Table S3. Comprehensive list of enriched functional categories based 253 experimentally verified gene targets of differentially expressed microRNAs in ACR. Enrichment *P*-values were adjusted for multiple hypothesis testing using Benjamini-Hochberg method (adjusted *P*-value cutoff < 0.01).

Database	**Functional term**	**Adjusted P-value**
GOTERM_BP_ALL	GO:0042127~regulation of cell proliferation	4.86E-27
GOTERM_BP_ALL	GO:0009893~positive regulation of metabolic process	3.20E-23
GOTERM_BP_ALL	GO:0048856~anatomical structure development	1.14E-22
GOTERM_BP_ALL	GO:0048513~organ development	1.59E-22
GOTERM_BP_ALL	GO:0019222~regulation of metabolic process	1.95E-22
KEGG_PATHWAY	hsa05200:Pathways in cancer	2.64E-22
GOTERM_BP_ALL	GO:0032502~developmental process	7.35E-22
GOTERM_BP_ALL	GO:0008284~positive regulation of cell proliferation	1.56E-21
GOTERM_BP_ALL	GO:0048731~system development	6.53E-21
KEGG_PATHWAY	hsa05215:Prostate cancer	1.57E-20
GOTERM_BP_ALL	GO:0007275~multicellular organismal development	2.91E-20
GOTERM_BP_ALL	GO:0048869~cellular developmental process	4.60E-20
GOTERM_BP_ALL	GO:0030154~cell differentiation	5.71E-20
GOTERM_BP_ALL	GO:0045595~regulation of cell differentiation	1.38E-19
GOTERM_BP_ALL	GO:0006357~regulation of transcription from RNA polymerase II promoter	6.77E-19
GOTERM_BP_ALL	GO:0050793~regulation of developmental process	4.36E-18
GOTERM_BP_ALL	GO:0010628~positive regulation of gene expression	1.19E-17
GOTERM_BP_ALL	GO:0051254~positive regulation of RNA metabolic process	9.30E-17
GOTERM_BP_ALL	GO:0010468~regulation of gene expression	9.37E-17
GOTERM_MF_ALL	GO:0043565~sequence-specific DNA binding	1.41E-16
KEGG_PATHWAY	hsa05220:Chronic myeloid leukemia	2.45E-16
GOTERM_BP_ALL	GO:0045941~positive regulation of transcription	7.04E-16
GOTERM_BP_ALL	GO:0009790~embryonic development	8.93E-16
GOTERM_MF_ALL	GO:0003700~transcription factor activity	1.22E-15
KEGG_PATHWAY	hsa05212:Pancreatic cancer	1.26E-15
GOTERM_BP_ALL	GO:0022008~neurogenesis	5.77E-15
GOTERM_BP_ALL	GO:0051252~regulation of RNA metabolic process	6.00E-15
KEGG_PATHWAY	hsa05210:Colorectal cancer	3.42E-14
GOTERM_BP_ALL	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	7.06E-14
GOTERM_BP_ALL	GO:0042221~response to chemical stimulus	8.53E-14
GOTERM_BP_ALL	GO:0009887~organ morphogenesis	1.13E-13
KEGG_PATHWAY	hsa05214:Glioma	2.71E-13
GOTERM_BP_ALL	GO:0010646~regulation of cell communication	4.28E-13
GOTERM_BP_ALL	GO:0045449~regulation of transcription	5.17E-13
GOTERM_BP_ALL	GO:0007399~nervous system development	7.28E-13
GOTERM_BP_ALL	GO:0048699~generation of neurons	2.01E-12
KEGG_PATHWAY	hsa05218:Melanoma	2.32E-12
GOTERM_BP_ALL	GO:0051338~regulation of transferase activity	2.50E-12
KEGG_PATHWAY	hsa05222:Small cell lung cancer	3.87E-12
GOTERM_BP_ALL	GO:0043549~regulation of kinase activity	4.91E-12
