

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 11:32:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/BB016.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/BB016-BiooBarcode_33_CAGGCG_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/BB016-BiooBarcode_33_CAGGCG_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 11:32:56 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/BB016.sorted.bam.b

am

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	15,011,025
Mapped reads	12,816,958 / 85.38%
Unmapped reads	2,194,067 / 14.62%
Mapped paired reads	12,816,958 / 85.38%
Mapped reads, first in pair	6,378,902 / 42.49%
Mapped reads, second in pair	6,438,056 / 42.89%
Mapped reads, both in pair	12,686,575 / 84.52%
Mapped reads, singletons	130,383 / 0.87%
Read min/max/mean length	30 / 100 / 99.81
Duplicated reads (estimated)	3,873,332 / 25.8%
Duplication rate	30.63%
Clipped reads	813,799 / 5.42%

2.2. ACGT Content

Number/percentage of A's	335,653,458 / 26.73%
Number/percentage of C's	292,318,223 / 23.28%
Number/percentage of T's	336,915,687 / 26.83%
Number/percentage of G's	291,044,489 / 23.17%
Number/percentage of N's	107,303 / 0.01%
GC Percentage	46.45%

2.3. Coverage

Mean	52.4705
Standard Deviation	31.7003

2.4. Mapping Quality

Mean Mapping Quality	58.56
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2.5. Insert size

Mean	981.53
Standard Deviation	27,787.8
P25/Median/P75	273 / 335 / 397

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	6,589,951
Insertions	212,404
Mapped reads with at least one insertion	1.6%
Deletions	302,120
Mapped reads with at least one deletion	2.29%
Homopolymer indels	75.22%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

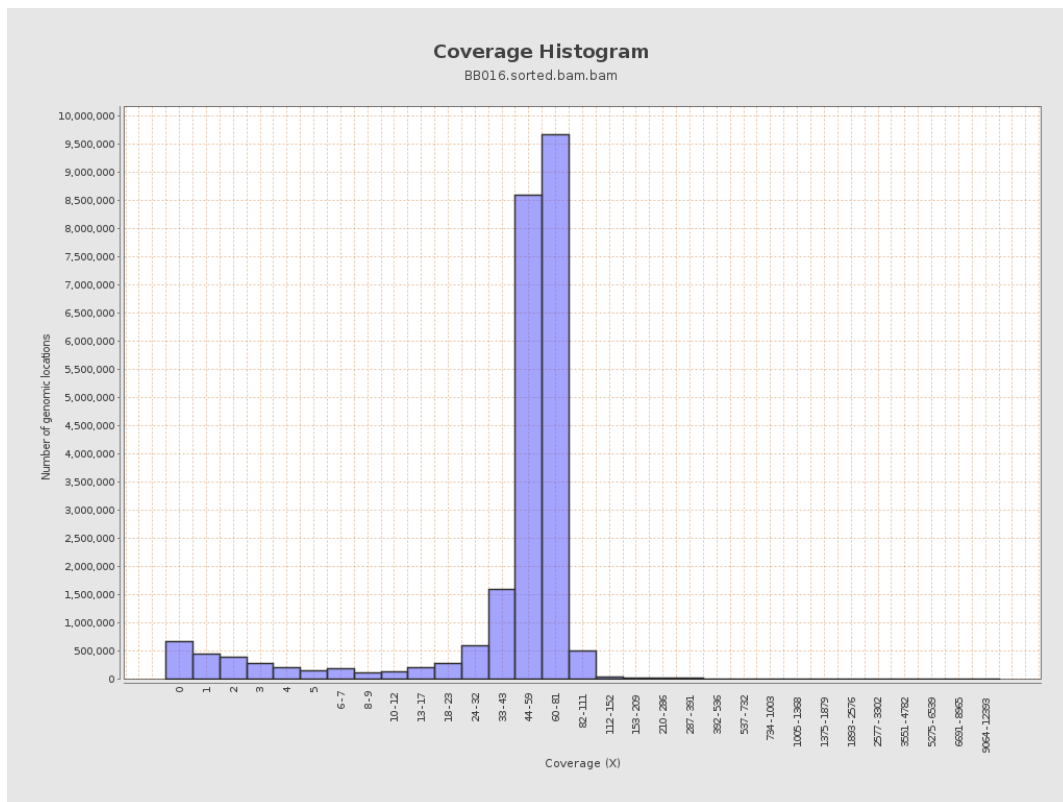
gi 1074120478 emb LT615256.1	977217	54539786	55.8113	18.1116
gi 1074120682 emb LT615257.1	860454	39929705	46.4054	25.415
gi 1074120865 emb LT615258.1	989719	46483843	46.9667	28.7882
gi 1074121086 emb LT615259.1	935450	47245920	50.5061	34.3266
gi 1074121301 emb LT615260.1	1432239	72778002	50.8141	29.413
gi 1074121615 emb LT615261.1	1080962	55254705	51.1162	22.8073
gi 1074121871 emb LT615262.1	1545099	84537125	54.7131	18.899
gi 1074122235 emb LT615263.1	1585108	86047134	54.2847	22.5255
gi 1074122590 emb LT615264.1	2122358	112707053	53.1046	21.3763
gi 1074123050 emb LT615265.1	1754192	82411276	46.9796	27.3873
gi 1074123421 emb LT615	2150147	120347162	55.9716	74.1732

