

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:47:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549097.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_SRR1549097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549097.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:47:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,073,546
Mapped reads	9,406,118 / 84.94%
Unmapped reads	1,667,428 / 15.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	527,801 / 4.77%
Duplication rate	3.38%
Clipped reads	618,383 / 5.58%

2.2. ACGT Content

Number/percentage of A's	109,076,389 / 29.29%
Number/percentage of C's	76,141,170 / 20.44%
Number/percentage of T's	110,647,273 / 29.71%
Number/percentage of G's	76,593,182 / 20.56%
Number/percentage of N's	1,506 / 0%
GC Percentage	41.01%

2.3. Coverage

Mean	0.1203
Standard Deviation	1.2287

2.4. Mapping Quality

Mean Mapping Quality	40.86
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2.5. Mismatches and indels

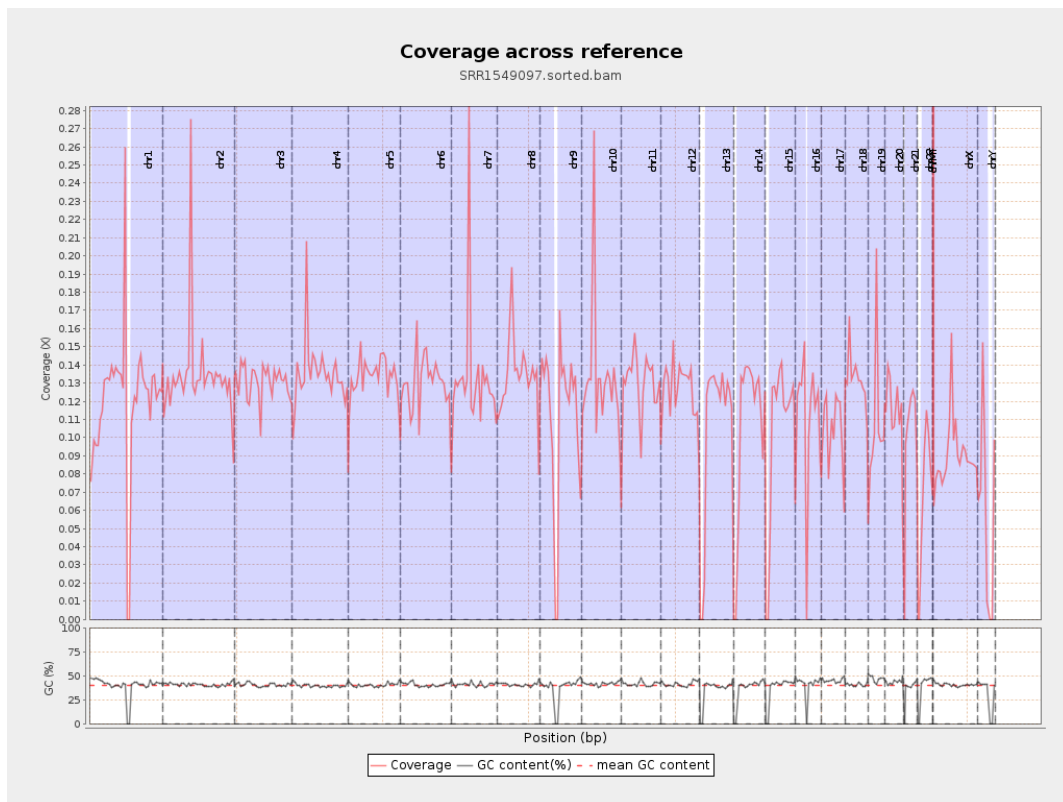
General error rate	0.34%
Mismatches	1,262,130
Insertions	10,624
Mapped reads with at least one insertion	0.11%
Deletions	27,958
Mapped reads with at least one deletion	0.3%
Homopolymer indels	43.21%

