SUPPLEMENTAL MATERIAL

Supplemental Methods

Materials and Methods

All animal protocols conformed to the *Guidelines for the Care and Use of Laboratory Animals* prepared by the National Academy of Sciences and published by the National Institutes of Health, and were approved by the University of Cincinnati Animal Care and Use Committee.

Regional Ischemia *In Vivo*

Male adult mice (10-12 weeks old) were anesthetized with sodium pentobarbital (90 mg/kg IP), intubated with PE 90 tubing, and ventilated by use of a mouse miniventilator (Harvard Apparatus) with room air supplemented with oxygen. ECG electrodes were placed subcutaneously, and data were recorded with a Digi-Med Sinus Rhythm Analyzer (Micro-Med). A lateral thoracotomy (1.5-cm incision between the second and third ribs) was performed to provide exposure of the left anterior descending coronary artery (LAD), while avoiding rib and sternal resection, retraction, and rotation of the heart. Vascular bundles in the vicinity were coagulated by use of a microcoagulator (Medical Industries). An 8-0 nylon suture was placed around the LAD at 2 to 3 mm from the tip of the left auricle, and a piece of soft silicon tubing (0.64 mm ID, 1.19 mm OD) was placed over the artery. All mice were subjected to a 30-minute coronary occlusion by tightening and tying the suture. Ischemia was confirmed by visual observation (cyanosis) and continuous ECG monitoring. After 24 hours of reperfusion, the aorta was cannulated, and the hearts were quick frozen in liquid N_2 for further experiments or perfused with 1% TTC (37°C, 60 mmHg) as previously described. [1, 2] The occluder, which had been left in place, was retied, and the heart was perfused with 5% phthalo blue. Hearts were cut into 5 to 6 transverse sections, with 1 section made at the site of the ligature. Infarct sizes were determined and expressed as a percentage of the region at risk.

microRNA (miR) Extraction and Quantitative Stem-Loop RT-PCR

miRs were isolated from mouse hearts (B6129SF2/JF2, 10~12-weeks old) subjected to 30-min ischemia via left anterior descending (LAD) coronary artery occlusion followed by reperfusion for 1h, 4h, or 24h or from mouse hearts (FVB/N) subjected to 45-min no-flow global ischemia and 2-h reperfusion *ex vivo*, using the miRNeasy Mini kit (Qiagen) according to the manufacturer's protocol. The concentration of RNA was determined by a NanoDrop ND-1000 Spectrophotometer (NanoDrop Tech., Rockland, DE). All stem-loop RT reactions (the supplemental Figure S3), including no-template controls and RT minus controls, were run in triplicate in a GeneAmp PCR 9700 Thermocycler (Applied Biosystems). U6 was used as an internal control. Relative expression was calculated using the comparative threshold cycle (Ct) method, as previously described.[1]

Generation of a miR-494 Transgenic Mouse Model

Transgenic (TG) mice (FVB/N) were constructed by using a 372-bp DNA fragment containing murine primary miR-494 DNA under the control of the α-myosin heavy chain promoter (α-MHCp). The following primer set including *Sal*I and *Hind*III sites (underlined) was used to generate the murine primary miR-494. Forward primer: 5'-CAG AGT CGA CTG TCA AAT TGC ACA G -3'; Reverse primer: 5'-CTGTAAGCTTAGGGAGTAGCCTCAGGCCAC-3'. Expression levels of miR-494 in TG hearts were detected by Northern blot, as previously described.[1] U6 was used as a loading control to normalize expression levels. MiR-494 probe sequence: 5'- GAG GTT TCC CGT GTA TGT TTC A-3'; U6 probe sequence: 5′-GCA GGG GCC ATG CTA ATC TTC TCT GTA TCG-3′.

Global Ischemia *Ex Vivo* and Cardiac Injury Analysis

The cellular and functional responses to I/R were assessed in mice using an isolated perfused heart model, as previously described.[1, 2] After a 30-min equilibration period, hearts were subjected to 45 min of no-flow global ischemia, followed by 60 min of reperfusion. The left ventricular end diastolic pressure (LVEDP), left ventricular developed pressure (LVDP), maximum rate of contraction (+dP/dt), and maximum rate of relaxation (–dP/dt) were monitored during this process. Cardiac injury was assessed by measuring lactate dehydrogenase (LDH) release. Perfusion effluent was collected every 10 minutes pre-ischemia and also during reperfusion. Total LDH released from the heart was determined using an *in vitro* Toxicology Assay Kit (Sigma) and expressed as units per ml of wet heart weight (U/ml/g). PK/LDH enzyme (Sigma, #P-0294) was used as a standard control. In situ DNA fragmentation was assessed using the DeadEnd Fluorometric TUNEL system (Promega), followed by staining with an anti–α-sarcomeric actin antibody (Sigma-Aldrich) and 4', 6-diamidino-2-phenylindole (DAPI) (Invitrogen).[3] TUNEL-positive (green) nuclei were counted from 10 randomly-chosen microscope fields of the midventricular section and were expressed as a percentage of total nuclei (both blue and green staining nuclei) from the same fields, using five hearts for each group and two sections for each heart. For more accurate quantification of apoptosis in the I/R hearts, DNA fragmentation was determined by a cell-death-detection ELISA kit (Roche Applied Science). Results were normalized to the standard provided in the kit and expressed as a fold increase over control. Caspase-3 activity was determined in cardiac lysates (100 µg) using Caspase-3/CPP32 Fluorometric Assay kit (BioVision).

Cell Culture and Construction of Adenoviral Vectors

HEK293 cells were cultured in Dulbecco's Modified Eagle Medium (DMEM), supplemented with 10% fetal bovine serum and 100 µg/ml penicillin/streptomycin. Primary miR-494 DNA was PCR-amplified from mouse genomic DNA using high fidelity AccuPrime Taq DNA polymerase (Invitrogen). After sequencing, the amplified fragment (372 bp) was first subcloned in pcDNA3 (Invitrogen), then inserted under the CMV promoter into the AdEasy-1/Shuttle backbone, similar to our previous construction of adenoviral vectors.[1, 4]

Preparation and Infection of Adult Rat Cardiomyocytes

Adult rat ventricular myocytes were isolated from Langendorff-perfused hearts of 6-week-old male Sprague-Dawley rats (Harlan Laboratory) at 37°C, as described before.[1, 4-6] Isolated cardiomyocytes were plated on laminin-coated dishes. After 1-2 hours, cardiomyocytes were infected with adenoviruses at a multiplicity of infection of 500 for 2 hours. For detection the expression levels of miR-494 and its target proteins, the cultured rat cardiomyocytes were harvested after 60 hours of adenoviral infection.

Simulated Ischemia/Reperfusion Treatment and Cell Survival Assay

To mimic *in vivo* I/R conditions, adenovirus-infected cardiomyocytes were cultured in ischemia buffer (1.13 mM $CaCl_2$, 5 mM KCl, 0.3 mM KH_2PO_4, 0.5 mM $MgCl_2$, 0.4 mM $MgSO_4$, 128 mM NaCl, 4 mM $NaHCO_3$, 10 mM HEPES, pH 6.8), and placed into a hypoxic chamber (37°C, 1% O_2, 20% CO_2 and 79% N_2) for 1-h, followed by reperfusion for 3-h under normal culture conditions, as previously described.[1] Cardiomyocyte cell viability assessment was performed with the CellTiter 96 AQueous One Solution Cell Proliferation Assay Kit (Promega), per manufacturer's instructions. DNA fragmentation and caspase-3 activity were determined as described above.

Western Blot Analysis

Protein samples were extracted from hearts or cultured cells, using the procedures described in detail elsewhere.[1,5,7] Protein samples (100μg) were fractionated by SDS-PAGE. Binding of the primary antibody was detected by peroxidase-conjugated secondary antibodies and enhanced chemiluminescence (Amersham). The corresponding bands were quantified by densitometry. The antibodies used in this study were as follows: rabbit anti-ROCK1 (H85) (1:200 dilution), rabbit anti-PTEN (A2B1) (1:300 dilution), rabbit anti-ILF (M179) (1:200 dilution) (Santa Cruz Biotech Inc); rabbit anti-FGFR2 (1:300 dilution), rabbit anti-CaMKIIδ (1:1000 dilution), and rabbit anti-apoptosis inhibitor 5 (Api5) (1:300 dilution) (Abcam Inc); rabbit anti-Akt and its phosphorylation ($pS^{473}Akt$ and $pT^{308}Akt$) antibodies (1:1000 dilution), rabbit anti-BAD and its phosphorylation (Ser136) (1:250 dilution), rabbit anti-Bcl-2 and Bcl-xL (1:500 dilution), (Cell Signaling Technology, Inc.). α-actin (1:1000 dilution, Sigma-Aldrich) was used as an internal control.

Luciferase Reporter Assay for miR-494 targets

For luciferase reporter experiments, a ROCK1, PTEN, CAMKIIδ, FGFR2, LIF, or Api5 3'-UTR segment of ~120 bp and its respective mutant was amplified by foot-print two-step PCR (supplemental Figure S1) and inserted into the pMIR-REPORT™ luciferase miRNA expression reporter vector (Ambion) at sites of *Spe*I and *Hind*III (supplemental Figure S2). HEK293 cells were cotransfected in 12-well plates using DharmaFECT Duo Transfection Reagent (Thermo Fisher Scientific Inc) according to the protocol of the manufacturer, with 0.4 μg of the 3'-UTR luciferase reporter vector and 0.08 μg of the control vector pMIR-β-gal (Ambion, Inc.). For each well, 100 nM mimic miR-494 or mimic miR control (Thermo Fisher Scientific Inc) was used. Cell lysates were prepared 48-h later. Luciferase activity was measured, using a Monolight 3010 luminometer (Pharmingen), and expressed as relative light units using a luciferase assay kit (Promega). β-galactosidase activity was measured with a commercially available kit (Promega). 3'UTR activity of each construct was expressed as the ratio of luciferase/β-galactosidase activity. All transfections were performed in triplicate from three independent experiments.

In Vivo Administration of AntagomiR-494

Chemically modified antisense oligonucleotides (antagomiR) have been used to inhibit microRNA expression in vivo [1, 8-10]. AntagomiRs were synthesized by Dharmacon (www.dharmacon.com). Sequences are 5'—$g_Sa_Sgguuucccguguauguu_Su_Sc_Sa_S$—Chol-3' (antagomiR-494); 5'—$g_Sa_Sgguuucccgugu\underline{uacug_Sg_Sa_S}c_S$—Chol-3' (antagomiR-494 mutant as a control). Lower case letters represent 2′-O-Methyl-modified oligonucleotides, subscript 's' represents a phosphorothioate linkage, 'Chol' represents linked cholesterol, and underlined letters are a mutated seed sequence. AntagomiR oligonucleotides were deprotected, desalted and purified by high-performance liquid chromatography. FVB/N male mice (6-week old) received either antagomiR-494, or mutant antagomiR-494, or a comparable volume of saline (200 μl) through three consecutive daily injections via tail vein (3x40 mg/kg body weight). Global no-flow ischemia/reperfusion was performed at the third day after final injection.

mRNA Microarray Analysis for miR-494 hearts

Total RNA was isolated from miR-494 mouse hearts and WT hearts using a RNeasy Mini Kit (Qiagene). Affymetrix Gene Chip Mouse Gene 1.0 ST array (#901168) (www.affymetrix.com) was performed at the University of Cincinnati Genomics and Microarray Core. The microarray data was analyzed using statistical software R and the limma package of Bioconductor[11] with custom CDF downloaded from the previous literature [12]. Data preprocessing, including background correction and normalization, was performed using RMA. Array quality was assessed using the arrayQualityMetrics package of Bioconductor [13]. Estimated fold change for each comparison was calculated using ANOVA, and resulting t-statistics were modified using an intensity-based empirical Bayes method (IBMT) [14]. Genes with p-value < 0.05 were considered significantly differentially expressed. The list of miR-494 predicted targets was downloaded from TargetScan[15].

Statistical Analysis

Data are expressed as mean ± SD. ANOVA was conducted first across all investigated groups in Fig.3 and Fig. 8C-E. We performed Shapiro-Wilk test for the normality, and there was no evidence of deviation from normality for all variables. Then, Post hoc pairwise tests were performed with assessment of statistical significance after Bonferroni correction of the P values. In these figures, alpha level =0.05, only a p value from pairwise test for each time point less than $0.05/6=0.008$ would be considered significant. $P< 0.05$ was considered statistically significant, when Student t-test was used for two-group comparisons in other figures.

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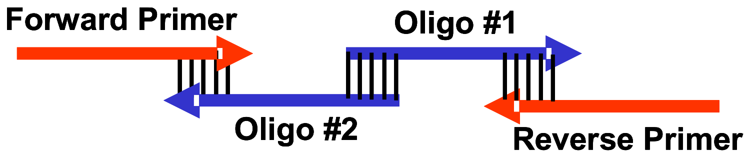
Supplemental Figures

Figure S1: Diagram of foot-print two-step PCR



Step 1: extend the overlapping oligos (mixture of forward primer, reverse primer, oligo#1, and oligo#2) using Taq under the following conditions: 94° C for 15 s, 55° C for 30 s, 72° C for 50 s, for a total of 5 cycles, then 72° C extension for 5 min.

Step 2: Take 2 μl of the Step 1 PCR product as template, add the forward primer and reverse primer under same PCR conditions for a total of 30 cycles, then 72° C extension for 5 min.

Figure S2: Diagram of Luciferase-Reporter Plasmid Construction

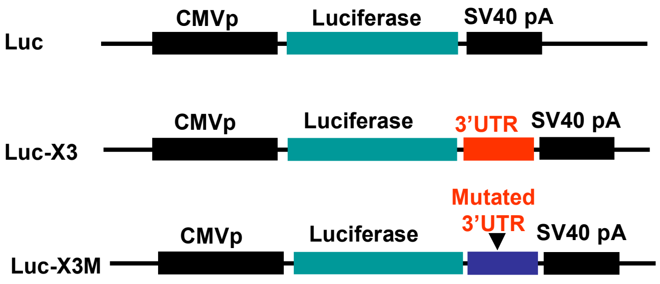
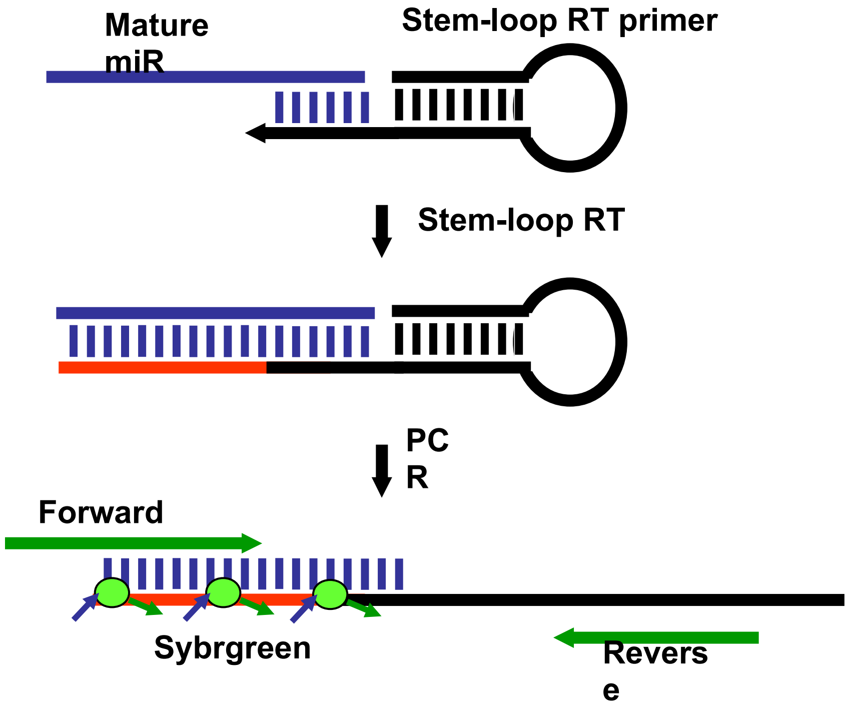


Figure S2: A segment of Gene X (ROCK1, PTEN, CaMKIIδ, FGFR2, LIF, and Api5) 3' UTR or its mutated segment was cloned downstream of the luciferase-coding region.

