Table 3. Quality distribution of a total of the 17,490,205 sequenced bp in the database

| Phred score | Error probability | Accuracy, % | No. of bp in database | Percentage of total |
|-------------|-------------------|-------------|-----------------------|---------------------|
| 1-10        | 1 in 10           | 90          | 377,214               | 2.1                 |
| 11-20       | 1 in 100          | 99          | 1,108,410             | 6.3                 |
| 21-30       | 1 in 1,000        | 99.9        | 1,704,845             | 9.6                 |
| 31-40       | 1 in 10,000       | 99.99       | 2,992,367             | 11.6                |
| 41-50       | 1 in 100,000      | 99.999      | 5,171,875             | 30.4                |
| >51         | 1 in 1,000,000    | 99.9999     | 6,135,494             | 40.1                |
| Total       |                   |             | 17,490,205            | 100                 |

Color-coding is the same as quality graphs in the database (Fig. 12*E*). Only 2.1% of the sequences are low in quality (scores 1-10), and these passed trimming because they were within stretches of regions of high quality or were at the 5' and 3' primer ends, where trimming would have shortened the zebra finch-specific sequences.