| **Metric (field name)** | **Pass rule** |
| --- | --- |
| **CheckM completeness** (Completeness) | **≥ 90 %** |
| **CheckM contamination** (Contamination) | **≤ 5 %** |
| **Depth of coverage** (qc\_final\_coverage) | **≥ 20** |
| **Genome size** (assembler\_total\_contig\_length) | *Within species band* (see table 2) |
| **GC content** (GC\_Content \* 100) | ± 2 % of species median |
| **Contig count** (assembler\_total\_contig) | **< 500** |
| **Mean read Q-score** (qc\_final\_qual\_mean) | **≥ 30** |
| **N50** (assembler\_n50\_contig\_length) | **> 20 kb** (short-read); aim for > 100 kb if hybrid/ONT |

\*\*not included until further advise

|  |  |
| --- | --- |
|  |  |
| **L50** (assembler\_l50\_contig\_count) | **≤ 50** |
| **Largest contig** (assembler\_max\_contig\_length) | **> 200 kb** |
| **%N / non-ACGT bases** (assembler\_contig\_percent\_n) | **< 1 %** |
| **Bases in contigs > 10 kb** (assembler\_percent\_contigs\_greater\_10k) | **≥ 90 %** |

Table 2 – genome-size & GC qualifiers (use ±10 % for size, ±2 % for GC)

| **Organism** | **Org Code** | **Typical size (Mb)** | **GC %** |
| --- | --- | --- | --- |
| *Acinetobacter baumannii* | aba | **3.4 – 4.2** | **≈ 39 %** |
| *Pseudomonas aeruginosa* | pae | **5.5 – 7.0** | **65 – 67 %** |
| *Klebsiella pneumoniae* | kpn | **5.0 – 5.7** | **≈ 57 %** |
| *Escherichia coli* | eco | **4.5 – 5.5** | **≈ 51 %** |
| *Enterococcus faecalis* | efa | **2.8 – 3.2** | **≈ 37 %** |
| *Enterococcus faecium* | efm | **2.6 – 3.1** | **≈ 38 %** |
| *Staphylococcus aureus* | sau | **2.7 – 3.0** | **≈ 33 %** |
| *Streptococcus pneumoniae* | spn | **2.0 – 2.3** | **≈ 40 %** |
| *Haemophilus influenzae* | hin | **1.7 – 1.9** | **≈ 38 %** |
| *Neisseria gonorrhoeae* | ngo | **2.1 – 2.3** | **≈ 52 %** |
| *Salmonella enterica* (non-Typhi) | sal | **4.5 – 5.3** | **≈ 52 %** |
| *Salmonella Typhi* | sat | **4.6 – 4.8** | **≈ 52 %** |