Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 11:42:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/KP014.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/KP014-BiooBarcode_22_CGTACG_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/KP014-BiooBarcode_22_CGTACG_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:42:02 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/KP014.sorted.bam.b

	am

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	14,550,393
Mapped reads	9,901,431 / 68.05%
Unmapped reads	4,648,962 / 31.95%
Mapped paired reads	9,901,431 / 68.05%
Mapped reads, first in pair	4,920,657 / 33.82%
Mapped reads, second in pair	4,980,774 / 34.23%
Mapped reads, both in pair	9,685,312 / 66.56%
Mapped reads, singletons	216,119 / 1.49%
Read min/max/mean length	30 / 100 / 99.87
Duplicated reads (estimated)	3,581,045 / 24.61%
Duplication rate	34.48%
Clipped reads	960,114 / 6.6%

2.2. ACGT Content

Number/percentage of A's	275,174,891 / 28.69%
Number/percentage of C's	204,056,940 / 21.28%
Number/percentage of T's	276,234,909 / 28.8%
Number/percentage of G's	203,526,967 / 21.22%
Number/percentage of N's	80,208 / 0.01%
GC Percentage	42.5%

2.3. Coverage

Mean	40.0696
Standard Deviation	27.8506

2.4. Mapping Quality

Mean Mapping Quality	58.76

2.5. Insert size

Mean	1,333.97
Standard Deviation	34,841.81
P25/Median/P75	311 / 399 / 491

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	9,631,633
Insertions	242,167
Mapped reads with at least one insertion	2.33%
Deletions	319,773
Mapped reads with at least one deletion	3.08%
Homopolymer indels	65.78%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	38107030	38.9955	18.1432
gi|1074120682|emb|LT615257.1|	860454	34867557	40.5223	24.8451
gi|1074120865|emb|LT615258.1|	989719	43297043	43.7468	48.7175
gi|1074121086|emb|LT615259.1|	935450	38977455	41.6671	44.9462
gi|1074121301|emb|LT615260.1|	1432239	56873194	39.7093	21.0011
gi|1074121615|emb|LT615261.1|	1080962	43457344	40.2025	23.6398
gi|1074121871|emb|LT615262.1|	1545099	60238979	38.9871	10.4374
gi|1074122235|emb|LT615263.1|	1585108	63273020	39.9172	17.9835
gi|1074122590|emb|LT615264.1|	2122358	82867673	39.0451	15.2917
gi|1074123050|emb|LT615265.1|	1754192	69937747	39.8689	31.2648
gi|1074123421|emb|LT615	2150147	91400330	42.5089	54.3466

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	119744976	39.5063	12.495
gi|1074124588|emb|LT615268.1|	2359348	91935174	38.9663	30.4582
gi|1074125065|emb|LT615269.1|	3135668	125049483	39.8797	10.0093

