

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 13:07:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM114.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/OM-114_CAGATC_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM-114_CAGATC_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:07:10 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM114.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	60,685,392
Mapped reads	3,348,435 / 5.52%
Unmapped reads	57,336,957 / 94.48%
Mapped paired reads	3,348,435 / 5.52%
Mapped reads, first in pair	1,676,112 / 2.76%
Mapped reads, second in pair	1,672,323 / 2.76%
Mapped reads, both in pair	2,883,128 / 4.75%
Mapped reads, singletons	465,307 / 0.77%
Read min/max/mean length	30 / 100 / 99.97
Duplicated reads (estimated)	896,049 / 1.48%
Duplication rate	14.43%
Clipped reads	766,953 / 1.26%

2.2. ACGT Content

Number/percentage of A's	88,192,218 / 29.73%
Number/percentage of C's	59,098,566 / 19.92%
Number/percentage of T's	90,306,902 / 30.45%
Number/percentage of G's	59,025,140 / 19.9%
Number/percentage of N's	10,006 / 0%
GC Percentage	39.82%

2.3. Coverage

Mean	12.3956
Standard Deviation	74.0861

2.4. Mapping Quality

Mean Mapping Quality	55.78
----------------------	-------

2.5. Insert size

Mean	1,121.6
Standard Deviation	33,655.11
P25/Median/P75	217 / 228 / 251

2.6. Mismatches and indels

General error rate	1.25%
Mismatches	3,404,299
Insertions	122,207
Mapped reads with at least one insertion	3.36%
Deletions	140,024
Mapped reads with at least one deletion	3.56%
Homopolymer indels	60.67%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

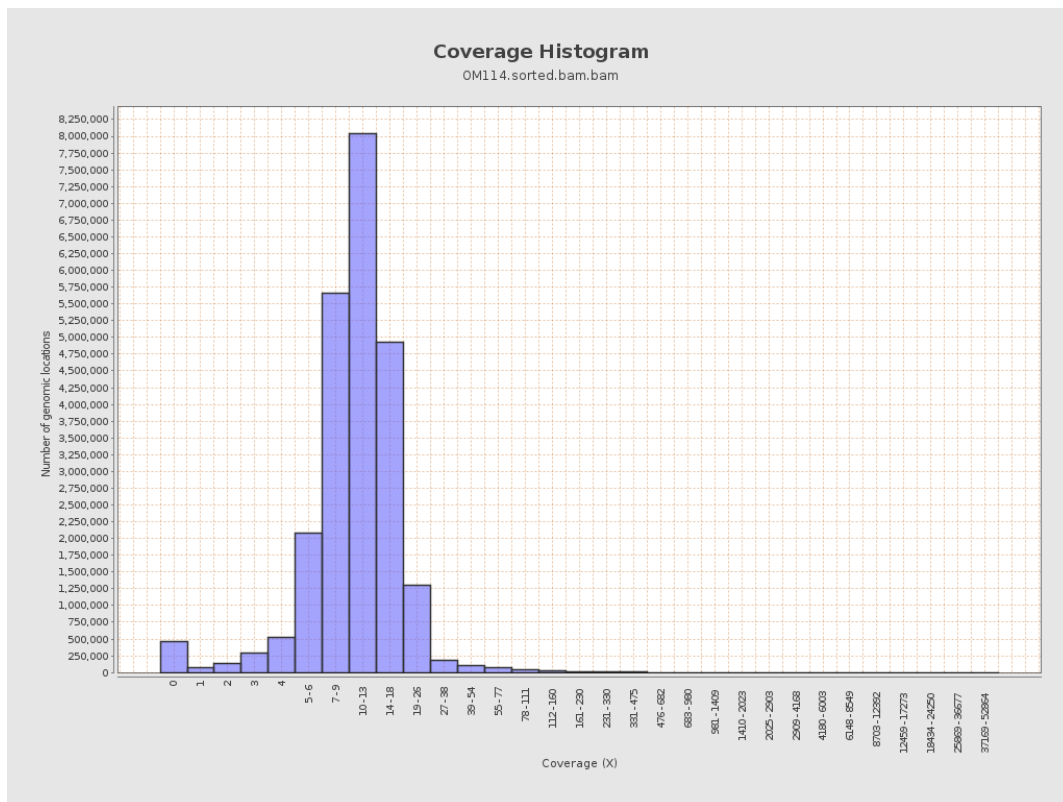
gi 1074120478 emb LT615256.1	977217	11008826	11.2655	17.124
gi 1074120682 emb LT615257.1	860454	11051492	12.8438	31.4841
gi 1074120865 emb LT615258.1	989719	13293015	13.4311	34.866
gi 1074121086 emb LT615259.1	935450	12579601	13.4476	20.9075
gi 1074121301 emb LT615260.1	1432239	18313072	12.7863	41.7723
gi 1074121615 emb LT615261.1	1080962	13302922	12.3066	28.3246
gi 1074121871 emb LT615262.1	1545099	17880197	11.5722	17.6265
gi 1074122235 emb LT615263.1	1585108	20771746	13.1043	107.1027
gi 1074122590 emb LT615264.1	2122358	24848803	11.7081	12.7826
gi 1074123050 emb LT615265.1	1754192	24846275	14.1639	226.9033
gi 1074123421 emb LT615	2150147	27448219	12.7657	30.2421

266.1				
gi 107412389 8 emb LT615 267.1	3031036	36900149	12.1741	63.6024
gi 107412458 8 emb LT615 268.1	2359348	27090060	11.482	19.6799
gi 107412506 5 emb LT615 269.1	3135668	37652413	12.0078	16.9992

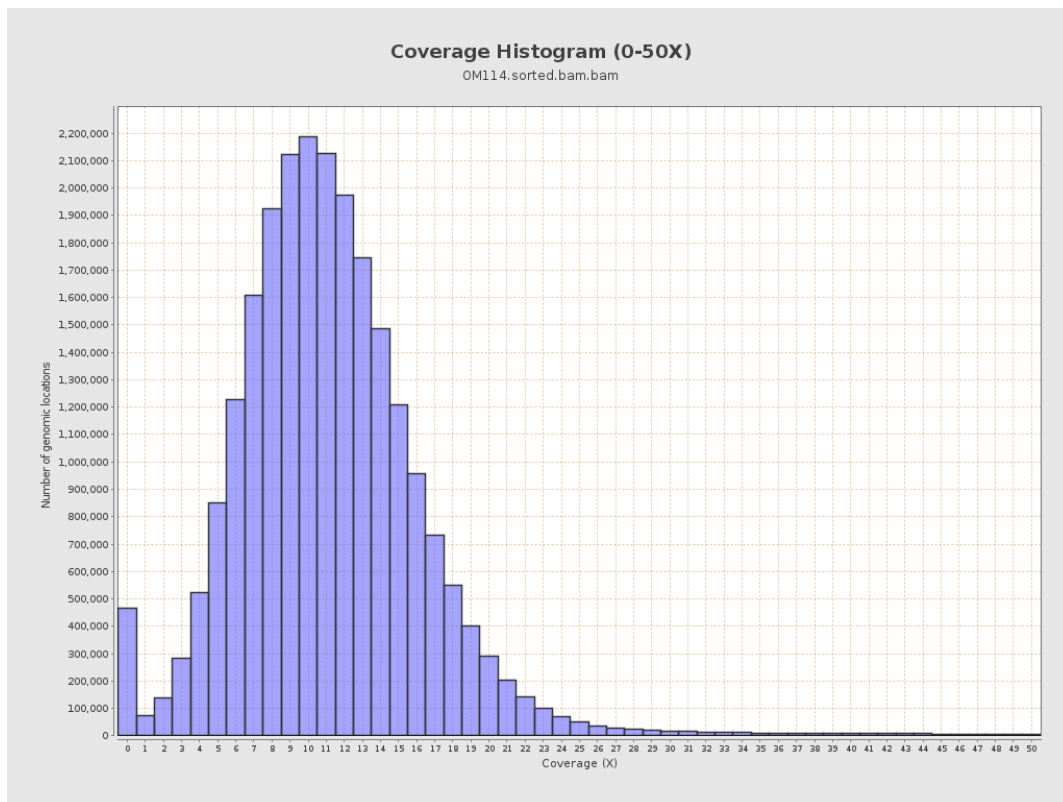
3. Results : Coverage across reference



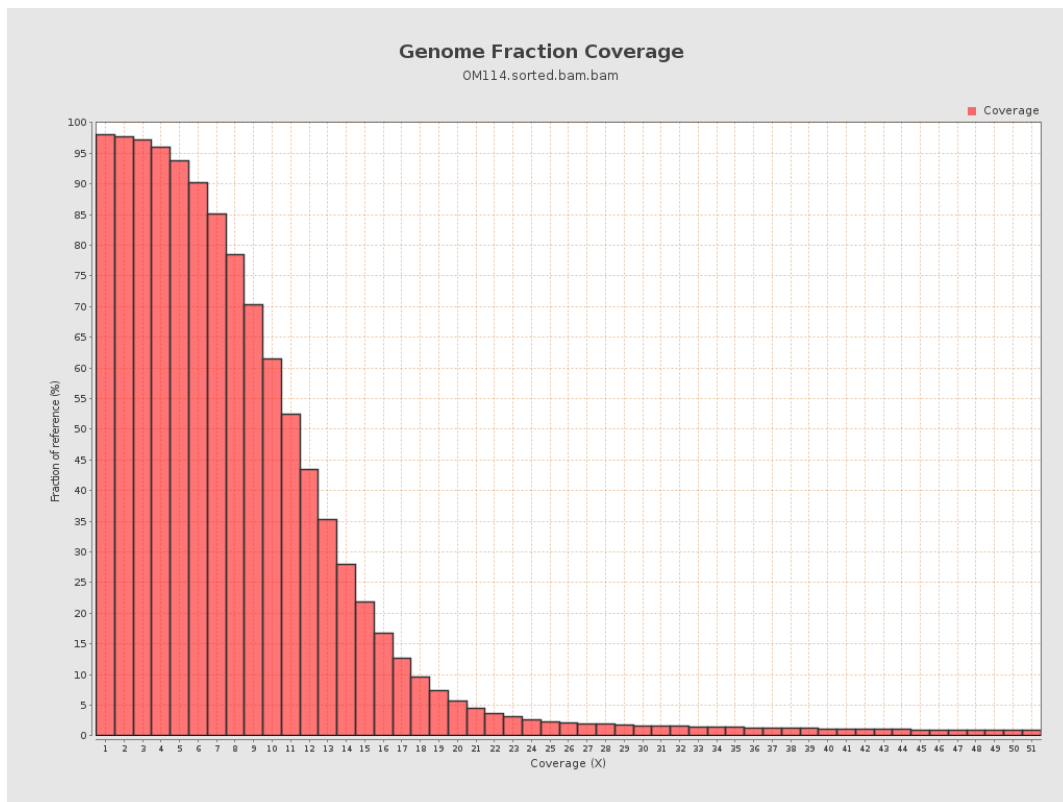
4. Results : Coverage Histogram



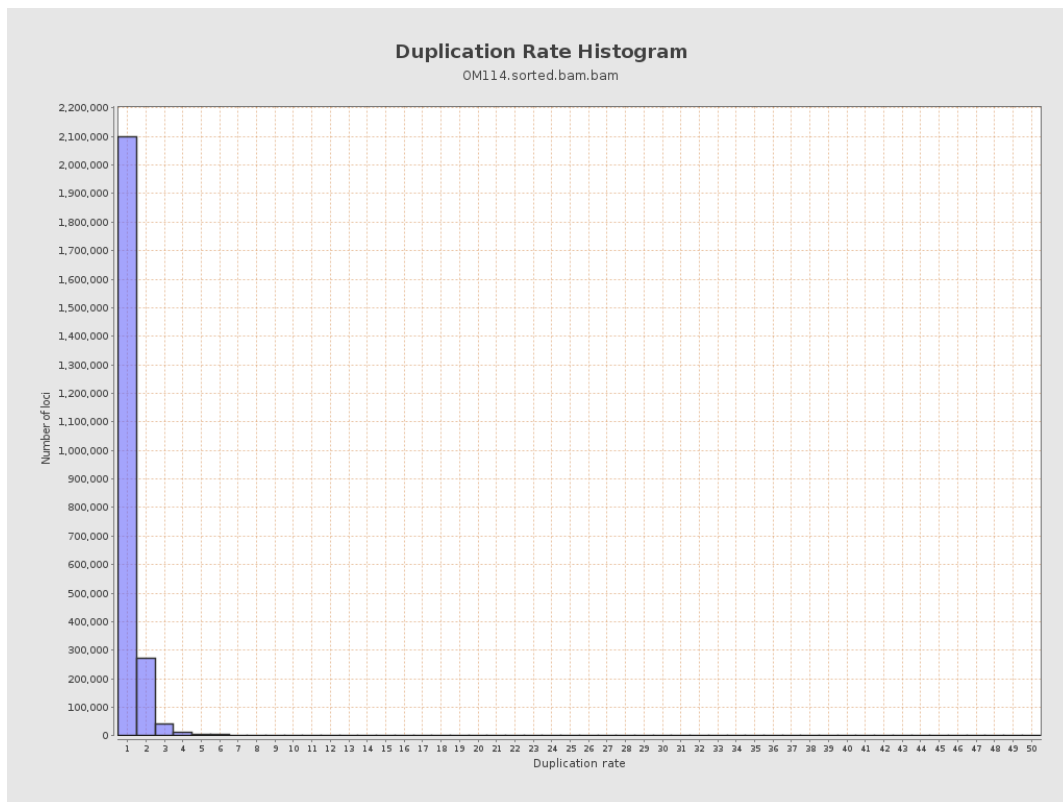
5. Results : Coverage Histogram (0-50X)



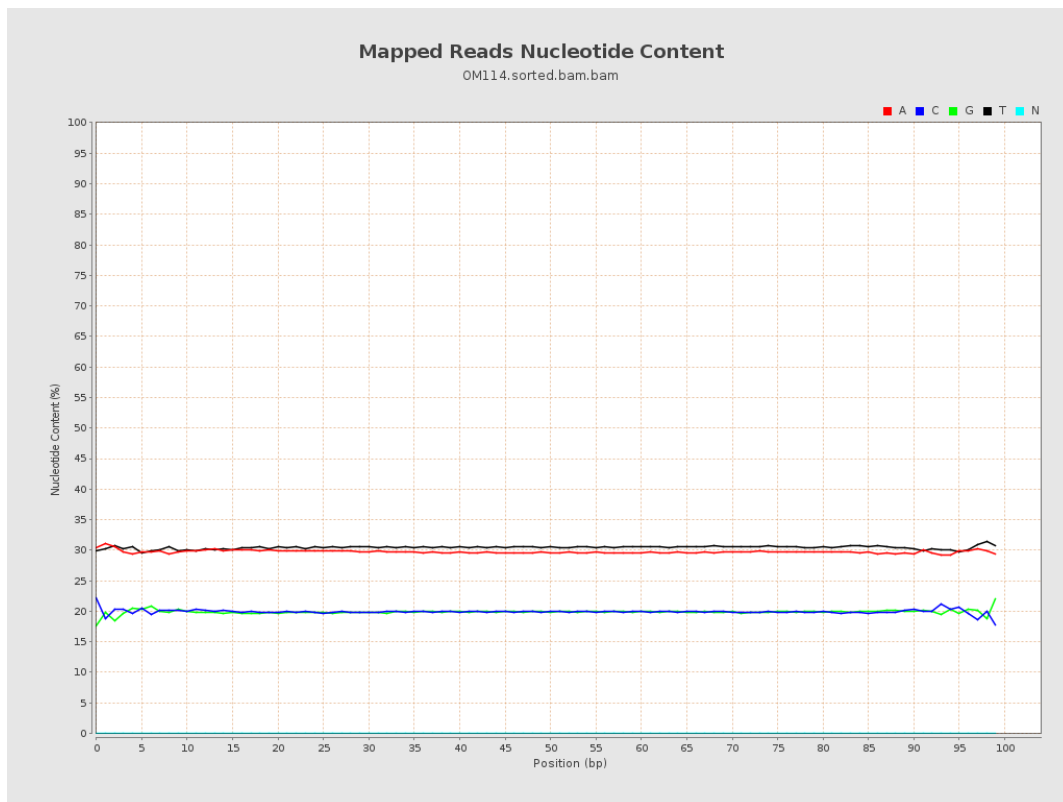
6. Results : Genome Fraction Coverage



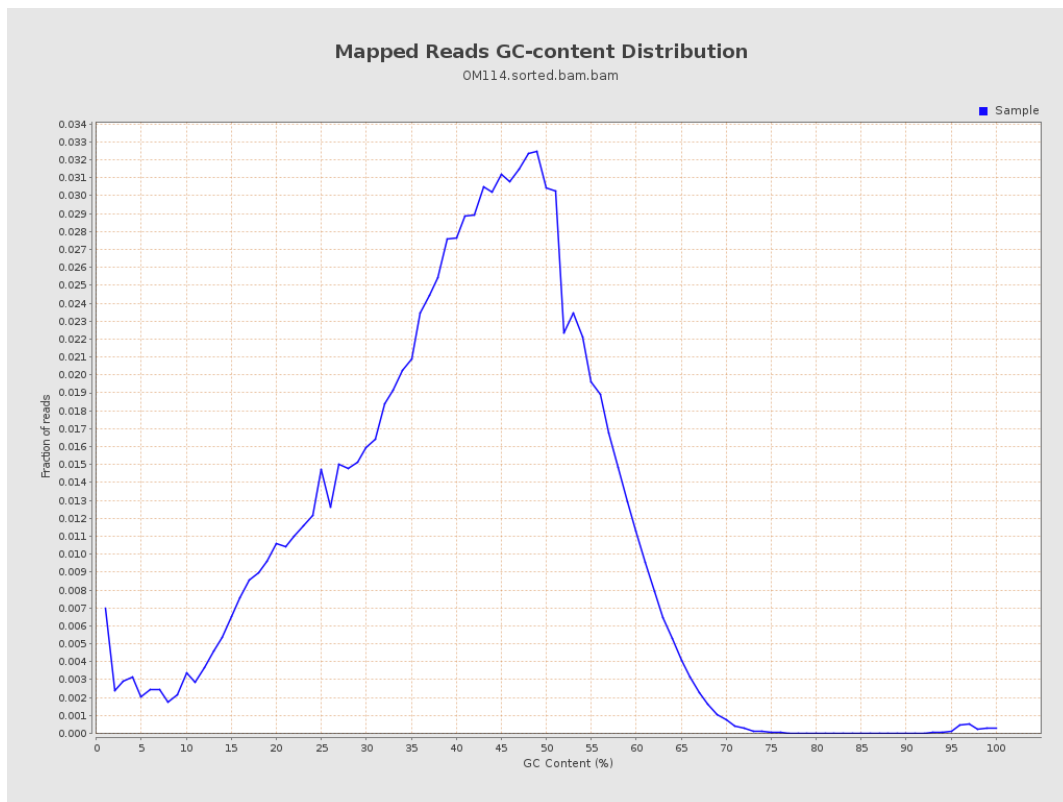
