Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 11:39:14

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/BB034.sorted.bam.bam -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/BB034-BiooBarcode_38_CTAGCT_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/BB034-BiooBarcode_38_CTAGCT_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:39:14 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/BB034.sorted.bam.b

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	20,206,430
Mapped reads	12,821,917 / 63.45%
Unmapped reads	7,384,513 / 36.55%
Mapped paired reads	12,821,917 / 63.45%
Mapped reads, first in pair	6,390,527 / 31.63%
Mapped reads, second in pair	6,431,390 / 31.83%
Mapped reads, both in pair	12,576,528 / 62.24%
Mapped reads, singletons	245,389 / 1.21%
Read min/max/mean length	30 / 100 / 99.87
Duplicated reads (estimated)	4,719,648 / 23.36%
Duplication rate	35.64%
Clipped reads	1,069,317 / 5.29%

2.2. ACGT Content

Number/percentage of A's	351,894,871 / 28.19%
Number/percentage of C's	271,999,540 / 21.79%
Number/percentage of T's	352,889,794 / 28.27%
Number/percentage of G's	271,342,092 / 21.74%
Number/percentage of N's	104,421 / 0.01%
GC Percentage	43.53%

2.3. Coverage

Mean	52.1477
Standard Deviation	36.156

2.4. Mapping Quality

Mean Mapping Quality	58.79

2.5. Insert size

Mean	955.97
Standard Deviation	28,376.44
P25/Median/P75	303 / 341 / 380

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	10,596,677
Insertions	289,085
Mapped reads with at least one insertion	2.15%
Deletions	377,822
Mapped reads with at least one deletion	2.82%
Homopolymer indels	68.01%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|107412047 8|emb|LT615 256.1|	977217	51185967	52.3793	16.6278
gi|107412068 2|emb|LT615 257.1|	860454	42548809	49.4493	20.6095
gi|107412086 5|emb|LT615 258.1|	989719	55923002	56.5039	52.8618
gi|107412108 6|emb|LT615 259.1|	935450	52445426	56.0644	53.2393
gi|107412130 1|emb|LT615 260.1|	1432239	76026511	53.0823	32.3086
gi|107412161 5|emb|LT615 261.1|	1080962	55486188	51.3304	21.8807
gi|107412187 1|emb|LT615 262.1|	1545099	82103651	53.1381	15.0394
gi|107412223 5|emb|LT615 263.1|	1585108	82637357	52.1336	19.2801
gi|107412259 0|emb|LT615 264.1|	2122358	108331467	51.043	17.3621
gi|107412305 0|emb|LT615 265.1|	1754192	87307526	49.7708	29.466
gi|107412342 1|emb|LT615	2150147	118018283	54.8885	87.0011

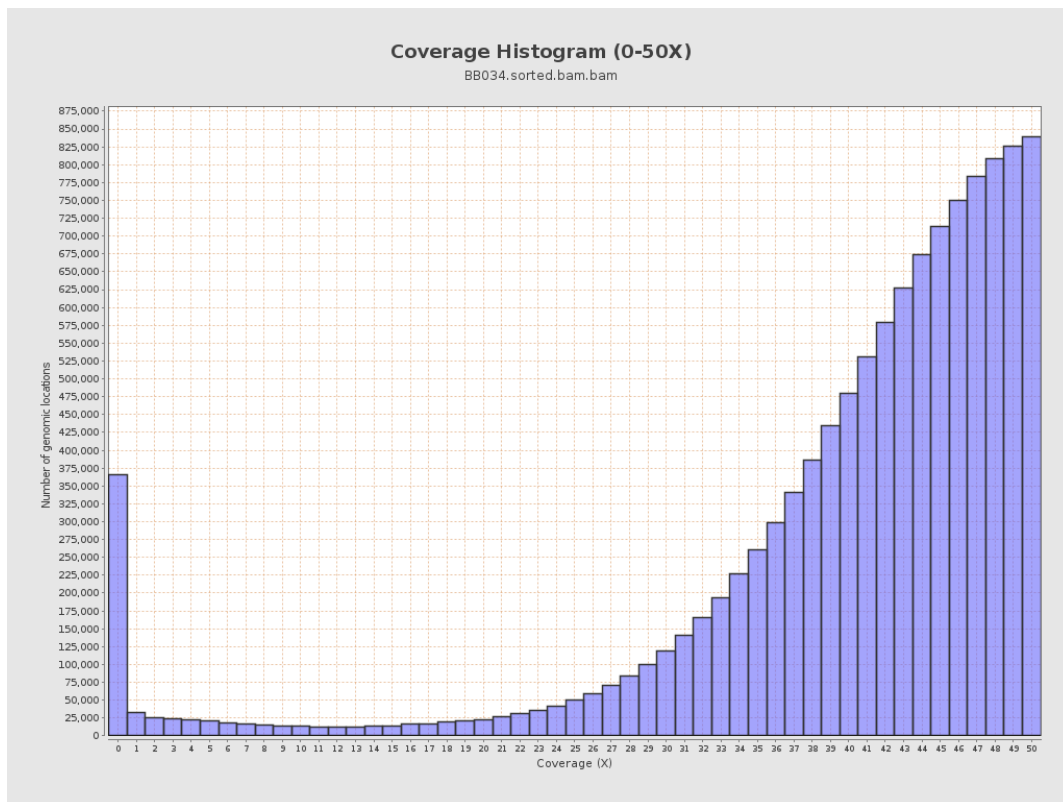|				
266.1|				
gi|1074123898|emb|LT615267.1|	3031036	158375411	52.2512	17.4781
gi|1074124588|emb|LT615268.1|	2359348	117938927	49.9879	32.0189
gi|1074125065|emb|LT615269.1|	3135668	161077281	51.3694	11.9819

