Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 11:54:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/KP070.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/KP070-BiooBarcode_29_CAACTA_R2.fastq. gz /home/vdp5/data/cambodia_samples/ sequences_gz/KP070-BiooBarcode_29_CAACTA_R1.fastq. gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:54:06 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/ sequences_bam/KP070.sorted.bam.b

am

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	20,342,248
Mapped reads	7,983,298 / 39.24%
Unmapped reads	12,358,950 / 60.76%
Mapped paired reads	7,983,298 / 39.24%
Mapped reads, first in pair	3,969,262 / 19.51%
Mapped reads, second in pair	4,014,036 / 19.73%
Mapped reads, both in pair	7,740,834 / 38.05%
Mapped reads, singletons	242,464 / 1.19%
Read min/max/mean length	30 / 100 / 99.92
Duplicated reads (estimated)	4,416,096 / 21.71%
Duplication rate	56.47%
Clipped reads	917,308 / 4.51%

2.2. ACGT Content

Number/percentage of A's	222,354,230 / 29.06%
Number/percentage of C's	159,894,971 / 20.9%
Number/percentage of T's	223,175,058 / 29.17%
Number/percentage of G's	159,775,640 / 20.88%
Number/percentage of N's	62,224 / 0.01%
GC Percentage	41.78%

2.3. Coverage

Mean	31.9719
Standard Deviation	32.4335

2.4. Mapping Quality

Mean Mapping Quality	58.57

2.5. Insert size

Mean	992.27
Standard Deviation	29,396.13
P25/Median/P75	297 / 385 / 471

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	8,283,674
Insertions	203,269
Mapped reads with at least one insertion	2.41%
Deletions	264,648
Mapped reads with at least one deletion	3.14%
Homopolymer indels	63.29%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|107412047 8|emb|LT615 256.1|	977217	28791050	29.4623	16.0146
gi|107412068 2|emb|LT615 257.1|	860454	26343005	30.6152	21.4548
gi|107412086 5|emb|LT615 258.1|	989719	35603006	35.9728	41.1053
gi|107412108 6|emb|LT615 259.1|	935450	33197042	35.4878	47.0189
gi|107412130 1|emb|LT615 260.1|	1432239	46873907	32.7277	26.1318
gi|107412161 5|emb|LT615 261.1|	1080962	35400836	32.7494	26.6757
gi|107412187 1|emb|LT615 262.1|	1545099	47433146	30.6991	11.8843
gi|107412223 5|emb|LT615 263.1|	1585108	50208542	31.6752	25.6641
gi|107412259 0|emb|LT615 264.1|	2122358	65923341	31.0614	49.9102
gi|107412305 0|emb|LT615 265.1|	1754192	52961596	30.1914	42.8759
gi|107412342 1|emb|LT615	2150147	72939318	33.9229	48.4988

|				
266.1|				
gi|1074123898|emb|LT615267.1|	3031036	95755121	31.5915	20.565
gi|1074124588|emb|LT615268.1|	2359348	74973986	31.7774	32.4154
gi|1074125065|emb|LT615269.1|	3135668	99610356	31.7669	11.5956

