Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:58:21

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM275.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/OM275-BiooBarcode27_ATTCCT_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM275-BiooBarcode27_ATTCCT_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:58:20 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM275.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	2,629,578
Mapped reads	1,555,746 / 59.16%
Unmapped reads	1,073,832 / 40.84%
Mapped paired reads	1,555,746 / 59.16%
Mapped reads, first in pair	776,190 / 29.52%
Mapped reads, second in pair	779,556 / 29.65%
Mapped reads, both in pair	1,526,527 / 58.05%
Mapped reads, singletons	29,219 / 1.11%
Read min/max/mean length	30 / 100 / 99.9
Duplicated reads (estimated)	159,986 / 6.08%
Duplication rate	7.53%
Clipped reads	177,389 / 6.75%

2.2. ACGT Content

Number/percentage of A's	44,826,148 / 29.85%
Number/percentage of C's	30,238,847 / 20.13%
Number/percentage of T's	45,021,759 / 29.98%
Number/percentage of G's	30,095,208 / 20.04%
Number/percentage of N's	12,569 / 0.01%
GC Percentage	40.17%

2.3. Coverage

Mean	6.2754
Standard Deviation	7.4448

2.4. Mapping Quality

Mean Mapping Quality	58.69

2.5. Insert size

Mean	740.14
Standard Deviation	25,527.97
P25/Median/P75	268 / 281 / 291

