Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 11:36:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /home/vdp5/data/cambodia_samples/sequences_bam/BB021.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/BB021-BiooBarcode_36_CCAACA_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/BB021-BiooBarcode_36_CCAACA_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:36:25 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/BB021.sorted.bam.b

	am

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	22,482,767
Mapped reads	15,208,434 / 67.64%
Unmapped reads	7,274,333 / 32.36%
Mapped paired reads	15,208,434 / 67.64%
Mapped reads, first in pair	7,537,670 / 33.53%
Mapped reads, second in pair	7,670,764 / 34.12%
Mapped reads, both in pair	14,797,290 / 65.82%
Mapped reads, singletons	411,144 / 1.83%
Read min/max/mean length	30 / 100 / 99.85
Duplicated reads (estimated)	8,966,981 / 39.88%
Duplication rate	60.67%
Clipped reads	1,529,878 / 6.8%

2.2. ACGT Content

Number/percentage of A's	418,295,572 / 28.48%
Number/percentage of C's	315,867,551 / 21.51%
Number/percentage of T's	419,564,765 / 28.57%
Number/percentage of G's	315,078,560 / 21.45%
Number/percentage of N's	121,830 / 0.01%
GC Percentage	42.96%

2.3. Coverage

Mean	61.3693
Standard Deviation	43.082

2.4. Mapping Quality

Mean Mapping Quality	58.71

2.5. Insert size

Mean	1,553.88
Standard Deviation	39,415.46
P25/Median/P75	265 / 360 / 464

2.6. Mismatches and indels

General error rate	1.02%
Mismatches	13,947,299
Insertions	357,724
Mapped reads with at least one insertion	2.24%
Deletions	471,731
Mapped reads with at least one deletion	2.96%
Homopolymer indels	66.65%

2.7. Chromosome stats

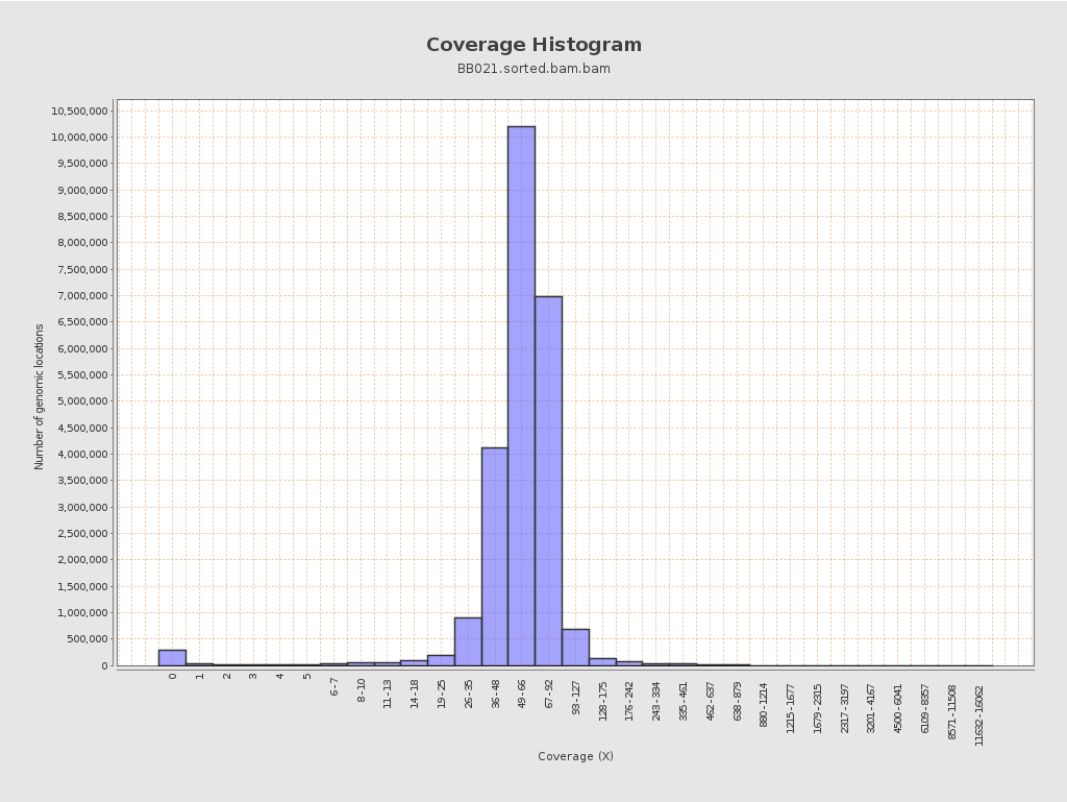
Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	59003286	60.3789	22.3285
gi|1074120682|emb|LT615257.1|	860454	49784101	57.8579	29.6237
gi|1074120865|emb|LT615258.1|	989719	65208359	65.8857	57.341
gi|1074121086|emb|LT615259.1|	935450	60293411	64.4539	61.2424
gi|1074121301|emb|LT615260.1|	1432239	90849477	63.4318	47.9789
gi|1074121615|emb|LT615261.1|	1080962	67149913	62.1205	32.6881
gi|1074121871|emb|LT615262.1|	1545099	95990250	62.1256	20.4801
gi|1074122235|emb|LT615263.1|	1585108	97040637	61.2202	25.9844
gi|1074122590|emb|LT615264.1|	2122358	127804334	60.2181	25.4545
gi|1074123050|emb|LT615265.1|	1754192	104210436	59.4065	33.974
gi|1074123421|emb|LT615	2150147	138600316	64.4609	97.7049

