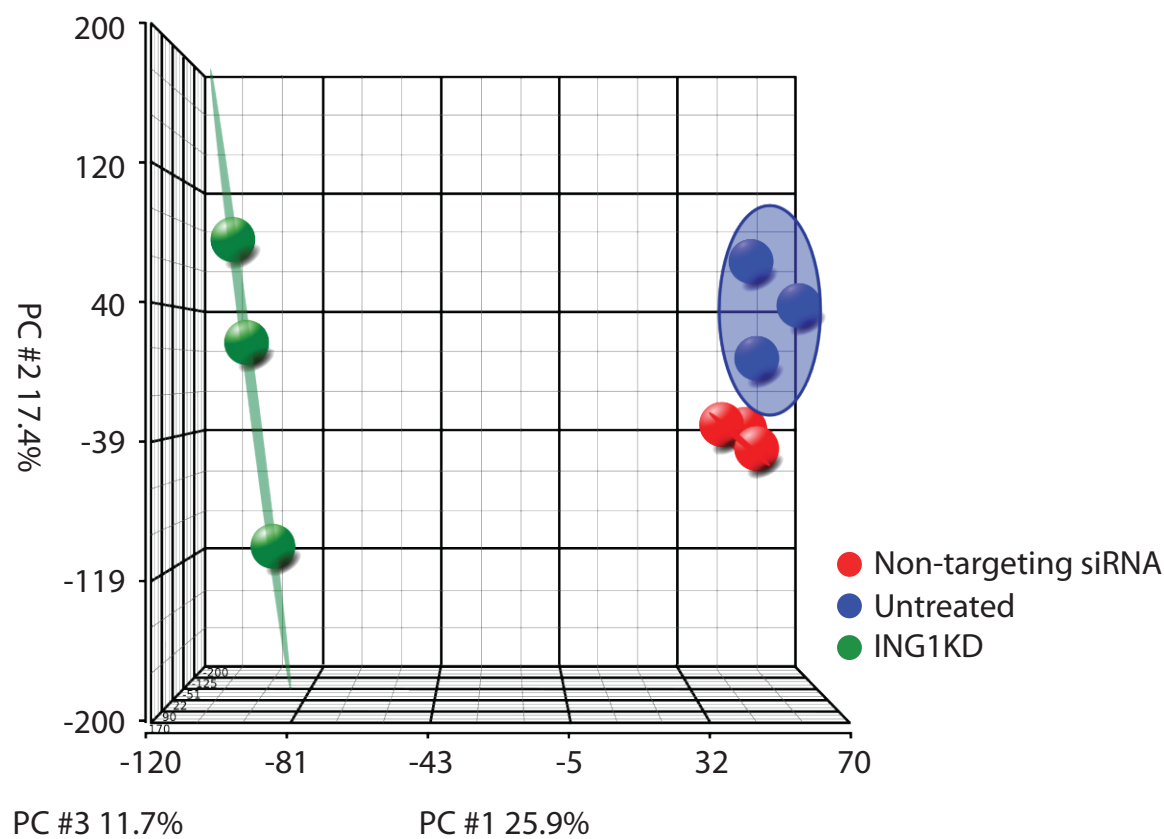
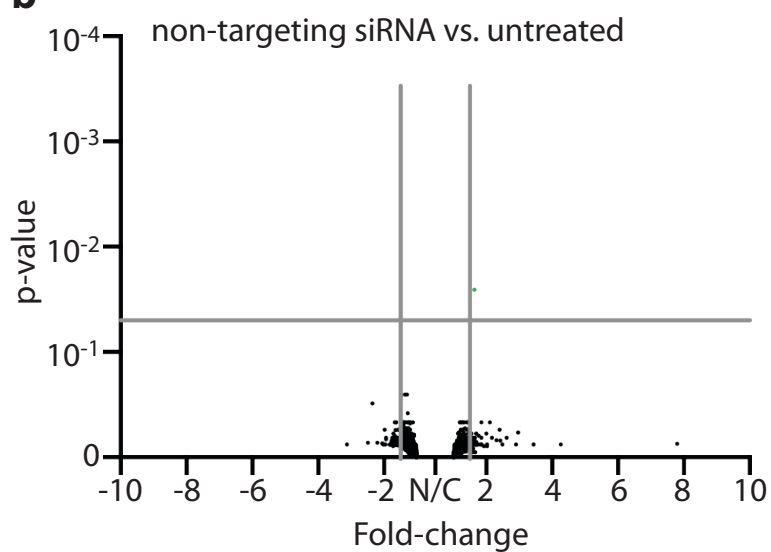
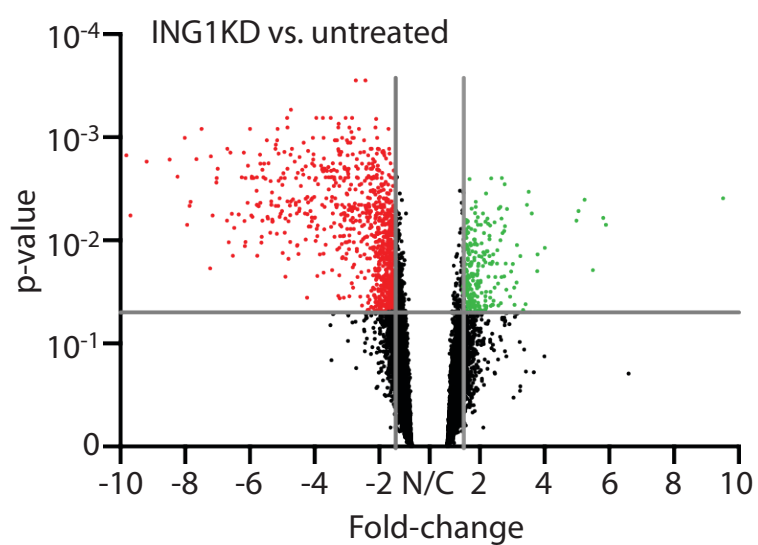
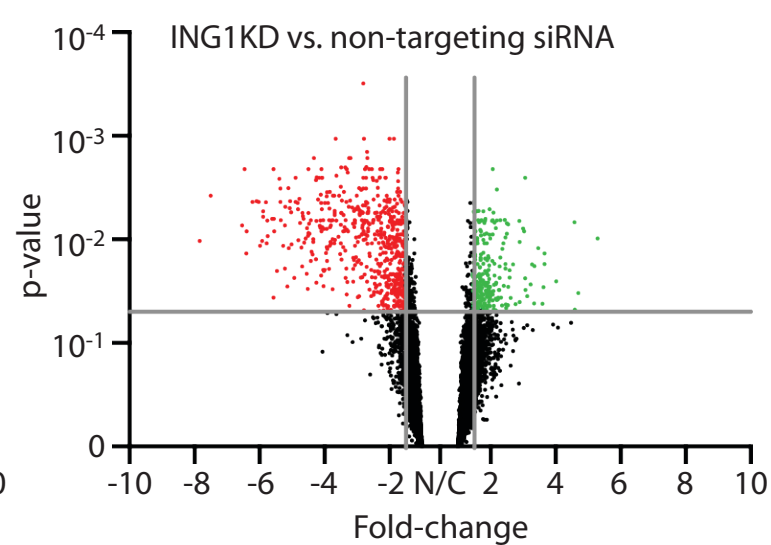


**Figure S4****a****b****c****d**

**Figure S4: Identification of differences in gene expression induced by ING1KD through microarray analysis of the MCF7 transcriptome**

**(a)** PCA analysis of genome-wide mRNA expression shows that samples clearly cluster together based on the experimental conditions used: transfection with ING1 siRNA (green), non-targeting siRNA (red) or no treatment (blue). Each dot represents one sample. **(b-d)** Volcano plot of significance level versus fold change in genetic expression from treated and untreated MCF7 cells. Each black dot represents a gene that had no significant change in expression (grey lines represent cut-off points:  $FC \in [-1.5; 1.5]$ ,  $p < 0.01$  and  $FDR < 0.05$ ). Each red and green dot represents a gene that was downregulated or upregulated, respectively, compared to the control. Differentially expressed genes between ING1KD cells and UNT or NON-T MCF7 cells are shown in (c) and (d) respectively; (b) is the negative control. Two-way ANOVA analysis was performed to determine statistical significance.