

Supplementary Table ST1: Deregulated microRNAs in diabetic retinopathy						
MicroRNA	Detected in	Altered	In	Compared with	Comment	References
let-7a-5p	serum	Increased	DR	T2DM patients with noDR		[1]
let-7b	Aqueous and vitreous humor or plasma	Increased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
let-7b-5p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal		[4]
let-7b-5p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal		[4]
let-7c	Vitreous humor	Decreased	PDR	MH patients		[1]
let-7c-5p	Aqueous humor	Decreased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
let-7f-5p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal		[4]
let-7g	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
let7g-5p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
let-7i	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-100-5p	Aqueous humor	Decreased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
miR-101a-3p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
miR-102	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
miR-106a	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-106a	Retina and serum of animal	Decreased	diabetic C57BL/6J mice	Control mice		[6]
miR-106a-5p	Cells treated with high glucose	Decreased	Cell model for diabetic retinopathy	Control cells (-treatemt with high glucose)	Involves in angiogenesis	[7]
miR-106b	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-1179	serum	Increased	PDR	NPDR		[1]
miR-122	serum	Increased	NDR and from NDR to NPDR	Healthy control		[8]
miR-122	retinal pigment epithelial cells treated with high glucose	Increased	retinal pigment epithelial cells treated with high glucose	Control cells (-treatemt with high glucose)	miR-122 targets metalloproteinases-3 (TIMP3) and modulates cell viability and apoptosis	[9]
miR-124-3p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal		[4]
miR-125a-5p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
miR-126	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-126	serum	Decreased	DR/NPDR	DM patients with no DR.	The level of expression of miR-126 in the PDR group was significantly lower than that in the combined NDR and NPDR group.	[1]

miR-126	Rat model and Retina of diabetic rat, serum	Decreased	Retina of diabetic rat, serum	Nondiabetic rat	miR-126 targets PLK4 and the intravitreal delivery of miR-126 alleviated retinopathy, suppresses endothelial cell proliferation and migration	[10]
miR-126a-5p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal	Involves in angiogenesis, apoptosis, inflammation	[4]
miR-130a	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-135a-5p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal		[4]
miR-142-3p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
miR-143-3p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal	Involves in angiogenesis, apoptosis, inflammation	[4]
miR-148-3p	Human retinal microvascular endothelial cells (HRECs) treated with different concentration gradients of high glucose	Decreased	Retinal cells treated with high glucose	Cells without treatment with high glucose	miR-148a-3p targets TGFB2 and FGF2. Over expression of miR-148a-3p caused increased cell viability and decreased apoptosis, modulated angiogenesis mediated through TGFB2	[11]
miR-148a-3p	serum	Decreased	DR	T2DM-noDR		[1]
miR-150	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-151a-5p	serum	Decreased	DR	T2DM-noDR		[1]
miR-152-3p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal		[4]
miR-155	PBMC	Increased	PDR and Background Retinopathy (BDR, early stage DR)	Nondiabetic retinopathy, healthy control	Expression of miR-155 was negatively related to Treg cells ($r = -0.835$ $p = 0.000$) and TGF- β ($r = -0.771$, $p = 0.000$).	[12]
miR-155	Plasma	Increased	BDR and PDR	T2DM patients without DR		[1]
miR-15a	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-15a	Vitreous humor	Increased	PDR	MH eyes		[1]
miR-15b	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-15b	Serum/plasma	Decreased	PDR	DM or NPDR	miR-15b targets VEGF and regulates vascular abnormalities in vivo in diabetic rats inhibiting endothelial tube formation	[13]
miR-16-1	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-16-2	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-17	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-181C	serum	Increased	PDR	NPDR		[1]
miR-18a	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-18a-5p	Mouse model of oxygen-induced proliferative retinopathy (OIR)	Increased	Increased in pathologic neovascularization in the retinas of OIR mice	Control mice	miR-18a-5p directly decreased FGF1 and HIF1A	[14]
miR-18b	serum	Increased	DR	Nondiabetic retinopathy	AUC values with 95% CI calculated by ROC curves was 0.779	[1]
miR-192	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-193a-5p	Aqueous humor	Decreased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]

miR-194-1	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-194-2	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-199a-5p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal	Involves in angiogenesis, apoptosis, inflammation	[4]
miR-19b	serum	Increased	DR	Nondiabetic retinopathy	AUC values with 95% CI calculated by ROC curves was 0.744	[1]
miR-19b-3p	Aqueous humor	Decreased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
miR-1b-5p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal	Involves in angiogenesis, apoptosis, inflammation	[4]
miR-200-3p	Retina tissues of DR rats and cultured cells treated with high glucose	Decreased	Retina	Control mice	miR-200a-3p targets TGF- β 2. overexpression of miR-200a-3p promoted cell proliferation, reduced apoptosis, as well as inhibited the levels of inflammatory cytokines secreted, matrix metalloproteinase 2/9 (MMP2/9), and vascular endothelial growth factor (VEGF) in HG-injured ARPE-19 cells.	[15]
miR-200b	serum	Decreased	DR	Healthy control	VEGFA was confirmed as a target of miR-200b	[16]
miR-200b	Retinal tissue	Decreased	DR	Decreased level was first identified in mouse model and confirmed in human retinal tissue by in situ hybridization	VEGFA was confirmed as a target of miR-200b	[17]
miR-200b-3p	Aqueous humor	Decreased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
miR-204	Vitreous humor	Decreased	PDR	MH patients		[1]
miR-204-5p	Aqueous humor	Decreased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
miR-206-3p	Retina and serum of animal	Increased	diabetic C57BL/6J mice	Control mice		[6]
miR-20a	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-20a-3p	Retina and serum of animal	Decreased	diabetic C57BL/6J mice	Control mice		[6]
miR-20a-3p	Cells treated with high glucose	Decreased	Cell model for diabetic retinopathy	Control cells (-treatment with high glucose)	Involves in angiogenesis	[7]
miR-20a-5p	Cells treated with high glucose	Decreased	Cell model for diabetic retinopathy	Control cells (-treatment with high glucose)	Involves in angiogenesis	[7]
miR-20a-5p	Retina and serum of animal	Decreased	diabetic C57BL/6J mice	Control mice		[6]
miR-20b	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-20b	Retina and serum of animal	Decreased	diabetic C57BL/6J mice	Control mice		[6]
miR-20b	Cells treated with high glucose	Decreased	Cell model for diabetic retinopathy	Control cells (-treatment with high glucose)	Involves in angiogenesis	[7]
miR-21	serum	Increased	PDR	NPDR		[1]
miR-21	Plasma	Increased	BDR and PDR	T2DM patients without DR	expression in the PDR group was significantly greater than in the BDR group	[1]
miR-21	Vitreous humor	Increased	PDR	macular hole (MH) patients		[1]
miR-210	Serum	Increased	DR	DM without DR and healthy controls	overexpression of miR-210 promoted HUVEC proliferation, while the knockdown of miR-210 resulted in the opposite effect under a high-glucose condition	[18]
miR-211	serum	Increased	DR	Nondiabetic retinopathy	AUC values with 95% CI calculated by ROC curves was 0.864	[1]
miR-2116-5p	serum	Increased	DR	T2DM	NOTCH2 was the target gene of miR-2116-5p	[19]
miR-216a	Retinal tissues of DR rats and cells treated with high glucose	Decreased	DR rats	Control rat	miR-216a targets NOS2 and played a protective role in the retina of DR rats. Moreover, in cell experiments, overexpression of miR-216a promoted the viability of HRMECs under d-glucose treatment, and inhibited NOS2 expression and the JAK/STAT signaling pathway activation.	[20]
miR-221	Serum	Increased	T2DM, NDR,	Healthy control	Serum miR-221 was positively correlated with metabolic parameters like glycated hemoglobin	[21]

			NPDR, PDR		($r=0.310$, $P=0.002$) and homeostasis model assessment for insulin resistance ($r=0.413$, $P<0.001$), as well as serum markers for instance Ang II ($r=0.667$, $P<0.001$) and VEGF ($r=0.499$, $P<0.001$). Furthermore, serum miR-221 (AUC, 0.894; 95%CI, 0.833-0.955; $P<0.001$), Ang II (AUC, 0.888; 95%CI, 0.828-0.949; $P<0.001$) and VEGF (AUC, 0.785; 95%CI, 0.695-0.875; $P<0.001$)	
miR-222	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-25	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-27a	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR- 27a- 3 p	Retina and serum of animal	Increased	diabetic C57BL/6J mice	Control mice		[6]
miR- 27a- 5 p	Retina and serum of animal	Increased	diabetic C57BL/6J mice	Control mice		[6]
miR-27b	serum	Decreased	DR (T1DM)	T1D-noDR		[1]
miR-27b	serum	Decreased	DR (T1DM)	Healthy control	Odds ratios for higher miR-27b ranged from 0.570-78 in different cohorts, the miRNA was implicated in angiogenesis	[22]
miR-28-3p	serum	Increased	DR	T2DM patients with noDR		[1]
miR-29a	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-29a	Vitreous humor	Increased	PDR	MH eyes		[1]
miR-29c-3p	Plasma	Decreased	diabetic patients with retinopathy and without retinopathy	Healthy control	Changes in plasma miR-29c-3p levels are an independent risk factor for the development of DR.	[23]
miR-30a-5p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal	Involves in angiogenesis, apoptosis, inflammation	[4]
miR-30b-5p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
miR-30d	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-30e	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-30e-3p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
miR-3197	serum	Increased	DR	T2DM		[24]
miR-320a	serum	Increased	DR (T1DM)	T1D-noDR		[1]
miR-320a	Vitreous humor	Increased	DR (T1DM)	T1D-noDR		[1]
miR-320a	serum	Increased	DR (T1DM)	Healthy control	Odds ratios for higher miR-320a ranged from 1.43-1.57 in different cohorts, the miRNA was implicated in angiogenesis	[22]
miR-320a	Aqueous and vitreous humor or plasma	Increased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-320a	Plasma	Decreased	DR	DM patients without DR and healthy subjects		[25]
miR-320d-1	Aqueous and vitreous humor or plasma	Increased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-320d-2	Aqueous and vitreous humor or plasma	Increased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-335	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
miR-335	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal	Involves in angiogenesis , apoptosis, inflammation	[4]
miR-34a	Retinal tissues of DR rats and rat retinal vascular endothelial cells	Increased	Retinal tissues of DR rats	Untreated control	miR-34a promotes apoptosis of RVECs by targeting SIRT1 in DR rats	[26]

	treated with high glucose					
miR-34a-5p	Aqueous humor	Increased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
miR-363	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-365	retinal tissues of DR mice	Increased	retinal tissues of DR mice	Control mice	miR-365 targeted SIRT1, results in increased β -catenin and GLUT1 expression and subsequent enhancement of Retinal microvascular endothelial cells proliferation and tube formation in vitro	[27]
miR-365-3p	Aqueous humor	Decreased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
miR-374-5p	Aqueous humor	Increased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
miR-381-3p	Retina and serum of animal	Increased	diabetic C57BL/6J mice	Control mice		[6]
miR-411	Rat model and Retina of diabetic rat	Decreased	Retina of diabetic rat	Nondiabetic rat	ROBO4 is a target of miR-411. ROBO4 and could partially reverse the effects of high glucose and hypoxia on ARPE-19 cell viability and monolayer cell permeability	[28]
miR-423	Plasma	Decreased	PDR	Healthy control	Lowered miR-423 levels in diabetic patients showed a correlation with VEGF and an inverse correlation between NO and eNOS expression	[29]
miR-423-5p	Vitreous humor	Increased	PDR	MH eyes		[1]
miR-429	Aqueous humor	Decreased	diabetic macular edema (DME)	non-diabetic patients (CTR)		[5]
miR-451	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-455	Aqueous and vitreous humor or plasma	Increased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-486	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-502	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-532	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-660	Aqueous and vitreous humor or plasma	Decreased	DR/NPDR/PDR (mixed)	Normal (without diabetic retinopathy)	Result in GSE140959 (Aqueous and vitreous humor, plasma from DR/NPDR/PDR and compared with macular pucker or macular hole patients as normal, Ref. N6) was reanalysed	[2, 3]
miR-92a	CD34+ cells from individuals with DR	Decreased	DR	control subjects and patients with diabetes with no DR		[30]
miR-93	Plasma	Increased	DR	T2DM patients without DR		[1]
miR-93	Vitreous humor	Increased	PDR	MH eyes		[1]
miR-96-5p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal	Involves in angiogenesis, apoptosis, inflammation	[4]
miR-9a-5p	Retina during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Decreased	Model for PDR	Control animal		[4]
miR-9a-5p	Choroid during vasodegenerative phases of oxygen-induced retinopathy (OIR)	Increased	Model for PDR	Control animal		[4]
References						
1	Martinez B, Peplow P. MicroRNAs as biomarkers of diabetic retinopathy and disease progression. <i>Neural Regeneration Research</i> 2019; 14(11):1858-69.					
2	Smit-McBride Z, Nguyen AT, Yu AK, Modjtahedi SP, Hunter AA, Rashid S, Moisseiev E, Morse LS. Unique molecular signatures of microRNAs in ocular fluids and plasma in diabetic retinopathy. <i>PLoS One</i> 2020; 15(7):e0235541.					
3	Kumari N, Karmakar A, Chakrabarti S, Ganesan SK. Integrative Computational Approach Revealed Crucial Genes Associated With Different Stages of Diabetic Retinopathy. <i>Front Genet</i> 2020; 11:576442.					
4	Desjarlais M, Rivera JC, Lahaie I, Cagnone G, Wirt M, Omri S, Chemtob S. MicroRNA expression profile in retina and choroid in oxygen-induced retinopathy model. <i>PLoS one</i> 2019; 14(6):e0218282-e.					

5	Grieco GE, Sebastiani G, Eandi CM, Neri G, Nigi L, Brusco N, D'Aurizio R, Posarelli M, Bacci T, Benedetto E, Fruschelli M, Orlandini M, Galvagni F, Dotta F, Tosi GM. MicroRNA Expression in the Aqueous Humor of Patients with Diabetic Macular Edema. <i>International journal of molecular sciences</i> 2020; 21(19).
6	Platania CBM, Maisto R, Trotta MC, D'Amico M, Rossi S, Gesualdo C, D'Amico G, Balta C, Herman H, Hermenean A, Ferraraccio F, Panarese I, Drago F, Bucolo C. Retinal and circulating miRNA expression patterns in diabetic retinopathy: An in silico and in vivo approach. <i>Br J Pharmacol</i> 2019; 176(13):2179-94.
7	Maisto R, Trotta MC, Petrillo F, Izzo S, Cuomo G, Alfano R, Hermenean A, Barcia JM, Galdiero M, Platania CBM, Bucolo C, D'Amico M. Resolvin D1 Modulates the Intracellular VEGF-Related miRNAs of Retinal Photoreceptors Challenged With High Glucose. <i>Front Pharmacol</i> 2020; 11:235.
8	Pastukh N, Meerson A, Kalish D, Jabaly H, Blum A. Serum miR-122 levels correlate with diabetic retinopathy. <i>Clinical and Experimental Medicine</i> 2019; 19(2):255-60.
9	Wang M, Zheng H, Zhou X, Zhang J, Shao G. miR-122 promotes diabetic retinopathy through targeting TIMP3. <i>Animal Cells and Systems</i> 2020; 24(5):275-81.
10	Zheng Y, Liu Y, Wang L, Xu H, Lu Z, Xuan Y, Meng W, Ye L, Fang D, Zhou Y, Ke K, Liu Y, An M. MicroRNA126 suppresses the proliferation and migration of endothelial cells in experimental diabetic retinopathy by targeting pololike kinase 4. <i>Int J Mol Med</i> 2021; 47(1):151-60.
11	Wang J, Yao Y, Wang K, Li J, Chu T, Shen H. MicroRNA-148a-3p alleviates high glucose-induced diabetic retinopathy by targeting TGFB2 and FGF2. <i>Acta diabetologica</i> 2020; 57(12):1435-43.
12	Yang TT, Song SJ, Xue HB, Shi DF, Liu CM, Liu H. Regulatory T cells in the pathogenesis of type 2 diabetes mellitus retinopathy by miR-155. <i>Eur Rev Med Pharmacol Sci</i> 2015; 19(11):2010-5.
13	Yang Y, Liu Y, Li Y, Chen Z, Xiong Y, Zhou T, Tao W, Xu F, Yang H, Yla-Herttuala S, Chaurasia SS, Adam WC, Yang K. MicroRNA-15b Targets VEGF and Inhibits Angiogenesis in Proliferative Diabetic Retinopathy. <i>The Journal of clinical endocrinology and metabolism</i> 2020; 105(11).
14	Guan JT, Li XX, Peng DW, Zhang WM, Qu J, Lu F, D'Amato RJ, Chi ZL. MicroRNA-18a-5p Administration Suppresses Retinal Neovascularization by Targeting FGF1 and HIF1A. <i>Front Pharmacol</i> 2020; 11:276.
15	Xue L, Xiong C, Li J, Ren Y, Zhang L, Jiao K, Chen C, Ding P. miR-200-3p suppresses cell proliferation and reduces apoptosis in diabetic retinopathy via blocking the TGF-beta2/Smad pathway. <i>Biosci Rep</i> 2020; 40(11).
16	Li EH, Huang QZ, Li GC, Xiang ZY, Zhang X. Effects of miRNA-200b on the development of diabetic retinopathy by targeting VEGFA gene. <i>Biosci Rep</i> 2017; 37(2).
17	McArthur K, Feng B, Wu Y, Chen S, Chakrabarti S. MicroRNA-200b regulates vascular endothelial growth factor-mediated alterations in diabetic retinopathy. <i>Diabetes</i> 2011; 60(4):1314-23.
18	Yin C, Lin X, Sun Y, Ji X. Dysregulation of miR-210 is involved in the development of diabetic retinopathy and serves a regulatory role in retinal vascular endothelial cell proliferation. <i>Eur J Med Res</i> 2020; 25(1):20.
19	Ji H, Yi Q, Chen L, Wong L, Liu Y, Xu G, Zhao J, Huang T, Li B, Yang Y, Li W, Han L, Duan S. Circulating miR-3197 and miR-2116-5p as novel biomarkers for diabetic retinopathy. <i>Clinica chimica acta; international journal of clinical chemistry</i> 2020; 501:147-53.
20	Liu Y, Xiao J, Zhao Y, Zhao C, Yang Q, Du X, Wang X. microRNA-216a protects against human retinal microvascular endothelial cell injury in diabetic retinopathy by suppressing the NOS2/JAK/STAT axis. <i>Experimental and Molecular Pathology</i> 2020; 115:104445.
21	Liu HN, Li X, Wu N, Tong MM, Chen S, Zhu SS, Qian W, Chen XL. Serum microRNA-221 as a biomarker for diabetic retinopathy in patients associated with type 2 diabetes. <i>Int J Ophthalmol</i> 2018; 11(12):1889-94.
22	Zampetaki A, Willeit P, Burr S, Yin X, Langley SR, Kiechl S, Klein R, Rossing P, Chaturvedi N, Mayr M. Angiogenic microRNAs Linked to Incidence and Progression of Diabetic Retinopathy in Type 1 Diabetes. <i>Diabetes</i> 2016; 65(1):216.
23	Torus B, Korkmaz H, Ozturk KH, FB SI, Argun M, Sevi KS, L TO. Downregulation of plasma microRNA-29c-3p expression may be a new risk factor for diabetic retinopathy. <i>Minerva Endocrinol</i> 2020.
24	Ji H, Yi Q, Chen L, Wong L, Liu Y, Xu G, Zhao J, Huang T, Li B, Yang Y, Li W, Han L, Duan S. Circulating miR-3197 and miR-2116-5p as novel biomarkers for diabetic retinopathy. <i>Clinica Chimica Acta</i> 2019.
25	Prado MSG, de Jesus ML, de Goes TC, Mendonca LSO, Kaneto CM. Downregulation of circulating miR-320a and target gene prediction in patients with diabetic retinopathy. <i>BMC Res Notes</i> 2020; 13(1):155.
26	Ji Q, Han J, Wang L, Liu J, Dong Y, Zhu K, Shi L. MicroRNA-34a promotes apoptosis of retinal vascular endothelial cells by targeting SIRT1 in rats with diabetic retinopathy. <i>Cell cycle</i> 2020; 19(21):2886-96.
27	Wang J, Liang S, Guangming W, Zhao D, Qian C, Dong Y, Minghang P. A novel microRNA-365/SIRT1/beta-catenin/GLUT1 signaling axis affects the initiation of diabetic retinopathy. <i>Diabetes Metab Res Rev</i> 2020:e3428.
28	Hu K, Li JL, Yuan XW. MicroRNA-45xUdHPiFHQ7xbKh19G45saF1raB2ot5pag8p1Hnk4yrfXRJZskr8TMbFpVfC5tDk8eQQg63TqkW9gKhwagx6HePTaK2yXbMed <i>Pharmacol Sci</i> 2019; 23(21):9171-9.
29	Blum A, Meerson A, Rohana H, Jabaly H, Nahul N, Celesh D, Romanenko O, Tamir S. MicroRNA-423 may regulate diabetic vasculopathy. <i>Clinical and Experimental Medicine</i> 2019; 19(4):469-77.
30	Bhatwadekar AD, Yan Y, Stepps V, Hazra S, Korah M, Bartelmez S, Chaqour B, Grant MB. miR-92a Corrects CD34+ Cell Dysfunction in Diabetes by Modulating Core Circadian Genes Involved in Progenitor Differentiation. <i>Diabetes</i> 2015; 64(12):4226-37.

Supplementary Table ST2: PCR primer sequence used in the study

Primer name	Sequence (5' to 3')	References
Universal stem-loop primer:	5'GAAAGAAGGCGAGGAGCAGATCGAGGAAGAAGACGGAAGAAT GTGCGTCTCGCCTTCTTTCNNNNNNNNN3'	[1]
U6 RT primer:	5'CGCTTCACGAATTTGCGTGTCAB3'	[1]
U6 qRT-PCR Forward primer:	5'GCTTCGGCAGCACATATACTAAAAT3'	[1]
U6 qRT-PCR Reverse Primer:	5'CGCTTCACGAATTTGCGTGTCAT3'	[1]
Universal Reverse Primer:	5'CGAGGAAGAAGACGGAAGAAT3'	[1]
miR-126 Forward primer:	5'ACACTCCAGCTGGGTCGTACCGTGAGTAA3'	[2]
miR132 Forward primer#:	5'ACACTCCAGCTGGGTAACAGTCTACAGCCA3'	[2].

#Sequence of miR-132 was taken from miRBase (<https://www.mirbase.org/index.shtml>). miR132 forward primer is self-designed but concept was adopted from Chen et al 2008 [2].