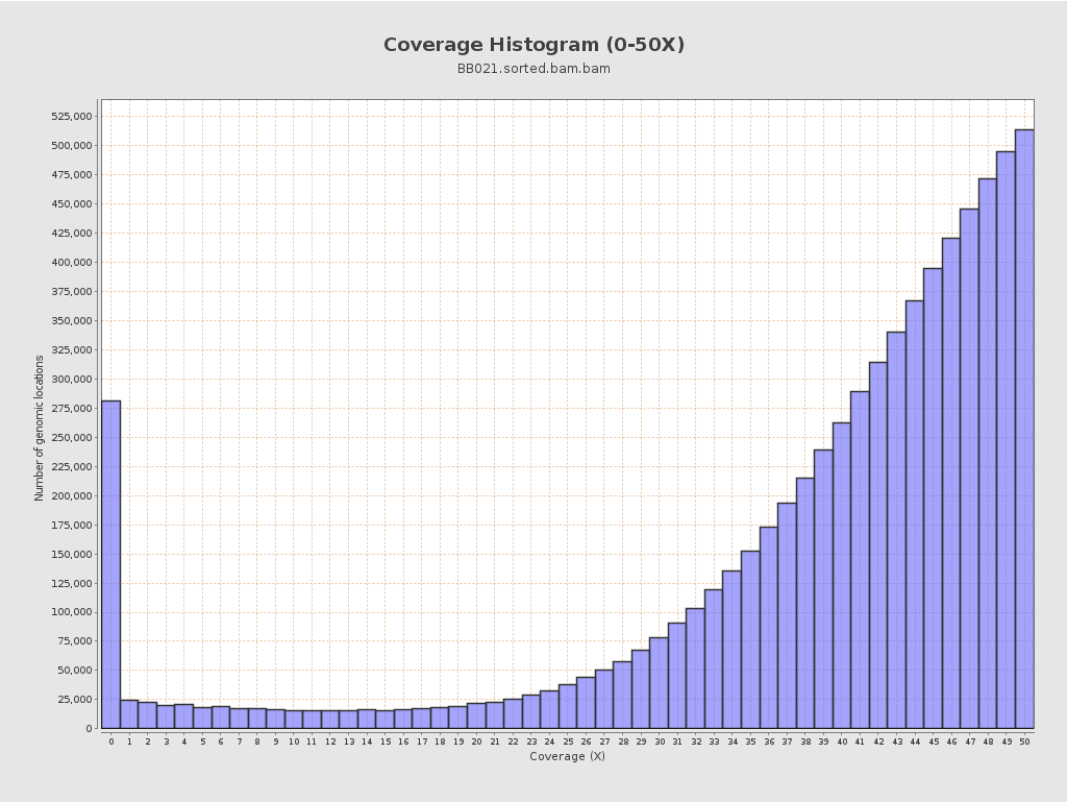
266.1|				
gi|107412389 8|emb|LT615 267.1|	3031036	186215062	61.4361	23.5513
gi|107412458 8|emb|LT615 268.1|	2359348	136247968	57.7481	39.6112
gi|107412506 5|emb|LT615 269.1|	3135668	191950288	61.2151	16.717

