**Supplemental Table S1 Illumina read alignment to H1706 reference assembly and genome coverage metrics.** *S. gal = S. galapagense*; *S. pim = S. pimpinellifolium.*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | ***S. lycopersicum*** | | **Wild species** | |
| **Reference-guided assembly** | **H1706** | **YP-1** | ***S. gal*** | ***S. pim*** |
| filtered reads in millions | 462.7 | 420.3 | 363.9 | 281.5 |
| mapped reads *(%mapped)* | 426.1 *(92.1%)* | 393.1 *(93.5%)* | 324.7 *(89.0%)* | 247.7 *(88.0%)* |
| coverage depth1 | 39.3x | 45x | 32x | 25x |
| coverage of tomato gen | 99.2% | 99.3% 2 | 95.4% 2 | 95.0% 2 |
| no of gaps *(total size in mb)* | 76,276  *(5.9)* | 51,980  *(5.4)* 2 | 227,699 *(36.1)*2 | 209,919 *(38.9)* 2 |
| no of gaps > 500 bp | 1,660 | 1,926 2 | 10,751 2 | 14,396 2 |

1 after removal of duplicate reads and reads with mapping quality less than 30.

2 gaps in Heinz assembly (“N”) removed from calculation.