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	2,213,599
Insertions	51,906
Mapped reads with at least one insertion	3.16%
Deletions	58,844
Mapped reads with at least one deletion	3.56%
Homopolymer indels	62.93%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	5532755	5.6617	3.7679
gi|1074120682|emb|LT615257.1|	860454	5342162	6.2085	5.0458
gi|1074120865|emb|LT615258.1|	989719	7549221	7.6276	11.7604
gi|1074121086|emb|LT615259.1|	935450	6878995	7.3537	12.6656
gi|1074121301|emb|LT615260.1|	1432239	9596948	6.7007	7.6027
gi|1074121615|emb|LT615261.1|	1080962	6730009	6.2259	5.8919
gi|1074121871|emb|LT615262.1|	1545099	9087549	5.8815	3.5281
gi|1074122235|emb|LT615263.1|	1585108	9756243	6.1549	4.9969
gi|1074122590|emb|LT615264.1|	2122358	12655288	5.9628	4.3554
gi|1074123050|emb|LT615265.1|	1754192	11092836	6.3236	5.9607
gi|1074123421|emb|LT615	2150147	14266703	6.6352	14.836

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	17943365	5.9199	3.4987
gi|1074124588|emb|LT615268.1|	2359348	14674541	6.2197	8.7016
gi|1074125065|emb|LT615269.1|	3135668	19244949	6.1374	3.0821

3. Results : Coverage across reference

Coverage across reference
0M275.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM275.sorted.bam.bam
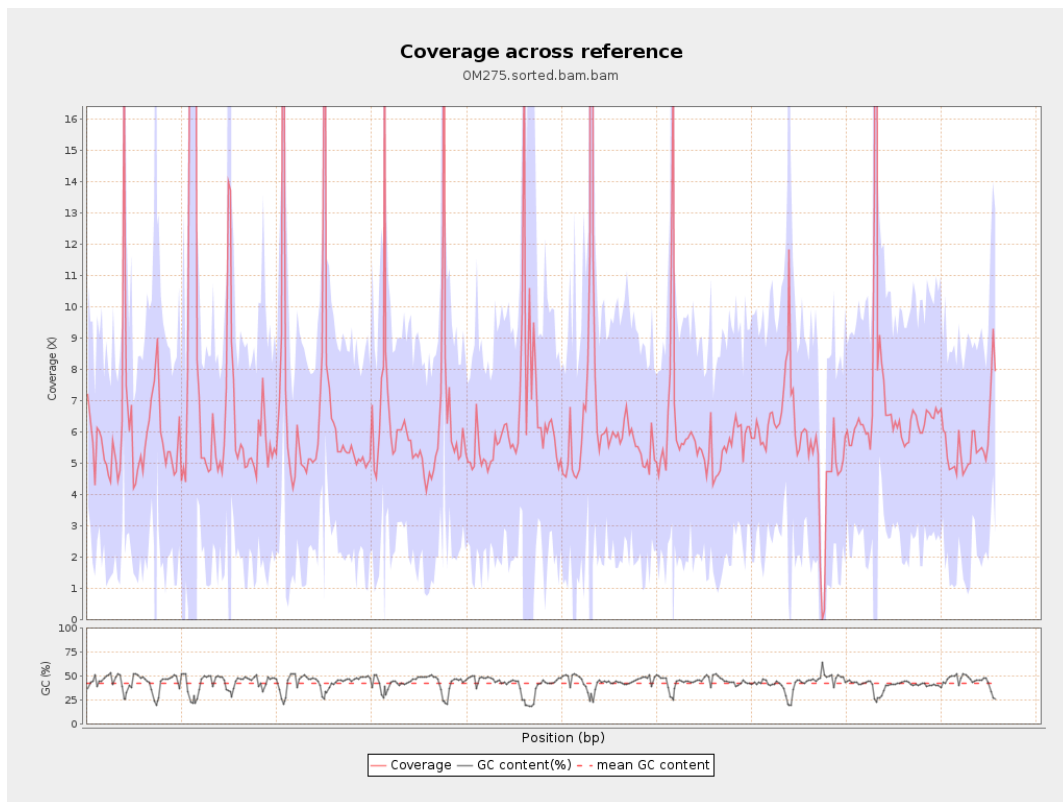
5. Results : Coverage Histogram (0-50X)
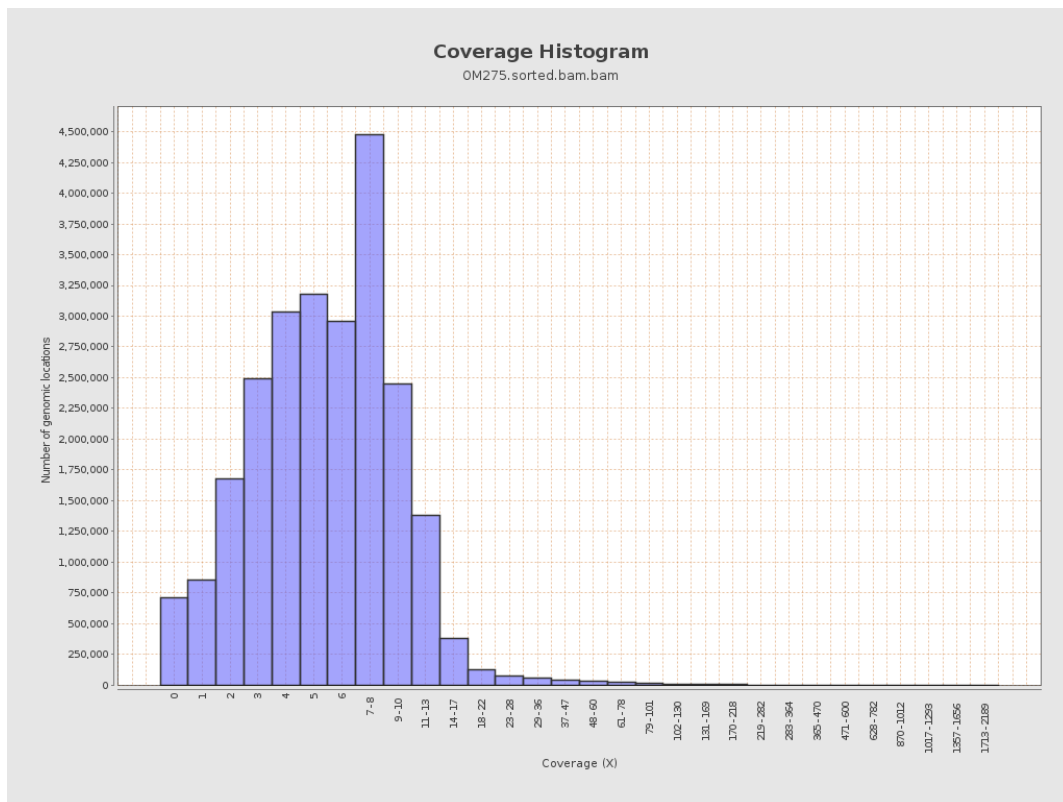