Figure S3: Diagram of Stem-Loop RT-PCR



Supplemental Figure S4

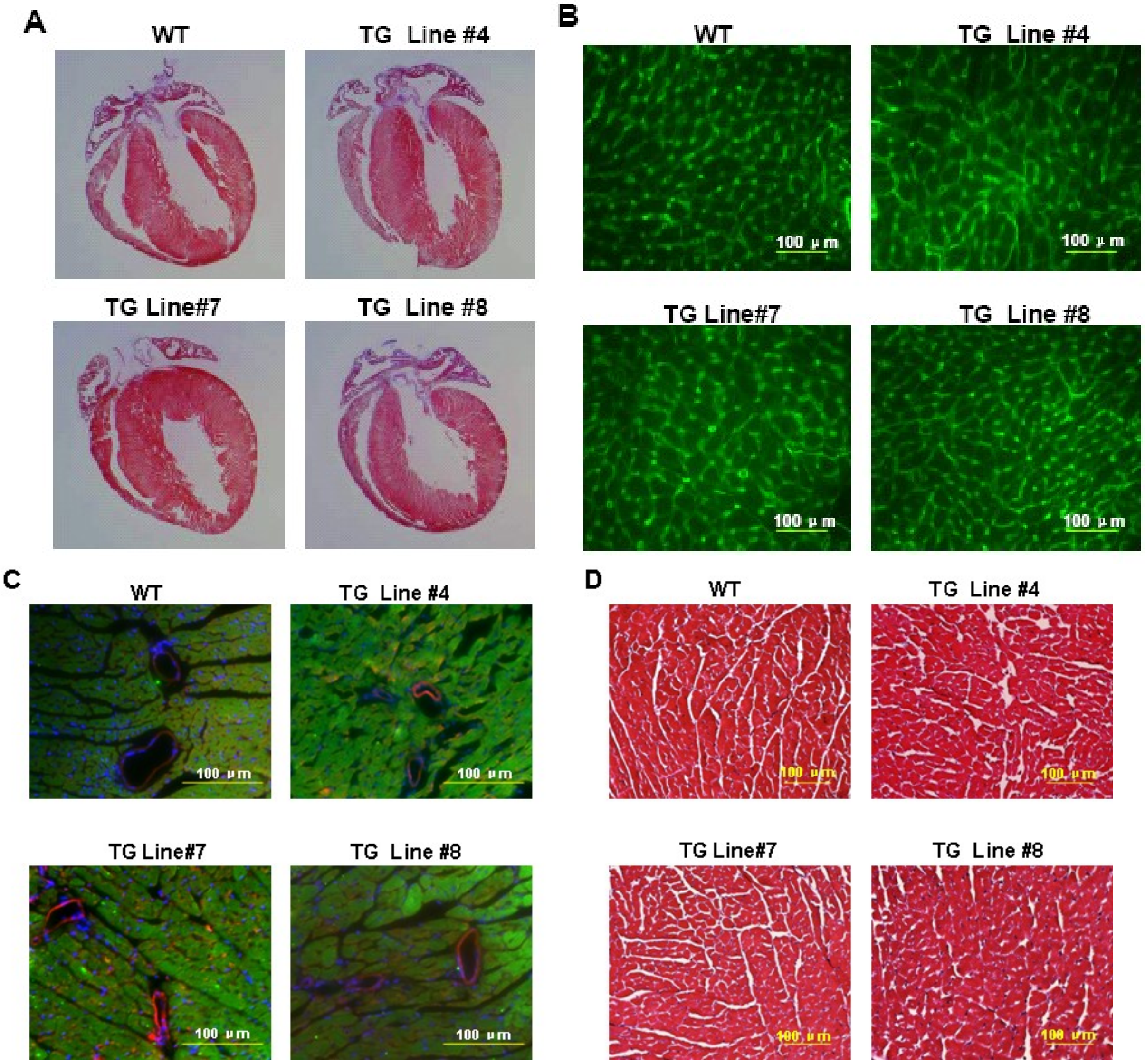


Figure S4 Models of cardiac-specific overexpression of miR-494 showed no apparent cardiac morphological abnormalities. (A) Representative global heart section photographs from WT and miR-494 TG mice. (B) Immunostaining of heart sections from WT and TG mice with fluorescence labeled wheat germ agglutinin (Oregon Green 488 conjugated WGA, 1:50). (C) Blood vessels were stained for CD-31 (capillary density) in heart sections of WT and miR-494 TG mice. Green: α-Actin (1:50), Alexa Fluor® 488 goat anti-mouse 2nd Ab (1:250); red: CD31 (1:100, purchased from BioLegend), Alexa Fluor® 594 goat anti-rabbit 2nd Ab (1:250); blue: DAPI. Original magnification: x400. (D) Representative images of Masson's Trichrome staining.

Supplemental Figure S5

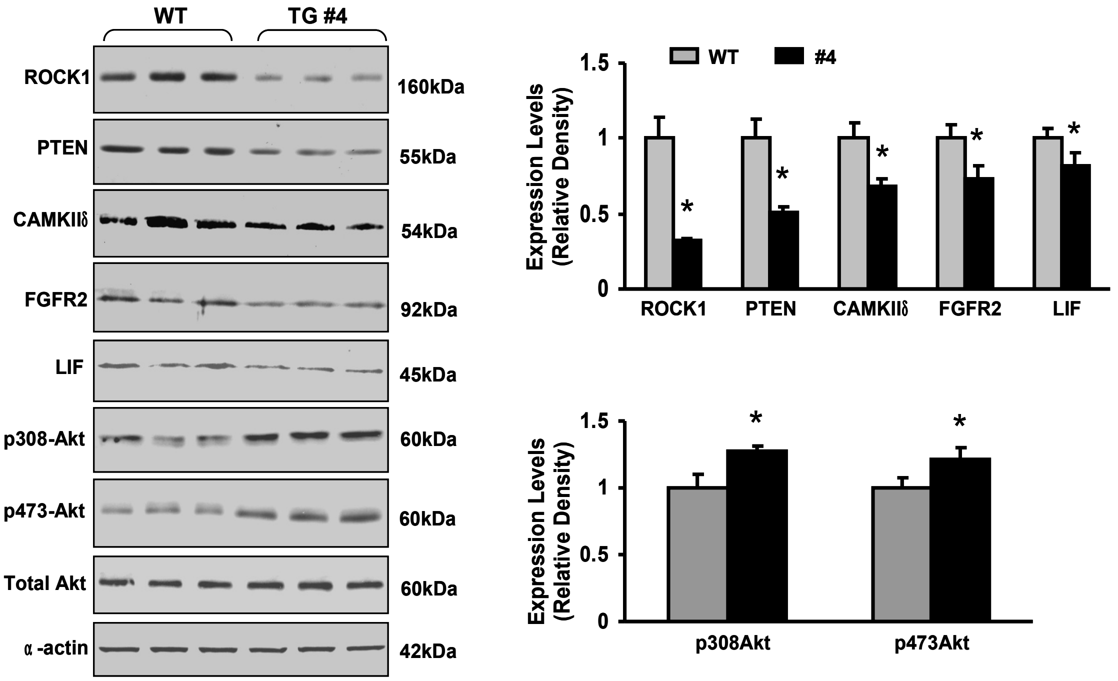


Figure S5 Overexpression of miR-494 downregulated protein levels of ROCK1, PTEN, CAMKIIδ, FGFR2, and LIF. Consequently, Akt was activated, as evidenced by the increased phosphorylated Akt (T308 and S473). n=3 hearts; * $p<0.05$ vs WT controls.

Supplemental Figure S6: Sequence alignments of miR-494 and 3'-UTR of PTEN, ROCK1, CAMK2D, FGFR2, LIF, and Api5

3'-UTR of PTEN

Position 2800-2806 of PTEN 3' UTR

mmu-miR-494

```
5'...UACCGGCAGCAUCAAAUGUUUC
A...
                       |||||||
3'   CUCCAAAGGGCACAUACAAAGU
```

```
    ......2780....... 2790........2800........2810
Mmu AAGUGGAGUUUACCGGCAGCAUCAAAUGUUUCAGCUUU
Hsa AAGUGGAGUUUACCGGCAGCAUCAAAUGUUUCAGCUUU
Rno AAGUGGAGUUUACCGGCAGCAUCAAAUGUUUCAGCUUU
Cfa AAGUGGAGUUUACCGGCAGCAUCAAAUGUUUCAGCUUU
```

3'-UTR of ROCK1

Position 1393-1399 of ROCK1 3' UTR

mmu-miR-494

```
5'   ...UCUAGGGUGAUAUGCAUGUUUCA...
                       |||||||
 3'     CUCCAAAGGGCACAUACAAAGU
```

```
    ........1380.........1390........1400.........
Mmu CUUCUCUAGGGUGAUA-UGCAUGUUUCAAGUGGUAUU
Hsa CGUCUCUAGGAUGAUA-UGCAUGUUUCAAGUGGUAUU
Rno CUUCUCUAGGGUGACA-UGCAUGUUUCAAGUGGUAUU
Cfa UGUCUCUAGGAUGAUA-UGCAUGUUUCAAGUGGUAUU
```

3'-UTR of CAMK2D

Position 116-122 of CAMK2D 3' UTR

mmu-miR-494

```
5'    ...CUCUCCUCUUCAUGCAUGUUUCU...
                        |||||||
 3'      CUCCAAAGGGCACAUACAAAGU
```

```
    100............110........120.........130.........140
Mmu CCUCUCCUC-- - -UUCAUGCAUGUU-UCUGAGUGCAUGAAGUUGUGAA
Hsa CCUCUCCUCCUCUUCAUGCAUGUU-UCUGAGUGCAUGAAGUUGUGAA
Rno CCUCUCCUC------UUCAUGCAUGUU-UCUGAGUGCAUGAAGUUGUGAA
Cfa CCUCUCCCCC--CUUCAUGCAUGUU-UCUGAGUGCAUGAAGUUGUGAA
```

3'-UTR of FGFR2

```
Position 1446-1452 of FGFR2 3' UTR   5'  ...AUACUGACAAUAAAAAUGUUUCU...
                                                          |||||||
mmu-miR-494                          3'     CUCCAAAGGGCACAUACAAAGU

          1420.......1430........1440........1450........1460
     Mmu  UGUUAAUUUUUAUACUGACAAUAAAAA-UGUUUCUACAGAUAUUA
     Hsa  UGUUAAUUUUUAUACUGACAAUAAAAA-UGUUUCUACAGAUAUUA
     Rno  UGUUAAUUUUUAUACUGACAAUAAAAA-UGUUUCUACAGAUAUUA
     Cfa  UGUUAAUUUUUAUACUGACAAUAAAAA-UGUUUCUACAGAUAUUA
```

3'-UTR of LIF

```
Position 2934-2940 of LIF 3' UTR   5'   ...AUGUACCCUGUGGGAAUGUUUCA...
                                                          |||||||
mmu-miR-494                        3'      CUCCAAAGGGCACAUACAAAGU

          ...........2920........2930........2940........2950......
     Mmu  UUUGAUGAAUGUACCCUGUGGGAAUGUUUCAUACUGACAGAUUAUUU
     Hsa  UUUGAUGAAUGUACCCUGUGGGGAUGUUUCAUACUGACAGAUUAUUU
     Rno  UUUGAUGAAUGUACCCUGUGGGAAUGUUUCAUACUGACAGAUUAUUU
     Cfa  UUUGAUGAAUGUACCCUGUGGGAAUGUUUCAUACUGACAGAUUAUUU
```

3'-UTR of Api5

```
Position 1269-1275 of API5 3' UTR   5'  ...CUGUUCUUCAUUUGAAUGUUUCA...
                                                          |||||||
mmu-miR-494                         3'     CUCCAAAGGGCACAUACAAAGU

          .........1260.........1270.........1280........
     Mmu  CUCUGUUCUU-CAUUUGAAUGUUU-C--ACACA-UUUUUGUU
     Hsa  CUUUGUUCUG-CAUUUGAAUGUUU-C--GUAUA-UUUUUGUU
     Rno  CUCUGUUCUU-CAUUUGAAUGUUU-C--AUAAA-UUUUUGUU
     Cfa  CUUUGCUCUG-CAUUCGAAUGUUU-C -AUAUA-UUUUUGUU
```

Figure S6: The putative miR-494-binding sites within these targets are conserved among mammalian species (mouse, human, rat, and dog), where the crucial seed regions are highlighted.

List of Primers for 3’-UTR Segment (Seed Sequence is Underlined) and miR-494

ROCK1 3’UTR
Forward: 5’-GAC AAC TAGT GCA GTAATGTGTA TC AAATAAGC AC
Reverse: 5’- CTG TAA GCT T TC AATACCAC
Oligo #1: 5’-GCA TATCACCCTAGAGAAGATCGGTTTTCCAGTGCTTATTTGA
Oligo#2: 5’-CTAGGGTGATA TGC**ATGTTTC** AAGTGGTATT GAAAGC
Mutated Oligo#2: 5’-CTAGGGTGATA TGC**TACCAAT** AAGTGGTATT GAAAGC

PTEN 3’UTR
Forward: 5’-GAC A AC TAG T GT CACCATTCTT TGCTGTGGCAC
Reverse: 5’-- CTG T AA GCT T GTAACTTGTAACCTAC
Oligo #1: 5’ –GATGCTG CCGGTAAACTCCACTTAAGTTTATAACCTGTGCCACAGC
Oligo #2:
5’- GTTTACCGG CAGCATCAA**ATGTTTC**AGCTTTAAAAATAAAAGTAGGT TAC
Mutated Oligo #2:
5’- GTTTACCGG CAGCATCAA**T** **ACGAGA**AGCT TTAAAAATAA AAGTAGGTTAC

CaMKIIδ 3’UTR
Forward: 5’-GAC AAC TAG T CAACAGTGCC ACTTC TTCAT TCTG
Reverse: 5’-- CTG TAA G CT T CAC AAC TTC ATG CAC
Oligo #1:
5’-GTCCCA GGATC ACCCG CCTGGTGCCT TGAGGACAGAATGAAGAAG
Oligo #2:
5’-GATCC TGGGACGTCC TCTCCTCTTC ATGCATGTTT CTGAGTGCATGAAG
Mutated Oligo#2 :
5’-GATCC TGGGACGTCC TCTCCTCTTC ATGCCACTAC ATGAGTGCATGAAG

FGFR2 3’UTR
Forward: 5’ -GACA ACTAGT TGTATGCAGA TTACACTG
Reverse: 5’-CTGT AAGCTTGT TAACATTAAT ATCTGTAGAA ACATTTTTATTGTC
Oligo #1 :
5’- G AGAAAGTATT TAATAAAACC TGTTAATTTT TATACTGACA ATAAAA **ATGTTTC** TACAG
Mutated Oligo #1:
5’- G AGAAAGTATT TAATAAAACC TGTTAATTTT TATACTGACA ATAAAA**CAGCCAC**TACAG
Oligo#2 :
5’ –GGTTTTATTA AATACTTTCT CCAATTCCAA AA CACATAAA AT CAGTGTAATCTGC

LIF 3’UTR
Forward: 5’- GACA ACTAGT TGGAAGGGA CTTGGCCTTG
Reverse: 5’ – CTGT AAGCTT ATAATCTGTC
Oligo #1: 5’-GAATGTACC CTGTGGGA**AT** **GTTTC**ATACT GACAGATTAT AAGC

Mutated Oligo #1:
5’-GAATGTACC CTGTGGGA**CA** **CGACT**ATACT GACAGATTAT AAGC
Oligo#2: 5’- CAGGGTACATTCATCAAAGAGGAATTTGTCACCCAAGGCCAAGTC

Api5 3’UTR

Forward: 5’-GACA ACTA G TTCGTGGAGT GTCTCATG
Reverse: 5’-CTGT AAGCTTGGA AGATTAACTG TG
Oligo #1: 5’- G ACTCTGTTCT TCATTTGA**ATGTTTC**ACACA TTTTTGTTCA CAGTTAATCT
Mutated Oligo#1: 5’- GACTCTGTTCT TCATTTGA**CCAACGC**ACACA TTTTTGTTCA CAGTTAATCT
Oligo#2: 5’-GAAGCCAGAGT CTGGGCTACT AAAAATGCCCAACAT GAGAC AC

Stem-Loop RT-PCR Primers for miR-494

miR-494/stem-loop RT primer:
5’-GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC gaggtt—3’
Forward: 5’— GCAGAG tga aac ata cac gg
Reverse: 5' - GTGCAGGGTCCGAGGT-3'

Supplemental Table S1. Upregulated genes in miR-494 hearts (292, P<0.05)

