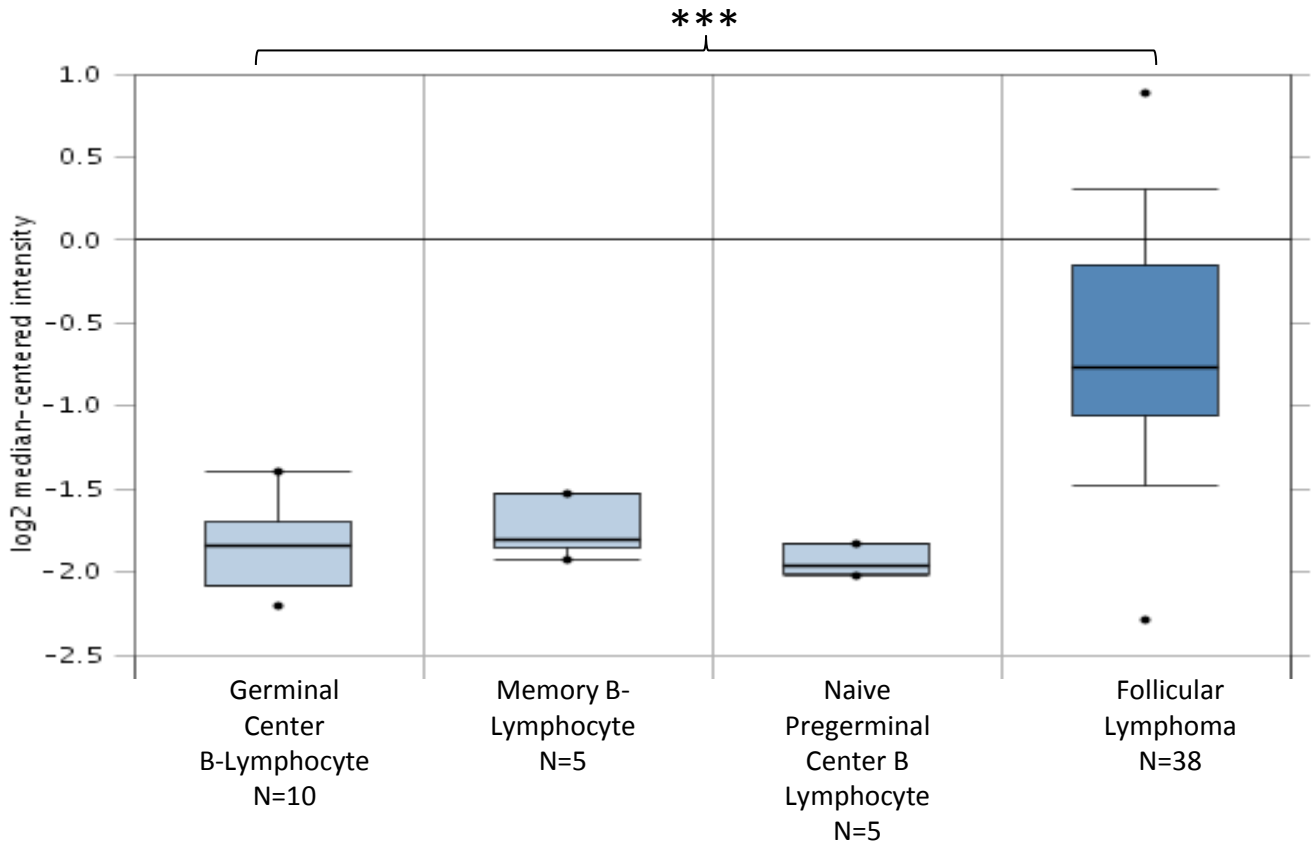
KDM4C expression in Hairy cell Leukemia, *Basso et al., Nat Genet 2005*



