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# **ORIGINAL ARTICLE**

# Region-specific microRNA signatures in the human epididymis

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The epithelium of the human epididymis maintains an appropriate luminal environment for sperm maturation that is essential for male fertility. Regional expression of small noncoding RNAs such as microRNAs contributes to segment-specific gene expression and differentiated functions. MicroRNA profiles were reported in human epididymal tissues but not specifically in the epithelial cells derived from those regions. Here, we reveal miRNA signatures of primary cultures of caput, corpus, and cauda epididymis epithelial cells and of the tissues from which they were derived. We identify 324 epithelial cell-derived microRNAs and 259 tissue-derived microRNAs in the epididymis, some of which displayed regionalized expression patterns in cells and/or tissues. Caput cell-enriched miRNAs included miR-573 and miR-155. Cauda cell-enriched miRNAs included miR-1204 and miR-770. Next, we determined the gene ontology pathways associated with *in silico* predicted target genes of the differentially expressed miRNAs. The effect of androgen receptor stimulation on miRNA expression was also investigated. These data show novel epithelial cell-derived miRNAs that may regulate the expression of important gene networks that are responsible for the regionalized gene expression and function of the epididymis.

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#### INTRODUCTION

The epididymis epithelium supports a luminal environment that promotes sperm maturation, and each region of the duct (caput, corpus, and cauda) has a unique role in the process. These region-specific functions are maintained by distinct gene expression signatures,<sup>1-3</sup> which are coordinated by a network of transcription factors and also by noncoding RNAs. MicroRNAs (miRNAs) are one family of small noncoding RNAs that regulate gene expression posttranscriptionally, generally by binding to specific motifs in the 3'-untranslated regions (3'UTRs) of target genes (reviewed by Bartel<sup>4</sup>). miRNAs coordinate diverse biological processes including stem cell maintenance,<sup>5</sup> development, metabolism,<sup>6</sup> proliferation,<sup>7</sup> differentiation,8 and apoptosis.9 In the epididymis, miRNAs may have tissue-specific roles and also be released from the epididymis epithelium in exosomes, which can be taken up by transiting sperm.<sup>10,11</sup> Conditional deletion of Dicer, a critical component of the mature miRNA processing pathway, from epididymal principal cells of the mouse has a dramatic effect on the epithelium and impairs male fertility.<sup>12,13</sup> Androgens are required for normal epididymal structure and function (reviewed by Robaire and Hamzeh<sup>14</sup>) and have been shown to regulate miRNA expression in rodents.<sup>15,16</sup> Region-specific miRNA profiles were characterized in rodents<sup>17,18</sup> and in whole human epididymis tissue by microarray analysis<sup>19</sup> and RNA-seq.<sup>20</sup> We recently described the transcriptome of human caput, corpus, and cauda epididymis tissues and primary epithelial cell cultures derived

from each region,<sup>3</sup> though miRNAs were not discussed. Here, we describe the region-specific expression of microRNAs in the caput, corpus, and cauda epididymal cells and tissues. Further, we use *in silico* prediction methods to identify candidate targets of several abundant miRNAs, which may directly impact regional functions of the epididymal epithelium.

#### PATIENTS AND METHODS

#### Preparation of primary cultures

Human epididymis tissue was obtained with the institutional review board permission from institutions listed in the author affiliations, and with informed consent from patients undergoing inguinal radical orchiectomy for a clinical diagnosis of testicular cancer. None of the epididymides had extension of the testicular cancer, and no donors were receiving hormone or drug treatments before surgery. Efferent ducts were removed and the three anatomical regions of the epididymis: caput, corpus, and cauda, were separated and segments of each were either snap frozen in liquid nitrogen or epithelial cells were isolated and established in culture as described previously.<sup>21</sup> For the experiments to test androgen receptor (AR) function, cells were cultured in phenol-red-free CMRL-1066 medium containing 10% fetal bovine serum (FBS), hormone depleted with dextran coated-charcoal (C6241; Sigma, St. Louis, MO, USA), for 72 h before stimulation with vehicle or the synthetic androgen R1881 (1 nmol l<sup>-1</sup>, methyltrienolone, NLP005005MG; PerkinElmer, Waltham, MA, USA) for a further 16 h.

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#### RNA sequencing

RNA was extracted using TRIzol (Life Technologies, Carlsbad, CA, USA) as per the manufacturer's protocol. RNA quality was confirmed by NanoDrop (NanoDrop<sup>™</sup> One, Thermo Fisher Scientific, Waltham, MA, USA) measurement of OD 260/280 and 260/230 ratios, and the RNA was stored at  $-80^{\circ}$ C under ethanol. RNA integrity was verified by the Bioanalyzer (Agilent, Santa Clara, CA, USA), and RNA-seq libraries were prepared using the TruSeq RNA Sample Preparation Kit v2 as per the manufacturer's Low-throughput protocol (Illumina, San Diego, CA, USA). The libraries were sequenced on Illumina HiSeq2500 machines and generated  $1.9 \times 10^7 - 3.9 \times 10^7$  reads per library from the cultured cells (95%–99% mapping to the genome) and  $1.4 \times 10^7 - 3.9 \times 10^7$  reads per library from tissues (84%–99% mapping to the genome). Data were analyzed using TopHat and Cufflinks.<sup>22</sup> All data are deposited at GEO (http://www.ncbi.nlm.nih.gov/geo/GSE72986).

#### In silico analysis of miRNAs and target prediction

Putative mRNA targets of differentially expressed miRNAs were predicted using TargetScan 7.0 (http://www.targetscan.org/)<sup>23,24</sup> and miRecords.<sup>25</sup> Only data generated with TargetScan are presented here, as the miRecord database was incomplete with respect to miRNAs of interest. Gene ontology process enrichment analysis<sup>26,27</sup> was performed to identify statistically significant biological processes associated with the miRNA targets (as shown by both *P* value and false discovery rate [FDR]).

#### RESULTS

#### Regional miRNA expression in the human epididymis

To identify the regional microRNA signature of the epididymis epithelium, we examined RNA-seq data from both cultured human epididymal epithelial (HEE) cells and tissues from the caput, corpus, and cauda segments.<sup>3</sup> The majority of the 324 miRNAs identified in HEE cells (**Supplementary Table 1**) were expressed in more than one region, as were most of the 259 tissue miRNAs (**Supplementary Table 2**). Fifty-seven percent (185/324) of the HEE cell miRNAs were also present in the tissues they were derived from. Regionally restricted miRNAs were defined by differential expression of at least 2.5-fold change between caput, corpus, and cauda HEE cells and minimum gene expression levels of  $\geq$ 0.3 fragments per kilobase of transcript per million mapped reads (FPKM; **Table 1**). The same parameters were used in a comparison of differential gene expression for the miRNAs of the caput, corpus, and cauda tissues (**Table 2**).

#### Caput-enriched miRNAs of the cells and tissues

Two microRNAs (miR-573 and miR-155) were significantly more abundant in caput cells than in corpus or cauda HEE cells (**A** and **B** in **Table 1**). miR-30c2 was also enriched in the caput compared to corpus cells, and miR-196A1 was enhanced in the caput over the cauda cells. The most significant differentially expressed miRNAs observed in intact tissues were distinct from those seen in HEE cells, with miR-1247 more abundant in the caput tissue compared to both the corpus and cauda (A and B in **Table 2**). Likewise, miR-4461 was enriched in the caput in comparison to the corpus and cauda tissues though it was abundant in all tissue regions (A and B in **Table 2**). Sixteen other miRNAs were more highly expressed in the caput than the cauda tissue (**B** in **Table 2**).

#### Corpus-enriched miRNAs of the cells and tissues

Although our analysis did not identify any corpus-specific cell-derived miRNAs, four miRNAs (miR-4730, miR-196a1, miR-let7d, and miR-3916) were enriched in the corpus over the cauda cells (**C** in **Table 1**). In the tissues, miR-662 and miR-3936 were more abundant in the corpus than either the caput or cauda.

miRNA FPKN		omparison	Log2 fold change	Actual fold change	Differential
Α.	Caput	Corpus			
miR-573	10.28	0.40	-4.68	25.7	Cap>Corp
miR-155	3.11	0.61	-2.36	5.1	Cap>Corp
miR-30c2	3.92	1.10	-1.83	3.6	Cap>Corp
В.	Caput	Cauda			
miR-196a1	15.03	0.44	-5.10	34.4	Cap>Cau
miR-573	10.28	0.58	-4.15	17.8	Cap>Cau
miR-155	3.11	0.45	-2.77	6.8	Cap>Cau
miR-let7i	0.72	8.67	3.59	12.0	Cau>Cap
miR-770	2.12	24.47	3.53	11.5	Cau>Cap
miR-1204	8.54	89.13	3.38	10.4	Cau>Cap
С.	Corpus	Cauda			
miR-4730	21.14	0.00	infinity	infinity	Corp>Cau
miR-196a1	72.23	0.44	-7.37	165.2	Corp>Cau
miR-let7d	12.80	1.64	-2.97	7.8	Corp>Cau
miR-3916	34.98	9.98	-1.81	3.5	Corp>Cau
miR-1204	7.84	89.13	3.51	11.4	Cau>Corp
miR-675	0.42	2.90	2.79	6.9	Cau>Corp

A: caput vs corpus; B: caput vs cauda; C: corpus vs cauda. Cap: caput; Corp: corpus; Cau: cauda; FPKM: fragments per kilobase of transcript per million mapped reads

Three other miRNAs (miR-33b, miR-135b, and miR-3074) were enriched in the corpus over the caput tissues (**A** in **Table 2**). Multiple other tissue-derived miRNAs were enriched in the corpus over the cauda tissues, including the highly expressed miR-205, miR-141, and miR-3648-miR-3687 (**C** in **Table 2**).

#### Cauda-enriched miRNAs of the cells and tissues

In HEE cells, miR-1204 showed enhanced expression in the cauda compared to both the caput and corpus cells (**Table 1**). H19-miR-675 was also enriched in the cauda over the corpus cells. miR-770 and miR-let7i were higher in the cauda than the caput cells (**B** in **Table 1**). In the tissues, miR-146a was more abundant in the cauda compared to the caput and corpus (**B** in **Table 2**).

Also of note, but solely in the tissues, miR-135b and miR-3074 were more abundant in both the corpus and the cauda (A in Table 2) than in the caput (B in Table 2).

# In silico analysis of microRNA-regulated processes of human epididymal epithelial cells

Putative target genes of the differentially expressed miRNAs were predicted using TargetScan 7.0 (http://www.targetscan.org/).<sup>23,24</sup> We chose this *in silico* prediction tool since it was one of the few such resources that were recently updated and included all the differentially expressed miRNAs in the HEE cells. Moreover, it was a robust predictive tool in our recent work on other miRNAs.<sup>28–30</sup> Target genes (<–0.2 total context score) were then subjected to gene ontology process enrichment analysis using the Database for Annotation, Visualization, and Integrated Discovery (DAVID).<sup>26,27</sup> The top 10 predicted targets and their associated processes are shown in **Table 3** and **4**.

#### MicroRNA-regulated processes of the caput

Processes enriched among the predicted targets of the caput cell-enriched miRNAs (miR-155 and miR-573) were identified first. For miR-155-3p and miR-155-5p, these included predominantly aspects of transcriptional regulation and membrane-enclosed lumens of both nuclei and intracellular organelles (**A** and **B** in **Table 3**). Processes associated with miR-573 included

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# Table 2: Differentially expressed miRNAs comparing the caput, corpus and cauda epididymis tissues

miRNA	FPKM сог	nparison	Log2 fold change	Actual fold change	Differential
Α.	Caput	Corpus			
miR-1247	67.97	0.00	infinity	infinity	Cap>Corp
miR-4461	3.58E+6	5.26E+5	-2.77	6.81	Cap>Corp
miR-33b	0.00	10.82	infinity	infinity	Corp>Cap
miR-3074	2.08	44.72	4.43	21.54	Corp>Cap
miR-135b	0.15	2.59	4.14	17.61	Corp>Cap
miR-3936	39.97	263.65	2.72	6.60	Corp>Cap
miR-662	4.84	16.07	1.73	3.32	Corp>Cap
В.	Caput	Cauda			
miR-1247	67.97	0.00	infinity	infinity	Cap>Cau
miR-1324	5.20	0.00	infinity	infinity	Cap>Cau
miR-770	45.74	0.27	-7.42	171.75	Cap>Cau
miR-205	466.77	5.06	-6.53	92.31	Cap>Cau
miR-135a2	201.75	2.41	-6.39	83.88	Cap>Cau
miR-4674	62.96	0.80	-6.30	79.03	Cap>Cau
miR-141	337.14	6.92	-5.61	48.73	Cap>Cau
miR-3675	16.77	0.41	-5.35	40.91	Cap>Cau
miR-424	61.67	3.05	-4.34	20.20	Cap>Cau
miR-374c	19.10	1.22	-3.96	15.61	Cap>Cau
miR-100	44.27	3.18	-3.80	13.93	Cap>Cau
miR-4461	3.58E+6	4.13E+5	-3.12	8.68	Cap>Cau
miR-662	4.84	0.62	-2.97	7.84	Cap>Cau
miR-let7d	17.86	2.37	-2.92	7.55	Cap>Cau
miR-3648-miR-3687	12 117.00	1614.22	-2.91	7.51	Cap>Cau
miR-4458	7.05	1.63	-2.12	4.34	Cap>Cau
miR-3916	0.81	28.96	5.15	35.57	Cau>Cap
miR-135b	0.15	4.85	5.04	32.94	Cau>Cap
miR-3074	2.08	54.46	4.71	26.23	Cau>Cap
miR-24-2	5.55	60.77	3.45	10.95	Cau>Cap
miR-4435-1	0.28	3.07	3.44	10.87	Cau>Cap
miR-146a	0.82	6.83	3.07	8.37	Cau>Cap
С.	Corpus	Cauda			
miR-1324	3.32	0.00	infinity	infinity	Corp>Cau
miR-4491	6.22	0.00	infinity	infinity	Corp>Cau
miR-205	1770.51	5.06	-8.45	350.16	Corp>Cau
miR-770	92.56	0.27	-8.44	347.54	Corp>Cau
miR-135a2	198.86	2.41	-6.37	82.68	Corp>Cau
miR-141	487.46	6.92	-6.14	70.46	Corp>Cau
miR-4674	48.73	0.80	-5.93	61.17	Corp>Cau
miR-3675	11.42	0.41	-4.80	27.87	Corp>Cau
miR-662	16.07	0.62	-4.70	26.01	Corp>Cau
miR-424	49.11	3.05	-4.01	16.08	Corp>Cau
miR-3936	263.65	18.89	-3.80	13.96	Corp>Cau
miR-3648-miR-3687	17 315 50	1614.22	-3.42	10.73	Corp>Cau
miR-374c	12.58	1.22	-3.36	10.28	Corp>Cau
miR-100	27.17	3.18	-3.10	8.55	Corp>Cau
miR-let7d	15.18	2.37	-2.68	6.41	Corp>Cau
miR-143-miR-145	2.72	0.48	-2.50	5.67	Corp>Cau
miR-4458	5.02	1.63	-1.63	3.09	Corp>Cau
miR-24-2	7.16	60 77	3.09	8.49	Call>Corp
miR-1462	1.00	6.83	2 77	6.84	
	1.00	0.00	2.11	0.04	000/001P

A: caput vs corpus; B: caput vs cauda; C: corpus vs cauda. Cap: caput; Corp: corpus; Cau: cauda; FPKM: fragments per kilobase of transcript per million mapped reads

some relevant to modification-dependent protein catabolic processes and as for miR-155, to the lumens of nuclei and intracellular organelles including the mitochondrion (C in Table 3).

# MicroRNA-regulated processes in the corpus and cauda

Although no corpus-specific HEE cell miRNAs were identified here, processes associated with the predicted targets of cauda cell-enriched miRNAs (miR-1204, miR-770, and miR-let7i) are shown in **Table 4**. miR-1204-associated processes include "small GTPase-mediated intracellular signaling" and "regulation of cell motion" (**A** in **Table 4**). The diverse processes associated with miR-770 included those relevant to metal ion binding (including zinc), transcription, and DNA (**B** in **Table 4**). Transcriptional regulation was also enriched in the miR-let7i-associated processes, together with multiple processes of less obvious relevance to HEE cell function including "regulation of neuron differentiation" and "blood vessel development" (**C** in **Table 4**).

#### Androgen-regulated miRNAs of the epididymis

To investigate whether any miRNAs were regulated by androgens in the human epididymis epithelium, caput HEE cells were treated with vehicle or R1881 (1 nmol l<sup>-1</sup>) for 18 h and gene expression was analyzed by RNA-seq (Yang *et al.*, manuscript in review). Eight miRNAs were differentially expressed following R1881 treatment. Of these, four miRNAs were downregulated (miR-137, miR-3074, miR-3190, and miR-3916) and four were upregulated (miR-4740, miR-506, miR-573, and miR-let7d;  $P = 5 \times 10^{-5}$ , q = 0.007, **Table 5**).

#### DISCUSSION

Mechanisms that control gene expression along the human epididymis epithelium are pivotal to coordinating its role in sperm maturation and male fertility. One aspect of this coordination likely involves noncoding RNAs including microRNAs. miRNAs were profiled previously in tissue samples from the human epididymis that contained many cell types.<sup>19,20,31</sup> In order to focus on the specific functions of cells within the epithelial layer lining the epididymis, we established the HEE cell culture model.<sup>21</sup> Here, we use RNA-seq analysis to reveal the miRNA signatures of caput, corpus, and cauda HEE cells and the tissues from which they were derived.

#### Tissue-derived miRNAs

Among the epididymis tissue-derived miRNAs identified in this study, we detected approximately 22.0%  $(116/527)^{20}$  and approximately 24.1%  $(81/336)^{19}$ , respectively of the tissue-derived miRNAs previously reported by others. As previously noted by Belleannee *et al.*<sup>19</sup> most of the tissue miRNAs were present in all three regions, with similar observations of HEE cell-derived miRNAs. Furthermore, most of the HEE cell-derived miRNAs were also evident in the tissues.

