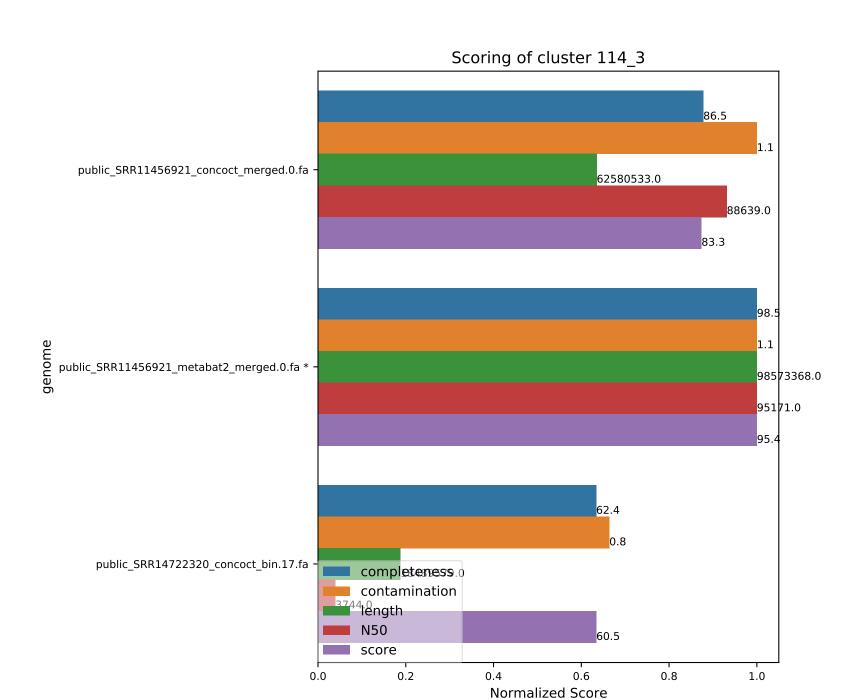
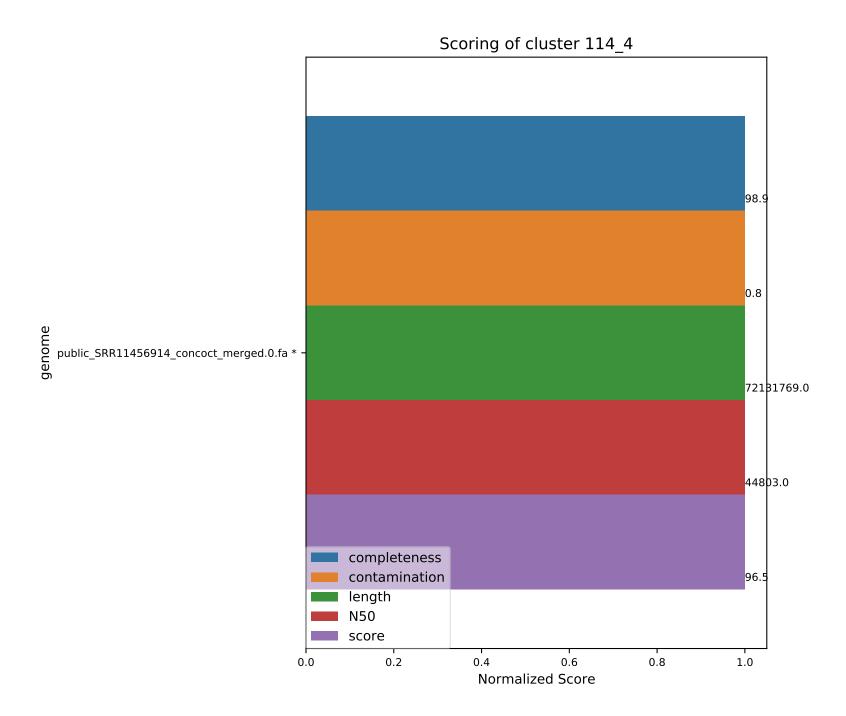
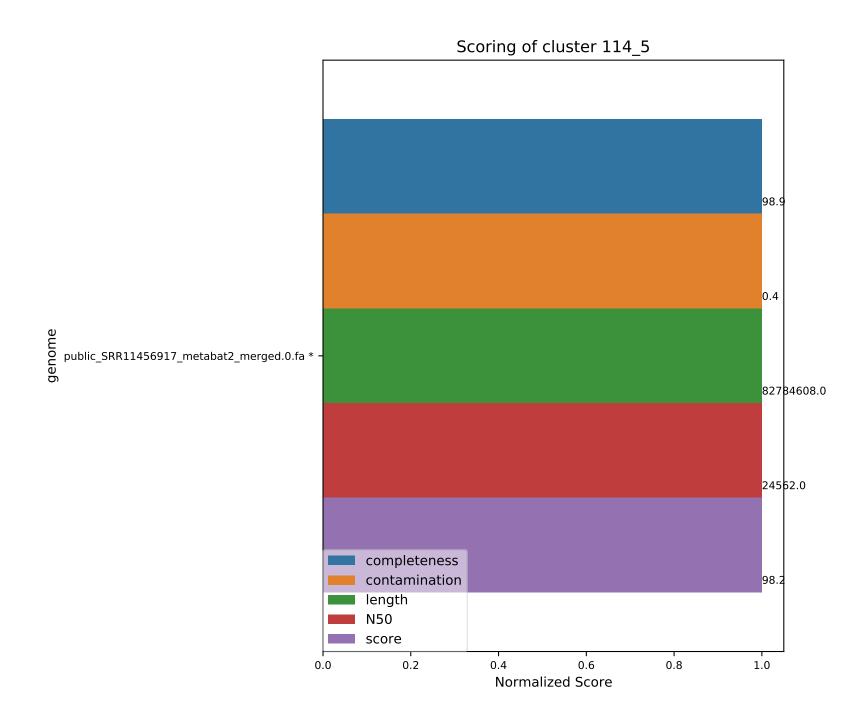


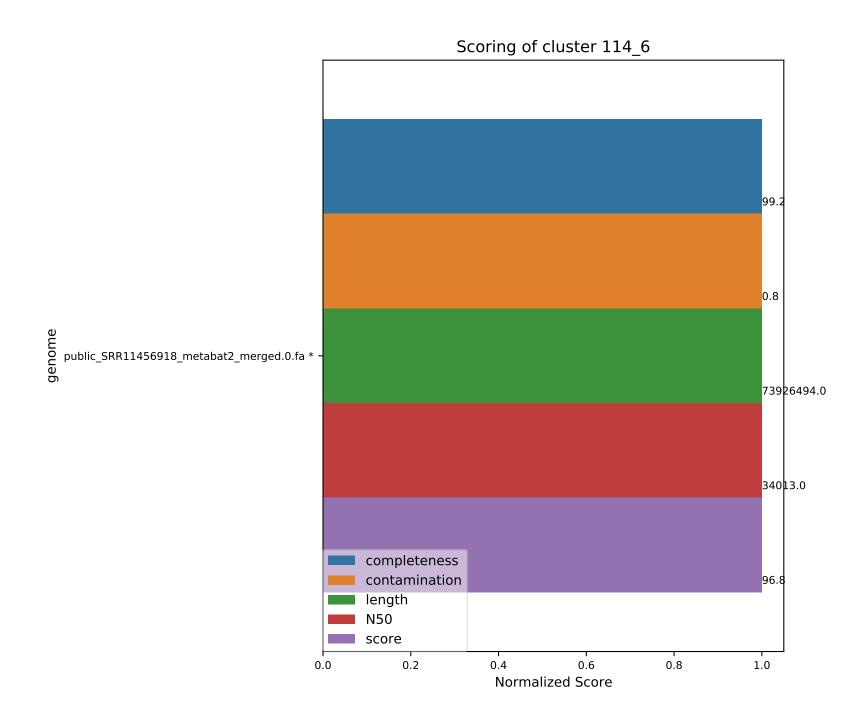
Scoring of cluster 114_2 88.3 1.9 public_SRR11456913_concoct_bin.13.fa -43163750.0 22249.0 81.: genome 95.9 3.4 public_SRR11456915_metabat2_merged.0.fa * -88820417.0 completeness 23392.0 contamination length 81.1 N50 score 0.0 0.2 0.4 0.6 0.8 1.0

