**Table S1. Statistics of Illumina short reads coverage**

|  |  |
| --- | --- |
| Genome assembly | Parameter |
| Average sequencing depth | 87.11 |
| Mapping rate (%) | 93.93 |
| Coverage (%) | 88.90 |
| Coverage at least 4X (%) | 86.67 |
| Coverage at least 10X (%) | 85.18 |
| Coverage at least 20X (%) | 83.65 |

**Table S2. Summary genomic completeness by CEGMA.**

|  |  |  |
| --- | --- | --- |
| Number of core eukaryotic genes | Complete | Complete and Partial |
| Number | Percentage (%) | Number | Percentage |
| 248 | 198 | 79.84 | 227 | 91.53 |

**Table S3. Summary genomic completeness by BUSCO.**

|  |  |  |  |
| --- | --- | --- | --- |
| Number of core metazoan genes | Complete | Fragmented | Missing |
| single copy | duplicated |
| 978 | 832 | 36 | 40 | 70 |

**Table S4. Statistics of the repetitive sequences**

|  |  |  |
| --- | --- | --- |
| Annotation Method | Repeat Size(bp) | % ofGenome |
| Trf | 347,649,222 | 26.10 |
| Repeatmasker | 486,560,380 | 36.53 |
| Proteinmask | 43,792,830 | 3.29 |
| Total | 675,404,889 | 50.71 |

**Table S5. Summary of the gene prediction results**

|  |  |  |  |
| --- | --- | --- | --- |
| Method | Software | Species | Gene number |
| *Ab initio* | Augustus | - | 72,557 |
| GlimmerHMM | - | 231,927 |
| Genscan | - | 53,981 |
| GeneID | - | 35,803 |
| SNAP | - | 127,520 |
| Homology-based | GeMoMa | *Branchiostoma floridae* | 39,275 |
| *Caenorhabditis elegans* | 5,479 |
| *Crassostrea gigas* | 27,530 |
| *Ciona intestinalis* | 10,680 |
| *Drosophila melanogaster* | 5,741 |
| *Helobdella robusta* | 27,467 |
| *Homo sapiens* | 12,495 |
| *Lottia gigantea* | 61,176 |
| *Octopus bimaculoides* | 18,868 |
| *Patinopecten yessoensis* | 41,949 |
| *Strongylocentrotus purpuratus* | 20,929 |
| RNA-seq | Full-length seq | - | 75,225 |
| Cufflinks |  | 69,612 |
| PASA | - | 30,235 |
| Integration | EVM | - | 40,123 |
| PASA-update |  | 26,270 |

**Table S6. Statistics of gene annotation to different databases.**

|  |  |  |
| --- | --- | --- |
| Annotation database | Number of annotated genes | Percentage |
| NR | 23,844 | 90.88 |
| Swiss-Prot | 18,131 | 69.1 |
| KEGG | 18,928 | 72.14 |
| InterProScan | 25,475 | 97.1 |
| Pfam | 15,391 | 58.66 |
| GO | 22,956 | 87.49 |
| Total | 26,140 | 99.50 |

**Table S7. Summary of the non-coding RNA annotation**

|  |  |  |  |
| --- | --- | --- | --- |
| Type | Copy | Average length (bp) | Total length (bp) |
| miRNA | 968 | 102.75 | 99,462 |
| tRNA | 3354 | 74.58 | 250,141 |
| 18S rRNA | 516 | 321 | 165,636 |
| 28S rRNA | 65 | 115.95 | 7,537 |
| 5S rRNA | 241 | 90.95 | 21,919 |
| CD-box snRNA | 67 | 88.73 | 5,945 |
| HACA-box snRNA | 37 | 183.56 | 6,792 |
| Splicing snRNA | 193 | 147.58 | 28,483 |