GOTERM_BP_ALL	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	6.85E-12
GOTERM_BP_ALL	GO:0009725~response to hormone stimulus	9.62E-12
GOTERM_BP_ALL	GO:0016477~cell migration	1.55E-11
KEGG_PATHWAY	hsa05219:Bladder cancer	1.67E-11
GOTERM_BP_ALL	GO:0009888~tissue development	1.80E-11
KEGG_PATHWAY	hsa05213:Endometrial cancer	2.50E-11
GOTERM_BP_ALL	GO:0051726~regulation of cell cycle	2.53E-11
GOTERM_BP_ALL	GO:0042981~regulation of apoptosis	2.61E-11
GOTERM_BP_ALL	GO:0009966~regulation of signal transduction	3.30E-11
GOTERM_BP_ALL	GO:0043067~regulation of programmed cell death	3.55E-11
GOTERM_BP_ALL	GO:0010941~regulation of cell death	3.98E-11
GOTERM_BP_ALL	GO:0045859~regulation of protein kinase activity	6.48E-11
GOTERM_BP_ALL	GO:0008361~regulation of cell size	7.65E-11
GOTERM_BP_ALL	GO:0045597~positive regulation of cell differentiation	8.57E-11
GOTERM_BP_ALL	GO:0048870~cell motility	1.54E-10

GOTERM_BP_ALL	GO:0006928~cell motion	2.25E-10
GOTERM_BP_ALL	GO:0050896~response to stimulus	2.51E-10
GOTERM_BP_ALL	GO:0045165~cell fate commitment	2.91E-10
GOTERM_BP_ALL	GO:0050790~regulation of catalytic activity	4.86E-10
KEGG_PATHWAY	hsa05223:Non-small cell lung cancer	6.38E-10
GOTERM_BP_ALL	GO:0051094~positive regulation of developmental process	6.46E-10
GOTERM_BP_ALL	GO:0030334~regulation of cell migration	8.95E-10
GOTERM_BP_ALL	GO:0040012~regulation of locomotion	1.08E-09
GOTERM_CC_ALL	GO:0005654~nucleoplasm	1.11E-09
GOTERM_BP_ALL	GO:0051270~regulation of cell motion	1.18E-09
GOTERM_BP_ALL	GO:0035295~tube development	1.79E-09
GOTERM_CC_ALL	GO:0005667~transcription factor complex	2.14E-09
GOTERM_BP_ALL	GO:0010647~positive regulation of cell communication	3.52E-09
KEGG_PATHWAY	hsa04110:Cell cycle	4.21E-09
GOTERM_MF_ALL	GO:0046983~protein dimerization activity	4.85E-09
GOTERM_BP_ALL	GO:0007417~central nervous system development	7.07E-09
GOTERM_BP_ALL	GO:0040011~locomotion	9.48E-09
GOTERM_BP_ALL	GO:0030182~neuron differentiation	1.34E-08
GOTERM_BP_ALL	GO:0009314~response to radiation	1.43E-08
KEGG_PATHWAY	hsa04510:Focal adhesion	1.65E-08
GOTERM_BP_ALL	GO:0001568~blood vessel development	6.83E-08
GOTERM_BP_ALL	GO:0003002~regionalization	7.22E-08
GOTERM_CC_ALL	GO:0043229~intracellular organelle	9.48E-08
GOTERM_BP_ALL	GO:0001944~vasculature development	1.02E-07
GOTERM_BP_ALL	GO:0006950~response to stress	1.29E-07
GOTERM_BP_ALL	GO:0022414~reproductive process	1.44E-07
GOTERM_BP_ALL	GO:0033674~positive regulation of kinase activity	1.46E-07
GOTERM_BP_ALL	GO:0014031~mesenchymal cell development	1.50E-07
GOTERM_BP_ALL	GO:0048762~mesenchymal cell differentiation	1.50E-07
GOTERM_BP_ALL	GO:0060485~mesenchyme development	1.79E-07
GOTERM_BP_ALL	GO:0009611~response to wounding	1.96E-07
GOTERM_BP_ALL	GO:0007420~brain development	2.01E-07
KEGG_PATHWAY	hsa05221:Acute myeloid leukemia	2.02E-07
GOTERM_MF_ALL	GO:0004672~protein kinase activity	2.45E-07
