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# 1. Samples

Sample name
Ctrl_L002 (trimmed)
test_1_L001 (trimmed)
test_2_L001 (trimmed)
test_3_L001 (trimmed)
test_4_L001 (trimmed)
PAH_68_L001 (trimmed)

# 2. UMI Statistics

No UMI read creation information included.

# 3. Map and Annotate

## 3.1 Summary

Sample	Sequence type	Total	Annotated with record	% of total
test_1_L001 (trimmed)	Unique search sequence	411,031	53,657	13.05
test_1_L001 (trimmed)	Read	19,535,836	16,202,028	82.93
test_2_L001 (trimmed)	Unique search sequence	597,309	76,823	12.86
test_2_L001 (trimmed)	Read	25,487,037	19,355,301	75.94
test_3_L001 (trimmed)	Unique search sequence	1,756,490	71,925	4.09
test_3_L001 (trimmed)	Read	24,987,933	7,000,777	28.02
test_4_L001 (trimmed)	Unique search sequence	1,026,685	39,676	3.86
test_4_L001 (trimmed)	Read	15,872,410	7,144,530	45.01
Ctrl_L002 (trimmed)	Unique search sequence	706,656	42,972	6.08
Ctrl_L002 (trimmed)	Read	29,014,651	14,139,137	48.73
PAH_68_L001 (trimmed)	Unique search sequence	905,892	71,262	7.87

Sample	Sequence type	Total	Annotated with record	% of total
PAH_68_L001 (trimmed)	Read	18,758,423	10,932,257	58.28

Sample	Ambiguously annotated	% of total
test_1_L001 (trimmed)	9,928	2.42
test_1_L001 (trimmed)	3,560,935	18.23
test_2_L001 (trimmed)	13,233	2.22
test_2_L001 (trimmed)	4,710,518	18.48
test_3_L001 (trimmed)	11,124	0.63
test_3_L001 (trimmed)	2,057,125	8.23
test_4_L001 (trimmed)	6,861	0.67
test_4_L001 (trimmed)	683,547	4.31
Ctrl_L002 (trimmed)	8,279	1.17
Ctrl_L002 (trimmed)	7,354,362	25.35
PAH_68_L001 (trimmed)	12,074	1.33
PAH_68_L001 (trimmed)	3,362,712	17.93

## 4. Spike-ins

No spike-in information present. The input reports were either not made by the Quantify miRNA tool or spike-ins were disabled.

## 5. Reference sequences

### 5.1 Top 20 mature sequences

Mature	Species	Average %	test_1_L001 (trimmed)	test_2_L001 (trimmed)
hsa-miR-451a	Homo sapiens	16.29	9,197,022	8,096,081
hsa-miR-486-5p	Homo sapiens	11.47	2,595,309	2,492,500
hsa-miR-122-5p	Homo sapiens	6.71	145,192	141,392
hsa-miR-148a-3p	Homo sapiens	2.51	253,489	630,399
hsa-miR-320a-3p	Homo sapiens	1.70	414,575	293,796
hsa-let-7i-5p	Homo sapiens	1.39	190,576	368,331
hsa-miR-151a-3p	Homo sapiens	1.33	202,499	469,513
hsa-miR-26a-5p	Homo sapiens	1.05	245,937	965,302

Mature	Species	Average %	test_1_L001 (trimmed)	test_2_L001 (trimmed)
hsa-miR-92a-3p	Homo sapiens	1.02	255,739	347,586
hsa-miR-99a-5p	Homo sapiens	0.95	205,404	343,632
hsa-miR-30d-5p	Homo sapiens	0.87	124,672	363,809
hsa-miR-126-3p	Homo sapiens	0.85	202,751	564,172
hsa-miR-21-5p	Homo sapiens	0.62	115,736	386,316
hsa-let-7b-5p	Homo sapiens	0.48	97,266	110,462
hsa-let-7a-5p	Homo sapiens	0.36	85,289	185,861
hsa-let-7f-5p	Homo sapiens	0.29	71,405	201,449
hsa-miR-423-5p	Homo sapiens	0.29	60,276	?
hsa-miR-24-3p	Homo sapiens	0.28	71,562	165,580
hsa-miR-128-3p	Homo sapiens	0.24	64,268	193,687
hsa-miR-22-3p	Homo sapiens	0.17	86,480	?

test_3_L001 (trimmed)	test_4_L001 (trimmed)	Ctrl_L002 (trimmed)	PAH_68_L001 (trimmed)
309,800	102,690	1,158,367	2,441,429
1,361,951	458,850	6,822,038	2,608,083
215,321	4,760,623	2,099,270	165,013
335,985	454,164	1,181,309	559,468
577,639	90,663	151,333	655,723
859,421	112,303	127,194	249,639
264,195	47,151	282,243	517,803
97,048	27,808	?	132,950
258,654	86,791	277,612	165,391
162,144	140,916	120,396	255,497
192,984	78,621	141,283	262,387
76,023	16,299	?	275,275
89,559	20,308	?	212,115
248,699	93,097	?	63,648
138,687	45,938	50,028	?
82,235	16,707	48,943	?
116,435	?	50,152	150,288
?	?	?	129,191
?	?	?	68,179
?	?	?	107,025

? is printed when a feature is not among the top 20 features for the given sample.

