Qualimap Analysis Results

Multi-sample BAM QC analysis
Generated by Qualimap v.2.0
2016/05/27 17:12:03

# 1. Input data & parameters

1.1. Samples

ori_mapped	/export/home/amirh/novoalign_testing/blacklast/black_sorted_stats
t50	/export/home/amirh/novoalign_testing/blacklast/psorted50.bam_stats
t60	/export/home/amirh/novoalign_testing/blacklast/psorted60.bam_stats
t80	/export/home/amirh/novoalign_testing/blacklast/psorted80.bam_stats
t100	/export/home/amirh/novoalign_testing/blacklast/psorted100.bam_stats
t30	/export/home/amirh/novoalign_testing/blacklast/psorted30.bam_stats
t40	/export/home/amirh/novoalign_testing/blacklast/psorted40.bam_stats
t70	/export/home/amirh/novoalign_testing/blacklast/psorted70.bam_stats
t90	/export/home/amirh/novoalign_testing/blacklast/psorted90.bam_stats
t150	/export/home/amirh/novoalign_testing/blacklast/psorted150.bam_stats
t110	/export/home/amirh/novoalign_testing/blacklast/psorted110.bam_stats
t130	/export/home/amirh/novoalign_testing/blacklast/psorted130.bam_stats
t140	/export/home/amirh/novoalign_testing/blacklast/psorted140.bam_stats

ori_ART	/export/home/amirh/art_bin_GreatSmokyMountains/testing/old/black/black_sorted.bam_stats
t120	/export/home/amirh/novoalign_testing/blacklast/psorted120.bam_stats

