Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 12:05:36

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM032.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/OM032-BiooBarcode7_ATCACG_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM032-BiooBarcode7_ATCACG_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:05:35 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM032.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	16,169,831
Mapped reads	8,355,931 / 51.68%
Unmapped reads	7,813,900 / 48.32%
Mapped paired reads	8,355,931 / 51.68%
Mapped reads, first in pair	4,183,560 / 25.87%
Mapped reads, second in pair	4,172,371 / 25.8%
Mapped reads, both in pair	8,244,754 / 50.99%
Mapped reads, singletons	111,177 / 0.69%
Read min/max/mean length	30 / 100 / 99.91
Duplicated reads (estimated)	1,921,087 / 11.88%
Duplication rate	19.83%
Clipped reads	879,642 / 5.44%

2.2. ACGT Content

Number/percentage of A's	239,818,410 / 29.7%
Number/percentage of C's	163,699,307 / 20.28%
Number/percentage of T's	240,492,555 / 29.79%
Number/percentage of G's	163,326,442 / 20.23%
Number/percentage of N's	71,906 / 0.01%
GC Percentage	40.51%

2.3. Coverage

Mean	33.7318
Standard Deviation	27.1323

2.4. Mapping Quality

Mean Mapping Quality	58.67

2.5. Insert size

Mean	551.72
Standard Deviation	22,208.5
P25/Median/P75	172 / 187 / 204

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	10,255,065
Insertions	251,303
Mapped reads with at least one insertion	2.85%
Deletions	283,154
Mapped reads with at least one deletion	3.2%
Homopolymer indels	64.07%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	30085154	30.7866	13.1919
gi|1074120682|emb|LT615257.1|	860454	26934225	31.3023	20.096
gi|1074120865|emb|LT615258.1|	989719	37779563	38.172	46.6673
gi|1074121086|emb|LT615259.1|	935450	34913765	37.323	47.4536
gi|1074121301|emb|LT615260.1|	1432239	50335332	35.1445	29.2409
gi|1074121615|emb|LT615261.1|	1080962	36620130	33.8774	23.1503
gi|1074121871|emb|LT615262.1|	1545099	50506230	32.688	12.8407
gi|1074122235|emb|LT615263.1|	1585108	52839653	33.335	20.3209
gi|1074122590|emb|LT615264.1|	2122358	70265832	33.1074	16.9892
gi|1074123050|emb|LT615265.1|	1754192	61778102	35.2174	29.3067
gi|1074123421|emb|LT615	2150147	75851905	35.2775	50.9489

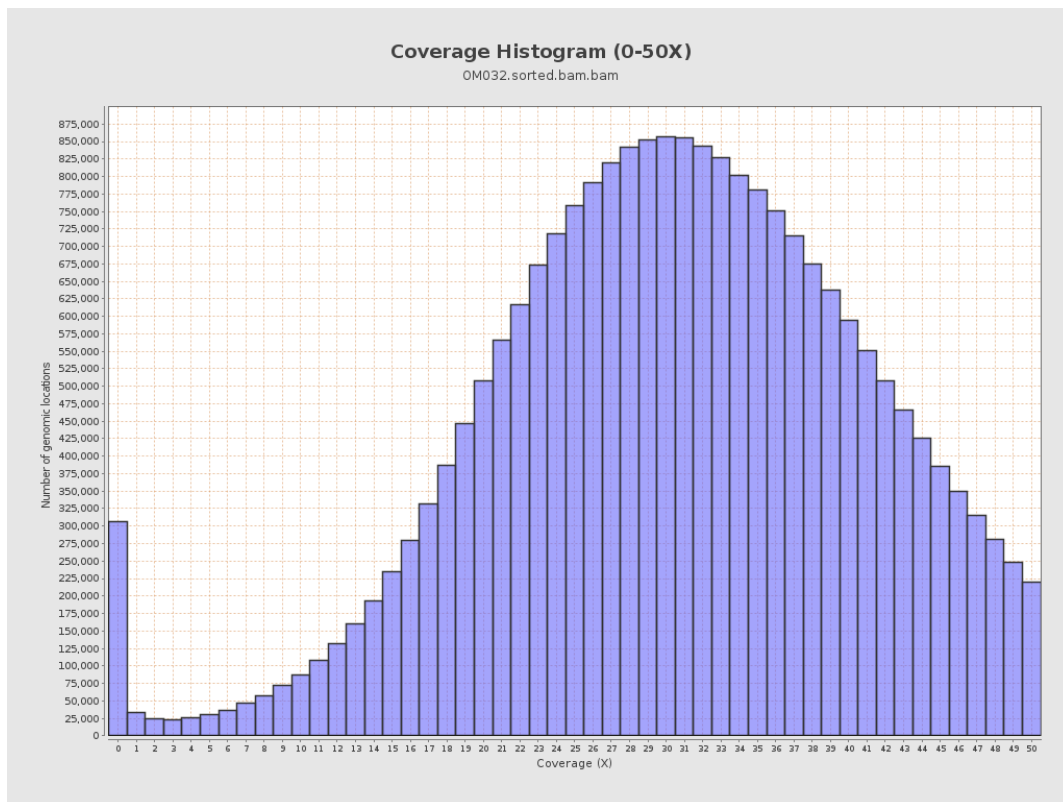|				
266.1|				
gi|1074123898|emb|LT615267.1|	3031036	99283966	32.7558	13.1918
gi|1074124588|emb|LT615268.1|	2359348	74199545	31.4492	24.5708
gi|1074125065|emb|LT615269.1|	3135668	106786462	34.0554	11.5434