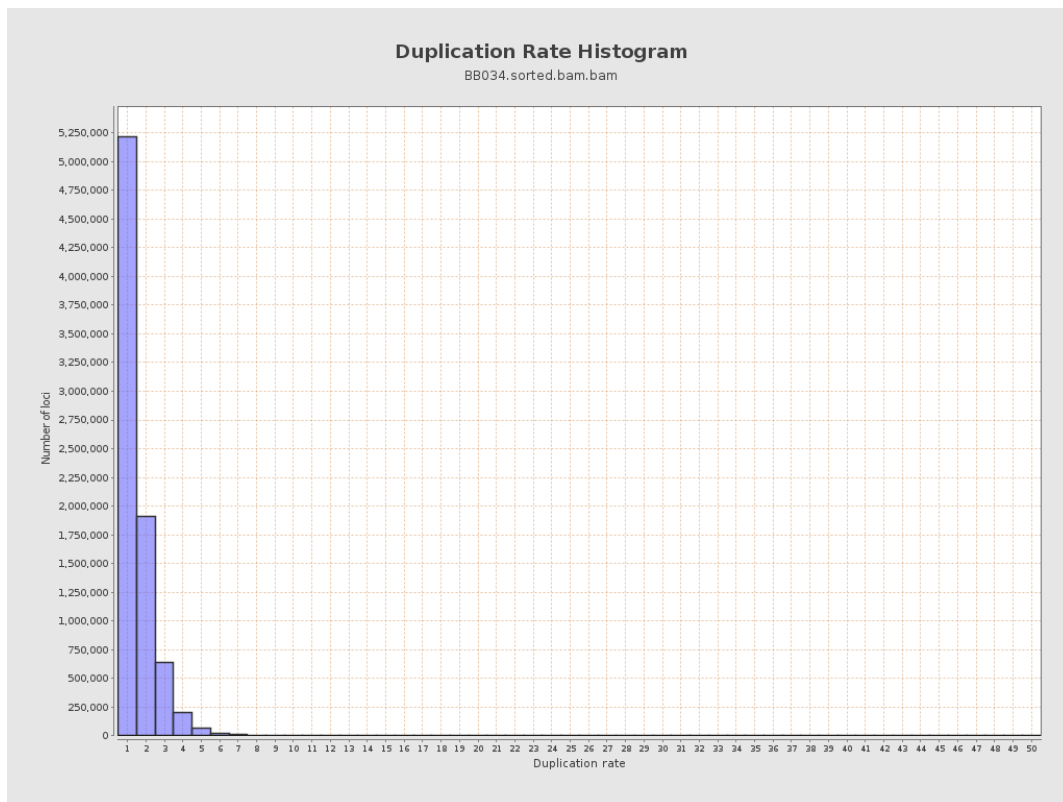# 3. Results : Coverage across reference

4. Results : Coverage Histogram
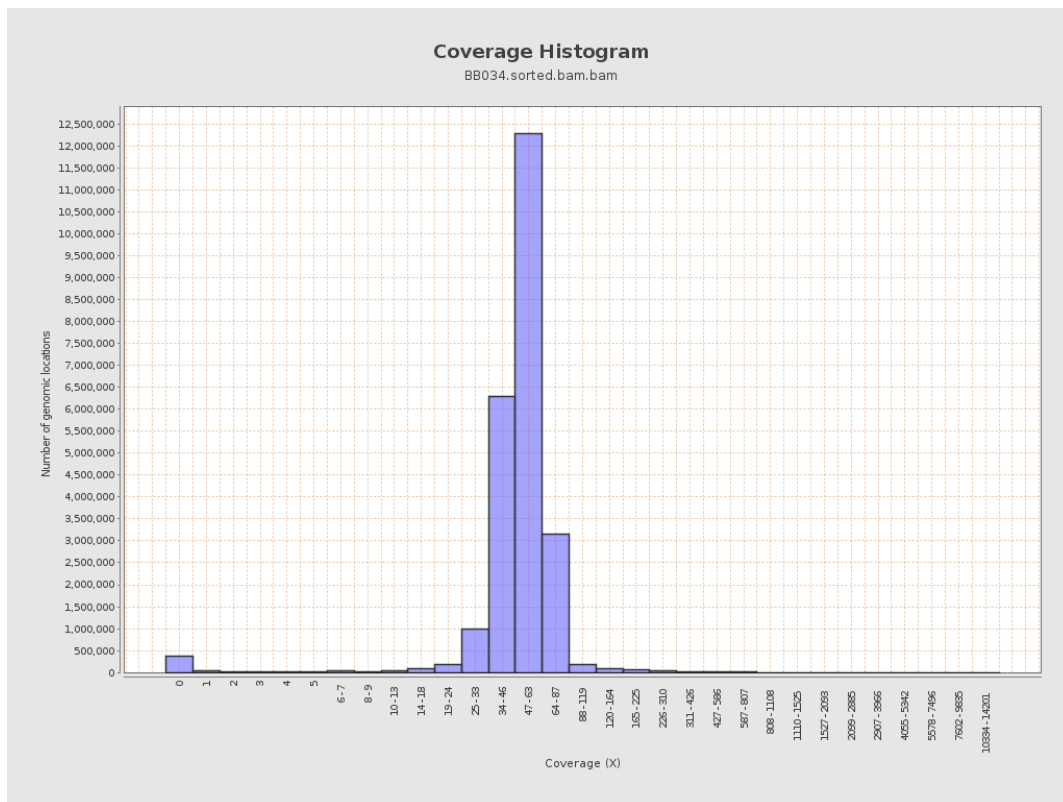
5. Results : Coverage Histogram (0-50X)