3. Results : Coverage across reference
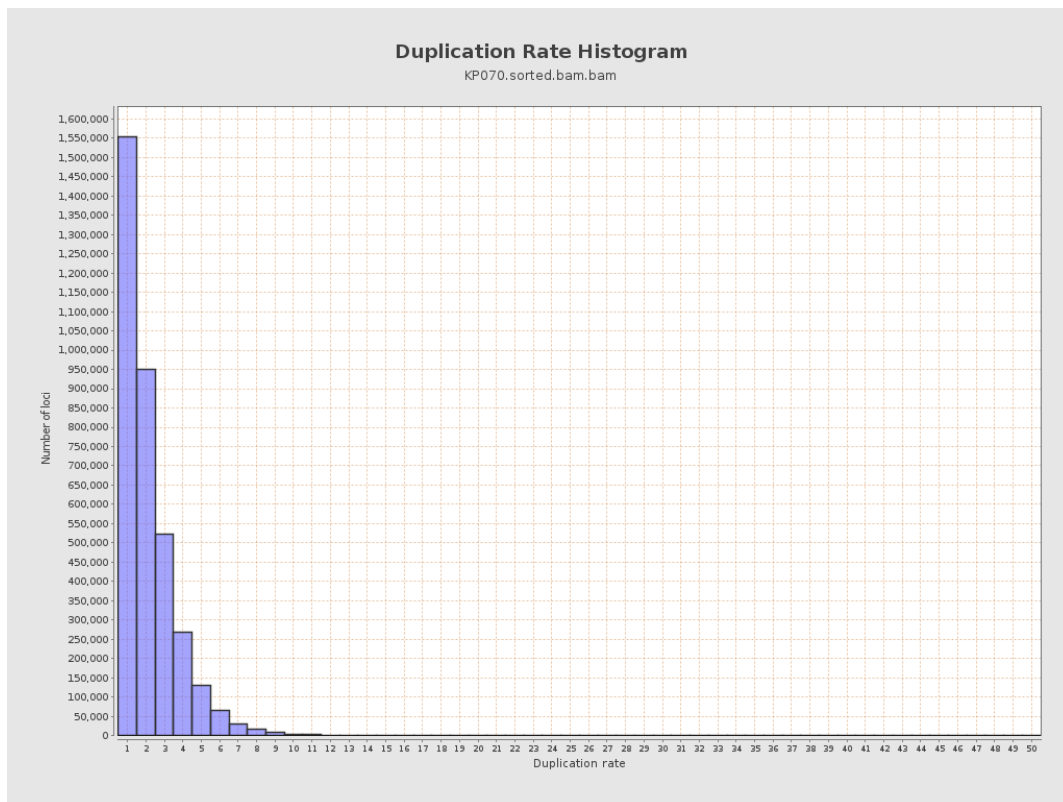
4. Results : Coverage Histogram

Coverage Histogram
KP070.