Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:59:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM283.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_SAME A2376790.fasta /home/vdp5/data/cambodia_samples/ sequences_gz/OM283-BiooBarcode29_CAACTA_R2.fastq.g z /home/vdp5/data/cambodia_samples/ sequences_gz/OM283-BiooBarcode29_CAACTA_R1.fastq.g z
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:59:01 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/ sequences_bam/OM283.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	2,399,618
Mapped reads	1,339,299 / 55.81%
Unmapped reads	1,060,319 / 44.19%
Mapped paired reads	1,339,299 / 55.81%
Mapped reads, first in pair	666,830 / 27.79%
Mapped reads, second in pair	672,469 / 28.02%
Mapped reads, both in pair	1,308,754 / 54.54%
Mapped reads, singletons	30,545 / 1.27%
Read min/max/mean length	30 / 100 / 99.91
Duplicated reads (estimated)	108,148 / 4.51%
Duplication rate	6.01%
Clipped reads	149,870 / 6.25%

2.2. ACGT Content

Number/percentage of A's	38,699,677 / 29.91%
Number/percentage of C's	25,993,092 / 20.09%
Number/percentage of T's	38,764,379 / 29.96%
Number/percentage of G's	25,948,734 / 20.05%
Number/percentage of N's	10,589 / 0.01%
GC Percentage	40.14%

2.3. Coverage

Mean	5.407
Standard Deviation	5.6057

2.4. Mapping Quality

Mean Mapping Quality	58.6

2.5. Insert size

Mean	855.66
Standard Deviation	26,548.54
P25/Median/P75	307 / 319 / 328

2.6. Mismatches and indels

General error rate	1.57%
Mismatches	1,934,507
Insertions	42,386
Mapped reads with at least one insertion	3.01%
Deletions	48,277
Mapped reads with at least one deletion	3.4%
Homopolymer indels	63.71%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|107412047 8|emb|LT615 256.1|	977217	4727327	4.8375	3.1775
gi|107412068 2|emb|LT615 257.1|	860454	4609235	5.3567	4.4012
gi|107412086 5|emb|LT615 258.1|	989719	6305001	6.3705	9.5726
gi|107412108 6|emb|LT615 259.1|	935450	5498751	5.8782	8.6015
gi|107412130 1|emb|LT615 260.1|	1432239	8183017	5.7134	6.0625
gi|107412161 5|emb|LT615 261.1|	1080962	6072405	5.6176	6.3169
gi|107412187 1|emb|LT615 262.1|	1545099	8463203	5.4775	3.6928
gi|107412223 5|emb|LT615 263.1|	1585108	8361859	5.2753	4.6252
gi|107412259 0|emb|LT615 264.1|	2122358	10950486	5.1596	3.3427
gi|107412305 0|emb|LT615 265.1|	1754192	9458399	5.3919	5.4465
gi|107412342 1|emb|LT615	2150147	12273791	5.7083	9.9729

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	15821815	5.2199	3.3219
gi|1074124588|emb|LT615268.1|	2359348	12143784	5.1471	5.2486
gi|1074125065|emb|LT615269.1|	3135668	16676404	5.3183	2.8462

