Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 12:03:11

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam /home/vdp5/data/cambodia_samples/sequences_bam/OM015.sorted.bam.bam -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/OM015-BiooBarcode5_CAGATC_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM015-BiooBarcode5_CAGATC_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:03:10 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM015.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	65,302,351
Mapped reads	15,350,362 / 23.51%
Unmapped reads	49,951,989 / 76.49%
Mapped paired reads	15,350,362 / 23.51%
Mapped reads, first in pair	7,660,200 / 11.73%
Mapped reads, second in pair	7,690,162 / 11.78%
Mapped reads, both in pair	14,856,696 / 22.75%
Mapped reads, singletons	493,666 / 0.76%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	5,772,048 / 8.84%
Duplication rate	33.91%
Clipped reads	1,853,245 / 2.84%

2.2. ACGT Content

Number/percentage of A's	437,298,509 / 29.76%
Number/percentage of C's	296,437,177 / 20.18%
Number/percentage of T's	439,787,328 / 29.93%
Number/percentage of G's	295,664,017 / 20.12%
Number/percentage of N's	128,114 / 0.01%
GC Percentage	40.3%

2.3. Coverage

Mean	61.3871
Standard Deviation	69.127

2.4. Mapping Quality

Mean Mapping Quality	58.21

2.5. Insert size

Mean	754.83
Standard Deviation	27,293.58
P25/Median/P75	238 / 249 / 261

2.6. Mismatches and indels

General error rate	1.42%
Mismatches	19,685,901
Insertions	468,930
Mapped reads with at least one insertion	2.89%
Deletions	536,945
Mapped reads with at least one deletion	3.28%
Homopolymer indels	62.87%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	53705940	54.958	23.6545
gi|1074120682|emb|LT615257.1|	860454	57870008	67.2552	58.8071
gi|1074120865|emb|LT615258.1|	989719	69315319	70.0354	82.8778
gi|1074121086|emb|LT615259.1|	935450	59759536	63.8832	84.4565
gi|1074121301|emb|LT615260.1|	1432239	90113377	62.9178	58.8941
gi|1074121615|emb|LT615261.1|	1080962	68294615	63.1795	63.3917
gi|1074121871|emb|LT615262.1|	1545099	89531029	57.9452	23.92
gi|1074122235|emb|LT615263.1|	1585108	97103387	61.2598	82.5582
gi|1074122590|emb|LT615264.1|	2122358	122131794	57.5453	27.2045
gi|1074123050|emb|LT615265.1|	1754192	114804679	65.4459	152.8651
gi|1074123421|emb|LT615	2150147	139742064	64.9919	97.1235

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	179776263	59.3118	42.7864
gi|1074124588|emb|LT615268.1|	2359348	136128912	57.6977	51.2065
gi|1074125065|emb|LT615269.1|	3135668	192496817	61.3894	22.6629