7. Results : Duplication Rate Histogram



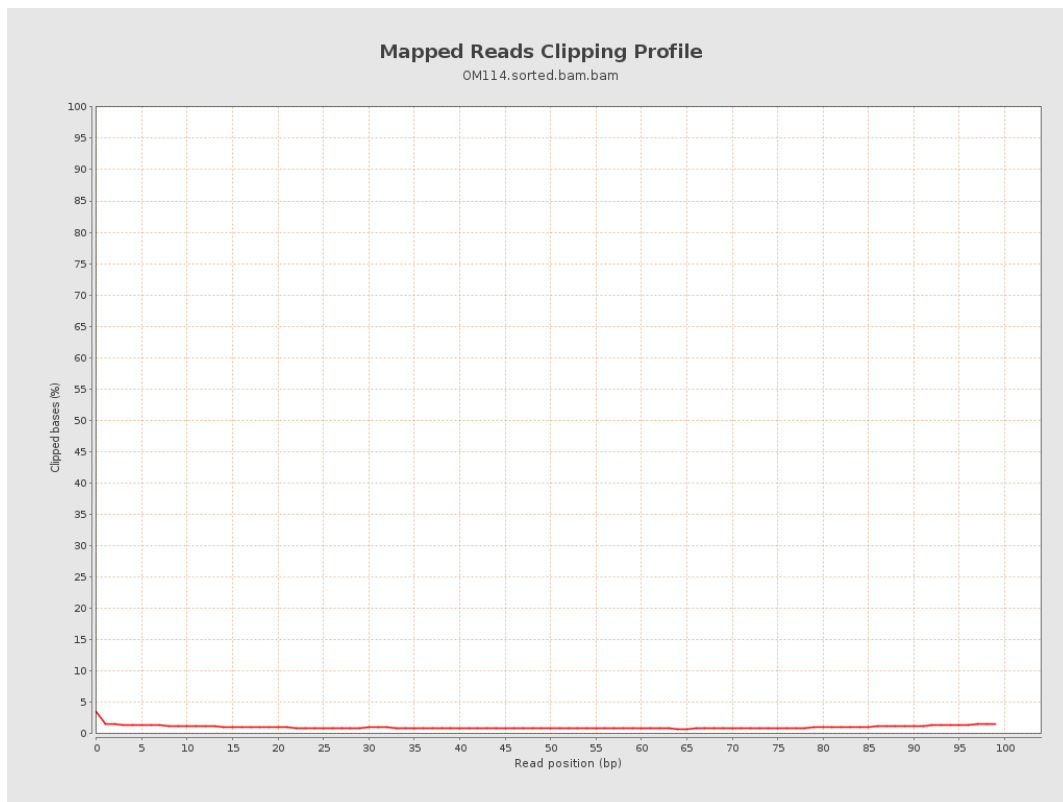
8. Results : Mapped Reads Nucleotide Content



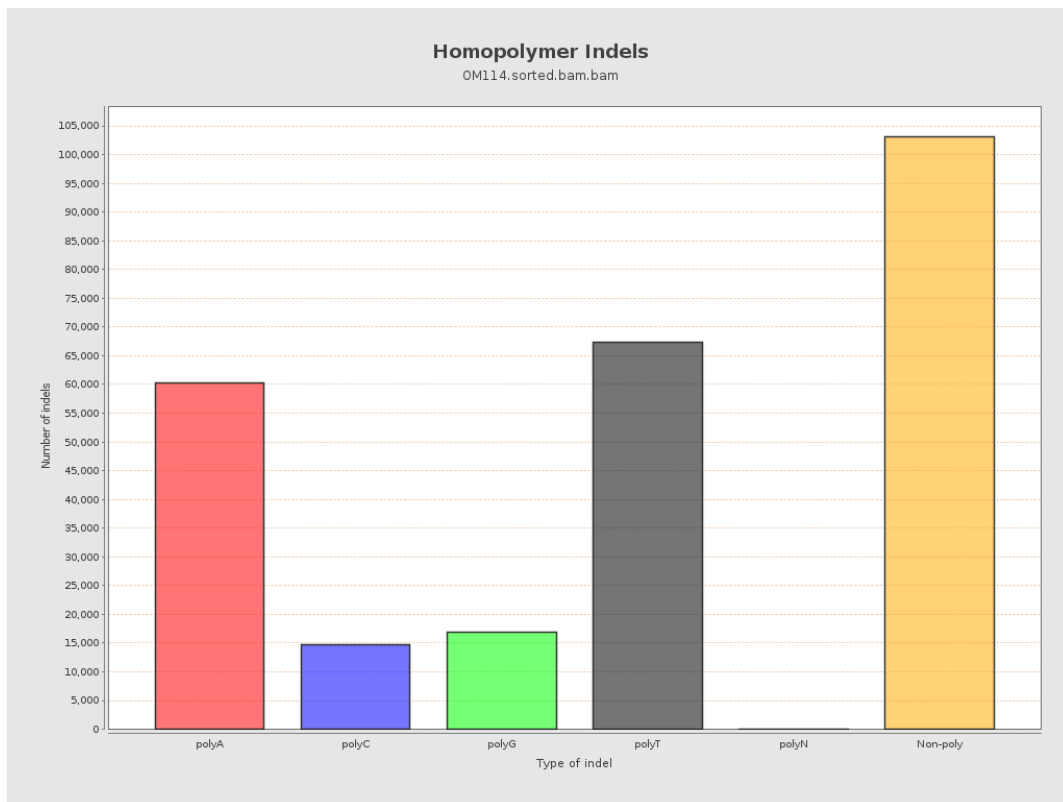
9. Results : Mapped Reads GC-content Distribution