GOTERM_MF_ALL	GO:0003677~DNA binding	2.46E-07
GOTERM_MF_ALL	GO:0016563~transcription activator activity	2.54E-07
GOTERM_MF_ALL	GO:0016301~kinase activity	2.54E-07
GOTERM_BP_ALL	GO:0000079~regulation of cyclin-dependent protein kinase activity	2.58E-07
GOTERM_MF_ALL	GO:0008134~transcription factor binding	2.69E-07
GOTERM_BP_ALL	GO:0009967~positive regulation of signal transduction	2.82E-07
GOTERM_BP_ALL	GO:0048545~response to steroid hormone stimulus	2.88E-07
GOTERM_BP_ALL	GO:0035239~tube morphogenesis	3.44E-07
GOTERM_CC_ALL	GO:0042995~cell projection	4.40E-07
GOTERM_BP_ALL	GO:0008285~negative regulation of cell proliferation	4.40E-07
GOTERM_BP_ALL	GO:0002376~immune system process	5.58E-07
GOTERM_BP_ALL	GO:0048729~tissue morphogenesis	6.98E-07
GOTERM_MF_ALL	GO:0016773~phosphotransferase activity, alcohol group as acceptor	6.99E-07
GOTERM_BP_ALL	GO:0048732~gland development	7.20E-07
GOTERM_BP_ALL	GO:0060284~regulation of cell development	7.20E-07
GOTERM_BP_ALL	GO:0001709~cell fate determination	7.32E-07
KEGG_PATHWAY	hsa04722:Neurotrophin signaling pathway	9.67E-07
GOTERM_BP_ALL	GO:0051272~positive regulation of cell motion	1.02E-06
GOTERM_BP_ALL	GO:0048514~blood vessel morphogenesis	1.04E-06
GOTERM_BP_ALL	GO:0009952~anterior/posterior pattern formation	1.07E-06
GOTERM_BP_ALL	GO:0048754~branching morphogenesis of a tube	1.40E-06
GOTERM_BP_ALL	GO:0007049~cell cycle	1.95E-06
GOTERM_BP_ALL	GO:0031960~response to corticosteroid stimulus	1.96E-06
GOTERM_BP_ALL	GO:0002520~immune system development	2.01E-06
GOTERM_BP_ALL	GO:0045860~positive regulation of protein kinase activity	2.20E-06
GOTERM_BP_ALL	GO:0048598~embryonic morphogenesis	2.26E-06
GOTERM_BP_ALL	GO:0031099~regeneration	2.41E-06
GOTERM_BP_ALL	GO:0006915~apoptosis	2.47E-06
GOTERM_BP_ALL	GO:0008283~cell proliferation	2.84E-06
GOTERM_BP_ALL	GO:0030335~positive regulation of cell migration	2.99E-06

GOTERM_BP_ALL	GO:0008219~cell death	3.18E-06
GOTERM_BP_ALL	GO:0043434~response to peptide hormone stimulus	3.20E-06
GOTERM_BP_ALL	GO:0012501~programmed cell death	3.29E-06
GOTERM_BP_ALL	GO:0048534~hemopoietic or lymphoid organ development	3.73E-06
KEGG_PATHWAY	hsa05216:Thyroid cancer	3.92E-06
KEGG_PATHWAY	hsa04520:Adherens junction	4.43E-06
GOTERM_BP_ALL	GO:0001763~morphogenesis of a branching structure	4.47E-06
KEGG_PATHWAY	hsa04115:p53 signaling pathway	8.52E-06
GOTERM_BP_ALL	GO:0010648~negative regulation of cell communication	8.94E-06
GOTERM_BP_ALL	GO:0045937~positive regulation of phosphate metabolic process	9.23E-06
GOTERM_BP_ALL	GO:0010562~positive regulation of phosphorus metabolic process	9.23E-06
GOTERM_BP_ALL	GO:0000278~mitotic cell cycle	9.63E-06
GOTERM_BP_ALL	GO:0060541~respiratory system development	1.88E-05
GOTERM_BP_ALL	GO:0030097~hemopoiesis	2.07E-05
GOTERM_MF_ALL	GO:0003702~RNA polymerase II transcription factor activity	3.60E-05
