Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:30:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081201.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_SRR3081201 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081201.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:30:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081201.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,098,912
Mapped reads	3,995,395 / 78.36%
Unmapped reads	1,103,517 / 21.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,612 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	384,773 / 7.55%
Duplication rate	7.01%
Clipped reads	1,912,316 / 37.5%

2.2. ACGT Content

Number/percentage of A's	74,151,178 / 28.02%
Number/percentage of C's	49,990,988 / 18.89%
Number/percentage of T's	83,130,164 / 31.41%
Number/percentage of G's	57,238,360 / 21.63%
Number/percentage of N's	150,852 / 0.06%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0855

Standard Deviation	0.9864

2.4. Mapping Quality

Mean Mapping Quality	46.23

2.5. Mismatches and indels

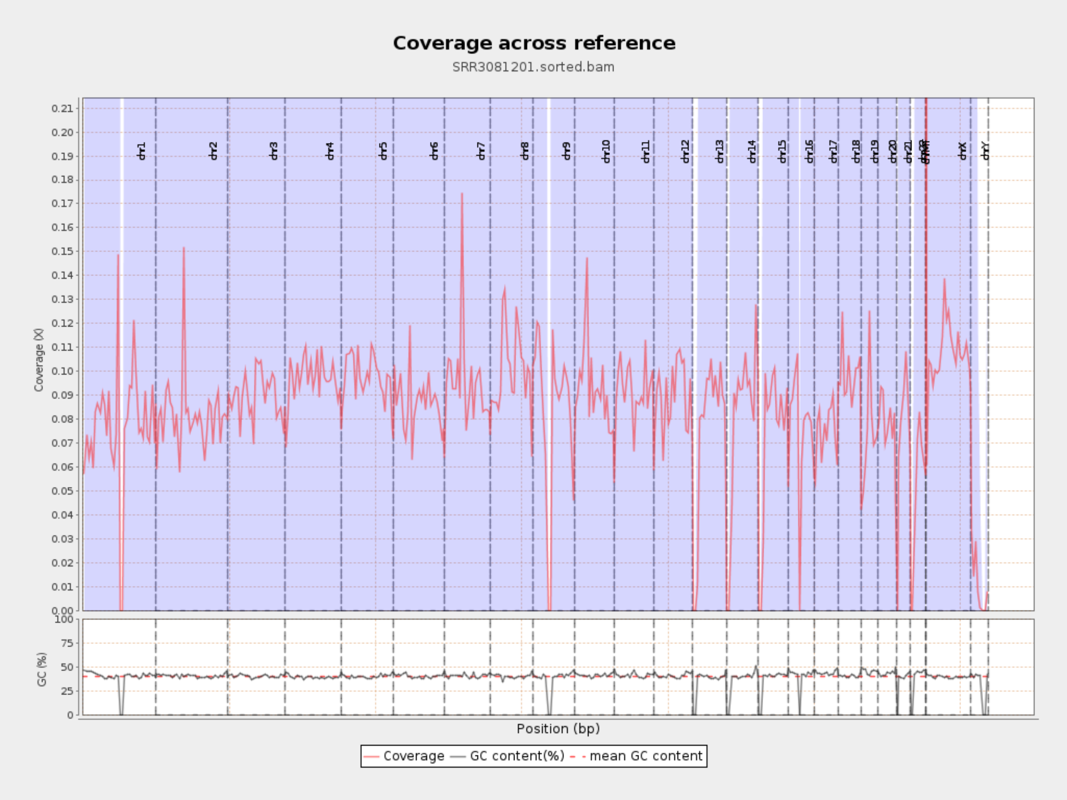
General error rate	1.04%
Mismatches	2,725,602
Insertions	19,567
Mapped reads with at least one insertion	0.49%
Deletions	54,488
Mapped reads with at least one deletion	1.35%
Homopolymer indels	44.63%