Coverage Histogram (0-50X)
0M275.sorted.bam.bam
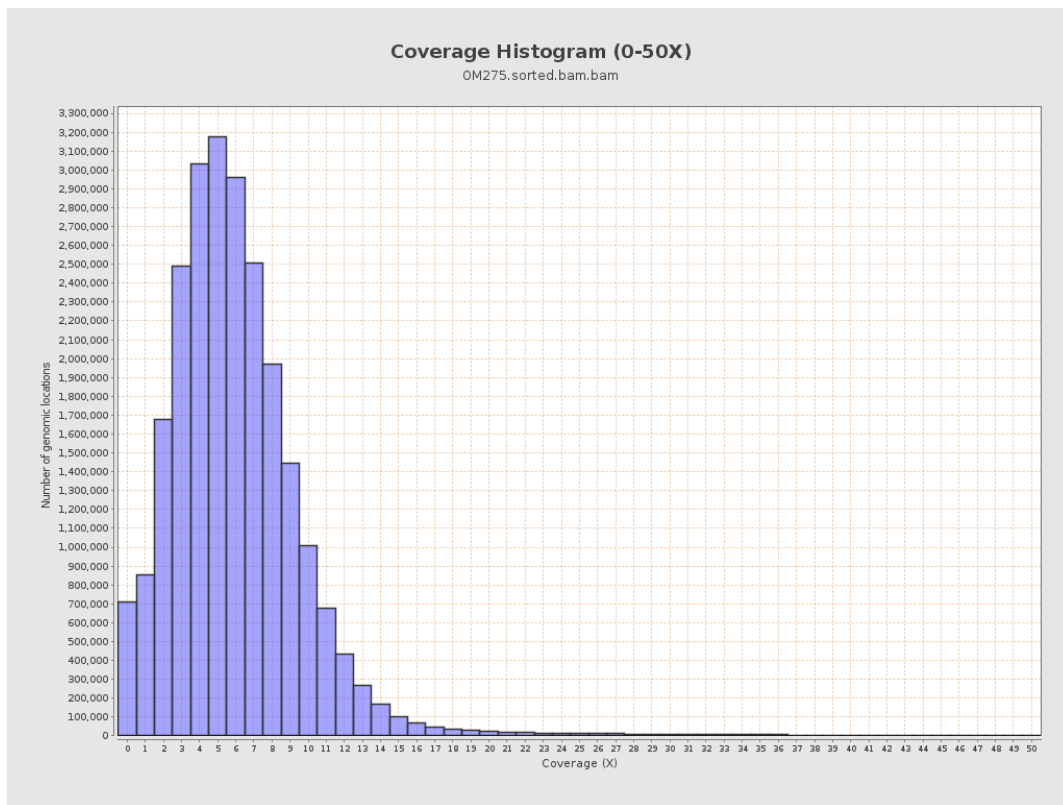
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
0M275.sorted.bam.bam
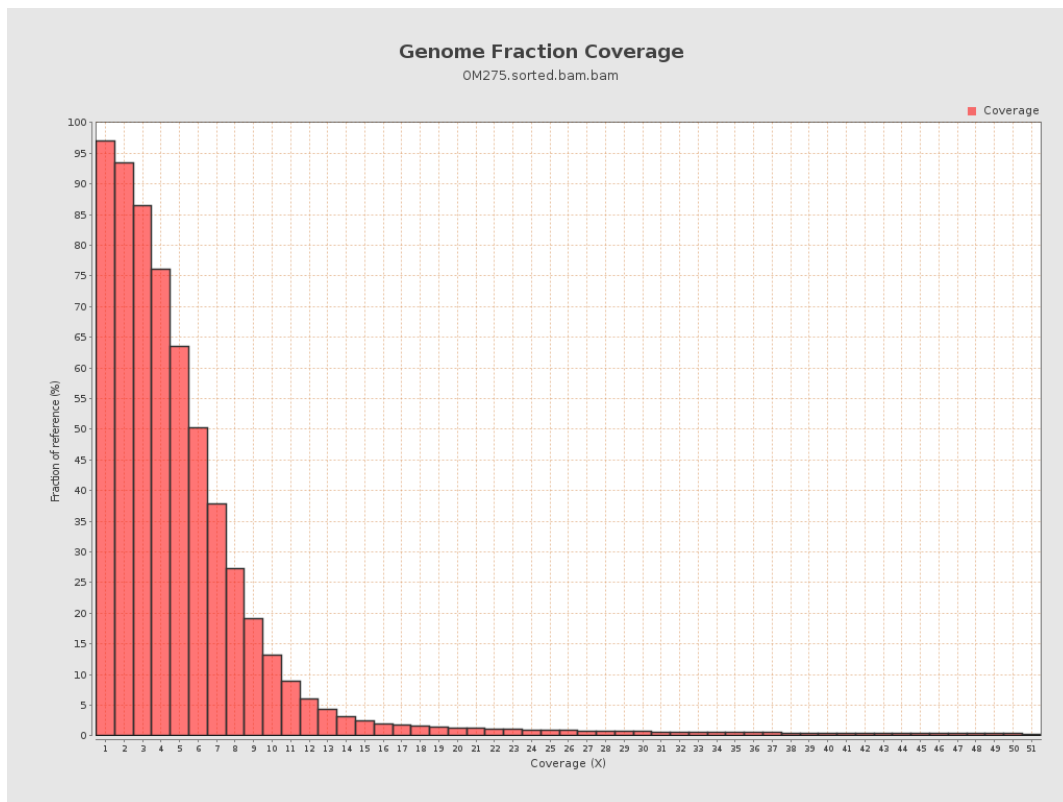
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
OM275.sorted.bam.bam
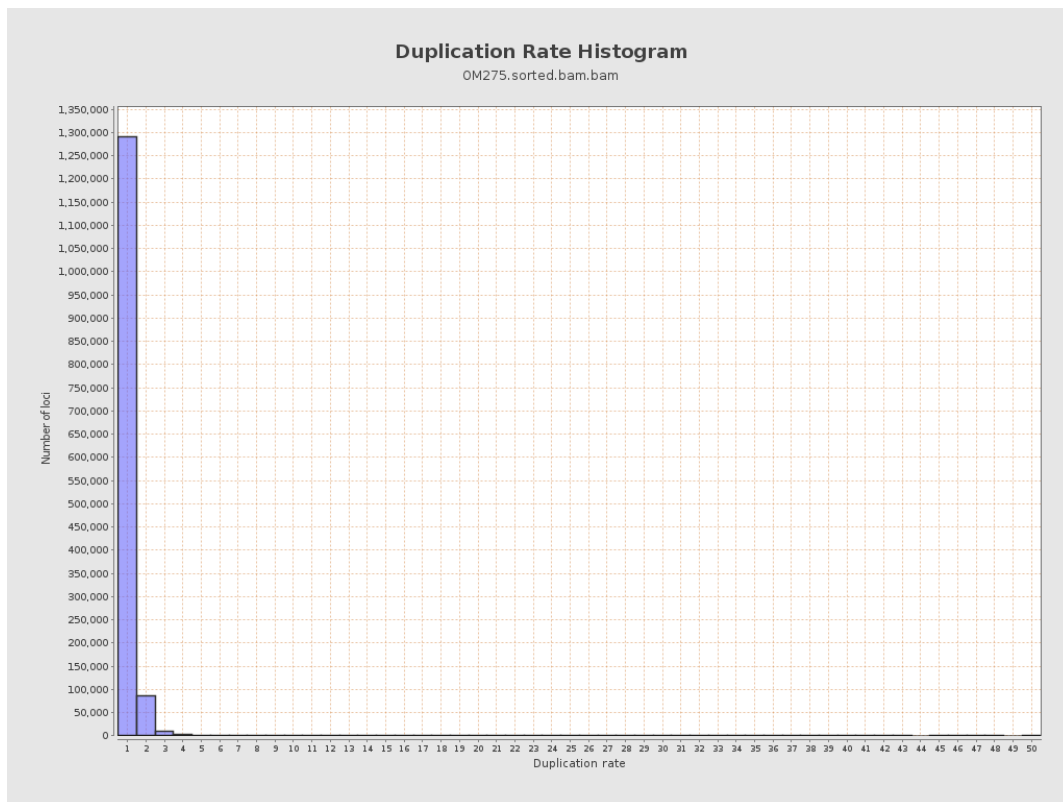
8. Results : Mapped Reads Nucleotide Content
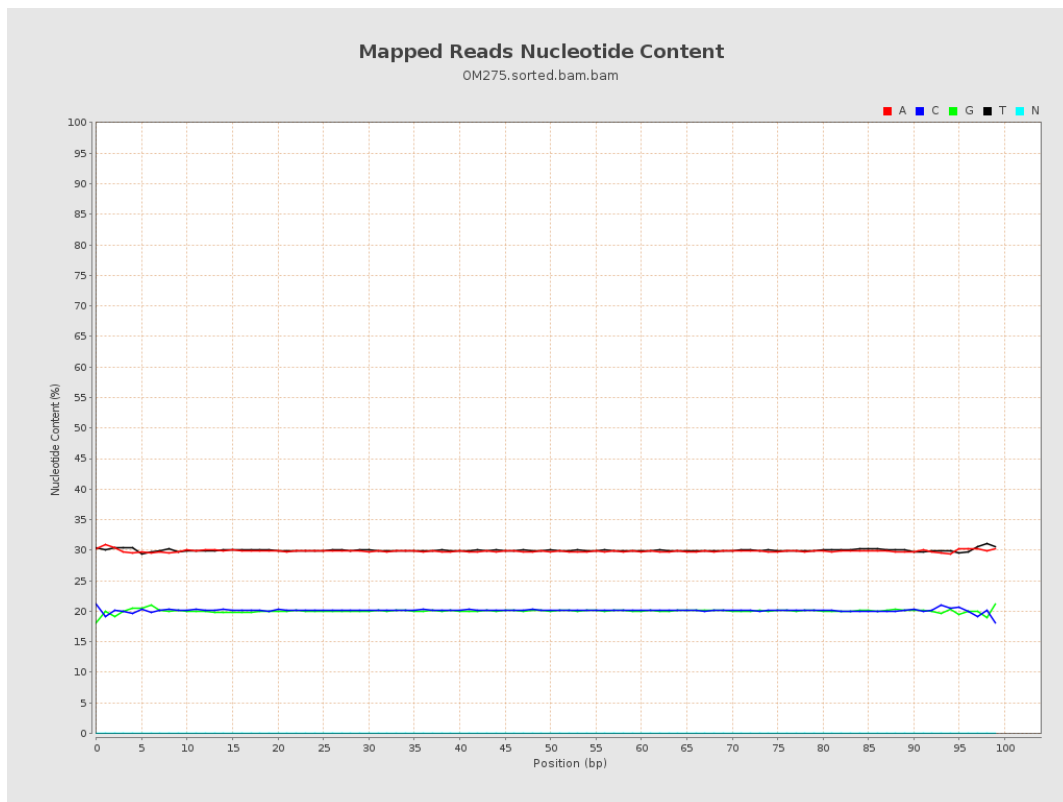
9. Results : Mapped Reads GC-content Distribution
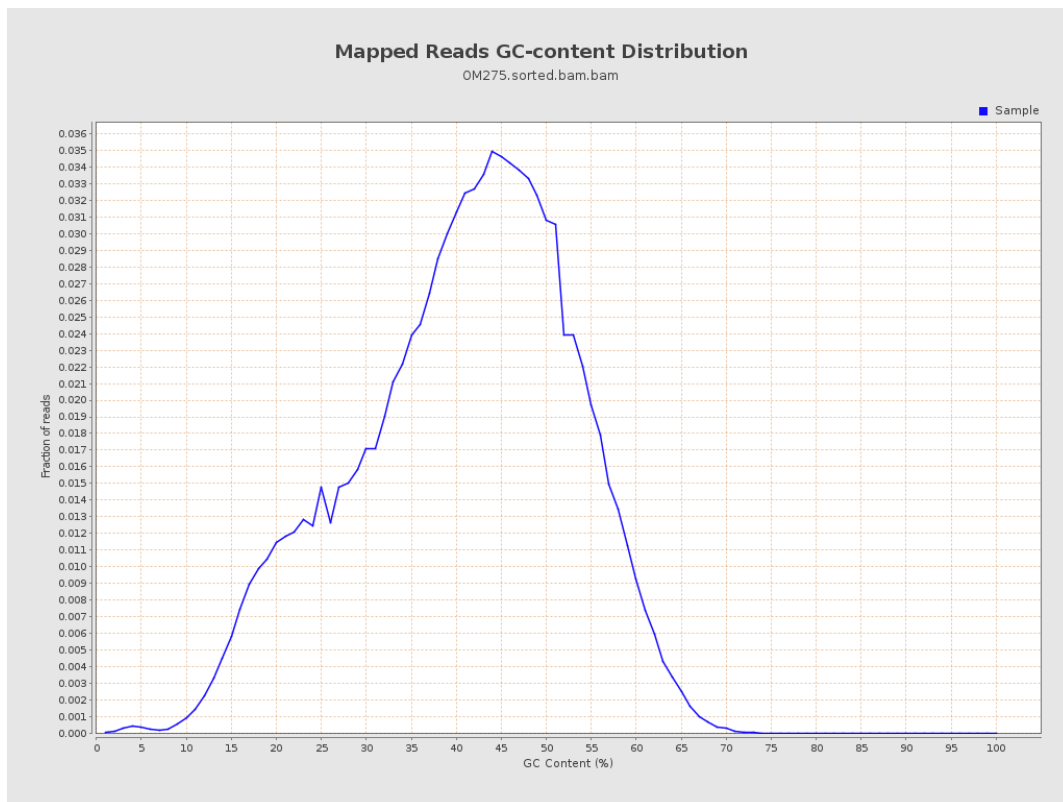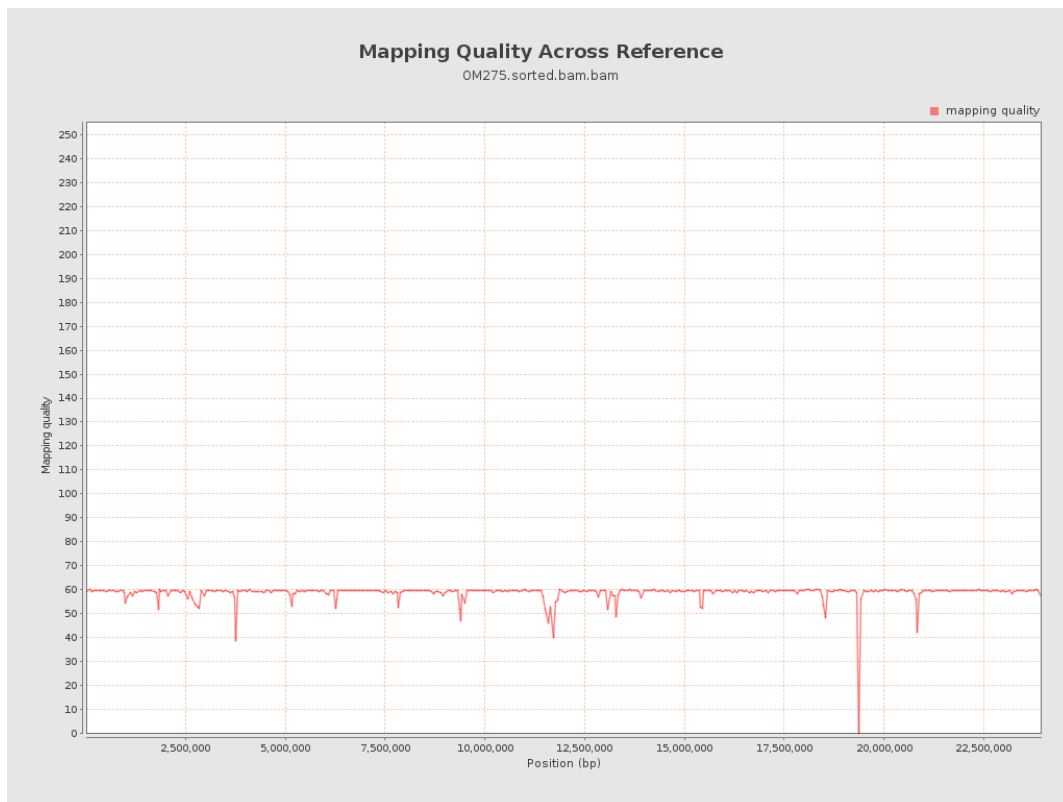
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
OM275.sorted.bam.bam
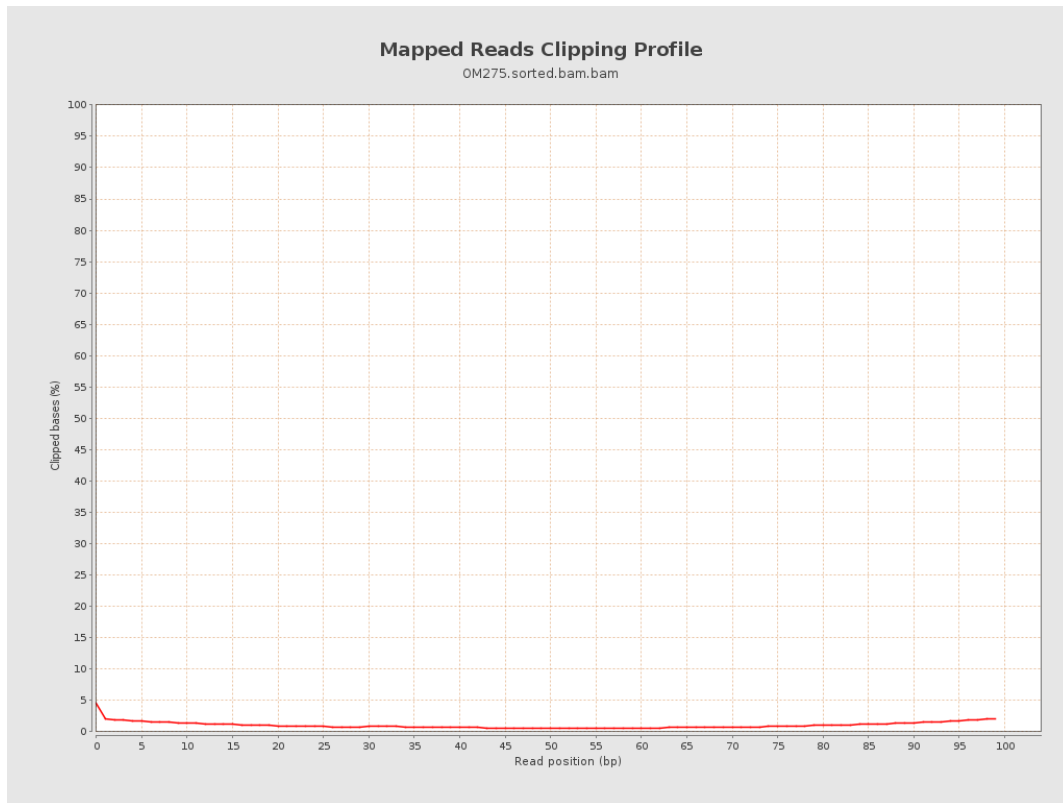
11. Results : Homopolymer Indels
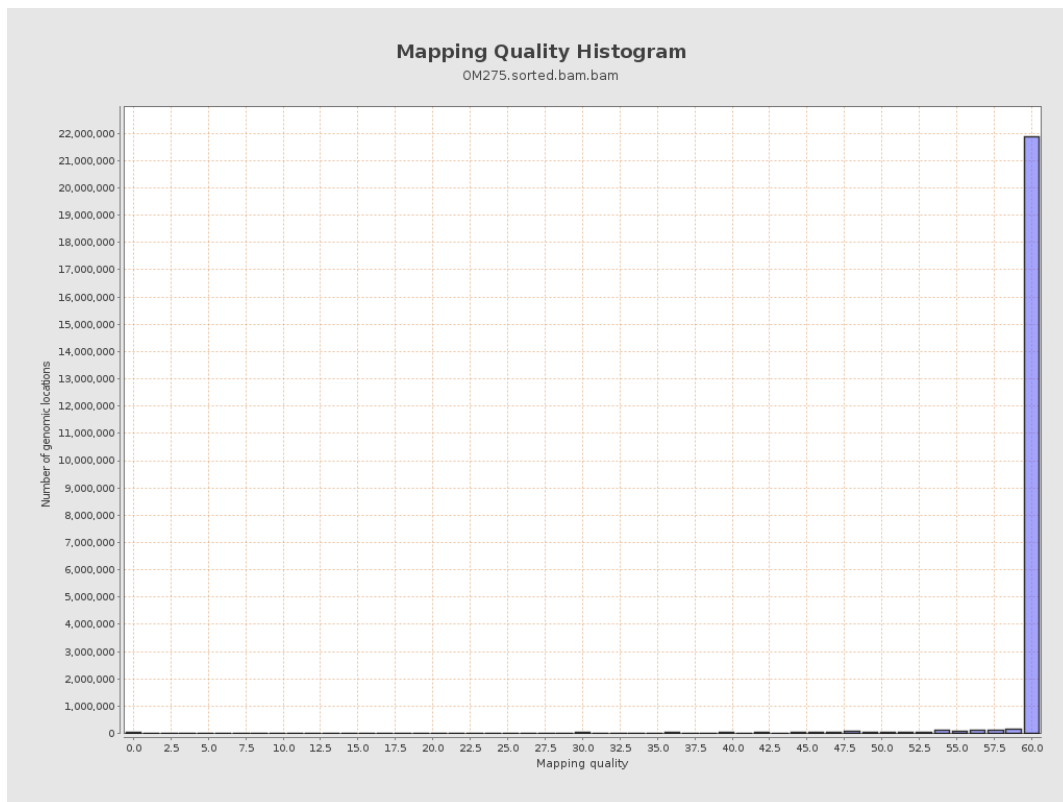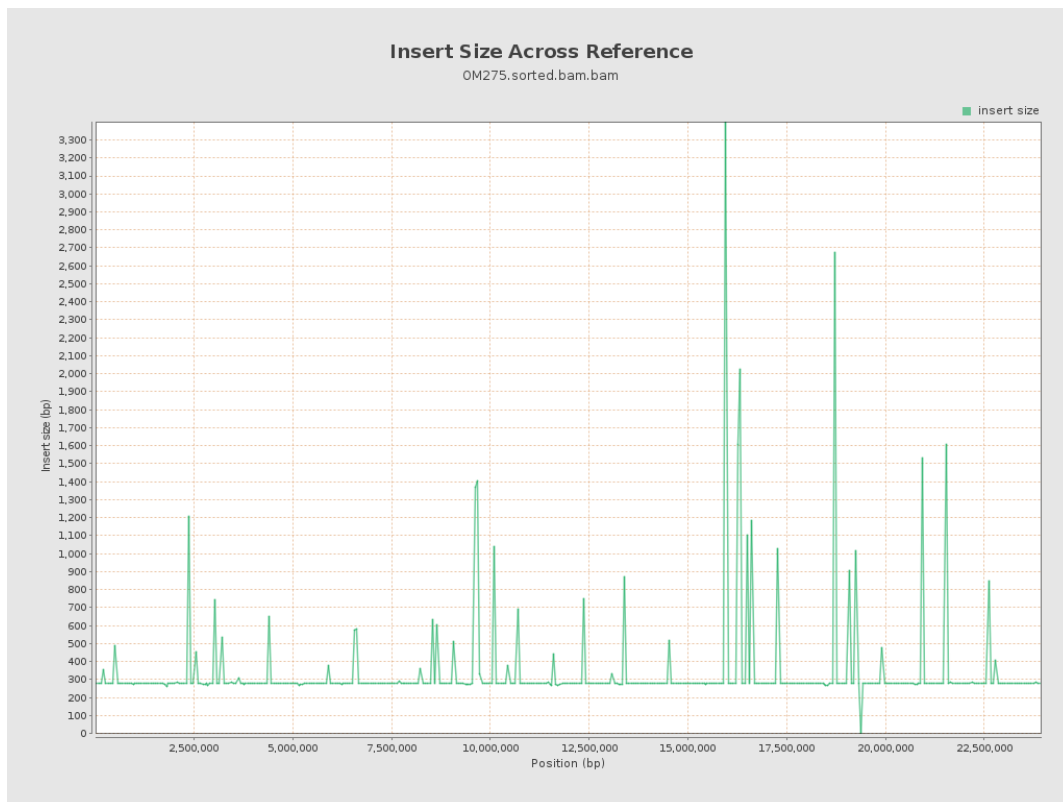

Homopolymer Indels
0M275.sorted.bam.bam
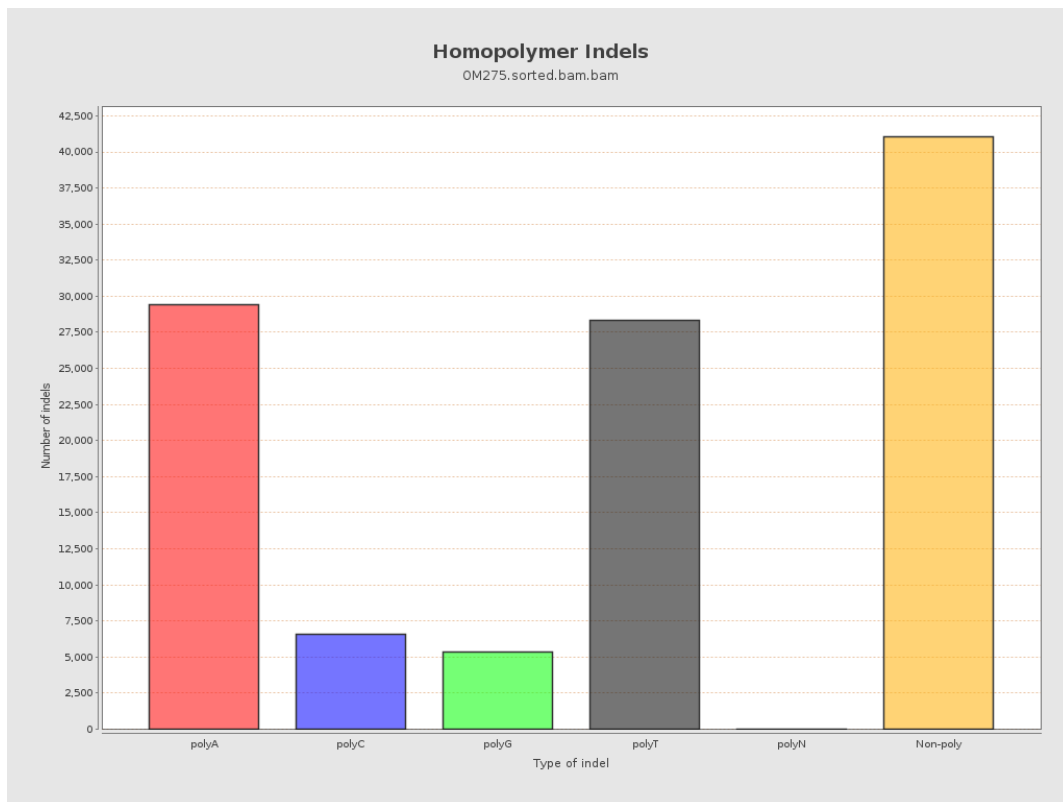
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram