Supplementary Table 1. Statistics of the distribution for small RNAs during a series of filters in order

By counts of sequences	Average of % (by count#)	Ovary		Testis	
		# counts	% of raw	# counts	% of raw
raw	\	17,620,539	\	18,616,809	\
(1) Adapters	0.31	67,860	0.39	45,152	0.24
(2) More than 80% A, C, G, or T	0.00	0	0.00	0	0.00
(3) More than two N (undermined bases)	0.00	306	0.00	249	0.00
(4) Only A and C or G and T	0.03	7,947	0.05	4,155	0.02
(5) Stretches of A7, C8, G6, or T7	0.08	16,990	0.10	13,517	0.07
(6) Shorter than 15 nt and longer than 26 nt	21.70	2,352,975	13.35	5,592,543	30.04
(7) More than ten dimers, six trimers and five tetrames	0.00	94	0.00	106	0.00
(8) Lower than three copy number	3.78	633,323	3.59	737,453	3.96
(9) Hit mRNA, RFam, Repbase	13.65	2,530,191	14.36	2,408,610	12.94
(10) Mappable	60.44	12,010,853	68.16	9,815,024	52.72

Supplementary Table 2. Proportion of sequ-seqs mapping to known RNA classes

There is overlapping in mapping of sequ-seqs with **mRNA, rRNA, tRNA, snRNA, snoRNA** and **repeats.**

RNA class	Ovary	Testis
	# counts	# counts
mRNA	2,009,560	2,000,614
rRNA	146,988	98,401
tRNA	74,838	63,693
snRNA	9,387	8,109
snoRNA	39,135	33,318
repeats	678,731	521,619
total	2,530,191	2,408,610

Supplementary Table 3. Statistics based on the counts and kinds of the mappable sequences

There is overlapping with the sequ-seqs mapped to pre-miRNAs (i.e., one specific sequ-seq may both mapped to porcine and other mammalian pre-miRNAs).

By counts of sequences	Average of % (by count#)	Ovary		Testis	
		# counts	% of mappable	# counts	% of mappable
mappable	\	12,010,853	\	9,815,024	\
Group 1. mapped to knonw porcine pre-miRNAs (with genome location)	80.48	7,942,616	66.129	5,407,333	55.092
Group 2: mapped to knonw porcine pre-miRNAs (without genome location)	1.33	134,483	1.120	86,833	0.885
Group 3: mapped to mammalian (excluded pig) pre-miRNAs, which map to pig genome (PN(a))	1.27	117,331	0.977	90,679	0.924
Group 4: the most abundant sequ-seqs encoding from pre-miRNAs in group1 or 3 were originate from the novel predicted hairpins in genome (PN(b))	0.00	255	0.002	201	0.002
Group 5: mapped to mammalian (excluded pig) pre-miRNAs, which do not map to pig genome, but the sequ-seqs were mapped to genome and encompassing predicted hairpins (PN(c))	0.00	341	0.003	147	0.001
Group 6: unmapped to any mammalian pre-miRNAs, but the sequ-seqs (longer than 18 nt) were mapped to genome and encompassing predicted hairpins (PC)	0.22	29,129	0.243	9,306	0.095
Group 7. not accounted for by the above categories (remain)	37.27	3786953	31.529	4,220,726	43.003
By kinds of sequences	**Average of % (by sequence#)**	**Ovary**		**Testis**	
		# sequences	**% of mappable**	**# sequences**	**% of mappable**
mappable	\	55,329	\	56,873	\
Group 1. mapped to knonw porcine pre-miRNAs (with genome location)	12.36	7,714	13.942	6,132	10.782
Group 2: mapped to knonw porcine pre-miRNAs (without genome location)	0.70	458	0.828	330	0.580
Group 3: mapped to mammalian (excluded pig) pre-miRNAs, which map to pig genome (PN(a))	1.33	856	1.547	638	1.122
Group 4: the most abundant sequ-seqs encoding from pre-miRNAs in group1 or 3 were originate from the novel predicted hairpins in genome (PN(b))	0.00	3	0.005	2	0.004
Group 5: mapped to mammalian (excluded pig) pre-miRNAs, which do not map to pig genome, but the sequ-seqs were mapped to genome and encompassing predicted hairpins (PN(c))	0.02	17	0.031	6	0.011
Group 6: unmapped to any mammalian pre-miRNAs, but the sequ-seqs (longer than 18 nt) were mapped to genome and encompassing predicted hairpins (PC)	0.55	162	0.293	459	0.807
Group 7. not accounted for by the above categories (remain)	85.04	46129	83.372	49,314	86.709

Supplementary Table 4.1. Profile of the known porcine miRNAs (miRBase 15.0) with genome locations

(1). In "sequence in miRBase" column, "New", miRNA identified in this study and not reported in miRBase 15.0; "Diff", confirming miRNA sequences in miRBase 15.0, but different sequences are reported in our study; and "Yes", confirming miRNA sequences in miRBase15.0.(2) The genome locations of mir-28, mir-29c and mir-139 were absent in miRBase 15.0, while been annotated in Ensemble database (release 59, Aug 2010).(3) "Consensus miRNA sequence" is the assembly sequence of the most abundance sequences in ovary and testis libraries, which was chosen as a report reference sequence in our study.

Pre-miRNA ID	Pre-miRNA name	Genomic location of pre-miRNA based on Sscrofa9 genome assembly								miRNA name	Consensus miRNA sequence	Length (nt)	Sequence in miRBase	Ovary					Testis				
		1st location				2nd location																	
		Chromosome	Strand	Start	End	Chromosome	Strand	Start	End					Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs	Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs
1	mir-30c	1	-	53,819,906	53,819,985					miR-30c-5p	TGTAAACATCCTACACTCTCAGCT	24	diff	TGTAAACATCCTACACTCTCAGCT	24	6,573	11,757	46	TGTAAACATCCTACACTCTCAGCT	24	4,266	6,982	34
1	mir-30c	1	-	53,819,906	53,819,985					miR-30c-3p	CTGGGAGAAGGCTGTTTACTCT	22	new	CTGGGAGAAGGCTGTTTACTCT	22	35	47	3	CTGGGAGAAGGCTGTTTACTCT	22	15	15	1
2	mir-30a	1	-	53,848,998	53,849,104					miR-30a-5p	TGTAAACATCCTCGACTGGAAGCT	24	diff	TGTAAACATCCTCGACTGGAAGCT	24	6,965	13,816	64	TGTAAACATCCTCGACTGGAAGCT	24	2,545	5,759	34
2	mir-30a	1	-	53,848,998	53,849,104					miR-30a-3p	CTTTCAGTCGGATGTTTGCAGC	22	yes	CTTTCAGTCGGATGTTTGCAGC	22	150	590	15	CTTTCAGTCGGATGTTTGCAGC	22	62	270	14
3	mir-122	1	-	169,284,211	169,284,295					miR-122-5p	TGGAGTGTGACAATGGTGTTTGT	23	yes	TGGAGTGTGACAATGGTGTTTGT	23	335	1,477	13	TGGAGTGTGACAATGGTGTTTG	22	223	1,073	11
4	mir-101-1	1	-	227,255,282	227,255,372					miR-101-1-5p	TCGGTTATCATGGTACCGATGCTG	24	new	TCGGTTATCATGGTACCGATGCT	23	4	7	2	CGGTTATCATGGTACCGATGCTG	23	6	6	1
4	mir-101-1	1	-	227,255,282	227,255,372					miR-101-1-3p	TACAGTACTGTGATAACTGAAG	22	diff	TACAGTACTGTGATAACTGAAG	22	83,429	191,018	283	TACAGTACTGTGATAACTGAAG	22	69,188	152,498	236
5	mir-204	1	-	234,511,625	234,511,733					miR-204-5p	TTCCCTTTGTCATCCTATGCCT	22	yes	TTCCCTTTGTCATCCTATGCCT	22	147	185	5	TTCCCTTTGTCATCCTATGCCT	22	64	76	4
5	mir-204	1	-	234,511,625	234,511,733					miR-204-3p	GCTGGGAAGGCAAAGGGACGT	21	new	GCTGGGAAGGCAAAGGGACGT	21	10	10	1	GCTGGGAAGGCAAAGGGACGT	21	5	5	1
6	mir-455	1	+	267,848,307	267,848,386					miR-455-5p	TATGTGCCTTTGGACTACATCGT	23	new	TATGTGCCTTTGGACTACATCGT	23	451	1,207	27	TATGTGCCTTTGGACTACATCGT	23	293	643	16
6	mir-455	1	+	267,848,307	267,848,386					miR-455-3p	GCAGTCCATGGGCATATACAC	21	yes	GCAGTCCATGGGCATATACAC	21	345	1,539	39	GCAGTCCATGGGCATATACAC	21	22	306	19
7	mir-181a-2	1	+	280,334,006	280,334,085					miR-181a-2-5p	AACGCTGTCGGTGAGT	16	diff	AACGCTGTCGGTGAGT	16	5	181	12	AACGCTGTCGGTGAGT	16	3	124	11
8	mir-181b-2	1	+	280,335,868	280,335,953					miR-181b-2-5p	AACATTCATTGCTGTCG	17	diff	AACATTCATTGCTGTCG	17	3	812	9	AACATTCATTGCTGTCGGTGGGGT	24	438	560	8
9	mir-199b	1	-	283,325,992	283,326,065					miR-199b-5p	CCCAGTGTTTAGACTATCTGTTC	23	new	CCCAGTGTTTAGACTATCTGTTC	23	2,015	3,650	26	CCCAGTGTTTAGACTATCTGTTC	23	257	478	11
9	mir-199b	1	-	283,325,992	283,326,065					miR-199b-3p	ACAGTAGTCTGCACATTGGTT	21	diff	ACAGTAGTCTGCACATTGGTT	21	14,605	33,568	111	ACAGTAGTCTGCACATTGGTT	21	2,422	5,222	35
10	mir-210	2	+	331,306	331,381					miR-210-5p	AGCCACTGCCCACCGCACACTG	22	new	AGCCACTGCCCACCGCACACTG	22	11	14	2	AGCCACTGCCCACCGCACACTG	22	6	6	1
10	mir-210	2	+	331,306	331,381					miR-210-3p	CTGTGCGTGTGACAGCGGCTGA	22	yes	CTGTGCGTGTGACAGCGGCTGA	22	396	617	19	CTGTGCGTGTGACAGCGGCTGA	22	349	533	15
11	mir-192	2	+	5,685,412	5,685,491					miR-192-5p	CTGACCTATGAATTGACAGCC	21	yes	CTGACCTATGAATTGACAGCC	21	312	1,554	27	CTGACCTATGAATTGACAGCC	21	237	1,141	20
11	mir-192	2	+	5,685,412	5,685,491					miR-192-3p	CTGCCAATTCCATAGGTCACA	21	new	CTGCCAATTCCATAGGTCACA	21	5	17	3					
12	mir-130a	2	-	11,301,854	11,301,932					miR-130a-5p	GCTCTTTTCACATTGTGCTACT	22	new	GCTCTTTTCACATTGTGCTACT	22	54	71	4	GCTCTTTTCACATTGTGCTACT	22	38	49	3
12	mir-130a	2	-	11,301,854	11,301,932					miR-130a-3p	CAGTGCAATGTTAAAAGGGCATT	23	diff	CAGTGCAATGTTAAAAGGGCATT	23	7,828	15,711	49	CAGTGCAATGTTAAAAGGGCATT	23	6,659	13,182	39
13	mir-129	2	-	17,100,324	17,100,403					miR-129-5p	CTTTTTGCGGTCTGGGCTTGC	21	new	CTTTTTGCGGTCTGGGCTTGC	21	178	231	7	CTTTTTGCGGTCTGGGCTTGC	21	89	138	6
13	mir-129	2	-	17,100,324	17,100,403					miR-129-3p	AAGCCCTTACCCCAAAAAGCAT	22	yes	AAGCCCTTACCCCAAAAAGCAT	22	78	94	3	AAGCCCTTACCCCAAAAAGCAT	22	38	65	3
14	mir-199a	2	-	52,684,957	52,685,036					miR-199a-5p	CCCAGTGTTCAGACTACCTGTTC	23	yes	CCCAGTGTTCAGACTACCTGTTC	23	27,112	48,699	124	CCCAGTGTTCAGACTACCTGTTC	23	3,253	9,023	36
14	mir-199a	2	-	52,684,957	52,685,036					miR-199a-3p	ACAGTAGTCTGCACATTGGTT	21	diff	ACAGTAGTCTGCACATTGGTT	21	14,605	33,564	110	ACAGTAGTCTGCACATTGGTT	21	2,422	5,222	35
15	mir-24-1	2	-	56,860,821	56,860,892					miR-24-1-5p	GTGCCTACTGAGCTGAAACA	20	diff	GTGCCTACTGAGCTGAAAC	19	28	122	14	GTGCCTACTGAGCTGAAACA	20	28	73	5
15	mir-24-1	2	-	56,860,821	56,860,892					miR-24-1-3p	TGGCTCAGTTCAGCAGGAACAG	22	yes	TGGCTCAGTTCAGCAGGAACAG	22	141,747	210,439	177	TGGCTCAGTTCAGCAGGAACAG	22	128,462	190,423	159
16	mir-27a	2	-	56,860,970	56,861,051					miR-27a-5p	AGGGCTTAGCTGCTTGTGAGCA	22	new	AGGGCTTAGCTGCTTGTGAGCA	22	5,179	5,589	20	AGGGCTTAGCTGCTTGTGAGCA	22	5,188	5,556	23
16	mir-27a	2	-	56,860,970	56,861,051					miR-27a-3p	TTCACAGTGGCTAAGTTCCGC	21	yes	TTCACAGTGGCTAAGTTCCGC	21	18,594	48,884	102	TTCACAGTGGCTAAGTTCCGC	21	15,445	40,700	93
17	mir-23a	2	-	56,861,159	56,861,228					miR-23a-3p	ATCACATTGCCAGGGATTTCCA	22	diff	ATCACATTGCCAGGGATTTCCA	22	28,630	64,293	158	ATCACATTGCCAGGGATTTCCA	22	20,750	51,432	128
18	mir-181c	2	+	56,889,316	56,889,402					miR-181c-5p	AACATTCAACCTGTCGGTGAGT	22	yes	AACATTCAACCTGTCGGTGAGT	22	630	882	12	AACATTCAACCTGTCGGTGAGT	22	678	908	9
18	mir-181c	2	+	56,889,316	56,889,402					miR-181c-3p	ACCATCGACCGTTGAGTGGACC	22	new	ACCATCGACCGTTGAGTGGACC	22	243	458	12	ACCATCGACCGTTGAGTGGACC	22	225	426	12
19	mir-181d	2	+	56,889,500	56,889,579					miR-181d-5p	AACATTCATTGTTGTCGGT	19	diff	AACATTCATTGTTGTCGGT	19	16	367	26	AACATTCATTGTTGTCGGT	19	19	315	21
19	mir-181d	2	+	56,889,500	56,889,579					miR-181d-3p	CCCACCGGGGGATGAATGTCA	21	new	CCCACCGGGGGATGAATGTCA	21	4	4	1					
20	mir-340	2	+	67,820,612	67,820,691	2	+	67,919,929	67,920,008	miR-340-5p	TTATAAAGCAATGAGACTGATT	22	yes	TTATAAAGCAATGAGACTGATT	22	67	124	5	TTATAAAGCAATGAGACTGATT	22	45	77	4
20	mir-340	2	+	67,820,612	67,820,691	2	+	67,919,929	67,920,008	miR-340-3p	TCCGTCTCAGTTACTTTATAGCC	23	new	TCCGTCTCAGTTACTTTATAGCC	23	25	35	2	TCCGTCTCAGTTACTTTATAGCC	23	16	19	2
21	mir-143	2	+	136,030,752	136,030,831					miR-143-5p	GGTGCAGTGCTGCATCTCTGG	21	new	GGTGCAGTGCTGCATCTCTGG	21	1,154	1,990	14	GGTGCAGTGCTGCATCTCTGG	21	138	260	6
21	mir-143	2	+	136,030,752	136,030,831					miR-143-3p	TGAGATGAAGCACTGTAGCTCG	22	diff	TGAGATGAAGCACTGTAGCTCG	22	390,545	2,512,314	328	TGAGATGAAGCACTGTAGCTCG	22	154,700	825,639	228
22	mir-145	2	+	136,032,141	136,032,226					miR-145-5p	GTCCAGTTTTCCCAGGAATCCCT	23	diff	GTCCAGTTTTCCCAGGAATCCCT	23	14,311	20,969	75	GTCCAGTTTTCCCAGGAATCCCT	23	1,618	2,525	17
22	mir-145	2	+	136,032,141	136,032,226					miR-145-3p	ATTCCTGGAAATACTGTTCTT	21	new	ATTCCTGGAAATACTGTTCTT	21	226	475	13	ATTCCTGGAAATACTGTTCTT	21	30	65	7
23	mir-378	2	+	136,265,603	136,265,682					miR-378-5p	CCTGACTCCAGGTCCTGTGTGT	22	diff	CTCCTGACTCCAGGTCCTGTGA	22	3	3	1	CCTGACTCCAGGTCCTGTGTGT	22	4	4	1
23	mir-378	2	+	136,265,603	136,265,682					miR-378-3p	CACTGGACTTGGAGTCAGAAGGC	23	new	CACTGGACTTGGAGTCAGAAGGC	23	715	42,705	158	CACTGGACTTGGAGTCAGAAGGC	23	616	47,070	164
24	mir-339	3	+	406,870	406,949					miR-339-5p	TCCCTGTCCTCCAGGAGCTCACT	23	diff	TCCCTGTCCTCCAGGAGCTCACT	23	65	107	5	TCCCTGTCCTCCAGGAGCTCACT	23	30	44	4
24	mir-339	3	+	406,870	406,949					miR-339-3p	AGCTCCTCGAGGCCAGAGCCC	21	new	AGCTCCTCGAGGCCAGAGCCC	21	3	3	1					
25	mir-365-1	3	+	26,344,192	26,344,271					miR-365-1-5p	AGGGACTTTTGGGGGCAGATGTG	23	new	AGGGACTTTTGGGGGCAGATGTG	23	6	10	2	AGGGACTTTTGGGGGCAGATGTG	23	4	7	2
25	mir-365-1	3	+	26,344,192	26,344,271					miR-365-1-3p	TAATGCCCCTAAAAATCCTTAT	22	yes	TAATGCCCCTAAAAATCCTTAT	22	255	349	7	TAATGCCCCTAAAAATCCTTAT	22	202	283	8
26	mir-216	3	+	79,165,852	79,165,956	3	-	79,385,092	79,385,196	miR-216-5p	TAATCTCAGCTGGCAACTGTGA	22	diff						TAATCTCAGCTGGCAACTGTGA	22	7	7	1
27	mir-217	3	+	79,172,584	79,172,690	3	-	79,378,361	79,378,467	miR-217-5p	TACTGCATCAGGAACTGATTGGA	23	diff	TACTGCATCAGGAACTGATTGGA	23	6	6	1	TACTGCATCAGGAACTGATTGGA	23	20	33	4
28	mir-30d	4	+	5,729,459	5,729,537					miR-30d-5p	TGTAAACATCCCCGACTGGAAGC	23	diff	TGTAAACATCCCCGACTGGAAGC	23	28,240	48,044	127	TGTAAACATCCCCGACTGGAAGC	23	25,106	40,144	96
28	mir-30d	4	+	5,729,459	5,729,537					miR-30d-3p	CTTTCAGTCAGATGTTTGCTGC	22	new	CTTTCAGTCAGATGTTTGCTGC	22	44	71	5	CTTTCAGTCAGATGTTTGCTGC	22	37	61	5
29	mir-30b	4	+	5,733,584	5,733,659					miR-30b-5p	TGTAAACATCCTACACTCAGCT	22	yes	TGTAAACATCCTACACTCAGCT	22	6,732	8,104	36	TGTAAACATCCTACACTCAGCT	22	5,318	6,368	30
29	mir-30b	4	+	5,733,584	5,733,659					miR-30b-3p	CTGGGAGGTGGATGTTTACTTC	22	diff	CTGGGAGGTGGATGTTTACTTC	22	5	5	1					
30	mir-124a-1	4	-	72,452,797	72,452,901					miR-124a-1-3p	TAAGGCACGCGGTGAATGCCAA	22	diff	TAAGGCACGCGGTGAATGCCAA	22	425	1,177	23	TAAGGCACGCGGTGAATGCCAA	22	437	1,175	30
31	mir-92b	4	-	98,703,325	98,703,404					miR-92b-5p	AGGGACGGGACGCGGTGCAGTGT	23	new	AGGGACGGGACGCGGTGCAGTGT	23	9	14	2	AGGGACGGGACGCGGTGCAGTGT	23	6	6	1
31	mir-92b	4	-	98,703,325	98,703,404					miR-92b-3p	TATTGCACTCGTCCCGGCCTCC	22	yes	TATTGCACTCGTCCCGGCCTCC	22	240	428	12	TATTGCACTCGTCCCGGCCTCC	22	53	87	6
32	mir-148b	5	+	18,088,734	18,088,813					miR-148b-3p	TCAGTGCATCACAGAACTTTGTTT	24	diff	TCAGTGCATCACAGAACTTTGTTT	24	317	352	4	TCAGTGCATCACAGAACTTTGTTT	24	289	318	5
33	let-7i	5	+	26,807,364	26,807,448					let-7i-5p	TGAGGTAGTAGTTTGTGCTGTT	22	diff	TGAGGTAGTAGTTTGTGCTGTT	22	357,715	444,799	190	TGAGGTAGTAGTTTGTGCTGTT	22	460,146	566,030	199
33	let-7i	5	+	26,807,364	26,807,448					let-7i-3p	CTGCGCAAGCTACTGCCTTGCT	22	new	CTGCGCAAGCTACTGCCTTGCT	22	101	236	7	CTGCGCAAGCTACTGCCTTGCT	22	82	204	7
34	mir-135-2	5	-	81,615,635	81,615,734					miR-135-2-5p	TATGGCTTTTTATTCCTATGTGA	23	yes	TATGGCTTTTTATTCCTATGTGA	23	227	372	6	TATGGCTTTTTATTCCTATGTGA	23	92	112	4
34	mir-135-2	5	-	81,615,635	81,615,734					miR-135-2-3p	ATGTAGGGATGGAAGCCATGAAA	23	new	TGTAGGGATGGAAGCCATGAAA	22	3	3	1	ATGTAGGGATGGAAGCCATGA	21	3	3	1
35	mir-331	5	+	82,983,750	82,983,829					miR-331-5p	TCTAGGTATGGTCCCAGGGATC	22	diff	TCTAGGTATGGTCCCAGGGATC	22	97	196	8	TCTAGGTATGGTCCCAGGGATC	22	37	80	5
35	mir-331	5	+	82,983,750	82,983,829					miR-331-3p	GCCCCTGGGCCTATCCTAGA	20	diff	GCCCCTGGGCCTATCCTAGA	20	409	1,085	17	GCCCCTGGGCCTATCCTAGA	20	273	661	14
36	mir-328	6	+	13,347,429	13,347,508					miR-328-5p	GTTTCGGAGCCTGGAGCG	18	new	TGTCTCGGAGCCTGGAGCG	19	9	9	1	GTTTCGGAGCCTGGAGCG	18	5	16	4
36	mir-328	6	+	13,347,429	13,347,508					miR-328-3p	CTGGCCCTCTCTGCCCTTCCGT	22	yes	CTGGCCCTCTCTGCCCTTCCGT	22	217	475	7	CTGGCCCTCTCTGCCCTTCCGT	22	173	383	7
37	mir-769	6	-	36,259,104	36,259,183					miR-769-5p	TGAGACCTCTGGGTTCTGAGCT	22	new	TGAGACCTCTGGGTTCTGAGCT	22	204	428	10	TGAGACCTCTGGGTTCTGAGC	21	85	158	4
37	mir-769	6	-	36,259,104	36,259,183					miR-769-3p	CTGGGATCTCTGGGGTCTTGGTT	23	yes	CTGGGATCTCTGGGGTCTTGGTT	23	17	27	4					
38	mir-99b	6	+	39,533,216	39,533,285					miR-99b-5p	CACCCGTAGAACCGACCTTGCG	22	yes	CACCCGTAGAACCGACCTTGCG	22	7,888	12,838	54	CACCCGTAGAACCGACCTTGCG	22	6,115	9,803	33
38	mir-99b	6	+	39,533,216	39,533,285					miR-99b-3p	CAAGCTCGTGTCTGTGGGTCCGT	23	new	CAAGCTCGTGTCTGTGGGTCCGT	23	98	339	11	CAAGCTCGTGTCTGTGGGTCCGT	23	94	277	9
39	let-7e	6	+	39,533,375	39,533,454					let-7e-5p	TGAGGTAGGAGGTTGTATAGTT	22	yes	TGAGGTAGGAGGTTGTATAGTT	22	2,963	4,961	40	TGAGGTAGGAGGTTGTATAGTT	22	1,471	2,602	32
39	let-7e	6	+	39,533,375	39,533,454					let-7e-3p	CTATACGGCCTCCTAGCTTTCC	22	new	CTATACGGCCTCCTAGCTTTCC	22	37	78	8	CTATACGGCCTCCTAGCTTTCC	22	12	20	3
40	mir-125a	6	+	39,533,851	39,533,930					miR-125a-5p	TCCCTGAGACCCTTTAACCTGT	22	diff	TCCCTGAGACCCTTTAACCTGT	22	2,312	3,973	30	TCCCTGAGACCCTTTAACCTGT	22	605	1,039	11
40	mir-125a	6	+	39,533,851	39,533,930					miR-125a-3p	ACAGGTGAGGTTCTTGGGA	19	new	ACAGGTGAGGTTCTTGGGA	19	4	7	2					
41	mir-935	6	+	40,293,236	40,293,315	6	+	40,351,581	40,351,660	miR-935-3p	CAGTTACCGCTTCCGCTACCG	21	diff	CAGTTACCGCTTCCGCTACCG	21	8	12	2					
42	mir-186	6	+	99,703,517	99,703,598					miR-186-5p	CAAAGAATTCTCCTTTTGGGCTT	23	yes	CAAAGAATTCTCCTTTTGGGCTT	23	12,221	17,855	69	CAAAGAATTCTCCTTTTGGGCTT	23	8,212	12,467	47
42	mir-186	6	+	99,703,517	99,703,598					miR-186-3p	CCAAAGGTGAATTTTTTGGGA	21	new	CCAAAGGTGAATTTTTTGGGA	21	32	76	4	CCAAAGGTGAATTTTTTGGGA	21	21	52	5
43	mir-101-2	6	+	103,818,808	103,818,888					miR-101-2-5p	TCAGTTATCACAGTGCTGATGC	22	new	CAGTTATCACAGTGCTGATGC	21	4	12	2	TCAGTTATCACAGTGCTGATG	21	6	6	1
43	mir-101-2	6	+	103,818,808	103,818,888					miR-101-2-3p	TACAGTACTGTGATAACTGAAG	22	diff	TACAGTACTGTGATAACTGAAG	22	83,429	183,178	247	TACAGTACTGTGATAACTGAAG	22	69,188	147,538	210
44	mir-30e	6	-	121,824,301	121,824,380					miR-30e-5p	TGTAAACATCCTTGACTGGAAGCT	24	yes	TGTAAACATCCTTGACTGGAAGCT	24	16,053	29,524	100	TGTAAACATCCTTGACTGGAAGCT	24	11,433	20,494	74
44	mir-30e	6	-	121,824,301	121,824,380					miR-30e-3p	CTTTCAGTCGGATGTTTACAGC	22	yes	CTTTCAGTCGGATGTTTACAGC	22	1,198	4,232	30	CTTTCAGTCGGATGTTTACAGC	22	830	2,530	22
45	mir-133b	7	+	53,115,236	53,115,315					miR-133b-3p	TTGGTCCCCTTCAACCAGCTGTTA	24	diff	TTGGTCCCCTTCAACCAGCTGTTA	24	4	7	2					
46	mir-184	7	+	54,379,989	54,380,071					miR-184-3p	TGGACGGAGAACTGATAAGGGAA	23	diff	TGGACGGAGAACTGATAAGGGAA	23	3	3	1	TGGACGGAGAACTGATAAGGGAA	23	5	5	1
47	mir-744	7	+	108,483,610	108,483,689	12	+	53,485,953	53,486,032	miR-744-5p	TGCGGGGCTAGGGCTAACAGCA	22	yes	TGCGGGGCTAGGGCTAACAGCA	22	7,153	8,393	39	TGCGGGGCTAGGGCTAACAGCA	22	6,080	7,093	31
47	mir-744	7	+	108,483,610	108,483,689	12	+	53,485,953	53,486,032	miR-744-3p	CTGTTGCCACTAACCTCAACC	21	new	CTGTTGCCACTAACCTCAACC	21	17	29	3	CTGTTGCCACTAACCTCAACC	21	6	11	2
48	mir-342	7	-	130,281,629	130,281,708					miR-342-5p	AGGGTGCTATCTGTGACTGAGGGAC	25	new	AGGGTGCTATCTGTGACTGAGGGAC	25	13	30	4					
48	mir-342	7	-	130,281,629	130,281,708					miR-342-3p	TCTCACACAGAAATCGCACCCGT	23	diff	TCTCACACAGAAATCGCACCCGT	23	84	190	6	TCTCACACAGAAATCGCACCCGT	23	28	51	4
49	mir-345	7	+	130,435,923	130,436,002	7	-	130,622,836	130,622,915	miR-345-5p	GCTGACTCCTAGTCCAGTGCTT	22	diff	GCTGACTCCTAGTCCAGTGCTT	22	5	14	3	GCTGACTCCTAGTCCAGTGCTA	22	11	18	3
49	mir-345	7	+	130,435,923	130,436,002	7	-	130,622,836	130,622,915	miR-345-3p	CCCTGAACTAGGGGTCTGGAG	21	yes	CCCTGAACTAGGGGTCTGGAG	21	7	34	3	CCCTGAACTAGGGGTCTGGAG	21	8	23	3
50	mir-432	7	+	133,834,157	133,834,236					miR-432-5p	TCTTGGAGTAGGTCATTGGGT	21	yes	TCTTGGAGTAGGTCATTGGGT	21	9	26	4					
51	mir-136	7	+	133,834,348	133,834,429					miR-136-5p	ACTCCATTTGTTTTGATGATGG	22	diff	ACTCCATTTGTTTTGATGATGG	22	100	103	2	ACTCCATTTGTTTTGATGATGG	22	5	5	1
51	mir-136	7	+	133,834,348	133,834,429					miR-136-3p	CATCATCGTCTCAAATGAGTCT	22	new	CATCATCGTCTCAAATGAGTCT	22	15	15	1					
52	mir-127	7	+	133,929,738	133,929,817					miR-127-5p	CTGAAGCTCAGAGGGCTCTGAT	22	new	CTGAAGCTCAGAGGGCTCTGAT	22	82	159	7					
52	mir-127	7	+	133,929,738	133,929,817					miR-127-3p	TCGGATCCGTCTGAGCTTGGCT	22	yes	TCGGATCCGTCTGAGCTTGGCT	22	626	1,313	15	TCGGATCCGTCTGAGCTTGGCT	22	81	215	10
53	mir-95	8	-	3,350,578	3,350,658					miR-95-3p	AACGGGTATTTATTGAGC	18	diff	AACGGGTATTTATTGAGC	18	5	5	1					
54	mir-574	8	+	25,753,375	25,753,454					miR-574-3p	CACGCTCATGCACACACCCACA	22	yes	CACGCTCATGCACACACCCACA	22	2,906	3,775	18	CACGCTCATGCACACACCCACA	22	452	600	6
55	mir-139	9	-	6,808,359	6,808,426					miR-139-5p	TCTACAGTGCACGTGTCTCCAGT	23	diff	TCTACAGTGCACGTGTCTCCAGT	23	3,225	4,634	27	TCTACAGTGCACGTGTCTCCAGT	23	2,863	4,001	24
55	mir-139	9	-	6,808,359	6,808,426					miR-139-3p	TGGAGACGCGGCCCTGTTGGAGT	23	new	TGGAGACGCGGCCCTGTTGGAGT	23	331	505	14	TGGAGACGCGGCCCTGTTGGAGT	23	264	428	14
56	mir-326	9	-	9,132,230	9,132,320					miR-326-3p	CCTCTGGGCCCTTCCTCCAGT	21	diff	CCTCTGGGCCCTTCCTCCA	19	5	1,525	4	CCTCTGGGCCCTTCCTCCAGT	21	985	994	3
57	mir-708	9	-	13,711,347	13,711,426					miR-708-5p	AAGGAGCTTACAATCTAGCTGGGT	24	diff	AAGGAGCTTACAATCTAGCTGGGT	24	208	368	11	AAGGAGCTTACAATCTAGCTGGGT	20	184	322	7
57	mir-708	9	-	13,711,347	13,711,426					miR-708-3p	CAACTAGACTGTGAGCTTCTAG	22	new	CAACTAGACTGTGAGCTTCTAG	22	473	1,540	15	CAACTAGACTGTGAGCTTCTAG	22	406	1,353	10
58	mir-34c	9	+	38,211,158	38,211,237	9	+	38,328,136	38,328,215	miR-34c-5p	AGGCAGTGTAGTTAGCTGATTGC	23	yes	AGGCAGTGTAGTTAGCTGATTGC	23	130,113	152,665	146	AGGCAGTGTAGTTAGCTGATTGC	23	153,583	194,512	172
58	mir-34c	9	+	38,211,158	38,211,237	9	+	38,328,136	38,328,215	miR-34c-3p	AATCACTAACCACACGGCCAGG	22	new	AATCACTAACCACACGGCCAGG	22	974	1,588	17	AATCACTAACCACACGGCCAGG	22	1,112	1,924	24
59	mir-1308	9	+	46,759,497	46,759,576					miR-1308-3p	GCATTGTGGTTCAGTG	16	diff	GCATTGTGGTTCAGTG	16	3	3	1	GCATTGTGGTTCAGTG	16	3	3	1
60	mir-125b-1	9	-	47,573,167	47,573,246	9	-	47,654,247	47,654,326	miR-125b-1-5p	TCCCTGAGACCCTAACTTGTGA	22	yes	TCCCTGAGACCCTAACTTGTGA	22	34,713	52,195	111	TCCCTGAGACCCTAACTTGTGA	22	18,800	24,649	72
60	mir-125b-1	9	-	47,573,167	47,573,246	9	-	47,654,247	47,654,326	miR-125b-1-3p	ACGGGTTAGGCTCTTGGGAGCT	22	new	ACGGGTTAGGCTCTTGGGAGC	21	453	1,859	25	ACGGGTTAGGCTCTTGGGAGCT	22	409	1,644	17
61	let-7a	9	-	47,697,398	47,697,477					let-7a-5p	TGAGGTAGTAGGTTGTATAGTT	22	yes	TGAGGTAGTAGGTTGTATAGTT	22	181,948	245,139	201	TGAGGTAGTAGGTTGTATAGTT	22	187,951	251,361	200
61	let-7a	9	-	47,697,398	47,697,477					let-7a-3p	CTGTACAGCCTCCTAGCTTTCC	22	new	CTGTACAGCCTCCTAGCTTTCC	22	20	23	2	CTGTACAGCCTCCTAGCTTTCC	22	9	12	2
62	mir-100	9	-	47,702,721	47,702,800					miR-100-5p	AACCCGTAGATCCGAACTTGTG	22	yes	AACCCGTAGATCCGAACTTGTG	22	13,403	57,850	87	AACCCGTAGATCCGAACTTGTG	22	12,641	51,307	74
62	mir-100	9	-	47,702,721	47,702,800					miR-100-3p	ACAAGCTTGTGTCTATAGGTAT	22	new	ACAAGCTTGTGTCTATAGGTAT	22	15	18	2	ACAAGCTTGTGTCTATAGGTAT	22	13	13	1
63	mir-214	9	-	107,639,153	107,639,262					miR-214-5p	TGCCTGTCTACACTTGCTGTGC	22	new	TGCCTGTCTACACTTGCTGTGC	22	227	363	12	TGCCTGTCTACACTTGCTGTGC	22	56	109	7
63	mir-214	9	-	107,639,153	107,639,262					miR-214-3p	ACAGCAGGCACAGACAGGCAGT	22	diff	ACAGCAGGCACAGACAGGCAGT	22	78	677	27	ACAGCAGGCACAGACAGGCAGT	22	68	403	22
64	mir-205	9	-	126,011,588	126,011,656					miR-205-5p	TCCTTCATTCCACCGGAGTCTGT	23	diff	TCCTTCATTCCACCGGAGTCTG	22	16	31	3	TCCTTCATTCCACCGGAGTCTGT	23	7	7	1
65	mir-29c	9	+	127,174,326	127,174,413					miR-29c-5p	TGACCGATTTCTCCTGGTGTTCAG	24	new	ACCGATTTCTCCTGGTGTTCAG	22	39	214	14	TGACCGATTTCTCCTGGTGTTC	22	33	205	15
65	mir-29c	9	+	127,174,326	127,174,413					miR-29c-3p	TAGCACCATTTGAAATCGGTT	21	diff	TAGCACCATTTGAAATCGGTT	21	719	1,301	17	TAGCACCATTTGAAATCGGTT	21	385	759	16
66	mir-215	10	-	9,750,609	9,750,704					miR-215-5p	ATGACCTATGAATTGACAGACA	22	diff	ATGACCTATGAATTGACAGACA	22	144	222	7	ATGACCTATGAATTGACAGACA	22	124	171	3
67	mir-181b-1	10	-	22,839,191	22,839,270					miR-181b-1-5p	AACATTCATTGCTGTCG	17	diff	AACATTCATTGCTGTCG	17	3	798	10	AACATTCATTGCTGTCGGTGGGGT	24	438	537	8
67	mir-181b-1	10	-	22,839,191	22,839,270					miR-181b-1-3p	CTCACTGAACAATGAATGCAT	21	new	CTCACTGAACAATGAATGCAT	21	4	4	1					
68	mir-181a-1	10	-	22,839,352	22,839,455					miR-181a-1-5p	AACGCTGTCGGTGAGT	16	diff	AACGCTGTCGGTGAGT	16	5	181	12	AACGCTGTCGGTGAGT	16	3	124	11
68	mir-181a-1	10	-	22,839,352	22,839,455					miR-181a-1-3p	ACCATCGACCGTTGATTGTACC	22	new	ACCATCGACCGTTGATTGTACC	22	574	704	10	ACCATCGACCGTTGATTGTACC	22	526	645	11
69	mir-24-2	10	-	26,148,230	26,148,309					miR-24-2-5p	GTGCCTACTGAGCTGATATCAGT	23	diff	GTGCCTACTGAGCTGATATCAGT	23	42	68	5	GTGCCTACTGAGCTGATATCAGT	23	29	32	2
69	mir-24-2	10	-	26,148,230	26,148,309					miR-24-2-3p	TGGCTCAGTTCAGCAGGAACAG	22	yes	TGGCTCAGTTCAGCAGGAACAG	22	141,747	303,438	227	TGGCTCAGTTCAGCAGGAACAG	22	128,462	269,815	204
70	mir-27b	10	-	26,148,776	26,148,855					miR-27b-5p	AGAGCTTAGCTGATTGGTGAAC	22	diff	AGAGCTTAGCTGATTGGTGAAC	22	184	253	4	AGAGCTTAGCTGATTGGTGAAC	22	145	204	5
70	mir-27b	10	-	26,148,776	26,148,855					miR-27b-3p	TTCACAGTGGCTAAGTTCTGC	21	yes	TTCACAGTGGCTAAGTTCTGC	21	53,837	80,075	123	TTCACAGTGGCTAAGTTCTGC	21	17,545	26,868	78
71	mir-23b	10	-	26,149,010	26,149,089					miR-23b-5p	TGGGTTCCTGGCATGCTGATTT	22	new	TGGGTTCCTGGCATGCTGATTT	22	3	3	1					
71	mir-23b	10	-	26,149,010	26,149,089					miR-23b-3p	ATCACATTGCCAGGGATTACCA	22	yes	ATCACATTGCCAGGGATTACCA	22	4,993	23,548	75	ATCACATTGCCAGGGATTACCA	22	1,835	8,412	41
72	mir-15a	11	+	17,602,978	17,603,056					miR-15a-5p	TAGCAGCACATAATGGTTTGTG	22	diff	TAGCAGCACATAATGGTTTGTG	22	1,246	2,241	18	TAGCAGCACATAATGGTTTGTG	22	937	1,671	16
72	mir-15a	11	+	17,602,978	17,603,056					miR-15a-3p	CAGGCCATATTGTGCTGCCTCA	22	new	CAGGCCATATTGTGCTGCCTCA	22	14	22	2	CAGGCCATATTGTGCTGCCTCA	22	14	23	2
73	mir-16-2	11	+	17,603,121	17,603,199					miR-16-2-5p	GCACGTAAATATTGGCG	17	diff	GCACGTAAATATTGGCG	17	20	184	12	CACGTAAATATTGGCG	16	5	140	12
73	mir-16-2	11	+	17,603,121	17,603,199					miR-16-2-3p	CCAGTATTAACTGTGCTGCTGAA	23	new	CCAGTATTAACTGTGCTGCTGAA	23	38	49	2	CCAGTATTAACTGTGCTGCTGAA	23	38	55	3
74	mir-17	11	+	60,972,458	60,972,534					miR-17-5p	GCTTACAGTGCAGGTAG	17	diff	GCTTACAGTGCAGGTAG	17	3	27	6	CAAAGTGCTTACAGTGCAGGTATT	24	14	18	2
74	mir-17	11	+	60,972,458	60,972,534					miR-17-3p	TGAAGGCACTTGTAGC	16	diff	TGAAGGCACTTGTAGC	16	3	7	2	ACTGCAGTGAAGGCACTTGTAGAA	24	8	8	1
75	mir-18	11	+	60,972,593	60,972,684					miR-18-5p	TAAGGTGCATCTAGTGC	17	diff	TAAGGTGCATCTAGTGC	17	3	3	1					
76	mir-19a	11	+	60,972,741	60,972,822					miR-19a-3p	ATTTGTGCAAATCTATGCAAAACTGA	26	diff	ATTTGTGCAAATCTATGCAAAACTGA	26	192	192	1	ATTTGTGCAAATCTATGCAAAACTGA	26	125	131	3
77	mir-20	11	+	60,972,911	60,972,981					miR-20-5p	GCTTATAGTGCAGGTAG	17	diff	TAAAGTGCTTATAGTGCAGGTATT	24	9	20	3	GCTTATAGTGCAGGTAG	17	3	17	4
78	mir-19b-1	11	+	60,973,040	60,973,119					miR-19b-1-3p	TATGCAAATCCATGCAAAACTGA	23	diff	TATGCAAATCCATGCAAAACTGA	23	13	22	4	TATGCAAATCCATGCAAAACTGA	23	8	17	4
79	mir-92a-1	11	+	60,973,160	60,973,239					miR-92a-1-3p	TATTGCACTTGTCCCGG	17	diff	TATTGCACTTGTCCCGG	17	36	359	20	TATTGCACTTGTCCCGG	17	26	277	14
80	mir-152	12	+	21,743,215	21,743,294					miR-152-5p	AGGTTCTGTGATACACTCCGACT	23	new	AGGTTCTGTGATACACTCCGACT	23	37	48	3	AGGTTCTGTGATACACTCCGACT	23	16	16	1
80	mir-152	12	+	21,743,215	21,743,294					miR-152-3p	TCAGTGCATGACAGAACTTGG	21	yes	TCAGTGCATGACAGAACTTGG	21	4,977	9,121	33	TCAGTGCATGACAGAACTTGG	21	1,591	2,833	14
81	mir-10a	12	-	22,389,424	22,389,503					miR-10a-5p	TACCCTGTAGATCCGAATTTGTGTA	25	diff	TACCCTGTAGATCCGAATT	19	13	13,030	185	ACCCTGTAGATCCGAATTTGTGTA	24	9	11,020	166
81	mir-10a	12	-	22,389,424	22,389,503					miR-10a-3p	CAAATTCGTATCTAGGGGAAT	21	new	CAAATTCGTATCTAGGGGAAT	21	113	155	7	CAAATTCGTATCTAGGGGAAT	21	98	116	3
82	mir-142	12	-	32,630,403	32,630,482					miR-142-5p	CATAAAGTAGAAAGCACTACT	21	yes	CATAAAGTAGAAAGCACTACT	21	188	293	9	CATAAAGTAGAAAGCACTACT	21	28	53	6
82	mir-142	12	-	32,630,403	32,630,482					miR-142-3p	TGTAGTGTTTCCTACTTTATGG	22	new	TGTAGTGTTTCCTACTTTATGG	22	1,176	3,133	20	TGTAGTGTTTCCTACTTTATGG	22	124	326	10
83	mir-21	12	+	34,201,565	34,201,656					miR-21-5p	TAGCTTATCAGACTGATGTTGAC	23	diff	TAGCTTATCAGACTGATGTTGAC	23	901,056	1,498,660	366	TAGCTTATCAGACTGATGTTGAC	23	728,247	1,050,829	301
83	mir-21	12	+	34,201,565	34,201,656					miR-21-3p	CAACAGCAGTCGATGGGCTGTC	22	new	CAACAGCAGTCGATGGGCTGTC	22	1,113	2,323	24	CAACAGCAGTCGATGGGCTGTC	22	893	1,430	16
84	mir-365-2	12	-	41,107,186	41,107,265					miR-365-2-5p	AGGGACTTTCAGGGGCAGCTGTG	23	new	AGGGACTTTCAGGGGCAGCTGTG	23	195	406	11	AGGGACTTTCAGGGGCAGCTGTG	23	181	376	11
84	mir-365-2	12	-	41,107,186	41,107,265					miR-365-2-3p	TAATGCCCCTAAAAATCCTTAT	22	yes	TAATGCCCCTAAAAATCCTTAT	22	255	349	7	TAATGCCCCTAAAAATCCTTAT	22	202	283	8
85	mir-193a	12	-	41,119,432	41,119,511					miR-193a-5p	TGGGTCTTTGCGGGCGAGATGA	22	yes	TGGGTCTTTGCGGGCGAGATGA	22	85	199	8	TGGGTCTTTGCGGGCGAGATGA	22	21	104	5
85	mir-193a	12	-	41,119,432	41,119,511					miR-193a-3p	AACTGGCCTACAAAGTCCCAGT	22	yes	AACTGGCCTACAAAGTCCCAGT	22	2,283	5,399	32	AACTGGCCTACAAAGTCCCAGT	22	1,677	3,976	24
86	mir-423	12	+	44,150,500	44,150,579					miR-423-5p	TGAGGGGCAGAGAGCGAGACTTT	23	yes	TGAGGGGCAGAGAGCGAGACTTT	23	1,581	2,490	19	TGAGGGGCAGAGAGCGAGACTTT	23	1,532	2,366	17
86	mir-423	12	+	44,150,500	44,150,579					miR-423-3p	AGCTCGGTCTGAGGCCCCTCAGT	23	yes	AGCTCGGTCTGAGGCCCCTCAGT	23	9,556	13,658	89	AGCTCGGTCTGAGGCCCCTCAGT	23	6,967	9,941	79
87	mir-22	12	+	45,319,043	45,319,122					miR-22-5p	AGTTCTTCAGTGGCAAGCTTT	21	diff	AGTTCTTCAGTGGCAAGCTTT	21	272	493	6	AGTTCTTCAGTGGCAAGCTTT	21	266	494	7
87	mir-22	12	+	45,319,043	45,319,122					miR-22-3p	AAGCTGCCAGTTGAAGAACTGT	22	yes	AAGCTGCCAGTTGAAGAACTGT	22	5,338	6,817	36	AAGCTGCCAGTTGAAGAACTGT	22	4,725	5,830	32
88	mir-497	12	+	49,575,594	49,575,673					miR-497-5p	CAGCAGCACACTGTGGTTTGTA	22	diff	CAGCAGCACACTGTGGTTTGTA	22	758	1,518	18	CAGCAGCACACTGTGGTTTGTA	22	444	913	12
88	mir-497	12	+	49,575,594	49,575,673					miR-497-3p	CAAACCACACTGTGGTGTTAGA	22	new	CAAACCACACTGTGGTGTTAGA	22	71	121	4	CAAACCACACTGTGGTGTTAGA	22	36	48	2
89	mir-195	12	+	49,575,884	49,575,963					miR-195-5p	TAGCAGCACAGAAATATTGGCA	22	diff	TAGCAGCACAGAAATATTGGCA	22	2,674	3,514	13	TAGCAGCACAGAAATATTGGCA	22	1,783	2,315	8
90	mir-324	12	+	49,872,807	49,872,886					miR-324-5p	CGCATCCCCTAGGGCATTGGTGT	23	yes	CGCATCCCCTAGGGCATTGGTGT	23	473	652	9	CGCATCCCCTAGGGCATTGGTGT	23	395	521	10
90	mir-324	12	+	49,872,807	49,872,886					miR-324-3p	CCACTGCCCCAGGTGCTGCTGG	22	new	CCACTGCCCCAGGTGCTGCTGG	22	78	548	16	CCACTGCCCCAGGTGCTGCTGG	22	59	442	13
91	mir-128-2	13	+	17,766,863	17,766,942					miR-128-2-3p	TCACAGTGAACCGGTCTCTTT	21	yes	TCACAGTGAACCGGTCTCTTT	21	271	356	8	TCACAGTGAACCGGTCTCTTT	21	210	271	5
92	mir-425	13	-	26,605,151	26,605,230					miR-425-5p	AATGACACGATCACTCCCGTTGA	23	yes	AATGACACGATCACTCCCGTTGA	23	4,094	9,722	54	AATGACACGATCACTCCCGTTGA	23	4,453	9,986	49
92	mir-425	13	-	26,605,151	26,605,230					miR-425-3p	CATCGGGAATGTCGTGTCCGCC	22	diff	CATCGGGAATGTCGTGTCCGCC	22	143	515	22	CATCGGGAATGTCGTGTCCGCC	22	110	373	19
93	mir-191	13	-	26,605,641	26,605,720					miR-191-5p	CAACGGAATCCCAAAAGCAGCTGT	24	diff	CAACGGAATCCCAAAAGCAGCTG	23	5,315	21,842	90	CAACGGAATCCCAAAAGCAGCTGT	24	3,482	16,145	62

93	mir-191	13	-	26,605,641	26,605,720					miR-191-3p	CTGCACTTGGATTTCGTTCCC	21	new	CTGCACTTGGATTTCGTTCCC	21	8	249	13	CTGCACTTGGATTTCGTTCCC	21	5	226	11
94	mir-135-1	13	+	28,964,466	28,964,555					miR-135-1-5p	TATGGCTTTTTATTCCTATGTGA	23	yes	TATGGCTTTTTATTCCTATGTGA	23	227	336	5	TATGGCTTTTTATTCCTATGTGA	23	92	103	3
95	let-7g	13	+	28,999,419	28,999,498					let-7g-5p	TGAGGTAGTAGTTTGTACAGTT	22	yes	TGAGGTAGTAGTTTGTACAGTT	22	30,971	38,455	96	TGAGGTAGTAGTTTGTACAGTT	22	31,834	39,288	86
95	let-7g	13	+	28,999,419	28,999,498					let-7g-3p	CTGTACAGGCCACTGCCTTGC	21	new	CTGTACAGGCCACTGCCTTGC	21	14	67	4	CTGTACAGGCCACTGCCTTGC	21	4	20	2
96	mir-885	13	-	55,826,401	55,826,480					miR-885-5p	TCCATTACACTACCCTGCCTCT	22	26	TCCATTACACTACCCTGCCTCT	22	26	26	1	TCCATTACACTACCCTGCCTCT	22	3	3	1
96	mir-885	13	-	55,826,401	55,826,480					miR-885-3p	AGGCAGCGGGGTGTAGTGGAT	21	yes	AGGCAGCGGGGTGTAGTGGAT	21	8	8	1	AGGCAGCGGGGTGTAGTGGAT	21	5	5	1
97	mir-15b	13	+	78,787,511	78,787,608					miR-15b-5p	GCACATCATGGTTTACA	17	diff	GCACATCATGGTTTACA	17	5	23	5	GCACATCATGGTTTACA	17	3	21	6
97	mir-15b	13	+	78,787,511	78,787,608					miR-15b-3p	CGAATCATTATTTGCTGCTCTAAA	24	new						CGAATCATTATTTGCTGCTCTAAA	24	4	4	1
98	mir-16-1	13	+	78,787,668	78,787,744					miR-16-1-5p	GCACGTAAATATTGGCG	17	diff	GCACGTAAATATTGGCG	17	20	74	7	GCACGTAAATATTGGCG	17	5	62	9
99	mir-28	13	-	95,264,193	95,264,278					miR-28-5p	AAGGAGCTCACAGTCTATTGAGT	23	diff	AAGGAGCTCACAGTCTATTGAGT	23	159	1,070	9	AAGGAGCTCACAGTCTATTGAGT	23	136	854	6
99	mir-28	13	-	95,264,193	95,264,278					miR-28-3p	CACTAGATTGTGAGCTCCTGGA	22	29	CACTAGATTGTGAGCTCCTGGA	22	4,105	6,694	34	CACTAGATTGTGAGCTCCTGGA	22	2,597	4,316	26
100	mir-99a	13	+	130,664,295	130,664,374					miR-99a-5p	AACCCGTAGATCCGATCTTGT	21	diff	AACCCGTAGATCCGATCTTGT	21	22,631	89,823	122	AACCCGTAGATCCGATCTTGT	21	4,268	17,474	39
100	mir-99a	13	+	130,664,295	130,664,374					miR-99a-3p	CAAGCTCGCTTCTATGGGTCTGT	23	new	CAAGCTCGCTTCTATGGGTCTGT	23	194	590	12	CAAGCTCGCTTCTATGGGTCTGT	23	38	79	6
101	let-7c	13	+	130,665,021	130,665,114					let-7c-5p	TGAGGTAGTAGGTTGTATGGTT	22	yes	TGAGGTAGTAGGTTGTATGGTT	22	157,247	205,724	210	TGAGGTAGTAGGTTGTATGGTT	22	182,862	235,623	200
101	let-7c	13	+	130,665,021	130,665,114					let-7c-3p	CTGTACAACCTTCTAGCTTTCC	22	new	CTGTACAACCTTCTAGCTTTCC	22	17	30	4	CTGTACAACCTTCTAGCTTTCC	22	5	5	1
102	mir-320	14	-	6,473,891	6,473,970					miR-320-3p	AAAAGCTGGGTTGAGAGGGCGA	22	diff	AAAAGCTGGGTTGAGAGGGCGA	22	23,359	35,048	120	AAAAGCTGGGTTGAGAGGGCGA	22	25,308	37,543	115
103	mir-124a-2	14	-	13,279,339	13,279,423					miR-124a-2-3p	TAAGGCACGCGGTGAATGCCAA	22	diff	TAAGGCACGCGGTGAATGCCAA	22	425	1,177	23	TAAGGCACGCGGTGAATGCCAA	22	437	1,175	30
104	mir-130b	14	-	51,318,779	51,318,858					miR-130b-5p	ACTCTTTCCCTGTTGCACTACT	22	new	ACTCTTTCCCTGTTGCACTACT	22	33	41	3	ACTCTTTCCCTGTTGCACTACT	22	3	3	1
104	mir-130b	14	-	51,318,779	51,318,858					miR-130b-3p	CAGTGCAATGATGAAAGGGCAT	22	yes	CAGTGCAATGATGAAAGGGCAT	22	88	170	6	CAGTGCAATGATGAAAGGGCAT	22	17	88	4
105	mir-185	14	+	52,703,712	52,703,787					miR-185-5p	TGGAGAGAAAGGCAGTTCCTGTT	23	diff	TGGAGAGAAAGGCAGTTCCTGTT	23	7	10	2	TGGAGAGAAAGGCAGTTCCTGTT	23	8	8	1
106	mir-1306	14	+	52,728,146	52,728,225					miR-1306-5p	CCACCTCCCCTGCAAACGTCCATT	24	diff	CCACCTCCCCTGCAAACGTCCATT	24	4	4	1					
107	mir-107	14	-	106,321,702	106,321,788					miR-107-3p	AGCAGCATTGTACAGGGCTAT	21	diff	AGCAGCATTGTACAGGGCTAT	21	458	1,246	19	AGCAGCATTGTACAGGGCTAT	21	440	1,265	20
107	mir-107	14	-	106,321,702	106,321,788					miR-107-5p	AGCTTCTTTACAGTGTTGCCTTG	23	new						AGCTTCTTTACAGTGTTGCCTTG	23	6	6	1
108	mir-146b	14	+	118,471,588	118,471,686					miR-146b-5p	TGAGAACTGAATTCCATAGGCTAT	24	diff	TGAGAACTGAATTCCA	16	3	66	8	TGAGAACTGAATTCCATAGGCTAT	24	19	44	4
109	mir-1307	14	-	119,440,203	119,440,282					miR-1307-5p	TCGACCGGACCTGCGACCGGCT	21	30	TCGACCGGACCTGCGACCGGCT	21	1,130	2,715	22	TCGACCGGACCTGCGACCGGCT	21	404	946	12
109	mir-1307	14	-	119,440,203	119,440,282					miR-1307-3p	ACTCGGCGTGGCGTCGGTCGTGG	23	diff	ACTCGGCGTGGCGTCGGTCGTGG	23	204	898	24	ACTCGGCGTGGCGTCGGTCGTGG	23	81	352	19
110	mir-202	14	-	147,952,465	147,952,544					miR-202-5p	CTTCCTATGCATATACTTCTTT	22	diff	CTTCCTATGCATATACTTCTTT	22	1,035	2,360	38	CTTCCTATGCATATACTTCTTT	22	1,252	3,059	45
110	mir-202	14	-	147,952,465	147,952,544					miR-202-3p	AGAGGTGTAGGCATGGGAAAC	21	new	AGAGGTGTAGGCATGGGAAAC	21	61	109	8	AGAGGTGTAGGCATGGGAAAC	21	29	58	7
111	mir-128-1	15	-	14,550,874	14,550,955					miR-128-1-5p	CGGGGCCGTAGCACTGTCTGAGA	23	6	CGGGGCCGTAGCACTGTCTGAGA	23	6	6	1	CGGGGCCGTAGCACTGTCTGAGA	23	13	13	1
111	mir-128-1	15	-	14,550,874	14,550,955					miR-128-1-3p	TCACAGTGAACCGGTCTCTTT	21	yes	TCACAGTGAACCGGTCTCTTT	21	271	452	10	TCACAGTGAACCGGTCTCTTT	21	210	366	6
112	mir-10b	15	+	77,060,704	77,060,783					miR-10b-5p	ACCCTGTAGAACCGAAT	17	diff	ACCCTGTAGAACCGAAT	17	12	825	42	ACCCTGTAGAACCGAAT	17	8	742	42
113	mir-103-1	16	-	52,667,657	52,667,738					miR-103-1-5p	GGCTTCTTTACAGTGCTGCCTTG	23	new	GGCTTCTTTACAGTGCTGCCTTG	23	3	4	1	GGCTTCTTTACAGTGCTGCCTTG	23	4	4	1
113	mir-103-1	16	-	52,667,657	52,667,738					miR-103-1-3p	AGCAGCATTGTACAGGGCTATGA	23	yes	AGCAGCATTGTACAGGGCTATGA	23	11,325	16,874	68	AGCAGCATTGTACAGGGCTATGA	23	9,750	14,526	55
114	mir-486	17	+	10,558,722	10,558,801	17	+	10,710,522	10,710,601	miR-486-5p	TCCTGTACTGAGCTGCCCCGAG	22	yes	TCCTGTACTGAGCTGCCCCGAG	22	573	1,728	13	TCCTGTACTGAGCTGCCCCGAG	22	550	1,719	14
115	mir-103-2	17	-	33,406,489	33,406,568	17	-	33,574,977	33,575,056	miR-103-2-5p	AGCTTCTTTACAGTGCTGCCTTG	23	new	AGCTTCTTTACAGTGCTGCCTTG	23	14	35	4	AGCTTCTTTACAGTGCTGCCTTG	23	14	23	2
115	mir-103-2	17	-	33,406,489	33,406,568	17	-	33,574,977	33,575,056	miR-103-2-3p	AGCAGCATTGTACAGGGCTATGA	23	yes	AGCAGCATTGTACAGGGCTATGA	23	11,325	18,400	86	AGCAGCATTGTACAGGGCTATGA	23	9,750	16,064	70
116	mir-499	17	-	40,405,262	40,405,341					miR-499-5p	TAAGACTTGCAGTGATGTTTAGC	23	diff	TAAGACTTGCAGTGATGTTTAGC	23	13	13	1	TAAGACTTGCAGTGATGTTTAGC	23	14	21	2
117	mir-133a	17	-	64,053,943	64,054,045					miR-133a-3p	TTTGGTCCCCTTCAACCAGCTGT	22	diff	TTGGTCCCCTTCAACCAGCTGT	22	647	1,001	9	TTGGTCCCCTTCAACCAGCTGT	22	194	313	5
118	mir-1	17	+	64,096,222	64,096,329					miR-1-3p	TGGAATGTAAAGAAGTATGTACT	23	diff	TGGAATGTAAAGAAGT	16	3	36	3	TGGAATGTAAAGAAGTATGTACT	23	11	15	2
119	mir-29b	18	+	16,054,349	16,054,429					miR-29b-5p	GCTGGTTTCATATGGTGGTTTAGA	24	new	GCTGGTTTCATATGGTGGTTTAGA	24	35	118	6	GCTGGTTTCATATGGTGGTTTAGA	24	31	93	6
119	mir-29b	18	+	16,054,349	16,054,429					miR-29b-3p	TAGCACCATTTGAAATCAGTGTT	23	diff	TAGCACCATTTGAAATCAGTGTT	23	18,091	19,712	64	TAGCACCATTTGAAATCAGTGTT	23	16,914	18,330	51
120	mir-29a	18	+	16,054,752	16,054,837					miR-29a-5p	ACTGATTTTCTTTTGGTGTTCAG	22	new	ACTGATTTTCTTTTGGTGTTCAG	22	188	459	8	ACTGATTTTCTTTTGGTGTTCAG	22	132	339	8
120	mir-29a	18	+	16,054,752	16,054,837					miR-29a-3p	TAGCACCATCTGAAATCGGTT	21	diff	TAGCACCATCTGAAATCGGTT	21	101,184	176,303	197	TAGCACCATCTGAAATCGGTT	21	96,154	171,344	199
121	mir-335	18	-	16,506,711	16,506,790					miR-335-5p	TCAAGAGCAATAACGAAAAATGT	23	diff	TCAAGAGCAATAACGAAAAATGT	23	37	71	4	TCAAGAGCAATAACGAAAAATGT	23	8	14	2
121	mir-335	18	-	16,506,711	16,506,790					miR-335-3p	TTTTTCATTATTGCTCTGACC	22	new	TTTTTCATTATTGCTCTGACC	22	44	77	6	TTTTTCATTATTGCTCTGACC	22	25	44	5
122	mir-183	18	-	17,172,238	17,172,307					miR-183-5p	TATGGCACTGGTAGAATTCACT	22	diff	TATGGCACTGGTAGAATTCACT	22	853	2,376	14	TATGGCACTGGTAGAATTCACT	22	382	1,331	18
123	mir-196b	18	+	44,179,792	44,179,871	18	+	44,205,846	44,205,925	miR-196b-5p	TAGGTAGTTTCCTGTTGTTGGG	22	yes	TAGGTAGTTTCCTGTTGTTGGG	22	67	200	7	TAGGTAGTTTCCTGTTGTTGG	21	8	18	3
124	mir-148a	18	-	45,214,548	45,214,615					miR-148a-5p	AAAGTTCTGAGACACTCCGACT	22	new	AAAGTTCTGAGACACTCCGACT	22	334	359	5	AAAGTTCTGAGACACTCCGACT	22	174	192	3
124	mir-148a	18	-	45,214,548	45,214,615					miR-148a-3p	TCAGTGCACTTTGAAACTTTGT	22	yes	TCAGTGCACTTTGAAACTTTGT	22	213,739	223,834	94	TCAGTGCACTACAGAACTTTGT	22	125,809	131,046	83
125	mir-221	X	-	40,478,094	40,478,163					miR-221-5p	ACCTGGCATACAATGTAGATTTCTGT	26	new	ACCTGGCATACAATGTAGATTTCTGT	26	10,314	10,980	46	ACCTGGCATACAATGTAGATTTCTGT	26	9,027	9,503	37
125	mir-221	X	-	40,478,094	40,478,163					miR-221-3p	AGCTACATTGTCTGCTGGGTTTC	23	diff	AGCTACATTGTCTGCTGGGTTTC	23	3,418	8,452	53	AGCTACATTGTCTGCTGGGTTTC	23	3,646	8,783	48
126	mir-222	X	-	40,478,834	40,478,913					miR-222-5p	GGCTCAGTAGCCAGTGTAGATC	22	new	GGCTCAGTAGCCAGTGTAGATC	22	39	122	11	GGCTCAGTAGCCAGTGTAGATC	22	38	119	12
126	mir-222	X	-	40,478,834	40,478,913					miR-222-3p	AGCTACATCTGGCTACTGGGTCTCT	25	diff	AGCTACATCTGGCTACTGGGTCTCT	25	773	2,971	34	AGCTACATCTGGCTACTGGGTCTCT	25	750	3,020	33
127	mir-98	X	-	45,719,499	45,719,578					miR-98-5p	TGAGGTAGTAAGTTGTATTGTT	22	yes	TGAGGTAGTAAGTTGTATTGTT	22	2,322	3,128	22	TGAGGTAGTAAGTTGTATTGTT	22	1,657	2,262	16
127	mir-98	X	-	45,719,499	45,719,578					miR-98-3p	CTATACAACTTACTACTTTCCT	22	new	CTATACAACTTACTACTTTCCT	22	16	16	1					
128	let-7f	X	-	45,720,363	45,720,445					let-7f-5p	TGAGGTAGTAGATTGTATAGTT	22	yes	TGAGGTAGTAGATTGTATAGTT	22	351,377	461,911	210	TGAGGTAGTAGATTGTATAGTT	22	397,795	519,025	210
128	let-7f	X	-	45,720,363	45,720,445					let-7f-3p	CTATACAGTCTACTGTCTTTCT	22	15	CTATACAGTCTACTGTCTTTCT	22	15	15	1	CTATACAGTCTACTGTCTTTCT	22	15	15	1
129	mir-676	X	-	55,113,034	55,113,113	X	-	55,165,137	55,165,216	miR-676-3p	CCGTCCTAAGGTTGTTGAGTT	21	yes	CCGTCCTAAGGTTGTTGAGTT	21	1,135	1,632	5	CCGTCCTAAGGTTGTTGAGTT	21	76	124	3
130	mir-374b	X	+	58,683,650	58,683,729					miR-374b-5p	ATATAATACAACCTGCTAAGTG	22	yes	ATATAATACAACCTGCTAAGTG	22	1,632	2,022	10	ATATAATACAACCTGCTAAGTG	22	1,282	1,573	6
130	mir-374b	X	+	58,683,650	58,683,729					miR-374b-3p	CTTATCAGGTTGTATTATCATT	22	new	CTTATCAGGTTGTATTATCATT	22	13	13	1	CTTATCAGGTTGTATTATCATT	22	11	11	1
131	mir-374a	X	-	58,793,654	58,793,733					miR-374a-5p	ATTTTATAATACAACCTGATAAGTGA	26	diff	ATTTTATAATACAACCTGATAAGTGA	26	16	16	1	ATTTTATAATACAACCTGATAAGTGA	26	3	3	1
132	mir-325	X	+	60,496,392	60,496,485	X	-	60,552,421	60,552,514	miR-325-5p	CCTAGTAGGTGCTCAGTAAGTGT	23	diff	CCTAGTAGGTGCTCAGTAAGTGT	23	6	6	1					
132	mir-325	X	+	60,496,392	60,496,485	X	-	60,552,421	60,552,514	miR-325-3p	TTTATTGAGCACCTCCTATCA	21	new	TTTATTGAGCACCTCCTATCA	21	31	35	2	TTTATTGAGCACCTCCTATCA	21	25	29	2
133	mir-361	X	-	67,904,186	67,904,265					miR-361-5p	TTATCAGAATCTCCAGGGGTAC	22	yes	TTATCAGAATCTCCAGGGGTAC	22	127	272	9	TTATCAGAATCTCCAGGGGTAC	22	49	134	8
133	mir-361	X	-	67,904,186	67,904,265					miR-361-3p	CCCCCAGGTGTGATTCTGATTTGC	24	yes	CCCCCAGGTGTGATTCTGATTTGC	24	17	57	8	CCCCCAGGTGTGATTCTGATTTGC	24	4	11	3
134	mir-1277	X	-	97,562,457	97,562,536					miR-1277-3p	TACGTAGATATATATGTATTT	21	diff	TACGTAGATATATATGTATTT	21	12	15	2	TACGTAGATATATATGTATTT	21	8	8	1
135	mir-363	X	-	108,178,321	108,178,400	X	-	108,212,243	108,212,322	miR-363-3p	AATTGCACGGTATCCATCTGTA	22	diff	AATTGCACGGTATCCATCTGTA	22	41	79	5	AATTGCACGGTATCCATCTGTA	22	16	30	2
136	mir-92a-2	X	-	108,178,486	108,178,565	X	-	108,212,408	108,212,487	miR-92a-2-3p	TATTGCACTTGTCCCGG	17	diff	TATTGCACTTGTCCCGG	17	36	352	18	TATTGCACTTGTCCCGG	17	26	265	13
137	mir-19b-2	X	-	108,178,624	108,178,703	X	-	108,212,546	108,212,625	miR-19b-2-3p	TGTGCAAATCCATGCAAACTGATT	25	4	TGTGCAAATCCATGCAAACTGATT	25	4	42	6	TGTGCAAATCCATGCAAACTGATT	24	15	35	6
138	mir-106a	X	-	108,213,079	108,213,159					miR-106a-5p	AAAAGTGCTTACAGTGCAGGTAGA	24	diff	GCTTACAGTGCAGGTAG	17	3	3	1	AAAAGTGCTTACAGTGCAGGTAGA	24	4	4	1
139	mir-450a	X	-	108,480,688	108,480,793					miR-450a-5p	TTTTGCGATGTGTTCCT	17	diff	TTTTGCGATGTGTTCCT	17	11	17	3	TTTTGCGATGTGTTCCT	17	6	6	1
140	mir-450c	X	-	108,480,833	108,480,913					miR-450c-5p	TTTTGCGATGTGTTCCT	17	diff	TTTTGCGATGTGTTCCT	17	11	17	3	TTTTGCGATGTGTTCCT	17	6	6	1
141	mir-542	X	+	108,481,539	108,481,618					miR-542-5p	TTGGGGATCATCATGTCACGAGA	23	diff	TTGGGGATCATCATGTCACGAGA	23	4	4	1					
141	mir-542	X	+	108,481,539	108,481,618					miR-542-3p	TGTGACAGATTGATAACTGAAGG	22	3	TGTGACAGATTGATAACTGAAGG	22	3	3	1	TGTGACAGATTGATAACTGAAGG	23	3	3	1
142	mir-503	X	-	108,498,665	108,498,773					miR-503-5p	TAGCAGCGGGAACAGTACTGCAG	23	yes	TAGCAGCGGGAACAGTACTGCAG	23	93	467	13	TAGCAGCGGGAACAGTACTGCAG	23	16	57	5
142	mir-503	X	-	108,498,665	108,498,773					miR-503-3p	GGGGTATTGTTTCTGCTGCCCGG	23	new	GGGGTATTGTTTCTGCTGCCCGG	23	14	14	1	GGGGTATTGTTTCTGCTGCCCGG	23	5	5	1
143	mir-424	X	-	108,499,011	108,499,090					miR-424-5p	CAGCAGCAATTCATGTTTTGA	21	diff	CAGCAGCAATTCATGTTTTGA	21	14,618	19,368	27	CAGCAGCAATTCATGTTTTGA	21	4,296	7,057	41
143	mir-424	X	-	108,499,011	108,499,090					miR-424-3p	CAAAACGTGAGGCGCTGCTAT	21	yes	CAAAACGTGAGGCGCTGCTAT	21	28	44	2	CAAAACGTGAGGCGCTGCTAT	21	10	13	2
144	mir-504	X	+	111,416,461	111,416,540					miR-504-5p	AGACCCTGGTCTGCACTCTATC	22	diff	AGACCCTGGTCTGCACTCTATC	22	122	420	14	GACCCTGGTCTGCACTCTATC	21	9	19	3
145	mir-505	X	+	112,590,812	112,590,891					miR-505-5p	GGGAGCCAGGAAGTATTGATGTT	23	new	GGGAGCCAGGAAGTATTGATGTT	23	4	7	2	GGGAGCCAGGAAGTATTGATGTT	23	4	12	3
145	mir-505	X	+	112,590,812	112,590,891					miR-505-3p	GTCAACACTTGCTGGTTTCCTCT	23	diff	GTCAACACTTGCTGGTTTCCTCT	23	632	2,312	32	GTCAACACTTGCTGGTTTCCTCT	23	537	1,989	30
146	mir-224	X	-	121,480,634	121,480,714					miR-224-5p	CAAGTCACTAGTGGTTCCGTTTAG	24	diff	CAAGTCACTAGTGGTTCCGTTTAG	24	31	59	4					
146	mir-224	X	-	121,480,634	121,480,714					miR-224-3p	AATGGTGCCCTAGTGACTAC	20	new						AATGGTGCCCTAGTGACTAC	20	3	3	1

Supplementary Table 4.2. Profile of the known porcine miRNAs (miRBase 15.0) without genome locations

(1). In "sequence in miRBase" column, "New", miRNA identified in this study and not reported in miRBase 15.0; "Diff", confirming miRNA sequences in miRBase 15.0, but different sequences are reported in our study; and "Yes", confirming miRNA sequences in miRBase 15.0. (2) "Consensus miRNA sequence" is the assembly sequence of the most abundance sequences in ovary and testis libraries, which was chosen as a report reference sequence in our study.