^[1]Yang L-h, Wang S-l, Tang L-l, Liu B, Ye W-l, Wang L-l, et al. (2014) Universal Stem-Loop Primer Method for Screening and Quantification of MicroRNA. PLoS ONE 9: e115293. <https://doi.org/10.1371/journal.pone.0115293>

^[2]Chen, X., Ba, Y., Ma, L. *et al.* (2008) Characterization of microRNAs in serum: a novel class of biomarkers for diagnosis of cancer and other diseases. *Cell Res* 18, 997–1006. <https://doi.org/10.1038/cr.2008.282>

Supplementary Table ST3A Validated targets of miR-132 collected from miRTarBase (<http://mirtarbase.mbc.nctu.edu.tw/>)

miRTarBase ID	miRNA	Target Gene	Target Gene (Entrez Gene ID)	Experiments	References (PMID)
MIRT000333	hsa-miR-132-3p	SIRT1	23411	Luciferase reporter assay//Western blot	19819989
MIRT000333	hsa-miR-132-3p	SIRT1	23411	ChIP-seq//Immunoprecipitation//Luciferase reporter assay//Microarray//qRT-PCR//Western blot	28383763
MIRT000601	hsa-miR-132-3p	CDKN1A	1026	qRT-PCR//Luciferase reporter assay//Western blot	20190813
MIRT000601	hsa-miR-132-3p	CDKN1A	1026	PAR-CLIP	26701625
MIRT000601	hsa-miR-132-3p	CDKN1A	1026	PAR-CLIP	27292025
MIRT003926	hsa-miR-132-3p	ARHGAP32	9743	qRT-PCR	18082412
MIRT003926	hsa-miR-132-3p	ARHGAP32	9743	Luciferase reporter assay//Western blot	18577589
MIRT003926	hsa-miR-132-3p	ARHGAP32	9743	Luciferase reporter assay	19850129
MIRT006503	hsa-miR-132-3p	RB1	5925	Luciferase reporter assay//Western blot//Reporter assay;Western blot;qRT-PCR	21329664
MIRT006659	hsa-miR-132-3p	HBEGF	1839	Luciferase reporter assay//Microarray//qRT-PCR//Western blot	21853268
MIRT006659	hsa-miR-132-3p	HBEGF	1839	Luciferase reporter assay	22310291
MIRT006659	hsa-miR-132-3p	HBEGF	1839	Microarray	17612493
MIRT007010	hsa-miR-132-3p	RASA1	5921	Immunoblot//Western blot	21868695
MIRT007166	hsa-miR-132-3p	CRK	1398	Luciferase reporter assay	23184980
MIRT007166	hsa-miR-132-3p	CRK	1398	Microarray	17612493
MIRT007167	hsa-miR-132-3p	TJAP1	93643	Luciferase reporter assay	23184980
MIRT007167	hsa-miR-132-3p	TJAP1	93643	PAR-CLIP	21572407
MIRT007167	hsa-miR-132-3p	TJAP1	93643	PAR-CLIP	26701625
MIRT007253	hsa-miR-132-3p	TLN2	83660	Luciferase reporter assay	22310291
MIRT007253	hsa-miR-132-3p	TLN2	83660	Luciferase reporter assay	22330136
MIRT021716	hsa-miR-132-3p	ARL6IP6	151188	Microarray	17612493
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MIRT021718	hsa-miR-132-3p	PIP5K1A	8394	Microarray	17612493
MIRT021719	hsa-miR-132-3p	CDH3	1001	Microarray	17612493
MIRT021720	hsa-miR-132-3p	LOXL1	4016	Microarray	17612493
MIRT021721	hsa-miR-132-3p	TNFRSF17	608	Microarray	17612493
MIRT021722	hsa-miR-132-3p	ADH1A	124	Microarray	17612493
MIRT021723	hsa-miR-132-3p	KCTD4	386618	Microarray	17612493
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MIRT021725	hsa-miR-132-3p	WNT3A	89780	Microarray	17612493
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MIRT021730	hsa-miR-132-3p	PLSCR1	5359	Microarray	17612493
MIRT021731	hsa-miR-132-3p	CSTF2T	23283	Microarray	17612493
MIRT021732	hsa-miR-132-3p	TAF15	8148	Microarray	17612493
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MIRT021860	hsa-miR-132-3p	MUC13	56667	Microarray	17612493
MIRT021860	hsa-miR-132-3p	MUC13	56667	Immunohistochemistry//Luciferase reporter assay//qRT-PCR//Western blot	28339011
MIRT021861	hsa-miR-132-3p	TSPAN6	7105	Microarray	17612493
MIRT021862	hsa-miR-132-3p	GTF2H1	2965	Microarray	17612493
MIRT021863	hsa-miR-132-3p	CALU	813	Microarray	17612493
MIRT021864	hsa-miR-132-3p	CAMSAP2	23271	Microarray	17612493
MIRT021865	hsa-miR-132-3p	CCNA2	890	Western blot;qRT-PCR	21329664
MIRT021866	hsa-miR-132-3p	CCNB1	891	Western blot;qRT-PCR	21329664
MIRT045838	hsa-miR-132-3p	PARP10	84875	CLASH	23622248
MIRT045839	hsa-miR-132-3p	RPL7	6129	CLASH	23622248
MIRT045840	hsa-miR-132-3p	FOXO1	2308	CLASH	23622248
MIRT045840	hsa-miR-132-3p	FOXO1	2308	Luciferase reporter assay//qRT-PCR//Western blot	26298723
MIRT045840	hsa-miR-132-3p	FOXO1	2308	Luciferase reporter assay//Western blot	27556448
MIRT045841	hsa-miR-132-3p	RACK1	10399	CLASH	23622248
MIRT045842	hsa-miR-132-3p	CSTF3	1479	CLASH	23622248
MIRT045843	hsa-miR-132-3p	RPSA	3921	CLASH	23622248
MIRT045844	hsa-miR-132-3p	ANXA2	302	CLASH	23622248
MIRT045845	hsa-miR-132-3p	NCKAP1	10787	CLASH	23622248
MIRT045846	hsa-miR-132-3p	RPS5	6193	CLASH	23622248
MIRT045847	hsa-miR-132-3p	IRAK1	3654	CLASH	23622248
MIRT045848	hsa-miR-132-3p	PDLIM7	9260	CLASH	23622248
MIRT054502	hsa-miR-132-3p	BDNF	627	qRT-PCR//Western blotting	23704927
MIRT054835	hsa-miR-132-3p	JPT1	51155	Luciferase reporter assay//QRTPCR//Microarray//Western blot	25538559
MIRT054836	hsa-miR-132-3p	KLHL11	55175	Luciferase reporter assay//QRTPCR//Microarray//Western blot	25538559
MIRT054837	hsa-miR-132-3p	MAPK1	5594	Luciferase reporter assay//QRTPCR//Microarray//Western blot	25538559
MIRT054894	hsa-miR-132-3p	SOX5	6660	Luciferase reporter assay//Western blot	25305446
MIRT091255	hsa-miR-132-3p	FXR1	8087	PAR-CLIP	23446348
MIRT091255	hsa-miR-132-3p	FXR1	8087	PAR-CLIP	20371350
MIRT091255	hsa-miR-132-3p	FXR1	8087	PAR-CLIP	26701625
MIRT100367	hsa-miR-132-3p	HSPA1B	3304	PAR-CLIP	21572407
MIRT106174	hsa-miR-132-3p	RRS1	23212	PAR-CLIP	21572407
MIRT149855	hsa-miR-132-3p	LDLR	3949	PAR-CLIP	21572407
MIRT217679	hsa-miR-132-3p	ASF1A	25842	PAR-CLIP	21572407
MIRT259587	hsa-miR-132-3p	EIF2S3	1968	PAR-CLIP	20371350
MIRT289307	hsa-miR-132-3p	TNRC6C	57690	HITS-CLIP	19536157
MIRT368374	hsa-miR-132-3p	ARID2	196528	PAR-CLIP	23592263
MIRT438882	hsa-miR-132-3p	IRAK4	51135	Luciferase reporter assay	23264652
MIRT442189	hsa-miR-132-3p	HOOK3	84376	PAR-CLIP	22100165
MIRT449483	hsa-miR-132-3p	STAG1	10274	PAR-CLIP	22100165
MIRT453131	hsa-miR-132-3p	HOXC4	3221	PAR-CLIP	23592263
MIRT455372	hsa-miR-132-3p	KDM5C	8242	PAR-CLIP	23592263

MIRT455526	hsa-miR-132-3p	C6orf106	64771	PAR-CLIP	23592263
MIRT458882	hsa-miR-132-3p	PFAS	5198	PAR-CLIP	23592263
MIRT464180	hsa-miR-132-3p	VMP1	81671	PAR-CLIP	23592263
MIRT464180	hsa-miR-132-3p	VMP1	81671	PAR-CLIP	23446348
MIRT464180	hsa-miR-132-3p	VMP1	81671	PAR-CLIP//HITS-CLIP	21572407
MIRT464180	hsa-miR-132-3p	VMP1	81671	PAR-CLIP	20371350
MIRT464180	hsa-miR-132-3p	VMP1	81671	HITS-CLIP	24906430
MIRT464180	hsa-miR-132-3p	VMP1	81671	HITS-CLIP	23824327
MIRT464180	hsa-miR-132-3p	VMP1	81671	HITS-CLIP	23706177
MIRT464180	hsa-miR-132-3p	VMP1	81671	HITS-CLIP	23313552
MIRT464180	hsa-miR-132-3p	VMP1	81671	HITS-CLIP	22927820
MIRT464180	hsa-miR-132-3p	VMP1	81671	HITS-CLIP	19536157
MIRT464180	hsa-miR-132-3p	VMP1	81671	PAR-CLIP	26701625
MIRT464180	hsa-miR-132-3p	VMP1	81671	PAR-CLIP	27292025
MIRT464180	hsa-miR-132-3p	VMP1	81671	HITS-CLIP	27418678
MIRT464180	hsa-miR-132-3p	VMP1	81671	HITS-CLIP	28735896
MIRT467690	hsa-miR-132-3p	SLC38A2	54407	PAR-CLIP	23592263
MIRT467690	hsa-miR-132-3p	SLC38A2	54407	PAR-CLIP	21572407
MIRT476656	hsa-miR-132-3p	FZD6	8323	PAR-CLIP	23592263
MIRT476656	hsa-miR-132-3p	FZD6	8323	PAR-CLIP	21572407
MIRT477439	hsa-miR-132-3p	EML4	27436	PAR-CLIP	23592263
MIRT477439	hsa-miR-132-3p	EML4	27436	PAR-CLIP	21572407
MIRT479294	hsa-miR-132-3p	CHAC1	79094	PAR-CLIP	23592263
MIRT485291	hsa-miR-132-3p	PLAGL2	5326	PAR-CLIP	23592263
MIRT485291	hsa-miR-132-3p	PLAGL2	5326	PAR-CLIP	26701625
MIRT495258	hsa-miR-132-3p	BMPER	168667	PAR-CLIP	23708386
MIRT497153	hsa-miR-132-3p	PRDM15	63977	PAR-CLIP	22291592
MIRT500830	hsa-miR-132-3p	ELOC	6921	PAR-CLIP	24398324
MIRT500830	hsa-miR-132-3p	ELOC	6921	PAR-CLIP	26701625
MIRT500830	hsa-miR-132-3p	ELOC	6921	PAR-CLIP	27292025
MIRT506948	hsa-miR-132-3p	HS3ST3B1	9953	PAR-CLIP	23446348
MIRT506948	hsa-miR-132-3p	HS3ST3B1	9953	PAR-CLIP	22012620
MIRT506948	hsa-miR-132-3p	HS3ST3B1	9953	PAR-CLIP	26701625
MIRT506948	hsa-miR-132-3p	HS3ST3B1	9953	PAR-CLIP	27292025
MIRT507623	hsa-miR-132-3p	CRTC1	23373	PAR-CLIP	23446348
MIRT508137	hsa-miR-132-3p	AMD1	262	PAR-CLIP	23446348
MIRT508137	hsa-miR-132-3p	AMD1	262	PAR-CLIP	27292025
MIRT526271	hsa-miR-132-3p	CCDC169	728591	PAR-CLIP	22012620
MIRT526867	hsa-miR-132-3p	PARP11	57097	PAR-CLIP	22012620
MIRT532420	hsa-miR-132-3p	ART4	420	PAR-CLIP	22012620
MIRT532508	hsa-miR-132-3p	TWISTNB	221830	PAR-CLIP	22012620
MIRT532508	hsa-miR-132-3p	TWISTNB	221830	PAR-CLIP	20371350

MIRT534833	hsa-miR-132-3p	RAB18	22931	PAR-CLIP	22012620
MIRT542577	hsa-miR-132-3p	ZNF280B	140883	PAR-CLIP	21572407
MIRT546160	hsa-miR-132-3p	TSPAN12	23554	PAR-CLIP	21572407
MIRT547255	hsa-miR-132-3p	NUP50	10762	PAR-CLIP	21572407
MIRT547255	hsa-miR-132-3p	NUP50	10762	PAR-CLIP	20371350
MIRT547614	hsa-miR-132-3p	LIFR	3977	PAR-CLIP	21572407
MIRT547705	hsa-miR-132-3p	KPNA1	3836	PAR-CLIP	21572407
MIRT547705	hsa-miR-132-3p	KPNA1	3836	PAR-CLIP	20371350
MIRT549141	hsa-miR-132-3p	BRWD1	54014	PAR-CLIP	21572407
MIRT549455	hsa-miR-132-3p	ACSL4	2182	PAR-CLIP//HITS-CLIP	21572407
MIRT551640	hsa-miR-132-3p	TRUB1	142940	PAR-CLIP	21572407
MIRT551640	hsa-miR-132-3p	TRUB1	142940	PAR-CLIP	20371350
MIRT554985	hsa-miR-132-3p	RAB5B	5869	PAR-CLIP	21572407
MIRT554985	hsa-miR-132-3p	RAB5B	5869	PAR-CLIP	26701625
MIRT555924	hsa-miR-132-3p	OCLN	100506658	PAR-CLIP	21572407
MIRT555924	hsa-miR-132-3p	OCLN	100506658	PAR-CLIP	20371350
MIRT557610	hsa-miR-132-3p	GNB1	2782	PAR-CLIP	21572407
MIRT571512	hsa-miR-132-3p	ZNF711	7552	PAR-CLIP	20371350
MIRT572928	hsa-miR-132-3p	PRAMEF1	65121	PAR-CLIP	20371350
MIRT573617	hsa-miR-132-3p	ZNF724	440519	PAR-CLIP	20371350
MIRT614465	hsa-miR-132-3p	ALKBH4	54784	HITS-CLIP	23824327
MIRT623025	hsa-miR-132-3p	OLFML2A	169611	HITS-CLIP	23824327
MIRT639080	hsa-miR-132-3p	CD226	10666	HITS-CLIP	23824327
MIRT642134	hsa-miR-132-3p	CYP20A1	57404	HITS-CLIP	23824327
MIRT653734	hsa-miR-132-3p	SLC25A32	81034	HITS-CLIP	23824327
MIRT655167	hsa-miR-132-3p	PHF20L1	51105	HITS-CLIP	23824327
MIRT680989	hsa-miR-132-3p	DCAF17	80067	HITS-CLIP	23706177
MIRT681564	hsa-miR-132-3p	UBXN2A	165324	HITS-CLIP	23706177
MIRT681564	hsa-miR-132-3p	UBXN2A	165324	PAR-CLIP	27292025
MIRT696294	hsa-miR-132-3p	IER3IP1	51124	HITS-CLIP	23313552
MIRT697724	hsa-miR-132-3p	USP8	9101	HITS-CLIP	23313552
MIRT703296	hsa-miR-132-3p	GID4	79018	HITS-CLIP	23313552
MIRT718422	hsa-miR-132-3p	CALN1	83698	HITS-CLIP	19536157
MIRT719460	hsa-miR-132-3p	APBA1	320	HITS-CLIP	19536157
MIRT731713	hsa-miR-132-3p	EGFR	1956	Immunohistochemistry//Luciferase reporter assay//qRT-PCR//Western blot	26452132
MIRT731714	hsa-miR-132-3p	RAF1	5894	Immunohistochemistry//Luciferase reporter assay//qRT-PCR//Western blot	26452132
MIRT732559	hsa-miR-132-3p	SOX4	6659	Immunoprecipitaion//Luciferase reporter assay//qRT-PCR//Western blot	26377202
MIRT732595	hsa-miR-132-3p	FGF2	2247	qRT-PCR	25864118
MIRT733351	hsa-miR-132-3p	SPRY1	10252	Luciferase reporter assay//Western blot	25945589
MIRT733764	hsa-miR-132-3p	MMP9	4318	Luciferase reporter assay	26319558
MIRT733928	hsa-miR-132-3p	YY1AP1	55249	Luciferase reporter assay//qRT-PCR//Western blot	26096363
MIRT734062	hsa-miR-132-3p	AGO2	27161	Immunoblot//Luciferase reporter assay//qRT-PCR	26475020

MIRT734812	hsa-miR-132-3p	SOX6	55553	Luciferase reporter assay//Western blot	27556448
MIRT734813	hsa-miR-132-3p	GDF5	8200	Luciferase reporter assay//Western blot	27556448
MIRT734832	hsa-miR-132-3p	PIK3R3	8503	Luciferase reporter assay//qRT-PCR//Western blot	26252738
MIRT735158	hsa-miR-132-3p	SMAD2	4087	GFP reporter assay//qRT-PCR//Western blot	25988335
MIRT735435	hsa-miR-132-3p	SLC2A1	6513	Luciferase reporter assay//qRT-PCR//Western blot	27398313
MIRT737386	hsa-miR-132-3p	DAZAP2	9802	PAR-CLIP	26701625
MIRT737386	hsa-miR-132-3p	DAZAP2	9802	PAR-CLIP	27292025
MIRT737387	hsa-miR-132-3p	SETD5	55209	PAR-CLIP	26701625
MIRT762535	hsa-miR-132-3p	GMNN	51053	PAR-CLIP	27292025
MIRT762536	hsa-miR-132-3p	MTO1	25821	PAR-CLIP	27292025
MIRT762537	hsa-miR-132-3p	OTUD3	23252	PAR-CLIP	27292025
MIRT762538	hsa-miR-132-3p	SH3TC2	79628	PAR-CLIP	27292025
MIRT762539	hsa-miR-132-3p	SLC10A7	84068	PAR-CLIP	27292025

Supplementary Table ST3B Validated targets of miR-126 collected from miRTarBase (http://mirtarbase.mbc.nctu.edu.tw/)					
miRTarBase ID	miRNA	Target Gene	Target Gene (Entrez Gene ID)	Experiments	References (PMID)
MIRT613368	hsa-miR-126-3p	ACVR2B	93	HITS-CLIP	23824327
MIRT007266	hsa-miR-126-3p	ADAM9	8754	Luciferase reporter assay	23437250
MIRT007266	hsa-miR-126-3p	ADAM9	8754	Immunohistochemistry//In situ hybridization//Microarray//qRT-PCR//Western blot	22064652
MIRT007266	hsa-miR-126-3p	ADAM9	8754	Western blot	24823697
MIRT007266	hsa-miR-126-3p	ADAM9	8754	In situ hybridization//Microarray//Luciferase reporter assay	25512445
MIRT007266	hsa-miR-126-3p	ADAM9	8754	Luciferase reporter assay//Western blot	26244545
MIRT007266	hsa-miR-126-3p	ADAM9	8754	Luciferase reporter assay//qRT-PCR//Western blot	28260063
MIRT438175	hsa-miR-126-3p	ADGRE5	976	FACS//Flow//GFP reporter assay//Luciferase reporter assay//qRT-PCR	24274104
MIRT438600	hsa-miR-126-3p	ADM	133	Luciferase reporter assay	24037526
MIRT735543	hsa-miR-126-3p	AKT1	207	qRT-PCR//Western blot	26659078
MIRT568554	hsa-miR-126-3p	AKT2	208	PAR-CLIP	20371350
MIRT053253	hsa-miR-126-3p	BCL2	596	In situ hybridization//Luciferase reporter assay//Microarray//Northern blot//qRT-PCR//Western blot	23603512
MIRT732065	hsa-miR-126-3p	CADM1	23705	Luciferase reporter assay//qRT-PCR//Western blot	26464628
MIRT000965	hsa-miR-126-3p	CCNE2	9134	Luciferase reporter assay	18834857
MIRT438412	hsa-miR-126-3p	Cdkn1b	83571	Immunoblot//qRT-PCR	25133421
MIRT002993	hsa-miR-126-3p	CRK	1398	Luciferase reporter assay//Western blot//qRT-PCR	18602365
MIRT002993	hsa-miR-126-3p	CRK	1398	Western blot	19767772
MIRT002993	hsa-miR-126-3p	CRK	1398	Immunohistochemistry//Luciferase reporter assay//Western blot	20619534
MIRT002993	hsa-miR-126-3p	CRK	1398	Sequencing	20371350
MIRT002993	hsa-miR-126-3p	CRK	1398	qRT-PCR//Western blot	24969300
MIRT002993	hsa-miR-126-3p	CRK	1398	qRT-PCR//Western blot	25027343
MIRT002993	hsa-miR-126-3p	CRK	1398	qRT-PCR	27785060
MIRT021281	hsa-miR-126-3p	CRKL	1399	Immunohistochemistry//Luciferase reporter assay//qRT-PCR//Western blot	24055140

