

Table SXII. GO analysis for mRNAs in hsa_circ_0043278-microRNA-mRNA axis.

ID	Description	GeneRatio	P-value
GO:0000982	Transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding	39/634	5.23E-08
GO:0001227	Transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific DNA binding	24/634	4.12E-06
GO:0000987	Proximal promoter sequence-specific DNA binding	36/634	7.90E-06
GO:0000978	RNA polymerase II proximal promoter sequence-specific DNA binding	34/634	2.29E-05
GO:0001077	Transcriptional activator activity, RNA polymerase II proximal promoter sequence-specific DNA binding	24/634	8.09E-05
GO:0004721	Phosphoprotein phosphatase activity	18/634	8.81E-05
GO:0043021	Ribonucleoprotein complex binding	14/634	0.00011
GO:0001228	Transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific DNA binding	31/634	0.000126
GO:0003727	Single-stranded RNA binding	11/634	0.000137
GO:0019787	Ubiquitin-like protein transferase activity	33/634	0.000241
GO:0046332	SMAD binding	10/634	0.000315
GO:0031625	Ubiquitin protein ligase binding	24/634	0.000378
GO:0050839	Cell adhesion molecule binding	33/634	0.000454
GO:0019888	Protein phosphatase regulator activity	10/634	0.000485
GO:0003713	Transcription coactivator activity	24/634	0.000546

GO:0003730	Mrna 3'-UTR binding	9/634	0.000583
GO:0043022	Ribosome binding	8/634	0.000585
GO:0001078	Transcriptional repressor activity, RNA polymerase II proximal promoter sequence-specific DNA binding	14/634	0.000593
GO:0044389	Ubiquitin-like protein ligase binding	24/634	0.000711
GO:0008013	Beta-catenin binding	10/634	0.000725
GO:0004842	Ubiquitin-protein transferase activity	30/634	0.000855
GO:0001046	Core promoter sequence-specific DNA binding	10/634	0.001155

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