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
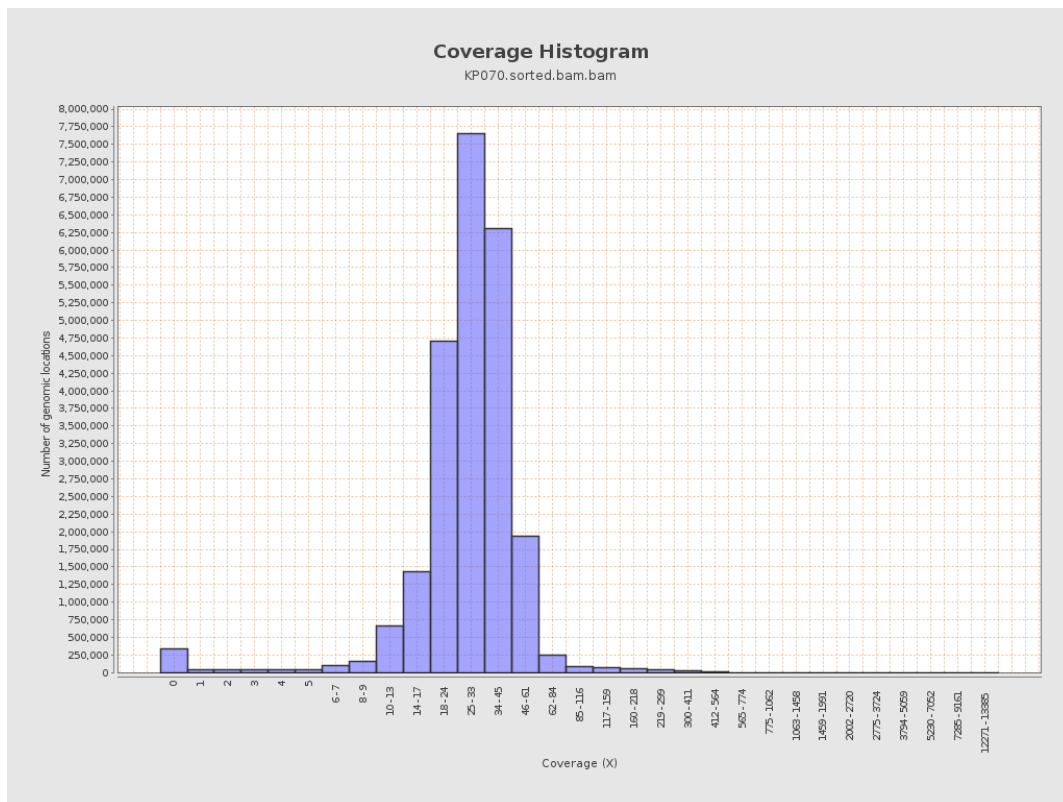
Coverage Histogram (0-50X)
KP070.sorted.bam.bam
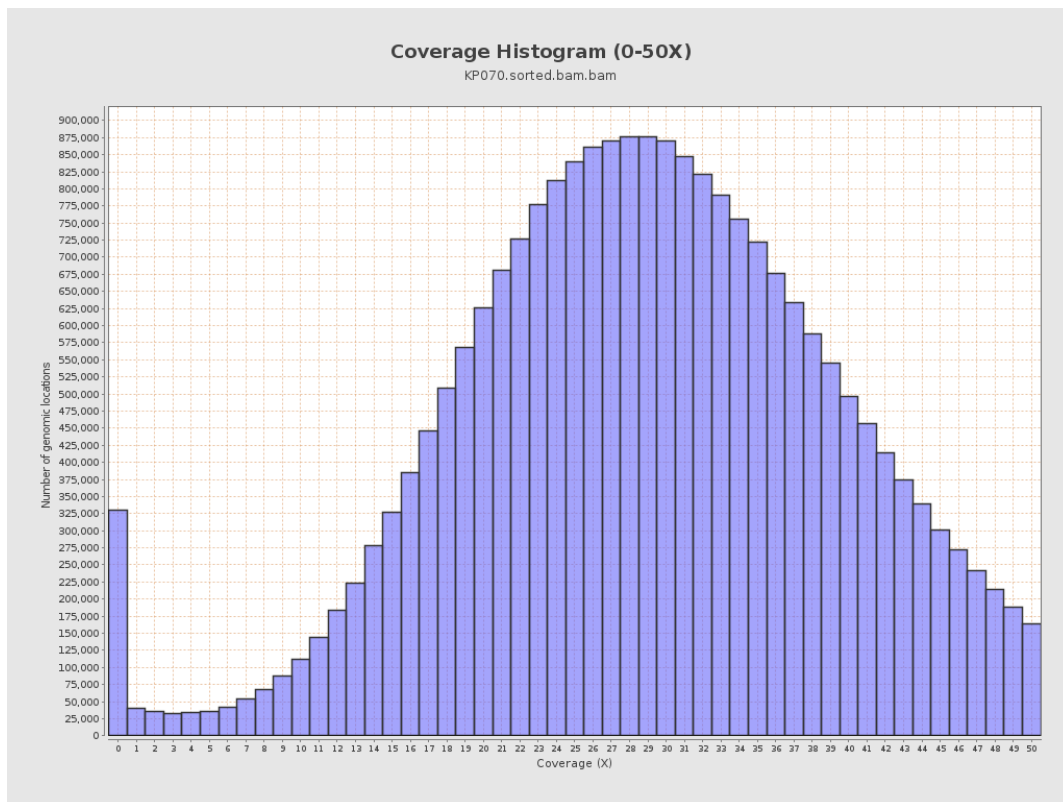
