Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:44:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM208.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/OM208-BiooBarcode19_GTGAAA_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM208-BiooBarcode19_GTGAAA_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:44:00 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM208.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	17,086,772
Mapped reads	4,128,426 / 24.16%
Unmapped reads	12,958,346 / 75.84%
Mapped paired reads	4,128,426 / 24.16%
Mapped reads, first in pair	2,068,052 / 12.1%
Mapped reads, second in pair	2,060,374 / 12.06%
Mapped reads, both in pair	3,999,316 / 23.41%
Mapped reads, singletons	129,110 / 0.76%
Read min/max/mean length	30 / 100 / 99.95
Duplicated reads (estimated)	673,699 / 3.94%
Duplication rate	12.7%
Clipped reads	493,202 / 2.89%

2.2. ACGT Content

Number/percentage of A's	117,975,050 / 29.84%
Number/percentage of C's	79,486,972 / 20.1%
Number/percentage of T's	118,602,420 / 30%
Number/percentage of G's	79,314,578 / 20.06%
Number/percentage of N's	35,809 / 0.01%
GC Percentage	40.16%

2.3. Coverage

Mean	16.5198
Standard Deviation	17.7781

2.4. Mapping Quality

Mean Mapping Quality	58.29

2.5. Insert size

Mean	725.31
Standard Deviation	29,192.18
P25/Median/P75	184 / 192 / 202

2.6. Mismatches and indels

General error rate	1.38%
Mismatches	5,155,838
Insertions	128,980
Mapped reads with at least one insertion	2.95%
Deletions	146,400
Mapped reads with at least one deletion	3.32%
Homopolymer indels	63.76%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	14514728	14.8531	7.66
gi|1074120682|emb|LT615257.1|	860454	13228792	15.3742	10.8385
gi|1074120865|emb|LT615258.1|	989719	18209437	18.3986	22.6575
gi|1074121086|emb|LT615259.1|	935450	17002111	18.1753	22.4898
gi|1074121301|emb|LT615260.1|	1432239	25067522	17.5023	16.303
gi|1074121615|emb|LT615261.1|	1080962	18195663	16.8328	14.1883
gi|1074121871|emb|LT615262.1|	1545099	24908848	16.1212	7.9888
gi|1074122235|emb|LT615263.1|	1585108	26170442	16.5102	24.7114
gi|1074122590|emb|LT615264.1|	2122358	33777168	15.9149	7.9351
gi|1074123050|emb|LT615265.1|	1754192	29259955	16.68	37.6682
gi|1074123421|emb|LT615	2150147	36700024	17.0686	19.477

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	49051654	16.1831	14.8991
gi|1074124588|emb|LT615268.1|	2359348	37622520	15.9462	14.0892
gi|1074125065|emb|LT615269.1|	3135668	52087784	16.6114	7.4576

