Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 12:54:36

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM105.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/OM-105_ACAGTG_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM-105_ACAGTG_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:54:36 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM105.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	84,177,858
Mapped reads	1,652,976 / 1.96%
Unmapped reads	82,524,882 / 98.04%
Mapped paired reads	1,652,976 / 1.96%
Mapped reads, first in pair	822,185 / 0.98%
Mapped reads, second in pair	830,791 / 0.99%
Mapped reads, both in pair	993,151 / 1.18%
Mapped reads, singletons	659,825 / 0.78%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	765,923 / 0.91%
Duplication rate	13.3%
Clipped reads	828,735 / 0.98%

2.2. ACGT Content

Number/percentage of A's	36,535,402 / 30.96%
Number/percentage of C's	21,100,975 / 17.88%
Number/percentage of T's	39,184,310 / 33.21%
Number/percentage of G's	21,169,090 / 17.94%
Number/percentage of N's	3,120 / 0%
GC Percentage	35.83%

2.3. Coverage

Mean	4.933
Standard Deviation	105.9811

2.4. Mapping Quality

Mean Mapping Quality	48.86

2.5. Insert size

Mean	2,764.59
Standard Deviation	55,994.73
P25/Median/P75	217 / 230 / 257

2.6. Mismatches and indels

General error rate	1.54%
Mismatches	1,602,670
Insertions	82,272
Mapped reads with at least one insertion	4.4%
Deletions	88,277
Mapped reads with at least one deletion	4.02%
Homopolymer indels	53.61%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|107412047 8|emb|LT615 256.1|	977217	4236134	4.3349	25.2749
gi|107412068 2|emb|LT615 257.1|	860454	4706633	5.4699	44.9799
gi|107412086 5|emb|LT615 258.1|	989719	5482392	5.5393	45.9674
gi|107412108 6|emb|LT615 259.1|	935450	4248826	4.542	17.0805
gi|107412130 1|emb|LT615 260.1|	1432239	7849006	5.4802	56.3318
gi|107412161 5|emb|LT615 261.1|	1080962	5125590	4.7417	39.2284
gi|107412187 1|emb|LT615 262.1|	1545099	6757139	4.3733	25.3839
gi|107412223 5|emb|LT615 263.1|	1585108	9531933	6.0134	161.8548
gi|107412259 0|emb|LT615 264.1|	2122358	9089639	4.2828	18.1787
gi|107412305 0|emb|LT615 265.1|	1754192	12076488	6.8844	322.9299
gi|107412342 1|emb|LT615	2150147	10175997	4.7327	32.2265

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	14712047	4.8538	93.4644
gi|1074124588|emb|LT615268.1|	2359348	10357546	4.39	24.3677
gi|1074125065|emb|LT615269.1|	3135668	13840164	4.4138	24.5455