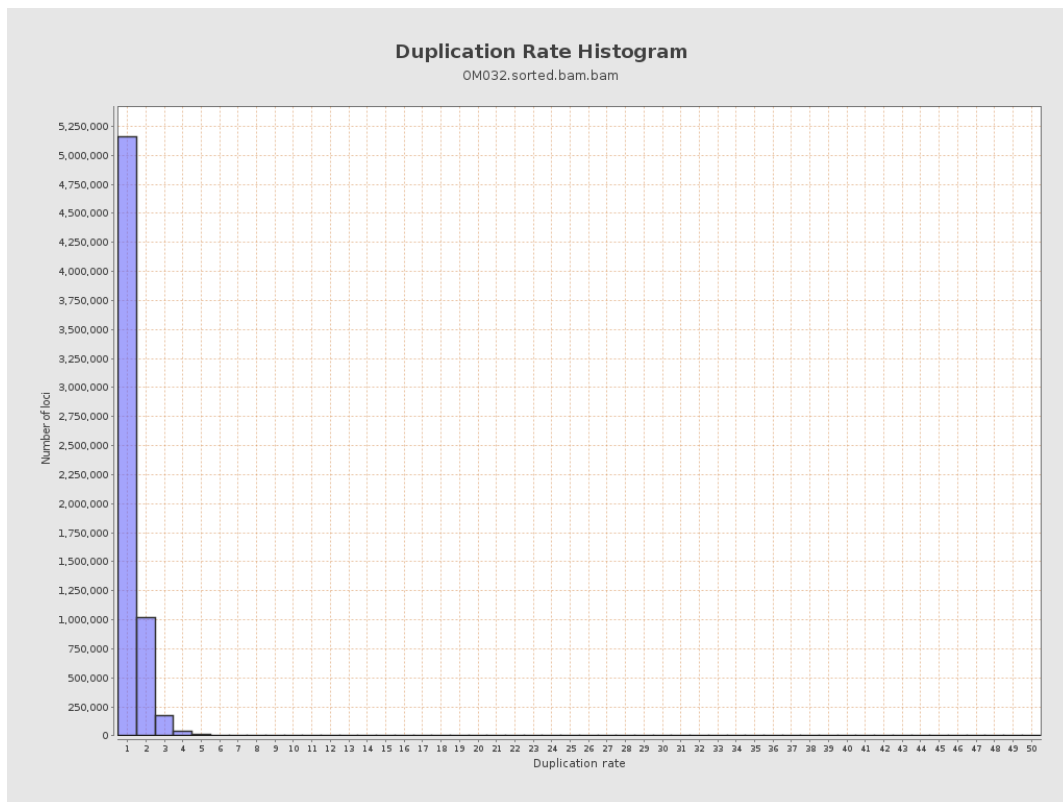# 3. Results : Coverage across reference

4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
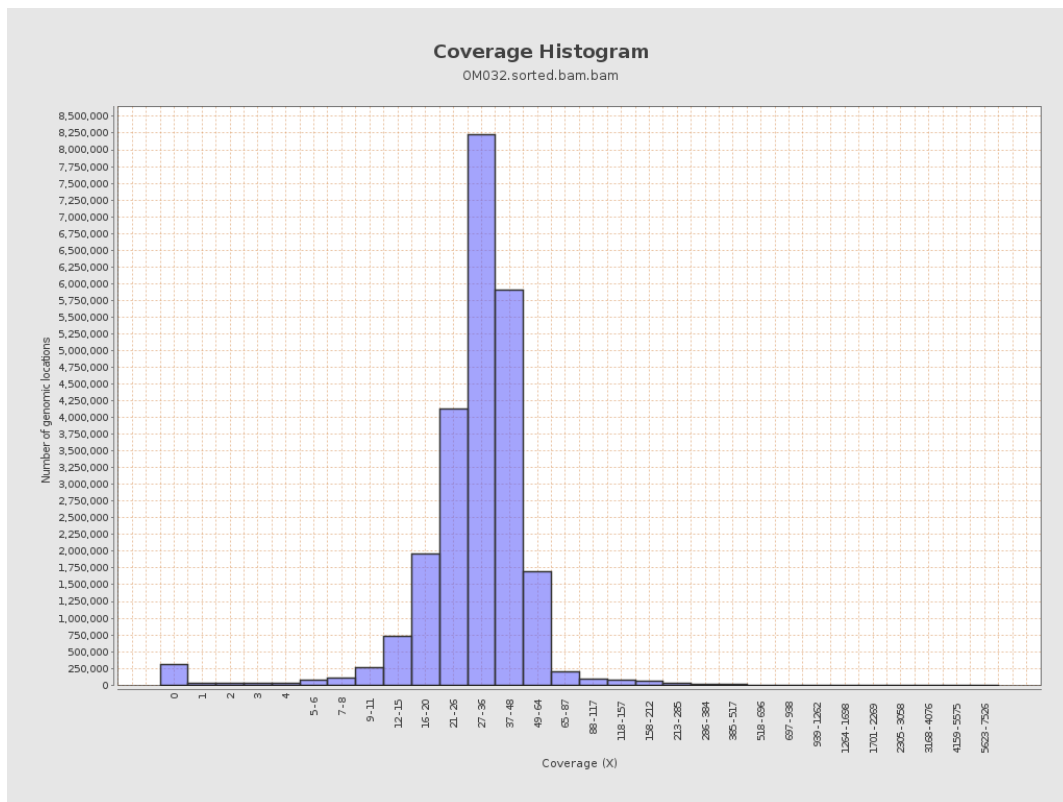
Coverage Histogram (0-50X)
OM032.sorted.bam.bam

