

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 13:33:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM142.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/OM142-BiooBarcode16_CCGTCC_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM142-BiooBarcode16_CCGTCC_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:33:01 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM142.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	21,455,942
Mapped reads	12,299,087 / 57.32%
Unmapped reads	9,156,855 / 42.68%
Mapped paired reads	12,299,087 / 57.32%
Mapped reads, first in pair	6,141,971 / 28.63%
Mapped reads, second in pair	6,157,116 / 28.7%
Mapped reads, both in pair	12,114,038 / 56.46%
Mapped reads, singletons	185,049 / 0.86%
Read min/max/mean length	30 / 100 / 99.89
Duplicated reads (estimated)	3,625,990 / 16.9%
Duplication rate	27.17%
Clipped reads	1,177,078 / 5.49%

2.2. ACGT Content

Number/percentage of A's	351,382,045 / 29.45%
Number/percentage of C's	245,091,382 / 20.54%
Number/percentage of T's	352,434,194 / 29.53%
Number/percentage of G's	244,400,395 / 20.48%
Number/percentage of N's	63,768 / 0.01%
GC Percentage	41.02%

2.3. Coverage

Mean	49.8567
Standard Deviation	37.1887

2.4. Mapping Quality

Mean Mapping Quality	58.67
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2.5. Insert size

Mean	633.58
Standard Deviation	23,179.16
P25/Median/P75	179 / 187 / 195

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	13,226,265
Insertions	362,166
Mapped reads with at least one insertion	2.79%
Deletions	410,060
Mapped reads with at least one deletion	3.15%
Homopolymer indels	64.03%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

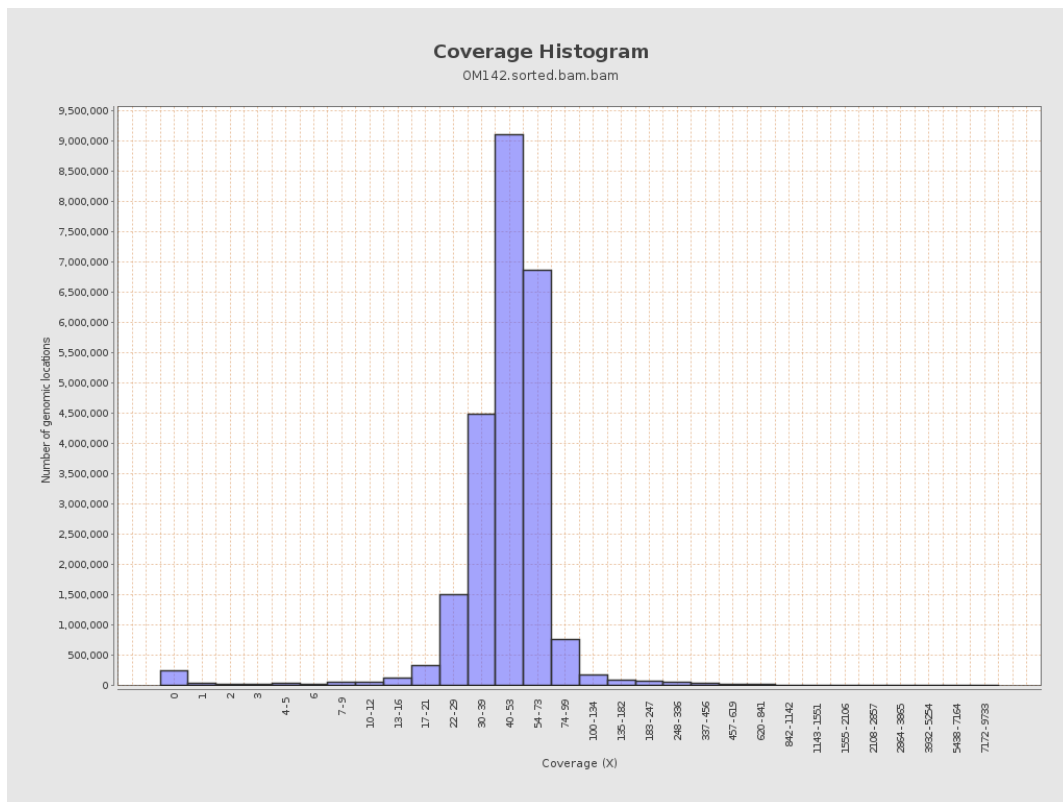
gi 1074120478 emb LT615256.1	977217	45341491	46.3986	20.2153
gi 1074120682 emb LT615257.1	860454	42574576	49.4792	27.7248
gi 1074120865 emb LT615258.1	989719	53055129	53.6063	58.3354
gi 1074121086 emb LT615259.1	935450	50999922	54.5191	65.9431
gi 1074121301 emb LT615260.1	1432239	73551553	51.3542	43.3252
gi 1074121615 emb LT615261.1	1080962	54115519	50.0624	31.5704
gi 1074121871 emb LT615262.1	1545099	75606567	48.9332	17.5276
gi 1074122235 emb LT615263.1	1585108	77826317	49.0984	26.9107
gi 1074122590 emb LT615264.1	2122358	103093034	48.5748	20.3927
gi 1074123050 emb LT615265.1	1754192	91527686	52.1765	43.5209
gi 1074123421 emb LT615	2150147	111163860	51.7006	66.2728

