

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 14:07:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM300.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/OM300-BiooBarcode4_GCCAAT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM300-BiooBarcode4_GCCAAT_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:07:04 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM300.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	49,519,315
Mapped reads	7,620,761 / 15.39%
Unmapped reads	41,898,554 / 84.61%
Mapped paired reads	7,620,761 / 15.39%
Mapped reads, first in pair	3,816,868 / 7.71%
Mapped reads, second in pair	3,803,893 / 7.68%
Mapped reads, both in pair	7,237,748 / 14.62%
Mapped reads, singletons	383,013 / 0.77%
Read min/max/mean length	30 / 100 / 99.96
Duplicated reads (estimated)	2,738,436 / 5.53%
Duplication rate	31.58%
Clipped reads	1,036,589 / 2.09%

2.2. ACGT Content

Number/percentage of A's	214,595,510 / 29.75%
Number/percentage of C's	145,424,833 / 20.16%
Number/percentage of T's	216,215,230 / 29.97%
Number/percentage of G's	145,189,234 / 20.13%
Number/percentage of N's	36,253 / 0.01%
GC Percentage	40.28%

2.3. Coverage

Mean	30.1433
Standard Deviation	52.9064

2.4. Mapping Quality

Mean Mapping Quality	57.93
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2.5. Insert size

Mean	773.03
Standard Deviation	24,375.03
P25/Median/P75	254 / 266 / 278

2.6. Mismatches and indels

General error rate	1.31%
Mismatches	8,871,268
Insertions	242,241
Mapped reads with at least one insertion	2.99%
Deletions	277,018
Mapped reads with at least one deletion	3.37%
Homopolymer indels	62.68%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

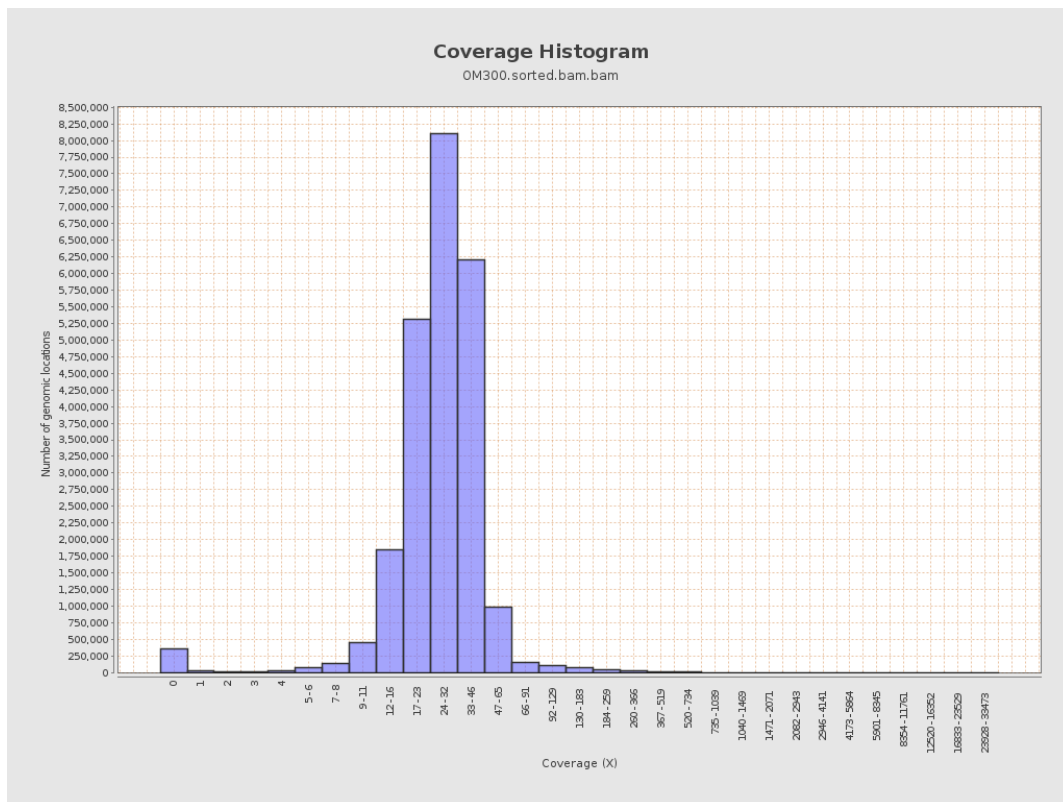
gi 1074120478 emb LT615256.1	977217	26267586	26.88	15.2892
gi 1074120682 emb LT615257.1	860454	25557722	29.7026	26.1002
gi 1074120865 emb LT615258.1	989719	34334880	34.6915	53.5032
gi 1074121086 emb LT615259.1	935450	31349608	33.5129	45.4163
gi 1074121301 emb LT615260.1	1432239	45020533	31.4337	35.3976
gi 1074121615 emb LT615261.1	1080962	32776094	30.3212	31.4834
gi 1074121871 emb LT615262.1	1545099	44068230	28.5213	15.2715
gi 1074122235 emb LT615263.1	1585108	48132546	30.3655	68.4269
gi 1074122590 emb LT615264.1	2122358	61381947	28.9216	17.6222
gi 1074123050 emb LT615265.1	1754192	54474289	31.0538	144.7392
gi 1074123421 emb LT615	2150147	66458930	30.909	51.9147