#### MicroRNA-regulated processes of the caput cells

miR-573 and miR-155, which are differentially expressed in caput HEE cells compared to corpus or cauda cells, were investigated previously in other contexts. miR-573 is downregulated by the inflammatory cytokine tumor necrosis factor (TNF)-alpha in primary human airway epithelial cells.32 More relevant to the male reproductive tract, miR-573 is downregulated in testicular tissue from patients with nonobstructive azoospermia.33 It is perhaps of relevance that we observed miR-573 among miRNAs that were upregulated in androgen-stimulated caput HEE cells. Gene ontology process enrichment analysis on the mRNA targets of miR-573 identified processes related to protein modification by small protein conjugation or removal and modification-dependent protein catabolic process, both of which might be relevant to maintenance of optimal luminal environment in the epididymis. The role of miR-155 in the male reproductive tract has yet to be explored, but it is well characterized as a pleiotropic regulator of both immunity and cancer.34-36



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#### Table 3: Predicted target genes of caput-enriched microRNAs (left) and their enriched processes (right)

A. mR-159-3p         1. Zinc finger protein 140 (ZNF140)         -1.7         1. GO:0031974-membrane-enclosed lumen         2.4E-09         3.4E-06           2. Zinc finger protein 334 (ZNF340)         -1.3         2. GO:00043233-organelle lumen         2.1E-05         0.6E-06           3. ELL associated factor 1 (EAF1)         -1.3         3. GO:0003307-transcription         1.1E-08         1.6E-05           5. ZFP14 zinc finger protein (ZFP14)         -1.0         5. GO:00051252-regulation of RM metabolic process         2.6E-07         3.6E-07         6.5E-04           6. Mitchchndrial rubsomment 2 (AGO2)         -0.9         6. GO:00051252-regulation of transcription, DNA-dependent         3.6E-07         6.5E-04           8. Chornorssom 12 open reading frame 49 (C12ar/49)         -0.8         8. GO:00054564-nucleoplasm         1.3E-06         1.9E-03           10. Molydeatum cofactor synthesis 2 (MOCS2)         -0.8         1. GO:0005730-nucleolus         8.7E-06         1.2E-02           9. mR-155-5p         1.2m (finger protein 3850 (ZNF3850)         -0.8         1. GO:0005352-regulation of transcription         1.5E-11         2.6E-08           2. Abpribosylation factor-like 58 (ARL5B)         -0.7         3. GO:0006350-transcription         6.5E-08         1.1E-04           3. Casair kinasa 1, alpha 1 (CNFA1)         -0.7         6. GO:00035357-regulation of transcription <td< th=""><th>Top 10 target genes</th><th>TCS</th><th>Top 10 enriched GO terms</th><th>Р</th><th>FDR</th></td<>	Top 10 target genes	TCS	Top 10 enriched GO terms	Р	FDR
1. Zinc finger protein 1340 (ZWF140)       -1.7       1. 60:0031974-membrane-enclosed lumen       2.4E.09       3.4E.04         2. Zinc finger protein 334 (ZMF334)       -1.3       3. G0:0006350-transcription       1.1E.08       1.9E-05         3. ELL associated factor 1 ( <i>LFL</i> 1)       -1.0       4. G0:0070013-intracellular ognale lumen       1.1E.08       1.9E-05         5. ZFP14 zinc finger protein (ZFP14)       -0.9       5. G0:00051252-regulation of RNA metabolic process       2.6E-07       4.8E-04         7. Argonaute RISC catalytic component 2 (AGO2)       -0.9       7. G0:0005355-regulation of transcription       3.8E-06       5.9E-07         8. Chromosome 12 open reading frame 49 ( <i>C12ar449</i> )       -0.8       8. G0:00054249-regulation of transcription       3.8E-06       1.9E-03         10. Molybdenum cofactor synthesis 2 (MOCS2)       -0.8       1.0.G0:005730-nucleolus       8.7E-06       1.2E-02         2. ADP-ribosylation factor-like 5B (ARL5B)       -0.8       1.0.G0:005700-mucleolus       8.7E-06       1.2E-04         3. Zinc finger protein 35D (ZWF382D)       -0.7       4. G0:00033052-transcription factor activity       4.4E-08       6.1E-05         4. Cadd family interacting protein 1 (NDF/PI)       -0.7       5. G0:00033050-transcription factor activity       4.4E-08       6.1E-05         7. Cel division factor (IAWJ3)       -0.6       7.6	A. miR-155-3p				
2. Zinc finger protein 334 (2NF334)         -1.3         2. 60:004323-organelle lumen         2. 56:00         3. 16.00           3. ELL associated factor 1 ( <i>EAF1</i> )         -1.3         3. 60:0006350-transcription         1.16:08         1.66:05           5. <i>PEPL4</i> zinc finger protein ( <i>ZFP14</i> )         -1.0         5. 60:0031981-nuclear lumen         1.26:08         1.76:00           6. Mitochondrial inbosomal protein ( <i>ZFP14</i> )         -1.0         5. 60:003525-regulation of RNA metabolic process         2.66:07         4.86:04           7. Argonaute RISC catalytic component 2 ( <i>AGO2</i> )         -0.9         7. 60:0005635-regulation of transcription         5.96:70         1.16:03           9. Tropomyssin 1 alpha ( <i>TPM1</i> )         -0.8         9. 60:0005730-nucleolus         8.76:06         1.26:08           0. Molydołenum cofactor synthesis 2 ( <i>MOCS2</i> )         -0.8         1.60:00045449-regulation of transcription         1.56:11         2.66:03           1. Zinc finger protein 35D ( <i>ZNF385D</i> )         -0.8         1.60:0004530-regulation of transcription         1.26:08         1.26:08           2. ADP-ribosylation factor-like 5B ( <i>ARL5B</i> )         -0.8         1.60:0006350-transcription factor activity         2.26:10         3.06:07           3. Red family interacting protein 1 ( <i>NDFIP1</i> )         -0.7         5.60:0003535-regulation of transcription from RNA         1.26:07         1.26:07	1. Zinc finger protein 140 (ZNF140)	-1.7	1. GO:0031974~membrane-enclosed lumen	2.4E-09	3.4E-06
3. EL. associated factor 1 ( <i>EAF</i> )         -1.3         3. G0:0006350-transcription         1.1E-08         1.6E-05           4. NADH dehydrogenase ubiquinone flavoprotein 3, 10kDa ( <i>NUUFV</i> )         -1.0         5. G0:0031981-nuclear lumen         1.1E-08         1.6E-05           5. ZFP14 zinc finger protein ( <i>ZFP14</i> )         -1.0         5. G0:0051525-regulation of RNA metabolic process         2.6E-07         4.8E-04           7. Argonaute RISC catalytic component 2 ( <i>AGO2</i> )         -0.9         7. G0:00063554-regulation of transcription         5.9E-07         1.1E-03           9. Topoponyosin 1 alpha ( <i>TPMI</i> )         -0.8         8. G0:0005564-nucleoplasm         3.8E-06         1.2E-02           9. Infenter protein 3850 ( <i>ZNF385D</i> )         -0.8         1. G0:0005730-nucleolus         8.7E-06         1.2E-02           9. Tipoponyosin 1 alpha ( <i>CSNK1A1</i> )         -0.8         2.60:00352E-transcription frageritator activity         2.4E-08         6.1E-05           1.2. Kine finger protein 3850 ( <i>ZNF385D</i> )         -0.8         1.60:0045449-regulation of transcription         1.5E-11         2.6E-03           4. Obeld family interacting protein 1 ( <i>NDFP1</i> )         -0.7         5. G0:000352E-transcription frageritator activity         4.4E-08         6.1E-05           6. Sphingosine-1-phosphate receptor 1 ( <i>SIPR1</i> )         -0.7         6. G0:0001252E-regulation of transcription, 1.7E-07         2.8E-04 <td>2. Zinc finger protein 334 (ZNF334)</td> <td>-1.3</td> <td>2. G0:0043233~organelle lumen</td> <td>2.5E-09</td> <td>3.6E-06</td>	2. Zinc finger protein 334 (ZNF334)	-1.3	2. G0:0043233~organelle lumen	2.5E-09	3.6E-06
4. NADH dehydrogenase ubiquinone flavoprotein 3, 10kDa (NDUFV3)         -1.0         4. G0:070013-intracellular organelle lumen         1.12:08         1.72:03           5. ZFP14 zinc finger protein (ZFP14)         -1.0         5. G0:0031981-nuclear lumen         1.22:08         1.72:03           6. Mitochondrial ribosomal protein L19 (MRPL19)         -0.9         7. G0:0005355-regulation of transcription         5.96:07         1.16:03           9. Topornyosin 1 alpha (TPM)         -0.8         8. G0:0005730-nucleolus         8.76:06         1.96:03           9. Topornyosin 1 alpha (TPM)         -0.8         9. G0:0005730-nucleolus         8.76:06         1.96:03           1. Zinc finger protein 385D (ZNF385D)         -0.8         1. G0:0005730-nucleolus         8.76:06         1.26:08           2. ADPritosylation factor-like 58 (ARL5B)         -0.8         1. G0:0005370-transcription fractar activity         4.26:08         6.16:05           4. Casein kinase 1, alpha 1 (CSNK1A1)         -0.7         4. G0:0003502-transcription factor activity         4.26:08         1.16:04           5. Nedd4 family interacting protein 1 (NDFIP1)         -0.7         4. G0:0003502-transcription form RNA         1.26:07         2.86:04           4. Gasin kinase 1, alpha 1 (CSNK1A1)         -0.7         6. G0:0031981-nuclear lumen         1.86:07         3.16:04           5. Adplicatinger protein	3. ELL associated factor 1 (EAF1)	-1.3	3. G0:0006350~transcription	1.1E-08	1.9E-05
5. ZPT14 zinc finger protein (ZFP14)         -1.0         5. G0:0031981-nuclear lumen         1.26:08         1.76:05           6. Mitochondrial ribosomal protein 119 (MRPL19)         -0.9         7. G0:0003555-regulation of RNA metabolic process         2.66:07         4.86:04           7. Argonaute RISC catalytic component 2 (AGO2)         -0.9         7. G0:00003555-regulation of transcription, DNA-dependent         5.96:07         1.16:03           9. Topoproyosin 1 alpha (TPM1)         -0.8         9. G0:0005730-nucleolus         8.76:-06         1.26:08           10. Molydehum cofactor synthesis 2 (MOCS2)         -0.8         1. G0:00045449-regulation of transcription         1.56:-11         2.66:03           2. ADP-ribosylatin fator-like SB (ARL5B)         -0.8         1. G0:0003700-transcription form of transcription         1.56:-11         2.66:03           3. Zinc finger protein 552 (ZNF652)         -0.7         3. G0:0003700-transcription form RNA         1.26:07         1.26:08           4. Casein kinase 1, alpha 1 (CSMKIAI)         -0.7         4. G0:0006350-regulation of transcription from RNA         1.26:07         1.26:07           5. Nedd4 family interacting protein 1 (NDF/PI)         -0.7         6. G0:0006355-regulation of transcription, NA-dependent         1.86:-07         3.86:04           6. Sphingosine-1-phosphate receptor 1 (SIPR1)         -0.6         6. G0:0004355-regulation of transcription, N	4. NADH dehydrogenase ubiquinone flavoprotein 3, 10kDa (NDUFV3)	-1.0	4. G0:0070013~intracellular organelle lumen	1.1E-08	1.6E-05
6. Micchondrial ribosomal protein L19 (MRP.L19)         -0.9         6. G0:0051252-regulation of RNA metabolic process         2.6E-07         A.8E-04           7. Argonaute RISC catalytic component 2 (AGO2)         -0.9         7. G0:0006355-regulation of transcription, DNA-dependent         5.6-07         1.E-03           9. Tropomyosin 1 alpha ( <i>TPM1</i> )         -0.8         8. G0:0045449-regulation of transcription         5.7-07         1.E-03           10. Molybdenum cofactor synthesis 2 (MOCS2)         -0.8         10. G0:0005730-nucleolus         8.7E-01         1.2E-02           8. miR-155-5         -         -         3.00-07         3.00-07         3.00-07           2. ADP-ribosylation factor-like 50 (ARL5B)         -0.7         3. G0:0003700-rucleolus         4.4E-08         6.1E-06           3. Zinc finger protein 52 (ZVF562)         -0.7         3. G0:0003700-transcription regulator activity         2.2E-10         3.0E-07           5. Nedd4 family interacting protein 1 (NDF/PI)         -0.7         5. G0:0006357-regulation of transcription from RNA         1.2E-07         1.E-04           6. Sphingsnine-1-phosphate receptor 1 (SIPR1)         -0.7         6. G0:0006355-regulation of transcription, NA-dependent         1.8E-07         3.0E-04           9. Teshingt sinc rule active act	5. ZFP14 zinc finger protein (ZFP14)	-1.0	5. GO:0031981~nuclear lumen	1.2E-08	1.7E-05
7. Argonaute RISC catalytic component 2 (AGO2)       -0.9       7. 60:0006355-regulation of transcription, DNA-dependent       3.6E-07       6.5E-04         8. Chromosome 12 open reading frame 49 (C12or/49)       -0.8       8. G0:0045449-regulation of transcription       5.9E-07       1.1E-03         9. Tropomyosin 1 alpha (TPM1)       -0.8       9. G0:0005654-nucleolpasm       8.7E-06       1.2E-02         B. mR-155-50       -0.8       1. G0:0005730-nucleolus       8.7E-01       2.6E-03         2. ADP-ribosylation factor-like 5B (ARL5B)       -0.8       1. G0:0003700-transcription regulator activity       2.2E-10       3.0E-07         3. Cric finger protein 652 (ZNF652)       -0.7       3. G0:0003700-transcription factor activity       4.4E-08       6.1E-05         5. Nedd4 family interacting protein 1 (NDF/P1)       -0.7       5. G0:0006357-regulation of transcription from RNA       1.2E-07       2.1E-04         6. Sphingosine-1-phosphate receptor 1 (SIPR1)       -0.7       6. G0:0031981-nuclear lumen       1.3E-07       3.0E-04         7. Cold dvision cycle 73 (CDC73)       -0.6       7. G0:0045832-regulation of transcription, DNA-dependent       1.8E-07       3.0E-04         0. Wets avian erythroblastosi virus E26 oncogene homolog 1 (ETS)       -0.6       9. G0:0006355-regulation of RNA metabolic process       2.8E-04         1. Dynactin associated protein (DYNAP) <t< td=""><td>6. Mitochondrial ribosomal protein L19 (MRPL19)</td><td>-0.9</td><td>6. G0:0051252~regulation of RNA metabolic process</td><td>2.6E-07</td><td>4.8E-04</td></t<>	6. Mitochondrial ribosomal protein L19 (MRPL19)	-0.9	6. G0:0051252~regulation of RNA metabolic process	2.6E-07	4.8E-04
8. Chromosome 12 open reading frame 49 ( <i>C12orf49</i> )       -0.8       8. G0:0045449-regulation of transcription       5.9E-07       1.1E-03         9. Tropomyosin 1 alpha ( <i>TPM1</i> )       -0.8       9. G0:000564-nucleoplasm       1.3E-06       1.2E-03         10. Molybdemum cofactor synthesis 2 ( <i>MOCS2</i> )       -0.8       1. G0:0045449-regulation of transcription       1.5E-11       2.6E-08         2. ADP-ribosylation factor-like 5B ( <i>ARL5B</i> )       -0.8       2. G0:0003700-transcription reactor activity       2.2E-10       3.0E-07         3. Zinc finger protein 652 ( <i>ZNF652</i> )       -0.7       3. G0:0003700-transcription factor activity       2.4E-08       6.1E-05         4. Casein kinase 1, alpha 1 ( <i>CSNK1A1</i> )       -0.7       4. G0:0006350-transcription factor activity       2.1E-04         5. Nedd4 family interacting protein 1 ( <i>NDF/P1</i> )       -0.7       5. G0:0006357-regulation of transcription, from RNA       1.2E-07       2.1E-04         6. Sphingosine-1-phosphate receptor 1 ( <i>S1PR1</i> )       -0.7       6. G0:0031981-nuclear lumen       1.3E-07       2.8E-04         10. Vets avian enveltoride exchange factor ( <i>VW3</i> )       -0.6       7. G0:0045893-positive regulation of transcription, DNA-dependent       1.8E-07       3.1E-04         10. Vets avian enveltorio ( <i>DYMAP</i> )       -0.6       9. G0:001252-regulation of RNA metabolic process       3.6E-06         coniguation ar moreval <td< td=""><td>7. Argonaute RISC catalytic component 2 (AGO2)</td><td>-0.9</td><td>7. GO:0006355~regulation of transcription, DNA-dependent</td><td>3.6E-07</td><td>6.5E-04</td></td<>	7. Argonaute RISC catalytic component 2 (AGO2)	-0.9	7. GO:0006355~regulation of transcription, DNA-dependent	3.6E-07	6.5E-04
9. Tropomyosin 1 alpha ( <i>TPM1</i> )       -0.8       9. G0:0005654nucleoplasm       1.3E-06       1.9E-03         10. Molybdenum cofactor synthesis 2 ( <i>MOCS2</i> )       -0.8       10. G0:0005730-nucleolus       8.7E-05       1.2E-05         1. Zinc finger protein 385D ( <i>ZNF385D</i> )       -0.8       1. G0:0005730-nucleolus       1.5E-11       2.6E-08         2. ADP-ribosylation factor-like 58 ( <i>ARL5B</i> )       -0.8       2. G0:0003620-transcription regulator activity       2.4E-08       3.1E-04         4. Casein kinase 1, alpha 1 ( <i>CSNK1A1</i> )       -0.7       4. G0:0006357-regulation of transcription from RNA       1.2E-07       2.1E-04         5. Nedd4 family interacting protein 1 ( <i>NDFIP1</i> )       -0.7       6. G0:0006357-regulation of transcription, from RNA       1.2E-07       2.1E-04         7. Cell division cycle 73 ( <i>CDC73</i> )       -0.6       6. G0:0005252-regulation of transcription, NA-dependent       1.8E-07       3.4E-04         8. Vav 3 guanine nucleotide exchange factor ( <i>VAV3</i> )       -0.6       8. G0:00051252-regulation of RNA metabolic process       1.8E-07       3.4E-04         0. Vest avian erythroblastosis virus E26 oncogene homolog 1 ( <i>ETS</i> )       -0.6       1.0G:00070647-protein modification by small protein       2.4E-09       3.4E-06         2. Argonaute RISC catalytic component 2 ( <i>AGO2</i> )       -1.5       2. G0:00031941-membrane-enclosed lumen       1.1E-08       1.9E-05       3.	8. Chromosome 12 open reading frame 49 (C12orf49)	-0.8	8. GO:0045449~regulation of transcription	5.9E-07	1.1E-03
10. Molybdenum cofactor synthesis 2 (MOCS2)       -0.8       1.0. G0.0005730-nucleolus       8.7E-06       1.2E-02         B. miR-155-5p       -       -       8.1 G0.00045449-regulation of transcription       1.5E-11       2.6E-08         2. ADP-ribosylation factor-like 5B (ARL5B)       -0.8       2.60:0030528-transcription regulator activity       2.2E1       3.0E-07         3. Zinc finger protein 652 (ZNF652)       -0.7       3. G0:0003700-transcription factor activity       4.4E-08       6.1E-05         4. Casein kinase 1, alpha 1 (CSNK1A1)       -0.7       4. G0:0006350-transcription of transcription from RNA       1.2E-07       2.1E-04         5. Nedd4 family interacting protein 1 (NDF/P1)       -0.7       5. G0:00031981-nuclear lumen       1.3E-07       1.7E-04         6. Sphingosine-1-phosphate receptor 1 (SIPR1)       -0.6       7. G0:0045893-positive regulation of transcription, DNA-dependent       1.3E-07       3.0E-04         8. Vav 3 guanine nucleotide exchange factor (VAV3)       -0.6       8. G0:0051252-regulation of RNA metabolic process       2.0E-07       3.4E-04         0.1. Unsettin associated protein (DYNAP)       -0.6       9. G0:0006352-regulation of transcription, DNA-dependent       1.8E-07       3.1E-04         1. Opnactin associated protein (DYNAP)       -0.6       9. G0:00015254-regulation of transcription, DNA-dependent       3.6E-07       3.4E-04	9. Tropomyosin 1 alpha (TPM1)	-0.8	9. GO:0005654~nucleoplasm	1.3E-06	1.9E-03
B. miR-155-5p         1. Cinc finger protein 3850 (ZNF385D)         -0.8         1. G:00045449-regulation of transcription         1.5E-1         2.6E-08           2. ADP-ribosylation factor-like 5B (ARL5B)         -0.8         2. G0:0003028-transcription regulator activity         2.2E-10         3.0E-07           3. Zinc finger protein 552 (ZNF652)         -0.7         3. G0:0003700-transcription factor activity         4.6E-08         1.E-04           5. Nedd4 family interacting protein 1 (NDFIP1)         -0.7         5. G0:0006355-regulation of transcription from RNA         1.2E-07         2.1E-04           6. Sphingosine-1-phosphate receptor 1 (SIPR1)         -0.7         6. G0:0031981-nuclear lumen         1.3E-07         2.8E-04           7. Cell division cycle 73 (CDC73)         -0.6         7. G0:0006355-regulation of RNA metabolic process         1.8E-07         3.1E-04           9. Teashirt zinc finger homeobox 3 (TSH23)         -0.6         8. G0:0031252-regulation of RNA metabolic process         2.8E-07         3.4E-07           1. Dynactin associated protein (DYNAP)         -0.6         1.0:00051252-regulation of RNA metabolic process         2.0E-07         3.4E-07           3. Solute carrier family 25, member 26 (SLC25A26)         -0.6         1.0:00032446-protein modification by small protein         2.4E-09         3.6E-05           5. Fanconi anemia, complementation group M (FANCM)         -0.9	10. Molybdenum cofactor synthesis 2 (MOCS2)	-0.8	10. G0:0005730~nucleolus	8.7E-06	1.2E-02
1. Zinc finger protein 385D (ZNF385D)       -0.8       1. G0.0045449-regulation of transcription       1.5E-11       2.6E-08         2. ADP-ribosylation factor-like 5B (ARL5B)       -0.8       2. G0.0003700-transcription factor activity       2.2E-10       3.0E-07         3. Zinc finger protein 652 (ZNF652)       -0.7       3. G0.0003700-transcription factor activity       4.4E-08       6.1E-06         4. Casein kinase 1, alpha 1 (CSNK1A1)       -0.7       4. G0.0006350-transcription factor activity       4.2E-07       2.1E-04         5. Nedd4 family interacting protein 1 (NDF/P1)       -0.7       5. G0.00031981-nuclear lumen       1.3E-07       1.7E-04         7. Cell division cycle 73 (CDC73)       -0.6       7. G0.00051252-regulation of RNA metabolic process       1.8E-07       3.0E-04         9. Teashirt zinc finger homeobox 3 (TSH23)       -0.6       8. G0:00051252-regulation of RNA metabolic process       1.8E-07       3.4E-04         C. miR-573       -0.6       8. G0:00051252-regulation of RNA metabolic process       2.0E-07       3.4E-06         3. Solute carrier family 25, member 26 (SLC25A26)       -0.6       1.0C:0051254-positive regulation of RNA metabolic process       3.6E-06         3. Solute carrier family 25, member 26 (SLC25A26)       -1.0       3. G0:0031941-membrane-enclosed lumen       1.8E-07       3.4E-06         5. Ranconi anemia, complementation group M (FA	B. miR-155-5p				
2. ADP-ribosylation factor-like 5B (ARL5B)       -0.8       2. G0:0003528-transcription regulator activity       2.2E-10       3.0E-07         3. Zinc finger protein 652 (2Nr652)       -0.7       3. G0:0003700-transcription factor activity       4.4E-08       6.1E-05         4. Casein kinase 1, alpha 1 (CSNK1A1)       -0.7       4. G0:0006357-transcription factor activity       6.5E-08       1.1E-04         5. Nedd4 family interacting protein 1 (NDFIP1)       -0.7       6. G0:0005357-regulation of transcription from RNA       1.2E-07       2.1E-04         6. Sphingosine-1-phosphate receptor 1 (S1PR1)       -0.7       6. G0:0031981-nuclear lumen       1.3E-07       2.8E-04         7. Cell division cycle 73 (CDC73)       -0.6       7. G0:00045893-positive regulation of transcription, DNA-dependent       1.8E-07       3.0E-04         8. Vav 3 guanine nucleotide exchange factor (VAV3)       -0.6       8. G0:0051254-positive regulation of RNA metabolic process       1.8E-07       3.1E-04         10. Vets avian enythroblastosis virus E26 oncogene homolog 1 (ETS1)       -0.6       10. G0:0051254-positive regulation of RNA metabolic process       2.0E-07       3.4E-06         2. Argonaute RISC catalytic component 2 (AGO2)       -1.5       2. G0:0032446-protein modification by small protein       2.5E-09       3.6E-05         3. Solute carrier family 25, member 26 (SLC25A26)       -1.0       3. G0:0031374-membrane-enclosed l	1. Zinc finger protein 385D (ZNF385D)	-0.8	1. GO:0045449~regulation of transcription	1.5E-11	2.6E-08
