

Supplementary Table 2. Functional annotation table of the miRNA-720 target genes using DAVID

MN1	MN1 ptoto-oncogene, transcriptional regulator (MN1)	Homo sapiens
GOTERM_BP_DIRECT	intramembranous ossification, regulation of transcription, DNA-templated, negative regulation of osteoblast proliferation, positive regulation of vitamin D receptor signaling pathway, regulation of cell cycle G1/S phase transition,	
GOTERM_CC_DIRECT	nucleus	
GOTERM_MF_DIRECT	protein binding	
OMIM_DISEASE	Meningioma, CEBALID syndrome	
UP_KW_BIOLOGICAL_PROCESS	Transcription, Transcription regulation	
UP_KW_CELLULAR_COMPONENT	Nucleus	
UP_KW_DISEASE	Tumor suppressor, Disease variant, Intellectual disability	
UP_KW_MOLECULAR_PROCESS	Activator, Developmental protein, Developmental protein	
UP_KW_PTM	Acetylation, Phosphoprotein	
UP_SEQ_FEATURE	COMPBias:Polar residues, COMPBias:Pro residues, REGION:Disordered	
STARD13	StAR related lipid transfer domain containing 13 (STARD13)	Homo sapiens
GOTERM_BP_DIRECT	signal transduction, actin cytoskeleton organization, regulation of Rho protein signal transduction, endothelial cell migration, regulation of small GTPase mediated signal transduction, negative regulation of cell migration involved in sprouting angiogenesis, endothelial tube lumen extension	
GOTERM_CC_DIRECT	cytoplasm, lipid particle, cytosol, mitochondrial membrane	
GOTERM_MF_DIRECT	GTPase activator activity, protein binding, lipid binding	
INTERPRO	Rho GTPase-activating protein domain, Sterile alpha motif domain, START domain, Rho GTPase activation protein, Sterile alpha motif/pointed domain, START-like domain	
SMART	START, RhoGAP	
UP_KW_CELLULAR_COMPONENT	Membrane, Mitochondrion, Lipid droplet, Cytoplasm	
UP_KW_DISEASE	Tumor suppressor	
UP_KW_MOLECULAR_PROCESS	GTPase activation	
UP_KW_PTM	Acetylation, Phosphoprotein	
UP_SEQ_FEATURE	COMPBias:Polar residues, DOMAIN:Rho-GAP, DOMAIN:SAM, DOMAIN:START, MUTAGEN:K->E: Loss of RhoGAP activity., MUTAGEN:R->A: Loss of RhoGAP activity., MUTAGEN:R->E: Loss of RhoGAP activity., REGION:Disordered	
SUSD2	sushi domain containing 2 (SUSD2)	Homo sapiens
GOTERM_BP_DIRECT	negative regulation of cell division, negative regulation of cell cycle G1/S phase transition	
GOTERM_CC_DIRECT	extracellular space, plasma membrane, integral component of membrane, extracellular exosome	
GOTERM_MF_DIRECT	protein binding	
INTERPRO	Sushi/SCR/CCP, Somatomedin B domain, von Willebrand factor, type D domain, AMOP	
SMART	CCP, VWD, AMOP	
UP_KW_CELLULAR_COMPONENT	Membrane, Cell membrane	
UP_KW_DISEASE	Tumor suppressor	
UP_KW_DOMAIN	Signal, Sushi, Transmembrane, Transmembrane helix	
UP_KW_MOLECULAR_PROCESS	Receptor	
UP_KW_PTM	Glycoprotein, Disulfide bond	
UP_SEQ_FEATURE	CARBOHYD:N-linked (GlcNAc...) asparagine, DISULFID:Alternate, DOMAIN:AMOP, DOMAIN:SMB, DOMAIN:Sushi, DOMAIN:VWFD, TOPO_DOM:Cytoplasmic, TOPO_DOM:Extracellular, TRANSMEM:Helical	

DAVID, Database for Annotation, Visualization, and Integrated Discovery.