6. Results : Genome Fraction Coverage
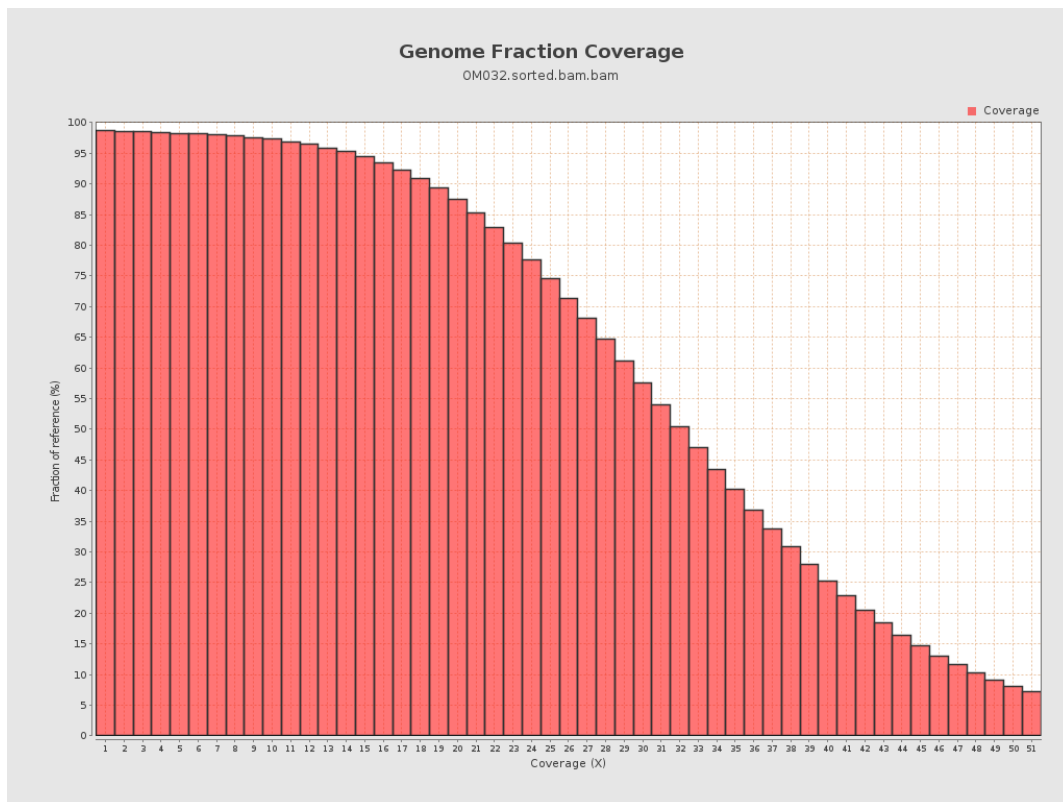
7. Results : Duplication Rate Histogram

