Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 12:36:46

1. Input data & parameters

1.1. QualiMap command line

> qualimap bamqc -bam
> /home/vdp5/data/cambodia_samples/sequences_bam/OM093.sorted.bam.ba
> m -nw 400 -hm 3

1.2. Alignment

Command line:	bwa mem -M /home/vdp5/data/salvador_vivax_asia_2016/first-SAMEA2376790/pvivax_sal1_SAMEA2376790.fasta /home/vdp5/data/cambodia_samples/sequences_gz/OM-093_CGATGT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM-093_CGATGT_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:36:45 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM093.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	86,172,059
Mapped reads	3,955,334 / 4.59%
Unmapped reads	82,216,725 / 95.41%
Mapped paired reads	3,955,334 / 4.59%
Mapped reads, first in pair	1,975,276 / 2.29%
Mapped reads, second in pair	1,980,058 / 2.3%
Mapped reads, both in pair	3,328,219 / 3.86%
Mapped reads, singletons	627,115 / 0.73%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	1,279,245 / 1.48%
Duplication rate	17.56%
Clipped reads	1,045,245 / 1.21%

2.2. ACGT Content

Number/percentage of A's	100,240,551 / 29.45%
Number/percentage of C's	68,336,805 / 20.08%
Number/percentage of T's	103,315,793 / 30.36%
Number/percentage of G's	68,432,554 / 20.11%
Number/percentage of N's	10,914 / 0%
GC Percentage	40.19%

2.3. Coverage

Mean	14.2232
Standard Deviation	113.9469

2.4. Mapping Quality

Mean Mapping Quality	55.12

2.5. Insert size

Mean	1,511.28
Standard Deviation	41,734.45
P25/Median/P75	183 / 198 / 228

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	3,653,198
Insertions	153,421
Mapped reads with at least one insertion	3.48%
Deletions	169,643
Mapped reads with at least one deletion	3.49%
Homopolymer indels	58.21%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|107412047 8|emb|LT615 256.1|	977217	12878812	13.1791	23.9902
gi|107412068 2|emb|LT615 257.1|	860454	12650609	14.7022	45.5146
gi|107412086 5|emb|LT615 258.1|	989719	15022501	15.1786	46.443
gi|107412108 6|emb|LT615 259.1|	935450	13228104	14.1409	19.5123
gi|107412130 1|emb|LT615 260.1|	1432239	21826414	15.2394	60.9312
gi|107412161 5|emb|LT615 261.1|	1080962	14981524	13.8594	40.0556
gi|107412187 1|emb|LT615 262.1|	1545099	20870313	13.5074	26.0677
gi|107412223 5|emb|LT615 263.1|	1585108	24114744	15.2133	173.7475
gi|107412259 0|emb|LT615 264.1|	2122358	29736178	14.0109	78.9938
gi|107412305 0|emb|LT615 265.1|	1754192	28137924	16.0404	333.7621
gi|107412342 1|emb|LT615	2150147	30767206	14.3094	37.8777

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	42616673	14.0601	107.1199
gi|1074124588|emb|LT615268.1|	2359348	30914054	13.1028	25.9041
gi|1074125065|emb|LT615269.1|	3135668	43027448	13.7219	26.3244

