Table SXI. GO analysis for mRNAs in hsa_circ_0000977-microRNA-mRNA axis.

ID	Description	GeneRatio	P-value
GO:0000982	Transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding	22/283	1.12E-06
GO:0035035	Histone acetyltransferase binding	6/283	5.80E-06
GO:0000987	Proximal promoter sequence-specific DNA binding	21/283	1.46E-05
GO:0001228	Transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific DNA binding	20/283	1.53E-05
GO:0001047	Core promoter binding	10/283	0.000104
GO:0001077	Transcriptional activator activity, RNA polymerase II proximal promoter sequence-specific DNA binding	14/283	0.000184
GO:0000978	RNA polymerase II proximal promoter sequence-specific DNA binding	18/283	0.000269
GO:0005112	Notch binding	4/283	0.000385
GO:0042826	Histone deacetylase binding	8/283	0.000386
GO:0070491	Repressing transcription factor binding	6/283	0.000571
GO:0004842	Ubiquitin-protein transferase activity	17/283	0.000967
GO:0008022	Protein C-terminus binding	10/283	0.001016
GO:0034450	Ubiquitin-ubiquitin ligase activity	3/283	0.001053
GO:0000980	RNA polymerase II distal enhancer sequence-specific DNA binding	6/283	0.001324

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