Pre-miRNA ID	Pre-miRNA name	miRNA name	Consensus miRNA sequence	Length (nt)	Sequence in miRBase	Ovary					Testis				
						Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs	Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs
1	mir-7	miR-7-5p	TGGAAGACTAGTGATTTTGTTGTTT	25	diff	TGGAAGACTAGTGATTTTGTTGTTT	25	206	225	4	TGGAAGACTAGTGATTTTGTTGTTT	25	157	168	3
1	mir-7	miR-7-3p	CAACAAATCACAGTCTGCCATA	22	new	CAACAAATCACAGTCTGCCATA	22	53	84	4	CAACAAATCACAGTCTGCCATA	22	28	34	2
2	mir-26a	miR-26a-5p	TTCAAGTAATCCAGGATAGGCT	22	yes	TTCAAGTAATCCAGGATAGGCT	22	17,587	37,082	106	TTCAAGTAATCCAGGATAGGCT	22	7,673	18,495	62
2	mir-26a	miR-26a-3p	CCTATTCTTGGTTACTTGCACG	22	new	CCTATTCTTGGTTACTTGCACG	22	39	39	1	CCTATTCTTGGTTACTTGCACG	22	29	29	1
3	mir-32	miR-32-5p	TATTGCACATTACTAAGTTGC	21	yes	TATTGCACATTACTAAGTTGC	21	92	189	4	TATTGCACATTACTAAGTTGC	21	58	121	5
3	mir-32	miR-32-3p	CAATTTAGTGTGTGTGATATT	21	new	CAATTTAGTGTGTGTGATATT	21	9	9	1	CAATTTAGTGTGTGTGATATT	21	6	6	1
4	mir-34a	miR-34a-5p	TGGCAGTGTCTTAGCTGGTTGT	22	yes	TGGCAGTGTCTTAGCTGGTTGT	22	309	600	12	TGGCAGTGTCTTAGCTGGTTGT	22	45	74	3
5	mir-140	miR-140-5p	CAGTGGTTTTACCCTATGGTAG	22	diff	CAGTGGTTTTACCCTATGGTAG	22	3,634	5,478	26	CAGTGGTTTTACCCTATGGTAG	22	1,351	2,095	14
5	mir-140	miR-140-3p	ACCACAGGGTAGAACCACGGAC	22	diff	ACCACAGGGTAGAACCACGGAC	22	24,195	82,828	203	ACCACAGGGTAGAACCACGGAC	22	19,008	56,053	123
6	mir-151	miR-151-5p	TCGAGGAGCTCACAGTCTAGTA	22	diff						TCGAGGAGCTCACAGTCTAGTA	22	3,327	4,436	45
6	mir-151	miR-151-3p	CTAGACTGAAGCTCCTTGAGGA	22	yes						CTAGACTGAAGCTCCTTGAGGA	22	1,206	3,162	24
7	mir-299	miR-299-5p	TGGTTTACCGTCCCACATACAT	22	diff	TGGTTTACCGTCCCACATACAT	22	20	75	6					
7	mir-299	miR-299-3p	TATGTGGGACGGTAAACCGCTT	22	new	TATGTGGGACGGTAAACCGCTT	22	166	401	11	TATGTGGGACGGTAAACCGCTT	22	9	17	3
8	mir-301	miR-301-5p	GCTCTGACTTTATTGCACTACT	22	new	GCTCTGACTTTATTGCACTACT	22	18	18	1	GCTCTGACTTTATTGCACTACT	22	16	16	1
9	mir-323	miR-323-5p	AGGTGGTCCGTGGCGCGTTCG	21	new						AGGTGGTCCGTGGCGCGTTCG	21	4	4	1
9	mir-323	miR-323-3p	GCACATTACACGGTCGACCTCT	22	yes	GCACATTACACGGTCGACCTCT	22	12	24	2	GCACATTACACGGTCGACCTCT	22	3	3	1
10	mir-338	miR-338-5p	AACAATATCCTGGTGCTGAGT	21	new	AACAATATCCTGGTGCTGAGT	21	6	9	2	AACAACATCCTGGTGCTGAGT	21	3	3	1
10	mir-338	miR-338-3p	TCCAGCATCAGTGATTTTGTTGA	23	diff	TCCAGCATCAGTGATTTTGTTGA	23	3	3	1	TCCAGCATCAGTGATTTTGTTGA	23	7	7	1
11	mir-369	miR-369-5p	AGATCGACCGTGTTATATTCGC	22	new	AGATCGACCGTGTTATATTCGC	22	108	400	10	AGATCGACCGTGTTATATTCGC	22	97	352	6
11	mir-369	miR-369-3p	AATAATACATGGTTGATCTTT	21	yes	AATAATACATGGTTGATCTTT	21	134	360	12	AATAATACATGGTTGATCTTT	21	91	222	10
12	mir-376a	miR-376a-5p	GTAGATTCTCCTTCTATGAGTA	22	diff	GTAGATTCTCCTTCTATGAGTA	22	29	56	3					
13	mir-500	miR-500-5p	TAATCCTTGCTACCTGGGTGAGA	23	new	TAATCCTTGCTACCTGGGTGAGA	23	815	1,321	12	TAATCCTTGCTACCTGGGTGAGA	23	199	317	6
13	mir-500	miR-500-3p	ATGCACCTGGGCAAGGATTCTGA	23	diff	ATGCACCTGGGCAAGGATTCTGA	23	279	528	13	ATGCACCTGGGCAAGGATTCTGA	23	57	124	6
14	mir-532	miR-532-5p	CATGCCTTGAGTGTAGGACCGT	22	yes	CATGCCTTGAGTGTAGGACCGT	22	3,983	4,538	18	CATGCCTTGAGTGTAGGACCGT	22	881	1,058	9
14	mir-532	miR-532-3p	CCTCCCACACCCAAGGCTTGCA	22	yes	CCTCCCACACCCAAGGCTTGCA	22	184	208	4	CCTCCCACACCCAAGGCTTGCA	22	34	34	1
15	mir-758	miR-758-3p	TTTGTGACCTGGTCCACTAAC	21	yes	TTTGTGACCTGGTCCACTAAC	21	4	8	2	TTTGTGACCTGGTCCACTAAC	21	3	3	1

Supplementary Table 4.3. Profile of novle miRNAs originating from PN(a) type pre-miRNAs

Pre-miRNA ID	Pre-miRNA name	Pre-miRNA sequence	Length (nt)	Conserved pre-miRNAs in mammalian cluster	Genomic location of pre-miRNA based on Sscrofa9 genome assembly								miRNA name	Consensus miRNA sequence	Length (nt)	Ovary					Testis				
					1st location				2nd location																
					Chromosome	Strand	Start	End	Chromosome	Strand	Start	End				Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs	Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs
1	PN(a)-1	tgcaggcctctgtgTGATATGTTTGATATATTAGGTTGttatttaatccaactatatatcaaacatattcctacagtgtcttgcc	85	hsa-mir-190;mmu-mir-190;mdo-mir-190a;rno-mir-190;oan-mir-190a;eca-mir-190;	1	-	112,612,943	##########					PN(a)-1-5p	TGATATGTTTGATATATTAGGTTG	24	TGATATGTTTGATATATTAGGTTG	24	178	683	14	TGATATGTTTGATATATTAGGTTG	24	138	397	9
2	PN(a)-2	ccccagggtcctcttgtctgagccccagaaaggaggagagagcgcTGGGTCACAGAAGAGGGTCTGGGgg	69	bta-mir-2366;	1	+	134,062,654	##########	1	-	##########	##########	PN(a)-2-3p	TGGGTCACAGAAGAGGGTCTGGA	23	TGGGTCACAGAAGAGGGTCTGG	22	3	44	3	TGGGTCACAGAAGAGGGTCTGGA	23	3	3	1
3	PN(a)-3	cagcagccccatcTGGAAGACTAGTGATTTTGTTGTTgtctcactgcgctcaacaacaagtcccagtctgccgcatggtgccggccactgca	93	bta-mir-7-1;eca-mir-7;cfa-mir-7-2;	1	-	200,316,390	##########					PN(a)-3-5p	TGGAAGACTAGTGATTTTGTTGTT	24	TGGAAGACTAGTGATTTTGTTGT	24	8,092	11,207	45	TGGAAGACTAGTGATTTTGTTGTT	24	6,552	9,094	39
4	PN(a)-4	tgctcctgtaacttggaactggagaggAGGCAAGATGCTGGCAtagctgttaaactgagaacctgctatgccaacatattgccatcttcttgtctgacagcagc	105	hsa-mir-31;mmu-mir-31;rno-mir-31;bta-mir-31;eca-mir-31;cfa-mir-31;	1	+	209,939,196	##########					PN(a)-4-5p	AGGCAAGATGCTGGCATAGCTTT	23	AGGCAAGATGCTGGCA	16	8	16	3	AGGCAAGATGCTGGCATAGCTTT	23	5	5	1
5	PN(a)-5	aattgacttagctgggtAGTGGGGAACCCTTCCATGAGGagtagaacactccttatgcaagattcccttctacctgactgggttgg	86	hsa-mir-491;mmu-mir-491;bta-mir-491;ptr-mir-491;cfa-mir-491;	1	-	210,973,875	##########					PN(a)-5-5p	AGTGGGGAACCCTTCCATGAGG	22	AGTGGGGAACCCTTCCATGAGG	22	29	35	3	AGTGGGGAACCCTTCCATGAGG	22	30	33	2
5	PN(a)-5	aattgacttagctgggtAGTGGGGAACCCTTCCATGAGGagtagaacactccttatgcaagattcccttctacctgactgggttgg	86	hsa-mir-491;mmu-mir-491;bta-mir-491;ptr-mir-491;cfa-mir-491;	1	-	210,973,875	##########					PN(a)-5-3p	CTTATGCAAGATTCCCTTCTAC	22	CTTATGCAAGATTCCCTTCTAC	22	22	29	3	CTTATGCAAGATTCCCTTCTAC	22	20	20	1
6	PN(a)-6	actcaggggcttcgccactgattgtccaaacgcaattcttgtacgagtctgcggccaaccgAGAATTGTGGCTGGACATCTGTggctgagctccggg	97	hsa-mir-219-2;mmu-mir-219-2;ptr-mir-219-2;bta-mir-219-1;rno-mir-219-2;bta-mir-219-2;mdo-mir-219;cfa-mir-219-2;	1	-	283,451,013	##########	1	-	##########	##########	PN(a)-6-3p	AGAATTGTGGCTGGACATCTGT	22	AGAATTGTGGCTGGACATCTGT	22	10	10	1	AGAATTGTGGCTGGACATCTGT	22	9	9	1
7	PN(a)-7	cgctggcgacgggacattattactttttggtacgcgctgtgacacttcaaacTCGTACCGTGAGTAATAATGCGctgtcggcagc	84	hsa-mir-126;mmu-mir-126;mml-mir-126;ppy-mir-126;ptr-mir-126;bta-mir-126;eca-mir-126;rno-mir-126;cfa-mir-126;	1	+	294,113,063	##########					PN(a)-7-5p	CATTATTACTTTTGGTACGCG	21	CATTATTACTTTTGGTACGCG	21	2,276	2,861	18	CATTATTACTTTTGGTACGCG	21	988	1,456	10
7	PN(a)-7	cgctggcgacgggacattattactttttggtacgcgctgtgacacttcaaacTCGTACCGTGAGTAATAATGCGctgtcggcagc	84	hsa-mir-126;mmu-mir-126;mml-mir-126;ppy-mir-126;ptr-mir-126;bta-mir-126;eca-mir-126;rno-mir-126;cfa-mir-126;	1	+	294,113,063	##########					PN(a)-7-3p	TCGTACCGTGAGTAATAATGCG	22	TCGTACCGTGAGTAATAATGCG	22	13,020	19,197	65	TCGTACCGTGAGTAATAATGCG	22	2,697	4,547	28
8	PN(a)-8	tggctgccaccccctGTAACAGCAACTCCATGTGGAagtgcccactagttccagtggggctgctgttatctggggtgggggccag	85	hsa-mir-194-2;mmu-mir-194-2;eca-mir-194;rno-mir-194-2;bta-mir-194-2;	2	+	5,685,207	5,685,291					PN(a)-8-5p	TGTAACAGCAACTCCATGTGGA	22	TGTAACAGCAACTCCATGTGGA	22	929	1,575	9	TGTAACAGCAACTCCATGTGGA	22	756	1,289	10
8	PN(a)-8	tggctgccaccccctGTAACAGCAACTCCATGTGGAagtgcccactagttccagtggggctgctgttatctggggtgggggccag	85	hsa-mir-194-2;mmu-mir-194-2;eca-mir-194;rno-mir-194-2;bta-mir-194-2;	2	+	5,685,207	5,685,291					PN(a)-8-3p	CCAGTGGGGCTGCTGTTATCTG	22	CCAGTGGGGCTGCTGTTATCTG	22	4	8	2	CCAGTGGGGCTGCTGTTATCTG	22	6	9	2
9	PN(a)-9	ggtttcggggtggatctgacatccctgagtgtatgtggtgaacctgaatttgccttgggTTTCCTCATATTCATTCAGGAGTGtcagttccccttcact	100	hsa-mir-670;eca-mir-670;mml-mir-670;ptr-mir-670;	2	-	17,122,268	17,122,367					PN(a)-9-3p	TTTCCTCATATTCATTCAGGAGTG	25						TTTCCTCATATTCATTCAGGAGTGA	25	4	4	1
10	PN(a)-10	ggcttcggtgctggggagcggcccccgggcgggcctctgctctggcccCTCCTGGGGCCCGCACTCTCGCTccggg	76	bta-mir-1343;	2	-	24,490,873	24,490,948					PN(a)-10-3p	CCTCCTGGGGCCCGCACTCTCG	24	CCTCCTGGGGCCCGCACTCTCG	23	4	58	5	CTCCTGGGGCCCGCACTCTCGCA	23	15	30	3
11	PN(a)-11	TCTTTGGTTATCTAGCTGTATGAgtgtattggtcttcataaagctagataaccgaaagta	60	cfa-mir-9-2;cfa-mir-9-1;	2	-	85,597,109	85,597,168					PN(a)-11-5p	ATTTCTTTGGTTATCTAGCTGTAT	26	ATTTCTTTGGTTATCTAGCTGTAT	26	3	3	1	ATTTCTTTGGTTATCTAGCTGTATG	26	3	3	1
12	PN(a)-12	ttagccctgcggccccacgcaccagggtaagagagactctcgcttcCTGCCCTGGCCCGAGGGACCGACtggctgggc	78	hsa-mir-874;mmu-mir-874;ptr-mir-874;mml-mir-874;rno-mir-874;eca-mir-874;	2	-	126,729,110	##########					PN(a)-12-5p	CGGCCCCACGCACCAGGGTAAG	23	CGGCCCCACGCACCAGGGTAA	23	13	24	3	CGGCCCCACGCACCAGGGTAAGA	23	3	3	1
12	PN(a)-12	ttagccctgcggccccacgcaccagggtaagagagactctcgcttcCTGCCCTGGCCCGAGGGACCGACtggctgggc	78	hsa-mir-874;mmu-mir-874;ptr-mir-874;mml-mir-874;rno-mir-874;eca-mir-874;	2	-	126,729,110	##########					PN(a)-12-3p	CTGCCCTGGCCCGAGGGACCGA	23	CTGCCCTGGCCCGAGGGACCG	23	115	319	11	CTGCCCTGGCCCGAGGGACCGAC	23	25	72	5
13	PN(a)-13	tcttcactgtgggaTGAGGTAGTAGGTTGTATAGTTttagggtcacacccaccactgggagataactatacaatctactgtctttcctaacgtgat	96	hsa-let-7a-1;mmu-let-7a-1;mdo-let-7a-1;ptr-let-7a-1;	3	+	38,549,756	38,549,851					PN(a)-13-5p	TGAGGTAGTAGGTTGTATAGTTT	24	TGAGGTAGTAGGTTGTATAGTTT	24	126	399	14	TGAGGTAGTAGGTTGTATAGTTTT	24	116	375	18
13	PN(a)-13	tcttcactgtgggaTGAGGTAGTAGGTTGTATAGTTttagggtcacacccaccactgggagataactatacaatctactgtctttcctaacgtgat	96	hsa-let-7a-1;mmu-let-7a-1;mdo-let-7a-1;ptr-let-7a-1;	3	+	38,549,756	38,549,851					PN(a)-13-3p	CTATACAATCTACTGTCTTTC	21	CTATACAATCTACTGTCTTTC	21	13	189	9	CTATACAATCTACTGTCTTTC	21	11	77	7
14	PN(a)-14	atcagagTGAGGTAGTAGATTGTATAGTTgtggggtagtgatttacccctgttcaggagataactatacaatctattgccttccctgag	89	hsa-let-7f-1;mmu-let-7f-1;ptr-let-7f-1;eca-let-7f;cfa-let-7f;	3	+	38,550,130	38,550,218					PN(a)-14-5p	TGAGGTAGTAGATTGTATAGTTG	23	TGAGGTAGTAGATTGTATAGTTG	23	328	1,441	13	TGAGGTAGTAGATTGTATAGTTG	23	351	1,401	13
14	PN(a)-14	atcagagTGAGGTAGTAGATTGTATAGTTgtggggtagtgatttacccctgttcaggagataactatacaatctattgccttccctgag	89	hsa-let-7f-1;mmu-let-7f-1;ptr-let-7f-1;eca-let-7f;cfa-let-7f;	3	+	38,550,130	38,550,218					PN(a)-14-3p	CTATACAATCTATTGCCTTCCT	22	CTATACAATCTATTGCCTTCC	21	3	43	4	CTATACAATCTATTGCCTTCCT	22	17	17	1
15	PN(a)-15	aatgggttcctaggaAGAGGTAGTAGGTTGCATAGTTttagggcagagattttgcccacaaggaggtaactatacgacctgctgcctttcttagggccttattatt	106	hsa-let-7d;mmu-let-7d;rno-let-7d;mdo-let-7d;ptr-let-7d;eca-let-7d;bta-let-7d;	3	+	38,552,589	38,552,694					PN(a)-15-5p	AGAGGTAGTAGGTTGCATAGTT	22	AGAGGTAGTAGGTTGCATAGTT	22	13,111	19,074	67	AGAGGTAGTAGGTTGCATAGTT	22	13,128	18,931	65
15	PN(a)-15	aatgggttcctaggaAGAGGTAGTAGGTTGCATAGTTttagggcagagattttgcccacaaggaggtaactatacgacctgctgcctttcttagggccttattatt	106	hsa-let-7d;mmu-let-7d;rno-let-7d;mdo-let-7d;ptr-let-7d;eca-let-7d;bta-let-7d;	3	+	38,552,589	38,552,694					PN(a)-15-3p	CTATACGACCTGCTGCCTTTCT	22	CTATACGACCTGCTGCCTTTCT	22	492	815	14	CTATACGACCTGCTGCCTTTCT	22	269	443	12
16	PN(a)-16	gtggcagactggaAAATCTCTGCAGGCAAATGTGAtgttactaaagaaatcacacacttacctgtagagattcatacagtctgacat	86	hsa-mir-216b;mmu-mir-216b;eca-mir-216b;bta-mir-216b;mml-mir-216b;ptr-mir-216b;cfa-mir-216b;	3	+	79,154,190	79,154,275					PN(a)-16-5p	AAATCTCTGCAGGCAAATGTGA	22						AAATCTCTGCAGGCAAATGTGA	22	3	3	1
17	PN(a)-17	TCTTTGGTTATCTAGCTGTATGAgtggtgtggagtcttcataaagctagataaccgaaagta	62	cfa-mir-9-1;cfa-mir-9-2;	4	+	97,531,341	97,531,402	4	-	97,746,803	97,746,864	PN(a)-17-5p	ATTTCTTTGGTTATCTAGCTGTAT	26	ATTTCTTTGGTTATCTAGCTGTAT	26	3	3	1	ATTTCTTTGGTTATCTAGCTGTATG	26	3	3	1
18	PN(a)-18	gaggcaatggagtgactgtcagatgcagccatcagaataggtgatttggcTGAACTGTCATACTCCCACATCCtc	77	bta-mir-2411;	4	-	99,530,701	99,530,777					PN(a)-18-5p	TGGAGTGACTGTCAGATGCAGC	24	TGGAGTGACTGTCAGATGCAGC	24	3	3	1					
18	PN(a)-18	gaggcaatggagtgactgtcagatgcagccatcagaataggtgatttggcTGAACTGTCATACTCCCACATCCtc	77	bta-mir-2411;	4	-	99,530,701	99,530,777					PN(a)-18-3p	TGAACTGTCATACTCCCACATCC	23	TGAACTGTCATACTCCCACATCC	23	6	9	2					
19	PN(a)-19	tgcttctgtgTGATATGTTTGATATTGGGTTGtttaattaggaaccaactaaatgtcaaacatattcttacagcagtagg	80	hsa-mir-190b;mmu-mir-190b;bta-mir-190b;mml-mir-190b;ptr-mir-190b;eca-mir-190b;cfa-mir-190b;mdo-mir-190b;	4	+	99,584,645	99,584,724					PN(a)-19-5p	TGATATGTTTGATATTGGGTTG	22	TGATATGTTTGATATTGGGTTG	22	516	606	7	TGATATGTTTGATATTGGGTTG	22	501	597	6
20	PN(a)-20	ggctgtgccgggtagagagggccacgggagataagagcttttcacccCTCACCACCTTCTCCACCCAGCatggcc	75	hsa-mir-197;cfa-mir-197;	4	-	115,043,656	##########					PN(a)-20-3p	TTCACCACCTTCTCCACCCAGC	22	TTCACCACCTTCTCCACCCAGC	22	18	21	2	TTCACCACCTTCTCCACCCAGC	22	16	16	1
21	PN(a)-21	gggtattcttgggtggataatacggattacgttgtTATTGCTTAAGAATACGCGT	55	cfa-mir-137;	4	-	124,680,227	##########					PN(a)-21-3p	TATTGCTTAAGAATACGCGTACC	23	TATTGCTTAAGAATACGCGTACC	23	7	7	1					
22	PN(a)-22	gggaggagggaggagatgggccaagttccctctgcctggaACGCCCTTCCCCCCCTTCTTCAcct	65	hsa-mir-1249;ptr-mir-1249;bta-mir-1249;	5	+	927,612	927,676	5	-	875,657	875,721	PN(a)-22-3p	ACGCCCTTCCCCCCCTTCTTCA	22	ACGCCCTTCCCCCCCTTCTTCA	22	152	254	10	ACGCCCTTCCCCCCCTTCTTCA	22	40	85	6
22	PN(a)-22	gggaggagggaggagatgggccaagttccctctgcctggaACGCCCTTCCCCCCCTTCTTCAcct	65	hsa-mir-1249;ptr-mir-1249;bta-mir-1249;	5	+	927,612	927,676	5	-	875,657	875,721	PN(a)-22-5p	AGGAGGGAGGGGATGGGCCAAG	24	AGGAGGGAGGGGATGGGCCAA	24	4	4	1					
23	PN(a)-23	actcgggaggggcgggaggggctccccggtgctcggatctcgaggtgcttattgcggTCCGAGCCTGGGTCTCCCTCTccccccaccccc	95	hsa-mir-615;mmu-mir-615;ptr-mir-615;bta-mir-615;eca-mir-615;mml-mir-615;	5	-	17,933,485	17,933,579					PN(a)-23-5p	GGGGGTCCCCGGTGCTCGGATC	22	GGGGGTCCCCGGTGCTCGGATC	22	4	4	1	GGGGGTCCCCGGTGCTCGGATC	22	7	7	1
23	PN(a)-23	actcgggaggggcgggaggggctccccggtgctcggatctcgaggtgcttattgcggTCCGAGCCTGGGTCTCCCTCTccccccaccccc	95	hsa-mir-615;mmu-mir-615;ptr-mir-615;bta-mir-615;eca-mir-615;mml-mir-615;	5	-	17,933,485	17,933,579					PN(a)-23-3p	TCCGAGCCTGGGTCTCCCTCT	21	TCCGAGCCTGGGTCTCCCTCT	21	19	31	3	TCCGAGCCTGGGTCTCCCTCT	21	12	18	2
24	PN(a)-24	cgtcggaccgggGTCCGGTGCGGAGAGCccttcgtcctgggaaacggggcgcggcc	57	bta-mir-2887-1;	6	-	248,247	248,303					PN(a)-24-5p	GTCCGGTGCGGAGAGC	16	GTCCGGTGCGGAGAGC	16	22	118	15	GTCCGGTGCGGAGAGC	16	9	56	10
25	PN(a)-25	acggcagcgccgcgggagcctcggttggcctcggatagccGGTCCCCCGCCGTCCCcgccggcgggccg	69	bta-mir-2904-1;	6	-	248,338	248,406					PN(a)-25-5p	GCAGCGCCGCGGGAGC	16	GCAGCGCCGCGGGAGC	16	10	37	8	CGCCGCGGGAGCCTCG	16	3	3	1
25	PN(a)-25	acggcagcgccgcgggagcctcggttggcctcggatagccGGTCCCCCGCCGTCCCcgccggcgggccg	69	bta-mir-2904-1;	6	-	248,338	248,406					PN(a)-25-3p	GGTCCCCCGCCGTCCC	16	GGTCCCCCGCCGTCCC	16	36	76	9	GGTCCCCCGCCGTCCC	16	4	11	3
26	PN(a)-26	cgggtggagccgccgcaggtgcagatcttggtggtagtagcaaatattcaAACGAGAACTTTGAAGGCCGAAGtggagaagggttccatgtg	92	mdo-mir-739;	6	-	250,392	250,483					PN(a)-26-3p	AACGAGAACTTTGAAGGCCGAC	23	AACGAGAACTTTGAAGGCCGAC	23	3	3	1					
26	PN(a)-26	cgggtggagccgccgcagGTGCAGATCTTGGTGGTAGTAGCAaatattcaaacgagaactttgaaggccgaagtggagaagggttccatgtg	92	mmu-mir-2140;mdo-mir-739;	6	-	250,392	250,483					PN(a)-26-5p	GCGCAGATCTTGGTGGTAGTAG	24						GCGCAGATCTTGGTGGTAGTAGCA	24	3	3	1
27	PN(a)-27	ccctaTCTCCCAACCCTTGTACCAGTGcgtgcctcagtccctggtacaggaatggggggcaggg	64	eca-mir-150;cfa-mir-150;	6	+	38,211,395	38,211,458	6	-	38,390,208	38,390,271	PN(a)-27-5p	TCTCCCAACCCTTGTACCAGTG	22	TCTCCCAACCCTTGTACCAGTG	22	124	190	4	TCTCCCAACCCTTGTACCAGTG	22	38	63	3
28	PN(a)-28	ACTCAAACTGTGGGGGCACTTTctggtctagggagggaagtgccgccatttttgagtgt	60	eca-mir-371;	6	+	40,022,202	40,022,261	6	-	39,872,470	39,872,529	PN(a)-28-5p	ACTCAAACTGTGGGGGCACTTT	22	ACTCAAACTGTGGGGGCACTTT	22	3	3	1					
29	PN(a)-29	gggtgtcttaccaggcacggttagatctggttcttctgtcTAATACTGTCTGGTAATGCCGTccat	66	eca-mir-429;	6	-	42,894,055	42,894,120					PN(a)-29-3p	TAATACTGTCTGGTAATGCCGT	22	TAATACTGTCTGGTAATGCCGT	22	14	14	1	TAATACTGTCTGGTAATGCCGT	22	14	17	2
30	PN(a)-30	ggggaccgcctggtgaccctggaaatccagagcgggtgaggcctgtctgactgtttctagGCGACCCACTCTTGGTTTCCAtggttgccctggaaa	96	hsa-mir-551a;ppy-mir-551a;ptr-mir-551a;cfa-mir-551a;mml-mir-551a;eca-mir-551a;	6	-	43,640,508	43,640,603					PN(a)-30-3p	GCGACCCACTCTTGGTTTCCA	21	GCGACCCACTCTTGGTTTCCA	21	7	7	1					
31	PN(a)-31	tgtccccaTGGCACAGGGTCCAGCTGTCGGCtgtaatacccgatgggtcgatgatggtccctgtgtttgggg	72	bta-mir-2320;	6	-	43,886,642	43,886,713					PN(a)-31-5p	TGGCACAGGGTCCAGCTGTCGG	23	TGGCACAGGGTCCAGCTGTCGG	23	252	982	7	TGGCACAGGGTCCAGCTGTCGGC	23	132	447	9
31	PN(a)-31	tgtccccaTGGCACAGGGTCCAGCTGTCGGCtgtaatacccgatgggtcgatgatggtccctgtgtttgggg	72	bta-mir-2320;	6	-	43,886,642	43,886,713					PN(a)-31-3p	TCGATGATGGTCCCTGTGTTTG	22	TCGATGATGGTCCCTGTGTTTG	22	3	3	1					
32	PN(a)-32	ggccaggctcaccatgacaccgtgtgagacctcgggctacaacacgggactcgggcgctgctctgacccTCGTGTCTTGTGTTGCAGCCGGAgggacgcaggtctgca	109	hsa-mir-187;mmu-mir-187;mml-mir-187;ppy-mir-187;ptr-mir-187;bta-mir-187;cfa-mir-187;eca-mir-187;	6	-	83,322,546	83,322,654					PN(a)-32-3p	TCGTGTCTTGTGTTGCAGCCGGA	23	TCGTGTCTTGTGTTGCAGCCGG	23	3	29	3					
33	PN(a)-33	gtaaccatgccgtagtgcgTGTAAACATCCTACACTCTCAGCTgtgagctcgaggtgcctgggagaggggttgtttactccttctgccatggaaaacg	97	hsa-mir-30c-1;mmu-mir-30c-1;bta-mir-30c;ptr-mir-30c-1;cfa-mir-30c-1;	6	-	121,821,234	##########					PN(a)-33-3p	CTGGGAGAGGGTTGTTTACTCC	22	CTGGGAGAGGGTTGTTTACTCC	22	18	18	1	CTGGGAGAGGGTTGTTTACTCC	22	11	11	1
34	PN(a)-34	GAAAGCATGCTCCAGTGGCGCaatcggttagcgcgcggtacttatacagcagtatatgtgcgggtgatgccgaggttgtgagttcgagcctcacctggagcatgttttcttcccctttacg	120	mmu-mir-1983;	7	+	22,803,533	22,803,652					PN(a)-34-5p	AAAAAGCATGCTCCAGTGGCGC	22	AAAAAGCATGCTCCAGTGGCGC	22	58	97	3	AAAAAGCATGCTCCAGTGGCGC	22	48	68	2
34	PN(a)-34	GAAAGCATGCTCCAGTGGCGCaatcggttagcgcgcggtacttatacagcagtatatgtgcgggtgatgccgaggttgtgagttcgagcctcacctggagcatgttttcttcccctttacg	120	mmu-mir-1983;	7	+	22,803,533	22,803,652					PN(a)-34-3p	CTCACCTGGAGCATGTTTTTT	21	CTCACCTGGAGCATGTTTTTT	21	8	8	1	CTCACCTGGAGCATGTTTTTT	21	8	8	1
35	PN(a)-35	ccgccccgggccgcggctcttgattgtccaaacgcaattctcgagtctatagctctggccgAGAGTTGAGTCTGGACGTCccgagccgtcgcccccaaacctcgagggg	109	mmu-mir-219-1;rno-mir-219-1;cfa-mir-219-1;	7	+	29,626,546	29,626,654					PN(a)-35-3p	AGAGTTGCGTCTGGACGTC	19	AGAGTTGCGTCTGGACGTC	19	29	29	1	AGAGTTGCGTCTGGACGTC	19	30	30	1
36	PN(a)-36	TCTTTGGTTATCTAGCTGTATGAgtgccacagagccgtcataaagctagataaccgaaagt	61	cfa-mir-9-3;	7	+	60,349,141	60,349,201					PN(a)-36-5p	ATTTCTTTGGTTATCTAGCTGTAT	26	ATTTCTTTGGTTATCTAGCTGTAT	26	3	3	1	ATTTCTTTGGTTATCTAGCTGTATG	26	3	3	1
37	PN(a)-37	agacagagaagccaggtcacgtctctgcagttacacagctcacgagtGCCTGCTGGGGTGGAACCTGGTctgtctgtct	79	hsa-mir-370;mmu-mir-370;cfa-mir-370;ptr-mir-370;mml-mir-370;rno-mir-370;eca-mir-370;bta-mir-370;	7	+	133,847,438	##########					PN(a)-37-3p	GCCTGCTGGGGTGGAACCTGGT	22	GCCTGCTGGGGTGGAACCTGGT	22	21	34	3	GCCTGCTGGGGTGGAACCTGGT	22	6	6	1
38	PN(a)-38	tcctgctcgtcctgcgaggTGTCTTGCAGGCCGTCATGCaggccacactgacggtaacgttgcaggtcgtcttgcagggcttctcgcaagacgacatcctcgtcgtcgacgacg	114	hsa-mir-431;mmu-mir-431;rno-mir-431;ptr-mir-431;bta-mir-431;eca-mir-431;oar-mir-431;	7	+	133,927,744	##########					PN(a)-38-5p	TGTCTTGCAGGCCGTCATGC	20	TGTCTTGCAGGCCGTCATGC	20	3	3	1					
39	PN(a)-39	gtggttatgtagcgagattttctgTTGTGCTTGATCTAACCATGTggttgccaggtatgagtaaaacatggttctgtcaagcaccatggaacgtcacgcagctttctaca	110	hsa-mir-218-1;mmu-mir-218-1;bta-mir-218-1;lca-mir-218;mdo-mir-218;mne-mir-218-1;mml-mir-218-1;rno-mir-218-1;cfa-mir-218-1;eca-mir-	8	+	11,840,680	11,840,789	8	-	12,027,376	12,027,485	PN(a)-39-5p	TTGTGCTTGATCTAACCATGT	21	TTGTGCTTGATCTAACCATGT	21	265	525	9	TTGTGCTTGATCTAACCATGT	21	40	59	5
39	PN(a)-39	gtggttatgtagcgagattttctgTTGTGCTTGATCTAACCATGTggttgccaggtatgagtaaaacatggttctgtcaagcaccatggaacgtcacgcagctttctaca	110	hsa-mir-218-1;mmu-mir-218-1;bta-mir-218-1;lca-mir-218;mdo-mir-218;mne-mir-218-1;mml-mir-218-1;rno-mir-218-1;cfa-mir-218-1;eca-mir-	8	+	11,840,680	11,840,789	8	-	12,027,376	12,027,485	PN(a)-39-3p	AAACATGGTTCTGTCAAGCAC	21	AAACATGGTTCTGTCAAGCAC	21	3	3	1					
40	PN(a)-40	cccaccacttaaacgtggatgtacttgctttcaaactctaaaagTAAGTGCTTCCATGTTTTAGTGAtgg	70	cfa-mir-302a;eca-mir-302a;bta-mir-302a;	8	+	92,257,711	92,257,780					PN(a)-40-3p	TAAGTGCTTCCATGTTTTAGTGA	23	TAAGTGCTTCCATGTTTTAGTGA	23	4	4	1					
41	PN(a)-41	ccatgactgttgctaatatgcaactctgttcaatacaaactggaATTGCACTTTAGCAATGGTGAtgg	68	hsa-mir-367;cfa-mir-367;eca-mir-367;bta-mir-367;ppy-mir-367;ptr-mir-367;mml-mir-367;mdo-mir-367;	8	+	92,258,012	92,258,079					PN(a)-41-3p	ATTGCACTTTAGCAATGGTGA	21	ATTGCACTTTAGCAATGGTGA	21	3	3	1					
42	PN(a)-42	gtgctcggtttgtaggcagtgtaattagctgattgtactctggcgcttacAATCACTAATTCCACTGCCATCaaaacaaggcac	84	hsa-mir-34b;mmu-mir-34b;eca-mir-34b;cfa-mir-34b;bta-mir-34b;ptr-mir-34b;ppy-mir-34b;	9	+	38,210,599	38,210,682	9	+	38,327,577	38,327,660	PN(a)-42-5p	AGGCAGTGTAATTAGCTGATTGT	23	AGGCAGTGTAATTAGCTGATTGT	23	1,424	2,331	18	AGGCAGTGTAATTAGCTGATTGT	23	2,871	4,453	30
42	PN(a)-42	gtgctcggtttgtaggcagtgtaattagctgattgtactctggcgcttacAATCACTAATTCCACTGCCATCaaaacaaggcac	84	hsa-mir-34b;mmu-mir-34b;eca-mir-34b;cfa-mir-34b;bta-mir-34b;ptr-mir-34b;ppy-mir-34b;	9	+	38,210,599	38,210,682	9	+	38,327,577	38,327,660	PN(a)-42-3p	AATCACTAATTCCACTGCCATC	22	AATCACTAATTCCACTGCCATC	22	151	10,272	23	AATCACTAATTCCACTGCCATC	22	2,055	13,896	31
43	PN(a)-43	gctctgctgtggccTATGGCTTTTCATTCCTATGTGAttactgttccaaactcatgtaggctaaaagccatgggctacagtgaggggcgtgctcc	96	hsa-mir-135b;mmu-mir-135b;bta-mir-135b;ptr-mir-135b;rno-mir-135b;ppy-mir-135b;eca-mir-135b;cfa-mir-135b;	9	+	63,365,115	63,365,210					PN(a)-43-5p	TATGGCTTTTCATTCCTATGTGA	23	TATGGCTTTTCATTCCTATGTGA	23	203	305	5	TATGGCTTTTCATTCCTATGTGA	23	9	13	2
44	PN(a)-44	tggaagcttctggagatcctgctccgtcgcCCCAGTGTTCAGACTACCTGTTCaggacaatgccgttgtacagtagtctgcacattggtagactgggcaagggaaagcaacgcca	118	hsa-mir-199a-2;mmu-mir-199a-2;rno-mir-199a;lla-mir-199a;bta-mir-199a-1;oan-mir-199;eca-mir-199a;cfa-mir-199-2;	9	-	107,644,923	##########					PN(a)-44-3p	ACAGTAGTCTGCACATTGGTAAG	24	ACAGTAGTCTGCACATTGGTTA	24	10	599	8	ACAGTAGTCTGCACATTGGTA	21	36	45	2
44	PN(a)-44	tggaagcttctggagatcctgctccgtcgcCCCAGTGTTCAGACTACCTGTTCaggacaatgccgttgtacagtagtctgcacattggtagactgggcaagggaaagcaacgcca	118	hsa-mir-199a-2;mmu-mir-199a-2;rno-mir-199a;lla-mir-199a;bta-mir-199a-1;oan-mir-199;eca-mir-199a;cfa-mir-199-2;	9	-	107,644,923	##########					PN(a)-44-5p	CCCCAGTGTTCAGACTACCTGTT	24	CCCCAGTGTTCAGACTACCTGTT	24	20	35	3					
45	PN(a)-45	gagaatcatctctcccagataatggcactctcaaacaagtttccaagttgTTGAAAGGCTATTTCTTGGTCAgaagactctcagtgccttctgga	96	hsa-mir-488;bta-mir-488;eca-mir-488;cfa-mir-488;mml-mir-488;ptr-mir-488;rno-mir-488;	9	+	111,719,026	##########					PN(a)-45-3p	TTGAAAGGCTATTTCTTGGTC	21						TTGAAAGGCTATTTCTTGGTC	21	9	27	5
46	PN(a)-46	cttctggaagctggtttcacatggtggcttagattttccatctttgtatcTAGCACCATTTGAAATCAGTGTTttaggag	81	hsa-mir-29b-2;oan-mir-29b-2;bta-mir-29e;cfa-mir-29b-2;	9	+	127,173,767	##########					PN(a)-46-5p	CTGGTTTCACATGGTGGCTTAGA	23	CTGGTTTCACATGGTGGCTTAGA	23	17	17	1	CTGGTTTCACATGGTGGCTTAGA	23	7	10	2
46	PN(a)-46	cttctggaagctggtttcacatggtggcttagattttccatctttgtatcTAGCACCATTTGAAATCAGTGTTttaggag	81	hsa-mir-29b-2;oan-mir-29b-2;bta-mir-29e;cfa-mir-29b-2;	9	+	127,173,767	##########					PN(a)-46-3p	TAGCACCATTTGAAATCAGTGTTT	24	TAGCACCATTTGAAATCAGTGTT	24	154	172	4	TAGCACCATTTGAAATCAGTGTTT	24	118	135	3
47	PN(a)-47	TGTAACAGCAACTCCATGTGGActgtgcccaatttccagtggagatgctgttacctt	58	cfa-mir-194;	10	-	9,750,923	9,750,980					PN(a)-47-5p	TGTAACAGCAACTCCATGTGGA	22	TGTAACAGCAACTCCATGTGG	21	18	42	4	TGTAACAGCAACTCCATGTGGA	22	5	5	1
48	PN(a)-48	gctcgactcctGTTCCTGCTGAACTGAGCCAGTgtgtaaaatgagaactgatatcagctcagtaggcaccggagggcgggt	81	hsa-mir-3074;	10	+	26,148,228	26,148,308					PN(a)-48-5p	GTTCCTGCTGAACTGAGCCAGT	22	GTTCCTGCTGAACTGAGCCAGT	22	3	3	1					
49	PN(a)-49	GTGTGCATTTGCAGGAACttgtgagtctcctattgaaaatgaacaggagactgataagttcccgggaacaccccacaa	77	hsa-mir-873;mmu-mir-873;ptr-mir-873;rno-mir-873;bta-mir-873;	10	-	36,097,479	36,097,555					PN(a)-49-5p	TATATGTGTGTATTTGCAGGAAC	23						TATATGTGTGTATTTGCAGGAAC	23	19	34	2
50	PN(a)-50	tgaagtgctgtggatttctttgtgaatcaccatatctaagctaatgtggtgGTGGTTTACAAAGTAATTCATAgtgcttca	81	hsa-mir-876;ptr-mir-876;eca-mir-876;	10	+	36,141,559	36,141,639	10	-	36,311,908	36,311,988	PN(a)-50-5p	TGGATTTCTTTGTGAATCACCA	22	TGGATTTCTTTGTGAATCACCA	22	3	3	1					
50	PN(a)-50	tgaagtgctgtggatttctttgtgaatcaccatatctaagctaatgtggtgGTGGTTTACAAAGTAATTCATAgtgcttca	81	hsa-mir-876;ptr-mir-876;eca-mir-876;	10	+	36,141,559	36,141,639	10	-	36,311,908	36,311,988	PN(a)-50-3p	GTGGTTTACAAAGTAATTCATA	22	GTGGTTTACAAAGTAATTCATA	22	3	3	1					
51	PN(a)-51	tgaactggacgtgctgagtgaatTAGGTAGTTTCATGTTGTTGGGcctggatttctgaacacaacgacattaaaccacccgactcacggcagttactgctcc	102	hsa-mir-196a-1;bta-mir-196a-1;cfa-mir-196a-1;eca-mir-196a;ptr-mir-196a-1;	12	+	22,434,918	22,435,019					PN(a)-51-5p	TAGGTAGTTTCATGTTGTTGGG	22	TAGGTAGTTTCATGTTGTTGGG	22	451	918	10	TAGGTAGTTTCATGTTGTTGGG	22	365	739	9
52	PN(a)-52	ctgtttatcaccagatcctagaaccctatcgatattgtctctgctgtgtaaatagctctgagTAGTGCAATATTGCTTATAGGGTtttggtgtttgggaagaactatgggca	112	hsa-mir-454;bta-mir-454;mml-mir-454;ptr-mir-454;oan-mir-454;cfa-mir-454;eca-mir-454;	12	-	33,457,315	33,457,426					PN(a)-52-3p	TAGTGCAATATTGCTTATAGGGT	23	TAGTGCAATATTGCTTATAGGGT	23	13	45	6	TAGTGCAATATTGCTTATAGGG	22	4	4	1
53	PN(a)-53	cttgggggtggcgagcAAACCGTTACCATTACTGAGTTtagtaatggtaacggttctcttgctgcacccaga	72	hsa-mir-451;mmu-mir-451;bta-mir-451;cfa-mir-451;eca-mir-451;ptr-mir-451;	12	-	42,820,762	42,820,833					PN(a)-53-5p	AAACCGTTACCATTACTGAGTT	22	AAACCGTTACCATTACTGAGTT	22	5,259	11,027	48	AAACCGTTACCATTACTGAGTT	22	3,319	7,477	27
54	PN(a)-54	gggccctggctgggatatcatcatatactgtaagtttgcgatgagacacTACAGTATAGATGATGtactagtccgggtgctccc	84	hsa-mir-144;mmu-mir-144;bta-mir-144;ppy-mir-144;mml-mir-144;rno-mir-144;eca-mir-144;cfa-mir-144;	12	-	42,820,910	42,820,993					PN(a)-54-5p	GGATATCATCATATACTGTAAGT	23	GGATATCATCATATACTGTAAGT	23	41	45	2	GGATATCATCATATACTGTAAGT	23	27	30	2
54	PN(a)-54	gggccctggctgggatatcatcatatactgtaagtttgcgatgagacacTACAGTATAGATGATGtactagtccgggtgctccc	84	hsa-mir-144;mmu-mir-144;bta-mir-144;ppy-mir-144;mml-mir-144;rno-mir-144;eca-mir-144;cfa-mir-144;	12	-	42,820,910	42,820,993					PN(a)-54-3p	TACAGTATAGATGATG	16	TACAGTATAGATGATG	16	54	124	4	TACAGTATAGATGATG	16	20	60	4
55	PN(a)-55	aagcaagacTGAGGGGCCTCAGACCGAGCTTTtggaaaatagaaaagtctcgctctctgcccctcagcctaactt	75	hsa-mir-3184;	12	-	44,150,500	44,150,574					PN(a)-55-5p	TGAGGGGCCTCAGACCGAGCTT	23	TGAGGGGCCTCAGACCGAGCTT	23	6	6	1	TGAGGGGCCTCAGACCGAGCTTT	23	3	3	1
56	PN(a)-56	ccgcccccgcgtctccagggcaaccgtggcttttcgattgttactgtgggaaccggaggTAACAGTCTACAGCCATGGTCGccccgcagcacgcccacgcgc	101	hsa-mir-132;mmu-mir-132;bta-mir-132;rno-mir-132;eca-mir-132;mdo-mir-132;cfa-mir-132;	12	-	45,599,472	45,599,572					PN(a)-56-5p	ACCGTGGCTTTCGATTGTTACT	22	ACCGTGGCTTTCGATTGTTACT	22	74	196	10	ACCGTGGCTTTCGATTGTTACT	22	16	27	3
56	PN(a)-56	ccgcccccgcgtctccagggcaaccgtggcttttcgattgttactgtgggaaccggaggTAACAGTCTACAGCCATGGTCGccccgcagcacgcccacgcgc	101	hsa-mir-132;mmu-mir-132;bta-mir-132;rno-mir-132;eca-mir-132;mdo-mir-132;cfa-mir-132;	12	-	45,599,472	45,599,572					PN(a)-56-3p	TAACAGTCTACAGCCATGGTCG	22	TAACAGTCTACAGCCATGGTCG	22	5,526	8,551	42	TAACAGTCTACAGCCATGGTCG	22	676	933	13
57	PN(a)-57	ggagccaccacgcccgggcagcgcgccggcaccttggctctagactgcttactgcccgggccgccctcagTAACAGTCTCCAGTCACGGCCAccgacgcctggccccgcc	110	hsa-mir-212;mmu-mir-212;bta-mir-212;rno-mir-212;mml-mir-212;mdo-mir-212;cfa-mir-212;eca-mir-212;	12	-	45,599,904	45,600,013					PN(a)-57-5p	ACCTTGGCTCTAGACTGCTTACT	23	ACCTTGGCTCTAGACTGCTTACT	23	49	60	3	ACCTTGGCTCTAGACTGCTTACT	23	7	7	1
57	PN(a)-57	ggagccaccacgcccgggcagcgcgccggcaccttggctctagactgcttactgcccgggccgccctcagTAACAGTCTCCAGTCACGGCCAccgacgcctggccccgcc	110	hsa-mir-212;mmu-mir-212;bta-mir-212;rno-mir-212;mml-mir-212;mdo-mir-212;cfa-mir-212;eca-mir-212;	12	-	45,599,904	45,600,013					PN(a)-57-3p	TAACAGTCTCCAGTCACGGCCA	22	TAACAGTCTCCAGTCACGGCCA	22	72	230	11	TAACAGTCTCCAGTCACGGCCA	22	7	12	2
58	PN(a)-58	ggtgcggtggggcAGCTGGTGTTGTGAATCAGGCCGttgccaatcagagaacggctacttcacaacaccagggtcacaccccaccacagg	90	bta-mir-138-1;cfa-mir-138a;eca-mir-138-2;	13	+	23,336,877	23,336,966					PN(a)-58-5p	AGCTGGTGTTGTGAATCAGGCCG	23	AGCTGGTGTTGTGAATCAGGCC	23	7	13	3	AGCTGGTGTTGTGAATCAGGC	21	6	6	1
59	PN(a)-59	ctgTTAATGCTAATTGTGATAGGGGTTttacctccgtctgactcctacatgttagcattaacag	65	hsa-mir-155;mmu-mir-155;mml-mir-155;eca-mir-155;bta-mir-155;cfa-mir-155;ptr-mir-155;	13	-	135,049,642	##########					PN(a)-59-5p	TTAATGCTAATTGTGATAGGGGT	24	TTAATGCTAATTGTGATAGGGGT	24	283	1,560	24	TTAATGCTAATTGTGATAGGGGT	23	15	297	12
60	PN(a)-60	ccccctgctggccgcaggtgctctgacgaggttgcactactgtgctttgaggagCAGTGCAATGATATTGTCAAAGCatctgggaccagccttgggg	97	hsa-mir-301b;bta-mir-301b;eca-mir-301b;mml-mir-301b;cfa-mir-301b;	14	-	51,319,104	51,319,200					PN(a)-60-3p	CAGTGCAATGATATTGTCAAAGC	23	CAGTGCAATGATATTGTCAAAG	23	7	10	2					
61	PN(a)-61	acctacctaactgggTTAGGGCCCTGGCTCCATCTCCtttaggaaaaccttctgtggggagtggggttttgaccctaacccagctgggctgt	92	hsa-mir-1296;bta-mir-1296;eca-mir-1296;ptr-mir-1296;	14	-	69,493,246	69,493,337					PN(a)-61-5p	TTAGGGCCCTGGCTCCATCTCC	22	TTAGGGCCCTGGCTCCATCTCC	22	11	14	2	TTAGGGCCCTGGCTCCATCTCC	22	8	8	1
62	PN(a)-62	gccggcgcccaggcTCTGGCTCCGTGTCTTCACTCCcgtgtgtgtccgaggagggagggagggacgggggctgtgctggggcgaacgga	89	mmu-mir-149;eca-mir-149;mml-mir-149;ppy-mir-149;ptr-mir-149;cfa-mir-149;	15	-	131,645,445	##########					PN(a)-62-5p	TCTGGCTCCGTGTCTTCACTCC	22	TCTGGCTCCGTGTCTTCACTCC	22	1,873	7,377	43	TCTGGCTCCGTGTCTTCACTCC	22	1,727	6,929	36
62	PN(a)-62	gccggcgcccaggcTCTGGCTCCGTGTCTTCACTCCcgtgtgtgtccgaggagggagggagggacgggggctgtgctggggcgaacgga	89	mmu-mir-149;eca-mir-149;mml-mir-149;ppy-mir-149;ptr-mir-149;cfa-mir-149;	15	-	131,645,445	##########					PN(a)-62-3p	GAGGGAGGGACGGGGGCGGTG	22	GAGGGAGGGACGGGGGCGGTG	22	128	179	4	GAGGGAGGGACGGGGGCGGTGC	22	100	146	3
63	PN(a)-63	gacctgaatcaggtAGGCAGTGTATTGTTAGCTGGCtgctttggatcagttcagcagccacgactaccctgccacttgcttctggataaattcttct	97	hsa-mir-449b;bta-mir-449b;ppy-mir-449b;ptr-mir-449b;mml-mir-449b;	16	+	31,984,173	31,984,269	16	-	31,831,951	31,832,047	PN(a)-63-5p	AGGCAGTGTATTGTTAGCTGGCT	26	AGGCAGTGTATTGTTAGCTGG	21	13	19	2	AGGCAGTGTATTGTTAGCTGGCTG	26	174	278	8
63	PN(a)-63	gacctgaatcaggtAGGCAGTGTATTGTTAGCTGGCTGCTttggatcagttcagcagccacgactaccctgccacttgcttctggataaattcttct	97	hsa-mir-449b;bta-mir-449b;ppy-mir-449b;ptr-mir-449b;mml-mir-449b;	16	+	31,984,173	31,984,269	16	-	31,831,951	31,832,047	PN(a)-63-3p	CAGCCACGACTACCCTGCCACT	22						CAGCCACGACTACCCTGCCACT	22	31	37	2
64	PN(a)-64	ctgtgtgtgatgggtTGGCAGTGTATTGTTAGCTGGTtgagtatatgagtagcatcagctaacatgcaactgctgtcttattgcatata	89	hsa-mir-449a;cfa-mir-449;mml-mir-449a;bta-mir-449a;eca-mir-449a;	16	+	31,984,293	31,984,381	16	-	31,831,839	31,831,927	PN(a)-64-5p	TGGCAGTGTATTGTTAGCTGGT	22	TGGCAGTGTATTGTTAGCTGGT	22	122	231	8	TGGCAGTGTATTGTTAGCTGGT	22	2,428	4,890	26
64	PN(a)-64	ctgtgtgtgatgggtTGGCAGTGTATTGTTAGCTGGTtgagtatatgagtagcatcagctaacatgcaactgctgtcttattgcatata	89	hsa-mir-449a;cfa-mir-449;mml-mir-449a;bta-mir-449a;eca-mir-449a;	16	+	31,984,293	31,984,381					PN(a)-64-3p	TCAGCTAACATGCAACTGCTGT	22	TCAGCTAACATGCAACTGCTGT	22	10	13	2	TCAGCTAACATGCAACTGCTGT	22	725	1,123	13
65	PN(a)-65	atctgtgctctttggtTACAGTTGTTCAACCAGTTACTaatctaactaactgtaaccggttgaacaactgaacccaaagggtgcaaagtggaaacatt	98	hsa-mir-582;mmu-mir-582;ptr-mir-582;mml-mir-582;bta-mir-582;cfa-mir-582;eca-mir-582;	16	+	36,589,521	36,589,618					PN(a)-65-5p	TACAGTTGTTCAACCAGTTACT	22	TACAGTTGTTCAACCAGTTACT	22	12	17	2	TACAGTTGTTCAACCAGTTACT	22	4	4	1
65	PN(a)-65	atctgtgctctttggtTACAGTTGTTCAACCAGTTACTaatctaactaactgtaaccggttgaacaactgaacccaaagggtgcaaagtggaaacatt	98	hsa-mir-582;mmu-mir-582;ptr-mir-582;mml-mir-582;bta-mir-582;cfa-mir-582;eca-mir-582;	16	+	36,589,521	36,589,618					PN(a)-65-3p	TAACCKGTTGAACAACTGAACCC	23	TAACCGGTTGAACAACTGAACC	23	7	28	6	AACCTGTTGAACAACTGAAC	20	4	7	2
66	PN(a)-66	gaccagtcgccgcggggctttcctTTGTGCTTGATCTAACCATGTggtggaacgatggaaacggaacatggttctgtcaagcaccgcggaaagctccgcgctctcctgca	110	hsa-mir-218-2;mmu-mir-218-2;sla-mir-218-2;oan-mir-218-2;cfa-mir-218-2;bta-mir-218-2;eca-mir-218-2;	16	+	52,396,946	52,397,055					PN(a)-66-5p	TTGTGCTTGATCTAACCATGT	21	TTGTGCTTGATCTAACCATGT	21	265	525	9	TTGTGCTTGATCTAACCATGT	21	40	59	5
67	PN(a)-67	cctatgtgtatactcagcttTGAGAACTGAATTCCATGGGTTgtgtcattgtcagacctgtgaagtttagttcttcagctgggatatctctatcatc	97	hsa-mir-146a;mmu-mir-146a;bta-mir-146a;mml-mir-146a;ptr-mir-146a;eca-mir-146a;cfa-mir-146a;	16	+	60,604,380	60,604,476					PN(a)-67-5p	TGAGAACTGAATTCCATGGGTT	22	TGAGAACTGAATTCCATGGGTT	22	602	1,116	20	TGAGAACTGAATTCCATGGGTT	22	161	260	8
68	PN(a)-68	aggacccttccggagggccccccccaatcctgttgtgctggattcagAGGGTTGGGCGGAGGCTTTCCTgaaggctct	78	bta-mir-296;eca-mir-296;	17	-	61,587,159	61,587,236					PN(a)-68-3p	AGGGTTGGGCGGAGGCTTTCCT	22	AGGGTTGGGCGGAGGCTTTCCT	22	87	210	14	AGGGTTGGGCGGAGGCTTTCCT	22	23	63	7
69	PN(a)-69	gctggtgaactggcaggccaggaagaggAGGAAGCCCTGGAGGGGCTGGAGGtgatggatgttttcctccggttctcagggctccaccttttccgggccgtggagccagggctg	118	hsa-mir-671;mmu-mir-671;bta-mir-671;ptr-mir-671;eca-mir-671;rno-mir-671;cfa-mir-671;	18	-	5,054,287	5,054,404					PN(a)-69-5p	AGGAAGCCCTGGAGGGGCTGGA	24	AGGAAGCCCTGGAGGGGCTGG	24	203	303	8	AGGAAGCCCTGGAGGGGCTGGAG	24	132	216	9
69	PN(a)-69	gctggtgaactggcaggccaggaagaggAGGAAGCCCTGGAGGGGCTGGAGGtgatggatgttttcctccggttctcagggctccaccttttccgggccgtggagccagggctg	118	hsa-mir-671;mmu-mir-671;bta-mir-671;ptr-mir-671;eca-mir-671;rno-mir-671;cfa-mir-671;	18	-	5,054,287	5,054,404					PN(a)-69-3p	TCCGGTTCTCAGGGCTCCACC	21	TCCGGTTCTCAGGGCTCCACC	21	61	127	10	TCCGGTTCTCAGGGCTCCACC	21	55	102	6
70	PN(a)-70	tggatacctttggctggtttggaaagttcattgttcgacaccatggatccccaggtgggtcacgtttcaagatacacCAACCTGGAGGACTCCATGCTGTtgagctgttcacaagcagc	129	hsa-mir-490;mmu-mir-490;bta-mir-490;ptr-mir-490;ppy-mir-490;cfa-mir-490;eca-mir-490;	18	+	10,924,533	10,924,661	18	-	10,994,278	10,994,406	PN(a)-70-3p	CAACCTGGAGGACTCCATGCTGT	23	CAACCTGGAGGACTCCATGCTG	23	7	10	2	CAACCTGGAGGACTCCATGCTGT	23	7	10	2
70	PN(a)-70	tggatacctttggctggtttggaaagttcattgttcgacaccatggatccccaggtgggtcacgtttcaagatacacCAACCTGGAGGACTCCATGCTGTtgagctgttcacaagcagc	129	hsa-mir-490;mmu-mir-490;bta-mir-490;ptr-mir-490;ppy-mir-490;cfa-mir-490;eca-mir-490;	18	+	10,924,533	10,924,661	18	-	10,994,278	10,994,406	PN(a)-70-5p	CCATGGATCCCCAGGTGGGT	20						CCATGGATCCCCAGGTGGGT	20	3	3	1
71	PN(a)-71	gccgccacttgcctcgcaccgttTTTGGCAATGGTAGAACTCACACTggtgagataatgggatccggtggttctagacttgccaactatggtgcgagggctcagcaagca	110	mmu-mir-182;bta-mir-182;cfa-mir-182;eca-mir-182;mdo-mir-182;	18	-	17,167,650	17,167,759					PN(a)-71-5p	TTTGGCAATGGTAGAACTCACAC	24	TTTGGCAATGGTAGAACTCACA	24	4,897	9,090	43	TTTGGCAATGGTAGAACTCACACT	24	2,997	7,499	32
72	PN(a)-72	ccacgaccacctgctgggccgatTTTGGCACTAGCACATTTTTGCTtgtgtctctccgctctgagcaattatgtgcagtgccaatatgggaaagcaggatgctgc	105	hsa-mir-96;mmu-mir-96;rno-mir-96;bta-mir-96;cfa-mir-96;sla-mir-96;	18	-	17,171,979	17,172,083					PN(a)-72-5p	TTTGGCACTAGCACATTTTTGCT	23	TTTGGCACTAGCACATTTTTGCT	23	55	63	3	TTTGGCACTAGCACATTTTTGCT	23	79	86	2
73	PN(a)-73	tggatCTTTTTGCGGTCTGGGCTTGCtgttcctctctacagtagtcaggaagcccttaccccaaaaagtatct	73	hsa-mir-129-1;mmu-mir-129-1;bta-mir-129-1;eca-mir-129a;ptr-mir-129-1;rno-mir-129-1;cfa-mir-129-1;mdo-mir-129;	18	+	18,269,493	18,269,565					PN(a)-73-3p	AAGCCCTTACCCCAAAAAGTAT	22	AAGCCCTTACCCCAAAAAGTAT	22	8	8	1					
74	PN(a)-74	gctggttggcattctgggcctggtttatgccaactctgttgttaacTATACCAGGATGCCAGCATAGTt	69	mmu-mir-1949;	X	+	48,289,631	48,289,699					PN(a)-74-3p	TATACCAGGATGTCAGCATAGTT	23	TATACCAGGATGTCAGCATAGT	22	4	7	2	TATACCAGGATGTCAGCATAGTT	23	4	4	1
75	PN(a)-75	gcacattgtaggcctcattaaatgtttgttgaatgaaaaaatgaatcATCAACAGACATTAATTGGGCGCctgctctgtgatctc	85	hsa-mir-421;mmu-mir-421;ptr-mir-421;mml-mir-421;rno-mir-421;ppy-mir-421;cfa-mir-421;	X	+	58,683,804	58,683,888					PN(a)-75-3p	ATCAACAGACATTAATTGGGCGC	23	ATCAACAGACATTAATTGGGCG	23	16	23	3	ATCAACAGACATTAATTGGGCGC	23	4	7	2
76	PN(a)-76	tgttaaatcaggaattgtaaacaattcctaggtaatgtgtataatgtttgtaagTCATTCCTAGAAATTGTTCACAatgcctgtaaca	88	mmu-mir-384;eca-mir-384;rno-mir-384;cfa-mir-384;	X	+	60,374,121	60,374,208					PN(a)-76-5p	TGTAAACAATTCCTAGGCAATGT	23	TGTAAACAATTCCTAGGCAATGT	23	9	9	1	TGTAAACAATTCCTAGGCAATGT	23	9	9	1
76	PN(a)-76	tgttaaatcaggaattgtaaacaattcctaggtaatgtgtataatgtttgtaagTCATTCCTAGAAATTGTTCACAatgcctgtaaca	88	mmu-mir-384;eca-mir-384;rno-mir-384;cfa-mir-384;	X	+	60,374,121	60,374,208					PN(a)-76-3p	TCATTCCTAGAAATTGTTCACA	22	TCATTCCTAGAAATTGTTCACA	22	9	32	7	TCATTCCTAGAAATTGTTCACA	22	11	22	4
77	PN(a)-77	gagtgaaaagttccgtcaaccatccagctgtttggggtgatgcaaacAAACATCTGGTTGGTTGAGAGAAtttttttactt	80	bta-mir-2483;	X	-	100,547,916	##########					PN(a)-77-5p	CGTCAACCATCCAGCTGTTTGG	22	CGTCAACCATCCAGCTGTTTGG	22	27	50	4	CGTCAACCATCCAGCTGTTTGG	22	10	16	3
77	PN(a)-77	gagtgaaaagttccgtcaaccatccagctgtttggggtgatgcaaacAAACATCTGGTTGGTTGAGAGAAtttttttactt	80	bta-mir-2483;	X	-	100,547,916	##########					PN(a)-77-3p	AAACATCTGGTTGGTTGAGAGA	22	AACATCTGGTTGGTTGAGAGA	21	29	64	4	AAACATCTGGTTGGTTGAGAGA	22	4	7	2
78	PN(a)-78	agtacCAAAGTGCTCACAGTGCAGGTAGgttttgcattactctactgtagtgtgggcacttccagtact	69	hsa-mir-20b;eca-mir-20b;mml-mir-20b;bta-mir-20b;ptr-mir-20b;	X	-	108,178,755	##########	X	-	##########	##########	PN(a)-78-5p	CAAAGTGCTCAYAGTGCAGGTAG	23	CAAAGTGCTCACAGTGCAGGTA	23	18	21	2	CAAAGTGCTCATAGTGCAGGTAG	23	7	21	4
79	PN(a)-79	atgctgtgtgcggtgctccacttcaagaagtgccatccatgtggctagaaataTGATTGGCACCTCTTTGAGTGAcgtaacacacaacaggtac	94	eca-mir-507;	X	-	118,219,037	##########					PN(a)-79-3p	TGATTGGCACCTCTTTGAGTGA	22	TGATTGGCACCTCTTTGAGTGA	22	8	14	3	TGATTGGCACCTCTTTGAGTGA	22	508	914	9
79	PN(a)-79	atgctgtgtgcggtgctccacttcaagaagtgccatccatgtggctagaaataTGATTGGCACCTCTTTGAGTGAcgtaacacacaacaggtac	94	eca-mir-507;	X	-	118,219,037	##########					PN(a)-79-5p	CACTTCAAGAAGTGCCATCCA	21						CACTTCAAGAAGTGCCATCCA	21	3	3	1
80	PN(a)-80	gctaagcacttacaactgtttgcagaggaaactgagactttgtaactacatcTCAGTCTCAACTGCAAAGAAGTaagtgcttagc	85	hsa-mir-452;mmu-mir-452;cfa-mir-452;bta-mir-452;ptr-mir-452;	X	-	121,481,685	##########					PN(a)-80-5p	AACTGTTTGCAGAGGAAACTGAG	24	TGTTTGCAGAGGAAACTGAGA	21	14	39	5	AACTGTTTGCAGAGGAAACTGA	22	5	11	3
80	PN(a)-80	gctaagcacttacaactgtttgcagaggaaactgagactttgtaactacatcTCAGTCTCAACTGCAAAGAAGTaagtgcttagc	85	hsa-mir-452;mmu-mir-452;cfa-mir-452;bta-mir-452;ptr-mir-452;	X	-	121,481,685	##########					PN(a)-80-3p	TCAGTCTCAACTGCAAAGAAGT	22	TCAGTCTCAACTGCAAAGAAGT	22	14	14	1					