3. Zinc finger protein 652 (ZNF652)       -0.7       3. G0:0003700-transcription factor activity       4.4E-08       6.1E-05         4. Casein kinase 1, alpha 1 (CSNK1A1)       -0.7       4. G0:0006350-transcription       6.5E-08       1.1E-04         5. Nedd4 family interacting protein 1 (NDF/P1)       -0.7       5. G0:000350-transcription       for solution       2.1E-04         6. Sphingosine-1-phosphate receptor 1 (SIPR1)       -0.7       6. G0:0031981-nuclear lumen       1.3E-07       1.7E-04         7. Cell division cycle 73 (CDC73)       -0.6       7. G0:0045352-regulation of transcription, DNA-dependent       1.8E-07       3.0E-04         9. Teashirt zinc finger homeobox 3 (TSH23)       -0.6       8. G0:0051254-regulation of transcription, DNA-dependent       1.8E-07       3.4E-04         10. V-ets avian erythroblastosis virus E26 oncogene homolog 1 (ETS1)       -0.6       10. G0:0051254-rostilve regulation of transcription, DNA-dependent       1.8E-07       3.4E-04         c. miR-573       -2.4       1. G0:0070647-protein modification by small protein       2.4E-09       3.4E-06         c. Argonaute RISC catalytic component 2 (AGO2)       -1.5       2. G0:0032446-protein modification by small protein       2.4E-09       3.6E-05         4. RNA binding motif protein 23 (RBM23)       -0.9       4. G0:0013233-organelle lumen       1.1E-08       1.6E-05         5. Fanc	2. ADP-ribosylation factor-like 5B (ARL5B)	-0.8	2. GO:0030528~transcription regulator activity	2.2E-10	3.0E-07
4. Casein kinase 1, alpha 1 (CSNKTA1)       -0.7       4. G0:0006350-transcription       6. 5E-08       1.1E-04         5. Nedd4 family interacting protein 1 (NDF/P1)       -0.7       5. G0:0006357-regulation of transcription from RNA       1.2E-07       2.1E-04         6. Sphingosine-1-phosphate receptor 1 (SIPR1)       -0.7       6. G0:0031981-nuclear lumen       1.3E-07       1.7E-04         7. Cell division cycle 73 (CDC73)       -0.6       6. G0:0051252-regulation of RNA metabolic process       1.8E-07       3.1E-04         9. Teashirt zinc finger homeobox 3 (TSHZ3)       -0.6       9. G0:0005355-regulation of transcription, DNA-dependent       1.8E-07       3.1E-04         10. V-ets avian erythroblastosis virus E26 oncogene homolog 1 (ETS1)       -0.6       9. G0:0005355-regulation of RNA metabolic process       2.0E-07       3.4E-04         2. Argonaute RISC catalytic component 2 (AGO2)       -0.6       1.0G:0070647-protein modification by small protein       2.4E-09       3.4E-06         3. Solute carrier family 25, member 26 (SLC25A26)       -1.0       3. G0:0031974-membrane-enclosed lumen       1.1E-08       1.5E-05         4. RNA binding motif protein 23 (RBM23)       -0.9       4. G0:0043632-modification-dependent macromolecule       2.6E-07       3.6E-06         5. Fanconi anemia, complementation group M (FANCM)       -0.9       5. G0:0019914-membrane-enclosed lumen       1.1E-08 <td< td=""><td>3. Zinc finger protein 652 (ZNF652)</td><td>-0.7</td><td>3. G0:0003700~transcription factor activity</td><td>4.4E-08</td><td>6.1E-05</td></td<>	3. Zinc finger protein 652 (ZNF652)	-0.7	3. G0:0003700~transcription factor activity	4.4E-08	6.1E-05
5. Nedd4 family interacting protein 1 (NDF/P1)-0.75. G0:0006357-regulation of transcription from RNA polymerase II promoter1.2E-072.1E-046. Sphingosine-1-phosphate receptor 1 (S1PR1)-0.76. G0:0031981-nuclear lumen1.3E-072.8E-047. Cell division cycle 73 (CDC73)-0.67. G0:0045893-positive regulation of transcription, DNA-dependent1.8E-073.0E-048. Vav 3 guanine nucleotide exchange factor (VAV3)-0.68. G0:0051252-regulation of RNA metabolic process1.8E-073.1E-0410. Vets avian erythroblastosis virus E26 oncogene homolog 1 (ETS)-0.610. G0:0051254-positive regulation of RNA metabolic process3.4E-042. miR-5731.60:0070647-protein modification by small protein conjugation or removal2.4E-093.4E-062. Argonaute RISC catalytic component 2 (AGO2)-1.52. G0:0032446-protein modification by small protein conjugation or removal1.1E-081.9E-053. Solute carrier family 25, member 26 (SLC25A26)-1.03. G0:0031974-membrane-enclosed lumen1.1E-081.9E-054. RNA binding motif protein 23 (RBM23)-0.94. G0:0043632-modification-dependent protein catabolic process1.2E-051.2E-055. Fanconi anemia, complementation group M (FANCM)-0.86. G0:0043632-modification-dependent macromolecule catabolic process2.6E-074.8E-077. Enhancer of yellow 2 homolog Drosophila (ENY2)-0.87. G0:001901-guanyl nucleotide binding3.6E-075.E-048. Family with sequence similarity 104, member B (FAM104B)-0.88. G0:0035551-grupanyl fibonucleotid	4. Casein kinase 1, alpha 1 (CSNK1A1)	-0.7	4. GO:0006350~transcription	6.5E-08	1.1E-04
6. Sphingosine-1-phosphate receptor 1 (SIPRI)       -0.7       6. G0:0031981-nuclear lumen       1.3E-07       1.7E-04         7. Cell division cycle 73 (CDC73)       -0.6       7. G0:0045893-positive regulation of transcription, DNA-dependent       1.8E-07       3.8E-04         8. Vav 3 guanine nucleotide exchange factor (VAV3)       -0.6       8. G0:0051252-regulation of RNA metabolic process       1.8E-07       3.1E-04         9. Teashirt zinc finger homeobox 3 ( <i>TSHZ3</i> )       -0.6       9. G0:0006355-regulation of transcription, DNA-dependent       1.8E-07       3.4E-04         C. miR-573       -0.6       1.0. G0:0070647-protein modification by small protein conjugation or removal       2.4E-09       3.4E-04         2. Argonaute RISC catalytic component 2 (AGO2)       -1.5       2. G0:0032446-protein modification by small protein conjugation       1.1E-08       1.9E-05         3. Solute carrier family 25, member 26 ( <i>SLC25A26</i> )       -1.0       3. G0:0013974-membrane-enclosed lumen       1.1E-08       1.9E-05         5. Fanconi anemia, complementation group M ( <i>FANCM</i> )       -0.9       5. G0:0034333-organelle lumen       1.1E-08       1.7E-05         6. Melan-A ( <i>MLANA</i> )       -0.8       6. G0:00043233-organelle lumen       1.1E-08       1.7E-05         7. Enhancer of yellow 2 homolog Drosophila ( <i>ENY2</i> )       -0.8       6. G0:00043632-modification-dependent macromolecule catabolic process       2.6E-07	5. Nedd4 family interacting protein 1 (NDFIP1)	-0.7	5. GO:0006357~regulation of transcription from RNA polymerase II promoter	1.2E-07	2.1E-04
7. Cell division cycle 73 (CDC73)-0.67. G0:0045893-positive regulation of transcription, DNA-dependent1.7E-072.8E-048. Vav 3 guanine nucleotide exchange factor (VAV3)-0.68. G0:0051252-regulation of RNA metabolic process1.8E-073.1E-049. Teashirt zinc finger homeobox 3 (TSHZ3)-0.69. G0:0006355-regulation of transcription, DNA-dependent1.8E-073.4E-0410. V-ets avian erythroblastosis virus E26 oncogene homolog 1 (ETS1)-0.61.0G:0070647-protein modification by small protein conjugation or removal2.4E-093.4E-062. Argonaute RISC catalytic component 2 (AGO2)-1.52. G0:0031974-membrane-enclosed lumen1.1E-081.9E-053. Solute carrier family 25, member 26 (SLC25A26)-1.03. G0:0031974-membrane-enclosed lumen1.1E-081.9E-054. RNA binding motif protein 23 (RBM23)-0.94. G0:0043233-organelle lumen1.1E-081.7E-055. Fanconi anemia, complementation group M (FANCM)-0.86. G0:0019941-modification-dependent macromolecule catabolic process2.6E-074.8E-047. Enhancer of yellow 2 homolog Drosophila (ENY2)-0.87. G0:0019001-guanyl nucleotide binding3.6E-074.8E-048. Family with sequence similarity 104, member B (FAM104B)-0.88.G0:0032561-guanyl ribonucleotide binding5.9E-071.1E-039. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BR/X1)-0.710. G0:0005525-GTP binding8.7E-061.2E-0810. Killer cell lectin-like receptor subfamily F, member 1 (KLRFI)-0.710. G0:0005525-GTP binding8.7E-061.2E-08	6. Sphingosine-1-phosphate receptor 1 (S1PR1)	-0.7	6. G0:0031981~nuclear lumen	1.3E-07	1.7E-04
8. Vav 3 guanine nucleotide exchange factor (VAV3)       -0.6       8. G0:0051252-regulation of RNA metabolic process       1.8E-07       3.0E-04         9. Teashirt zinc finger homeobox 3 (TSHZ3)       -0.6       9. G0:0006355-regulation of transcription, DNA-dependent       1.8E-07       3.1E-04         10. V-ets avian erythroblastosis virus E26 oncogene homolog 1 (ETS1)       -0.6       10. G0:0051254-positive regulation of RNA metabolic process       2.0E-07       3.4E-04         C. miR-573       .       .       G0:0070647-protein modification by small protein conjugation or removal       2.4E-09       3.4E-06         2. Argonaute RISC catalytic component 2 (AGO2)       -1.5       2. G0:0032446-protein modification by small protein conjugation or removal       2.5E-09       3.6E-06         3. Solute carrier family 25, member 26 (SLC25A26)       -1.0       3. G0:0031974-membrane-enclosed lumen       1.1E-08       1.6E-05         5. Fanconi anemia, complementation group M (FANCM)       -0.9       5. G0:0019941-modification-dependent protein catabolic process       1.7E-05         7. Enhancer of yellow 2 homolog Drosophila (ENY2)       -0.8       6. G0:0043632-modification-dependent macromolecule catabolic process       3.6E-07       4.8E-04         8. Family with sequence similarity 104, member B (FAM104B)       -0.8       8. G0:0032561-guanyl ribonucleotide binding       5.6E-04         9. BRX1, biogenesis of ribosomes, homolog (S. cerevis	7. Cell division cycle 73 (CDC73)	-0.6	7. GO:0045893~positive regulation of transcription, DNA-dependent	1.7E-07	2.8E-04
9. Teashirt zinc finger homeobox 3 ( <i>TSHZ3</i> )-0.69. G0:0006355~regulation of transcription, DNA-dependent1.8E-073.1E-0410. V-ets avian erythroblastosis virus E26 oncogene homolog 1 ( <i>ETS1</i> )-0.610. G0:0051254~positive regulation of RNA metabolic process2.0E-073.4E-04C. miR-573-2.41. G0:0070647~protein modification by small protein conjugation or removal2.4E-093.4E-062. Argonaute RISC catalytic component 2 ( <i>AGO2</i> )-1.52. G0:0032446~protein modification by small protein conjugation2.5E-093.6E-063. Solute carrier family 25, member 26 ( <i>SLC25A26</i> )-1.03. G0:0031974~membrane-enclosed lumen1.1E-081.9E-054. RNA binding motif protein 23 ( <i>RBM23</i> )-0.94. G0:0043233~organelle lumen1.1E-081.6E-055. Fanconi anemia, complementation group M ( <i>FANCM</i> )-0.86. G0:0043632~modification-dependent macromolecule catabolic process2.6E-074.8E-047. Enhancer of yellow 2 homolog Drosophila ( <i>ENY2</i> )-0.87. G0:001901~guanyl nucleotide binding3.6E-076.5E-048. Family with sequence similarity 104, member B ( <i>FAM104B</i> )-0.88. G0:0032561~guanyl ribonucleotide binding5.9E-071.1E-039. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) ( <i>BRIX1</i> )-0.710. G0:0005525~GTP binding8.7E-061.2E-0810. Killer cell lectin-like receptor subfamily F, member 1 ( <i>KLRF1</i> )-0.710. G0:0005525~GTP binding8.7E-061.2E-08	8. Vav 3 guanine nucleotide exchange factor (VAV3)	-0.6	8. GO:0051252~regulation of RNA metabolic process	1.8E-07	3.0E-04
10. V-ets avian erythroblastosis virus E26 oncogene homolog 1 ( <i>ETS1</i> )-0.610. G0:0051254~positive regulation of RNA metabolic process2.0E-073.4E-04C. miR-5731. Dynactin associated protein ( <i>DYNAP</i> )-2.41. G0:0070647~protein modification by small protein conjugation or removal2.4E-093.4E-062. Argonaute RISC catalytic component 2 ( <i>AGO2</i> )-1.52. G0:0032446~protein modification by small protein conjugation2.5E-093.6E-063. Solute carrier family 25, member 26 ( <i>SLC25A26</i> )-1.03. G0:0031974~membrane-enclosed lumen1.1E-081.9E-054. RNA binding motif protein 23 ( <i>RBM23</i> )-0.94. G0:0043233~organelle lumen1.1E-081.6E-055. Fanconi anemia, complementation group M ( <i>FANCM</i> )-0.95. G0:0019941~modification-dependent protein catabolic process2.6E-074.8E-047. Enhancer of yellow 2 homolog Drosophila ( <i>ENY2</i> )-0.87. G0:0019001~guanyl nucleotide binding3.6E-076.5E-048. Family with sequence similarity 104, member B ( <i>FAM104B</i> )-0.88. G0:0032561~guanyl ribonucleotide binding5.9E-071.1E-039. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) ( <i>BRIX1</i> )-0.710. G0:0005525~GTP binding8.7E-061.2E-0610. Killer cell lectin-like receptor subfamily F, member 1 ( <i>KLRF1</i> )-0.710. G0:0005525~GTP binding8.7E-061.2E-02	9. Teashirt zinc finger homeobox 3 (TSHZ3)	-0.6	9. GO:0006355~regulation of transcription, DNA-dependent	1.8E-07	3.1E-04
C. miR-5731. Dynactin associated protein (DYNAP)-2.41. GO:0070647-protein modification by small protein conjugation or removal2.4E-093.4E-092. Argonaute RISC catalytic component 2 (AGO2)-1.52. GO:0032446-protein modification by small protein conjugation2.5E-093.6E-063. Solute carrier family 25, member 26 (SLC25A26)-1.03. GO:0031974-membrane-enclosed lumen1.1E-081.9E-054. RNA binding motif protein 23 (RBM23)-0.94. GO:0043233-organelle lumen1.1E-081.7E-055. Fanconi anemia, complementation group M (FANCM)-0.95. GO:0019941-modification-dependent protein catabolic process1.2E-081.7E-056. Melan-A (MLANA)-0.86. GO:0043632-modification-dependent macromolecule catabolic process2.6E-074.8E-047. Enhancer of yellow 2 homolog Drosophila (ENY2)-0.87. GO:0019001-guanyl nucleotide binding3.6E-076.5E-048. Family with sequence similarity 104, member B (FAM104B)-0.88. GO:0032561-guanyl ribonucleotide binding5.9E-071.1E-039. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BRIX1)-0.79. GO:0051603-proteolysis involved in cellular protein catabolic process1.3E-061.9E-0310. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)-0.710. GO:0005525-GTP binding8.7E-061.2E-06	10. V-ets avian erythroblastosis virus E26 oncogene homolog 1 (ETS1)	-0.6	10. G0:0051254~positive regulation of RNA metabolic process	2.0E-07	3.4E-04
1. Dynactin associated protein (DYNAP)-2.41. G0:0070647~protein modification by small protein conjugation or removal2.4E-093.4E-062. Argonaute RISC catalytic component 2 (AGO2)-1.52. G0:0032446~protein modification by small protein conjugation2.5E-093.6E-063. Solute carrier family 25, member 26 (SLC25A26)-1.03. G0:0031974~membrane-enclosed lumen1.1E-081.9E-054. RNA binding motif protein 23 (RBM23)-0.94. G0:0043233~organelle lumen1.1E-081.6E-055. Fanconi anemia, complementation group M (FANCM)-0.95. G0:0019941~modification-dependent protein catabolic process1.2E-081.7E-056. Melan-A (MLANA)-0.86. G0:0043632~modification-dependent macromolecule catabolic process2.6E-074.8E-047. Enhancer of yellow 2 homolog Drosophila (ENY2)-0.87. G0:0019001~guanyl nucleotide binding3.6E-076.5E-048. Family with sequence similarity 104, member B (FAM104B) 9. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BRIX1)-0.79. G0:0051603~proteolysis involved in cellular protein catabolic process1.3E-061.9E-0310. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)-0.710. G0:0005525~GTP binding8.7E-061.2E-081.2E-08	C. miR-573				
2. Argonaute RISC catalytic component 2 (AGO2)-1.52. G0:0032446~protein modification by small protein conjugation2.5E-093.6E-063. Solute carrier family 25, member 26 (SLC25A26)-1.03. G0:0031974~membrane-enclosed lumen1.1E-081.9E-054. RNA binding motif protein 23 (RBM23)-0.94. G0:0043233~organelle lumen1.1E-081.6E-055. Fanconi anemia, complementation group M (FANCM)-0.95. G0:0019941~modification-dependent protein catabolic process1.2E-081.7E-056. Melan-A (MLANA)-0.86. G0:0043632~modification-dependent macromolecule catabolic process2.6E-074.8E-047. Enhancer of yellow 2 homolog Drosophila (ENY2)-0.87. G0:0019001~guanyl nucleotide binding3.6E-076.5E-048. Family with sequence similarity 104, member B (FAM104B)-0.88. G0:0032561~guanyl ribonucleotide binding5.9E-071.1E-039. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BRIXI)-0.79. G0:0051603~proteolysis involved in cellular protein catabolic process1.3E-061.9E-0310. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)-0.710. G0:0005525~GTP binding8.7E-061.2E-02	1. Dynactin associated protein (DYNAP)	-2.4	1. GO:0070647~protein modification by small protein conjugation or removal	2.4E-09	3.4E-06
3. Solute carrier family 25, member 26 ( <i>SLC25A26</i> )-1.03. G0:0031974~membrane-enclosed lumen1.1E-081.9E-054. RNA binding motif protein 23 ( <i>RBM23</i> )-0.94. G0:0043233~organelle lumen1.1E-081.6E-055. Fanconi anemia, complementation group M ( <i>FANCM</i> )-0.95. G0:0019941~modification-dependent protein catabolic process1.2E-081.7E-056. Melan-A ( <i>MLANA</i> )-0.86. G0:0043632~modification-dependent macromolecule catabolic process2.6E-074.8E-047. Enhancer of yellow 2 homolog Drosophila ( <i>ENY2</i> )-0.87. G0:0019001~guanyl nucleotide binding3.6E-076.5E-048. Family with sequence similarity 104, member B ( <i>FAM104B</i> )-0.88. G0:0032561~guanyl ribonucleotide binding5.9E-071.1E-039. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) ( <i>BRIXI</i> )-0.710. G0:0005525~GTP binding8.7E-061.2E-0310. Killer cell lectin-like receptor subfamily F, member 1 ( <i>KLRF1</i> )-0.710. G0:0005525~GTP binding8.7E-061.2E-02	2. Argonaute RISC catalytic component 2 (AGO2)	-1.5	2. G0:0032446~protein modification by small protein conjugation	2.5E-09	3.6E-06
4. RNA binding motif protein 23 ( <i>RBM23</i> )       -0.9       4. G0:0043233~organelle lumen       1.1E-08       1.6E-05         5. Fanconi anemia, complementation group M ( <i>FANCM</i> )       -0.9       5. G0:0019941~modification-dependent protein catabolic process       1.2E-08       1.7E-05         6. Melan-A ( <i>MLANA</i> )       -0.8       6. G0:0043632~modification-dependent macromolecule catabolic process       2.6E-07       4.8E-04         7. Enhancer of yellow 2 homolog Drosophila ( <i>ENY2</i> )       -0.8       7. G0:0019001~guanyl nucleotide binding       3.6E-07       6.5E-04         8. Family with sequence similarity 104, member B ( <i>FAM104B</i> )       -0.8       8. G0:0032561~guanyl ribonucleotide binding       5.9E-07       1.1E-03         9. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) ( <i>BRIX1</i> )       -0.7       9. G0:0051603~proteolysis involved in cellular protein catabolic process       1.3E-06       1.9E-03         10. Killer cell lectin-like receptor subfamily F, member 1 ( <i>KLRF1</i> )       -0.7       10. G0:0005525~GTP binding       8.7E-06       1.2E-02	3. Solute carrier family 25, member 26 (SLC25A26)	-1.0	3. G0:0031974~membrane-enclosed lumen	1.1E-08	1.9E-05
5. Fanconi anemia, complementation group M (FANCM)       -0.9       5. G0:0019941~modification-dependent protein catabolic process       1.2E-08       1.7E-05         6. Melan-A (MLANA)       -0.8       6. G0:0043632~modification-dependent macromolecule catabolic process       2.6E-07       4.8E-04         7. Enhancer of yellow 2 homolog Drosophila (ENY2)       -0.8       7. G0:0019001~guanyl nucleotide binding       3.6E-07       6.5E-04         8. Family with sequence similarity 104, member B (FAM104B)       -0.8       8. G0:0032561~guanyl ribonucleotide binding       5.9E-07       1.1E-03         9. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BRIXI)       -0.7       9. G0:0051603~proteolysis involved in cellular protein catabolic process       1.3E-06       1.9E-03         10. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)       -0.7       10. G0:0005525~GTP binding       8.7E-06       1.2E-08	4. RNA binding motif protein 23 (RBM23)	-0.9	4. GO:0043233~organelle lumen	1.1E-08	1.6E-05
6. Melan-A (MLANA)-0.86. G0:0043632~modification-dependent macromolecule catabolic process2.6E-074.8E-047. Enhancer of yellow 2 homolog Drosophila (ENY2)-0.87. G0:0019001~guanyl nucleotide binding3.6E-076.5E-048. Family with sequence similarity 104, member B (FAM104B)-0.88. G0:0032561~guanyl ribonucleotide binding5.9E-071.1E-039. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BRIX1)-0.79. G0:0051603~proteolysis involved in cellular protein catabolic process1.3E-061.9E-0310. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)-0.710. G0:0005525~GTP binding8.7E-061.2E-02	5. Fanconi anemia, complementation group M (FANCM)	-0.9	5. G0:0019941~modification-dependent protein catabolic process	1.2E-08	1.7E-05
7. Enhancer of yellow 2 homolog Drosophila (ENY2)       -0.8       7. G0:0019001~guanyl nucleotide binding       3.6E-07       6.5E-04         8. Family with sequence similarity 104, member B (FAM104B)       -0.8       8. G0:0032561~guanyl ribonucleotide binding       5.9E-07       1.1E-03         9. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BRIX1)       -0.7       9. G0:0051603~proteolysis involved in cellular protein catabolic process       1.3E-06       1.9E-03         10. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)       -0.7       10. G0:0005525~GTP binding       8.7E-06       1.2E-02	6. Melan-A ( <i>MLANA</i> )	-0.8	6. G0:0043632~modification-dependent macromolecule catabolic process	2.6E-07	4.8E-04
8. Family with sequence similarity 104, member B (FAM104B)       -0.8       8. G0:0032561~guanyl ribonucleotide binding       5.9E-07       1.1E-03         9. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BRIX1)       -0.7       9. G0:0051603~proteolysis involved in cellular protein catabolic process       1.3E-06       1.9E-03         10. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)       -0.7       10. G0:0005525~GTP binding       8.7E-06       1.2E-02	7. Enhancer of yellow 2 homolog Drosophila (ENY2)	-0.8	7. GO:0019001~guanyl nucleotide binding	3.6E-07	6.5E-04
9. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) (BRIX1)       -0.7       9. G0:0051603~proteolysis involved in cellular protein catabolic process       1.3E-06       1.9E-03         10. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)       -0.7       10. G0:0005525~GTP binding       8.7E-06       1.2E-02	8. Family with sequence similarity 104, member B (FAM104B)	-0.8	8. GO:0032561~guanyl ribonucleotide binding	5.9E-07	1.1E-03
10. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)-0.710. G0:0005525~GTP binding8.7E-061.2E-02	9. BRX1, biogenesis of ribosomes, homolog (S. cerevisiae) ( <i>BRIX1</i> )	-0.7	9. G0:0051603~proteolysis involved in cellular protein catabolic process	1.3E-06	1.9E-03
	10. Killer cell lectin-like receptor subfamily F, member 1 (KLRF1)	-0.7	10. G0:0005525~GTP binding	8.7E-06	1.2E-02

