

Table S1 Primer sequences for real-time PCR

miRNA	Primer	Sequence
<i>U6</i>	Up primer	CGCTTCGGCAGCACATATAC
	Down primer	TCACGAATTTGCGTGTCAT
<i>chi-let-7b-5p</i>	Up primer	CCGTGAGGTAGTAGGTTGTGTGGTT
<i>chi-miR-107-3p</i>	Up primer	CGAGCAGCATTGTACAGGGCTAT
<i>chi-miR-30b-5p</i>	Up primer	CCGCTGTAAACATCCTACACTCAGCT
<i>chi-miR-1271-3p</i>	Up primer	CGTCACAGTGAACCGGTCTCTTT
<i>chi-miR-92a-5p</i>	Up primer	AGGTTGGGATCAGTTGCAATGCT
<i>chi-miR-412-3p</i>	Up primer	TATACGCTTCACCTGGTCCACTAGC

Table S2: Overview of reads from raw data to cleaned sequences of small RNA sequences.

Type	D10_1		D10_2		D10_3		D10_4		D10_5	
	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq
Raw reads	863442	100.00	1023031	100.00	1349392	100.00	1307004	100.00	949935	100.00
3ADT&length filter	476498	55.19	547130	53.48	793297	58.79	848030	64.88	544110	57.28
Junk reads	6163	0.71	7110	0.69	6798	0.50	6861	0.52	5921	0.62
Rfam	11680	1.35	12669	1.24	14641	1.09	14884	1.14	12709	1.34
mRNA	18716	2.17	17626	1.72	21711	1.61	18720	1.43	14504	1.53
Repeats	1324	0.15	1582	0.15	1753	0.13	1931	0.15	1634	0.17
Valid reads	353058	40.89	440934	43.10	515858	38.23	421672	32.26	375327	39.51

Type	D25_1		D25_2		D25_3		D25_4		D25_5	
	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq
Raw reads	998568	100.00	917367	100.00	1489136	100.00	1064340	100.00	1187114	100.00
3ADT&length filter	518623	51.94	512348	55.85	759610	51.01	626571	58.87	539346	45.43
Junk reads	8583	0.86	4263	0.46	12349	0.83	6927	0.65	9931	0.84
Rfam	11863	1.19	10411	1.13	16740	1.12	14807	1.39	14443	1.22
mRNA	16088	1.61	15852	1.73	27692	1.86	20096	1.89	22255	1.87
Repeats	1305	0.13	1338	0.15	1686	0.11	1561	0.15	1697	0.14
Valid reads	445955	44.66	376668	41.06	676188	45.41	398934	37.48	604124	50.89

Type	D31_1		D31_2		D31_3		D31_4		D31_5	
	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq	Uniq	% of uniq
Raw reads	1215693	100.00	1090285	100.00	1058913	100.00	1546792	100.00	1800286	100.00
3ADT&length filter	601086	49.44	550849	50.52	502707	47.47	685778	44.34	1028346	57.12
Junk reads	9399	0.77	6572	0.60	7709	0.73	14981	0.97	13989	0.78
Rfam	15045	1.24	14985	1.37	11486	1.08	18371	1.19	16436	0.91
mRNA	22095	1.82	19174	1.76	18500	1.75	35054	2.27	30393	1.69
Repeats	1606	0.13	1488	0.14	1442	0.14	2103	0.14	1900	0.11
Valid reads	570984	46.97	501582	46.00	521044	49.21	796524	51.50	714684	39.70

Table S3: Information of the highly expressed miRNAs in the goat colon of three different periods.

miR_name	Sequence	D10_1 (norm)	D10_2 (norm)	D10_3 (norm)	D10_4 (norm)	D10_5 (norm)	D25_1 (norm)	D25_2 (norm)	D25_3 (norm)	D25_4 (norm)	D25_5 (norm)	D31_1 (norm)	D31_2 (norm)	D31_3 (norm)	D31_4 (norm)	D31_5 (norm)
chi-let-7f-5p	TGAGGTAGTAGAT TGTATAGTT	31245. 66	31577. 41	24545. 72	22108. 92	40557. 50	31878. 85	68705. 39	37339. 47	31208. 06	27579. 35	28455. 72	29908. 99	24931. 13	17577. 23	23287. 28
chi-let-7d-5p	AGAGGTAGTAGGT TGCATAGTT	17727. 73	20104. 59	18721. 97	21742. 38	19750. 87	19055. 95	18598. 87	19642. 49	19593. 06	21274. 85	22562. 20	20098. 75	19962. 66	19492. 20	16406. 29
chi-let-7d-3p	CTATACGACCTGC TGCCTTTCT	4844.6 1	7089.7 3	6341.1 9	6762.0 8	5883.0 3	3801.4 7	14170. 87	6507.7 6	5145.3 6	9214.9 8	5528.7 3	7017.1 3	6903.8 0	7994.4 9	5557.4 7
chi-let-7e-5p	TGAGGTAGGAGGT TGTATAGTT	32213. 65	40306. 38	40948. 79	39775. 16	33621. 36	32349. 50	34276. 18	31642. 95	39923. 47	33233. 69	41543. 94	50541. 23	36741. 77	29093. 51	27127. 68
chi-let-7a-5p	TGAGGTAGTAGGT TGTGTGGTT	273674 .80	308517 .33	296359 .97	317003 .02	330373 .78	311181 .55	521287 .55	306841 .98	352508 .62	303980 .85	399522 .55	392244 .07	339988 .32	255973 .03	245615 .70
chi-let-7i-5p	TGAGGTAGTAGTT TGTGCTGTT	32712. 21	31512. 86	26314. 27	25278. 73	34437. 59	31221. 13	79115. 93	37108. 08	29293. 70	28501. 77	28455. 99	31761. 57	27101. 97	22835. 44	20823. 23
chi-let-7g-5p	TGAGGTAGTAGTT TGTACAGTT	20827. 40	27945. 82	19867. 21	20364. 65	31014. 77	20261. 49	53386. 92	22753. 72	24312. 68	20075. 23	24907. 09	27355. 42	20522. 19	15088. 47	16710. 72
chi-let-7c-5p	TGAGGTAGTAGGT TGTATGGTT	19998. 78	19328. 18	22494. 28	25363. 75	15374. 01	17784. 34	27865. 21	14034. 72	20558. 67	15736. 86	22688. 46	29583. 58	24529. 86	19915. 93	15916. 33
chi-let-7b-5p	TGAGGTAGTAGGT TGTGTGGTT	176240 .70	173168 .72	187498 .46	222957 .97	151793 .56	227617 .78	245458 .22	194446 .03	201309 .73	256727 .74	242442 .15	267225 .59	239427 .19	275758 .49	213294 .50
chi-miR-10a-5p	TACCCTGTAGATC CGAATTTGT	61275. 44	62140. 88	37246. 00	27586. 79	28542. 14	68528. 90	324180 .62	59130. 15	66710. 19	48078. 30	40605. 32	71483. 46	62414. 76	28559. 75	54096. 73
chi-miR-10b-5p	TACCCTGTAGAAC CGAATTTGT	83940. 80	144259 .68	65070. 37	50191. 29	107257 .26	112533 .55	496302 .40	115090 .28	122741 .97	71568. 14	91293. 33	124972 .55	94762. 61	36804. 97	109924 .35
chi-miR-15b-5p	TAGCAGCACATCA TGGTTTACA	11208. 64	13415. 82	14560. 07	14409. 52	9032.5 9	15375. 47	6677.4 4	11321. 83	15858. 47	14897. 83	17803. 06	12090. 30	17598. 22	18493. 66	16968. 02
chi-miR-16a-5p	TAGCAGCACGTAA ATATTGGAG	35752. 62	34798. 93	33487. 76	35944. 45	38726. 32	45266. 57	15268. 46	41279. 50	42988. 96	37575. 85	54593. 67	42767. 59	45125. 23	32024. 41	37342. 72
chi-miR-16b-5p	TAGCAGCACGTAA ATATTGGGGT	35517. 99	35954. 43	34295. 88	29418. 16	28622. 87	45564. 78	17434. 25	44566. 09	45192. 76	43874. 74	51678. 97	43648. 03	46939. 85	39158. 87	42668. 67
chi-miR-21-5p	TAGCTTATCAGAC TGATGTTGAC	74169. 93	45746. 10	38806. 10	31978. 46	75424. 49	101040 .06	93761. 21	161189 .87	46105. 82	59979. 95	50154. 74	40877. 89	51023. 21	41172. 61	63962. 63

