Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:45:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM214.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/OM214-BiooBarcode3_ACAGTG_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM214-BiooBarcode3_ACAGTG_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:45:12 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM214.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	8,642,274
Mapped reads	1,976,802 / 22.87%
Unmapped reads	6,665,472 / 77.13%
Mapped paired reads	1,976,802 / 22.87%
Mapped reads, first in pair	985,539 / 11.4%
Mapped reads, second in pair	991,263 / 11.47%
Mapped reads, both in pair	1,906,941 / 22.07%
Mapped reads, singletons	69,861 / 0.81%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	219,687 / 2.54%
Duplication rate	7.85%
Clipped reads	247,760 / 2.87%

2.2. ACGT Content

Number/percentage of A's	56,518,027 / 29.92%
Number/percentage of C's	37,777,169 / 20%
Number/percentage of T's	56,905,884 / 30.13%
Number/percentage of G's	37,683,794 / 19.95%
Number/percentage of N's	16,483 / 0.01%
GC Percentage	39.95%

2.3. Coverage

Mean	7.8921
Standard Deviation	9.2259

2.4. Mapping Quality

Mean Mapping Quality	58.24

2.5. Insert size

Mean	819.73
Standard Deviation	27,128.41
P25/Median/P75	294 / 307 / 320

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	2,651,007
Insertions	61,780
Mapped reads with at least one insertion	2.96%
Deletions	70,037
Mapped reads with at least one deletion	3.34%
Homopolymer indels	63.22%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	6935903	7.0976	4.4625
gi|1074120682|emb|LT615257.1|	860454	6748606	7.8431	6.3781
gi|1074120865|emb|LT615258.1|	989719	8346203	8.4329	10.2585
