Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:12:57

1. Input data & parameters

1.1. QualiMap command line

> qualimap bamqc -bam
> /home/vdp5/data/cambodia_samples/sequences_bam/OM118.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/OM118-BiooBarcode15_ATGTCA_R2.fastq.gz /home/vdp5/data/cambodia_samples/ sequences_gz/OM118-BiooBarcode15_ATGTCA_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:12:56 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/ sequences_bam/OM118.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	31,125,160
Mapped reads	5,132,280 / 16.49%
Unmapped reads	25,992,880 / 83.51%
Mapped paired reads	5,132,280 / 16.49%
Mapped reads, first in pair	2,560,817 / 8.23%
Mapped reads, second in pair	2,571,463 / 8.26%
Mapped reads, both in pair	4,908,146 / 15.77%
Mapped reads, singletons	224,134 / 0.72%
Read min/max/mean length	30 / 100 / 99.97
Duplicated reads (estimated)	1,074,627 / 3.45%
Duplication rate	16.32%
Clipped reads	654,687 / 2.1%

2.2. ACGT Content

Number/percentage of A's	144,940,099 / 29.68%
Number/percentage of C's	98,691,681 / 20.21%
Number/percentage of T's	146,117,840 / 29.93%
Number/percentage of G's	98,522,362 / 20.18%
Number/percentage of N's	41,573 / 0.01%
GC Percentage	40.39%

2.3. Coverage

Mean	20.4008
Standard Deviation	30.0294

2.4. Mapping Quality

Mean Mapping Quality	58.06

2.5. Insert size

Mean	775.14
Standard Deviation	27,221.87
P25/Median/P75	251 / 262 / 272

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	6,300,596
Insertions	155,827
Mapped reads with at least one insertion	2.87%
Deletions	175,872
Mapped reads with at least one deletion	3.2%
Homopolymer indels	62.79%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	18212432	18.637	10.6897
gi|1074120682|emb|LT615257.1|	860454	15977716	18.5689	16.0591
gi|1074120865|emb|LT615258.1|	989719	23071162	23.3108	28.9755
gi|1074121086|emb|LT615259.1|	935450	21285002	22.7538	24.5495
gi|1074121301|emb|LT615260.1|	1432239	30476579	21.279	21.0573
gi|1074121615|emb|LT615261.1|	1080962	21545341	19.9316	16.8892
gi|1074121871|emb|LT615262.1|	1545099	30284837	19.6006	10.4602
gi|1074122235|emb|LT615263.1|	1585108	32063571	20.228	42.3083
gi|1074122590|emb|LT615264.1|	2122358	42022994	19.8001	10.9625
gi|1074123050|emb|LT615265.1|	1754192	36183272	20.6267	81.0438
gi|1074123421|emb|LT615	2150147	45910646	21.3523	28.2012

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	60675501	20.0181	21.8389
gi|1074124588|emb|LT615268.1|	2359348	46002049	19.4978	16.7924
gi|1074125065|emb|LT615269.1|	3135668	65071846	20.7521	9.8188