266.1				
gi 107412389 8 emb LT615 267.1	3031036	171247942	56.4982	18.6528
gi 107412458 8 emb LT615 268.1	2359348	118453330	50.206	25.0444
gi 107412506 5 emb LT615 269.1	3135668	165157945	52.6707	19.8417

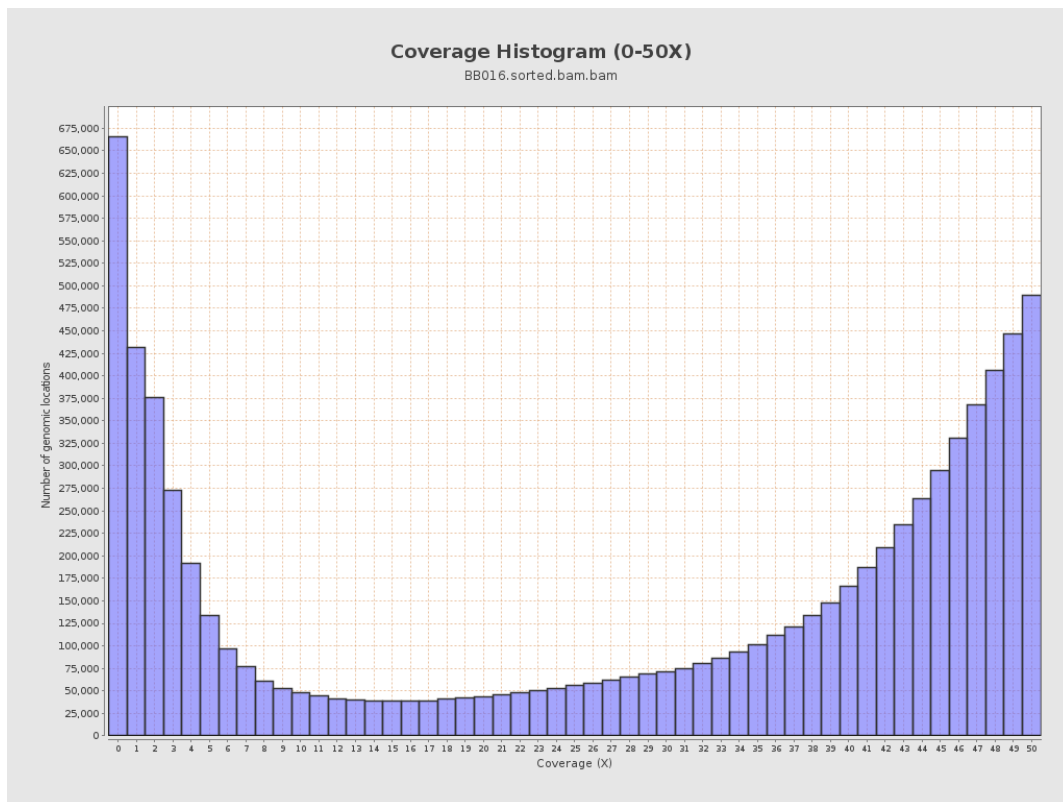
3. Results : Coverage across reference



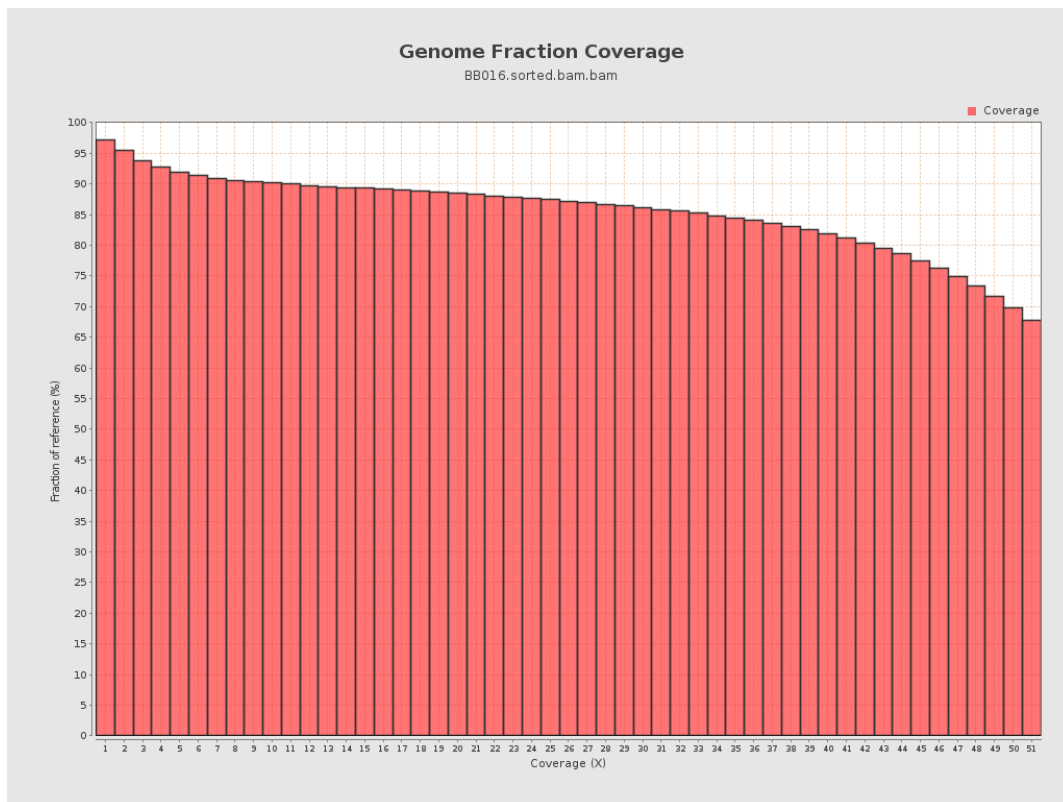
4. Results : Coverage Histogram



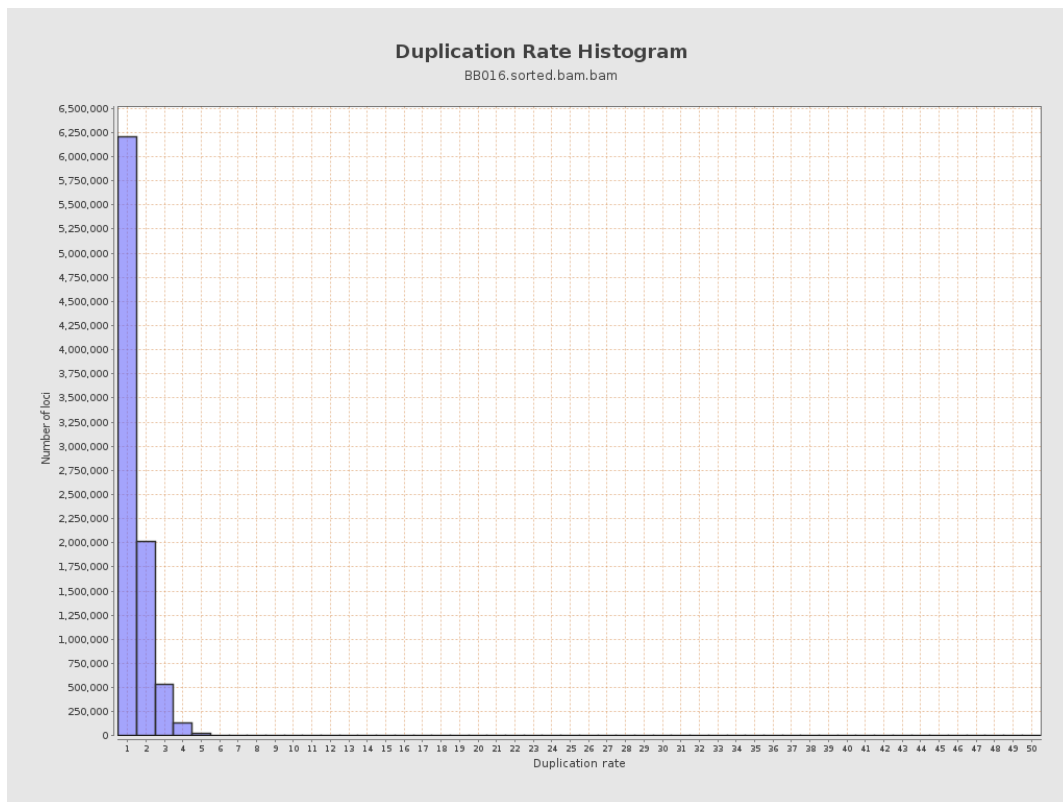
5. Results : Coverage Histogram (0-50X)



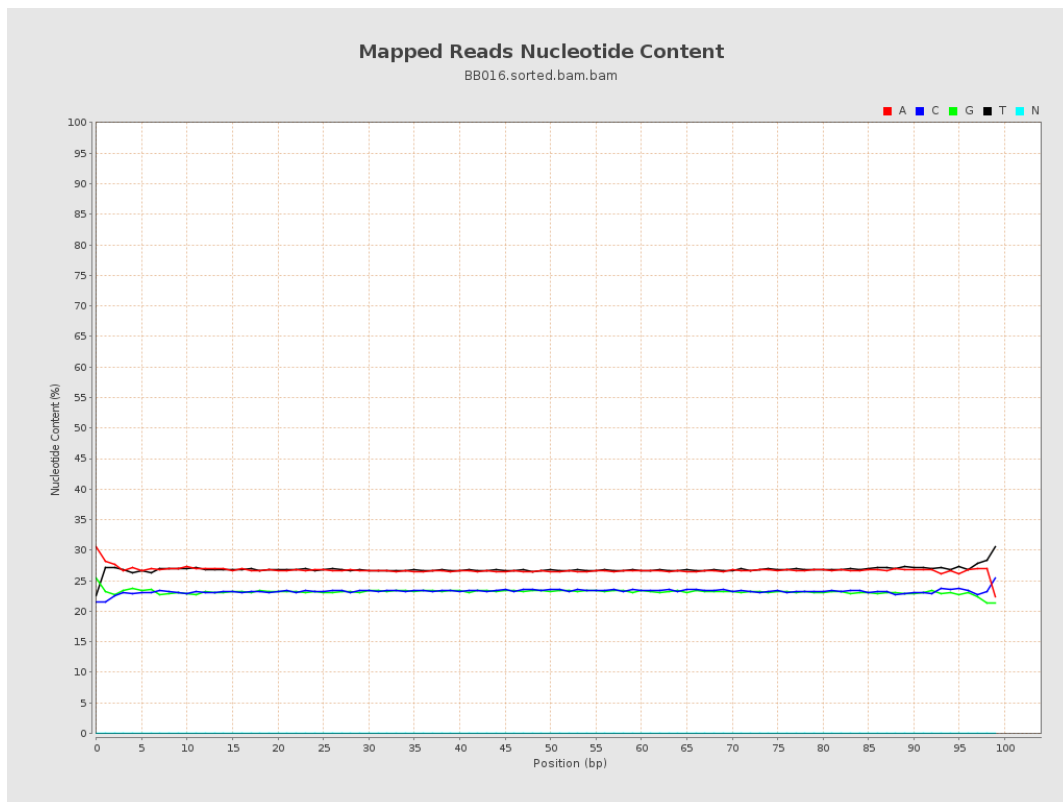
6. Results : Genome Fraction Coverage



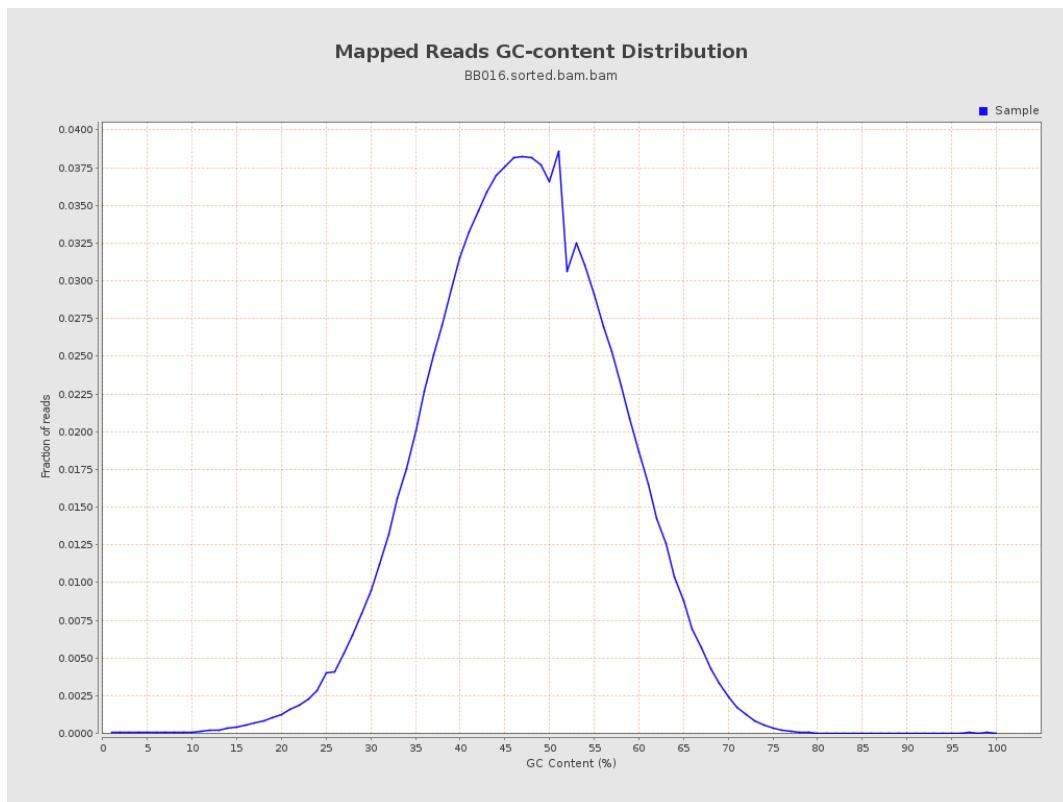
7. Results : Duplication Rate Histogram



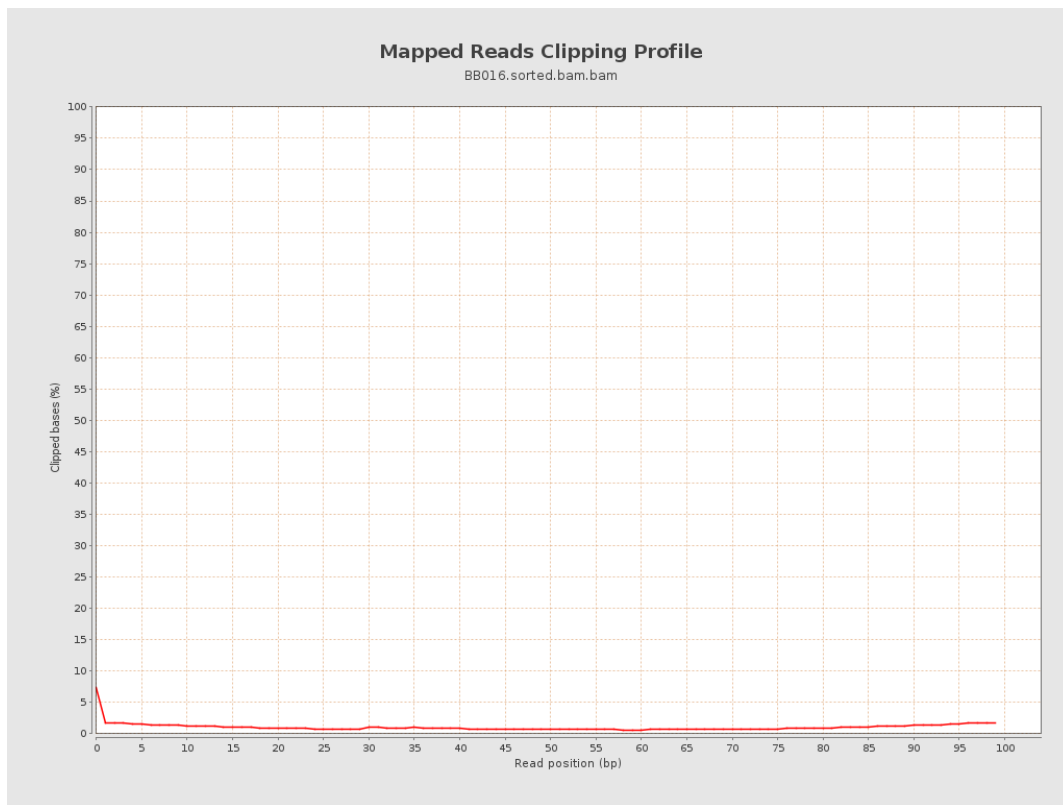
8. Results : Mapped Reads Nucleotide Content



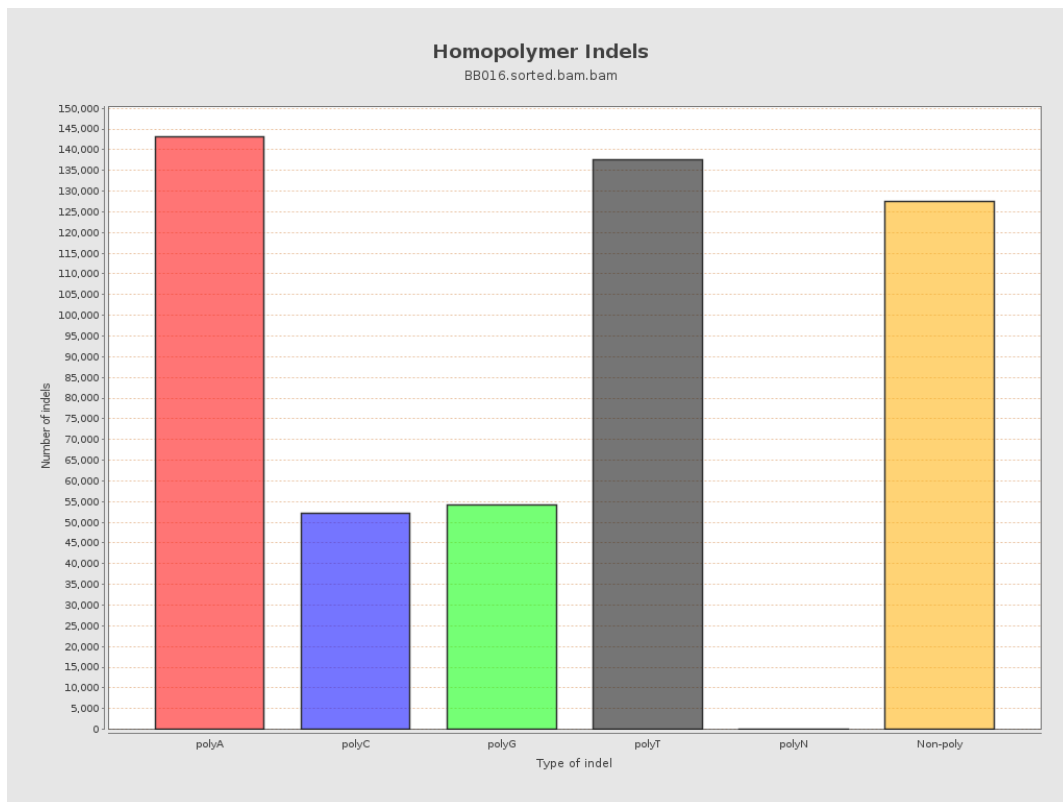
9. Results : Mapped Reads GC-content Distribution



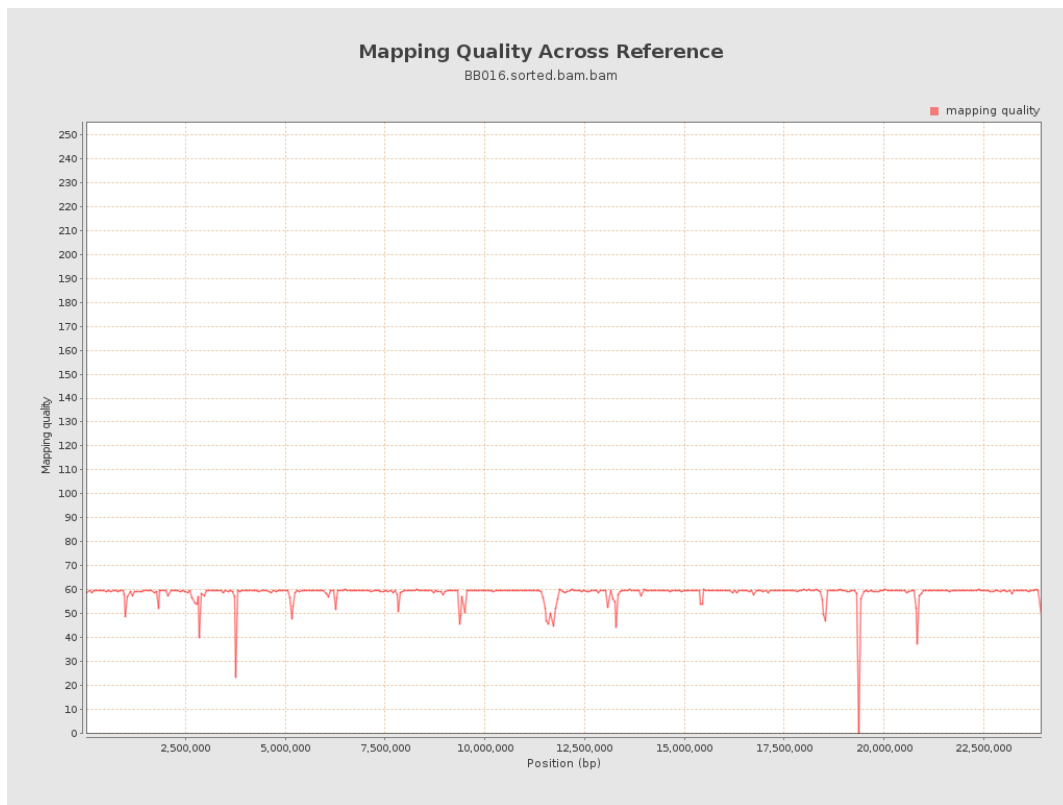
10. Results : Mapped Reads Clipping Profile



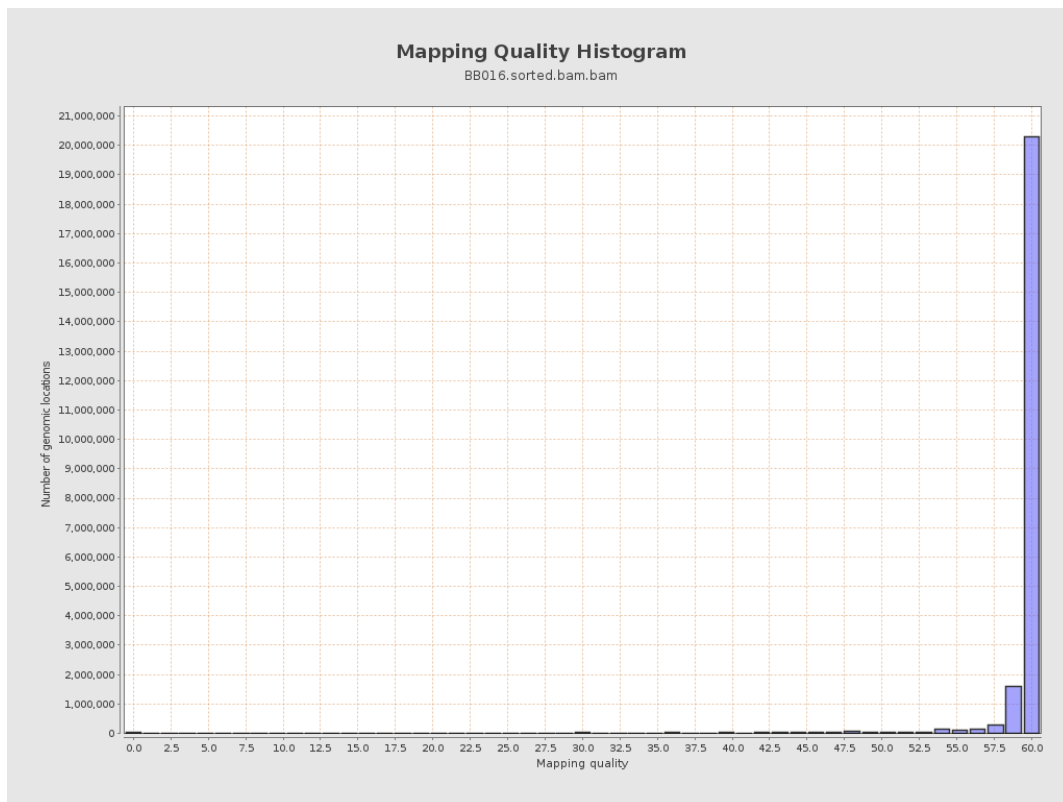
11. Results : Homopolymer Indels



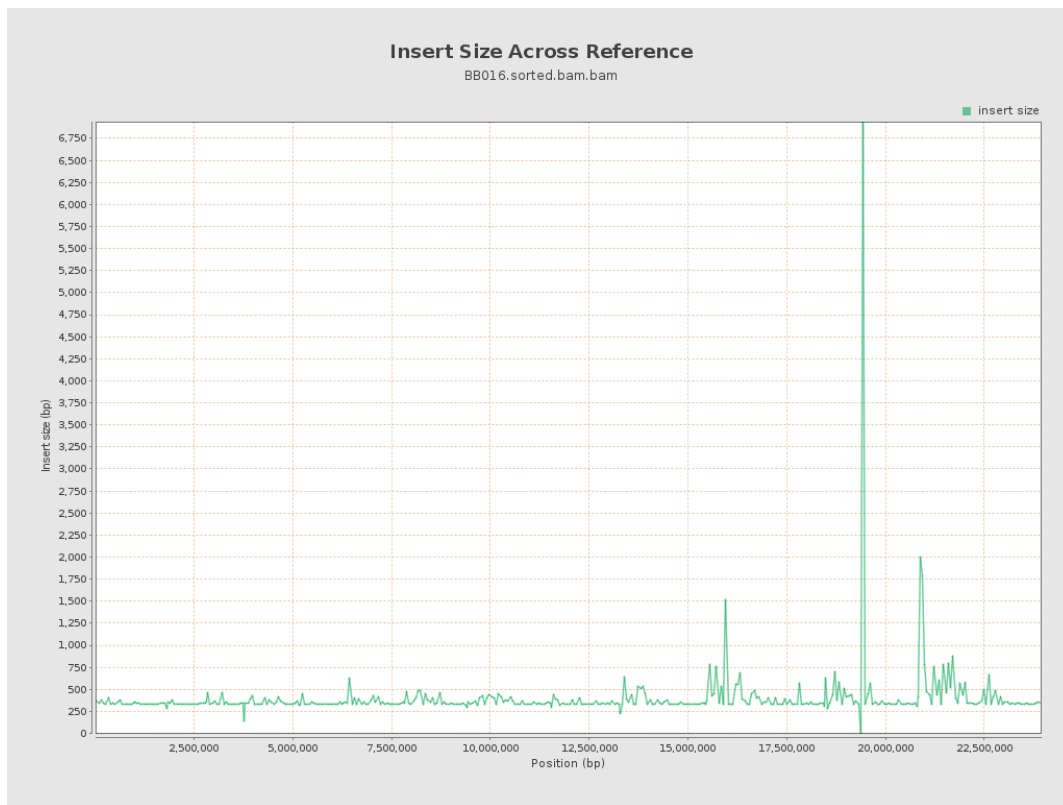
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