2. Results : PCA
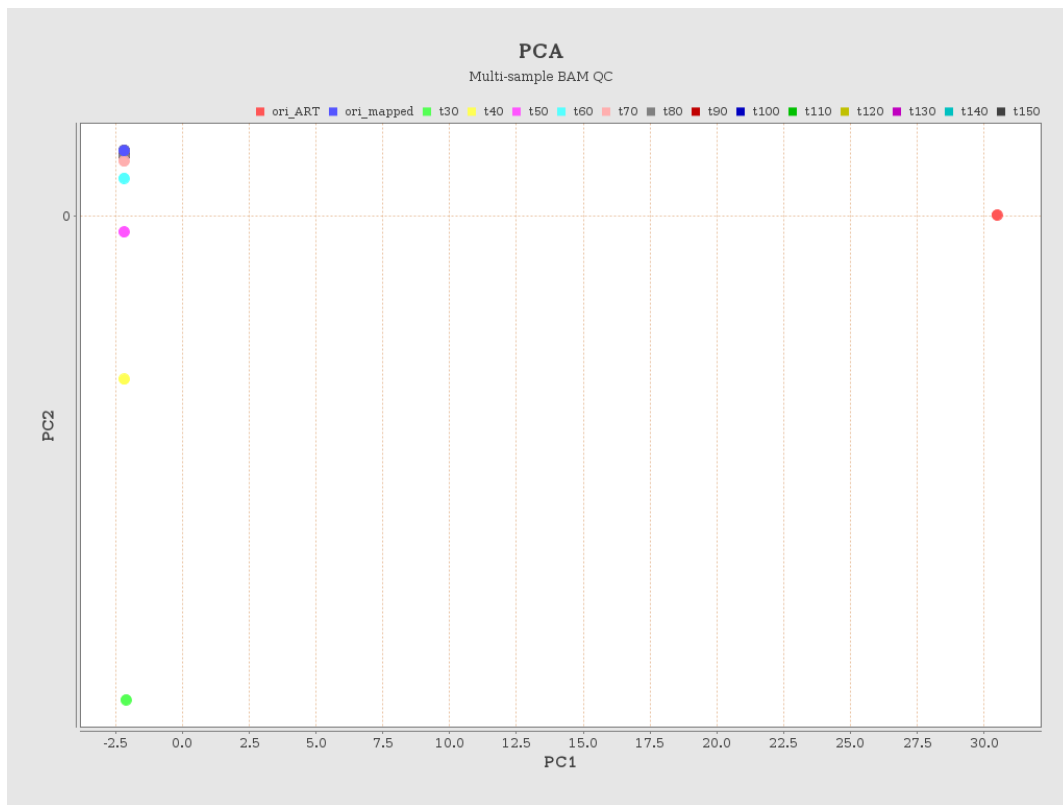
3. Results : Coverage Across Reference

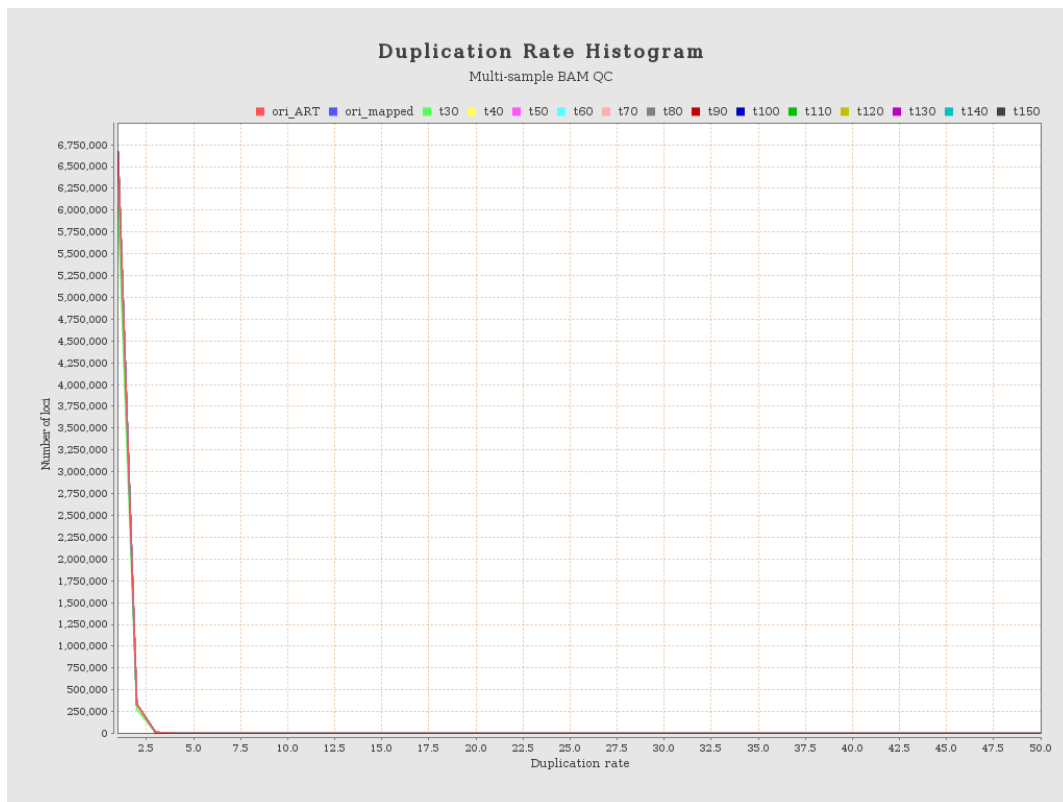