

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:40:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549051.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_SRR1549051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:40:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,692,433
Mapped reads	3,202,507 / 86.73%
Unmapped reads	489,926 / 13.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	101,970 / 2.76%
Duplication rate	2.49%
Clipped reads	214,811 / 5.82%

2.2. ACGT Content

Number/percentage of A's	36,278,078 / 28.59%
Number/percentage of C's	26,707,097 / 21.05%
Number/percentage of T's	36,861,286 / 29.05%
Number/percentage of G's	27,024,242 / 21.3%
Number/percentage of N's	1,129 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.041
Standard Deviation	0.4147

2.4. Mapping Quality

Mean Mapping Quality	43.92
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2.5. Mismatches and indels

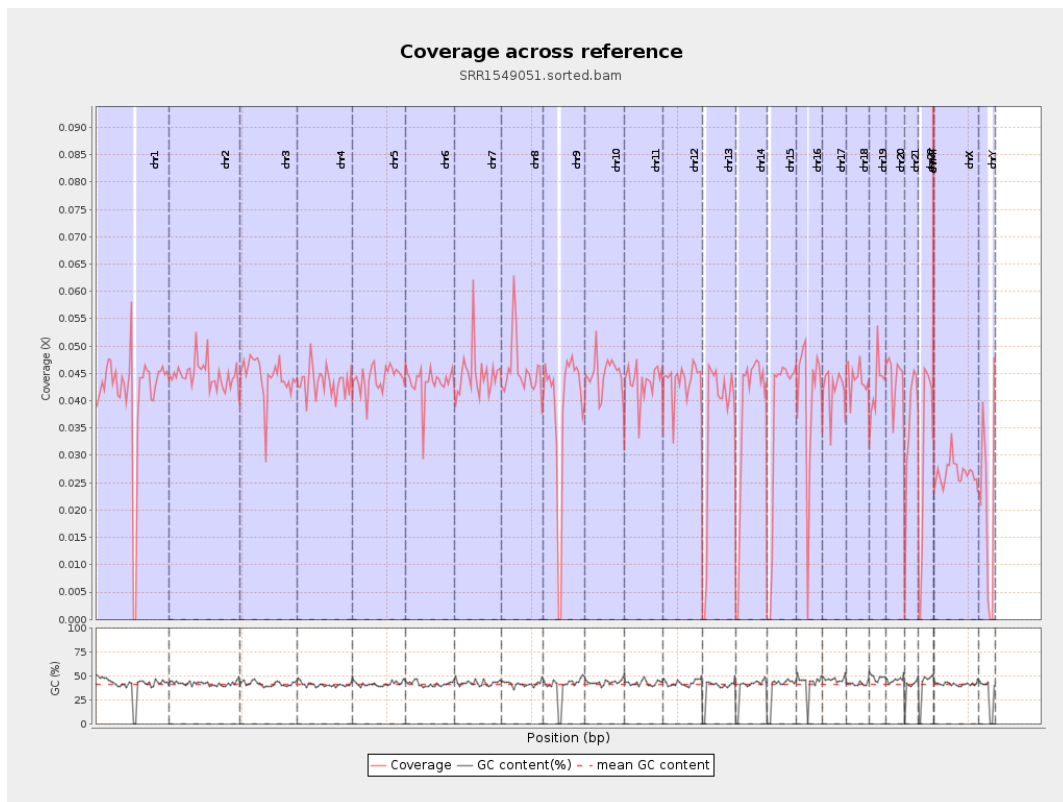
General error rate	0.23%
Mismatches	293,899
Insertions	3,514
Mapped reads with at least one insertion	0.11%
Deletions	10,197
Mapped reads with at least one deletion	0.32%
Homopolymer indels	42.16%