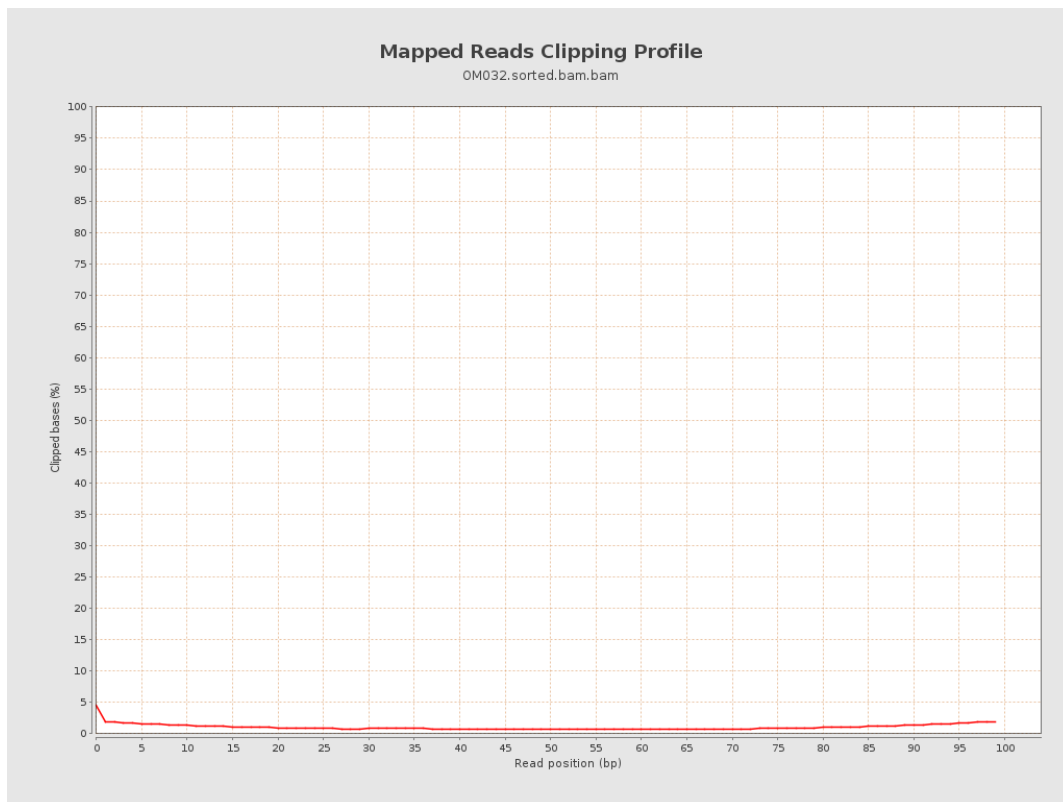
Duplication Rate Histogram
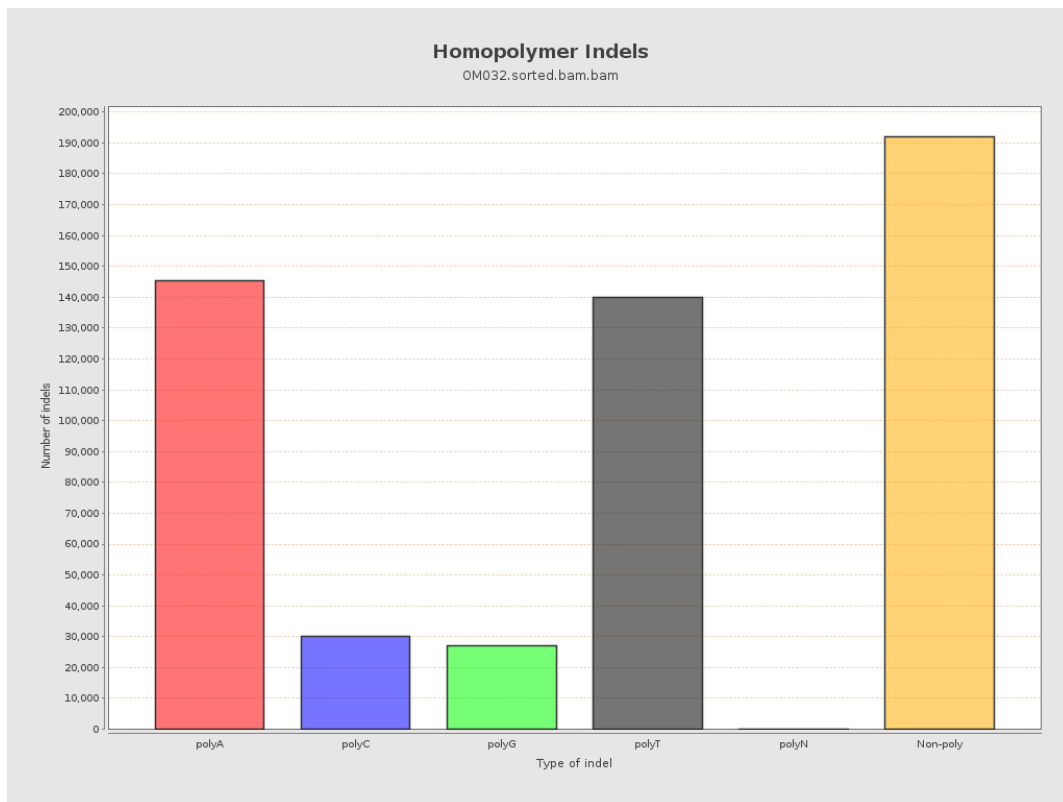
OM032.sorted.bam.bam

