

Supplementary Tables

Table 1. Human, Mouse and Rat miRNAs Changes during Liver Regeneration

Post-PH (hrs)	Up-regulated	No Change	Down-regulated	Total
3	198 (44%)	214 (47%)	39 (9%)	451
6	140 (28%)	199 (39%)	166 (33%)	505
12	106 (31%)	194 (57%)	40 (12%)	340
18	192 (38%)	233 (46%)	86 (17%)	511
24	40 (11%)	64 (18%)	244 (70%)	348
36	83 (20%)	232 (55%)	104 (25%)	419
48	35 (11%)	151 (47%)	133 (42%)	319
72	62 (16%)	187 (47%)	147 (37%)	396

Table 2. The Correlation Between qRT-PCR and Microarray Results

Post-PH (hrs)	Selected genes			Genome-wide	
	Microarray	Real-time	Correlation	Microarray	Correlation
3 hrs					
Up-regulated	9	6	67%	47%	31%
No change	14	12	86%	44%	38%
Down-regulated	1	1	100%	9%	9%
Total	24	19	79%	100%	78%

24 hrs	Selected genes			Genome-wide	
	Microarray	Real-time	Correlation	Microarray	Correlation
Up-regulated	3	1	33%	11%	4%
No change	3	1	33%	18%	6%
Down-regulated	16	16	100%	71%	71%
Total	22	18	82%	100%	81%

Table 3. Primers Used for qRT-PCR and Cloning

primer name	cloning	miR primers	miRNA expression
DROSHA-3'UTR-F	ataata gctagc aggaggcatcaagtgt	rno-miR-21	ccttagcttatcagactgatgtga
DROSHA-3'UTR-R	aattat ctcgag ttgtttacaagaagtttgc	rno-miR-653	gtgttgaacattctctactg
TRBP-3'UTR-F	ataata gctagc gctctctgaggagcagc	rno-let-7a	gcgtgaggtagtaggtgtatagtt
TRBP-3'UTR-R	aattat ctcgag aaaaatccacaagcagcatat	rno-miR-29a	tagcaccatctgaatcggtta
PACT-3'UTR-F	ataata tctaga atctggagcaacttaaaaaatc	rno-miR-292-5p	actcaaactgggggctcttttg
PACT-3'UTR-R	aattat ctcgag atgtttgtaattttacttaggc	rno-miR-30	tgtaaacatcctcagctggaag
let-7a-1 CLU-F	aattat aagctt tgcattgagccaaatgttc	rno-miR-376	atcgttagaggaaaatccactg
let-7a-1 CLU-R	attaat tctaga ttttgcttaactcaaatctg	rno-miR-183	tatggcactgtagaattcact
miR-15a CLU-F	aattat aagctt ggcacagaatggacttcagtt	rno-miR-411	ggg tagtagaccgtatagcgtacg
miR-15a CLU-R	attaattctagattgcaattacagattttaagagatga	rno-miR-106b	taaagtctgacagtgcagat
miR-21-F	aattat aagctt tttgtttgcttgggagga	rno-miR-107	agcagcattgtacaggctatca
miR-21-R	ttaat tctaga gaagactatccccatttctcca	rno-miR-125a-5p	tcctcgagacccttaaacctgtga
miR-25 CLU-F	aattat aagctt gcttgggctagtaaggatgc	rno-miR-93	caaagtctgtctgtagcaggtag
miR-25 CLU-R	attaat tctaga gfgcctaagggaaggttagg	rno-miR-15b	tagcagcacatcatggtttaca
miR-29 CLU-F	aattat gctagc ggcattgctctccatcaata	rno-miR-148b	gaagttctgtatacactcagg
miR-29 CLU-R	aattat ctcgag accacatgcaattcaggta	hsa-miR-106a	aaaagtcttacagtgcaggtag
miR-107-F	aattat aagctt ggcactggatgataatgaatga	rno-miR-17-5p	caaagtcttacagtgcaggtag
miR-107-R	attaat tctaga tccatgctcaactctctt	rno-miR-20b	actgcagtgtagcacttctgg
miR-125A CLU-F	aattat aagctt ggtgaggaaggcctagact	hsa-miR-424	cagcagcaattcatgtttgaa
miR-125A CLU-R	attaat tctaga ccagtggctctgggctcag	rno-miR-27a	ttcagctggctaaagtccgc
miR-424 CLU-F	aattataagcttcaaatggtgaagtataagaagtacc	rno-miR-365	taatgccctaaaaatccttat
miR-424 CLU-R	attaat tctaga ggggtccaaaatgaagcat	rno-miR-181	aacattcattgctgctgggggt
miR-653-F	aattat aagctt atgccccaatgggtatgta	rno-miR-519d	caaagtgcctcccttagagtg
miR-653-R	attaat tctaga ggcaaatagtatgccaggat	Has-miR-494	gggtgaaacatacacgggaaac
	gene expression	rno-miR-98	ggggtgaggtagtaagttgattgtt
R-DICER-F	tgagctctccacgtcattg	rno-miR-377	atcacacaaggcaacttttgg
R-DICER-R	gtacacctgccagaccact		
R-DROSHA-F	gagcgcattgattcaaggat		
R-DROSHA-R	ctcagattttgggacctgta		
R-DGCR-8-F	agacaagtgtgcagccaatg		
R-DGCR-8-R	gtctggaccaggtgaccact		
R-PACT-F	acggcatgaagaccaagaac		
R-PACT-R	ctttggctgtttggatgat		
R-TRBP-F	cggaattctgtgggagaaaa		
R-TRBP-R	cactcaggctcagttcctcaata		
R-AGO2-F	gcgagagctgctcattcagt		
R-AGO2-R	tgatccctggctgatagtc		
R-18S-F	gtgatccccgagaagtttca		
R-18S-R	ttggtgaggtcaatgtctgc		

Table 4. Candidate miRNAs Selected for Cloning

	miRNAs/cluster name	All miRNAs in the cluster		
1	let-7a-1 cluster	let-7a-1	let-7f-1	
2	miR-15a cluster	miR-15a	miR-16-1	
3	miR-15b cluster	miR-15b	miR-16-2	
4	miR-21	miR-21		
5	miR-25 cluster	miR-25	miR-93	miR-106b
6	miR-29a cluster	miR-29a	miR-29b-1	
7	miR-107	miR-107		
8	miR-125a cluster	let-7e	miR-99b	miR-125a
9	miR-424 cluster	miR-424	miR-503	
10	miR-653	miR-653		

Table 5. miRNA Changes Associated with miRNA Biogenesis Genes by Microarray

	Total	Detected	Detected		
			Up-regulated	no change	Down-regulated
Dicer	131	83 (63%)	28 (34%)	55 (66%)	0
Drosha	41	28 (68%)	10 (36%)	18 (64%)	0
Dgcr8	61	40 (66%)	15 (38%)	24 (60%)	1 (3%)
TRBP	8	8 (100%)	2 (25%)	6 (75%)	0
PACT	22	15 (68%)	9 (60%)	6 (40%)	0