

		Pos	Name	Id
mIGF-IR	ATGAAGTCTGGCTCCGGAGGAGGGTCCCCGACCTCGC---TGTGGGGGCTCGTGTTC	57	KSG	0.42
mINS-R	ATGGGCTTCGGGAGAGGATGTGAGACGACGGCTGTGCCATTGCTGGTGGCCGTGGCCCG	60		
	*** * ** *			
mIGF-IR	//ATCCGCAACGACTATCAGCAGCTGAAGCGCCTGGAAAACGCACGGTGATCGAGGGCTTC	174	DYQ	0.37
mINS-R	//ATCCGGAACAACCTGACCAGGTACATGAGCTGGAGAACTGCTCAGTCATGAGGGCCAT	177		
	***** ** *			
mIGF-IR	//CTGGTCATCTTCGAGATGACCAATCTCAAGGATATTGGGGCTTTATAATCTGAGGAACATT	408	MTN/LKD	
mINS-R	//CTGGTTATCTTCGAGATGGTCCACCTGAAGGAGCTGGGGCTTTATAACCTCATGAACATC	417	0.68/0.73	
	***** ***** *			
mIGF-IR	//TGGTCTCTCATCTTGGATGCGGTGTCCAATAACTACATTGTGGGGAACAA-GCCCCCGA-	526	LDA	0.69
mINS-R	//TGGTCCCCTATCCTGGATTCTGTGGAGGACAACACTACATTGTAAGTGAACAAAGATGACAAC	537		
	***** * ** *			
mIGF-IR	//ACCATCAACAATGAGTACAACCTACCCTGCTGGACCACAAATCGCTGCCAGAAAATGTGC	645	NNE	0.31
mINS-R	//GTCATCAATGGGCAGTTTGTGGAACGGTGTGGACACACAGTCATGTGAGAAAGTTTGC	657		
	***** *			
mIGF-IR	//CGCCAGAGCAAAGGGACATAAACACCAGGAACAACGGAGAGCGAGCTTCCTGTGAAAGT	1473	DIN	0.58
mINS-R	//CGTCAGGAGAGGAACGACATTGCCCTGAAGACCAATGGGGACCAGGCATCGTGTGAAAT	1491		
	** *			
mIGF-IR	//CCAACACGACCATGTCCAGCCGAAGCAGGAACACCACGGTAGCTGACACCTACAATATCA	2299	ADT	0.52
mINS-R	//GGAATGTGACAG---CCACCACACTCACACTTCCAGATTTCCCAACGCTCTCCTTACCA	2383		
	** *			
mIGF-IR	//CAGAGACCTTGCTGCTAGGAAGTGCATGGTAGCCGAAGATTTCACAGTCAAAATTGGAGA	3464	CMV	0.84
mINS-R	//CCGGGACCTGGCAGCTCGAACTGCATGGTTGCCCATGATTTACTGTCAAATTTGGAGA	3500		
	* *			

Figure S1. Alignment of mouse IGF-IR and INS-R mRNAs.

Clustal 2.0.12 multiple alignments of mIGF-IR (Genbank NM_010513) and mouse insulin receptor (Genbank NM_010568) were performed using the EMBL-EBI web site. Start positions refer to the translation initiation codons. For clarity, only regions with siRNA binding sites are shown and these binding sites are highlighted in gray. The LKD siRNA sequence is underlined. There is a global similarity of 0.62 between mIGF-IR and mINS-R: similarity in siRNA sites are indicated in percentages (Id).