

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:28:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549031.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_SRR1549031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549031.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:28:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,810,048
Mapped reads	7,637,018 / 86.69%
Unmapped reads	1,173,030 / 13.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	464,848 / 5.28%
Duplication rate	5.03%
Clipped reads	573,393 / 6.51%

2.2. ACGT Content

Number/percentage of A's	87,813,741 / 29.06%
Number/percentage of C's	62,377,419 / 20.64%
Number/percentage of T's	88,778,315 / 29.38%
Number/percentage of G's	63,249,591 / 20.93%
Number/percentage of N's	3,026 / 0%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0976
Standard Deviation	1.3135

2.4. Mapping Quality

Mean Mapping Quality	42.44
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2.5. Mismatches and indels

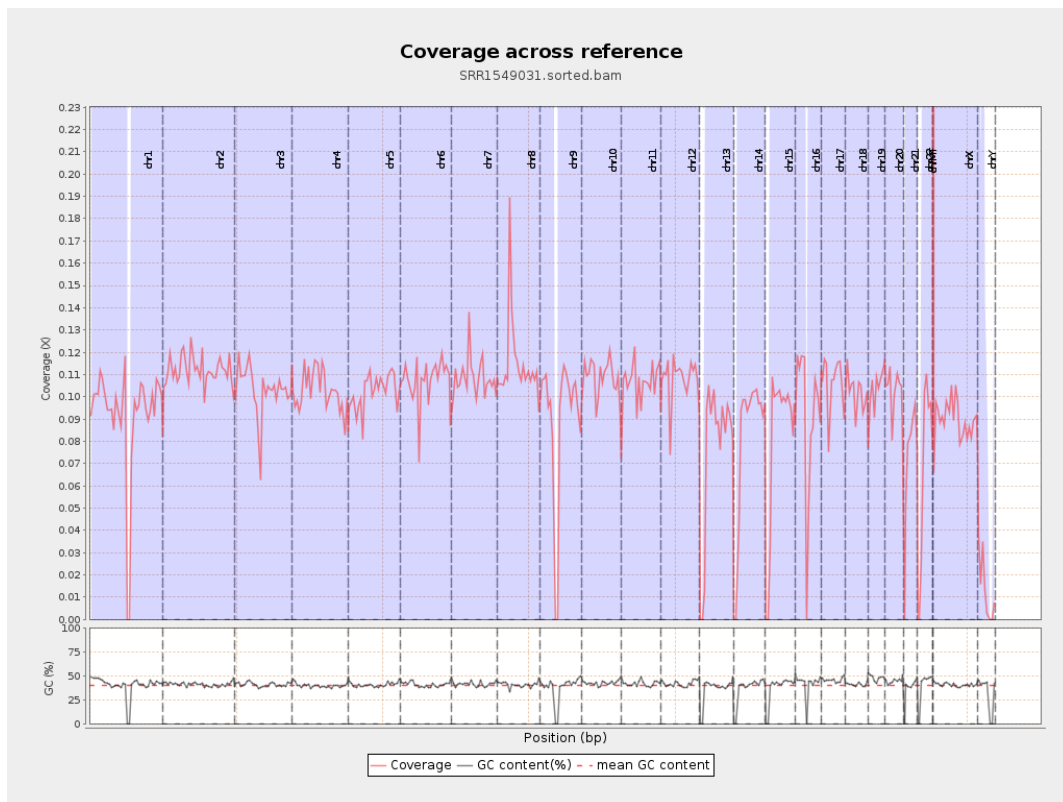
General error rate	0.27%
Mismatches	793,150
Insertions	9,514
Mapped reads with at least one insertion	0.12%
Deletions	24,500
Mapped reads with at least one deletion	0.32%
Homopolymer indels	42.09%

