

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 13:25:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM125.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-125_ATCACG_R2.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM-125_ATCACG_R1.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:25:00 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM125.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	60,519,116
Mapped reads	1,610,475 / 2.66%
Unmapped reads	58,908,641 / 97.34%
Mapped paired reads	1,610,475 / 2.66%
Mapped reads, first in pair	807,308 / 1.33%
Mapped reads, second in pair	803,167 / 1.33%
Mapped reads, both in pair	1,145,638 / 1.89%
Mapped reads, singletons	464,837 / 0.77%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	564,093 / 0.93%
Duplication rate	11.71%
Clipped reads	608,211 / 1%

2.2. ACGT Content

Number/percentage of A's	38,372,251 / 30.1%
Number/percentage of C's	24,382,623 / 19.13%
Number/percentage of T's	40,279,472 / 31.6%
Number/percentage of G's	24,432,138 / 19.17%
Number/percentage of N's	3,689 / 0%
GC Percentage	38.3%

2.3. Coverage

Mean	5.3277
Standard Deviation	75.776

2.4. Mapping Quality

Mean Mapping Quality	52.32
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2.5. Insert size

Mean	1,637.38
Standard Deviation	41,051.53
P25/Median/P75	214 / 225 / 240

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	1,499,957
Insertions	68,639
Mapped reads with at least one insertion	3.83%
Deletions	73,672
Mapped reads with at least one deletion	3.71%
Homopolymer indels	55.7%

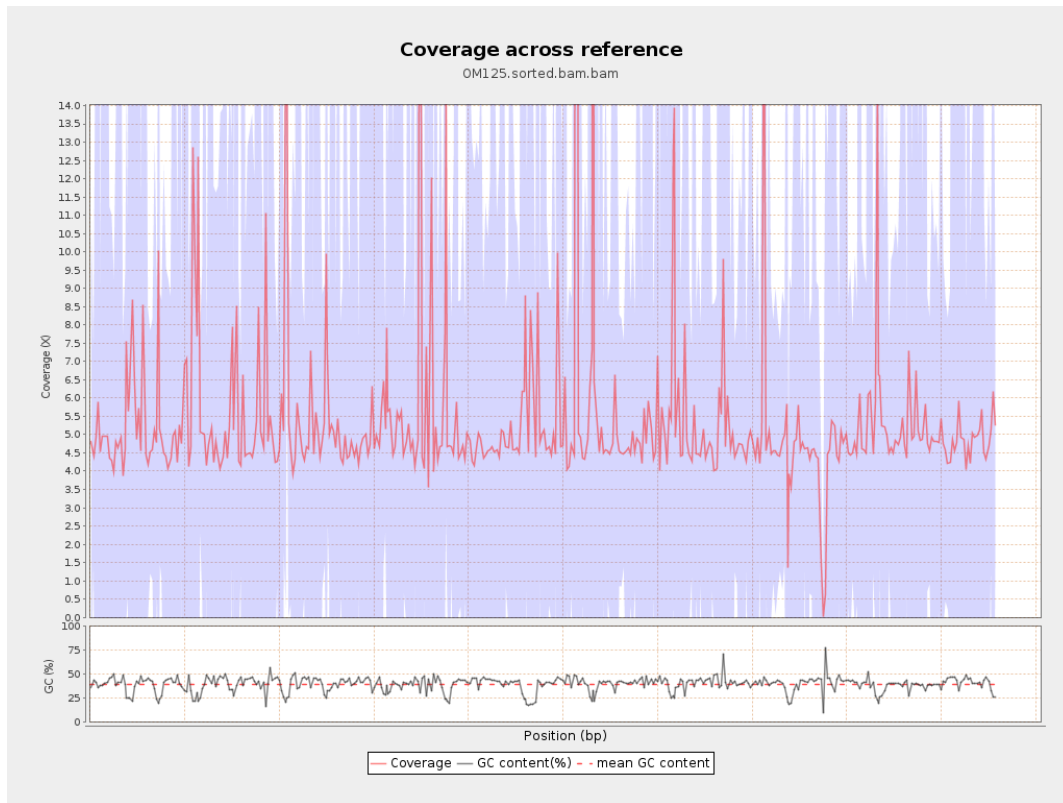
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

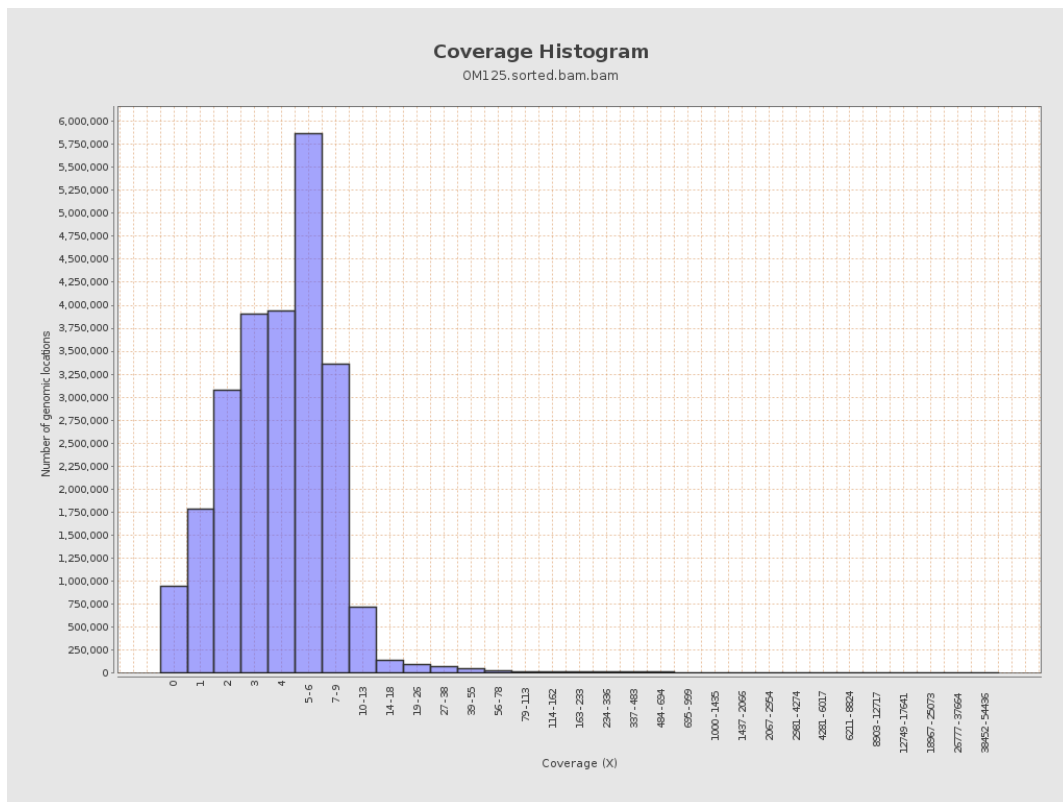
gi 1074120478 emb LT615256.1	977217	4629206	4.7371	17.4054
gi 1074120682 emb LT615257.1	860454	4988376	5.7974	31.1445
gi 1074120865 emb LT615258.1	989719	5704827	5.7641	33.3265
gi 1074121086 emb LT615259.1	935450	4895140	5.2329	12.7346
gi 1074121301 emb LT615260.1	1432239	8296857	5.7929	38.3672
gi 1074121615 emb LT615261.1	1080962	5772721	5.3404	27.9195
gi 1074121871 emb LT615262.1	1545099	7602989	4.9207	18.0787
gi 1074122235 emb LT615263.1	1585108	9670856	6.1011	110.4619
gi 1074122590 emb LT615264.1	2122358	10232948	4.8215	12.6272
gi 1074123050 emb LT615265.1	1754192	11714995	6.6783	233.6772
gi 1074123421 emb LT615	2150147	11483806	5.3409	23.3645

266.1				
gi 107412389 8 emb LT615 267.1	3031036	15975806	5.2707	66.7406
gi 107412458 8 emb LT615 268.1	2359348	10964544	4.6473	17.0336
gi 107412506 5 emb LT615 269.1	3135668	15712908	5.011	16.9496