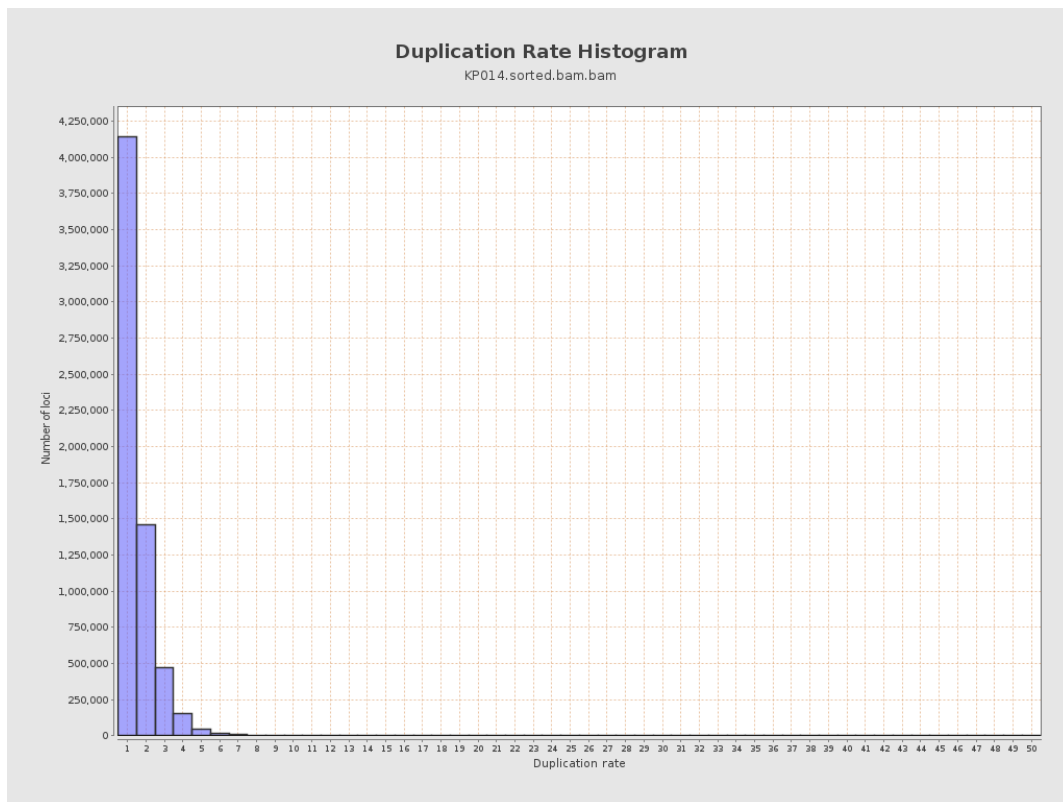# 3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
KP014.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