3. Results : Coverage across reference

Coverage across reference
OM208.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
0M208.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
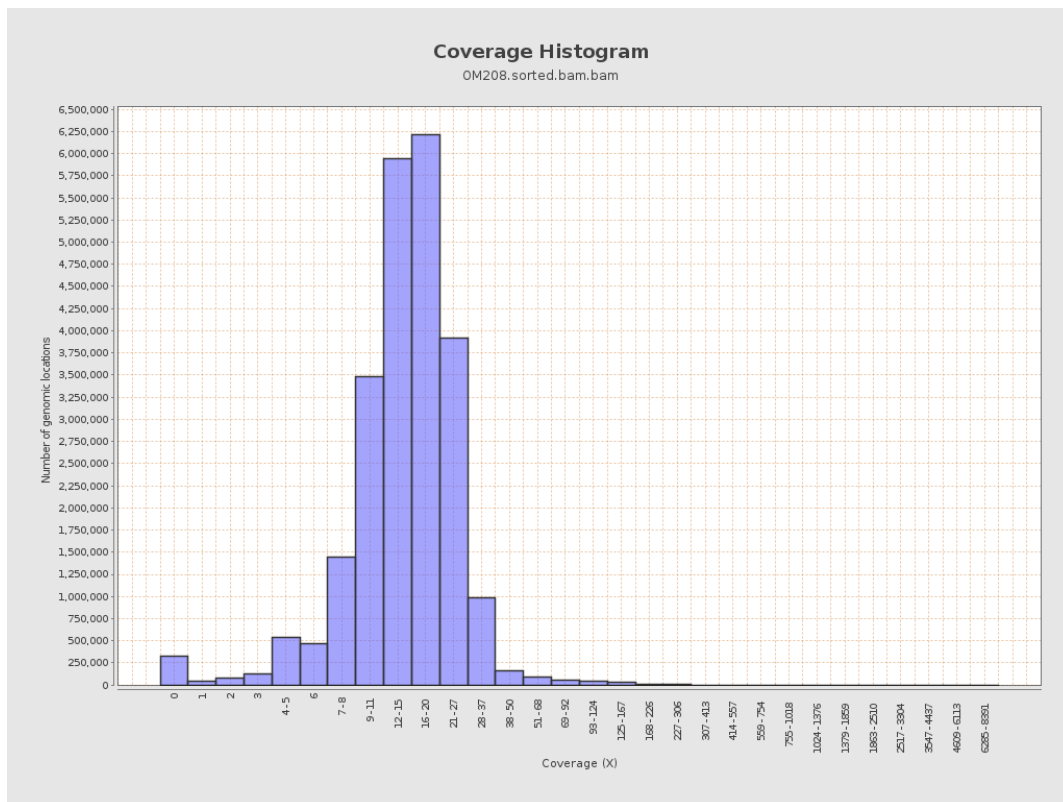
Coverage Histogram (0-50X)
OM208.sorted.bam.bam
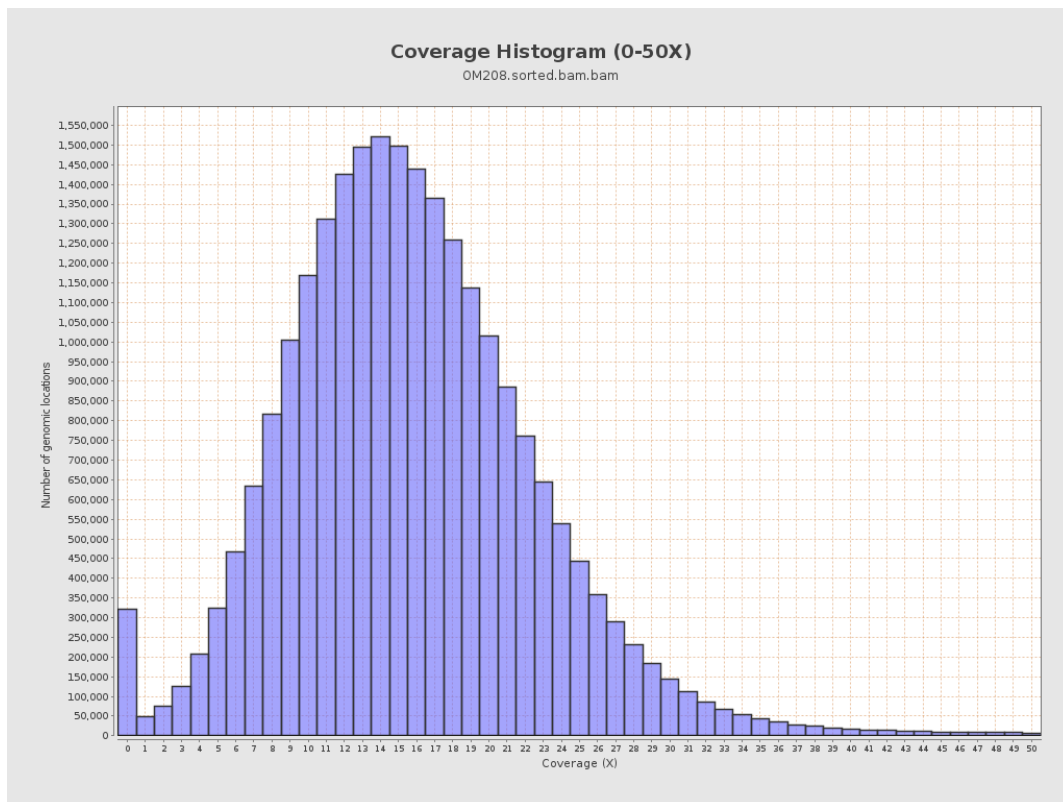
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM208.sorted.bam.bam
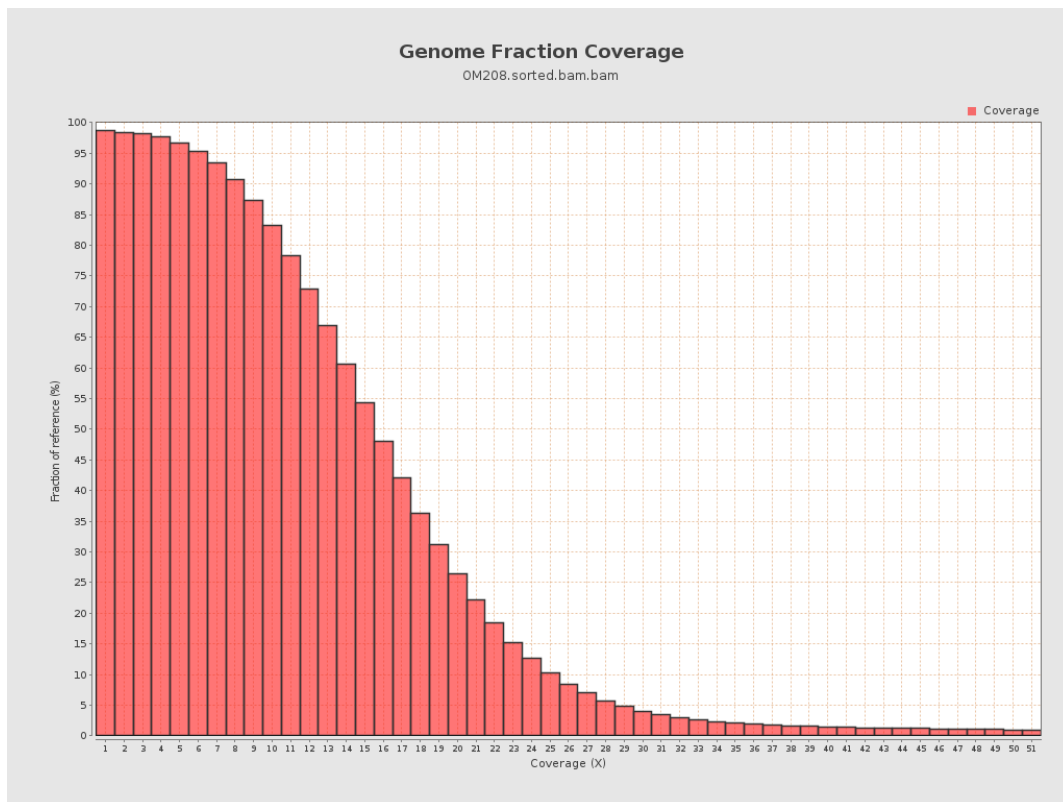
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
OM208.sorted.bam.bam