MIRT007381	hsa-miR-126-3p	CXCL12	6387	Luciferase reporter assay	23396050
MIRT054425	hsa-miR-126-3p	CXCR4	7852	qRT-PCR//Western blot	24532280
MIRT054425	hsa-miR-126-3p	CXCR4	7852	Luciferase reporter assay	24189753
MIRT054425	hsa-miR-126-3p	CXCR4	7852	Luciferase reporter assay//Western blot	23744532
MIRT005729	hsa-miR-126-3p	DNMT1	1786	Flow//Luciferase reporter assay//Microarray//qRT-PCR//Western blot	21538319
MIRT005020	hsa-miR-126-3p	E2F1	1869	qRT-PCR	18521848
MIRT006558	hsa-miR-126-3p	EGFL7	51162	Flow//Immunoblot//Immunohistochemistry//Luciferase reporter assay//qRT-PCR//Western blot//Western blot;qRT-PCR;Other	20034472
MIRT006558	hsa-miR-126-3p	EGFL7	51162	Reporter assay	21249429
MIRT736681	hsa-miR-126-3p	EVI5	7813	PAR-CLIP	26701625
MIRT733311	hsa-miR-126-3p	EZH2	2146	Luciferase reporter assay//qRT-PCR//Western blot	27622325
MIRT053249	hsa-miR-126-3p	FOXO3	2309	In situ hybridization//Luciferase reporter assay//Northern blot//qRT-PCR//Western blot	23603512
MIRT623746	hsa-miR-126-3p	GRIN2B	2904	HITS-CLIP	23824327
MIRT001918	hsa-miR-126-3p	HOXA9	3205	GFP reporter assay//qRT-PCR//Western blot//Luciferase reporter assay	18474618
MIRT006543	hsa-miR-126-3p	IGFBP2	3485	ELISA//Flow//Immunohistochemistry//Luciferase reporter assay//Microarray//qRT-PCR//Western blot	22170610
MIRT004355	hsa-miR-126-3p	IRS1	3667	qRT-PCR//Luciferase reporter assay//Western blot	18834857
MIRT004355	hsa-miR-126-3p	IRS1	3667	Luciferase reporter assay	21464990
MIRT004355	hsa-miR-126-3p	IRS1	3667	Luciferase reporter assay//Northern blot//qRT-PCR//Western blot	23603512
MIRT004355	hsa-miR-126-3p	IRS1	3667	Luciferase reporter assay//qRT-PCR//Western blot	23893300
MIRT004355	hsa-miR-126-3p	IRS1	3667	Luciferase reporter assay	26893711
MIRT004355	hsa-miR-126-3p	IRS1	3667	Luciferase reporter assay//qRT-PCR//Western blot	26617742
MIRT004355	hsa-miR-126-3p	IRS1	3667	Microarray//qRT-PCR//Western blot	27119351
MIRT527649	hsa-miR-126-3p	KCNJ1	3758	PAR-CLIP	22012620
MIRT006450	hsa-miR-126-3p	KRAS	3845	Immunohistochemistry//Luciferase reporter assay//Microarray//qRT-PCR//Western blot	22384141
MIRT761730	hsa-miR-126-3p	L2HGDH	79944	PAR-CLIP	27292025
MIRT438575	hsa-miR-126-3p	LRP6	4040	Luciferase reporter assay//qRT-PCR//Western blot	23811937
MIRT438575	hsa-miR-126-3p	LRP6	4040	Luciferase reporter assay//qRT-PCR//Western blot	26239517
MIRT006545	hsa-miR-126-3p	MERTK	10461	ELISA//Flow//Immunohistochemistry//Luciferase reporter assay//Microarray//qRT-PCR//Western blot	22170610
MIRT007269	hsa-miR-126-3p	MMP7	4316	Luciferase reporter assay	23437250
MIRT438759	hsa-miR-126-3p	NFKBIA	4792	Immunofluorescence//Luciferase reporter assay//qRT-PCR//Western blot	23285182
MIRT021282	hsa-miR-126-3p	PGR	5241	Reporter assay;Western blot	21526342
MIRT006831	hsa-miR-126-3p	PIK3CG	5294	Immunocytochemistry//Luciferase reporter assay//qRT-PCR//Western blot	22900072
MIRT006831	hsa-miR-126-3p	PIK3CG	5294	Microarray//qRT-PCR//Western blot//SILAC (Stable Isotope Labeling of Amino acids in Culture)	23142521
MIRT006831	hsa-miR-126-3p	PIK3CG	5294	Luciferase reporter assay	27729613
MIRT006831	hsa-miR-126-3p	PIK3CG	5294	qRT-PCR//Western blot	26659078
MIRT736682	hsa-miR-126-3p	PIK3R1	5295	PAR-CLIP	26701625
MIRT003894	hsa-miR-126-3p	PIK3R2	5296	Luciferase reporter assay//Western blot	18987025
MIRT003894	hsa-miR-126-3p	PIK3R2	5296	Western blot//qRT-PCR//Luciferase reporter assay	18663744
MIRT003894	hsa-miR-126-3p	PIK3R2	5296	Luciferase reporter assay//Western blot//Reporter assay;Western blot	21249429
MIRT003894	hsa-miR-126-3p	PIK3R2	5296	qRT-PCR//Western blot	24969300
MIRT003894	hsa-miR-126-3p	PIK3R2	5296	Immunohistochemistry//In situ hybridization//qRT-PCR//Western blot	26381870
MIRT003894	hsa-miR-126-3p	PIK3R2	5296	Luciferase reporter assay//qRT-PCR//Western blot	27191494

MIRT006544	hsa-miR-126-3p	PITPNC1	26207	ELISA//Flow//Immunohistochemistry//Luciferase reporter assay//Microarray//qRT-PCR//Western blot	22170610
MIRT761731	hsa-miR-126-3p	PLAGL2	5326	PAR-CLIP	27292025
MIRT000344	hsa-miR-126-3p	PLK2	10769	Luciferase reporter assay//qRT-PCR	18832181
MIRT000344	hsa-miR-126-3p	PLK2	10769	Luciferase reporter assay//qRT-PCR//Western blot	24969300
MIRT005727	hsa-miR-126-3p	PTPN7	5778	Flow//Immunoprecipitation//Luciferase reporter assay//qRT-PCR//Western blot	21163928
MIRT045695	hsa-miR-126-3p	RBMX	27316	CLASH	23622248
MIRT000966	hsa-miR-126-3p	RGS3	5998	Luciferase reporter assay	18834857
MIRT000966	hsa-miR-126-3p	RGS3	5998	Reporter assay	21249429
MIRT000966	hsa-miR-126-3p	RGS3	5998	Immunohistochemistry//Luciferase reporter assay//qRT-PCR//Western blot	27754994
MIRT438574	hsa-miR-126-3p	RHOU	58480	Luciferase reporter assay//qRT-PCR//Western blot	23811937
MIRT734471	hsa-miR-126-3p	ROCK1	6093	Luciferase reporter assay//qRT-PCR//Western blot	27108693
MIRT438651	hsa-miR-126-3p	SIRT1	23411	Luciferase reporter assay//qRT-PCR//Western blot	23877372
MIRT545417	hsa-miR-126-3p	SLC39A6	25800	PAR-CLIP	21572407
MIRT614772	hsa-miR-126-3p	SLC41A2	84102	HITS-CLIP	23824327
MIRT614772	hsa-miR-126-3p	SLC41A2	84102	HITS-CLIP	19536157
MIRT614772	hsa-miR-126-3p	SLC41A2	84102	HITS-CLIP	27418678
MIRT000798	hsa-miR-126-3p	SLC45A3	85414	Western blot//Luciferase reporter assay//Reporter assay;Other	18193184
MIRT006679	hsa-miR-126-3p	SLC7A5	8140	Immunohistochemistry//Luciferase reporter assay//qRT-PCR//Western blot	21439283
MIRT006679	hsa-miR-126-3p	SLC7A5	8140	PAR-CLIP	20371350
MIRT006679	hsa-miR-126-3p	SLC7A5	8140	Flow//Immunohistochemistry//Luciferase reporter assay//qRT-PCR//Western blot	26054677
MIRT006679	hsa-miR-126-3p	SLC7A5	8140	Luciferase reporter assay//Western blot	26244545
MIRT005370	hsa-miR-126-3p	SOX2	6657	Immunohistochemistry//Luciferase reporter assay//Microarray//qRT-PCR//Western blot	21304604
MIRT005370	hsa-miR-126-3p	SOX2	6657	Luciferase reporter assay	24384842
MIRT000343	hsa-miR-126-3p	SPRED1	161742	Luciferase reporter assay//Western blot	18987025
MIRT000343	hsa-miR-126-3p	SPRED1	161742	Luciferase reporter assay	18694566
MIRT000343	hsa-miR-126-3p	SPRED1	161742	Luciferase reporter assay	18832181
MIRT000343	hsa-miR-126-3p	SPRED1	161742	Flow//Luciferase reporter assay//qRT-PCR//Western blot	22525256
MIRT000343	hsa-miR-126-3p	SPRED1	161742	qRT-PCR//Western blot	23811937
MIRT000343	hsa-miR-126-3p	SPRED1	161742	Immunohistochemistry//In situ hybridization//qRT-PCR//Western blot	26381870
MIRT736683	hsa-miR-126-3p	SZRD1	26099	PAR-CLIP	26701625
MIRT438192	hsa-miR-126-3p	TCF4	6925	Luciferase reporter assay	24190507
MIRT006883	hsa-miR-126-3p	TEK	7010	Luciferase reporter assay//qRT-PCR//Western blot	22867989
MIRT000967	hsa-miR-126-3p	TOM1	10043	Luciferase reporter assay	18834857
MIRT000967	hsa-miR-126-3p	TOM1	10043	Luciferase reporter assay//qRT-PCR//Western blot//Reporter assay;Western blot	20083669
MIRT000967	hsa-miR-126-3p	TOM1	10043	Microarray//qRT-PCR	22815788
MIRT005538	hsa-miR-126-3p	TWF1	5756	Luciferase reporter assay//Microarray//Northern blot//qRT-PCR//Western blot	20571053
MIRT005540	hsa-miR-126-3p	TWF2	11344	Luciferase reporter assay//Microarray//Northern blot//qRT-PCR//Western blot	20571053
MIRT004081	hsa-miR-126-3p	VCAM1	7412	Luciferase reporter assay//Western blot//Reporter assay;Other	18227515
MIRT003428	hsa-miR-126-3p	VEGFA	7422	Luciferase reporter assay//Reporter assay	19223090
MIRT003428	hsa-miR-126-3p	VEGFA	7422	Luciferase reporter assay//qRT-PCR//Western blot	22510476
MIRT003428	hsa-miR-126-3p	VEGFA	7422	Luciferase reporter assay//Western blot//Reporter assay;Western blot	21249429
MIRT003428	hsa-miR-126-3p	VEGFA	7422	Luciferase reporter assay//qRT-PCR//Western blot	25428912

MIRT003428	hsa-miR-126-3p	VEGFA	7422	PAR-CLIP	21572407
MIRT003428	hsa-miR-126-3p	VEGFA	7422	Luciferase reporter assay	24140635
MIRT003428	hsa-miR-126-3p	VEGFA	7422	Luciferase reporter assay//qRT-PCR//Western blot	23900443

Supplementary Table ST4A: Significantly enriched biological processes having at least 3 genes in a category (<https://genecodis.genyo.es/>)

Description	Anno tation_id	Genes_f ound among validate d targets	Inp ut_size	No of genes with the GO term	Total number of genes in the genome (genes_univ erse)	Relative _enrich ment	pval	pval _adj	genes
signal transduction	GO:0 0071 65	46	309	1540	61686	5.96300 593	3.25 E- 22	3.94 E- 19	PITPNC1,CHRNA5,CHL1,CD226,ADGRE5,TOM1,ACVR2B,ARHGAP32,CD164,CNTNAP1,PIP5K1A,FZD6,CXCR4,VEGFA,TEK,BDNF,CXCL12,TN FRSF17,ROCK1,RGS3,RASA1,RAF1,MAPK1,PIK3R2,PIK3R1,PGR,ARR3,STMN1,KRAS,IRS1,IRAK1,IMPA1,IGFBP2,GNB1,GATA3,ADGRF4,ALK, FGF2,CMTM3,AKT2,AKT1,EGFR,HBEGF,LGR4,IRAK4,ADM
multicellular organism development	GO:0 0072 75	37	309	1102	61686	6.70267 651	1.18 E- 19	9.56 E- 17	CADM1,SIRT1,RAB18,CHL1,MERTK,RACK1,SPRY1,PDLIM7,CD164,FZD6,FXR1,VEGFA,TEK,SPAST,SOX2,TNFRSF17,MEF2A,LRP6,LFNG,STM N1,HOXC4,HOXA9,GRIN2B,ALK,SPRED1,FGF2,AKT2,AKT1,FAT3,EYA4,WNT3A,EPHA4,EGFR,PRDM15,SOX6,LGR4,EGFL7
positive regulation of transcription by RNA polymerase II	GO:0 0459 44	34	309	1064	61686	6.37918 826	1.73 E- 17	1.05 E- 14	SIRT1,CRTC1,ACTR2,NR1D2,MLLT10,ZNF148,VEGFA,TCF4,SOX4,SOX2,RB1,RAF1,PLSCR1,PLAGL2,PIK3R2,PIK3R1,PGR,NFKBIA,MEF2A,S MAD2,LRP6,HOXC4,HOXA9,GATA3,FOXO3,FOXO1,FGF2,AKT1,WNT3A,EGFR,E2F1,PRDM15,RBMX,AGO2
viral process	GO:0 0160 32	31	309	576	61686	10.7440 332	1.91 E- 22	4.64 E- 19	CADM1,SIRT1,CRTC1,RAB18,NCKAP1,NUP50,RACK1,CCNA2,PLA2G4C,CXCR4,ELOC,STAU1,CXCL12,RB1,MAPK1,PLSCR1,PIK3R1,NFKBIA,N BN,LDLR,RPSA,TRIM23,KPNA1,IRAK1,HSPA1B,ANXA2,EGFR,E2F1,CD55,MDFIC,CR2
cell differentiation	GO:0 0301 54	31	309	940	61686	6.58357 777	2.08 E- 16	7.20 E- 14	CADM1,SIRT1,CHL1,NR1D2,PDLIM7,FXR1,VEGFA,TCF4,SPAST,SOX5,SOX4,SOX2,RB1,RAF1,NAP1L1,MEF2A,SMAD2,ARF6,STMN1,FOXO1, FGF2,AKT1,EYA4,EGFR,ECT2,PARP11,SOX6,LGR4,YY1AP1,EGFL7,FGF22
regulation of transcription by RNA polymerase II	GO:0 0063 57	29	309	1101	61686	5.25822 068	5.64 E- 13	1.05 E- 10	ZNF652,CDKN1A,ZNF236,ZNF148,VEGFA,TCF4,ELOC,SOX5,RB1,PLAGL2,PGR,MEF2A,SMAD2,HOXC4,HOXA9,ZNF724,GATA3,CC2D1B,FOX O3,FOXO1,ZNF280B,EZH2,EGFR,E2F1,PRDM15,SOX6,BRWD1,PHF20L1,CRK
regulation of transcription, DNA-templated	GO:0 0063 55	25	309	999	61686	4.99577 247	7.00 E- 11	7.38 E- 09	NR1D2,ACVR2B,TAF15,ZNF711,SOX4,SOX2,RB1,PGR,MEF2A,SMAD2,LRP6,HOXC4,HOXA9,ZNF724,GATA3,ARID2,FOXO3,FOXO1,ZNF280 B,EZH2,E2F1,SOX6,YY1AP1,PHF20L1,AGO2
positive regulation of transcription, DNA-templated	GO:0 0458 93	24	309	698	61686	6.86410 549	2.40 E- 13	4.84 E- 11	NR1D2,CCNA2,TAF15,ZNF711,TCF4,SOX4,SOX2,MAPK1,NFKBIA,MEF2A,SMAD2,LRP6,GTF2H1,GATA3,FOXO3,FOXO1,FGF2,AKT1,WNT3A ,EGFR,E2F1,LGR4,MDFIC,RBMX
nervous system development	GO:0 0073 99	22	309	507	61686	8.66249 21	2.41 E- 14	6.48 E- 12	CHL1,MERTK,VEGFA,TCF4,SPAST,SMN1,BDNF,NAP1L1,MEF2A,MAP1B,ARF6,STMN1,APBA1,GATA3,ALK,FGF2,AKT1,FABP7,EPHA4,ECT2, CHAC1,RTN4
positive regulation of cell population proliferation	GO:0 0082 84	22	309	519	61686	8.46220 327	3.86 E- 14	9.35 E- 12	SIRT1,VEGFA,THBS1,SOX4,CXCL12,BCL2,MAPK1,NAP1L1,LIFR,KRAS,IRS1,FGF2,AKT2,AKT1,EZH2,WNT3A,EGFR,HBEGF,PRAMEF1,CRKL,AD M,FGF22
apoptotic process	GO:0 0069 15	22	309	674	61686	6.51614 762	6.72 E- 12	8.57 E- 10	CADM1,SIRT1,NCKAP1,RACK1,CASP7,FXR1,CXCR4,BNIP2,BCL2,ROCK1,RAF1,MAPK1,PLSCR1,NFKBIA,MEF2A,FOXO3,FOXO1,AKT2,AKT 1,E2F1,CHAC1,RTN4
positive regulation of gene expression	GO:0 0106 28	21	309	485	61686	8.64381 944	9.88 E- 14	2.18 E- 11	CDH3,PIK3R3,VEGFA,ROCK1,MAPK1,PLSCR1,OCLN,MEF2A,SMAD2,KRAS,HSPA1B,GATA3,FGF2,AKT1,WNT3A,E2F1,DNMT1,TNRC6C,SLC3 8A2,AGO2,FGF22
phosphorylation	GO:0 0163 10	21	309	677	61686	6.19239 65	5.22 E- 11	5.75 E- 09	CDKN1A,PLK2,MERTK,ACVR2B,PIK3R3,PIP5K1A,TEK,ROCK1,RAF1,MAPK1,PIK3CG,MAP3K3,IRAK1,GK,ALK,AKT2,AKT1,EPHA4,EGFR,ETNK 2,IRAK4
cytokine-mediated signaling pathway	GO:0 0192 21	20	309	283	61686	14.1082 027	3.66 E- 17	1.78 E- 14	CDKN1A,VEGFA,VCAM1,SOX2,BCL2,PTGS2,PIK3R1,MMP9,LIFR,KRAS,IRAK1,GATA3,FOXO3,FOXO1,FGF2,AKT1,RHOU,IRAK4,CRKL,CRK
negative regulation of gene expression	GO:0 0106	20	309	289	61686	13.8152 988	5.50 E-	2.22 E-	SIRT1,CDKN1A,RACK1,CCNB1,SLC7A5,ZNF148,VEGFA,RB1,PGR,OCLN,SMAD2,GATA3,FGF2,AKT1,EZH2,PARP10,DNMT1,TNRC6C,CRKL,AG O2

	29						17	14	
negative regulation of apoptotic process	GO:0043066	20	309	511	61686	7.81334904	2.44E-12	3.70E-10	SIRT1,CDKN1A,PLK2,VEGFA,THBS1,TEK,BNIP2,BCL2,RASA1,RAF1,PIK3R1,NFKBIA,MMP9,IRAK1,HSPA1B,FOXO1,AKT2,AKT1,EGFR,PRAMEF1
cell adhesion	GO:0007155	20	309	579	61686	6.8957191	2.29E-11	2.78E-09	CADM1,CHL1,CD226,CDH3,ADGRE5,CD164,ADAM9,CNTNAP1,VCAM1,THBS1,CXCL12,ARF6,RPSA,APBA1,FAT3,EPHA4,TLN2,VMP1,FAT4,EGFL7
protein phosphorylation	GO:0006468	19	309	588	61686	6.45066376	2.24E-10	2.17E-08	PLK2,MERTK,ACVR2B,CCNB1,TEK,ROCK1,RAF1,MAPK1,PIK3R1,PIK3CG,MAP3K3,SMAD2,IRAK1,ALK,AKT2,AKT1,EPHA4,EGFR,IRAK4
cell cycle	GO:0007049	18	309	626	61686	5.74019045	4.16E-09	3.25E-07	TUSC2,CDKN1A,RACK1,STAG1,CCNB1,CCNA2,CCNE2,USP8,EVI5,SPAST,RB1,MAPK1,NBN,LIG4,ARF6,ECT2,E2F1,GMNN
intracellular signal transduction	GO:0035556	17	309	426	61686	7.96649802	8.22E-11	8.30E-09	PLA2G4C,S100A1,ROCK1,RASA1,RAF1,MAPK1,MAP3K3,SMAD2,STMN1,IRAK1,AKT2,AKT1,DEPDC7,EGFR,ECT2,IRAK4,CRKL
protein transport	GO:0015031	17	309	613	61686	5.53626126	1.91E-08	1.29E-06	RAB18,NUP50,YKT6,EXOC5,TOM1,RAB5B,PIK3R2,PIK3R1,ARF6,KPNA1,APBA1,LCA5,HOOK3,ECT2,PARP11,SNX7,SEC61A1
positive regulation of protein phosphorylation	GO:0001934	16	309	202	61686	15.8123618	9.20E-15	2.79E-12	SIRT1,RACK1,PIK3R3,FXR1,VEGFA,TEK,RAF1,MMP9,KRAS,FGF2,AKT2,AKT1,WNT3A,EGFR,CRKL,FGF22
MAPK cascade	GO:0000165	16	309	276	61686	11.5728155	1.15E-12	1.86E-10	TEK,RASA1,RAF1,PSMD12,PSMA2,MAPK1,MAP3K3,MEF2A,KRAS,IRS1,GRIN2B,SPRED1,FGF2,EGFR,HBEGF,FGF22
negative regulation of transcription, DNA-templated	GO:0045892	16	309	549	61686	5.81802748	2.54E-08	1.67E-06	SIRT1,NR1D2,KDM5C,ZNF148,RB1,SMAD2,GATA3,FOXO1,EZH2,PARP10,E2F1,PRAMEF1,SOX6,LGR4,GMNN,MDFIC
negative regulation of transcription by RNA polymerase II	GO:0000122	15	309	766	61686	3.90922457	9.47E-06	0.0001978	SIRT1,NR1D2,ACVR2B,ZNF148,VEGFA,SOX2,RB1,MEF2A,SMAD2,GATA3,CC2D1B,FOXO3,EZH2,E2F1,DNMT1
positive regulation of protein kinase B signaling	GO:0051897	14	309	181	61686	15.4410771	6.11E-13	1.06E-10	VEGFA,THBS1,TEK,PIK3R2,PIK3R1,PIK3CG,IRS1,GATA3,FGF2,OSBPL8,EGFR,HBEGF,RTN4,FGF22
positive regulation of cell migration	GO:0030335	14	309	250	61686	11.1793398	4.78E-11	5.51E-09	RACK1,ADAM9,PIK3R3,CXCR4,VEGFA,THBS1,CXCL12,MAPK1,PIK3R1,MMP9,MMP7,AKT2,EGFR,HBEGF
cellular response to DNA damage stimulus	GO:0006974	14	309	496	61686	5.63474789	2.81E-07	1.22E-05	SIRT1,SMCHD1,CDKN1A,BCL2,MAPK1,NBN,LIG4,GTF2H1,FOXO1,AKT1,EYA4,PARP10,UBE2W,POLK
transmembrane transport	GO:0055085	14	309	558	61686	5.00866479	1.13E-06	3.39E-05	SLC39A6,CFTR,ATP6V0E1,SLC7A5,VDAC2,SLC2A1,BCL2,PSMD12,PSMA2,GJE1,SFXN2,SLC45A3,SLC10A7,EIF2S3
G protein-coupled receptor signaling pathway	GO:0007186	14	309	672	61686	4.15898058	9.46E-06	0.0001993	ADGRE5,FZD6,CXCR4,CXCL12,ROCK1,RGS3,PIK3R1,PIK3CG,GNB1,ADGRF4,AKT1,ECT2,LGR4,ADM
chromatin organization	GO:0006325	13	309	322	61686	8.05963939	1.23E-08	8.75E-07	ASF1A,SIRT1,SMCHD1,KDM5C,SOX2,RB1,ARID2,EZH2,EYA4,DNMT1,SETD5,ALKBH4,BRWD1
negative regulation of cell population	GO:00082	13	309	438	61686	5.92512302	4.27E-	1.64E-	CDKN1A,SPRY1,CD164,SOX4,BCL2,RB1,RAF1,SMAD2,HSPA1B,GATA3,ARID2,FABP7,ADM