3. Results : Coverage across reference

Coverage across reference
0M093.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM093.sorted.bam.bam
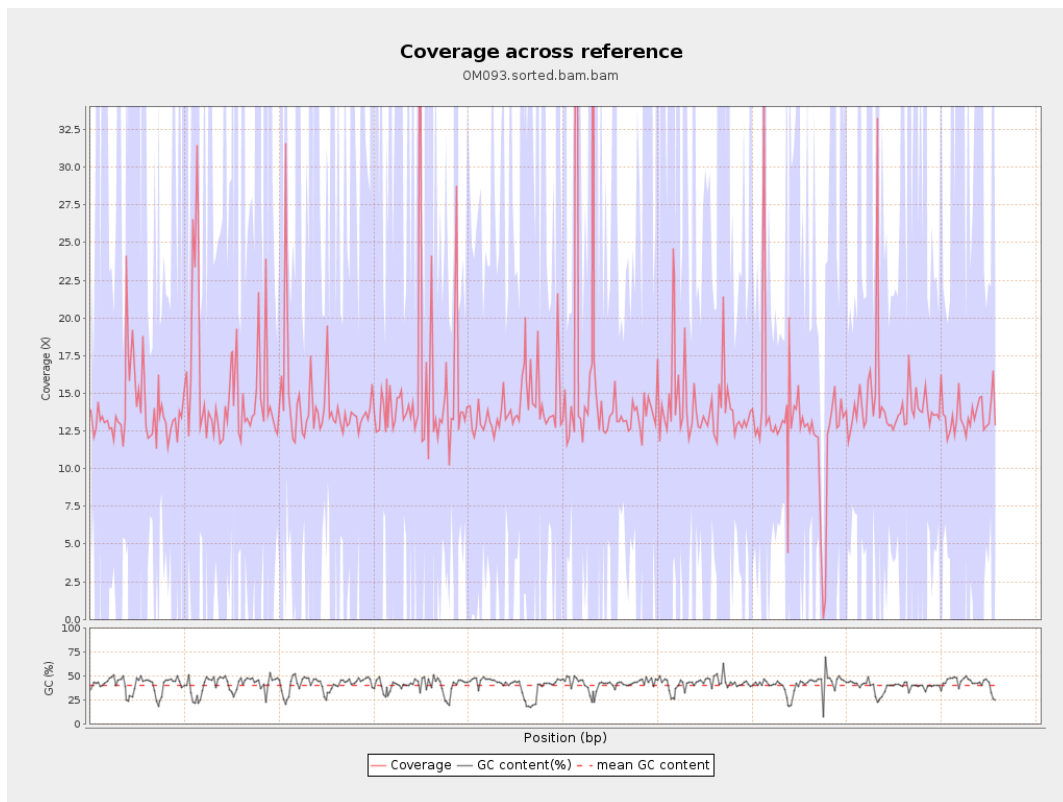
5. Results : Coverage Histogram (0-50X)
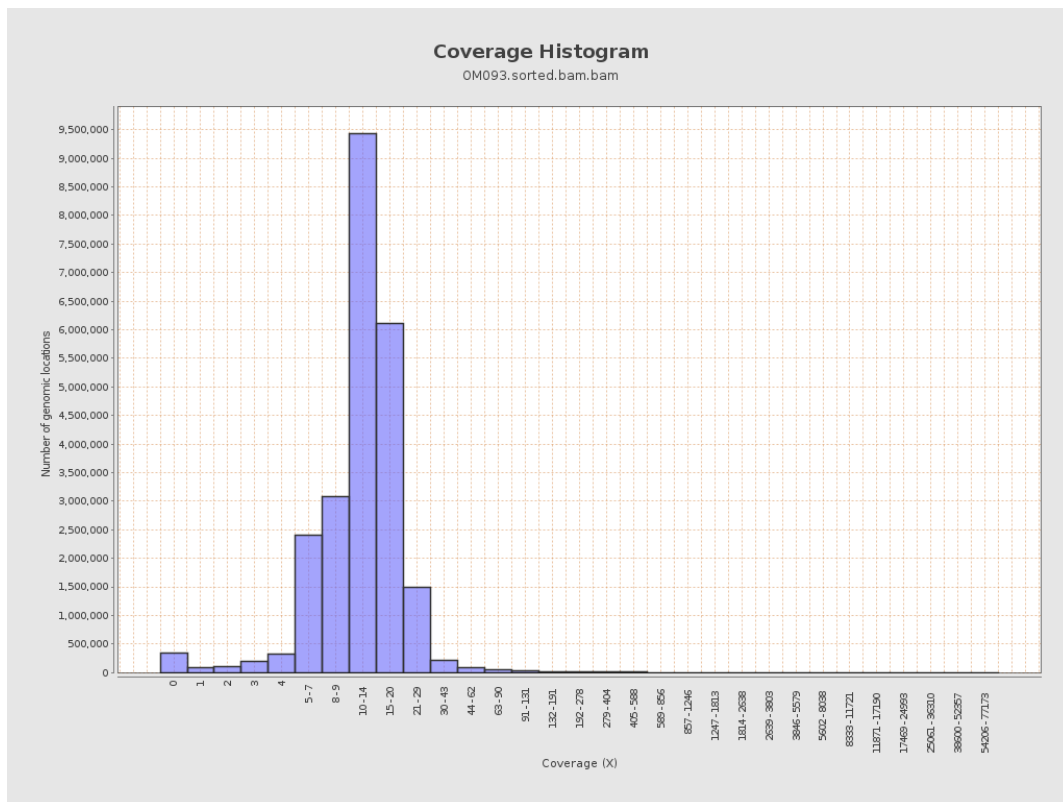
Coverage Histogram (0-50X)
OM093.sorted.bam.bam