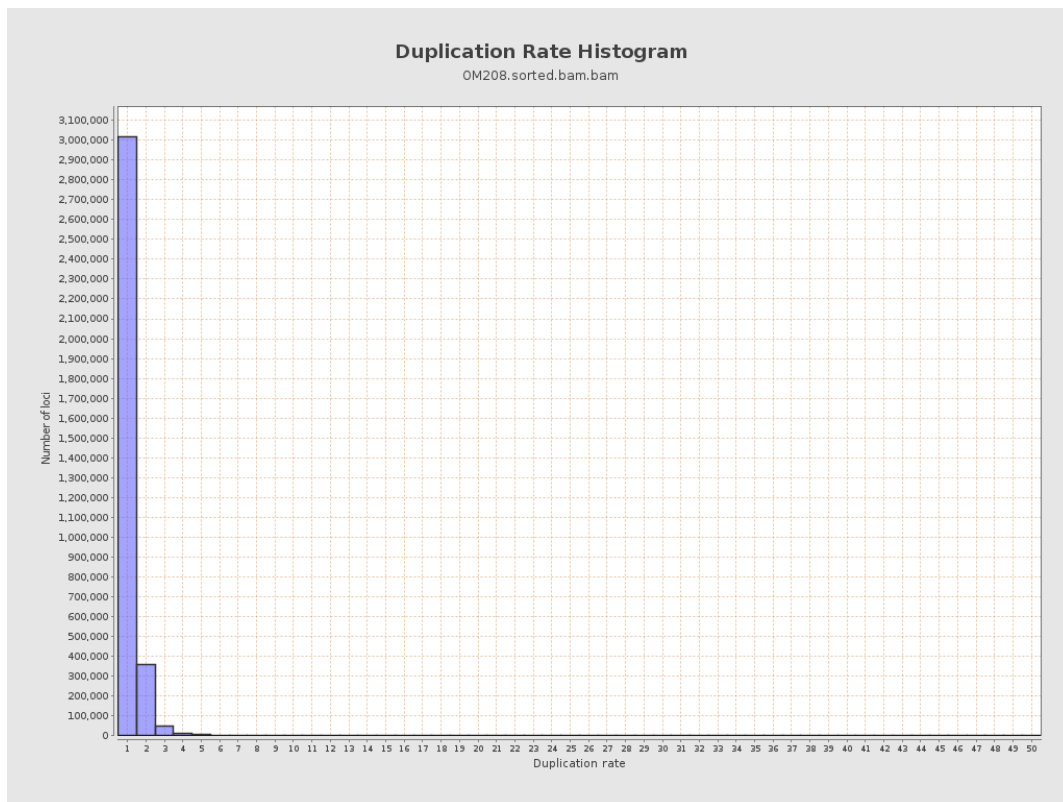
8. Results : Mapped Reads Nucleotide Content
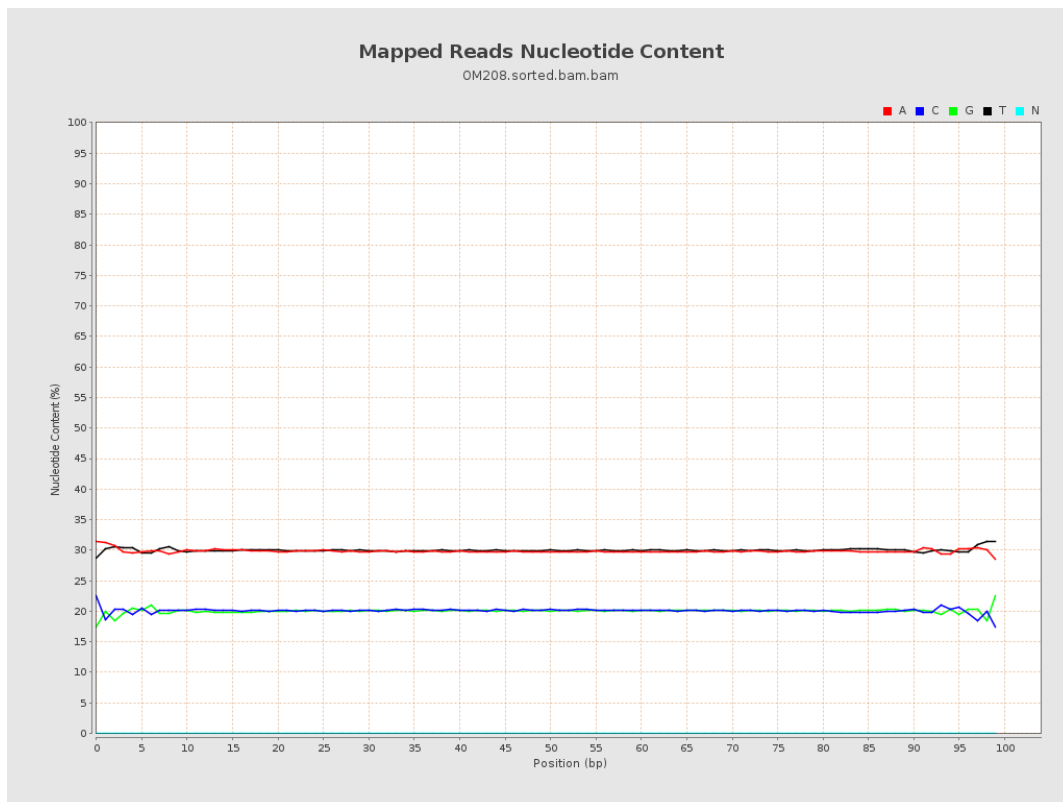
9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
