Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 11:37:17

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/BB023.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/BB023-BiooBarcode_37_CGGAAT_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/BB023-BiooBarcode_37_CGGAAT_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:37:17 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/BB023.sorted.bam.b

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	16,004,271
Mapped reads	6,600,014 / 41.24%
Unmapped reads	9,404,257 / 58.76%
Mapped paired reads	6,600,014 / 41.24%
Mapped reads, first in pair	3,277,880 / 20.48%
Mapped reads, second in pair	3,322,134 / 20.76%
Mapped reads, both in pair	6,339,515 / 39.61%
Mapped reads, singletons	260,499 / 1.63%
Read min/max/mean length	30 / 100 / 99.92
Duplicated reads (estimated)	1,947,280 / 12.17%
Duplication rate	27.83%
Clipped reads	599,045 / 3.74%

2.2. ACGT Content

Number/percentage of A's	179,916,923 / 28.14%
Number/percentage of C's	139,687,037 / 21.84%
Number/percentage of T's	180,681,392 / 28.25%
Number/percentage of G's	139,187,200 / 21.77%
Number/percentage of N's	53,276 / 0.01%
GC Percentage	43.61%

2.3. Coverage

Mean	26.7182
Standard Deviation	22.9101

2.4. Mapping Quality

Mean Mapping Quality	58.57

2.5. Insert size

Mean	963.54
Standard Deviation	27,854.85
P25/Median/P75	315 / 357 / 401

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	5,520,839
Insertions	151,654
Mapped reads with at least one insertion	2.18%
Deletions	197,683
Mapped reads with at least one deletion	2.84%
Homopolymer indels	67.37%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	26493190	27.1109	10.3022
gi|1074120682|emb|LT615257.1|	860454	20792550	24.1646	11.535
gi|1074120865|emb|LT615258.1|	989719	27559470	27.8458	19.0485
gi|1074121086|emb|LT615259.1|	935450	25843279	27.6266	25.2836
gi|1074121301|emb|LT615260.1|	1432239	38398264	26.81	18.3089
gi|1074121615|emb|LT615261.1|	1080962	28768963	26.6142	11.4191
gi|1074121871|emb|LT615262.1|	1545099	43533403	28.1752	9.9214
gi|1074122235|emb|LT615263.1|	1585108	42500784	26.8125	16.35
gi|1074122590|emb|LT615264.1|	2122358	54158975	25.5183	10.9222
gi|1074123050|emb|LT615265.1|	1754192	47109322	26.8553	35.3905
gi|1074123421|emb|LT615	2150147	60420726	28.1007	54.7323

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	82213686	27.124	13.3821
gi|1074124588|emb|LT615268.1|	2359348	59006287	25.0096	14.8445
gi|1074125065|emb|LT615269.1|	3135668	83343224	26.5791	8.4437