3. Results : Coverage across reference

Coverage across reference
OM118.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM118.sorted.bam.bam
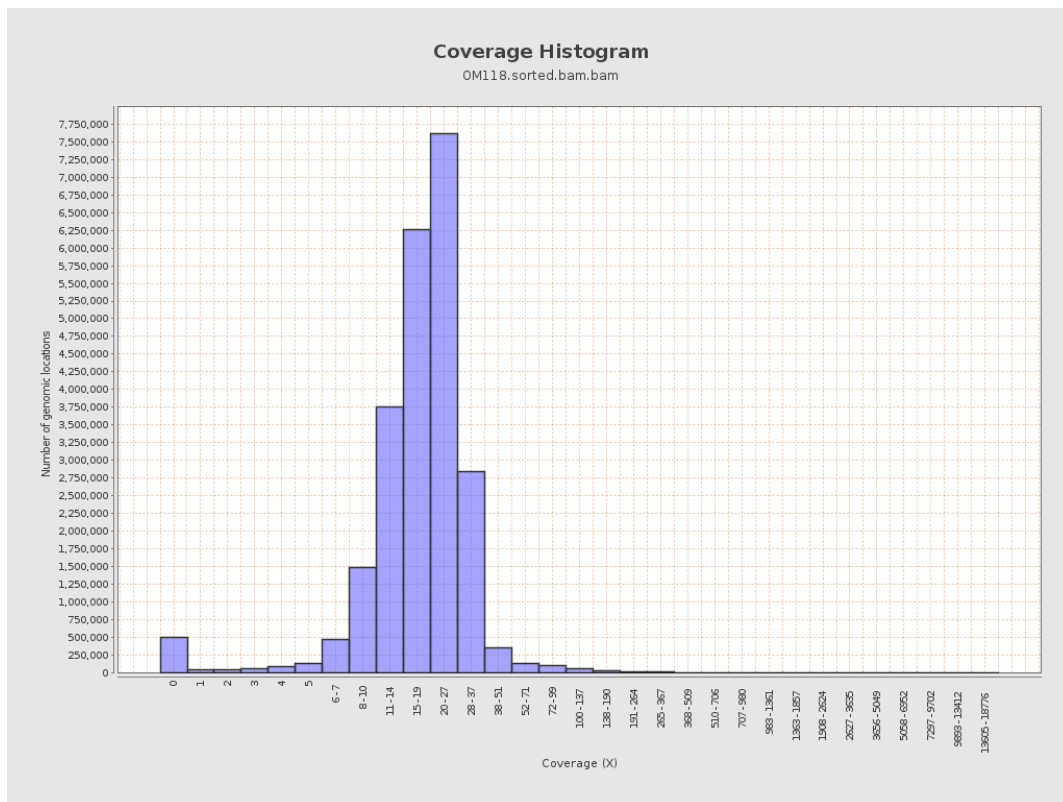
5. Results : Coverage Histogram (0-50X)
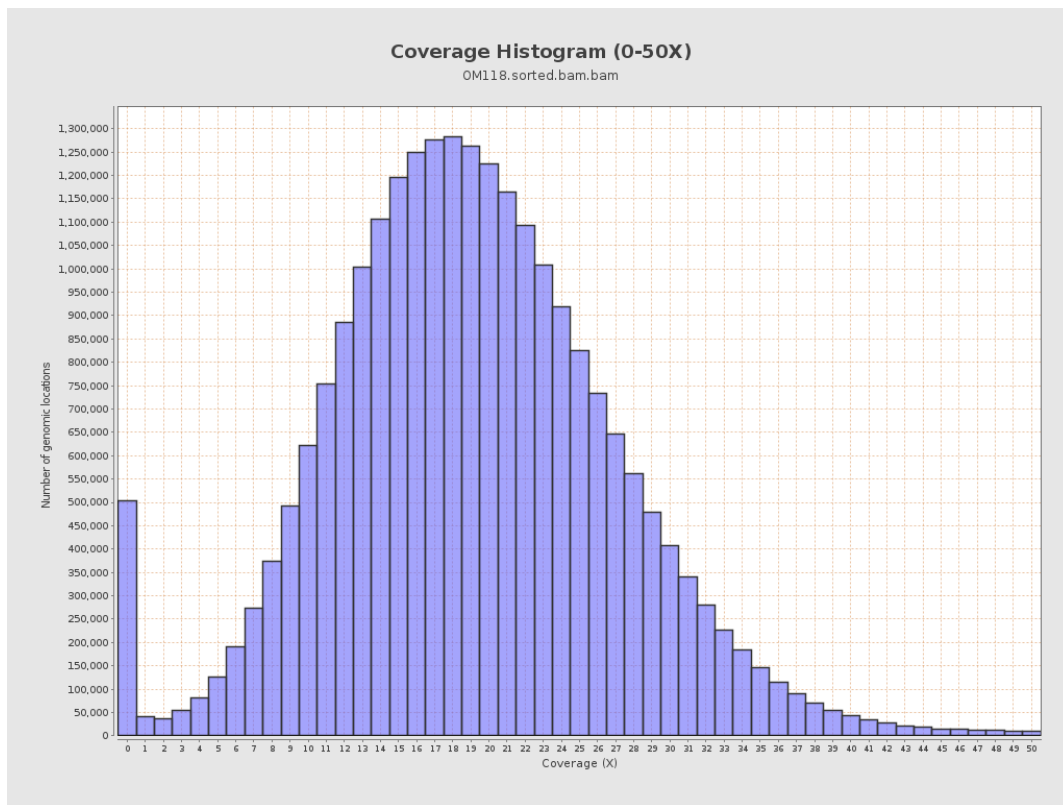