chi-miR-22-3p	AAGCTGCCAGTTG AAGAACTGT	22087. 56	16599. 82	18985. 88	22805. 15	23012. 22	26298. 75	19557. 26	29765. 13	22556. 97	19791. 59	19415. 33	15278. 96	17003. 36	14130. 40	17773. 66
chi-miR-23a	ATCACATTGCCAG GGATTTCCA	82978. 49	65670. 25	78868. 63	66701. 42	64283. 02	110036. .40	51555. 06	95555. 34	103646. .03	80819. 71	113583. .50	95078. 51	95547. 00	103799. .89	87428. 33
chi-miR-23b-3p	ATCACATTGCCAG GGATTACCAC	133104 .20	131714 .13	156157 .08	138250 .22	138852 .26	147873 .90	93665. 43	115966 .83	192298 .40	144988 .38	209574 .50	204187 .50	165829 .17	163783 .52	135452 .42
chi-miR-24-3p	TGGCTCAGTTCAG CAGGAACAGT	40784. 83	32631. 91	36585. 00	38759. 81	38466. 37	45744. 37	22724. 22	33964. 00	41356. 99	37496. 74	43184. 03	41366. 71	39540. 64	36327. 18	36777. 58
chi-miR-25-3p	CATTGCACTTGTCT CGGTCTGA	50610. 48	55247. 98	68050. 82	63119. 16	74336. 78	45852. 03	58881. 21	58094. 53	60706. 49	53001. 72	72787. 13	76805. 29	63806. 22	47145. 46	46415. 37
chi-miR-26a-5p	TTCAAGTAATCCA GGATAGGCT	290462 .96	208818 .18	253956 .68	249888 .01	277753 .75	279325 .25	389337 .65	262252 .32	309618 .50	212521 .57	329445 .51	350132 .17	322036 .37	179724 .71	214181 .88
chi-miR-26b-5p	TTCAAGTAATTCA GGATAGGTT	18240. 92	15065. 23	13079. 89	12754. 99	17737. 36	17301. 93	9211.6 4	13334. 40	17061. 57	12223. 52	16673. 81	13915. 83	13812. 30	11225. 95	13402. 87
chi-miR-27b-3p	TTCACAGTGGCTA AGTTCTGC	196235 .00	194481 .06	185781 .28	197366 .55	304629 .28	159991 .92	508343 .24	140905 .10	179853 .30	151888 .49	186223 .19	197298 .71	174079 .39	126295 .61	124029 .06
chi-miR-27a-3p	TTCACAGTGGCTA AGTTCTGCT	20014. 11	13022. 15	15879. 62	16467. 05	19137. 81	24138. 39	12577. 18	18811. 44	15647. 86	16372. 19	18301. 44	14880. 73	17844. 05	17755. 05	16910. 35
chi-miR-28-3p	CACTAGATTGAGA GCTCCTGGA	15879. 60	16288. 16	15023. 14	14849. 37	15532. 23	14658. 05	47860. 70	18328. 23	14833. 64	18357. 78	17489. 08	17543. 77	18095. 50	18356. 02	15894. 97
chi-miR-29a-3p	TAGCACCATCTGA AATCGGTTA	10120. 24	8025.6 2	7902.5 2	7020.5 5	9810.6 7	10653. 65	7762.8 9	14072. 20	10641. 34	13441. 28	14468. 05	11016. 40	14605. 13	10578. 95	12817. 64
chi-miR-30b-5p	TGTAAACATCCTA CACTCAGCT	19374. 29	14295. 20	14427. 30	13312. 17	14965. 75	19186. 47	7321.0 4	11105. 24	17476. 32	12181. 99	19552. 38	18930. 96	19215. 80	9939.8 5	16795. 87
chi-miR-30c-5p	TGTAAACATCCTA CACTCTCAGCT	112280 .76	110130 .08	88273. 05	74750. 73	84263. 23	115693 .35	98426. 09	99048. 38	147437 .44	111663 .05	132038 .19	139418 .72	128165 .07	88494. 73	136830 .90
chi-miR-30f-5p	TGTAAACACCCTA CACTCTCAGCT	17991. 30	19253. 00	14830. 95	17673. 80	12309. 91	26754. 16	27423. 58	18099. 59	21949. 83	23521. 49	26039. 67	27240. 92	26595. 31	29144. 06	39820. 30
chi-miR-30a-5p	TGTAAACATCCTC GACTGGAAGCT	23002. 32	17309. 70	14127. 74	13110. 95	16340. 47	32243. 43	91366. 83	23928. 98	20376. 10	19140. 44	21426. 72	23769. 63	20341. 73	14469. 68	18929. 16
chi-miR-30e-5p	TGTAAACATCCTT GACTGGAAGCT	14812. 38	9288.6 4	7471.0 0	5836.4 7	11345. 52	19004. 97	40769. 52	18016. 49	13041. 65	12156. 78	12047. 57	10962. 61	9515.9 5	7526.7 8	10695. 47
chi-miR-92b	TATTGCACTTGTCC CGGCCTGT	66963. 48	64004. 44	73273. 27	81684. 55	83213. 67	60723. 50	92643. 19	78797. 46	65935. 38	84666. 29	80895. 82	67022. 26	88932. 19	115874 .02	86577. 84

chi-miR-92b	TATTGCACTTGTCC CGGCCTGT	66963. 48	64004. 44	73273. 27	81684. 55	83213. 67	60723. 50	92643. 19	78797. 46	65935. 38	84666. 29	80895. 82	67022. 26	88932. 19	115874 .02	86577. 84
chi-miR-93-5p	CAAAGTGCTGTTC GTGCAGGTAG	25222. 55	24945. 29	28047. 30	20722. 68	26230. 98	27005. 69	17167. 99	31709. 26	34650. 26	27812. 06	38161. 16	33031. 27	25425. 28	22381. 76	22610. 08
chi-miR-99a-5p	AACCCGTAGATCC GATCTTGT	167177 .69	157458 .61	143857 .86	162109 .08	121271 .04	147777 .19	539839 .18	131113 .75	158757 .69	127848 .85	152753 .89	228667 .24	178494 .90	118130 .17	128140 .14
chi-miR-99b-5p	CACCCGTAGAACC GACCTTGCG	115796 .13	151188 .12	119575 .36	107430 .33	84552. 90	85275. 86	563668 .01	93788. 32	91129. 15	129596 .13	89483. 79	139628 .22	127225 .87	142445 .46	141938 .13
chi-miR-100-5p	AACCCGTAGATCC GATCTTGT	167177 .69	157458 .61	143857 .86	162109 .08	121271 .04	147777 .19	539839 .18	131113 .75	158757 .69	127848 .85	152753 .89	228667 .24	178494 .90	118130 .17	128140 .14
chi-miR-103-3p	AGCAGCATTGTAC AGGGCTATGA	54320. 17	57872. 46	56674. 46	47463. 22	68170. 29	61571. 45	80161. 79	76525. 80	67447. 34	57381. 78	68465. 74	62166. 61	55252. 00	42961. 93	39428. 59
chi-miR-106b-3p	CCGCACTGTGGGT ACTTGCTGC	4595.5 0	6311.5 0	5110.1 6	5189.7 4	5193.6 7	3475.6 3	10996. 25	4867.4 7	4364.0 8	5277.4 3	4087.5 7	4257.8 4	5286.2 2	5549.4 1	5595.0 6
chi-miR-125b-5p	TCCCTGAGACCCT AACTTGTA	325308 .05	366963 .89	357392 .61	410646 .95	214696 .39	306550 .07	811122 .60	315553 .84	354191 .78	503747 .73	372845 .10	489928 .83	482108 .30	482556 .10	573169 .90
chi-miR-125a-5p	TCCCTGAGACCCT TTAACCTGT	76423. 23	73473. 52	69836. 71	83714. 88	44604. 91	77510. 95	172388 .68	69580. 32	81558. 53	127075 .58	86828. 24	102271 .16	113921 .17	135995 .69	121615 .98
chi-miR-126-3p	TCGTACCGTGAGT AATAATGCG	22155. 78	20079. 99	16552. 50	20647. 86	22652. 90	27067. 62	18944. 30	24143. 32	23704. 17	17441. 13	23834. 32	22610. 33	18744. 79	14363. 60	20422. 97
chi-miR-127-3p	TCGGATCCGTCTG AGCTTGGCT	159180 .53	198602 .76	190836 .53	179957 .46	160685 .38	119067 .03	490227 .71	130713 .27	127489 .04	127811 .27	107991 .23	172715 .17	160027 .84	175085 .30	122465 .19
chi-miR-133a-3p	TTGGTCCCCTTCA ACCAGCTGT	63330. 29	46415. 43	57773. 53	52680. 17	23719. 76	74072. 95	35867. 11	47496. 95	69303. 46	66436. 07	58866. 47	83550. 64	51673. 43	76644. 15	66789. 64
chi-miR-140-3p	ACCACAGGGTAGA ACCACGGAC	31624. 83	30640. 77	28587. 41	29835. 90	28506. 65	28652. 04	119940 .99	35911. 89	26175. 07	39225. 23	32540. 24	44156. 20	41441. 58	35936. 18	30350. 38
chi-miR-143-5p	GGTGCAGTGCTGC ATCTCTGG	7447.2 8	7232.8 0	7442.7 3	7400.3 1	5505.0 8	9562.7 5	14938. 35	8685.7 9	6923.2 3	9599.6 4	7505.6 4	8307.1 3	5753.4 8	5523.9 9	6399.8 5
chi-miR-143-3p	TGAGATGAAGCAC TGTAGCTC	126544 2.91	978624 .76	118518 9.08	122397 0.31	100438 2.33	174863 7.71	331278 5.67	148840 2.37	118380 7.11	137814 9.54	143433 8.82	182169 3.24	123469 5.89	681185 .63	823166 .51
chi-miR-145-5p	GTCCAGTTTTCCC AGGAATCCCT	413928 .08	273737 .54	305373 .85	259564 .08	158024 .67	793964 .42	638968 .89	541464 .83	631723 .29	709422 .09	752564 .55	708834 .75	619420 .59	683159 .93	806093 .40
chi-miR-148b-3p	TCAGTGCATCACA GAACTTTGT	11716. 15	16633. 54	15764. 87	14707. 66	18941. 74	12204. 72	29471. 89	13071. 93	15800. 23	11653. 46	18318. 89	13771. 45	16121. 38	10127. 90	9856.5 1

chi-miR-148a-3p	TCAGTGC ACTACA GAACTTTGT	17993. 37	13478. 70	12347. 17	9831.9 4	19812. 08	20308. 81	63178. 32	25952. 08	16426. 19	14153. 24	14891. 68	16023. 04	14462. 52	7909.0 1	11173. 04
chi-miR-150	TCTCCCAACCCCTT GTACCAGTG	7238.4 9	7862.5 0	10018. 71	5326.9 1	3185.0 5	7577.2 2	4807.9 1	8794.0 9	8113.9 7	11637. 64	8922.7 1	9453.6 8	18551. 50	17071. 68	17578. 87
chi-miR-151-5p	TCGAGGAGCTCAC AGTCTAGT	39841. 64	59860. 41	50657. 82	56378. 05	60594. 93	37213. 45	112601 .43	42147. 40	45274. 54	42107. 69	51792. 35	57195. 83	47958. 81	36867. 21	40825. 43
chi-miR-151-3p	CTAGACTGAAGCT CCTTGAGG	12902. 76	17417. 23	12956. 13	14128. 38	16357. 32	10902. 31	32350. 25	13511. 90	12716. 90	13176. 27	12666. 40	16005. 58	13610. 57	9682.1 0	13138. 88
chi-miR-181b-5p	AACATTCATTGCT GTCGGTGGGTT	19062. 65	19039. 31	21285. 24	15153. 75	14940. 91	23146. 58	25074. 54	22894. 49	24424. 85	21651. 10	26571. 69	32499. 99	22415. 31	21861. 88	17587. 42
chi-miR-186-5p	CAAAGAATTCTCC TTTTGGGCTT	23493. 29	20199. 36	17199. 16	16012. 47	21252. 01	30013. 52	38970. 22	26861. 34	29226. 04	23320. 76	26362. 78	22464. 06	24708. 44	16435. 20	21047. 49
chi-miR-191-5p	CAACGGAATCCCA AAAGCAGCTG	91284. 71	82650. 08	87009. 65	94805. 14	102237 .48	99899. 62	322962 .36	134048 .00	98190. 04	136355 .82	129039 .59	101344 .48	138137 .96	109419 .87	103426 .25
chi-miR-192-5p	CTGACCTATGAAT TGACAGCC	88187. 97	103572 .54	73356. 46	81439. 12	199865 .94	56505. 68	219895 .65	64759. 11	82610. 43	56386. 51	65916. 93	58206. 50	58216. 93	30809. 32	48731. 06
chi-miR-193b-3p	AACTGGCCACAA AGTCCCCT	17306. 01	10998. 20	12463. 55	16264. 13	7850.8 4	14316. 02	14785. 11	16803. 76	13027. 53	14312. 44	13013. 60	10673. 85	16444. 15	27350. 80	18504. 98
chi-miR-194	TGTAACAGCAACT CCATGTGGA	130256 .56	105981 .50	95792. 41	116805 .42	194800 .92	89265. 02	67951. 75	86648. 06	115745 .20	86480. 81	104781 .64	78949. 30	89398. 51	55807. 98	91344. 19
chi-miR-196b	TAGGTAGTTTCCT GTTGTTGGG	10525. 42	12794. 33	8681.9 5	12941. 47	18458. 21	7630.5 7	5245.9 2	5897.0 7	12588. 65	9848.8 3	16154. 25	9389.5 1	10613. 73	5947.4 3	8258.8 9
chi-miR-197-3p	TTCACCACCTTCTC CACCCAGC	13850. 59	15759. 62	17677. 80	17327. 47	15088. 62	11520. 65	21781. 80	13946. 60	14717. 15	18705. 85	14222. 18	15416. 73	15342. 62	28061. 80	21572. 91
chi-miR-199c-5p	CCCAGTGTTTCAGA CTACCTGTTC	45779. 83	38312. 81	29670. 09	33933. 39	40887. 54	41187. 37	174491 .90	42558. 79	36835. 24	31436. 15	34419. 56	37742. 07	44641. 08	22696. 49	27605. 82
chi-miR-199a-3p	ACAGTAGTCTGCA CATTGGTT	30784. 49	33963. 74	25116. 43	28068. 01	33597. 85	26143. 45	28798. 91	23614. 23	24792. 54	19997. 77	23068. 89	27623. 10	26479. 90	17244. 38	23479. 37
chi-miR-199a-5p	CCCAGTGTTTCAGA CTACCTGTTC	45779. 83	38312. 81	29670. 09	33933. 39	40887. 54	41187. 37	174491 .90	42558. 79	36835. 24	31436. 15	34419. 56	37742. 07	44641. 08	22696. 49	27605. 82
chi-miR-199a-3p	ACAGTAGTCTGCA CATTGGTT	30784. 49	33963. 74	25116. 43	28068. 01	33597. 85	26143. 45	28798. 91	23614. 23	24792. 54	19997. 77	23068. 89	27623. 10	26479. 90	17244. 38	23479. 37
chi-miR-200b	TAATACTGCCTGG TAATGATGAC	250913 .83	231979 .19	188729 .36	185024 .20	398711 .61	180883 .34	373249 .36	242647 .06	311846 .43	225913 .40	305546 .82	216668 .48	270118 .99	169230 .80	192533 .36

chi-miR-200a	TAACACTGTCTGG	50695.	37807.	33054.	28554.	77658.	40612.	28076.	43769.	50536.	34507.	49615.	34638.	32443.	23711.	30001.
	TAACGATGTT	24	96	19	91	46	38	13	64	97	48	25	34	55	69	39
chi-miR-200c	TAATACTGCCGGG	142744	132646	106194	100223	177858	111039	113744	126130	133042	145257	127252	102610	139025	129327	134852
	TAATGATGGA	.83	.37	.69	.31	.04	.17	.99	.08	.68	.84	.06	.88	.57	.63	.68
chi-miR-214-3p	ACAGCAGGCACAG	29364.	34544.	38456.	43015.	23157.	24843.	13465.	17963.	25620.	30410.	30744.	32777.	36853.	50807.	41848.
	ACAGGCAGT	29	68	13	44	72	90	97	47	88	73	40	43	43	38	93
chi-miR-215-5p	ATGACCTATGAAT	2464.1	1118.5	1260.1	1635.2	4034.9	1610.1	19151.	3194.4	2159.1	1939.1	2397.2	2237.4	1554.7	1038.8	1200.7
	TGACAGACA	7	9	2	6	9	5	18	7	0	1	2	4	2	7	7
chi-miR-221-3p	AGCTACATTGTCT	16843.	14266.	12956.	11271.	15225.	15008.	11370.	18014.	16745.	12938.	20840.	14848.	16023.	15299.	12810.
	GCTGGGTTTC	98	04	13	64	25	67	41	61	64	95	70	64	80	02	81
chi-miR-222-3p	AGCTACATCTGGC	15056.	10456.	9171.2	7226.8	9756.5	14923.	22731.	20286.	13787.	16338.	17420.	11729.	15184.	19621.	17206.
	TACTGGGTCTCT	84	90	5	7	5	87	89	65	62	57	14	82	99	08	38
chi-miR-224-5p	CAAGTCACTAGTG	9299.5	10005.	9085.1	8088.4	10942.	7452.4	21543.	9239.3	9649.4	7582.4	9872.1	11455.	8354.3	7009.9	6885.1
	GTTCCGTTT	4	82	9	2	74	1	00	2	5	1	3	21	7	7	2
chi-miR-320-3p	AAAAGCTGGGTTG	49012.	53214.	56629.	59097.	56655.	51449.	58260.	64067.	56247.	70089.	83169.	84691.	69709.	109690	65181.
	AGAGGGCGA	49	01	79	06	76	44	59	57	10	83	28	54	82	.77	78
chi-miR-342-3p	TCTCACACAGAAA	57838.	49887.	45589.	44033.	40630.	73595.	41295.	56338.	73986.	61717.	70126.	60650.	79353.	63958.	75358.
	TCGCACCCATC	63	85	87	43	25	15	64	42	99	34	60	60	38	52	66
chi-miR-361-5p	TTATCAGAATCTC	12656.	9718.7	11030.	11624.	10516.	12854.	16515.	12337.	13042.	11626.	13201.	9756.6	14807.	11435.	11194.
	CAGGGGTAC	75	7	08	20	88	50	45	14	82	76	33	0	80	47	40
chi-miR-365-3p	TAATGCCCTAAA	12878.	8581.4	8618.0	10524.	5145.7	15033.	6987.7	12211.	13105.	11095.	12110.	8383.5	15200.	16126.	15834.
	AATCCTTAT	98	9	2	58	6	44	5	55	18	75	70	6	00	61	31
chi-miR-378-3p	ACTGGACTTGAG	117211	165700	128123	129840	161087	116524	399160	134281	132729	142785	177164	151023	126942	134739	150798
	TCAGAAGGC	.16	.20	.72	.99	.28	.14	.97	.89	.70	.25	.26	.97	.51	.40	.48
chi-miR-380-3p	TATGTAATGTGGT	11687.	9819.9	12592.	14123.	9256.1	8922.5	6402.8	6379.9	8004.5	7093.9	7232.3	7372.8	11338.	8198.7	7904.3
	CCACGTCT	21	2	23	85	7	0	8	1	4	2	6	9	07	5	4
chi-miR-409-5p	AGGTTACCCGAGC	4650.2	4406.0	3750.4	2998.4	3530.1	3809.0	18641.	5020.9	3599.2	3712.1	2649.7	3177.3	3644.2	3494.4	2604.8
	AACTTTGCAT	8	2	6	4	7	9	65	0	8	0	3	4	5	6	8
chi-miR-409-3p_R+1	GAATGTTGCTCGG	16353.	17111.	18988.	16487.	14681.	12701.	32168.	20048.	13080.	13335.	10898.	12287.	12482.	15791.	12090.
	TGAACCCCT	00	05	33	46	40	11	92	99	48	47	80	52	76	72	60
chi-miR-423-5p	TGAGGGGCAGAGA	25229.	26387.	27903.	23292.	25257.	27293.	59727.	42902.	30520.	45913.	39892.	36880.	40463.	43376.	33302.
	GCGAGACTTT	79	84	87	61	72	42	87	49	32	73	21	50	90	60	98

chi-miR-423-3p	AGCTCGGTCTGAG GCCCCTCAGT	45392. 74	61522. 12	47283. 15	41076. 94	44643. 06	42981. 40	93362. 78	68795. 15	52951. 39	80568. 55	60626. 60	59735. 24	60208. 88	84922. 68	73601. 28
chi-miR-455-3p_R-1	GCAGTCCATGGGC ATATACAC	10201. 89	14532. 13	14596. 95	17046. 33	10243. 62	14674. 25	9845.6 7	13137. 36	12152. 12	15240. 96	17659. 36	14293. 77	12987. 55	19230. 95	16381. 95
chi-miR-490	CAACCTGGAGGAC TCCATGCTGT	7649.8 7	4271.1 5	4968.3 7	2670.8 2	1683.9 1	4637.9 9	17129. 68	5105.1 3	4242.8 9	5685.8 2	3089.1 4	5528.0 2	3115.0 6	4993.6 0	3983.7 8
chi-miR-500-3p	ATGCACCTGGGCA AGGATTCTGA	2681.2 3	3180.8 1	3125.9 3	2657.2 2	3243.1 6	2369.4 9	14198. 33	3253.8 8	3192.1 7	3338.8 1	3150.6 1	3314.6 4	2905.8 3	2749.2 8	2346.0 1
chi-miR-532-5p	CATGCCTTGAGTG TAGGACCGT	5591.9 2	5445.7 9	6647.7 2	7069.2 9	8028.2 8	5440.2 0	12748. 30	7238.7 8	5364.2 1	5678.9 0	6710.7 2	6678.3 5	4513.0 9	4388.6 8	4420.3 5
chi-miR-3431-5p	CCTCAGTCAGCCT TGTGGATGT	12515. 15	12208. 38	12572. 56	10588. 07	17275. 57	9865.7 2	15921. 64	12849. 31	11335. 55	11145. 19	13085. 04	14699. 54	11338. 07	11818. 58	9932.5 4

Table S4: The dynamic miRNAs in goat colon from D10 to D31

miRNA	D10	D25	D31	<i>P</i> -values
Gene Table for Profile 0 (0.0, -1.0, -2.0)				0.024
1 CHI-MIR-1197-3P	0	-19.41	-36.53	
2 CHI-MIR-758_R-1	0	-273.70	-465.43	
3 CHI-MIR-411A-3P	0	-543.55	-912.93	
4 CHI-MIR-493-3P	0	-179.44	-255.48	
5 CHI-MIR-382-3P_R+1	0	-39.17	-139.70	
6 CHI-MIR-412-5P	0	-109.14	-269.07	
7 CHI-MIR-130B-5P	0	-628.74	-1169.07	
8 CHI-MIR-665_R+2	0	-202.00	-388.48	
9 CHI-MIR-3959-3P	0	-28.94	-62.77	
10 CHI-MIR-379-5P	0	-397.83	-1442.10	
11 CHI-MIR-381_1SS4AG	0	-59.05	-204.99	
12 CHI-MIR-301A-5P_R+1	0	-8.89	-14.47	
Gene Table for Profile 1 (0.0, -1.0, -1.0)				0.023
1 CHI-MIR-493-5P	0	-2929.6	-2,829.03	
2 CHI-MIR-124A_R-1	0	-493.19	-289.55	
3 CHI-MIR-410-3P	0	-865.49	-1,140.76	
4 CHI-MIR-323B	0	-593.06	-792.81	
5 CHI-MIR-411B-3P_1SS6CA	0	-29.82	-21.65	
6 CHI-MIR-1271-3P	0	-18.92	-14.78	
7 CHI-MIR-134_R-1	0	-45.65	-60.83	
8 CHI-MIR-592	0	-18.00	-15.46	
9 CHI-MIR-380-3P	0	-4,135.12	-3,086.59	
10 CHI-MIR-382-5P	0	-705.72	-663.6	
11 CHI-MIR-1306-3P_1SS22GT	0	-100.07	-71.03	
12 CHI-MIR-379-3P	0	-613	-638.01	
13 CHI-MIR-412-3P_L-1	0	-20.49	-21.53	
14 CHI-MIR-128-3P	0	-2,059.22	-2,097.99	
15 CHI-MIR-496-5P	0	-7.67	-5.96	
16 CHI-MIR-1307-5P_R+5	0	-201.20	-115.13	
17 CHI-MIR-496-3P_R+1	0	-35.19	-46.13	
18 CHI-MIR-107-3P	0	-1,473.39	-1,902.38	

19	CHI-MIR-199A-3P	0	-5,636.73	-6,726.98	
20	CHI-MIR-432-5P_1SS23GT	0	-1,046.70	-808.66	
21	CHI-MIR-194	0	-39,509.19	-44,671.03	
22	CHI-MIR-34C-5P	0	-61.30	-73.78	
23	PC-3P-37101_116	0	-19.28	-21.60	
24	PC-3P-3191_2100	0	-74.51	-63.31	
Gene Table for Profile 2 (0.0, -1.0,0.0)					0.982
1	CHI-MIR-211	0	-57.63	18.19	
2	CHI-MIR-214-3P_L-1R+3	0	-11,246.66	4,898.66	
3	CHI-MIR-214-5P	0	-102.99	-4.06	
4	CHI-MIR-329B-3P_R+1	0	-549.76	-247.17	
5	CHI-MIR-329A-3P_R+1_1SS19TC	0	-549.76	-247.17	
Gene Table for Profile 3 (0.0,0.0, -1.0)					0.805
1	CHI-MIR-98-5P	0	112.63	-284.83	
2	CHI-MIR-22-3P_R+3	0	2,895.81	-3,977.78	
3	CHI-MIR-494	0	1,290.21	-1,402.23	
4	CHI-MIR-340-5P	0	56.26	-95.29	
5	CHI-MIR-3959-5P	0	6.41	-202.94	
Gene Table for Profile 4 (0.0,0.0,1.0)					0.999
1	CHI-MIR-320-3P	0	5,101.08	27,566.81	
2	CHI-MIR-129-3P	0	-411.06	1,765.55	
3	CHI-MIR-150	0	1,459.83	7,589.36	
4	CHI-MIR-99A-3P	0	-53.36	110.12	
5	PC-3P-89392_15	0	0	3.92	
6	PC-5P-27762_176	0	-1.03	6.01	
Gene Table for Profile 5 (0.0,1.0,0.0)					0.794
1	CHI-MIR-186-5P_R+1	0	10,047.12	2,572.34	
2	CHI-MIR-146A	0	883.38	83.51	
3	CHI-MIR-146B-5P	0	1,726.04	63.26	
4	CHI-MIR-374B-3P	0	3.42	-1.24	
5	CHI-MIR-145-3P_L+2R-1	0	2,032.56	449.18	
6	CHI-MIR-33B-3P	0	10.7	-5.88	
7	CHI-MIR-1	0	1,889.91	106.05	
8	CHI-MIR-143-5P	0	2,936.31	-307.62	

9	CHI-MIR-30C-3P_R+1	0	50.96	11.68	
10	CHI-MIR-146B-3P	0	122.14	13.16	
11	PC-5P-62000_42	0	8.21	0	
12	PC-5P-18419_285	0	33.04	-9.76	
13	PC-3P-80363_21	0	4.18	0	
14	PC-3P-43684_88	0	6.85	-0.12	
15	PC-5P-3628_1784	0	161.3	37.74	
Gene Table for Profile 6 (0.0,1.0,1.0)					0.503
1	CHI-MIR-145-5P	0	380,983.06	431,889.00	
2	CHI-MIR-29B-5P	0	121.01	155.44	
3	CHI-MIR-222-3P_R+1	0	7,280.04	5,898.80	
4	CHI-MIR-423-5P	0	15,657.20	13,168.87	
5	CHI-MIR-181B-5P_R+1	0	5,541.94	6,290.89	
6	CHI-MIR-195-3P_R+1	0	288.78	194.9	
7	CHI-MIR-342-5P	0	88.3	75.06	
Gene Table for Profile 7 (0.0,1.0,2.0)					0.024
1	CHI-MIR-29C-5P_1SS23AT	0	162.94	239.2	
2	CHI-MIR-30F-5P_R+1	0	7,137.94	13,356.26	
3	CHI-LET-7B-5P	0	42,780.02	65,297.70	
4	CHI-MIR-92A-5P	0	15.46	25.16	
5	CHI-MIR-342-3P_R+2	0	13,790.70	22,293.55	
6	CHI-MIR-29A-3P_R+1	0	2,738.35	4,121.32	
7	CHI-MIR-671-5P	0	19.24	35.54	
8	CHI-MIR-425-5P_L-1R+2	0	354.58	625.13	
9	CHI-MIR-193B-5P	0	36.21	80.45	
10	CHI-MIR-491-5P_R+1	0	62.6	175.79	
11	CHI-MIR-23A_R+1	0	16,622.14	27,387.08	
12	PC-3P-20760_249	0	8.06	17.26	

Table S5: The identified DEmiRNAs in the goat colon.

miR_ name	miR_seq	D10_1 (norm)	D10_2 (norm)	D10_3 (norm)	D10_4 (norm)	D10_5 (norm)	D25_1 (norm)	D25_2 (norm)	D25_3 (norm)	D25_4 (norm)	D25_5 (norm)	D31_1 (norm)	D31_2 (norm)	D31_3 (norm)	D31_4 (norm)	D31_5 (norm)
	ATATACA															
chi-miR-1185-3p	GAGGGAG	81.656	84.748	58.191	46.478	65.652	104.80	24.263	72.199	44.711	24.720	15.782	18.873	18.765	35.067	67.492
	ACTCTTAT	48211	74639	11424	66561	86255	24656	00884	82339	5274	95152	11941	39635	43041	38123	76279
	TAGGACA															
chi-miR-1197-3p	CATGGTC	68.219	63.789	63.108	68.017	84.284	51.448	62.573	47.381	49.418	39.553	25.749	31.141	43.160	25.423	39.299
	TACTTCT	33949	379	6732	55943	0803	4831	0228	1341	00397	52244	77378	10398	48995	85139	5834
	TAAGGCA															
chi-miR-124a	CGCGGTG	566.42	780.96	885.98	1122.2	868.56	412.54	291.15	219.60	392.99	442.01	528.28	619.99	437.23	571.59	619.39
	AATGC	7243	42544	02042	89731	96276	06145	61061	77961	07934	06133	56814	10701	45286	8314	56079
	AGTGCCT															
chi-miR-1271-3p	GCTATGT	18.605	16.402	27.866	34.008	29.277	8.5747	0	9.0249	7.0597	6.9218	5.8144	17.929	0	12.273	16.232
	GCCAGG	27441	98317	16738	77972	6279	47183		77923	14852	66427	65047	72653		58343	43662
	GTCCAGT															
	TTTCCCAG															
chi-miR-145-5p	GAATCCC	413928	273737	305373	259564	158024	793964	638968	541464	631723	709422	752564	708834	619420	683159	806093
	T	.0777	.5396	.8541	.0758	.6658	.4242	.8918	.8317	.2875	.0901	.5498	.7524	.5864	.9272	.4048
	TGAGAAC															
	TGAATTC															
chi-miR-146a	CATAGGT	575.72	414.63	298.33	253.93	347.78	1424.3	1678.6	2107.3	423.58	673.39	539.08	334.05	394.07	307.71	733.02
	T	98802	09635	19097	22219	27314	60782	17112	32345	28911	87195	39737	91154	40387	62703	26642
	TCTCCCA															
chi-miR-150	ACCCTTGT	7238.4	7862.4	10018.	5326.9	3185.0	7577.2	4807.9	8794.0	8113.9	11637.	8922.7	9453.6	18551.	17071.	17578.
	ACCAGTG	8537	96601	70677	08529	51035	18261	06752	88905	65603	63514	11934	84232	50451	67787	87452

	TGTCAGTT															
chi-miR-223-3p	TGTCAAA	275.97	1420.6	475.36	671.10	1208.3	5258.2	247.73	7662.9	1151.9	2003.3	2901.4	451.07	2071.7	2537.1	3501.9
	TACCCCA	8237	80598	40319	65864	67551	25523	80903	58338	1014	85912	18059	41728	03518	25032	34616
	CCTATTCT															
chi-miR-26a-3p	CGGTTAC	7.2353	6.3789	4.0979	10.202	4.4360	4.7637	7.6620	4.5124	8.2363	0	4.1531	4.7183	0	0	4.2716
	TTGCACG	84491	379	65792	63391	04227	48435	02792	88962	33994		89319	49088			93847
	ACTGATTT															
	CTTTTGGT															
chi-miR-29a-5p	GTTCAGA	6.2017	6.3789	4.9175		11.533	30.487	0	26.322	14.119	0	47.346	12.267	9.3827	28.053	28.193
	GT	58135	379	5895	0	61099	98999		85228	4297		35824	70763	15207	90498	17939
	CTAGCAC															
	CATTTGA															
chi-miR-29b-3p	AATCAGT	27.907	15.491	31.964	5.6681	23.954	92.416	7.6620	72.199	18.825	62.296	45.685	57.563	35.654	35.944	69.201
	G	91161	70633	13318	29953	42282	71964	02792	82339	90627	79784	08251	85887	31779	06576	44033
	CTGGTTTC															
	ACATGGT															
chi-miR-29b-5p	GGCTTAG	185.01	143.98	154.08	113.36	123.32	297.25	201.76	285.79	223.55	316.42	299.86	433.14	283.35	252.48	228.10
	A	91177	17412	35138	25991	09175	79024	60735	09676	7637	81795	02689	44463	79992	51448	84515
	TGACCGA															
chi-miR-29c-5p	TTTCTCCT															
	GGTGTTC	231.53	232.38	188.51	190.45	147.28	476.37	257.95	311.36	382.40	376.75	430.27	523.74	365.93	431.33	434.86
	CACAATA															
chi-miR-323b	CACGGTC	1368.5	1368.7	1870.3	1953.2	1209.2	774.58	1236.1	1116.0	829.51	848.42	575.63	529.39	793.77	1118.6	788.55
	GGCCTCT	21295	37818	11587	37582	54752	54956	3645	88936	64951	30563	20397	87676	77065	49461	46842
	CTTATCA															
chi-miR-374b-3p	GGTTGTA	6.2017					5.7164	0	6.7687	5.8830	4.9441	0	0	0	0	0
	TTATCATT	58135	0	0	0	0	98122		33442	9571	90305					