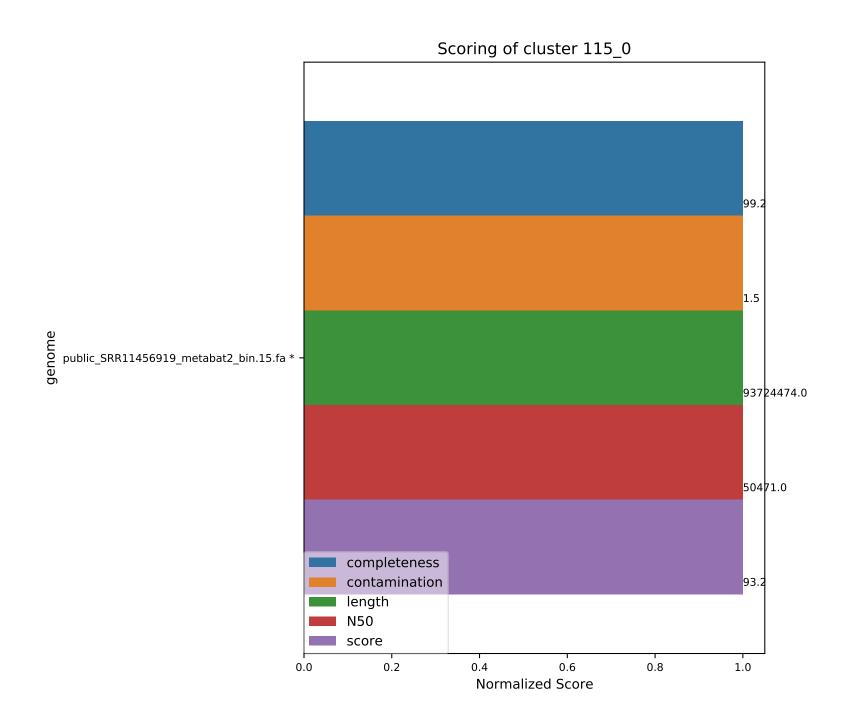
Normalized Score

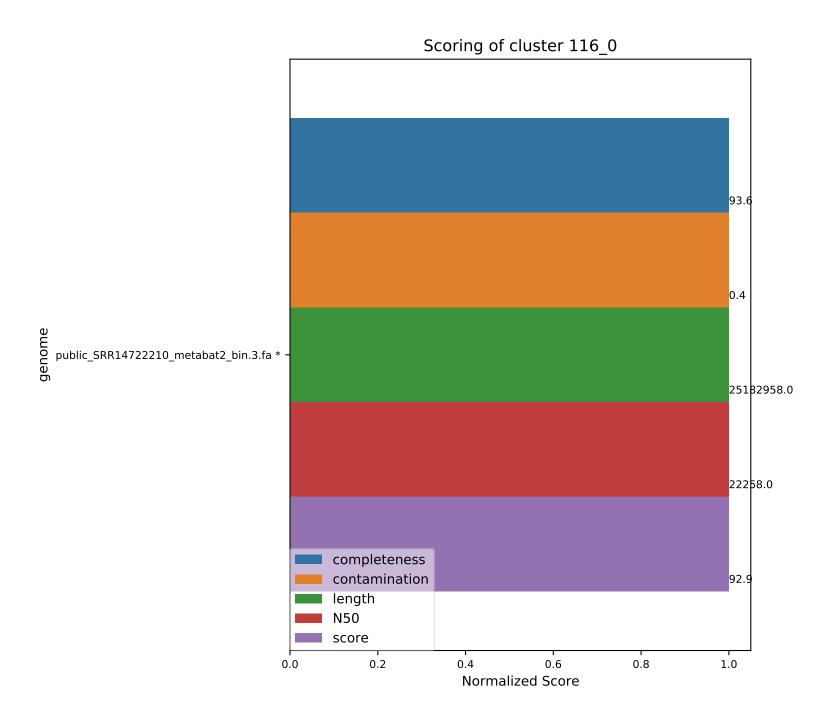


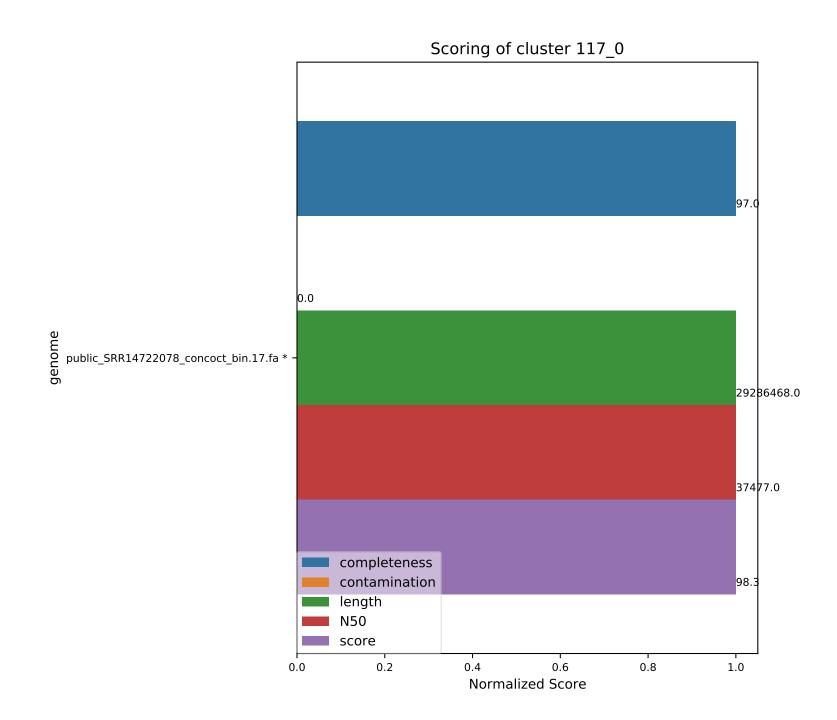


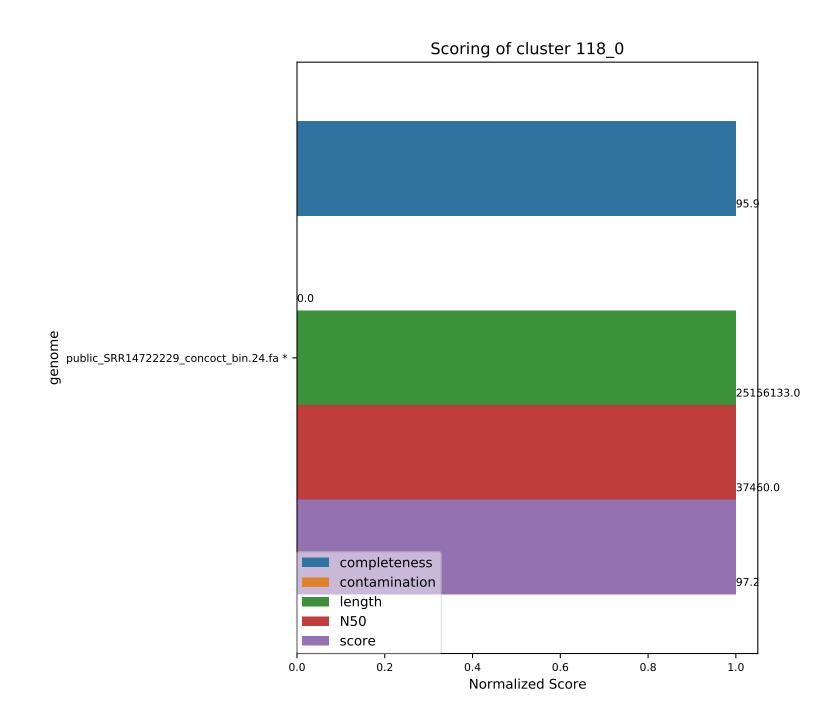


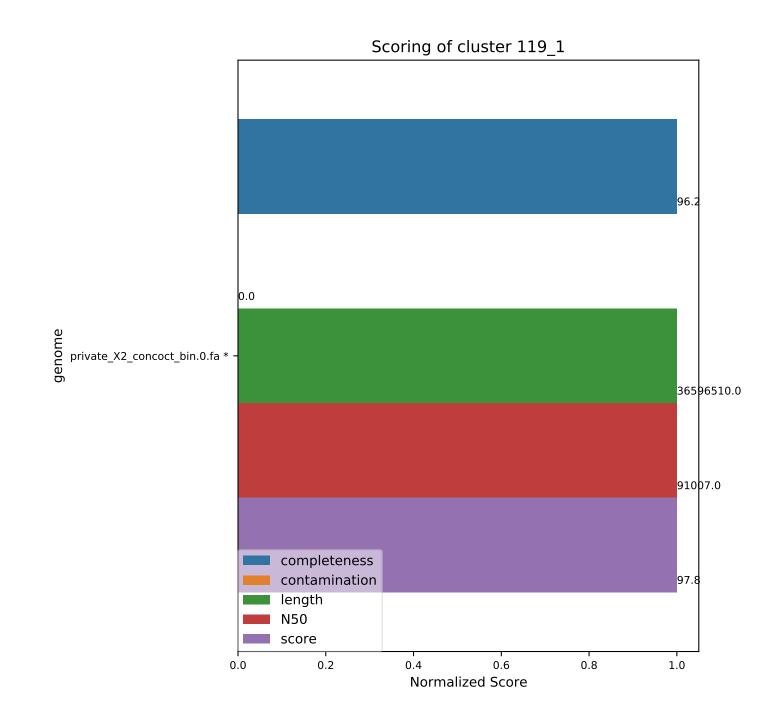


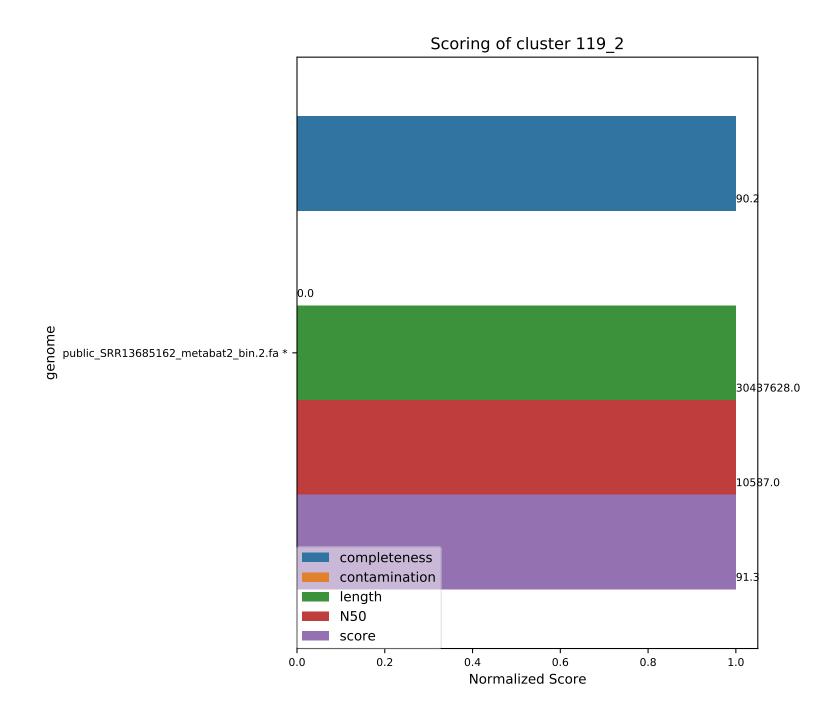


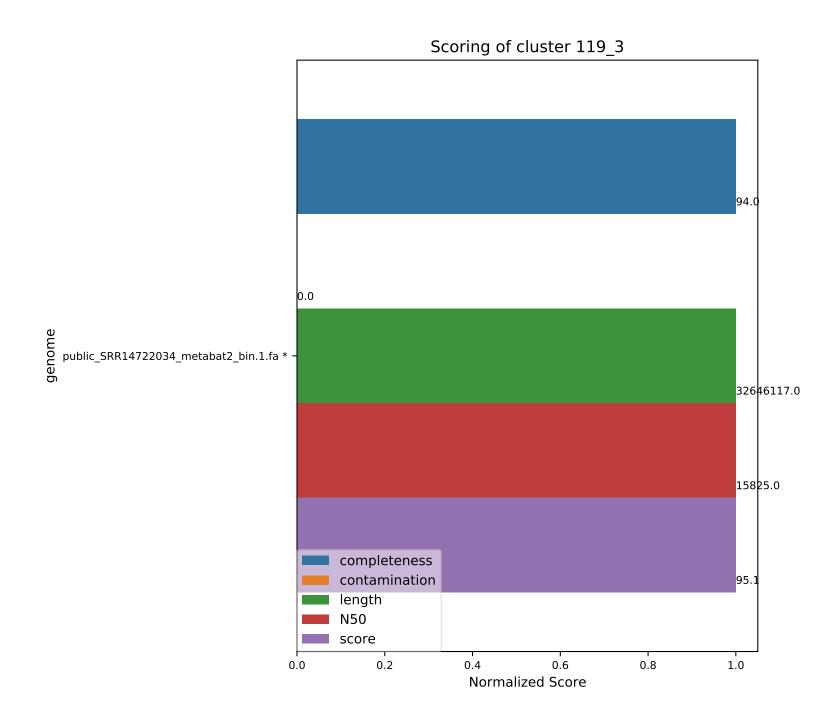


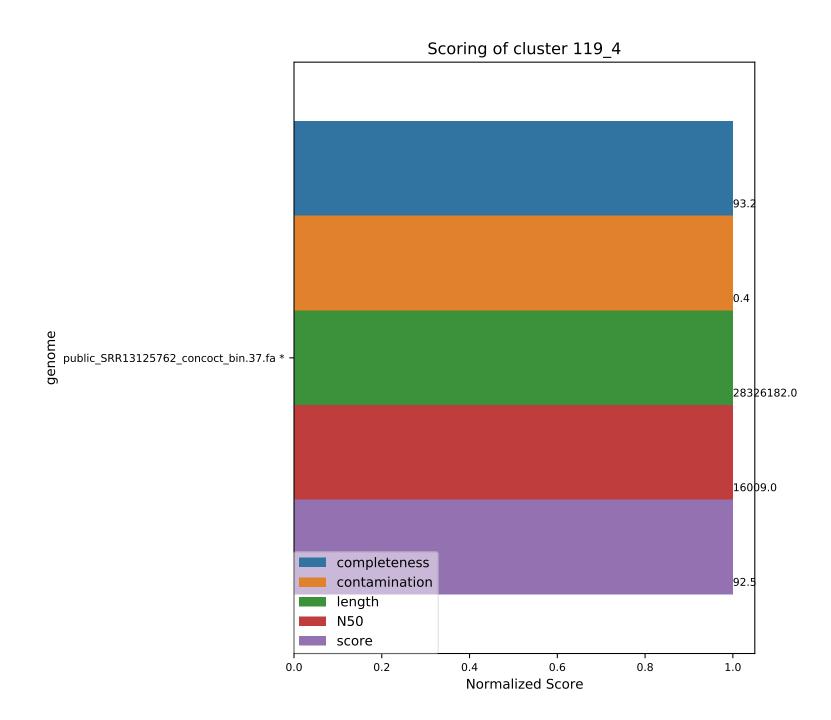


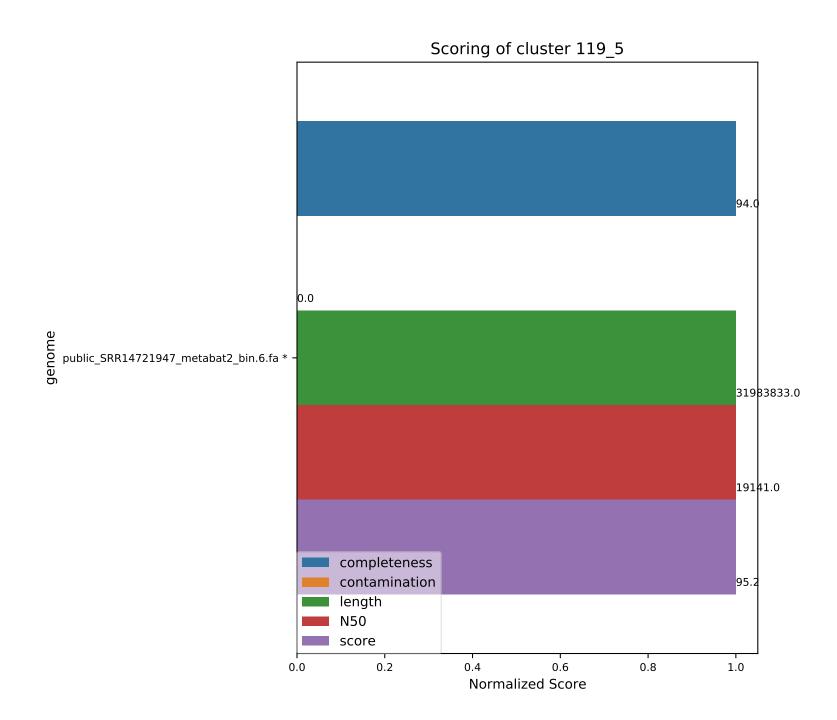


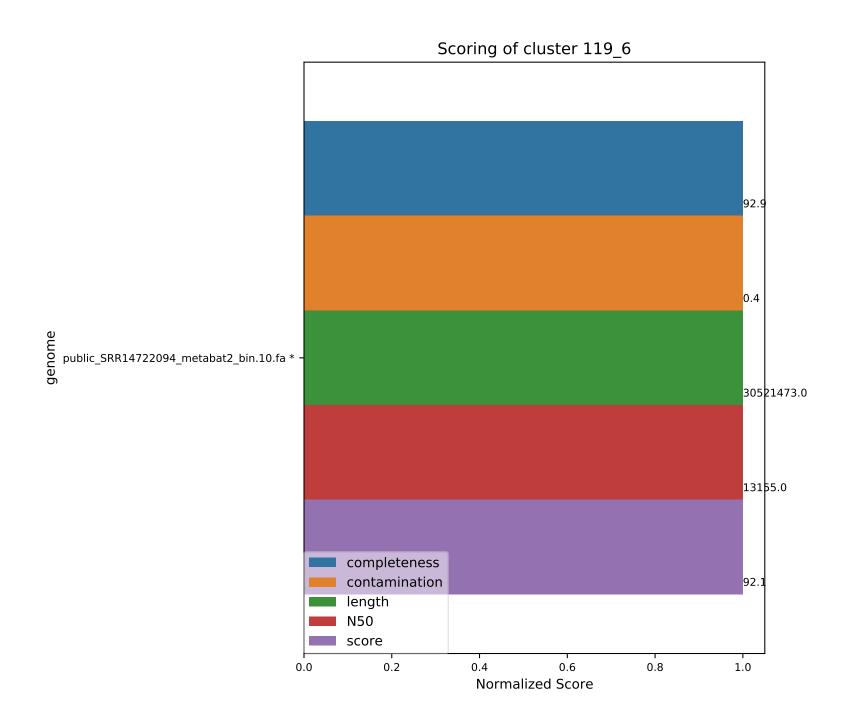


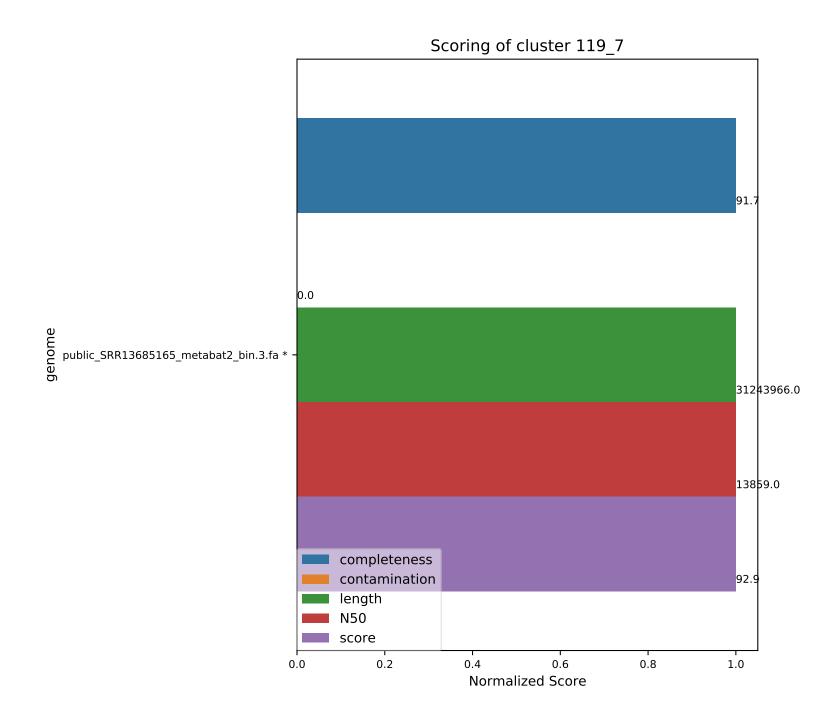


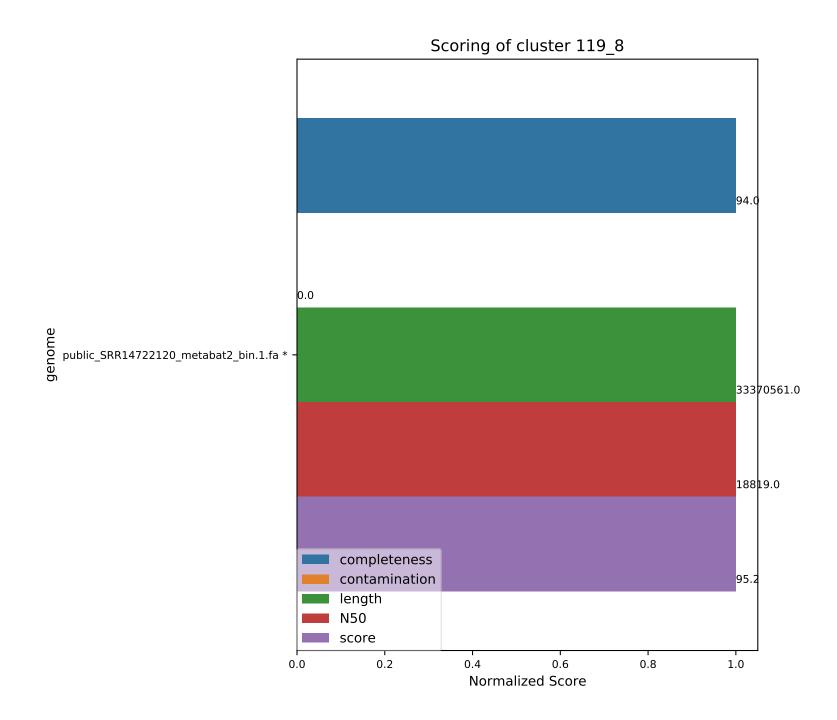


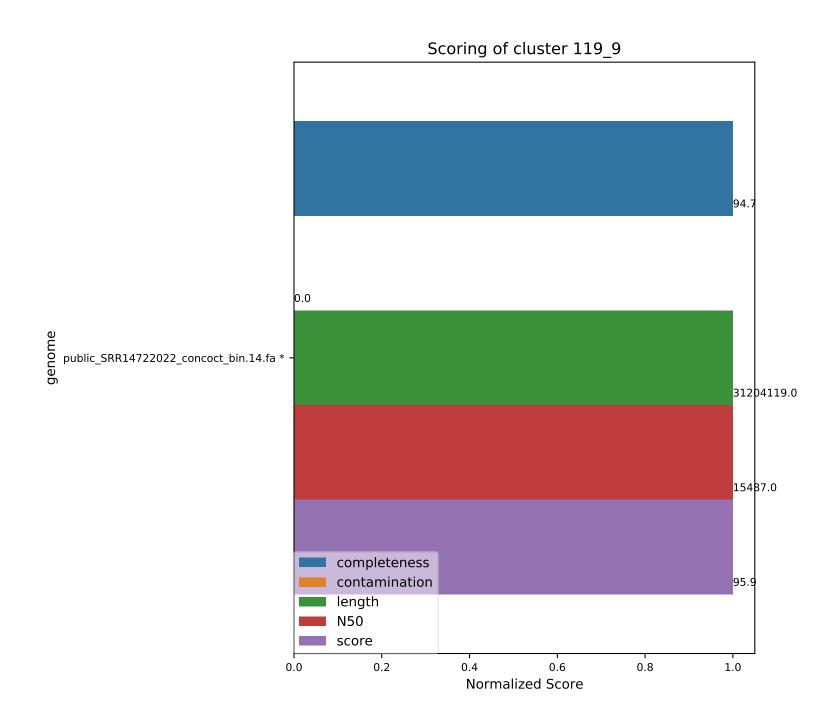


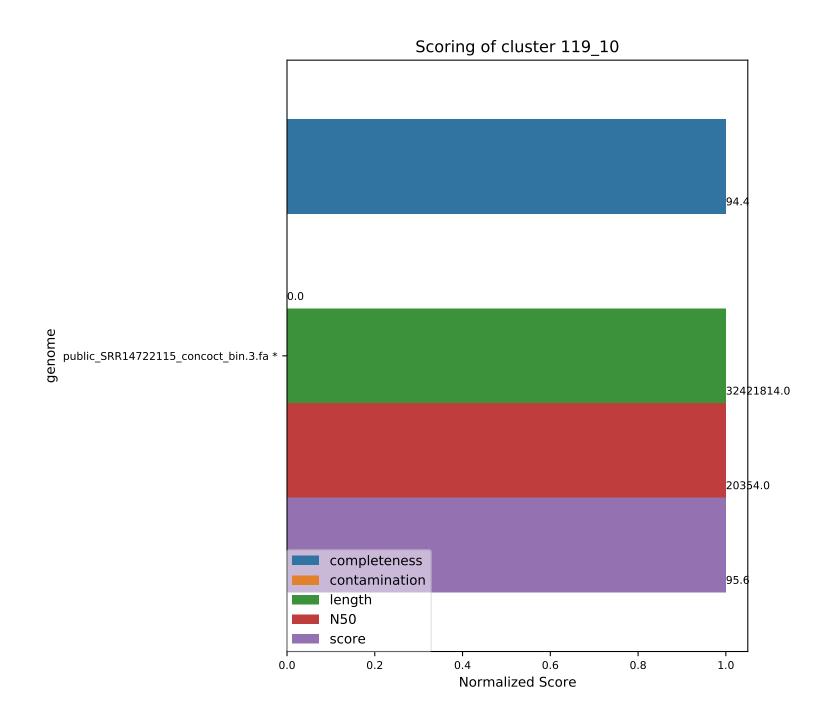


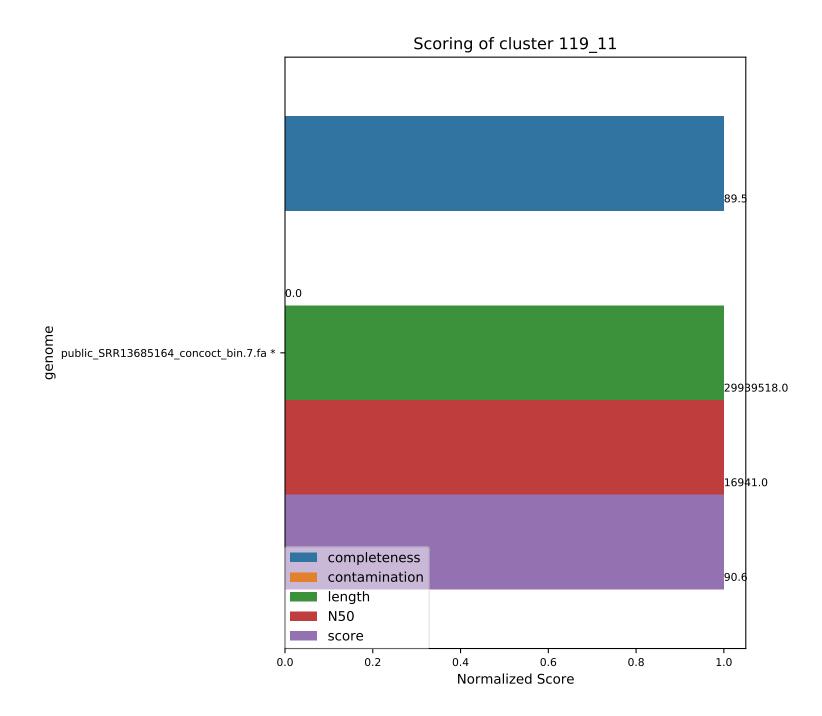


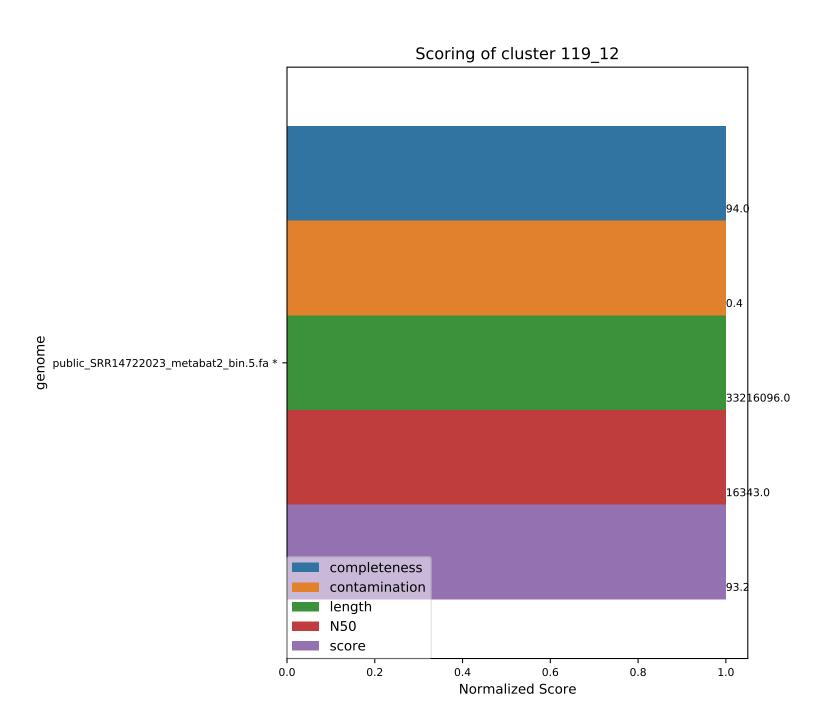


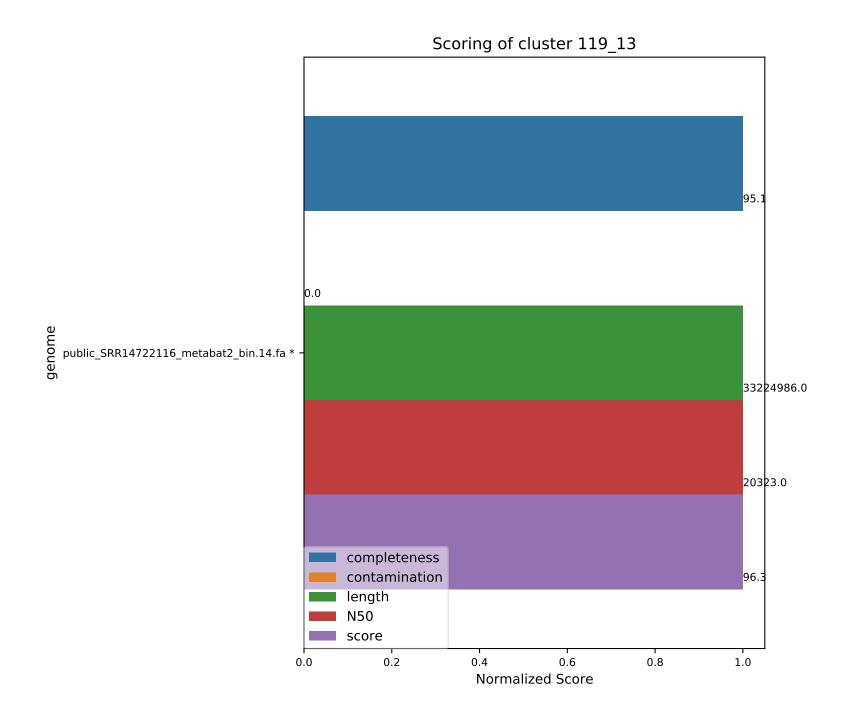


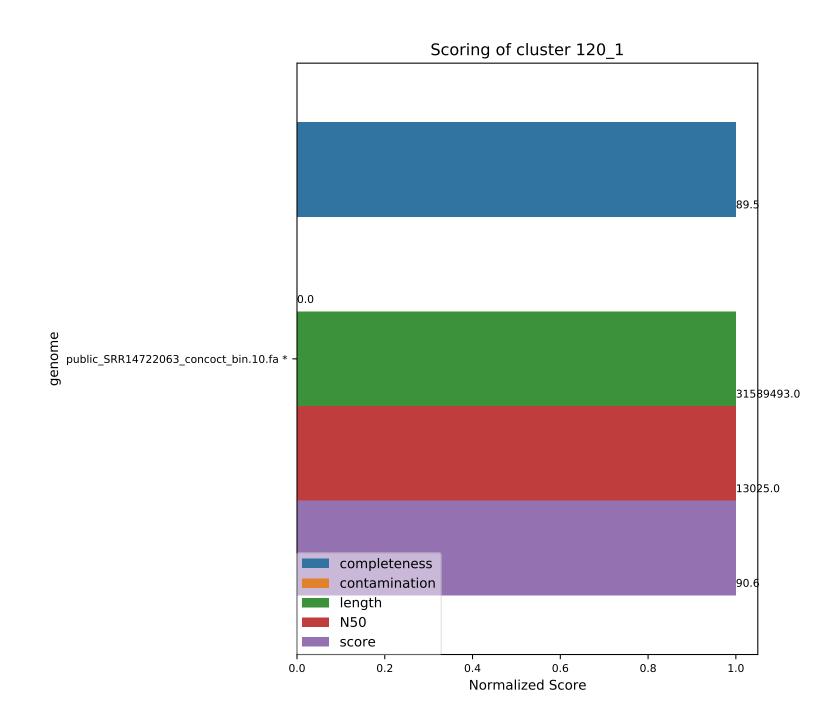


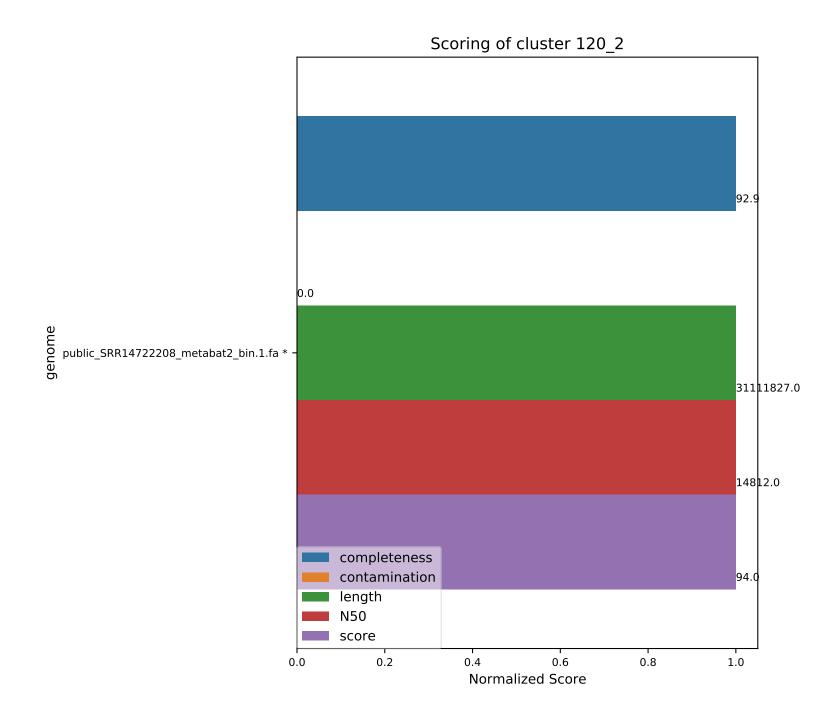


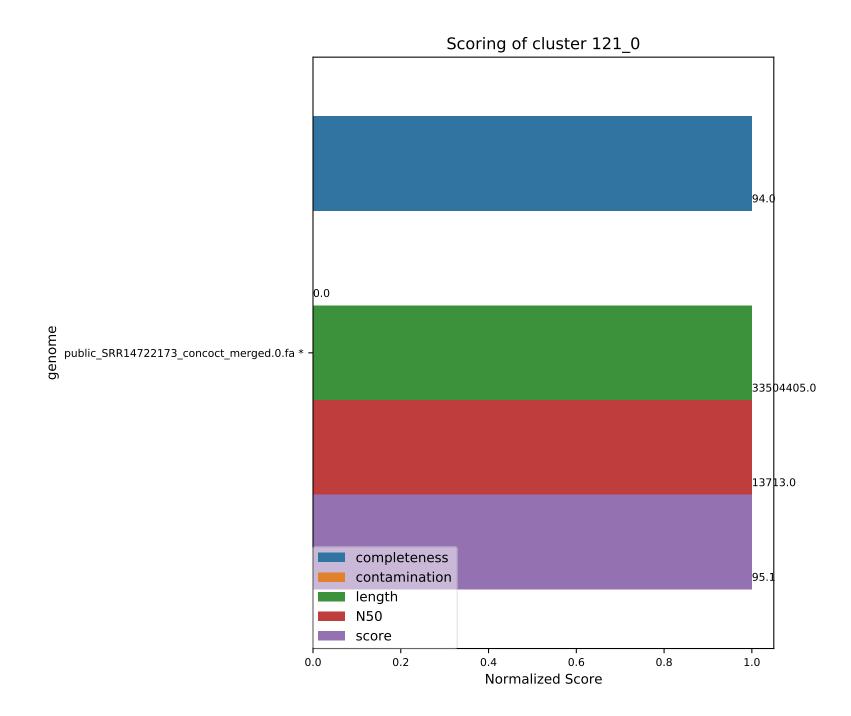


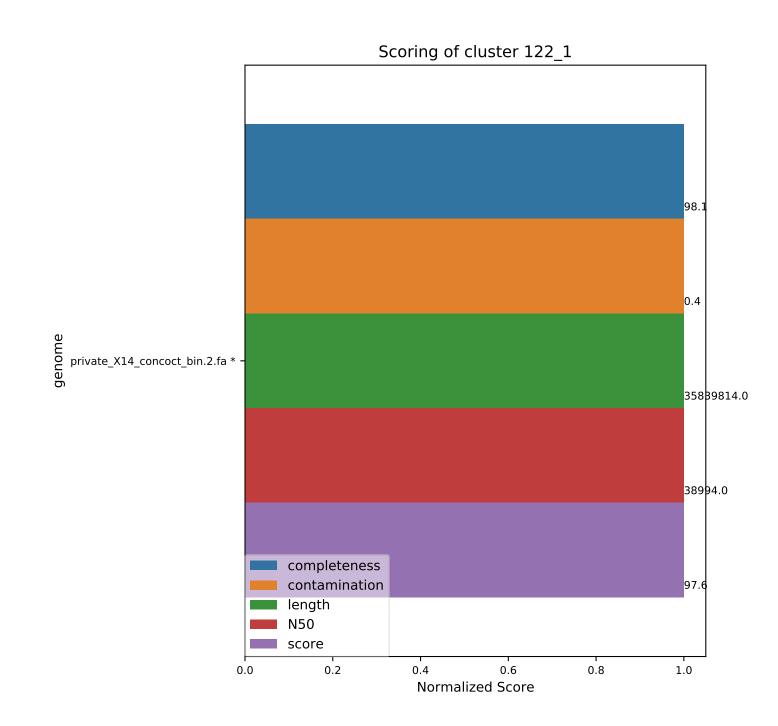


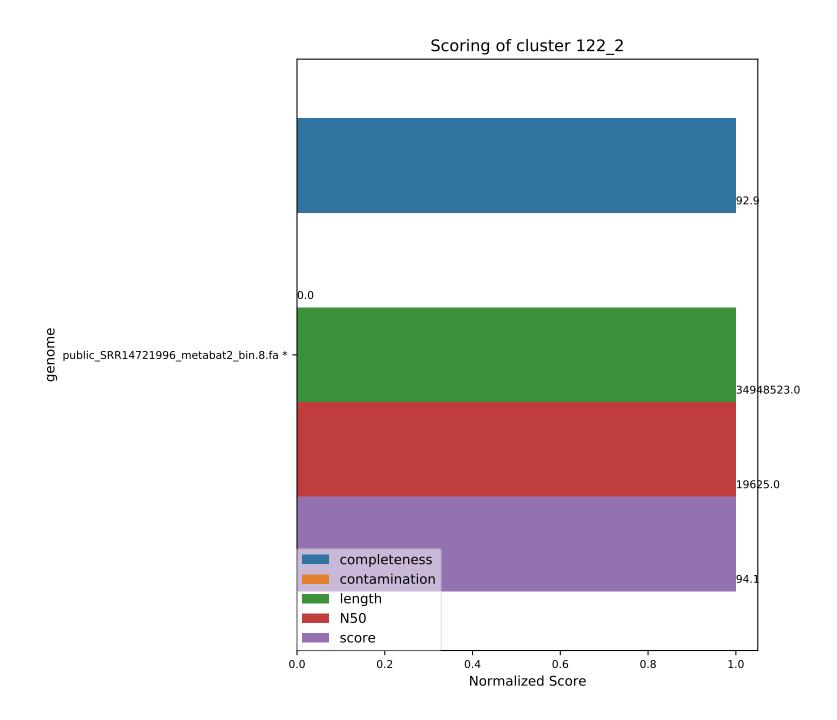


