Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 12:03:54

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM018.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/OM018-BiooBarcode6_CTTGTA_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM018-BiooBarcode6_CTTGTA_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:03:54 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM018.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	5,880,165
Mapped reads	2,159,552 / 36.73%
Unmapped reads	3,720,613 / 63.27%
Mapped paired reads	2,159,552 / 36.73%
Mapped reads, first in pair	1,082,656 / 18.41%
Mapped reads, second in pair	1,076,896 / 18.31%
Mapped reads, both in pair	2,107,090 / 35.83%
Mapped reads, singletons	52,462 / 0.89%
Read min/max/mean length	30 / 100 / 99.94
Duplicated reads (estimated)	236,582 / 4.02%
Duplication rate	8.37%
Clipped reads	239,904 / 4.08%

2.2. ACGT Content

Number/percentage of A's	61,723,579 / 29.66%
Number/percentage of C's	42,239,527 / 20.3%
Number/percentage of T's	61,982,690 / 29.78%
Number/percentage of G's	42,157,372 / 20.26%
Number/percentage of N's	18,100 / 0.01%
GC Percentage	40.56%

2.3. Coverage

Mean	8.695
Standard Deviation	8.4199

2.4. Mapping Quality

Mean Mapping Quality	58.54

2.5. Insert size

Mean	726.16
Standard Deviation	24,598.11
P25/Median/P75	255 / 267 / 278

2.6. Mismatches and indels

General error rate	1.43%
Mismatches	2,811,265
Insertions	65,621
Mapped reads with at least one insertion	2.88%
Deletions	74,801
Mapped reads with at least one deletion	3.26%
Homopolymer indels	63.89%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	7695445	7.8749	4.3432
gi|1074120682|emb|LT615257.1|	860454	7218257	8.3889	6.7981
gi|1074120865|emb|LT615258.1|	989719	9474434	9.5729	12.6
gi|1074121086|emb|LT615259.1|	935450	8814178	9.4224	12.3156
gi|1074121301|emb|LT615260.1|	1432239	12802437	8.9388	8.2654
gi|1074121615|emb|LT615261.1|	1080962	9896514	9.1553	8.7516
gi|1074121871|emb|LT615262.1|	1545099	13509894	8.7437	4.7313
gi|1074122235|emb|LT615263.1|	1585108	13656792	8.6157	7.2946
gi|1074122590|emb|LT615264.1|	2122358	17822097	8.3973	4.8163
gi|1074123050|emb|LT615265.1|	1754192	15516591	8.8454	11.8613
gi|1074123421|emb|LT615	2150147	19750434	9.1856	14.6711

266.1|				
gi|107412389 8|emb|LT615 267.1|	3031036	25489497	8.4095	4.8617
gi|107412458 8|emb|LT615 268.1|	2359348	19395880	8.2209	8.215
gi|107412506 5|emb|LT615 269.1|	3135668	27281525	8.7004	3.9241

