Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 11:49:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/KP063.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/KP063-BiooBarcode_26_ATGAGC_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/KP063-BiooBarcode_26_ATGAGC_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:49:22 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/KP063.sorted.bam.b

am

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	16,783,434
Mapped reads	12,193,402 / 72.65%
Unmapped reads	4,590,032 / 27.35%
Mapped paired reads	12,193,402 / 72.65%
Mapped reads, first in pair	6,120,695 / 36.47%
Mapped reads, second in pair	6,072,707 / 36.18%
Mapped reads, both in pair	11,979,037 / 71.37%
Mapped reads, singletons	214,365 / 1.28%
Read min/max/mean length	30 / 100 / 99.82
Duplicated reads (estimated)	4,751,354 / 28.31%
Duplication rate	38.23%
Clipped reads	1,145,640 / 6.83%

2.2. ACGT Content

Number/percentage of A's	336,231,174 / 28.44%
Number/percentage of C's	254,652,589 / 21.54%
Number/percentage of T's	337,530,634 / 28.55%
Number/percentage of G's	253,982,976 / 21.48%
Number/percentage of N's	97,077 / 0.01%
GC Percentage	43.02%

2.3. Coverage

Mean	49.402
Standard Deviation	29.1005

2.4. Mapping Quality

Mean Mapping Quality	58.78

2.5. Insert size

Mean	1,424.55
Standard Deviation	37,890.68
P25/Median/P75	265 / 351 / 435

2.6. Mismatches and indels

| General error rate	0.96%
Mismatches	10,606,752
Insertions	276,370
Mapped reads with at least one insertion	2.17%
Deletions	370,292
Mapped reads with at least one deletion	2.9%
Homopolymer indels	66.55%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|107412047 8|emb|LT615 256.1|	977217	47011923	48.108	13.5715
gi|107412068 2|emb|LT615 257.1|	860454	41769077	48.5431	21.2179
gi|107412086 5|emb|LT615 258.1|	989719	51905270	52.4445	38.8305
gi|107412108 6|emb|LT615 259.1|	935450	48350391	51.6868	41.0102
gi|107412130 1|emb|LT615 260.1|	1432239	71693511	50.0569	23.1607
gi|107412161 5|emb|LT615 261.1|	1080962	55356590	51.2105	24.6774
gi|107412187 1|emb|LT615 262.1|	1545099	75848694	49.0899	14.8901
gi|107412223 5|emb|LT615 263.1|	1585108	80099849	50.5327	25.7661
gi|107412259 0|emb|LT615 264.1|	2122358	103347097	48.6945	17.9935
gi|107412305 0|emb|LT615 265.1|	1754192	83857734	47.8042	26.6795
gi|107412342 1|emb|LT615	2150147	110121666	51.2159	63.3323

|				
266.1|				
gi|1074123898|emb|LT615267.1|	3031036	149519381	49.3295	15.1771
gi|1074124588|emb|LT615268.1|	2359348	109275267	46.3159	29.513
gi|1074125065|emb|LT615269.1|	3135668	155466304	49.58	12.167

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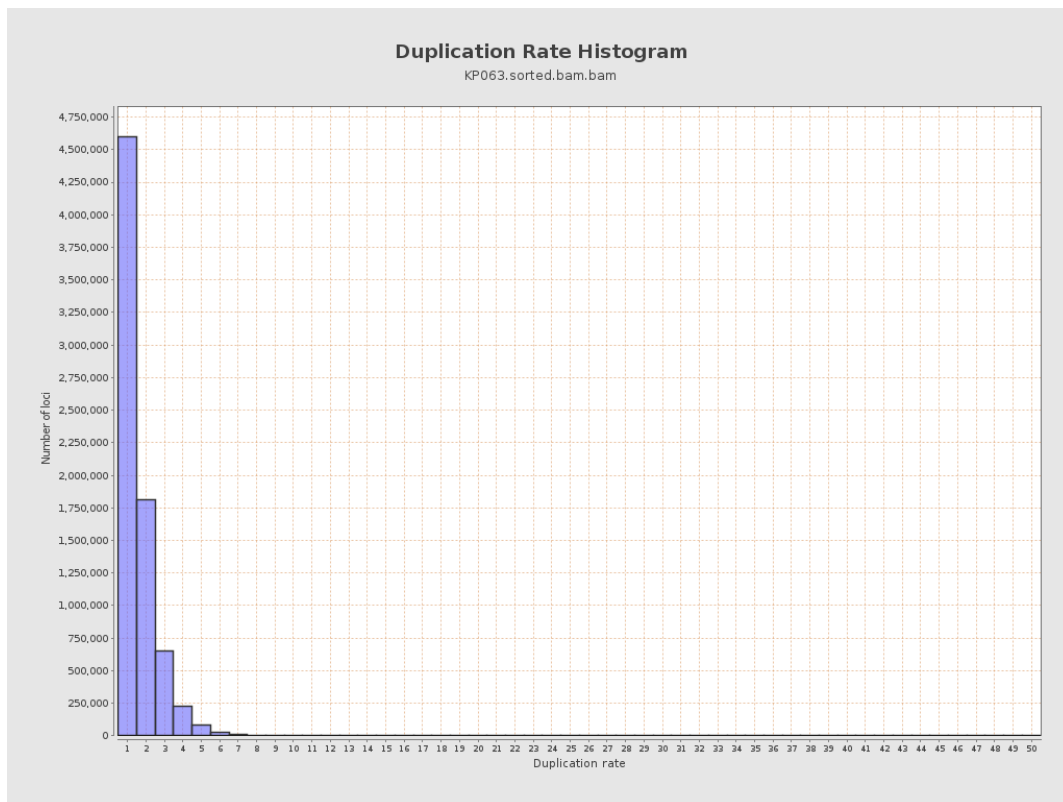
4. Results : Coverage Histogram