3. Results : Coverage across reference

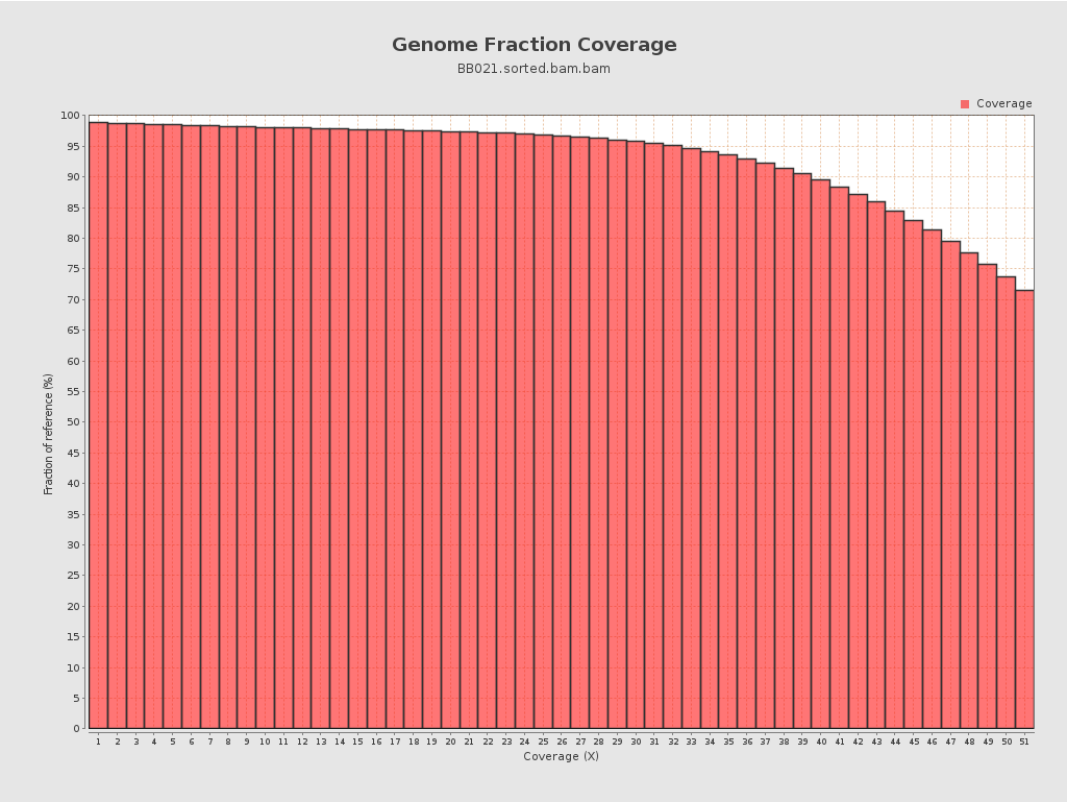
4. Results : Coverage Histogram



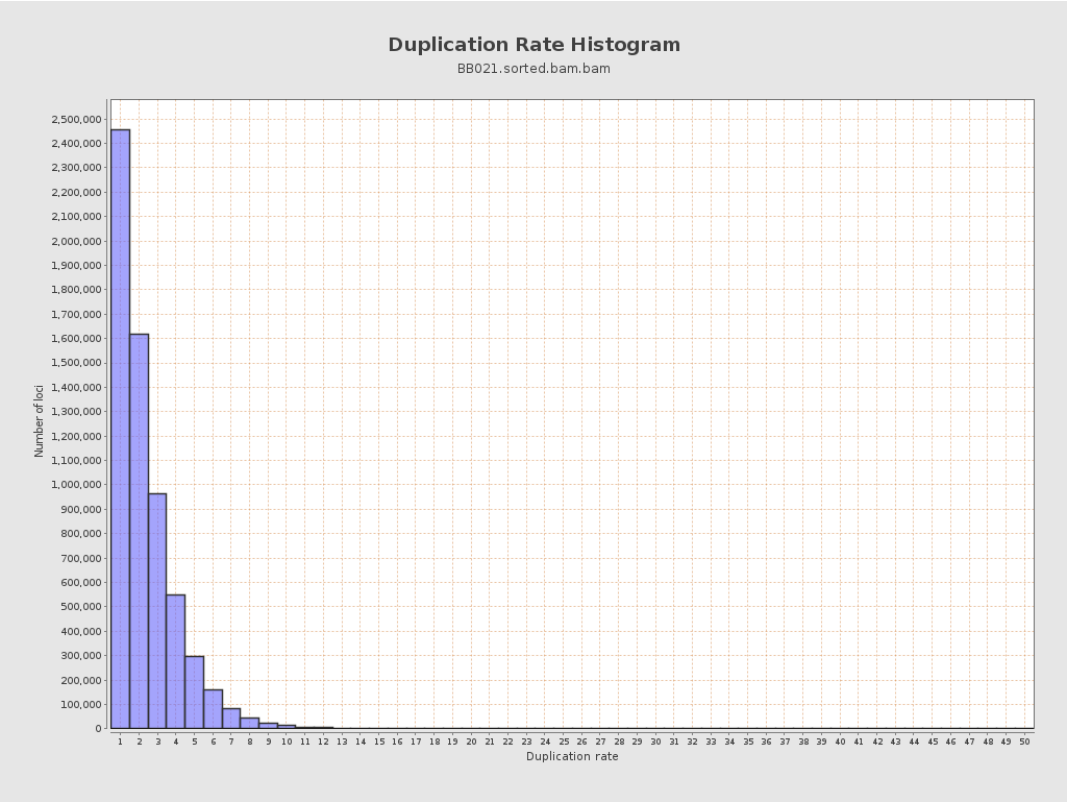
5. Results : Coverage Histogram (0-50X)



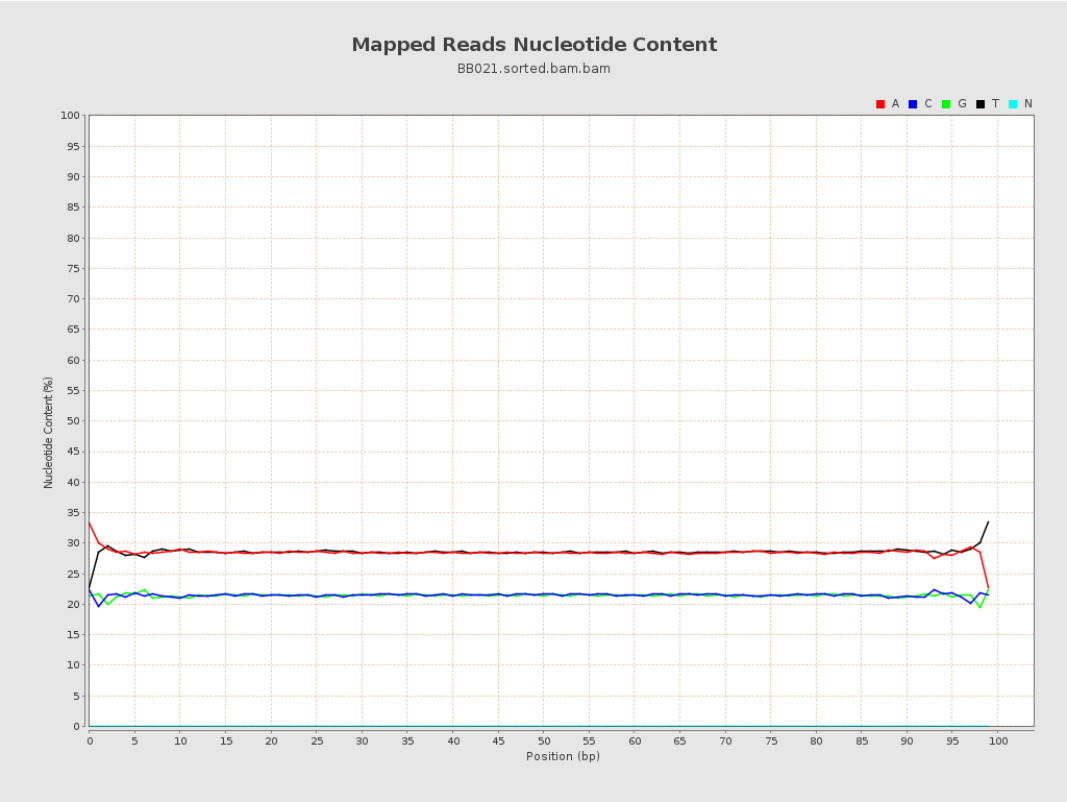
6. Results : Genome Fraction Coverage



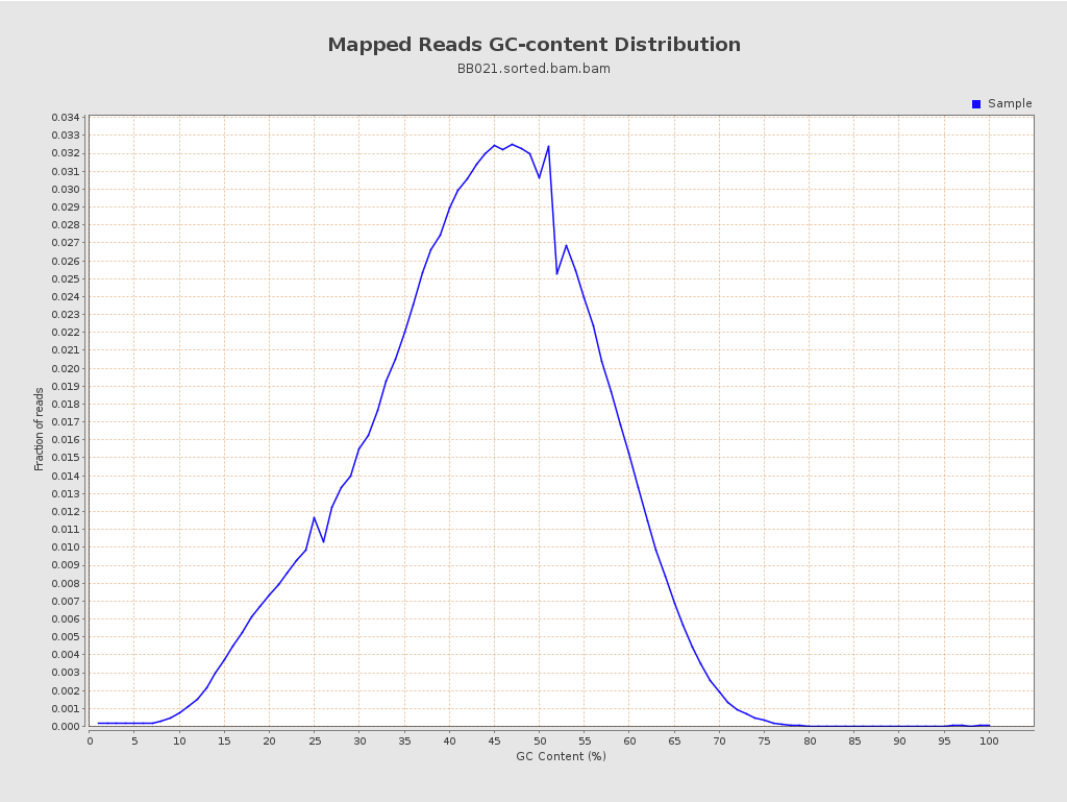
