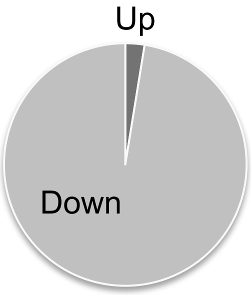
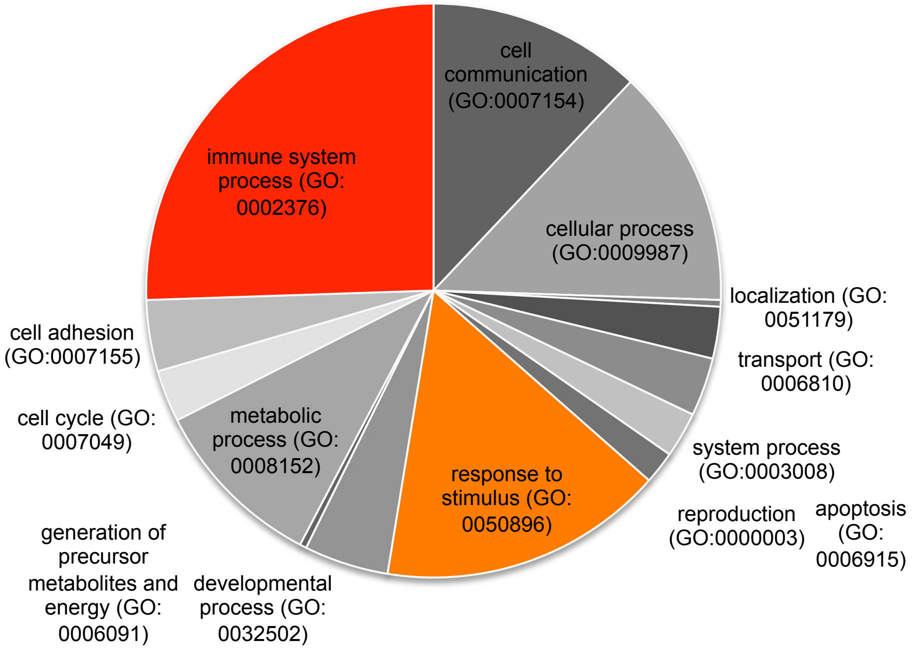
Figure S2

A

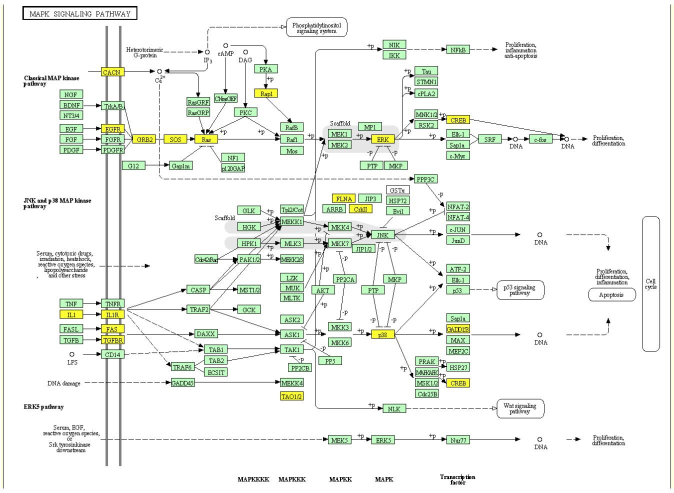


Up-regulated	Down-regulated	Total
28 (2.6%)	**1068** (97.4%)	**1096**

B



C



D

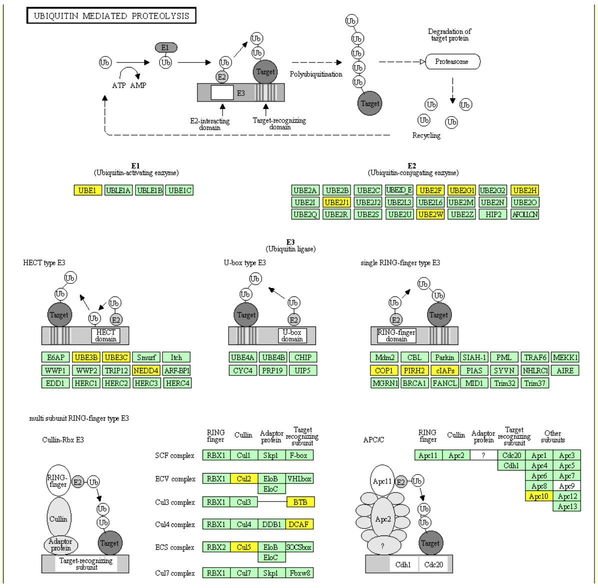


Fig S2 DYRK1A functions as a transcriptional activator. The transcriptome of DYRK1A-depleted HeLa cells was compared to that of HeLa cells transfected with a non-targeted siRNA using Affimetrix Exon arrays in biological triplicates. The threshold was set at a 1.5-fold change in expression. (**A**) Chart showing up-regulated vs. down-regulated genes. (**B**) Chart generated with the PANTHER classification system showing the main GO terms associated with down-regulated genes. Listed below are statistic details for each category (# genes; Percent of gene hit against total # genes; Percent of gene hit against total # Function hits). Cell communication (GO:0007154): 33, 44.6%, 12.0%; cellular process (GO:0009987): 37, 50.0%; 13.5%; localization (GO:0051179):1, 1.4%, 0.4%; transport (GO:0006810): 8, 10.8%, 2.9%; apoptosis (GO:0006915): 9, 12.2%, 3.3%; system process (GO:0003008): 7, 9.5%, 2.6%; reproduction (GO:0000003): 5, 6.8%, 1.8%; response to stimulus (GO:0050896): 44, 59.5%, 16.1%; developmental process (GO:0032502): 13, 17.6%, 4.7%; generation of precursor metabolites and energy (GO:0006091): 1, 1.4%, 0.4%; metabolic process (GO:0008152): 27, 36.5%, 9.9%; cell cycle (GO:0007049): 8, 10.8%, 2.9%; cell adhesion (GO:0007155): 11, 14.9%, 4.0%; immune system process (GO:0002376): 70; 94.6%, 25.5%. (**C**-**D**) Diagrams representing the MAPK signaling, and the ubiquitin-mediated proteolysis pathways. Genes regulated by DYRK1A are represented in yellow.