**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 | log2  Fold\_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 | log2  Fold\_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.