Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 12:22:39

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM076.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/OM076-BiooBarcode11_TAGCTT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM076-BiooBarcode11_TAGCTT_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:22:38 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM076.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	38,095,441
Mapped reads	6,187,626 / 16.24%
Unmapped reads	31,907,815 / 83.76%
Mapped paired reads	6,187,626 / 16.24%
Mapped reads, first in pair	3,099,640 / 8.14%
Mapped reads, second in pair	3,087,986 / 8.11%
Mapped reads, both in pair	5,894,805 / 15.47%
Mapped reads, singletons	292,821 / 0.77%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	1,432,150 / 3.76%
Duplication rate	17.56%
Clipped reads	857,052 / 2.25%

2.2. ACGT Content

Number/percentage of A's	176,111,547 / 30.05%
Number/percentage of C's	116,445,116 / 19.87%
Number/percentage of T's	177,325,694 / 30.25%
Number/percentage of G's	116,262,514 / 19.84%
Number/percentage of N's	51,483 / 0.01%
GC Percentage	39.7%

2.3. Coverage

Mean	24.4918
Standard Deviation	37.456

2.4. Mapping Quality

Mean Mapping Quality	57.9

2.5. Insert size

Mean	782.33
Standard Deviation	27,216.37
P25/Median/P75	199 / 208 / 217

2.6. Mismatches and indels

General error rate	1.45%
Mismatches	8,009,631
Insertions	206,571
Mapped reads with at least one insertion	3.15%
Deletions	233,737
Mapped reads with at least one deletion	3.51%
Homopolymer indels	62.5%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|107412047 8|emb|LT615 256.1|	977217	21751466	22.2586	13.6776
gi|107412068 2|emb|LT615 257.1|	860454	19951610	23.1873	20.7077
gi|107412086 5|emb|LT615 258.1|	989719	28343489	28.6379	45.9244
gi|107412108 6|emb|LT615 259.1|	935450	23993684	25.6493	32.1517
gi|107412130 1|emb|LT615 260.1|	1432239	36754235	25.6621	26.6294
gi|107412161 5|emb|LT615 261.1|	1080962	26341790	24.3688	22.6041
gi|107412187 1|emb|LT615 262.1|	1545099	36456988	23.5952	13.5806
gi|107412223 5|emb|LT615 263.1|	1585108	38549414	24.3197	55.353
gi|107412259 0|emb|LT615 264.1|	2122358	50003050	23.5601	14.0877
gi|107412305 0|emb|LT615 265.1|	1754192	46522446	26.5207	95.0325
gi|107412342 1|emb|LT615	2150147	54218916	25.2164	34.5739

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	71631629	23.6327	28.1988
gi|1074124588|emb|LT615268.1|	2359348	55915563	23.6996	25.5375
gi|1074125065|emb|LT615269.1|	3135668	76364747	24.3536	12.2858