2.6. Chromosome stats

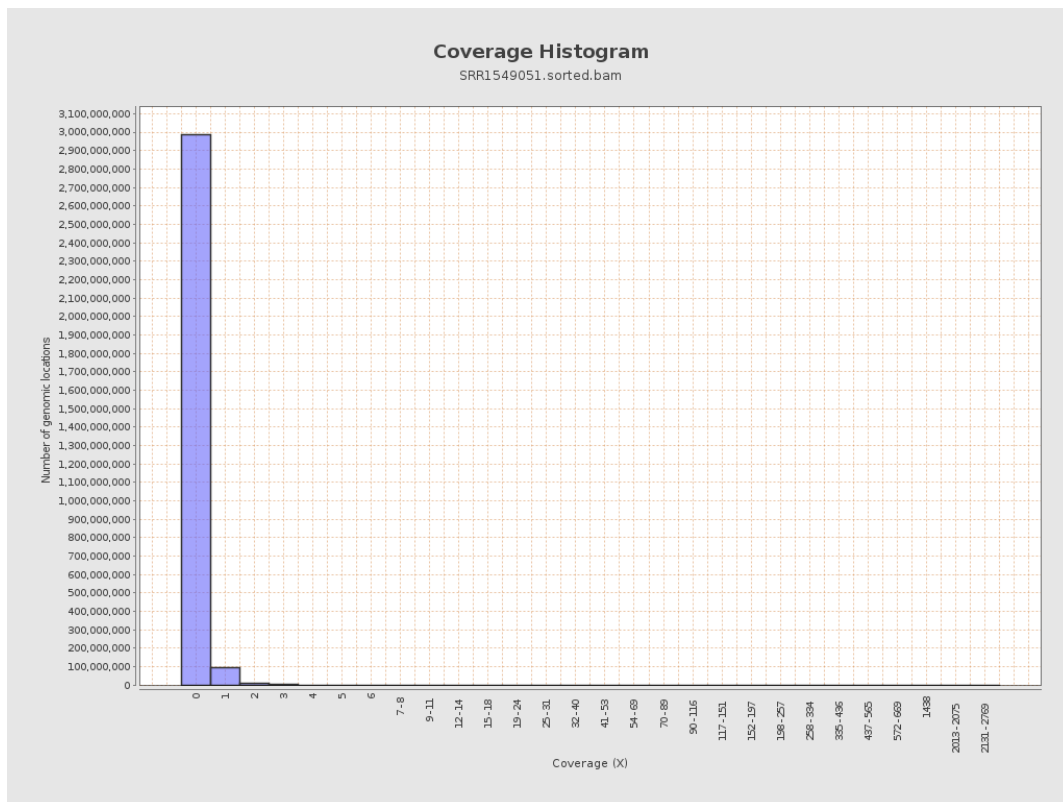
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10281582	0.0412	0.5107
chr2	243199373	10889829	0.0448	0.2799
chr3	198022430	8783438	0.0444	0.2393
chr4	191154276	8274331	0.0433	0.2441
chr5	180915260	7966365	0.044	0.2383
chr6	171115067	7432219	0.0434	0.2405
chr7	159138663	7141731	0.0449	0.3989
chr8	146364022	6642625	0.0454	1.3647

chr9	141213431	5448703	0.0386	0.2639
chr10	135534747	6085754	0.0449	0.2809
chr11	135006516	5848041	0.0433	0.2783
chr12	133851895	5839270	0.0436	0.2389
chr13	115169878	4099407	0.0356	0.2128
chr14	107349540	4009470	0.0373	0.2299
chr15	102531392	3706726	0.0362	0.2142
chr16	90354753	3680619	0.0407	0.2361
chr17	81195210	3411688	0.042	0.239
chr18	78077248	3434515	0.044	0.395
chr19	59128983	2536321	0.0429	0.4322
chr20	63025520	2762277	0.0438	0.2432
chr21	48129895	1686282	0.035	0.2348
chr22	51304566	1549434	0.0302	0.2556
chrMT	16571	4961	0.2994	0.6321
chrX	155270560	4160693	0.0268	0.2059
chrY	59373566	1209300	0.0204	0.255