**Coverage Across Reference**
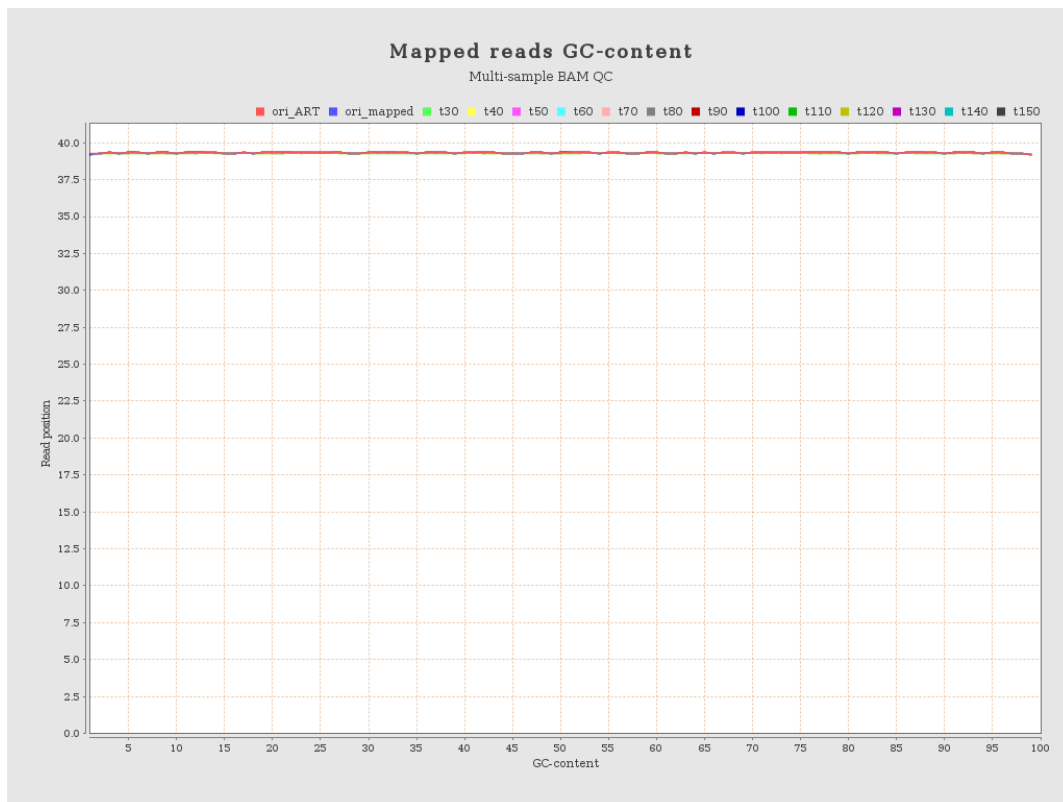Multi-sample BAM QC
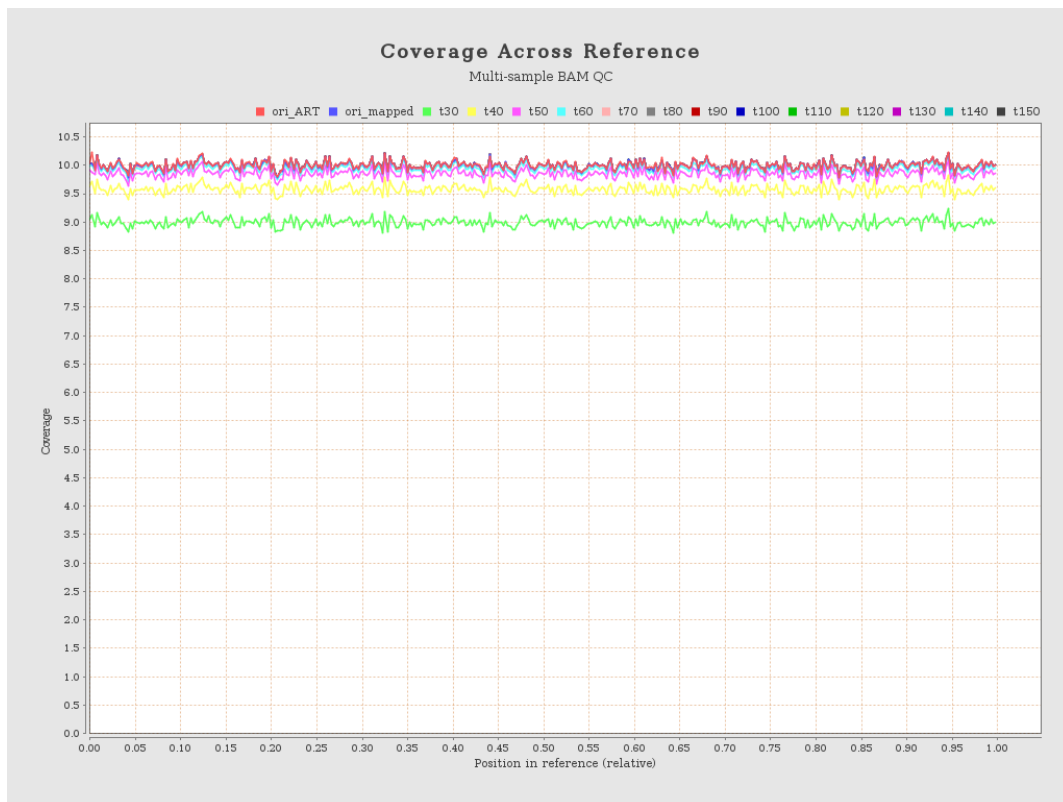