GOTERM_BP_ALL	GO:0048666~neuron development	3.61E-05
GOTERM_BP_ALL	GO:0010551~regulation of specific transcription from RNA polymerase II promoter	3.61E-05
GOTERM_BP_ALL	GO:0051960~regulation of nervous system development	3.82E-05
GOTERM_BP_ALL	GO:0050767~regulation of neurogenesis	3.91E-05
GOTERM_MF_ALL	GO:0016564~transcription repressor activity	5.21E-05
GOTERM_MF_ALL	GO:0003705~RNA polymerase II transcription factor activity, enhancer binding	5.47E-05
GOTERM_BP_ALL	GO:0031175~neuron projection development	5.51E-05
GOTERM_BP_ALL	GO:0048663~neuron fate commitment	5.52E-05
GOTERM_BP_ALL	GO:0030324~lung development	5.64E-05
GOTERM_BP_ALL	GO:0060348~bone development	6.14E-05
GOTERM_BP_ALL	GO:0000902~cell morphogenesis	6.90E-05
GOTERM_BP_ALL	GO:0016049~cell growth	7.04E-05
GOTERM_BP_ALL	GO:0030323~respiratory tube development	7.10E-05
REACTOME_PATHWAY	REACT_11061:Signalling by NGF	9.24E-05
KEGG_PATHWAY	hsa04350:TGF-beta signaling pathway	9.55E-05
GOTERM_BP_ALL	GO:0010942~positive regulation of cell death	1.00E-04
GOTERM_BP_ALL	GO:0007507~heart development	1.25E-04
GOTERM_BP_ALL	GO:0043193~positive regulation of gene-specific transcription	1.26E-04
GOTERM_BP_ALL	GO:0006873~cellular ion homeostasis	1.29E-04
GOTERM_BP_ALL	GO:0001655~urogenital system development	1.30E-04
GOTERM_BP_ALL	GO:0042493~response to drug	1.30E-04
GOTERM_BP_ALL	GO:0042060~wound healing	1.54E-04
GOTERM_BP_ALL	GO:0055082~cellular chemical homeostasis	1.54E-04
GOTERM_BP_ALL	GO:0007154~cell communication	1.55E-04
GOTERM_BP_ALL	GO:0010720~positive regulation of cell development	1.59E-04
GOTERM_BP_ALL	GO:0050678~regulation of epithelial cell proliferation	1.93E-04
GOTERM_BP_ALL	GO:0070482~response to oxygen levels	1.93E-04
GOTERM_BP_ALL	GO:0043405~regulation of MAP kinase activity	1.93E-04
GOTERM_BP_ALL	GO:0001775~cell activation	1.93E-04
KEGG_PATHWAY	hsa04310:Wnt signaling pathway	2.22E-04
GOTERM_BP_ALL	GO:0007398~ectoderm development	2.29E-04
GOTERM_BP_ALL	GO:0051301~cell division	2.66E-04
GOTERM_BP_ALL	GO:0042692~muscle cell differentiation	2.75E-04
GOTERM_BP_ALL	GO:0045767~regulation of anti-apoptosis	3.03E-04
GOTERM_BP_ALL	GO:0010467~gene expression	3.45E-04
GOTERM_BP_ALL	GO:0007243~protein kinase cascade	3.51E-04
GOTERM_BP_ALL	GO:0048812~neuron projection morphogenesis	4.40E-04
GOTERM_BP_ALL	GO:0008544~epidermis development	4.53E-04
KEGG_PATHWAY	hsa04012:ErbB signaling pathway	4.65E-04
GOTERM_BP_ALL	GO:0031100~organ regeneration	5.05E-04
GOTERM_BP_ALL	GO:0001952~regulation of cell-matrix adhesion	6.01E-04
GOTERM_BP_ALL	GO:0060429~epithelium development	8.01E-04
BIOCARTA	h_cellcyclePathway:Cyclins and Cell Cycle Regulation	8.03E-04
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	1.10E-03
GOTERM_BP_ALL	GO:0008637~apoptotic mitochondrial changes	1.14E-03
