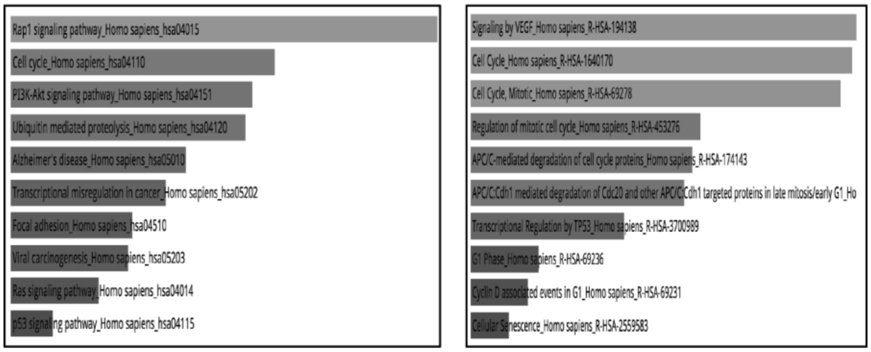
Supplementary Figure 2



Supplementary Fig. S2.

All negatively altered genes were subjected to enrichment analysis via the online gene analysis tool EnrichR, and were assigned to different pathways according to KEGG and Reactome. The figure shows the pathways from KEGG and Reactome with significant p-values (starting from lowest p-value on top).