4. Results : Coverage Histogram (0-50X)
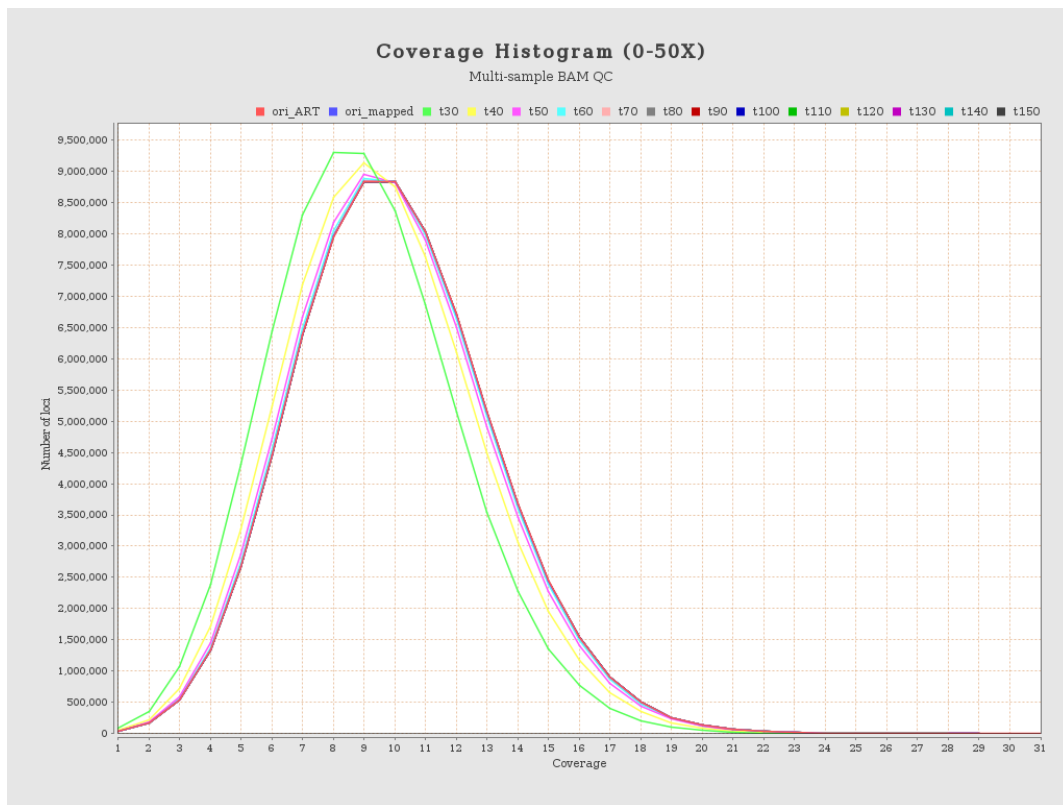
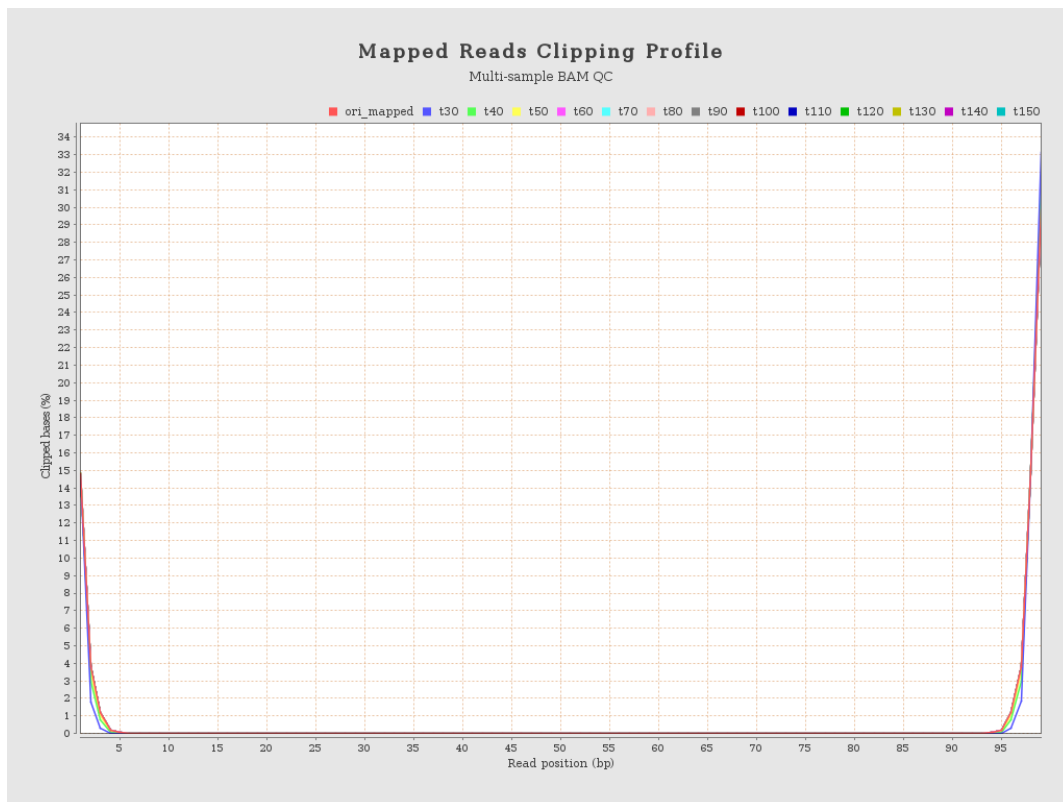# 