**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  |