SUPPLEMENTAL MATERIAL

1. Methods

MicroRNA TaqMan Low Density Array

MiRNAs were reverse transcribed and amplified using the multiplex RT TaqMan MicroRNA Low Density Array (TLDA) (Life Technologies). Global miRNA profiling for 754 human miRNAs was performed by using the TLDA Human microRNA Panel A v2.1+ Panel B v3.0 (Life Technologies). TLDAs were run on an ABI7900 HT analyzer with TLDA upgrade and analyzed by RQ Manager software (Applied Biosystems). All quality control tests were validated: blanks and reproducibility [standard deviation of cycle threshold (Ct) < 1] of the two small nucleolar house-keeping RNAs, RNU48 and RNU44. The amount of RNA from each sample was calibrated to the more stable (between the different arrays) small nucleolar housekeeping RNA, RNU48. To find consistently differentially expressed genes, the data were subjected to significance analysis of microarrays (SAM). Genes showing at least 1.7-fold regulation and a FDR value less than 5% were considered to be differentially expressed.

In situ hybridization

In situ hybridization was performed on frozen sections (10 µm in thickness) of skin biopsies. Briefly, after fixed in 4% formaldehyde for 10 minutes and incubated in acetylation solution (0.06M HCl, 1.3% Trietanolamin and 0.6% Acetic anhydride in DEPC treated water) for 10 minutes at room temperature, sections were treated with 2 ug/mL Proteinase K for 5 minutes at 37 °C, washed, and prehybridized for 30 minutes at 50 °C. Hybridization with digoxygenin (DIG)-labeled miRCURY LNA probes (Exiqon) was performed 2 hours at 50°C. Slides were then washed twice with 2 × SCC buffer followed by one time with 0.1× SCC buffer at 55°C. The probe binding was detected by incubating the sections with alkaline phosphatase (AP) - conjugated sheep anti-DIG Fab fragments [1:1000 (Roche)] for 1 hour at room temperature. Sections were visualized by adding BM purple AP substrate (Roche) according to the manufacturer's instructions.

Treatments of the cells

Keratinocytes were treated with TNF-α (50 ng/mL, Immuno tools), EGF (15 ng/mL, Immuno tools) or TGF-β1 (10 ng/mL, Immuno tools) or TGF-β2 (10 ng/mL, Immuno tools) at the indicated time points. TGF-β receptor inhibitor, SB431542 (15 µM, Tocris), was applied 15 min before adding TGF-β2 (Figure 2H). For the analysis of signalling pathways mediating the effect of miR-132 on cell proliferation (Figure 5F), primary human keratinocytes transfected with pre-miR-132 or pre-miR-Ctrl for 24 hours were treated with various inhibitors or dimethylsulfoxide (DMSO) for another 24 hours: p38-inhibitor SB203580 (10 µM, Merck), JNK-inhibitor SP600125 (10 µM, Santa Cruz Biotechnology), ERK-inhibitor U0126 (10 µM, Calbiochem), STAT3-inhibitor WP1066 (5 µM, Calbiochem), PKC-inhibitor Ro-31-8220 (100 nM, Santa Cruz Biotechnology), PI3K-inhibitor Wortmannin (1 µM, Calbiochem) and EGFR-inhibitor PD153035 (500 nM, Calbiochem).

Leukocyte chemotaxis assay

Human or murine neutrophils and mononuclear cells were isolated from 0.2% EDTA anti-coagulated whole blood collected by venipuncture from healthy human donors (n=4) or by cardiac puncture from miR-132 KO mice (n=7) and WT mice (n=5). Erythrocytes were removed using dextran sedimentation (1:1 mixture of blood: 6% dextran/0.9% NaCl), followed by one or two rounds of hypotonic lysis using ddH$_2$O. Neutrophils and mononuclear cells were isolated from the resulting cell suspension using Ficoll-Histopaque (Sigma) density centrifugation (1). The entire isolation was done at 4°C. Purified neutrophils and mononuclear cells were suspended in EpiLife® serum-free keratinocyte growth medium and 3×10^5 cells were added to the inner chamber of BD Falcon™ Cell Culture Insert. The human neutrophils or mononuclear cells migrate through a 3 μm porosity polyethylene terephthalate (PET) membrane toward outer chambers containing culture medium from keratinocytes, which were transfected with pre-miR-132 or pre-miR-Ctrl for 72 hours. To induce the chemotaxis of murine neutrophils or mononuclear cells, the bacterial formylpeptide fMLP (8 uM, Sigma) were used (2). After incubation for 1.5 hours at 37°C in 5% CO_2, the migrating cells in the medium of the outer chamber were quantified by flow cytometry.

Gene expression microarray

Expression profiling of primary human keratinocytes transfected with 10 nM pre-miR-132 or pre-miR-Ctrl for 48 hours (in triplicates) was performed using Affymetrix Genechip system at the Microarray core facility of Karolinska Institute. In brief, total RNA was extracted using the miRNeasy Mini Kit (Qiagen) and RNA quality and quantity were determined using Agilent 2100 Bioanalyzer and Nanodrop ND-1000. 100 ng of total RNA were used to prepare cDNA following the Affymetrix 3'IVT Express Kit labelling protocol. Standardized array processing procedures recommended by Affymetrix including hybridization, fluidics processing and scanning were used. Genes showing at least 1.2-fold regulation and FDR less than 5% were considered to be differentially expressed. Gene ontology analysis was performed according to the Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7 (3). Gene set enrichment analysis (GSEA) was performed using public software from Broad Institute (4, 5).

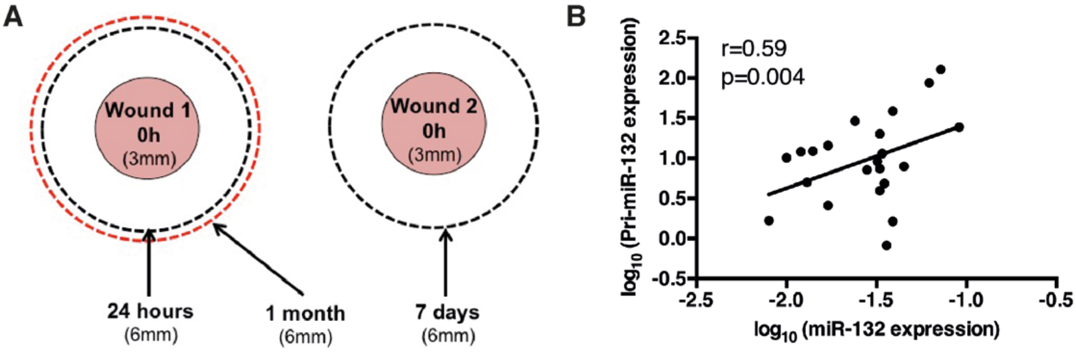
Collagen gel contraction assay

The contraction ability of dermal fibroblasts was analyzed by using cell contraction assay kit (Cell Biolabs). 6×10^4 mouse dermal fibroblasts transfected with 20 nM miR-132 miRCURY LNA Power inhibitor (Anti-miR-132) or negative control A (Anti-miR-Ctrl) were mixed with collagen gel and seeded in each well of 24-well cell culture plate. After incubated for 2 days, the gels were released from the walls of wells using a syringe tip and the pictures were taken 24 hours later. The area of the gel lattice was measured with Image J software. The relative gel area was determined by dividing the gel area at 24 hours after detachment with the initial area of the gel.

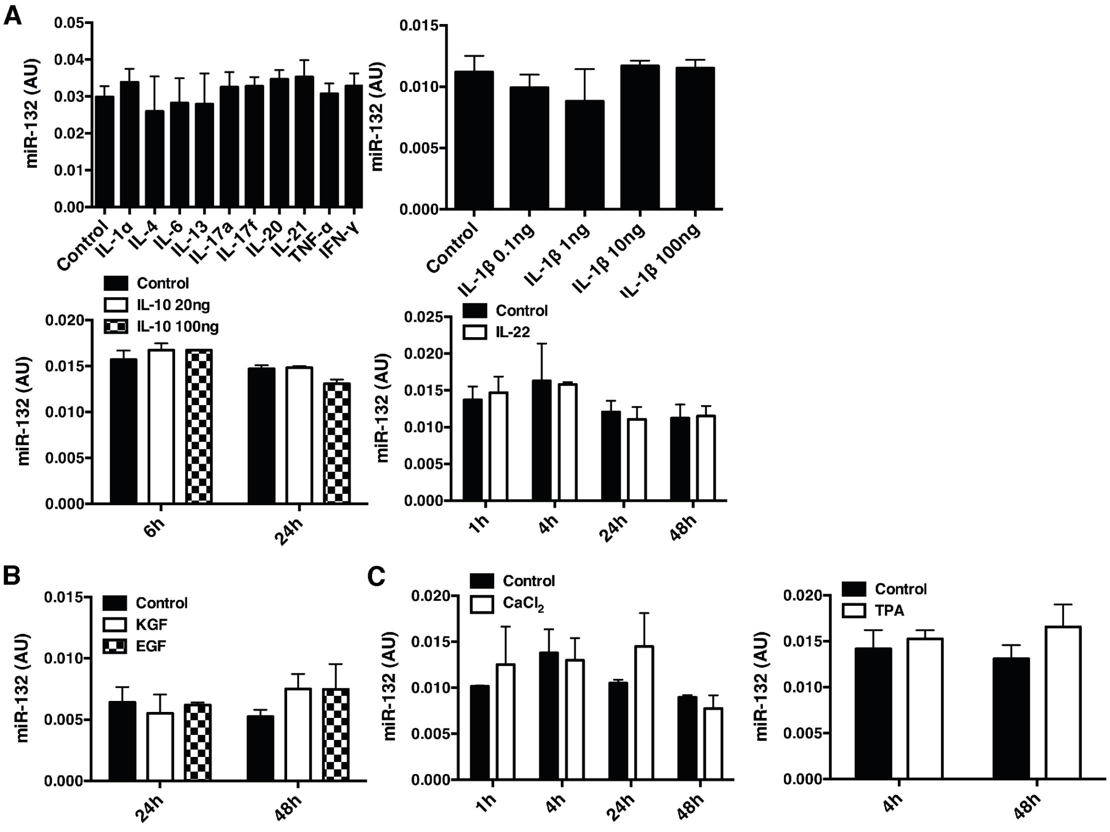
In vivo wound model

In this study, all the mice were caged individually for one week, handled daily, and then wounded. General anesthesia was performed with 3% isoflurane (Abbott). The hair of the back was shaved with an electric clipper followed by a depilatory cream. The skin was rinsed with alcohol and two full-thickness wounds extending through the panniculus carnosus were made on the dorsum on each side of midline, using a 6-mm biopsy punch. Following the surgical procedure, the animals were individually housed. During the first 2 days, the animals received s.c. buprenorphine (0.03 mg/kg) twice a day for relief of any possible distress caused by the procedure. The size of wound area was photographed and measured every other day until approximately 90% of wound area was healed. A circular reference was placed alongside to permit correction for the distance between the camera and the animals. The wound area was calculated in pixels with ImageJ 1.32 software (National Institutes of Health), corrected for the area of the reference circle and expressed as percentage of the original area. Alternatively, the mice were sacrificed at the specified time points after injury and skin biopsies at wound site and intact area were collected to analyze histology and gene expression.

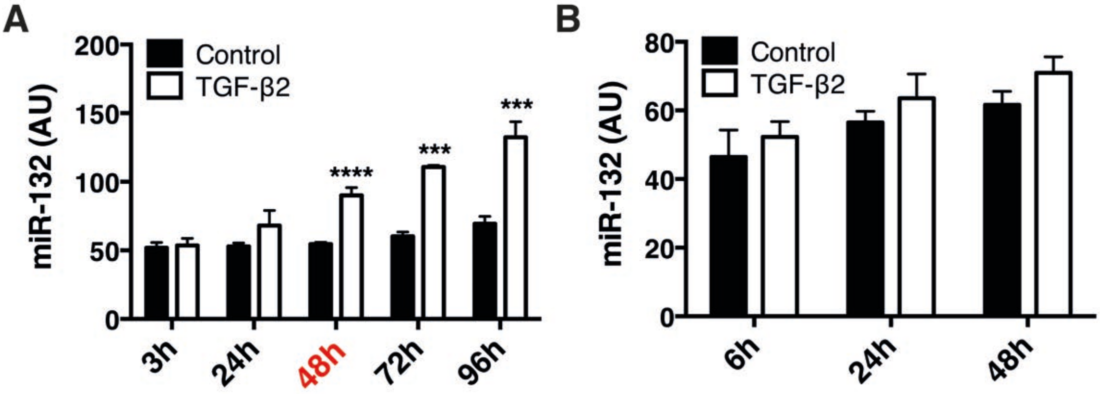
2. Figures



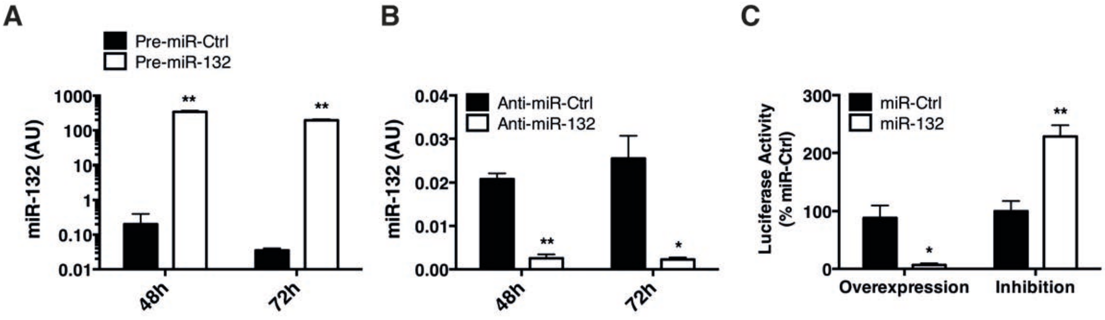
Supplementary Figure 1: The expression of miR-132 in human skin wounds. (A) Two 3 mm surgical wounds were created on the abdominal skin of each healthy volunteer (n=14). The wound edge was excised with a 6 mm biopsy punch at 24 hours, 7 days and 1 month after injury. **(B)** Correlation of miR-132 with its primary transcript (pri-miR-132) expression in human wound biopsies, Spearman-correlation on log-transformed values.