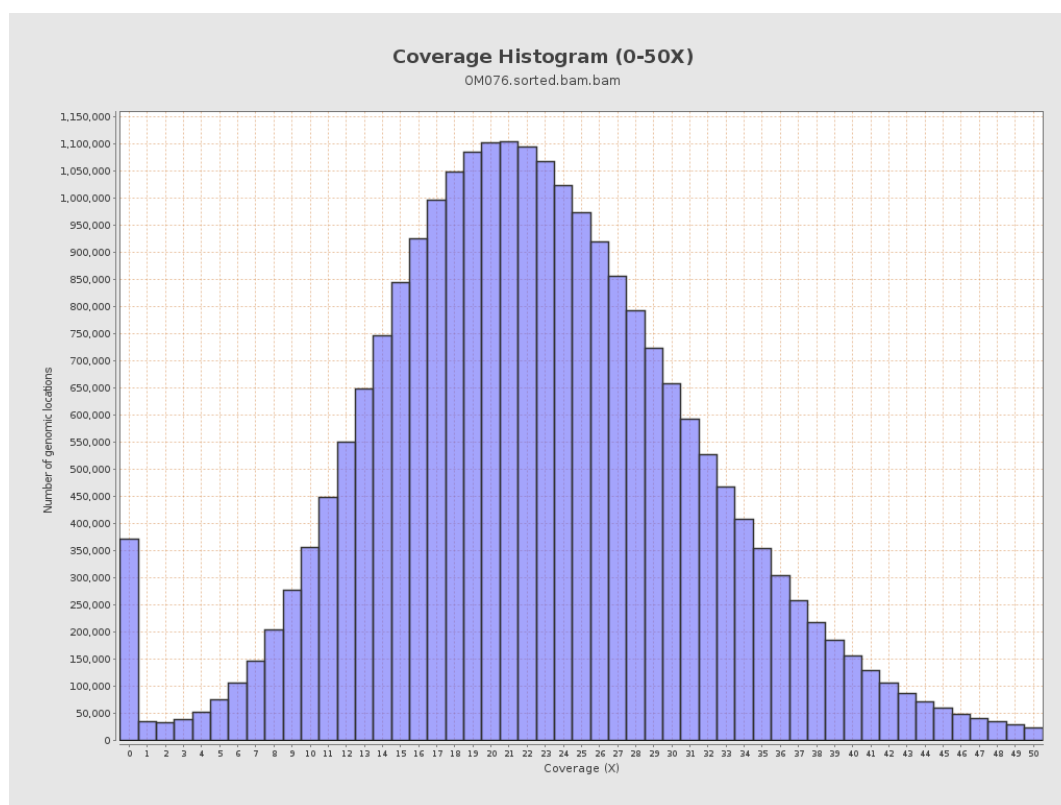# 3. Results : Coverage across reference
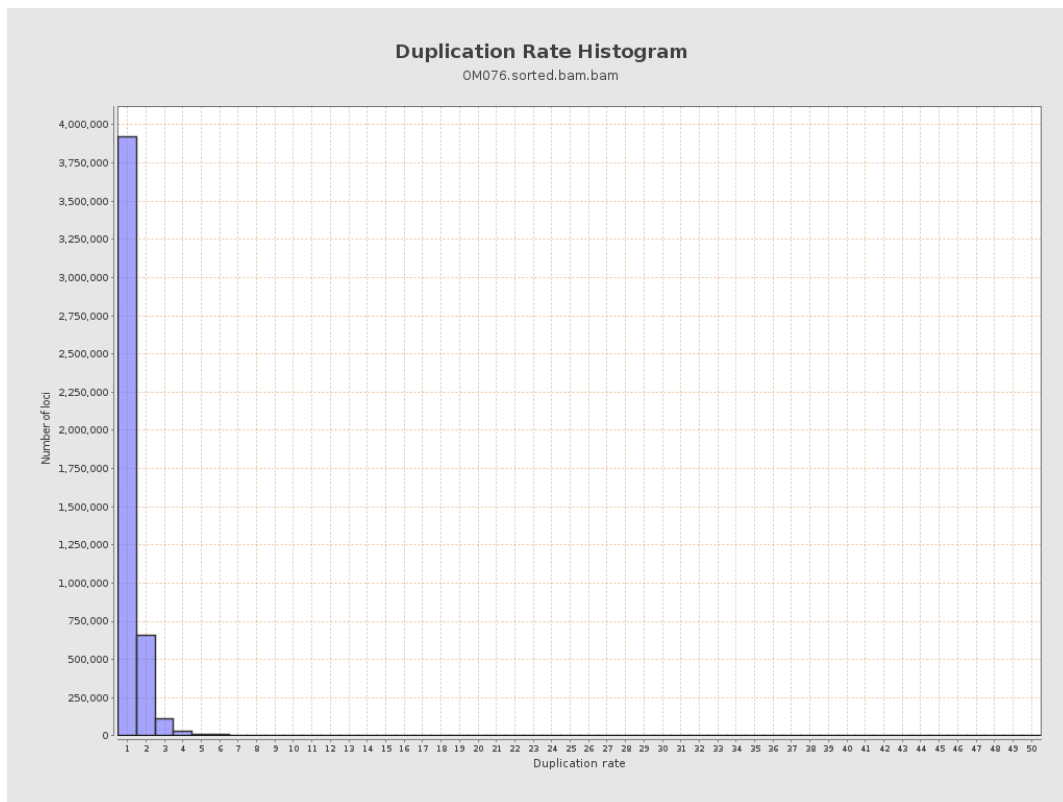
4. Results : Coverage Histogram