Coverage Histogram
KP063.sorted.bam.bam
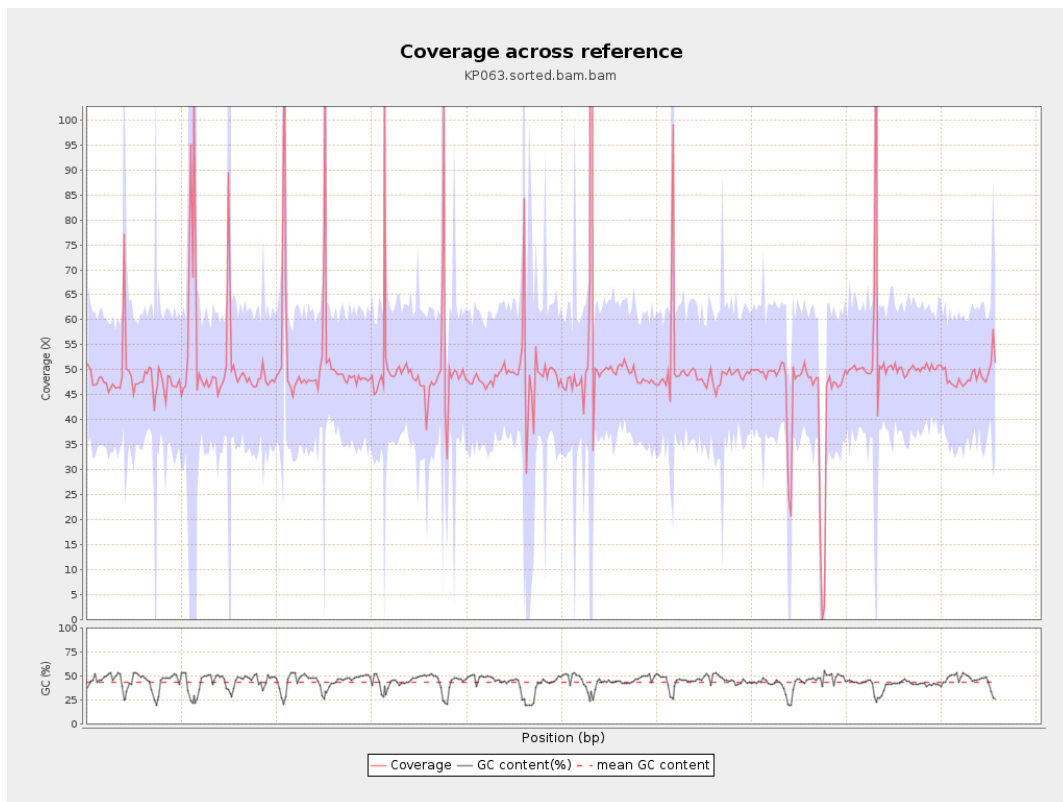
5. Results : Coverage Histogram (0-50X)
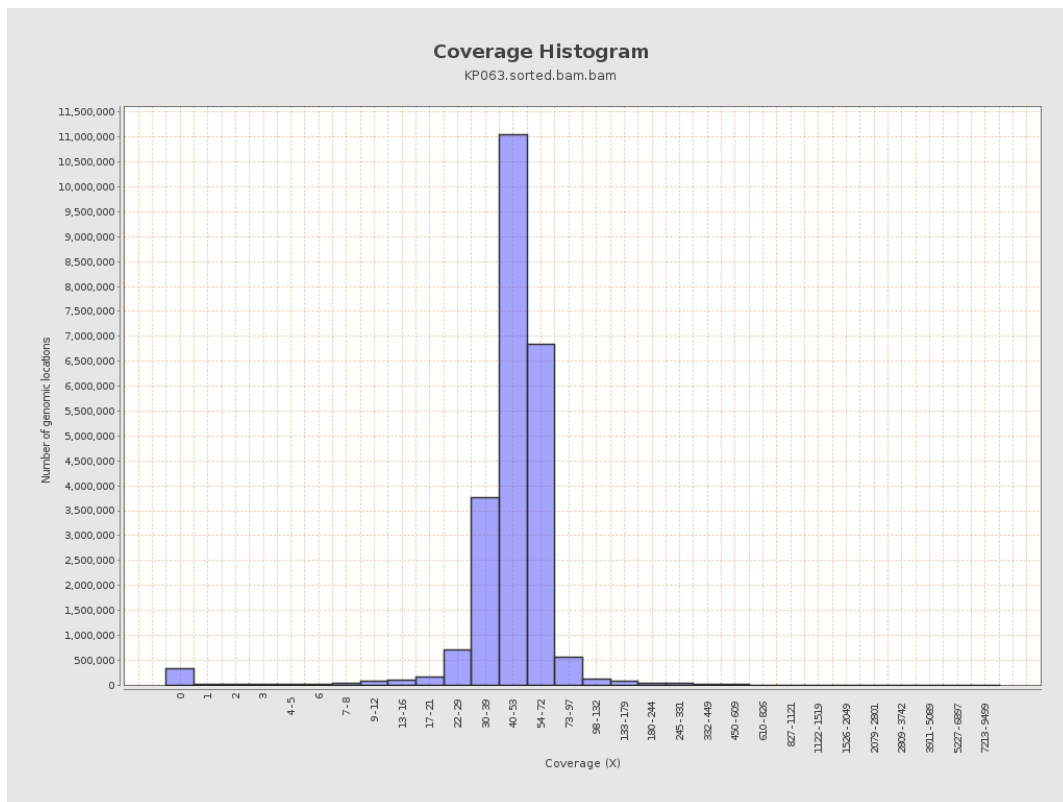