6. Results : Genome Fraction Coverage

Genome Fraction Coverage
BB034.sorted.bam.bam
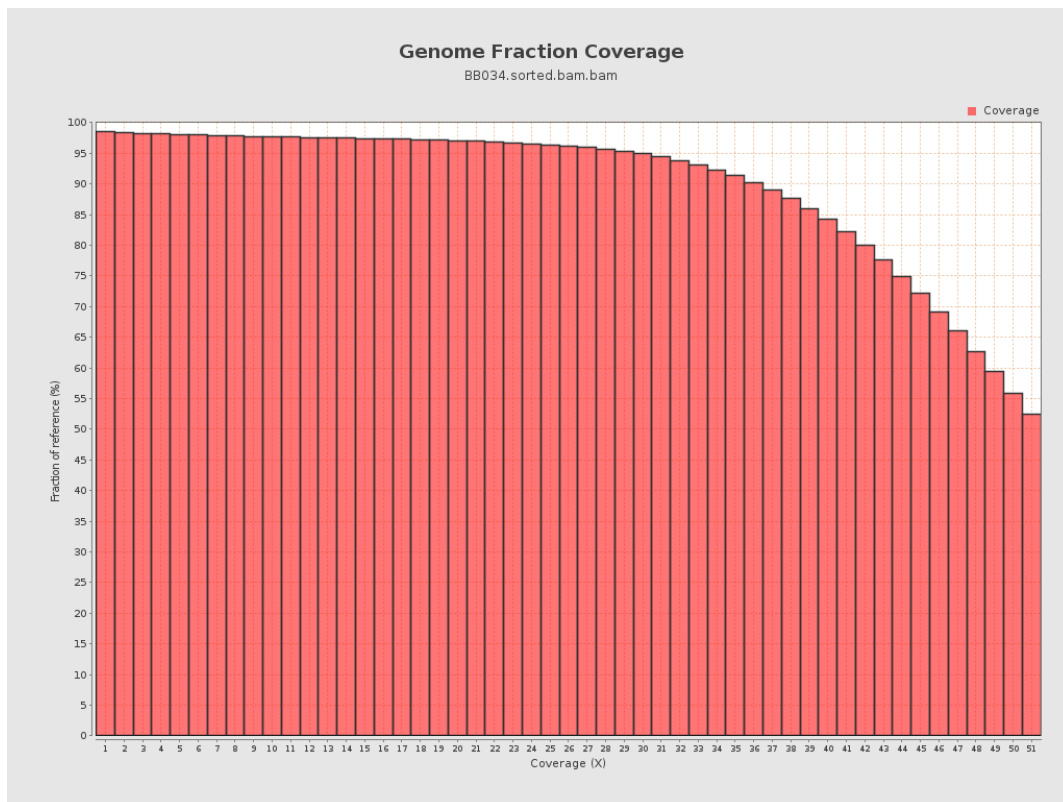
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