Coverage Histogram
OM076.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
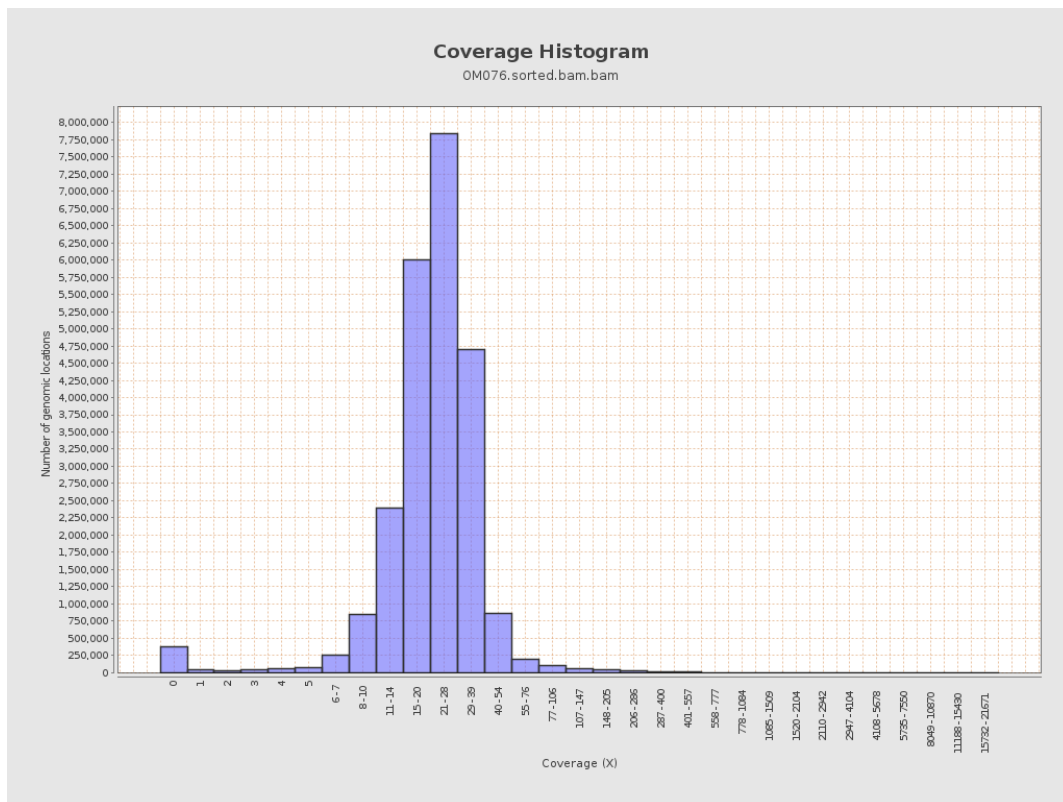
Coverage Histogram (0-50X)
OM076.sorted.bam.bam

6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM076.sorted.bam.bam
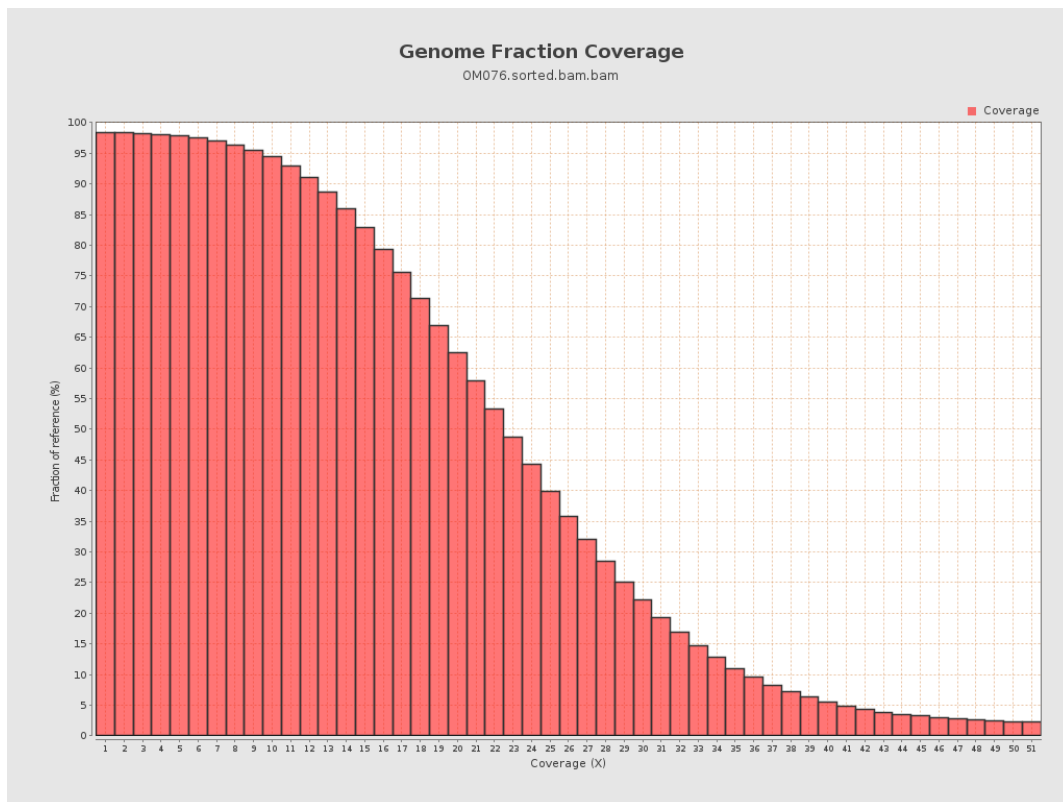
7. Results : Duplication Rate Histogram

8. Results : Mapped Reads Nucleotide Content
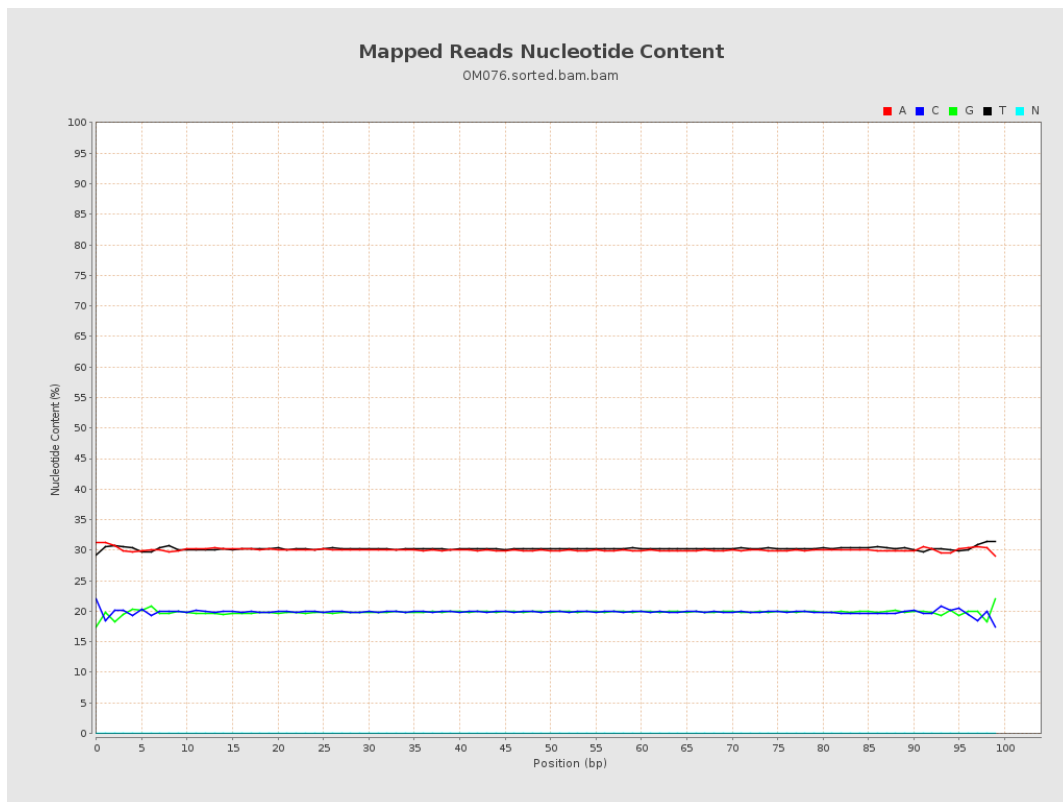
9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
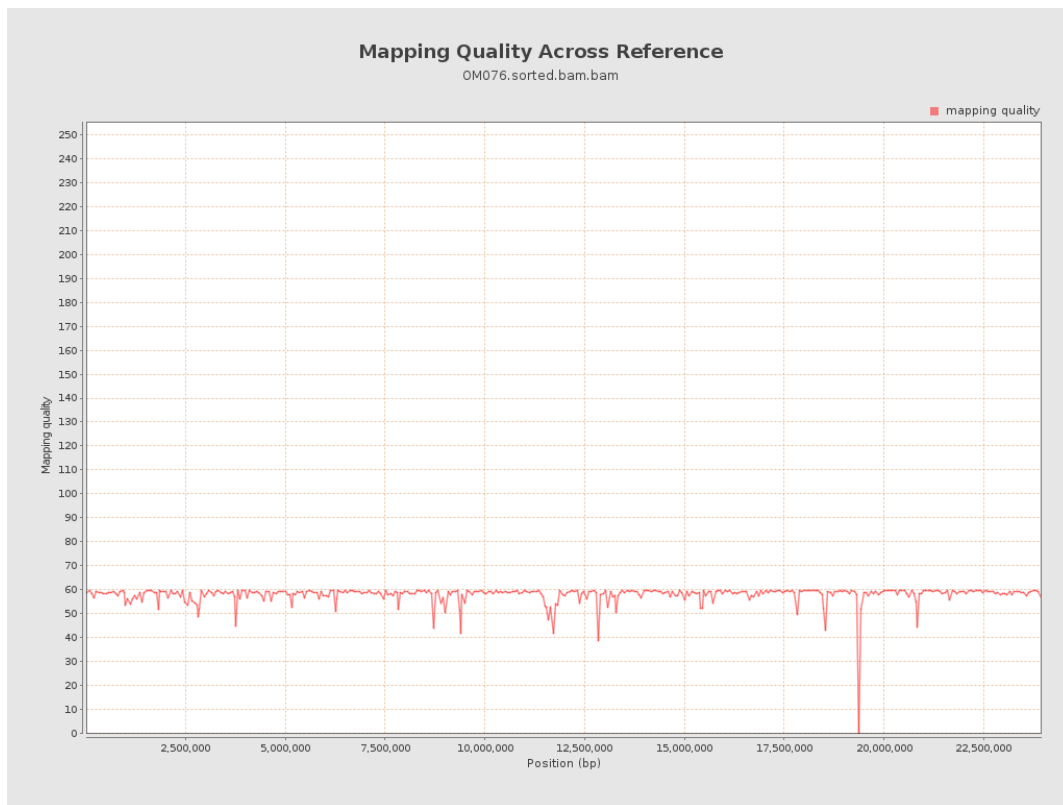0M076.sorted.bam.bam
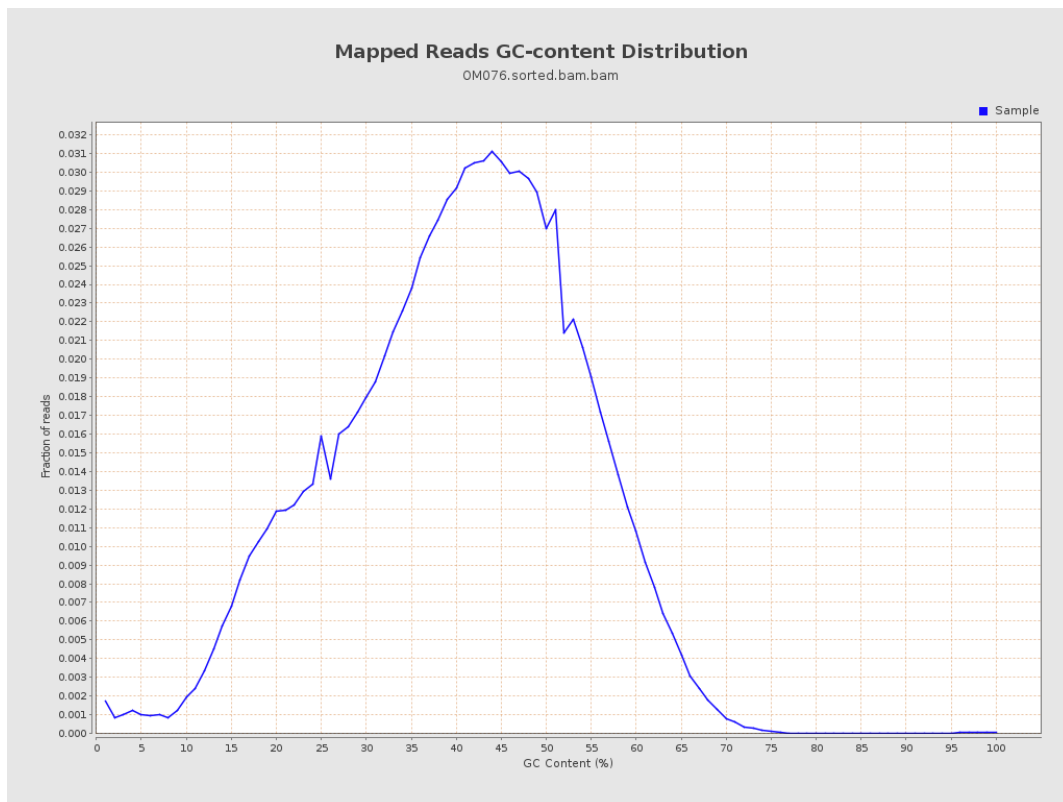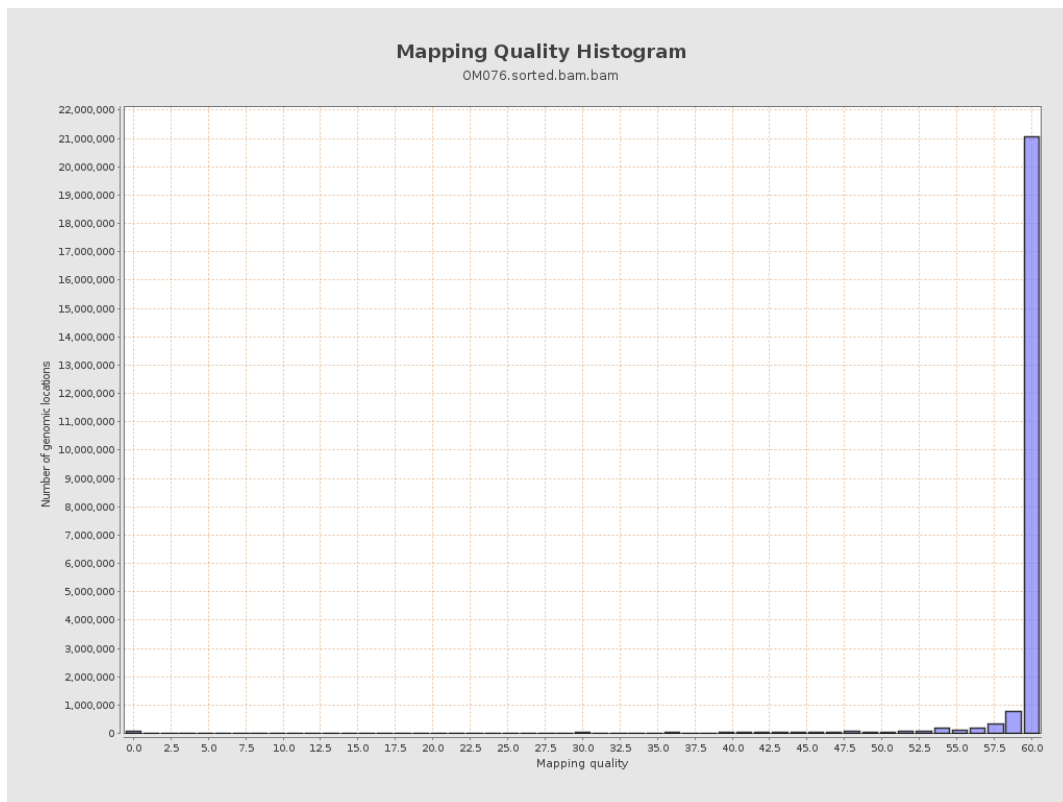
10. Results : Mapped Reads Clipping Profile
