Supplementary Material

The value of reference genomes in the conservation of threatened species

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Table S1. Comparison of model and non-model mammalian/marsupial reference genomes to the G10K and EBP minimum reference genome quality standards. Green: metrics matching the G10K standards, Yellow: metrics matching the EBP Phase I standards, RED: metrics matching the EBP Phase II standards, Grey: metrics which fall below all VGP and EBP standards.

Reference Genome Minimum Quality Standards

| Project | Phase | Contig N50 | Scaffold N50 | % Genome assembled into chromosomes | Inter-chromosomal rearrangements validated by >2 data sources | QV Cut-off Score* | Genome Quality Metric [^] |
|---------|-------|------------|--------------|-------------------------------------|---|----------------------|------------------------------------|
| G10K | - | 1Mb | 10Mb | >90% | Yes | 40 | 3.4.2.QV40 |
| EBP | 1 | 0.1Mb | 1Mb | >90% | Yes | 40 | 2.3.2QV40 |
| EBP | II | 0.01Mb | 0.1Mb | >90% | No | 40 | 1.2.1QV40 |

Current Mammalian/Marsupial Reference Genome Metrics

| Species | Genome | Contig (Mb) | N50 | Scaffold N50 | % Genome assembled into chromosomes | rearrangements validated by >2 data sources | QV Cut-off Score | Genome Quality | Date Published to |
|-----------------|----------------------------|----------------|-----|--------------|-------------------------------------|---|---------------------|----------------------|-------------------|
| Human | GRCh38.p13 | 57.9 | | 67.8 | 99.86% | Yes | ND | 4.4.2QV? | 28/2/19 |
| Mouse | GRCm38.p6 | 32.8 | | 54.5 | 99.97% | Yes | ND | 4.4.2QV? | 15/9/17 |
| Dog Koala | CanFam3.1 phaCin_unsw_v4.1 | 0.267 | | 45.9 | 96.54% | Yes | ND ND | 2.4.2QV? 4.4.0QV? | 2/11/11 |
| Tasmanian Devil | Devil_ref v7.0 | 0.0201 | | 1.85 | 99.96% | Yes | 30 | 1.3.2QV30 | 17/2/11 |

^{*} ND = Not Determined.

[^] The genome quality metric summarises all of the minimum standards from the previous columns whereby the first three numbers are the exponents of the N50 contig, N50 scaffold and level of chromosomal assembly and QV represents the minimum base-call quality error.