Coverage Histogram (0-50X)
KP063.sorted.bam.bam
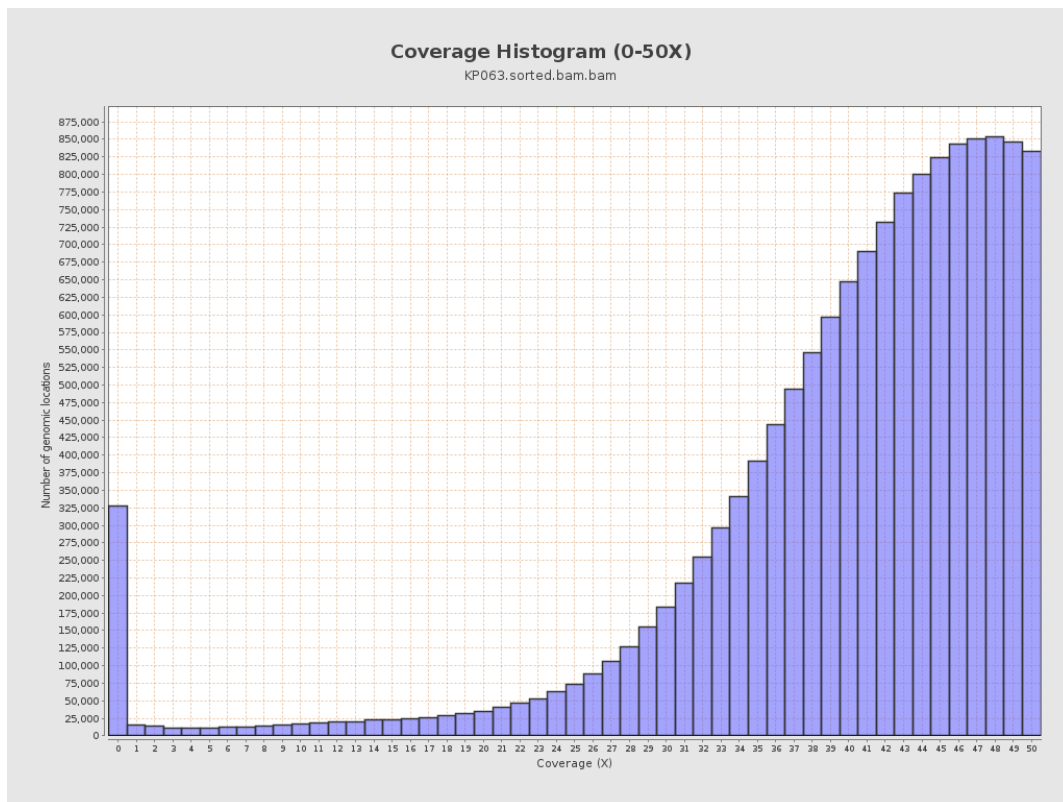
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