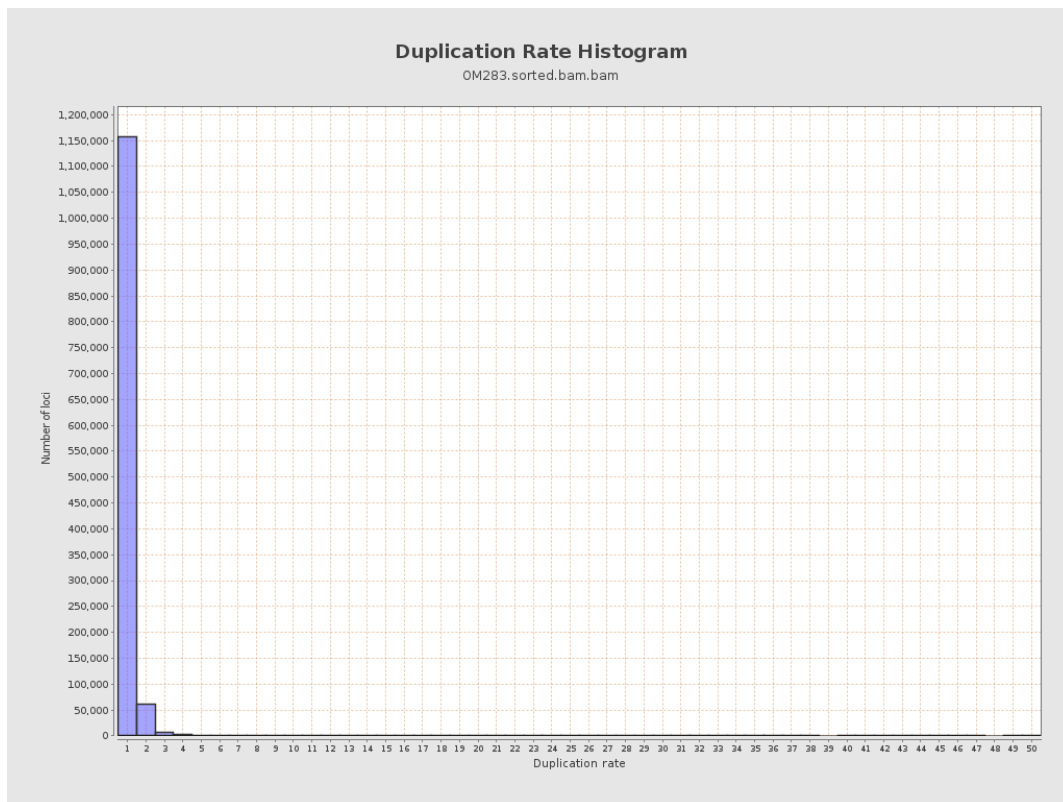# 3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
OM283.sorted.bam.bam
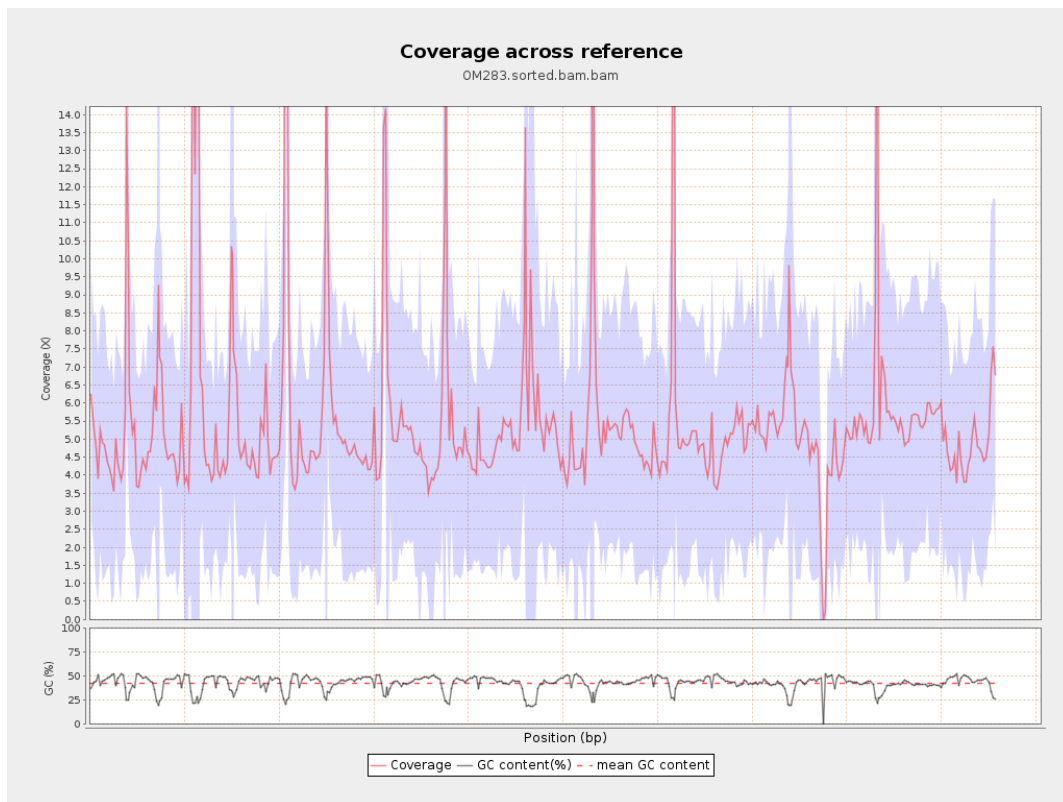