7. Results : Duplication Rate Histogram



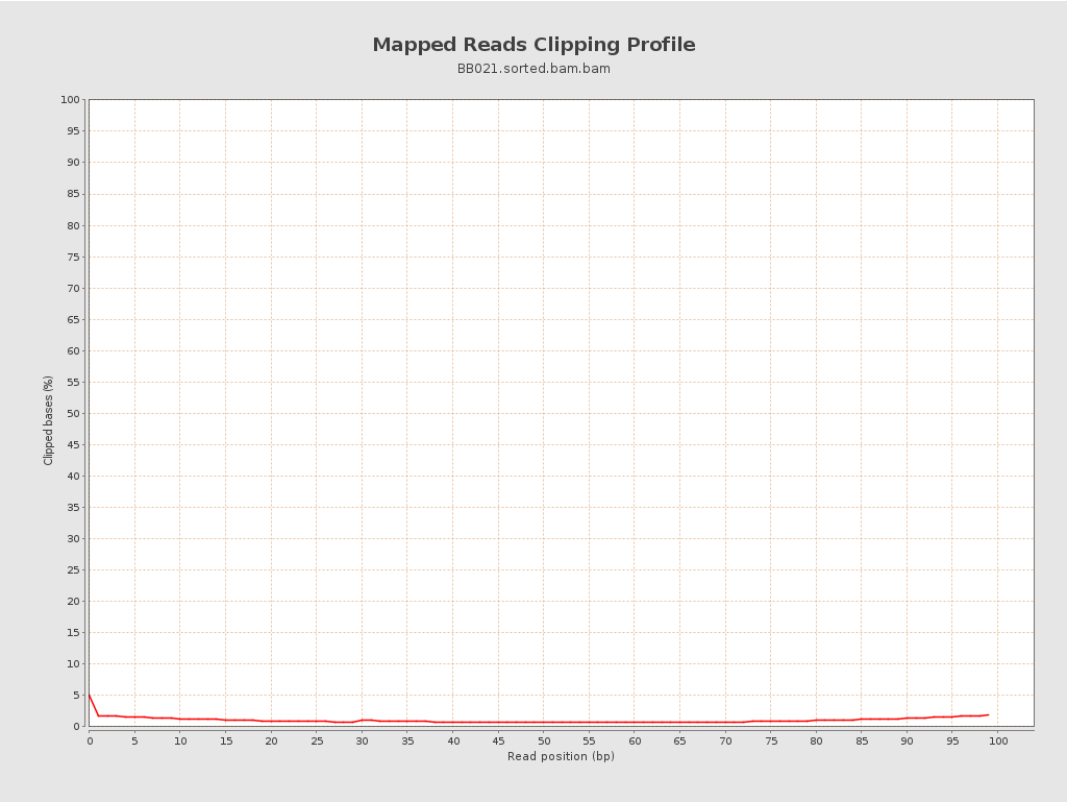
8. Results : Mapped Reads Nucleotide Content



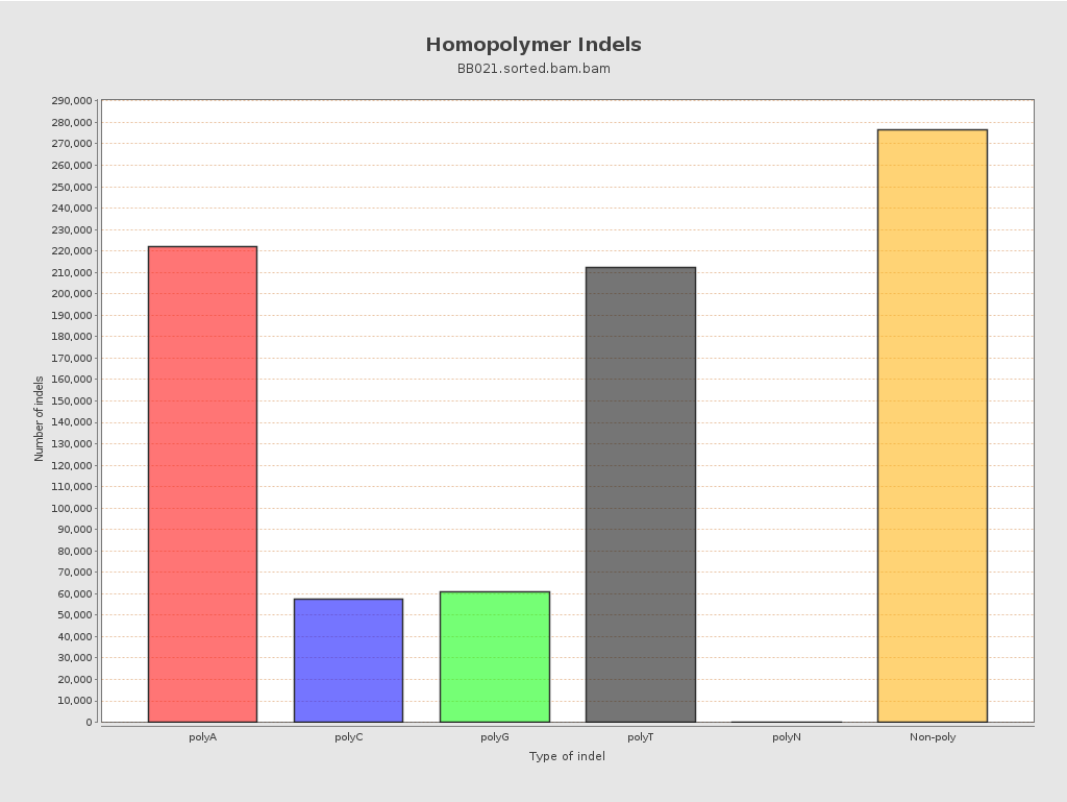
9. Results : Mapped Reads GC-content Distribution



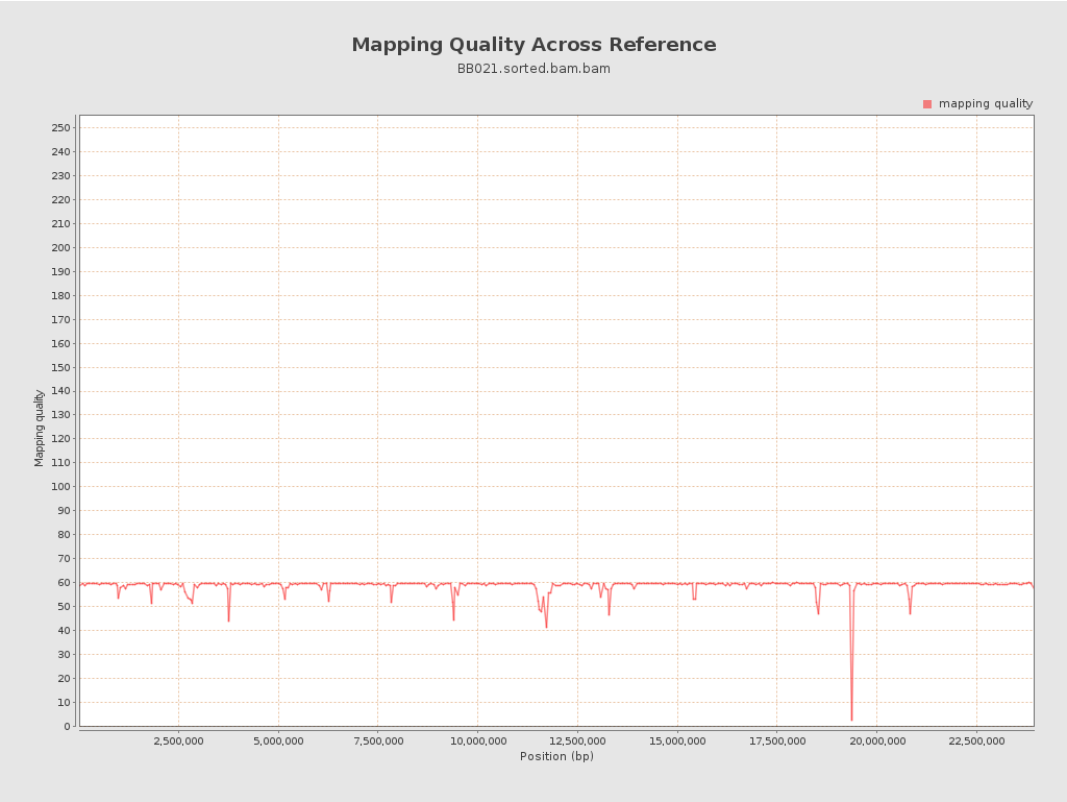
10. Results : Mapped Reads Clipping Profile



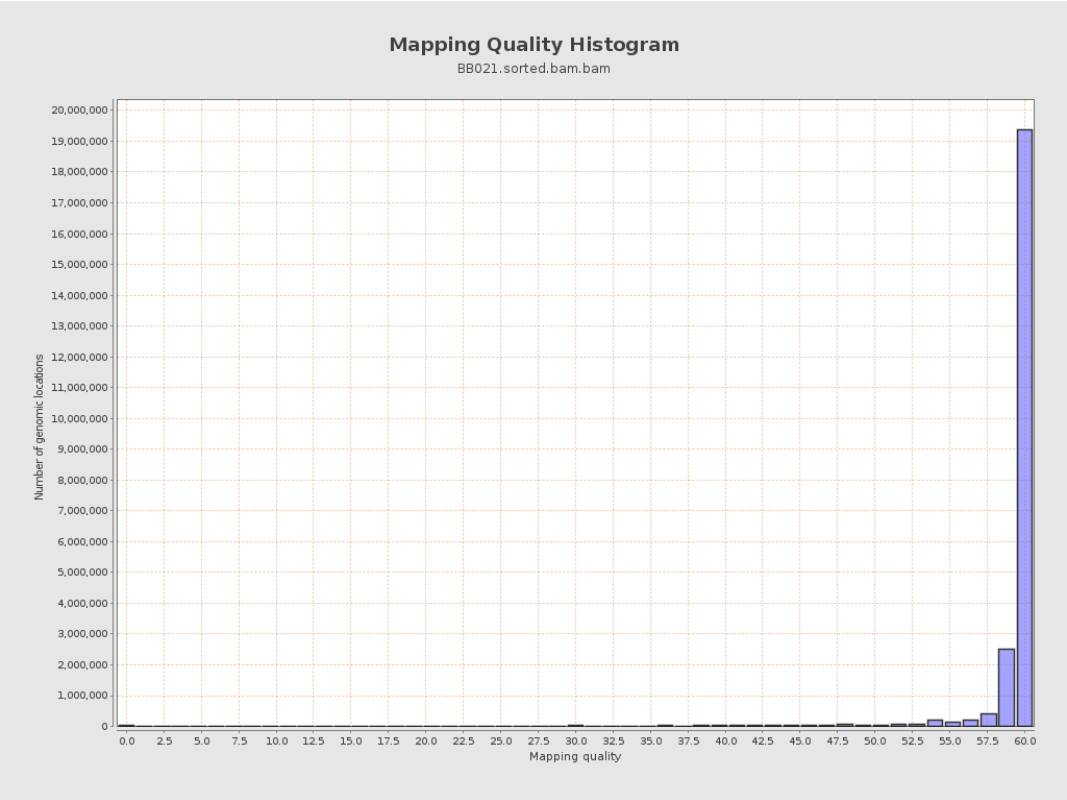
11. Results : Homopolymer Indels



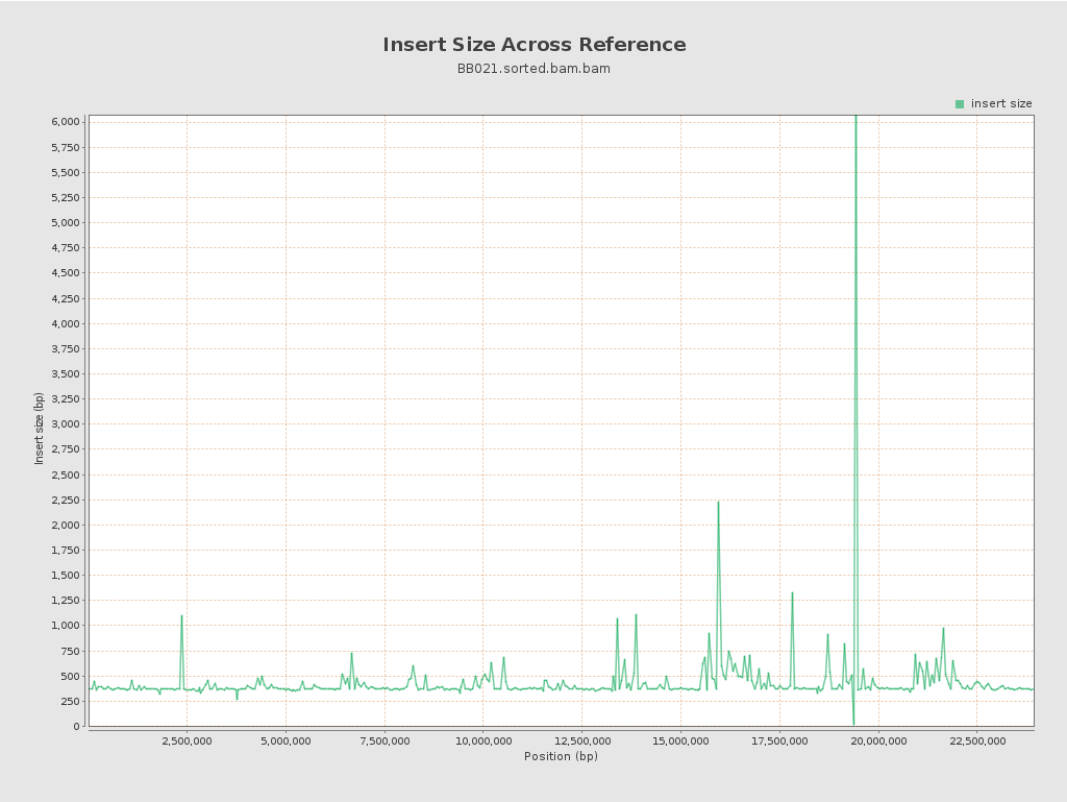