KP063.sorted.bam.bam
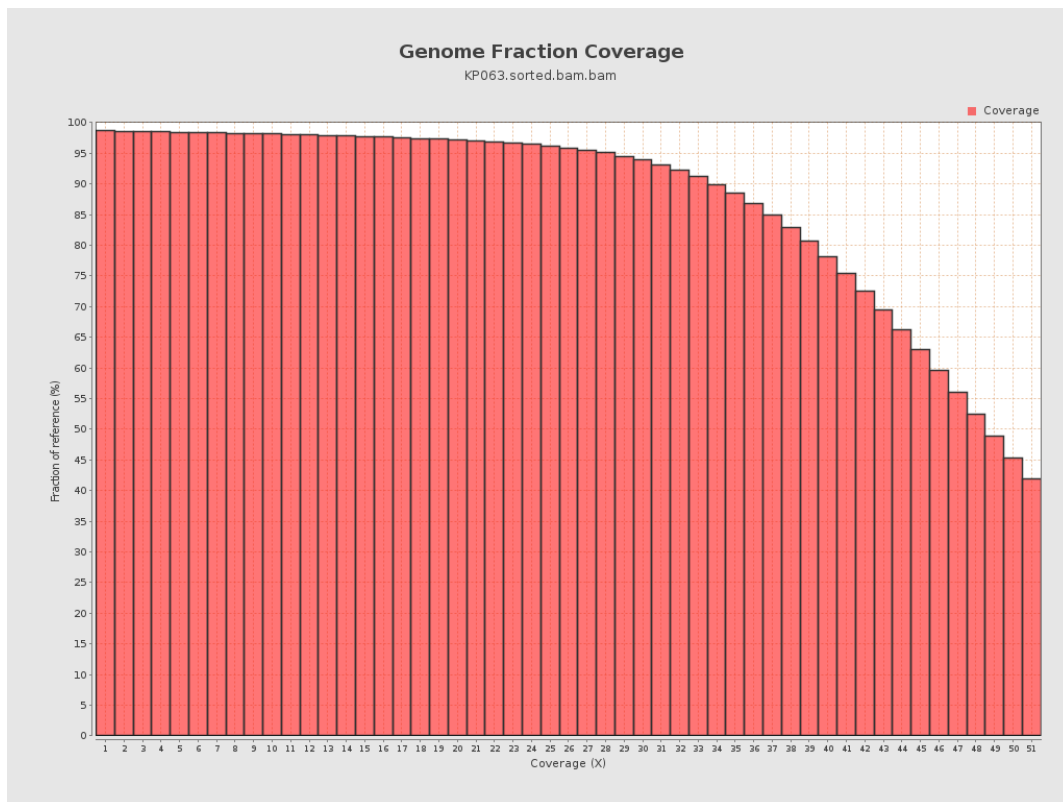
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
KP063.sorted.bam.bam