5. Results : Coverage Histogram (0-50X)
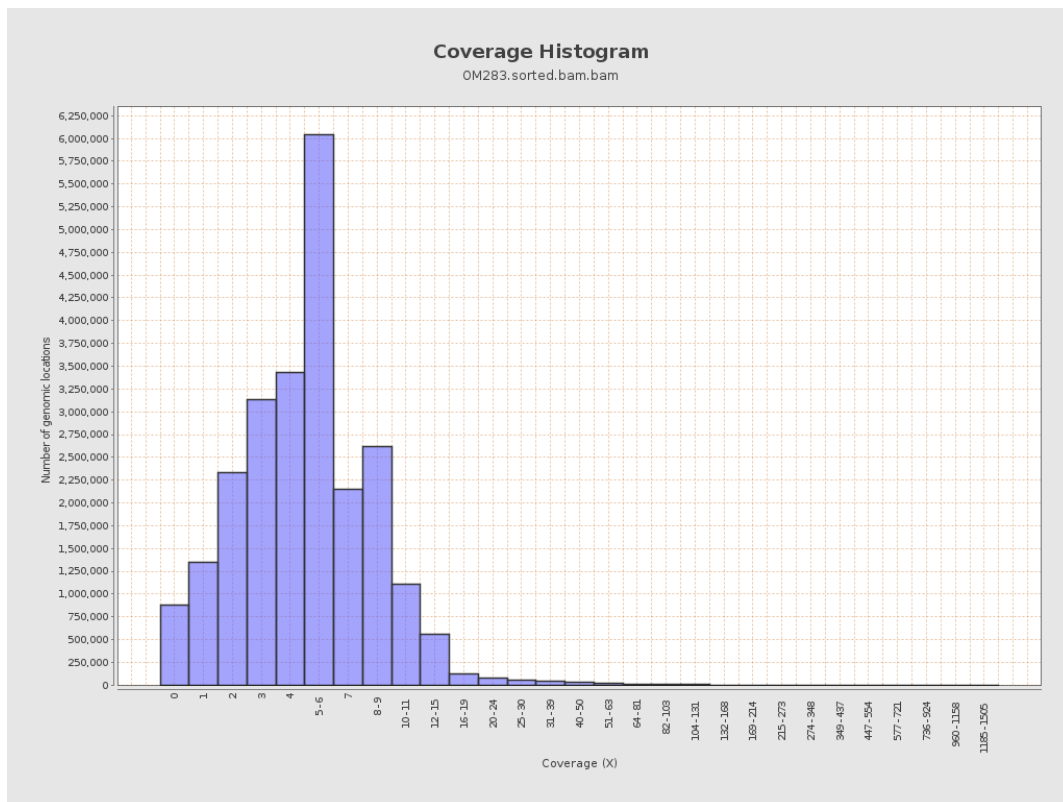
Coverage Histogram (0-50X)
0M283.sorted.bam.bam
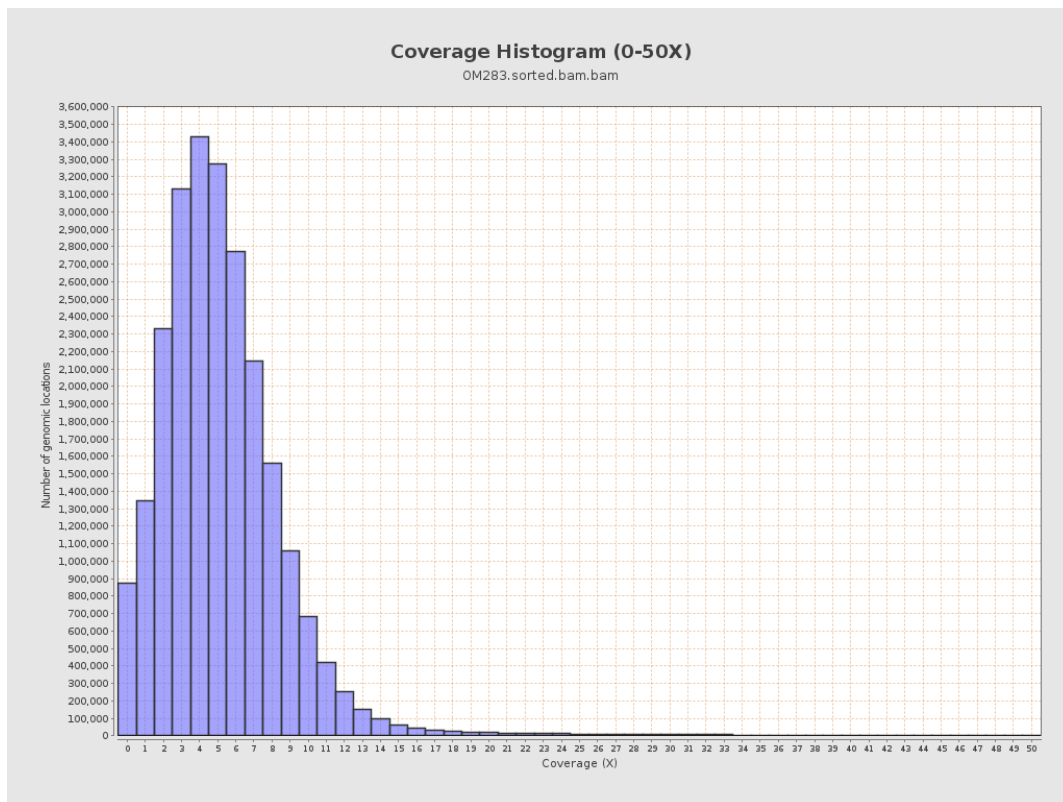