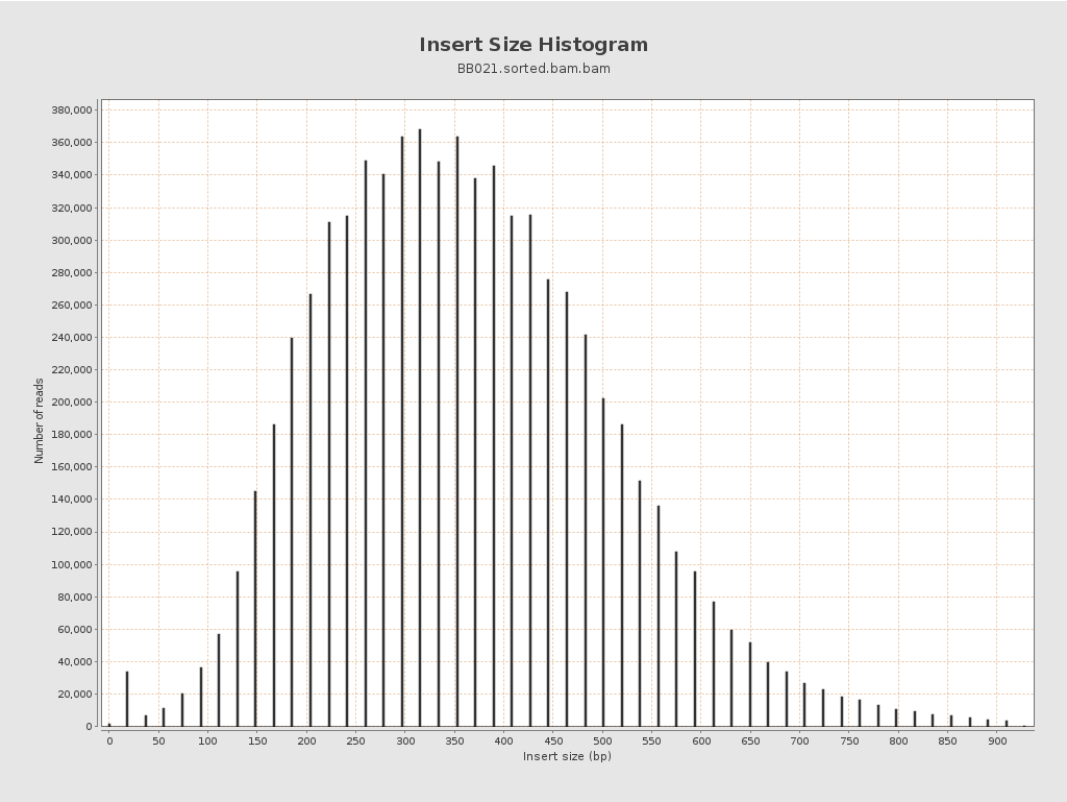
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram