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## Table of contents

1. Summary ........................................................ 3
2. Resources ........................................................ 3
3. Reads ........................................................ 3
4. Small RNAs ........................................................ 4
5. Read count proportions ........................................................ 5
6. Annotations (miRBase) ........................................................ 6

# 1. Summary

| Name | Small RNAs | Annotated | Percentage | Ambiguously annotated |
|---|---|---|---|---|
| RMI-2-OHS-PIT- RNA-SmRNA_S8_clip_R1 Small RNA sample | 1,602,410 | 77,802 | 4.9% | 11,070 |

| Name | Percentage | Reads | Annotated | Percentage |
|---|---|---|---|---|
| RMI-2-OHS-PIT- RNA-SmRNA_S8_clip_R1 Small RNA sample | 0.7% | 18,428,630 | 8,268,916 | 44.9% |

| Name | Ambiguously annotated | Percentage |
|---|---|---|
| RMI-2-OHS-PIT- RNA-SmRNA_S8_clip_R1 Small RNA sample | 2,182,285 | 11.8% |

# 2. Resources

| Resource | Sequences in resource | Sequences found | Percentage found |
|---|---|---|---|
| miRBase (Macaca mulatta) | 619 | 469 | 75.8% |
| miRBase (Macaca nemestrina) | 74 | 10 | 13.5% |
| miRBase (Homo sapiens) | 1,881 | 597 | 31.7% |

# 3. Reads

| Annotation | Count | Percentage | Perfect matches | % |
|---|---|---|---|---|
| Annotated | 8,268,916 | 44.9% | 6,312,179 | 76.3% |
| - with miRBase (Macaca mulatta) | 7,883,719 | 95.3% | 6,023,216 | 76.4% |
| - with miRBase (Macaca nemestrina) | 25,690 | 0.3% | 21,684 | 84.4% |
| - with miRBase (Homo sapiens) | 359,507 | 4.3% | 267,279 | 74.3% |
| Unannotated | 10,159,714 | 55.1% | | |

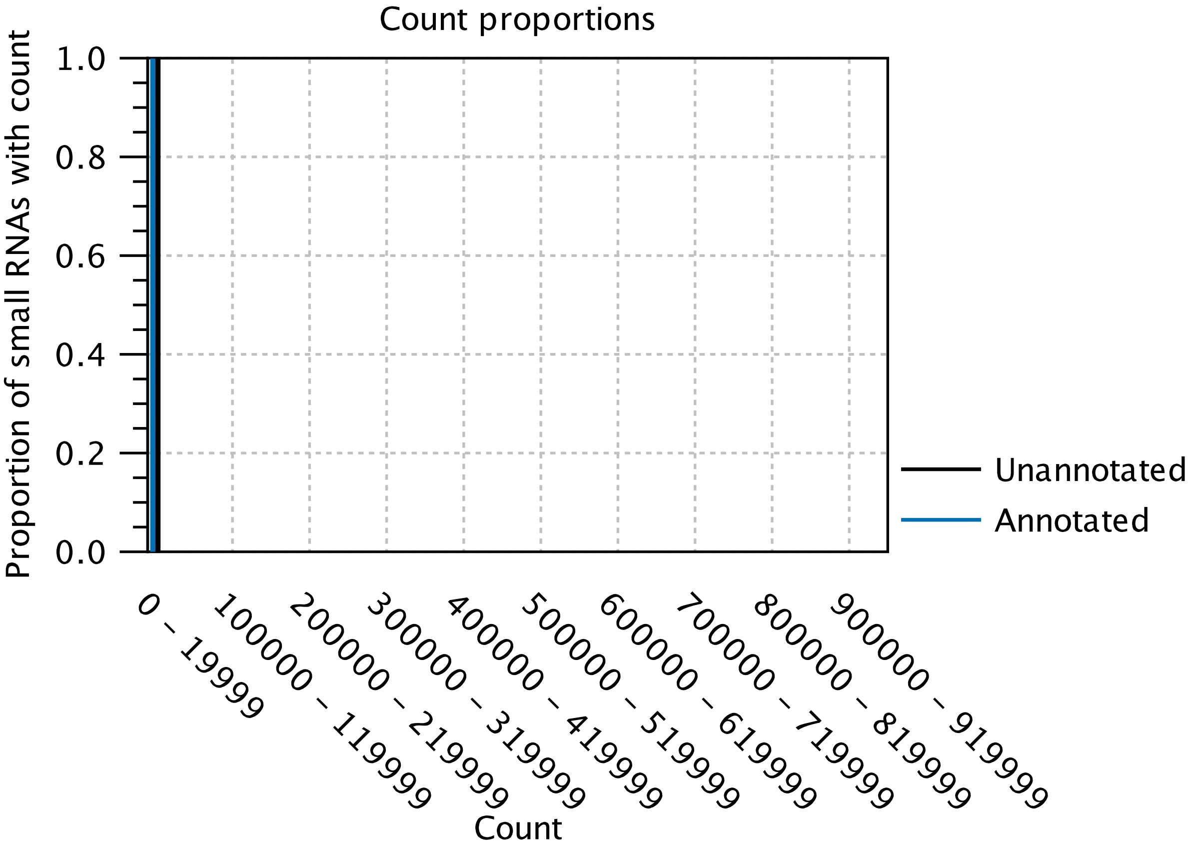
| Annotation | Count | Percentage | Perfect matches | % |
|---|---|---|---|---|
| Total | 18,428,630 | 100.0% | | |

| 1 mismatch | % | 2 mismatches | % |
|---|---|---|---|
| 1,506,675 | 18.2% | 450,062 | 5.4% |
| 1,430,993 | 18.2% | 429,510 | 5.4% |
| 3,325 | 12.9% | 681 | 2.7% |
| 72,357 | 20.1% | 19,871 | 5.5% |

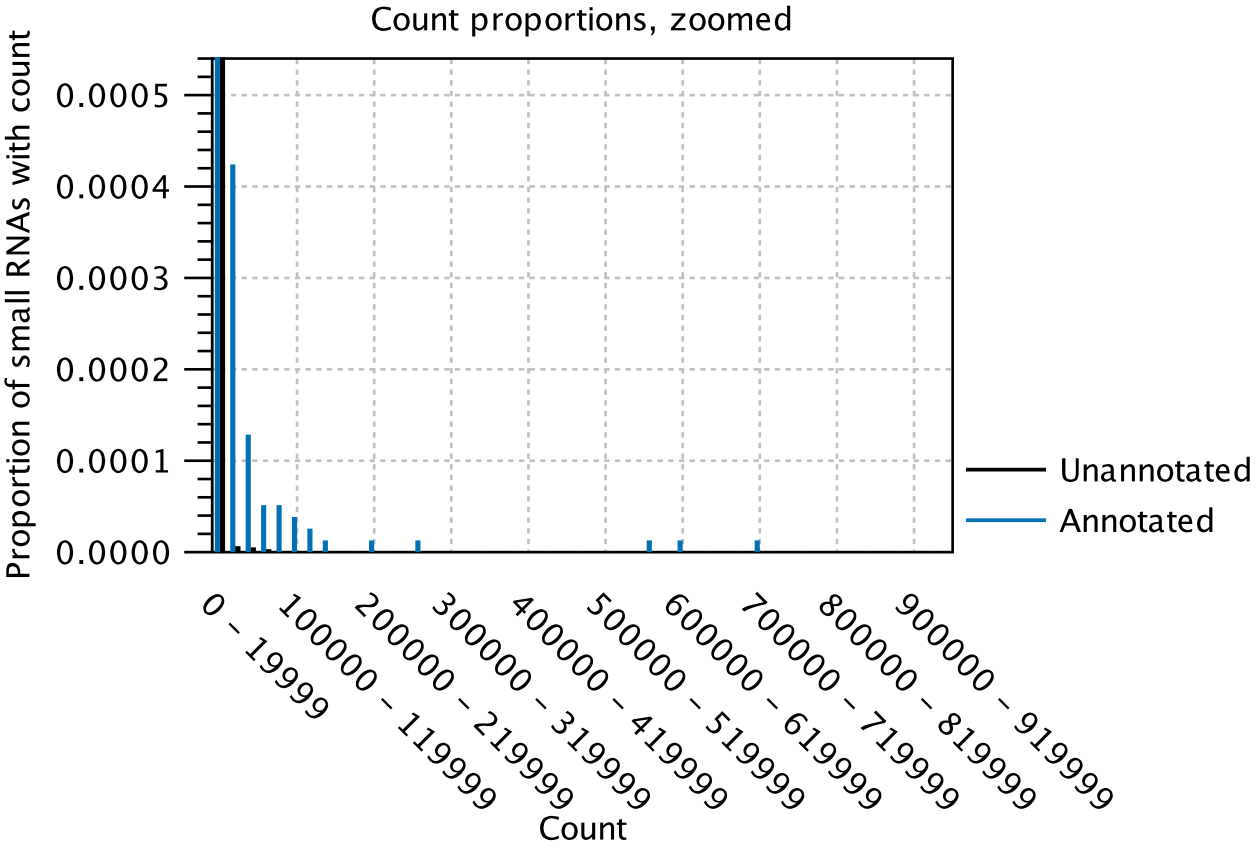
# 4. Small RNAs

| Annotation | Count | Percentage |
|---|---|---|
| Annotated | 77,802 | 4.9% |
| - with miRBase (Macaca mulatta) | 63,955 | 82.2% |
| - with miRBase (Macaca nemestrina) | 524 | 0.7% |
| - with miRBase (Homo sapiens) | 13,323 | 17.1% |
| Unannotated | 1,524,608 | 95.1% |
| Total | 1,602,410 | 100.0% |

## 5. Read count proportions



The histogram shows, for each interval of read counts, the proportion of annotated (respec tively, unannotated) small RNAs with a read count in that interval. Annotated small RNAs may be expected to be associated with higher counts.



Zoomed version of the read count proportions histogram. Note that some bars extend beyond the plotting area.

## 6. Annotations (miRBase)

| Organism | Total | Mature 5' total | Mature 5' exact matches | Mature 5' length variants |
|---|---|---|---|---|
| Macaca mulatta | 7,883,719 | 4,137,577 | 2,024,208 | 1,289,109 |
| Macaca nemestrina | 25,690 | 22,378 | 3,636 | 15,760 |
| Homo sapiens | 359,507 | 143,455 | 103,984 | 18,077 |

| Organism | Mature 5' mutant variants | Non-mature total | Mature 3' | Precursor |
|---|---|---|---|---|
| Macaca mulatta | 824,260 | 3,746,142 | 3,443,251 | 302,891 |
| Macaca nemestrina | 2,982 | 3,312 | 3,064 | 248 |
| Homo sapiens | 21,394 | 216,052 | 189,974 | 26,078 |