Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 11:55:58

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/KP076.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/KP076-BiooBarcode_30_CACCGG_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/KP076-BiooBarcode_30_CACCGG_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:55:57 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/KP076.sorted.bam.b

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	21,557,260
Mapped reads	9,907,308 / 45.96%
Unmapped reads	11,649,952 / 54.04%
Mapped paired reads	9,907,308 / 45.96%
Mapped reads, first in pair	4,981,208 / 23.11%
Mapped reads, second in pair	4,926,100 / 22.85%
Mapped reads, both in pair	9,695,753 / 44.98%
Mapped reads, singletons	211,555 / 0.98%
Read min/max/mean length	30 / 100 / 99.9
Duplicated reads (estimated)	4,333,661 / 20.1%
Duplication rate	44.31%
Clipped reads	859,006 / 3.98%

2.2. ACGT Content

Number/percentage of A's	263,839,654 / 27.49%
Number/percentage of C's	215,898,102 / 22.49%
Number/percentage of T's	264,804,389 / 27.59%
Number/percentage of G's	215,271,773 / 22.43%
Number/percentage of N's	81,248 / 0.01%
GC Percentage	44.92%

2.3. Coverage

Mean	40.1015
Standard Deviation	33.9921

2.4. Mapping Quality

Mean Mapping Quality	58.48

2.5. Insert size

Mean	873.72
Standard Deviation	25,800.7
P25/Median/P75	261 / 344 / 426

2.6. Mismatches and indels

General error rate	0.74%
Mismatches	6,526,202
Insertions	190,391
Mapped reads with at least one insertion	1.83%
Deletions	260,641
Mapped reads with at least one deletion	2.52%
Homopolymer indels	71.77%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	41124313	42.0831	13.2129
gi|1074120682|emb|LT615257.1|	860454	31333704	36.4153	17.9207
gi|1074120865|emb|LT615258.1|	989719	39145515	39.5522	23.1805
gi|1074121086|emb|LT615259.1|	935450	37852820	40.4648	28.6125
gi|1074121301|emb|LT615260.1|	1432239	57334925	40.0317	23.553
gi|1074121615|emb|LT615261.1|	1080962	43691961	40.4195	16.1646
gi|1074121871|emb|LT615262.1|	1545099	66272854	42.8923	13.1827
gi|1074122235|emb|LT615263.1|	1585108	65445712	41.2879	23.3446
gi|1074122590|emb|LT615264.1|	2122358	84570821	39.8476	41.03
gi|1074123050|emb|LT615265.1|	1754192	63267378	36.0664	43.1475
gi|1074123421|emb|LT615	2150147	91309637	42.4667	80.6905

|				
266.1|				
gi|1074123898|emb|LT615267.1|	3031036	125955002	41.5551	21.0535
gi|1074124588|emb|LT615268.1|	2359348	88510353	37.5148	20.3862
gi|1074125065|emb|LT615269.1|	3135668	124977782	39.8568	12.2997