6. Results : Genome Fraction Coverage
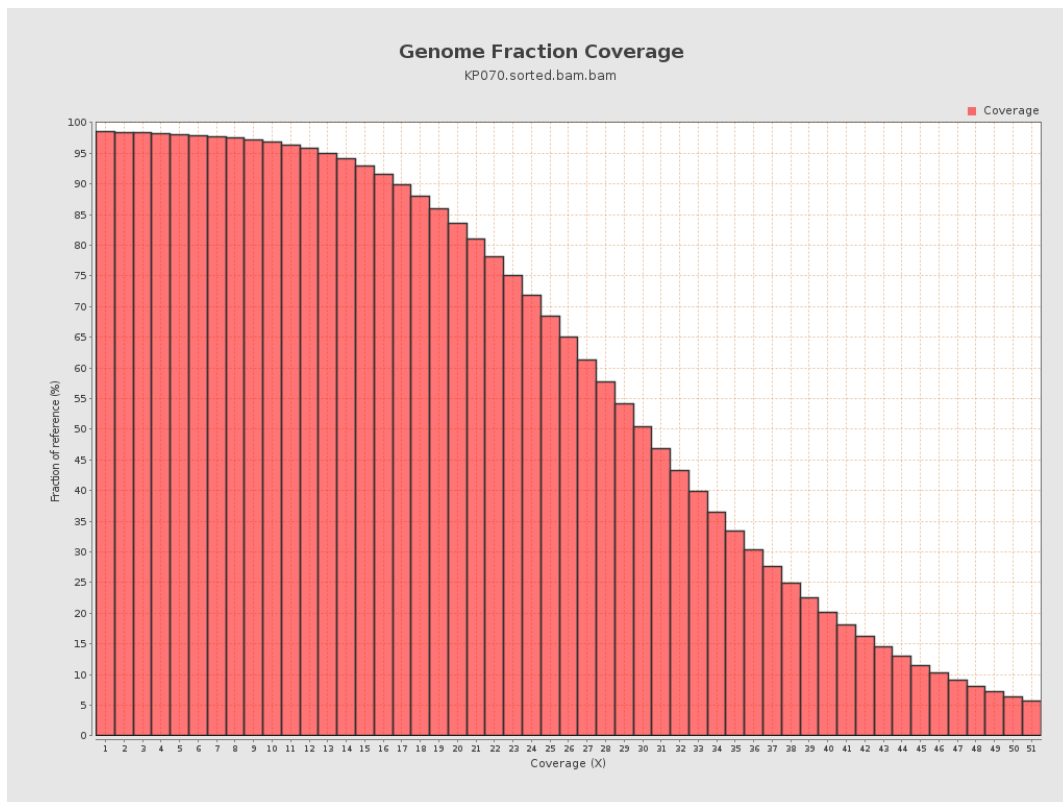
7. Results : Duplication Rate Histogram
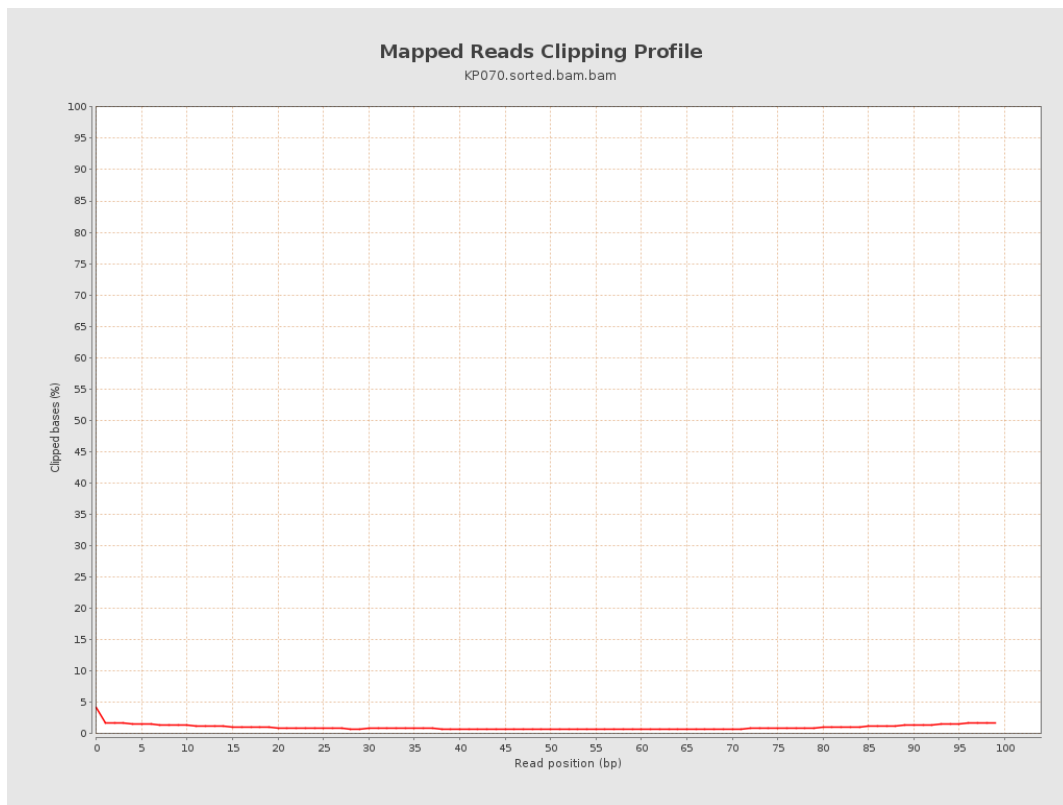

