

Table SX. GO analysis for mRNAs in the hsa_circ_0006220-microRNA-mRNA axis.

ID	Description	GeneRatio	P-value
GO:0001046	Core promoter sequence-specific DNA binding	11/483	2.60E-05
GO:0005200	Structural constituent of cytoskeleton	12/483	3.82E-05
GO:0019887	Protein kinase regulator activity	17/483	4.02E-05
GO:0019207	Kinase regulator activity	18/483	4.49E-05
GO:0000987	Proximal promoter sequence-specific DNA binding	28/483	5.71E-05
GO:0000978	RNA polymerase II proximal promoter sequence-specific DNA binding	27/483	8.07E-05
GO:0001047	Core promoter binding	13/483	0.000153
GO:0031490	Chromatin DNA binding	11/483	0.000191
GO:0000982	Transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding	25/483	0.000225
GO:0001227	Transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific DNA binding	17/483	0.00026
GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase activity	4/483	0.000333
GO:0003727	Single-stranded RNA binding	9/483	0.000345
GO:0033549	MAP kinase phosphatase activity	4/483	0.000456
GO:0019208	Phosphatase regulator activity	9/483	0.000894

GO, Gene Ontology; MAP, mitogen-activated protein; circ, circular RNA; hsa, Homo sapiens.