2.6. Chromosome stats

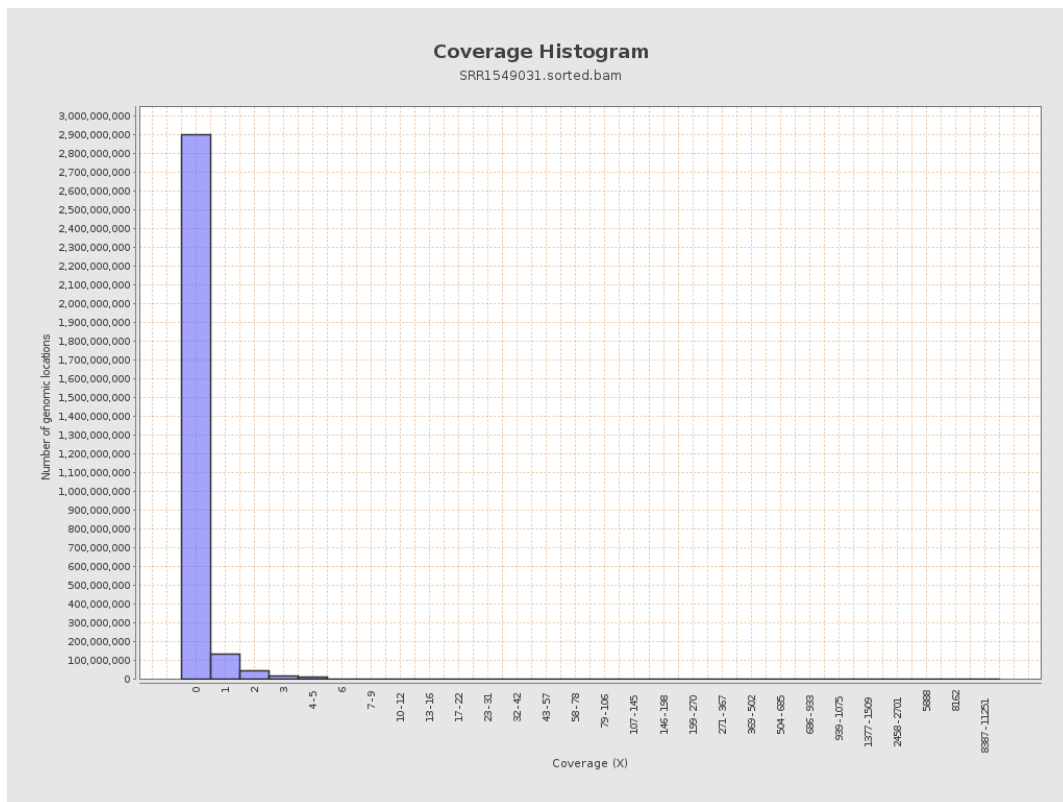
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	22917707	0.0919	0.8317
chr2	243199373	27258403	0.1121	0.5968
chr3	198022430	20398947	0.103	0.4619
chr4	191154276	19639867	0.1027	0.4718
chr5	180915260	18522771	0.1024	0.4644
chr6	171115067	18376280	0.1074	0.503
chr7	159138663	17231064	0.1083	0.7657
chr8	146364022	16805329	0.1148	5.454

chr9	141213431	12716908	0.0901	0.5479
chr10	135534747	14737475	0.1087	0.536
chr11	135006516	14374306	0.1065	0.7987
chr12	133851895	14535181	0.1086	0.4836
chr13	115169878	8805285	0.0765	0.3991
chr14	107349540	8733667	0.0814	0.4601
chr15	102531392	8168343	0.0797	0.4035
chr16	90354753	8082883	0.0895	0.4497
chr17	81195210	8676550	0.1069	0.5165
chr18	78077248	7961696	0.102	0.9038
chr19	59128983	6133114	0.1037	0.7702
chr20	63025520	6432476	0.1021	0.4729
chr21	48129895	3484664	0.0724	0.4132
chr22	51304566	3495850	0.0681	0.4213
chrMT	16571	62721	3.785	4.6466
chrX	155270560	13936032	0.0898	0.4903
chrY	59373566	766793	0.0129	0.1876

