

## SUPPLEMENTARY ONLINE DATA

## Identification of four novel serum protein biomarkers in sepsis patients encoded by target genes of sepsis-related miRNAs

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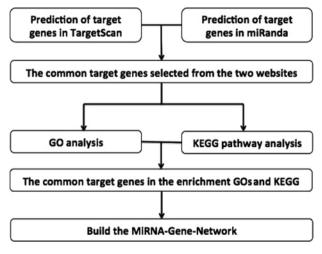


Figure S1 The flow diagram of the bioinformatics analysis

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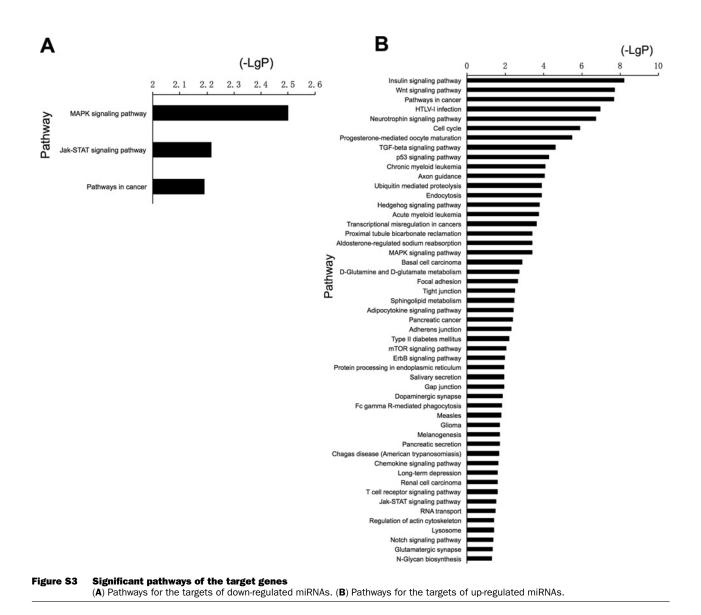
	Α	Targetge	ene Sig GO	(-LgP)		В		Targetge	ene S	Sig GO	) (-Lg	gP)		
		negative regulation of apoptosis		3 4 5	6			(	0	5	10	15	20	25
		f siRNA involved in RNA interference patterning of blood vessels					regulation of transcription	on, DNA-dependent		1			-	
		rphogenesis of a branching structure peptidyl-serine phosphorylation						cell differentiation			_			
		otein serine/threonine kinase activity bearing substrate import into nucleus					alin-like growth factor recepto			_				
	negative re	intracellular protein kinase cascade guiation of ERK1 and ERK2 cascade			positive	e regulation of	f transcription from RNA poly ubiquitin-dependent protei							
		inactivation of MAPK activity protein deubiquitination		=				ulation of translation						
		branching morphogenesis of a tube gene silencing by RNA.		=		nega	ative regulation of transcription	on, DNA-dependent						
		neuroprotection on from RNA polymerase II promoter						NA damage stimulus						
~		rmal growth factor receptor signaling multicellular organism growth						n of cell proliferation						
		insport, vesicle recycling within Goigi glucosamine catabolic process						romatin modification lar organism growth						
	pyri	midine nucleoside metabolic process selenocysteine biosynthetic process						e to insulin stimulus						
	periphe	riboflavin transport and nervous system myelin formation						mitotic cell cycle						
		regulation of Rab GTPase activity In transmembrane transporter activity						n of cell proliferation						
	camara-bine era	pative regulation of eye pigmentation a photoreceptor cell fate commitment						ulation of apoptosis		-				
	5 negi	hair folicle cell proliferation ative regulation of signal transduction				fibr	cotranslational protein targ							
	positive re	egative regulation of cell proliferation gulation of epithelial cell proliferation			protein u	ubiquitination i	involved in ubiquitin-depende							
	R	in utero embryonic development endocardium development						oblast differentiation						
	net net	epithelial cell morphogenesis inal pigment epithelium development						to glucose stimulus						
		glycolipid metabolic process syncytium formation						ophilic cell adhesion						
	positive reg	zygote asymmetric cell division lation of Schwann cell differentiation					neuron project olfactory bulb interne	tion morphogenesis						
		intein-mediated protein splicing actory bulb interneuron differentiation					axis elongation involve							
		truction involved in RNA interference vitelline membrane formation						cell adhesion						
		activation of phospholipase D activity positive regulation of myelination					central nervous s	system development						
	regulation of odon	togenesis of dentine-containing tooth cardiac muscle cell development.						eural tube formation						
		primitive hemopolesis lung growth			2	posit	tive regulation of Ras protein	axis specification						
		intestinal epithelial cell development regulation of enamel mineralization			ogo			protein folding						
		tion of transcription, DNA-dependent peptidyl-tyrosine dephosphorylation			cate			transport						
	regulation of transcripti	on from RNA polymerase II promoter			ALC: N		production of siRNA involved i							
					òlo	Wnt recep	ptor signaling pathway involve							
					Gene ontology category		positive regulation of cellular lipic	d metabolic process						
					Je c		positive regulation o							
					Ger		sy	maptic transmission						
					0			glutamate secretion						
						transformin		3 signaling pathway						
						transformin	ng growth factor beta recepto positive regulation	on of anti-apoptosis						
								on target recognition						
						neg	ative regulation of multicellul	lar organism growth						
						nega	ative regulation of ubiquitin-pr							
								2 signaling pathway						
						MyD8	gastrulation with mo 8-dependent toll-like recepto							
								onse to retinoic acid						
							toll-like receptor 4	4 signaling pathway						
								of exit from mitosis						
							steroid hormone recepto							
								vary gland cavitation						
								ion of MAPK activity						
							odontogenesis of denti	ine-containing tooth						
								oblast differentiation						
							tri othelial growth factor recepto	anslational initiation						
					2	vascular enoc		e to manganese ion						
						positive regul	lation of cyclin-dependent pre	-						
						neural tube development Notch signaling pathway								
					pancreas development N-glycan processing positive regulation of fatty acid beta-oxidation									
				positive regulation of positive chemotaxis										
					cartilage	e development	t involved in endochondral bo							
								oderm development						
								n of cell proliferation						
								n metabolic process in targeting to Golgi						
						reg	gulation of I-kappaB kinase/N							
								stone H3 acetylation						
								hemopolesis						
							response	e to insulin stimulus						

Figure S2

Significant GO terms of the target genes (A) GO terms for the targets of down-regulated miRNAs. (B) GO terms for the targets of up-regulated miRNAs.

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