3. Results : Coverage across reference

Coverage across reference
BB023.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
BB023.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
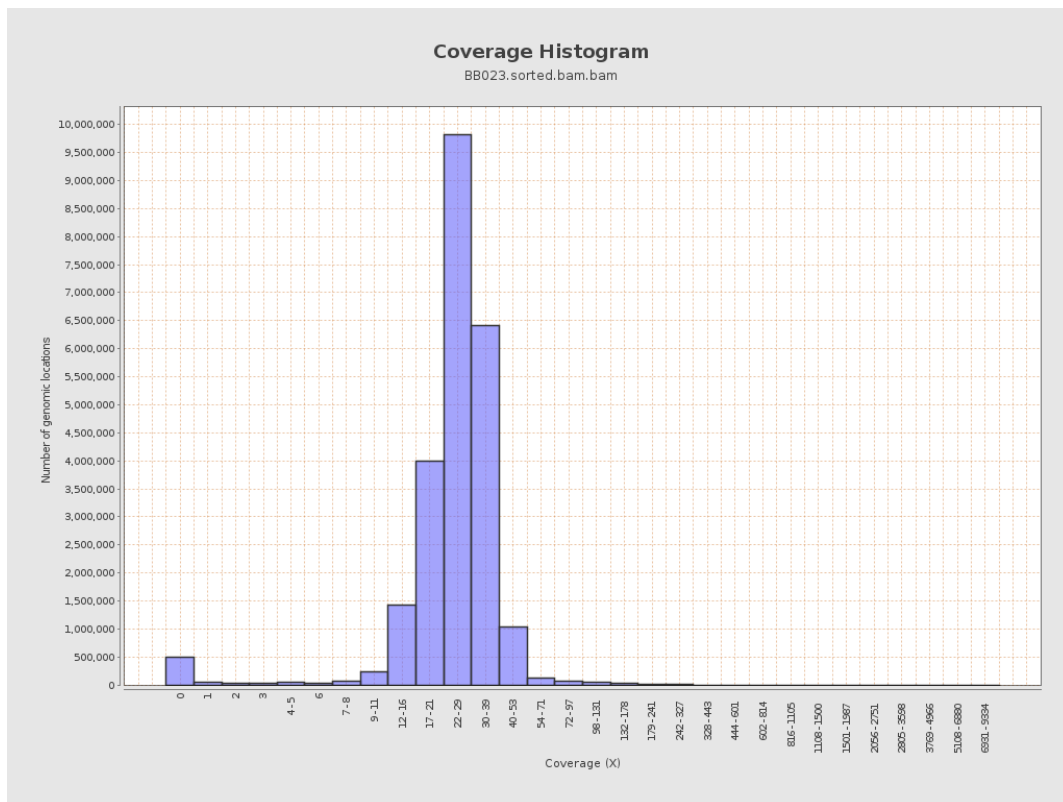
Coverage Histogram (0-50X)
BB023.sorted.bam.bam
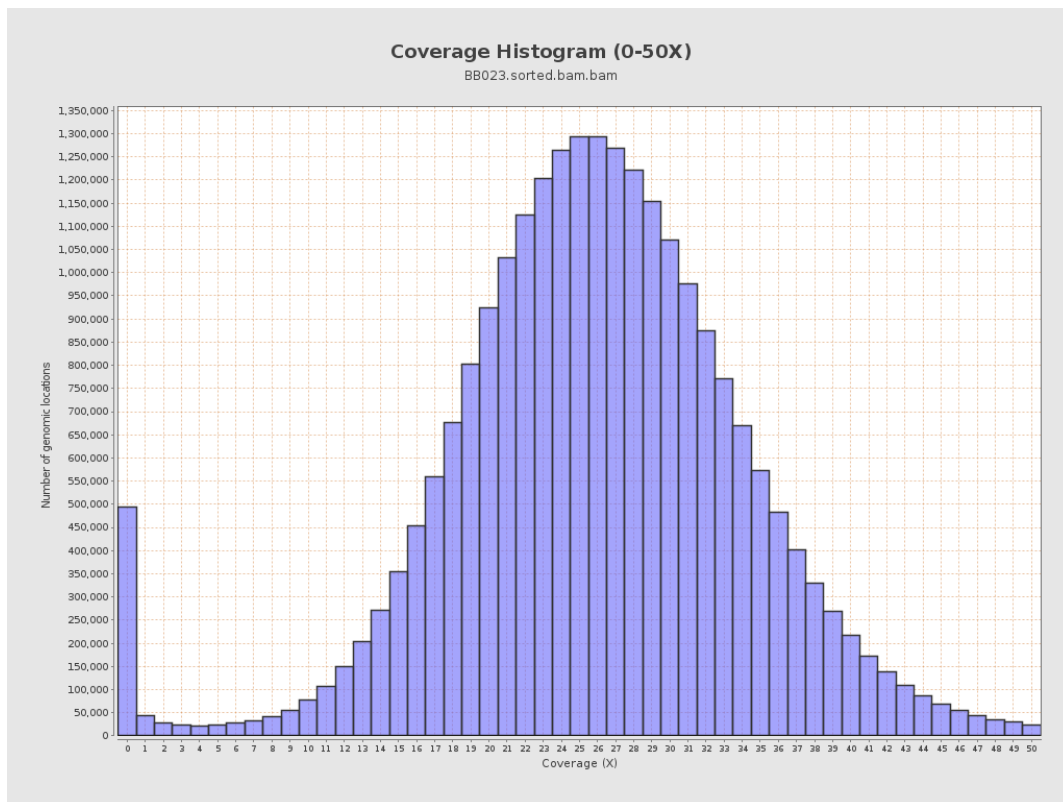
