**Table S1 Data summary of three small RNA sequencing libraries**

|  |  |  |  |
| --- | --- | --- | --- |
| Type | mock-treated | emu-treated 6h | emu-treated 12h |
| Total reads | 13,792,508 | 12,090,305 | 14,921,792 |
| Clean readsa | 13,324,762 (96.61%) | 11,519,818 (95.28%) | 14,300,790 (95.84%) |
| Number of known miRNAs identified | 585 | 661 | 573 |
| Reads mapped to the genomeb | 8,867,794 (83.75%) | 11,357,549 (90.48%) | 10,177,416 (81.52%) |
| Total reads of known miRNAs | 12,553,020 | 10,588,918 | 12,485,306 |
| a Calculated by reads mapped to the genome/clean reads ×100%. |
| b Calculated by total reads of known miRNAs/reads mapped to the genome ×100%. |

**Table S2 Summary of the differentially expressed miRNAs in** [**emu-treated 6h**](http://www.sciencedirect.com/science/article/pii/S0001706X16307021#tblfn0005)**-library compared to mock-treated library**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| miRNA | mock-treated | emu-treated 6h | log2Fold\_change | *P* value  |
| mmu-miR-21a-5p | 235382 | 16787.13 | 1.2672 | 0 |
| mmu-miR-155-5p | 934.1146 | 4492.764 | 2.2659 | 0 |
| mmu-miR-146a-5p | 5197.685 | 566549.5 | 1.6914 | 0 |
| mmu-miR-146b-5p | 2542.09 | 7644.847 | 1.5885 | 2.74E-280 |
| mmu-miR-221-5p | 1311.454 | 4521.039 | 1.7855 | 5.53E-216 |
| mmu-miR-30a-5p | 4396.999 | 9073.972 | 1.0452 | 2.63E-102 |
| mmu-miR-1981-5p | 322.8264 | 151.5533 | -1.0909 | 1.55E-31 |
| mmu-miR-99b-3p | 94.92261 | 375.4903 | 1.984 | 7.40E-24 |
| mmu-miR-21a-3p | 12.0892 | 96.58696 | 2.9981 | 5.52E-13 |
| mmu-miR-155-3p | 10.96983 | 83.91982 | 2.9355 | 3.47E-11 |
| mmu-miR-125a-5p | 129.5112 | 336.1317 | 1.376 | 4.09E-10 |
| mmu-let-7c-1-3p | 93.57937 | 44.5612 | -1.0704 | 4.64E-10 |
| mmu-miR-146b-3p | 5.372978 | 51.12097 | 3.2501 | 3.22E-08 |
| mmu-miR-378d | 5.820726 | 46.59699 | 3.001 | 5.38E-07 |
| mmu-miR-222-5p | 126.7127 | 295.6421 | 1.2223 | 6.89E-07 |
| mmu-miR-125b-1-3p | 47.79712 | 23.52469 | -1.0227 | 1.34E-05 |
| mmu-miR-125a-3p | 8.619152 | 47.27559 | 2.4555 | 1.43E-05 |
| mmu-miR-146a-3p | 1.343245 | 16.28633 | 3.5999 | 0.00093 |

**Table S3 Summary of the differentially expressed miRNAs in** [**emu-treated 12h**](http://www.sciencedirect.com/science/article/pii/S0001706X16307021#tblfn0005)**-library compared to mock-treated library**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| miRNA | mock-treated | emu-treated 12h | log2Fold\_change | *P* value |
|

|  |
| --- |
| mmu-miR-146b-5p |
| mmu-miR-146a-5p |
| mmu-miR-21a-5p |
| mmu-let-7c-5p |
| mmu-let-7b-5p |
| mmu-miR-374b-5p |
| mmu-miR-374c-3p |
| mmu-miR-155-5p |
| mmu-miR-99b-5p |
| mmu-miR-96-5p |
| mmu-let-7e-5p |
| mmu-miR-339-5p |
| mmu-miR-107-3p |
| mmu-miR-99b-3p |
| mmu-let-7c-1-3p |
| mmu-miR-155-3p |
| mmu-miR-16-2-3p |
| mmu-miR-125a-3p |
| mmu-miR-125a-5p |
| mmu-miR-421-3p |
| mmu-let-7a-1-3p |
| mmu-miR-301a-5p |
| mmu-miR-322-5p |
| mmu-miR-378d |
| mmu-miR-210-5p |
| mmu-miR-935 |
| mmu-miR-146b-3p |
| mmu-miR-210-3p |
| mmu-miR-3473b |
| mmu-miR-301b-5p |
| mmu-miR-21a-3p |
| mmu-miR-1981-5p |

 |

|  |
| --- |
| 2370.905 |
| 4847.671 |
| 219531.3 |
| 24050.96 |
| 4177.219 |
| 2880.477 |
| 2878.18 |
| 871.211 |
| 2480.628 |
| 540.8921 |
| 493.5992 |
| 340.7589 |
| 387.7385 |
| 88.53049 |
| 87.2777 |
| 10.23112 |
| 67.65066 |
| 8.038735 |
| 120.7898 |
| 78.61257 |
| 78.71697 |
| 50.1116 |
| 55.85355 |
| 5.428756 |
| 5.01116 |
| 35.91331 |
| 5.01116 |
| 58.56793 |
| 11.48391 |
| 19.20945 |
| 11.27511 |
| 16.59947 |

 |

|  |
| --- |
| 10928.3 |
| 18010.74 |
| 698935.3 |
| 11550.98 |
| 1871.668 |
| 1013.87 |
| 1011.664 |
| 4492.204 |
| 7452.369 |
| 262.3946 |
| 1728.234 |
| 127.787 |
| 169.1121 |
| 446.5524 |
| 30.09113 |
| 99.90255 |
| 22.46804 |
| 81.84787 |
| 367.513 |
| 37.313 |
| 37.71421 |
| 20.86318 |
| 27.08202 |
| 51.75674 |
| 45.3373 |
| 17.25225 |
| 39.31907 |
| 169.3128 |
| 57.37375 |
| 7.021263 |
| 50.7537 |
| 6.820656 |

 |

|  |
| --- |
| 2.2046 |
| 1.8935 |
| 1.6707 |
| -1.0581 |
| -1.1582 |
| -1.5064 |
| -1.5084 |
| 2.3663 |
| 1.587 |
| -1.0436 |
| 1.8079 |
| -1.415 |
| -1.1971 |
| 2.3346 |
| -1.5363 |
| 3.2876 |
| -1.5902 |
| 3.3479 |
| 1.6053 |
| -1.0751 |
| -1.0616 |
| -1.2642 |
| -1.0443 |
| 3.2531 |
| 3.1775 |
| -1.0577 |
| 2.972 |
| 1.5315 |
| 2.3208 |
| -1.452 |
| 2.1704 |
| -1.2832 |

 |

|  |
| --- |
| 0 |
| 0 |
| 0 |
| 0 |
| 0 |
| 0 |
| 0 |
| 1.06E-297 |
| 2.13E-184 |
| 1.18E-63 |
| 6.73E-63 |
| 3.38E-52 |
| 1.45E-51 |
| 2.14E-30 |
| 1.65E-15 |
| 3.49E-13 |
| 1.12E-12 |
| 2.60E-11 |
| 6.59E-11 |
| 8.01E-11 |
| 9.78E-11 |
| 2.74E-08 |
| 6.20E-08 |
| 2.03E-07 |
| 1.74E-06 |
| 1.28E-05 |
| 2.32E-05 |
| 3.75E-05 |
| 4.47E-05 |
| 0.000263 |
| 0.000351 |
| 0.001288 |

 |

**Table S4 KEGG enrichment analysis of validated targets of differentially expressed miRNAs. According to *P* value, the top 20 significantly enriched pathway terms were shown in the** [**emu-treated 6h**](http://www.sciencedirect.com/science/article/pii/S0001706X16307021#tblfn0005)**- (A) and emu-treated 12h-libraries (B), respectively.**

|  |  |
| --- | --- |
| **emu-treated 6h vs mock-treated** | **emu-treated 12h vs mock-treated** |
| **Term** | **Number** | ***p* Value** | **Term** | **Number** | ***p* Value** |
| TNF signaling pathway | 28 | 0.000 | TNF signaling pathway | 29 | 0.000  |
| NF-kappa B signaling pathway | 25 | 0.000 | NF-kappa B signaling pathway | 24 | 0.001  |
| Osteoclast differentiation | 28 | 0.000 | Osteoclast differentiation | 35 | 0.008  |
| Tuberculosis | 29 | 0.013 | Cell cycle | 28 | 0.008  |
| Leishmaniasis | 15 | 0.018 | Leishmaniasis | 19 | 0.008  |
| Rheumatoid arthritis | 17 | 0.019 | B cell receptor signaling pathway | 19 | 0.012  |
| p53 signaling pathway | 15 | 0.019 | Tuberculosis | 34 | 0.012  |
| Hematopoietic cell lineage | 16 | 0.049 | Chagas disease  | 22 | 0.037  |
| Malaria | 11 | 0.049 | p53 signaling pathway | 16 | 0.061  |
| B cell receptor signaling pathway | 14 | 0.049 | Rheumatoid arthritis | 18 | 0.061  |
| Cell cycle | 20 | 0.049 | HIF-1 signaling pathway | 22 | 0.061  |
| Apoptosis | 15 | 0.049 | Small cell lung cancer | 18 | 0.066  |
| Hepatitis B | 22 | 0.049 | NOD-like receptor signaling pathway | 14 | 0.066  |
| Legionellosis | 12 | 0.049 | Pancreatic cancer | 15 | 0.070  |
| NOD-like receptor signaling pathway | 12 | 0.049 | Mismatch repair | 8 | 0.070  |
| Toll-like receptor signaling pathway | 17 | 0.051 | Pertussis | 16 | 0.073  |
| HIF-1 signaling pathway | 18 | 0.052 | Apoptosis | 17 | 0.077  |
| Viral carcinogenesis | 30 | 0.057 | Proteoglycans in cancer | 33 | 0.077  |
| Influenza A | 24 | 0.057 | FoxO signaling pathway | 24 | 0.077  |
| Transcriptional misregulation in cancer | 24 | 0.089 | Acute myeloid leukemia | 13 | 0.086  |



Fig. S1Correlation between miRNA and their target mRNA expression levels was represented by a logarithmic curve. X represents the relative expression of miRNA and Y represents the relative expression of the corresponding target mRNA.