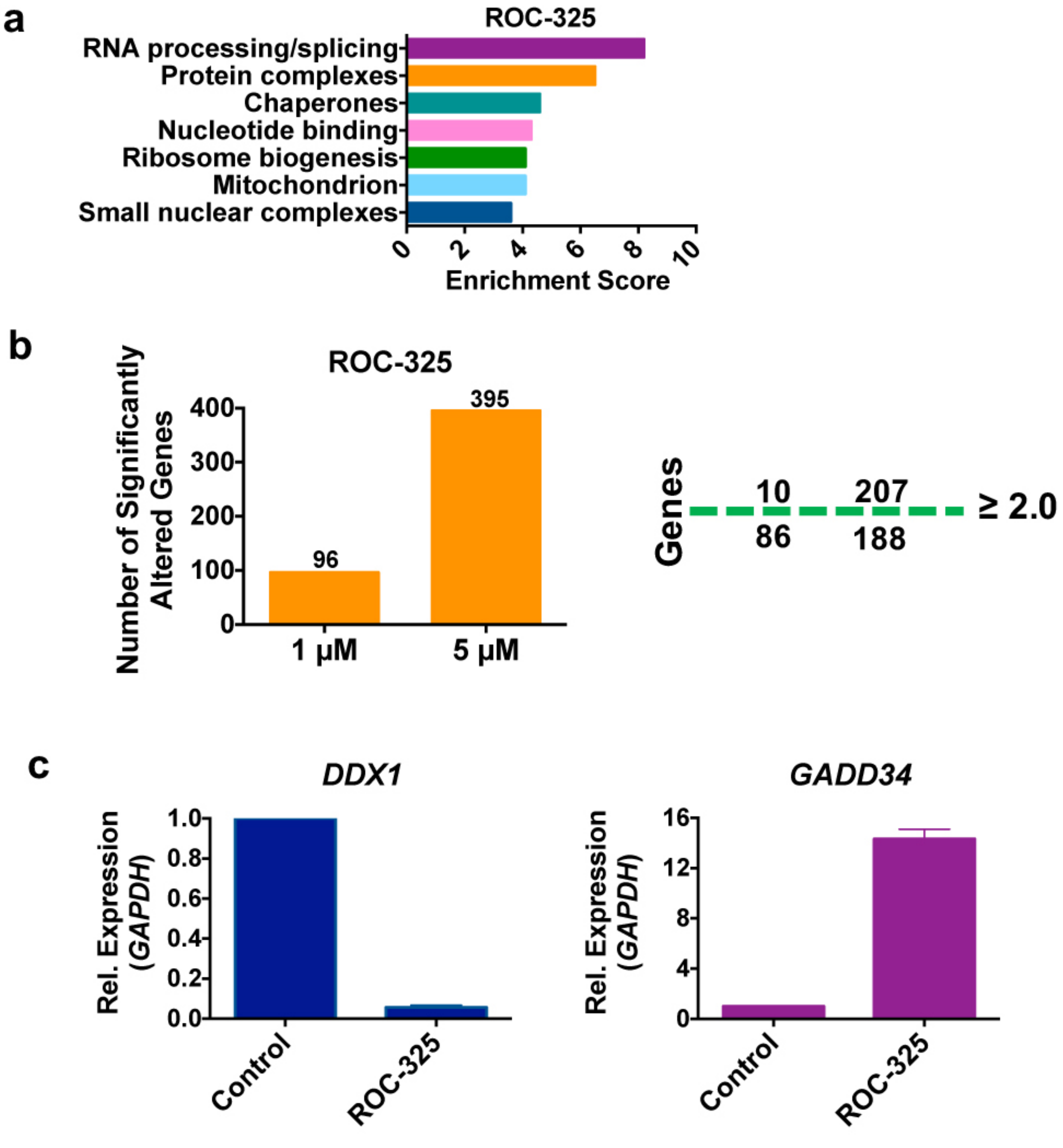
Supplemental Figure 4



Supplemental Figure 4. Transcriptome analysis of the effects of ROC-325. (a) Effects of drug treatment on major pathways. RNASeq was conducted on MV4-11 AML cells treated with ROC-325 as described in the Materials and Methods. Pathway enrichment is shown. RNA processing/splicing; P = 2.22 x 10^{-16}, Q = 0.032; Protein complexes: P = 1.82 x 10^{-8}, Q = 0.011; Chaperones: P = 2.55 x 10^{-8}, Q = 0.046; Nucleotide binding: P = 1.06 x 10^{-6}, Q = 0.002; Ribosome biogenesis; P = 9.64 x 10^{-12}, Q = 0.023; Mitochondrion: P = 3.34 x 10^{-9}, Q = 0.033; Small nuclear complexes: P = 3.45 x 10^{-7}, Q = 0.025. **(b)** Quantification of ROC-325 induced gene expression changes. Left, the number of significantly altered genes for each treatment group. Right, Breakdown of the number of genes significantly upregulated and downregulated for each treatment group. **(c)** Selected qRT-PCR validation of RNASeq results. Two representative genes are shown: DDX1 (significantly downregulated) and GADD34 (significantly upregulated).