2.6. Chromosome stats

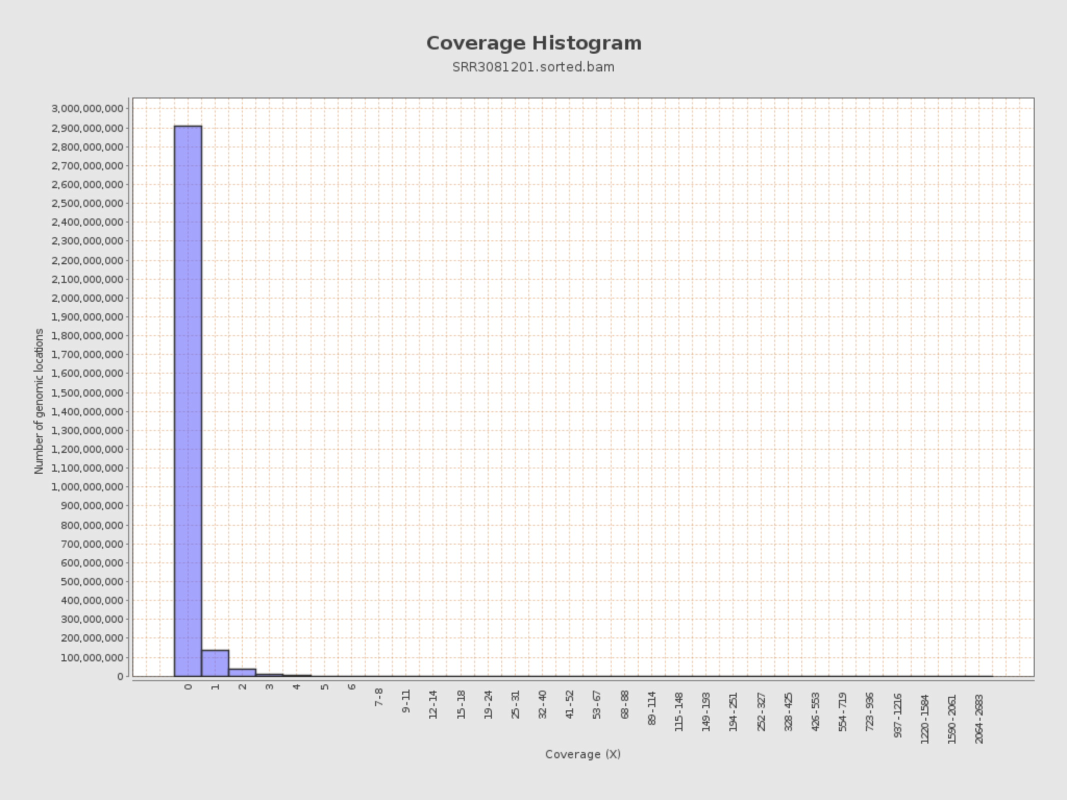
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19143445	0.0768	1.8654
chr2	243199373	19899263	0.0818	0.7227
chr3	198022430	17719498	0.0895	0.4018
chr4	191154276	18572738	0.0972	0.4257
chr5	180915260	17613680	0.0974	0.4344
chr6	171115067	14886301	0.087	0.6143
chr7	159138663	15277963	0.096	1.3335

chr8	146364022	14677035	0.1003	1.6203
chr9	141213431	11765721	0.0833	0.7731
chr10	135534747	12618008	0.0931	0.8377
chr11	135006516	12445215	0.0922	0.7077
chr12	133851895	12042915	0.09	0.4439
chr13	115169878	8673679	0.0753	0.3629
chr14	107349540	8558414	0.0797	2.1215
chr15	102531392	7279421	0.071	0.3522
chr16	90354753	6682193	0.074	0.4459
chr17	81195210	6108571	0.0752	0.4513
chr18	78077248	7728129	0.099	1.6579
chr19	59128983	4417726	0.0747	1.1787
chr20	63025520	4984618	0.0791	0.4179
chr21	48129895	3664598	0.0761	0.4129
chr22	51304566	2550534	0.0497	0.2954
chrMT	16571	155954	9.4113	6.9393
chrX	155270560	16648352	0.1072	0.5121
chrY	59373566	631735	0.0106	0.1889

