

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:47:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013245.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013245.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:47:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,410,290
Mapped reads	1,085,417 / 76.96%
Unmapped reads	324,873 / 23.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,501 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	151,197 / 10.72%
Duplication rate	10.99%
Clipped reads	663,072 / 47.02%

2.2. ACGT Content

Number/percentage of A's	19,462,389 / 28.54%
Number/percentage of C's	11,595,629 / 17%
Number/percentage of T's	22,795,596 / 33.42%
Number/percentage of G's	14,336,927 / 21.02%
Number/percentage of N's	14,455 / 0.02%
GC Percentage	38.02%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.3034
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2.4. Mapping Quality

Mean Mapping Quality	41.18
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2.5. Mismatches and indels

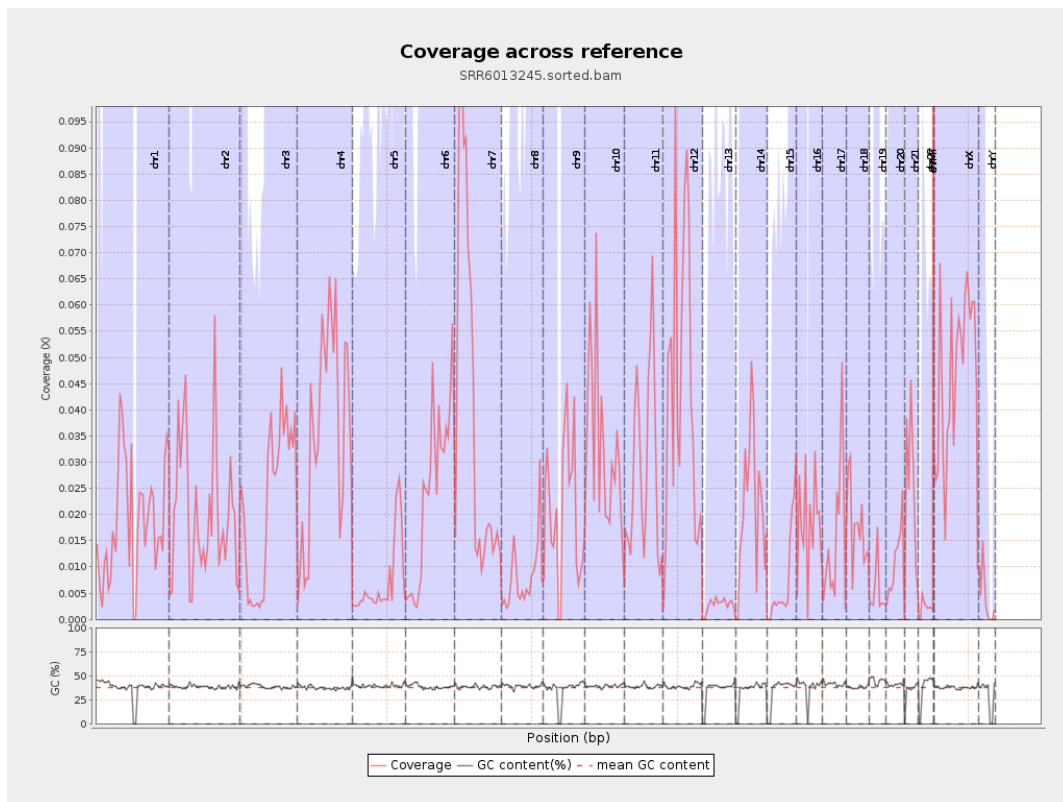
General error rate	1.08%
Mismatches	724,560
Insertions	5,702
Mapped reads with at least one insertion	0.52%
Deletions	41,658
Mapped reads with at least one deletion	3.75%
Homopolymer indels	41.35%