6. Results : Genome Fraction Coverage
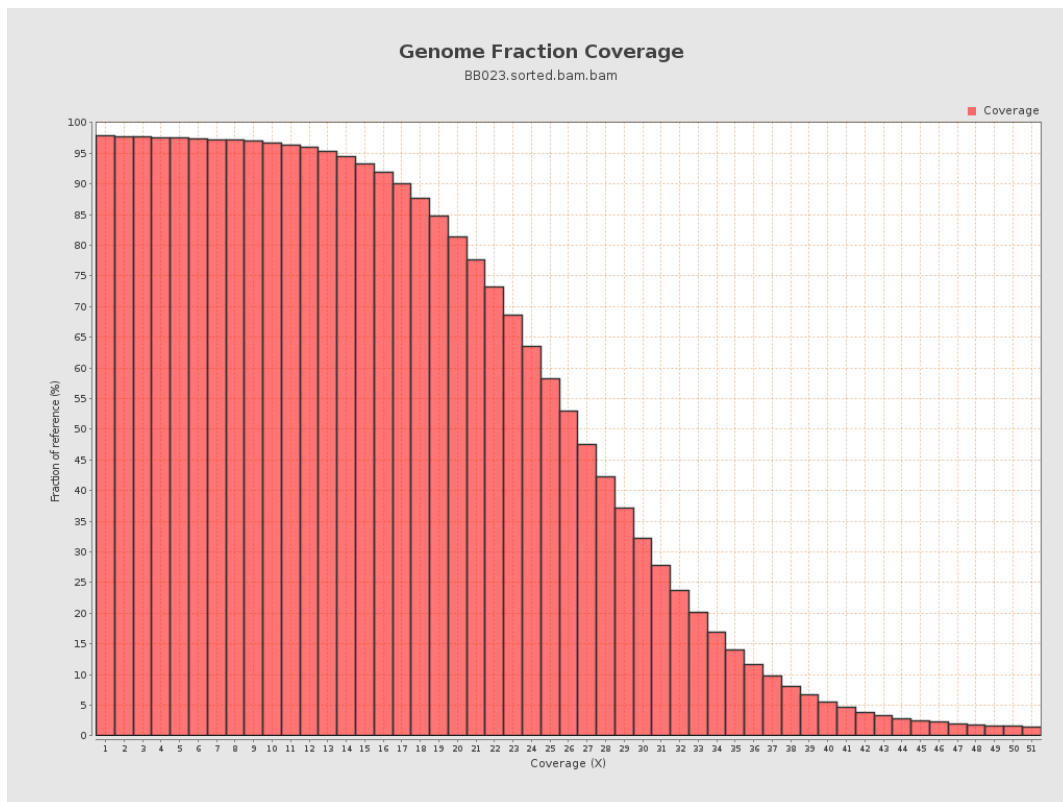
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