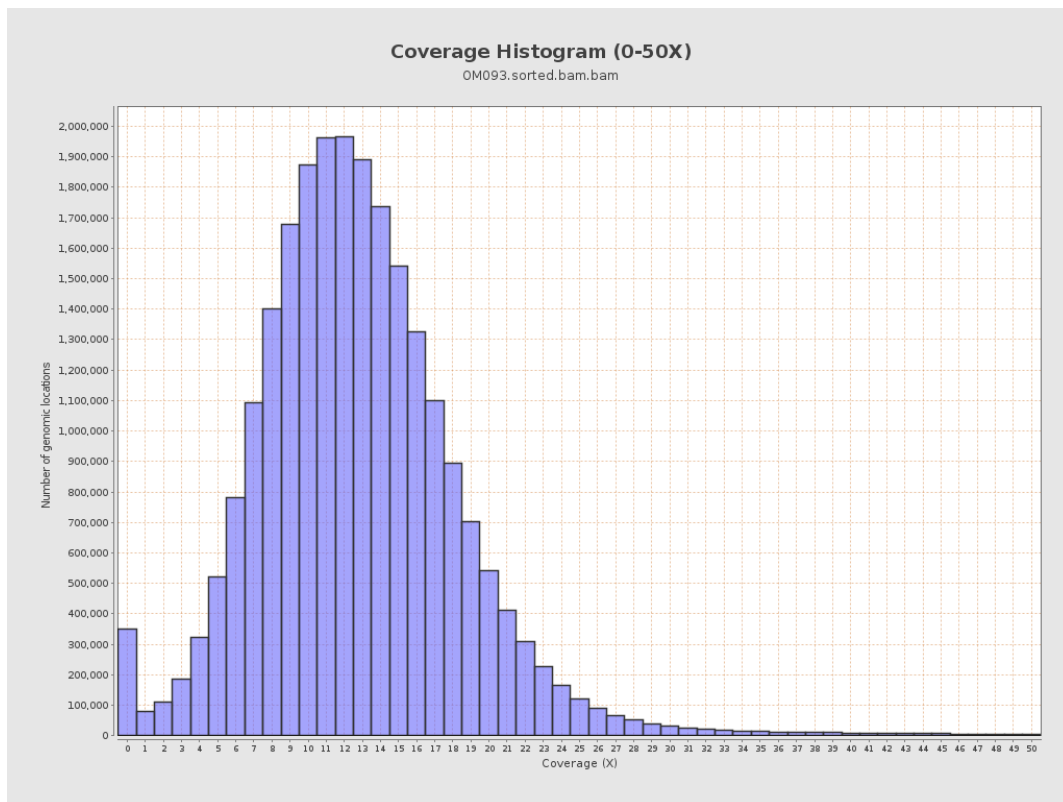
6. Results : Genome Fraction Coverage
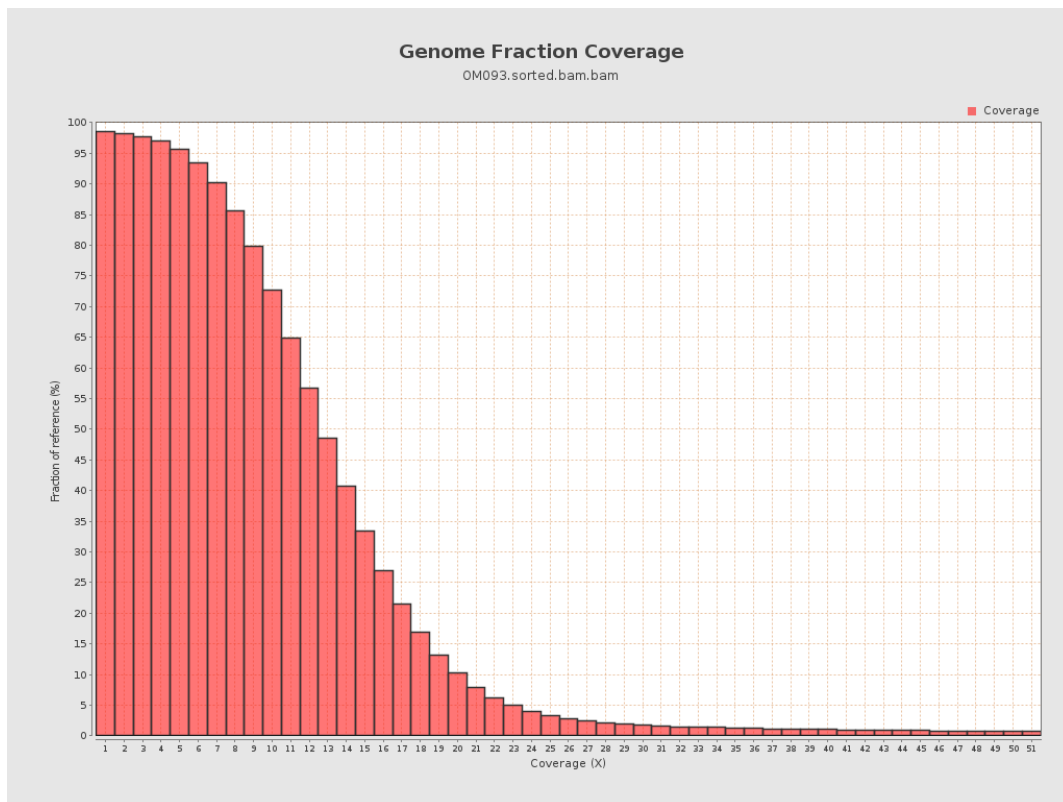
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