Duplication Rate Histogram
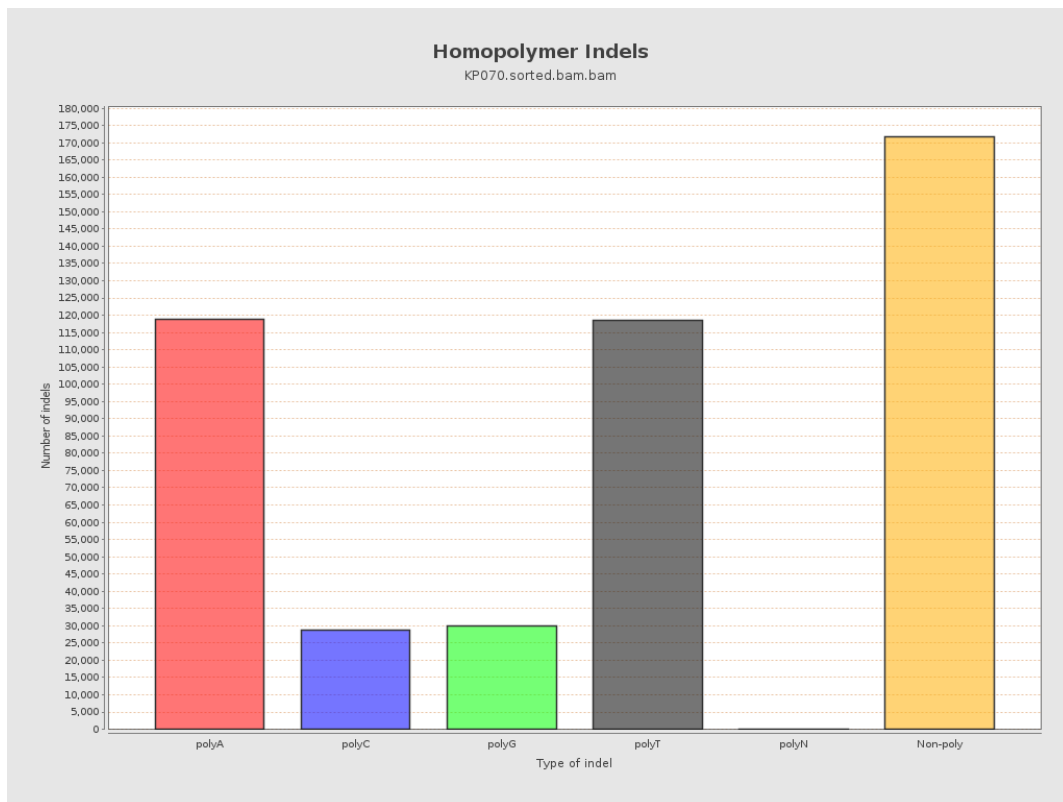KP070.sorted.bam.bam