Probe ID	Gene ID	Symbol	Name	Intensity	Fold	P value	Std.err
20301_at	20301	Ccl27a	chemokine (C-C motif) ligand 27A	181.2	1.597	0.0001	0.11
238756_at	238756	Gm4936	predicted gene 4936	81.01	1.651	0.0002	0.12
258769_at	258769	Olfr508	olfactory receptor 508	20.42	1.345	0.0007	0.08
623475_at	623475	Gm6434	predicted gene 6434	43.72	1.453	0.0009	0.1
629079_at	629079	Vmn2r56	vomeronasal 2, receptor 56	24.62	1.383	0.0016	0.1
258783_at	258783	Olfr920	olfactory receptor 920	28.15	1.366	0.0018	0.1
433216_at	433216	Gm5510	predicted gene 5510	40.15	1.402	0.002	0.1
208111_at	208111	C330019L16Rik	RIKEN cDNA C330019L16 gene	58.03	1.547	0.002	0.14
667147_at	667147	Gm8481	ribosomal protein L7a pseudogene	66.37	1.369	0.0022	0.1
620078_at	620078	C130026I21Rik	RIKEN cDNA C130026I21 gene	34.05	1.482	0.0024	0.13
74568_at	74568	Mlkl	mixed lineage kinase domain-like	133.9	1.355	0.0024	0.1
667597_at	667597	BC023105	cDNA sequence BC023105	52.68	1.644	0.0028	0.18
258752_at	258752	Olfr583	olfactory receptor 583	10.41	1.4	0.0029	0.12
212090_at	212090	Tmem60	transmembrane protein 60	148.9	1.329	0.0035	0.1
66358_at	66358	2310004I24Rik	RIKEN cDNA 2310004I24 gene	235.4	1.23	0.0035	0.08
171252_at	171252	V1rh9	vomeronasal 1 receptor, H9	34.8	1.431	0.0039	0.13
15957_at	15957	Ifit1	interferon-induced protein with tetratricopeptide repeats 1	65.54	1.346	0.0041	0.1
22441_at	22441	Xlr	X-linked lymphocyte-regulated complex	33.91	1.619	0.0042	0.18
225594_at	225594	Gm4841	predicted gene 4841	24.69	1.261	0.005	0.08
66206_at	66206	1110059E24Rik	RIKEN cDNA 1110059E24 gene	248.9	1.249	0.0053	0.09
665434_at	665434	Gm7634	predicted gene 7634	15.87	1.346	0.0054	0.12
631323_at	631323	Gm12250	predicted gene 12250	170.9	1.486	0.0055	0.16
258898_at	258898	Olfr1203	olfactory receptor 1203	17.49	1.238	0.0057	0.08
628705_at	628705	Gm6907	predicted gene 6907	36.86	1.396	0.0065	0.13
12314_at	12314	Calm2	calmodulin 2	2248	1.184	0.0068	0.08
73736_at	73736	Fcf1	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	430.6	1.232	0.0069	0.09
54123_at	54123	Irf7	interferon regulatory factor 7	132.7	1.353	0.008	0.13
52653_at	52653	Nudcd2	NudC domain containing 2	582.7	1.216	0.008	0.09
235459_at	235459	Gtf2a2	general transcription factor II A, 2	697.3	1.177	0.0081	0.08
266690_at	266690	Cyb5r4	cytochrome b5 reductase 4	405.1	1.24	0.0086	0.1
76630_at	76630	Stambpl1	STAM binding protein like 1	164.1	1.259	0.0086	0.1
382236_at	382236	Brwd3	bromodomain and WD repeat domain containing 3	218.9	1.193	0.0088	0.08
209786_at	209786	Vmn2r-ps88	vomeronasal 2, receptor, pseudogene 88	16.67	1.297	0.0089	0.11
11498_at	11498	Adam4	a disintegrin and metallopeptidase domain 4	111.6	1.362	0.009	0.13
545938_at	545938	Zfp607	zinc finger proten 607	142.2	1.249	0.0095	0.09
76273_at	76273	Ndfip2	Nedd4 family interacting protein 2	580.9	1.178	0.0097	0.08
17993_at	17993	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	1885	1.21	0.0097	0.1
54364_at	54364	Rpp30	ribonuclease P/MRP 30 subunit (human)	362	1.193	0.0098	0.08

319800_at	319800	C730048C13Rik	RIKEN cDNA C730048C13 gene	10.5	1.273	0.0102	0.11
100041449_at	1E+08	Cyp3a59	cytochrome P450, subfamily 3A, polypeptide 59	24.41	1.325	0.0104	0.12
22717_at	22717	Zfp59	zinc finger protein 59	166.2	1.364	0.0104	0.14
22773_at	22773	Zic3	zinc finger protein of the cerebellum 3	41.29	1.231	0.0104	0.08
73233_at	73233	3110048L19Rik	zinc finger pseudogene	166.9	1.206	0.0107	0.08
17022_at	17022	Lum	lumican	1814	1.362	0.0107	0.15
66202_at	66202	1110059G10Rik	RIKEN cDNA 1110059G10 gene	246	1.208	0.0108	0.09
19889_at	19889	Rp2h	retinitis pigmentosa 2 homolog (human)	327.7	1.194	0.0108	0.08
68212_at	68212	Tmbim4	transmembrane BAX inhibitor motif containing 4	2065	1.156	0.0111	0.08
109054_at	109054	Pfdn4	prefoldin 4	164.6	1.219	0.0113	0.09
76561_at	76561	Snx7	sorting nexin 7	297.5	1.198	0.0114	0.09
71538_at	71538	Fbxo9	f-box protein 9	537.5	1.199	0.0114	0.09
20823_at	20823	Ssb	Sjogren syndrome antigen B	974.4	1.16	0.0115	0.08
16145_at	16145	Igtp	interferon gamma induced GTPase	251.1	1.616	0.0115	0.23
75623_at	75623	1700029F09Rik	RIKEN cDNA 1700029F09 gene	344.2	1.213	0.0115	0.09
66226_at	66226	Trappc2	trafficking protein particle complex 2	1247	1.251	0.0116	0.11
223499_at	223499	Dcaf13	DDB1 and CUL4 associated factor 13	389.1	1.193	0.0117	0.09
97112_at	97112	Nmd3	NMD3 homolog (S. cerevisiae)	993.4	1.172	0.0118	0.08
240880_at	240880	Scyl3	SCY1-like 3 (S. cerevisiae)	220.8	1.223	0.0119	0.09
664952_at	664952	Gm7422	predicted gene 7422	25.56	1.313	0.0126	0.12
100043759_at	1E+08	Gm14335	predicted gene 14335	81.29	1.451	0.0126	0.17
22700_at	22700	Zfp40	zinc finger protein 40	110.6	1.256	0.0131	0.1
269831_at	269831	Tspan12	tetraspanin 12	1507	1.188	0.0131	0.09
73112_at	73112	3110003A17Rik	RIKEN cDNA 3110003A17 gene	638.2	1.663	0.0134	0.25
106869_at	106869	Tnfaip8	tumor necrosis factor, alpha-induced protein 8	580.5	1.225	0.0136	0.1
15401_at	15401	Hoxa4	homeo box A4	135.5	1.194	0.0138	0.08
72748_at	72748	Hdhd3	haloacid dehalogenase-like hydrolase domain containing 3	170.9	1.276	0.0141	0.12
258924_at	258924	Olfr376	olfactory receptor 376	14.13	1.227	0.0148	0.1
19167_at	19167	Psma3	proteasome (prosome, macropain) subunit, alpha type 3	434.8	1.212	0.0148	0.1
636177_at	636177	Rhox4f	reproductive homeobox 4F	30.72	1.46	0.0151	0.18
12540_at	12540	Cdc42	cell division cycle 42 homolog (S. cerevisiae)	5273	1.132	0.0151	0.08
66836_at	66836	Tmem223	transmembrane protein 223	1991	1.161	0.0157	0.09
13110_at	13110	Cyp2j6	cytochrome P450, family 2, subfamily j, polypeptide 6	231.9	1.194	0.0158	0.09
71690_at	71690	Esm1	endothelial cell-specific molecule 1	77.2	1.23	0.0158	0.09
546500_at	546500	Gm12211	ribosomal protein L9 pseudogene	27.38	1.271	0.0166	0.11
67168_at	67168	Lpar6	lysophosphatidic acid receptor 6	527.5	1.32	0.0166	0.15
56221_at	56221	Ccl24	chemokine (C-C motif) ligand 24	147.9	1.215	0.0166	0.09
26888_at	26888	Clec4a2	C-type lectin domain family 4, member a2	39.5	1.271	0.0167	0.11
237411_at	237411	B230315N10Rik	RIKEN cDNA B230315N10 gene	1298	1.169	0.0168	0.09
15042_at	15042	H2-T24	histocompatibility 2, T region locus 24	364.3	1.208	0.0168	0.1
66061_at	66061	Tctex1d2	Tctex1 domain containing 2	199.9	1.218	0.0169	0.1
19106_at	19106	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	240.3	1.193	0.0172	0.09

257956_at	257956	Olfr1307	olfactory receptor 1307	13.25	1.25	0.0172	0.11
227615_at	227615	C730025P13Rik	RIKEN cDNA C730025P13 gene	418.9	1.169	0.0173	0.08
449631_at	449631	Gm5775	predicted gene 5775	280.7	1.184	0.0176	0.09
18968_at	18968	Pola1	polymerase (DNA directed), alpha 1	180.1	1.177	0.0179	0.08
19988_at	19988	Rpl6	ribosomal protein L6	98.49	1.251	0.018	0.1
16616_at	16616	Klk1b21	kallikrein 1-related peptidase b21	26.47	1.327	0.0182	0.14
107701_at	107701	Sf3b4	splicing factor 3b, subunit 4	93.19	1.256	0.0185	0.11
383619_at	383619	Aim2	absent in melanoma 2	90.3	1.245	0.0185	0.1
630294_at	630294	H2-t9	MHC class Ib T9	29.23	1.477	0.0187	0.2
22381_at	22381	Wbp5	WW domain binding protein 5	303.3	1.376	0.0187	0.17
214804_at	214804	Syde2	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	583.2	1.154	0.0187	0.08
66310_at	66310	Dpy30	dpy-30 homolog (C. elegans)	863.4	1.164	0.0194	0.09
13482_at	13482	Dpp4	dipeptidylpeptidase 4	231.3	1.281	0.0194	0.13
68735_at	68735	Mrps18c	mitochondrial ribosomal protein S18C	3086	1.144	0.0197	0.09
56220_at	56220	Zfp386	zinc finger protein 386 (Kruppel-like)	557	1.151	0.02	0.08
330908_at	330908	Opcml	opioid binding protein/cell adhesion molecule-like	68.33	1.239	0.0203	0.1
258659_at	258659	Olfr732	olfactory receptor 732	27.08	1.219	0.0207	0.09
66195_at	66195	Lce1g	late cornified envelope 1G	12.29	1.178	0.0208	0.08
68036_at	68036	Zfp706	zinc finger protein 706	700.9	1.165	0.0211	0.09
68404_at	68404	Nrn1	neuritin 1	138.9	1.379	0.0215	0.17
59048_at	59048	C1galt1c1	C1GALT1-specific chaperone 1	386.1	1.16	0.0216	0.08
101772_at	101772	Ano1	anoctamin 1, calcium activated chloride channel	195.8	1.175	0.0218	0.08
258089_at	258089	Olfr304	olfactory receptor 304	11.28	1.185	0.022	0.09
338346_at	338346	Gpr21	G protein-coupled receptor 21	76.25	1.286	0.022	0.12
17936_at	17936	Nab1	Ngfi-A binding protein 1	533	1.166	0.0221	0.09
620603_at	620603	Gm6166	predicted gene 6166	472.4	1.366	0.0223	0.17
228094_at	228094	Cerkl	ceramide kinase-like	32.65	1.203	0.0225	0.09
67371_at	67371	Gtf3c6	general transcription factor IIIC, polypeptide 6, alpha	453.2	1.174	0.0227	0.09
258519_at	258519	Olfr859	olfactory receptor 859	18.24	1.254	0.023	0.12
621080_at	621080	AI429214	expressed sequence AI429214	32.34	1.259	0.0231	0.12
668724_at	668724	Gm9320	predicted gene 9320	3469	1.224	0.0232	0.12
233276_at	233276	Tubgcp5	tubulin, gamma complex associated protein 5	225.7	1.168	0.0235	0.08
67628_at	67628	Anp32b	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	2286	1.202	0.0236	0.11
52700_at	52700	Txndc17	thioredoxin domain containing 17	1214	1.15	0.0236	0.09
331004_at	331004	Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	218.5	1.236	0.0237	0.12
19941_at	19941	Rpl26	ribosomal protein L26	1350	1.182	0.0237	0.1
217578_at	217578	Baz1a	bromodomain adjacent to zinc finger domain 1A	207.8	1.191	0.0244	0.09
228662_at	228662	Btbd3	BTB (POZ) domain containing 3	461.2	1.161	0.0247	0.09
241732_at	241732	Tspyl3	TSPY-like 3	107.4	1.24	0.025	0.11
74245_at	74245	Ctbs	chitobiase, di-N-acetyl-	138.9	1.168	0.0253	0.08
68705_at	68705	Gtf2f2	general transcription factor IIF, polypeptide 2	179	1.166	0.0253	0.08
224585_at	224585	Zfp160	zinc finger protein 160	267.4	1.173	0.0253	0.09

67606_at	67606	Fibin	fin bud initiation factor homolog (zebrafish)	245.1	1.374	0.0254	0.18
66440_at	66440	Cdc26	cell division cycle 26	918.5	1.141	0.0254	0.08
67005_at	67005	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K	337.3	1.157	0.0255	0.08
16182_at	16182	Il18r1	interleukin 18 receptor 1	26.94	1.229	0.0258	0.11
404308_at	404308	Olfr118	olfactory receptor 118	23.77	1.239	0.0259	0.11
211550_at	211550	Tifa	TRAF-interacting protein with forkhead-associated domain	111.5	1.224	0.026	0.1
258606_at	258606	Olfr973	olfactory receptor 973	12.95	1.166	0.026	0.08
66787_at	66787	4933433P14Rik	RIKEN cDNA 4933433P14 gene	319.7	1.154	0.0262	0.08
13051_at	13051	Cx3cr1	chemokine (C-X3-C) receptor 1	217	1.219	0.0262	0.11
666113_at	666113	Gm7935	predicted gene 7935	130	1.273	0.0263	0.13
107868_at	107868	Usp9y	ubiquitin specific peptidase 9, Y chromosome	14.73	1.193	0.0264	0.09
13197_at	13197	Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	668.4	1.174	0.0264	0.1
269623_at	269623	C030048B08Rik	RIKEN cDNA C030048B08 gene	233.5	1.154	0.0266	0.08
73692_at	73692	2410089E03Rik	RIKEN cDNA 2410089E03 gene	258.7	1.166	0.0267	0.09
16653_at	16653	Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	715.3	1.141	0.0267	0.08
241226_at	241226	Itga8	integrin alpha 8	177.4	1.207	0.0268	0.1
11958_at	11958	Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	1275	1.152	0.0269	0.09
22169_at	22169	Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	117.2	1.351	0.0271	0.17
67775_at	67775	Rtp4	receptor transporter protein 4	214.3	1.269	0.0274	0.13
625534_at	625534	Gm6597	predicted gene 6597	22.6	1.253	0.0274	0.12
66403_at	66403	Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	423.4	1.148	0.0275	0.08
22327_at	22327	Vbp1	von Hippel-Lindau binding protein 1	825.5	1.168	0.0279	0.09
210162_at	210162	Zkscan2	zinc finger with KRAB and SCAN domains 2	47.48	1.183	0.0281	0.08
12571_at	12571	Cdk6	cyclin-dependent kinase 6	485.9	1.171	0.0282	0.09
67980_at	67980	Gnpda2	glucosamine-6-phosphate deaminase 2	264.5	1.191	0.0284	0.1
234086_at	234086	Erich1	glutamate-rich 1	175.8	1.174	0.0286	0.09
50933_at	50933	Uchl3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	965.8	1.217	0.0287	0.12
72560_at	72560	Naalad2	N-acetylated alpha-linked acidic dipeptidase 2	299.1	1.258	0.0288	0.13
259148_at	259148	Olfr329	olfactory receptor 329	13.26	1.211	0.029	0.11
66200_at	66200	Commd6	COMM domain containing 6	472.3	1.2	0.0292	0.11
24110_at	24110	Usp18	ubiquitin specific peptidase 18	127	1.181	0.0292	0.09
56517_at	56517	Slc22a21	solute carrier family 22 (organic cation transporter), member 21	53.5	1.202	0.0293	0.09
16617_at	16617	Klk1b24	kallikrein 1-related peptidase b24	36.49	1.221	0.0296	0.1
77604_at	77604	C430048L16Rik	RIKEN cDNA C430048L16 gene	646	1.196	0.0296	0.11
77805_at	77805	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	347.1	1.153	0.0296	0.08
17763_at	17763	Mtcp1	mature T-cell proliferation 1	275.6	1.152	0.0296	0.08
66140_at	66140	Fam33a	family with sequence similarity 33, member A	890.1	1.135	0.0297	0.08
235956_at	235956	Zfp825	zinc finger protein 825	288.3	1.188	0.0301	0.1
67698_at	67698	Fam174a	family with sequence similarity 174, member A	689.5	1.154	0.0303	0.09
18108_at	18108	Nmt2	N-myristoyltransferase 2	367.2	1.176	0.0303	0.1