2.6. Chromosome stats

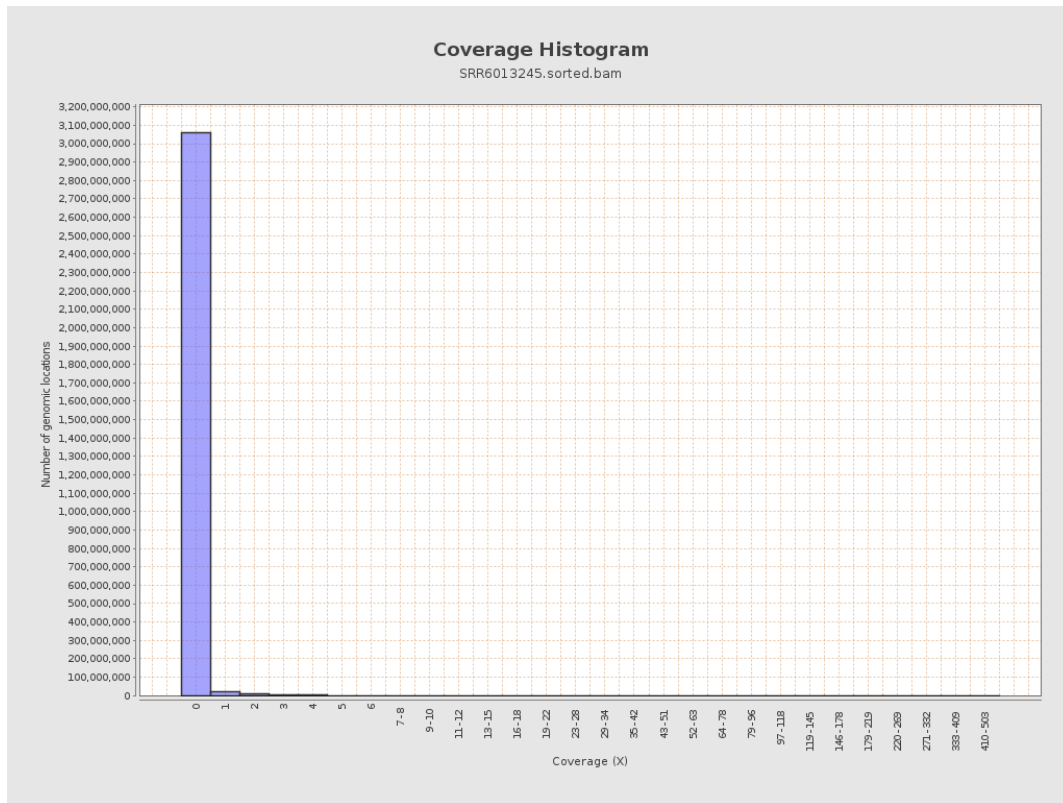
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4642717	0.0186	0.3946
chr2	243199373	4860676	0.02	0.3467
chr3	198022430	4353988	0.022	0.2389
chr4	191154276	6907170	0.0361	0.3372
chr5	180915260	1310946	0.0072	0.1322
chr6	171115067	4149402	0.0242	0.2595
chr7	159138663	6379491	0.0401	0.421

chr8	146364022	1190381	0.0081	0.3179
chr9	141213431	2984600	0.0211	0.2681
chr10	135534747	4435406	0.0327	0.4367
chr11	135006516	3856949	0.0286	0.3019
chr12	133851895	5829797	0.0436	0.3473
chr13	115169878	313605	0.0027	0.0774
chr14	107349540	2337105	0.0218	0.2453
chr15	102531392	750532	0.0073	0.132
chr16	90354753	1649558	0.0183	0.2318
chr17	81195210	1212937	0.0149	0.2077
chr18	78077248	1394323	0.0179	0.341
chr19	59128983	327132	0.0055	0.3355
chr20	63025520	707772	0.0112	0.1677
chr21	48129895	1123190	0.0233	0.2722
chr22	51304566	116785	0.0023	0.0632
chrMT	16571	9840	0.5938	1.1023
chrX	155270560	7194577	0.0463	0.37
chrY	59373566	240048	0.004	0.1595