3. Results : Coverage across reference

Coverage across reference
OM105.sorted.bam.bam
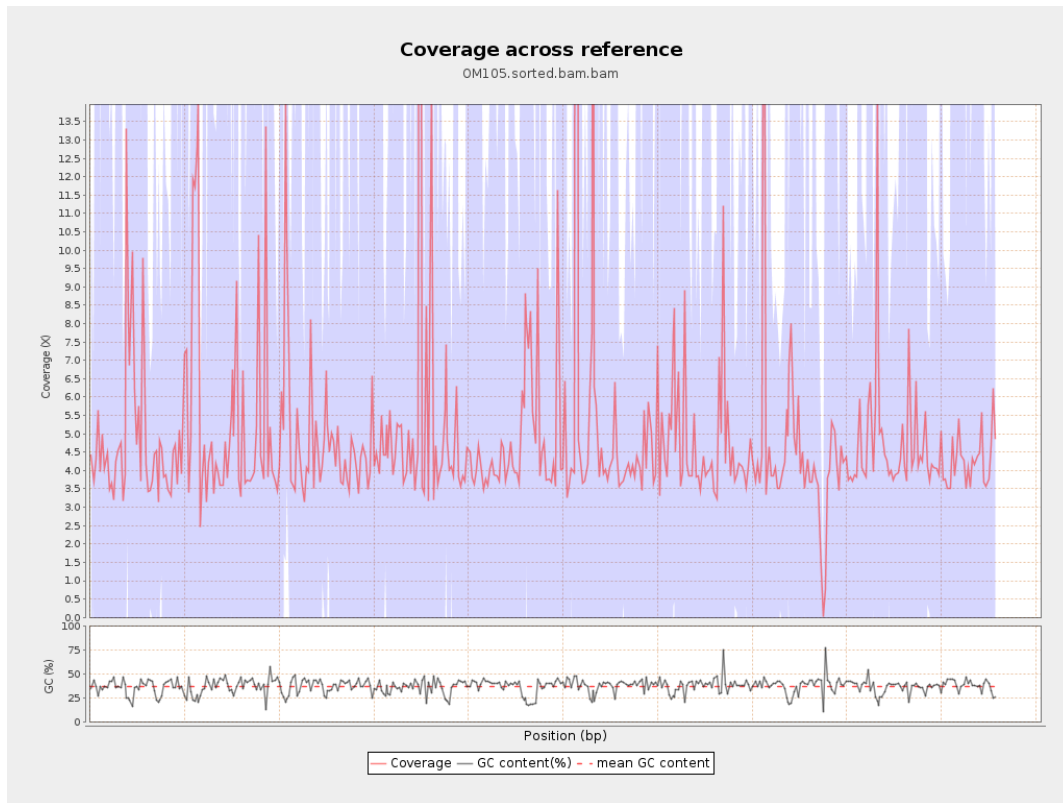
4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