proliferation	85						07	05	
neutrophil degranulation	GO:0043312	13	309	476	61686	5.452109	1.08E-06	3.31E-05	RAB18,ADGRE5,ACTR2,TOM1,ROCK1,RAB5B,PSMD12,PSMA2,MAPK1,MMP9,HSPA1B,ANXA2,CD55
cellular response to hypoxia	GO:0071456	12	309	128	61686	18.7154126	2.85E-12	4.06E-10	SIRT1,CCNB1,CCNA2,VEGFA,BCL2,PTGS2,IRAK1,GNB1,AKT1,E2F1,RTN4,B3GAT1
immune system process	GO:0002376	12	309	541	61686	4.42804587	2.23E-05	0.0003923	CADM1,TNFRSF17,PIK3CG,OAS2,TRIM23,IRAK1,GATA3,C6orf106,CD55,LGR4,IRAK4,CR2
ion transport	GO:0006811	12	309	587	61686	4.08104398	4.90E-05	0.0007071	SLC39A6,CHRNA5,CFTR,ATP6V0E1,VDAC2,KCNJ9,KCNJ1,GRIN2B,SFXN2,SLC41A2,SLC10A7,SLC38A2
cell-cell adhesion	GO:0098609	11	309	164	61686	13.3898887	8.68E-10	7.79E-08	CDH3,VCAM1,BCL2,LRP6,ANXA2,FAT3,TLN2,EGFR,TMEM47,VMP1,FAT4
heart development	GO:0007507	11	309	234	61686	9.38436644	3.53E-08	2.14E-06	CDKN1A,PDLIM7,CASP7,TEK,SOX4,RAF1,MAPK1,MEF2A,SMAD2,CRKL,ADM
Ras protein signal transduction	GO:0007265	10	309	72	61686	27.7265372	3.50E-12	4.72E-10	CDKN1A,PLK2,CCNA2,USP8,RB1,KRAS,GNB1,FGF2,DNMT1,CRKL
in utero embryonic development	GO:0001701	10	309	202	61686	9.88272614	9.16E-08	4.73E-06	CCNB1,VEGFA,NBN,SMAD2,LIG4,APBA1,GATA3,WNT3A,FKBP10,ETNK2
axon guidance	GO:0007411	10	309	224	61686	8.91210125	2.39E-07	1.12E-05	CHL1,PDLIM7,CXCR4,BDNF,CXCL12,MAPK1,PIK3R1,GATA3,WNT3A,EPHA4
protein deubiquitination	GO:0016579	10	309	236	61686	8.45894356	3.87E-07	1.54E-05	OTUD3,CFTR,CCNA2,USP8,PSMD12,PSMA2,NFKBIA,SMAD2,GATA3,RNF128
extracellular matrix organization	GO:0030198	10	309	245	61686	8.14820686	5.44E-07	1.94E-05	VCAM1,THBS1,MMP13,MMP9,MMP7,LOXL1,OLFML2A,FGF2,ADAMTSL1,WNT3A
response to drug	GO:0042493	10	309	278	61686	7.18097367	1.70E-06	4.92E-05	CDKN1A,CDH3,CCNB1,THBS1,BCL2,PFAS,MAP1B,IGFBP2,GATA3,CYP2E1
positive regulation of GTPase activity	GO:0043547	10	309	303	61686	6.58848409	3.66E-06	9.24E-05	RACK1,ARHGAP32,EVI5,BNIP2,RGS3,RASA1,EZH2,ECT2,DOCK10,HACD3
regulation of gene expression	GO:0010468	10	309	313	61686	6.37798939	4.87E-06	0.0001146	ZNF711,SOX2,BCL2,MAPK1,NFKBIA,APBA1,HOXA9,UBXN2A,EZH2,CRKL
positive regulation of apoptotic process	GO:0043065	10	309	370	61686	5.39543427	2.07E-05	0.0003687	SIRT1,RACK1,SOX4,MMP9,FOXO3,FOXO1,AKT1,ECT2,E2F1,ADM
cell division	GO:00051301	10	309	385	61686	5.18522254	2.90E-05	0.0004559	STAG1,CCNB1,CCNA2,CCNE2,EVI5,SPAST,RB1,LIG4,ARF6,ECT2
protein ubiquitination	GO:00165	10	309	503	61686	3.96880851	0.00025	0.00254	SIRT1,RACK1,ELOC,TRIM23,AKT1,DCAF17,RNF128,GID4,TRIM36,UBE2W

	67						79	13	
innate immune response	GO:0045087	10	309	505	61686	3.95309045	0.0002661	0.0025802	PIK3CG,OAS2,TRIM23,IRAK1,GATA3,C6orf106,CD55,LGR4,IRAK4,CR2
lipid metabolic process	GO:0006629	10	309	578	61686	3.45382471	0.0007561	0.0055368	PLA2G4C,PTGS2,PLAGL2,LDLR,ACSL4,CYP2E1,ETNK2,HACD3,CRKL,CRK
platelet activation	GO:0030168	9	309	107	61686	16.7913982	4.12E-09	3.33E-07	MERTK,FZD6,RAF1,MAPK1,PLSCR1,PIK3R1,PIK3CG,GNB1,WNT3A
positive regulation of canonical Wnt signaling pathway	GO:0090263	9	309	144	61686	12.4769417	5.56E-08	3.21E-06	CDH3,USP8,SOX4,PSMD12,PSMA2,WNT3A,EGFR,PRDM15,LGR4
regulation of cell cycle	GO:0051726	9	309	149	61686	12.0582524	7.46E-08	4.21E-06	CDKN1A,RACK1,CCNB1,CCNE2,BCL2,RB1,E2F1,TRIM36,YY1AP1
response to hypoxia	GO:0001666	9	309	170	61686	10.5687036	2.30E-07	1.09E-05	CXCR4,VEGFA,VCAM1,THBS1,TEK,SLC2A1,CXCL12,RAF1,ADM
cell migration	GO:0016477	9	309	248	61686	7.24467585	5.25E-06	0.0001223	NCKAP1,MERTK,ADAM9,PIP5K1A,CXCR4,THBS1,PIK3CG,HBEGF,RHOU
DNA repair	GO:0006281	9	309	380	61686	4.72810424	0.0001451	0.0017152	ASF1A,SMCHD1,NBN,LIG4,GTF2H1,EYA4,PARP10,UBE2W,POLK
inflammatory response	GO:0006954	9	309	402	61686	4.46935227	0.00022	0.0023088	TUSC2,ADGRE5,PLA2G4C,CXCR4,THBS1,PTGS2,PIK3CG,AKT1,ADM
spermatogenesis	GO:0007283	9	309	413	61686	4.35031383	0.0002681	0.0025896	CADM1,SIRT1,MERTK,CCNB1,HOXA9,E2F1,PARP11,LGR4,CRKL
proteolysis	GO:0006508	9	309	509	61686	3.52982242	0.0011823	0.0076223	OTUD3,USP8,CASP7,ADAM9,MMP13,MMP9,MMP7,ADAMTSL1,PRSS22
positive regulation of endothelial cell migration	GO:0010595	8	309	66	61686	24.1977052	1.62E-09	1.40E-07	VEGFA,THBS1,TEK,PIK3CG,GATA3,FUT1,FGF2,AKT1
insulin receptor signaling pathway	GO:0008286	8	309	79	61686	20.2158044	6.94E-09	5.26E-07	ATP6V0E1,PIK3R3,PIK3R2,PIK3R1,IRS1,FOXO1,AKT2,AKT1
cellular response to tumor necrosis factor	GO:00071356	8	309	139	61686	11.4895579	5.77E-07	2.00E-05	SIRT1,VCAM1,THBS1,MAPK1,NFKBIA,OCLN,GATA3,AKT1
positive regulation of angiogenesis	GO:0045766	8	309	151	61686	10.5764804	1.08E-06	3.28E-05	SIRT1,VEGFA,THBS1,TEK,FGF2,RTN4,ADM,AGO2
aging	GO:0007568	8	309	167	61686	9.56316493	2.30E-06	6.27E-05	CASP7,VCAM1,MAPK1,MMP7,IRAK1,IGFBP2,AKT1,ADM
cell surface receptor signaling pathway	GO:00071	8	309	251	61686	6.3627432	4.42E-	0.00066	TSPAN12,MERTK,ADGRE5,FZD6,MAPK1,LIFR,ADGRF4,EGFR

	66						05	94	
angiogenesis	GO:0001525	8	309	252	61686	6.33749422	4.54E-05	0.0006798	TSPAN12,SIRT1,VEGFA,TEK,PIK3CG,ANXA2,FGF2,EGFL7
intracellular protein transport	GO:0006886	8	309	286	61686	5.58408582	0.0001095	0.0013616	TBC1D9,RAB18,TOM1,EVI5,RAB5B,ARF6,TRIM23,APBA1
positive regulation of glucose import	GO:0046326	7	309	38	61686	36.7741441	8.17E-10	7.62E-08	PIK3R1,OCLN,MEF2A,IRS1,AKT2,AKT1,OSBPL8
activation of MAPKK activity	GO:0000186	7	309	46	61686	30.3786408	3.35E-09	2.80E-07	ADAM9,RAF1,MAPK1,MAP3K3,EGFR,CRKL,CRK
mitotic cytokinesis	GO:0000281	7	309	51	61686	27.4003427	7.09E-09	5.21E-07	USP8,SPAST,ROCK1,RASA1,STMN1,ECT2,TRIM36
positive regulation of MAP kinase activity	GO:0043406	7	309	57	61686	24.5160961	1.58E-08	1.09E-06	VEGFA,PIK3CG,KRAS,IRAK1,FGF2,EZH2,EGFR
cellular response to growth factor stimulus	GO:0071363	7	309	63	61686	22.1812298	3.22E-08	2.00E-06	TWF2,RACK1,ACVR2B,THBS1,MAP1B,AKT1,EGFR
positive regulation of endothelial cell proliferation	GO:0001938	7	309	71	61686	19.6819363	7.47E-08	4.12E-06	SIRT1,VEGFA,TEK,CXCL12,FGF2,AKT1,EGFL7
response to insulin	GO:0032868	7	309	73	61686	19.1427051	9.08E-08	4.78E-06	SIRT1,SLC2A1,IRS1,IGFBP2,GCNT1,FOXO1,ADM
phosphatidylinositol biosynthetic process	GO:0006661	7	309	77	61686	18.1482789	1.32E-07	6.52E-06	PIK3R3,PIP5K1A,PIK3R2,PIK3R1,PIK3CG,IMPA1,FGF2
cell chemotaxis	GO:0060326	7	309	80	61686	17.4677184	1.72E-07	8.33E-06	PIP5K1A,CXCR4,VCAM1,CXCL12,HBEGF,CRKL,CRK
ephrin receptor signaling pathway	GO:0048013	7	309	84	61686	16.6359223	2.41E-07	1.10E-05	ACTR2,ROCK1,RASA1,MMP9,GRIN2B,EPHA4,CRK
regulation of protein stability	GO:0031647	7	309	86	61686	16.2490404	2.83E-07	1.20E-05	USP8,SOX4,BCL2,MAPK1,KRAS,RNF128,GNL3L
positive regulation of peptidyl-serine phosphorylation	GO:0033138	7	309	88	61686	15.879744	3.32E-07	1.34E-05	VEGFA,BDNF,BCL2,RAF1,AKT1,WNT3A,EGFR
viral entry into host cell	GO:0046718	7	309	91	61686	15.356236	4.18E-07	1.63E-05	PLSCR1,LDLR,RPSA,HSPA1B,EGFR,CD55,CR2
activation of GTPase activity	GO:0090630	7	309	95	61686	14.7096576	5.60E-07	1.97E-05	TBC1D9,PIP5K1A,EVI5,AKT2,ECT2,CRKL,CRK
regulation of cell migration	GO:00303	7	309	101	61686	13.8358166	8.50E-	2.79E-	ROCK1,FGF2,AKT2,AKT1,RTN4,DOCK10,FGF22

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wound healing	GO:0042060	7	309	101	61686	13.8358166	8.50E-07	2.79E-05	CDKN1A,CDH3,RAF1,SMAD2,FGF2,EGFR,FKBP10
negative regulation of cell growth	GO:0030308	7	309	126	61686	11.0906149	3.75E-06	9.37E-05	SIRT1,CDKN1A,RACK1,BCL2,RB1,HSPA1B,RTN4
activation of MAPK activity	GO:0000187	7	309	129	61686	10.8326936	4.38E-06	0.0001052	CXCR4,THBS1,MAPK1,IRAK1,ALK,FGF2,CRKL
leukocyte migration	GO:0050900	7	309	141	61686	9.91076224	7.88E-06	0.0001768	MERTK,SLC7A5,TEK,ROCK1,PIK3R2,PIK3R1,MMP9
cell population proliferation	GO:0008283	7	309	144	61686	9.70428803	9.04E-06	0.0001922	BCL2,NBN,LIG4,GNB1,AKT1,WNT3A,YY1AP1
rhythmic process	GO:0048511	7	309	148	61686	9.44200997	1.08E-05	0.0002202	SIRT1,CRTC1,RACK1,NR1D2,KDM5C,EZH2,LGR4
regulation of translation	GO:0006417	7	309	152	61686	9.19353602	1.29E-05	0.0002493	RACK1,FXR1,FOXO3,AKT2,AKT1,TNRC6C,AGO2
animal organ morphogenesis	GO:0009887	7	309	163	61686	8.57311335	2.02E-05	0.0003627	BCL2,MAPK1,LFNG,FGF2,GMNN,CRKL,FGF22
T cell receptor signaling pathway	GO:0050852	7	309	165	61686	8.46919682	2.19E-05	0.0003866	PSMD12,PSMA2,MAPK1,PIK3R2,PIK3R1,GATA3,CRKL
protein autophosphorylation	GO:0046777	7	309	172	61686	8.12452021	2.85E-05	0.0004548	TEK,MAP3K3,IRAK1,ALK,AKT1,EPHA4,EGFR
response to lipopolysaccharide	GO:0032496	7	309	172	61686	8.12452021	2.85E-05	0.0004548	VCAM1,TFPI,MAPK1,NFKBIA,LOXL1,IRAK1,ADM
protein stabilization	GO:0050821	7	309	194	61686	7.20318286	6.12E-05	0.0008475	OTUD3,CDKN1A,SOX4,PIK3R1,HSPA1B,EPHA4,RTN4
endocytosis	GO:0006897	7	309	228	61686	6.12902402	0.0001668	0.0018715	TOM1,RAB5B,PIK3CG,ARR3,LRP6,LDLR,RHOU
translation	GO:0006412	7	309	233	61686	5.9974999	0.0001904	0.000207	RPS5,RPL7,RPSA,AKT1,EIF2S3,EGFR,AGO2
regulation of apoptotic process	GO:0042981	7	309	240	61686	5.82257282	0.0002208	0.00023623	SIRT1,BCL2,RAF1,KPNA1,ALK,AKT1,RTN4
protein phosphotransferase activity	GO:0018215	7	309	287	61686	4.86905044	0.0006634	0.00050411	OTUD3,YKT6,USP8,LOXL1,GCNT1,EOGT,ZDHHC2
immune response	GO:00069	7	309	377	61686	3.70667765	0.000312	0.000613	ADGRE5,CD164,CXCR4,THBS1,CXCL12,KIR3DL1,CR2

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phosphatidylinositol 3-kinase signaling	GO:0014065	6	309	37	61686	32.3726056	3.07E-08	1.96E-06	PIK3R2,PIK3R1,PIK3CG,IRS1,GATA3,AKT1
phosphatidylinositol phosphorylation	GO:0046854	6	309	52	61686	23.034354	2.52E-07	1.13E-05	PIK3R3,PIP5K1A,PIK3R2,PIK3R1,PIK3CG,IMPA1
somatic stem cell population maintenance	GO:0035019	6	309	58	61686	20.6514898	4.89E-07	1.82E-05	SOX4,SOX2,RAF1,SMAD2,LIG4,FGF2
positive regulation of smooth muscle cell proliferation	GO:0048661	6	309	59	61686	20.3014645	5.42E-07	1.96E-05	THBS1,IRAK1,AKT1,EGFR,HBEGF,IRAK4
response to mechanical stimulus	GO:0009612	6	309	61	61686	19.6358428	6.63E-07	2.26E-05	CCNB1,GDF5,THBS1,CXCL12,MAP1B,IGFBP2
response to glucocorticoid	GO:0051384	6	309	64	61686	18.7154126	8.84E-07	2.82E-05	CDKN1A,ADAM9,BCL2,KRAS,IGFBP2,ADM
post-embryonic development	GO:0009791	6	309	64	61686	18.7154126	8.84E-07	2.82E-05	BCL2,PLAGL2,SMAD2,GATA3,ETNK2,AGO2
vascular endothelial growth factor receptor signaling pathway	GO:0048010	6	309	65	61686	18.4274832	9.70E-07	3.05E-05	NCKAP1,VEGFA,ROCK1,PIK3R2,PIK3R1,CRK
cell fate commitment	GO:0045165	6	309	67	61686	17.8774091	1.16E-06	3.43E-05	SOX5,SOX2,SMAD2,GATA3,WNT3A,SOX6
cerebral cortex development	GO:0021987	6	309	72	61686	16.6359223	1.78E-06	5.02E-05	SLC2A1,LRP6,FAT4,SLC38A2,CRKL,CRK
positive regulation of kinase activity	GO:0033674	6	309	72	61686	16.6359223	1.78E-06	5.02E-05	MERTK,TEK,NBN,ALK,EPHA4,EGFR
protein import into nucleus	GO:0006606	6	309	75	61686	15.9704854	2.27E-06	6.24E-05	CDKN1A,NUP50,PIK3R1,NFKBIA,KPNA1,AKT1
fibroblast growth factor receptor signaling pathway	GO:0008543	6	309	78	61686	15.356236	2.86E-06	7.52E-05	MAPK1,SPRED1,FGF2,FAT4,CRKL,FGF22
cell morphogenesis	GO:0000902	6	309	78	61686	15.356236	2.86E-06	7.52E-05	NCKAP1,FRY,BCL2,GJE1,GATA3,ECT2
Fc-gamma receptor signaling pathway involved in phagocytosis	GO:0038096	6	309	80	61686	14.9723301	3.31E-06	8.45E-05	NCKAP1,ACTR2,MAPK1,PIK3R2,PIK3R1,CRK
positive regulation of cell growth	GO:0030307	6	309	83	61686	14.4311615	4.11E-06	0.00016	BCL2,ACSL4,AKT1,EGFR,HBEGF,CRK

female pregnancy	GO:0007565	6	309	84	61686	14.259362	4.41E-06	0.0001047	SLC2A1,BCL2,KRAS,IGFBP2,SLC38A2,ADM
positive regulation of phosphatidylinositol 3-kinase signaling	GO:0014068	6	309	92	61686	13.0194175	7.47E-06	0.0001693	SIRT1,VEGFA,TEK,PIK3R1,PIK3CG,FGF2
interleukin-1-mediated signaling pathway	GO:0070498	6	309	94	61686	12.7424086	8.46E-06	0.0001848	PSMD12,PSMA2,NFKBIA,MAP3K3,IRAK1,IRAK4
G1/S transition of mitotic cell cycle	GO:000082	6	309	95	61686	12.608278	9.00E-06	0.000193	CDKN1A,PLK2,CCNE2,RB1,E2F1,GMNN
response to estradiol	GO:0032355	6	309	99	61686	12.0988526	1.14E-05	0.0002285	CCNA2,TFPI,MAP1B,IGFBP2,EZH2,EGFR
neuron migration	GO:0001764	6	309	100	61686	11.9778641	1.21E-05	0.0002381	CXCR4,CXCL12,MAP1B,GATA3,CRKL,CRK
muscle organ development	GO:0007517	6	309	100	61686	11.9778641	1.21E-05	0.0002381	SIRT1,CD164,FXR1,MEF2A,HBEGF,SOX6
cellular response to insulin stimulus	GO:0032869	6	309	101	61686	11.8592714	1.28E-05	0.0002501	PIK3R2,PIK3R1,IRS1,FOXO1,AKT2,AKT1
osteoblast differentiation	GO:0001649	6	309	104	61686	11.517177	1.51E-05	0.0002864	ASF1A,SOX2,AKT1,WNT3A,LGR4,RBMX
anterior/posterior pattern specification	GO:0009952	6	309	105	61686	11.4074896	1.60E-05	0.0002956	ACVR2B,SMAD2,HOXC4,HOXA9,WNT3A,CRKL
stimulatory C-type lectin receptor signaling pathway	GO:0002223	6	309	105	61686	11.4074896	1.60E-05	0.0002956	RAF1,PSMD12,PSMA2,KRAS,MUC17,MUC13
response to virus	GO:0009615	6	309	115	61686	10.415534	2.68E-05	0.0004358	CXCR4,CXCL12,PSMA2,OAS2,STMN1,GATA3
peptidyl-tyrosine phosphorylation	GO:00018108	6	309	126	61686	9.50624133	4.48E-05	0.0006742	MERTK,TEK,TWF1,ALK,EPHA4,EGFR
transmembrane receptor protein tyrosine kinase signaling pathway	GO:0007169	6	309	127	61686	9.43138904	4.68E-05	0.0006917	MERTK,TEK,BDNF,ALK,EPHA4,EGFR
protein-containing complex assembly	GO:0006503	6	309	127	61686	9.43138904	4.68E-05	0.0006917	CCNB1,ZNF148,SLC2A1,OCLN,APBA1,GMNN
anatomical structure morphogenesis	GO:0009653	6	309	129	61686	9.28516595	5.11E-05	0.0007325	SOX4,SOX2,SMAD2,GATA3,EYA4,FBN3
neuron projection	GO:0000000	6	309	130	61686	9.21374	5.33E-05	0.0000000	CAMSAP2,FRY,CNTNAP1,ROCK1,RB1,STMN1