BB034.sorted.bam.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
BB034.sorted.bam.bam
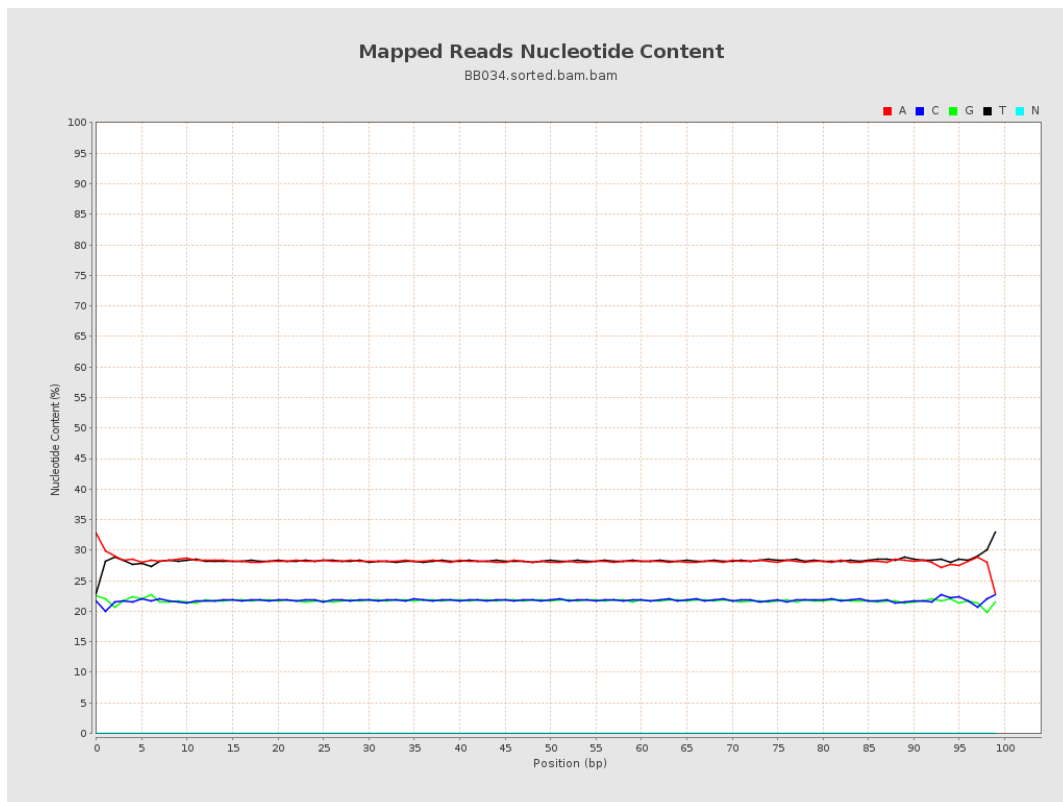
9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