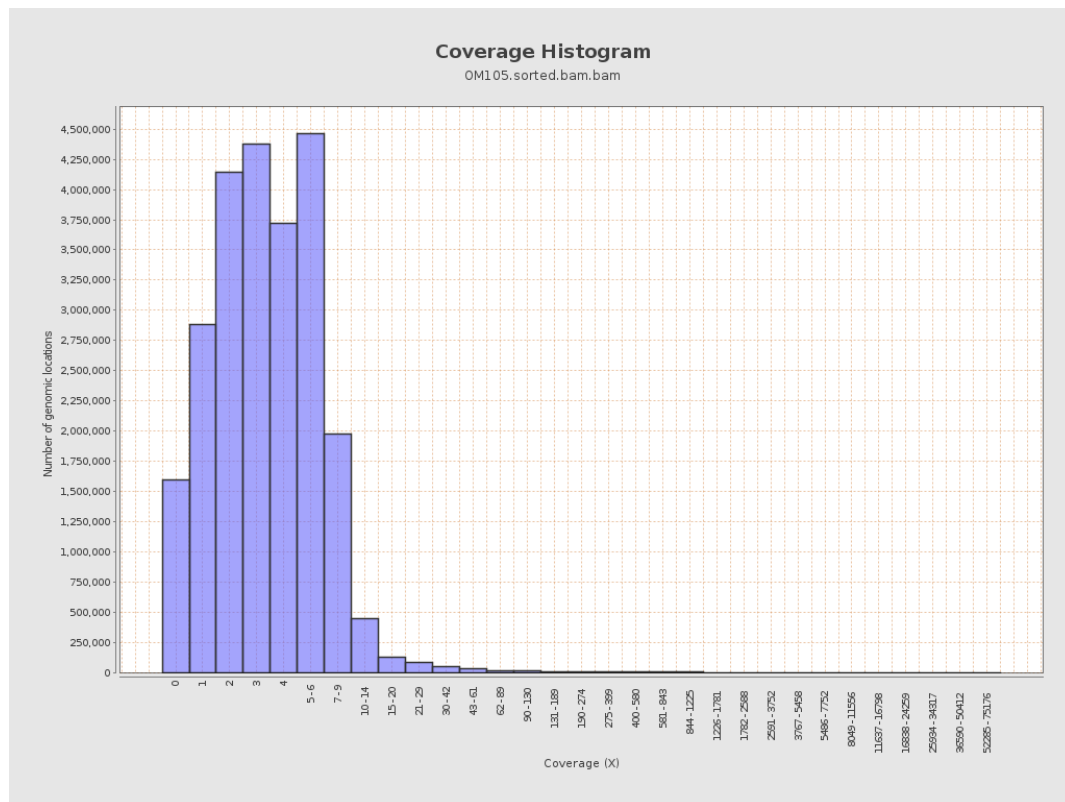
Coverage Histogram (0-50X)
OM105.sorted.bam.bam
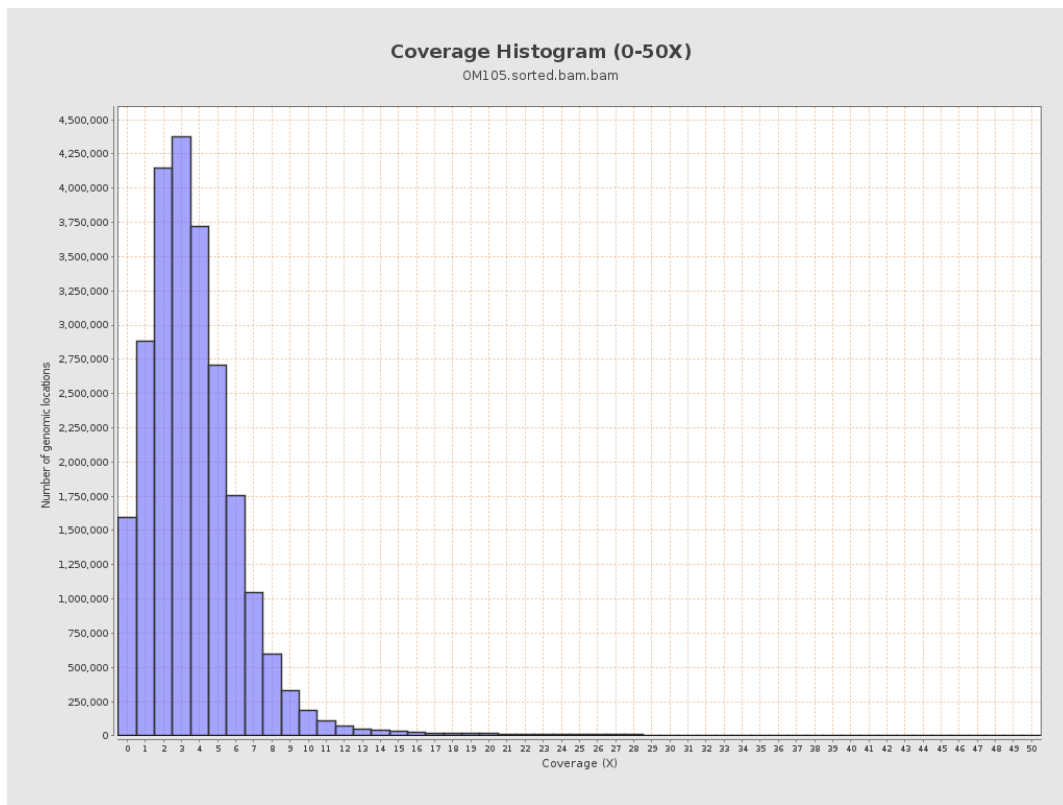