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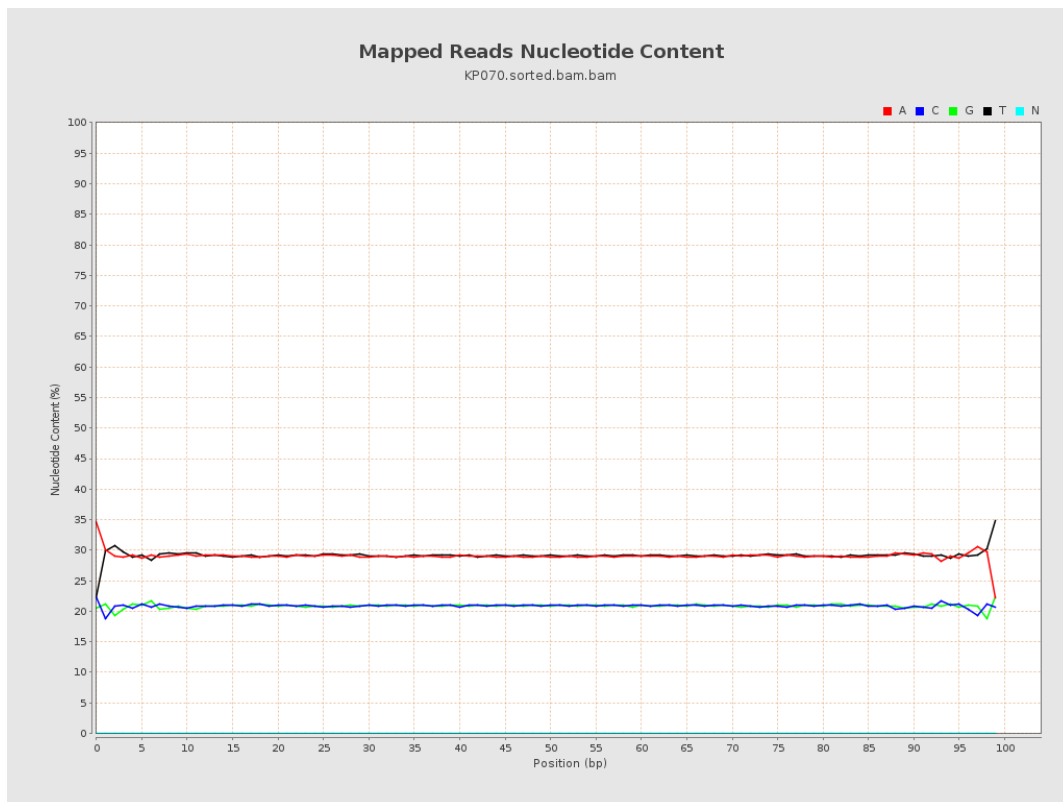
9. Results : Mapped Reads GC-content Distribution
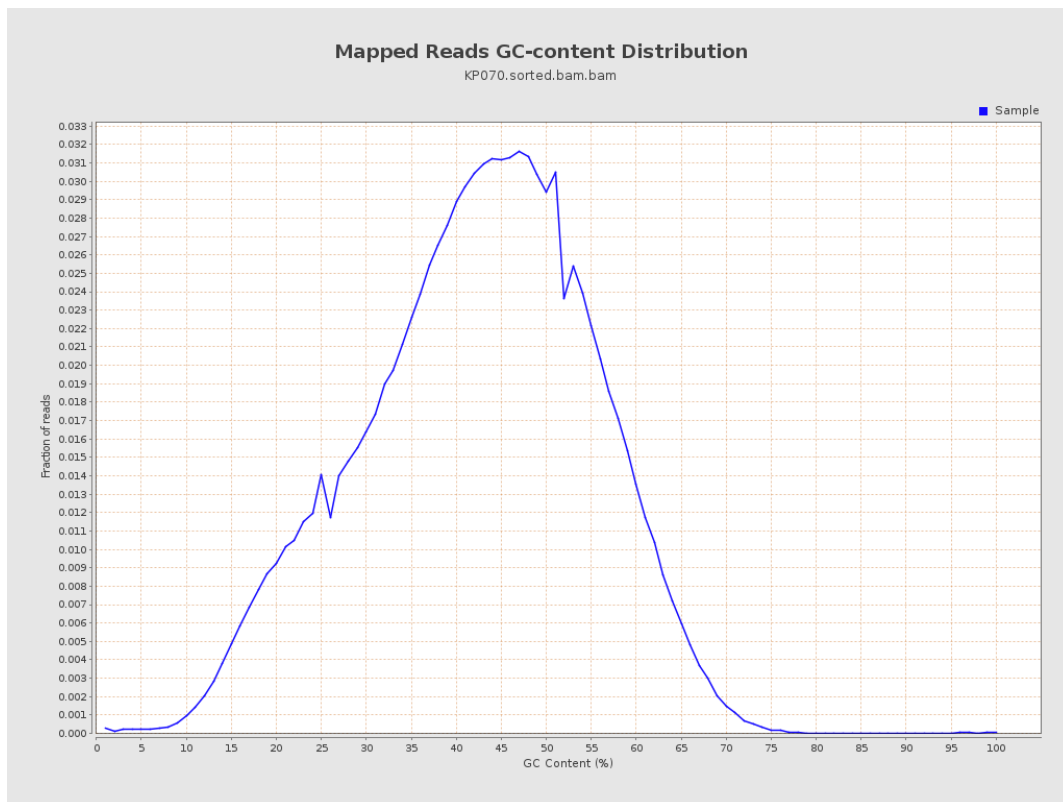
10. Results : Mapped Reads Clipping Profile