5. Results : Genome Fraction Coverage
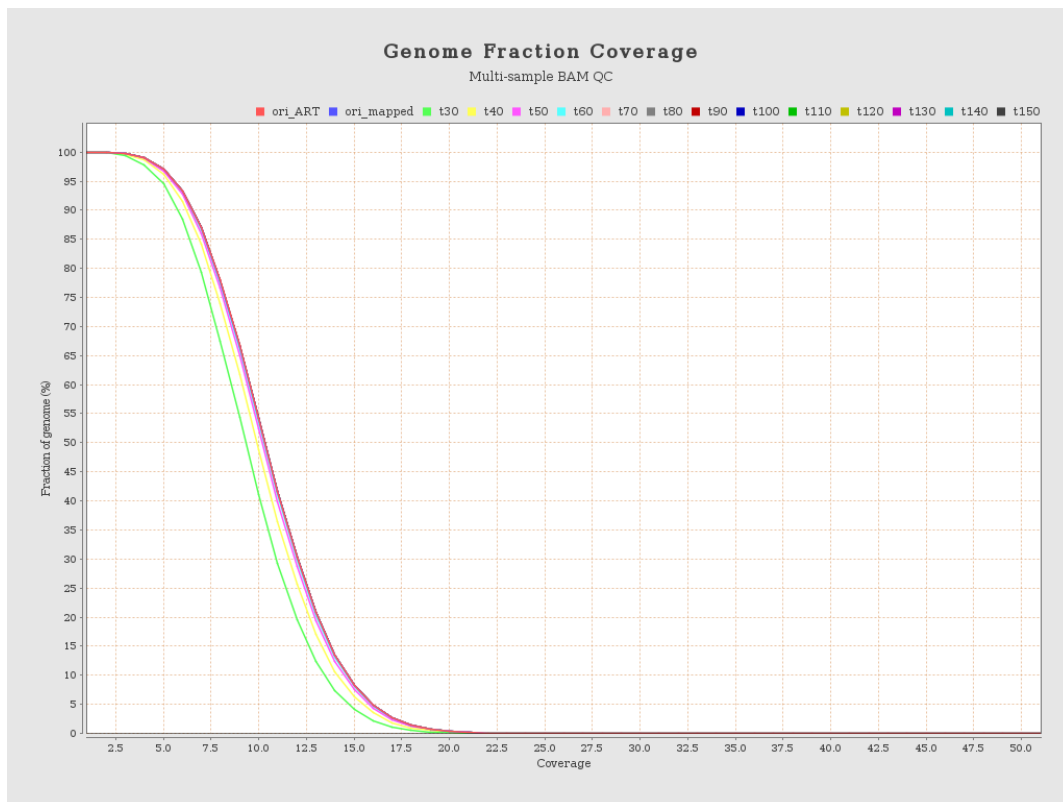
6. Results : Duplication Rate Histogram