gi|1074121086|emb|LT615259.1|	935450	7688541	8.2191	9.6418
gi|1074121301|emb|LT615260.1|	1432239	12182382	8.5058	9.4388
gi|1074121615|emb|LT615261.1|	1080962	8281865	7.6616	6.9871
gi|1074121871|emb|LT615262.1|	1545099	11498966	7.4422	4.2048
gi|1074122235|emb|LT615263.1|	1585108	12545697	7.9147	11.2743
gi|1074122590|emb|LT615264.1|	2122358	16087368	7.58	4.6866
gi|1074123050|emb|LT615265.1|	1754192	14363603	8.1882	19.7308
gi|1074123421|emb|LT615	2150147	17725164	8.2437	11.8348

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	23158904	7.6406	7.1091
gi|1074124588|emb|LT615268.1|	2359348	18046466	7.6489	7.7466
gi|1074125065|emb|LT615269.1|	3135668	25478215	8.1253	4.229

3. Results : Coverage across reference

Coverage across reference
OM214.sorted.bam.bam
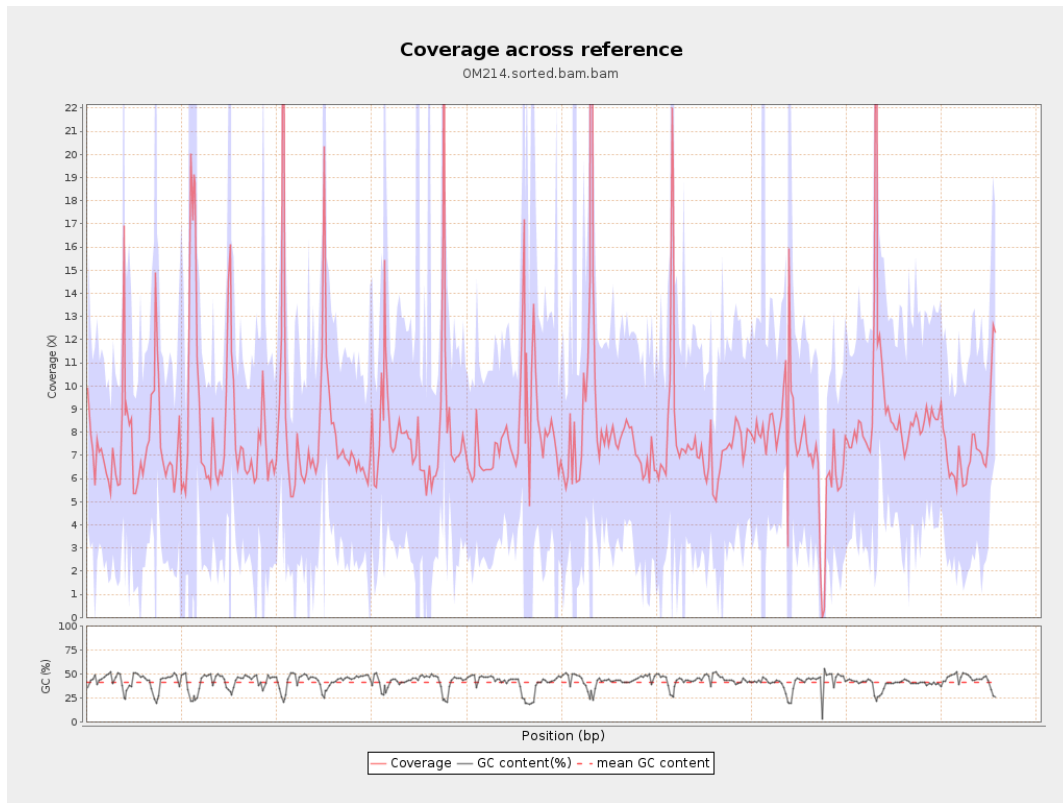
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