8. Results : Mapped Reads Nucleotide Content
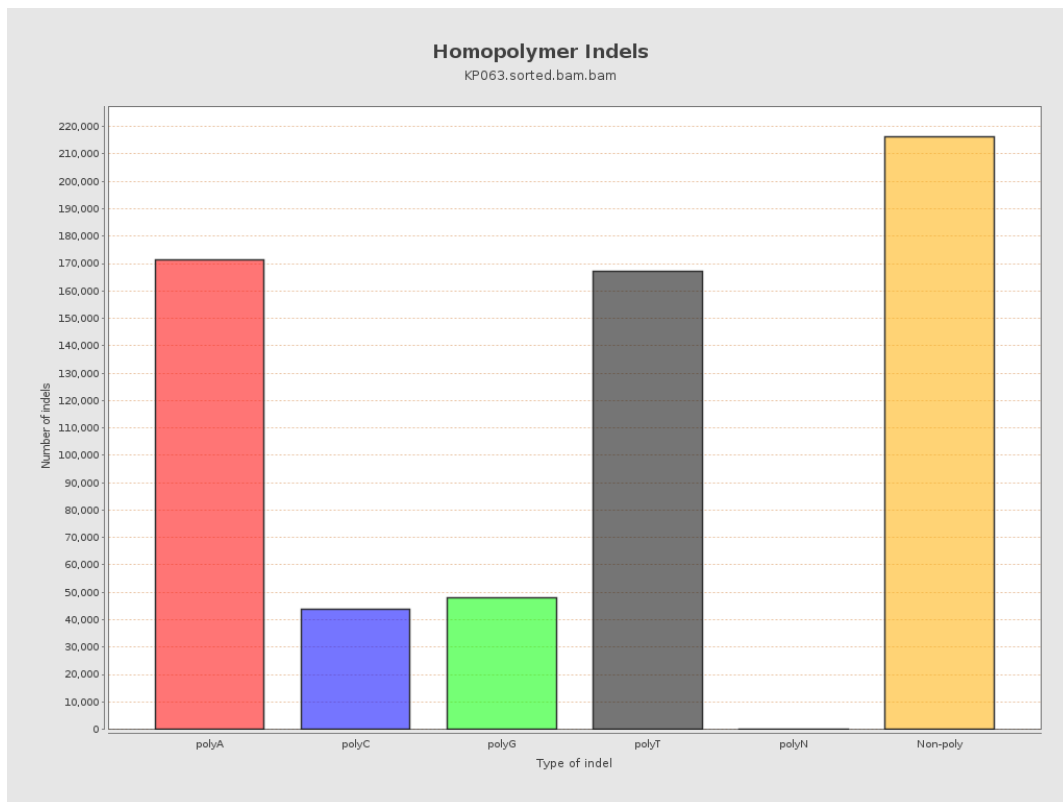

Mapped Reads Nucleotide Content
KP063.sorted.bam.bam
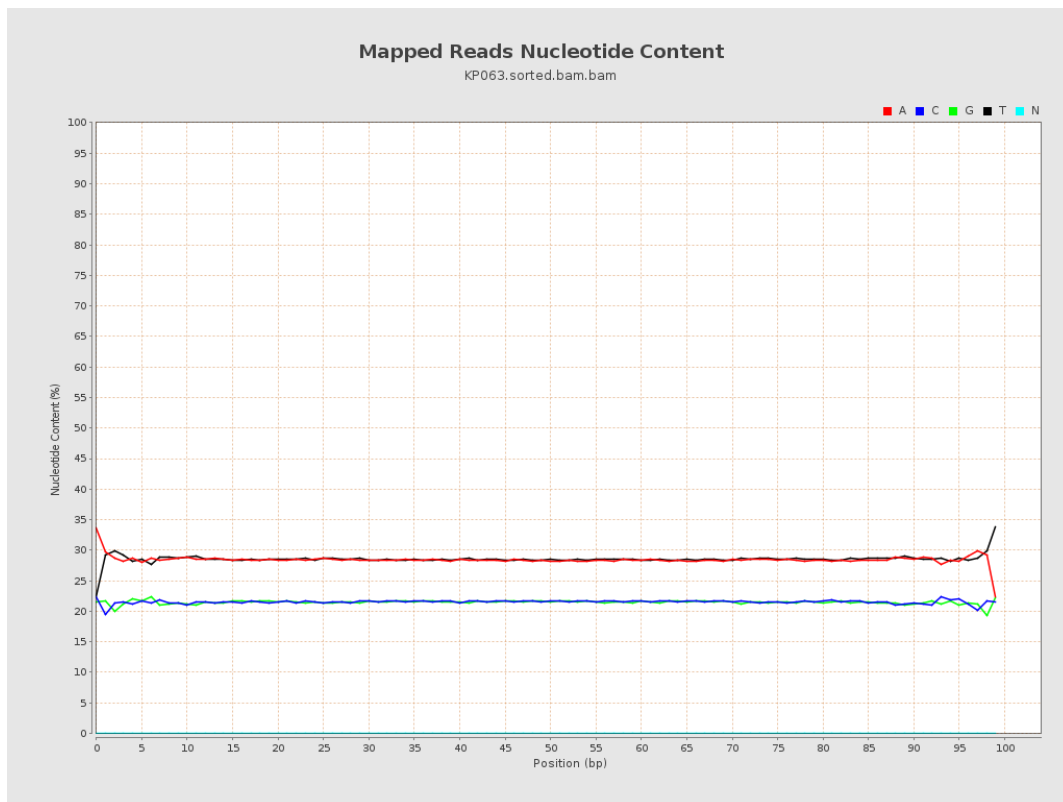
9. Results : Mapped Reads GC-content Distribution
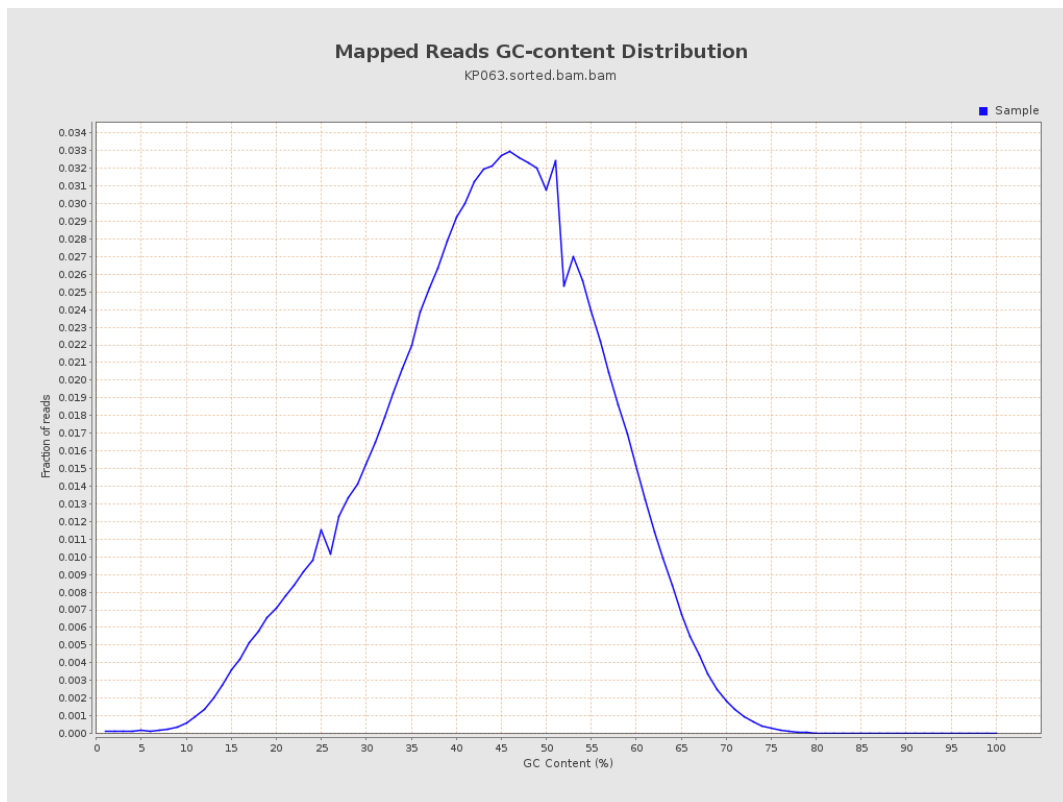
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
KP063.sorted.bam.bam
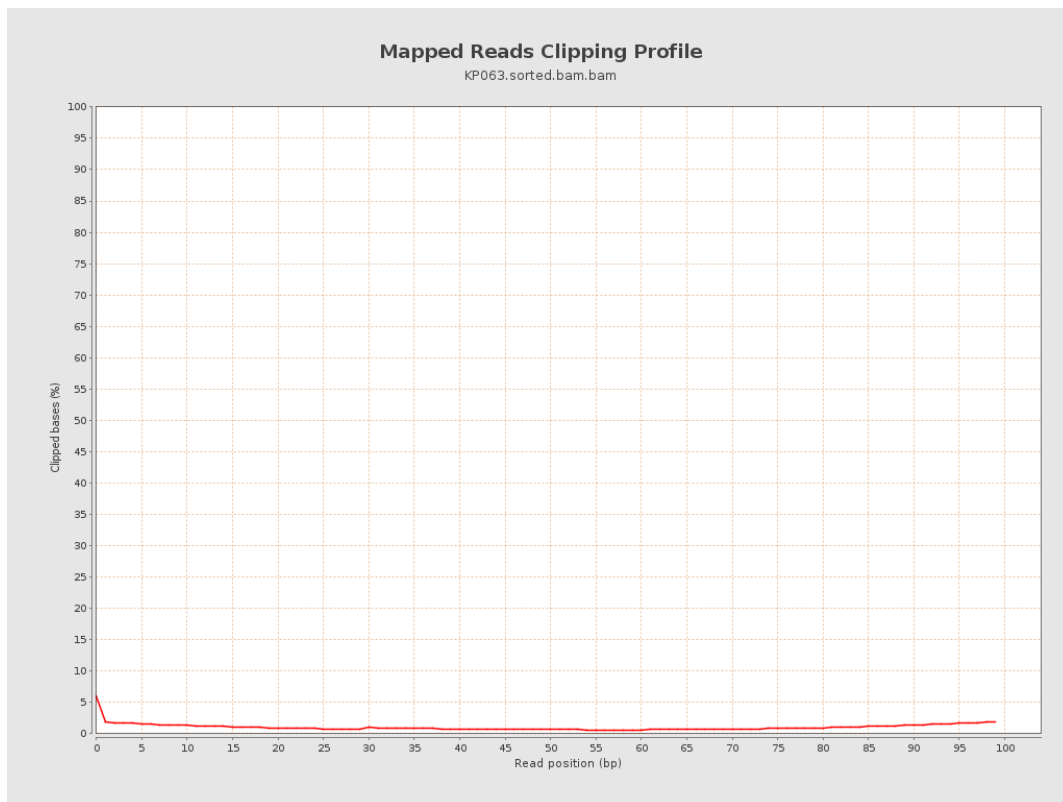
11. Results : Homopolymer Indels