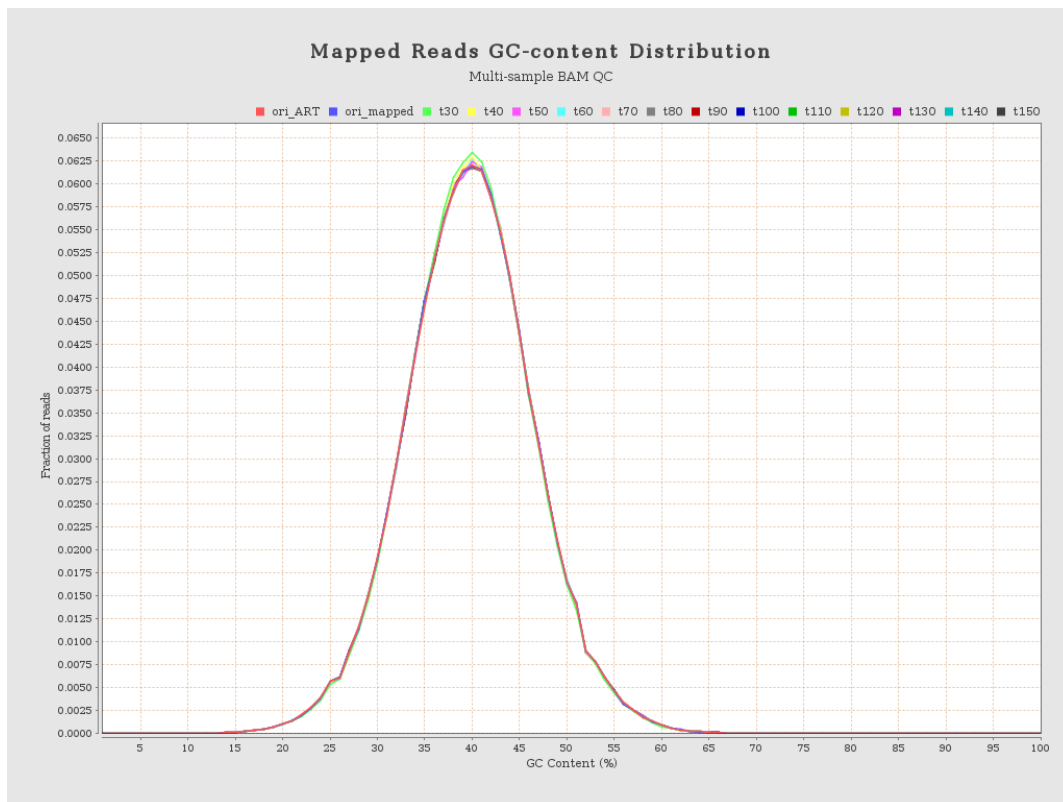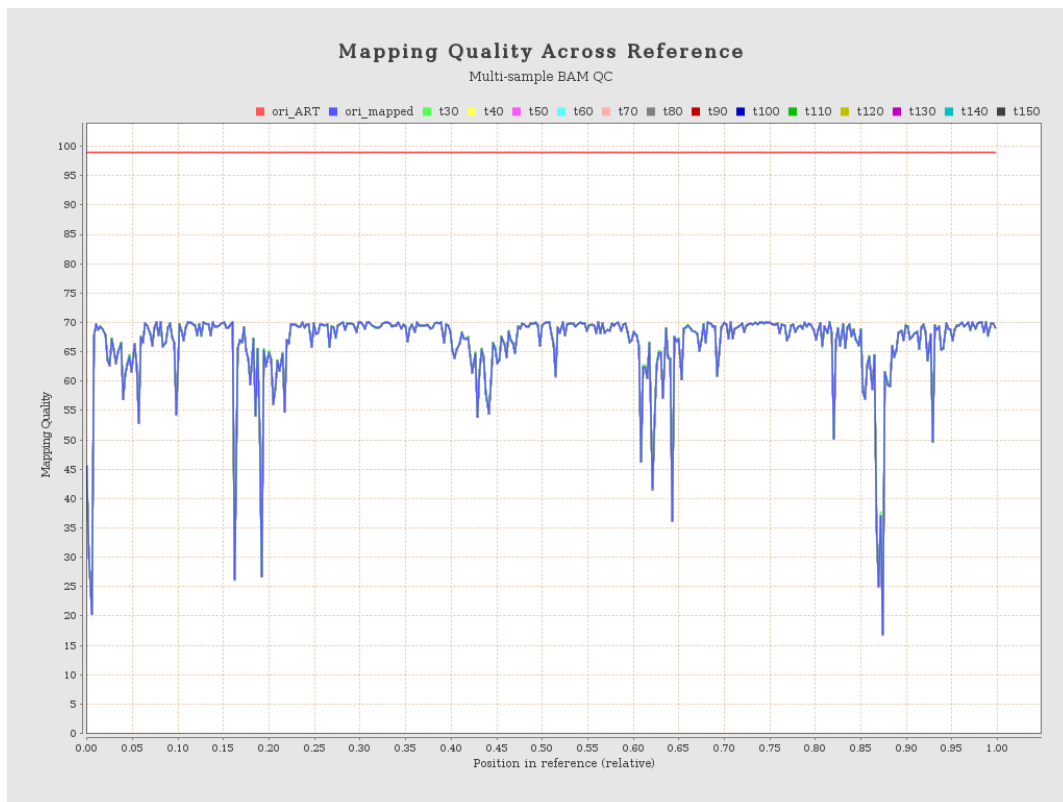# 7. Results : Mapped reads GC-content
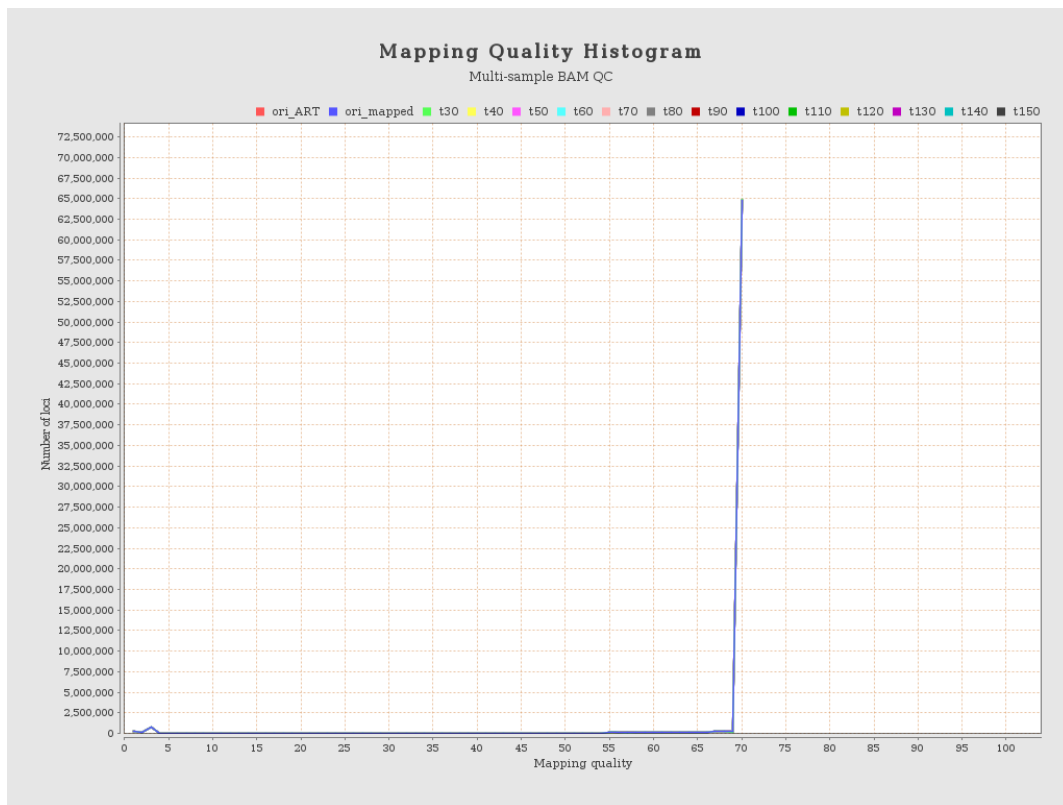
8. Results : Mapped Reads Clipping Profile

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
Multi-sample BAM QC

10. Results : Mapping Quality Across Reference

11. Results : Mapping Quality Histogram

12. Results : Insert Size Across Reference

Insert Size Across Reference

Multi-sample BAM QC

No data available.

13. Results : Insert Size Histogram

Insert Size Histogram
Multi-sample BAM QC

No data available.