6. Results : Genome Fraction Coverage
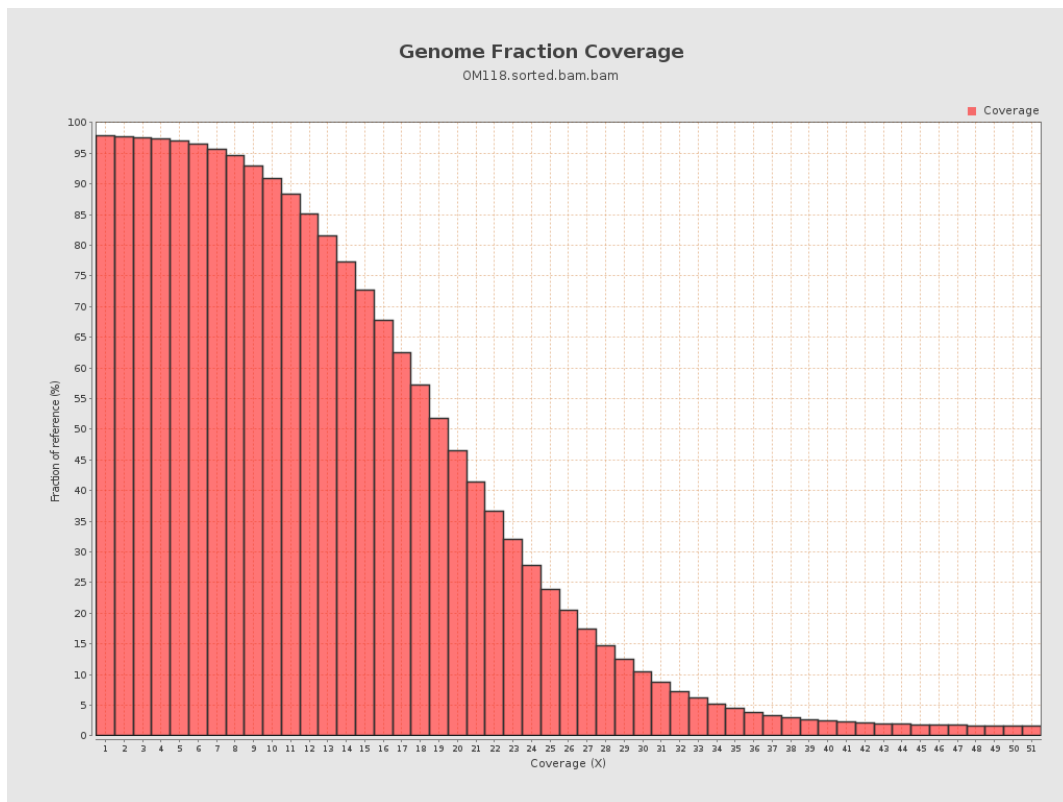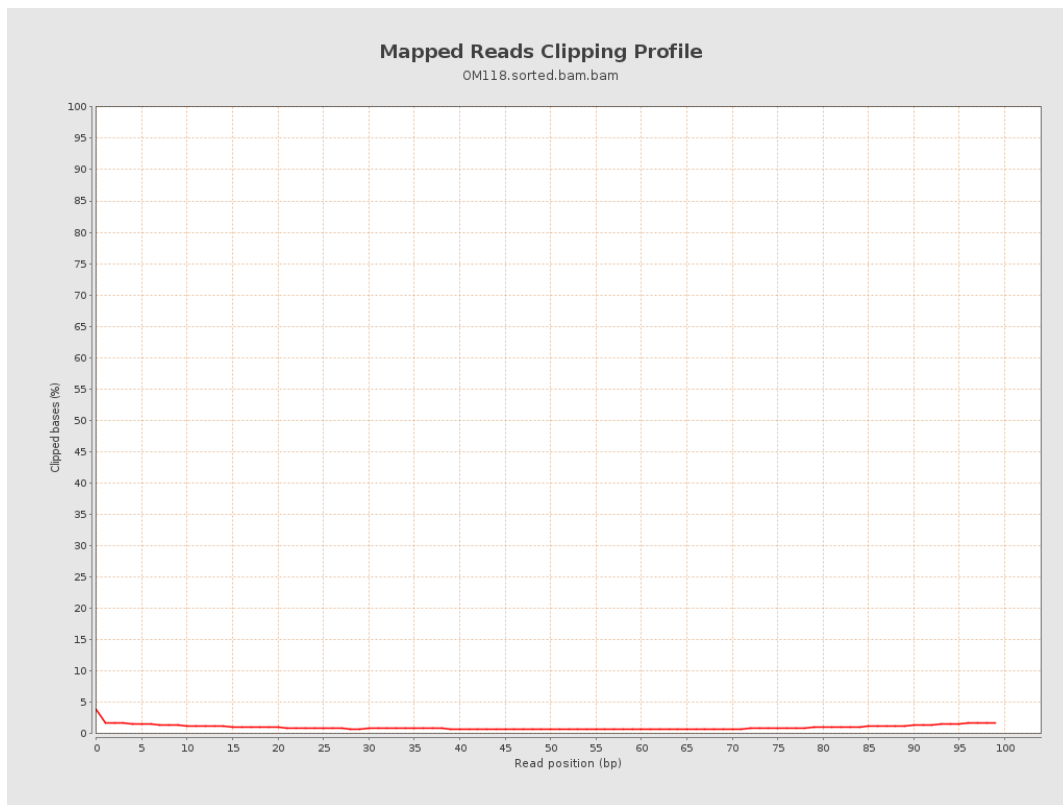
7. Results : Duplication Rate Histogram