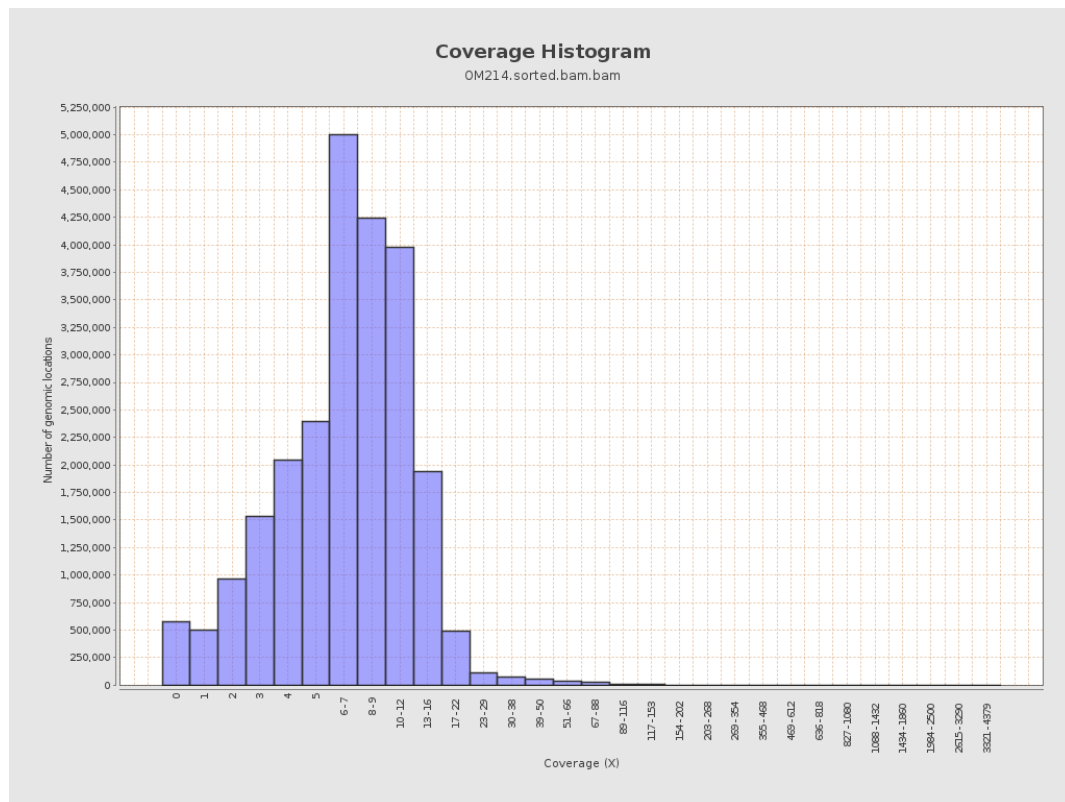
Coverage Histogram (0-50X)
OM214.sorted.bam.bam
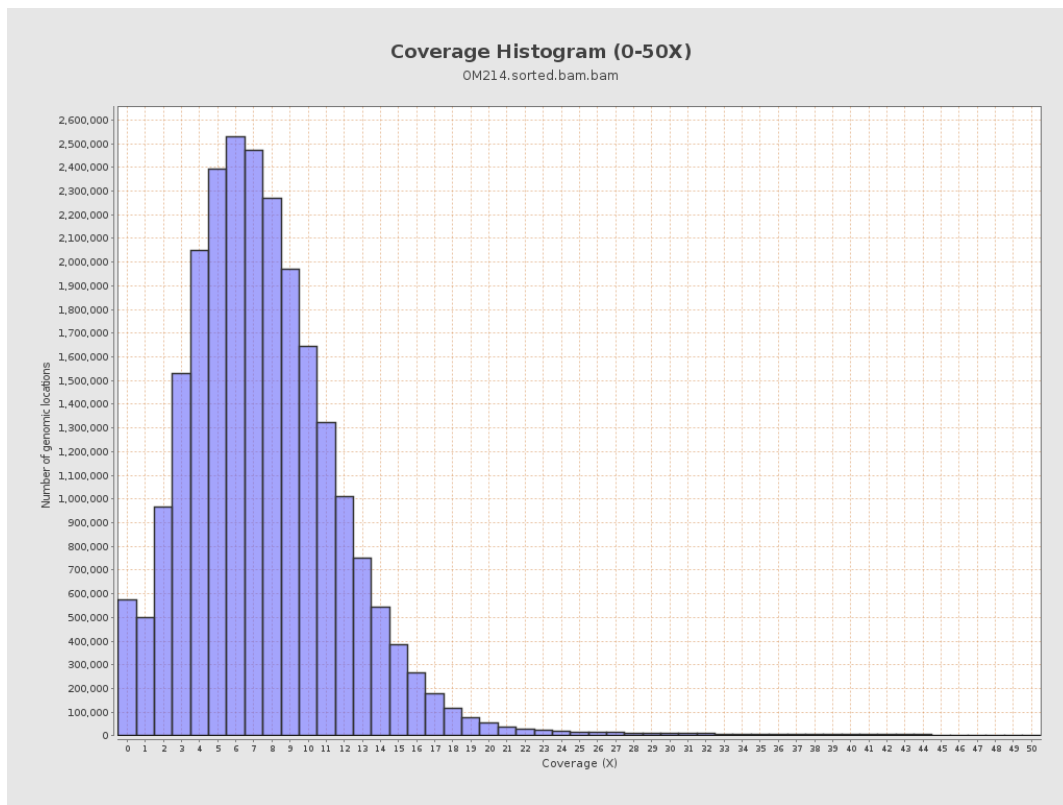
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
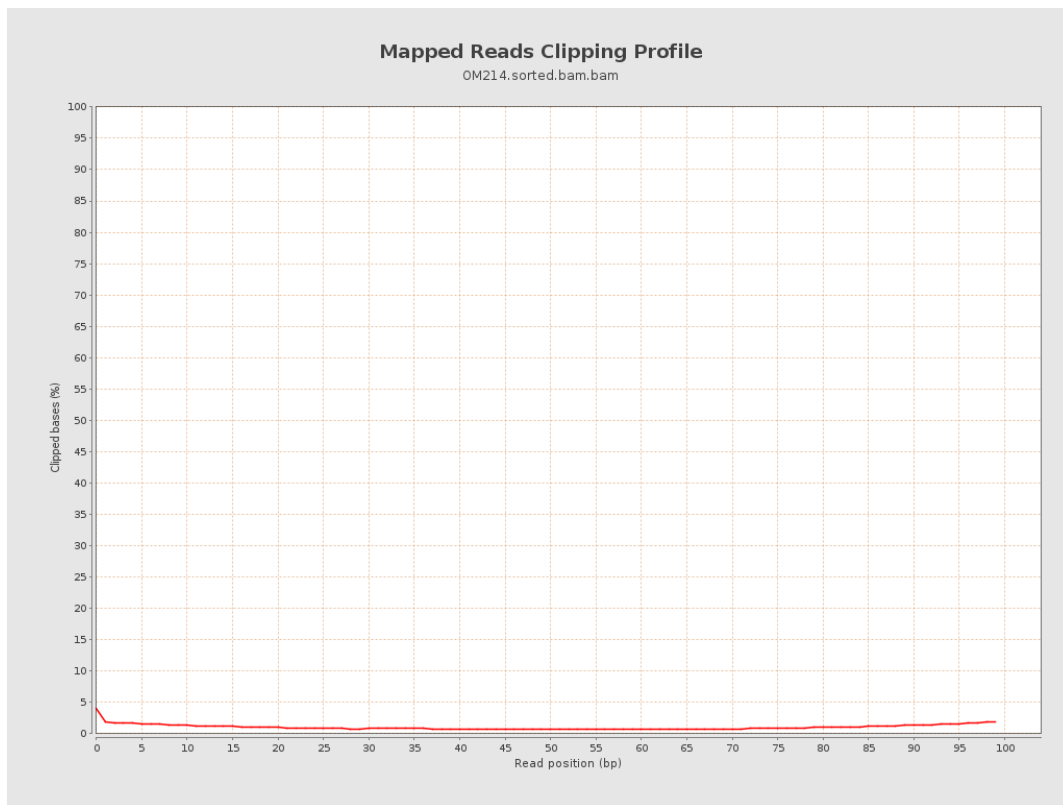OM214.sorted.bam.bam
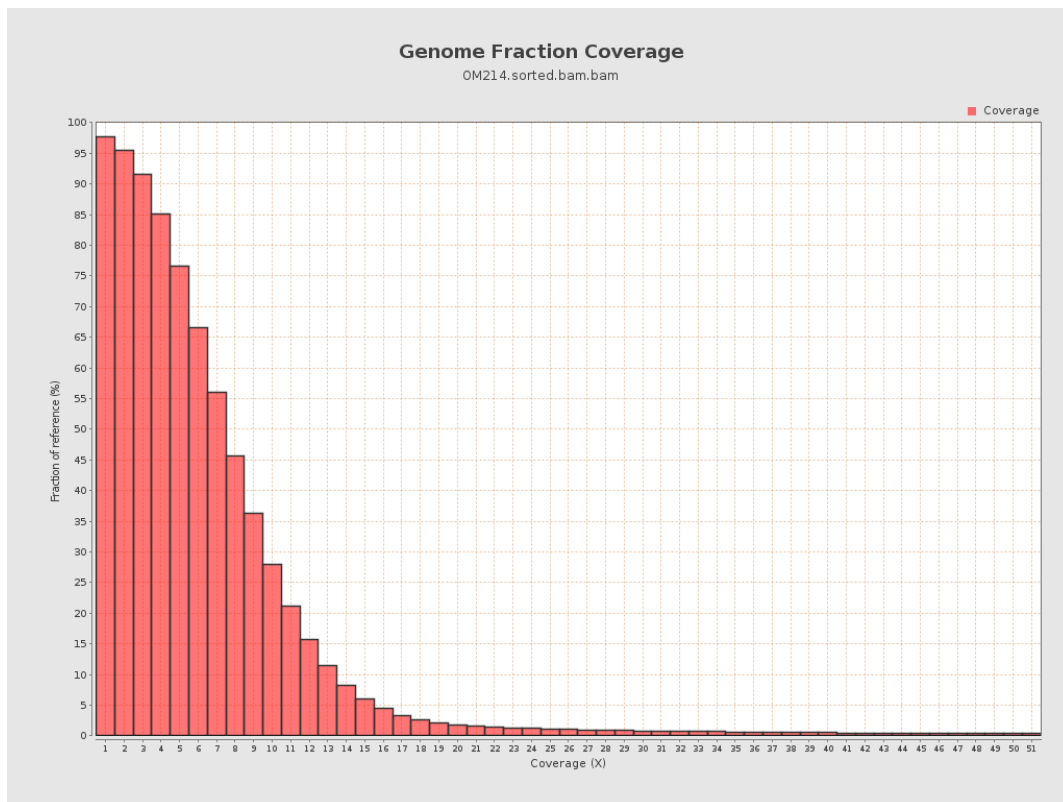
7. Results : Duplication Rate Histogram
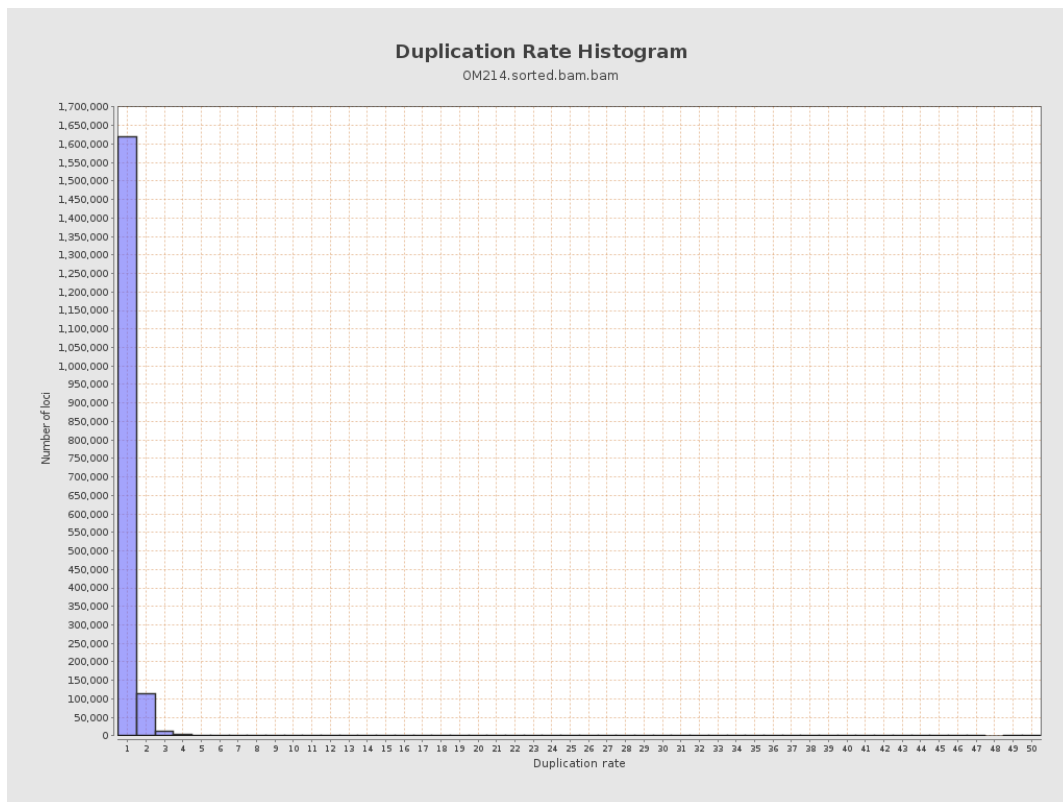
8. Results : Mapped Reads Nucleotide Content
