Summary of Quality Control

Short read quality assessment was performed by Genome Analyzer on RNA-seq samples at the different time points. Most sample had nearly 70 milion total reads with 65%-82% mapping ratio after filtering. Data from the 120h\_antenna\_2.sorted.bam were not analyzed further. For other samples, GC content, read distribution and read quality were all sufficient further computational analysis.

|  |  |  |  |
| --- | --- | --- | --- |
| name | readsBeforeMap | readsAfterMap | mapRatio |
| 120h\_antenna\_1.sorted.bam | 53823482.0 | 40021313 | 0.74356603313 |
| 120h\_antenna\_2.sorted.bam | 7387554.0 | 1028296 | 0.139193026542 |
| 120h\_eye.sorted.bam | 70190990.0 | 54296487 | 0.77355351449 |
| 120h\_eye\_antenna.sorted.bam | 64739818.0 | 53447516 | 0.82557408487 |
| 120h\_whole\_animal.sorted.bam | 71826692.0 | 54025446 | 0.752163917002 |
| 72h\_eye\_antenna.sorted.bam | 87111417.0 | 64575504 | 0.741297825519 |
| 72h\_eye\_antenna\_mouthpart.sorted.bam | 67915869.0 | 48769280 | 0.718083722083 |
| 72h\_whole\_animal.sorted.bam | 78565136.0 | 56483233 | 0.71893508846 |
| 96h\_antenna.sorted.bam | 70276795.0 | 53100557 | 0.755591614558 |
| 96h\_eye.sorted.bam | 75090827.0 | 59127681 | 0.787415498833 |
| 96h\_eye\_antenna.sorted.bam | 58089605.0 | 46926164 | 0.807823775011 |
| 96h\_whole\_animal.sorted.bam | 78499741.0 | 51353464 | 0.654186413176 |