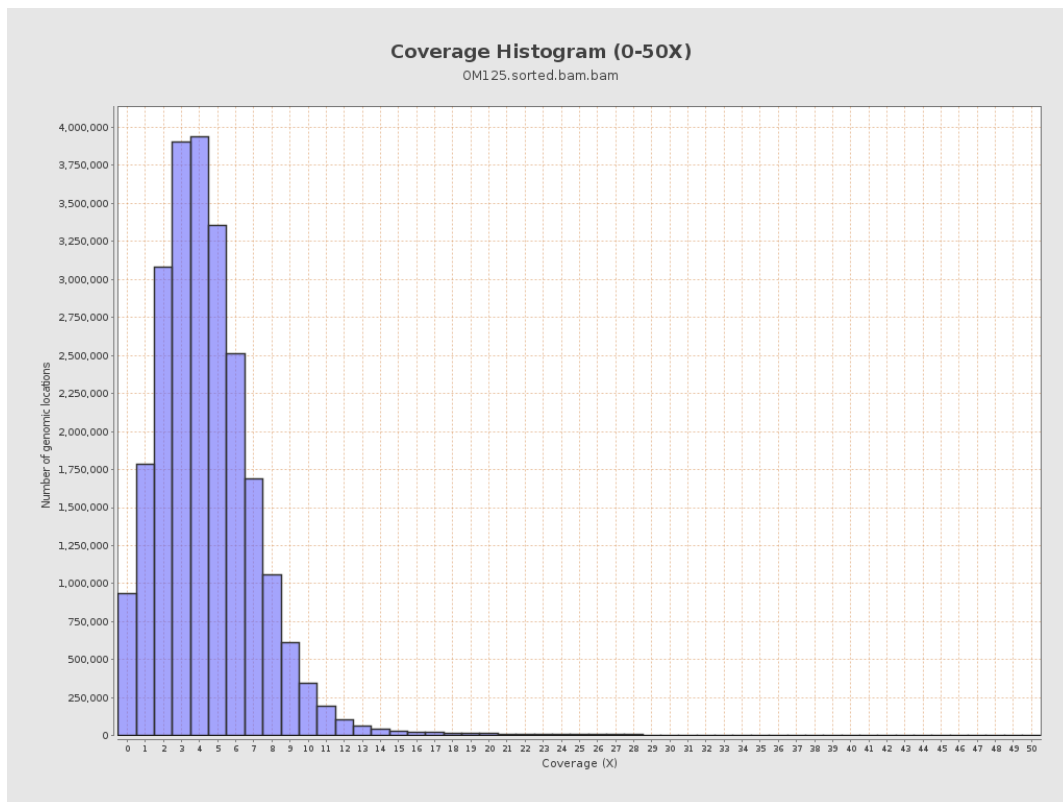
3. Results : Coverage across reference



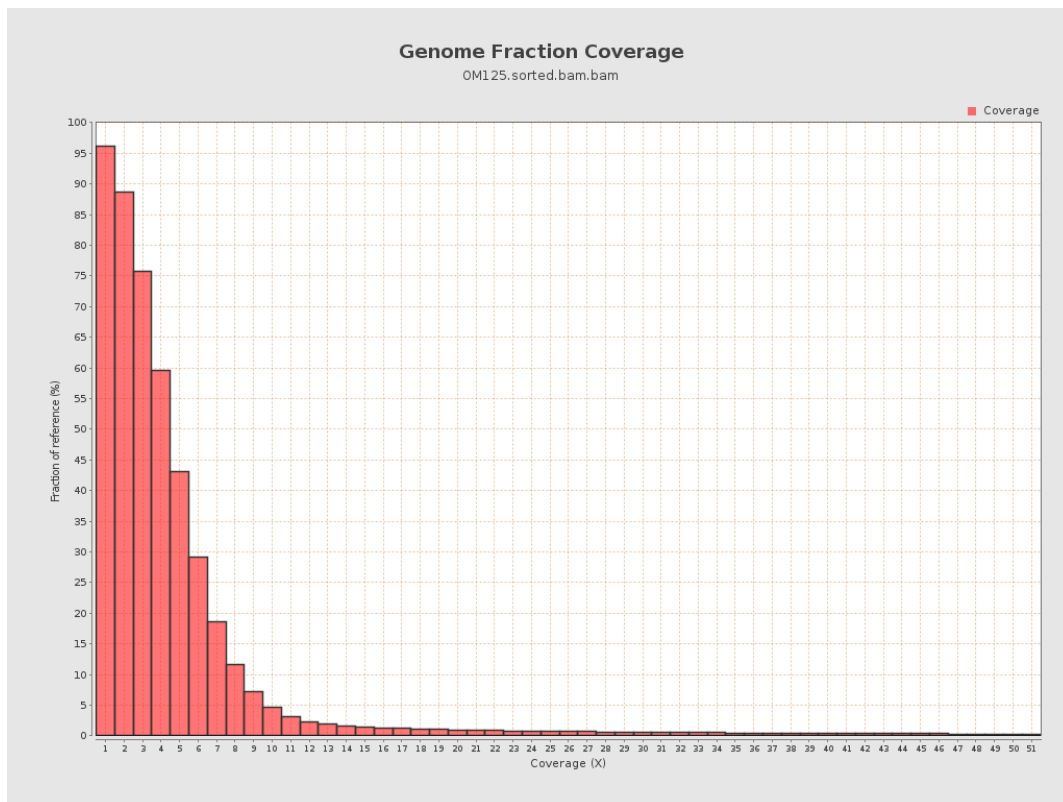
4. Results : Coverage Histogram



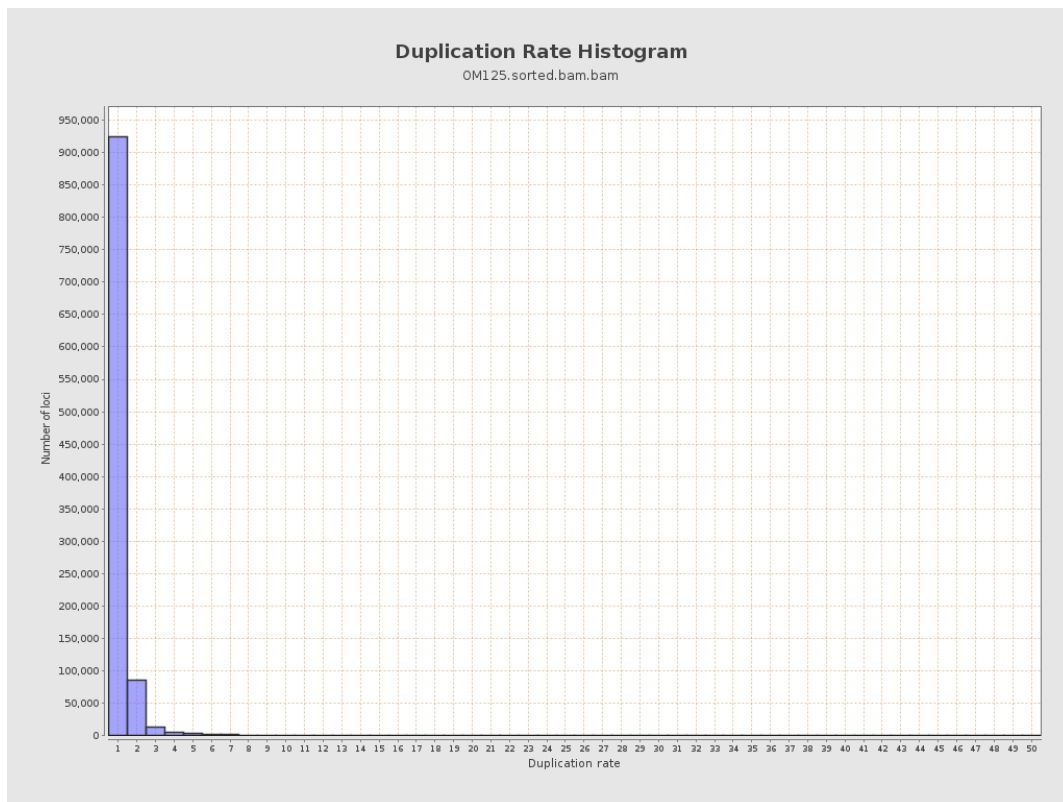
5. Results : Coverage Histogram (0-50X)