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM105.sorted.bam.bam
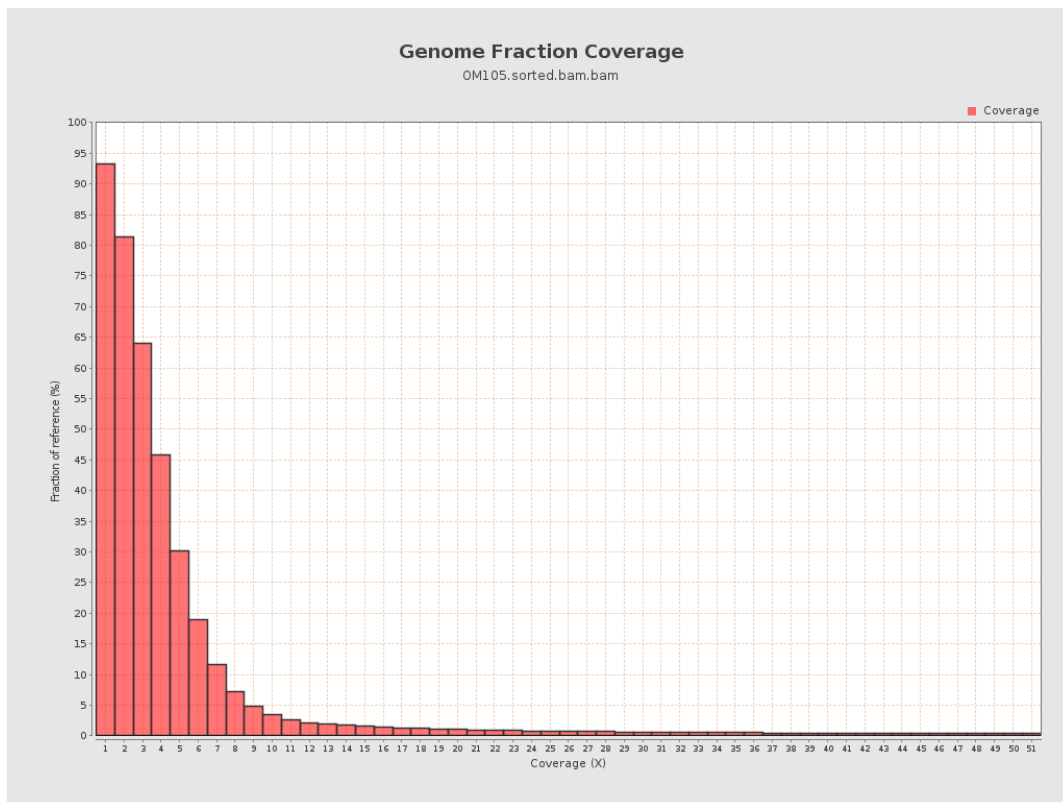
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
OM105.sorted.bam.bam
