

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2016/10/23 14:15:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM313.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/OM313-BiooBarcode39_CTATAC_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM313-BiooBarcode39_CTATAC_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:15:26 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM313.sorted.bam.

	bam
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2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	4,434,021
Mapped reads	1,796,536 / 40.52%
Unmapped reads	2,637,485 / 59.48%
Mapped paired reads	1,796,536 / 40.52%
Mapped reads, first in pair	902,093 / 20.34%
Mapped reads, second in pair	894,443 / 20.17%
Mapped reads, both in pair	1,746,951 / 39.4%
Mapped reads, singletons	49,585 / 1.12%
Read min/max/mean length	30 / 100 / 99.93
Duplicated reads (estimated)	184,656 / 4.16%
Duplication rate	7.29%
Clipped reads	219,222 / 4.94%

2.2. ACGT Content

Number/percentage of A's	52,067,746 / 30.15%
Number/percentage of C's	34,241,428 / 19.83%
Number/percentage of T's	52,214,731 / 30.24%
Number/percentage of G's	34,169,171 / 19.79%
Number/percentage of N's	13,925 / 0.01%
GC Percentage	39.61%

2.3. Coverage

Mean	7.2157
Standard Deviation	7.9361

2.4. Mapping Quality

Mean Mapping Quality	58.47
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2.5. Insert size

Mean	1,029.69
Standard Deviation	32,440.84
P25/Median/P75	337 / 350 / 360

2.6. Mismatches and indels

General error rate	1.65%
Mismatches	2,712,123
Insertions	59,446
Mapped reads with at least one insertion	3.12%
Deletions	66,864
Mapped reads with at least one deletion	3.51%
Homopolymer indels	62.22%

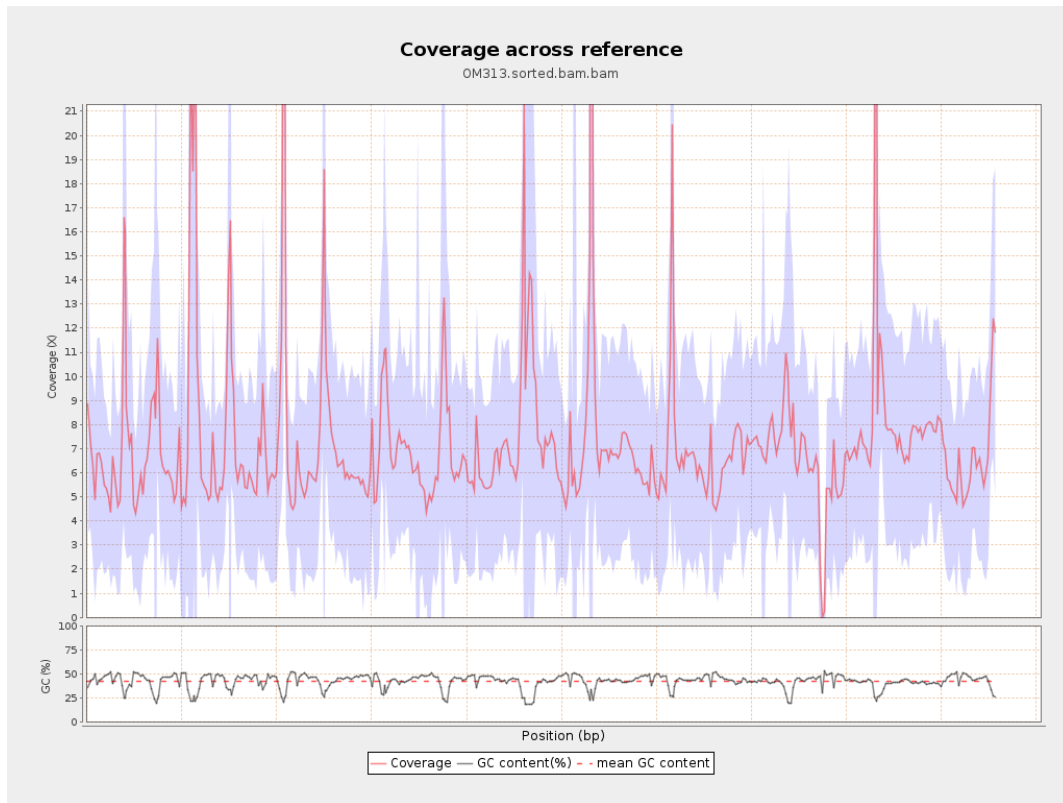
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

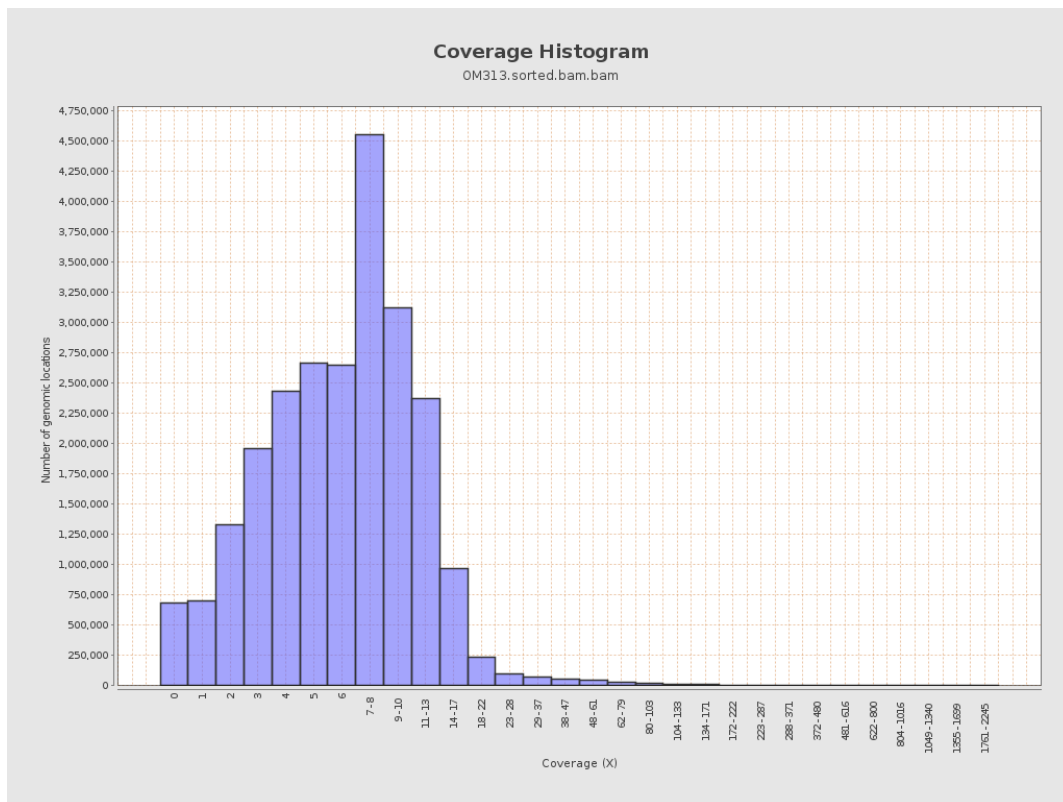
gi 1074120478 emb LT615256.1	977217	6097420	6.2396	4.0499
gi 1074120682 emb LT615257.1	860454	6197762	7.2029	6.3913
gi 1074120865 emb LT615258.1	989719	8159003	8.2438	11.8962
gi 1074121086 emb LT615259.1	935450	7426895	7.9394	13.2541
gi 1074121301 emb LT615260.1	1432239	10928815	7.6306	8.2544
gi 1074121615 emb LT615261.1	1080962	8055492	7.4522	7.682
gi 1074121871 emb LT615262.1	1545099	10284620	6.6563	3.7448
gi 1074122235 emb LT615263.1	1585108	10885325	6.8672	5.8594
gi 1074122590 emb LT615264.1	2122358	14747422	6.9486	4.8943
gi 1074123050 emb LT615265.1	1754192	13603734	7.755	9.7455
gi 1074123421 emb LT615	2150147	16129960	7.5018	14.2966

266.1				
gi 107412389 8 emb LT615 267.1	3031036	21008007	6.931	4.0249
gi 107412458 8 emb LT615 268.1	2359348	16303953	6.9104	8.2309
gi 107412506 5 emb LT615 269.1	3135668	23053113	7.3519	3.8017

