

ESM Table 3 Pathway analysis of predicted miR-222 target genes generated by TargetScan and the MiRanda algorithm

Pathway	Number of times represented TargetScan	FDR-corrected <i>p</i> value	Number of times represented miRanda	FDR-corrected <i>p</i> value
Amyotrophic lateral sclerosis	1	4.94×10^{-2}	0	N/A
Antigen processing and presentation	0	N/A	1	2.62×10^{-2}
Cell adhesion molecules	0	N/A	1	4.00×10^{-2}
ECM–receptor interaction	0	N/A	1	3.52×10^{-2}
Jak-STAT signalling pathway	1	1.78×10^{-2}	0	N/A
MAPK signalling pathway	1	4.84×10^{-2}	3	2.62×10^{-2}
Melanoma	0	N/A	1	3.43×10^{-2}
Natural killer cell-mediated cytotoxicity	1	4.64×10^{-2}		
Pathways in cancer	0	N/A	3	2.62×10^{-2}
Regulation of actin cytoskeleton	0	N/A	2	3.43×10^{-2}
Renal cell carcinoma	1	6.36×10^{-3}	0	N/A
T-cell receptor signalling pathway	0	N/A	1	4.64×10^{-2}
Toll-like receptor signalling pathway	0	N/A	1	4.61×10^{-2}

KEGG pathways were tested for enrichment among target genes using GENECODIS (<http://genecodis2.dacya.ucm.es/>)

ECM, extracellular matrix; Jak-STAT, Janus kinase–signal transducers and activators of transcription; MAPK, mitogen-activated protein kinase