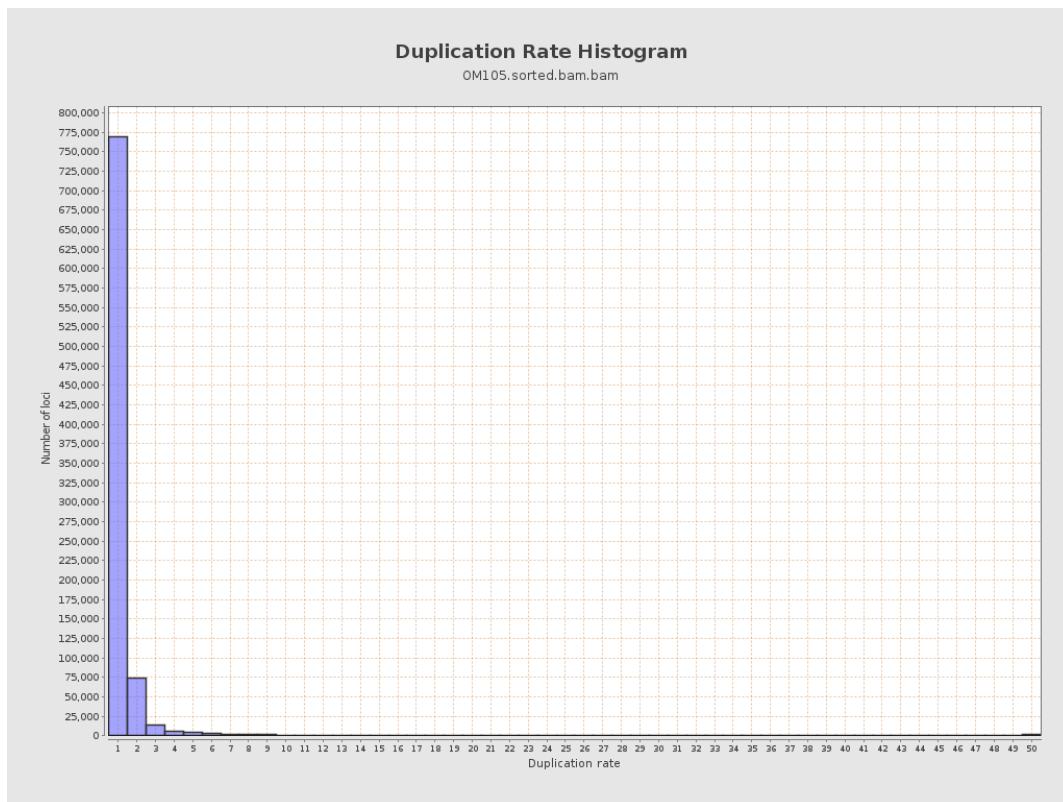
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution
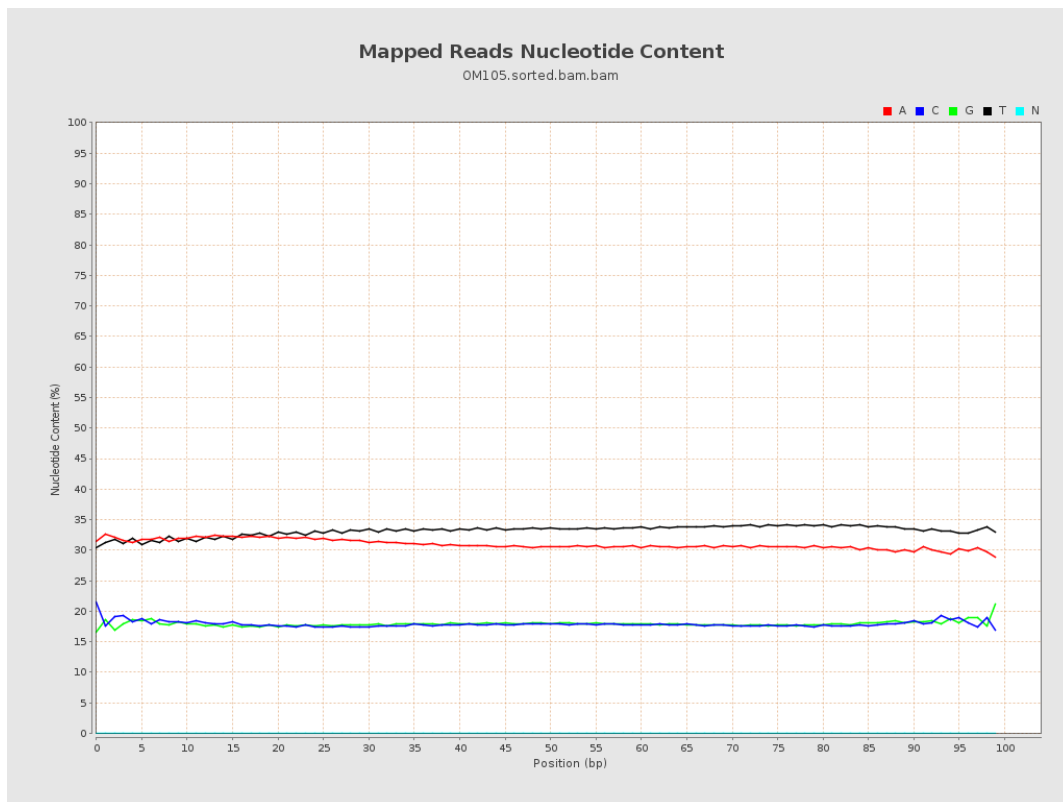
Mapped Reads GC-content Distribution