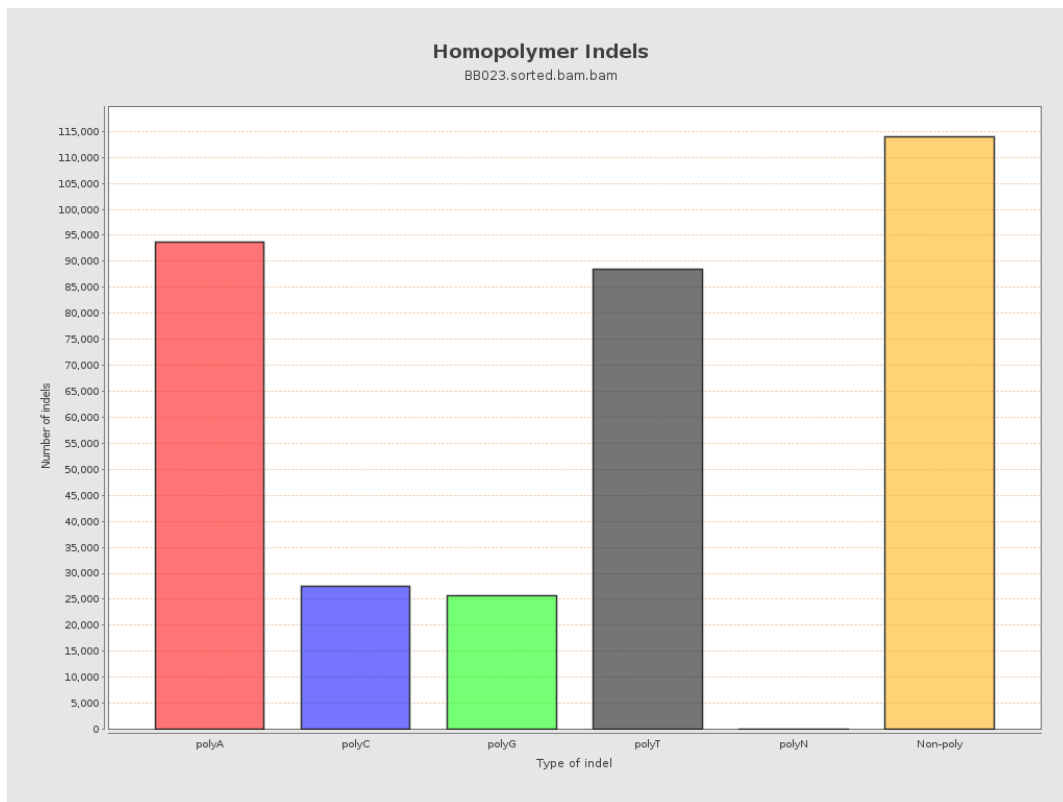BB023.sorted.bam.bam
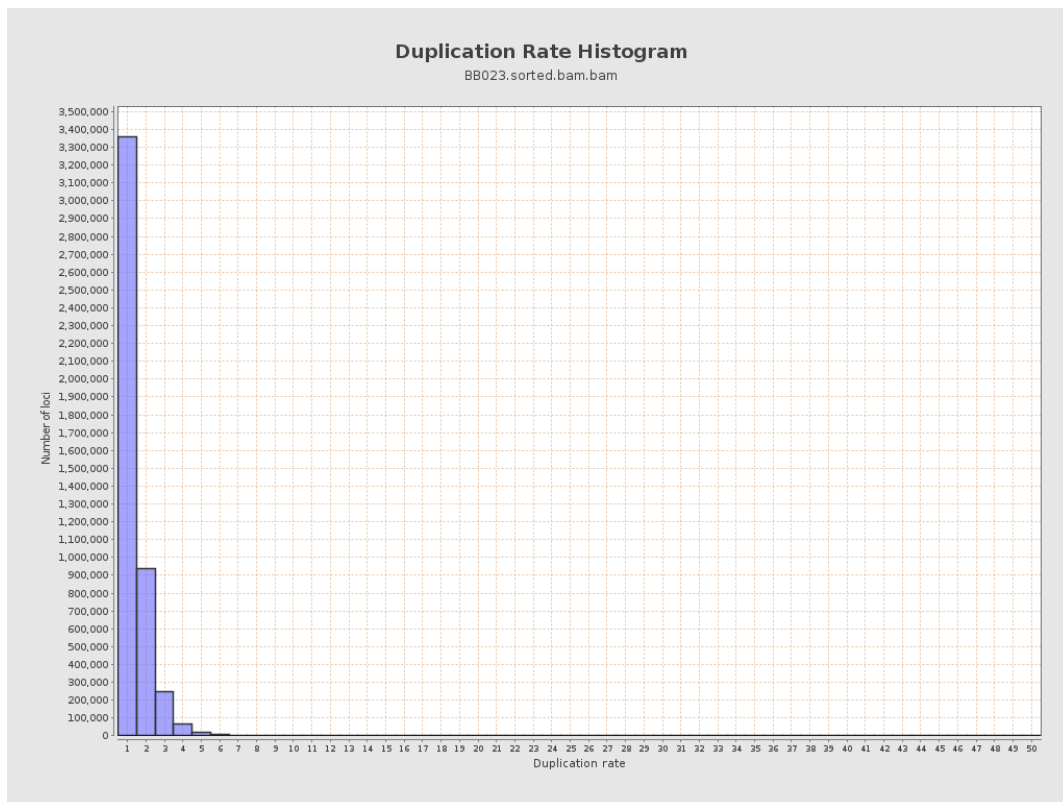
8. Results : Mapped Reads Nucleotide Content
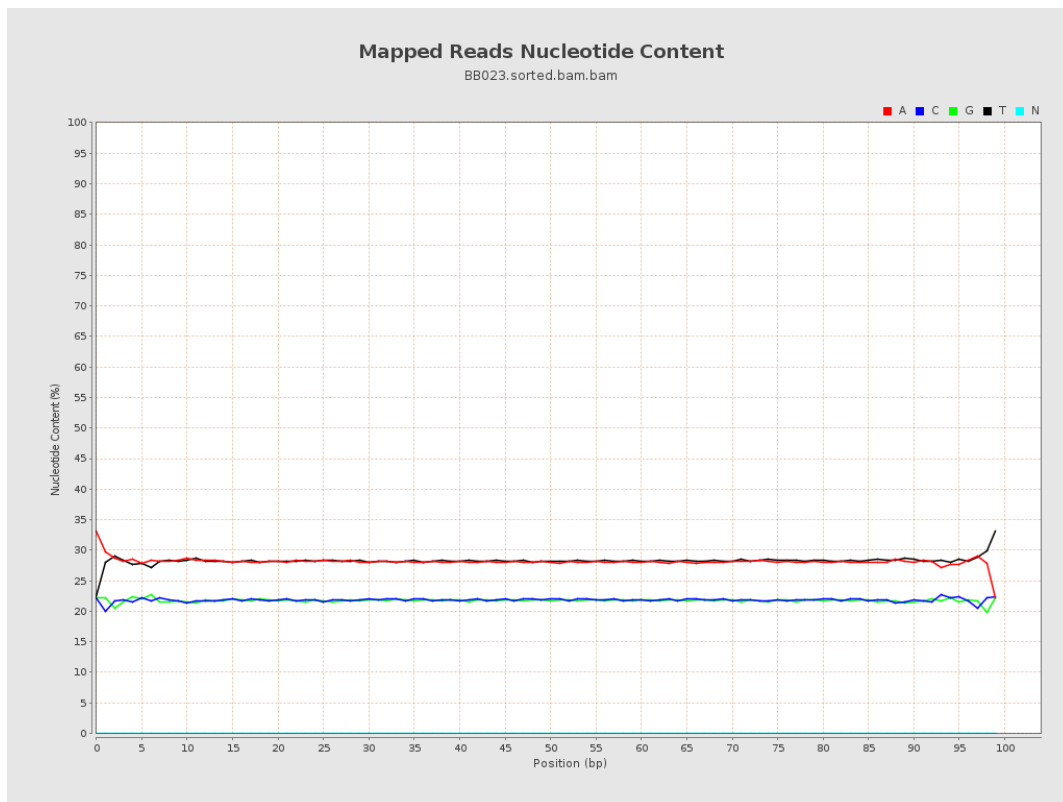