3. Results : Coverage across reference

Coverage across reference
OM018.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM018.sorted.bam.bam
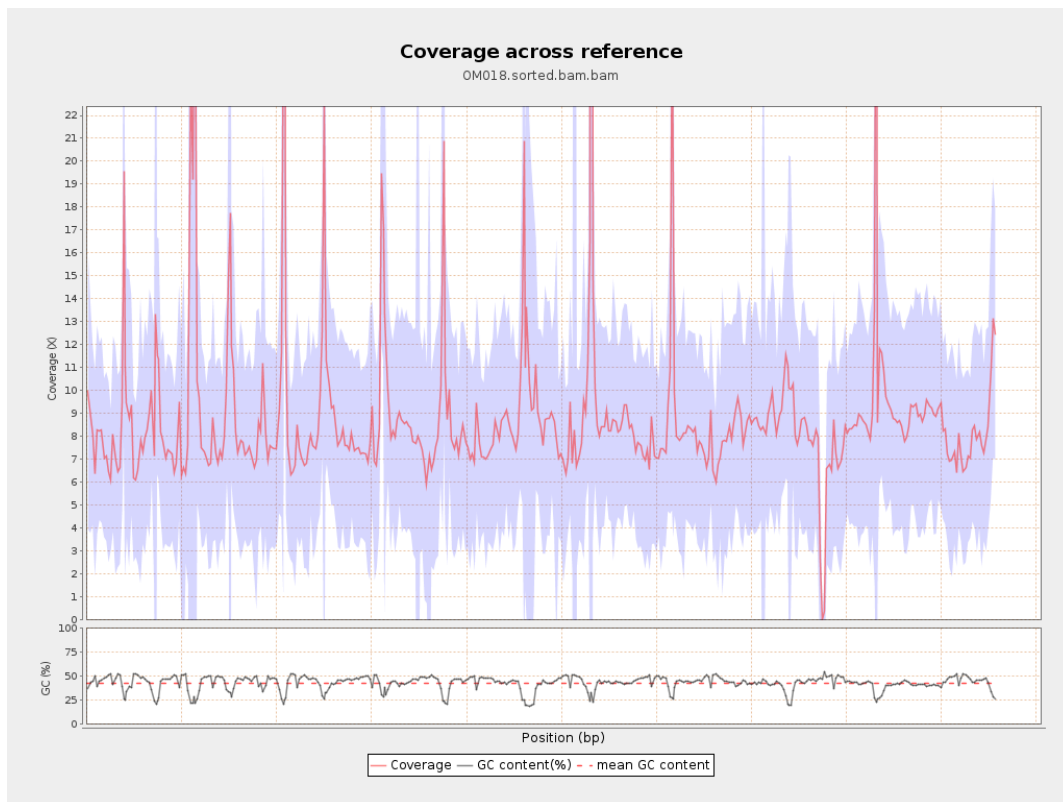