0M105.sorted.bam.bam
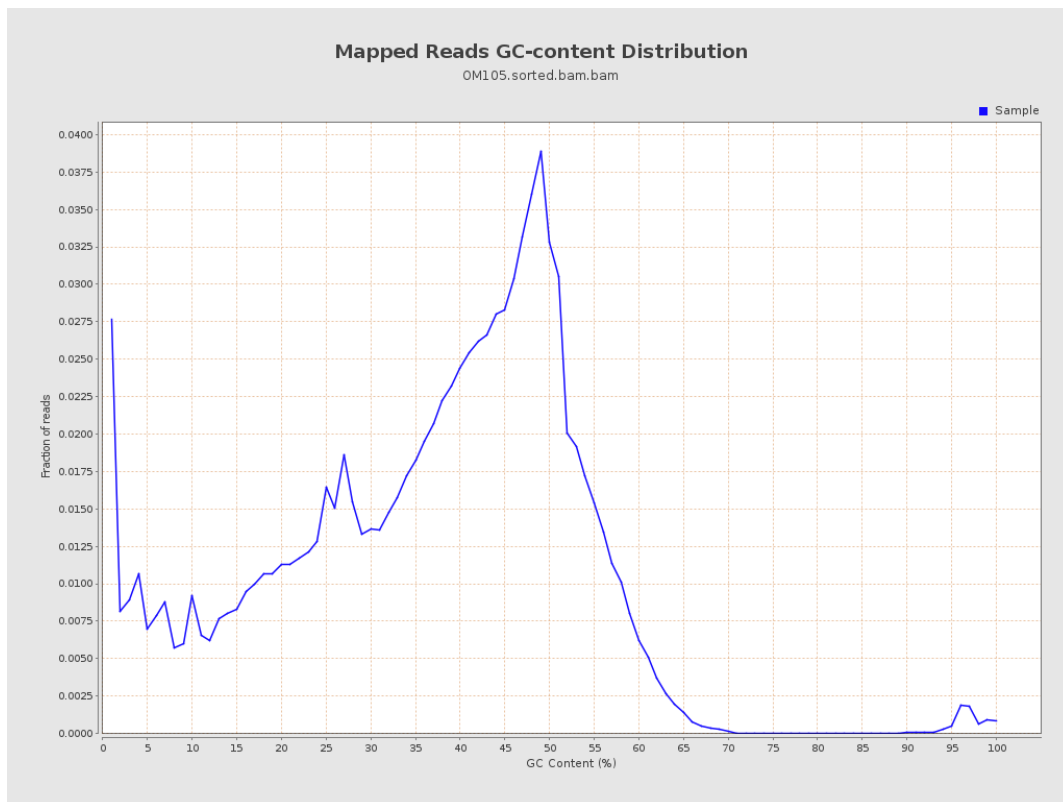
10. Results : Mapped Reads Clipping Profile
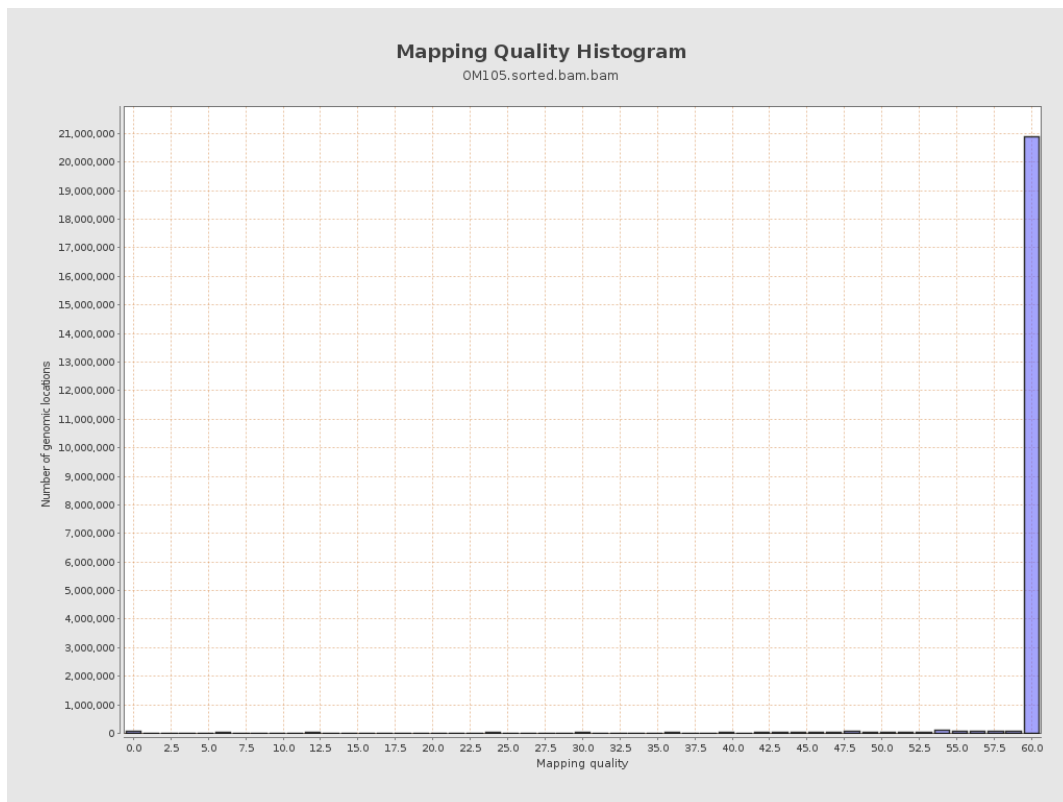