3. Results : Coverage across reference

Coverage across reference
OM015.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM015.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
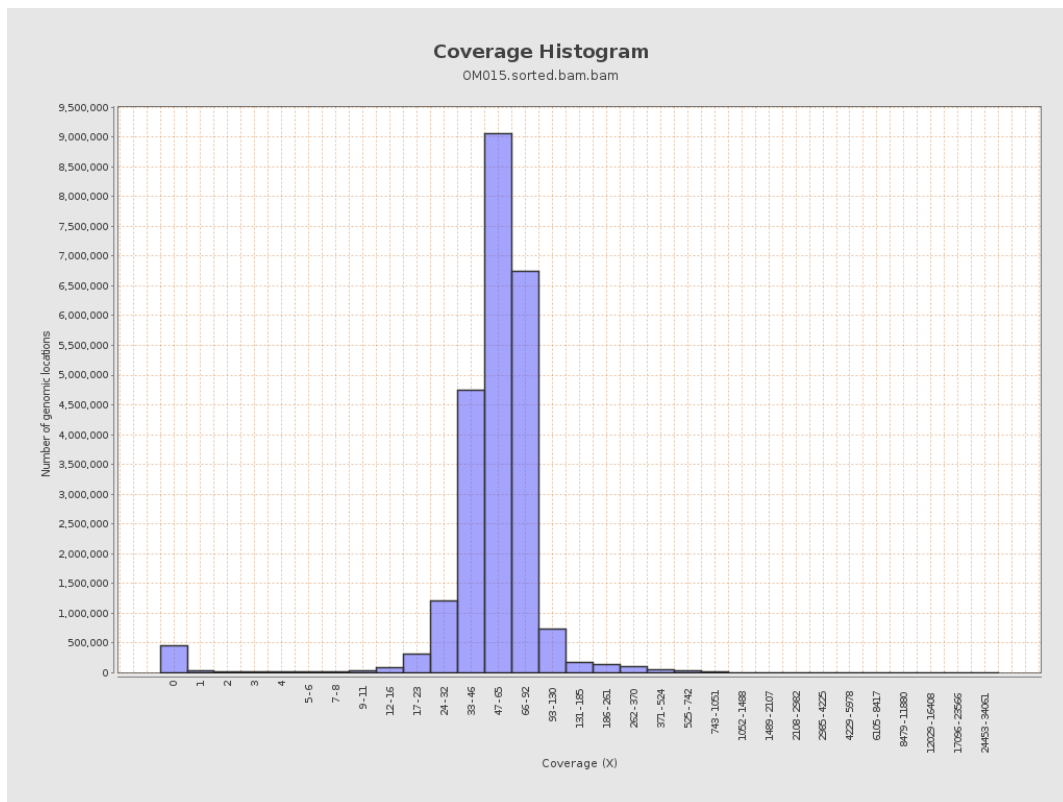
Coverage Histogram (0-50X)
OM015.sorted.bam.bam
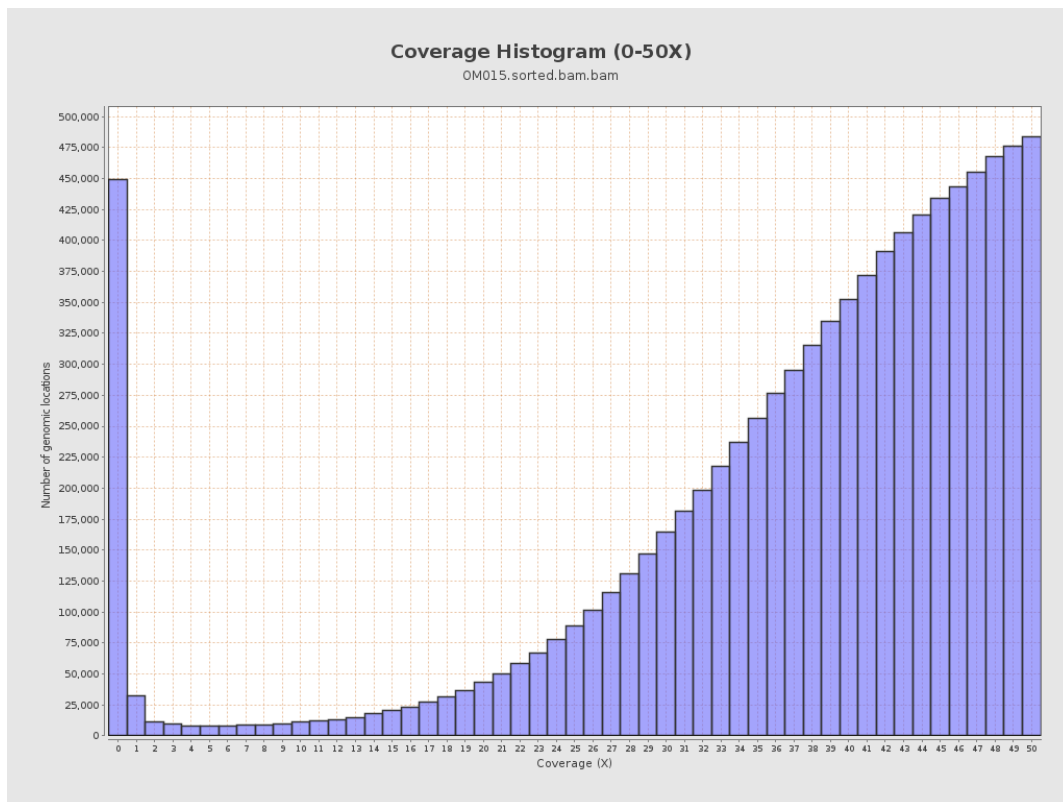
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM015.sorted.bam.bam