8. Results : Mapped Reads Nucleotide Content
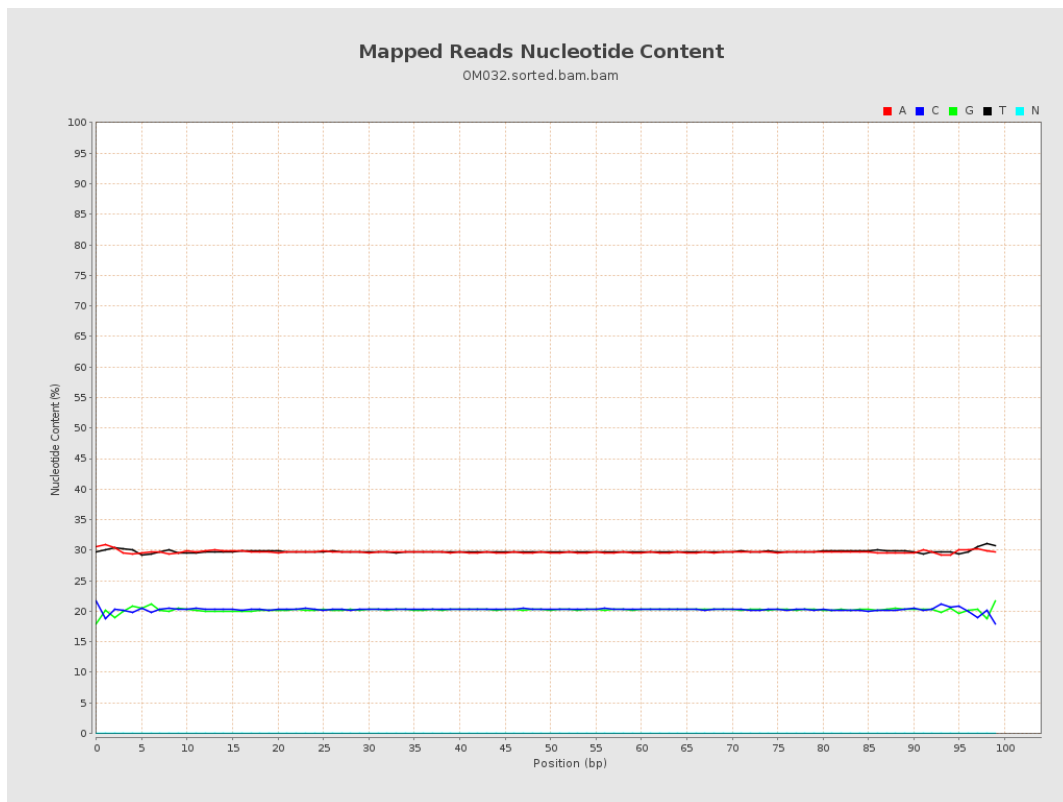
9. Results : Mapped Reads GC-content Distribution
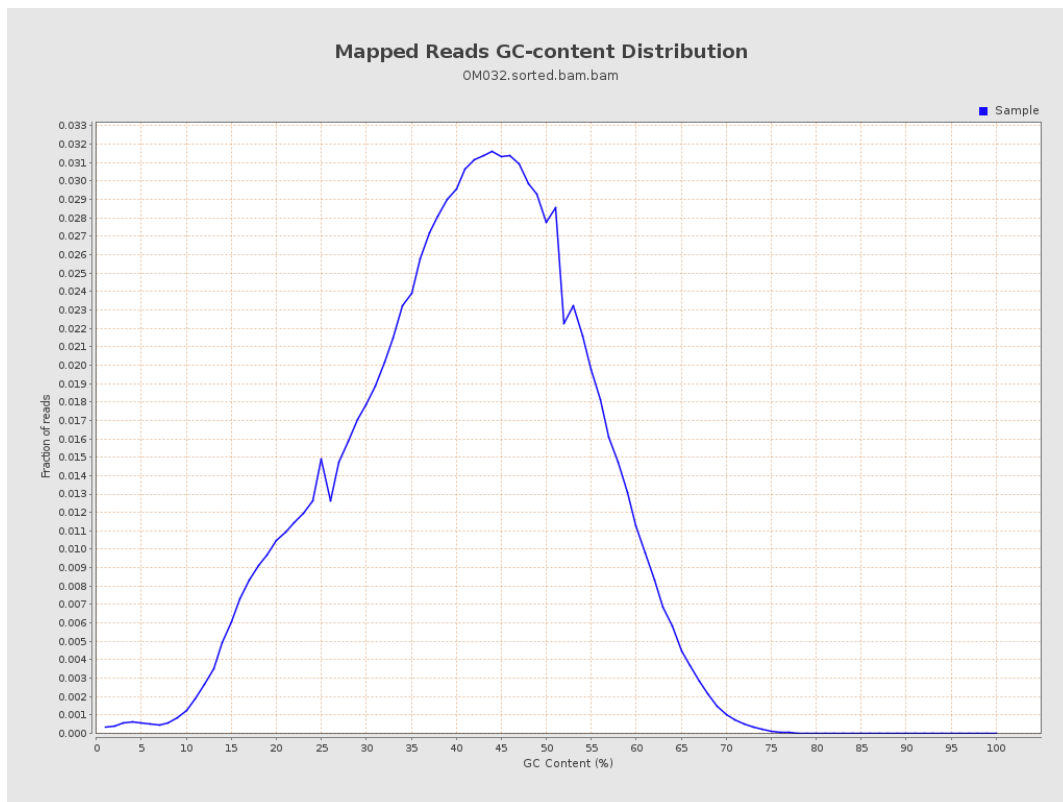
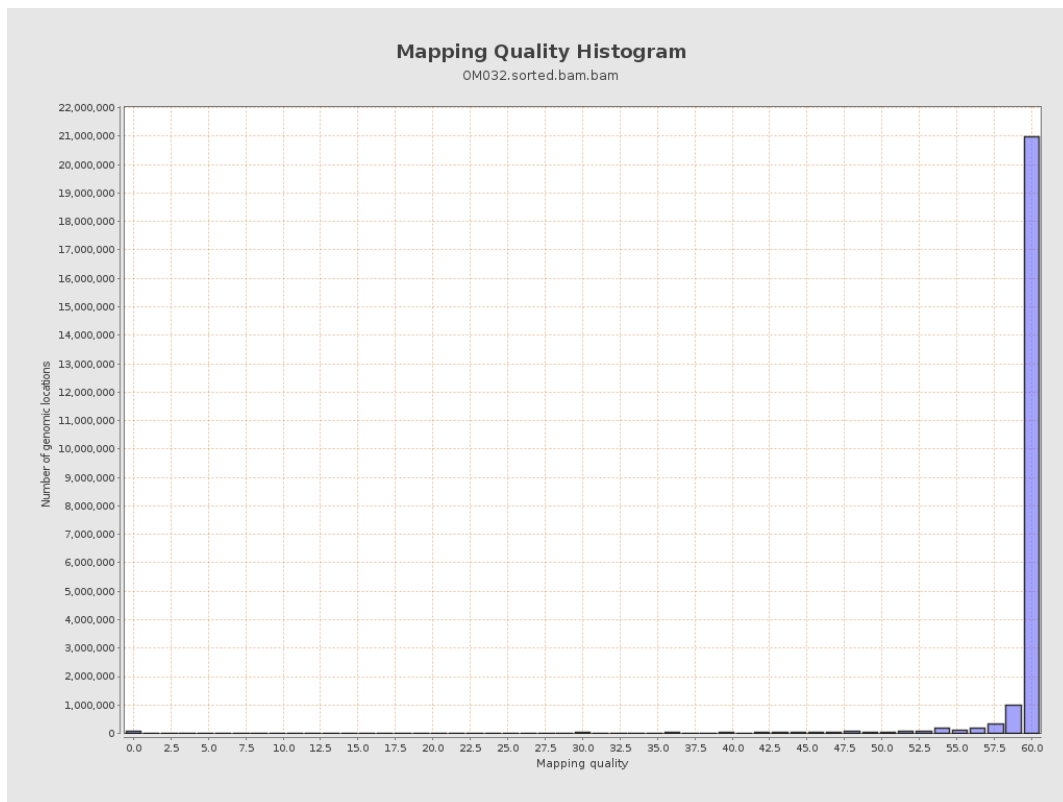# 10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
OM032.sorted.bam.bam