20585_at	20585	Hltf	helicase-like transcription factor	314	1.155	0.0306	0.08
66695_at	66695	Aspn	asporin	1487	1.329	0.0308	0.17
75698_at	75698	Fam35a	family with sequence similarity 35, member A	152.2	1.188	0.0312	0.09
20639_at	20639	Snrpb2	U2 small nuclear ribonucleoprotein B	1066	1.137	0.0312	0.08
217558_at	217558	G2e3	G2/M-phase specific E3 ubiquitin ligase	229	1.15	0.0315	0.08
77951_at	77951	Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1	365.7	1.153	0.0317	0.08
27528_at	27528	D0H4S114	DNA segment, human D4S114	488.1	1.253	0.032	0.14
435766_at	435766	Tnni3k	TNNI3 interacting kinase	803.6	1.134	0.0324	0.08
66143_at	66143	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	657.4	1.198	0.0324	0.11
59029_at	59029	Psmd14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	1244	1.141	0.0327	0.09
229782_at	229782	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	521.5	1.134	0.0327	0.08
56515_at	56515	Rnf138	ring finger protein 138	229.3	1.152	0.0328	0.08
218294_at	218294	Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	560.7	1.152	0.0329	0.09
69149_at	69149	Kbtbd3	kelch repeat and BTB (POZ) domain containing 3	141.2	1.248	0.0331	0.13
114893_at	114893	Dcun1d1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	1019	1.14	0.0333	0.09
238693_at	238693	Zfp58	zinc finger protein 58	97.99	1.217	0.0336	0.11
69792_at	69792	Med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	359.2	1.152	0.0337	0.09
70611_at	70611	Fbxo33	F-box protein 33	199.5	1.18	0.0338	0.1
54394_at	54394	Crlf3	cytokine receptor-like factor 3	412.9	1.163	0.0339	0.09
68262_at	68262	Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	94.35	1.188	0.0342	0.09
622486_at	622486	Smok3c	sperm motility kinase 3C	26.88	1.226	0.0343	0.11
387512_at	387512	Tas2r135	taste receptor, type 2, member 135	61.28	1.21	0.0343	0.1
20104_at	20104	Rps6	ribosomal protein S6	153.9	1.419	0.0345	0.21
66209_at	66209	1110054O05Rik	RIKEN cDNA 1110054O05 gene	261.2	1.194	0.0345	0.11
280668_at	280668	Adam1a	a disintegrin and metallopeptidase domain 1a	123.4	1.224	0.0346	0.11
319189_at	319189	Hist2h2bb	histone cluster 2, H2bb	124.5	1.186	0.0348	0.09
71911_at	71911	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	1780	1.194	0.0348	0.11
67529_at	67529	Fgfr1op2	FGFR1 oncogene partner 2	525.7	1.129	0.0348	0.08
381535_at	381535	Gm12800	predicted gene 12800	12.19	1.172	0.0351	0.09
100040853_at	1E+08	LOC100040853	CASP8 and FADD-like apoptosis regulator pseudogene	244.2	1.257	0.0353	0.14
74653_at	74653	4930444A02Rik	RIKEN cDNA 4930444A02 gene	253.4	1.148	0.0354	0.08
26611_at	26611	Rcn2	reticulocalbin 2	548.7	1.132	0.0356	0.08
381481_at	381481	Samd13	sterile alpha motif domain containing 13	85.18	1.6	0.0359	0.28
73300_at	73300	1700031F05Rik	RIKEN cDNA 1700031F05 gene	81.05	1.253	0.0364	0.13
18295_at	18295	Ogn	osteoglycin	1376	1.207	0.0364	0.12
12269_at	12269	C4bp	complement component 4 binding protein	29.73	1.203	0.0364	0.1
20620_at	20620	Plk2	polo-like kinase 2 (Drosophila)	590.8	1.144	0.0364	0.09
171209_at	171209	Accn3	amiloride-sensitive cation channel 3	56.52	1.213	0.0366	0.1
93765_at	93765	Ube2n	ubiquitin-conjugating enzyme E2N	421.7	1.189	0.0369	0.11

18193_at	18193	Nsd1	nuclear receptor-binding SET-domain protein 1	915.9	1.121	0.0376	0.08
58521_at	58521	Eid1	EP300 interacting inhibitor of differentiation 1	552	1.146	0.0381	0.09
54561_at	54561	Nap1l3	nucleosome assembly protein 1-like 3	54.13	1.194	0.0381	0.09
252837_at	252837	Ccrl1	chemokine (C-C motif) receptor-like 1	169.8	1.259	0.0382	0.14
432760_at	432760	Gm5449	small nuclear ribonucleoprotein D2 pseudogene	21.42	1.184	0.0383	0.09
15953_at	15953	Ifi47	interferon gamma inducible protein 47	223.3	1.888	0.0384	0.4
434394_at	434394	Gm5614	predicted gene 5614	130.1	1.182	0.0387	0.09
17141_at	17141	Magea5	melanoma antigen, family A, 5	9.663	1.27	0.0387	0.15
97884_at	97884	B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	935	1.151	0.0389	0.09
76983_at	76983	Scfd1	Sec1 family domain containing 1	430.6	1.143	0.0389	0.08
546511_at	546511	Gm11555	predicted gene 11555	692.2	1.32	0.0392	0.18
319615_at	319615	6330416L07Rik	RIKEN cDNA 6330416L07 gene	123.4	1.236	0.0392	0.12
69215_at	69215	Sat2	spermidine/spermine N1-acetyl transferase 2	126.7	1.169	0.0392	0.09
98363_at	98363	Efhd1	EF hand domain containing 1	163.3	1.22	0.0394	0.12
30057_at	30057	Timm8b	translocase of inner mitochondrial membrane 8 homolog b (yeast)	1215	1.161	0.0395	0.1
67636_at	67636	Lyrm5	LYR motif containing 5	1290	1.163	0.0395	0.1
245282_at	245282	Apol10a	apolipoprotein L 10a	19.25	1.181	0.0396	0.1
56382_at	56382	Rab9	RAB9, member RAS oncogene family	209.1	1.166	0.0396	0.09
67693_at	67693	2310003F16Rik	RIKEN cDNA 2310003F16 gene	2102	1.141	0.0398	0.09
624866_at	624866	Gm6534	predicted gene 6534	218.5	1.173	0.04	0.1
98258_at	98258	Txndc9	thioredoxin domain containing 9	636.5	1.138	0.04	0.09
13136_at	13136	Cd55	CD55 antigen	171.6	1.279	0.0401	0.15
74492_at	74492	5430433E21Rik	RIKEN cDNA 5430433E21 gene	50.54	1.208	0.0401	0.1
327959_at	327959	Xaf1	XIAP associated factor 1	128.7	1.236	0.0403	0.13
69069_at	69069	1810011H11Rik	RIKEN cDNA 1810011H11 gene	92.65	1.303	0.0404	0.16
21399_at	21399	Tcea1	transcription elongation factor A (SII) 1	1570	1.118	0.0405	0.08
212898_at	212898	Dse	dermatan sulfate epimerase	302.4	1.212	0.0406	0.12
107350_at	107350	AW112010	expressed sequence AW112010	396.2	1.37	0.0407	0.2
14727_at	14727	Gp49a	glycoprotein 49 A	105.2	1.192	0.0407	0.1
630499_at	630499	Gm7035	predicted gene 7035	66.04	1.226	0.0408	0.11
245575_at	245575	Gm4992	predicted gene 4992	211.2	1.264	0.041	0.15
15959_at	15959	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	46.08	1.247	0.0411	0.13
76522_at	76522	Lsm8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	259.4	1.185	0.0412	0.11
20821_at	20821	Trim21	tripartite motif-containing 21	247.5	1.209	0.0415	0.12
73656_at	73656	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	426.4	1.147	0.0417	0.09
404285_at	404285	V1rd11	vomeronasal 1 receptor, D11	21.53	1.249	0.042	0.13
17126_at	17126	Smad2	MAD homolog 2 (Drosophila)	484	1.165	0.0423	0.1
80287_at	80287	Apobec3	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 3	100.9	1.183	0.0424	0.09
320713_at	320713	Mysm1	myb-like, SWIRM and MPN domains 1	384.8	1.138	0.0424	0.08
51813_at	51813	Ccnc	cyclin C	373.3	1.154	0.0426	0.09
26874_at	26874	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	345.3	1.199	0.0429	0.12

239337_at	239337	Adamts12	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 12	189.6	1.182	0.043	0.1
237504_at	237504	Rassf9	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	309.7	1.408	0.043	0.22
12768_at	12768	Ccr1	chemokine (C-C motif) receptor 1	17.51	1.217	0.0435	0.12
20910_at	20910	Stxbp1	syntaxin binding protein 1	329.3	1.128	0.0437	0.08
26388_at	26388	Ifi202b	interferon activated gene 202B	60.75	1.277	0.0437	0.15
240327_at	240327	Gm4951	predicted gene 4951	120	1.413	0.0438	0.22
68852_at	68852	Lrrn4cl	LRRN4 C-terminal like	130.2	1.191	0.0438	0.1
68197_at	68197	Ndufc2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	3348	1.167	0.044	0.11
11745_at	11745	Anxa3	annexin A3	605.9	1.148	0.0441	0.09
22755_at	22755	Zfp93	zinc finger protein 93	199	1.136	0.0441	0.08
404324_at	404324	Olfr1051	olfactory receptor 1051	9.775	1.155	0.0441	0.09
57438_at	57438	7-Mar	membrane-associated ring finger (C3HC4) 7	676.9	1.122	0.0444	0.08
13008_at	13008	Csrp2	cysteine and glycine-rich protein 2	410	1.183	0.0446	0.11
74117_at	74117	Actr3	ARP3 actin-related protein 3 homolog (yeast)	2799	1.114	0.0448	0.08
100042485_at	1E+08	Gm3867	predicted gene 3867	9.442	1.148	0.0448	0.09
258921_at	258921	Olfr1188	olfactory receptor 1188	18.62	1.213	0.045	0.12
66979_at	66979	Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	486	1.123	0.045	0.08
52570_at	52570	Ccdc69	coiled-coil domain containing 69	172.5	1.223	0.0452	0.13
67011_at	67011	Mettl6	methyltransferase like 6	532.1	1.133	0.0452	0.08
225358_at	225358	Fam13b	family with sequence similarity 13, member B	408.5	1.143	0.0454	0.09
26930_at	26930	Ppnr	per-pentamer repeat gene	80.28	1.245	0.0458	0.13
70984_at	70984	4931406C07Rik	RIKEN cDNA 4931406C07 gene	240.7	1.154	0.046	0.09
75731_at	75731	5133401N09Rik	RIKEN cDNA 5133401N09 gene	648.7	1.156	0.0462	0.1
12368_at	12368	Casp6	caspase 6	271.1	1.163	0.0463	0.1
637800_at	637800	Gm7222	predicted gene 7222	24.58	1.278	0.0464	0.15
76959_at	76959	Chmp5	chromatin modifying protein 5	1193	1.113	0.0469	0.08
257912_at	257912	Olfr948	olfactory receptor 948	9.812	1.137	0.0469	0.08
12506_at	12506	Cd48	CD48 antigen	52.06	1.279	0.0471	0.15
252875_at	252875	Mios	missing oocyte, meiosis regulator, homolog (Drosophila)	399.7	1.125	0.0471	0.08
22370_at	22370	Vtn	vitronectin	625.5	1.141	0.0471	0.09
18974_at	18974	Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)	45.99	1.192	0.0472	0.1
170780_at	170780	Cd209e	CD209e antigen	36.79	1.165	0.0472	0.08
240614_at	240614	Ranbp6	RAN binding protein 6	746.7	1.137	0.0477	0.09
69352_at	69352	Necab1	N-terminal EF-hand calcium binding protein 1	80.33	1.184	0.0478	0.09
780960_at	780960	Gm10885	predicted gene 10885	14.54	1.325	0.0481	0.18
100554_at	100554	AA792892	expressed sequence AA792892	37.33	1.374	0.0482	0.2
13382_at	13382	Dld	dihydrolipoamide dehydrogenase	6271	1.088	0.0483	0.08
666704_at	666704	Samd1	sterile alpha motif domain containing 1	114.9	1.216	0.0484	0.12
56726_at	56726	Sh3bgrl	SH3-binding domain glutamic acid-rich protein like	1194	1.17	0.0486	0.11
258648_at	258648	Olfr438	olfactory receptor 438	18.63	1.205	0.0488	0.12
70349_at	70349	Copb1	coatomer protein complex, subunit beta 1	1440	1.106	0.0488	0.08

67463_at	67463	1200014M14Rik	RIKEN cDNA 1200014M14 gene	226.2	1.18	0.0489	0.11
67006_at	67006	Cisd2	CDGSH iron sulfur domain 2	718	1.116	0.049	0.08
22035_at	22035	Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10	286.7	1.65	0.0493	0.33
68833_at	68833	Pdcl3	phosducin-like 3	633.7	1.133	0.0493	0.09
18570_at	18570	Pdcd6	programmed cell death 6	462.5	1.17	0.0495	0.11
72085_at	72085	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	1239	1.13	0.0496	0.09
16431_at	16431	Itm2a	integral membrane protein 2A	849.9	1.223	0.0498	0.14
23961_at	23961	Oas1b	2'-5' oligoadenylate synthetase 1B	44.48	1.206	0.0499	0.11
66254_at	66254	Dimt1	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	309.2	1.181	0.05	0.11

Table S2. Downregulated genes in miR-494 hearts (393, $p<0.05$)

Probe	Gene	Symbol	Name	Intensity	Fold	p.value	std.err
209351_at	209351	Wfdc6a	WAP four-disulfide core domain 6A	33.4853	-1.4843	0.00033	0.09259
668131_at	668131	Gm8991	predicted gene 8991	15.6834	-1.5709	0.00045	0.12419
626347_at	626347	Igk-V21-4	immunoglobulin kappa chain variable 21 (V21)-4	21.6778	-1.3942	0.00081	0.0924
269919_at	269919	Gm660	predicted gene 660	27.1176	-1.9831	0.00118	0.21913
21817_at	21817	Tgm2	transglutaminase 2, C polypeptide	1990.29	-1.3281	0.00131	0.10258
67160_at	67160	Eef1g	eukaryotic translation elongation factor 1 gamma	112.567	-1.4723	0.00155	0.12281
545792_at	545792	Gm5871	predicted gene 5871	50.4872	-1.4579	0.00179	0.1169
194231_at	194231	Cnksr1	connector enhancer of kinase suppressor of Ras 1	185.152	-1.4837	0.00194	0.13625
22339_at	22339	Vegfa	vascular endothelial growth factor A	2664.39	-1.248	0.00198	0.08968
258086_at	258086	Olfr967	olfactory receptor 967	19.1675	-1.3956	0.00199	0.11058
17347_at	17347	Mknk2	MAP kinase-interacting serine/threonine kinase 2	939.791	-1.3002	0.00206	0.09918
140781_at	140781	Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	2108.82	-1.5856	0.00222	0.17166
435528_at	435528	Gm5683	predicted gene 5683	23.9417	-1.4263	0.00225	0.11908
14645_at	14645	Glul	glutamate-ammonia ligase (glutamine synthetase)	1355.7	-1.2433	0.00259	0.08827
27279_at	27279	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	796.032	-1.2376	0.00314	0.08669
84506_at	84506	Hamp	hepcidin antimicrobial peptide	13.8806	-1.2601	0.00344	0.08322
328778_at	328778	Rab26	RAB26, member RAS oncogene family	85.2138	-1.3712	0.00348	0.10841
51897_at	51897	D2Ertd391e	DNA segment, Chr 2, ERATO Doi 391, expressed	1275.66	-1.2728	0.0039	0.1019
70948_at	70948	Wdr20b	WD repeat domain 20b	29.0969	-1.3429	0.00406	0.10456
69810_at	69810	Clec4b1	C-type lectin domain family 4, member b1	11.2659	-1.2768	0.00427	0.09476
15370_at	15370	Nr4a1	nuclear receptor subfamily 4, group A, member 1	979.887	-1.8545	0.00507	0.25816
13138_at	13138	Dag1	dystroglycan 1	1889.41	-1.2523	0.00512	0.1011
59069_at	59069	Tpm3	tropomyosin 3, gamma	250.969	-1.2747	0.0055	0.09948
328825_at	328825	Gm5093	predicted gene 5093	32.1539	-1.8172	0.00555	0.24518
245566_at	245566	Cypt2	cysteine-rich perinuclear theca 2	31.2554	-1.4299	0.0056	0.14019
69583_at	69583	Tnfsf13	tumor necrosis factor (ligand) superfamily, member 13	24.968	-1.325	0.00568	0.10781
17691_at	17691	Sik1	salt inducible kinase 1	1010.52	-1.3964	0.00588	0.14574

