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**Supplementary Fig. 1 Whole-genome CRISPR-Cas9 screen in NCI-H1373 cells.**
**A,** Histograms showing the of the frequency of all sgRNA counts in DMSO and RBN-2397 treated samples. **B,** Volcano plot for hits from the DMSO *vs* RBN-2397(20 nM) CRISPR screen. x axis shows gene-level LFC (median of LFC for all sgRNAs per gene, scaled). y axis shows the -log10(adjp) as calculated by MAGeCK. Positive hits (enriched in 20nM RBN-2397 treated cells, LFC > 0.6 and -log10(adjp) > 2 are in blue and negative hits (depleted in 20nM RBN-2397 treated cells, LFC < 0.6 and -log10(adjp) > 2 are in red. **C,** Venn diagram of significantly enriched genes in RBN-2397(10 nM) vs DMSO and RBN-2397(20 nM) vs DMSO (P < 0.05) analyses **D,** Venn diagram of significantly depleted genes in RBN-2397(10 nM) vs DMSO and RBN-2397(20 nM) vs DMSO analyses (P < 0.05). **E,** Pathway analysis of the 346 shared hits in (**D**).