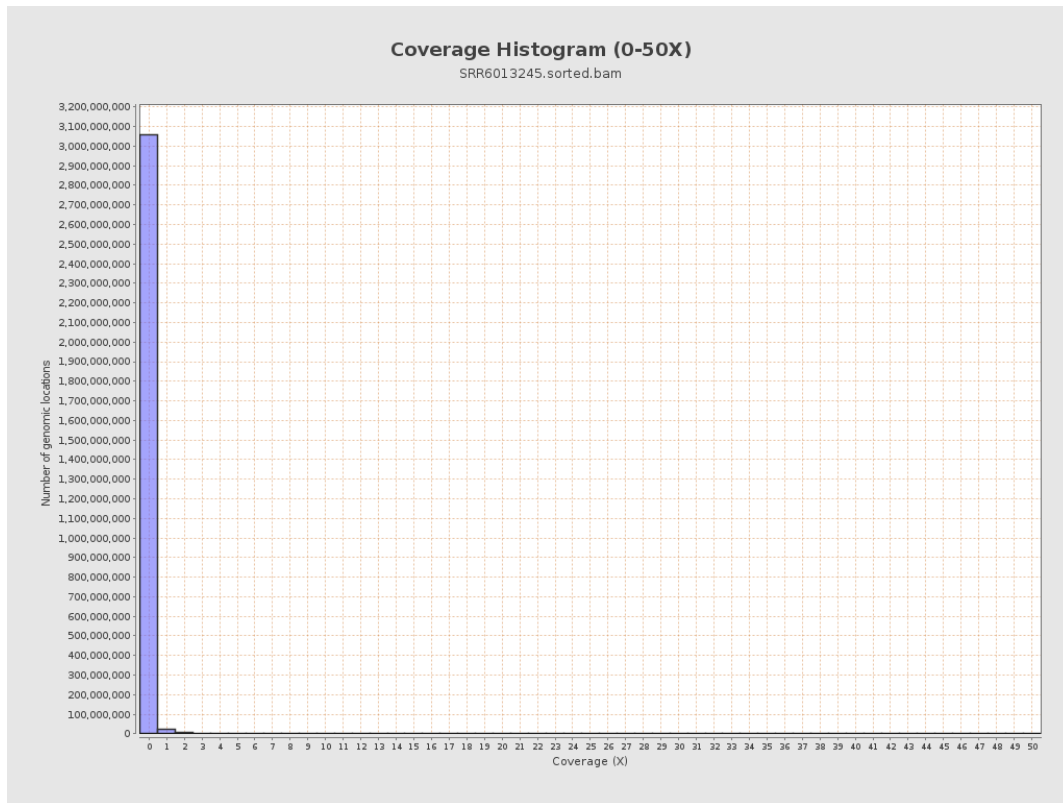
3. Results : Coverage across reference



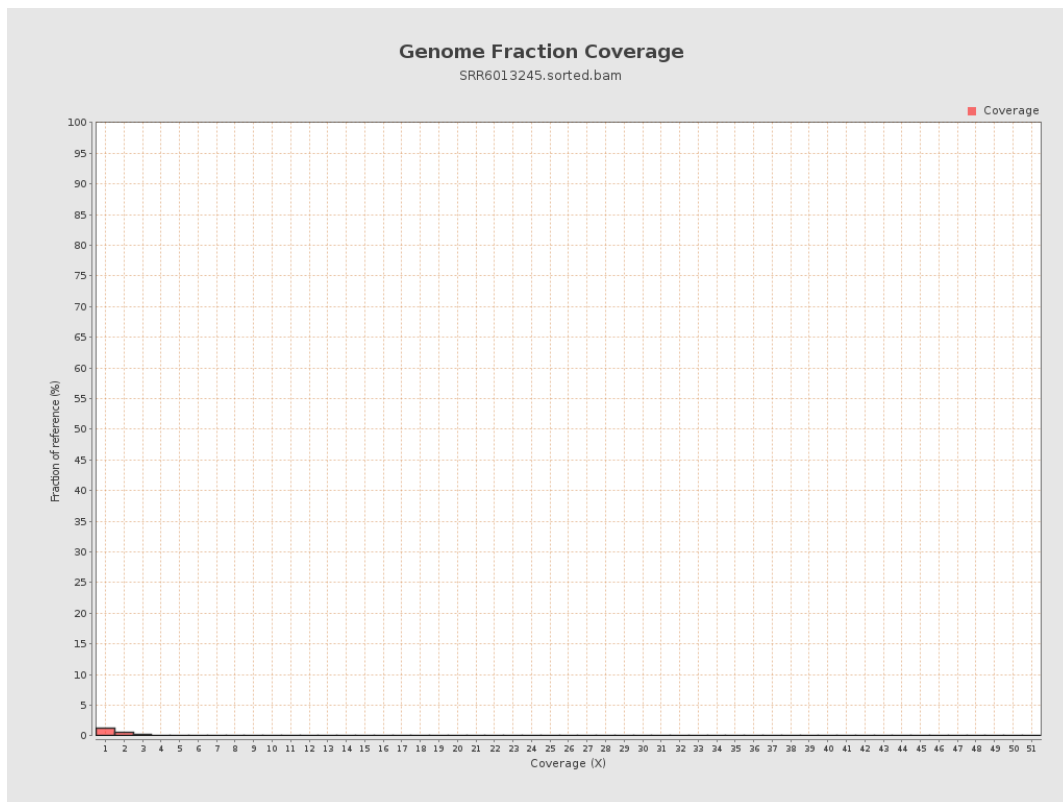