2.6. Chromosome stats

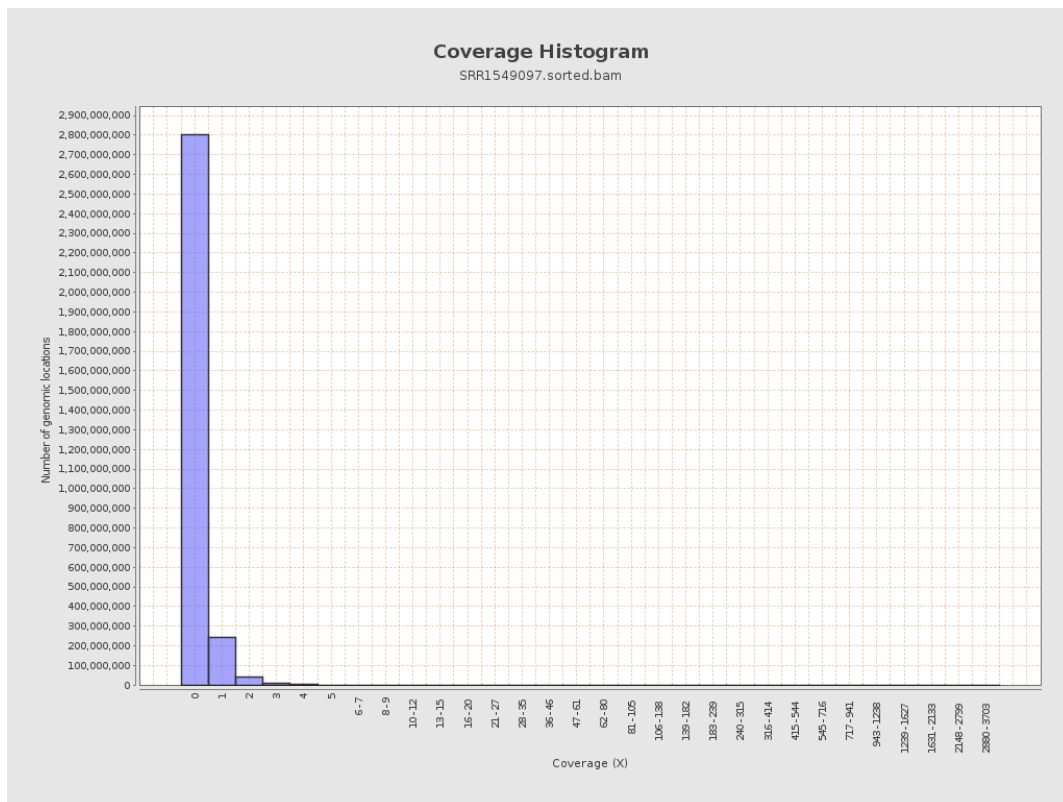
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29877720	0.1199	2.6761
chr2	243199373	32651431	0.1343	1.1655
chr3	198022430	25923608	0.1309	0.4486
chr4	191154276	25917546	0.1356	0.5993
chr5	180915260	24097849	0.1332	0.4852
chr6	171115067	22352748	0.1306	0.5523
chr7	159138663	21047124	0.1323	1.7512
chr8	146364022	19689178	0.1345	1.5009

chr9	141213431	15859480	0.1123	1.0747
chr10	135534747	17921616	0.1322	1.1482
chr11	135006516	17552026	0.13	0.8901
chr12	133851895	16992928	0.127	0.5375
chr13	115169878	12104714	0.1051	0.38
chr14	107349540	11456844	0.1067	0.6818
chr15	102531392	10468462	0.1021	0.3865
chr16	90354753	9796516	0.1084	0.5967
chr17	81195210	8577310	0.1056	0.4884
chr18	78077248	10400286	0.1332	2.4785
chr19	59128983	6426880	0.1087	2.2337
chr20	63025520	7319519	0.1161	0.5472
chr21	48129895	4840361	0.1006	0.6516
chr22	51304566	3510030	0.0684	0.3201
chrMT	16571	47653	2.8757	3.4544
chrX	155270560	14021525	0.0903	0.6804
chrY	59373566	3640571	0.0613	0.6344

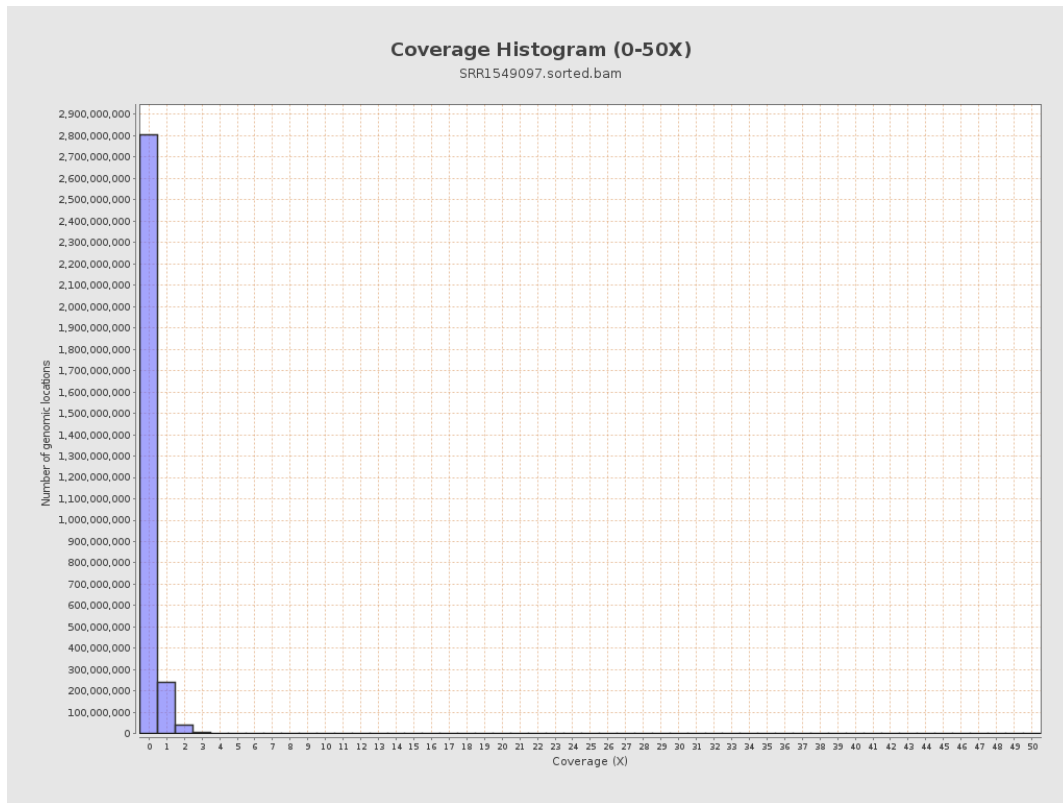
3. Results : Coverage across reference



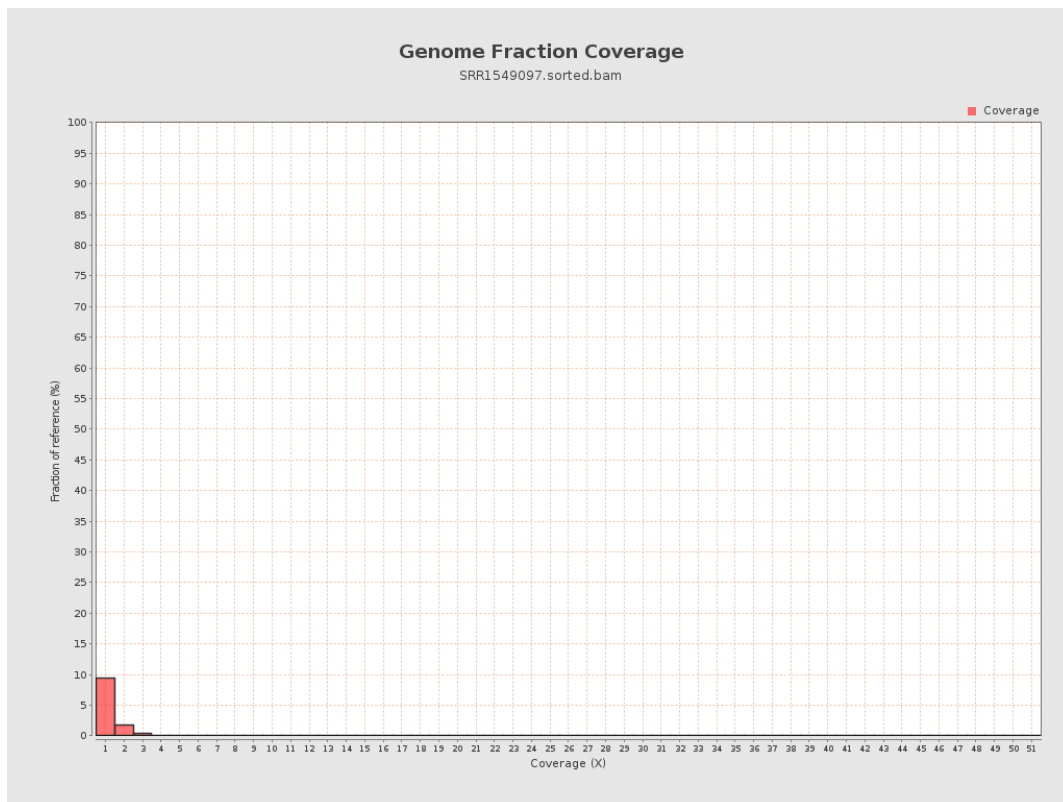
