

Supplementary Material

1 Supplementary Figures and Tables

1.1 Supplementary Tables

Supplementary Table 1. Differentially expressed miRNA qRT-PCR verified miRNA and primer sequences

Primer Name	Sequence(5'-3')
rno-miR-19a-3p Forward	GCGTGTGCAAATCTATGCAA
rno-miR-19a-3p Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-21-3p Forward	CGCAACAGCAGTCGATGG
rno-miR-21-3p Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-122-5p Forward	CGCGTGGAGTGTGACAATGG
rno-miR-122-5p Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-142-3p Forward	GCGCGTGTAGTGTTTCCTACTT
rno-miR-142-3p Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-184 Forward	CGCGTGGACGGAGAACTGAT
rno-miR-184 Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-200a-5p Forward	CGCGCATCTTACCGGACAG
rno-miR-200a-5p Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-378b Forward	CGCGAGTGGACTTGGAGTC
rno-miR-378b Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-451-5p Forward	CGCGAAACCGTTACCATTAC
rno-miR-451-5p Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-484 Forward	GCGTCAGGCTCAGTCCCCT
rno-miR-484 Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-1247-3p Forward	CGCGGGAACGTCGAGAC
rno-miR-1247-3p Reverse	AGTGCAGGGTCCGAGGTATT
rno-miR-3548 Forward	CGCAGCACTGTCCGGTAA

mo-miR-3548 Reverse	AGTGCAGGGTCCGAGGTATT
U6 Forward	AGAGAAGATTAGCATGGCCCCTG
U6 Reverse	AGTGCAGGGTCCGAGGTATT

Supplementary Table 2. Lipid-related biochemical indicators in rats' blood and liver samples (Mean \pm SD, n=7).

Group	Serum TC	Serum TG	Serum HDL-C	Serum LDL-C	Liver TC	Liver TG
CON	1.43 \pm 0.12	0.60 \pm 0.11***	1.54 \pm 0.20***	0.50 \pm 0.05	0.77 \pm 0.19**	1.46 \pm 0.12***
MOD	1.55 \pm 0.22	0.89 \pm 0.21	1.30 \pm 0.08	0.55 \pm 0.07	1.17 \pm 0.22	2.83 \pm 0.71
PSF.L	1.43 \pm 0.04	0.96 \pm 0.18	1.40 \pm 0.06	0.45 \pm 0.05*	0.94 \pm 0.17*	2.48 \pm 0.19
PSF.M	1.53 \pm 0.21	1.07 \pm 0.21*	1.56 \pm 0.17***	0.45 \pm 0.13*	0.89 \pm 0.14**	2.55 \pm 0.21
PSF.H	1.50 \pm 0.08	0.84 \pm 0.14	1.54 \pm 0.19***	0.44 \pm 0.05**	1.22 \pm 0.20	2.81 \pm 0.39
PS.L	1.42 \pm 0.18	0.62 \pm 0.21**	1.45 \pm 0.10*	0.48 \pm 0.08	0.94 \pm 0.17*	2.45 \pm 0.49
PS.M	1.44 \pm 0.09	0.67 \pm 0.10*	1.45 \pm 0.11*	0.49 \pm 0.05	0.78 \pm 0.15**	1.97 \pm 0.08***
PS.H	1.50 \pm 0.08	0.69 \pm 0.15*	1.47 \pm 0.08*	0.51 \pm 0.05	0.99 \pm 0.07	2.33 \pm 0.27*
PWE.L	1.46 \pm 0.22	0.87 \pm 0.16	1.53 \pm 0.21**	0.42 \pm 0.09*	1.48 \pm 0.30**	2.88 \pm 0.47
PWE.M	1.45 \pm 0.23	0.78 \pm 0.14	1.53 \pm 0.22**	0.48 \pm 0.08	1.04 \pm 0.20	2.28 \pm 0.30**
PWE.H	1.51 \pm 0.13	0.76 \pm 0.16	1.50 \pm 0.12*	0.49 \pm 0.11	0.95 \pm 0.15*	1.20 \pm 0.28***
SIM	1.55 \pm 0.12	0.76 \pm 0.13	1.60 \pm 0.12***	0.53 \pm 0.05	0.94 \pm 0.15*	1.37 \pm 0.43***

* indicates a significant difference compared to the model group, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Supplementary Table 3. Data output quality status list

Sample	Reads	Bases	Error rate	Q20	Q30	GC content
A4	12421004	0.621G	0.01%	97.75%	95.24%	49.12%
A5	12747475	0.637G	0.01%	97.95%	95.47%	49.46%
A7	13296982	0.665G	0.01%	97.74%	95.18%	50.27%
B2	12360128	0.618G	0.01%	98.01%	95.64%	49.51%
B3	13058584	0.653G	0.01%	97.66%	95.03%	50.42%
B8	15247335	0.762G	0.01%	97.52%	94.47%	48.75%
C3	14352960	0.718G	0.01%	98.08%	95.81%	48.70%
C7	12720262	0.636G	0.01%	98.13%	95.84%	49.31%
C10	13779509	0.689G	0.01%	98.08%	95.85%	48.54%
D1	12027228	0.601G	0.01%	97.31%	94.17%	48.66%
D2	13012192	0.651G	0.01%	97.70%	95.14%	48.90%
D3	16546825	0.827G	0.01%	97.76%	94.93%	48.72%
E1	11086312	0.554G	0.01%	97.64%	94.93%	48.17%
E6	11829462	0.591G	0.01%	97.31%	94.19%	48.70%
E9	12183363	0.609G	0.01%	97.41%	94.36%	48.77%
F5	11739384	0.587G	0.01%	97.24%	94.04%	48.93%
F7	14832062	0.742G	0.01%	97.62%	94.94%	49.46%
F10	12638910	0.632G	0.01%	97.72%	95.18%	48.79%
G1	12676623	0.634G	0.01%	97.23%	94.02%	49.33%
G2	12916298	0.646G	0.01%	97.26%	94.10%	49.16%
G8	11043558	0.552G	0.01%	97.49%	94.60%	49.45%
H1	13622367	0.681G	0.01%	97.75%	95.23%	48.80%
H4	14490965	0.725G	0.01%	97.85%	95.28%	49.47%
H9	13594326	0.680G	0.01%	97.61%	94.66%	48.71%
I2	13228996	0.661G	0.01%	97.69%	95.12%	49.04%
I4	15247587	0.762G	0.01%	98.41%	96.55%	48.71%
I7	14030572	0.702G	0.01%	98.46%	96.65%	48.88%

J2	13766445	0.688G	0.01%	98.04%	95.66%	49.77%
J6	13506671	0.675G	0.01%	97.71%	95.16%	49.78%
J7	15373809	0.769G	0.01%	98.31%	96.34%	49.22%
K1	14135749	0.707G	0.01%	98.13%	95.91%	48.91%
K5	11535959	0.577G	0.01%	98.33%	96.40%	49.01%
K6	13257891	0.663G	0.01%	98.08%	95.69%	51.80%
L1	15645729	0.782G	0.01%	97.68%	95.09%	49.21%
L9	12913291	0.646G	0.01%	98.06%	95.74%	49.24%
L10	13345779	0.667G	0.01%	98.08%	95.80%	49.77%

Note:

- (1) Sample: samples id.
- (2) Reads: The original sequence data is counted, and the number of sequencing sequences of each sequencing file is counted in one unit of four behaviors.
- (3) Bases: The number of sequencing sequences is multiplied by the length of the sequencing sequence and converted to G.
- (4) Error rate: Refers to the sequencing error rate, calculated by the formula 1.
- (5) Q20: The base of the Phred value greater than 20 is a percentage of the total base.
- (6) Q30: Bases with a Phred value greater than 30 as a percentage of the total base.
- (7) GC content: Calculate the sum of the number of bases G and C as a percentage of the total number of bases

Supplementary Table 4. Data filtering situation list.

Sample	Total reads	N%>10%	Low quality	5 adapter contaminate	3 adapter null or insert null	With plopA/T/G/C	Clean reads
A4	12421004 (100.00%)	6 (0.00%)	47077 (0.38%)	1724 (0.01%)	582532 (4.69%)	15281 (0.12%)	11774384 (94.79%)
A5	12747475 (100.00%)	1575 (0.01%)	25834 (0.20%)	1065(0.01%)	530824 (4.16%)	39828 (0.31%)	12148349 (95.30%)
A7	13296982 (100.00%)	7(0.00%)	48455 (0.36%)	1441 (0.01%)	785760 (5.91%)	17485 (0.13%)	12443834 (93.58%)
B2	12360128 (100.00%)	1494 (0.01%)	23924 (0.19%)	1003(0.01%)	458162 (3.71%)	24201 (0.20%)	11851344 (95.88%)
B3	13058584 (100.00%)	4 (0.00%)	57440 (0.44%)	2761(0.02%)	464905 (3.65%)	11015 (0.08%)	12522459 (95.89%)
B8	15247335 (100.00%)	4691 (0.03%)	33136 (0.22%)	423(0.00%)	453725 (2.98%)	11945 (0.08%)	14743415 (96.70%)
C3	14353960 (100.00%)	1773 (0.01%)	30813 (0.21%)	531 (0.00%)	457958 (3.19%)	13483 (0.09%)	13848402 (96.48%)
C7	12720262 (100.00%)	1600 (0.01%)	23718 (0.19%)	614 (0.00%)	409989 (3.22%)	19290 (0.15%)	12265051 (96.42%)
C10	13779509 (100.00%)	1703 (0.01%)	26979 (0.20%)	343 (0.00%)	569349 (4.13%)	7775 (0.06%)	13173360 (95.60%)
D1	12027228 (100.00%)	416 (0.00%)	104372 (0.87%)	282 (0.00%)	297642 (2.47%)	6408 (0.05%)	11618108 (96.60%)
D2	13012192 (100.00%)	6 (0.00%)	56766 (0.44%)	534 (0.00%)	358024 (2.75%)	8400 (0.06%)	12588462(96.74%)

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D3	16546825 (100.00%)	3097 (0.02%)	15042 (0.09%)	361 (0.00%)	560212 (3.39%)	10505 (0.06%)	15957608 (96.44%)
E1	11086312 (100.00%)	405 (0.00%)	66357 (0.60%)	111 (0.00%)	271624 (2.45%)	2624 (0.02%)	10745191 (96.44%)
E6	11829462 (100.00%)	442 (0.00%)	110822 (0.94%)	303 (0.00%)	378150 (3.20%)	9273(0.08%)	11330472 (95.78%)
E9	12183363 (100.00%)	445 (0.00%)	110251 (0.90%)	412 (0.00%)	387636 (3.18%)	6468 (0.05%)	11678151 (95.85%)
F5	11739384 (100.00%)	442 (0.00%)	97003 (0.83%)	408 (0.00%)	404921 (3.45%)	11861 (0.10%)	11224749 (95.62%)
F7	14832062 (100.00%)	357 (0.00%)	45345 (0.31%)	2872(0.02%)	581680 (3.92%)	12418 (0.08%)	14189390 (95.67%)
F10	12638910 (100.00%)	320 (0.00%)	37795 (0.30%)	603 (0.00%)	392886 (3.11%)	20671 (0.16%)	12186635 (96.42%)
G1	12676623 (100.00%)	479 (0.00%)	108109 (0.85%)	678 (0.01%)	602912 (4.76%)	16634 (0.13%)	11947811 (94.25%)
G2	12916298 (100.00%)	485 (0.00%)	111623 (0.86%)	749 (0.01%)	467450 (3.62%)	18579 (0.14%)	12317412 (95.36%)
G8	11043558 (100.00%)	411 (0.00%)	65508 (0.59%)	370 (0.00%)	394403 (3.57%)	7898(0.07%)	10574968 (95.76%)
H1	13622367 (100.00%)	10 (0.00%)	57329 (0.42%)	630 (0.00%)	478369 (3.51%)	10069 (0.07%)	13075960 (95.99%)
H4	14490965 (100.00%)	1787 (0.01%)	30435 (0.21%)	1135 (0.01%)	496149 (3.42%)	19645(0.14%)	13941814 (96.21%)
H9	13594326 (100.00%)	1697 (0.01%)	28910 (0.21%)	734 (0.01%)	427041 (3.73%)	10452(0.08%)	13125492 (96.55%)
I2	13228996 (100.00%)	14 (0.00%)	53939 (0.41%)	719 (0.01%)	493499 (3.73%)	17861 (0.14%)	12662964 (95.72%)

I4	15247587 (100.00%)	2361 (0.02%)	44480 (0.29%)	698 (0.00%)	385331 (2.53%)	12993 (0.09%)	14801724 (97.08%)
I7	14030572 (100.00%)	2109 (0.02%)	33465 (0.24%)	783 (0.01%)	436204 (3.11%)	10082 (0.07%)	13547929 (96.56%)
J2	13766445 (100.00%)	1667 (0.01%)	26873 (0.20%)	1101 (0.01%)	493111 (3.58%)	12036 (0.09%)	13231657(96.12%)
J6	13506671 (100.00%)	8(0.00%)	64474 (0.48%)	2141(0.02%)	513341 (3.80%)	13724 (0.10%)	12912983 (95.60%)
J7	15373809 (100.00%)	2334 (0.02%)	40429 (0.26%)	962 (0.01%)	576533 (3.75%)	10229 (0.07%)	14743322 (95.90%)
K1	14135749 (100.00%)	1704 (0.01%)	26427 (0.19%)	634 (0.00%)	493985 (3,49%)	11003 (0.08%)	13601996 (96.22%)
K5	11535959 (100.00%)	1701 (0.01%)	31139 (0.27%)	680 (0.01%)	407006 (3.53%)	8764 (0.08%)	11086669 (96.11%)
K6	13257891 (100.00%)	1621 (0.01%)	21821 (0.16%)	1167 (0.01%)	412921 (3.11%)	46797 (0.35%)	12773564 (96.35%)
L1	15645729 (100.00%)	10(0.00%)	51957 (0.33%)	2529(0.02%)	664894 (4.25%)	27934 (0.18%)	14898405 (95.22%)
L9	12913291 (100.00%)	1601 (0.01%)	24133 (0.19%)	905(0.01%)	42661 (3.30%)	17996 (0.14%)	12442040 (96.35%)
L10	13345779 (100.00%)	1602 (0.01%)	26494 (0.20%)	1158(0.01%)	489044 (3,66%)	21224 (0.16%)	12806257 (95.96%)

Note:

- (1) Sample: sample id.
- (2) total_reads: Count the number of original sequence data.
- (3) N% > 10%: The ratio of the number of reads filtered out and the total number of raw reads due to the N content exceeding 10%.
- (4) low quality: Due to low quality, the number of copies that are filtered out and their proportion to the total number of raw reads.
- (5) 5_adapter_contamine: The number of reads that are filtered out and their proportion to the total number of raw reads due to the 5' joint.

(6) 3_adapter_null or insert_null: The number of reads that are filtered out and their proportion to the total number of raw reads, since there are no 3' connectors or no inserts.

(7) with polyA/T/G/C: The number of reads filtered and their proportion to the total number of raw reads due to the inclusion of polyA/T/G/C.

(8) clean reads: The resulting number of clean reads and their proportion to the total number of raw read

Supplementary Table 5. Alignment with reference genome.