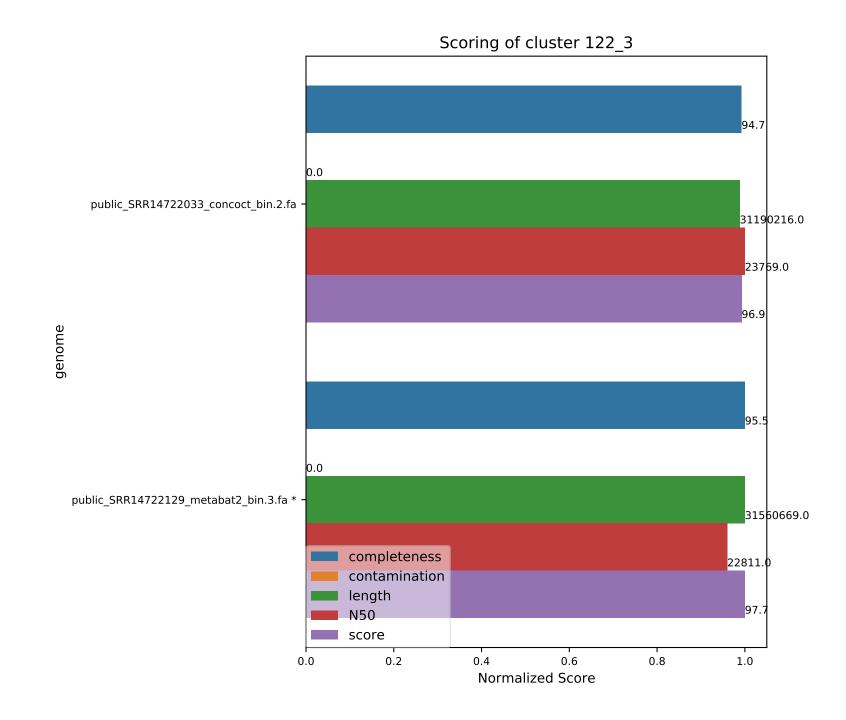


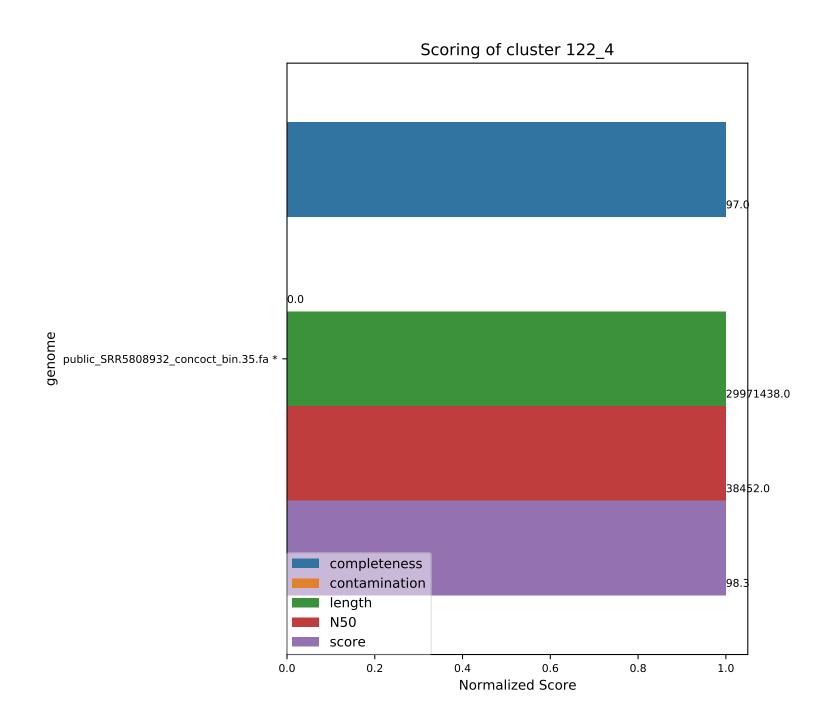


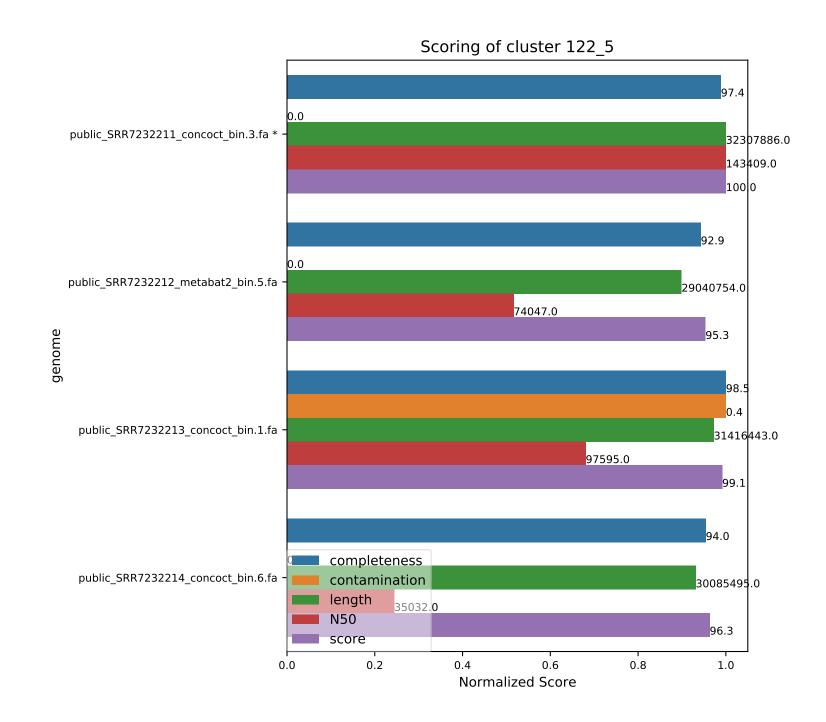


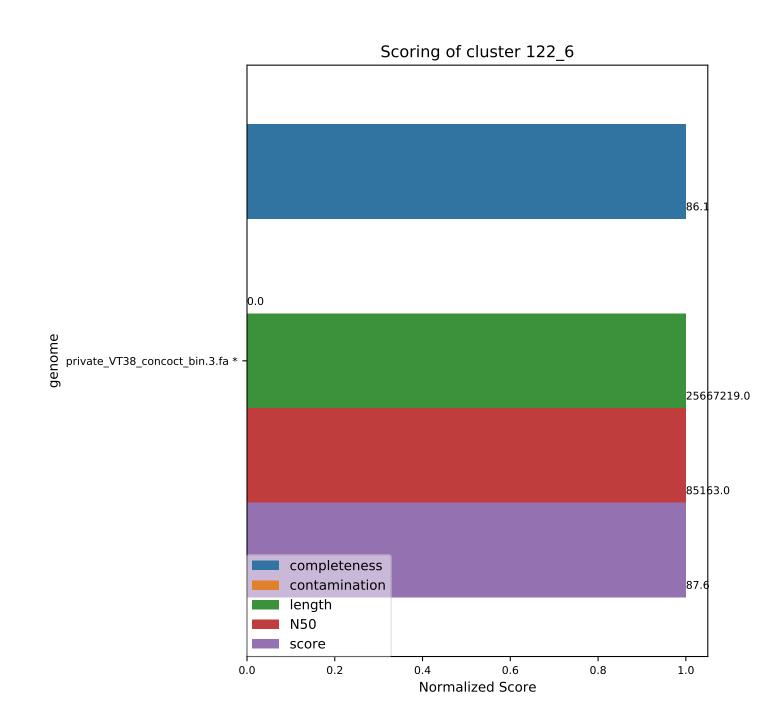


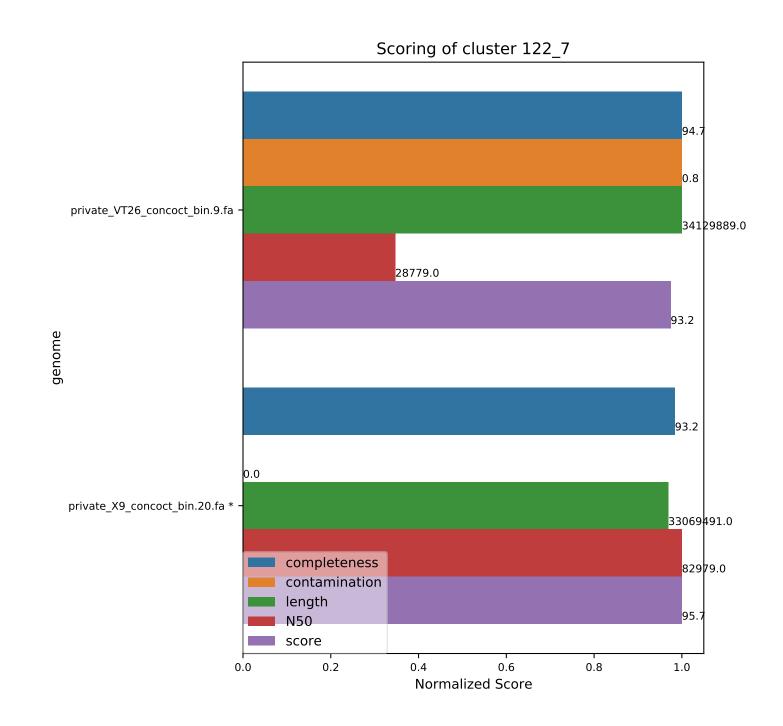


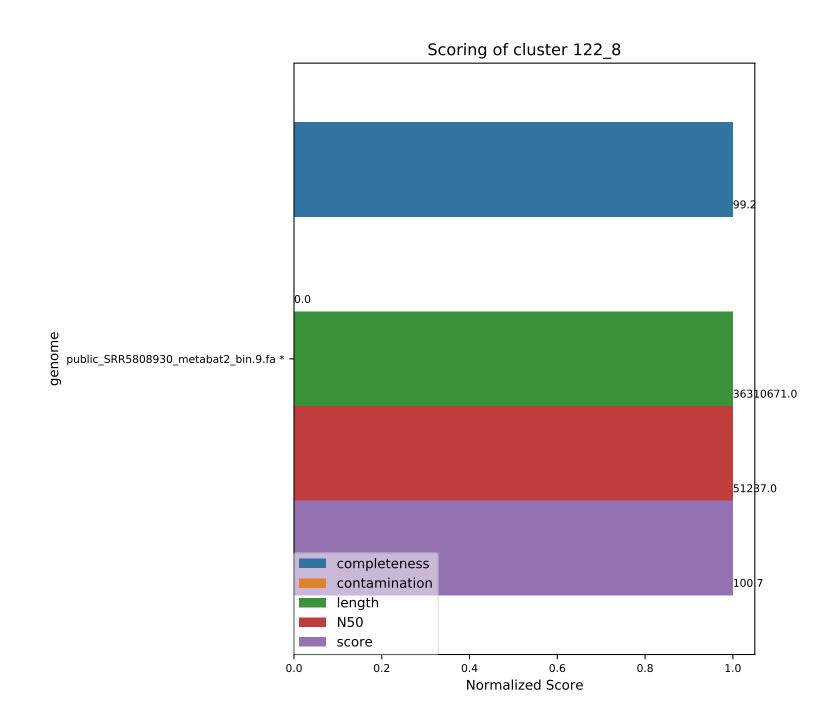


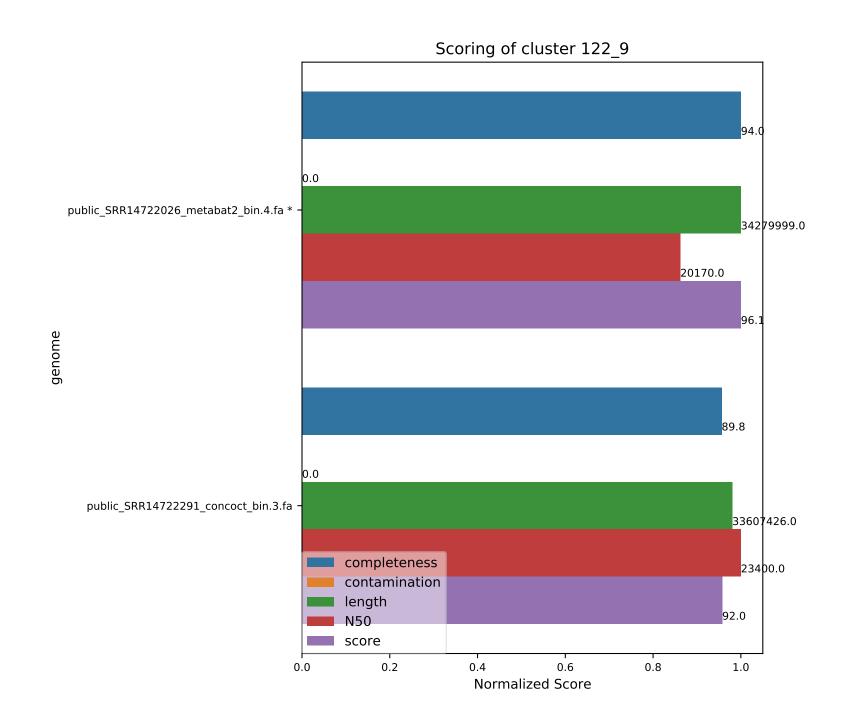


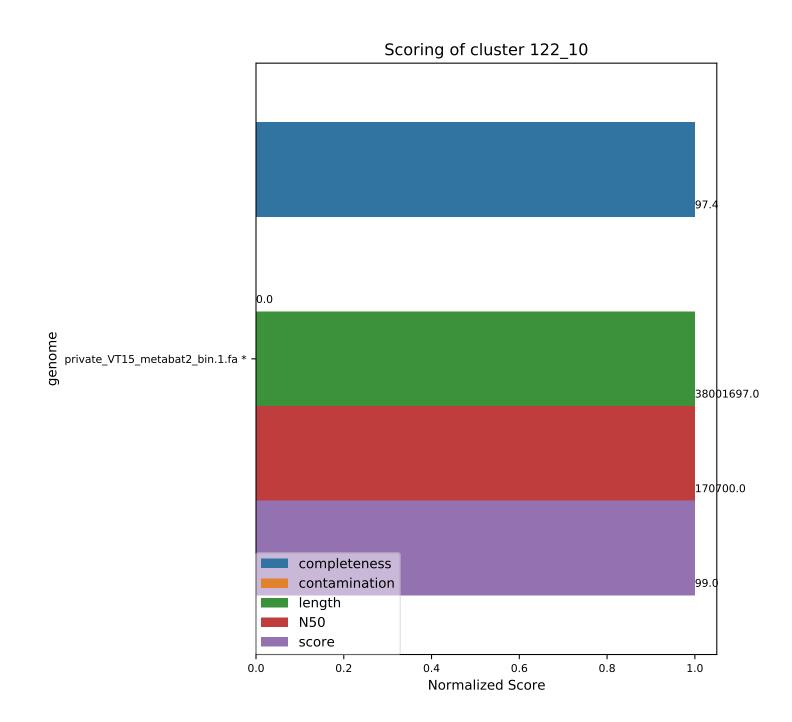


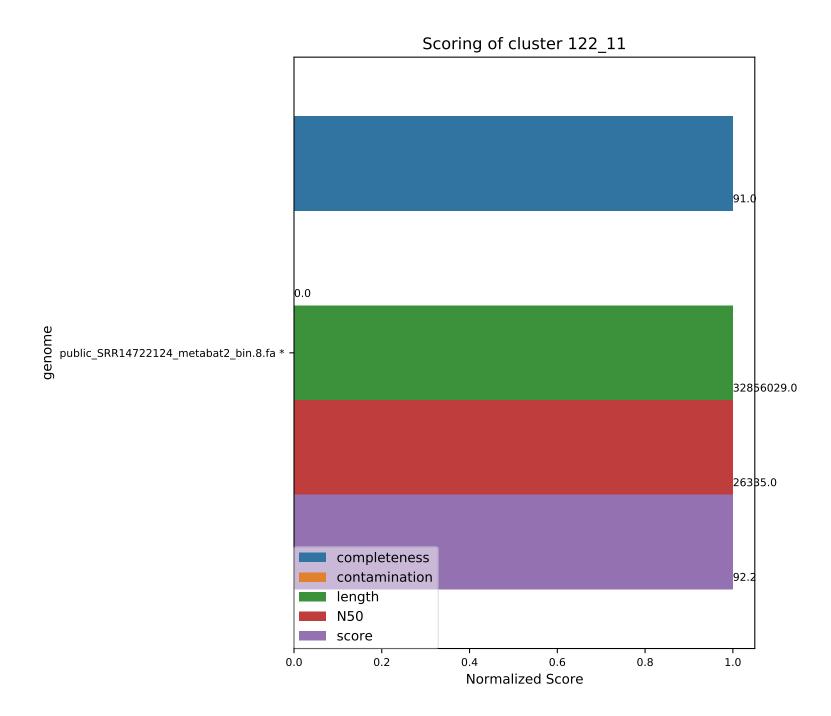


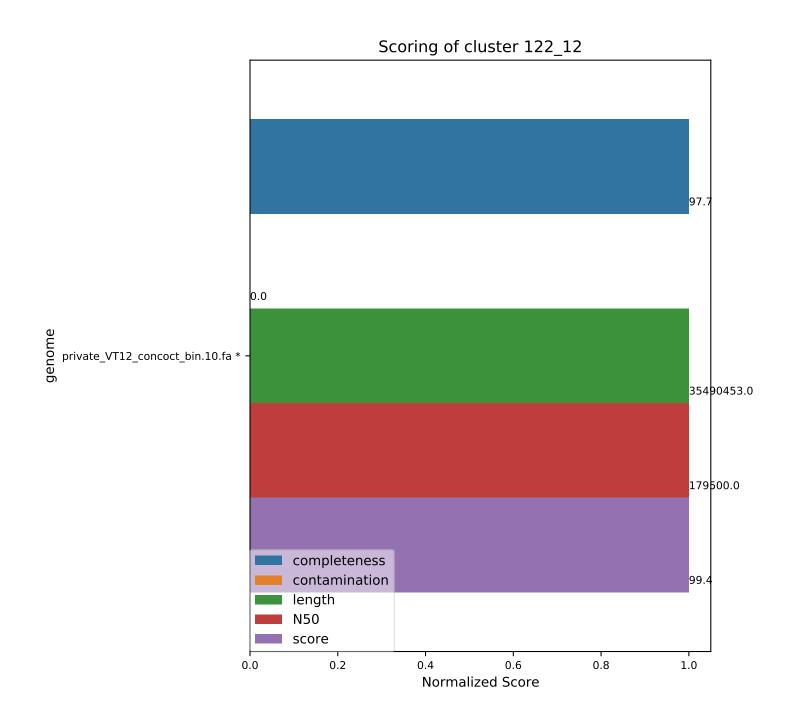


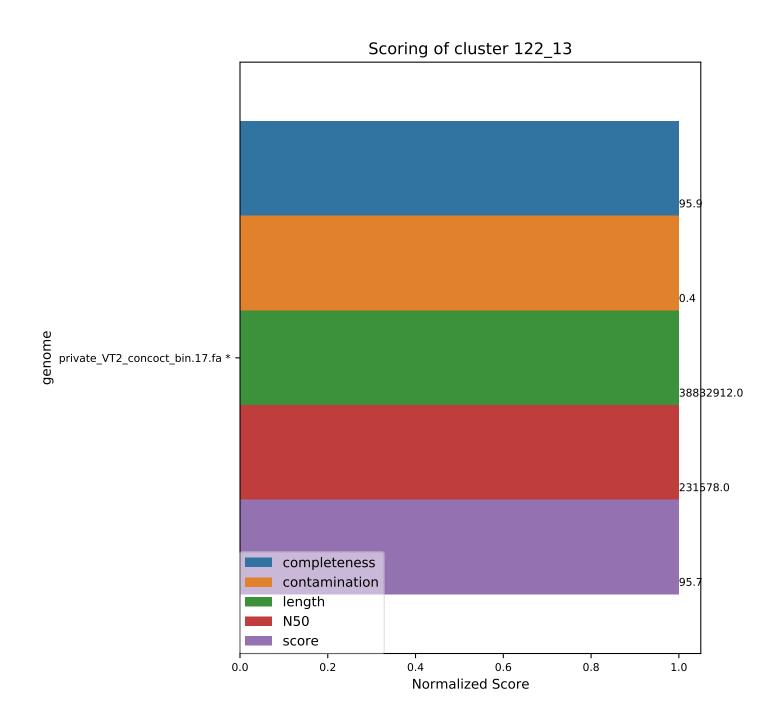


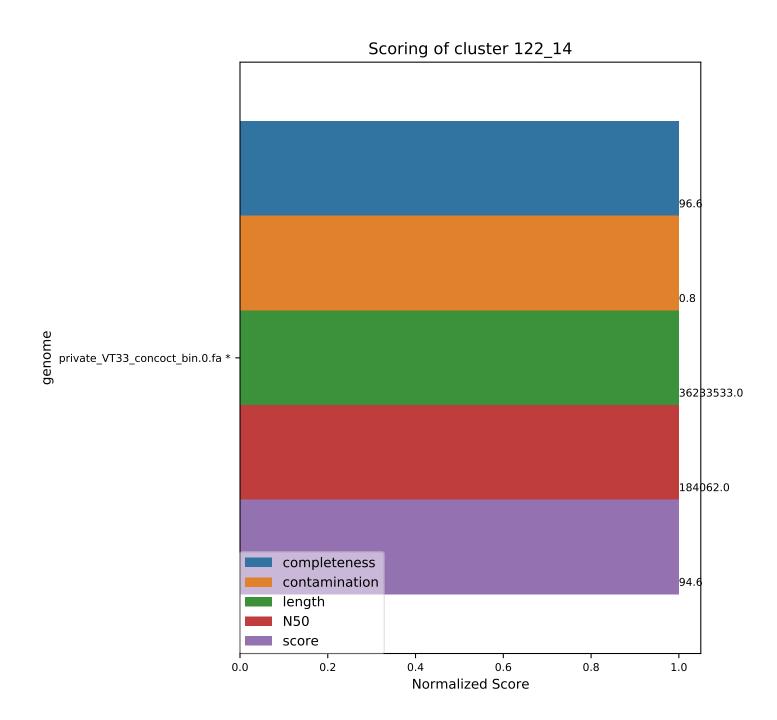