development	031175					16	E-05	07602	
negative regulation of neuron apoptotic process	GO:0043524	6	309	133	61686	9.00591284	6.05E-05	0.0008434	GDF5,BDNF,BCL2,RASA1,LIG4,KRAS
regulation of cell shape	GO:0008360	6	309	143	61686	8.37612873	9.04E-05	0.0011598	VEGFA,RASA1,SYNE3,RHOU,BRWD1,CRK
transcription initiation from RNA polymerase II promoter	GO:0006367	6	309	154	61686	7.77783382	0.0001358	0.0016294	CDKN1A,NR1D2,CCNB1,TAF15,PGR,GTF2H1
positive regulation of cytosolic calcium ion concentration	GO:0007204	6	309	155	61686	7.72765424	0.0001407	0.0016714	CXCR4,PIK3CG,LRP6,GNB1,CD55,ADM
chemotaxis	GO:0006935	6	309	155	61686	7.72765424	0.0001407	0.0016714	CXCR4,CXCL12,MAPK1,PIK3CG,FGF2,CMTM3
peptidyl-serine phosphorylation	GO:0018105	6	309	162	61686	7.39374326	0.0001788	0.0019616	PLK2,BCL2,ROCK1,MAPK1,AKT2,AKT1
proteasome-mediated ubiquitin-dependent protein catabolic process	GO:0043161	6	309	174	61686	6.88382993	0.0002629	0.0025801	SIRT1,PSMD12,PSMA2,UBXN2A,GID4,UBE2W
negative regulation of canonical Wnt signaling pathway	GO:0090090	6	309	177	61686	6.76715485	0.0002881	0.0027388	FZD6,SOX2,PSMD12,PSMA2,LRP6,IGFBP2
positive regulation of I-kappaB kinase/NF-kappaB signaling	GO:0043123	6	309	183	61686	6.54528092	0.0003442	0.0031486	PLK2,TSPAN6,MAP3K3,IRAK1,ECT2,IRAK4
positive regulation of ERK1 and ERK2 cascade	GO:0070374	6	309	216	61686	5.54530744	0.000822	0.0059656	VEGFA,TEK,BMPER,FGF2,EGFR,CRKL
cell-cell signaling	GO:0007267	6	309	231	61686	5.18522254	0.001161	0.0075044	MERTK,ADGRE5,GDF5,TEK,PGR,GJE1
protein polyubiquitination	GO:0000209	6	309	248	61686	4.8297839	0.0016644	0.0100613	FBXO28,BCL2,PSMD12,PSMA2,TRIM36,UBE2W
brain development	GO:0007420	6	309	253	61686	4.73433363	0.0018401	0.0108523	RAB18,CXCR4,CXCL12,STMN1,GRIN2B,ALK
post-translational protein modification	GO:0043687	6	309	304	61686	3.94008687	0.0045335	0.0212968	CALU,ELOC,PSMD12,PSMA2,DCAF17,KLHL11
biological_process	GO:0008150	6	309	318	61686	3.76662392	0.0056199	0.0218661	PLPBP,CALU,DEPDC7,TMEM47,GSTCD,ETNK2
cellular glucose	GO:0	5	309	22	61686	45.3706	7.50	4.04	SIRT1,RAF1,PIK3R2,PIK3R1,FOXO1

homeostasis	001678					973	E-08	E-06	
positive regulation of sprouting angiogenesis	GO:1903672	5	309	28	61686	35.648405	2.73E-07	1.20E-05	VEGFA,S100A1,FUT1,BMPER,FGF2
positive regulation of lamellipodium assembly	GO:0010592	5	309	29	61686	34.4191496	3.29E-07	1.35E-05	TWF2,NCKAP1,ACTR2,PIK3R1,OCLN
regulation of cell motility	GO:2000145	5	309	31	61686	32.1985593	4.66E-07	1.77E-05	ROCK1,RAF1,EGFR,HBEGF,CRK
positive regulation of cell migration involved in sprouting angiogenesis	GO:0090050	5	309	34	61686	29.35751	7.54E-07	2.54E-05	PLK2,VEGFA,PTGS2,MAP3K3,FGF2
cellular response to nerve growth factor stimulus	GO:1990090	5	309	36	61686	27.7265372	1.01E-06	3.15E-05	USP8,ARF6,AKT1,E2F1,CRK
negative regulation of Notch signaling pathway	GO:0045746	5	309	39	61686	25.5937267	1.53E-06	4.47E-05	NFKBIA,AKT1,EGFR,CHAC1,EGFL7
thymus development	GO:0048538	5	309	45	61686	22.1812298	3.17E-06	8.16E-05	BCL2,RAF1,MAPK1,GATA3,CRKL
positive regulation of fibroblast proliferation	GO:0048146	5	309	45	61686	22.1812298	3.17E-06	8.16E-05	CDKN1A,CCNB1,CCNA2,LIG4,E2F1
positive regulation of blood vessel endothelial cell migration	GO:0043536	5	309	51	61686	19.5716733	5.94E-06	0.0001371	SIRT1,VEGFA,THBS1,FGF2,AKT1
negative regulation of fat cell differentiation	GO:0045599	5	309	52	61686	19.195295	6.54E-06	0.0001496	SIRT1,GATA3,FOXO1,WNT3A,E2F1
phosphatidylinositol-mediated signaling	GO:0048015	5	309	54	61686	18.4843581	7.90E-06	0.0001756	NCS1,PIK3R2,PIK3R1,PIK3CG,IRS1
regulation of cyclin-dependent protein serine/threonine kinase activity	GO:0000079	5	309	55	61686	18.1482789	8.65E-06	0.0001872	CDKN1A,CCNB1,CCNA2,CCNE2,GTF2H1
positive regulation of protein localization to plasma membrane	GO:1903078	5	309	57	61686	17.5114972	1.03E-05	0.0002122	PIK3R1,ARF6,AKT1,WNT3A,EGFR
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	GO:0006977	5	309	58	61686	17.2095748	1.13E-05	0.0002274	CDKN1A,PLK2,CCNB1,SOX4,E2F1

hippocampus development	GO:0021766	5	309	64	61686	15.5961772	1.83E-05	0.0003356	ALK,EZH2,WNT3A,CRKL,CRK
SRP-dependent cotranslational protein targeting to membrane	GO:0006614	5	309	67	61686	14.8978409	2.29E-05	0.0003959	SSR3,RPS5,RPL7,RPSA,SEC61A1
B cell differentiation	GO:0030183	5	309	70	61686	14.259362	2.83E-05	0.0004575	VCAM1,BCL2,PIK3R1,EZH2,CR2
negative regulation of protein binding	GO:0032091	5	309	73	61686	13.6733608	3.47E-05	0.0005392	CDKN1A,RACK1,ROCK1,AKT1,GNL3L
cellular response to mechanical stimulus	GO:0071260	5	309	75	61686	13.3087379	3.96E-05	0.000603	SLC2A1,MMP7,AKT1,EGFR,SLC38A2
negative regulation of transforming growth factor beta receptor signaling pathway	GO:0030512	5	309	86	61686	11.6064574	7.63E-05	0.0009944	SIRT1,SPRY1,SMAD2,HSPA1B,SPRED1
response to toxic substance	GO:0009636	5	309	88	61686	11.3426743	8.51E-05	0.0010977	CDKN1A,CCNB1,KDM5C,BCL2,MAPK1
positive regulation of neuron differentiation	GO:0045666	5	309	91	61686	10.96874	9.98E-05	0.001267	GDF5,TCF4,CXCL12,MAP1B,ECT2
axonogenesis	GO:0007409	5	309	92	61686	10.8495146	0.0001051	0.0013138	SPAST,BCL2,MAP1B,STMN1,WNT3A
transcription, DNA-templated	GO:0006351	5	309	105	61686	9.50624133	0.0001958	0.0021189	PLAGL2,MEF2A,HOXA9,GTF2H1,E2F1
regulation of mRNA stability	GO:0043488	5	309	112	61686	8.91210125	0.0002644	0.0025739	FXR1,PSMD12,PSMA2,HSPA1B,AKT1
small GTPase mediated signal transduction	GO:0007264	5	309	113	61686	8.8332331	0.0002755	0.0026397	RAB18,ARHGAP32,RHOA,DOCK10,HACD3
Fc-epsilon receptor signaling pathway	GO:0038095	5	309	114	61686	8.75574859	0.000287	0.0027388	PSMD12,PSMA2,MAPK1,PIK3R2,PIK3R1
response to ethanol	GO:0045471	5	309	117	61686	8.53124222	0.0003236	0.0030051	ACTR2,VCAM1,GRIN2B,GATA3,CYP2E1
translational initiation	GO:0006413	5	309	117	61686	8.53124222	0.0003236	0.0030051	RPS5,RPL7,RPSA,EIF2S3,AGO2
response to oxidative stress	GO:0006979	5	309	119	61686	8.38786	0.0003498	0.0031761	SIRT1,BCL2,PTGS2,AKT1,EGFR

positive regulation of MAPK cascade	GO:0043410	5	309	121	61686	8.24921768	0.0003777	0.0032816	VEGFA,TEK,SOX2,ROCK1,FGF2
tumor necrosis factor-mediated signaling pathway	GO:0033209	5	309	121	61686	8.24921768	0.0003777	0.0032816	TNFRSF17,PSMD12,PSMA2,NFKBIA,FOXO3
negative regulation of angiogenesis	GO:0016525	5	309	122	61686	8.18160115	0.0003923	0.0033837	PLK2,THBS1,TEK,ROCK1,SPRED1
regulation of small GTPase mediated signal transduction	GO:0051056	5	309	127	61686	7.85949086	0.0004714	0.0039269	ARHGAP32,PIK3R2,DEPDC7,ECT2,RHOU
negative regulation of endopeptidase activity	GO:0010951	5	309	128	61686	7.79808859	0.0004886	0.0040422	TFPI,ROCK1,ANXA2,CST9L,AKT1
kidney development	GO:0001822	5	309	131	61686	7.61950641	0.000543	0.0043151	VEGFA,BCL2,GATA3,FAT4,CYP26A1
cell cycle arrest	GO:0007050	5	309	132	61686	7.56178288	0.000562	0.004409	CDKN1A,THBS1,SOX2,RB1,NBN
membrane organization	GO:0061024	5	309	136	61686	7.3393775	0.0006435	0.0049361	CFTR,ACTR2,LDLR,EGFR,HBEGF
protein localization to plasma membrane	GO:007259	5	309	145	61686	6.88382993	0.0008587	0.0061223	PIP5K1A,ROCK1,LRP6,AKT2,ZDHHC2
cytoskeleton organization	GO:0007010	5	309	151	61686	6.61030026	0.0010294	0.0069698	CNTNAP1,SYNE3,TLN2,RHOU,BRWD1
actin cytoskeleton organization	GO:0030036	5	309	171	61686	5.83716573	0.0017823	0.0106147	ACTR2,PDLIM7,ROCK1,KRAS,CRK
transcription by RNA polymerase II	GO:0006366	5	309	176	61686	5.67133716	0.0020208	0.0116352	TAF15,ELOC,SOX5,GTF2H1,RBMX
Wnt signaling pathway	GO:0016055	5	309	226	61686	4.41661655	0.0058436	0.0225917	TSPAN12,FZD6,LRP6,WNT3A,LGR4
chemical synaptic transmission	GO:0007268	5	309	228	61686	4.3778743	0.0060604	0.0231346	CHRNA5,MAPK1,LRP6,APBA1,GRIN2B
carbohydrate metabolic process	GO:0005975	5	309	230	61686	4.33980583	0.0062828	0.0237591	GK,FUT1,AKT2,AKT1,B3GAT1
ion transmembrane transport	GO:0034220	5	309	237	61686	4.21162591	0.0071063	0.0261789	CHRNA5,ATP6V0E1,RAF1,KCNJ1,SFXN2
peripheral nervous system myelin maintenance	GO:0032287	4	309	8	61686	99.815534	4.25E-08	2.52E-06	AKT2,AKT1,SH3TC2,PRX

positive regulation of glucose metabolic process	GO:0010907	4	309	10	61686	79.8524272	1.27E-07	6.40E-06	IRS1,AKT2,AKT1,SLC45A3
positive regulation of keratinocyte migration	GO:0051549	4	309	12	61686	66.5436893	2.96E-07	1.24E-05	ADAM9,MMP9,ARF6,HBEGF
striated muscle cell differentiation	GO:0051146	4	309	18	61686	44.3624595	1.79E-06	4.98E-05	CASP7,RB1,KRAS,AKT1
cell migration involved in sprouting angiogenesis	GO:0002042	4	309	20	61686	39.9262136	2.81E-06	7.56E-05	PIK3R3,VEGFA,FGF2,AKT1
developmental growth	GO:0048589	4	309	26	61686	30.712472	8.46E-06	0.0001865	BCL2,SMAD2,GATA3,ADM
negative regulation of intrinsic apoptotic signaling pathway	GO:2001243	4	309	27	61686	29.574973	9.90E-06	0.000205	VDAC2,BCL2,MMP9,AKT1
digestive tract development	GO:0048565	4	309	30	61686	26.6174757	1.53E-05	0.0002869	CCNB1,RB1,FAT4,LGR4
positive regulation of DNA repair	GO:0045739	4	309	32	61686	24.9538835	1.99E-05	0.0003596	SIRT1,SMCHD1,EYA4,EGFR
response to nicotine	GO:0035094	4	309	32	61686	24.9538835	1.99E-05	0.0003596	CHRNA5,VCAM1,BCL2,MAPK1
cellular response to cadmium ion	GO:0071276	4	309	33	61686	24.1977052	2.25E-05	0.0003929	MAPK1,MMP9,AKT1,EGFR
negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	GO:2001240	4	309	34	61686	23.486008	2.54E-05	0.0004194	BCL2,HSPA1B,AKT1,EYA4
lipopolysaccharide-mediated signaling pathway	GO:0031663	4	309	34	61686	23.486008	2.54E-05	0.0004194	MAPK1,NFKBIA,IRAK1,AKT1
T cell differentiation	GO:0030217	4	309	34	61686	23.486008	2.54E-05	0.0004194	SOX4,BCL2,LFNG,GATA3
cellular response to ionizing radiation	GO:0071479	4	309	34	61686	23.486008	2.54E-05	0.0004194	SIRT1,CDKN1A,LIG4,ECT2
energy homeostasis	GO:0097009	4	309	35	61686	22.8149792	2.86E-05	0.0004532	CRTC1,NR1D2,ALK,FOXO1
Wnt signaling pathway, calcium modulating pathway	GO:0007223	4	309	37	61686	21.5817371	3.58E-05	0.0005492	FZD6,GNB1,TNRC6C,AGO2
ureteric bud	GO:0000000	4	309	37	61686	21.5817371	3.58E-05	0.0005492	SPRY1,BCL2,SMAD2,BMPER

development	001657					371	E-05	05492	
regulation of neuron projection development	GO:0010975	4	309	40	61686	19.9631068	4.90E-05	0.0007105	NCS1,ARF6,GATA3,AKT1
positive regulation of protein import into nucleus	GO:0042307	4	309	40	61686	19.9631068	4.90E-05	0.0007105	MAPK1,PIK3R2,PIK3R1,ECT2
cellular response to reactive oxygen species	GO:0034614	4	309	40	61686	19.9631068	4.90E-05	0.0007105	MAPK1,MMP9,AKT1,EGFR
neuron apoptotic process	GO:0051402	4	309	41	61686	19.4762018	5.40E-05	0.0007659	CASP7,BCL2,RB1,LIG4
animal organ regeneration	GO:0031100	4	309	43	61686	18.5703319	6.53E-05	0.0008997	CDKN1A,CCNA2,CXCL12,ADM
intrinsic apoptotic signaling pathway in response to DNA damage	GO:0008630	4	309	45	61686	17.7449838	7.82E-05	0.0010143	SIRT1,BCL2,PIK3R1,E2F1
epidermal growth factor receptor signaling pathway	GO:0007173	4	309	48	61686	16.6359223	0.000101	0.0012684	PIK3R1,AKT1,EGFR,HBEGF
heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	GO:0007157	4	309	48	61686	16.6359223	0.000101	0.0012684	CADM1,CD164,VCAM1,FAT4
cellular response to heat	GO:0034605	4	309	49	61686	16.2964137	0.0001095	0.0013546	CDKN1A,THBS1,IRAK1,HSPA1B
response to hydrogen peroxide	GO:0042542	4	309	53	61686	15.0664957	0.000149	0.0017535	SIRT1,ADAM9,BCL2,CRK
negative regulation of protein ubiquitination	GO:0031397	4	309	54	61686	14.7874865	0.0001603	0.0018074	SOX4,HSPA1B,AKT1,GNL3L
blood vessel development	GO:0001568	4	309	55	61686	14.5186231	0.0001722	0.0019236	MAP3K3,BMPER,EGFL7,CRKL
neurogenesis	GO:0022008	4	309	56	61686	14.259362	0.0001847	0.002017	CXCR4,WNT3A,FAT4,CHAC1
response to peptide hormone	GO:0043434	4	309	58	61686	13.7676599	0.0002117	0.0022312	TEK,CXCL12,LRP6,IRS1
negative regulation of G1/S transition of mitotic cell cycle	GO:2000134	4	309	59	61686	13.5343097	0.0002262	0.0023534	CDKN1A,BCL2,RB1,EZH2
cellular response to transforming growth	GO:00715	4	309	59	61686	13.5343097	0.00022	0.00235	SOX5,SOX6,CRKL,CRK

factor beta stimulus	60					62	34		
response to estrogen	GO:0043627	4	309	61	61686	13.0905618	0.0002573	0.0025462	TEK,MAPK1,IGFBP2,GATA3
vasculogenesis	GO:0001570	4	309	61	61686	13.0905618	0.0002573	0.0025462	VEGFA,RASA1,EGFL7,ADM
negative regulation of protein kinase B signaling	GO:0051898	4	309	61	61686	13.0905618	0.0002573	0.0025462	SIRT1,OTUD3,RACK1,AKT1
positive regulation of autophagy	GO:0010508	4	309	62	61686	12.8794237	0.000274	0.0026358	PLK2,ROCK1,FOXO3,FOXO1
negative regulation of neuron death	GO:1901215	4	309	63	61686	12.6749884	0.0002914	0.0027597	SIRT1,KIR3DL2,AKT1,WNT3A
I-kappaB kinase/NF-kappaB signaling	GO:0007249	4	309	64	61686	12.4769417	0.0003097	0.0028981	ROCK1,NFKBIA,AKT1,HACD3
NIK/NF-kappaB signaling	GO:0038061	4	309	65	61686	12.2849888	0.0003287	0.0030293	PSMD12,PSMA2,ALK,AKT1
cellular response to hydrogen peroxide	GO:0070301	4	309	65	61686	12.2849888	0.0003287	0.0030293	SIRT1,FOXO1,EZH2,ECT2
neuron projection morphogenesis	GO:0048812	4	309	66	61686	12.0988526	0.0003485	0.0031759	NCKAP1,CNTNAP1,BDNF,EGFR
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	GO:0043154	4	309	67	61686	11.9182727	0.0003692	0.0033268	VEGFA,THBS1,RAF1,AKT1
peptidyl-threonine phosphorylation	GO:0018107	4	309	67	61686	11.9182727	0.0003692	0.0033268	BCL2,ROCK1,MAPK1,AKT1
regulation of transcription from RNA polymerase II promoter in response to hypoxia	GO:0061418	4	309	68	61686	11.743004	0.0003907	0.0033825	VEGFA,ELOC,PSMD12,PSMA2
regulation of protein localization	GO:0032880	4	309	69	61686	11.5728155	0.0004131	0.0035139	RACK1,USP8,BCL2,AKT1
positive regulation of proteasomal ubiquitin-dependent protein catabolic process	GO:0032436	4	309	72	61686	11.0906149	0.0004859	0.0040337	PLK2,RACK1,HSPA1B,AKT1
cartilage development	GO:00512	4	309	74	61686	10.7908685	0.00053	0.00429	GDF5,SOX5,HOXC4,SOX6

	16						92	94	
regulation of cellular response to heat	GO:1900034	4	309	75	61686	10.6469903	0.0005673	0.0044363	SIRT1,NUP50,MAPK1,HSPA1B
phagocytosis	GO:0006909	4	309	76	61686	10.5068983	0.0005965	0.0046495	TUSC2,MERTK,PIP5K1A,LDLR
positive regulation of translation	GO:0045727	4	309	78	61686	10.2374907	0.000658	0.0050161	FXR1,THBS1,SOX4,MAPK1
negative regulation of protein phosphorylation	GO:0001933	4	309	78	61686	10.2374907	0.000658	0.0050161	CCNB1,OCLN,LRP6,CRKL
negative regulation of DNA-binding transcription factor activity	GO:0043433	4	309	84	61686	9.50624133	0.0008695	0.0061806	SIRT1,FZD6,RB1,EZH2
regulation of GTPase activity	GO:0043087	4	309	85	61686	9.3944032	0.0009088	0.0063124	EVI5,RASA1,EPHA4,CRK
response to organic substance	GO:0010033	4	309	85	61686	9.3944032	0.0009088	0.0063124	CDKN1A,TEK,AKT1,ADM
negative regulation of protein kinase activity	GO:0006469	4	309	86	61686	9.28516595	0.0009494	0.0064648	RB1,LRP6,SPRED1,AKT1
viral transcription	GO:0019083	4	309	86	61686	9.28516595	0.0009494	0.0064648	NUP50,RPS5,RPL7,RPSA
response to endoplasmic reticulum stress	GO:0034976	4	309	87	61686	9.17843991	0.0009913	0.0067309	CFTR,THBS1,PIK3R2,PIK3R1
negative regulation of NF-kappaB transcription factor activity	GO:0032088	4	309	89	61686	8.97218283	0.0010789	0.0072647	SIRT1,NFKBIA,IRAK1,PARP10
lung development	GO:0030324	4	309	93	61686	8.58628249	0.0012702	0.0081024	VEGFA,SMAD2,FGF2,EGFR
protein homooligomerization	GO:0051260	4	309	95	61686	8.40551865	0.0013742	0.0084973	SPAST,KCTD4,ECT2,RBMX
cellular response to oxidative stress	GO:0034599	4	309	101	61686	7.90618091	0.0017216	0.0102785	STAU1,HSPA1B,FOXO3,FOXO1
male gonad development	GO:0008584	4	309	105	61686	7.60499307	0.0019844	0.0114526	BCL2,HOXA9,GATA3,CRKL
ossification	GO:0001503	4	309	106	61686	7.53324785	0.0020542	0.0117714	PDLIM7,BCL2,MMP9,EGFR

transforming growth factor beta receptor signaling pathway	GO:007179	4	309	107	61686	7.46284366	0.0021256	0.0121522	SIRT1,ADAM9,GDF5,SMAD2
homophilic cell adhesion via plasma membrane adhesion molecules	GO:007156	4	309	114	61686	7.00459888	0.0026746	0.0142487	CADM1,CDH3,FAT3,FAT4
negative regulation of inflammatory response	GO:0050728	4	309	124	61686	6.43971187	0.0036167	0.0181883	NR1D2,TEK,RB1,GATA3
regulation of signal transduction by p53 class mediator	GO:1901796	4	309	130	61686	6.1424944	0.0042782	0.0205759	RRS1,TAF15,NBN,AKT1
central nervous system development	GO:0007417	4	309	144	61686	5.54530744	0.0061283	0.0233201	NCKAP1,SLC2A1,LIG4,SOX6
negative regulation of cell migration	GO:0030336	4	309	144	61686	5.54530744	0.0061283	0.0233201	BCL2,ARID2,FOXO3,OSBPL8
regulation of immune response	GO:0050776	4	309	145	61686	5.50706394	0.0062777	0.023777	CD226,VCAM1,KIR3DL2,KIR3DL1
DNA replication	GO:0006260	4	309	152	61686	5.25344916	0.0073923	0.0271912	NBN,NAP1L1,LIG4,POLK
protein dephosphorylation	GO:0006470	4	309	168	61686	4.75312067	0.0104103	0.0307738	BCL2,PTPN7,EYA4,CTDSPL2
neuron differentiation	GO:0030182	4	309	172	61686	4.64258298	0.0112722	0.0326448	RB1,GATA3,ACSL4,WNT3A
positive regulation of NF-kappaB transcription factor activity	GO:0051092	4	309	163	61686	4.89892191	0.0093945	0.0328603	KRAS,IRAK1,HSPA1B,ALK
endoplasmic reticulum to Golgi vesicle-mediated transport	GO:0006888	4	309	180	61686	4.43624595	0.0131307	0.0373138	YKT6,SPAST,CD55,IER3IP1
methylation	GO:0032259	4	309	180	61686	4.43624595	0.0131307	0.0373138	EZH2,DNMT1,PRDM15,SETD5
fatty acid metabolic process	GO:0006631	4	309	188	61686	4.24746953	0.0151737	0.0381151	PTGS2,ACSL4,CYP2E1,HACD3
cellular protein metabolic process	GO:0044267	4	309	199	61686	4.01268478	0.0182941	0.0449745	CALU,IGFBP2,L2HGDH,ZDHHC2
regulation of cell population proliferation	GO:0042127	4	309	201	61686	3.97275757	0.018901	0.0464195	SIRT1,NFKBIA,ALK,EZH2