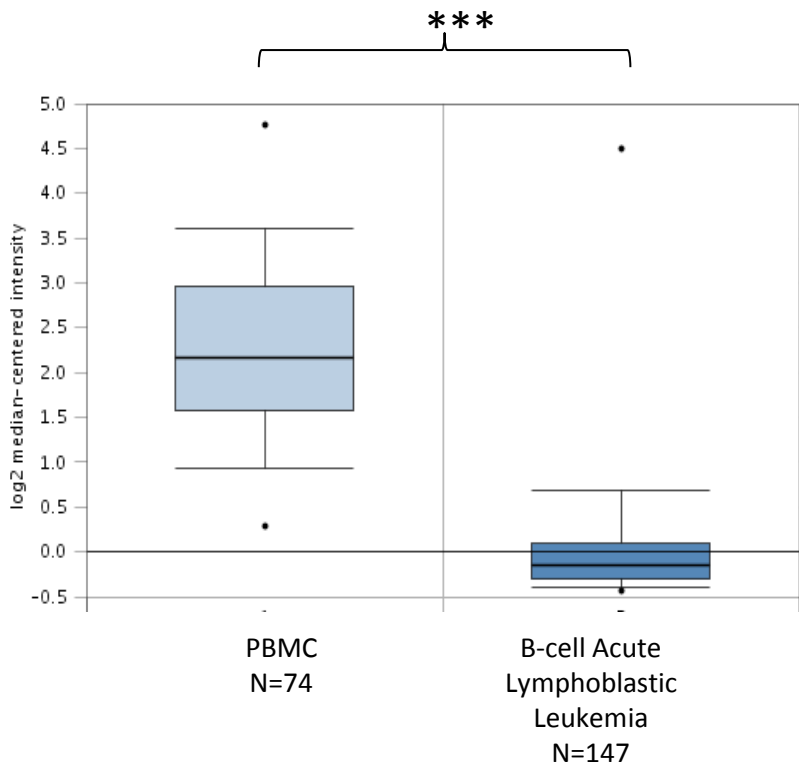
MEF2C expression in B-cell Acute Lymphoblastic Leukemia, *Haferlach et al., J Clin Oncol 2010*



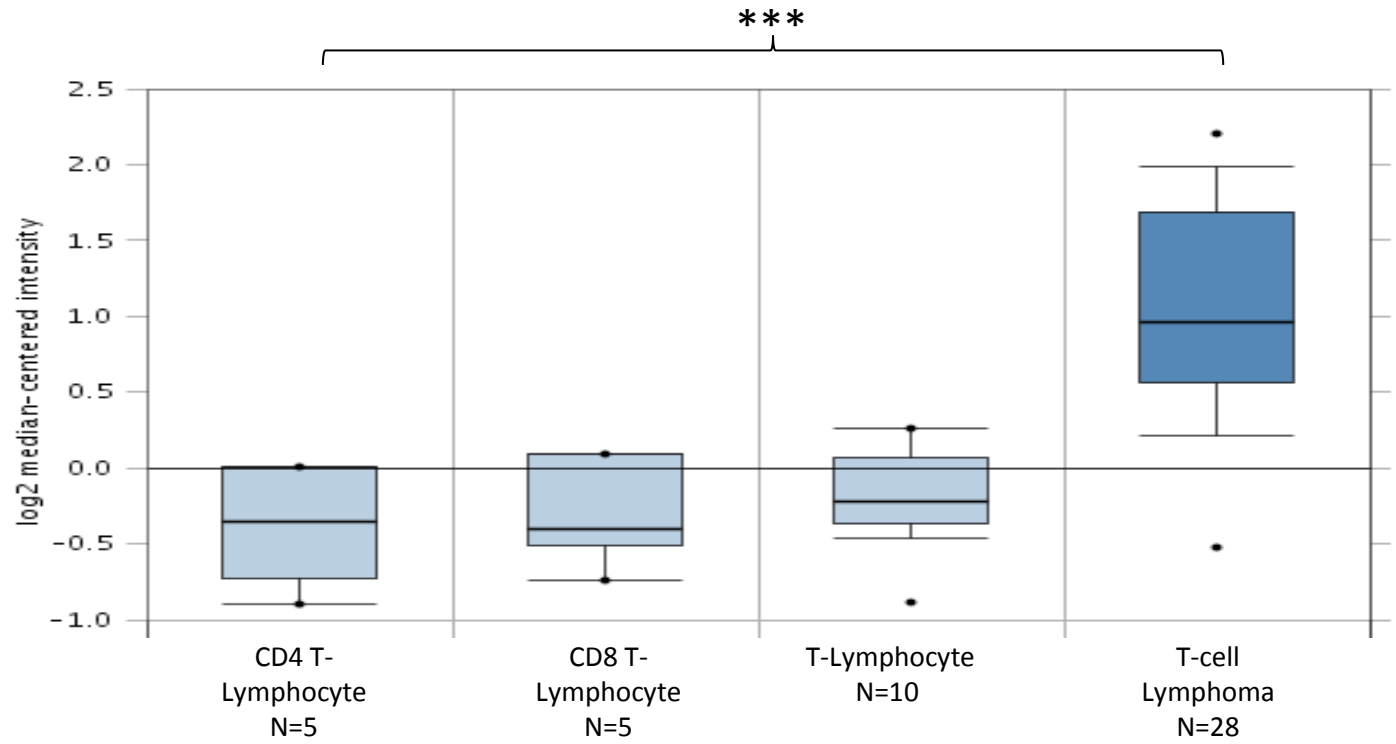
PLA2G4A expression in Follicular Lymphoma, *Compagno et al., Nature 2009*