4. Results : Coverage Histogram



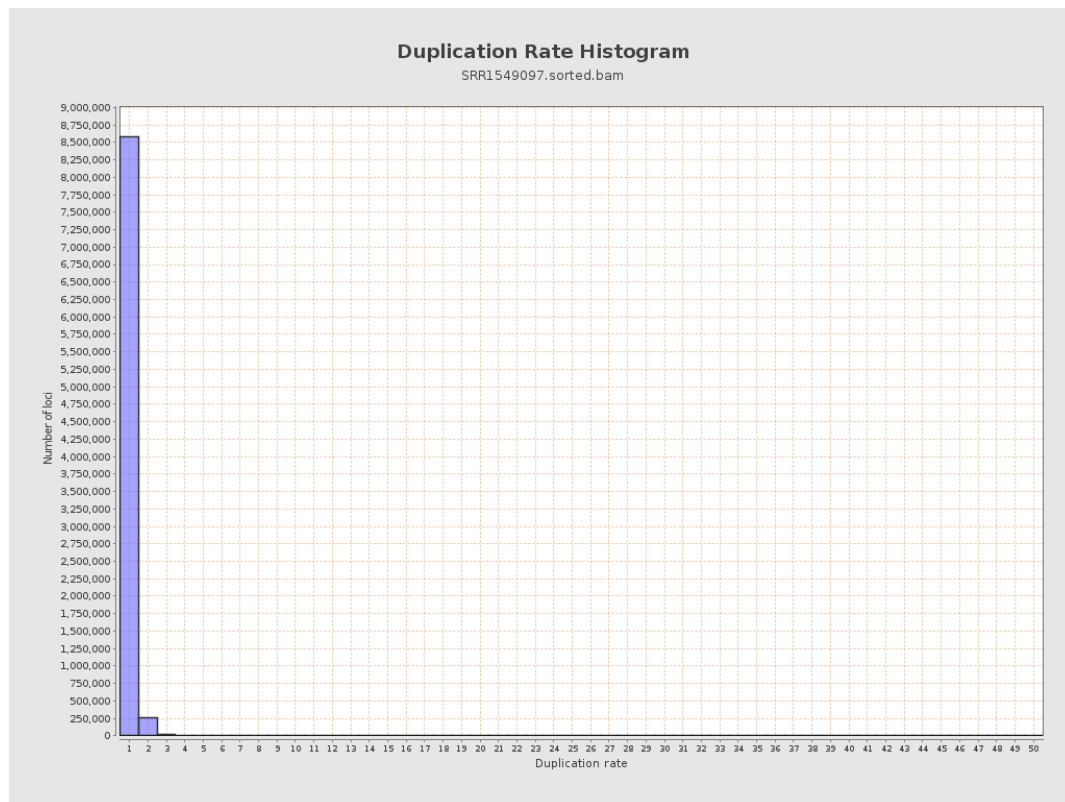
5. Results : Coverage Histogram (0-50X)