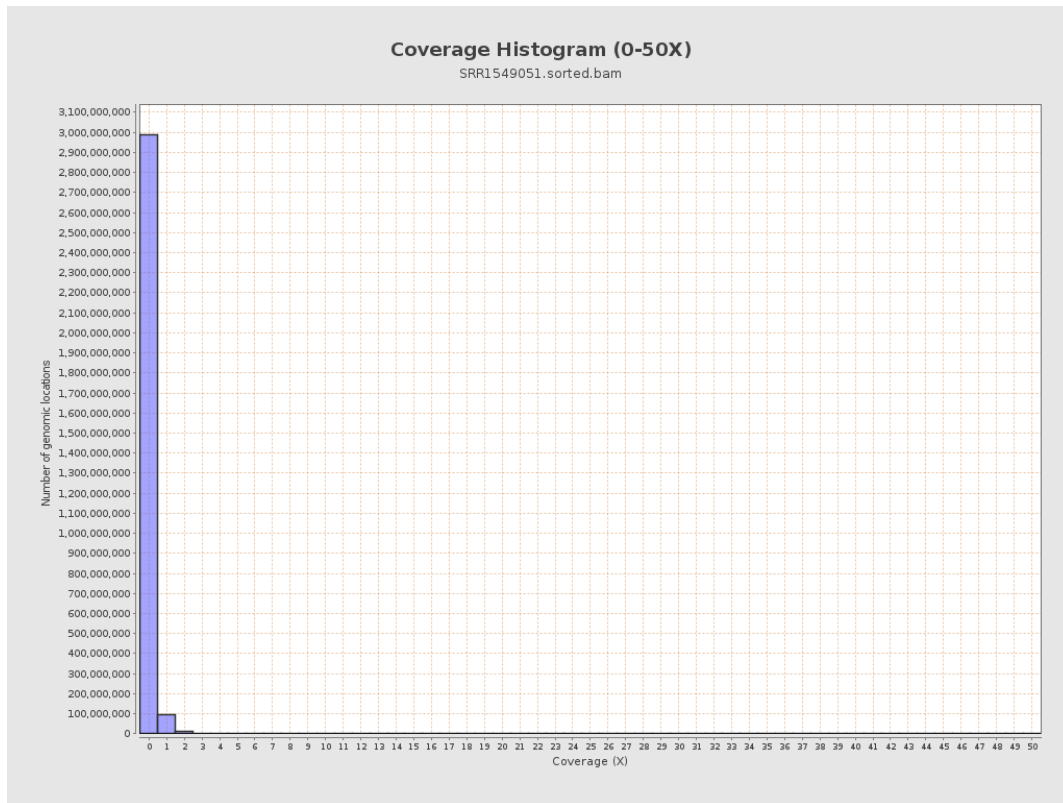
3. Results : Coverage across reference



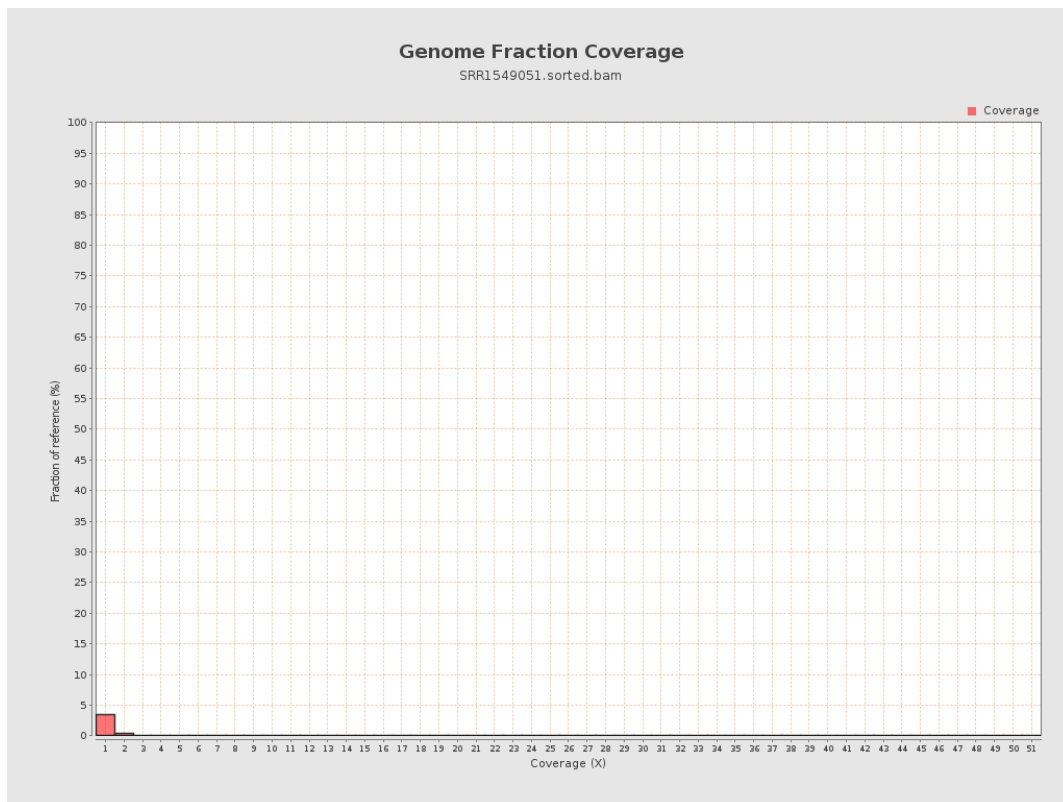