Homopolymer Indels
KP063.sorted.bam.bam

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram
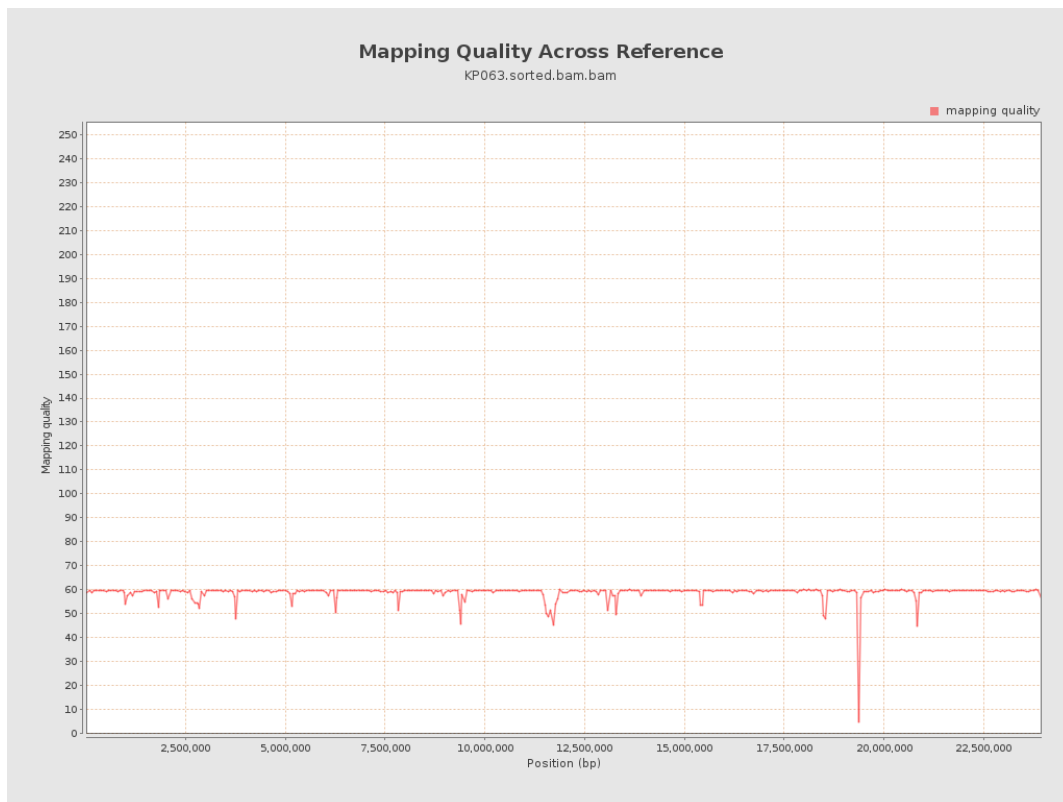
Mapping Quality Histogram
KP063.sorted.bam.bam
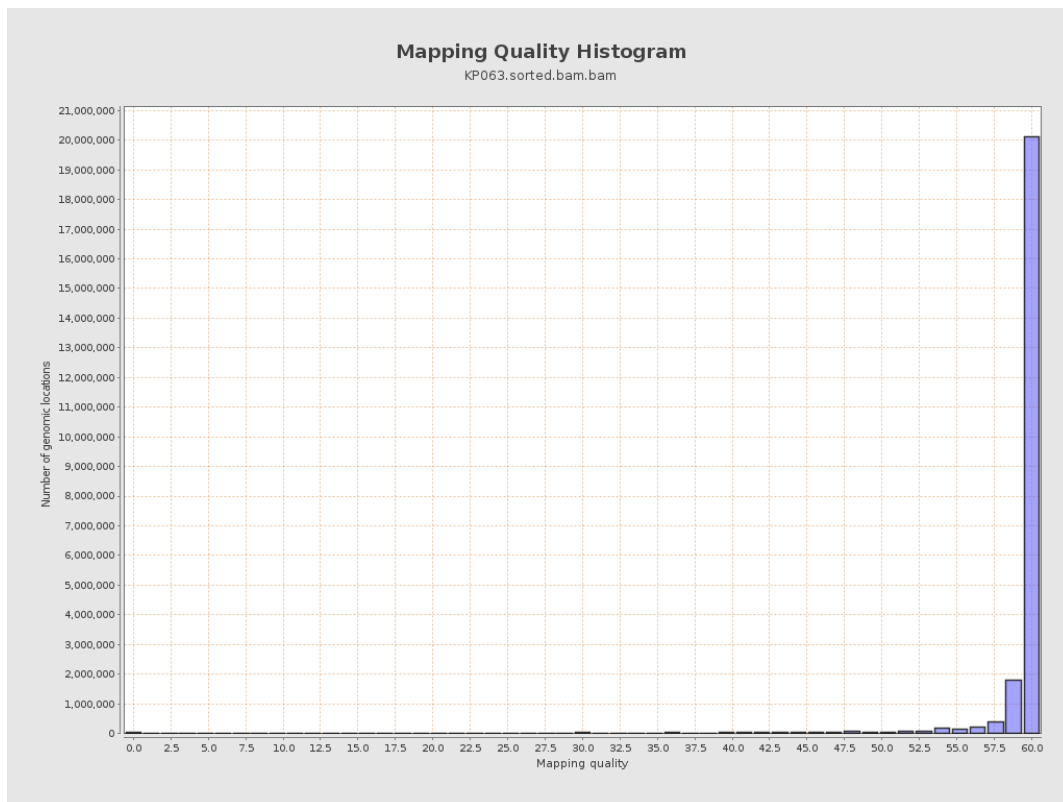
14. Results : Insert Size Across Reference