266.1				
gi 107412389 8 emb LT615 267.1	3031036	88949069	29.3461	39.0662
gi 107412458 8 emb LT615 268.1	2359348	69682332	29.5346	31.2556
gi 107412506 5 emb LT615 269.1	3135668	93749804	29.8979	14.3673

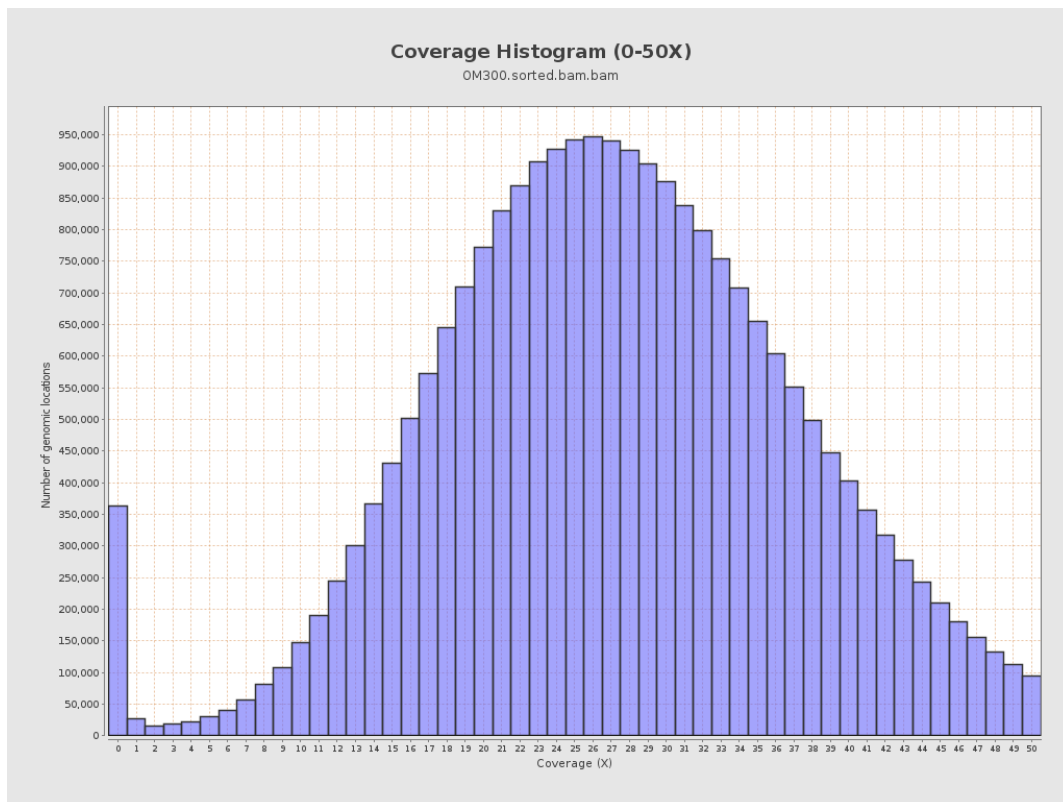
3. Results : Coverage across reference



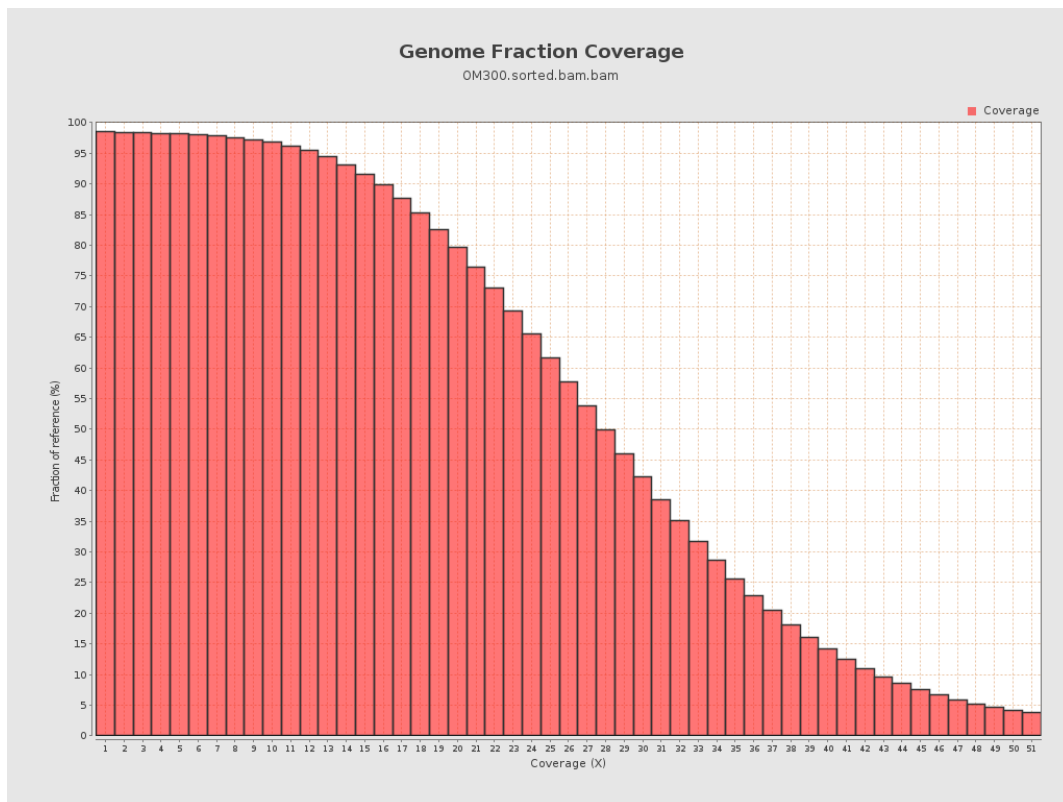
4. Results : Coverage Histogram



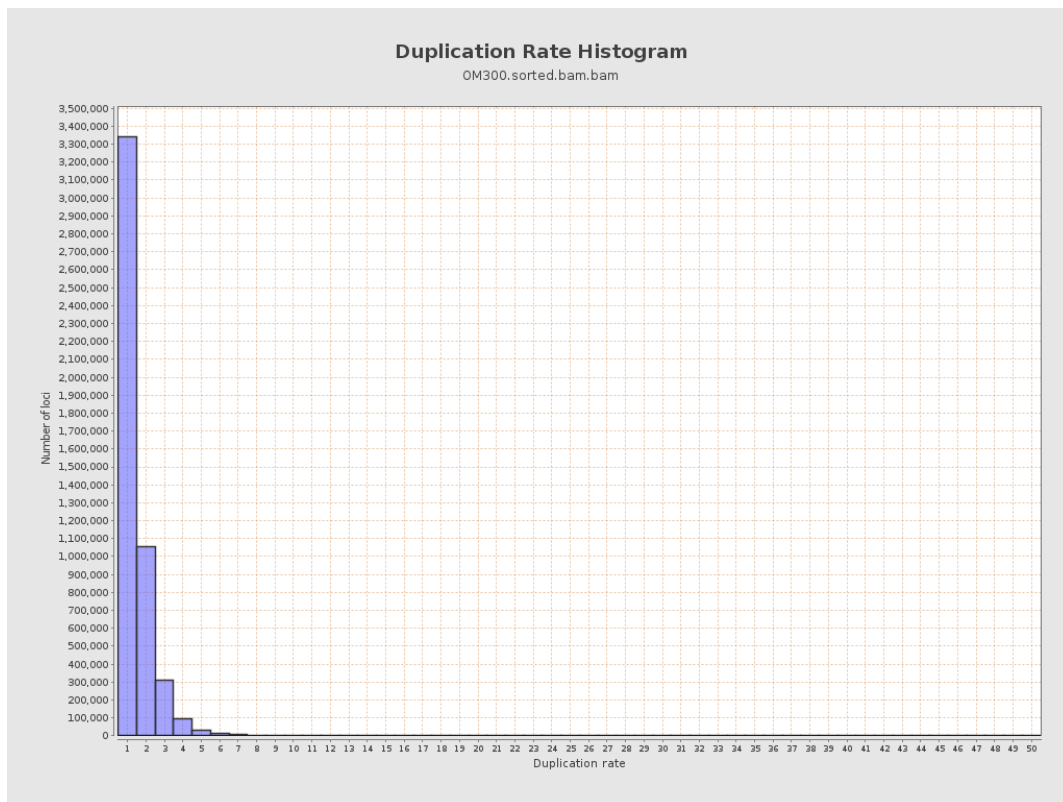
5. Results : Coverage Histogram (0-50X)



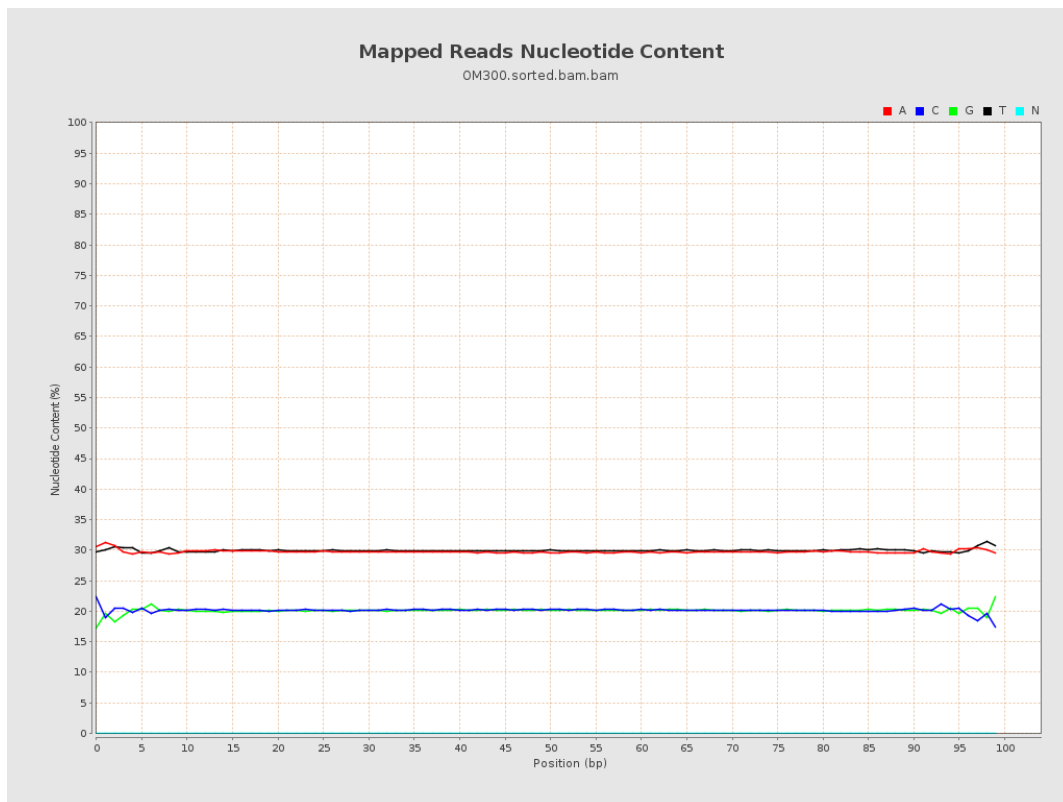
6. Results : Genome Fraction Coverage



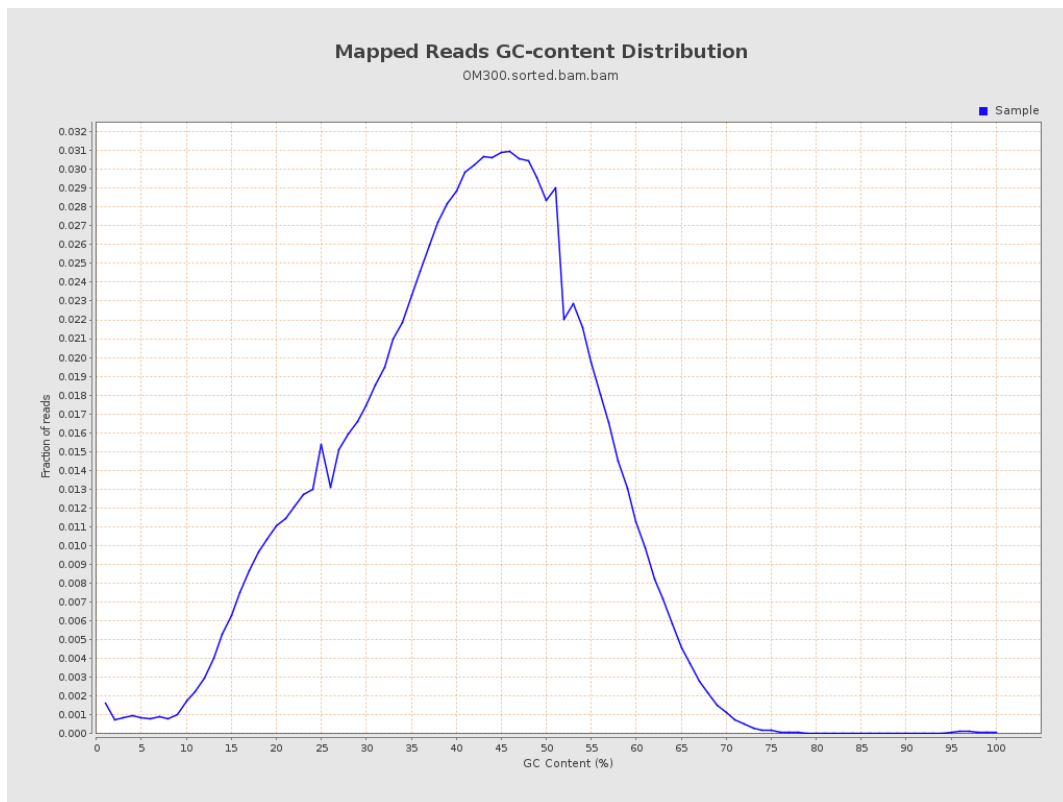
7. Results : Duplication Rate Histogram



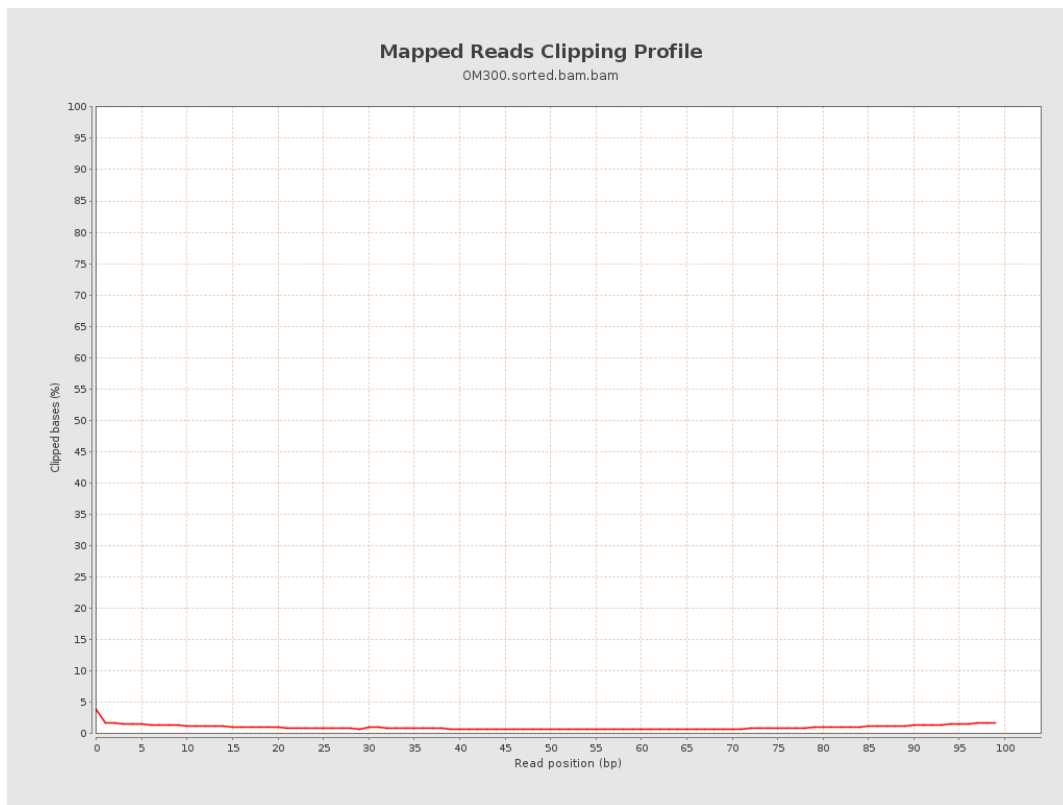
8. Results : Mapped Reads