4. Results : Coverage Histogram



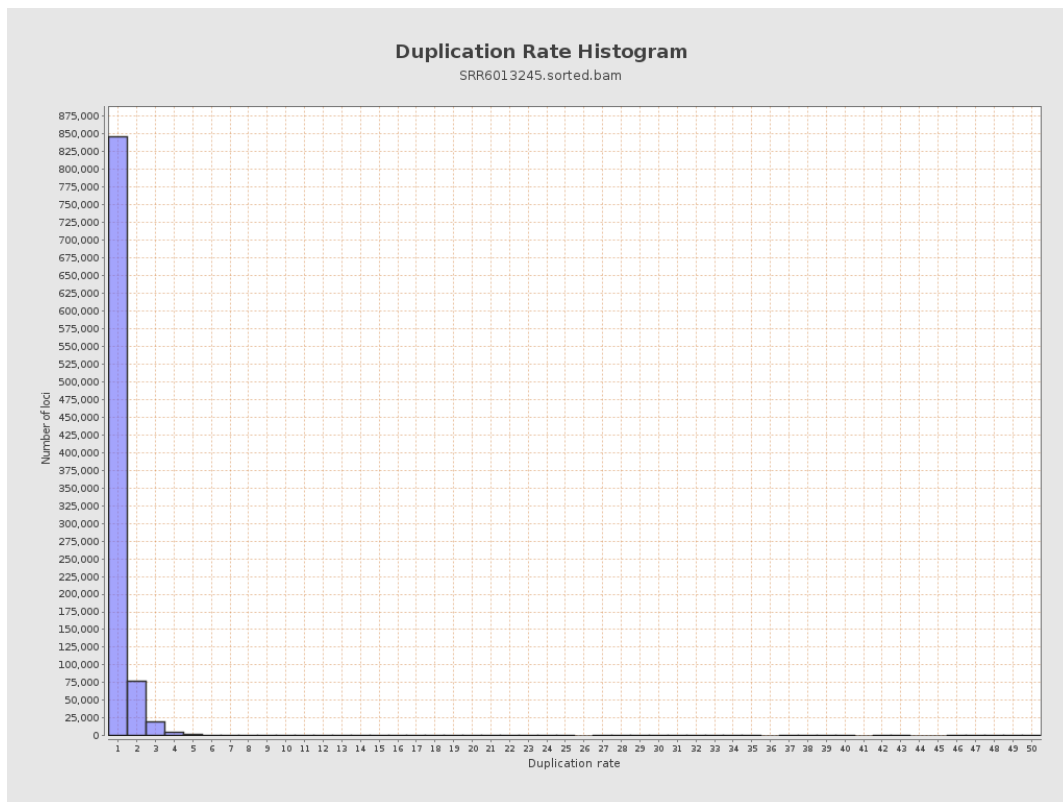
5. Results : Coverage Histogram (0-50X)