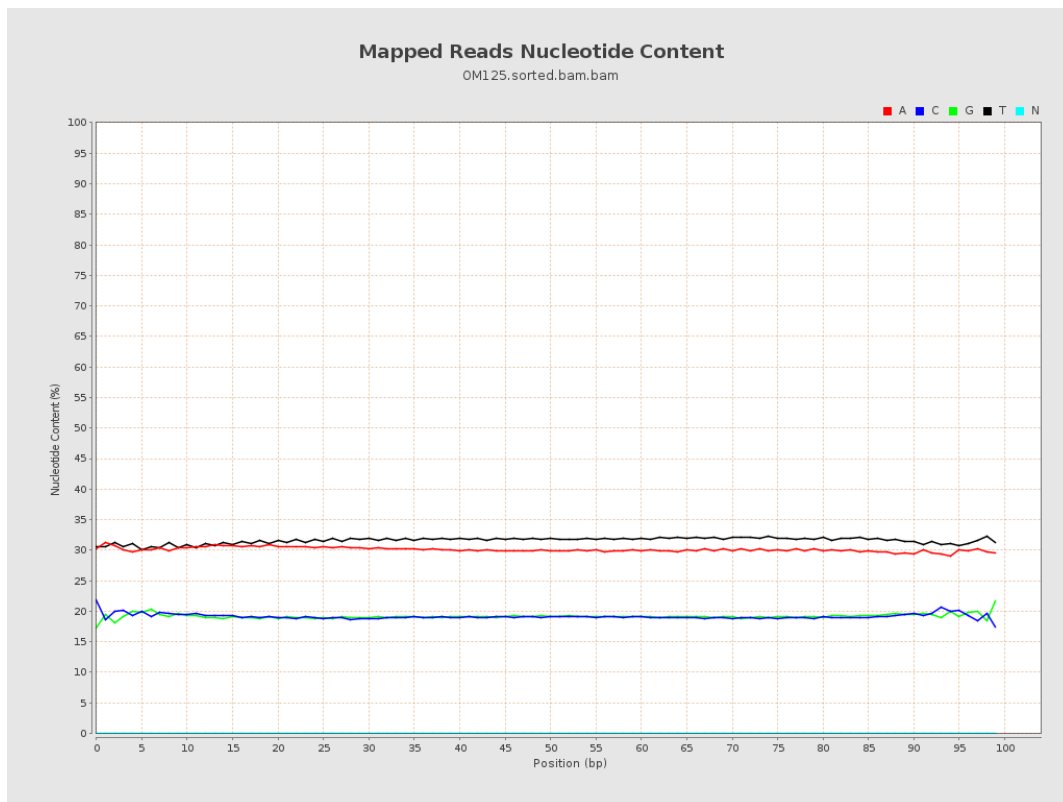
6. Results : Genome Fraction Coverage



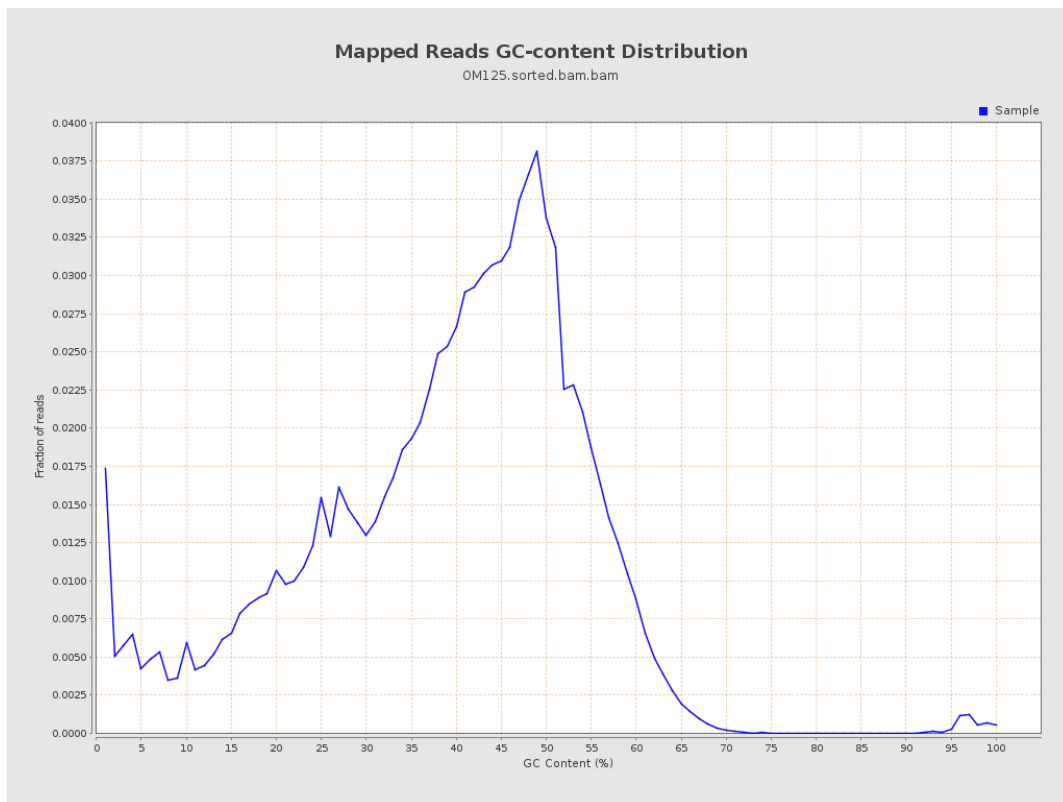