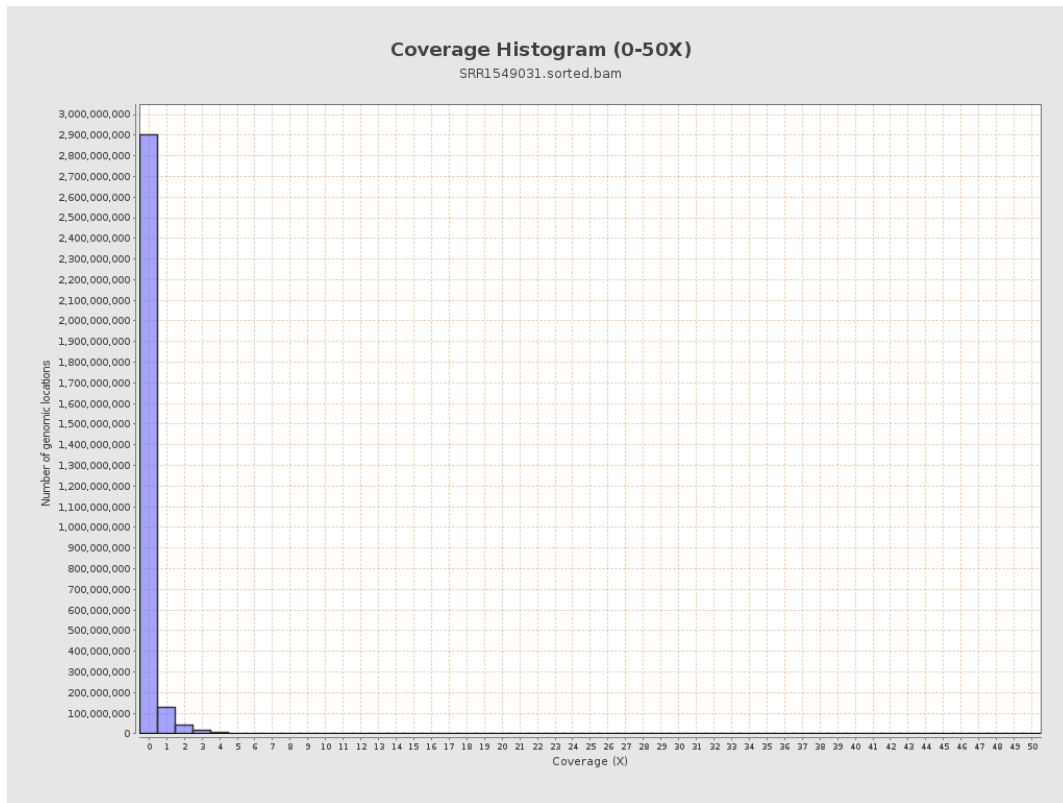
3. Results : Coverage across reference



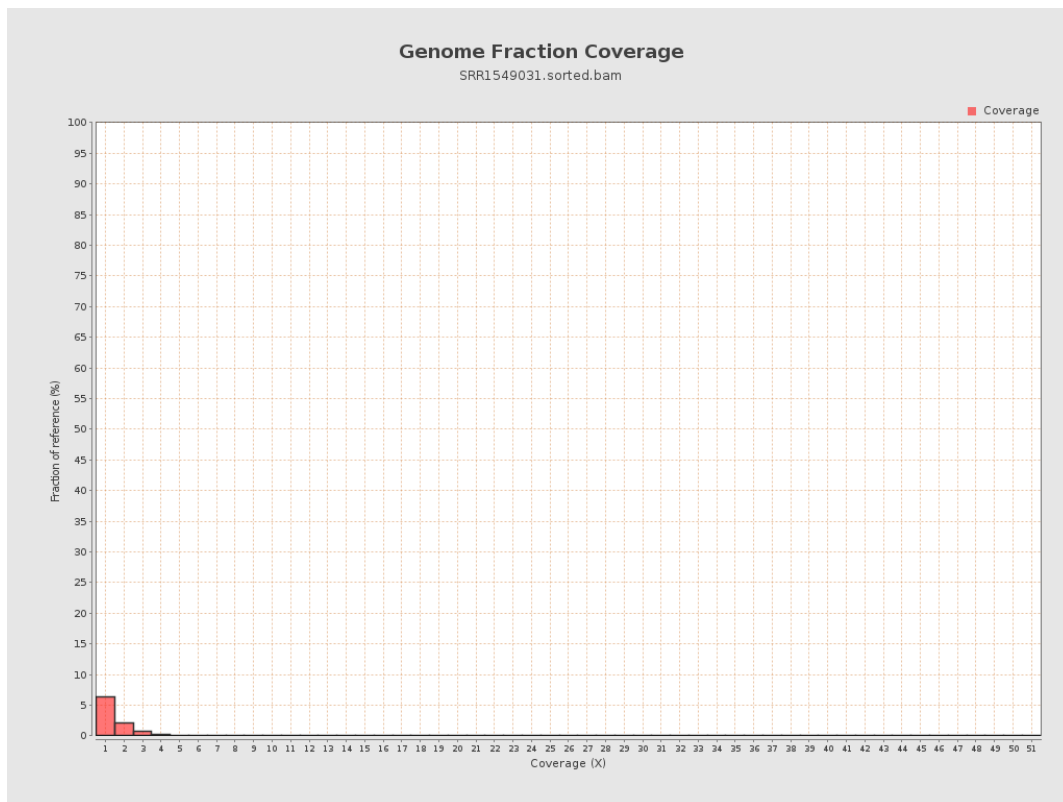