266.1				
gi 107412389 8 emb LT615 267.1	3031036	147371864	48.621	20.0859
gi 107412458 8 emb LT615 268.1	2359348	112120719	47.5219	39.1431
gi 107412506 5 emb LT615 269.1	3135668	156168341	49.8039	14.6767

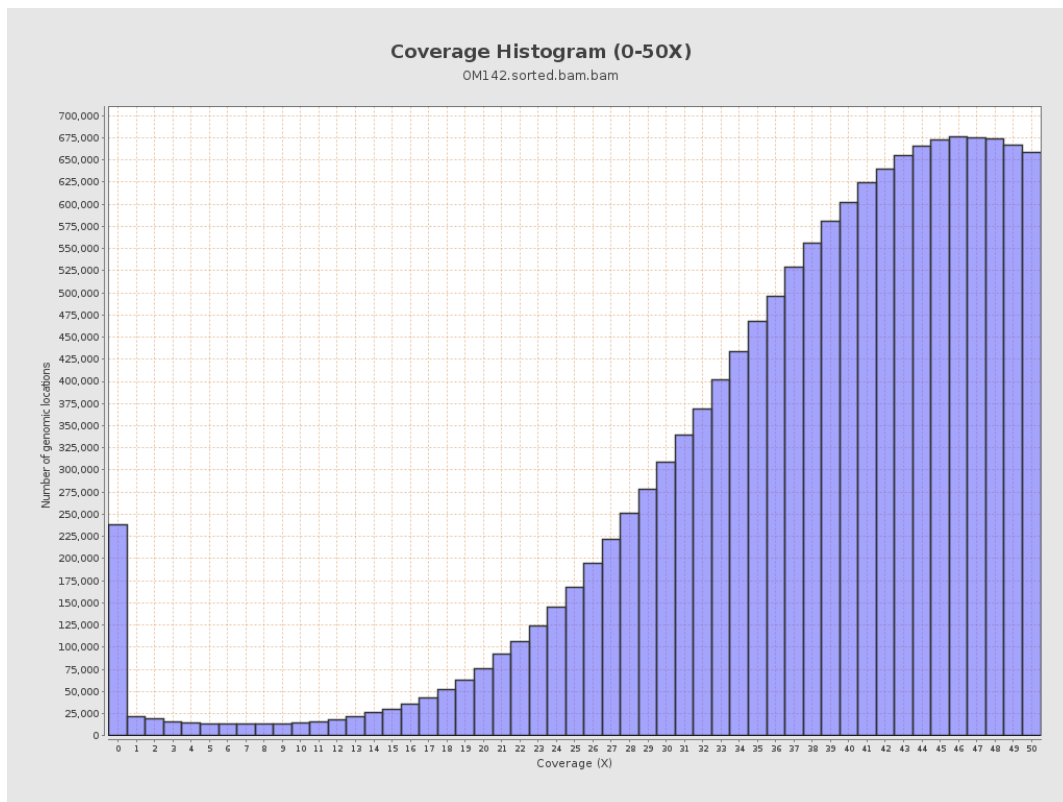
3. Results : Coverage across reference



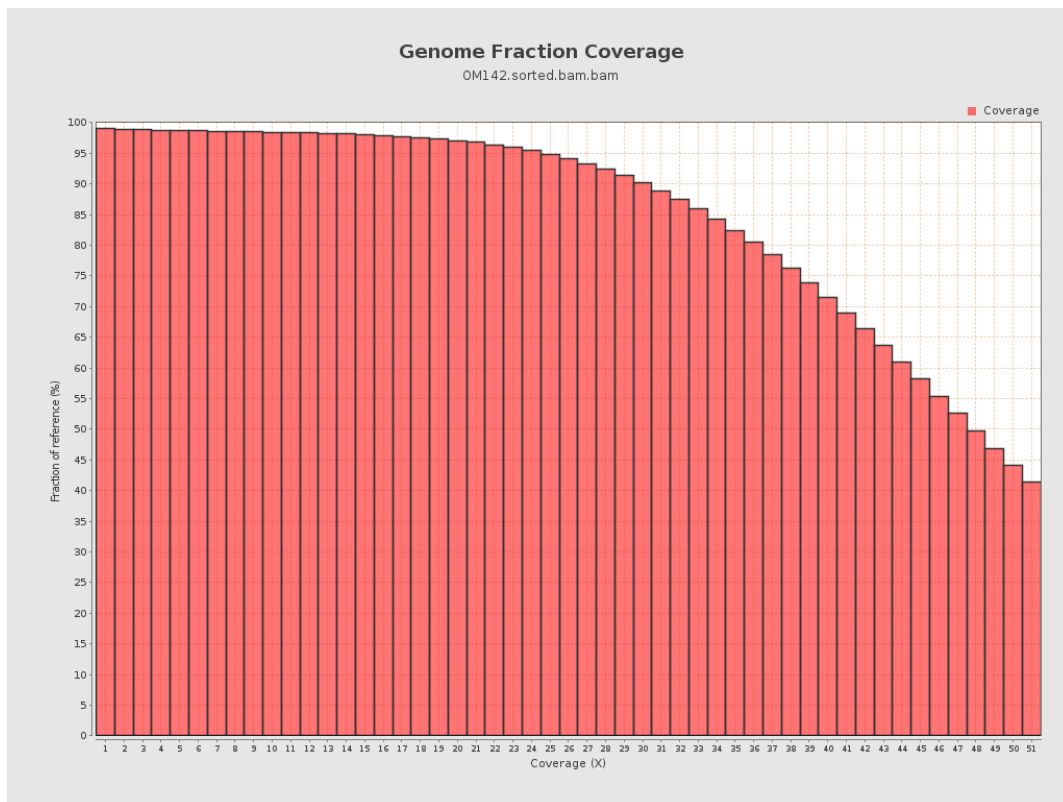
4. Results : Coverage Histogram



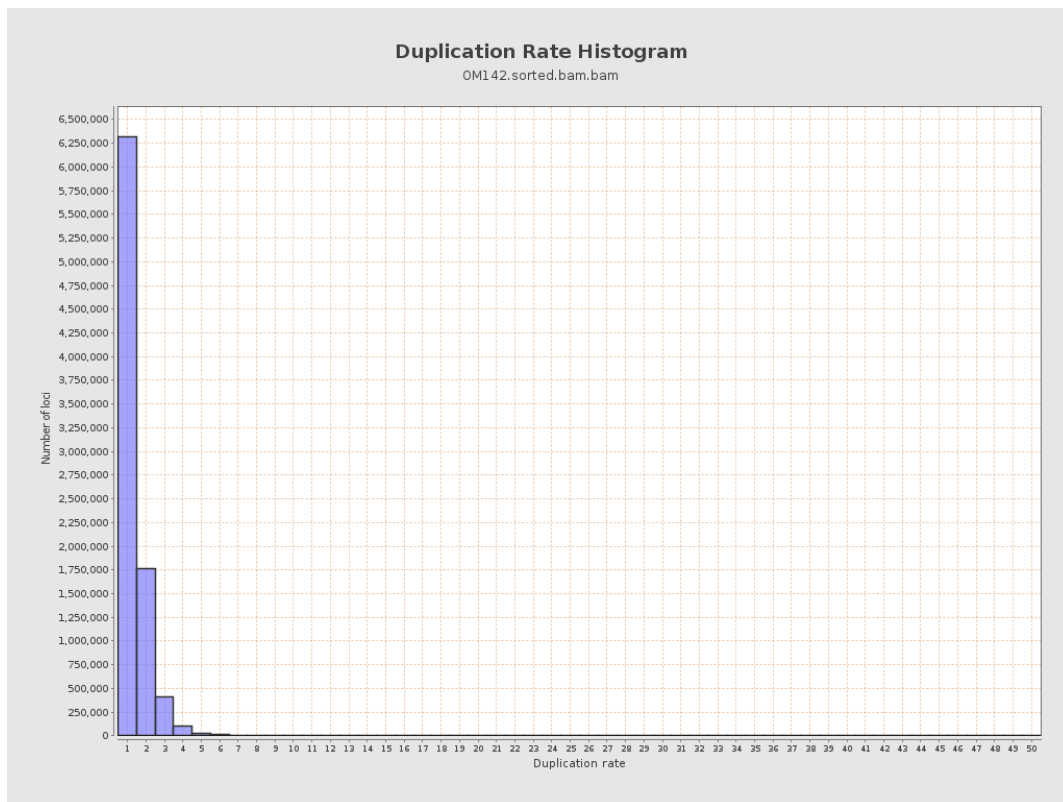
5. Results : Coverage Histogram (0-50X)



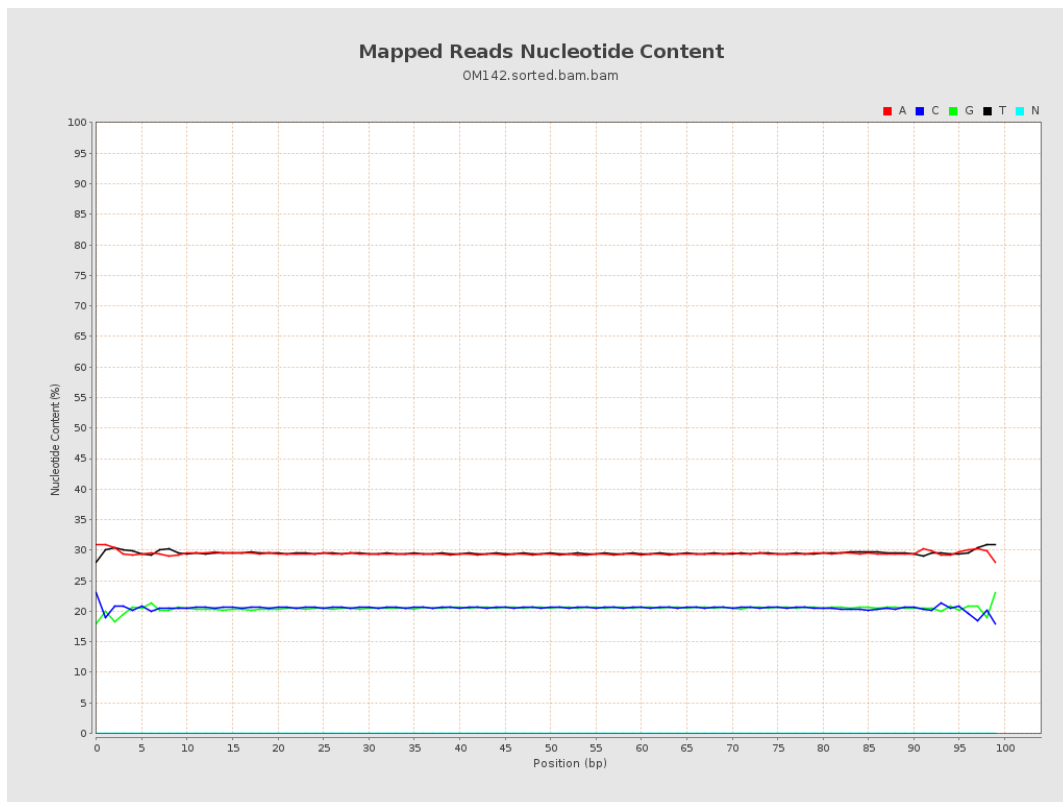
6. Results : Genome Fraction Coverage



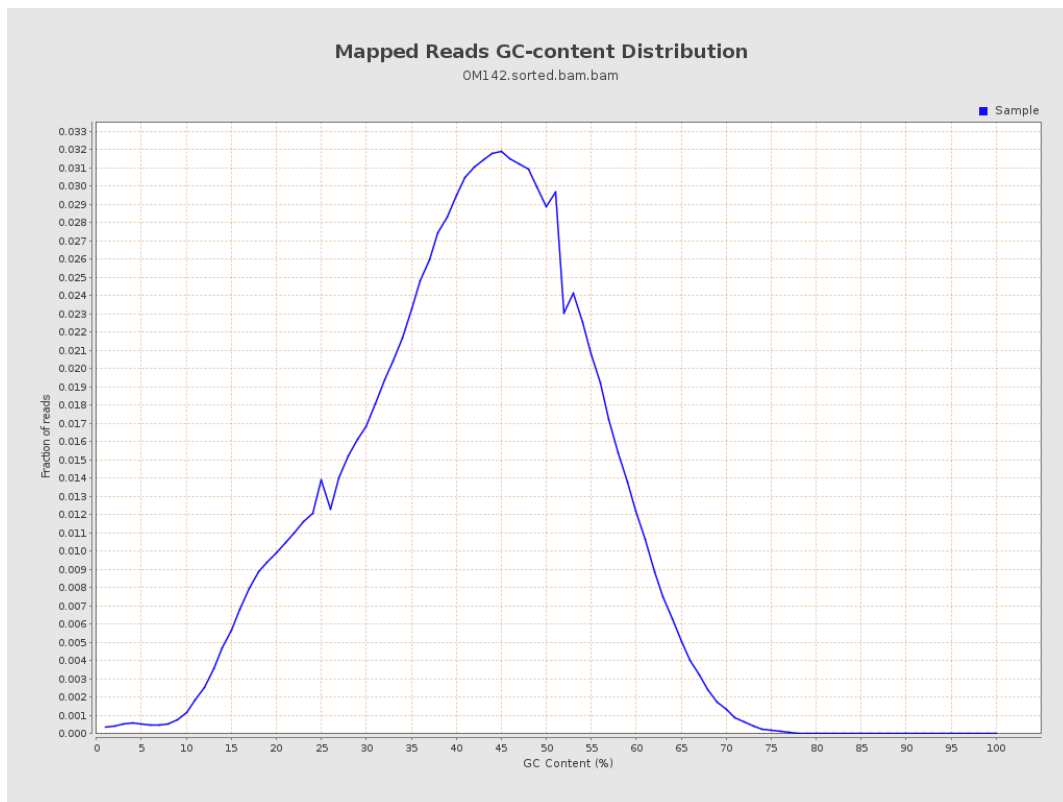