5. Results : Coverage Histogram (0-50X)
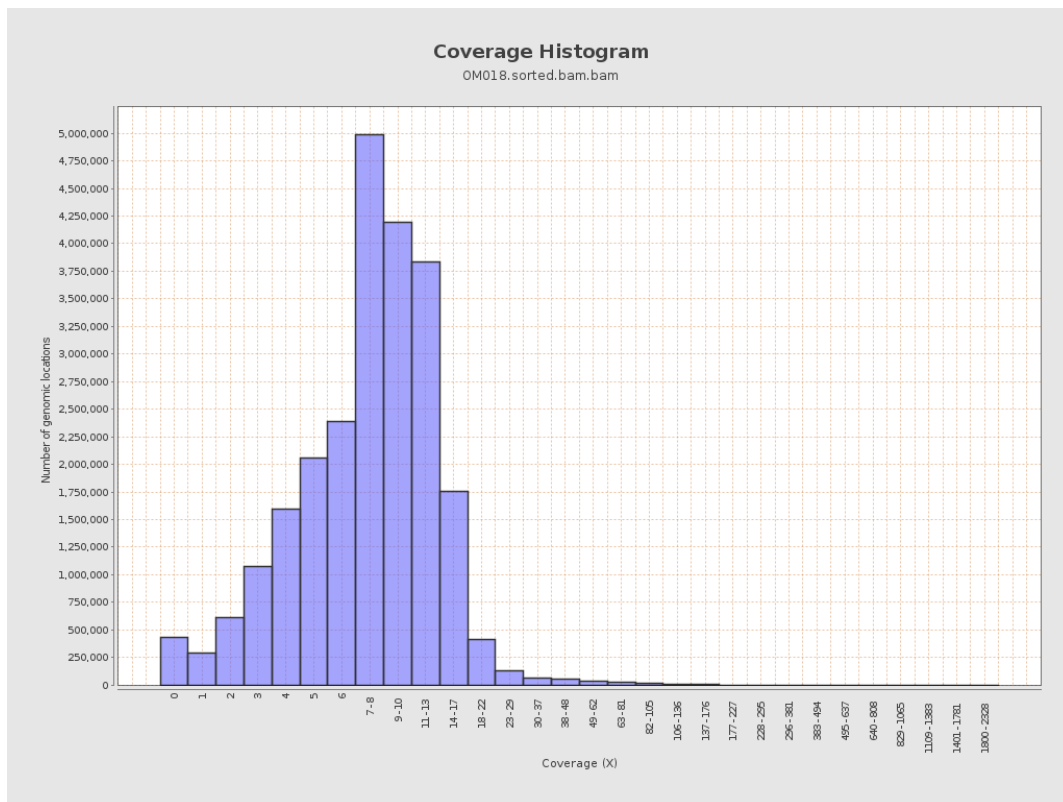
Coverage Histogram (0-50X)
OM018.sorted.bam.bam
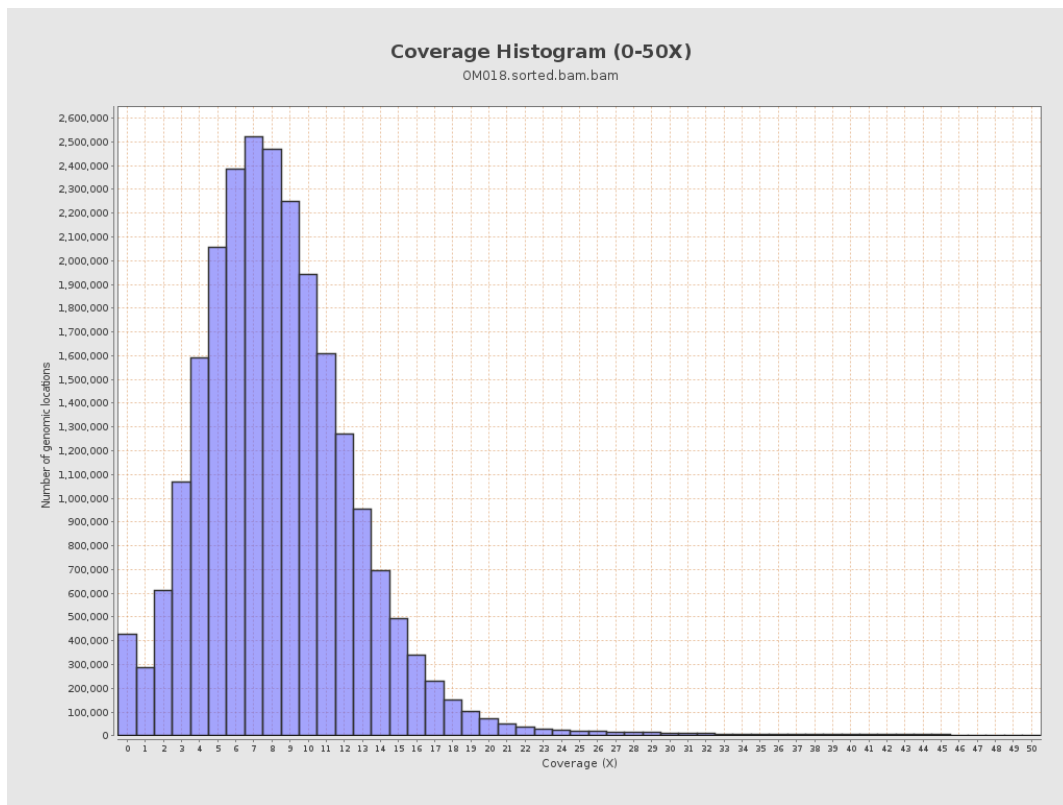