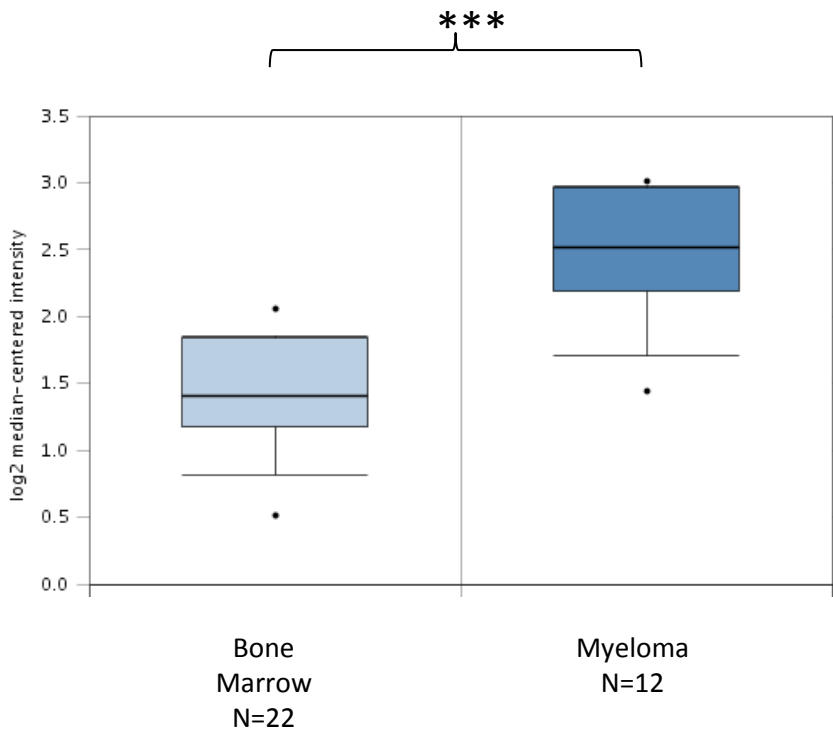
SERPINB2 expression in B-cell Acute Lymphoblastic Leukemia, *Haferlach et al., J Clin Oncol 2010*



WDR33 expression in Peripheral T-Cell Lymphoma, *Piccaluga et al., J Clin Invest 2007*



TMEM135 expression Myeloma, *Zhan et al., Blood 2010*



Supplemental Figure 4. Representative expression of some CIS gene in human hematopoietic tumors. Datamining on Oncomine web resource showed that 53 out of 67 CIS gene are significantly deregulated in human hematopoietic tumor. The name of the deregulated CIS gene and the reference for each study are reported for each graph. Box plots show log₂ of the median centered intensity in non-tumoral tissues (pale blue) and tumors (blue). Dots represent maximum (upper) and minimum (lower) of expression, the whisker lines represent 90th (upper) and 10th (lower) percentile, the box represents from 25th (lower side) to 75th (upper side) percentiles, the thicker line within the box represents the median. Number of samples (N) is indicated below the graph; significance is calculated by unpaired t-test and tumor type is outlined above the graphs.