**Table S1. Sequencing statistics for *Hydra viridissima* A99**

A. Genome sequencing

|  |  |  |  |
| --- | --- | --- | --- |
| **Method** | **Average insert size (kbp)** | **Number of reads** | **Total sequence bases (bp)** |
| paired-end | 0.54 | 22,898,708 | 7,070,567,877 |
| mate-pair | 3.2 | 16,396,858 | 4,765,376,261 |
| mate-pair | 4.6 | 15,675,862 | 4,769,208,860 |
| mate-pair | 7.8 | 11,955,526 | 3,669,733,399 |
| mate-pair | 15.2 | 11,583,414 | 3,551,259,973 |
| 　 | **(Total)** | 78,510,368 | 23,826,146,370 |

B. RNA-sequencing

|  |  |  |  |
| --- | --- | --- | --- |
| **Method** | **Sample** | **Number of reads** | **Total sequence bases (bp)** |
| paired-end | Symbiotic hydra in the light | 82,359,812 | 11,036,214,808 |
| Symbiotic hydra in the dark | 85,506,198 | 11,457,830,532 |
| Symbiotic hydra treated with DMCU | 77,803,532 | 10,425,673,288 |
| Symbiotic hydra treated with antibiotics | 81,479,328 | 10,918,229,952 |
| Aposymbiotic hydra in the light | 93,821,528 | 12,572,084,752 |
| Aposymbiotic hydra in the dark | 81,565,856 | 10,929,824,704 |
|  | **(Total)** | 502,536,254 | 67,339,858,036 |