BB034.sorted.bam.bam
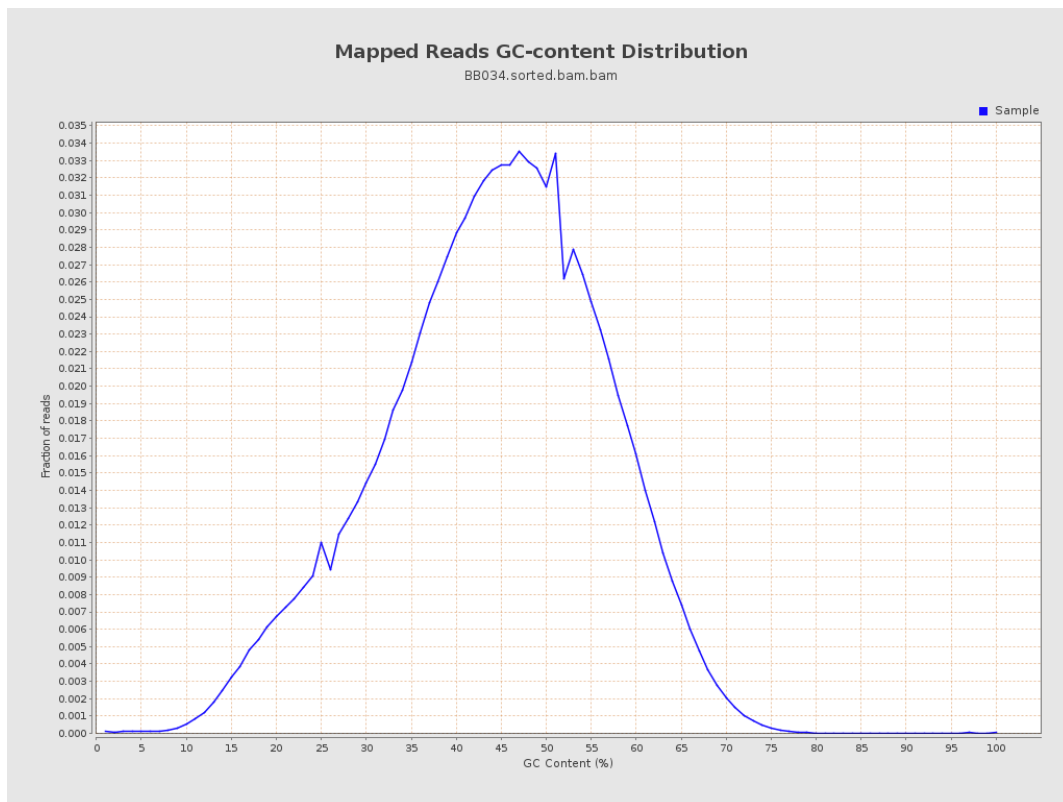
10. Results : Mapped Reads Clipping Profile
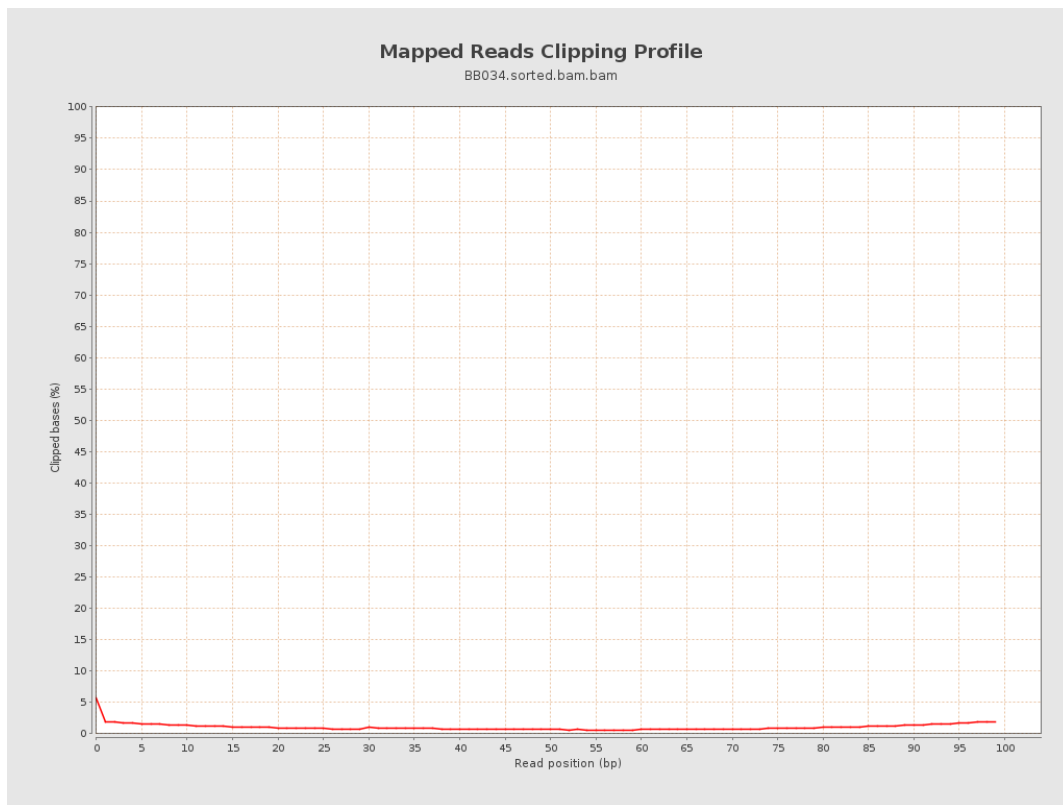
11. Results : Homopolymer Indels

Homopolymer Indels
BB034.sorted.bam.bam
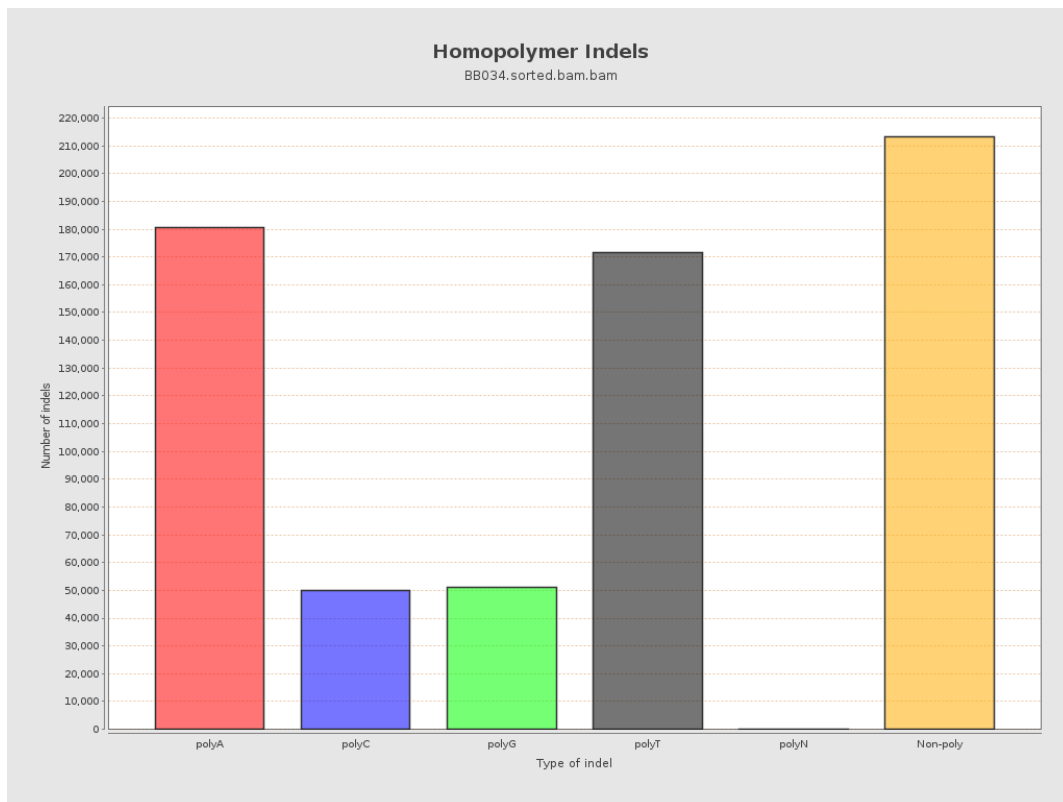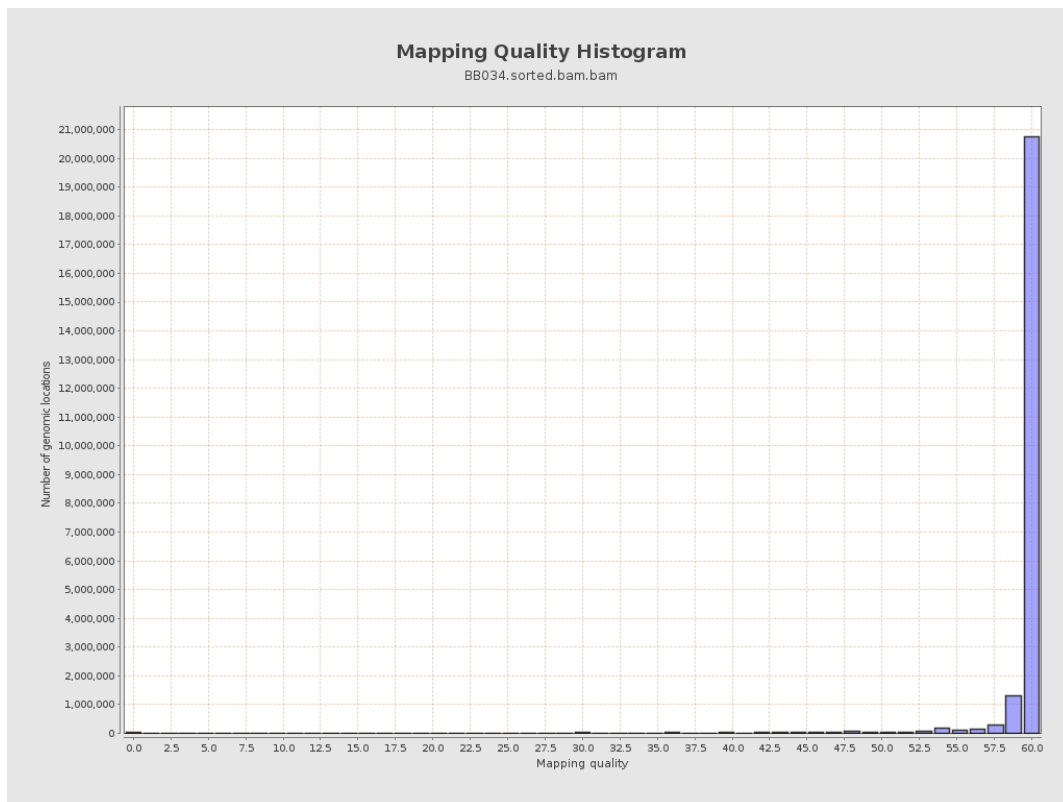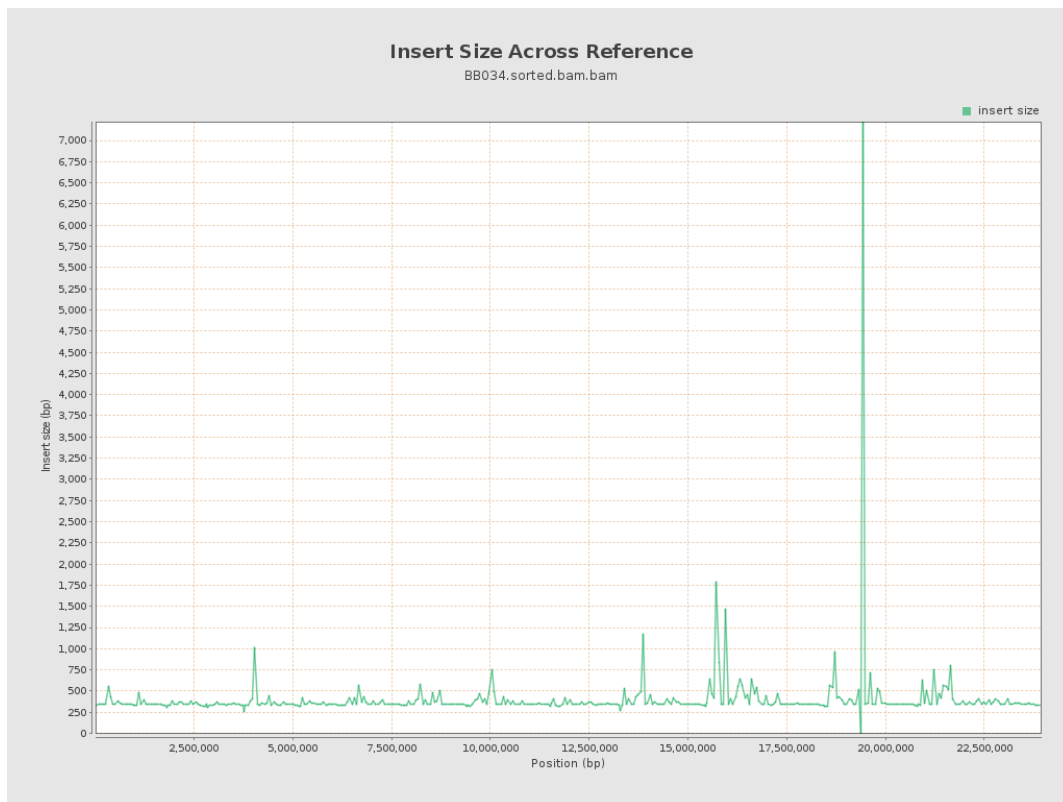
12. Results : Mapping Quality Across Reference
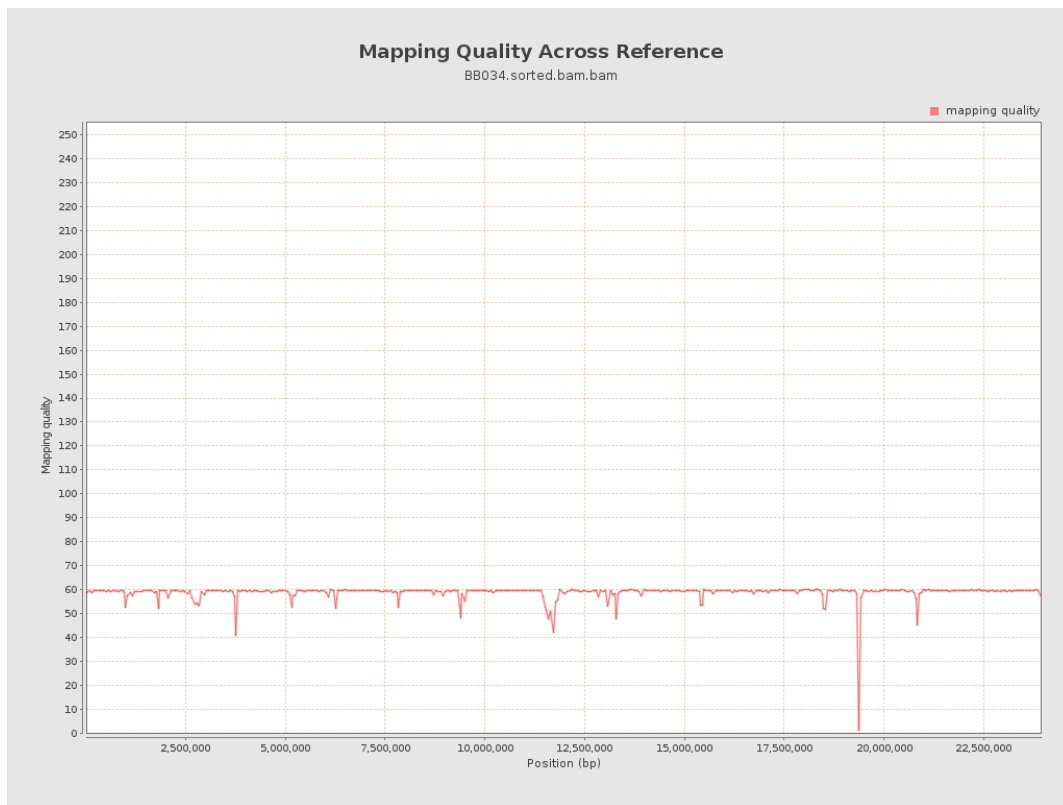
13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
BB034.sorted.bam.bam

15. Results : Insert Size Histogram

Insert Size Histogram
BB034.sorted.bam.bam