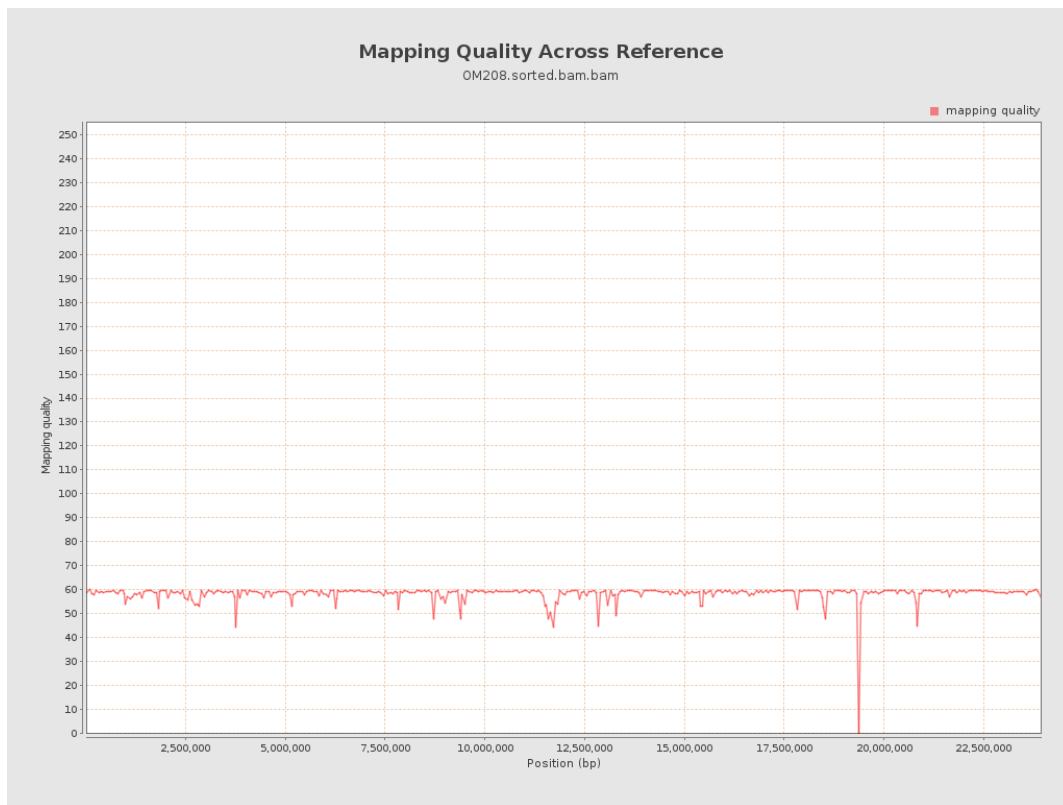OM208.sorted.bam.bam
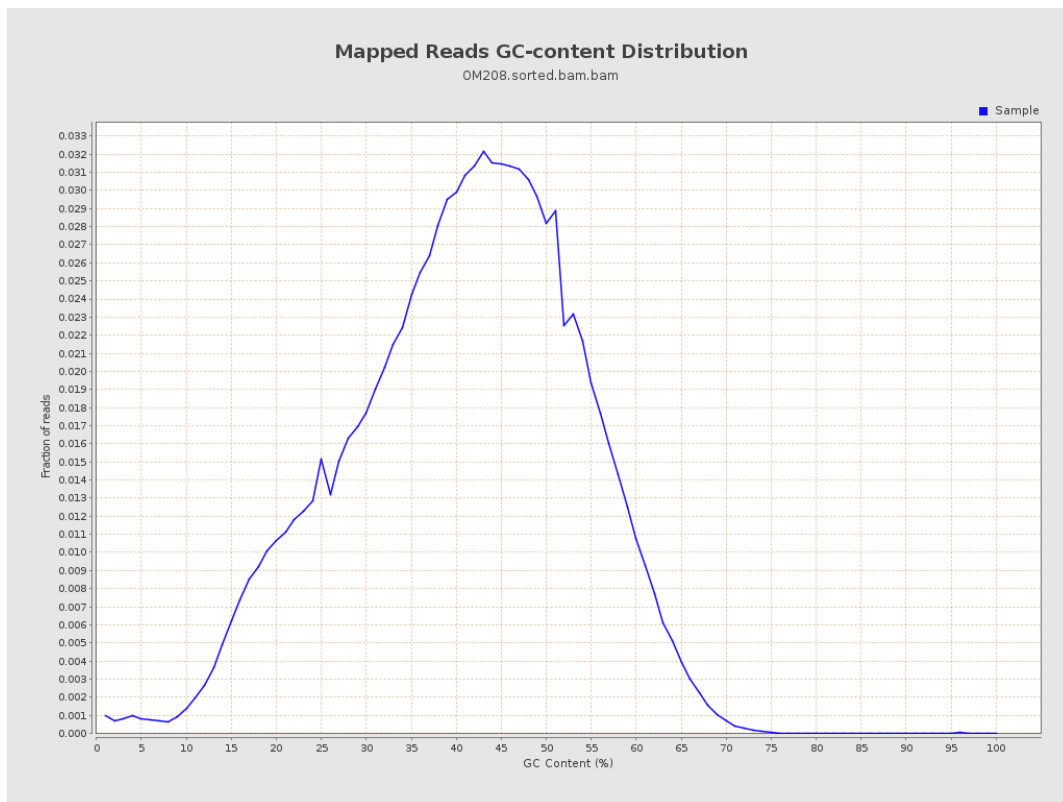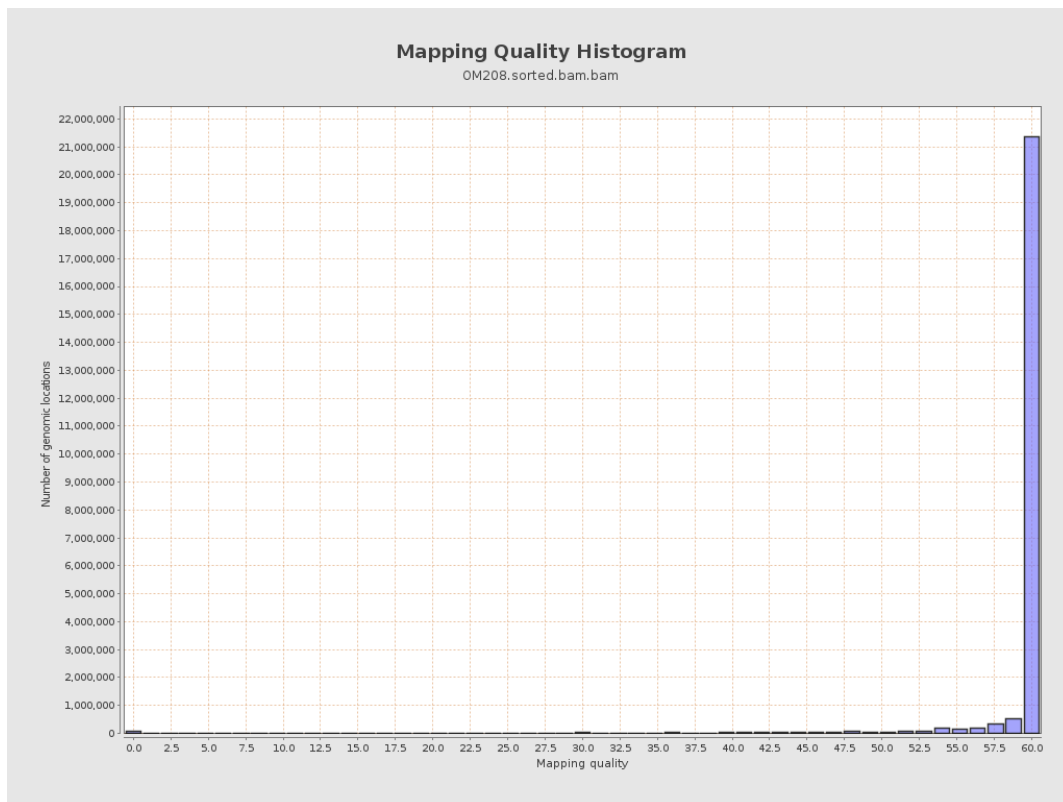