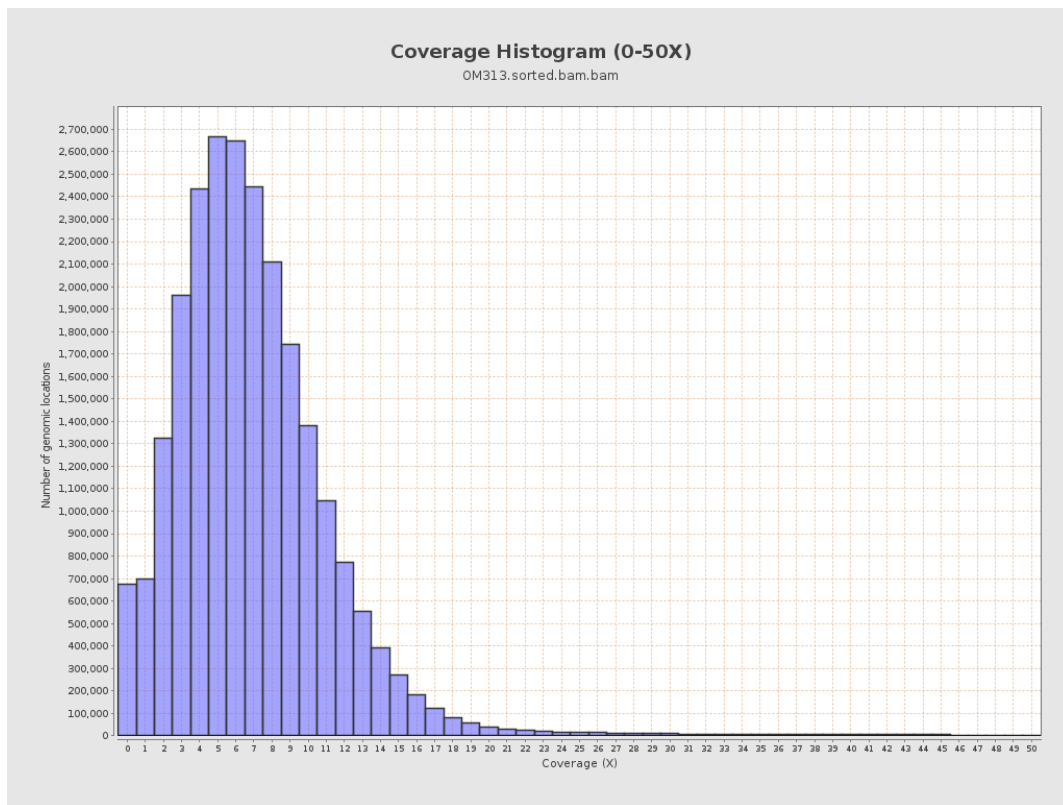
3. Results : Coverage across reference



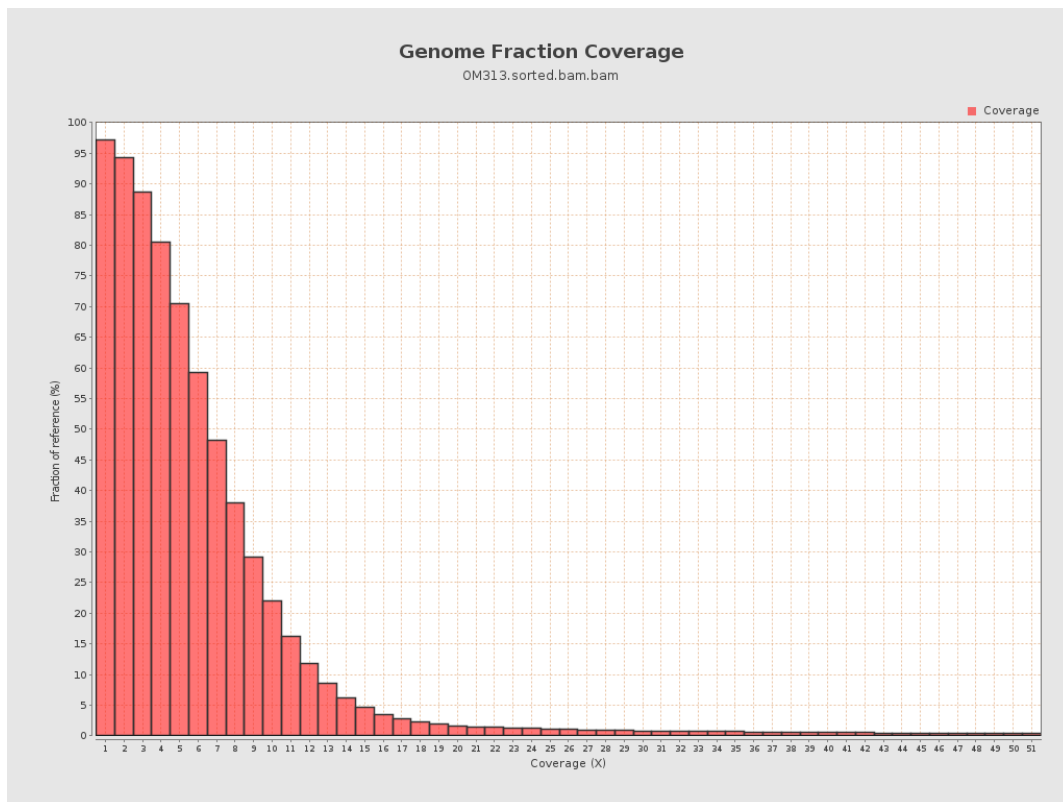