4. Results : Coverage Histogram



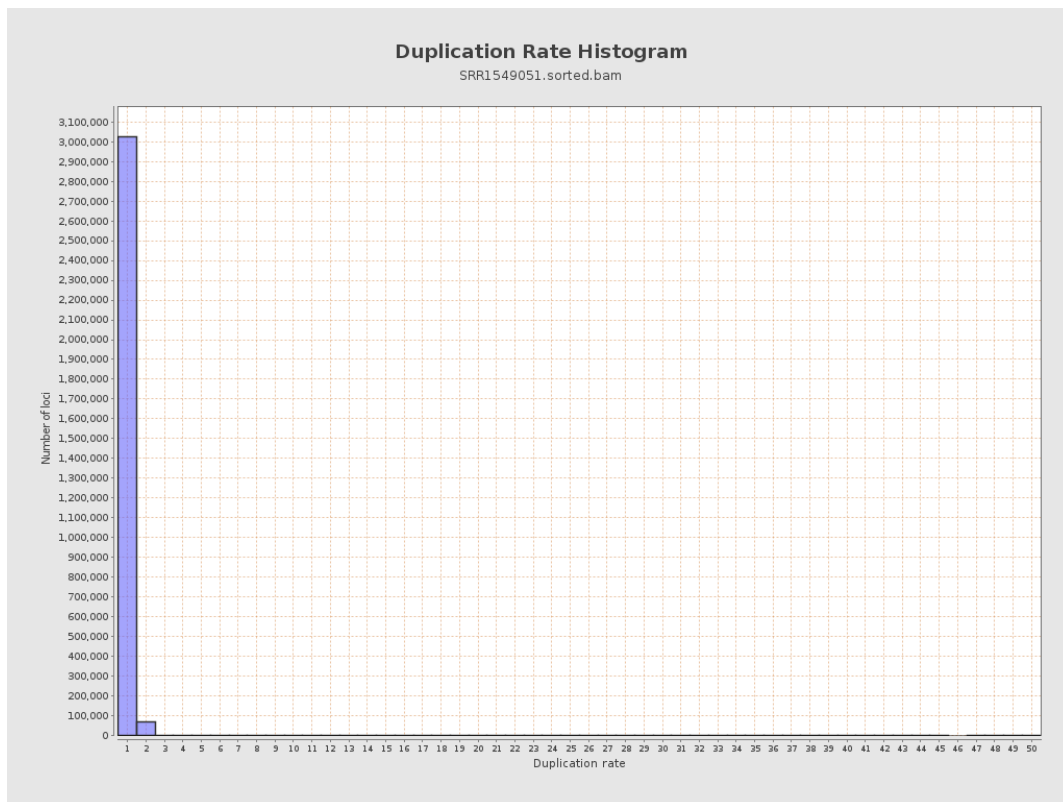
5. Results : Coverage Histogram (0-50X)



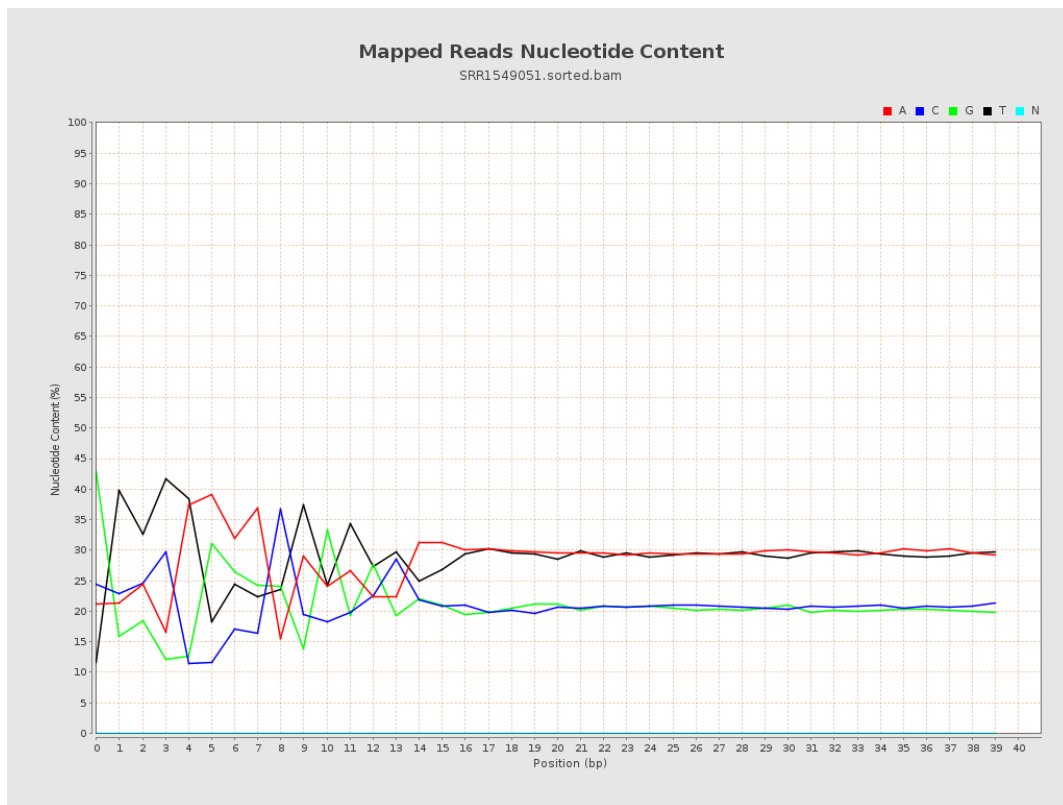
6. Results : Genome Fraction Coverage



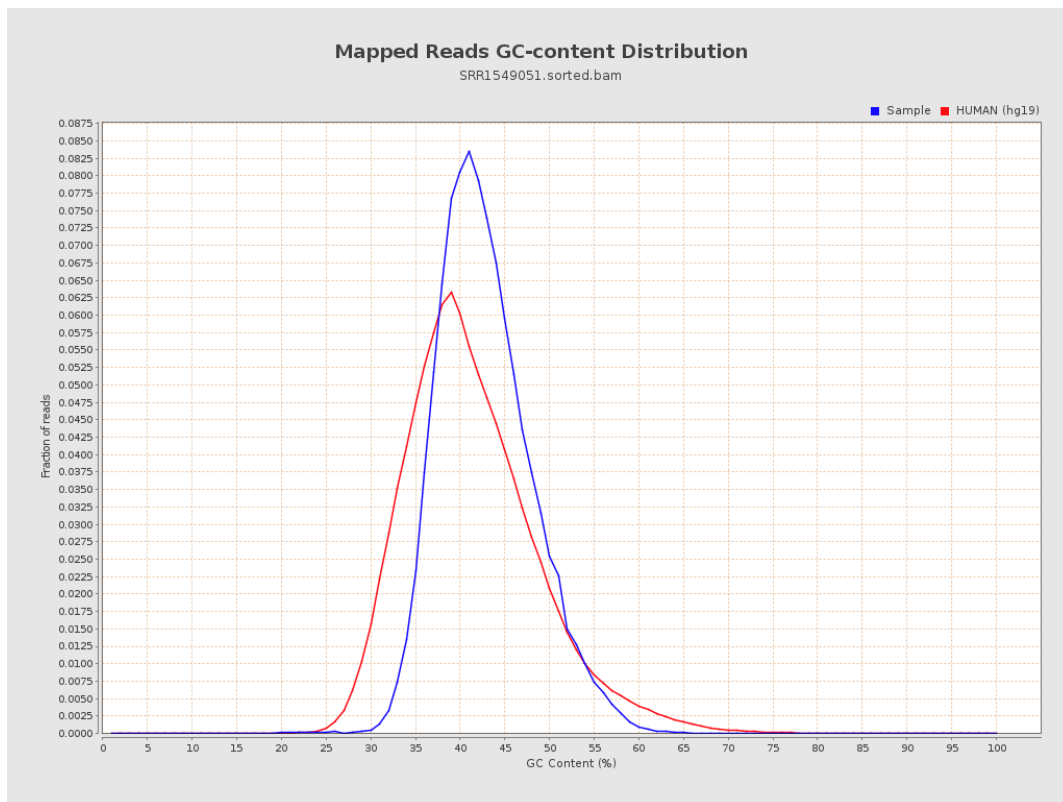
