

ESM Table 2 Pathway analysis of predicted miR-222, miR-487b, miR-10b, miR-125b and miR-103 target genes generated by theTargetScan 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
Adherens junction	4	9.62×10^{-9}	2	1.31×10^{-2}
Adipocytokine signalling pathway	1	1.26×10^{-5}	1	1.31×10^{-2}
Apoptosis	1	1.26×10^{-5}	0	N/A
Axon guidance	10	7.98×10^{-5}	1	9.30×10^{-3}
B-cell receptor signalling pathway	3	1.75×10^{-4}	0	N/A
Calcium signalling pathway	11	2.60×10^{-4}	3	8.40×10^{-3}
Cell adhesion molecules	0	N/A	1	1.11×10^{-2}
Cell communication	0	N/A	1	8.40×10^{-3}
Circadian rhythm	2	8.64×10^{-4}	0	N/A
Colorectal cancer	18	9.03×10^{-4}	3	8.40×10^{-3}
Cytokine–cytokine receptor interaction	0	N/A	1	1.48×10^{-2}
Dorsoventral axis formation	2	2.01×10^{-3}	5	8.40×10^{-3}
ECM–receptor interaction	0	N/A	4	7.83×10^{-3}
Fcε RI signalling pathway	14	2.24×10^{-3}	10	1.32×10^{-3}
Focal adhesion	22	3.49×10^{-3}	17	6.30×10^{-3}
Gap junction	9	6.67×10^{-3}	4	8.40×10^{-3}
Glutathione metabolism	0	N/A	1	1.31×10^{-2}
Glycan structures: biosynthesis 1	2	8.54×10^{-3}	0	N/A
Glycan structures: biosynthesis 2	0	N/A	1	8.40×10^{-3}
Glycerophospholipid metabolism	1	9.76×10^{-3}	0	N/A
Glycosylphosphatidylinositol anchor biosynthesis	0	N/A	2	8.27×10^{-3}
GnRH signalling pathway	24	9.62×10^{-9}	18	6.30×10^{-3}
Hedgehog signalling pathway	2	7.98×10^{-5}	0	N/A
Histidine metabolism	0	N/A	1	1.95×10^{-2}
Huntington’s disease	1	8.81×10^{-5}	0	N/A

Pathway	Number of times represented TargetScan	FDR- corrected <i>p</i> value	Number of times represented miRanda	FDR- corrected <i>p</i> value
Inositol phosphate metabolism	0	N/A	1	7.83×10^{-3}
Insulin signalling pathway	14	1.13×10^{-4}	4	6.30×10^{-3}
Jak-STAT signalling pathway	3	4.04×10^{-4}	1	1.52×10^{-2}
Leucocyte transendothelial migration	2	5.94×10^{-4}	5	8.40×10^{-3}
Long-term potentiation	11	6.46×10^{-4}	0	N/A
MAPK signalling pathway	33	1.21×10^{-3}	20	1.32×10^{-3}
Metabolism of xenobiotics by cytochrome P450	1	1.56×10^{-2}	0	N/A
mTOR signalling pathway	3	4.29×10^{-3}	0	N/A
Neuroactive ligand–receptor interaction	1	4.29×10^{-3}	0	N/A
Neurodegenerative disorders	1	4.29×10^{-3}	0	N/A
O-Glycan biosynthesis	1	4.29×10^{-3}	0	N/A
Olfactory transduction	3	4.29×10^{-3}	1	9.05×10^{-3}
Phenylalanine metabolism	0	N/A	2	1.31×10^{-2}
Phosphatidylinositol signalling system	1	4.39×10^{-3}	3	7.83×10^{-3}
Purine metabolism	0	N/A	2	1.26×10^{-2}
Pyrimidine metabolism	0	N/A	2	6.30×10^{-3}
Regulation of actin cytoskeleton	19	9.62×10^{-9}	9	5.45×10^{-3}
RNA polymerase	1	1.48×10^{-2}	0	N/A
T-cell receptor signalling pathway	25	1.54×10^{-4}	3	2.08×10^{-3}
TGF- β signalling pathway	1	1.21×10^{-3}	0	N/A
Tight junction	4	1.21×10^{-3}	1	1.52×10^{-2}
Toll-like receptor signalling pathway	2	9.62×10^{-9}	1	1.95×10^{-2}
Type 2 diabetes mellitus	4	6.23×10^{-7}	0	N/A
Tyrosine metabolism	4	1.31×10^{-2}	0	N/A

Pathway	Number of times represented TargetScan	FDR- corrected <i>p</i> value	Number of times represented miRanda	FDR- corrected <i>p</i> value
VEGF signalling pathway	9	7.98×10^{-5}	8	8.40×10^{-3}
WNT signalling pathway	5	9.62×10^{-9}	1	1.95×10^{-2}

KEGG pathways were tested for enrichment among target genes using GENECODIS

(<http://genecodis2.dacya.ucm.es/>). All KEGG pathway analysis results are in alphabetical order

ECM, extracellular matrix; GnRH, gonadotropin-releasing hormone; Jak-STAT, Janus kinase–signal transducers and activators of transcription; MAPK, mitogen-activated protein kinase; mTOR, mammalian target of rapamycin; VEGF, vascular endothelial growth factor