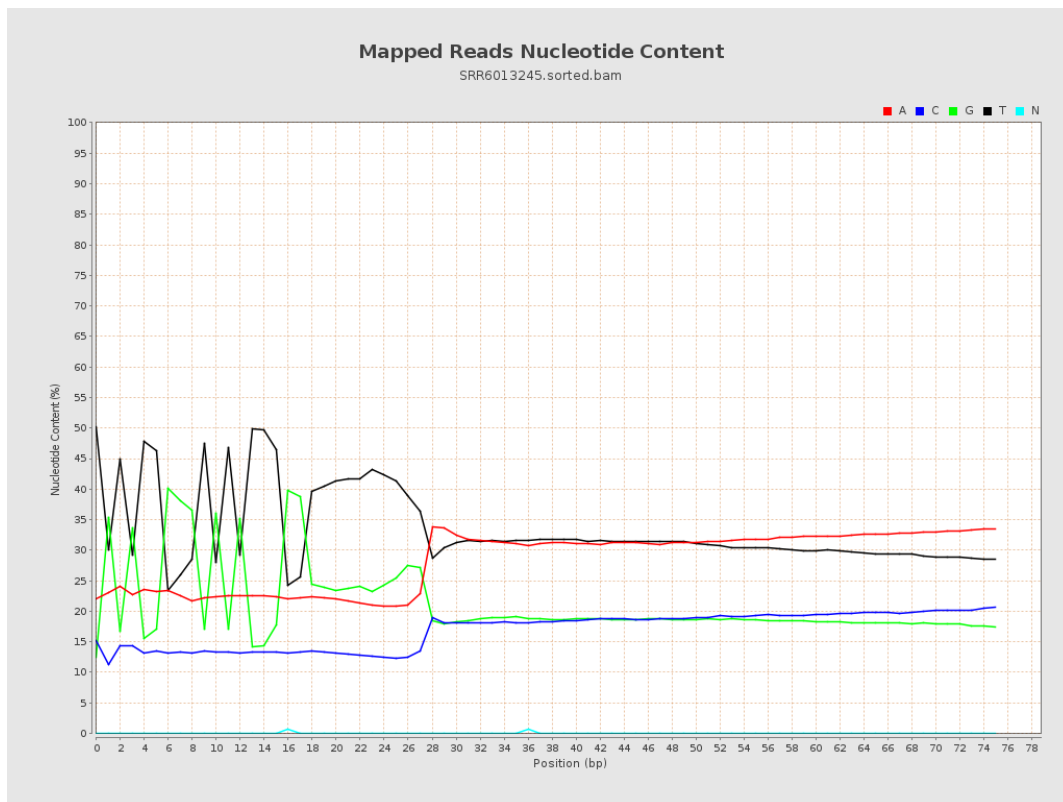
6. Results : Genome Fraction Coverage



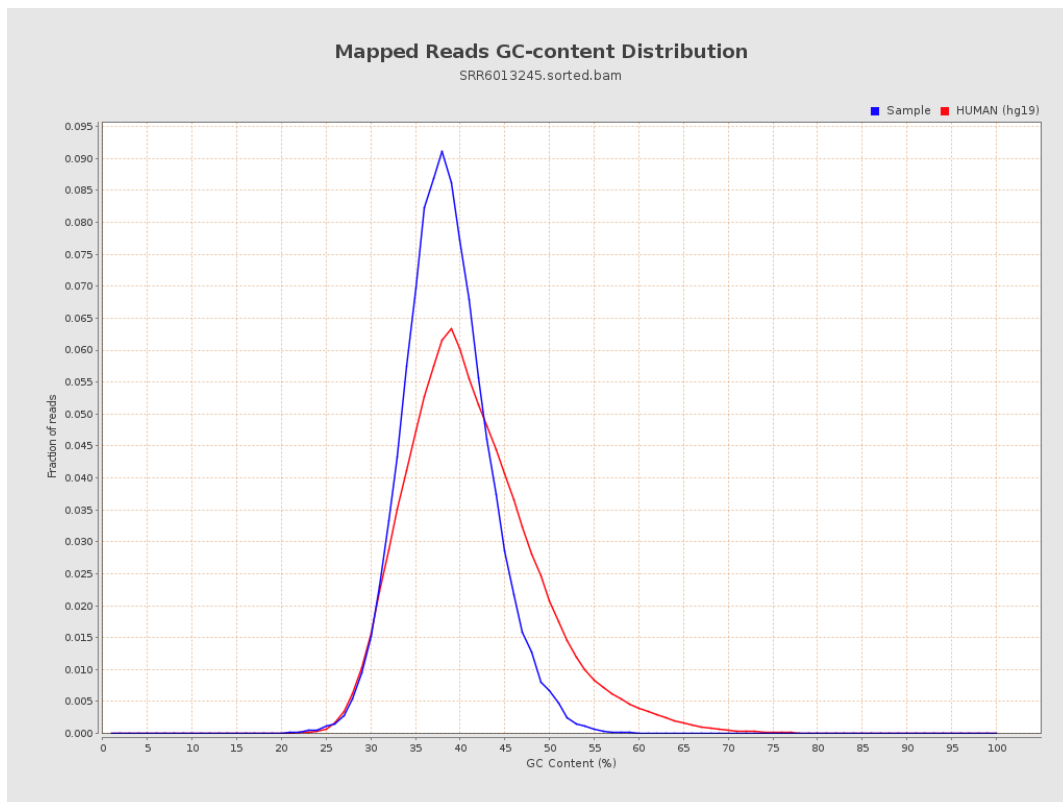
