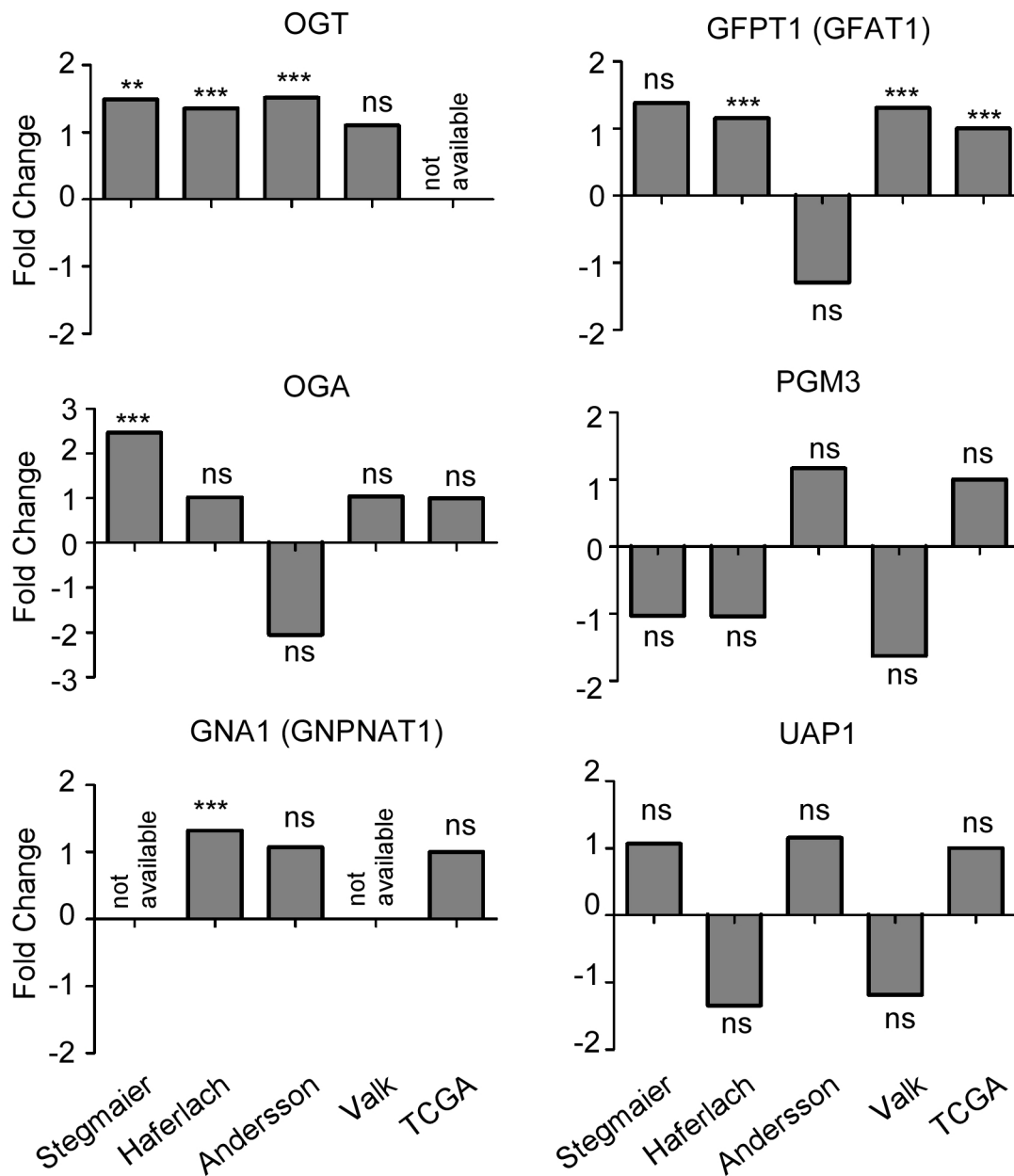


FIGURE S1



**Figure S1. Comparative expression of genes involved in O-GlcNAcylation.**

Fold change mRNA expression levels of normal samples were compared to that of Acute Myeloid Leukemia samples for genes involved in protein O-GlcNAcylation machinery. Fold change and significance was derived by data mining from Oncomine database. Stegmaier, Haferlach, Andersson, Valk, and TCGA leukemia statistics were used to compare the fold change mRNA expression in normal vs AML samples for each gene as indicated in the graph. Statistical significance was determined using t-test. ns= not significant, \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.