

## A Downregulated genes

GO Term	Count	P-Value	Benjamini
TOR signaling	3	1.1E-3	3.6E-1
cellular response to corticotropin-releasing hormone stimulus	2	1.1E-2	8.9E-1
protein localization	3	1.1E-2	7.8E-1
positive regulation of transcription from RNA polymerase II promoter	7	1.6E-2	8.1E-1
negative regulation of transcription from RNA polymerase II promoter	6	1.6E-2	7.4E-1
negative regulation of hormone secretion	2	2.1E-2	7.7E-1
negative regulation of pri-miRNA transcription from RNA polymerase II promoter	2	2.1E-2	7.7E-1
post-embryonic development	3	2.4E-2	7.6E-1
negative regulation of cAMP-dependent protein kinase activity	2	3.1E-2	8.1E-1
neuron maturation	2	3.1E-2	8.1E-1
clathrin coat assembly	2	3.1E-2	8.1E-1

## B Upregulated genes

GO Term	Count	P-Value	Benjamini
heart development	10	5.8E-5	4.5E-2
protein phosphorylation	12	1.5E-3	4.5E-1
positive regulation of telomere capping	3	4.9E-3	7.3E-1
organ morphogenesis	5	5.8E-3	6.9E-1
negative regulation of MAPK cascade	3	6.8E-3	6.7E-1
regulation of JNK cascade	3	6.8E-3	6.7E-1
protein glycosylation	5	7.3E-3	6.2E-1
protein ADP-ribosylation	3	7.6E-3	5.8E-1
transcription elongation from RNA polymerase II promoter	3	9.1E-3	6.0E-1
response to calcium ion	4	1.0E-2	6.0E-1

## C Upregulated genes\_Telomerase pathway

GENE NAME
epidermal growth factor receptor(Egfr)
insulin-like growth factor I receptor(Igf1r)
tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase(Tnks)

Figure S3