|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **Avg. read  length** | **total reads** | **Mapped reads1** | **% endogenous** | **final  % clonality** | **Avg. depth of  coverage** |
| D01 | 59.81 | 134225056 | 70269208 | 51.6% | 8.6% | 3.26 |
| D02 | 59.69 | 85951800 | 46100496 | 54.0% | 6.8% | 2.17 |
| D03 | 56.38 | 99242513 | 52731138 | 53.2% | 7.5% | 2.33 |
| D04 | 72.97 | 102941745 | 61754874 | 58.8% | 6.1% | 3.58 |
| D05 | 58.80 | 127746794 | 65461446 | 50.2% | 8.9% | 2.97 |
| D06 | 68.34 | 130927829 | 76908293 | 56.5% | 8.2% | 4.09 |
| D07 | 59.63 | 108202859 | 57289986 | 52.7% | 7.3% | 2.68 |
| D08 | 60.27 | 142816603 | 74810241 | 51.0% | 7.8% | 3.52 |
| D09 | 69.11 | 109176502 | 62749114 | 55.4% | 7.6% | 3.39 |
| D10 | 72.07 | 278338659 | 156096544 | 52.0% | 11.2% | 8.47 |
| D11 | 62.77 | 95764414 | 50811776 | 53.0% | 6.9% | 2.51 |
| D12 | 53.58 | 91045649 | 43588302 | 46.5% | 11.3% | 1.75 |
| D13 | 51.41 | 155280278 | 74151486 | 48.7% | 8.5% | 2.96 |
| D14 | 52.26 | 141127547 | 68026962 | 49.7% | 7.1% | 2.80 |
| D15 | 50.54 | 107528836 | 49753642 | 46.0% | 8.4% | 1.95 |
| D16 | 51.44 | 138748840 | 61670366 | 44.9% | 9.4% | 2.43 |
| D17 | 44.35 | 176039417 | 70208931 | 22.4% | 53.6% | 1.22 |
| D18 | 64.02 | 106838495 | 54759839 | 49.2% | 8.4% | 2.72 |
| D19 | 61.86 | 120278923 | 68268801 | 54.5% | 9.6% | 3.24 |
| D20 | 68.92 | 238271223 | 136966371 | 53.6% | 10.4% | 7.17 |
| D21 | 51.72 | 218486584 | 112063256 | 50.1% | 12.4% | 4.30 |
| D22 | 60.07 | 129704818 | 71338711 | 52.8% | 8.3% | 3.33 |
| D23 | 61.82 | 133771693 | 63202688 | 46.2% | 8.1% | 3.04 |
| D24 | 81.09 | 120502346 | 69954485 | 55.3% | 6.6% | 4.49 |
| D25 | 80.13 | 126946626 | 74271614 | 56.1% | 6.1% | 4.74 |
| D26 | 80.20 | 126355430 | 71656043 | 54.2% | 6.5% | 4.56 |

Supplementary Table 2. Sequencing data generated for all the *Streptopelia* samples used for this study. 1 Final reads used in the analyses after removing PCR duplicates and quality filtering.