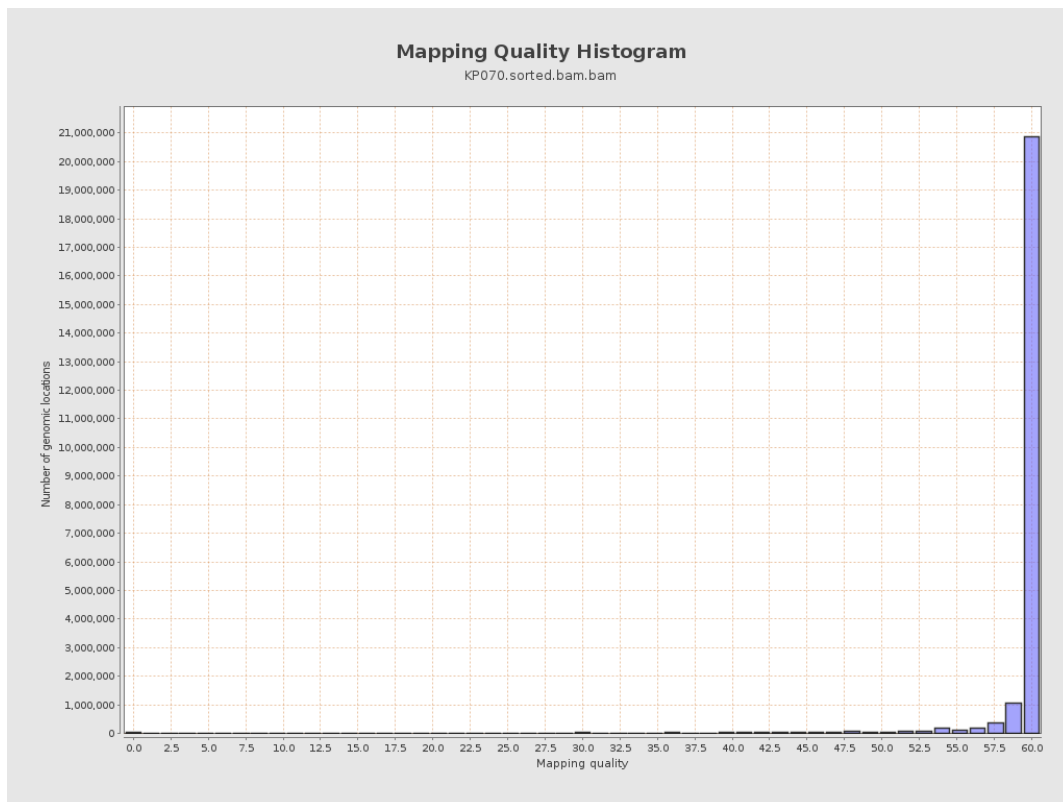
Mapped Reads Clipping Profile
KP070.sorted.bam.bam