Supplementary Table 4.4. Profile of novle miRNAs originating from PN(b) type pre-miRNAs

Pre-miRNA ID	Pre-miRNA name	Pre-miRNA sequence	Length (nt)	Conserved pre-miRNAs in mammalian cluster	Genomic location of pre-miRNA based on Sscrofa9 genome assembly				miRNA name	Consensus miRNA sequence	Length (nt)	Ovary					Ovary				
					1st location																
					Chromosome	Strand	Start	End				Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs	Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs
1	PN(b)-1	ttatcaggcACAGGAGAGGTTCTTGGGAttttttcccaggcaaaaaccatcctctgaggctgaact	65	ssc-mir-125a;hsa-mir-125a;mmu-mir-125a;ptr-mir-125a;mml-mir-125a;eca-mir-125a;bta-mir-125a;rno-mir-125a;cfa-mir-125a	3	-	29,674,061	29,674,125	PN(b)-1-5p	ACAGGTGAGGTTCTTGGGA	19	ACAGGTGAGGTTCTTGGGA	19	4	4	1					
2	PN(b)-2	gctcctcatCTGGCCCTCTCTGCCCTGCCGTCtgcattgcacaggtttgcatagtttgcaggtttgcgcattaag	67	ssc-mir-328;hsa-mir-328;mmu-mir-328;bta-mir-328;ptr-mir-328;eca-mir-328;rno-mir-328;ppy-mir-328;cfa-mir-328;	9	+	59,116,508	59,116,574	PN(b)-2-5p	CTGGCCCTCTCTGCCCTTCCGT	22	CTGGCCCTCTCTGCCCTTCCGT	22	217	251	2	CTGGCCCTCTCTGCCCTTCCGT	22	173	201	2

Supplementary Table 4.5. Profile of novle miRNAs originating from PN(c) type pre-miRNAs

Pre-miRNA ID	Pre-miRNA name	Pre-miRNA sequence	Length (nt)	Conserved miRNAs in mammalian cluster	Genomic location of pre-miRNA based on Sscrofa9 genome assembly								miRNA name	Consensus miRNA sequence	Length (nt)	Ovary					Testis				
					1st location				2nd location																
					Chromosome	Strand	Start	End	Chromosome	Strand	Start	End				Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs	Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs
1	PN(c)-1	cTCCAGGAGCTCACAGTCTAggaggctagtttatagtacattcaatagaagggctgctgctt	62	hsa-mir-151;mmu-mir-151;ptr-mir-151;mo-mir-151;eca-mir-151;bta-mir	1	+	71,257,795	71,257,856					PN(c)-1-5p	TCGAGGAGCTCACAGTCTA	19	TCGAGGAGCTCACAGTCTA	19	11	11	1					
2	PN(c)-2	ctgttccggtggctccaggggcagaacagttggaaTCTCGCTGGGGCCTCCAgaaatg	59	hsa-mir-720;mmu-mir-720;ptr-mir-720;	1	+	206,000,024	206,000,082	1	+	206,124,051	206,124,109	PN(c)-2-3p	TCTCGCTGGGGCCTCCA	17	TCTCGCTGGGGCCTCCA	17	135	135	1	TCTCGCTGGGGCCTCCA	17	53	53	1
3	PN(c)-3	ctccacaaaatgCTTGGCACGCTAGTAAGCACtcaataaatgtttgctacatatctagtttaagtagtgagt	71	cfa-mir-1271;	1	+	234,748,918	234,748,988					PN(c)-3-5p	CTTGGCACCTAGTAAGCAC	19	CTTGGCACCTAGTAAGCAC	19	5	9	2					
4	PN(c)-4	agctccataaactcagagatttgtgatagtgcctggcacatgTTGGGAACATTTTGAATATttgtggaaag	71	hsa-mir-450a-1;mmu-mir-450a-1;mo-mir-450a;ptr-mir-450a-1;ppy-mir-	2	+	28,657,309	28,657,379					PN(c)-4-3p	TTGGGAACATTTTGCATAT	19	TTGGGAACATTTTGCATAT	19	3	3	1					
5	PN(c)-5	gcagggctgcagcggagtcaaactcgagtcgggttcttgcagatCATCCCTGGCATGGTGGAGcgagtgcagctcggc	79	hsa-mir-188;mmu-mir-188;cfa-mir-188;bta-mir-188;ptr-mir-188;mml-mi	3	+	112,795,739	112,795,817					PN(c)-5-3p	CATCCGTTGCATGGTGGA	18						CATCCCTTGCATGGTGGA		112,795,802	3	1
6	PN(c)-6	ttgctgcagctgtgatgtacattgctgctgtgactgagattcaatcacagaactgcatGTGCTGCCAGTGCACATA	77	hsa-mir-106b;mmu-mir-106b;eca-mir-106b;tla-mir-106b;bta-mir-106b;c	6	+	18,297,569	18,297,645					PN(c)-6-3p	GTGCTGACAGTGCAGATA	18	GTGCTGACAGTGCAGATA	18	43	43	1	GTGCTGACAGTGCAGATA	18	23	23	1
7	PN(c)-7	agcggcggggacggggaggcgagtcgcgtgtgacgcCTCCTGGCTGCCTCGCCAgg	57	oan-mir-1386;	6	+	38,030,592	38,030,648					PN(c)-7-3p	CTCCTGGCTGGCTCGCCA	18	CTCCTGGCTGGCTCGCCA	18	53	53	1	CTCCTGGCTGGCTCGCCA	18	37	37	1
8	PN(c)-8	ctagatccttatttagttgtaaattcatgacatcatcacttacggCTAGACTGAGGCTCCTG	62	mmu-mir-151;cfa-mir-151;mo-mir-151;	6	+	109,113,891	109,113,952					PN(c)-8-3p	CTAGACTGAGGCTCCT	16	CTAGACTGAGGCTCCT	16	3	8	2					
9	PN(c)-9	ccccctccccgcccccggCTGCTGCCTGGCTCGCCGcccacccccccagtgccgcccaaggtgagcccggccagggctggcagaggcca	91	oan-mir-1386;	6	+	118,011,934	118,012,024					PN(c)-9-5p	CTGCTGCCTGGCTCGCCA	18	CTGCTGCCTGGCTCGCCA	18	3	21	4	CTGCTGCCTGGCTCGCCA	18	9	9	1
10	PN(c)-10	ctcccgccTCGAGAAGCCCACAGTCTAGTAggaaaggaagcagttacaacacagtgtggcagcggccactgggaaggtttccagaggg	90	hsa-mir-151;mmu-mir-151;ptr-mir-151;mo-mir-151;eca-mir-151;bta-mir	12	+	47,219,122	47,219,211					PN(c)-10-5p	TCGAGGAGCCCACAGTCTAGTA	22	TCGAGGAGCCCACAGTCTAGT	22	4	4	1					
11	PN(c)-11	acctgcttcccctgtaaacctccagaactccagttccgtccttgggatggatgagaatAACAGCTCCCATCTCAGAggactgtaggaattgaaaagaggtggagaagtgcttagt	124	mmu-mir-674;mo-mir-674;	16	+	65,985,474	65,985,597					PN(c)-11-3p	CACAGCTCCCATCTCAGA	18	CACAGCTCCCATCTCAGA	18	6	6	1					
12	PN(c)-12	ggACAAGTCAGGCTCTGGGGAaaggagacagggattgatctggtcagtgttctggagcctggatgaac	70	bta-mir-125b-2;eca-mir-125b-2;mo-mir-125b-2;cfa-mir-125b-2;	17	+	10,529,440	10,529,509	17	+	10,822,768	10,822,837	PN(c)-12-5p	ACAAGTCAGGCTCTTGGGA	19	ACAAGTCAGGCTCTTGGGA	19	39	48	2	ACAAGTCAGGCTCTTGGGA	19	22	22	1

Supplementary Table 4.6. Profile of candidate miRNAs originating from PC type pre-miRNAs

Pre-miRNA ID	Pre-miRNA name	Pre-miRNA sequence	Length (nt)	Genomic location of pre-miRNA based on Sscrofa9 genome assembly: 1st location				2nd location				3rd location			
				Chromosome	Strand	Start	End	Chromosome	Strand	Start	End	Chromosome	Strand	Start	End
1	PC-1	ctcgCCTAATGACGAAACTCTGAGGagctgggcgtttgactctttcccttcgtttctgcatttcttggctct	73	1	-	1258879	1258951	1	-	1364889	1364961	1	-	1514176	1514248
2	PC-2	gcccacccgccgagccgggttctgtcccgacacgtccctCGGCCCCCGGCGCTTCGGGtgact	63	1	+	2518268	2518330	1	-	3359786	3359848				
3	PC-3	aacggtgatttcctaaGATGGAGGATGATTCTGACAaagtcctgtcagccacccttcccttgtaaactcacttc	75	1	-	29438821	29438895								
4	PC-4	actgtgctgggctagggattgaaacccatgtctcagcagcaacccatgccactgaagtcaGATTCCTAACCCACCGGACcacagtggg	88	1	-	30606651	30606738								
5	PC-5	gtgactagaacacacagaatgaccttgctgtaattgctcttgaatggttctttaaagaatGAAGCTACCAGGCGTAGGAaattcttcagctggcctgtcacgtcgtgtgcagtcatctg	119	1	+	54908027	54908145								
6	PC-6	ggcgggGCGGGGCGGGCGGTCGCCCGGGgcgggcggcggcggcggcggcggccgttggggtgcgaccgtccccgccccttt	80	1	+	106652033	106652112								
7	PC-7	gtcacagagctaATTAGTGGCAGAGCCAGGAacagatctgggtcacctgatgctctgtcca	61	1	-	112234267	112234327								
8	PC-8	aatgtcatctgagcggggaggttcattatcctgaattacattttcaaatgggagtGCAATTTAGGTTAATGACTGTCttgctcctgactca	91	1	-	124579963	124580053								
9	PC-9	cGTGACATGGTGTGATTTGCcccttactttgctcattgccacctgcttctgtggctgggctgggctgtctcaggatgttc	80	1	+	128995206	128995285								
10	PC-10	gcctccagaaggaatgcaggtctgccaattctttgattttatccagtgagagccaTGGCTGACTTCTGACCTCCagaatggaata	85	1	-	140033943	140034027								
11	PC-11	gcccccggcccggccggcgcccgggggngcccCGGCCGGGCCCGCCCCCCGCcccccggggcgcccgggcggccgcggcncgccgccccccgcccgcgggcccggccgcg	110	1	+	149525673	149525782								
12	PC-12	ggtcccgggtacccagatgtggggatgtctgttgtggagcaggGGTCCCAGCTGGGGTGCCAaggttg	69	1	+	163547048	163547116								
13	PC-13	gtctcatgtattttattcatgtctgttcaatttgggatgtggtcaagagcattataaatgATTGATTTAGGTTGGGACAca	81	1	-	207240580	207240660								
14	PC-14	cttgggactgtgatGTGGGCTGGAGAGAAGGCTccaaggccccttccatgtactgcccttgtccagtgtcctgtttctgtgaatagtcccca	93	1	-	268094086	268094178								
15	PC-15	cggttgcacacccaggagttttgggctccgccgacctgcttcccgttccctggccattccCTCCTGGGTTTCGGCACCAaa	81	1	-	273707759	273707839								
16	PC-16	acatactgtgttctgttcagatagctgaaccctgggctgaccttggggagttTATAGTCTGGAGGATGTAGTACTACC	79	2	+	4174427	4174505								
17	PC-17	ggcgcccacaGCGCGCGGCCGCCCGGGGAatgagtcctcgggaacgtctgcctgggcctc	62	2	+	4857494	4857555	2	-	4667122	4667183				
18	PC-18	ggcaggaggaaaagggcctcaggagggaggccaggtgggggctgggcacccgatgacccTGCCCACACTCCTCTCTCCAGTgtggcagcaatcccctcccggg	104	2	-	5079854	5079957								
19	PC-19	tctcgcttcagttcccccgccgccgcctgtgagagagatgctgccattaaccccTTGGACGGATGAGGACACTGAGGCGTgg	82	2	+	5178771	5178852								
20	PC-20	tttaggttcctttttcactctccgaggggccttcaagggcaagttcttgtcaccTTTGTTGGCTCCTCTGAAGTGAgaaggaaaccttcc	90	2	-	6684275	6684364								
21	PC-21	gaaccagtaggcacccctcatcgctgcctgtgtgtccacactggagcaCGAGGCAGCGCTGAGGATGAACcgctgggag	79	2	+	8421890	8421968								
22	PC-22	gtcTTTTGTCTCTGAACTCTGCGCTTTTcagcccaggtaccagtgggggtgggggaggtggtgaggaggcgagaaca	77	2	-	15100864	15100940								
23	PC-23	tttcACTTCTCTGAGCCTGCTTCTTcatttgaaaaatgggaataagacttagcttgaagtgcta	64	2	-	15108433	15108496								
24	PC-24	tcttgtacttcaccaAAGTAGGAAGAATATGATCTCAGAATacacaccgttttacgaatttttttaggttttttatttttctattatagtttgatttacat	101	2	-	15119677	15119777								
25	PC-25	ctttcatatattccactgtatccccagcatctggcacatagtaagtgcccaggcaacagcTGGACGATGCATTGAATATTTGAGCg	86	2	+	15169332	15169417	2	-	15113347	15113432				
26	PC-26	tcaacTGAGGTAGTCAGGACCAGACCAAGGCatctgatgtctgatgttggagttaatcaggtctgggtttgaaccctgagtgcctctgtgt	91	2	+	15174303	15174393	2	-	15108515	15108605				
27	PC-27	tttgcaatgtatcagtgtcttgtattcagccttagtttgtAAACTGGTAGACTTAAGTAaagaatatgttaggaatgtatttatatctatctttatatatctggcttactgatttgcca	119	2	+	20499654	20499772								
28	PC-28	gaacaggttctttaatctccgtctacctcagtttcttatctgtaaAATGGAGAGGGGAGTAGGACctgact	72	2	+	26867438	26867509								
29	PC-29	catggaggttcccaggctagaggTCAAATCGGAGCTACGGCTgctggcctacaccacagccatagcaacgcaggatctgagccttgtctgggacctacccca	102	2	+	38741521	38741622								
30	PC-30	atgagctgcagtgtaggtcatagactcagcttggatctggtgttgcTGTGTCTGTGACATCTGCTGGCAgctata	75	2	+	43890115	43890189								
31	PC-31	gggaggcgtggaggtcccagccgcgggggtGGGGGGCGCGGCGGCCGCCtcctttgcctgcgtccccgccggcttccgcatctgcttggctgccccctctgcgtctggc	109	2	-	46479632	46479740								
32	PC-32	ctccagtgcccgcccctcgcgcGCCGGCCCCGCCCCCGCGGgggggagcgagcgctcgcgggccccgtggtgggttcggctgcgcggcggggctgagg	98	2	+	47333618	47333715								
33	PC-33	tgaccctagggagcagtgtaacccagagcctgggccatgcccaagagaggtgagtgTGGGGGATGCCAAGGCTCTggtcctgcccagggccc	92	2	-	49359225	49359316								
34	PC-34	gttcggtctctggcctcactcagtgggtgggggaatccagcattgctgtgagctgtggtgTAGGTCACAGACACGGCGTggatcccttgttcctgtggctgtggtgtaggccagaagctgta	127	2	-	52814443	52814569								
35	PC-35	ggagcatgtgtgtgtgcacgcgtgcgcgcgcccacgtgtgCATGTGTGTGCATGTGCACgcaaa	64	2	-	61429973	61430036								
36	PC-36	ttttgctttttagggccacaggtgtggtatgtggaagttctcaggctggaggTCAAATCGGAGCTACGGCTgctggccgtagcaatgtgggatccaagctgtgtctgcaacctacaccacg	131	2	+	68799996	68800126	2	+	68800592	68800722				
37	PC-37	gaaacgctcttctttcagcccctTGCGTGGCTTCTCTGTGCAGTCttttcttctgggacctgcacaggaaggccacggaggggccggagaaagagatgtacc	101	2	+	76418882	76418982								
38	PC-38	ccttcacagaaaaatttacatatgagtgtatggttaaaACAGTGTAATTTCATGTGAtgc	60	2	+	78556717	78556776								
39	PC-39	tttttaggtgagaaAACTGAAGTGTAGAACATTtaaggccataaaattagtaaattaggaagccaggttttgaaatcagttggactaatct	92	2	+	91849127	91849218								
40	PC-40	catgggtccagtgttgccatgagctgtgatgtaggtcacagatgtggctcagatcctgcATTGCTGTGGCCATTGCGTagaccagcagctctaggtctgatttgaccccta	111	2	-	95662202	95662312								
41	PC-41	actgcagctgccaagccttgatacaccctgaaaagagctcaaggtggagatCAGGAGTGAGGCACTCTGTgct	73	2	+	96802823	96802895								
42	PC-42	atctgttttcctgcacacagtaaaactgaactactgaCAGAAGGCTGTGGTGAAGGaaggtacag	65	2	-	99465444	99465508								
43	PC-43	agatagttatgtatttTTAGGAGAAGATTTTATGAacccaattcttgcatcccctcatatgtagaaaacactaaaatctgccaatgatgactaat	95	2	-	100052886	100052980								
44	PC-44	ggggaagctgagcgagagctccggggagtcagtaccagccCGGCGCGACTGAACTCCGGAccgctcctcgctccaccttcggt	83	2	-	104855985	104856067								
45	PC-45	ataggattacaattataatttaatggctaaaaagtcaatctgtcttagaagattatttTTATGTGGCTATTCTGATAtataatgtacccaga	92	2	-	108075703	108075794								
46	PC-46	ggagacCAGGAGTGAGGCACTCTGTgctctgggaaatctggaagaacagaccttcagatggtcaga	66	2	+	113207729	113207794								
47	PC-47	tgactccGCCTCTGCTTGAGAGAAGGaatttcttagagatccaccccgtcataagaggtttttctgattattggaggcggggann	85	2	-	114720073	114720157								
48	PC-48	ccAGGGGCGGGGCGGGGCGGGgcgtcccaggctgggccccacctctctgtcctcct	57	2	-	124406188	124406244								
49	PC-49	tttcccagccaccccagggcttgctcggtggacccatgaatcaaggagccatgGTGGCACGGATGCAGGCTCTGCAGgggtctggggcc	89	2	+	125269176	125269264								
50	PC-50	ccagcgcGCAGAACTTGGGGAGCCGCCGCcgccgccgccgacagctgccgccgccgccgccgccgacagctgccgccac	79	2	+	127484068	127484146	2	+	127525736	127525814				
51	PC-51	acactttctatgctaccaagcgtctcataggccggCGATATGATGACCCTGAAGTAcagaaagaca	66	2	-	127612667	127612732								
52	PC-52	caggggaggccctggcTCTCACTCTGAGGCATGAGccctcatccaggagtgggaactgggagtcccaca	69	2	+	128590030	128590098								
53	PC-53	ccaggagctctgtgtcttcttgctacctgctgccctgagtcccAAGGGCTGGAGGCAGGAGcagccaaaccagacacagaatccggc	88	2	+	129116291	129116378								
54	PC-54	caagaagaaaggggaaaaaaAGACGGATGACCTTGCTGTTTacatttagaaaggataagcagcaaggttgtctgtcttttttttcctctctgttcttcagc	100	2	-	131648312	131648411								
55	PC-55	cctgctgcgatggcgccttcttctgctcacttctctgctgtaccatttcgaggaGCCAGGCACTGAGAGGGCAgggaggttgcagctca	89	2	-	135910191	135910279								
56	PC-56	ctgtgagctgtggcgtaggtcaaagacgtggcttggagctggcgttgatggctgtggtGTAGGCCTGCGACTATAGCtccgatt	86	3	+	5360718	5360803								
57	PC-57	agacaaaggaTATCACTAGGGACGGACGTAGCTGCGaagggaagtagggcgtcagtttggggtggtgggctttggtt	77	3	+	6689611	6689688								
58	PC-58	ttaactgctaggccacgggggaactcccagaccagcttccactcccttcaagaAGCTGGTCTGGGAGTTCCCGGGtggcctagtagtgac	90	3	+	9289226	9289315								
58	PC-58	ttaactgctaggccacgggggaactcccagaccagcttccactcccttcaagaAGCTGGTCTGGGAGTTCCCGGGtggcctagtagtgac	90	3	+	9289226	9289315								
59	PC-59	aatgcatgaatacagacggggcctggtctaggctTGGCAGAGACTGTCCTGGAcgtgaggaggtgctgg	69	3	-	10306072	10306140								
60	PC-60	aAGGCATGGCTGAATACTGTGttcttttatcagtaatttacacagccagacaccatgcaaa	62	3	-	15359737	15359798	3	-	15384758	15384819				
61	PC-61	caagtctctgagacactgactgtgggggtatgtgtgtgtccATCTGTCTGTGTCTCTGAGCAGG	64	3	+	25819331	25819394								
61	PC-61	caagtctctgagacactgactgtgggggtatgtgtgtgtccATCTGTCTGTGTCTCTGAGCAGG	64	3	+	25819331	25819394								
62	PC-62	ccaggattgtgggttCGAGTCCCACCCGGGGTAGAaaagagttgtattttaaaacctctggggaaacatgggcgaggacaaacccgat	90	3	-	35061542	35061631								
63	PC-63	gagctggAGCATACTCTGTCTAATGGgggcgtggaatgagagggtatagtcagaaa	56	3	-	38667463	38667518	3	-	38800661	38800716				
64	PC-64	gaactggtgagTGTCCAGAGGGCTGAATGGtaccaaagcagctctccatccccagagt	58	3	-	38716142	38716199								
65	PC-65	tgccaggtcattcacagggttcagttgcctgagggtaACAGTGTTATTTCCTGTGAaagtcttgtga	67	3	+	41088681	41088747								
66	PC-66	atgCAGGGAGCCTGCACAAGAGgctgttcctaccatgtccccatcagcttcccgggctcctctgacc	67	3	+	41090685	41090751								
67	PC-67	tcGGATTTCCTTGTGACTGTGGGACTtaggaagagactggttggaagcaagccaggatcgccgtacagtcacagggatcaaa	82	3	-	41092230	41092311								
68	PC-68	tgATCCCTGTGACTGTACGGCgatcctggcttgcttccaaccagtctcttcctaagtcccacagtcacaaggaaat	76	3	+	41092232	41092307								
69	PC-69	tttgatttttggtgagcctctttgaagatgttgctcTGGAGATGAGGACCGATGAAGTCctc	63	3	+	41624237	41624299								
70	PC-70	gaggagTAGGATGAGAAATAGAGCCttgaaaggtaagcttccacgttcagccctgtgcgccctgagaatctgcttccatctctc	84	3	-	41626515	41626598								
71	PC-71	ggcgccccagacccgcttcctgggtggatgaaaccatcctcgcctTGGTGTGTGGACTGGGGCTct	66	3	-	41627418	41627483								
72	PC-72	agggaaaTGAGGGTTGATTGTATAGTTattcatctggaaccaacctcatccctcccttcatc	62	3	-	43740583	43740644								
73	PC-73	catggctcggatcccgagttgctgtggctatggtgtaggccggcagctgtagctccaattAAACCCTTAGCCTGAGAACTtccacatgccatgggt	96	3	-	51172480	51172575								
74	PC-74	cttcagtCTGGAGGACATCTGATGGCtcccacagtggctgtcacctttctcagtactgttc	61	3	-	54103022	54103082								
75	PC-75	agggcTGGAGTGGGAATCAGAAGAcagaagcagcgggtttttttttttgttttagttttagtttt	67	3	-	75256016	75256082								
76	PC-76	taacagtgccttcttgaagaatattggctgaaagAATGAATGTCAGGAAGAATtgaaa	58	3	-	75974603	75974660	3	-	76126373	76126430				
77	PC-77	ttggtAGAACCTTGGGCCTGTGAAacttatttgcagattttcttcacaagcctatattacact	64	3	-	80676447	80676510								
78	PC-78	cagccgaaaacattaattaaacaactactgtatgcaagaggcttTGTTGGGCACAGTGTGTGTgtgtgtgtgtgtggggg	80	3	+	80958108	80958187								
79	PC-79	tgttacaggccctcgcaccccaattaacctggggggtgGGGAGCGGAGGGCCTGTGGGt	59	3	+	88700641	88700699								
80	PC-80	agacaggctggaGGAGCAGGGGCTGTAGCCCctggtagggggttctggcaggttccggtgcctgggg	67	3	+	90728599	90728665								
81	PC-81	ccctttatagccacagattcaaccaaccccagaaggaaatttaatcTTCAGGCCAAGCTTGGTTGAATccctaatgtaaaacc	83	3	+	91722859	91722941								
82	PC-82	ttCGATTCCCGGCCAATGCAGCgggctgtctcttggagttcccatcttggctcagtggtaaatgaatctga	71	3	-	102331759	102331829	3	-	102598324	102598394	3	+	102154824	102154894
83	PC-83	ttcctggtgctctagcggttaggattaggtgctttcaccgctgtggcccgcgttcaaccCCTGGTCTGAGAACTGAGAtcctacatcaagccgctgctgcatccagcag	109	3	+	104700413	104700521								
84	PC-84	tgtgcgctcggtacacctgaggacttatgacatgcagattctgactcactaggCTGGGGTGTGGATTCTGCGtttctaacaagctctcaagtgatgccggcgctgc	106	3	-	107185259	107185364								
85	PC-85	caagaaccattgtagttattatctgtgtgtgtacatgtttgTATATGTGTGTATGTGCAGGAttaaatcacaatagtttaca	84	3	-	116265943	116266026								
86	PC-86	atatacggtcggccctccatgtccgcgggttccctatcccgggttggttgagttcgcggATGCGGAACCTGCGGATACGGagggctgattgtactc	96	5	-	4391274	4391369								
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87	PC-87	tcacatctggggctgatccagctgcgagaggcaaggcaggcccctgcattTGGGCGGGATGGCAGGTGGgg	71	5	+	7858579	7858649	5	-	7937006	7937076				
88	PC-88	cgactcaccctgcagctcctTGCGTTCATTCTGTTTGGCCTGGtgttctttcagcaggcgggacagcatggtcgcagtgggctgggggtagggcgc	96	5	-	20064090	20064185	5	-	20108111	20108206				
89	PC-89	gtgggtcagagaggaaggatgtgatttgagcagatggttcTCATTCTCCTTCTTTGACCAGA	62	5	-	21622111	21622172								
90	PC-90	gaagcttttgaaaaattcctggtgcctgggtcccctccccagaggttcaaatttaattgcTCTGAGATGTGACCTGGGCATCcggatttttaaagtcct	99	5	-	26991012	26991110								
91	PC-91	gaaagcagaccaaatatatattcctaagaaagggatgagggagggagagAGTATGTCTTTGGGGGTTGgg	70	5	-	32152374	32152443								
92	PC-92	tccggtgaaatggtcaccactgaactggTCTCCAGTGAGACAGTCTCTGGtgaactggtctccagtgactcactccctggtgtaccagtccctggtgaatcagtctccac	110	5	-	55170859	55170968								
93	PC-93	aatgggggcacctGGGGGCTGGAGGAGGGAGGGCtggaggagggaggcctggatctgcttcagaccctagagccgcccccggc	83	5	-	61083977	61084059	5	-	61164139	61164221				
94	PC-94	caggacctcgtggcgcaacggtagcgcgtctgactccagatcagaaggctgcgtgttCGAATCACGTCGGGGTCATGGg	79	5	-	80874736	80874814								
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96	PC-96	gtccgcgagcgggtgctccgggccgccaccggcGCGGGGTGGTGGTCTGTGGGtgcgtgctccagcgtgg	70	6	-	247465	247534								
97	PC-97	cGCCGGCCTTGCGGGCCGCCGGtgaaatccactactctgatcggtttttcactgacccggtgaggcggg	70	6	-	249044	249113								
98	PC-98	atacccggccgtcgccggcagtcggagcagcgcgcgagagggacgggagcggggcgCGCGGTCGCCCGGGGACGCCGGGGtcgc	84	6	-	250690	250773								
99	PC-99	ccaccccggcctcgcctcctcccccccttcccggggtgtggggagGGCCACGGTGCGGGTCGGGGCgg	71	6	-	251649	251719								
100	PC-100	cgcgccgggtttttcTTGGTGGGGGCCGGGCCGCCcctcccacggcgcgaccgctctccccaccccggcctc	71	6	-	251707	251777								
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108	PC-108	AGTGCCTGCTGTGTACCAAGGTtgttctgggtgttctgggttttacagataagccatctgcctgtggtgcacacagctggaa	82	6	+	32774401	32774482								
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116	PC-116	cctgagtctgcaTGTACACGTCAAAAAGGACCagccgactttcctggtgccaagacttgaccctgacatcaaggctccac	80	6	-	66475127	66475206								
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120	PC-120	ggtGCGCGCGCACGTGTGCGCGGGcaaaagggggcggggaagctctggggcggacgacgggcgcgcgtcg	73	6	+	94621902	94621974								
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123	PC-123	acacgccgcgcccgggctcggccggcggggcGGGCCGGGCGGTGGTGGCGgcgggg	56	6	+	103808631	103808686								
124	PC-124	tgcctgataggcacctctcccggagtgatgttcgaaatagtccataacctgtgtgacaCGAGCATACCAGTTGGGACagatcctgccctgccaccaggccaa	104	6	-	106940778	106940881								
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126	PC-126	ttagccacgacgggaactccagaaatcttacatattaaagtgagacCTGGAGTTTTTGTCATGGCaca	68	6	-	113778937	113779004								
127	PC-127	atttctgcaggagtttccattgTGGCTCAGCGGCAATGAACctgactagcatctgtgagtccggcattgccgtgagctgtggtgtaggtcgcagatac	98	6	-	121989562	121989659								
128	PC-128	tgagtcctgagacatcgctTCTGGTCCAGACACTGTGGAGCtgaagagaccaacacttctcagtgtttgaaccagaagctgtctgcagaacaat	96	7	-	8508435	8508530								
129	PC-129	ctgcatttagagatgacatcagttagtgctcatgatgtgtcaccttttgaccatttttAAATGGGTGACGGGCAACAtgttatgacattggtcatagatgaatgctac	110	7	+	17776790	17776899								
130	PC-130	aggcctTCGGTGTCAGGATGGCCGAGTGGtctaaggcgccagactcaagcggcagcttcccaccttgggcggttctggtctccgaatggag	90	7	-	22793682	22793771								
131	PC-131	atcaagttcctcctgctggatataggcagagtaggaTGTTTTCAGTGTCTGTGTTCTGGgagaatgtacttaaa	74	7	-	31617508	31617581								
132	PC-132	catcagggagcccgtgtggttgagctgggcaaaggacagttTGGCAGTAGGACCATAAGCACGGtgttccttgttc	76	7	-	34450857	34450932								
133	PC-133	agttttccggagcgaagtgatttatcttcattctgtgcagaaaatgagtTGACTGCACGGAGTGAGGATGAAAGAacggcggggcgggggtgg	93	7	-	34464588	34464680								
134	PC-134	tctgtcccctcctccccagtggggaggctgaacctcgtaattatcttcattctcctgCTGGGTCTCGGCTGGGATCaact	81	7	-	34466641	34466721								
135	PC-135	agagcacagtgcagggaaactaaggctcaagtcaccagcaagggtacagggccatcccttttctTCCTGACTCTGACATTGCGccgagtatcaggaccacttgtcac	106	7	-	34484784	34484889								
136	PC-136	taATCATGAGGACATGGATTTGAGCCctgatcttgcacagtgggttaaggatccggtgttgccatgagct	70	7	-	40634472	40634541								
137	PC-137	cccgggaaacagcAGGGTGTGTGTTTTTATTTtgcaaaatattaaatcacagtattgattatgcttttgcagacagcacacttctctctcccc	92	7	+	45307051	45307142								
138	PC-138	ccagactctccagaaacaggaagAAGCTACTCTGGTACCATCtccaatagtacctttgttgtcctttttctgtgtctgctacgttagc	89	7	-	47856717	47856805								
139	PC-139	cAAGCCTTGCCTTCTTGACCAtgaccgctcctttgggttccgggctaatgaatggtaaattgtttaagaggcatgcgtg	78	7	+	54374344	54374421								
140	PC-140	acctggcaacccccttttaccctcctgataaaaatagaaAGGGCTGAAGTGGGGAAAGccatgg	64	7	-	59814924	59814987								
141	PC-141	tcctctggcaggagggctcgggctgagtatgagggtggtgattggtcccctttcTCAGCCCGCATTCTCCACCAgacac	79	7	-	63696327	63696405								
142	PC-142	taaggcttgtagtgtttccccctctgcttgggattgtcgtggaaggcttctaccagtaataACACAGGTAGTGGAGGAGAaatacgctgga	90	7	+	75040376	75040465								
143	PC-143	taaTGGGACCAGTCTCTGGCCTctgcctttaactggggataccaaggaggcagcttccagacagatcccagct	75	7	-	90893972	90894046								
144	PC-144	gctgggaTCGTGTCTGGAAGCTGCCTCCTTGGTatccccagttaaaaggcagaggccagagactggtcccatt	73	7	+	90893973	90894045								
145	PC-145	ggcgtttcaccaaggtggttcttccTGCCATCATCCGGCCTGGTAGAggaggaacttggttccttcctcagcccaggagagttgggggggatggatgggagagccaggtggagc	111	7	+	90894127	90894237								
146	PC-146	ccagatgctgagtttggcaaggcagctgtcctactgggagagggacccagggtactcccTGCCAGTGTGCAGACACGGGGtctgaaa	88	7	+	90894674	90894761								
147	PC-147	ataggATTGTTGTGAAGGTTCTATGAATTaatttttatatagaatacttagaacagccaga	61	7	-	93560699	93560759								
148	PC-148	tggcaaaggccatgagttttcatcctcggggcagacttcccacgtggacacacaaaggtcAGCAAGGTCTGCCTTAAGGccacctgataacgatggctgtgccccc	106	7	-	95895079	95895184								
149	PC-149	atctgttcagatttggaaatttcctcggcatcccttgagaataaaagactgcttgccaggGTGCAAGGCTGAATTAGACac	81	7	-	95897924	95898004								
150	PC-150	tatgggaatctcagcacatctggctctggcacggaggacGGAGTCCACCTGTGCCTGAGtccactggatggcttggtcccccct	84	7	-	97085759	97085842								
151	PC-151	tcaggagaaaacgctttgagctctggttggatttttTCCAAGATAGTTTTCAGCCCTTCTCcatg	66	7	-	117947019	117947084								
152	PC-152	cagtcaggctttcccctctgtgatgcgaccagtcaagctagctcTAATTGTAGACAGTCCTGAGAGTCTggaag	74	7	-	117950334	117950407								
153	PC-153	ccTGAGACCTGGTCCAGAGCCTCGACTTtaaaagaatttaggctttgaatcctagtttccaa	62	7	-	117952163	117952224								
154	PC-154	tgggactaagtcctttcgtgtagaagttgcccagtgccatgactgaagcatctggaacaaTAGGATATGAGGGCCTCAGTTTCtag	86	7	-	117963458	117963543								
155	PC-155	tgattttttagtggctgcactcTATGTAGTTTCGCTCCACTaagaagtgggcgtaaatgggcatatgcatctgatgaaagaggg	83	7	-	117965108	117965190								
156	PC-156	gtgggagcttgttagaaatcccagatcctagaccccagctcgcaccTAAGGATCTGCGGTTTACCAAGAtctccagg	77	7	-	117966638	117966714								
156	PC-156	gtgggagcttgttagaaatcccagatcctagaccccagctcgcaccTAAGGATCTGCGGTTTACCAAGAtctccagg	77	7	-	117966638	117966714								
157	PC-157	tttggattccaagagaaagtagtTAAGAGAATCAGCAGCTCTGTAGCTCtgttgcatatctgttctggttctgtttctgaagttcttttggtgtctttt	99	7	-	117967067	117967165								
158	PC-158	TCCTATTCCTGAGACGGTGATtcgtagctggattctcagtttctgcacctctttcaggaatcta	64	7	-	117967900	117967963								
159	PC-159	tctgggtctgtctactggagacCTGCTGGTCATTTGTAAGCtcttgtttcatttgtatctgtatgtcagctttccagttgtcttaccctct	91	7	-	117971856	117971946								
160	PC-160	tctggcgttgctgtgaactgtggtgTAGGTCACAGACACGGCGTggatcccacattgctgtggctgtggtgtagcccagcagctgtagctccgat	95	7	-	120949888	120949982								
161	PC-161	gcGATTGGTGGAGAGACCTGAccaccatcatccttgactgtgcggtcaaggtcaccttcaccaatgat	67	7	+	124374252	124374318								
162	PC-162	agagcccccacccgcccatggggcaggGCCAGGATAGACTTGACCTgaccgaacagttagcatcctgttaactcctggtgaactgcagtgggagtgaggctggtggca	108	7	-	127129134	127129241								
163	PC-163	aggaggggagtgggagagggaggggggtGAGGGAAGGGAGGGTGGGCtgcccggagagaggaggaccgccctggctcctccagacctgtgctccccagcacccctgc	107	7	+	134000412	134000518	7	+	134289662	134289768				
164	PC-164	cttagtctattgCTGTCCTTTGCATCCAACAggtagttattgcatatcacatatgtagcaggcactgttctaggctctt	79	7	+	136080734	136080812								
165	PC-165	tgctcaggttctaagggtcagttttcctgcgaTTCCGCGGACAAGGCCTTTggtctgaaga	61	8	+	2376898	2376958								
166	PC-166	aaggcgtcacgtggtgcccctcagacgggaccCGCCCCCGCGGTCCTCCTCtgtgagacctcggtgcccggaccccggggggcgccatcgcggg	94	8	-	3763031	3763124								
167	PC-167	ttagtgtttttttttttcagatataTAACCAGGAGTAGAATTGCtgggtcattcggtacgtctactttcgttttctgagaaacctccacacaaa	97	8	-	8634350	8634446								
168	PC-168	tggaggtttccaggctacaggTCAAATCGGAGCTACGGCTttggccctctgccacagccacagcagctccggatctgagccgagcctgtg	90	8	+	18324589	18324678								
169	PC-169	gaggctggatcattctcctccaaaccccacagctgctatggcaaggaatggaatGGAGGCTGCAGAGTGAACCtcaggtctgc	90	8	+	25394642	25394731								
170	PC-170	tcggcagcctcttgggagcaCTGGGACCCAGGCTCCATCactggtccacaacggtggattaaagtgggttaaggttccagcgttgcttggctgcagc	98	8	-	33558121	33558218								
171	PC-171	taatgtgtacgtgtgtctacatatatgtatgtgctatgcatgtatGTGTATGTATGTGTATATGTATAtacat	76	8	-	66520502	66520577								
172	PC-172	agaggtacaaatctatcctggtacaattATTGTGATTTTCCTTGTAAatatatggaaaatatatattttgtcttttagggctgcacccat	93	8	-	67706089	67706181								
173	PC-173	taattttaaagtagcaacaataagatagtaactgacttctcaatagaaaTGCTGGAAATCAGGAGACTaagccataattttaaagtgctgaaagaaaaacc	101	8	+	82552014	82552114								
174	PC-174	acactacctctgccacactgttaagacccagatcttctgtgTTGGATCTGAGCTCAGGCAgtgtcagtttgtggaag	77	8	-	82901157	82901233								
175	PC-175	tcttacacagctttccagaggtttccagcttataggatattcatatggtagtTCTGTGAACTAGAAACCTCTGGaaagtggtgtacat	88	8	-	97945306	97945393								
176	PC-176	ctttttacattgtactgctgtcctgtgacttctcctgcaatctgaattgtaaagtaacatAGGATGgTAGACATAGAAGGAGc	83	8	+	102390022	102390104								
177	PC-177	gTGGACTGGATGACAATCTGCAGGctggccatgccgtagatgggaatccggtcgct	56	8	+	112041388	112041443								
178	PC-178	gtttcgctcctccacgtgtggttttagccttcacagaataaggagaccaaggcagggtgaGTGGTGCGTGTGGGTGGGTggggtgt	86	8	-	113270933	113271018								

Pre-miRNA ID	miRNA name	Consensus miRNA sequence	Length (nt)	Ovary					Testis				
				Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs	Most abundant sequences	Length (nt)	Counts of most abundant sequences	Counts of all isomiRs	Kinds of all isomiRs
1	PC-1-5p	CCTAATGATGAAACTCTGAGG	21	CCTAATGATGAAACTCTGAGG	21	9	9	1					
2	PC-2-3p	CGGCCCCCGGCGCGTCGGG	19	CGGCCCCCGGCGCGTCGGG	19	8	15	2					
3	PC-3-5p	GATGGATGATGATTCTGACA	20	GATGGATGATGATTCTGACA	20	13	13	1					
4	PC-4-3p	GATTCCTAACTCACCGGAC	19	GATTCCTAACTCACCGGAC	19	3	3	1					
5	PC-5-3p	GAAGCTACCATGCGTAGGA	19	GAAGCTACCATGCGTAGGA	19	3	3	1					
6	PC-6-5p	GCGGGGCGCGCGGTCGCCCGGG	22	GCGGGGCGCGCGGTCGCCCGGG	22	9	49	8					
7	PC-7-5p	ATTAGTGGCAGAGCCCGGA	19	ATTAGTGGCAGAGCCCGGA	19	10	10	1					
8	PC-8-3p	GCAATTTAGGTTAATGACTGTC	22	GCAATTTAGGTTAATGACTGTC	22	4	4	1					
9	PC-9-5p	GTGACATGGTGTGAATTGC	19	GTGACATGGTGTGAATTGC	19	3	3	1					
10	PC-10-3p	TGGCTGACCTCTGACCTCC	19	TGGCTGACCTCTGACCTCC	19	88	88	1					
11	PC-11-5p	CGGCCGGGCCCGCCCCCGC	19	CGGCCGGGCCCGCCCCCGC	19	3	3	1					
12	PC-12-3p	GGTCCCATCTGGGGTGCCA	19	GGTCCCATCTGGGGTGCCA	19	20	37	3					
13	PC-13-3p	ATTGATTTCGGTTGGGACA	19	ATTGATTTCGGTTGGGACA	19	12	12	1					
14	PC-14-5p	GTGGGCTGGAGAGACGGCT	19	GTGGGCTGGAGAGACGGCT	19	3	3	1					
15	PC-15-3p	CTCCCGGGTTTCGGCACCA	19	CTCCCGGGTTTCGGCACCA	19	18	18	1					
16	PC-16-3p	TATAGTCTGGAGGATGTAGTACTACC	26						TATAGTCTGGAGGATGTAGTACTACC	26	3	3	1
17	PC-17-5p	GCGCGCGGTCGCCCGGGGA	19	GCGCGCGGTCGCCCGGGGA	19	62	62	1	GCGCGCGGTCGCCCGGGGA	19	22	22	1
18	PC-18-3p	TGCCCACACTCCTCTCTCCAGT	22	TGCCCACACTCCTCTCTCCAGT	22	3	3	1					
19	PC-19-3p	TTGGACGGATGAGGACACTGAGGCGT	26						TTGGACGGATGAGGACACTGAGGCGT	26	3	3	1
20	PC-20-3p	TTTGTTGGCTCCTCTGAAGTGA	22	TTTGTTGGCTCCTCTGAAGTGA	22	14	22	3	TTTGTTGGCTCCTCTGAAGTGA	22	7	10	2
21	PC-21-3p	CGAGGCAGCGCTGAGGATGAAC	22	CGAGGCAGCGCTGAGGATGAAC	22	4	4	1					
22	PC-22-5p	TTTTGTCTCTGAACTCTGCGCTTTT	25						TTTTGTCTCTGAACTCTGCGCTTTT	25	8	33	6
23	PC-23-5p	ACTTCTCTGAGCCTGCTTCTT	21						ACTTCTCTGAGCCTGCTTCTT	21	3	3	1
24	PC-24-5p	AAGTAGGAAGAATATGATCTCAGAAT	26						AAGTAGGAAGAATATGATCTCAGAAT	26	3	3	1
25	PC-25-3p	TGGACGATGCATTGAATATTTGAGC	25						TGGACGATGCATTGAATATTTGAGC	25	11	11	1
26	PC-26-5p	TGAGGTAGTCAGGACCAGACCAAGGC	26						TGAGGTAGTCAGGACCAGACCAAGGC	26	5	5	1
27	PC-27-5p	AAACTGGTAGACTTGAGTA	19	AAACTGGTAGACTTGAGTA	19	4	4	1					
28	PC-28-3p	AATGGAGAGGGCAGTAGGAC	20	AATGGAGAGGGCAGTAGGAC	20	4	4	1					
29	PC-29-5p	TCAAATCGGACCTACGGCT	19						TCAAATCGGACCTACGGCT	19	7	7	1
30	PC-30-3p	TGTGTCTGTGACATCTGCTGGCA	23	TGTGTCTGTGACATCTGCTGGCA	23	16	24	3	TGTGTCTGTGACATCTGCTGGCA	23	5	5	1
31	PC-31-5p	GGAGGGCGCGGCGGCCGCC	19	GGAGGGCGCGGCGGCCGCC	19	4	4	1	GGAGGGCGCGGCGGCCGCC	19	5	5	1
32	PC-32-5p	GCCGGGCCCGCCCCCGCGG	19	GCCGGGCCCGCCCCCGCGG	19	10	10	1	GCCGGGCCCGCCCCCGCGG	19	3	3	1
33	PC-33-3p	TGGGGGATGCCTAGGCTCT	19	TGGGGGATGCCTAGGCTCT	19	13	13	1	TGGGGGATGCCTAGGCTCT	19	8	8	1
34	PC-34-3p	TAGGTCAAAGACACGGCGT	19						TAGGTCAAAGACACGGCGT	19	4	4	1
35	PC-35-3p	CATGTGTCTGCATGTGCAC	19						CATGTGTCTGCATGTGCAC	19	3	3	1
36	PC-36-5p	TCAAATCGGACCTACGGCT	19						TCAAATCGGACCTACGGCT	19	7	7	1
37	PC-37-5p	TGCGTGGCTTCTCTGTGCAGTC	22	TGCGTGGCTTCTCTGTGCAGTC	22	33	72	5					
38	PC-38-3p	ACAGTGTTATTTCATGTGA	19						ACAGTGTTATTTCATGTGA	19	3	3	1
39	PC-39-5p	AACTGAAGTGTAGAACATT	19						AACTGAAGTGTAGAACATT	19	4	4	1
40	PC-40-3p	ATTGCTGTGGCCACTGCGT	19	ATTGCTGTGGCCACTGCGT	19	6	6	1	ATTGCTGTGGCCACTGCGT	19	8	8	1
41	PC-41-3p	CAGGCGTGAGGCACTCTGT	19						CAGGCGTGAGGCACTCTGT	19	4	4	1
42	PC-42-3p	CAGCAGGCTGTGGTGAAGG	19						CAGCAGGCTGTGGTGAAGG	19	41	41	1
43	PC-43-5p	TTAGGACAAGATTTTATGA	19						TTAGGACAAGATTTTATGA	19	3	3	1
44	PC-44-3p	CGGCGCGACTGAACTCCGGA	20						CGGCGCGACTGAACTCCGGA	20	3	3	1
45	PC-45-3p	TTACGTGGCTATTCTGATA	19	TTACGTGGCTATTCTGATA	19	17	23	3	TTACGTGGCTATTCTGATA	19	29	32	2
46	PC-46-5p	CAGGCGTGAGGCACTCTGT	19						CAGGCGTGAGGCACTCTGT	19	4	4	1
47	PC-47-5p	GCCTCTGCTTGAGAGATGG	19						GCCTCTGCTTGAGAGATGG	19	12	12	1
48	PC-48-5p	AGGGGCGGCGCGGGGCGGG	19	AGGGGCGGCGCGGGGCGGG	19	32	32	1					
49	PC-49-3p	GTGGCACGGATGCAGGCTCTGCAA	24	GTGGCACGGATGCAGGCTCTGCAA	24	4	4	1					
50	PC-50-5p	GCAGAACTTGGGGAGCCGCCGC	22	GCAGAACTTGGGGAGCCGCCGC	22	3	3	1					
51	PC-51-3p	CGATATGATGACCCTGAAGTA	21	CGATATGATGACCCTGAAGTA	21	3	3	1					
52	PC-52-5p	TCTCACTCTGAGGCAGGAG	19						TCTCACTCTGAGGCAGGAG	19	4	4	1
53	PC-53-3p	AAGGGCTGGAGGCAGCAGG	19						AAGGGCTGGAGGCAGCAGG	19	6	6	1
54	PC-54-5p	AGACGGATGACCTTGCTGTTT	21	AGACGGATGACCTTGCTGTTT	21	4	4	1					
55	PC-55-3p	GCCCGGCACTGAGAGGGCA	19						GCCCGGCACTGAGAGGGCA	19	8	8	1
56	PC-56-3p	GTAGGCCTGCGACTCTAGC	19						GTAGGCCTGCGACTCTAGC	19	3	3	1
57	PC-57-5p	TATCACTAGGGACGGACGTAGCTGCG	26						TATCACTAGGGACGGACGTAGCTGCG	26	12	25	3
58	PC-58-5p	AGCTGGTCTGGGAGTTCCCGGG	22						AGCTGGTCTGGGAGTTCCCGGG	22	9	9	1
58	PC-58-3p	GGGGAACTCCCAGACCAGCTTC	22						GGGGAACTCCCAGACCAGCTTC	22	5	8	2
59	PC-59-3p	TGGAAGAGACTGTCCTGGA	19						TGGAAGAGACTGTCCTGGA	19	16	16	1
60	PC-60-5p	AGGCATGGCTGAATACTGT	19						AGGCATGGCTGAATACTGT	19	3	6	2
61	PC-61-5p	ATCTGTCTGTGTCTCTGAGCAGA	23						ATCTGTCTGTGTCTCTGAGCAGA	23	4	4	1
61	PC-61-3p	TCTGAGACACTGACTGTTGG	20						TCTGAGACACTGACTGTTGG	20	3	3	1
62	PC-62-5p	CGAGTCCCACCCGGGGTAGG	20						CGAGTCCCACCCGGGGTAGG	20	40	43	2
63	PC-63-5p	AGCATACTCTGGCTAATGG	19						AGCATACTCTGGCTAATGG	19	4	4	1
64	PC-64-5p	TGTCCAGAGGGCTGAACGG	19						TGTCCAGAGGGCTGAACGG	19	4	4	1
65	PC-65-3p	ACAGTGTTATTTCATGTGA	19						ACAGTGTTATTTCATGTGA	19	3	3	1
66	PC-66-5p	CAGGGAGCCTGCACAAGAG	19						CAGGGAGCCTGCACAAGAG	19	3	3	1
67	PC-67-5p	TGATTTCCTTGTGACTGTGGGACT	24						TGATTTCCTTGTGACTGTGGGACT	24	3	3	1
68	PC-68-5p	ATCCCTGTGACTGTACGGC	19						ATCCCTGTGACTGTACGGC	19	7	7	1
69	PC-69-3p	TGGAGATGAGGACTGATGAAGTC	23						TGGAGATGAGGACTGATGAAGTC	23	3	3	1
70	PC-70-5p	TAGGATGAGAAATAGAGCC	19						TAGGATGAGAAATAGAGCC	19	25	28	2
71	PC-71-3p	TGGTGTGTGGACTGGGGCT	19						TGGTGTGTGGACTGGGGCT	19	20	29	3
72	PC-72-5p	TGAGGGTAGATTGTATAGTT	20						TGAGGGTAGATTGTATAGTT	20	3	3	1
73	PC-73-3p	AAACCCTTTGCCTGAGAACT	20						AAACCCTTTGCCTGAGAACT	20	4	4	1
74	PC-74-5p	CTGGAGGACATATGATGGC	19						CTGGAGGACATATGATGGC	19	9	9	1
75	PC-75-5p	TGGACTGGGAATCAGAAGAC	20						TGGACTGGGAATCAGAAGAC	20	9	9	1
76	PC-76-3p	TATGAATGTCAGGAAGAAT	19						TATGAATGTCAGGAAGAAT	19	3	3	1
77	PC-77-5p	AGAACCTTGGGACTGTGAA	19						AGAACCTTGGGACTGTGAA	19	6	6	1
78	PC-78-3p	TGTTGGGCTCAGTGTGTGT	19						TGTTGGGCTCAGTGTGTGT	19	4	4	1
79	PC-79-3p	GGGGGCGGAGGGCCTGTGGG	20						GGGGGCGGAGGGCCTGTGGG	20	8	8	1
80	PC-80-5p	GGAGTAGGGGCTGTAGCCC	19						GGAGTAGGGGCTGTAGCCC	19	3	3	1
81	PC-81-3p	TTTAGGCCAAGCTTGGTTGAAT	22						TTTAGGCCAAGCTTGGTTGAAT	22	5	5	1
82	PC-82-5p	CGATTCCCGGCCAACGCAGC	20						CGATTCCCGGCCAACGCAGC	20	5	5	1
83	PC-83-3p	CCTGGTCTGAGAACTCAGA	19						CCTGGTCTGAGAACTCAGA	19	3	3	1
84	PC-84-3p	CTGGGGTGTGGATTCGGCG	19						CTGGGGTGTGGATTCGGCG	19	17	30	4
85	PC-85-3p	TATATGTGTGTATTTGCAGGA	21						TATATGTGTGTATTTGCAGGA	21	3	3	1
86	PC-86-5p	ATGTCCGCGGGTTCCCTATCC	21	ATGTCCGCGGGTTCCCTATCC	21	322	588	16					
86	PC-86-3p	ATGCGGAACCTGCGGATACGG	21	ATGCGGAACCTGCGGATACGG	21	18663	26759	13					
87	PC-87-3p	TGGGCGGGATGGGAGGTGG	19	TGGGCGGGATGGGAGGTGG	19	14	14	1					
88	PC-88-5p	TGCGTTCATTCTGTTTGGCCTGT	23	TGCGTTCATTCTGTTTGGCCTGT	23	5	5	1					
89	PC-89-3p	TCATTCTCCTTCTTTGACCAGT	22	TCATTCTCCTTCTTTGACCAGT	22	11	11	1					
90	PC-90-3p	TCTGAGATGTGACCTGGGCATC	22	TCTGAGATGTGACCTGGGCATC	22	6	6	1					
91	PC-91-3p	AGTATGTCTTTGGGGATTG	19	AGTATGTCTTTGGGGATTG	19	3	3	1					
92	PC-92-5p	TCTCCAGTGAGACAGTCTCTGG	22	TCTCCAGTGAGACAGTCTCTGG	22	4	4	1					
93	PC-93-5p	CGGGGCTGGAGGAGGGAGGGC	21	CGGGGCTGGAGGAGGGAGGGC	21	17	17	1					
94	PC-94-3p	CGAATCACGTCGGGGTCATGG	21	CGAATCACGTCGGGGTCATGG	21	44	74	3					
95	PC-95-3p	ACACGTAGCCTTTAAGTAGTGA	22	ACACGTAGCCTTTAAGTAGTGA	22	3	3	1					
96	PC-96-3p	CGGGGTGGTGGTCTGTGGG	19	CGGGGTGGTGGTCTGTGGG	19	3	6	2					
97	PC-97-5p	GCCGGCCTTGCGGGCCGCCGG	21						GCCGGCCTTGCGGGCCGCCGG	21	17	40	4
98	PC-98-3p	CGCGGTCGCCCGGGGACGCCGGGG	24	CGCGGTCGCCCGGGGACGCCGGGG	24	34	206	5					
99	PC-99-3p	CCCCCCCTTCCCGGGGTGTGGGGA	24						CCCCCCCTTCCCGGGGTGTGGGGA	24	3	12	5
100	PC-100-5p	TTGGTGGGGGCCGGGCCGCC	20	TTGGTGGGGGCCGGGCCGCC	20	11	40	8					
101	PC-101-5p	CCCGGCGCTCCCCCCCGCGGGGG	23						CCCGGCGCTCCCCCCCGCGGGGG	23	4	15	4
102	PC-102-5p	TTGTCCGTGCCCCACCCACTCA	22	TTGTCCGTGCCCCACCCACTCA	22	15	30	3					
103	PC-103-5p	TGGGCCGTCTGTCTGTGCAGC	21						TGGGCCGTCTGTCTGTGCAGC	21	4	4	1
104	PC-104-5p	TGTTTCTTTGACAAGCAGCCTGGTCC	26						TGTTTCTTTGACAAGCAGCCTGGTCC	26	34	44	3
105	PC-105-5p	TTGGAGCTGTTTAGAGAGACATGGCT	26						TTGGAGCTGTTTAGAGAGACATGGCT	26	48	58	2
106	PC-106-5p	TGTGCATTGCAGGATGATT	19						TGTGCATTGCAGGATGATT	19	7	7	1
107	PC-107-3p	TGAGGAATAAGAAGAACCGATGGTGT	26						TGAGGAATAAGAAGAACCGATGGTGT	26	7	7	1
108	PC-108-5p	GTGCCTGCTGTGTGCCAAGG	20						GTGCCTGCTGTGTGCCAAGG	20	7	14	2
109	PC-109-5p	CGGCTGGACTGTGAAAAGA	19						CGGCTGGACTGTGAAAAGA	19	7	7	1
110	PC-110-3p	AGGGGGCGGAGGGCCTGTGG	20	AGGGGGCGGAGGGCCTGTGG	20	19	19	1	AGGGGGCGGAGGGCCTGTGG	20	18	18	1
111	PC-111-3p	GAAGGAGGCAGAGGCAGGA	19						GAAGGAGGCAGAGGCAGGA	19	18	32	4
112	PC-112-3p	CGATGATGGTCCCTGTGTTTGT	22						CGATGATGGTCCCTGTGTTTGT	22	13	16	2
113	PC-113-3p	GCTTGTGATGACTGAACTGAGG	22	GCTTGTGATGACTGAACTGAGG	22	4	4	1					
114	PC-114-5p	GGGGACTGGAGAGATGGCT	19						GGGGACTGGAGAGATGGCT	19	4	7	2
115	PC-115-3p	GGTCCTGCCGCGGGCGCCA	19	GGTCCTGCCGCGGGCGCCA	19	5	5	1	GGTCCTGCCGCGGGCGCCA	19	4	4	1
116	PC-116-5p	TGTACACGTCAAAAAGGACC	20						TGTACACGTCAAAAAGGACC	20	3	3	1
117	PC-117-3p	GTATTCTGAAGCTCTGAAATGCT	23	GTATTCTGAAGCTCTGAAATGCT	23	3	3	1					
118	PC-118-3p	TGGAACTGTGCTGTCTGAAGCAAG	24						TGGAACTGTGCTGTCTGAAGCAAG	24	7	33	7
119	PC-119-5p	CACCTGTGGTTCTGAGGGG	19						CACCTGTGGTTCTGAGGGG	19	3	3	1
120	PC-120-5p	GCGCGCGCGCGTGTGCGCGGG	21	GCGCGCGCGCGTGTGCGCGGG	21	81	180	4	GCGCGCGCGCGTGTGCGCGGG	21	26	48	3
121	PC-121-3p	CCTGGTCTGAGAACTCAGA	19						CCTGGTCTGAGAACTCAGA	19	3	3	1
122	PC-122-3p	CTGGAGTTGTTGTCATGGC	19						CTGGAGTTGTTGTCATGGC	19	3	3	1
123	PC-123-3p	GGGCCGGGCGGTGGTGGCG	19	GGGCCGGGCGGTGGTGGCG	19	8	8	1	GGGCCGGGCGGTGGTGGCG	19	3	3	1
124	PC-124-3p	CGAGCATACCTGTTGGGAC	19						CGAGCATACCTGTTGGGAC	19	3	3	1
125	PC-125-5p	TTAGGACAAGATTTTATGA	19						TTAGGACAAGATTTTATGA	19	3	3	1
126	PC-126-3p	CTGGAGTTGTTGTCATGGC	19						CTGGAGTTGTTGTCATGGC	19	3	3	1
127	PC-127-5p	TGGCTCATCGGCAATGAAC	19						TGGCTCATCGGCAATGAAC	19	4	4	1
128	PC-128-5p	TCTGGTCCAGACACTGTGGAGC	22						TCTGGTCCAGACACTGTGGAGC	22	4	4	1
129	PC-129-3p	AAGTGGGTGACGGGCAACA	19						AAGTGGGTGACGGGCAACA	19	3	3	1
130	PC-130-5p	TCTGTGTCAGGATGGCCGAGTGG	23						TCTGTGTCAGGATGGCCGAGTGG	23	9	12	2
131	PC-131-3p	TGTTTTCAGTATCTGTGTTCTGG	23						TGTTTTCAGTATCTGTGTTCTGG	23	3	3	1
132	PC-132-3p	TGGCAGTAGGACCATAAGCACGG	23						TGGCAGTAGGACCATAAGCACGG	23	4	10	3
133	PC-133-3p	TGACTGCACGGAGTGAGGATGAAAGA	26						TGACTGCACGGAGTGAGGATGAAAGA	26	4	7	2
134	PC-134-3p	CTGGGTCTCGGCTGGGATC	19						CTGGGTCTCGGCTGGGATC	19	6	9	2
135	PC-135-3p	TCCTGACTCTGACATTGCG	19						TCCTGACTCTGACATTGCG	19	14	21	2
136	PC-136-5p	ATCATGAGGACATGGATTTGAGCC	24	ATCATGAGGACATGGATTTGAGCC	24	8	19	4					
137	PC-137-5p	AGGTGTCTGTTTTTATTT	19	AGGTGTCTGTTTTTATTT	19	3	3	1					
138	PC-138-5p	AAGCTACTCTGGCACCATC	19						AAGCTACTCTGGCACCATC	19	36	36	1
139	PC-139-5p	AAGCCTTCCTTCTTGACCA	19	AAGCCTTCCTTCTTGACCA	19	6	6	1					
140	PC-140-3p	AGGACTGAAGTGGGGAAAG	19	AGGACTGAAGTGGGGAAAG	19	5	5	1					
141	PC-141-3p	TCTGCCCGCATTCTCCACCA	20	TCTGCCCGCATTCTCCACCA	20	9	9	1	TCTGCCCGCATTCTCCACCA	20	9	9	1
142	PC-142-3p	ACACAGGTAGTCGAGGAGA	19	ACACAGGTAGTCGAGGAGA	19	3	3	1	ACACAGGTAGTCGAGGAGA	19	5	5	1
143	PC-143-5p	TGGGACCAGTCTCTGGCCT	19						TGGGACCAGTCTCTGGCCT	19	4	4	1
144	PC-144-5p	TCGTGTCTGGAAGCTGCCTCCTTGGT	26						TCGTGTCTGGAAGCTGCCTCCTTGGT	26	47	71	4
145	PC-145-5p	TGCCATCATCCGGCCTGGTAGA	22						TGCCATCATCCGGCCTGGTAGA	22	14	31	5
146	PC-146-3p	TGCCAGTGTGCAGACACGGGG	21						TGCCAGTGTGCAGACACGGGG	21	3	3	1
147	PC-147-5p	ATTGTTGTGAAGGTTCTATGAATT	24						ATTGTTGTGAAGGTTCTATGAATT	24	32	43	3
148	PC-148-3p	AGCAAGGTCTGCCTTAAGG	19						AGCAAGGTCTGCCTTAAGG	19	4	4	1
149	PC-149-3p	GTGCAAGGCTGAATTAGAC	19						GTGCAAGGCTGAATTAGAC	19	28	28	1
150	PC-150-3p	GAGTCCACCTGTGCCTGAG	19						GAGTCCACCTGTGCCTGAG	19	17	38	2
151	PC-151-3p	TCCAAGATAGTTTTCAGCCCTTCTC	25						TCCAAGATAGTTTTCAGCCCTTCTC	25	14	24	3
152	PC-152-3p	TAATTGTAGACAGTCCTGAGAGTCT	25						TAATTGTAGACAGTCCTGAGAGTCT	25	3	3	1
153	PC-153-5p	TGAGACCTGGTCCAGAGCCTCGACTT	26						TGAGACCTGGTCCAGAGCCTCGACTT	26	12	12	1
154	PC-154-3p	TAGGATATGAGGGCCTCAGTTTC	23						TAGGATATGAGGGCCTCAGTTTC	23	5	11	3
155	PC-155-5p	TATGTAGTTTCGCTCCACT	19						TATGTAGTTTCGCTCCACT	19	6	6	1
156	PC-156-5p	TAAGGATCTGCGGTTTACCAAGA	23						TAAGGATCTGCGGTTTACCAAGA	23	15	33	3
156	PC-156-3p	CTTGTTAGAAATCCCAGATCCTAGAC	26						CTTGTTAGAAATCCCAGATCCTAGAC	26	3	3	1
157	PC-157-5p	TAAGAGAATCAGCAGCTCTGTAGCTC	26						TAAGAGAATCAGCAGCTCTGTAGCTC	26	6	6	1
158	PC-158-5p	TCCTATTCCTGAGACGGTGAT	21						TCCTATTCCTGAGACGGTGAT	21	5	5	1
159	PC-159-5p	CTGCTGGTCATTTGTAAGC	19						CTGCTGGTCATTTGTAAGC	19	5	5	1
160	PC-160-5p	TAGGTCAAAGACACGGCGT	19						TAGGTCAAAGACACGGCGT	19	4	4	1
161	PC-161-5p	GAATGGTGGAGAGACCTGA	19	GAATGGTGGAGAGACCTGA	19	3	3	1					
162	PC-162-5p	GCCAGGATAGACTTGAACT	19						GCCAGGATAGACTTGAACT	19	6	11	2
163	PC-163-5p	GAGGGAAGGGAGGGCGGGC	19						GAGGGAAGGGAGGGCGGGC	19	3	3	1
164	PC-164-5p	CTGTCATTTGCATCCAACA	19						CTGTCATTTGCATCCAACA	19	3	3	1
165	PC-165-3p	TTCCGCGGACGAGGCCTTT	19						TTCCGCGGACGAGGCCTTT	19	3	3	1
166	PC-166-5p	CGCCCCCGCGGTCCTCCTC	19						CGCCCCCGCGGTCCTCCTC	19	7	11	2
167	PC-167-5p	TAACCAGGAGTAGAAATGC	19						TAACCAGGAGTAGAAATGC	19	3	3	1
168	PC-168-5p	TCAAATCGGACCTACGGCT	19						TCAAATCGGACCTACGGCT	19	7	7	1
169	PC-169-3p	GGGGGCTGCAGAGTGAACC	19						GGGGGCTGCAGAGTGAACC	19	3	3	1
170	PC-170-5p	CTGGCACCCAGGCTCCATC	19						CTGGCACCCAGGCTCCATC	19	3	3	1
171	PC-171-3p	GTTTATGTATGTGTATATGTATA	23						GTTTATGTATGTGTATATGTATA	23	28	28	1
172	PC-172-5p	ATTGTGATTTTCCTTGGAA	19						ATTGTGATTTTCCTTGGAA	19	38	49	2
173	PC-173-3p	TGCTGGACATCAGGAGACT	19						TGCTGGACATCAGGAGACT	19	3	3	1
174	PC-174-3p	TTGGACCTGAGCTCAGGCA	19						TTGGACCTGAGCTCAGGCA	19	3	3	1
175	PC-175-3p	TCTGTGAACTAGAAACCTCTGG	22						TCTGTGAACTAGAAACCTCTGG	22	4	4	1
176	PC-176-3p	AGGATGTAGACATAGAAGGAG	21						AGGATGTAGACATAGAAGGAG	21	9	9	1
177	PC-177-5p	TGGACTGGATGACAATCTGCAGG	23						TGGACTGGATGACAATCTGCAGG	23	27	36	2
178	PC-178-3p	GTGGTGCGGGTGGGTGGGT	19						GTGGTGCGGGTGGGTGGGT	19	3	3	1