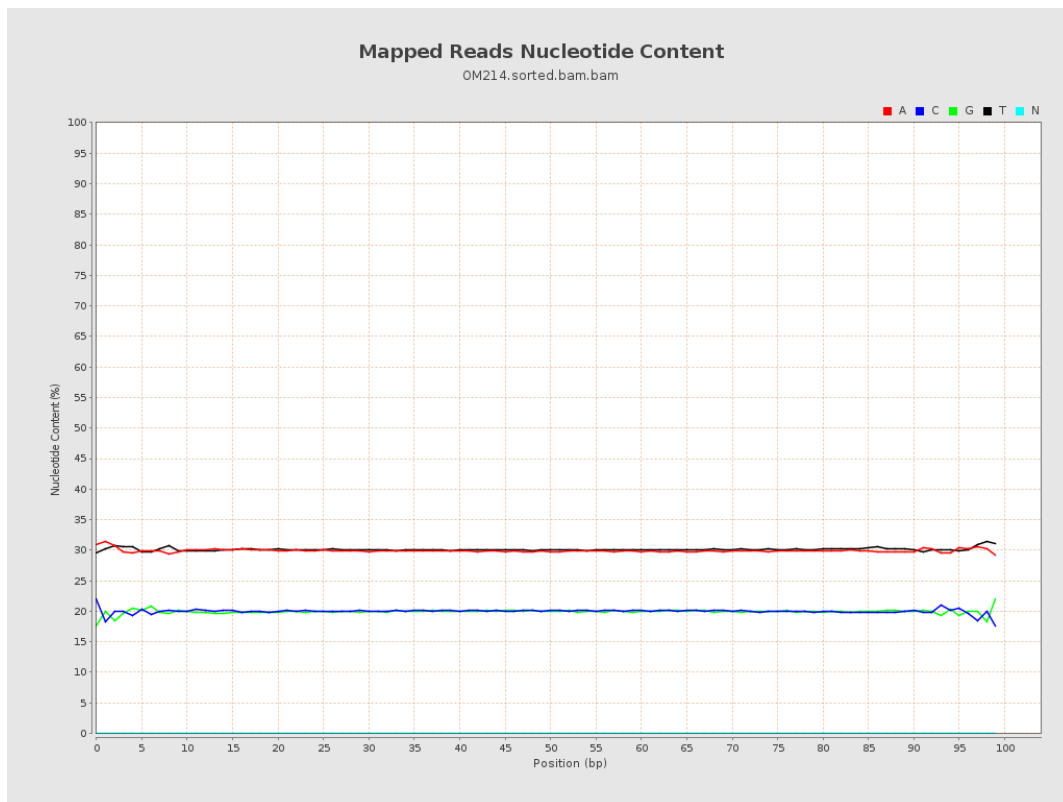
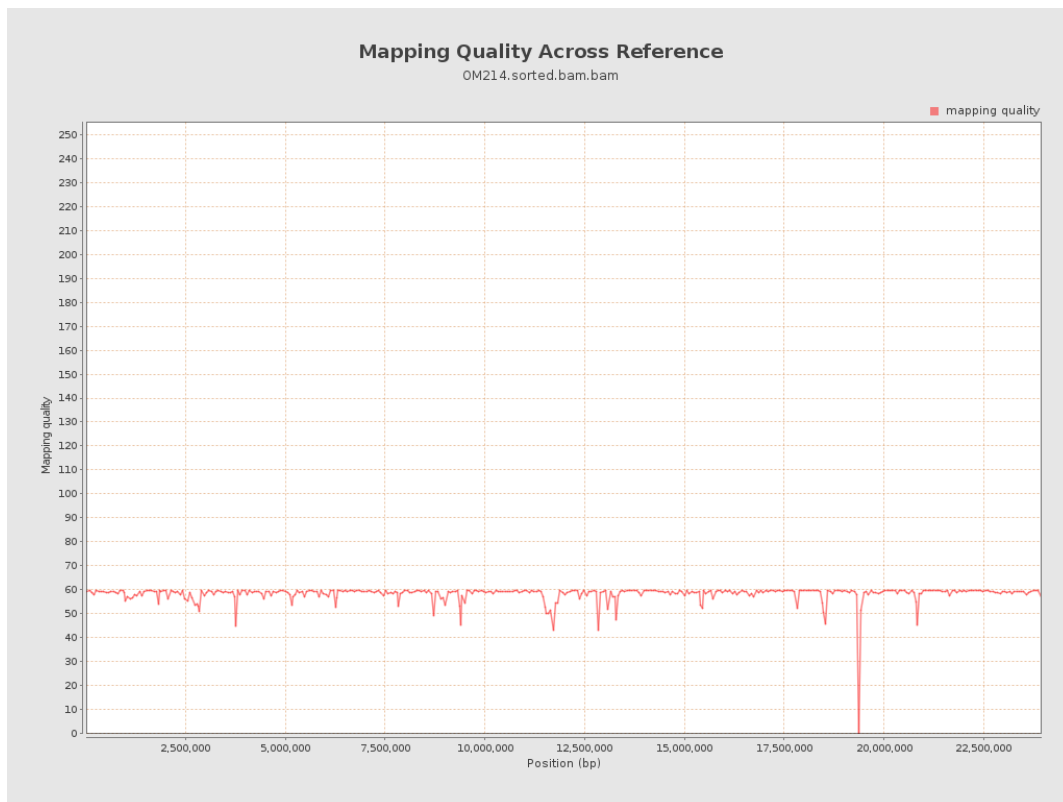# 9. Results : Mapped Reads GC-content Distribution
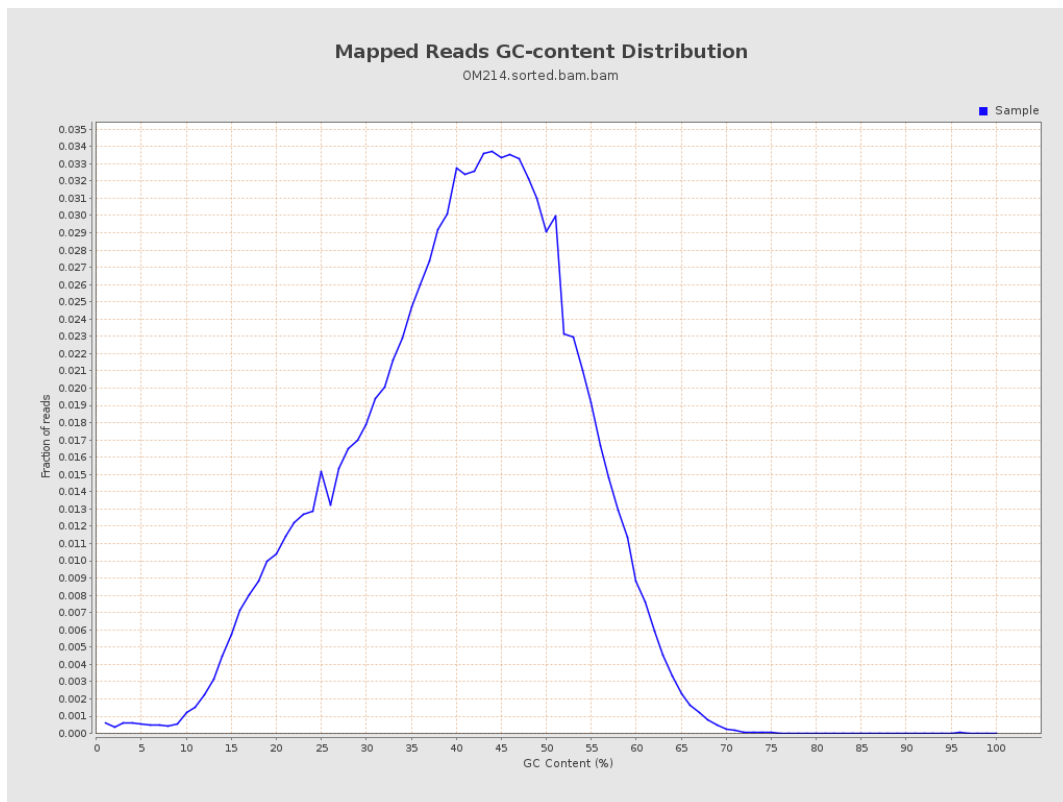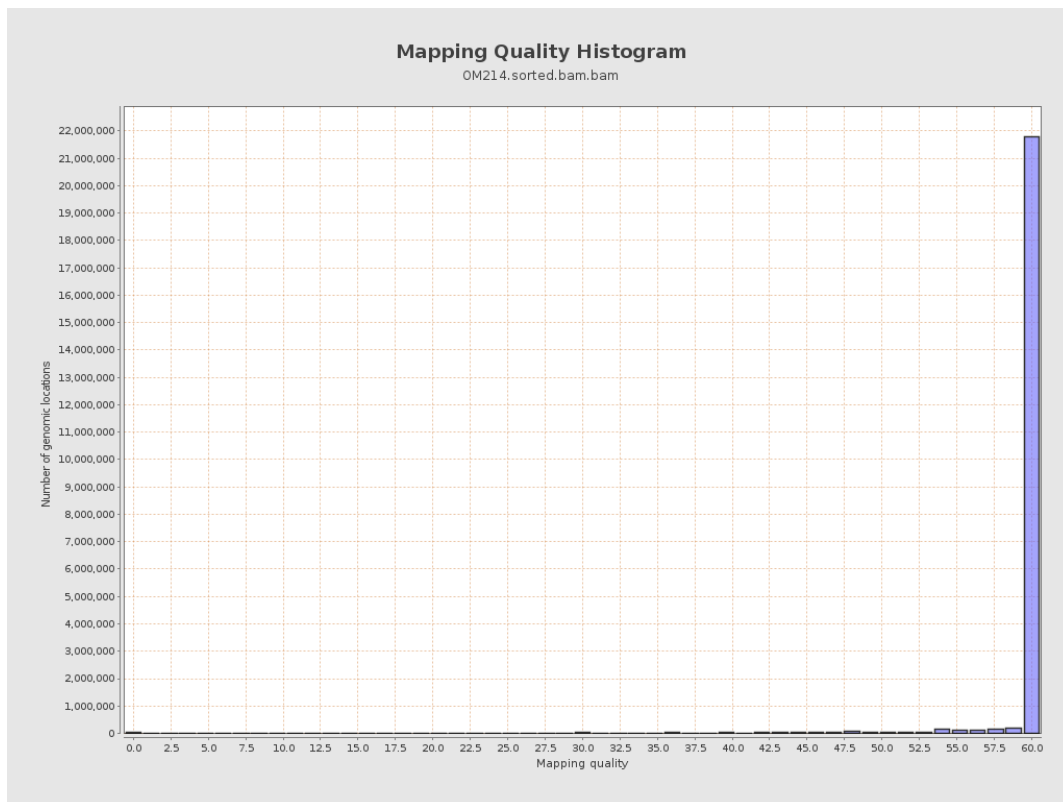
10. Results : Mapped Reads Clipping Profile

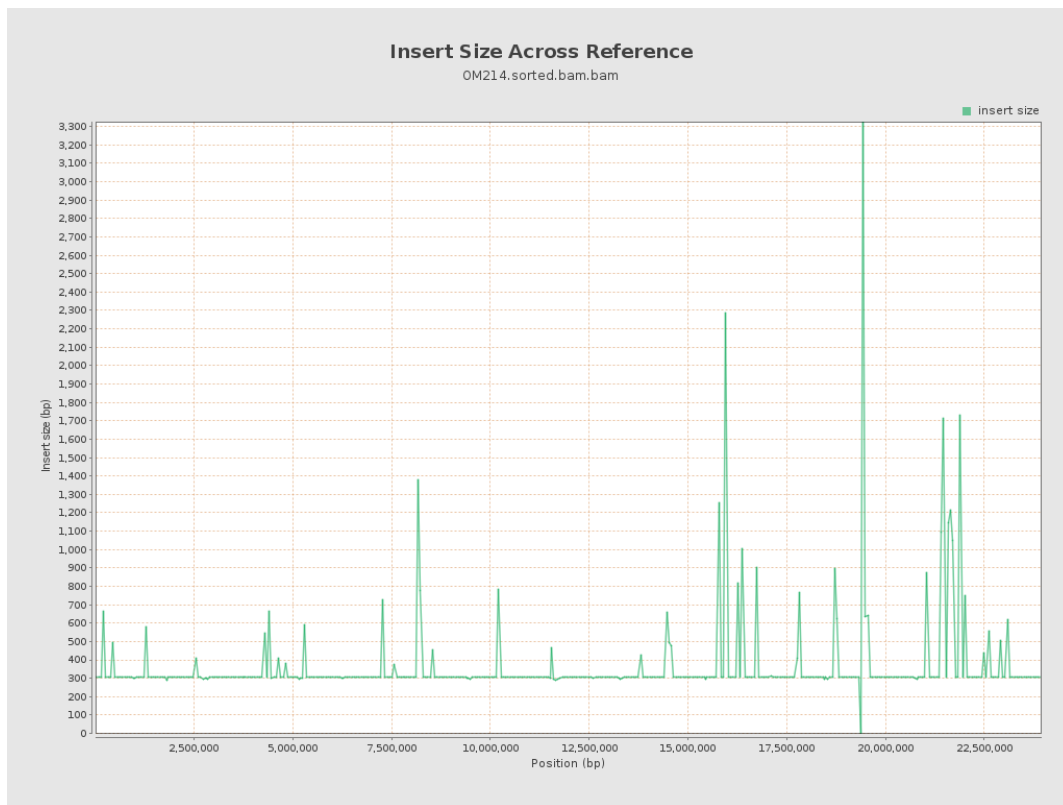# 11. Results : Homopolymer Indels
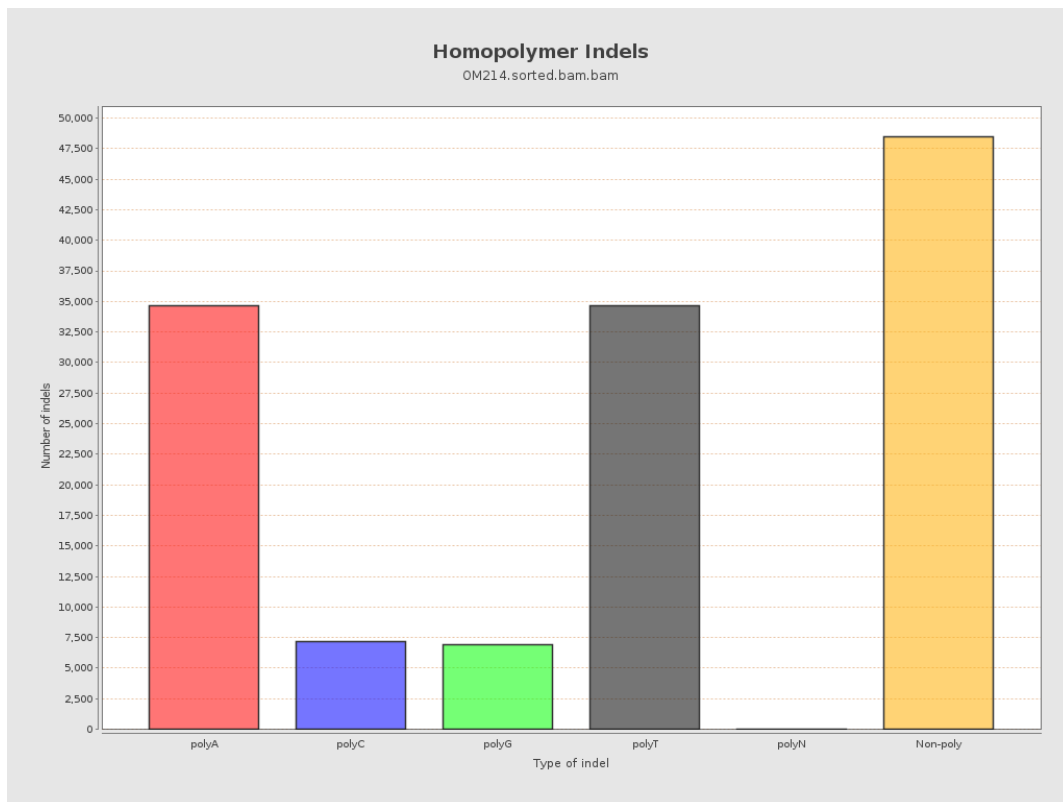
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
OM214.sorted.bam.bam