Nucleotide Content



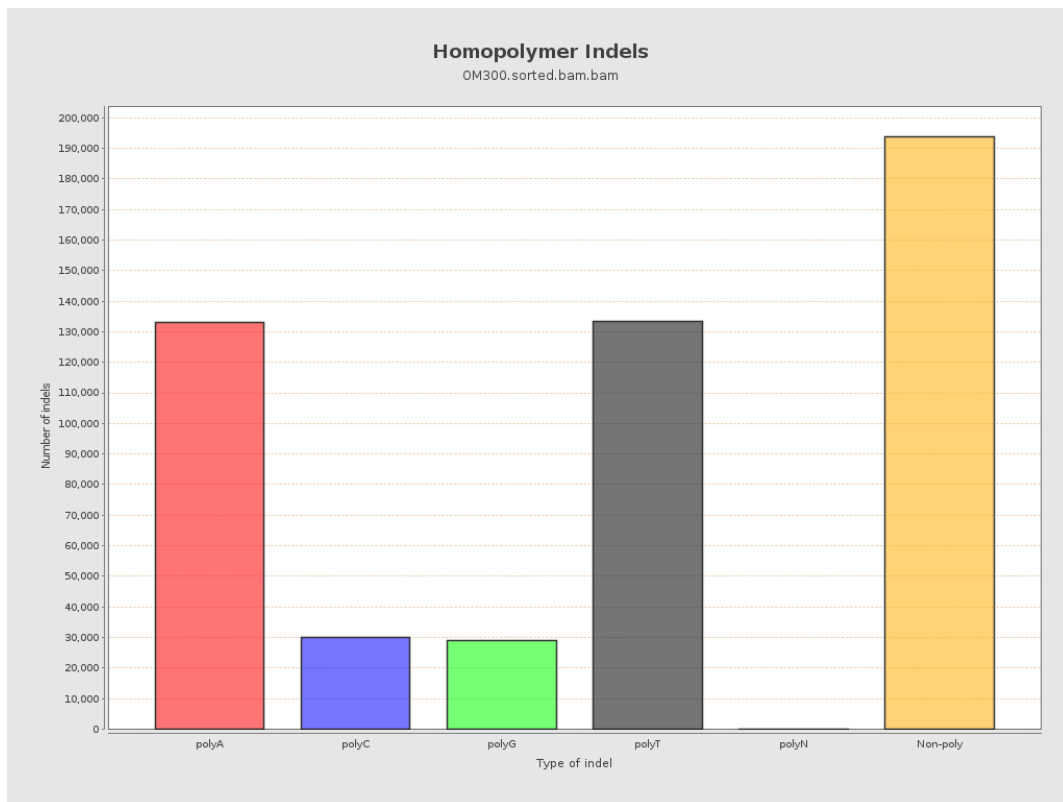
9. Results : Mapped Reads GC-content Distribution



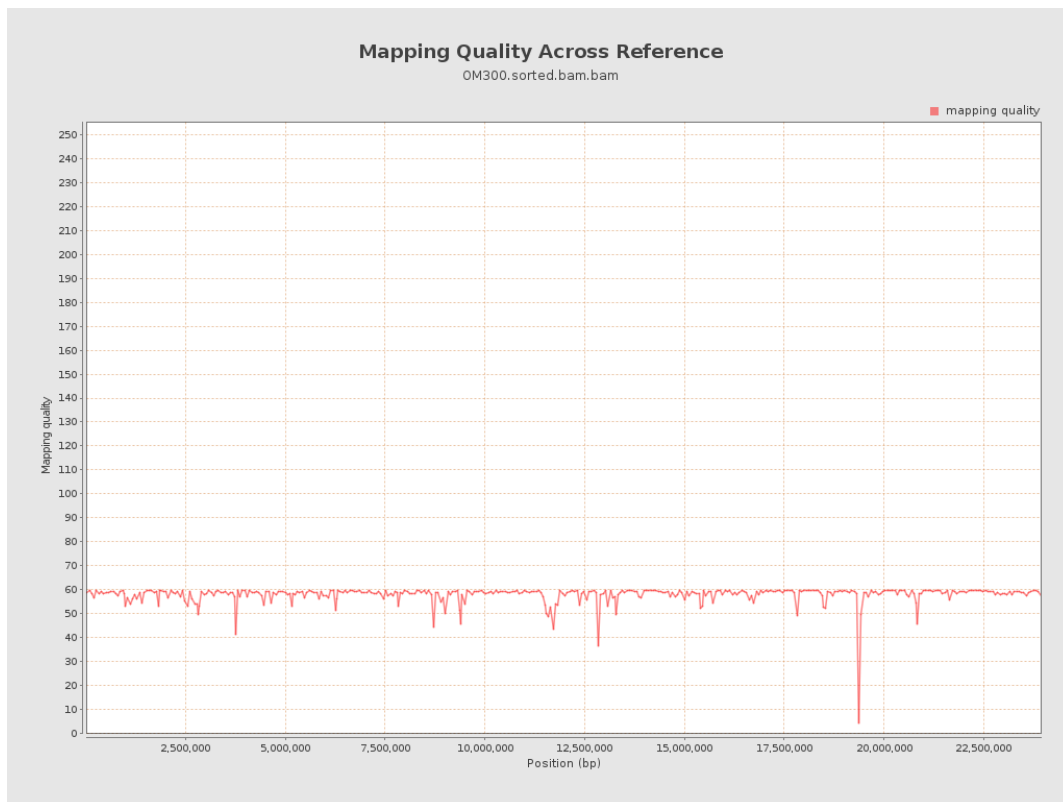
10. Results : Mapped Reads Clipping Profile



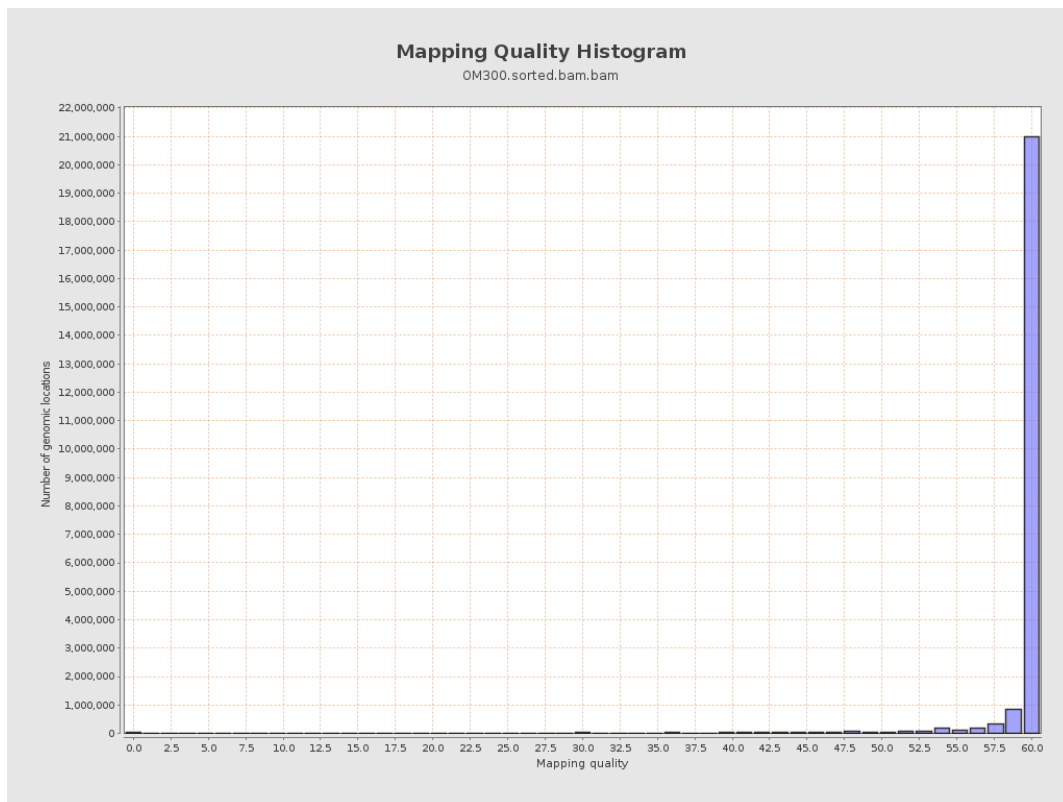
11. Results : Homopolymer Indels



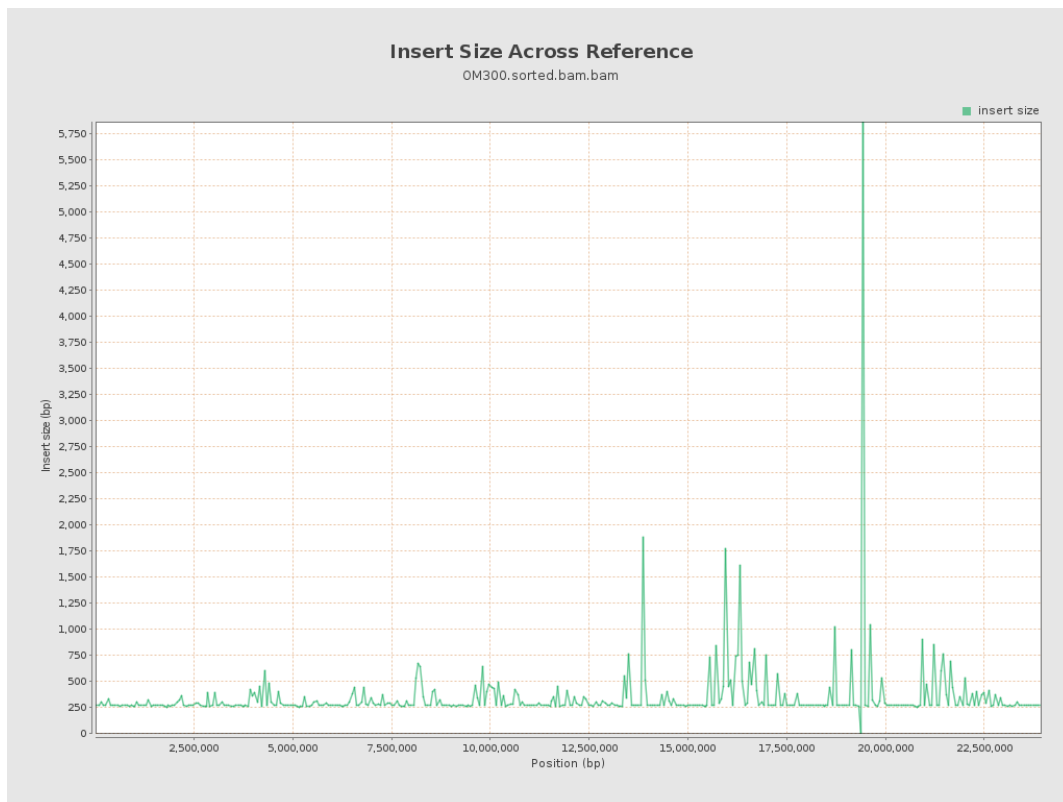
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