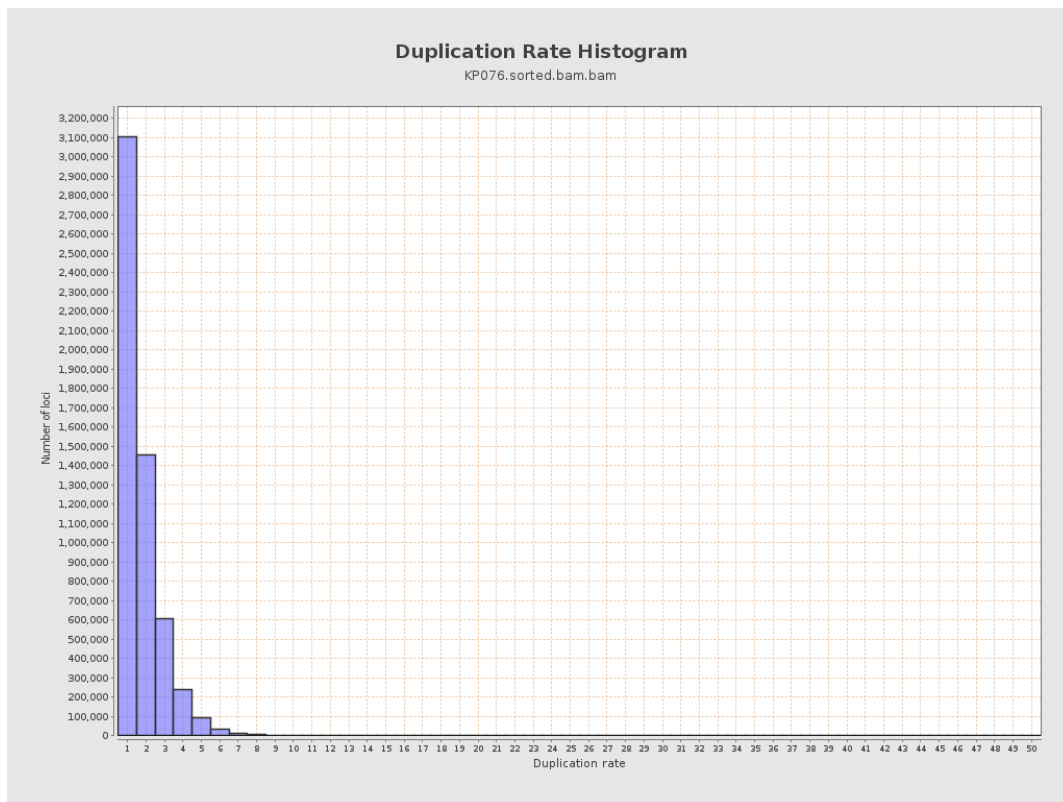# 3. Results : Coverage across reference

4. Results : Coverage Histogram

Coverage Histogram
KP076.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