negative regulation of long-chain fatty acid import across plasma membrane	GO:0010748	3	309	4	61686	149.723301	4.96E-07	1.82E-05	THBS1,AKT2,AKT1
positive regulation of Rac protein signal transduction	GO:0035022	3	309	7	61686	85.556172	4.29E-06	0.000104	PIK3CG,KRAS,RTN4
postsynapse to nucleus signaling pathway	GO:0099527	3	309	7	61686	85.556172	4.29E-06	0.000104	CRTC1,KPNA1,WNT3A
organ growth	GO:0035265	3	309	10	61686	59.8893204	1.46E-05	0.000278	BCL2,SMAD2,GJE1
hepatocyte apoptotic process	GO:0097284	3	309	10	61686	59.8893204	1.46E-05	0.000278	RB1,PIK3CG,ARF6
insulin-like growth factor receptor signaling pathway	GO:0048009	3	309	12	61686	49.907767	2.65E-05	0.000438	PIK3R1,IRS1,AKT1
regulation of cell adhesion mediated by integrin	GO:0033628	3	309	13	61686	46.068708	3.43E-05	0.0005364	PIK3CG,CRKL,CRK
cellular response to nitric oxide	GO:0071732	3	309	15	61686	39.9262136	5.42E-05	0.0007589	CCNA2,FOXO1,CRK
positive regulation of RNA splicing	GO:0033120	3	309	15	61686	39.9262136	5.42E-05	0.0007589	PIK3R1,HSPA1B,SLC38A2
positive regulation of dendrite development	GO:0090006	3	309	16	61686	37.4308252	6.64E-05	0.0008994	CRTC1,ALK,EZH2
positive regulation of glycogen biosynthetic process	GO:0045725	3	309	16	61686	37.4308252	6.64E-05	0.0008994	IRS1,AKT2,AKT1
positive regulation of chondrocyte differentiation	GO:0032332	3	309	16	61686	37.4308252	6.64E-05	0.0008994	GDF5,SOX5,SOX6
negative regulation of phosphorylation	GO:0042326	3	309	18	61686	33.2718447	9.61E-05	0.0012256	SIRT1,CDKN1A,ROCK1
regulation of establishment of cell polarity	GO:0000114	3	309	19	61686	31.5206949	0.0001137	0.0003775	RACK1,ROCK1,GATA3
mitotic cell cycle phase transition	GO:0044772	3	309	19	61686	31.5206949	0.0001137	0.0003775	CCNB1,CCNA2,CCNE2
regulation of dendrite development	GO:0050773	3	309	19	61686	31.5206949	0.0001137	0.0003775	CAMSAP2,CRKL,CRK
regulation of phosphatidylinositol	GO:00435	3	309	19	61686	31.5206949	0.0001137	0.0003775	PIK3R3,PIK3R2,PIK3R1

3-kinase activity	51						37	75	
leukocyte tethering or rolling	GO:0050901	3	309	20	61686	29.9446602	0.0001332	0.0016065	VCAM1,ROCK1,GCNT1
negative regulation of cell-matrix adhesion	GO:0001953	3	309	21	61686	28.518724	0.0001548	0.0017539	THBS1,RASA1,PIK3R1
regulation of phosphatidylinositol 3-kinase signaling	GO:0014066	3	309	21	61686	28.518724	0.0001548	0.0017539	PIP5K1A,MAPK1,EGFR
macrophage differentiation	GO:0030225	3	309	22	61686	27.2224184	0.0001786	0.0019681	SIRT1,VEGFA,MMP9
negative regulation of fibroblast growth factor receptor signaling pathway	GO:0040037	3	309	22	61686	27.2224184	0.0001786	0.0019681	SPRY1,THBS1,FGF2
membrane protein ectodomain proteolysis	GO:0006509	3	309	22	61686	27.2224184	0.0001786	0.0019681	ADAM9,MMP7,RBMX
positive regulation of insulin receptor signaling pathway	GO:0046628	3	309	23	61686	26.038835	0.0002047	0.0021663	SIRT1,IRS1,OSBPL8
protein ADP-ribosylation	GO:0006471	3	309	23	61686	26.038835	0.0002047	0.0021663	SIRT1,ART4,PARP10
positive regulation of long-term synaptic potentiation	GO:00900273	3	309	23	61686	26.038835	0.0002047	0.0021663	CRTC1,STAU1,ZDHHC2
tissue regeneration	GO:0042246	3	309	23	61686	26.038835	0.0002047	0.0021663	CDKN1A,CCNB1,SOX2
positive regulation of nitric-oxide synthase activity	GO:0005100	3	309	23	61686	26.038835	0.0002047	0.0021663	S100A1,KRAS,AKT1
negative regulation of protein serine/threonine kinase activity	GO:00071901	3	309	24	61686	24.9538835	0.000233	0.0023935	RB1,LRP6,AKT1
negative regulation of cellular senescence	GO:0000773	3	309	24	61686	24.9538835	0.000233	0.0023935	SIRT1,PLK2,MAP3K3
positive regulation of focal adhesion assembly	GO:00051894	3	309	25	61686	23.9557282	0.0002638	0.0025787	VEGFA,TEK,ROCK1
endocrine pancreas development	GO:00031018	3	309	26	61686	23.034354	0.0002971	0.0027916	SOX4,FOXO1,AKT1
cellular response to fatty acid	GO:000713	3	309	26	61686	23.034354	0.0002971	0.0027916	CCNB1,IRS1,E2F1

	98					71	16		
response to gamma radiation	GO:0010332	3	309	27	61686	22.1812298	0.000333	0.0030579	BCL2,LIG4,GATA3
cochlea development	GO:0090102	3	309	28	61686	21.389043	0.0003716	0.003252	CCNA2,GATA3,EPHA4
regulation of calcium ion transport	GO:0051924	3	309	29	61686	20.6514898	0.000413	0.0035247	CXCR4,CXCL12,BCL2
cortical actin cytoskeleton organization	GO:0030866	3	309	29	61686	20.6514898	0.000413	0.0035247	NCKAP1,ROCK1,ARF6
negative regulation of MAPK cascade	GO:0043409	3	309	29	61686	20.6514898	0.000413	0.0035247	PIK3R2,SPRED1,PRDM15
negative regulation of apoptotic signaling pathway	GO:2001234	3	309	30	61686	19.9631068	0.0004572	0.0038212	BDNF,BCL2,RB1
midbrain development	GO:0030901	3	309	30	61686	19.9631068	0.0004572	0.0038212	FZD6,LRP6,WNT3A
positive regulation of cardiac muscle cell proliferation	GO:0060045	3	309	30	61686	19.9631068	0.0004572	0.0038212	CCNB1,MAPK1,FGF2
positive regulation of cyclin-dependent protein serine/threonine kinase activity	GO:0045737	3	309	30	61686	19.9631068	0.0004572	0.0038212	CCNB1,AKT1,EGFR
cellular response to dexamethasone stimulus	GO:0071549	3	309	30	61686	19.9631068	0.0004572	0.0038212	USP8,FOXO1,EGFR
positive regulation of phosphorylation	GO:0042327	3	309	31	61686	19.3191356	0.0005043	0.0041156	VEGFA,THBS1,EGFR
ERBB2 signaling pathway	GO:0038128	3	309	31	61686	19.3191356	0.0005043	0.0041156	PIK3R1,EGFR,HBEGF
mammary gland development	GO:0030879	3	309	31	61686	19.3191356	0.0005043	0.0041156	PGR,HOXA9,WNT3A
aortic valve morphogenesis	GO:0003180	3	309	31	61686	19.3191356	0.0005043	0.0041156	ROCK1,RB1,GATA3
regulation of microtubule cytoskeleton organization	GO:0070507	3	309	32	61686	18.7154126	0.0005544	0.004363	ROCK1,WNT3A,TRIM36
regulation of neuron differentiation	GO:00456	3	309	32	61686	18.7154126	0.0005544	0.004363	BDNF,ROCK1,ALK

	64						44	3	
positive regulation of phosphatidylinositol 3-kinase activity	GO:0043552	3	309	32	61686	18.7154126	0.0005544	0.004363	TEK,IRS1,FGF2
microtubule bundle formation	GO:0001578	3	309	33	61686	18.1482789	0.0006076	0.0046753	SPAST,MAP1B,CCSER2
T cell differentiation in thymus	GO:0033077	3	309	33	61686	18.1482789	0.0006076	0.0046753	BCL2,LIG4,GATA3
negative regulation of DNA binding	GO:0043392	3	309	33	61686	18.1482789	0.0006076	0.0046753	NFKBIA,E2F1,C6orf106
positive regulation of neurogenesis	GO:0050769	3	309	33	61686	18.1482789	0.0006076	0.0046753	CXCR4,NAP1L1,LIG4
cell maturation	GO:0048469	3	309	34	61686	17.614506	0.0006639	0.0049977	TUSC2,VEGFA,GATA3
sprouting angiogenesis	GO:0002040	3	309	34	61686	17.614506	0.0006639	0.0049977	VEGFA,THBS1,TEK
cellular response to vascular endothelial growth factor stimulus	GO:0035924	3	309	34	61686	17.614506	0.0006639	0.0049977	VEGFA,VCAM1,AKT1
endosome organization	GO:0007032	3	309	35	61686	17.1112344	0.0007234	0.005314	USP8,RAB5B,HOOK3
negative regulation of cytokine production	GO:0001818	3	309	36	61686	16.6359223	0.0007863	0.0057237	MERTK,RNF128,LGR4
regulation of angiogenesis	GO:0045765	3	309	36	61686	16.6359223	0.0007863	0.0057237	TSPAN12,BMPER,FGF2
negative regulation of epidermal growth factor receptor signaling pathway	GO:0042059	3	309	37	61686	16.1863028	0.0008525	0.0060959	SPRY1,EGFR,HBEGF
negative regulation of epithelial to mesenchymal transition	GO:0010719	3	309	37	61686	16.1863028	0.0008525	0.0060959	SPRY1,GATA3,SPRED1
adherens junction organization	GO:0034332	3	309	37	61686	16.1863028	0.0008525	0.0060959	CADM1,CDH3,EPHA4
negative regulation of mitotic cell cycle	GO:0045930	3	309	37	61686	16.1863028	0.0008525	0.0060959	BCL2,RB1,EGFR

dendrite development	GO:0016358	3	309	37	61686	16.1863028	0.0008525	0.0060959	MAP1B,CRKL,CRK
carbohydrate transport	GO:0008643	3	309	38	61686	15.7603475	0.0009222	0.0063146	SLC2A1,AKT2,AKT1
branching involved in ureteric bud morphogenesis	GO:0001658	3	309	38	61686	15.7603475	0.0009222	0.0063146	BCL2,FGF2,FAT4
hair follicle development	GO:0001942	3	309	38	61686	15.7603475	0.0009222	0.0063146	FZD6,EGFR,LGR4
negative regulation of cell differentiation	GO:0004596	3	309	38	61686	15.7603475	0.0009222	0.0063146	MAPK1,KRAS,PRAMEF1
protein kinase B signaling	GO:0004391	3	309	38	61686	15.7603475	0.0009222	0.0063146	MERTK,PIK3R3,AKT1
positive regulation of intrinsic apoptotic signaling pathway	GO:2001244	3	309	40	61686	14.9723301	0.0010721	0.0072388	RACK1,BCL2,PLAGL2
phospholipid transport	GO:0001594	3	309	41	61686	14.6071513	0.0011525	0.0074693	PITPNC1,LDLR,OSBPL8
positive regulation of B cell proliferation	GO:0003090	3	309	41	61686	14.6071513	0.0011525	0.0074693	CDKN1A,BCL2,WNT3A
long-term synaptic potentiation	GO:0006091	3	309	42	61686	14.259362	0.0012365	0.0079085	PLK2,MAPK1,GRIN2B
positive regulation of pri-miRNA transcription by RNA polymerase II	GO:1902895	3	309	42	61686	14.259362	0.0012365	0.0079085	GATA3,FOXO3,FGF2
negative regulation of viral genome replication	GO:0004571	3	309	42	61686	14.259362	0.0012365	0.0079085	PLSCR1,OAS2,PARP10
collagen catabolic process	GO:0003074	3	309	43	61686	13.9277489	0.0013244	0.0083819	MMP13,MMP9,MMP7
regulation of synaptic vesicle exocytosis	GO:2000300	3	309	43	61686	13.9277489	0.0013244	0.0083819	CHRNA5,NCS1,APBA1
mitotic metaphase plate congression	GO:0007080	3	309	43	61686	13.9277489	0.0013244	0.0083819	RRS1,CCNB1,EML4
O-glycan processing	GO:0001666	3	309	44	61686	13.6112092	0.001416	0.008734	GCNT1,MUC17,MUC13
cellular response to amino acid	GO:000341	3	309	45	61686	13.3087379	0.00151	0.00927	CDKN1A,MAPK1,SLC38A2

starvation	98						16	62	
toll-like receptor signaling pathway	GO:002224	3	309	45	61686	13.3087379	0.0015116	0.0092762	S100A1,IRAK1,IRAK4
cytoplasmic microtubule organization	GO:0031122	3	309	46	61686	13.0194175	0.0016111	0.0097632	CAMSAP2,SPAST,HOOK3
regulation of signal transduction	GO:0009966	3	309	47	61686	12.7424086	0.0017146	0.0102622	SPRY1,SPRED1,CRK
negative regulation of cold-induced thermogenesis	GO:0120163	3	309	47	61686	12.7424086	0.0017146	0.0102622	ACVR2B,RB1,LGR4
cellular response to glucose starvation	GO:0042149	3	309	47	61686	12.7424086	0.0017146	0.0102622	SLC2A1,BCL2,FOXO3
regulation of mitotic cell cycle	GO:0007346	3	309	47	61686	12.7424086	0.0017146	0.0102622	SIRT1,CDKN1A,RB1
negative regulation of cell adhesion	GO:0007162	3	309	48	61686	12.4769417	0.0018222	0.010773	CD164,RASA1,PIK3R1
positive regulation of vascular associated smooth muscle cell proliferation	GO:1904707	3	309	48	61686	12.4769417	0.0018222	0.010773	MMP9,FGF2,DNMT1
hormone-mediated signaling pathway	GO:0009755	3	309	48	61686	12.4769417	0.0018222	0.010773	NR1D2,GTF2H1,LGR4
inner ear development	GO:0048839	3	309	49	61686	12.2223103	0.0019339	0.0111878	SOX2,BMPER,EYA4
negative regulation of cell cycle	GO:0045786	3	309	49	61686	12.2223103	0.0019339	0.0111878	RB1,GATA3,GMNN
mitotic spindle organization	GO:0007052	3	309	50	61686	11.9778641	0.0020497	0.0117738	PLK2,CCNB1,STMN1
pattern specification process	GO:0007389	3	309	52	61686	11.517177	0.0022942	0.012639	SMAD2,LFNG,CRKL
JNK cascade	GO:0007254	3	309	53	61686	11.2998718	0.0024229	0.0132279	IRAK1,IRAK4,CRKL
heart morphogenesis	GO:0003007	3	309	53	61686	11.2998718	0.0024229	0.0132279	VEGFA,ARID2,FAT4
regulation of cell adhesion	GO:0030155	3	309	53	61686	11.2998718	0.0024229	0.0132279	CXCR4,ROCK1,FUT1

positive regulation of protein-containing complex assembly	GO:0031334	3	309	53	61686	11.2998718	0.0024229	0.0132279	RACK1,VEGFA,GNL3L
synapse assembly	GO:0007416	3	309	54	61686	11.0906149	0.002556	0.0136471	BDNF,MAP1B,CRKL
inner ear morphogenesis	GO:0042472	3	309	54	61686	11.0906149	0.002556	0.0136471	FZD6,GATA3,WNT3A
positive regulation of cytokine production	GO:0001819	3	309	55	61686	10.8889673	0.0026936	0.0143183	CADM1,GATA3,WNT3A
amino acid transport	GO:0006865	3	309	56	61686	10.6945215	0.0028356	0.0150074	SLC7A5,SFXN2,SLC38A2
substrate adhesion-dependent cell spreading	GO:0034446	3	309	56	61686	10.6945215	0.0028356	0.0150074	MERTK,TEK,PIK3R1
cellular response to cytokine stimulus	GO:0071345	3	309	57	61686	10.5068983	0.0029821	0.0154457	CXCR4,PTPN7,GATA3
excitatory postsynaptic potential	GO:0060079	3	309	58	61686	10.3257449	0.0031332	0.0161593	CHRNA5,GRIN2B,AKT1
response to calcium ion	GO:0051592	3	309	59	61686	10.1507323	0.0032889	0.0166786	ADAM9,THBS1,EGFR
negative regulation of epithelial cell proliferation	GO:0050680	3	309	60	61686	9.9815534	0.0034493	0.0174191	GDF5,SOX2,RB1
positive regulation of epithelial cell proliferation	GO:0050679	3	309	60	61686	9.9815534	0.0034493	0.0174191	VEGFA,FGF2,EGFR
cellular response to glucose stimulus	GO:0071333	3	309	61	61686	9.81792138	0.0036144	0.0182149	RACK1,ZNF236,SOX4
learning or memory	GO:0007611	3	309	62	61686	9.6595678	0.0037843	0.0187589	MAPK1,GRIN2B,EGFR
cellular response to organic cyclic compound	GO:0071407	3	309	63	61686	9.50624133	0.0039589	0.0195846	CCNB1,CCNA2,AKT1
extracellular matrix disassembly	GO:0022617	3	309	64	61686	9.35770631	0.0041384	0.0199433	MMP13,MMP9,MMP7
cellular response to drug	GO:0035690	3	309	64	61686	9.35770631	0.0041384	0.0199433	CXCR4,EGFR,CRKL
regulation of hematopoietic stem	GO:19020	3	309	65	61686	9.2137416	0.00432	0.02070	PSMD12,PSMA2,GATA3

cell differentiation	36					27	82		
double-strand break repair	GO:0006302	3	309	65	61686	9.2137416	0.0043227	0.0207082	SMCHD1,NBN,LIG4
regulation of protein phosphorylation	GO:0001932	3	309	66	61686	9.07413945	0.004512	0.021237	PIK3CG,ARR3,EZH2
response to unfolded protein	GO:0006986	3	309	67	61686	8.93870454	0.0047062	0.0220654	THBS1,HSPA1B,CHAC1
regulation of autophagy	GO:0010506	3	309	72	61686	8.31796117	0.0057526	0.0222751	BCL2,ROCK1,PIK3R2
negative regulation of cell death	GO:00060548	3	309	72	61686	8.31796117	0.0057526	0.0222751	SOX4,HSPA1B,FGF2
modulation of chemical synaptic transmission	GO:00050804	3	309	72	61686	8.31796117	0.0057526	0.0222751	STAU1,BDNF,WNT3A
response to wounding	GO:0009611	3	309	73	61686	8.20401649	0.0059772	0.0228527	SOX2,MAP1B,ADM
fat cell differentiation	GO:00045444	3	309	68	61686	8.807253	0.0049054	0.0228665	FOXO1,AKT2,OSBPL8
hemopoiesis	GO:00030097	3	309	68	61686	8.807253	0.0049054	0.0228665	CD164,BCL2,WNT3A
canonical Wnt signaling pathway	GO:00060070	3	309	68	61686	8.807253	0.0049054	0.0228665	FZD6,LRP6,WNT3A
regulation of actin cytoskeleton organization	GO:00032956	3	309	74	61686	8.0931514	0.0062069	0.0235456	TWF2,ROCK1,CRK
keratinization	GO:00031424	3	309	74	61686	8.0931514	0.0062069	0.0235456	CDH3,KRTAP4-11,KRT6C
response to nutrient	GO:00007584	3	309	75	61686	7.98524272	0.0064419	0.0240604	VCAM1,IGFBP2,ACSL4
regulation of growth	GO:00040008	3	309	75	61686	7.98524272	0.0064419	0.0240604	RACK1,BCL2,IGFBP2
memory	GO:00007613	3	309	76	61686	7.88017374	0.0066821	0.024881	CRTC1,PLK2,BDNF
regulation of mitotic cell cycle phase transition	GO:000901990	3	309	76	61686	7.88017374	0.0066821	0.024881	CCNB1,PSMD12,PSMA2
neural tube closure	GO:000018	3	309	77	61686	7.77783382	0.00692	0.02575	FZD6,LRP6,ADM

	43						76	55	
anaphase-promoting complex-dependent catabolic process	GO:0031145	3	309	79	61686	7.58092663	0.0074345	0.0273049	CCNB1,PSMD12,PSMA2
circadian rhythm	GO:0007623	3	309	83	61686	7.21558077	0.0085127	0.0304796	SIRT1,EGFR,LGR4
transport across blood-brain barrier	GO:0150104	3	309	84	61686	7.129681	0.0087957	0.0312622	SLC7A5,SLC2A1,SLC38A2
BMP signaling pathway	GO:0030509	3	309	85	61686	7.0458024	0.0090843	0.0322405	ACVR2B,GDF5,SMAD2
liver development	GO:0001889	3	309	86	61686	6.96387446	0.0093783	0.0328512	ARF6,KRAS,EGFR
Wnt signaling pathway, planar cell polarity pathway	GO:0060071	3	309	87	61686	6.88382993	0.0096778	0.0338027	FZD6,PSMD12,PSMA2
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	GO:0000184	3	309	95	61686	6.30413899	0.0122745	0.0352529	RPS5,RPL7,RPSA
Golgi organization	GO:0007030	3	309	97	61686	6.17415674	0.0129799	0.0369722	UBXN2A,TJAP1,VMP1
cellular calcium ion homeostasis	GO:0006874	3	309	104	61686	5.7585885	0.0156285	0.039055	CXCL12,BCL2,SLC10A7
chromatin remodeling	GO:0006338	3	309	100	61686	5.98893204	0.0140807	0.0398734	KDM5C,RB1,GATA3
receptor-mediated endocytosis	GO:0006898	3	309	110	61686	5.44448367	0.0181228	0.0445986	PDLIM7,LDLR,EGFR
glucose homeostasis	GO:00042593	3	309	112	61686	5.34726075	0.0190004	0.0465694	SOX4,IRS1,AKT1
adenylate cyclase-activating G protein-coupled receptor signaling pathway	GO:0007189	3	309	112	61686	5.34726075	0.0190004	0.0465694	ADGRE5,LGR4,ADM
positive regulation of DNA-binding transcription factor activity	GO:00051091	3	309	113	61686	5.29993986	0.019448	0.0476181	LRP6,AKT1,WNT3A

Supplementary materials

Supplementary Table ST4B: Significantly enriched KEGG pathways having at least 3 genes in a category (https://genecodis.genyo.es/)									
description	annotation_id	genes_found	input_size	term_genes	genes_universe	relative_enrichment	pval	pval_adj	genes
Pathways in cancer	hsa05200	38	309	378	61686	20.0687317	2.09E-37	5.38E-35	CDKN1A,CCNA2,CCNE2,CASP7,PIK3R3,FZD6,CXCR4,VEGFA,ELOC,SLC2A1,CXCL12,BCL2,ROCK1,RB1,RAF1,PTGS2,MAPK1,PIK3R2,PIK3R1,NFKBIA,MMP9,SMAD2,LRP6,KRAS,GNB1,ALK,FOXO1,FGF2,AKT2,AKT1,WNT3A,EGFR,E2F1,POLK,CRKL,CRK,EML4,FGF22
Metabolic pathways	hsa01100	27	309	553	61686	9.746905669	1.30E-18	9.79E-18	SIRT1,ATP6V0E1,PLA2G4C,PIP5K1A,CA1,PTGS2,PIK3CG,PFAS,NDUFB10,IMPA1,GK,COX8C,AMD1,GCNT1,FUT1,ACSL4,EZH2,L2HGDH,CHAC1,DNMT1,CYP26A1,CYP2E1,ETNK2,HACD3,DMGDH,ADH1A,B3GAT1
MicroRNAs in cancer	hsa05206	26	309	124	61686	41.85812715	1.37E-34	1.76E-32	SIRT1,CDKN1A,CCNE2,PIK3R3,VEGFA,THBS1,SOX4,BCL2,ROCK1,RAF1,PTGS2,MAPK1,PIK3R2,PIK3R1,MMP9,STMN1,KRAS,IRS1,EZH2,WNT3A,SLC45A3,EGFR,E2F1,DNMT1,CRKL,CRK
Human papillomavirus infection	hsa05165	22	309	187	61686	23.486008	1.31E-23	4.79E-22	CDKN1A,CCNA2,CCNE2,ATP6V0E1,PIK3R3,FZD6,VEGFA,THBS1,RB1,RAF1,PTGS2,MAPK1,PIK3R2,PIK3R1,LFNG,KRAS,FOXO1,AKT2,AKT1,WNT3A,EGFR,E2F1
PI3K-Akt signaling pathway	hsa04151	22	309	229	61686	19.17853055	1.19E-21	1.91E-20	CDKN1A,CCNE2,PIK3R3,VEGFA,THBS1,TEK,BDNF,BCL2,RAF1,MAPK1,PIK3R2,PIK3R1,PIK3CG,KRAS,IRS1,GNB1,FOXO3,FGF2,AKT2,AKT1,EGFR,FGF22
Gastric cancer	hsa05226	21	309	96	61686	43.66929612	1.39E-28	1.19E-26	CDKN1A,CCNE2,PIK3R3,FZD6,BCL2,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,SMAD2,LRP6,KRAS,FGF2,AKT2,AKT1,WNT3A,EGFR,E2F1,POLK,FGF22
Alzheimer disease	hsa05010	21	309	162	61686	25.8781014	1.68E-23	5.38E-22	CASP7,PIK3R3,FZD6,VDAC2,RAF1,PTGS2,PSMD12,PSMA2,MAPK1,PIK3R2,PIK3R1,NDUFB10,LRP6,KRAS,IRS1,GRIN2B,COX8C,AKT2,AKT1,WNT3A,RTN4
Human cytomegalovirus infection	hsa05163	21	309	165	61686	25.40759047	2.49E-23	6.41E-22	CDKN1A,PIK3R3,CXCR4,VEGFA,CXCL12,ROCK1,RB1,RAF1,PTGS2,MAPK1,PIK3R2,PIK3R1,NFKBIA,KRAS,GNB1,AKT2,AKT1,EGFR,E2F1,CRKL,CRK
MAPK signaling pathway	hsa04010	21	309	201	61686	20.85697725	1.71E-21	2.59E-20	PLA2G4C,VEGFA,TEK,BDNF,RASA1,RAF1,PTPN7,MAPK1,MAP3K3,STMN1,KRAS,IRAK1,HSPA1B,FGF2,AKT2,AKT1,EGFR,IRAK4,CRKL,CRK,FGF22
Cellular senescence	hsa04218	20	309	111	61686	35.96956179	1.89E-25	1.21E-23	SIRT1,CDKN1A,CCNB1,CCNA2,CCNE2,PIK3R3,VDAC2,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,NBN,SMAD2,KRAS,FOXO3,FOXO1,AKT2,AKT1,E2F1
Ras signaling pathway	hsa04014	20	309	159	61686	25.11082616	3.58E-22	6.57E-21	PLA2G4C,PIK3R3,VEGFA,TEK,BDNF,RASA1,RAF1,RAB5B,MAPK1,PIK3R2,PIK3R1,ARF6,KRAS,GRIN2B,GNB1,FGF2,AKT2,AKT1,EGFR,FGF22
Human T-cell leukemia virus 1 infection	hsa05166	20	309	162	61686	24.64581086	5.26E-22	9.01E-21	CRTC1,CDKN1A,CCNA2,CCNE2,PIK3R3,VDAC2,SLC2A1,RB1,MAPK1,PIK3R2,PIK3R1,NFKBIA,MMP7,MAP3K3,SMAD2,KRAS,AKT2,AKT1,TLN2,E2F1
Breast cancer	hsa05224	19	309	93	61686	40.78484184	2.32E-25	1.19E-23	CDKN1A,PIK3R3,FZD6,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,PGR,LRP6,KRAS,FGF2,AKT2,AKT1,WNT3A,EGFR,E2F1,POLK,FGF22
Proteoglycans in cancer	hsa05205	19	309	146	61686	25.97938556	2.04E-21	2.92E-20	CDKN1A,PIK3R3,FZD6,VEGFA,THBS1,ROCK1,RAF1,MAPK1,PIK3R2,PIK3R1,MMP9,SMAD2,KRAS,FGF2,AKT2,AKT1,WNT3A,EGFR,HBEGF
Neurotrophin signaling pathway	hsa04722	18	309	87	61686	41.30297958	3.37E-24	1.44E-22	PIK3R3,BDNF,BCL2,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,MAP3K3,KRAS,IRS1,IRAK1,FOXO3,AKT2,AKT1,IRAK4,CRKL,CRK
Hepatocellular carcinoma	hsa05225	18	309	96	61686	37.43082524	2.30E-23	6.57E-22	CDKN1A,PIK3R3,FZD6,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,SMAD2,LRP6,KRAS,ARID2,AKT2,AKT1,WNT3A,EGFR,E2F1,POLK
Hepatitis B	hsa05161	18	309	134	61686	26.81611361	1.30E-20	1.52E-19	CDKN1A,CCNA2,CCNE2,PIK3R3,BCL2,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,MMP9,KRAS,IRAK1,AKT2,AKT1,E2F1,IRAK4
Epstein-Barr virus infection	hsa05169	18	309	139	61686	25.8515052	2.57E-20	2.88E-19	CDKN1A,CCNA2,CCNE2,PIK3R3,BCL2,RB1,PSMD12,PIK3R2,PIK3R1,OAS2,NFKBIA,IRAK1,AKT2,AKT1,E2F1,POLK,IRAK4,CR2
Human immunodeficiency virus 1 infection	hsa05170	18	309	141	61686	25.48481719	3.36E-20	3.59E-19	CCNB1,PIK3R3,CXCR4,ELOC,BCL2,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,KRAS,IRAK1,GNB1,AKT2,AKT1,IRAK4,CRKL,CRK
Rap1 signaling pathway	hsa04015	18	309	156	61686	23.034354	2.17E-19	1.80E-18	PIK3R3,VEGFA,THBS1,TEK,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,GRIN2B,FGF2,AKT2,AKT1,TLN2,EGFR,CRKL,CRK,FGF22
Prostate cancer	hsa05215	17	309	82	61686	41.38692872	6.10E-23	1.31E-21	CDKN1A,CCNE2,PIK3R3,BCL2,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,MMP9,KRAS,FOXO1,AKT2,AKT1,EGFR,E2F1
Chemokine signaling pathway	hsa04062	17	309	124	61686	27.36877545	1.08E-19	9.89E-19	PIK3R3,CXCR4,CXCL12,ROCK1,RAF1,MAPK1,PIK3R2,PIK3R1,PIK3CG,NFKBIA,KRAS,GNB1,FOXO3,AKT2,AKT1,CRKL,CRK

Kaposi sarcoma-associated herpesvirus infection	hsa05167	17	309	137	61686	24.77173836	6.20E-19	4.83E-18	CDKN1A,PIK3R3,VEGFA,RB1,RAF1,PTGS2,MAPK1,PIK3R2,PIK3R1,PIK3CG,NFKBIA,KRAS,GNB1,FGF2,AKT2,AKT1,E2F1
Salmonella infection	hsa05132	17	309	143	61686	23.73236472	1.31E-18	9.34E-18	NCKAP1,EXOC5,ACTR2,CASP7,BCL2,RAF1,RAB5B,MAPK1,PIK3CG,NFKBIA,ARF6,KPNA1,IRAK1,ANXA2,AKT2,AKT1,IRAK4
Regulation of actin cytoskeleton	hsa04810	17	309	143	61686	23.73236472	1.31E-18	9.34E-18	NCKAP1,ACTR2,PIK3R3,PIP5K1A,CXCR4,CXCL12,ROCK1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,FGF2,EGFR,CRKL,CRK,FGF22
Shigellosis	hsa05131	17	309	158	61686	21.47929212	7.35E-18	4.97E-17	ACTR2,PIK3R3,BCL2,ROCK1,MAPK1,PIK3R2,PIK3R1,NFKBIA,ARF6,FOXO3,FOXO1,AKT2,AKT1,TLN2,EGFR,CRKL,CRK
Non-small cell lung cancer	hsa05223	16	309	63	61686	50.69995377	3.15E-23	7.36E-22	CDKN1A,PIK3R3,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,ALK,FOXO3,AKT2,AKT1,EGFR,E2F1,POLK,EML4
FoxO signaling pathway	hsa04068	16	309	100	61686	31.94097087	9.80E-20	9.33E-19	SIRT1,CDKN1A,PLK2,CCNB1,PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,IRS1,FOXO3,FOXO1,AKT2,AKT1,EGFR
Hepatitis C	hsa05160	16	309	108	61686	29.57497303	3.58E-19	2.87E-18	CDKN1A,PIK3R3,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,OAS2,NFKBIA,OCLN,LDLR,KRAS,AKT2,AKT1,EGFR,E2F1
Focal adhesion	hsa04510	16	309	135	61686	23.65997843	1.44E-17	9.22E-17	PIK3R3,PIP5K1A,VEGFA,THBS1,BCL2,ROCK1,RAF1,MAPK1,PIK3R2,PIK3R1,AKT2,AKT1,TLN2,EGFR,CRKL,CRK
Pathways of neurodegeneration - multiple diseases	hsa05022	16	309	208	61686	15.356236	1.46E-14	6.57E-14	CASP7,FZD6,VDAC2,BDNF,BCL2,RAF1,PTGS2,PSMD12,PSMA2,MAPK1,NDUFB10,LRP6,KRAS,GRIN2B,COX8C,WNT3A
Melanoma	hsa05218	15	309	54	61686	55.45307443	1.62E-22	3.20E-21	CDKN1A,PIK3R3,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,FGF2,AKT2,AKT1,EGFR,E2F1,POLK,FGF22
Pancreatic cancer	hsa05212	15	309	67	61686	44.69352268	6.10E-21	7.83E-20	CDKN1A,PIK3R3,VEGFA,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,SMAD2,KRAS,AKT2,AKT1,EGFR,E2F1,POLK
Chronic myeloid leukemia	hsa05220	15	309	67	61686	44.69352268	6.10E-21	7.83E-20	CDKN1A,PIK3R3,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,KRAS,AKT2,AKT1,E2F1,POLK,CRKL,CRK
Signaling pathways regulating pluripotency of stem cells	hsa04550	15	309	69	61686	43.39805825	9.90E-21	1.21E-19	ACVR2B,PIK3R3,FZD6,SOX2,RAF1,MAPK1,PIK3R2,PIK3R1,SMAD2,LIFR,KRAS,FGF2,AKT2,AKT1,WNT3A
Endocrine resistance	hsa01522	15	309	78	61686	38.39058999	7.33E-20	7.25E-19	CDKN1A,PIK3R3,BCL2,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,MMP9,KRAS,AKT2,AKT1,EGFR,E2F1,HBEGF
Estrogen signaling pathway	hsa04915	15	309	80	61686	37.43082524	1.10E-19	9.78E-19	PIK3R3,BCL2,RAF1,MAPK1,PIK3R2,PIK3R1,PGR,MMP9,KRAS,KCNJ9,HSPA1B,AKT2,AKT1,EGFR,HBEGF
Relaxin signaling pathway	hsa04926	15	309	83	61686	36.07790385	2.00E-19	1.71E-18	PIK3R3,VEGFA,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,MMP13,MMP9,SMAD2,KRAS,GNB1,AKT2,AKT1,EGFR
Yersinia infection	hsa05135	15	309	109	61686	27.47216532	1.48E-17	9.30E-17	ACTR2,PIK3R3,PIP5K1A,ROCK1,MAPK1,PIK3R2,PIK3R1,NFKBIA,ARF6,IRAK1,AKT2,AKT1,IRAK4,CRKL,CRK
Renal cell carcinoma	hsa05211	14	309	60	61686	46.58058252	6.57E-20	6.75E-19	CDKN1A,PIK3R3,VEGFA,ELOC,SLC2A1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1,CRKL,CRK
Glioma	hsa05214	13	309	57	61686	45.52989269	1.95E-18	1.35E-17	CDKN1A,PIK3R3,RB1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1,EGFR,E2F1,POLK
Fc gamma R-mediated phagocytosis	hsa04666	13	309	66	61686	39.32127096	1.56E-17	9.57E-17	ACTR2,PLA2G4C,PIK3R3,PIP5K1A,RAF1,MAPK1,PIK3R2,PIK3R1,ARF6,AKT2,AKT1,CRKL,CRK
EGFR tyrosine kinase inhibitor resistance	hsa01521	13	309	69	61686	37.61165049	2.92E-17	1.74E-16	PIK3R3,VEGFA,BCL2,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,FOXO3,FGF2,AKT2,AKT1,EGFR
ErbB signaling pathway	hsa04012	13	309	70	61686	37.07434119	3.57E-17	2.08E-16	CDKN1A,PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1,EGFR,HBEGF,CRKL,CRK
Small cell lung cancer	hsa05222	13	309	71	61686	36.55216737	4.35E-17	2.48E-16	CDKN1A,CCNE2,PIK3R3,BCL2,RB1,PTGS2,PIK3R2,PIK3R1,NFKBIA,AKT2,AKT1,E2F1,POLK
Colorectal cancer	hsa05210	13	309	73	61686	35.55073813	6.40E-17	3.50E-16	CDKN1A,PIK3R3,BCL2,RAF1,MAPK1,PIK3R2,PIK3R1,SMAD2,KRAS,AKT2,AKT1,EGFR,POLK

PD-L1 expression and PD-1 checkpoint pathway in cancer	hsa05235	13	309	74	61686	35.07032275	7.73E-17	4.14E-16	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,MAP3K3,KRAS,ALK,AKT2,AKT1,EGFR,EML4
HIF-1 signaling pathway	hsa04066	13	309	79	61686	32.85068207	1.91E-16	9.99E-16	CDKN1A,PIK3R3,VEGFA,TEK,ELOC,SLC2A1,BCL2,MAPK1,PIK3R2,PIK3R1,AKT2,AKT1,EGFR
mTOR signaling pathway	hsa04150	13	309	80	61686	32.44004854	2.26E-16	1.16E-15	PIK3R3,FZD6,SLC7A5,RAF1,MAPK1,PIK3R2,PIK3R1,LRP6,KRAS,IRS1,AKT2,AKT1,WNT3A
Phospholipase D signaling pathway	hsa04072	13	309	107	61686	24.2542419	1.15E-14	5.30E-14	PLA2G4C,PIK3R3,PIP5K1A,RAF1,MAPK1,PIK3R2,PIK3R1,PIK3CG,ARF6,KRAS,AKT2,AKT1,EGFR
Measles	hsa05162	13	309	111	61686	23.38021517	1.88E-14	8.19E-14	RACK1,CCNE2,PIK3R3,BCL2,PIK3R2,PIK3R1,OAS2,NFKBIA,IRAK1,HSPA1B,AKT2,AKT1,IRAK4
Coronavirus disease - COVID-19	hsa05171	13	309	113	61686	22.96640605	2.38E-14	9.87E-14	PIK3R3,RPS5,RPL7,MAPK1,PIK3R2,PIK3R1,OAS2,NFKBIA,RPSA,IRAK1,EGFR,HBEGF,IRAK4
Endometrial cancer	hsa05213	12	309	48	61686	49.90776699	1.19E-17	7.87E-17	CDKN1A,PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,FOXO3,AKT2,AKT1,EGFR,POLK
AGE-RAGE signaling pathway in diabetic complications	hsa04933	12	309	81	61686	29.57497303	1.05E-14	4.89E-14	PIK3R3,VEGFA,VCAM1,BCL2,MAPK1,PIK3R2,PIK3R1,SMAD2,KRAS,FOXO1,AKT2,AKT1
Axon guidance	hsa04360	12	309	85	61686	28.18320959	1.91E-14	8.19E-14	PIK3R3,CXCR4,CXCL12,ROCK1,RGS3,RASA1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,EPHA4
Insulin signaling pathway	hsa04910	12	309	86	61686	27.85549786	2.21E-14	9.33E-14	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,IRS1,FOXO1,AKT2,AKT1,CRKL,CRK
cAMP signaling pathway	hsa04024	12	309	143	61686	16.75225745	1.07E-11	3.39E-11	CFTR,PIK3R3,BDNF,ROCK1,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,GRIN2B,AKT2,AKT1
Bladder cancer	hsa05219	11	309	38	61686	57.78794073	4.45E-17	2.48E-16	CDKN1A,VEGFA,THBS1,RB1,RAF1,MAPK1,MMP9,KRAS,EGFR,E2F1,HBEGF
VEGF signaling pathway	hsa04370	11	309	45	61686	48.7987055	3.64E-16	1.83E-15	PLA2G4C,PIK3R3,VEGFA,RAF1,PTGS2,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1
Longevity regulating pathway - multiple species	hsa04213	11	309	47	61686	46.72216484	6.18E-16	3.06E-15	SIRT1,PIK3R3,PIK3R2,PIK3R1,KRAS,IRS1,HSPA1B,FOXO3,FOXO1,AKT2,AKT1
Central carbon metabolism in cancer	hsa05230	11	309	52	61686	42.22964899	2.10E-15	1.02E-14	PIK3R3,SLC7A5,SLC2A1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1,EGFR
Progesterone-mediated oocyte maturation	hsa04914	11	309	56	61686	39.21324549	5.08E-15	2.42E-14	CCNB1,CCNA2,PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,PGR,KRAS,AKT2,AKT1
Choline metabolism in cancer	hsa05231	11	309	62	61686	35.41841528	1.69E-14	7.48E-14	PLA2G4C,PIK3R3,PIP5K1A,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1,EGFR
AMPK signaling pathway	hsa04152	11	309	80	61686	27.44927184	3.21E-13	1.31E-12	SIRT1,CFTR,CCNA2,PIK3R3,PIK3R2,PIK3R1,IRS1,FOXO3,FOXO1,AKT2,AKT1
Growth hormone synthesis, secretion and action	hsa04935	11	309	86	61686	25.53420637	7.31E-13	2.89E-12	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,IRS1,AKT2,AKT1,CRKL,CRK
TNF signaling pathway	hsa04668	11	309	96	61686	22.8743932	2.52E-12	9.52E-12	CASP7,PIK3R3,VCAM1,PTGS2,MAPK1,PIK3R2,PIK3R1,NFKBIA,MMP9,AKT2,AKT1
Prion disease	hsa05020	11	309	97	61686	22.63857472	2.83E-12	1.04E-11	PIK3R3,VDAC2,PSMD12,PSMA2,MAPK1,PIK3R2,PIK3R1,NDUFB10,HSPA1B,GRIN2B,COX8C
Autophagy - animal	hsa04140	11	309	98	61686	22.40756885	3.17E-12	1.15E-11	PIK3R3,BCL2,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,IRS1,AKT2,AKT1,VMP1
Fluid shear stress and atherosclerosis	hsa05418	11	309	100	61686	21.95941748	3.98E-12	1.38E-11	ACVR2B,PIK3R3,VEGFA,VCAM1,BCL2,PIK3R2,PIK3R1,MMP9,MEF2A,AKT2,AKT1

Apoptosis	hsa04210	11	309	100	61686	21.95941748	3.98E-12	1.38E-11	CASP7,PIK3R3,BCL2,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,KRAS,AKT2,AKT1
Influenza A	hsa05164	11	309	115	61686	19.09514563	1.87E-11	5.72E-11	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,OAS2,NFKBIA,KPNA1,AKT2,AKT1,IRAK4
Viral carcinogenesis	hsa05203	11	309	124	61686	17.70920764	4.27E-11	1.23E-10	CDKN1A,CCNA2,CCNE2,PIK3R3,RB1,MAPK1,PIK3R2,PIK3R1,NFKBIA,KRAS,GTF2H1
B cell receptor signaling pathway	hsa04662	10	309	59	61686	33.83577423	4.35E-13	1.75E-12	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,KRAS,AKT2,AKT1,CR2
Non-alcoholic fatty liver disease	hsa04932	10	309	67	61686	29.79568179	1.66E-12	6.45E-12	CASP7,PIK3R3,PIK3R2,PIK3R1,NDUFB10,IRS1,COX8C,AKT2,AKT1,CYP2E1
Longevity regulating pathway	hsa04211	10	309	69	61686	28.93203883	2.25E-12	8.64E-12	SIRT1,PIK3R3,PIK3R2,PIK3R1,KRAS,IRS1,FOXO3,FOXO1,AKT2,AKT1
Sphingolipid signaling pathway	hsa04071	10	309	70	61686	28.51872399	2.62E-12	9.74E-12	PIK3R3,BCL2,ROCK1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1
Cholinergic synapse	hsa04725	10	309	75	61686	26.61747573	5.35E-12	1.83E-11	PIK3R3,BCL2,MAPK1,PIK3R2,PIK3R1,PIK3CG,KRAS,GNB1,AKT2,AKT1
Toxoplasmosis	hsa05145	10	309	77	61686	25.92611272	7.01E-12	2.34E-11	BCL2,MAPK1,PIK3CG,NFKBIA,LDLR,IRAK1,HSPA1B,AKT2,AKT1,IRAK4
Thyroid hormone signaling pathway	hsa04919	10	309	78	61686	25.59372666	8.01E-12	2.61E-11	PIK3R3,SLC2A1,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,FOXO1,AKT2,AKT1
Parathyroid hormone synthesis, secretion and action	hsa04928	10	309	78	61686	25.59372666	8.01E-12	2.61E-11	CDKN1A,BCL2,RAF1,MAPK1,MMP13,MEF2A,LRP6,GATA3,EGFR,HBEGF
Chagas disease	hsa05142	10	309	80	61686	24.9538835	1.04E-11	3.34E-11	PIK3R3,MAPK1,PIK3R2,PIK3R1,NFKBIA,SMAD2,IRAK1,AKT2,AKT1,IRAK4
C-type lectin receptor signaling pathway	hsa04625	10	309	83	61686	24.0519359	1.51E-11	4.69E-11	PIK3R3,RAF1,PTGS2,MAPK1,PIK3R2,PIK3R1,NFKBIA,KRAS,AKT2,AKT1
Endocytosis	hsa04144	10	309	88	61686	22.68534863	2.75E-11	8.12E-11	ACTR2,USP8,PIP5K1A,CXCR4,RAB5B,SMAD2,ARF6,LDLR,HSPA1B,EGFR
Platelet activation	hsa04611	10	309	91	61686	21.93748	3.86E-11	1.13E-10	PLA2G4C,PIK3R3,ROCK1,MAPK1,PIK3R2,PIK3R1,PIK3CG,AKT2,AKT1,TLN2
Oxytocin signaling pathway	hsa04921	10	309	92	61686	21.69902913	4.31E-11	1.23E-10	CDKN1A,PLA2G4C,ROCK1,RAF1,PTGS2,MAPK1,PIK3CG,KRAS,KCNJ9,EGFR
Cushing syndrome	hsa04934	10	309	101	61686	19.76545227	1.10E-10	3.02E-10	CDKN1A,CCNE2,USP8,FZD6,RB1,MAPK1,LDLR,WNT3A,EGFR,E2F1
JAK-STAT signaling pathway	hsa04630	10	309	106	61686	18.83311962	1.79E-10	4.80E-10	CDKN1A,PIK3R3,BCL2,RAF1,PIK3R2,PIK3R1,LIFR,AKT2,AKT1,EGFR
Pathogenic Escherichia coli infection	hsa05130	10	309	110	61686	18.14827891	2.59E-10	6.87E-10	NCKAP1,ACTR2,CASP7,ROCK1,MAPK1,NFKBIA,OCLN,ARF6,IRAK1,IRAK4
Herpes simplex virus 1 infection	hsa05168	10	309	121	61686	16.49843537	6.66E-10	1.71E-09	PIK3R3,BCL2,PIK3R2,PIK3R1,OAS2,NFKBIA,IRAK1,AKT2,AKT1,IRAK4
GnRH secretion	hsa04929	9	309	50	61686	35.93359223	3.70E-12	1.32E-11	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,KCNJ9,AKT2,AKT1
Fc epsilon RI signaling pathway	hsa04664	9	309	52	61686	34.55153099	5.38E-12	1.82E-11	PLA2G4C,PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1
Prolactin signaling pathway	hsa04917	9	309	56	61686	32.08356449	1.09E-11	3.41E-11	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,FOXO3,AKT2,AKT1
Acute myeloid leukemia	hsa05221	9	309	61	61686	29.45376413	2.44E-11	7.29E-11	CCNA2,PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,AKT2,AKT1
Insulin resistance	hsa04931	9	309	69	61686	26.03883495	7.70E-11	2.17E-10	PIK3R3,SLC2A1,PIK3R2,PIK3R1,NFKBIA,IRS1,FOXO1,AKT2,AKT1

Leukocyte transendothelial migration	hsa04670	9	309	71	61686	25.30534664	1.00E-10	2.77E-10	PIK3R3,CXCR4,VCAM1,CXCL12,ROCK1,PIK3R2,PIK3R1,OCLN,MMP9
Spinocerebellar ataxia	hsa05017	9	309	75	61686	23.95572816	1.66E-10	4.49E-10	PIK3R3,VDAC2,PSMD12,PSMA2,PIK3R2,PIK3R1,GRIN2B,AKT2,AKT1
Toll-like receptor signaling pathway	hsa04620	9	309	79	61686	22.74277989	2.68E-10	7.02E-10	PIK3R3,MAPK1,PIK3R2,PIK3R1,NFKBIA,IRAK1,AKT2,AKT1,IRAK4
T cell receptor signaling pathway	hsa04660	9	309	84	61686	21.389043	4.68E-10	1.22E-09	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,NFKBIA,KRAS,AKT2,AKT1
Apelin signaling pathway	hsa04371	9	309	94	61686	19.11361289	1.29E-09	3.29E-09	RAF1,MAPK1,PIK3CG,MEF2A,SMAD2,KRAS,GNB1,AKT2,AKT1
cGMP-PKG signaling pathway	hsa04022	9	309	112	61686	16.04178225	6.18E-09	1.51E-08	VDAC2,ROCK1,RAF1,MAPK1,PIK3CG,MEF2A,IRS1,AKT2,AKT1
Platinum drug resistance	hsa01524	8	309	47	61686	33.97975625	9.61E-11	2.68E-10	CDKN1A,PIK3R3,BCL2,MAPK1,PIK3R2,PIK3R1,AKT2,AKT1
Natural killer cell mediated cytotoxicity	hsa04650	8	309	76	61686	21.01379663	5.08E-09	1.27E-08	PIK3R3,RAF1,MAPK1,PIK3R2,PIK3R1,KRAS,KIR3DL2,KIR3DL1
Cell cycle	hsa04110	8	309	77	61686	20.74089018	5.65E-09	1.40E-08	CDKN1A,STAG1,CCNB1,CCNA2,CCNE2,RB1,SMAD2,E2F1
Neutrophil extracellular trap formation	hsa04613	8	309	85	61686	18.7888064	1.25E-08	3.02E-08	PIK3R3,VDAC2,RAF1,MAPK1,PIK3R2,PIK3R1,AKT2,AKT1
Transcriptional misregulation in cancer	hsa05202	8	309	112	61686	14.259362	1.10E-07	2.56E-07	CDKN1A,CCNA2,TAF15,MMP9,HOXA9,FOXO1,SLC45A3,POLK
Tuberculosis	hsa05152	8	309	119	61686	13.420576	1.75E-07	4.03E-07	BCL2,RAF1,RAB5B,MAPK1,IRAK1,AKT2,AKT1,IRAK4
Aldosterone-regulated sodium reabsorption	hsa04960	7	309	24	61686	58.22572816	2.38E-11	7.19E-11	PIK3R3,MAPK1,PIK3R2,PIK3R1,KRAS,KCNJ1,IRS1
Regulation of lipolysis in adipocytes	hsa04923	7	309	47	61686	29.73228672	3.92E-09	9.87E-09	PIK3R3,PTGS2,PIK3R2,PIK3R1,IRS1,AKT2,AKT1
GnRH signaling pathway	hsa04912	7	309	65	61686	21.4987304	4.01E-08	9.64E-08	PLA2G4C,RAF1,MAPK1,MAP3K3,KRAS,EGFR,HBEGF
Serotonergic synapse	hsa04726	7	309	71	61686	19.68193628	7.47E-08	1.76E-07	PLA2G4C,RAF1,PTGS2,MAPK1,KRAS,KCNJ9,GNB1
NF-kappa B signaling pathway	hsa04064	7	309	86	61686	16.24904042	2.83E-07	6.38E-07	VCAM1,CXCL12,BCL2,PTGS2,NFKBIA,IRAK1,IRAK4
Huntington disease	hsa05016	7	309	92	61686	15.18932039	4.50E-07	9.89E-07	VDAC2,BDNF,PSMD12,PSMA2,NDUFB10,GRIN2B,COX8C
Osteoclast differentiation	hsa04380	7	309	100	61686	13.97417476	7.95E-07	1.73E-06	PIK3R3,MAPK1,PIK3R2,PIK3R1,NFKBIA,AKT2,AKT1
Amyotrophic lateral sclerosis	hsa05014	7	309	122	61686	11.4542416	3.03E-06	6.38E-06	NUP50,BCL2,PSMD12,PSMA2,NDUFB10,GRIN2B,COX8C
Bacterial invasion of epithelial cells	hsa05100	6	309	47	61686	25.48481719	1.36E-07	3.15E-07	ACTR2,PIK3R3,PIK3R2,PIK3R1,CRKL,CRK
Adipocytokine signaling pathway	hsa04920	6	309	51	61686	23.486008	2.24E-07	5.10E-07	SLC2A1,NFKBIA,IRS1,AKT2,ACSL4,AKT1
TGF-beta signaling pathway	hsa04350	6	309	54	61686	22.18122977	3.18E-07	7.10E-07	ACVR2B,GDF5,THBS1,ROCK1,MAPK1,SMAD2
Cell adhesion molecules	hsa04514	6	309	56	61686	21.389043	3.96E-07	8.77E-07	CADM1,CD226,CDH3,CNTNAP1,VCAM1,OCLN

Alcoholism	hsa05034	6	309	67	61686	17.87740907	1.16E-06	2.49E-06	BDNF,RAF1,MAPK1,KRAS,GRIN2B,GNB1
NOD-like receptor signaling pathway	hsa04621	6	309	113	61686	10.59987971	2.43E-05	4.72E-05	VDAC2,BCL2,MAPK1,OAS2,NFKBIA,IRAK4
Cytokine-cytokine receptor interaction	hsa04060	6	309	143	61686	8.376128726	9.04E-05	0.000158104	ACVR2B,GDF5,CXCR4,CXCL12,TNFRSF17,LIFR
Calcium signaling pathway	hsa04020	6	309	148	61686	8.093151404	0.000109	0.000189702	CXCR4,VEGFA,VDAC2,FGF2,EGFR,FGF22
Carbohydrate digestion and absorption	hsa04973	5	309	21	61686	47.53120666	5.82E-08	1.38E-07	PIK3R3,PIK3R2,PIK3R1,AKT2,AKT1
Phosphatidylinositol signaling system	hsa04070	5	309	36	61686	27.72653722	1.01E-06	2.19E-06	PIK3R3,PIP5K1A,PIK3R2,PIK3R1,IMPA1
Type II diabetes mellitus	hsa04930	5	309	39	61686	25.59372666	1.53E-06	3.25E-06	PIK3R3,MAPK1,PIK3R2,PIK3R1,IRS1
Glucagon signaling pathway	hsa04922	5	309	52	61686	19.195295	6.54E-06	1.37E-05	SIRT1,SLC2A1,FOXO1,AKT2,AKT1
p53 signaling pathway	hsa04115	5	309	54	61686	18.48435814	7.90E-06	1.62E-05	CDKN1A,CCNB1,CCNE2,THBS1,BCL2
Melanogenesis	hsa04916	5	309	54	61686	18.48435814	7.90E-06	1.62E-05	FZD6,RAF1,MAPK1,KRAS,WNT3A
Leishmaniasis	hsa05140	5	309	58	61686	17.20957482	1.13E-05	2.26E-05	PTGS2,MAPK1,NFKBIA,IRAK1,IRAK4
Protein processing in endoplasmic reticulum	hsa04141	5	309	58	61686	17.20957482	1.13E-05	2.26E-05	SSR3,BCL2,HSPA1B,UBXN2A,SEC61A1
Retrograde endocannabinoid signaling	hsa04723	5	309	60	61686	16.63592233	1.33E-05	2.65E-05	PTGS2,MAPK1,NDUFB10,KCNJ9,GNB1
Wnt signaling pathway	hsa04310	5	309	69	61686	14.46601942	2.64E-05	5.06E-05	FZD6,MMP7,LRP6,WNT3A,LGR4
IL-17 signaling pathway	hsa04657	5	309	69	61686	14.46601942	2.64E-05	5.06E-05	PTGS2,MAPK1,NFKBIA,MMP13,MMP9
Glutamatergic synapse	hsa04724	5	309	70	61686	14.259362	2.83E-05	5.39E-05	PLA2G4C,MAPK1,GRIN2B,GNB1,SLC38A2
Adrenergic signaling in cardiomyocytes	hsa04261	5	309	72	61686	13.86326861	3.25E-05	6.13E-05	BCL2,MAPK1,PIK3CG,AKT2,AKT1
Dopaminergic synapse	hsa04728	5	309	73	61686	13.67336082	3.47E-05	6.51E-05	KCNJ9,GRIN2B,GNB1,AKT2,AKT1
Parkinson disease	hsa05012	5	309	75	61686	13.30873786	3.96E-05	7.37E-05	VDAC2,PSMD12,PSMA2,NDUFB10,COX8C
Tight junction	hsa04530	5	309	76	61686	13.13362289	4.22E-05	7.74E-05	CFTR,ACTR2,ROCK1,OCLN,TJAP1
Vascular smooth muscle contraction	hsa04270	5	309	80	61686	12.47694175	5.40E-05	9.84E-05	PLA2G4C,ROCK1,RAF1,MAPK1,ADM
Hippo signaling pathway	hsa04390	5	309	82	61686	12.1726261	6.08E-05	0.000109979	FZD6,GDF5,SOX2,SMAD2,WNT3A
Basal cell carcinoma	hsa05217	4	309	31	61686	25.75884748	1.75E-05	3.45E-05	CDKN1A,FZD6,WNT3A,POLK

Thyroid cancer	hsa05216	4	309	32	61686	24.9538835	1.99E-05	3.90E-05	CDKN1A,MAPK1,KRAS,POLK
RNA transport	hsa03013	4	309	38	61686	21.01379663	3.99E-05	7.37E-05	NUP50,FXR1,SMN1,EIF2S3
Long-term potentiation	hsa04720	4	309	43	61686	18.5703319	6.53E-05	0.000117402	RAF1,MAPK1,KRAS,GRIN2B
Mitophagy - animal	hsa04137	4	309	44	61686	18.14827891	7.16E-05	0.00012686	USP8,KRAS,FOXO3,E2F1
Epithelial cell signaling in Helicobacter pylori infection	hsa05120	4	309	44	61686	18.14827891	7.16E-05	0.00012686	ATP6V0E1,NFKBIA,EGFR,HBEGF
Long-term depression	hsa04730	4	309	45	61686	17.74498382	7.82E-05	0.000137739	PLA2G4C,RAF1,MAPK1,KRAS
Pertussis	hsa05133	4	309	53	61686	15.0664957	0.000149	0.000255317	CASP7,MAPK1,IRAK1,IRAK4
Gap junction	hsa04540	4	309	59	61686	13.53430969	0.000226	0.000382478	RAF1,MAPK1,KRAS,EGFR
Rheumatoid arthritis	hsa05323	4	309	59	61686	13.53430969	0.000226	0.000382478	ATP6V0E1,VEGFA,TEK,CXCL12
Oocyte meiosis	hsa04114	4	309	60	61686	13.30873786	0.000241	0.000405523	CCNB1,CCNE2,MAPK1,PGR
Inflammatory mediator regulation of TRP channels	hsa04750	4	309	61	61686	13.09056183	0.000257	0.000429472	PLA2G4C,PIK3R3,PIK3R2,PIK3R1
Circadian entrainment	hsa04713	4	309	64	61686	12.47694175	0.00031	0.000513437	MAPK1,KCNJ9,GRIN2B,GNB1
Amoebiasis	hsa05146	4	309	65	61686	12.2849888	0.000329	0.000541468	PIK3R3,RAB5B,PIK3R2,PIK3R1
Thermogenesis	hsa04714	4	309	74	61686	10.79086854	0.000539	0.000860711	NDUFB10,KRAS,COX8C,ACSL4
Phagosome	hsa04145	4	309	77	61686	10.37044509	0.000627	0.000988192	ATP6V0E1,THBS1,RAB5B,SEC61A1
Th17 cell differentiation	hsa04659	4	309	81	61686	9.858324344	0.000759	0.001188729	MAPK1,NFKBIA,SMAD2,GATA3
Ribosome	hsa03010	3	309	9	61686	66.54368932	1.02E-05	2.09E-05	RPS5,RPL7,RPSA
Oxidative phosphorylation	hsa00190	3	309	20	61686	29.94466019	0.000133	0.000229769	ATP6V0E1,NDUFB10,COX8C
Vibrio cholerae	hsa051	3	309	27	61686	22.181229	0.00	0.000	CFTR,ATP6V0E1,SEC61A1

infection	10					77	033 3	54515 7	
Arachidonic acid metabolism	hsa005 90	3	309	28	61686	21.389043	0.00 037 2	0.000 60446 7	PLA2G4C,PTGS2,CYP2E1
Inositol phosphate metabolism	hsa005 62	3	309	30	61686	19.963106 8	0.00 045 7	0.000 73891 9	PIP5K1A,PIK3CG,IMPA1
Intestinal immune network for IgA production	hsa046 72	3	309	31	61686	19.319135 61	0.00 050 4	0.000 80997 1	CXCR4,CXCL12,TNFRSF17
Chemical carcinogenesis	hsa052 04	3	309	32	61686	18.715412 62	0.00 055 4	0.000 87946 4	PTGS2,CYP2E1,ADH1A
Antigen processing and presentation	hsa046 12	3	309	37	61686	16.186302 81	0.00 085 3	0.001 32787	KIR3DL2,KIR3DL1,HSPA1B
Ovarian steroidogenesis	hsa049 13	3	309	38	61686	15.760347 47	0.00 092 2	0.001 42771	PLA2G4C,PTGS2,LDLR
Complement and coagulation cascades	hsa046 10	3	309	43	61686	13.927748 93	0.00 132 4	0.002 02596	TFPI,CD55,CR2
Legionellosis	hsa051 34	3	309	44	61686	13.611209 18	0.00 141 6	0.002 1407	CASP7,NFKBIA,HSPA1B
Bile secretion	hsa049 76	3	309	47	61686	12.742408 59	0.00 171 5	0.002 56193	CFTR,SLC2A1,LDLR
PPAR signaling pathway	hsa033 20	3	309	50	61686	11.977864 08	0.00 205	0.003 04498	GK,ACSL4,FABP7
Th1 and Th2 cell differentiation	hsa046 58	3	309	64	61686	9.3577063 11	0.00 413 8	0.006 04301	MAPK1,NFKBIA,GATA3
Necroptosis	hsa042 17	3	309	84	61686	7.1296809 99	0.00 879 6	0.012 1532	PLA2G4C,VDAC2,BCL2
Neuroactive ligand-receptor interaction	hsa040 80	3	309	148	61686	4.0465757 02	0.03 875 5	0.048 5858	CHRNA5,GRIN2B,ADM

Supplementary Table ST5: Genes associated with cholesterol, triglyceride and lipid metabolism as well as oxidative stress and validated targets of miR-126 and miR-132 (taken from ST3A and ST3B)						
Genes	Category	MicroRNA	Term	ID		
ANXA2	cholesterol	hsa-miR-132-3p	positive regulation of receptor-mediated endocytosis involved in cholesterol transport	GO:1905602		
LRP6	cholesterol	hsa-miR-126-3p	receptor-mediated endocytosis involved in cholesterol transport	GO:0090118		
SIRT1	cholesterol	hsa-miR-126-3p	positive regulation of cholesterol efflux	GO:0010875		
NFKBIA	cholesterol	hsa-miR-126-3p	positive regulation of cholesterol efflux	GO:0010875		
CFTR	cholesterol	hsa-miR-132-3p	cholesterol transport	GO:0030301		
VDAC2	cholesterol	hsa-miR-132-3p	Cholesterol metabolism	hsa04979		
LDLR	cholesterol	hsa-miR-132-3p	receptor-mediated endocytosis involved in cholesterol transport	GO:0090118	cholesterol transport	GO:0030301
GK	triglyceride	hsa-miR-132-3p	triglyceride biosynthetic process	GO:0019432	triglyceride metabolic process	GO:0006641
ACSL4	triglyceride	hsa-miR-132-3p	triglyceride biosynthetic process	GO:0019432		
CYP2E1	triglyceride	hsa-miR-132-3p	triglyceride metabolic process	GO:0006641		
SIRT1	triglyceride	hsa-miR-126-3p	triglyceride mobilization	GO:0006642		
PIK3CG	triglyceride	hsa-miR-126-3p	negative regulation of triglyceride catabolic process	GO:0010897		
SIRT1	oxidative stress	hsa-miR-126-3p	response to oxidative stress	GO:0006979		
BCL2	oxidative stress	hsa-miR-126-3p	response to oxidative stress	GO:0006979		
PTGS2	oxidative stress	hsa-miR-132-3p	response to oxidative stress	GO:0006979		
AKT1	oxidative stress	hsa-miR-126-3p	response to oxidative stress	GO:0006979		
EGFR	oxidative stress	hsa-miR-132-3p	response to oxidative stress	GO:0006979		
STAU1	oxidative stress	hsa-miR-132-3p	cellular response to oxidative stress	GO:0034599		
HSPA1B	oxidative stress	hsa-miR-132-3p	cellular response to oxidative stress	GO:0034599		
FOXO3	oxidative stress	hsa-miR-126-3p	cellular response to oxidative stress	GO:0034599		
FOXO1	oxidative stress	hsa-miR-132-3p	cellular response to oxidative stress	GO:0034599		
PLA2G4C	lipid metabolic process	hsa-miR-132-3p	lipid metabolic process	GO:0006629		
PTGS2	lipid metabolic process	hsa-miR-132-3p	lipid metabolic process	GO:0006629		
PLAGL2	lipid metabolic process	hsa-miR-132-3p	lipid metabolic process	GO:0006629		
LDLR	lipid metabolic process	hsa-miR-132-3p	lipid metabolic process	GO:0006629		
ACSL4	lipid metabolic process	hsa-miR-132-3p	lipid metabolic process	GO:0006629		
CYP2E1	lipid metabolic process	hsa-miR-132-3p	lipid metabolic process	GO:0006629		
ETNK2	lipid metabolic process	hsa-miR-132-3p	lipid metabolic process	GO:0006629		
HACD3	lipid metabolic process	hsa-miR-132-3p	lipid metabolic process	GO:0006629		
CRKL	lipid metabolic process	hsa-miR-126-3p	lipid metabolic process	GO:0006629		
CRK	lipid metabolic process	hsa-miR-126-3p	lipid metabolic process	GO:0006629		
ANXA2	low-density lipoprotein	hsa-miR-132-3p	positive regulation of low-density lipoprotein particle receptor binding	GO:1905597		