4. Results : Coverage Histogram



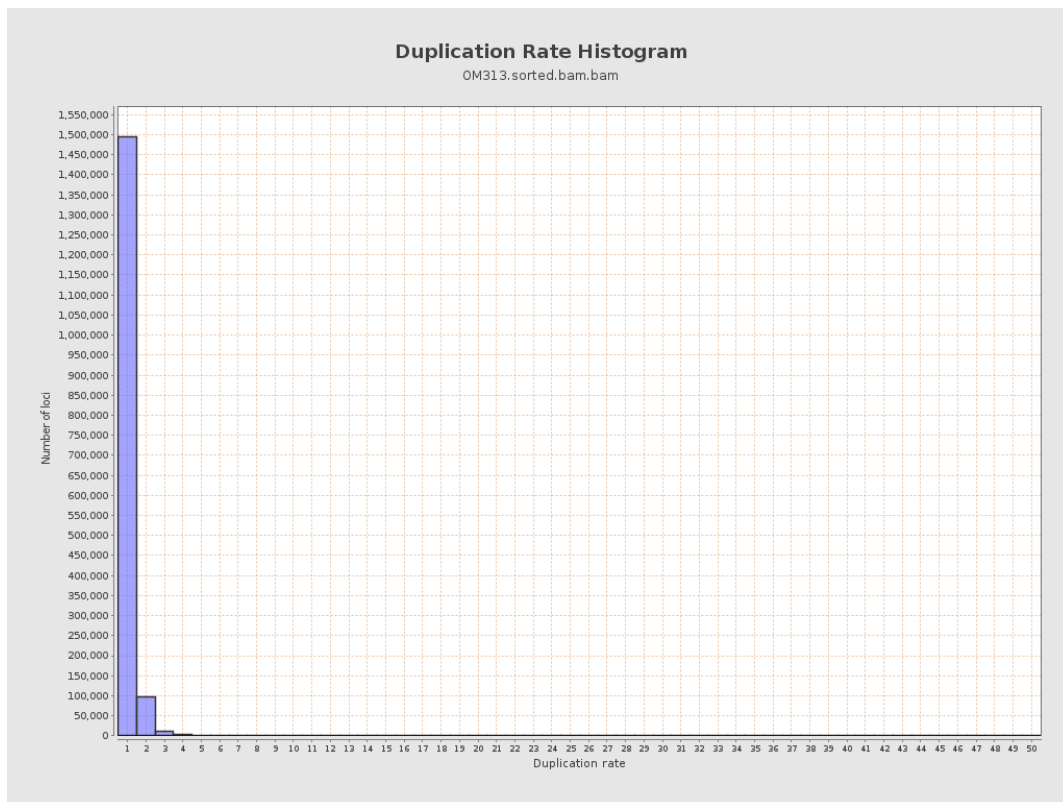
5. Results : Coverage Histogram (0-50X)



