**Table S3. Data from 454 Sequencing Runs Newbler Assembler**

|  |  |
| --- | --- |
| Reads | |
| Total # of reads | 826,176 |
| Total # of clean reads | 514,412 (62.3%) |
| Total # of bases | 95,486,897 |
| Total # of clean bases | 49,857,586 (52.2%) |
| # of fully assembled reads | 70,828 |
| # of partially assembled reads | 64,823 |
| # of singletons | 276,760 |
| # of repeat reads | 93,504 |
| # of outlier reads | 8,497 |
| All Contigs | |
| # of all contigs | 16,895 |
| # of bases covered | 4,720,747 |
| Avg. contig size | 279.4 |
| Min. contig size | 93 |
| Max contig size | 2,827 |
| Large Contigs | |
| # of large contigs | 1,902 |
| # of bases covered | 1,557,286 |
| Avg. large contig size | 818 |
| Min. large contig size | 500 |
| Max. large contig size | 2,827 |