4. Results : Coverage Histogram



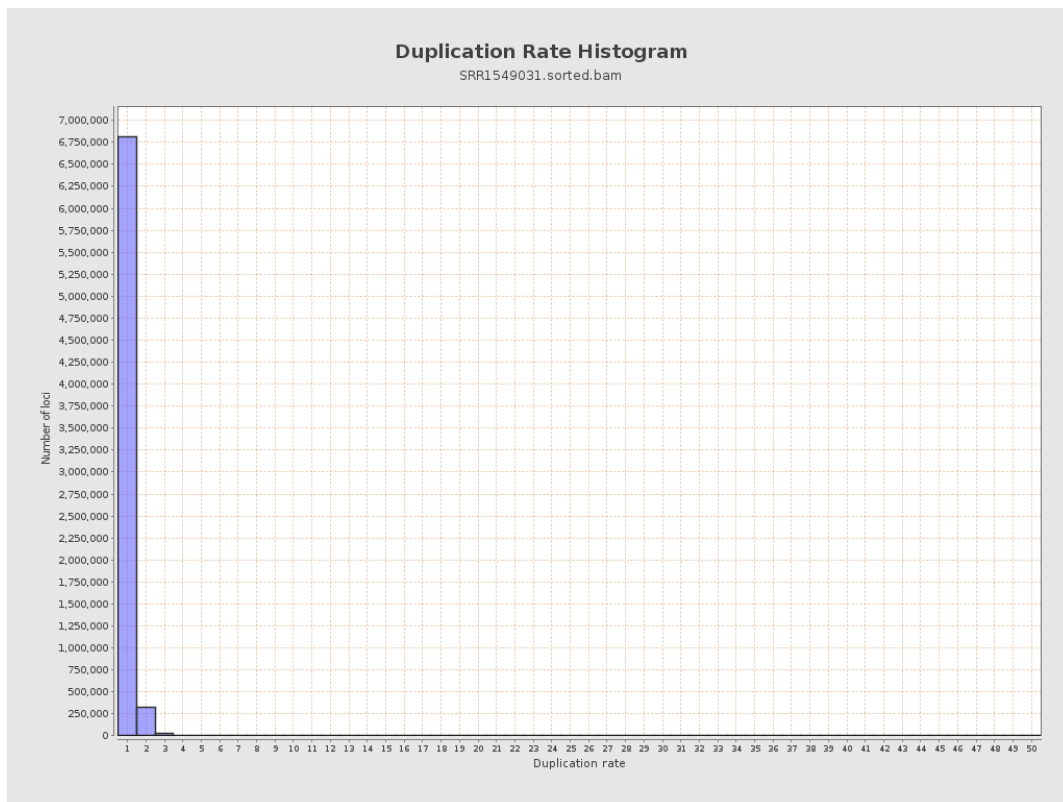
5. Results : Coverage Histogram (0-50X)



