Table SIX. GO analysis for mRNAs in hsa_circ_0000520-microRNA-mRNA axis.

ID	Description	GeneRatio	P-value
GO:0042826	Histone deacetylase binding	20/714	1.41E-08
GO:0001047	Core promoter binding	21/714	2.97E-07
GO:0001228	Transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific DNA binding	40/714	4.69E-07
GO:0001046	Core promoter sequence-specific DNA binding	15/714	2.06E-06
GO:0000982	Transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding	35/714	3.96E-05
GO:0001158	Enhancer sequence-specific DNA binding	13/714	0.00010835
GO:0035035	Histone acetyltransferase binding	7/714	0.00012774
GO:0000987	Proximal promoter sequence-specific DNA binding	35/714	0.00020548
GO:0001221	Transcription cofactor binding	8/714	0.00020951
GO:0001227	Transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific DNA binding	22/714	0.00022204
GO:0003713	Transcription coactivator activity	27/714	0.00025121
GO:0035326	Enhancer binding	13/714	0.00044017

GO, Gene Ontology; circ, circular RNA; hsa, Homo sapiens.