6. Results : Genome Fraction Coverage
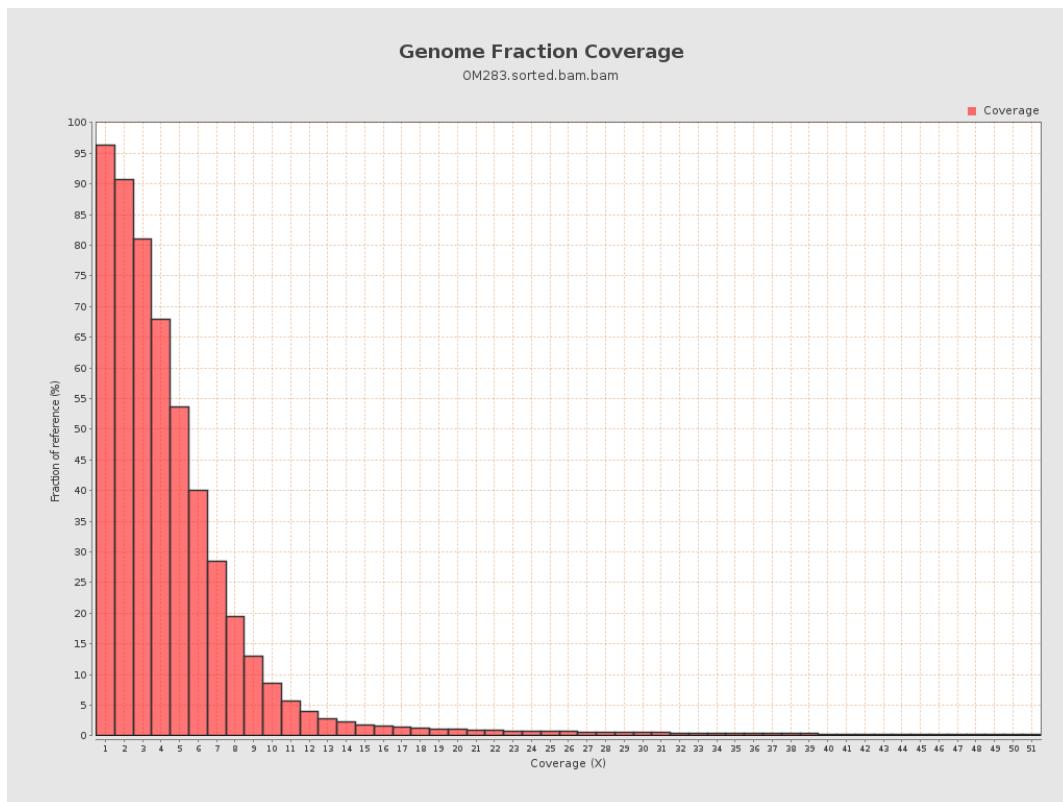
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
0M283.sorted.bam.bam