11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram
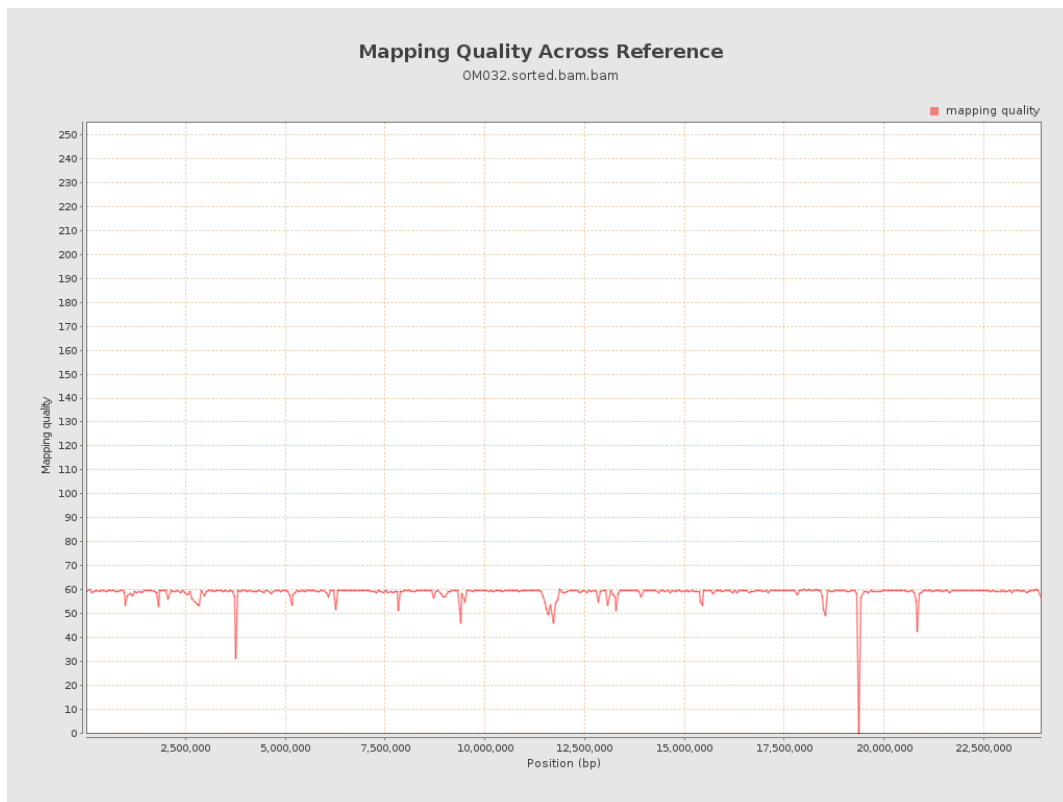
Mapping Quality Histogram