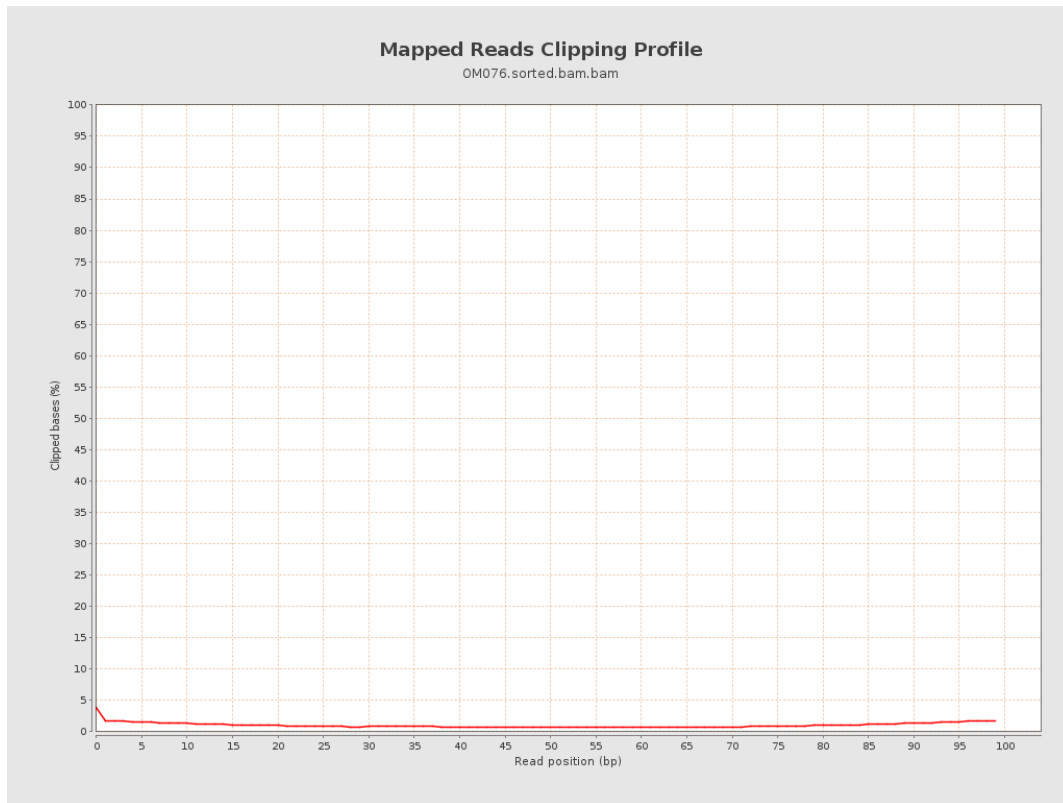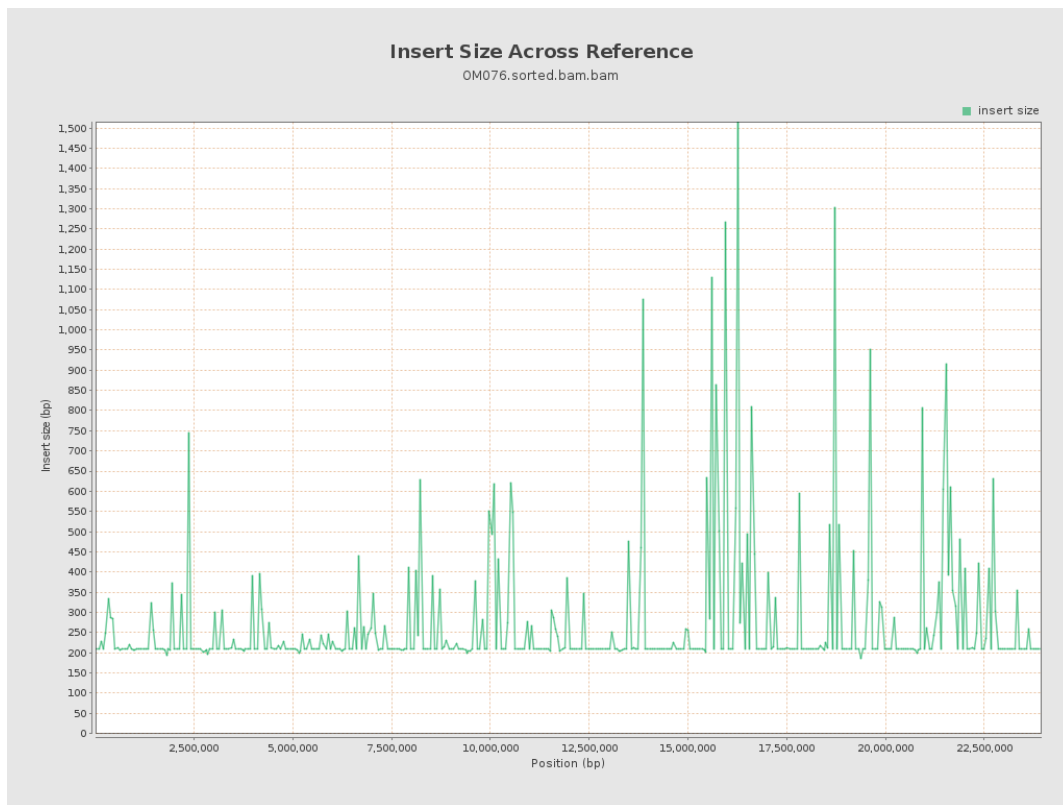
11. Results : Homopolymer Indels
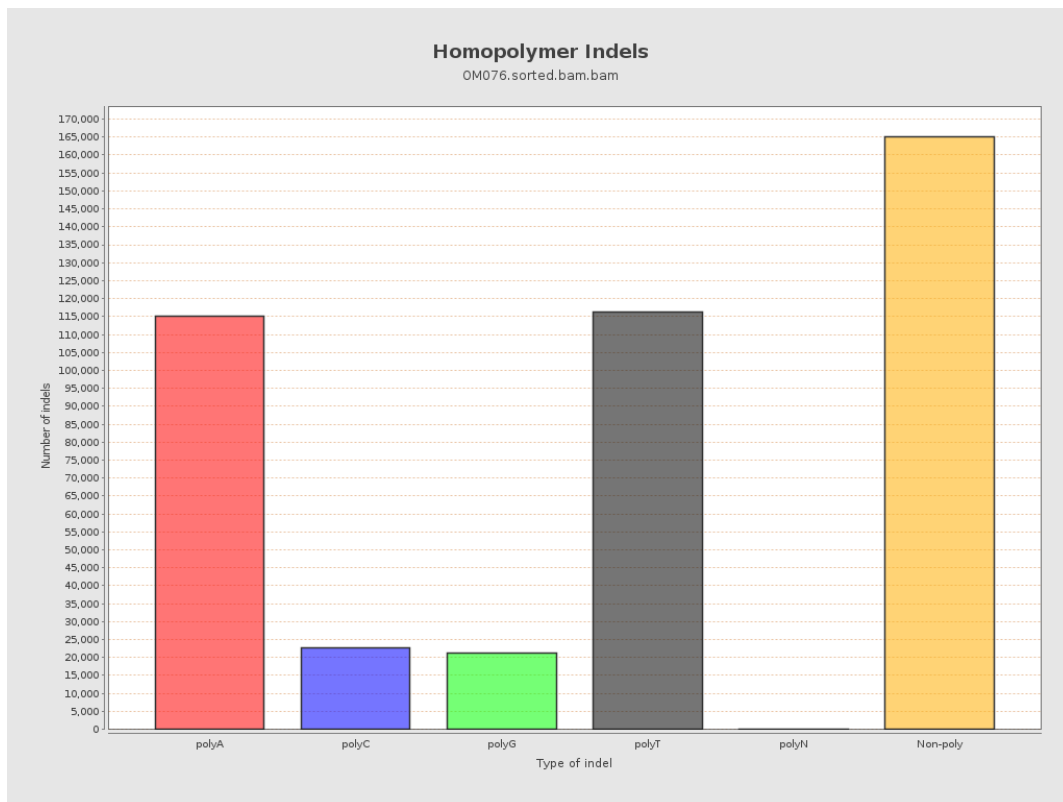
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM076.sorted.bam.bam

15. Results : Insert Size Histogram

Insert Size Histogram
OM076.sorted.bam.bam