**Table S2. Mapping of transcriptome sequencing reads.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample\_name** | **Total reads** | **Total****mapped** | **Multiple mapped** | **Uniquely****mapped** |
| **RGD+\_1** | 47440128 | 38377287(80.9%) | 3173709 (6.69%) | 35203578(74.21%) |
| **RGD+\_2** | 50692828 | 40137002 (79.18%) | 3198800 (6.31%) | 36938202(72.87%) |
| **RGD+\_3** | 55637472 | 34043741 (61.19%) | 2254946 (4.05%) | 31788795(57.14%) |
| **RGD+(+)\_1** | 52990832 | 37715459 (71.17%) | 2470539 (4.66%) | 35244920(66.51%) |
| **RGD+(+)\_2** | 56046684 | 40371632 (72.03%) | 2669564 (4.76%) | 37702068(67.27%) |
| **RGD+(+)\_3** | 48655340 | 34636902 (71.19%) | 2275437 (4.68%) | 32361465(66.51%) |
| **RGD-\_1** | 49723784 | 38251337 (76.93%) | 2536607 (5.1%) | 35714730(71.83%) |
| **RGD-\_2** | 53740516 | 41508266 (77.24%) | 2824793 (5.26%) | 38683473(71.98%) |
| **RGD-\_3** | 50506374 | 39138132 (77.49%) | 2632295 (5.21%) | 36505837(72.28%) |

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