## 6. Seeds report

## 6.1 Top 20 seeds (reference)

Seeds	Example mature miRNA	Species	Average %	test_1_L001 (trimmed)
GAGTGTG	hsa-miR-574-5p	Homo sapiens	6.50	146,180
AGGTAGT	hsa-miR-196a-5p	Homo sapiens	2.98	524,862
AAGCTGG	hsa-miR-320e	Homo sapiens	1.67	447,595
AGACTGA	hsa-miR-4499	Homo sapiens	1.22	185,325
CTGGTCC	hsa-miR-7152-3p	Homo sapiens	0.81	88,692
TTGGTCC	hsa-miR-133a-3p	Homo sapiens	0.40	43,418
AGGGGCA	hsa-miR-4688	Homo sapiens	0.33	63,370
CACAGTG	hsa-miR-128-3p	Homo sapiens	0.14	54,303
TGGACTT	hsa-miR-5009-5p	Homo sapiens	0.12	10,486
CGGGGCT	hsa-miR-4508	Homo sapiens	0.11	28,118
AGTTCTA	hsa-miR-3168	Homo sapiens	0.10	?
GGCTGGG	hsa-miR-4505	Homo sapiens	0.09	35,819
GAGAGTG	hsa-miR-4693-3p	Homo sapiens	0.09	?
CCCCACT	hsa-miR-4286	Homo sapiens	0.09	70,555
CCTGAGA	hsa-miR-4324	Homo sapiens	0.08	13,376
CGTACCG	hsa-miR-126-3p	Homo sapiens	0.07	16,917
GAGAAGG	hsa-miR-6770-5p	Homo sapiens	0.07	?
GGCACGG	hsa-miR-564	Homo sapiens	0.06	?
GGAGAAG	hsa-miR-4434	Homo sapiens	0.06	?
GCTCGGT	hsa-miR-423-3p	Homo sapiens	0.06	?

test_2_L001 (trimmed)	test_3_L001 (trimmed)	test_4_L001 (trimmed)	Ctrl_L002 (trimmed)	PAH_68_L001 (trimmed)
141,918	210,162	4,571,850	2,086,664	163,644
1,024,668	1,395,250	293,321	347,660	477,627
307,268	555,254	86,859	152,975	605,802
424,886	239,004	45,195	275,748	476,337
155,045	215,946	49,035	151,551	397,916
81,825	268,282	44,081	32,137	73,474
42,521	113,549	12,119	50,871	150,786
97,679	?	?	?	37,803
25,279	?	26,911	55,231	35,655
62,471	47,981	?	?	14,626
?	?	92,482	?	?
18,318	?	?	60,347	19,785
?	?	85,612	?	?
24,461	?	?	?	13,167

test_2_L001 (trimmed)	test_3_L001 (trimmed)	test_4_L001 (trimmed)	Ctrl_L002 (trimmed)	PAH_68_L001 (trimmed)
29,941	23,390	?	19,623	23,061
59,228	?	?	?	24,107
?	62,724	26,056	?	?
?	61,221	20,104	?	?
?	49,693	23,115	?	?
?	42,375	14,299	?	15,333

? is printed when a feature is not among the top 20 features for the given sample.

## 6.2 Top 20 novel seeds

Seeds	Average %	test_1_L001 (trimmed)	test_2_L001 (trimmed)	test_3_L001 (trimmed)
CTGTACT	0.02	3,102	3,552	4,138
TAAACAT	0.01	1,381	2,272	2,949
TTGCACT	0.01	1,605	2,071	2,439
CGACCTC	0.01	844	1,164	2,679
AGAACTG	0.01	741	1,200	3,040
ACCGTTA	0.01	2,553	2,248	?
CCCGTAG	0.01	851	1,192	1,538
CAGTACT	0.01	857	930	1,709
AGTGCAC	0.00	?	778	?
CAGAACT	0.00	?	?	2,092
CAAGTAA	0.00	1,124	2,391	?
CTCGGTC	0.00	605	854	1,780
TGTCCTG	0.00	?	?	2,390
GAGTGAG	0.00	?	?	?
TGTCGGC	0.00	?	?	2,166
GTCGGCT	0.00	?	?	2,132
TGTAGGT	0.00	?	?	1,861
GCTTATC	0.00	654	1,090	?
GATGTCG	0.00	?	?	2,023
ACAGTGA	0.00	724	1,221	?

test_4_L001 (trimmed)	Ctrl_L002 (trimmed)	PAH_68_L001 (trimmed)
2,032	5,910	4,681
1,745	1,489	3,291
1,349	1,845	1,932
1,850	1,837	1,257
1,679	971	1,390

test_4_L001 (trimmed)	Ctrl_L002 (trimmed)	PAH_68_L001 (trimmed)
?	1,494	2,493
1,696	1,254	1,877
?	2,015	2,227
1,328	1,636	1,342
1,174	716	1,065
?	?	1,114
?	?	1,030
1,505	?	?
3,016	?	?
1,325	?	?
1,260	?	?
1,246	?	?
?	?	1,366
1,063	?	?
?	?	1,126

? is printed when a feature is not among the top 20 features for the given sample.