TCS: total context score; FDR: false discovery rate; GO: gene ontology

#### MicroRNA-regulated processes of the corpus/cauda cells

The role of miR-1204 was investigated in human carcinoma cell lines,<sup>37,38</sup> though to date there is no information on its involvement in processes relevant to the male reproductive tract. miR-770 is downregulated in testicular tissue from patients with nonobstructive azoospermia.<sup>33</sup> miR-let7i negatively regulates cardiac inflammation and fibrosis<sup>39</sup> and is downregulated in the serum from ovarian cancer patients.<sup>40</sup> However, deciphering its role in the epididymis will require further study.

#### Androgen-regulated miRNAs in the caput epididymis

Androgens are important for epididymal epithelial structure and function (reviewed by Robaire and Hamzeh<sup>14</sup>) and regulate their effects via the AR. We previously showed enrichment of AR protein in caput HEE cells and its nuclear accumulation in these cells in response to R1881.<sup>3,21</sup> Hence, here, we also examined the effect of R1881 on miRNA expression in caput HEE cells. Among the

miRNAs that were differentially regulated in response to R1881, miR-137 is of interest since this miRNA is differentially expressed after androgen treatment in the prostate adenocarcinoma cell line, LnCaP.<sup>41</sup> Of note, in LnCaP cells, androgen treatment increases miR-137 in contrast to the repression observed here in HEE cells. However, the overamplification of AR in LnCaP cells compared to normal prostate epithelium and the strong context-dependence of AR cofactors could account for these differences. Another androgen-regulated miRNA in the caput epididymis is miR-506, which plays a complex role in cancer. It is oncogenic in melanomas,<sup>42</sup> a tumor suppressor in ovarian cancer,<sup>43</sup> and confers chemoresistance in colon cancer.<sup>44</sup>

In conclusion, our data suggest that further investigation of regionalized miRNA expression along the epididymis may contribute to the understanding of mechanisms controlling segment-specific epididymal epithelial function.

#### Table 4: Predicted target genes of cauda-enriched microRNAs (left) and their enriched processes (right)

Top 10 target genes	TCS	Top 10 enriched GO terms	Р	FDR
A. miR-1204				
1. Von Willebrand factor A domain containing 1 (VWA1)	-1.4	1. GO:0007242~intracellular signaling cascade	3.2E-04	5.7E-01
2. N-acetyltransferase 8-like (GCN5-related, putative) (NAT8L)	-1.2	2. GO:0051270~regulation of cell motion	1.2E-03	2.1E+00
3. Solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 ( <i>SLC25A10</i> )	-1.2	3. GO:0030036~actin cytoskeleton organization	1.2E-03	2.2E+00
<ol> <li>Mitochondrial dicarboxylate carrier; Uncharacterized protein; cDNA FLJ60124 (ENSG0000262660)</li> </ol>	-1.1	<ol> <li>GO:0051056~regulation of small GTPase signal transduction</li> </ol>	2.0E-03	3.5E+00
5. Leucine-rich repeat containing 56 (LRRC56)	-1.1	5. GO:0030695~GTPase regulator activity	2.0E-03	3.0E+00
6. Zinc finger, AN1-type domain 3 (ZFAND3)	-1.0	6. G0:0051129~negative regulation of cellular component organization	2.4E-03	4.1E+00
7. Coiled-coil domain containing 127 (CCDC127)	-1.0	7. GO:0000271~polysaccharide biosynthetic process	2.4E-03	4.1E+00
8. Matrix metallopeptidase 11 (stromelysin 3) (MMP11)	-0.9	8. G0:0030029~actin filament-based process	2.6E-03	4.6E+00
9. Protein ITFG3; Uncharacterized protein; cDNA FLJ60496 ( <i>ITFG3</i> )	-0.9	9. G0:0060589~nucleoside-triphosphatase regulator activity	2.8E-03	4.1E+00
10. Transmembrane protein 141 ( <i>TMEM141</i> )	-0.8	10. G0:0005089~Rho guanyl-nucleotide exchange factor activity	2.9E-03	4.3E+00
B. miR-770-5p				
1. zinc finger, DHHC-type containing 11 (ZDHHC11)	-2.9	1. GO:0008270~zinc ion binding	3.62E-09	5.6E-06
2. zinc finger protein 138 (ZNF138)	-1.5	2. GO:0046914~transition metal ion binding	2.23E-08	3.4E-05
3. zinc finger protein 83 (ZNF83)	-1.4	<ol> <li>GO:0006355~regulation of transcription, DNA-dependent</li> </ol>	6.03E-07	1.1E-03
4. glia maturation factor, beta (GMFB)	-1.1	4. GO:0006350~transcription	6.15E-07	1.1E-03
5. zinc finger protein 480 (ZNF480)	-1.0	5. GO:0003677~DNA binding	1.24E-06	1.9E-03
6. zinc finger protein 140 (ZNF140)	-0.9	6. GO:0051252~regulation of RNA metabolic process	2.00E-06	3.5E-03
7. zinc finger protein 107 (ZNF107)	-0.9	7. GO:0045449~regulation of transcription	3.02E-06	5.4E-03
8. motor neuron and pancreas homeobox 1 (MNX1)	-0.8	8. GO:0005794~Golgi apparatus	8.52E-05	1.2E-01
9. zinc finger protein 616 (ZNF616)	-0.8	9. GO:0070013~intracellular organelle lumen	2.46E-04	3.5E-01
10. zinc finger protein 676 (ZNF676)	-0.8	10. GO:0043233~organelle lumen	2.49E-04	3.5E-01
C. miR-let7i-3p				
1. Histone cluster 3, H3 (HIST3H3)	-0.9	1. GO:0001568~blood vessel development	4.7E-04	7.8E-01
2. Calcium/calmodulin-dependent protein kinase II inhibitor 1 (CAMK2N1)	-0.9	2. G0:0048514~blood vessel morphogenesis	4.8E-04	8.0E-01
3. Peptidylprolyl isomerase (cyclophilin)-like 4 (PPIL4)	-0.8	3. GO:0001944~vasculature development	5.9E-04	9.8E-01
4. IQ motif containing B1 ( <i>IQCB1</i> )	-0.8	4. G0:0045893~positive regulation of transcription, DNA-dependent	1.3E-03	2.2E+00
5. Coiled-coil domain containing 151 (CCDC151)	-0.8	5. GO:0007411~axon guidance	1.4E-03	2.3E+00
6. Ribonuclease, RNase A family, 7 (RNASE7)	-0.8	6. G0:0051254~positive regulation of RNA metabolic process	1.5E-03	2.4E+00
7. RAB, member of RAS oncogene family-like 3 (RABL3)	-0.7	7. GO:0045446~endothelial cell differentiation	1.8E-03	3.0E+00
8. Paraspeckle component 1 (PSPC1)	-0.7	8. GO:0030030~cell projection organization	1.9E-03	3.2E+00
9. X-prolyl aminopeptidase (aminopeptidase P) 3, putative (XPNPEP3)	-0.7	9. GO:0031175~neuron projection development	2.3E-03	3.8E+00
10. Fatty acyl CoA reductase 1 (FAR1)	-0.7	10. G0:0043065~positive regulation of apoptosis	3.1E-03	5.0E+00
TCS, total context score, EDP, false discovery rate, CO, gone entellegy				

ore; FDR: false discovery rate; GO: gene ontology

#### Table 5: Differentially expressed microRNAs in caput human epididymal epithelial cells after R1881 treatment compared to vehicle

miRNAs	Vehicle	R1881	Log2 fold change	Actual fold change
miR-137	4.55	0.06	-6.17	72.2
miR-4740	24.04	1.55	-3.95	15.5
miR-let7d	22.58	1.96	-3.53	11.5
miR-125a	3.85	23.98	2.64	6.2
miR-573	0.76	7.81	3.36	10.3
miR-3177	1.52	18.16	3.58	11.9

Average of 4 RNA-seq replicas. HEE: human epididymal epithelial; miRNAs: microRNAs

#### AUTHOR CONTRIBUTIONS

JAB, SHL, SEE, and AH acquired, analyzed, and interpreted data. JAB

and AH wrote the manuscript. All authors read and approved the final manuscript.

#### **COMPETING INTERESTS**

All authors declared no competing interests.

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Supplementary Information is linked to the online version of the paper on the Asian Journal of Andrology website.

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Supplementary	Table	1: List	t of	microRNAs	in	primary	human	epididymal	epithelial	cells	(fragments	per	kilobase	of	transcript	per	million	mapped
reads [FPKM] :	>0.1)																	

miRNAs	Caput cell	Corpus cell	Cauda cell
miR-4461	1.7E+05	1.8E+05	1.6E+05
miR-548AJ2	1966.26	0.00	0.00
miR-3648, miR-3687	1671.15	957.40	1148.85
miR-3661	1102.61	1940.27	1845.95
miR-1281	1101.70	387.63	1734.55
miR-1282	1014.31	924.35	847.09
miR-4426, RPS27A	777.37	652.50	691.22
miR-1244-3, PTMA	711.12	298.98	326.28
miR-1279	573.42	272.52	146.82
miR-1304, SNORA1, SNORA18, SNORA25, SNORA32, SNORA40, SNORA8, SNORD5, SNORD6, TAF1D	526.49	447.01	460.93
miR-3918	444.70	89.37	33.48
miR-612. NEAT1	395.09	323.26	298.88
miR-762	281.14	261.52	474.86
miR-611_TMFM258	275 76	161.24	219.19
miR-3658 LICK2	274.04	11.72	11.40
miR-663A	261.77	474.04	606.03
miR-4750	247 77	0.00	0.00
miR-1307_LISMG5	237 72	299.19	290 34
miR-4722	201.60	250.98	0.00
miR_3650	201.00	0.00	0.00
miR-1/89	182.15	0.00	0.00
miR 4405	168.00	0.00	68 57
min-4035	164.02	106.90	0.00
miR-4720	164.03	06.09	106.67
	162.52	76.91	100.07
miR-1914, miR-047, UCKL1	103.32	76.81	99.04 106.04
miR-4/09, NFO2	147.87	96.90	106.94
miR-4273	144.19	125.18	42.10
MIR-1229	134.65	0.00	131.72
MIR-4517, NFAICZIP	128.76	106.77	15.63
MIR-3605, PHU2	124.66	91.17	99.54
MIR-4746	124.34	31.59	32.04
MIR-4/21, TUFM	115.52	92.37	89.91
miR-1292, NOP56, SNORD86	112.86	179.88	/5.91
miR-4449	111.43	51.91	52.65
miR-4/84	108.83	38.87	57.11
miR-25	107.56	12.16	54.35
miR-4/00, UNC119B	105.79	20.00	41.59
miR-4263	101.36	155.52	60.15
miR-4292	100.02	121.06	336.41
miR-4516	99.53	108.04	150.05
miR-4/85	94.02	170.49	153.80
miR-637	93.21	36.40	72.98
miR-103B2	91.08	0.00	128.09
miR-639, TECR	90.46	78.54	85.37
miR-631	88.55	0.00	0.00
miR-21, VMP1	86.68	60.45	63.40
miR-3684	86.61	0.00	0.00
miR-1260B	86.36	29.21	62.99
miR-636, SRSF2	82.81	63.90	89.84
miR-632, ZNF207	82.38	122.83	112.16
miR-4492	82.05	53.39	98.15
miR-1226	80.00	0.00	22.94
miR-3917, STMN1	77.23	42.78	46.43
miR-196B	73.74	76.55	32.98
miR-4440	67.99	5.78	10.01

miRNAs	Caput cell	Corpus cell	Cauda cell
miR-135A1	64.30	0.00	23.67
miR-1248, SNORA81	62.48	33.60	16.85
miR-210	61.67	13.90	17.62
miR-1251	61.23	0.00	0.00
miR-4680, PDCD4	61.21	14.30	14.34
miR-641	60.96	17.72	16.81
miR-3615, SLC9A3R1	57.49	21.56	21.93
miR-4441	54.35	33.48	5.35
miR-3607	54.25	0.00	17.09
miR-4647, SLC35B2	52.83	40.44	40.56
miR-661	51.10	0.00	0.00
miR-3665	50.96	0.00	0.00
miR-937, SCRIB	50.60	52.30	18.96
miR-3191	50.36	57.65	70.64
miR-24-1	49.35	42.02	0.00
miR-553	45.10	42.02	42.62
miR-4253	45.10	0.00	0.00
miR-200C	45.10	0.00	0.00
miR-4312	44.95	20.94	53.39
miR-943, NELFA	44.12	19.36	20.06
miR-4678	43.31	0.00	0.00
miR-324	42.63	29.48	56.10
miR-4741, RBBP8	42.26	42.51	36.76
miR-4754	41.99	0.00	63.03
miR-1180	40.85	84.02	0.00
miR-302A	40.85	0.00	0.00
miR-621, SLC25A15	40.14	28.67	29.08
miR-564, TMEM42	39.32	68.50	12.89
miR-3074	38.91	1.36	1.66
miR-29C	36.62	40.50	47.39
miR-3610, RAD21	36.50	31.86	31.41
miR-93	35.95	0.00	15.95
miR-761, NRD1	33.99	43.41	43.15
miR-4742	33.24	36.73	0.00
miR-663B	30.71	20.74	37.43
miR-3177	29.60	0.00	13.99
miR-3189	28.53	164.97	118.92
miR-5690	28.53	0.00	0.00
miR-4688	28.52	12.94	22.39
miR-604	28.42	0.00	0.00
miR-568	28.32	6.93	15.56
miR-3614, TRIM25	28.24	33.82	31.11
miR-LET7G	27.88	0.00	0.00
miR-4668, UGCG	27.78	28.78	28.47
miR-1227	27.38	9.63	23.97
miR-4687, STIM1	27.24	298.95	247.37
miR-3916	26.91	34.98	9.98
miR-1915	26.78	0.00	0.00
miR-29B2	26.03	0.00	14.93
miR-1278	26.03	0.00	0.00
miR-2467	26.03	0.00	0.00
miR-4497	25.88	0.00	0.00
miR-938	24.70	0.00	0.00
miR-320A	24.39	0.00	0.00
miR-4800, MXD4	24.32	26.93	33.59
miR-27B	23.89	14.56	10.49

miRNAs	Caput cell	Corpus cell	Cauda cell
miR-4258	23.30	8.18	16.59
miR-186	23.17	10.79	18.67
miR-4442, TOP2B	22.66	65.67	99.63
miR-4730	22.66	21.14	0.00
miR-26A2	22.19	0.00	28.25
miR-4691	22.02	32.76	13.94
miR-3192	20.86	42.90	0.00
miR-940	20.74	15.48	21.34
miR-1203	20.25	0.00	0.00
miR-5193, UBA7	19.14	28.36	26.92
miR-2117	19.14	23.51	27.37
miR-140	18.66	0.00	0.00
miR-106B	18.54	0.00	27.97
miR-4640	18.52	27.58	56.09
miR-22, miR-22HG	18.24	21.85	24.39
miR-3134, PTBP3	18.13	18.67	17.58
miR-5685	18.11	0.00	0.00
miR-3620	18.08	16.85	29.15
miR-635	17.89	56.60	25.88
miR-4420	17.66	0.00	0.00
miR-193A	17.03	21.25	0.00
miR-298	17.03	0.00	0.00
miR-130A	16.11	0.00	0.00
miR-181B2	16.11	0.00	0.00
miR-192	16.02	0.00	0.00
miR-3120	15.80	0.00	0.00
miR-4308	15 79	0.00	14 93
miR-4723	15.79	0.00	0.00
miR-941-2 miR-941-3 miR-941-4	15.50	19.85	10.06
miR-3909	15.00	8.00	0.00
miR-181B1	15 35	0.00	0.00
miR-152-1	15.00	0.00	0.00
miR-100HG	15.15	25.61	51.07
miR-196A1	15.03	72.23	0.44
miR-638	15.00	5 28	0.00
miR-7-1	14.92	10.42	21.14
miR-54841	14.82	0.00	0.00
miR-4748	14.80	0.00	0.00
miR-4999	14 47	0.00	0.00
miR-662	14.33	119.82	27.08
miR-4484	13.89	0.00	0.00
miR-1236	13 75	40.74	43.23
miR-30F	13.74	0.00	0.00
miR-378D2	12.42	5 78	10.01
miR-339	12.12	0.00	0.00
miR-135B	12.10	0.00	0.00
miR-3190	12.00	12 37	25.38
miR-1909 RFX01	11.84	58 58	81 37
miR-559	11.25	0.00	0.00
miR-219-1	11 19	12 78	0.00
miR-5006_VWA8	11 16	9.64	9.06
miR-3176	10.93	1 59	1 22
miR-3613	10.93	0.00	0.00
miR-598	10.72	0.00	0.00
miR-4523 TAOK1	10.42	13 25	11 83
miR-708	10.33	0.00	0.00

miRNAs	Caput cell	Corpus cell	Cauda cell
miR-4296	10.33	0.00	0.00
miR-573	10.28	0.40	0.58
miR-744	10.23	0.00	0.00
miR-148B	9.80	0.00	0.00
miR-10A	9.71	2.33	9.67
miR-146A	9.40	1.11	1.10
miR-4315-2, PLEKHM1	9.39	11.30	10.37
miR-1225	9.26	0.00	0.00
miR-205, miR-205HG	8.99	104.08	149.66
miR-1204, PVT1	8.54	7.84	89.13
miR-210HG	8.15	4.65	4.91
miR-3911	7.76	15.65	8.27
miR-941-1, miR-941-3, miR-941-4	7.61	15.41	28.02
miR-3939	7.21	0.00	4.14
miR-200A. miR-200B. miR-429	7.19	24.14	8.31
miR-4469. RNF170	6.85	10.56	26.39
miR-3653	6.83	73.59	39.59
miR-1287. PYROXD2	6.72	4.46	7.00
miR-23B	6.51	12.12	0.00
miR-590	6.51	46.23	30.39
miR-499A	6.40	0.00	7.88
miR-484_NDF1	6.26	7.56	8 98
miR-3651_SNOR484	6.22	20.52	18 15
miR-567	6.21	0.00	6.91
miR-345	6.21	0.00	0.00
miR-1763 miR-1 ET7A3 miR-1 ET7R miR-1 ET7RHG	5.85	39.49	41.06
miR-4/03, miR-EEF/D, miR-EEF/DHd	5.05	16 11	11.75
miR-141 miR-570 SDHAP2	5.14	6.57	11.75
miR-370, 301Ai 2	1 97	4.63	11.70
miR-3541	4.97	4.03	4.09
miR-221, miR-222	4.74	12 70	11.09
miR-4707, 515	4.04	0.00	0.00
miR-709	4.57	3.76	0.00
	4.54	5.70	4.15
miR-3107, TOWIW40L	4.07	1.10	22.80
	3.9Z	1.10	0.90
miR-5004, STNGAL1	2.75	1 70	1.25
miR-3387	3.75	1.79	2.76
miR-34A	3.03	2.73	2.70
	3.04	0.95	1.09
	3.21	2.00	2.63
	3.20	0.00	0.00
miR-100, miR-100mG	2.00	0.01	0.45
	3.09	0.00	0.00
miR-4/24, RADIIFIF4	2.75	3.95	25.00
miR-3194	2.59	0.00	0.00
	2.43	0.00	0.00
miR-5001, HGD1	2.00	2.30	2.30
min-LL170	1.90	1 74	1.04
1000-7010	1.//	1./4	1.91
	1./2	1.63	0.00
min-3/14, FLUL2	1.00	0.17	0.23
min-0100-4	1.62	0.00	0.00
HIIT-1200, SLU20A00	1.58	1.20	1.30
1111-1231, SINUKAS4	1.42	5.94	3.50
ППК-IOIA2ПU	1.29	0.03	0.88
ник-17, ник-17пь, ник-10а, ник-19А, ник-19В1, МК-2UA, МК-9ZA1	1.10	0./3	0.84

miRNAs	Caput cell	Corpus cell	Cauda cell
miR-54812	1.09	0.00	0.00
miR-4720	0.97	1.25	33.19
miR-548AA1, PALMD	0.91	0.77	0.69
miR-600HG	0.81	0.45	0.39
miR-3619	0.76	0.63	22.01
miR-3677	0.73	0.84	0.40
miR-LET7I	0.72	10.14	8.67
miR-4632, TNFRSF1B	0.72	0.22	0.25
miR-320B2	0.70	0.00	1.39
miR-4324, SLC6A16	0.64	0.12	0.10
miR-548N, OSBPL6	0.50	2.68	2.77
miR-374C	0.48	0.68	3.19
miR-374B, miR-421	0.43	3.57	8.80
miR-143, miR-143HG, miR-145	0.40	0.64	9.23
miR-137, miR-137HG	0.07	0.16	0.15
miR-4690	0.00	251.25	412.35
miR-4749	0.00	97.76	0.00
miR-4669	0.00	84.86	0.00
miR-199A1	0.00	83.60	0.00
miR-149	0.00	67.76	35.79
miR-4665	0.00	67.39	63.32
miR-4651	0.00	58.67	0.00
miR-3136	0.00	39.90	31.28
miR-1972-2	0.00	38.87	0.00
miR-4685	0.00	38.06	0.00
miR-4782	0.00	37.19	29.15
miR-3125	0.00	36.15	0.00
miR-2116	0.00	34.73	0.00
miR-5087	0.00	34.62	21.24
miR-548D2	0.00	28.57	0.00
miR-933	0.00	27.47	0.00
miR-1266	0.00	26.91	0.00
miR-3682	0.00	26.85	0.00
miR-593	0.00	26.73	0.00
miR-4505	0.00	26.58	0.00
miR-4656	0.00	22.65	62.11
miR-3184	0.00	22.61	0.00
miR-622	0.00	22.17	22.00
miR-3132	0.00	21.19	0.00
miR-LET7F2	0.00	19.84	0.00
miR-3138	0.00	19.48	0.00
miR-4653	0.00	16.30	54.72
miR-4786	0.00	15.73	15.95
miR-5192	0.00	15.53	0.00
miR-572	0.00	14.73	27.08
miR-3153	0.00	13.79	13.99
miR-624	0.00	13.38	0.00
miR-5088	0.00	12.18	0.00
miR-4787	0.00	12.16	0.00
miR-877	0.00	10.79	0.00
miR-142	0.00	10.19	0.00
miR-1207	0.00	10.19	0.00
miR-152	0.00	10.19	0.00
miR-3944	0.00	8.30	10.32
miR-5188	0.00	8.00	0.00
miR-4314	0.00	7.76	0.00

miRNAs	Caput cell	Corpus cell	Cauda cell
miR-5008	0.00	7.01	0.00
miR-645	0.00	7.01	0.00
miR-3662	0.00	6.69	0.00
miR-615	0.00	6.54	0.00
miR-1324	0.00	6.36	0.00
miR-597	0.00	6.09	0.00
miR-218-2	0.00	4.87	3.52
miR-3973	0.00	3.91	0.00
miR-548F4	0.00	3.90	0.00
miR-98	0.00	3.83	0.00
miR-181A2	0.00	3.47	0.00
miR-365B	0.00	3.34	0.00
miR-548K	0.00	2.78	2.82
miR-181C	0.00	2.55	0.00
miR-3180-5	0.00	2.21	2.52
miR-4519	0.00	0.00	851.22
miR-1249	0.00	0.00	180.16
miR-4701	0.00	0.00	128.52
miR-5581	0.00	0.00	115.31
miR-4520A	0.00	0.00	59.89
miR-4271	0.00	0.00	47.26
miR-302C	0.00	0.00	42.62
miR-2909	0.00	0.00	38.60
miR-4524A	0.00	0.00	38.60
miR-4479	0.00	0.00	32.12
miR-4284	0.00	0.00	29.85
miR-3157	0.00	0.00	28.94
miR-328	0.00	0.00	22.94
miR-363	0.00	0.00	22.94
miR-1-2	0.00	0.00	17.04
miR-LET7A1	0.00	0.00	15.95
miR-3162	0.00	0.00	13.99
miR-92B	0.00	0.00	13.90
miR-554	0.00	0.00	12.90
miR-4644	0.00	0.00	12.34
miR-659	0.00	0.00	12.30
miR-330	0.00	0.00	12.14
miR-5094	0.00	0.00	11.61
miR-644A	0.00	0.00	9.40
miR-4306	0.00	0.00	8.29
miR-648	0.00	0.00	7.12
miR-4313	0.00	0.00	5.12
miR-1250	0.00	0.00	3.15
miR-664, SNORA36B	0.00	0.00	2.94
miR-3689B	0.00	0.00	1.06

miRNAs: microRNAs

Supplementary	Table	2:	List	of r	microRNAs	in	primary	human	epididymal	tissues	(fragments	per	kilobase	of	transcript	per	million	mapped	reads
[FPKM] >0.1)																			

mil-4441         34.6.6/s         5.37.40/s         4.16.070           miR-4205, MPC2         1150.700         12315.000         164.85           miR-4205, MPC2         12117.00         17315.50         164.53           miR-1282         1565.40         1400.44         1665.53           miR-1284         1565.40         1400.44         1665.53           miR-1282         1565.40         1400.44         1665.53           miR-1282         1565.40         140.70         799.30           miR-464, Strand         862.17         797.60         799.30           miR-462, RISZ7A         733.05         350.24         954.78           miR-462, Str32         438.79         18.75         miR-257           miR-462, Str32         438.77         170.51         5.06           miR-463, Str32         455.79         7.66         0.00           miR-1302, UMG5         445.79         7.66         0.00           miR-1302, UMG5         445.79         7.66         0.00           miR-1302, UMG5         436.64         1374.74         272.55           miR-469         134.38         7.87         77.149         204.53           miR-468         366.64         1374.7	miRNAs	Caput tissue	Corpus tissue	Cauda tissue
miR-400, NPC2         112.00         128.50           miR-3648, miR-3637         1121.00         1215.50         1164.22           miR-3648, miR-3637         126.60         100.4         166.33           miR-363         1438.89         1222.82         7.97.80           miR-363         4.67         2.23         7.97.80           miR-365         36.21         6.50.3         390.24         9.43           miR-365         51.81         105.79         1.87.5         1.87.5           miR-265         51.82         100.79         1.87.5         1.77.5           miR-265, miR-205H6         466.77         1.77.05         1.56.6           miR-270         455.71         7.46         0.00           miR-265, miR-205H6         466.77         1.77.5         1.86.6           miR-111         3.57.14         489.86         0.62.1           miR-361         466.77         7.7.6         0.00           miR-362         7.0.5         1.00.7         1.7.6           miR-363         7.87.4         2.57.7         1.7.6           miR-364         7.87.4         2.57.7         1.7.6           miR-365         7.6.6         0.00         0.00		3.6E+06	5.3E+05	4.1E+05
miR-3687 121.00 173.63 165.43 165.43 165.43 165.43 165.43 165.43 165.43 165.43 165.43 165.93 173.75	miR-4709, NPC2	41160.70	121350.00	188.55
miR-1282156.5.4.0143.8.8.01222.8.247.05.0miR-4634. PTMA162.1.71222.8.247.0.5miR-4643. PTMA163.2.11222.8.210.3.3miR-4617. INTENC28-113.0.533.0.533.0.530.0.7miR-417. INTENC28-11108.7.718.7.51108.7.718.7.5miR-205. miR-205.49.8.7.77.77.0.5.15.0.60.0.0miR-205. miR-205.466.7.717.70.5.15.0.60.0.0miR-205. miR-205.466.7.77.76.60.0.00.0.0miR-205. miR-205.7.76.60.0.00.0.00.0.0miR-305.1455.77.76.60.0.00.0.0miR-305.130.6.6.417.4.427.1.2.60.0.1miR-305.130.7.1487.466.22.10.0.0miR-307.130.7.1487.466.22.10.0.0miR-307.130.7.1487.466.22.10.0.0miR-307.130.7.1487.466.22.10.0.0miR-4630.131.2.10.0.00.0.00.0.0miR-150.miR-150.130.7.22.9.1.2.314.8.2miR-150.131.2.10.0.00.0.00.0.0miR-150.131.2.10.0.00.0.00.0.0miR-150.131.2.10.0.00.0.00.0.0miR-150.131.2.132.8.812.1.20.0.0miR-150.131.2.132.8.812.1.20.0.0miR-150.131.2.131.4.80.0.00.0.0 <td< td=""><td>miR-3648, miR-3687</td><td>12117.00</td><td>17315.50</td><td>1614.22</td></td<>	miR-3648, miR-3687	12117.00	17315.50	1614.22
mik-6ab.1438.891438.89179.29247.05mik-2464.87733.05739.50739.50739.50mik-2465.85514.21652.57244.28mik-250514.21652.57244.28mik-260516.181105.79145.75mik-260466.77172.6870.51mik-250465.71144.440.00mik-250465.71144.440.00mik-307.0500465.71144.440.00mik-307.0500455.797.060.00mik-307.0500455.797.060.00mik-307.0500452.71144.460.00mik-307.0500452.71144.470.02mik-307.0500420.02512.42389.86mik-307.0500420.02512.42389.86mik-307.0500326.470.000.00mik-309.0500326.470.000.00mik-466412.10204.5521.42204.55mik-469326.470.000.000.00mik-469.0500326.470.000.000.00mik-309.05000326.470.000.000.00mik-309.05000326.470.000.000.00mik-309.05000326.870.000.000.00mik-309.05000326.870.000.000.00mik-309.05000116.0734.800.000.00mik-309.05001116.0734.800.000.00mik-309.05001 <td< td=""><td>miR-1282</td><td>1565.40</td><td>1400.44</td><td>1605.93</td></td<>	miR-1282	1565.40	1400.44	1605.93
miR-3450862.1777.0079.30miR-3450813.3694.470.23miR-3451.11MEN22851.481105.79248.28miR-427, SLC5552498.7773.26577.77miR-250, miR-205H0466.7717270.5150.68miR-1537465.71174.460.00miR-355457.977.060.00miR-355455.797.060.00miR-356456.797.060.00miR-353456.797.060.00miR-356476.0257.24283.86miR-365476.0278.74221.26miR-36613374.4425.72124.2miR-36536.641344.74255.72miR-36536.641344.746.92miR-365355.100.000.00miR-365355.100.000.00miR-365355.100.000.00miR-365355.120.000.00miR-365155.1079.32147.62miR-155.miR-155H0295.7279.32147.62miR-1350.155H0295.7279.32147.62miR-1350.155H0295.7279.32147.62miR-1350.155H0295.7279.32147.62miR-1350.155H0295.7279.32147.62miR-1350.155H0295.72149.200.00miR-1350.1550.000.000.00miR-1350.155155.070.000.00miR-1350.1550.000.00	miR-663A	1438.89	1222.82	47.05
miR-365083.3.64.70.2.3miR-4026, PS27A390.2.4954.78miR-4026, PS27A390.2.4954.78miR-4026, MS27A501.88105.91.74.8miR-4026, MS205C466.777.72.8.677.57miR-205, miR-205H0466.771.74.4.60.00miR-1279466.771.74.4.60.00miR-1279465.711.44.4.60.00miR-1307, USMS5456.12389.863.73.7miR-205, USMS5456.12389.863.74.23.74.2miR-206, USMS5356.141.74.742.55.723.74.2miR-307, USMS5366.41.374.742.55.723.74.2miR-308, USMS5326.470.001.29.053.74.2miR-406326.470.001.29.053.74.24.59.72miR-407, MSNGA1, SNORA15, SNORA2, SNORA6, SNORA5, SNORA5326.470.001.29.05miR-408326.470.001.29.053.74.24.59.72miR-1305, USA72.02.82.12.21.47.621.29.2miR-1305, USA72.02.82.12.21.47.621.29.2miR-1305, USA72.03.72.00.00.001.29.05miR-1305, USA72.02.77.9.21.47.622.00.0miR-1305, USA72.02.77.9.21.47.622.00.0miR-1305, USA71.29.41.00.01.00.01.00.0miR-1305, USA71.29.41.00.01.00.0miR-1305, USA71.29.41.00.01.00.	miR-1244-3, PTMA	862.17	797.60	799.30
mik-4.26, KPS27A953, 05902, 43954, 78mik-6.11, TMKM258501, 881105, 7918, 75mik-6.26, mik-72, SL05B2465, 771770, 5116, 06mik-205, mik-205HG465, 71170, 5116, 06mik-305, mik-205HG455, 7070, 60000mik-305, mik-307, USM65426, 02512, 42398, 86mik-307, USM65426, 02512, 42398, 86mik-307, USM65366, 641374, 74255, 72mik-307, USM65366, 641374, 746, 92mik-4690321, 20, 000, 00mik-4690322, 470, 000, 00mik-4690322, 470, 000, 00mik-469, 01, SNORA15, SNORA52, SNORA52, SNORA53, SNORA6, SNORA5, SNORA5285, 7271, 49mik-155, mik-155, mik-155, mik-155, mik-163332, 88112, 000, 00mik-136, USA7, SNORA15, SNORA52, SNORA52, SNORA52, SNORA53, SNORA54, SNOR5	miR-3650	833.36	4.67	0.23
mik-Bit514.21626.27248.28miR-20C51.8105.7317.57miR-20S498.77732.8577.57miR-20S, miR-20BHG465.7714.440.00miR-1379455.797.660.00miR-1379455.797.660.00miR-30S, USMOS426.0251.24498.98miR-30S436.64137.4271.26miR-30S366.64137.4271.26miR-30S366.64137.4271.26miR-30A357.14487.466.92miR-4669326.470.001.200miR-4690312.120.000.00miR-30A, SNORA15, SNORA25, SNORA32, SNORA6, SNOR66, TAF1D298.208.98miR-313A, SNORA15, SNORA25, SNORA32, SNORA60, SNOR66, TAF1D298.208.98miR-313A, SNORA15, SNORA25, SNORA32, SNORA60, SNOR66, TAF1D298.602.41miR-313A, SNORA1, SNORA15, SNORA26, SNOR6159.876.6170.00miR-326, CMST120.2411.61012.52miR-326, SNST2159.876.6170.000.00miR-639, TCCA120.2416.1012.520.00miR-326, SNST210.000.000.000.00miR-326, SNST20.000.000.00	miR-4426, RPS27A	733.05	390.24	954.78
mR-267501.88105.7917.87mR-467, SIGSBC466.77177.0515.06mR-1279466.77177.0515.06mR-1253465.777.060.00mR-361426.02512.42399.86mR-365426.0247.74215.72mR-36537.74215.72366.641374.74mR-37237.14487.466.92mR-4668321.120.000.00mR-4668321.210.000.00mR-135, mR-155326.470.00129.06mR-4568321.210.000.00mR-1369, SN0RA1, SN0RA1, SN0RA2, SN0RA2, SN0RA40, SN0RA6, SN0RD5, TAF1D395.7727.149MR-155, mR-155285.727.9.32147.62mR-1639, TECR201.75198.862.41mR-639, TECR151.607.3.480.00mR-639, TECR151.607.3.480.00mR-639, TECR151.607.3.480.00mR-639, TECR124.240.000.00mR-636, SISF2124.240.000.00mR-636, SISF2124.240.000.00mR-636, SISF2126.471.95.441.95.44mR-64624.11.61.011.55.27mR-636, SISF2124.240.000.00mR-636, SISF2124.240.000.00mR-636, SISF2124.240.000.00mR-64624.411.61.011.55.27mR-647124.240.000.00 </td <td>miR-611, TMEM258</td> <td>514.21</td> <td>652.57</td> <td>248.28</td>	miR-611, TMEM258	514.21	652.57	248.28
miR-407, SLC3B2498,77732.8577.57miR-205, miR-205HQ465,71144.460.00miR-137, USM05455,797.060.00miR-305, miR-3661413.867.87.4271.26miR-305466,71144.460.00miR-305466,4137.4275.72miR-3061337.14487.466.52miR-468364,70.00129.06miR-4690327.14487.466.52miR-1304, SNORA18, SNORA25, SNORA32, SNORA40, SNORA8, SNORD6, TAF1D305.727.192.00miR-1304, SNORA1, SNORA18, SNORA25, SNORA32, SNORA6, SNORD6, TAF1D203.782.61.231.4.82miR-1304, SNORA1, SNORA18, SNORA25, SNORA32, SNORA40, SNORA8, SNORD6, TAF1D33.22.81.17.62miR-1304, SNORA1, SNORA18, SNORA25, SNORA32, SNORA40, SNORA8, SNORD6, TAF1D203.782.61.731.4.82miR-1304, SNORA1, SNORA18, SNORA25, SNORA32, SNORA40, SNORA8, SNORD6, TAF1D33.22.81.17.621.4.82miR-1304, SNORA1, SNORA18, SNORA25, SNORA32, SNORA40, SNORA8, SNORD6, TAF1D203.782.61.731.4.82miR-1304, SNORA1, SNORA14, SNORA14, SNORA8, SNORD6, TAF1D203.782.61.731.4.82miR-1304, SNORA1, SNORA14, SNORA25, SNORA32, SNORA40, SNORA8, SNORD6, TAF1D203.782.61.731.4.82miR-1304, SNORA1, SNORA14, SNORA1	miR-29C	501.88	1105.79	18.75
mR-205/mR-205/mG466.771770.515.06mR-1279455.797.060.00mR-1538455.797.060.00mR-36614126.02512.42389.86mR-367426.02512.42389.86mR-367366.641374.74255.72mR-72918366.641374.74255.72mR-74668326.470.00129.06mR-4668326.470.00129.06mR-154, MR-155MG305.77271.49204.53mR-154, MR-155MG255.7279.32147.62mR-154, MR-155MG203.28251.72147.62mR-4663203.28251.7314.82mR-135A2, RMST203.28251.7314.82mR-533, TECR151.93332.88121.02mR-6363151.6073.480.00mR-6467124.520.000.00mR-636, SNSF2104.450.000.00mR-75966.70.000.00mR-7690104.45151.600.00mR-7691104.45155.520.00mR-7691104.45155.520.00mR-7691104.45155.510.00mR-7692121.5241.200.00mR-769367.750.000.00mR-769367.750.000.00mR-769367.750.000.00mR-769367.750.000.00mR-769367.750.000.00mR-7693<	miR-4647, SLC35B2	498.77	732.85	77.57
mR-1279455.71144.460.00mR-1538455.727.060.00mR-1307, USMG5426.02512.42389.86mR-3661413.8678.74271.26mR-752347.98705.2850.41mR-141337.14487.466.92mR-4668326.470.001.20.66mR-4690312.120.000.00mR-1304, SNORA18, SNORA25, SNORA32, SNORA40, SNORA6, SNORD6, TAF1D298.208.981.85mR-1304, SNORA18, SNORA25, SNORA32, SNORA40, SNORA6, SNORD6, TAF1D298.208.981.85mR-1304, SNORA18, SNORA25, SNORA32, SNORA40, SNORA6, SNORD6, TAF1D298.208.981.85mR-1428255.7279.321.47.62mR-1530, IUBA7201.75198.862.41mR-539, TEGR151.607.3480.00mR-639, TEGR151.607.3480.00mR-639, TEGR151.607.3480.00mR-636, SRSF2124.200.000.00mR-636, SRSF2120.24116.101.25.52mR-530, TEGR94.990.000.00mR-636, SRSF2115.460.000.00mR-636, SRSF2120.24116.101.25.52mR-530, TEGR2.350.000.00mR-636, SRSF210.677.160.00mR-637, TEGR2.363.550.00mR-638, SRSF210.310.000.00mR-7457.285.3520.00mR-7457.365.35	miR-205, miR-205HG	466.77	1770.51	5.06
mik-1358455.797.060.00mik-1307, USM055456.641374.74221.26mik-3661413.8678.74221.26mik-3661366.641374.74255.72mik-75237.14487.466.92mik-140337.14487.466.92mik-4690312.120.000.00mik-1403, SNORA1, SNORA15, SNORA32, SNORA40, SNORA6, SNORD6, TAFLD305.77271.49204.53mik-155, mik-155M6255.7279.32147.62148.22mik-154, Mik-155M6201.75198.862.41148.22mik-1353, USA72, SNORA32, SNORA32	miR-1279	465.71	144.46	0.00
miR.307, USMG5         426.0         51.2.4         89.86           miR.3661         413.86         78.74         271.26           miR.3918         366.64         1374.74         255.72           miR.462         347.98         705.28         6.041           miR.411         337.14         487.46         6.92           miR.468         326.47         0.00         0.00           miR.4690         326.17         0.00         20.05           miR.405, SNORA15, SNORA25, SNORA32, SNORA6, SNORD6, TAF1D         305.77         271.49         204.53           miR.450, TESDirk         255.72         7.9.32         147.62           miR.453, TESDirk         159.87         66.17         0.00           miR.459, TECR         151.60         7.3.48         0.00           miR.4667         161.93         32.88         21.02           miR.4667         142.45         0.00         0.00	miR-1538	455.79	7.06	0.00
mR-3661     413.66     78.74     215.72       mR-3918     366.64     1374.74     255.72       mR-762     347.98     705.28     50.41       mR-141     337.14     487.46     6.92       mR-4690     312.12     0.00     0.00       mR-4690.     312.12     0.00     0.00       mR-15.00.4, SNORA15, SNORA55, SNORA52, SNORA52, SNORA5, SNORA5, SNORD5, TAF1D     305.77     271.49     204.53       mR-15.5m RR-155M6     305.77     73.52     147.62       mR-15.5m RR-155M6     255.72     73.52     147.62       mR-5193, UBA7     201.75     198.86     2.41       mR-539, TECR     161.93     332.88     121.02       mR-6453     151.60     73.48     0.00       mR-4667     142.42     4.00     0.00       mR-4667     142.42     4.00     0.00       mR-4667     124.20     0.00     0.00       mR-4667     124.42     4.00     0.00       mR-4667     124.42     4.10     1.05       mR-458, NSF2     241     0.00     0.00       mR-4667     124.42     4.10     0.00       mR-4674     6.70     0.00     0.00       mR-518, NSF2     24.10     0.00	miR-1307, USMG5	426.02	512.42	389.86
mR-3918         36.6         137.4/74         255.72           mR-762         347.98         705.28         50.41           mR-468         326.47         0.00         0.00           mR-4680         326.47         0.00         0.00           mR-4590         312.12         0.00         0.00           mR-155, mR-155H6         286.27         271.49         204.53           mR-4728         255.72         79.32         147.62           mR-4728         226.72         79.32         147.62           mR-1539, UBA7         201.75         198.86         2.41           mR-639, TECR         161.93         332.88         121.02           mR-639, TECR         151.60         73.48         0.00           mR-4657         124.25         0.00         0.00           mR-4658         151.60         73.48         0.00           mR-4657         124.24         0.00         0.00           mR-4657         124.24         0.00         0.00           mR-4657         124.24         0.00         0.00           mR-4657         124.24         0.00         0.00           mR-4658         0.00         0.00         0.	miR-3661	413.86	78.74	271.26
miR-7c2     37.14     487.46     6.92       miR-4668     326.47     0.00     129.06       miR-4690     312.12     0.00     0.00       miR-1304, SNORA15, SNORA25, SNORA32, SNORA40, SNORA6, SNORD6, TAFLD     305.77     271.49     204.53       miR-1304, SNORA1, SNORA15, SNORA25, SNORA32, SNORA40, SNORA6, SNORD6, TAFLD     305.77     271.49     204.53       miR-1304, SNORA1, SNORA15, SNORA25, SNORA32, SNORA60, SNORA6, SNORD6, TAFLD     305.77     271.49     204.53       miR-1304, SNORA1, SNORA15, SNORA25, SNORA32, SNORA60, SNORA6, SNORD6, TAFLD     305.77     271.49     204.53       miR-155, miR-155H6     298.20     8.98     1.85       miR-4503, UBA7     203.28     251.23     1.4.82       miR-519, SIBA7     KBAT     201.75     198.86     2.41       miR-6363, TECR     159.87     66.17     0.00       miR-6363, TECR     159.87     66.17     0.00       miR-6363, SISF2     124.20     429.02     0.00       miR-6364     159.87     0.00     0.00       miR-6365, SISF2     124.24     429.02     0.00       miR-6369     124.20     429.02     0.00       miR-6369     124.20     429.02     0.00       miR-6369     94.99     0.00     0.00	miR-3918	366.64	1374.74	255.72
miR-141     37.1     487.46     6.92       miR-4568     326.47     0.00     129.06       miR-4568     326.47     0.00     0.00       miR-4569     312.12     0.00     0.00       miR-155.miR-155H6     352.7     271.49     204.53       miR-1728     255.72     79.32     147.62       miR-17393, UBA7     203.7     271.49     204.53       miR-17394, RMST     201.75     198.86     2.41       miR-639, TECR     161.93     332.88     121.02       miR-639, TECR     151.60     73.48     0.00       miR-667     142.45     0.00     0.00       miR-4566     142.45     0.00     0.00       miR-356, SFSF2     120.24     116.10     125.52       miR-6591     115.46     0.00     0.00       miR-1909, RX01     104.45     195.44     81.03       miR-1909, RX01     104.45     195.44     81.03       miR-1908     94.99     0.00     0.00       miR-2982     80.76     75.16     0.00       miR-2982     85.79     0.00     0.00       miR-3584     62.66     14.43     0.83       miR-4667     1.23     0.00     0.00       miR	miR-762	347.98	705.28	50.41
miR-4686         326.17         0.00         129.06           miR-4690         312.12         0.00         0.00           miR-1304, SNORA1, SNORA15, SNORA32, SNORA40, SNORA6, SNORD6, TAF1D         305.77         271.49         204.53           miR-1555, miR-155HG         295.27         79.32         147.62           miR-4528         251.23         14.82           miR-1513, UBA7         203.28         251.23         14.82           miR-639, TECR         161.93         332.86         2.10.02           miR-639, TECR         159.87         66.17         0.00           miR-636         159.87         66.17         0.00           miR-636         124.25         0.00         0.00           miR-636, StSF2         120.24         16.10         125.52           miR-636, StSF2         120.42         16.10         125.52           miR-636, StSF2         104.65         195.44         81.03           miR-636, StSF2         104.65         0.00         0.00           miR-1200         0.00         0.00         0.00           miR-3507         9.00         0.00         0.00           miR-458         66.76         75.16         0.00	miR-141	337.14	487.46	6.92
miR-450     312.12     0.00     0.00       miR-1304, SNORA1, SNORA25, SNORA32, SNORA40, SNORA6, SNORD6, TAF1D     305.77     271.49     204.53       miR-155, miR-155HG     298.20     8.98     1.85       miR-4728     255.72     79.32     147.62       miR-151, UBA7     201.75     198.86     2.41       miR-353, TCR     161.93     332.88     121.02       miR-659, TCCR     161.93     332.86     121.02       miR-658     151.60     73.48     0.00       miR-656     152.02     429.02     0.00       miR-4567     124.24     429.02     0.00       miR-4565     151.60     73.48     0.00       miR-1226     120.24     116.10     125.52       miR-8581     116.00     0.00     0.00       miR-4567     120.24     151.60     0.00       miR-350, SKSF2     120.24     151.60     0.00       miR-36607     92.46     57.36     0.00       miR-368     65.70     0.00     0.00       miR-368     65.70     0.00     0.00       miR-369     94.99     0.00     0.00       miR-3607     22.66     57.35     0.00       miR-3607     0.00     0.00	miR-4668	326.47	0.00	129.06
miR-1304, SNORA1, SNORA18, SNORA32, SNORA32, SNORA3, SNORD6, TAF1D         305.77         271.49         204.53           miR-155, miR-155HG         298.20         8.98         1.85           miR-4728         255.72         79.32         147.62           miR-15193, UBA7         203.28         251.23         14.82           miR-135A2, RMST         201.75         198.86         2.41           miR-639, TECR         161.93         32.28         121.02           miR-596         155.87         66.17         0.00           miR-4568         151.60         73.48         0.00           miR-4567         124.20         429.02         0.00           miR-363, SIS72         120.24         116.10         125.52           miR-366, SIS72         120.24         116.10         125.52           miR-369, SIS7         100.4         100.45         0.00           miR-369         94.99         0.00         0.00           miR-360, SIS7         75.16         0.00         0.00           miR-360, SIS7         75.16         0.00         0.00           miR-363         55.5         0.00         0.00           miR-360, SIS7         75.16         0.00         0.00<	miR-4690	312.12	0.00	0.00
miR-155         miR-156         miR-156 <t< td=""><td>miR-1304, SNORA1, SNORA18, SNORA25, SNORA32, SNORA40, SNORA8, SNORD6, TAF1D</td><td>305.77</td><td>271.49</td><td>204.53</td></t<>	miR-1304, SNORA1, SNORA18, SNORA25, SNORA32, SNORA40, SNORA8, SNORD6, TAF1D	305.77	271.49	204.53
miR-4228     255.72     79.32     147.62       miR-5193, UBA7     203.28     251.23     14.82       miR-359, TECR     161.93     332.88     121.02       miR-639, TECR     159.87     66.17     0.00       miR-636     151.60     73.48     0.00       miR-4667     142.45     0.00     0.00       miR-31520     121.5     241.20     0.00       miR-636, SRSF2     120.24     116.10     125.52       miR-5991     115.46     0.00     0.00       miR-3607     92.46     57.36     0.00       miR-3607     92.46     57.36     0.00       miR-622     76.83     53.55     0.00       miR-624     79.33     0.00     0.00       miR-503     72.36     53.55     0.00       miR-626     75.16     0.00     0.00       miR-627     76.83     53.55     0.00       miR-628     79.36     0.00     0.00       miR-5093     72.36     53.92     0.00       miR-548D2     71.03     0.00     0.00       miR-548D2     71.03     0.00     0.00       miR-548D2     71.33     0.00     0.00       miR-548D2     62.66     0.00	miR-155, miR-155HG	298.20	8.98	1.85
miR-1393, UBA7     203.28     251.23     14.82       miR-135A2, RMST     201.75     198.86     2.41       miR-639, TECR     151.93     332.88     121.02       miR-596     159.87     66.17     0.00       miR-637, TECR     124.26     0.00     0.00       miR-636, Sass     124.20     429.02     0.00       miR-636, Sass     124.20     429.02     0.00       miR-636, Sass     120.24     116.10     125.52       miR-591     115.46     0.00     0.00       miR-1290, REX01     104.45     195.44     81.03       miR-380, TESP     94.99     0.00     0.00       miR-188     86.70     0.00     0.00       miR-1892     80.76     75.16     0.00       miR-593     72.36     53.92     0.00       miR-593     72.36     53.92     0.00       miR-593     72.36     53.92     0.00       miR-593     66.76     174.39     18.63       miR-4674     62.96     48.73     0.80       miR-458     62.96     48.73     0.80       miR-4591     62.96     48.73     0.80       miR-4674     62.96     48.73     0.80       miR-4674	miR-4728	255.72	79.32	147.62
miR-135A2, RMST     201.75     198.86     2.41       miR-639, TECR     161.93     332.88     121.02       miR-639     161.93     332.88     121.02       miR-6638     151.60     73.48     0.00       miR-6637     142.45     0.00     0.00       miR-1226     142.42     42.90     42.90     0.00       miR-3120     121.15     241.20     0.00       miR-5691     115.46     0.00     0.00       miR-1296, REX01     104.45     195.44     81.03       miR-1998     94.99     0.00     0.00       miR-3667     0.00     0.00     0.00       miR-1898     94.99     0.00     0.00       miR-1998     94.99     0.00     0.00       miR-1980     86.70     0.00     0.00       miR-1980     75.16     0.00     0.00       miR-1980     72.93     0.00     0.00       miR-4662     71.03     0.00     0.00       miR-503     72.93     0.00     0.00       miR-504     67.97     0.00     0.00       miR-4674     62.96     38.50     0.00       miR-4674     62.96     38.50     0.00       miR-363     62.06	miR-5193, UBA7	203.28	251.23	14.82
mR-839, TECR     161.93     332.88     121.02       mR-639     159.87     66.17     0.00       mR-636     161.60     73.48     0.00       mR-4667     142.45     0.00     0.00       mR-3120     124.20     429.02     0.00       mR-636, SRSF2     120.24     116.10     125.52       mR-5691     115.46     0.00     0.00       mR-909, REX01     104.45     195.44     81.03       mR-909, REX01     104.45     10.00     0.00       mR-908, REX01     86.70     0.00     0.00       mR-188     86.70     0.00     0.00       mR-4785     72.93     0.00     0.00       mR-4785     72.93     0.00     0.00       mR-14674     62.96     48.73     0.80	miR-135A2, RMST	201.75	198.86	2.41
mR-856     159.87     66.17     0.00       mR-663B     151.60     73.48     0.00       mR-4667     124.20     429.02     0.00       mR-3120     121.15     241.20     0.00       mR-563 SRSF2     120.24     116.10     125.52       mR-5691     104.45     195.44     81.03       mR-998     94.99     0.00     0.00       mR-1880     86.70     0.00     0.00       mR-662     76.83     53.55     0.00       mR-563     53.55     0.00     0.00       mR-662     76.83     53.55     0.00       mR-563     75.16     0.00     0.00       mR-564     7.93     0.00     0.00       mR-662     76.83     53.55     0.00       mR-563     53.92     0.00     0.00       mR-564     7.93     0.00     0.00       mR-562     7.103     0.00     0.00       mR-562     7.683     53.55     0.00       mR-562     7.03     0.00     0.00       mR-562     7.03     0.00     0.00       mR-562     7.97     0.00     0.00       mR-562     53.39     0.00     0.00       mR-562	miR-639, TECR	161.93	332.88	121.02
mR-663B     151.60     73.48     0.00       mR-4667     142.45     0.00     0.00       mR-1226     124.20     429.02     0.00       mR-3120     121.15     241.20     0.00       mR-5691     120.24     116.10     125.52       mR-998, REX01     104.45     195.44     81.03       mR-998     94.99     0.00     0.00       mR-807     92.46     57.36     0.00       mR-8282     80.76     75.16     0.00       mR-622     76.83     53.55     0.00       mR-593     72.36     53.92     0.00       mR-4785     72.93     0.00     0.00       mR-548D2     71.03     0.00     0.00       mR-4785     72.96     33.35     0.00       mR-474     62.96     48.73     48.63       mR-474     62.96     48.73     0.80       mR-474     62.96     0.00     0.00       mR-474     62.96     0.00     0.00       mR-474     62.96     0.00     0.00       mR-474     62.96     0.00     0.00       mR-475     52.33     0.00     0.00       mR-476     52.33     0.00     0.00    mR-4674	miR-596	159.87	66.17	0.00
miR-4667       142.45       0.00       0.00         miR-1226       124.20       429.02       0.00         miR-3120       121.15       241.20       0.00         miR-636, SRSF2       120.24       116.10       125.52         miR-5691       104.45       195.44       81.03         miR-998       94.99       0.00       0.00         miR-300, REX01       104.45       195.44       81.03         miR-398       94.99       0.00       0.00         miR-307       92.46       57.36       0.00         miR-188       86.70       0.00       0.00         miR-4802       76.83       53.55       0.00         miR-4785       72.93       0.00       0.00         miR-54802       71.03       0.00       0.00         miR-54802       71.03       0.00       0.00         miR-54802       71.03       0.00       0.00         miR-54802       62.96       48.73       0.80         miR-4691       62.96       48.73       0.80         miR-4691       62.96       38.50       0.00         miR-4516       52.33       0.00       0.00         mi	miR-663B	151.60	73.48	0.00
mR-1226     124.20     429.02     0.00       mR-3120     121.15     241.20     0.00       mR-356, SRSF2     120.24     116.10     125.52       mR-5691     115.46     0.00     0.00       mR-98     94.99     0.00     0.00       mR-3007     92.46     57.36     0.00       mR-2982     80.76     75.16     0.00       mR-4662     76.83     53.55     0.00       mR-4785     0.00     0.00     0.00       mR-548D2     71.03     0.00     0.00       mR-4785     71.03     0.00     0.00       mR-4674     67.97     0.00     0.00       mR-4674     62.96     48.73     0.80       mR-4674     62.96     38.50     0.00       mR-363     0.00     0.00     0.00       mR-364     52.32     0.63     0.00       mR-363     0	miR-4667	142.45	0.00	0.00
miR-3120       121.15       241.20       0.00         miR-636, SRSP2       120.24       116.10       125.52         miR-5691       115.46       0.00       0.00         miR-998       94.99       0.00       0.00         miR-3607       92.46       57.36       0.00         miR-3807       86.70       0.00       0.00         miR-3807       80.76       75.16       0.00         miR-2982       76.83       53.55       0.00         miR-4785       72.93       0.00       0.00         miR-5093       72.36       53.92       0.00         miR-548D2       71.03       0.00       0.00         miR-474       62.96       48.73       0.80         miR-4691       62.84       19.49       132.11         miR-363       62.06       38.50       0.00         miR-4516       52.33       0.00       0.00         miR-3912       62.06       38.50       0.00         miR-363       62.06       0.00       0.00         miR-363       0.00       0.00       0.00         miR-3912       52.42       0.00       0.00         miR-3912	miR-1226	124.20	429.02	0.00
miR-636, SR5F2     120.24     116.10     125.52       miR-5691     115.46     0.00     0.00       miR-1909, REX01     104.45     195.44     81.03       miR-99B     94.99     0.00     0.00       miR-3607     92.46     57.36     0.00       miR-29B2     80.76     75.16     0.00       miR-662     76.83     53.55     0.00       miR-5093     72.93     0.00     0.00       miR-548D2     71.03     0.00     0.00       miR-3682     66.76     174.39     18.63       miR-474     62.96     48.73     0.80       miR-363     62.66     0.00     0.00       miR-363     62.06     0.00     0.00       miR-364     62.96     48.73     0.80       miR-4691     62.06     0.00     0.00       miR-363     62.06     0.00     0.00       miR-364     59.23     92.82     16.63       miR-340     53.33     0.00     0.00       miR-3912     52.76     146.28       miR-1225     47.34     14.68     0.00       miR-1245     19.30     52.76     146.28	miR-3120	121.15	241.20	0.00
mR-5991       115.46       0.00       0.00         mR-1909, REX01       104.45       195.44       81.03         mR-998       94.99       0.00       0.00         mR-3607       92.46       57.36       0.00         mR-2982       86.70       0.00       0.00         mR-2982       80.76       75.16       0.00         mR-4785       72.93       0.00       0.00         mR-5093       72.36       53.92       0.00         mR-14785       0.00       0.00       0.00         mR-4785       66.76       174.39       18.63         mR-1474       67.97       0.00       0.00         mR-3682       66.76       174.39       18.63         mR-4674       62.96       48.73       0.80         mR-4691       62.06       0.00       0.00         mR-3633       0.00       0.00       0.00         mR-92A2       62.06       0.00       0.00         mR-3404       53.33       0.00       0.00         mR-3416       59.23       92.82       16.63         mR-3416       53.33       0.00       0.00         mR-3912       52.42	miR-636, SRSF2	120.24	116.10	125.52
mR-1909, REX01     104.45     195.44     81.03       miR-99B     94.99     0.00     0.00       miR-3607     92.46     57.36     0.00       miR-18B     86.70     0.00     0.00       miR-29B2     80.76     75.16     0.00       miR-4785     72.93     0.00     0.00       miR-5093     72.36     53.92     0.00       miR-548D2     71.03     0.00     0.00       miR-474     67.97     0.00     0.00       miR-4674     62.96     48.73     0.80       miR-4691     62.84     19.49     132.11       miR-4516     59.23     92.82     16.63       miR-4516     59.23     92.82     16.63       miR-3912     53.33     0.00     0.00       miR-3912     52.42     0.00     0.00       miR-4516     59.23     92.82     16.63       miR-3912     52.42     0.00     0.00       miR-3912     52.42     0.00     0.00       miR-1225     47.34     14.68     0.00       miR-1245     50.76     146.28     0.00	miR-5691	115.46	0.00	0.00
miR-39B     94.99     0.00     0.00       miR-3607     92.46     57.36     0.00       miR-18B     86.70     0.00     0.00       miR-29B2     80.76     75.16     0.00       miR-4785     72.93     0.00     0.00       miR-5093     72.36     53.92     0.00       miR-548D2     71.03     0.00     0.00       miR-474     67.97     0.00     0.00       miR-4674     62.96     48.73     0.80       miR-4691     62.84     19.49     132.11       miR-4691     62.06     38.50     0.00       miR-4516     59.23     92.82     16.63       miR-3912     53.33     0.00     0.00       miR-3912     52.42     0.00     0.00       miR-1245     50.76     146.28     16.81	miR-1909, REX01	104.45	195.44	81.03
miR-3607     92.46     57.36     0.00       miR-188     86.70     0.00     0.00       miR-29B2     80.76     75.16     0.00       miR-662     76.83     53.55     0.00       miR-4785     72.93     0.00     0.00       miR-5093     72.36     53.92     0.00       miR-1247     67.97     0.00     0.00       miR-4682     66.76     174.39     18.63       miR-4674     62.96     48.73     0.80       miR-363     62.06     0.00     0.00       miR-363     62.06     0.00     0.00       miR-4516     59.23     92.82     16.63       miR-3912     52.42     0.00     0.00       miR-3912     52.42     0.00     0.00       miR-1225     47.34     14.68     0.80	mik-99B	94.99	0.00	0.00
miR-18B     86.70     0.00     0.00       miR-29B2     80.76     75.16     0.00       miR-662     76.83     53.55     0.00       miR-4785     72.93     0.00     0.00       miR-5093     72.36     53.92     0.00       miR-1247     67.97     0.00     0.00       miR-4682     66.76     174.39     18.63       miR-4674     62.96     48.73     0.80       miR-4691     62.84     19.49     132.11       miR-363     62.06     38.50     0.00       miR-4516     59.23     92.82     16.63       miR-3912     53.33     0.00     0.00       miR-1225     46.51     29.13     68.95	miR-3607	92.46	57.36	0.00
miR-2982       80.76       75.16       0.00         miR-662       76.83       53.55       0.00         miR-785       72.93       0.00       0.00         miR-5093       72.36       53.92       0.00         miR-548D2       71.03       0.00       0.00         miR-548D2       67.97       0.00       0.00         miR-1247       67.97       0.00       0.00         miR-664       174.39       18.63         miR-674       62.96       48.73       0.80         miR-691       62.84       19.49       132.11         miR-363       62.06       38.50       0.00         miR-4516       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-3912       52.42       0.00       0.00         miR-1225       47.34       14.68       0.00         miR-1248       SNORA81       46.51       29.13       68.95	miR-18B	86.70	0.00	0.00
miR-662       76.83       53.55       0.00         miR-7785       72.93       0.00       0.00         miR-5093       72.36       53.92       0.00         miR-548D2       71.03       0.00       0.00         miR-548D2       67.97       0.00       0.00         miR-5682       66.76       174.39       18.63         miR-4674       62.96       48.73       0.80         miR-4691       62.84       19.49       132.11         miR-363       62.06       38.50       0.00         miR-4516       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-312, VMP1       49.30       52.76       146.28         miR-1225       47.34       14.68       0.00	miR-2982	80.76	75.16	0.00
miR-4785       72.95       0.00       0.00         miR-5093       72.36       53.92       0.00         miR-548D2       71.03       0.00       0.00         miR-1247       67.97       0.00       0.00         miR-3682       66.76       174.39       18.63         miR-4674       62.96       48.73       0.80         miR-4691       62.84       19.49       132.11         miR-363       62.06       38.50       0.00         miR-4516       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-21, VMP1       49.30       52.76       146.28         miR-1225       47.34       14.68       0.00	miR-002	70.00	0.00	0.00
miR-5053       72.50       53.52       0.00         miR-548D2       71.03       0.00       0.00         miR-1247       67.97       0.00       0.00         miR-3682       66.76       174.39       18.63         miR-4674       62.96       48.73       0.80         miR-4691       62.84       19.49       132.11         miR-363       62.06       38.50       0.00         miR-4516       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-3912       52.42       0.00       0.00         miR-1225       47.34       14.68       0.00         miR-1248       SNORA81       46.51       29.13       68.95	miR-4765	72.35	53 92	0.00
min-340271.030.000.00miR-124767.970.000.00miR-368266.76174.3918.63miR-467462.9648.730.80miR-469162.8419.49132.11miR-36362.0638.500.00miR-92A262.060.000.00miR-34C59.2392.8216.63miR-391252.420.000.00miR-21, VMP149.3052.76146.28miR-122547.3414.680.00	miR-5095	72.30	0.00	0.00
miR-1247       67.57       6.00       6.00         miR-3682       66.76       174.39       18.63         miR-4674       62.96       48.73       0.80         miR-4691       62.84       19.49       132.11         miR-363       62.06       38.50       0.00         miR-92A2       62.06       0.00       0.00         miR-316       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-21, VMP1       49.30       52.76       146.28         miR-1225       47.34       14.68       0.00	min-54602	67.07	0.00	0.00
miR-4674       62.96       48.73       0.80         miR-4691       62.84       19.49       132.11         miR-363       62.06       38.50       0.00         miR-4516       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-21, VMP1       49.30       52.76       146.28         miR-1225       47.34       14.68       0.00	miR-1247	66.76	174 30	18.63
miR-4691       62.84       19.49       132.11         miR-363       62.06       38.50       0.00         miR-92A2       62.06       0.00       0.00         miR-316       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-1225       47.34       14.68       0.00         miR-1248_SNORA81       46.51       29.13       68.95	miR-1674	62.96	174.39	0.80
miR-451       62.64       10.45       152.11         miR-363       62.06       38.50       0.00         miR-92A2       62.06       0.00       0.00         miR-4516       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-21, VMP1       49.30       52.76       146.28         miR-1225       47.34       14.68       0.00	miR-4691	62.90	19.79	132 11
miR-92A2       62.00       50.50       0.00         miR-92A2       62.06       0.00       0.00         miR-4516       59.23       92.82       16.63         miR-3912       52.42       0.00       0.00         miR-1225       47.34       14.68       0.00         miR-1248_SNORA81       46.51       29.13       68.95	miR-363	62.04	38.50	0.00
miR-4516       59.23       92.82       16.63         miR-34C       53.33       0.00       0.00         miR-3912       52.42       0.00       0.00         miR-125       47.34       14.68       0.00         miR-1248_SNORA81       46.51       29.13       68.95	miR-9242	62.00	0.00	0.00
miR 410       53.25       51.02       10.05         miR-34C       53.33       0.00       0.00         miR-3912       52.42       0.00       0.00         miR-21, VMP1       49.30       52.76       146.28         miR-1225       47.34       14.68       0.00         miR-1248_SNORA81       46.51       29.13       68.95	miR-4516	59.23	92.82	16.63
miR-3912     52.42     0.00     0.00       miR-21, VMP1     49.30     52.76     146.28       miR-1225     47.34     14.68     0.00       miR-1248_SNORA81     46.51     29.13     68.95	miR-34C	53 33	0.00	0.00
miR-21, VMP1     49.30     52.76     146.28       miR-1225     47.34     14.68     0.00       miR-1248_SNORA81     46.51     29.13     68.95	miR-3912	52 42	0.00	0.00
miR-1225 47.34 14.68 0.00 miR-1248_SNORA81 46.51 29.13 68.95	miR-21_VMP1	49 30	52 76	146.28
miR-1248_SN0R481 46.51 29.13 68.95	miR-1225	47 34	14 68	0.00
	miR-1248_SNORA81	46 51	29.13	68 95
miR-3620 46.23 0.00 98.43	miR-3620	46.23	0.00	98.43