	GTAGATT															
chi-miR-376a	CTCCTTCT	119.90	91.127	70.485	46.478	39.924	94.322	0	33.843	54.124	23.732	27.411	19.817	28.148	32.437	47.842
	ATGAGT	06573	68429	01162	66561	03804	21902		66721	48053	11346	04951	06617	14562	32763	97109
	ATGGTTG															
	ACCACAG															
chi-miR-380-5p	AACATGC	7.2353	8.2014	6.5567		5.3232	4.7637		10.529						4.3834	
	G	84491	91586	45267	0	05072	48435	0	14091	0	0	0	0	0	22653	0
	AATATAA															
chi-miR-410-3p	CACAGAT	2767.0	1924.6	2273.5	2535.9	1837.3	2004.5	1154.4	1331.9	1354.2	1165.8	928.65	870.06	1352.9	1084.4	1398.5
	GGCCTGT	17755	16692	51421	21341	92951	85342	08421	36325	88632	40074	31318	35718	87533	58764	52566
	CTTCACCT															
chi-miR-412-3p	GGTCCAC	20.672	19.136	54.093	31.741	26.616	12.385	6.3850	8.2728	0	22.743	0	0	15.012	21.040	8.5433
	TAGCT	52712	8137	14845	52773	02536	74593	02327	9643		2754			34433	42874	87695
	TCACTCCT															
chi-miR-483	CTCCTCCC	262.54	375.44	375.37	637.09	226.23	263.91	90.667	217.35	220.02	233.36	313.15	208.55	501.03	621.56	524.56
	GTCTTCT	10944	60593	36665	78067	62156	16633	03304	15516	77796	57824	04747	10297	69921	93322	40045
	TTGTACAT															
chi-miR-493-5p	GGTAGGC	4999.6	7253.7	6637.8	4949.4	4818.3	2541.9	3025.2	3008.3	3475.7	1959.8	2622.3	3930.3	3009.9	2527.4	2423.7
	TTTCATT	50683	6367	8499	11075	87791	36165	14102	25974	32946	77037	23736	8479	75038	81502	59089
	GAGTCGG															
chi-miR-496-5p	GTACTION		7.2902	14.752	5.6681	10.646	0	0	0	0	0	0	0	0	0	8.5433
	AATGGA	0	14743	67685	29953	41014										87695
	TCTTGTTA															
chi-miR-544-5p	AAAGGCA	36.176	6.3789	18.850	15.870	26.616	27.629	26.817	21.058	20.002	12.854	7.4757	6.6056	0	19.287	16.232
	GATTCT	92245	379	64264	76387	02536	74092	00977	28182	52541	89479	40775	88723		05967	43662
	TTGTGTCA															
chi-miR-592	ATATGCG	28.941	19.136	18.850		23.067	0	0	0	0	0	0	5.6620	0	7.0134	0
	ATGATGT	53796	8137	64264	0	22198							18905		76245	

chi-miR-656	AATATTA															
	TACAGTC	24.807	11.846	5.7371	12.469	15.082	18.102	0	6.7687	12.942	6.9218	8.3063	0	0	4.3834	6.8347
	AACCTCT	03254	59896	52109	8859	41437	24405		33442	81056	66427	78639			22653	10156
chi-miR-758	TTTGTGAC															
	CTGGTCC	981.94	677.07	954.82	919.37	981.24	759.34	759.81	588.87	598.89	439.04	387.07	453.90	463.50	412.91	469.88
	ACTAAC	5038	86943	60295	06783	41349	15006	52769	98095	91433	40991	72446	51822	61312	84139	63232
PC-3p-34697_129	TCACGGC															
	CTCTCTGC		9.1127			6.2104	11.432	17.878	12.033	0	12.854	18.274	5.6620	15.012	9.6435	8.5433
	CCCCAGT	0	68429	0	0	05917	99624	00651	3039		89479	03301	18905	34433	29837	87695
PC-3p-37101_116	GCGTCTC															
	ACTGAGC	28.941	25.515	60.649	34.008	33.713	23.818	0	9.0249	25.885	27.687	13.290	7.5493	16.888	14.903	22.212
	AGCATGT	53796	7516	89372	77972	63212	74218		77923	62112	46571	20582	5854	88737	63702	80801
PC-3p-37151_116	TGGTGCT															
	CCCTGGA															
	GCTGAGC	9.3026	15.491	9.8351	10.202	19.518	9.5274	6.3850	12.033	0	10.877	12.459	4.7183	0	0	6.8347
PC-3p-37745_113	A	37203	70633	17901	63391	4186	9687	02327	3039		21867	56796	49088			10156
PC-3p-37745_113	TGTACTCT						18.578	84.920	26.698	5.8830	28.181	6.2297	6.6056	13.135	4.3834	0
	GGGACTC						6189	53094	89302	9571	88474	83979	88723	80129	22653	
	GGGTGTC	13.953	19.592	6.5567	12.469	15.969										
PC-3p-43684_8	T	9558	45212	45267	8859	61522										
	AAAACCC															
	GCATGAA															
PC-3p-43684_8	CTTTTTTG	7.2353	6.3789	4.0979		0	10.480	19.155	6.0166	9.4129	6.9218	4.9838	0	0	7.0134	5.1260
	G	84491	379	65792	0		24656	00698	51949	53136	66427	27183			76245	32617

PC-5p- 18419_2	AGTTGAG GCTCCGA	17.571	48.297	22.129	19.271	29.277	40.968	103.43	61.670	54.124	41.531	14.120	22.648	15.012	35.944	0
85	GCTTTGGT	64805	67267	01528	64184	6279	23654	70377	68247	48053	19856	84369	07562	34433	06576	
PC-5p- 24127_2	CTATGGTT TTCTGAG	13.437	29.160	24.587	32.875	50.570	16.196	12.770	15.793	0	19.776	21.596	13.211	9.3827	29.807	23.921
09	GAT GAGGGTT	14263	85897	79475	15373	44818	74468	00465	71137		76122	58446	37745	15207	27404	48555
PC-5p- 3628_17	TGGGTTT GGTCGTG	200.52	68.345	116.38	97.491	86.945	235.32	287.32	459.52	108.24	285.77	115.45	66.056	91.950	255.11	229.81
84	GGA	3513	76322	22285	83519	68284	91727	51047	17926	89611	41996	86631	88723	60903	51984	7129
PC-5p- 43003_9	TGGTGGG ACCGAGT	5.1681	6.3789	7.3763	10.202	8.8720	5.7164	0	10.529	10.589	7.9107	0	0	0	6.1367	5.9803
1	CCTGGGT	31779	379	38425	63391	08453	98122		14091	57228	04488				91714	71386
PC-5p- 48419_7	CGCAGAG GCGGGAG															
2	GTATGAC CT	5.1681	9.1127	13.113	17.004	11.533	8.5747	28.094	3.7604	8.2363	6.9218	7.4757	0	0	7.0134	5.1260
		31779	68429	49053	38986	61099	47183	01024	07468	33994	66427	40775			76245	32617
PC-5p- 49834_6	AACCCGG TCCGCCTC			4.0979			0	6.3850	29.331	0	11.866	7.4757	4.7183	15.012	23.670	34.173
8	CCCCCG	0	0	65792	0	0		02327	17825		05673	40775	49088	34433	48233	55078
PC-5p- 53455_5	AAGAGGG TAACTAT															
9	ACAGTGA			2.8685			6.1928	0	5.2645	3.5298	2.9665	5.3991	0	0	2.1917	0
	A	0	0	76054	0	0	72966		70455	57426	14183	46115			11327	
PC-5p- 62000_4	AGCTGGA GACTACT															
2	GAAGTGA C	0	0	0	0	0	0	7.6620	13.537	12.942	6.9218	0	0	0	0	0
								02792	46688	81056	66427					

Table S6: The enriched KEGG pathway of differentially expressed miRNAs in goat colon from D10 to D31

Pathway Id	Pathway description	S gene number	TS gene number	B gene number	TB gene number	<i>P</i> -value of Fisher's Exact Test
ko04010	MAPK signaling pathway	1,254	18,333	1,719	29,837	3.44E-25
ko04931	Insulin resistance	470	18,333	605	29,837	5.46E-18
ko04910	Insulin signaling pathway	439	18,333	566	29,837	1.13E-16
ko04810	Regulation of actin cytoskeleton	1,074	18,333	1,511	29,837	5.51E-16
ko05166	HTLV-I infection	533	18,333	725	29,837	2.76E-12
ko04510	Focal adhesion	1,074	18,333	1,542	29,837	3.14E-12
ko04360	Axon guidance	516	18,333	702	29,837	6.46E-12
ko04390	Hippo signaling pathway	403	18,333	536	29,837	7.53E-12
ko05100	Bacterial invasion of epithelial cells	229	18,333	286	29,837	7.92E-12
ko05205	Proteoglycans in cancer	524	18,333	717	29,837	2.12E-11
ko04012	ErbB signaling pathway	669	18,333	934	29,837	2.18E-11
ko04514	Cell adhesion molecules	508	18,333	694	29,837	2.83E-11
ko04310	Wnt signaling pathway	505	18,333	690	29,837	3.36E-11
ko05200	Pathways in cancer	834	18,333	1,188	29,837	7.66E-11
ko05202	Transcriptional misregulation in cancers	613	18,333	855	29,837	1.16E-10
ko04071	Sphingolipid signaling pathway	273	18,333	356	29,837	5.59E-10
ko04068	FoxO signaling pathway	454	18,333	625	29,837	1.81E-09
ko00562	Inositol phosphate metabolism	202	18,333	258	29,837	4.77E-09
ko04320	Dorso-ventral axis formation	263	18,333	346	29,837	5.25E-09
ko04520	Adherens junction	445	18,333	615	29,837	6.04E-09
ko04666	Fc gamma R-mediated phagocytosis	238	18,333	311	29,837	9.65E-09
ko00310	Lysine degradation	228	18,333	297	29,837	1.21E-08
ko03420	Nucleotide excision repair	290	18,333	389	29,837	2.66E-08
ko04550	Signaling pathways regulating pluripotency of stem cells	424	18,333	590	29,837	5.29E-08
ko05217	Basal cell carcinoma	134	18,333	167	29,837	1.30E-07
ko04660	T cell receptor signaling pathway	218	18,333	290	29,837	4.66E-07
ko04070	Phosphatidylinositol signaling system	298	18,333	412	29,837	1.94E-06
ko04380	Osteoclast differentiation	267	18,333	366	29,837	2.11E-06