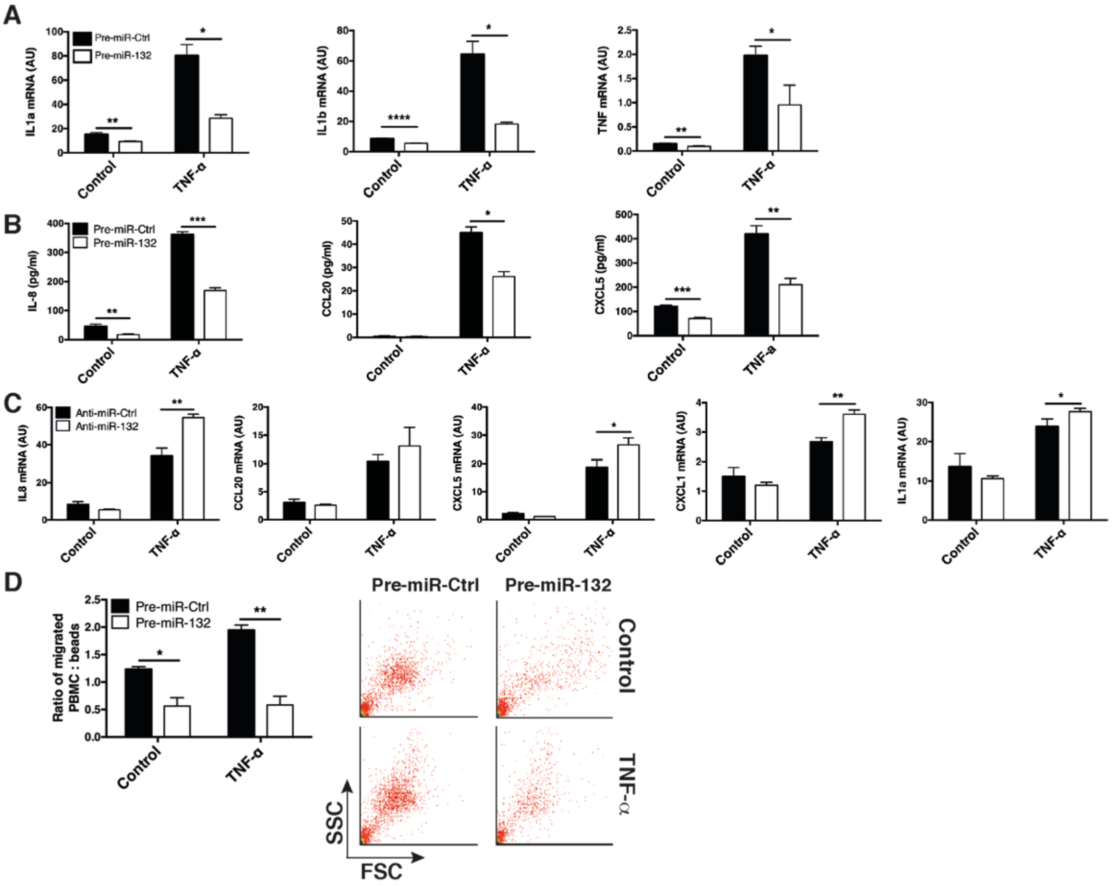
Supplementary Figure 2: The effect of skin wound healing related factors on miR-132 expression in keratinocytes. (A) Human primary keratinocytes were treated with cytokines, including IL-1α (20 ng/mL for 24h), IL-4 (20 ng/mL for 24h), IL-6 (20 ng/mL for 24h), IL-13 (20 ng/mL for 24h), IL-17a (10 ng/mL for 24h), IL-17f (10 ng/mL for 24h), IL-20 (20 ng/mL for 24h), IL-21 (150 ng/mL for 24h), TNF-α (20 ng/mL for 24h), IFN-γ (10 ng/mL for 24h), IL-1β (0.1-100 ng/mL for 24h), IL-10 (20-100 ng/mL for 6h and 24h) and IL-22 (20 ng/mL for 1, 4, 24 and 48h). (**B**) Human primary keratinocytes were treated with KGF (20 ng/mL) and EGF (10 ng/mL) for 24 and 48h. (**C**) Keratinocytes were treated with $CaCl_2$ (1.5 mM) for 1-48h or TPA (50 ng/mL) for 4 and 48h. The expression of miR-132 was analyzed by using qRT-PCR.



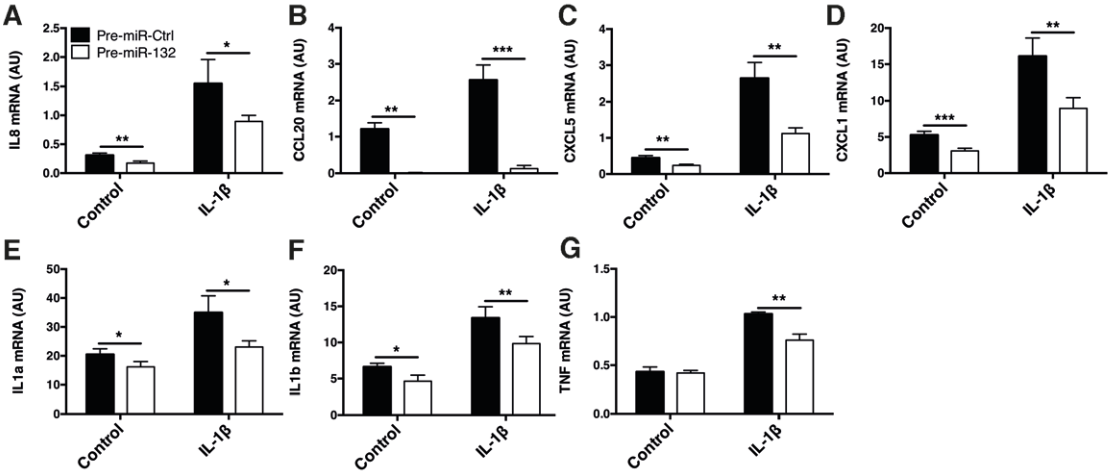
Supplementary Figure 3: TGF-β-inducible miR-132 expression in keratinocytes. (A) Human primary keratinocytes were treated with or not with TGF-β2 (10 ng/mL) for 3-96 hours and miR-132 expression was analysed by qRT-PCR. (**B**) The conditioned medium from the keratinocytes incubated with TGF-β2 for 48 hours was collected and added to the normal human keratinocytes. After 6-48 hours, RNA was extracted from the cells treated with conditioned medium and miR-132 expression was analysed by qRT-PCR. ***$P < 0.001$, ****$P < 0.0001$; Student's t test.



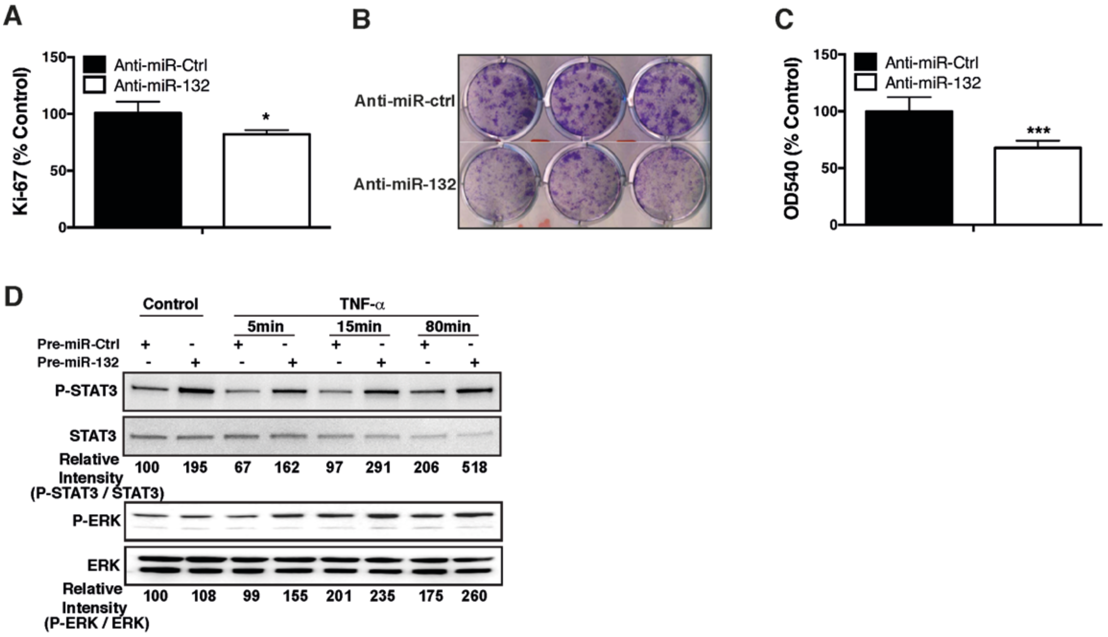
Supplementary Figure 4: Overexpression or inhibition of miR-132 in human keratinocytes. (A) 20 nM miR-132 miRNA precursor (Pre-miR-132) or miRNA precursor negative control #1 (Pre-miR-Ctrl); **(B)** 20 nM miR-132 miRCURY LNA Power inhibitor (Anti-miR-132) or negative control A (Anti-miR-Ctrl) were transfected to human primary keratinocytes for 48-72 hours and the level of miR-132 was analysed by qRT-PCR. (**C**) Luciferase activity was measured in keratinocytes co-transfected with luciferase reporter plasmids containing synthetic sequence repeats that are fully complementary to miR-132 (miR-132 sensor) together with pre-miR-132/pre-miR-Ctrl/anti-miR-132/anti-miR-Ctrl for 24h. *$P < 0.05$, **$P < 0.01$; Student's t test.



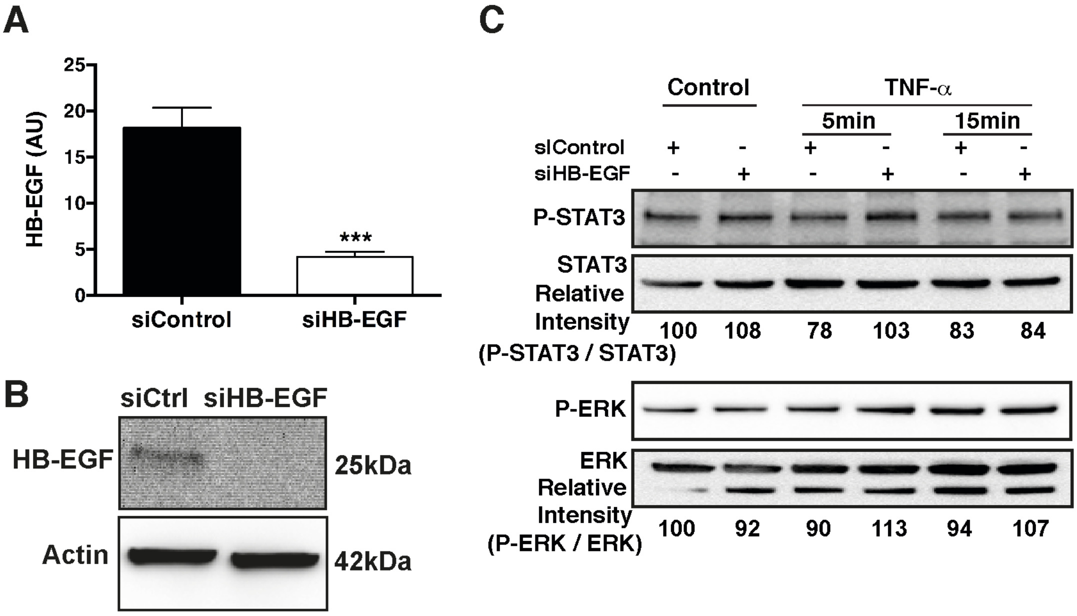
Supplementary Figure 5: MiR-132 regulates keratinocyte chemokine/cytokine production. **(A)** The expression of *IL1A, IL1B* and *TNF* was analysed by qRT-PCR in keratinocytes transfected with pre-miR-132/pre–miR-Ctrl for 48h and then treated with or not with TNF-α for 24h. (**B**) The secretion of IL-8, CXCL5 and CCL20 by keratinocytes treated as described above was analysed using ELISA. (**C**) The expression of *IL8, CXCL5, CCL20, CXCL1* and *IL1A* was analysed by qRT-PCR in keratinocytes transfected with anti-miR-132/anti–miR-Ctrl for 48h and then treated with or not with TNF-α for 24h. (**D**) Human peripheral blood mononuclear cells (PBMC) chemotaxis toward the conditioned medium from cultured keratinocytes transfected with pre-miR-132/pre–miR-Ctrl for 48h and then treated with or not with TNF-α for 24h. The migrating cells were quantified by flow cytometry. Plots showing forward/side scatter (FSC/SSC) of migrated cells.*$P < 0.05$, **$P < 0.01$, ***$P < 0.001$; Student's t test.



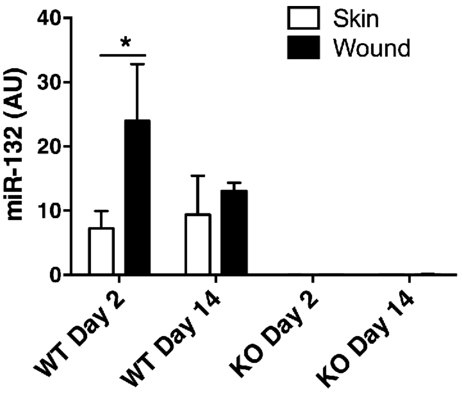
Supplementary Figure 6: MiR-132 regulates keratinocyte chemokine/cytokine production induced by IL-1β. The expression of *IL8* (**A**), *CCL20* (**B**), *CXCL5* (**C**), *CXCL1* (**D**), *IL1A* (**E**), *IL1B* (**F**) and *TNF* (**G**) was analysed by qRT-PCR in keratinocytes transfected with pre-miR-132/pre–miR-Ctrl for 48h and then treated with or not with IL-1β for 24h. .**P* < 0.05, ***P* < 0.01, ****P* < 0.001; Student's t test.



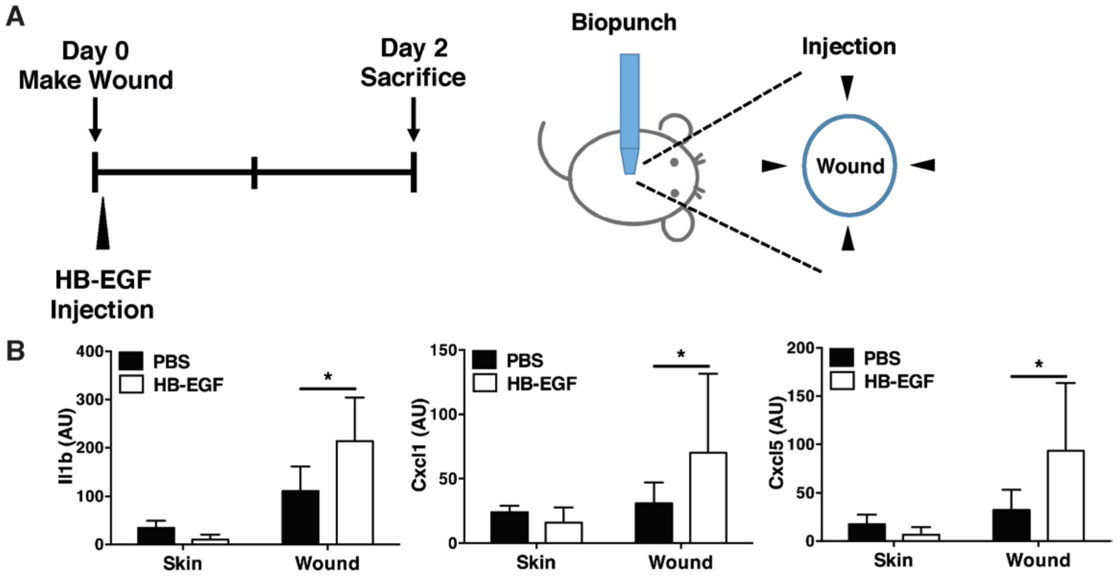
Supplementary Figure 7: The effects of miR-132 on keratinocyte growth. (A) The expression of proliferation marker Ki-67 was analysed in keratinocytes transfected with Anti-miR-132 or Anti-miR-Ctrl for 48h using qRT-PCR. **(B)** Colonies formed by the transfected keratinocytes were stained with crystal violet 8 days after transfection. **(C)** Crystal violet was dissolved with methanol and absorbance value was measured at 540 nm. $*P < 0.05$, $***P < 0.001$; Student's t test. (**D**) Keratinocytes transfected with pre-miR-132/pre-miR-Ctrl for 48h were treated with TNF-α for 5-80 min. Phosphorylated (P-) and total STAT3 and ERK were detected by Western blotting.



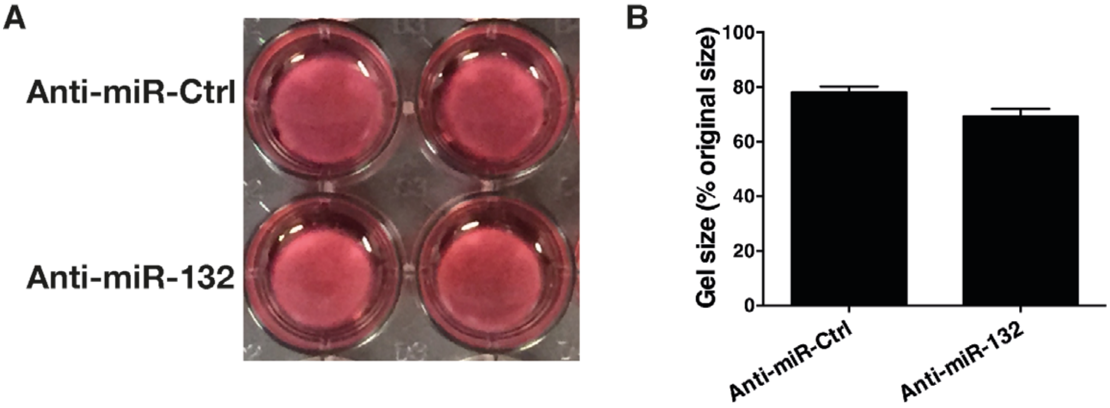
Supplementary Figure 8: Silencing the expression of HB-EGF in human keratinocytes and its effect on STAT3 and ERK signalling. Human primary keratinocytes were transfected with 30 nM Silencer® select pre-designed siRNA for HB-EGF (siRNA ID: s4353) or siRNA negative control #1 for 48 hours. The mRNA **(A)** and protein levels **(B)** of HB-EGF was analysed by qRT-PCR and Western blotting respectively. ***$P < 0.001$; Student's t test. (**C**) Both phosphorylated (P-) and total STAT3 and ERK were detected in TNF-α treated keratinocytes with silenced HB-EGF expression by Western blotting.



Supplementary Figure 9: The expression of miR-132 during skin wound healing process of mice. RNA was extracted from the biopsies of the intact skin and wound edge from WT (n=5) and KO mice (n=9) at 2 and 14 days after injury. The expression of miR-132 was analysed by using qRT-PCR. *$P < 0.05$; Student's t test.



Supplementary Figure 10: Intradermal injection of HB-EGF protein into mouse skin wounds. (A) HB-EGF protein or phosphate-buffered saline (PBS) were injected into the wound edges of mice (5 vs. 5) immediately after wounding. (**B**) The expression of *Il1b, Cxcl1* and *Cxcl5* in intact skin and 2-day wound was analysed using qRT-PCR. * $P < 0.05$; Student's t test.



Supplementary Figure 11: Mouse dermal fibroblast-mediated collagen gel contraction. (A) Mouse dermal fibroblasts transfected with 20 nM Anti-miR-132 or Anti-miR-Ctrl were mixed with collagen gel and seeded in cell culture plate. After incubated for 2 days, the gels were released from the well walls and the pictures were taken 24 hours later. **(B)** The relative gel size was determined by dividing the gel area at 24 hours after detachment with the initial gel area.

3. References

1. Heit B, Liu L, Colarusso P, Puri KD, and Kubes P. PI3K accelerates, but is not required for, neutrophil chemotaxis to fMLP. *Journal of cell science.* 2008;121(Pt 2):205-14.
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3. Huang da W, Sherman BT, and Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. *Nature protocols.* 2009;4(1):44-57.
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Supplementary table 1: miR-132 regulated transcripts in human primary keratinocytes

The presence of miR-132 target sites was predicted by TargetScan; The NF-kB target genes were defined on the website http://bioinfo.lifl.fr/NF-KB.

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
11,000	10,980	10,890	1988,486	9,810	9,810	9,760	887,452	-2,241	0,000	0,023	NM_001945	HBEGF	heparin-binding EGF-like growth factor	Yes	
10,510	10,430	10,460	1415,450	9,290	9,300	9,490	658,471	-2,150	0,000	0,023	NM_015497	TMEM87A	transmembrane protein 87A		
10,380	10,390	10,370	1332,595	9,470	9,350	9,270	659,708	-2,020	0,000	0,023	AK131040	LOC388022	hypothetical gene supported by AK131040		
11,140	11,090	11,110	2215,597	10,140	10,180	10,100	1128,640	-1,963	0,000	0,023	NM_000963	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)		Yes
9,160	9,010	8,960	528,537	8,130	8,300	8,110	290,531	-1,819	0,001	0,036	NM_144601	CMTM3	CKLF-like MARVEL transmembrane domain containing 3		
8,600	8,580	8,450	373,470	7,810	7,670	7,680	211,047	-1,770	0,000	0,028	NM_000425	L1CAM	L1 cell adhesion molecule		
10,510	10,540	10,440	1445,419	9,710	9,740	9,590	821,116	-1,760	0,000	0,024	NM_021727	FADS3	fatty acid desaturase 3		
7,570	7,520	7,450	182,806	6,630	6,780	6,790	106,534	-1,716	0,000	0,024	NR_026825	RPSAP52	ribosomal protein SA pseudogene 52		
9,990	9,760	9,940	955,427	9,250	8,980	9,130	558,034	-1,712	0,002	0,049	NM_030666	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1		Yes
10,290	10,210	10,180	1198,835	9,420	9,500	9,460	704,458	-1,702	0,000	0,023	NM_001040056	MAPK3	mitogen-activated protein kinase 3	Yes	
9,970	9,930	10,020	1005,574	9,200	9,150	9,270	591,203	-1,701	0,000	0,023	NM_203401	STMN1	stathmin 1		
10,250	10,190	10,210	1190,113	9,370	9,420	9,570	702,260	-1,695	0,000	0,024	NM_015379	BRI3	brain protein I3		
9,540	9,550	9,580	753,136	8,710	8,810	8,910	449,541	-1,675	0,000	0,024	NM_024039	MIS12	MIS12, MIND kinetochore complex component, homolog (S. pombe)		
10,370	10,360	10,310	1302,353	9,560	9,610	9,670	783,633	-1,662	0,000	0,023	NM_002890	RASA1	RAS p21 protein activator (GTPase activating protein) 1	Yes	
9,170	9,110	9,110	560,387	8,300	8,390	8,510	338,397	-1,656	0,000	0,024	NM_006832	FERMT2	fermitin family homolog 2 (Drosophila)		
8,720	8,660	8,770	420,910	8,030	7,980	7,970	254,862	-1,652	0,000	0,023	NM_006923	SDF2	stromal cell-derived factor 2		
8,330	8,300	8,340	320,334	7,760	7,700	7,440	199,450	-1,606	0,001	0,038	NM_003046	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2		
9,200	9,090	9,160	568,381	8,410	8,480	8,530	355,615	-1,598	0,000	0,024	NM_014992	DAAM1	dishevelled associated activator of morphogenesis 1		
11,790	11,820	11,820	3590,749	11,240	11,140	11,020	2250,655	-1,595	0,000	0,024	NM_138689	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B		
9,750	9,690	9,620	824,653	9,070	9,130	8,840	518,662	-1,590	0,001	0,043	NM_000240	MAOA	monoamine oxidase A		
9,270	9,320	9,130	605,599	8,690	8,560	8,470	381,667	-1,587	0,002	0,046	NM_001511	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)		Yes
11,180	11,120	11,180	2288,642	10,520	10,500	10,510	1458,251	-1,569	0,000	0,023	NM_001020818	MYADM	myeloid-associated differentiation marker		
10,450	10,340	10,340	1330,365	9,730	9,750	9,720	851,219	-1,563	0,000	0,024	NM_014049	ACAD9	acyl-CoA dehydrogenase family, member 9		
11,910	11,900	11,770	3720,794	11,260	11,280	11,180	2419,751	-1,538	0,000	0,032	NM_001415	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	Yes	
9,950	9,910	9,900	968,872	9,370	9,290	9,240	630,782	-1,536	0,000	0,023	NM_175852	TXLNA	taxilin alpha		
10,280	10,140	10,250	1196,478	9,700	9,620	9,490	779,234	-1,536	0,001	0,039	NM_015169	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)		
8,700	8,830	8,720	430,880	8,050	8,280	8,080	282,153	-1,527	0,001	0,045	NM_032449	CC2D1B	coiled-coil and C2 domain containing 1B	Yes	
10,530	10,420	10,420	1406,220	9,770	9,890	9,890	923,583	-1,523	0,000	0,029	NM_004124	GMFB	glia maturation factor, beta	Yes	
7,920	7,810	7,830	231,382	7,350	7,310	7,110	153,323	-1,509	0,001	0,042	NM_000387	SLC25A20	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20		
9,580	9,380	9,420	705,556	8,860	8,910	8,840	467,980	-1,508	0,002	0,046	NM_004548	NDUFB10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa		
10,820	10,730	10,840	1779,744	10,270	10,260	10,090	1183,627	-1,504	0,001	0,036	NM_000930	PLAT	plasminogen activator, tissue		
11,430	11,320	11,270	2595,070	10,850	10,700	10,720	1731,989	-1,498	0,001	0,042	NM_144975	SLFN5	schlafen family member 5		
11,770	11,700	11,770	3437,257	11,140	11,220	11,130	2294,397	-1,498	0,000	0,024	NM_014764	DAZAP2	DAZ associated protein 2	Yes	
8,650	8,470	8,580	379,659	7,970	7,990	8,000	253,655	-1,497	0,001	0,037	NM_032415	CARD11	caspase recruitment domain family, member 11		
6,050	5,910	5,870	61,624	5,380	5,340	5,380	41,263	-1,493	0,001	0,041	NM_000640	IL13RA2	interleukin 13 receptor, alpha 2		
10,830	10,750	10,810	1779,265	10,210	10,330	10,130	1197,396	-1,486	0,001	0,032	NM_000687	AHCY	adenosylhomocysteinase		
10,530	10,510	10,440	1441,991	9,840	9,970	9,960	971,810	-1,484	0,000	0,026	NM_003330	TXNRD1	thioredoxin reductase 1		
9,580	9,560	9,610	767,211	8,920	9,080	9,040	517,323	-1,483	0,000	0,024	NM_019067	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like		
8,410	8,320	8,360	329,425	7,850	7,760	7,780	222,427	-1,481	0,000	0,024	NM_175918	CRIPAK	cysteine-rich PAK1 inhibitor		
9,290	9,250	9,160	602,306	8,580	8,740	8,680	406,798	-1,481	0,001	0,036	NM_015106	RAD54L2	RAD54-like 2 (S. cerevisiae)		
7,040	6,870	6,950	124,070	6,340	6,330	6,510	84,199	-1,474	0,002	0,049	NM_001017372	SLC27A6	solute carrier family 27 (fatty acid transporter), member 6		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
7,230	7,180	7,270	149,825	6,830	6,560	6,610	101,935	-1,470	0,002	0,049	NM_153345	TMEM139	transmembrane protein 139		
8,960	8,810	8,830	467,303	8,360	8,190	8,390	318,685	-1,466	0,002	0,049	NM_197965	SLC10A6	solute carrier family 10 (sodium/bile acid cotransporter family), member 6		
10,230	10,170	10,130	1157,867	9,730	9,600	9,550	791,627	-1,463	0,001	0,036	NM_134268	CYGB	cytoglobin		
10,380	10,410	10,440	1360,770	9,760	9,900	9,930	932,665	-1,459	0,000	0,028	NM_001135599	TGFB2	transforming growth factor, beta 2		
8,440	8,450	8,460	349,712	7,870	8,040	7,820	241,037	-1,451	0,001	0,036	NM_139314	ANGPTL4	angiopoietin-like 4		
9,440	9,390	9,460	689,926	8,860	8,910	8,910	475,574	-1,451	0,000	0,023	NM_015993	PLLP	plasma membrane proteolipid (plasmolipin)		
9,140	9,070	9,080	547,608	8,550	8,520	8,610	377,540	-1,451	0,000	0,024	NM_003786	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3		
8,890	8,860	8,890	471,159	8,310	8,420	8,300	325,016	-1,450	0,000	0,024	NM_053279	FAM167A	family with sequence similarity 167, member A	Yes	
9,640	9,600	9,550	774,508	9,040	9,150	8,990	534,319	-1,450	0,000	0,030	NM_031283	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)	Yes	
10,580	10,510	10,560	1499,535	10,050	10,030	10,000	1043,209	-1,437	0,000	0,023	NM_000576	IL1B	interleukin 1, beta		Yes
10,370	10,280	10,240	1258,680	9,810	9,840	9,680	878,149	-1,433	0,001	0,041	NM_001098672	HEPHL1	hephaestin-like 1		
8,560	8,550	8,530	373,955	8,020	8,090	7,970	260,928	-1,433	0,000	0,023	NM_022765	MICAL1	microtubule associated monoxygenase, calponin and LIM domain containing 1		
8,730	8,600	8,660	405,712	8,220	8,180	8,030	283,190	-1,433	0,001	0,043	NM_130766	INPP5K	inositol polyphosphate-5-phosphatase K		
10,210	10,100	10,130	1134,167	9,620	9,630	9,650	794,216	-1,428	0,000	0,024	NM_178354	LCE1F	late cornified envelope 1F		
8,290	8,320	8,290	315,188	7,860	7,750	7,770	221,956	-1,420	0,000	0,024	NR_026717	STK19	serine/threonine kinase 19		
8,410	8,370	8,500	344,342	8,020	7,870	7,880	243,028	-1,417	0,001	0,043	NM_007074	CORO1A	coronin, actin binding protein, 1A		
9,720	9,640	9,670	818,617	9,220	9,100	9,210	579,105	-1,414	0,000	0,028	NM_005504	BCAT1	branched chain amino-acid transaminase 1, cytosolic		
8,290	8,300	8,260	311,575	7,750	7,880	7,720	220,559	-1,413	0,000	0,029	NM_203351	MAP3K3	mitogen-activated protein kinase kinase kinase 3	Yes	
8,500	8,490	8,430	355,490	7,960	7,930	8,040	252,024	-1,411	0,000	0,024	NM_031419	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta		Yes
8,680	8,700	8,700	413,965	8,120	8,320	8,150	293,942	-1,408	0,001	0,037	NM_033338	CASP7	caspase 7, apoptosis-related cysteine peptidase		
9,150	9,170	9,050	558,062	8,530	8,670	8,690	396,654	-1,407	0,001	0,042	NM_001042685	LGALS9B	lectin, galactoside-binding, soluble, 9B		
9,470	9,460	9,460	705,910	9,020	9,050	8,850	503,548	-1,402	0,001	0,036	NM_001876	CPT1A	carnitine palmitoyltransferase 1A (liver)		
8,870	8,850	8,910	470,119	8,390	8,410	8,370	335,482	-1,401	0,000	0,023	NM_000725	CACNB3	calcium channel, voltage-dependent, beta 3 subunit		
9,780	9,730	9,750	863,157	9,190	9,310	9,300	616,382	-1,400	0,000	0,024	NM_173470	MMGT1	membrane magnesium transporter 1	Yes	
10,080	10,030	9,930	1034,468	9,440	9,590	9,560	740,031	-1,398	0,002	0,047	NM_003828	MTMR1	myotubularin related protein 1		
9,440	9,330	9,350	663,582	9,000	8,890	8,790	476,352	-1,393	0,002	0,049	NM_001141	ALOX15B	arachidonate 15-lipoxygenase, type B		
10,170	10,100	10,160	1131,219	9,660	9,650	9,700	814,721	-1,389	0,000	0,023	NM_014286	NCS1	neuronal calcium sensor 1		
9,640	9,660	9,650	803,427	9,190	9,280	9,060	579,827	-1,386	0,001	0,040	NM_002350	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog		
10,410	10,320	10,350	1314,671	9,770	9,910	9,990	950,699	-1,383	0,002	0,047	NM_003821	RIPK2	receptor-interacting serine-threonine kinase 2		Yes
12,480	12,570	12,520	5888,987	12,030	12,090	12,050	4260,724	-1,382	0,000	0,024	NM_000527	LDLR	low density lipoprotein receptor		
8,210	8,240	8,240	300,260	7,830	7,700	7,770	217,919	-1,378	0,000	0,024	NR_026717	STK19	serine/threonine kinase 19		
8,210	8,240	8,240	300,260	7,830	7,700	7,770	217,919	-1,378	0,000	0,024	NR_026717	STK19	serine/threonine kinase 19		
10,080	10,050	10,050	1067,536	9,530	9,740	9,520	776,202	-1,375	0,002	0,049	NM_005698	SCAMP3	secretory carrier membrane protein 3		
9,350	9,390	9,400	666,361	9,030	8,860	8,880	486,181	-1,371	0,001	0,037	NM_017583	TRIM44	tripartite motif-containing 44		
9,210	9,230	9,160	588,255	8,740	8,790	8,710	429,658	-1,369	0,000	0,024	NM_001389	DSCAM	Down syndrome cell adhesion molecule		
10,100	10,000	9,990	1046,141	9,560	9,630	9,550	765,597	-1,366	0,001	0,036	NM_015176	FBXO28	F-box protein 28	Yes	
11,620	11,610	11,540	3083,678	11,220	11,130	11,070	2258,769	-1,365	0,001	0,036	NM_001130145	YAP1	Yes-associated protein 1		
7,600	7,450	7,590	187,179	7,160	7,060	7,080	137,249	-1,364	0,002	0,049	NM_207627	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1		
9,690	9,820	9,680	850,062	9,260	9,340	9,250	623,350	-1,364	0,002	0,046	NM_004036	ADCY3	adenylate cyclase 3	Yes	
7,890	7,950	7,940	243,353	7,500	7,480	7,460	178,538	-1,363	0,000	0,023	NM_003739	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)		
9,140	9,030	8,990	531,799	8,590	8,670	8,570	390,899	-1,361	0,002	0,047	NM_001040445	ASB1	ankyrin repeat and SOCS box-containing 1	Yes	
8,720	8,690	8,740	420,748	8,300	8,230	8,290	309,472	-1,360	0,000	0,023	NM_014945	ABLIM3	actin binding LIM protein family, member 3		
9,230	9,110	9,210	581,760	8,750	8,760	8,720	428,584	-1,357	0,001	0,033	NM_005536	IMPA1	inositol(myo)-1(or 4)-monophosphatase 1		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
9,660	9,670	9,680	814,642	9,290	9,270	9,130	601,215	-1,355	0,001	0,032	NM_001042454	TGFB1I1	transforming growth factor beta 1 induced transcript 1		
12,000	12,010	12,000	4105,497	11,550	11,630	11,530	3041,676	-1,350	0,000	0,024	NM_016441	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)		
11,700	11,720	11,640	3297,291	11,210	11,360	11,190	2444,546	-1,349	0,001	0,044	NM_005988	SPRR2A	small proline-rich protein 2A		
10,830	10,870	10,850	1845,879	10,390	10,460	10,410	1370,324	-1,347	0,000	0,023	NM_016823	CRK	v-crk sarcoma virus CT10 oncogene homolog (avian)	Yes	
11,300	11,260	11,230	2458,595	10,800	10,840	10,870	1829,142	-1,344	0,000	0,024	NM_203459	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1	Yes	
10,400	10,430	10,460	1379,766	9,950	10,060	10,000	1026,868	-1,344	0,000	0,025	NM_052855	ANKRD40	ankyrin repeat domain 40	Yes	
10,950	10,820	10,870	1885,847	10,370	10,460	10,530	1403,502	-1,344	0,002	0,049	NM_001025231	KPRP	keratinocyte proline-rich protein		
7,870	7,860	7,880	233,945	7,420	7,400	7,530	174,992	-1,337	0,000	0,028	NM_005639	SYT1	synaptotagmin I		
10,870	10,790	10,800	1808,329	10,430	10,470	10,310	1355,793	-1,334	0,001	0,042	NM_001146069	MFSD10	major facilitator superfamily domain containing 10		
10,110	10,100	10,050	1087,579	9,710	9,650	9,660	816,649	-1,332	0,000	0,024	NR_024386	PLEKHM1P	pleckstrin homology domain containing, family M (with RUN domain) member 1 pseudoge		
10,830	10,810	10,820	1807,805	10,400	10,420	10,400	1357,463	-1,332	0,000	0,023	NM_016626	MEX3C	mex-3 homolog C (C. elegans)	Yes	
10,450	10,480	10,540	1438,637	10,040	10,130	10,060	1080,277	-1,332	0,000	0,030	NM_001099415	POM121C	POM121 membrane glycoprotein C	Yes	
10,500	10,460	10,480	1428,309	10,030	10,050	10,120	1072,814	-1,331	0,000	0,024	NM_017958	PLEKHB2	pleckstrin homology domain containing, family B (evectins) member 2		
8,320	8,360	8,270	318,939	7,860	7,900	7,960	240,060	-1,329	0,000	0,031	NM_002185	IL7R	interleukin 7 receptor		
10,780	10,810	10,680	1731,407	10,360	10,400	10,290	1305,796	-1,326	0,001	0,046	NM_002192	INHBA	inhibin, beta A		Yes
10,290	10,170	10,200	1193,437	9,770	9,870	9,800	900,102	-1,326	0,001	0,042	NM_024662	NAT10	N-acetyltransferase 10 (GCN5-related)		
9,500	9,620	9,530	750,083	9,090	9,140	9,200	565,756	-1,326	0,001	0,043	NM_015062	PPRC1	peroxisome proliferator-activated receptor gamma, coactivator-related 1		
10,690	10,760	10,670	1671,798	10,280	10,280	10,340	1260,936	-1,326	0,000	0,029	NM_001137552	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	Yes	
10,980	11,070	10,980	2063,143	10,550	10,670	10,590	1556,619	-1,325	0,001	0,039	NM_001219	CALU	calumenin	Yes	
6,640	6,580	6,630	98,149	6,240	6,240	6,160	74,225	-1,322	0,000	0,024	ENST000003793	LOC727963	similar to elongation factor Tu GTP binding domain containing 1		
10,250	10,220	10,250	1209,394	9,710	9,910	9,890	916,143	-1,320	0,002	0,049	NM_001164446	C6orf132	chromosome 6 open reading frame 132		
9,670	9,560	9,600	781,834	9,280	9,180	9,170	592,578	-1,319	0,001	0,042	NM_007150	ZNF185	zinc finger protein 185 (LIM domain)		
7,930	7,930	7,880	241,106	7,420	7,530	7,590	182,917	-1,318	0,001	0,041	NM_016546	C1RL	complement component 1, r subcomponent-like		
10,720	10,790	10,810	1750,858	10,360	10,420	10,350	1329,805	-1,317	0,000	0,029	NM_172020	POM121	POM121 membrane glycoprotein (rat)	Yes	
8,820	8,830	8,870	458,304	8,450	8,430	8,450	348,101	-1,317	0,000	0,023	NM_201574	SLC4A3	solute carrier family 4, anion exchanger, member 3		
7,840	7,830	7,800	226,510	7,420	7,450	7,410	172,060	-1,317	0,000	0,023	NM_006045	ATP9A	ATPase, class II, type 9A		
7,470	7,400	7,400	171,696	7,090	7,010	6,980	130,456	-1,316	0,001	0,033	NM_002288	LAIR2	leukocyte-associated immunoglobulin-like receptor 2		
9,660	9,680	9,630	807,217	9,180	9,260	9,340	613,738	-1,315	0,001	0,037	NM_014903	NAV3	neuron navigator 3		
8,280	8,310	8,280	313,011	7,880	7,940	7,870	238,360	-1,313	0,000	0,023	NM_005581	BCAM	basal cell adhesion molecule (Lutheran blood group)		
8,910	8,830	8,900	471,279	8,430	8,590	8,460	360,791	-1,306	0,002	0,048	NM_005823	MSLN	mesothelin		
8,440	8,400	8,430	343,326	8,120	8,000	8,000	263,401	-1,303	0,001	0,033	NM_013246	CLCF1	cardiotrophin-like cytokine factor 1		
11,270	11,290	11,270	2480,985	10,810	11,000	10,870	1904,939	-1,302	0,002	0,047	AK302302	ODZ2	odz, odd Oz/ten-m homolog 2 (Drosophila)		
11,020	11,010	10,990	2057,562	10,600	10,620	10,660	1581,286	-1,301	0,000	0,023	NM_006379	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C		
10,820	10,720	10,740	1734,917	10,370	10,460	10,320	1336,738	-1,298	0,002	0,047	NM_022825	PORCN	porcupine homolog (Drosophila)		
9,470	9,430	9,430	696,248	9,130	9,100	8,970	536,830	-1,297	0,001	0,042	NM_001964	EGR1	early growth response 1	Yes	Yes
8,980	8,950	9,000	503,837	8,620	8,610	8,580	388,948	-1,295	0,000	0,023	NM_022900	CASD1	CAS1 domain containing 1		
9,030	8,990	9,000	514,407	8,680	8,690	8,530	397,598	-1,294	0,001	0,043	NM_018110	DOK4	docking protein 4	Yes	
7,220	7,190	7,190	147,041	6,720	6,900	6,860	113,670	-1,294	0,002	0,046	AK127420	LOC400464	similar to FLJ43276 protein		
8,470	8,430	8,550	358,095	8,160	8,110	8,070	277,012	-1,293	0,001	0,043	NM_001012631	IL32	interleukin 32		
8,050	8,080	7,980	262,700	7,690	7,620	7,690	203,240	-1,293	0,001	0,036	NM_024676	C1orf113	chromosome 1 open reading frame 113		
7,940	7,900	7,970	245,053	7,560	7,540	7,600	189,609	-1,292	0,000	0,024	AF005082	C1orf46	chromosome 1 open reading frame 46		
9,420	9,390	9,380	674,076	9,110	9,040	8,930	522,237	-1,291	0,002	0,046	NM_007275	TUSC2	tumor suppressor candidate 2	Yes	
8,710	8,640	8,750	416,079	8,310	8,340	8,350	322,562	-1,290	0,001	0,035	NM_022367	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytopl		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
11,830	11,730	11,760	3501,954	11,450	11,420	11,350	2716,009	-1,289	0,001	0,040	NM_001135242	NDRG1	N-myc downstream regulated 1		
9,840	9,780	9,840	904,061	9,420	9,500	9,440	701,226	-1,289	0,000	0,028	NM_019096	GTPBP2	GTP binding protein 2		
9,890	9,850	9,930	949,069	9,490	9,540	9,550	737,707	-1,287	0,000	0,028	NM_001668	ARNT	aryl hydrocarbon receptor nuclear translocator		
9,290	9,330	9,270	628,986	8,960	8,900	8,940	488,952	-1,286	0,000	0,024	NM_181552	CUX1	cut-like homeobox 1	Yes	
8,680	8,650	8,650	404,521	8,230	8,400	8,270	315,576	-1,282	0,002	0,047	NM_005490	SH2D3A	SH2 domain containing 3A		
10,560	10,610	10,540	1520,470	10,190	10,280	10,170	1187,846	-1,280	0,001	0,036	NM_002224	ITPR3	inositol 1,4,5-triphosphate receptor, type 3		
10,710	10,690	10,740	1679,108	10,400	10,380	10,290	1311,911	-1,280	0,000	0,031	NM_020360	PLSCR3	phospholipid scramblase 3		
11,350	11,350	11,340	2604,290	11,010	11,040	10,920	2035,116	-1,280	0,000	0,029	NM_001080779	MYO1C	myosin IC		
9,980	9,950	9,940	993,769	9,560	9,580	9,670	778,273	-1,277	0,000	0,030	NM_001042537	SLC9A6	solute carrier family 9 (sodium/hydrogen exchanger), member 6		
10,930	10,820	10,900	1889,877	10,530	10,570	10,500	1482,297	-1,275	0,001	0,040	NM_020387	RAB25	RAB25, member RAS oncogene family		
12,280	12,260	12,290	4962,050	11,890	11,920	11,970	3894,021	-1,274	0,000	0,024	NM_002539	ODC1	ornithine decarboxylase 1		
8,000	7,940	8,080	257,390	7,650	7,680	7,650	202,261	-1,273	0,002	0,047	NM_019034	RHOF	ras homolog gene family, member F (in filopodia)		
9,260	9,140	9,270	598,219	8,900	8,880	8,850	470,096	-1,273	0,002	0,049	NM_003325	HIRA	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)		
6,300	6,370	6,400	81,984	6,060	5,990	5,980	64,465	-1,272	0,001	0,040	NM_016118	NUB1	negative regulator of ubiquitin-like proteins 1		
10,900	10,940	10,930	1942,143	10,600	10,600	10,530	1527,590	-1,271	0,000	0,024	NM_015368	PANX1	pannexin 1		
8,910	8,840	8,890	471,234	8,480	8,510	8,610	370,778	-1,271	0,001	0,042	NM_024577	SH3TC2	SH3 domain and tetratricopeptide repeats 2		
8,560	8,540	8,550	374,812	8,160	8,210	8,250	295,525	-1,268	0,000	0,024	NM_153229	TMEM92	transmembrane protein 92		
10,020	9,990	9,970	1019,383	9,630	9,580	9,740	804,282	-1,267	0,002	0,047	NM_015252	EHBP1	EH domain binding protein 1		
8,830	8,930	8,810	463,887	8,520	8,510	8,520	366,248	-1,267	0,001	0,043	NM_022489	INF2	inverted formin, FH2 and WH2 domain containing		
8,550	8,570	8,450	368,183	8,190	8,210	8,150	290,733	-1,266	0,002	0,046	NM_001570	IRAK2	interleukin-1 receptor-associated kinase 2		
11,300	11,350	11,230	2511,217	10,900	10,990	10,970	1983,519	-1,266	0,002	0,047	NM_018222	PARVA	parvin, alpha		
9,820	9,870	9,880	927,308	9,470	9,580	9,500	732,872	-1,265	0,001	0,036	NM_182705	FAM101B	family with sequence similarity 101, member B		
8,670	8,610	8,580	393,573	8,250	8,290	8,310	311,599	-1,263	0,001	0,033	NM_198236	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	Yes	
7,730	7,710	7,690	209,396	7,400	7,330	7,390	165,842	-1,263	0,000	0,024	NM_024734	CLMN	calmin (calponin-like, transmembrane)	Yes	
6,070	6,080	6,180	69,112	5,810	5,760	5,760	54,829	-1,261	0,001	0,045	NM_000206	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)		
8,560	8,580	8,530	376,580	8,200	8,300	8,170	299,085	-1,259	0,001	0,040	NM_001142397	KIAA0427	KIAA0427		
11,080	11,050	11,160	2191,067	10,790	10,740	10,770	1742,343	-1,258	0,001	0,041	NM_002776	KLK10	kallikrein-related peptidase 10		
12,910	12,870	12,890	7591,095	12,560	12,580	12,540	6038,994	-1,257	0,000	0,023	NM_003486	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5		
12,120	12,060	12,070	4340,282	11,740	11,710	11,810	3453,741	-1,257	0,001	0,035	NM_005978	S100A2	S100 calcium binding protein A2		
9,370	9,410	9,370	667,886	9,080	9,100	8,990	532,801	-1,254	0,001	0,035	NR_026590	CDYL	chromodomain protein, Y-like		
11,630	11,660	11,660	3213,810	11,300	11,400	11,270	2564,410	-1,253	0,001	0,039	NM_014225	PPP2R1A	protein phosphatase 2, regulatory subunit A, alpha		
8,510	8,520	8,460	361,263	8,090	8,180	8,240	288,277	-1,253	0,002	0,048	NM_004726	REPS2	RALBP1 associated Eps domain containing 2		
11,560	11,540	11,560	3005,447	11,270	11,210	11,220	2407,922	-1,248	0,000	0,023	NM_016185	HN1	hematological and neurological expressed 1	Yes	
11,050	10,990	10,980	2057,960	10,720	10,710	10,630	1648,828	-1,248	0,001	0,037	NM_032237	SGK196	protein kinase-like protein SgK196		
11,060	11,050	11,090	2145,008	10,700	10,830	10,720	1723,519	-1,245	0,001	0,043	NM_006456	ST6GALNAC2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6		
7,990	7,920	7,950	247,901	7,690	7,640	7,590	199,546	-1,242	0,001	0,037	NM_194285	SPTY2D1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)		
10,400	10,420	10,400	1357,463	10,070	10,170	10,040	1093,253	-1,242	0,001	0,040	NM_032899	FAM83A	family with sequence similarity 83, member A		
6,280	6,250	6,260	76,819	6,020	5,880	5,950	61,868	-1,242	0,001	0,042	NM_152670	C2orf51	chromosome 2 open reading frame 51		
9,370	9,380	9,360	661,695	9,000	9,150	9,020	533,082	-1,241	0,002	0,049	NM_001145642	KIAA0226	KIAA0226		
8,410	8,320	8,430	334,870	8,060	8,120	8,050	270,034	-1,240	0,002	0,048	NM_032727	INA	internexin neuronal intermediate filament protein, alpha		
8,770	8,750	8,830	440,725	8,490	8,460	8,470	355,422	-1,240	0,000	0,029	BC047380	CRYBB2P1	crystallin, beta B2 pseudogene 1		
9,770	9,710	9,750	857,236	9,430	9,430	9,440	691,383	-1,240	0,000	0,024	NM_006141	DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2	Yes	
11,610	11,540	11,620	3083,678	11,270	11,320	11,260	2492,837	-1,237	0,001	0,036	NM_005727	TSPAN1	tetraspanin 1		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)			Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average		p-value	q-value	Public id	Symbol	Name		
9,390	9,340	9,360	658,701	9,050	9,070	9,050	532,522	-1,237	0,000	0,023	NM_013441	RCAN3	RCAN family member 3		
11,620	11,570	11,550	3062,091	11,300	11,280	11,240	2475,576	-1,237	0,000	0,029	NM_007350	PHLDA1	pleckstrin homology-like domain, family A, member 1		
8,120	8,120	8,110	277,563	7,810	7,790	7,830	224,426	-1,237	0,000	0,023	NM_018271	THNSL2	threonine synthase-like 2 (S. cerevisiae)		
12,310	12,260	12,250	4951,236	11,970	12,000	11,930	4003,237	-1,237	0,000	0,029	NM_013336	SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)		
10,200	10,160	10,180	1160,147	9,860	9,910	9,850	938,084	-1,237	0,000	0,024	NM_001013642	TRNP1	TMF1-regulated nuclear protein 1		
10,480	10,470	10,520	1438,313	10,150	10,210	10,200	1165,638	-1,234	0,000	0,024	NM_001025366	VEGFA	vascular endothelial growth factor A		
8,700	8,710	8,680	414,929	8,330	8,370	8,480	336,564	-1,233	0,002	0,049	NM_024650	C11orf80	chromosome 11 open reading frame 80		
10,920	10,920	10,940	1946,542	10,610	10,640	10,630	1581,108	-1,231	0,000	0,023	NM_002340	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)		
10,600	10,530	10,580	1520,468	10,240	10,260	10,310	1235,005	-1,231	0,001	0,033	NM_001432	EREG	epiregulin		
9,940	9,860	9,920	960,116	9,580	9,670	9,580	781,785	-1,228	0,001	0,045	NM_002648	PIM1	pim-1 oncogene		Yes
9,170	9,150	9,140	569,435	8,820	8,900	8,850	463,699	-1,228	0,000	0,024	NM_005419	STAT2	signal transducer and activator of transcription 2, 113kDa		
9,600	9,570	9,640	777,996	9,240	9,350	9,330	633,611	-1,228	0,001	0,044	NM_198282	TMEM173	transmembrane protein 173		
10,230	10,210	10,220	1192,706	9,990	9,890	9,890	971,526	-1,228	0,001	0,036	NM_138795	ARL8A	ADP-ribosylation factor-like 8A		
9,400	9,370	9,300	655,873	9,100	9,040	9,050	535,066	-1,226	0,001	0,043	NM_003417	ZNF264	zinc finger protein 264		
10,670	10,670	10,650	1621,782	10,370	10,380	10,360	1323,390	-1,226	0,000	0,023	NM_033631	LUZP1	leucine zipper protein 1		
9,410	9,480	9,390	688,439	9,090	9,190	9,120	561,812	-1,225	0,002	0,049	NM_006306	SMC1A	structural maintenance of chromosomes 1A		
11,630	11,630	11,590	3140,524	11,340	11,290	11,340	2562,836	-1,225	0,000	0,024	NM_024422	DSC2	desmocollin 2		
8,430	8,480	8,550	358,917	8,180	8,190	8,220	293,409	-1,223	0,002	0,049	NR_026052	MGC2752	hypothetical LOC65996		
11,800	11,780	11,810	3557,679	11,530	11,500	11,490	2909,926	-1,223	0,000	0,023	NM_001128619	LUZP6	leucine zipper protein 6		
5,020	5,040	5,040	32,749	4,760	4,690	4,780	26,794	-1,222	0,000	0,029	NM_205859	OR2K2	olfactory receptor, family 2, subfamily K, member 2		
8,970	8,960	8,970	500,308	8,650	8,720	8,670	410,234	-1,220	0,000	0,024	NM_001079872	CUL4B	cullin 4B		
7,090	7,100	7,130	137,832	6,860	6,760	6,840	113,036	-1,219	0,001	0,036	NM_001030060	SAMD5	sterile alpha motif domain containing 5		
11,250	11,290	11,250	2458,320	10,910	10,990	11,030	2016,343	-1,219	0,001	0,043	NM_138420	AHNAK2	AHNAK nucleoprotein 2		
9,470	9,460	9,480	709,187	9,190	9,240	9,120	581,716	-1,219	0,001	0,038	NM_017694	MFSD6	major facilitator superfamily domain containing 6		
7,850	7,870	7,890	233,956	7,520	7,610	7,630	192,332	-1,216	0,001	0,040	NM_001932	MPP3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)		
10,570	10,500	10,550	1489,177	10,250	10,310	10,220	1226,632	-1,214	0,001	0,041	NM_016229	CYB5R2	cytochrome b5 reductase 2		
8,620	8,570	8,610	388,067	8,370	8,310	8,290	320,401	-1,211	0,001	0,033	NM_006454	MXD4	MAX dimerization protein 4		
11,900	11,890	11,850	3769,510	11,640	11,610	11,560	3112,180	-1,211	0,001	0,032	NM_001080412	ZBTB38	zinc finger and BTB domain containing 38		
8,110	8,160	8,110	279,530	7,910	7,830	7,810	230,824	-1,211	0,001	0,042	NM_021916	ZNF70	zinc finger protein 70		
10,720	10,760	10,750	1714,335	10,440	10,470	10,500	1418,557	-1,209	0,000	0,024	NM_003165	STXBP1	syntaxin binding protein 1		
8,960	8,890	8,920	485,598	8,620	8,700	8,630	401,830	-1,209	0,001	0,041	NM_032112	MRPL43	mitochondrial ribosomal protein L43		
10,030	10,070	10,050	1060,179	9,820	9,780	9,730	877,427	-1,208	0,001	0,033	NM_003370	VASP	vasodilator-stimulated phosphoprotein		
11,370	11,410	11,390	2683,858	11,120	11,180	11,050	2222,001	-1,208	0,002	0,047	NM_003045	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1		
10,570	10,580	10,530	1509,820	10,250	10,340	10,280	1252,406	-1,206	0,001	0,037	NM_015137	EFR3A	EFR3 homolog A (S. cerevisiae)		
12,520	12,540	12,490	5860,519	12,290	12,270	12,180	4862,405	-1,205	0,001	0,045	NM_001164317	FLNB	filamin B, beta		
5,710	5,660	5,660	51,157	5,400	5,430	5,400	42,520	-1,203	0,000	0,024	NM_003697	OR5F1	olfactory receptor, family 5, subfamily F, member 1		
9,550	9,550	9,500	741,100	9,240	9,300	9,260	616,041	-1,203	0,000	0,029	NM_001012761	RGMB	RGM domain family, member B		
12,700	12,740	12,710	6731,755	12,440	12,420	12,490	5596,469	-1,203	0,000	0,028	NM_001007553	CSDE1	cold shock domain containing E1, RNA-binding	Yes	
11,430	11,360	11,370	2678,110	11,130	11,150	11,090	2231,114	-1,200	0,001	0,037	NM_001493	GDI1	GDP dissociation inhibitor 1		
8,330	8,330	8,300	319,588	8,050	8,080	8,040	266,274	-1,200	0,000	0,023	NM_178169	RASSF3	Ras association (RalGDS/AF-6) domain family member 3	Yes	
11,090	11,040	11,100	2160,133	11,310	11,380	11,330	2592,811	1,200	0,001	0,037	NM_139279	MCFD2	multiple coagulation factor deficiency 2		
9,790	9,740	9,770	871,171	10,050	10,000	10,040	1045,633	1,200	0,000	0,025	NM_173517	VKORC1L1	vitamin K epoxide reductase complex, subunit 1-like 1		
10,310	10,200	10,210	1210,059	10,490	10,530	10,500	1454,963	1,202	0,002	0,047	NM_001160210	SLC25A13	solute carrier family 25, member 13 (citrin)		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
10,360	10,320	10,410	1317,697	10,600	10,630	10,660	1584,935	1,203	0,001	0,039	NM_003720	PSMG1	proteasome (prosome, macropain) assembly chaperone 1		
11,040	11,030	11,030	2095,881	11,270	11,290	11,340	2521,910	1,203	0,000	0,028	NM_018290	PGM2	phosphoglucomutase 2		
6,870	6,800	6,830	114,057	7,140	7,070	7,100	137,532	1,206	0,001	0,036	NM_021186	ZP4	zona pellucida glycoprotein 4		
9,930	9,920	9,910	968,778	10,170	10,170	10,230	1168,368	1,206	0,000	0,027	NM_000436	OXCT1	3-oxoacid CoA transferase 1		
9,100	9,040	9,030	532,633	9,310	9,290	9,380	642,336	1,206	0,002	0,047	NM_001173984	BRD7	bromodomain containing 7		
10,650	10,670	10,660	1618,031	10,890	10,930	10,980	1956,153	1,209	0,001	0,036	NM_002139	RBMX	RNA binding motif protein, X-linked		
11,180	11,100	11,150	2262,512	11,380	11,440	11,440	2740,600	1,211	0,001	0,037	NM_004964	HDAC1	histone deacetylase 1		
7,770	7,710	7,710	212,347	7,970	8,000	8,050	257,253	1,212	0,001	0,039	NM_019002	ETAA1	Ewing tumor-associated antigen 1		
9,550	9,550	9,500	741,100	9,840	9,750	9,840	898,030	1,212	0,002	0,046	NM_138287	DTX3L	deltex 3-like (Drosophila)		
9,550	9,470	9,510	729,301	9,790	9,780	9,800	885,300	1,214	0,000	0,024	NM_006979	SLC39A7	solute carrier family 39 (zinc transporter), member 7		
9,550	9,470	9,510	729,301	9,790	9,780	9,800	885,300	1,214	0,000	0,024	NM_006979	SLC39A7	solute carrier family 39 (zinc transporter), member 7		
9,550	9,470	9,510	729,301	9,790	9,780	9,800	885,300	1,214	0,000	0,024	NM_006979	SLC39A7	solute carrier family 39 (zinc transporter), member 7		
9,290	9,280	9,370	636,448	9,580	9,640	9,560	772,685	1,214	0,002	0,047	NM_032193	RNASEH2C	ribonuclease H2, subunit C		
8,060	8,110	8,100	272,509	8,330	8,430	8,350	330,992	1,215	0,002	0,046	NM_004629	FANCG	Fanconi anemia, complementation group G		
10,550	10,480	10,600	1493,179	10,810	10,820	10,850	1816,275	1,216	0,001	0,042	NR_027363	C12orf32	chromosome 12 open reading frame 32		
10,680	10,790	10,730	1703,203	10,970	11,050	11,030	2072,370	1,217	0,002	0,049	NM_175065	HIST2H2AB	histone cluster 2, H2ab		
10,600	10,530	10,590	1524,017	10,870	10,870	10,830	1854,468	1,217	0,000	0,028	NM_013242	C16orf80	chromosome 16 open reading frame 80		
8,640	8,620	8,690	401,791	8,900	8,970	8,930	488,976	1,217	0,001	0,036	NM_016824	ADD3	adducin 3 (gamma)		
10,850	10,780	10,840	1812,371	11,050	11,140	11,140	2211,209	1,220	0,002	0,047	NM_133259	LRPPRC	leucine-rich PPR-motif containing		
7,680	7,550	7,620	196,399	7,910	7,890	7,930	240,533	1,225	0,001	0,043	NM_017956	TRMT12	tRNA methyltransferase 12 homolog (S. cerevisiae)		
9,760	9,670	9,670	832,108	9,950	10,020	10,010	1019,512	1,225	0,001	0,043	NM_016001	UTP18	UTP18, small subunit (SSU) processome component, homolog (yeast)		
11,040	11,010	11,020	2081,470	11,300	11,350	11,300	2551,023	1,226	0,000	0,024	NM_001693	ATP6V1B2	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2		
8,930	8,940	8,930	488,882	9,180	9,240	9,260	599,271	1,226	0,000	0,029	NM_000466	PEX1	peroxisomal biogenesis factor 1		
9,840	9,820	9,870	918,719	10,150	10,080	10,180	1126,219	1,226	0,001	0,042	NM_002053	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa		Yes
10,610	10,590	10,600	1552,119	10,820	10,930	10,930	1903,261	1,226	0,002	0,049	NM_032839	DIRC2	disrupted in renal carcinoma 2		
9,650	9,650	9,550	785,480	9,890	9,930	9,920	964,363	1,228	0,001	0,037	NM_022470	ZMAT3	zinc finger, matrin type 3		
7,350	7,360	7,290	161,307	7,600	7,640	7,650	198,111	1,228	0,000	0,028	NM_145231	C14orf143	chromosome 14 open reading frame 143		
11,110	11,110	11,130	2220,544	11,440	11,420	11,380	2727,850	1,229	0,000	0,024	NM_005034	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa		
9,630	9,620	9,560	778,020	9,860	9,960	9,880	955,857	1,229	0,002	0,047	NM_022459	XPO4	exportin 4		
7,270	7,310	7,300	156,871	7,620	7,620	7,530	192,754	1,229	0,001	0,040	NM_005386	NNAT	neuronatin		
7,900	7,930	7,940	242,768	8,160	8,280	8,220	298,344	1,229	0,002	0,047	NM_002462	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)		Yes
8,510	8,510	8,610	373,279	8,880	8,830	8,820	459,389	1,231	0,001	0,043	NM_001040694	INCENP	inner centromere protein antigens 135/155kDa		
9,920	9,890	9,830	942,588	10,170	10,210	10,160	1160,204	1,231	0,001	0,032	NM_014633	CTR9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)		
11,170	11,180	11,230	2342,077	11,500	11,520	11,460	2883,386	1,231	0,000	0,028	NM_001255	CDC20	cell division cycle 20 homolog (S. cerevisiae)		
9,930	9,930	9,880	964,425	10,180	10,260	10,200	1187,519	1,231	0,001	0,035	NM_006307	SRPX	sushi-repeat-containing protein, X-linked		
10,290	10,280	10,260	1240,513	10,530	10,630	10,570	1527,814	1,232	0,001	0,038	NM_018319	TDP1	tyrosyl-DNA phosphodiesterase 1		
9,630	9,590	9,610	781,495	9,970	9,900	9,860	962,551	1,232	0,001	0,043	NM_005333	HCCS	holocytochrome c synthase		
10,610	10,520	10,650	1546,029	10,910	10,920	10,860	1906,756	1,233	0,002	0,047	NM_021074	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa		
9,530	9,590	9,490	743,018	9,790	9,840	9,890	916,873	1,234	0,002	0,049	NM_006810	PDIA5	protein disulfide isomerase family A, member 5		
11,710	11,720	11,750	3389,289	12,040	12,000	12,050	4182,533	1,234	0,000	0,024	NM_005896	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble		
11,060	11,020	10,960	2067,852	11,260	11,330	11,360	2551,752	1,234	0,002	0,049	NM_032047	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5		
9,160	9,150	9,200	576,095	9,430	9,490	9,500	710,979	1,234	0,000	0,029	NM_014679	CEP57	centrosomal protein 57kDa		
9,480	9,490	9,420	706,068	9,730	9,750	9,820	871,396	1,234	0,001	0,042	NM_001018067	SERBP1	SERPINE1 mRNA binding protein 1		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
9,360	9,370	9,410	666,362	9,620	9,710	9,720	822,590	1,234	0,001	0,043	NM_178042	ACTL6A	actin-like 6A		
11,160	11,120	11,160	2267,347	11,380	11,490	11,480	2799,295	1,235	0,002	0,047	NM_014573	TMEM97	transmembrane protein 97		
8,650	8,730	8,670	411,211	8,960	9,000	9,010	508,520	1,237	0,000	0,029	NM_003518	HIST1H2BG	histone cluster 1, H2bg		
7,990	7,960	8,010	253,671	8,240	8,340	8,300	313,847	1,237	0,001	0,039	NM_138340	ABHD3	abhydrolase domain containing 3		
9,070	9,070	9,180	551,649	9,380	9,450	9,420	683,573	1,239	0,002	0,046	NM_005003	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa		
11,170	11,180	11,080	2263,013	11,410	11,470	11,480	2804,763	1,239	0,001	0,042	NM_014278	HSPA4L	heat shock 70kDa protein 4-like		
10,570	10,480	10,540	1479,079	10,840	10,820	10,860	1833,129	1,239	0,000	0,028	NM_016026	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)		
8,180	8,190	8,230	294,100	8,500	8,580	8,460	365,620	1,243	0,002	0,047	NM_024032	C17orf53	chromosome 17 open reading frame 53		
9,350	9,270	9,340	639,339	9,590	9,670	9,650	796,243	1,245	0,001	0,037	NM_052965	TSEN15	tRNA splicing endonuclease 15 homolog (S. cerevisiae)		
7,760	7,750	7,790	217,786	8,020	8,130	8,100	271,362	1,246	0,001	0,042	NM_001002814	RAB11FIP1	RAB11 family interacting protein 1 (class I)		
10,540	10,500	10,550	1478,749	10,850	10,780	10,910	1842,749	1,246	0,002	0,049	NM_007085	FSTL1	follistatin-like 1		
9,580	9,430	9,490	724,741	9,830	9,820	9,810	903,902	1,247	0,001	0,043	NM_018361	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsi		
10,400	10,330	10,450	1345,728	10,730	10,730	10,680	1679,161	1,248	0,001	0,039	NM_021074	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa		
6,980	6,900	6,940	122,817	7,260	7,260	7,260	153,277	1,248	0,000	0,024	NM_001010860	C14orf174	chromosome 14 open reading frame 174		
9,180	9,170	9,200	581,400	9,430	9,540	9,540	726,217	1,249	0,001	0,045	NM_032016	STARD3NL	STARD3 N-terminal like		
10,360	10,370	10,330	1308,260	10,640	10,690	10,700	1637,075	1,251	0,000	0,024	NM_001002030	ECHDC1	enoyl CoA hydratase domain containing 1		
8,620	8,550	8,490	375,928	8,900	8,860	8,880	471,166	1,253	0,001	0,037	NM_145698	ACBD5	acyl-CoA binding domain containing 5		
8,610	8,580	8,650	391,703	8,920	8,960	8,940	491,175	1,254	0,000	0,024	NM_033276	XRCC6BP1	XRCC6 binding protein 1		
6,170	6,240	6,180	73,364	6,540	6,470	6,560	92,018	1,254	0,001	0,037	NR_002590	SNORA41	small nucleolar RNA, H/ACA box 41		
11,740	11,750	11,740	3428,451	12,000	12,080	12,130	4302,591	1,255	0,001	0,046	NM_001316	CSE1L	CSE1 chromosome segregation 1-like (yeast)		
9,750	9,640	9,660	822,648	10,010	9,980	10,050	1033,712	1,257	0,001	0,040	NM_001995	ACSL1	acyl-CoA synthetase long-chain family member 1		
9,740	9,670	9,750	843,612	10,010	10,080	10,060	1060,331	1,257	0,001	0,032	NM_005964	MYH10	myosin, heavy chain 10, non-muscle		
9,540	9,630	9,610	772,744	9,880	9,920	9,970	971,320	1,257	0,001	0,039	NM_001102396	SIKE1	suppressor of IKBKE 1		
7,340	7,370	7,330	162,779	7,630	7,720	7,680	204,667	1,257	0,000	0,030	NM_016483	PHF7	PHD finger protein 7		
12,490	12,490	12,490	5752,606	12,840	12,800	12,830	7248,331	1,260	0,000	0,023	NM_002266	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)		
8,130	7,980	8,090	268,365	8,370	8,440	8,410	339,426	1,265	0,002	0,047	NM_014252	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15		
12,720	12,710	12,730	6746,966	13,080	13,040	13,060	8540,427	1,266	0,000	0,023	NM_002266	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)		
9,230	9,160	9,170	582,857	9,540	9,570	9,470	737,895	1,266	0,001	0,039	NM_002168	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial		
10,660	10,630	10,690	1618,238	10,970	10,970	11,060	2048,892	1,266	0,001	0,037	NM_015602	TOR1AIP1	torsin A interacting protein 1		
10,310	10,290	10,350	1275,532	10,610	10,640	10,720	1615,111	1,266	0,001	0,041	NM_032864	PRPF38A	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A		
9,080	9,050	9,090	538,736	9,390	9,480	9,390	685,317	1,272	0,001	0,035	NM_018706	DHTKD1	dehydrogenase E1 and transketolase domain containing 1		
9,710	9,640	9,620	807,426	9,990	10,000	10,040	1031,239	1,277	0,000	0,028	NM_001263	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1		
8,490	8,490	8,560	365,496	8,870	8,870	8,860	466,805	1,277	0,000	0,023	NM_016426	GTSE1	G-2 and S-phase expressed 1		
10,420	10,270	10,410	1321,786	10,690	10,740	10,740	1690,841	1,279	0,002	0,046	NM_005916	MCM7	minichromosome maintenance complex component 7		
7,220	7,110	7,100	141,471	7,460	7,520	7,520	181,054	1,280	0,001	0,040	NM_017414	USP18	ubiquitin specific peptidase 18		
11,550	11,550	11,540	2991,544	11,870	11,920	11,920	3831,053	1,281	0,000	0,023	NM_002128	HMGB1	high-mobility group box 1		
12,370	12,330	12,320	5185,122	12,720	12,640	12,730	6641,187	1,281	0,000	0,032	NM_015161	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1		
7,320	7,180	7,270	153,046	7,600	7,630	7,620	196,273	1,282	0,001	0,036	NM_000849	GSTM3	glutathione S-transferase mu 3 (brain)		
11,920	11,880	11,950	3866,872	12,240	12,290	12,300	4962,683	1,283	0,000	0,024	NM_016551	TM7SF3	transmembrane 7 superfamily member 3		
9,550	9,370	9,500	711,791	9,810	9,860	9,840	914,483	1,285	0,002	0,049	NM_004887	CXCL14	chemokine (C-X-C motif) ligand 14		
8,140	8,110	8,250	287,602	8,530	8,520	8,540	369,652	1,285	0,001	0,036	NM_138809	CMBL	carboxymethylenebutenolidase homolog (Pseudomonas)		
8,730	8,720	8,670	417,869	9,030	9,130	9,050	537,697	1,287	0,001	0,036	NM_002806	PSMC6	proteasome (prosome, macropain) 26S subunit, ATPase, 6		
11,140	11,090	11,070	2195,451	11,400	11,540	11,450	2825,913	1,287	0,002	0,049	NM_000310	PPT1	palmitoyl-protein thioesterase 1		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
7,860	7,750	7,920	229,928	8,230	8,190	8,210	296,131	1,288	0,001	0,043	NM_182513	SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)		
9,340	9,230	9,310	627,763	9,590	9,710	9,680	809,505	1,290	0,002	0,048	NM_032231	FAM96A	family with sequence similarity 96, member A		
10,030	9,930	10,080	1034,468	10,330	10,430	10,390	1336,197	1,292	0,002	0,049	NM_004237	TRIP13	thyroid hormone receptor interactor 13		
9,530	9,510	9,560	741,077	9,890	9,880	9,940	957,795	1,292	0,000	0,024	NM_001034194	EXOSC9	exosome component 9		
9,620	9,630	9,650	794,216	9,960	10,050	10,000	1026,703	1,293	0,000	0,026	NM_002105	H2AFX	H2A histone family, member X		
10,790	10,820	10,780	1778,897	11,100	11,200	11,200	2300,020	1,293	0,001	0,036	NM_153485	NUP155	nucleoporin 155kDa		
8,020	7,990	8,000	256,602	8,390	8,390	8,350	332,403	1,295	0,000	0,023	NM_018137	PRMT6	protein arginine methyltransferase 6		
9,730	9,800	9,830	883,614	10,080	10,190	10,210	1144,992	1,296	0,002	0,050	NM_017426	NUP54	nucleoporin 54kDa		
8,240	8,170	8,150	291,466	8,480	8,600	8,600	377,700	1,296	0,002	0,049	NM_020236	MRPL1	mitochondrial ribosomal protein L1		
9,120	9,080	9,160	556,551	9,430	9,480	9,570	721,323	1,296	0,002	0,049	NM_001013660	FRRS1	ferric-chelate reductase 1		
8,660	8,720	8,760	419,905	9,050	9,140	9,080	545,141	1,298	0,001	0,036	NM_015448	DPCD	deleted in primary ciliary dyskinesia homolog (mouse)		
8,400	8,410	8,420	340,149	8,810	8,780	8,770	441,652	1,298	0,000	0,023	NM_005320	HIST1H1D	histone cluster 1, H1d		
10,640	10,520	10,630	1549,602	10,980	10,990	10,960	2015,218	1,301	0,000	0,029	NM_001182	ALDH7A1	aldehyde dehydrogenase 7 family, member A1		
7,390	7,360	7,310	163,564	7,700	7,760	7,740	212,829	1,301	0,000	0,024	NM_022745	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1		
9,530	9,440	9,450	711,095	9,780	9,860	9,920	925,745	1,302	0,002	0,049	NM_004456	EZH2	enhancer of zeste homolog 2 (Drosophila)		
9,150	9,110	9,140	561,613	9,450	9,580	9,510	731,297	1,302	0,001	0,040	NM_005441	CHAF1B	chromatin assembly factor 1, subunit B (p60)		
7,810	7,770	7,800	221,849	8,140	8,260	8,130	289,594	1,305	0,001	0,045	NM_001845	COL4A1	collagen, type IV, alpha 1		
8,200	8,100	8,140	283,510	8,550	8,520	8,540	371,372	1,310	0,000	0,024	NM_004242	HMGN3	high mobility group nucleosomal binding domain 3		
10,390	10,260	10,310	1279,174	10,730	10,720	10,690	1679,054	1,313	0,000	0,029	NM_033286	C15orf23	chromosome 15 open reading frame 23		
8,630	8,620	8,620	394,352	9,030	9,050	8,970	518,092	1,314	0,000	0,024	NM_020362	C1orf128	chromosome 1 open reading frame 128		
7,750	7,810	7,770	219,318	8,080	8,200	8,230	288,303	1,315	0,002	0,049	NM_005573	LMNB1	lamin B1		
9,060	8,970	9,010	516,922	9,440	9,410	9,380	680,385	1,316	0,000	0,024	NM_006347	PPIH	peptidylprolyl isomerase H (cyclophilin H)		
6,790	6,750	6,740	108,396	7,120	7,210	7,140	142,734	1,317	0,000	0,028	NM_024539	RNF128	ring finger protein 128		
9,760	9,780	9,760	871,102	10,130	10,220	10,140	1147,198	1,317	0,000	0,027	NM_002466	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2		
7,040	7,050	7,110	134,085	7,380	7,510	7,500	176,623	1,317	0,001	0,045	NM_024680	E2F8	E2F transcription factor 8		
8,610	8,590	8,700	397,313	8,980	9,090	9,030	524,222	1,319	0,001	0,041	NM_018283	NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15		
9,130	9,060	9,100	547,589	9,510	9,470	9,510	722,468	1,319	0,000	0,023	NM_024843	CYBRD1	cytochrome b reductase 1		
9,490	9,540	9,600	746,519	9,860	10,000	9,970	985,409	1,320	0,002	0,049	NM_182751	MCM10	minichromosome maintenance complex component 10		
9,500	9,450	9,430	704,425	9,780	9,890	9,910	930,023	1,320	0,001	0,043	NM_021982	SEC24A	SEC24 family, member A (S. cerevisiae)		
9,130	8,980	9,020	528,125	9,420	9,510	9,410	698,140	1,322	0,002	0,047	NM_024657	MORC4	MORC family CW-type zinc finger 4		
10,000	9,890	9,900	976,084	10,270	10,350	10,380	1290,824	1,323	0,001	0,042	NM_001008661	CCBL2	cysteine conjugate-beta lyase 2		
9,470	9,340	9,500	693,773	9,800	9,880	9,850	918,865	1,324	0,001	0,043	NM_016048	ISOC1	isochorismatase domain containing 1		
9,480	9,380	9,520	704,860	9,800	9,880	9,920	934,160	1,325	0,002	0,047	NM_001843	CNTN1	contactin 1		
9,750	9,730	9,760	859,123	10,130	10,210	10,120	1139,274	1,326	0,000	0,027	NM_005914	MCM4	minichromosome maintenance complex component 4		
11,600	11,620	11,630	3140,374	11,950	12,020	12,100	4166,546	1,327	0,001	0,043	NM_003100	SNX2	sorting nexin 2		
11,200	11,190	11,190	2341,701	11,580	11,610	11,620	3111,583	1,329	0,000	0,023	NM_018837	SULF2	sulfatase 2		
11,140	10,970	11,090	2147,462	11,450	11,460	11,530	2857,309	1,331	0,001	0,044	NM_018407	LAPTM4B	lysosomal protein transmembrane 4 beta		
7,990	7,840	7,910	241,292	8,290	8,360	8,330	321,116	1,331	0,001	0,036	NM_015920	RPS27L	ribosomal protein S27-like		
10,030	10,090	9,990	1050,786	10,380	10,460	10,510	1399,785	1,332	0,001	0,042	NM_005872	BCAS2	breast carcinoma amplified sequence 2		
8,000	8,000	8,050	259,009	8,380	8,490	8,420	345,064	1,332	0,000	0,032	NM_003920	TIMELESS	timeless homolog (Drosophila)		
9,700	9,690	9,650	820,387	10,030	10,140	10,110	1092,999	1,332	0,000	0,031	NM_173163	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3		
9,220	9,170	9,250	593,749	9,570	9,600	9,710	791,218	1,333	0,001	0,046	NM_021105	PLSCR1	phospholipid scramblase 1		
8,890	8,850	8,830	463,647	9,190	9,330	9,290	617,885	1,333	0,001	0,042	NM_002354	EPCAM	epithelial cell adhesion molecule		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
10,290	10,310	10,330	1269,542	10,730	10,650	10,790	1691,949	1,333	0,001	0,039	NM_138555	KIF23	kinesin family member 23		
8,550	8,440	8,480	359,717	8,830	8,930	8,960	480,279	1,335	0,001	0,044	NM_001142725	ERI2	ERI1 exoribonuclease family member 2		
9,530	9,560	9,610	758,521	9,960	10,050	9,940	1012,799	1,335	0,001	0,036	NM_030919	FAM83D	family with sequence similarity 83, member D		
8,150	8,260	8,200	294,891	8,610	8,600	8,660	394,415	1,338	0,000	0,027	NM_001012515	FECH	ferrochelatase		
9,450	9,360	9,460	686,935	9,870	9,870	9,790	918,937	1,338	0,001	0,032	NM_016399	TRIAP1	TP53 regulated inhibitor of apoptosis 1		
9,670	9,600	9,620	792,519	10,050	10,090	10,010	1060,383	1,338	0,000	0,024	NM_000696	ALDH9A1	aldehyde dehydrogenase 9 family, member A1		
8,450	8,390	8,510	349,908	8,860	8,940	8,810	468,205	1,338	0,001	0,044	NM_001080443	KIF18B	kinesin family member 18B		
9,500	9,480	9,480	717,432	9,870	9,910	9,940	960,040	1,338	0,000	0,023	NM_004661	CDC23	cell division cycle 23 homolog (S. cerevisiae)		
11,460	11,480	11,470	2836,750	11,840	11,900	11,930	3796,577	1,338	0,000	0,024	NM_015172	BAT2L2	HLA-B associated transcript 2-like 2		
11,100	11,100	11,100	2194,992	11,440	11,580	11,540	2939,171	1,339	0,001	0,039	NM_004096	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2		
8,200	8,240	8,220	298,191	8,600	8,730	8,600	400,219	1,342	0,001	0,042	NM_006342	TACC3	transforming, acidic coiled-coil containing protein 3		
8,460	8,420	8,420	345,719	8,790	8,940	8,850	465,075	1,345	0,001	0,042	NM_002535	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa		
9,980	9,910	9,980	993,958	10,330	10,440	10,390	1339,396	1,348	0,000	0,032	NM_001100624	CENPN	centromere protein N		
8,570	8,560	8,550	377,419	8,950	9,030	8,990	508,593	1,348	0,000	0,024	NM_001024674	LIN52	lin-52 homolog (C. elegans)		
9,110	9,190	9,210	576,287	9,600	9,670	9,530	776,656	1,348	0,001	0,043	NM_018101	CDCA8	cell division cycle associated 8		
6,840	6,830	6,900	115,921	7,250	7,300	7,320	156,530	1,350	0,000	0,024	NM_003243	TGFBR3	transforming growth factor, beta receptor III		
9,410	9,400	9,460	686,717	9,820	9,910	9,840	927,488	1,351	0,000	0,026	NM_003338	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)		
9,770	9,770	9,770	873,098	10,120	10,230	10,260	1180,006	1,352	0,001	0,038	NM_001113378	FANCI	Fanconi anemia, complementation group I		
11,350	11,420	11,290	2618,114	11,800	11,800	11,770	3541,314	1,353	0,000	0,024	NM_003542	HIST1H4C	histone cluster 1, H4c		
10,170	10,180	10,190	1160,092	10,560	10,650	10,640	1570,736	1,354	0,000	0,024	NM_018087	TMEM48	transmembrane protein 48		
7,300	7,410	7,500	169,559	7,800	7,880	7,850	229,716	1,355	0,001	0,045	NM_003841	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular do		
10,220	10,200	10,290	1206,979	10,610	10,700	10,720	1637,699	1,357	0,001	0,036	NM_018304	PRR11	proline rich 11		
7,880	7,730	7,880	227,814	8,210	8,340	8,270	309,611	1,359	0,002	0,049	NM_005621	S100A12	S100 calcium binding protein A12		
10,290	10,220	10,310	1238,044	10,770	10,690	10,690	1683,400	1,360	0,000	0,029	NM_012412	H2AFV	H2A histone family, member V		
9,600	9,590	9,530	762,008	9,960	10,060	10,030	1036,333	1,360	0,000	0,029	NM_005327	HADH	hydroxyacyl-CoA dehydrogenase		
9,110	9,230	9,140	572,410	9,550	9,580	9,690	780,325	1,363	0,002	0,047	NM_001042551	SMC2	structural maintenance of chromosomes 2		
9,580	9,530	9,570	754,910	9,950	10,080	9,990	1029,477	1,364	0,001	0,036	NM_025205	MED28	mediator complex subunit 28		
8,410	8,370	8,490	343,508	8,870	8,850	8,900	469,012	1,365	0,000	0,024	NM_018944	C21orf45	chromosome 21 open reading frame 45		
9,880	9,790	9,850	916,813	10,230	10,350	10,290	1252,706	1,366	0,001	0,035	NM_022346	NCAPG	non-SMC condensin I complex, subunit G		
5,990	6,070	6,070	65,974	6,450	6,550	6,490	90,337	1,369	0,000	0,029	NM_138801	GALM	galactose mutarotase (aldose 1-epimerase)		
7,490	7,640	7,620	191,985	7,990	8,020	8,110	263,363	1,372	0,001	0,044	NM_004864	GDF15	growth differentiation factor 15		
11,010	10,970	10,950	2015,445	11,390	11,470	11,440	2766,239	1,373	0,000	0,024	NM_014774	KIAA0494	KIAA0494		
10,370	10,370	10,340	1314,291	10,770	10,820	10,860	1804,190	1,373	0,000	0,024	NM_001033	RRM1	ribonucleotide reductase M1		
6,900	6,860	6,840	116,718	7,380	7,340	7,250	160,269	1,373	0,001	0,035	NM_001166131	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)		
10,240	10,030	10,150	1130,350	10,560	10,590	10,650	1552,618	1,374	0,002	0,046	NM_004925	AQP3	aquaporin 3 (Gill blood group)		
8,280	8,290	8,420	322,113	8,750	8,870	8,760	443,985	1,378	0,002	0,046	NM_018048	MAGOHB	mago-nashi homolog B (Drosophila)		
8,790	8,580	8,590	403,556	9,090	9,110	9,160	556,525	1,379	0,002	0,049	NM_001134658	TMEM20	transmembrane protein 20		
8,660	8,760	8,820	429,993	9,170	9,290	9,180	594,020	1,382	0,001	0,046	NM_024592	SRD5A3	steroid 5 alpha-reductase 3		
9,980	9,840	9,900	960,611	10,340	10,460	10,320	1327,660	1,382	0,002	0,047	NM_018154	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)		
7,310	7,380	7,440	166,300	7,760	7,890	7,880	229,847	1,382	0,001	0,043	NM_133374	ZNF618	zinc finger protein 618		
10,490	10,430	10,500	1421,958	10,880	10,990	10,950	1965,545	1,382	0,000	0,029	NM_001071	TYMS	thymidylate synthetase		
9,860	9,800	9,800	904,063	10,190	10,310	10,360	1250,610	1,383	0,002	0,046	NM_000043	FAS	Fas (TNF receptor superfamily, member 6)		Yes
8,400	8,290	8,350	325,693	8,770	8,900	8,780	451,283	1,386	0,001	0,042	NM_001706	BCL6	B-cell CLL/lymphoma 6		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
8,950	8,830	8,810	466,156	9,300	9,360	9,350	646,678	1,387	0,000	0,029	NM_001098802	CEP78	centrosomal protein 78kDa		
9,080	8,970	9,080	527,950	9,520	9,480	9,550	732,635	1,388	0,000	0,026	NM_001122665	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked		
9,900	9,860	9,930	953,409	10,340	10,400	10,370	1323,560	1,388	0,000	0,023	NM_018131	CEP55	centrosomal protein 55kDa		
8,660	8,600	8,520	386,539	8,980	9,110	9,110	536,694	1,389	0,001	0,045	NM_014711	CP110	CP110 protein		
6,640	6,570	6,650	98,390	7,050	7,140	7,100	136,915	1,392	0,000	0,024	NM_020682	AS3MT	arsenic (+3 oxidation state) methyltransferase		
6,730	6,640	6,560	100,080	7,060	7,180	7,150	140,157	1,401	0,001	0,042	NM_021052	HIST1H2AE	histone cluster 1, H2ae		
8,840	8,810	8,810	451,966	9,290	9,330	9,300	633,310	1,401	0,000	0,023	NM_005325	HIST1H1A	histone cluster 1, H1a		
9,560	9,450	9,460	719,505	9,910	10,050	9,980	1010,695	1,405	0,001	0,039	NM_001690	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A		
9,800	9,850	9,750	891,801	10,230	10,310	10,340	1255,526	1,408	0,000	0,030	NM_020354	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7		
8,650	8,720	8,580	402,022	9,070	9,240	9,130	567,467	1,412	0,002	0,049	NM_130398	EXO1	exonuclease 1		
9,300	9,200	9,150	595,527	9,640	9,760	9,750	842,003	1,414	0,001	0,040	NM_030816	ANKRD13C	ankyrin repeat domain 13C		
7,310	7,110	7,210	148,293	7,660	7,750	7,730	209,942	1,416	0,001	0,040	NM_001790	CDC25C	cell division cycle 25 homolog C (S. pombe)		
10,140	10,010	10,120	1090,763	10,520	10,680	10,580	1546,562	1,418	0,001	0,046	NM_002490	NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa		
8,420	8,390	8,350	334,753	8,820	8,920	8,930	474,692	1,418	0,000	0,029	NM_020147	THAP10	THAP domain containing 10		
8,200	8,280	8,240	302,412	8,790	8,640	8,800	429,099	1,419	0,001	0,043	NM_012310	KIF4A	kinesin family member 4A		
8,350	8,190	8,270	309,004	8,740	8,840	8,770	440,789	1,427	0,001	0,035	NM_001761	CCNF	cyclin F		
12,530	12,570	12,580	6039,282	13,020	13,150	13,050	8625,613	1,428	0,000	0,031	NM_003521	HIST1H2BM	histone cluster 1, H2bm		
11,130	11,070	11,050	2170,386	11,600	11,600	11,600	3104,188	1,430	0,000	0,023	NM_139276	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)		
9,490	9,490	9,450	712,522	9,930	10,010	10,040	1019,804	1,431	0,000	0,024	NM_001048166	STIL	SCL/TAL1 interrupting locus		
7,800	7,730	7,740	216,317	8,190	8,250	8,380	309,872	1,433	0,002	0,048	NM_012449	STEAP1	six transmembrane epithelial antigen of the prostate 1		
8,760	8,730	8,760	430,560	9,230	9,370	9,210	618,133	1,436	0,001	0,041	NM_003544	HIST1H4B	histone cluster 1, H4b		
8,870	8,790	8,910	463,854	9,360	9,420	9,360	666,416	1,437	0,000	0,024	NM_005915	MCM6	minichromosome maintenance complex component 6		
7,770	7,830	7,750	220,363	8,200	8,370	8,350	317,066	1,439	0,001	0,044	NM_001012267	CENPP	centromere protein P		
6,220	6,350	6,350	79,229	6,810	6,840	6,860	114,310	1,443	0,000	0,024	NM_006823	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha		
7,640	7,720	7,620	202,342	8,160	8,230	8,180	292,097	1,444	0,000	0,024	NM_001037332	CYFIP2	cytoplasmic FMR1 interacting protein 2		
8,570	8,620	8,580	385,386	9,090	9,120	9,150	556,489	1,444	0,000	0,023	NM_001333	CTSL2	cathepsin L2		
10,440	10,450	10,620	1453,916	11,000	11,070	11,040	2101,132	1,445	0,001	0,036	NM_002402	MEST	mesoderm specific transcript homolog (mouse)		
9,460	9,450	9,610	728,378	10,050	10,010	10,060	1052,906	1,446	0,000	0,029	NM_003385	VSNL1	visinin-like 1		
9,100	8,970	9,060	527,984	9,530	9,620	9,580	763,845	1,447	0,000	0,027	NM_006243	PPP2R5A	protein phosphatase 2, regulatory subunit B', alpha		
9,310	9,210	9,230	609,148	9,720	9,810	9,820	881,630	1,447	0,000	0,028	NM_012416	RANBP6	RAN binding protein 6		
9,900	9,820	9,970	954,080	10,480	10,390	10,430	1383,209	1,450	0,000	0,029	NM_003981	PRC1	protein regulator of cytokinesis 1		
7,900	8,080	8,040	257,550	8,480	8,520	8,630	373,441	1,450	0,002	0,046	NM_003372	VBP1	von Hippel-Lindau binding protein 1		
10,100	10,050	10,070	1077,506	10,580	10,650	10,600	1563,216	1,451	0,000	0,023	NM_021067	GINS1	GINS complex subunit 1 (Psf1 homolog)		
7,980	7,870	8,060	251,096	8,450	8,550	8,530	364,719	1,453	0,001	0,036	NM_007175	ERLIN2	ER lipid raft associated 2		
8,850	8,910	8,800	462,733	9,320	9,450	9,430	676,114	1,461	0,001	0,033	NM_007174	CIT	citron (rho-interacting, serine/threonine kinase 21)		
8,800	8,800	8,770	442,664	9,240	9,350	9,420	647,421	1,463	0,001	0,040	NM_033084	FANCD2	Fanconi anemia, complementation group D2		
9,540	9,480	9,510	729,219	9,960	10,060	10,170	1071,848	1,470	0,002	0,047	NM_003384	VRK1	vaccinia related kinase 1		
9,130	8,980	9,040	530,541	9,600	9,540	9,680	780,259	1,471	0,001	0,037	NM_007086	WDHD1	WD repeat and HMG-box DNA binding protein 1		
6,840	6,700	6,640	106,088	7,290	7,240	7,330	156,188	1,472	0,001	0,036	NM_015595	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor		
10,510	10,550	10,570	1492,534	11,050	11,160	11,120	2211,353	1,482	0,000	0,024	NM_022754	SFXN1	sideroflexin 1		
9,420	9,360	9,340	663,400	10,000	9,890	9,940	985,037	1,485	0,000	0,024	NM_024745	SHCBP1	SHC SH2-domain binding protein 1		
8,360	8,380	8,340	328,578	8,860	8,980	8,950	488,053	1,485	0,000	0,024	NM_003513	HIST1H2AB	histone cluster 1, H2ab		
10,370	10,270	10,370	1293,828	10,840	11,010	10,870	1922,261	1,486	0,001	0,043	NM_014865	NCAPD2	non-SMC condensin I complex, subunit D2		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
9,500	9,520	9,570	739,446	9,970	10,180	10,150	1099,733	1,487	0,002	0,049	NM_145061	SKA3	spindle and kinetochore associated complex subunit 3		
11,150	11,130	11,220	2299,629	11,640	11,820	11,760	3425,093	1,489	0,001	0,040	NM_005030	PLK1	polo-like kinase 1 (Drosophila)		
10,120	10,140	10,140	1123,173	10,630	10,690	10,810	1677,333	1,493	0,001	0,038	NM_002906	RDX	radixin		
10,110	10,250	10,180	1160,984	10,680	10,810	10,800	1739,589	1,498	0,001	0,035	NM_002417	MKI67	antigen identified by monoclonal antibody Ki-67		
8,750	8,640	8,780	423,019	9,200	9,350	9,370	634,131	1,499	0,001	0,043	AB096683	FAM72D	family with sequence similarity 72, member D		
7,290	7,130	7,180	147,192	7,780	7,820	7,770	221,347	1,504	0,000	0,024	NM_001548	IFIT1	interferon-induced protein with tetratricopeptide repeats 1		
6,500	6,460	6,510	89,895	7,100	7,140	7,000	135,410	1,506	0,000	0,029	NM_032898	C3orf34	chromosome 3 open reading frame 34		
9,170	8,960	9,180	551,355	9,640	9,750	9,720	834,100	1,513	0,001	0,040	NM_138285	NUP35	nucleoporin 35kDa		
8,720	8,560	8,580	393,924	9,160	9,220	9,280	596,688	1,515	0,001	0,033	NM_003548	HIST2H4A	histone cluster 2, H4a		
8,720	8,560	8,580	393,924	9,160	9,220	9,280	596,688	1,515	0,001	0,033	NM_003548	HIST2H4A	histone cluster 2, H4a		
9,090	9,020	9,030	528,954	9,620	9,720	9,600	802,095	1,516	0,000	0,026	NM_020840	FNIP2	folliculin interacting protein 2		
9,760	9,730	9,720	853,216	10,230	10,360	10,420	1295,083	1,518	0,001	0,039	NM_031966	CCNB1	cyclin B1		
8,480	8,390	8,550	355,774	9,020	9,080	9,140	541,505	1,522	0,000	0,030	NM_003318	TTK	TTK protein kinase	Yes	
8,780	8,700	8,660	419,987	9,270	9,340	9,350	639,339	1,522	0,000	0,024	NM_032900	ARHGAP19	Rho GTPase activating protein 19		
8,450	8,420	8,340	338,750	8,940	9,050	9,040	515,864	1,523	0,000	0,026	NM_017760	NCAPG2	non-SMC condensin II complex, subunit G2		
9,900	9,900	9,910	957,641	10,390	10,560	10,580	1460,740	1,525	0,001	0,041	NM_170589	CASC5	cancer susceptibility candidate 5		
8,440	8,550	8,530	363,914	9,050	9,110	9,190	555,564	1,527	0,000	0,030	NM_001008708	CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)		
10,160	10,230	10,200	1173,784	10,770	10,750	10,900	1793,068	1,528	0,001	0,033	NM_005496	SMC4	structural maintenance of chromosomes 4		
9,040	9,080	9,030	530,115	9,610	9,680	9,700	811,162	1,530	0,000	0,023	NM_152562	CDCA2	cell division cycle associated 2		
9,120	9,140	9,250	576,486	9,730	9,720	9,900	882,669	1,531	0,002	0,046	NM_058216	RAD51C	RAD51 homolog C (S. cerevisiae)		
9,120	9,130	9,150	561,595	9,730	9,710	9,810	861,466	1,534	0,000	0,024	NM_016530	RAB8B	RAB8B, member RAS oncogene family		
10,040	10,000	10,060	1048,091	10,560	10,690	10,700	1608,382	1,535	0,000	0,029	NM_018204	CKAP2	cytoskeleton associated protein 2		
9,190	9,010	9,090	548,197	9,660	9,720	9,770	841,819	1,536	0,000	0,030	NM_003093	SNRPC	small nuclear ribonucleoprotein polypeptide C		
9,260	9,100	9,230	587,449	9,770	9,800	9,890	904,456	1,540	0,000	0,031	NM_001211	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)		
7,570	7,740	7,680	202,959	8,260	8,330	8,280	313,061	1,543	0,000	0,024	NM_004153	ORC1L	origin recognition complex, subunit 1-like (yeast)		
9,770	9,570	9,690	819,725	10,230	10,270	10,410	1265,435	1,544	0,002	0,047	NM_198433	AURKA	aurora kinase A		
10,280	10,170	10,160	1179,833	10,750	10,880	10,860	1821,766	1,544	0,000	0,030	NM_012112	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)		
10,190	10,050	10,220	1140,313	10,850	10,750	10,750	1763,358	1,546	0,000	0,030	NM_002275	KRT15	keratin 15		Yes
8,860	8,840	8,800	456,208	9,380	9,450	9,580	710,354	1,557	0,001	0,040	NM_014875	KIF14	kinesin family member 14		
8,710	8,710	8,750	422,690	9,310	9,390	9,390	658,857	1,559	0,000	0,023	NM_018394	ABHD10	abhydrolase domain containing 10		
9,680	9,710	9,850	860,236	10,290	10,430	10,460	1346,702	1,566	0,001	0,041	NM_001165931	RRM2	ribonucleotide reductase M2		
8,170	8,100	8,120	280,198	8,710	8,800	8,830	439,858	1,570	0,000	0,024	NM_001142556	HMMR	hyaluronan-mediated motility receptor (RHAMM)		
10,030	10,040	10,110	1067,812	10,660	10,720	10,770	1683,638	1,577	0,000	0,024	NM_002592	PCNA	proliferating cell nuclear antigen		
7,910	7,940	7,910	242,203	8,520	8,600	8,610	381,946	1,577	0,000	0,023	NM_004447	EPS8	epidermal growth factor receptor pathway substrate 8		
9,150	9,140	9,090	559,078	9,680	9,810	9,870	884,568	1,582	0,001	0,036	NM_018136	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)		
9,610	9,510	9,630	767,637	10,170	10,220	10,350	1216,632	1,585	0,001	0,038	NM_016343	CENPF	centromere protein F, 350/400ka (mitosin)		
10,950	11,050	11,130	2113,192	11,620	11,740	11,770	3353,478	1,587	0,001	0,036	NM_018685	ANLN	anillin, actin binding protein		
6,360	6,340	6,340	81,385	6,960	7,000	7,080	129,266	1,588	0,000	0,024	NM_001935	DPP4	dipeptidyl-peptidase 4		
9,730	9,800	9,850	887,849	10,430	10,480	10,510	1422,004	1,602	0,000	0,023	NM_004336	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)		
10,570	10,460	10,510	1462,311	11,150	11,130	11,330	2362,625	1,616	0,001	0,043	NM_001237	CCNA2	cyclin A2		
8,740	8,730	8,650	417,961	9,330	9,520	9,380	681,354	1,630	0,001	0,037	NM_001130914	BTG3	BTG family, member 3		
8,060	8,000	8,000	259,624	8,700	8,810	8,690	425,899	1,640	0,000	0,024	NM_002497	NEK2	NIMA (never in mitosis gene a)-related kinase 2		
8,160	8,120	8,040	275,809	8,710	8,880	8,880	453,679	1,645	0,001	0,036	NM_001001664	SPOPL	speckle-type POZ protein-like		