71088_at	71088	4933412E24Rik	RIKEN cDNA 4933412E24 gene	71.6216	-1.2702	0.00622	0.08286
100042456_at	NA	NA	NA	52.0371	-1.2667	0.00622	0.08067
545152_at	545152	Gm5809	predicted gene 5809	105.42	-1.5162	0.00652	0.17259
668771_at	668771	Gm9347	predicted gene 9347	391.212	-1.3636	0.00681	0.13562
383490_at	383490	Gm16393	predicted gene 16393	35.3473	-1.3845	0.00711	0.13092
18997_at	18997	Pou4f2	POU domain, class 4, transcription factor 2	114.712	-1.2646	0.00712	0.0908
14537_at	14537	Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	572.586	-1.261	0.00715	0.10464
57837_at	57837	Eral1	Era (G-protein)-like 1 (E. coli)	557.026	-1.1789	0.00737	0.07611
11910_at	11910	Atf3	activating transcription factor 3	322.256	-1.4498	0.00744	0.1642
60425_at	60425	Doc2g	double C2, gamma	1529.96	-1.2099	0.0075	0.09218
18175_at	18175	Nrap	nebulin-related anchoring protein	5023.19	-1.148	0.00775	0.07988
667731_at	667731	Gm12215	ribosomal protein S2 pseudogene	52.0591	-1.3934	0.00776	0.13486
94244_at	94244	Fkbp6	FK506 binding protein 6	60.4913	-1.2957	0.00793	0.09832
68867_at	68867	Rnf122	ring finger protein 122	317.513	-1.3317	0.0081	0.12822
14177_at	14177	Fgf6	fibroblast growth factor 6	75.5568	-1.2622	0.00814	0.08612
66277_at	66277	Klf15	Kruppel-like factor 15	623.763	-1.3096	0.00827	0.12451
628098_at	628098	Gm6839	predicted gene 6839	46.0174	-1.2483	0.00827	0.0797
15939_at	15939	Ier5	immediate early response 5	424.202	-1.3655	0.00837	0.14176
194655_at	194655	Klf11	Kruppel-like factor 11	361.774	-1.2553	0.00838	0.10287
78321_at	78321	Ankrd23	ankyrin repeat domain 23	5702.13	-1.1734	0.00866	0.08958
68760_at	68760	Synpo2l	synaptopodin 2-like	1133.05	-1.2437	0.00871	0.10519
12846_at	12846	Comt1	catechol-O-methyltransferase 1	2271.74	-1.2364	0.00889	0.1054
237560_at	237560	Lrrc10	leucine rich repeat containing 10	1046.25	-1.2927	0.00896	0.12238
384783_at	384783	Irs2	insulin receptor substrate 2	226.612	-1.5014	0.009	0.18491
668668_at	668668	Gm9294	predicted gene 9294	586.831	-1.256	0.00941	0.10812
13508_at	13508	Dscam	Down syndrome cell adhesion molecule	47.456	-1.2735	0.00942	0.09387
435962_at	435962	Gm5731	predicted gene 5731	87.4497	-1.2774	0.00965	0.09846
13392_at	13392	Dlx2	distal-less homeobox 2	77.8666	-1.2821	0.00971	0.09927
636952_at	636952	Gm7194	predicted gene 7194	21.4444	-1.2741	0.00982	0.10317
70652_at	70652	Tmem144	transmembrane protein 144	1599.4	-1.2588	0.00986	0.11372
100041924_at	1E+08	Gm3576	predicted gene 3576	17.3029	-1.4174	0.00997	0.15826
243642_at	243642	Gm4968	predicted gene 4968	697.663	-1.2786	0.00998	0.11825
20411_at	20411	Sorbs1	sorbin and SH3 domain containing 1	2573.45	-1.1981	0.01004	0.09468
83557_at	83557	Lin28	lin-28 homolog (C. elegans)	126.571	-1.2598	0.01008	0.09831
57436_at	57436	Gabarapl1	gamma-aminobutyric acid (GABA) A receptor-associated protein-like 1	1217.08	-1.1787	0.01008	0.08455
227638_at	227638	Qsox2	quiescin Q6 sulfhydryl oxidase 2	269.202	-1.2293	0.01047	0.09535
232887_at	232887	Gm4879	WD repeat domain 12 pseudogene	138.128	-1.3919	0.0105	0.15056
223513_at	223513	Abra	actin-binding Rho activating protein	1124.31	-1.2379	0.01052	0.10649
74840_at	74840	Manf	mesencephalic astrocyte-derived neurotrophic factor	630.194	-1.2133	0.01059	0.09496
13838_at	13838	Epha4	Eph receptor A4	777.342	-1.3655	0.01089	0.15112
208449_at	208449	Sgms1	sphingomyelin synthase 1	1052.95	-1.2993	0.01093	0.12907
272381_at	272381	Lrrc4b	leucine rich repeat containing 4B	407.187	-1.205	0.011	0.08957
104175_at	104175	Sbk1	SH3-binding kinase 1	610.623	-1.2137	0.01105	0.09563
268807_at	268807	Klhl38	kelch-like 38 (Drosophila)	652.024	-1.2726	0.0112	0.11826

64209_at	64209	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	3400.96	-1.2306	0.01125	0.1096
12125_at	12125	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	213.021	-1.272	0.01136	0.11216
17965_at	17965	Nbl1	neuroblastoma, suppression of tumorigenicity 1	188.438	-1.1967	0.01156	0.08057
432681_at	432681	Gm5437	ribosomal protein L31 pseudogene	15.0635	-1.5637	0.0117	0.21274
320292_at	320292	Rasgef1b	RasGEF domain family, member 1B	144.817	-1.5169	0.01181	0.19742
21898_at	21898	Tlr4	toll-like receptor 4	776.673	-1.1864	0.01196	0.08778
17748_at	17748	Mt1	metallothionein 1	3471.53	-1.2168	0.01198	0.10588
215748_at	215748	Cnksr3	Cnksr family member 3	639.03	-1.2842	0.01201	0.12402
68794_at	68794	Flnc	filamin C, gamma	1753.14	-1.2125	0.01203	0.10086
67379_at	67379	Dedd2	death effector domain-containing DNA binding protein 2	321.914	-1.2135	0.01209	0.093
100043368_at	1E+08	Gm10361	predicted gene 10361	15.9646	-1.3271	0.01214	0.13226
258405_at	258405	Olfr1420	olfactory receptor 1420	45.6696	-1.3279	0.01219	0.12389
213989_at	213989	Tmem82	transmembrane protein 82	258.92	-1.5267	0.01221	0.20481
17750_at	17750	Mt2	metallothionein 2	1012.06	-1.389	0.01229	0.16345
545812_at	545812	Pilrb2	paired immunoglobin-like type 2 receptor beta 2	24.9546	-1.2645	0.0123	0.10271
140742_at	140742	Sesn1	sestrin 1	2528.39	-1.1968	0.01233	0.09718
433022_at	433022	Plcxd2	phosphatidylinositol-specific phospholipase C, X domain containing 2	59.7781	-1.2237	0.01262	0.07707
76585_at	76585	Lce1i	late cornified envelope 1I	21.894	-1.328	0.01299	0.13166
69314_at	69314	1700011H22Rik	RIKEN cDNA 1700011H22 gene	13.6865	-1.21	0.01314	0.08804
279618_at	279618	Gm715	predicted gene 715	137.683	-1.2023	0.01316	0.08055
100039265_at	1E+08	LOC100039265	hypothetical protein LOC100039265	79.1954	-1.4631	0.01328	0.17879
664817_at	664817	Gm7353	zinc finger CCCH type containing 3 pseudogene	22.0705	-1.3335	0.0137	0.13534
56219_at	56219	Extl1	exostoses (multiple)-like 1	345.232	-1.1997	0.01385	0.09028
74284_at	74284	1700086L19Rik	RIKEN cDNA 1700086L19 gene	30.7375	-1.223	0.01387	0.08389
381591_at	381591	L1td1	LINE-1 type transposase domain containing 1	42.4153	-1.2539	0.01417	0.0961
12235_at	12235	Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	35.4981	-1.3013	0.0142	0.11865
68943_at	68943	Pink1	PTEN induced putative kinase 1	3307.62	-1.2183	0.01451	0.10947
26912_at	26912	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	148.155	-1.2025	0.0147	0.08425
23927_at	23927	Krtap14	keratin associated protein 14	35.4588	-1.2475	0.01502	0.09603
319188_at	319188	Hist1h2bp	histone cluster 1, H2bp	265.224	-1.194	0.01539	0.08791
29818_at	29818	Hspb7	heat shock protein family, member 7 (cardiovascular)	3435.49	-1.1696	0.01543	0.09233
14120_at	14120	Fbp2	fructose bisphosphatase 2	369.53	-1.1839	0.01543	0.08604
15277_at	15277	Hk2	hexokinase 2	3461.03	-1.1864	0.01552	0.09881
104183_at	104183	Chi3l4	chitinase 3-like 4	12.1286	-1.2039	0.01579	0.09046
16156_at	16156	Il11	interleukin 11	50.2977	-1.2349	0.01583	0.08901
21859_at	21859	Timp3	tissue inhibitor of metalloproteinase 3	973.94	-1.1773	0.01593	0.08975
194225_at	194225	Gm13103	predicted gene 13103	42.462	-1.3514	0.01599	0.14248
57435_at	57435	Plin4	perilipin 4	583.121	-1.2103	0.01622	0.10105
56018_at	56018	Stard10	START domain containing 10	514.876	-1.2301	0.01633	0.10864
16007_at	16007	Cyr61	cysteine rich protein 61	1395.48	-1.1789	0.01634	0.09215

14776_at	14776	Gpx2	glutathione peroxidase 2	33.9369	-1.3543	0.01641	0.14581
18787_at	18787	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	560.575	-1.2553	0.01651	0.11965
239017_at	239017	Ogdhl	oxoglutarate dehydrogenase-like	1094.99	-1.2123	0.01677	0.10537
71720_at	71720	Osbpl3	oxysterol binding protein-like 3	1008.32	-1.2011	0.01736	0.10114
56722_at	56722	Litaf	LPS-induced TN factor	652.614	-1.1893	0.01748	0.09434
18984_at	18984	Por	P450 (cytochrome) oxidoreductase	584.72	-1.1865	0.01753	0.09253
223726_at	223726	Mpped1	metallophosphoesterase domain containing 1	108.822	-1.2065	0.01765	0.08411
20510_at	20510	Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	130.67	-1.25	0.01789	0.10861
12020_at	12020	Nkx3-2	NK3 homeobox 2	88.7163	-1.3032	0.01789	0.12706
208634_at	208634	Tspan10	tetraspanin 10	91.5816	-1.3007	0.01795	0.12636
272428_at	272428	Acsm5	acyl-CoA synthetase medium-chain family member 5	103.82	-1.2827	0.01806	0.1201
67760_at	67760	Slc38a2	solute carrier family 38, member 2	5427.29	-1.1544	0.01817	0.09162
338350_at	338350	9330129D05Rik	RIKEN cDNA 9330129D05 gene	775.49	-1.251	0.01821	0.12171
97187_at	97187	C87977	expressed sequence C87977	46.2402	-1.2974	0.01835	0.12343
59001_at	59001	Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	205.802	-1.1865	0.01837	0.0858
16615_at	16615	Klk1b16	kallikrein 1-related peptidase b16	12.6282	-1.254	0.01853	0.1159
252906_at	252906	V1rh2	vomeronasal 1 receptor, H2	14.6005	-1.2556	0.01869	0.11547
116913_at	116913	Tpbpb	trophoblast specific protein beta	10.5903	-1.1944	0.01872	0.09114
18550_at	18550	Furin	furin (paired basic amino acid cleaving enzyme)	498.863	-1.2508	0.01874	0.12028
225638_at	225638	Alpk2	alpha-kinase 2	1514.04	-1.2126	0.01881	0.10872
434246_at	434246	Trim72	tripartite motif-containing 72	2637.2	-1.2202	0.019	0.11421
16917_at	16917	Lmx1b	LIM homeobox transcription factor 1 beta	220.307	-1.2377	0.01902	0.11044
407789_at	407789	BC048644	cDNA sequence BC048644	25.3664	-1.2519	0.01903	0.10838
320159_at	320159	Fam179a	family with sequence similarity 179, member A	130.878	-1.3433	0.01906	0.1509
268420_at	268420	Alkbh5	alkB, alkylation repair homolog 5 (E. coli)	1676.77	-1.1657	0.01921	0.08997
52331_at	52331	Stbd1	starch binding domain 1	46.9219	-1.2303	0.01925	0.09233
13845_at	13845	Ephb3	Eph receptor B3	223.735	-1.2615	0.01938	0.12147
432836_at	432836	3425401B19Rik	RIKEN cDNA 3425401B19 gene	544.971	-1.2599	0.01948	0.12551
27419_at	27419	Naglu	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	217.301	-1.17	0.01954	0.07967
11354_at	11354	Abpa	androgen binding protein alpha	73.1696	-1.2218	0.01956	0.08869
208522_at	208522	Gm4754	predicted gene 4754	37.0456	-1.4854	0.01959	0.20382
75628_at	75628	1700010L13Rik	RIKEN cDNA 1700010L13 gene	145.239	-1.1881	0.01983	0.08331
382639_at	382639	Gm5188	predicted gene 5188	144.052	-1.216	0.02005	0.09714
18124_at	18124	Nr4a3	nuclear receptor subfamily 4, group A, member 3	144.962	-1.6207	0.0201	0.25705
76737_at	76737	Creld2	cysteine-rich with EGF-like domains 2	451.465	-1.1553	0.02054	0.07963
22433_at	22433	Xbp1	X-box binding protein 1	1242.55	-1.1718	0.02071	0.09278
16477_at	16477	Junb	Jun-B oncogene	118.3	-1.1822	0.02078	0.07706
76454_at	76454	Fbxo31	F-box protein 31	1271.31	-1.3073	0.02091	0.1498
546913_at	546913	Vmn2r22	vomeronasal 2, receptor 22	24.9987	-1.6225	0.02091	0.2582
16627_at	16627	Klra1	killer cell lectin-like receptor, subfamily A, member 1	12.0757	-1.3003	0.02094	0.13978

244199_at	244199	Ovch2	ovochymase 2	31.7641	-1.2278	0.02124	0.0969
12957_at	12957	Cryba1	crystallin, beta A1	32.4919	-1.2462	0.02135	0.10611
75475_at	75475	Oplah	5-oxoprolinase (ATP-hydrolysing)	545.079	-1.1638	0.02164	0.08577
22147_at	22147	Tuba3b	tubulin, alpha 3B	17.2212	-1.2152	0.02185	0.09909
104156_at	104156	Etv5	ets variant gene 5	145.256	-1.2711	0.02192	0.12538
100041819_at	1E+08	Gm10167	predicted gene 10167	59.2328	-1.3715	0.02211	0.16238
20404_at	20404	Sh3gl2	SH3-domain GRB2-like 2	87.9742	-1.2206	0.02235	0.09387
258700_at	258700	Olfr1451	olfactory receptor 1451	15.6615	-1.1726	0.02239	0.07943
100043538_at	1E+08	LOC100043538	hypothetical protein LOC100043538	48.2128	-1.2192	0.02271	0.091
56437_at	56437	Rrad	Ras-related associated with diabetes	1958.31	-1.1911	0.02274	0.10435
666048_at	666048	Gm12824	predicted gene 12824	167.546	-1.2041	0.02284	0.09663
404336_at	404336	Olfr1380	olfactory receptor 1380	69.6747	-1.3625	0.02295	0.16032
11606_at	11606	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	147.005	-1.3265	0.02307	0.15172
627734_at	627734	Gm6783	predicted gene 6783	28.5363	-1.2657	0.02317	0.11945
269109_at	269109	Dpp10	dipeptidylpeptidase 10	14.558	-1.1842	0.02323	0.08713
225058_at	225058	Gm4832	predicted gene 4832	184.987	-1.1946	0.02331	0.09367
26457_at	26457	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	1958.47	-1.1683	0.02334	0.09493
12399_at	12399	Runx3	runt related transcription factor 3	104.003	-1.2003	0.02351	0.08712
171183_at	171183	V1rc10	vomeronasal 1 receptor, C10	8.47245	-1.1622	0.02375	0.08306
11859_at	11859	Phox2a	paired-like homeobox 2a	65.3583	-1.2292	0.02389	0.09766
19416_at	19416	Rasd1	RAS, dexamethasone-induced 1	229.901	-1.27	0.02397	0.13146
268860_at	268860	Abat	4-aminobutyrate aminotransferase	359.444	-1.3153	0.02403	0.15342
208144_at	208144	Dhx37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	429.006	-1.1727	0.02414	0.09032
16601_at	16601	Klf9	Kruppel-like factor 9	1415.64	-1.1963	0.02429	0.10686
230815_at	230815	Man1c1	mannosidase, alpha, class 1C, member 1	594.62	-1.1747	0.02436	0.09353
236285_at	236285	Lancl3	LanC lantibiotic synthetase component C-like 3 (bacterial)	129.968	-1.2667	0.02446	0.12534
414094_at	414094	A930013B10Rik	RIKEN cDNA A930013B10 gene	90.566	-1.2207	0.02465	0.09713
93721_at	93721	Cpn1	carboxypeptidase N, polypeptide 1	38.8527	-1.2178	0.02484	0.09407
665612_at	665612	Gm7712	predicted gene 7712	89.6152	-1.1962	0.02485	0.08369
17928_at	17928	Myog	myogenin	60.1799	-1.2243	0.02493	0.09605
211468_at	211468	Kcnh8	potassium voltage-gated channel, subfamily H (eag-related), member 8	38.9275	-1.2652	0.02506	0.11908
269615_at	269615	Plch2	phospholipase C, eta 2	82.3573	-1.2915	0.02508	0.13234
17870_at	17870	Mycs	myc-like oncogene, s-myc protein	83.7053	-1.2376	0.02544	0.10603
21756_at	21756	Tesp2	testicular serine protease 2	33.0107	-1.2138	0.0255	0.09424
338348_at	338348	Ttc16	tetratricopeptide repeat domain 16	115.857	-1.2168	0.02557	0.10018
18361_at	18361	Olfr60	olfactory receptor 60	19.274	-1.1827	0.02568	0.085
210274_at	210274	Shank2	SH3/ankyrin domain gene 2	86.3023	-1.2544	0.02616	0.11593
114666_at	114666	Krtap5-5	keratin associated protein 5-5	29.0818	-1.2152	0.02626	0.09743
229499_at	229499	Fcrl1	Fc receptor-like 1	33.3226	-1.2109	0.02628	0.09344
626150_at	626150	Gm12271	predicted gene 12271	20.2598	-1.2464	0.02642	0.11783
258120_at	258120	Olfr1463	olfactory receptor 1463	45.7625	-1.2684	0.02643	0.12174
30951_at	30951	Cbx8	chromobox homolog 8 (Drosophila Pc class)	178.206	-1.1947	0.02667	0.09644
218215_at	218215	Rnf144b	ring finger protein 144B	687.82	-1.3875	0.02686	0.19007

17830_at	17830	Prol1	proline rich, lacrimal 1	11.7046	-1.2004	0.0269	0.10117
12311_at	12311	Calcr	calcitonin receptor	30.7119	-1.2069	0.02694	0.09293
83429_at	83429	Ctns	cystinosis, nephropathic	312.946	-1.1473	0.02724	0.07776
72043_at	72043	Sulf2	sulfatase 2	566.03	-1.1656	0.02727	0.09114
104885_at	104885	Tmem179	transmembrane protein 179	146.695	-1.2061	0.02763	0.10069
237987_at	237987	Otop2	otopetrin 2	151.086	-1.2508	0.02782	0.12358
330222_at	330222	Sdk1	sidekick homolog 1 (chicken)	90.8042	-1.2218	0.02786	0.10137
216505_at	216505	Pik3ip1	phosphoinositide-3-kinase interacting protein 1	610.567	-1.1738	0.02788	0.09599
14874_at	14874	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	515.89	-1.2129	0.02803	0.11369
623519_at	623519	Gm6438	predicted gene 6438	289.724	-1.2159	0.02832	0.11225
19245_at	19245	Ptp4a3	protein tyrosine phosphatase 4a3	1632.96	-1.1817	0.0284	0.10399
58805_at	58805	Mlxipl	MLX interacting protein-like	261.21	-1.2529	0.02842	0.12944
233199_at	233199	Mybpc2	myosin binding protein C, fast-type	360.99	-1.2542	0.02849	0.13176
14281_at	14281	Fos	FBJ osteosarcoma oncogene	120.161	-1.263	0.02852	0.12744
384071_at	384071	Slc25a34	solute carrier family 25, member 34	1228.84	-1.2202	0.02855	0.12104
71820_at	71820	Wdr34	WD repeat domain 34	320.746	-1.1497	0.02877	0.08022
258008_at	258008	Olfr1513	olfactory receptor 1513	18.1519	-1.2948	0.029	0.14518
69288_at	69288	Rhobtb1	Rho-related BTB domain containing 1	1341.83	-1.2401	0.02901	0.13074
216082_at	216082	Gm4798	ets variant gene 5 pseudogene	10.8202	-1.2099	0.02947	0.10897
17869_at	17869	Myc	myelocytomatosis oncogene	119.179	-1.3375	0.02962	0.16404
414801_at	414801	Itprip	inositol 1,4,5-triphosphate receptor interacting protein	210.341	-1.1775	0.02974	0.09196
72029_at	72029	Cnpy3	canopy 3 homolog (zebrafish)	286.124	-1.1726	0.02984	0.09184
243373_at	243373	AI854703	expressed sequence AI854703	53.4576	-1.2058	0.02985	0.09122
72654_at	72654	Ccdc12	coiled-coil domain containing 12	151.958	-1.2416	0.0299	0.12137
12778_at	12778	Cxcr7	chemokine (C-X-C motif) receptor 7	299.39	-1.1932	0.03018	0.10285
258491_at	258491	Olfr490	olfactory receptor 490	10.1538	-1.1784	0.03018	0.09425
17930_at	17930	Myom2	myomesin 2	6089.03	-1.2285	0.0302	0.13242
12590_at	12590	Cdx1	caudal type homeo box 1	145.827	-1.1731	0.03024	0.08522
19752_at	19752	Rnase1	ribonuclease, RNase A family, 1 (pancreatic)	87.6447	-1.2513	0.03037	0.11948
20762_at	20762	Sprr2h	small proline-rich protein 2H	24.3094	-1.298	0.03074	0.14642
93882_at	93882	Pcdhb11	protocadherin beta 11	72.9698	-1.251	0.0308	0.11821
12765_at	12765	Il8rb	interleukin 8 receptor, beta	17.3083	-1.1734	0.03088	0.08583
75815_at	75815	4930470H14Rik	RIKEN cDNA 4930470H14 gene	21.8301	-1.1716	0.03091	0.0815
75751_at	75751	Ipo4	importin 4	649.239	-1.1653	0.03098	0.09441
11551_at	11551	Adra2a	adrenergic receptor, alpha 2a	54.345	-1.1987	0.03132	0.08841
100039724_at	1E+08	Gm16509	predicted gene 16509	15.1995	-1.1594	0.03135	0.08012
433715_at	433715	Gm11249	predicted gene 11249	9833.68	-1.1182	0.03141	0.08743
16337_at	16337	Insr	insulin receptor	1653.27	-1.1551	0.03148	0.09367
66270_at	66270	Fam134b	family with sequence similarity 134, member B	1892.58	-1.1926	0.03169	0.11203
621127_at	621127	Mup-ps14	major urinary protein, pseudogene 14	9.01398	-1.2335	0.03173	0.12423
69582_at	69582	Plekhm2	pleckstrin homology domain containing, family M (with RUN domain) member 2	607.009	-1.2566	0.03174	0.13858
20779_at	20779	Src	Rous sarcoma oncogene	136.751	-1.1788	0.03195	0.08869
270150_at	270150	Ccdc153	coiled-coil domain containing 153	170.078	-1.1914	0.032	0.09882

15013_at	15013	H2-Q2	histocompatibility 2, Q region locus 2	70.7957	-1.2417	0.03201	0.11437
545743_at	545743	Gm5864	predicted gene 5864	1557.83	-1.1847	0.03202	0.10789
258113_at	258113	Olfr748	olfactory receptor 748	13.5093	-1.227	0.03214	0.11802
57752_at	57752	Tacc2	transforming, acidic coiled-coil containing protein 2	1607.3	-1.2054	0.03214	0.11787
233038_at	233038	Nccrp1	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	104.598	-1.2216	0.03233	0.10801
80906_at	80906	Kcnip2	Kv channel-interacting protein 2	2335.22	-1.1623	0.03237	0.09908
233977_at	233977	Ppfia1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein, alpha 1	661.955	-1.2273	0.03259	0.12586
21678_at	21678	Tead3	TEA domain family member 3	213.891	-1.1644	0.03264	0.08733
319187_at	319187	Hist1h2bn	histone cluster 1, H2bn	140.151	-1.2366	0.03322	0.12125
327799_at	327799	Usp44	ubiquitin specific peptidase 44	32.4472	-1.208	0.03322	0.09916
98878_at	98878	Ehd4	EH-domain containing 4	4994.79	-1.1291	0.03336	0.08922
11549_at	11549	Adra1a	adrenergic receptor, alpha 1a	463.033	-1.3532	0.03344	0.18365
434339_at	434339	Gm5610	adaptor-related protein complex 3, sigma 1 subunit pseudogene	1126.95	-1.1486	0.03361	0.09045
628900_at	628900	Gm6930	predicted gene 6930	76.2541	-1.4431	0.03372	0.21404
56323_at	56323	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	1252.71	-1.1533	0.03373	0.0932
242939_at	242939	Cpz	carboxypeptidase Z	95.684	-1.2139	0.03373	0.10374
320593_at	320593	A230051N06Rik	RIKEN cDNA A230051N06 gene	104.854	-1.2182	0.03409	0.10786
16706_at	16706	Ksr1	kinase suppressor of ras 1	146.526	-1.1597	0.03418	0.08064
258649_at	258649	Olfr441	olfactory receptor 441	11.9889	-1.3198	0.03426	0.16629
18640_at	18640	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	2331.51	-1.1745	0.03442	0.10617
94045_at	94045	P2rx5	purinergic receptor P2X, ligand-gated ion channel, 5	363.141	-1.2205	0.03458	0.12135
242022_at	242022	Frem2	Fras1 related extracellular matrix protein 2	265.974	-1.2152	0.03467	0.11701
677858_at	677858	Igkv8-24	immunoglobulin kappa chain variable 8-24	9.37903	-1.2065	0.03478	0.11305
320321_at	320321	9430077A04Rik	RIKEN cDNA 9430077A04 gene	109.935	-1.1929	0.03492	0.09504
18217_at	18217	Ntsr2	neurotensin receptor 2	173.535	-1.2356	0.03501	0.12478
75695_at	75695	Rilpl1	Rab interacting lysosomal protein-like 1	1747.77	-1.1501	0.03504	0.0935
11451_at	11451	Acrv1	acrosomal vesicle protein 1	31.6888	-1.2033	0.03525	0.09859
20289_at	20289	Scx	scleraxis	252.746	-1.2061	0.03532	0.1126
215928_at	215928	BC021785	cDNA sequence BC021785	90.4314	-1.2097	0.03534	0.10203
50913_at	50913	Olig2	oligodendrocyte transcription factor 2	39.3499	-1.2394	0.03541	0.11741
76399_at	76399	Il31	interleukin 31	104.209	-1.1793	0.03542	0.08639
216805_at	216805	Flcn	folliculin	1186.94	-1.2336	0.03555	0.13336
93961_at	93961	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	25.8292	-1.1673	0.03575	0.08009
235493_at	235493	BC031353	cDNA sequence BC031353	688.444	-1.1456	0.03601	0.08788
16559_at	16559	Kif17	kinesin family member 17	70.7258	-1.2091	0.03605	0.09982
15551_at	15551	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	49.383	-1.1724	0.03607	0.07632
20525_at	20525	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	519.761	-1.1709	0.03612	0.09924
58916_at	58916	Myot	myotilin	1121.92	-1.5053	0.03614	0.25428
435804_at	435804	Olfr1335	olfactory receptor 1335	128.528	-1.2495	0.03641	0.12993
622589_at	622589	Gm6336	predicted gene 6336	1744.31	-1.1446	0.03659	0.09163
546166_at	546166	Gm5922	predicted gene 5922	42.0744	-1.2042	0.03678	0.09798

19661_at	19661	Rbp3	retinol binding protein 3, interstitial	35.5832	-1.2063	0.0368	0.10053
240156_at	240156	Gm4947	predicted gene 4947	212.45	-1.1963	0.03687	0.10753
230674_at	230674	Kdm4a	lysine (K)-specific demethylase 4A	758.877	-1.1499	0.037	0.09118
171185_at	171185	V1rc12	vomeronasal 1 receptor, C12	11.6727	-1.2057	0.03703	0.11255
100043129_at	1E+08	Gm4248	high mobility group nucleosomal binding domain 2 pseudogene	46.8302	-1.2311	0.0371	0.1136
67731_at	67731	Fbxo32	F-box protein 32	1539.2	-1.2855	0.03713	0.16003
11504_at	11504	Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	515.424	-1.1864	0.03719	0.10788
71986_at	71986	Ddx28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	112.931	-1.178	0.0372	0.08861
14104_at	14104	Fasn	fatty acid synthase	235.109	-1.1676	0.03754	0.09318
72224_at	72224	1700001J11Rik	RIKEN cDNA 1700001J11 gene	59.8156	-1.1812	0.03763	0.08303
209776_at	209776	Gpr139	G protein-coupled receptor 139	88.1782	-1.3195	0.03783	0.16306
100041826_at	1E+08	Gm10182	predicted gene 10182	783.574	-1.1225	0.03802	0.07777
73259_at	73259	Cib4	calcium and integrin binding family member 4	45.453	-1.2889	0.0381	0.14631
100042605_at	1E+08	Gm3925	predicted gene 3925	105.745	-1.2224	0.03833	0.11421
18145_at	18145	Npc1	Niemann Pick type C1	1603.04	-1.1519	0.03834	0.09582
17433_at	17433	Mobp	myelin-associated oligodendrocytic basic protein	46.3334	-1.201	0.03846	0.09708
70065_at	70065	Ankrd60	ankyrin repeat domain 60	40.8336	-1.1873	0.03853	0.08919
72330_at	72330	Kbtbd5	kelch repeat and BTB (POZ) domain containing 5	116.776	-1.261	0.03867	0.13691
228801_at	228801	U46068	cDNA sequence U46068	44.3387	-1.2297	0.03872	0.11456
71889_at	71889	Epn3	epsin 3	700.438	-1.2678	0.03884	0.1513
20202_at	20202	S100a9	S100 calcium binding protein A9 (calgranulin B)	55.9205	-1.199	0.03887	0.0955
258238_at	258238	Olfr417	olfactory receptor 417	114.813	-1.2116	0.03888	0.10991
20211_at	20211	Saa4	serum amyloid A 4	22.5647	-1.3035	0.03889	0.15931
18845_at	18845	Plxna2	plexin A2	431.571	-1.1624	0.0389	0.09535
24131_at	24131	Ldb3	LIM domain binding 3	2524.51	-1.1316	0.03907	0.08829
216749_at	216749	Nmur2	neuromedin U receptor 2	30.9594	-1.2068	0.03914	0.1043
12759_at	12759	Clu	clusterin	2644.01	-1.3668	0.0392	0.20106
211482_at	211482	Efhb	EF hand domain family, member B	19.1164	-1.1798	0.03929	0.09465
99571_at	99571	Fgg	fibrinogen gamma chain	17.8682	-1.1973	0.03948	0.1056
381707_at	381707	LOC381707	hypothetical LOC381707	155.121	-1.3512	0.03948	0.18574
257926_at	257926	Olfr544	olfactory receptor 544	24.0053	-1.192	0.03954	0.09901
170758_at	170758	Rac3	RAS-related C3 botulinum substrate 3	80.112	-1.2071	0.03955	0.10285
18583_at	18583	Pde7a	phosphodiesterase 7A	1168.61	-1.1383	0.0396	0.08855
11512_at	11512	Adcy6	adenylate cyclase 6	1272.71	-1.2111	0.03968	0.12575
244668_at	244668	Sipa1l2	signal-induced proliferation-associated 1 like 2	397.62	-1.1756	0.03975	0.10247
545683_at	545683	Gm13213	predicted gene 13213	286.039	-1.1675	0.03975	0.09592
433766_at	433766	Trim63	tripartite motif-containing 63	1351.23	-1.227	0.03998	0.13404
666244_at	666244	Tmsb15b1	thymosin beta 15b1	9.84223	-1.1387	0.04051	0.07963
234072_at	234072	Adprhl1	ADP-ribosylhydrolase like 1	4681	-1.1372	0.04058	0.09565
381823_at	381823	Apold1	apolipoprotein L domain containing 1	541.891	-1.1994	0.04082	0.11741
68738_at	68738	Acss1	acyl-CoA synthetase short-chain family member 1	3768.08	-1.1389	0.04146	0.09555
74178_at	74178	Stk40	serine/threonine kinase 40	702.185	-1.1366	0.04152	0.08611

216439_at	216439	Agap2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	154.947	-1.1852	0.04182	0.10167
332131_at	332131	Krt78	keratin 78	57.2441	-1.2043	0.04182	0.1013
12984_at	12984	Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	48.1038	-1.2944	0.04186	0.15319
72555_at	72555	2700045P11Rik	RIKEN cDNA 2700045P11 gene	160.087	-1.1831	0.04196	0.101
209294_at	209294	Csta	cystatin A	8.95412	-1.1365	0.04206	0.08026
71375_at	71375	Foxn3	forkhead box N3	465.937	-1.1569	0.04209	0.09471
231885_at	231885	Gm4871	predicted gene 4871	27.1325	-1.3366	0.0421	0.17817
241489_at	241489	Pde11a	phosphodiesterase 11A	119.925	-1.2632	0.04213	0.1418
11634_at	11634	Aire	autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy)	123.08	-1.2175	0.04214	0.11707
16660_at	16660	Krt31	keratin 31	60.0266	-1.2944	0.04237	0.15342
16514_at	16514	Kcnj11	potassium inwardly rectifying channel, subfamily J, member 11	976.725	-1.1651	0.04238	0.10311
27261_at	27261	Dok3	docking protein 3	158.686	-1.152	0.04252	0.08277
545989_at	545989	Gm5901	predicted gene 5901	69.6387	-1.2739	0.04255	0.1429
319848_at	319848	Slc17a4	solute carrier family 17 (sodium phosphate), member 4	48.3233	-1.1785	0.04258	0.08584
100705_at	100705	Acacb	acetyl-Coenzyme A carboxylase beta	1617.62	-1.1503	0.04278	0.0973
12335_at	12335	Capn3	calpain 3	136.866	-1.2507	0.0429	0.13743
26366_at	26366	Ceacam10	carcinoembryonic antigen-related cell adhesion molecule 10	31.3429	-1.1739	0.0431	0.08693
12155_at	12155	Bmp15	bone morphogenetic protein 15	32.9446	-1.2577	0.04314	0.13635
55983_at	55983	Pdzrn3	PDZ domain containing RING finger 3	395.546	-1.1924	0.0434	0.11382
258541_at	258541	Olfr800	olfactory receptor 800	26.9774	-1.5067	0.04351	0.25944
217212_at	217212	Pyy	peptide YY	138.723	-1.1953	0.04376	0.10739
26380_at	26380	Esrrb	estrogen related receptor, beta	248.74	-1.224	0.0438	0.12864
20400_at	20400	Sh2d1a	SH2 domain protein 1A	27.6394	-1.1843	0.04382	0.09577
12348_at	12348	Car11	carbonic anhydrase 11	223.715	-1.1431	0.04389	0.08251
14613_at	14613	Gja5	gap junction membrane channel protein alpha 5	140.843	-1.1833	0.0439	0.10064
384813_at	384813	Gm5346	predicted gene 5346	69.8966	-1.2832	0.04392	0.14937
12608_at	12608	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	325.803	-1.2649	0.04397	0.15153
16779_at	16779	Lamb2	laminin, beta 2	2626.52	-1.1328	0.04406	0.09126
14526_at	14526	Gcg	glucagon	33.713	-1.188	0.04433	0.09604
100042747_at	1E+08	Gm4005	predicted gene 4005	35.5718	-1.1998	0.04459	0.1031
235320_at	235320	Zbtb16	zinc finger and BTB domain containing 16	929.987	-1.409	0.04471	0.22516
14284_at	14284	Fosl2	fos-like antigen 2	342.327	-1.1999	0.04481	0.11809
237781_at	237781	Smcr7	Smith-Magenis syndrome chromosome region, candidate 7 homolog (human)	283.159	-1.1531	0.04502	0.09079
76263_at	76263	Gstk1	glutathione S-transferase kappa 1	1649.66	-1.1492	0.04504	0.09794
67255_at	67255	Zfp422	zinc finger protein 422	105.69	-1.272	0.04538	0.14811
627009_at	627009	Gm13125	predicted gene 13125	33.2043	-1.219	0.04541	0.11607
11732_at	11732	Ank	progressive ankylosis	1879.92	-1.1613	0.04564	0.10505
75136_at	75136	Rsph10b2	radial spoke head 10 homolog B (Chlamydomonas)	43.7713	-1.2134	0.04583	0.11111
338374_at	338374	Il28b	interleukin 28B	173.654	-1.3892	0.04608	0.21266
100038380_at	1E+08	Gm10837	predicted gene 10837	186.015	-1.2297	0.04635	0.13191

17962_at	17962	Nat3	N-acetyltransferase 3	12.9297	-1.1478	0.04636	0.08477
629750_at	629750	Gm11517	predicted gene 11517	86.2125	-1.2478	0.04653	0.13351
212943_at	212943	Fam46a	family with sequence similarity 46, member A	465.529	-1.2159	0.04659	0.12947
64657_at	64657	Mrps10	mitochondrial ribosomal protein S10	159.429	-1.2948	0.0469	0.16597
675815_at	NA	NA	NA	206.12	-1.158	0.04694	0.09228
626067_at	626067	Gm6650	predicted gene 6650	11.4129	-1.233	0.04713	0.13537
209588_at	209588	Sectm1a	secreted and transmembrane 1A	32.0934	-1.1806	0.04733	0.09401
434440_at	434440	Fbxw12	F-box and WD-40 domain protein 12	27.5288	-1.2422	0.04738	0.13305
100042548_at	1E+08	Gm3898	predicted gene 3898	80.4573	-1.1846	0.04738	0.09496
66853_at	66853	Pnpla2	patatin-like phospholipase domain containing 2	2131.4	-1.1437	0.0476	0.09727
545548_at	545548	Lce3a	late cornified envelope 3A	44.1194	-1.2445	0.04764	0.13125
12497_at	12497	Entpd6	ectonucleoside triphosphate diphosphohydrolase 6	504.484	-1.1936	0.04769	0.11857
13629_at	13629	Eef2	eukaryotic translation elongation factor 2	4965.18	-1.0919	0.04785	0.07715
67224_at	67224	Med29	mediator complex subunit 29	381.692	-1.1389	0.04788	0.08626
227580_at	227580	C1ql3	C1q-like 3	26.7586	-1.2153	0.04788	0.11807
227731_at	227731	Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	208.562	-1.2085	0.0479	0.12216
210582_at	210582	Coq10a	coenzyme Q10 homolog A (yeast)	814.9	-1.1357	0.04796	0.08931
20848_at	20848	Stat3	signal transducer and activator of transcription 3	2072.18	-1.1833	0.048	0.11828
406176_at	406176	Olfr151	olfactory receptor 151	14.2865	-1.1878	0.04837	0.10881
13009_at	13009	Csrp3	cysteine and glycine-rich protein 3	6601.41	-1.0873	0.04851	0.07707
67838_at	67838	Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	862.674	-1.1246	0.04855	0.08378
12614_at	12614	Celsr1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	172.366	-1.134	0.0486	0.07613
18125_at	18125	Nos1	nitric oxide synthase 1, neuronal	75.1423	-1.1948	0.04876	0.10198
574403_at	574403	Gm6041	predicted gene 6041	54.0292	-1.2512	0.04901	0.13581
20480_at	20480	Clpb	ClpB caseinolytic peptidase B homolog (E. coli)	868.791	-1.1481	0.04908	0.09697
193740_at	193740	Hspa1a	heat shock protein 1A	348.283	-1.4228	0.04911	0.23481
15407_at	15407	Hoxb1	homeo box B1	108.25	-1.203	0.04915	0.11198
668539_at	668539	Gm9229	predicted gene 9229	39.2477	-1.561	0.04947	0.29129
433224_at	433224	Gm5512	required for meiotic nuclear division 1 pseudogene	17.5981	-1.2564	0.04975	0.14701
20536_at	20536	Slc4a3	solute carrier family 4 (anion exchanger), member 3	2199.18	-1.1442	0.04976	0.09866
230126_at	230126	Shb	src homology 2 domain-containing transforming protein B	234.84	-1.1345	0.04979	0.08074
665772_at	665772	Gm7780	predicted gene 7780	300.414	-1.176	0.04994	0.10717
665716_at	665716	Gm7755	predicted gene 7755	178.843	-1.1754	0.04997	0.10296

Table S3. Alteration of predicted miR-494 target genes (Target-Scan) in miR-494 hearts

Probe	Gene	Symbol	Name	Intensity	Fold (TG/WT)	P value	Std
11910_at	11910	Atf3	activating transcription factor 3	322.26	-1.45	0.01	0.16
12125_at	12125	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	213.02	-1.27	0.01	0.11
268860_at	268860	Abat	4-aminobutyrate aminotransferase	359.44	-1.32	0.02	0.15
57752_at	57752	Tacc2	transforming, acidic coiled-coil containing protein 2	1607.3	-1.21	0.03	0.12
70611_at	70611	Fbxo33	F-box protein 33	199.5	1.18	0.03	0.1
18193_at	18193	Nsd1	nuclear receptor-binding SET-domain protein 1	915.91	1.12	0.04	0.08
319653_at	319653	Slc25a40	solute carrier family 25, member 40	443.2	1.13	0.06	0.09
268902_at	268902	Robo2	roundabout homolog 2 (Drosophila)	94.17	1.16	0.07	0.1
68107_at	68107	Cntd1	cyclin N-terminal domain containing 1	30.87	1.16	0.11	0.12
60611_at	60611	Foxj2	forkhead box J2	471.2	-1.12	0.11	0.1
20893_at	20893	Bhlhe40	basic helix-loop-helix family, member e40	484.52	-1.26	0.12	0.2
80889_at	80889	Mesdc1	mesoderm development candidate 1	119.77	1.14	0.12	0.11
74148_at	74148	1300001I01Rik	RIKEN cDNA 1300001I01 gene	2851.8	-1.1	0.13	0.09
234267_at	234267	Gpm6a	glycoprotein m6a	289.12	1.28	0.13	0.22
13803_at	13803	Enc1	ectodermal-neural cortex 1	282.43	-1.12	0.13	0.11
54446_at	54446	Nfat5	nuclear factor of activated T-cells 5	539.74	1.1	0.14	0.09
66704_at	66704	Rbm4b	RNA binding motif protein 4B	281.55	-1.11	0.14	0.1
230233_at	230233	Ikbkap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	545.14	-1.1	0.14	0.09
319478_at	319478	Cxxc4	CXXC finger 4	57.03	1.11	0.14	0.08
16878_at	16878	Lif	leukemia inhibitory factor	45.85	-1.18	0.15	0.14
17153_at	17153	Mal	myelin and lymphocyte protein, T-cell differentiation protein	251.68	-1.21	0.15	0.18
28018_at	28018	Ubfd1	ubiquitin family domain containing 1	927	-1.1	0.16	0.09
16911_at	16911	Lmo4	LIM domain only 4	597.66	1.11	0.16	0.1
67886_at	67886	Camsap1l1	calmodulin regulated spectrin-associated protein 1-like 1	610.86	1.09	0.16	0.09
12013_at	12013	Bach1	BTB and CNC homology 1	616.65	-1.09	0.17	0.09
170791_at	170791	Rbm39	RNA binding motif protein 39	2368.9	1.07	0.18	0.08
16210_at	16210	Impact	imprinted and ancient	1250.3	-1.14	0.18	0.14
14536_at	14536	Nr6a1	nuclear receptor subfamily 6, group A, member 1	120.03	-1.11	0.18	0.1
68292_at	68292	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	1313.1	-1.07	0.18	0.08
14007_at	14007	Cugbp2	CUG triplet repeat, RNA binding protein 2	376.07	-1.09	0.18	0.09
21841_at	21841	Tia1	cytotoxic granule-associated RNA binding protein 1	623.72	1.08	0.19	0.08
53622_at	53622	Krt85	keratin 85	57.26	1.26	0.19	0.24
22589_at	22589	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	957.54	1.08	0.19	0.09
15191_at	15191	Hdgf	hepatoma-derived growth factor	866.18	-1.09	0.19	0.1
19877_at	19877	Rock1	Rho-associated coiled-coil containing protein kinase 1	1293.7	1.07	0.2	0.08
215449_at	215449	Rap1b	RAS related protein 1b	2863.3	1.08	0.2	0.09
241694_at	241694	A230067G21Rik	RIKEN cDNA A230067G21 gene	1025.2	1.09	0.2	0.1

18935_at	18935	Phox2b	paired-like homeobox 2b	67.01	-1.11	0.21	0.09
66975_at	66975	2410002O22Rik	RIKEN cDNA 2410002O22 gene	1041.5	1.07	0.21	0.08
217869_at	217869	Eif5	eukaryotic translation initiation factor 5	2199	1.06	0.21	0.08
16001_at	16001	Igf1r	insulin-like growth factor I receptor	320.85	-1.09	0.21	0.09
22196_at	22196	Ube2i	ubiquitin-conjugating enzyme E2I	1582	-1.11	0.21	0.13
211255_at	211255	Kbtbd7	kelch repeat and BTB (POZ) domain containing 7	228.7	-1.13	0.22	0.14
15078_at	15078	H3f3a	H3 histone, family 3A	15.48	1.18	0.23	0.19
105855_at	105855	Nckap1l	NCK associated protein 1 like	242.8	1.09	0.25	0.1
245572_at	245572	Tbx22	T-box 22	26.83	-1.1	0.25	0.11
18488_at	18488	Cntn3	contactin 3	26.31	-1.09	0.25	0.1
226518_at	226518	Nmnat2	nicotinamide nucleotide adenylyltransferase 2	112.43	-1.11	0.25	0.11
52348_at	52348	Vps37a	vacuolar protein sorting 37A (yeast)	371.26	1.07	0.26	0.08
69257_at	69257	Elf2	E74-like factor 2	885.15	-1.06	0.27	0.08
15081_at	15081	H3f3b	H3 histone, family 3B	2552.4	1.1	0.28	0.14
226409_at	226409	Zranb3	zinc finger, RAN-binding domain containing 3	198.13	1.08	0.28	0.09
140486_at	140486	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	54.34	-1.11	0.28	0.12
18751_at	18751	Prkcb	protein kinase C, beta	101.13	-1.09	0.29	0.11
228491_at	228491	Zfp770	zinc finger protein 770	412.27	1.1	0.3	0.14
245555_at	245555	C77370	expressed sequence C77370	20.27	-1.08	0.3	0.1
77799_at	77799	Sla2	Src-like-adaptor 2	95.03	-1.1	0.3	0.12
56363_at	56363	Tmeff2	transmembrane protein with EGF-like and two follistatin-like domains 2	29.06	-1.1	0.3	0.12
320924_at	320924	Ccbe1	collagen and calcium binding EGF domains 1	138.48	-1.1	0.31	0.12
70571_at	70571	Tcerg1l	transcription elongation regulator 1-like	77.37	-1.09	0.33	0.11
12934_at	12934	Dpysl2	dihydropyrimidinase-like 2	1883	1.07	0.33	0.11
215280_at	215280	Wipf1	WAS/WASL interacting protein family, member 1	159.56	1.07	0.34	0.09
100017_at	100017	Ldlrap1	low density lipoprotein receptor adaptor protein 1	288.75	1.06	0.34	0.08
21780_at	21780	Tfam	transcription factor A, mitochondrial	473.8	1.07	0.34	0.11
269275_at	269275	Acvr1c	activin A receptor, type IC	23.18	1.08	0.35	0.11
16324_at	16324	Inhbb	inhibin beta-B	82.37	-1.09	0.35	0.12
328949_at	328949	Mcc	mutated in colorectal cancers	686.23	1.08	0.36	0.12
207212_at	207212	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	331.07	1.05	0.36	0.08
213491_at	213491	D4Ertd22e	DNA segment, Chr 4, ERATO Doi 22, expressed	972.2	-1.06	0.37	0.1
13593_at	13593	Ebf3	early B-cell factor 3	224.69	1.07	0.37	0.1
110611_at	110611	Hdlbp	high density lipoprotein (HDL) binding protein	5514.7	-1.05	0.37	0.09
20269_at	20269	Scn3a	sodium channel, voltage-gated, type III, alpha	84.48	-1.1	0.37	0.15
13487_at	13487	Slc26a3	solute carrier family 26, member 3	36.09	1.1	0.37	0.14
56403_at	56403	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	1872.3	1.05	0.38	0.09
212391_at	212391	Lcor	ligand dependent nuclear receptor corepressor	525.52	1.05	0.38	0.08
240660_at	240660	Tmem20	transmembrane protein 20	252.48	-1.05	0.38	0.08
59125_at	59125	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	1733.9	-1.04	0.39	0.08
78521_at	78521	B230219D22Rik	RIKEN cDNA B230219D22 gene	1625.4	1.04	0.39	0.08