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM018.sorted.bam.bam
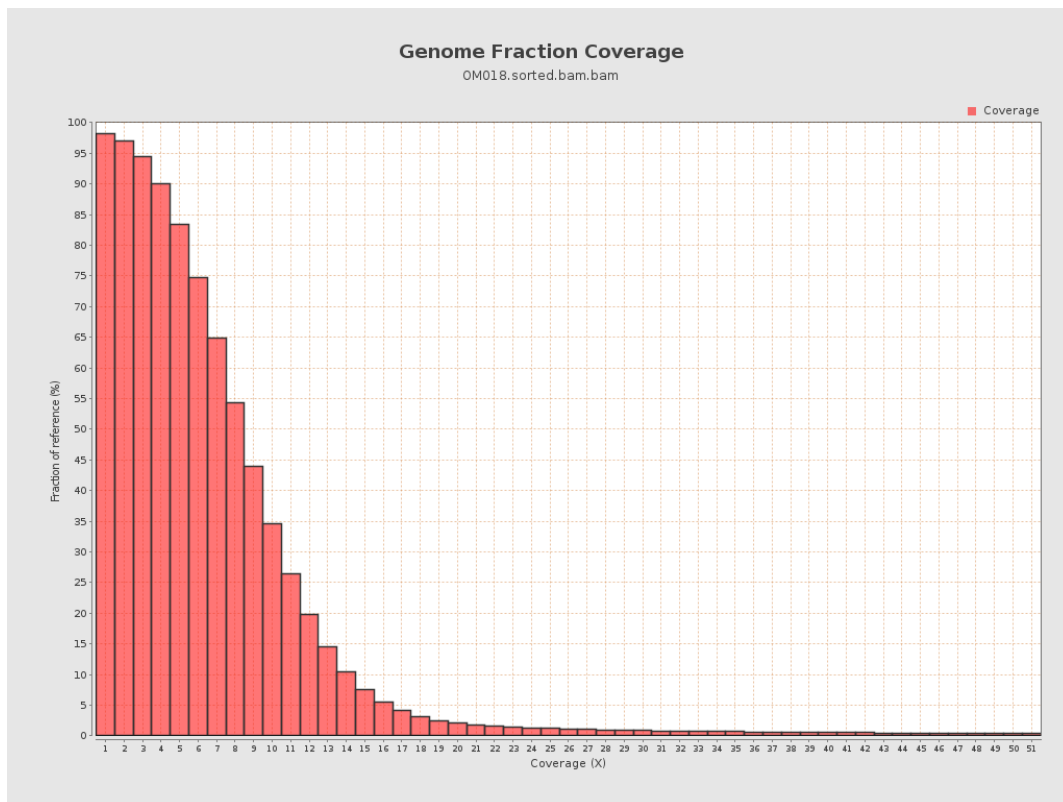
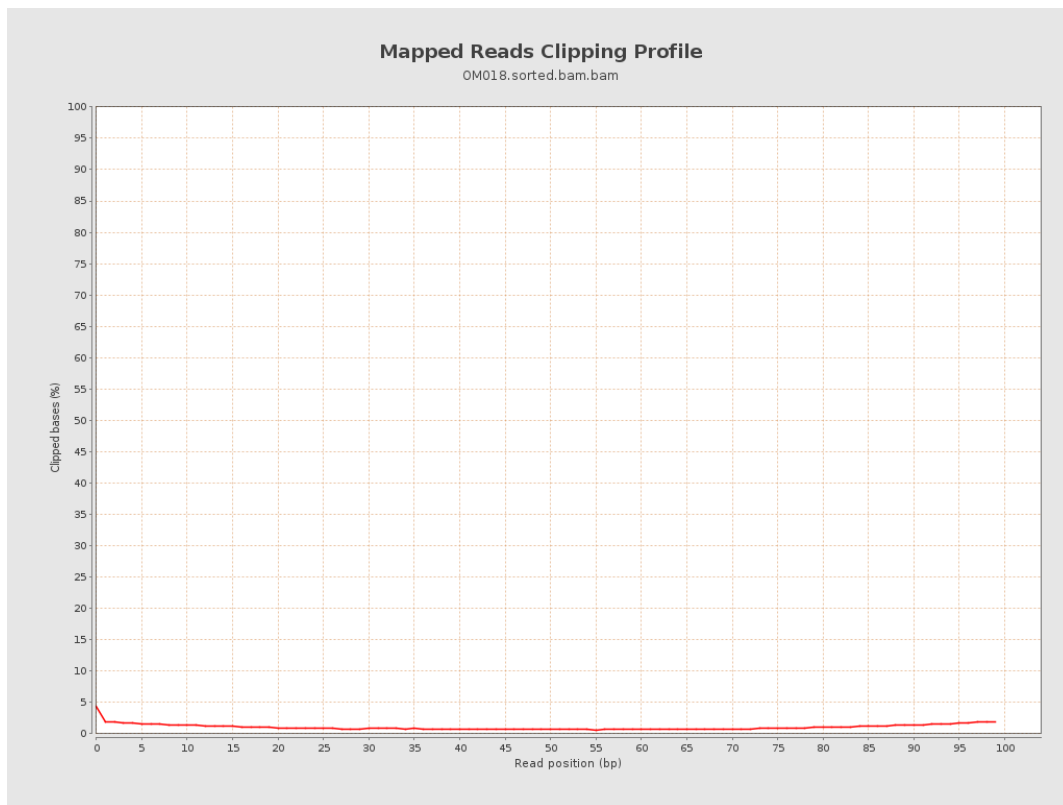# 7. Results : Duplication Rate Histogram