10. Results : Mapped Reads Clipping Profile
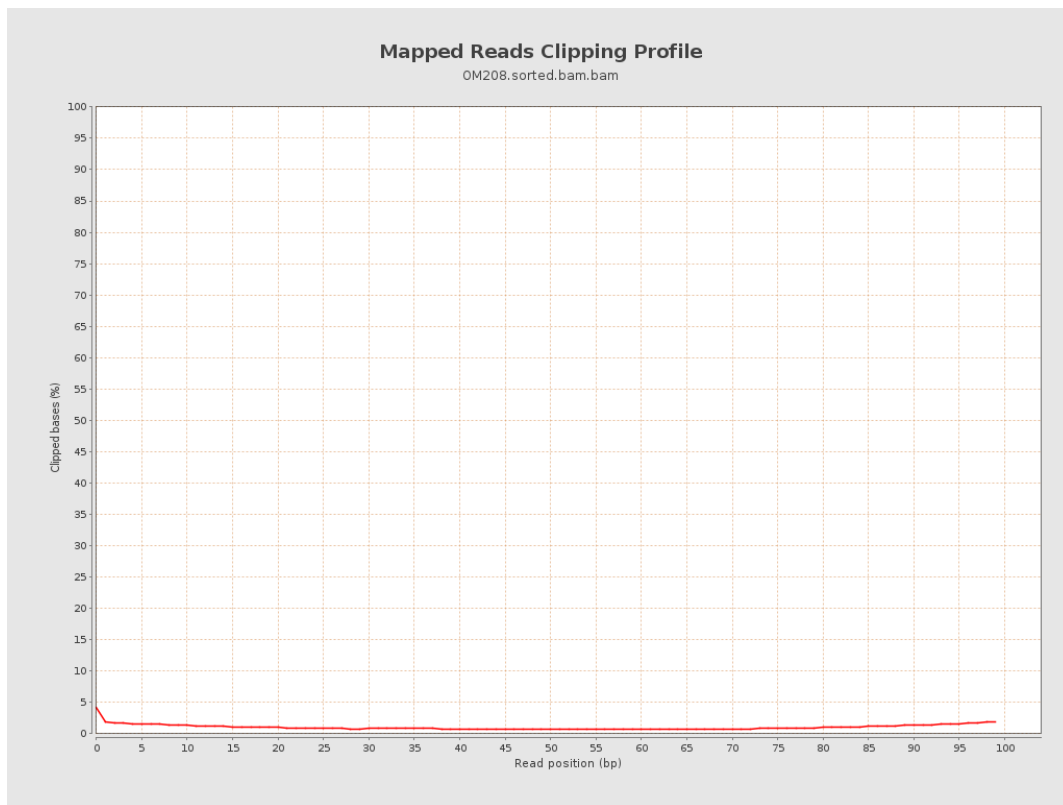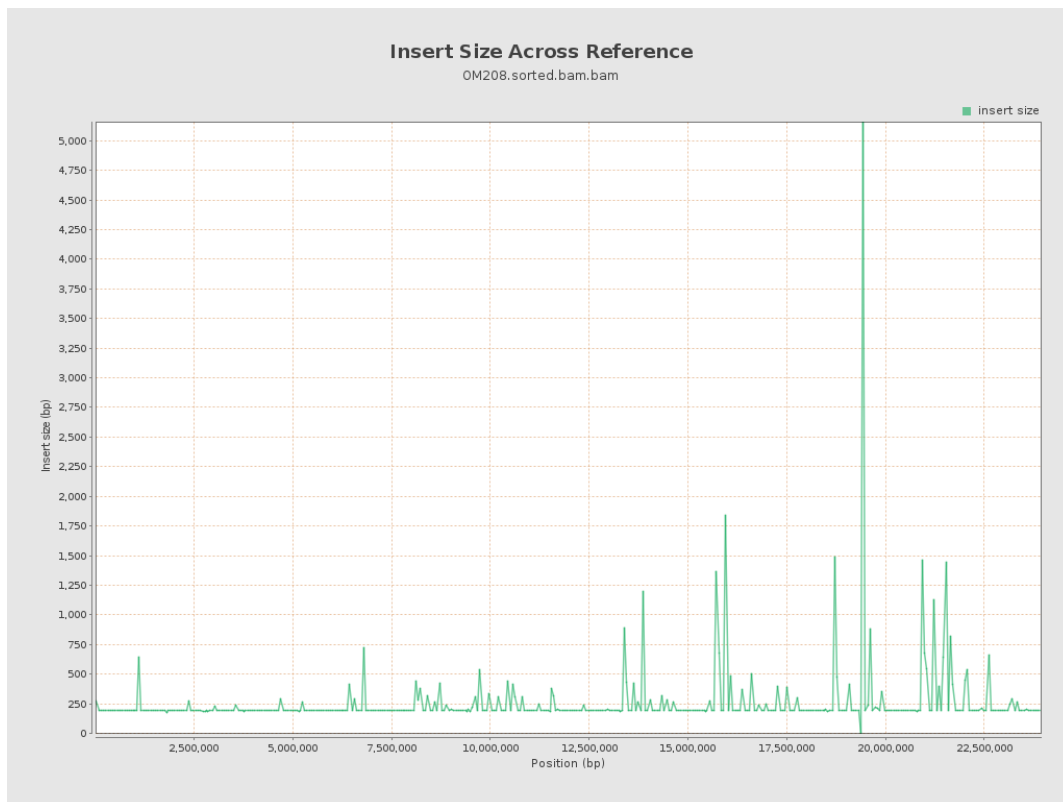
11. Results : Homopolymer Indels
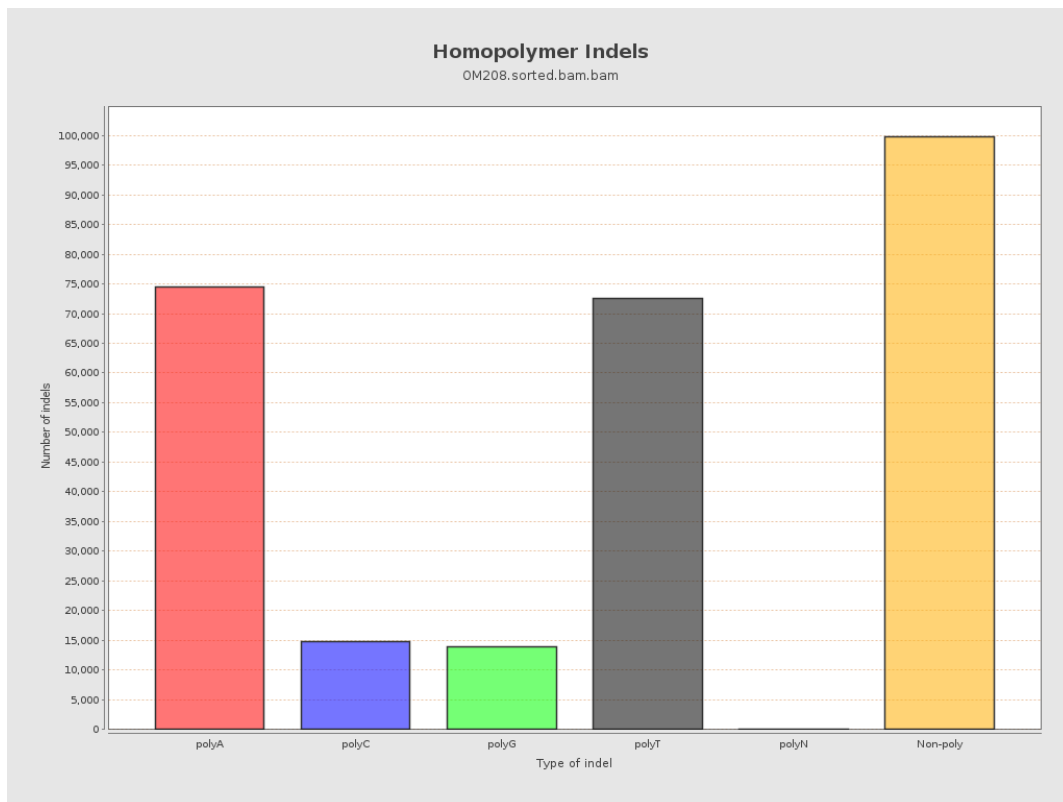
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM208.sorted.bam.bam

15. Results : Insert Size Histogram

Insert Size Histogram
OM208.sorted.bam.bam