7. Results : Duplication Rate Histogram



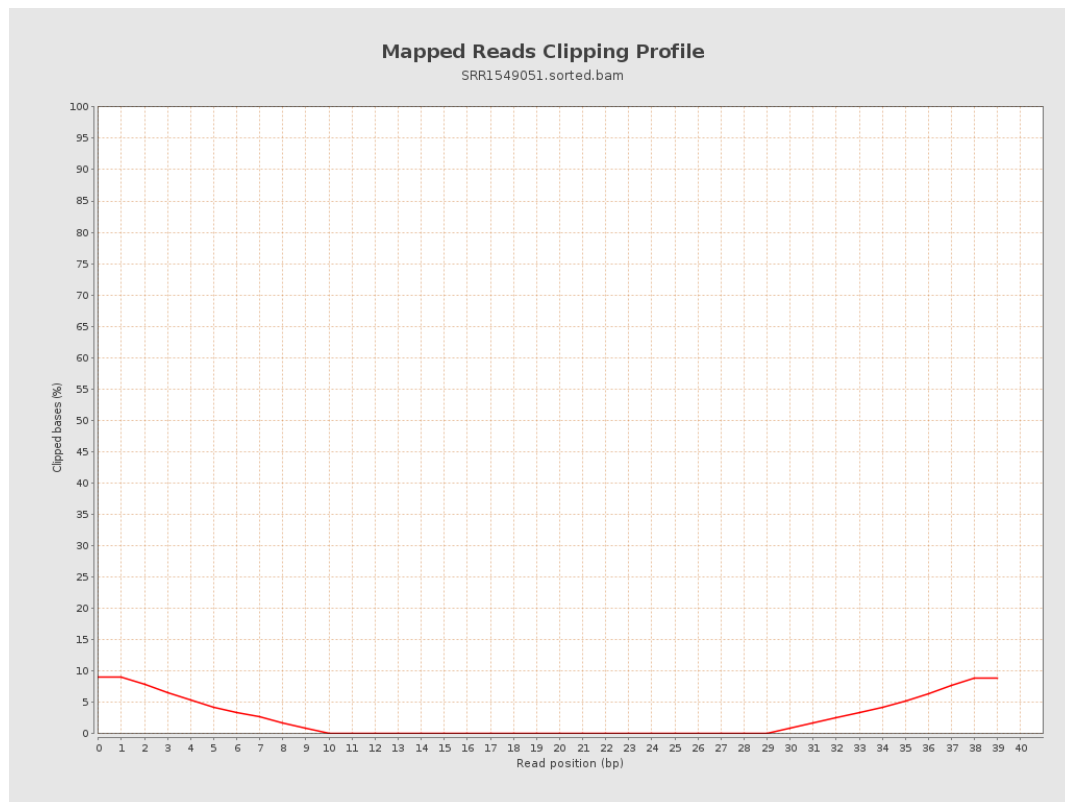
8. Results : Mapped Reads Nucleotide Content