11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
KP070.sorted.bam.bam

13. Results : Mapping Quality Histogram
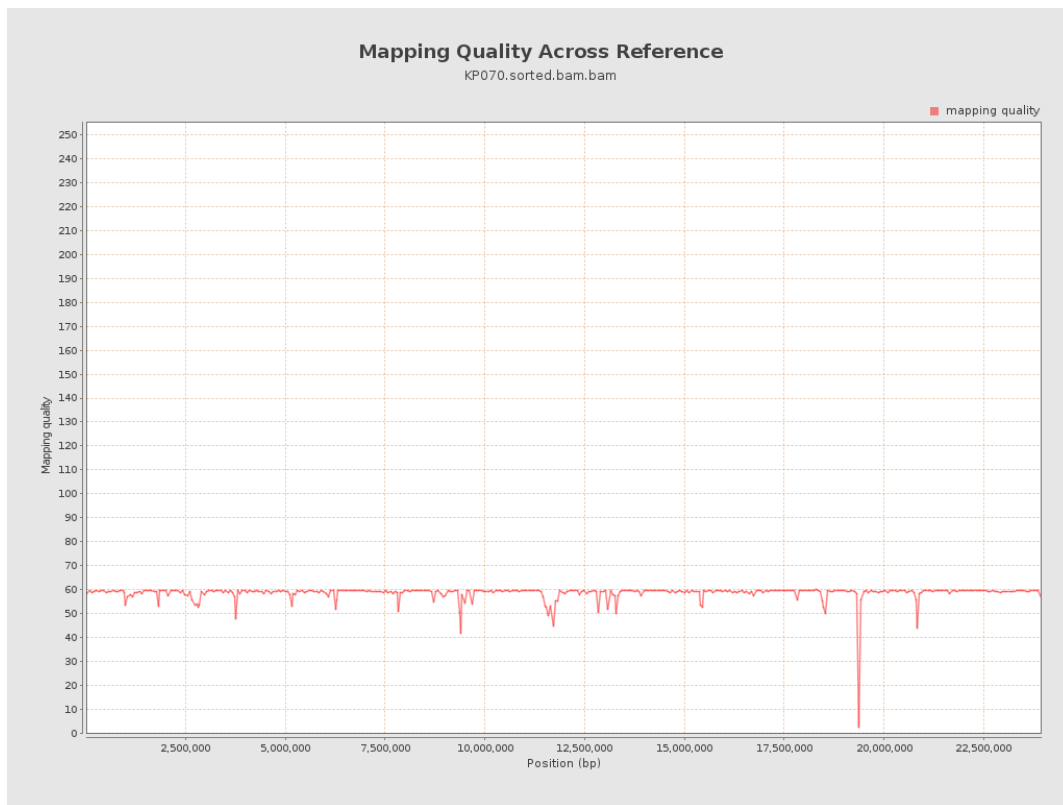
Mapping Quality Histogram
KP070.sorted.bam.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
KP070.sorted.bam.bam
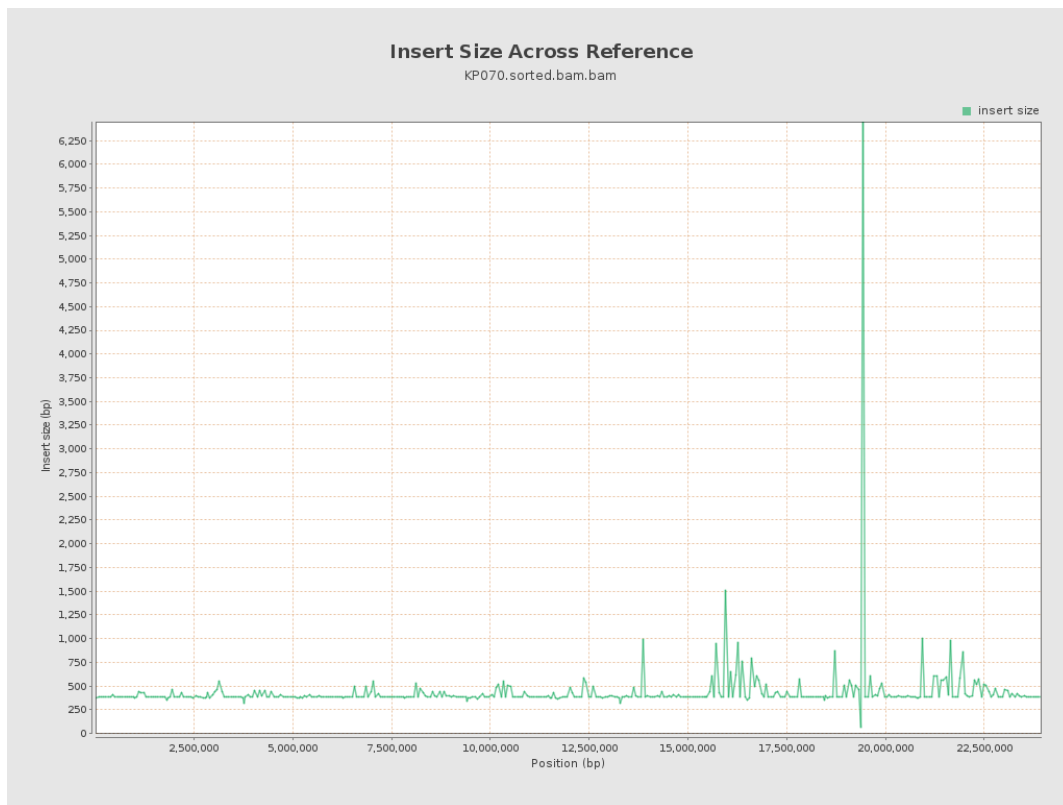
15. Results : Insert Size Histogram