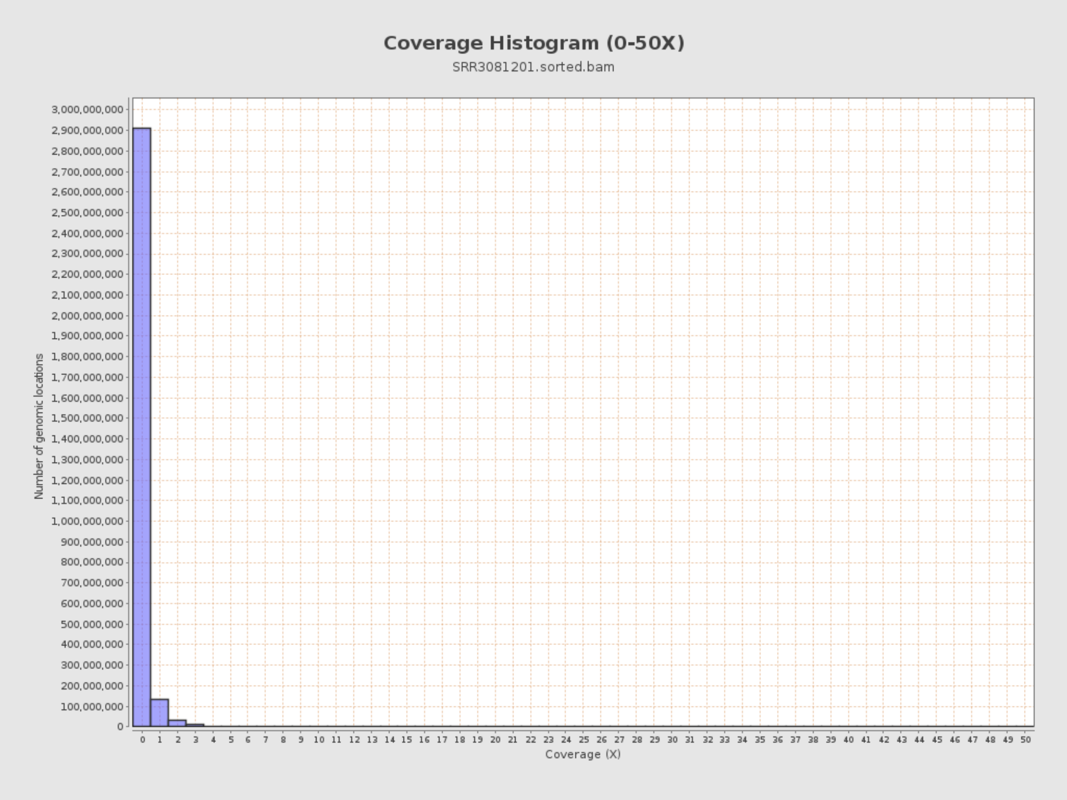
3. Results : Coverage across reference



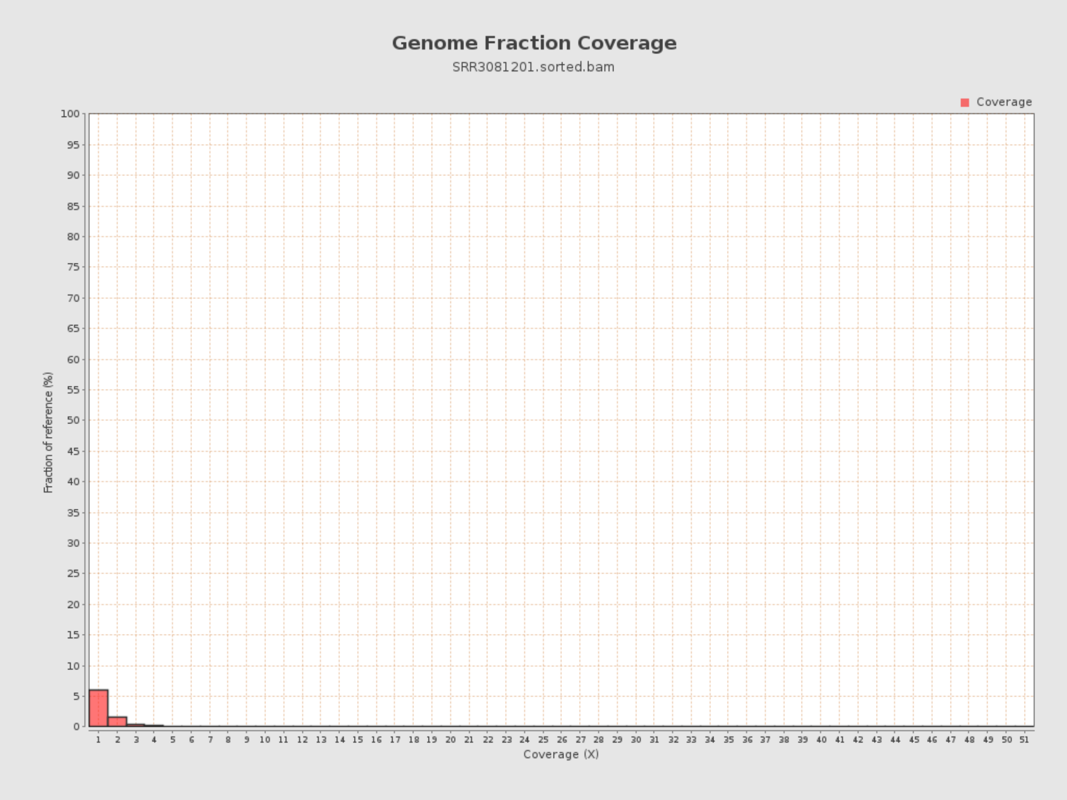
4. Results : Coverage Histogram



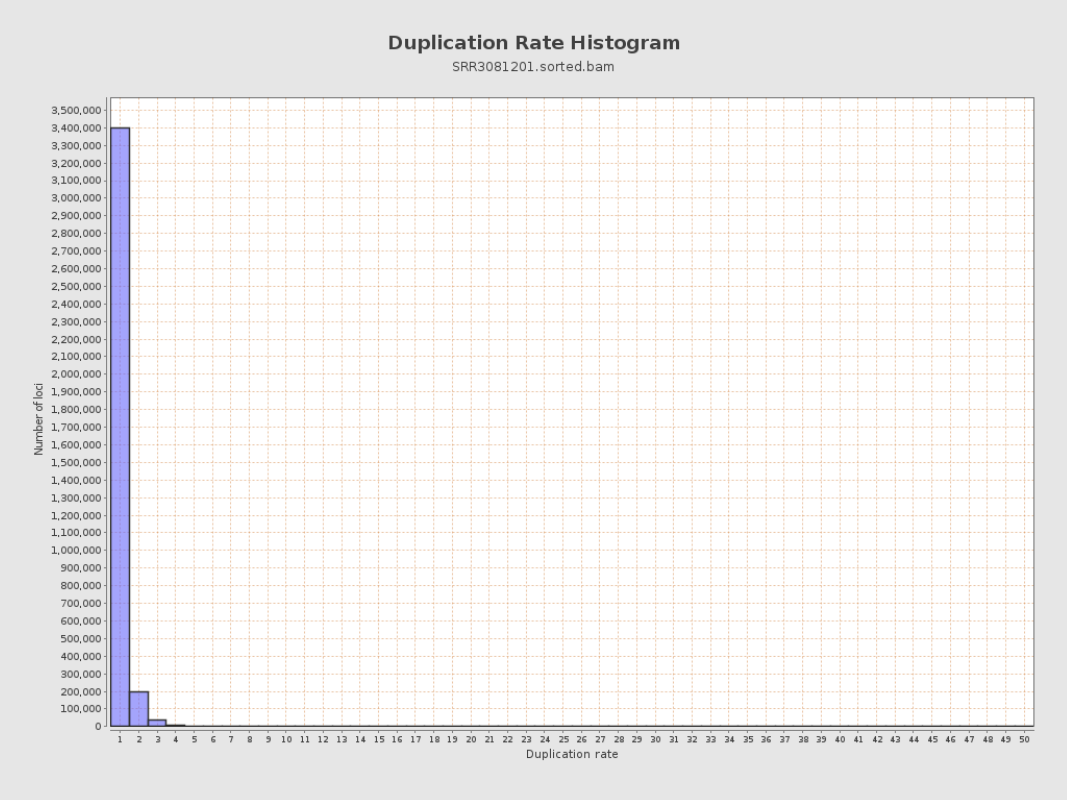
5. Results : Coverage Histogram (0-50X)



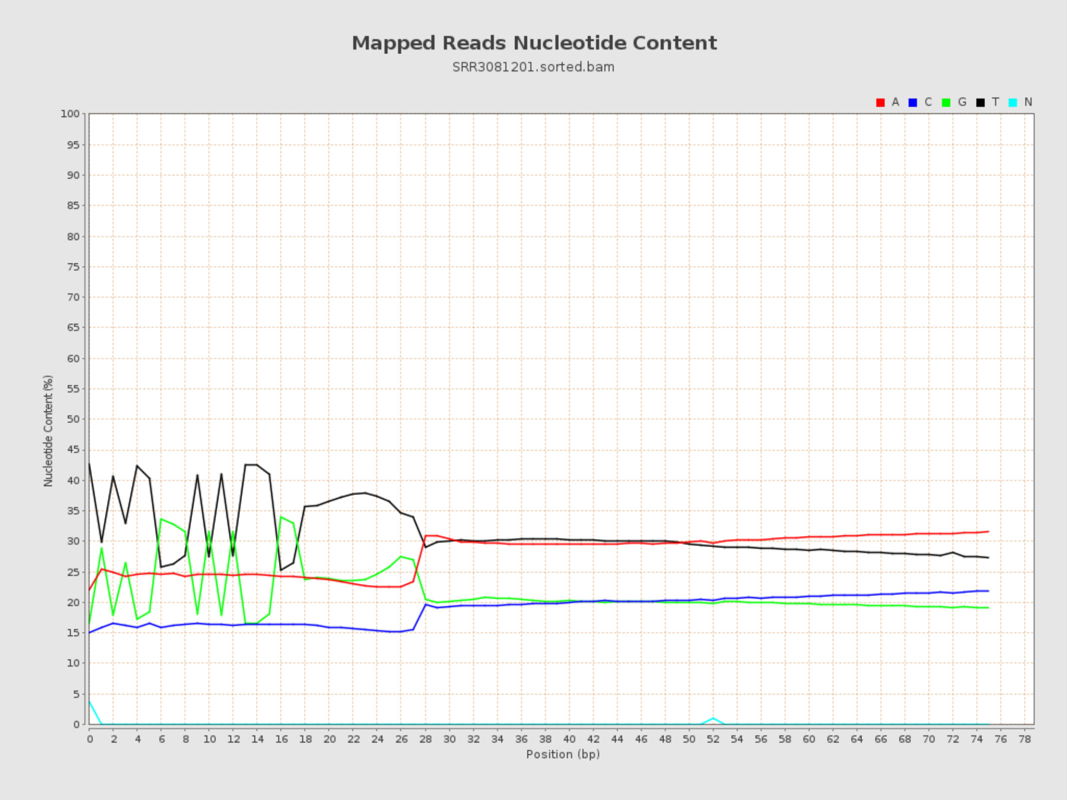
6. Results : Genome Fraction Coverage



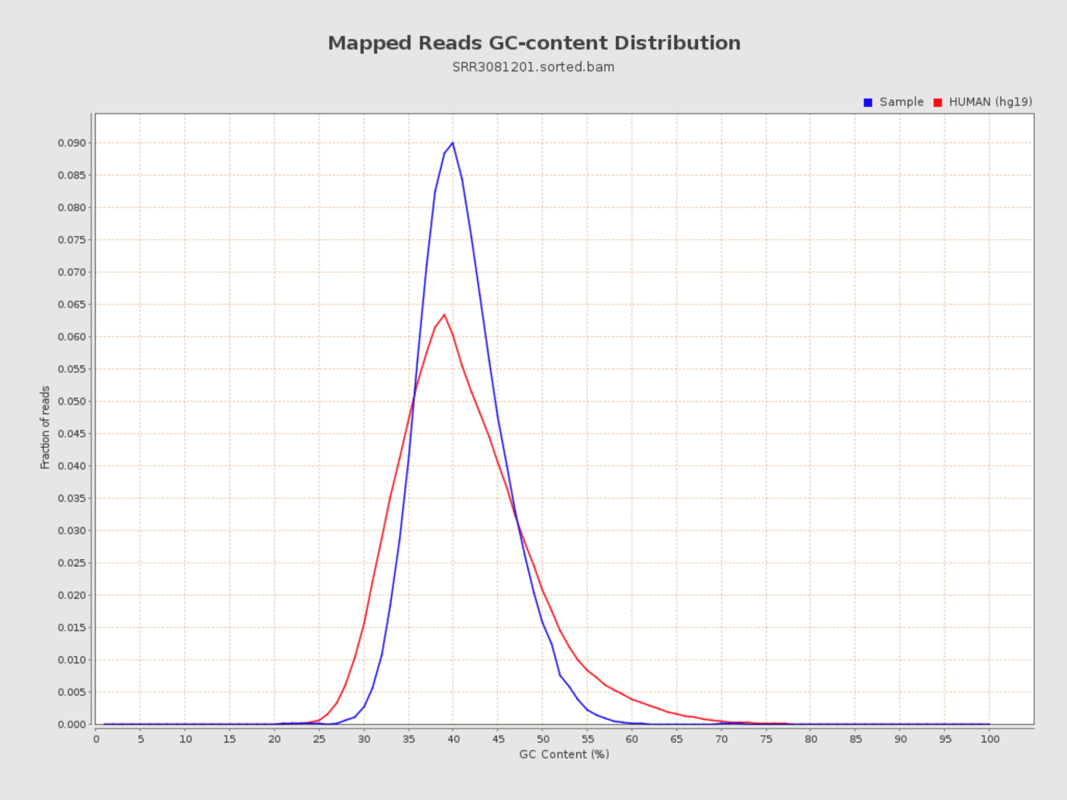