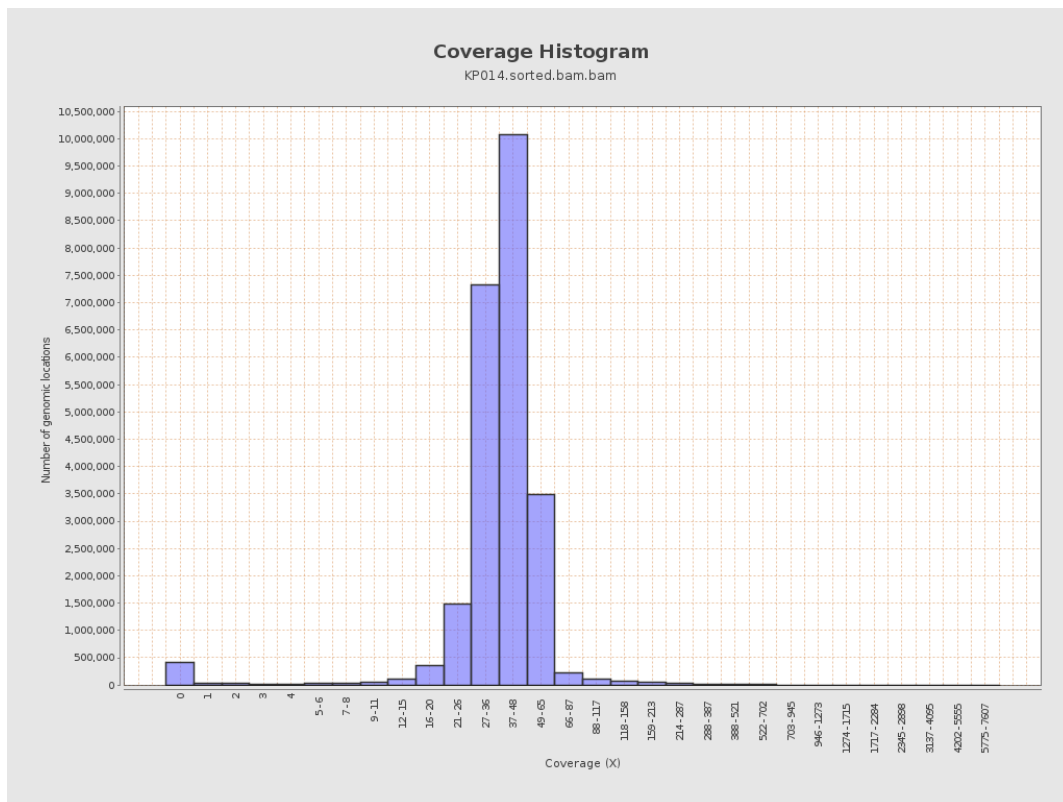
Coverage Histogram (0-50X)
KP014.sorted.bam.bam
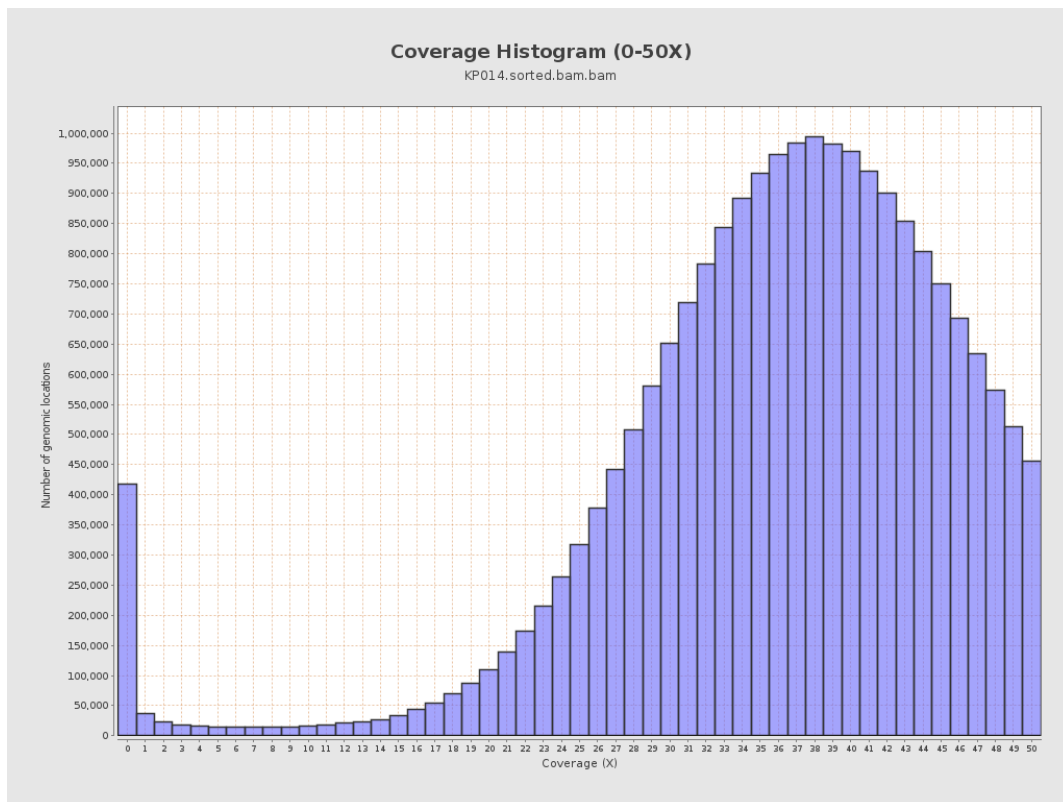
6. Results : Genome Fraction Coverage