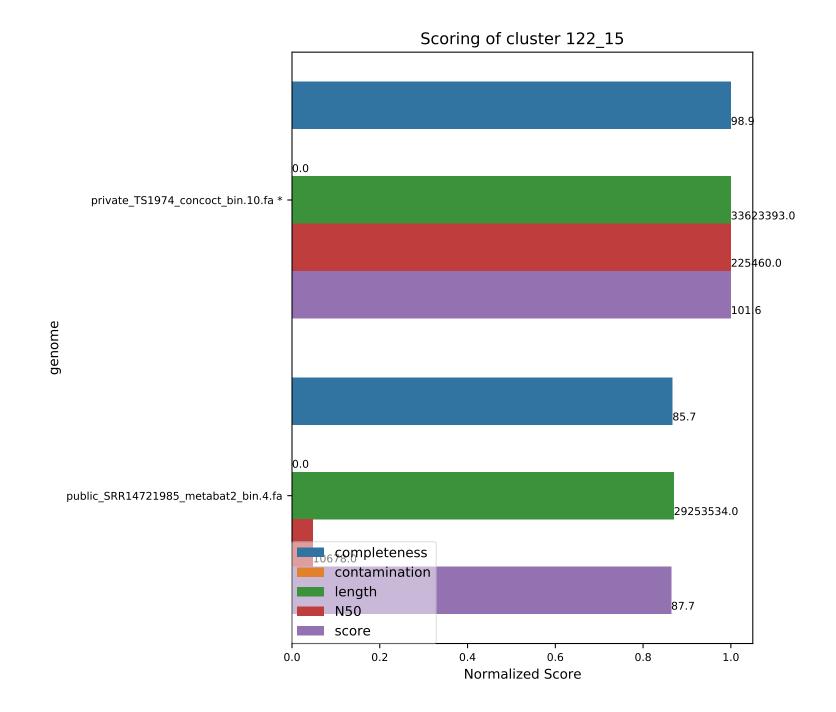


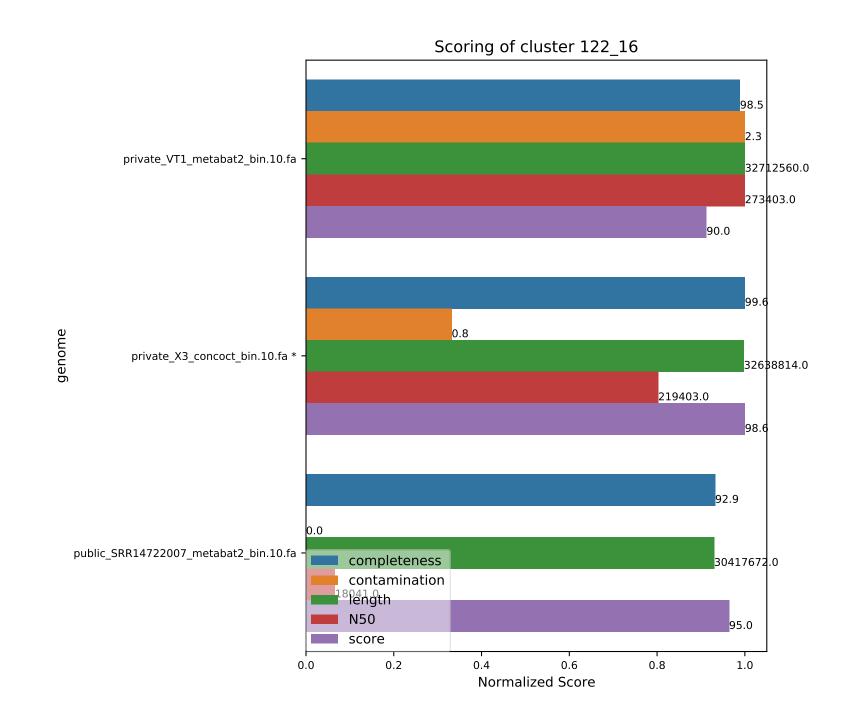


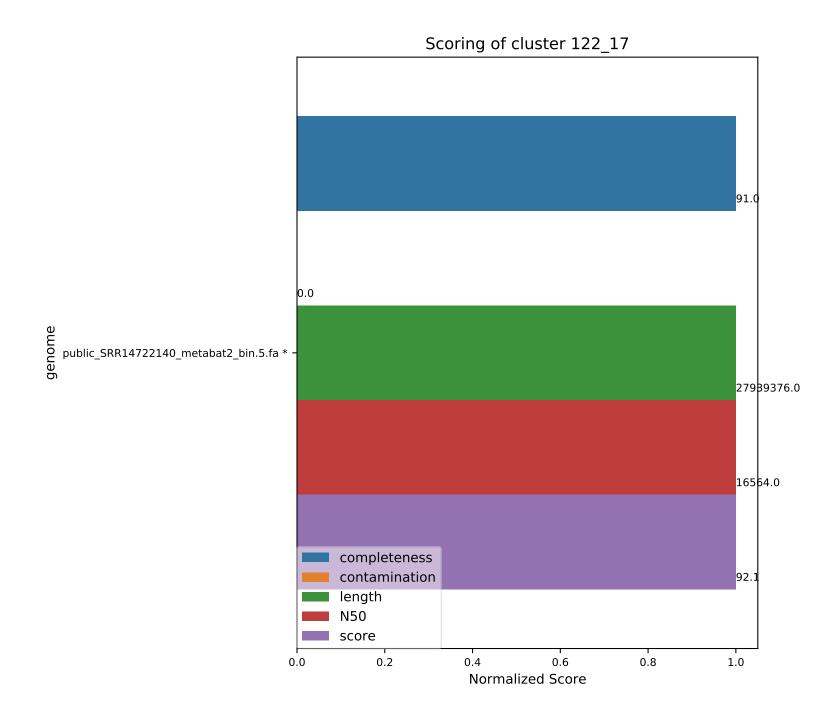


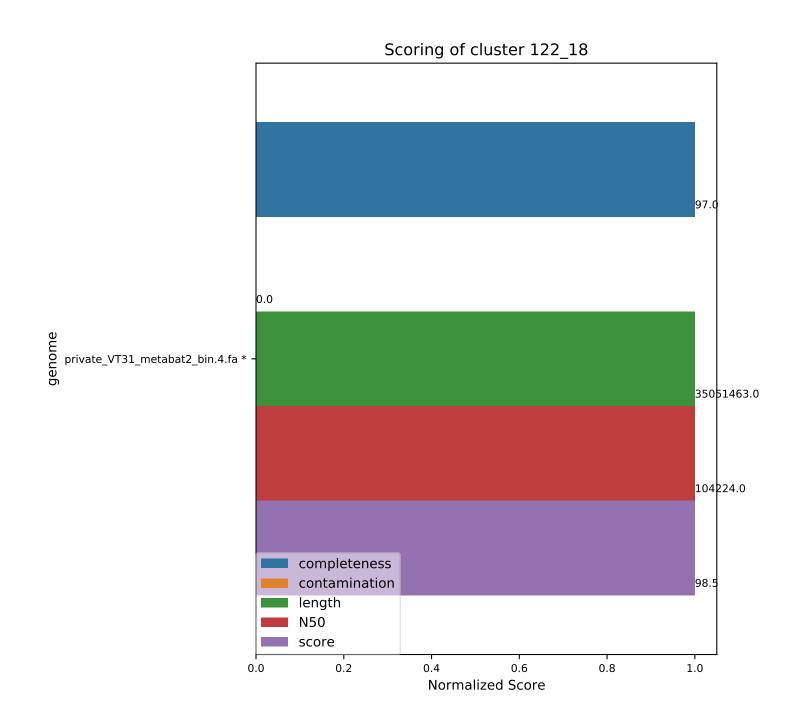


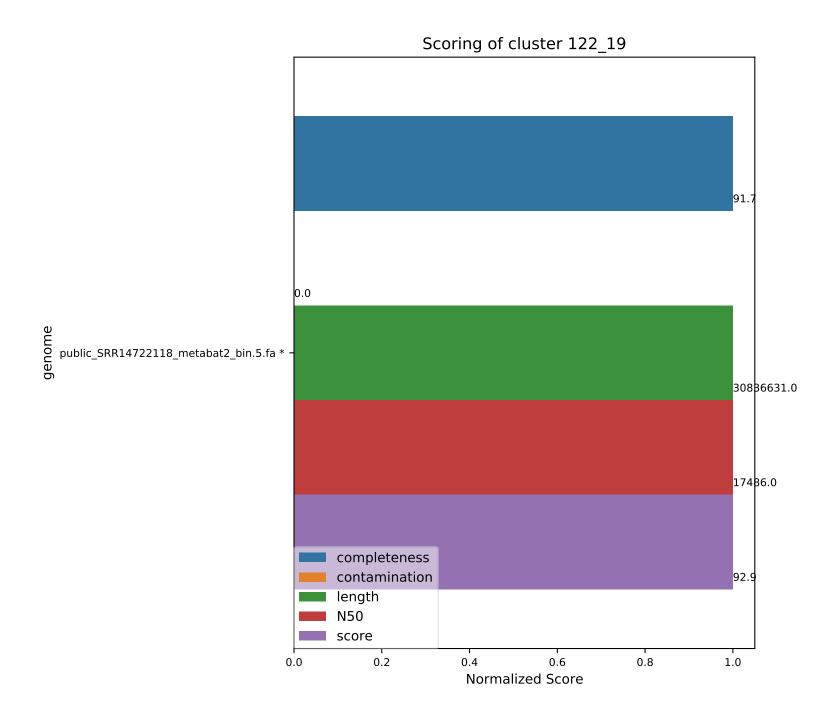


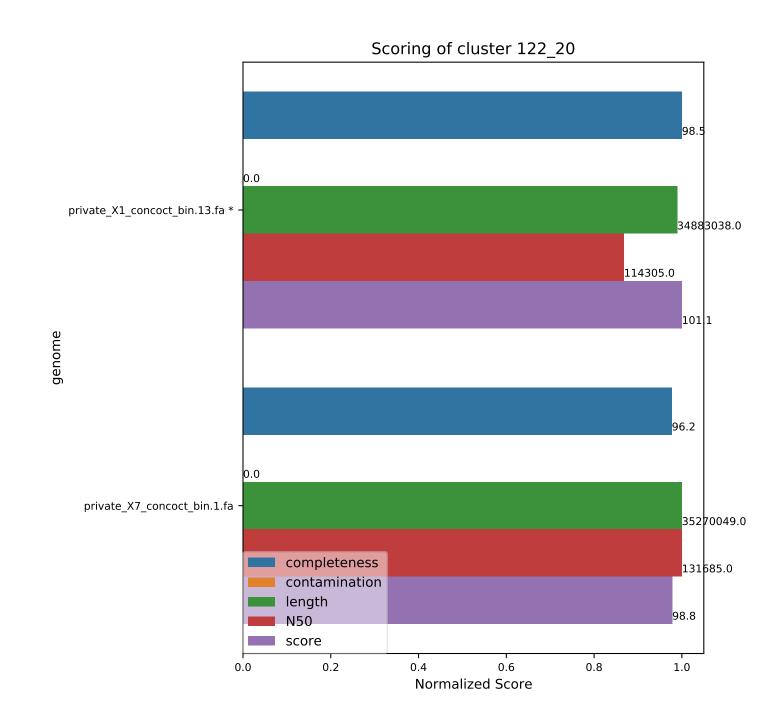


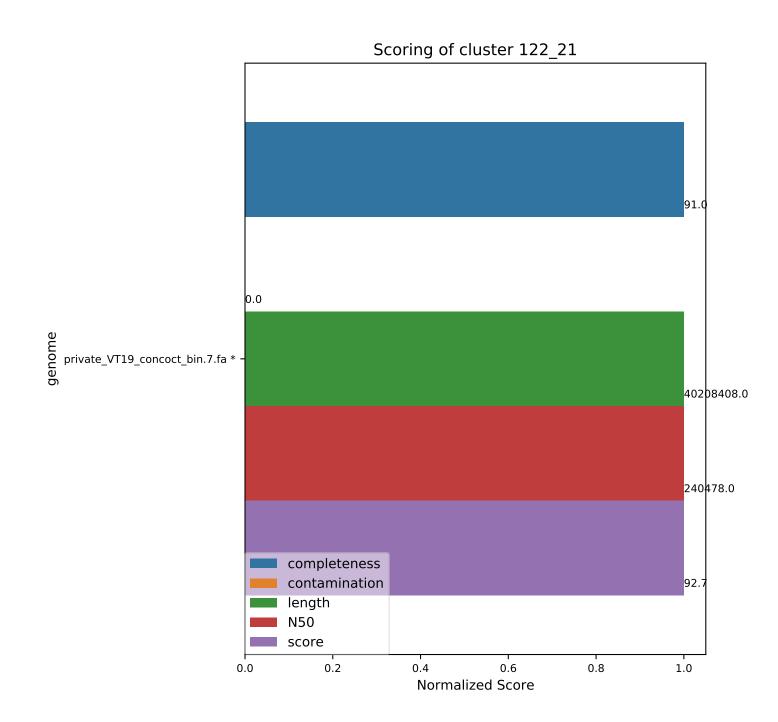


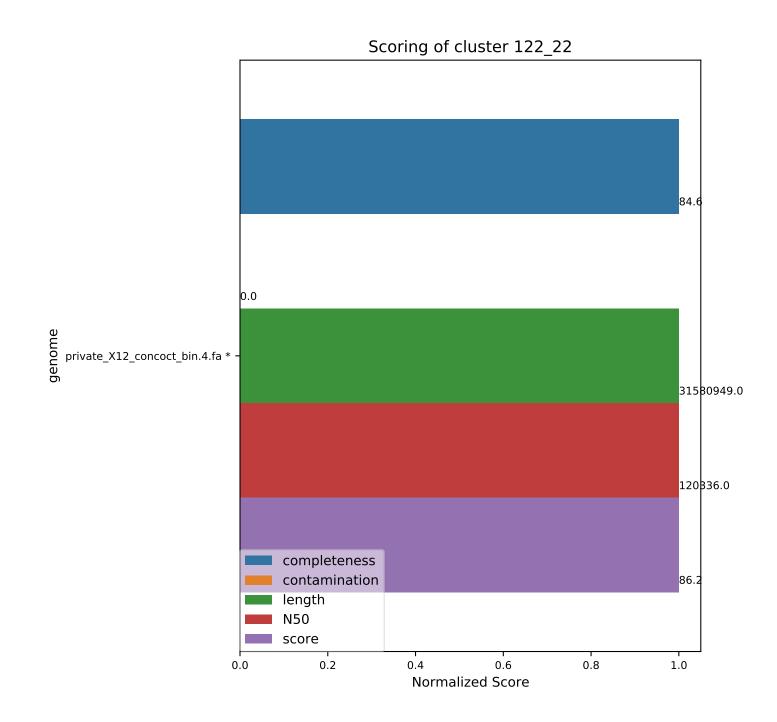


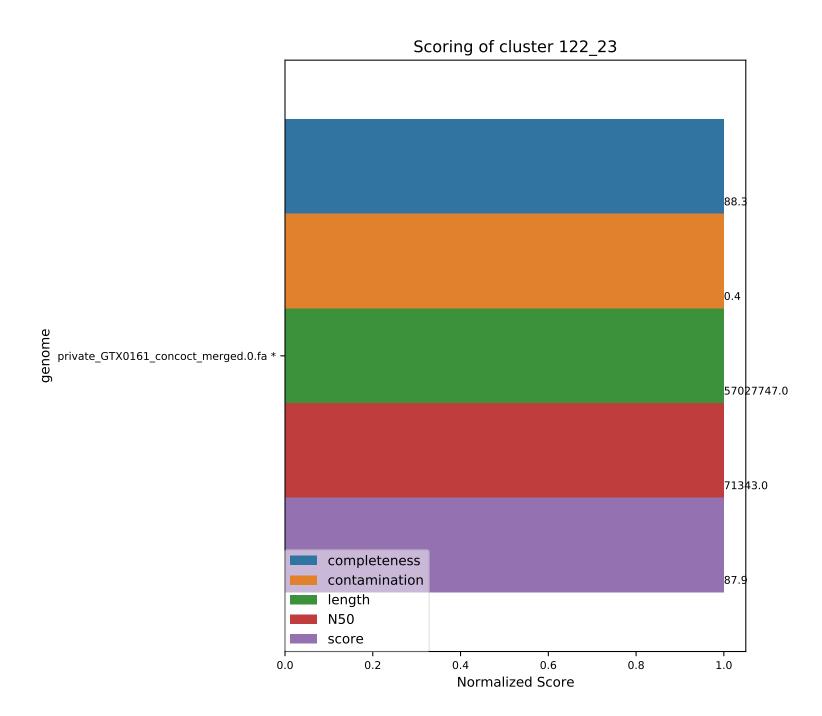


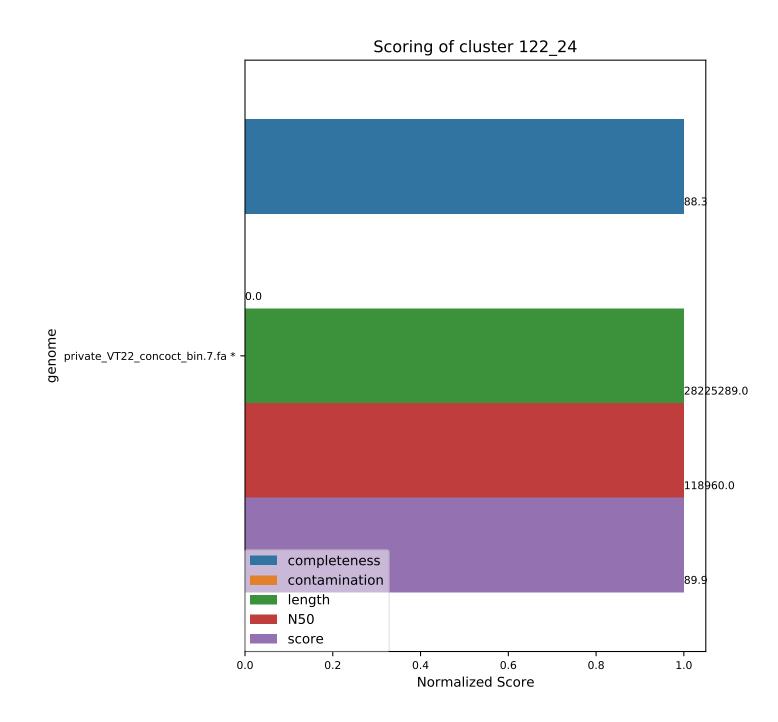


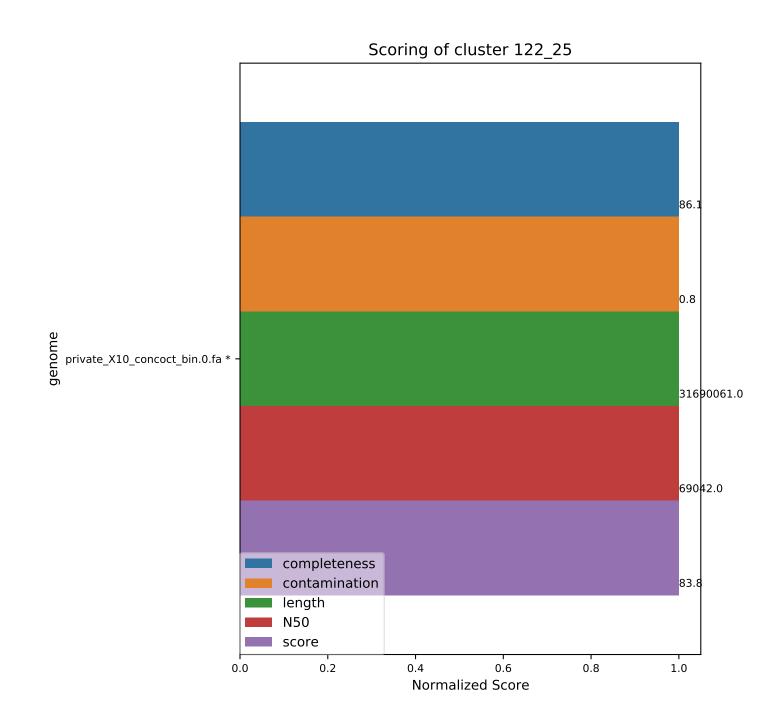


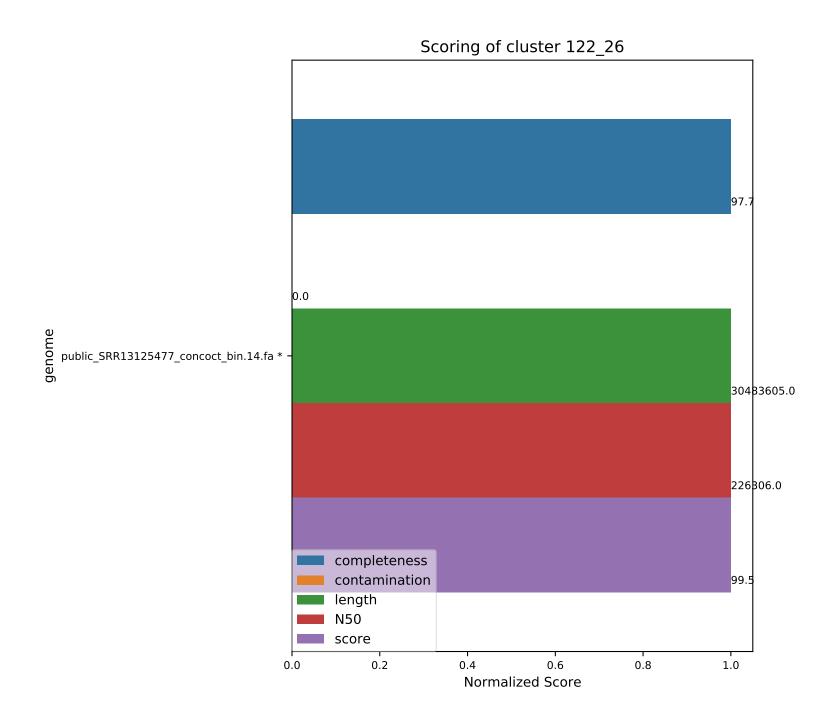


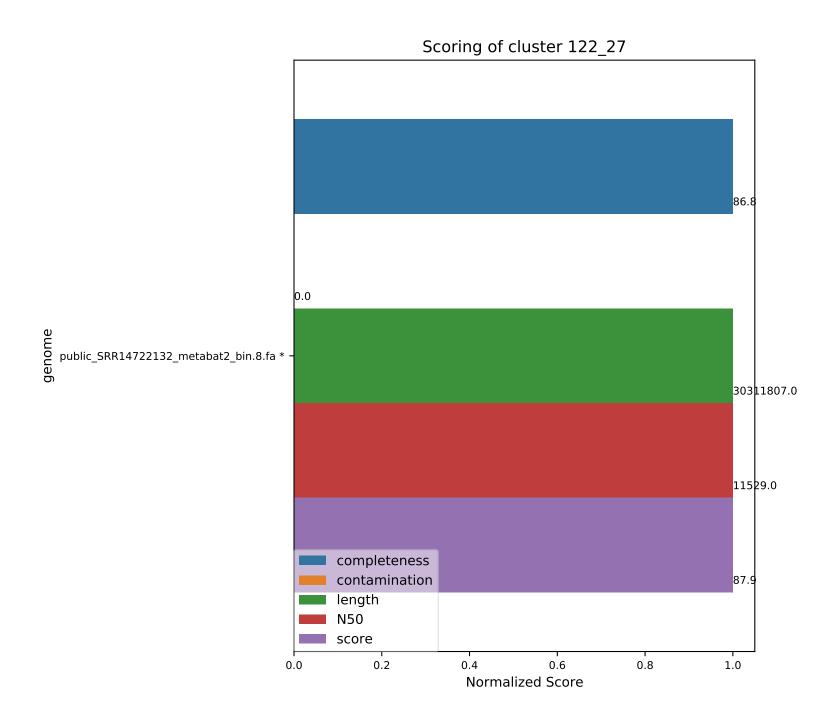


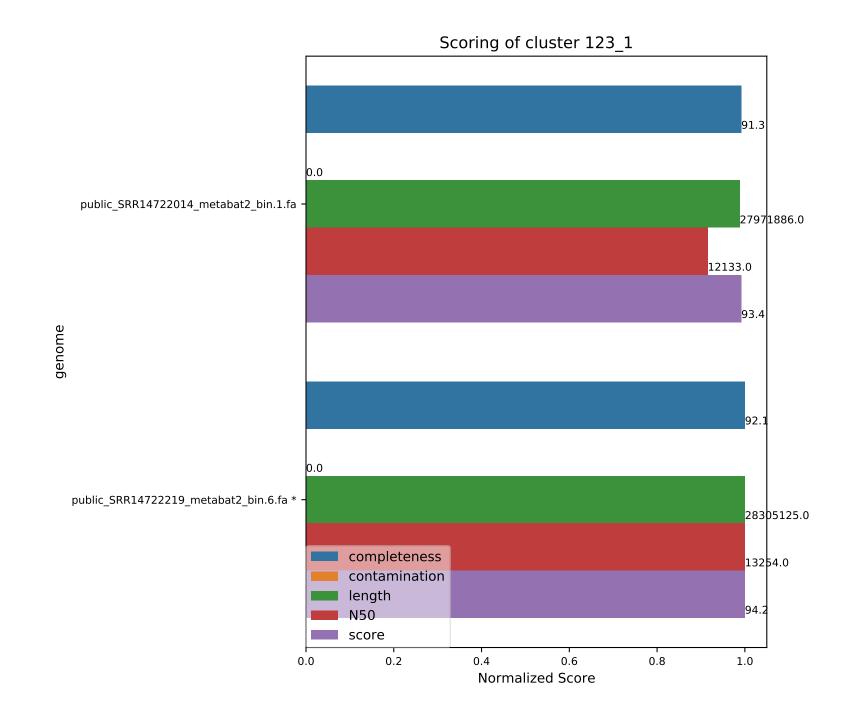


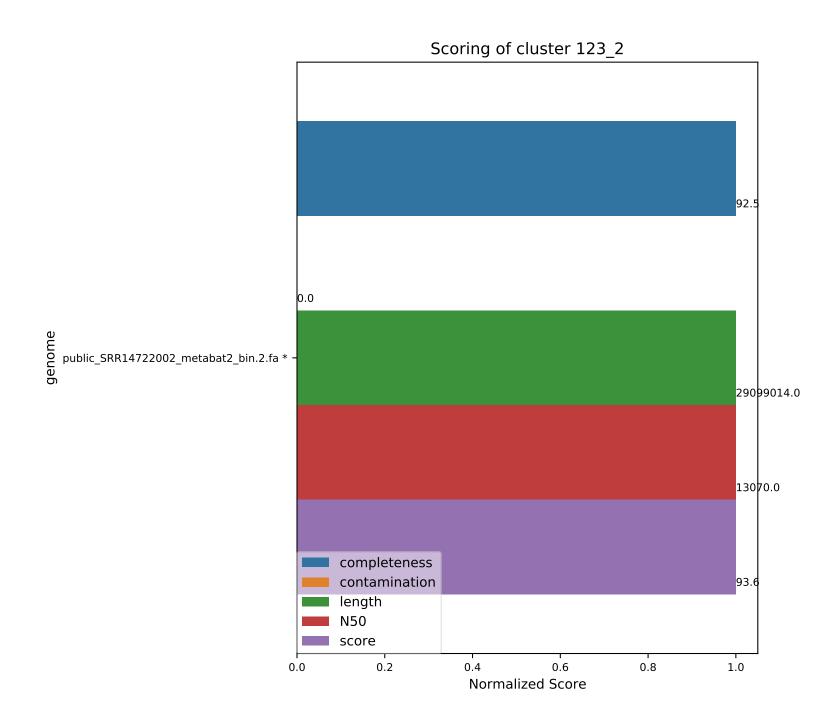


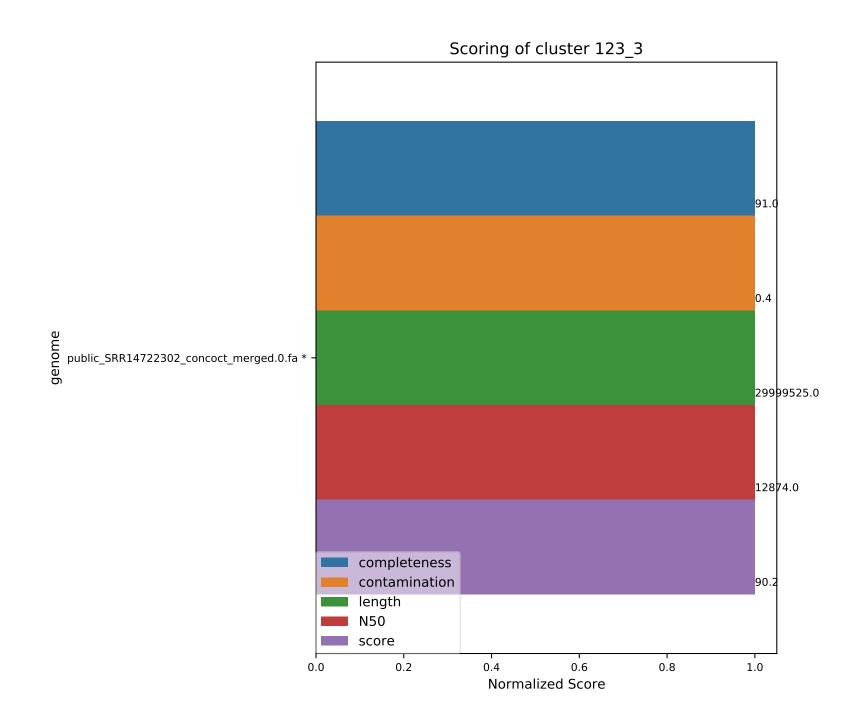


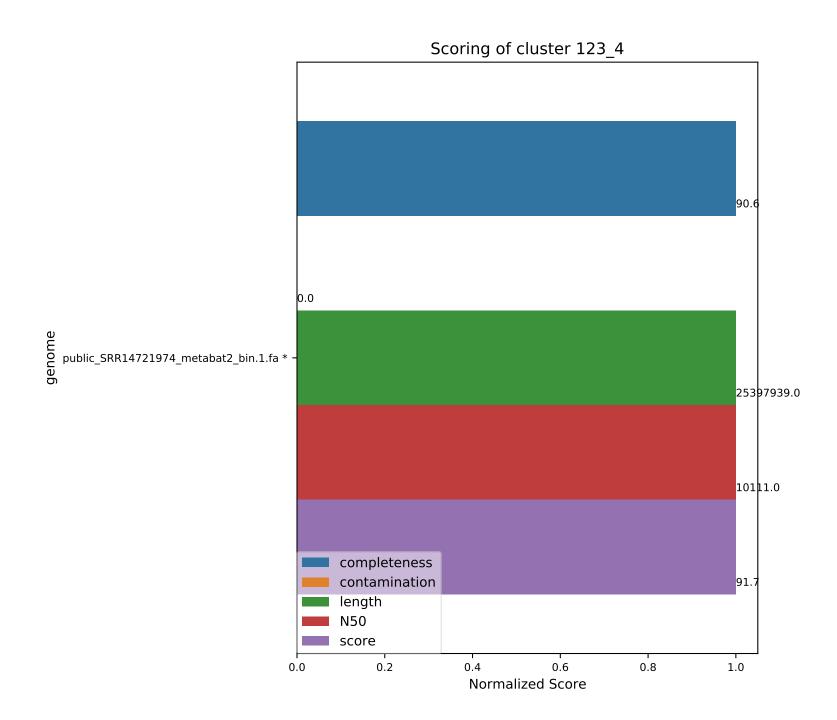


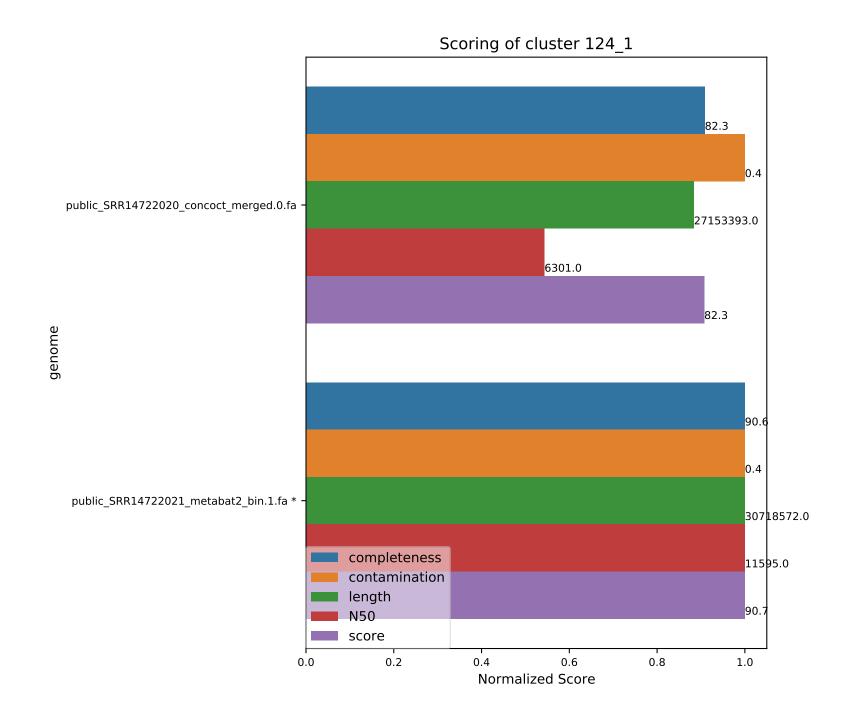


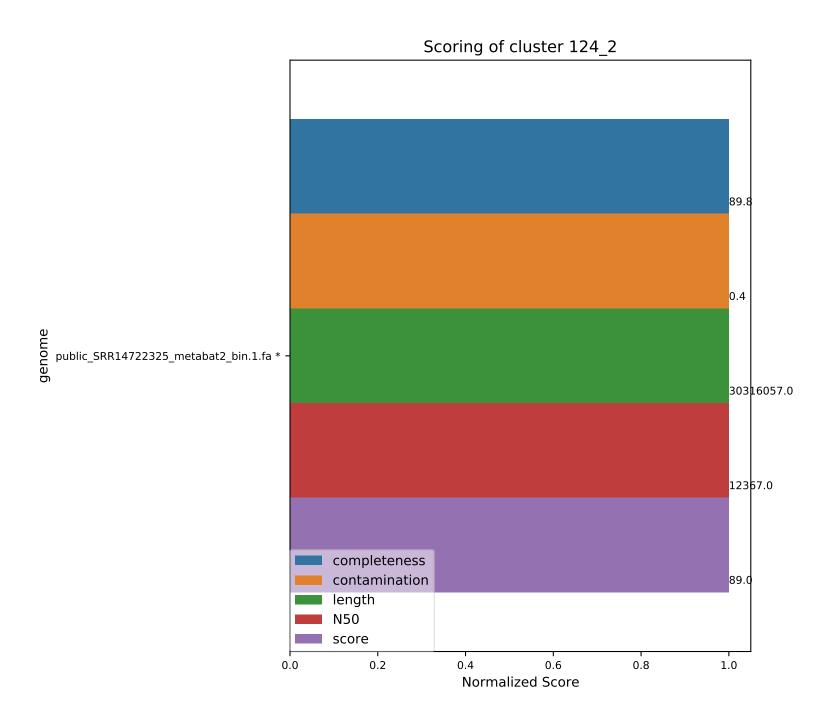


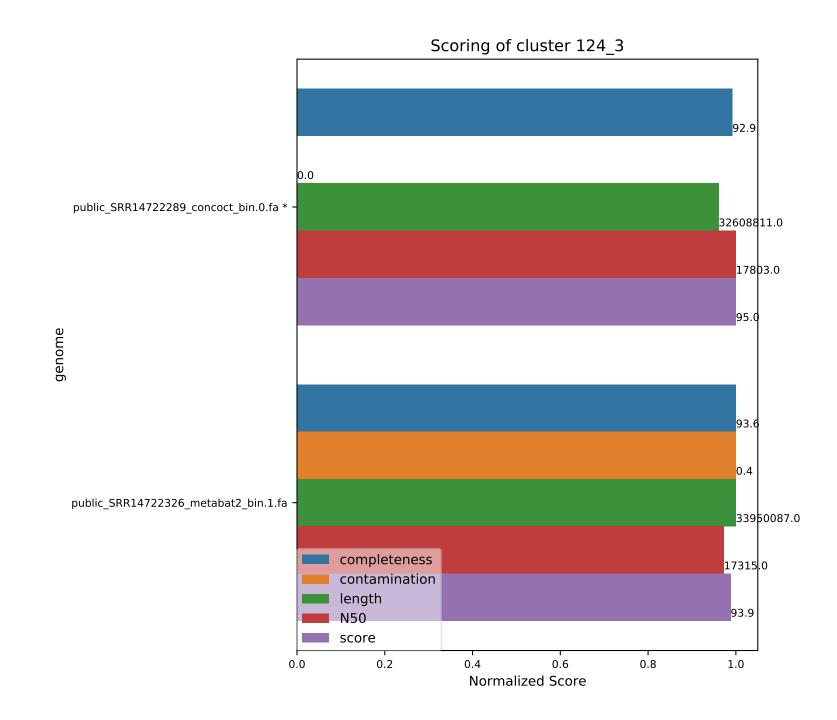


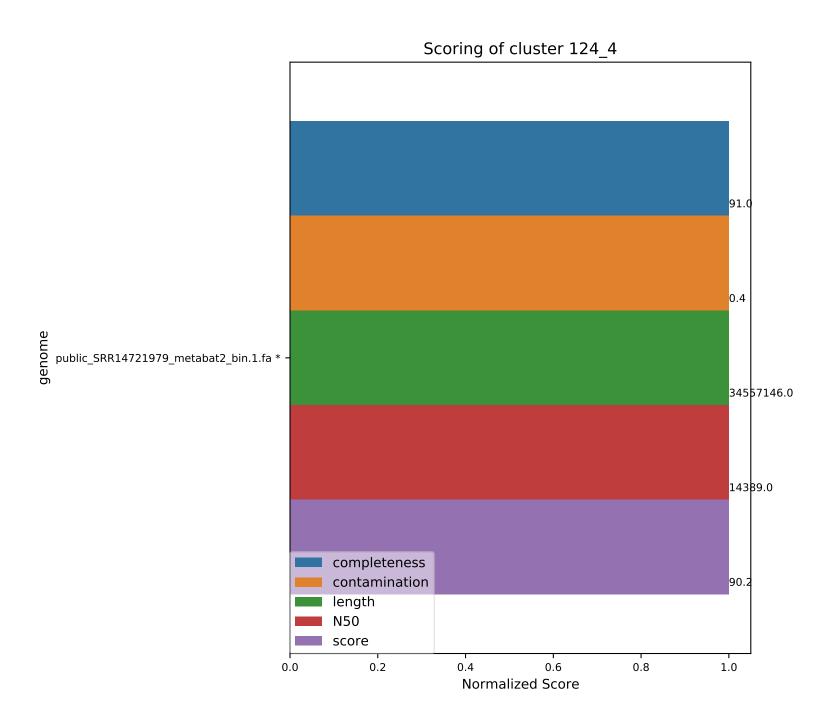


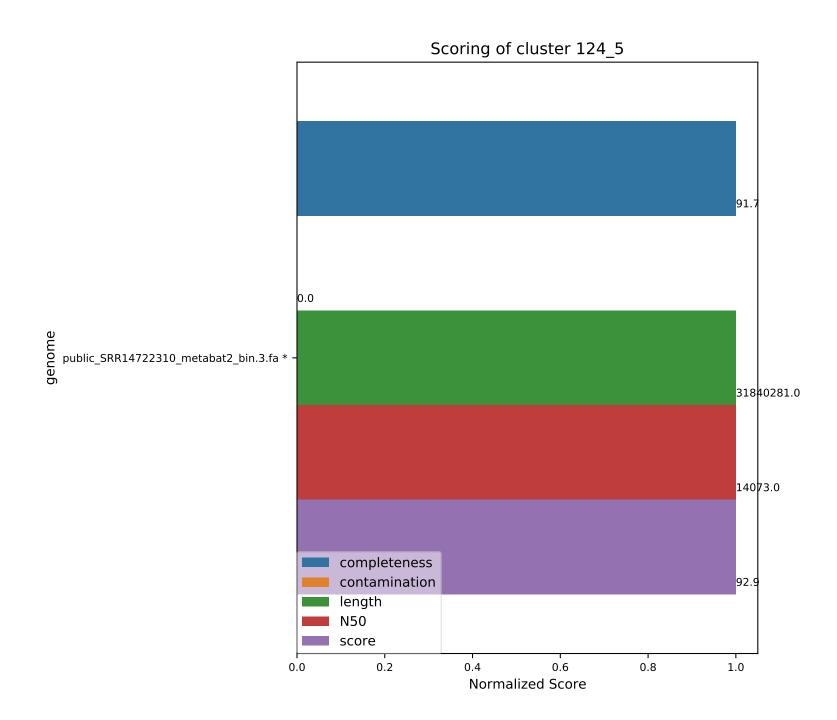


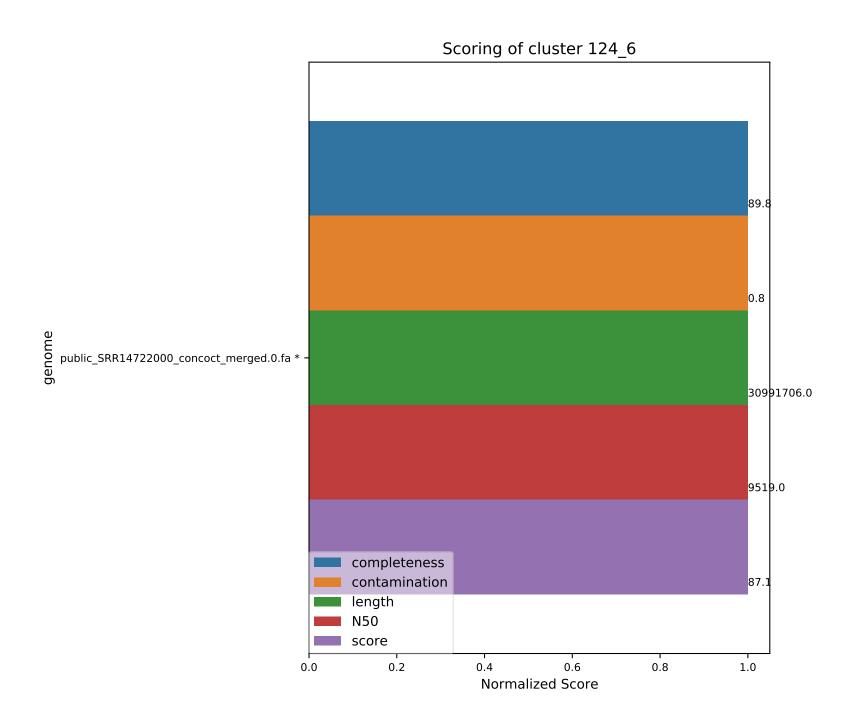


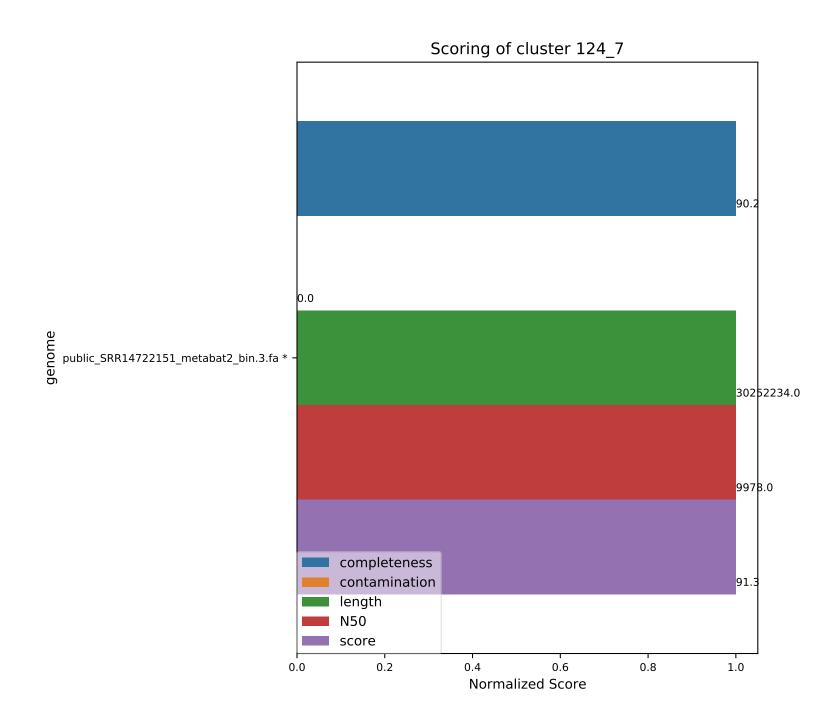


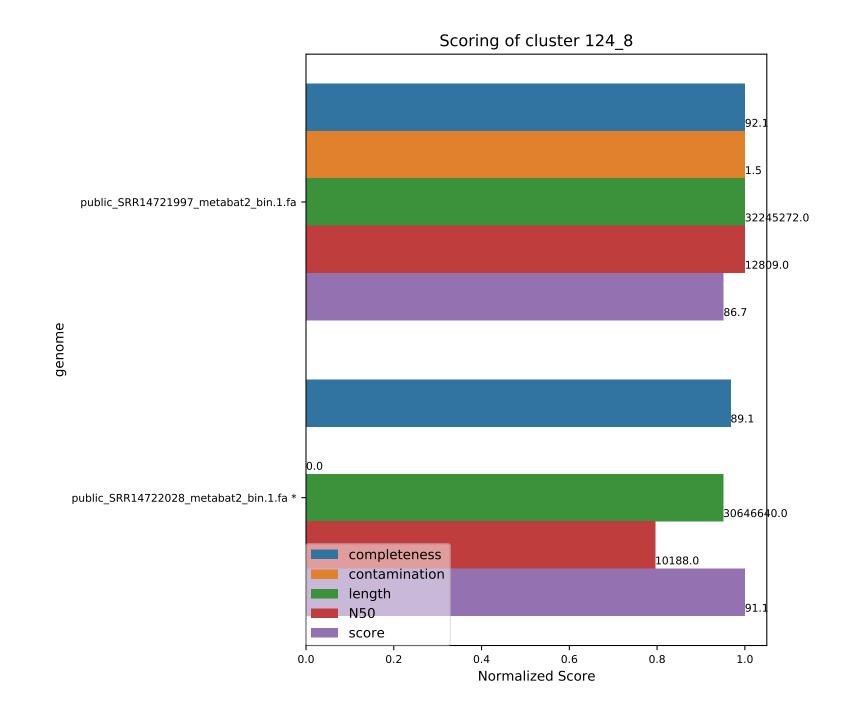


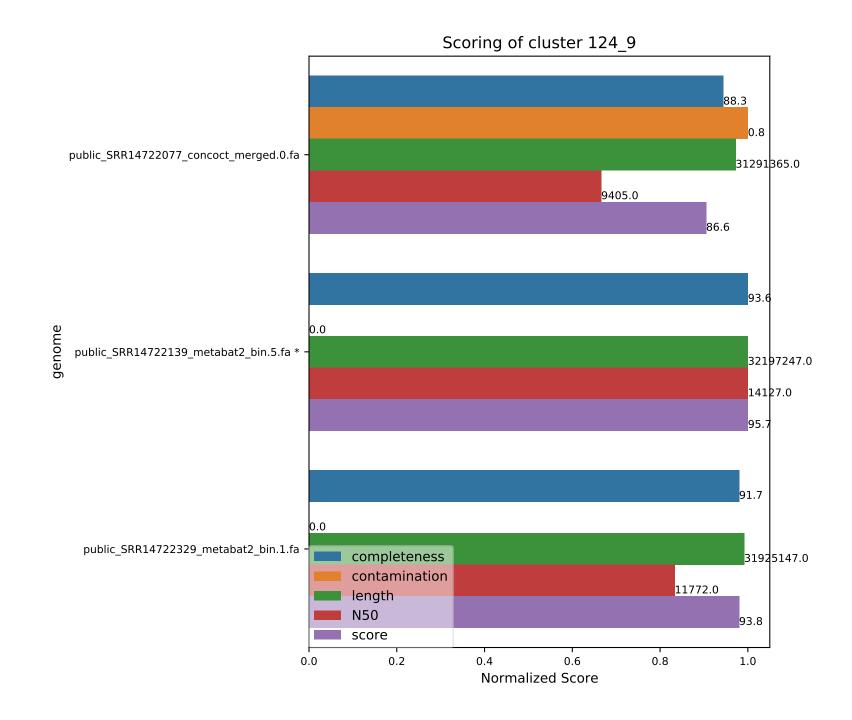


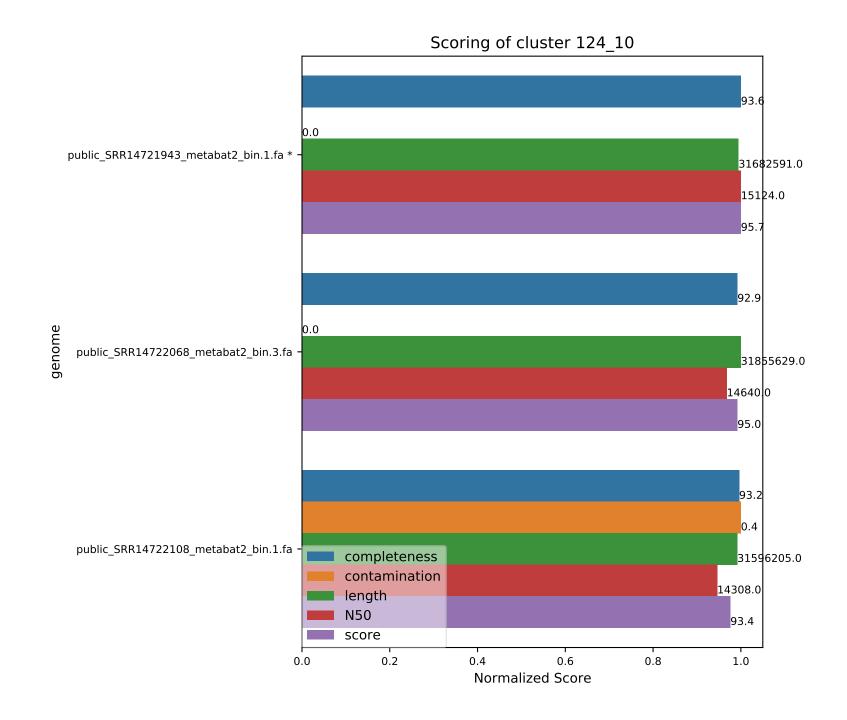


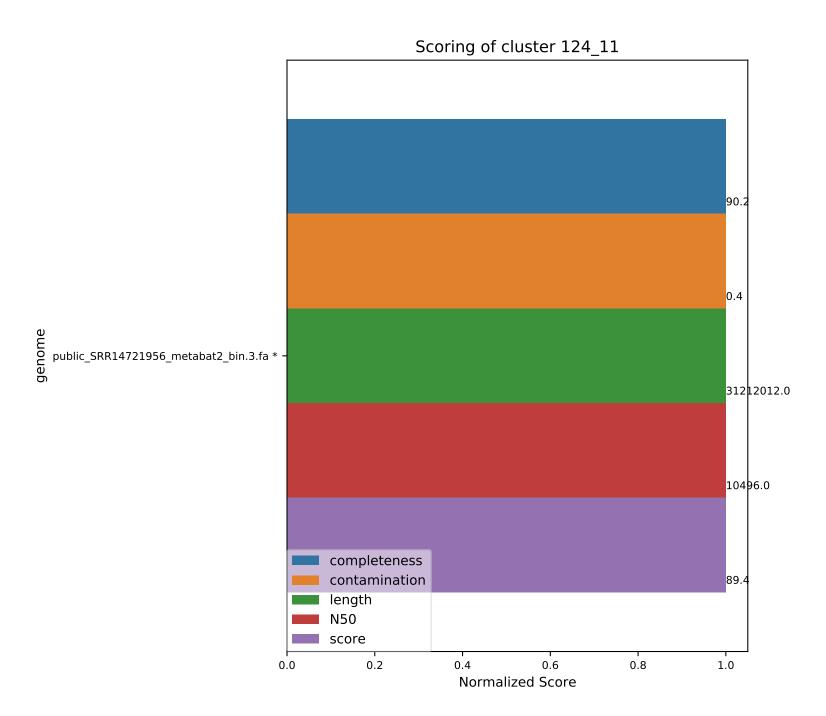


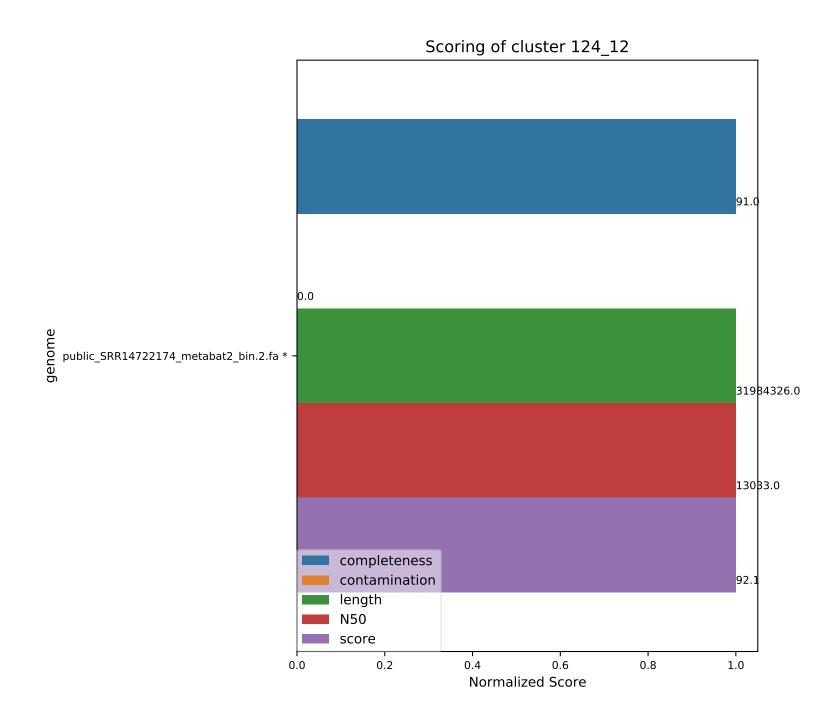


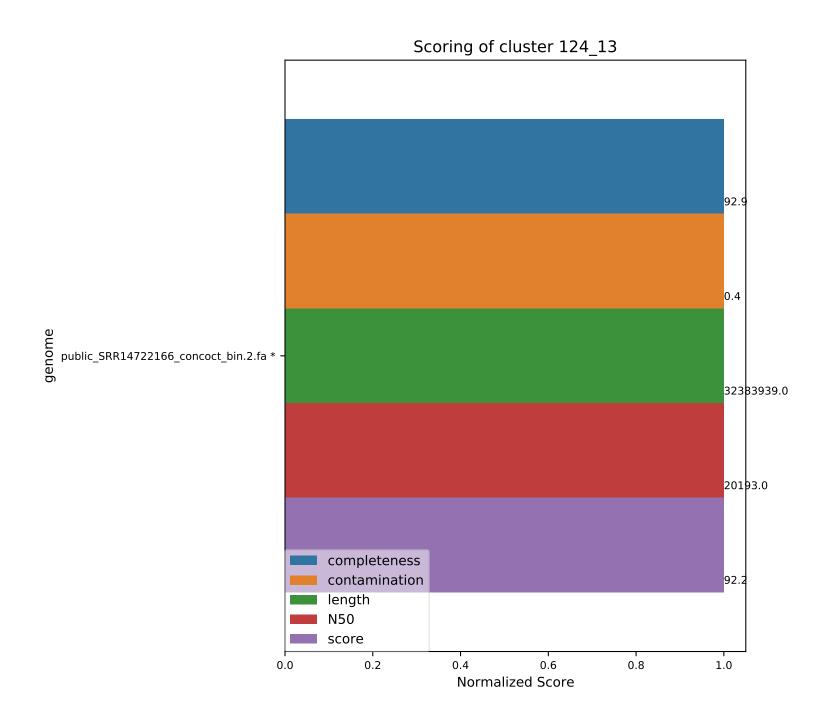


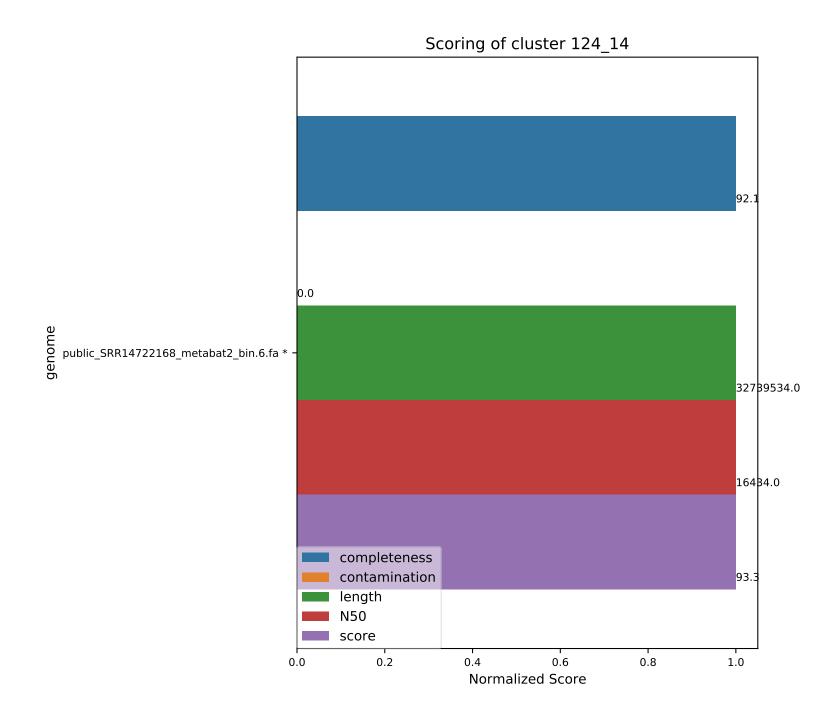


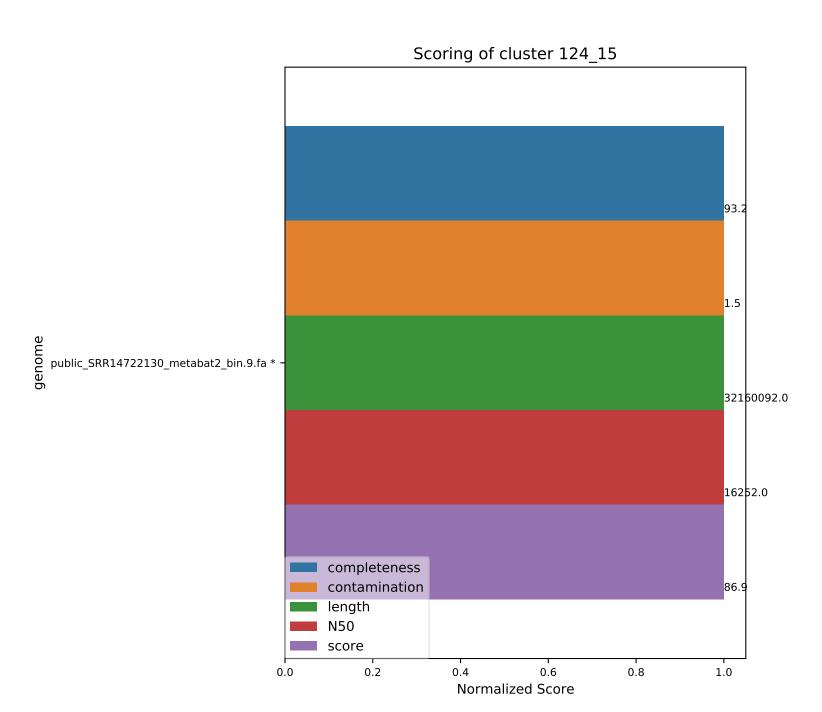


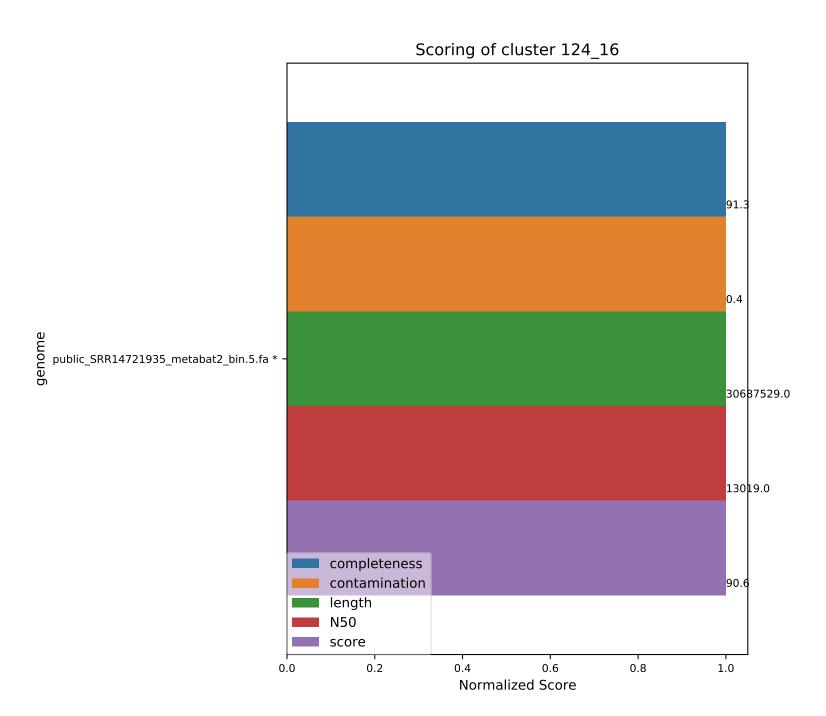


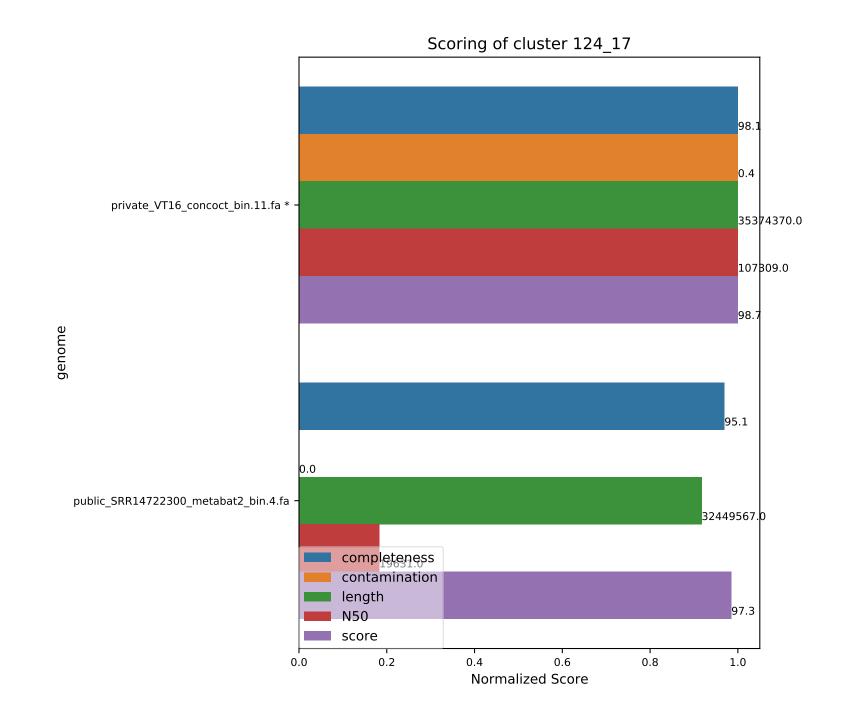