Sample	Total sRNA	Mapped sRNA	“+” Mapped sRNA	“ - ” Mapped sRNA
A4	9957773 (100.00%)	9171075 (92.10%)	5827771 (58.52%)	3343304 (33.57%)
A5	9929824 (100.00%)	8989999 (90.54%)	5093774 (51.30%)	3896225 (39.24%)
A7	9062665 (100.00%)	8386298 (92.54%)	5508280 (60.28%)	2878018 (31.76%)
B2	9877613 (100.00%)	9058975 (91.71%)	4969564 (50.31%)	4098411 (41.40%)
B3	10903089 (100.00%)	10199924 (93.55%)	7411371 (67.97%)	2788553 (25.58%)
B8	14215131 (100.00%)	13073698 (91.97%)	7264916 (51.11%)	5808782 (40.86%)
C7	11789813 (100.00%)	10265833 (87.07%)	5450452 (46.23%)	4815381 (40.84%)
C10	12544891 (100.00%)	11648895 (92.86%)	6067417 (48.37%)	5581478 (44.49%)
D1	10995598 (100.00%)	10092981 (91.79%)	5821993 (52.95%)	4270988 (38.84%)
D2	11785873 (100.00%)	10980277 (93.16%)	6115128 (51.89%)	4865149 (41.28%)
D3	15162458(100.00%)	13899690 (91.67%)	8161808 (53.83%)	5737882 (37.84%)
E1	10531734(100.00%)	9807608 (93.12%)	3263862 (30.99%)	6543746 (62.13%)
E6	10656185 (100.00%)	9661029 (90.66%)	5337571 (50.09%)	4323458 (40.57%)
E9	10999441 (100.00%)	10171968 (92.48%)	5244069 (47.68%)	4927899 (44.80%)
F5	10285683 (100.00%)	9236454 (90.06%)	5058089 (49.18%)	4205405 (40.89%)
F7	12806146 (100.00%)	11498360 (89.79%)	7307487 (57.06%)	4190873 (32.73%)
F10	11705711 (100.00%)	10878172 (92.93%)	6097979 (52.09%)	4780193 (40.84%)

G1	10488619 (100.00%)	9543915 (90.99%)	5345553 (50.97%)	4632411 (40.88%)
G2	1133087 (100.00%)	10179499 (89.84%)	5547088 (48.96%)	4198362 (40.03%)
G8	10193191 (100.00%)	9000777 (88.30%)	4356897 (42.74%)	4643880 (45.56%)
H1	12344375 (100.00%)	11407697 (92.41%)	5830137 (47.23%)	5577560 (45.18%)
H4	12887729 (100.00%)	11935831 (92.61%)	7129792 (55.32%)	4806039 (37.29%)
H9	12466355 (100.00%)	11588383 (92.96%)	6222783 (49.92%)	5365600 (43.04%)
I2	11859522 (100.00%)	10609054 (89.46%)	5279823 (44.52%)	5329231 (44.94%)
I4	13863420 (100.00%)	12804597 (92.36%)	7061094 (50.93%)	5743503 (41.43%)
I7	12803089 (100.00%)	11548265 (90.20%)	5818854 (45.45%)	5729411 (44.75%)
J2	11703399 (100.00%)	10803163 (92.31%)	6412740 (54.79%)	4390423 (37.51%)
J6	11334709(100.00%)	10483748 (92.49%)	6734790 (59.42%)	3748959 (33.08%)
J7	13656246 (100.00%)	12661944 (92.72%)	6656399 (48.74%)	6005545 (43.98%)
K1	12633606 (100.00%)	11742813 (92.95%)	5912644 (46.80%)	5830169 (46.15%)
K5	10496375(100.00%)	9610236 (91.56%)	5089336 (48.49%)	4520900 (43.07%)
K6	12052339 (100.00%)	10509833 (87.20%)	7829142 (64.96%)	2680691 (22.24%)
L1	12682274 (100.00%)	11549158 (91.07%)	7145029 (56.34%)	4041129 (34.73%)
L9	11170677 (100.00%)	10360595(92.75%)	5237357 (46.88%)	5123238 (45.86%)
L10	11873978 (100.00%)	10925397 (92.01%)	6402049 (53.92%)	4523348 (38.09%)

Note: (1) Sample: sample id.

(2) Total sRNA: The total number of reads obtained for each sample after analysis of "sRNA length screening".

(3) Mapped sRNA: The number of reads and percentages that can be mapped to the reference sequence in the sample reads.

(4) “+” Mapped sRNA: The number of reads and the percentage of the same chain that can be mapped to the reference sequence in the sample reads.

(5) “-” Mapped sRNA: The sample reads mapped to the number of reads in the opposite direction of the reference sequence and the percentage

Supplementary Table 6. sRNA classification statistics table

Types	total	Known-miRNA	rRN A	tRNA	snRN A	snoRN A	repeat	Novel-miRNA	Exon:+	Exon:-	Intron:+	Intron :-	other
A4	9171075	4204528	3426 7	20391 9	10172	61383	201227	656	249226	31834	182887	68993	3921983
A4	100.00%	45.85%	0.37 %	2.22%	0.11%	0.67%	2.19%	0.01%	2.72%	0.35%	1.99%	0.75%	42.76%
A5	8989999	2778375	4454 8	29834 4	24059	79704	436643	407	1092458	51478	361607	61667	3760709
A5	100.00%	30.91%	0.50 %	3.32%	0.27%	0.89%	4.86%	0.00%	12.15%	0.57%	4.02%	0.69%	41.83%
A7	8386298	3903214	3810 2	15859 5	8552	57769	258959	767	320828	36934	199888	71437	3331253
A7 (percent)	100.00%	46.54%	0.45 %	1.89%	0.10%	0.69%	3.09%	0.01%	3.83%	0.44%	2.38%	0.85%	39.72%
B2	9058975	3546089	5041 6	12855 4	14240	72761	417005	653	826165	65150	296003	99042	3542897
B2	100.00%	39.14%	0.56 %	1.42%	0.16%	0.80%	4.60%	0.01%	9.12%	0.72%	3.27%	1.09%	39.11%
B3	1019992 4	3968744	1042 73	13909	10859	87033	295361	937	220353	100324	501140	228401	4668590
B3 (percent)	100.00%	38.91%	1.02 %	0.14%	0.11%	0.85%	2.90%	0.01%	2.16%	0.98%	4.91%	2.24%	45.77%
B8	1307369 8	6831682	3114 9	26799	8817	107581	365228	776	171375	40742	200158	80529	5217862

B8 (percent)	100.00%	52.26%	0.24 %	0.20%	0.07%	0.82%	2.72%	0.01%	1.31%	1.53%	0.62%	0.62%	39.91%
C3	1188668 5	5583766	4094 5	16110 3	6661	127456	310086	820	273182	39880	204752	87903	5050031
C3 (percent)	100.00%	46.97%	0.34 %	1.36%	0.06%	1.07%	2.61%	0.01%	2.30%	0.34%	1.72%	0.74%	42.48%
C7	1026583 3	3720987	3065 9	15659 6	8880	155388	109447 1	516	526740	24591	241638	53017	4252350
C7 (percent)	100.00%	36.25%	0.30 %	1.53%	0.09%	1.51%	10.66 %	0.01%	5.13%	0.24%	2.35%	0.52%	41.42%
C10	1164889 5	6122783	3118 1	17684	4081	130417	168951	653	142429	30510	164445	63332	4772429
C10	100.00%	52.56%	0.27 %	0.15%	0.04%	1.12%	1.45%	0.01%	1.22%	0.26%	1.41%	0.54%	40.97%
D1	1009298 1	5825375	1948 7	28060	3637	54518	85816	648	113869	14531	89757	33016	3824267
D1 (percent)	100.00%	57.72%	0.19 %	0.28%	0.04%	0.54%	0.85%	0.01%	1.13%	0.14%	0.89%	0.33%	37.89%
D2	1098027 7	5506507	5541 14	19839	5940	123810	295301	868	168381	59717	309541	132925	4303334
D2 (percent)	100.00%	50.15%	0.49 %	0.18%	0.05%	1.13%	2.69%	0.01%	1.53%	0.54%	2.82%	1.21%	39.19%
D3	1389969 0	7263692	3964 3	67429	5784	104998	296517	878	178336	32047	201774	62058	5646534
D3 (percent)	100.00%	52.26%	0.29 %	0.49%	0.04%	0.76%	2.13%	0.01%	1.28%	0.23%	1.45%	0.45%	40.62%
E1	9807608	6212784	1062 1	3238	1636	52028	72301	369	27990	11631	70721	56473	3277816

E1 (percent)	100.00%	63.35%	0.11 %	0.03%	0.02%	0.53%	0.74%	0.00%	0.39%	0.12%	0.72%	0.58%	33.42%
E6	9661029	5123747	2854 5	75351	6327	75574	160480	771	171946	21427	141435	39386	3816040
E6 (percent)	100.00%	53.04%	0.30 %	0.78%	0.07%	0.78%	1.66%	0.01%	1.78%	0.22%	1.46%	0.41%	39.50%
E9	1017196 8	5512522	3880 9	11289	3897	60299	138366	832	121393	47183	210237	99861	39272279
E9 (percent)	100.00%	54.19%	0.38 %	0.11%	0.04%	0.59%	1.36%	0.01%	1.19%	0.46%	2.07%	0.98%	38.61%
F5	9263494	4637459	2482 3	55995	6476	106484	225660	718	250534	19753	139438	47125	3749029
F5 (percent)	100.00%	50.06%	0.27 %	0.60%	0.07%	1.15%	2.44%	0.01%	2.70%	0.21%	1.51%	0.51%	40.47%
F7	1149836 0	4386525	8530 7	25036 8	15708	108376	580561	573	283608	38234	351264	79459	5318377
F7 (percent)	100.00%	38.15%	0.74 %	2.18%	0.14%	0.94%	5.05%	0.00%	2.47%	0.33%	3.05%	0.69%	46.25%
F10	1087817 2	6196044	1802 7	12468	7503	126535	302076	591	131528	39780	121884	47831	3873905
F10 (percent)	100.00%	56.96%	0.17 %	0.11%	0.07 %	1.16%	2.78%	0.01%	1.21%	0.37%	1.12%	0.44%	35.61%
G1	9543915	4432083	4334 1	66308	13539	101871	287886	720	361246	45208	245434	94028	3852251
G1 (percent)	100.00%	46.44%	0.45 %	0.69%	0.14%	1.07%	3.02%	0.01%	3.79%	0.47%	2.57%	0.99%	40.36%

G2	1017949 9	4347371	4511 9	45119	13713	129654	339322	785	472886	49994	307474	112198	4307953
G2 (percent)	100.00%	42.71%	0.44 %	0.52%	0.13%	1.27%	3.33%	0.01%	4.65%	0.49%	3.02%	1.10%	43.32%
G8	9000777	4298224	1787 4	4828	6959	89223	104360 8	367	94949	32965	200393	53731	3157656
G8 (percent)	100.00%	47.75%	0.20 %	0.05%	0.08%	0.99%	11.59 %	0.00%	1.05%	0.37%	2.23%	0.60%	35.08%
H1	1140769 7	5510667	2968 8	39334	6166	91689	173302	756	201718	27832	161974	69701	5094870
H1 (percent)	100.00%	48.31%	0.26 %	0.34%	0.05%	0.80%	1.52%	0.01%	1.77%	0.24%	1.42%	0.61%	44.66%
H4	1193583 1	4615265	1011 32	52811	17705	146698	419309	757	536660	116568	612353	276510	5040063
H4 (percent)	100.00%	38.67%	0.85 %	0.44%	0.15%	1.23%	3.51%	0.01%	4.50%	0.98%	5.13%	2.32%	42.23%
H9	1158838 3	5650623	5790 6	30250	9585	134558	211005	851	259547	56155	303262	134116	4740525
H9 (percent)	100.00%	48.76%	0.50 %	0.26%	0.08%	1.16%	1.82%	0.01%	2.24%	0.48%	2.62%	1.16%	40.91%
I2	1060905 4	4309058	2265 7	67631	10883	121601	449848	570	426596	20348	222883	49493	4907486
I2 (percent)	100.00%	40.62%	0.21 %	0.64%	0.10%	1.15%	4.24%	0.01%	4.02%	0.19%	2.10%	0.47%	46.26%
I4	1280459 7	6454381	3343 9	54707	9917	101670	201840	875	209406	34731	208570	74042	5421092
I4 (percent)	100.00%	50.41%	0.26 %	0.43%	0.08%	0.79%	1.58%	0.01%	1.64%	0.27%	1.63%	0.58%	42.34%

I7	1154826 5	4851303	4450 4	57796	7554	85585	334233	792	229085	45044	285772	106891	5499706
I7 (percent)	100.00%	42.01%	0.39 %	0.50%	0.07%	0.74%	2.89%	0.01%	1.98%	0.39%	2.47%	0.93%	47.62%
J2	1080316 3	4265750	8298 7	16619	11236	114573	401294	1087	233455	93272	445349	197157	4940384
J2 (percent)	100.00%	39.49%	0.77 %	0.15%	0.10%	1.06%	3.71%	0.01%	2.16%	0.86%	4.12%	1.82%	45.73%
J6	1048374 9	4854940	5404 1	23719	5666	117066	270253	825	137414	43309	248659	95348	4632509
J6 (percent)	100.00%	46.31%	0.52 %	0.23%	0.05%	1.12%	2.58%	0.01%	1.31%	0.41%	2.37%	0.91%	44.19%
J7	1266194	5524136	8761 0	12684	8269	126937	288270	984	180639	88913	443552	190770	5709180
J7 (percent)	100.00%	43.63%	0.69 %	0.10%	0.07%	1.00%	2.28%	0.01%	1.43%	0.70%	3.50%	1.51%	45.09%
K1	1174281 3	5813863	4464 6	64883	8983	134745	282638	794	208819	50835	264058	105690	4762859
K1 (percent)	100.00%	49.51%	0.38 %	0.55%	0.08%	1.15%	2.41%	0.01%	1.78%	0.43%	2.25%	0.90%	40.56%
K5	9610236	4316483	5522 0	2764	4728	90957	269267	735	116912	57841	288958	120055	4286316
K5 (percent)	100.00%	44.92%	0.57 %	0.03%	0.05%	0.95%	2.80%	0.01%	1.22%	0.60%	3.01%	1.25%	44.60%
K6	1050983 3	3267238	1010 37	1553	23438	147016	801247	426	246649	154164	1014171	214581	4538313

K6 (percent)	100.00%	31.09%	0.96 %	0.01%	0.22%	1.40%	7.62%	0.00%	2.35%	1.47%	9,65%	2.04%	43.18%
L1	1154915 8	4742850	3852 4	23235 9	24562	127099	532106	699	632988	32881	302033	66349	4810408
L1 (percent)	100.00%	41.07%	0.33 %	2.01%	0.21%	1.10%	4.61%	0.01%	5.54%	0.28%	2.62%	0.57%	41.65%
L9	1036059 5	4647723	4260 9	53178	16186	104978	388417	830	415239	52345	341389	107633	4190068
L9 (percent)	100.00%	44.86%	0.41 %	0.51%	0.16%	1.01%	3.75%	0.01%	4.01%	0.51%	3.30%	1.04%	40.44%
L10	1092539 7	3975475	1088 56	85895	14080	162498	439963	797	413565	123115	620475	241249	4739429
L10 (percent)	100.00%	36.39%	1.00 %	0.79%	0.13%	1.49%	4.03%	0.01%	3.79%	1.13%	5.68%	2.21%	43.38%

Note: > total: Refers to the number of sRNAs in each sample compared to the reference sequence, followed by a reference to calculate the proportion of each type of sRNA.

> known_miRNA: Refers to the number and proportion of sRNAs that are compared to known miRNAs for each sample.

> rRNA/tRNA/snRNA/snoRNA: Refers to the number and proportion of rRNA/tRNA/snRNA/snoRNA sRNA in each sample.

> novel_miRNA: Refers to the number and proportion of sRNA in each sample compared to the new miRNA.

> exon: +/exon: -/intron: +/intron: - : Refers to a sample comparison to the number of exon/intron positive and negative chains and their proportion.