7. Results : Duplication Rate Histogram



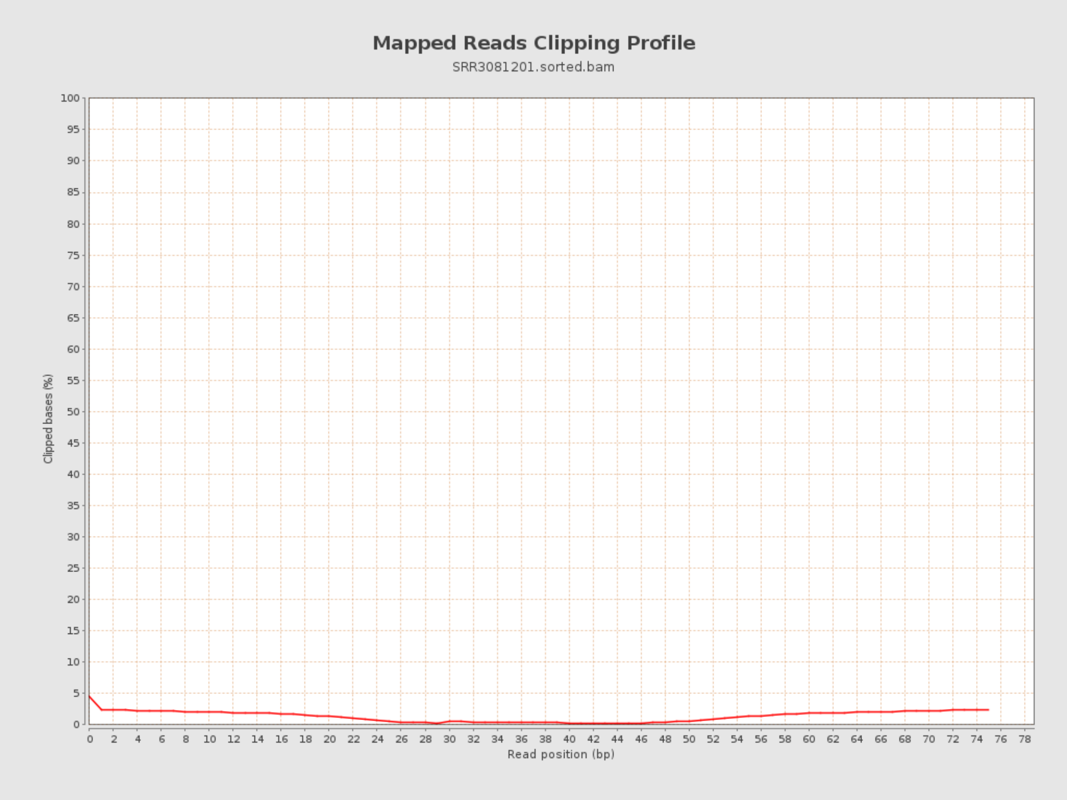
8. Results : Mapped Reads