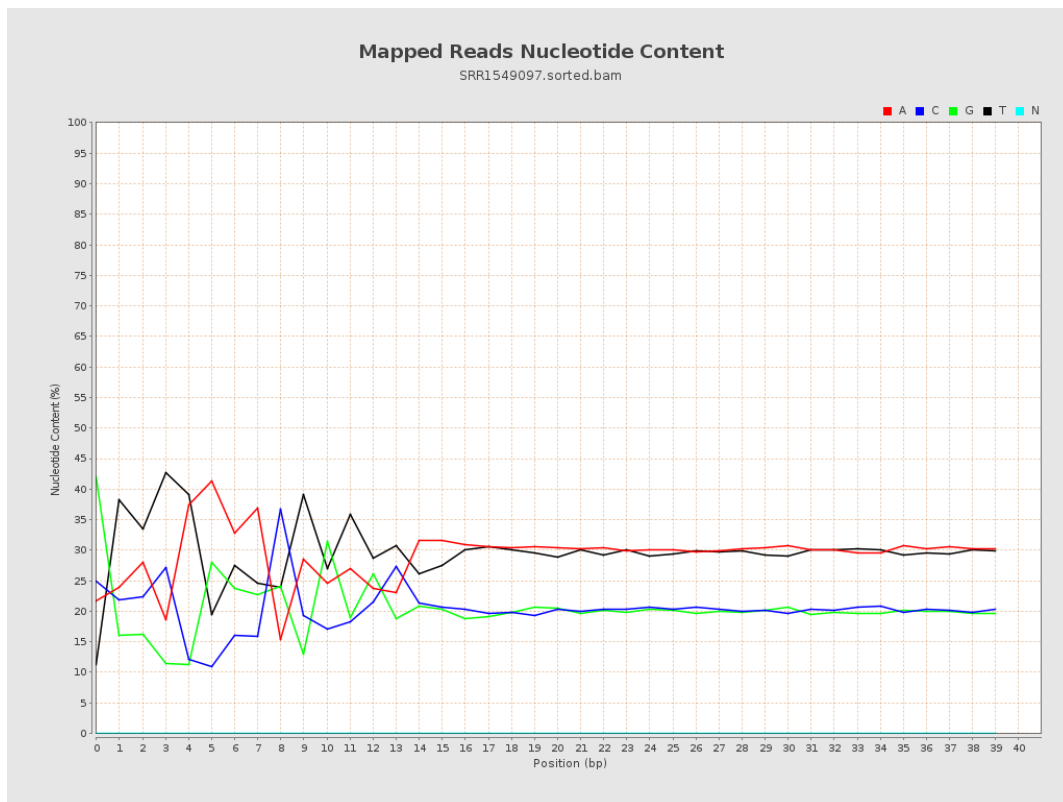
6. Results : Genome Fraction Coverage



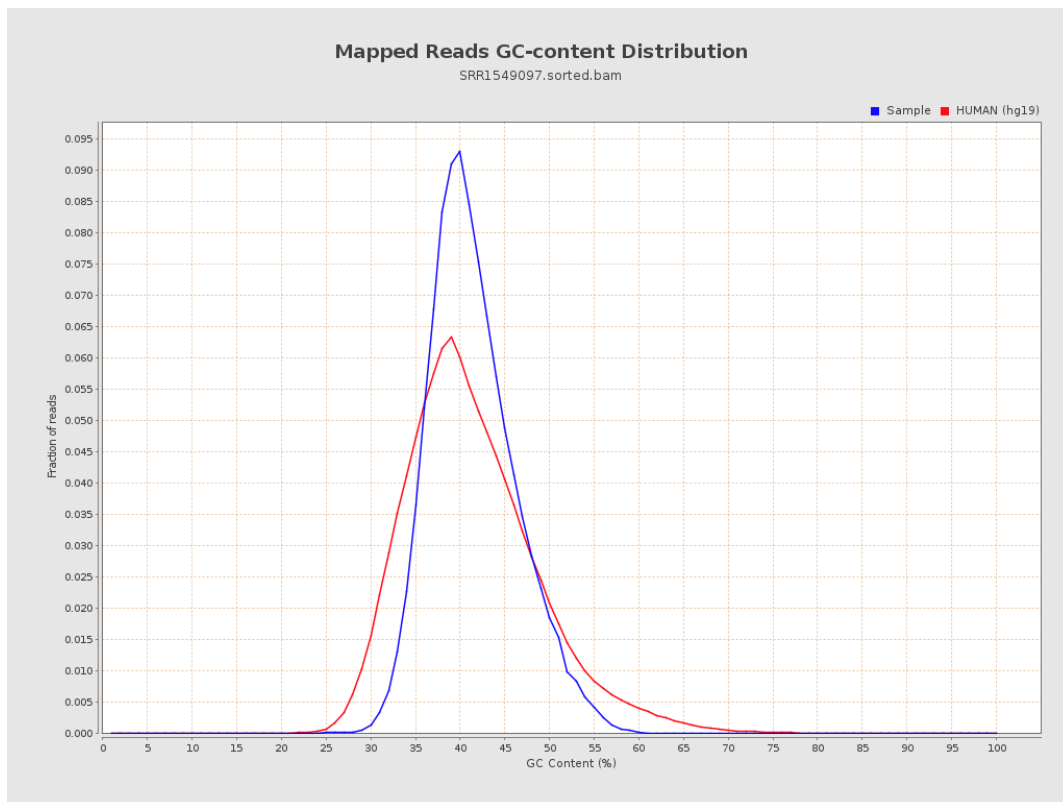
