|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **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.