9. Results : Mapped Reads GC-content Distribution
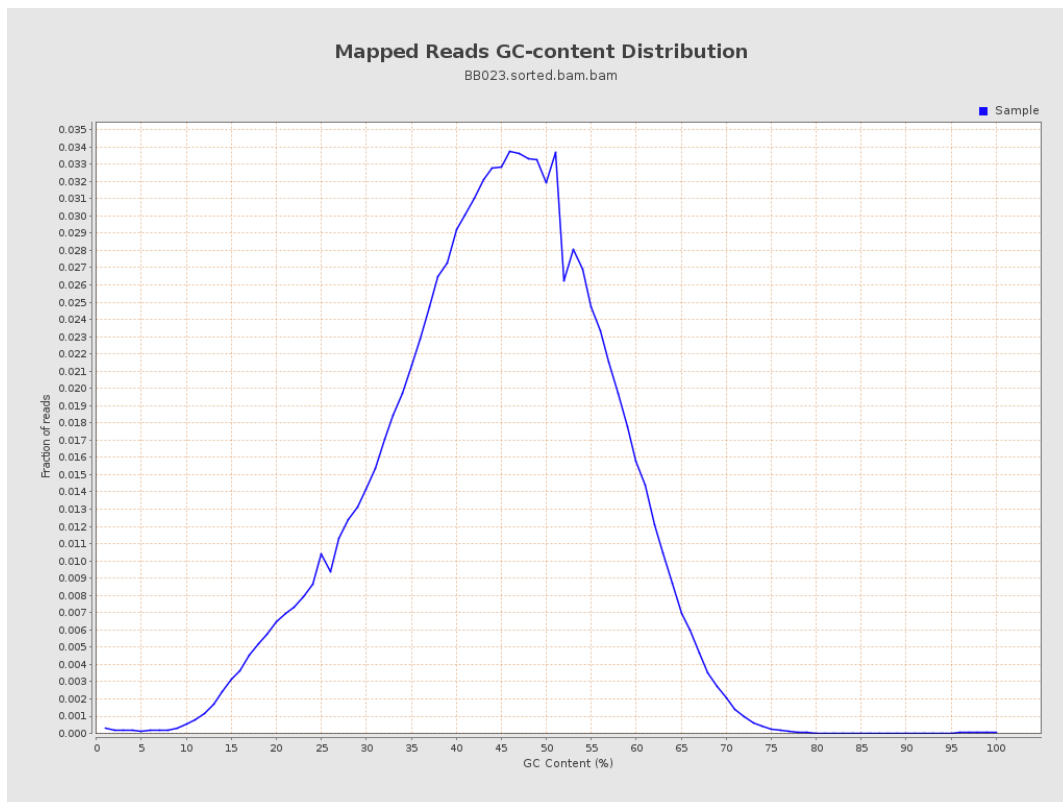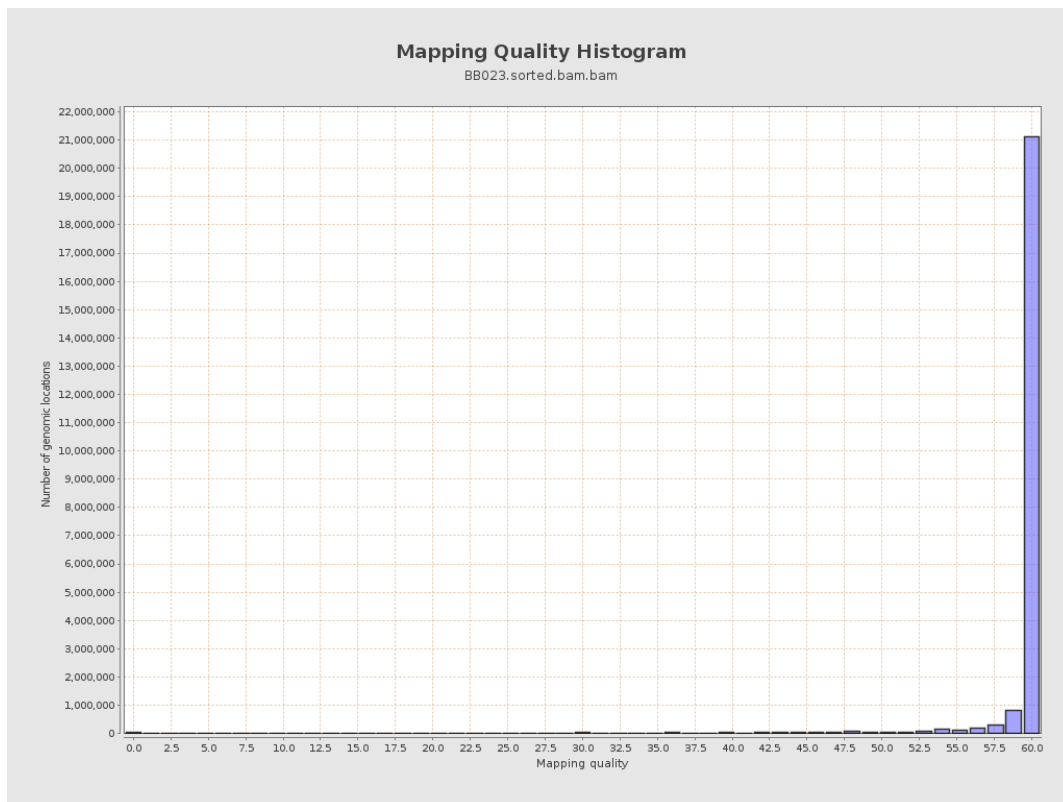