OM032.sorted.bam.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM032.sorted.bam.bam
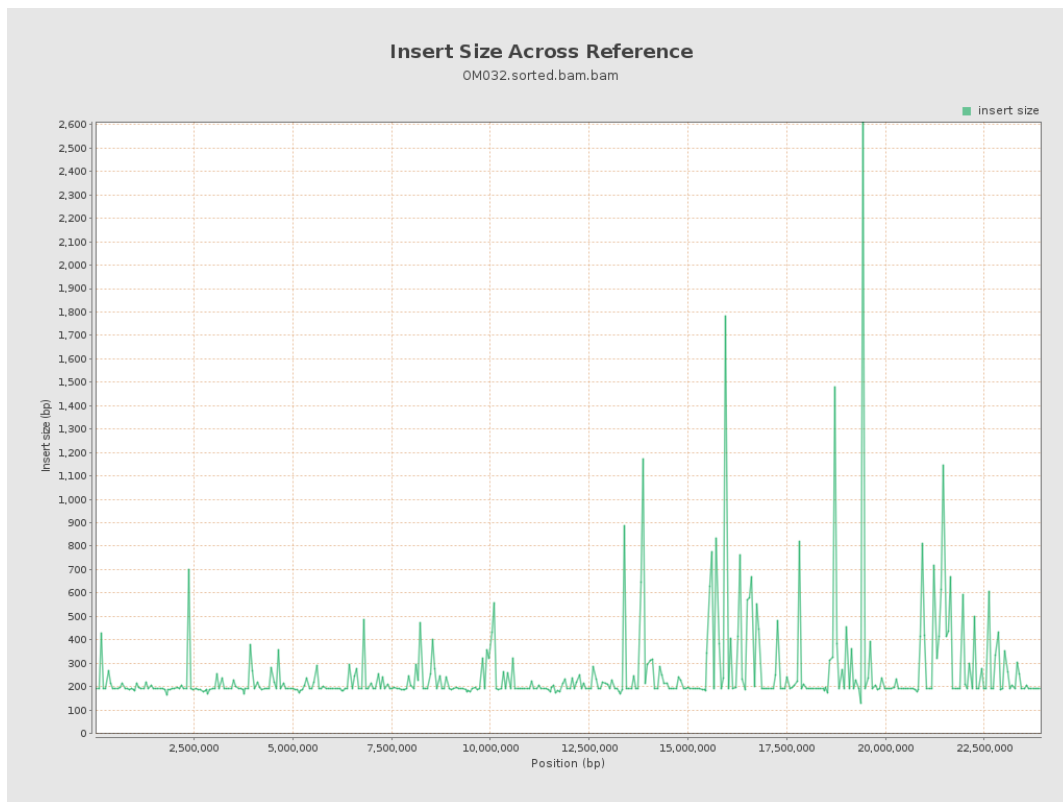
15. Results : Insert Size Histogram