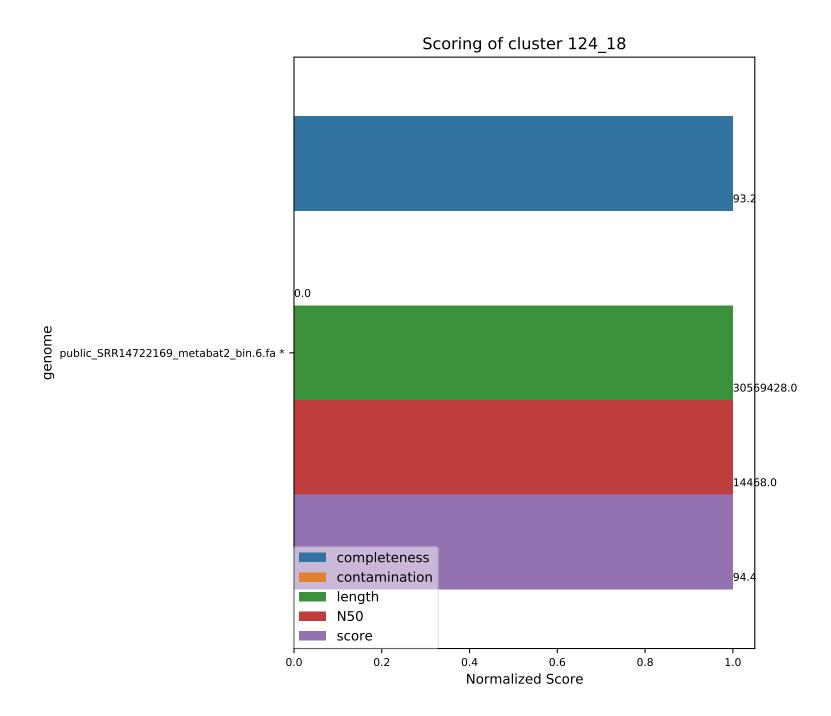


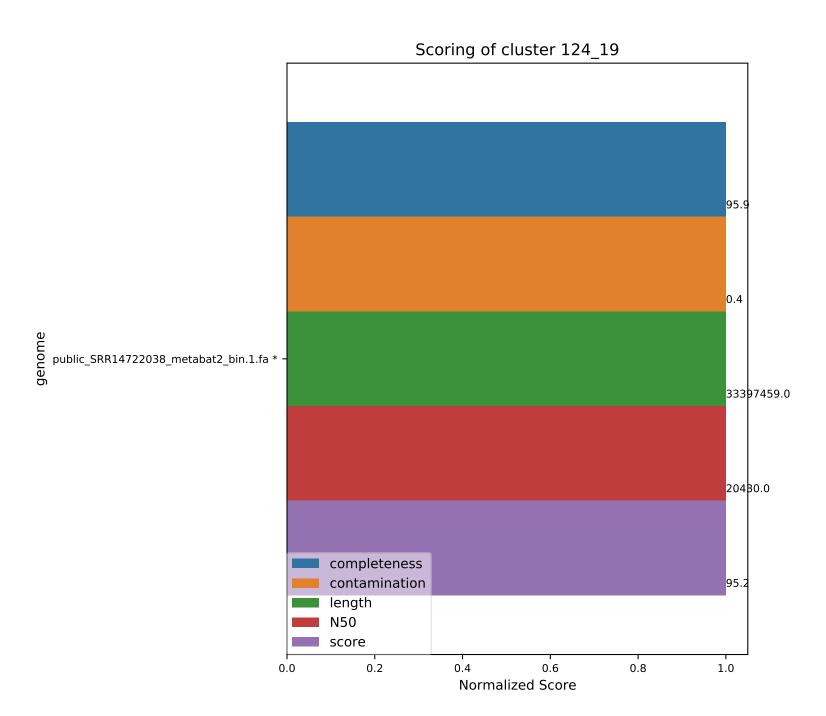


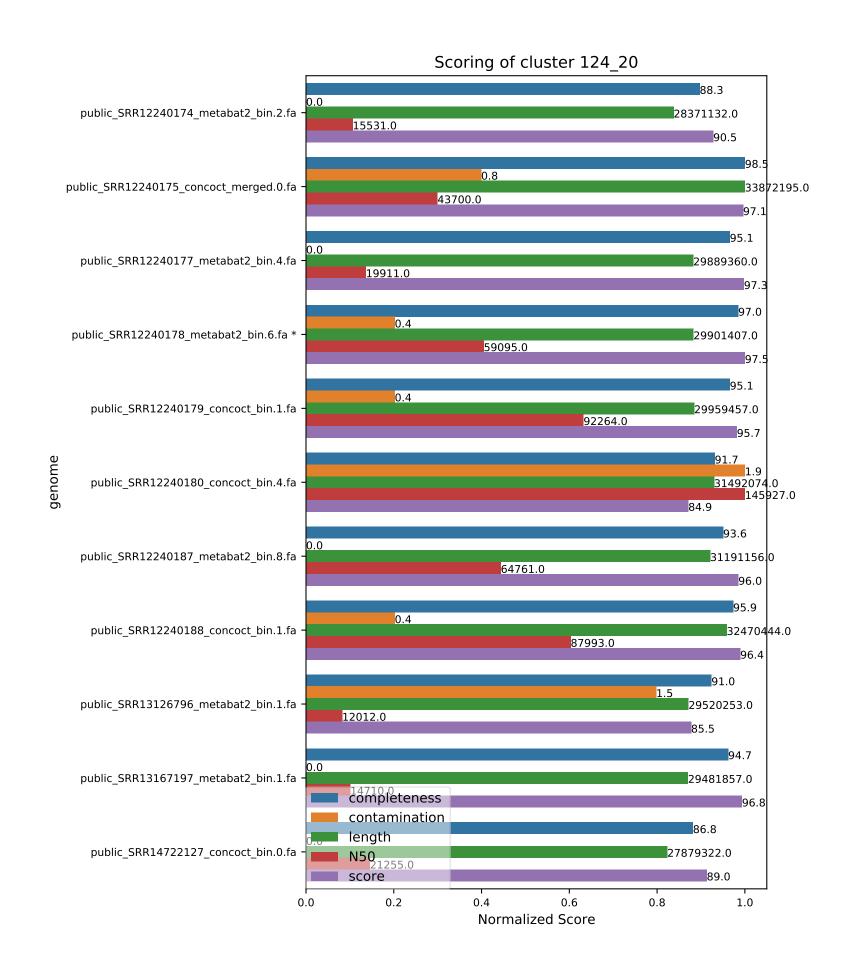


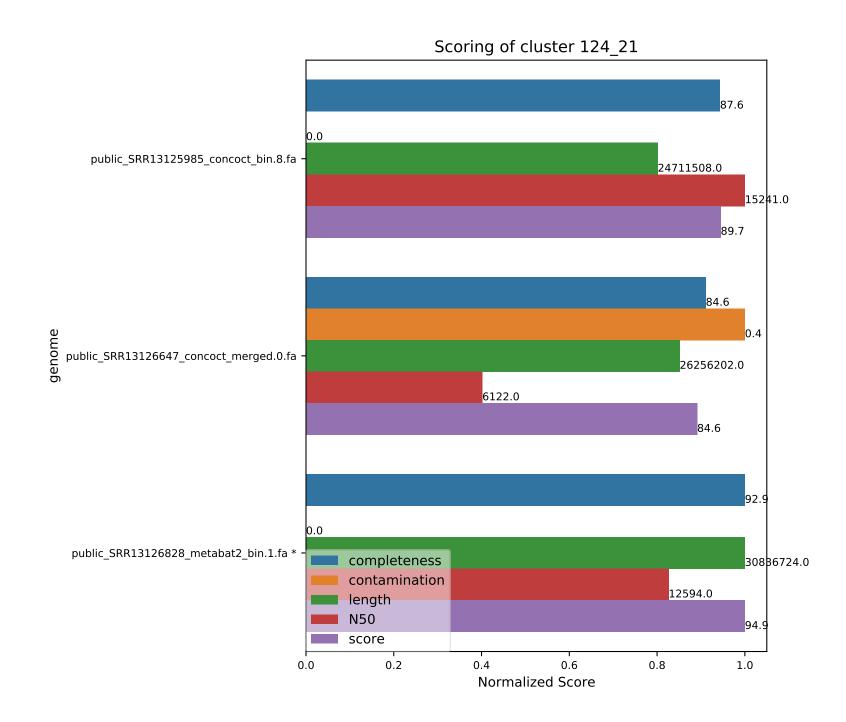


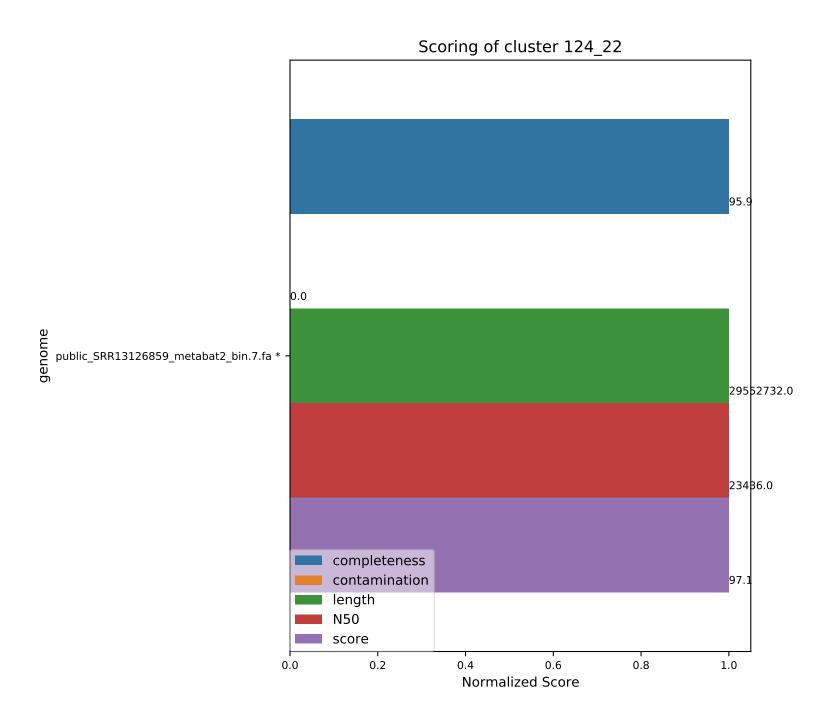












Scoring of cluster 124_23 72.9 0.4 public_SRR14721992_concoct_merged.0.fa -28661687.0 5472.0 72.9 genome 0.0 public_SRR14722106_metabat2_bin.2.fa * -34593352.0 completeness 14550.0 contamination length 95.3 N50 score 0.0 0.2 0.4 0.6 0.8 1.0

Normalized Score