ko04933	AGE-RAGE signaling pathway in diabetic complications	277	18,333	382	29,837	3.13E-06
ko05213	Endometrial cancer	131	18,333	169	29,837	6.03E-06
ko04152	AMPK signaling pathway	265	18,333	366	29,837	6.14E-06
ko04062	Chemokine signaling pathway	324	18,333	455	29,837	7.03E-06
ko04144	Endocytosis	1,033	18,333	1,550	29,837	7.43E-06
ko05220	Chronic myeloid leukemia	167	18,333	222	29,837	9.11E-06
ko04664	Fc epsilon RI signaling pathway	149	18,333	196	29,837	1.01E-05
ko04022	cGMP - PKG signaling pathway	347	18,333	492	29,837	1.35E-05
ko04014	Ras signaling pathway	504	18,333	733	29,837	1.78E-05
ko04370	VEGF signaling pathway	185	18,333	250	29,837	1.79E-05
ko04072	Phospholipase D signaling pathway	307	18,333	433	29,837	2.12E-05
ko04150	mTOR signaling pathway	217	18,333	298	29,837	2.21E-05
ko04120	Ubiquitin mediated proteolysis	588	18,333	864	29,837	2.43E-05
ko04151	PI3K-Akt signaling pathway	618	18,333	911	29,837	2.72E-05
ko04611	Platelet activation	252	18,333	351	29,837	2.78E-05
ko05210	Colorectal cancer	156	18,333	209	29,837	3.65E-05
ko05215	Prostate cancer	209	18,333	289	29,837	6.30E-05
ko04214	Apoptosis - fly	64	18,333	78	29,837	6.98E-05
ko05206	MicroRNAs in cancer	419	18,333	610	29,837	1.00E-04
ko04020	Calcium signaling pathway	466	18,333	685	29,837	1.70E-04
ko04211	Longevity regulating pathway - mammal	191	18,333	265	29,837	1.73E-04
ko04723	Retrograde endocannabinoid signaling	203	18,333	284	29,837	2.38E-04
ko04015	Rap1 signaling pathway	492	18,333	727	29,837	2.40E-04
ko05218	Melanoma	152	18,333	208	29,837	2.67E-04
ko05032	Morphine addiction	166	18,333	229	29,837	2.81E-04
ko04916	Melanogenesis	254	18,333	362	29,837	3.04E-04
ko04662	B cell receptor signaling pathway	165	18,333	228	29,837	3.34E-04
ko04921	Oxytocin signaling pathway	336	18,333	488	29,837	3.55E-04
ko05222	Small cell lung cancer	189	18,333	265	29,837	4.61E-04
ko05014	Amyotrophic lateral sclerosis	107	18,333	143	29,837	4.94E-04
ko05212	Pancreatic cancer	134	18,333	183	29,837	5.20E-04
ko04728	Dopaminergic synapse	278	18,333	403	29,837	9.10E-04

ko00532	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	50	18,333	62	29,837	9.51E-04
ko00460	Cyanoamino acid metabolism	36	18,333	43	29,837	1.37E-03
ko05216	Thyroid cancer	101	18,333	137	29,837	1.66E-03
ko00230	Purine metabolism	359	18,333	531	29,837	1.70E-03
ko04110	Cell cycle	395	18,333	588	29,837	2.07E-03
ko04710	Circadian rhythm	80	18,333	107	29,837	2.51E-03
ko05120	Epithelial cell signaling in Helicobacter pylori infection	16	18,333	17	29,837	2.95E-03
ko05231	Choline metabolism in cancer	210	18,333	304	29,837	3.23E-03
ko00603	Glycosphingolipid biosynthesis - globo series	43	18,333	54	29,837	3.42E-03
ko04350	TGF-beta signaling pathway	263	18,333	386	29,837	3.53E-03
ko05211	Renal cell carcinoma	123	18,333	172	29,837	3.60E-03
ko05219	Bladder cancer	79	18,333	107	29,837	4.75E-03
ko05223	Non-small cell lung cancer	127	18,333	179	29,837	4.88E-03
ko05230	Central carbon metabolism in cancer	146	18,333	208	29,837	5.14E-03
ko00232	Caffeine metabolism	34	18,333	42	29,837	5.58E-03
ko04261	Adrenergic signaling in cardiomyocytes	407	18,333	613	29,837	5.85E-03
ko05221	Acute myeloid leukemia	143	18,333	204	29,837	6.02E-03
ko04914	Progesterone-mediated oocyte maturation	227	18,333	333	29,837	6.13E-03
ko00920	Sulfur metabolism	36	18,333	45	29,837	6.31E-03
ko04919	Thyroid hormone signaling pathway	243	18,333	358	29,837	6.47E-03
ko00750	Vitamin B6 metabolism	14	18,333	15	29,837	6.98E-03
ko05412	Arrhythmogenic right ventricular cardiomyopathy	227	18,333	334	29,837	7.56E-03
ko04960	Aldosterone-regulated sodium reabsorption	101	18,333	142	29,837	1.00E-02
ko04064	NF-kappa B signaling pathway	191	18,333	280	29,837	1.07E-02
ko05214	Glioma	146	18,333	211	29,837	1.14E-02
ko00730	Thiamine metabolism	9	18,333	9	29,837	1.25E-02
ko03018	RNA degradation	262	18,333	391	29,837	1.25E-02
ko00430	Taurine and hypotaurine metabolism	21	18,333	25	29,837	1.37E-02
ko00062	Fatty acid elongation	53	18,333	72	29,837	2.07E-02
ko05132	Salmonella infection	210	18,333	313	29,837	2.16E-02
ko04725	Cholinergic synapse	206	18,333	307	29,837	2.26E-02
ko04530	Tight junction	648	18,333	1,005	29,837	2.36E-02

ko00270	Cysteine and methionine metabolism	99	18,333	142	29,837	2.46E-02
ko00534	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	52	18,333	71	29,837	2.52E-02
ko04912	GnRH signaling pathway	234	18,333	352	29,837	2.81E-02
ko00670	One carbon pool by folate	39	18,333	52	29,837	2.84E-02
ko05142	Chagas disease	185	18,333	276	29,837	3.10E-02
ko04727	GABAergic synapse	169	18,333	252	29,837	3.69E-02
ko04721	Synaptic vesicle cycle	142	18,333	210	29,837	3.69E-02
ko04668	TNF signaling pathway	211	18,333	318	29,837	3.92E-02
ko04141	Protein processing in endoplasmic reticulum	416	18,333	642	29,837	4.18E-02
ko04130	SNARE interactions in vesicular transport	51	18,333	71	29,837	4.46E-02
ko05033	Nicotine addiction	74	18,333	106	29,837	4.55E-02

Table S7: The enriched KEGG pathway of highly expressed miRNAs in goat colon from D10 to D31

Pathway	S gene	TS gene	B gene	TB gene	<i>P</i> -value of Fisher's Exact	
Id	Pathway description	number	number	number	Test	
ko04310	Wnt signaling pathway	609	21,529	690	29,837	3.12E-25
ko04514	Cell adhesion molecules	606	21,529	694	29,837	2.03E-22
ko04010	MAPK signaling pathway	1,392	21,529	1,719	29,837	1.91E-18
ko04520	Adherens junction	531	21,529	615	29,837	1.61E-17
ko04530	Tight junction	824	21,529	1,005	29,837	1.07E-13
ko04360	Axon guidance	582	21,529	702	29,837	1.09E-11
ko04931	Insulin resistance	506	21,529	605	29,837	1.48E-11
ko05200	Pathways in cancer	955	21,529	1,188	29,837	1.52E-11
ko05166	HTLV-I infection	599	21,529	725	29,837	1.87E-11
ko04320	Dorso-ventral axis formation	301	21,529	346	29,837	2.21E-11
ko04390	Hippo signaling pathway	449	21,529	536	29,837	1.29E-10
ko04070	Phosphatidylinositol signaling system	350	21,529	412	29,837	4.47E-10
ko04510	Focal adhesion	1,215	21,529	1,542	29,837	5.43E-10
ko05212	Pancreatic cancer	165	21,529	183	29,837	1.83E-09
ko04120	Ubiquitin mediated proteolysis	695	21,529	864	29,837	7.51E-09
ko04910	Insulin signaling pathway	466	21,529	566	29,837	8.24E-09
ko04810	Regulation of actin cytoskeleton	1,184	21,529	1,511	29,837	9.42E-09
ko05205	Proteoglycans in cancer	582	21,529	717	29,837	9.83E-09
ko03420	Nucleotide excision repair	327	21,529	389	29,837	1.91E-08
ko00562	Inositol phosphate metabolism	223	21,529	258	29,837	2.97E-08
ko04014	Ras signaling pathway	592	21,529	733	29,837	3.16E-08
ko04068	FoxO signaling pathway	509	21,529	625	29,837	3.48E-08
ko04660	T cell receptor signaling pathway	248	21,529	290	29,837	4.31E-08
ko05215	Prostate cancer	247	21,529	289	29,837	5.13E-08
ko05220	Chronic myeloid leukemia	193	21,529	222	29,837	9.49E-08
ko04720	Long-term potentiation	200	21,529	231	29,837	1.14E-07
ko05211	Renal cell carcinoma	152	21,529	172	29,837	2.10E-07
ko04921	Oxytocin signaling pathway	400	21,529	488	29,837	2.49E-07
ko04012	ErbB signaling pathway	739	21,529	934	29,837	4.32E-07
ko05206	MicroRNAs in cancer	492	21,529	610	29,837	6.15E-07
ko04114	Oocyte meiosis	355	21,529	434	29,837	1.73E-06