7. Results : Duplication Rate Histogram



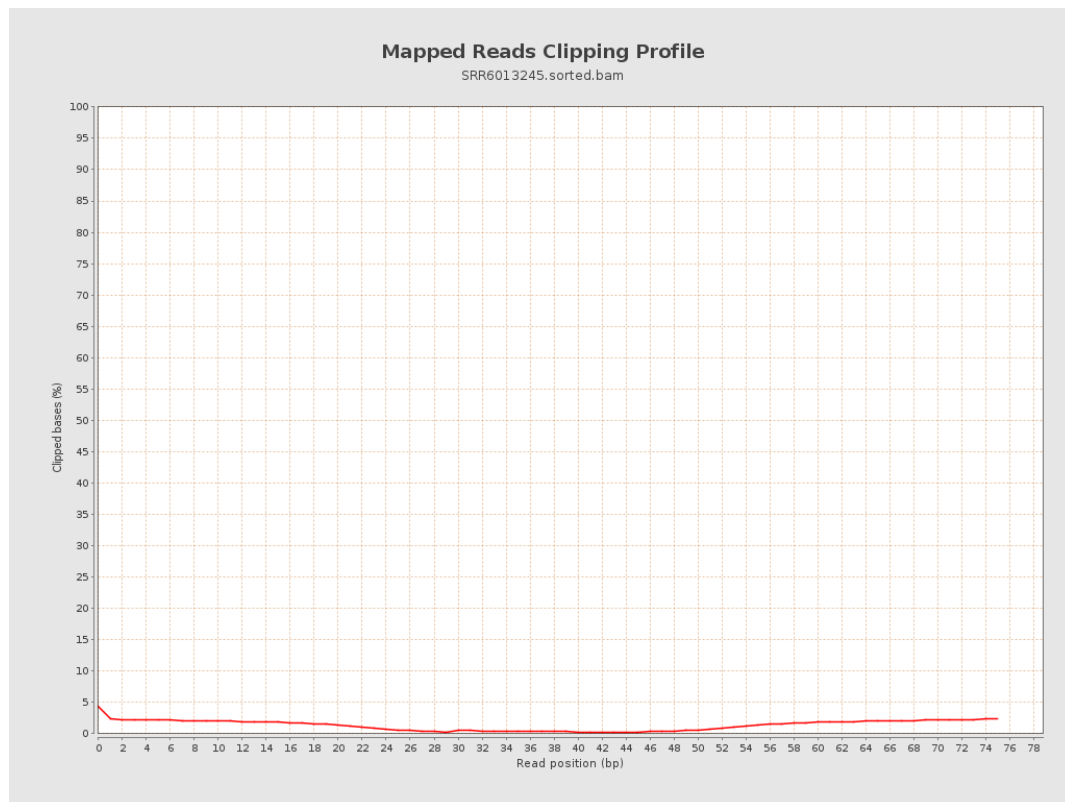
8. Results : Mapped Reads Nucleotide Content