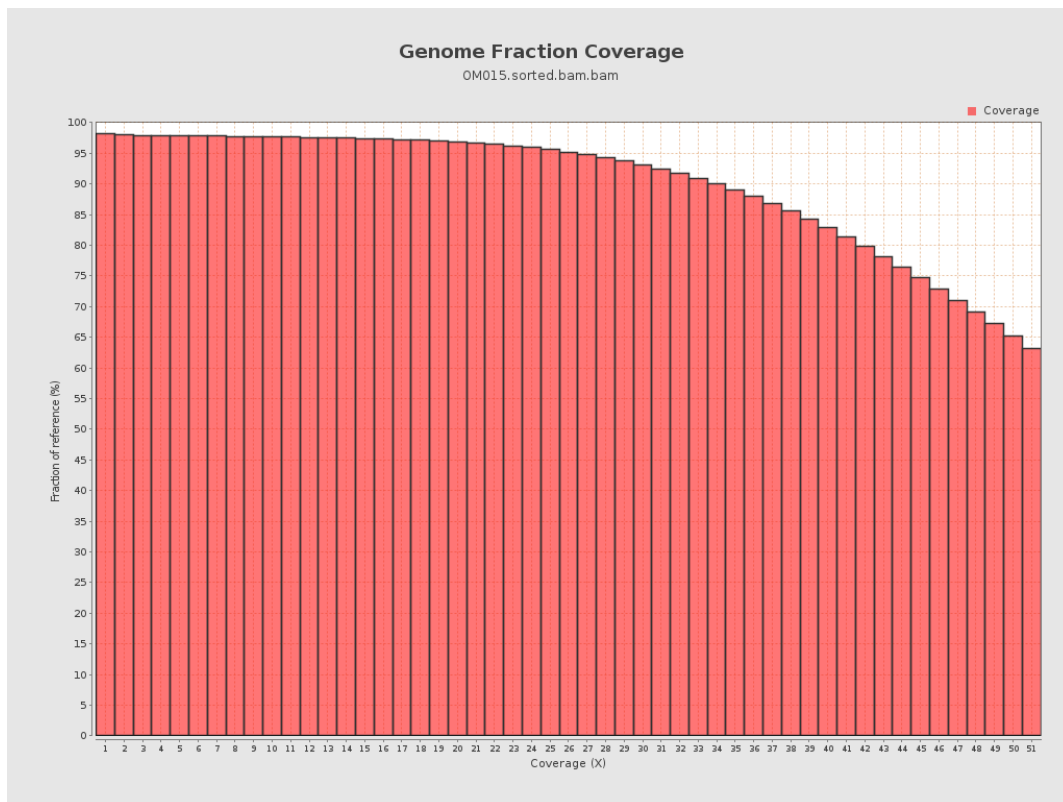
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
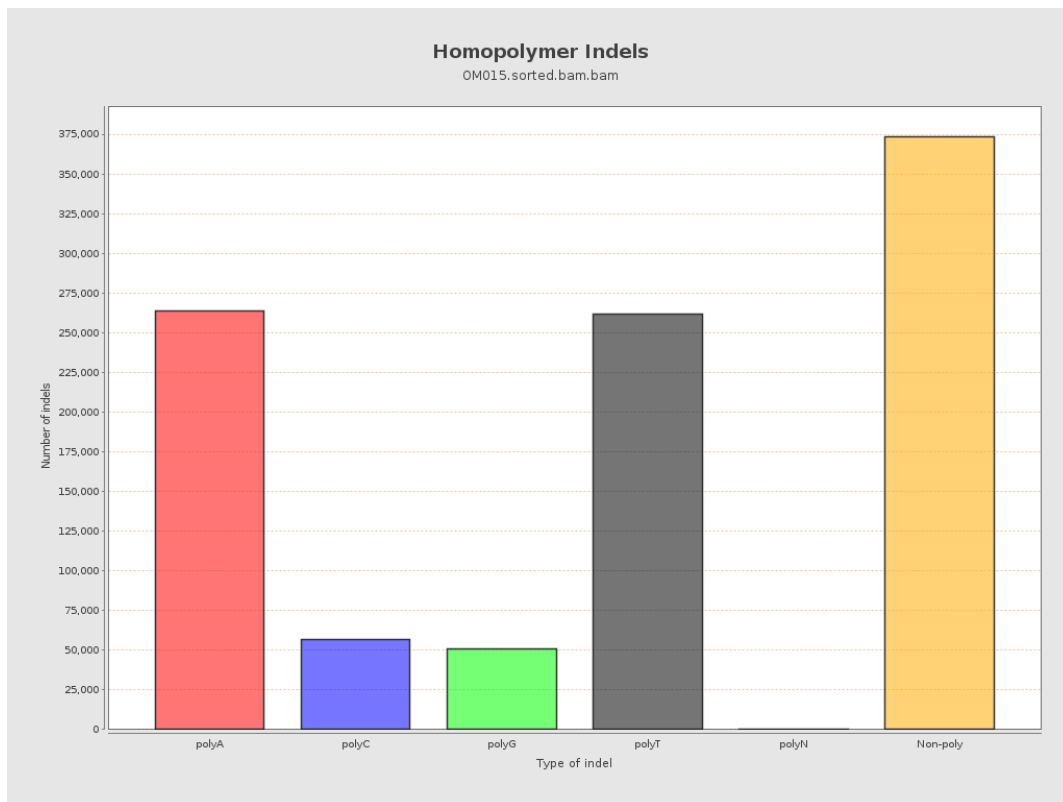OM015.sorted.bam.bam
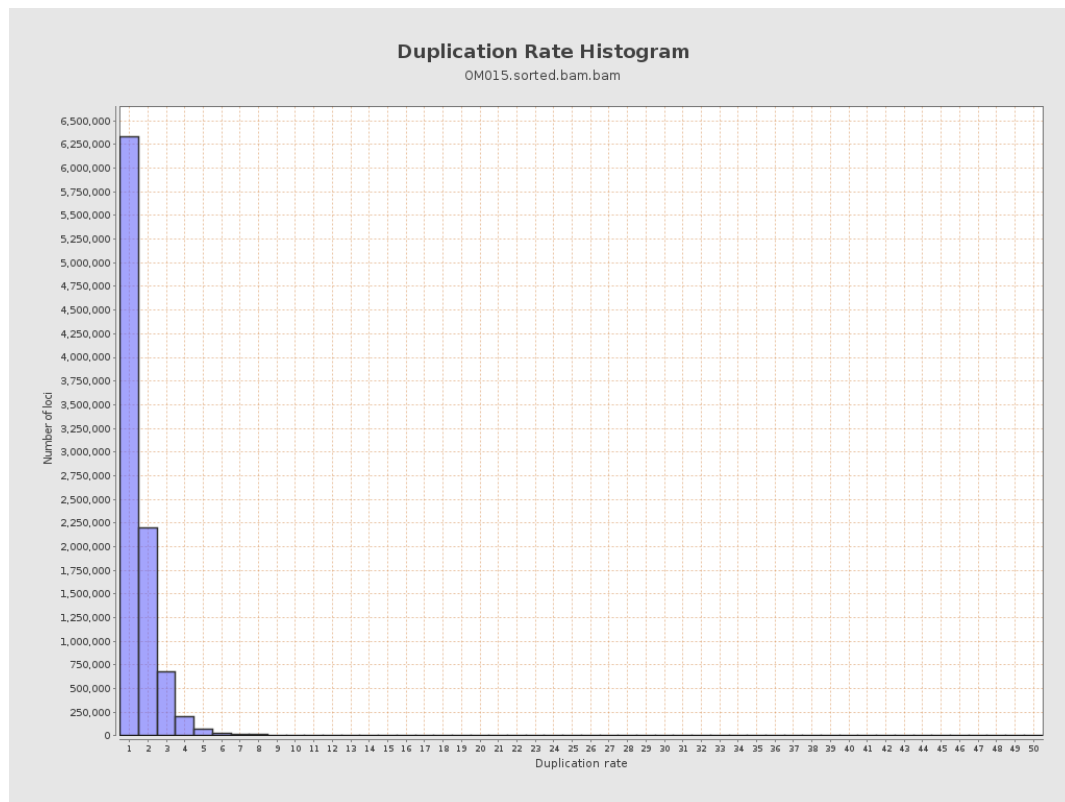