10. Results : Mapped Reads Clipping Profile
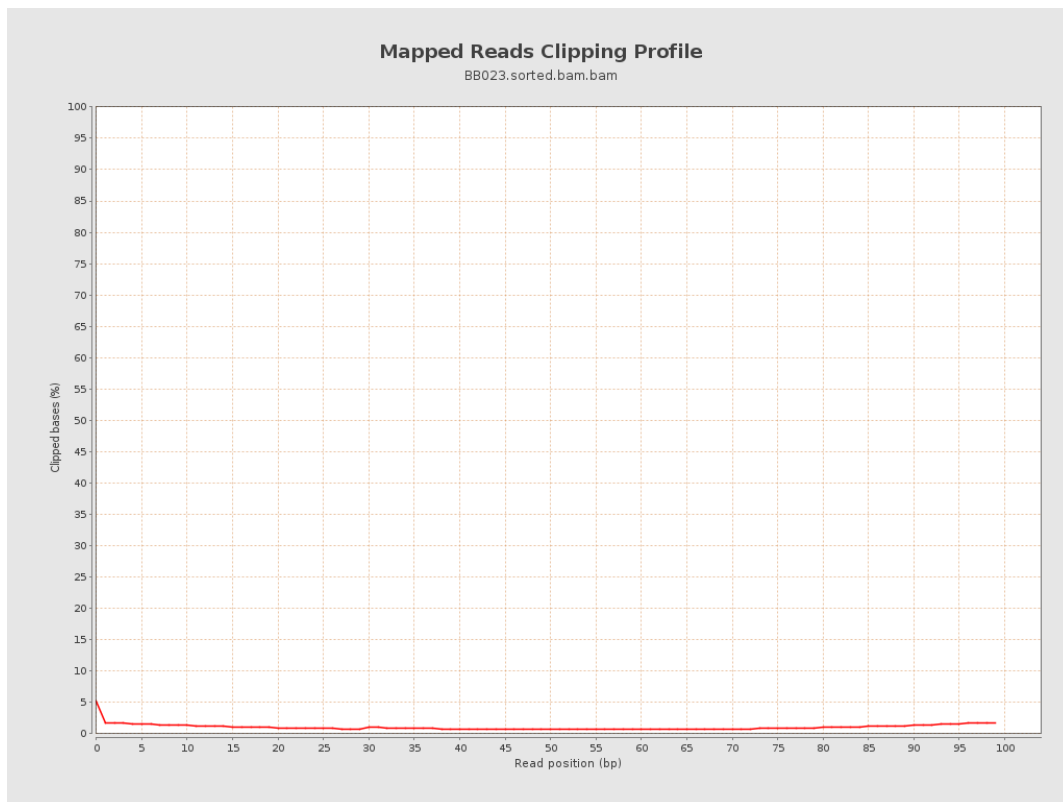
11. Results : Homopolymer Indels
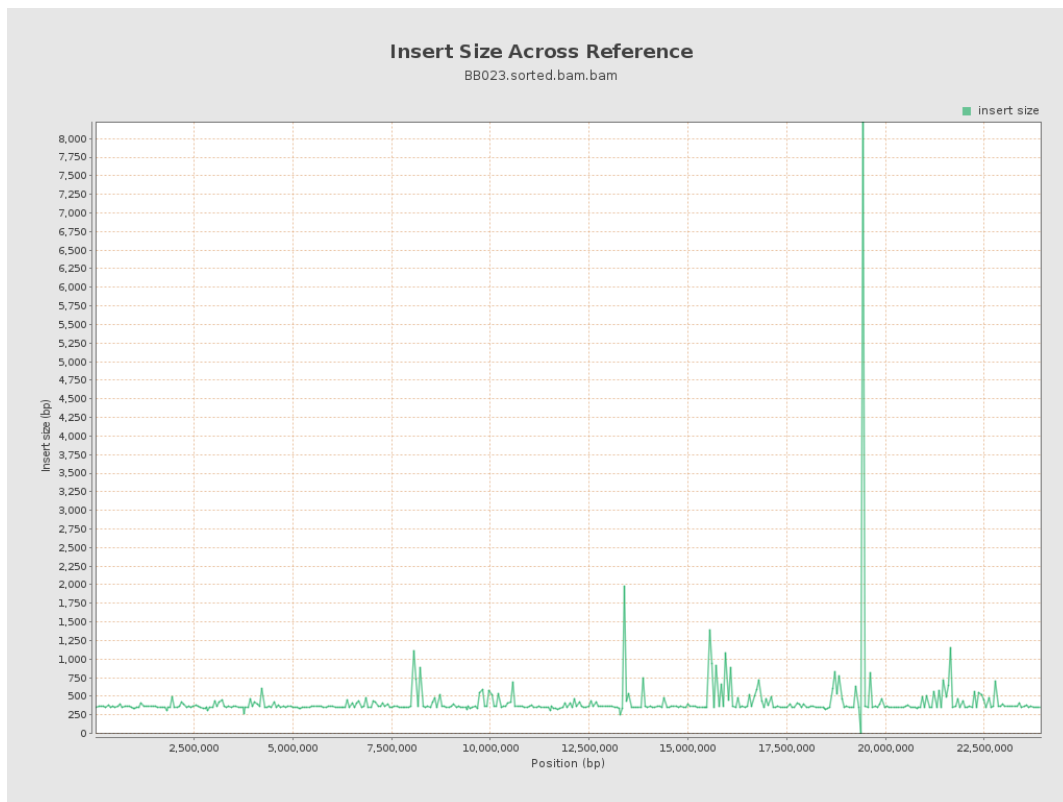

Homopolymer Indels
BB023.sorted.bam.bam

12. Results : Mapping Quality Across Reference
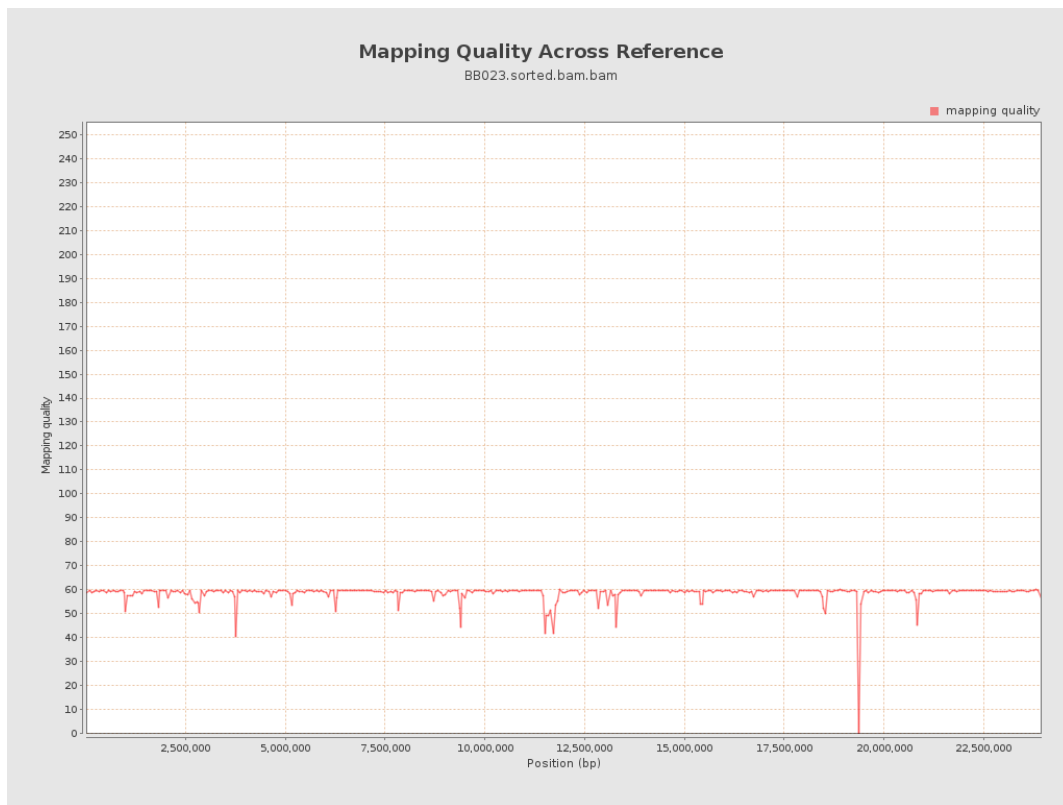
13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
BB023.sorted.bam.bam

15. Results : Insert Size Histogram

Insert Size Histogram
BB023.sorted.bam.bam