Mapped Reads Clipping Profile
OM105.sorted.bam.bam
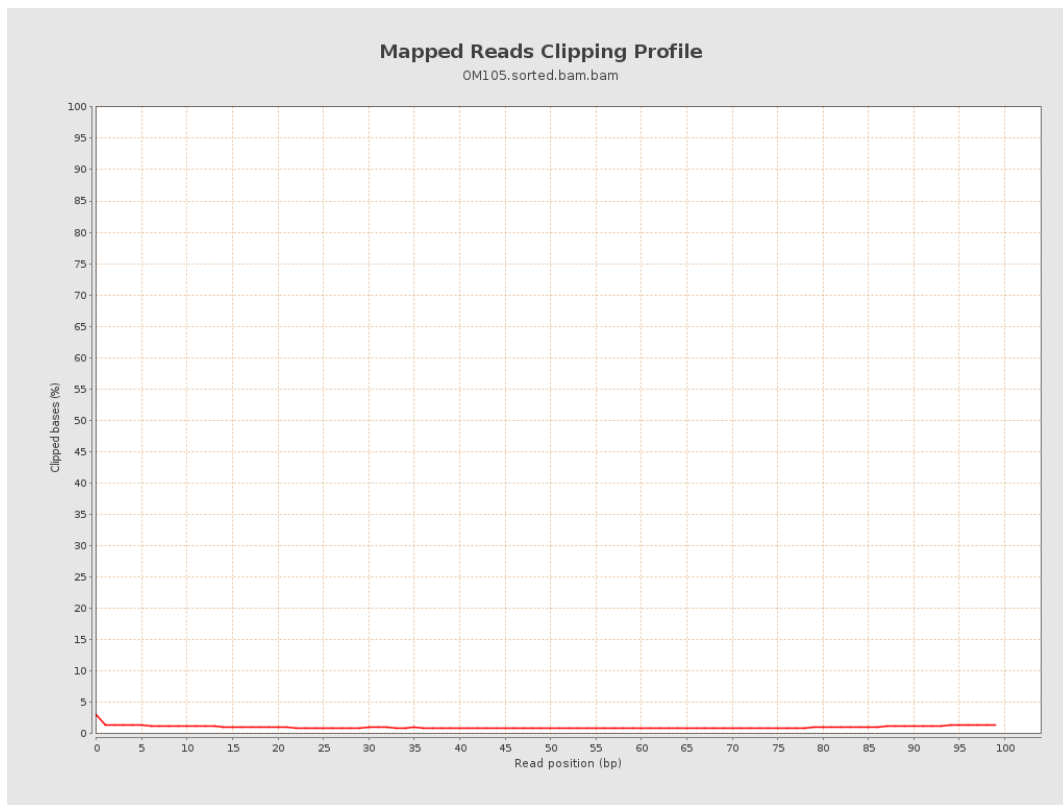
11. Results : Homopolymer Indels
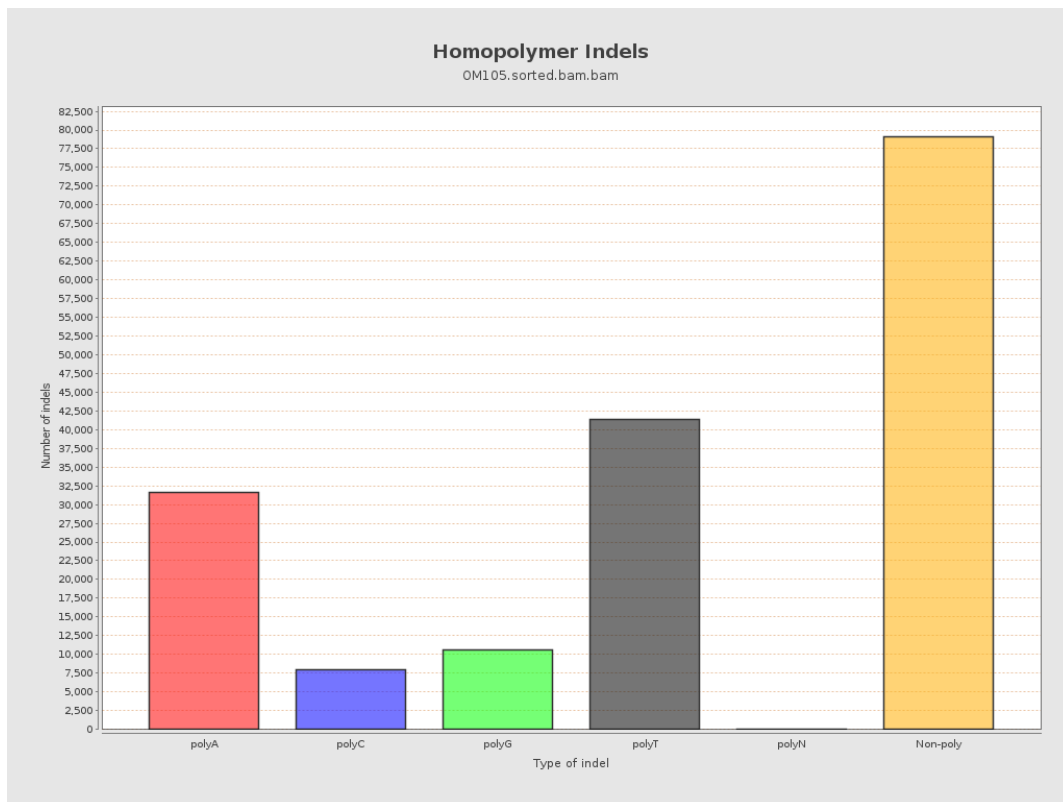
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