7. Results : Duplication Rate Histogram



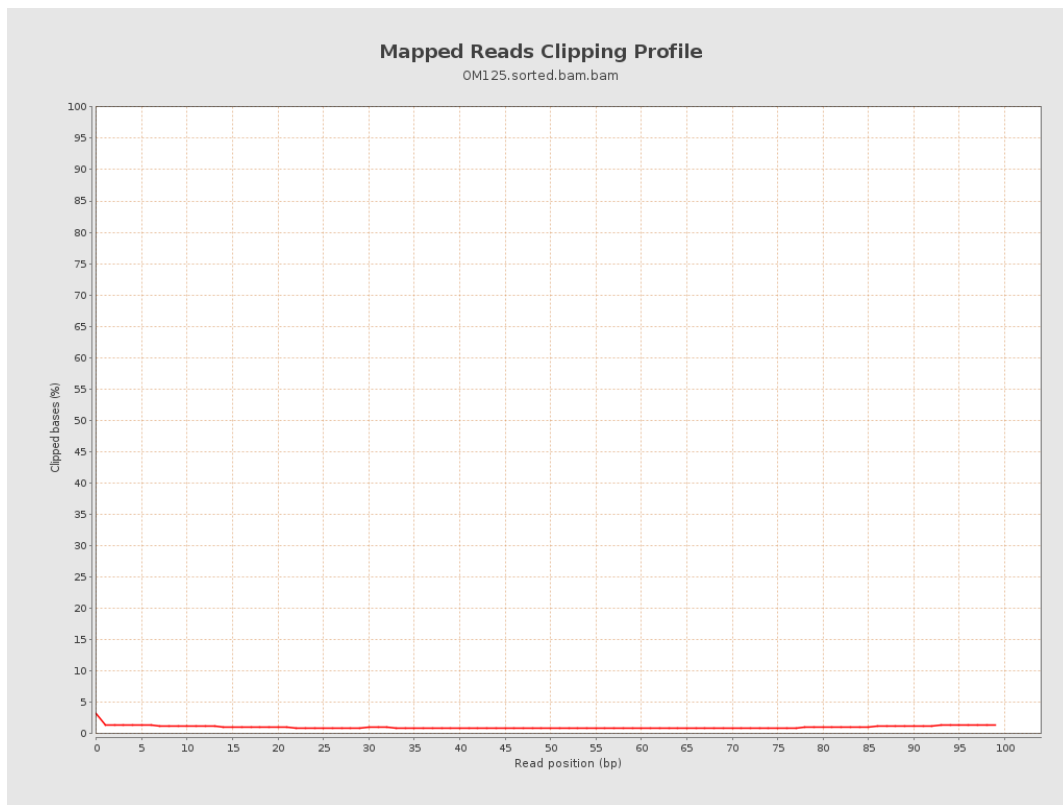
8. Results : Mapped Reads Nucleotide Content