Duplication Rate Histogram
OM018.sorted.bam.bam
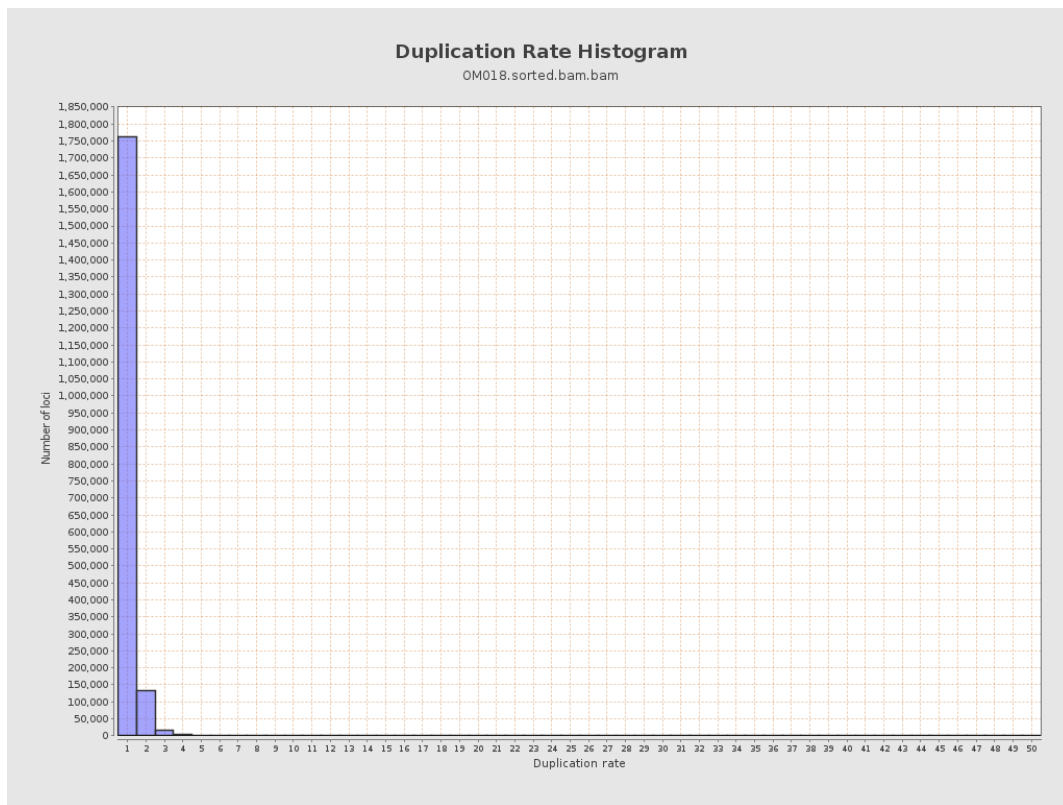
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution
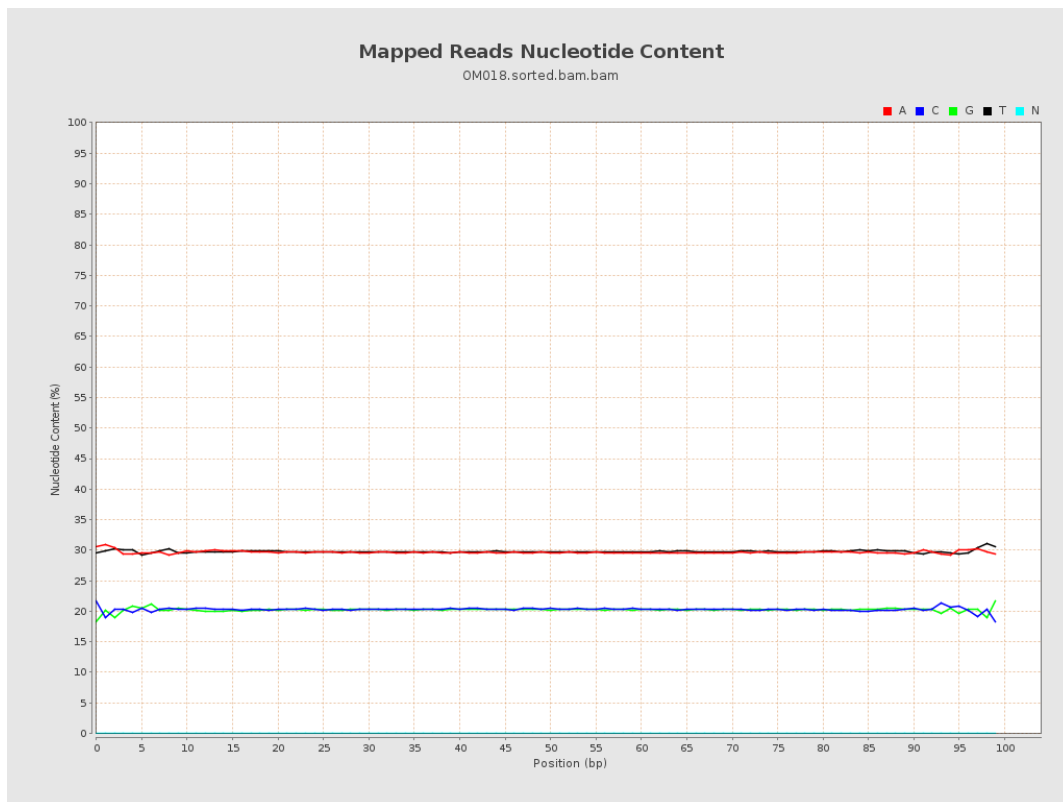
Mapped Reads GC-content Distribution
OM018.sorted.bam.bam
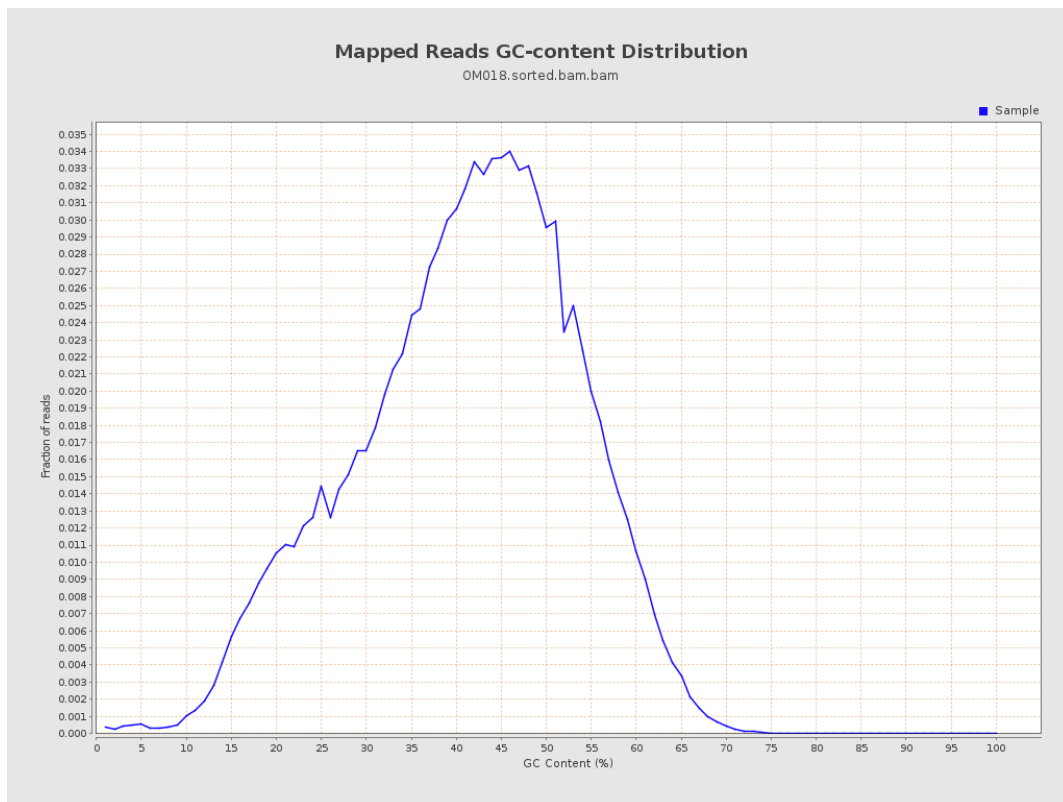
10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels

Homopolymer Indels
OM018.sorted.bam.bam
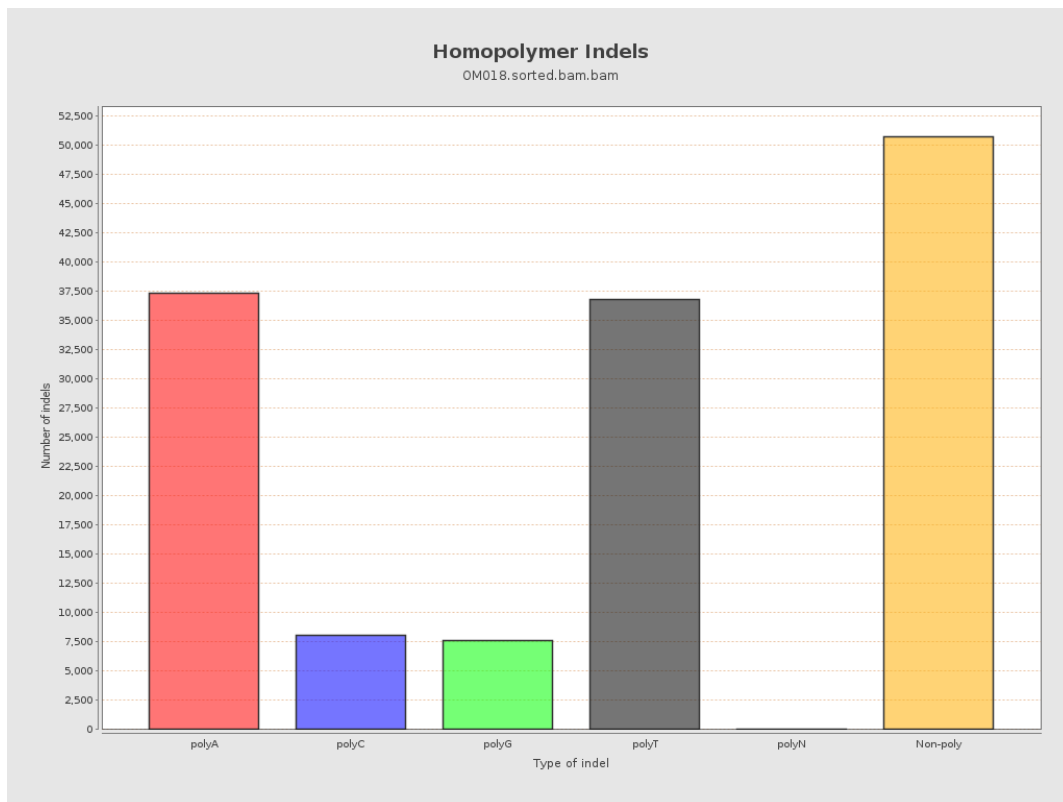
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram
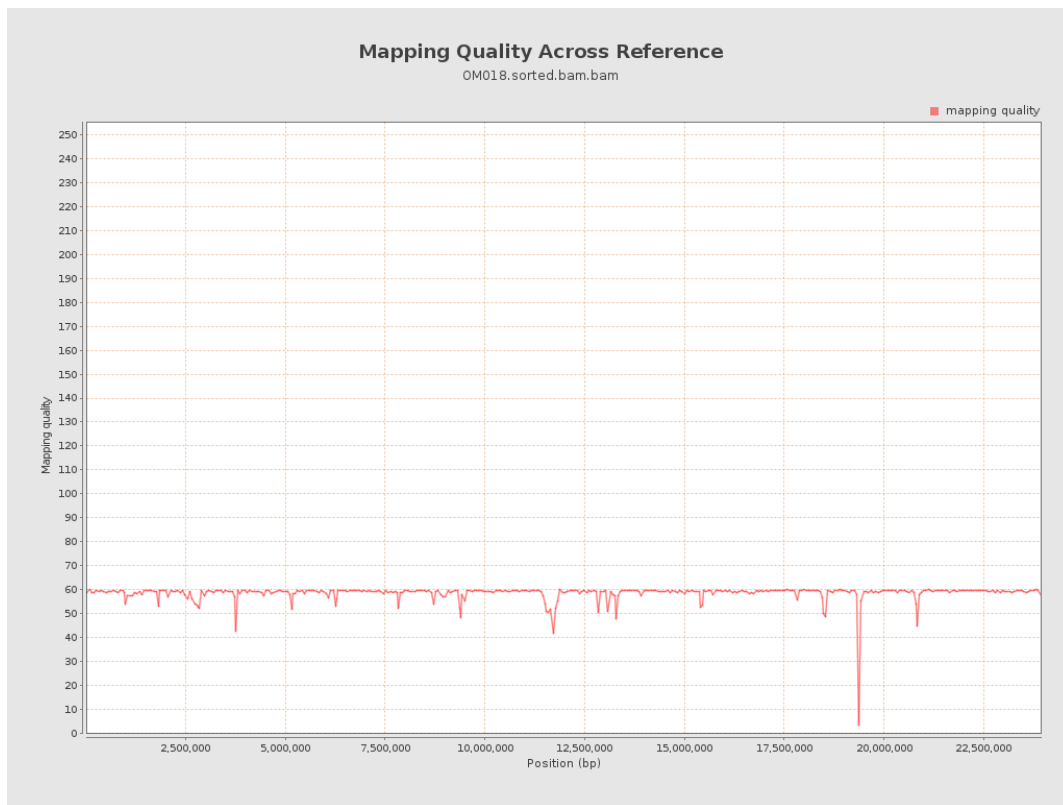
Mapping Quality Histogram
OM018.sorted.bam.bam
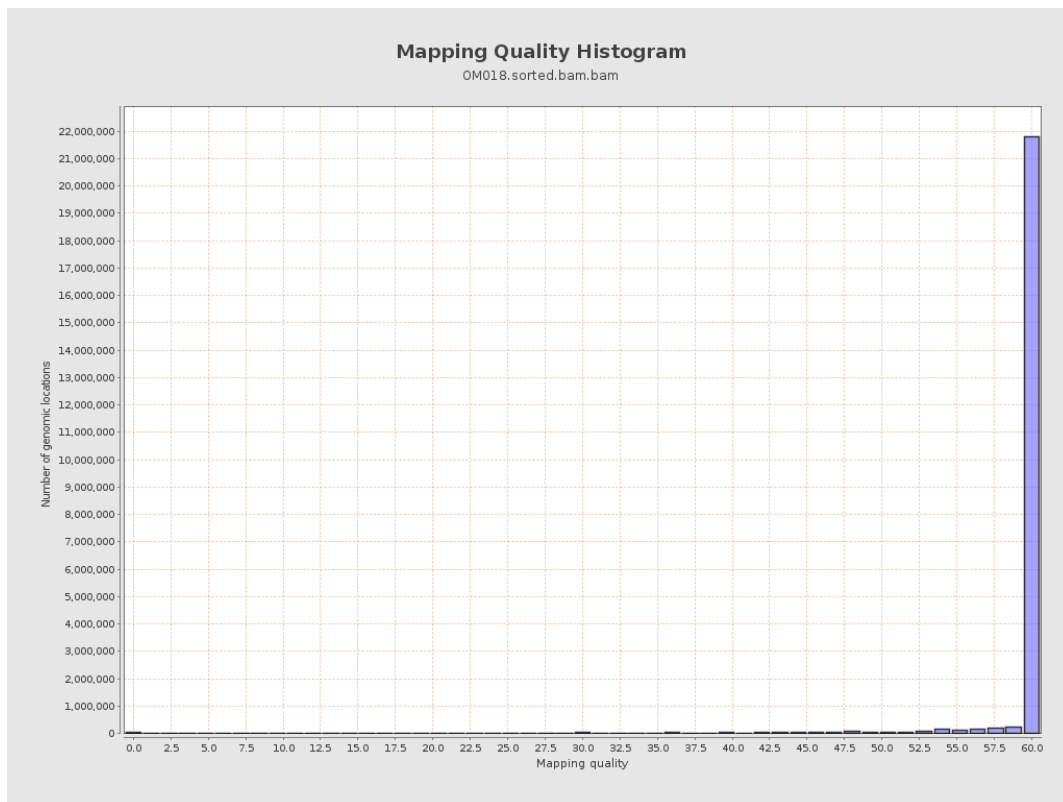
14. Results : Insert Size Across Reference
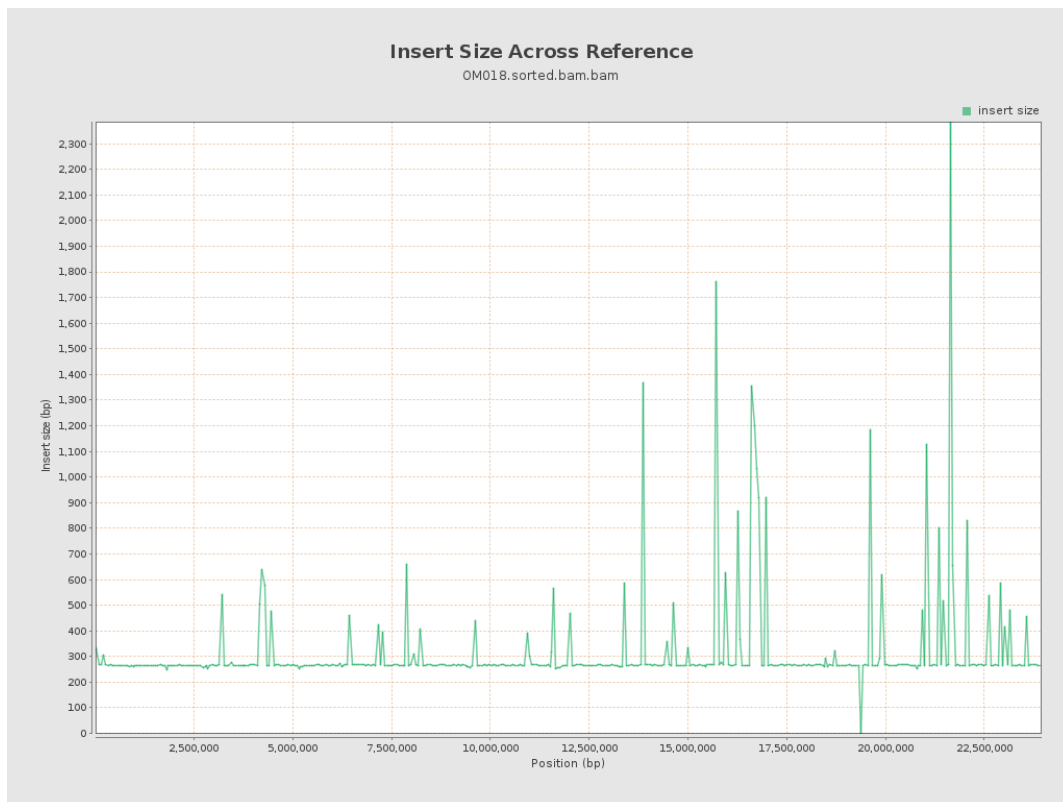
15. Results : Insert Size Histogram

Insert Size Histogram
OM018.sorted.bam.bam