Table S1. List of 117 differentially expressed microRNAs in airway epithelial cells of lung transplantation patients with acute cellular rejection (Q-value < 0.05).

microRNA	Q-value
hsa-miR-1205	0.0000
hsa-miR-125a-3p	0.0000
hsa-miR-149-3p	0.0000
hsa-miR-1538	0.0000
hsa-miR-1914-5p	0.0000
hsa-miR-1972	0.0000
hsa-miR-21-3p	0.0000
hsa-miR-22-5p	0.0000
hsa-miR-298	0.0000
hsa-miR-34b-5p	0.0000
hsa-miR-371a-5p	0.0000
hsa-miR-431-5p	0.0000
hsa-miR-490-3p	0.0000
hsa-miR-514a-3p	0.0000
hsa-miR-515-3p	0.0000
hsa-miR-524-3p	0.0000
hsa-miR-552-3p	0.0000
hsa-miR-593-3p	0.0000
hsa-miR-593-5p	0.0000
hsa-miR-615-5p	0.0000
hsa-miR-622	0.0000
hsa-miR-659-3p	0.0000
hsa-miR-665	0.0000
hsa-miR-668-3p	0.0000
hsa-miR-671-5p	0.0000
hsa-miR-885-5p	0.0000
hsa-miR-891b	0.0000
hsa-miR-133a-3p	0.0124
hsa-miR-202-3p	0.0124
hsa-miR-224-5p	0.0124
hsa-miR-30c-2-3p	0.0124
hsa-miR-520h	0.0124
hsa-miR-302d-5p	0.0139
hsa-miR-433	0.0142
hsa-miR-506-3p	0.0142
hsa-miR-128-3p	0.0150
hsa-miR-1909-3p	0.0150
hsa-miR-195-3p	0.0150
hsa-miR-329-3p	0.0150

hsa-miR-34a-5p	0.0150
hsa-miR-361-3p	0.0150
hsa-miR-579-3p	0.0150
hsa-miR-937-3p	0.0150
hsa-miRPlus-A1027	0.0150
hsa-miR-1200	0.0200
hsa-miR-198	0.0200
hsa-miR-526b-3p	0.0200
hsa-miR-124-3p	0.0211
hsa-miR-326	0.0211
hsa-miR-432-3p	0.0211
hsa-miR-516a-3p	0.0211
hsa-miR-611	0.0211
hsa-miR-646	0.0211
hsa-miRPlus-C1066	0.0211
hsa-miR-135b-3p	0.0242
hsa-miR-10b-5p	0.0278
hsa-miR-1203	0.0278
hsa-miR-1254	0.0278
hsa-miR-181a-3p	0.0278
hsa-miR-564	0.0278
hsa-let-7i-3p	0.0296
hsa-miR-1236-3p	0.0296
hsa-miR-1248	0.0296
hsa-miR-1258	0.0296
hsa-miR-1260a	0.0296
hsa-miR-143-5p	0.0296
hsa-miR-147b	0.0296
hsa-miR-155-3p	0.0296
hsa-miR-214-3p	0.0296
hsa-miR-297	0.0296
hsa-miR-30c-1-3p	0.0296
hsa-miR-365a-3p	0.0296
hsa-miR-373-5p	0.0296
hsa-miR-410-3p	0.0296
hsa-miR-496	0.0296
hsa-miR-554	0.0296
hsa-miR-623	0.0296
hsa-miR-7-2-3p	0.0296
hsa-miR-765	0.0296
hsa-miR-1237-3p	0.0309
hsa-miR-148a-3p	0.0309
hsa-miR-331-5p	0.0309