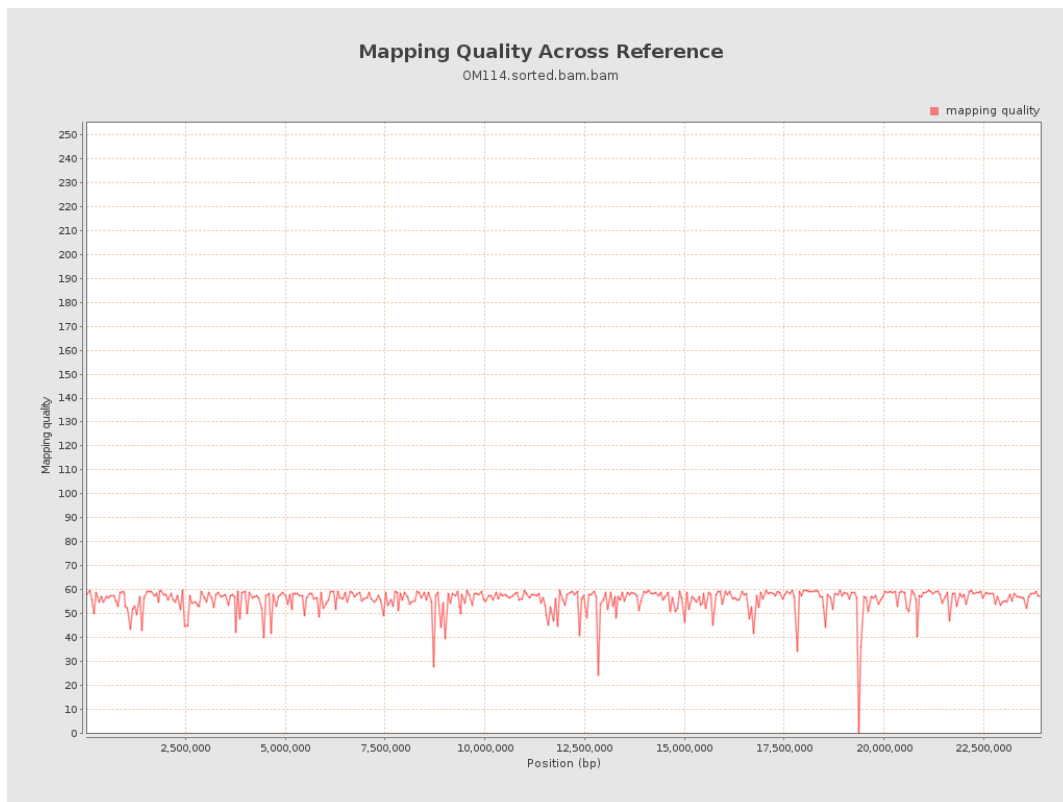
10. Results : Mapped Reads Clipping Profile