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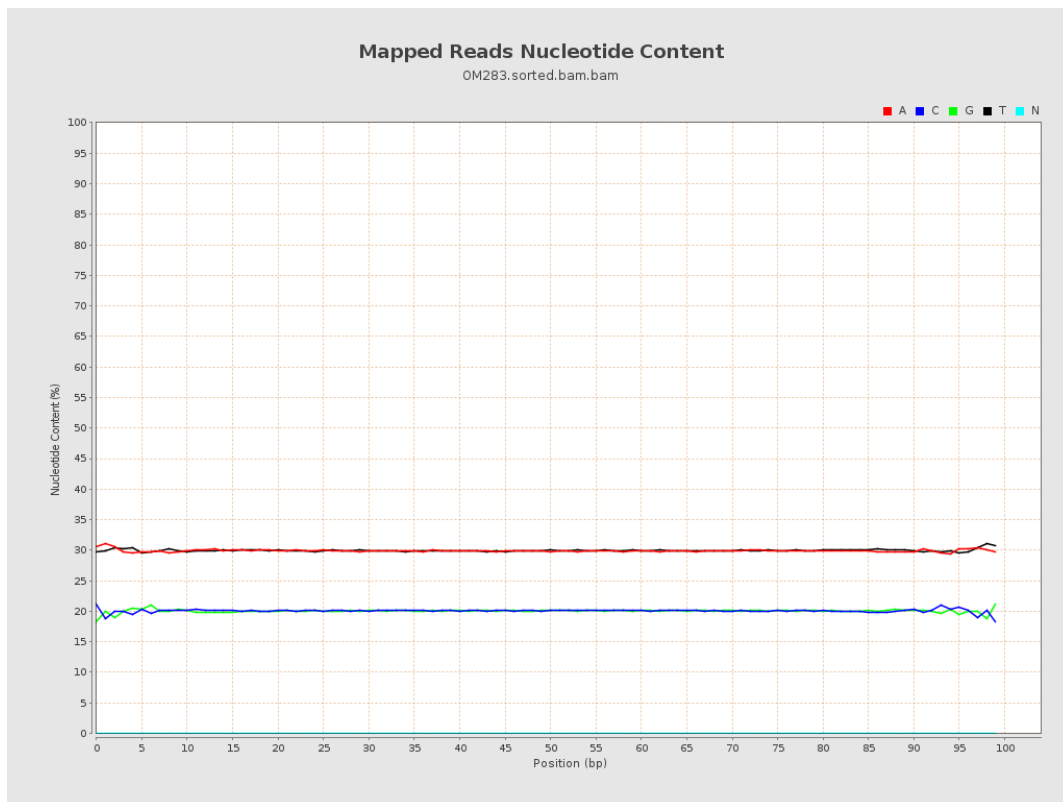
9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
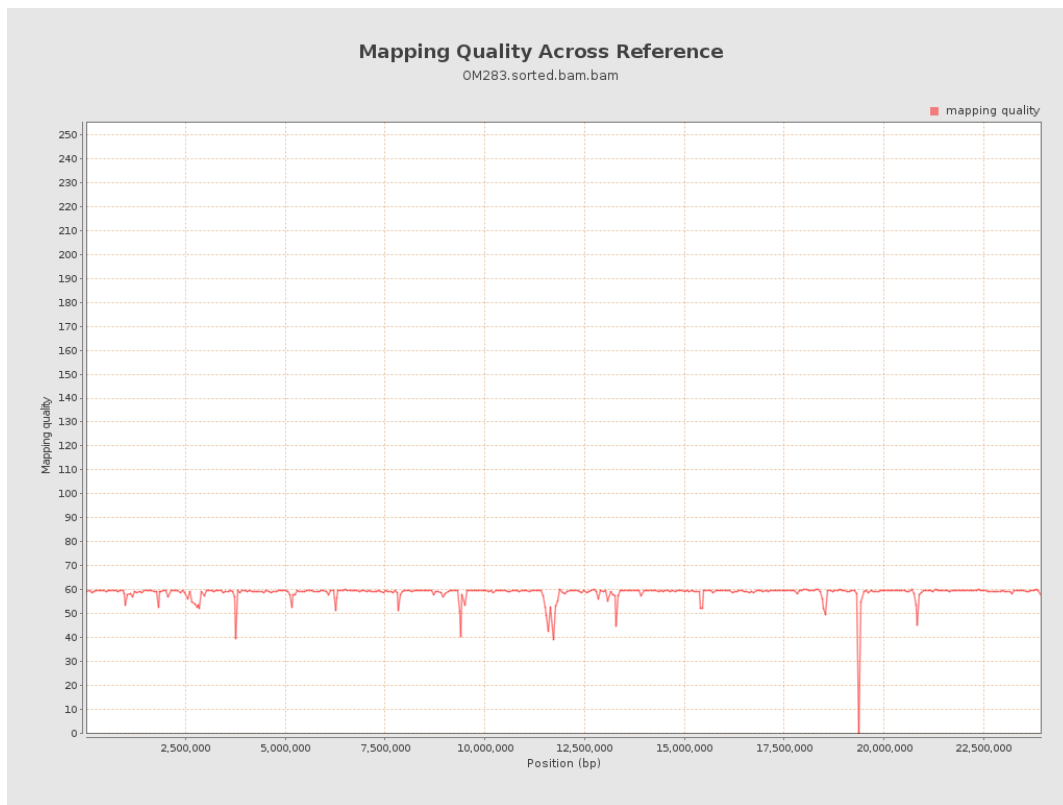OM283.sorted.bam.bam
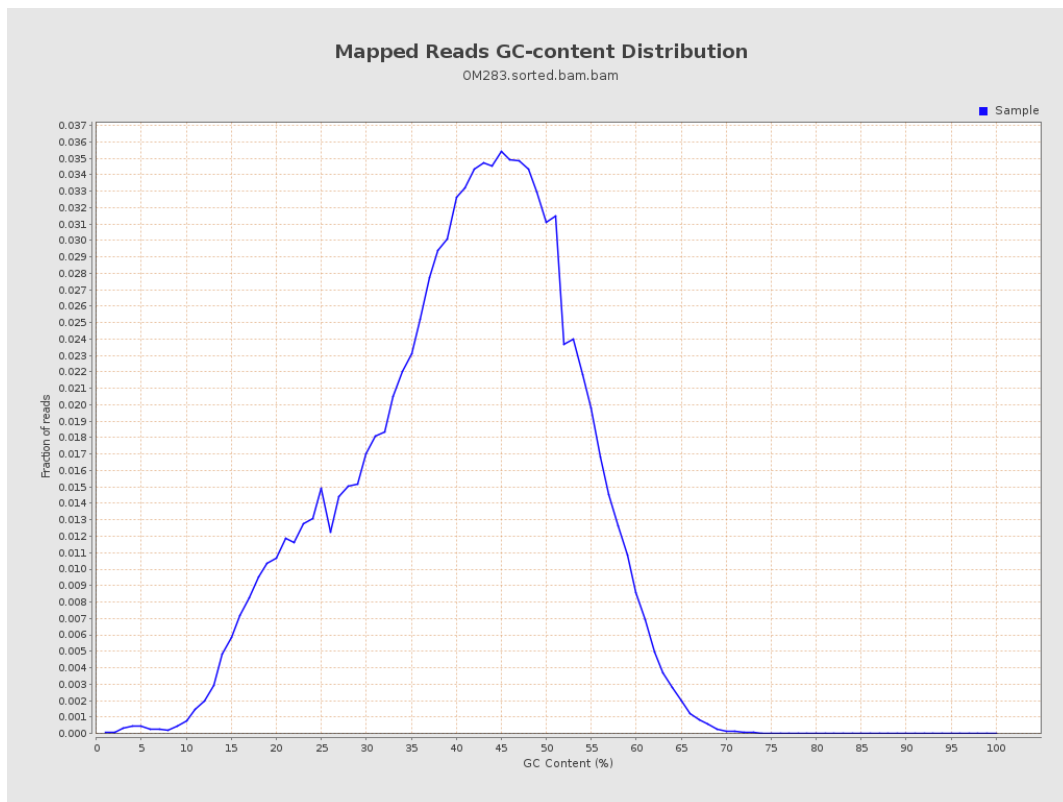
10. Results : Mapped Reads Clipping Profile
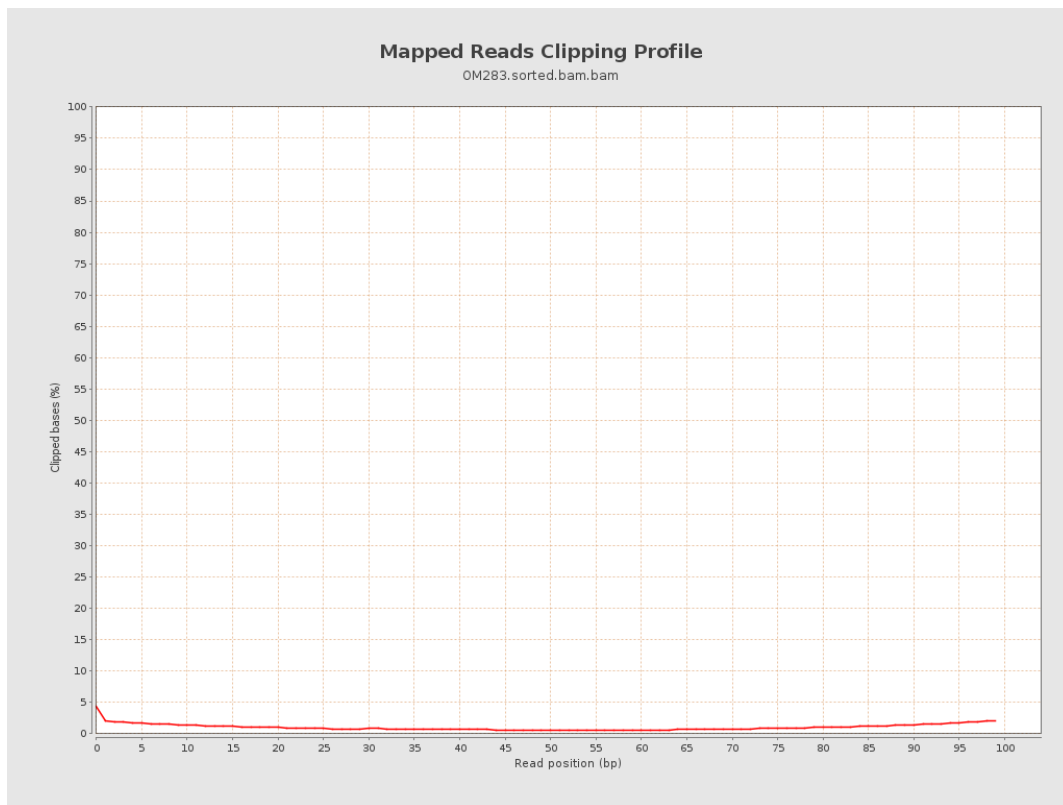
11. Results : Homopolymer Indels
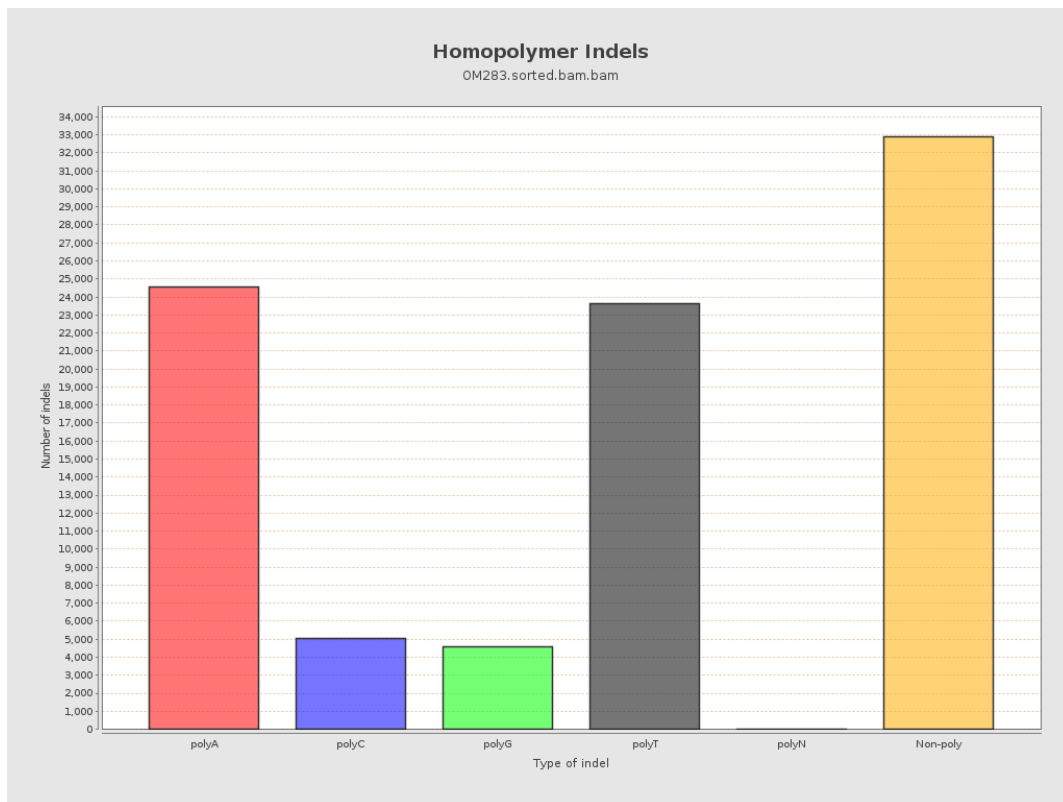
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
OM283.sorted.bam.bam
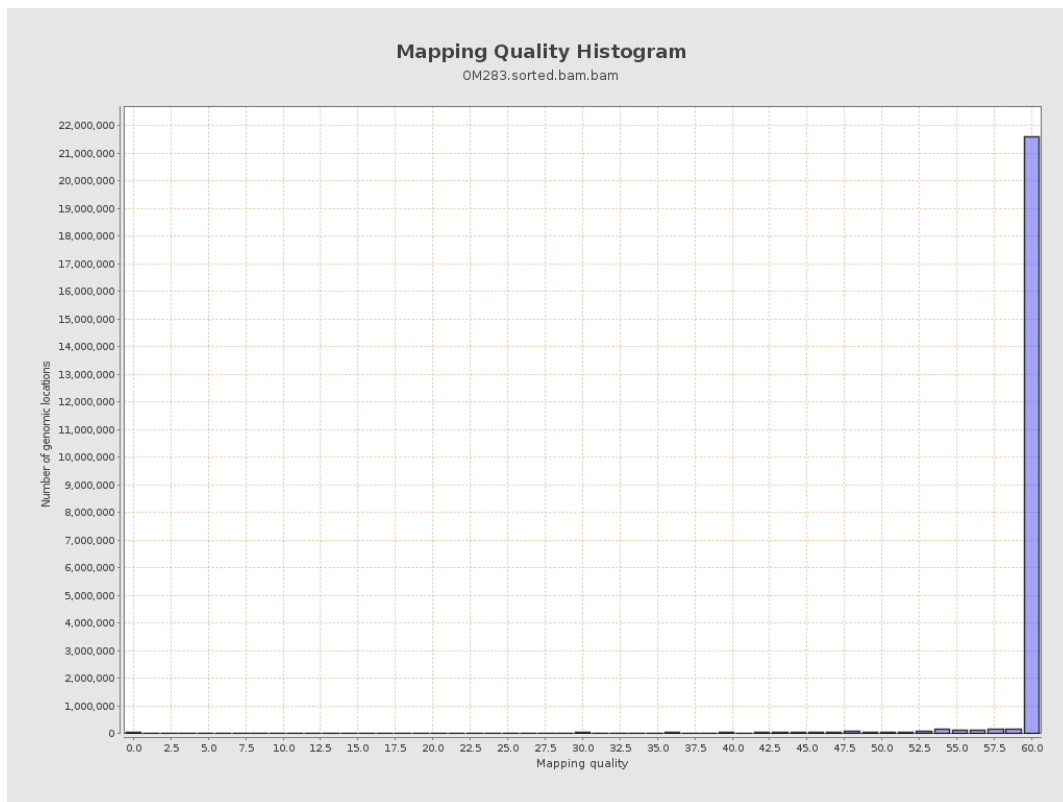
14. Results : Insert Size Across Reference

Insert Size Across Reference
OM283.sorted.bam.bam
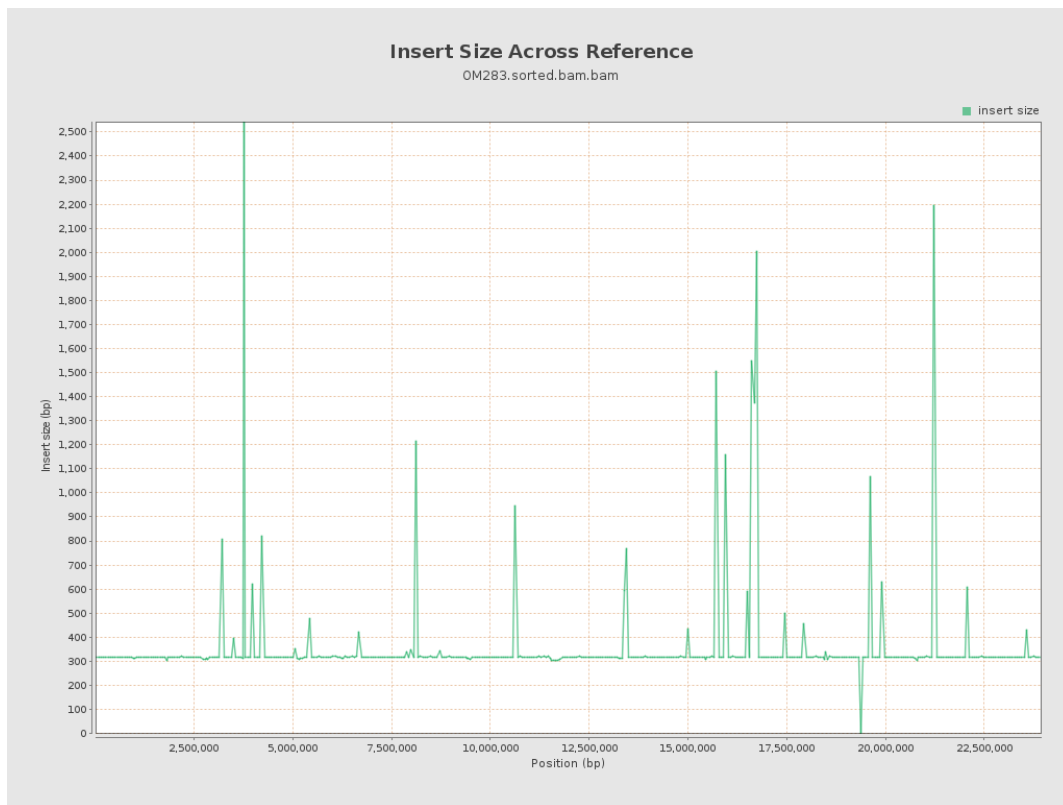
15. Results : Insert Size Histogram

Insert Size Histogram
OM283.sorted.bam.bam