7. Results : Duplication Rate Histogram



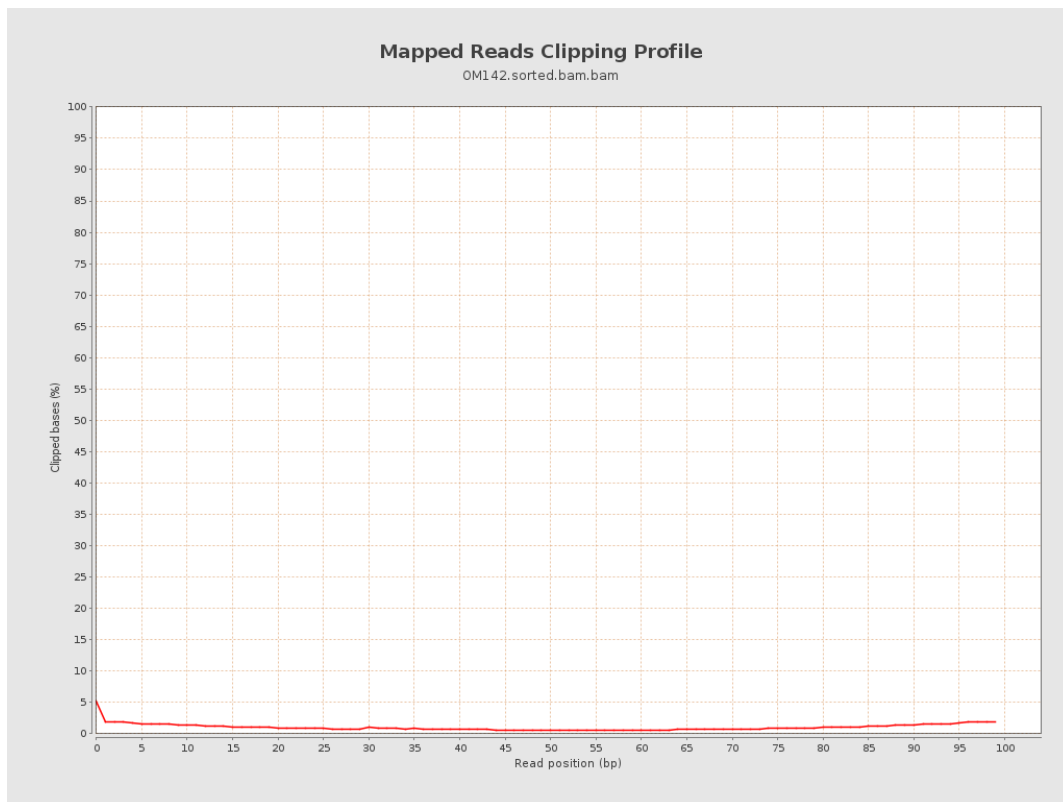
8. Results : Mapped Reads Nucleotide Content



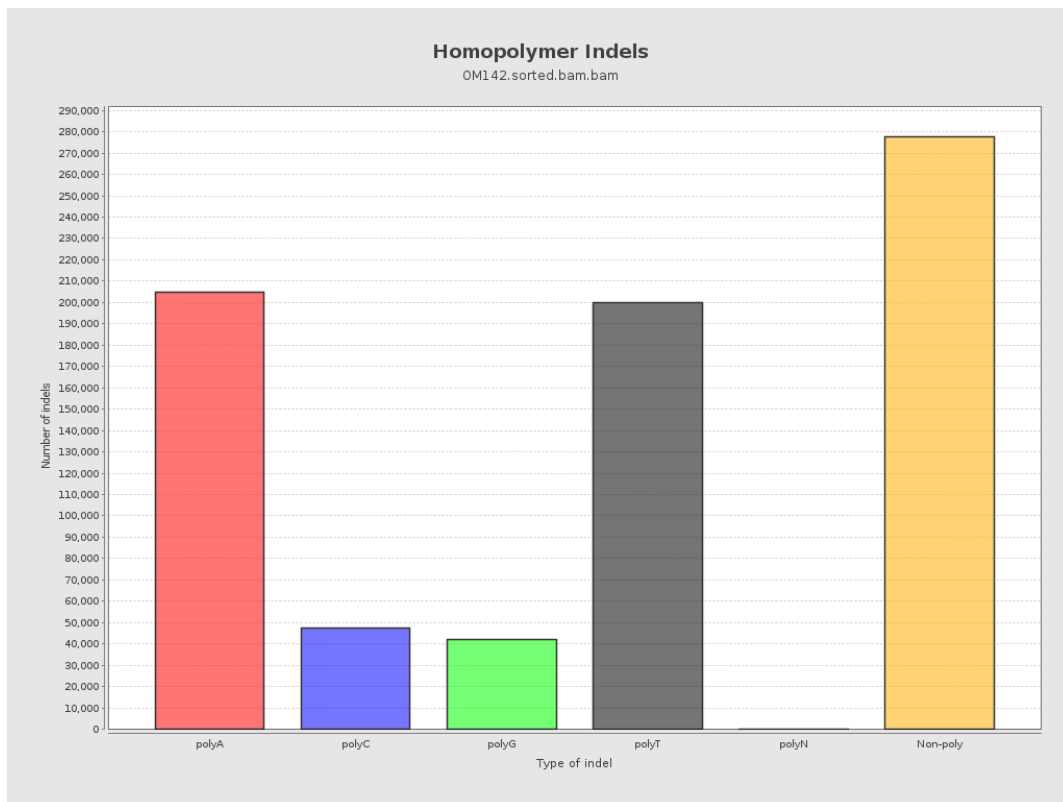
9. Results : Mapped Reads GC-content Distribution



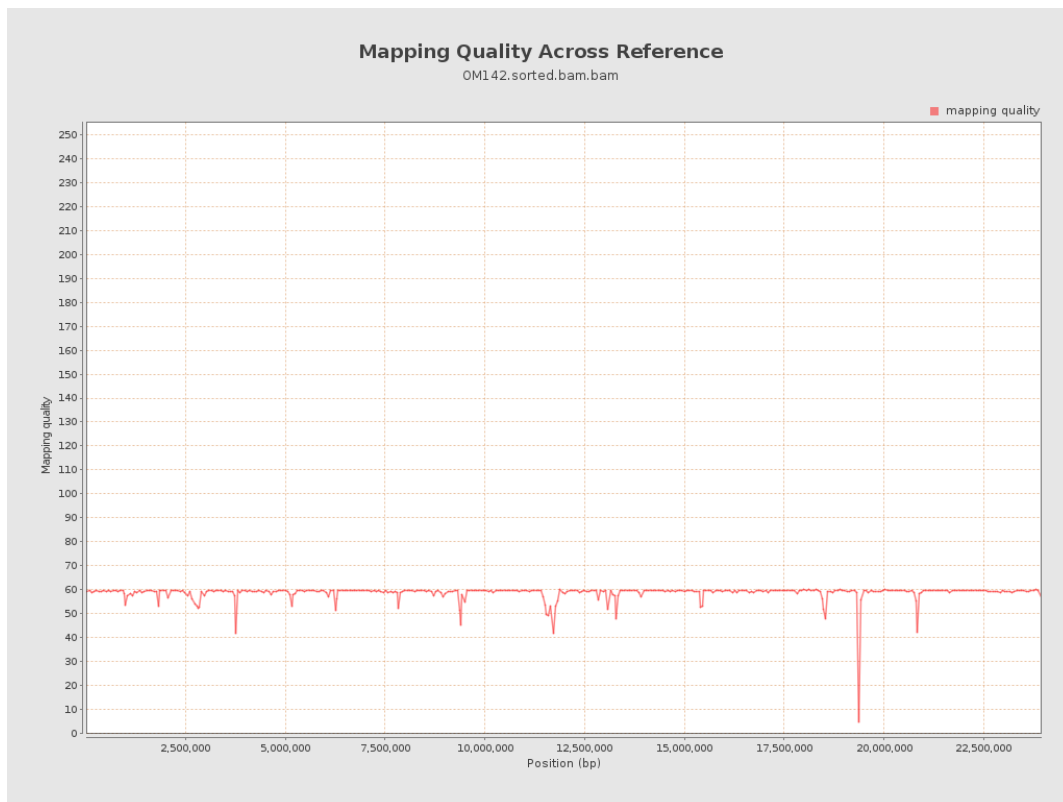
10. Results : Mapped Reads Clipping Profile



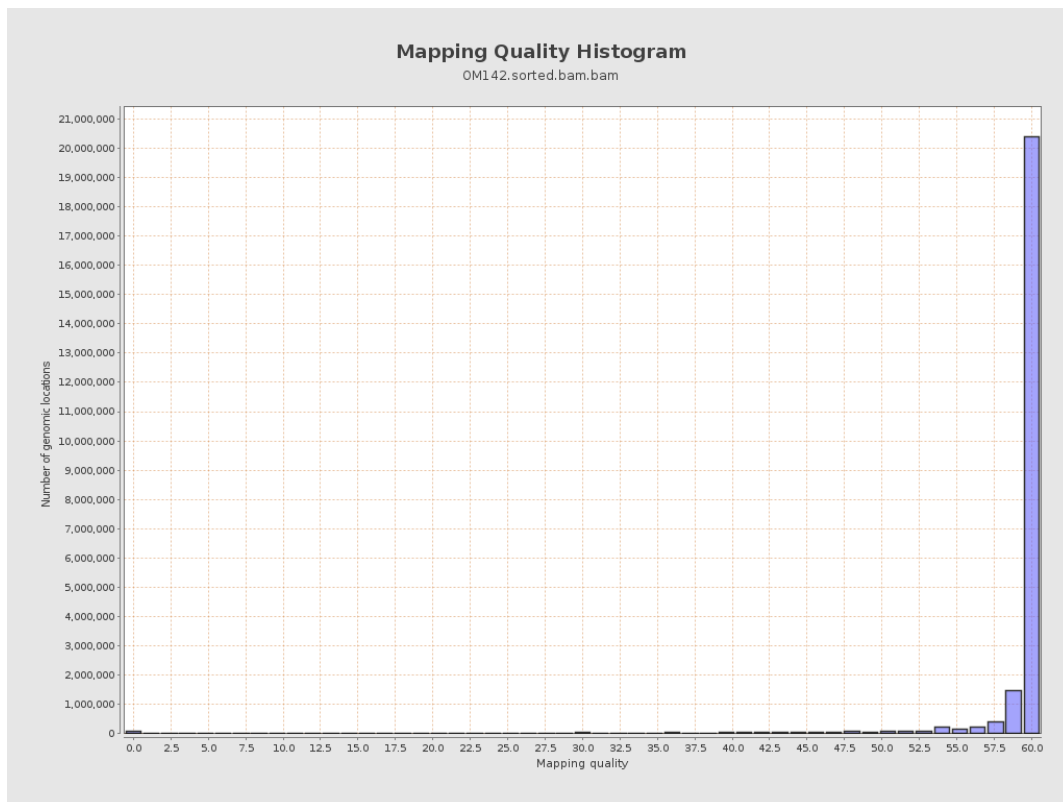
11. Results : Homopolymer Indels



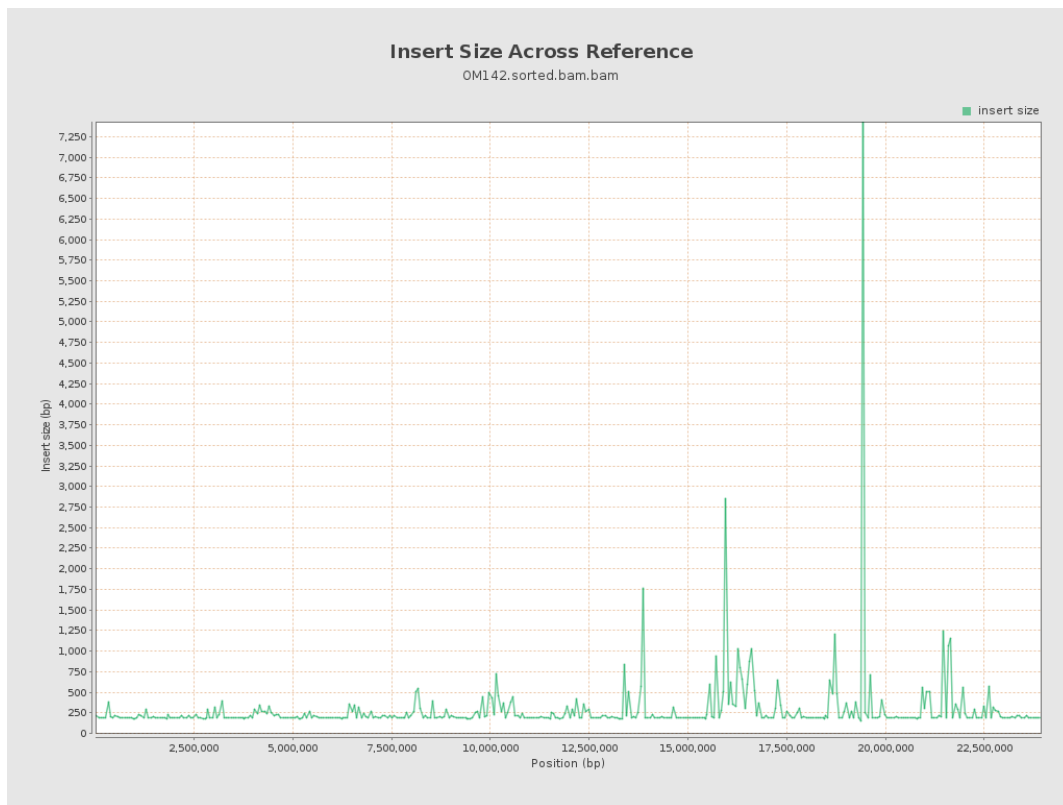
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