Pre-miR-Ctrl				Pre-miR-132				Fold change (pre-miR-132 vs pre-miR-Ctrl)	p-value	q-value	Gene Assignment			miR-132 target sites	NF-κB target genes
Sample 1	Sample 2	Sample 3	Average	Sample 1	Sample 2	Sample 3	Average				Public id	Symbol	Name		
8,340	8,230	8,190	305,439	8,860	8,980	9,080	503,598	1,649	0,001	0,042	NM_002493	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa		
6,590	6,610	6,470	94,221	7,240	7,250	7,390	157,039	1,667	0,000	0,032	NM_012114	CASP14	caspase 14, apoptosis-related cysteine peptidase		
8,170	8,030	8,220	282,522	8,830	8,990	8,840	473,934	1,678	0,001	0,036	NM_003534	HIST1H3G	histone cluster 1, H3g		
9,670	9,760	9,790	855,661	10,480	10,470	10,520	1438,313	1,681	0,000	0,023	NM_016359	NUSAP1	nucleolar and spindle associated protein 1		
8,770	8,760	8,790	437,575	9,450	9,580	9,570	741,617	1,695	0,000	0,024	NM_006461	SPAG5	sperm associated antigen 5		
7,080	7,170	7,240	143,491	7,830	7,900	8,090	246,293	1,716	0,002	0,049	NM_001012507	CENPW	centromere protein W		
7,910	7,830	8,060	244,978	8,590	8,770	8,790	421,512	1,721	0,001	0,043	NM_001037540	SCML1	sex comb on midleg-like 1 (Drosophila)		
9,180	9,230	9,250	596,467	9,860	10,110	10,040	1029,073	1,725	0,001	0,043	NM_014736	KIAA0101	KIAA0101		
10,130	10,120	10,110	1112,834	10,880	10,850	10,990	1921,386	1,727	0,000	0,024	NM_001067	TOP2A	topoisomerase (DNA) II alpha 170kDa		
7,180	7,100	7,140	141,080	7,800	7,910	8,080	244,659	1,734	0,002	0,049	NM_020675	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)		
7,850	7,610	7,640	208,516	8,470	8,510	8,560	365,519	1,753	0,000	0,026	NM_024089	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1		
6,190	6,130	6,260	73,228	6,920	7,100	7,040	129,960	1,775	0,000	0,029	NM_016323	HERC5	hect domain and RLD 5		
7,940	7,880	7,920	241,110	8,730	8,810	8,730	432,682	1,795	0,000	0,023	NM_005643	TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa		
9,690	9,540	9,690	798,812	10,390	10,610	10,530	1461,105	1,829	0,001	0,036	NM_001040152	PEG10	paternally expressed 10		
9,480	9,370	9,550	708,469	10,310	10,510	10,520	1398,686	1,974	0,001	0,034	NM_005733	KIF20A	kinesin family member 20A		
9,100	9,010	9,100	537,686	10,030	9,960	10,250	1086,421	2,021	0,001	0,043	NM_014750	DLGAP5	discs, large (Drosophila) homolog-associated protein 5		
10,420	10,090	10,520	1309,441	11,360	11,340	11,590	2767,824	2,114	0,002	0,047	NM_000421	KRT10	keratin 10		
6,790	6,720	6,870	111,017	7,780	8,020	7,940	241,646	2,177	0,000	0,030	NM_001128424	FAM198B	family with sequence similarity 198, member B		