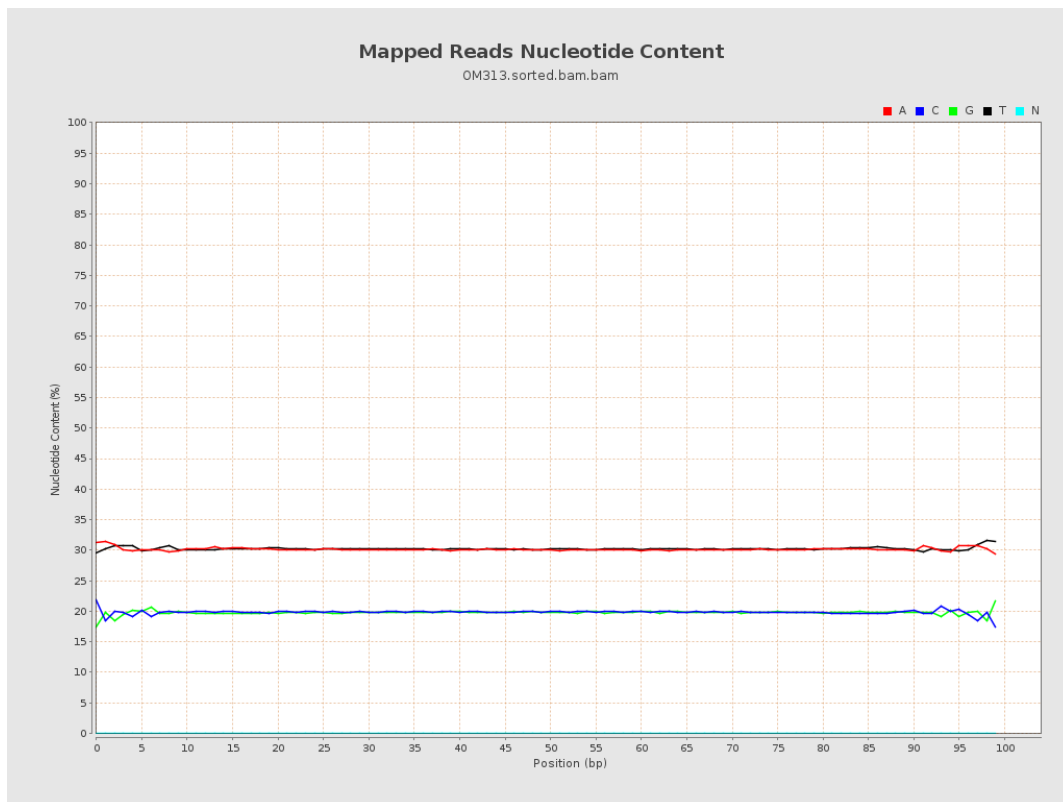
6. Results : Genome Fraction Coverage



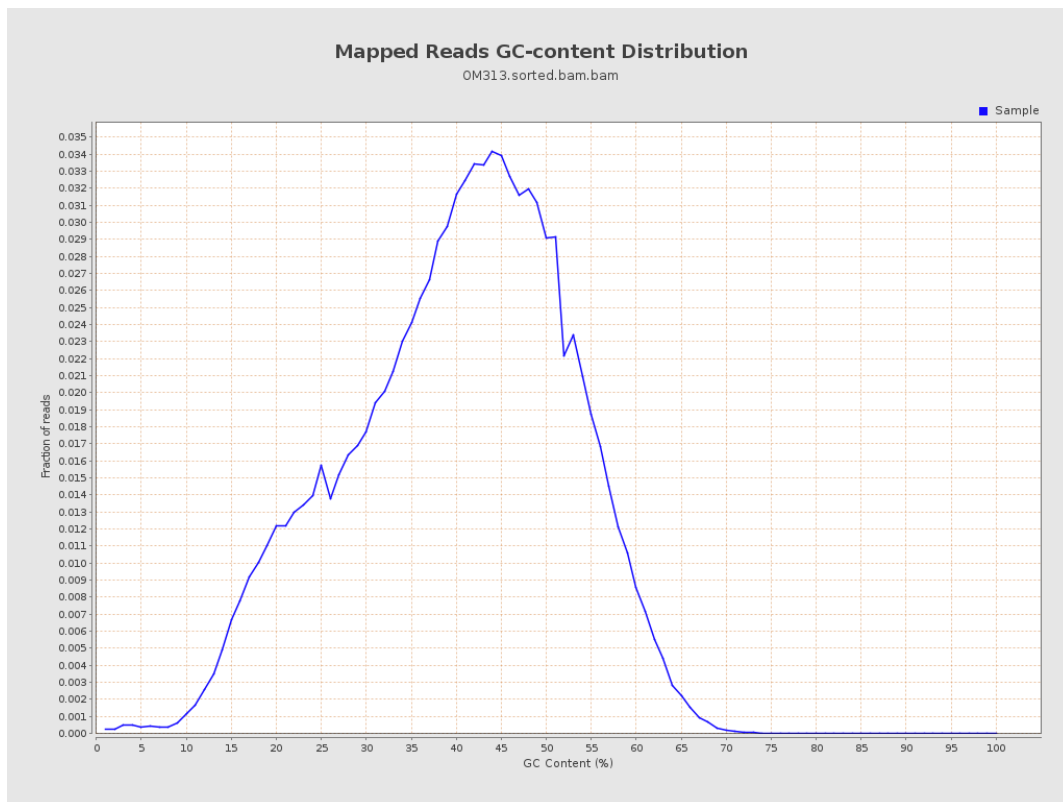