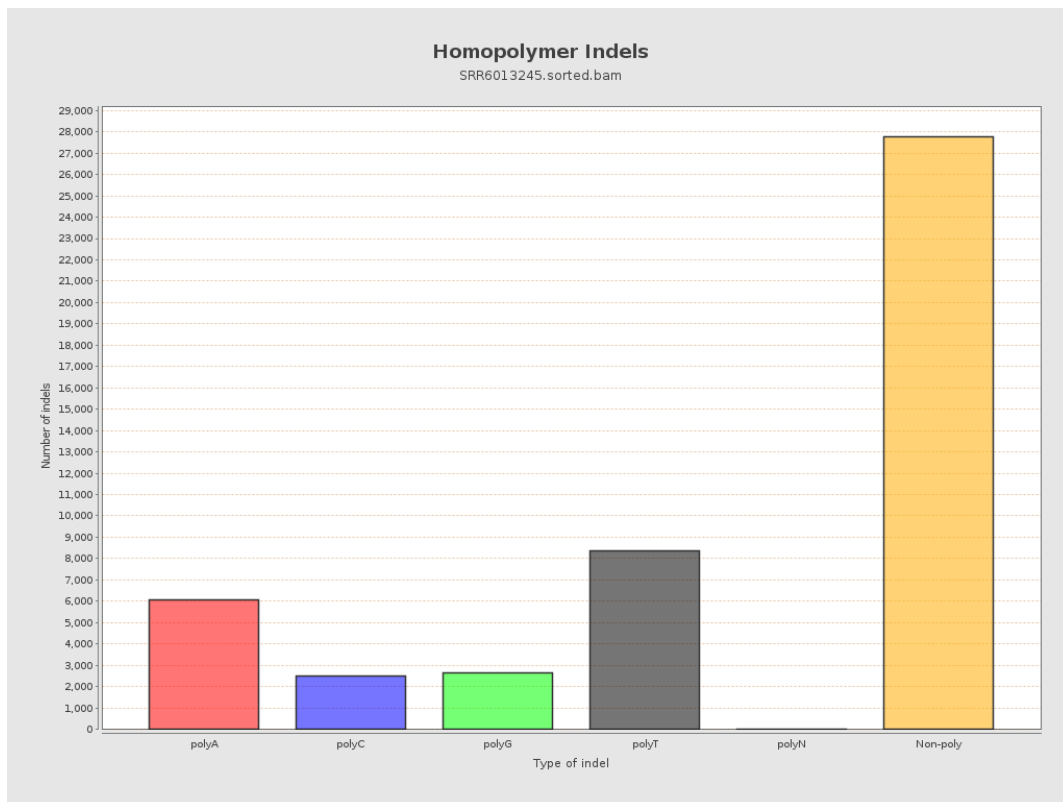
9. Results : Mapped Reads GC-content Distribution



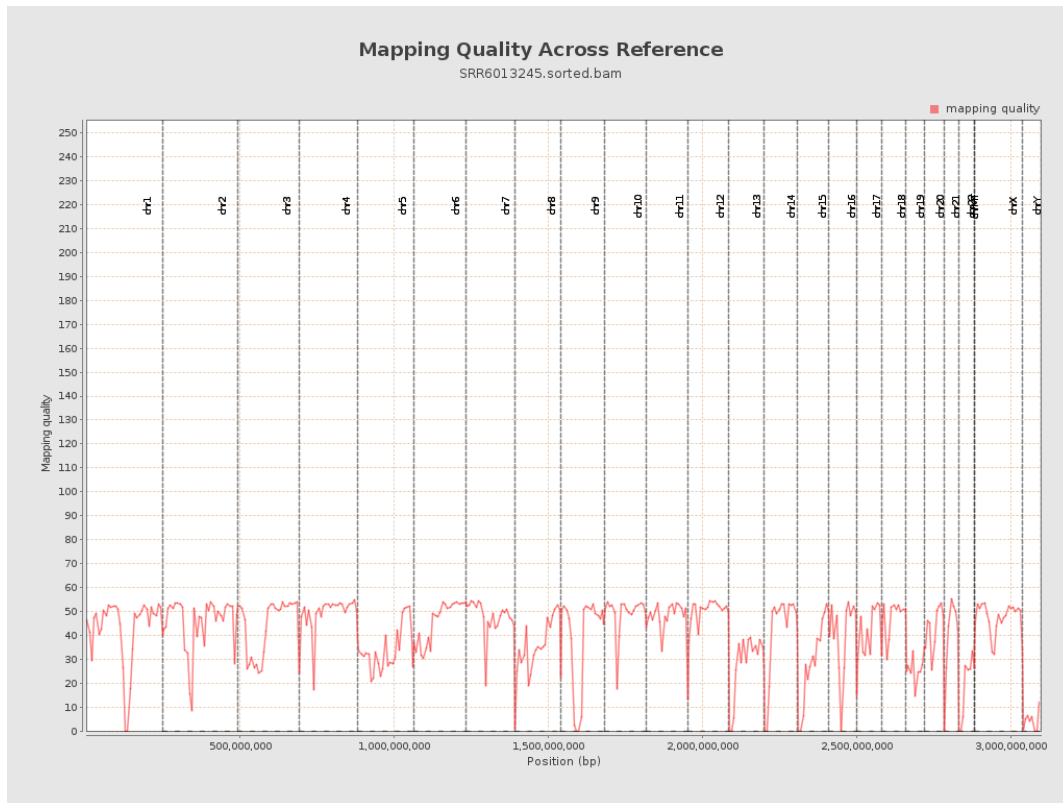
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