miRNAs	Caput tissue	Corpus tissue	Cauda tissue
miR-1914, miR-647, UCKL1	45.88	32.86	53.33
miR-100HG	44.27	27.17	3.18
miR-4492	43.19	0.00	171.29
miR-760	43.17	0.00	0.00
miR-2117	43.17	0.00	0.00
miR-4672	40.38	0.00	0.00
miR-761, NRD1	39.38	41.00	38.81
miR-564. TMEM42	36.73	102.04	14.21
miR-4721, TUFM	35.57	40.49	101.44
miR-1238	35.51	44.06	25.20
miR-4750. TBC1D17	33.73	982.62	15.97
miR-505	33.38	0.00	0.00
miR-568	32.26	31.31	15.49
miR-378D2	31.75	19.70	0.00
miR-632. ZNE207	31.60	34.27	99.60
miR-3621	31.42	0.00	0.00
miR-3610 RAD21	31.30	34.26	49.89
miR-3615_SLC9A3R1	30.40	50.69	76.26
miR-22 miR-22HG	30.06	36.51	29.73
miR-3942	29.75	18.46	7 04
miR-3180-4	29.53	16.72	1 39
miR-3917_STMN1	28.96	36.46	168.86
miR-221 miR-222	28.50	28.33	8 73
miR-221, miR-222	27.47	20.33	113 30
miR-3671	26.41	19.16	0.00
miR-1287 PVROYD2	25.93	28.19	13.40
miR-1207, 1 TROAD2	25.55	7.82	230.06
miR-4007; 511111	23.38	9.57	5 45
miR-3000, WAO	23.70	14.69	31.42
miR-130A1	23.07	14.00	90.01
miR-1292, NOF 30, SNOR 200	22.34	19.47	140.30
miR-3003, FH62	22.13	20.77	0.00
miR-191	21.50	0.00	110.52
miR-4000, MAD4	10.24	21.04	12.66
miR-045	19.24	12.59	1.22
miR-5740	19.10	12.50	1.22
miR-4000, 10004	17.04	15 19	2 27
miR-LET7D	17.00	10.10	2.37
miR-343, NELLA	17.00	11 70	20.01
miR-4/41, RDDF0	17.23	152 56	20.43
miP 2004 miP 2008 miP 420	14.24	0.23	12.86
miR-200A, miR-200B, miR-423	14.24	55.40	20.69
miR-210, miR-21010	13.41	11 02	40.31
miR-3134, 11013	10.12	16.11	40.31
	10.12	14.52	7.07
miR-937; SURID	9.80	14.55	90.00
miR-4/24, RADIIFIF4	9.00	25.42	22.94
miR-3077; miR-940	9.00	120.00	10.04
min-4517; NFAIGZIF	0.92	11.00	10.75
mir-570, SDRAFZ	8.24	11.09	7.02
בנט-אוווו איפ ארט געוניז אין אין ארט אין	8.13	2.47	0.57
	8.00	4.02	222.21
1111R-4403, RIVET/U mid LETZDUC	/.38	9.17	9.75
	7.33	4.88	5.47
	7.00	/.08	15.60
mik-4/05, mik-LET/A3, mik-LET/B, mik-LET/BHG	6.58 5.50	17.98	0.43
	5.58	3.90	1.34

miRNAs	Caput tissue	Corpus tissue	Cauda tissue
miR-3685	5.06	5.17	5.23
miR-664, SNORA36B	4.63	2.87	0.00
miR-3614, TRIM25	4.62	4.94	25.36
miR-5001, TIGD1	4.58	4.34	3.49
miR-132	4.51	9.33	0.12
miR-5004, SYNGAP1	4.26	2.49	2.63
miR-3911	4.04	10.32	8.18
miR-1291, SNORA34	3.87	2.41	7.39
miR-612	3.54	38.31	7.24
miR-3658, UCK2	3.24	1016.70	7.48
miR-3714, PLCL2	3.18	2.84	2.26
miR-31HG	3.06	4.16	6.69
miR-1256, SLC25A53	2.89	3.00	2.67
miR-4315-2, PLEKHM1	2.77	2.80	9.67
miR-548AA1, PALMD	2.72	2.85	0.28
miR-621, SLC25A15	2.53	1.98	21.57
miR-143, miR-143HG, miR-145	2.39	2.72	0.48
miR-4740	2.25	1.55	0.88
miR-31	2.16	3.20	6.27
miR-3074	2.08	44.72	54.46
miR-17, miR-17HG, miR-18A, miR-19A, miR-19B1, miR-20A, miR-92A1	2.01	1.81	1.29
miR-320E	1.71	1.61	0.60
miR-5187, TOMM40L	1.55	1.82	5.64
miR-146B	1.46	2.19	0.01
miR-600HG	1.46	1.17	1.50
miR-548N, OSBPL6	1.27	1.24	0.27
miR-LET7I	1.14	1.41	1.83
miR-4632, TNFRSF1B	1.14	1.49	0.40
miR-1972-2	1.13	0.94	0.09
miR-484, NDE1	0.90	1.32	4.41
miR-146A	0.82	1.00	6.83
miR-3916	0.81	1.21	28.96
miR-4712	0.71	1.06	1.92
miR-3688-2	0.65	0.87	11.27
miR-4720	0.51	0.78	1.70
miR-30C2	0.34	0.11	10.52
miR-4491	0.28	6.22	0.00
miR-7-3HG	0.26	0.22	0.00
miR-573	0.25	0.09	47.53
miR-196A1	0.17	0.15	139.54
miR-135B	0.15	2.59	4.85
miR-5587	0.06	0.28	2.58
miR-631	0.00	230.99	0.00
miR-4489	0.00	144.46	165.26
miR-4714	0.00	137.92	0.00
miR-4467	0.00	126.45	0.00
miR-4256	0.00	111.51	0.00
miR-4449	0.00	88.37	0.00
miR-4292	0.00	79.32	271.37
miR-328	0.00	77.00	0.00
miR-200C	0.00	71.54	0.00
miR-20B	0.00	64.80	0.00
miR-4306	0.00	58.24	0.00
miR-4746	0.00	53.78	61.53
miR-4725	0.00	52.49	0.00
miR-330	0.00	49.30	0.00

miRNAs	Caput tissue	Corpus tissue	Cauda tissue
miR-572	0.00	48.06	0.00
miR-339	0.00	47.46	0.00
miR-4804	0.00	45.24	0.00
miR-5690	0.00	45.24	0.00
miR-324	0.00	44.08	176.20
miR-4768	0.00	41.68	0.00
miR-641	0.00	39.91	79.97
miR-4784	0.00	33.09	168.92
miR-3125	0.00	30.78	0.00
miR-LET7A1	0.00	26.78	0.00
miR-1236	0.00	23.96	21.25
miR-4642	0.00	23.47	31.43
miR-5188	0.00	20.90	3.96
miR-196B	0.00	20.74	71.06
miR-4513	0.00	18.37	0.00
miR-1227	0.00	16.39	52.50
miR-133A1	0.00	16.39	0.00
miR-604	0.00	11.94	28.32
miR-331	0.00	11.94	0.00
miR-33B	0.00	10.82	16.51
miR-1324	0.00	10.82	0.00
miR-5002	0.00	10.32	0.00
miR-561	0.00	10.32	0.00
miR-27B	0.00	10.32	0.00
miR-4440	0.00	9.85	25.01
miR-345	0.00	9.85	0.00
miR-4441	0.00	8.99	25.83
miR-593	0.00	8.99	10.28
miR-5000	0.00	7.88	0.00
miR-765	0.00	5.10	0.00
miR-941-1, miR-941-3, miR-941-4	0.00	4.56	15.64
miR-3651, SNORA84	0.00	2.71	0.00
miR-320B2	0.00	2.34	3.73
miR-54811	0.00	1.73	0.00
miR-54812	0.00	1.73	0.00
miR-3907	0.00	1.64	0.00
miR-137, miR-137HG	0.00	0.07	0.14
miR-1260B	0.00	0.00	450.62
miR-4701	0.00	0.00	261.36
miR-4273	0.00	0.00	199.26
miR-553	0.00	0.00	163.23
miR-25	0.00	0.00	145.65
miR-3189	0.00	0.00	96.63
miR-4253	0.00	0.00	93.04
miR-302C	0.00	0.00	81.84
miR-4284	0.00	0.00	74.31
miR-4685	0.00	0.00	74.13
miR-1229	0.00	0.00	74.13
miR-4482-1	0.00	0.00	67.41
miR-2/A	0.00	0.00	65.58
mik-590	0.00	0.00	52.91
miR-23A	0.00	0.00	48.97
miR-4640	0.00	0.00	47.57
miR-3/4B	0.00	0.00	42.76
miR-4/66	0.00	0.00	40.78
miR-3191	0.00	0.00	39.63

miRNAs	Caput tissue	Corpus tissue	Cauda tissue
miR-5687	0.00	0.00	37.85
miR-3117	0.00	0.00	35.21
miR-4742	0.00	0.00	33.32
miR-3153	0.00	0.00	29.95
miR-5087	0.00	0.00	26.92
miR-3138	0.00	0.00	26.86
miR-3662	0.00	0.00	26.00
miR-4263	0.00	0.00	25.28
miR-4653	0.00	0.00	25.20
miR-938	0.00	0.00	24.53
miR-3188	0.00	0.00	22.30
miR-186	0.00	0.00	21.02
miR-149	0.00	0.00	19.32
miR-193A	0.00	0.00	18.75
miR-661	0.00	0.00	18.39
miR-1231	0.00	0.00	16.16
miR-LET7G	0.00	0.00	14.62
miR-421	0.00	0.00	14.11
miR-507	0.00	0.00	13.66
miR-219-1	0.00	0.00	13.53
miR-941-2, miR-941-3, miR-941-4	0.00	0.00	13.16
miR-199B	0.00	0.00	12.15
miR-634	0.00	0.00	11.81
miR-455	0.00	0.00	11.27
miR-7-1	0.00	0.00	11.17
miR-423	0.00	0.00	11.14
miR-622	0.00	0.00	10.70
miR-140	0.00	0.00	10.28
miR-3622B	0.00	0.00	9.14
miR-4311	0.00	0.00	8.35
miR-181A2	0.00	0.00	5.53
miR-769	0.00	0.00	5.03
miR-3909	0.00	0.00	4.86
miR-499A	0.00	0.00	4.47
miR-4524B	0.00	0.00	4.40

miRNAs: microRNAs