8. Results : Mapped Reads Nucleotide Content
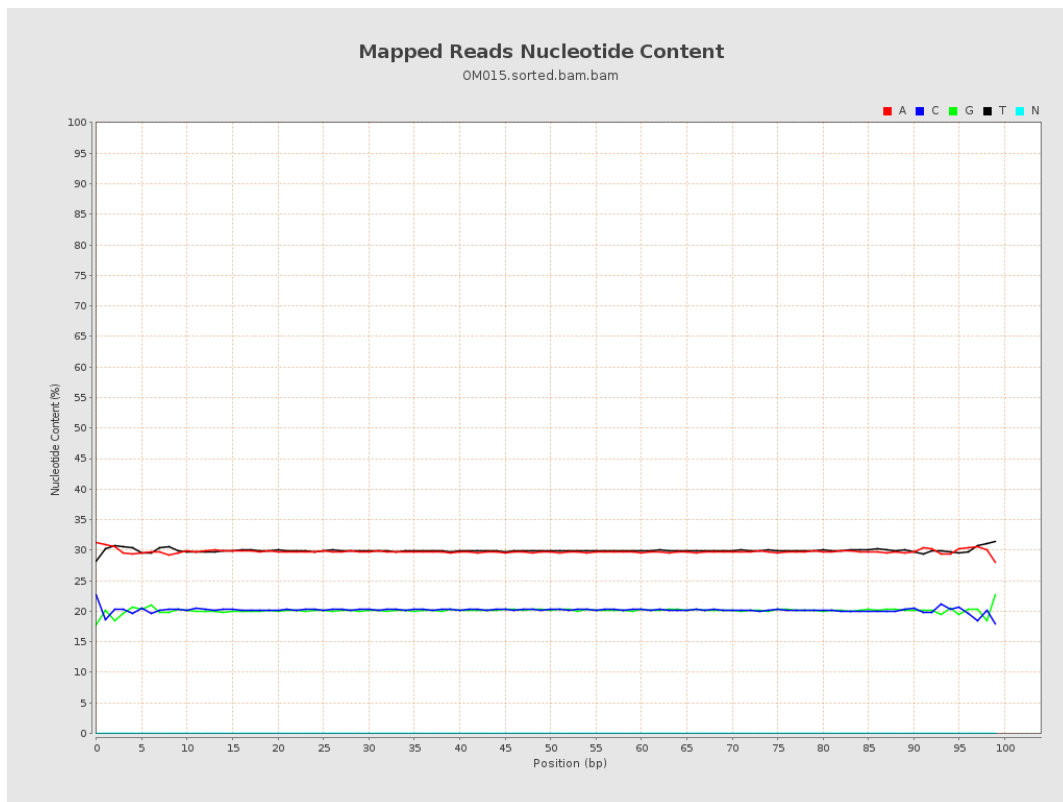
9. Results : Mapped Reads GC-content Distribution
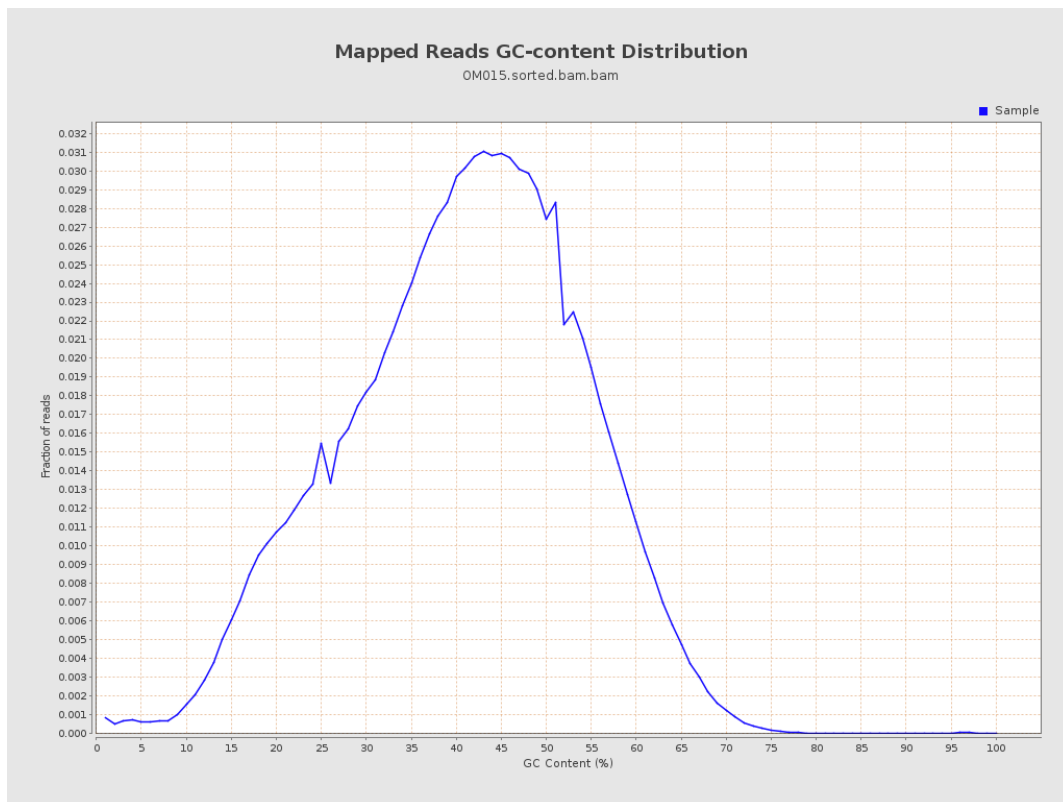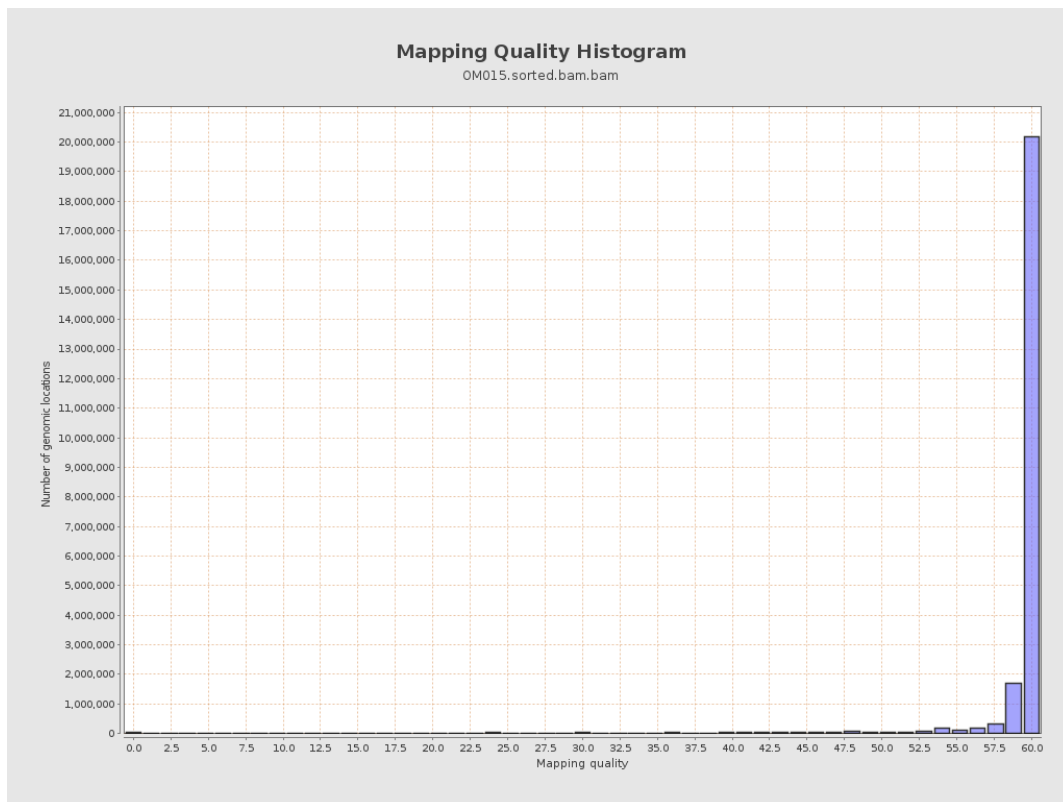
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
OM015.sorted.bam.bam
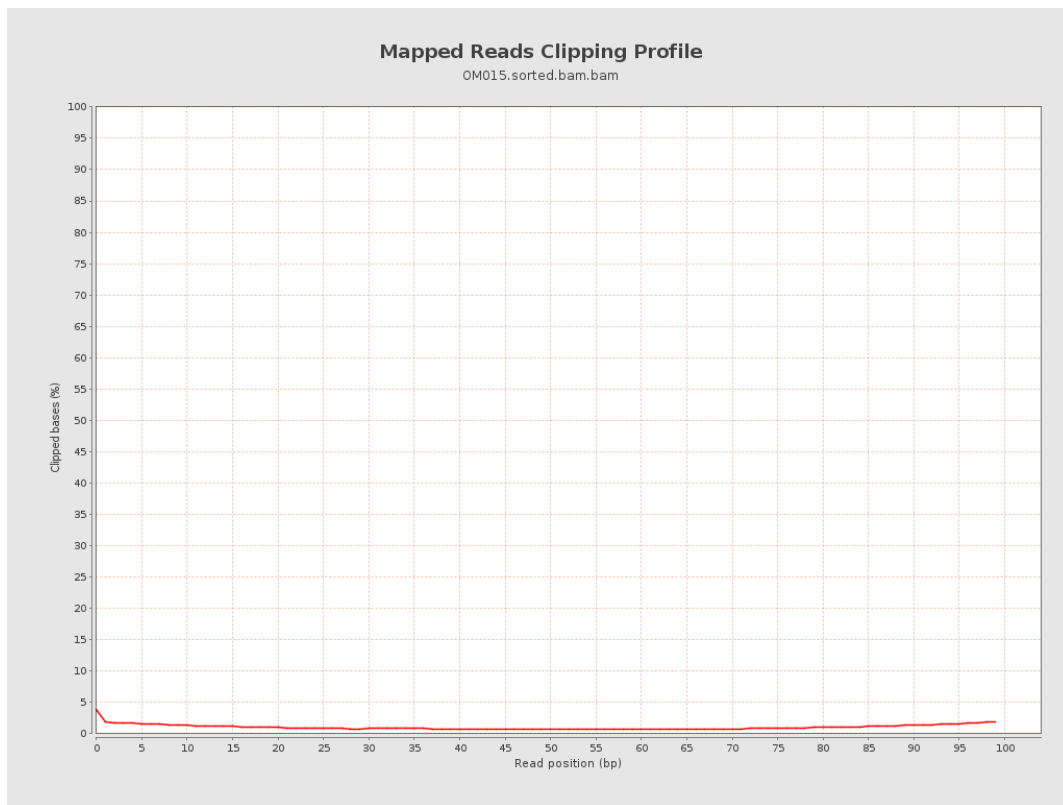
11. Results : Homopolymer Indels

Homopolymer Indels
OM015.sorted.bam.bam

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram
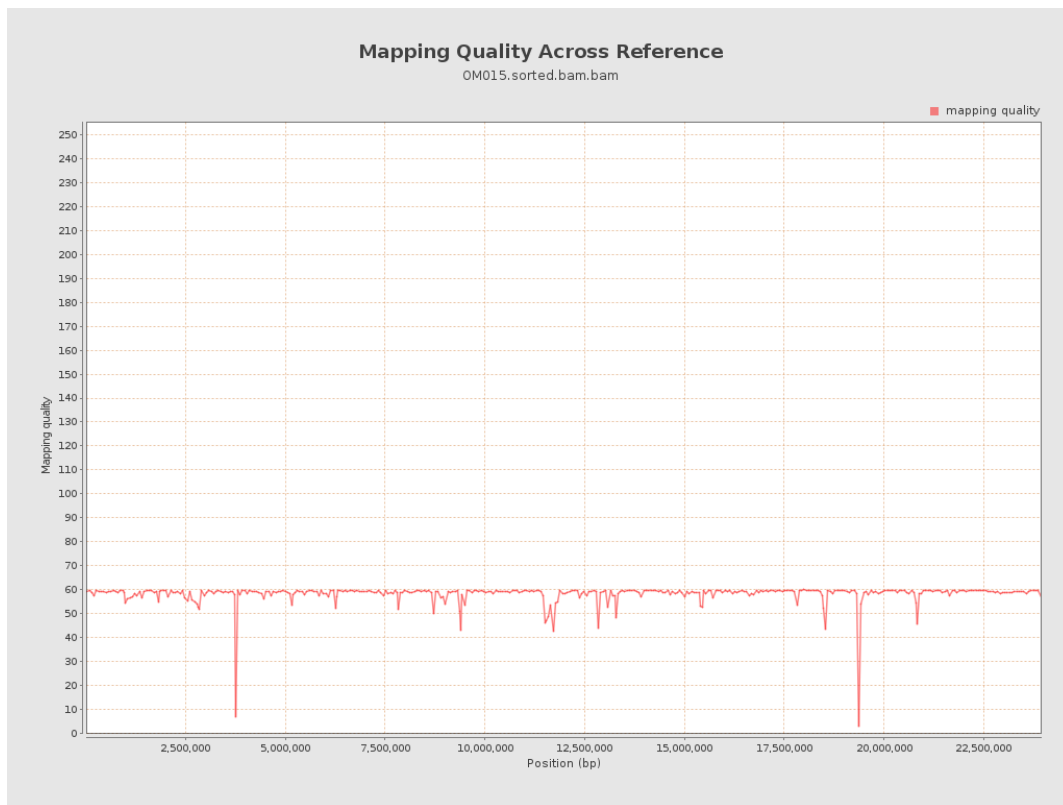
Mapping Quality Histogram
OM015.sorted.bam.bam

14. Results : Insert Size Across Reference
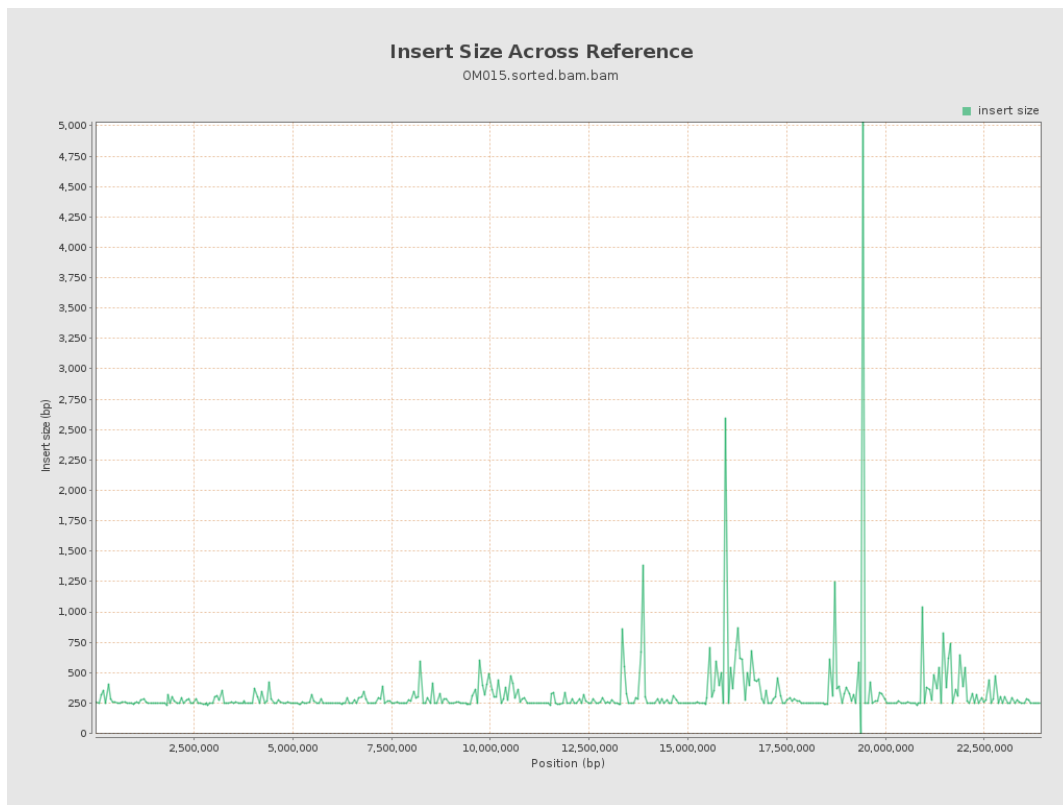
15. Results : Insert Size Histogram