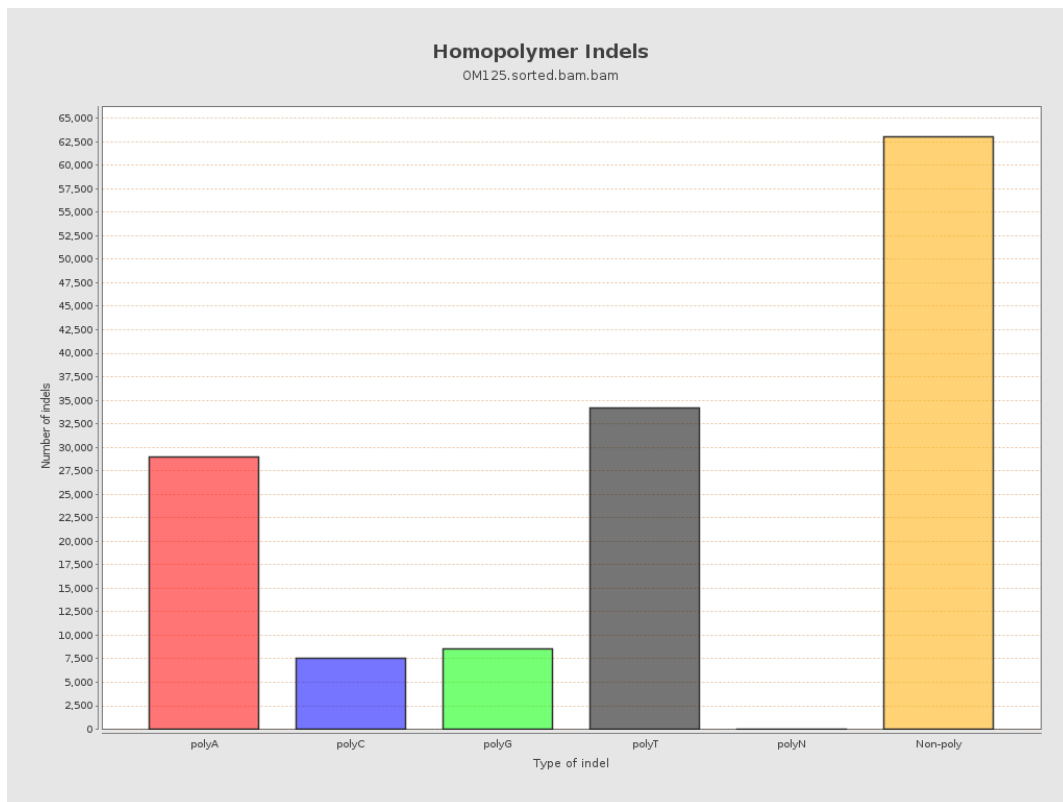
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



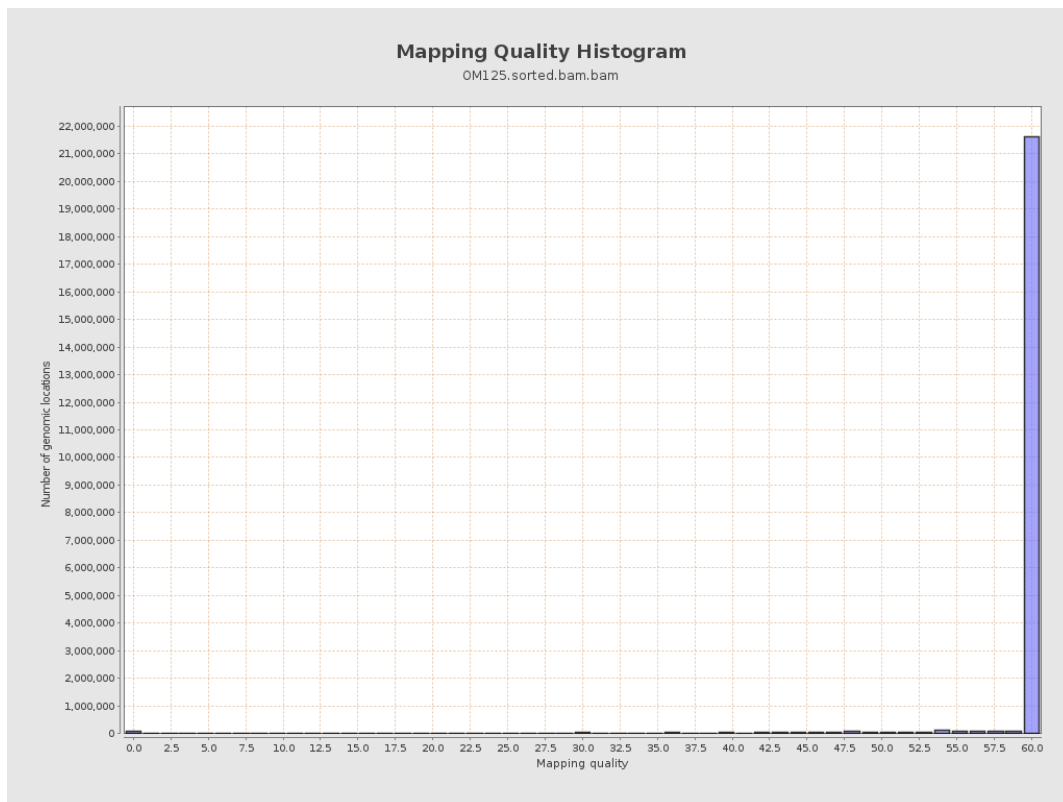
11. Results : Homopolymer Indels



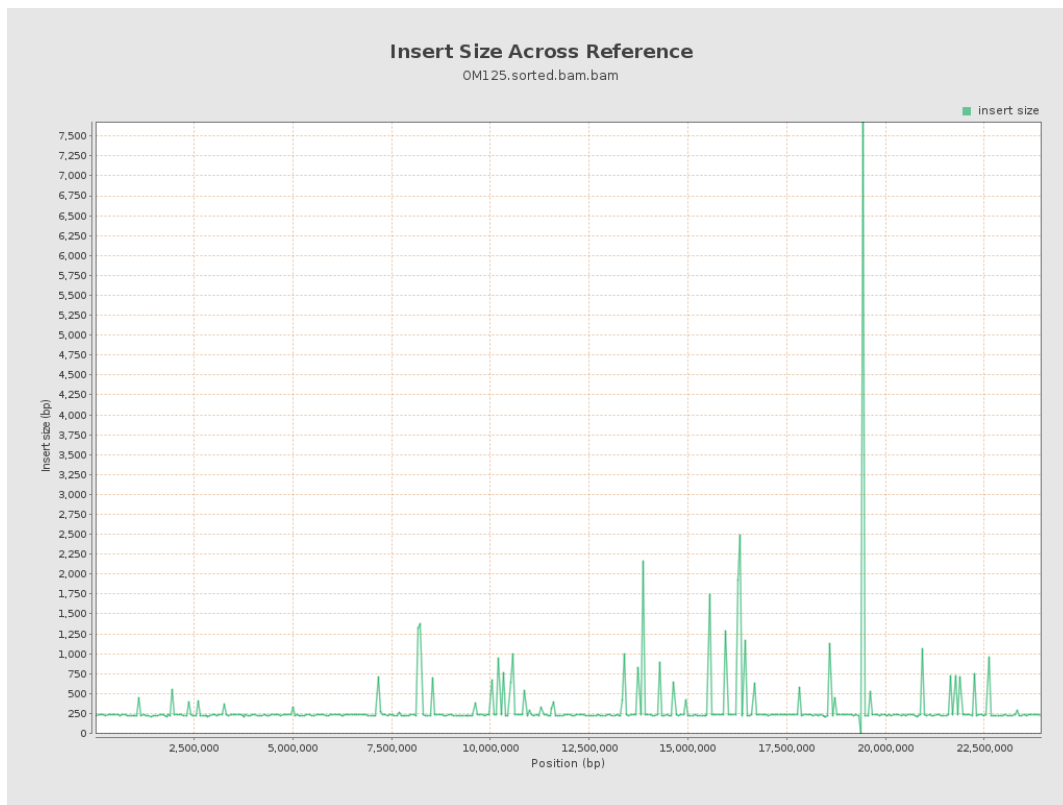
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