0M093.sorted.bam.bam
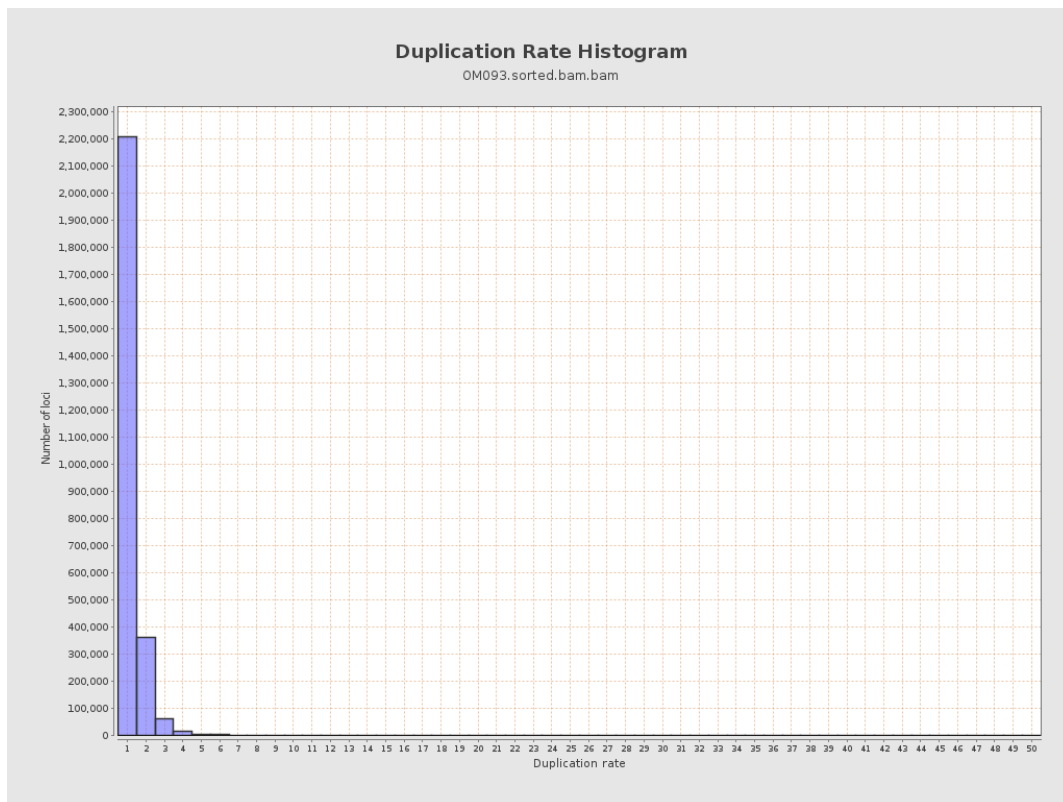
8. Results : Mapped Reads Nucleotide Content
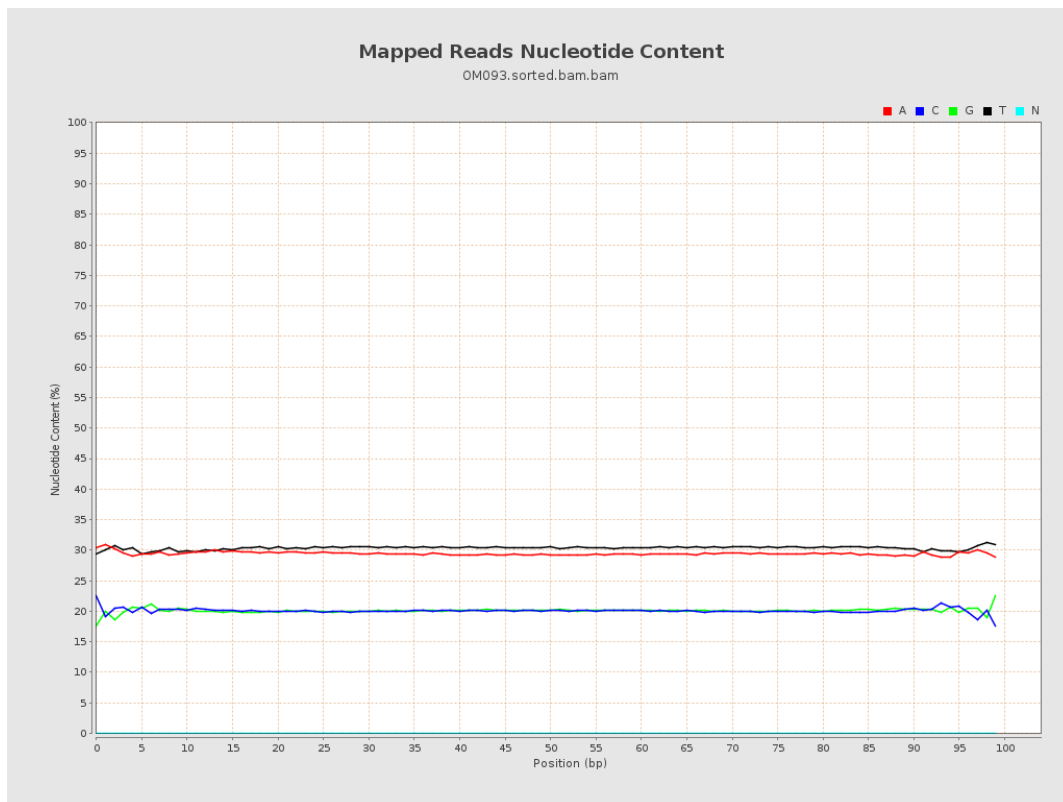
9. Results : Mapped Reads GC-content Distribution
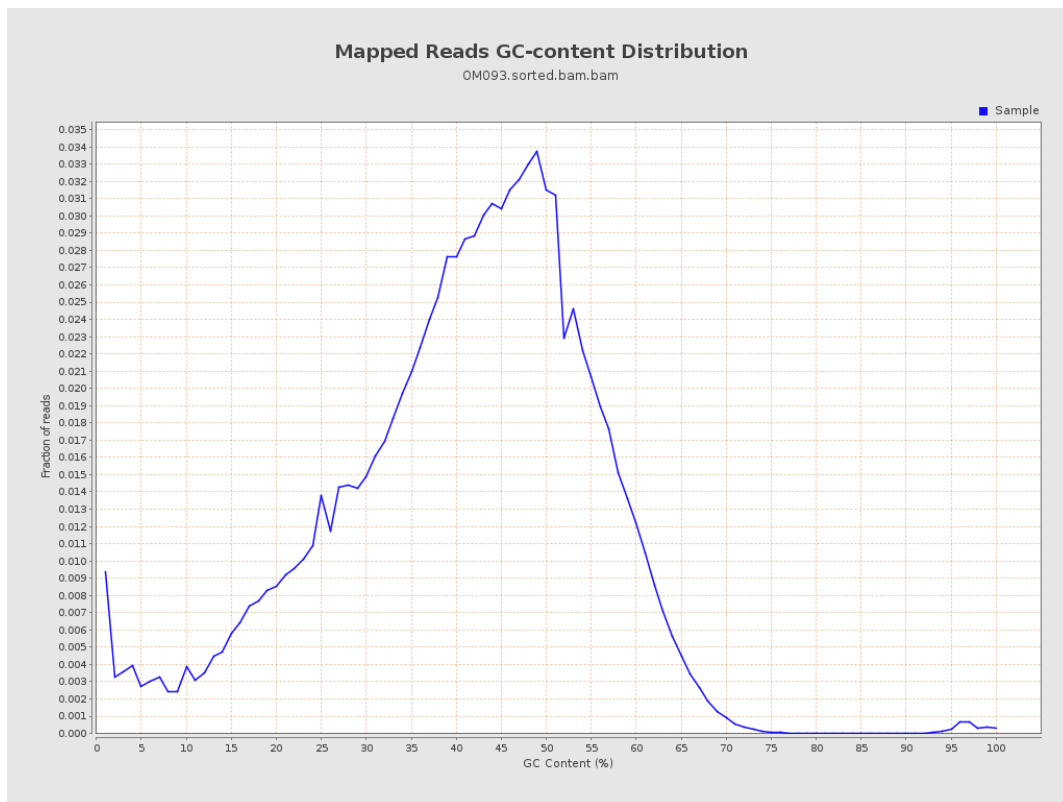
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
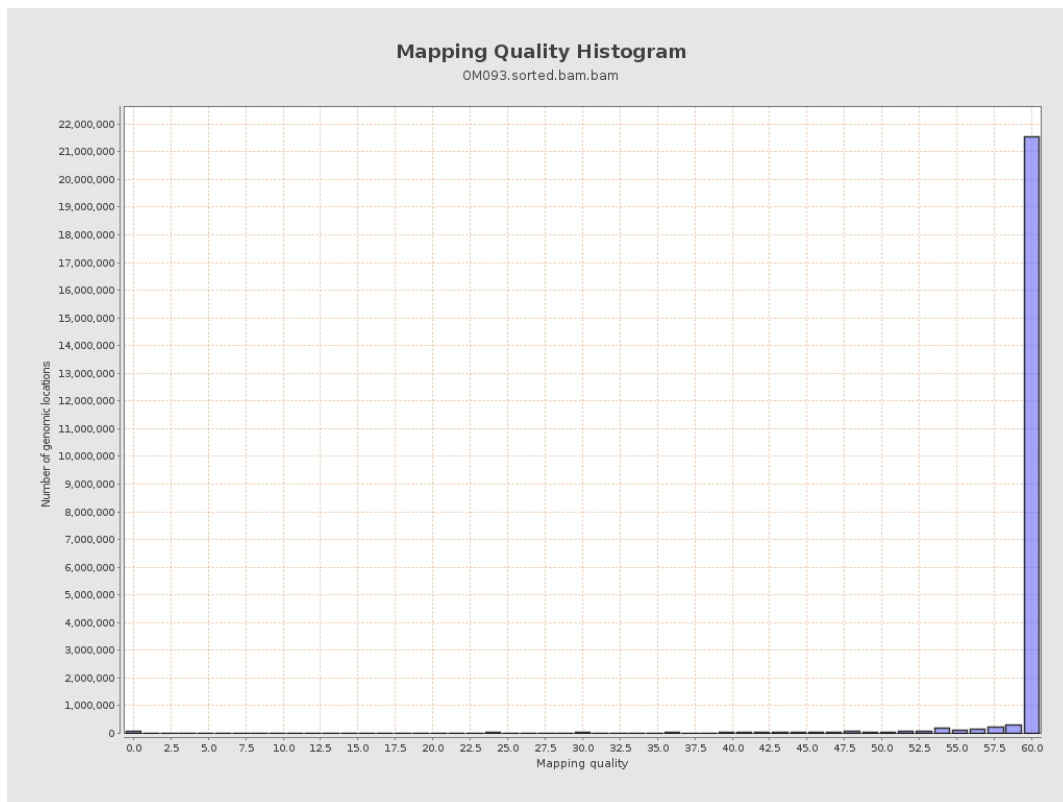OM093.sorted.bam.bam
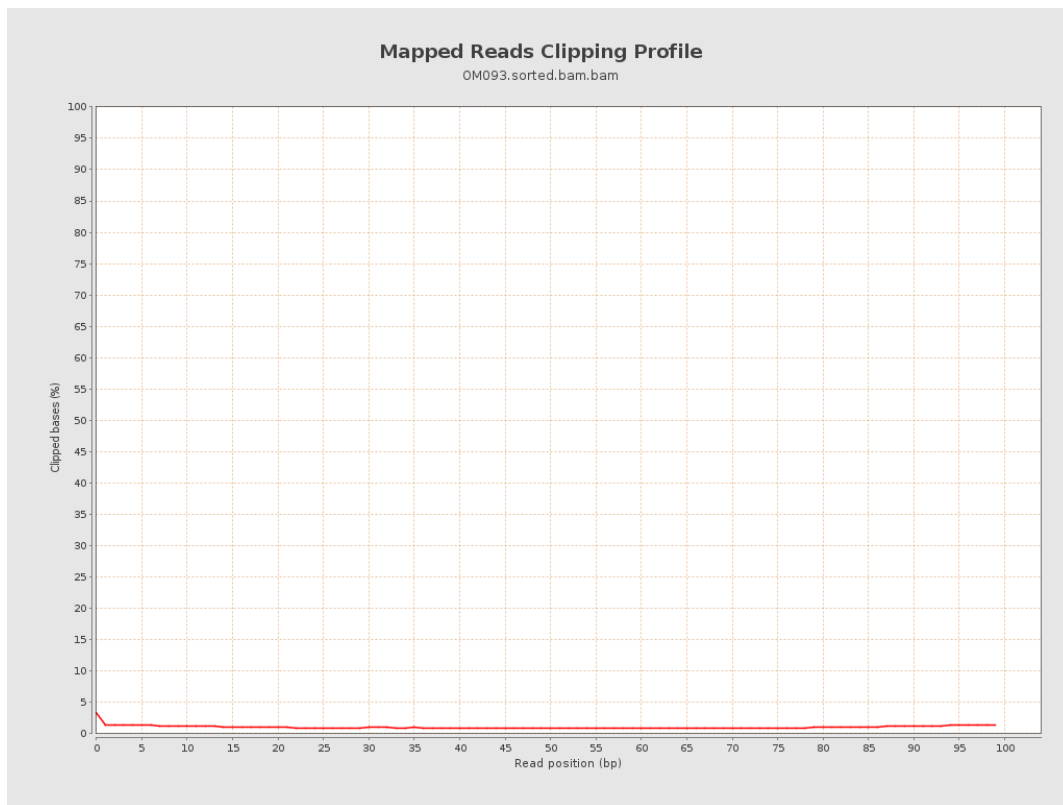
11. Results : Homopolymer Indels
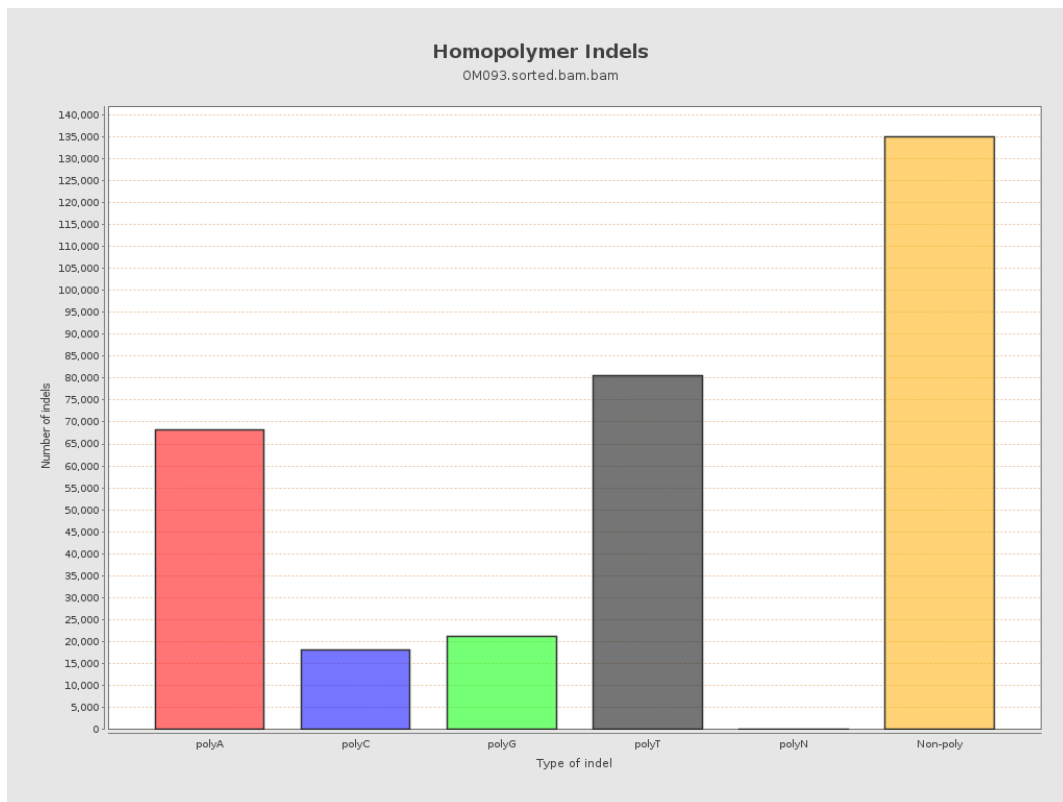
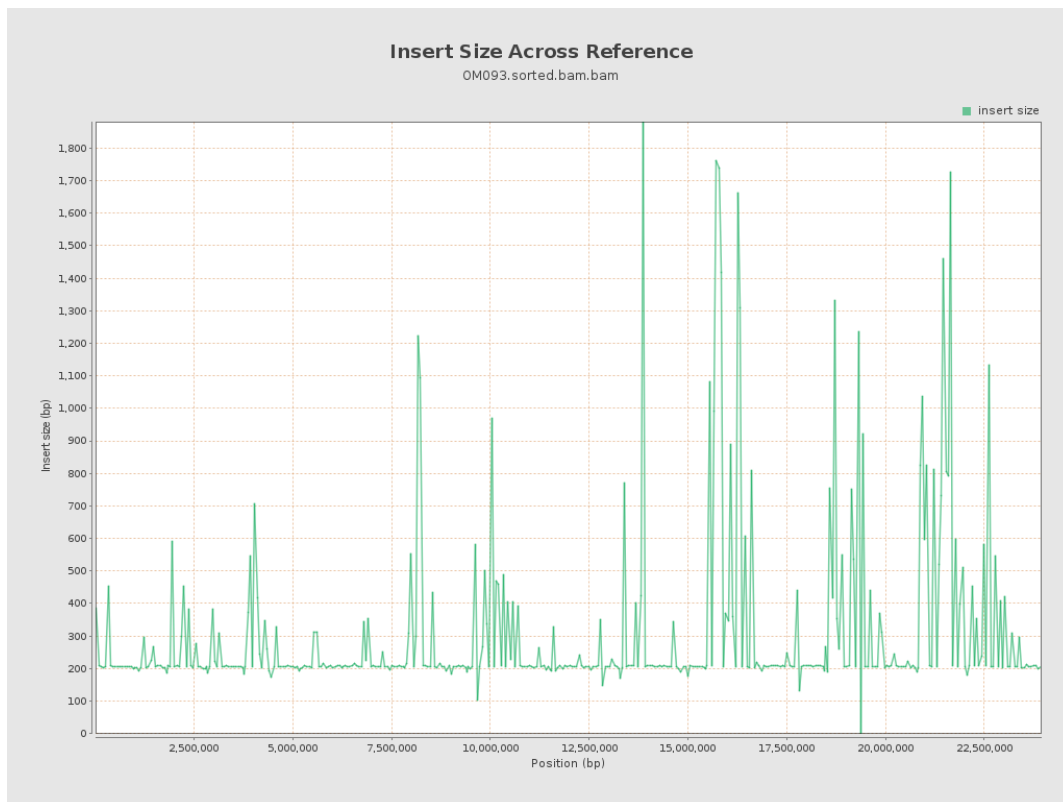# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM093.sorted.bam.bam

15. Results : Insert Size Histogram