**Table S8. Summary of Illumina short-read transcriptome sequencing.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sample type | Sample name | Raw reads | Clean reads | Clean bases (Gb) | Total mapped | Mapping rate |
| Development stages | Egg | 43,935,046  | 42,881,284  | 6.43 | 24,187,623  | 56.41% |
|  | Four cells | 43,085,794  | 42,600,768  | 6.39 | 20,200,370  | 47.42% |
|  | Blastulae | 47,526,530  | 46,718,170  | 7.01 | 25,396,271  | 54.36% |
|  | Gastrulae | 43,935,046  | 42,881,284  | 6.43 | 24,187,626  | 56.41% |
|  | Trochophore | 43,935,046  | 42,881,284  | 6.43 | 24,187,619  | 56.41% |
|  | D-stage larvae | 36,806,136  | 36,163,274  | 5.42 | 6,791,195  | 18.78% |
|  | Umbo larvae | 43,492,564  | 43,044,208  | 6.46 | 24,011,371  | 55.78% |
| 　 | Juvenile | 44,296,144  | 43,739,942  | 6.56 | 25,315,001  | 57.88% |
| Adult tissues | Gill | 58,314,622  | 52,571,902  | 5.31 | 42,408,674  | 80.67% |
|  | Foot | 57,279,662  | 51,774,716  | 5.23 | 43,445,527  | 83.91% |
|  | Adductor muscle | 50,833,380  | 45,661,534  |  4.61 | 40,224,430  | 88.09% |
|  | Digestive gland | 50,796,292  | 45,624,660  | 4.61 | 36,325,819  | 79.62% |
|  | Mantle | 54,234,040  | 48,455,080  | 4.89 | 38,728,162  | 79.93% |
|  | Siphon | 54,593,774  | 49,368,016  | 4.99 | 41,079,077  | 83.21% |
|  | Ovary01 | 34,903,986  | 34,468,792  | 4.33 | 25,108,177  | 72.84% |
|  | Ovary02 | 36,188,356  | 35,741,542  | 4.50 | 25,149,497  | 70.36% |
|  | Ovary03 | 36,718,496  | 36,258,132  | 4.56 | 25,481,341  | 70.28% |
|  | Testis01 | 32,433,246  | 32,024,558  | 4.03 | 21,917,877  | 68.44% |
|  | Testis02 | 28,685,592  | 28,336,062  | 3.56 | 20,012,672  | 70.63% |
| 　 | Testis03 | 28,626,282  | 28,264,944  | 3.56 | 19,934,211  | 70.53% |
| Salt stress | N\_salt01 | 40,034,734  | 39,581,252  | 5.83 | 27,870,270  | 70.41% |
|  | N\_salt02 | 44,533,952  | 44,056,944  | 6.48 | 29,653,739  | 67.31% |
|  | N\_salt03 | 44,718,238  | 44,227,004  | 6.50 | 30,710,518  | 69.44% |
|  | H\_salt01 | 40,847,898  | 40,374,444  | 5.92 | 27,098,825  | 67.12% |
|  | H\_salt02 | 39,929,882  | 39,491,552  | 5.80 | 27,423,141  | 69.44% |
|  | H\_salt03 | 39,319,852  | 38,959,456  | 5.71 | 26,790,941  | 68.77% |
|  | L\_salt01 | 40,036,290  | 39,619,590  | 5.82 | 27,108,102  | 68.42% |
|  | L\_salt02 | 43,389,812  | 42,822,802  | 6.31 | 29,175,853  | 68.13% |
| 　 | L\_salt03 | 49,465,626  | 48,917,228  | 7.22 | 33,534,046  | 68.55% |
| Ammonia nitrogen stress | CK\_gill01 | 46,352,328  | 44,879,776  | 6.72 | 32,665,206  | 72.78% |
|  | CK\_gill02 | 41,173,924  | 39,806,810  | 5.96 | 28,375,170  | 71.28% |
|  | CK\_gill03 | 53,350,356  | 52,349,692  | 7.8 | 38,794,212  | 74.11% |
|  | CK\_liver01 | 48,457,610  | 47,321,004  | 7.07 | 34,385,645  | 72.66% |
|  | CK\_liver02 | 51,489,774  | 50,275,468  | 7.52 | 35,885,565  | 71.38% |
|  | CK\_liver03 | 47,243,064  | 46,163,320  | 6.91 | 32,758,689  | 70.96% |
|  | TG\_gill01 | 49,728,640  | 48,603,280  | 7.27 | 34,880,190  | 71.77% |
|  | TG\_gill02 | 45,918,180  | 44,886,696  | 6.72 | 33,194,601  | 73.95% |
|  | TG\_gill03 | 55,087,602  | 53,844,418  | 8.06 | 38,983,895  | 72.40% |
|  | TG\_liver01 | 48,314,008  | 47,190,368  | 7.04 | 33,925,631  | 71.89% |
|  | TG\_liver02 | 48,330,144  | 47,191,178  | 7.06 | 33,663,638  | 71.33% |
|  | TG\_liver03 | 48,063,138  | 46,949,294  | 7.03 | 33,861,230  | 72.12% |