hsa-miR-583	0.0309
hsa-miR-216a-5p	0.0323
hsa-miR-376a-5p	0.0323
hsa-miR-486-3p	0.0323
hsa-miR-504-5p	0.0323
hsa-miR-658	0.0323
hsa-miR-675-3p	0.0323
hsa-miR-302a-3p	0.0345
hsa-miR-551b-3p	0.0345
hsa-miR-663b	0.0345
hsa-miR-758-3p	0.0345
hsa-miR-1471	0.0360
hsa-miR-323a-5p	0.0360
hsa-miR-602	0.0360
hsa-miR-382-5p	0.0387
hsa-miR-429	0.0387
hsa-miR-517-5p	0.0395
hsa-miR-216b-5p	0.0399
hsa-miR-640	0.0410
hsa-miRPlus-C1076	0.0410
hsa-miR-1227-3p	0.0418
hsa-miR-147a	0.0418
hsa-miR-518d-5p	0.0418
hsa-miR-596	0.0418
hsa-miR-649	0.0418
hsa-miR-877-5p	0.0418
hsa-miR-518d-3p	0.0442
hsa-miR-558	0.0442
hsa-miR-182-3p	0.0449
hsa-miR-296-3p	0.0453
hsa-miR-487a	0.0453
hsa-miR-127-5p	0.0474
hsa-miR-148b-3p	0.0474
hsa-miR-518c-5p	0.0474
hsa-miR-642a-5p	0.0474

Table S2. List of 40 differentially expressed microRNAs (Q-value < 0.05) in acute cellular rejection with their experimentally validated targets.

microRNA		Target Gene
1.	hsa-miR-10b-5p	BCL2L11
		CDK2
		CDKN1A
		CDKN2A
		CSNK2A1
		HOXD10
		KLF4
		LAMC1
		MAPRE1
		NCOR2
		NF1
		NOTCH1
		NR4A3
		NRP2
		PAX6
		PIEZO1
		PPARA
		SDC1
		SRSF1
		TFAP2C
		TP53
		TRA2B
2.	hsa-miR-124-3p	ADIPOR2
		AHR
		AR
		BACE1
		CCL2
		CDK2
		CDK4
		CDK6
		CDKN2A
		CEBPA
		COL1A1
		CTDSP1
		E2F6
		EFNB1
		ELK3
		EYA4
		EZH2

		FXN
		HCN2
		HMGA1
		IL6
		IL6R
		IQGAP1
		IRAK3
		ITGB1
		KLF4
		LAMC1
		MAP2K3
		MECP2
		MSN
		MTPN
		NFKBIZ
		NR3C1
		NR4A3
		PEA15
		PNP
		PPARA
		PRPS1
		QKI
		RASSF2
		RDH10
		RELA
		ROCK2
		SHC1
		SIRT1
		SLC16A1
		SMYD3
		SNAI2
		SP1
		SULF1
		VIM
		VKORC1
3.	hsa-miR-1258	HPSE
4.	hsa-miR-128-3p	BMI1
		CTDSP1
		DCX
		E2F3
		EGFR
		EYA4
		FBXW7

		KLF4
		MAP2K1
		NTRK3
		POU5F1
		RELN
		RPS6KA5
		SIRT1
		SLC16A1
		SOX2
		TGFBR1
5.	hsa-miR-133a-3p	BCL2L1
		CACNA1C
		CASP9
		COL1A1
		EGFL7
		EGFR
		FSCN1
		GSTP1
		HCN2
		HCN4
		KCNH2
		KCNQ1
		KRT7
		LASP1
		MCL1
		MSN
		PIK3R2
		PKM
		PNP
		PRDM16
		RGS3
		SP1
		TAGLN2
		VEGFA
		VKORC1
6.	hsa-miR-147a	ACVR1C
		VEGFA
7.	hsa-miR-148a-3p	ACVR1
		BCL2
		CCKBR
		CDC25B
		DNMT1
		DNMT3B

		HLA-G
		IRS1
		NR1I2
		RPS6KA5
		TGIF2
		TMED7
8.	hsa-miR-148b-3p	CCKBR
		CSF1
		EYA4
		HLA-G
		ITGA5
		MECP2
		NR3C2
		NRAS
		PIK3CA
		ROCK1
		SNAI2
9.	hsa-miR-149-3p	AKT1
		E2F1
		MYBL2
		TGIF2
10.	hsa-miR-155-3p	IRAK3
11.	hsa-miR-181a-3p	NANOG
12.	hsa-miR-198	CCNT1
		MYB
		NTRK3
13.	hsa-miR-202-3p	MYCN
14.	hsa-miR-214-3p	ASF1B
		ATF4
		BCL2L2
		CTNNB1
		MAP2K3
		MAPK8
		PLXNB1
		POU4F2
		PSMD10
		PTEN
		QKI
		SRGAP1
		SRGAP2
		TP53
		TWIST1

		XBP1
15.	hsa-miR-216a-5p	CD44 CDC42 PTEN SIRT1 SMAD7 CSNK2A1
16.	hsa-miR-216b-5p	CSNK2A1
17.	hsa-miR-224-5p	AP2M1 API5 CDC42 CXCR4 EDNRA EYA4 FOSB KLK10 NCOA6 NIT1 PEBP1 SMAD4
18.	hsa-miR-296-3p	CDC25B CDKN2A HMGA1 KCNH1 LGALS3BP PIK3R2 PKM SPI1
19.	hsa-miR-298	BACE1 CDKN1A
20.	hsa-miR-302a-3p	AKT1 CCND1 CDKN1A DAZAP2 LEFTY1 LEFTY2 NR2F2 SLAIN1 TAC1 TOB2
21.	hsa-miR-30c-1-3p	HMBOX1
22.	hsa-miR-326	CD9

		GLI1
		MSH3
		NOTCH1
		NOTCH2
		PKM
		SMO
		VKORC1
23.	hsa-miR-34a-5p	ACSL1
		ACSL4
		AP2M1
		AXIN2
		AXL
		BCL2
		BMP7
		CCL22
		CCND1
		CCND3
		CCNE2
		CD44
		CDC25A
		CDK4
		CDK6
		CDKN2A
		CDKN2C
		CEBPB
		CTNNB1
		DLL1
		E2F1
		E2F3
		EFNB1
		EPHA5
		FOSL1
		FOXP1
		GRM7
		HDAC1
		HNF4A
		IFNB1
		IMPA1
		IMPDH2
		JAG1
		KLB
		LDHA
		LEF1

		MAGEA12
		MAGEA2
		MAGEA3
		MAGEA6
		MAP2K1
		MAP3K9
		MCM5
		MET
		MTA2
		MYB
		MYC
		MYCN
		NANOG
		NOTCH1
		NOTCH2
		PDGFRA
		PEA15
		PPP1R10
		SEPT7
		SIRT1
		SOX2
		SPI1
		STX1A
		SYT1
		TP53
		ULBP2
		VAMP2
		VEGFA
		WNT1
		YY1
		ZAP70
24.	hsa-miR-34b-5p	BCL2
		CCNE2
		CDK4
		CREB1
		HNF4A
		MET
		MYB
		MYC
25.	hsa-miR-365a-3p	BCL2
		CCND1
		IL6
		IMPA1

		MTA2
26.	hsa-miR-376a-5p	ACVR1C
		PRPS1
		SLC16A1
		SNX19
		SRSF11
		TTK
		ZNF513
27.	hsa-miR-429	BAP1
		BCL2
		ELMO2
		ERBB2IP
		HOXB5
		KLF11
		KLHL20
		MYC
		OSTF1
		PTPRD
		RASSF2
		RERE
		RIN2
		SEPT7
		SHC1
		SOX2
		TCF7L1
		VAC14
		WASF3
		WDR37
		XIAP
		ZEB1
		ZEB2
		ZFPM2
28.	hsa-miR-490-3p	ERGIC3
29.	hsa-miR-504-5p	DRD1
		MDM2
		TCEAL1
		TP53
		VEGFA
30.	hsa-miR-506-3p	FXN
31.	hsa-miR-515-3p	CDKN1A
32.	hsa-miR-516a-3p	SULF1
33.	hsa-miR-520h	ABCG2

		VEGFA
34.	hsa-miR-596	LGALS3BP
35.	hsa-miR-615-5p	IGF2
36.	hsa-miR-622	KRAS
37.	hsa-miR-642a-5p	DOHH
38.	hsa-miR-659-3p	GRN
39.	hsa-miR-765	HNF4A NTRK3
40.	hsa-miR-885-5p	CDK2 MCM5

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