7. Results : Duplication Rate Histogram



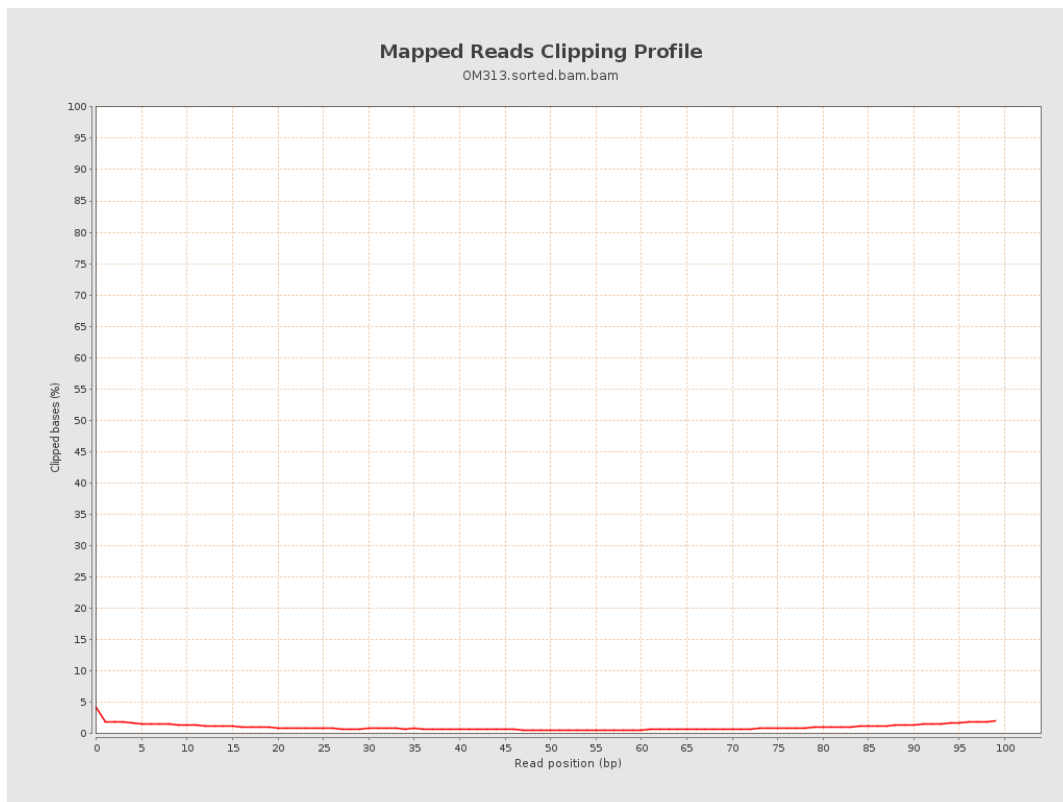
8. Results : Mapped Reads Nucleotide Content



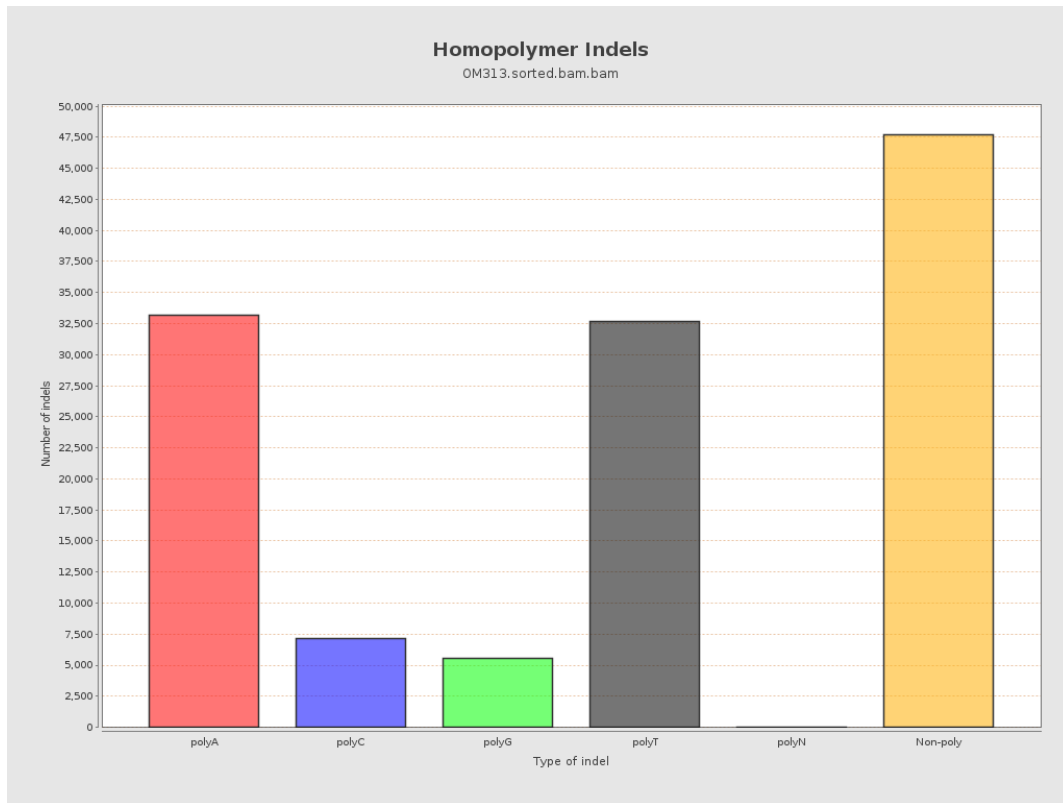
9. Results : Mapped Reads GC-content Distribution



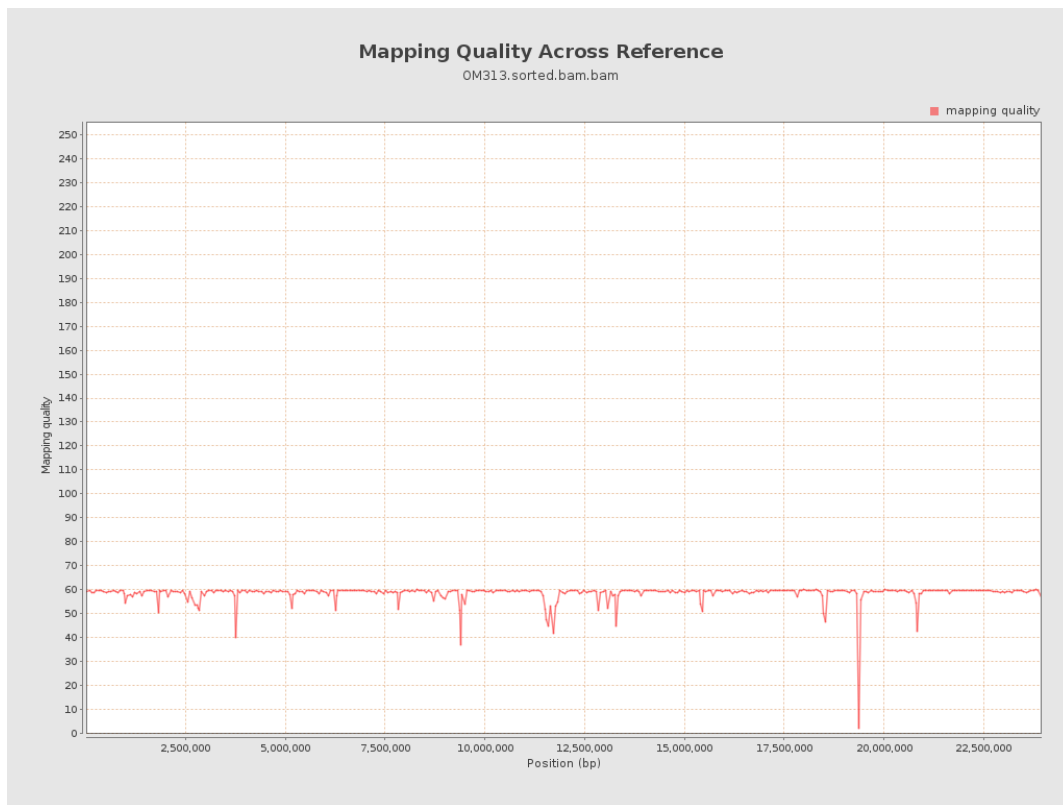
10. Results : Mapped Reads Clipping Profile



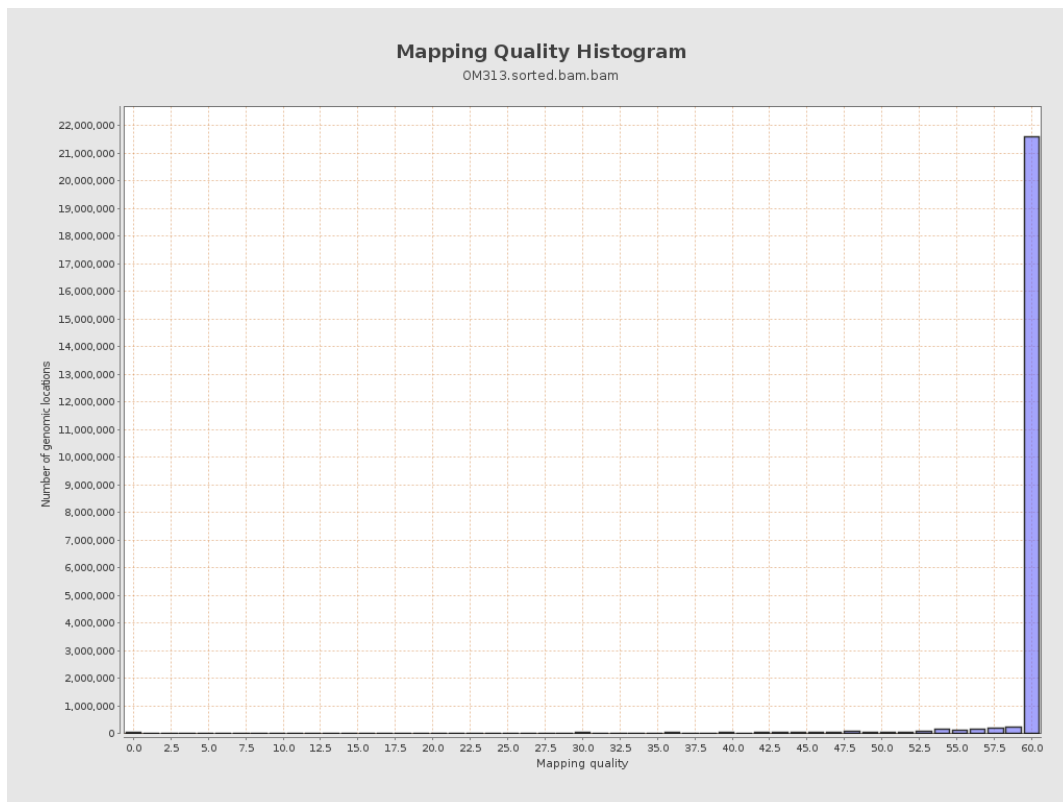
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