GOTERM_BP_ALL	GO:0060393~regulation of pathway-restricted SMAD protein phosphorylation	1.19E-03
GOTERM_BP_ALL	GO:0051057~positive regulation of small GTPase mediated signal transduction	1.19E-03
GOTERM_MF_ALL	GO:0046332~SMAD binding	1.22E-03
REACTOME_PATHWAY	REACT_498:Signaling by Insulin receptor	1.30E-03

GOTERM_BP_ALL	GO:0016202~regulation of striated muscle tissue development	1.31E-03
GOTERM_BP_ALL	GO:0001525~angiogenesis	1.32E-03
GOTERM_BP_ALL	GO:0001822~kidney development	1.43E-03
GOTERM_BP_ALL	GO:0014033~neural crest cell differentiation	1.50E-03
GOTERM_BP_ALL	GO:0014032~neural crest cell development	1.50E-03
GOTERM_BP_ALL	GO:0007569~cell aging	1.50E-03
GOTERM_BP_ALL	GO:0000904~cell morphogenesis involved in differentiation	1.54E-03
GOTERM_BP_ALL	GO:0051240~positive regulation of multicellular organismal process	1.54E-03
GOTERM_MF_ALL	GO:0003682~chromatin binding	1.72E-03
GOTERM_MF_ALL	GO:0016538~cyclin-dependent protein kinase regulator activity	1.72E-03
GOTERM_BP_ALL	GO:0045792~negative regulation of cell size	1.73E-03
GOTERM_BP_ALL	GO:0001889~liver development	1.73E-03
GOTERM_BP_ALL	GO:0010001~glial cell differentiation	1.73E-03
GOTERM_BP_ALL	GO:0007165~signal transduction	1.74E-03
GOTERM_BP_ALL	GO:0000165~MAPKKK cascade	1.76E-03
KEGG_PATHWAY	hsa04210:Apoptosis	2.07E-03
BIOCARTA	h_p53Pathway:p53 Signaling Pathway	2.15E-03
GOTERM_BP_ALL	GO:0034330~cell junction organization	2.47E-03
GOTERM_BP_ALL	GO:0045927~positive regulation of growth	2.50E-03
BIOCARTA	h_RacCycDPathway:Influence of Ras and Rho proteins on G1 to S Transition	2.55E-03
GOTERM_BP_ALL	GO:0001569~patterning of blood vessels	2.56E-03
GOTERM_BP_ALL	GO:0001666~response to hypoxia	2.66E-03
KEGG_PATHWAY	hsa04370:VEGF signaling pathway	3.12E-03
GOTERM_BP_ALL	GO:0007179~transforming growth factor beta receptor signaling pathway	3.14E-03
GOTERM_BP_ALL	GO:0046649~lymphocyte activation	3.15E-03
GOTERM_BP_ALL	GO:0070663~regulation of leukocyte proliferation	3.20E-03
GOTERM_BP_ALL	GO:0032944~regulation of mononuclear cell proliferation	3.20E-03
GOTERM_BP_ALL	GO:0006952~defense response	3.37E-03
GOTERM_BP_ALL	GO:0040014~regulation of multicellular organism growth	3.37E-03
GOTERM_BP_ALL	GO:0046651~lymphocyte proliferation	4.09E-03
GOTERM_BP_ALL	GO:0051591~response to cAMP	4.09E-03
GOTERM_BP_ALL	GO:0001764~neuron migration	4.26E-03
GOTERM_BP_ALL	GO:0045321~leukocyte activation	4.50E-03
GOTERM_BP_ALL	GO:0070661~leukocyte proliferation	5.00E-03
GOTERM_BP_ALL	GO:0042306~regulation of protein import into nucleus	5.00E-03
GOTERM_BP_ALL	GO:0032943~mononuclear cell proliferation	5.00E-03
KEGG_PATHWAY	hsa04620:Toll-like receptor signaling pathway	5.10E-03
KEGG_PATHWAY	hsa04062:Chemokine signaling pathway	5.12E-03
GOTERM_BP_ALL	GO:0006954~inflammatory response	6.24E-03
GOTERM_BP_ALL	GO:0002521~leukocyte differentiation	9.03E-03
GOTERM_BP_ALL	GO:0006325~chromatin organization	9.05E-03