Insert Size Across Reference
KP063.sorted.bam.bam
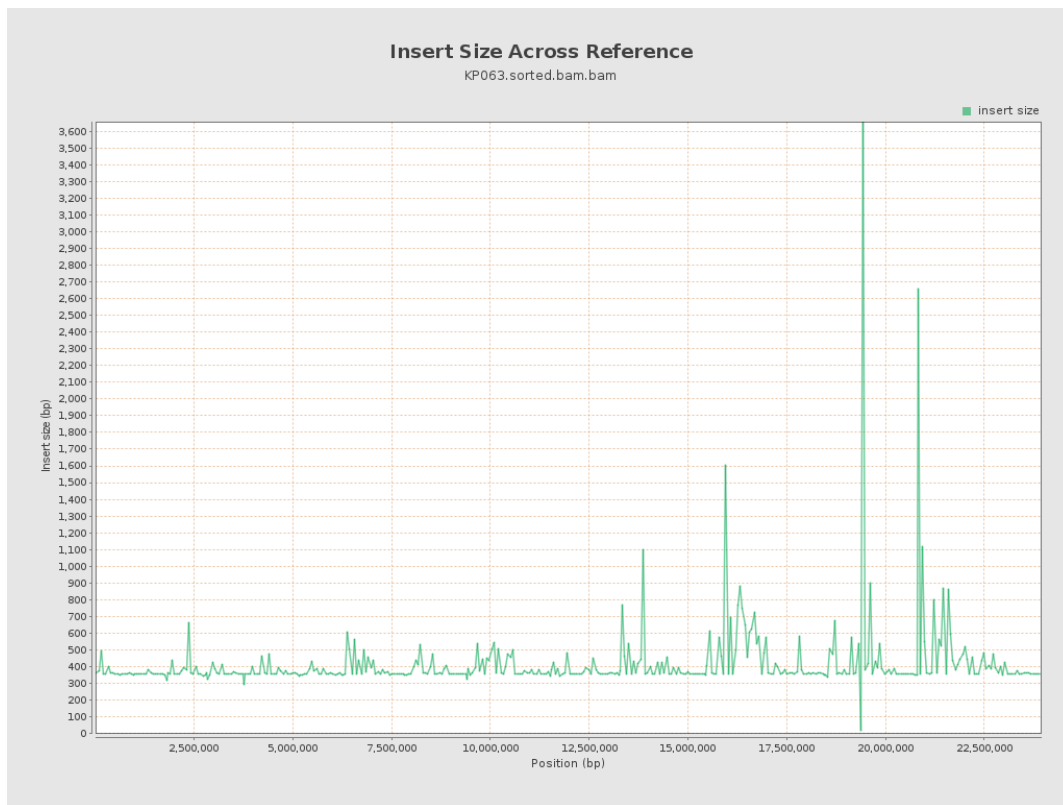
15. Results : Insert Size Histogram

Insert Size Histogram
KP063.sorted.bam.bam