23859_at	23859	Dlg2	discs, large homolog 2 (Drosophila)	87.36	-1.07	0.39	0.11
103268_at	103268	2410017P07Rik	RIKEN cDNA 2410017P07 gene	69.4	-1.06	0.4	0.08
214162_at	214162	Mll1	myeloid/lymphoid or mixed-lineage leukemia 1	611.22	-1.06	0.41	0.11
71777_at	71777	Ing3	inhibitor of growth family, member 3	326.8	-1.05	0.42	0.08
109594_at	109594	Lmo1	LIM domain only 1	48.66	1.07	0.42	0.1
68465_at	68465	Adipor2	adiponectin receptor 2	965.34	-1.06	0.42	0.11
76901_at	76901	Phf15	PHD finger protein 15	213.74	-1.08	0.42	0.14
70900_at	70900	4921517D22Rik	RIKEN cDNA 4921517D22 gene	53.29	-1.08	0.42	0.12
213988_at	213988	Tnrc6b	trinucleotide repeat containing 6b	790.94	-1.05	0.42	0.09
241568_at	241568	Lrrc4c	leucine rich repeat containing 4C	19.88	-1.07	0.43	0.12
74206_at	74206	Sipa1l3	signal-induced proliferation-associated 1 like 3	198.94	-1.07	0.44	0.13
106143_at	106143	Cggbp1	CGG triplet repeat binding protein 1	468.42	1.05	0.44	0.09
54710_at	54710	Hs3st3b1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	120.6	-1.06	0.44	0.11
140780_at	140780	Bmp2k	BMP2 inducible kinase	170.46	1.07	0.44	0.12
14183_at	14183	Fgfr2	fibroblast growth factor receptor 2	35.39	-1.06	0.44	0.1
218335_at	218335	Clptm1l	CLPTM1-like	1133	-1.05	0.45	0.1
11855_at	11855	Arhgap5	Rho GTPase activating protein 5	1115	1.04	0.45	0.09
320165_at	320165	Tacc1	transforming, acidic coiled-coil containing protein 1	929.39	-1.04	0.46	0.08
217039_at	217039	Ggnbp2	gametogenetin binding protein 2	1098.3	1.05	0.47	0.1
54124_at	54124	Cks1b	CDC28 protein kinase 1b	112.88	1.06	0.47	0.1
22415_at	22415	Wnt3	wingless-related MMTV integration site 3	57.52	-1.05	0.47	0.09
234135_at	234135	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	486.71	1.06	0.47	0.12
18542_at	18542	Pcolce	procollagen C-endopeptidase enhancer protein	983.93	-1.04	0.47	0.08
69053_at	69053	1810013L24Rik	RIKEN cDNA 1810013L24 gene	1551.5	-1.04	0.48	0.09
18771_at	18771	Pknox1	Pbx/knotted 1 homeobox	225.22	-1.05	0.48	0.1
217082_at	217082	Hlf	hepatic leukemia factor	310.44	1.06	0.48	0.11
12032_at	12032	Bcan	brevican	38.9	-1.08	0.5	0.15
67684_at	67684	3300001P08Rik	RIKEN cDNA 3300001P08 gene	2123.5	1.05	0.5	0.11
22031_at	22031	Traf3	TNF receptor-associated factor 3	229.06	1.04	0.5	0.09
99031_at	99031	Osbpl6	oxysterol binding protein-like 6	342.76	-1.06	0.52	0.13
53323_at	53323	Ube2k	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	1919.4	1.03	0.53	0.08
224224_at	224224	Impg2	interphotoreceptor matrix proteoglycan 2	17.96	-1.05	0.53	0.12
76707_at	76707	Clasp1	CLIP associating protein 1	2931.3	-1.03	0.53	0.09
71902_at	71902	Cand1	cullin associated and neddylation disassociated 1	721.23	1.04	0.55	0.09
73379_at	73379	Dcbld2	discoidin, CUB and LCCL domain containing 2	396.36	1.04	0.56	0.09
16478_at	16478	Jund	Jun proto-oncogene related gene d	509.57	-1.05	0.57	0.12
17476_at	17476	Mpeg1	macrophage expressed gene 1	228.13	1.04	0.58	0.11
11431_at	11431	Acp1	acid phosphatase 1, soluble	191.89	-1.05	0.59	0.14
18741_at	18741	Pitx2	paired-like homeodomain transcription factor 2	50.14	-1.04	0.59	0.09
17933_at	17933	Myt1l	myelin transcription factor 1-like	86.83	-1.04	0.61	0.1
53860_at	53860	9-Sep	septin 9	382.79	-1.03	0.61	0.09
14806_at	14806	Grik2	glutamate receptor, ionotropic, kainate 2 (beta 2)	49.32	-1.04	0.61	0.1

30791_at	30791	Slc39a1	solute carrier family 39 (zinc transporter), member 1	836.71	-1.04	0.61	0.1
71653_at	71653	4930506M07Rik	RIKEN cDNA 4930506M07 gene	112.62	1.04	0.61	0.11
330409_at	330409	Cecr2	cat eye syndrome chromosome region, candidate 2 homolog (human)	198.92	-1.04	0.62	0.12
12638_at	12638	Cftr	cystic fibrosis transmembrane conductance regulator homolog	22.62	-1.04	0.62	0.09
217371_at	217371	Rab40b	Rab40b, member RAS oncogene family	133.38	-1.03	0.62	0.09
230753_at	230753	Thrap3	thyroid hormone receptor associated protein 3	1733.7	1.03	0.63	0.09
70640_at	70640	Dcp2	DCP2 decapping enzyme homolog (S. cerevisiae)	216.17	1.04	0.63	0.1
225027_at	225027	Sfrs7	splicing factor, arginine/serine-rich 7	1266.5	1.03	0.64	0.09
320538_at	320538	Ubn2	ubinuclein 2	588.28	-1.03	0.64	0.09
239555_at	239555	Smcr7l	Smith-Magenis syndrome chromosome region, candidate 7-like (human)	385.74	1.04	0.64	0.11
245386_at	245386	Fam70a	family with sequence similarity 70, member A	56.36	-1.03	0.65	0.08
76884_at	76884	Cyfip2	cytoplasmic FMR1 interacting protein 2	338.2	1.08	0.66	0.24
83925_at	83925	Trps1	trichorhinophalangeal syndrome I (human)	355.36	1.06	0.66	0.18
272027_at	272027	BC057893	cDNA sequence BC057893	373.17	1.03	0.67	0.1
18072_at	18072	Nhlh2	nescient helix loop helix 2	58.48	-1.04	0.67	0.14
12033_at	12033	Bcap29	B-cell receptor-associated protein 29	1263.4	-1.03	0.68	0.12
108946_at	108946	Zzz3	zinc finger, ZZ domain containing 3	640.06	1.03	0.68	0.1
223881_at	223881	Rnd1	Rho family GTPase 1	69.98	-1.03	0.68	0.1
18197_at	18197	Nsg2	neuron specific gene family member 2	43.45	-1.03	0.68	0.11
67468_at	67468	Mmd	monocyte to macrophage differentiation-associated	478.47	1.04	0.69	0.13
69091_at	69091	Vps26b	vacuolar protein sorting 26 homolog B (yeast)	715.34	1.03	0.69	0.1
16443_at	16443	Itsn1	intersectin 1 (SH3 domain protein 1A)	479.89	-1.02	0.7	0.09
55980_at	55980	Impa1	inositol (myo)-1(or 4)-monophosphatase 1	328.73	1.03	0.7	0.11
232798_at	232798	Leng8	leukocyte receptor cluster (LRC) member 8	649.91	1.03	0.7	0.13
231769_at	231769	Sfrs8	splicing factor, arginine/serine-rich 8	423.62	-1.02	0.7	0.09
13511_at	13511	Dsg2	desmoglein 2	578.69	-1.03	0.71	0.1
68051_at	68051	Nutf2	nuclear transport factor 2	325.28	-1.04	0.71	0.16
381695_at	381695	N4bp2l2	NEDD4 binding protein 2-like 2	659.3	1.02	0.72	0.09
17536_at	17536	Meis2	Meis homeobox 2	566.44	1.02	0.72	0.1
320595_at	320595	Phf8	PHD finger protein 8	286.39	1.02	0.72	0.09
71833_at	71833	Dcaf7	DDB1 and CUL4 associated factor 7	1012.8	-1.02	0.73	0.1
11906_at	11906	Zfhx3	zinc finger homeobox 3	230.02	-1.03	0.73	0.12
77286_at	77286	Nkrf	NF-kappaB repressing factor	141.99	1.02	0.73	0.09
80892_at	80892	Zfhx4	zinc finger homeodomain 4	65.65	-1.03	0.74	0.12
11800_at	11800	Api5	apoptosis inhibitor 5	702.43	-1.02	0.74	0.08
15354_at	15354	Hmgb3	high mobility group box 3	694.88	1.05	0.74	0.21
17749_at	17749	Polr2k	polymerase (RNA) II (DNA directed) polypeptide K	53.07	-1.04	0.74	0.17
78808_at	78808	Stxbp5	syntaxin binding protein 5 (tomosyn)	465.34	-1.03	0.75	0.13
22221_at	22221	Ubp1	upstream binding protein 1	609.32	1.02	0.75	0.08
68801_at	68801	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	1035.2	1.02	0.75	0.08
12151_at	12151	Bmi1	Bmi1 polycomb ring finger oncogene	1548.4	1.02	0.76	0.08

108058_at	108058	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	2427.2	-1.02	0.76	0.09
11977_at	11977	Atp7a	ATPase, Cu++ transporting, alpha polypeptide	293.21	-1.02	0.76	0.1
109205_at	109205	Sobp	sine oculis-binding protein homolog (Drosophila)	289.17	1.02	0.77	0.08
230700_at	230700	Foxj3	forkhead box J3	340.58	1.02	0.77	0.11
14634_at	14634	Gli3	GLI-Kruppel family member GLI3	73.08	1.04	0.77	0.16
22608_at	22608	Ybx1	Y box protein 1	691.94	1.02	0.78	0.09
78798_at	78798	Eml4	echinoderm microtubule associated protein like 4	272.36	1.02	0.78	0.08
170707_at	170707	Usp48	ubiquitin specific peptidase 48	526.94	-1.02	0.78	0.1
12444_at	12444	Ccnd2	cyclin D2	2169.1	1.02	0.79	0.1
11982_at	11982	Atp10a	ATPase, class V, type 10A	91.36	1.02	0.79	0.11
19211_at	19211	Pten	phosphatase and tensin homolog	2633.6	-1.01	0.79	0.08
77531_at	77531	Anks1b	ankyrin repeat and sterile alpha motif domain containing 1B	45.53	-1.02	0.8	0.11
73251_at	73251	Setd7	SET domain containing (lysine methyltransferase) 7	404.96	-1.01	0.8	0.08
216965_at	216965	Taok1	TAO kinase 1	1567.9	1.01	0.8	0.08
110648_at	110648	Lmx1a	LIM homeobox transcription factor 1 alpha	71.47	1.02	0.81	0.09
56809_at	56809	Gmeb1	glucocorticoid modulatory element binding protein 1	226.95	1.01	0.81	0.09
217517_at	217517	Stxbp6	syntaxin binding protein 6 (amisyn)	236.85	1.02	0.81	0.11
226442_at	226442	Zfp281	zinc finger protein 281	470.86	-1.01	0.82	0.1
242481_at	242481	Palm2	paralemmin 2	400.97	-1.01	0.83	0.08
192185_at	192185	Nadk	NAD kinase	666.49	-1.01	0.83	0.1
14897_at	14897	Trip12	thyroid hormone receptor interactor 12	2304.3	1.01	0.84	0.08
69632_at	69632	Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	2569.1	-1.01	0.86	0.08
65962_at	65962	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	636.59	-1.01	0.86	0.08
109241_at	109241	Mbd5	methyl-CpG binding domain protein 5	199.28	-1.01	0.87	0.09
99375_at	99375	Cul4a	cullin 4A	580.75	-1.01	0.87	0.12
18028_at	18028	Nfib	nuclear factor I/B	2109.9	-1.01	0.89	0.09
227960_at	227960	Gca	grancalcin	559.07	1.01	0.89	0.14
22780_at	22780	Ikzf3	IKAROS family zinc finger 3	43.77	1.01	0.89	0.12
22764_at	22764	Zfx	zinc finger protein X-linked	913.06	1.01	0.9	0.08
54610_at	54610	Tbc1d8	TBC1 domain family, member 8	131.44	1.01	0.91	0.1
226757_at	226757	Wdr26	WD repeat domain 26	1207.8	-1.01	0.91	0.09
22680_at	22680	Zfp207	zinc finger protein 207	1681.2	-1.01	0.91	0.08
71835_at	71835	Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2	585.32	-1.01	0.91	0.1
114873_at	114873	Dscaml1	Down syndrome cell adhesion molecule-like 1	59.3	-1.01	0.91	0.12
27386_at	27386	Npas3	neuronal PAS domain protein 3	30.7	-1.01	0.92	0.09
29808_at	29808	Mga	MAX gene associated	628.16	-1.01	0.92	0.08
12145_at	12145	Cxcr5	chemochine (C-X-C motif) receptor 5	20.29	-1.01	0.93	0.12
67475_at	67475	Ero1lb	ERO1-like beta (S. cerevisiae)	148.34	-1.01	0.93	0.11
80985_at	80985	Trim44	tripartite motif-containing 44	619.2	1	0.94	0.08
68010_at	68010	Bambi	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	561.81	1.01	0.94	0.15
57376_at	57376	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	1552.2	-1.01	0.94	0.17

14701_at	14701	Gng12	guanine nucleotide binding protein (G protein), gamma 12	910.56	1	0.95	0.09
66923_at	66923	Pbrm1	polybromo 1	1170.4	1	0.95	0.08
56364_at	56364	Zmym3	zinc finger, MYM-type 3	262.21	1	0.95	0.09
170770_at	170770	Bbc3	BCL2 binding component 3	65.47	-1	0.96	0.11
224997_at	224997	Dlgap1	discs, large (Drosophila) homolog-associated protein 1	38.17	-1	0.96	0.1
140810_at	140810	Ttbk2	tau tubulin kinase 2	285.76	1	0.97	0.08
93690_at	93690	Gpr45	G protein-coupled receptor 45	46.94	1	0.97	0.11
71834_at	71834	Zbtb43	zinc finger and BTB domain containing 43	359.92	-1	0.97	0.11
19267_at	19267	Ptpre	protein tyrosine phosphatase, receptor type, E	117.62	-1	0.97	0.08
15245_at	15245	Hhip	Hedgehog-interacting protein	27.97	1	0.98	0.08
81000_at	81000	Rad54l2	RAD54 like 2 (S. cerevisiae)	238.57	1	0.99	0.09
26965_at	26965	Cul1	cullin 1	1296.2	1	0.99	0.08
19212_at	19212	Pter	phosphotriesterase related	340.81	-1	0.99	0.1
12753_at	12753	Clock	circadian locomoter output cycles kaput	981.35	-1	1	0.1