OM105.sorted.bam.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM105.sorted.bam.bam
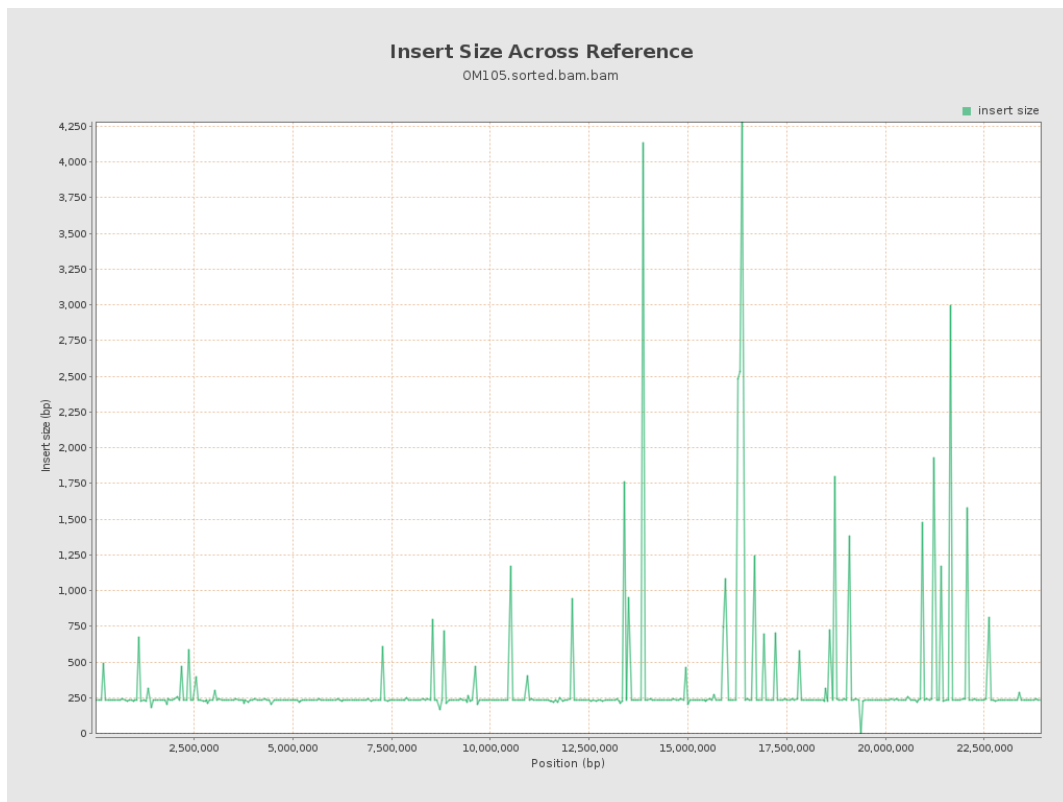
15. Results : Insert Size Histogram

Insert Size Histogram
OM105.sorted.bam.bam