> other: Refers to the comparison of each sample to the reference sequence, but does not compare the number and proportion of sRNAs to known miRNAs, ncRNAs, new miRNAs, and exons and intron regions

Supplementary Table 7. 135 (partially repeated) differentially expressed miRNA expression levels between groups

miRNA	CON	MOD	PSF.L	PSF.M	PSF.H	PS.L	PS.M	PS.H	WE.L	WE.M	WE.H	SIM
rno-miR-200a-5p	81.91	276.75	620.04	400.67	386.67	495.67	462.00	270.00	390.00	314.67	372.33	401.00
rno-miR-3548	68.81	224.32	500.89	312.67	310.33	398.67	360.00	205.00	312.67	256.67	282.33	324.33
rno-miR-455-3p	99.07	200.60	184.67	319.00	187.67	256.67	204.33	187.33	193.33	277.00	418.00	157.00
rno-miR-155-5p	76.38	124.64	166.33	105.07	100.00	96.00	94.00	105.33	139.67	145.00	277.82	112.33
rno-miR-139-5p	1158.96	1701.24	2105.00	1955.33	1683.33	2347.00	2039.00	1989.67	2264.00	2525.67	3363.00	1916.00
rno-miR-200b-5p	12.68	33.93	41.00	50.33	25.33	42.00	39.67	25.33	25.33	31.67	64.67	35.67
rno-let-7g-3p	0.79	6.48	2.67	4.00	4.00	3.33	2.67	2.67	3.67	2.67	2.33	4.33
rno-miR-184	28.41	77.23	81.00	193.67	58.00	146.00	46.00	88.00	57.67	9.29	37.67	47.00
rno-miR-375-3p	1227.95	2132.58	3181.00	3307.33	3012.00	3838.00	2546.00	2396.33	2438.00	3168.67	2622.00	3351.33
rno-miR-126b	97.58	59.45	76.67	65.00	72.67	76.33	52.33	64.67	70.67	86.00	53.33	77.00
rno-miR-101a-3p	33591.11	22931.01	27996.33	31088.00	31374.67	30197.00	18560.67	27828.67	26014.00	29140.67	23893.33	33227.67
rno-miR-455-5p	876.80	1547.60	2488.67	1886.33	1693.67	1980.33	1591.33	2314.67	2666.67	2460.33	1146.33	1534.00

rno-miR-204-5p	35.71	12.79	48.67	42.00	41.67	32.67	24.67	42.33	43.67	42.33	36.00	47.33
rno-miR-144-5p	231.32	122.39	252.33	184.33	222.33	429.00	257.33	212.33	153.00	246.00	194.33	134.00
rno-miR-451-5p	1689.67	1608.98	5138.57	2480.33	2106.33	7869.33	6667.33	3802.33	2646.33	3025.33	3362.33	2310.67
rno-miR-27a-5p	148.33	129.96	355.80	164.00	165.00	148.00	172.00	180.67	249.67	258.33	221.00	110.00
rno-miR-486	644.67	731.48	1866.79	1192.33	1665.33	6529.67	3689.33	979.00	766.33	1087.33	1600.67	911.67
rno-miR-193b-3p	85.00	150.68	81.38	175.33	125.33	150.33	93.00	136.00	143.33	233.33	175.33	176.67
rno-miR-218a-5p	235.00	257.96	396.82	259.00	303.67	459.67	275.33	282.33	334.33	351.00	232.33	262.00
rno-miR-218b	220.00	241.68	369.71	241.67	288.00	436.33	260.67	265.67	318.33	334.00	218.00	249.00
rno-miR-6329	77.00	88.17	150.34	141.61	109.00	129.67	141.61	161.69	136.60	142.00	123.00	126.67
novel_380	96.33	152.08	69.97	113.67	86.00	68.81	85.00	110.33	73.96	168.00	166.33	137.33
rno-miR-674-5p	100.67	144.02	74.62	142.67	72.00	120.67	81.00	95.33	103.33	155.00	136.33	94.00
rno-miR-34a-5p	295.00	594.17	1008.10	1082.67	1037.31	1168.33	423.67	722.33	862.67	1037.31	663.33	884.00
rno-miR-27b-5p	30.67	33.11	63.66	64.67	46.00	43.67	42.00	56.00	55.67	62.25	51.33	45.67
rno-miR-872-3p	54.33	67.10	36.17	55.33	41.67	64.67	39.67	44.67	62.67	103.00	46.33	71.33

rno-miR-3591	570349.00	678984.32	441138.29	919571.0 0	458747.33	695366.67	404941.6 7	559518.3 3	444524.91	457994.27	640041.33	486635.0 0
rno-miR-194-5p	58675.33	77880.16	51100.88	75951.67	52896.33	60330.00	46669.00	64133.33	61899.00	84747.67	40791.33	66772.33
rno-miR-122-5p	924354.33	1045670.2 7	643091.25	1273570. 33	630795.67	1078007.00	588732.6 7	837387.0 0	748935.00	842153.33	1007918.3 3	761266.3 3
rno-miR-1247-3p	31.67	24.10	52.61	74.28	47.00	22.00	21.67	28.00	45.33	33.67	113.67	15.33
rno-miR-146b-5p	540.33	683.49	1116.24	881.33	629.33	954.00	650.00	640.67	832.33	746.33	1085.33	612.00
rno-miR-3556b	396.00	433.77	260.74	410.33	305.67	385.67	278.33	373.00	417.00	643.00	246.33	474.33
rno-miR-29c-3p	410.33	447.12	269.89	423.33	312.00	396.67	285.67	388.00	427.67	659.00	250.00	489.33
rno-miR-21-3p	54.67	54.94	64.00	13.21	29.67	32.67	20.82	34.33	39.33	46.67	37.33	40.00
rno-miR-142-3p	387.33	697.61	884.67	256.23	322.05	840.67	441.67	713.00	840.67	1160.67	968.33	668.33
rno-miR-32-5p	178.67	226.89	257.67	114.40	144.00	217.33	124.00	202.00	240.00	329.33	176.67	238.00
rno-miR-19a-3p	54.00	62.52	86.67	18.37	22.67	58.00	29.67	62.67	70.33	89.00	32.00	65.33
rno-miR-130a-3p	76.33	94.25	90.67	51.27	67.33	85.00	61.67	76.67	88.33	87.67	77.33	104.33
rno-miR-3590-5p	76.33	94.25	90.67	51.27	67.33	85.00	61.67	76.67	88.33	87.67	77.33	104.33

rno-miR-203b-5p	2798.67	3085.61	3362.67	4594.62	3752.67	3249.33	2058.67	3388.67	3043.33	3056.00	1764.00	2892.33
rno-miR-3065-5p	22.00	29.81	27.00	15.06	17.33	28.67	12.33	27.33	37.67	38.00	19.33	22.33
rno-miR-338-3p	22.00	29.81	27.00	15.06	17.33	28.67	12.33	27.33	37.67	38.00	19.33	22.33
rno-miR-1843a-5p	974.67	1044.50	1196.00	1512.91	1341.33	1174.67	918.33	1392.00	1495.00	1579.00	1235.00	1222.00
rno-miR-107-3p	690.67	868.80	676.67	617.08	578.33	791.33	498.00	778.00	814.67	1045.67	606.67	877.33
rno-miR-203a-3p	4105.33	4763.84	5281.33	6758.27	5787.67	4946.33	3118.00	5487.67	4847.67	4721.67	2681.33	4344.00
rno-miR-144-3p	137.00	116.69	222.67	59.58	134.67	377.67	139.33	157.00	155.00	316.45	219.33	183.67
rno-miR-181a-1-3p	75.33	105.57	158.33	170.73	142.67	117.00	91.33	130.67	111.00	119.33	118.33	105.00
rno-miR-3570	75.33	105.57	158.33	170.73	142.67	117.00	91.33	130.67	111.00	119.33	118.33	105.00
rno-miR-181a-2-3p	13.33	8.94	11.67	20.01	10.00	7.00	11.67	15.33	15.00	11.67	15.67	9.67
rno-miR-3120	30.67	48.06	53.67	26.48	33.67	61.00	42.33	51.00	43.33	55.67	64.33	51.67
rno-miR-19b-3p	761.00	995.54	802.67	539.22	497.33	997.67	527.67	852.00	715.33	1114.33	453.00	923.67
rno-miR-653-5p	1.33	0.00	1.67	2.81	0.67	1.33	1.00	1.00	1.33	0.67	0.67	0.33

rno-miR-362-3p	113.00	131.72	102.67	78.52	71.67	113.33	54.64	95.33	85.33	159.67	67.00	135.67
rno-miR-186-5p	1673.33	2332.57	1910.00	1567.44	1136.86	2664.33	1186.67	1822.67	2018.67	2830.67	1620.00	2258.67
rno-miR-15a-3p	0.33	2.43	0.00	0.00	0.33	0.33	0.33	0.67	0.67	0.00	0.67	0.67
rno-miR-33-5p	22.33	17.75	7.67	5.61	7.00	9.67	4.33	12.00	19.00	20.00	7.67	13.67
rno-miR-1843b-5p	169.00	176.26	192.67	240.11	208.67	206.00	158.33	226.67	237.67	282.33	222.33	214.00
rno-miR-378b	8.33	11.23	15.67	111.33	199.71	101.00	243.52	13.00	17.00	18.33	23.67	14.00
rno-miR-542-3p	909.67	799.28	1376.00	1201.67	1597.65	1028.00	846.00	1135.67	1109.33	1209.33	1076.67	1229.67
rno-miR-203a-5p	637.33	648.07	886.33	1303.67	1465.35	783.00	572.67	839.33	918.67	792.00	526.33	952.67
novel_536	49.33	114.89	21.33	46.67	30.02	28.00	43.33	80.00	39.33	124.33	33.33	50.67
rno-miR-203b-3p	825.33	838.41	1150.33	1635.67	1740.82	989.67	705.00	1096.00	1210.67	1026.67	681.67	1222.00
rno-miR-421-3p	5.00	2.81	5.67	4.33	5.67	12.86	5.00	5.00	5.00	6.67	8.33	7.00
rno-miR-93-3p	5.33	3.94	9.67	11.67	8.33	15.40	6.67	6.00	7.33	8.67	10.67	6.67
rno-miR-98-3p	2.00	3.50	2.00	1.67	1.67	0.34	1.33	2.00	1.67	2.00	2.33	4.15
rno-miR-106b-3p	192.67	248.53	354.33	450.33	367.67	532.00	499.01	332.33	329.33	359.33	556.00	328.33

rno-miR-490-3p	18.33	20.60	13.33	21.67	25.00	23.00	8.74	13.67	22.33	27.67	20.67	20.67
rno-miR-96-5p	203.33	238.69	148.67	188.67	166.67	335.67	102.21	152.00	446.33	289.33	277.33	149.67
rno-miR-429	188.33	339.16	441.33	338.00	419.00	535.00	336.33	236.61	393.67	467.33	352.33	504.33
rno-miR-148a-5p	4487.00	6030.83	8861.67	8273.00	7145.67	7050.67	6889.00	9719.31	11180.73	10375.67	6962.00	7855.67
rno-miR-31a-3p	116.00	109.54	127.33	172.67	176.33	156.67	109.67	178.65	174.00	170.33	113.00	174.33
rno-miR-217-5p	15.33	13.29	29.33	12.33	23.00	124.00	23.33	4.47	6.00	13.33	19.00	14.00
rno-miR-183-5p	276.67	314.03	213.67	403.00	384.33	407.67	188.00	267.00	575.28	388.00	539.33	233.33
rno-miR-3553	276.67	314.03	213.67	403.00	384.33	407.67	188.00	267.00	575.28	388.00	539.33	233.33
rno-miR-7b	14.33	19.00	26.00	27.33	24.67	27.67	21.00	31.33	40.86	32.00	33.33	20.67
rno-miR-98-5p	328.00	406.49	390.33	423.33	307.00	602.00	340.67	355.33	282.21	400.67	285.00	323.00
rno-miR-182	1095.33	1186.15	810.00	1458.67	1487.33	1220.33	709.33	970.00	1722.14	1135.00	1464.67	892.00
rno-miR-200c-3p	76.33	103.43	112.33	89.33	55.33	154.33	56.00	70.00	70.33	55.17	87.00	51.08
rno-miR-379-5p	10.33	15.73	21.33	9.33	8.33	26.00	4.00	14.33	13.67	4.17	7.67	6.67
rno-miR-200b-3p	2283.67	5447.73	5296.33	5120.33	3902.33	5683.67	4797.33	3779.67	3540.67	3445.98	3953.33	4611.33

rno-miR-411-5p	5.33	4.83	6.33	3.33	2.00	4.33	2.67	5.67	3.67	0.83	2.00	1.33
rno-miR-6216	21.33	38.28	48.33	37.67	31.00	40.67	22.67	32.67	32.00	15.82	68.67	23.67
rno-miR-484	7.67	4.17	7.00	11.33	7.33	11.00	8.33	8.00	9.00	12.94	15.56	9.67
rno-miR-1b	784.33	896.10	1266.33	1897.33	1142.00	2594.67	3693.67	488.00	604.00	283.46	1011.67	276.67
rno-miR-127-3p	37.00	50.89	76.33	56.67	45.67	94.67	31.67	57.00	60.00	26.94	72.33	27.33
rno-miR-92b-3p	2.00	10.22	3.00	3.00	3.33	4.67	3.33	4.00	4.33	5.00	10.22	2.00
rno-miR-138-1-3p	1.33	3.03	1.00	1.33	1.33	1.33	0.33	0.00	1.33	0.33	3.03	3.33
rno-miR-3574	313.33	216.37	322.67	365.67	259.00	372.33	302.33	362.33	325.67	603.67	216.37	361.67
rno-miR-342-5p	4.33	9.22	6.67	2.00	2.67	3.67	3.00	3.33	2.00	2.33	9.22	3.33
rno-miR-210-3p	314.00	217.09	322.67	366.00	259.00	372.67	303.33	362.33	326.67	604.67	217.09	361.67
rno-miR-99a-3p	47.67	31.19	50.33	81.33	63.33	60.00	45.00	79.67	74.67	81.00	31.19	54.67
rno-miR-138-1-3p	1.33	0.00	1.00	1.33	1.33	1.33	0.33	0.00	1.33	0.33	3.00	3.27
rno-miR-150-3p	4.67	14.07	8.33	11.00	8.33	7.33	6.33	11.67	8.67	13.67	17.67	5.80

rno-miR-1843a-3p	32.00	37.48	48.00	61.00	39.67	57.67	34.67	46.33	46.00	71.67	85.00	59.89
rno-miR-582-5p	5.67	10.70	11.00	8.67	5.67	8.67	8.33	6.33	6.33	9.33	4.00	4.15
rno-miR-547-5p	1.33	2.49	0.67	2.00	0.00	1.67	1.00	2.00	0.67	1.00	2.00	0.00
rno-miR-122-3p	2113.33	2676.75	3290.33	3446.33	3122.67	2985.00	2737.67	3226.00	3063.00	3416.00	2797.67	3700.92

Supplementary Table 8. Groups of 11 miRNAs that are significantly different from the MOD group

miRNA	TEST
miR-19a-3p	PSF.M
miR-21-3p	PSF.M
miR-142-3p	PSF.M
miR-1247-3p	PSF.M
miR-200a-5p	CON
miR-3548	CON
miR-122-5p	PSF.L
miR-451-5p	PSF.L
miR-378b	PS.M
miR-184	PWE.M
miR-484	PWE.H

Supplementary Table 9. Three software predicts the correspondence between the analyzed miRNA and the target gene (partial).

Target::miRNA	RNAhybrid	PITA	miRanda
ENSRNOT00000000008::rno-miR-101a-3p	0	0	1
ENSRNOT00000000008::rno-miR-124-5p	0	0	1
ENSRNOT00000000008::rno-miR-150-3p	1	0	0
ENSRNOT00000000008::rno-miR-188-5p	1	1	0
ENSRNOT00000000008::rno-miR-350	0	1	1
ENSRNOT00000000008::rno-miR-3541	0	1	0
ENSRNOT00000000008::rno-miR-674-5p	1	1	0
ENSRNOT00000000008::rno-miR-872-3p	0	1	0
ENSRNOT00000000009::novel_392	1	0	0
ENSRNOT00000000010::novel_549	1	0	0
ENSRNOT00000000008::novel_150	0	0	1
ENSRNOT00000000008::novel_183	0	1	0
ENSRNOT00000000008::novel_239	0	1	0
ENSRNOT00000000008::novel_226	1	1	0

Note: 0 means unpredicted, 1 means predicted.