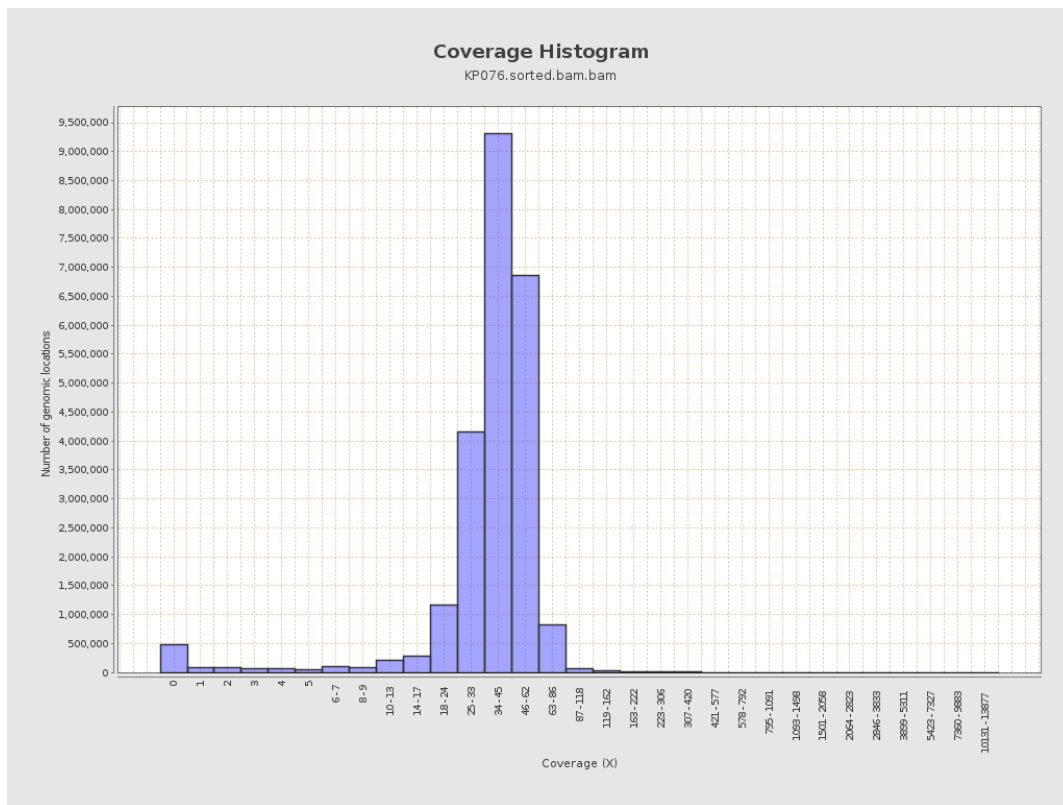
Coverage Histogram (0-50X)
KP076.sorted.bam.bam
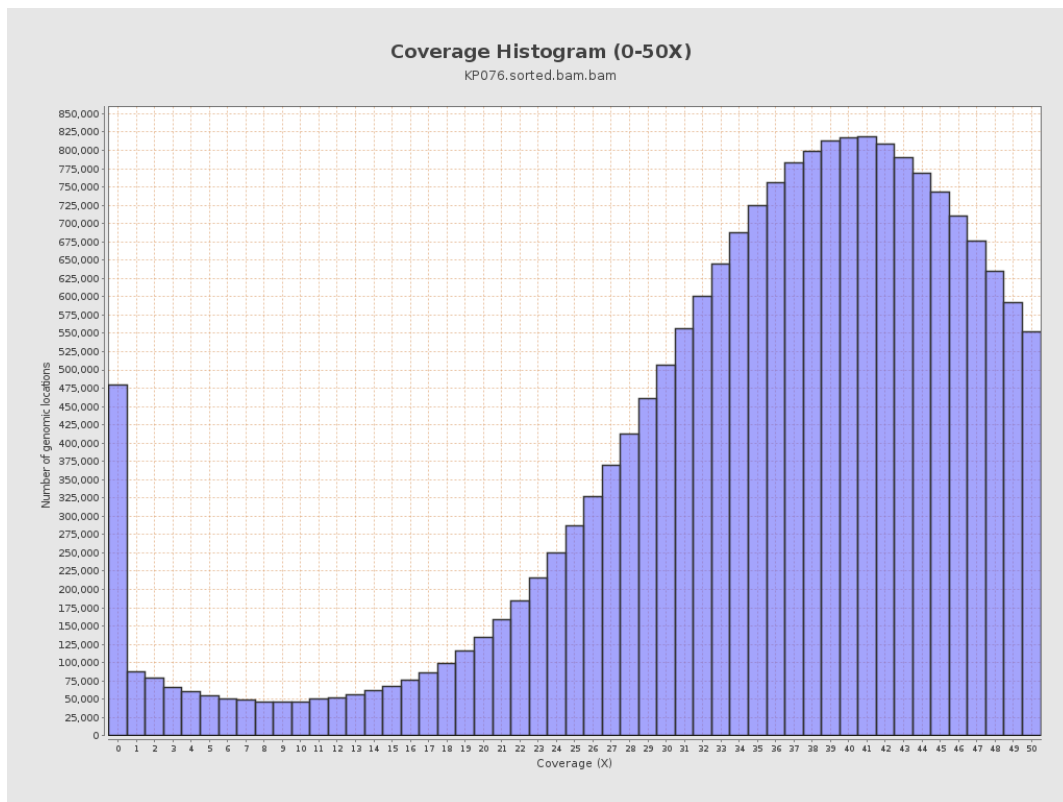
6. Results : Genome Fraction Coverage
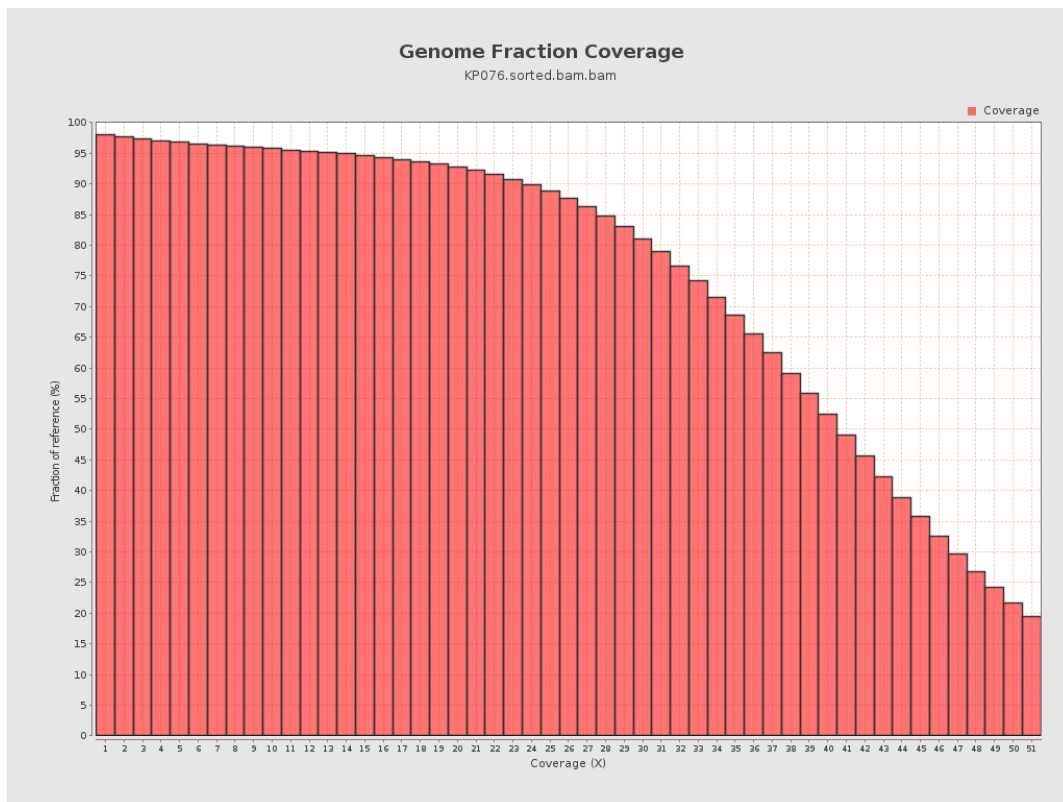
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
KP076.sorted.bam.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
KP076.sorted.bam.bam
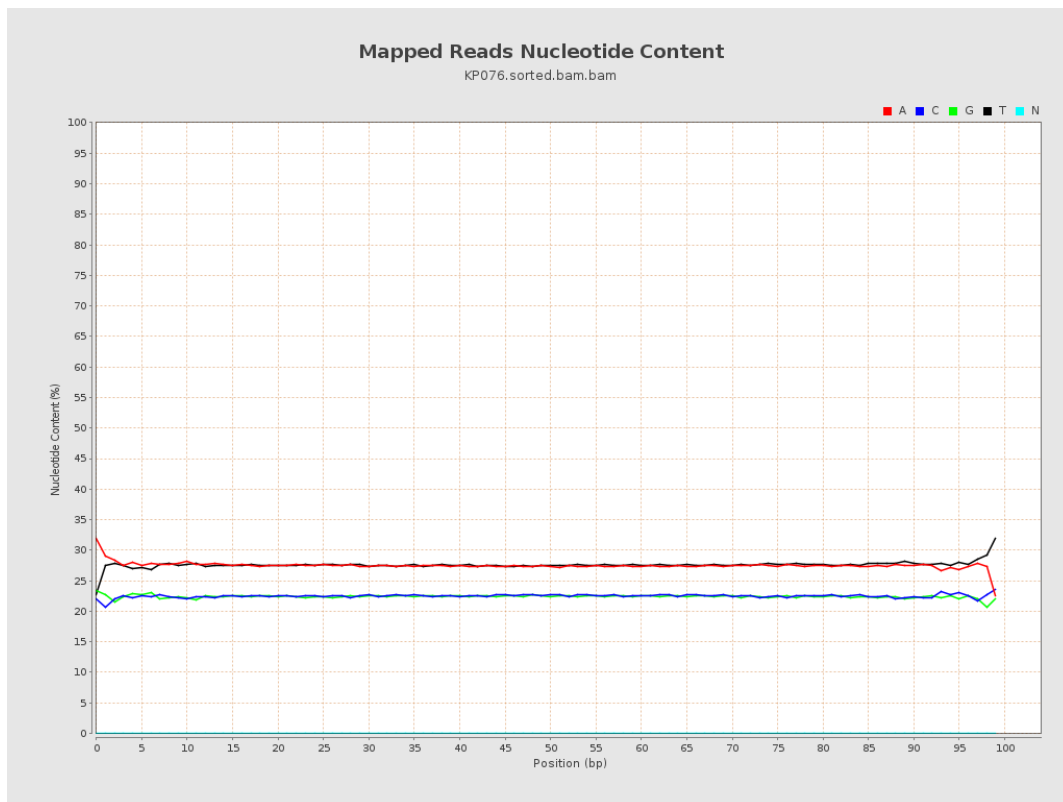
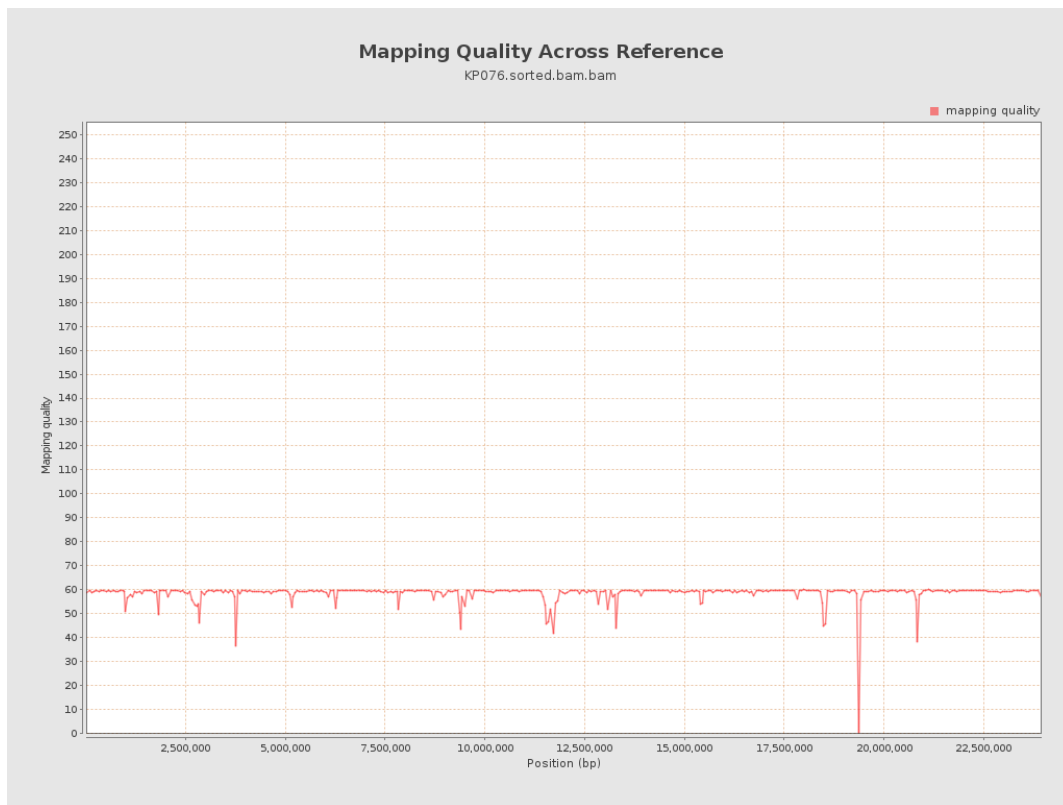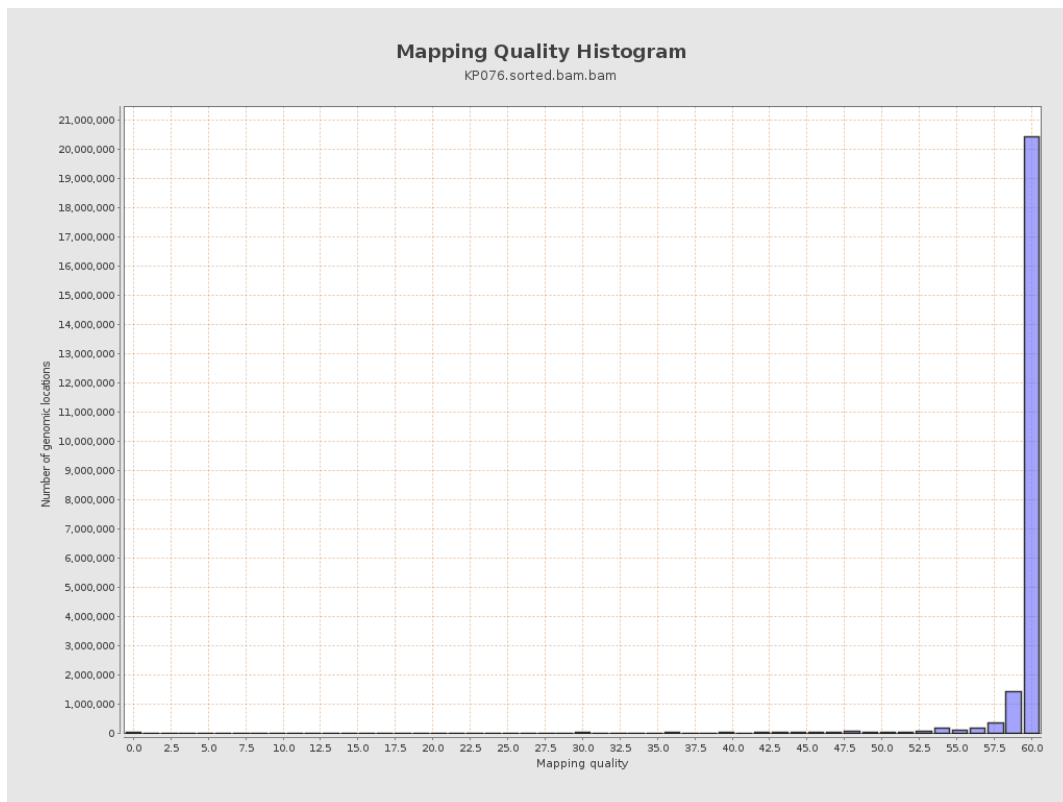# 9. Results : Mapped Reads GC-content Distribution
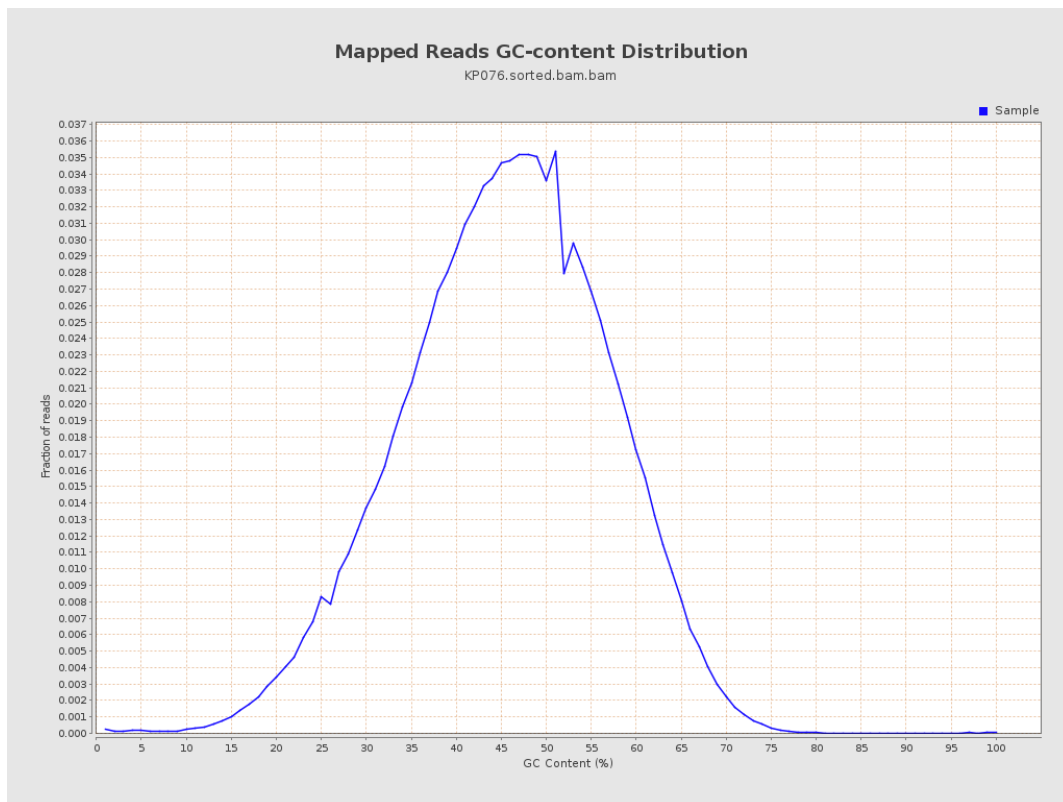
10. Results : Mapped Reads Clipping Profile
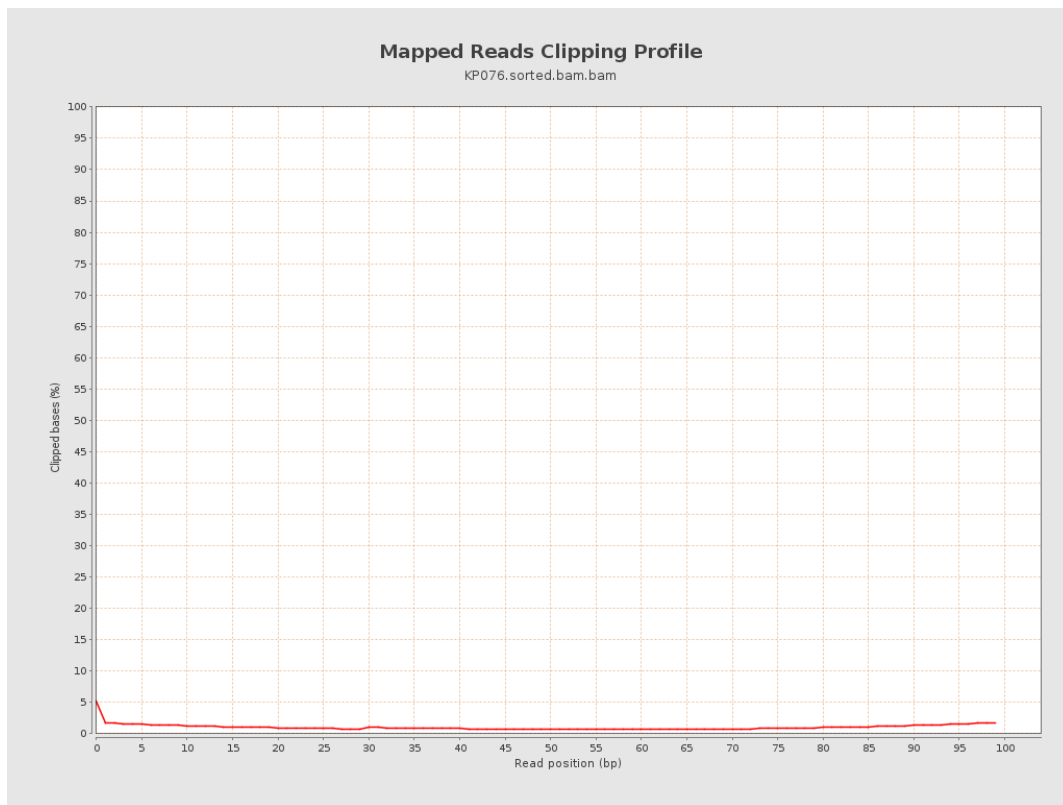
11. Results : Homopolymer Indels
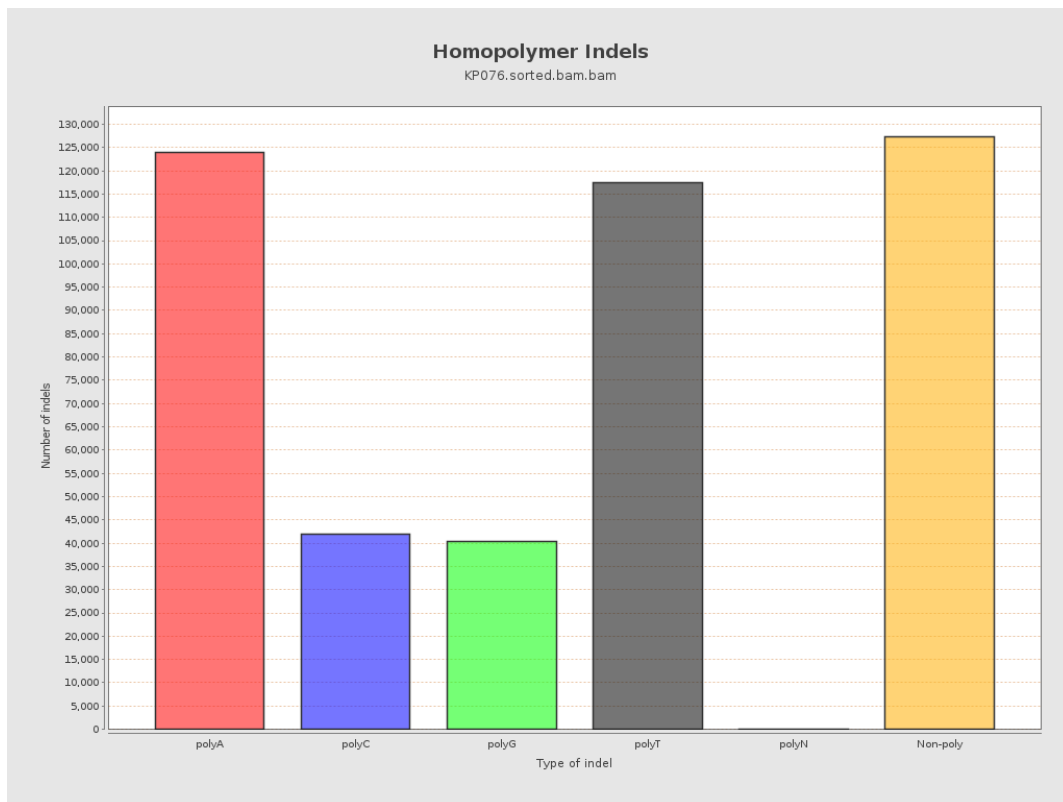
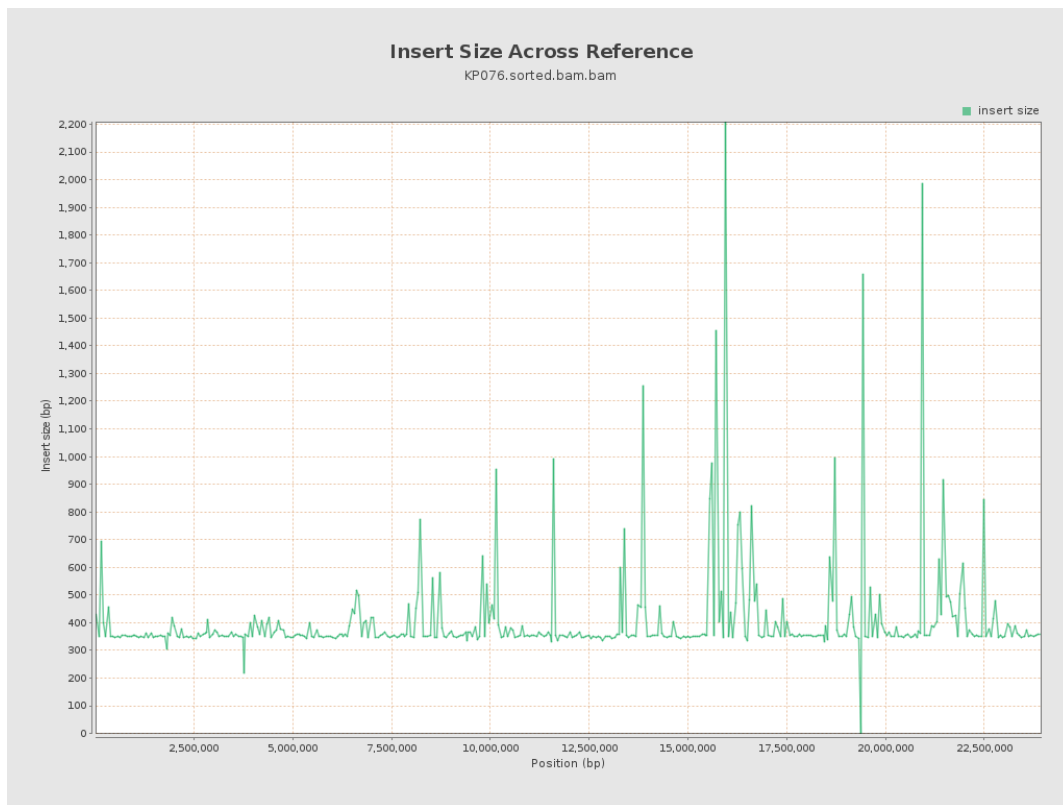# 12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
KP076.sorted.bam.bam

14. Results : Insert Size Across Reference

Insert Size Across Reference
KP076.sorted.bam.bam

15. Results : Insert Size Histogram