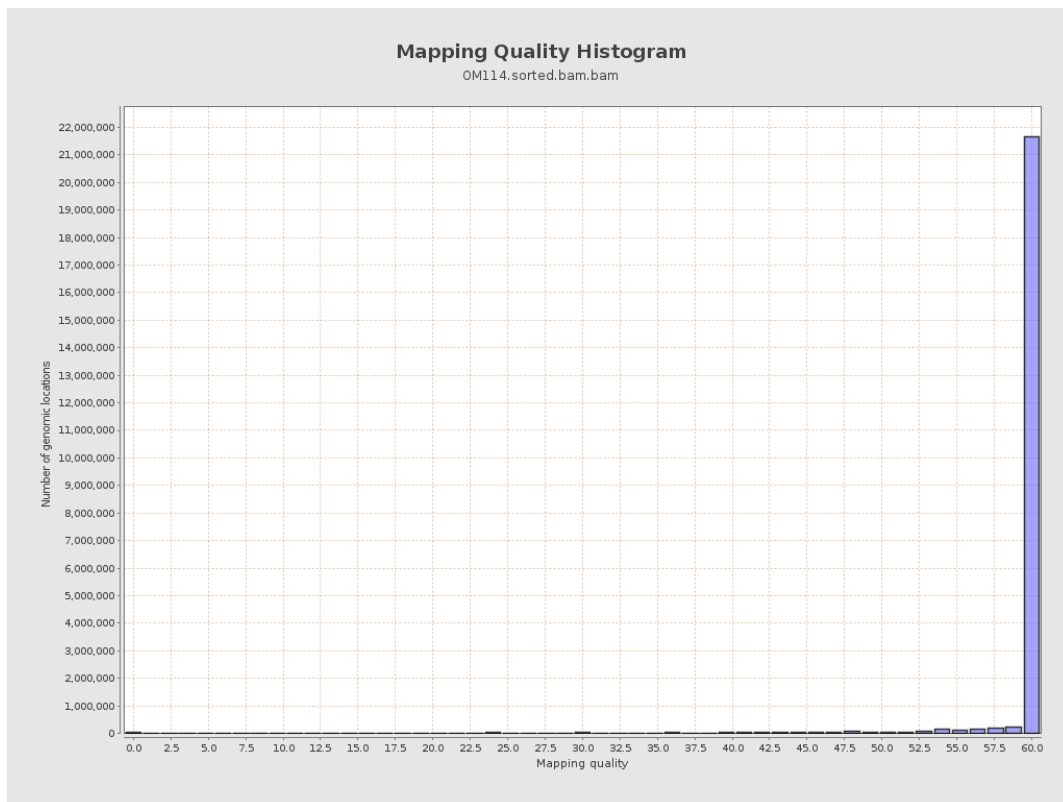
11. Results : Homopolymer Indels



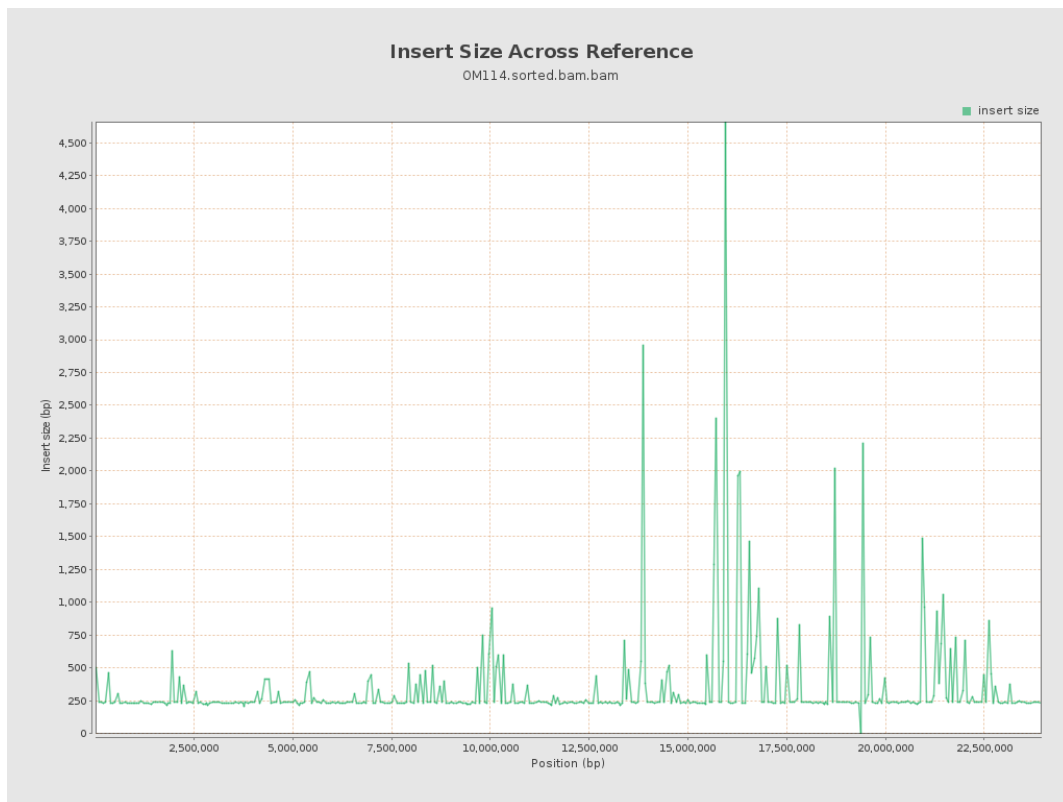
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

