**Table S1. Overall profiles of transcriptome sequencing.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample name** | **Raw reads** | **Clean reads** | **Clean bases** | **Error rate (%)** | **Q20 (%)** | **Q30 (%)** | **GC content(%)** |
| **RGD+\_1** | 48981606 | 47440128 | 7.12G | 0.02 | 98.72 | 95.79 | 39.3 |
| **RGD+\_2** | 51740698 | 50692828 | 7.6G | 0.03 | 96.72 | 91.49 | 39 |
| **RGD+\_3** | 56969438 | 55637472 | 8.35G | 0.03 | 96.86 | 91.68 | 37.06 |
| **RGD+(+)\_1** | 53922048 | 52990832 | 7.95G | 0.03 | 96.76 | 91.66 | 41.25 |
| **RGD+(+)\_2** | 57428746 | 56046684 | 8.41G | 0.03 | 96.63 | 91.4 | 41.25 |
| **RGD+(+)\_3** | 49733092 | 48655340 | 7.3G | 0.03 | 96.43 | 91.02 | 41.23 |
| **RGD-\_1** | 50683788 | 49723784 | 7.46G | 0.03 | 97.24 | 92.49 | 40.99 |
| **RGD-\_2** | 54829856 | 53740516 | 8.06G | 0.03 | 97.29 | 92.64 | 41.36 |
| **RGD-\_3** | 51354490 | 50506374 | 7.58G | 0.03 | 97.5 | 93.08 | 41.35 |

Note: RGD+ represents the resting RGD+ hemocytes; RGD- represents the resting RGD- hemocytes; RGD+(+) represents the activated RGD+ hemocytes.