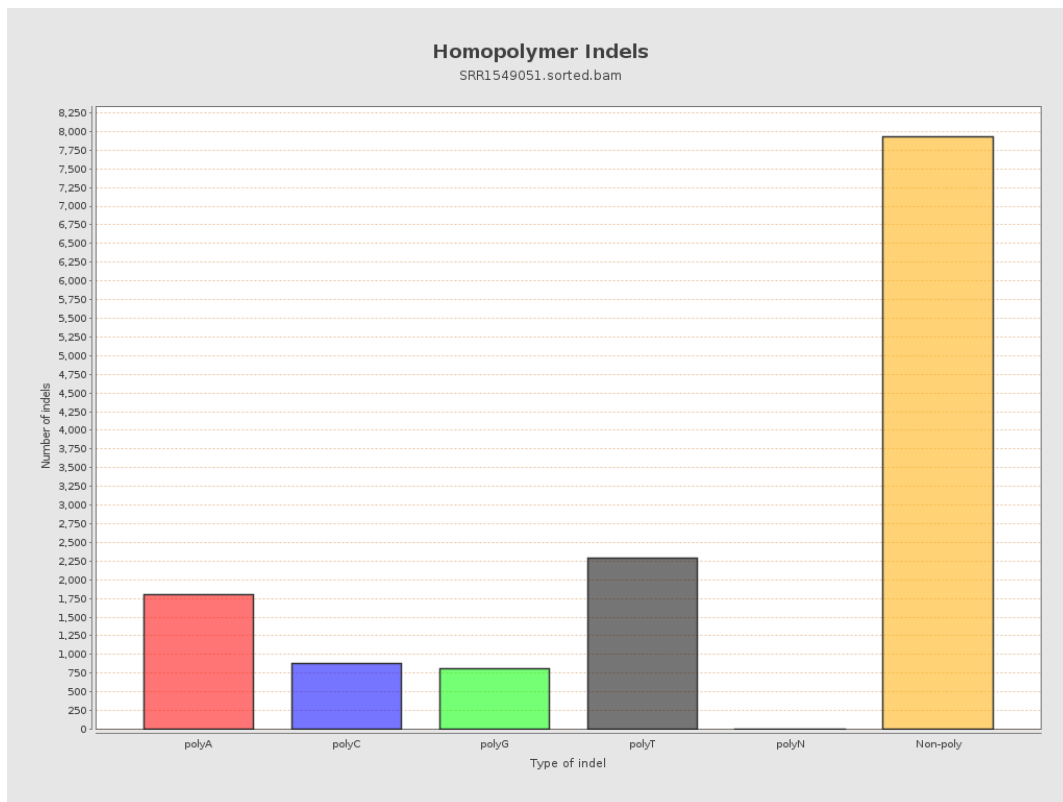
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