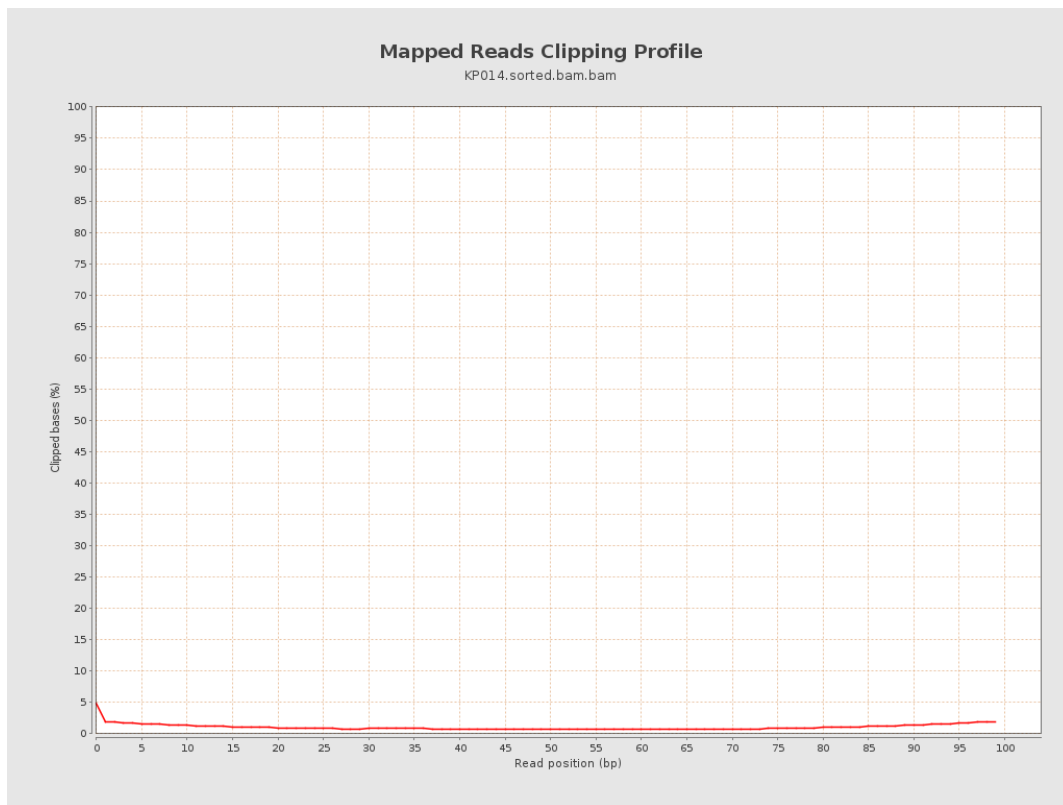

Genome Fraction Coverage
KP014.sorted.bam.bam
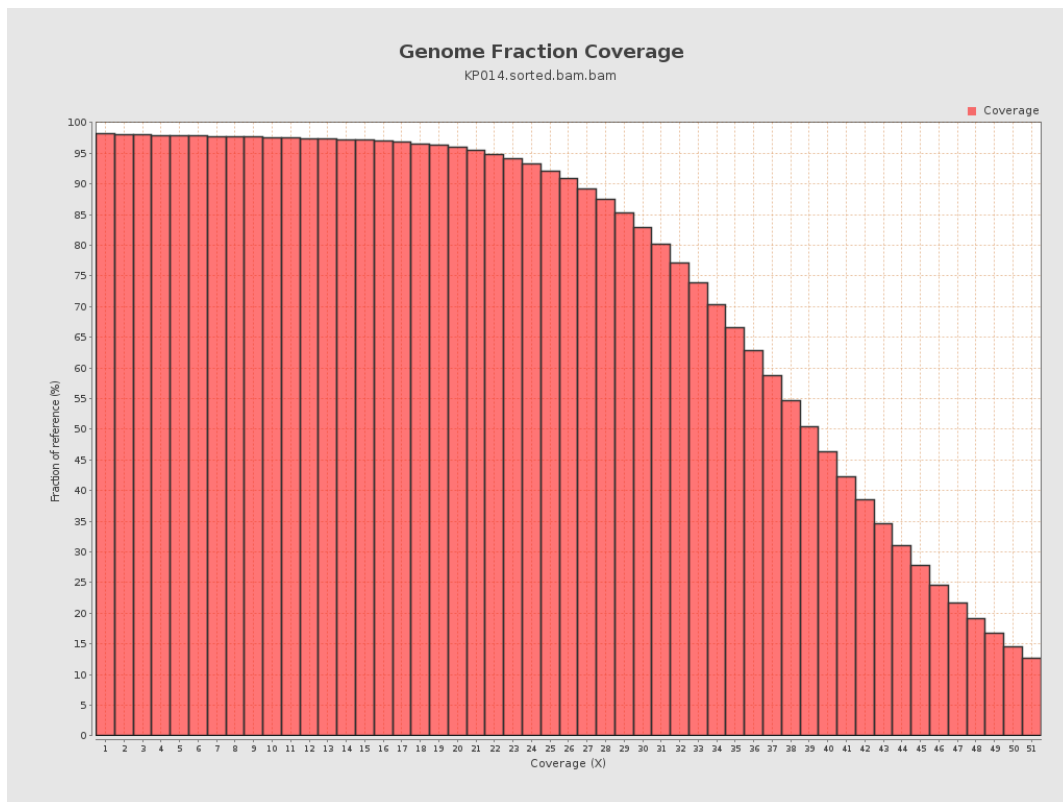
7. Results : Duplication Rate Histogram