7. Results : Duplication Rate Histogram



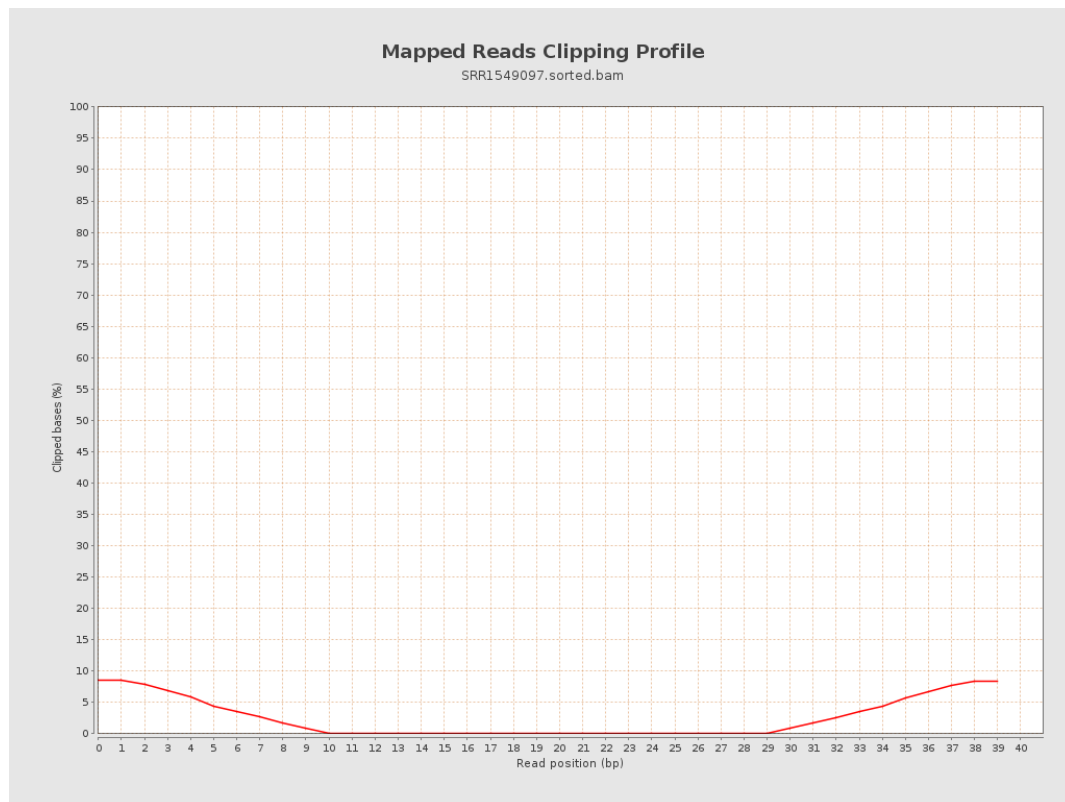
8. Results : Mapped Reads Nucleotide Content



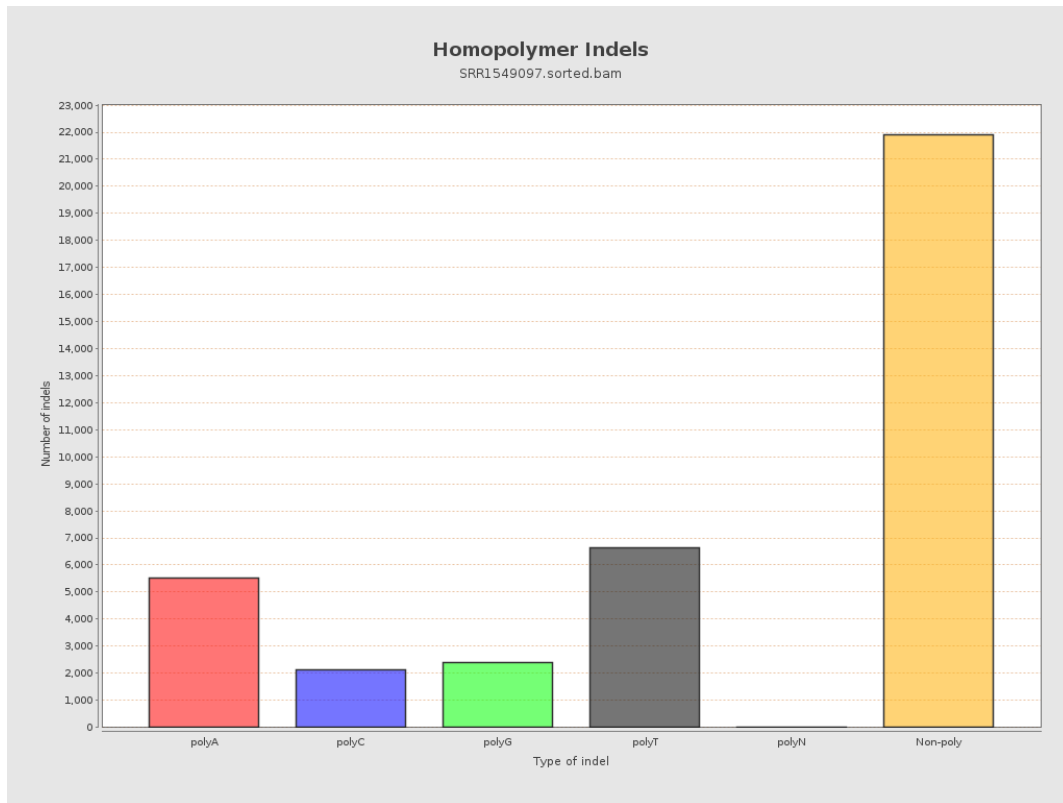
9. Results : Mapped Reads GC-content Distribution



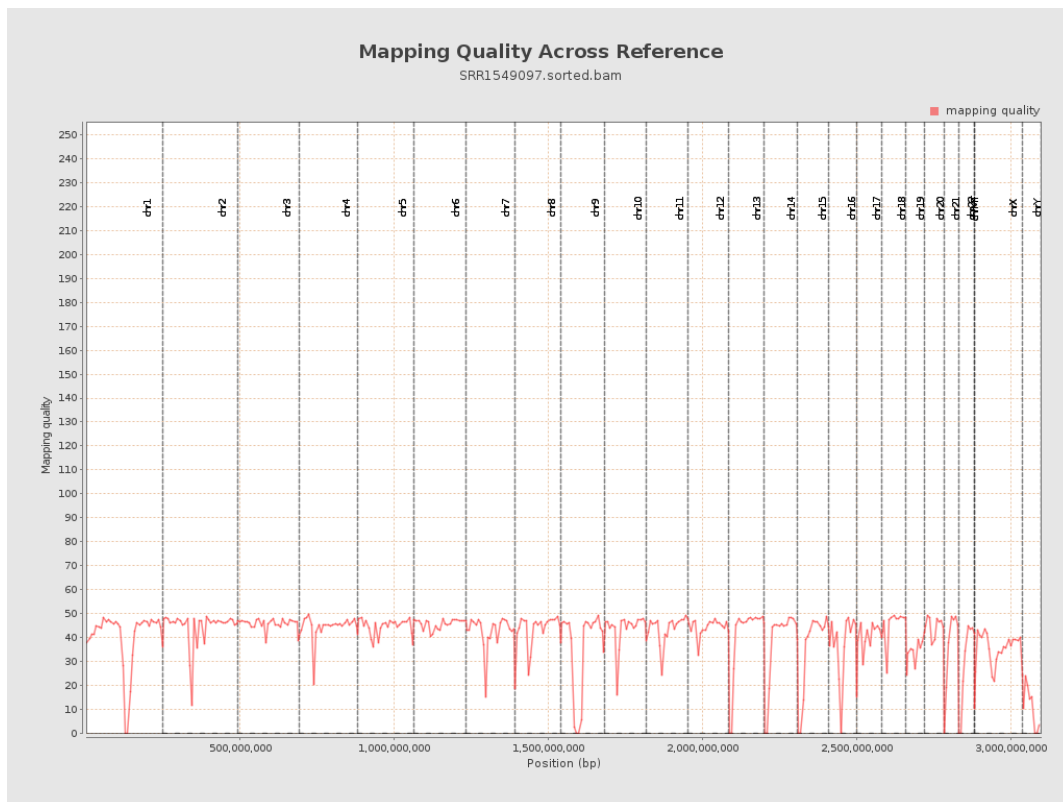
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