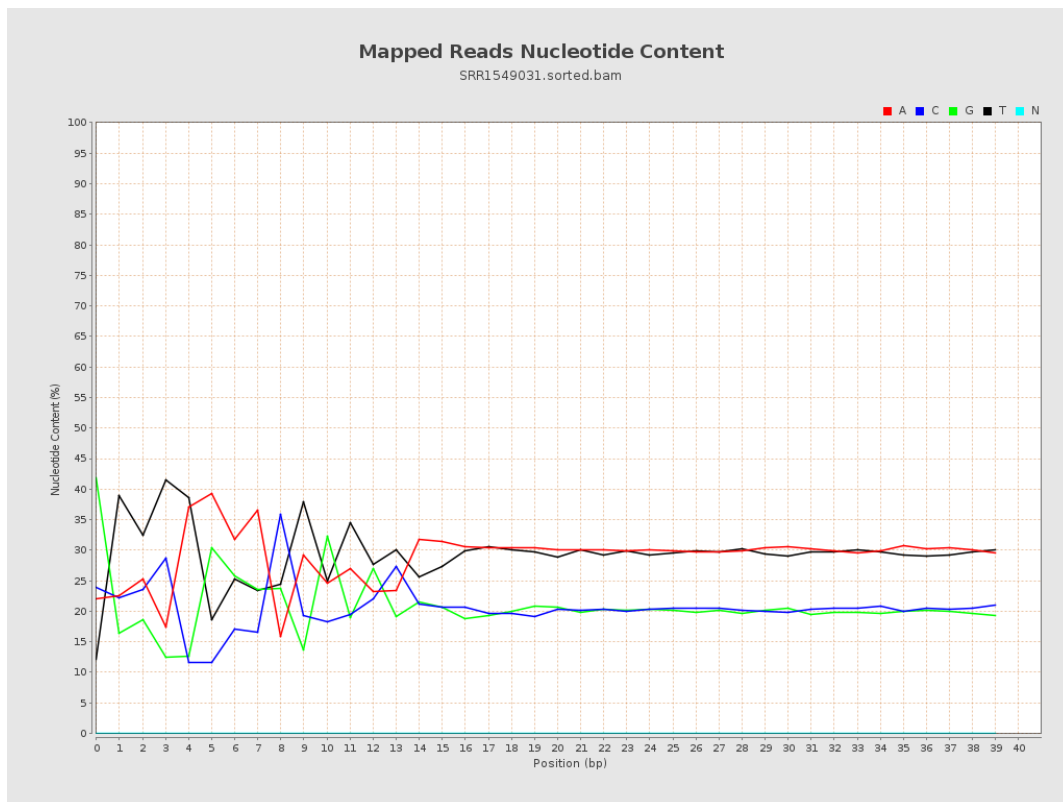
6. Results : Genome Fraction Coverage



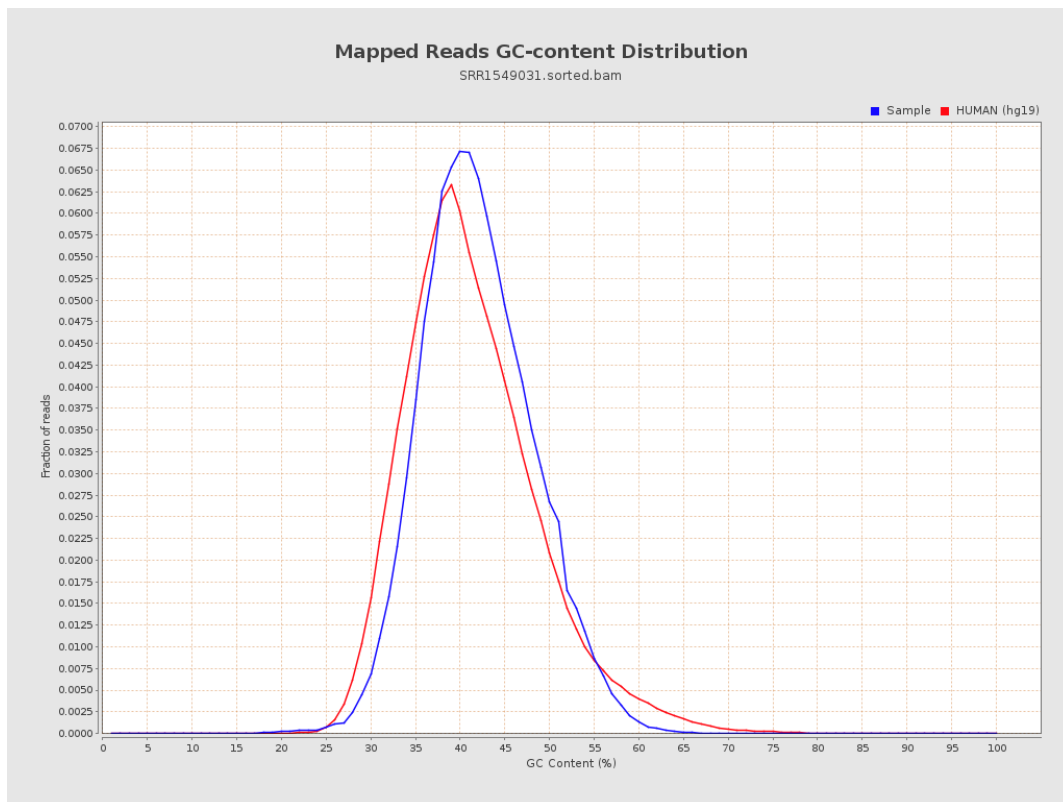
7. Results : Duplication Rate Histogram



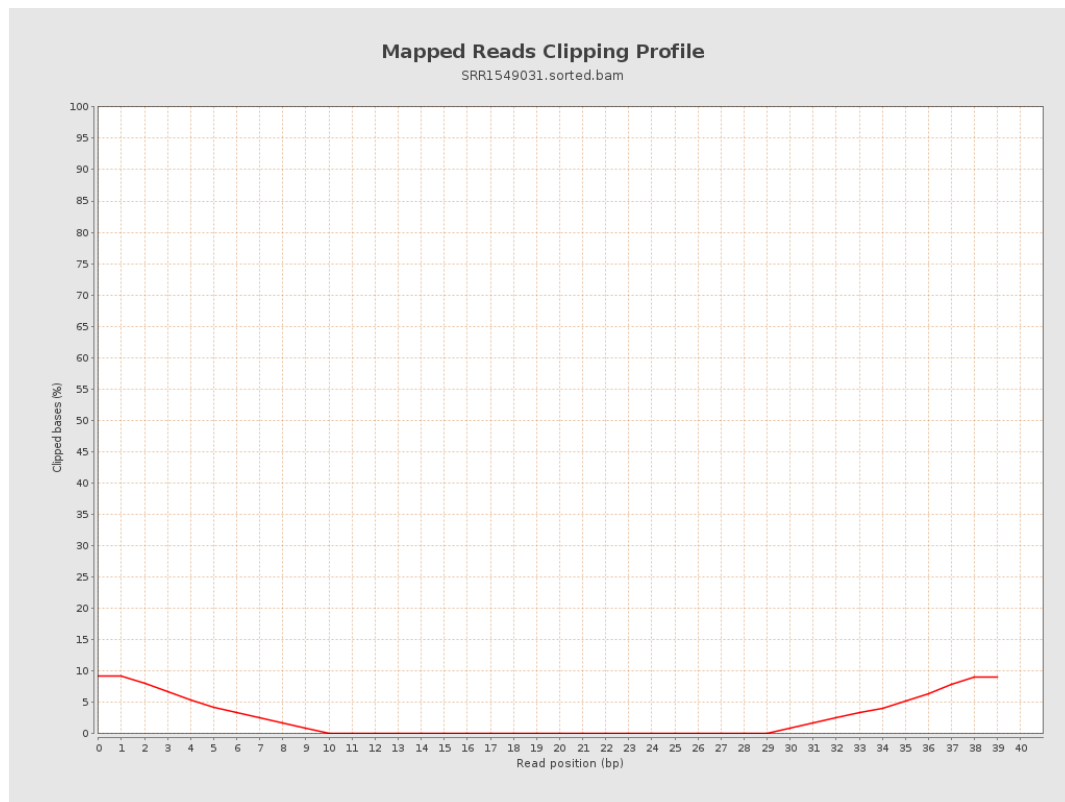
8. Results : Mapped Reads Nucleotide Content



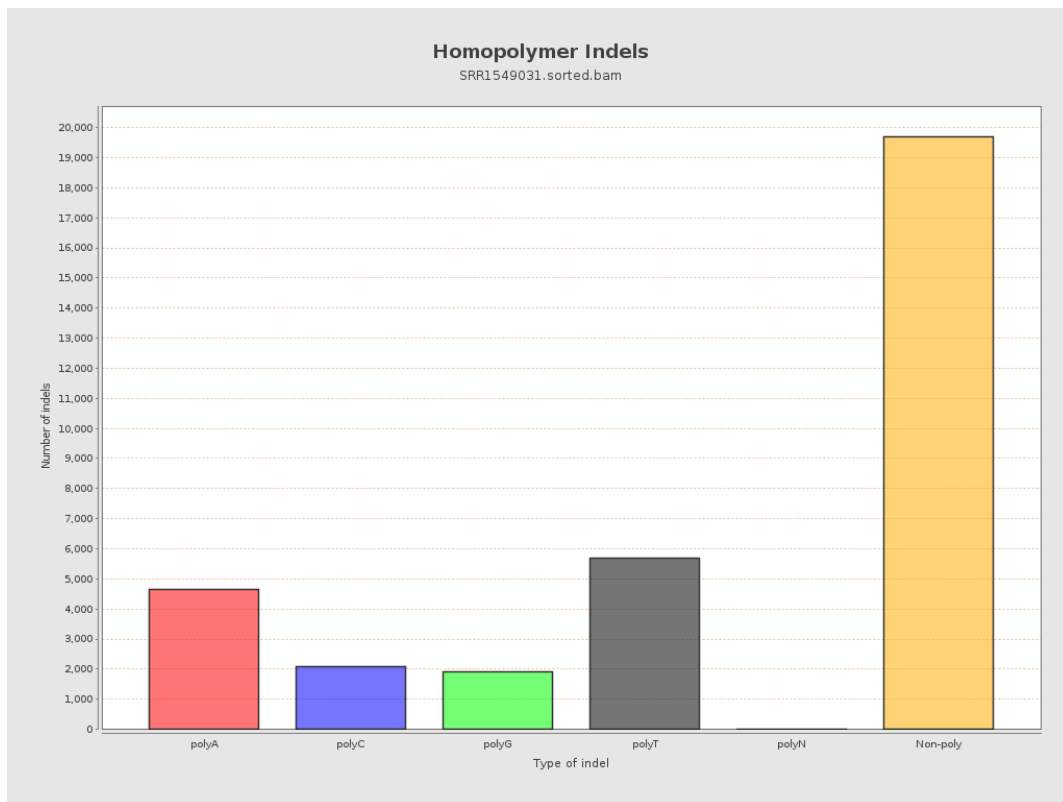
9. Results : Mapped Reads GC-content Distribution



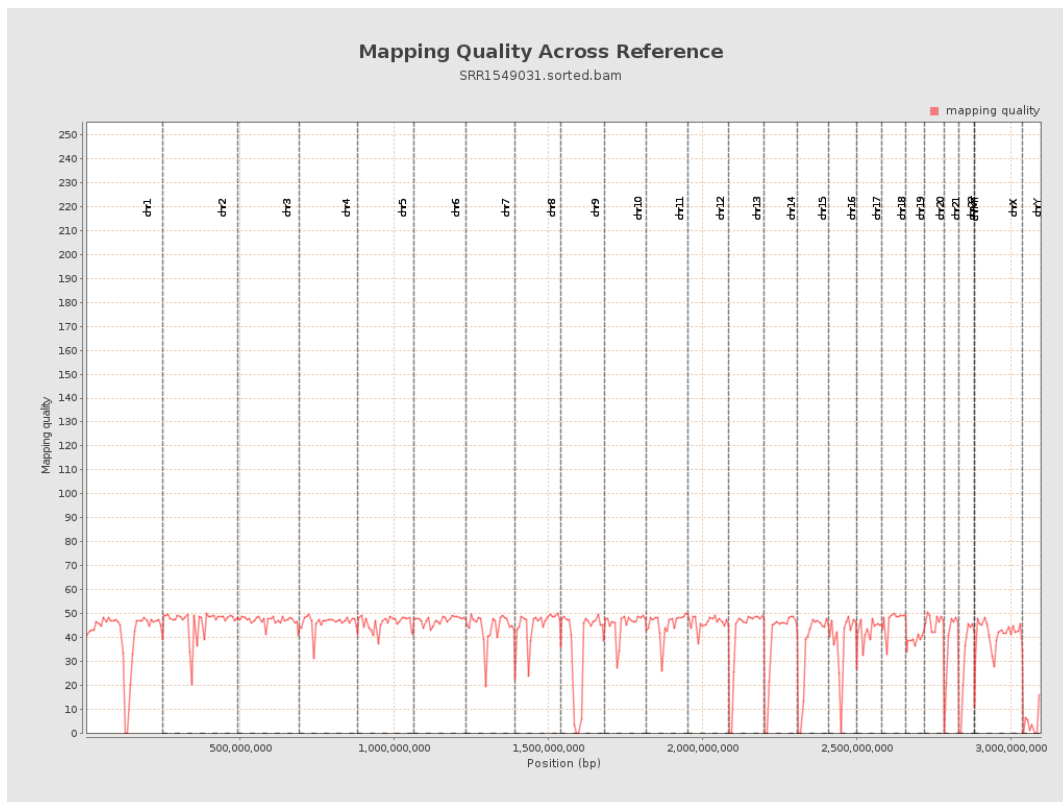
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