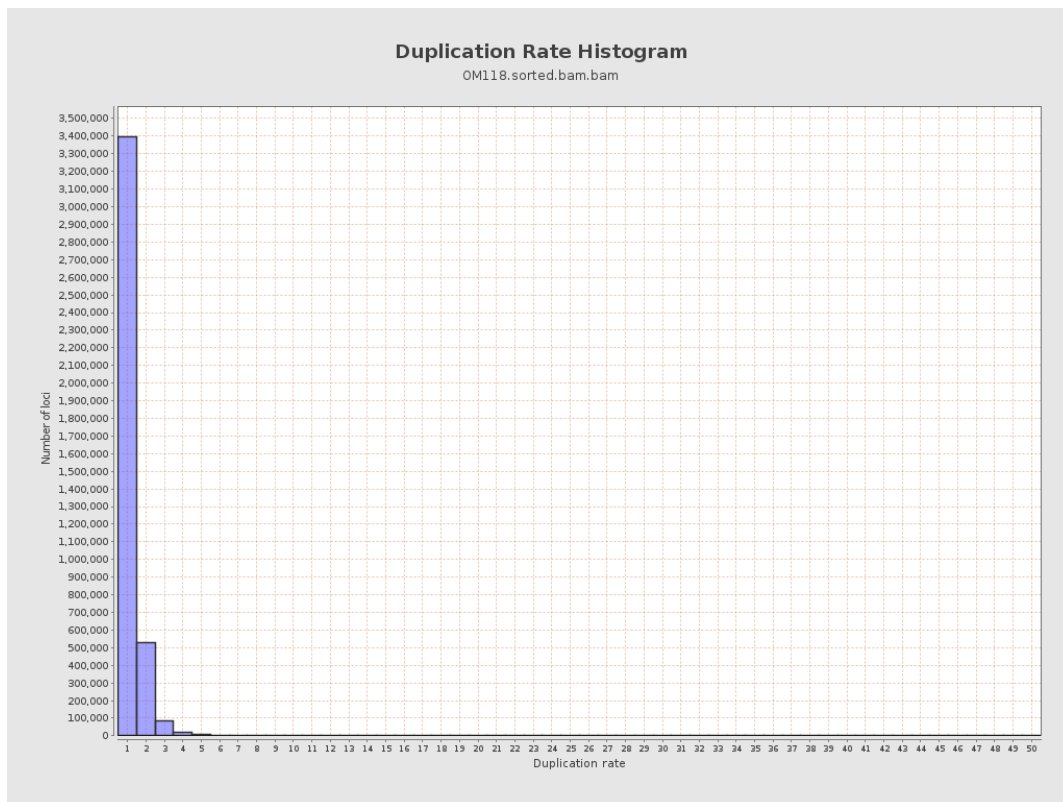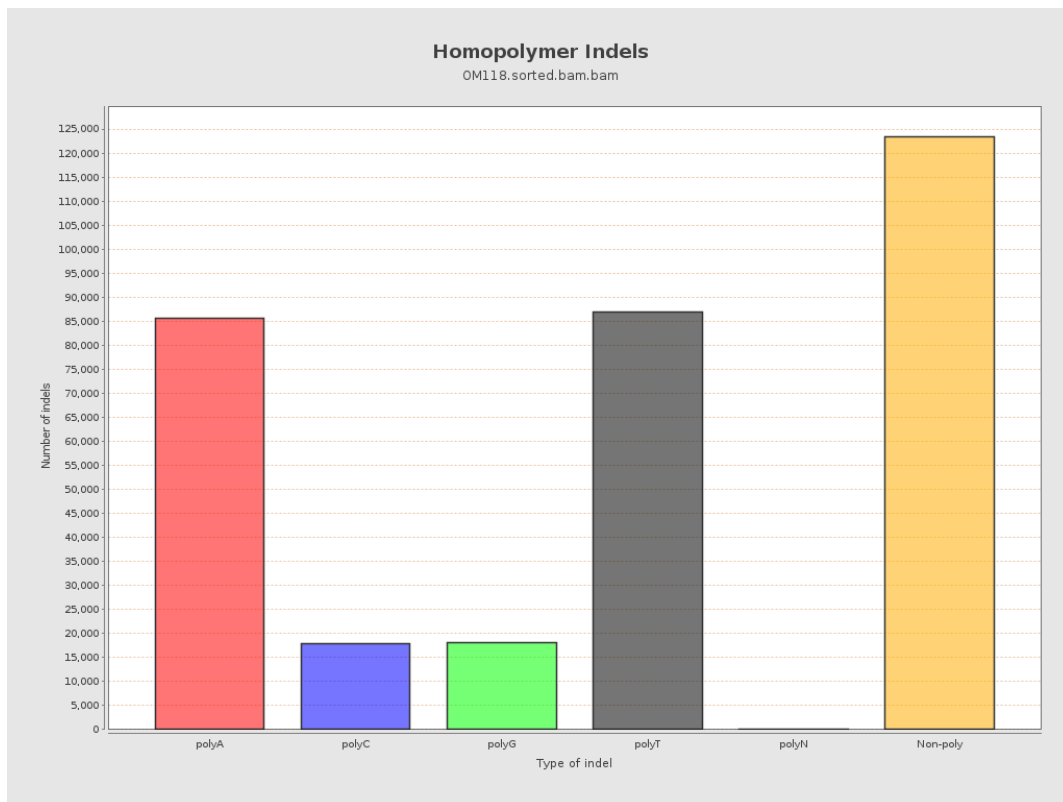
8. Results : Mapped Reads Nucleotide Content
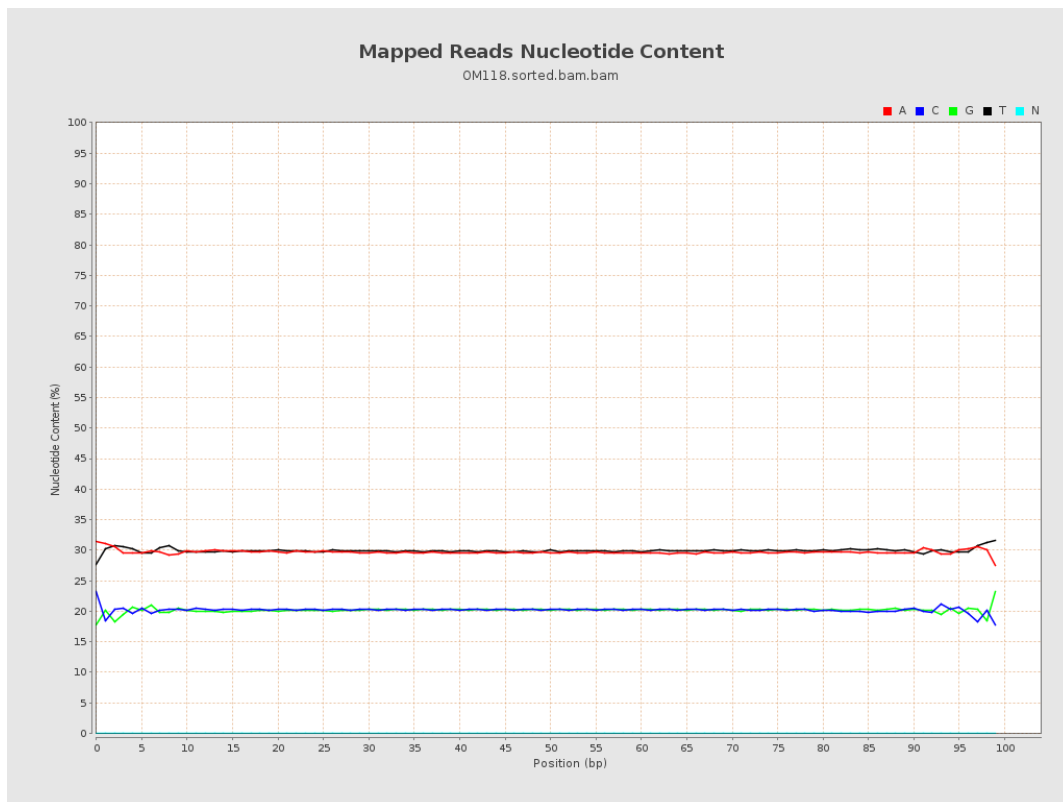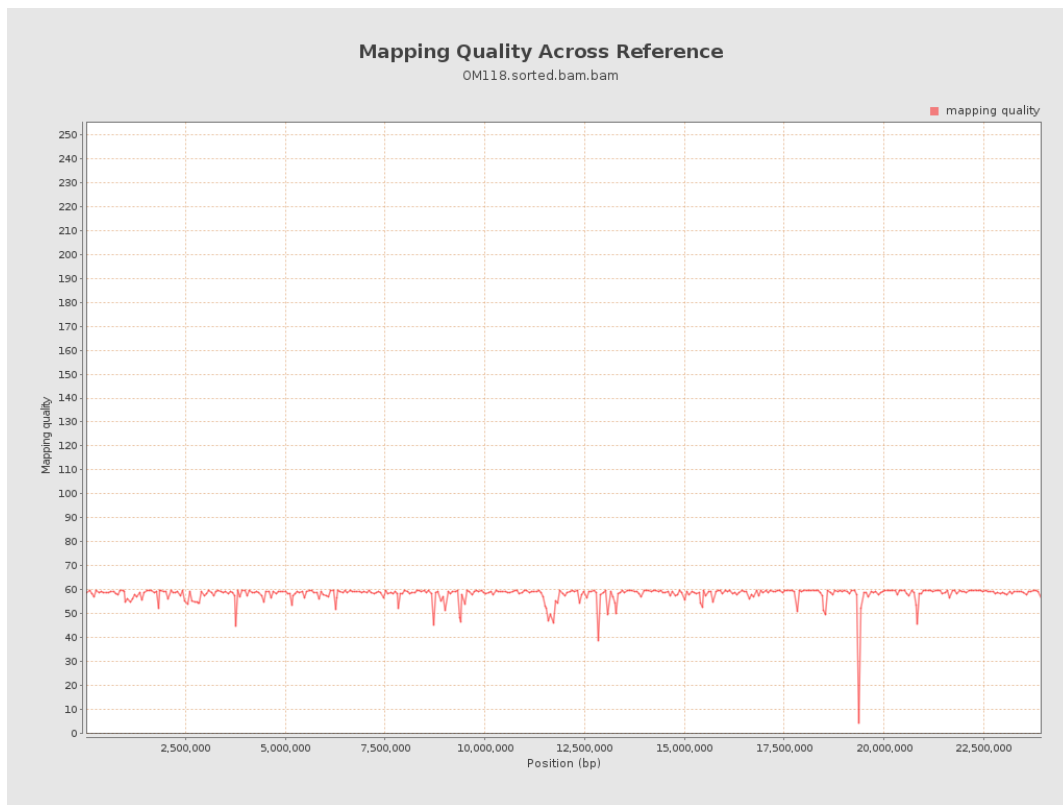
9. Results : Mapped Reads GC-content Distribution
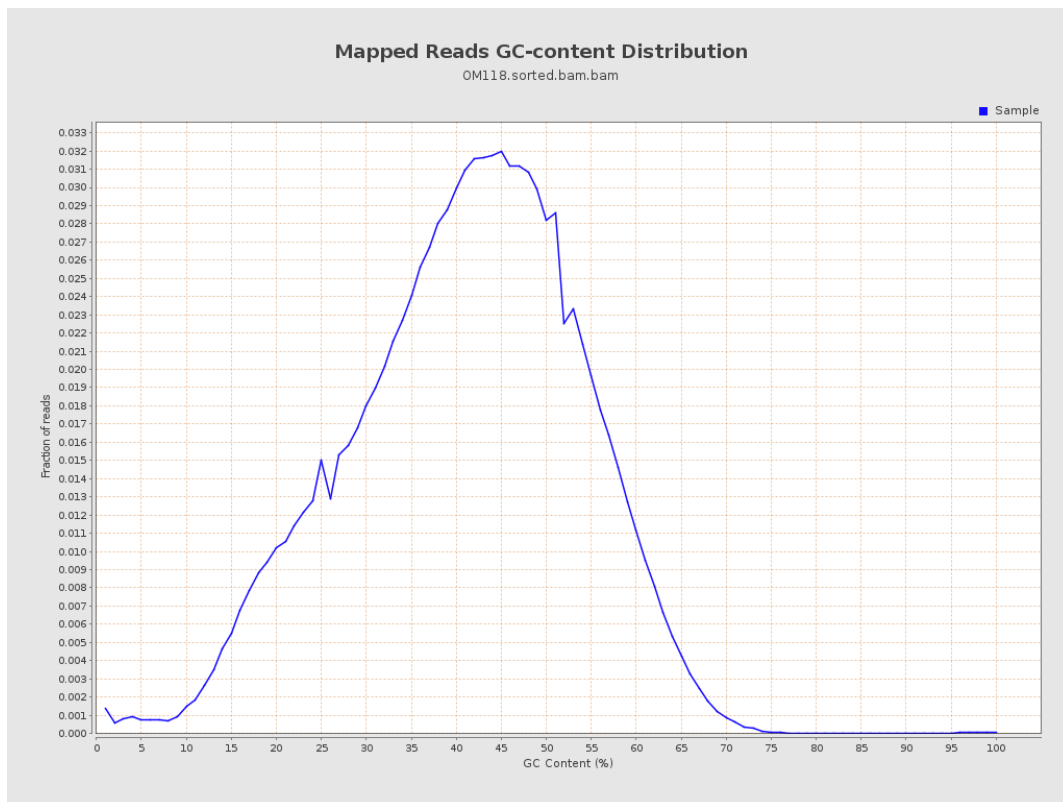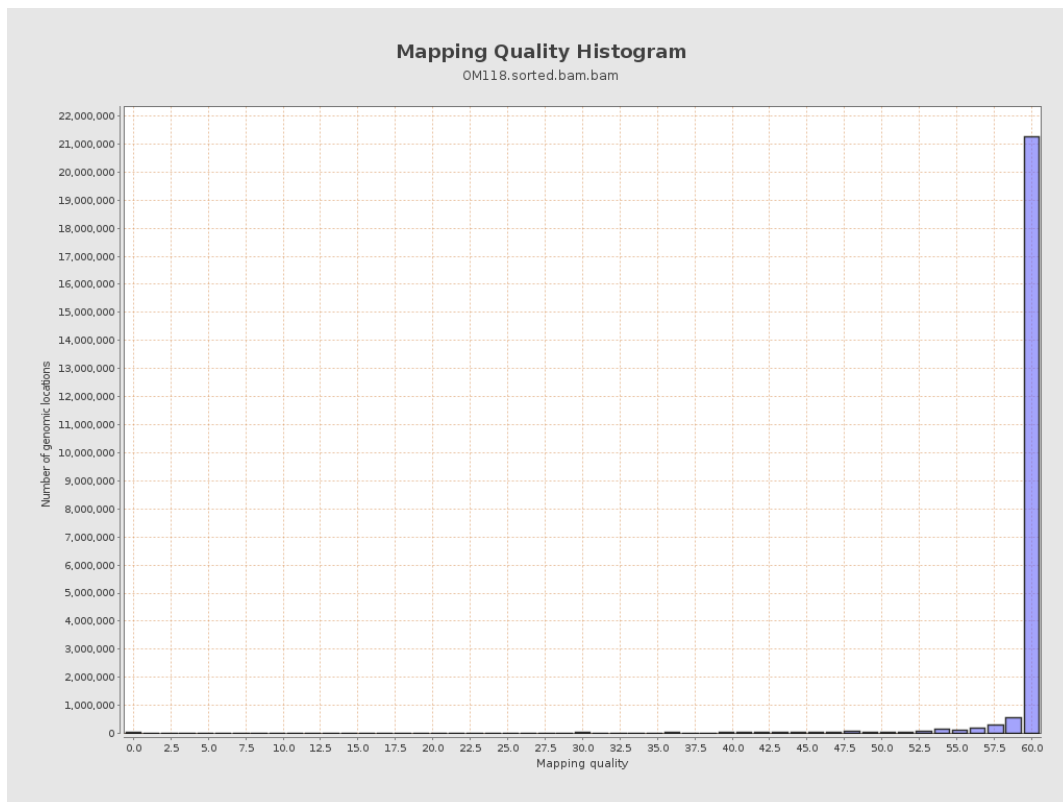
10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels

Homopolymer Indels
OM118.sorted.bam.bam

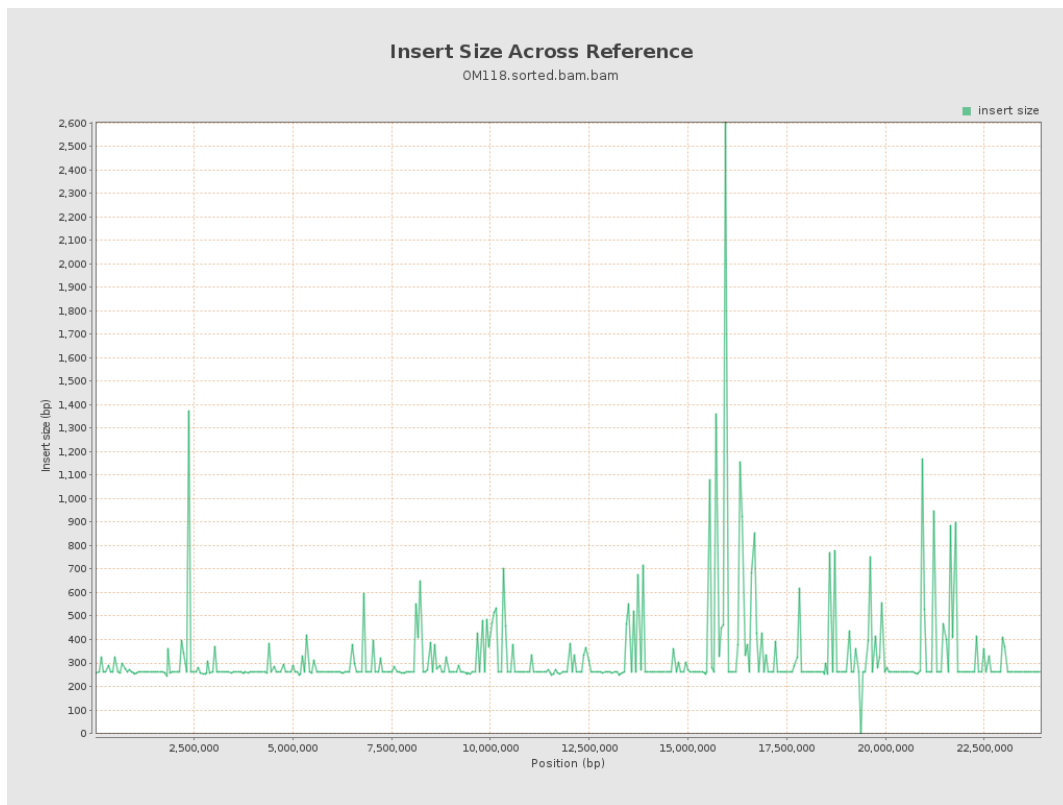# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM118.sorted.bam.bam

15. Results : Insert Size Histogram