Nucleotide Content



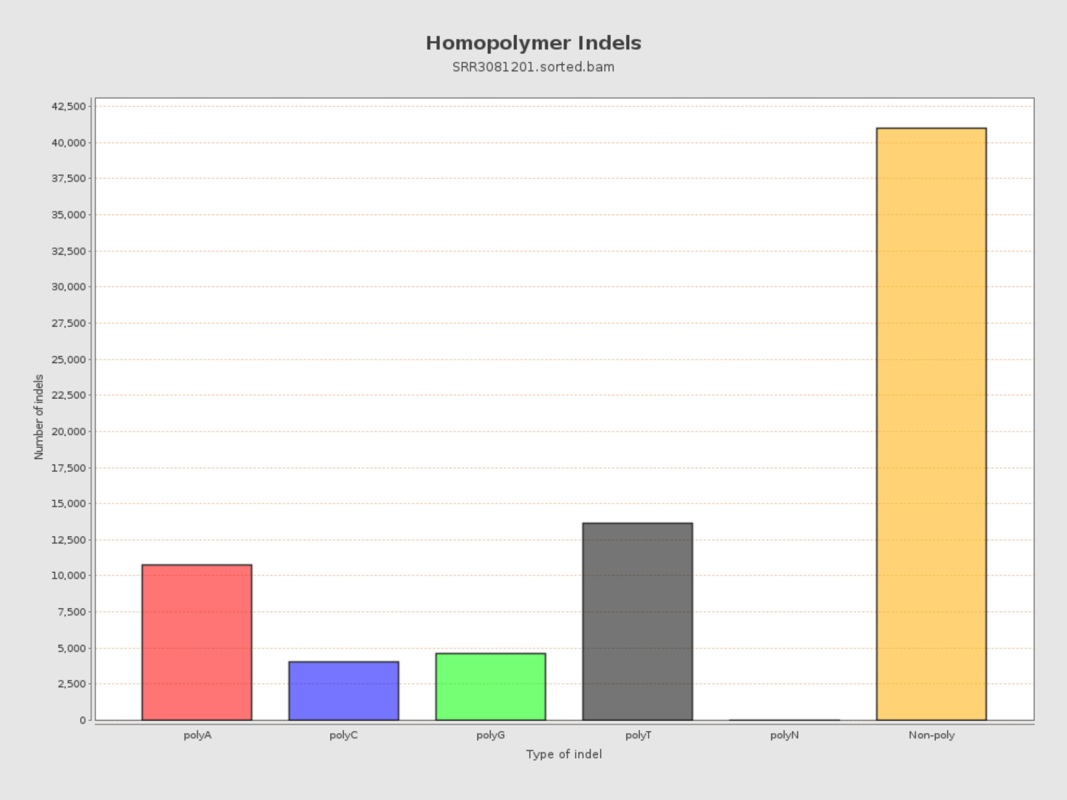
9. Results : Mapped Reads GC-content Distribution