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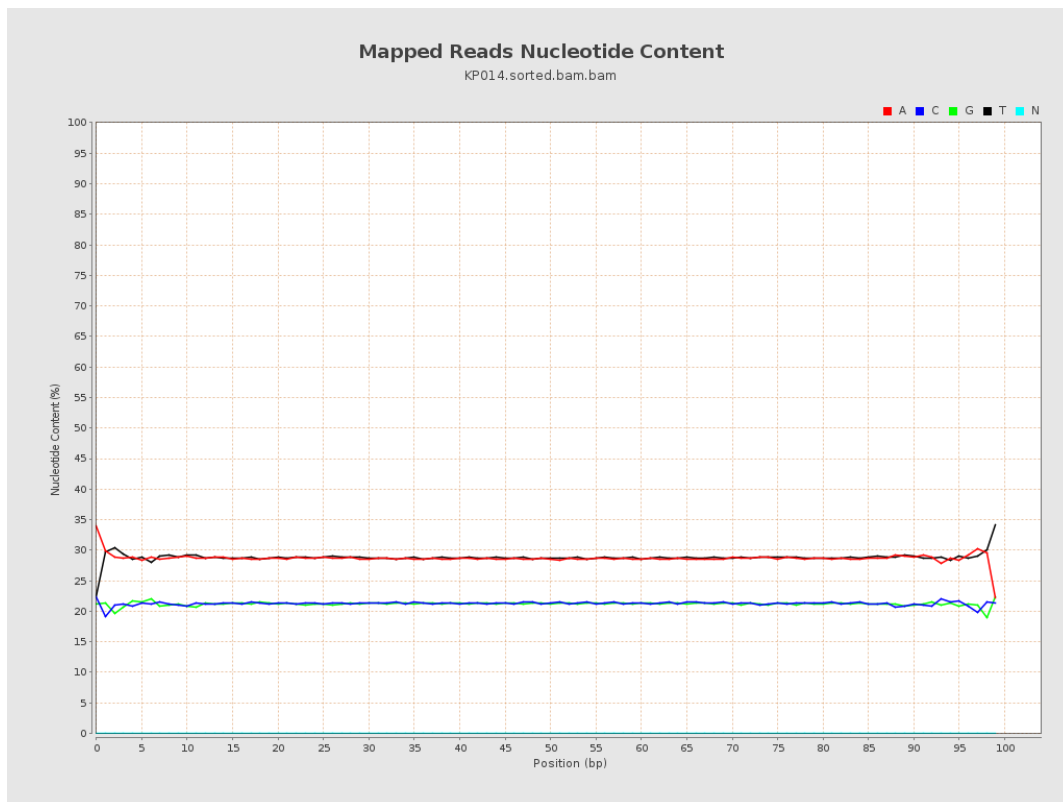
9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
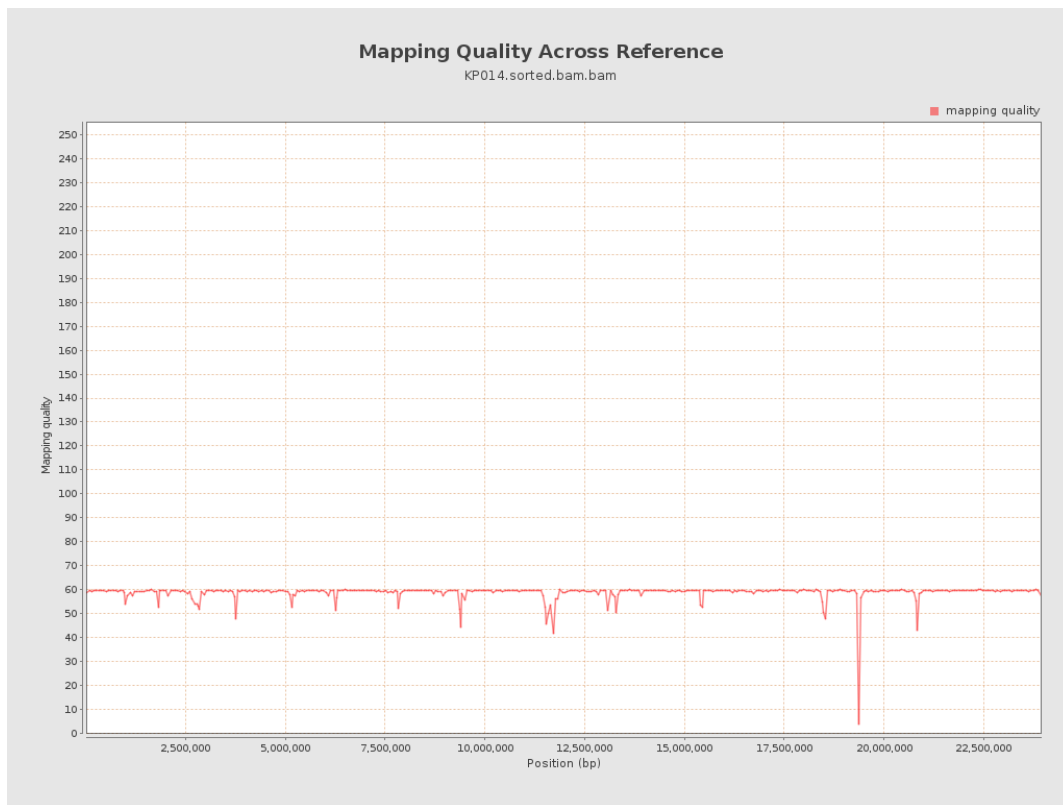KP014.sorted.bam.bam
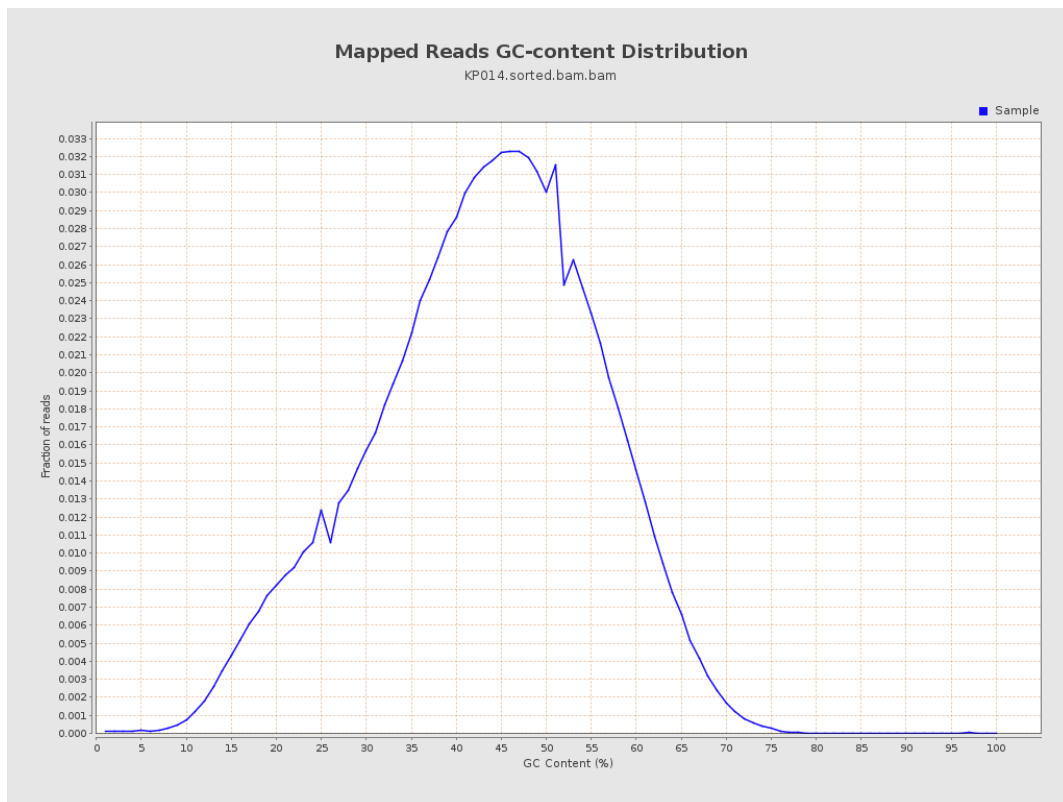
10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels
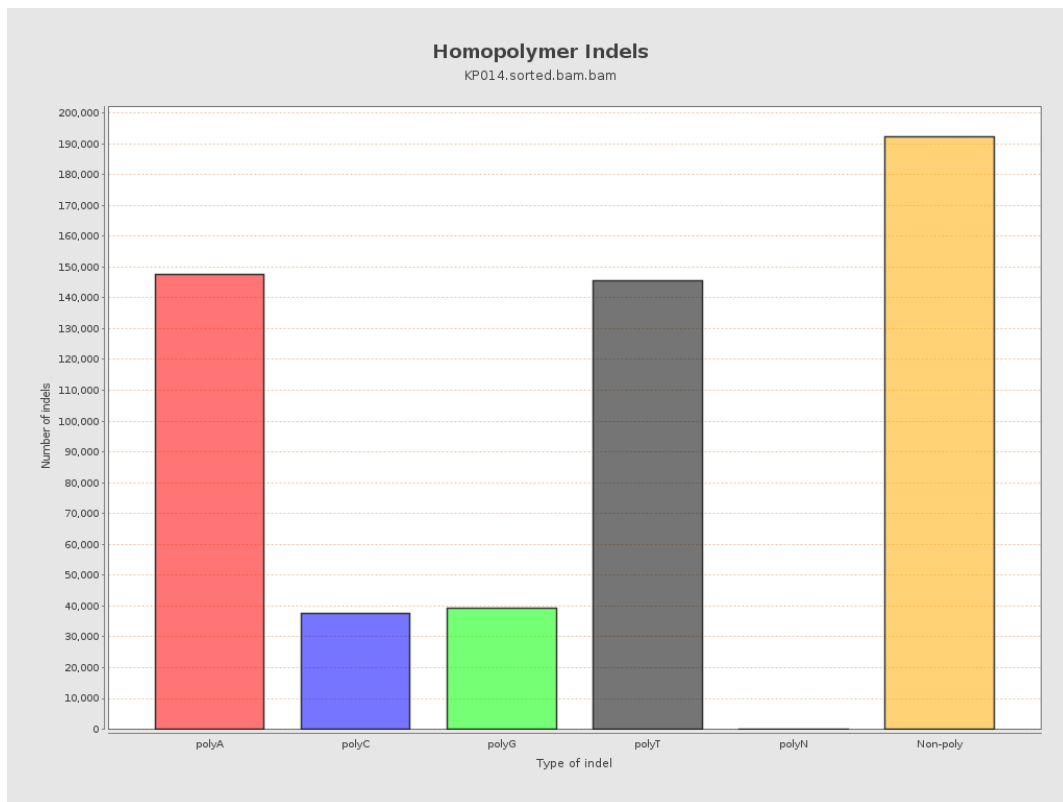
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
KP014.sorted.bam.bam
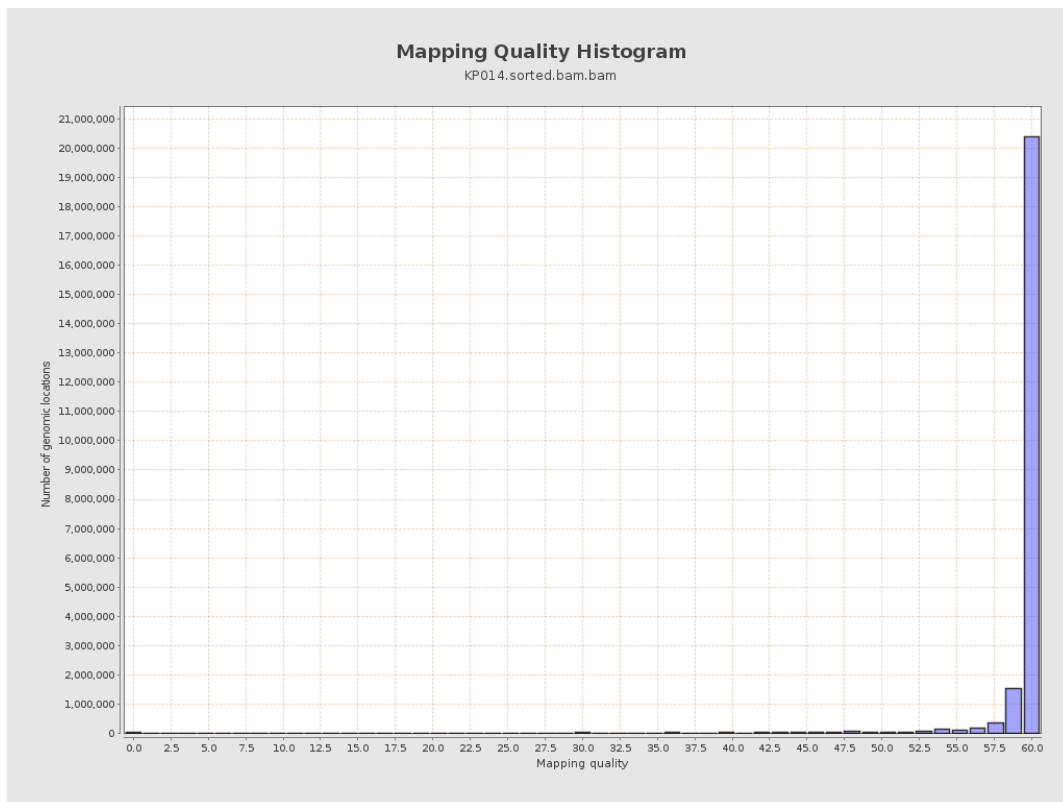
14. Results : Insert Size Across Reference

Insert Size Across Reference
KP014.sorted.bam.bam
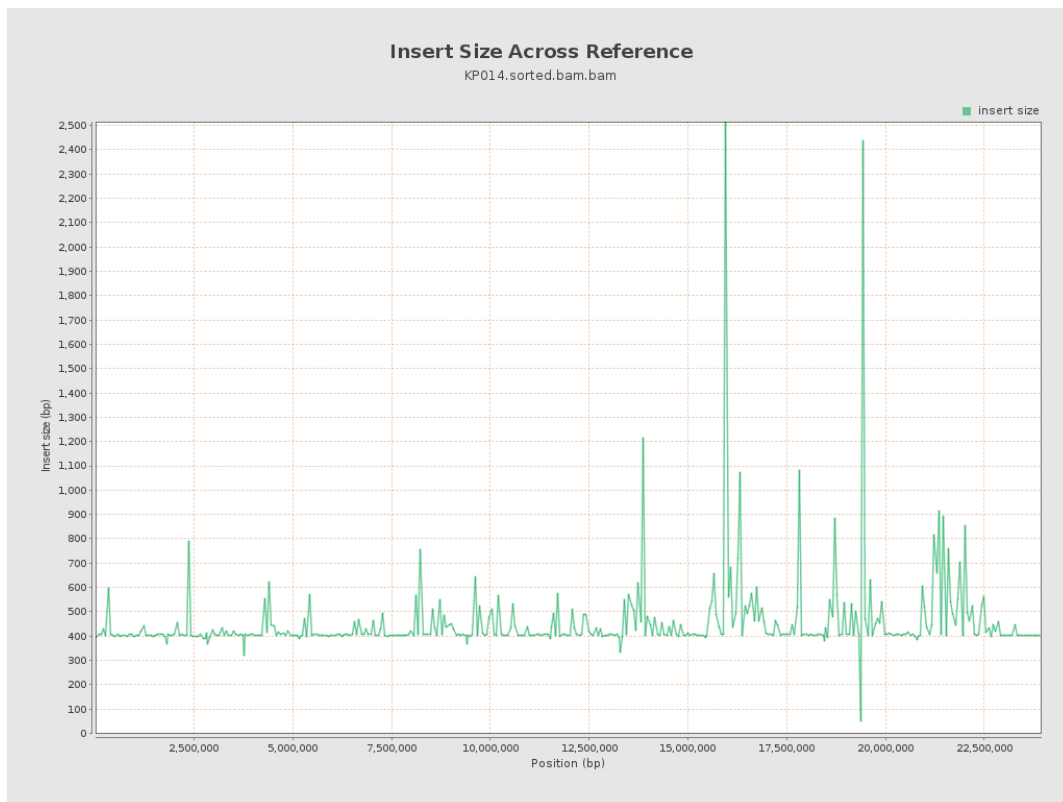
15. Results : Insert Size Histogram

Insert Size Histogram
KP014.sorted.bam.bam