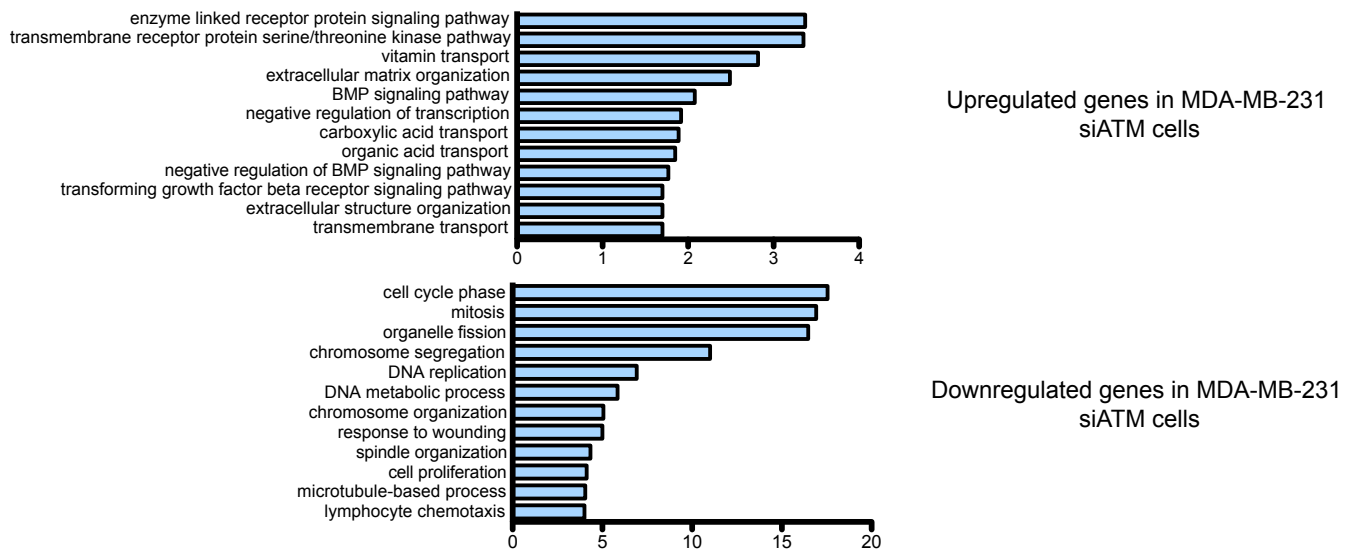


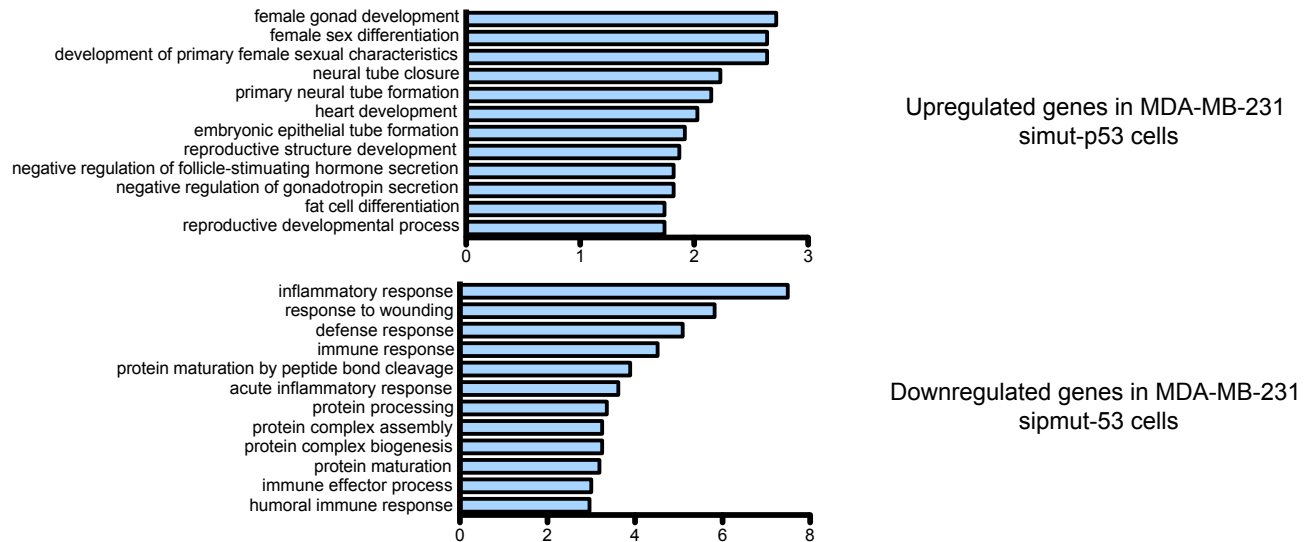
Figure 4-figure supplement 1

Gene ontology (GO) analysis

A



B



C

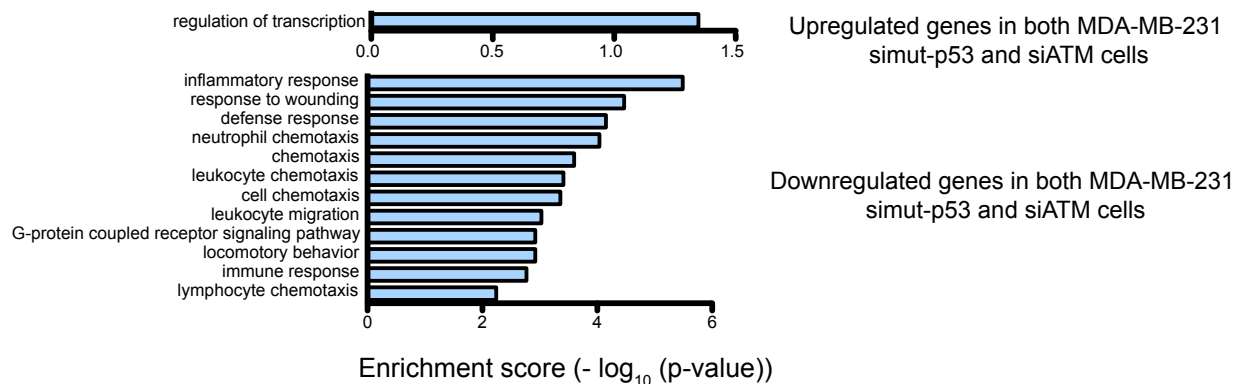


Figure 4—figure supplement 1. Gene ontology analysis of ATM and mutant p53 regulated genes in MDA-MB-231 cells. (A-C) Functional classification of regulated genes in MDA-MB-231 from siATM (A), simut-p53 (B) and genes regulated similarly in both siATM and simut-p53 by more than 1.5 fold (C). Gene ontology analysis was analyzed using the “Functional Annotation Tool” in DAVID (<http://david.abcc.ncifcrf.gov/home.jsp>) and biological process terms are shown. Gene ontology pathways are shown for the upregulated genes (top) and downregulated genes (bottom). X-axis plots $-\log_{10}$ p-values obtained by the gene ontology analysis. The top twelve pathways are shown for each data set.