179	PC-179	cttgtgcctaagtgtcacgtcacagtttctaatctctgtcatatccTGTGATGATGGGCAGCTTAGCtgattatgtgccgg	81	8	-	118720077	118720157									PC-179-3p	TGTGATGATGGGCAGCTGAGC	21						TGTGATGATGGGCAGCTGAGC	21	5	5	1
180	PC-180	cgcccgttacgtcgGCCGCCGGCCGCGCGCGCGCccgcctcccccgcgaccgcggctccgggagccgcttccggcggcgtgaggttctggttc	93	9	-	137827	137919									PC-180-5p	GCCCCCGGCCGCGCGCGCGC	20	GCCCCCGGCCGCGCGCGCGC	20	6	6	1	GCCCCCGGCCGCGCGCGCGC	20	3	3	1
181	PC-181	gttcCCATTGTGGAGCAGCAGAAatgaacccaactatggactataaggttcaggttcaatctctggcttcgctcagtgggtt	83	9	-	1149380	1149462									PC-181-5p	CCATTGTGGACCAGCAGAA	19						CCATTGTGGACCAGCAGAA	19	9	9	1
182	PC-182	acagccaggcgctgctgcacgcccagcccatcgtcagcatccgcgTGTGGGGCGTCGGGCGGGACagcggaaggtgggggcgcg	84	9	-	2620488	2620571									PC-182-3p	TGAGGGGCGTCGGGCGGGAC	20	TGAGGGGCGTCGGGCGGGA	19	4	8	2	TGAGGGGCGTCGGGCGGGAC	20	6	10	2
183	PC-183	tcAGTCTCCTGGCTGGCTCGCCAgttgctgggctgcgccctaccggcctgcaagccctgtactggctcagcctcaagaccaa	82	9	+	6137609	6137690									PC-183-5p	CGTCTCCTGGCTGGCTCGCCA	21	CGTCTCCTGGCTGGCTCGCCA	21	12	12	1	CGTCTCCTGGCTGGCTCGCCA	21	10	10	1
184	PC-184	gcatcagttgttactccaacagggccgcgtctccagcctccgagccacACTGGAGACACGTGCACTGTAGAaatacacctgagcc	84	9	+	6808350	6808433									PC-184-3p	ACTGGAGACACGTGCACTGTAGA	23						ACTGGAGACACGTGCACTGTAGA	23	3	3	1
185	PC-185	cggctgtgcaacacgggtattcacttctgcacacgttaaGAATATGTCAGGGCTGGAGttcccatcgtggcgcagcgga	80	9	+	10181129	10181208									PC-185-3p	GAATTTGTCAGGGCTGGAG	19						GAATTTGTCAGGGCTGGAG	19	23	23	1
186	PC-186	gtttggacaacccatgcacagccagagtgaaggcttcctCTCCACCTGAGCAGGGGTTcagtccatca	68	9	+	20919179	20919246									PC-186-3p	CTCCACCTGAGCAGAGGTT	19						CTCCACCTGAGCAGAGGTT	19	5	5	1
187	PC-187	tatgagttgtggtataggtcacagacccagctcagatctggtgttgctgtggctgtggTGTAGGCCTGAGCTATAGCtccga	82	9	+	34656689	34656770									PC-187-3p	TGTAAGCCTGAGCTATAGC	19						TGTAAGCCTGAGCTATAGC	19	5	5	1
188	PC-188	gaaGGGGAAGGGCGGGAGGGGCttgtgttccccaccaccgagaacagagcccttgcagccctcacccaaa	70	9	+	38167345	38167414	9	-	38355285	38355354					PC-188-5p	GGGGAAGGGCGGGAGCGGC	19	GGGGAAGGGCGGGAGCGGC	19	5	5	1					
189	PC-189	aagaagaacaccggggcagggtgtgtgtgtgtgtgtgtgtgtGCGCGCGCGCGCGTGTGCACGGcggtgtctttcc	78	9	+	45200560	45200637	9	+	45292749	45292826					PC-189-3p	GCGCGCGCGCGCGTGTGCGCGG	22	GCGCGCGCGCGCGTGTGCGCGG	22	23	23	1	GCGCGCGCGCGCGTGTGCGCGG	22	9	9	1
190	PC-190	GCTTGGCTTGGAGTCAGAAGGCctgggtcccagtggctcaccactgtgtgacctggggcctgacattgaacatccccgagcc	82	9	+	45484804	45484885									PC-190-5p	GCTGGGCTTGGAGTCAGAAGGC	22	GCTGGGCTTGGAGTCAGAAGGC	22	3	3	1	GCTGGGCTTGGAGTCAGAAGGC	22	3	3	1
191	PC-191	ttttggacttaatccctgaaacgaatacttaagacaggtttaattggttctgtacgTGTCTCAGTGGGACCTCCAtcg	78	9	+	53870457	53870534	9	-	53921770	53921847					PC-191-3p	TGTCTCGGTGGGACCTCCA	19	TGTCTCGGTGGGACCTCCA	19	4	4	1	TGTCTCGGTGGGACCTCCA	19	3	3	1
192	PC-192	ccagggcgcgcccccgccGCCCTCGGCCGCGCGCGCGCtctgcccgccctcctcgcgcgtgctcgtgctcgcggccgcggcggcgcgcctctt	93	9	-	54632020	54632112									PC-192-5p	GCCCCCGGCCGCGCGCGCGC	20	GCCCCCGGCCGCGCGCGCGC	20	6	6	1	GCCCCCGGCCGCGCGCGCGC	20	3	3	1
193	PC-193	ctaagcaaagggaggaatttaacattaaatCTAATTCAGAATTGTGATTactgtcttcaactggacattgcagtttctgaattgaggctgttagggactaatgtgttg	110	9	-	55593342	55593451									PC-193-5p	GTAATTCAGAATTGTGATT	19						GTAATTCAGAATTGTGATT	19	3	3	1
194	PC-194	ccaggagaaaCTCATGGTTGGGCTGAAGGaaaacactcatcttcagccatgtatggaatggctctgtc	68	9	-	61437426	61437493									PC-194-5p	CTCATGGTTGGGCTGCAGG	19						CTCATGGTTGGGCTGCAGG	19	32	42	3
195	PC-195	tcagctttttacgtgtttacatgaggtttgcagagtgtgggTCTAAGTAGGCATAGGAAGAgcaag	66	9	+	72529977	72530042									PC-195-3p	TCTAAGTAGGCGTAGGAAGA	20	TCTAAGTAGGCGTAGGAAGA	20	3	3	1					
196	PC-196	atcactaatataaCAAATTGGATCAGACAAAAatgcccttatttccctggtatcttgttatttcactattacaatgttttaattagtaag	91	9	+	79211129	79211219									PC-196-5p	CATATTGGATCAGACAAAA	19						CATATTGGATCAGACAAAA	19	3	3	1
197	PC-197	ccaggTGGCTCAGTCGTAACGAACcagactagtatccatgaggatgcaggttcaatccctggccccact	69	9	-	94977928	94977996									PC-197-5p	TGGCTCAGTCGTAACGAAC	19						TGGCTCAGTCGTAACGAAC	19	5	5	1
198	PC-198	tgacaggtgaggcttgaaaatattagtattcttgttctagaATACATGATGATCTCACCCTaacttgaac	72	9	+	108993733	108993804									PC-198-3p	ATACATGATGATCTCACCCT	20	ATACATGATGATCTCACCCT	20	5	5	1					
199	PC-199	gcatgcggagtttcccaggctagggTCAAATCGGAGCTACGGCTgccggcctatgccacagccacagccacgctgatcgagccatgtctgagacctacacca	104	9	+	115972854	115972957									PC-199-5p	TCAAATCGGACCTACGGCT	19						TCAAATCGGACCTACGGCT	19	7	7	1
200	PC-200	agaggtctggtctgcactgaGGGCAGGTGGATCTGGAGTaacggtgctgtgaagtccagcaaacaccagcgctctaactggacaggcgtgaccaca	95	9	-	128187949	128188043	9	-	128376476	128376570					PC-200-5p	AGGCAGGTGGATCTGGAGT	19	AGGCAGGTGGATCTGGAGT	19	3	3	1					
201	PC-201	ggtgctgattcTGGAGACTGGGAAGACATAattgtttaaccctctgtgttgtcctctgctccagaatacatgcttt	77	9	+	131098991	131099067									PC-201-5p	TGGAGACTTGGAAGACATA	19						TGGAGACTTGGAAGACATA	19	11	11	1
202	PC-202	agaggtatctgaattttaaaaAAGGGAGTTGATTGATTAAttgattgattgattgattgtcttttctagggctgtacccga	81	9	+	132262428	132262508									PC-202-5p	AAGGGTGTTGATTGATTAA	19	AAGGGTGTTGATTGATTAA	19	3	3	1					
203	PC-203	tcacTCAGTCTCCATGGCCTTCCctgagctctaaggggcgggttcaacagaggctgatcagggaagggaggggacgctgaga	83	10	-	8177008	8177090									PC-203-5p	TCAGTCTCCATGGCCTTCC	19						TCAGTCTCCATGGCCTTCC	19	4	4	1
204	PC-204	tgccctcatagctctggcaaacacaacattggatcaacctcattatattttactgactCTTGAGTTGTTGTCATGGCctgattatttggact	93	10	-	9079852	9079944									PC-204-3p	CTGGAGTTGTTGTCATGGC	19						CTGGAGTTGTTGTCATGGC	19	3	3	1
205	PC-205	taaagatgggctTGATTTCAGATAAACTGTTgtcacaacattttatcatcagtttttcttagcaaaatctaca	73	10	+	16301388	16301460									PC-205-5p	TGATTTCAGAAAAACTGTT	19						TGATTTCAGAAAAACTGTT	19	3	3	1
206	PC-206	gatggcggcggcgtcggaggagcggATGGCTGAGGAAGGAGGCGGCGgccacggcgacggcggctcctcttcggctatcggctgcacccagcgactgcccccaccgc	107	10	+	21123019	21123125									PC-206-5p	ATGGCTGAGGAAGGAGGCGGC	21						ATGGCTGAGGAAGGAGGCGGC	21	3	6	2
207	PC-207	cccaaagCAAGAAGGATTTGTAGAAAagttaatttaaaacttggtaaatgggctcttctgcaaggtttgttttaac	75	10	+	36281835	36281909									PC-207-5p	CAAGAAGGATTAGTAGAAA	19						CAAGAAGGATTAGTAGAAA	19	6	6	1
208	PC-208	acgtggctcagatctggtggtgttgtggctgtggtGTAGGCCGGCGCCTGTAGCtctgattcaacc	66	10	-	57005556	57005621									PC-208-3p	GTAGGCCGCCGCCTGTAGC	19						GTAGGCCGCCGCCTGTAGC	19	5	5	1
209	PC-209	ttaaggatctggcgttgctgtgagctggggtgTAGGTCACAGACACGGCGTggatcctgtg	61	10	+	61345224	61345284									PC-209-3p	TAGGTCAAAGACACGGCGT	19						TAGGTCAAAGACACGGCGT	19	4	4	1
210	PC-210	aagctggccgtgtccgctgtgggggcagcaccCAGGGCAGGGCAGGGCGGGGcagagccgtctcagagcacatgtcctgggcgcccgctccacacctcggaccacggtcag	111	11	+	2375881	2375991									PC-210-5p	CAGGGCAGGGCAGGGCGGGA	20						CAGGGCAGGGCAGGGCGGGA	20	4	4	1
211	PC-211	gggtttgcagtggttgagttccggacgttacttcttaaggacttccccacatcaagggttgTCTGATCAAGGTTGTTACCCAGCC	84	11	-	7423052	7423135									PC-211-3p	TCTGATCAAGGTTGTTACCCAGCC	24						TCTGATCAAGGTTGTTACCCAGCC	24	3	3	1
212	PC-212	gttTCAAGATTGCAGGTATCCTCTGTAttgcgatgcttttggagaaagactcccaggatggggcatgagggagggtttgcagtgttgag	89	11	-	7423119	7423207									PC-212-5p	TCAAGATTGCAGGTATCCTCTGTA	24						TCAAGATTGCAGGTATCCTCTGTA	24	18	36	4
213	PC-213	tcctccctcaTGTGTCCTCTGATTGCTTTCCATGGTctggagcgttttcatccatgttcttaaagccatgagcaatcgcagggactttggaggaa	96	11	-	7511699	7511794									PC-213-5p	TGTGTCCTCTGATTGCTTTCCATGGT	26						TGTGTCCTCTGATTGCTTTCCATGGT	26	3	3	1
214	PC-214	aaagagaccagatggCTCTGACACCATCAGGATAaaatccaaattccctcaggtgccattcaggcctttgcacaatctggtctcagt	87	11	+	9966839	9966925									PC-214-5p	CTCTGGCACCATCAGGATA	19						CTCTGGCACCATCAGGATA	19	4	4	1
215	PC-215	aatctcttacttggaatatggattgagtttggcgctaactcagaggactacaggcaagtaTTCAGGACATAGCCAGAGGgatatt	85	11	+	17606545	17606629									PC-215-3p	TTCAGGACATAACCAGAGG	19						TTCAGGACATAACCAGAGG	19	3	3	1
216	PC-216	gttcccattgTGGCTCAGCGGCAATGAACccaaccagtatccatgaggacgtgggttcaatccccggctttgctcagtgggtta	84	11	+	19873929	19874012									PC-216-5p	TGGCTCATCGGCAATGAAC	19						TGGCTCATCGGCAATGAAC	19	4	4	1
217	PC-217	agcagcacttcccatatggtctagcggttaggatttcctggtttcacccaggcggcccggGTTCGACTCCCGGTATGGGAACGttgcaac	90	11	+	24760354	24760443									PC-217-3p	GTTCGACTCCCGGTATGGGAACC	23						GTTCGACTCCCGGTATGGGAACC	23	3	3	1
218	PC-218	gtctctctgagggGATCCCACTGGGGCCTCCAggatatgttgtagaatacccagaaatcacctcagagaaca	72	11	-	33534925	33534996	11	-	33632117	33632188					PC-218-5p	GATCCCAGTGGGGCCTCCA	19						GATCCCAGTGGGGCCTCCA	19	8	8	1
219	PC-219	ctactctagtggttcgggttgggtgcttcacccctacagcctgggttcaattCCTGGTCTGAGAACTGAGAtcccacatcaagccgctgcacactggggcca	103	11	-	68033653	68033755	11	-	68153156	68153258					PC-219-3p	CCTGGTCTGAGAACTCAGA	19						CCTGGTCTGAGAACTCAGA	19	3	3	1
220	PC-220	agtggaattacattaatatgaaggaaatcacatatgattgCATGTGTGTGCATGTGCACatgtgtgtatgtgtgtgcgtgcgtgtggttttaaacgtttctgtaatgagttcccaa	116	11	-	69581588	69581703									PC-220-5p	CATGTGTCTGCATGTGCAC	19						CATGTGTCTGCATGTGCAC	19	3	3	1
221	PC-221	gcagggagCGGGGCTGGAGGTGGGAGGGCtcggagagctcaactggggctgctcgagggccggcgatcagacctcagatccgctgcttt	89	11	+	79607387	79607475									PC-221-5p	CGGGGCTGGAGGAGGGAGGGC	21						CGGGGCTGGAGGAGGGAGGGC	21	15	15	1
222	PC-222	cgtgagctgtggtgtaggtcacagatgcagctcggatcccatgctgctgtggctgtggtGTAGGCCTGCGACTGTAGCttcaa	83	12	-	3749393	3749475									PC-222-3p	GTAGGCCTGCGACTCTAGC	19						GTAGGCCTGCGACTCTAGC	19	3	3	1
223	PC-223	cgagcgacgagagccaccgtcacccgcggctcaaggacactcgcgatgcggCGGCGGCGGCGGCGACTCCGGGcggc	77	12	-	4609395	4609471									PC-223-3p	CGGCGGCGGCGGCGACTCTGGG	22						CGGCGGCGGCGGCGACTCTGGG	22	3	3	1
224	PC-224	taccaccttgcctgaatttcttgctggcttcatcagtttctattgATCCAGGAAGGCCAAGAACcctggtccgtgata	79	12	-	13651628	13651706									PC-224-3p	ATCGAGGAAGGCCAAGAAC	19						ATCGAGGAAGGCCAAGAAC	19	3	3	1
225	PC-225	cagctgcagtccctcatccccaacaatgacgtgagggggctcatttctcatgttatccggACGTTGAAGATGGACTGCTCTGAGC	85	12	+	15837537	15837621									PC-225-3p	ACGTTGAAGATGGACTGCTCCGAGC	25						ACGTTGAAGATGGACTGCTCCGAGC	25	4	4	1
226	PC-226	cgtctgtcacTCTCACTCTGAGGCTGGAGaaggagactggaattgacagtgcagaggggcaggaggacagcag	73	12	+	16259952	16260024									PC-226-5p	TCTCACTCTGAGGCAGGAG	19						TCTCACTCTGAGGCAGGAG	19	4	4	1
227	PC-227	gcagccgcctcatggctcgctcataatcctccgggtccgggggctgcggcggcgagcggcGCGGCGCGGGCGGGAGGAGgggcgggcggggaggcgcgggctgcggg	107	12	-	16480765	16480871									PC-227-3p	GCGGCGCGGGCGGGTGGAG	19						GCGGCGCGGGCGGGTGGAG	19	4	4	1
228	PC-228	tgtggtgTAGGTCACAGACACGGCGTggatctggcattgccgtggctgtggcgtagaccagc	62	12	-	20823931	20823992	12	-	20895608	20895669					PC-228-5p	TAGGTCAAAGACACGGCGT	19						TAGGTCAAAGACACGGCGT	19	4	4	1
229	PC-229	taagcagctcttaagccctgcaagtcagagcctcactctgtgCCTTCCAGGACTGAAGAAGctgccag	68	12	-	23105346	23105413									PC-229-3p	CCTACCAGGACTGAAGAAG	19						CCTACCAGGACTGAAGAAG	19	5	5	1
230	PC-230	acccTGAATCCGGCACGTCAGGTtatacaaataaattgaggcaactccgttttctggaaaatttgttagatgcagaaa	78	12	+	24439602	24439679									PC-230-5p	TGAATCCGGCACGTCAGGT	19						TGAATCCGGCACGTCAGGT	19	6	6	1
231	PC-231	tatcgtgcagcttctctgccatgttttcttgcgcgTAGCACTGAGAGGTCTGTACGTATCC	62	12	-	24443832	24443893									PC-231-3p	TAGCACTGAGAGGTCTGTATGTATCC	26						TAGCACTGAGAGGTCTGTATGTATCC	26	6	6	1
232	PC-232	acaagctTGGCTGGACTGTGAAAAGAtctgcctactttctcagacagtccctccaagttggg	62	12	+	27163466	27163527									PC-232-5p	CGGCTGGACTGTGAAAAGA	19						CGGCTGGACTGTGAAAAGA	19	7	7	1
233	PC-233	gggagtTCCCTGGTCTAGTGGTTAGGATTTGGtgtgctcactgctgcagcctaggtttaagccctggtctgggaactgag	80	12	-	40808305	40808384									PC-233-5p	TCCCTGGTCTAGTGGTTAGGATTCGG	26						TCCCTGGTCTAGTGGTTAGGATTCGG	26	158	158	1
234	PC-234	aaaatctattggactgaagatgccctgggcctggccttagccCGGATTCCAGGCTGCAACTtcctcacttgatcct	76	12	+	45042670	45042745									PC-234-3p	CGGATTGCAGGCTGCAACT	19						CGGATTGCAGGCTGCAACT	19	3	3	1
235	PC-235	ccctggtggtctggtggttaggatttggcactttcactactgcagtccaggttcaatcCCTGGTCTGAGAACTGAGAccccacatcaagctgctgcactctgtggccaaaa	111	12	+	46400192	46400302									PC-235-3p	CCTGGTCTGAGAACTCAGA	19						CCTGGTCTGAGAACTCAGA	19	3	3	1
236	PC-236	tggtctgggtcagagtcagtctggggtcaaggccagggttGTGGTGCTGGTGGGTGGGTgagactcagcctggtacctcgtctgggcagggactggggctcagtggcggtgaagta	119	12	+	48081172	48081290									PC-236-5p	GTGGTGCGGGTGGGTGGGT	19						GTGGTGCGGGTGGGTGGGT	19	3	3	1
237	PC-237	cagcgaagactcAGGGGCTTGAGAAATGGCTaggaagccaacccaccctattggttgagagctgtggtctcagaggctccgaggattcgggg	91	12	-	50606828	50606918									PC-237-5p	AGGGGCTGGAGAAATGGCT	19						AGGGGCTGGAGAAATGGCT	19	7	7	1
238	PC-238	ATAGGCCAGCCGCTATAGCtctgattggaccccctagcctgggaacctccatatgctgtgagtgtggcccta	71	14	+	3354384	3354454									PC-238-5p	ATAGGCCAGCCGCTATTGC	19						ATAGGCCAGCCGCTATTGC	19	3	3	1
239	PC-239	caacgggcactcctaatgttttgttttgttgtttttttaattataaaAAGGAACCTGAAAAGAGAGccttggggagtctgatc	85	14	+	9572326	9572410									PC-239-3p	AAGGAACCTGAAAACAGAG	19						AAGGAACCTGAAAACAGAG	19	3	3	1
240	PC-240	actttcctctatttctacACTCTGCAGAGCAAGCTGGcaaattactagcattcttaggcagtttagaaagggagggagga	80	14	-	11939845	11939924									PC-240-5p	ACTCTGTAGAGCAAGCTGG	19						ACTCTGTAGAGCAAGCTGG	19	3	3	1
241	PC-241	ccctgaaatcacttatggcctggaatgggctcattccaactaagggCCCTGGGCTGTAGATTTCGata	68	14	+	16319123	16319190									PC-241-3p	CCCTGGGCTGTAGATTTCA	19						CCCTGGGCTGTAGATTTCA	19	6	6	1
242	PC-242	aaccgtcactgtaaatcatcaaaagcttaacaaacGTGGAGTTGTTGTCATGGCtcagcggtgacgaac	69	14	+	17508038	17508106									PC-242-3p	CTGGAGTTGTTGTCATGGC	19						CTGGAGTTGTTGTCATGGC	19	3	3	1
243	PC-243	caacatgtaaaacattacgtcctttgctccttgcaaaacttttttAGGGTGTCTGCTTTTATTTTcatgggc	71	14	+	36957400	36957470									PC-243-3p	AGGGTGTCTGTTTTTATTT	19	AGGGTGTCTGTTTTTATTT	19	3	3	1					
244	PC-244	ctggtggtctagtggttaggactcagtgctttcagtgctgcaagctgagttcaatcCCTGGTCTGAGAACTGAGAttctatattaagctacagc	94	14	-	40612326	40612419									PC-244-3p	CCTGGTCTGAGAACTCAGA	19						CCTGGTCTGAGAACTCAGA	19	3	3	1
245	PC-245	tggcagaagctgggggtcttcgacttgtttttttTAGTTGAAGTGGAACTCGTTTCTGGAa	61	14	+	40701684	40701744									PC-245-3p	TAGTTGAAGTGGAACTCGTTTCTGGT	26						TAGTTGAAGTGGAACTCGTTTCTGGT	26	3	3	1
246	PC-246	gtATAGGCCGGAAGCTGTAGCtcagattcaacccctagcctgggaaccttcatatgctgtgcgtgccgccctaaaa	76	14	+	41026092	41026167									PC-246-5p	ATAGGCCGCAAGCTGTAGC	19						ATAGGCCGCAAGCTGTAGC	19	5	5	1
247	PC-247	gcagacttttcttggtggaagagatttgactgtaggcagtgaatcctgctgtgcttgtTTGAGACTCTTTCGCCATGAAGATagtcaaa	89	14	-	42961929	42962017									PC-247-5p	TTGAGACTCTTTCGCCATGAAGAT	24						TTGAGACTCTTTCGCCATGAAGAT	24	4	4	1
248	PC-248	ccggggggaaggttacaatgttatgcttacagctTGTGAAGAATATCTGTTATCGTCTCCtgtg	65	14	+	43084470	43084534	14	-	42970651	42970715					PC-248-3p	TGTGAAGAATATCTGTTATCGTCTCC	26						TGTGAAGAATATCTGTTATCGTCTCC	26	8	8	1
249	PC-249	cgggacagggcagtctggctggagcagtggggtctgagagagcagtaaccctctagcccTGCTACCTGGAGGCTCTGTCCTGGg	85	14	+	43089470	43089554	14	-	42965615	42965699					PC-249-3p	TGCTACCTGGAGGCTCTGTCCTGG	24						TGCTACCTGGAGGCTCTGTCCTGG	24	5	5	1
250	PC-250	acgtagggccaagcgcgccgctggagtcagagccaatggcggCGGCGGCGGCGGCTCTGGAa	62	14	+	44815938	44815999									PC-250-3p	CGGCGGCGGCGACTCTGGA	19	CGGCGGCGGCGACTCTGGA	19	299	299	1	CGGCGGCGGCGACTCTGGA	19	99	99	1
251	PC-251	aactatggTTTTCTCTGAATAGATGCCCAGAATtgggatcaatggatcatacggtagttcttttaatttttctgagaaacctccatactc	90	14	+	51963459	51963548	14	-	8198199	8198288					PC-251-5p	TTTTCTCTGAATAGATGCCCAGAAC	25						TTTTCTCTGAATAGATGCCCAGAAC	25	15	15	1
252	PC-252	acccagggttaggacaggatccacaactcctgcagggagATCCTGTATCAGATCCTGAaa	60	14	+	54585542	54585601									PC-252-3p	ATCCTGTATCAGATCCTGA	19						ATCCTGTATCAGATCCTGA	19	15	15	1
253	PC-253	ttgatctttTTTGGATCCATGTGGTACTtgccaatgatggatcctttagaagatgat	57	14	-	54679464	54679520									PC-253-5p	TTTGGATCGATGTGGTACT	19	TTTGGATCGATGTGGTACT	19	3	3	1	TTTGGATCGATGTGGTACT	19	3	3	1
254	PC-254	ccaggaGTGGGAAGGACCAGAGGTGcggtcaagggcaaagagctgctatttccaaatagccctctgctccccatcctgctcccac	85	14	-	77864669	77864753									PC-254-5p	GTGGGAAGGAGCAGAGGTG	19	GTGGGAAGGAGCAGAGGTG	19	3	3	1					
255	PC-255	cacgtgttacttTGTGAAGCTTTGCTAGACTCTCTCTggaagtttctctctcacagggctctagtgtagccatttttacaagttctgtaatgcctg	96	14	+	83584887	83584982									PC-255-5p	TGTGAAGCTTTGCTAGACTCTCTCT	25						TGTGAAGCTTTGCTAGACTCTCTCT	25	4	4	1
256	PC-256	ttctgccgcagaggccaaaggctaagagcaaattcaaggtatctttcttttccagcccTAGAAGCTTAGAGTTTTGTTCTAGActtttacccacacaggcaagg	104	14	+	83596598	83596701									PC-256-3p	TAGAAGCTTAGAGTTTTGTTCTAGA	25						TAGAAGCTTAGAGTTTTGTTCTAGA	25	3	3	1
257	PC-257	ctctgaagagctgtagagcatttcagcagcacctcctttgtcacattaacaggctccaTGTGATGGGACTGATTCCTTgtgccctatttctaggctcatcacct	104	14	+	83602614	83602717									PC-257-3p	TGTGATGGGACTGATTCCTT	20						TGTGATGGGACTGATTCCTT	20	3	3	1
258	PC-258	tttttttttttctgtaatttggatggttttacagaggtgtcatcAAGCCTCAAGCTACAGACTcattattgaagaagaaacac	84	14	-	87667820	87667903									PC-258-3p	AAGGCTCAAGCTACAGACT	19						AAGGCTCAAGCTACAGACT	19	3	3	1
259	PC-259	cttctggtctggactctgagctccagcctccccattctcctggctgaagccCCATCCTTCCAGGCACAGCtc	72	14	+	110282677	110282748									PC-259-3p	CCATCCTTCCAGGCCCAGC	19						CCATCCTTCCAGGCCCAGC	19	4	4	1
260	PC-260	agtgtggtgtaggtcacagatacagcttggatccagtgttggctgtggctgtggctatggcATAGGCCGGAAGCTGTAGCtctgattgacccctagcctgaacctc	106	14	+	118385291	118385396									PC-260-3p	ATAGGCCGCAAGCTGTAGC	19						ATAGGCCGCAAGCTGTAGC	19	5	5	1
261	PC-261	ttCTGTGTGTTATTGTTAACAcattgtgcatttatgttgggtctcagtttccttctgcacagtgtgatgcagttcagcata	81	14	-	124927456	124927536									PC-261-5p	CTGTGGGTTATTGTTAACA	19	CTGTGGGTTATTGTTAACA	19	26	26	1	CTGTGGGTTATTGTTAACA	19	5	5	1
262	PC-262	tcaatccagaaaaCAAGAAAGATTAGTAGAAAtaaactttgattaaaaaaaaaaaaaggtttaaaaaaaattaaacatttttctctgtagggt	92	14	+	125589337	125589428									PC-262-5p	CAAGAAGGATTAGTAGAAA	19						CAAGAAGGATTAGTAGAAA	19	6	10	2
263	PC-263	ttccattgccatgggtgcagccattaaaaaaaaaaaaaaaaaaagatggagttcctgttgTGGCTCAGCGGCAATGAAC	78	14	-	134018935	134019012									PC-263-3p	TGGCTCATCGGCAATGAAC	19						TGGCTCATCGGCAATGAAC	19	4	4	1
264	PC-264	ctccctggtgatctagtggtcaggactcagctctttcaccactatggcctggactcaatgCCTGGTCTGAGAACTGAGAtcctacatcaagccactgcacactatggcca	110	14	-	141832329	141832438	14	-	141905608	141905717					PC-264-3p	CCTGGTCTGAGAACTCAGA	19						CCTGGTCTGAGAACTCAGA	19	3	3	1
265	PC-265	cctctcttcacttccggcctcgctcggtgccctcCTGGGCTGGATGGGAGGTGaggggtca	61	14	-	147755794	147755854									PC-265-3p	CTGGGCGGGATGGGAGGTG	19						CTGGGCGGGATGGGAGGTG	19	7	7	1
266	PC-266	gcagccagGGGTTGTGATGAGGACTCAgggggcttccgtcctggaaagcctcatcctcctggtgtt	66	15	+	23522146	23522211									PC-266-5p	GGGATGTGATGAGGACTCA	19						GGGATGTGATGAGGACTCA	19	5	5	1
267	PC-267	gcagttcccatatggtctagcggttaggattcctggttttcacccaggcggcccggGTTCGACTCCCGGTATGGGAACAcg	81	15	-	29171436	29171516									PC-267-3p	GTTCGACTCCCGGTATGGGAACC	23						GTTCGACTCCCGGTATGGGAACC	23	3	3	1
268	PC-268	gtacctcagaatgtgactttatttggaaattgggtctttacagagacatgCTAAAATGAGGTCACAGGAgggac	74	15	-	42519943	42520016									PC-268-3p	CTAAAATGAGGACACAGGA	19						CTAAAATGAGGACACAGGA	19	4	4	1
269	PC-269	tTAGGAAAGGACATGTGACTgagagaaaggaagtaaacgagtgaactctacagtcacctggactttctgcc	71	15	+	43096080	43096150									PC-269-5p	TAGGAAAGGACGTGTGACT	19						TAGGAAAGGACGTGTGACT	19	4	4	1
270	PC-270	tttttcttttACATTCTCTGCTCCTTTTTTtcgttattgttataaagtagtgattgtggagagaattgggagaaaagtatgaaaaagga	89	15	+	55174428	55174516	15	-	55124427	55124515					PC-270-5p	ACATTCTCTGTTCCTTTTT	19						ACATTCTCTGTTCCTTTTT	19	27	27	1
271	PC-271	ctgctgtgagctgtggtgtatgtcgcagatgtggcttgaatctagcattgctgtggctctGGCATAGGCTGATTAGACCcatagcctgggaacttccatagttcgcaggtgcggccc	117	15	+	70274482	70274598	15	+	70442174	70442290					PC-271-3p	GGCATGGGCTGATTAGACC	19						GGCATGGGCTGATTAGACC	19	16	20	2
272	PC-272	ttaaccactgagccaTGACGGGAACTCCTTACCATTCagattttagaaaatgactaggttgggagttcctgttgtggctcagtggtaac	89	15	+	71640343	71640431									PC-272-5p	TGACGGGAACTCCTTACCATTC	22						TGACGGGAACTCCTTACCATTC	22	5	5	1
273	PC-273	aatgcagatctcagtgtcatcatggccctttacaagatcaaaaaggaattttttttcgttTAAGGACTTGGTGATGGTAggagaatgtcgc	90	15	+	82309250	82309339	15	-	82510573	82510662					PC-273-3p	TAAGGACTTGATGATGGTA	19						TAAGGACTTGATGATGGTA	19	61	61	1
274	PC-274	atacggaagacagagaaagacagAGTTGTTCTGGTAGGGGAGCtaagagtctgttgggttttcctgaccagctcaaacctctttttcccaccttgcggac	100	15	+	102867585	102867684	15	-	102721025	102721124					PC-274-5p	AGTTGATCTGGTAGGGGAGC	20						AGTTGATCTGGTAGGGGAGC	20	4	7	2
275	PC-275	gtaggctgcagatggatctggcattgctgtggctgtggcATAGGCCGGAAGCTGTAGCtcta	62	15	-	106146587	106146648									PC-275-3p	ATAGGCCGCAAGCTGTAGC	19						ATAGGCCGCAAGCTGTAGC	19	5	5	1
276	PC-276	GGAGAATTTAGTAGTAAATctgtcacagtataatttaaaagcaagatgtgcccaatatttataatttcattcagg	75	15	+	108547214	108547288									PC-276-5p	GGAGGATTTAGTAGTAAAT	19						GGAGGATTTAGTAGTAAAT	19	3	3	1
277	PC-277	aaagccatcatttttggaagttccctggtggcctgGTGGTTAGGAGCTTTCACTgctgaggccaa	65	15	-	121165858	121165922									PC-277-3p	GTGGTGAGGAGCTTTCACT	19						GTGGTGAGGAGCTTTCACT	19	119	119	1
278	PC-278	tccctggtggtctagtggttaggattggtgcttcactgctgtggcccaggttcCCTGGTCTGAGAACTGAGAgctcacatcaaatccctacaggctgcaaccagatt	109	15	+	129673201	129673309									PC-278-3p	CCTGGTCTGAGAACTCAGA	19						CCTGGTCTGAGAACTCAGA	19	3	3	1
279	PC-279	ggagggaatgcctgggGGGCCGGGCGGTGGTGGCGgcggcgcccgagggccagcgccaccccccccccccccccgggaacccgcg	85	15	-	131466125	131466209									PC-279-5p	GGGCCGGGCGGTGGTGGCG	19	GGGCCGGGCGGTGGTGGCG	19	8	8	1	GGGCCGGGCGGTGGTGGCG	19	3	3	1
280	PC-280	ctagaggtaagggctgcctccagcctccattctcatgactggtgagTGTCCAGAGGGCGGAACGGcacaaaagcagctctccatctccag	90	15	-	132643979	132644068									PC-280-3p	TGTCCAGAGGGCTGAACGG	19						TGTCCAGAGGGCTGAACGG	19	4	7	2
281	PC-281	ctctcaggccctcattagctcagctggagccttcgcatatACAGGACCTTGGCATGGACaccctgctaatgtttccaggcatcctttcacctcgagagaaggaggggttgacag	113	15	-	132673789	132673901									PC-281-5p	ACAGGACCTTGGCATGGAC	19						ACAGGACCTTGGCATGGAC	19	8	8	1
282	PC-282	ggaactacagcccagCCCATGGACCTCTCTGATCccacatggtagtcctgtatcccctcccgggatgtgtggaggtagggggttgtaagtggta	94	15	+	133832625	133832718									PC-282-5p	CCCAGGGACCTCTCTGATC	19						CCCAGGGACCTCTCTGATC	19	7	7	1
283	PC-283	ttaggattcagtgttttcactgctatggtctaggttcagtcCCTGGTCTGAGAACTAAGAacccaca	67	16	-	8436462	8436528									PC-283-3p	CCTGGTCTGAGAACTCAGA	19						CCTGGTCTGAGAACTCAGA	19	3	3	1
284	PC-284	gtagcattcagaagttctagtggatataggagttcctgtcatggctcaGGGGATGATGTATCTGACTagggtccatgaggatgcagg	87	16	+	25008563	25008649									PC-284-3p	TGGGATGATGTATCTGACT	19						TGGGATGATGTATCTGACT	19	16	16	1
285	PC-285	ccttgtcatggtAGGGTTTTGTCTGCTTTGTcaccactgtacatctagccttagaaacacattgacaaat	70	16	+	28893231	28893300									PC-285-5p	AGGGTTTTGTCTGCTCTGT	19						AGGGTTTTGTCTGCTCTGT	19	5	5	1
286	PC-286	aatgggcccaggaatctatattgttaagaagtagcacccgataattctgacatgcTGGGAACTACTGCTTTGCAGCAagaatatccctttttggtcctca	99	16	+	49529363	49529461									PC-286-3p	TGAGAACTACTGCTTTGCAGCA	22						TGAGAACTACTGCTTTGCAGCA	22	3	3	1
287	PC-287	ctttcCACCATCCCTTCCTTCCTTaaaaatactttgacaggattgagatggtggagga	58	16	+	58716707	58716764									PC-287-5p	CACCATGCCTTCCTTCCTT	19						CACCATGCCTTCCTTCCTT	19	5	5	1
288	PC-288	agcaaaggcgcttccctgaatcactgcaccatccaaggctgccaggtgacagctggcatctTTGGCTGCTGTAGTGGACCaggcagtgtatgttgctcca	100	16	-	66332556	66332655									PC-288-3p	TTGGCTGCTGTAATGGACC	19						TTGGCTGCTGTAATGGACC	19	7	12	2
289	PC-289	tctttatgtcttcatccattcatggacatttaaGTTGTTCCTGAACCTTGGCtactaggcataatgc	67	16	+	71084744	71084810									PC-289-3p	GTAGTTCCTGAACCTTGGC	19						GTAGTTCCTGAACCTTGGC	19	6	6	1
290	PC-290	gagagctgatagtcaatgaatctgaagtttgaaagcgcagcatcccgcagaatcaggtCAGGGTTATGTGACTGAGCtgct	81	16	-	74241218	74241298									PC-290-3p	CAGGGTTATGTGACAGAGC	19						CAGGGTTATGTGACAGAGC	19	78	78	1
291	PC-291	gaaattcactaagagagtagacttaagttttcccactacacatacacacaattgaaccatATGATGTGAAGGATAGGTTaatttgcttgattggggcaatcatt	104	17	+	4030704	4030807									PC-291-3p	ATGATGTGTAGGATAGGTT	19	ATGATGTGTAGGATAGGTT	19	5	5	1					
292	PC-292	gcTGTGGGGCGTCGGGCGGGAtcccattatcgcggtgtttgcttggggctgcccagcgcctccgccta	68	17	+	30731396	30731463									PC-292-5p	TGAGGGGCGTCGGGCGGGA	19	TGAGGGGCGTCGGGCGGGA	19	4	4	1					
293	PC-293	acaggatttagcttatttaaaagtgtttgatttgcattcaATTGATGTAGGATGAGTCCaca	61	17	-	31542493	31542553									PC-293-3p	ATTGATGTAGGATGAATCC	19	ATTGATGTAGGATGAATCC	19	3	3	1					
294	PC-294	CCACTAGCCCTGCTGTGGCcgtcttaccattggcatggaagtccagggtggaggacgcattcccaagagaactgctggc	79	17	+	33520810	33520888									PC-294-5p	CCACTAGCCCTGCTGGGGC	19	CCACTAGCCCTGCTGGGGC	19	16	16	1					
295	PC-295	cttccgcagggggcgcccttgcccaaccctccctaaatccctgggctcctgcccCCGGTGCGCCCCCGCCGGCtg	75	17	+	43396695	43396769	17	-	43689890	43689964					PC-295-3p	CCGGTGCGCCCCCGGCGGC	19	CCGGTGCGCCCCCGGCGGC	19	3	3	1					
296	PC-296	gtagaaaGAAGGAGGCAGAGACAGGAtactggtctgcctgaggctggatgcagacagaatcctggagctggctgcctgagtcatc	85	17	-	48914488	48914572									PC-296-5p	GAAGGAGGCAGAGACAGGA	19	GAAGGAGGCAGAGACAGGA	19	31	31	1					
297	PC-297	cagtcAGGGACCCAGGAGACAAATctagatggacgttgactgggaaccacctgaggg	57	17	-	50402325	50402381									PC-297-5p	AGGGACCTAGGAGACAAAT	19	AGGGACCTAGGAGACAAAT	19	19	19	1					
298	PC-298	ttggcgctgctcctcgctCAGAGCTGTGGGCACGGTGgccagcgtgcttccagactctcacgctccgtccgcagcgcggg	80	18	-	638836	638915									PC-298-5p	CAGAGCTGTGAGCACGGTG	19	CAGAGCTGTGAGCACGGTG	19	5	5	1					
299	PC-299	aaaATCTACAGATTGTCGAGATGGAGAaaatagtagagttttgcagacgagctgtaggtcat	62	18	+	8777643	8777704									PC-299-5p	ATCTACAGATTGTCGAGATGGAGA	24	ATCTACAGATTGTCGAGATGGAGA	24	4	4	1					
300	PC-300	ggtgctctgtcatgGACTCTGTTGCCCACTGGAtgatgatctcattcttcttattggcttactttgggtttttgagcctt	81	18	+	9936632	9936712									PC-300-5p	GACTCTGTTGCCCAATGGA	19	GACTCTGTTGCCCAATGGA	19	3	3	1					
301	PC-301	aggggagatgggacacttggtaatgtctgcggCACCTGCCCTCTGCACGTGGGCtgtgaggatgggtagcccagggcaggggtcaggaaccctgggcttacttctagatccaca	114	18	-	15647628	15647741									PC-301-5p	CACCTGCCCTCTGCACGTGGGC	22	CACCTGCCCTCTGCACGTGGGC	22	5	5	1					
302	PC-302	atATTGGCACTGCACATAATTGCtcagagcggagagacacaagcaaaaatgtgctagtgccaaaat	66	18	+	17171997	17172062									PC-302-5p	ATTGGCACTGCACATGATTGC	21	ATTGGCACTGCACATGATTGC	21	6	6	1					
303	PC-303	gtctctgctctgtTTATGGCCCTTCGGTAATTCACTgaccgagactgttcacagtgaattctaccagtgccatacacagaacaggagt	88	18	+	17172229	17172316									PC-303-5p	TTATGGCCCTTCGGTAATTCACT	23	TTATGGCCCTTCGGTAATTCACT	23	6	6	1					
304	PC-304	tgtggtgtggtgtgtgggtgtgggtgtGGGTGTGGTGTGGGTGTGGGtttgtcctgactgctgtgaccttgactaaatgatctttgcacttggacctct	99	18	+	41660291	41660389									PC-304-5p	CGGTGTGGTGTGGGTGTGGG	20	CGGTGTGGTGTGGGTGTGGG	20	4	4	1					
305	PC-305	accctgtagatcttcaaagagtagggactagatgaaatccaacataacattcaggagttcCCATTGTGGAGCAGCAGAAa	80	X	-	9559780	9559859									PC-305-3p	CCATTGTGGACCAGCAGAA	19						CCATTGTGGACCAGCAGAA	19	9	9	1
306	PC-306	taactttctagcagacctcagttctctcaagagtTCTACTGTGAGGGCTGAGGtcggttaccaaggat	68	X	-	9857208	9857275	X	-	10007257	10007324					PC-306-3p	TCTACTGTGAGGACTGAGG	19						TCTACTGTGAGGACTGAGG	19	3	3	1
307	PC-307	ccgccacccaatatggcagaactcaagctatttctaaactcggggcctgcCTGGAGTTCTTGTCATGGCtcagtggtta	79	X	+	14901779	14901857									PC-307-3p	CTGGAGTTGTTGTCATGGC	19						CTGGAGTTGTTGTCATGGC	19	3	3	1
308	PC-308	acctgcttaaacgcgtgtgtacgcacatgtatgcacgtgtacACATGTGTACGCATGTGTActgcattc	69	X	+	20900275	20900343	X	-	21036978	21037046					PC-308-3p	GCATGTGTACGCATGTGTA	19						GCATGTGTACGCATGTGTA	19	29	29	1
309	PC-309	ttcccagtgtttgtgagtctcctggtccttctaattttctcatttttctgaatgtagcccATGAGAAGGTCCTGGTAGAtcctgctgggcca	92	X	+	55669052	55669143	X	-	55385622	55385713	X	-	55520745	55520836	PC-309-3p	ATGAGAAGGTCCTGGCAGA	19						ATGAGAAGGTCCTGGCAGA	19	7	7	1
310	PC-310	tgcatgtgtctttttgagttagcgtttctgtttttttctggatataTAACCAGGAGTAGAACTGCtgggccataat	76	X	-	68738973	68739048									PC-310-3p	TAACCAGGAGTAGAAATGC	19						TAACCAGGAGTAGAAATGC	19	3	3	1
311	PC-311	TGTGTGTGTGTGTGTGAGTGTGAATgaattaatccaggtatatcatttcatataatg	57	X	+	73931162	73931218									PC-311-5p	TGAGTGTGTGTGTGTGAGTGTGAAT	25						TGAGTGTGTGTGTGTGAGTGTGAAT	25	4	4	1
312	PC-312	caATCTACCAAAATCGCTTGGccttagattatttacttgtttctgaaggaggggttttgtggaaaa	66	X	+	74667082	74667147									PC-312-5p	ATCTACAAAAATCGCTTGG	19						ATCTACAAAAATCGCTTGG	19	5	5	1
313	PC-313	actttgcaatcaaactgaatccctttttattttatagttttgctagtaataaaagcaaAAAGACTATAAAATAAAAAGGaattcagtttgatttgtcaacac	102	X	-	76729946	76730047									PC-313-3p	AAAGACTATAAAATAAAAAGG	21						AAAGACTATAAAATAAAAAGG	21	8	8	1
314	PC-314	aaaggtgttctggagAGGGAACCTGGAAAAGCTGAAGgtgtaatatgaaaacctcagcaattcttggttctcatttttaggacatcaat	89	X	-	76730882	76730970									PC-314-5p	TCAGCAATTCTTGGTTCTCATTT	23						TCAGCAATTCTTGGTTCTCATTT	23	13	30	4
314	PC-314	aaaggtgttctggagAGGGAACCTGGAAAAGCTGAAGgtgtaatatgaaaacctcagcaattcttggttctcatttttaggacatcaat	89	X	-	76730882	76730970									PC-314-3p	AGGGAACCTGGAAAAGCTGAAG	22						AGGGAACCTGGAAAAGCTGAAG	22	41	78	3
315	PC-315	cgtggctcagatccctcagatgctgtggctgtggctgtggctgtggctgtggctgtggcATAGGCCGGAAGCTGTAGCtgtgatgtgaccctta	94	X	+	85144244	85144337									PC-315-3p	ATAGGCCGCAAGCTGTAGC	19						ATAGGCCGCAAGCTGTAGC	19	5	5	1
316	PC-316	cagtctgtcagttctatcagtactgttgataattcaatcaagtttgggtttctggagttcCCATTGTGGATCAGCAGAAatgaactggactagt	94	X	+	93065671	93065764									PC-316-3p	CCATTGTGGACCAGCAGAA	19						CCATTGTGGACCAGCAGAA	19	9	9	1
317	PC-317	tttccacctccattttggcagTACAGATGTCCTGAGAAACacacacctgtgccaggagtggagatgctgaagagggatttgtggaagatggagcagtggc	100	X	-	99435849	99435948									PC-317-5p	TACATATGTCCTGAGAAAC	19						TACATATGTCCTGAGAAAC	19	4	4	1
318	PC-318	gttcCCATTGTGGATCAGCAGAAacggatcaaactaggaagcataaggttgcaagtttgatccctggcctcactcagtgggtt	83	X	-	100110551	100110633									PC-318-5p	CCATTGTGGACCAGCAGAA	19						CCATTGTGGACCAGCAGAA	19	9	9	1
319	PC-319	tatttgaGATTCAGATTTGTATAGTGgttaatagcgtagactctaaagactctggagccagatatcctgaaatttgaatcttggccc	86	X	+	100680341	100680426									PC-319-5p	GATTCAGATTTGTATAGTG	19						GATTCAGATTTGTATAGTG	19	5	5	1
320	PC-320	ggtgcagtgccctgcccaggcaggtgctgatcacttagtctctgggtCAACAGTCCCTGCCTGGGTAGAgtaaggctca	79	X	+	117267529	117267607									PC-320-3p	CAACAGTCCCTGCCTGGGTAGA	22						CAACAGTCCCTGCCTGGGTAGA	22	409	935	6
321	PC-321	ccaacccagggaggtgctgttcacctagactgcatgTGAACAGGGCCTTTCTGGGTCGAgt	61	X	+	117268042	117268102									PC-321-5p	TGAACAGGGCCTTTCTGGGTCGA	23						TGAACAGGGCCTTTCTGGGTCGA	23	531	1611	13
321	PC-321	ccaacccagggaggtgctgttcacctagactgcatgTGAACAGGGCCTTTCTGGGTCGAgt	61	X	+	117268042	117268102									PC-321-3p	AACCCAGGGAGGTGCTGTTCACC	23						AACCCAGGGAGGTGCTGTTCACC	23	193	500	11
322	PC-322	cggtgccctatccagacaggtgctgttctcttgacgactgcTGAACGGCGCCTGTGTGGTTAGAgcaagg	70	X	+	117270803	117270872									PC-322-5p	TGAACGGCGCCTGTGTGGTTAGA	23						TGAACGGCGCCTGTGTGGTTAGA	23	388	938	14
322	PC-322	cggtgccctatccagacaggtgctgttctcttgacgactgcTGAACGGCGCCTGTGTGGTTAGAgcaagg	70	X	+	117270803	117270872									PC-322-3p	TATCCAGACAGGTGCTGTTCT	21						TATCCAGACAGGTGCTGTTCT	21	199	856	13
323	PC-323	gccgtgctgtgtgtggtgcccTGACCAGGCAGGTGCTGTTCTCTcgacgagtagtgaacggtgcctgtgtggctagagtaaggctcacaagaacatc	97	X	+	117271810	117271906									PC-323-5p	TGACCAGGCAGGTGCTGTTCTCT	23						TGACCAGGCAGGTGCTGTTCTCT	23	47	115	6
324	PC-324	gagccattcagcgtgcagtgcttttcacaagaaggtgtcaattcaggtggactaaaatatgAATGGCGCTTTTTTGTGAAGAgtaatggaccaccatgtaaggcaca	106	X	-	118198291	118198396									PC-324-5p	AATGGCGCTTTTTTGTGAAGA	21						AATGGCGCTTTTTTGTGAAGA	21	332	646	7
324	PC-324	gagccattcagcgtgcagtgcttttcacaagaaggtgtcaattcaggtggactaaaatatgAATGGCGCTTTTTTGTGAAGAgtaatggaccaccatgtaaggcaca	106	X	-	118198291	118198396									PC-324-3p	TTCACAAGAAGGTGTCAATTCA	22						TTCACAAGAAGGTGTCAATTCA	22	27	34	2
325	PC-325	cagtgcccTACTCAGGAAGGCATTATTCACAtagttggaaatatgaatggcgcctttctgagtagagcaatg	72	X	-	118218736	118218807									PC-325-5p	TGAATGGCGCCTTTCTGAGTAGAA	24						TGAATGGCGCCTTTCTGAGTAGAA	24	18	64	6
325	PC-325	cagtgcccTACTCAGGAAGGCATTATTCACAtagttggaaatatgaatggcgcctttctgagtagagcaatg	72	X	-	118218736	118218807									PC-325-3p	TACTCAGGAAGGCATTATTCACA	23						TACTCAGGAAGGCATTATTCACA	23	20	56	4
326	PC-326	aacttcagttgagtgtggtgccctactccaaagggtgtcattcatacagactaatacatgACTGTCACCTTTTTGAGTAGAGtaatgcacatcatttgtgaaata	105	X	-	118227198	118227302									PC-326-5p	ACTGTCACCTTTTTGAGTAGAA	22						ACTGTCACCTTTTTGAGTAGAA	22	68	272	29
326	PC-326	aacttcagttgagtgtggtgccctactccaaagggtgtcattcatacagactaatacatgACTGTCACCTTTTTGAGTAGAGtaatgcacatcatttgtgaaata	105	X	-	118227198	118227302									PC-326-3p	TACTCCAAAGGGTGTCATTCAT	22						TACTCCAAAGGGTGTCATTCAT	22	16	16	1
327	PC-327	tctgtgcagtgcctcactccaaagagtgccaatcaggtacattaaaatatgATTGGCACTTTTTAGAGTGTGGtaattcacagc	84	X	-	118233387	118233470									PC-327-3p	ATTGGCACTTTTTAGAGTGTGA	22						ATTGGCACTTTTTAGAGTGTGA	22	295	307	3

Supplementary Table 5. Porcine unique miRNAs

The list of unique miRNAs ranked by the average percent of the most abundant isomiR (i.e., unique miRNA) counts against the total counts of the mappable sequences (i.e., the "% average" column).

ID	miRNA name	Consensus miRNA sequence	% average	Ovary		Testis	
				counts of mappable sequences: 12,010,853		counts of mappable sequences: 9,815,024	
				# counts	% of mappable	# counts	% of mappable
1	miR-21-5p	TAGCTTATCAGACTGATGTTGAC	7.46	901,056	7.50	728,247	7.42
2	let-7i-5p	TGAGGTAGTAGTTTGTGCTGTT	3.83	357,715	2.98	460,146	4.69
3	let-7f-5p	TGAGGTAGTAGATTGTATAGTT	3.49	351,377	2.93	397,795	4.05
4	miR-143-3p	TGAGATGAAGCACTGTAGCTCG	2.41	390,545	3.25	154,700	1.58
5	let-7a-5p	TGAGGTAGTAGGTTGTATAGTT	1.71	181,948	1.51	187,951	1.91
6	let-7c-5p	TGAGGTAGTAGGTTGTATGGTT	1.59	157,247	1.31	182,862	1.86
7	miR-148a-3p	TCAGTGCACTACAGAACTTTGT	1.53	213,739	1.78	125,809	1.28
8	miR-34c-5p	AGGCAGTGTAGTTAGCTGATTGC	1.32	130,113	1.08	153,583	1.56
9	miR-24-1-3p, miR-24-2-3p	TGGCTCAGTTCAGCAGGAACAG	1.24	141,747	1.18	128,462	1.31
10	miR-29a-3p	TAGCACCATCTGAAATCGGTT	0.91	101,184	0.84	96,154	0.98
11	miR-101-1-3p, miR-101-2-3p	TACAGTACTGTGATAACTGAAG	0.70	83,429	0.69	69,188	0.70
12	miR-27b-3p	TTCACAGTGGCTAAGTTCTGC	0.31	53,837	0.45	17,545	0.18
13	let-7g-5p	TGAGGTAGTAGTTTGTACAGTT	0.29	30,971	0.26	31,834	0.32
14	miR-30d-5p	TGTAAACATCCCCGACTGGAAGC	0.25	28,240	0.24	25,106	0.26
15	miR-125b-1-5p	TCCCTGAGACCCTAACTTGTGA	0.24	34,713	0.29	18,800	0.19
16	miR-320-3p	AAAAGCTGGGTTGAGAGGGCGA	0.23	23,359	0.19	25,308	0.26
17	miR-23a-3p	ATCACATTGCCAGGGATTTCCA	0.22	28,630	0.24	20,750	0.21
18	miR-140-3p	ACCACAGGGTAGAACCACGGAC	0.20	24,195	0.20	19,008	0.19
19	miR-29b-3p	TAGCACCATTTGAAATCAGTGTT	0.16	18,091	0.15	16,914	0.17
20	miR-27a-3p	TTCACAGTGGCTAAGTTCCGC	0.16	18,594	0.15	15,445	0.16
21	miR-199a-5p	CCCAGTGTTCAGACTACCTGTTC	0.13	27,112	0.23	3,253	0.03
22	miR-30e-5p	TGTAAACATCCTTGACTGGAAGCT	0.13	16,053	0.13	11,433	0.12
23	PN(a)-15-5p	AGAGGTAGTAGGTTGCATAGTT	0.12	13,111	0.11	13,128	0.13
24	miR-100-5p	AACCCGTAGATCCGAACTTGTG	0.12	13,403	0.11	12,641	0.13
25	miR-99a-5p	AACCCGTAGATCCGATCTTGT	0.12	22,631	0.19	4,268	0.04
26	miR-26a-5p	TTCAAGTAATCCAGGATAGGCT	0.11	17,587	0.15	7,673	0.08
27	miR-103-1-3p, miR-103-2-3p	AGCAGCATTGTACAGGGCTATGA	0.10	11,325	0.09	9,750	0.10
28	miR-186-5p	CAAAGAATTCTCCTTTTGGGCTT	0.09	12,221	0.10	8,212	0.08
29	miR-221-5p	ACCTGGCATACAATGTAGATTTCT	0.09	10,314	0.09	9,027	0.09
30	miR-424-5p	CAGCAGCAATTCATGTTTTGA	0.08	14,618	0.12	4,296	0.04
31	PC-86-3p	ATGCGGAACCTGCGGATACGG	0.08	18,663	0.16		\
32	miR-423-3p	AGCTCGGTCTGAGGCCCCTCAGT	0.08	9,556	0.08	6,967	0.07
33	miR-199a-3p, miR-199b-3p	ACAGTAGTCTGCACATTGGTT	0.07	14,605	0.12	2,422	0.02
34	PN(a)-7-3p	TCGTACCGTGAGTAATAATGCG	0.07	13,020	0.11	2,697	0.03
35	miR-145-5p	GTCCAGTTTTCCCAGGAATCCCT	0.07	14,311	0.12	1,618	0.02
36	PN(a)-3-5p	TGGAAGACTAGTGATTTTGTTGTT	0.07	8,092	0.07	6,552	0.07
37	miR-130a-3p	CAGTGCAATGTTAAAAGGGCATT	0.07	7,828	0.07	6,659	0.07
38	miR-99b-5p	CACCCGTAGAACCGACCTTGCG	0.06	7,888	0.07	6,115	0.06
39	miR-744-5p	TGCGGGGCTAGGGCTAACAGCA	0.06	7,153	0.06	6,080	0.06
40	miR-30b-5p	TGTAAACATCCTACACTCAGCT	0.06	6,732	0.06	5,318	0.05
41	miR-30c-5p	TGTAAACATCCTACACTCTCAGCT	0.05	6,573	0.05	4,266	0.04
42	miR-27a-5p	AGGGCTTAGCTGCTTGTGAGCA	0.05	5,179	0.04	5,188	0.05
43	miR-22-3p	AAGCTGCCAGTTGAAGAACTGT	0.05	5,338	0.04	4,725	0.05
44	miR-30a-5p	TGTAAACATCCTCGACTGGAAGCT	0.04	6,965	0.06	2,545	0.03
45	miR-191-5p	CAACGGAATCCCAAAAGCAGCTGT	0.04	5,315	0.04	3,482	0.04
46	miR-425-5p	AATGACACGATCACTCCCGTTGA	0.04	4,094	0.03	4,453	0.05
47	PN(a)-53-5p	AAACCGTTACCATTACTGAGTT	0.04	5,259	0.04	3,319	0.03
48	PN(a)-71-5p	TTTGGCAATGGTAGAACTCACACT	0.04	4,897	0.04	2,997	0.03
49	miR-221-3p	AGCTACATTGTCTGCTGGGTTTC	0.03	3,418	0.03	3,646	0.04
50	miR-28-3p	CACTAGATTGTGAGCTCCTGGA	0.03	4,105	0.03	2,597	0.03
51	miR-23b-3p	ATCACATTGCCAGGGATTACCA	0.03	4,993	0.04	1,835	0.02
52	miR-152-3p	TCAGTGCATGACAGAACTTGG	0.03	4,977	0.04	1,591	0.02
53	miR-139-5p	TCTACAGTGCACGTGTCTCCAGT	0.03	3,225	0.03	2,863	0.03
54	PN(a)-56-3p	TAACAGTCTACAGCCATGGTCG	0.03	5,526	0.05	676	0.01
55	miR-140-5p	CAGTGGTTTTACCCTATGGTAG	0.02	3,634	0.03	1,351	0.01
56	miR-532-5p	CATGCCTTGAGTGTAGGACCGT	0.02	3,983	0.03	881	0.01
57	PN(a)-42-5p	AGGCAGTGTAATTAGCTGATTGT	0.02	1,424	0.01	2,871	0.03
58	miR-195-5p	TAGCAGCACAGAAATATTGGCA	0.02	2,674	0.02	1,783	0.02
59	let-7e-5p	TGAGGTAGGAGGTTGTATAGTT	0.02	2,963	0.02	1,471	0.01
60	miR-98-5p	TGAGGTAGTAAGTTGTATTGTT	0.02	2,322	0.02	1,657	0.02
61	miR-193a-3p	AACTGGCCTACAAAGTCCCAGT	0.02	2,283	0.02	1,677	0.02
62	miR-151-5p	TCGAGGAGCTCACAGTCTAGTA	0.02		\	3,327	0.03
63	PN(a)-62-5p	TCTGGCTCCGTGTCTTCACTCC	0.02	1,873	0.02	1,727	0.02
64	PN(a)-7-5p	CATTATTACTTTTGGTACGCG	0.01	2,276	0.02	988	0.01
65	miR-574-3p	CACGCTCATGCACACACCCACA	0.01	2,906	0.02	452	0.00
66	miR-423-5p	TGAGGGGCAGAGAGCGAGACTTT	0.01	1,581	0.01	1,532	0.02
67	miR-374b-5p	ATATAATACAACCTGCTAAGTG	0.01	1,632	0.01	1,282	0.01
68	PN(a)-64-5p	TGGCAGTGTATTGTTAGCTGGT	0.01	122	0.00	2,428	0.02
69	miR-125a-5p	TCCCTGAGACCCTTTAACCTGT	0.01	2,312	0.02	605	0.01
70	PN(a)-42-3p	AATCACTAATTCCACTGCCATC	0.01	151	0.00	2,055	0.02
71	miR-202-5p	CTTCCTATGCATATACTTCTTT	0.01	1,035	0.01	1,252	0.01
72	miR-15a-5p	TAGCAGCACATAATGGTTTGTG	0.01	1,246	0.01	937	0.01
73	miR-34c-3p	AATCACTAACCACACGGCCAGG	0.01	974	0.01	1,112	0.01
74	miR-199b-5p	CCCAGTGTTTAGACTATCTGTTC	0.01	2,015	0.02	257	0.00
75	miR-30e-3p	CTTTCAGTCGGATGTTTACAGC	0.01	1,198	0.01	830	0.01
76	miR-21-3p	CAACAGCAGTCGATGGGCTGTC	0.01	1,113	0.01	893	0.01
77	PN(a)-8-5p	TGTAACAGCAACTCCATGTGGA	0.01	929	0.01	756	0.01
78	miR-222-3p	AGCTACATCTGGCTACTGGGTCTC	0.01	773	0.01	750	0.01
79	miR-1307-5p	TCGACCGGACCTCGACCGGCT	0.01	1,130	0.01	404	0.00
80	miR-151-3p	CTAGACTGAAGCTCCTTGAGGA	0.01		\	1,206	0.01
81	miR-378-3p	CACTGGACTTGGAGTCAGAAGGC	0.01	715	0.01	616	0.01
82	miR-181c-5p	AACATTCAACCTGTCGGTGAGT	0.01	630	0.01	678	0.01
83	miR-142-3p	TGTAGTGTTTCCTACTTTATGG	0.01	1,176	0.01	124	0.00
84	miR-143-5p	GGTGCAGTGCTGCATCTCTGG	0.01	1,154	0.01	138	0.00
85	miR-183-5p	TATGGCACTGGTAGAATTCACT	0.01	853	0.01	382	0.00
86	miR-497-5p	CAGCAGCACACTGTGGTTTGTA	0.01	758	0.01	444	0.00
87	miR-505-3p	GTCAACACTTGCTGGTTTCCTCT	0.01	632	0.01	537	0.01
88	miR-486-5p	TCCTGTACTGAGCTGCCCCGAG	0.01	573	0.00	550	0.01
89	miR-676-3p	CCGTCCTAAGGTTGTTGAGTT	0.01	1,135	0.01	76	0.00
90	miR-181a-1-3p	ACCATCGACCGTTGATTGTACC	0.01	574	0.00	526	0.01
91	miR-326-3p	CCTCTGGGCCCTTCCTCCAGT	0.01	5	0.00	985	0.01
92	miR-29c-3p	TAGCACCATTTGAAATCGGTT	0.00	719	0.01	385	0.00
93	PN(a)-19-5p	TGATATGTTTGATATTGGGTTG	0.00	516	0.00	501	0.01
94	miR-500-5p	TAATCCTTGCTACCTGGGTGAGA	0.00	815	0.01	199	0.00
95	miR-107-3p	AGCAGCATTGTACAGGGCTAT	0.00	458	0.00	440	0.00
96	miR-708-3p	CAACTAGACTGTGAGCTTCTAG	0.00	473	0.00	406	0.00
97	miR-124a-1-3p, miR-124a-2-3p	TAAGGCACGCGGTGAATGCCAA	0.00	425	0.00	437	0.00
98	miR-324-5p	CGCATCCCCTAGGGCATTGGTGT	0.00	473	0.00	395	0.00
99	miR-125b-1-3p	ACGGGTTAGGCTCTTGGGAGCT	0.00	453	0.00	409	0.00
100	PN(a)-51-5p	TAGGTAGTTTCATGTTGTTGGG	0.00	451	0.00	365	0.00
101	PN(a)-64-3p	TCAGCTAACATGCAACTGCTGT	0.00	10	0.00	725	0.01
102	miR-133a-3p	TTGGTCCCCTTCAACCAGCTGT	0.00	647	0.01	194	0.00

103	miR-210-3p	CTGTGCGTGTGACAGCGGCTGA	0.00	396	0.00	349	0.00
104	PN(a)-15-3p	CTATACGACCTGCTGCCTTTCT	0.00	492	0.00	269	0.00
105	miR-455-5p	TATGTGCCTTTGGACTACATCGT	0.00	451	0.00	293	0.00
106	PN(a)-67-5p	TGAGAACTGAATTCCATGGGTT	0.00	602	0.01	161	0.00
107	PN(a)-14-5p	TGAGGTAGTAGATTGTATAGTTG	0.00	328	0.00	351	0.00
108	miR-331-3p	GCCCCTGGGCCTATCCTAGA	0.00	409	0.00	273	0.00
109	miR-127-3p	TCGGATCCGTCTGAGCTTGGCT	0.00	626	0.01	81	0.00
110	miR-148b-3p	TCAGTGCATCACAGAACTTTGTTT	0.00	317	0.00	289	0.00
111	miR-139-3p	TGGAGACGCGGCCCTGTTGGAGT	0.00	331	0.00	264	0.00
112	PC-321-5p	TGAACAGGGCCTTTCTGGGTCGA	0.00		\	531	0.01
113	PN(a)-79-3p	TGATTGGCACCTCTTTGAGTGA	0.00	8	0.00	508	0.01
114	miR-122-5p	TGGAGTGTGACAATGGTGTTTGT	0.00	335	0.00	223	0.00
115	miR-192-5p	CTGACCTATGAATTGACAGCC	0.00	312	0.00	237	0.00
116	miR-22-5p	AGTTCTTCAGTGGCAAGCTTT	0.00	272	0.00	266	0.00
117	miR-148a-5p	AAAGTTCTGAGACACTCCGACT	0.00	334	0.00	174	0.00
118	miR-181b-1-5p, miR-181b-2-5p	AACATTCATTGCTGTCG	0.00	3	0.00	438	0.00
119	miR-128-1-3p, miR-128-2-3p	TCACAGTGAACCGGTCTCTTT	0.00	271	0.00	210	0.00
120	miR-181c-3p	ACCATCGACCGTTGAGTGGACC	0.00	243	0.00	225	0.00
121	miR-365-1-3p, miR-365-2-3p	TAATGCCCCTAAAAATCCTTAT	0.00	255	0.00	202	0.00
122	PC-320-3p	CAACAGTCCCTGCCTGGGTAGA	0.00		\	409	0.00
123	PC-322-5p	TGAACGGCGCCTGTGTGGTTAGA	0.00		\	388	0.00
124	miR-708-5p	AAGGAGCTTACAATCTAGCTGGGT	0.00	208	0.00	184	0.00
125	miR-328-3p, PN(b)-2-5p	CTGGCCCTCTCTGCCCTTCCGT	0.00	217	0.00	173	0.00
126	PC-250-3p	CGGCGGCGGCGACTCTGGA	0.00	299	0.00	99	0.00
127	miR-365-2-5p	AGGGACTTTCAGGGGCAGCTGTG	0.00	195	0.00	181	0.00
128	PN(a)-31-5p	TGGCACAGGGTCCAGCTGTCGGC	0.00	252	0.00	132	0.00
129	PC-324-5p	AATGGCGCTTTTTTGTGAAGA	0.00		\	332	0.00
130	miR-7-5p	TGGAAGACTAGTGATTTTGTTGTT	0.00	206	0.00	157	0.00
131	miR-455-3p	GCAGTCCATGGGCATATACAC	0.00	345	0.00	22	0.00
132	PN(a)-69-5p	AGGAAGCCCTGGAGGGGCTGGAC	0.00	203	0.00	132	0.00
133	miR-34a-5p	TGGCAGTGTCTTAGCTGGTTGT	0.00	309	0.00	45	0.00
134	miR-27b-5p	AGAGCTTAGCTGATTGGTGAAC	0.00	184	0.00	145	0.00
135	PC-327-3p	ATTGGCACTTTTTAGAGTGTGA	0.00		\	295	0.00
136	miR-29a-5p	ACTGATTTCTTTTGGTGTTCAG	0.00	188	0.00	132	0.00
137	miR-500-3p	ATGCACCTGGGCAAGGATTCTGA	0.00	279	0.00	57	0.00
138	PN(a)-1-5p	TGATATGTTTGATATATTAGGTTG	0.00	178	0.00	138	0.00
139	miR-19a-3p	ATTTGTGCAAATCTATGCAAAACTC	0.00	192	0.00	125	0.00
140	miR-135-1-5p, miR-135-2-5p	TATGGCTTTTTATTCCTATGTGA	0.00	227	0.00	92	0.00
141	miR-28-5p	AAGGAGCTCACAGTCTATTGAGT	0.00	159	0.00	136	0.00
142	PC-86-5p	ATGTCCGCGGGTTCCCTATCC	0.00	322	0.00		\
143	PN(a)-39-5p, PN(a)-66-5p	TTGTGCTTGATCTAACCATGT	0.00	265	0.00	40	0.00
144	miR-769-5p	TGAGACCTCTGGGTTCTGAGCT	0.00	204	0.00	85	0.00
145	miR-92b-3p	TATTGCACTCGTCCCGGCCTCC	0.00	240	0.00	53	0.00
146	miR-1307-3p	ACTCGGCGTGGCGTCGGTCGTGG	0.00	204	0.00	81	0.00
147	PN(a)-59-5p	TTAATGCTAATTGTGATAGGGGTT	0.00	283	0.00	15	0.00
148	PN(a)-46-3p	TAGCACCATTTGAAATCAGTGTTT	0.00	154	0.00	118	0.00
149	miR-215-5p	ATGACCTATGAATTGACAGACA	0.00	144	0.00	124	0.00
150	miR-214-5p	TGCCTGTCTACACTTGCTGTGC	0.00	227	0.00	56	0.00
151	miR-129-5p	CTTTTTGCGGTCTGGGCTTGC	0.00	178	0.00	89	0.00
152	miR-425-3p	CATCGGGAATGTCGTGTCCGCC	0.00	143	0.00	110	0.00
153	PN(a)-13-5p	TGAGGTAGTAGGTTGTATAGTTTT	0.00	126	0.00	116	0.00
154	miR-145-3p	ATTCCTGGAAATACTGTTCTT	0.00	226	0.00	30	0.00
155	PN(a)-62-3p	GAGGGAGGGACGGGGGCGGTGC	0.00	128	0.00	100	0.00
156	miR-369-3p	AATAATACATGGTTGATCTTT	0.00	134	0.00	91	0.00
157	PC-322-3p	TATCCAGACAGGTGCTGTTCT	0.00		\	199	0.00
158	miR-99a-3p	CAAGCTCGCTTCTATGGGTCTGT	0.00	194	0.00	38	0.00
159	PC-321-3p	AACCCAGGGAGGTGCTGTTCACC	0.00		\	193	0.00
160	miR-10a-3p	CAAATTCGTATCTAGGGGAAT	0.00	113	0.00	98	0.00
161	miR-369-5p	AGATCGACCGTGTTATATTCGC	0.00	108	0.00	97	0.00
162	PN(a)-63-5p	AGGCAGTGTATTGTTAGCTGGCTC	0.00	13	0.00	174	0.00
163	miR-30a-3p	CTTTCAGTCGGATGTTTGCAGC	0.00	150	0.00	62	0.00
164	miR-532-3p	CCTCCCACACCCAAGGCTTGCA	0.00	184	0.00	34	0.00
165	miR-204-5p	TTCCCTTTGTCATCCTATGCCT	0.00	147	0.00	64	0.00
166	miR-142-5p	CATAAAGTAGAAAGCACTACT	0.00	188	0.00	28	0.00
167	PN(a)-43-5p	TATGGCTTTTCATTCCTATGTGA	0.00	203	0.00	9	0.00
168	miR-99b-3p	CAAGCTCGTGTCTGTGGGTCCGT	0.00	98	0.00	94	0.00
169	let-7i-3p	CTGCGCAAGCTACTGCCTTGCT	0.00	101	0.00	82	0.00
170	PN(a)-22-3p	ACGCCCTTCCCCCCCTTCTTCA	0.00	152	0.00	40	0.00
171	PN(c)-2-3p	TCTCGCTGGGGCCTCCA	0.00	135	0.00	53	0.00
172	PC-233-5p	TCCCTGGTCTAGTGGTTAGGATTC	0.00		\	158	0.00
173	miR-361-5p	TTATCAGAATCTCCAGGGGTAC	0.00	127	0.00	49	0.00
174	miR-299-3p	TATGTGGGACGGTAAACCGCTT	0.00	166	0.00	9	0.00
175	PN(a)-27-5p	TCTCCCAACCCTTGTACCAGTG	0.00	124	0.00	38	0.00
176	miR-32-5p	TATTGCACATTACTAAGTTGC	0.00	92	0.00	58	0.00
177	miR-214-3p	ACAGCAGGCACAGACAGGCAGT	0.00	78	0.00	68	0.00
178	PN(a)-72-5p	TTTGGCACTAGCACATTTTTGCT	0.00	55	0.00	79	0.00
179	miR-324-3p	CCACTGCCCCAGGTGCTGCTGG	0.00	78	0.00	59	0.00
180	PC-277-3p	GTGGTGAGGAGCTTTCACT	0.00		\	119	0.00
181	PN(a)-12-3p	CTGCCCTGGCCCGAGGGACCGAC	0.00	115	0.00	25	0.00
182	miR-331-5p	TCTAGGTATGGTCCCAGGGATC	0.00	97	0.00	37	0.00
183	miR-504-5p	AGACCCTGGTCTGCACTCTATC	0.00	122	0.00	9	0.00
184	PN(a)-69-3p	TCCGGTTCTCAGGGCTCCACC	0.00	61	0.00	55	0.00
185	miR-129-3p	AAGCCCTTACCCCAAAAAGCAT	0.00	78	0.00	38	0.00
186	miR-340-5p	TTATAAAGCAATGAGACTGATT	0.00	67	0.00	45	0.00
187	miR-342-3p	TCTCACACAGAAATCGCACCCGT	0.00	84	0.00	28	0.00
188	PN(a)-34-5p	AAAAAGCATGCTCCAGTGGCGC	0.00	58	0.00	48	0.00
189	PN(a)-68-3p	AGGGTTGGGCGGAGGCTTTCCT	0.00	87	0.00	23	0.00
190	miR-497-3p	CAAACCACACTGTGGTGTTAGA	0.00	71	0.00	36	0.00
191	PC-120-5p	GCGCGCGCGCGTGTGCGCGGG	0.00	81	0.00	26	0.00
192	miR-503-5p	TAGCAGCGGGAACAGTACTGCAG	0.00	93	0.00	16	0.00
193	miR-193a-5p	TGGGTCTTTGCGGGCGAGATGA	0.00	85	0.00	21	0.00
194	miR-130b-3p	CAGTGCAATGATGAAAGGGCAT	0.00	88	0.00	17	0.00
195	miR-136-5p	ACTCCATTTGTTTTGATGATGG	0.00	100	0.00	5	0.00
196	miR-339-5p	TCCCTGTCCTCCAGGAGCTCACT	0.00	65	0.00	30	0.00
197	miR-130a-5p	GCTCTTTTCACATTGTGCTACT	0.00	54	0.00	38	0.00
198	PN(c)-7-3p	CTCCTGGCTGGCTCGCCA	0.00	53	0.00	37	0.00
199	miR-202-3p	AGAGGTGTAGGCATGGGAAAC	0.00	61	0.00	29	0.00
200	PC-290-3p	CAGGGTTATGTGACAGAGC	0.00		\	78	0.00
201	PN(a)-56-5p	ACCGTGGCTTTCGATTGTTACT	0.00	74	0.00	16	0.00
202	miR-30d-3p	CTTTCAGTCAGATGTTTGCTGC	0.00	44	0.00	37	0.00
203	PC-17-5p	GCGCGCGGTCGCCCGGGGA	0.00	62	0.00	22	0.00
204	PC-10-3p	TGGCTGACCTCTGACCTCC	0.00	88	0.00		\
205	miR-7-3p	CAACAAATCACAGTCTGCCATA	0.00	53	0.00	28	0.00
206	miR-222-5p	GGCTCAGTAGCCAGTGTAGATC	0.00	39	0.00	38	0.00
207	miR-16-2-3p	CCAGTATTAACTGTGCTGCTGAA	0.00	38	0.00	38	0.00
208	PC-326-5p	ACTGTCACCTTTTTGAGTAGAA	0.00		\	68	0.00
209	miR-127-5p	CTGAAGCTCAGAGGGCTCTGAT	0.00	82	0.00		\
210	PN(a)-57-3p	TAACAGTCTCCAGTCACGGCCA	0.00	72	0.00	7	0.00
211	miR-29c-5p	TGACCGATTTCTCCTGGTGTTCAG	0.00	39	0.00	33	0.00
212	PN(a)-54-3p	TACAGTATAGATGATG	0.00	54	0.00	20	0.00

213	miR-24-2-5p	GTGCCTACTGAGCTGATATCAGT	0.00	42	0.00	29	0.00
214	miR-196b-5p	TAGGTAGTTTCCTGTTGTTGGG	0.00	67	0.00	8	0.00
215	PC-273-3p	TAAGGACTTGATGATGGTA	0.00		\	61	0.00
216	miR-335-3p	TTTTTCATTATTGCTCCTGACC	0.00	44	0.00	25	0.00
217	miR-26a-3p	CCTATTCTTGGTTACTTGCACG	0.00	39	0.00	29	0.00
218	PN(a)-54-5p	GGATATCATCATATACTGTAAGT	0.00	41	0.00	27	0.00
219	miR-29b-5p	GCTGGTTTCATATGGTGGTTTAGA	0.00	35	0.00	31	0.00
220	PN(c)-6-3p	GTGCTGACAGTGCAGATA	0.00	43	0.00	23	0.00
221	miR-92a-1-3p, miR-92a-2-3p	TATTGCACTTGTCCCGG	0.00	36	0.00	26	0.00
222	PN(c)-12-5p	ACAAGTCAGGCTCTTGGGA	0.00	39	0.00	22	0.00
223	PN(a)-5-5p	AGTGGGGAACCCTTCCATGAGG	0.00	29	0.00	30	0.00
224	PN(a)-35-3p	AGAGTTGCGTCTGGACGTC	0.00	29	0.00	30	0.00
225	miR-24-1-5p	GTGCCTACTGAGCTGAAACA	0.00	28	0.00	28	0.00
226	miR-325-3p	TTTATTGAGCACCTCCTATCA	0.00	31	0.00	25	0.00
227	miR-363-3p	AATTGCACGGTATCCATCTGTA	0.00	41	0.00	16	0.00
228	PC-105-5p	TTGGAGCTGTTTAGAGAGACATGC	0.00		\	48	0.00
229	miR-186-3p	CCAAAGGTGAATTTTTTGGGA	0.00	32	0.00	21	0.00
230	PN(a)-57-5p	ACCTTGGCTCTAGACTGCTTACT	0.00	49	0.00	7	0.00
231	PC-144-5p	TCGTGTCTGGAAGCTGCCTCCTTC	0.00		\	47	0.00
232	PC-323-5p	TGACCAGGCAGGTGCTGTTCTCT	0.00		\	47	0.00
233	miR-152-5p	AGGTTCTGTGATACACTCCGACT	0.00	37	0.00	16	0.00
234	PN(a)-44-3p	ACAGTAGTCTGCACATTGGTAAGA	0.00	10	0.00	36	0.00
235	miR-30c-3p	CTGGGAGAAGGCTGTTTACTCT	0.00	35	0.00	15	0.00
236	PC-45-3p	TTACGTGGCTATTCTGATA	0.00	17	0.00	29	0.00
237	let-7e-3p	CTATACGGCCTCCTAGCTTTCC	0.00	37	0.00	12	0.00
238	PC-42-3p	CAGCAGGCTGTGGTGAAGG	0.00		\	41	0.00
239	PC-314-3p	AGGGAACCTGGAAAAGCTGAAG	0.00		\	41	0.00
240	PC-62-5p	CGAGTCCCACCCGGGGTAGG	0.00		\	40	0.00
241	miR-335-5p	TCAAGAGCAATAACGAAAAATGT	0.00	37	0.00	8	0.00
242	PC-172-5p	ATTGTGATTTTCCTTGGAA	0.00		\	38	0.00
243	PN(a)-5-3p	CTTATGCAAGATTCCCTTCTAC	0.00	22	0.00	20	0.00
244	miR-340-3p	TCCGTCTCAGTTACTTTATAGCC	0.00	25	0.00	16	0.00
245	PC-138-5p	AAGCTACTCTGGCACCATC	0.00		\	36	0.00
246	PC-94-3p	CGAATCACGTCGGGGTCATGG	0.00	44	0.00		\
247	PC-104-5p	TGTTTCTTTGACAAGCAGCCTGGT	0.00		\	34	0.00
248	PC-110-3p	AGGGGGCGGAGGGCCTGTGG	0.00	19	0.00	18	0.00
249	PN(a)-25-3p	GGTCCCCCGCCGTCCC	0.00	36	0.00	4	0.00
250	miR-424-3p	CAAAACGTGAGGCGCTGCTAT	0.00	28	0.00	10	0.00
251	miR-181d-5p	AACATTCATTGTTGTCGGT	0.00	16	0.00	19	0.00
252	PN(a)-77-5p	CGTCAACCATCCAGCTGTTTGG	0.00	27	0.00	10	0.00
253	PC-147-5p	ATTGTTGTGAAGGTTCTATGAATT	0.00		\	32	0.00
254	PC-194-5p	CTCATGGTTGGGCTGCAGG	0.00		\	32	0.00
255	PN(a)-63-3p	CAGCCACGACTACCCTGCCACT	0.00		\	31	0.00
256	PN(a)-20-3p	TTCACCACCTTCTCCACCCAGC	0.00	18	0.00	16	0.00
257	miR-301-5p	GCTCTGACTTTATTGCACTACT	0.00	18	0.00	16	0.00
258	miR-130b-5p	ACTCTTTCCCTGTTGCACTACT	0.00	33	0.00	3	0.00
259	PC-308-3p	GCATGTGTACGCATGTGTA	0.00		\	29	0.00
260	PC-93-5p, PC-221-5p	CGGGGCTGGAGGAGGGAGGGC	0.00	17	0.00	15	0.00
261	PC-149-3p	GTGCAAGGCTGAATTAGAC	0.00		\	28	0.00
262	PC-171-3p	GTTTATGTATGTGTATATGTATA	0.00		\	28	0.00
263	PC-189-3p	GCGCGCGCGCGCGTGTGCGCGG	0.00	23	0.00	9	0.00
264	PC-98-3p	CGCGGTCGCCCGGGGACGCCGG	0.00	34	0.00		\
265	PN(a)-77-3p	AAACATCTGGTTGGTTGAGAGA	0.00	29	0.00	4	0.00
266	PN(a)-23-3p	TCCGAGCCTGGGTCTCCCTCT	0.00	19	0.00	12	0.00
267	let-7f-3p	CTATACAGTCTACTGTCTTTCT	0.00	15	0.00	15	0.00
268	PC-177-5p	TGGACTGGATGACAATCTGCAGG	0.00		\	27	0.00
269	PC-270-5p	ACATTCTCTGTTCCTTTTT	0.00		\	27	0.00
270	PC-324-3p	TTCACAAGAAGGTGTCAATTCA	0.00		\	27	0.00
271	PN(a)-24-5p	GTCCGGTGCGGAGAGC	0.00	22	0.00	9	0.00
272	PC-37-5p	TGCGTGGCTTCTCTGTGCAGTC	0.00	33	0.00		\
273	PC-261-5p	CTGTGGGTTATTGTTAACA	0.00	26	0.00	5	0.00
274	PC-48-5p	AGGGGCGGCGCGGGGCGGG	0.00	32	0.00		\
275	PN(a)-33-3p	CTGGGAGAGGGTTGTTTACTCC	0.00	18	0.00	11	0.00
276	miR-15a-3p	CAGGCCATATTGTGCTGCCTCA	0.00	14	0.00	14	0.00
277	miR-103-2-5p	AGCTTCTTTACAGTGCTGCCTTG	0.00	14	0.00	14	0.00
278	PN(a)-29-3p	TAATACTGTCTGGTAATGCCGT	0.00	14	0.00	14	0.00
279	let-7a-3p	CTGTACAGCCTCCTAGCTTTCC	0.00	20	0.00	9	0.00
280	PC-296-5p	GAAGGAGGCAGAGACAGGA	0.00	31	0.00		
281	miR-224-5p	CAAGTCACTAGTGGTTCCGTTTAG	0.00	31	0.00		\
282	miR-100-3p	ACAAGCTTGTGTCTATAGGTAT	0.00	15	0.00	13	0.00
283	PC-70-5p	TAGGATGAGAAATAGAGCC	0.00		\	25	0.00
284	miR-217-5p	TACTGCATCAGGAACTGATTGGA	0.00	6	0.00	20	0.00
285	miR-499-5p	TAAGACTTGCAGTGATGTTTAGC	0.00	13	0.00	14	0.00
286	miR-885-5p	TCCATTACACTACCCTGCCTCT	0.00	26	0.00	3	0.00
287	miR-376a-5p	GTAGATTCTCCTTCTATGAGTA	0.00	29	0.00		\
288	PN(a)-37-3p	GCCTGCTGGGGTGGAACCTGGT	0.00	21	0.00	6	0.00
289	PC-185-3p	GAATTTGTCAGGGCTGGAG	0.00		\	23	0.00
290	PN(a)-78-5p	CAAAGTGCTCAYAGTGCAGGTAG	0.00	18	0.00	7	0.00
291	miR-374b-3p	CTTATCAGGTTGTATTATCATT	0.00	13	0.00	11	0.00
292	PN(a)-13-3p	CTATACAATCTACTGTCTTTC	0.00	13	0.00	11	0.00
293	miR-146b-5p	TGAGAACTGAATTCCATAGGCTAT	0.00	3	0.00	19	0.00
294	miR-16-1-5p, miR-16-2-5p	GCACGTAAATATTGGCG	0.00	20	0.00	5	0.00
295	PN(a)-46-5p	CTGGTTTCACATGGTGGCTTAGA	0.00	17	0.00	7	0.00
296	miR-205-5p	TCCTTCATTCCACCGGAGTCTGT	0.00	16	0.00	7	0.00
297	PC-71-3p	TGGTGTGTGGACTGGGGCT	0.00		\	20	0.00
298	PC-325-3p	TACTCAGGAAGGCATTATTCACA	0.00		\	20	0.00
299	miR-744-3p	CTGTTGCCACTAACCTCAACC	0.00	17	0.00	6	0.00
300	PC-183-5p	CGTCTCCTGGCTGGCTCGCCA	0.00	12	0.00	10	0.00
301	PN(a)-47-5p	TTATGTAACAGCAACTCCATGTGG	0.00	18	0.00	5	0.00
302	miR-10a-5p	TACCCTGTAGATCCGAATTTGTGT	0.00	13	0.00	9	0.00
303	PN(a)-14-3p	CTATACAATCTATTGCCTTCCT	0.00	3	0.00	17	0.00
304	PN(a)-49-5p	TATATGTGTGTATTTGCAGGAAC	0.00		\	19	0.00
305	let-7c-3p	CTGTACAACCTTCTAGCTTTCC	0.00	17	0.00	5	0.00
306	miR-19b-1-3p	TATGCAAATCCATGCAAAACTGA	0.00	13	0.00	8	0.00
307	PC-33-3p	TGGGGGATGCCTAGGCTCT	0.00	13	0.00	8	0.00
308	PC-20-3p	TTTGTTGGCTCCTCTGAAGTGA	0.00	14	0.00	7	0.00
309	PN(a)-76-3p	TCATTCCTAGAAATTGTTCACA	0.00	9	0.00	11	0.00
310	miR-19b-2-3p	TGTGCAAATCCATGCAAAACTGAT	0.00	4	0.00	15	0.00
311	PN(a)-10-3p	CCTCCTGGGGCCCGCACTCTCGC	0.00	4	0.00	15	0.00
312	PC-30-3p	TGTGTCTGTGACATCTGCTGGCA	0.00	16	0.00	5	0.00
313	PC-111-3p	GAAGGAGGCAGAGGCAGGA	0.00			18	0.00
314	PC-212-5p	TCAAGATTGCAGGTATCCTCTGTA	0.00		\	18	0.00
315	PC-325-5p	TGAATGGCGCCTTTCTGAGTAGAA	0.00		\	18	0.00
316	miR-128-1-5p	CGGGGCCGTAGCACTGTCTGAGA	0.00	6	0.00	13	0.00
317	miR-361-3p	CCCCCAGGTGTGATTCTGATTTGC	0.00	17	0.00	4	0.00
318	miR-10b-5p	ACCCTGTAGAACCGAAT	0.00	12	0.00	8	0.00
319	miR-1277-3p	TACGTAGATATATATGTATTT	0.00	12	0.00	8	0.00
320	PN(a)-6-3p	AGAATTGTGGCTGGACATCTGT	0.00	10	0.00	9	0.00
321	PN(a)-75-3p	ATCAACAGACATTAATTGGGCGC	0.00	16	0.00	4	0.00
322	PC-84-3p	CTGGGGTGTGGATTCGGCG	0.00		\	17	0.00

323	PC-97-5p	GCCGGCCTTGCGGGCCGCCGG	0.00		\	17	0.00
324	PC-150-3p	GAGTCCACCTGTGCCTGAG	0.00		\	17	0.00
325	PN(a)-61-5p	TTAGGGCCCTGGCTCCATCTCC	0.00	11	0.00	8	0.00
326	miR-17-5p	GCTTACAGTGCAGGTAG	0.00	3	0.00	14	0.00
327	miR-503-3p	GGGGTATTGTTTCTGCTGCCCGG	0.00	14	0.00	5	0.00
328	PN(a)-80-5p	AACTGTTTGCAGAGGAAACTGAGA	0.00	14	0.00	5	0.00
329	PN(a)-76-5p	TGTAAACAATTCCTAGGCAATGT	0.00	9	0.00	9	0.00
330	PC-141-3p	TCTGCCCGCATTCTCCACCA	0.00	9	0.00	9	0.00
331	PN(a)-44-5p	CCCCAGTGTTCAGACTACCTGTTC	0.00	20	0.00		\
332	miR-299-5p	TGGTTTACCGTCCCACATACAT	0.00	20	0.00		\
333	PC-12-3p	GGTCCCATCTGGGGTGCCA	0.00	20	0.00		\
334	miR-374a-5p	ATTTTATAATACAACCTGATAAGTG	0.00	16	0.00	3	0.00
335	PC-59-3p	TGGAAGAGACTGTCCTGGA	0.00		\	16	0.00
336	PC-271-3p	GGCATGGGCTGATTAGACC	0.00		\	16	0.00
337	PC-284-3p	TGGGATGATGTATCTGACT	0.00		\	16	0.00
338	PC-326-3p	TACTCCAAAGGGTGTCATTCAT	0.00		\	16	0.00
339	PC-297-5p	AGGGACCTAGGAGACAAAT	0.00	19	0.00		\
340	let-7g-3p	CTGTACAGGCCACTGCCTTGC	0.00	14	0.00	4	0.00
341	miR-345-5p	GCTGACTCCTAGTCCAGTGCTT	0.00	5	0.00	11	0.00
342	PC-156-5p	TAAGGATCTGCGGTTTACCAAGA	0.00		\	15	0.00
343	PC-251-5p	TTTTCTCTGAATAGATGCCCAGAA	0.00		\	15	0.00
344	PC-252-3p	ATCCTGTATCAGATCCTGA	0.00		\	15	0.00
345	miR-450a-5p, miR-450c-5p	TTTTGCGATGTGTTCCT	0.00	11	0.00	6	0.00
346	miR-210-5p	AGCCACTGCCCACCGCACACTG	0.00	11	0.00	6	0.00
347	PC-15-3p	CTCCCGGGTTTCGGCACCA	0.00	18	0.00		\
348	PN(a)-52-3p	TAGTGCAATATTGCTTATAGGGT	0.00	13	0.00	4	0.00
349	PN(a)-34-3p	CTCACCTGGAGCATGTTTTTT	0.00	8	0.00	8	0.00
350	PC-135-3p	TCCTGACTCTGACATTGCG	0.00		\	14	0.00
351	PC-145-5p	TGCCATCATCCGGCCTGGTAGA	0.00		\	14	0.00
352	PC-151-3p	TCCAAGATAGTTTTCAGCCCTTCT	0.00		\	14	0.00
353	miR-769-3p	CTGGGATCTCTGGGGTCTTGGTT	0.00	17	0.00		\
354	PN(a)-65-5p	TACAGTTGTTCAACCAGTTACT	0.00	12	0.00	4	0.00
355	miR-345-3p	CCCTGAACTAGGGGTCTGGAG	0.00	7	0.00	8	0.00
356	miR-185-5p	TGGAGAGAAAGGCAGTTCCTGTT	0.00	7	0.00	8	0.00
357	PN(a)-12-5p	CGGCCCCACGCACCAGGGTAAGA	0.00	13	0.00	3	0.00
358	miR-1-3p	TGGAATGTAAAGAAGTATGTACT	0.00	3	0.00	11	0.00
359	miR-92b-5p	AGGGACGGGACGCGGTGCAGTGT	0.00	9	0.00	6	0.00
360	miR-32-3p	CAATTTAGTGTGTGTGATATT	0.00	9	0.00	6	0.00
361	miR-204-3p	GCTGGGAAGGCAAAGGGACGT	0.00	10	0.00	5	0.00
362	miR-98-3p	CTATACAACTTACTACTTTCCT	0.00	16	0.00		\
363	PC-294-5p	CCACTAGCCCTGCTGGGGC	0.00	16	0.00		\
364	PC-112-3p	CGATGATGGTCCCTGTGTTTGT	0.00		\	13	0.00
365	PC-314-5p	TCAGCAATTCTTGGTTCTCATTT	0.00		\	13	0.00
366	PC-40-3p	ATTGCTGTGGCCACTGCGT	0.00	6	0.00	8	0.00
367	miR-323-3p	GCACATTACACGGTCGACCTCT	0.00	12	0.00	3	0.00
368	PN(a)-70-3p	CAACCTGGAGGACTCCATGCTGT	0.00	7	0.00	7	0.00
369	miR-328-5p	GTTTCGGAGCCTGGAGCG	0.00	9	0.00	5	0.00
370	miR-136-3p	CATCATCGTCTCAAATGAGTCT	0.00	15	0.00		\
371	PC-102-5p	TTGTCCGTGCCCCACCCACTCA	0.00	15	0.00		\
372	PC-47-5p	GCCTCTGCTTGAGAGATGG	0.00		\	12	0.00
373	PC-57-5p	TATCACTAGGGACGGACGTAGCTC	0.00		\	12	0.00
374	PC-153-5p	TGAGACCTGGTCCAGAGCCTCGA	0.00		\	12	0.00
375	PN(a)-58-5p	AGCTGGTGTTGTGAATCAGGCCG	0.00	7	0.00	6	0.00
376	miR-191-3p	CTGCACTTGGATTTCGTTCCC	0.00	8	0.00	5	0.00
377	miR-885-3p	AGGCAGCGGGGTGTAGTGGAT	0.00	8	0.00	5	0.00
378	PN(a)-4-5p	AGGCAAGATGCTGGCATAGCTTT	0.00	8	0.00	5	0.00
379	PN(c)-9-5p	CTCCTGCCTGGCTCGCCA	0.00	3	0.00	9	0.00
380	PN(a)-80-3p	TCAGTCTCAACTGCAAAGAAGT	0.00	14	0.00		\
381	PC-87-3p	TGGGCGGGATGGGAGGTGG	0.00	14	0.00		\
382	PN(a)-25-5p	GCAGCGCCGCGGGAGC	0.00	10	0.00	3	0.00
383	PC-32-5p	GCCGGGCCCGCCCCCGCGG	0.00	10	0.00	3	0.00
384	PC-25-3p	TGGACGATGCATTGAATATTTGAG	0.00		\	11	0.00
385	PC-201-5p	TGGAGACTTGGAAGACATA	0.00		\	11	0.00
386	miR-342-5p	AGGGTGCTATCTGTGACTGAGGG	0.00	13	0.00		\
387	PC-3-5p	GATGGATGATGATTCTGACA	0.00	13	0.00		\
388	miR-17-3p	TGAAGGCACTTGTAGC	0.00	3	0.00	8	0.00
389	miR-20-5p	GCTTATAGTGCAGGTAG	0.00	9	0.00	3	0.00
390	PN(a)-23-5p	GGGGGTCCCCGGTGCTCGGATC	0.00	4	0.00	7	0.00
391	PC-13-3p	ATTGATTTCGGTTGGGACA	0.00	12	0.00		\
392	PN(a)-65-3p	TAACCKGTTGAACAACTGAACCC	0.00	7	0.00	4	0.00
393	PC-123-3p, PC-279-5p	GGGCCGGGCGGTGGTGGCG	0.00	8	0.00	3	0.00
394	miR-338-3p	TCCAGCATCAGTGATTTTGTTGA	0.00	3	0.00	7	0.00
395	miR-101-1-5p	TCGGTTATCATGGTACCGATGCTG	0.00	4	0.00	6	0.00
396	miR-101-2-5p	TCAGTTATCACAGTGCTGATGC	0.00	4	0.00	6	0.00
397	PN(a)-8-3p	CCAGTGGGGCTGCTGTTATCTG	0.00	4	0.00	6	0.00
398	PC-182-3p	TGAGGGGCGTCGGGCGGGAC	0.00	4	0.00	6	0.00
399	PC-181-5p, PC-305-3p, PC-316-3p, PC-318	CCATTGTGGACCAGCAGAA	0.00		\	9	0.00
400	PN(a)-45-3p	TTGAAAGGCTATTTCTTGGTC	0.00		\	9	0.00
401	PC-58-5p	AGCTGGTCTGGGAGTTCCCGGG	0.00		\	9	0.00
402	PC-74-5p	CTGGAGGACATATGATGGC	0.00		\	9	0.00
403	PC-75-5p	TGGACTGGGAATCAGAAGAC	0.00		\	9	0.00
404	PC-130-5p	TCTGTGTCAGGATGGCCGAGTGG	0.00		\	9	0.00
405	PC-176-3p	AGGATGTAGACATAGAAGGAG	0.00		\	9	0.00
406	PN(c)-1-5p	TCGAGGAGCTCACAGTCTA	0.00	11	0.00		\
407	PC-89-3p	TCATTCTCCTTCTTTGACCAGT	0.00	11	0.00		\
408	PC-100-5p	TTGGTGGGGGCCGGGCCGCC	0.00	11	0.00		\
409	miR-365-1-5p	AGGGACTTTTGGGGGCAGATGTG	0.00	6	0.00	4	0.00
410	PC-31-5p	GGAGGGCGCGGCGGCCGCC	0.00	4	0.00	5	0.00
411	PC-7-5p	ATTAGTGGCAGAGCCCGGA	0.00	10	0.00		\
412	PC-115-3p	GGTCCTGCCGCGGGCGCCA	0.00	5	0.00	4	0.00
413	PC-22-5p	TTTTGTCTCTGAACTCTGCGCTTTT	0.00		\	8	0.00
414	PC-55-3p	GCCCGGCACTGAGAGGGCA	0.00		\	8	0.00
415	PC-79-3p	GGGGGCGGAGGGCCTGTGGG	0.00		\	8	0.00
416	PC-218-5p	GATCCCAGTGGGGCCTCCA	0.00		\	8	0.00
417	PC-248-3p	TGTGAAGAATATCTGTTATCGTCT	0.00		\	8	0.00
418	PC-281-5p	ACAGGACCTTGGCATGGAC	0.00		\	8	0.00
419	PC-313-3p	AAAGACTATAAAATAAAAAGG	0.00		\	8	0.00
420	PC-180-5p, PC-192-5p	GCCCCCGGCCGCGCGCGCGC	0.00	6	0.00	3	0.00
421	PN(a)-55-5p	TGAGGGGCCTCAGACCGAGCTTT	0.00	6	0.00	3	0.00
422	miR-338-5p	AACAATATCCTGGTGCTGAGT	0.00	6	0.00	3	0.00
423	miR-184-3p	TGGACGGAGAACTGATAAGGGAA	0.00	3	0.00	5	0.00
424	PC-142-3p	ACACAGGTAGTCGAGGAGA	0.00	3	0.00	5	0.00
425	miR-432-5p	TCTTGGAGTAGGTCATTGGGT	0.00	9	0.00		\
426	PC-1-5p	CCTAATGATGAAACTCTGAGG	0.00	9	0.00		\
427	PC-6-5p	GCGGGGCGCGCGGTCGCCCGGG	0.00	9	0.00		\
428	miR-505-5p	GGGAGCCAGGAAGTATTGATGTT	0.00	4	0.00	4	0.00
429	PN(a)-74-3p	TATACCAGGATGTCAGCATAGTT	0.00	4	0.00	4	0.00
430	miR-181a-1-5p, miR-181a-2-5p	AACGCTGTCGGTGAGT	0.00	5	0.00	3	0.00
431	miR-15b-5p	GCACATCATGGTTTACA	0.00	5	0.00	3	0.00
432	PC-29-5p, PC-36-5p, PC-168-5p, PC-199-5	TCAAATCGGACCTACGGCT	0.00		\	7	0.00

433	PC-109-5p, PC-232-5p	CGGCTGGACTGTGAAAAGA	0.00		\	7	0.00
434	miR-216-5p	TAATCTCAGCTGGCAACTGTGA	0.00		\	7	0.00
435	PC-68-5p	ATCCCTGTGACTGTACGGC	0.00		\	7	0.00
436	PC-106-5p	TGTGCATTGCAGGATGATT	0.00		\	7	0.00
437	PC-107-3p	TGAGGAATAAGAAGAACCGATGGT	0.00		\	7	0.00
438	PC-108-5p	GTGCCTGCTGTGTGCCAAGG	0.00		\	7	0.00
439	PC-118-3p	TGGAACTGTGCTGTCTGAAGCAAC	0.00		\	7	0.00
440	PC-166-5p	CGCCCCCGCGGTCCTCCTC	0.00		\	7	0.00
441	PC-237-5p	AGGGGCTGGAGAAATGGCT	0.00		\	7	0.00
442	PC-265-3p	CTGGGCGGGATGGGAGGTG	0.00		\	7	0.00
443	PC-282-5p	CCCAGGGACCTCTCTGATC	0.00		\	7	0.00
444	PC-288-3p	TTGGCTGCTGTAATGGACC	0.00		\	7	0.00
445	PC-309-3p	ATGAGAAGGTCCTGGCAGA	0.00		\	7	0.00
446	miR-935-3p	CAGTTACCGCTTCCGCTACCG	0.00	8	0.00		\
447	PN(a)-73-3p	AAGCCCTTACCCCAAAAAGTAT	0.00	8	0.00		\
448	PC-2-3p	CGGCCCCCGGCGCGTCGGG	0.00	8	0.00		\
449	PC-136-5p	ATCATGAGGACATGGATTTGAGCC	0.00	8	0.00		\
450	miR-378-5p	CCTGACTCCAGGTCCTGTGTGT	0.00	3	0.00	4	0.00
451	miR-103-1-5p	GGCTTCTTTACAGTGCTGCCTTG	0.00	3	0.00	4	0.00
452	miR-106a-5p	AAAAGTGCTTACAGTGCAGGTAGA	0.00	3	0.00	4	0.00
453	miR-758-3p	TTTGTGACCTGGTCCACTAAC	0.00	4	0.00	3	0.00
454	PC-191-3p	TGTCTCGGTGGGACCTCCA	0.00	4	0.00	3	0.00
455	PC-207-5p, PC-262-5p	CAAGAAGGATTAGTAGAAA	0.00		\	6	0.00
456	miR-107-5p	AGCTTCTTTACAGTGTTGCCTTG	0.00		\	6	0.00
457	PC-53-3p	AAGGGCTGGAGGCAGCAGG	0.00		\	6	0.00
458	PC-77-5p	AGAACCTTGGGACTGTGAA	0.00		\	6	0.00
459	PC-134-3p	CTGGGTCTCGGCTGGGATC	0.00		\	6	0.00
460	PC-155-5p	TATGTAGTTTCGCTCCACT	0.00		\	6	0.00
461	PC-157-5p	TAAGAGAATCAGCAGCTCTGTAGC	0.00		\	6	0.00
462	PC-162-5p	GCCAGGATAGACTTGAACT	0.00		\	6	0.00
463	PC-230-5p	TGAATCCGGCACGTCAGGT	0.00		\	6	0.00
464	PC-231-3p	TAGCACTGAGAGGTCTGTATGTAT	0.00		\	6	0.00
465	PC-241-3p	CCCTGGGCTGTAGATTTCA	0.00		\	6	0.00
466	PC-289-3p	GTAGTTCCTGAACCTTGGC	0.00		\	6	0.00
467	PN(a)-21-3p	TATTGCTTAAGAATACGCGTACC	0.00	7	0.00		\
468	PN(a)-30-3p	GCGACCCACTCTTGGTTTCCA	0.00	7	0.00		\
469	PN(a)-60-3p	CAGTGCAATGATATTGTCAAAGC	0.00	7	0.00		\
470	PN(a)-11-5p, PN(a)-17-5p, PN(a)-36-5p	ATTTCTTTGGTTATCTAGCTGTATG	0.00	3	0.00	3	0.00
471	miR-135-2-3p	ATGTAGGGATGGAAGCCATGAAA	0.00	3	0.00	3	0.00
472	miR-1308-3p	GCATTGTGGTTCAGTG	0.00	3	0.00	3	0.00
473	miR-542-3p	TGTGACAGATTGATAACTGAAGG	0.00	3	0.00	3	0.00
474	PN(a)-2-3p	TGGGTCACAGAAGAGGGTCTGGA	0.00	3	0.00	3	0.00
475	PC-190-5p	GCTGGGCTTGGAGTCAGAAGGC	0.00	3	0.00	3	0.00
476	PC-253-5p	TTTGGATCGATGTGGTACT	0.00	3	0.00	3	0.00
477	PC-246-5p, PC-260-3p, PC-275-3p, PC-315	ATAGGCCGCAAGCTGTAGC	0.00		\	5	0.00
478	PC-26-5p	TGAGGTAGTCAGGACCAGACCAA	0.00		\	5	0.00
479	PC-58-3p	GGGGAACTCCCAGACCAGCTTC	0.00		\	5	0.00
480	PC-81-3p	TTTAGGCCAAGCTTGGTTGAAT	0.00		\	5	0.00
481	PC-82-5p	CGATTCCCGGCCAACGCAGC	0.00		\	5	0.00
482	PC-154-3p	TAGGATATGAGGGCCTCAGTTTC	0.00		\	5	0.00
483	PC-158-5p	TCCTATTCCTGAGACGGTGAT	0.00		\	5	0.00
484	PC-159-5p	CTGCTGGTCATTTGTAAGC	0.00		\	5	0.00
485	PC-179-3p	TGTGATGATGGGCAGCTGAGC	0.00		\	5	0.00
486	PC-186-3p	CTCCACCTGAGCAGAGGTT	0.00		\	5	0.00
487	PC-187-3p	TGTAAGCCTGAGCTATAGC	0.00		\	5	0.00
488	PC-197-5p	TGGCTCAGTCGTAACGAAC	0.00		\	5	0.00
489	PC-208-3p	GTAGGCCGCCGCCTGTAGC	0.00		\	5	0.00
490	PC-229-3p	CCTACCAGGACTGAAGAAG	0.00		\	5	0.00
491	PC-249-3p	TGCTACCTGGAGGCTCTGTCCTGC	0.00		\	5	0.00
492	PC-266-5p	GGGATGTGATGAGGACTCA	0.00		\	5	0.00
493	PC-272-5p	TGACGGGAACTCCTTACCATTC	0.00		\	5	0.00
494	PC-285-5p	AGGGTTTTGTCTGCTCTGT	0.00		\	5	0.00
495	PC-287-5p	CACCATGCCTTCCTTCCTT	0.00		\	5	0.00
496	PC-312-5p	ATCTACAAAAATCGCTTGG	0.00		\	5	0.00
497	PC-319-5p	GATTCAGATTTGTATAGTG	0.00		\	5	0.00
498	miR-325-5p	CCTAGTAGGTGCTCAGTAAGTGT	0.00	6	0.00		\
499	PN(a)-18-3p	TGAACTGTCATACTCCCACATCC	0.00	6	0.00		\
500	PN(c)-11-3p	CACAGCTCCCATCTCAGA	0.00	6	0.00		\
501	PC-90-3p	TCTGAGATGTGACCTGGGCATC	0.00	6	0.00		\
502	PC-139-5p	AAGCCTTCCTTCTTGACCA	0.00	6	0.00		\
503	PC-302-5p	ATTGGCACTGCACATGATTGC	0.00	6	0.00		\
504	PC-303-5p	TTATGGCCCTTCGGTAATTCACT	0.00	6	0.00		\
505	miR-192-3p	CTGCCAATTCCATAGGTCACA	0.00	5	0.00		\
506	miR-30b-3p	CTGGGAGGTGGATGTTTACTTC	0.00	5	0.00		\
507	miR-95-3p	AACGGGTATTTATTGAGC	0.00	5	0.00		\
508	PN(c)-3-5p	CTTGGCACCTAGTAAGCAC	0.00	5	0.00		\
509	PC-88-5p	TGCGTTCATTCTGTTTGGCCTGT	0.00	5	0.00		\
510	PC-140-3p	AGGACTGAAGTGGGGAAAG	0.00	5	0.00		\
511	PC-188-5p	GGGGAAGGGCGGGAGCGGC	0.00	5	0.00		\
512	PC-198-3p	ATACATGATGATCTCACCCT	0.00	5	0.00		\
513	PC-291-3p	ATGATGTGTAGGATAGGTT	0.00	5	0.00		\
514	PC-298-5p	CAGAGCTGTGAGCACGGTG	0.00	5	0.00		\
515	PC-301-5p	CACCTGCCCTCTGCACGTGGGC	0.00	5	0.00		\
516	PC-34-3p, PC-160-5p, PC-209-3p, PC-228-	TAGGTCAAAGACACGGCGT	0.00		\	4	0.00
517	PC-41-3p, PC-46-5p	CAGGCGTGAGGCACTCTGT	0.00		\	4	0.00
518	PC-52-5p, PC-226-5p	TCTCACTCTGAGGCAGGAG	0.00		\	4	0.00
519	PC-64-5p, PC-280-3p	TGTCCAGAGGGCTGAACGG	0.00		\	4	0.00
520	PC-127-5p, PC-216-5p, PC-263-3p	TGGCTCATCGGCAATGAAC	0.00		\	4	0.00
521	miR-15b-3p	CGAATCATTATTTGCTGCTCTAAA	0.00		\	4	0.00
522	PN(a)-9-3p	TTTCCTCATATTCATTCAGGAGTG	0.00		\	4	0.00
523	miR-323-5p	AGGTGGTCCGTGGCGCGTTCG	0.00		\	4	0.00
524	PC-39-5p	AACTGAAGTGTAGAACATT	0.00		\	4	0.00
525	PC-61-5p	ATCTGTCTGTGTCTCTGAGCAGA	0.00		\	4	0.00
526	PC-63-5p	AGCATACTCTGGCTAATGG	0.00		\	4	0.00
527	PC-73-3p	AAACCCTTTGCCTGAGAACT	0.00		\	4	0.00
528	PC-78-3p	TGTTGGGCTCAGTGTGTGT	0.00		\	4	0.00
529	PC-101-5p	CCCGGCGCTCCCCCCCGCGGGG	0.00		\	4	0.00
530	PC-103-5p	TGGGCCGTCTGTCTGTGCAGC	0.00		\	4	0.00
531	PC-114-5p	GGGGACTGGAGAGATGGCT	0.00		\	4	0.00
532	PC-128-5p	TCTGGTCCAGACACTGTGGAGC	0.00		\	4	0.00
533	PC-132-3p	TGGCAGTAGGACCATAAGCACGG	0.00		\	4	0.00
534	PC-133-3p	TGACTGCACGGAGTGAGGATGAA	0.00		\	4	0.00
535	PC-143-5p	TGGGACCAGTCTCTGGCCT	0.00		\	4	0.00
536	PC-148-3p	AGCAAGGTCTGCCTTAAGG	0.00		\	4	0.00
537	PC-175-3p	TCTGTGAACTAGAAACCTCTGG	0.00		\	4	0.00
538	PC-203-5p	TCAGTCTCCATGGCCTTCC	0.00		\	4	0.00
539	PC-210-5p	CAGGGCAGGGCAGGGCGGGA	0.00		\	4	0.00
540	PC-214-5p	CTCTGGCACCATCAGGATA	0.00		\	4	0.00
541	PC-225-3p	ACGTTGAAGATGGACTGCTCCGAC	0.00		\	4	0.00
542	PC-227-3p	GCGGCGCGGGCGGGTGGAG	0.00		\	4	0.00

543	PC-247-3p	TTGAGACTCTTTCGCCATGAAGAT	0.00		\	4	0.00
544	PC-255-5p	TGTGAAGCTTTGCTAGACTCTCTC	0.00		\	4	0.00
545	PC-259-3p	CCATCCTTCCAGGCCCAGC	0.00		\	4	0.00
546	PC-268-3p	CTAAAATGAGGACACAGGA	0.00		\	4	0.00
547	PC-269-5p	TAGGAAAGGACGTGTGACT	0.00		\	4	0.00
548	PC-274-5p	AGTTGATCTGGTAGGGGAGC	0.00		\	4	0.00
549	PC-311-5p	TGAGTGTGTGTGTGTGAGTGTGAA	0.00		\	4	0.00
550	PC-317-5p	TACATATGTCCTGAGAAAC	0.00		\	4	0.00
551	miR-125a-3p, PN(b)-1-5p	TCCCTGAGACCCTTTAACCTGT	0.00	4	0.00		\
552	miR-181d-3p	CCCACCGGGGGATGAATGTCA	0.00	4	0.00		\
553	miR-133b-3p	TTGGTCCCCTTCAACCAGCTGTTA	0.00	4	0.00		\
554	miR-181b-1-3p	CTCACTGAACAATGAATGCAT	0.00	4	0.00		\
555	miR-1306-5p	CCACCTCCCCTGCAAACGTCCATT	0.00	4	0.00		\
556	miR-542-5p	TTGGGGATCATCATGTCACGAGA	0.00	4	0.00		\
557	PN(a)-22-5p	AGGAGGGAGGGGATGGGCCAAGT	0.00	4	0.00		\
558	PN(a)-40-3p	TAAGTGCTTCCATGTTTTAGTGA	0.00	4	0.00		\
559	PN(c)-10-5p	TCGAGGAGCCCACAGTCTAGTA	0.00	4	0.00		\
560	PC-8-3p	GCAATTTAGGTTAATGACTGTC	0.00	4	0.00		\
561	PC-21-3p	CGAGGCAGCGCTGAGGATGAAC	0.00	4	0.00		\
562	PC-27-5p	AAACTGGTAGACTTGAGTA	0.00	4	0.00		\
563	PC-28-3p	AATGGAGAGGGCAGTAGGAC	0.00	4	0.00		\
564	PC-49-3p	GTGGCACGGATGCAGGCTCTGCA	0.00	4	0.00		\
565	PC-54-5p	AGACGGATGACCTTGCTGTTT	0.00	4	0.00		\
566	PC-92-5p	TCTCCAGTGAGACAGTCTCTGG	0.00	4	0.00		\
567	PC-113-3p	GCTTGTGATGACTGAACTGAGG	0.00	4	0.00		\
568	PC-292-5p	TGAGGGGCGTCGGGCGGGA	0.00	4	0.00		\
569	PC-299-5p	ATCTACAGATTGTCGAGATGGAGA	0.00	4	0.00		\
570	PC-304-5p	CGGTGTGGTGTGGGTGTGGG	0.00	4	0.00		\
571	PC-35-3p, PC-220-5p	CATGTGTCTGCATGTGCAC	0.00		\	3	0.00
572	PC-38-3p, PC-65-3p	ACAGTGTTATTTCATGTGA	0.00		\	3	0.00
573	PC-43-5p, PC-125-5p	TTAGGACAAGATTTTATGA	0.00		\	3	0.00
574	PC-56-3p, PC-222-3p	GTAGGCCTGCGACTCTAGC	0.00		\	3	0.00
575	PC-83-3p, PC-121-3p, PC-219-3p, PC-235-	CCTGGTCTGAGAACTCAGA	0.00		\	3	0.00
576	PC-122-3p, PC-126-3p, PC-204-3p, PC-242	CTGGAGTTGTTGTCATGGC	0.00		\	3	0.00
577	PC-167-5p, PC-310-3p	TAACCAGGAGTAGAAATGC	0.00		\	3	0.00
578	PC-178-3p, PC-236-5p	GTGGTGCGGGTGGGTGGGT	0.00		\	3	0.00
579	PC-217-3p, PC-267-3p	GTTCGACTCCCGGTATGGGAACC	0.00		\	3	0.00
580	miR-224-3p	AATGGTGCCCTAGTGACTAC	0.00		\	3	0.00
581	PN(a)-16-5p	AAATCTCTGCAGGCAAATGTGA	0.00		\	3	0.00
582	PN(a)-26-5p	GCGCAGATCTTGGTGGTAGTAGC	0.00		\	3	0.00
583	PN(a)-70-5p	CCATGGATCCCCAGGTGGGT	0.00		\	3	0.00
584	PN(a)-79-5p	CACTTCAAGAAGTGCCATCCA	0.00		\	3	0.00
585	PN(c)-5-3p	CATCCCTTGCATGGTGGA	0.00		\	3	0.00
586	PC-16-3p	TATAGTCTGGAGGATGTAGTACTA	0.00		\	3	0.00
587	PC-19-3p	TTGGACGGATGAGGACACTGAGG	0.00		\	3	0.00
588	PC-23-5p	ACTTCTCTGAGCCTGCTTCTT	0.00		\	3	0.00
589	PC-24-5p	AAGTAGGAAGAATATGATCTCAGA	0.00		\	3	0.00
590	PC-44-3p	CGGCGCGACTGAACTCCGGA	0.00		\	3	0.00
591	PC-60-5p	AGGCATGGCTGAATACTGT	0.00		\	3	0.00
592	PC-61-3p	TCTGAGACACTGACTGTTGG	0.00		\	3	0.00
593	PC-66-5p	CAGGGAGCCTGCACAAGAG	0.00		\	3	0.00
594	PC-67-5p	TGATTTCCTTGTGACTGTGGGACT	0.00		\	3	0.00
595	PC-69-3p	TGGAGATGAGGACTGATGAAGTC	0.00		\	3	0.00
596	PC-72-5p	TGAGGGTAGATTGTATAGTT	0.00		\	3	0.00
597	PC-76-3p	TATGAATGTCAGGAAGAAT	0.00		\	3	0.00
598	PC-80-5p	GGAGTAGGGGCTGTAGCCC	0.00		\	3	0.00
599	PC-85-3p	TATATGTGTGTATTTGCAGGA	0.00		\	3	0.00
600	PC-99-3p	CCCCCCCTTCCCGGGGTGTGGGG	0.00		\	3	0.00
601	PC-116-5p	TGTACACGTCAAAAAGGACC	0.00		\	3	0.00
602	PC-119-5p	CACCTGTGGTTCTGAGGGG	0.00		\	3	0.00
603	PC-124-3p	CGAGCATACCTGTTGGGAC	0.00		\	3	0.00
604	PC-129-3p	AAGTGGGTGACGGGCAACA	0.00		\	3	0.00
605	PC-131-3p	TGTTTTCAGTATCTGTGTTCTGG	0.00		\	3	0.00
606	PC-146-3p	TGCCAGTGTGCAGACACGGGG	0.00		\	3	0.00
607	PC-152-3p	TAATTGTAGACAGTCCTGAGAGTC	0.00		\	3	0.00
608	PC-156-3p	CTTGTTAGAAATCCCAGATCCTAG	0.00		\	3	0.00
609	PC-163-5p	GAGGGAAGGGAGGGCGGGC	0.00		\	3	0.00
610	PC-164-5p	CTGTCATTTGCATCCAACA	0.00		\	3	0.00
611	PC-165-3p	TTCCGCGGACGAGGCCTTT	0.00		\	3	0.00
612	PC-169-3p	GGGGGCTGCAGAGTGAACC	0.00		\	3	0.00
613	PC-170-5p	CTGGCACCCAGGCTCCATC	0.00		\	3	0.00
614	PC-173-3p	TGCTGGACATCAGGAGACT	0.00		\	3	0.00
615	PC-174-3p	TTGGACCTGAGCTCAGGCA	0.00		\	3	0.00
616	PC-184-3p	ACTGGAGACACGTGCACTGTAGA	0.00		\	3	0.00
617	PC-193-5p	GTAATTCAGAATTGTGATT	0.00		\	3	0.00
618	PC-196-5p	CATATTGGATCAGACAAAA	0.00		\	3	0.00
619	PC-205-5p	TGATTTCAGAAAAACTGTT	0.00		\	3	0.00
620	PC-206-5p	ATGGCTGAGGAAGGAGGCGGC	0.00		\	3	0.00
621	PC-211-3p	TCTGATCAAGGTTGTTACCCAGCC	0.00		\	3	0.00
622	PC-213-5p	TGTGTCCTCTGATTGCTTTCCATG	0.00		\	3	0.00
623	PC-215-3p	TTCAGGACATAACCAGAGG	0.00		\	3	0.00
624	PC-223-3p	CGGCGGCGGCGGCGACTCTGGG	0.00		\	3	0.00
625	PC-224-3p	ATCGAGGAAGGCCAAGAAC	0.00		\	3	0.00
626	PC-234-3p	CGGATTGCAGGCTGCAACT	0.00		\	3	0.00
627	PC-238-5p	ATAGGCCAGCCGCTATTGC	0.00		\	3	0.00
628	PC-239-3p	AAGGAACCTGAAAACAGAG	0.00		\	3	0.00
629	PC-240-5p	ACTCTGTAGAGCAAGCTGG	0.00		\	3	0.00
630	PC-245-3p	TAGTTGAAGTGGAACTCGTTTCTG	0.00		\	3	0.00
631	PC-256-3p	TAGAAGCTTAGAGTTTTGTTCTAG	0.00		\	3	0.00
632	PC-257-3p	TGTGATGGGACTGATTCCTT	0.00		\	3	0.00
633	PC-258-3p	AAGGCTCAAGCTACAGACT	0.00		\	3	0.00
634	PC-276-5p	GGAGGATTTAGTAGTAAAT	0.00		\	3	0.00
635	PC-286-3p	TGAGAACTACTGCTTTGCAGCA	0.00		\	3	0.00
636	PC-306-3p	TCTACTGTGAGGACTGAGG	0.00		\	3	0.00
637	PC-137-5p, PC-243-3p	AGGGTGTCTGTTTTTATTT	0.00	3	0.00		\
638	miR-339-3p	AGCTCCTCGAGGCCAGAGCCC	0.00	3	0.00		\
639	miR-23b-5p	TGGGTTCCTGGCATGCTGATTT	0.00	3	0.00		\
640	miR-18-5p	TAAGGTGCATCTAGTGC	0.00	3	0.00		\
641	PN(a)-18-5p	TGGAGTGACTGTCAGATGCAGCCT	0.00	3	0.00		\
642	PN(a)-26-3p	AACGAGAACTTTGAAGGCCGACG	0.00	3	0.00		\
643	PN(a)-28-5p	ACTCAAACTGTGGGGGCACTTT	0.00	3	0.00		\
644	PN(a)-31-3p	TCGATGATGGTCCCTGTGTTTG	0.00	3	0.00		\
645	PN(a)-32-3p	TCGTGTCTTGTGTTGCAGCCGGA	0.00	3	0.00		\
646	PN(a)-38-5p	TGTCTTGCAGGCCGTCATGC	0.00	3	0.00		\
647	PN(a)-39-3p	AAACATGGTTCTGTCAAGCAC	0.00	3	0.00		\
648	PN(a)-41-3p	ATTGCACTTTAGCAATGGTGA	0.00	3	0.00		\
649	PN(a)-48-5p	GTTCCTGCTGAACTGAGCCAGT	0.00	3	0.00		\
650	PN(a)-50-5p	TGGATTTCTTTGTGAATCACCA	0.00	3	0.00		\
651	PN(a)-50-3p	GTGGTTTACAAAGTAATTCATA	0.00	3	0.00		\
652	PN(c)-4-3p	TTGGGAACATTTTGCATAT	0.00	3	0.00		\

653	PN(c)-8-3p	CTAGACTGAGGCTCCT	0.00	3	0.00		\
654	PC-4-3p	GATTCCTAACTCACCGGAC	0.00	3	0.00		\
655	PC-5-3p	GAAGCTACCATGCGTAGGA	0.00	3	0.00		\
656	PC-9-5p	GTGACATGGTGTGAATTGC	0.00	3	0.00		\
657	PC-11-5p	CGGCCGGGCCCGCCCCCGC	0.00	3	0.00		\
658	PC-14-5p	GTGGGCTGGAGAGACGGCT	0.00	3	0.00		\
659	PC-18-3p	TGCCCACACTCCTCTCTCCAGT	0.00	3	0.00		\
660	PC-50-5p	GCAGAACTTGGGGAGCCGCCGC	0.00	3	0.00		\
661	PC-51-3p	CGATATGATGACCCTGAAGTA	0.00	3	0.00		\
662	PC-91-3p	AGTATGTCTTTGGGGATTG	0.00	3	0.00		\
663	PC-95-3p	ACACGTAGCCTTTAAGTAGTGA	0.00	3	0.00		\
664	PC-96-3p	CGGGGTGGTGGTCTGTGGG	0.00	3	0.00		\
665	PC-117-3p	GTATTCTGAAGCTCTGAAATGCT	0.00	3	0.00		\
666	PC-161-5p	GAATGGTGGAGAGACCTGA	0.00	3	0.00		\
667	PC-195-3p	TCTAAGTAGGCGTAGGAAGA	0.00	3	0.00		\
668	PC-200-5p	AGGCAGGTGGATCTGGAGT	0.00	3	0.00		\
669	PC-202-5p	AAGGGTGTTGATTGATTAA	0.00	3	0.00		\
670	PC-254-5p	GTGGGAAGGAGCAGAGGTG	0.00	3	0.00		\
671	PC-293-3p	ATTGATGTAGGATGAATCC	0.00	3	0.00		\
672	PC-295-3p	CCGGTGCGCCCCCGGCGGC	0.00	3	0.00		\
673	PC-300-5p	GACTCTGTTGCCCAATGGA	0.00	3	0.00		\

Supplementary Table 6. miRNAs differentially expressed (DE) between porcine adult ovary and testis

Unique miR ID	miRNA name	Consensus miRNA sequence	Chromosome	Type (ovary versus testis)	Ovary	Testis	Audic-Claverie test	Fisher exact test	Chi-squared 2×2 test
					Counts of most abundant sequences (normalized	Counts of most abundant sequences	*P* value	*P* value	*P* value
1	miR-181b-2-5p	AACATTCATTGCTGTCG	1	Up	2	438	0	0	0
1	miR-181b-1-5p	AACATTCATTGCTGTCG	10	Up	2	438	0	0	0
2	miR-199b-3p	ACAGTAGTCTGCACATTGGTT	1	Down	11,935	2,422	0	0	0
2	miR-199a-3p	ACAGTAGTCTGCACATTGGTT	2	Down	11,935	2,422	0	0	0
3	miR-103-1-3p	AGCAGCATTGTACAGGGCTATGA	16	Up	9,255	9,750	0.000002	0.000164	0.000159
3	miR-103-2-3p	AGCAGCATTGTACAGGGCTATGA	17	Up	9,255	9,750	0.000002	0.000164	0.000159
4	PC-181-5p	CCATTGTGGACCAGCAGAA	9	Up	0	9	0.000414	0.000752	0.000905
4	PC-305-3p	CCATTGTGGACCAGCAGAA	X	Up	0	9	0.000414	0.000752	0.000905
4	PC-316-3p	CCATTGTGGACCAGCAGAA	X	Up	0	9	0.000414	0.000752	0.000905
4	PC-318-5p	CCATTGTGGACCAGCAGAA	X	Up	0	9	0.000414	0.000752	0.000905
5	PC-93-5p	CGGGGCTGGAGGAGGGAGGGC	5	Down	14	0	0.000021	0.000066	0.000194
5	PC-221-5p	CGGGGCTGGAGGAGGGAGGGC	11	Up	0	15	0.000003	0.000006	0.000018
6	miR-124a-1-3p	TAAGGCACGCGGTGAATGCCAA	4	Up	347	437	0.000051	0.000786	0.000726
6	miR-124a-2-3p	TAAGGCACGCGGTGAATGCCAA	14	Up	347	437	0.000051	0.000786	0.000726
7	miR-135-2-5p	TATGGCTTTTTATTCCTATGTGA	5	Down	185	92	0	0	0
7	miR-135-1-5p	TATGGCTTTTTATTCCTATGTGA	13	Down	185	92	0	0	0
8	miR-24-1-3p	TGGCTCAGTTCAGCAGGAACAG	2	Up	115,833	128,462	0	0	0
8	miR-24-2-3p	TGGCTCAGTTCAGCAGGAACAG	10	Up	115,833	128,462	0	0	0
9	PN(a)-39-5p	TTGTGCTTGATCTAACCATGT	8	Down	217	40	0	0	0
9	PN(a)-66-5p	TTGTGCTTGATCTAACCATGT	16	Down	217	40	0	0	0
10	miR-320-3p	AAAAGCTGGGTTGAGAGGGCGA	14	Up	19,088	25,308	0	0	0
11	PN(a)-77-3p	AAACATCTGGTTGGTTGAGAGA	X	Down	24	4	0.000028	0.000075	0.000149
12	PN(a)-53-5p	AAACCGTTACCATTACTGAGTT	12	Down	4,298	3,319	0	0	0
13	miR-148a-5p	AAAGTTCTGAGACACTCCGACT	18	Down	273	174	0	0.000001	0.000001
14	miR-181c-5p	AACATTCAACCTGTCGGTGAGT	2	Up	515	678	0	0.000001	0.000001
15	PC-321-3p	AACCCAGGGAGGTGCTGTTCACC	X	Up	0	193	0	0	0
16	miR-100-5p	AACCCGTAGATCCGAACTTGTG	9	Up	10,953	12,641	0	0	0
17	miR-99a-5p	AACCCGTAGATCCGATCTTGT	13	Down	18,494	4,268	0	0	0
18	miR-193a-3p	AACTGGCCTACAAAGTCCCAGT	12	Down	1,866	1,677	0.000028	0.000942	0.000913
19	PC-138-5p	AAGCTACTCTGGCACCATC	7	Up	0	36	0	0	0
20	miR-22-3p	AAGCTGCCAGTTGAAGAACTGT	12	Up	4,362	4,725	0.000001	0.000066	0.000063
21	miR-34c-3p	AATCACTAACCACACGGCCAGG	9	Up	796	1,112	0	0	0
22	PN(a)-42-3p	AATCACTAATTCCACTGCCATC	9	Up	123	2,055	0	0	0
23	miR-425-5p	AATGACACGATCACTCCCGTTGA	13	Up	3,346	4,453	0	0	0
24	PC-324-5p	AATGGCGCTTTTTTGTGAAGA	X	Up	0	332	0	0	0
25	PN(a)-44-3p	ACAGTAGTCTGCACATTGGTAAGA	9	Up	8	36	0.000002	0.000008	0.000006
26	PC-270-5p	ACATTCTCTGTTCCTTTTT	15	Up	0	27	0	0	0
27	miR-140-3p	ACCACAGGGTAGAACCACGGAC	N	Down	19,772	19,008	0.000001	0.000048	0.000047
28	PN(a)-56-5p	ACCGTGGCTTTCGATTGTTACT	12	Down	60	16	0	0	0
29	miR-221-5p	ACCTGGCATACAATGTAGATTTCT	X	Up	8,428	9,027	0	0.000002	0.000002
30	PN(a)-57-5p	ACCTTGGCTCTAGACTGCTTACT	12	Down	40	7	0	0	0.000001
31	PN(a)-22-3p	ACGCCCTTCCCCCCCTTCTTCA	5	Down	124	40	0	0	0
32	miR-136-5p	ACTCCATTTGTTTTGATGATGG	7	Down	82	5	0	0	0
33	miR-1307-3p	ACTCGGCGTGGCGTCGGTCGTGG	14	Down	167	81	0	0	0
34	miR-130b-5p	ACTCTTTCCCTGTTGCACTACT	14	Down	27	3	0.000001	0.000002	0.00001
35	PC-326-5p	ACTGTCACCTTTTTGAGTAGAA	X	Up	0	68	0	0	0
36	miR-504-5p	AGACCCTGGTCTGCACTCTATC	X	Down	100	9	0	0	0
37	PN(a)-15-5p	AGAGGTAGTAGGTTGCATAGTT	3	Up	10,714	13,128	0	0	0
38	miR-222-3p	AGCTACATCTGGCTACTGGGTCTC	X	Up	632	750	0.000042	0.000886	0.000796
39	miR-221-3p	AGCTACATTGTCTGCTGGGTTTC	X	Up	2,793	3,646	0	0	0
40	miR-423-3p	AGCTCGGTCTGAGGCCCCTCAGT	12	Down	7,809	6,967	0	0	0
41	PC-58-5p	AGCTGGTCTGGGAGTTCCCGGG	3	Up	0	9	0.000414	0.000752	0.000905
42	PC-176-3p	AGGATGTAGACATAGAAGGAG	8	Up	0	9	0.000414	0.000752	0.000905
43	PN(a)-42-5p	AGGCAGTGTAATTAGCTGATTGT	9	Up	1,164	2,871	0	0	0
44	miR-34c-5p	AGGCAGTGTAGTTAGCTGATTGC	9	Up	106,326	153,583	0	0	0
45	PN(a)-63-5p	AGGCAGTGTATTGTTAGCTGGCTC	16	Up	11	174	0	0	0
46	PC-314-3p	AGGGAACCTGGAAAAGCTGAAG	X	Up	0	41	0	0	0
47	PC-297-5p	AGGGACCTAGGAGACAAAT	17	Down	16	0	0.000006	0.000018	0.000081
48	miR-27a-5p	AGGGCTTAGCTGCTTGTGAGCA	2	Up	4,232	5,188	0	0	0
49	PC-48-5p	AGGGGCGGCGCGGGGCGGG	2	Down	26	0	0	0	0
50	PN(a)-68-3p	AGGGTTGGGCGGAGGCTTTCCT	17	Down	71	23	0	0	0
51	miR-23b-3p	ATCACATTGCCAGGGATTACCA	10	Down	4,080	1,835	0	0	0
52	miR-23a-3p	ATCACATTGCCAGGGATTTCCA	2	Down	23,396	20,750	0	0	0
53	PC-252-3p	ATCCTGTATCAGATCCTGA	14	Up	0	15	0.000003	0.000006	0.000018
54	miR-500-3p	ATGCACCTGGGCAAGGATTCTGA	N	Down	228	57	0	0	0
55	PC-86-3p	ATGCGGAACCTGCGGATACGG	5	Down	15,251	0	0	0	0
56	PC-86-5p	ATGTCCGCGGGTTCCCTATCC	5	Down	263	0	0	0	0

57	miR-145-3p	ATTCCTGGAAATACTGTTCTT	2	Down	185	30	0	0	0
58	PC-327-3p	ATTGGCACTTTTTAGAGTGTGA	X	Up	0	295	0	0	0
59	PC-172-5p	ATTGTGATTTTCCTTGGAA	8	Up	0	38	0	0	0
60	PC-147-5p	ATTGTTGTGAAGGTTCTATGAATT	7	Up	0	32	0	0	0
61	miR-186-5p	CAAAGAATTCTCCTTTTGGGCTT	6	Down	9,987	8,212	0	0	0
62	PC-320-3p	CAACAGTCCCTGCCTGGGTAGA	X	Up	0	409	0	0	0
63	miR-191-5p	CAACGGAATCCCAAAAGCAGCTG	13	Down	4,343	3,482	0	0	0
64	miR-99a-3p	CAAGCTCGCTTCTATGGGTCTGT	13	Down	159	38	0	0	0
65	miR-224-5p	CAAGTCACTAGTGGTTCCGTTTAG	X	Down	25	0	0	0	0
66	miR-574-3p	CACGCTCATGCACACACCCACA	8	Down	2,375	452	0	0	0
67	miR-28-3p	CACTAGATTGTGAGCTCCTGGA	13	Down	3,355	2,597	0	0	0
68	miR-424-5p	CAGCAGCAATTCATGTTTTGA	X	Down	11,946	4,296	0	0	0
69	miR-497-5p	CAGCAGCACACTGTGGTTTGTA	12	Down	619	444	0	0	0
70	PC-42-3p	CAGCAGGCTGTGGTGAAGG	2	Up	0	41	0	0	0
71	PN(a)-63-3p	CAGCCACGACTACCCTGCCACT	16	Up	0	31	0	0	0
72	PC-290-3p	CAGGGTTATGTGACAGAGC	16	Up	0	78	0	0	0
73	miR-130b-3p	CAGTGCAATGATGAAAGGGCAT	14	Down	72	17	0	0	0
74	miR-140-5p	CAGTGGTTTTACCCTATGGTAG	N	Down	2,970	1,351	0	0	0
75	miR-142-5p	CATAAAGTAGAAAGCACTACT	12	Down	154	28	0	0	0
76	miR-136-3p	CATCATCGTCTCAAATGAGTCT	7	Down	12	0	0.000071	0.000249	0.000463
77	miR-532-5p	CATGCCTTGAGTGTAGGACCGT	N	Down	3,255	881	0	0	0
78	PN(a)-7-5p	CATTATTACTTTTGGTACGCG	1	Down	1,860	988	0	0	0
79	PC-294-5p	CCACTAGCCCTGCTGGGGC	17	Down	13	0	0.000039	0.000128	0.000299
80	miR-199a-5p	CCCAGTGTTCAGACTACCTGTTC	2	Down	22,155	3,253	0	0	0
81	miR-199b-5p	CCCAGTGTTTAGACTATCTGTTC	1	Down	1,647	257	0	0	0
82	PN(a)-44-5p	CCCCAGTGTTCAGACTACCTGTTC	9	Down	16	0	0.000004	0.000009	0.000053
83	miR-676-3p	CCGTCCTAAGGTTGTTGAGTT	X	Down	927	76	0	0	0
84	miR-532-3p	CCTCCCACACCCAAGGCTTGCA	N	Down	150	34	0	0	0
85	miR-326-3p	CCTCTGGGCCCTTCCTCCAGT	9	Up	4	985	0	0	0
86	PC-94-3p	CGAATCACGTCGGGGTCATGG	5	Down	36	0	0	0	0
87	PC-62-5p	CGAGTCCCACCCGGGGTAGG	3	Up	0	40	0	0	0
88	PC-112-3p	CGATGATGGTCCCTGTGTTTGT	6	Up	0	13	0.000017	0.000031	0.000066
89	PC-98-3p	CGCGGTCGCCCGGGGACGCCGG	6	Down	28	0	0	0	0
90	PC-250-3p	CGGCGGCGGCGACTCTGGA	14	Down	244	99	0	0	0
91	miR-151-3p	CTAGACTGAAGCTCCTTGAGGA	N	Up	0	1,206	0	0	0
92	miR-98-3p	CTATACAACTTACTACTTTCCT	X	Down	13	0	0.000039	0.000128	0.000299
93	PN(a)-14-3p	CTATACAATCTATTGCCTTCCT	3	Up	2	17	0.000132	0.000387	0.00032
94	PN(a)-15-3p	CTATACGACCTGCTGCCTTTCT	3	Down	402	269	0	0	0
95	PC-194-5p	CTCATGGTTGGGCTGCAGG	9	Up	0	32	0	0	0
96	PC-15-3p	CTCCCGGGTTTCGGCACCA	1	Down	15	0	0.000012	0.000034	0.000125
97	miR-127-5p	CTGAAGCTCAGAGGGCTCTGAT	7	Down	67	0	0	0	0
98	PN(a)-12-3p	CTGCCCTGGCCCGAGGGACCGAC	2	Down	94	25	0	0	0
99	PC-74-5p	CTGGAGGACATATGATGGC	3	Up	0	9	0.000414	0.000752	0.000905
100	miR-769-3p	CTGGGATCTCTGGGGTCTTGGTT	6	Down	14	0	0.000021	0.000066	0.000194
101	PC-84-3p	CTGGGGTGTGGATTCGGCG	3	Up	0	17	0.000001	0.000001	0.000005
102	miR-202-5p	CTTCCTATGCATATACTTCTTT	14	Up	846	1,252	0	0	0
103	miR-30e-3p	CTTTCAGTCGGATGTTTACAGC	6	Down	979	830	0.000012	0.00025	0.000252
104	miR-30a-3p	CTTTCAGTCGGATGTTTGCAGC	1	Down	123	62	0.000001	0.000003	0.000004
105	miR-129-5p	CTTTTTGCGGTCTGGGCTTGC	2	Down	145	89	0.000016	0.000129	0.000132
106	PC-296-5p	GAAGGAGGCAGAGACAGGA	17	Down	25	0	0	0	0
107	PC-111-3p	GAAGGAGGCAGAGGCAGGA	6	Up	0	18	0	0.000001	0.000003
108	PC-185-3p	GAATTTGTCAGGGCTGGAG	9	Up	0	23	0	0	0
109	PC-150-3p	GAGTCCACCTGTGCCTGAG	7	Up	0	17	0.000001	0.000001	0.000005
110	miR-455-3p	GCAGTCCATGGGCATATACAC	1	Down	282	22	0	0	0
111	PC-308-3p	GCATGTGTACGCATGTGTA	X	Up	0	29	0	0	0
112	PC-97-5p	GCCGGCCTTGCGGGCCGCCGG	6	Up	0	17	0.000001	0.000001	0.000005
113	PC-47-5p	GCCTCTGCTTGAGAGATGG	2	Up	0	12	0.000038	0.000068	0.000127
114	PC-120-5p	GCGCGCGCGCGTGTGCGCGGG	6	Down	66	26	0.000003	0.000014	0.000017
115	PC-17-5p	GCGCGCGGTCGCCCGGGGA	2	Down	51	22	0.000099	0.000588	0.00054
116	PC-271-3p	GGCATGGGCTGATTAGACC	15	Up	0	16	0.000002	0.000003	0.00001
117	PC-12-3p	GGTCCCATCTGGGGTGCCA	1	Down	16	0	0.000004	0.000009	0.000053
118	PN(a)-25-3p	GGTCCCCCGCCGTCCC	6	Down	29	4	0.000001	0.000003	0.000009
119	miR-143-5p	GGTGCAGTGCTGCATCTCTGG	2	Down	943	138	0	0	0
120	miR-376a-5p	GTAGATTCTCCTTCTATGAGTA	N	Down	24	0	0	0	0.000001
121	miR-145-5p	GTCCAGTTTTCCCAGGAATCCCT	2	Down	11,695	1,618	0	0	0
122	PC-149-3p	GTGCAAGGCTGAATTAGAC	7	Up	0	28	0	0	0
123	PC-277-3p	GTGGTGAGGAGCTTTCACT	15	Up	0	119	0	0	0
124	PC-171-3p	GTTTATGTATGTGTATATGTATA	8	Up	0	28	0	0	0
125	PN(a)-56-3p	TAACAGTCTACAGCCATGGTCG	12	Down	4,516	676	0	0	0
126	PN(a)-57-3p	TAACAGTCTCCAGTCACGGCCA	12	Down	59	7	0	0	0
127	PC-273-3p	TAAGGACTTGATGATGGTA	15	Up	0	61	0	0	0

128	PC-156-5p	TAAGGATCTGCGGTTTACCAAGA	7	Up	0	15	0.000003	0.000006	0.000018
129	miR-500-5p	TAATCCTTGCTACCTGGGTGAGA	N	Down	666	199	0	0	0
130	PC-325-3p	TACTCAGGAAGGCATTATTCACA	X	Up	0	20	0	0	0.000001
131	PC-326-3p	TACTCCAAAGGGTGTCATTCAT	X	Up	0	16	0.000002	0.000003	0.00001
132	miR-29a-3p	TAGCACCATCTGAAATCGGTT	18	Up	82,686	96,154	0	0	0
133	miR-29b-3p	TAGCACCATTTGAAATCAGTGTT	18	Up	14,784	16,914	0	0	0
134	miR-29c-3p	TAGCACCATTTGAAATCGGTT	9	Down	588	385	0	0	0
135	miR-195-5p	TAGCAGCACAGAAATATTGGCA	12	Down	2,185	1,783	0	0	0
136	miR-503-5p	TAGCAGCGGGAACAGTACTGCAG	X	Down	76	16	0	0	0
137	miR-21-5p	TAGCTTATCAGACTGATGTTGAC	12	Down	736,325	728,247	0	0	0
138	PC-70-5p	TAGGATGAGAAATAGAGCC	3	Up	0	25	0	0	0
139	miR-196b-5p	TAGGTAGTTTCCTGTTGTTGGG	18	Down	55	8	0	0	0
140	PN(a)-49-5p	TATATGTGTGTATTTGCAGGAAC	10	Up	0	19	0	0	0.000001
141	PC-57-5p	TATCACTAGGGACGGACGTAGCT	3	Up	0	12	0.000038	0.000068	0.000127
142	PC-322-3p	TATCCAGACAGGTGCTGTTCT	X	Up	0	199	0	0	0
143	miR-183-5p	TATGGCACTGGTAGAATTCACT	18	Down	697	382	0	0	0
144	PN(a)-43-5p	TATGGCTTTTCATTCCTATGTGA	9	Down	166	9	0	0	0
145	miR-299-3p	TATGTGGGACGGTAAACCGCTT	N	Down	136	9	0	0	0
146	miR-92b-3p	TATTGCACTCGTCCCGGCCTCC	4	Down	196	53	0	0	0
147	miR-335-5p	TCAAGAGCAATAACGAAAAATGT	18	Down	30	8	0.00005	0.000229	0.000246
148	PC-212-5p	TCAAGATTGCAGGTATCCTCTGTA	11	Up	0	18	0	0.000001	0.000003
149	PC-314-5p	TCAGCAATTCTTGGTTCTCATTT	X	Up	0	13	0.000017	0.000031	0.000066
150	PN(a)-64-3p	TCAGCTAACATGCAACTGCTGT	16	Up	8	725	0	0	0
151	PN(a)-80-3p	TCAGTCTCAACTGCAAAGAAGT	X	Down	11	0	0.000129	0.000247	0.000719
152	miR-148a-3p	TCAGTGCACTACAGAACTTTGT	18	Down	174,663	125,809	0	0	0
153	miR-152-3p	TCAGTGCATGACAGAACTTGG	12	Down	4,067	1,591	0	0	0
154	PC-151-3p	TCCAAGATAGTTTTCAGCCCTTCT	7	Up	0	14	0.000008	0.000014	0.000035
155	miR-885-5p	TCCATTACACTACCCTGCCTCT	13	Down	21	3	0.000033	0.000102	0.000178
156	miR-125b-1-5p	TCCCTGAGACCCTAACTTGTGA	9	Down	28,367	18,800	0	0	0
157	miR-125a-5p	TCCCTGAGACCCTTTAACCTGT	6	Down	1,889	605	0	0	0
158	PC-233-5p	TCCCTGGTCTAGTGGTTAGGATTC	12	Up	0	158	0	0	0
159	PC-135-3p	TCCTGACTCTGACATTGCG	7	Up	0	14	0.000008	0.000014	0.000035
160	miR-1307-5p	TCGACCGGACCTCGACCGGCT	14	Down	923	404	0	0	0
161	miR-151-5p	TCGAGGAGCTCACAGTCTAGTA	N	Up	0	3,327	0	0	0
162	miR-127-3p	TCGGATCCGTCTGAGCTTGGCT	7	Down	512	81	0	0	0
163	PN(a)-7-3p	TCGTACCGTGAGTAATAATGCG	1	Down	10,640	2,697	0	0	0
164	PC-144-5p	TCGTGTCTGGAAGCTGCCTCCTTC	7	Up	0	47	0	0	0
165	miR-331-5p	TCTAGGTATGGTCCCAGGGATC	5	Down	79	37	0.000008	0.000055	0.000054
166	miR-342-3p	TCTCACACAGAAATCGCACCCGT	7	Down	69	28	0.000003	0.000015	0.000022
167	PN(a)-27-5p	TCTCCCAACCCTTGTACCAGTG	6	Down	101	38	0	0	0
168	PN(c)-2-3p	TCTCGCTGGGGCCTCCA	1	Down	110	53	0	0.000003	0.000004
169	PN(a)-62-5p	TCTGGCTCCGTGTCTTCACTCC	15	Up	1,531	1,727	0.000011	0.000315	0.000293
170	PC-130-5p	TCTGTGTCAGGATGGCCGAGTGG	7	Up	0	9	0.000414	0.000752	0.000905
171	PC-321-5p	TGAACAGGGCCTTTCTGGGTCGA	X	Up	0	531	0	0	0
172	PC-322-5p	TGAACGGCGCCTGTGTGGTTAGA	X	Up	0	388	0	0	0
173	PC-325-5p	TGAATGGCGCCTTTCTGAGTAGAA	X	Up	0	18	0	0.000001	0.000003
174	PC-323-5p	TGACCAGGCAGGTGCTGTTCTCT	X	Up	0	47	0	0	0
175	miR-146b-5p	TGAGAACTGAATTCCATAGGCTAT	14	Up	2	19	0.000036	0.000111	0.000095
176	PN(a)-67-5p	TGAGAACTGAATTCCATGGGTT	16	Down	492	161	0	0	0
177	miR-769-5p	TGAGACCTCTGGGTTCTGAGCT	6	Down	167	85	0	0	0
178	PC-153-5p	TGAGACCTGGTCCAGAGCCTCGA	7	Up	0	12	0.000038	0.000068	0.000127
179	miR-143-3p	TGAGATGAAGCACTGTAGCTCG	2	Down	319,145	154,700	0	0	0
180	miR-423-5p	TGAGGGGCAGAGAGCGAGACTTT	12	Up	1,292	1,532	0	0.000002	0.000002
181	let-7e-5p	TGAGGTAGGAGGTTGTATAGTT	6	Down	2,421	1,471	0	0	0
182	miR-98-5p	TGAGGTAGTAAGTTGTATTGTT	X	Down	1,897	1,657	0.000001	0.000024	0.000025
183	let-7f-5p	TGAGGTAGTAGATTGTATAGTT	X	Up	287,138	397,795	0	0	0
184	PN(a)-14-5p	TGAGGTAGTAGATTGTATAGTTG	3	Up	268	351	0.000035	0.000508	0.000428
185	let-7a-5p	TGAGGTAGTAGGTTGTATAGTT	9	Up	148,684	187,951	0	0	0
186	let-7c-5p	TGAGGTAGTAGGTTGTATGGTT	13	Up	128,499	182,862	0	0	0
187	let-7g-5p	TGAGGTAGTAGTTTGTACAGTT	13	Up	25,309	31,834	0	0	0
188	let-7i-5p	TGAGGTAGTAGTTTGTGCTGTT	5	Up	292,317	460,146	0	0	0
189	PN(a)-79-3p	TGATTGGCACCTCTTTGAGTGA	X	Up	7	508	0	0	0
190	PC-145-5p	TGCCATCATCCGGCCTGGTAGA	7	Up	0	14	0.000008	0.000014	0.000035
191	miR-214-5p	TGCCTGTCTACACTTGCTGTGC	9	Down	185	56	0	0	0
192	PC-37-5p	TGCGTGGCTTCTCTGTGCAGTC	2	Down	27	0	0	0	0
193	PC-59-3p	TGGAAGAGACTGTCCTGGA	3	Up	0	16	0.000002	0.000003	0.00001
194	PC-25-3p	TGGACGATGCATTGAATATTTGAG	2	Up	0	11	0.000084	0.000152	0.000244
195	PC-177-5p	TGGACTGGATGACAATCTGCAGG	8	Up	0	27	0	0	0
196	PC-75-5p	TGGACTGGGAATCAGAAGAC	3	Up	0	9	0.000414	0.000752	0.000905
197	PC-201-5p	TGGAGACTTGGAAGACATA	9	Up	0	11	0.000084	0.000152	0.000244
198	PN(a)-31-5p	TGGCACAGGGTCCAGCTGTCGGC	6	Down	206	132	0.000003	0.000031	0.00003

199	PN(a)-64-5p	TGGCAGTGTATTGTTAGCTGGT	16	Up	100	2,428	0	0	0
200	miR-34a-5p	TGGCAGTGTCTTAGCTGGTTGT	N	Down	253	45	0	0	0
201	PC-10-3p	TGGCTGACCTCTGACCTCC	1	Down	72	0	0	0	0
202	PC-284-3p	TGGGATGATGTATCTGACT	16	Up	0	16	0.000002	0.000003	0.00001
203	PC-87-3p	TGGGCGGGATGGGAGGTGG	5	Down	11	0	0.000129	0.000247	0.000719
204	miR-193a-5p	TGGGTCTTTGCGGGCGAGATGA	12	Down	69	21	0	0	0
205	PC-71-3p	TGGTGTGTGGACTGGGGCT	3	Up	0	20	0	0	0.000001
206	miR-299-5p	TGGTTTACCGTCCCACATACAT	N	Down	16	0	0.000004	0.000009	0.000053
207	miR-30d-5p	TGTAAACATCCCCGACTGGAAGC	4	Up	23,077	25,106	0	0	0
208	miR-30c-5p	TGTAAACATCCTACACTCTCAGCT	1	Down	5,371	4,266	0	0	0
209	miR-30a-5p	TGTAAACATCCTCGACTGGAAGCT	1	Down	5,692	2,545	0	0	0
210	miR-30e-5p	TGTAAACATCCTTGACTGGAAGCT	6	Down	13,118	11,433	0	0	0
211	miR-142-3p	TGTAGTGTTTCCTACTTTATGG	12	Down	961	124	0	0	0
212	PC-104-5p	TGTTTCTTTGACAAGCAGCCTGGT	6	Up	0	34	0	0	0
213	PN(a)-59-5p	TTAATGCTAATTGTGATAGGGGTT	13	Down	231	15	0	0	0
214	miR-361-5p	TTATCAGAATCTCCAGGGGTAC	X	Down	104	49	0.000001	0.000004	0.000005
215	miR-26a-5p	TTCAAGTAATCCAGGATAGGCT	N	Down	14,372	7,673	0	0	0
216	PC-324-3p	TTCACAAGAAGGTGTCAATTCA	X	Up	0	27	0	0	0
217	miR-27b-3p	TTCACAGTGGCTAAGTTCTGC	10	Down	43,994	17,545	0	0	0
218	miR-204-5p	TTCCCTTTGTCATCCTATGCCT	1	Down	120	64	0.000003	0.000016	0.000019
219	PN(a)-45-3p	TTGAAAGGCTATTTCTTGGTC	9	Up	0	9	0.000414	0.000752	0.000905
220	PC-105-5p	TTGGAGCTGTTTAGAGAGACATGC	6	Up	0	48	0	0	0
221	miR-133a-3p	TTGGTCCCCTTCAACCAGCTGT	17	Down	529	194	0	0	0
222	PC-102-5p	TTGTCCGTGCCCCACCCACTCA	6	Down	12	0	0.000071	0.000249	0.000463
223	PN(a)-71-5p	TTTGGCAATGGTAGAACTCACACT	18	Down	4,002	2,997	0	0	0
224	PC-251-5p	TTTTCTCTGAATAGATGCCCAGAA	14	Up	0	15	0.000003	0.000006	0.000018

Supplementary Table 7. Porcine pre-miRNA annotations

The pig genome annotations were obtained from pig genome assembly (Sscrofa9) in Ensembl release 59. Pre-miRNAs located outside of Ensembl transcripts were classified as "intergenic", while those overlapping the intron or exon of annotated transcripts were classified as "intronic" or "exonic", respectively. Infrequently, pre-miRNAs matched both introns and exons, depending on the alternative splicing patterns were categorized as "mixed"

Pre-miRNA ID	Group	Pre-miRNA name	Pre-miRNA sequence	Length (nt)	Location No.	Chromosome	Strand	Start	End	Genomic context (Ensembl BLAT)
1	miRBase 15.0 (with genome loctaion)	mir-30c	gacagatacTGTAAACATCCTACACTCTCAGCTgtggaaagtaagaaagctgggagaaggctgtttactctctctgcctt	80	1	1	-	53,819,906	53,819,985	Intergenic
2	miRBase 15.0 (with genome loctaion)	mir-30a	tccctgcgacagtgagcggcTGTAAACATCCTCGACTGGAAGCTgtgaggctgaagacgggctttcagtcggatgttttgcagccgccgcctgcctcccgcatcagga	107	1	1	-	53,848,998	53,849,104	Intergenic
3	miRBase 15.0 (with genome loctaion)	mir-122	ccttagcagagctgTGGAGTGTGACAATGGTGTTTGTgtccaaactatcaaacgccattatcacactaaatagctactgttaggc	85	1	1	-	169,284,211	169,284,295	Intergenic
4	miRBase 15.0 (with genome loctaion)	mir-101-1	gactgaactgtccttttcggttatcatggtaccgatgctgtatatctgaaaggTACAGTACTGTGATAACTGAAGaatggtggtgccatc	91	1	1	-	227,255,282	227,255,372	Intronic
5	miRBase 15.0 (with genome loctaion)	mir-204	ggctacagtccttctcatgtgactcgtggacTTCCCTTTGTCATCCTATGCCTgagaatatatgaaggaggctgggaaggcaaagggacgttcaattgtcatcactggc	109	1	1	-	234,511,625	234,511,733	Intronic
6	miRBase 15.0 (with genome loctaion)	mir-455	tggcgtgagggTATGTGCCTTTGGACTACATCGTggaagccagcaccatgcagtccatgggcatatacacttgcctcaag	80	1	1	+	267,848,307	267,848,386	Intronic
7	miRBase 15.0 (with genome loctaion)	mir-181a-2	actccaaggAACATTCAACGCTGTCGGTGagtttgggatttgaaaaaaccaccgaccgttgactgtacctttggggttctt	80	1	1	+	280,334,006	280,334,085	Intergenic
8	miRBase 15.0 (with genome loctaion)	mir-181b-2	atggctgcactcAACATTCATTGCTGTCGGTGGGTTtgagtctgaatcaactcactgatcaatgaatgcaaactgcggaccaaaca	86	1	1	+	280,335,868	280,335,953	Intergenic
9	miRBase 15.0 (with genome loctaion)	mir-199b	ccgtctacccagtgtttagactatctgttcaggactcccaaattgtACAGTAGTCTGCACATTGGTTaggctgg	74	1	1	-	283,325,992	283,326,065	Intergenic
10	miRBase 15.0 (with genome loctaion)	mir-210	gcgcagggcagccactgcccaccgcacactgcgctgctccggacccaCTGTGCGTGTGACAGCGGCTGAtctgtcc	76	1	2	+	331,306	331,381	Intergenic
11	miRBase 15.0 (with genome loctaion)	mir-192	gcacagggctCTGACCTATGAATTGACAGCCagtgctctcatctcccctctggctgccaattccataggtcacaggtatg	80	1	2	+	5,685,412	5,685,491	Intergenic
12	miRBase 15.0 (with genome loctaion)	mir-130a	cgggccggagctcttttcacattgtgctactgtctgcacctatcactagCAGTGCAATGTTAAAAGGGCATTggccacg	79	1	2	-	11,301,854	11,301,932	Intergenic
13	miRBase 15.0 (with genome loctaion)	mir-129	cttcgtgaatCTTTTTGCGGTCTGGGCTTGCtgtacataactcaatagccggaagcccttaccccaaaaagcattcgcgg	80	1	2	-	17,100,324	17,100,403	Intergenic
14	miRBase 15.0 (with genome loctaion)	mir-199a	ccccgccaaCCCAGTGTTCAGACTACCTGTTCaggggGctctgaatgtgtacagtagtctgcacattggttaggctgggc	80	1	2	-	52,684,957	52,685,036	Intergenic
15	miRBase 15.0 (with genome loctaion)	mir-24-1	ctctgcctcccgtgcctactgagctgaaacacagttgatttgtgcagacTGGCTCAGTTCAGCAGGAACAGg	72	1	2	-	56,860,821	56,860,892	Intergenic
16	miRBase 15.0 (with genome loctaion)	mir-27a	tggcctgggggagcagggcttagctgcttgtgagcaggtccacagcaagtcgtgTTCACAGTGGCTAAGTTCCGCcccctgga	82	1	2	-	56,860,970	56,861,051	Intergenic
17	miRBase 15.0 (with genome loctaion)	mir-23a	cggctgggGttcctgggatgggatttgctgcctgtcacaaATCACATTGCCAGGGATTTCCAatcgacc	70	1	2	-	56,861,159	56,861,228	Intergenic
18	miRBase 15.0 (with genome loctaion)	mir-181c	caaggggttgggggAACATTCAACCTGTCGGTGAGTttgggcagctcaggcaaaccatcgaccgttgagtggaccccgaggcctgga	87	1	2	+	56,889,316	56,889,402	Intergenic
19	miRBase 15.0 (with genome loctaion)	mir-181d	tcacaatcAACATTCATTGTTGTCGGTGGGTgtgagacggaggccagacccaccgagggatgaatgtcactgtggctgg	80	1	2	+	56,889,500	56,889,579	Intergenic
20	miRBase 15.0 (with genome loctaion)	mir-340	tacctggtgtgaTTATAAAGCAATGAGACTGATTGtcatatgtcgttttgtgggatccgtctcagttactttatagccata	80	1	2	+	67,820,612	67,820,691	Intergenic
20	miRBase 15.0 (with genome loctaion)	mir-340	tacctggtgtgaTTATAAAGCAATGAGACTGATTGtcatatgtcgttttgtgggatccgtctcagttactttatagccata	80	2	2	+	67,919,929	67,920,008	Intergenic
21	miRBase 15.0 (with genome loctaion)	mir-143	gtcccccagccggaggtgcagtgctgcatctctggtcagctgggagtcTGAGATGAAGCACTGTAGCTCGggaagggaga	80	1	2	+	136,030,752	136,030,831	Intergenic
22	miRBase 15.0 (with genome loctaion)	mir-145	caccttgtcctcacgGTCCAGTTTTCCCAGGAATCCCTtagatgctgagatggggattcctggaaatactgttcttgaggtcatgg	86	1	2	+	136,032,141	136,032,226	Intergenic
23	miRBase 15.0 (with genome loctaion)	mir-378	ccacccagggctcctgactccaggtcctgtgtgttgcctggaaatagcACTGGACTTGGAGTCAGAAGGCctgcgtggag	80	1	2	+	136,265,603	136,265,682	Intergenic
24	miRBase 15.0 (with genome loctaion)	mir-339	gcagccgccgTCCCTGTCCTCCAGGAGCTCACTtaccttgggccgtgagctcctcgaggccagagcccgtgtctgcctct	80	1	3	+	406,870	406,949	Intronic
25	miRBase 15.0 (with genome loctaion)	mir-365-1	cgcagggaaaatgagggacttttgggggcagatgtgtttccattccactatcaTAATGCCCCTAAAAATCCTTATtgctc	80	1	3	+	26,344,192	26,344,271	Intergenic
26	miRBase 15.0 (with genome loctaion)	mir-216	gatggctgtgagttggcTAATCTCAGCTGGCAACTGTGAgatgttcatacaatcccccacagtggtctctgggattatgctaaacagagcaatttccttgccct	105	1	3	+	79,165,852	79,165,956	Intergenic
26	miRBase 15.0 (with genome loctaion)	mir-216	gatggctgtgagttggcTAATCTCAGCTGGCAACTGTGAgatgttcatacaatcccccacagtggtctctgggattatgctaaacagagcaatttccttgccct	105	2	3	-	79,385,092	79,385,196	Intergenic
27	miRBase 15.0 (with genome loctaion)	mir-217	ataattattacagagtttttgatgtcgcagaTACTGCATCAGGAACTGATTGGAtaagaattggtcaccatcagttcttaatgcattgccttcagcatctaaacaag	107	1	3	+	79,172,584	79,172,690	Intergenic
27	miRBase 15.0 (with genome loctaion)	mir-217	ataattattacagagtttttgatgtcgcagaTACTGCATCAGGAACTGATTGGAtaagaattggtcaccatcagttcttaatgcattgccttcagcatctaaacaag	107	2	3	-	79,378,361	79,378,467	Intergenic
28	miRBase 15.0 (with genome loctaion)	mir-30d	ctgttgtTGTAAACATCCCCGACTGGAAGCtgtaagacatagctaagctttcagtcagatgtttgctgccaccgactct	79	1	4	+	5,729,459	5,729,537	Intergenic
29	miRBase 15.0 (with genome loctaion)	mir-30b	tttcagttcgTGTAAACATCCTACACTCAGCTgtaatacatggattggctgggaggtggatgtttacttcagctga	76	1	4	+	5,733,584	5,733,659	Intergenic
30	miRBase 15.0 (with genome loctaion)	mir-124a-1	tcaagaccagactctgccctccgtgttcacagcggaccttgatttaatgtcatacaatTAAGGCACGCGGTGAATGCCAAgagcggagcctacggctgcacttga	105	1	4	-	72,452,797	72,452,901	Intergenic
31	miRBase 15.0 (with genome loctaion)	mir-92b	gcgggcgggagggacgggacgcggtgcagtgttgttctttccccTgccaaTATTGCACTCGTCCCGGCCTCCggcccccc	80	1	4	-	98,703,325	98,703,404	Intergenic
32	miRBase 15.0 (with genome loctaion)	mir-148b	atttgaggtgaagttctgttatacactcaggctgtggctctctgaaagTCAGTGCATCACAGAACTTTGTCTcgaaagct	80	1	5	+	18,088,734	18,088,813	Intronic
33	miRBase 15.0 (with genome loctaion)	let-7i	ctggcTGAGGTAGTAGTTTGTGCTGTTggtcgggttgtgacattgcccgctgtggagataactgcgcaagctactgccttgctag	85	1	5	+	26,807,364	26,807,448	Intergenic
34	miRBase 15.0 (with genome loctaion)	mir-135-2	agataaattcactctagtgcttTATGGCTTTTTATTCCTATGTGAtagtaataaagtctcatgtagggatggaagccatgaaatacattgtgaaaaatca	100	1	5	-	81,615,635	81,615,734	Intergenic
35	miRBase 15.0 (with genome loctaion)	mir-331	ttgtttgggtttgttctaggtatggtcccagggatcccagatcaaaccagGCCCCTGGGCCTATCCTAGAaccaacctaa	80	1	5	+	82,983,750	82,983,829	Intergenic
36	miRBase 15.0 (with genome loctaion)	mir-328	ggagcgggggggcaggaggggctcagggagaaagtgtgtgccgcccCTGGCCCTCTCTGCCCTTCCGTcccccgttcctg	80	1	6	+	13,347,429	13,347,508	Intergenic
37	miRBase 15.0 (with genome loctaion)	mir-769	tgcgctctgaccTGAGACCTCTGGGTTCTGAGCTgtgatgttgcttccaagctgggatctctggggtcttggttcagggt	80	1	6	-	36,259,104	36,259,183	Intergenic
38	miRBase 15.0 (with genome loctaion)	mir-99b	ggcacccCACCCGTAGAACCGACCTTGCGgggccttcgccgcacacaagctcgtgtctgtgggtccgtgtc	70	1	6	+	39,533,216	39,533,285	Intergenic
39	miRBase 15.0 (with genome loctaion)	let-7e	gccccgggcTGAGGTAGGAGGTTGTATAGTTgaggaggacacccacggagatcactatacggcctcctagctttccccag	80	1	6	+	39,533,375	39,533,454	Intergenic
40	miRBase 15.0 (with genome loctaion)	mir-125a	ggccctctgagTCCCTGAGACCCTTTAACCTGTgaggacatcagggtcacaggtgaggttcttgggagcctggcgtccgg	80	1	6	+	39,533,851	39,533,930	Intergenic
41	miRBase 15.0 (with genome loctaion)	mir-935	ggcgcaggcggcagtggcgggagcggcccctcggccatcctccgtctgccCAGTTACCGCTTCCGCTACCGccgccgctc	80	1	6	+	40,293,236	40,293,315	Exonicic
41	miRBase 15.0 (with genome loctaion)	mir-935	ggcgcaggcggcagtggcgggagcggcccctcggccatcctccgtctgccCAGTTACCGCTTCCGCTACCGccgccgctc	80	2	6	+	40,351,581	40,351,660	Exonicic
42	miRBase 15.0 (with genome loctaion)	mir-186	tgcttataacctttcCAAAGAATTCTCCTTTTTGGGCTTtatgattttattttaagcccaaaggtgaatttttttgggaagtttg	82	1	6	+	99,703,517	99,703,598	Intronic
43	miRBase 15.0 (with genome loctaion)	mir-101-2	ggctgccctggctcagttatcacagtgctgatgctgtccattctaaaggTACAGTACTGTGATAACTGAAGgatggcagcc	81	1	6	+	103,818,808	103,818,888	Intergenic
44	miRBase 15.0 (with genome loctaion)	mir-30e	tttgccacTGTAAACATCCTTGACTGGAAGCTgtgaggcgttcccaggagctttcagtcggatgtttacagcggcaggct	80	1	6	-	121,824,301	121,824,380	Intronic
45	miRBase 15.0 (with genome loctaion)	mir-133b	cctgctctggctggtcaaacggaaccaagtccgtcttcctgagaggTTTGGTCCCCTTCAACCAGCTATagcagggctgg	80	1	7	+	53,115,236	53,115,315	Intergenic
46	miRBase 15.0 (with genome loctaion)	mir-184	ccagtcacatccccttatcacttttccagccagctttgtgactctaaatgtTGGACGGAGAACTGATAAGGGTAggtgattga	83	1	7	+	54,379,989	54,380,071	Intergenic
47	miRBase 15.0 (with genome loctaion)	mir-744	gcagggTGCGGGGCTAGGGCTAACAGCAgtcttactgaaggtttccctggaaaccacgcacatgctgttgccactaacctc	80	1	7	+	108,483,610	108,483,689	Intronic
47	miRBase 15.0 (with genome loctaion)	mir-744	gcagggTGCGGGGCTAGGGCTAACAGCAgtcttactgaaggtttccctggaaaccacgcacatgctgttgccactaacctc	80	2	12	+	53,485,953	53,486,032	Intronic
48	miRBase 15.0 (with genome loctaion)	mir-342	aaggtgagggtgctatctgtgactgagggacatggcgcatagaactgTCTCACACAGAAATCGCACCCGTcaccttggcc	80	1	7	-	130,281,629	130,281,708	Intronic
49	miRBase 15.0 (with genome loctaion)	mir-345	aacccaggtctgctgactcctagtccagtgcttgtgatggctggtgggcCCTGAACTAGGGGTCTGGAGGcctgggtttg	80	1	7	+	130,435,923	130,436,002	Intergenic
49	miRBase 15.0 (with genome loctaion)	mir-345	aacccaggtctgctgactcctagtccagtgcttgtgatggctggtgggcCCTGAACTAGGGGTCTGGAGGcctgggtttg	80	2	7	-	130,622,836	130,622,915	Intergenic
50	miRBase 15.0 (with genome loctaion)	mir-432	tccaggTCTTGGAGTAGGTCATTGGGTggatcctttatttccctatgtgggccactggatggctcctccatggcttggag	80	1	7	+	133,834,157	133,834,236	Intergenic
51	miRBase 15.0 (with genome loctaion)	mir-136	tgagccctcggaggACTCCATTTGTTTTGATGATGGattcttacgctccatcatcgtctcaaatgagtcttcagagggttct	82	1	7	+	133,834,348	133,834,429	Intergenic
52	miRBase 15.0 (with genome loctaion)	mir-127	atcgctgtctccagcctgctgaagctcagagggctctgattcagaaagatcaTCGGATCCGTCTGAGCTTGGCTggtcgg	80	1	7	+	133,929,738	133,929,817	Intergenic
53	miRBase 15.0 (with genome loctaion)	mir-95	aacacagtgggcgctcaataaatgtttgttgaattgagatgcgttaaattcAACGGGTATTTATTGAGCacccactctgtg	81	1	8	-	3,350,578	3,350,658	Intronic
54	miRBase 15.0 (with genome loctaion)	mir-574	tgggtgcgggcgtgtgagtgtgtgtgtgagtgtgtgtcgctccgggtcCACGCTCATGCACACACCCACAcgcccgca	80	1	8	+	25,753,375	25,753,454	Intronic
55	Ensemble (with genome loctaion)	mir-139	gtgtatTCTACAGTGCACGTGTCTCCAGTgtggctcggaggctggagacgcggccctgttggagtaac	68	1	9	-	6,808,359	6,808,426	Intergenic
56	miRBase 15.0 (with genome loctaion)	mir-326	tctgtctgttgggctggaggcagggcctttgtgcaggcgggttgtgctcagatcgCCTCTGGGCCCTTCCTCCAGCCcagaggcggattca	91	1	9	-	9,132,230	9,132,320	Intergenic
57	miRBase 15.0 (with genome loctaion)	mir-708	ccctcaaggagcttacaatctagctgggggtgaatgacttgcacatgaacgCAACTAGACTGTGAGCTTCTAGagggcag	80	1	9	-	13,711,347	13,711,426	Intergenic
58	miRBase 15.0 (with genome loctaion)	mir-34c	agtctagttactAGGCAGTGTAGTTAGCTGATTGCtgataaaaccaatcactaaccacaggccaggtaaaaagatttgg	80	1	9	+	38,211,158	38,211,237	Intergenic
58	miRBase 15.0 (with genome loctaion)	mir-34c	agtctagttactAGGCAGTGTAGTTAGCTGATTGCtgataaaaccaatcactaaccacaggccaggtaaaaagatttgg	80	2	9	+	38,328,136	38,328,215	Intronic
59	miRBase 15.0 (with genome loctaion)	mir-1308	gagggagaaactagtcactccaaaatagaacaccatcagGCATTGgTGGTTCAGTGgtagaattcttgccggccagaac	80	1	9	+	46,759,497	46,759,576	Intergenic
60	miRBase 15.0 (with genome loctaion)	mir-125b-1	cctctcagTCCCTGAGACCCTAACTTGTGAtgtttaccgtttaaatccacgggttaggctcttgggagctgcgagccgtg	80	1	9	-	47,573,167	47,573,246	Intergenic
60	miRBase 15.0 (with genome loctaion)	mir-125b-1	cctctcagTCCCTGAGACCCTAACTTGTGAtgtttaccgtttaaatccacgggttaggctcttgggagctgcgagccgtg	80	2	9	-	47,654,247	47,654,326	Intergenic
61	miRBase 15.0 (with genome loctaion)	let-7a	cccaggtTGAGGTAGTAGGTTGTATAGTTagaattgtatcaagggagataactgtacagcctcctagctttcctTgggt	80	1	9	-	47,697,398	47,697,477	Intergenic
62	miRBase 15.0 (with genome loctaion)	mir-100	aggcctgttgccacaACCCCGTAGATCCGAACTTGTGCtgatagtgcacacaagcttgtgtctataggtatgtgtctgtg	80	1	9	-	47,702,721	47,702,800	Intergenic
63	miRBase 15.0 (with genome loctaion)	mir-214	ggcctggctggacggagttgtcatgtgtcTGCCTGTCTACACTTGCTGTGCagaacatccgctcacctgtacagcaggcacagacaggcagtcacatgacaacccagcct	110	1	9	-	107,639,153	107,639,262	Intergenic
64	miRBase 15.0 (with genome loctaion)	mir-205	ctcttgTCCTTCATTCCACCGGAGTCTGtctcatacccaaccagatttcagtggagtgaagctcaggag	69	1	9	-	126,011,588	126,011,656	Intergenic
65	Ensemble (with genome loctaion)	mir-29c	atctcttacacaggctgaccgatttctcctggtgttcagagtctgtttttgtcTAGCACCATTTGAAATCGGTTatgatgtaggggga	88	1	9	+	127,174,326	127,174,413	Intergenic
66	miRBase 15.0 (with genome loctaion)	mir-215	agagatggtgtacaggaaaATGACCTATGAATTGACAGACAatgtggctaaatctgtctgtcatttctgtaggccaatattctgtatatctctgct	96	1	10	-	9,750,609	9,750,704	Intergenic
67	miRBase 15.0 (with genome loctaion)	mir-181b-1	ggtcacaatcAACATTCATTGCTGTCGGTGGGTTgaactgtgtagacaagctcactgaacaatgaatgcaactgtggccc	80	1	10	-	22,839,191	22,839,270	Intergenic
68	miRBase 15.0 (with genome loctaion)	mir-181a-1	gagtttagaggttgcttcagtgaacattcaacgctgtcggtgagtttggaattcaaatcaaaACCATCGACCGTTGATTGTACCctatggccaaccatcagctc	104	1	10	-	22,839,352	22,839,455	Intergenic
69	miRBase 15.0 (with genome loctaion)	mir-24-2	gacccgccctccggtgcctactgagctgatatcagttctcattttacacacTGGCTCAGTTCAGCAGGAACAGgagtcga	80	1	10	-	26,148,230	26,148,309	Intronic
70	miRBase 15.0 (with genome loctaion)	mir-27b	acgaggtgcagagcttagctgattggtgaacagtgactggtttccgctttgTTCACAGTGGCTAAGTTCTGCacctgaag	80	1	10	-	26,148,776	26,148,855	Intronic
71	miRBase 15.0 (with genome loctaion)	mir-23b	ctctggctgcttgggttcctggcatgctgatttgtgacttaagattaaaATCACATTGCCAGGGATTACCACGcagccac	80	1	10	-	26,149,010	26,149,089	Intronic
72	miRBase 15.0 (with genome loctaion)	mir-15a	ttggagtaaagTAGCAGCACATAATGGTTTGTGgatttttgaaaaggtgcaggccatattgtgctgcctcaaaaatacaa	79	1	11	+	17,602,978	17,603,056	Intergenic
73	miRBase 15.0 (with genome loctaion)	mir-16-2	cagtgccttagcagcacgtaaatattggcgTTAAGATTCTAAAATTATCTccagtattaactgtgctgctgaagtaagg	79	1	11	+	17,603,121	17,603,199	Intergenic
74	miRBase 15.0 (with genome loctaion)	mir-17	gaataatgtCAAAGTGCTTACAGTGCAGGTAGTgataatgtgcatctactgcagtgaaggcacttgtagcattatgg	77	1	11	+	60,972,458	60,972,534	Intergenic
75	miRBase 15.0 (with genome loctaion)	mir-18	gtgctttttgttcTAAGGTGCATCTAGTGCagatagtgaagtagattagcatctactgccctaagtgctccttctggcataagaagttatgt	92	1	11	+	60,972,593	60,972,684	Intergenic
76	miRBase 15.0 (with genome loctaion)	mir-19a	gcagtcctctgttagttttgcatagttgcactacaagaagaatgtAGTTGTGCAAATCTATGCAAAACTGAtggtggcctgc	82	1	11	+	60,972,741	60,972,822	Intergenic
77	miRBase 15.0 (with genome loctaion)	mir-20	gtagcacTAAAGTGCTTATAGTGCAGGTAGTgtttagttatctactgcattatgagcacttaaagtactgc	71	1	11	+	60,972,911	60,972,981	Intergenic
78	miRBase 15.0 (with genome loctaion)	mir-19b-1	ctgttctatggttagttttgcaggtttgcatccagctgtgtgatattctgcTGTGCAAATCCATGCAAAACTGActgtgg	80	1	11	+	60,973,040	60,973,119	Intergenic
79	miRBase 15.0 (with genome loctaion)	mir-92a-1	ctttctacacaggttgggatcggttgcaatgctgtgtttctgtatggTATTGCACTTGTCCCGGCCTGTTGagtttggtg	80	1	11	+	60,973,160	60,973,239	Intergenic
80	miRBase 15.0 (with genome loctaion)	mir-152	cggcccaggttctgtgatacacctccgactcgggctctggagcagTCAGTGCATGACAGAACTTGGgcccggacggacctt	80	1	12	+	21,743,215	21,743,294	Intergenic
81	miRBase 15.0 (with genome loctaion)	mir-10a	tctgtatatACCCTGTAGATCCGAATTTGTGTaaggaattttgtggtcacaaattcgtatctaggggaatatgtagttga	80	1	12	-	22,389,424	22,389,503	Intergenic
82	miRBase 15.0 (with genome loctaion)	mir-142	gtgcagtcacccataaagtagaaagcactactaacagcactggagggTGTAGTGTTTCCTACTTTATGGatgagtgtact	80	1	12	-	32,630,403	32,630,482	Intergenic
83	miRBase 15.0 (with genome loctaion)	mir-21	tgtaccaccttgtcgggTAGCTTATCAGACTGATGTTGACtgttgaatctcatggcaacagcagtcgatgggctgtctgacattttggtatc	92	1	12	+	34,201,565	34,201,656	Intergenic
84	miRBase 15.0 (with genome loctaion)	mir-365-2	aaaaatgagggactttcaggggcagctgtgttttctgactcagtcaTAATGCCCCTAAAAATCCTTATtgttcttgcagt	80	1	12	-	41,107,186	41,107,265	Intergenic
85	miRBase 15.0 (with genome loctaion)	mir-193a	gcgggagctgagggctgggtctttgcgggcgagatgagggtgttggttcAACTGGCCTACAAAGTCCCAGTcctcggccc	80	1	12	-	41,119,432	41,119,511	Intergenic
86	miRBase 15.0 (with genome loctaion)	mir-423	aagttaggctgaggggcagagagcgagacttttctattttccaaaAGCTCGGTCTGAGGCCCCTCAGTcttgcttcctac	80	1	12	+	44,150,500	44,150,579	Intronic
87	miRBase 15.0 (with genome loctaion)	mir-22	gagccgcagtagttcttcagtggcaagctttatgtcctgacccagctaAAGCTGCCAGTTGAAGAACTGTTgccctctgc	80	1	12	+	45,319,043	45,319,122	Intergenic
88	miRBase 15.0 (with genome loctaion)	mir-497	cccgcccCAGCAGCACACTGTGGTTTGTAcggcactgtggccagtccaaaccacactgtggtgttagagcgagggtggg	80	1	12	+	49,575,594	49,575,673	Intergenic
89	miRBase 15.0 (with genome loctaion)	mir-195	cagcccccctggctcTAGCAGCACAGAAATATTGGCAccgggcggagagtctgccagtattggctgtgctgccccaggca	80	1	12	+	49,575,884	49,575,963	Intergenic
90	miRBase 15.0 (with genome loctaion)	mir-324	ctatgcctcccCGCATCCCCTAGGGCATTGGTGTgaagctggagacccactgccccaggtgctgctgggggttgtagtct	80	1	12	+	49,872,807	49,872,886	Intergenic
91	miRBase 15.0 (with genome loctaion)	mir-128-2	gcagtgggaagggggccgaggcactgtccgagagtgagtagcaggtcTCACAGTGAACCGGTCTCTTTccctactgtgt	80	1	13	+	17,766,863	17,766,942	Intronic
92	miRBase 15.0 (with genome loctaion)	mir-425	aagtgctttggAATGACACGATCACTCCCGTTGAgtgggcacccaagtagccatcgggaatgtcgtgtccgcccagtgct	80	1	13	-	26,605,151	26,605,230	Intronic
93	miRBase 15.0 (with genome loctaion)	mir-191	acagcgggCAACGGAATCCCAAAAGCAGCTGttgtctccagagcattccagctgcacttggatttcgttccctgctctct	80	1	13	-	26,605,641	26,605,720	Intronic
94	miRBase 15.0 (with genome loctaion)	mir-135-1	aggcctcgctgttctcTATGGCTTTTTATTCCTATGTGAttctactgctcattcatatagggattggagccgtggcgcacggcggggaca	90	1	13	+	28,964,466	28,964,555	Intergenic
95	miRBase 15.0 (with genome loctaion)	let-7g	ggcTGAGGTAGTAGTTTGTACAGTTtgagggtctatgataccacccggtacaggagataactgtacaggccactgcttg	80	1	13	+	28,999,419	28,999,498	Intronic
96	miRBase 15.0 (with genome loctaion)	mir-885	cactcggcccgcgctctcTCCATTACACTACCCTGCCTCTtctccacgagaggcagcgggggtgtagtggatagagcacgg	80	1	13	-	55,826,401	55,826,480	Intronic
97	miRBase 15.0 (with genome loctaion)	mir-15b	ttgaggccttaaagtactgTAGCAGCACATCATGGTTTACAtactacaatcaagatgcgaatcattatttgctgctctagaaatttaaggaaattcat	98	1	13	+	78,787,511	78,787,608	Intronic

98	miRBase 15.0 (with genome loctaion)	mir-16-1	tccgctcTATGCAGCACGTAAATATTGGCGtagtaaaataaatattaaacaccaatattattgtgctgctttagcgtg	77	1	13	+	78,787,668	78,787,744	Intronic
99	Ensemble (with genome loctaion)	mir-28	ggtccttgccctcaaggagctcacagtctattgagttgcctttctgtcttcccCACTAGATTGTGAGCTCCTGGAgggcaggcact	86	1	13	-	95,264,193	95,264,278	Intergenic
100	miRBase 15.0 (with genome loctaion)	mir-99a	ccattggcataAACCCGTAGATCCGATCTTGTGGtgaagtggaccgcacaagctcgcttctatgggtctgtgtcagtgtg	80	1	13	+	130,664,295	130,664,374	Intergenic
101	miRBase 15.0 (with genome loctaion)	let-7c	tgtgtgcatccgggtTGAGGTAGTAGGTTGTATGGTTtagagttacaccgtgggagttaactgtacaaccttctagctttccttggagcacact	94	1	13	+	130,665,021	130,665,114	Intergenic
102	miRBase 15.0 (with genome loctaion)	mir-320	gctcccctccgcctctctctcccggttcttcccggagtcgggAAAAGCTGGGTTGAGAGGGCGAaaaaggaagaaggggac	80	1	14	-	6,473,891	6,473,970	Intergenic
103	miRBase 15.0 (with genome loctaion)	mir-124a-2	aggcctctctctccgtgttcacagcggacctgattaaatgtccatacaatTAAGGCACGCGGTGAATGCCAAgaatgggcctg	85	1	14	-	13,279,339	13,279,423	Intergenic
104	miRBase 15.0 (with genome loctaion)	mir-130b	gcctgcctgacactctttccctgttgcactactgtgggccactgggaagCAGTGCAATGATGAAAGGGCATcagtcaggc	80	1	14	-	51,318,779	51,318,858	Intergenic
105	miRBase 15.0 (with genome loctaion)	mir-185	ggtgagggatTGGAGAGAAAGGCAGTTCCTGATggtcccctcccccagggctggctttcctctggtcctttccctcc	76	1	14	+	52,703,712	52,703,787	Intergenic
106	miRBase 15.0 (with genome loctaion)	mir-1306	gtctccaCCACCTCCCCTGCAAACGTCCAGTgatgcagaggtaatggacgttggctctggtggtgatggacaggccgaac	80	1	14	+	52,728,146	52,728,225	Exonicic
107	miRBase 15.0 (with genome loctaion)	mir-107	ttctctctgctttcagctttttacagtgttgcctttgtggcatggagttcaAGCAGCATTGTACAGGGCTATcaaagcacagagagc	87	1	14	-	106,321,702	106,321,788	Intronic
108	miRBase 15.0 (with genome loctaion)	mir-146b	gaacttggccacctggctcTGAGAACTGAATTCCATAGGCTGTgagctctagcaaatgccctaggaactcagttctggtgcccggctgtgctatagtc	99	1	14	+	118,471,588	118,471,686	Intergenic
109	miRBase 15.0 (with genome loctaion)	mir-1307	ctaccaatcTCGACCGGACCTCGACCGGCTcgtctatgttgccaatcgactcggcgtggcgtcggtcgtggtagataggc	80	1	14	-	119,440,203	119,440,282	Intronic
110	miRBase 15.0 (with genome loctaion)	mir-202	cgccgttccgcCTTCCTATGCATATACTTCTTTgagggtctggcctgaagaggtgtaggcatgggaaaccgggggcgacga	80	1	14	-	147,952,465	147,952,544	Intergenic
111	miRBase 15.0 (with genome loctaion)	mir-128-1	tgagctgttggattcggggccgtagcacttctgagaggtttacatttcTCACAGTGAACCGGTCTCTTTtcagctgcttc	82	1	15	-	14,550,874	14,550,955	Intronic
112	miRBase 15.0 (with genome loctaion)	mir-10b	gtctatataTACCCTGTAGAACCGAATTTGTgtggtatccacatagtcacagattcgattctagggggaatatatgtcga	80	1	15	+	77,060,704	77,060,783	Intergenic
113	miRBase 15.0 (with genome loctaion)	mir-103-1	cttactgccctcggcttctttacagtgctgccttgttgcatatggatcaAGCAGCATTGTACAGGGCTATGAaggcactgag	82	1	16	-	52,667,657	52,667,738	Intronic
114	miRBase 15.0 (with genome loctaion)	mir-486	gctggggcttcagggccagctcggacctctgacctccctgacgggTCCTGTACTGAGCTGCCCCGAGgccctcactgtgc	80	1	17	+	10,558,722	10,558,801	Intronic
114	miRBase 15.0 (with genome loctaion)	mir-486	gctggggcttcagggccagctcggacctctgacctccctgacgggTCCTGTACTGAGCTGCCCCGAGgccctcactgtgc	80	2	17	+	10,710,522	10,710,601	Intronic
115	miRBase 15.0 (with genome loctaion)	mir-103-2	tgtgctttcagcttctttacagtgctgccttgtagcattcaggtcaAGCAGCATTGTACAGGGCTATGAaagaactaaga	80	1	17	-	33,406,489	33,406,568	Intergenic
115	miRBase 15.0 (with genome loctaion)	mir-103-2	tgtgctttcagcttctttacagtgctgccttgtagcattcaggtcaAGCAGCATTGTACAGGGCTATGAaagaactaaga	80	2	17	-	33,574,977	33,575,056	Intergenic
116	miRBase 15.0 (with genome loctaion)	mir-499	tgggcgggcggccgTTAAGACTTGCAGTGATGTTTaactcctctccacgtgaacatcacagcaagtctgtgctgcttccc	80	1	17	-	40,405,262	40,405,341	Intronic
117	miRBase 15.0 (with genome loctaion)	mir-133a	cgggacccaaatgctttgctaaagctggtaaaatggaaccaaatcaactgttgaatggatTTGGTCCCCTTCAACCAGCTGTagctgcgcattgacagcgccg	103	1	17	-	64,053,943	64,054,045	Intergenic
118	miRBase 15.0 (with genome loctaion)	mir-1	ccggttgacgtacctgcttgggggacatacttctttatgtgcccatatggacctgctaagctaTGGAATGTAAAGAAGTATGTATTtcaggctgggaactctcaccgg	108	1	17	+	64,096,222	64,096,329	Intergenic
119	miRBase 15.0 (with genome loctaion)	mir-29b	cttcaggaagctggtttcatatggtggtttagatttaaaaagtgattgtcTAGCACCATTTGAAATCAGTGTTcttggggg	81	1	18	+	16,054,349	16,054,429	Intergenic
120	miRBase 15.0 (with genome loctaion)	mir-29a	cccctagaggatgactgatttcttttggtgttcagagtcaatataattttcTAGCACCATCTGAAATCGGTTataatgattgggg	86	1	18	+	16,054,752	16,054,837	Intergenic
121	miRBase 15.0 (with genome loctaion)	mir-335	cttttgggcgggggtcaagagcaataacgaaaaatgtttgtcataaaccgTTTTTCATTATTGCTCCTGACCtcctctca	80	1	18	-	16,506,711	16,506,790	Intronic
122	miRBase 15.0 (with genome loctaion)	mir-183	ctgtgTATGGCACTGGTAGAATTCACTgtgaacagtctcggtcagtgaattaccgaagggccataaacag	70	1	18	-	17,172,238	17,172,307	Intergenic
123	miRBase 15.0 (with genome loctaion)	mir-196b	ctggtcggtgattTAGGTAGTTTCCTGTTGTTGGGatccaccttttctctcgacagcacgacactgccttcattacttcag	80	1	18	+	44,179,792	44,179,871	Intronic
123	miRBase 15.0 (with genome loctaion)	mir-196b	ctggtcggtgattTAGGTAGTTTCCTGTTGTTGGGatccaccttttctctcgacagcacgacactgccttcattacttcag	80	2	18	+	44,205,846	44,205,925	Intronic
124	miRBase 15.0 (with genome loctaion)	mir-148a	gaggcaaagttctgagacactccgactctgaatatgatagaagTCAGTGCACTACAGAACTTTGTctc	68	1	18	-	45,214,548	45,214,615	Intergenic
125	miRBase 15.0 (with genome loctaion)	mir-221	tgaACCTGGCATACAATGTAGATTTCTGTgtttgttgggcaacagctacattgtctgctgggtttcaggc	70	1	X	-	40,478,094	40,478,163	Intergenic
126	miRBase 15.0 (with genome loctaion)	mir-222	tgccctcaatggctcagtagccagtgtagatcctgtcatttgtaatcagtAGCTACATCTGGCTACTGGGTCTCTgatgg	80	1	X	-	40,478,834	40,478,913	Intergenic
127	miRBase 15.0 (with genome loctaion)	mir-98	gggTGAGGTAGTAAGTTGTATTGTTgtgggggtagggatttttaggccccaattagaagataactatacaacttactacttt	80	1	X	-	45,719,499	45,719,578	Intronic
128	miRBase 15.0 (with genome loctaion)	let-7f	tgtgggaTGAGGTAGTAGATTGTATAGTTttagggtcataccccatcttggagataactatacagtctactgtctttcccacg	83	1	X	-	45,720,363	45,720,445	Intronic
129	miRBase 15.0 (with genome loctaion)	mir-676	aacgcgtgactcttcaatctcaggactcgcataattagcagaatgCCGTCCTAAGGTTGTTGAGTTctgcgtttctgggc	80	1	X	-	55,113,034	55,113,113	Intronic
129	miRBase 15.0 (with genome loctaion)	mir-676	aacgcgtgactcttcaatctcaggactcgcataattagcagaatgCCGTCCTAAGGTTGTTGAGTTctgcgtttctgggc	80	2	X	-	55,165,137	55,165,216	Intronic
130	miRBase 15.0 (with genome loctaion)	mir-374b	tcggatggATATAATACAACCTGCTAAGTGtcctagcacttatcaggttgtattatcattgtccgtgtctatggctctcg	80	1	X	+	58,683,650	58,683,729	Intergenic
131	miRBase 15.0 (with genome loctaion)	mir-374a	catcggccaTTATAATACAACCTGATAAGTGttacagcacttatcaggttgtattgtaattgtctgtgtatatatgcc	80	1	X	-	58,793,654	58,793,733	Intergenic
132	miRBase 15.0 (with genome loctaion)	mir-325	agtgcttggttcctagtaggtgttcagtaagtgtttgtgacataattcgTTTATTGAGCACCTCCTATCAatcaagcactgtgctaggttctgg	94	1	X	+	60,496,392	60,496,485	Intergenic
132	miRBase 15.0 (with genome loctaion)	mir-325	agtgcttggttcctagtaggtgttcagtaagtgtttgtgacataattcgTTTATTGAGCACCTCCTATCAatcaagcactgtgctaggttctgg	94	2	X	-	60,552,421	60,552,514	Intergenic
133	miRBase 15.0 (with genome loctaion)	mir-361	ggagcTTATCAGAATCTCCAGGGGTACttataatttgaaaaagtcccccaggtgtgattctgatttgcttcctcctcctc	80	1	X	-	67,904,186	67,904,265	Intronic
134	miRBase 15.0 (with genome loctaion)	mir-1277	tagcctcccaaatatatatatatgtacgtatgtgtatatgaatgtaTACGTAGATATATATGTATTTttggtgggttt	80	1	X	-	97,562,457	97,562,536	Intronic
135	miRBase 15.0 (with genome loctaion)	mir-363	gctgttgtcgggtggatcacgatgcaattttgattagtatcataggagaaaAATTGCACGGTATCCATCTGTAaaccgca	80	1	X	-	108,178,321	108,178,400	Intergenic
135	miRBase 15.0 (with genome loctaion)	mir-363	gctgttgtcgggtggatcacgatgcaattttgattagtatcataggagaaaAATTGCACGGTATCCATCTGTAaaccgca	80	2	X	-	108,212,243	108,212,322	Intergenic
136	miRBase 15.0 (with genome loctaion)	mir-92a-2	ctttcatccgtgggtgggattttgttgcattacttgtggtgtgtataaagTATTGCACTTGTCCCGGCCTGTGGaagaaa	80	1	X	-	108,178,486	108,178,565	Intergenic
136	miRBase 15.0 (with genome loctaion)	mir-92a-2	ctttcatccgtgggtgggattttgttgcattacttgtggtgtgtataaagTATTGCACTTGTCCCGGCCTGTGGaagaaa	80	2	X	-	108,212,408	108,212,487	Intergenic
137	miRBase 15.0 (with genome loctaion)	mir-19b-2	tacagttagttttgcaggtttgcatttcagcgtatgtatgtgtatatggcTGTGCAAATCCATGCAAAACTGATtgtgat	80	1	X	-	108,178,624	108,178,703	Intergenic
137	miRBase 15.0 (with genome loctaion)	mir-19b-2	tacagttagttttgcaggtttgcatttcagcgtatgtatgtgtatatggcTGTGCAAATCCATGCAAAACTGATtgtgat	80	2	X	-	108,212,546	108,212,625	Intergenic
138	miRBase 15.0 (with genome loctaion)	mir-106a	ccttggccgtgtaaaagtGCTTACAGTGCAGGTAGctttttgagatctactgcaatgcaagcacttcttacattaccatgg	81	1	X	-	108,213,079	108,213,159	Intergenic
139	miRBase 15.0 (with genome loctaion)	mir-450a	gtctgtcaaagaaagatgctaaactggTTTTGCGATGTGTTCCTaatatgcagtataaaatatattgggagcattttgcatgcatggttttgtatcactatacagat	106	1	X	-	108,480,688	108,480,793	Intergenic
140	miRBase 15.0 (with genome loctaion)	mir-450c	ggcactaaactatTTTTGCGATGTGTTCCTaatacgtaatctaagtgtattgggaacattttgcattcgtagttttgtgtc	81	1	X	-	108,480,833	108,480,913	Intergenic
141	miRBase 15.0 (with genome loctaion)	mir-542	cctcagacgtcTCGGGGATCATCATGTCACGAGAgaccactgtgcacttgtgacagattgataactgaaaggtctgggag	80	1	X	-	108,481,539	108,481,618	Intergenic
142	miRBase 15.0 (with genome loctaion)	mir-503	gccccgcactcagccgtgcccTAGCAGCGGGAACAGTACTGCAGTgggcgatcggtactctggggtattgtttctgctgcccgggcaaggctgggactcccgccggggc	109	1	X	-	108,498,665	108,498,773	Intergenic
143	miRBase 15.0 (with genome loctaion)	mir-424	tccgaggggatgCAGCAGCAATTCATGTTTTGAagggctttaaatggttcaaaacgtgaggcgctgctataccccctcgc	80	1	X	-	108,499,011	108,499,090	Intergenic
144	miRBase 15.0 (with genome loctaion)	mir-504	gctgttgggAGACCCTGGTCTGCACTCTATCtgtatgcttactgaagggagcgcagggcagggtttcccacacagagggc	80	1	X	+	111,416,461	111,416,540	Intergenic
145	miRBase 15.0 (with genome loctaion)	mir-505	gcactcagtgggggagccaggaagtattgatgtttctgccaggttagcGTCAACACTTGCTGGTTTCCTCTctggagcat	80	1	X	+	112,590,812	112,590,891	Intronic
146	miRBase 15.0 (with genome loctaion)	mir-224	gggctttCAAGTCACTAGTGGTTCCGTTTAGtagaaggttttgcattgtttcaaaatggtgccctagtgactacaaagccc	81	1	X	-	121,480,634	121,480,714	Intronic
147	miRBase 15.0 (without genome loctaion)	mir-7	gcctgtagaatatagaagatttcagtggacgttggtctagttctgtgTGGAAGACTAGTGATTTTGTTGTTTgtagataactaaatcgacaacaaatcgcagtctgccatatggcacagaccatgcctctacaggac	139						
148	miRBase 15.0 (without genome loctaion)	mir-26a	aaggccgtggcctcgTTCAAGTAATCCAGGATAGGCTgtgcaggtcccaggggcctattctcggttacttgcacgcggacgcgggcctg	90						
149	miRBase 15.0 (without genome loctaion)	mir-32	ttcccattctgctagctctggtggagaTATTGCACATTACTAAGTTGCatgttgtcaaggcctctgtgcaatttagtgtgtgcgatattttcacatgagtgcatgcaccccggttg	116						
150	miRBase 15.0 (without genome loctaion)	mir-34a	ggccagctgtgagtgtttcttTGGCAGTGTCTTAGCTGGTTGTtgtgagtaatagataaggaagcaatcagcaagtatactgccctagaagtgctgcacgttgttaggccc	111						
151	miRBase 15.0 (without genome loctaion)	mir-140	gtgtctctctctgtgtcctgccagtggttttaccctatggtaggttacatcatgctgttctACCACAGGGTAGAACCACGGACaggatactggagcacc	99						
152	miRBase 15.0 (without genome loctaion)	mir-151	tttcctgcccTCGAGGAGCTCACAGTCTAGTAtgtctcatccccctactagactgaagctccttgaggacagggatggtcatactcacctc	90						
153	miRBase 15.0 (without genome loctaion)	mir-299	cggtacttgaagaaatggtttaccgtcccacatacattttgcatatgTATGTGGGACGGTAAACCGCTTcttggtatcc	79						
154	miRBase 15.0 (without genome loctaion)	mir-301	gctaacaaatGCTCTGACTTTATTGCACTACTgtacttacagctaccagtcccaatagtattgtcaaagcatctgagagcag	82						
155	miRBase 15.0 (without genome loctaion)	mir-323	ttggtacttggagagAGGTGGTCCGTGGCGCGTTCGctttatttatggcgcacattacacggtcgacctctttgcggtatctaatc	86						
156	miRBase 15.0 (without genome loctaion)	mir-338	caacgctgcacaggccgtcctccccAACAATATCCTGGTGCTGAGTgggtgcacagtgactccagcatcagtgattttgttgaagagggcagctgcca	98						
157	miRBase 15.0 (without genome loctaion)	mir-369	ttgaagggagatcgaccgtgttatattcgctttatggtactTgaagggagatcgaccgtgttatattcgcttggctgacttcgAATAATACATGGTTGATCTTTTctcagtatctgacttcgaataatacatggttgatcttttctcag	149						
158	miRBase 15.0 (without genome loctaion)	mir-376a	aatccttctttggtatttaaaaggTAGATTCTCCTTCTATGAGTAcattatttacgattaatcatagaggaaaatccacgttttcagtatcaaatgctg	99						
159	miRBase 15.0 (without genome loctaion)	mir-500	cccctctcTAATCCTTGCTACCTGGGTGAGAgtgctgtgtgaatgcaatgcacctgggcaaggattctgagagtgagagc	80						
160	miRBase 15.0 (without genome loctaion)	mir-532	cagatttgctttttctcttcCATGCCTTGAGTGTAGGACCGTgacatcttaattaccctcccacacccaaggcttgcaggagagcaagccttctc	96						
161	miRBase 15.0 (without genome loctaion)	mir-758	gcctgggtacatgagatggttgaccagagagcacacgctttattttgtgccgTTTGTGACCTGGTCCACTAACCctcagtatctaatcc	88						
162	PN(a)	PN(a)-1	tgcaggcctctgtgTGATATGTTTGATATATTAGGTTGttatttaatccaactatatatcaaacatattcctacagtgtcttgcc	85	1	1	-	112,612,943	112,613,027	Intronic
163	PN(a)	PN(a)-2	ccccagggtcctcttgtctgagccccagaaagaggagagagcgcTGGGTCACAGAAGAGGGTCTGGGgg	69	1	1	+	134,062,654	134,062,722	Intronic
163	PN(a)	PN(a)-2	ccccagggtcctcttgtctgagccccagaaagaggagagagcgcTGGGTCACAGAAGAGGGTCTGGGgg	69	2	1	-	134,001,047	134,001,115	Intronic
164	PN(a)	PN(a)-3	cagccagccccatcTGGAAGACTAGTGATTTTGTTGTTgtctcactgcgctcaacaacaagtcccagtctgccgcatggtgccggccactgca	93	1	1	-	200,316,390	200,316,482	Intergenic
165	PN(a)	PN(a)-4	tgctcctgtaacttggaactggagaggAGGCAAGATGCTGGCAtagctgttaaactgagaacctgctatgccaacatattgccatctttcttgtctgacagcagc	105	1	1	+	209,939,196	209,939,300	Intergenic
166	PN(a)	PN(a)-5	aattgacttagctgggtAGTGGGGAACCCTTCCATGAGGagtagaacactccttatgcaagattcccttctacctgactgggttgg	86	1	1	-	210,973,875	210,973,960	Intergenic
167	PN(a)	PN(a)-6	actcaggggcttcgccactgattgtccaaacgcaattcttgtacgagtctgcggccaaccgAGAATTGTGGCTGGACATCTGTggctgagctccggg	97	1	1	-	283,451,013	283,451,109	Intergenic
167	PN(a)	PN(a)-6	actcaggggcttcgccactgattgtccaaacgcaattcttgtacgagtctgcggccaaccgAGAATTGTGGCTGGACATCTGTggctgagctccggg	97	2	1	-	283,497,677	283,497,773	Intergenic
168	PN(a)	PN(a)-7	cgctggcgacgggacattattacttttggtacgcgctgtgacacttcaaacTCGTACCGTGAGTAATAATGCGctgtcggcagc	84	1	1	+	294,113,063	294,113,146	Intronic
169	PN(a)	PN(a)-8	tggctgccaccccctGTAACAGCAACTCCATGTGGAagtgcccactagttccagtggggctgctgttatctgggtgggggccag	85	1	2	+	5,685,207	5,685,291	Intergenic
170	PN(a)	PN(a)-9	ggtttcgggggtggatctgacatccctgagtgtatgtggtgaacctgaatttgccttgggTTTCCTCATATTCATTCAGGAGTGTcagttccccttcact	100	1	2	-	17,122,268	17,122,367	Intergenic
171	PN(a)	PN(a)-10	ggcttcggtgctgggagcggccccccggcgggcctctgctctggcccCTCCTGGGGCCCGCACTCTCGCTccggg	76	1	2	-	24,490,873	24,490,948	Intronic
172	PN(a)	PN(a)-11	TCTTTGGTTATCTAGCTGTATGAgtgtattggtcttcataaagctagataaccgaaagta	60	1	2	-	85,597,109	85,597,168	Intergenic
173	PN(a)	PN(a)-12	ttagccctgcggccccacgcaccagggtaagagagactctcgcttcCTGCCCTGGCCCGAGGGACCGACtggctgggc	78	1	2	-	126,729,110	126,729,187	Intronic
174	PN(a)	PN(a)-13	tcttcactgtgggaTGAGGTAGTAGGTTGTATAGTTttagggtcacaccccaccactgggagataactatacaatctactgtctttcctaacgtgat	96	1	3	+	38,549,756	38,549,851	Intergenic
175	PN(a)	PN(a)-14	atcagagTGAGGTAGTAGATTGTATAGTTgtggggtagtgattttaccctgttcaggagataactatacaatctattgccttccctgag	89	1	3	+	38,550,130	38,550,218	Intergenic
176	PN(a)	PN(a)-15	aatgggttcctaggaAGAGGTAGTAGGTTGCATAGTTttagggcagagattttgcccacaaggaggtaactatacgacctgctgcctttcttagggccttattatt	106	1	3	+	38,552,589	38,552,694	Intergenic
177	PN(a)	PN(a)-16	gtggcagactggaAAATCTCTGCAGGCAAATGTGAtgttactaaagaaatcacacacttacctgtagagattctacagtctgacat	86	1	3	+	79,154,190	79,154,275	Intergenic
178	PN(a)	PN(a)-17	TCTTTGGTTATCTAGCTGTATGAgtggtgtggagtcttcataaagctagataaccgaaagta	62	1	4	+	97,531,341	97,531,402	Intergenic
178	PN(a)	PN(a)-17	TCTTTGGTTATCTAGCTGTATGAgtggtgtggagtcttcataaagctagataaccgaaagta	62	2	4	-	97,746,803	97,746,864	Intergenic
179	PN(a)	PN(a)-18	gaggcaatgtggagtgactgtcagatgcagccatcagaataggtgatttggcTGAACTGTCATACTCCCACATCCtc	77	1	4	-	99,530,701	99,530,777	Intronic
180	PN(a)	PN(a)-19	tgcttctgtgTGATATGTTTGATATTGGGTTGtttaattaggaaccaactaaatgtcaaacatattcttacagcagtagg	80	1	4	+	99,584,645	99,584,724	Intergenic
181	PN(a)	PN(a)-20	ggctgtgccgggtagagagggccacgggagataagagcttttcacccCTCACCACCTTCTCCACCCAGCatggcc	75	1	4	-	115,043,656	115,043,730	Intergenic
182	PN(a)	PN(a)-21	gggtattcttgggtggataatacggattacgttgtTATTGCTTAAGAATACGCGT	55	1	4	-	124,680,227	124,680,281	Intergenic
183	PN(a)	PN(a)-22	gggaggagggaggagatgggccaagttccctctgcctggaACGCCCTTCCCCCCCTTCTTCAcct	65	1	5	+	927,612	927,676	Intronic
183	PN(a)	PN(a)-22	gggaggagggaggagatgggccaagttccctctgcctggaACGCCCTTCCCCCCCTTCTTCAcct	65	2	5	-	875,657	875,721	Intronic
184	PN(a)	PN(a)-23	actcgggagggcgggaggggggctccccggtgctcggatctcgagggtgcttattgttcggTCCGAGCCTGGGTCTCCCTCTccccccaccccc	95	1	5	-	17,933,485	17,933,579	Intronic
185	PN(a)	PN(a)-24	cgtcgggaccgggGTCCGGTGCGGAGAGCccttcgtcctgggaaacggggcgcggcc	57	1	6	-	248,247	248,303	Intergenic
186	PN(a)	PN(a)-25	acggcagcgccgcgggagcctcggttggcctcggatagccGGTCCCCCGCCGTCCCcgccggcgggccg	69	1	6	-	248,338	248,406	Intergenic
187	PN(a)	PN(a)-26	cgggtggagccgccgcaggtgcagatcttggtggtagtagcaaatattcaAACGAGAACTTTGAAGGCCGAAGtggagaaggttccatgtg	92	1	6	-	250,392	250,483	Intergenic
188	PN(a)	PN(a)-27	ccctaTCTCCCAACCCTTGTACCAGTGcgtgcctcagtccctggtacaggaatgggggggcaggg	64	2	6	-	38,390,208	38,390,271	Intergenic
188	PN(a)	PN(a)-27	ccctaTCTCCCAACCCTTGTACCAGTGcgtgcctcagtccctggtacaggaatgggggggcaggg	64	1	6	+	38,211,395	38,211,458	Intronic
189	PN(a)	PN(a)-28	ACTCAAACTGTGGGGGCACTTTctggtctagggagggaagtgccgccatttttttgagtgt	60	1	6	+	40,022,202	40,022,261	Intergenic
189	PN(a)	PN(a)-28	ACTCAAACTGTGGGGGCACTTTctggtctagggagggaagtgccgccatttttttgagtgt	60	2	6	-	39,872,470	39,872,529	Intergenic
190	PN(a)	PN(a)-29	gggtgtcttaccaggcacggttagatctggttcttctgtcTAATACTGTCTGGTAATGCCGTccat	66	1	6	-	42,894,055	42,894,120	Intergenic
191	PN(a)	PN(a)-30	ggggaccgcctggtgacctcgaaatccagagcgggtgaggcctgtctgactgttttctagGCGACCCACTCTTGGTTTCCAtggttgccctggaaa	96	1	6	-	43,640,508	43,640,603	Intronic
192	PN(a)	PN(a)-31	tgtccccaTGGCACAGGGTCCAGCTGTCGGCtgtaatacccgatgggtcgatgatggtccctgtgtttgggg	72	1	6	-	43,886,642	43,886,713	Intronic
193	PN(a)	PN(a)-32	ggccaggctcaccatgacaccgtgtgagacctcgggctacaacacgggactcgggcgctgctctgaccccTCGTGTCTTGTGTTGCAGCCGGAgggacgcaggtctgca	109	1	6	-	83,322,546	83,322,654	Intergenic

194	PN(a)	PN(a)-33	gtaaccatgccgtagtgcgTGTAAACATCCTACACTCTCAGCTgtgagctcgaggtggctgggagagggttgtttactccttctgccatggaaaacg	97	1	6	-	121,821,234	121,821,330	Intronic
195	PN(a)	PN(a)-34	GAAAGCATGCTCCAGTGGCGCaatcggttagcgcgcggtacttatacagcagtatatgtgcgggtgatgccgaggttgtgagttcgagcctcacctggagcatgttttcttccctttacg	120	1	7	+	22,803,533	22,803,652	Intergenic
196	PN(a)	PN(a)-35	ccgccccgggccgcggctcttgattgtccaaacgcaattctcgagtctatagctctggccgAGAGTTGAGTCTGGACGTCccgagccgtcgcccccaaacctcgagggg	109	1	7	+	29,626,546	29,626,654	Intergenic
197	PN(a)	PN(a)-36	TCTTTGGTTATCTAGCTGTATGAgtgccacagagccgtcataaagctagataaccgaaagt	61	1	7	+	60,349,141	60,349,201	Intergenic
198	PN(a)	PN(a)-37	agacagagaagccaggtcacgtctctgcagttacacagctcacgagtGCCTGCTGGGGTGGAACCTGGTctgtctgtct	79	1	7	+	133,847,438	133,847,516	Intergenic
199	PN(a)	PN(a)-38	tcctgctcgtcctgcgaggTGTCTTGCAGGCCGTCATGCaggccacactgacggtaacgttgcaggtcgtcttgcagggcttctcgcaagacgacatcctcgtcgtcgacgacg	114	1	7	+	133,927,744	133,927,857	Intergenic
200	PN(a)	PN(a)-39	gtggttatgtagcgagattttctgTTGTGCTTGATCTAACCATGTggttgccaggtatgagtaaaacatggttctgtcaagcaccatggaacgtcacgcagctttctaca	110	2	8	-	12,027,376	12,027,485	Intergenic
200	PN(a)	PN(a)-39	gtggttatgtagcgagattttctgTTGTGCTTGATCTAACCATGTggttgccaggtatgagtaaaacatggttctgtcaagcaccatggaacgtcacgcagctttctaca	110	1	8	+	11,840,680	11,840,789	Intronic
201	PN(a)	PN(a)-40	cccaccacttaaacgtggatgtacttgctttcaaactctaaaagTAAGTGCTTCCATGTTTTAGTGAtgg	70	1	8	+	92,257,711	92,257,780	Intergenic
202	PN(a)	PN(a)-41	ccatgactgttgctaatatgcaactctgttcaatacaaactggaATTGCACTTTAGCAATGGTGAtgg	68	1	8	+	92,258,012	92,258,079	Intergenic
203	PN(a)	PN(a)-42	gtgctcggtttgtaggcagtgtaattagctgattgtactctggcgcttacAATCACTAATTCCACTGCCATCaaaacaaggcac	84	1	9	+	38,210,599	38,210,682	Intergenic
203	PN(a)	PN(a)-42	gtgctcggtttgtaggcagtgtaattagctgattgtactctggcgcttacAATCACTAATTCCACTGCCATCaaaacaaggcac	84	2	9	+	38,327,577	38,327,660	Intronic
204	PN(a)	PN(a)-43	gctctgctgtggccTATGGCTTTTCATTCCTATGTGAttactgttccaaactcatgtagggctaaaagccatgggctacagtgaggggcgtgctcc	96	1	9	+	63,365,115	63,365,210	Intergenic
205	PN(a)	PN(a)-44	tggaagcttctggagatcctgctccgtcgcCCCAGTGTTCAGACTACCTGTTCaggacaatgccgttgtacagtagtctgcacattggttagactgggcaagggaaagcaacgccatg	118	1	9	-	107,644,923	107,645,040	Intergenic
206	PN(a)	PN(a)-45	gagaatcatctctcccagataatggcactctcaaacaagtttccaagttgtTTGAAAGGCTATTTCTTGGTCAgaagactctcagtgccttctgga	96	1	9	+	111,719,026	111,719,121	Intergenic
207	PN(a)	PN(a)-46	cttctggaagctggtttcacatggtggcttagatttttccatctttgtatcTAGCACCATTTGAAATCAGTGTTttaggag	81	1	9	+	127,173,767	127,173,847	Intergenic
208	PN(a)	PN(a)-47	TGTAACAGCGACTCCATGTGGactgtgccccaatttccagtggagatgctgttacctt	58	1	10	-	9,750,923	9,750,980	Intergenic
209	PN(a)	PN(a)-48	gctcgactcctGTTCCTGCTGAACTGAGCCAGTgtgtaaaatgagaactgatatcagctcagtaggcaccggagggcgggt	81	1	10	+	26,148,228	26,148,308	Intergenic
210	PN(a)	PN(a)-49	GTGTGCATTTGCAGGAACttgtgagtctcctattgaaaatgaacaggagactgataagttcccgggaacacccacaa	77	1	10	-	36,097,479	36,097,555	Intergenic
211	PN(a)	PN(a)-50	tgaagtgctgtggatttctttgtgaatcaccatatctaagctaatgtggtgGTGGTTTACAAAGTAATTCATAgtgcttca	81	1	10	+	36,141,559	36,141,639	Intergenic
211	PN(a)	PN(a)-50	tgaagtgctgtggatttctttgtgaatcaccatatctaagctaatgtggtgGTGGTTTACAAAGTAATTCATAgtgcttca	81	2	10	-	36,311,908	36,311,988	Intergenic
212	PN(a)	PN(a)-51	tgaactggaactgctgagtgaatTAGGTAGTTTCATGTTGTTGGGcctggatttctgaacacaacgacattaaaccacccgactcacggcagttactgctcc	102	1	12	+	22,434,918	22,435,019	Intergenic
213	PN(a)	PN(a)-52	ctgtttatcaccagatcctagaaccctatcgatattgtctctgctgtgtaaatagctctgagTAGTGCAATATTGCTTATAGGGTtttggtgtttgggaagaactatgggca	112	1	12	-	33,457,315	33,457,426	Intergenic
214	PN(a)	PN(a)-53	cttgggggtggcgagcAAACCGTTACCATTACTGAGTTtagtaatggtaacggttctcttgctgcacccaga	72	1	12	-	42,820,762	42,820,833	Intergenic
215	PN(a)	PN(a)-54	gggccctggctgggatatcatcatatactgtaagtttgcgatgagacacTACAGTATAGATGATGtactagtccgggtgctccc	84	1	12	-	42,820,910	42,820,993	Intergenic
216	PN(a)	PN(a)-55	aagcaagacTGAGGGGCCTCAGACCGAGCTTTtggaaaatagaaaagtctcgctctctgcccctcagcctaactt	75	1	12	-	44,150,500	44,150,574	Intronic
217	PN(a)	PN(a)-56	ccgcccccgcgtctccagggcaaccgtggctttcgattgttactgtgggaaccggaggTAACAGTCTACAGCCATGGTCGccccgcagcacgcccacgcgc	101	1	12	-	45,599,472	45,599,572	Intergenic
218	PN(a)	PN(a)-57	ggagccaccacgcccgggcagcgcgccggcaccttggctctagactgcttactgcccgggccgccctcagTAACAGTCTCCAGTCACGGCCAccgacgcctggccccgcc	110	1	12	-	45,599,904	45,600,013	Intergenic
219	PN(a)	PN(a)-58	ggtgcggtggggcAGCTGGTGTTGTGAATCAGGCCGttgccaatcagagaacggctacttcacaacaccagggtcacaccccaccacagg	90	1	13	+	23,336,877	23,336,966	Intergenic
220	PN(a)	PN(a)-59	ctgTTAATGCTAATTGTGATAGGGGTTtttacctccgtctgactcctacatgttagcattaacag	65	1	13	-	135,049,642	135,049,706	Intergenic
221	PN(a)	PN(a)-60	ccccctgctggccgcaggtgctctgacgaggttgcactactgtgctttgaggagCAGTGCAATGATATTGTCAAAGCatctgggaccagccttgggg	97	1	14	-	51,319,104	51,319,200	Intergenic
222	PN(a)	PN(a)-61	acctacctaactgggTTAGGGCCCTGGCTCCATCTCCtttaggaaaaccttctgtggggagtggggttttgaccctaacccagctgggctgt	92	1	14	-	69,493,246	69,493,337	Intergenic
223	PN(a)	PN(a)-62	gccggcgcccaggcTCTGGCTCCGTGTCTTCACTCCcgtgtgtgtccgaggagggagggagggacgggggctgtgctggggcgaacgga	89	1	15	-	131,645,445	131,645,533	Intergenic
224	PN(a)	PN(a)-63	gacctgaatcaggtAGGCAGTGTATTGTTAGCTGGctgctttggatcagttcagcagccacgactaccctgccacttgcttctggataaattcttct	97	1	16	+	31,984,173	31,984,269	Intergenic
224	PN(a)	PN(a)-63	gacctgaatcaggtAGGCAGTGTATTGTTAGCTGGctgctttggatcagttcagcagccacgactaccctgccacttgcttctggataaattcttct	97	2	16	-	31,831,951	31,832,047	Intronic
225	PN(a)	PN(a)-64	ctgtgtgtgatgggtTGGCAGTGTATTGTTAGCTGGTtgagtatatgagtagcatcagctaacatgcaactgctgtcttattgcatata	89	1	16	+	31,984,293	31,984,381	Intergenic
225	PN(a)	PN(a)-64	ctgtgtgtgatgggtTGGCAGTGTATTGTTAGCTGGTtgagtatatgagtagcatcagctaacatgcaactgctgtcttattgcatata	89	2	16	-	31,831,839	31,831,927	Intronic
226	PN(a)	PN(a)-65	atctgtgctctttggtTACAGTTGTTCAACCAGTTACTaatctaactaactgtaaccggttgaacaactgaacccaaagggtgcaaagtggaaacatt	98	1	16	+	36,589,521	36,589,618	Intergenic
227	PN(a)	PN(a)-66	gaccagtcgccgcggggctttcctTTGTGCTTGATCTAACCATGTggtggaacgatggaaacggaacatggttctgtcaagcaccgcggaaagctccgcgctctcctgca	110	1	16	+	52,396,946	52,397,055	Intronic
228	PN(a)	PN(a)-67	cctatgtgtatactcagcttTGAGAACTGAATTCCATGGGTTgtgtcattgtcagacctgtgaagtttagttcttcagctgggatatctctatcatc	97	1	16	+	60,604,380	60,604,476	Intronic
229	PN(a)	PN(a)-68	aggacccttccggagggcccccccaatcctgttgtgctggattcagAGGGTTGGGCGGAGGCTTTCCTgaaggctct	78	1	17	-	61,587,159	61,587,236	Intergenic
230	PN(a)	PN(a)-69	gctggtgaactggcaggccaggaagaggAGGAAGCCCTGGAGGGGCTGGAGGtgatggatgttttcctccggttctcagggctccaccttttccgggccgtggagccagggctggtgc	118	1	18	-	5,054,287	5,054,404	Exonicic
231	PN(a)	PN(a)-70	tggataccttggctggtttggaaagttcattgttcgacaccatggatccccaggtgggtcacgtttcaagatacacCAACCTGGAGGACTCCATGCTGTtgagctgttcacaagcagcggacacttcta	129	1	18	+	10,924,533	10,924,661	Intergenic
231	PN(a)	PN(a)-70	tggataccttggctggtttggaaagttcattgttcgacaccatggatccccaggtgggtcacgtttcaagatacacCAACCTGGAGGACTCCATGCTGTtgagctgttcacaagcagcggacacttcta	129	2	18	-	10,994,278	10,994,406	Intergenic
232	PN(a)	PN(a)-71	gccgccacttgcctcgcaccgttTTTGGCAATGGTAGAACTCACACTggtgagataatgggatccggtggttctagacttgccaactatggtgcgagggctcagcaagca	110	1	18	-	17,167,650	17,167,759	Intergenic
233	PN(a)	PN(a)-72	ccacgaccacctgctgggccgatTTTGGCACTAGCACATTTTTGCTtgtgtctctccgctctgagcaattatgtgcagtgccaatatgggaaagcaggatgctgc	105	1	18	-	17,171,979	17,172,083	Intergenic
234	PN(a)	PN(a)-73	tggatCTTTTTGCGGTCTGGGCTTGCtgttcctctctacagtagtcaggaagcccttaccccaaaaagtatct	73	1	18	+	18,269,493	18,269,565	Intergenic
235	PN(a)	PN(a)-74	gctggttggcattctgggcctggtttatgccaactctgttgttaacTATACCAGGATGCCAGCATAGTt	69	1	X	+	48,289,631	48,289,699	Intergenic
236	PN(a)	PN(a)-75	gcacattgtaggcctcattaaatgtttgttgaatgaaaaaatgaatcATCAACAGACATTAATTGGGCGCctgctctgtgatctc	85	1	X	+	58,683,804	58,683,888	Intergenic
237	PN(a)	PN(a)-76	tgttaaatcaggaattgtaaacaattcctaggtaatgtgtataatgtttgtaagTCATTCCTAGAAATTGTTCACAatgcctgtaaca	88	1	X	+	60,374,121	60,374,208	Intergenic
238	PN(a)	PN(a)-77	gagtgaaaagttccgtcaaccatccagctgtttggggtgatgcaaacAAACATCTGGTTGGTTGAGAGAattttttactt	80	1	X	-	100,547,916	100,547,995	Intergenic
239	PN(a)	PN(a)-78	agtacCAAAGTGCTCACAGTGCAGGTAGgttttgcattactctactgtagtgtgggcacttccagtact	69	1	X	-	108,178,755	108,178,823	Intergenic
239	PN(a)	PN(a)-78	agtacCAAAGTGCTCACAGTGCAGGTAGgttttgcattactctactgtagtgtgggcacttccagtact	69	2	X	-	108,212,677	108,212,745	Intergenic
240	PN(a)	PN(a)-79	atgctgtgtgcggtgctccacttcaagaagtgccatccatgtggctagaaataTGATTGGCACCTCTTTGAGTGAcgtaacacacaacaggtac	94	1	X	-	118,219,037	118,219,130	Intergenic
241	PN(a)	PN(a)-80	gctaagcacttacaactgtttgcagaggaaactgagactttgtaactacatcTCAGTCTCAACTGCAAAGAAGTaagtgcttagc	85	1	X	-	121,481,685	121,481,769	Intronic
242	PN(b)	PN(b)-1	ttatcaggcACAGGAGAGGTTCTTGGGAtttttcccaggcaaaaccatcctctgaggctgaact	65	1	3	-	29,674,061	29,674,125	Intergenic
243	PN(b)	PN(b)-2	gctcctcatCTGGCCCTCTCTGCCCTGCCGTctggatggcagggttggtaggttgggcatgaggtac	67	1	9	+	59,116,508	59,116,574	Intergenic
244	PN(c)	PN(c)-1	cTCCAGGAGCTCACAGTCTAggaggctagtttatagtacattccatagaagggctgctgctt	62	1	1	+	71,257,795	71,257,856	Intergenic
245	PN(c)	PN(c)-2	ctgttccggtggctccaggggccagaacagttggaaTCTCGCTGGGGCCTCCAgaaatg	59	1	1	+	206,000,024	206,000,082	Intergenic
245	PN(c)	PN(c)-2	ctgttccggtggctccaggggccagaacagttggaaTCTCGCTGGGGCCTCCAgaaatg	59	2	1	+	206,124,051	206,124,109	Intergenic
246	PN(c)	PN(c)-3	ctccacaaaatgCTTGGCAGCTAGTAAGCACtcaataaatgtttgctacatatctagtttaagtagtgagt	71	1	1	+	234,748,918	234,748,988	Intergenic
247	PN(c)	PN(c)-4	agctccataaactcagagatttgtgatagtgcctggcacatgTTGGGAACATTTTGAATATttgtggaaag	71	1	2	+	28,657,309	28,657,379	Intergenic
248	PN(c)	PN(c)-5	gcagggctgcagcgagtcaaactcgaggtcggggttcttgcagatCATCCCTGGCATGGTGGAcgcggtgcagctcggc	79	1	3	+	112,795,739	112,795,817	Intergenic
249	PN(c)	PN(c)-6	ttgctgcagctgtgatgtacattgctgctgtgactgagattcaatcacagaacttgcatGTGCTGCCAGTGCAGATA	77	1	6	+	18,297,569	18,297,645	Intergenic
250	PN(c)	PN(c)-7	agcggcggggacgggggaggcgagtcgcgtgtgacgcCTCCTGGCTGCCTCGCCAgg	57	1	6	+	38,030,592	38,030,648	Mixed
251	PN(c)	PN(c)-8	ctagatccttatttagttgtaaattcatgacatcatcacttacgaCTAGACTGAGGCTCCTG	62	1	6	+	109,113,891	109,113,952	Intronic
252	PN(c)	PN(c)-9	ccccctcccccgccccggCTCCTGCCTGGCTCGCCCcccacccccccagtgccgcccaaggtgagcccggccagggcctggcagaggcca	91	1	6	+	118,011,934	118,012,024	Intergenic
253	PN(c)	PN(c)-10	ctcccgccTCGAGAAGCCCACAGTCTAGTAggaaaggaagcagttacaacacagtgtggcgacggccactgggaagggtttccagagggg	90	1	12	+	47,219,122	47,219,211	Intergenic
254	PN(c)	PN(c)-11	acctgcttcccctgtaaactccagaactccagttccgtccttgggatggagatgagaatAACAGCTCCCATCTCAGAggactgtgaggaatgaaaagaggtggagaaagtgcttagcatggaac	124	1	16	+	65,985,474	65,985,597	Intergenic
255	PN(c)	PN(c)-12	ggACAAGTCAGGCTCTGGGGAaaggagacaggggatggatcctggtcagtgtctggagcctgggatgaac	70	1	17	+	10,529,440	10,529,509	Intergenic
255	PN(c)	PN(c)-12	ggACAAGTCAGGCTCTGGGGAaaggagacaggggatggatcctggtcagtgtctggagcctgggatgaac	70	2	17	+	10,822,768	10,822,837	Mixed
256	PC	PC-1	ctcgCCTAATGACGAAACTCTGAGGagctgggcgtttgactctttcccttcgtttctgcattttcttggctct	73	1	1	-	1,258,879	1,258,951	Intronic
256	PC	PC-1	ctcgCCTAATGACGAAACTCTGAGGagctgggcgtttgactctttcccttcgtttctgcattttcttggctct	73	2	1	-	1,364,889	1,364,961	Intronic
256	PC	PC-1	ctcgCCTAATGACGAAACTCTGAGGagctgggcgtttgactctttcccttcgtttctgcattttcttggctct	73	3	1	-	1,514,176	1,514,248	Intronic
257	PC	PC-2	gcccacccgccgagccgggttctgtcccgacacgtccctCGGCCCCCGGCGCTTCGGGtgact	63	1	1	+	2,518,268	2,518,330	Intergenic
257	PC	PC-2	gcccacccgccgagccgggttctgtcccgacacgtccctCGGCCCCCGGCGCTTCGGGtgact	63	2	1	-	3,359,786	3,359,848	Intergenic
258	PC	PC-3	aacggtgatttcctaaGATGGAGGATGATTCTGACAaagtcctgtcagccacccttcccttgtaaactcaccttc	75	1	1	-	29,438,821	29,438,895	Intronic
259	PC	PC-4	actgtgctgggctagggattgaaacccatgtctcagcagcaacccatgccactgaagtcaGATTCCTAACCCACCGGACcacagtggg	88	1	1	-	30,606,651	30,606,738	Intergenic
260	PC	PC-5	gtgactagaacacacagaatgaccttgctgtaattgctcttgaatggttctttaaagaatGAAGCTACCAGGCGTAGGAaattcttcagctggcctgtcacgtcgtgtgcagtcatctg	119	1	1	+	54,908,027	54,908,145	Intergenic
261	PC	PC-6	ggcgggGCGGGGCGGGCGGTCGCCCGGGgcggcggcggcggcggcggcggccgttggggtgcgaccgtccccgccccttt	80	1	1	+	106,652,033	106,652,112	Intronic
262	PC	PC-7	gtcacagagctaATTAGTGGCAGAGCCAGGAacagatctgggtcacctgatgctctgtcca	61	1	1	-	112,234,267	112,234,327	Intergenic
263	PC	PC-8	aatgtcatctgagcggggaggttcattatcctgaattacattttcaaatgggagtGCAATTTAGGTTAATGACTGTCttgctcctgactca	91	1	1	-	124,579,963	124,580,053	Intergenic
264	PC	PC-9	cGTGACATGGTGTGATTTGCcccttactttgctcattgccacctgcttctgtggctgggctgggctgtctcaggatgttc	80	1	1	+	128,995,206	128,995,285	Intergenic
265	PC	PC-10	gcctccagaaggaatgcaggtctgccaattctttgattttatccagtgagagccaTGGCTGACTTCTGACCTCCagaatggaata	85	1	1	-	140,033,943	140,034,027	Intergenic
266	PC	PC-11	gcccccggcccggccggcgcccgggggngccCGGCCGGGGCCGCCCCCGCcccccggggcgcccgggcggccgcggcncgccgccccccgcccgcgggcccggccgcggc	110	1	1	+	149,525,673	149,525,782	Intergenic
267	PC	PC-12	ggtcccgggtaccccagatgtggggatgtctgttgtggagcaggGGTCCCAGCTGGGGTGCCAaggttg	69	1	1	+	163,547,048	163,547,116	Intergenic
268	PC	PC-13	gtctcatgtattttattcatgtctgttcaatttgggatgtggtcaagagcattataaatgATTGATTTAGGTTGGGACAca	81	1	1	-	207,240,580	207,240,660	Intergenic
269	PC	PC-14	cttgggactgtgatGTGGGCTGGAGAGAAGGCTccaaggccccttccatgtactgcccttgtccagtgtcctcgtttctgtgaatagtcccca	93	1	1	-	268,094,086	268,094,178	Intronic
270	PC	PC-15	cggttgcacacccaggagttttgggctccgccgacctgcttcccgttccctggccattccCTCCTGGGTTTCGGCACCAaa	81	1	1	-	273,707,759	273,707,839	Intergenic
271	PC	PC-16	acatactgtgttctgttcagatagctgaacccttgggctgaccttggggagttTATAGTCTGGAGGATGTAGTACTACC	79	1	2	+	4,174,427	4,174,505	Intergenic
272	PC	PC-17	ggcgcccacaGCGCGCGGCCGCCCGGGGAatgagtcctcgggaacgtctgcgcctgggcctc	62	2	2	-	4,667,122	4,667,183	Intergenic
272	PC	PC-17	ggcgcccacaGCGCGCGGCCGCCCGGGGAatgagtcctcgggaacgtctgcgcctgggcctc	62	1	2	+	4,857,494	4,857,555	Intronic
273	PC	PC-18	ggcaggaggaaaagggcctcaggagggaggccaggtgggggctgggcacccgatgaccccTGCCCACACTCCTCTCTCCAGTgtggcagcaatcccctcccggg	104	1	2	-	5,079,854	5,079,957	Mixed
274	PC	PC-19	tctcgcttcagttcccccgccgccgcctgtgagagagatgctgccattaaccccTTGGACGGATGAGGACACTGAGGCGTgg	82	1	2	+	5,178,771	5,178,852	Intergenic
275	PC	PC-20	tttaggttcctttttcactctccgaggggccttcaagggcaagttcttgtcaccTTTGTTGGCTCCTCTGAAGTGAgaaggaaaccttcc	90	1	2	-	6,684,275	6,684,364	Intergenic
276	PC	PC-21	gaaccagtaggccaccctcatcgctgcctgtgtgtccacactggagcaCGAGGCAGCGCTGAGGATGAACcgctgggag	79	1	2	+	8,421,890	8,421,968	Intergenic
277	PC	PC-22	gtcTTTTGTCTCTGAACTCTGCGCTTTTcagcccaggtaccagtgggggtgggggaggtggtgaggaggcgagaaca	77	1	2	-	15,100,864	15,100,940	Intergenic
278	PC	PC-23	tttcACTTCTCTGAGCCTGCTTCTTcatttgaaaaatgggaataagacttagcttgaagtgcta	64	1	2	-	15,108,433	15,108,496	Intergenic
279	PC	PC-24	tcttgtacttcaccaAAGTAGGAAGAATATGATCTCAGAATacacaccgtttttacgaatttttttaggtttttatttttctattatagttgatttacat	101	1	2	-	15,119,677	15,119,777	Intergenic
280	PC	PC-25	ctttcatatattccactgtatccccagcatctggcacatagtaagtgcccaggcaacagcTGGACGATGCATTGAATATTTGAGCg	86	1	2	+	15,169,332	15,169,417	Intergenic
280	PC	PC-25	ctttcatatattccactgtatccccagcatctggcacatagtaagtgcccaggcaacagcTGGACGATGCATTGAATATTTGAGCg	86	2	2	-	15,113,347	15,113,432	Intergenic
281	PC	PC-26	tcaacTGAGGTAGTCAGGACCAGACCAAGGCatctgatgtctgatgttggagttaatcaggtctgggtttgaaccctgagtgcctctgtgt	91	1	2	+	15,174,303	15,174,393	Intergenic
281	PC	PC-26	tcaacTGAGGTAGTCAGGACCAGACCAAGGCatctgatgtctgatgttggagttaatcaggtctgggtttgaaccctgagtgcctctgtgt	91	2	2	-	15,108,515	15,108,605	Intergenic
282	PC	PC-27	tttgcaatgtatcagtgtcttgtattcagccttagtttgtAAACTGGTAGACTTAAGTAaagaatatgttaggaatgtatttatatctatctttatatatctggcttactgatttgcca	119	1	2	+	20,499,654	20,499,772	Intergenic
283	PC	PC-28	gaacaggttctttaatctccgtctacctcagtttctttatctgtaaAATGGAGAGGGGAGTAGGACctgact	72	1	2	+	26,867,438	26,867,509	Intergenic
284	PC	PC-29	catggaggttcccaggctagaggTCAAATCGGAGCTACGGCTgctggcctacaccacagccatagcaacgcaggatctgagccttgtctgggacctacccca	102	1	2	+	38,741,521	38,741,622	Intergenic
285	PC	PC-30	atgagctgcagtgtaggtcatagactcagcttggatctggtgttgcTGTGTCTGTGACATCTGCTGGCAgctata	75	1	2	+	43,890,115	43,890,189	Intronic
286	PC	PC-31	gggaggcgtggaggtcccagccgcgggggtGGGGGGCGCGGCGGCCGCCtcctttgcctgcgtccccgccggcttccgcatctgcttggctgccccctctgcgtctggc	109	1	2	-	46,479,632	46,479,740	Intergenic
287	PC	PC-32	ctccagtgcccgcccctcgcgcGCCGGCCCCGCCCCCGCGGgggggagcgagcgctcgcgggccccgtggtgggttcggctgcgcggcggggctgagg	98	1	2	+	47,333,618	47,333,715	Intergenic
288	PC	PC-33	tgaccctagggagcagtgtaacccagagcctgggccatgcccaagagaggtgagtgTGGGGGATGCCAAGGCTCTggtcctgcccagggccc	92	1	2	-	49,359,225	49,359,316	Intergenic
289	PC	PC-34	gttcggtctctggcctcactcagtgggtgggggaatccagcattgctgtgagctgtggtgTAGGTCACAGACACGGCGTggatcccttgttcctgtggctgtggtgtaggccagaagctgtagctct	127	1	2	-	52,814,443	52,814,569	Intronic

290	PC	PC-35	ggagcatgtgtgtgtgcacgcgtgcgcgcgcccacgtgtgCATGTGTGTGCATGTGCACgcaaa	64	1	2	-	61,429,973	61,430,036	Intronic
291	PC	PC-36	ttttgctttttagggccacaggtgtggtatgtggaagttctcaggctggaggTCAAATCGGAGCTACGGCTgctggccgtagcaatgtgggatccaagctgtgtctgcaacctacaccacggcgcacagca	131	1	2	+	68,799,996	68,800,126	Intronic
291	PC	PC-36	ttttgctttttagggccacaggtgtggtatgtggaagttctcaggctggaggTCAAATCGGAGCTACGGCTgctggccgtagcaatgtgggatccaagctgtgtctgcaacctacaccacggcgcacagca	131	2	2	+	68,800,592	68,800,722	Intronic
292	PC	PC-37	gaaacgctcttcttttcagccccTGCGTGGCTTCTCTGTGCAGTCttttcttctgggacctgcacaggaaggccacggaggggccggagaaagagatgtacc	101	1	2	-	76,418,882	76,418,982	Intergenic
293	PC	PC-38	ccttcacagaaaaatttacatatgagtgtatggttaaaACAGTGTAATTTCATGTGAtgc	60	1	2	+	78,556,717	78,556,776	Intergenic
294	PC	PC-39	tttttaggtgagaaAACTGAAGTGTAGAACATTtaaggccataaaattagtaaattaggaagccaggtttttgaaatcagttggacctaatct	92	1	2	+	91,849,127	91,849,218	Intergenic
295	PC	PC-40	catgggtccagtgttgccatgagctgtgatgtaggtcacagatgtggctcagatcctgcATTGCTGTGGCCATTGCGTagaccagcagctctaggtctgatttgacccccta	111	1	2	-	95,662,202	95,662,312	Intergenic
296	PC	PC-41	actgcagctgccaagccttgatacaccctgaaaagagctcaaggtggagatCAGGAGTGAGGCACTCTGTgct	73	1	2	+	96,802,823	96,802,895	Intergenic
297	PC	PC-42	atctgttttcctgcacacagtaaaactgaactactgaCAGAAGGCTGTGGTGAAGGaaggtacag	65	1	2	-	99,465,444	99,465,508	Intergenic
298	PC	PC-43	agatagttatgtatttTTAGGAGAAGATTTTTATGAacccaattcttgcatcccctcatatgtagaaaacactaaaatctgccaatgatgactaat	95	1	2	-	100,052,886	100,052,980	Intergenic
299	PC	PC-44	ggggaagctgagcgagagctccgggggagtcagtaccagccCGGCGCGACTGAACTCCGGAccgctcctcgctccaccttcggt	83	1	2	-	104,855,985	104,856,067	Exonicic
300	PC	PC-45	ataggattacaattataatttaatggctaaaaagtcaatctgtcttagaagattatttTTATGTGGCTATTCTGATAtataatgtacccaga	92	1	2	+	108,075,703	108,075,794	Intergenic
301	PC	PC-46	ggagacCAGGAGTGAGGCACTCTGTgctctgggaaatctggaagaacagaccttcagatggtcaga	66	1	2	+	113,207,729	113,207,794	Intergenic
302	PC	PC-47	tgactccGCCTCTGCTTGAGAGAAGGaatttcttagagatccaccccgtcataagaggtttttctgattattggaggcggggann	85	1	2	-	114,720,073	114,720,157	Intergenic
303	PC	PC-48	ccAGGGGCGGGGCGGGGCGGGGcgtcccaggctgggccccacctcctctgtcctcct	57	1	2	-	124,406,188	124,406,244	Intergenic
304	PC	PC-49	tttcccagccaccccagggcttgctcggtggacccatgaatcaaggagccatgGTGGCACGGATGCAGGCTCTGCAGgggtctggggcc	89	1	2	+	125,269,176	125,269,264	Intergenic
305	PC	PC-50	ccagcgcGCAGAACTTGGGGAGCCGCCGCcgccgccgccgacagctgccgccgccgccgccgccgacagctgccgccac	79	1	2	+	127,484,068	127,484,146	Intergenic
305	PC	PC-50	ccagcgcGCAGAACTTGGGGAGCCGCCGCcgccgccgccgacagctgccgccgccgccgccgccgacagctgccgccac	79	2	2	+	127,525,736	127,525,814	Intergenic
306	PC	PC-51	acacttttctatgctaccaagcgtctcataggccggCGATATGATGACCCTGAAGTAcagaaagaca	66	1	2	-	127,612,667	127,612,732	Exonicic
307	PC	PC-52	caggggaggccctggcTCTCACTCTGAGGCATGAGccctcatccaggagtgggaactgggagtcccaca	69	1	2	+	128,590,030	128,590,098	Intergenic
308	PC	PC-53	ccaggagctctgtctcttgctacctgctgccctgagtcccAAGGGCTGGAGGCAGGAGGcagccaaaccagacacagaatccggc	88	1	2	+	129,116,291	129,116,378	Intergenic
309	PC	PC-54	caagaagaaaggggaaaaaaaAGACGGATGACCTTGCTGTTTacatttagaaaggataagcagcaaggttgtctgtctttttttcctctctgttcttcagc	100	1	2	-	131,648,312	131,648,411	Intergenic
310	PC	PC-55	cctgctgcgatggcgccttcttctgctcacttctctgctgtaccatttcgaggaGCCAGGCACTGAGAGGGCAgggaggttgcagctca	89	1	2	-	135,910,191	135,910,279	Intergenic
311	PC	PC-56	ctgtgagctgtggcgtaggtcaaagacgtggcttggagctggcgttgatgtggctgtggtGTAGGCCTGCGACTATAGCtccgatt	86	1	3	+	5,360,718	5,360,803	Intronic
312	PC	PC-57	agacaaaggaTATCACTAGGGACGGACGTAGCTGCGaagggaagtagggcgtcagtttggggtggtgggcttggtt	77	1	3	+	6,689,611	6,689,688	Intergenic
313	PC	PC-58	ttaactgctaggccaccgggggaactcccagaccagcttccactcccttcaagaAGCTGGTCTGGGAGTTCCCGGGtggcctagtagtgac	90	1	3	+	9,289,226	9,289,315	Intronic
314	PC	PC-59	aatgcatgaatacagacggggcctggtctaggctTGGCAGAGACTGTCCTGGAcgtgaggaggtgctgg	69	1	3	-	10,306,072	10,306,140	Intergenic
315	PC	PC-60	aAGGCATGGCTGAATACTGTGttctttttatcagtaatttacacagccagacaccatgcaaa	62	1	3	-	15,359,737	15,359,798	Intronic
315	PC	PC-60	aAGGCATGGCTGAATACTGTGttctttttatcagtaatttacacagccagacaccatgcaaa	62	2	3	-	15,384,758	15,384,819	Intronic
316	PC	PC-61	caagtctctgagacactgactgtgggggtatgtgtgtgtccATCTGTCTGTGTCTCTGAGCAGG	64	1	3	+	25,819,331	25,819,394	Intergenic
317	PC	PC-62	ccagggattgtgggttCGAGTCCCACCCCGGGGTAGAAaagagttgtattttaaaacctctgggggaaacatgggcgaggacaaacccgat	90	1	3	-	35,061,542	35,061,631	Intergenic
318	PC	PC-63	gagctggAGCATACTCTGTCTAATGGggggcgtggaatgagagggtatagtcagaaa	56	1	3	-	38,667,463	38,667,518	Intergenic
318	PC	PC-63	gagctggAGCATACTCTGTCTAATGGggggcgtggaatgagagggtatagtcagaaa	56	2	3	-	38,800,661	38,800,716	Intergenic
319	PC	PC-64	gaactggtgagTGTCCAGAGGGCTGAATGGtaccaaagcagctctccatccccagagt	58	1	3	-	38,716,142	38,716,199	Intergenic
320	PC	PC-65	tgccaggtcattcacagggttcagttgcctgaggggtaACAGTGTTATTTCCTGTGAaagtcttgtga	67	1	3	+	41,088,681	41,088,747	Intergenic
321	PC	PC-66	atgCAGGGAGCCTGCACAAGAGgctgttcctaccatgtccccatcagcttcccgggctcctctgacc	67	1	3	+	41,090,685	41,090,751	Exonicic
322	PC	PC-67	tcGGATTTCCTTGTGACTGTGGGACTtaggaagagactggttggaagcaagccaggatcgccgtacagtcacagggatcaaa	82	1	3	-	41,092,230	41,092,311	Intergenic
323	PC	PC-68	tgATCCCTGTGACTGTACGGCgatcctggcttgcttccaaccagtctcttcctaagtcccacagtcacaaggaaat	76	1	3	+	41,092,232	41,092,307	Exonicic
324	PC	PC-69	tttgatttttggtgagcctcttttgaagatgttgctcTGGAGATGAGGACCGATGAAGTCctc	63	1	3	+	41,624,237	41,624,299	Intergenic
325	PC	PC-70	gaggagTAGGATGAGAAATAGAGCCttgaaaggtaagcttccacgttcagccctgtgcgccctgagaatctgcttccatctctc	84	1	3	-	41,626,515	41,626,598	Intergenic
326	PC	PC-71	ggcgccccagacccgcttcctgggtggatgaaaccatcctcgcctTGGTGTGTGGACTGGGGCTct	66	1	3	-	41,627,418	41,627,483	Intergenic
327	PC	PC-72	agggaaaTGAGGGTTGATTGTATAGTTattcatctggaaccaacctcatccctccccttcatc	62	1	3	-	43,740,583	43,740,644	Intergenic
328	PC	PC-73	catggctcggatcccgagttgctgtggctatggtgtaggccggcagctgtagctccaattAAACCCTTAGCCTGAGAACTtccacatgccatgggt	96	1	3	-	51,172,480	51,172,575	Intergenic
329	PC	PC-74	cttcagtCTGGAGGACATCTGATGGCtcccacagtggctgtcacctttctcagtactgttc	61	1	3	-	54,103,022	54,103,082	Intronic
330	PC	PC-75	agggcTGGAGTGGGAATCAGAAGACagaagcagcgggttttttttttgttttagttttagtttt	67	1	3	-	75,256,016	75,256,082	Intergenic
331	PC	PC-76	taacagtgccttcttgaagaatattggctgaaagAATGAATGTCAGGAAGAATtgaaa	58	1	3	-	75,974,603	75,974,660	Intergenic
331	PC	PC-76	taacagtgccttcttgaagaatattggctgaaagAATGAATGTCAGGAAGAATtgaaa	58	2	3	-	76,126,373	76,126,430	Intergenic
332	PC	PC-77	ttggtAGAACCTTGGGCCTGTGAAacttatttgcagatttttcttcacaagcctatattacact	64	1	3	-	80,676,447	80,676,510	Intergenic
333	PC	PC-78	cagccgaaaacattaattaaacaactactgtatgcaagaggcttTGTTGGGCACAGTGTGTGTgtgtgtgtgtggggg	80	1	3	+	80,958,108	80,958,187	Intergenic
334	PC	PC-79	tgttacaggccctcgcaccccaattaacctgggggggtgGGGAGCGGAGGGCCTGTGGGt	59	1	3	+	88,700,641	88,700,199	Intergenic
335	PC	PC-80	agacaggctggaGGAGCAGGGGCTGTAGCCCctggtagggggttctggcaggttccggtgcctgggg	67	1	3	+	90,728,599	90,728,665	Intergenic
336	PC	PC-81	ccctttatagccacagattcaaccaaccccagaaggaaatttaatcTTCAGGCCAAGCTTGGTTGAATccctaatgtaaaacc	83	1	3	+	91,722,859	91,722,941	Intergenic
337	PC	PC-82	ttCGATTCCCGGCCAATGCAGCgggctgtctcttggagttcccatcttggctcagtggtaaatgaatctga	71	1	3	-	102,331,759	102,331,829	Intergenic
337	PC	PC-82	ttCGATTCCCGGCCAATGCAGCgggctgtctcttggagttcccatcttggctcagtggtaaatgaatctga	71	2	3	-	102,598,324	102,598,394	Intergenic
337	PC	PC-82	ttCGATTCCCGGCCAATGCAGCgggctgtctcttggagttcccatcttggctcagtggtaaatgaatctga	71	3	3	+	102,154,824	102,154,894	Intergenic
338	PC	PC-83	ttcctggtgctctagcggttaggattaggtgctttcaccgctgtggcccgcgttcaacccCCTGGTCTGAGAACTGAGAtcctacatcaagccgctgctgcatccagcag	109	1	3	+	104,700,413	104,700,521	Intergenic
339	PC	PC-84	tgtgcgctcggtacacctgaggacttatgacatgcagattctgactcactaggCTGGGGTGTGGATTCTGCGtttctaacaagctctcaagtgatgccggcgctgc	106	1	3	-	107,185,259	107,185,364	Intergenic
340	PC	PC-85	caagaaccattgtagttattatctgtgtgtgtgtacatgtttgTATATGTGTGTATGTGCAGGAttaaatcacaatagtttaca	84	1	3	-	116,265,943	116,266,026	Intergenic
341	PC	PC-86	atatacggtcggccctccatgtccgcgggttccctatcccgggttggttgagttcgcggATGCGGAACCTGCGGATACGGagggctgattgtactc	96	1	5	-	4,391,274	4,391,369	Intergenic
342	PC	PC-87	tcacatctggggctgatccagctgcagaggggcaaggcaggcccctgcattTGGGCGGGATGGCAGGTGGGg	71	1	5	+	7,858,579	7,858,649	Intronic
342	PC	PC-87	tcacatctggggctgatccagctgcagaggggcaaggcaggcccctgcattTGGGCGGGATGGCAGGTGGGg	71	2	5	-	7,937,006	7,937,076	Intronic
343	PC	PC-88	cgactcaccctgcagctcctTGCGTTCATTCTGTTTGGCCTGGtgttctttcagcaggcgggacagcatggtcgcagtgggctgggggtagggcgc	96	1	5	-	20,064,090	20,064,185	Intergenic
343	PC	PC-88	cgactcaccctgcagctcctTGCGTTCATTCTGTTTGGCCTGGtgttctttcagcaggcgggacagcatggtcgcagtgggctgggggtagggcgc	96	2	5	-	20,108,111	20,108,206	Intronic
344	PC	PC-89	gtgggtcagagaggaaggatgtgatttgagcagatggttcTCATTCTCCTTCTTTGACCAGA	62	1	5	-	21,622,111	21,622,172	Intergenic
345	PC	PC-90	gaagcttttgaaaaattcctggtgcctgggtcccctccccagaggttcaaattttaattgcTCTGAGATGTGACCTGGGCATCcggattttttaaagtcct	99	1	5	-	26,991,012	26,991,110	Intergenic
346	PC	PC-91	gaaagcagaccaaatatatattcctaagaaagggatgagggagggagagAGTATGTCTTTGGGGGTTGgg	70	1	5	-	32,152,374	32,152,443	Intergenic
347	PC	PC-92	tccggtgaaatggtcaccactgaactggTCTCCAGTGAGACAGTCTCTGGtgaactggtctccagtgactcactccctggtgtaccagtccctggtgaatcagtctccac	110	1	5	-	55,170,859	55,170,968	Exonicic
348	PC	PC-93	aatgggggcacctGGGGGCTGGAGGAGGGAGGGCtggaggagggaggcctggatctgcttcagaccctagagccgcccccggc	83	1	5	-	61,083,977	61,084,059	Intergenic
348	PC	PC-93	aatgggggcacctGGGGGCTGGAGGAGGGAGGGCtggaggagggaggcctggatctgcttcagaccctagagccgcccccggc	83	2	5	-	61,164,139	61,164,221	Intergenic
349	PC	PC-94	caggacctcgtggcgcaacggtagcgcgtctgactccagatcagaaggctgcgtgttCGAATCACGTCGGGGTCATGGg	79	1	5	-	80,874,736	80,874,814	Intergenic
350	PC	PC-95	gttagattctattattgctacttaaaggctacatgcgctaacattaataatcgcACACGTAGCCTTTAAGTAGTGAtaatagattctcgt	90	1	5	+	83,900,122	83,900,211	Intronic
351	PC	PC-96	gtccgcgagcgggtgctccgggccgccaccggcGCGGGGTGGTGGTCTGTGGGtgcgtgctccagcgtgg	70	1	6	-	247,465	247,534	Intergenic
352	PC	PC-97	cGCCGGCCTTGCGGGCCGCCGGtgaaataccactactctgatcgtttttcactgacccggtgaggcggg	70	1	6	-	249,044	249,113	Intergenic
353	PC	PC-98	atacccggccgtcgccggcagtcggagcagcgcgcgagagggacgggagcggggcgCGCGGTCGCCCGGGGACGCCGGGGtcgc	84	1	6	-	250,690	250,773	Intergenic
354	PC	PC-99	ccaccccggcctcgcctcctcctccccccttcccggggtgtgggggagGGCCACGGTGCGGGTCGGGGCgg	71	1	6	-	251,649	251,719	Intergenic
355	PC	PC-100	cgcgccgggtttttcTTGGTGGGGGCCGGGCCGCCcctcccacggcgcgaccgctctccccacccggcctc	71	1	6	-	251,707	251,777	Intergenic
356	PC	PC-101	ctccccccCCCGGCGCTCCCCCCCGCGGGGGCgcttccccgccagggggggtgtccctcgcgggggcgcgccgggttttcttggtgggggcc	94	1	6	-	251,751	251,844	Intergenic
357	PC	PC-102	ccgggcgcctgtggggTTGTCCGTGCCCCACCCACTCAcccgtgtgtgtgtgtgtgtgtgggcgccggacgcccccgtcgtgtgaagccttc	91	1	6	-	255,386	255,476	Intergenic
358	PC	PC-103	ccTGGGCCTTCTGTCTGTGCAGCgcgctttctctggacgccgctggctgatgggcccccc	60	1	6	-	842,777	842,836	Intronic
359	PC	PC-104	aacttggtgacccagctgaatgacagcgaaatcTGTTTCTTTGACAAGCAGCCTGGTCCagatggtcagggtgctggttaagcggaaaccggcgggtgatttggtttggtgaccaacac	119	1	6	-	10,153,594	10,153,712	Intergenic
360	PC	PC-105	tgactgctcacttcTTGGAGCTGTTTAGAGAGACATGGCTggtggaagcgtctctctgtttctggctgtgtttgtcctaaaacatgtctcaagttcgcag	100	1	6	-	10,156,459	10,156,558	Intergenic
361	PC	PC-106	tccctgtttgtgccgggggtggctgtccTGTGCATTGCAGGATGATTagcagcatccctagctctcctcttgcaaagccaggagcatcccctcccagtttgtgacag	107	1	6	-	10,159,080	10,159,186	Intergenic
362	PC	PC-107	ttccctctggttcagtctttttcttccaggcaTGAGGAATAAGAAGAACCGATGGTGT	57	1	6	-	10,518,648	10,518,704	Intergenic
363	PC	PC-108	AGTGCCTGCTGTGTACCAAGGTTtgttctgggtgttctgggttttacagataagccatctgcctgtggtcacacagctggaa	82	1	6	+	32,774,401	32,774,482	Intergenic
364	PC	PC-109	acaagctCGGCCGGACTGTGAAAAGAtccacctacattctcaggctgtccttctgagttggg	62	1	6	+	39,700,905	39,700,966	Intergenic
365	PC	PC-110	tccgcgctgatgaccagcggctcgctgcgctgggacagcacgtAGGGGGCGGAGGGCGTGTGGtagtagcagctgt	76	1	6	-	40,429,042	40,429,117	Intergenic
366	PC	PC-111	aaagttcgtctggtgttttcttttgttttgttgttgttagaacagcagggaaGAAGGAGGCAGAGGCAGGAgcaat	76	1	6	+	42,202,593	42,202,668	Intergenic
366	PC	PC-111	aaagttcgtctggtgttttcttttgttttgttgttgttagaacagcagggaaGAAGGAGGCAGAGGCAGGAgcaat	76	2	6	+	42,373,513	42,373,588	Intronic
367	PC	PC-112	caagggggctgtccccatggcacagggtccagctgtcggctgtaataccccgatgggtCGATGATGGTCCCTGTGTTTGGggcgagcactccgaa	94	1	6	-	43,886,629	43,886,722	Intronic
368	PC	PC-113	ccttggccccagttccagcgaccagtacctagtatgggctcagaaaatGCTTGTtGATGACTGAACTGAGGgctatag	78	1	6	+	54,234,662	54,234,739	Intronic
369	PC	PC-114	aattGGGGAATGGAGAGATGGCTaatacaggatccggcccctccagggactccctcttttccatcttccagcccctacag	79	1	6	-	55,492,609	55,492,687	Intergenic
370	PC	PC-115	gttcagagcagccatggccccccgcctcttgcccttgcctccgccggGGTCCGGCCGCGGGCGCCAgggacgctctggga	80	2	6	+	63,785,046	63,785,125	Intergenic
370	PC	PC-115	gttcagagcagccatggccccccgcctcttgcccttgcctccgccggGGTCCGGCCGCGGGCGCCAgggacgctctggga	80	1	6	-	63,563,867	63,563,946	Intronic
371	PC	PC-116	cctgagtctgcaTGTACACGTCAAAAAGGACCagccgactttcctggtgccaagacttgaccctgacatcaaggctccac	80	1	6	-	66,475,127	66,475,206	Intergenic
372	PC	PC-117	agtgtatgccttctccatgggaatttatacttaagtagttaagggcttttgatattaaagGTATTCTGAAGCTCTGAAATGCTagaaaaaacttggaatggggtatatgctaaa	114	1	6	-	67,374,246	67,374,359	Intergenic
373	PC	PC-118	gccttttttattctctgcttcagggagcatggccaggcccaagAGATGGAACTGTGCTCTCTGAAGCAagagaataaaaagact	85	1	6	-	68,915,145	68,915,229	Intergenic
374	PC	PC-119	aaaaatatatttgCACCTGAGGTTCTGAGGGGacaaaaaaaccaaatgaaaagctggttttcaccacagatactttgaaatatattgtt	89	1	6	+	90,088,087	90,088,175	Intergenic
375	PC	PC-120	ggtGCGCGCGCACGTGTGCGCGGGcaaaaggggggcggggaagtctctggggcggacgacgggcgcgcgctcg	73	1	6	+	94,621,902	94,621,974	Intergenic
376	PC	PC-121	ctggtggtctagtggttaagatttggtgctttcagtgccgcagcccaggttcaatcaataCCTGGTCTGAGAACTGAGAtctgacaatcaagccgcttcatactacagcaggaa	114	1	6	-	96,211,101	96,211,214	Intergenic
377	PC	PC-122	tttcctccataatgatctcagtgggtttaaataagtgattagaaataCTGGAGTTCTTGTCATGGCtc	68	1	6	+	98,571,653	98,571,720	Intergenic
378	PC	PC-123	acacgccgccgccgggctcgccggcggggcGGGCCGGGCGGTGGTGGCGcgggg	56	1	6	+	103,808,631	103,808,686	Intergenic
379	PC	PC-124	tgcctgataggcacctctctcccggagtgatgttcgaaatagtccataacctgtgtgacaCGAGCATACCAGTTGGGACagatcctgccctgccaccaggccaa	104	1	6	-	106,940,778	106,940,881	Intergenic
380	PC	PC-125	ttaggtagctatcTTAGGAGAAGATTTTATGAacccaattcttacatttccttgtgtttagaaaagcactaaaatccttaatggtgatatct	93	1	6	+	111,647,013	111,647,105	Intergenic
381	PC	PC-126	ttagccacgacgggaactccagaaatcttacatattaaagtgagacCTGGAGTTTTTGTCATGGCaca	68	1	6	-	113,778,937	113,779,004	Intronic
382	PC	PC-127	atttctgcaggagtttccattgTGGCTCAGCGGCAATGAACctgactagcatctgtgagtccggcattgccgtgagctgtggtgtaggtcgcagatac	98	1	6	-	121,989,562	121,989,659	Intergenic
383	PC	PC-128	tgagtcctgagacatcgctTCTGGTCCAGACACTGTGGAGCtgaagagaccaacacttctcagtgtttgaaccagaagctctgtctgcagaacaat	96	1	7	-	8,508,435	8,508,530	Intergenic
384	PC	PC-129	ctgcatttagagatgacatcagttagtgctcatgatgtgtcacctccttttgaccatttttAAATGGGTGACGGGCAACAtgttatgacattggtcatagatgaatgctac	110	1	7	+	17,776,790	17,776,899	Intergenic
385	PC	PC-130	aggcctTCGGTGTCAGGATGGCCGAGTGGtctaaggcgccagactcaagcggcagcttcccacctggggcgttctggtctccgaatggag	90	1	7	-	22,793,682	22,793,771	Intergenic
386	PC	PC-131	atcaagttcctccctgctggatataggcagagtaggaTGTTTTCAGTGTCTGTGTTCTGGgagaatgtacttaaa	74	1	7	-	31,617,508	31,617,581	Intergenic
387	PC	PC-132	catcagggagcccgtgtggttgagctgggcaaaggacagttTGGCAGTAGGACCATAAGCACGGtgttccttgttc	76	1	7	-	34,450,857	34,450,932	Intronic
388	PC	PC-133	agttttccggagcgaagtgatttatcttcattctgtgcagaaaatgagttGACTGCACGGAGTGAGGATGAAAGAacggcggggcgggggtgg	93	1	7	-	34,464,588	34,464,680	Intronic

389	PC	PC-134	tctgtcccctcctccccagtggggaggctgaacctcgtaattatctttcattctcctgCTGGGTCTCGGCTGGGATCaact	81	1	7	-	34,466,641	34,466,721	Intronic
390	PC	PC-135	agagcacagtgcagggaaactaaggctcaagtcaccagcaagggtacagggccatccctttctTCCTGACTCTGACATTGCGccgagtatcaggaccacttgtcac	106	1	7	-	34,484,784	34,484,889	Intronic
391	PC	PC-136	taATCATGAGGACATGGATTTGAGCCctgatcttgcacagtgggttaaggatccggtgttgccatgagct	70	1	7	-	40,634,472	40,634,541	Intergenic
392	PC	PC-137	cccgggaaacagcAGGGTGTGTGTTTTTATTTtgcaaatattaaatcacagtattgattatgcttttgcagacagcacacttctctctcccc	92	1	7	+	45,307,051	45,307,142	Intergenic
393	PC	PC-138	ccagactctccagaaacaggaagAAGCTACTCTGGTACCATCtccaatagtacctttgttgtcctttttctgtgtctgctacgttagc	89	1	7	-	47,856,717	47,856,805	Intergenic
394	PC	PC-139	cAAGCCTGCCTTCTTGACCAtgaccgtcctttgggttccgggctaatgaatggtaaattgttttaagaggcatgcgtg	78	1	7	+	54,374,344	54,374,421	Intergenic
395	PC	PC-140	acctggcaacccccttttaccctcctgataaaaatagaaAGGGCTGAAGTGGGGAAAGccatgg	64	1	7	-	59,814,924	59,814,987	Intergenic
396	PC	PC-141	tcctctggcaggagggctctgggctgagtatgagggtggtgattggtccccttcTCAGCCCGCATTCTCCACCAgacac	79	1	7	-	63,696,327	63,696,405	Intergenic
397	PC	PC-142	taaggcttgtagtgtttcccctctgcttgggattgtcgtggaaggcttctaccagtaataACACAGGTAGTGGAGGAGAaatacgctgga	90	1	7	+	75,040,376	75,040,465	Intergenic
398	PC	PC-143	taaTGGGACCAGTCTCTGGCCTctgccttttaactggggataccaaggaggcagcttccagacacgatcccagct	75	1	7	-	90,893,972	90,894,046	Intergenic
399	PC	PC-144	gctgggaTCGTGTCTGGAAGCTGCCTCCTTGGTatccccagttaaaaggcagaggccagagactggtcccatt	73	1	7	+	90,893,973	90,894,045	Intergenic
400	PC	PC-145	ggcgtttcaccaaggtggttcttccTGCCATCATCCGGCCTGGTAGAggaggaacttgttccttcctcagccaggagagttgggggggatggatgggagagccaggtggagc	111	1	7	+	90,894,127	90,894,237	Intergenic
401	PC	PC-146	ccagatgctgagtttggcaagggcagctgtcctactgggagagggacccagggtactcccTGCCAGTGTGCAGACACGGGGtctgaaa	88	1	7	+	90,894,674	90,894,761	Intergenic
402	PC	PC-147	ataggATTGTTGTGAAGGTTCTATGAATTaatttttatatagaatacttagaacagccaga	61	1	7	-	93,560,699	93,560,759	Intergenic
403	PC	PC-148	tggcaaaggccatgagttttcatcctcggggcagacttcccacgtggacacacaaaggtcAGCAAGGTCTGCCTTAAGGccacctgataacgatggctgtgccccc	106	1	7	-	95,895,079	95,895,184	Intergenic
404	PC	PC-149	atctgttcagatttggaaatttcctcggcatcccttgagaataaaagactgcttgccaggGTGCAAGGCTGAATTAGACac	81	1	7	-	95,897,924	95,898,004	Intergenic
405	PC	PC-150	tatgggaatctcagcacatctggctctggcacggaggacGGAGTCCACCTGTGCCTGAgtccactggatggcttggtcccccct	84	1	7	-	97,085,759	97,085,842	Intergenic
406	PC	PC-151	tcaggagaaaacgctttgagctctggttggattttttTCCAAGATAGTTTTCAGCCCTTCTCcatg	66	1	7	-	117,947,019	117,947,084	Intergenic
407	PC	PC-152	cagtcaggctttcccctctgtgatgcgaccagtcaagctagctcTAATTGTAGACAGTCCTGAGAGTCTggaag	74	1	7	-	117,950,334	117,950,407	Intergenic
408	PC	PC-153	ccTGAGACCTGGTCCAGAGCCTCGACTTtaaaagaatttaggctttgaatcctagtttccaa	62	1	7	-	117,952,163	117,952,224	Intergenic
409	PC	PC-154	tgggactaagtcctttcgtgtagaagttgcccagtgccatgactgaagcatctggaacaaTAGGATATGAGGGCCTCAGTTTCtag	86	1	7	-	117,963,458	117,963,543	Intergenic
410	PC	PC-155	tgatttttagtggctgcactctTATGTAGTTTCGCTCCACTaagaagtgggcgtaatgggcatatgcatctgatgaaagaggg	83	1	7	-	117,965,108	117,965,190	Intergenic
411	PC	PC-156	gtgggagcttgttagaaatcccagatcctagaccccagcctgcaccTAAGGATCTGCGGTTTACCAAGAtctccagg	77	1	7	-	117,966,638	117,966,714	Intergenic
412	PC	PC-157	tttggattccaagagaaagtagtTAAGAGAATCAGCAGCTCTGTAGCTCtgttgcatatctgttctggttctgtttctgaagttcttttggtgtctttt	99	1	7	-	117,967,067	117,967,165	Intergenic
413	PC	PC-158	TCCTATTCCTGAGACGGTGATtcgtagctggattctcagtttctgcacctctttcaggaatcta	64	1	7	-	117,967,900	117,967,963	Intergenic
414	PC	PC-159	tctgggtctgtctactggagacCTGCTGGTCATTTGTAAGCtcttgtttcatttgtatctgtatgtcagctttccagttgtcttaccctct	91	1	7	-	117,971,856	117,971,946	Intergenic
415	PC	PC-160	tctggcgttgctgtgaactgtggtgTAGGTCACAGACACGGCGTggatcccacattgctgtggctgtggtgtagcccagcagctgtagctccgat	95	1	7	-	120,949,888	120,949,982	Intergenic
416	PC	PC-161	gcGATTGGTGGAGAGACCTGAcacccatatccttgactgtgcggtcaaggtcaccttcaccaatgat	67	1	7	+	124,374,252	124,374,318	Intergenic
417	PC	PC-162	agagcccccaccccgcccatggggcagGCCAGGATAGACTTGACCTgaccgaacagttagcatcctgttaactcctggtgaactgcagtgggagtgaggctggtggca	108	1	7	-	127,129,134	127,129,241	Intergenic
418	PC	PC-163	aggaggggagtgggagagggaggggggtgGAGGGAAGGGAGGGTGGGCtgcccggagagaggaggaccgccctggctcctccagacctgtgctccccagcacccctgc	107	1	7	+	134,000,412	134,000,518	Intergenic
418	PC	PC-163	aggaggggagtgggagagggaggggggtgGAGGGAAGGGAGGGTGGGCtgcccggagagaggaggaccgccctggctcctccagacctgtgctccccagcacccctgc	107	2	7	+	134,289,662	134,289,768	Intronic
419	PC	PC-164	cttagtctattgCTGTCCTTTGCATCCAACAggtagttattgcatatccactatgtagcaggcactgttctaggctctt	79	1	7	+	136,080,734	136,080,812	Intergenic
420	PC	PC-165	tgctcaggttctaagggtcagttttcctgcgaTTCCGCGGACAAGGCCTTTggtctgaaga	61	1	8	+	2,376,898	2,376,958	Intergenic
421	PC	PC-166	aaggcgtcacgtggtgcccctcagacgggaccCGCCCCCGGGGTCCTCCTCtgtgagacctcggtgcccggaccccgggggcgccatcgcggg	94	1	8	-	3,763,031	3,763,124	Intergenic
422	PC	PC-167	ttagtgtttttttttttcagatataTAACCAGGAGTAGAATTGCtgggtcattcggtacgtctacttttcgttttctgagaaacctccacacaaa	97	1	8	-	8,634,350	8,634,446	Intergenic
423	PC	PC-168	tggaggtttccaggctacaggTCAAATCGGAGCTACGGCTtttggcctctgccacagccacagcagctccggatctgagccgagcctgtg	90	1	8	+	18,324,589	18,324,678	Intergenic
424	PC	PC-169	gaggctggatcattctcctccaaaccccacagctgctatggcacatggaaggaatggaatGGAGGCTGCAGAGTGAACCtcagtgtctgc	90	1	8	+	25,394,642	25,394,731	Intergenic
425	PC	PC-170	tcggcagcctcttgggagcaCTGGGACCCAGGCTCCATCactggtccacaacggtggattaaagtgggttaaggttccagcgttgctttggctgcagc	98	1	8	-	33,558,121	33,558,218	Intergenic
426	PC	PC-171	taatgtgtacgtgtgctatctacatatatgtatgtgctatgcatgtatGTGTATGTATGTGTATATGTATAtacat	76	1	8	-	66,520,502	66,520,577	Intergenic
427	PC	PC-172	agaggtacaaatctatcctggtacaattATTGTGATTTTCCTTGTAAatatatggaaaatatatatattttgtctttttagggctgcacccat	93	1	8	-	67,706,089	67,706,181	Intergenic
428	PC	PC-173	taattttaaagtagcaacaataagatagtaactgacttctcaatagaaaTGCTGGAAATCAGGAGACTaagccataattttaaagtgctgaaagaaaaacc	101	1	8	+	82,552,014	82,552,114	Intronic
429	PC	PC-174	acactacctctgccacactgttaagacccagatcttctgtgTTGGATCTGAGCTCAGGCAgtgtcagtttgtggaag	77	1	8	-	82,901,157	82,901,233	Intergenic
430	PC	PC-175	tcttacacagctttccagaggtttccagcttataggatattcatatggtagtTCTGTGAACTAGAAACCTCTGGaaagtggtgtacat	88	1	8	-	97,945,306	97,945,393	Intronic
431	PC	PC-176	ctttttacattgtactgctgtcctgtgacttctcctgcaatctgaattgtaaagtaacatAGGATGgTAGACATAGAAGGAGc	83	1	8	+	102,390,022	102,390,104	Intergenic
432	PC	PC-177	gTGGACTGGATGACAATCTGCAGGctggccatgccgtagatgggaatccggtcgct	56	1	8	+	112,041,388	112,041,443	Intergenic
433	PC	PC-178	gtttcgctcctccacgtgtggttttagccttcacagaataaggagaccaaggcagggtgaGTGGTGCGTGTGGGTGGGTggggtgt	86	1	8	-	113,270,933	113,271,018	Intronic
434	PC	PC-179	cttgtgcctaagtgtcacgtcacagtttctaatctctgtcatatccTGTGATGATGGGCAGCTTAGCtgattatgtgccgg	81	1	8	-	118,720,077	118,720,157	Intergenic
435	PC	PC-180	cgcccgttacgtcgGCCGCCGGCCGCGCGCGCGCccgcctcccccgcgaccgcggctccgggagccgcttccggcggcgtgaggttctggttc	93	1	9	-	137,827	137,919	Intergenic
436	PC	PC-181	gttcCCATTGTGGAGCAGCAGAAatgaacccaactatggactataaggttgcaggttcaatctctggcttcgctcagtgggtt	83	1	9	-	1,149,380	1,149,462	Intergenic
437	PC	PC-182	acagccaggcgctgctgcacgcccagcccatcgtcagcatccgcgTGTGGGGCGTCGGGCGGGACagcggaaggtgggggcgcg	84	1	9	-	2,620,488	2,620,571	Exonicic
438	PC	PC-183	tcAGTCTCCTGGCTGGCTCGCCAgttgctgggctgcgccctaccggcctgcaagccctgtactggctcagcctcaagaccaa	82	1	9	+	6,137,609	6,137,690	Intergenic
439	PC	PC-184	gcatcagttgttactccaacagggccgcgtctccagcctccgagccacACTGGAGACACGTGCACTGTAGAatacacctgagcc	84	1	9	+	6,808,350	6,808,433	Intergenic
440	PC	PC-185	cgggctgtgcaacacgggtattcacttctgcacacgttaaGAATATGTCAGGGCTGGAGttcccatcgtggcgcagcgga	80	1	9	+	10,181,129	10,181,208	Intergenic
441	PC	PC-186	gtttggacaacccatgcacagccagagtgaaggcttcctCTCCACCTGAGCAGGGGTTcagtccatca	68	1	9	+	20,919,179	20,919,246	Intergenic
442	PC	PC-187	tatgagttgtggtataggtcacagacccagctcagatctggtgttgctgtggctgtggTGTAGGCCTGAGCTATAGCtccga	82	1	9	+	34,656,689	34,656,770	Intergenic
443	PC	PC-188	gaaGGGGAAGGGCGGGAGGGGCttgtgttccccaccaccgagaacagagcccttgcagccctcacccaaa	70	1	9	+	38,167,345	38,167,414	Intergenic
443	PC	PC-188	gaaGGGGAAGGGCGGGAGGGGCttgtgttccccaccaccgagaacagagcccttgcagccctcacccaaa	70	2	9	-	38,355,285	38,355,354	Intergenic
444	PC	PC-189	aagaagaacaccggggcagggtgtgtgtgtgtgtgtgtgtgtGCGCGCGCGCGCGTGTGCACGGcggtgtctttcc	78	1	9	+	45,200,560	45,200,637	Intergenic
444	PC	PC-189	aagaagaacaccggggcagggtgtgtgtgtgtgtgtgtgtgtGCGCGCGCGCGCGTGTGCACGGcggtgtctttcc	78	2	9	+	45,292,749	45,292,826	Intergenic
445	PC	PC-190	GCTTGGCTTGGAGTCAGAAGGCctgggtcccagtggctcaccactgtgtgacctggggcctgacattgaacatccccgagcc	82	1	9	+	45,484,804	45,484,885	Intergenic
446	PC	PC-191	ttttggacttaatccctgaaacgaatacttaagacaggtttaattggttctgtacgTGTCTCAGTGGGACCTCCAtcg	78	1	9	+	53,870,457	53,870,534	Intergenic
446	PC	PC-191	ttttggacttaatccctgaaacgaatacttaagacaggtttaattggttctgtacgTGTCTCAGTGGGACCTCCAtcg	78	2	9	-	53,921,770	53,921,847	Intergenic
447	PC	PC-192	ccagggcgcgcccccgccGCCCTCGGCCGCGCGCGCGCtctgcccgccctcctcgcgcgtgctcgtgctcgcggccgcggcggcgcgcctctt	93	1	9	-	54,632,020	54,632,112	Intergenic
448	PC	PC-193	ctaagcaaagggaggaattttaacattaaatCTAATTCAGAATTGTGATTactgtcttcaactggacattgcagtttctgaattgaggctgttagggacttaatgtgttg	110	1	9	-	55,593,342	55,593,451	Intergenic
449	PC	PC-194	ccaggagaaaCTCATGGTTGGGCTGAAGGaaaacactcatcttcagccatgtatggaatggctctgtc	68	1	9	-	61,437,426	61,437,493	Intergenic
450	PC	PC-195	tcagctttttacgtgtttacatgaggtttgcagagtgtgggTCTAAGTAGGCATAGGAAGAgcaag	66	1	9	+	72,529,977	72,530,042	Intergenic
451	PC	PC-196	atcactaatataaCAAATTGGATCAGACAAAAatgcccttatttcccttggtatcttgttatttcactattacaatgttttaattagtaag	91	1	9	+	79,211,129	79,211,219	Intergenic
452	PC	PC-197	ccaggTGGCTCAGTCGTAACGAACcagactagtatccatgaggatgcaggttcaatccctggccccact	69	1	9	-	94,977,928	94,977,996	Intergenic
453	PC	PC-198	tgacaggtgaggcttgaaaatattagtattctcttgttctagaATACATGATGATCTCACCCTaacttgaac	72	1	9	+	108,993,733	108,993,804	Intronic
454	PC	PC-199	gcatgcggagtttcccaggctaggggTCAAATCGGAGCTACGGCTgccggcctatgccacagccacagccacgctgatccgagccatgtctgagacctacacca	104	1	9	+	115,972,854	115,972,957	Intergenic
455	PC	PC-200	agaggtctggtctgcactgaGGGCAGGTGGATCTGGAGTaacggtgctgtgaagtccagcaaacaccacgctctaactggacaggcgtgaccaca	95	1	9	-	128,187,949	128,188,043	Intergenic
455	PC	PC-200	agaggtctggtctgcactgaGGGCAGGTGGATCTGGAGTaacggtgctgtgaagtccagcaaacaccacgctctaactggacaggcgtgaccaca	95	2	9	-	128,376,476	128,376,570	Intergenic
456	PC	PC-201	ggtgctgattcTGGAGACTGGGAAGACATAattgtttaacccttctgtgttgtcctctgctccagaatacatgcttt	77	1	9	+	131,098,991	131,099,067	Intergenic
457	PC	PC-202	agaggtatctgaattttaaaaAAGGGAGTTGATTGATTAAttgattgattgattgattgtcttttctagggctgtacccga	81	1	9	+	132,262,428	132,262,508	Intergenic
458	PC	PC-203	tcacTCAGTCTCCATGGCCTTCCctgagctctaaggggcgggttccaacagaggctgatcagggaagggaggggacgctgaga	83	1	10	-	8,177,008	8,177,090	Intergenic
459	PC	PC-204	tgccctcatagctctggcaaacacaacattggatcaacctcattatattttactgactCTTGAGTTGTTGTCATGGCctgattatttggact	93	1	10	-	9,079,852	9,079,944	Intergenic
460	PC	PC-205	taaagatgggctTGATTTCAGATAAACTGTTgtcacaacattttatcatcagtttttcttagcaaaatctaca	73	1	10	+	16,301,388	16,301,460	Intergenic
461	PC	PC-206	gatggcggcggcgtcggaggagcggATGGCTGAGGAAGGAGGCGGCGgccacggcgacggcggctcctcttcggctatcggctgcacccagcgactgcccccaccgc	107	1	10	+	21,123,019	21,123,125	Exonicic
462	PC	PC-207	cccaaagCAAGAAGGATTTGTAGAAAagtttattaaaacttggtaaatgggctcttctgcaaggtttgttttaac	75	1	10	+	36,281,835	36,281,909	Intergenic
463	PC	PC-208	acgtggctcagatctggtggtgttgtggctgtggtGTAGGCCGGCGCCTGTAGCtctgattcaacc	66	1	10	-	57,005,556	57,005,621	Intergenic
464	PC	PC-209	ttaaggatctggcgttgctgtgagctggggtgTAGGTCACAGACACGGCGTggatcctgtg	61	1	10	+	61,345,224	61,345,284	Intergenic
465	PC	PC-210	aagctggccgtgtccgctgtgggggcagcacccAGGGCAGGGCAGGGCGGGGcagagccgtctcagagcacatgtcctgggcgcccgctccacacctcggaccacggtcag	111	1	11	+	2,375,881	2,375,991	Intergenic
466	PC	PC-211	gggtttgcagtgttgagttccggacgttacttcttaaggacttccccacatcaagggttgTCTGATCAAGGTTGTTACCCAGCC	84	1	11	-	7,423,052	7,423,135	Intergenic
467	PC	PC-212	gttTCAAGATTGCAGGTATCCTCTGTAttgcgatgcttttggagaaagactcccaggatggggcatgagggagggtttgcagtgttgag	89	1	11	-	7,423,119	7,423,207	Intergenic
468	PC	PC-213	tcctccctcaTGTGTCCTCTGATTGCTTTCCATGGTctggagcgttttcatccatgttcttaaagccatgagcaatcgcagggacttttggaggaa	96	1	11	-	7,511,699	7,511,794	Intergenic
469	PC	PC-214	aaagagaccagatggCTCTGACACCATCAGGATAaaatccaaattccctcaggtgccattcaggcctttgcacaatctggtctcagt	87	1	11	+	9,966,839	9,966,925	Intergenic
470	PC	PC-215	aatctcttacttggaatatggattgagtttggcgctaactcagaggactacaggcaagtaTTCAGGACATAGCCAGAGGgatatt	85	1	11	+	17,606,545	17,606,629	Intergenic
471	PC	PC-216	gttcccattgTGGCTCAGCGGCAATGAACccaaccagtatccatgaggacgtgggttcaatccccggctttgctcagtgggtta	84	1	11	+	19,873,929	19,874,012	Intergenic
472	PC	PC-217	agcagcacttcccatatggtctagcggttaggattcctggttttcacccaggcggcccggGTTCGACTCCCGGTATGGGAACGttgcaac	90	1	11	+	24,760,354	24,760,443	Intronic
473	PC	PC-218	gtctctctgagggGATCCCACTGGGGCCTCCAggatatgttgtagaatacccagaaatcacctcagagaaca	72	1	11	-	33,534,925	33,534,996	Intergenic
473	PC	PC-218	gtctctctgagggGATCCCACTGGGGCCTCCAggatatgttgtagaatacccagaaatcacctcagagaaca	72	2	11	-	33,632,117	33,632,188	Intergenic
474	PC	PC-219	ctactctagtggttcgggttgggtgctttcacccctacagcctgggttcaattCCTGGTCTGAGAACTGAGAtcccacatcaagccgctgcacactggggcca	103	2	11	-	68,153,156	68,153,258	Intergenic
474	PC	PC-219	ctactctagtggttcgggttgggtgctttcacccctacagcctgggttcaattCCTGGTCTGAGAACTGAGAtcccacatcaagccgctgcacactggggcca	103	1	11	+	68,033,653	68,033,755	Intronic
475	PC	PC-220	agtggaattacattaatatgaaggaaatcacatatgattgCATGTGTGTGCATGTGCACatgtgtgtatgtgtgtgcgtgcgtgtggttttaaacgtttctgtaatgagttcccaa	116	1	11	-	69,581,588	69,581,703	Intergenic
476	PC	PC-221	gcagggagCGGGGCTGGAGGTGGGAGGGCtcggagagctcaactggggctgctcgagggccggcgatcagacctcagatccgctgcttt	89	1	11	+	79,607,387	79,607,475	Intergenic
477	PC	PC-222	cgtgagctgtggtgtaggtcacagatgcagctcggatcccatgctgctgtggctgtggtGTAGGCCTGCGACTGTAGCttcaa	83	1	12	-	3,749,393	3,749,475	Intergenic
478	PC	PC-223	cgagcgacgagagccaccgtcacccgcggctcaaggacactcgcgatgcggCGGCGGCGGCGGCGACTCCGGGcggc	77	1	12	-	4,609,395	4,609,471	Intergenic
479	PC	PC-224	taccaccttgcctgaatttcttgtctggcttcatcagtttctattgATCCAGGAAGGCCAAGAACcctggtccgtgata	79	1	12	-	13,651,628	13,651,706	Intergenic
480	PC	PC-225	cagctgcagtccctcatccccaacaatgacgtgaggggggctcatttctcatgttatccggACGTTGAAGATGGACTGCTCTGAGC	85	1	12	+	15,837,537	15,837,621	Exonicic
481	PC	PC-226	cgtctgtcacTCTCACTCTGAGGCTGGAGaaggagactggaattgacagtgcagaggggcaggaggacagcag	73	1	12	+	16,259,952	16,260,024	Intergenic
482	PC	PC-227	gcagccgcctcatggctcgctcataatcctccgggtccgggggctgcggcggcgagcggcGCGGCGCGGGCGGGAGGAGgggcgggcggggaggcgcgggctgcggg	107	1	12	-	16,480,765	16,480,871	Intergenic
483	PC	PC-228	tgtggtgTAGGTCACAGACACGGCGTggatctggcattgccgtggctgtggcgtagaccagc	62	1	12	-	20,823,931	20,823,992	Intergenic
483	PC	PC-228	tgtggtgTAGGTCACAGACACGGCGTggatctggcattgccgtggctgtggcgtagaccagc	62	2	12	-	20,895,608	20,895,669	Intergenic
484	PC	PC-229	taagcagctcttaagccctgcaagtcagagcctcactctgtgCCTTCCAGGACTGAAGAAGctgccag	68	1	12	-	23,105,346	23,105,413	Intergenic
485	PC	PC-230	acccTGAATCCGGCACGTCAGGTtatacaaataaattgaggcaactccgttttctggaaaatttgttagatgcagaaa	78	1	12	+	24,439,602	24,439,679	Mixed
486	PC	PC-231	tatcgtgcagcttctctgccatgtttttcttgcgcgTAGCACTGAGAGGTCTGTACGTATCC	62	1	12	-	24,443,832	24,443,893	Intergenic
487	PC	PC-232	acaagctTGGCTGGACTGTGAAAAGAtctgcctactttctcagacagtccctccaagttggg	62	1	12	+	27,163,466	27,163,527	Intergenic
488	PC	PC-233	gggagtTCCCTGGTCTAGTGGTTAGGATTTGGtgtgctcactgctgcagcctaggtttaagccctggtctgggaactgag	80	1	12	-	40,808,305	40,808,384	Intronic
489	PC	PC-234	aaaatctattggactgaagatgccctgggcctggccttagcCGGATTCCAGGCTGCAACTtcctcactttgatcct	76	1	12	+	45,042,670	45,042,745	Intergenic
490	PC	PC-235	ccctggtggtctggtggttaggatttggcactttcactactgcagtccaggttcaatcCCTGGTCTGAGAACTGAGAccccacatcaagctgctgcactctgtggccaaaa	111	1	12	+	46,400,192	46,400,302	Intergenic
491	PC	PC-236	tggtctgggtcagagtcagtctggggtcaaggccagggttGTGGTGCTGGTGGGTGGGTgagactcagcctggtacctcgtctgggcagggactggggctcagtggcggtgaagtagat	119	1	12	+	48,081,172	48,081,290	Intronic

492	PC	PC-237	cagcgaagactcAGGGGCTTGAGAAATGGCTaggaagccaaccaccctattggttgagagctgtggtctcagaggctccgaggattcgggg	91	1	12	-	50,606,828	50,606,918	Intronic
493	PC	PC-238	ATAGGCCAGCCGCTATAGCtctgattggacccctagcctgggaacctccatatgctgtgagtgtggcccta	71	1	14	+	3,354,384	3,354,454	Intergenic
494	PC	PC-239	caacgggcactcctaatgttttgttttgttttttttaattataaaAAGGAACCTGAAAAGAGAGccttggggagtctgatc	85	1	14	+	9,572,326	9,572,410	Intergenic
495	PC	PC-240	actttcctctatttctacACTCTGCAGAGCAAGCTGGcaaattactagcattcttaggcagtttagaaagggagggagga	80	1	14	-	11,939,845	11,939,924	Intergenic
496	PC	PC-241	ccctgaaatcacttatggcctggaatgggctcattccaactaagggCCCTGGGCTGTAGATTTCGata	68	1	14	+	16,319,123	16,319,190	Intergenic
497	PC	PC-242	aaccgtcactgtaaatcatcaaaagcttaacaaacGTGGAGTTGTTGTCATGGCtcagcggtgacgaac	69	1	14	+	17,508,038	17,508,106	Intergenic
498	PC	PC-243	caacatgtaaaacattacgtccttgctccttgcaaaacttttAGGGTGTCTGCTTTTATTTtcatgggc	71	1	14	+	36,957,400	36,957,470	Intergenic
499	PC	PC-244	ctggtggtctagtggttaggactcagtgctttcagtgctgcaagctgagttcaatcCCTGGTCTGAGAACTGAGAttctatattaagctacagc	94	1	14	-	40,612,326	40,612,419	Intergenic
500	PC	PC-245	tggcagaagctggggggtcttcgacttgtttttttTAGTTGAAGTGGAACTCGTTTCTGGAa	61	1	14	+	40,701,684	40,701,744	Intergenic
501	PC	PC-246	gtATAGGCCGGAAGCTGTAGCtcagattcaacccctagcctgggaaccttcatatgctgtgcgtgccgccctaaaa	76	1	14	+	41,026,092	41,026,167	Intergenic
502	PC	PC-247	gcagacttttcttggtggaagagatttgactgtaggcagtgaatcctgctgtgcttgtTTGAGACTCTTTCGCCATGAAGATagtcaaa	89	1	14	-	42,961,929	42,962,017	Intergenic
503	PC	PC-248	ccgggggggaaggttacaatgttatgctttacagctTGTGAAGAATATCTGTTATCGTCTCCTgtg	65	1	14	+	43,084,470	43,084,534	Intergenic
503	PC	PC-248	ccgggggggaaggttacaatgttatgctttacagctTGTGAAGAATATCTGTTATCGTCTCCTgtg	65	2	14	-	42,970,651	42,970,715	Intergenic
504	PC	PC-249	cgggacagggcagtctggctggagcagtggggtctgagaagagcagtaaccctctagcccTGCTACCTGGAGGCTCTGTCCTGGg	85	1	14	+	43,089,470	43,089,554	Intergenic
504	PC	PC-249	cgggacagggcagtctggctggagcagtggggtctgagaagagcagtaaccctctagcccTGCTACCTGGAGGCTCTGTCCTGGg	85	2	14	-	42,965,615	42,965,699	Intergenic
505	PC	PC-250	acgtagggccaagcgcgccgctggagtcagagccaatggcggCGGCGGCGGCGGCTCTGGAa	62	1	14	+	44,815,938	44,815,999	Exonicic
506	PC	PC-251	aactatggTTTTCTCTGAATAGATGCCCAGAATtgggatcaatggatcatacggtagttcttttaatttttctgagaaacctccatactc	90	1	14	+	51,963,459	51,963,548	Intergenic
506	PC	PC-251	aactatggTTTTCTCTGAATAGATGCCCAGAATtgggatcaatggatcatacggtagttcttttaatttttctgagaaacctccatactc	90	2	14	-	8,198,199	8,198,288	Intergenic
507	PC	PC-252	acccagggttaggacaggatccacaactcctgcagggagATCCTGTATCAGATCCTGAaa	60	1	14	+	54,585,542	54,585,601	Intergenic
508	PC	PC-253	ttgatctttTTTGGATCCATGTGGTACTtgccaatgatggatcctttagaagatgat	57	1	14	-	54,679,464	54,679,520	Intergenic
509	PC	PC-254	ccaggaGTGGGAAGGACCAGAGGTGcggtcaagggcaaagagctgctatttccaaatagccctctgctccccatcctgctcccac	85	1	14	-	77,864,669	77,864,753	Intronic
510	PC	PC-255	cacgtgttacttTGTGAAGCTTTGCTAGACTCTCTCTggaagtttctctctcacagggctctagtgtagccatttttacaagttctgtaatgcctg	96	1	14	+	83,584,887	83,584,982	Intergenic
511	PC	PC-256	ttctgccgcagaggccaaaggctaagagcaaattcaaggtatctttcttttccagcccTAGAAGCTTTAGAGTTTTGTTCTAGActtttacccacacaggcaagg	104	1	14	+	83,596,598	83,596,701	Intergenic
512	PC	PC-257	ctctgaagagctgtagagcatttcagcagcacctccttttgtcacattaacaggctccaTGTGATGGGACTGATTCCTTgtgcccttatttctaggctcatcacct	104	1	14	+	83,602,614	83,602,717	Intergenic
513	PC	PC-258	ttttttttttttctgtaatttggatggttttacagaggtgtcatcAAGCCTCAAGCTACAGACTcattattgaagaagaaacac	84	1	14	-	87,667,820	87,667,903	Intergenic
514	PC	PC-259	cttctggtctggactctgagctccagcctcccccattctcctggctgaagcccCCATCCTTCCAGGCACAGCtc	72	1	14	+	110,282,677	110,282,748	Intronic
515	PC	PC-260	agtgtggtgtaggtcacagatacagcttggatccagttgctgtggctgtggctatggcATAGGCCGGAAGCTGTAGCtctgatttgacccctagcctgaacctc	106	1	14	+	118,385,291	118,385,396	Intergenic
516	PC	PC-261	ttCTGTGTGTTATTGTTAACAcattgtgcatttatgttgggtctcagtttccttctgcacagtgtgatgcagttcagcata	81	1	14	-	124,927,456	124,927,536	Intergenic
517	PC	PC-262	tcaatccagaaaaCAAGAAAGATTAGTAGAAATaaacttttgattaaaaaaaaaaaggtttaaaaaaaattaaacatttttctctgtagggt	92	1	14	+	125,589,337	125,589,428	Intergenic
518	PC	PC-263	ttccattgccatgggtgcagccattaaaaaaaaaaaaaaaaaagatggagttcctgttgTGGCTCAGCGGCAATGAAC	78	1	14	-	134,018,935	134,019,012	Intergenic
519	PC	PC-264	ctccctggtgatctagtggtcaggactcagctctttcaccactatggcctggactcaatgCCTGGTCTGAGAACTGAGAtcctacatcaagccactgcacactatggcca	110	1	14	-	141,832,329	141,832,438	Intergenic
519	PC	PC-264	ctccctggtgatctagtggtcaggactcagctctttcaccactatggcctggactcaatgCCTGGTCTGAGAACTGAGAtcctacatcaagccactgcacactatggcca	110	2	14	-	141,905,608	141,905,717	Intergenic
520	PC	PC-265	cctctcttcacttccggcctcgctcggtgccctcCTGGGCTGGATGGGAGGTGaggggtca	61	1	14	-	147,755,794	147,755,854	Intergenic
521	PC	PC-266	gcagccagGGGTTGTGATGAGGACTCAgggggcttccgtcctggaaagcctcatcctcctggtgtt	66	1	15	+	23,522,146	23,522,211	Intergenic
522	PC	PC-267	gcagttcccatatggtctagcggttaggattcctggttttcacccaggcggcccggGTTCGACTCCCGGTATGGGAACAcg	81	1	15	-	29,171,436	29,171,516	Intergenic
523	PC	PC-268	gtacctcagaatgtgactttatttggaaattgggtctttacagagacatgCTAAAATGAGGTCACAGGAgggac	74	1	15	-	42,519,943	42,520,016	Intergenic
524	PC	PC-269	tTAGGAAAGGACATGTGACTgagagaaaggaagtaaacgagtgaactctacagtcacctggactttctgcc	71	1	15	+	43,096,080	43,096,150	Intergenic
525	PC	PC-270	tttttctttttACATTCTCTGCTCCTTTTTTtcgttattgttataaagtagtgattgtggagagaattgggagaaaagtatgaaaaagga	89	2	15	-	55,124,427	55,124,515	Intergenic
525	PC	PC-270	tttttctttttACATTCTCTGCTCCTTTTTTtcgttattgttataaagtagtgattgtggagagaattgggagaaaagtatgaaaaagga	89	1	15	+	55,174,428	55,174,516	Intronic
526	PC	PC-271	ctgctgtgagctgtggtgtatgtcgcagatgtggcttgaatctagcattgctgtggctctGGCATAGGCTGATTAGACCcatagcctgggaacttccatagttcgcaggtgcggccc	117	1	15	+	70,274,482	70,274,598	Intergenic
526	PC	PC-271	ctgctgtgagctgtggtgtatgtcgcagatgtggcttgaatctagcattgctgtggctctGGCATAGGCTGATTAGACCcatagcctgggaacttccatagttcgcaggtgcggccc	117	2	15	+	70,442,174	70,442,290	Intergenic
527	PC	PC-272	ttaaccactgagccaTGACGGGAACTCCTTACCATTCagattttagaaaatgactaggttgggaggttcctgttgtggctcagtggtaac	89	1	15	+	71,640,343	71,640,431	Intronic
528	PC	PC-273	aatgcagatctcagtgtcatcatggccctttacaagatcaaaaaggaattttttttcgttTAAGGACTTGGTGATGGTAggagaatgtcgc	90	1	15	+	82,309,250	82,309,339	Intergenic
528	PC	PC-273	aatgcagatctcagtgtcatcatggccctttacaagatcaaaaaggaattttttttcgttTAAGGACTTGGTGATGGTAggagaatgtcgc	90	2	15	-	82,510,573	82,510,662	Intergenic
529	PC	PC-274	atacggaagacagagaaagacagAGTTGTTCTGGTAGGGGAGCtaagagtctgttgggttttcctgaccagctcaaacctctttttcccaccttgcggac	100	1	15	+	102,867,585	102,867,684	Intergenic
529	PC	PC-274	atacggaagacagagaaagacagAGTTGTTCTGGTAGGGGAGCtaagagtctgttgggttttcctgaccagctcaaacctctttttcccaccttgcggac	100	2	15	-	102,721,025	102,721,124	Intronic
530	PC	PC-275	gtaggctgcagatggatctggcattgctgtggctgtggcATAGGCCGGAAGCTGTAGCtcta	62	1	15	-	106,146,587	106,146,648	Intronic
531	PC	PC-276	GGAGAATTTAGTAGTAAATctgtcacagtataatttaaaagcaagatgtgcccaatatttataatttcattcagg	75	1	15	+	108,547,214	108,547,288	Intergenic
532	PC	PC-277	aaagccatcatttttggaagttccctggtggcctgGTGGTTAGGAGCTTTCACTgctgaggccaa	65	1	15	-	121,165,858	121,165,922	Intronic
533	PC	PC-278	tccctggtggtctagtggttaggatttggtgctttcactgctgtggcccaggttcCCTGGTCTGAGAACTGAGAgctcacatcaaatccctacaggctgcaaccagatt	109	1	15	+	129,673,201	129,673,309	Intergenic
534	PC	PC-279	ggagggaatgcctgggGGGCCGGGCGGTGGTGGCGgcggcgcccgagggccagcgccaccccccccccccccccgggaacccgcg	85	1	15	-	131,466,125	131,466,209	Intergenic
535	PC	PC-280	ctagaggtaagggctgcctccagcctccattctcatgactggtgagTGTCCAGAGGGCGGAACGGcacaaaagcagctctccatctccag	90	1	15	-	132,643,979	132,644,068	Intergenic
536	PC	PC-281	ctctcaggccctcattagctcagctggagccttcgcatatACAGGACCTTGGCATGGACcccctgctaatgtttccaggcatccttcacctcgagagaaggagggttgacag	113	1	15	-	132,673,789	132,673,901	Intergenic
537	PC	PC-282	ggaactacagcccagCCCATGGACCTCTCTGATCccacatggtagtcctgtatccccctcccgggatgtgtggaggtagggggttgtaagtggta	94	1	15	+	133,832,625	133,832,718	Intergenic
538	PC	PC-283	ttaggattcagtgttttcactgctatggtctaggttcagtcCCTGGTCTGAGAACTAAGAacccaca	67	1	16	-	8,436,462	8,436,528	Intergenic
539	PC	PC-284	gtagcattcagaagttctagtggatataggagttcctgtcatggctcaGGGGATGATGTATCTGACTagggtccatgaggatgcagg	87	1	16	+	25,008,563	25,008,649	Intronic
540	PC	PC-285	ccttgtcatggtAGGGTTTTGTCTGCTTTGTcaccactgtacatctagccttagaaacacattgacaaat	70	1	16	+	28,893,231	28,893,300	Intergenic
541	PC	PC-286	aatgggcccaggaatctatattgttaagaagtagcacccgataattctgacatgcTGGGAACTACTGCTTTGCAGCAagaatatccctttggtcctca	99	1	16	+	49,529,363	49,529,461	Intergenic
542	PC	PC-287	ctttcCACCATCCCTTCCTTCCTTaaaaatactttgacaggattgagatggtggagga	58	1	16	+	58,716,707	58,716,764	Intergenic
543	PC	PC-288	agcaaaggcgcttcccgaatcactgcaccatccaaggctgccaggtgacagctggcatctTTGGCTGCTGTAGTGGACCaggcagtgtatgttgctcca	100	1	16	-	66,332,556	66,332,655	Intergenic
544	PC	PC-289	tctttatgtcttcatccattcatggacatttaaGTTGTTCCTGAACCTTGGCtactaggcataatgc	67	1	16	+	71,084,744	71,084,810	Intergenic
545	PC	PC-290	gagagctgatagtcaatgaatctgaagtttgaaagcgcagcatcccgcagaatcaggtCAGGGTTATGTGACTGAGCtgct	81	1	16	-	74,241,218	74,241,298	Intergenic
546	PC	PC-291	gaaattcactaagagagtagacttaagtttcccactacacatacacacaattgaaccatATGATGTGAAGGATAGGTTaatttgcttgattggggcaatcatt	104	1	17	+	4,030,704	4,030,807	Intergenic
547	PC	PC-292	gcTGTGGGGCGTCGGGCGGGAtcccattatcgcggtgtttgcttggggctgcccagcgcctccgccta	68	1	17	+	30,731,396	30,731,463	Intergenic
548	PC	PC-293	acaggatttagcttatttaaagtgtttgatttgcattcaATTGATGTAGGATGAGTCCaca	61	1	17	-	31,542,493	31,542,553	Intergenic
549	PC	PC-294	CCACTAGCCCTGCTGTGGCcgtcttaccattggcatggaagtccagggtggaggacgcattcccaagagaactgctggc	79	1	17	+	33,520,810	33,520,888	Intergenic
550	PC	PC-295	cttccgcagggggcgcccttgcccaacccctccctaaatccctgggctcctgcccCCGGTGCGCCCCCGCCGGCtg	75	1	17	+	43,396,695	43,396,769	Intergenic
550	PC	PC-295	cttccgcagggggcgcccttgcccaacccctccctaaatccctgggctcctgcccCCGGTGCGCCCCCGCCGGCtg	75	2	17	-	43,689,890	43,689,964	Intergenic
551	PC	PC-296	gtagaaaGAAGGAGGCAGAGACAGGAtactggtctgcctgaggctggatgcagacagaatcctggagctggctgcctgagtcatc	85	1	17	-	48,914,488	48,914,572	Intergenic
552	PC	PC-297	cagtcAGGGACCCAGGAGACAAATctagatggacgttgactgggaaccacctgaggg	57	1	17	-	50,402,325	50,402,381	Intergenic
553	PC	PC-298	ttggcgctgctcctcgctCAGAGCTGTGGGCACGGTGgccagcgtgcttccagactctcacgctccgtccgcagcgcggg	80	1	18	-	638,836	638,915	Intergenic
554	PC	PC-299	aaaATCTACAGATTGTCGAGATGGAGAaaatagtagagttttgcagacgagctgtaggtcat	62	1	18	+	8,777,643	8,777,704	Intergenic
555	PC	PC-300	ggtgctctgtcatgGACTCTGTTGCCCACTGGAtgatgatctcattcttcttattggcttacttttgggtttttgagcctt	81	1	18	+	9,936,632	9,936,712	Intronic
556	PC	PC-301	aggggagatgggacacttggtaatgtctgcggCACCTGCCCTCTGCACGTGGGCtgtgaggatgggtagcccagggcaggggtcaggaaccctgggcttacttctagatccaca	114	1	18	-	15,647,628	15,647,741	Intergenic
557	PC	PC-302	atATTGGCACTGCACATAATTGCtcagagcggagagacacaagcaaaaatgtgctagtgccaaaat	66	1	18	+	17,171,997	17,172,062	Intergenic
558	PC	PC-303	gtctctgctctgtTTATGGCCCTTCGGTAATTCACTgaccgagactgttcacagtgaattctaccagtgcatacacagaacaggagt	88	1	18	+	17,172,229	17,172,316	Intergenic
559	PC	PC-304	tgtggtgtggtgtgggtgtgggtgtGGGTGTGGTGTGGGTGTGGGtttgtcctgactgctgtgaccttgactaaatgatctttgcacttggacctct	99	1	18	+	41,660,291	41,660,389	Intergenic
560	PC	PC-305	accctgtagatcttcaaagagtagggactagatgaaatccaacataacattcaggagttcCCATTGTGGAGCAGCAGAAa	80	1	X	-	9,559,780	9,559,859	Intronic
561	PC	PC-306	taactttctagcagacctcagttctctcaagagtTCTACTGTGAGGGCTGAGGtcggttaccaaggat	68	2	X	-	10,007,257	10,007,324	Intergenic
561	PC	PC-306	taactttctagcagacctcagttctctcaagagtTCTACTGTGAGGGCTGAGGtcggttaccaaggat	68	1	X	-	9,857,208	9,857,275	Intronic
562	PC	PC-307	ccgccacccaatatggcagaactcaagctatttctaaactcggggcctgcCTGGAGTTCTTGTCATGGCtcagtggtta	79	1	X	+	14,901,779	14,901,857	Intergenic
563	PC	PC-308	acctgcttaaacgcgtgtgtacgcacatgtatgcacgtgtacACATGTGTACGCATGTGTActgcattc	69	1	X	+	20,900,275	20,900,343	Intergenic
563	PC	PC-308	acctgcttaaacgcgtgtgtacgcacatgtatgcacgtgtacACATGTGTACGCATGTGTActgcattc	69	2	X	-	21,036,978	21,037,046	Intergenic
564	PC	PC-309	ttcccagtgtttgtgagtctcctggtccttctaattttctcattttctgaatgtagcccATGAGAAGGTCCTGGTAGAtcctgctgggcca	92	1	X	+	55,669,052	55,669,143	Intergenic
564	PC	PC-309	ttcccagtgtttgtgagtctcctggtccttctaattttctcattttctgaatgtagcccATGAGAAGGTCCTGGTAGAtcctgctgggcca	92	2	X	-	55,385,622	55,385,713	Intergenic
564	PC	PC-309	ttcccagtgtttgtgagtctcctggtccttctaattttctcattttctgaatgtagcccATGAGAAGGTCCTGGTAGAtcctgctgggcca	92	3	X	-	55,520,745	55,520,836	Intergenic
565	PC	PC-310	tgcatgtgtctttttgagttagcgtttctgtttttttctggatataTAACCAGGAGTAGAACTGCtgggccataat	76	1	X	-	68,738,973	68,739,048	Intergenic
566	PC	PC-311	TGTGTGTGTGTGTGTGAGTGTGAATgaattaatccaggtatatcatttcatataatg	57	1	X	+	73,931,162	73,931,218	Intergenic
567	PC	PC-312	caATCTACCAAAATCGCTTGGccttagattatttacttgtttctgaaggaggggttttgtggaaaa	66	1	X	+	74,667,082	74,667,147	Intergenic
568	PC	PC-313	actttgcaatcaaactgaatccctttttattttatagttttgctagtaataaaagcaaAAAGACTATAAAATAAAAAGGaattcagtttgatttgtcaacac	102	1	X	-	76,729,946	76,730,047	Intergenic
569	PC	PC-314	aaaggtgttctggagAGGGAACCTGGAAAAGCTGAAGgtgtaatatgaaaacctcagcaattcttggttctcatttttaggacatcaat	89	1	X	-	76,730,882	76,730,970	Intergenic
570	PC	PC-315	cgtggctcagatccctcagatgctgtggctgtggctgtggctgtggctgtggcATAGGCCGGAAGCTGTAGCtgtgatgtgacccttа	94	1	X	+	85,144,244	85,144,337	Intergenic
571	PC	PC-316	cagtctgtcagttctatcagtactgttgataattcaatcaagtttgggtttctggagttcCCATTGTGGATCAGCAGAAatgaactggactagt	94	1	X	+	93,065,671	93,065,764	Intergenic
572	PC	PC-317	tttccacctccattttggcagTACAGATGTCCTGAGAAACacacacctgtgccaggagtggagatgctgaagagggatttgtggaagatggagcagtggc	100	1	X	-	99,435,849	99,435,948	Intergenic
573	PC	PC-318	gttcCCATTGTGGATCAGCAGAAacggatcaaactaggaagcataaggttgcaagtttgatccctggcctcactcagtgggtt	83	1	X	-	100,110,551	100,110,633	Intergenic
574	PC	PC-319	tatttgaGATTCAGATTTGTATAGTGgttaatagcgtagactctaaagactctggagccagatatcctgaatttgaatcttggccc	86	1	X	+	100,680,341	100,680,426	Intergenic
575	PC	PC-320	ggtgcagtgccctgcccaggcaggtgctgatcacttagtctctgggtCAACAGTCCCTGCCTGGGTAGAgtaaggctca	79	1	X	+	117,267,529	117,267,607	Intergenic
576	PC	PC-321	ccaacccagggaggtgctgttcacctagactgcatgTGAACAGGGCCTTTCTGGGTCGAgt	61	1	X	+	117,268,042	117,268,102	Intergenic
577	PC	PC-322	cggtgccctatccagacaggtgctgttctcttgacgactgcTGAACGGCGCCTGTGTGGTTAGAgcaagg	70	1	X	+	117,270,803	117,270,872	Intergenic
578	PC	PC-323	gccgtgctgtgtgtggtgcccTGACCAGGCAGGTGCTGTTTCTCTcgacgagtagtgaacggtgcctgtgtggctaagggctcacaagaacatc	97	1	X	+	117,271,810	117,271,906	Intergenic
579	PC	PC-324	gagccattcagcgtgcagtgcttttcacaagaaggtgtcaattcaggtggactaaaaatatgAATGGCGCTTTTTTTGTGAAGAgtaatggacaccatgtaaggcaca	106	1	X	-	118,198,291	118,198,396	Intergenic
580	PC	PC-325	cagtgcccTACTCAGGAAGGCATTATTCACAtagttggaaatatgaatggcgcctttctgagtagagcaatg	72	1	X	-	118,218,736	118,218,807	Intergenic
581	PC	PC-326	aacttcagttgagtgtggtgccctactccaaagggtgtcattcatacagactaatacatgACTGTCACCTTTTTGAGTAGAGtaatgcacatcatttgtgaaata	105	1	X	-	118,227,198	118,227,302	Intergenic
582	PC	PC-327	tctgtgcagtgcctcactccaaagagtgccaatcaggtacattaaaatatgATTGGCACTTTTTAGAGTGTGGtaattcacagc	84	1	X	-	118,233,387	118,233,470	Intergenic

Supplementary Table 8. Genome location clusters of porcine pre-miRNAs					
Inter-distance <= 50,000 nts					
Cluster ID	Pre-miRNA name	Chromosome	Strand	Start	End
1	mir-30c	1	-	53,819,906	53,819,985
	mir-30a	1	-	53,848,998	53,849,104
2	mir-181a-2	1	+	280,334,006	280,334,085
	mir-181b-2	1	+	280,335,868	280,335,953
3	PN(a)-6	1	-	283,451,013	283,451,109
	PN(a)-6	1	-	283,497,677	283,497,773
4	PN(a)-8	2	+	5,685,207	5,685,291
	mir-192	2	+	5,685,412	5,685,491
5	PC-22	2	-	15,100,864	15,100,940
	PC-23	2	-	15,108,433	15,108,496
	PC-26	2	-	15,108,515	15,108,605
	PC-25	2	-	15,113,347	15,113,432
	PC-24	2	-	15,119,677	15,119,777
	PC-25	2	+	15,169,332	15,169,417
	PC-26	2	+	15,174,303	15,174,393
6	mir-129	2	-	17,100,324	17,100,403
	PN(a)-9	2	-	17,122,268	17,122,367
7	mir-24-1	2	-	56,860,821	56,860,892
	mir-27a	2	-	56,860,970	56,861,051
	mir-23a	2	-	56,861,159	56,861,228
	mir-181c	2	+	56,889,316	56,889,402
	mir-181d	2	+	56,889,500	56,889,579
8	PC-36	2	+	68,799,996	68,800,126
	PC-36	2	+	68,800,592	68,800,722
9	PC-50	2	+	127,484,068	127,484,146
	PC-50	2	+	127,525,736	127,525,814
10	mir-143	2	+	136,030,752	136,030,831
	mir-145	2	+	136,032,141	136,032,226
11	PC-60	3	-	15,359,737	15,359,798
	PC-60	3	-	15,384,758	15,384,819
12	PN(a)-13	3	+	38,549,756	38,549,851
	PN(a)-14	3	+	38,550,130	38,550,218
	PN(a)-15	3	+	38,552,589	38,552,694
13	PC-63	3	-	38,667,463	38,667,518
	PC-64	3	-	38,716,142	38,716,199
14	PC-65	3	+	41,088,681	41,088,747
	PC-66	3	+	41,090,685	41,090,751
	PC-67	3	-	41,092,230	41,092,311
	PC-68	3	+	41,092,232	41,092,307
15	PC-69	3	+	41,624,237	41,624,299
	PC-70	3	-	41,626,515	41,626,598
	PC-71	3	-	41,627,418	41,627,483
16	PN(a)-16	3	+	79,154,190	79,154,275
	mir-216	3	+	79,165,852	79,165,956
	mir-217	3	+	79,172,584	79,172,690
17	mir-217	3	-	79,378,361	79,378,467
	mir-216	3	-	79,385,092	79,385,196
18	mir-30d	4	+	5,729,459	5,729,537
	mir-30b	4	+	5,733,584	5,733,659
19	PC-88	5	-	20,064,090	20,064,185
	PC-88	5	-	20,108,111	20,108,206
20	PC-96	6	-	247,465	247,534
	PN(a)-24	6	-	248,247	248,303
	PN(a)-25	6	-	248,338	248,406
	PC-97	6	-	249,044	249,113
	PN(a)-26	6	-	250,392	250,483
	PC-98	6	-	250,690	250,773
	PC-99	6	-	251,649	251,719
	PC-100	6	-	251,707	251,777
	PC-101	6	-	251,751	251,844
	PC-102	6	-	255,386	255,476
21	PC-104	6	-	10,153,594	10,153,712
	PC-105	6	-	10,156,459	10,156,558
	PC-106	6	-	10,159,080	10,159,186
22	mir-99b	6	+	39,533,216	39,533,285
	let-7e	6	+	39,533,375	39,533,454
	mir-125a	6	+	39,533,851	39,533,930
23	PC-112	6	-	43,886,629	43,886,722
	PN(a)-31	6	-	43,886,642	43,886,713

24	PC-123	6	+	103,808,631	103,808,686
	mir-101-2	6	+	103,818,808	103,818,888
25	PN(a)-33	6	-	121,821,234	121,821,330
	mir-30e	6	-	121,824,301	121,824,380
26	PC-130	7	-	22,793,682	22,793,771
	PN(a)-34	7	+	22,803,533	22,803,652
27	PC-132	7	-	34,450,857	34,450,932
	PC-133	7	-	34,464,588	34,464,680
	PC-134	7	-	34,466,641	34,466,721
	PC-135	7	-	34,484,784	34,484,889
28	PC-139	7	+	54,374,344	54,374,421
	mir-184	7	+	54,379,989	54,380,071
29	PC-143	7	-	90,893,972	90,894,046
	PC-144	7	+	90,893,973	90,894,045
	PC-145	7	+	90,894,127	90,894,237
	PC-146	7	+	90,894,674	90,894,761
30	PC-148	7	-	95,895,079	95,895,184
	PC-149	7	-	95,897,924	95,898,004
31	PC-151	7	-	117,947,019	117,947,084
	PC-152	7	-	117,950,334	117,950,407
	PC-153	7	-	117,952,163	117,952,224
	PC-154	7	-	117,963,458	117,963,543
	PC-155	7	-	117,965,108	117,965,190
	PC-156	7	-	117,966,638	117,966,714
	PC-157	7	-	117,967,067	117,967,165
	PC-158	7	-	117,967,900	117,967,963
	PC-159	7	-	117,971,856	117,971,946
32	mir-432	7	+	133,834,157	133,834,236
	mir-136	7	+	133,834,348	133,834,429
	PN(a)-37	7	+	133,847,438	133,847,516
33	PN(a)-38	7	+	133,927,744	133,927,857
	mir-127	7	+	133,929,738	133,929,817
34	PN(a)-40	8	+	92,257,711	92,257,780
	PN(a)-41	8	+	92,258,012	92,258,079
35	PC-184	9	+	6,808,350	6,808,433
	mir-139	9	-	6,808,359	6,808,426
36	PC-188	9	+	38,167,345	38,167,414
	PN(a)-42	9	+	38,210,599	38,210,682
	mir-34c	9	+	38,211,158	38,211,237
37	PN(a)-42	9	+	38,327,577	38,327,660
	mir-34c	9	+	38,328,136	38,328,215
	PC-188	9	-	38,355,285	38,355,354
38	mir-125b-1	9	-	47,654,247	47,654,326
	let-7a	9	-	47,697,398	47,697,477
	mir-100	9	-	47,702,721	47,702,800
39	mir-214	9	-	107,639,153	107,639,262
	PN(a)-44	9	-	107,644,923	107,645,040
40	PN(a)-46	9	+	127,173,767	127,173,847
	mir-29c	9	+	127,174,326	127,174,413
41	mir-215	10	-	9,750,609	9,750,704
	PN(a)-47	10	-	9,750,923	9,750,980
42	mir-181b-1	10	-	22,839,191	22,839,270
	mir-181a-1	10	-	22,839,352	22,839,455
43	PN(a)-48	10	+	26,148,228	26,148,308
	mir-24-2	10	-	26,148,230	26,148,309
	mir-27b	10	-	26,148,776	26,148,855
	mir-23b	10	-	26,149,010	26,149,089
44	PN(a)-49	10	-	36,097,479	36,097,555
	PN(a)-50	10	+	36,141,559	36,141,639
45	PC-207	10	+	36,281,835	36,281,909
	PN(a)-50	10	-	36,311,908	36,311,988
46	PC-211	11	-	7,423,052	7,423,135
	PC-212	11	-	7,423,119	7,423,207
47	mir-15a	11	+	17,602,978	17,603,056
	mir-16-2	11	+	17,603,121	17,603,199
	PC-215	11	+	17,606,545	17,606,629
48	mir-17	11	+	60,972,458	60,972,534
	mir-18	11	+	60,972,593	60,972,684
	mir-19a	11	+	60,972,741	60,972,822
	mir-20	11	+	60,972,911	60,972,981
	mir-19b-1	11	+	60,973,040	60,973,119
	mir-92a-1	11	+	60,973,160	60,973,239

49	mir-10a	12	-	22,389,424	22,389,503
	PN(a)-51	12	+	22,434,918	22,435,019
50	PC-230	12	+	24,439,602	24,439,679
	PC-231	12	-	24,443,832	24,443,893
51	mir-365-2	12	-	41,107,186	41,107,265
	mir-193a	12	-	41,119,432	41,119,511
52	PN(a)-53	12	-	42,820,762	42,820,833
	PN(a)-54	12	-	42,820,910	42,820,993
53	mir-423	12	+	44,150,500	44,150,579
	PN(a)-55	12	-	44,150,500	44,150,574
54	PN(a)-56	12	-	45,599,472	45,599,572
	PN(a)-57	12	-	45,599,904	45,600,013
55	mir-497	12	+	49,575,594	49,575,673
	mir-195	12	+	49,575,884	49,575,963
56	mir-425	13	-	26,605,151	26,605,230
	mir-191	13	-	26,605,641	26,605,720
57	mir-135-1	13	+	28,964,466	28,964,555
	let-7g	13	+	28,999,419	28,999,498
58	mir-15b	13	+	78,787,511	78,787,608
	mir-16-1	13	+	78,787,668	78,787,744
59	mir-99a	13	+	130,664,295	130,664,374
	let-7c	13	+	130,665,021	130,665,114
60	PC-247	14	-	42,961,929	42,962,017
	PC-249	14	-	42,965,615	42,965,699
	PC-248	14	-	42,970,651	42,970,715
61	PC-248	14	+	43,084,470	43,084,534
	PC-249	14	+	43,089,470	43,089,554
62	mir-130b	14	-	51,318,779	51,318,858
	PN(a)-60	14	-	51,319,104	51,319,200
63	mir-185	14	+	52,703,712	52,703,787
	mir-1306	14	+	52,728,146	52,728,225
64	PC-255	14	+	83,584,887	83,584,982
	PC-256	14	+	83,596,598	83,596,701
	PC-257	14	+	83,602,614	83,602,717
65	PC-270	15	-	55,124,427	55,124,515
	PC-270	15	+	55,174,428	55,174,516
66	PC-280	15	-	132,643,975	132,644,064
	PC-281	15	-	132,673,789	132,673,901
67	PN(a)-64	16	-	31,831,839	31,831,927
	PN(a)-63	16	-	31,831,951	31,832,047
68	PN(a)-63	16	+	31,984,173	31,984,269
	PN(a)-64	16	+	31,984,293	31,984,381
69	PN(c)-12	17	+	10,529,440	10,529,509
	mir-486	17	+	10,558,722	10,558,801
70	mir-133a	17	-	64,053,943	64,054,045
	mir-1	17	+	64,096,222	64,096,329
71	mir-29b	18	+	16,054,349	16,054,429
	mir-29a	18	+	16,054,752	16,054,837
72	PN(a)-71	18	-	17,167,650	17,167,759
	PN(a)-72	18	-	17,171,979	17,172,083
	PC-302	18	+	17,171,997	17,172,062
	PC-303	18	+	17,172,229	17,172,316
	mir-183	18	-	17,172,238	17,172,307
73	mir-196b	18	+	44,179,792	44,179,871
	mir-196b	18	+	44,205,846	44,205,925
74	mir-221	X	-	40,478,094	40,478,163
	mir-222	X	-	40,478,834	40,478,913
75	mir-98	X	-	45,719,499	45,719,578
	let-7f	X	-	45,720,363	45,720,445
76	mir-374b	X	+	58,683,650	58,683,729
	PN(a)-75	X	+	58,683,804	58,683,888
77	PC-313	X	-	76,729,946	76,730,047
	PC-314	X	-	76,730,882	76,730,970
78	mir-363	X	-	108,178,321	108,178,400
	mir-92a-2	X	-	108,178,486	108,178,565
	mir-19b-2	X	-	108,178,624	108,178,703
	PN(a)-78	X	-	108,178,755	108,178,823
	mir-363	X	-	108,212,243	108,212,322
	mir-92a-2	X	-	108,212,408	108,212,487
	mir-19b-2	X	-	108,212,546	108,212,625
	PN(a)-78	X	-	108,212,677	108,212,745
	mir-106a	X	-	108,213,079	108,213,159

79	mir-450a	X	-	108,480,688	108,480,793
	mir-450c	X	-	108,480,833	108,480,913
	mir-542	X	-	108,481,539	108,481,618
	mir-503	X	-	108,498,665	108,498,773
	mir-424	X	-	108,499,011	108,499,090
80	PC-320	X	+	117,267,529	117,267,607
	PC-321	X	+	117,268,042	117,268,102
	PC-322	X	+	117,270,803	117,270,872
	PC-323	X	+	117,271,810	117,271,906
81	PC-324	X	-	118,198,291	118,198,396
	PC-325	X	-	118,218,736	118,218,807
	PN(a)-79	X	-	118,219,037	118,219,130
	PC-326	X	-	118,227,198	118,227,302
	PC-327	X	-	118,233,387	118,233,470
82	mir-224	X	-	121,480,634	121,480,714
	PN(a)-80	X	-	121,481,685	121,481,769