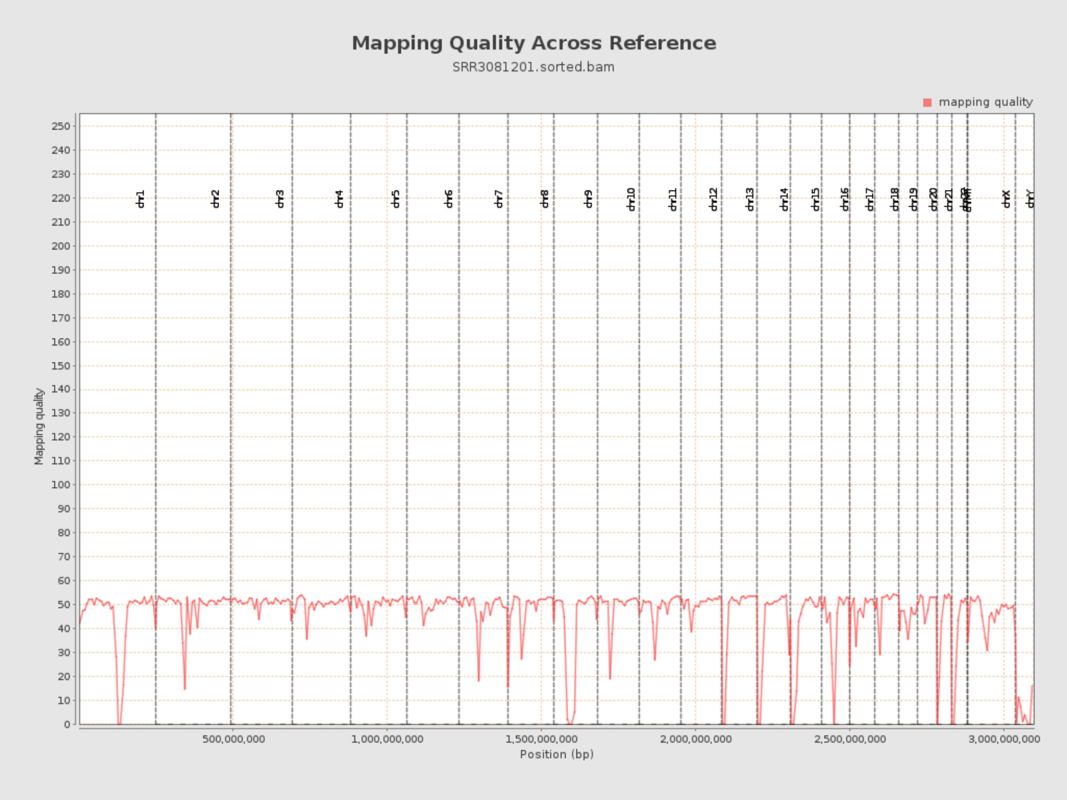
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram