



Supplementary Figure S6: Transcriptional analysis of primary AML patient samples. (A) GSEA was performed on expression data from GSE24505 [26] using the set of genes upregulated ≥ 1.5 -fold with an adjusted p-value of < 0.05 in TF-1 cells expressing R132H-mutant IDH1 ($IDH1^{R132H}$) when compared with TF-1 cells expressing empty vector control (Empty) ($n=341$ genes). **(B)** GSEA was performed on expression data from GSE24505 using the set of genes associated with H3K4me3 peaks that are enriched in both $IDH1^{R132H}$ -expressing TF-1 cells and TF-1 cells expressing Cas9 and sgRNAs targeting *KDM5A*, *KDM5C* and *KDM5D* (sgACD) when compared to empty vector control-expressing TF-1 cells and TF-1 cells expressing Cas9 and three non-targeting sgRNAs, respectively ($n=144$ genes). Expression data for the primary patient samples was derived from samples with an *IDH1* or *IDH2* mutation ($n=49$) and samples *wild-type* for *IDH1* and *IDH2* ($n=306$).