Supplementary Table 10. Gene Ontology Enrichment List of Candidate Target Genes in Samples (Partial)

GO_accession	Description	P-value
GO:0044241	lipid digestion	0.000894620
GO:0036146	cellular response to mycotoxin	0.000018207
GO:0009137	purine nucleoside diphosphate catabolic process	0.000025044
GO:0009191	ribonucleoside diphosphate catabolic process	0.000062470
GO:0009155	purine deoxyribonucleotide catabolic process	0.000062470
GO:0009181	purine ribonucleoside diphosphate catabolic process	0.000062119
GO:0009134	nucleoside diphosphate catabolic process	0.000087353
GO:0009151	purine deoxyribonucleotide metabolic process	0.000186490
GO:0046386	deoxyribose phosphate catabolic process	0.000227640
GO:0009264	deoxyribonucleotide catabolic process	0.000272820
GO:0016077	snoRNA catabolic process	0.002071700
GO:0072237	metanephric proximal tubule development	0.006202600
GO:0006195	purine nucleotide catabolic process	0.006457100
GO:0060548	negative regulation of cell death	0.006619600
GO:0034314	Arp2/3 complex-mediated actin nucleation	0.007808700
GO:0060587	regulation of lipoprotein lipid oxidation	0.008186600
GO:0034439	lipoprotein lipid oxidation	0.008186600
GO:0001635	calcitonin gene-related peptide receptor activity	0.008231000
GO:1902463	protein localization to cell leading edge	0.008564900
GO:2001025	positive regulation of response to drug	0.008564900

GO:0015670	carbon dioxide transport	0.010317000
GO:0043029	T cell homeostasis	0.015289000
GO:0090130	tissue migration	0.040841000

Supplementary Table 11. Regulation of Intestinal Microbial Composition of Rats with Abnormal Lipid Metabolism (abundance)

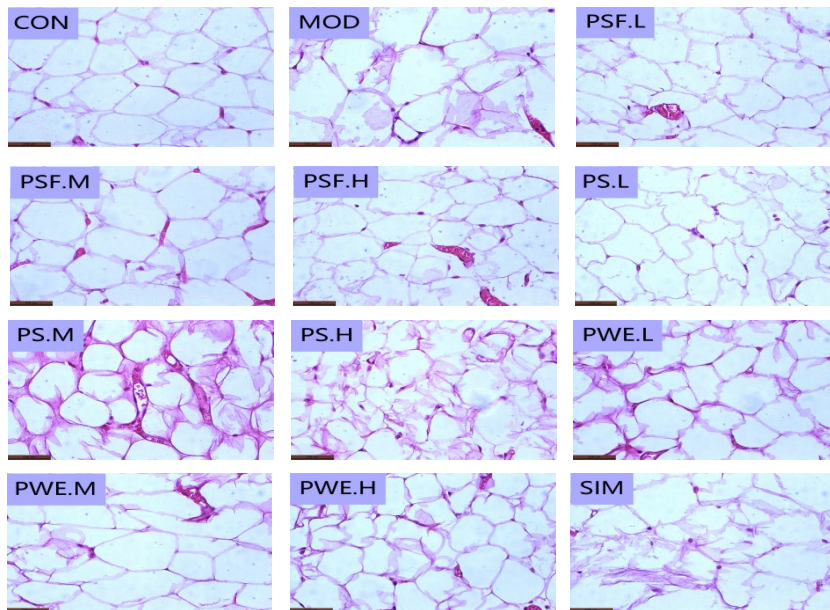
	CON	MOD	PSF.L	PSF.M	PSF.H	PS.L	PS.M	PS.H	WE.L	WE.M	WE.H	SIM
<i>Alloprevotella</i>	0.24±0.00	0.12±0.00	0.12±0.00	0.21±0.00	0.06±0.00	0.07±0.00	0.05±0.00	0.07±0.00	0.44±0.00**	0.26±0.00	0.18±0.00	0.14±0.00
<i>Allobaculum</i>	0.71±0.00	0.53±0.00	0.59±0.00	0.44±0.00	0.39±0.00	0.64±0.00	0.83±0.01	0.79±0.00	0.57±0.00	0.64±0.00	0.84±0.00*	0.75±0.00
<i>Bacteroides</i>	2.65±0.02	2.34±0.01	2.12±0.01	6.65±0.03**	3.35±0.00	3.42±0.01	2.59±0.01	3.10±0.01	2.76±0.01	2.76±0.01	5.61±0.02*	2.05±0.01
<i>Blautia</i>	0.77±0.00	0.62±0.00	0.87±0.00	1.27±0.00	0.73±0.00	1.23±0.01	1.40±0.01	1.52±0.00	0.67±0.00	1.12±0.00	2.08±0.00*	1.16±0.00
<i>Bacillus</i>	0.59±0.00	0.65±0.00	0.62±0.00	0.91±0.00	1.66±0.01	0.47±0.00	0.55±0.00	0.29±0.00	0.27±0.00	0.34±0.00	0.67±0.00	0.35±0.00
<i>Clostridium sensu stricto_1</i>	1.45±0.00	1.26±0.00	1.64±0.00	1.44±0.00	2.78±0.02	0.71±0.01	0.60±0.01	0.09±0.00	0.11±0.00	0.11±0.00	1.21±0.00	1.06±0.01
<i>Christensenellaceae_R-7</i>	0.39±0.00*	0.61±0.00	0.46±0.00	0.42±0.00*	0.44±0.00	0.52±0.00	0.58±0.00	0.59±0.00	0.35±0.00*	0.45±0.00	0.29±0.00**	0.39±0.00*
<i>Coprococcus_1</i>	0.20±0.00	0.17±0.00	0.18±0.00	0.21±0.00	0.15±0.00	0.17±0.00	0.19±0.00	0.20±0.00	0.15±0.00	0.20±0.00	0.24±0.00	0.22±0.00
<i>Desulfovibrio</i>	0.40±0.00	0.62±0.00	0.59±0.00	0.79±0.00	0.85±0.00	0.95±0.01	0.71±0.00	0.67±0.00	0.72±0.00	1.01±0.00	0.57±0.00	0.53±0.00
<i>[Eubacterium]_rumi nantium</i>	0.26±0.00	0.14±0.00	0.33±0.00	0.13±0.00	0.09±0.00	0.19±0.00	0.17±0.00	0.11±0.00	0.16±0.00	0.14±0.00	0.25±0.00	0.56±0.00*
<i>[Eubacterium]_copr ostanoligenes</i>	0.57±0.00	0.81±0.00	0.73±0.00	0.74±0.00	0.79±0.00	0.69±0.00	0.91±0.00	0.77±0.00	0.55±0.00	0.60±0.00	0.79±0.00	0.82±0.00

<i>Helicobacter</i>	0.32±0.00	0.17±0.00	0.52±0.00*	0.31±0.00	0.42±0.00	0.24±0.00	0.37±0.00	0.30±0.00	0.44±0.00	0.54±0.00*	0.43±0.00	0.60±0.00*
<i>Lactobacillus</i>	11.54±0.02*	15.08±0.02	8.67±0.01**	8.72±0.01**	7.40±0.02** *	12.08±0.03	9.77±0.03**	7.89±0.02** *	5.60±0.03** *	5.99±0.01** *	8.25±0.01**	9.41±0.03**
<i>Lachnospiraceae_N</i> K4A136	4.97±0.01	4.05±0.01	5.26±0.01	3.70±0.00	4.44±0.01	4.49±0.02	3.72±0.01	2.59±0.00	3.26±0.01	4.19±0.02	3.03±0.00	5.13±0.01
<i>Roseburia</i>	1.41±0.00	1.02±0.00	1.76±0.01	2.56±0.01	1.90±0.01	1.66±0.00	1.79±0.00	1.95±0.01	1.83±0.01	4.25±0.00**	3.63±0.01*	2.37±0.00
<i>Ruminococcus_1</i>	2.79±0.01	2.73±0.00	2.82±0.00	2.09±0.01*	1.74±0.00**	2.24±0.01	2.29±0.00	2.16±0.00	1.94±0.01*	1.88±0.00*	1.69±0.01**	2.28±0.00
<i>Ruminococcaceae_U</i> CG-014	1.87±0.01	1.76±0.00	2.25±0.00	1.69±0.01	1.71±0.00	1.80±0.00	2.26±0.00	1.93±0.00	1.66±0.00	1.71±0.00	1.93±0.00	1.93±0.00
<i>Ruminiclostridium_9</i>	0.94±0.00	0.69±0.00	1.14±0.00	0.99±0.00	0.71±0.00	0.67±0.00	0.85±0.00	0.69±0.00	0.73±0.00	1.00±0.00	1.32±0.00	1.36±0.00
<i>Ruminococcaceae_N</i> K4A214	0.55±0.00	0.66±0.00	0.60±0.00	0.54±0.00	0.48±0.00	0.58±0.00	0.65±0.00	0.64±0.00	0.52±0.00	0.56±0.00	0.54±0.00	0.66±0.00
<i>Prevotella_9</i>	2.23±0.01	2.26±0.01	2.33±0.01	4.35±0.01	3.51±0.01	3.41±0.02	1.72±0.01	3.27±0.02	2.40±0.01	3.54±0.01	5.46±0.01*	2.65±0.02
<i>Prevotellaceae_Ga6</i> A1	1.98±0.00	1.73±0.01	1.41±0.01	1.58±0.01	1.40±0.01	1.66±0.01	0.65±0.00	1.64±0.01	1.37±0.00	0.69±0.00	1.53±0.00	1.32±0.01
<i>Pseudoxanthomonas</i>	0.13±0.00	0.23±0.00	0.18±0.00	0.15±0.00	1.21±0.01	0.12±0.00	0.07±0.00	0.02±0.00	0.04±0.00	0.01±0.00	0.14±0.00	0.13±0.00
<i>Psychrobacter</i>	0.25±0.00*	0.57±0.00	0.27±0.00*	0.26±0.00*	0.23±0.00**	0.38±0.00	0.31±0.00**	0.23±0.00**	0.39±0.00	0.22±0.00**	0.39±0.00	0.24±0.00**
<i>Parabacteroides</i>	0.20±0.00	0.22±0.00	0.24±0.00	0.33±0.00	0.26±0.00	0.42±0.00	0.29±0.00	0.36±0.00	0.28±0.00	0.29±0.00	0.30±0.00	0.23±0.00

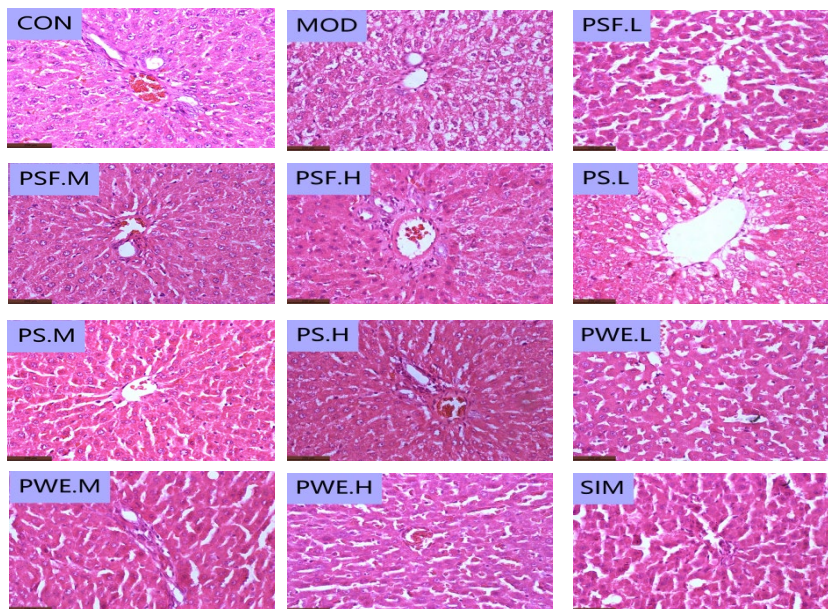
<i>Sutterella</i>	0.16±0.00	0.26±0.00	0.19±0.00	0.24±0.00	0.23±0.00	0.36±0.00	0.41±0.00	0.39±0.00	0.25±0.00	0.33±0.00	0.30±0.00	0.20±0.00
<i>Turicibacter</i>	0.57±0.00	0.47±0.00	0.56±0.00	0.63±0.00	1.16±0.01	0.27±0.00	0.25±0.00	0.16±0.00	0.15±0.00	0.22±0.00	0.53±0.00	0.41±0.00
<i>Terrisporobacter</i>	0.83±0.00	0.74±0.00	0.96±0.00	0.84±0.00	1.74±0.01	0.41±0.00	0.35±0.01	0.01±0.00	0.01±0.00	0.01±0.00	0.78±0.00	0.60±0.01
<i>Thermobacillus</i>	0.23±0.00	0.15±0.00	0.16±0.00	0.29±0.00	0.31±0.00	0.07±0.00	0.05±0.00	0.00±0.00	0.00±0.00	0.01±0.00	0.23±0.00	0.08±0.00
<i>Oscillibacter</i>	0.52±0.00	0.46±0.00	0.77±0.00	0.71±0.00	0.66±0.00	0.59±0.00	0.76±0.00	0.64±0.00	0.96±0.01*	0.96±0.00*	0.79±0.00	0.76±0.00

Note: * P <0.05, ** P <0.01, *** P <0.001 compared with model group

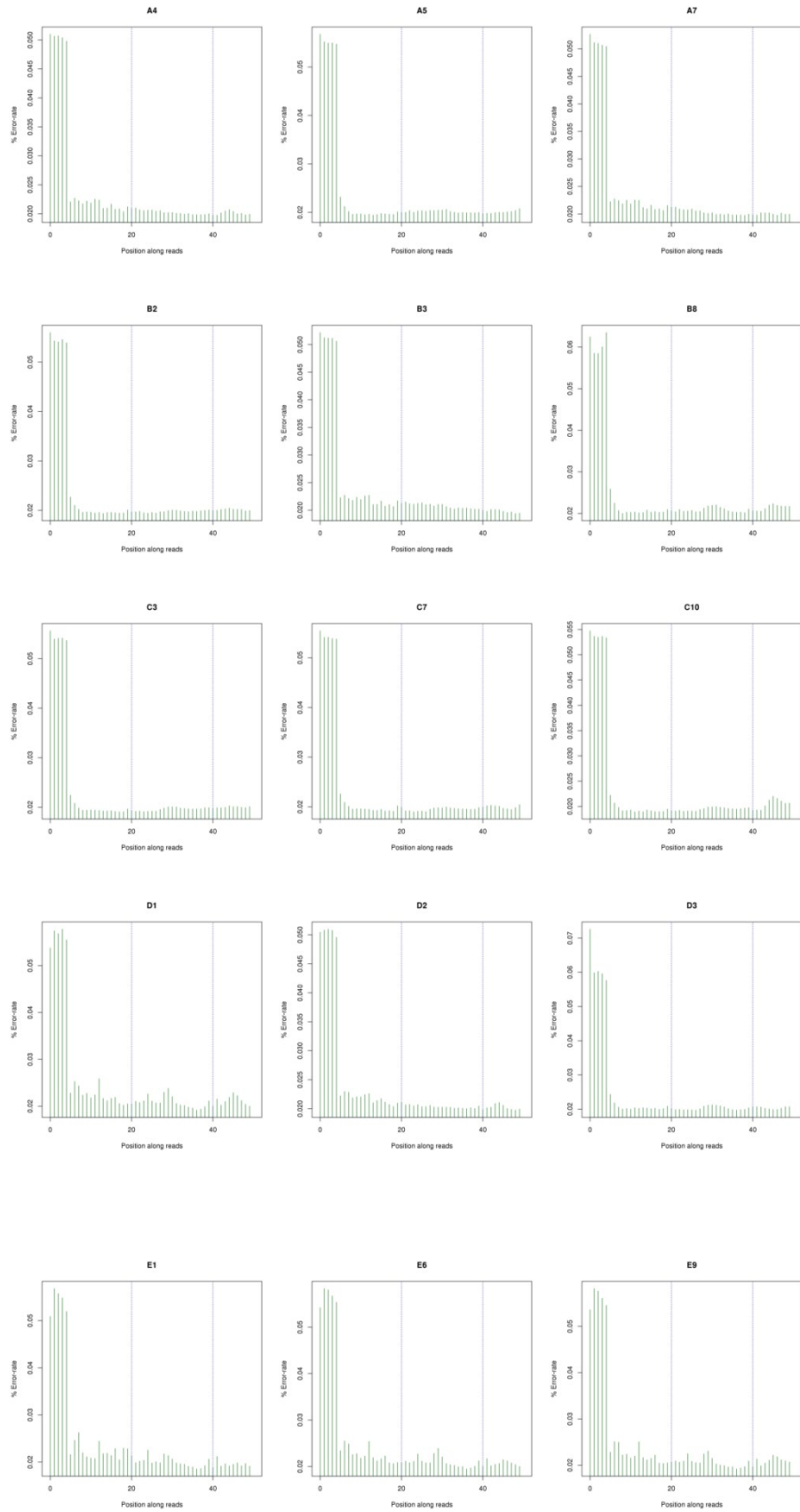
1.2 Supplementary Figures

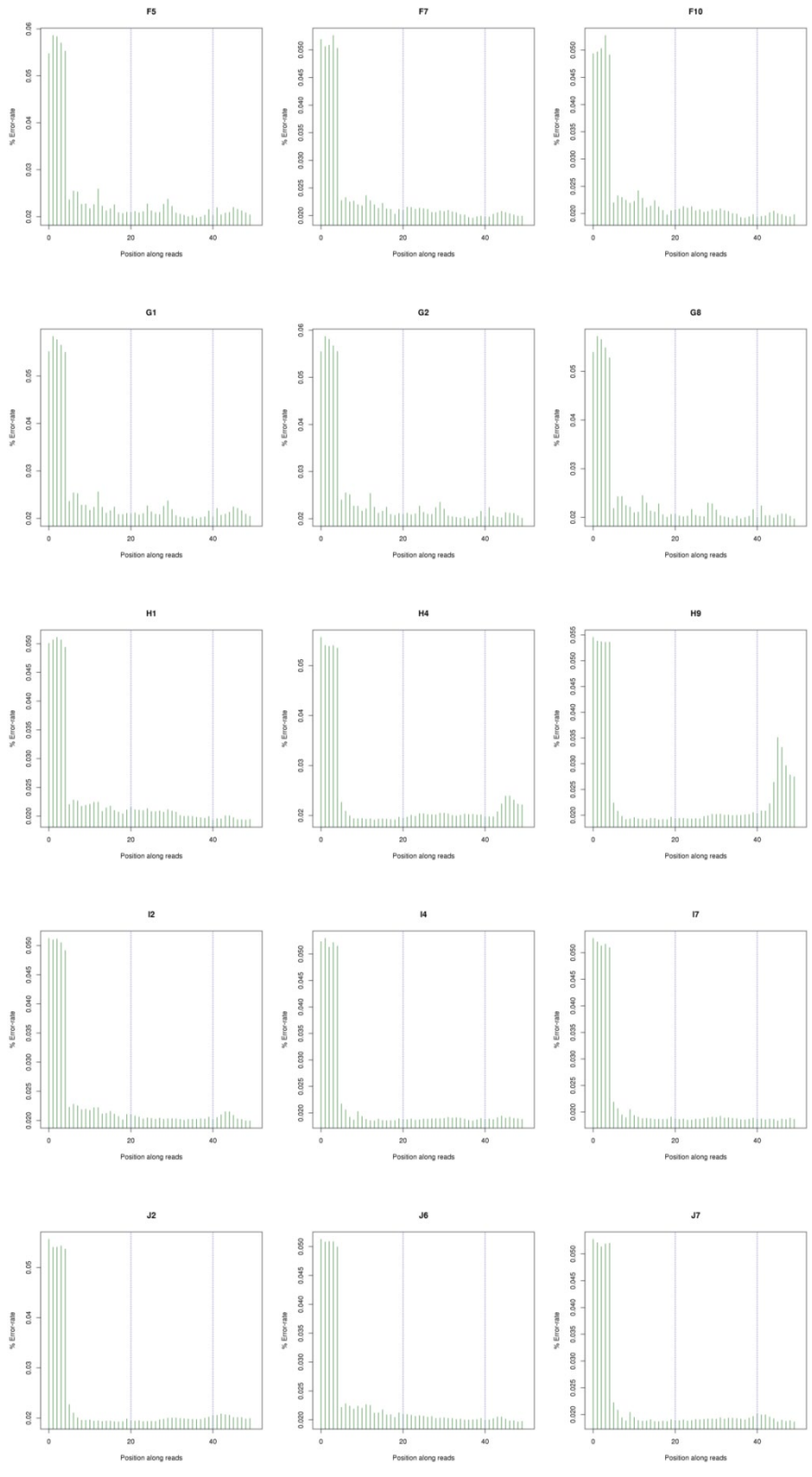


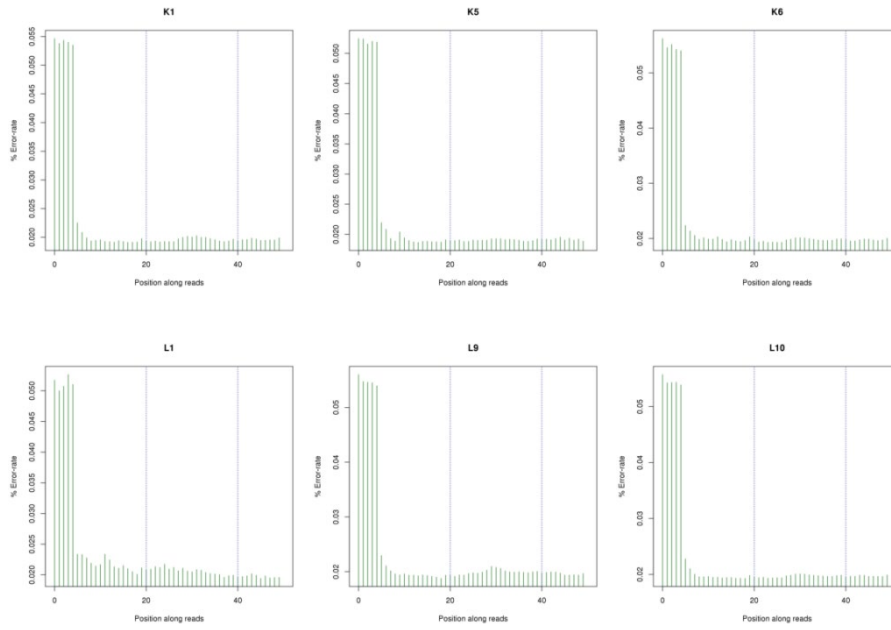
Supplementary Figure 1-1. HE staining of rat epididymal adipose tissue ($\times 400$)



Supplementary Figure 1-2. HE staining of rat liver tissue ($\times 200$)

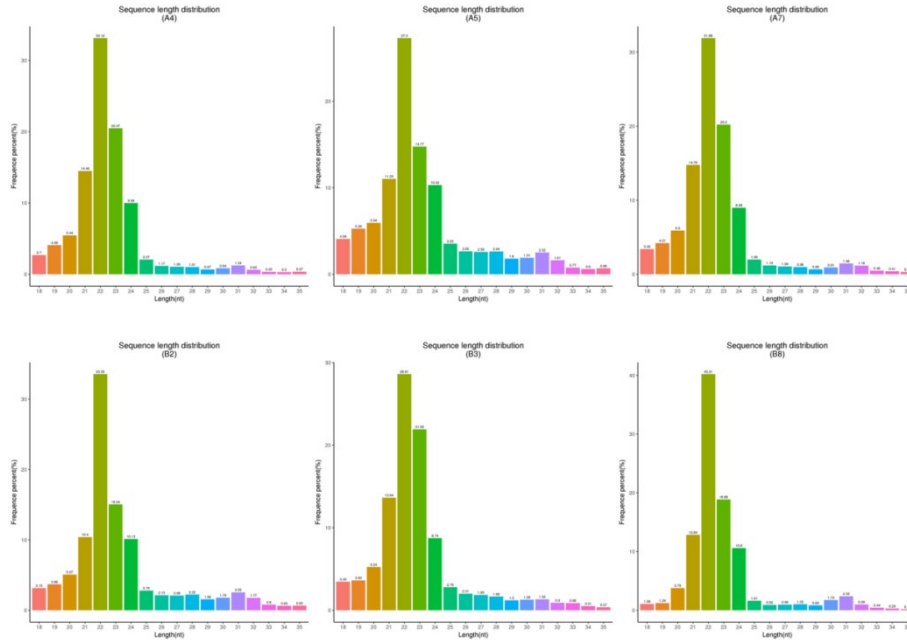


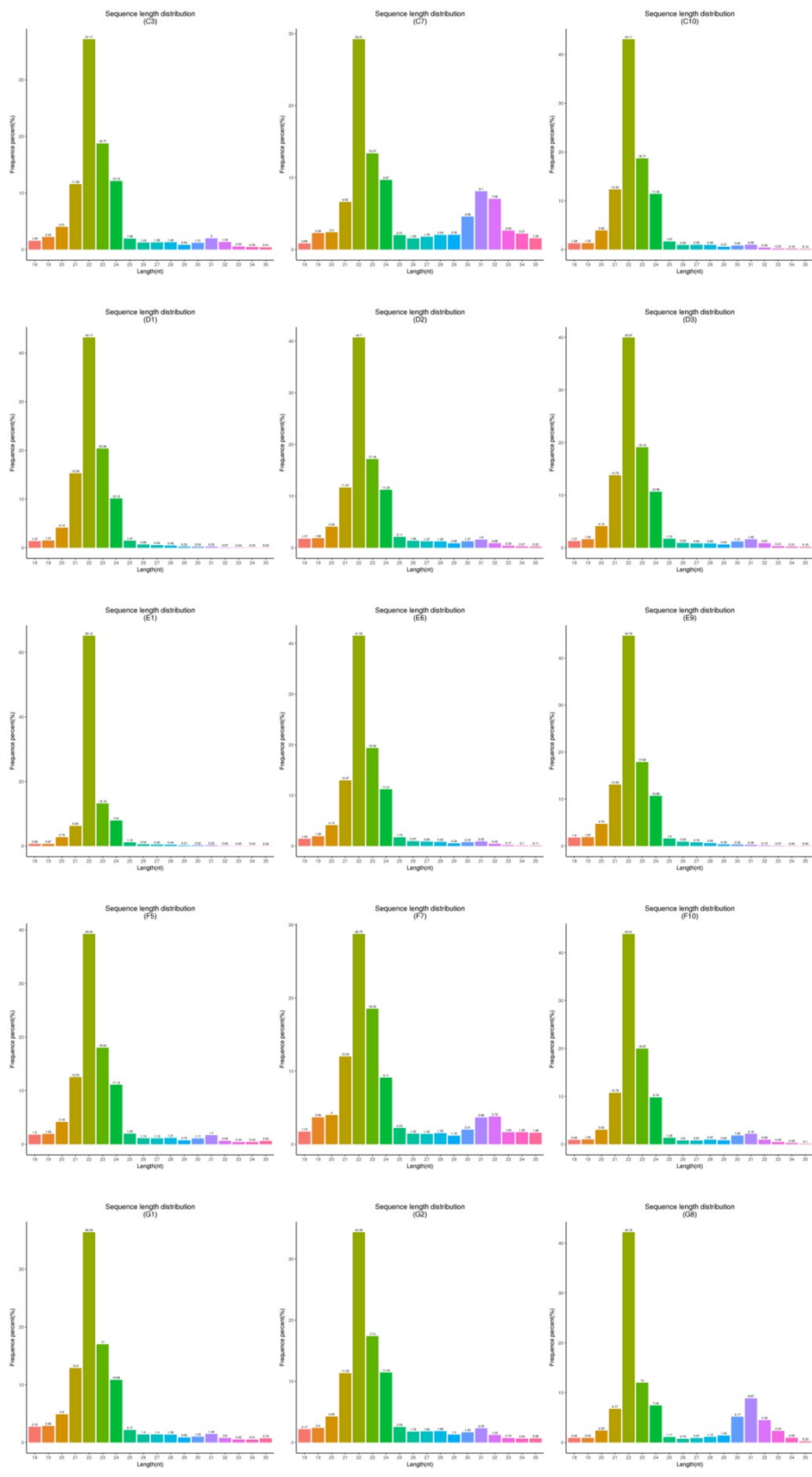


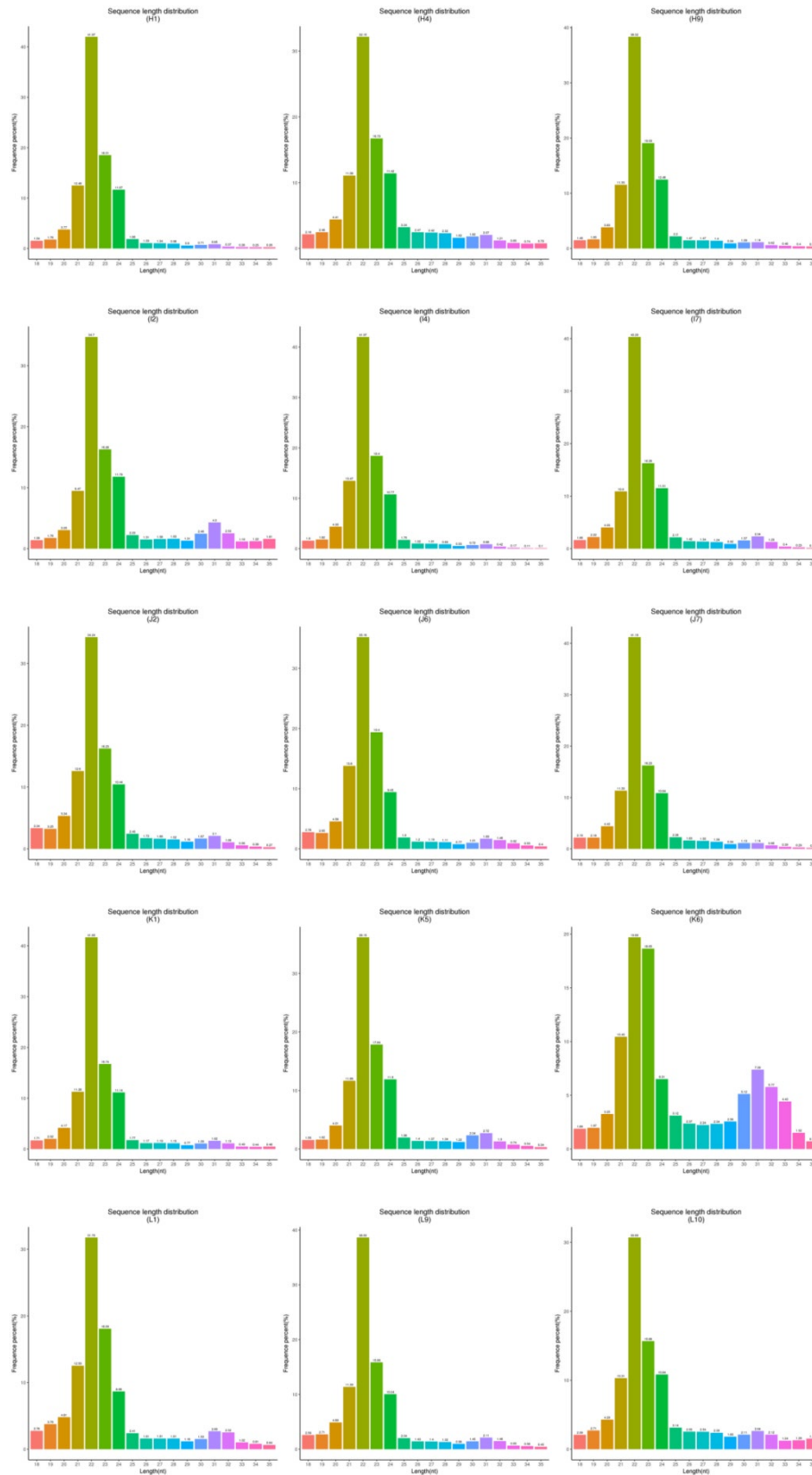


Supplementary Figure 2. Sequencing error rate distribution.

The abscissa is the base position of the reads, and the ordinate is the single base error rate







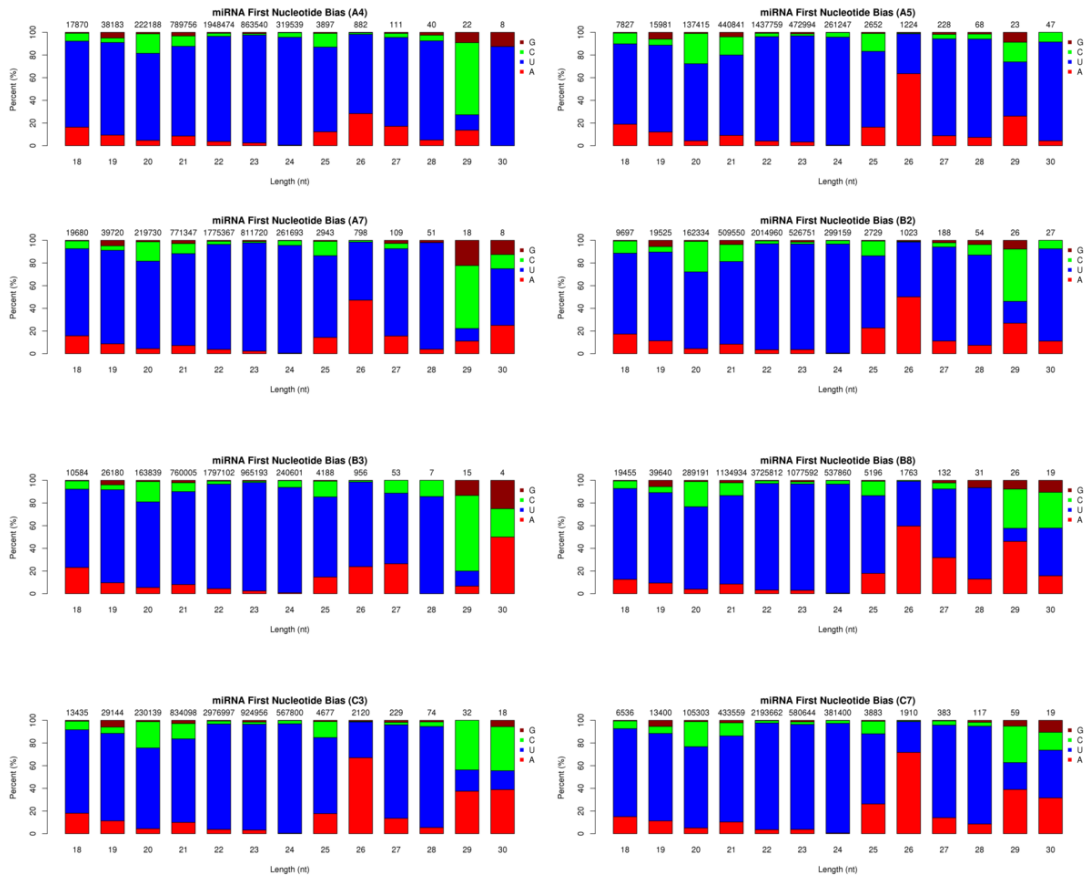
Supplementary Figure 3. Length distribution statistics of the obtained total sRNA fragments

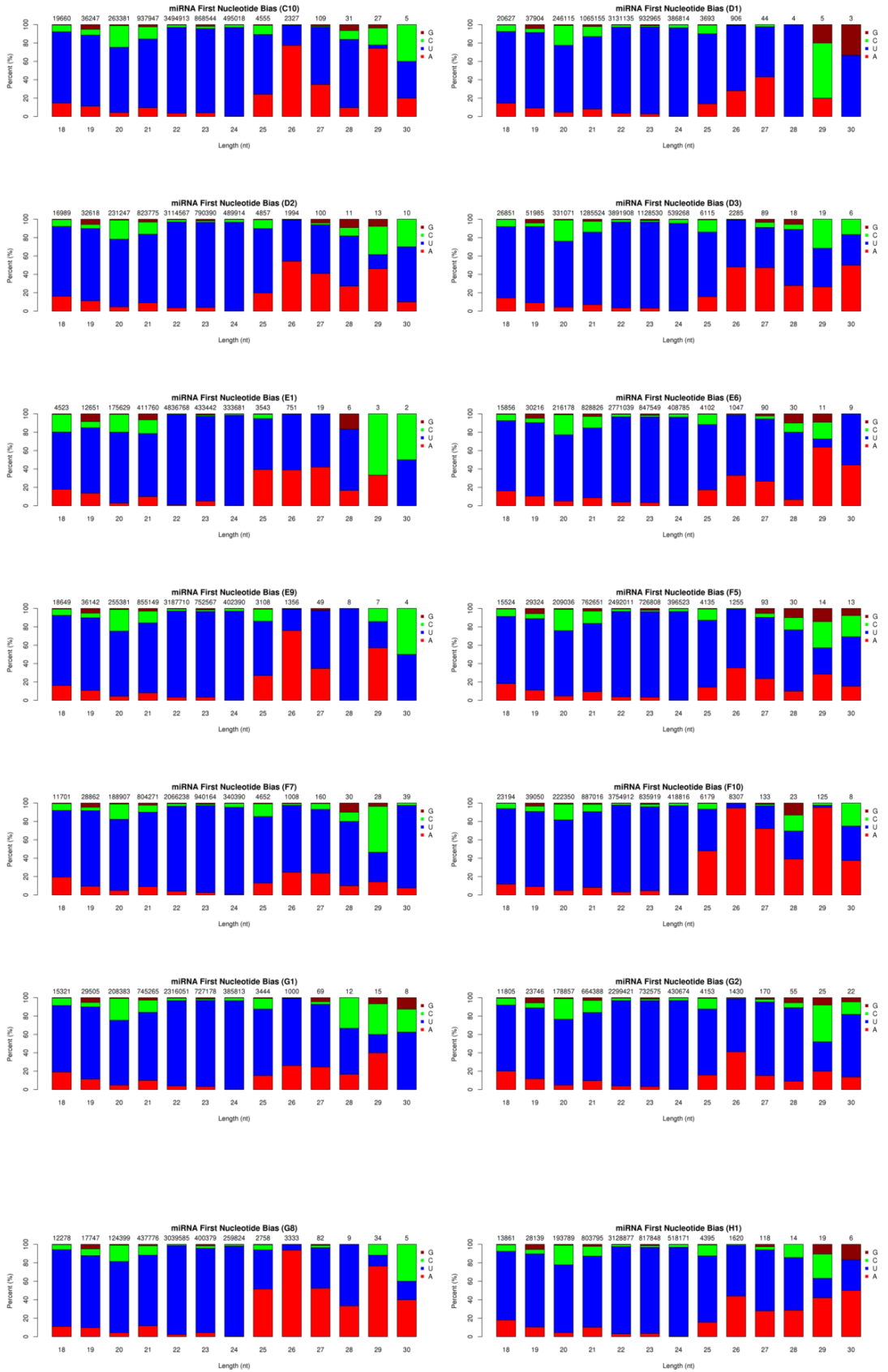
The abscissa is the length of the reads, and the ordinate is the proportion of the reads of the length.

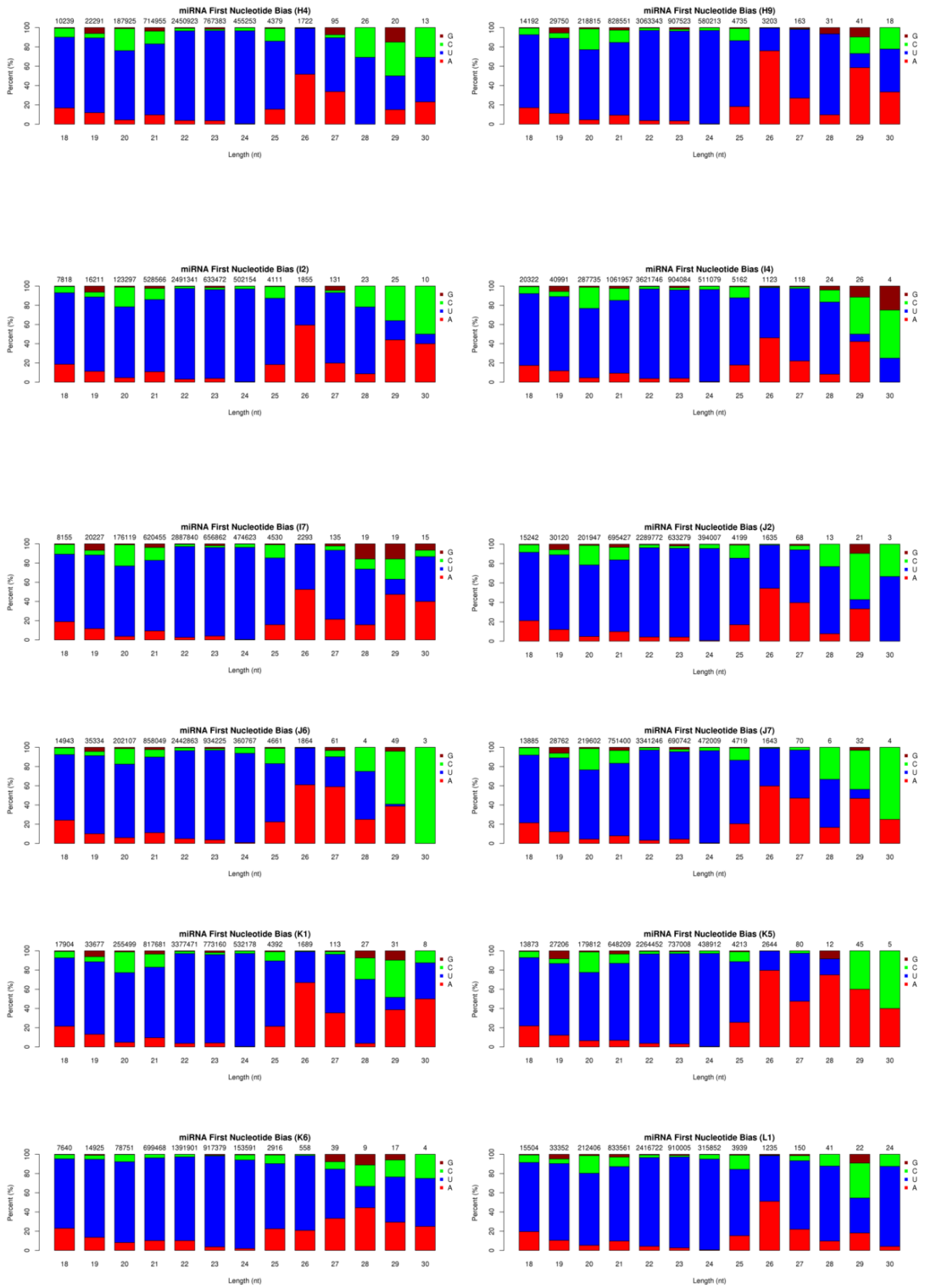


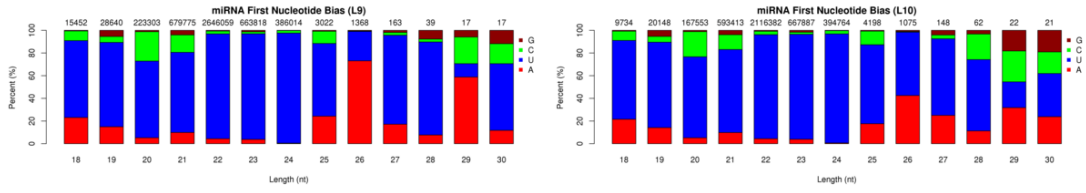
Supplementary Figure 4. Secondary structure of known miRNAs on partial matches

The entire sequence is the miRNA precursor, and the red highlight is the mature sequence.



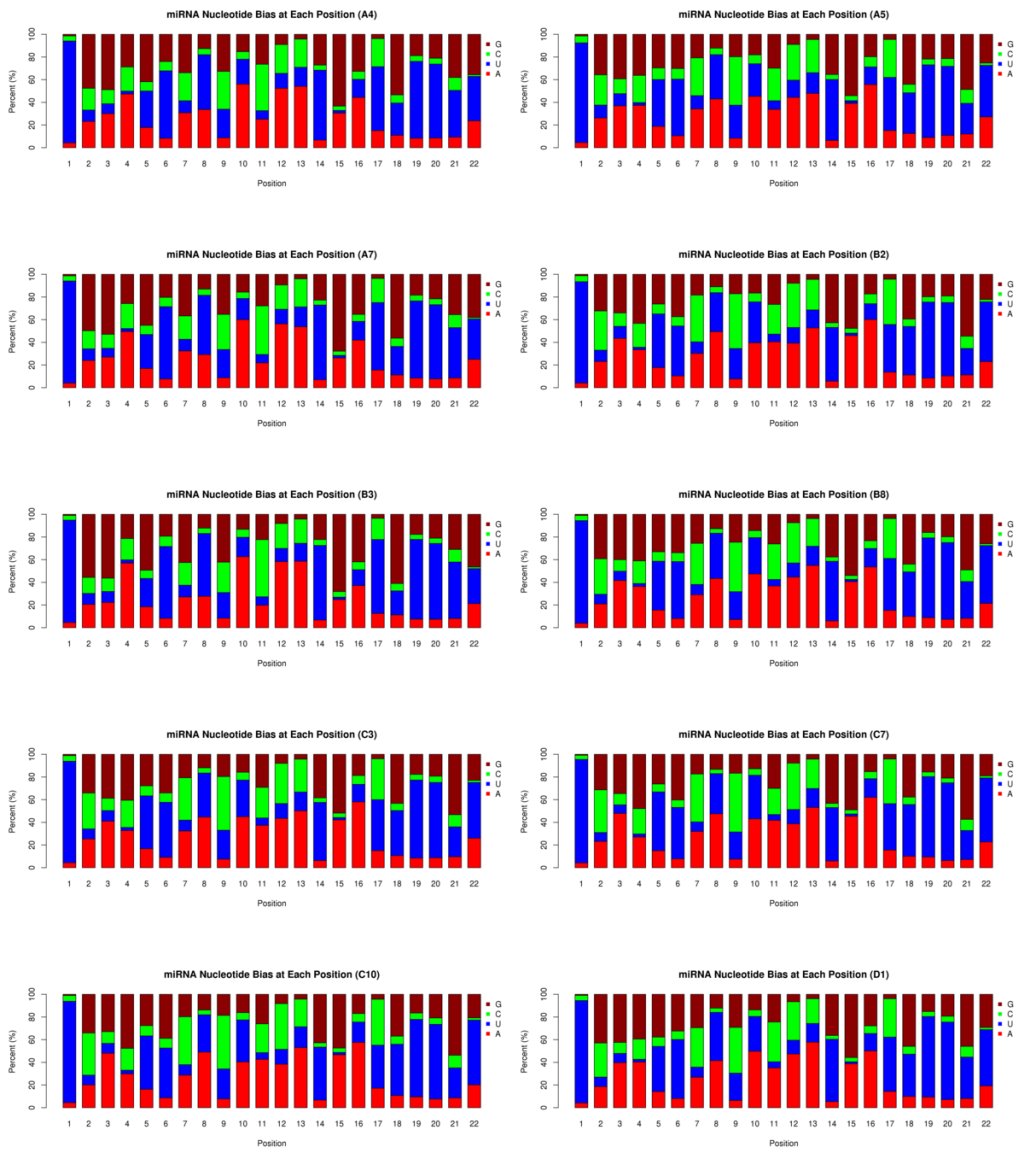


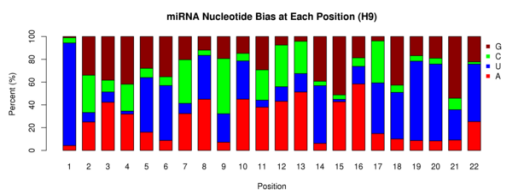
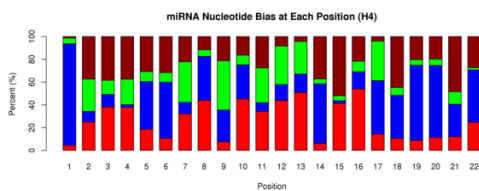
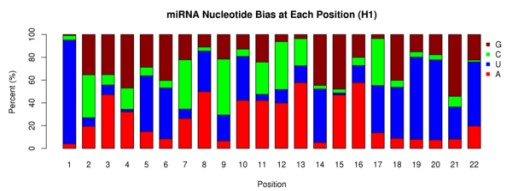
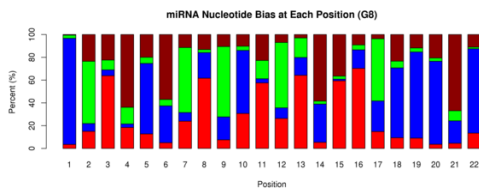
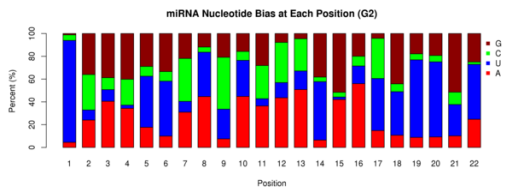
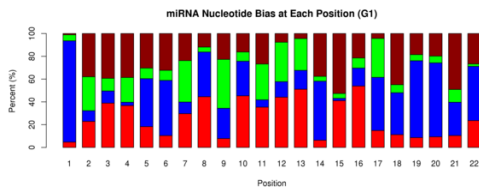
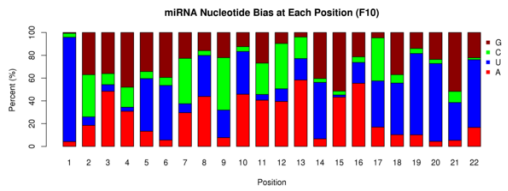
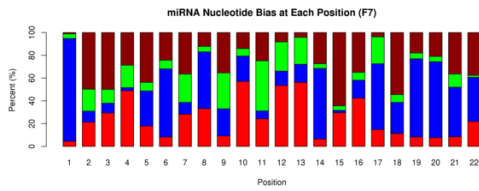
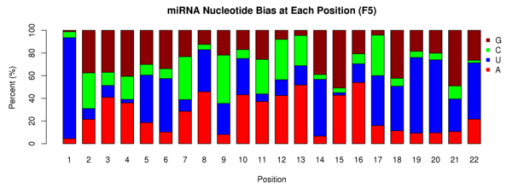
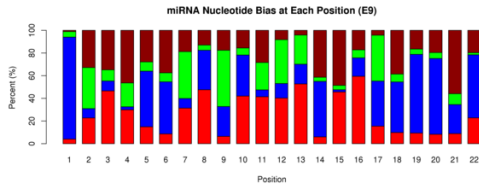
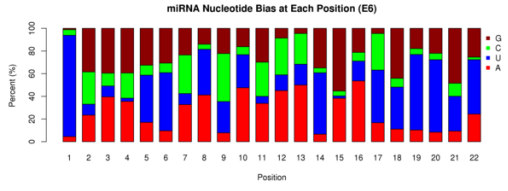
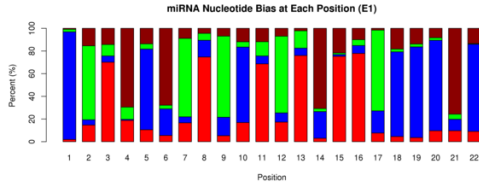
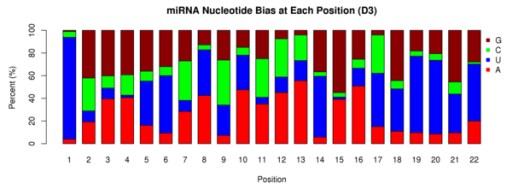
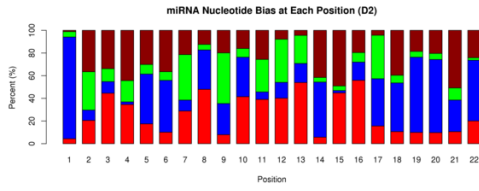


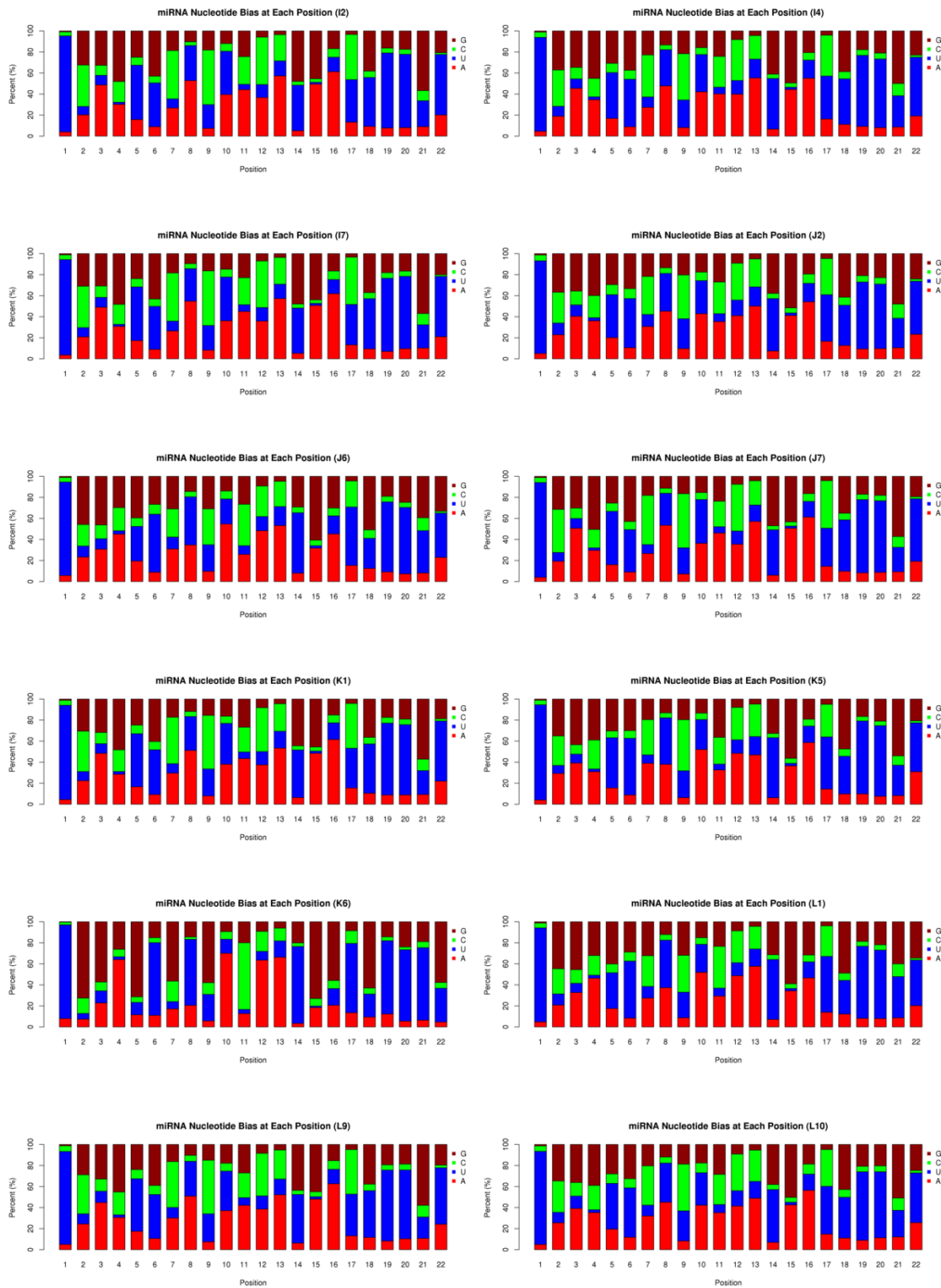


Supplementary Figure 5. Known miRNA first base preference of 18~30nt in length

The abscissa is the length of the miRNA, and the ordinate is the percentage of A/U/C/G in the first base of the miRNA in this length (the value above the histogram is the total number of miRNAs of this length)







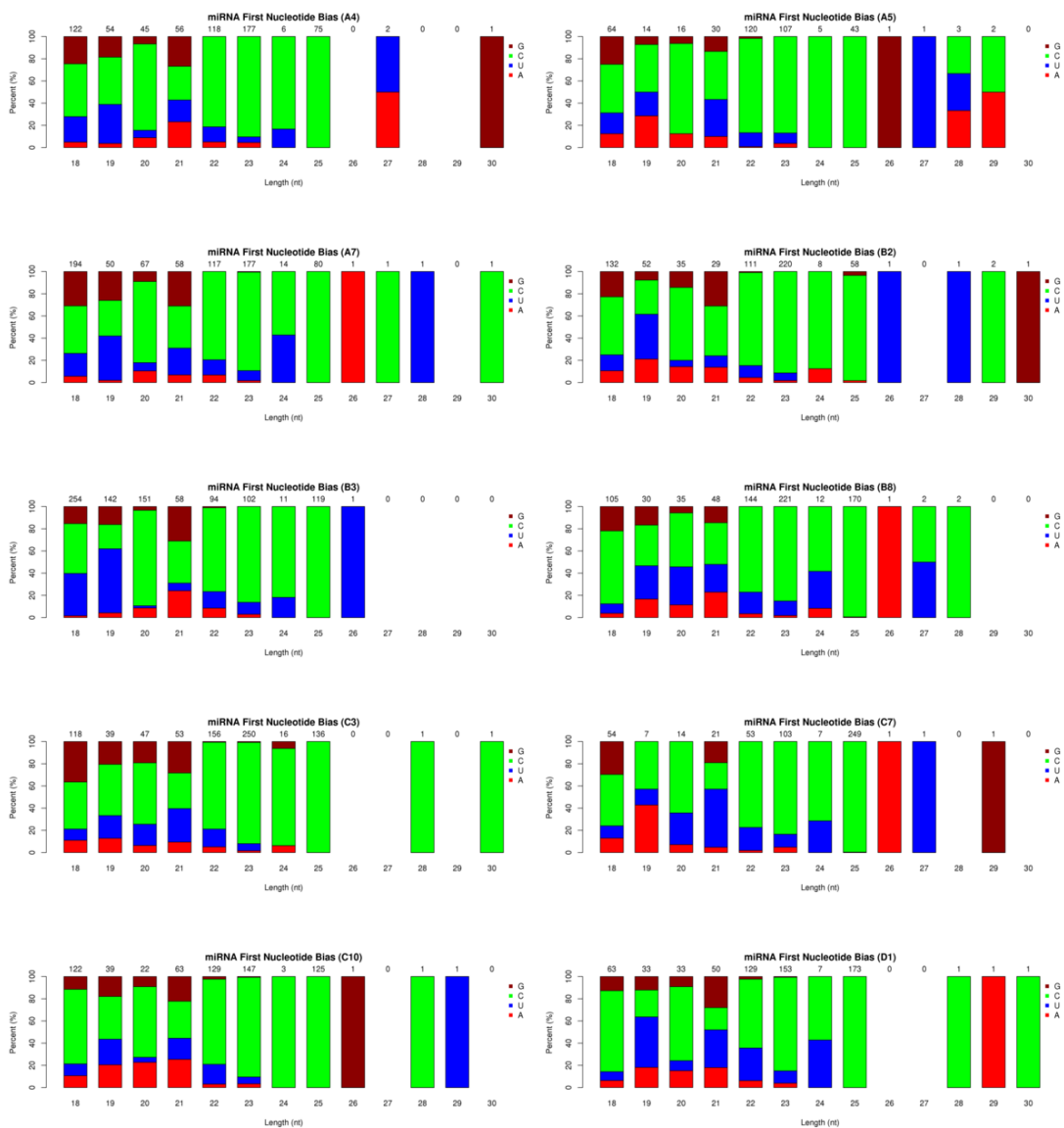
Supplementary Figure 6. Known miRNA base preference

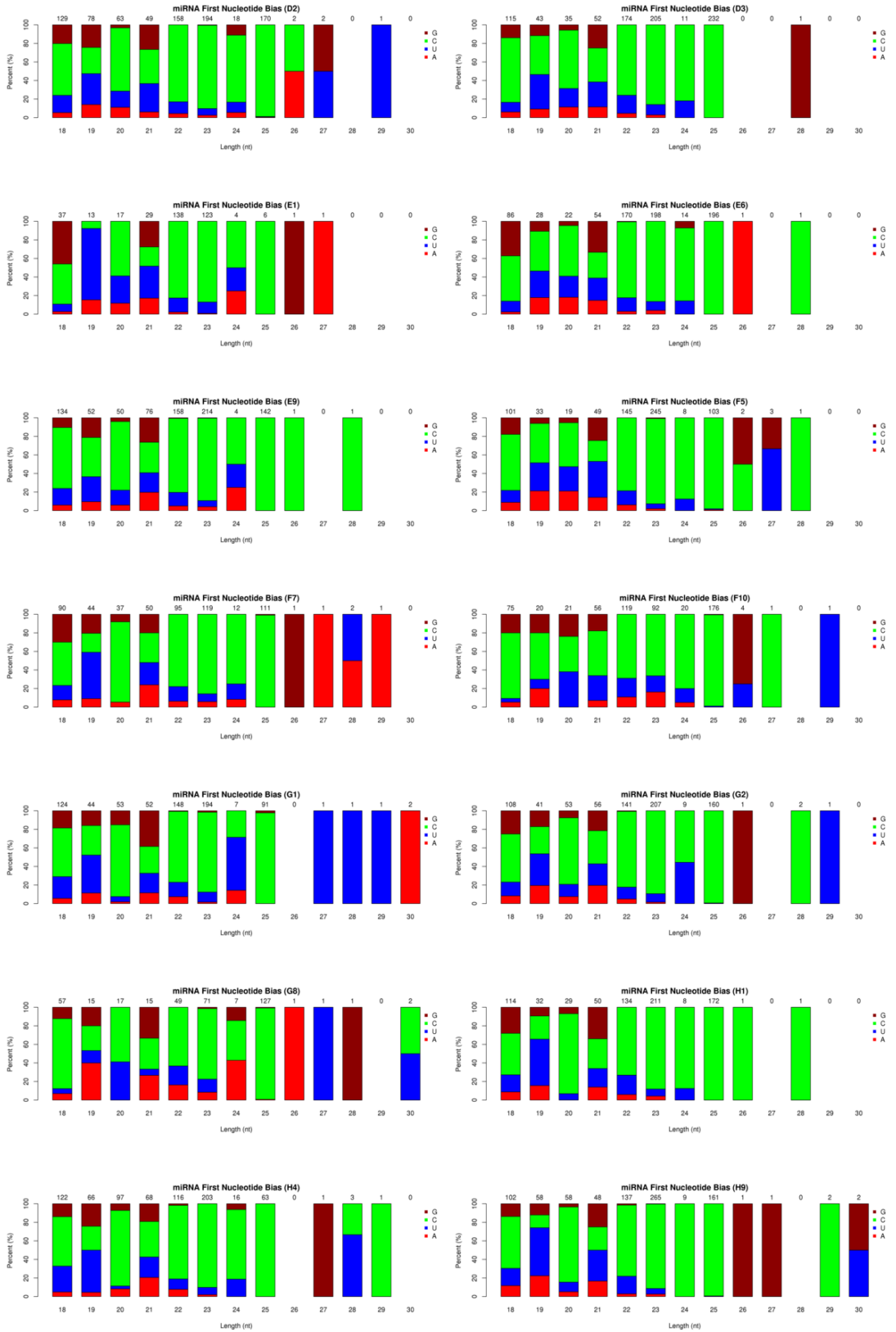
The abscissa is the base position of the miRNA, and the ordinate is the percentage of bases A/U/C/G in the miRNA at this position.

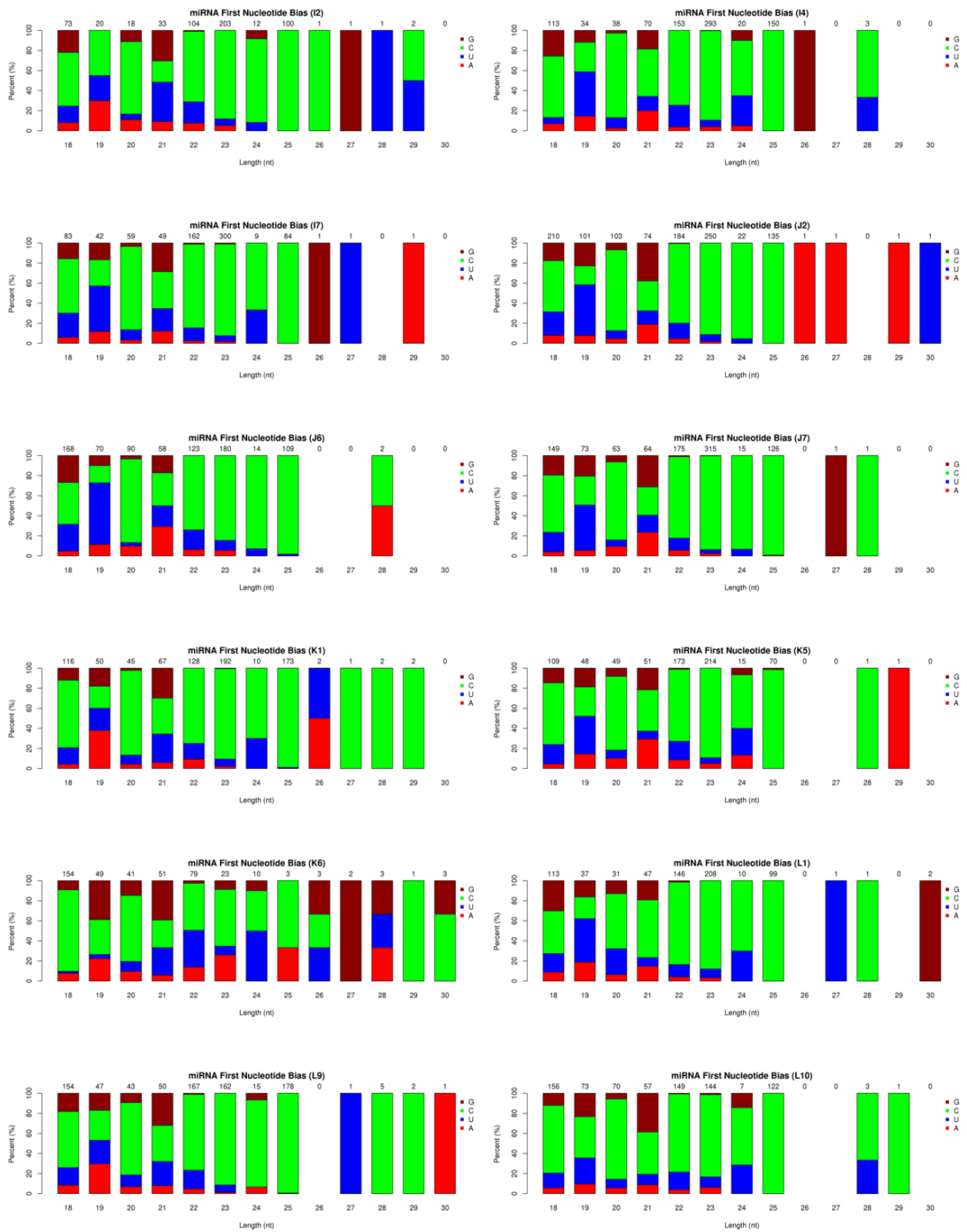


Supplementary Figure 7. Secondary structure of a partially predicted Novel miRNA.

The entire sequence is the miRNA precursor, and the red highlight is the mature sequence.

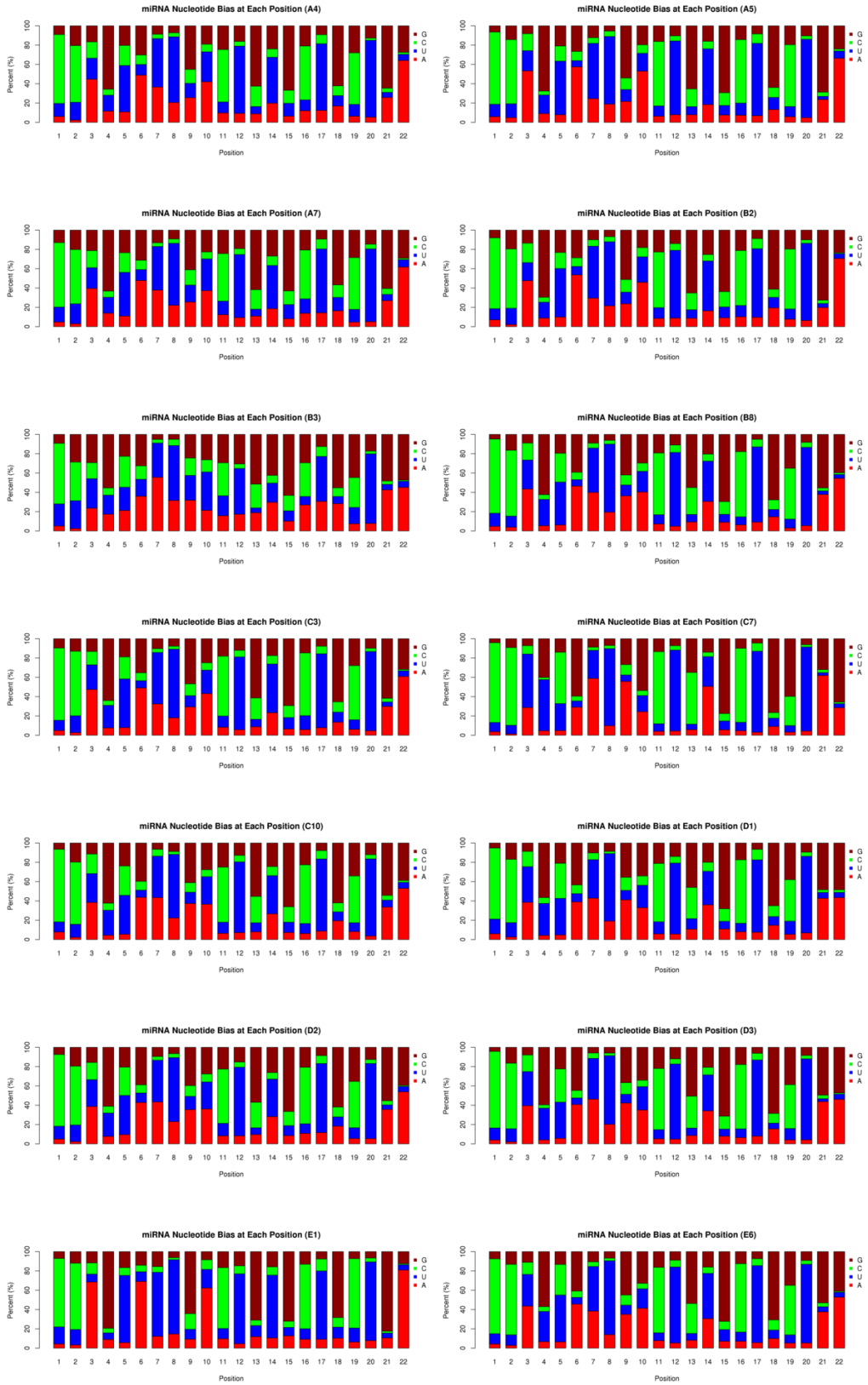


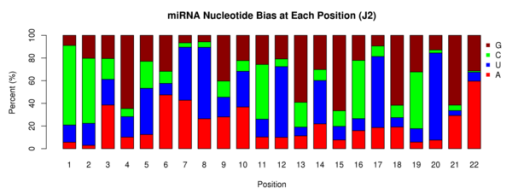
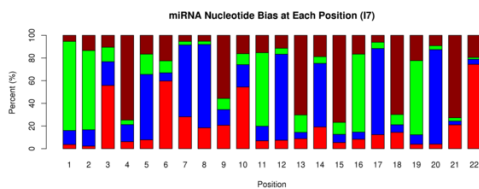
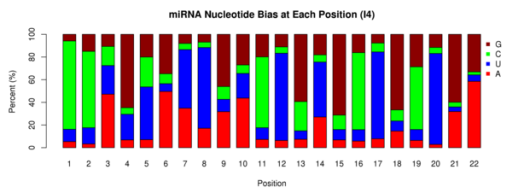
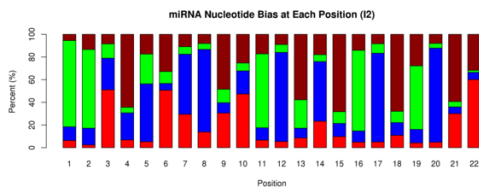
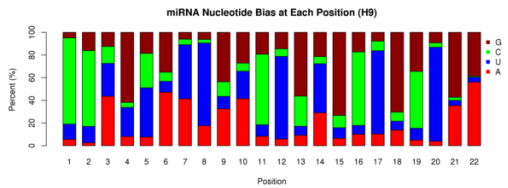
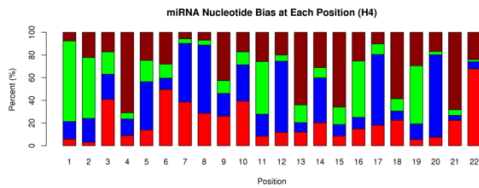
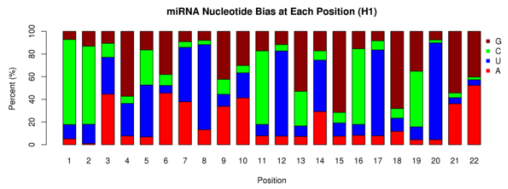
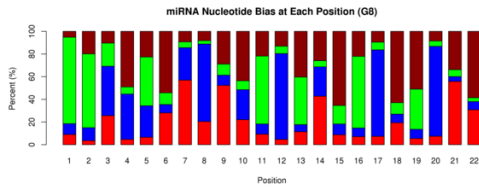
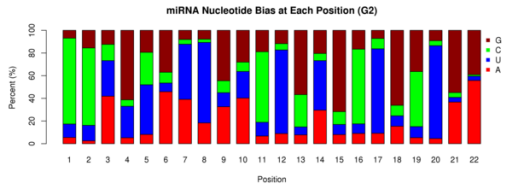
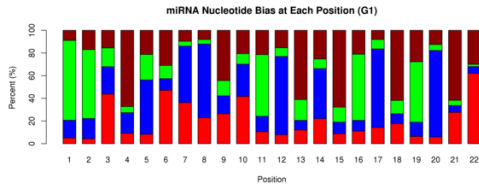
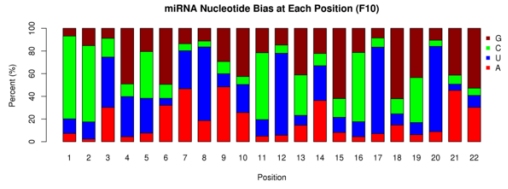
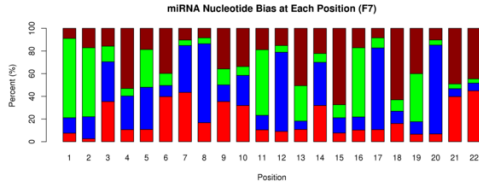
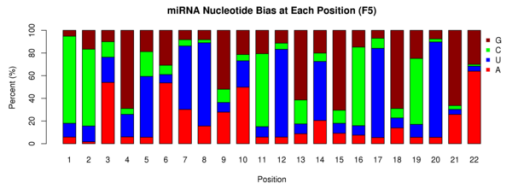
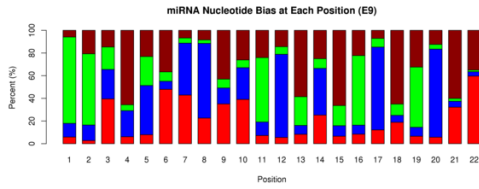


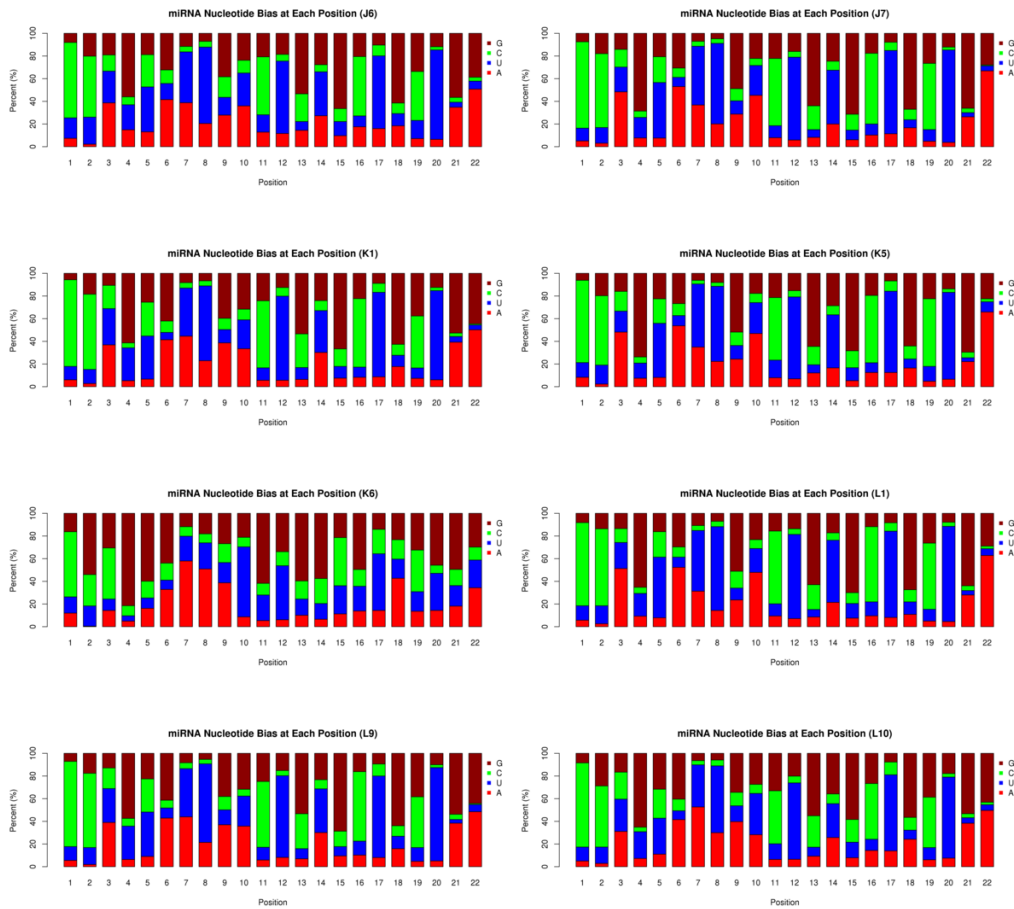


Supplementary Figure 8. First base preference of novel miRNAs with lengths from 18 to 30 nt.

The abscissa is the length of the miRNA, and the ordinate is the percentage of A/U/C/G in the first base of the length sRNA (the value above the bar graph is the total number of miRNAs of the length)

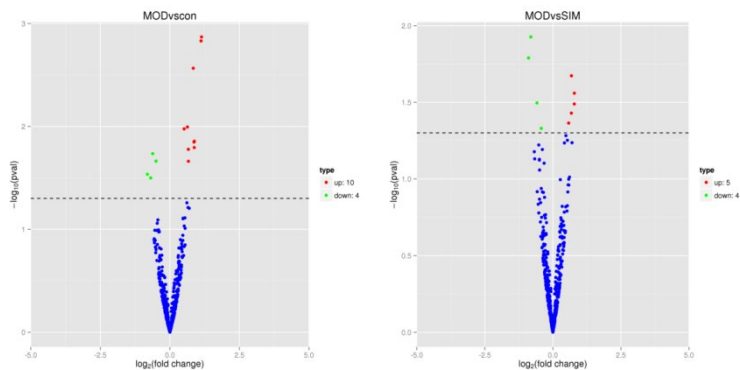


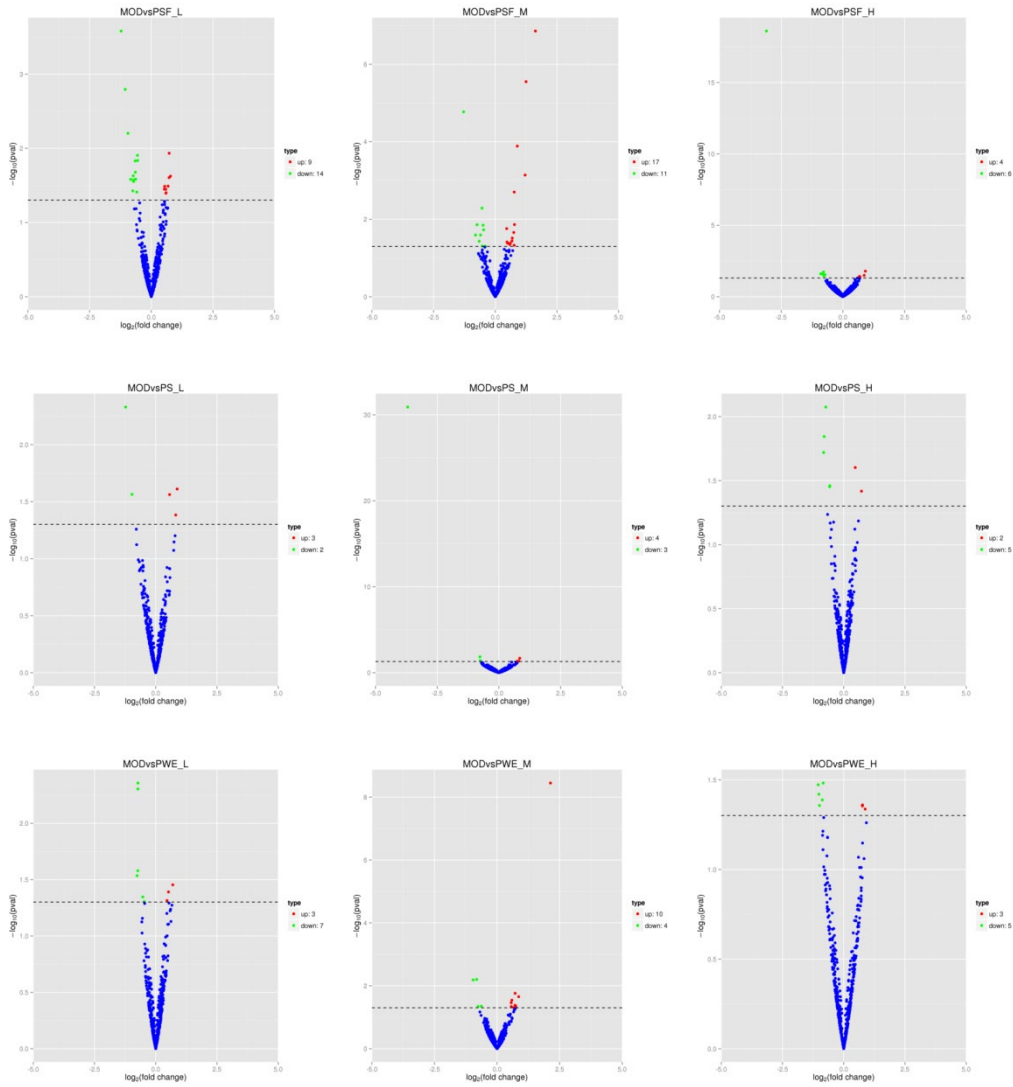




Supplementary Figure 9. Novel miRNA base preference.

The abscissa is the base position of the miRNA, and the ordinate is the percentage of bases A/U/C/G in the miRNA at this position

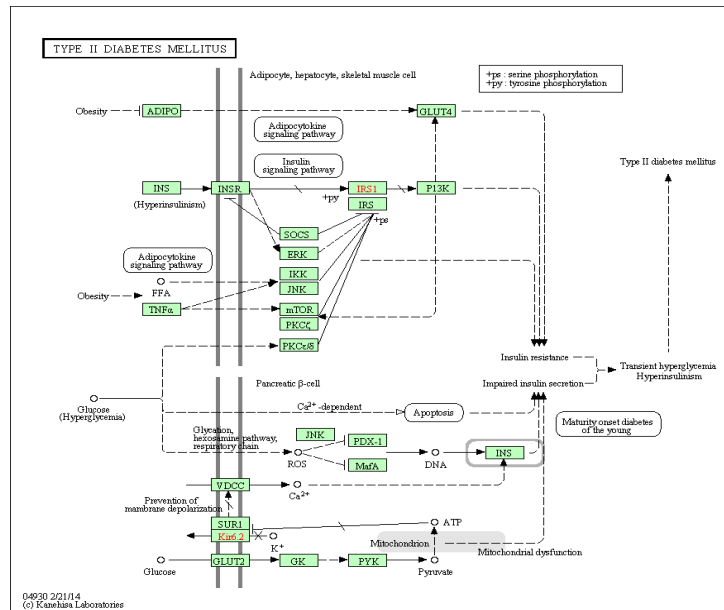




Supplementary Figure 10. Differential miRNA volcano map.

The abscissa represents the fold change in expression of miRNAs in different experimental groups/different samples, and the ordinate represents the statistical significance of the change in miRNA expression. The scatter points in the figure represent individual miRNAs, and the blue dots represent miRNAs with no significant differences. Red dots indicate significantly up-regulated differential miRNAs, and green dots indicate significantly down-regulated differential miRNAs

a



b