ko04916	Melanogenesis	299	21,529	362	29,837	2.13E-06
ko04330	Notch signaling pathway	248	21,529	297	29,837	2.88E-06
ko04350	TGF-beta signaling pathway	317	21,529	386	29,837	3.02E-06
ko00601	Glycosphingolipid biosynthesis - lacto and neolacto series	87	21,529	96	29,837	7.96E-06
ko04728	Dopaminergic synapse	327	21,529	403	29,837	1.71E-05
ko05214	Glioma	177	21,529	211	29,837	4.27E-05
ko00533	Glycosaminoglycan biosynthesis - keratan sulfate	50	21,529	53	29,837	4.79E-05
ko04550	Signaling pathways regulating pluripotency of stem cells	467	21,529	590	29,837	5.10E-05
ko04662	B cell receptor signaling pathway	190	21,529	228	29,837	5.15E-05
ko05217	Basal cell carcinoma	142	21,529	167	29,837	6.04E-05
ko04110	Cell cycle	465	21,529	588	29,837	6.21E-05
ko04919	Thyroid hormone signaling pathway	290	21,529	358	29,837	6.37E-05
ko04072	Phospholipase D signaling pathway	347	21,529	433	29,837	7.38E-05
ko04933	AGE-RAGE signaling pathway in diabetic complications	308	21,529	382	29,837	7.69E-05
ko05219	Bladder cancer	94	21,529	107	29,837	7.71E-05
ko04727	GABAergic synapse	208	21,529	252	29,837	7.84E-05
ko04724	Glutamatergic synapse	257	21,529	316	29,837	9.65E-05
ko04713	Circadian entrainment	249	21,529	306	29,837	1.15E-04
ko04723	Retrograde endocannabinoid signaling	232	21,529	284	29,837	1.20E-04
ko00062	Fatty acid elongation	65	21,529	72	29,837	1.56E-04
ko04144	Endocytosis	1,180	21,529	1,550	29,837	1.56E-04
ko00232	Caffeine metabolism	40	21,529	42	29,837	1.61E-04
ko04925	Aldosterone synthesis and secretion	226	21,529	277	29,837	1.70E-04
ko04380	Osteoclast differentiation	294	21,529	366	29,837	1.84E-04
ko00310	Lysine degradation	241	21,529	297	29,837	2.07E-04
ko04015	Rap1 signaling pathway	566	21,529	727	29,837	2.32E-04
ko05412	Arrhythmogenic right ventricular cardiomyopathy	269	21,529	334	29,837	2.44E-04
ko04668	TNF signaling pathway	256	21,529	318	29,837	3.59E-04
ko00920	Sulfur metabolism	42	21,529	45	29,837	4.08E-04
ko05210	Colorectal cancer	172	21,529	209	29,837	4.24E-04
ko05031	Amphetamine addiction	182	21,529	222	29,837	4.34E-04
ko04725	Cholinergic synapse	247	21,529	307	29,837	4.83E-04
ko05218	Melanoma	171	21,529	208	29,837	4.87E-04
ko05230	Central carbon metabolism in cancer	171	21,529	208	29,837	4.87E-04

ko04022	cGMP - PKG signaling pathway	386	21,529	492	29,837	7.78E-04
ko00770	Pantothenate and CoA biosynthesis	49	21,529	54	29,837	7.87E-04
ko05161	Hepatitis B	287	21,529	361	29,837	7.93E-04
ko05221	Acute myeloid leukemia	167	21,529	204	29,837	8.41E-04
ko04141	Protein processing in endoplasmic reticulum	498	21,529	642	29,837	9.40E-04
ko04664	Fc epsilon RI signaling pathway	160	21,529	196	29,837	1.37E-03
ko00532	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate	55	21,529	62	29,837	1.46E-03
ko05130	Pathogenic Escherichia coli infection	37	21,529	40	29,837	1.49E-03
ko04146	Peroxisome	227	21,529	284	29,837	1.57E-03
ko00270	Cysteine and methionine metabolism	118	21,529	142	29,837	1.61E-03
ko04922	Glucagon signaling pathway	288	21,529	365	29,837	1.84E-03
ko05202	Transcriptional misregulation in cancers	654	21,529	855	29,837	2.03E-03
ko05223	Non-small cell lung cancer	146	21,529	179	29,837	2.32E-03
ko00460	Cyanoamino acid metabolism	39	21,529	43	29,837	2.88E-03
ko04214	Apoptosis - fly	67	21,529	78	29,837	3.16E-03
ko04211	Longevity regulating pathway - mammal	211	21,529	265	29,837	3.20E-03
ko05120	Epithelial cell signaling in Helicobacter pylori infection	17	21,529	17	29,837	3.89E-03
ko00514	Other types of O-glycan biosynthesis	91	21,529	109	29,837	4.05E-03
ko04020	Calcium signaling pathway	525	21,529	685	29,837	4.07E-03
ko00564	Glycerophospholipid metabolism	261	21,529	332	29,837	4.18E-03
ko04071	Sphingolipid signaling pathway	279	21,529	356	29,837	4.30E-03
ko04611	Platelet activation	275	21,529	351	29,837	4.69E-03
ko04512	ECM-receptor interaction	344	21,529	443	29,837	4.74E-03
ko05213	Endometrial cancer	137	21,529	169	29,837	4.85E-03
ko05014	Amyotrophic lateral sclerosis	117	21,529	143	29,837	4.95E-03
ko05169	Epstein-Barr virus infection	423	21,529	549	29,837	5.01E-03
ko05160	Hepatitis C	250	21,529	319	29,837	6.61E-03
ko04540	Gap junction	224	21,529	285	29,837	7.71E-03
ko04914	Progesterone-mediated oocyte maturation	260	21,529	333	29,837	7.98E-03
ko05231	Choline metabolism in cancer	238	21,529	304	29,837	8.62E-03
ko04912	GnRH signaling pathway	274	21,529	352	29,837	8.71E-03
ko01040	Biosynthesis of unsaturated fatty acids	61	21,529	72	29,837	9.25E-03
ko05145	Toxoplasmosis	231	21,529	295	29,837	9.40E-03

ko05032	Morphine addiction	181	21,529	229	29,837	1.04E-02
ko04024	cAMP signaling pathway	476	21,529	624	29,837	1.05E-02
ko00534	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	60	21,529	71	29,837	1.10E-02
ko04130	SNARE interactions in vesicular transport	60	21,529	71	29,837	1.10E-02
ko00100	Steroid biosynthesis	66	21,529	79	29,837	1.32E-02
ko03013	RNA transport	552	21,529	728	29,837	1.33E-02
ko00512	Mucin type O-glycan biosynthesis	68	21,529	82	29,837	1.66E-02
ko05020	Prion diseases	71	21,529	86	29,837	1.76E-02
ko00410	beta-Alanine metabolism	67	21,529	81	29,837	1.93E-02
ko04710	Circadian rhythm	87	21,529	107	29,837	1.94E-02
ko04115	p53 signaling pathway	227	21,529	293	29,837	2.24E-02
ko04911	Insulin secretion	246	21,529	319	29,837	2.55E-02
ko00510	N-Glycan biosynthesis	126	21,529	159	29,837	2.55E-02
ko04340	Hedgehog signaling pathway	177	21,529	227	29,837	2.74E-02
ko04062	Chemokine signaling pathway	346	21,529	455	29,837	3.36E-02
ko03015	mRNA surveillance pathway	347	21,529	457	29,837	3.76E-02
ko04013	MAPK signaling pathway - fly	10	21,529	10	29,837	3.82E-02
ko05203	Viral carcinogenesis	481	21,529	639	29,837	4.03E-02
ko04730	Long-term depression	145	21,529	186	29,837	4.33E-02
ko00120	Primary bile acid biosynthesis	41	21,529	49	29,837	4.53E-02
ko04971	Gastric acid secretion	174	21,529	225	29,837	4.59E-02
ko04215	Apoptosis - multiple species	105	21,529	133	29,837	4.62E-02
ko00450	Selenocompound metabolism	54	21,529	66	29,837	4.88E-02
